SERVIÇO PÚBLICO FEDERAL
UNIVERSIDADE FEDERAL DE UBERLÂNDIA
INSTITUTO DE BIOTECNOLOGIA
PROGRAMA DE PÓS-GRADUAÇÃO EM GENÉTICA E BIOQUÍMICA

NEW INSIGHTS OF microRNAs AND METABOLIC PATHWAYS IN TOMATO SPECIES AND *Schistosoma haematobium*

Aluna: Thaís Cunha de Sousa Cardoso

Orientador: Matheus de Souza Gomes

UBERLÂNDIA - MG

2021

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Tese apresentada à Universidade Federal de Uberlândia como parte dos requisitos para obtenção do Título de Doutor em Genética e Bioquímica (Área Bioquímica)

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Aos vinte e oito dias do mês de janeiro de dois mil e vinte e um, às 14:00 horas, reuniu-se via web conferência pela plataforma Google Meet, em conformidade com a Portaria nº 36, de 19 de março de 2020 da Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – CAPES e Resolução de nº 06/2020 do Conselho de Pesquisa e Pós-graduação pela Universidade Federal de Uberlândia, a Banca Examinadora, designada pelo Colegiado do Programa de Pós-graduação em Genética e Bioquímica, assim composta: Prof. Dr. Antonio Chalfun Junior, Profª. Drª. Renata Guerra de Sá Cota, Prof. Dr. Aulus Estevão Anjos de Deus Barbosa, Profª. Drª. Enyara Rezende Morais e Prof. Dr. Matheus de Souza Gomes, orientador da candidata e demais convidados presentes conforme lista de presença. Iniciando os trabalhos o presidente da mesa, Prof. Dr. Matheus de Souza Gomes, apresentou a Comissão Examinadora e a candidata agradeceu a presença do público, e concedeu à discente a palavra para a exposição do seu trabalho. A duração da apresentação da discente e o tempo de arguição e resposta foram conforme as normas do Programa de Pós-graduação em Genética e Bioquímica. A seguir o presidente concedeu a palavra, pela ordem sucessivamente, aos examinadores, que passaram a arguir a candidata. Ultimada a arguição, que se desenvolveu dentro dos termos regimentais, a Banca, em sessão secreta, atribuiu os conceitos finais. Em face do resultado obtido, a Banca Examinadora considerou a candidata:

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Esta defesa de Tese de Doutorado é parte dos requisitos necessários à obtenção do título de Doutor. O competente diploma será expedido após cumprimento dos demais requisitos, conforme as normas do Programa, a legislação pertinente e a regulamentação interna da UFU. Nada mais havendo a tratar foram

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1 APRESENTAÇÃO

A família *Solanaceae* é uma das maiores famílias do reino vegetal, incluindo várias plantas de importância agronômica e médica, sobretudo o tomate, por seu alto consumo a nível mundial. Além de sua importância como alimento, o tomate possui características agronômicas interessantes, a saber, fruto carnoso e folhas compostas, que plantas modelo não possuem, ex. *Arabidopsis thaliana*. Nesse sentido, o tomate comum (*Solanum lycopersicum*) tem sido utilizado como modelo para espécies que também apresentam tais características.

Devido às características específicas e às condições de cultivo, as variedades de tomate são constantemente melhoradas. No entanto, essa cultura é suscetível a diversas pragas e patógenos. Para auxiliar no controle dessas doenças, a maioria dos produtores opta pelo uso de agentes químicos que, muitas vezes, são caros, às vezes ineficazes e têm efeitos deletérios ao meio ambiente. Uma alternativa para esses problemas é cruzar o tomate cultivado com espécies silvestres.

São várias as espécies conhecidas de tomate selvagem, constituídas por recursos genéticos pouco explorados e de grande importância para o melhoramento, pesquisa e desenvolvimento da cultura, como o *Solanum pennellii, Solanum galapagense, Solanum chilense, Solanum peruvianum* e *Solanum pimpinellifolium*. Algumas espécies de tomate selvagem têm sido amplamente utilizadas para a construção e mapeamento de populações devido a sua tolerância ao estresse ambiental. Nesse sentido, um melhor entendimento da base molecular do tomate é necessário para se atingir a eficiência e o sucesso na seleção de marcadores associados às características de interesse, como a tolerância biótica e abiótica.

Da mesma forma que é importante obter um maior conhecimento sobre as bases moleculares de muitas espécies de plantas, alguns animais, parasitas, bactérias e vírus também necessitam de estudos moleculares para auxiliarem no controle de doenças que acometem os serem humanos. Neste sentido, a esquistossomose humana é uma doença parasitária causada por helmintos do gênero *Schistosoma* que afeta milhões de pessoas em todo o mundo. Cinco espécies de *Schistosoma* são responsáveis pela maioria das infecções humanas:

Schistosoma mansoni, *Schistosoma japonicum*, *Schistosoma haematobium*, *Schistosoma mekongi* e *Schistosoma intercalatum*.

O *S. haematobium* afeta o sistema reprodutivo e urinário e tem sido considerado um grande problema de saúde pública na África. A disseminação da doença é dependente da interação entre o parasita e o hospedeiro intermediário. Esta interação é complexa e determinada por alguns genes envolvidos na infectividade do parasita e suscetibilidade do hospedeiro. Portanto, compreender os mecanismos de regulação gênica é extremamente importante para compreender as interações parasita-hospedeiro e quais genes podem contribuir para a infecção.

O progresso atual no sequenciamento do genoma de plantas e animais tem gerado informações úteis para auxiliar no estudo da diversidade genética de muitas espécies. Nos anos 2000 foram sequenciados os genomas de *S. galapagense, S. peruvianum*, *S. haematobium, S. lycopersicum*, *S. pennellii, S. pimpinellifolium* e *S. chilense*. A interpretação dos genomas do esquistossomo melhorou nosso entendimento da biologia molecular desses parasitas, permitindo a identificação e caracterização de genes ainda não descobertos.

A disponibilidade de um genoma de referência de tomate forneceu um arcabouço para a análise genômica da família *Solanaceae*, gerando uma fonte de informações importantes para seu melhoramento molecular. Além disso, o sequenciamento de genomas de espécies selvagens de tomate forneceu um recurso valioso para a compreensão de várias características proeminentes, como mudanças na resposta ao déficit hídrico, resistência biótica e abiótica e metabolismo. Entretanto, várias partes desses genomas precisam ser exaustivamente estudadas e anotadas, uma vez que o sequenciamento do genoma e o depósito das sequências em bancos de dados públicos são apenas os passos iniciais do estudo.

Estudos recentes têm mostrado a importância da regulação gênica envolvendo várias classes de pequenos RNAs, seu sistema de processamento e desempenho celular em diferentes organismos. Os principais representantes dessa classe de pequenos RNAs são os microRNAs (miRNAs), cujas formas de regulação podem envolver a inibição do processo de tradução, degradação de RNAm ou silenciamento de genes, seja por complementaridade de alvos ou por

sinalização de modificações no DNA em regiões específicas do genoma. Diferentes proteínas atuam para gerar miRNAs maduros específicos para a regulação pós-transcricional. Em plantas e animais estas vias de síntese dos miRNAs possuem algumas diferenças.

Estratégias computacionais têm sido usadas para identificar miRNAs e proteínas envolvidas em suas vias em vários organismos. Os métodos computacionais são amplamente utilizados na identificação de genes, uma vez que alguns transcritos são expressos apenas sob certas condições ou em células específicas. Assim, as técnicas computacionais auxiliam no processo de descoberta de novos miRNAs, utilizando todas as informações contidas no genoma e/ou no transcriptoma independentemente da amostragem. Além disso, tais métodos são úteis para a previsão de precursores de miRNA e seus alvos.

Diante da importância de tais RNAs não codificantes na regulação da expressão gênica, é importante estudarmos miRNAs maduros e precursores, bem como os genes envolvidos na via de miRNA nestas espécies de tomate cultivado e selvagens para auxiliar na elucidação de processos biológicos, bem como seus desempenhos no nível celular. Também em *S. haematobium,* o conhecimento destas pequenas moléculas e sua via de processamento pode ajudar a entender o ciclo de vida desse parasita, seu mecanismo de infectividade e na busca de novos métodos de controle da esquistossomose.

Além da via de produção dos miRNAs, outras vias de defesa são importantes em algumas plantas. Diferentes aleloquímicos presentes em espécies de *Solanum* têm sido associados à resistência a pragas, como metil-cetonas, sesquiterpenos e acilaçúcares. A seleção para altos teores destes aleloquímicos poderia, desta maneira, constituir-se uma técnica eficiente de seleção indireta para resistência a pragas. Esses fitoquímicos purificados podem agir contra as pragas reduzindo o desenvolvimento larval, prejudicando a alimentação e a ovoposição de muitas pragas do tomate.

Tendo em vista a grande importância do tomate e a alta taxa de aplicação de agrotóxicos na cultura, um maior conhecimento sobre as bases moleculares do tomate faz-se necessário na seleção de marcadores associados a características importantes em resposta ao estresse biótico e abiótico. Portanto, compreender os miRNAs, sua via de processamento e os genes relacionados com a produção de

metabólitos poderá auxiliar na compreensão do seu envolvimento na resistência a artrópodes, principalmente pela produção de acilaçúcar e a regulação pós transcricional mediada pelos miRNAs.

Tendo em vista essas questões, o Capítulo I apresentará a fundamentação teórica sobre os miRNAs, acilaçucares e suas vias, além da importância de estudar estas moléculas em *S. lycopersicum, S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium e S. haematobium.* No Capítulo II serão expostos os artigos publicados e submetidos referente às pesquisas realizadas durante o doutorado.

2 CAPÍTULO I: Fundamentação teórica

2.1 Os microRNAs

Diversos estudos têm mostrado a importância da regulação gênica, envolvendo várias classes de pequenos RNAs, suas vias de processamento e sua atuação a nível celular em diferentes organismos (AXTELL, 2013; FOURACRE; POETHIG, 2016; KANG *et al*., 2014; MOAZED, 2009b; VIDIGAL; VENTURA, 2015; WEN *et al*., 2014). Essas classes de pequenos RNAs incluem os pequenos RNAs de interferência (siRNAs), pequenos RNAs de interferência com repetições associadas (rasiRNAs), pequenos RNAs de interferência que atuam em "trans" (tasiRNAs), pequenos RNAs de interferência anti senso naturais (natsiRNAs), RNAs que interagem com a proteína PIWI (piRNAs) e microRNAs (miRNAs), que diferem em processamento, tamanho e função celular (AXTELL, 2013; BARTEL, 2004; FOURACRE; POETHIG, 2016; KIM, 2008; WEN *et al*., 2014).

Os principais representantes das classes de pequenos RNAs são os miRNAs, se destacando pelas suas diversas funções na regulação da expressão de RNAs mensageiros (RNAm) a nível celular. Essa regulação pode ocorrer a partir da inibição do processo de tradução, por degradação do RNAm ou por silenciamento do gene, seja por complementaridade do alvo, ou sinalizando modificações no DNA em regiões específicas do genoma, influenciando o processo de expressão gênica em diferentes organismos (AGRAWAL *et al*., 2003; BARTEL, 2004; BENTWICH, 2005; DOENCH; PETERSEN; SHARP, 2003; GOMES *et al*., 2009; RAO *et al*., 2009). Os miRNAs são uma classe de pequenos RNAs endógenos, presentes em plantas e animais, que não codificam proteínas, com aproximadamente 21 nucleotídeos de comprimento quando maduro (BARTEL, 2004; CARTHEW; SONTHEIMER, 2009; WAHID *et al*., 2010). Os genes precursores destes miRNAs são encontrados em plantas, principalmente em regiões intergênicas no genoma (BARTEL, 2004; CHEN, 2008; DE SOUSA CARDOSO *et al*., 2015; LANG *et al*., 2011; ZHOU *et al*., 2011a).

Em sua via de processamento, atuam diferentes proteínas capazes de gerar um miRNA específico, para que ocorra uma fina e característica regulação

ao nível de genoma e/ou transcriptoma (AXTELL, 2013; DHIR; PROUDFOOT, 2013; KIM; HAN; SIOMI, 2009).

Em plantas, o processamento do miRNA ocorre primeiramente no núcleo a partir da transcrição realizada pela RNA polimerase II (Pol II), resultando em um longo miRNA primário (pri-miRNA). Até pouco tempo, era considerado que os pri-miRNAs não possuíam a capacidade de codificar nenhuma proteína. No entanto, Lauressergues e colaboradores (2015) apresentaram que alguns pri-miRNAs codificam peptídeos que aumentam a produção de seus miRNAs (LAURESSERGUES *et al*., 2015; WATERHOUSE; HELLENS, 2015).

No processo de geração dos miRNAs maduros em plantas, as enzimas RIBONUCLEASE III (RNase III), DICER-LIKE 1 (DCL1), associadas a outras enzimas, SERRATE (SE) e HYPONASTIC LEAVES 1 (HYL1), clivam o pri-miRNA, gerando o precursor de miRNA (pré-miRNA) (AXTELL; WESTHOLM; LAI, 2011; BUDAK; AKPINAR, 2015; JONES-RHOADES; BARTEL; BARTEL, 2006; KAPOOR *et al*., 2008; WAHID *et al*., 2010; WATERHOUSE; HELLENS, 2015). O pré-miRNA possui uma estrutura secundária característica, formando um grampo (*hairpin*) a partir de uma complementaridade imperfeita, contendo de 200-300 nucleotídeos de comprimento (KIDNER; MARTIENSSEN, 2005; WINTER *et al*., 2009). Mais uma vez as enzimas DCL1 e HYL1 atuam, clivando o pré-miRNA na extremidade que possui o hairpin, formando um miRNA/miRNA fita dupla, sendo, em seguida, metilado por uma metiltransferase HUA ENHANCER (HEN1), estabilizando a molécula e impedindo a sua uridilação e degradação posterior pelas exonucleases SDN (*small RNA degrading nuclease*) (BUDAK; AKPINAR, 2015; LI *et al*., 2005; YANG *et al*., 2006). O miRNA maduro então é exportado para o citoplasma pela HASTY (HST), homóloga da proteína Exportina-5 (XPO5), proteína presente dos animais (BARTEL, 2004; BRODERSEN; VOINNET, 2006; WAHID *et al*., 2010). O miRNA fita dupla metilado é, na sequência, carregado por um complexo de enzimas liderado pela ARGONAUTA (AGO), momento em que ocorre o desanelamento da fita dupla, sendo uma fita degradada e a outra direcionada, junto ao complexo RISC, ao reconhecimento específico do RNAm alvo, com a finalidade de regular a expressão gênica: por inibição da tradução ou degradação do RNAm (AXTELL, 2013; KAPOOR *et al*., 2008; PETERS; MEISTER, 2007; WINTER *et al*., 2009).

Em animais, a diferença da via de processamento dos miRNAs é que os pri-miRNA são clivados por um complexo que envolve a enzima RNAse III de cadeia dupla (DROSHA) e a proteína de ligação DGCR8 (DiGeorge Syndrome Critical Region 8 protein) (RUBY *et al*., 2007). A DROSHA contém dois domínios de RNAse III, cada qual cliva uma fita do RNA sintetizando o pré-miRNA com aproximadamente 70 pares de bases (pb). O pré-miRNA é transferido para o citoplasma por meio da proteína XPO5, onde, então, é clivado pela DCL1.

Em plantas e em animais há diversos miRNAs que possuem alvos importantes no organismo. Isso faz com que essas pequenas moléculas consigam fazer uma regulação fina e específica de diversos processos biológicos dentro das células. Algumas das funções importantes que os miRNAs apresentam no organismo de plantas e animais estão relacionados a: diferenciação e crescimento de células, apoptose, florescimento, fertilidade, defesa contra patógenos, coordenação da homeostase, regulação do desenvolvimento foliar e floral, transdução de sinais, acumulação de fatores de transcrição e respostas ao estresse (AXTELL, 2013; JONES-RHOADES; BARTEL; BARTEL, 2006; LI; MAO, 2007; MALLORY; VAUCHERET, 2006; MARTÍNEZ DE ALBA; ELVIRA-MATELOT; VAUCHERET, 2013; WAHID *et al*., 2010). Diante disso, o estudo do genoma e transcriptoma de plantas e animais tem se tornado uma ferramenta muito poderosa para auxiliar na elucidação de processos biológicos bem como suas atuações a nível celular (AMBROS *et al*., 2003; SRIVASTAVA *et al*., 2014; ZHANG *et al*., 2005; ZHOU *et al*., 2008).

A publicação dos genomas de *S. galapagense, S. peruvianum*, *S. haematobium, S. lycopersicum*, *S. pennellii, S. pimpinellifolium* e *S. chilense* representou um grande avanço no estudo da biologia destas importantes espécies (BOLGER *et al*., 2014; FERNANDEZ-POZO *et al*., 2015; RAZALI *et al*., 2018; SATO; TABATA, 2016; SATO; TABATA; HIRAKAWA, 2012; STAM *et al*., 2019; STRICKLER *et al*., 2015; YOUNG *et al*., 2012). No entanto, várias partes destes genomas necessitam ser profundamente estudadas e anotadas, uma vez que o sequenciamento do genoma e o depósito das sequências em bancos de dados públicos representam apenas os passos iniciais neste estudo.

Diversas estratégias computacionais e experimentais têm sido utilizadas para identificação de miRNAs e as proteínas de seu processamento em vários

organismos (HUANG *et al*., 2011; LI *et al*., 2010; ZHANG *et al*., 2005). Os métodos computacionais têm sido bastante utilizados na identificação de genes uma vez que alguns transcritos são expressos apenas em determinadas condições, em células específicas, ou são pouco expressos, sendo impossível sua identificação *in vitro*. Assim, as técnicas computacionais auxiliam no processo de descoberta de novos miRNAs, utilizando todas as informações contidas no genoma e/ou transcriptoma independentemente da amostragem. Além disso, esses métodos são úteis para a predição de precursores de miRNA e seus alvos. Contudo, muitos genes de miRNAs e seus alvos ainda não foram identificados em vários organismo, principalmente em plantas (LI *et al*., 2010; SRIVASTAVA *et al*., 2014; ZHANG *et al*., 2005).

2.2 *Schistosoma haematobium*

A esquistossomose humana é uma doença parasitária, crônica e debilitante causada por helmintos do gênero *Schistosoma,* que afeta atualmente cerca de 240 milhões de pessoas em todo o mundo, segundo a Organização Mundial da Saúde (MOHAMMED *et al*., 2015; WHO, 2020). Os países da África e da América do Sul estão entre os mais afetados. Além disso, 700 milhões de pessoas vivem em áreas de risco de contrair a doença (MCMANUS *et al*., 2018). Cinco espécies de *Schistosoma* são responsáveis pela maioria das infecções humanas: *S. mansoni*, *S. japonicum*, *S. haematobium*, *S. mekongi* e *S. intercalatum* (MOHAMMED *et al*., 2015).

O ciclo de vida do esquistossomo ocorre em dois hospedeiros: caramujos e mamíferos. O tipo de reprodução (assexuada ou sexual) acontece de acordo com o hospedeiro. A reprodução assexuada ocorre em caramujos de água doce, iniciando com o desenvolvimento de miracídios em esporocistos, os quais se multiplicam e se transformam em cercarias. Nos hospedeiros mamíferos, os parasitas crescem para amadurecer, acasalar e produzir ovos (MOUAHID *et al*., 2018; NELWAN, 2019; VIANA *et al*., 2018). Hospedeiros mamíferos liberam ovos de vermes no ambiente externo por meio de fezes ou urina. Em água doce, esses ovos formam miracídios, que eclodem e infectam os caramujos. Os miracídios desenvolvem nos caramujos que, por sua vez, podem eliminar centenas de

cercarias diariamente. As cercárias penetram na pele humana e perdem sua cauda bifurcada, formando esquistossômulos, os quais migram pelos tecidos do corpo através da circulação sanguínea e se transformam em esquistossomos e vermes adultos (GEYER *et al*., 2018; GURARIE *et al*., 2018; MOUAHID *et al*., 2018; NELWAN, 2019; SHUJA *et al*., 2018).

O *S. haematobium* afeta o sistema reprodutivo e urinário e tem sido considerado um grande problema de saúde pública principalmente na África (MOHAMMED *et al*., 2015; RISIKAT; AYOADE, 2012). A infecção por esse parasita pode resultar em deficiências nutricionais e retardo de crescimento, podendo também levar à diminuição da sistema cognitivo (STEPHENSON, 1993). A propagação desta doença ocorre por água doce e pela presença de caramujos hospedeiros. Atividades em contato com a água, como a agricultura, podem facilitar a infecção pelo parasita (RISIKAT; AYOADE, 2012). Em *S. mansoni* e seu hospedeiro intermediário *Biomphalaria glabrata*, a interação é complexa e determinada por alguns genes envolvidos na infectividade do parasita e suscetibilidade do hospedeiro (LEWIS, F. A., RICHARDS, C. S., KNIGHT, M., COOPER, L. A., CLARK, 1993; RICHARDS, 1970; RICHARDS; SHADE, 1987). Assim, também é sugerida uma interação hospedeiro-parasita complexa, envolvendo vários genes entre *S. haematobium* e seu caramujo hospedeiro intermediário, do gênero *Bulinus*. Portanto, compreender os mecanismos de regulação gênica é extremamente importante para compreender as interações parasita-hospedeiro e quais genes podem contribuir para a infecção.

A regulação da expressão gênica em eucariotos compreende processos envolvidos na repressão da tradução e/ou degradação de genes alvo (BARTEL, 2009). Pequenos RNAs, como miRNAs, e suas vias de silenciamento têm sido considerados importantes em diversos organismos por realizarem uma regulação específica da expressão gênica mantendo a integridade do genoma (BARTEL, 2009; MOAZED, 2009a). Os genes envolvidos na via de silenciamento gênico mediada por miRNAs foram descritos em vários organismos modelo, como *Drosophila melanogaster*, *Caenorhabditis elegans* e *Homo sapiens* (AMBROS, 2003; LEE *et al*., 2004; SIOMI; SIOMI, 2008). Além disso, membros da via biosintética de miRNAs, como AGO e DCL, assim como moléculas de miRNA,

foram relatadas em algumas espécies de *Schistosoma*, incluindo *S. mansoni* e *S. japonicum* (GOMES *et al*., 2009; YOUNG *et al*., 2012).

Young *et al*., publicaram em 2012 a sequência do genoma completo de *S. haematobium* (YOUNG *et al*., 2012). A interpretação dos genomas do esquistossomo melhorou nosso entendimento da biologia molecular desses parasitas, permitindo a identificação e caracterização de genes ainda não descobertos. Diante da importância amplamente aumentada de tais RNAs não codificantes na regulação da expressão gênica, é importante estudarmos miRNAs maduros e precursores, bem como os genes envolvidos na via de miRNA em *S. haematobium*. Isso pode ajudar a entender o ciclo de vida desse parasita, seu mecanismo de infectividade e a busca de novos métodos de controle da esquistossomose.

2.3 O tomate

O tomate é uma das hortaliças mais importantes do mundo devido à sua importância na economia, na geração de empregos e renda, e no grande volume de mão de obra e recursos produzidos em sua cadeia produtiva e industrial (KNAPP, 2002; SATO; TABATA, 2016). Atualmente, o Brasil está entre os 10 maiores produtores do mundo, produzindo mais de 4 milhões de toneladas de frutos em 2019 (FAO, 2019; IBGE, 2020).

O gênero *Solanum* é um dos maiores entre as angiospermas e contém aproximadamente 1.500 espécies (BAUCHET; CAUSSE, 2012). *S. lycopersicum*, o tomate cultivado, tem maior destaque por ser uma dos frutos mais consumidas e estudadas (BAICHOO; JAUFEERALLY-FAKIM, 2016; KARKUTE *et al*., 2018; KIM *et al*., 2011; PEREZ-FONS *et al*., 2014). Além de ser um alimento nutritivo, o tomate possui muitas características interessantes como fruto carnudo com folhas compostas, tricomas multicelulares e glandulares, entre várias outras características importantes que outras plantas modelo (como por exemplo, *A. thaliana*) não possuem. Essas características fazem do tomate uma planta modelo para espécies que apresentam essas características (BEDINGER *et al*., 2011; CAMPOS *et al*., 2010; GAPPER; MCQUINN; GIOVANNONI, 2013; GIOVANNONI, 2004; KOBAYASHI *et al*., 2014).

A origem do tomate ocorreu na região ocidental das Américas Central e do Sul, envolvendo as regiões andinas do Equador, Bolívia, Peru, Colômbia e Chile (BAUCHET; CAUSSE, 2012; CARVALHO, 2014). A principal forma de consumo do fruto é *in natura*, caracterizando o tomate de mesa, o qual se destaca pelo seu alto valor nutritivo, apresentando 93% a 95% de água, baixo valor calórico, além de conter proteínas, carboidratos, cálcio, magnésio, ferro, zinco, fibras, vitamina C, potássio, licopeno e outros compostos essenciais na alimentação (BAUCHET; CAUSSE, 2012; KIM *et al*., 2011; TACO, 2011). O tomate possui também um grande mercado para o consumo do fruto processado de forma industrial, sobretudo na produção de molhos, extratos e sucos (MONTEIRO *et al*., 2008).

Devido às características específicas, as variedades de tomate são constantemente melhoradas de acordo com a região, a forma de cultivo e a finalidade do fruto após a colheita (CARVALHO, 2014). Estes fatores são essenciais para que pesquisadores e produtores possam melhorar a qualidade e produtividade de cultivares de tomateiro (GERSZBERG; HNATUSZKO-KONKA, 2015). Embora o tomateiro tenha se adaptado a diferentes ambientes, grande parte das variedades necessita de um clima ameno, com temperaturas em torno de 21° a 24°C, e de uma área ensolarada, que não ultrapasse os 35ºC para se obter uma produção de melhor qualidade (CAMARGO, 2006; CARVALHO, 2014; NAIKA *et al*., 2006). Em geral, as plantas comerciais de tomate *S. lycopersicum* são suscetíveis ao ataque de pragas e mais de 200 doenças causadas por diferentes tipos de patógenos, incluindo vírus, bactérias, fungos e nematoides (BAI; LINDHOUT, 2007; HAAPALAINEN, 2014; LUKYANENKO, 1991; MCGOVERN, 2015; NOWICKI *et al*., 2012). Seu controle é feito principalmente pelo uso de inseticidas e acaricidas, que, além de altos custos, envolvem aplicação intensiva, o que impacta negativamente o meio ambiente pela poluição ambiental e desequilíbrio ecológico (eliminação de inimigos naturais), e ainda são prejudiciais à saúde humana (ERCOLANO *et al*., 2012).

Uma alternativa para obter variedades melhoradas de tomateiro, com características desejadas pelos produtores e consumidores, tais como o aumento do potencial produtivo, precocidade, homeostase genética, uniformidade, qualidade do fruto e resistência a patógenos, insetos e estresses abióticos, além de minimizar a utilização de produtos químicos, é o cruzamento do tomate

cultivado com espécies selvagens (ALSEEKH *et al*., 2013; BOLGER *et al*., 2014; KAMENETZKY *et al*., 2010; KIMURA; SINHA, 2008; M. A. STEVENS; RICK C. M., 1986). Existem várias espécies conhecidas de tomate selvagem, consistindo em recursos genéticos subexplorados e de grande importância para o melhoramento, pesquisa e desenvolvimento da cultura (AFLITOS *et al*., 2014; BOLGER *et al*., 2014; KAMENETZKY *et al*., 2010; KIMURA; SINHA, 2008; MCDANIEL *et al*., 2016; MITTOVA; VOLOKITA; GUY, 2015; NOSENKO *et al*., 2016a; PERALTA; KNAPP; SPOONER, 2005; SPOONER; PERALTA; KNAPP, 2005).

S. pennellii é uma espécie de tomate selvagem, endêmica das regiões andinas da América do Sul, onde evoluiu para prosperar em ambientes áridos. Essa espécie é relativamente distante da espécie domesticada de *S. lycopersicum*, estimada em 2,7 milhões de anos, e tem sido largamente utilizado para a construção e mapeamento de populações e linhagens devido à sua tolerância ao estresse e morfologia incomum (BOLGER *et al*., 2014; FERNANDEZ-POZO *et al*., 2015; KAMENETZKY *et al*., 2010; RICK; TANKSLEY, 1981). O genoma nuclear de *S. lycopersicum* e *S. pennellii* possuem 12 cromossomos com aproximadamente 842 Mb e 1 Gb de tamanho, respectivamente (FERNANDEZ-POZO *et al*., 2015).

Essa espécie de tomate selvagem possui características bem específicas, como o sistema de acasalamento, a diversidade fitoquímica e a resistência a diferentes ambientes. Mesmo com essas especificidades, é sexualmente compatível com *S. lycopersicum*, oferecendo um conjunto de genes úteis para lidar com os desafios de reprodução existentes e gerando híbridos altamente produtivos possuindo as características almejadas. Nos dias de hoje, os produtores optam pelo plantio dessas cultivares híbridas, devido ao grande potencial dessas plantas que chegam ao mercado, ampliando a possibilidade de serem cultivadas com maior segurança (ALSEEKH *et al*., 2013; BAUCHET; CAUSSE, 2012).

A maioria das espécies selvagens possuem frutos verdes, exceto: *S. pimpinellifolium, S. galapagense e S. cheesmaniae.* Essas espécies também são consideradas as parentes mais próximas do tomate cultivado (DARWIN; KNAPP; PERALTA, 2003; SATO; TABATA; HIRAKAWA, 2012). *S. pimpinellifolium* é nativo de áreas de baixa elevação nas encostas ocidentais dos Andes no Peru e

Equador (GRANDILLO *et al*., 2011). É a espécie selvagem mais próxima proposta em relação ao tomate cultivado, contendo em seu gonema 12 cromossomos e ~807 – 923 Mb de tamanho, além de ser a única espécie selvagem de frutos vermelhos. *S. pimpinellifolium* tem sido usado para introduzir características como resistência à doenças e à sólidos solúveis, melhoradas em tomate cultivado (FERNANDEZ-POZO *et al*., 2015; GRANDILLO *et al*., 2011).

S. galapagense é uma espécie perene endêmicas das Ilhas Galápagos e possui um fruto de cor laranja. Recentemente, *S. galapagense* foi reconhecida como uma espécie separada de *S. cheesmaniae*, sendo que anteriormente, era nomeada como *S. lycopersicon cheesmaniae L. Riley var. menor (Hook.f)* (DARWIN; KNAPP; PERALTA, 2003). *S. galapagense* possui um genoma com ~742 Mb de tamanho e têm sido utilizado em programas de melhoramento, principalmente para melhorar a tolerância ao sal e à sólidos solúveis (GRANDILLO *et al*., 2011). A cor laranja do fruto nesta espécie é devido a uma variante dominante do gene *B* que resulta em aumento de 5 a 10 vezes no β-caroteno em comparação com o fruto vermelho (RONEN *et al*., 1999). Essas espécie possui outras diferenças fenotípicas do tomate cultivado, incluindo cheiro, resposta a patógenos, tricomas e morfologia foliar (DARWIN, 2009).

S. peruvianum é uma espécie de tomate selvagem mais distante incluído na seção *Lycopersicon* e possui um genoma com 12 cromossomos e ~25 Mb de tamanho (FERNANDEZ-POZO *et al*., 2015; PERALTA, I. E., SPOONER, D. M., AND KNAPP, 2008). Vários acessos de *S. peruvianum* foram identificados como resistentes a pragas, doenças e estresses abióticos, tornando-os uma fonte de novos genes para reprodução. No entanto, seu uso tem sido limitado devido a barreiras de incompatibilidade e problemas de fertilidade de suas progênies (RICK, 1986).

S. chilense é nativo da América do Sul, variando do sul do Peru ao norte do Chile, e colonizou uma ampla variedade de habitats. As populações de *S. chilense* são encontradas em regiões costeiras, mesmo em ambientes ligeiramente alcalinos, até regiões montanhosas de grande altitude. Também ocorre em habitats extremamente secos na borda do deserto do Atacama, bem como perto de rios e riachos (PERALTA, I. E., SPOONER, D. M., AND KNAPP, 2008). Esta espécie tem sido utilizada em estudos sobre seca (XIA *et al*., 2010),

salinidade (MARTÍNEZ *et al*., 2012; ZHOU *et al*., 2011b), tolerância ao frio (NOSENKO *et al*., 2016b), resistência a patógenos e evolução do gene de resistência (STAM; SCHEIKL; TELLIER, 2017), bem como adaptação a ambientes extremos (BÖNDEL; NOSENKO; STEPHAN, 2018). *S. chilense* possui um genoma com 12 cromossomos e ~930 Mb de tamanho (FERNANDEZ-POZO *et al*., 2015), também vem sendo usada no melhoramento do tomate, alguns de seus genes foram introduzidos com sucesso para aumentar a resistência ao patógeno fúngico *Verticilium dahliae* (TABAEIZADEH *et al*., 1999) e ao vírus Y do mosaico do tomate (VERLAAN *et al*., 2013).

Nesse sentido, um maior conhecimento sobre as bases moleculares dessas espécies de tomate é necessário, para obter eficiência e sucesso na seleção de marcadores associados a características de interesse (GERSZBERG; HNATUSZKO-KONKA, 2015).

2.4 Os acilaçucares

Muitas espécies selvagens de tomate possuem diversos aleloquímicos que têm sido associados com a resistência a diversos artrópodes e pragas, no entanto estas espécies não possuem valor comercial imediato (SILVA, 2009; WILLIAMS *et al*., 1980). *S pennellii*, relativamente distante da espécie domesticada de *S. lycopersicum*, e tem sido largamente utilizado para a construção de populações e linhagens devido a sua tolerância ao estresse, resistência a pragas e morfologia incomum (BOLGER *et al*., 2014; FERNANDEZ-POZO *et al*., 2015). Acessos de *S. pennellii,* entre os quais o denominado LA-716, apresentam alto nível de resistência à mosca branca, bem como a afídeos, ácaros rajados, lepidópteros, inclusive à traça-do-tomateiro, pragas relevantes do tomateiro e de importância mundial (GENTILE; WEBB; STONER, 1968, 1969; GOFFREDA *et al*., 1989).

Diferentes aleloquímicos presentes em espécies de *Solanum* têm sido associados à resistência a pragas: metil-cetonas como a 2-tridecanona em *S. habrochaites* var. *glabratum* (GONÇALVES *et al*., 1998; MALUF; BARBOSA; SANTA-CECÍLIA, 1997), sesquiterpenos em *S. habrochaites* var. *hirsutum* (EIGENBRODE *et al*., 1994) e acilaçúcares em *S. pennellii* (FREITAS *et al*., 2002; GOFFREDA *et al*., 1989). A seleção para altos teores destes aleloquímicos

poderia desta maneira, constituir-se uma técnica eficiente de seleção indireta para resistência a pragas, como a traça-do-tomateiro (GONÇALVES NETO *et al*., 2010; RESENDE *et al*., 2006), a mosca branca (FREITAS *et al*., 2002) e ácaros *Tetranychus* spp. (MALUF; CAMPOS; DAS GRAÇAS CARDOSO, 2001).

Esta resistência de amplo espectro é atribuída à presença de tricomas glandulares que ocupam a superfície da planta, principalmente tricomas do tipo IV, bem como aos aleloquímicos por eles secretados (GENTILE; WEBB; STONER, 1968; GOFFREDA *et al*., 1989). Os acilaçúcares são ésteres de ácidos graxos com 4 a 12 átomos de carbono, contendo glicose ou sacarose, constituem aproximadamente 90% do total secretado pelo tricoma tipo IV, e podem representar um importante papel na resistência a pragas do tomateiro. Esses fitoquímicos purificados podem agir contra as pragas reduzindo o desenvolvimento larval, prejudicando a alimentação e a ovoposição de muitas pragas do tomate (HAWTHORNE *et al*., 1992; JUVIK *et al*., 1982).

Acilaçúcares encontrados na família das *Solanaceae* possuem um conjunto característico de moléculas entre as espécies, os quais podem deferir de acordo com a porção de açúcar, como glicose ou sacarose, a porção de ácidos graxos e a disposição da acilação (SHAPIRO; STEFFENS; MUTSCHLER, 1994). A variedade de estruturas das moléculas de acilaçúcares está relacionada com uma diversidade de vias biossintéticas (GOFFREDA; STEFFENS; MUTSCHLER, 1990; SHAPIRO; STEFFENS; MUTSCHLER, 1994).

Alguns trabalhos mostram a contribuição de algumas proteínas no metabolismo de acilaçucares em plantas, como as enzimas acetyl-CoA synthase (KANDRA; SEVERSON; WAGNER, 1990), aldo keto reductase (AKR), acetolactate/acetohydroxyacid synthase (ALS/AHAS) (KROUMOVA; WAGNER, 2003; NING *et al*., 2015; SLOCOMBE *et al*., 2008; WALTERS; STEFFENS, 1990), acylsugar acyltransferase 2/4/3 (AT2/AT4/AT3) (KIM *et al*., 2012; LECKIE; HALITSCHKE, 2014; NING *et al*., 2015; SCHILMILLER; CHARBONNEAU; LAST, 2012), branched-chain aminotransferase 2/5 (BCAT) (NING *et al*., 2015), branched-chain keto acid dehydrogenase E1a/E1b/E2 (BCKD) (NING *et al*., 2015; SLOCOMBE *et al*., 2008; WALTERS; STEFFENS, 1990), dihydroxyacid dehydratase (DHAD) (LECKIE; HALITSCHKE, 2014; NING *et al*., 2015; WALTERS; STEFFENS, 1990), dihydrolipoyl dehydrogenase (IPD) (KANDRA; SEVERSON; WAGNER, 1990), isopropylmalate dehydratase/isopropylmalate

isomerase (IPDS/IPMI) (KANDRA; SEVERSON; WAGNER, 1990; KROUMOVA; WAGNER, 2003; SLOCOMBE *et al*., 2008), isopropylmalate dehydrogenase (IPMD) (KANDRA; SEVERSON; WAGNER, 1990; NING *et al*., 2015; SLOCOMBE *et al*., 2008; WALTERS; STEFFENS, 1990), 2-isopropylmalate synthase A/B (IPMSA/IPMSB) (HOEVEN *et al*., 2000; KANDRA; SEVERSON; WAGNER, 1990; LECKIE; HALITSCHKE, 2014; NING *et al*., 2015; SLOCOMBE *et al*., 2008), isovaleryl-CoA dehydrogenase 1 mitocondrial/methylacyl-CoA dehydrogenase, ketol acid/acetohydroxy-acid reductoisomerase I (KARI) (NING *et al*., 2015; WALTERS; STEFFENS, 1990), ketoacyl-ACP synthase I, II, III e mitocondrial (KAS) (SLOCOMBE *et al*., 2008), 3-ketoacyl-CoA reductase 2 (KCR2) (MCDOWELL *et al*., 2011), 3-ketoacyl-CoA synthase 3/19 (KCS3/KCS19) (LECKIE; HALITSCHKE, 2014; MCDOWELL *et al*., 2011) e threonine deaminase/dehydratase (TD) (NING *et al*., 2015; SLOCOMBE *et al*., 2008; WALTERS; STEFFENS, 1990).

Dentre as principais proteínas envolvidas na via de acilaçucar, o complexo multienzimático BCKD é composto por três subunidades de enzimas, 2-oxo acid dehydrogenase (E1), dihydrolipoyl acyltransferase (E2) e dihydrolipoamide dehydrogenase (E3), o qual desempenha um papel fundamental na regulação redox. E2, o componente central do complexo, catalisa a transferência do grupo acil do CoA a partir de E1 a E3 através de acetilação redutora de um grupo lipoil, covalentemente ligado a um resíduo de lisina (CDD, 2016). BCKD catalisa a conversão de cetoácidos de cadeia ramificada em acil-CoAs de cadeia ramificada com a perda de um carbono, num processo de descarboxilação (SLOCOMBE *et al*., 2008). Em plantas, BCKD está envolvido no primeiro passo do catabolismo de aminoácidos de cadeia ramificada (BCAA), além de também atuar de forma importante na via de síntese de ácidos graxos de cadeia ramificada (BCFA) (MOONEY; MIERNYK; RANDALL, 2002; SLOCOMBE *et al*., 2008; TAYLOR *et al*., 2004). A enzima ACYLSUGAR ACYLTRANSFERASE2 (ASAT2) catalisa a transferência de um grupo acetil via acetil-CoA para um receptor tri-acilsucrose para formar as tetra-acilsucroses acetiladas produzidas por tricomas de tomate cultivados. No tomate cultivado, a ACYLSUGAR ACYLTRANSFERASE3 (ASAT3), catalisa a acilação R3′ no anel furanose de cinco membros das di-acilsucroses nas células da ponta dos tricomas produtores de acilçucar (SCHILMILLER *et al*., 2015; SCHILMILLER; CHARBONNEAU; LAST, 2012).

A enzima IPMS é responsável por catalisar a condensação do tipo aldol de acetil-CoA-redutase e 2-oxoisovalerato, obtendo 2-isopropilmalato e CoA, sendo esse o primeiro passo envolvido na biossíntese de leucina (CDD, 2016; HOEVEN *et al*., 2000). Ning *et al*. (2015) observou que *S. lycopersicum* expressa um gene IPMS (Solyc08g014230) no cromossomo 8 de células apicais dos tricomas do tipo I/IV, o qual codifica uma proteína final funcional com menos 160 aminoácidos (a.a.) na região C-terminal quando comparada com a IPMS do cromossomo 6 (NING *et al*., 2015). Mesmo a proteína sendo ativa *in vitro*, ela é insensível a inibição alostérica mediada pela ligação à leucina no domínio regulador descrita em *Arabidopsis* (KRAKER; GERSHENZON, 2011) e microorganismos (CARVALHO; ARGYROU; BLANCHARD, 2005; KOON; SQUIRE; BAKER, 2004; NING *et al*., 2015). Por outro lado, um gene IPMS (Sopen08g005140), localizado no cromossomo 8 de *S. pennellii* codifica uma proteína IPMS truncada não-funcional com uma deleção maior na região C-terminal (51 a.a.). Essa deleção encontrada em *S. pennellii* faz com que não haja a regulação alostérica pela ligação de leucina, acumulando então grandes quantidades de ácido metilpropanóico para a síntese de acilaçucar (NING *et al*., 2015). Dessa forma, esses resultados auxiliam uma maior compreensão dos mecanismos naturais de defesa nas diferentes espécies de *Solanaceas* para avanços no melhoramento tradicional e em manipulações genéticas de espécies comercialmente importantes.

Tendo em vista a grande importância do tomate e a alta taxa de aplicação de agrotóxicos na cultura, um maior conhecimento sobre as bases moleculares do tomate faz-se necessário na seleção de marcadores associados a características importantes em resposta ao estresse biótico e abiótico. A publicação dos genomas de várias espécies de tomate representou um grande avanço no estudo da biologia destas espécies, possibilitando um aprofundamento nos estudos, na anotação e identificação de diversos genes. Portanto, compreender os genes relacionados com a produção de metabólitos nos tricomas de *S. galapagense, S. peruvianum*, *S. haematobium, S. lycopersicum*, *S. pennellii, S. pimpinellifolium* e *S. chilense* poderá auxiliar na compreensão do seu envolvimento na resistência a artrópodes, principalmente pela produção de acilaçúcar.

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3 CAPÍTULO II – Article: New insights into tomato microRNAs from Scientific Reports Journal

Algumas análises presentes no artigo *New insights into tomato microRNAs* a ser apresentado foram realizadas e defendidas no mestrado. No doutorado foram realizadas novas análises referentes a este trabalho para publicação.

Foram realizadas no mestrado:

- Predição dos genes e proteínas envolvidos na biogênese de pequenos RNAs, incluindo miRNAs em *S. lycopersicum* e *S. pennellii*;
- Predição de miRNAs maduros e precursores;
- Análise de domínios conservados, sítios ativos, filogenia e alinhamento de proteínas da via e precursores de miRNA em *S. lycopersicum* e *S. pennellii;*
- Predição dos genes alvos dos miRNAs identificados em *S. lycopersicum* e *S. pennellii.*

No doutorado:

- Expressão de miRNAs por PCR em tempo real:
    - Coleta das folhas, frutos e flores de *Solanum lycopersicum* e *Solanum pennellii;*
    - Extração e quantificação do RNA dos materiais vegetais;
    - Tratamento do RNA com DNAse;
    - Síntese do cDNA e expressão relativa dos miRNAs.
- Expressão de genes da via de miRNA em 18 bibliotecas de RNA-seq de tomate;
- Análise de miRNAs em 95 bibliotecas de smallRNAseq de *S. lycopersicum*;
- Análise estatística comparativa entre as variáveis estruturais e termodinâmicas de espécies e/ou famílias de miRNAs.

New insights into tomato microRNAs

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ABSTRACT

Cultivated tomato, *Solanum lycopersicum*, is one of the most common fruits in the global food industry and together with the wild tomato *Solanum pennellii*, are both species widely used in developing better cultivars. microRNAs act on mRNA regulation, inhibiting their translation and/or promoting its degradation. Important proteins involved in these processes are ARGONAUTA and DICER. This study aimed to identify and characterize genes involved in miRNA processing pathways, miRNAs molecules and target-genes in the genome of both species using in silico analysis. We also validated the genes and miRNAs expression in different NGS libraries, in addition to validating some miRNAs using quantitative RT-PCR. We

identified 70 putative proteins in *S. lycopersicum* and 108 in *S. pennellii* involved in small RNAs processing. Of these, 28 and 32 participate in miRNA processing pathways, respectively. We identified 343 mature miRNAs, 226 pre-miRNAs in 87 families, including 192 miRNAs not previously identified, belonging to 38 new families in *S. lycopersicum*. In *S. pennellii*, we found 388 mature miRNAs, 234 pre-miRNAs contained in 85 families. All miRNAs found in *S. pennellii* were unpublished, being first identified in our study. Furthermore, we identified 2471 and 3462 miRNA different target in *S. lycopersicum* and *S. pennellii*, respectively.

3.1 INTRODUCTION

The *Solanaceae* family is one of the largest families in the plant kingdom, including several plants of agronomic and medical importance. It is composed of about 100 genera and more than 3000 species that grow in all habitats, ranging from rainforests to deserts. The tomato is one of the most important fruit crop in the global food industry[1–5]. The genus *Solanum* is one of largest genera among the *Angiosperms*, containing approximately 1500 species[6]. *Solanum lycopersicum,* the cultivated tomato is one of the most consumed fruits worldwide[7,8]. Besides its importance as food, the tomato has important agronomic characteristics, including fleshy fruits and multicellular and glandular trichomes, which model plants like *Arabidopsis thaliana* do not have. Thus, the common tomato has beend used as a model for species that also have these characteristics[9–13].

Due to the specific characteristics and growing conditions, tomato varieties are constantly improved[14]. However, this crop is susceptible to insect attacks and more than 200 diseases caused by various types of pathogens, including viruses, bacteria, fungi and nematodes[15]. To aid in the control of these diseases, most producers opt for the use of chemical agents, which are often costly, at times ineffective, and have deleterious effects on the environment[16]. An alternative to these problems is to cross the cultivated tomato with wild species[12,17–20]. There are several known species of wild tomato, consisting of underexploited genetic resources and of great importance for the improvement, research and development of culture[12,18,20–26]. *Solanum pennellii* is a species of wild tomato that has been widely used for the construction and mapping of populations due to its

tolerance to environmental stress[18,20,27,28]. In this sense, a better understanding of the molecular basis of the tomato is required to achieve efficiency and success in the selection of markers associated with characteristics of interest[4].

The current progress in sequencing the tomato genome has generated useful information to assist in the study of their genetic diversity[12,23]. The sequencing of the genome of *S. lycopersicum* was completed in 2012[29]. Furthermore, the availability of a reference genome provided a framework for the genomic analysis of *Solanaceae* family, generating a source of important information for their molecular breeding[5,13,30]. In addition to *S. lycopersicum*, the *S. pennellii* genome was also sequenced, which provided a valuable resource for the understanding of several prominent features, such as changes in response to water deficit, biotic and abiotic resistance, and metabolism[20,28]. However, various parts of these genomes need to be thoroughly studied and annotated since the sequencing of the genome and the deposit of the sequences in public databases are only the initial steps for a thorough understanding.

Although much is known about tomato biology, relatively little is known about the regulation of gene expression involved in plant development. Recent studies have shown the importance of gene regulation, involving several classes of small RNAs, their processing system and cellular performance in different organisms[31–36]. The main representatives of this class of small RNAs are the microRNAs (miRNAs), whose way of regulation may involve inhibition of the translation process, degradation of mRNA or gene silencing, either by target complementarity or by signaling DNA modifications in specific regions of genome[37–42]. miRNAs are endogenous small RNAs with approximately 21 nucleotides in length in mature form[37,43,44].

Different proteins act to generate a specific mature miRNA for post-transcriptional regulation[32,45,46]. In plants, miRNA processing first occurs in nucleus from the transcription resulting in a long primary miRNA (pri-miRNA) which after cleaved generate the miRNA precursor (pre-miRNA)[43,47–54]. The pre-miRNA has a characteristic secondary structure, forming a hairpin from an imperfect complementarity, containing from 200-300 nucleotides in length[55,56]. The pre-miRNA is also cleaved at the end of the hairpin, forming a duplex of mature miRNAs (miRNA/miRNA double strand). The mature miRNA is exported to the

cytoplasm and then loaded in a RISC complex, to specific recognition of the target mRNA to regulate gene expression either by translation inhibition or mRNA degradation[32,48,55,57–59].

Important biological functions are mediated by miRNAs, which include the adaptation of plants to stress, regulation of leaf and floral development, defense, cell proliferation, apoptosis and signal transduction[32,43,47,60–62]. Due to important and complex regulation mediated by the miRNAs, the expression detection and quantification of these molecules in specific tissues is essential for a better understanding of their action. Although miRNAs have a high degree of transcription, their expression levels fluctuate widely between cells and in among tissues. A sensitive and rapid method for the detection and quantification of miRNAs expression is the quantitative real-time PCR (qRT-PCR)[63–65]. In addition, several computational strategies have been used to identify miRNAs and proteins of their pathway in various organisms[66–68]. Computational methods are widely used in the identification of genes since some transcripts are expressed only under certain conditions or in specific cells. Thus, computational techniques aid in the discovery process of new miRNAs, using all the information contained in the genome and/or the transcriptome independently of the sampling. Furthermore, such methods are useful for prediction of miRNA precursors and their targets.

Previous studies have identified miRNAs and proteins involved in miRNA biogenesis in *S. lycopersicum*[69–7273–87]. Many of these studies have shown important roles of tomato miRNAs such as those seen in fruit ripening[78], response to long-term RPM-treatment[88], response to curl *New Delhi virus* (ToLCNDV)[76], responses associated to *Botrytis cinerea* infection[83], male-sterility[85], salt-induced stress response[79], biotic[80], drought[84], and high-temperature stress response[87]. However, many of these genes, miRNAs and their respective targets have not yet been identified and characterized systematically in tomato species, especially in *S. pennellii*. Thus, the study of miRNAs in the plant genome and transcriptome has become a very powerful tool to assist in elucidation of biological processes as well as their performances at the cellular level[67,89–91].

The aims of this study were to identify and characterize by in silico analysis the genes involved in miRNA processing, the miRNA precursors, the miRNA targets as well as to validate such miRNAs in different tissues of *S. lycopersicum*

and *S. pennellii*, using genomic and transcriptomic sequences obtained from public databases and RT-PCR. This study allows for a better understanding of miRNAs, their processing pathways and their role in regulating the gene expression of these important species, as well as providing targets for future investigations.

3.2 RESULTS

3.2.1 The small RNAs processing pathway in *S. lycopersicum* and *S. pennellii*: analysis of conserved protein domains, active sites and phylogenetic trees

To understand the potential roles of small RNAs in the regulation of gene expression in the tomato, we sought to initially identify all possible components of small RNAs of the processing machinery in *S. lycopersicum* and *S. pennellii* genomes. Using local alignment, as well as the presence and arrangement of conserved domains, 70 putative proteins were identified in *S. lycopersicum* and 108 in *S. pennellii* involved in the biogenesis of small RNAs (siRNAs, tasiRNAs and miRNAs) (data not shown). Among these proteins, AGO and DCL family, are considered key proteins in processing machinery of small RNAs in plants[47,92]. We identified 15 and 16 proteins which belong to the ARGONAUTE family in *S. lycopersicum* and *S. pennellii* respectively (SlyAGO1.1, SlyAGO1.2, SlyAGO2.1, SlyAGO2.2, SlyAGO2.3, SlyAGO4.1, SlyAGO4.2, SlyAGO4.3, SlyAGO4.4, SlyAGO4.5, SlyAGO5, SlyAGO6, SlyAGO7, SlyAGO10.1, SlyAGO10.2, SpeAGO1.1, SpeAGO1.2, SpeAGO2.1, SpeAGO2.2, SpeAGO2.3, SpeAGO4.1, SpeAGO4.2, SpeAGO4.3, SpeAGO4.4, SpeAGO4.5, SpeAGO4.6, SpeAGO4.7, SpeAGO5, SpeAGO6, SpeAGO7, SpeAGO10). 8 and 11 DICER family proteins were found in *S. lycopersicum* and *S. pennellii* respectively (SlyDCL1, SlyDCL2.1, SlyDCL2.2, SlyDCL2.3, SlyDCL2.4, SlyDCL3.1, SlyDCL3.2, SlyDCL4, SpeDCL1, SpeDCL2.1, SpeDCL2.2, SpeDCL2.3, SpeDCL2.4, SpeDCL2.5, SpeDCL2.6, SpeDCL3, SpeDCL4.1, SpeDCL4.2, SpeDCL4.3).

Among the proteins involved in small RNAs processing, 28 (*S. lycopersicum*) and 32 (*S. pennellii*) putative proteins were identified by

participating in the miRNAs pathway (Supplementary Table S1 and Supplementary Table S2).

3.2.2 ARGONAUTE and DICER proteins in *S. lycopersicum* and *S. pennellii*

3.2.2.1 Analysis of conserved domains, active sites, phylogeny and pathway proteins and pre-miRNA alignment in *S. lycopersicum* and *S. pennellii*

We found 15 AGO proteins in the genome of *S. lycopersicum* and 16 in *S. pennellii*. The SlyAGO1.1/1.2 and SpeAGO1.1/1.2 proteins displayed the Gly-rich_Ago1, ArgoN, ArgoL1, PAZ, ArgoL2, ArgoMid and Piwi domains. Similar results were observed for SlyAGO10.1/10.2 and SpeAGO10 which displayed the domains ArgoN, ArgoL1, PAZ, ArgoL2, ArgoMid and Piwi (Supplementary Figure S1 and Supplementary Table S3).

The Piwi conserved domains, one of the main domains present in AGO proteins, was identified in the SlyAGO1.1, SlyAGO1.2, SpeAGO1.1, SpeAGO1.2, SlyAGO10.1, SlyAGO10.2 and SpeAGO10 proteins. These domains showed active sites regions containing an important catalytic triad DDH (aspartate/aspartate/histidine). The DDH catalytic triad of these proteins was found in Asp764-Asp850-His990, Asp690-Asp776-His916, Asp763-Asp849-His989, Asp862-Asp948-His1088, Asp704-Asp790-His930, Asp658-Asp744-His884, Asp704-Asp790-His930 positions, respectively (Figure 1a).

In *S. lycopersicum* and *S. pennellii,* we identified 8 and 11 putative proteins, respectively, belonging to the DCL protein family. We found DCL1 (DCL proteins are involved in the miRNAs processing) in *S. lycopersicum* and *S. pennellii*. Both proteins displayed the conserved domains ResIII (also known as DEAD-like), Helicase C, Dicer Dimer (also known as DUF283), PAZ, Ribonuclease IIIa (RNase IIIa), Ribonuclease IIIb (RNase IIIb), dsrm and DND1 DSRM (Supplementary Figure S1 and Supplementary Table S4).

We found two RNAse III domains in SlyDCL1 and SpeDCL1 proteins. The two domains (RNase IIIa and RNase IIIb) had the same catalytic residues in the two tomato species studied: glutamate (E), aspartate (D), aspartate (D), glutamate (E), representing the EDDE active site. These residues were located in RNase IIIa

domains at Glu1591-Asp1595-Asp1687-Glu1690 and Glu1617-Asp1621-Asp1713-Glu1716 positions and the RNase IIIb domains at Glu1390-Asp1394-Asp1465-Glu1468 and Glu1390-Asp1394-Asp1521-Glu1524 positions of the SlyDCL1 and SpeDCL1 proteins, respectively (Figure 1b).

To understand the diversification of AGO proteins in *S. lycopersicum* and *S. pennellii*, a phylogenetic analysis was performed using their amino acid sequences (Figure 2). The phylogeny of the Sly/SpeAGO1 and Sly/SpeAGO10 proteins showed that they were distributed in the phylogenetic tree closest to their respective orthologous proteins from the plant species *S. tuberosum* and *Nicotiniana sylvestris.* The phylogenetic tree was divided into seven distinct clades of paralogous (AGO1, AGO2, AGO4, AGO5, AGO6, AGO7 and AGO10). In addition, to determine the evolutionary relationship among the putative DCL proteins of *S. lycopersicum*, *S. pennellii* and their orthologous species, a phylogenetic analysis was also conducted (Figure 3). The proteins were grouped through global alignment in four distinct clades (DCL1, DCL2, DCL3 and DCL4).

3.2.3 Mature miRNAs and their precursors in *S. lycopersicum* and *S. pennellii*

To show that the miRNA processing machinery is well conserved in *S. lycopersicum* and *S. pennellii*, we sought to identify both mature and precursor sequences of miRNAs, in addition to predicting and defining the nature of their putative target genes using available public databases (Phytozome v12.1 and PlaBi). By applying an optimized and specific algorithm (see material and methods), we identified 343 sequences of mature miRNAs with 285 different sequences and 226 precursor miRNAs, distributed in 87 distinct miRNA families in *S. lycopersicum* genome (Supplementary Table S5). In *S. pennellii*, 388 sequences of mature miRNAs with 307 different sequences and 234 precursor miRNAs contained in 85 different miRNA families were identified (Supplementary Table S6).

Regarding the miRNA precursor genes localization and distribution in *S. lycopersicum* and *S. pennellii* genomes, 196 (86.73%) and 195 (81.59%) were found in intergenic regions and 30 (13.27%) and 44 (18.41%) within genes,

respectively, whereas in *S. pennellii*, 3 pre-miRNAs genes are located in more than one position in the genome (Supplementary Table S7). The spe-miR169-1 is located in the chromossomes 0 and 7, the spe-miR1919 is in two different positions in the chromossome 8 and the spe-miR5368 is in the chromossomes 6, 7 and in two different positions in the chromossome 9. In addition, it was possible identify that 72 miRNAs in *S. lycopersicum* and 73 in *S. pennellii* were organized in clusters (10kb as the maximum distance between two miRNAs genes to consider them clustered, see Material and Methods). Of these miRNAs in clusters, we identified 50 miRNAs in *S. lycopersicum* and 47 in *S. pennellii* that were organized in clusters, but are located in antiparallel strand (Supplementary Table S7).

All identified miRNAs were analyzed for their structural and thermodynamic characteristics. *S. lycopersicum* miRNA precursors displayed an MFE with a mean of -56.50 kcal/mol, having values between -98.2 and -21.8 kcal/mol. Other parameters as AMFE and MFEI, obtained an average of -39.38 kcal/mol and of 1.03, respectively (Supplementary Table S8). In *S. pennellii*, the pre-miRNAs showed an MFE with a mean of -55.60 kcal/mol, with values between -93.7 and -23.3 kcal/mol, the mean AMFE was -39.13 Kcal/mol and that of MFEI was 1.02 (Supplementary Table S9).

In addition, we performed statistical analyzes using thermodynamic and structural characteristics of the pre-miRNAs found in both tomato species compared to pre-miRNAs deposited in miRBase from *Solanaceae*, *Fabaceae* and *Brassicaceae* families. We compared the miRNA precursor characteristics from two tomato species (Supplementary Table S10) and *Solanaceae* family miRNA precursors (Supplementary Table S11) and no differences were observed among the characteristics analyzed ($p>0.05$). In the analysis performed among *S. lycopersicum* and *S. pennellii* against *Fabaceae* and *Brassicaceae* families, the pre-miRNA characteristics were significantly different ($p<0.05$).

3.2.3.1 Characterization of tomato miRNAs

Among the 172 miRNAs families identified in the two species of study, 71 were found in both tomato species. Of all 101 different miRNAs families indentified of *S. lycopersicum* and *S. pennellii*, we highlighted 10 families for more in-depth

characterization since MIR165/166, MIR167, MIR393, MIR530, MIR827 and MIR828 families are miRNAs conserved in plants and the MIR7983, MIR7990, MIR8011 and MIR8025 families were identified for the first time in *S. lycopersicum* and *S. pennellii*. For each of these families, we analyzed the conservation of sequences and phylogenetic distributions, as well as their putative target mRNAs.

We identified 8 precursors miRNAs in MIR165/166 family, 6 in MIR167 and MIR7983, 3 in MIR7990, 2 in MIR8011 and 1 in MIR393, MIR530, MIR827, MIR828 and MIR8025 families of *S. lycopersicum* (Supplementary Table S5). In turn, in *S. pennellii* were identified 7 pre-miRNAs in MIR7983 family, 6 in MIR165/166, 5 in MIR167, 3 in MIR8011, 2 in MIR7990 and 1 precursor sequence in MIR8025, MIR393, MIR530, MIR827 and MIR828 (Supplementary Table S6). We also identified mature miRNAs in these families, including 12 in MIR7983, 10 in MIR167 and MIR165/166, 3 mature sequences in MIR7990 and MIR8011, 2 in MIR393 and MIR827, in addition to 1 in each family MIR530, MIR828 and MIR8025 of *S. lycopersicum.* In *S. pennellii*, 14 mature miRNAs were found in MIR7983, 9 in MIR167, 10 in MIR165/166, 5 in MIR8011, 2 in MIR393, MIR828, MIR827, MIR7990, MIR8025 and 1 sequence in MIR530.

The precursor and mature miRNAs identified in our work presented great conservation in their sequences and secondary structures in relation to their orthologs, especially in the miRNAs mature region. As it was the case for the Sly/SpeMIR167 (Figure 4), Sly/SpeMIR165/166 (Figure 5 and Supplementary Figure S2), Sly/SpeMIR393 (Supplementary Figure S3), Sly/SpeMIR530 (Supplementary Figure S4), Sly/SpeMIR827 (Supplementary Figure S5), Sly/SpeMIR828 (Supplementary Figure S6), Sly/SpeMIR7983 (Supplementary Figure S7), Sly/SpeMIR7990 (Supplementary Figure S8), Sly/SpeMIR8011 (Supplementary Figure S9) and Sly/SpeMIR8025 families (Supplementary Figure S10).

The analysis of the MIR167 family showed a phylogenetic tree distributed in five distinct clades. The miRNAs from *S. lycopersicum* and *S. pennellii* were grouped together with miRNAs from *Solanaceae* species (Supplementary Figure S11). The phylogenetic tree of MIR165/166 family displayed two distinct clades of *Eudicot* and *Monocotyledon*. The miRNA sequences from both tomato species were distributed within *Solanaceae* in *Eudicot* clade (Figure 6). In the phylogenetic

trees of Sly/SpeMIR393 (Supplementary Figure S12), Sly/SpeMIR530 (Supplementary Figure S13) and Sly/SpeMIR827 (Supplementary Figure S14) were also distribued in two clades of *Eudicots* and *Monocotyledons* and the were observed miRNAs from tomato species within *Solanaceae* clade. The phylogenetic tree of Sly/SpeMIR828 family showed ten clades of different families of *Eudicots* (Supplementary Figure S15).

3.2.3.2 miRNAs target genes of *S. lycopersicum* and *S. pennellii*

To understand the putative roles of miRNAs in tomato, we identified their target genes. We identified 2471 different miRNA target genes from a total of 4197 in *S. lycopersicum* for 343 mature miRNAs (Supplementary Table S12) and 3462 different targets from a total of 5768 in *S. pennellii* for 388 mature miRNAs (Supplementary Table S13).

Notably, the Sly/SpeMIR167 family miRNAs showed 247 different target transcripts, being 37 of SlyMIR167 and 210 of SpeMIR167 family. Among these targets are: putative zinc finger in N-recognin (UBR box), retrotransposon gag proteins, magnesium transporter NIPA, annexin p34, BZIP transcription factor, cytochrome P450, RING/U-box superfamily protein, kinetochore protein and a proteins class related to disease resistance (CC-NBS-LRR). In addition, were identified 74 distinct targets in Sly/SpeMIR165/166 family, with 35 of SlyMIR165/166 and 39 of SpeMIR165/166 family. Targets comprise the homeobox-leucine zipper family, especially those with the MEKHLA domain, acyl-CoA N-acyltransferases (NAT) superfamily protein and retrotransposon gag protein. Interestingly, the Sly/SpeMIR393 family miRNA targets included 23 distinct transcripts, being 12 of SlyMIR393 and 11 of SpeMIR393 family. This target genes encode carbohydrate-binding protein of the ER, lipoxygenases and proteins containing the U-box and F-box domains, as transport inhibitor response 1 (TIR1) and a auxin receptor involved in a hormone-depleting mechanism. The Sly/SpeMIR530 family displayed 31 distinct targets, with 14 of SlyMIR530 and 17 of SpeMIR530 family. Among the targets are the DEAD/DEAH box helicase, ICP0-binding domain of Ubiquitin-specific protease 7, ethylene-responsive transcription factor, adenylate isopentenyltransferase, proteins containing the AP2 domain,

NAC domain protein, MULE transposase domain and tyrosine kinase type proteins. Sly/SpeMIR827 family miRNAs obtained 50 different mRNAs targets, being 29 of SlyMIR827 and 21 of SpeMIR827 family. These comprise reverse transcriptase (RNA-dependent DNA polymerase), cytochrome P450, OTU-like cysteine protease, no apical meristem (NAM) protein, cell-wall invertase, glyoxylate reductase and SPX domain-containing family protein.

The search for Sly/SpeMIR828 target, revealed 31 different genes, with 16 target gene of SlyMIR828 and 15 of SpeMIR828 family. Among them are MYB-type DNA binding domain, syntaxin of plants 51, F9H3-4 protein, TCP transcription factor 1 and reverse transcriptase (RNA-dependent DNA polymerase). The tomato Sly/SpeMIR7983 family showed 89 target genes, being 75 of SlyMIR7983 and 14 of SpeMIR7983 family. The targets contain transcripts encoding 2C phosphatases, serine carboxypeptidase, ribonuclease T2 family, glutathione S-transferase-like protein, ENTH/ANTH/VHS superfamily protein, alpha/beta-Hydrolases superfamily protein, UDP-glucuronate 4-epimerase 4 and Myb family transcription factor family protein. In addition, Sly/SpeMIR7990 miRNAs showed 15 target transcripts different, with 13 of SlyMIR7990 and 2 of SpeMIR7990 family, as GDSL esterase/lipase proteins, MADS-box transcription factor family protein, disease resistance protein (TIR-NBS-LRR class), WRKY DNA-binding protein 31, Nop53 protein, bHLH transcription factor GBOF-1 and permease family. Interestingly, we identifed 55 distinct target genes from miRNAs belonging to the Sly/SpeMIR8011 family, being 27 of SlyMIR8011 and 28 of SpeMIR8011 family. Among them, alpha/beta hydrolases family proteins, hAT family C-terminal dimerisation region, reverse transcriptase (RNA-dependent DNA polymerase), PHD-finger transcription factor, potassium transporter, ripening regulated protein and ARM repeat superfamily protein. Finally, the Sly/SpeMIR8025 family obtained the 11 miRNAs targets, with 5 of SlyMIR8025 and 6 of SpeMIR8025 family, which encode auxin response factor 9A (ARF9A), kinase proteins domain, FKBP-type peptidyl-prolyl cis-trans isomerase, NAD(P)-binding Rossmann-fold superfamily protein and telomerase activating protein Est1 (Supplementary Table S12 and Supplementary Table S13).

3.2.3.3 Expression of tomato miRNAs in *S. lycopersicum* and *S. pennellii*

We experimentally verified the expression of six miRNAs genes (miR165/166, miR167, miR530, miR827, miR828 and miR7983) in two different tissues: leaves and flowers of each tomato species. In leaves, the miR165/166 was 7.3 times more expressed in *S. lycopersicum* compared to *S. pennellii*. The miR167, miR530 and miR827 was, respectively, 26.7, 2.2 and 2.4 times more expressed in leaves *S. pennellii* compared to *S. lycopersicum* (Figure 7a). In tomato flowers, the miR167 showed an expression of 10.0 times also higher in *S. pennellii* compared to *S. lycopersicum* and the miR165/166, miR530 and miR7983 did not show a significant difference in the expression rate between the two tomato species (Figure 7b). In addition, the miR165/166 was 7.4 times more expressed in the leaves compared to the flowers and miR167, miR530 and miR7983 showed no difference in the two *S. lycopersicum* tissues (Figure 7c). Finally, the miR167 and miR530 was, respectively, 16.0 and 2.1 times more expressed in leaves than in *S. pennellii* flowers, but miR165/166 and miR7983 showed no difference in the two *S. pennellii* tissues (Figure 7d).

3.2.4 Transcriptomic changes in tomato leaves and flowers RNAseq-based

To confirm the expression of the RNA-silencing pathway components, we searched the RNAseq data of *S. lycopersicum* and *S. pennellii* publicly available in the Sequence Read Archive (SRA)[93]. The heatmap showed expression of all genes identified in the two species in the two analyzed tissues, except the *SpeEXO.2* gene that did not present expression in leaves (Figure 8, Supplementary Figure S16, Supplementary Figure S17 and Supplementary Table S14). In *S. lycopersicum* 10 (*ABH1, AGO1.1, AGO1.2, AGO10.1, AGO10.2, EXO.1, EXO.2, EXO.3, SQN.1* and *SQN.2*) of the 28 genes from the miRNA processing machinery were found to be differentially expressed (DE) between flowers and leaves. Among 10 genes DE, 8 up-regulated in flowers and 2 up-regulated in leaves, being these *SlyEXO.1* and *SlyEXO.3*. Considering the relative expression between *S. lycopersicum* flowers and leaves, *SlyAGO10.2* and *SlySQN.2* showed higher DE in flowers. When expressed in absolute expression

values (count per million - CPM), *SlyAGO1.2* was the most expressed gene both in the flower and leaf (Figure 8a, Supplementary Figure S16 and Supplementary Table S14). Similar results were found in *S. pennellii*, wherein 11 (*AGO1.1, AGO1.2, AGO10, DDL, EXO.1, EXO.5, EXO.6, EXO.8, HESO1.2, SE* and *SQN.2*) of the 30 genes identified from the same pathway were found to be DE between flowers and leaves. In this case, all the 11 genes were up-regulated in flowers, being *SpeSQN.2* and *SpeAGO10* the genes more DE in flowers compared with leaves. As regards, the absolute expression values, *SpeAGO1.2* and *SpeAGO1.1* were the genes most expressed in flowers and leaves, respectively (Figure 8b, Supplementary Figure S17 and Supplementary Table S14).

3.2.5 Validation of the tomato miRNAs in *S. lycopersicum* small RNAs libraries

To validate the miRNAs identified in this study, we retrieved 95 small RNAs libraries of *S. lycopersicum* available in the SRA and verified the presence of the mature miRNAs in each library (Supplementary Table S15, Supplementary Table S16, Supplementary Table S17 and Supplementary Table S18). A robust analysis of the presence of 285 different sequences of mature miRNAs found in *S. lycopersicum* was performed in the 95 different small RNAs libraries, in order to validate the miRNAs identified in this study. Among the 285 different mature miRNA sequences, 262 were found in at least one library analyzed and 23 mature miRNAs were not found in the searched libraries. Members of the MIR165/166, MIR167, MIR393, MIR530, MIR827, MIR828, MIR7983, MIR7990, MIR8011 and MIR8025 families were found in 69.5%, 64.2%, 43.2%, 95.8%, 27.4%, 14.7%, 62.1%, 31.6%, 54.7% and 1% of the libraries analyzed, respectively. Only one mature miRNA of the MIR7983 and MIR8025 families was not found in any studied library.

3.3 DISCUSSION

We identified 28 (*S. lycopersicum*) and 32 (*S. pennellii*) putative proteins involved in miRNAs pathway (Supplementary Table S1 and Supplementary Table

S2), which is in agreement with the description of miRNA biogenesis pathway in other plant species, such as in *A. thaliana*, *P. vulgaris* and *O. sativa*[43,92,94,95]. The presence of these proteins in different studies has shown a high conservation of the components of miRNA processing pathways in plants, performing essential functions for the post-transcriptional regulation of mRNAs in different cells[43,92]. All the proteins involved in miRNAs biogenesis were found in the two tomato species, except for the STABILIZED1 (STA1) protein that was found only in *S. pennellii*. Considering that STA1 part of a large miRNA processing/splicing complex that orchestrates pri-miRNA splicing and processing[96], this function may have been lost in the cultivated tomato as product of domestication since it is still present in the wild tomato (S*. pennellii*).

In fact, the analysis revealed that the components of this pathway were highly conserved at the amino acid level in the two species, as well as the distribution of domains, active sites location and phylogenetic distribution when compared to orthologous proteins in other plant species. This pattern was observed in both protein families, ARGONAUTE and DICER, both proteins considered to be critical in processing machinery of miRNAs in plants[47,92].

Among all proteins found, 15 and 16 proteins belong to the AGO family of *S. lycopersicum* and *S. pennellii*, respectively, compared to 19 identified in *O. sativa*[48], 17 in *P. vulgaris*[95]. In *A. thaliana* 10 AGO proteins have been found found[92,94]. Mirzaei et al. (2014) and Bai et al. (2012) found also 15 AGO proteins in *S. lycopersicum*, being all identified in this study[69,70]. However, in study of Bai et al. (2012) two classifications were different. Solyc02g069280 and Solyc03g111760 were considered by the authors to be SlyAGO3 and SlyAGO15, but in our analyzes they were classified as SLyAGO2 and SlyAGO4, respectively. Of all the AGO proteins identified in plants, only AGO1 and AGO10 showed activity in the biogenesis of miRNAs[92,94].

The conserved domains found in SlyAGO1.1/1.2, SpeAGO1.1/1.2, SlyAGO10.1/10.2 and SpeAGO10 (Supplementary Figure S1 and Supplementary Table S3) displayed the same domains and similar distribution of the domains compared to proteins from orthologous plant species[97–100]. The Piwi conserved domains of the AGO proteins showed an active site containing a DDH catalytic triad (Figure 1a), present in AGO proteins family and proteins with RNase H

function[48,94]. These results corroborated with AGO1 and AGO10 proteins found in *A. thaliana* and *P. vulgaris*[48,94,95]. The conserved domains and active sites found in Sly/SpeAGO1 and Sly/SpeAGO10 showed high conservation when compared to AGO1 and AGO10 proteins in *A. thaliana*, *O. sativa*, *S. tuberosum*, *G. Max* and *P. vulgaris*[48,95,99,101]. This high domain conservation may be directly related to the role played by AGO1 and AGO10 proteins in the miRNA processing pathway in different species.

Other important catalytic components of the miRNAs processing in plants are the DCL proteins[95,102–108]. In this study, we identified 8 and 11 putative DCL proteins of *S. lycopersicum* and *S. pennellii*, respectively. The number of DCL proteins found in tomato genome is in agreement with other plant species: 4 DCLs have been found in the *A. thaliana* genome[92,106], 6 in *P. vulgaris*[95] and in *O. sativa* were identified at least 5 DCL proteins[48,106,109]. Bai et al. (2012) and Wang et al. (2016) found only 7 DCL proteins in *S. lycopersicum*[69,71].

The DCL1 protein is the protein of the DCL family involved in the processing of miRNAs[58,110,111]. The conserved domains found in Sly/SpeDCL1 (Supplementary Figure S1 and Supplementary Table S4) was very similar to their orthologous proteins from plant species[95,106,109], suggesting a conserved function of DCL1 proteins in tomato species. According to recent studies, especially in DCL proteins, the distance between the RNase III and PAZ conserved domains is suggested to be the largest determinant of the resulting length of processed miRNAs[51,106,112]. This demonstrates the importance of the domain distribution and conservation in the performance of these proteins at the cellular level. The two RNAse III domains (RNase IIIa and RNase IIIb) found in Sly/SpeDCL1 proteins displayed an active site with the EDDE catalytic residues (Figure 1b), also identified in DCL1 proteins from other plant species[113]. These RNase III domains are required for the cleavage and processing function of dsRNAs (double-stranded RNA) in the miRNA pathway in plants[106,109].

A phylogenetic analysis of the Sly/SpeAGO (Figure 2) and Sly/SpeDCL (Figure 3) proteins was performed from their amino acid sequences, aiming at understand the evolutionary diversification of AGO and DCL proteins in the two tomato species. The distribution of the seven clades showed a relationship between some paralogous proteins specific of the AGO family, with a great

similarity among the AGO1, AGO5 and AGO10 proteins; AGO2 and AGO7; AGO6 and AGO4 corroborating the phylogenetic distribution in *A. thaliana* and *P. vulgaris*[92,95,114]. In general, the AGO proteins phylogeny distribution identified corroborates with current species protein phylogenies[115], which suggests that the conservation level of the member of the AGO family in *Angiosperms* is high. The phylogenetic tree of the AGO proteins showed a strong correlation between AGO1 and AGO10 proteins, being these two AGO proteins which participate in miRNAs pathway in plants[92,94]. AGO proteins have a key role in transcriptional and post-transcriptional silencing mediated by small RNAs in plants. The role of these proteins in miRNA regulation has been associated with the RISC complex (RNA-induced silencing complex), allowing degradation or inhibition of mRNA translation from the complementarity of bases between the miRNAs specific sequences and the target mRNA[92,94,116].

The analysis of Sly/SpeDCL proteins showed a great similarity to evolutionary tree of life of these species within each clade[115]. The distribution among the DCL family paralogs showed a strong correlation between the DCL2 and DCL4 proteins, being also close to DCL1 and further away from DCL3, corroborating with the distribution of DCL families in other plant species[48,106]. Thus, it was observed that DCL proteins of *S. lycopersicum* and *S. pennellii* are highly conserved in the same way as observed for the AGO proteins, highlighting their great importance in post-transcriptional silencing processes in plants.

The validation of the miRNAs pathway genes in libraries available in the SRA[93] showed the DE of 10 and 11 of the 28 and 30 genes identified in *S. lycopersicum* and *S. pennellii*, respectively (Figure 8, Supplementary Figure S16, Supplementary Figure S17 and Supplementary Table S14). Among the DE genes in the two species are the genes of *ABH1, AGO1, AGO10, DDL, EXO, HESO1, SE* and *SQN* family. In *S. lycopersicum*, of the 10 DE genes, 8 were up-regulated in flowers and 2 up-regulated in leaves, already in *S. pennellii* all 11 DE genes were up-regulated in flowers. This result shows a greater requirement of these genes in flowers, suggesting a great role of the miRNA in this tissue, and considering that several miRNAs targets are related to different roles in flowers[117–119]. Yamaguchi and Abe (2012) and Wang (2014) showed the important function of miR172, miR156 and miR159 in flowering time control in *A. thaliana*[118,119]. In

addition, Aukerman and Sakai (2003) demonstrated that miR172 causes early flowering and disrupts the specification of floral organism when overexpressed in *A. thaliana*[117].

In leaves, only the *SlyEXO.1* and *SlyEXO.3* genes were up-regulated whereas the *SpeEXO.2* gene presented not expression. This is because these genes were also involved in other pathways or have other functions, such as delivery of mRNAs, miRNAs and cell-specific proteins, considering that this family had greatest number of paralogous sequences[120,121]. In both species, *AGO10* and *SQN.2* were the most up-regulated genes in flowers, suggesting that the mechanism of use of these genes in flower is conserved in these two species. Ji et al. (2011) showed overlapping roles for *AGO10* and *AGO1* in the temporal regulation of floral stem cells[122]. Furthermore, Liu et al. (2014) reported that the role of miR168a in sweet orange is the accumulation of *AGO1* in leaf and fruit biology[123]. This may justify up-regulation of *AGO10* and *SNQ.2* in the leaves, considering that *AGO10* have important roles in this tissue and SQN has a direct relation with *AGO1* whereas *AGO1* has also important roles in flowers and is down-regulated by miR168 in leaves[122,123]. Considering the absolute expression values (CPM), *Sly/SpeAGO1.2* and *SpeAGO1.1* were the most expressed genes in both tissues, showing the great importance of this protein family in plant development and, consequently, in the post-transcriptional silencing machinery using miRNAs[124].

As for miRNAs sequences, we identified 343 and 388 mature miRNAs, 226 and 234 precursor miRNAs, distributed in 87 and 85 distinct miRNA families, besides 4197 and 5768 target genes in the *S. lycopersicum* genomes (Supplementary Table S5) and *S. pennellii* (Supplementary Table S6), respectively. In addition to predicting previously reported miRNAs, our study identified many additional novel miRNAs in the genomic sequences of *S. lycopersicum*, being that of the all miRNAs found, only 110 mature and 77 precursors were deposited in the miRBase (version 21)[125] (Supplementary Table S5). Thus, we identified 233 new mature miRNAs, 149 new precursors contained in 41 miRNAs families in comparison with miRNAs deposited in miRBase.

Some studies searched also miRNAs in *S. lycopersicum,* such as Moxon et al. (2008) that found only 30 miRNAs family, Yin et al. (2008), Kim et al. (2011),

Din and Barozai (2014), Luan, Wang and Liu (2014) and Fan et al. (2015) detected 21, 12, 109, 14 and 218 miRNAs, respectively[73–75,81,126]. In addition, other works found only six miRNAs responsive to long-term RPM-treatment[88], 69 miRNAs families link with phosphate and mycorrhizal signaling[82], 112 mature miRNAs responsive with curl *New Delhi virus* (ToLCNDV)[76], 143 miRNAs associated with *Botrytis cinerea* infection[83], 95 miRNAs salt-induced stress responsive[79] and only 69 putative miRNAs associated to biotic stress[80]. Further, our study identified 126 new mature miRNAs, 94 new precursors contained 29 miRNAs families of the *S. lycopersicum* in comparison with studies published to date[7,74–76,78,81,88,126–134]. Moreover, we identified for the first time in the literature mature miRNAs and their precursors in *S. pennellii* (Supplementary Table S6).

The miRNA precursor genes localization and distribution in *S. lycopersicum* and *S. pennellii* genomes showed that 86.73% and 81.59% of the genes were found in intergenic regions, respectively, and that, in *S. pennellii*, 3 them (spe-miR169-1, spe-miR1919 and spe-miR5368) are located in more than one position in the genome (Supplementary Table S7). This high percentage of intergenic miRNAs was also found in other plants as *A. thaliana, P. trichocarpa, O. sativa, P. vulgaris, Sorghum bicolor* and *Catharanthus roseus*[37,95,97,135–138]. Some of the miRNAs genes identified were organized in clusters (72 in *S. lycopersicum* and 73 in *S. pennellii*). The presence of miRNAs genes distributed in clusters in other plants has been reported before, e.g. 54 miRNAs in clusters were found in *A. thaliana*, 40 in *P. trichocarpa*, 103 in *O. sativa*, 32 in *S. bicolor*[138] and 25 in *P. vulgaris*[95]. Furthermore, 50 miRNAs genes in *S. lycopersicum* and 47 in *S. pennellii* also were organized in clusters but in antiparallel strand, agreeing with other plant genomes deposited in miRBase (version 21), such as the miR399a and miR399e from *O. sativa*, miR169e and miR169d from *A. thaliana* and miR167e and miR167i from *G. max*[125].

The structural and thermodynamic characteristics miRNAs of the *S. lycopersicum* and *S. pennellii* were similar to those reported in other plant studies[139–142]. In plants, the values for MFE in precursor miRNAs are typically smaller than -18kcal/mol[142]. Furthermore, studies have shown that the sequences of RNAs with mean AMFE -45.93 ± 9.43 kcal/mol are considered real miRNAs, knowing that these AMFE values found in miRNA precursors had a higher

negative value than in the other classes of non-coding RNAs, for example tRNAs and rRNAs. MFEI values with a mean value of 0.97, above 0.85 were suggested for potential precursors of plants miRNAs, which distinguishes them from other RNAs, corroborating with our results[139].

The statistical analyzes using thermodynamic and structural characteristics of the tomato pre-miRNAs, comparing the two tomato species (Supplementary Table S10) and *Solanaceae* family (Supplementary Table S11) showed no differences between the groups (p>0.05). Both displayed high conservation and similarity among pre-miRNAs from *S. lycopersicum*, *S. pennellii* and also species belonging to the *Solanaceae* family. However, the results among *S. lycopersicum* and *S. pennellii* against *Fabaceae* and *Brassicaceae* families were statistically significant (p<0.05), suggesting a great evolutionary conservation of the pre-miRNA characteristics within each plant family and a significant difference among different families (Supplementary Table S11). These differences using pre-miRNA characteristic were also observed using *Monocotyledons* and *Eudicotyledons*[143].

Several studies have shown the MIR165/166 and MIR167 families are highly conserved in different plant species, such as *A. thaliana, O. sativa, G. max*, *P. vulgaris* and *S. tuberosum*[95,140,144–148]. Members of the MIR393 family were also found in *Ferns, Gymnosperms, Angiosperms, Monocotyledons* and *Eudicots*, as *A. thaliana* and *P. vulgaris*[47,56,95,110,140,149–152]. The MIR530 family was also identified in orthologous plants, such as *S. tuberosum, O. sativa, C. sinensis, P. vulgaris* and *Z. mays*[95,107,140,150,153,154]. Furthermore, *P. trichocarpa, O. sativa, Z. mays, S. tuberosum, A. thaliana* and *Brassica spp* also possess miRNAs of the MIR827 family in their genomes[140,151,155–157], and studies have demonstrated the presence of miRNAs of the MIR828 family in other species as *A. thaliana*, *O. sativa, P. vulgaris, V. vinifera* and *Z. mays*[95,150,152,158–161]. On the other hand, the MIR7990 and MIR8025 families were identified in *S. tuberosum*[125,157], MIR7983 in *Solanum pimpinellifolium*[162] and the MIR8011 family has benn found in *Lycium chinense*[154] to date. In addition, the MIR7983, MIR7990, MIR8011 and MIR8025 families were identified for the first time in *S. lycopersicum* and *S. pennellii*, in this study, suggesting that these family can be restricted to *Solanaceae* (solanum-specific)[157].

The phylogenetic analysis performed of the MIR167 (Supplementary Figure S11), MIR165/166 (Figure 6), MIR393 (Supplementary Figure S12), MIR530

(Supplementary Figure S13), MIR827 (Supplementary Figure S14) and MIR828 miRNAs families (Supplementary Figure S15) of *S. lycopersicum* and *S. pennellii* highlighted an evolutionary distribution that highly corroborates with the accepted tree of life for plant species[163].

Several tomato miRNAs showed functions modulating important biological processes through gene expression control (Supplementary Table S12 and Supplementary Table S13). Many reports in plants demonstrate similar targets of Sly/SpemiR167, such as the proteins involved in disease resistance (CC-NBS-LRR) in *O. sativa* and the peptidase family proteins in *A. thaliana*[164]. Besides presenting other important targets of MIR167 family, as in the regulation of auxin response factors (ARF4, ARF6 and ARF8)[165–170]. The targets Sly/SpeMIR165/166 family are involved mainly with plants vascular development[171], including formation of axillary meristems, root lateral meristems, laminar outgrowth and differentiation in leaves, stems, and roots[145,172–176]. Several studies have also identified targets of miR165/166 in *A. thaliana* and *O. sativa*, agreeing with our results, also showing a great conservation of function in this family in plant miRNAs, as in retrotransposon, homeobox-leucine zipper family and kinase family proteins[100,146,164,172–174,177].

Interestingly, the Sly/SpeMIR393 family act on important proteins that regulate hormone-sensitive signaling in plant development[178–182]. The targets found for Sly/SpeMIR393, mainly the TIR1 proteins, are in line with with studies in *A. thaliana, O. sativa, Z. mays, P. vulgaris, Hordeum vulgare, Gossypium hirsutum* and *M. truncatula*[56,95,140,151,164,178–180,183–186]. In barley the miR393 acts as an integrator of environmental cues in auxin signaling, being able to act in approaches related to the aluminum toxicity[186]. In additional, the miR393 exhibited important roles in nitrate response, defense against pathogenic bacteria and plant development[181]. The Sly/SpeMIR530 family displayed targets also found in *N. tabacum*[187] and *O. sativa*[164], as plus-3 domain containing proteins. Additionally, this miRNA family was involved in the nitrogen regulation and high salinity[188,189], being pivotal in the plant physiological response to stress[190].

Other studies also present similar targets for Sly/SpeMIR827 family miRNAs, as SPX domain-containing family protein in *A. thaliana*[164] and *O. sativa*[191]. The targets found indicated that miR827 plays a key role in plant stress adaptation, especially in nitrogen and phosphorus deficiency[192–195]. In *A. thaliana*

the MYB-type DNA binding domain was also identified as miR828 target[164]. Sly/SpeMIR828 target genes showed a role important in cell proliferation, control of apical dominance and organ symmetry, as well as senescence, such as found in studies carried out in other plants[161,192,196,197]. Therefore, the targets found in this study showed the importance of the regulation performed by miRNAs (Supplementary Table S12 and Supplementary Table S13).

Expression analysis by real-time PCR of miR165/166, miR167, miR530, miR827, miR828 and miR7983 genes in leaves and flowers of the two species studied showed interesting differences (Figure 7). The miR165/166 expression was larger in *S. lycopersicum* leaves compared to *S. pennellii*, and in *S. lycopersicum*, the leaves expressed more miR165/166 that in flowers. The predicted targets for the tomato miR165/166 families are related to the HD-Zip proteins family, which participate in secondary development and vascular differentiation. In this sense, as there was a high expression of miR165/166 in *S. lycopersicum* leaves, our findings suggest a higher regulation of secondary and vascular development in the cultivated tomato species leaves compared to the wild species. The miR165/166 also showed a high expression in rice libraries after a short duration heat stress[198], potato[157] and in leaves, stems and roots of *Poncirus trifoliate*[199]. miRNAs from this family were also associated with a phenotype diversity involved with drought tolerance[200–202]. Furthermore, Guo et al. (2016) showed that during the establishment of Chinese kale seedlings, the miR165/166 expression was also regulated, showing its relation with leaf normal development[203].

The miR167 was more expressed in *S. pennellii* leaves and flowers compared to *S. lycopersicum,* and between *S. pennellii* tissues the leaves showed bigger expression. In rice seeds[198] and in *S. tuberosum* leaves and flowers[204], miR167 was also more abundant. Unlike *Citrus grandis*, which showed a low expression of the miR167 family members in the floral developmental stages, indicating an important role in the reproductive development[205]. In addition, miR167 was shown to be responsive to heat shock in *Arabidopsis*[206] and played an important role in nitrogen stress responses, being up-regulated in maize shoots and roots[207]. Furthermore, most of the observed miR167 targets in plants were related to the hormonal pathways regulation, as in *A. thaliana*, rice and

coffee[156,208,209]. Considering that miR167 plays these important roles, such as responses to heat shock, nitrogen stress and hormonal pathways regulation, a higher expression showed in *S. pennellii* suggests a higher resistance of wild plants to these abiotic stresses.

The bigger miR530 expression in *S. pennellii* suggest an important role in the plant physiological control, mainly related with response of plants to biotic and abiotic stresses, in which case it may need a higher expression in the wild species, according to their targets[210]. This miRNAs family was also more expressed in leaves of durum wheat[200]. Similarly to miR530, the miR827 was more expressed in *S. pennellii* leaves compared to *S. lycopersicum*. The miR827 also showed high expression in rice seeds[156]. Unlike maize, which showed a suppressed expression in nitrogen deficiency, corroborating with other studies that showed a involvement of miR827 with adaptive responses to low nitrogen and phosphorus conditions, showing important role in stress adaptation[188,189,192,193,207]. The miR828 was also expressed at higher levels in active bud in *Camellia sinensis*. In addition, the MYB-like DNA binding proteins, miR828 targets showed a role in regulating transcription and nucleotide metabolism[211] and were holistically expressed in grapevine[212]. The miR828 presence showed also a likely involvement with phenylpropanoid metabolism, biotic and abiotic stress, cell differentiation and hormone responses[213].

The validation of the mature miRNAs identified in this study, used 95 small RNAs libraries of *S. lycopersicum* available in the SRA (Supplementary Table S15, Supplementary Table S16, Supplementary Table S17 and Supplementary Table S18). From the robust analysis performed, 262 mature miRNAs of *S. lycopersicum* were found in at least one library analyzed. This result showed that the methods used in this study for the miRNAs prediction is quite effective. Only 23 mature miRNAs were not found in the libraries. Among these miRNAs are sly-miR172d-4-5p, sly-miR172d-9-3p, sly-miR2111a-3p, sly-miR403a-3p, sly-miR7983-6-3p, sly-miR7992-5p, sly-miR8008b-2-3p and sly-miR8025-5p, that the other mature miRNA of their pre-miRNAs were present among the libraries, suggesting that in these specific libraries only one mature miRNA was necessarily expressed. Moreover, the non-presence of the other mature miRNAs in the analyzed libraries may be because some miRNAs are expressed only under specific conditions

and/or tissues, which were not present in these libraries[214,215]. This validation analysis of the mature miRNAs could not be performed with *S. pennellii* due to the low number of small RNAs libraries available from this species, highlighting that our study was the first to identify miRNAs in *S. pennellii*.

3.4 CONCLUSION

Considering the global importance of the tomato culture and the problems generated by the susceptibility to the pests of the cultivated tomato (*S. lycopersicum*) and the differences with the wild tomato (*S. pennellii*), the obtained results elucidated several aspects of miRNAs in these two species. Our results expand the study of miRNAs in plants by providing a better understanding of essential roles in the regulation processes based on miRNAs in tomato, their processing pathways and gene expression, as well as providing targets for future investigations.

3.5 METHODS

3.5.1 Identification of putative proteins involved in the miRNA pathway in *S. lycopersicum* and *S. pennellii*

The proteins involved in small RNA pathways in *A. thaliana* and *Solanum tuberosum* were identified and retrieved from the reference protein database (refseq-protein) available at NCBI (National Center for Biotechnology Information). These sequences were used as query sequences to search putative proteins involved in the small RNA biogenesis (including miRNAs) in *S. lycopersicum* and *S. pennellii* using BLASTp (Basic Local Alignment Search Tool) (http://blast.ncbi.nlm.nih.gov/Blast.cgi)[216,217]. Using the reference sequences, the putative sRNA pathway proteins were searched for in the two tomato species using data from *S. lycopersicum* (ITAG3.0) 29 and *S. pennellii* (Spenn_v2.0) 20 of the Sol Genomics Network (https://solgenomics.net/)[28].

3.5.2 Prediction of mature and precursor miRNAs

Initially, the *S. lycopersicum* (ITAG3.0)[29] and *S. pennellii* (Spenn_v2.0)[20] assembly genome were obtained from Phytozome v12.1 (https://phytozome.jgi.doe.gov/)[218] and PlaBi dataBase (http://www.plabipd.de/project_spenn/start.ep), respectively. Genome annotation files were also obtained from the databases of the respective species. The putative miRNAs and their precursors were searched applying the method described by De Souza Gomes et al. (2011), adapted for both species[219]. First, we obtained the genome sequences and found the potential hairpin sequences or similarity to miRNA precursor structures using Blastn (NCBI) and Einverted (EMBOSS tool) programs[220] and the parameters of 336 nucleotides maximum repeat and threshold value 25. Several filters were applied to these sequences to discard undesirable sequences such as other non coding RNAs sequences and also to hold those corresponding to the putative miRNAs. The applied filters were based on precursors miRNA conserved characteristics, as well as characteristics of other known regions and which have no potential to originate precursor miRNAs. These filters were: GC content (guanine and cytosine) between 20% to 65%, Minimum Free Energy (MFE), homology with conserved mature miRNAs, homology with repetitive regions and nonconding RNAs except miRNAs[219].

The miRBase database (version 21 - http://www.mirbase.org/)[125,221] was used to compare with the putative hairpin sequences and find novel *S. lycopersicum* and *S. pennelli* miRNAs accepting a maximum of 5 mismatches in final mature sequence. Other RNA groups such as ribosomal RNA - rRNA, transporter RNA - tRNA, small nuclear RNA - snRNA, small nucleolar RNA - snoRNA, SL RNA, SRP, and RNase P were discarded based on RFAM database version 12.0[222] and repetitive sequences were discarded using RepeatMasker 4.0.5 (http://www.repeatmasker.org/). The putative precursor and mature miRNAs identified were used for further analysis.

The pre-miRNA sequences identified in *S. lycopersicum* and *S. pennellii* were characterized according to their thermodynamic structures and parameters: Minimum Free Energy (MFE), Adjusted Minimum Free Energy (AMFE), Free

Minimum Energy Index (MFEI), Size, content of A, content of U, content of C, content of G, of GC and AU, GC ratio, AU ratio, Minimum Free Energy Ensemble (MFEE), Ensemble Diversity (Diversity) and MFE Structure Frequency in the Ensemble (Frequency). The AMFE was determined with MFE of sequence length 100 nucleotides and the MFEI, measured from the equation: MFEI = [(AMFE) × 100] / (G% + C%)][130]. The pre-miRNA secondary structure prediction, in addition to the diversity calculation, MFE, ensemble frequency and MFE of the secondary structures were performed using the RNAfold (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi). GC content and other structural properties were defined using Perl scripts.

3.5.3 Analysis of conserved domains, active sites, phylogeny, primary and secondary alignments

For the conservation analyzes of domains, active sites and structure evaluation, putative protein sequences and precursor miRNAs we used the multiple alignment by ClustalX 2.1 and ClustalW[223]. In addition, we used RNAalifold (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAalifold.cgi) to analyze the primary and secondary structure alignment of precursor miRNAs with their respective orthologs[223]. Adjusted parameters (gap opening: 22.50; gap extension: 0.83) were used for the multiple alignments of precursor miRNA sequences[224]. The pre-miRNAs and proteins sequences logos were originated from WebLogo 2.8.2 (http://weblogo.berkeley.edu/logo.cgi)[225].

The conserved protein domains were recovered separately to verify, through multiple alignment, the presence of important amino acid residues. In addition, PFAM family protein database (http://pfam.xfam.org/)[226] was used to find conserved domains and their putative functions. The Conserved Domain Database (CDD) (http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi)[227] was used to identify amino acids from active sites of the putative proteins.

The phylogenetic analysis was performed using MEGA5.2 program and Neighbor-joining method for miRNA precursor sequence and also putative proteins[228,229]. The miRNAs evolutionary distance was calculated using the Kimura-2-parameter in site-replaced base units. For the putative proteins was

used the Jones-Taylor-Thornton (JTT) model[230]. A consensus tree was obtained using bootstrap of 5000 replicates for the precursor miRNAs and 1000 replicates for the proteins, representing the evolutionary history of the analyzed sequences group.

3.5.4 miRNA target prediction

The miRNA targets identified in *S. lycopersicum* and *S. pennellii* were predicted using psRNATarget tool (2017 Update) (http://plantgrn.noble.org/psRNATarget/)[231,232]. In order to obtain the false positives prediction rate lowest for miRNA target genes, the threshold was strict, being 3.0 for "Maximum expectation (Exp)". The other parameters used were the standard parameters: "Length for complementarity scoring (HSP size)" - 19 bp; "Top target genes for each small RNA" - 200; Target accessibility - allowed maximum energy to unpair target site (UPE) - 25; "Flanking length around target site for target accessibility analysis" - 17 bp before/13 bp after; "Range of central mismatch leading to translational inhibition", leading to inhibition of translation: 10-11 nucleotides. To analyze the miRNA target genes predicted in tomato, potential target candidate were retrieved by Phytozome v12.1 and Sol Genomics Network batabases.

3.5.5 miRNA expression by real-time PCR

3.5.5.1 Plant material

The plant material was harvested at the Experimental Station “HortiAgro Sementes S/A”, along to the Center of Development and Transference of Technology of the Federal University of Lavras (UFLA), at the municipality of Ijaci, MG. Leaves, flowers and fruits of *Solanum lycopersicum* and *Solanum pennellii* were harvested from three plants as biological replicates. The material was immediately frozen in liquid N_2 and stored in 50 mL tubes in -80ºC freezer until the RNA extraction.

3.5.5.2 RNA Extraction

The Total RNA was extracted using the QIAzol® Lysis Reagent (QIAGEN). Approximately 100 milligrams of tissue was grinded in liquid N_2 and transferred to a tube. 1mL of QIAzol was added and homogenized by vortex. The tubes were left at room temperature for five minutes. Afterwards, 300 µL of chloroform was added and homogenized by vortex. The mixture was left at room temperature for five minutes. Afterwards, the tubes were centrifuged at 12000 G at 4 ºC for 15 minutes, when three phases were formed, and 400 µL of the upper phase was collected and transferred to a new tube and 500 µL of Isopropanol was added and homogenized by vortex and left at room temperature for 10 minutes. The tubes were then centrifuged at 12000 G at 4 ºC for 10 minutes for precipitation of nucleic acids. The liquid was discarded and the pellet was washed with 1mL of 75% ethanol and centrifuged at 7500 G at 4 ºC for 10 minutes and the liquid was discarded carefully to preserve the pellet. Then, 500 µL of Isopropanol was added again and the steps were repeated. The pellet was dried at room temperature and then resuspended in 20 µL of autoclaved miliQ water.

The integrity of the RNA was visualized in 0.8% agarose gel, and the quantity and quality (ratio 260/280 and 260/230 between 1.8 and 2.2) were measured on Nanuvue spectrophotometer.

3.5.5.3 DNAse treatment

The Total RNA extracted was treated with the kit Turbo DNA-free™ (Life technologies™). 5 µg of RNA was used and the corresponding volume was completed to 22 µL with autoclaved milliQ water. Then, 2.5 µL of the 10x turbo DNAse Buffer and 0.5 µL of the turbo DNAse were added to each sample. The reaction was incubated for 30 minutes at 37 ºC. Afterwards, to stop the DNAse enzime activity, 2.5 µL of the DNAse Inactivation reagente was added. The samples were left at room temperature for 5 minutes, occasionally mixing the tubes, and then centrifuged at 10000 RPM for 2 minutes. After centrifugation, 15 µL were collected and transferred to a new tube. The samples were stored at -20 ºC until cDNA synthesis.

3.5.5.4 cDNA Synthesis and Relative Expression

The stem-loop method[63,233] was used for cDNA synthesis and expression analysis, following the steps described in[63,209]. In this method, three primers are needed – the stem-loop RT primer, the forward and the reverse primers. The stem-loop RT primers were designed according to Chen (2004)[233]. Sequence data are presented in Supplementary Table S19. The stem-loop primers contain 50 nucleotides, from which 44 nucleotides corresponds to a universal sequence, that in low temperatures form a stable stem-loop structure. The last 6 nucleotides at the 3' end of the stem-loop RT primer is a reverse complement of the last 6 nucleotides at the 3' end of the specific miRNA. The forward primers were designed with the exact sequence of the miRNA, excluding the last 6 nucleotides at the 3' end. To increase the melt temperature, nucleotides were randomly added (5-7 nucleotides) to the 5' end of the primer. Primer design software were used to calculate the melt temperature and verify the quality of the forward primers. The third primer is the reverse primer which is a reverse complement of the universal sequence of the stem-loop RT primer, and, therefore, is used for every miRNA.

The cDNA synthesis from total RNA (DNA-free) was performed using the *ImProm-II™ Reverse Transcriptase* (Promega). For each miRNA, 500 ng of RNA was used. The volume was completed to 7 µL with autoclaved miliQ water. To the RNA, 1 µL of oligodT primer; 2 µL of specific stem-loop RT primer (1 µM) and 1 µL of the dNTP mix were added. The samples were incubated at 70 °C for 10 min for denaturation of the secondary structures and later incubated at 4 °C for 10 min. Soon afterwards, 5 µl of Improm-II 5× reaction buffer, 2.4 µl of $MgCl_2$ 25 mM, 0.6 µl of RNase out (Invitrogen), and 1 µl of the Improm-II Reverse Transcriptase enzyme were added. The reactions were incubated in a thermocycler at 16 °C for 30 min, followed by reverse transcription of 60 cycles at 30 °C for 30 s, 42 °C for 30 s, and 50 °C for 1 s. For inactivation of the Improm-II Reverse Transcriptase enzyme, the reaction was incubated at 70 °C for 15 min. Subsequently, the reactions were stored at −20 °C.

Quantitative Real-time PCR (RT-qPCR) was performed using a standard SYBR Green PCR kit protocol on a Rotor-Gene Q (QIAGEN). The reactions were

performed in a final volume of 15 µl, using 1.5 µl cDNA, 1.5 µl of each primer at a final concentration of 1 µM, 7.5 µl of SYBR Green PCR Master Mix (QIAGEN), and 3.0 µl of water, for each reaction. The reaction was incubated at 95 °C for 5 min, followed by 40 cycles at 95 °C for 5 s and 60 °C for 10 s. Then, the samples were heated from 55 to 95 °C with an increase of 1 °C to acquire the denaturing curve of the amplified products. All reactions were run in triplicate.

The primer efficiency was calculated for each miRNA and the reference genes by a standard curve of a 1:5 serial dilution of a pool of cDNA of the respective miRNA. The primers efficiency is: miR165/166 (87%), sly-miR167 (97%), spe-miR167 (116%), miR827 (95%), miR7983(97%), miR530 (98%) and miR828 (96%).

To the relative expression experiment of the miRNAs in the selected tissues, the 1:25 dilution was chosen. To the calculation of relative expression, the normalized comparative Cq (quantitative Cycle) method was used[64], which takes into account the primers efficiency in the calculation. The normalization factor was the geometric mean of the U6 and 5.8S gene expression.

3.5.6 Expression of miRNA pathway genes in tomato RNA-seq libraries

Paired-end reads from leaves and flowers of both wild (*Solanum pennellii*) and cultivated (*Solanum lycopersicum*) tomato were retrieved from the Sequence Read Archive (SRA) under accessions numbers SRR786556, SRR786557, SRR786570, SRR786571, SRR786552, SRR786553, SRR786566, SRR786567, SRR786524, SRR786525, SRR786540, SRR786541, SRR786542, SRR786520, SRR786521, SRR786535, SRR786536, SRR786537[93]. In this way 10 libraries for *S. lycopersicum* and 8 libraries for *S. pennellii*, totalizing 77354968 paired-end reads, were used for differential expression analyses.

The quality of the libraries was evaluated using FastQC software[234]. Adapters were identified using minion[235] and removed with Trimmomatic[236] as well as reads with quality score and length below 20 and 35 bp, respectively. After quality control, 71703462 paired-end reads were used as input to STAR mapper tool (version 2.5.3a)[237] with default parameters to alignment against their respective genomes (*S. lycopersicum* version 3.2 and *S. pennellii* version 2.0)

retrieved from the Sol Genomics Network[28]. Approximately 88% and 87% of the *S. lycopersicum* and *S. pennellii* reads were uniquely mapped to their genomes, respectively.

The libraries were then sorted by query name using picard tools (version 2.18.0), and for each of them, raw read counts were obtained using the python script htseq-count (version 0.7.2)[238]. Differentially expressed (DE) genes were identified using the Bioconductor R package edgeR by comparing the normalized number of reads aligned to each gene in different tissues[239,240]. Benjamini and Hochberg's false discovery rate (FDR) below 0.05 and minimum fold change of two were the parameters used to consider a gene DE[241].

3.5.7 miRNAs in *S. lycopersicum* small RNAseq libraries

3.5.7.1 Sequencing analysis

95 raw small RNA data files were retrieved from NCBI Sequence Read Archive (SRA) with different accession number (Supplementary Table S15, Supplementary Table S16, Supplementary Table S17 and Supplementary Table S18). The library qualities were evaluated using FastQC software[234], adapters were removed with Trimmomatic[236] discarding reads with quality score below 20 and length less than 17 nucleotides and longer than 30 nucleotides. The filtered sequences were mapped and quantified using miRDeep2[242]. miRDeep2 and perl scripts were used to on each sequence separately to generate the numbers of the reads for each miRNAs identified.

3.5.8 Statistical analysis

For the statistical comparisons among the structural and thermodynamic variables of each category (species and/or families), a basic descriptive analysis was performed followed by non-parametric tests (Wilcoxon-Mann-Whitney). Median values were used to perform the statistical comparisons[243]. Statistical significance was set at $p<0.1$.

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Author contributions statement

Mat.S.G., W.R.M., L.A.A.G., T.C.S.C., C.M.C. and T.C.A. proposed the research.

Mat.S.G., A.C.J., A.A.L., C.N.F.B., L.R.A. and T.C.S.C. designed the experiments. W.R.M., L.A.A.G., M.M.D., G.L.R., C.N.F.B., D.R.G.S., C.M.C. and T.C.S.C. prepared samples. T.C.S.C., T.C.A., C.M.C., D.R.G.S., C.N.F.B., M.M.D. and G.L.R. performed experiments. Mar.S.G., P.E.G., T.H.C.R. and L.R.A. performed the statistical analyzes. D.R.G.S., C.M.C., T.C.S.C., T.C.A., T.H.C.R., M.M.D.G, L.R.A. and Mat.S.G. performed bioinformatic analysis. T.C.S.C., T.C.A., C.N.F.B., T.H.C.R., A.A.L., M.M.D.G and Mat.S.G. wrote manuscripts and prepared figures. Mat.S.G. supervised the project. All authors reviewed the manuscript.

Additional information

Competing Interests: The authors declare no competing financial interests.

FIGURES

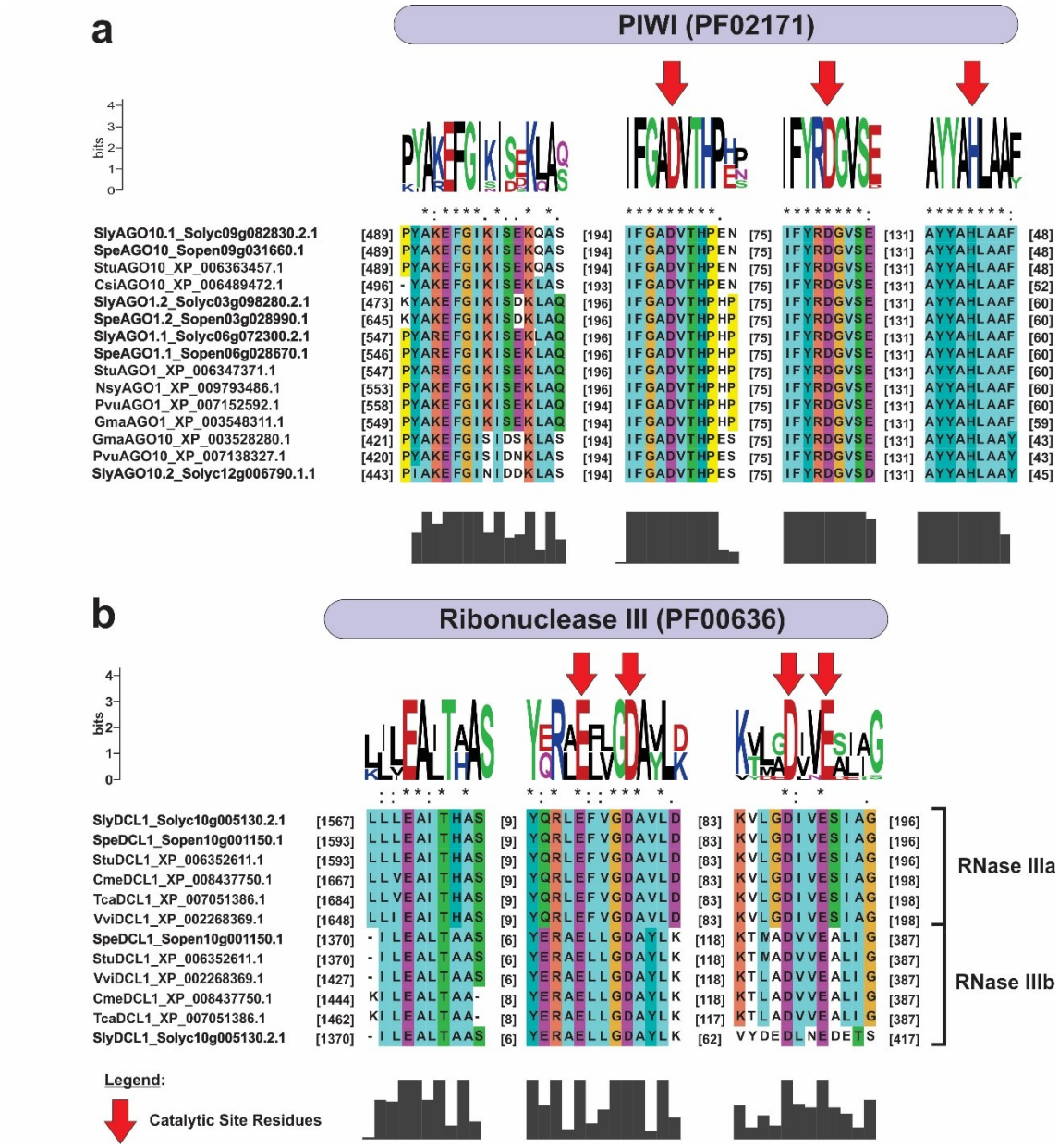

Figure 1. Weblogo analysis and sequence multiple alignment of active site amino acids and their flanking amino acid residues in the conserved domains of *S. lycopersicum, S. pennellii* and their orthologs. **(a)** PIWI domain (PF02171) from AGO proteins and **(b)** Ribonuclease III domain (PF00636) from DCL proteins. The red arrows show the amino acid residues of the active sites (catalytic triad AGO: Asp-Asp-His and DCL: Glu-Asp-Asp-Glu). The height of each amino acid symbol in Weblogo indicates amino acid residue conservation at a given position. The asterisk denotes 100% conserved amino acids at specific position. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Csi - *Citrus sinensis*, Gma - *Glycine max*, Pvu - *Phaseolus vulgaris*, Stu – *Solanum tuberosum* and Nsy - *Nicotiana sylvestris*, Cme - *Cucumis melo*, Tca - *Theobroma cacao*, Vvi – *Vitis vinifera*.

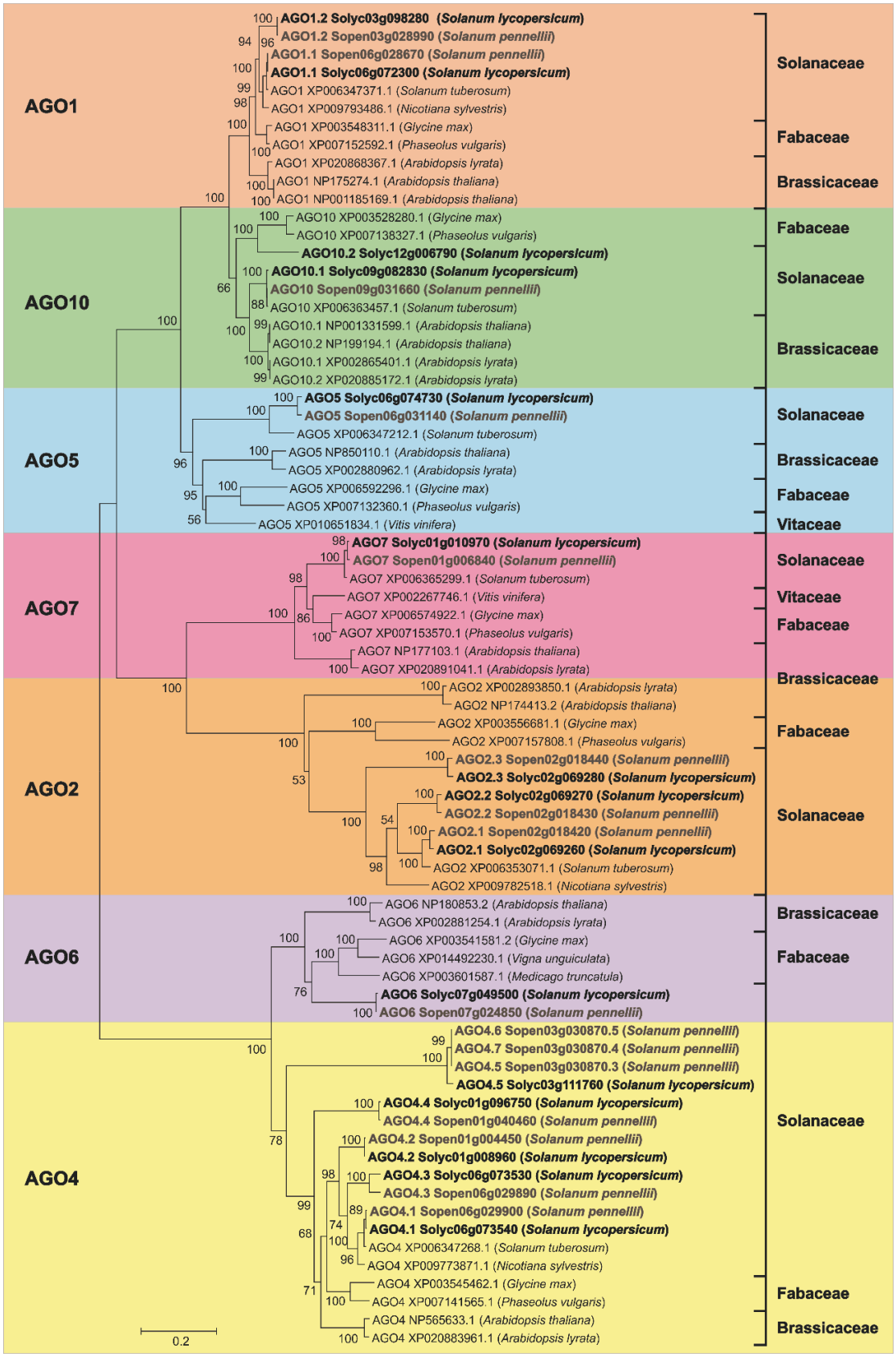

Figure 2. Phylogenetic tree of AGO proteins identified in *S. lycopersicum, S. pennellii* and their orthologs.

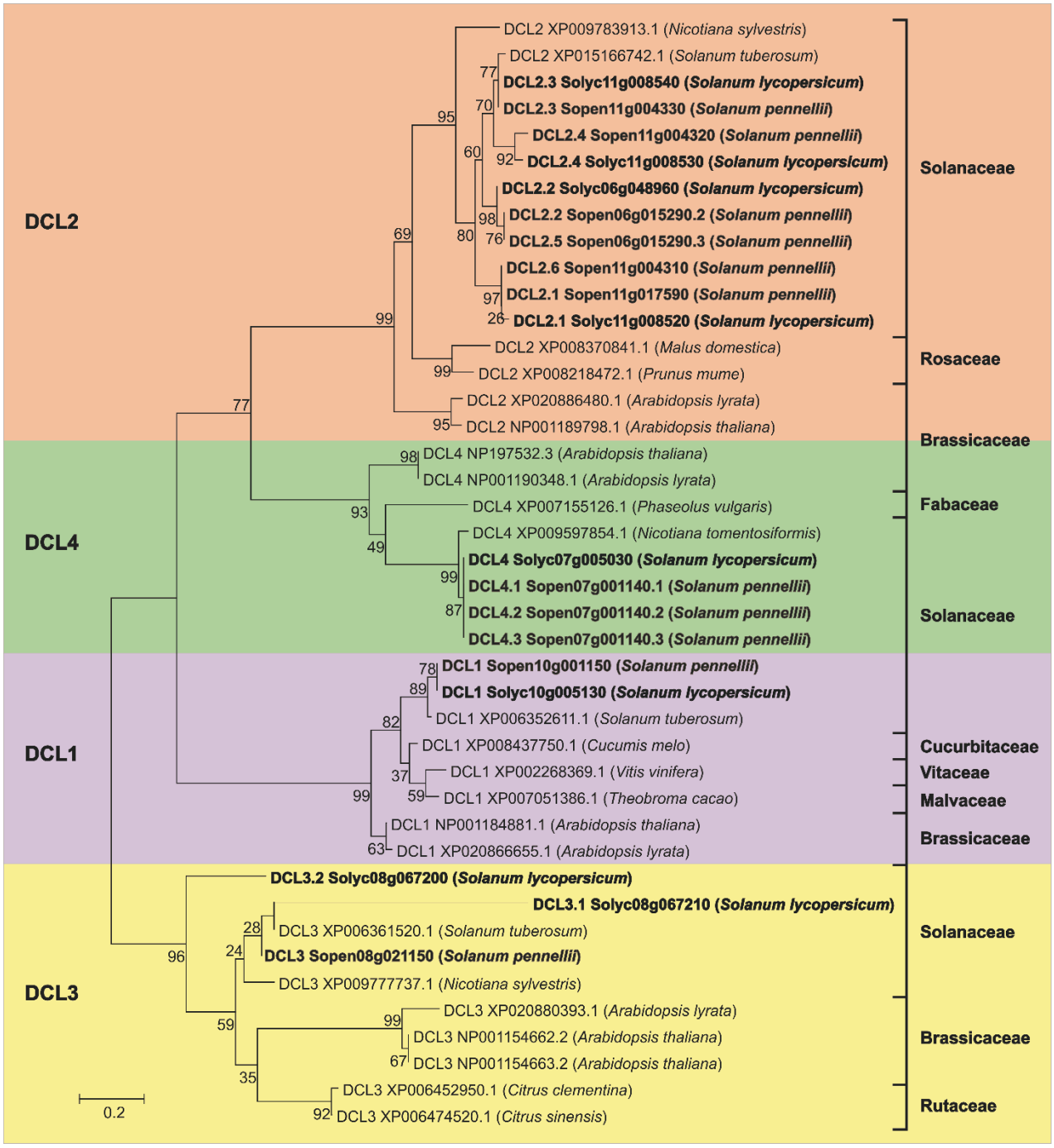

Figure 3. Phylogenetic tree of DCL proteins identified in *S. lycopersicum, S. pennellii* and their orthologs.

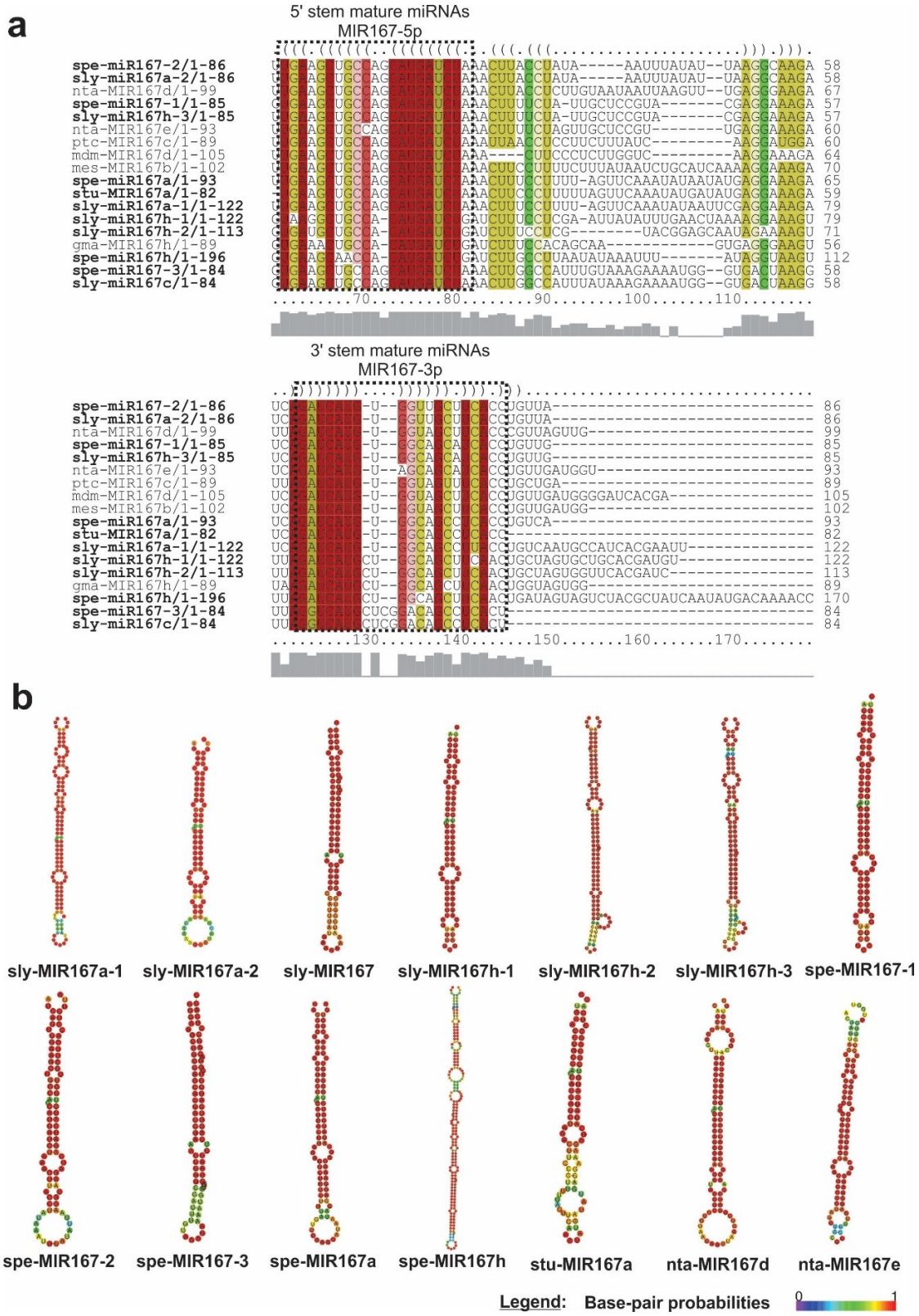

Figure 4. (a) Alignment of precursors from MIR167 family and **(b)** comparison of their predicted secondary structures in *S. lycopersicum* and *S. pennellii* to their orthologs. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Nta – *Nicotiana tabacum,* Ptc - *Populus trichocarpa*, Mdm - *Malus domestica*, Mes - *Manihot esculenta*, Gma - *Glycine max*, Stu – *Solanum tuberosum*.

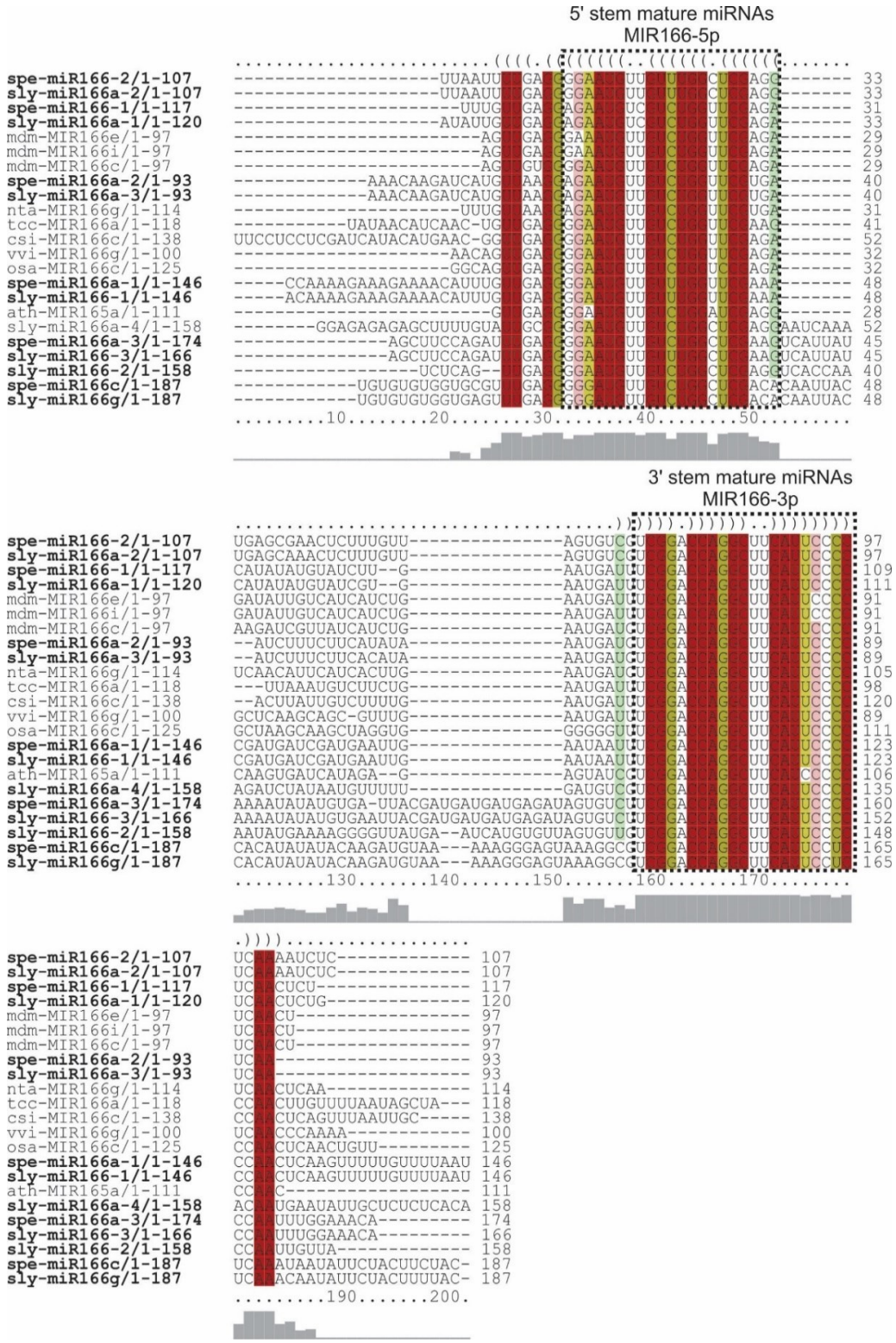

Figure 5. Alignment of precursors from MIR165/166 family in *S. lycopersicum* and *S. pennellii* to their orthologs. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Mdm - *Malus domestica*, Nta – *Nicotiana tabacum,* Tcc - *Theobroma cacao*, Csi - *Citrus sinensis,* Vvi – *Vitis vinifera,* Osa - *Oryza sativa*, Ath - *Arabidopsis thaliana*.

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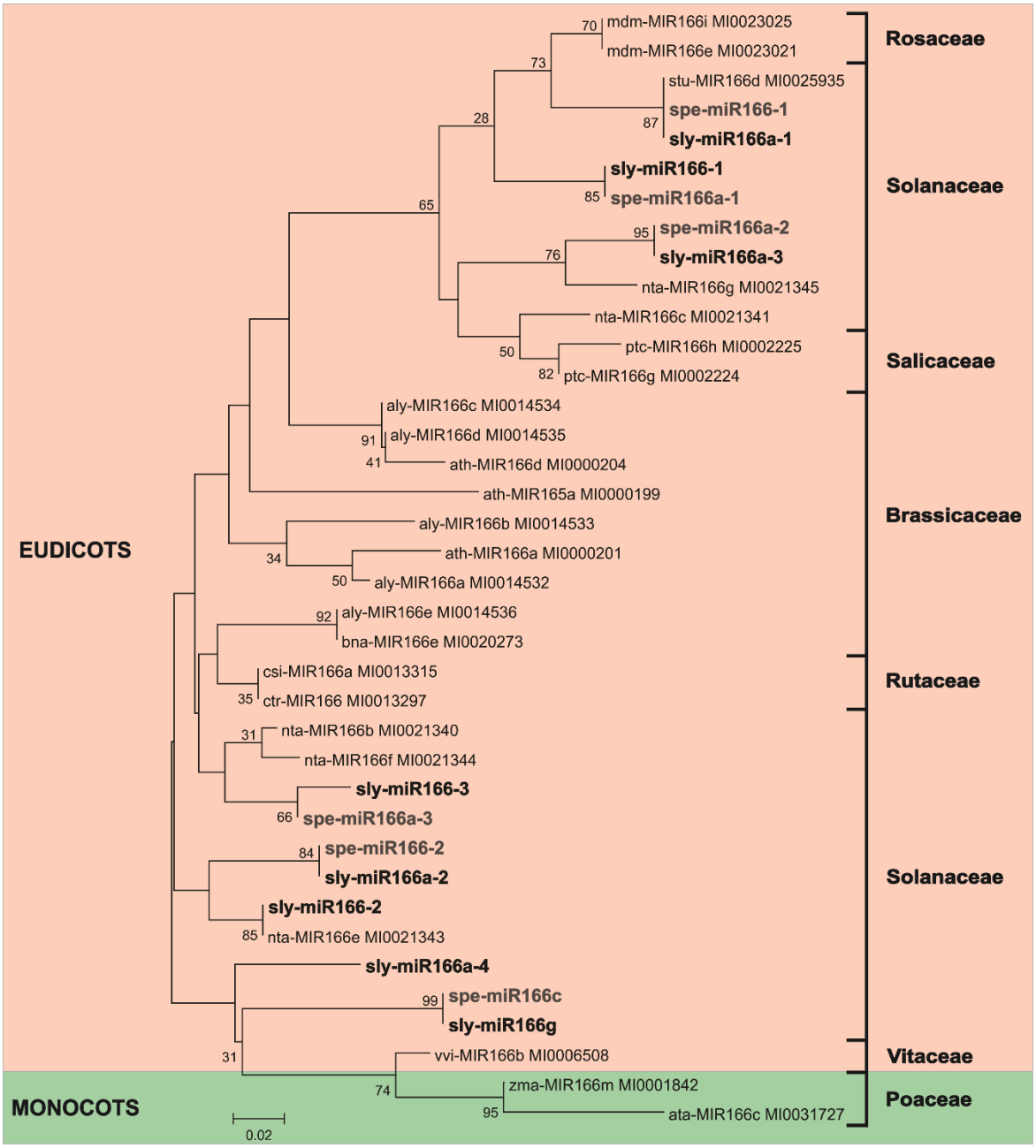


Figure 6. Phylogenetic tree of MIR165/166 family identified in *S. lycopersicum, S. pennellii* and their orthologs. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Mdm - *Malus domestica*, Stu – *Solanum tuberosum*, Nta – *Nicotiana tabacum,* Ptc - *Populus trichocarpa*, Aly - *Arabidopsis lyrata*, Ath - *Arabidopsis thaliana,* Bna - *Brassica napus*, Csi - *Citrus sinensis,* Ctr - *Citrus trifoliate,* Vvi – *Vitis vinifera,* Zma - *Zea mays*, Ata - *Aegilops tauschii*.

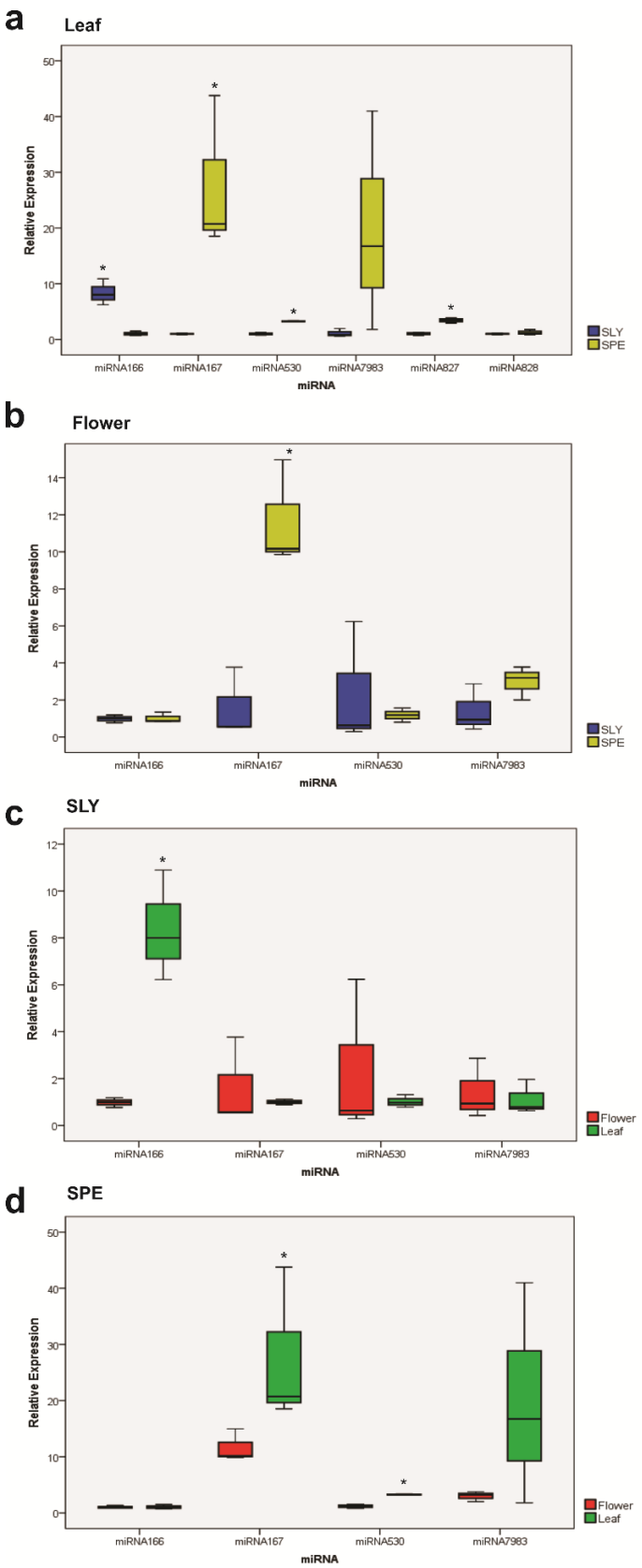


Figure 7. Relative expression profile of **(a)** miR165/166, miR167, miR530, miR7983, miR827 and miR828 in leaves and **(b)** the miR165/166, miR167, miR530 and miR7983 in flowers of **(c)** *S. lycopersicum* (SLY) and **(d)** *S. pennellii* (SPE).

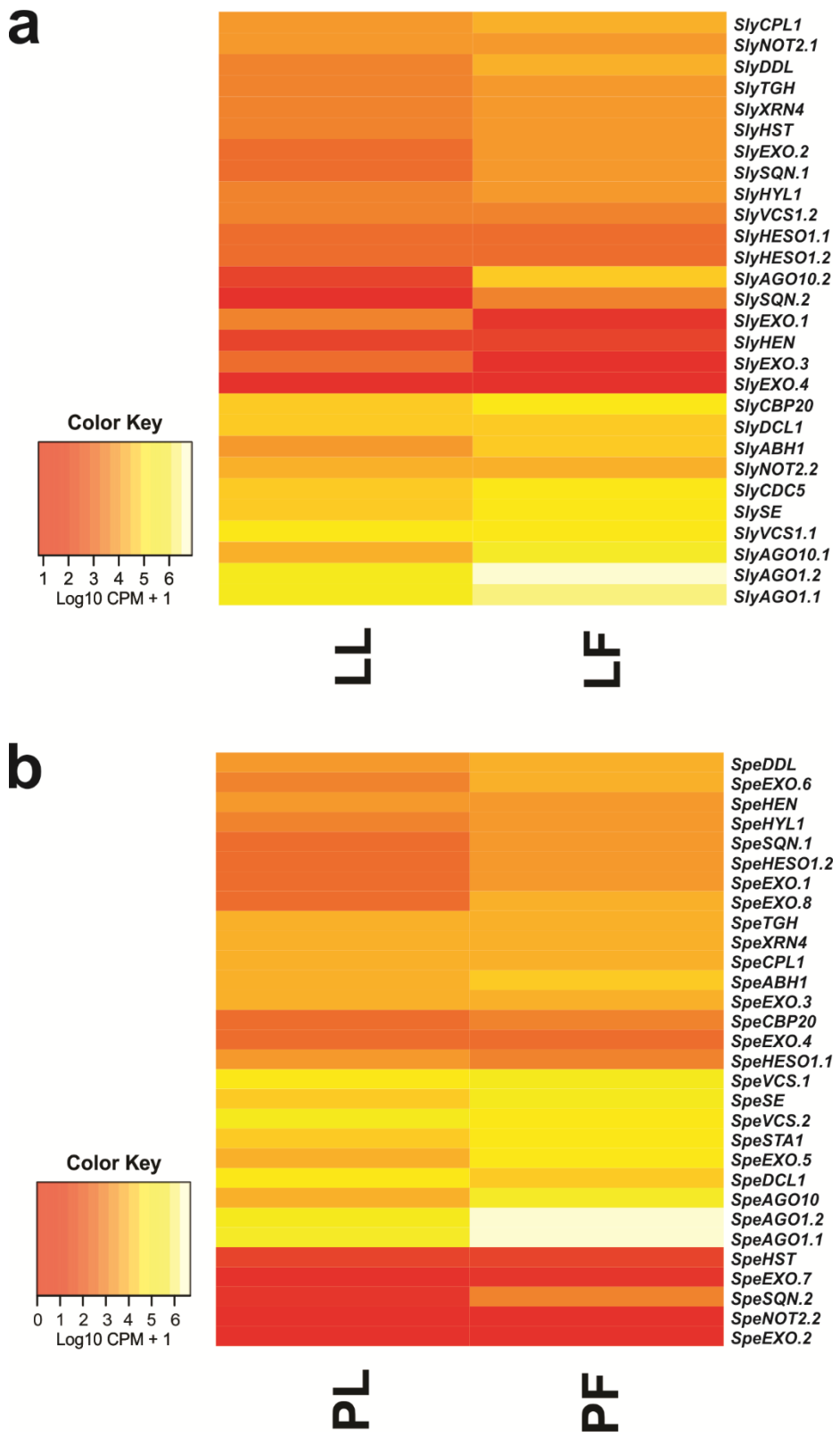
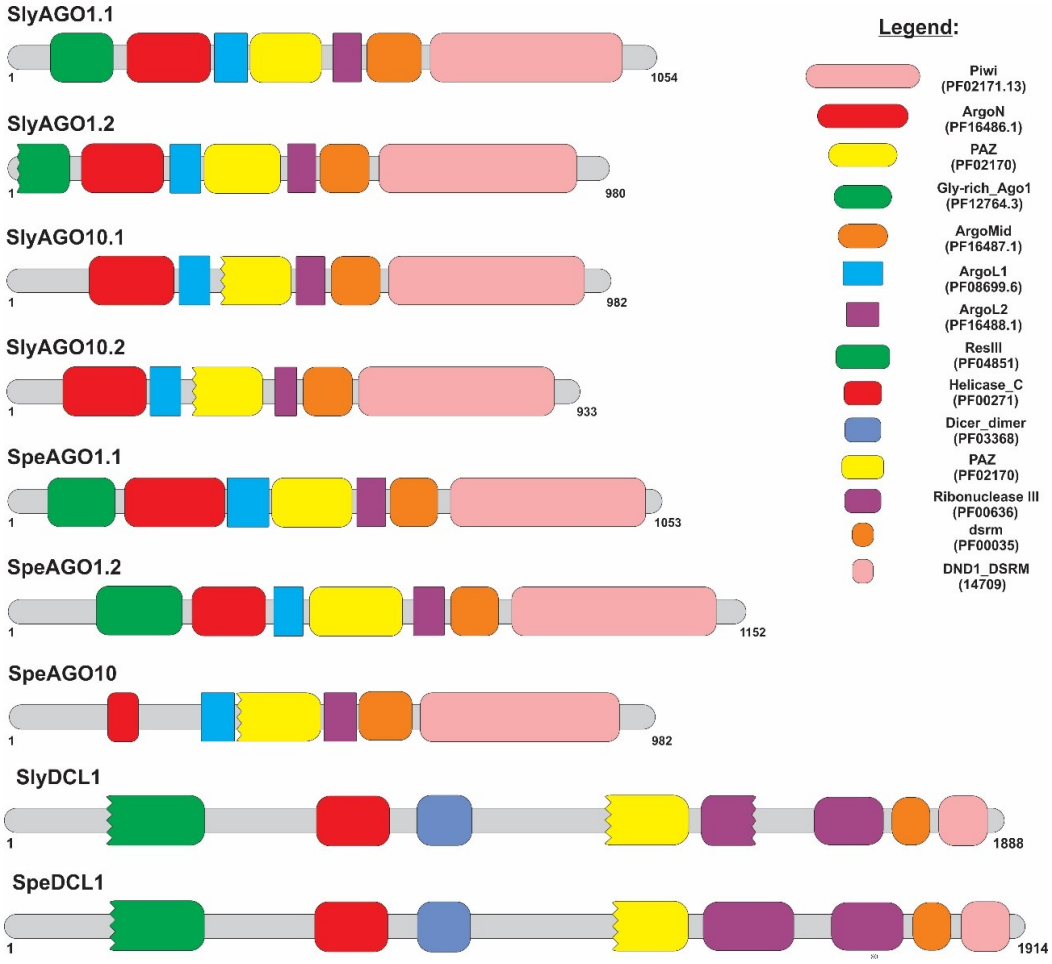
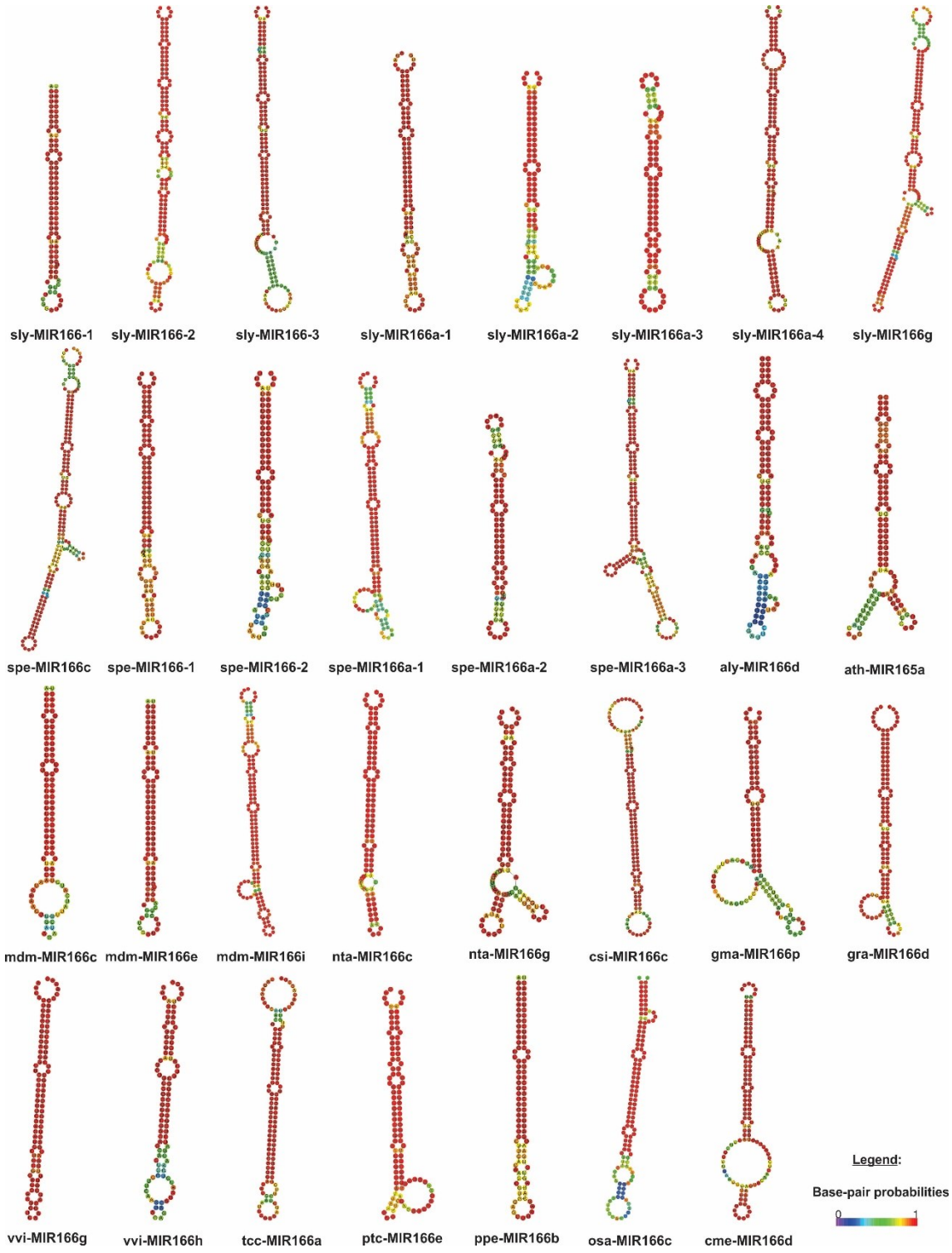


Figure 8. Heatmap analysis of the genes involved in the tomato miRNAs pathway from leaves and flowers RNA-seq libraries. Heatmap shows the expression profile of the **(a)** *S. lycopersicum* and **(b)** *S. pennellii* genes in two tissiues, being LL (*S. lycopersicum* leaves), LF (*S. lycopersicum* flowers), PL (*S. pennellii* leaves) and PF (*S. pennellii* flowers).

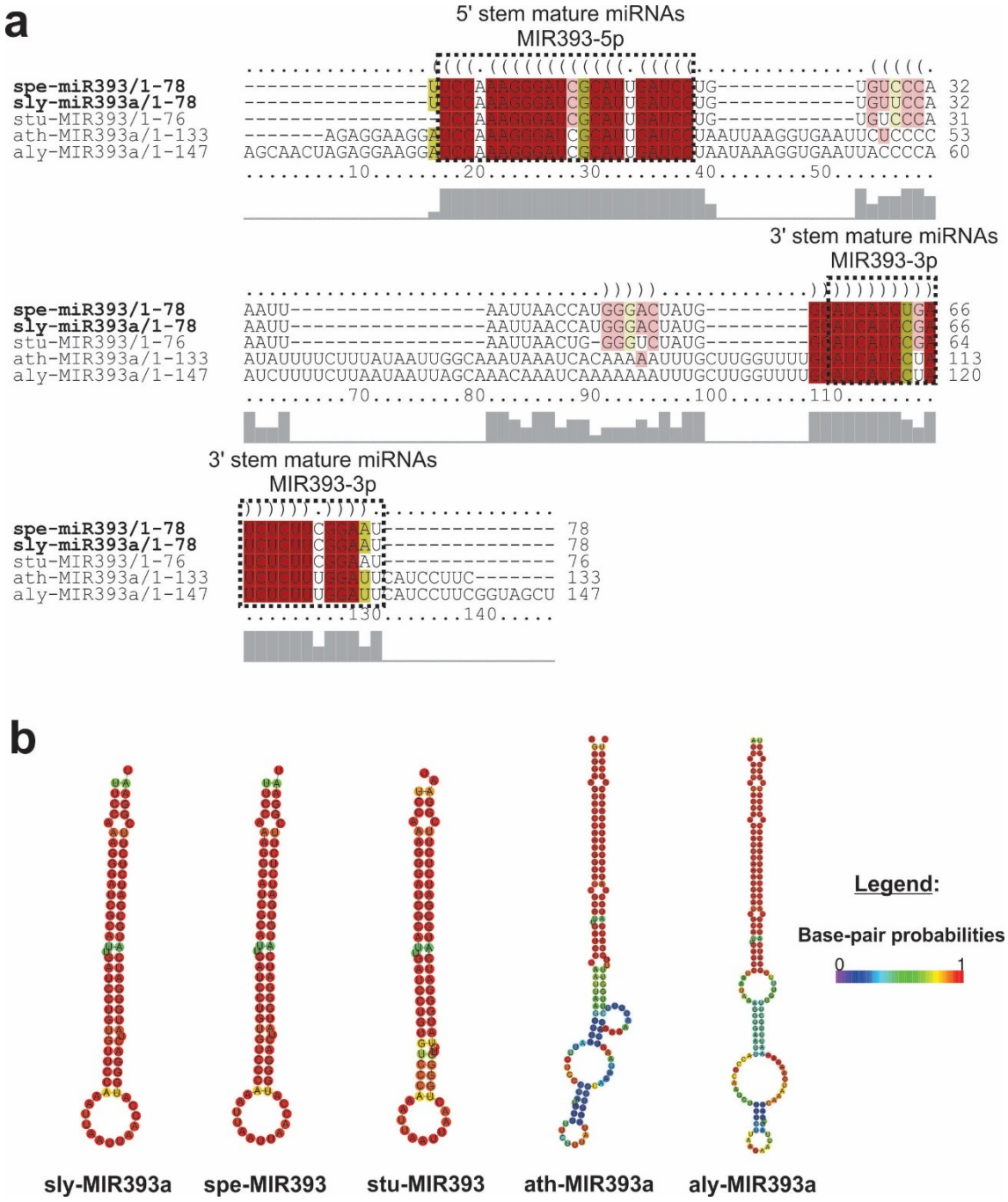
SUPPLEMENTARY FIGURES



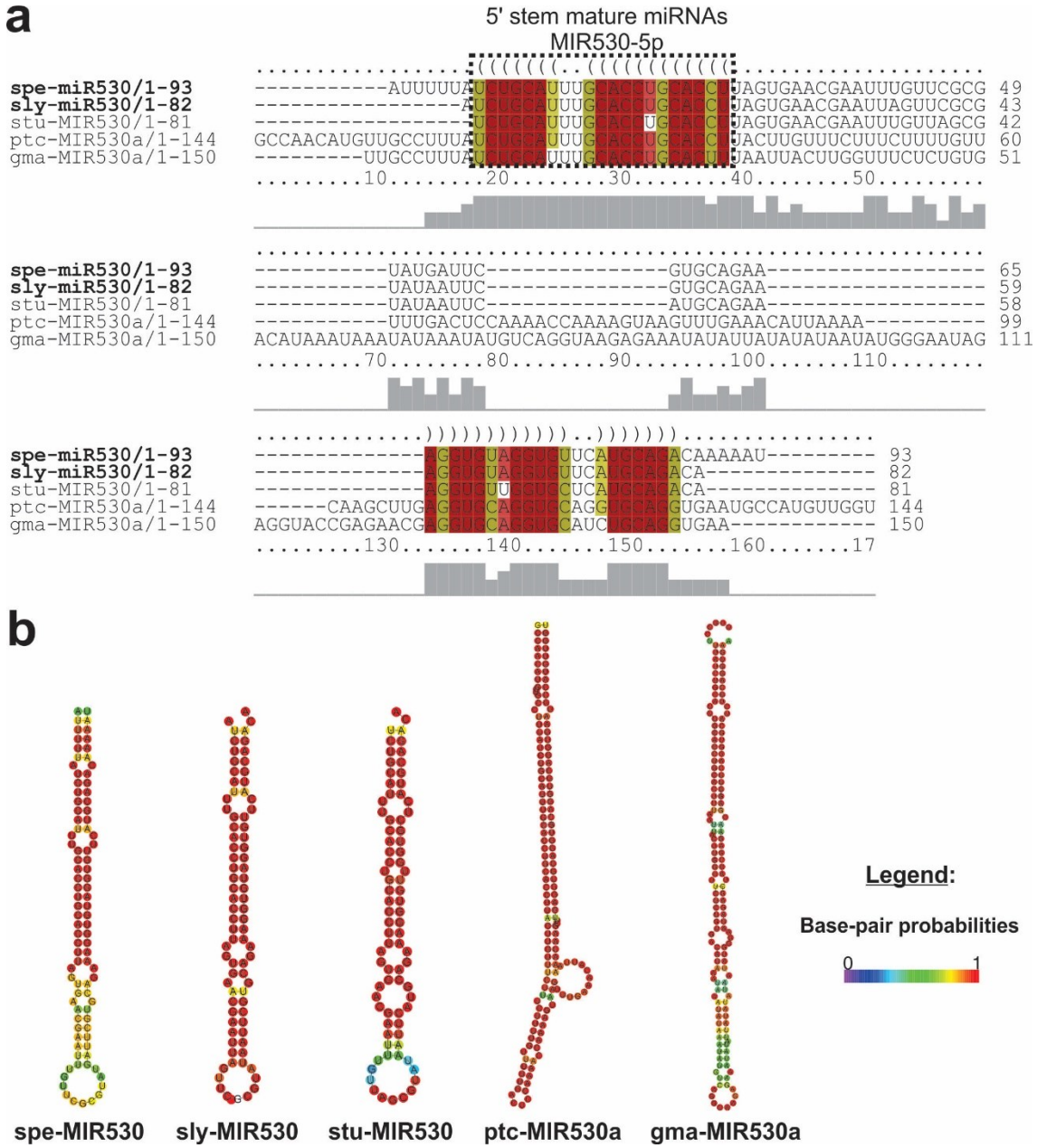
Supplementary Figure S1. Distribution of conserved domains in AGO and DCL putative proteins of *S. lycopersicum* and *S. pennellii*. The SlyAGO1.1/1.2 e SpeAGO1.1/1.2 proteins displayed the Gly-rich_Ago1, ArgoN, ArgoL1, PAZ, ArgoL2, ArgoMid and Piwi in positions 70-174, 185-328, 338-388, 394-520, 531-576, 587-661, 681-1000 / 18-100, 111-254, 264-314, 320-446, 457-502, 513-587, 607-926 e 69-173, 193-327, 337-387, 393-518, 529-575, 586-660, 680-999 / 160-272, 292-426, 436-486, 492-617, 685-759, 685-759, 779-1098, respectively. The same for SlyAGO10.1/10.2 and SpeAGO10 proteins which displayed the domains ArgoN, ArgoL1, PAZ, ArgoL2, ArgoMid and Piwi. The location these domains in SlyAGO10.1/10.2 and SpeAGO10 were at positions 127-270, 280-330, 342-462, 473-518, 529-606, 621-940 / 82-224, 234-284, 302-416, 429-472, 483-561, 575-891. The SlyDCL1 and SpeDCL1 proteins, only DCL involved in the processing of miRNAs, displayed the conserved domains ResIII (also known as DEAD-like), Helicase C, Dicer Dimer (also known as DUF283), PAZ, Ribonuclease IIIa (RNase IIIa), Ribonuclease IIIb (RNase IIIb), dsrm and DND1 DSRM, in 259-420, 656-773, 848-936, 1214-1349, 1386-1468, 1586-1699, 1726-1784, 1811-1883; e 256-420, 656-773, 848-936, 1214-1349, 1386-1534, 1612-1725, 1752-1810, 1837-1909 positions, respectively.



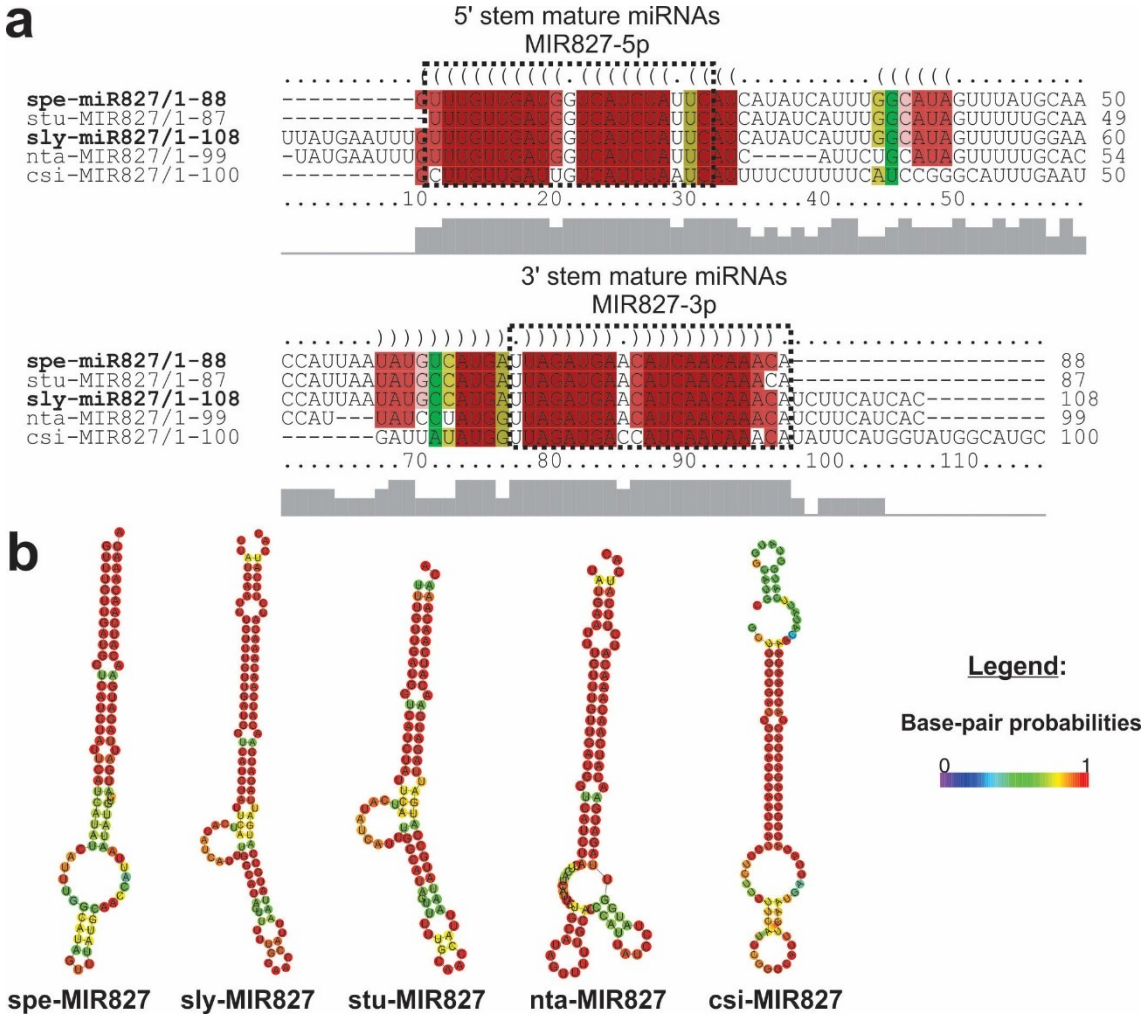
Supplementary Figure S2. Secondary structures of MIR165/166 family pre-miRNAs from *S. lycopersicum*, *S. pennellii* and their orthologs were draw by RNAfold.



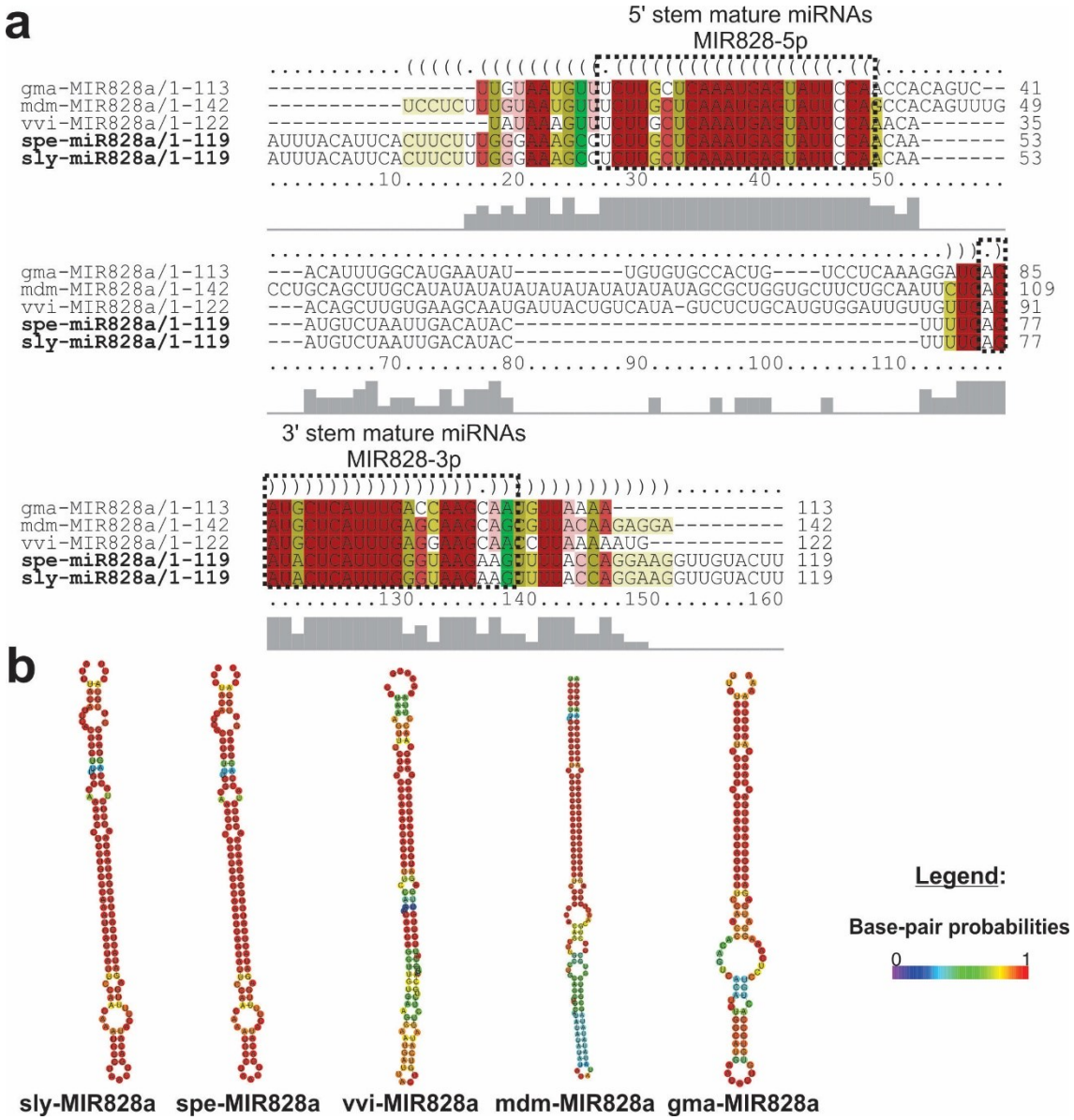
Supplementary Figure S3. (a) The high confidence of RNA alignments between MIR393 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' and 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR393 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum,* Ath - *Arabidopsis thaliana,* Aly - *Arabidopsis lyrata.*



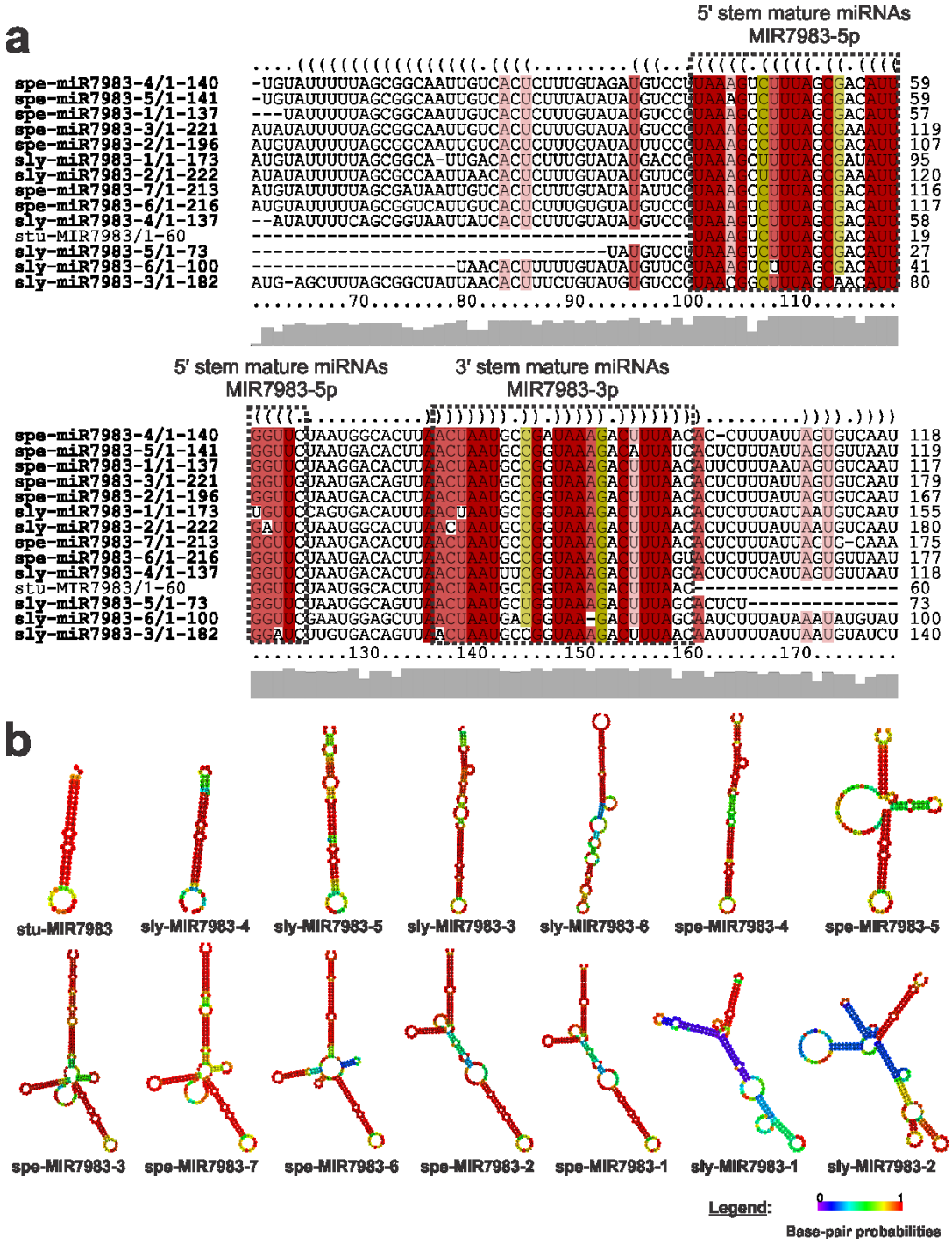
Supplementary Figure S4. (a) The high confidence of RNA alignments between MIR530 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR530 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum,* Ptc - *Populus trichocarpa*, Gma - *Glycine max.*



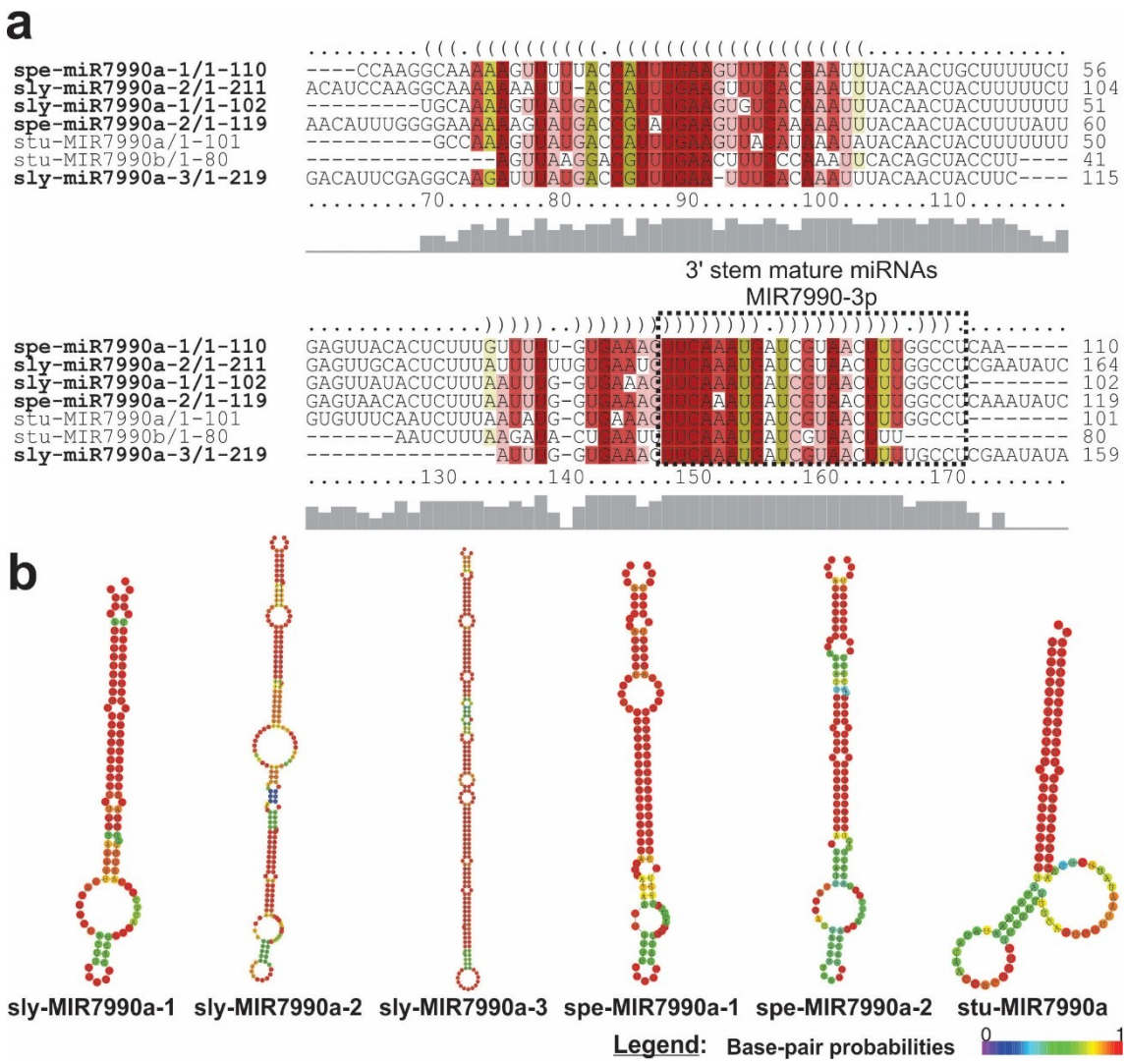
Supplementary Figure S5. (a) The high confidence of RNA alignments between MIR827 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' and 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR827 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum,* Nta – *Nicotiana tabacum,* Csi - *Citrus sinensis*.



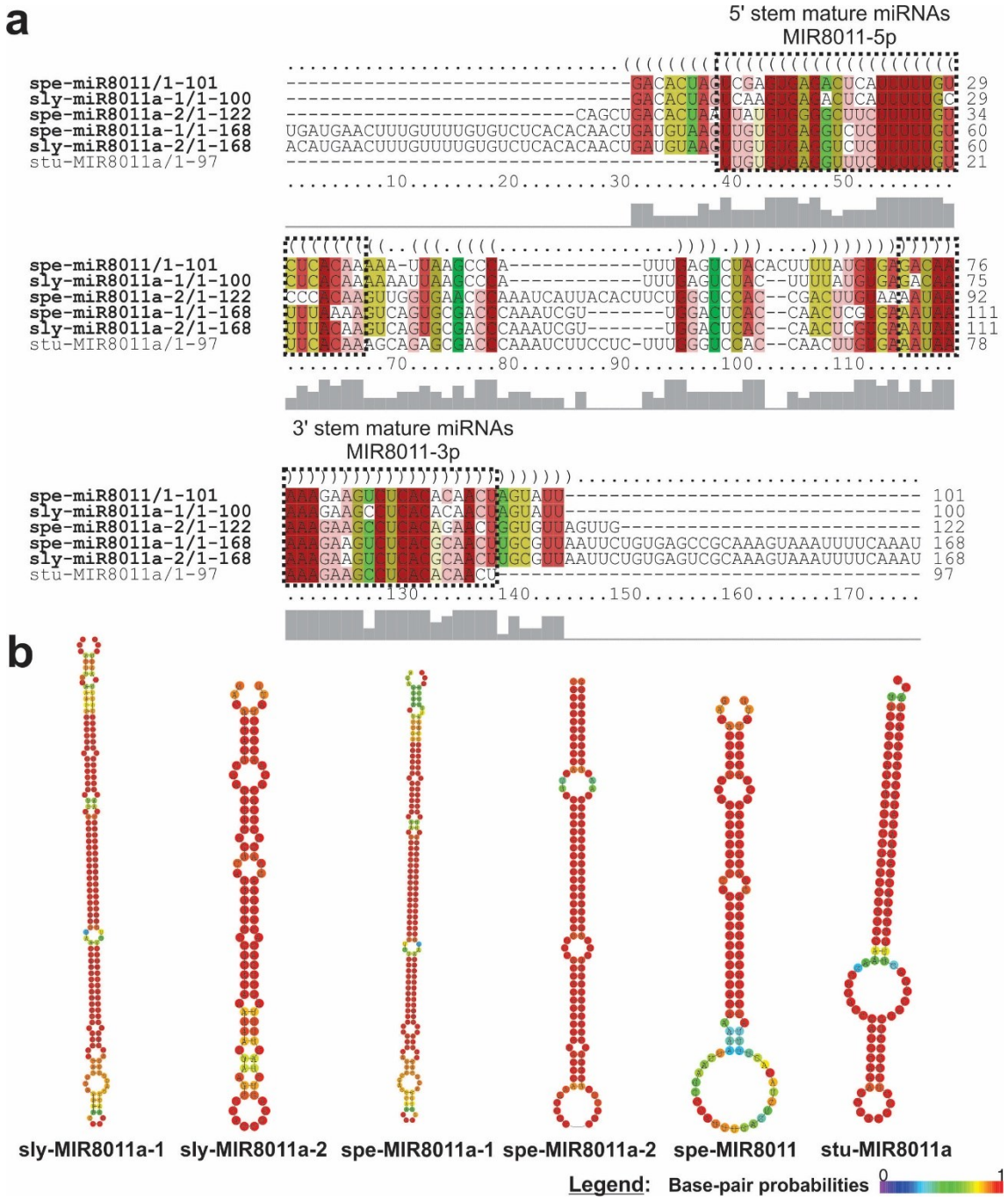
Supplementary Figure S6. (a) The high confidence of RNA alignments between MIR828 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' and 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR828 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Vvi – *Vitis vinifera*, Mdm - *Malus domestica*, Gma - *Glycine max*.



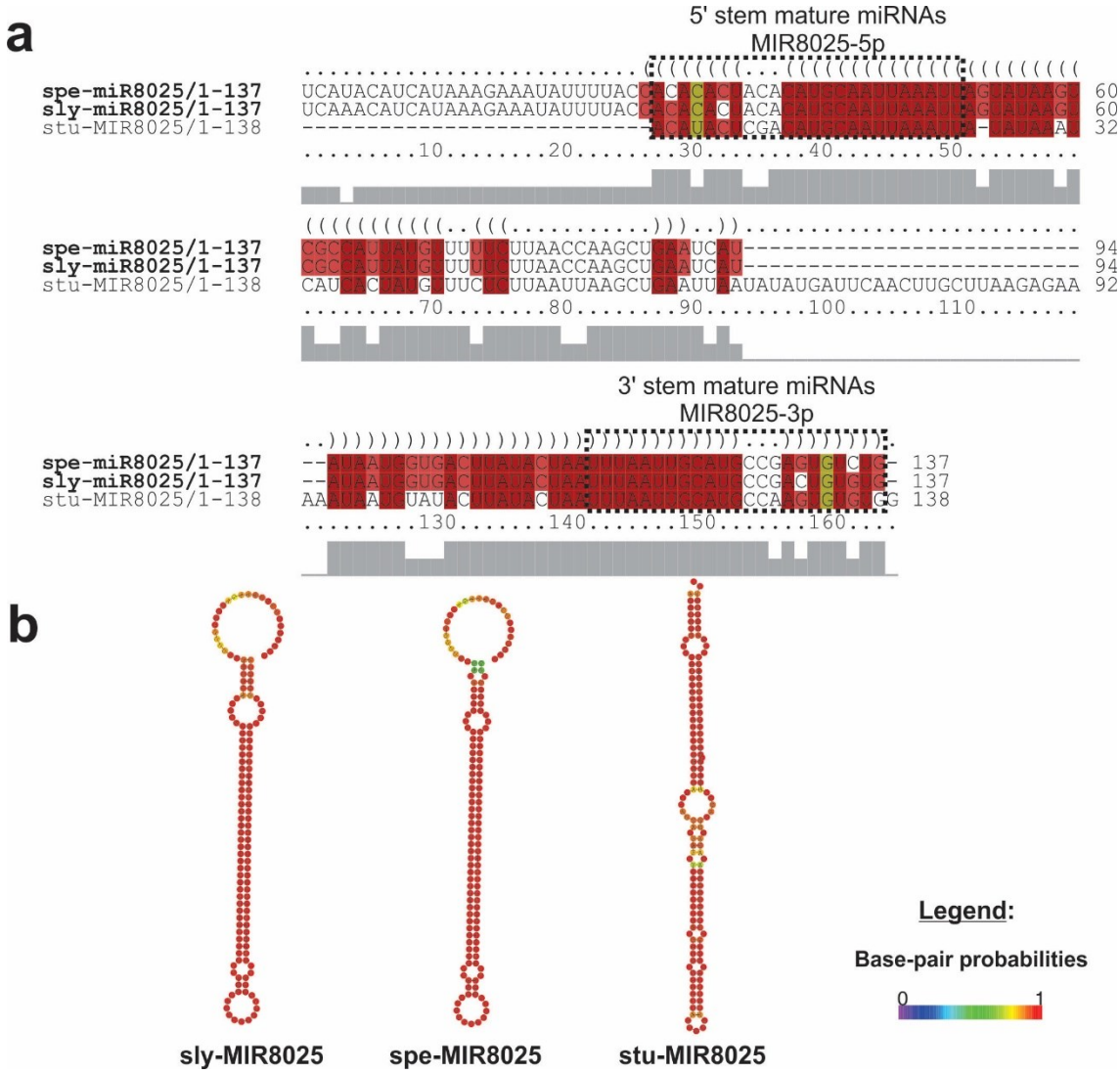
Supplementary Figure S7. (a) The high confidence of RNA alignments between MIR7983 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' and 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR7983 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum*.



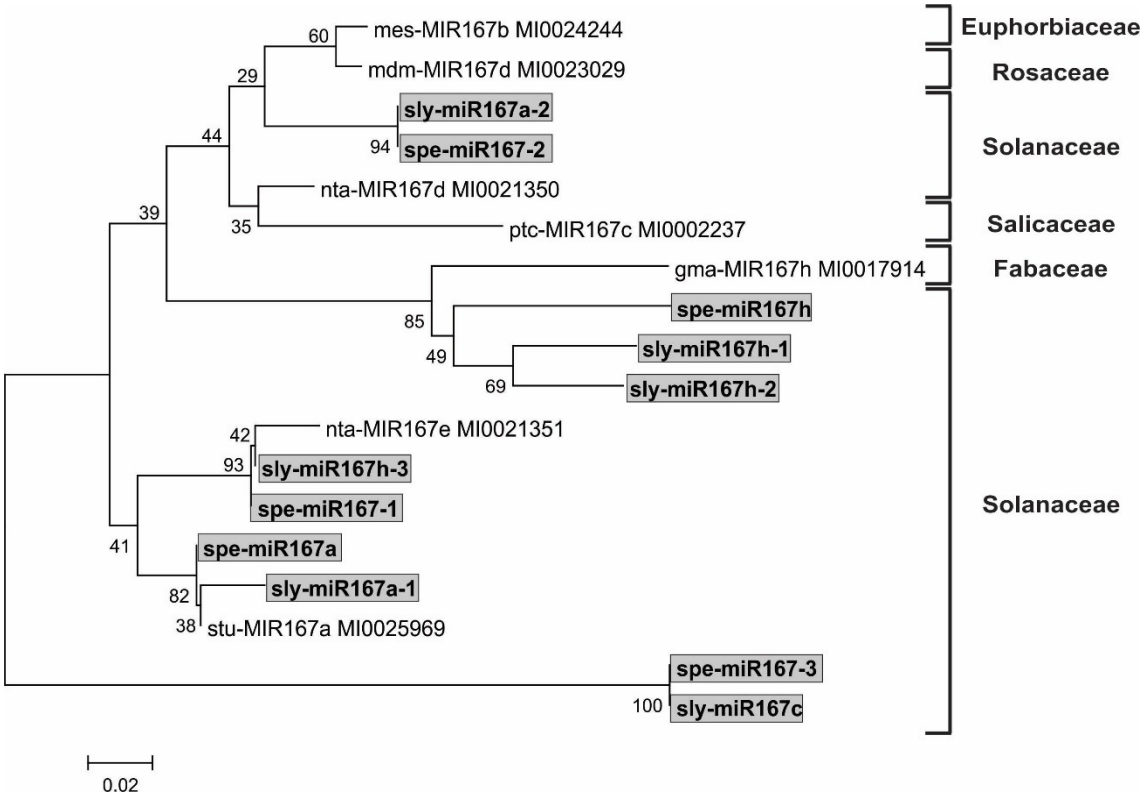
Supplementary Figure S8. (a) The high confidence of RNA alignments between MIR7990 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR7990 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum*.



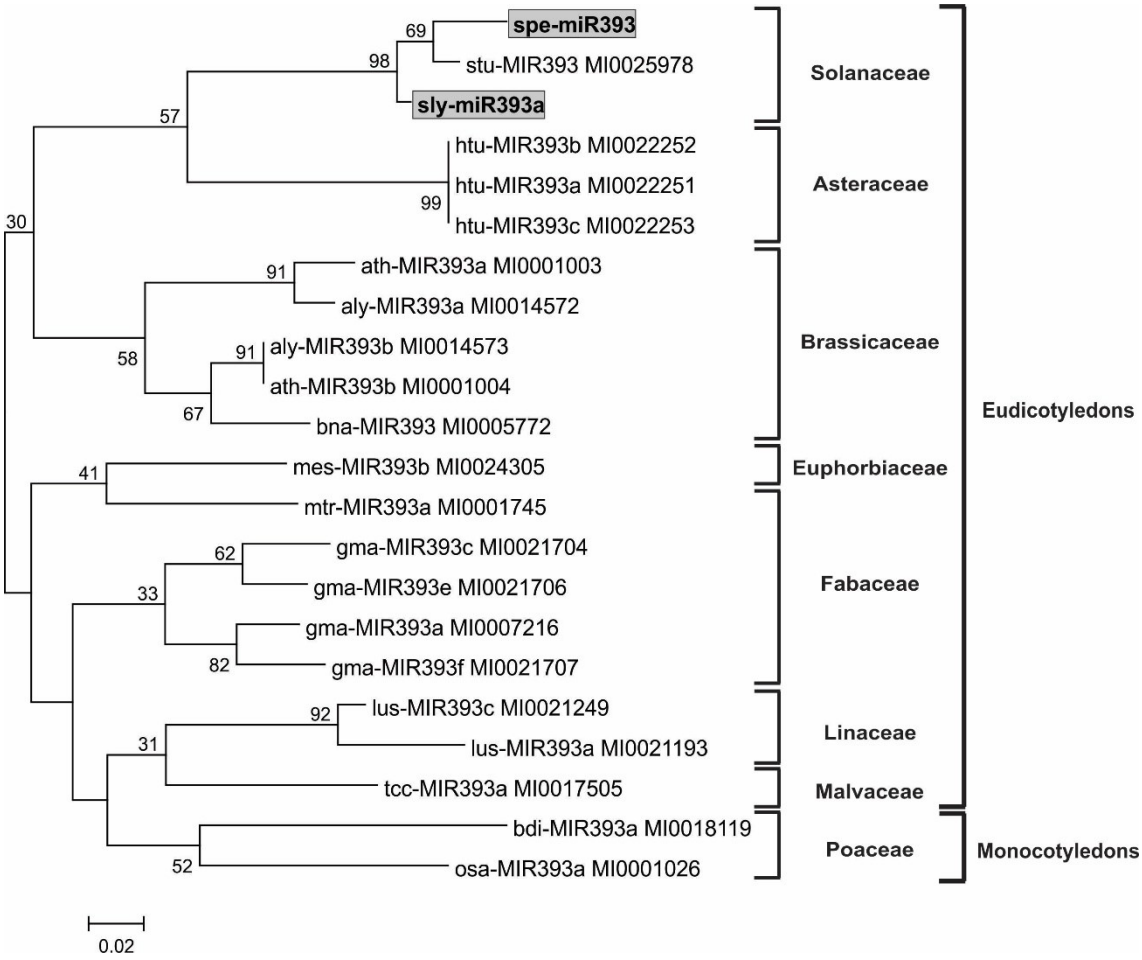
Supplementary Figure S9. (a) The high confidence of RNA alignments between MIR8011 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' and 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR8011 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum*.



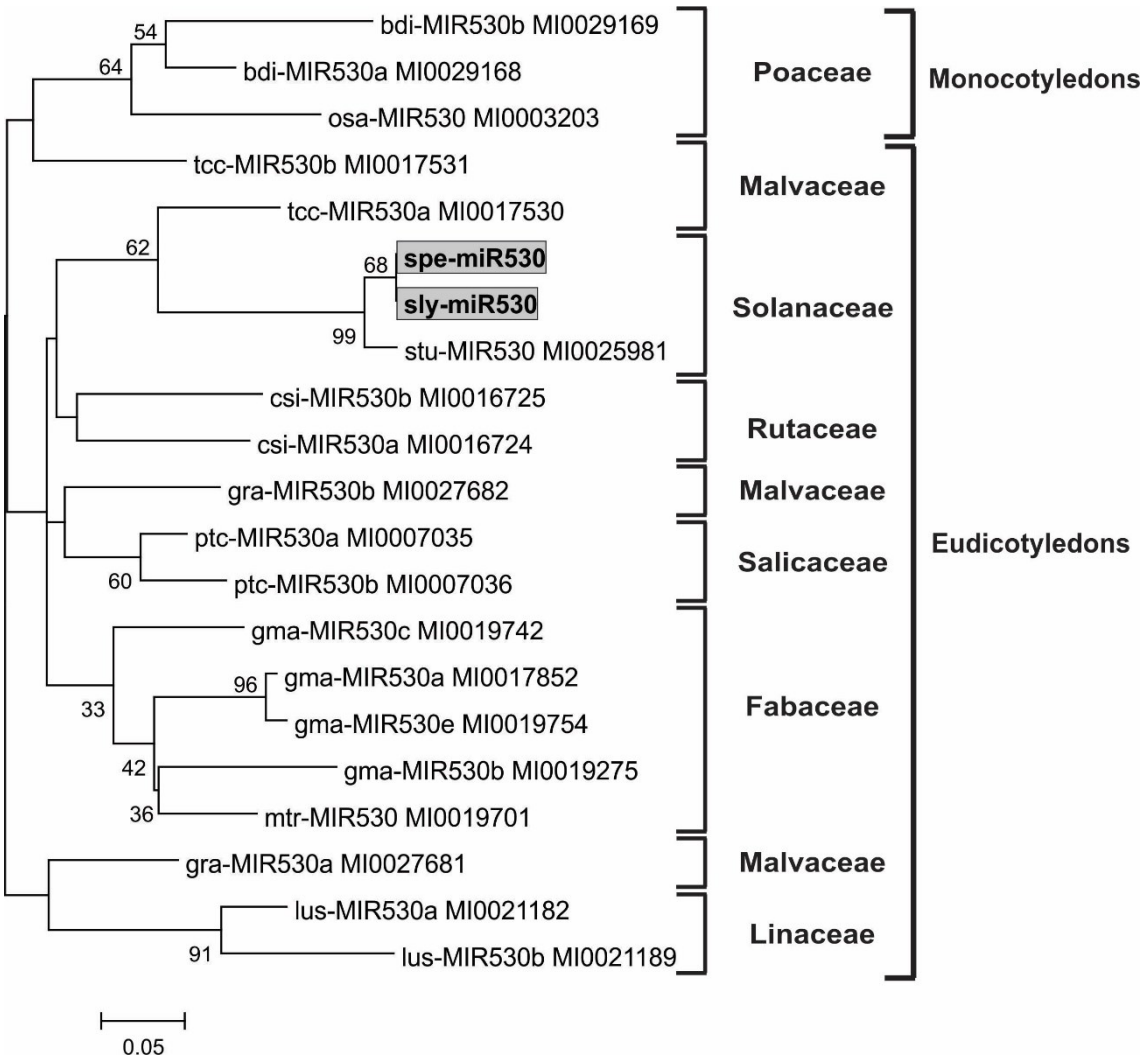
Supplementary Figure S10. (a) The high confidence of RNA alignments between MIR8025 family of *S. lycopersicum* and *S. pennellii* to their orthologs were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colors identify matching residues in 5' and 3' stems of hairpin structures. Level of nucleotide identity is indicated below the alignment. **(b)** Secondary structures of MIR8025 family from *S. lycopersicum, S. pennellii* and their orthologs were draw by RNAfold. Sly - *Solanum lycopersicum,* Spe - *Solanum pennellii,* Stu – *Solanum tuberosum*.



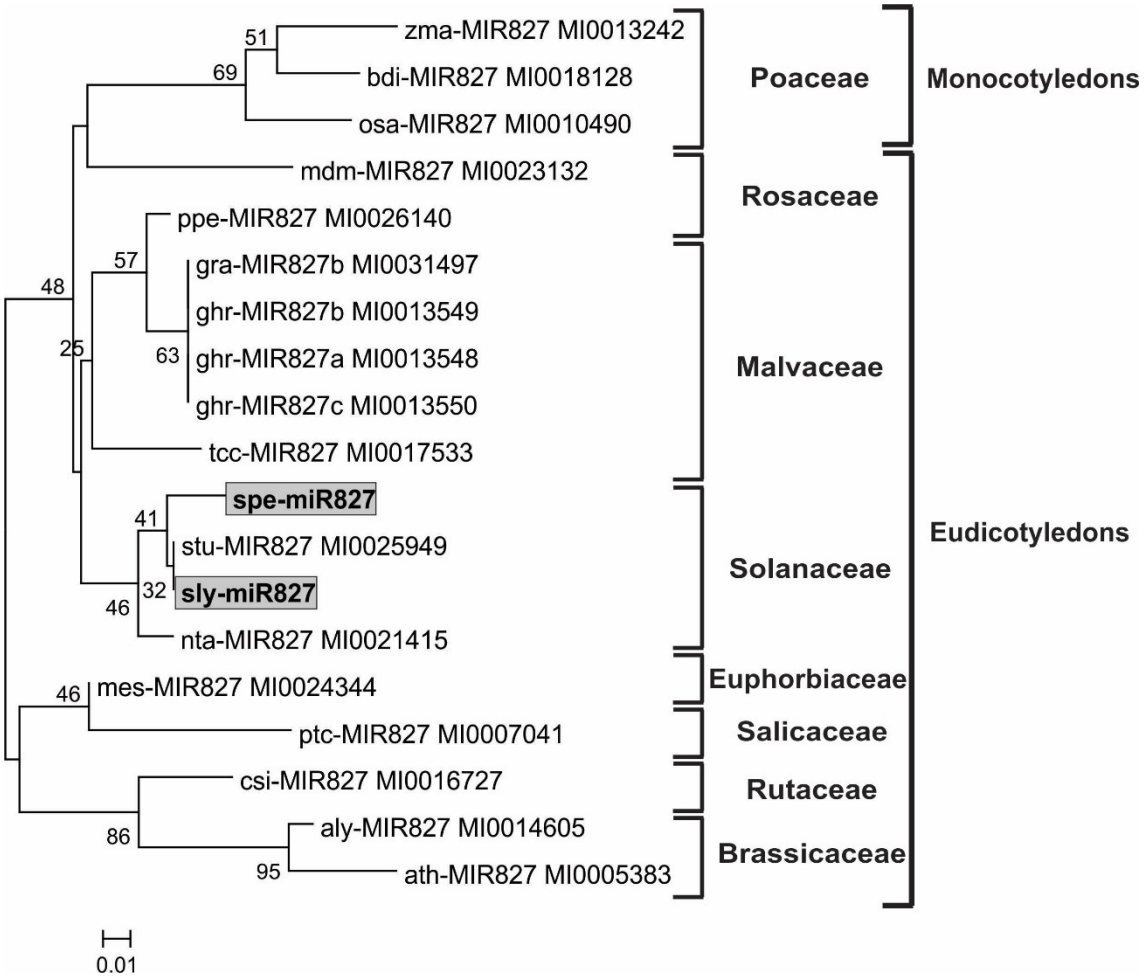
Supplementary Figure S11. Phylogenetic tree of MIR167 family identified in *S. lycopersicum, S. pennellii* and their orthologs.



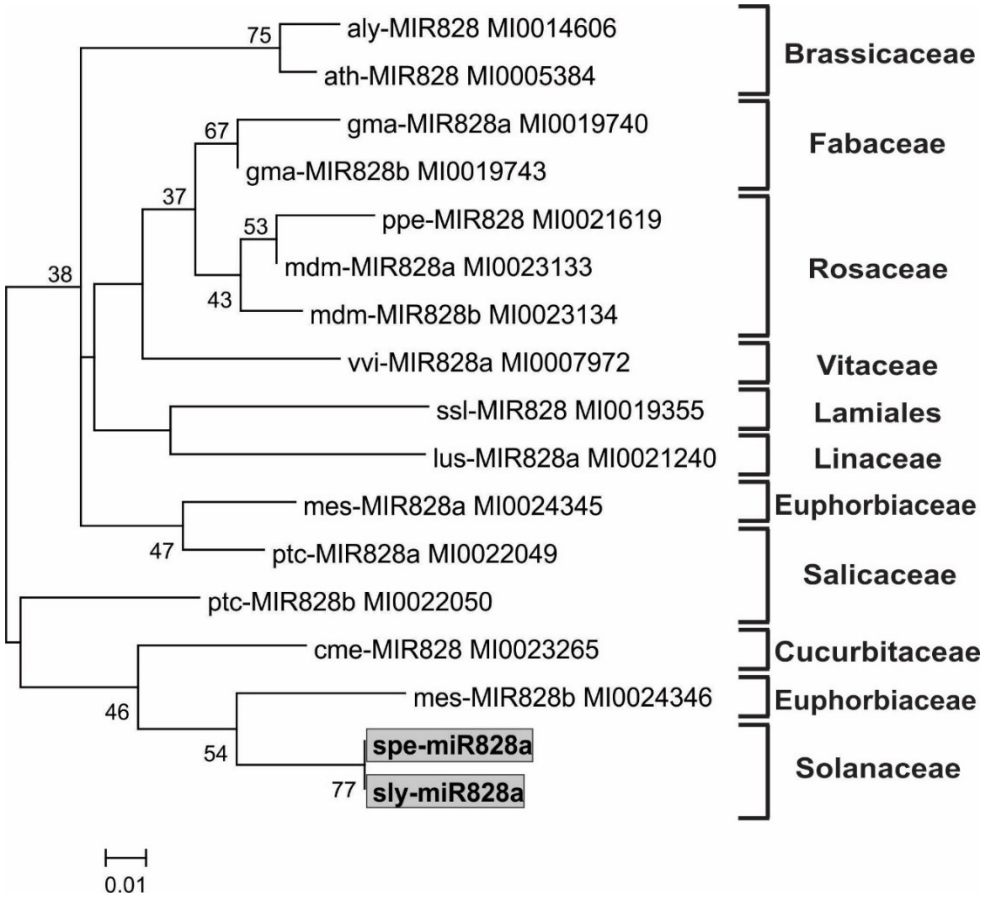
Supplementary Figure S12. Phylogenetic tree of MIR393 family identified in *S. lycopersicum, S. pennellii* and their orthologs.



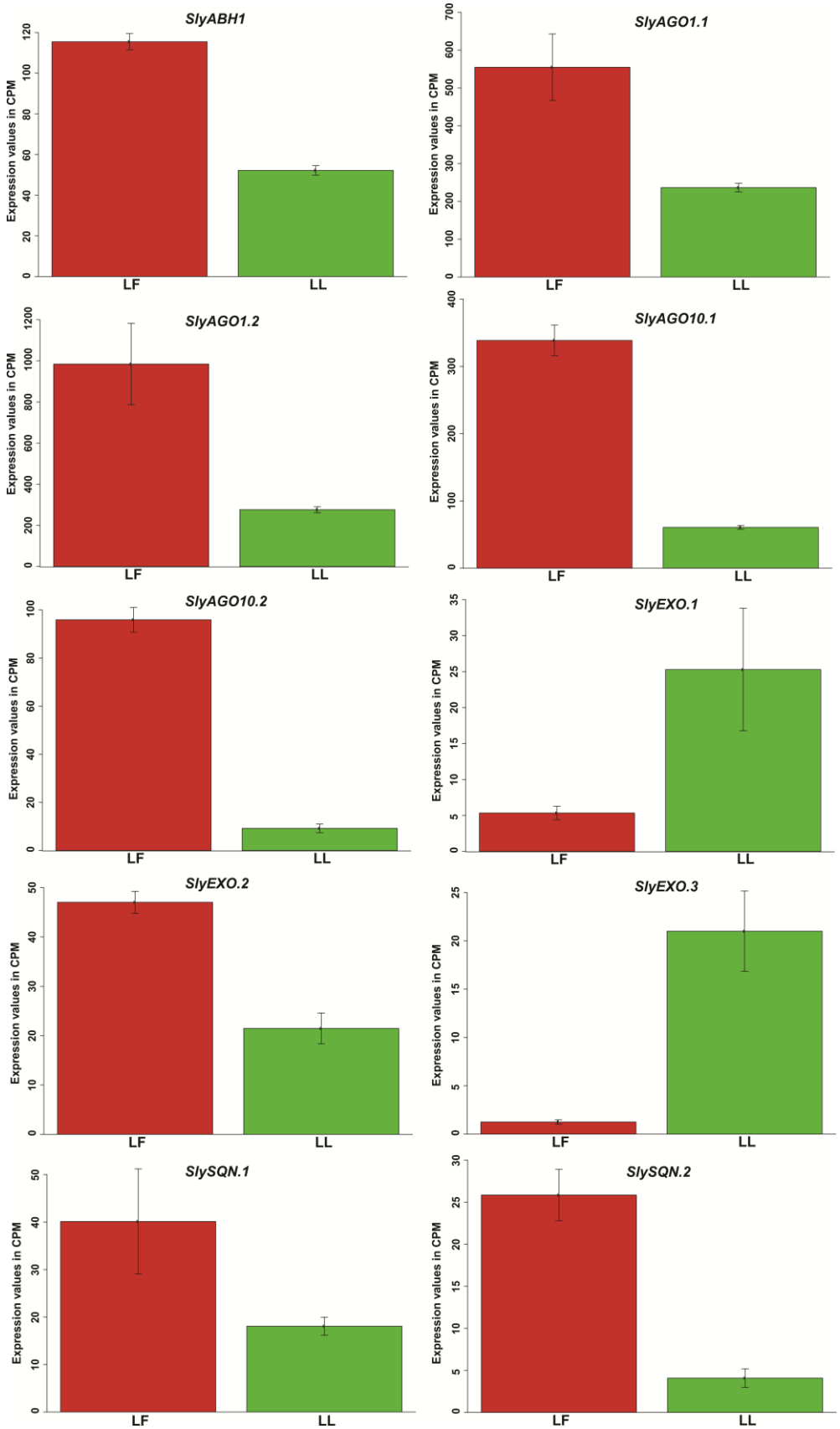
Supplementary Figure S13. Phylogenetic tree of MIR530 family identified in *S. lycopersicum, S. pennellii* and their orthologs.



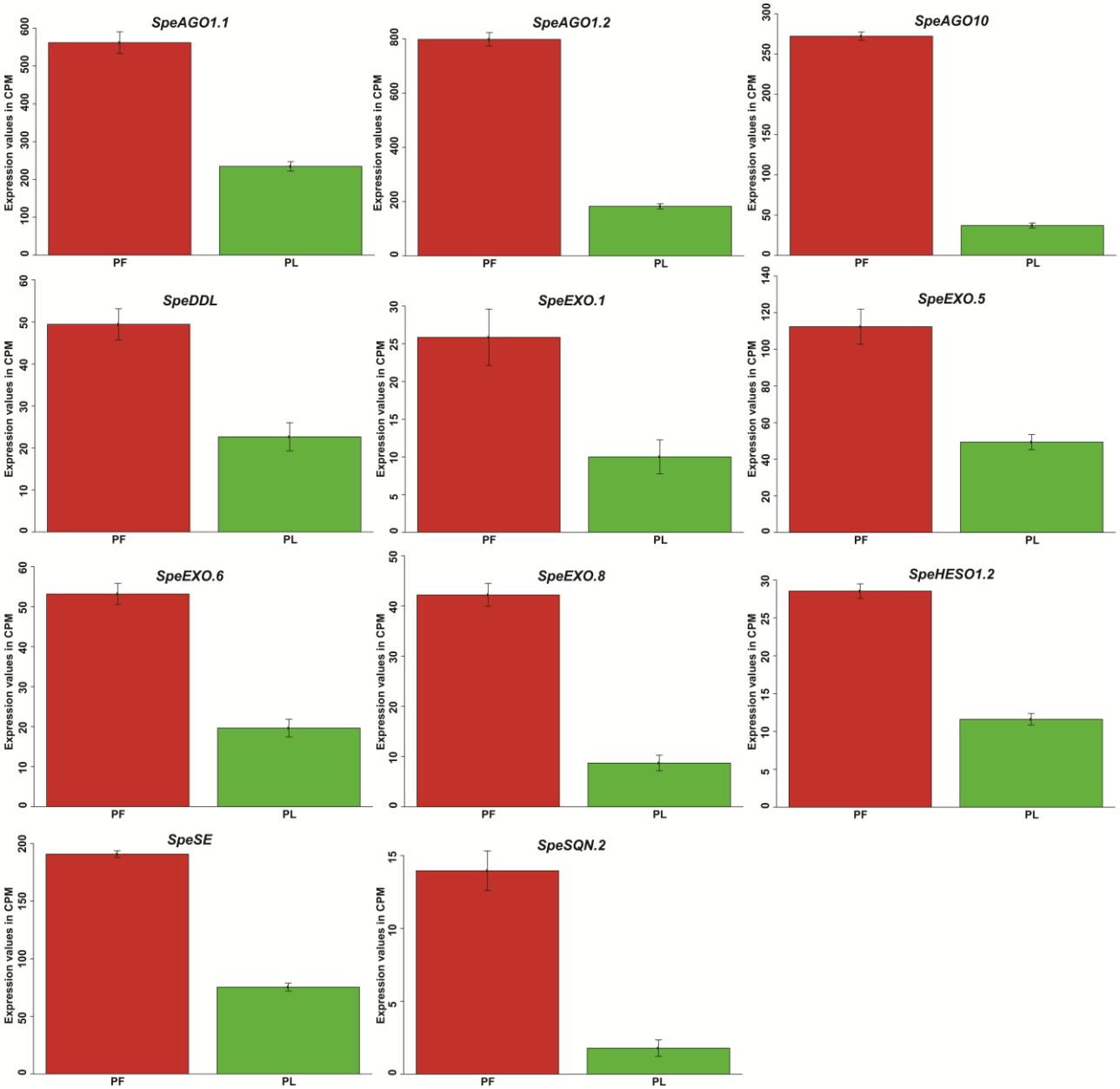
Supplementary Figure S14. Phylogenetic tree of MIR827 family identified in *S. lycopersicum, S. pennellii* and their orthologs.



Supplementary Figure S15. Phylogenetic tree of MIR828 family identified in *S. lycopersicum, S. pennellii* and their orthologs.



Supplementary Figure S16. Differential expression (DE) of the miRNAs pathway genes between *S. lycopersicum* flowers and leaves. LL (*S. lycopersicum* leaves in green), LF (*S. lycopersicum* flowers in red) and CPM (count per million).



Supplementary Figure S17. Differential expression (DE) of the miRNAs pathway genes between *S. pennellii* flowers and leaves. PL (*S. pennellii* leaves in green) and PF (*S. pennellii* flowers in red) and CPM (count per million).

4 CAPÍTULO II – Article: Computational prediction and characterisation of miRNAs and their pathway genes in human schistosomiasis caused by *Schistosoma haematobium* from Memórias do Instituto Oswaldo Cruz Journal

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ABSTRACT

BACKGROUND: Key genes control the infectivity of the *Schistosoma haematobium* causing schistosomiasis. A method for understanding the regulation of these genes might help in developing new strategies to control schistosomiasis, such as the silencing mediated by microRNAs (miRNAs). The miRNAs have been studied in schistosome species and they play important roles in the post-transcriptional regulation of genes, and in parasite-host interactions. However, genome-wide identification and characterization of novel miRNAs and their pathway genes and their gene expression have not been explored deeply in the genome and transcriptome of *S. haematobium.*

OBJECTIVES: Identify and characterize mature and precursor miRNAs and their pathway genes in the *S. haematobium* genome.

METHODS: Computational prediction and characterization of miRNAs and genes involved in miRNA pathway from *S. haematobium* genome on SchistoDB. Conserved domain analysis was performed using PFAM and CDD databases. A robust algorithm was applied to identify mature miRNAs and their precursors. The characterization of the precursor miRNAs was performed using RNAfold, RNAalifold and Perl scripts.

FINDINGS: We identified and characterized 14 putative proteins involved in miRNA pathway including ARGONAUTE and DICER in *S. haematobium*. Besides that, 149 mature miRNAs and 131 precursor miRNAs were identified in the genome including novel miRNAs.

MAIN CONCLUSIONS: miRNA pathway occurs in the *S. haematobium*, including endogenous miRNAs and miRNA pathway components, suggesting a role of this type of non-coding RNAs in gene regulation in the parasite. The results found in this work will open up a new avenue for studying miRNAs in the *S. haematobium* biology in helping to understand the mechanism of gene silencing in the human parasite *Schistosome*.

Key words: Human parasite, small RNAs, Bioinformatics, neglected diseases.

4.1 INTRODUCTION

The human schistosomiasis is a parasitic, chronic and debilitating disease caused by helminths of the *Schistosoma* genus that currently affects about 240 million people worldwide, according to the World Health Organization.[1] The countries of Africa and South America are among the most affected. In addition, 800 million people live in areas at risk of contracting the disease.[2] Five *Schistosoma* species are responsible for most of human infections: *Schistosoma mansoni*, *Schistosoma japonicum*, *S. haematobium*, *Schistosoma mekongi* and *Schistosoma intercalatum*.[1]

S. haematobium affects the reproductive and urinary system and it has been considered a major public health problem mainly in Africa.[1,3] The infection by this parasite can results in nutritional deficiencies and growth retardation, may also lead to a decrease in the cognitive system.[4] The spread of this disease occurs by fresh water and by the presence of host snails. Activities in water contact, such as agriculture, can facilitate the parasite infection.[3]

The dissemination of the disease is dependent of interaction between parasite and intermediate host. In *S. mansoni* and their intermediate host *Biomphalaria glabrata*, the interaction is complex and determined by some genes involved in the parasite infectivity and host susceptibility.[5,6] Thus, it is also suggested a complex host/parasite interation involving several genes between *S. haematobium* and its intermediate snail host, from the genus *Bulinus*. Therefore, understanding the mechanisms of gene regulation is critically important for understanding the host–parasite interactions and which genes might contribute to the infection.

The regulation of gene expression in eukaryotes comprises processes involved in translation repression and/or degradation of target genes.[7] Small RNAs, such as microRNAs (miRNAs), and their silencing pathways have been considered important in several organisms by performing a fine and specific regulation of gene expression maintaining genome integrity.[7,8]

The miRNAs are small non-coding endogenous RNAs with about 22 nucleotides in length of acting post-transcriptionally typically via imperfect complementary base pairing binding to the target genes.[7,9,10] To identify mature

miRNAs and their precursors several studies have been using experimental and computational strategies. The experimental approaches, despite presenting physical evidence of the miRNAs presence, can exclude molecules expressed in certain stages and tissues.[10,11,12] Thus, *in silico* analysis are useful for species with complete or incomplete sequenced genomes, allowing the discovery of new miRNAs using whole-genome DNA information.[11]

The genes involved in gene silencing pathway mediated by miRNAs have been described in several model organisms such as *Drosophila melanogaster*, *Caenorhabditis elegans* and *Homo sapiens*.[13,14] In addition, members of the biosynthetic pathway of miRNAs, such as ARGONAUTE and DICER, as well as miRNA molecules, have been reported in some *Schistosoma* species, including *S. mansoni*, *S. japonicum* and *S. haematobium*.[15]

Young et al., published in 2012 the whole-genome sequence of *S. haematobium*.[16] The interpretation of schistosome draft genomes has improved our understanding of the molecular biology of these parasites allowing the identification and characterization of undiscovered genes. In the face of the vastly increased importance of such non-coding RNAs in the gene expression regulation, it is important that we study mature and precursor miRNAs, as well as the genes involved in miRNA pathway in this *S. haematobium*. This might help to understand the life cycle of this parasite, its infectivity mechanism and for searching new methods of schistosomiasis control. In this work, we identified and characterized the miRNA pathway genes, the mature miRNAs and their precursors in the *S. haematobium* genome. The results found in this work will open up a new avenue for studying miRNAs in the *S. haematobium* biology in helping to understand the mechanism of gene silencing in the human parasite *Schistosome.*

4.2 MATERIALS AND METHODS

4.2.1 Prediction and characterization of genes involved in the miRNAs pathway

Firstly, to search the putative protein sequences involved in the miRNA pathway in *S. haematobium*, BLASTp tool was used (National Center for Biotechnology Information) (http://www.ncbi.nlm.nih.gov/) using as queries

sequence reference proteins from animal species, such as *D. melanogaster* and *C. elegans*, model organisms. The putative protein sequences in *S. haematobium* were found and collected from SchistoDB, *Schistosoma haematobium* Egypt genome (v 44, 2019-06-24) (http://schistodb.net). To improve the annotation of these predicted proteins involved in the miRNA pathway in *S. haematobium*, other gene prediction technique was used. The *Schistosoma haematobium* Egypt genome (v 44, 2019-06-24) was retrieved from the *Schistosoma* Genomic Resource database. To improve gene prediction of the putative genes involved in miRNA pathway in *S. haematobium* genome, single-end reads from a single cDNA library of *S. mansoni* were retrieved from SRA accession SRR629229. After quality control, approximately 63% of 36.836.649 reads were successfully mapped to the *S. haematobium* Egypt genome with STAR (v 2.5.3ab) using the parameter twopassMode.[17] The introns coordinates from this alignment were converted to GFF format to train GeneMark-ET algorithm (v 4.33).[18] In this way 19.686 putative genes were predicted. In addition, GeneMark-ES (v 4.33) was also applied to *S. haematobium* Egypt genome to predict genes without RNA-seq support, 18.622 putative genes were predicted with this approach. To identify the orthologous genes, BLAT (v 35) was applied to search query proteins against the reference genome.[19] The top 10 hits of each query were manually compared against the two sets of predicted genes using the Integrated Genome Browser (v 9.0.0).[20] In addition, Augustus web tool (http://augustus.gobics.de/) was used to improve gene prediction using the genomic locus around the BLAT results, setting the parameters to find similarities with *S. mansoni* genes. The consensus sequences, from the BLAT alignment, and the predicted genes were then aligned to their orthologous using CLUSTALX (v 2.1) (http://www.clustal.org/) and finally subjected to conserved domains searches with PFAM online tool (v 31.0) (http://pfam.xfam.org/).

The characterization and *in silico* validation of the putative protein sequences involved in the miRNA pathway in *S. haematobium* were performed using the position and the presence of the conserved domains and also of the amino acids from active sites using PFAM and Conserved Domains Database (CDD) (http://www.ncbi.nlm.nih.gov/cdd/).

4.2.2 Expression analysis

The transcripts of the genes involved in the miRNA pathway in *S. haematobium* were individually analysed using RNASeq data set, retrieved from NCBI Sequence Read Archive – SRA, of three different developmental stages of *S. haematobium*: adult female (SRR6655495), adult male (SRR6655497) and egg (SRR6655493)[16]. Quality control and adapter removal were conducted using Trimmomatic (v 0.36). Single-end reads were aligned against pre-selected sequences using bowtie2 (v 2.3.0) with the "--very-sensitive-local parameter". Alignment sam files were sorted and converted to bam files with samtools (v 1.6). Expression values were extracted from the alignment results using express (v 1.5.1) and RPKM (Reads Per Kilobase of transcript, per Million mapped reads) were calculated after library size normalization with the Bioconductor package edgeR in the R statistical environment. The results of the expression analysis were plotted in a heatmap, where the color system applied comprises an intense red color as the highest transcript expression and an intense blue color as the lowest transcript expression.

4.2.3 Prediction and characterization of mature miRNAs and their precursors (pre-miRNAs)

A robust algorithm used to predict miRNAs in *S. mansoni* genome[10] was also used for identification and characterization of mature miRNAs and their precursors in *S. haematobium* Egypt genome. The data was applied to Einverted (EMBOSS tool)[21] and BLASTN programs (http://www.ncbi.nlm.nih.gov/) to select sequences that show potential hairpin formation or similarities with precursor miRNAs. These sequences were applied in a set of filters accepting in the end of the algorithm putative real conserved miRNAs. These filters were based on conserved characteristics of precursor miRNAs and regions that have no potential formation of pre-miRNAs were discarded. The filters used were: GC content (guanine and cytosine), Minimal Energy Free (MFE), homology with mature miRNAs already identified, homology with protein coding region, homology to repetitive regions and homology with non-coding RNAs.

The miRNA cluster searching was optimized using information obtained from the position (start and the end position of the precursor miRNAs) each

miRNA identified in the *S. haematobium* Egypt genome. miRNAs found at a distance of less than 10k nucleotides downstream or upstream depending on the direction in the DNA strand were considered linked in a specific miRNA cluster. Each sequence portion was retrieved from the *S. haematobium* Egypt genome using information from the first and last nucleotides of the cluster. The secondary structure of each cluster was obtained using the RNAfold tool (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi).

miRNA sequences identified as putative real conserved miRNA precursors in *S. haematobium* genome were characterized structurally and thermodynamically using RNAfold, RNAalifold (Vienna RNA Package) (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAalifold.cgi) and homemade Perl scripts.[22]

4.2.4 miRNAs in *S. haematobium* Egypt small RNA-seq libraries

Two small RNA data files of adult male (SRR6655496) and adult female worms (SRR6655494) were retrieved from the NCBI Sequence Read Archive (SRA). The library qualities were evaluated using FastQC software.[23] The adapters were removed with Trimmomatic[24] discarding reads with quality score below 20 and length less than 17 nucleotides and longer than 30 nucleotides. The filtered sequences were mapped and quantified using miRDeep2.[25] miRDeep2 and perl scripts were used on each sequence separately to generate the numbers of the reads for each miRNAs identified.

4.2.5 Sequence alignments and phylogenetic analysis

The multiple sequence alignment (MSA) were performed to *S. haematobium* Egypt putative proteins involved in the miRNA pathway and also for the *S. haematobium* Egypt pre-miRNA sequences and their respective orthologs. These analyses were performed by CLUSTALX 2.0 with default parameters multiple sequence alignment of proteins and for the pre-miRNA sequences were used the following adjusted parameters: gap opening 22.50 and gap extension 0.83.

Phylogenetic analysis was performed using MEGA version X[26] and Neighbor-Joining.[27] A consensus tree was generated applying a bootstrap of

5.000 replicates for pre-miRNA sequences and 2.000 replicates for protein sequences. The calculation of their evolutionary distance was performed using Kimura-2-parameters for the pre-miRNA and JTT for protein sequences.[27]

4.2.6 Statistical analysis

For the statistical comparisons among the structural and thermodynamic variables of each category (superphylum, phylum and/or genus), a basic descriptive analysis was performed followed by non-parametric tests (Wilcoxon-Mann-Whitney). Median values were used to perform the statistical comparisons.[28] Statistical significance was set at $p<0.05$.

4.3 RESULTS

4.3.1 Identification, characterization, phylogenetic analysis of putative proteins involved in miRNA pathway

The predicted proteome version 44 of the *S. haematobium* genome obtained from SchistoDB was used to identify and characterize the predicted *S. haematobium* proteins involved in the miRNA pathway. Fourteen putative *S. haematobium* proteins involved in the miRNA pathway were identified and characterized according to their putative function based on homology, conserved domain distribution (and conservation) and protein size. These *S. haematobium* proteins were compared with their miRNA pathway orthologue proteins from related species such as *Schistosoma* species and model species (e.g. *C. elegans* and *D. melanogaster*) (Table 1). In order to confirm and improve the prediction of the proteome version 44 of the *S. haematobium* an alternative predicted genome-based proteome was performed using information from the *S. haematobium* genome and RNAseq sequences (SRR6655495, SRR6655497, SRR6655493). 18.622 putative genes were predicted with this alternative approach to predict the *S. haematobium* proteome. Comparing the proteins involved in the miRNA pathway predicted from *S. haematobium* version 44 to proteins obtained from the alternative predicted proteome only the DROSHA protein sequence was divergent. The putative DROSHA sequence predicted from proteome version 44 - SchistoDB showed 1041 amino acids in length and only one Ribonuclease III conserved

domain. The new prediction of DROSHA showed a protein with two Ribonuclease III and one DSRM conserved domains with 1581 amino acids in length corroborating with their orthologs and thus used for further analysis. Among the fourteen putative *S. haematobium* proteins involved in the miRNA pathway identified, two key protein families of the canonical miRNA biogenesis pathway were considered for the further analysis: ARGONAUTE and RNAse III proteins (DICER and DROSHA). We were able to identify and characterize in *S. haematobium* data and considered for the further analysis two AGO proteins (sht_Ago_MS3_08447/ sht_Ago_MS3_01142), two DICER proteins (sht_Dcr_MS3_05083 and sht_Dcr_MS3_09247) and one DROSHA protein (sht_Drsh_MS3_06910).

4.3.1.1 ARGONAUTE

The putative sht_Ago_MS3_08447 protein displayed only the PIWI and PAZ domains at positions 559-852 and 304-400, respectively. On the other hand, the putative protein sht_Ago_MS3_01142 showed the PAZ, PIWI, ARGOL1, ARGOL2, ARGON and ARGOMID domains. These *S. haematobium* Ago proteins and the distribution of their conserved domains corroborated with their orthologues in *S. mansoni* (Smp) and *S. japonicum* (Sjp)[15] (Figure 1).

The PIWI domain of these proteins showed a catalytic triad formed by DDH (aspartic acid, aspartic acid and histidine). In sht_Ago_MS3_08447, the catalytic triad was found at positions Asp621, Asp711 and His844. In sht_Ago_MS3_01142, the same triad was identified at positions Asp747, Asp819 and His957. Besides that, this triad showed high conservation in relation to ortholog AGO proteins (Figure 2).

The AGO protein family can be divided into two subfamilies, AGO and PIWI. AGO and PIWI orthologous proteins from animal species were used to compare with the putative *S. haematobium* AGO proteins. The organization of the AGO protein family clades in the phylogenetic analysis occurred as expected, in distinct clades, AGO subfamily grouped with AGO orthologous proteins including *S. haematobium* AGO proteins and PIWI subfamily with PIWI orthologous proteins. The distribution of the AGO and PIWI proteins from animal species corroborate with the species distribution in the tree of life (Figure 3). We observed that *S.*

haematobium putative proteins showed a suitable organization compared with their orthologs, in the Plathyhelminthe clade, with *S. haematobium, S. mansoni and S. japonicum* proteins clustering closest within the clade.

4.3.1.2 DICER and DROSHA

Two DICER proteins (sht_Dcr_MS3_05083 and sht_Dcr_MS3_09247) and one DROSHA protein (sht_Drsh_MS3_06910) were identified and characterized. The sht_Dcr_MS3_05083 displayed four domains, while sht_Dcr_MS3_09247 two conserved domains, and sht_Drsh_MS3_06910 three conserved domains. The putative sht_Dcr_MS3_05083 protein identified in the *S. haematobium* Egypt genome presented, in its structure, the conserved domains Dicer Dimer, PAZ, Ribonuclease III (Riboc I), Ribonuclease III (Riboc II), in the positions 896-1005, 1336-1508, 1926-2102, 2212-2474, respectively. The putative sht_Dcr_MS3_09247 presented only the Ribonuclease III (Riboc I) and Ribonuclease III (Riboc II) domains, in the positions 548-659 and 801-889. Finally, the putative sht_Drsh_MS3_06910 showed the Ribonuclease III (Riboc I), Ribonuclease III (Riboc II) and DSRM domains, at positions 941-1002, 1076-1229, 1258-1327, respectively, in its structure (Figure 4).

The two Ribonuclease III conserved domains identified in the putative DICER proteins (sht_Dcr_MS3_05083 and sht_Dcr_MS3_09247), showed an active site high conserved compared to their orthologs. Both domains displayed the conserved active site catalytic motif (EDDE): glutamic acid (E), aspartate (D), aspartate (D) and glutamic acid (E). The domains Riboc I in the sht_Dcr_MS3_05083 presented the catalytic residues conserved, at positions Glu2215, Asp2219, Asp2280 and Glu2283 and in sht_Dcr_MS3_09247 at positions Glu551, Asp555, Asp645 and Glu648. In the putative protein sht_Drs_MS3_06910 the catalytic residues of Riboc I domain showed in the positions Glu944, Asp948, Asp1017 and Glu1020 (Figure 5).

The phylogenetic analysis of DICER and DROSHA putative proteins displayed the evolutionary relationship with their orthologs and paralogues. The *S. haematobium* proteins clustered within Platyhelminthes clade closest to *S. mansoni* and *S. japonicum* DICER and DROSHA proteins. The phylogenetic tree

displayed two distinct clades (DICER and DROSHA clades) corroborating with the literature and the distribution of the species in the tree of life (Figure 6).

4.3.2 Expression Analysis of miRNA pathway transcripts

The genes involved in miRNA pathway identified in the genome data of *S. haematobium* were used to perform the expression analysis. This procedure occurred through submitting these transcripts individually to analyze against RNASeq data set for a library of three different stages of development in *S. haematobium,* adult female (SRR6655495), adult male (SRR6655497) and egg (SRR6655493). The heatmap showed the expression profile of the transcripts in the egg, adult female and adult male stages of the *S. haematobium* (Figure S1). The gene that showed a highest expression level was the VIG (MS3_11239) that showed a more intense red color in the heatmap for the three stages presented. The transcript of FMR1 (MS3_05484) also showed high level of expression in the three stages. The Expo1 transcript (MS3_06671) presented a high expression in egg and adult male, and a medium expression in adult female. The TSNA transcript (ID MS3_07205) presented a high expression in egg and adult female and a medium expression in adult male. The transcripts of the putative ARGONAUTE (sht_Ago_MS3_08447), showed a high level of expression in adult female and egg, and a low expression in the adult male. The others transcripts ARGONAUTE (sht_Ago_MS3_01142), DROSHA (sht_Drsh_MS3_06910) and DICER (sht_Dcr_MS3_05083 and sht_Dcr_MS3_09247), showed a low expression in all stages.

4.3.3 Identification and characterization of precursor and mature miRNAs in *S. haematobium* Egypt genome

We identified in the *S. haematobium* Egypt genome 149 mature miRNAs and 131 pre-miRNAs (Table S1). Regarding the miRNA precursor localization in *S. haematobium* Egypt genome, 98 (73.68%) were found in intergenic regions and 34 (26.32%) intragenic (Table S2). In addition, it was possible identify that 15 pre-miRNAs were organized in clusters (10kb as the maximum distance between two miRNAs genes to consider them clustered), such as sht-miR-71a/sht-miR-2a-1/sht-miR-2b/sht-miR-2e (Figure S2).

All pre-miRNAs identified were analyzed for their structural and thermodynamic characteristics. The *S. haematobium* Egypt pre-miRNAs displayed MFE with an average of -25.3 kcal/mol, with values between -48.5 and -18.5 kcal/mol; AMFE values averaging -27.91 kcal/mol and MFEI with -0.752 kcal/mol (Table S3).

In addition, we performed statistical analyses using thermodynamic and structural characteristics of pre-miRNAs found in *S. haematobium* Egypt compared to pre-miRNAs deposited in the miRBase from Ecdysozoa, Cnidaria, Polifera and Schistosoma clades (Table S4). We compared the miRNA precursor characteristics from genus *Schistosoma* miRNA precursors and no differences were observed among the characteristics analyzed ($p>0.05$). On the other hand, in the analysis performed among *S. haematobium* Egypt against Ecdysozoa, Cnidaria and Porifera phylum, the pre-miRNA characteristics were significantly different ($p<0.05$).

Results obtained using SRA data from male (SRR6655496) and female worms (SRR6655494) evidenced that all mature miRNAs were found in the genome, although some were not expressed in the libraries used for analysis. On the other hand, highly conserved miRNAs such as bantam, miR-2, let-7, miR-71, miR-125, miR-124 and miR-10 showed a greater amount of reads found in SRA data. In addition, some miRNAs were found only in the adult males library, suggesting possible targets for further studies (Table S5).

Of all precursor miRNAs, four families (miR-10, miR-8, miR-2 and miR-7) were selected to further analysis once they showed high conservation based on structural, thermodynamic characteristics and their phylogenetic distribution.

4.3.3.1 sht-miR-10

The sht-miR-10 precursor found in this study, showed two mature miRNAs, sht-miR-10-3p and sht-miR-10-5p. The sht-miR-10 precursor sequence presented a great conservation in the primary and secondary structures when compared to the ortholog sequences used for these analyses, as *S. mansoni, S. japonicum, Apis mellifera* and *D. melanogaster* (Figures 7 and 8).

Three clades were observed in the tree generated by phylogenetic analysis. The first clade was identified as Lophotrochozoa, showing sequences of Mollusca

and Platyhelminthes organisms. The second clade, called Ecdysozoa, was composed by arthropods organism sequences and the third clade presented Echinodermata organisms. This distribution showed similarity to the tree of life, where *S. haematobium* Egypt remained alongside others flatworms (Figure 9).

4.3.3.2 sht-miR-8

One precursor of miR-8 family was identified in the *S. haematobium* Egypt genome, sht-miR-8. Two mature miRNAs from this precursor also were found and named sht-miR-8-3p and sht-miR-8-5p. These sequences presented high conservation in relation to their orthologs in *S. mansoni, S. japonicum, Bombix mori, Heliconius melpomene, Anopheles gambiae, Daphnia pulex, Nasonia vitripennis, Ixodes scapularis* and *Lottia gigantea*, both for analyses of primary structure and secondary structures (Figures S3 and S4).

The phylogenetic analysis generated a tree divided in two clades: Lophotrochozoa and Ecdysozoa. The *S. haematobium* Egypt sequences were found closer to the main orthologs species, *S. japonicum* and *S. mansoni*, in the clade Lophotrochozoa, as well as organisms belonging to the Mollusca phylum. For the Escysozoa clade, the arthropod organisms were the only representative of this group. According to the conservation of the pre-miRNA sequences of these species, this distribution relation is also observed in the animal's tree of life (Figure S5).

4.3.3.3 sht-miR-2

In miR-2 family of *S. haematobium* Egypt were identified five precursor miRNAs (sht-miR-2a-1, sht-miR-2a-2, sht-miR-2b, sht-miR-2c and sht-miR-2e) and nine mature miRNAs: sht-miR-2a-1-3p, sht-miR-2a-1-5p, sht-miR-2a-2-3p, sht-miR-2b-3p, sht-miR-2b-5p, sht-miR-2c-3p, sht-miR-2c-5p, sht-miR-2e-3p and sht-miR-2e-5p.

The *S. haematobium* Egypt miRNAs from this family exhibited high conservation as mature miRNAs when compared with their orthologs in *S. mansoni* and *S. japonicum* (Figure S6). It was possible to observe that there is a great similarity between the secondary structures of the pre-miRNAs within the same family, as well as between *S. haematobium* and *S. mansoni* (Figure S7).

The tree generated from the phylogenetic analysis of miR-2 family showed a distribution into two clades. The clade Lophotrochozoa was composed by the Mollusca, Annelida and Platyhelminthe phylum, while the Ecdysozoa clade presented Arthropod organisms as its representative. Besides that, there was a correct grouping between all precursors sequences of this family (sht-miR-2a-1, sht-miR-2a-2, sht-miR-2b, sht-miR-2c and sht-miR-2e) with their respective orthologs species, mainly *S. mansoni* and *S. japonicum* (Figure S8).

4.3.3.4 sht-miR-7

Two precursor miRNAs of miR-7 family were identified: sht-miR-7 and sht-miR-7b. Besides that, three mature miRNAs also were found (sht-miR-7-5p and sht-miR-7b-5p) in *S. haematobium* Egypt genome. In the primary structure results of miR-7 family were observed a high conservation between the nucleotide sequences of *S. haematobium* miRNAs and their orthologs (Figure S9). The analysis performed for pre-miRNA secondary structures of miR-7 family also evidenced a great conservation between the *S. haematobium* miRNAs and their orthologous organisms (Figure S10).

Three well defined clades were observed in the phylogenetic analysis performed for sht-miR-7 family: the Deuterostome group and the Lophotrochozoa and Ecdysozoa clades formed the Protostome group. The first group was composed of Chordata and Hemichordata phylum, while the second group had the presence of flatworms and arthropod organisms. The species classification showed by this analysis corroborates with the distribution found in the animal tree of life (Figure S11).

4.4 DISCUSSION

The first version of *S. haematobium* genome published by Young et al. (2012) provided the conditions to researchers to study the genome and we were able to apply this robust analysis to identify and characterize miRNAs, and the putative proteins involved in miRNA processing pathway in the genome of this human parasite.[16] The miRNAs and proteins of their biosynthetic pathway were described in several organisms, including plants and animals. In animals, in the

model organisms *D. melanogaster* and *C. elegans,* were found mature and precursor miRNAs, pathway proteins and miRNA target genes.[29, 30] In addition, in species from *Schistosoma* genus*,* such as *S. mansoni* and *S. japonicum,* also were identified these regulatory molecules [10, 31, 32], showing that there have been an evolutionary conservation of these molecules.

Stroehlein et al. (2018) described mature and precursor miRNAs in *S. haematobium* genome data, however, they did not mention the identification, characterization and expression of the miRNA pathway genes in the organism under study, as observed in our results. In addition, we were able to identify conserved and novel miRNAs, being 149 mature miRNAs and 131 miRNA precursors. Stroehlein and colleagues found 36 conserved miRNAs and 53 new miRNAs, while we identified 41 conserved miRNAs in the *Schistosoma* genus and 108 conserved miRNAs in others animal species. Of all mature miRNAs identified in both studies, only 25 mature miRNAs were found in both studies. 124 novel conserved mature miRNAs were found in this study comparing to Stroehlein and colleagues (2018) work. We also have validated the presence of the mature *S. haematobium* miRNAs using public smallRNA-seq libraries of male and female *S. haematobium* parasites.[32]

In miRNA processing and maturation, the proteins ARGONAUTE, DICER and DROSHA play a several key roles. In the nucleus, DROSHA complex protein is responsible for the first step in this pathway. The pri-miRNA is the product of the transcription characterized mainly by the formation of a stem-loop. This structure is targeted by DROSHA complex, that acting by the cleavage generate the pre-miRNAs.[33] Protein DICER cleaves the pre-miRNAs removing the loop from the structure forming a miRNA duplex. In the RISC complex, DICER protein guides the miRNA duplex to ARGONAUTE proteins which one of the mature miRNA in the duplex target the target gene. A lot of others proteins are part of the RISC complex such as Fmr1, Tsn, VIG, among others.[34]

The family of ARGONAUTE proteins has two important subfamilies, AGO and PIWI. Both subfamilies play important roles in noncoding RNA pathways, being the AGO proteins the main protein of the RISC complex in the microRNA and small interfering RNA (siRNA) pathways, while PIWI proteins is responsible for specific RISC complex in PIWI-interecting RNAs (piRNA) pathway.[35] This both

ARGONAUTE subfamilies have shown two highly conserved domains, PIWI and PAZ domains. The PAZ domain has been presented at the N-terminal of the protein, while the C-terminal region has been composed by PIWI domain. The positions of theses domains are strategic, since they have the ability to position the small RNA in its target gene.[36, 37] The PIWI domain, in particular, has a catalytic site responsible for cleaving target messenger RNA (mRNA) of the miRNA. This active site has been composed by three amino acid residues: DDH (aspartate, aspartate and histidine) or DDD (three aspartates).[36]

All of these aspects in our analysis had a great importance. The putative ARGONAUTE genes found in *S. haematobium* Egypt showed the conserved domains, PAZ and PIWI. The phylogenetic tree showed two distinct clades. One clade showed only AGO orthologue proteins including sht_Ago_MS3_08447 and sht_Ago_MS3_0114 suggesting that these sequences are ARGONAUTE proteins. Furthermore, the catalytic site was identified in the PIWI domain of the *S. haematobium* Egypt ARGONAUTE proteins (DDH) corroborating with PIWI domain catalytic site reported by the literature. These proteins are considered one of the most important proteins involved in the miRNAs pathway, because they are catalytic component of RISC complex and help in the high silencing capacity of the miRNAs.[38, 39]

All conserved domains described for the DICER and DROSHA proteins were found in the analyses of this work, where DROSHA showed the same conserved domains reported by others studies and DICER presented, besides the mentioned domains for this protein, one Dicer Dimer domain. It is important to emphasize that this analysis was possible once we used the new gene prediction beyond the predicted proteome from SchistoDB. We were able to improve the prediction of putative protein *S. haematobium* DROSHA. The presence of these domains found in *S. haematobium* Egypt DICER and DROSHA confirm that these proteins are ortholog of DICER and DROSHA. The DICER protein contains three main conserved domains, one PAZ domain and two domains called RNase III.[15, 39] In *S. mansoni,* in the sequences identified as DROSHA, were found three conserved domains: two RNase III and one DSRM domain.[15]

In addition, the analyses performed to identify the active site of two RNase III domains of DICER showed the distribution of following amino acids: glutamic

acid (E), aspartate (D), aspartate (D) and glutamic acid (E), forming the site EDDE also present in *S. mansoni*.[15] These findings found in DICER, DROSHA and AGO-like proteins of *S. haematobium* corroborate with the literature in domain distribution, conservation of active site and phylogenetic distribution confirming Thais prediction within *S. haematobium* data.

In the expression analysis using RNAseq data – SRR6655495, SRR6655497, SRR6655493 – the *S. haematobium* transcripts of ARGONAUTE, DROSHA and DICER showed in general low expression level in all three stages of development analyzed. The highest expression way round for the VIG gene explained by the importance of this gene not only in the RISC complex of miRNA pathway but also in other mechanisms in the parasite such as the formation and maintenance of heterochromatin.[40]

24 mature miRNA sequences identified corroborated with Stroehlein et al. (2018) study such as bantam, let-7, miR-124 and others. Some studies involving *S. japonicum* were performed to identify miRNAs based on computational and experimental analysis. Xue et al. (2008) described 5 novel miRNAs while Huang et al. (2009) found 176 mature miRNAs using computational analyses.[41] In *S. mansoni* 67 mature miRNAs and 42 precursor miRNAs were identified by Gomes et al. (2011) and 11 mature miRNAs were confirmed by experimental analyses by Simões et al. (2011).[42] A comparison between *S. mansoni* and *S. haematobium* Egypt data showed that among the conserved miRNAs found in *S. mansoni*, only five of them were not identified in *S. haematobium* Egypt genome data in our study.

Most of the miRNA precursor genes was found in the intergenic regions of the *S. haematobium* Egypt genome (Table S2) corroborating with most animal species. We found 15 miRNAs in clusters. MiRNAs distributed in clusters has also been showed in other organisms such as in *S. japonicum*, *S. mansoni* and *B. glabrata.*[10, 41, 43, 44, 45] The miRNA cluster gene mir-71/2a-1/2b/2e found in this work (Figure S2) has been reported in other organisms such as *S. mansoni*.[10] The miRNA antiparallel clusters had been also occasionally found in other animals genomes deposited in miRBase version 22 (http://www.mirbase.org/), such as smp-miR-124b and smp-miR-124a from *S. mansoni*, mmu-miR-124-2 and mmu-

miR-124b from *Mus musculus*, and oni-miR-124a-3 and oni-miR-124b-1 from *Oreochromis niloticus,* corroborating to our results (Table S2).

The pre-miRNAs sequences of *S. haematobium* Egypt displayed a Minimal Energy Free (MFE) with a mean of -25.3 kcal/mol, with values between -48.5 and -18.5 kcal/mol, and, considering the structural and thermodynamic characteristics already reported for miRNAs, a precursor miRNA molecule is stable and can generate mature miRNA having a value of the MFE of -20 kcal/mol. Besides that, this data corroborating with the values found in others animals studies, beyond corresponding to the values used for the orthologs *S. mansoni* and *S. japonicum*.[10, 42] The pre-miRNA size (~70nt) of *S. haematobium* miRNAs corroborated to orthologous size, indicate a high probability that these sequences are real pre-miRNA sequences.

In addition, the guanine-cytosine (GC) content found in the results of this work showed a distribution between 21.28% and 45.94% of GC content, but the majority of the sequences presented a percentage greater than 25%. This is one of the main parameters for pre-miRNAs identification and the presence of these nucleotides is very important for the stability of pre-miRNA secondary structure. In animals, evaluation value of this parameter should be found between 20% and 55%. As showed, the results indicated that the sequences analysed satisfy the requirements to be considered miRNA precursors. Previous works have shown how important has been the use of these structural and thermodynamic characteristics for conserved miRNA elucidation and prediction in the genome.[10]

The statistical analyses using thermodynamic and structural characteristics of the *S. haematobium* Egypt pre-miRNAs, when comparing the genus *Schistosoma* showed no differences between the groups ($p>0.05$). Both displayed high conservation and similarity among pre-miRNAs from *S. haematobium* Egypt and species belonging to the genus *Schistosoma*. However, the results for *S. haematobium* Egypt were significantly different from results for other clades such as Ecdysozoa*,* Cnidaria and Porifera ($p<0.05$), suggesting an evolutionary conservation of the pre-miRNA characteristics within each animals clade (superphylum, phylum or genus) and a significant difference among different clades (Table S4). The studies based on specific characteristics of mature and

precursor miRNAs have been used in sequence groups in different species, from Protista to Metazoa and Plantae.[11, 46, 47, 48]

Our analyses using the libraries of small RNAs from male and female adult worms showed a validation of all 149 mature miRNAs found in the genome of *S. haematobium* Egypt (Table S5). Some conserved miRNAs such as bantam-3p, let-7-3p, miR-124-3p and miR-10-5p demonstrated a large number of reads in two libraries studied, corroborating with the results found in a previously published study[32], however, our findings refer to mature miRNAs. Other miRNAs have also identified in both studies, such as the miRNAs of the miR-2, miR-7 and miR-8 families demonstrating the importance of these molecules in both libraries, female and male adult worms.[32]

The miR-10 was found in *S. haematobium* Egypt genome containing two mature miRNAs (sht-miR-10-5p and sht-miR-10-3p), corroborating with results observed in studies with *D. melanogaster* and *S. japonicum.*[43, 49] Besides that, when compared to the pre-miR-10 sequences of *S. mansoni*, *S. haematobium* Egypt and *S. japonicum* had 100% identity in the region of their two mature miRNAs (Figure 7). Many different animal species have shown this miRNA and its presence in the HOX cluster, composed by miR-10 and HOX genes. This relationship was observed in organisms such as *S. mansoni, A. gambiae*, *Tribolium castaneum,* zebrafish and human.[10, 50] On the other hand, miR-10 was one of five miRNAs considered pathogen-specific found in rabbits infected with *S. japonicum*, which may offer a new biomarker to diagnose schistosomiasis.[51]

The results miR-8 precursor shown two mature miRNAs. Besides that, in *S. haematobium* a high conservation was observed among the species belonging to Lophotrochozoa and Ecdysozoa clades, being considered a Protostome-specific miRNA, corroborating with *S. mansoni* data.[52] This miRNA was found in several organisms, including the model organism *Drosophila* sp. that was also identified by computational analyses.[49] In another study, miR-8 was identified in two mosquito's vector: *Aedes albopictus* and *Culex quinquefasciatus*.[53] In *S. japonicum,* miR-8 also was identified and presented a greater expression in mature adult worms, but was observed with some nucleotide substitutions considered specific for *Schistosoma* sp.[43] MiR-8-3p was found 11 times more reads in the male library compared to the amount of reads found in the female

library which were 104 reads. For mature miRNA miR-8-5p, none read was found in the male library and in the female library.

The miR-2 family showed five precursors and ten mature miRNA in *S. haematobium* data. This family is specific of protostome organisms, since in the phylogenetic tree were found only organisms from Ecdysozoa and Lophotrochozoa clades, corroborating with the results shown by Gomes et al. (2013). Besides that, miR-2 family has considered one of the larger miRNA family found in *D. melanogaster* presenting eight miRNAs in the genome.[54] On the other hand, in *C. elegans*, another model organism, there is only one sequence of this family.[55] In *S. mansoni*, nine members belonging to the miR-2 family were identified and some were in the cluster with miR-71.[10] This cluster is located on a sexual chromosome in the parasite and therefore, may play a role in their sexual maturation.[44]

The sequences of miR-7 family corroborated with miRNAs found in *S. mansoni*. In addition, the secondary structures performed for miR-7b, in both studies, show a high conservation of these sequences.[52] This family is one of the most conserved miRNA families and was found in all Bilateria, including flatworms, nematodes, insects and vertebrates.[56] In *S. japonicum*, miR-7 was more expressed in male worms than in females; on the other hand, this miRNA is expressed in a specific stage of parasite life, mainly in cercariae stage. Data involving the validation of these miRNAs showed that in the small RNA library of adult male there were more reads of miR-7 compared to adult female library. The mature miRNA miR-7-5p demonstrates 25 times more reads in males library compared to females library. The miR-7 is related with different cellular processes. In *Drosophila* sp., it was reported its involvement in the formation of photoreceptor organs[57] and in a study with rat pancreas was observed that miR-7 is the miRNA most abundant in this cell type, confirming the performance flexibility of this miRNA.[58]

According to the results obtained in this work, through bioinformatics and computational analyses we were able to identify 14 key proteins involved in small RNA processing pathway. Our results showed that the miRNA pathway genes were transcriptionally active. In addition, we identified 149 mature miRNAs and 131 pre-miRNAs in the genome of this species, being highly conserved in their

sequences, corroborating with others studies involving *S. mansoni* and *S. japonicum*. The results found in this work will open up a new avenue for studying the miRNAs in the *Schistosome* biology and technologies involving the gene silencing control in this organism. In addition, will allow understanding many processes and mechanisms in their biology, since these molecules present a significant regulatory role for different mRNAs, affecting various characteristics of the organism in different stages and environmental conditions.

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AUTHOR'S CONTRIBUTION

M.S.G., T.C.S.C., C.B.A., L.G.P. and L.G.A.M. proposed the research. M.S.G., T.C.S.C., C.B.A., L.G.P. and L.G.A.M. designed the experiments. T.C.S.C., C.B.A., L.G.P., L.G.A.M., T.C.A. and L.R.A. prepared samples. T.C.S.C., C.B.A., L.G.P., T.C.A., G.C.S., T.H.C.R., P.E.G. and L.R.A. performed experiments. T.C.S.C., C.B.A., L.G.P. and E.R.M., wrote manuscripts and prepared figures. M.S.G. supervised the project. All authors reviewed the manuscript.

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COMPETING INTERESTS

We declare that there is no conflict of interest, whether financial or non-financial origin, involved in the publication of this article. The data present in this article have not been published and are not under consideration elsewhere, moreover we approved the submission of the manuscript.

TABLES

Table 1. Putative proteins involved in miRNA pathway identified in *Schistosoma haematobium* data compared with their orthologs from *Schistosoma mansoni* and *Schistosoma japonicum*.

ID protein *S. haematobium*	Putative name	Length (aa)	ID protein *S. mansoni*	E-value	Length (aa)	ID protein *S. japonicum*	E-value	Length (aa)
MS3_01142	Sht_Argonaute	1009	Smp_198380.1	0.0	928	Sjp_0044720	0.0	987
			Smp_102690.1	4 e^{-105}	783	Sjp_0103990	2 e^{-106}	904
			Smp_179320.2	1 e^{-118}	921	Sjp_0045200	2 e^{-115}	924
MS3_08447	Sht_Argonaute	882	Smp_198380.1	5 e^{-101}	928	Sjp_0044720	7 e^{-101}	987
			Smp_102690.1	0.0	783	Sjp_0103990	0.0	904
			Smp_179320.2	0.0	921	Sjp_0045200	0.0	924
MS3_06910	Sht_Drosha	1581	Smp_142510.1	0.0	1531	Sjp_0048900.1	0.0	1611
MS3_05083	Sht_Dicer	929	Smp_169750.2	0.0	2485	Sjp_0069770	4.2 e^{-129}	2480
			XP_018644375.1	0.0	2319	-	-	-
MS3_09247	Sht_Dicer	2588	Smp_033600	5 e^{-17}	954	Sjp_0043700	2e^{-17}	923
MS3_10205	Sht_Exportin 5	611	Smp_137650	0.0	1164	Sjp_0006510	0.0	695
MS3_11315	Sht_TSN	1162	Smp_246840	8.4 e^{-116}	992	Sjp_0048060	5 e^{-165}	1428
MS3_03052	Sht_Logs	284	Smp_023670	0.0	356	Sjp_0045700	6 e^{-178}	369
MS3_05484	Sht_FRX1	339	Smp_099630	0.0	598	Sjp_0017160	0.0	598
MS3_06671	Sht_Exportin-1	1031	Smp_124820	0.0	828	Sjp_0069890	0.0	1128
MS3_07205	Sht_TSN-a	718	Smp_166110	8 e^{-82}	378	Sjp_0100020	0.0	971
MS3_08368	Sht_DGCR8	298	Smp_087220	0.0	760	Sjp_0013270	0.0	760
MS3_10949	Sht_PASHA	395	Smp_087220	0.0	760	Sjp_0013270	2 e^{-129}	760
MS3_11239	Sht_VIG	237	Smp_009310	2 e^{-121}	417	Sjp_0074950	5 e^{-97}	414

FIGURES

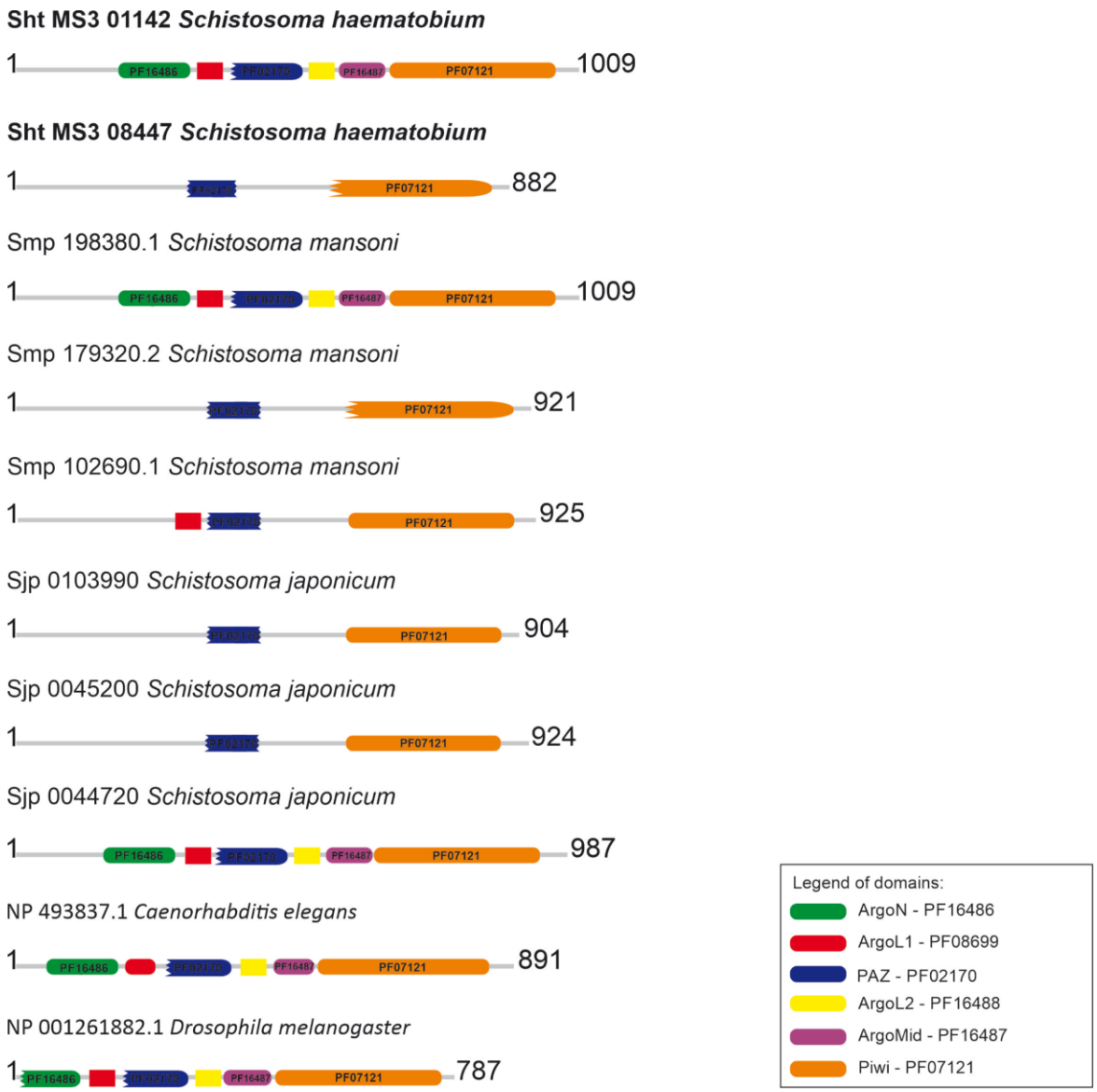


Figure 1. Conserved domains found in AGO proteins of *S. haematobium* Egypt versus their orthologous from *S. mansoni* and *S. japonicum*, and model organisms *C. elegans* and *D. melanogaster*.

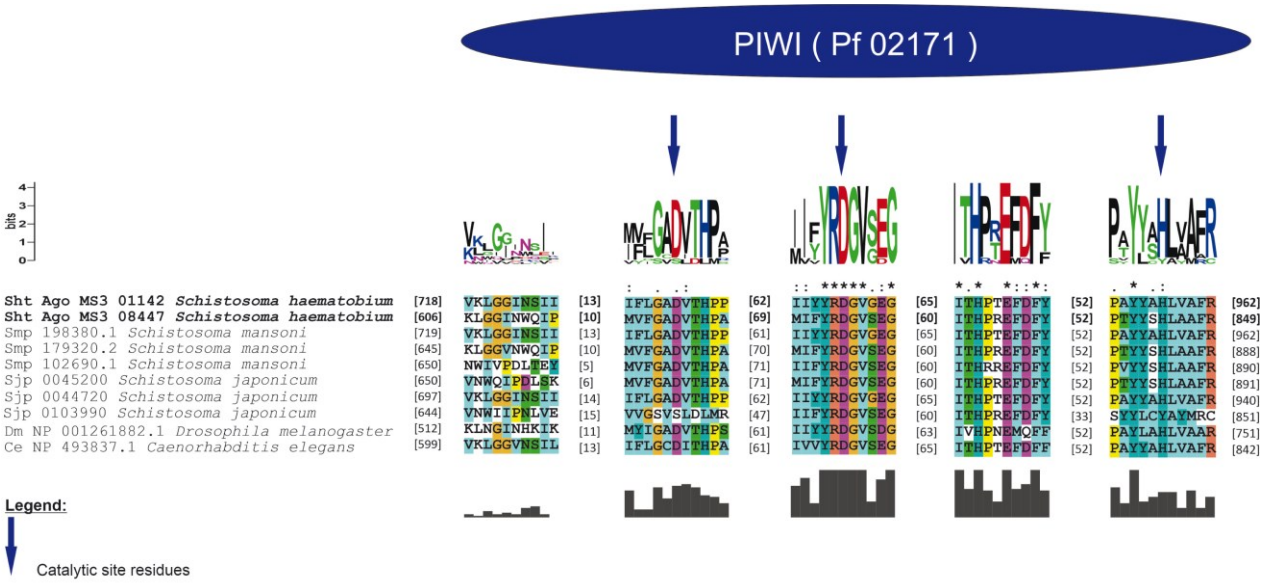


Figure 2. Analysis of PIWI conserved domain of *S. haematobium* AGO proteins.

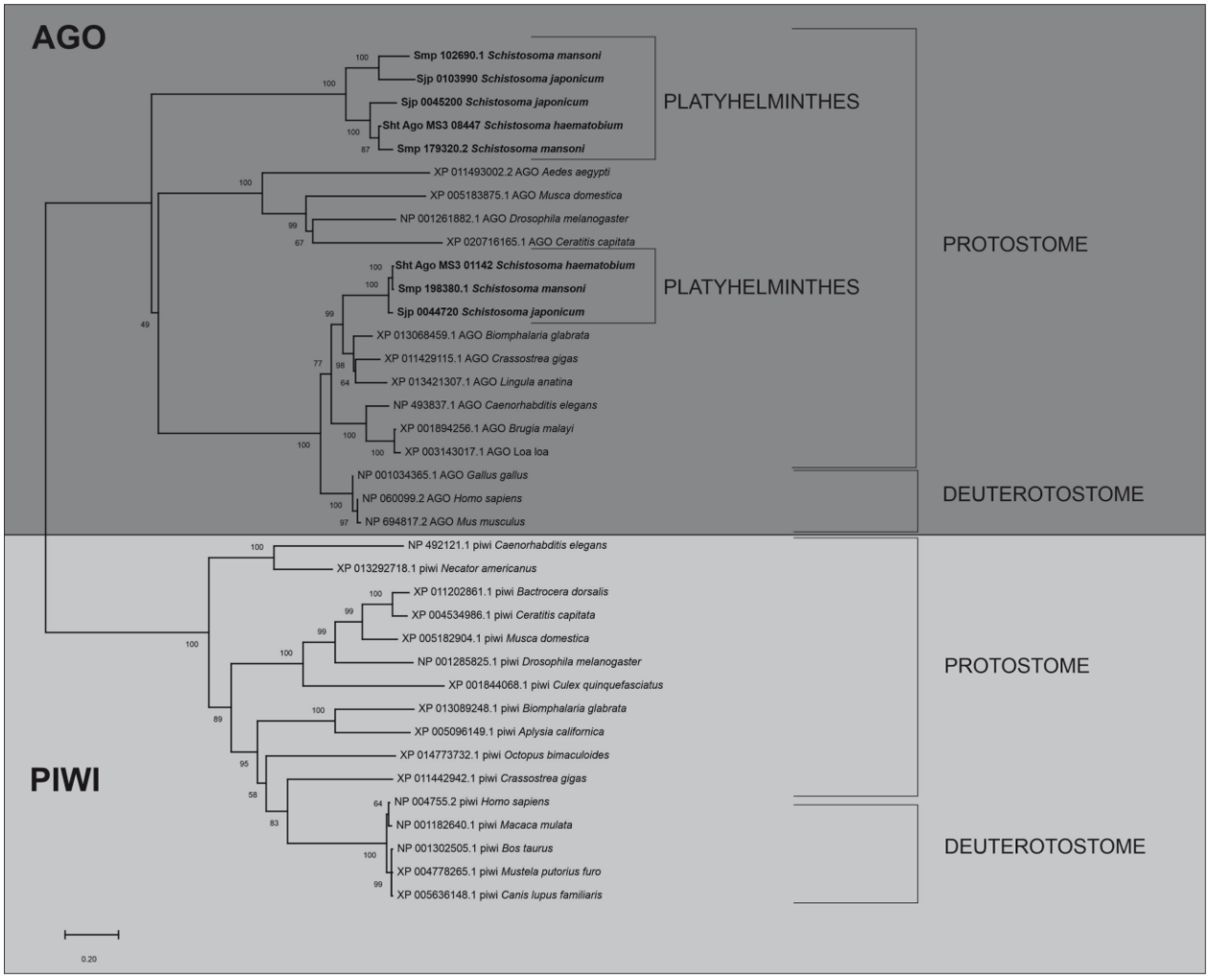


Figure 3. Phylogenetic analysis of *S. haematobium* AGO proteins and their orthologous.

Figure 4. Conserved domains of *S. haematobium* DICER/DROSHA proteins and their orthologous from *S. mansoni* and *S. japonicum*, and model organisms *C. elegans* and *D. melanogaster.*

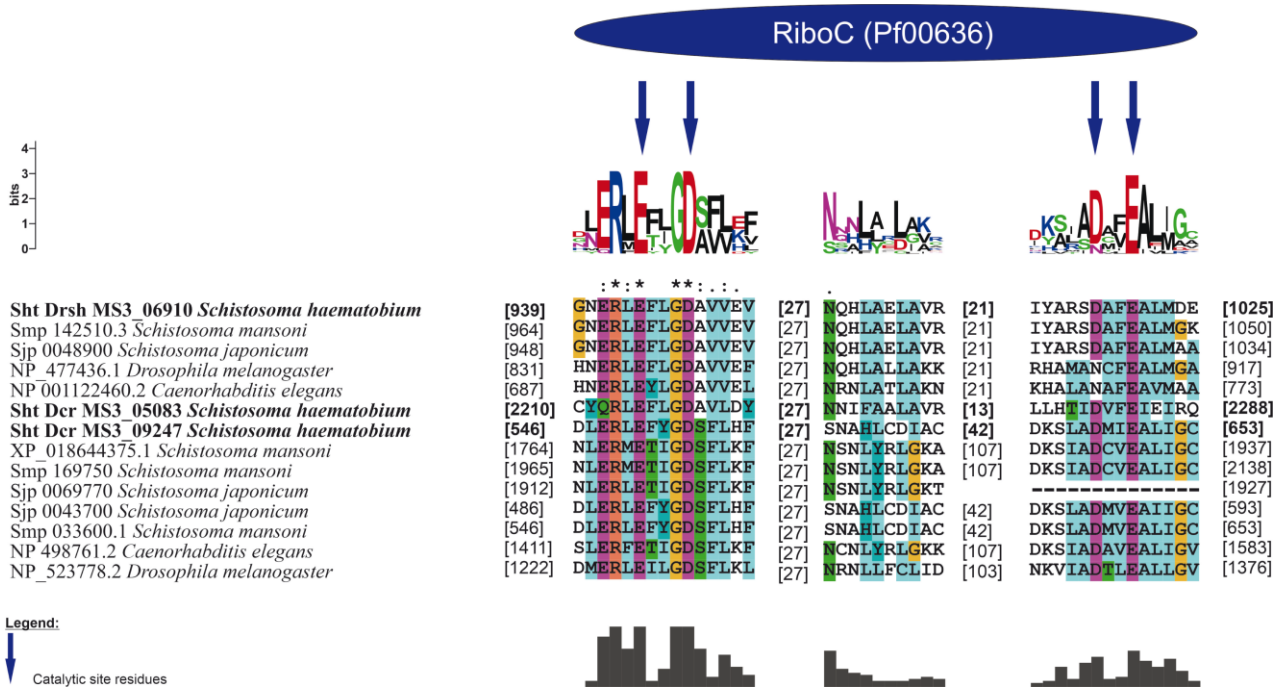


Figure 5. Analysis of Ribonuclease III (Riboc I and II) conserved domains of *S. haematobium* DICER and *S. haematobium* DROSHA proteins and their orthologous.

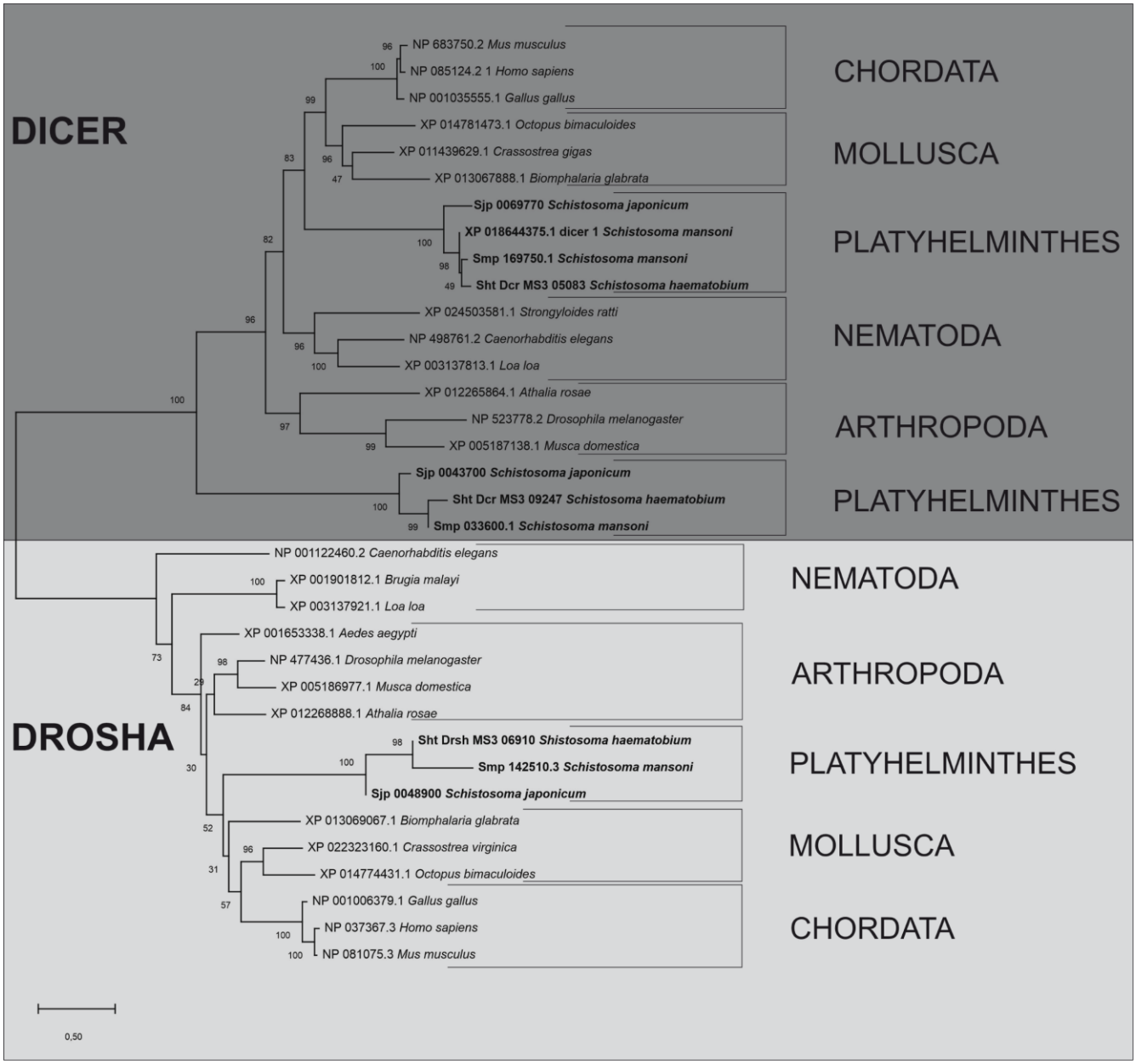


Figure 6. Phylogenetic analysis of the *S. haematobium* DICER and *S. haematobium* DROSHA proteins and their orthologous.

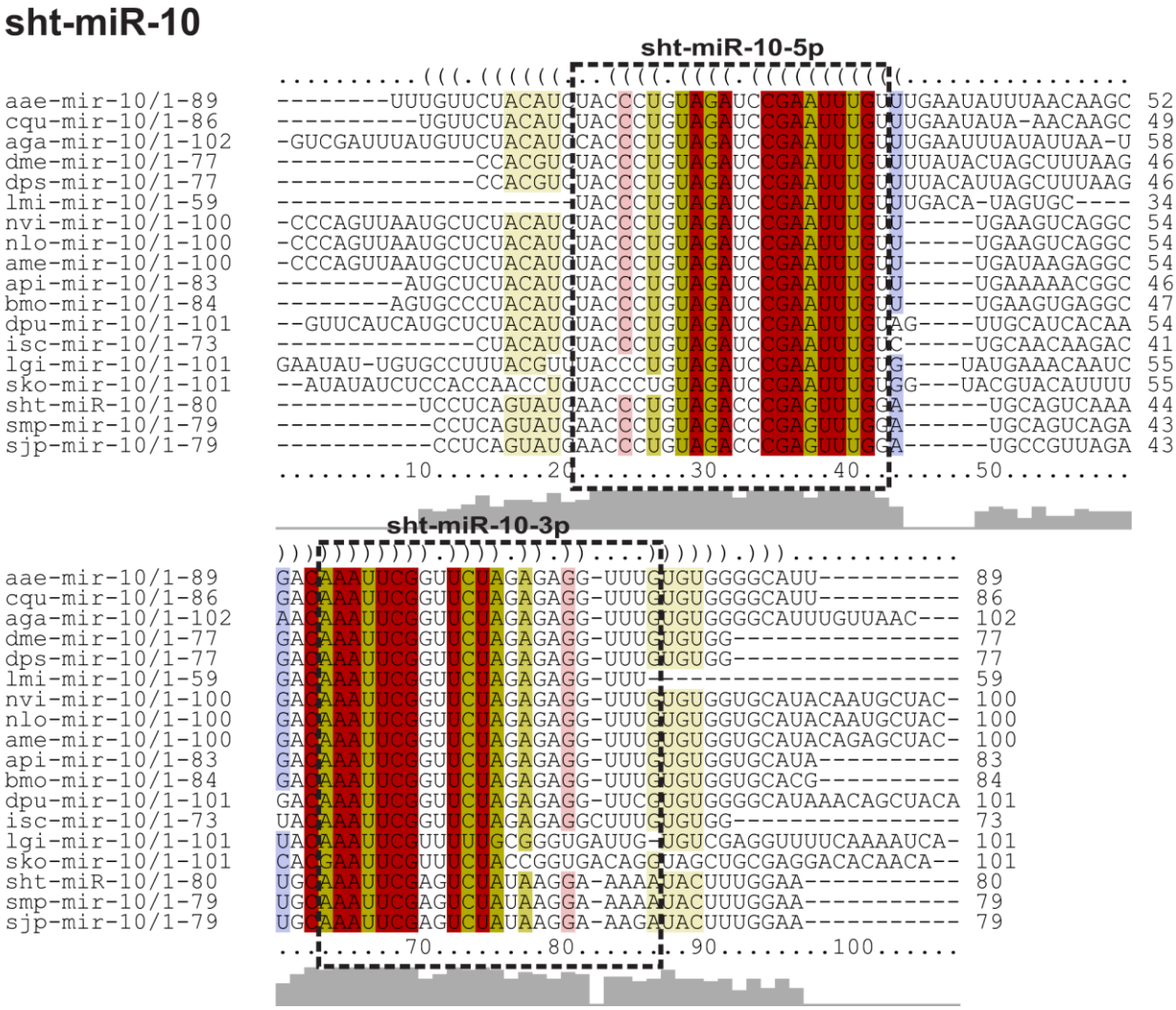


Figure 7. Alignment of the sht-miR-10 pre-miRNA and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum,* sko: *S. kowalevskii,* lgi: *L. gigantea,* isc: *I. scapularis,* dpu: *D. pulex,* bmo: *B. mori,* api: *A. pisum,* ame: *A. mellifera,* nvi: *N. vitripennis,* nlo: *N. longicornis,* lmi: *L. migratoria,* dps: *Drosophila pseudoobscura,* dme: *D. melanogaster,* aga: *A. gambiae,* cqu: *C. quinquefasciatus* and aae: *A. aegypti.*

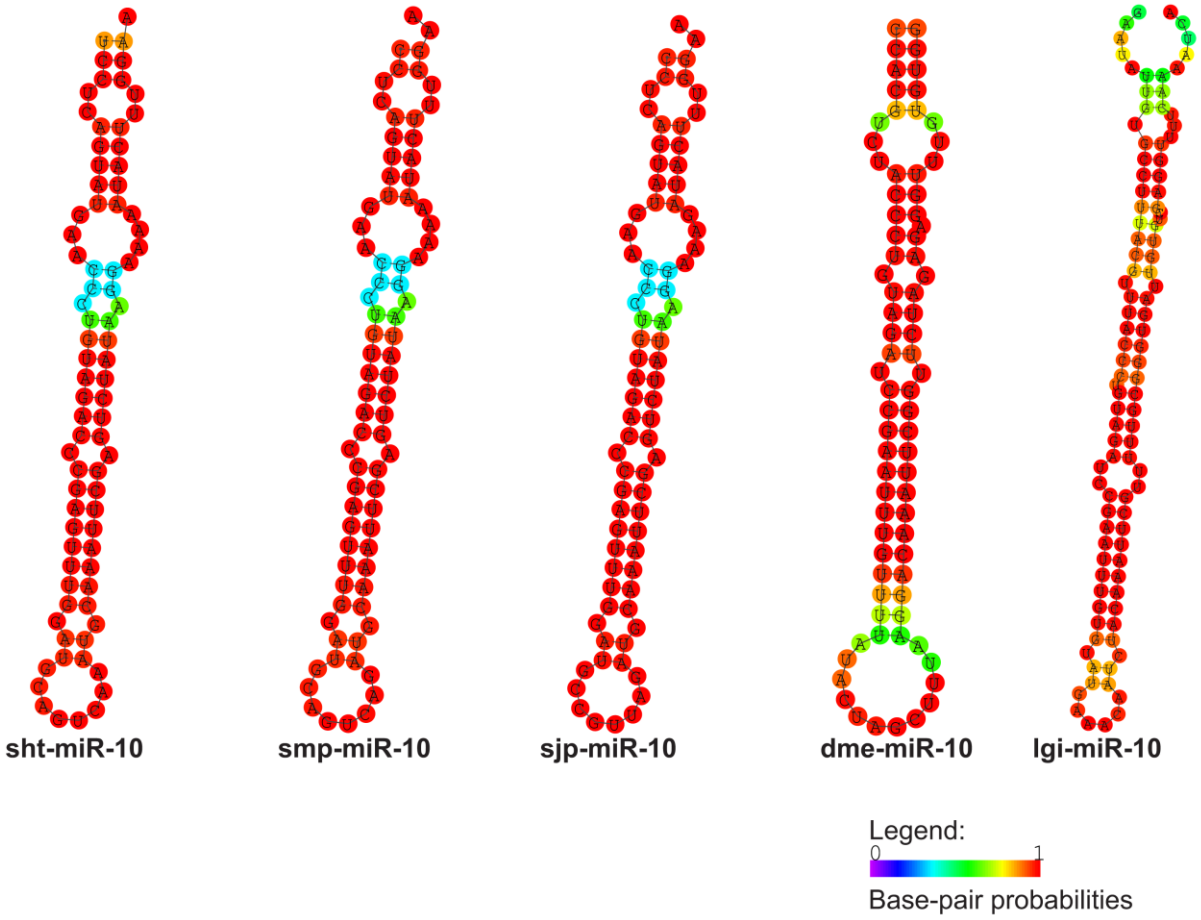


Figure 8. Secondary structures of the sht-miR-10 pre-miRNA and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum*, dme: *D. melanogaster* and lgi: *L. gigantea.*

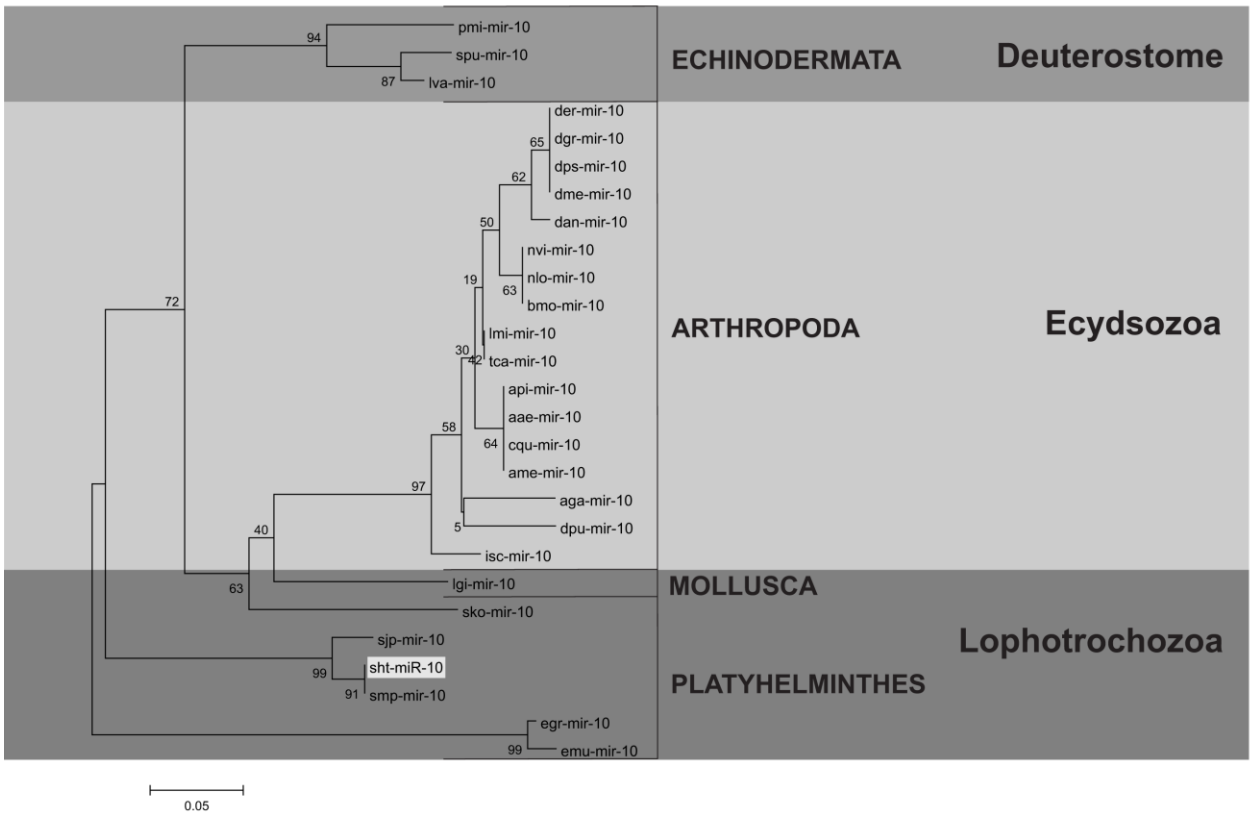


Figure 9. Phylogenetic tree performed to sht-miR-10 pre-miRNA identified in *S. haematobium* Egypt genome and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum*, egr: *E. granulosus*, emu: *E. multilocularis*, lgi: *L. gigantea,* isc: *I. scapularis,* dpu: *D. pulex*, aga: *A. gambiae,* ame: *A. mellifera,* cqu: *C. quinquefasciatus,* aae: *A. aegypti,* api: *A. pisum,* tca: *T. castaneum,* lmi: *L. migratoria,* bmo: *B. mori,* nvi: *N. vitripennis,* nlo: *N. longicornis,* dan: *D. ananassae,* dme: *D. melanogaster,* dgr: *D. grimshtwi,* dps: *D. pseudoobscura,* der: *Drosophila erecta*, lva: *Lytechinus variegatus,* spu: *Strongylocentrotus purpuratus* and and pmi: *Patiria miniata.*

SUPPLEMENTARY FIGURES

Figure S1- Expression profile of genes encoding the proteins involved in the miRNA pathway found in *S. haematobium* Egypt.

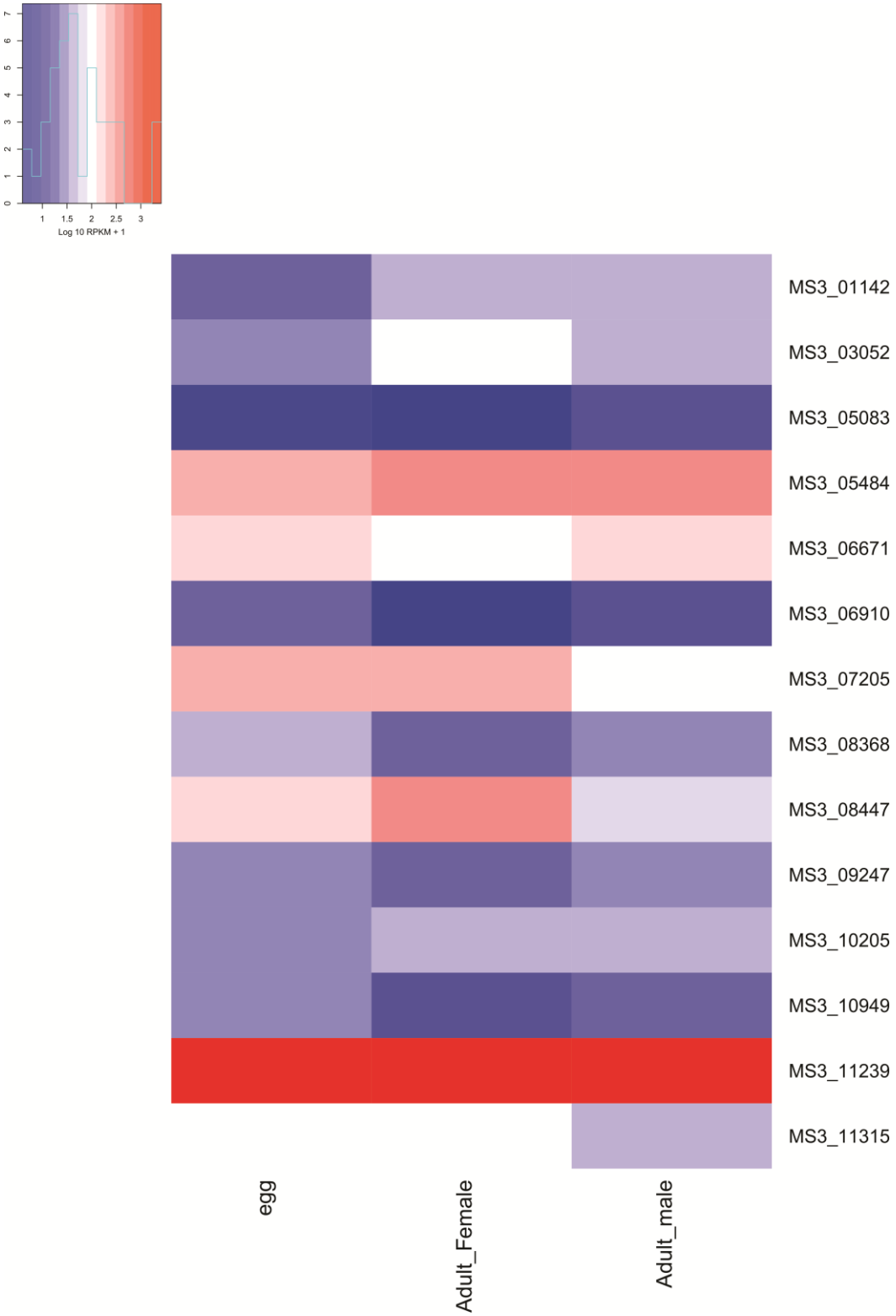


Figure S2 – RNA secondary structure of the cluster sht-miR-71a/sht-miR-2a-1/sht-miR-2b/sht-miR-2e; sht: *S. haematobium.*

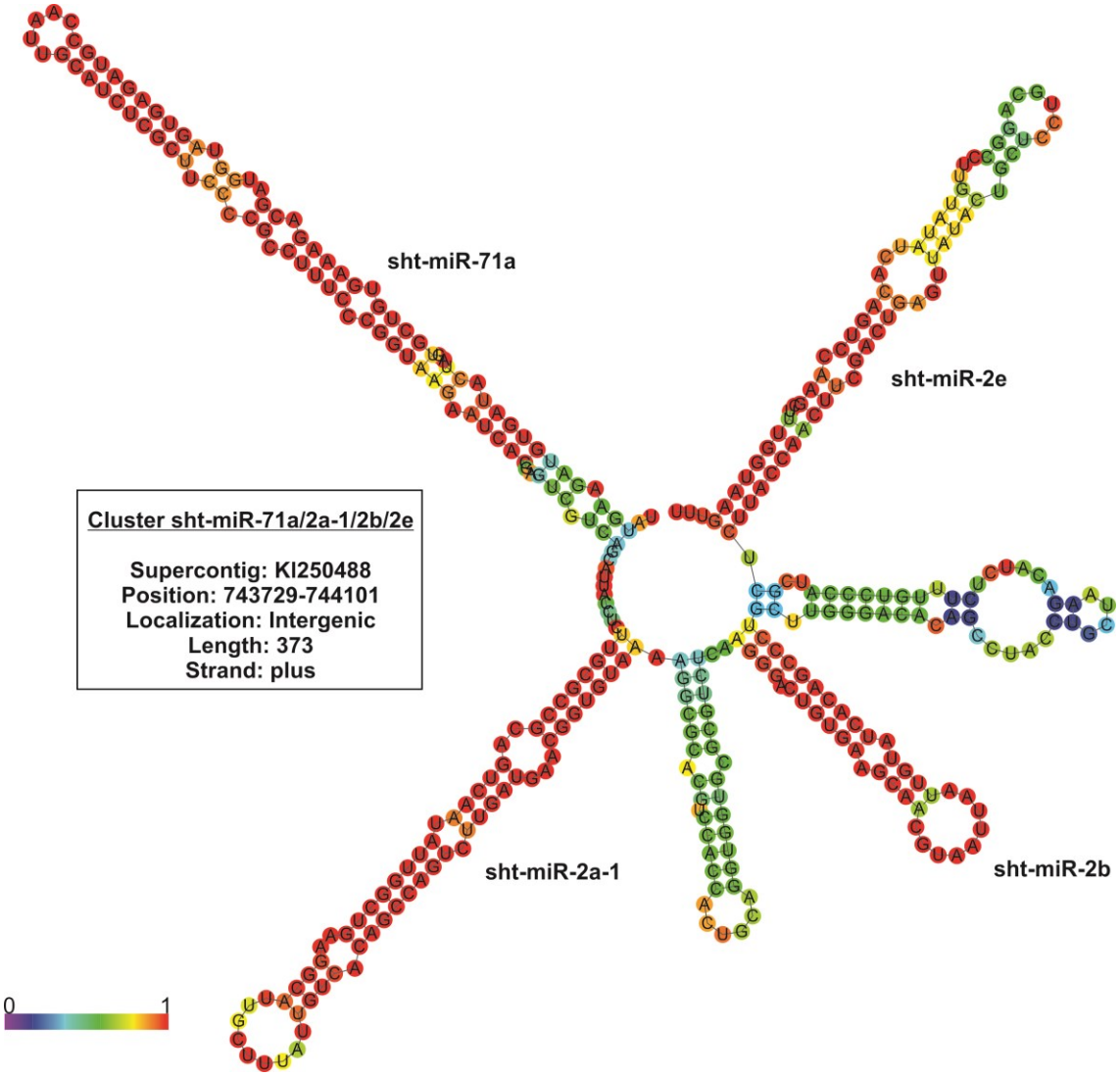


Figure S3 – Alignment of sht-miR-8 pre-miRNA and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum,* isc: *I. scapularis*, cte: *Capitella teleta*, ame: *Apis mellifera,* nlo: *Nasonia longicornis*, nvi: *N. vitripennis,* bmo: *Bombix mori,* hme: *Heliconius melpomene*, mse: *Manduca sexta,* dme: *D. melanogaster*, dpu: *D. pulex*, tca: *T. castaneum*, aga: *A. gambiae*, cqu: *C. quinquefasciatus* and aae: *A. aegypti*.

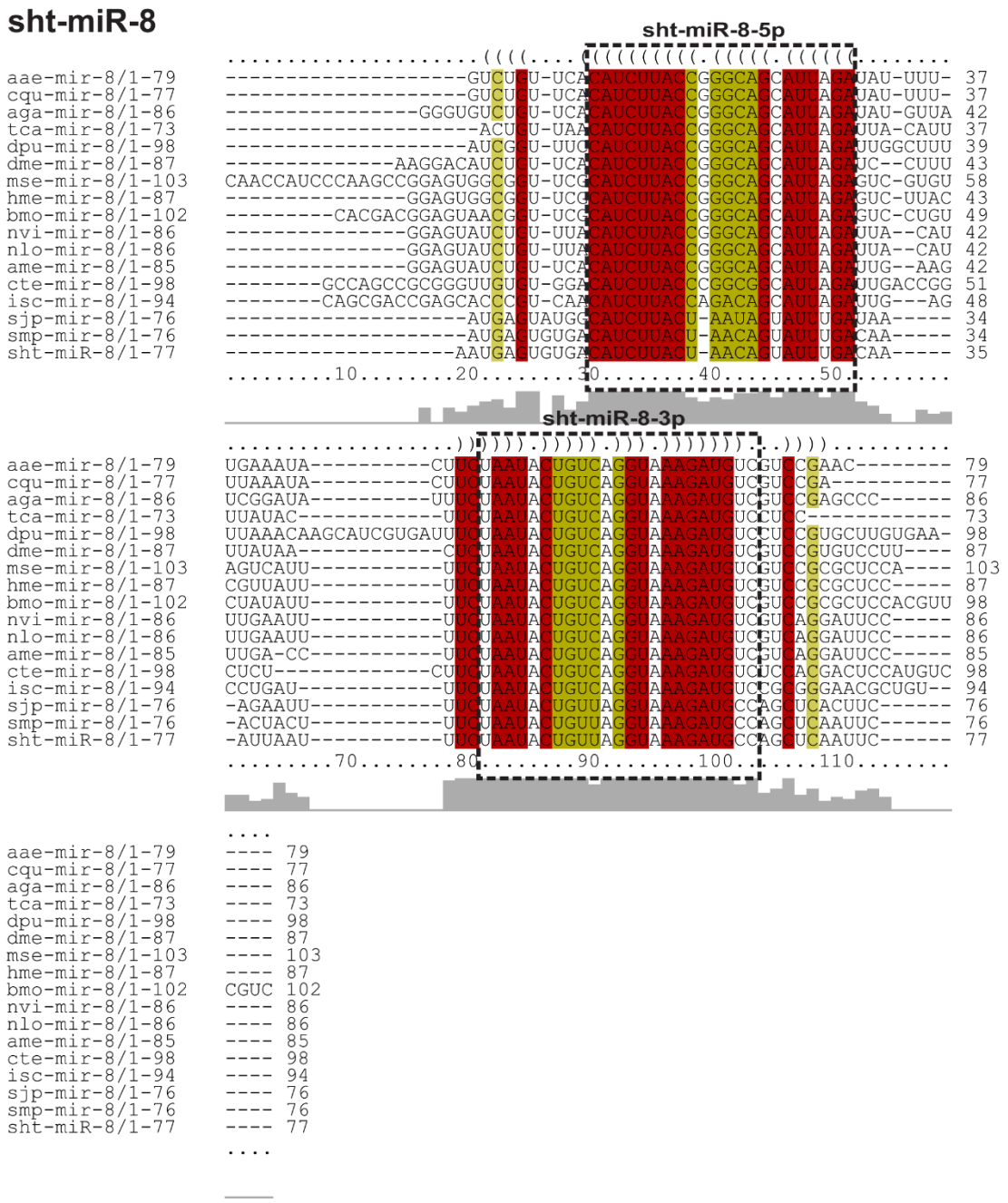


Figure S4 – Secondary structures of the sht-miR-8 pre-miRNA and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum,* dme: *D. melanogaster* and cte: *C. teleta.*

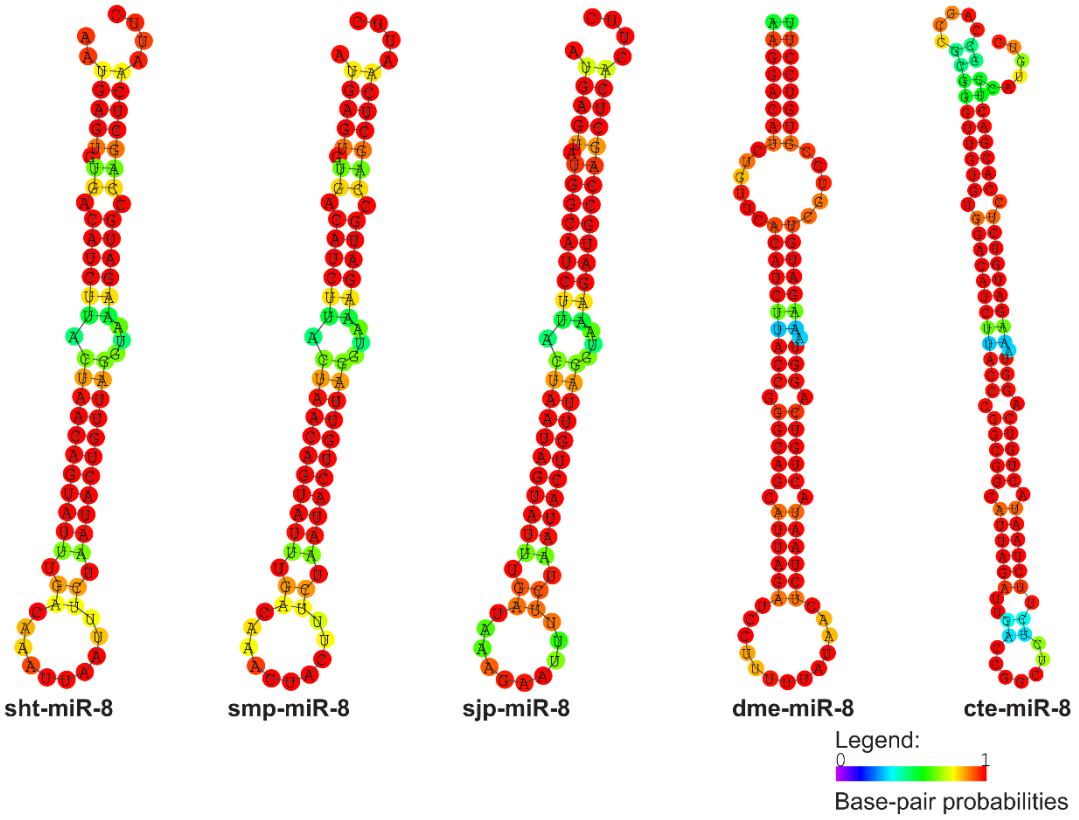


Figure S5 – Phylogenetic tree generated by phylogenetic analysis to sht-miR-8 precursor miRNAs found in *S. haematobium* Egypt and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum,* egr: *E. granulosus,* lgi: *Lottia gigantean,* lmi: *Locusta* migratoria, isc: *I. scapularis*, api: *A. pisum,* nlo: *Nasonia longicornis*, nvi: *N. vitripennis*, ame: *A. mellifera*, dpu: *D. pulex*, tca: *T. castaneum*, hme: *H. melpomene*, mse: *M. sexta,* bmo: *B. mori*, dmo: *Drosophila mojavensis,* dgr: *Drosophila grimshtwi,* dpe: *Drosophila persimilis*, dps: *Drosophila pseudoobscura*, dan: *Drosophila ananassae,* der: *Drosophila erecta*, dme: *D. melanogaster,* aae: *A. aegypti*, aga: *A. gambiae* and cqu: *C. quinquefasciatus*.

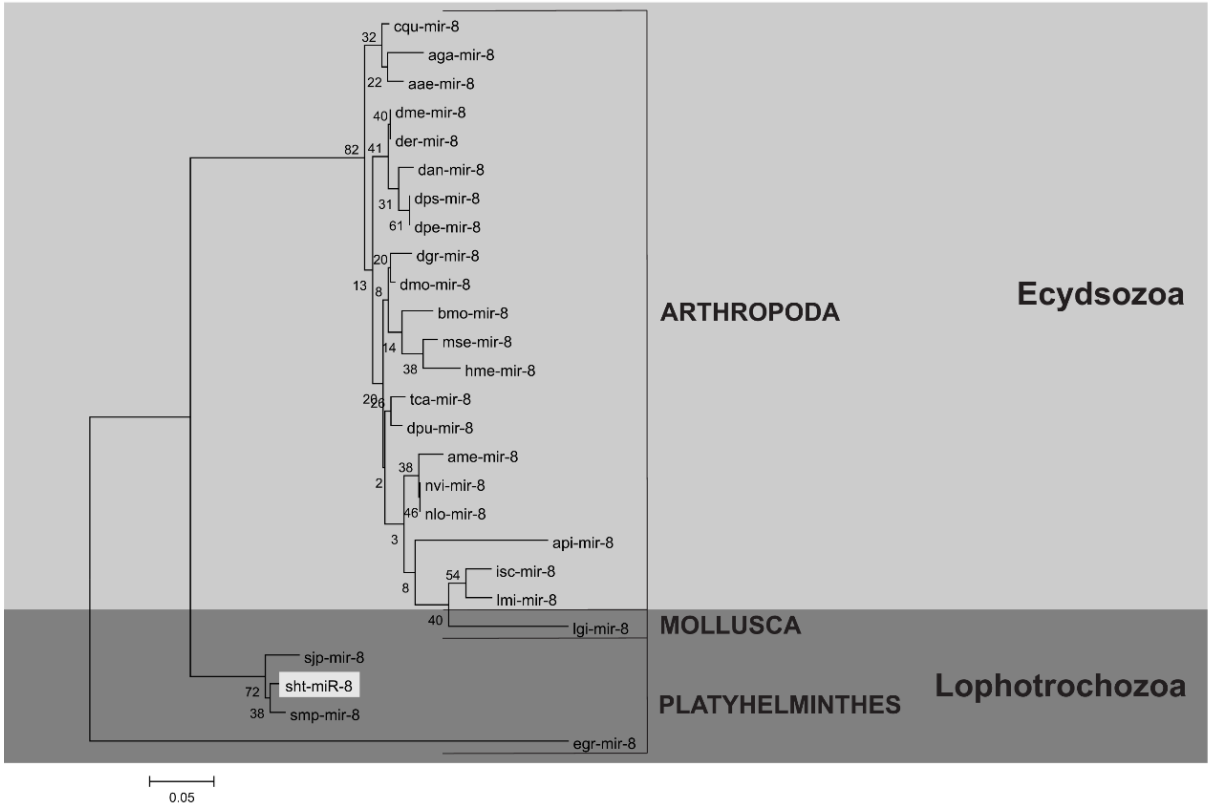


Figure S6 – Alignment of the sht-miR-2 family pre-miRNAs and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum.*

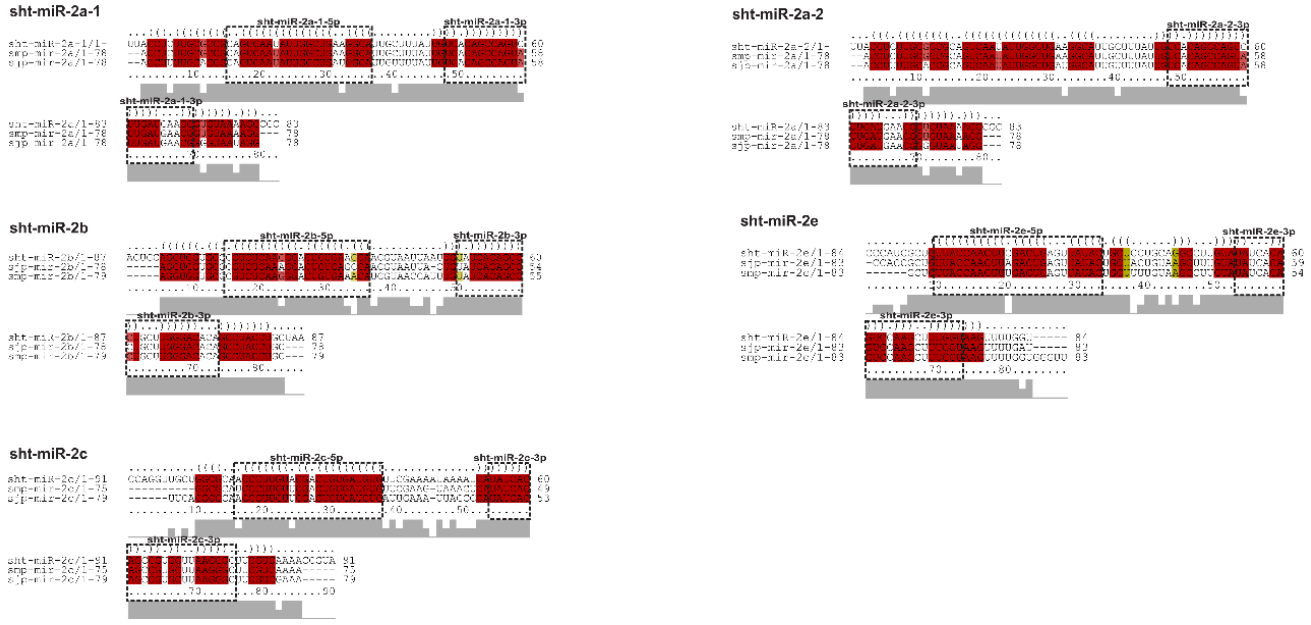


Figure S7 – Secondary structures of the sht-miR-2 family pre-miRNAs and their orthologs; smp: *S. mansoni*, sht: *S. haematobium*, gsa: *Gyrodactylus salaris.*

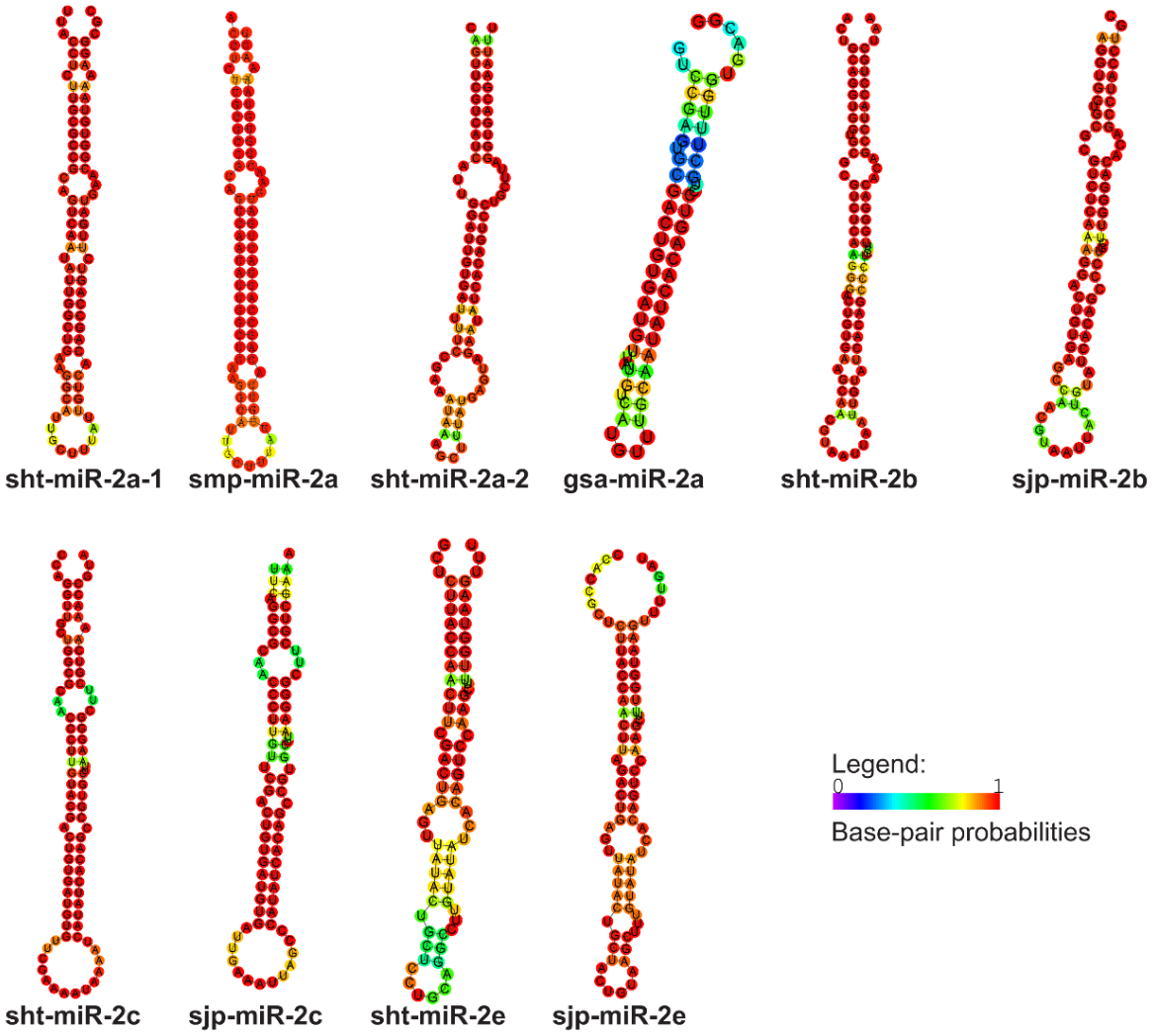


Figure S8 – Tree generated from the phylogenetic analysis to sht-miR-2 family precursor miRNAs and their orthologs; sht: *S. haematobium*, smp: *S. mansoni*, sjp: *S. japonicum,* emu: *E. multilocularis,* egr: *E. granulosus,* asu: *Ascaris suum*, isc: *I. scapularis*, tca: *T. castaneum*, api: *A. pisum*, nvi: *N. vitripennis*, mse: *M. sexta* and hme: *H. Melpomene.*

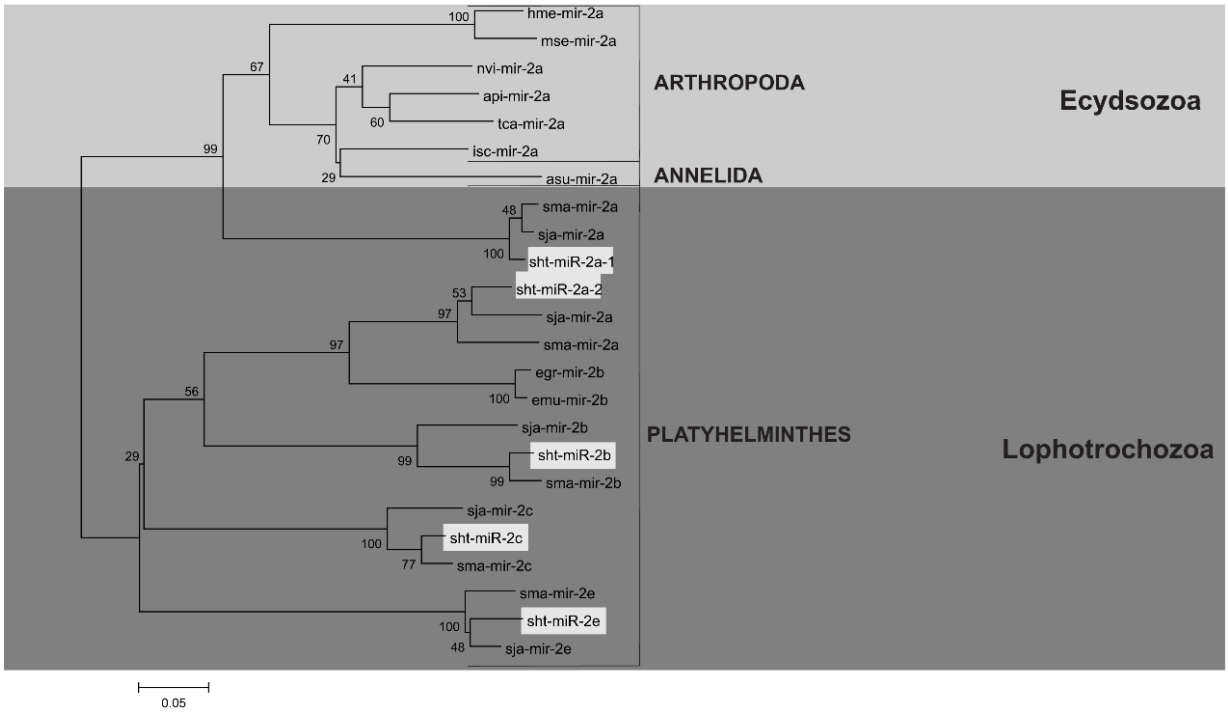


Figure S9 – Alignment of the sht-miR-7 and sht-miR-7b sequences and their orthologs*;* sht: *S. haematobium,* sjp: *S. japonicum,* mmu: *M. musculus,* rno: *R. norvegicus*, cgr: *C. griseus.*

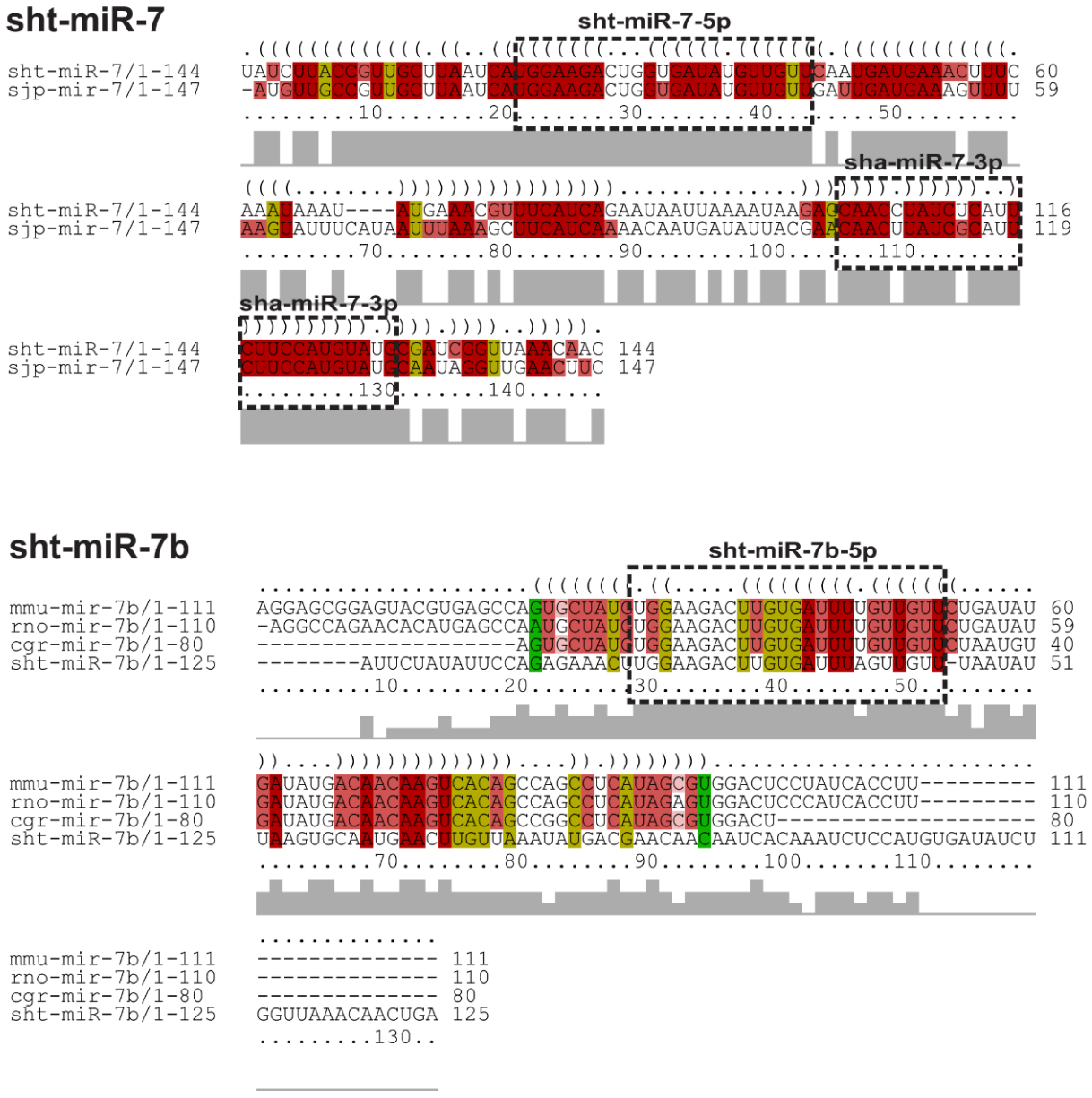


Figure S10 – Secondary structures of the sht-mir-7 and sht-mir-7b pre-miRNAs and their orthologs; sht: *S. haematobium*, sjp: *S. japonicum*, mmu: *M. musculus.*

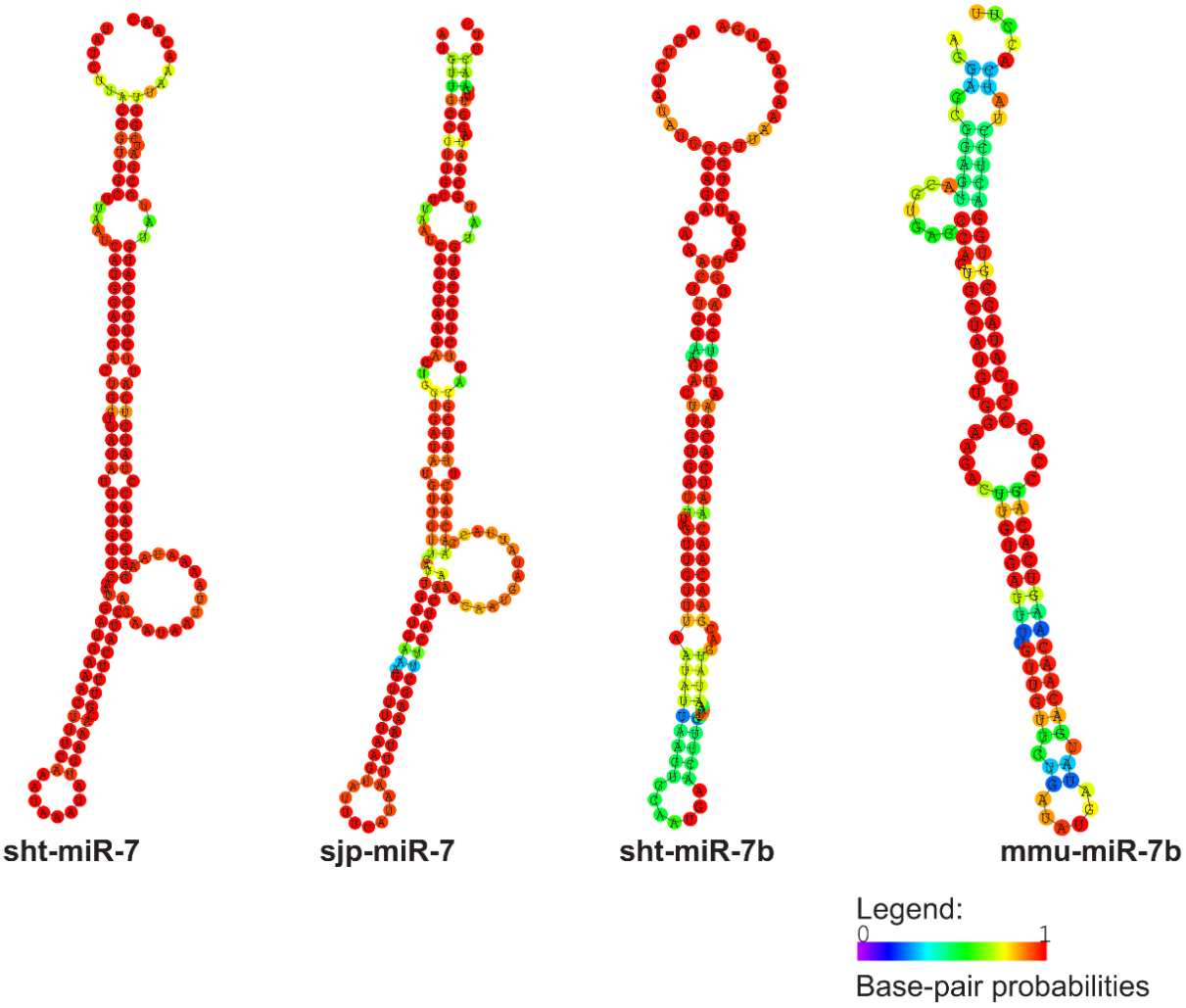
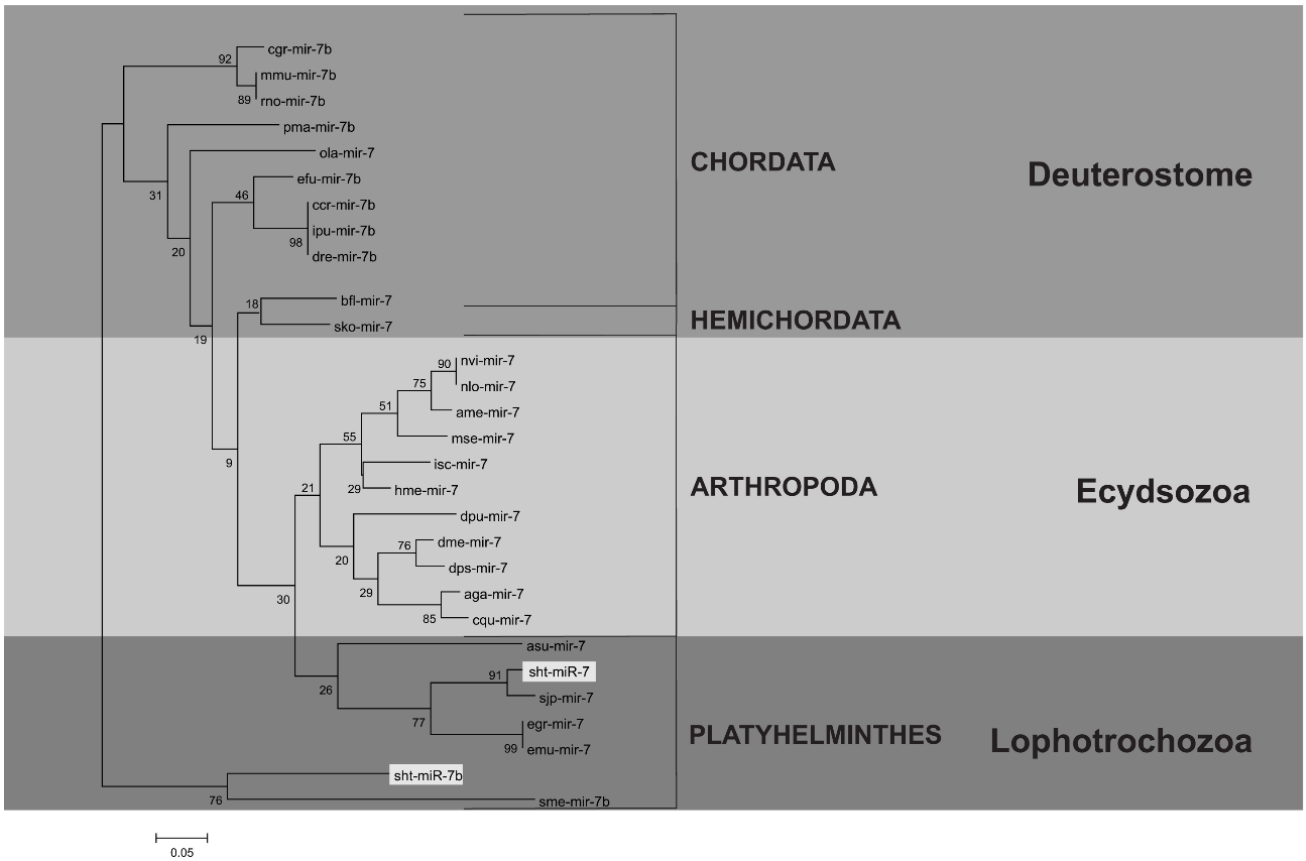


Figure S11. Phylogenetic tree of sht-miR-7 family precursor miRNAs and their orthologs; sht: *S. haematobium*, sjp: *S. japonicum,* sme: *S. mediterranea,* egr: *E. granulosus,* emu: *E. multilocularis,* asu: *A. suum*, cqu: *C. quinquefasciatus,* aga: *A. gambiae,* dps: *D. pseudoobscura*, dme: *D. melanogaster,* dpu: *D. pulex,* hme: *H. Melpomene,* isc: *I. scapularis,* mse: *M. sexta,* ame: *A. mellifera,* nlo: *N. longicornis*, nvi: *N. vitripennis,* sko: *Saccoglossus kowalevskii*, bfl: *Branchiostoma floridae*, dre: *Danio rerio*, ipu: *Ictalurus punctatus*, ccr: *Cyprinus carpio*, efu: *Eptesicus fuscus*, ola: *Oryzias latipes*, pma: *Petromyzon marinus*, rno: *Rattus norvegicus*, mmu: *M. musculus* and cgr: *Cricetulus griseus*.



5 CAPÍTULO II – Article: Genome-wide identification and characterization of genes involved in the acylsugar pathway in tomato - Manuscript Draft sob revision for Plant Gene Journal

Manuscript Number: PLANTGENE-D-20-00008R2

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ABSTRACT

Acylsugars are allelochemicals secreted by type IV trichomes in leaves and have been associated with resistance to arthropod pests in *Solanaceae* species. In this study, the putative genes involved in the acylsugar metabolism were identified, characterized, and validated in cultivated tomato, *Solanum lycopersicum*, and wild tomato, *Solanum pennellii*. Eighty-seven putative genes were identified in *S. lycopersicum* and 77 in *S. pennellii* involved in the acylsugar pathway, including the key proteins branched-chain keto acid dehydrogenase E2 (BCKD E2), 2-isopropylmalate synthase A (IPMSA), and threonine deaminase/dehydratase (TD). The putative tomato proteins displayed conservation using conserved domain distribution and active site comparing to ortholog proteins from the acylsugar pathway. Phylogenetic analysis of the putative proteins BCKD E2, IPMSA, and TD showed that all putative tomato proteins grouped with their orthologs from the *Solanaceae* species, corroborating with the distribution of the tree of life. The BCKD E2 and the IPMSA transcripts from *S. pennellii* showed higher gene expression compared to *S. lycopersicum* transcripts, suggesting that the acylsugar pathway is more active in wild than in cultivated tomato, corroborating with the literature. Given the important role of the allelochemicals produced in *Solanaceae*, the results contribute to a better understanding of acylsugars and their processing pathways and open up opportunities to study their relationship with biotic resistance in these important species and other *Solanaceae* species.

Keywords: Acylsugar; Allelochemicals; Trichomes; *Solanum lycopersicum*; *Solanum pennellii*; Resistance to pests; bioinformatics tools.

5.1 INTRODUCTION

Tomato is one of the most important vegetable crops in the world due to its significance in the economy, in generating jobs and income, and in the large volume of labor and resources produced through its production and industrial chain (Knapp, 2002; Sato and Tabata, 2016). Currently, Brazil ranks among the 10 largest producers in the world, producing more than 4 million tons of fruit in 2019 (FAO, 2019; IBGE, 2020).

The genus *Solanum* is one of the largest among the angiosperms and contains ~1500 species (Bauchet and Causse, 2012). *Solanum lycopersicum,* the cultivated tomato, has greater prominence for being one of the most consumed and studied fruits (Baichoo and Jaufeerally-Fakim, 2016; Karkute et al., 2018; Kim et al., 2011; Perez-Fons et al., 2014). Besides being a nutritious food, tomato, it has many interesting characteristics such as a fleshy fruit with compound leaves, multicellular and glandular trichomes, among several other important characteristics that other model plants (e.g., *Arabidopsis thaliana*) do not have. These traits make tomato a model plant for species that exhibit these characteristics (Bedinger et al., 2011; Campos et al., 2010; Gapper et al., 2013; Giovannoni, 2004; Kobayashi et al., 2014).

In general, commercial *S. lycopersicum* tomato plants are susceptible to pest attack and more than 200 diseases caused by different types of pathogens, including viruses, bacteria, fungi, and nematodes (Bai and Lindhout, 2007; Haapalainen, 2014; Lukyanenko, 1991; Mcgovern, 2015; Nowicki et al., 2012). Their control is mainly achieved by the use of insecticides and acaricides, which, in addition to high costs, involves intensive application, which has a negative impact on the environment through environmental pollution and ecological imbalance (elimination of natural enemies) (Ercolano et al., 2012).

Many wild tomato species produce several allelochemicals that have been associated with resistance to various arthropod pests (Bleeker et al., 2011; J. A. Freitas et al., 2002; Gonçalves et al., 1998; Gonçalves Neto et al., 2010; Maluf et al., 1997; Oliveira et al., 2009). However, these wild species have not shown immediate commercial value (Silva, 2009; Williams et al., 1980). *Solanum pennellii* is a wild tomato species relatively distant from the domesticated species *S.*

lycopersicum, with an estimated divergence time of 2.7 million years (Kamenetzky et al., 2010). They have been widely used in breeding programs to construct populations and lines due to their tolerance to stress, resistance to pests, and unusual morphology (A. Bolger et al., 2014; Fernandez-Pozo et al., 2015). *S. pennellii* lines, including LA-716, have a high level of resistance to whitefly, aphids, mites, Lepidoptera (such as the tomato moth), and other relevant tomato pests of importance around the world (Gentile et al., 1969, 1968; Goffreda et al., 1989).

Different allelochemicals found in *Solanum* species have been associated with resistance to pests such as 2-tridecanone, a methyl ketone found in *S. habrochaites* var. *glabratum* (Gonçalves et al., 1998; Maluf et al., 1997), the sesquiterpenes found in *S. lycopersicum* and *S. habrochaites* (Bleeker et al., 2011; Eigenbrode et al., 1994), and the acylsugars found in *S. pennellii* (J. A. De Freitas et al., 2002; Goffreda et al., 1989). Thus, the selection for high levels of these allelochemicals could be an efficient indirect screening technique to identify lines resistant to pests such as the tomato moth (Gonçalves Neto et al., 2010; Oliveira et al., 2009; Resende et al., 2006), whitefly (J. A. De Freitas et al., 2002) and *Tetranychus* spp. mites (Maluf et al., 2001).

The broad-spectrum disease resistance in wild tomato is attributed to the presence of glandular trichomes that occupy the plant surface, mainly type IV trichomes in leaves, and the allelochemicals they secrete (Gentile et al., 1968; Goffreda et al., 1989). Acylsugars are fatty acid esters with 4 to 12 carbon atoms that contain glucose or sucrose and constitute approximately 90% of the total of allelochemicals secreted by type IV trichomes. These allelochemicals may also play an important role in the resistance to tomato pests because of their sticky texture, acting as an insect trap by reducing larval development and impairing feeding and oviposition of the arthropods (Gomes et al., 2017; Hawthorne et al., 1992; Juvik et al., 1982; Kim et al., 2012).

The acylsugars found in the *Solanaceae* family is organized according to the sugar moiety, such as glucose or sucrose, the fatty acid moiety, and the acylation arrangement (Shapiro et al., 1994). The variety of acylsugar molecule structures is related to the diversity of biosynthetic pathways (Goffreda et al., 1990; Shapiro et al., 1994).

Several studies have shown the contribution of many proteins to the acylsugar metabolism in plants (Hoeven et al., 2000; Kandra et al., 1990; Kim et al., 2012; Kroumova and Wagner, 2003; Leckie and Halitschke, 2014; McDowell et al., 2011; Ning et al., 2015; Schilmiller et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990). Among all proteins involved in the acylsugar metabolism, thosefrom BCKD E2, IPMSA, and TD families have been considered the key proteins of the acylsugar pathway (Kandra et al., 1990; Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990).

The multi-enzymatic complex BCKD is composed of three subunits, 2-oxo acid dehydrogenase (E1), dihydrolipoyl acyltransferase (E2), and dihydrolipoamide dehydrogenase (E3), and plays a key role in redox regulation. E2, the central component of the complex, catalyzes the transfer of the acyl-CoA group from E1 to E3 via the reductive acetylation of a lipoyl group that is covalently attached to a lysine residue (CDD, 2016). BCKD catalyzes the conversion of the branched chain keto acids into the branched chain acyl-CoAs with the loss of one carbon in a decarboxylation process (Slocombe et al., 2008). In plants, BCKD is involved in the first step of branched chain amino acid (BCAA) catabolism and plays an important role in the synthesis of branched chain fatty acids (BCFA) (Mooney et al., 2002; Slocombe et al., 2008; Taylor et al., 2004). The enzyme TD is responsible for catalyzing the direct deamination of the alpha-amino group of threonine into $NH4^+$ in amino acid degradation, with pyridoxal phosphate (PLP) as the prosthetic group (CDD, 2016). Besides, TD is essential for the supply of ketoacid precursors (2-keto-3-methyl valerate and 2-ketoisovalerate) and precursors for acylsugar production and is involved in the first step of isoleucine and BCFA synthesis in trichomes (Slocombe et al., 2008). The enzyme IPMS is responsible for catalyzing the aldol type condensation of acetyl-CoA reductase and 2-oxoisovalerate, producing 2-isopropylmalate and CoA, which is the first step in leucine biosynthesis (CDD, 2016; Hoeven et al., 2000). In addition, the variation of 2-methylpropanoic acid (iC4) and 3-methylbutanoic acid (iC5) acyl chain in S. pennellii accessions is influenced by the variation in the activity of a set of truncated IPMS enzymes (Ning et al., 2015). Ning et al. (2015) observed that *S. lycopersicum* expresses an *IPMS* gene (Solyc08g014230 - chromosome 8) in the apical cells of type I/IV trichomes, which encodes a functional protein with 160

amino acids less at the end in the C-terminal region than the *IPMS* gene (Solyc06g053400) expressed from chromosome 6. Although the protein is active at *in vitro* conditions, it is insensitive to leucine-binding mediated inhibition in the regulatory domain as it has been described in Arabidopsis (Kraker and Gershenzon, 2011) and microorganisms (Carvalho et al., 2005; Koon et al., 2004; Ning et al., 2015). In contrast, an *IPMS* gene (Sopen08g005140) on chromosome 8 of *S. pennellii* encodes a non-functional truncated IPMS protein with a major deletion in the C-terminal region (51 aa.). The deletion found in *S. pennellii* means that there is no allosteric regulation by leucine binding, with large amounts of methylpropanoic acid accumulating for acylsugar synthesis instead (Ning et al., 2015). Taking into consideration these previous studies and the importance of these allelochemicals in mediating the resistance to tomato pests, a study that analyzes and characterizes the genes involved in the acylsugar metabolism supports a better understanding of the natural defense mechanisms in different *Solanaceae* species for advances in traditional breeding and the genetic manipulation of important commercial species.

Considering the importance of tomato crops and the rapid growth in agrochemical use in crops, a better understanding of the biology of the tomato is necessary for selecting markers associated with important characteristics in its response to biotic and abiotic stresses. The release of the *S. lycopersicum* (Sato et al., 2012) and *S. pennellii* genomes (A. Bolger et al., 2014) represented a great advance in the biological study of these species and deepened the annotation and identification studies of several genes. Therefore, identifying and characterizing the genes related to acylsugar pathway in *S. lycopersicum* and *S. pennellii* may help to understand the involvement of those genes in resistance to arthropods, which occurs mainly via acylsugar production. Thus, our study aimed to identify, characterize, and validate genes involved in the acylsugar metabolism in *S. lycopersicum* and *S. pennellii* genomes.

5.2 MATERIALS AND METHODS

5.2.1 Identification and characterization of putative genes involved in acylsugar metabolism in *S. lycopersicum* and *S. pennellii*

Based on literature, the genes involved in the acylsugar metabolism from model plant species (*A. thaliana*) and other species (*Solanum tuberosum, Glycine max, etc*) were searched in plant databases and retrieved as a protein FASTA file (Figure 1). These protein sequences were used as queries to search putative *S. lycopersicum* and *S. pennellii* proteins involved in the acylsugar pathway using the Blastp tool (Mcginnis and Madden, 2004). The Sol Genomics Network 2019 for both tomato species was used as a database to search the putative tomato proteins (Fernandez-Pozo et al., 2015). Other ortholog proteins from model plant species and other plants, that have been considered evolutionarily close and distant from tomato species, were retrieved using putative tomato sequences as queries and NCBI reference protein databases (RefSeq protein database 91) of the respective plant (*S. tuberosum*, *Capsicum annuum, Nicotiana sylvestris, Nicotiana tomentosiformis, Nicotiana tabacum, Glycine max, Theobroma cacao, Prunus mume, Cucumis melo, Vitis vinifera, Citrus sinensis, Nelumbo nucifera, Brassica napus, A. thaliana, Arabidopsis lyrata, Cucumis sativus, Vigna angularis, Vigna radiata, Nicotiana attenuate*, *Camelina sativa, Malus domestica, Cicer arietinum, Phaseolus vulgaris and Beta vulgaris*) (Leary et al., 2016). These protein sequences were retrieved as FASTA files and used for further analyses such as observation of sequence-structure conservation, presence of conserved domains and active sites, and phylogenetic analyses.

5.2.2 Alignment and phylogenetic analyses

Multiple Sequence Alignment (MSA) of the putative tomato proteins involved in the acylsugar pathway and their orthologs were performed by ClustalX 2.1 (Larkin et al., 2007). Conserved domains were identified and characterized using the Protein Family Database (Pfam) (El-gebali et al., 2019) and Conserved Domains Database (CDD) (Marchler-Bauer et al., 2015). Phylogenetic analysis was performed based on the putative tomato proteins and their ortholog proteins by the use of the MEGA 5.2 program using the Neighbor-joining method (Saitou and Nei, 1987; Tamura et al., 2011). A consensus tree was obtained through the Neighbor-joining (NJ) method using “2000 bootstraps”. The evolutionary distance was calculated using the JTT model (Jones et al., 1992).

5.2.3 Expression of acylsugar pathway genes in tomato RNA-seq libraries

Paired-end reads from leaves of both wild (*S. pennellii*) and cultivated (*S. lycopersicum*) tomato were retrieved from the Sequence Read Archive (SRA) under accessions numbers SRR786556, SRR786557, SRR786570, SRR786571, SRR786524, SRR786525, SRR786540, SRR786541, and SRR786542 (Dai et al., 2017).

The quality of the libraries was evaluated using the FastQC software (Kroll et al., 2014). Adapters were identified using the Minion tool from the Kraken suit for quality control of high-throughput sequence data (Davis et al., 2013), and removed using Trimmomatic (A. M. Bolger et al., 2014). Reads with a quality score below 20 and length below 35 bp were also removed using Trimmomatic. After the quality control, the library reads of *S. lycopersicum* (SRR786524, SRR786525 SRR786540, SRR786541 and SRR786542) and *S. pennellii* (SRR786556, SRR786557, SRR786570 and SRR786571) were used as input to the STAR mapper tool (version 2.5.3a) (Dobin et al., 2013) with the default parameters (Fernandez-Pozo et al., 2015). The libraries were then sorted by query name using Picard tools (version 2.18.0), and for each of them, raw read counts were obtained using the python script HTSeq-count (version 0.7.2) (Anders et al., 2015).

We searched for differentially expressed (DE) genes between leaf libraries of both species by contrasting the normalized number of counted reads aligned to the exons of genes in the *S. lycopersicum* genome. The comparisons were carried out with the Bioconductor package edgeR in the statistical environment R (Huber et al., 2015; Robinson et al., 2009). The Benjamini and Hochberg's false-discovery rate (FDR) below 0.05 and minimum fold-change of two were the parameters used to consider a gene DE (Benjamini and Hochberg, 1995).

5.2.4 Real-time PCR expression of the acylsugar pathway putative genes in *S. lycopersicum* and *S. pennellii*

The plant material was collected at the vegetable experimental station of HortiAgro Sementes SA. Two different lines were used to analyze the expression of the putative genes involved in the acylsugar processing. These lines are derived from *S. lycopersicum* and S. *pennellii*: LA-716 (*S. pennellii* wild strain with high acylsugars) and TOM-687 (pre-commercial strain of *S. lycopersicum*).

For RNA extraction, leaf trichomes of the two *S. lycopersicum* and *S. pennellii* lines were collected at three different times, under the same environmental conditions for expression analysis: 30, 60, and 90 days after planting to analyze the vegetative growth, flowering, and fruiting, respectively. The samples were immediately frozen in liquid nitrogen and stored at -80°C. The Concert ™ Plant RNA Reagent Kit (Invitrogen) was used following the manufacturer's recommendations. The samples were treated with the Turbo DNA-free Kit (Ambion) to eliminate residual DNA contamination. RNA integrity was checked on a 0.8% agarose gel. Samples were quantified in a spectrophotometer (Nanodrop® Spectrophotometer ND-1000) at A_{260}. Samples that showed a high degree of integrity and purity (OD260/OD280 = 1.8 a 2.0) were used for cDNA synthesis with the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). After cDNA synthesis, the samples were stored in a -20°C freezer until use.

The primers for real-time PCR of the putative tomato genes involved in the acylsugar pathway and reference genes were designed using the Primer Express v2.0 program (Applied Biosystems) (Supplementary Table S1). The gene expression analysis was performed in an ABI PRISM 7500 Real-Time PCR system (Applied Biosystems) using the SYBR Green qPCR method. The cycling parameters were 2 min at 50°C, 10 min at 95°C, followed by 40 cycles of 15 s at 95°C, 1 min at 60°C, and 15 s at 95°C. Data were collected and stored in the 7500 Fast Software program (Version 2.1). For each reaction, 80 ng of cDNA, 1.5 µM of each primer, and 5.0 µL of Master Mix SYBR green UDG with ROX (Invitrogen) were used in a final volume of 10.0 µL/sample. The reference genes *eukaryotic elongation factor 1* (*eEF-1*) and *glyceraldehyde-3- phosphate dehydrogenase* (*GAPDH*) were used as endogenous genes. The method used was the comparative C_T (Pfaffl, 2001). The normalization was calculated by the equation $\Delta C_T = C_T$ (target gene) - C_T (endogenous control), and the calibration was determined by the formula $\Delta\Delta C_T = \Delta C_T$ (sample) - ΔC_T (calibrator). Relative quantification was obtained by the formula $2^{-\Delta\Delta C_T}$.

For the statistical comparisons among the expressions of the three times of each gene analyzed, a basic descriptive analysis was performed followed by non-parametric tests (Wilcoxon-Mann-Whitney). Median values were used to perform

the statistical comparisons (Moses, 2005). Statistical significance was set at $p<0.05$.

5.3 RESULTS

5.3.1 *In silico* analysis of *S. lycopersicum* and *S. pennellii* acylsugar pathway genes

Initially, we conducted a review in the literature searching for genes involved in the acylsugar metabolism of the model plant species and other plant species (Table 1). Subsequently, these genes were compared with *the S. lycopersicum* and *S. pennellii* sequence databases using the BLASTp tool. Eighty-seven putative proteins involved in the acylsugar processing pathway were identified in the *S. lycopersicum* database and 77 in the *S. pennellii* database (Supplementary Table S2).

Our analysis revealed that the components of this pathway were highly conserved at the amino acid level in *S. lycopersicum* and *S. pennellii.* Supplementary Table S3 shows the conserved domains characterized in all putative proteins involved in the acylsugar pathway. Among all putative proteins identified, the putative protein families BCKD E2, IPMSA, and TD were considered key proteins in the processing machinery of acylsugars according to previous studies and were used for further analysis (Kandra et al., 1990; Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990). The distribution of the protein domains (Supplementary Figure S1 and Supplementary Table S3), the position of the amino acids from active sites (Figure 2), and the phylogenetic distribution of the putative tomato proteins BCKD E2, IPMSA and TD (Figure 3) were conserved compared to the reference ortholog proteins from other plant species.

5.3.2 BCKD E2 proteins

One putative BCKD E2 protein was found in *S. lycopersicum* (Solyc01g066520) and one in *S. pennellii* (Sopen01g028100) (Supplementary Table S2). The proteins Solyc01g066520 and Sopen01g028100 displayed the domains Biotin_lipoyl, E3_binding, and 2-oxoacid_dh at positions 90-163, 206-240, 272-502 and 90-163, 206-240, 272-502, respectively (Supplementary Figure

S1A and Supplementary Table S3). The Biotin_lipoyl conserved domain is one of the main domains contained in the BCKD E2 proteins. It was also shown that the active sites contained the important catalytic residue K (lysine) in a specific and conserved position (Figure 2A). The catalytic residues K of the BCKD E2 proteins from *S. lycopersicum* and *S. pennellii* were found at positions Lys130 on both proteins. The conserved domains and active sites found in Sly (*S. lycopersicum*)/Spe (*S. pennellii*) BCKD E2 showed high conservation compared to the BCKD E2 proteins in other plant species, such as *S. tuberosum, N. tabacum, T. cacao, A. thaliana*, *G. max,* and *V. vinifera*.

The phylogenetic distribution of BCKD E2 proteins was performed using amino acid sequences (Figure 3A). The phylogenetic analysis of the Solyc01g066520 and Sopen01g028100 proteins showed that these putative proteins were distributed in the phylogenetic tree closest to their respective ortholog proteins from other plant species. The phylogenetic tree was divided into clades of 9 distinct families: *Solanaceae, Fabaceae, Malvaceae, Rosaceae, Cucurbitaceae, Vitaceae, Rutaceae, Nelumbonaceae,* and *Brassicaceae*.

5.3.3 IPMSA proteins

Another important catalytic component of the acylsugar processing pathway in plants are the IPMSA proteins. Three putative proteins were identified in *S. lycopersicum* (Solyc08g014240, Solyc08g014230 and Solyc08g014130), and four putative proteins were identified in *S. pennellii* (Sopen08g005060, Sopen08g005140, Sopen10g006110 and Sopen08g005150) (Supplementary Table S2).

The Solyc08g014130.2.1 and Sopen08g005060 proteins showed the HMGL-like and LeuA_imer conserved domains in their structures. The HMGL-like domain was shown at positions 72-352 and 51-331, and the LeuA_imer domain was shown at positions 451-596 and 426-571 in the Solyc08g014130.2.1 and Sopen08g005060 proteins, respectively. The Solyc08g014240, Solyc08g014230, Sopen08g005140, Sopen10g006110, Sopen08g005150 proteins showed only the HMGL-like domain at positions 15-295, 15-331, 51-331, 51-331 and 15-295, respectively (Supplementary Figure S1B and Supplementary Table S3).

The HMGL-like domains in both tomato species showed the same catalytic residues, aspartate (D), arginine (R) and glutamate (E), and these of catalytic triad (DRE domain), corroborating with IPMSA proteins from other plant species (Figure 2B). These residues were found in the HMGL-like domains of the *S. lycopersicum* proteins Solyc08g014240 (Asp25-Arg94-Glu161), Solyc08g014230 (Asp61-Arg130-Glu197), and Solyc08g014130 (Asp82-Arg151-Glu218) and the *S. pennellii* proteins Sopen08g005060 (Asp57-Arg126-Glu193), Sopen08g005140 (Asp61-Arg130-Glu197), Sopen10g006110 (Asp61-Arg130-Glu197), and Sopen08g005150 (Asp25-Arg94-Glu1610).

To determine the evolutionary relationship among the putative IPMSA proteins of *S. lycopersicum* and *S. pennellii* and their orthologs, a phylogenetic analysis was performed to confirm the phylogenetic distribution of these putative proteins among their orthologs (Figure 3B). The proteins were grouped into 6 family clades (*Malvaceae, Brassicaceae, Cucurbitaceae, Fabaceae, Vitaceae,* and *Solanaceae*).

5.3.4 TD proteins

Three putative TD proteins were identified in *S. lycopersicum* (Solyc09g008670, Solyc10g083760, and Solyc10g083540) and three in *S. pennellii* (Sopen09g003470, Sopen10g033010, and Sopen10g033220) (Supplementary Table S2). The putative proteins Solyc09g008670, Solyc10g083760, Solyc10g083540, Sopen09g003470, Sopen10g033010, and Sopen10g033220 showed the PALP domain at positions 106-397, 117-409, 103-395, 68-359, 103-395, and 117-409, respectively. The same proteins showed the Thr_dehydrat_C I domain at positions 410-500, 422-512, 408-498, 372-462, and 408-498 and the Thr_dehydrat_C II domain at positions 504-593, 516-605, 503-591, 466-555, 503-591, and 422-512, respectively (Supplementary Figure S1C and Supplementary Table S3).

Almost all putative TD proteins from *S. lycopersicum* (Solyc09g008670 - Lys143, Solyc10g083760 - Lys154 and Solyc10g083540 - Lys140) and *S. pennellii* (Sopen09g003470 - Lys105, Sopen10g033010 - Lys140 and Sopen10g033220 - Lys154) showed at the PALP domain a catalytic K (lysine) residue (Figure 2C).

The phylogenetic analysis of the *S. lycopersicum* and *S. pennellii* TD proteins showed that they were distributed in the phylogenetic tree closest to their respective ortholog proteins of other plant species (Figure 3C). The phylogenetic tree showed 8 distinct clades distributed in 8 plant families: *Solanaceae, Vitaceae, Amaranthaceae, Cucurbitaceae, Malvaceae, Rosaceae, Fabaceae,* and *Brassicaceae*.

5.3.5 Transcriptomic changes in tomato leaves RNA-seq-based

To confirm the expression of the acylsugar pathway components, RNA-seq data of *S. lycopersicum* and *S. pennellii* were searched on the publicly available database Sequence Read Archive (SRA) (Dai et al., 2017). The results confirmed the expression of genes identified in the leaves of the two species (Figure 4). Eighteen genes (*Acetyl-CoA synthase, AT2, 3 AT3, 2 AKR, BCAT, BCKD E1a, 3 BCKD E2, IPDS, IPMD, IPMSA, Isovaleryl-CoA dehydrogenase 1, KAS II,* and *KAS III*) involved in the acylsugar processing pathway were found to be differentially expressed (DE) in *S. lycopersicum* and *S. pennellii* leaf samples.

Among 18 DE genes, 12 were up-regulated (*AT2,* three *AT3, AKR, BCAT,* two *BCKD E1a, BCKD E2, IPMSA, KAS II,* and *KAS III*) and 6 were down-regulated (*Acetyl-CoA synthase*, *AKR, BCKD E1a, IPDS, IPMD, Isovaleryl-CoA dehydrogenase 1*) in *S. pennellii*. Considering the relative expression in LogFC, *AT2* was the most expressed gene in *S. pennellii* leaves. Then, the *BCAT, AT3, IPMSA,* and *KAS III* genes showed the highest expression in the leaves of wild tomato compared to cultivated tomato. The down-regulated genes in *S. pennellii* and up-regulated in *S. lycopersicum* were *AKR, IPDS, BCKD E1a, Acetyl-CoA synthase,* and *Isovaleryl-CoA dehydrogenase 1*.

5.3.6 Real-time PCR validation of the BCKD E2, IPMSA and TD transcripts involved in the acylsugar pathway in *S. pennellii* (LA-716) and *S. lycopersicum* (TOM-687)

The leaf trichome samples from *S. pennellii* and *S. lycopersicum* were collected at three different times: 30, 60, and 90 days after planting to analyze the vegetative growth, flowering and fruiting, respectively. The real-time PCR analysis displayed different expression levels of the BCKD E2, IPMSA and TD transcripts.

The BCKD E2 transcripts had a different expression among the tomato species. *S. pennellii* BCKD E2 transcripts showed higher expression compared to *S. lycopersicum* BCKD E2 transcripts (p=0.000) (Figure 5A and Supplementary Table S4). Regarding the different times (30, 60, and 90 days), *S. pennellii* BCKD E2 transcripts showed higher expression (p<0.05) compared to *S. lycopersicum* BCKD E2 transcripts (Figure 5B and Supplementary Table S5).

Similar to BCKD E2, the IPMSA transcript showed higher expression in *S. pennellii* than in *S. lycopersicum* (p=0.000) (Figure 5C, 5D, and Supplementary Table S4). Regarding the three times studied, just as with the *BCKD E2* gene, the *S. pennellii* IPMSA transcript showed higher expression (p<0.05) at the three times (30, 60, and 90 days) than the *S. lycopersicum* IPMSA transcript at the three times. In addition, *S. pennellii* at 90 days showed higher expression than at 30 days (p=0.000), but showed lower expression than at 60 days (p=0.004). The *IPMSA* gene was more expressed at 60 days (p=0.004) compared to 90 days in *S. lycopersicum* (Figure 5D and Supplementary Table S6).

In contrast to BCKD E2 and IPMSA, the TD transcripts in the first analysis showed no different expression (p>0.05) between the two tomato species (Figure 5E and Supplementary Table S4). However, regarding the different times, it was observed a higher expression of the two tomato species at 60 days (flowering stage) compared to 30 days (vegetative growth stage), and 90 days (fruit set stage). Besides, the *S. pennellii TD* genes at the time of 60 days were more expressed than at 30 and 60 days (Figure 5F and Supplementary Table S7).

5.4 DISCUSSION

To better understand the biology, evolution, and domestication of the tomato regarding the acylsugars and the genes of their metabolic pathway, *in silico* and *in vitro* analysis were performed in cultivated tomato *S. lycopersicum* and the wild tomato *S. pennellii*. Overall, our results suggest that the acylsugar pathway genes are conserved in both tomato species, demonstrating a similar evolutionary pattern. However, a greater number of genes were found in cultivated tomato and higher levels of expression of these genes were found in the wild tomato. These findings suggest a possible gain of genes along the evolution and

domestication, together with a decrease in the expression of those genes due to the presence of isoforms, thus sharing or lacking their functions.

We identified 87 and 77 putative proteins involved in the acylsugar processing pathway in *S. lycopersicum* and *S. pennellii*, respectively (Supplementary Table S2). The analysis revealed that the components of this pathway in both tomato species were highly conserved at the amino acid level showing conserved domains (Supplementary Table S3 and Supplementary Figure S1), conserved amino acid residues in catalytic sites (Figure 2), and a phylogenetic distribution similar to the tree of life (Figure 3). These results were observed in the three protein families BCKD E2, IPMSA, and TD in both tomato species. These proteins play a key role in the acylsugar pathway according to other studies (Kandra et al., 1990; Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990). However, the complete pathway of acylsugar in plants has not been described yet in the literature (Kandra et al., 1990; Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990; Xu et al., 2013).

The genes BCKD E2, IPMSA, and TD perform important functions in the production of acylsugars. Among all proteins identified, one of the BCKD E2 family was found in both *S. lycopersicum* and *S. pennellii* genomes (Supplementary Table S2, Supplementary Figure S1A, and Supplementary Table S3). These genes have been also identified in other plant species (e.g., *Humulus lupulus* and *N. benthamiana*) (Slocombe et al., 2008; Walters and Steffens, 1990; Xu et al., 2013). The BCKD E2 protein active sites contained the important catalytic residue K (lysine) in a specific and conserved position (Figure 2A). This lysine residue is critical in the performance of these proteins because the BCKD E2 proteins catalyze the transfer of the acyl group of CoA to the reductive acetylation of a lipoyl group that is covalently attached to the lysine residue (CDD, 2016). This high conservation at the amino acid level in the active site might be directly related to the normal function of the BCKD E2 proteins in the acylsugar processing pathway in different species.

The IPMSA is another important catalytic component of the acylsugar processing pathway in plants. In *S. lycopersicum* and *S. pennellii,* three and four of these proteins were identified, respectively, and were also present in other plant species such as *N. benthamiana* (Slocombe et al., 2008). Members of the IPMS

protein family have a conserved HMGL-like triose-phosphate isomerase (TIM) domain (Supplementary Figure S1B and Supplementary Table S3). This catalytic domain contains a nucleus with a binding site at the divalent cation consisting of a conserved residue set that includes three invariant residues: one aspartate (D), one arginine (R), and one glutamate (E) (CDD, 2016), which were found in all IPMSA proteins of the two tomato species studied (Figure 2B).

In addition, four putative TD proteins were found in *S. lycopersicum* and three in *S. pennellii* (Supplementary Table S2, Supplementary Figure S1C, Figure 2C, and Supplementary Table S3). This protein family has also been found in other plants (e.g., *N. benthamiana*) (Slocombe et al., 2008). The PALP conserved domains identified in TD proteins had a catalytic K residue (Figure 2C). The members of this protein family are pyridoxal phosphate-dependent enzymes (PLP), which form an internal aldimine bond (Schiff base) for the action of the catalytic lysine residue (CDD, 2016). Thus, the high conservation of the domains and of the catalytic residues found in the Sly/Spe TD proteins suggest an important role of these proteins in plants, especially in the acylsugar pathway.

The phylogenetic analysis of the tomato proteins BCKD E2, IPMSA, and TD and their orthologs from other plant species corroborated with the distribution of species across the tree of life (Figure 3) (Stevens, 2001). These findings suggest high conservation among the members of the BCKD E2, IPMSA, and TD family in *Angiosperms*. Thus, it can be observed that the BCKD E2, IPMSA, and TD proteins of *S. lycopersicum* and *S. pennellii* are highly conserved, thus highlighting the great importance of these proteins in acylsugar processing in *Solanaceae*.

The validation of the acylsugar pathway genes in the libraries available in the SRA (Dai et al., 2017) showed the DE of 18 genes identified in *S. lycopersicum* and *S. pennellii* (Figure 4). The DE genes in the two species were *Acetyl-CoA synthase, AT2, AT3, AKR, BCAT, BCKD E1a, BCKD E2, IPDS, IPMD, IPMSA, Isovaleryl-CoA dehydrogenase 1, KAS II,* and *KAS III*. Twelve genes were up-regulated in *S. pennellii* and 6 were up-regulated in *S. lycopersicum*. The most expressed genes in *S. pennellii* leaves were *AT2, BCAT, AT3, IPMSA,* and *KAS III*. The AT3 and AT2 families belong to the BAHD class of acyltransferases and catalyze the third and fourth steps, respectively, of tetraacylsucrose biosynthesis in tomato, being required for adding the acetyl (C2) group found in the major

detectable tetra-acyl sucroses (Schilmiller et al., 2015, 2012). The BCAT family participates significantly in the leucine, isoleucine, and valine metabolism and is involved both in BCAA biosynthesis and degradation (Diebold et al., 2002). In addition, the KAS family is involved for both the branched and straight medium-chain fatty acid elongation in the trichome (Slocombe et al., 2008).

The BCKD E2 and IPMSA transcripts expressed differently between the species, with *S. pennellii* showing higher expression than *S. lycopersicum* at all three times (Figure 5A, 5B, 5C, 5D, Supplementary Tables S4, S5, and S6). However, the TD transcripts showed no different expression (p>0.05) between the different tomato species (Figure 5E and Supplementary Table S4), but had a different expression among the different times (Figure 5F and Supplementary Table S7). The 60-day plants showed higher expression of the gene in one species of tomato when compared to the 30 and 90 days of the other species, which indicates a greater production of metabolites in the flowering stage, suggesting that at this development stage the plant demands more defense against pests that may be attracted by flowers. These results show that, in the wild tomato, the BCKD E2 and IPMSA transcripts were more expressed compared to the cultivated tomato. In addition, the *TD* expression suggests that this gene plays an important role in tomato leaves, considering the high expression in both species, even though there is no DE. This suggests that *TD* gene might be important not only in acylsugar processing pathway but also in other metabolic pathways in tomato leaves.

The BCKD E2 and IPMSA proteins act on the acylsugar metabolism in the decarboxylation process in the keto acid conversion of the branched-chain acyl-CoAs and in the catalysis of the first step in leucine biosynthesis, producing 2-isopropylmalate and CoA (CDD, 2016; Hoeven et al., 2000; Slocombe et al., 2008). Therefore, this result shows a greater requirement of these genes in leaves, mainly in *S. pennellii*, suggesting an essential role in this tissue.

As these genes are important in the acylsugar synthesis in tomato trichomes, our results suggest that *S. pennellii* might display higher acylsugar production, which has been also shown in other studies (Gentile et al., 1968; Hoeven et al., 2000; Resende et al., 2002; Slocombe et al., 2008). Gentile et al. (1968) observed leaf resistance to whitefly in *S. pennellii* compared to other

tomato species. This resistance was observed by the sticky glandular exudate on the leaf surfaces, which is a death trap for the eggs laid on the leaves and for the adults moving on the leaves. These results indicate the presence of acylsugars, which offers resistance to arthropods in the tomato leaves (Gentile et al., 1968). Resende et al. (2002) confirmed the acylsugar presence on the leaf tomato surface of the genotype wild LA-716, which was also evaluated in our study (Resende et al., 2002). Resende et al. (2002), Neto (2008), and Lucini et al. (2015) found a higher acylsugar content in LA716 (63.75, 0.624, and 297.91 nmol/cm^2, respectively) compared to *S. lycopersicum* lines (28.26, 0.225, and 33.71 nmol/cm^2, respectively) using a colorimetric method (Lucini et al., 2015; Neto, 2008; Resende et al., 2002).

The *S. pennellii* lines used for the analysis (LA-716) showed higher acylsugar content compared to *S. lycopersicum* lines (TOM-687) in other studies (Lucini et al., 2015; Neiva et al., 2013; Neto, 2008; Talekar et al., 2006). Moreover, the expression of the pathway genes in *S. pennellii* was higher than the expression in *S. lycopersicum*.

Thus, our results demonstrate that the *BCKD E2* and *IPMSA* genes may surely be involved in acylsugar processing in tomatoes, especially in *S. pennellii*, which has a higher expression of these genes and higher production of these allelochemicals. In addition, the *TD* expression in the evaluated species suggests that this gene plays an important role in the tomato leaves. Our result suggests that these proteins are indeed important in the acylsugar processing in tomato leaves and may help to find new strategies to improve plant resistance to arthropod pests and to study the relationship between evolution, acylsugar synthesis, and biotic resistance in these two tomato species.

5.5 CONCLUSION

Considering the great importance of tomatoes and the high rate of application of agrochemicals, knowing the genes involved in the production of secondary metabolites that naturally protect the plant is necessary. In this way, the understanding of the possible involvement of acylsugars in resistance to arthropods and their association with markers related to important characteristics

will assist in the genetic improvement of these two tomato species seeking a response to the control of biotic stress. In this sense, bearing in mind the important role of allelochemical production in *Solanaceae*, our results contribute to a better understanding of acylsugars and their processing pathways and opens up opportunities to study their relationship with biotic resistance in these important vegetable crop species and other *Solanaceae* species.

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Conflict of interest

The authors declare that they have no conflict of interest.

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TABLES

Table 1. Studies that have shown the contribution of some genes to the acylsugar metabolism in plants.

Genes	References
Acetyl-CoA synthase	Kandra et al., 1990
Aldo keto reductase (AKR)	Sengupta et al., 2015
Acetolactate/acetohydroxyacid synthase (ALS/AHAS)	Kroumova and Wagner, 2003; Ning et al., 2015; Slocombe et al., 2008
Acylsugar acyltransferase 2/4/3 (AT2/AT4/AT3)	Kim et al., 2012; Leckie and Halitschke, 2014; Ning et al., 2015; Schilmiller et al., 2012
Branched-chain aminotransferase 2/5 (BCAT)	Ning et al., 2015
Branched-chain keto acid dehydrogenase E1a/E1b/E2 (BCKD)	Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990
Dihydroxyacid dehydratase (DHAD)	Leckie and Halitschke, 2014; Ning et al., 2015; Walters and Steffens, 1990
Dihydrolipoyl dehydrogenase (IPD)	Kandra et al., 1990
Isopropylmalate dehydratase/isopropylmalate isomerase (IPDS/IPMI)	Kandra et al., 1990; Kroumova and Wagner, 2003; Slocombe et al., 2008
Isopropylmalate dehydrogenase (IPMD)	Kandra et al., 1990; Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990
2-isopropylmalate synthase A/B (IPMSA/IPMSB)	Hoeven et al., 2000; Kandra et al., 1990; Leckie and Halitschke, 2014; Ning et al., 2015; Slocombe et al., 2008
Isovaleryl-CoA dehydrogenase 1 mitochondrial/methylacyl-CoA dehydrogenase	Walters and Steffens, 1990
Keto acid/acetohydroxyacid reductoisomerase I (KARI)	Ning et al., 2015; Walters and Steffens, 1990
Ketoacyl-ACP synthase (KAS) I, II, III; KAS mitocondrial	Slocombe et al., 2008
3-ketoacyl-CoA reductase 2 (KCR2)	Mcdowell et al., 2011
3-ketoacyl-CoA synthase 3/19 (KCS3/KCS19)	Leckie and Halitschke, 2014; Mcdowell et al., 2011
Threonine deaminase/dehydratase (TD)	Ning et al., 2015; Slocombe et al., 2008; Walters and Steffens, 1990

FIGURES

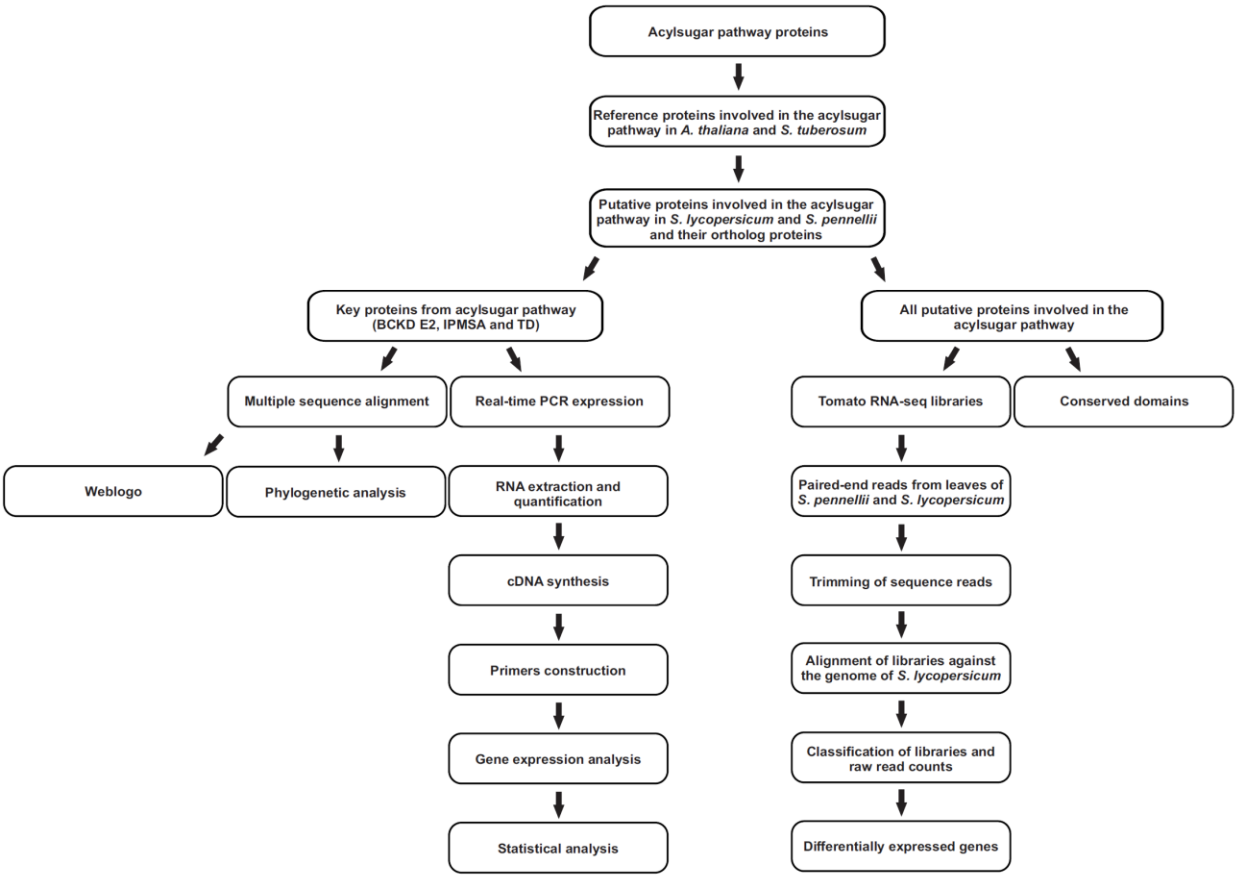


Figure 1. Flowchart of computational identification and characterization of acylsugar pathway genes in *S. lycopersicum* and *S. pennellii*.

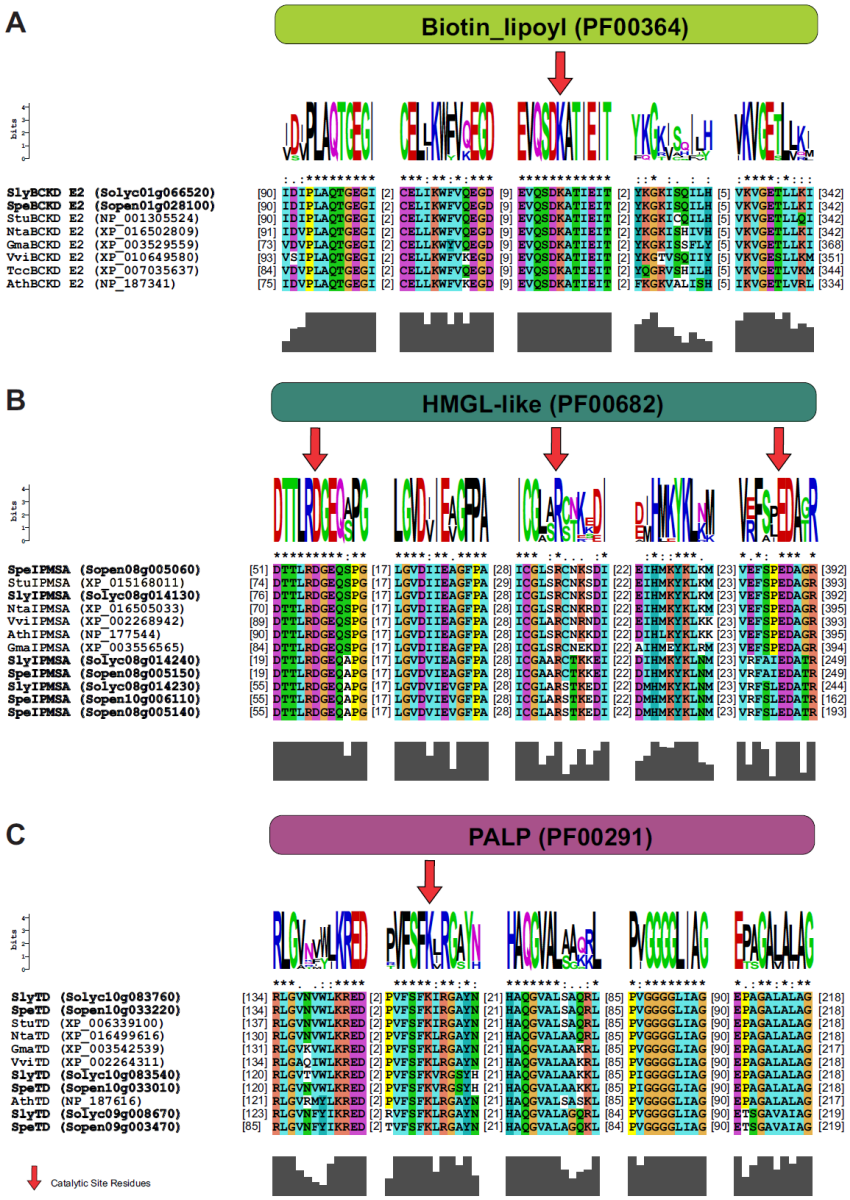


Figure 2. (A) Weblogo analysis and sequence multiple alignment of Biotin_lipoyl (PF00364) conserved domain from BCKD E2 proteins of *S. lycopersicum*, *S. pennellii* and their orthologs. The red arrow showed the amino acid residue of the active site (lysine - K). (B) Weblog analysis and sequence multiple alignment of conserved domain HMGL-like (PF00682) from the IPMSA proteins of *S. lycopersicum*, *S. pennellii* and their orthologs. The red arrows show the amino acid residues of the active site catalytic triad (aspartate - D, arginine - R and glutamate - E). (C) Weblogo analysis and sequence multiple alignment of domain PALP (PF00291) from the TD proteins of *S. lycopersicum*, *S. pennellii* and their orthologs. The red arrow shows the amino acid residue of the active site (lysine - K). The height of each amino acid symbol indicates the residue conservation in that position. Asterisks indicate the conserved amino acids in the specified position. Sly - *Solanum*

lycopersicum, Spe - *Solanum pennellii,* Stu – *Solanum tuberosum,* Nta – *Nicotiana tabacum,* Tcc - *Theobroma cacao,* Gma - *Glycine max*, Ath - *Arabidopsis thaliana* and Vvi - *Vitis vinifera.*

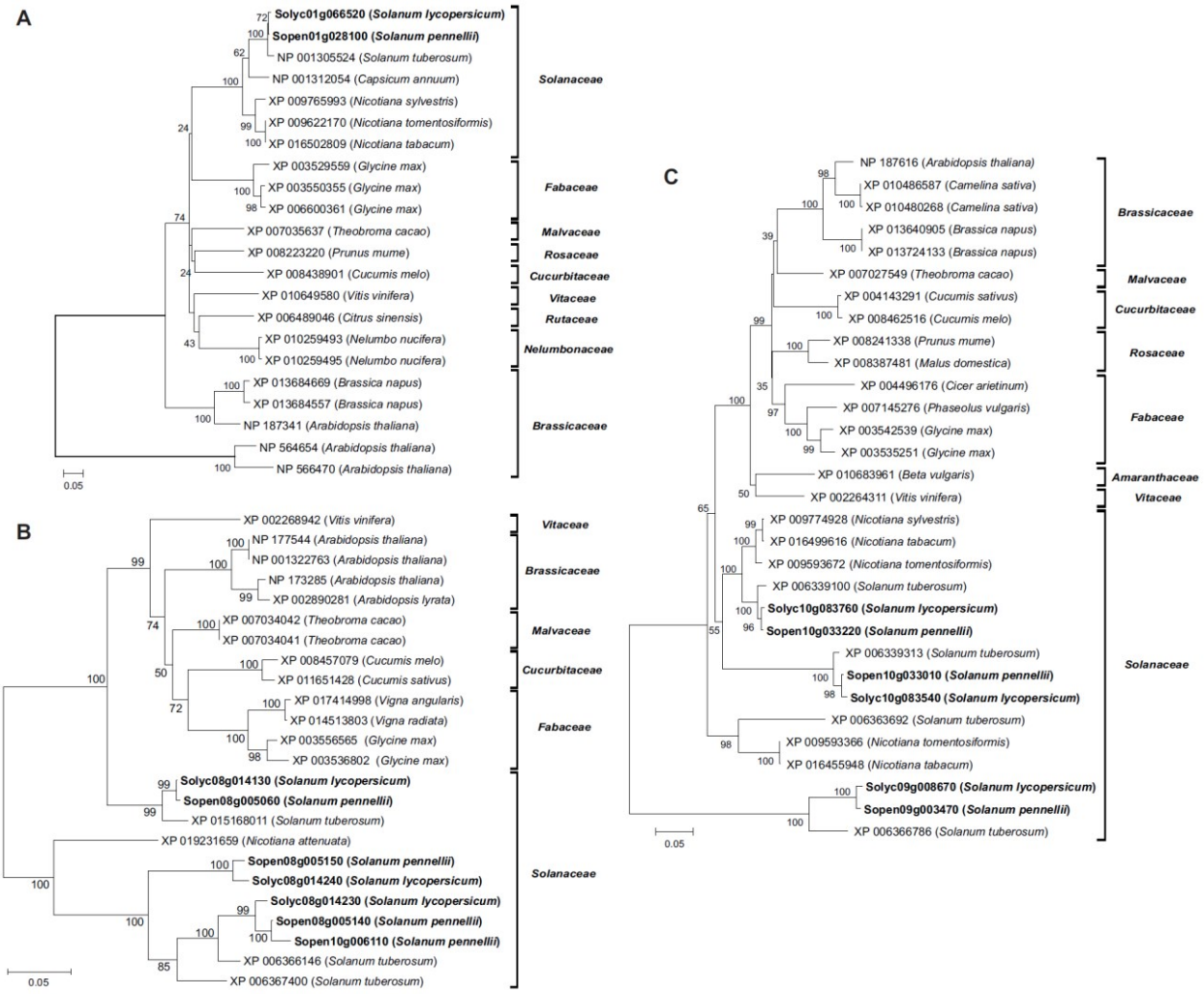


Figure 3. Phylogenetic tree of (A) BCKD E2, (B) IPMSA and (C) TD proteins identified in *S. lycopersicum*, *S. pennellii* and their orthologs.

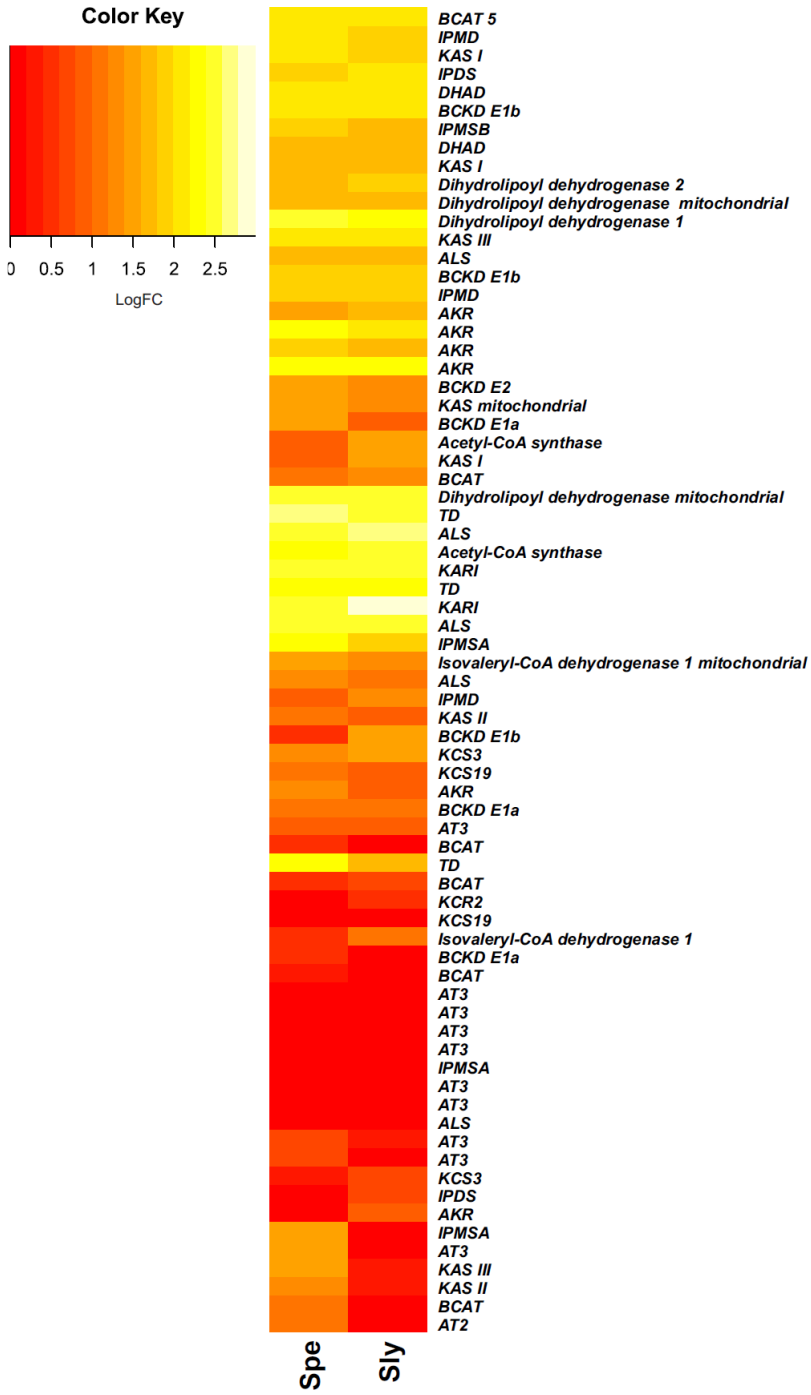


Figure 4. Heatmap analysis of the genes involved in the tomato acylsugar pathway from leaves RNA-seq libraries. Heatmap showed the expression profile of the *S. lycopersicum* (Sly) and *S. pennellii* (Spe) genes in leaves.

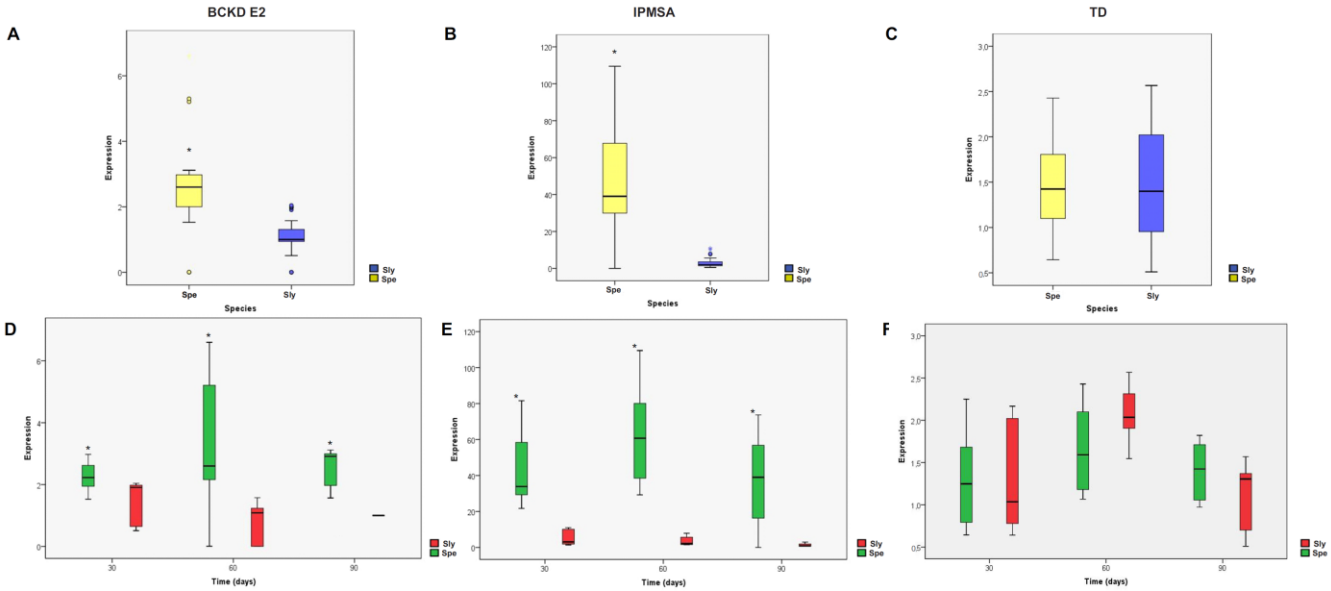
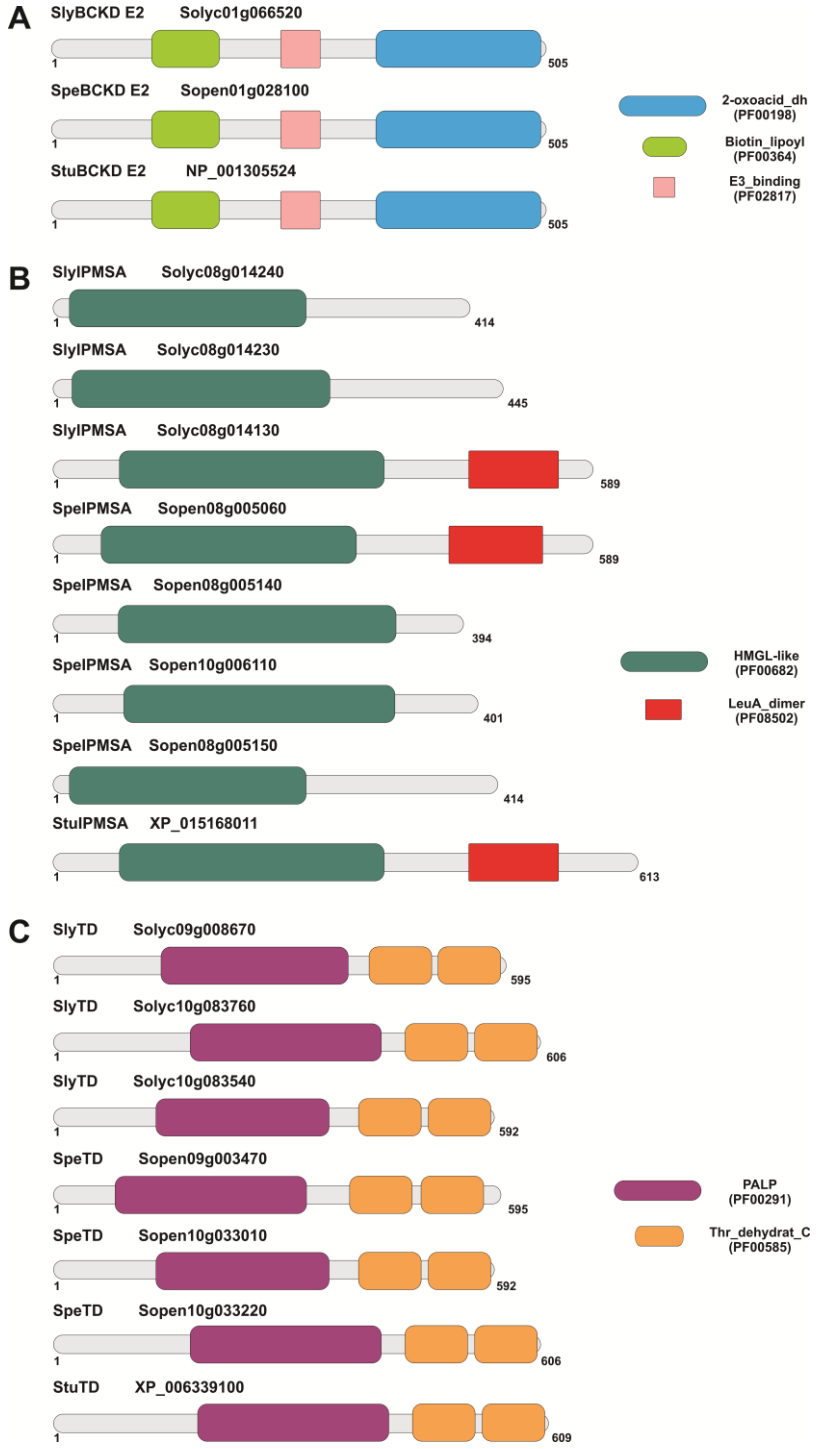


Figure 5. General relative expression of the (A) *BCKD E2,* (C) *IPMSA* and (E) *TD* genes in leaves of the *S. pennellii* (LA-716) and *S. lycopersicum* (TOM-687) and relative expression of the (B) *BCKD E2,* (D) *IPMSA* and (F) *TD* genes in three times (30, 60 and 90 days). Sly - *Solanum lycopersicum* and Spe - *Solanum pennellii.*

SUPPLEMENTARY FIGURE

Supplementary Figure S1. Conserved domain distribution in putative (A) BCKD E2, (B) IPMSA and (C) TD proteins of *S. lycopersicum*, *S. pennellii* and their ortholog of *S. tuberosum.*



6 RESULTADOS COMPLEMENTARES - Article: Description of acylsugar pathway, miRNA pathway and miRNA molecules in seven tomato species for submission in Molecular Genetics and Genomics Journal

6.1 The small RNAs processing and acylsugar pathway in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum* and *S. pimpinellifolium*: analysis of conserved protein domains, active sites and phylogenetic trees

6.1.1 AGO and DCL proteins

Using a local alignment of the 42 *S. lycopersicum* and *S. pennellii* mRNA, previously identified (Cardoso et al. 2018), against the *S. galapagense, S. chilense, S. peruvianum* and *S. pimpinellifolium* genomes, as well as the presence and arrangement of conserved domains, we predicted proteins involved in the biogenesis of small RNAs (siRNAs, tasiRNAs and miRNAs) (Jones-Rhoades et al. 2006; Bologna and Voinnet 2014). Were identified 18 AGO and 10 DCL proteins in *S. galapagense*, 11 AGO and 10 DCL proteins in 1 *S. peruvianum,* 16 AGO and 8 DCL proteins in *S. chilense,* 17 AGO and 10 DCL proteins in *S. pimpinellifolium* LA1589 and 18 AGO and 10 DCL proteins in *S. pimpinellifolium* LA0480 (Supplementary Table S1).

Among the proteins involved in small RNA processing, AGO1, AGO10 and DCL1 proteins participate in the miRNA pathways. We found 2 AGO1 proteins in *S. galapagense, S. chilense* and *S. pimpinellifolium* and 1 AGO1 in *S. peruvianum.* We also found 2 AGO10 proteins and 1 DCL1 protein in each specie analysed.

We search the conserved domains of the all AGO proteins in species studied (Figure 1, Figure 2 and Supplementary Table S2). The AGO1 proteins identified in all species displayed the Gly-richAgo1, ArgoN, ArgoL1, PAZ, ArgoL2, ArgoMid and Piwi domains, except the contig:385000:1:10591:1 protein of the *S. pimpinellifolium* LA1589 that did not have Gly-richAgo1 and ArgoL1 domains, probably because it was truncated at the beginning of the sequence due to the sequencing of the genome (Figure 1 and Supplementary Table S2). Similar results were observed for the AGO10 proteins, which displayed the ArgoN, ArgoL1, PAZ,

34 ArgoL2, ArgoMid and Piwi domains, except the scaffold28885_12.6 protein of the
35 *S. galapagense* that have Gly-rich domain; and scaffold1098 and
36 contig:6745152:1:10334:1 proteins of the *S. chilense* and
37 contig:6745152:1:10334:1 *S. pimpinellifolium* LA1589 that, respectively, did not
38 showed ArgoL1 domain (Figure 2 and Supplementary Table S2).
39

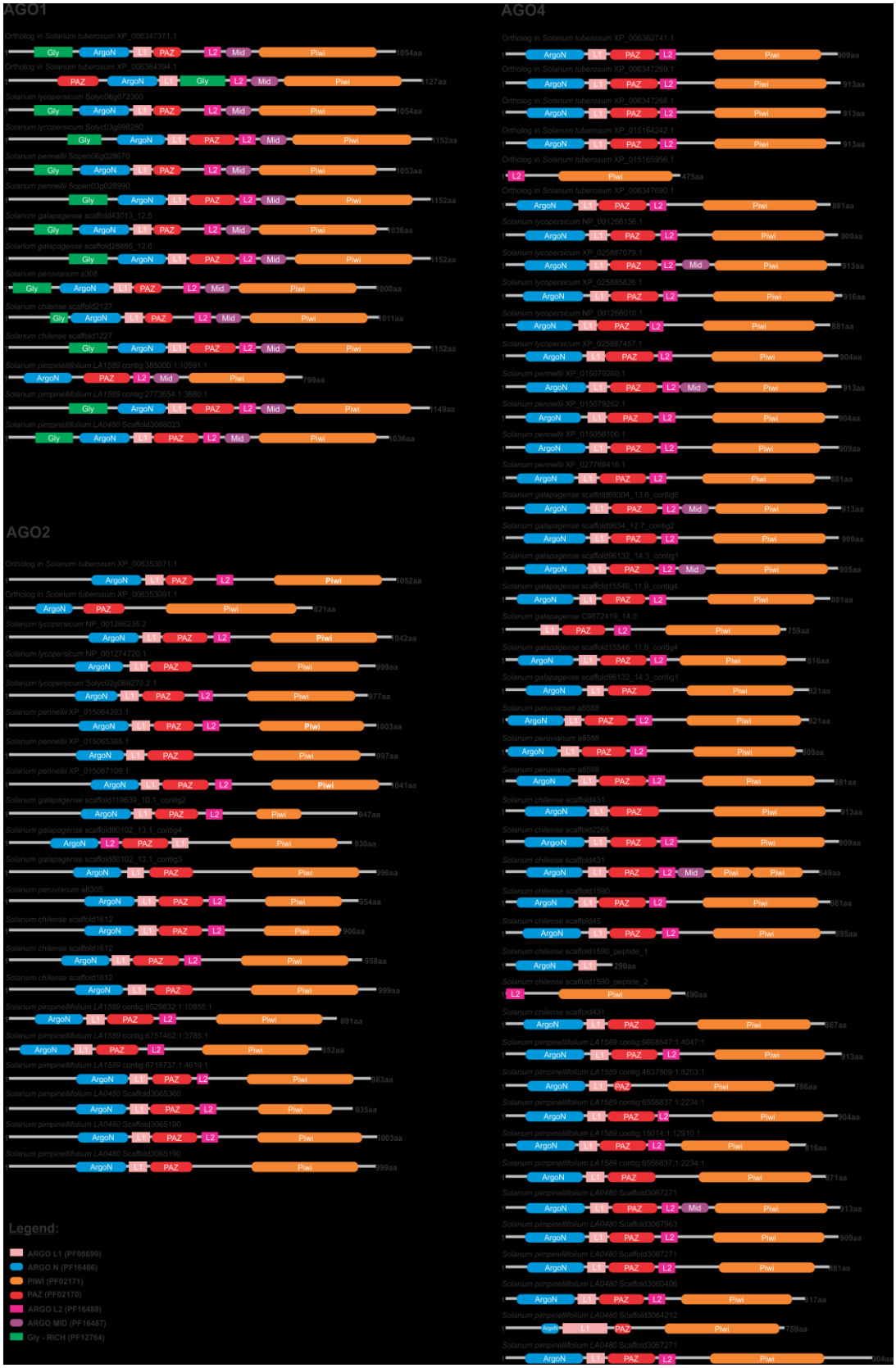


Figure 1 - Distribution of conserved domains in AGO1, AGO2 and AGO4 putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

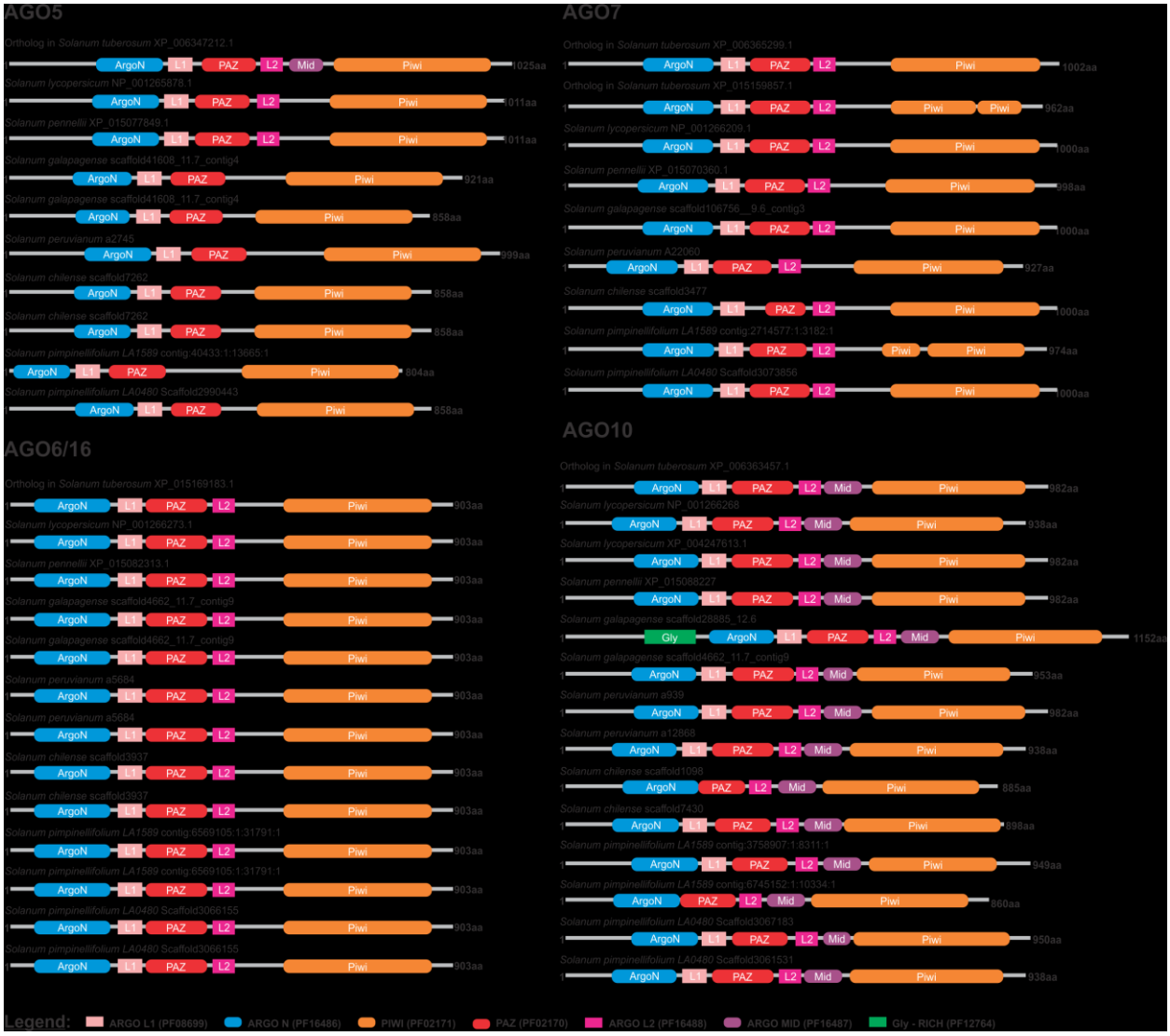
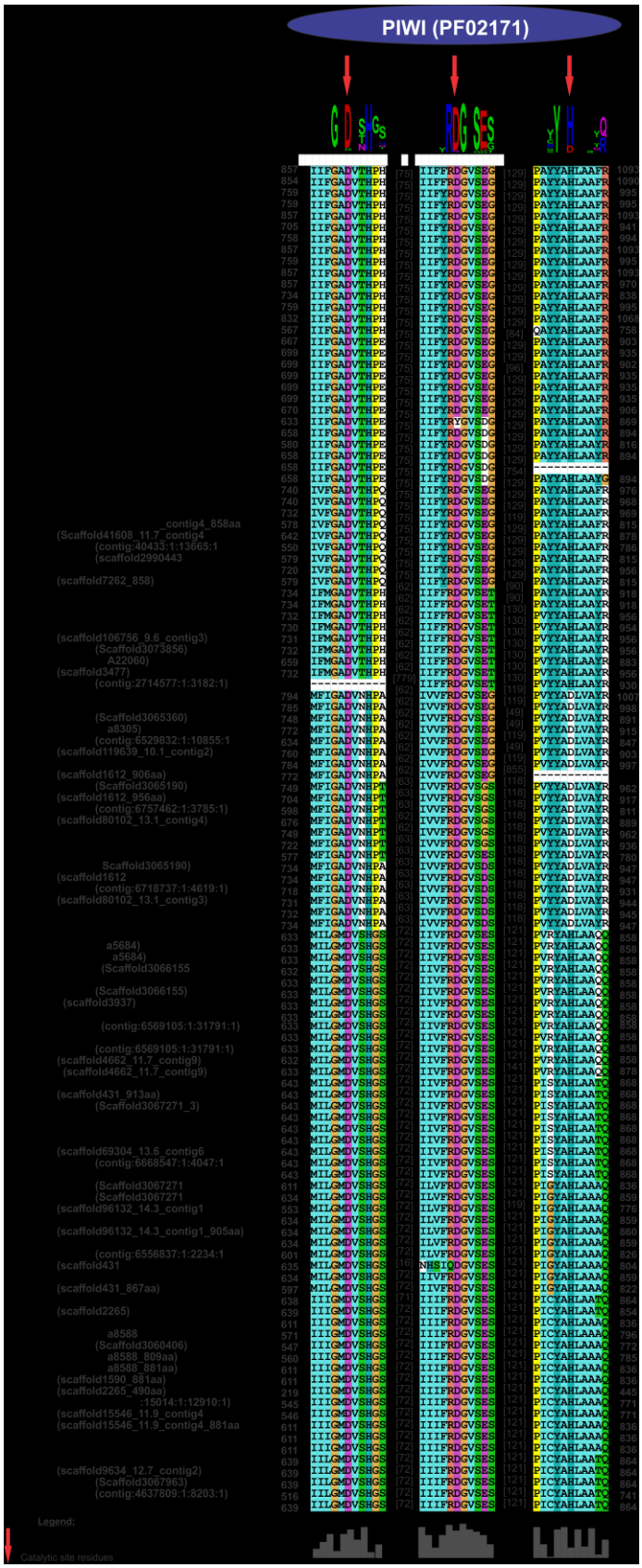


Figure 2 - Distribution of conserved domains in AGO5, AGO6/16, AGO7 and AGO10 putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

The Piwi conserved domain, one of the main domains present in AGO proteins, was identified in all AGO proteins of the species studied. These domains showed active site regions containing an important catalytic triad DDH (aspartate/aspartate/histidine) in all AGO pronteins, except AGO2 protein that showed active site regions the catalytic triad DDD (aspartate/aspartate/aspartate). The scaffold104755_11.7_contig5 of the SgaAGO10 exhibited the catalytic triad DYD (aspartate/tyrosine/histidine). Moreover, the SchAGO10 (scaffold7430) and

SchAGO2 (scaffold1612_906aa) showed truncated at the end and the SpiLA1589 AGO7 (contig:2714577:1:3182:1) at the beginning of the sequence (Figure 3).



60 **Figure 3 -** Weblogo analysis and sequence multiple alignment of active site amino
61 acids and their flanking amino acid residues in the PIWI conserved domain of *S.*
62 *lycopersicum* (Sly), *S. pennellii* (Spe), *S. galapagense* (Sga), *S. chilense* (Sch), *S.*
63 *peruvianum* (Spr), *S. pimpinellifolium* LA0480 (SpiLA0480), *S. pimpinellifolium* LA1589
64 (SpiLA1589) and their ortholog in *S. tuberosum*. The red arrows show the amino acid
65 residues of the active sites (catalytic triad: Asp-Asp-His). The height of each amino acid
66 symbol in Weblogo indicates amino acid residue conservation at a given position.
67
68 We also search the conserved domains of the all DCl proteins in species
69 studied (Figure 4, Figure 5, Figure 6 and Supplementary Table S3). The DCL1
70 proteins of the all species anlised displayed the conserved ResIII (also known as
71 DEAD-like), helicase C, Dicer dimer (also known as DUF283), PAZ, ribonuclease
72 IIIa (RNase IIIa), ribonuclease IIIb (RNase IIIb), dsrm and DND1 DSRM domains
73 (Figure 4 and Supplementary Figure S1 and Supplementary Table S4). We found
74 two RNAse III domains in DCL proteins of the all species of this work, except the
75 SgaDCL2 (Scaffold2617_14.2_contig6), SgaDCL2 (Scaffold2617_14.2_contig4),
76 SchDCL2 (Scaffold2617_14.2_contig7), SchDCL2 (Scaffold6549) and *S.*
77 *pimpinellifolium* LA1589 DCL2 (contig:6660195:1:6613:1). The two domains
78 (RNase IIIa and RNase IIIb) had the same catalytic residues in all tomato species
79 studied: glutamate (E), aspartate (D), aspartate (D), glutamate (E), representing
80 the EDDE active site. The SchDCL2 (Scaffold6549_1335aa) and StuDCL2
81 (XP_015169591.1) proteins did not showed the last catalytic residues (DE) of the
82 active site because it was truncated at the sequence end (Figure 7).
83

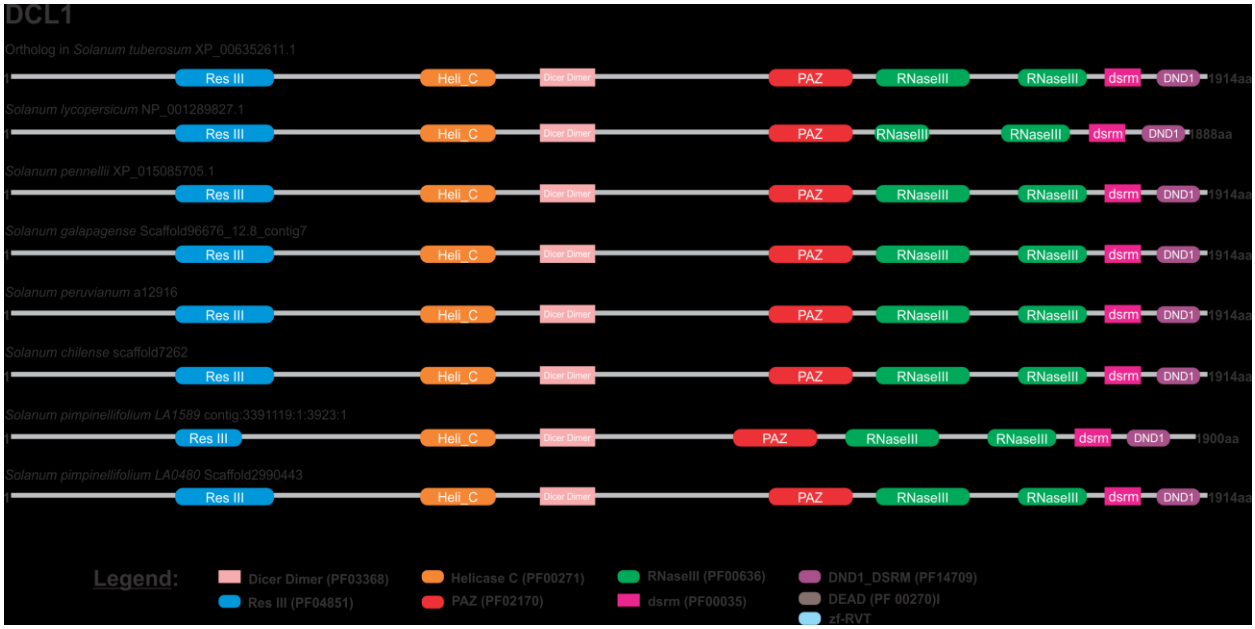


Figure 4 - Distribution of conserved domains in DCL1 putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

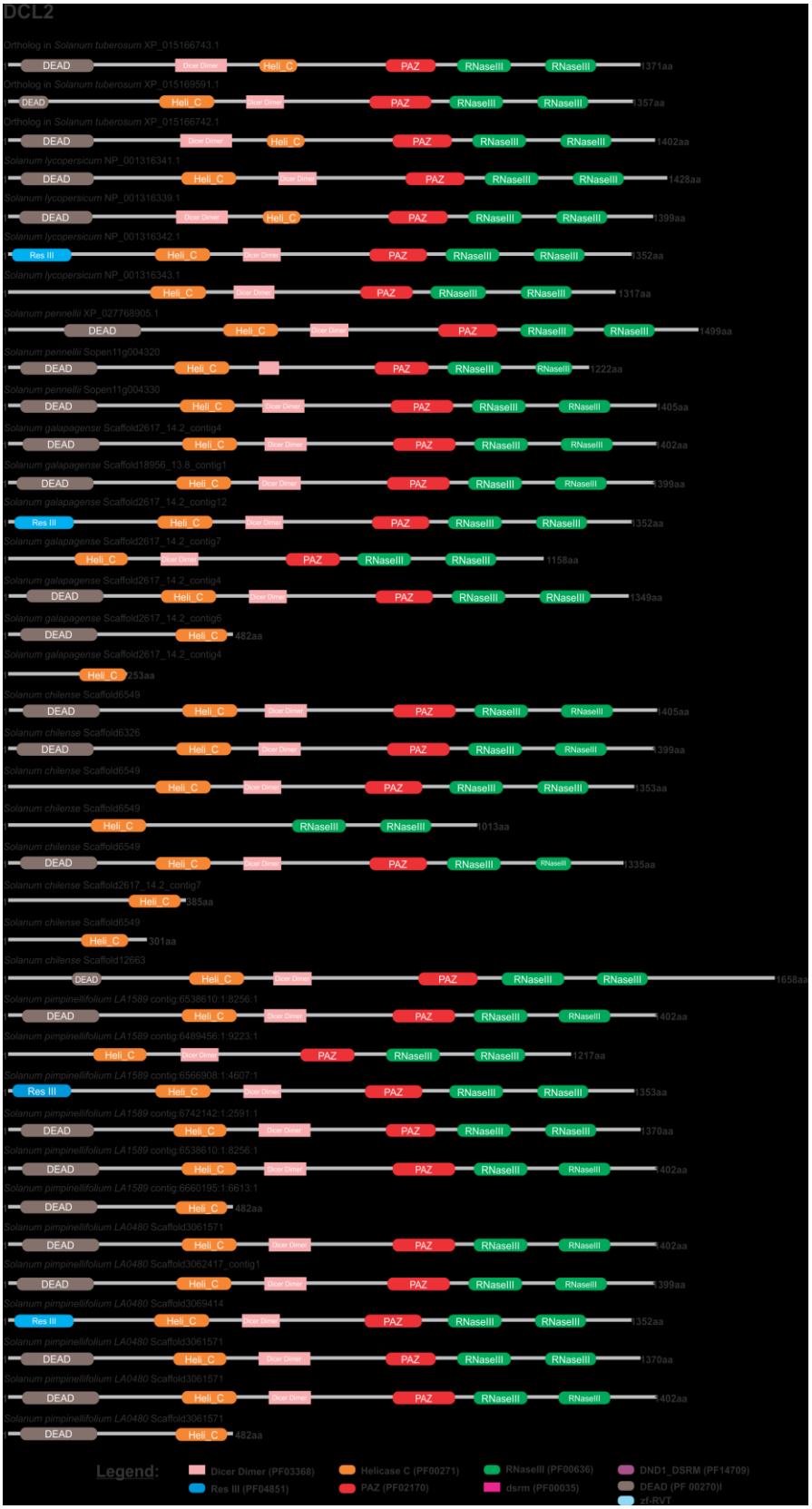


Figure 5 - Distribution of conserved domains in DCL2 putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

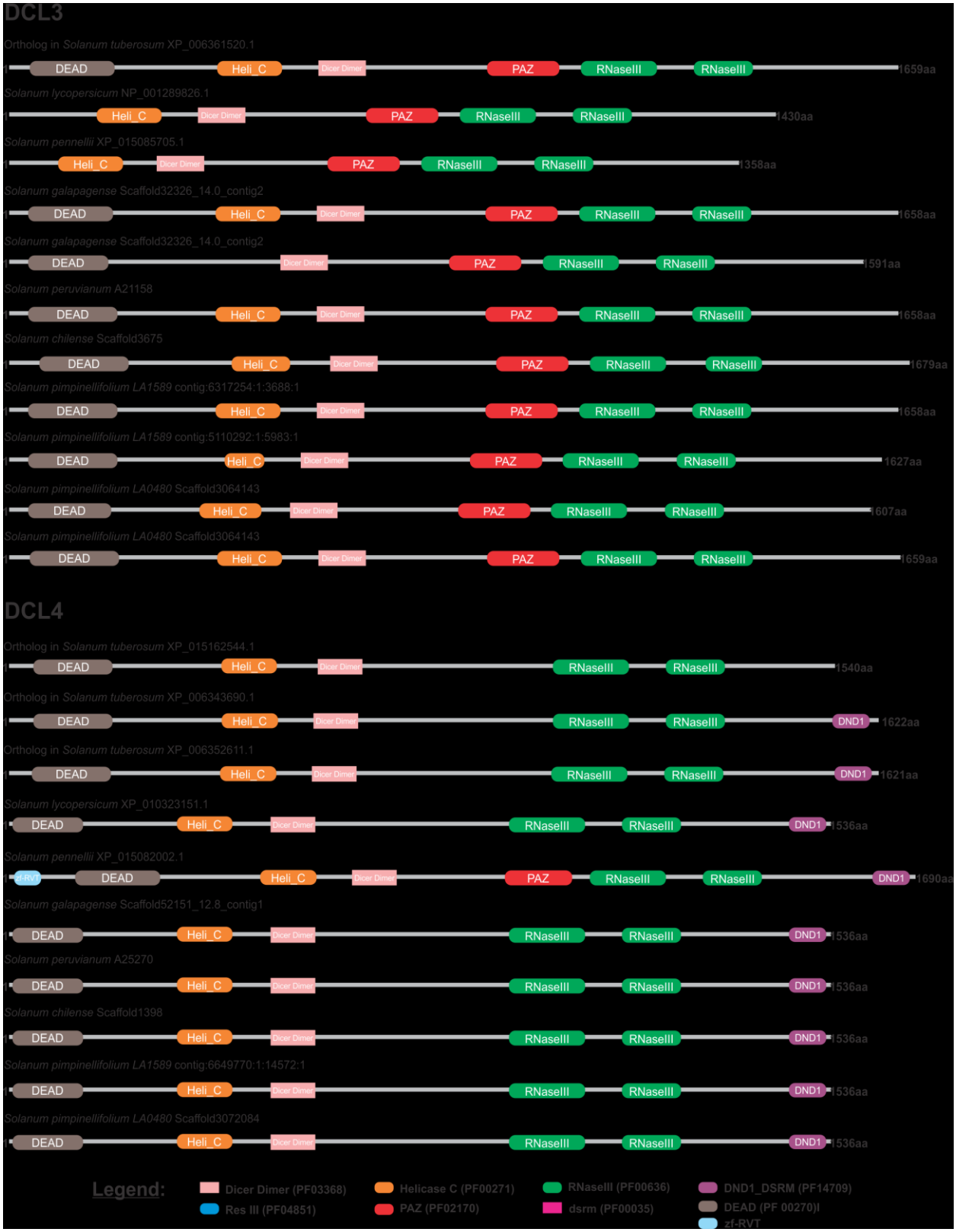


Figure 6 - Distribution of conserved domains in DCL3 and DCL4 putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

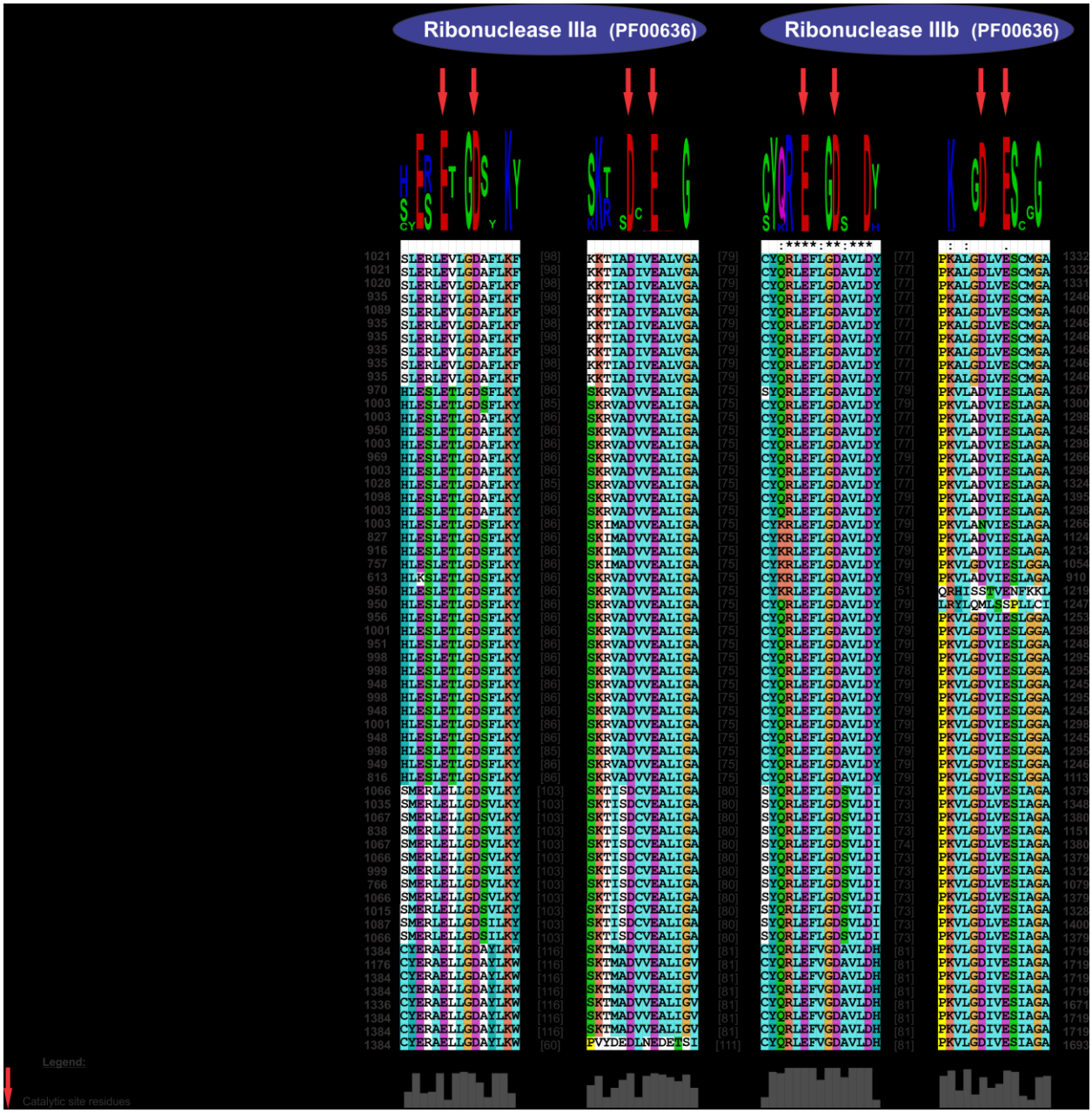


Figure 7 - Weblogo analysis and sequence multiple alignment of active site amino acids and their flanking amino acid residues in the Ribonuclease IIIa and Ribonuclease IIIb conserved domains of *S. lycopersicum* (Sly), *S. pennellii* (Spe), *S. galapagense* (Sga), *S. chilense* (Sch), *S. peruvianum* (Spr), *S. pimpinellifolium* LA0480 (SpiLA0480), *S. pimpinellifolium* LA1589 (SpiLA1589) and their ortholog in *S. tuberosum*. The red arrows show the amino acid residues of the active sites (Glu-Asp-Asp-Glu). The height of each amino acid symbol in Weblogo indicates amino acid residue conservation at a given position.

To understand the diversification of AGO proteins in *S. lycopersicum*, *S. pennellii*, *S. galapagense, S. chilense, S. peruvianum* and *S. pimpinellifolium,* a phylogenetic analysis was performed using their amino acid sequences (Figure 8). The phylogenetic tree was divided into seven distinct clades of paralogous AGOs (AGO1, AGO2, AGO4, AGO5, AGO6, AGO7 and AGO10). The distribution of the seven clades showed a relationship between some paralogous proteins specific to the AGO family, with a great similarity among the AGO1, AGO5 and AGO10 proteins; AGO6 and AGO4; AGO2 and AGO7. The tomato AGO1 and AGO10 proteins showed that they were distributed in the phylogenetic tree closest to their respective orthologous proteins from the plant species *S. tuberosum, Nicotiana attenuata* and *Nicotiniana sylvestris.*

In addition, to determine the evolutionary relationship among the putative DCL proteins of in *S. lycopersicum*, *S. pennellii*, *S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* and their homologous species, a phylogenetic analysis was also conducted. The proteins were grouped through global alignment in four distinct clades (DCL1, DCL2, DCL3 and DCL4). The distribution among the DCL family paralogous showed a strong correlation between the DCL1 and DCL2 proteins, being also close to DCL4 and further away from DCL3 (Figure 9).

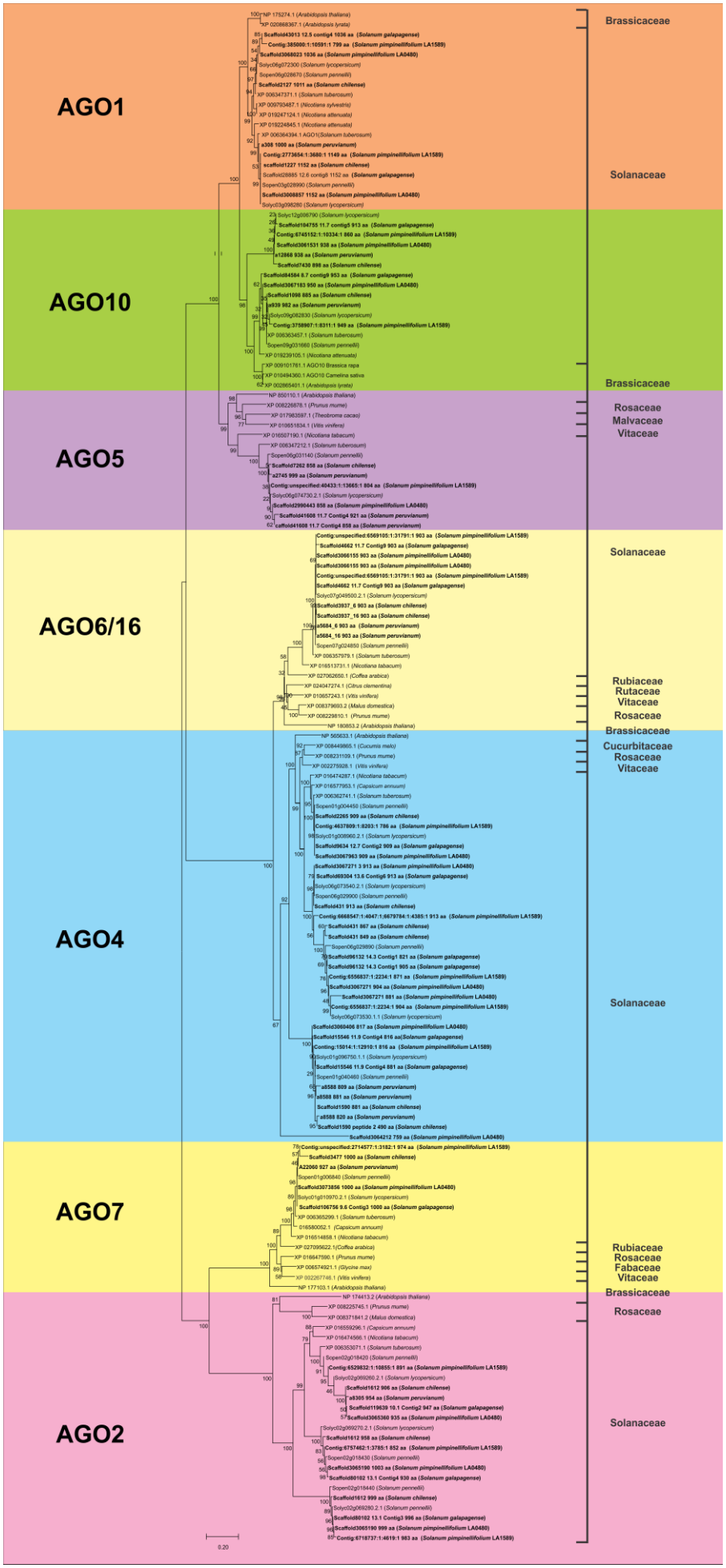

AGO1
AGO10
AGO5
AGO6/16
AGO4
AGO7
AGO2
Brassicaceae
Solanaceae
Brassicaceae
Rosaceae
Malvaceae
Vitaceae
Solanaceae
Rubiaceae
Rutaceae
Vitaceae
Rosaceae
Brassicaceae
Cucurbitaceae
Rosaceae
Vitaceae
Solanaceae
Rubiaceae
Rosaceae
Fabaceae
Vitaceae
Brassicaceae
Rosaceae
Solanaceae
0.20

Figure 8 - Phylogenetic tree of AGO proteins identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

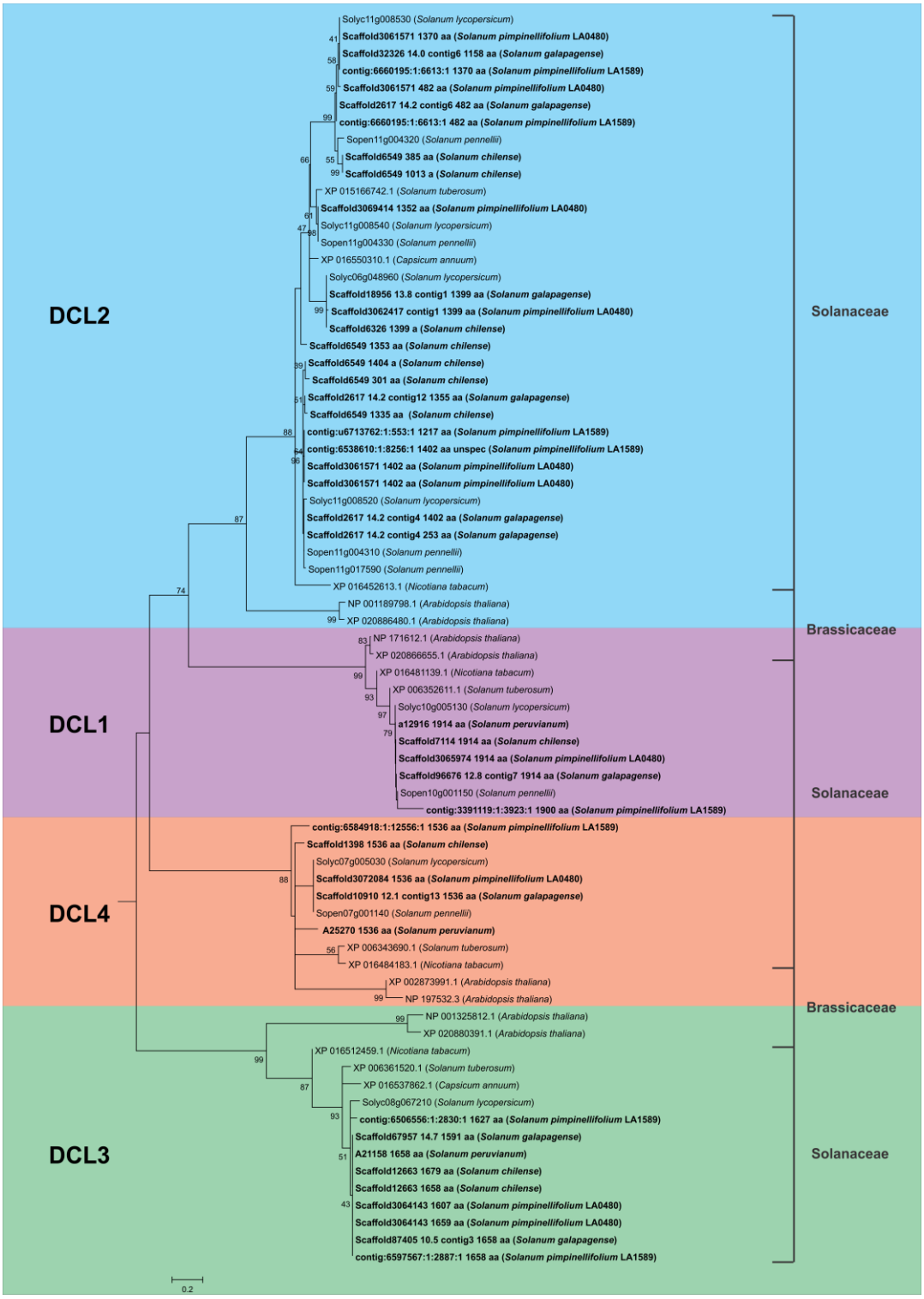


Figure 9 - Phylogenetic tree of DCL proteins identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

136 **BCKD, IPMS and AT proteins**

137

138 In the same way of the small RNA pathway proteins, through BLASTn tool,
139 we made the prediction and characterization of the acylsugar pathway proteins in
140 *S. galapagense, S. chilense, S. peruvianum* and *S. pimpinellifolium* genomes,
141 using 61 mRNA of *S. lycopersicum* and *S. pennellii*, previously identified
142 (Genome-wide identification and characterization of genes involved in the
143 acylsugar pathway in tomato). Were identified 5 IPMS, 11 BCKD and 21 AT
144 proteins in *S. galapagense*, 1 IPMS, 8 BCKD and 1 AT in *S. peruvianum,* 8 IPMS,
145 12 BCKD and 18 AT in *S. chilense,* 4 IPMS, 5 BCKD and 21 AT in *S.*
146 *pimpinellifolium* LA1589 and 4 IPMS, 10 BCKD and 21 AT proteins in *S.*
147 *pimpinellifolium* LA0480 (Supplementary Table S4).

148 Among all putative proteins identified, the putative protein families BCKD
149 E2, IPMSA, and AT were considered key proteins in the processing machinery of
150 acylsugars (Kandra et al. 1990; Walters and Steffens 1990; Slocombe et al. 2008;
151 Ning et al. 2015; Schilmiller et al. 2015; Fan et al. 2016, 2017). We found 1 BCKD
152 E2 proteins in all tomato species studied, 3 IPMSA proteins in *S. pimpinellifolium*
153 LA1589 and *S. pimpinellifolium* LA1589 as in *S. lycopersicum,* 4 in *S.*
154 *galapagense,* 6 in *S. chilense* and none in *S. peruvianum.* In addition, we also
155 found 2 AT2 proteins in *S. galapagense, S. chilense, S. pimpinellifolium,* none in
156 *S. peruvianum*; 19 AT3 proteins in *S. galapagense, S. pimpinellifolium* LA1589, *S.*
157 *pimpinellifolium* LA1589; 16 and 1 AT3 pronteins in *S. chilense* and *S.*
158 *peruvianum,* respectively (Supplementary Table S4).

159 The distribution of the conserved domains of the all BCKD and IPMS
160 proteins were search in the tomato species analised (Figure 10, Figure 11, Figure
161 12, Supplementary Figure S5 and Supplementary Table S6). Furthermore,
162 position of the amino acids from active sites (Figure 13 and Figure 14) and the
163 phylogenetic distribution (Figure 15 and Figure 16) of the putative tomato proteins
164 BCKD E2 and IPMS were obtained compared to the reference homologous
165 proteins from other plant species.

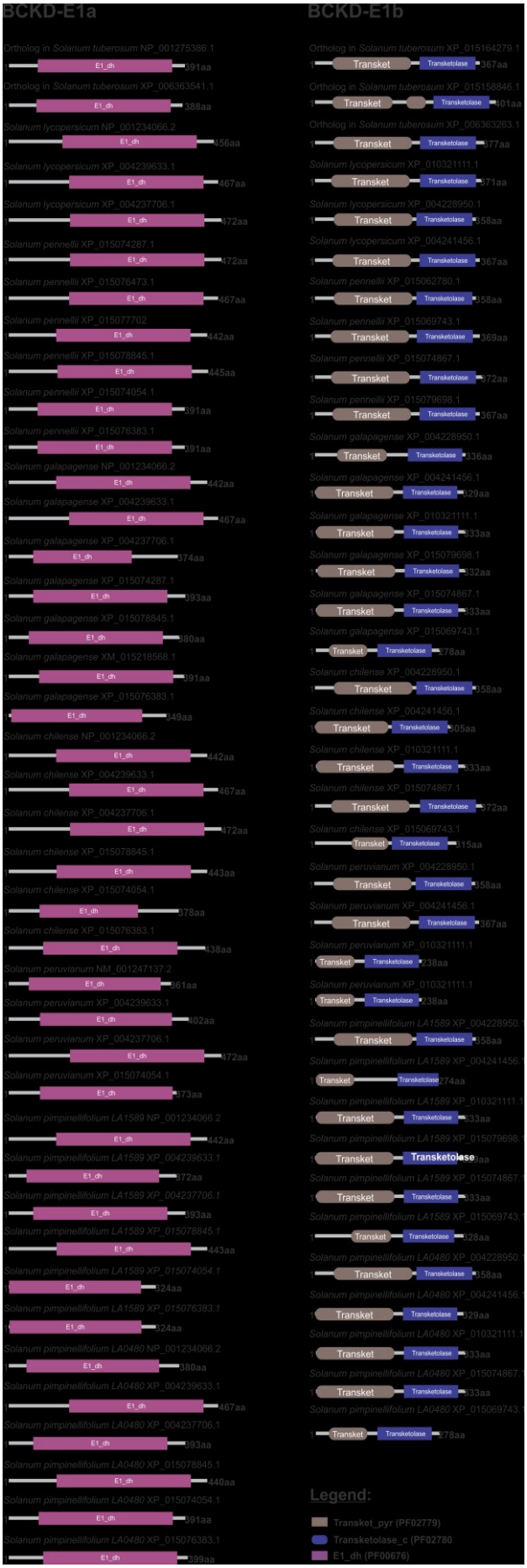

BCKD-E1a
BCKD-E1b
Legend:
Transket_pyr (PF02779)
Transketolase_c (PF02780
E1_dh (PF00676)

Figure 10 - Distribution of conserved domains in BCKD E1a and BCKD E1b putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

The BCKD E2 proteins of *S. lycopersicum*, *S. pennellii*, *S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* and ortholog *S. tuberosum* displayed the domains Biotin_lipoyl, E3_binding and 2-oxoacid_dh (Figure 11 and Supplementary Figure S5). The Biotin_lipoyl conserved domain is one of the main domains contained in the BCKD E2 proteins. It was also shown that the active sites contained the important catalytic residue K (lysine) in a specific and conserved position (Figure 13). The conserved domains and active sites found in BCKD E2 proteins of the all tomato species studied showed high conservation compared to the BCKD E2 proteins in other plant species, such as *S. tuberosum* and *A. thaliana*.

Figure 11 - Distribution of conserved domains in BCKD E2 putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

188 Another important catalytic component of the acylsugar processing pathway
189 in plants are the IPMSA proteins. The conserved domains HMGL-like and
190 LeuA_imer were the main domains found in tomato and *S. tuberosum* IPMSA and
191 IPMB proteins. In all IPMSB proteins and SlyIPMSA (NP_001316379.1),
192 SpeIPMSA (NP_001310380.1), SgaIPMSA (scaffold90874_8.2_contig_2 and
193 scaffold90874_8.2_contig_2), SchIPMSA (scaffold7114), SpiLA1589 IPMSA
194 (contig:921951:1:3418:1) and SpiLA0480 IPMSA (Scaffold2425123) contained the
195 HMGL-like and LeuA_imer domains; the other IPMSA proteins presented only the
196 HMGL-like domain (Figure 12 and Supplementary Table S6).

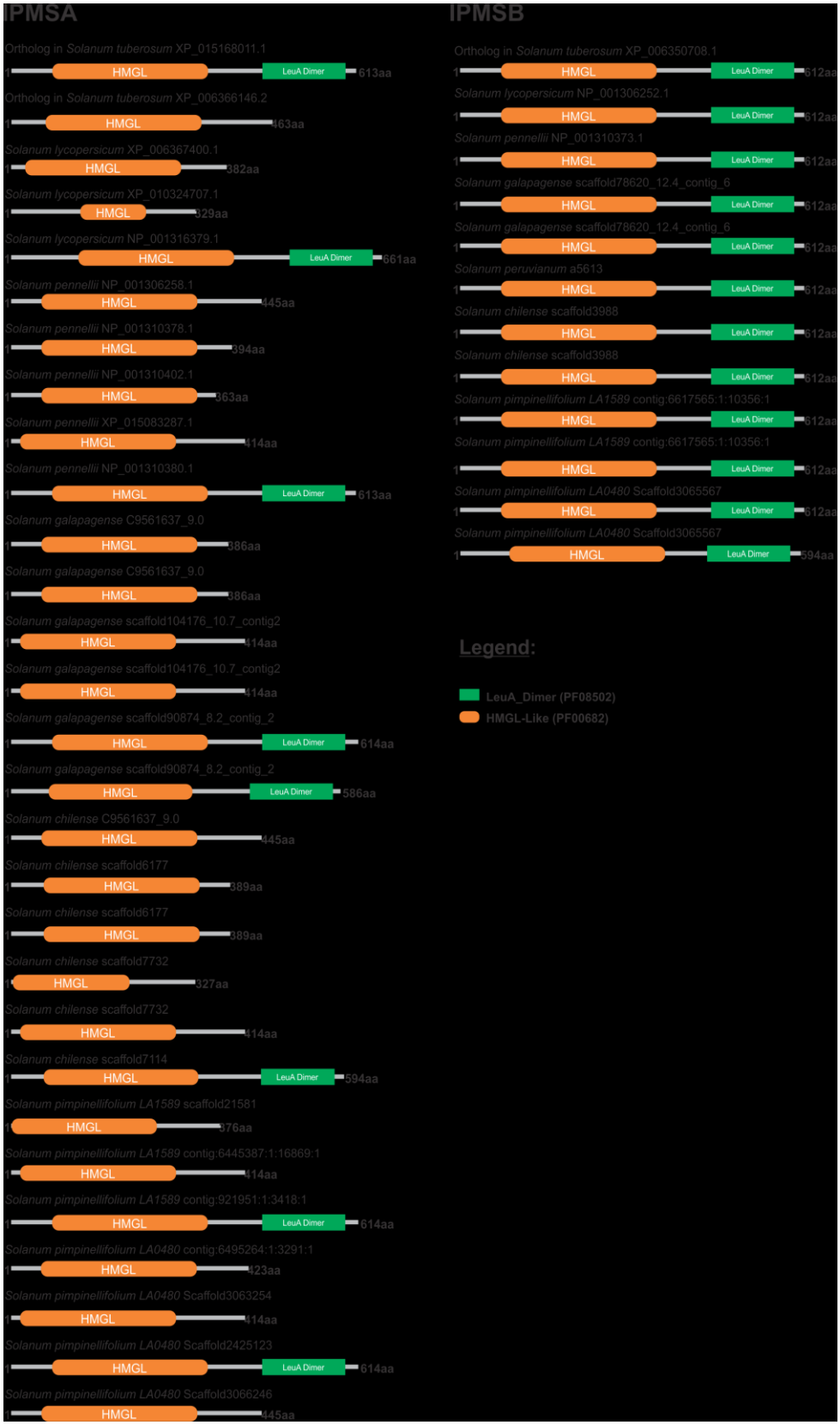


Figure 12 - Distribution of conserved domains in IPMSA and IPMSB putative proteins of *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their ortholog in *S. tuberosum.*

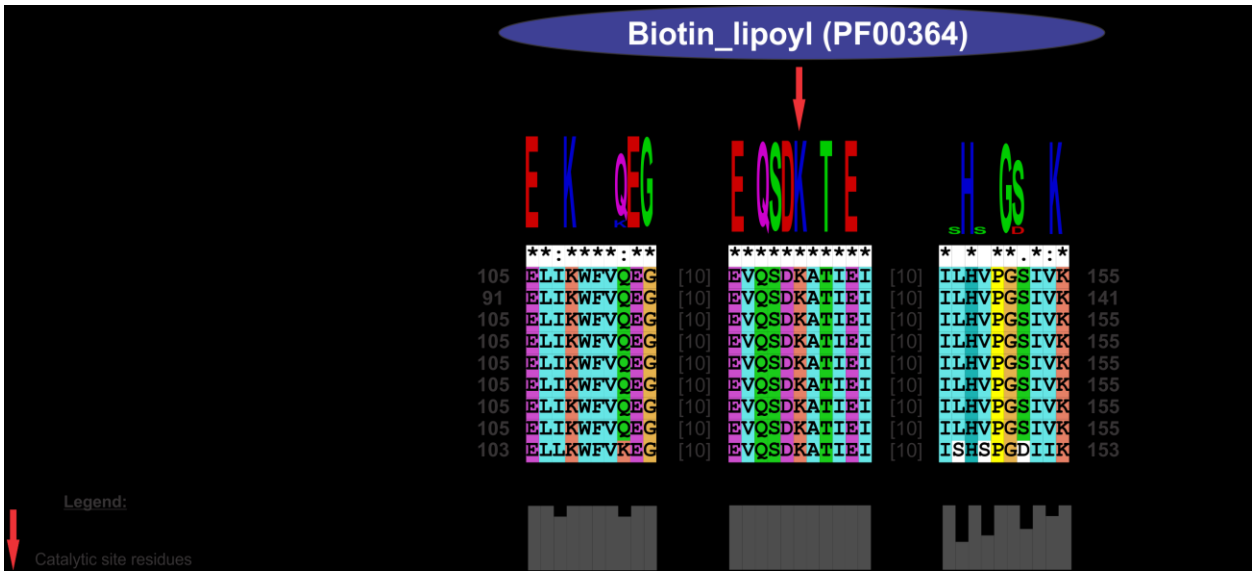


Figure 13 - Weblogo analysis and sequence multiple alignment of active site amino acids and their flanking amino acid residues in the Biotin_lipoyl conserved domains of *S. lycopersicum* (Sly), *S. pennellii* (Spe), *S. galapagense* (Sga), *S. chilense* (Sch), *S. peruvianum* (Spr), *S. pimpinellifolium* LA0480 (SpiLA0480), *S. pimpinellifolium* LA1589 (SpiLA1589) and their ortholog in *S. tuberosum*. The red arrows show the amino acid residues of the active sites (lysine). The height of each amino acid symbol in Weblogo indicates amino acid residue conservation at a given position.

The HMGL-like domains in all tomato species showed the same catalytic residues, aspartate (D), arginine (R) and glutamate (E), and these of catalytic triad (DRE), corroborating with IPMSA proteins of *S. tuberosum* (Figure 14). Only SchIPMSA (scaffold21581), SprIPMSA (a5613) and SchIPMSA (scaffold7732_327aa) proteins did not showed the first catalytic residue (D) of the active site because it was truncated at the beginning of the sequence.

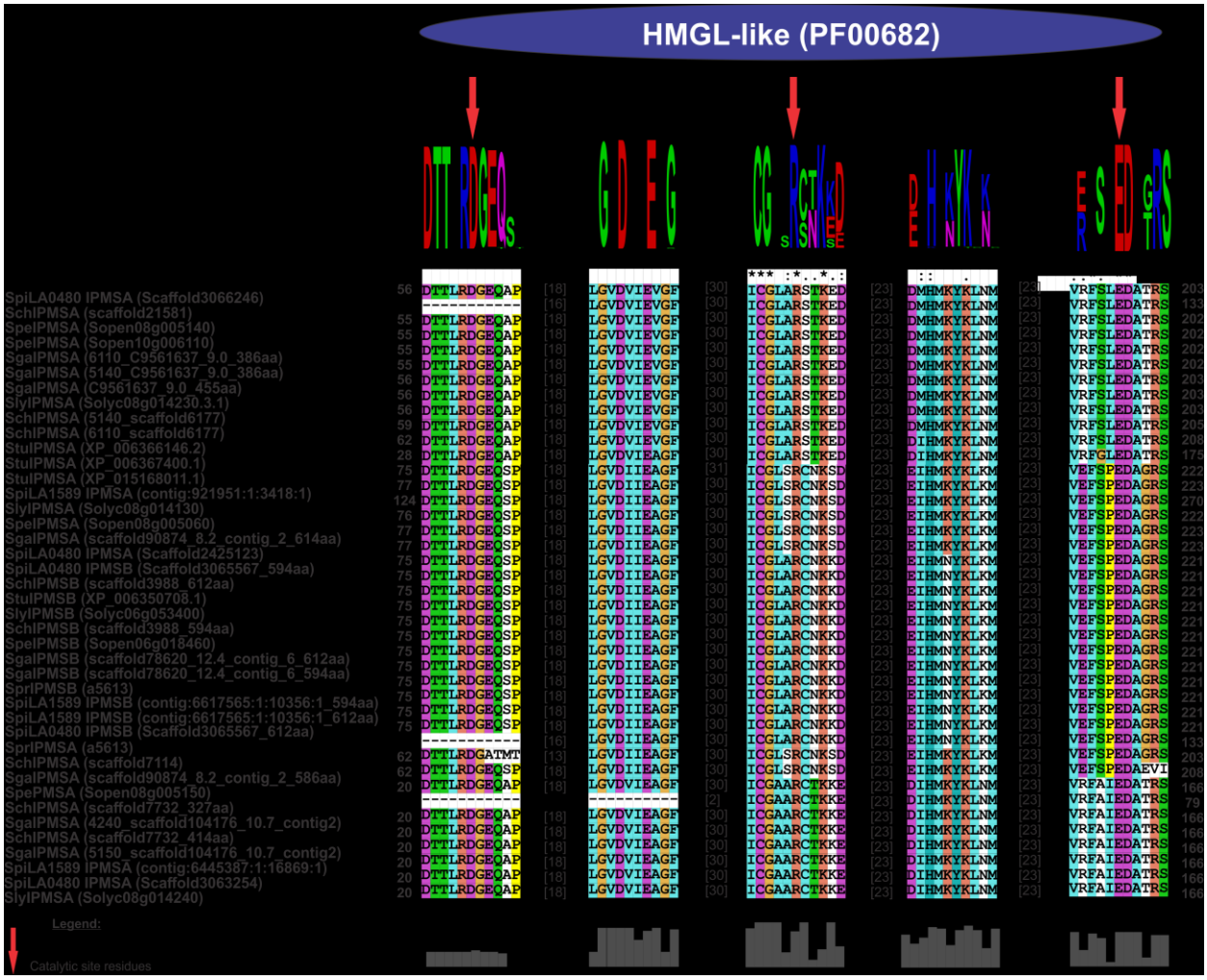


Figure 14 - Weblogo analysis and sequence multiple alignment of active site amino acids and their flanking amino acid residues in the HMGL-like conserved domains of *S. lycopersicum* (Sly), *S. pennellii* (Spe), *S. galapagense* (Sga), *S. chilense* (Sch), *S. peruvianum* (Spr), *S. pimpinellifolium* LA0480 (SpiLA0480), *S. pimpinellifolium* LA1589 (SpiLA1589) and their ortholog in *S. tuberosum*. The red arrows show the amino acid residues of the active sites (asp-arg-glu). The height of each amino acid symbol in Weblogo indicates amino acid residue conservation at a given position.

The phylogenetic distribution of BCKD (Figure 15) and IPMS (Figure 16) proteins was performed using amino acid sequences. The phylogenetic analysis of the BCKD proteins showed that these putative proteins were distributed in the phylogenetic tree closest to their respective ortholog proteins of the *Solanaceae,* as *Capsicum annuum*, *S. tuberosum, N. attenuate, N. tabacum* and *N. sylvestris.* The phylogenetic tree was divided into clades of 3 distinct: BCKD E2, BCKD E1a and BCKD E1b, and distributed among families *Solanaceae, Vitaceae, Rosaceae,*

233 *Malvaceae, Rubiaceae, Rutaceae, Myrtaceae, Fabaceae* and *Brassicaceae*
234 (Figure 15). To determine the evolutionary relationship among the putative tomato
235 IPMS proteins and their orthologs a phylogenetic analysis was performed (Figure
236 16). The proteins were grouped in IPMSA and IPMSB. The *Solanaceae* protein
237 family containing the tomato proteins and their orthologous of *S. tuberosum, N.*
238 *attenuate, N. tabacum* and *N. sylvestris* was well separated from the *Brassicaceae*
239 family on the tree.

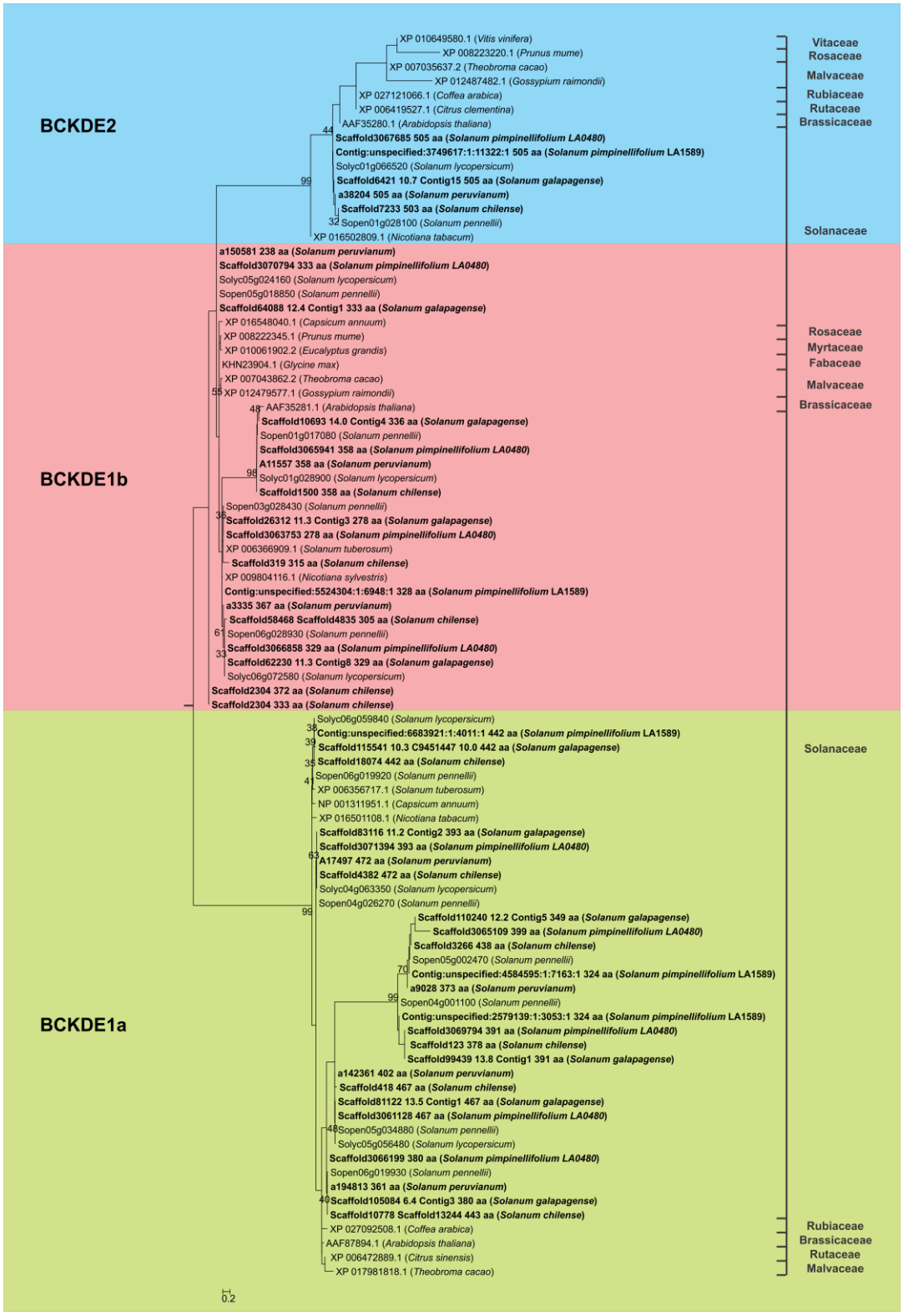


Figure 15 - Phylogenetic tree of BCKD proteins identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

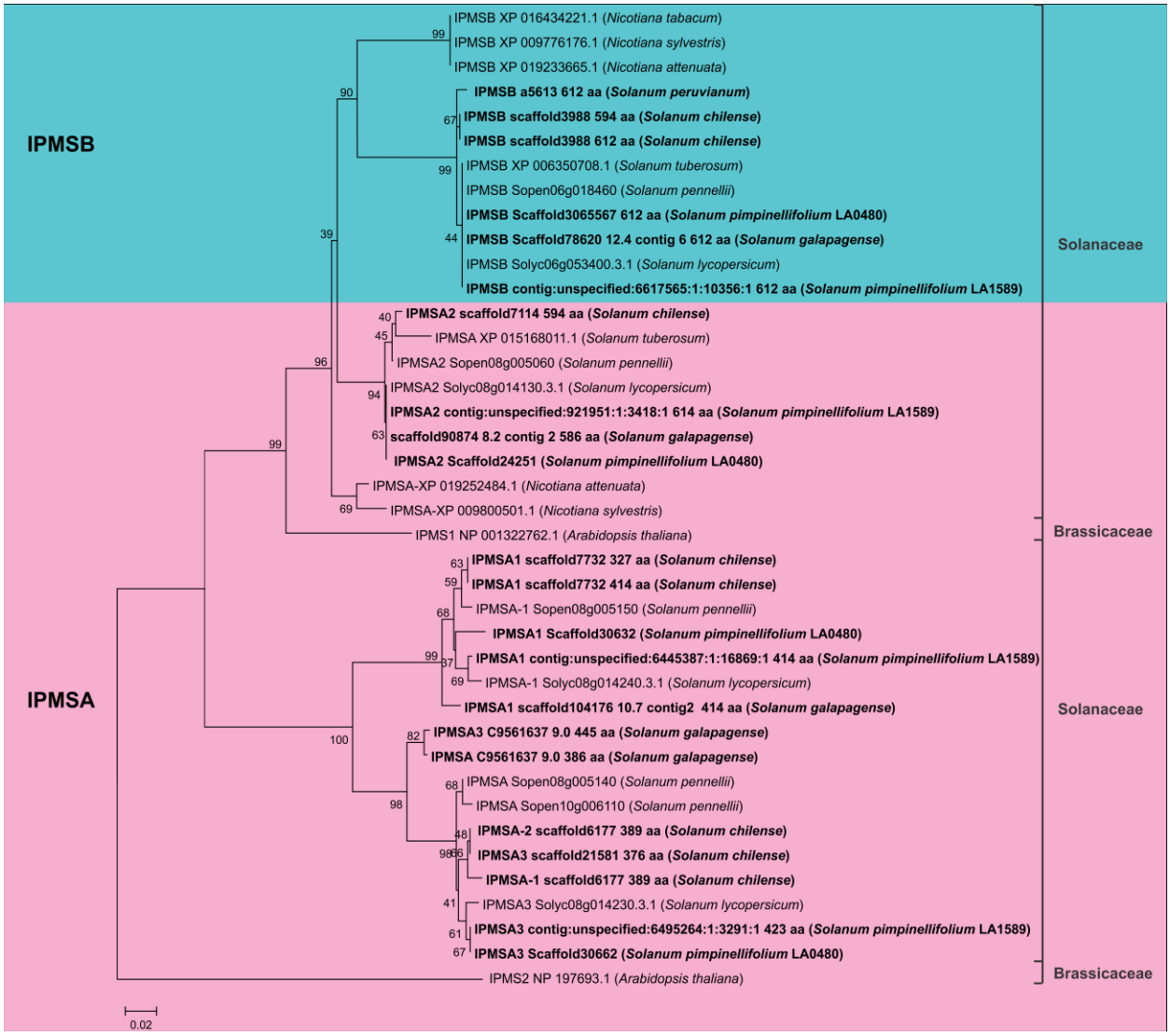


Figure 16 - Phylogenetic tree of IPMS proteins identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

Mature miRNAs and their precursors in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum* and *S. pimpinellifolium*

We identify both mature and precursor sequences of miRNAs in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480 and *S. pimpinellifolium* LA1589 genomes. By applying an optimized and specific algorithm, we identified 1081 sequences (3p and 5p) of mature miRNAs and 917 precursor miRNAs, distributed in 393 distinct miRNA families in *S. lycopersicum* genome (Supplementary Table S7). In *S. pennellii*,

258 1006 sequences of mature miRNAs were identified and 850 precursor miRNAs
259 were contained in 354 different miRNA families (Supplementary Table S8). *S.*
260 *galapagense* showed 909 mature miRNAs and 760 precursors in 373 families
261 (Supplementary Table S9). In addition, *S. chilense* exhibited 1424 mature miRNAs
262 and 889 precursors in 369 miRNA families (Supplementary Table S10) and *S.*
263 *peruvianum* presented 52 miRNAs mature sequences, 52 precursors in 32 families
264 (Supplementary Table S11). Finally, we searched 1170 mature miRNAs and 1005
265 pré-miRNAs in 446 *S. pimpinellifolium* LA0480 families (Supplementary Table
266 S12) and 1375 mature miRNAs sequences and 865 precursor in 365 different
267 miRNA families of *S. pimpinellifolium* LA1589 (Supplementary Table S13).
268 All identified miRNAs were analysed for their structural and thermodynamic
269 characteristics. *S. lycopersicum* miRNA precursors displayed an MFE with the
270 mean of -59.17 kcal/mol, spanning the values between -99.9 and -20.5 kcal/mol.
271 Such parameters as AMFE and MFEI, had the averages of -35.77 kcal/mol and of
272 -0.99, respectively (Supplementary Table S14). In *S. pennellii*, the pre-miRNAs
273 showed an MFE with the mean of -59.68 kcal/mol, with the values between -99.9
274 and -20.7 kcal/mol, the mean AMFE was -36.37 Kcal/mol and that of MFEI was -
275 0.99 (Supplementary Table S15). *S. galapagense* showed an average MFE,
276 AMFE and MFEI of the -56.36 kcal/mol, -35.60 kcal/mol and 0.97 kcal/mol,
277 respectively (Supplementary Table S16). *S. chilense* miRNA precursors exhibited
278 an MFE with the mean of -55.90 kcal/mol, spanning the values between -99.9 and
279 -20.6 kcal/mol, the mean AMFE was -36.43 Kcal/mol and that of MFEI was -0.99
280 (Supplementary Table S17). In addition, the pre-miRNAs of the *S. peruvianum*
281 (Supplementary Table S18), *S. pimpinellifolium* LA0480 (Supplementary Table
282 S19) and *S. pimpinellifolium* LA1589 (Supplementary Table S20) showed an
283 average MFE of the -51.49 Kcal/mol, -58.19 Kcal/mol and -57.70 Kcal/mol;
284 average AMFE of the -34.12 Kcal/mol, -36.27 Kcal/mol and -35.70 Kcal/mol; and
285 an average MFEI of the -0.85 Kcal/mol, -0.99 Kcal/mol and -0.96 Kcal/mol,
286 respectively.
287 Among the all miRNA families identified in the 7 species under study, we
288 highlighted 5 families for more in-depth characterization, since the MIR165/166
289 family are miRNAs conserved in plants, and the MIR5303, MIR6022 and MIR7981
290 are miRNAs found only in the *Solanaceae* family; and MIR10528 was found only in

tomato species. We analysed the sequences conservation of the MIR6022 (Figure 17) and MIR10528 (Figure 18) miRNAs families. In addition, we did the phylogenetic analysis of the MIR165/166 (Figure 19), MIR5303 (Figure 20), MIR6022 (Figure 21), MIR7981 (Figure 22) and MIR10528 (Figure 23) families.

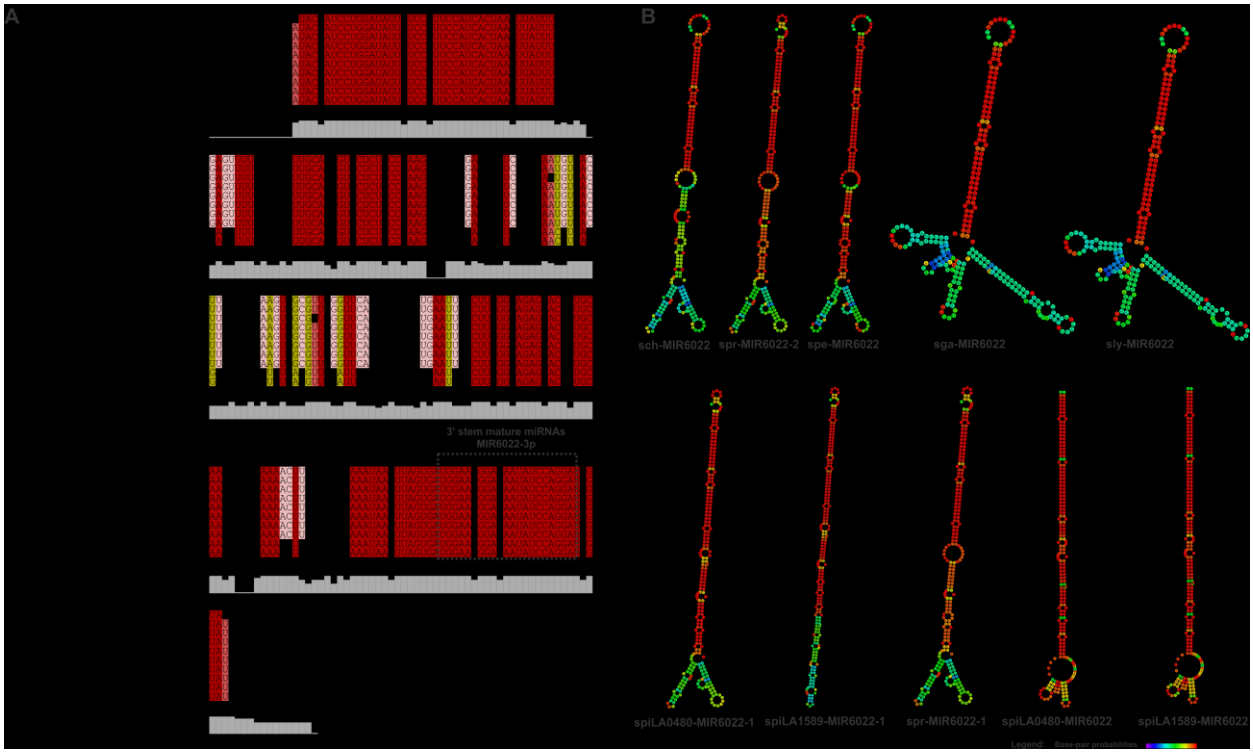


Figure 17 - (A) The high-confidence RNA alignments between MIR6022 families of *S. lycopersicum* (Sly), *S. pennellii* (Spe), *S. galapagense* (Sga), *S. chilense* (Sch), *S. peruvianum* (Spr), *S. pimpinellifolium* LA0480 (SpiLA0480) and *S. pimpinellifolium* LA1589 (SpiLA1589) were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colours identify matching residues in 3' stems of hairpin structures. Levels of nucleotide identity are indicated below the alignment. **(b)** Secondary structures of MIR6022 family from tomato were drawn by RNAfold.

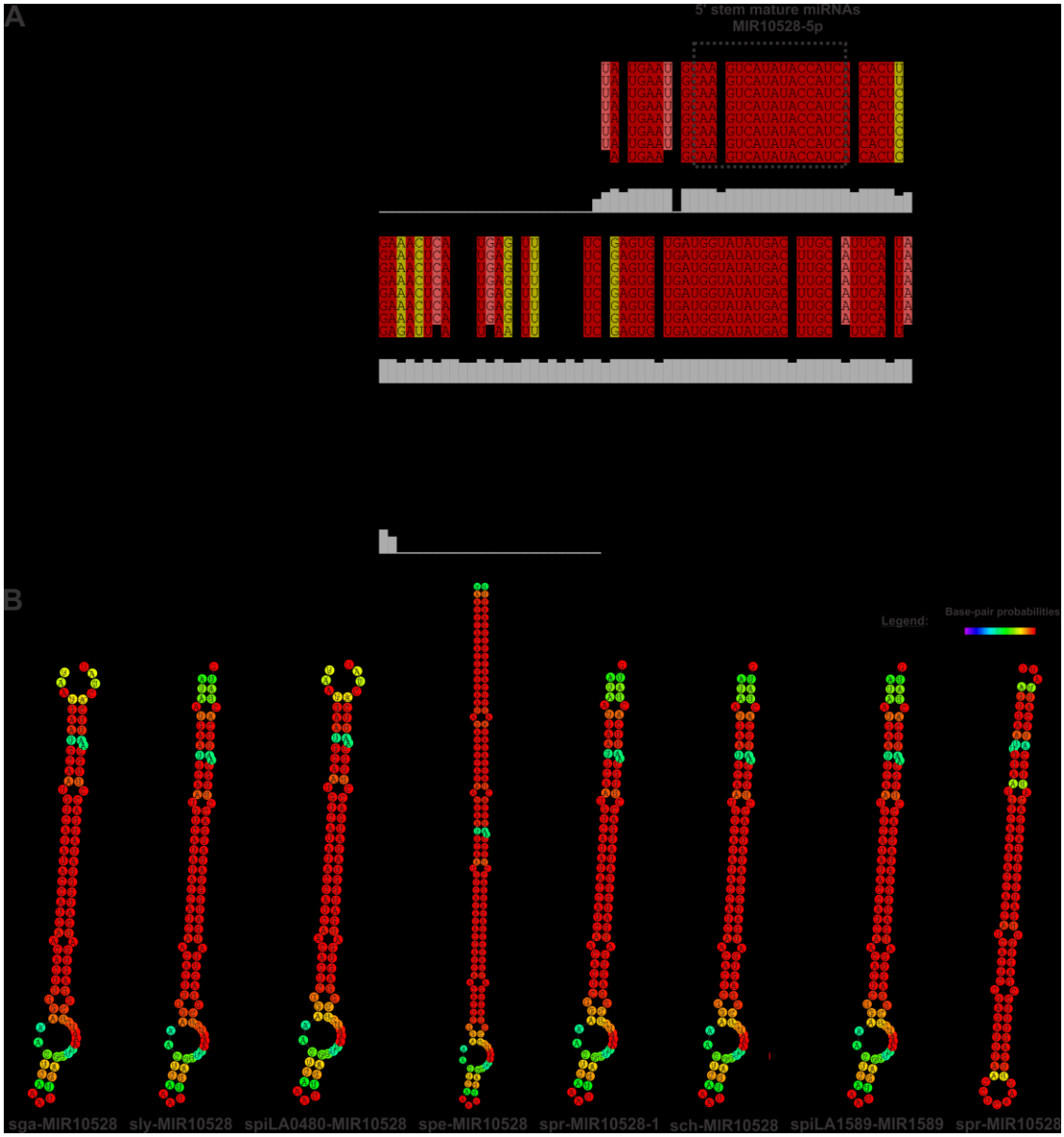


Figure 18 - (A) The high-confidence RNA alignments between MIR10528 families of *S. lycopersicum* (Sly), *S. pennellii* (Spe), *S. galapagense* (Sga), *S. chilense* (Sch), *S. peruvianum* (Spr), *S. pimpinellifolium* LA0480 (SpiLA0480) and *S. pimpinellifolium* LA1589 (SpiLA1589) were performed using RNAalifold. Mature miRNAs are shown as boxes. Brackets and colours identify matching residues in 3' stems of hairpin structures. Levels of nucleotide identity are indicated below the alignment. **(b)** Secondary structures of MIR10528 family from tomato were drawn by RNAfold.

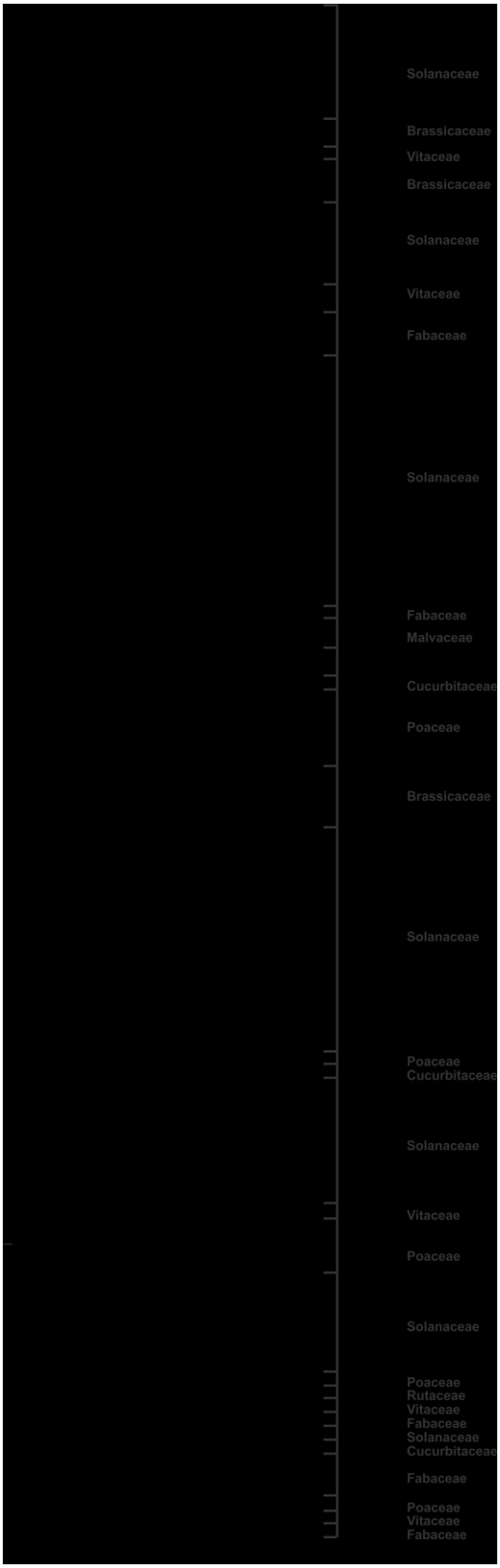


Figure 19 - Phylogenetic tree of MIR166 pre-miRNAs identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

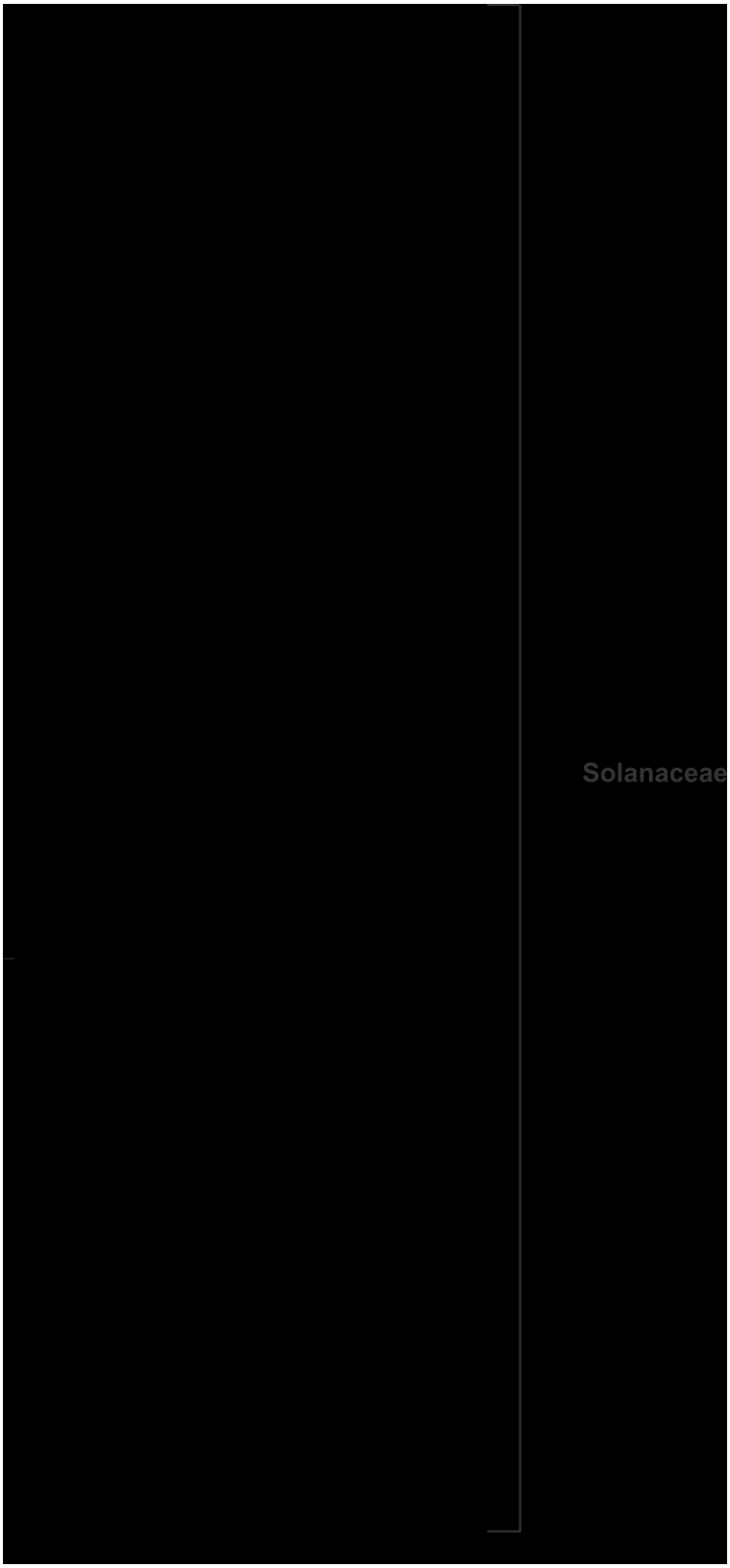


Figure 20 - Phylogenetic tree of MIR5303 pre-miRNAs identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

Figure 21 - Phylogenetic tree of MIR6022 pre-miRNAs identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

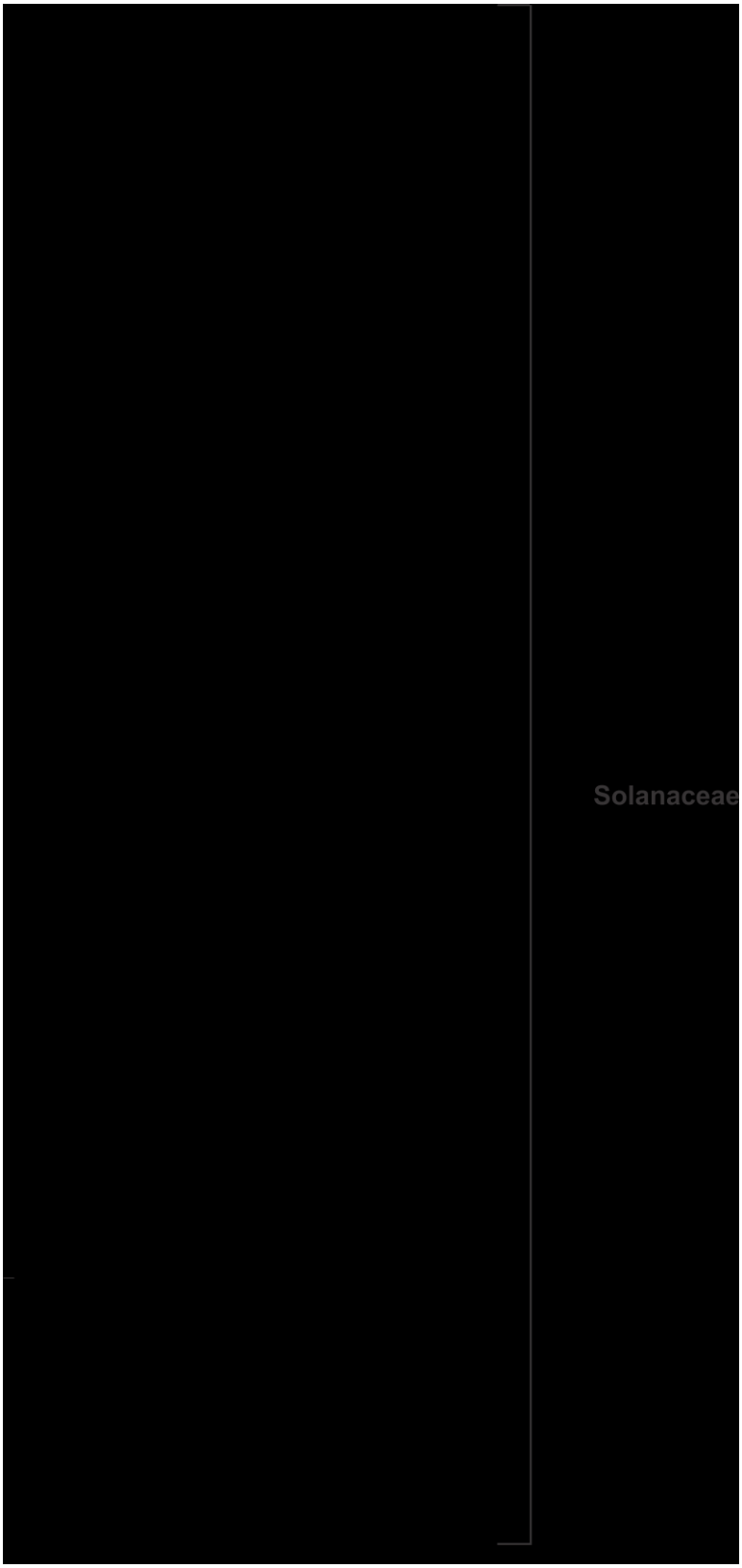


Figure 22 - Phylogenetic tree of MIR7981 pre-miRNAs identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

Figure 23 - Phylogenetic tree of MIR10528 pre-miRNAs identified in *S. lycopersicum*, *S. pennellii, S. galapagense, S. chilense, S. peruvianum*, *S. pimpinellifolium* LA0480, *S. pimpinellifolium* LA1589 and their orthologs.

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7 CONSIDERAÇÕES FINAIS

Considerando a importância global da cultura do tomateiro e os problemas gerados pela susceptibilidade às pragas do tomate cultivado e as diferenças com os tomates selvagens. Considerando a relevância de entender mais sobre os mecanismos de regulação gênica em *S. haematobium*. Nossos resultados expandem o estudo de miRNAs em plantas e animais ao fornecer um melhor entendimento dos papéis essenciais nos processos de regulação baseados em miRNAs em tomate e *S. haematobium*, suas vias de processamento e expressão gênica, além de fornecer alvos para investigações futuras. Além disso, estes resultados abrirão um novo caminho para o estudo dos miRNAs na biologia do esquistossomo e em tecnologias que envolvem o controle do silenciamento gênico neste organismo. Além disso, permitirá a compreensão de diversos processos e mecanismos em sua biologia, uma vez que essas moléculas apresentam importante papel regulatório para diferentes mRNAs, afetando diversas características do organismo em diferentes estágios e condições ambientais. Ainda, o entendimento do possível envolvimento dos acilaçucares na resistência aos artrópodes e sua associação com marcadores relacionados a características importantes auxiliará no melhoramento genético dessas espécies de tomate visando uma resposta ao controle do estresse biótico. Nesse sentido, tendo em vista o importante papel da produção de aleloquímicos em *Solanaceae*, nossos resultados contribuem para um melhor entendimento dos acilaçúcares e suas vias de processamento e abrem oportunidades para estudar sua relação com a resistência biótica nessas importantes espécies de vegetais e outras espécies de *Solanaceae*.

APÊNDICE I - SUPLEMENTARY TABLES - CAPÍTULO II – Article: New insights into tomato microRNAs from Scientific Reports Journal

Supplementary Table S1. Identification of putative proteins involved in the miRNA pathway in *Solanum lycopersicum*. Identity (Ident)

Gene	ID NCBI of *S. lycopersicum*	Size (aa)	ID NCBI of *Arabidopsis thaliana*	Size (aa)	Blastp e-value: *A. thaliana* and *S. lycopersicum*	Ident	Genome	Chromosome	Database	Start position	End position	Strand	ID/Name
SlyABH1	XP_004248287	861	NP_565356.1	848	0.0	67%	ITAG3.0	Chr10	Sol Genomics	428279	445465	-	Solyc10g005530
SlyAGO1.1	NP_001266057.1	1054	NP_001185169.1	1050	0.0	78%	ITAG3.0	Chr06	Sol Genomics	44710986	44721105	-	Solyc06g072300
SlyAGO1.2	NP_001266261.2	1152	NP_001185169.1	1050	0.0	78%	ITAG3.0	Chr03	Sol Genomics	62062318	62069468	+	Solyc03g098280
SlyAGO10.1	XP_004247613.1	982	NP_001190464.1	988	0.0	81%	ITAG3.0	Chr09	Sol Genomics	68916353	68924564	-	Solyc09g082830
SlyAGO10.2	NP_001266268.1	939	NP_001190464.1	988	0.0	73%	ITAG3.0	Chr12	Sol Genomics	1199288	1214285	-	Solyc12g006790
SlyCBP20	XP_004233527.1	257	NP_001078705.1	257	$2e^{-128}$	75%	ITAG3.0	Chr02	Sol Genomics	34895133	34912181	-	Solyc02g062620
SlyCDC5	NP_001234729.2	987	NP_172448.1	844	0.0	72%	ITAG3.0	Chr04	Sol Genomics	3261426	3266792	+	Solyc04g009950
SlyCPL1	XP_004232844.1	954	NP_193898.3	967	0.0	58%	ITAG3.0	Chr02	Sol Genomics	43775820	43786429	-	Solyc02g078550
SlyDDL	XP_004248371.2	519	NP_188691.1	314	$9e^{-110}$	60%	ITAG3.0	Chr10	Sol Genomics	996419	1004741	-	Solyc10g006390
SlyDCL1	NP_001289827.1	1914	NP_171612.1	1909	0.0	72%	ITAG3.0	Chr10	Sol Genomics	111695	125349	+	Solyc10g005130
SlyEXO.1	XP_010320183.1	314	NP_192634.1	314	$2e^{-162}$	72%	ITAG3.0	Chr04	Sol Genomics	60523838	60524782	-	Solyc04g074450
SlyEXO.2	XP_010320182.1	312	NP_192634.1	314	$2e^{-160}$	72%	ITAG3.0	Chr04	Sol Genomics	60507541	60516683	+	Solyc04g074410
SlyEXO.3	XP_004237932.1	315	NP_192634.1	314	$4e^{-157}$	70%	ITAG3.0	Chr04	Sol Genomics	60520286	60521233	-	Solyc04g074440

SlyEXO.4	XP_004237930.1	309	NP_192634.1	314	$2e^{-114}$	55%	ITAG3.0	Chr04	Sol Genomics	60492687	60493616	-	Solyc04g074400
SlyHEN	XP_004233884.1	936	NP_001190782.1	942	0.0	49%	ITAG3.0	Chr02	Sol Genomics	40384527	40384937	-	Solyc02g070030
SlyHESO1.1	NP_001310843.1	453	NP_001318386.1	511	$4e^{-147}$	52%	ITAG3.0	Chr06	Sol Genomics	35528135	35547246	+	Solyc06g051790
SlyHESO1.2	XP_004250756.1	552	NP_001318386.1	511	$4e^{-38}$	32%	ITAG3.0	Chr11	Sol Genomics	32288016	32302403	-	Solyc11g044900
SlyHST	XP_004230145.1	1199	NP_187155.2	1202	0.0	65%	ITAG3.0	Chr01	Sol Genomics	88619826	88632083	+	Solyc01g098170
SlyHYL1	XP_004238005.1	433	NP_563850.1	419	$1e^{-76}$	61%	ITAG3.0	Chr04	Sol Genomics	61402144	61407360	+	Solyc04g076420
SlyNOT2.1	XP_010313541.1	628	NP_001077478.1	614	0.0	60%	ITAG3.0	Chr11	Sol Genomics	56388283	56396735	+	Solyc11g072940
SlyNOT2.2	XP_004241255.1	658	NP_001077478.1	614	0.0	65%	ITAG3.0	Chr06	Sol Genomics	47119921	47134159	+	Solyc06g075590
SlySE	XP_004228474.1	748	NP_565635.1	720	0.0	69%	ITAG3.0	Chr01	Sol Genomics	3028724	3042442	-	Solyc01g009090
SlySQN.1	NP_001316807.1	362	NP_565381.1	361	0.0	76%	ITAG3.0	Chr01	Sol Genomics	95581585	95586349	+	Solyc01g108340
SlySQN.2	XP_004232050.1	361	NP_565381.1	361	0.0	68%	ITAG3.0	Chr02	Sol Genomics	52648116	52656092	+	Solyc02g090480
SlySTA1	XP_004243341.1	1019	OAO98779.1	1029	0.0	75%	ITAG3.0	Chr07	Sol Genomics	62685798	62688857	+	Solyc07g054200
SlyTGH	XP_004236099.1	984	NP_001031926.1	900	0.0	54%	ITAG3.0	Chr03	Sol Genomics	65890464	65905320	+	Solyc03g114410
SlyVCS1.1	XP_004244016.1	1407	NP_187938.2	1344	0.0	55%	ITAG3.0	Chr07	Sol Genomics	67656674	67666715	+	Solyc07g065950
SlyVCS1.2	XP_004248289.1	1418	NP_187938.2	1344	0.0	53%	ITAG3.0	Chr10	Sol Genomics	703110	706856	+	Solyc10g005920
SlyXRN4	NP_001233774.1	978	NP_175851.1	947	0.0	63%	ITAG3.0	Chr04	Sol Genomics	39105433	39147113	-	Solyc04g049010

403 **Supplementary Table S2.** Identification of putative proteins involved in the miRNA pathway in *Solanum pennellii*. Identity (Ident)

Gene	ID NCBI of *S. pennellii*	Size (aa)	ID NCBI of *Arabidopsis thaliana*	Size (aa)	Blastp e-value: *A. thaliana* and *S. pennellii*	Ident	Genome	Chromosome	Database	Start position	End position	Strand	ID/Name
SpeABH1	XP_015055991.1	861	NP_565356.1	848	0.0	67%	Spenn_v2.0	Chr10	Sol Genomics	470562	487876	-	Sopen10g001510
SpeAGO1.1	XP_015079116.1	1053	NP_001185169.1	1050	0.0	78%	Spenn_v2.0	Chr06	Sol Genomics	55270253	55279596	-	Sopen06g028670
SpeAGO1.2	XP_015069669.1	1152	NP_001185169.1	1050	0.0	78%	Spenn_v2.0	Chr03	Sol Genomics	64779141	64793113	+	Sopen03g028990
SpeAGO10	XP_015088227.1	982	NP_001190464.1	988	0.0	81%	Spenn_v2.0	Chr09	Sol Genomics	80029833	80037384	-	Sopen09g031660
SpeCBP20	XP_015066864.1	145	NP_001078705.1	257	$8e^{-128}$	77%	Spenn_v2.0	Chr02	Sol Genomics	37046624	37052022	-	Sopen02g013650
SpeCDC5	XP_015073427.1	1002	NP_172448.1	844	0.0	72%	Spenn_v2.0	Chr04	Sol Genomics	3448797	3454313	+	Sopen04g005080
SpeCPL1	XP_015065799.1	954	NP_193898.3	967	0.0	58%	Spenn_v2.0	Chr02	Sol Genomics	46784394	46794934	-	Sopen02g023400
SpeDDL	XP_015056276.1	519	NP_188691.1	314	$4e^{-112}$	60%	Spenn_v2.0	Chr10	Sol Genomics	1070258	1078336	-	Sopen10g002340
SpeDCL1	XP_015055701.1	1914	NP_171612.1	1909	0.0	72%	Spenn_v2.0	Chr10	Sol Genomics	140256	153832	+	Sopen10g001150
SpeEXO.1	XP_015072851.1	314	NP_192634.1	314	$7e^{-154}$	72%	Spenn_v2.0	Chr04	Sol Genomics	71013460	71014602	-	Sopen04g029470
SpeEXO.2	XP_015072850.1	315	NP_192634.1	314	$8e^{-150}$	70%	Spenn_v2.0	Chr04	Sol Genomics	71008901	71009992	-	Sopen04g029460
SpeEXO.3	XP_015074412.1	301	NP_192634.1	314	$8e^{-145}$	67%	Spenn_v2.0	Chr01	Sol Genomics	104235554	104236833	+	Sopen01g047900
SpeEXO.4	XP_015072852.1	309	NP_192634.1	314	$1e^{-133}$	62%	Spenn_v2.0	Chr04	Sol Genomics	71016771	71028199	+	Sopen04g029480
SpeEXO.5	XP_015056292.1	344	NP_192634.1	314	$6e^{-173}$	72%	Spenn_v2.0	Chr10	Sol Genomics	74630529	74631994	-	Sopen10g027040
SpeEXO.6	XP_015067414.1	349	NP_192634.1	314	$2e^{-180}$	77%	Spenn_v2.0	Chr03	Sol Genomics	54987335	54988714	+	Sopen03g023370

SpeEXO.7	XP_015064271.1	338	NP_192634.1	314	$3e^{-130}$	64%	Spenn_v2.0	Chr02	Sol Genomics	42023523	42024843	-	Sopen02g017980
SpeEXO.8	XP_015077362.1	348	NP_192634.1	314	$5e^{-172}$	75%	Spenn_v2.0	Chr06	Sol Genomics	29018255	29019378	-	Sopen06g011130
SpeHEN	XP_015066899.1	936	NP_001190782.1	942	0.0	49%	Spenn_v2.0	Chr02	Sol Genomics	43139412	43149375	-	Sopen02g019190
SpeHESO1.1	XP_015079772.1	453	NP_001318386.1	511	$4e^{-148}$	53%	Spenn_v2.0	Chr06	Sol Genomics	44896865	44916062	+	Sopen06g017790
SpeHESO1.2	XP_015086026.1	611	NP_190161.2	682	$5e^{-107}$	47%	Spenn_v2.0	Chr09	Sol Genomics	82784741	82791899	+	Sopen09g034750
SpeHST	XP_015062207.1	1199	NP_187155.2	1202	0.0	65%	Spenn_v2.0	Chr01	Sol Genomics	990095019	99104849	+	Sopen01g041740
SpeHYL1	XP_015071372.1	406	NP_563850.1	419	$4e^{-78}$	62%	Spenn_v2.0	Chr04	Sol Genomics	71813898	71819068	+	Sopen04g030180
SpeNOT2.1	XP_015058689.1	628	NP_001077478.1	614	0.0	60%	Spenn_v2.0	Chr11	Sol Genomics	65966414	65974981	+,	Sopen11g030600
SpeNOT2.2	XP_015079397.1	658	NP_001077478.1	614	0.0	66%	Spenn_v2.0	Chr06	Sol Genomics	57856903	57867863	+	Sopen06g031990
SpeSE	XP_015060466.1	749	NP_565635.1	720	0.0	69%	Spenn_v2.0	Chr01	Sol Genomics	3437801	3451620	-	Sopen01g004580
SpeSQN.1	XP_015067254.1	362	NP_565381.1	361	0.0	77%	Spenn_v2.0	Chr01	Sol Genomics	106469253	106473850	+	Sopen01g050560
SpeSQN.2	XP_015067196.1	361	NP_565381.1	361	0.0	69%	Spenn_v2.0	Chr02	Sol Genomics	56319127	56325887	+	Sopen02g035160
SpeSTA1	XP_015082387.1	1019	OAO98779.1	1029	0.0	75%	Spenn_v2.0	Chr07	Sol Genomics	73824806	73829303	+	Sopen07g028130
SpeTGH	XP_015070455.1	984	NP_001031926.1	900	0.0	54%	Spenn_v2.0	Chr03	Sol Genomics	68747090	68761834	+	Sopen03g033510
SpeVCS.1	XP_015082036.1	1405	NP_187938.2	1344	0.0	54%	Spenn_v2.0	Chr07	Sol Genomics	78737896	78747556	+	Sopen07g034150
SpeVCS.2	XP_015055595.1	1418	NP_187938.2	1344	0.0	55%	Spenn_v2.0	Chr10	Sol Genomics	749356	761206	+	Sopen10g001880
SpeXRN4	XP_015073528.1	978	NP_175851.1	947	0.0	63%	Spenn_v2.0	Chr04	Sol Genomics	44928340	44965197	-	Sopen04g018450

Supplementary Table S3. Distribution of conserved domains and their locations in putative AGO proteins identified in *Solanum lycopersicum* (Sly*), Solanum pennellii* (Spe) and their orthologs.

Family	Protein	ID	Conserved domain	Domain ID	Start and End	E-value
AGO1	**SlyAGO1.1**	Solyc06g072300	Gly-rich_Ago1	PF12764.4	70 – 174	$1.7e^{-27}$
			ArgoN	PF16486.2	185 – 328	$3.3e^{-24}$
			ArgoL1	PF08699.7	338 – 388	$1.1e^{-23}$
			PAZ	PF02170.19	394 – 520	$3.3e^{-28}$
			ArgoL2	PF16488.2	531 – 576	$7.6e^{-16}$
			ArgoMid	PF16487.2	587 – 661	$8e^{-08}$
			Piwi	PF02171.14	681 - 1000	$8.5e^{-113}$
	SlyAGO1.2	Solyc03g098280	Gly-rich_Ago1	PF12764.4	18 – 100	$3.5e^{-09}$
			ArgoN	PF16486.2	111 – 254	$9e^{-24}$
			ArgoL1	PF08699.7	264 – 314	$5.4e^{-23}$
			PAZ	PF02170.19	320 – 446	$5.2e^{-29}$
			ArgoL2	PF16488.2	457 – 502	$4.8e^{-15}$
			ArgoMid	PF16487.2	513 – 587	$8.6e^{-08}$
			Piwi	PF02171.14	607 – 926	$1.1e^{-112}$
	SpeAGO1.1	Sopen06g028670	Gly-rich_Ago1	PF12764.4	69 – 173	$2.7e^{-27}$
			ArgoN	PF16486.2	193 – 327	$8.4e^{-33}$
			ArgoL1	PF08699.7	337 – 387	$1.4e^{-23}$
			PAZ	PF02170.19	393 – 518	$5e^{-28}$
			ArgoL2	PF16488.2	529- 575	$2e^{-16}$
			ArgoMid	PF16487.2	586 – 660	$8.1e^{-08}$
			Piwi	PF02171.14	680 – 999	$8.5e^{-113}$
	SpeAGO1.2	Sopen03g028990	Gly-rich_Ago1	PF12764.4	160 - 272	$1.8e^{-26}$
			ArgoN	PF16486.2	292 – 426	$3e^{-32}$
			ArgoL1	PF08699.7	436 – 486	$8.6e^{-23}$
			PAZ	PF02170.19	492 – 617	$1.1e^{-28}$
			ArgoL2	PF16488.2	685 – 759	$1.9e^{-15}$
			ArgoMid	PF16487.2	685 – 759	$1.1e^{-07}$
			Piwi	PF02171.14	779 – 1098	$1.7e^{-112}$
	Ortólogo em *Glycine max*	XP_003548311.1	Gly-rich_Ago1	PF12764.4	69 – 169	$1.6e^{-10}$
			ArgoN	PF16486.2	196 – 330	$3.1e^{-32}$
			ArgoL1	PF08699.7	340 – 390	$1.4e^{-23}$
			PAZ	PF02170.19	395 – 523	$9e^{-29}$
			ArgoL2	PF16488.2	532 – 578	$4e^{-16}$
			ArgoMid	PF16487.2	589 – 664	$4.7e^{-08}$
			Piwi	PF02171.14	681 – 1000	$9.2e^{-112}$
	Ortólogo em *Phasolus vulgaris*	XP_007152592.1	Gly-rich_Ago1	PF12764.4	77 – 181	$2e^{-10}$

			ArgoN	PF16486.2	204 – 339	$3.6e^{-32}$
			ArgoL1	PF08699.7	349 – 399	$1.4e^{-23}$
			PAZ	PF02170.19	404 – 530	$2.9e^{-28}$
			ArgoL2	PF16488.2	541 – 587	$2.6e^{-15}$
			ArgoMid	PF16487.2	598 – 673	$5.7e^{-08}$
			Piwi	PF02171.14	690 – 1009	$5.8e^{-112}$
	Ortólogo em *Solanum tuberosum*	XP_006347371.1	Gly-rich_Ago1	PF12764.4	70 – 174	$9.7e^{-27}$
			ArgoN	PF16486.2	194 – 328	$8.4e^{-33}$
			ArgoL1	PF08699.7	338 – 388	$1.4e^{-23}$
			PAZ	PF02170.19	394 – 519	$3e^{-28}$
			ArgoL2	PF16488.2	530 – 576	$4.1e^{-16}$
			ArgoMid	PF16487.2	587 – 661	$8.1e^{-08}$
			Piwi	PF02171.14	681 - 1000	$6.8e^{-113}$
AGO2	**SlyAGO2.1**	Solyc02g069260	ArgoN	PF16486.2	206 – 352	$1.9e^{-18}$
			ArgoL1	PF08699.7	362 – 409	$1.8e^{-09}$
			PAZ	PF02170.19	417 – 539	$2.6e^{-19}$
			ArgoL2	PF16488.2	558 – 602	$3.7e^{-08}$
			Piwi	PF02171.14	710 - 1001	$2e^{-90}$
	SlyAGO2.2	Solyc02g069270	ArgoN	PF16486.2	169 – 294	$4.7e^{-15}$
			ArgoL1	PF08699.7	305 – 351	$5.7e^{-09}$
			PAZ	PF02170.19	361 – 480	$4.3e^{-20}$
			ArgoL2	PF16488.2	518 – 543	$4.1e^{-08}$
			Piwi	PF02171.14	648 - 939	$8.2e^{-87}$
	SlyAGO2.3	Solyc02g069280	ArgoN	PF16486.2	168 – 314	$7.2e^{-15}$
			ArgoL1	PF08699.7	324 – 366	$1.9e^{-08}$
			PAZ	PF02170.19	396 – 498	$5.8e^{-16}$
			Piwi	PF02171.14	659 - 950	$3.8e^{-85}$
	SpeAGO2.1	Sopen02g018420	ArgoN	PF16486.2	214 – 351	$6.8e^{-21}$
			ArgoL1	PF08699.7	361 – 408	$2.1e^{-09}$
			PAZ	PF02170.19	416 – 538	$6.3e^{-19}$
			ArgoL2	PF16488.2	557 – 601	$3.8e^{-08}$
			Piwi	PF02171.14	709 - 1000	$4.6e^{-90}$
	SpeAGO2.2	Sopen02g018430	ArgoN	PF16486.2	184 – 321	$4.1e^{-20}$
			ArgoL1	PF08699.7	331 – 376	$6.1e^{-09}$
			PAZ	PF02170.19	385 – 506	$4.1e-^{20}$
			ArgoL2	PF16488.2	524 – 569	$3.2e-^{09}$
			Piwi	PF02171.14	674 - 965	$1.4e^{-87}$
	SpeAGO2.3	Sopen02g018440	ArgoN	PF16486.2	178 – 314	$1e^{-16}$
			ArgoL1	PF08699.7	324 – 366	$2.2e^{-08}$

			PAZ	PF02170.19	379 – 498	$4.3e^{-16}$
			Piwi	PF02171.14	657 - 948	$2.7e^{-85}$
	Ortólogo em *Glycine max*	XP_003556681.1	ArgoN	PF16486.2	119 – 253	$3e^{-18}$
			ArgoL1	PF08699.7	265 – 315	$8.2e^{-09}$
			PAZ	PF02170.19	321 – 441	$1.9e^{-18}$
			ArgoL2	PF16488.2	475 – 505	$1.3e^{-07}$
			Piwi	PF02171.14	618 - 914	$8.1e^{-86}$
	Ortólogo em *Phasolus vulgaris*	XP_007157808.1	ArgoN	PF16486.2	144 – 274	$1.9e^{-17}$
			ArgoL1	PF08699.7	286 – 330	$5.5e^{-06}$
			PAZ	PF02170.19	349 – 459	$2.5e^{-16}$
			ArgoL2	PF16488.2	481 – 527	$3.3e^{-07}$
			Piwi	PF02171.14	637 - 928	$9.6e^{-86}$
	Ortólogo em *Solanum tuberosum*	XP_006353071.1	ArgoN	PF16486.2	224 – 361	$5e^{-21}$
			ArgoL1	PF08699.7	371 – 418	$3.8e^{-09}$
			PAZ	PF02170.19	426 – 548	$4e^{-19}$
			ArgoL2	PF16488.2	566 – 611	$2e^{-08}$
			Piwi	PF02171.14	719 - 1010	$1.7e^{-90}$
AGO4	**SlyAGO4.1**	Solyc06g073540	ArgoN	PF16486.2	44 – 217	$1.7e^{-24}$
			ArgoL1	PF08699.7	229 – 277	$2.6e^{-16}$
			PAZ	PF02170.19	283 – 413	$4.2e^{-28}$
			ArgoL2	PF16488.2	424 – 468	$5.1e^{-12}$
			ArgoMid	PF16487.2	478 – 556	$1.5e^{-07}$
			Piwi	PF02171.14	567 - 873	$8.2e^{-101}$
	SlyAGO4.2	Solyc01g008960	ArgoN	PF16486.2	45 – 214	$8.6e^{-25}$
			ArgoL1	PF08699.7	226 – 274	$1.1e^{-15}$
			PAZ	PF02170.19	280 – 410	$2.2e^{-27}$
			ArgoL2	PF16488.2	421 – 465	$1.4e^{-12}$
			ArgoMid	PF16487.2	473 – 524	$2.9e^{-06}$
			Piwi	PF02171.14	563 - 869	$1.2e^{-101}$
	SlyAGO4.3	Solyc06g073530	ArgoN	PF16486.2	44 – 208	$2.9e^{-23}$
			ArgoL1	PF08699.7	220 – 269	$7.4e^{-16}$
			PAZ	PF02170.19	274 – 404	$4e^{-27}$
			ArgoL2	PF16488.2	415 – 459	$4.5e^{-09}$
			Piwi	PF02171.14	558 – 864	$3e^{-99}$
	SlyAGO4.4	Solyc01g096750	ArgoN	PF16486.2	20 – 186	$4.3e^{-25}$
			ArgoL1	PF08699.7	198 – 247	$7.3e^{-16}$
			PAZ	PF02170.19	252 – 380	$1.3e^{-25}$
			ArgoL2	PF16488.2	391 – 435	$1.1e^{-10}$
			Piwi	PF02171.14	535 - 842	$1.7e^{-102}$

	SlyAGO4.5	Solyc03g111760	ArgoN	PF16486.2	37 – 205	$3.2e^{-14}$
			ArgoL1	PF08699.7	227 – 274	$7.9e^{-10}$
			PAZ	PF02170.19	282 – 408	$2.7e^{-19}$
			ArgoL2	PF16488.2	426 – 465	$6.3e^{-10}$
			Piwi	PF02171.14	565 - 895	$7.4e^{-72}$
	SpeAGO4.1	Sopen06g029900	ArgoN	PF16486.2	52 – 217	$1.8e^{-30}$
			ArgoL1	PF08699.7	229 – 277	$3e^{-16}$
			PAZ	PF02170.19	283 – 413	$6.8e^{-28}$
			ArgoL2	PF16488.2	423 – 468	$2.7e^{-13}$
			ArgoMid	PF16487.2	478 – 556	$1.5e\text{-}^{07}$
			Piwi	PF02171.14	567 - 873	$1.3e^{-100}$
	SpeAGO4.2	Sopen01g004450	ArgoN	PF16486.2	53 – 214	$1.2e^{-30}$
			ArgoL1	PF08699.7	226 – 274	$1.3e^{-15}$
			PAZ	PF02170.19	280 – 410	$6.2e^{-27}$
			ArgoL2	PF16488.2	420 – 465	$1.1e^{-14}$
			ArgoMid	PF16487.2	473 – 524	$2.9e^{-06}$
			Piwi	PF02171.14	563 - 869	$1.2e^{-101}$
	SpeAGO4.3	Sopen06g029890	ArgoN	PF16486.2	53 – 208	$2.3e^{-30}$
			ArgoL1	PF08699.7	220 – 268	$6.9e^{-17}$
			PAZ	PF02170.19	274 – 404	$2.3e^{-26}$
			ArgoL2	PF16488.2	414 – 459	$2.4e^{-09}$
			Piwi	PF02171.14	558 - 864	$1.4e^{-100}$
	SpeAGO4.4	Sopen01g040460	ArgoN	PF16486.2	28 – 186	$1.8e^{-29}$
			ArgoL1	PF08699.7	198 – 246	$8e^{-16}$
			PAZ	PF02170.19	252 – 380	$2.5e^{-26}$
			ArgoL2	PF16488.2	390 – 435	$8.5e^{-13}$
			Piwi	PF02171.14	535 – 842	$9.1e^{-103}$
	SpeAGO4.5	Sopen03g030870	ArgoN	PF16486.2	56 – 216	$2.3e^{-14}$
			ArgoL1	PF08699.7	229 – 276	$2.8e^{-09}$
			PAZ	PF02170.19	283 – 396	$6.1e^{-13}$
			ArgoL2	PF16488.2	417 - 455	$2.2e^{-10}$
			Piwi	PF02171.14	555 – 860	$3.3e^{-78}$
	SpeAGO4.6	Sopen03g030870	ArgoN	PF16486.2	56 – 216	$1.7e^{-14}$
			ArgoL1	PF08699.7	229 – 276	$2.2e^{-09}$
			PAZ	PF02170.19	283 – 396	$4.6e^{-13}$
			ArgoL2	PF16488.2	417 – 455	$1.8e^{-10}$
			Piwi	PF02171.14	555 - 860	$2.2e^{-78}$
	SpeAGO4.7	Sopen03g030870	ArgoN	PF16486.2	56 – 216	$1.7e^{-14}$
			ArgoL1	PF08699.7	229 – 276	$2.3e^{-09}$

			PAZ	PF02170.19	283 – 396	$4.7e^{-13}$
			ArgoL2	PF16488.2	417 – 455	$1.8e^{-10}$
			Piwi	PF02171.14	555 - 860	$2.3e^{-78}$
	Ortólogo em *Glycine max*	XP_003545462.1	ArgoN	PF16486.2	54 – 214	$3.4e^{-28}$
			ArgoL1	PF08699.7	226 – 274	$4.1e^{-16}$
			PAZ	PF02170.19	280 – 407	$3.7e^{-24}$
			ArgoL2	PF16488.2	417 – 463	$1.7e^{-13}$
			Piwi	PF02171.14	561 - 868	$2.3e^{-104}$
	Ortólogo em *Phasolus vulgaris*	XP_007141565.1	ArgoN	PF16486.2	54 – 215	$1.6e^{-28}$
			ArgoL1	PF08699.7	227 – 274	$4.3e^{-16}$
			PAZ	PF02170.19	281 – 409	$1.2e^{-25}$
			ArgoL2	PF16488.2	419 – 465	$2e^{-12}$
			ArgoMid	PF16487.2	472 – 525	$2e^{-6}$
			Piwi	PF02171.14	563 - 870	$4.9e^{-103}$
	Ortólogo em *Solanum tuberosum*	XP_006347268.1	ArgoN	PF16486.2	52 – 217	$1.9e^{-30}$
			ArgoL1	PF08699.7	229 – 277	$3e^{-16}$
			PAZ	PF02170.19	283 – 413	$3e^{-28}$
			ArgoL2	PF16488.2	423 – 468	$3.3e^{-14}$
			ArgoMid	PF16487.2	478 – 556	$3.2e^{-07}$
			Piwi	PF02171.14	567 – 873	$5.8e^{-101}$
AGO5	**SlyAGO5**	Solyc06g074730	ArgoN	PF16486.2	162 – 302	$2.2e^{-27}$
			ArgoL1	PF08699.7	313 – 363	$8.6e^{-20}$
			PAZ	PF02170.19	382 – 494	$7.8e^{-24}$
			ArgoL2	PF16488.2	504 – 549	$1.6e^{-11}$
			Piwi	PF02171.14	655 - 973	$2.2e^{-101}$
	SpeAGO5	Sopen06g031140	ArgoN	PF16486.2	170 – 302	$2.9e^{-31}$
			ArgoL1	PF08699.7	313 – 363	$9.1e^{-20}$
			PAZ	PF02170.19	382 – 494	$6.7e^{-25}$
			ArgoL2	PF16488.2	503 – 549	$6.9e^{-12}$
			Piwi	PF02171.14	655 - 973	$6.4e^{-102}$
	Ortólogo em *Glycine max*	XP_006592296.1	ArgoN	PF16486.2	116 – 257	$7.9e^{-32}$
			ArgoL1	PF08699.7	268 – 317	$5.1e^{-22}$
			PAZ	PF02170.19	323 – 448	$1.8e^{-25}$
			ArgoL2	PF16488.2	457 – 503	$2.6e^{-11}$
			ArgoMid	PF16487.2	514 – 592	$2.9e^{-08}$
			Piwi	PF02171.14	607 - 925	$1.2e^{-104}$
	Ortólogo em *Phasolus vulgaris*	XP_007132360.1	ArgoN	PF16486.2	151 – 293	$2.7e^{-35}$
			ArgoL1	PF08699.7	304 – 353	$9.6e^{-22}$
			PAZ	PF02170.19	361 – 482	$9.1e^{-25}$

			ArgoL2	PF16488.2	493 – 539	$2.4e^{-11}$
			Piwi	PF02171.14	639 - 957	$2.9e^{-104}$
	Ortólogo em *Solanum tuberosum*	XP_006347212.1	ArgoN	PF16486.2	178 – 310	$8.9e^{-31}$
			ArgoL1	PF08699.7	321 – 371	$7.7e^{-20}$
			PAZ	PF02170.19	384 – 502	$6.6e^{-23}$
			ArgoL2	PF16488.2	511 – 557	$1.8e^{-11}$
			ArgoMid	PF16487.2	568 – 642	$1.0e^{-06}$
			Piwi	PF02171.14	663 - 981	$1.3e^{-102}$
AGO6	**SlyAGO6**	Solyc07g049500	ArgoN	PF16486.2	40 – 206	$4.1e^{-24}$
			ArgoL1	PF08699.7	218 – 264	$2.9e^{-14}$
			PAZ	PF02170.19	272 – 403	$3.4e^{-26}$
			ArgoL2	PF16488.2	415 – 458	$1.6e^{-09}$
			Piwi	PF02171.14	557 - 862	$2.9e^{-97}$
	SpeAGO6	Sopen07g024850	ArgoN	PF16486.2	48 – 206	$7.7e^{-28}$
			ArgoL1	PF08699.7	218 – 265	3,00E-15
			PAZ	PF02170.19	272 – 403	$3.9e^{-26}$
			ArgoL2	PF16488.2	413 – 458	$5.3e^{-12}$
			Piwi	PF02171.14	557 – 862	$2.8e^{-97}$
	Ortólogo em *Glycine max*	XP_003541581.2	ArgoN	PF16486.2	66 – 225	$1.2e^{-25}$
			ArgoL1	PF08699.7	237 – 285	$1.2e^{-14}$
			PAZ	PF02170.19	291 – 421	$6.2e^{-28}$
			ArgoL2	PF16488.2	436 – 475	$6.6e^{-08}$
			Piwi	PF02171.14	573 - 880	$1.7e^{-95}$
	Ortólogo em *Medicago truncatula*	XP_003601587.1	ArgoN	PF16486.2	50 – 246	$9.3e^{-23}$
			ArgoL1	PF08699.7	258 – 306	$2.8e^{-14}$
			PAZ	PF02170.19	312 – 442	$1.1e^{-24}$
			ArgoL2	PF16488.2	457 – 497	$5.8e^{-11}$
			ArgoMid	PF16487.2	506 – 557	$8.9e^{-07}$
			Piwi	PF02171.14	595 - 910	$1.5e^{-96}$
AGO7	**SlyAGO7**	Solyc01g010970	ArgoN	PF16486.2	138 – 295	$6.1e^{-19}$
			ArgoL1	PF08699.7	306 – 355	$7.2e^{-18}$
			PAZ	PF02170.19	367 – 489	$2.7e^{-21}$
			ArgoL2	PF16488.2	515 – 545	$2.6e^{-08}$
			Piwi	PF02171.14	653 - 960	$2.6e^{-89}$
	SpeAGO7	Sopen01g006840	ArgoN	PF16486.2	147 – 293	$7.5e^{-22}$
			ArgoL1	PF08699.7	304 – 352	$8.4e^{-18}$
			PAZ	PF02170.19	365 – 487	$3.5e^{-21}$
			ArgoL2	PF16488.2	497 – 543	$2.1e^{-07}$
			Piwi	PF02171.14	651 - 958	$3.6e^{-89}$

	Ortólogo em *Glycine max*	_XP_006574922.1	ArgoN	PF16486.2	189 – 335	$8e^{-27}$
			ArgoL1	PF08699.7	345 – 394	$9.6e^{-19}$
			PAZ	PF02170.19	408 – 529	$5.6e^{-22}$
			Piwi	PF02171.14	692 - 1001	$5.4e^{-91}$
	Ortólogo em *Phasolus vulgaris*	XP_007153570.1	ArgoN	PF16486.2	45 – 191	$2e^{-26}$
			ArgoL1	PF08699.7	201 – 250	$8e^{-19}$
			PAZ	PF02170.19	264 – 385	$1.4e^{-22}$
			Piwi	PF02171.14	549 - 856	$6.1e^{-92}$
	Ortólogo em *Solanum tuberosum*	XP_006365299.1	ArgoN	PF16486.2	150 – 297	$1.5e^{-22}$
			ArgoL1	PF08699.7	308 – 356	$9.9e^{-18}$
			PAZ	PF02170.19	369 – 491	$2.3e^{-21}$
			ArgoL2	PF16488.2	501 – 547	$2.7e^{-07}$
			Piwi	PF02171.14	655 - 962	$1.3e^{-88}$
AGO10	**SlyAGO10.1**	Solyc09g082830	ArgoN	PF16486.2	127 – 270	$1.8e^{-23}$
			ArgoL1	PF08699.7	280 – 330	$1.4e^{-22}$
			PAZ	PF02170.19	342 – 462	$1.2e^{-27}$
			ArgoL2	PF16488.2	473 – 518	$4.6e^{-16}$
			ArgoMid	PF16487.2	529 – 606	$2.4e^{-13}$
			Piwi	PF02171.14	621 – 940	$2.4e^{-114}$
	SlyAGO10.2	Solyc12g006790	ArgoN	PF16486.2	82 – 224	$3.7e^{-18}$
			ArgoL1	PF08699.7	234 – 284	$1.1e^{-21}$
			PAZ	PF02170.19	302 – 416	$1.3e^{-25}$
			ArgoL2	PF16488.2	429 – 472	$6.7e^{-15}$
			ArgoMid	PF16487.2	483 – 561	$2.8e^{-11}$
			Piwi	PF02171.14	575 - 891	$3.9e^{-109}$
	SpeAGO10	Sopen09g031660	ArgoN	PF16486.2	136 – 270	$4.5e^{-30}$
			ArgoL1	PF08699.7	280 – 330	$1.7e^{-22}$
			PAZ	PF02170.19	343 – 462	$1.8e^{-27}$
			ArgoL2	PF16488.2	472 – 518	$1e^{-15}$
			ArgoMid	PF16487.2	529 – 606	$2e^{-13}$
			Piwi	PF02171.14	621 - 940	$2.4e^{-114}$
	Ortólogo em *Glycine max*	XP_003528280.1	ArgoN	PF16486.2	69 – 202	$6.7e^{-26}$
			ArgoL1	PF08699.7	212 – 262	$1.1e^{-20}$
			PAZ	PF02170.19	268 – 394	$2.8e^{-25}$
			ArgoL2	PF16488.2	406 – 450	$2.6e^{-15}$
			ArgoMid	PF16487.2	461 – 538	$2.2e^{-12}$
			Piwi	PF02171.14	553 - 872	$5.4e^{-109}$
	Ortólogo em *Phasolus vulgaris*	XP_007138327.1	ArgoN	PF16486.2	68 – 201	$4.3e^{-25}$
			ArgoL1	PF08699.7	211 – 261	$1.1e^{-20}$

			PAZ	PF02170.19	267 – 393	$4.3e^{-26}$
			ArgoL2	PF16488.2	405 – 449	$7.1e^{-17}$
			ArgoMid	PF16487.2	460 – 537	$1.9e^{-12}$
			Piwi	PF02171.14	552 - 871	$3.5e^{-110}$
	Ortólogo em *Solanum tuberosum*	XP_006363457.1	ArgoN	PF16486.2	136 – 270	$4.^{5e-30}$
			ArgoL1	PF08699.7	280 -330	$1.7e^{-22}$
			PAZ	PF02170.19	343 – 462	$1.8e^{-27}$
			ArgoL2	PF16488.2	472 – 518	$1e^{-15}$
			ArgoMid	PF16487.2	529 – 606	$2e^{-13}$
			Piwi	PF02171.14	621 - 940	$2.4e^{-114}$

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410 **Supplementary Table S4.** Distribution of conserved domains and their locations in putative DCL proteins identified in
411 *Solanum lycopersicum* (Sly), *Solanum pennellii* (Spe) and their orthologs.

Family	Protein	ID	Conserved domain	Domain ID	Start and End	E-value
DCL1	**SlyDCL1**	Solyc10g005130	ResIII	PF04851.12	259 - 420	$2.5e^{-14}$
			Helicase C	PF00271.28	656 – 773	$1.7e^{-17}$
			Dicer dimer	PF03368.11	848 – 936	$1e^{-21}$
			PAZ	PF02170.19	1214 – 1349	$5e^{-22}$
			Ribonuclease 3	PF00636.23	1386 – 1468	$2.8e^{-21}$
			Ribonuclease 3	PF00636.23	1586 – 1699	$2.6e^{-24}$
			dsrm	PF00035.23	1726 – 1784	$7.2e^{-05}$
			DND1 DSRM	PF14709.4	1811 – 1883	$7.8e^{-14}$
	SpeDCL1	Sopen10g001150	ResIII	PF04851.12	256 - 420	$2.2e^{-14}$
			Helicase C	PF00271.28	656 – 773	$9.2e^{-17}$
			Dicer dimer	PF03368.11	848 – 936	$7.1e^{-24}$
			PAZ	PF02170.19	1214 – 1349	$4.9e^{-22}$
			Ribonuclease 3	PF00636.23	1386 – 1534	$2.5e^{-29}$
			Ribonuclease 3	PF00636.23	1612 – 1725	$2.7e^{-24}$
			dsrm	PF00035.23	1752 – 1810	$7.3e^{-05}$
			DND1 DSRM	PF14709.4	1837 – 1909	$7.9e^{-14}$
	Ortólogo em *Vitis vinífera*	XP_002268369.1	ResIII	PF04851.12	318 – 478	$1.3e^{-13}$
			Helicase C	PF00271.28	715 – 832	$9.9e^{-17}$
			Dicer dimer	PF03368.11	907 – 995	$6.2e^{-24}$
			PAZ	PF02170.19	1268 – 1406	$2.7e^{-24}$
			Ribonuclease 3	PF00636.23	1443 – 1591	$2.3e^{-28}$
			Ribonuclease 3	PF00636.23	1667 – 1780	$1.6e^{-24}$
			DND1 DSRM	PF14709.4	1893 - 1966	$5.4e^{-14}$
	Ortólogo em *Solanum tuberosum*	XP_006352611.1	ResIII	PF04851.12	260 – 420	$3.7e^{-14}$
			Helicase C	PF00271.28	656 – 773	$9.2e^{-17}$
			Dicer dimer	PF03368.11	848 – 936	$7.4e^{-24}$
			PAZ	PF02170.19	1214 – 1349	$4.9e^{-22}$
			Ribonuclease 3	PF00636.23	1386 – 1534	$2.5e^{-29}$
			Ribonuclease 3	PF00636.23	1612 – 1725	$1.4e^{-24}$
			dsrm	PF00035.23	1752 – 1810	$1.3e^{-04}$
			DND1 DSRM	PF14709.4	1837 - 1909	$7.9e^{-14}$
	Ortólogo em *Theobroma cacao*	XP_007051386.1	ResIII	PF04851.12	356 – 516	$5.2e^{-13}$
			Helicase C	PF00271.28	753 – 870	$5.4e^{-17}$
			Dicer dimer	PF03368.11	945 – 1033	$8e^{-24}$
			PAZ	PF02170.19	1312 – 1443	$9.9e^{-25}$
			Ribonuclease 3	PF00636.23	1480 – 1627	$1.8e^{-28}$

			Ribonuclease 3	PF00636.23	1703 – 1816	$3.3e^{-24}$
			dsrm	PF00035.23	1843 – 1903	$2.2e^{-04}$
			DND1 DSRM	PF14709.4	1929 - 2002	$1.1e^{-13}$
DCL2	**SlyDCL2.1**	Solyc11g008520	DEAD	PF00270.26	26 – 192	$1.9e^{-13}$
			Helicase C	PF00271.28	375 – 492	$2.9e^{-18}$
			Dicer dimer	PF03368.11	588 – 668	$2e^{-19}$
			PAZ	PF02170.19	863 – 989	$2.2e^{-13}$
			Ribonuclease 3	PF00636.23	1031 – 1149	$2.8e^{-22}$
			Ribonuclease 3	PF00636.23	1221 – 1330	$2e^{-21}$
	SlyDCL2.2	Solyc06g048960	DEAD	PF00270.26	22 -187	$7.2e^{-13}$
			Helicase C	PF00271.28	372 – 487	$1.4e^{-17}$
			Dicer dimer	PF03368.11	557 – 637	$1.7e^{-20}$
			PAZ	PF02170.19	826 – 958	$4.5e^{-14}$
			Ribonuclease 3	PF00636.23	1000 – 1118	$4.5e^{-22}$
			Ribonuclease 3	PF00636.23	1190 - 1301	$3.4e^{-20}$
	SlyDCL2.3	Solyc11g008540	ResIII	PF00270.26	8 – 137	$9.1e^{-05}$
			Helicase C	PF00271.28	318 – 437	$2.4e^{-18}$
			Dicer dimer	PF03368.11	507 – 586	$2.6e^{-20}$
			PAZ	PF02170.19	777- 908	$4.8e^{-14}$
			Ribonuclease 3	PF00636.23	950 – 1068	$3.1e^{-22}$
			Ribonuclease 3	PF00636.23	1140 - 1251	$7.9e^{-20}$
	SlyDCL2.4	Solyc11g008530	Helicase C	PF00271.28	307 – 420	$3.1e^{-19}$
			Dicer dimer	PF03368.11	489 - 568	$2.2e^{-20}$
			PAZ	PF02170.19	764 – 875	$2.3e^{-13}$
			Ribonuclease 3	PF00636.23	918 – 1036	$7.7e^{-22}$
			Ribonuclease 3	PF00636.23	1109 - 1219	$3.3e^{-19}$
	SpeDCL2.1	Sopen11g004310	DEAD	PF00270.26	121 – 287	$1.6e^{-13}$
			Helicase C	PF00271.28	468 – 587	$6.7e^{-18}$
			Dicer dimer	PF03368.11	657 – 738	$2.5e^{-23}$
			PAZ	PF02170.19	933 – 1057	$2.3e^{-13}$
			Ribonuclease 3	PF00636.23	1100 – 1218	$2.6e^{-22}$
			Ribonuclease 3	PF00636.23	1290 -1401	$1.8e^{-20}$
	SpeDCL2.2	Sopen06g015290	DEAD	PF00270.26	24 – 190	$1.1e^{-12}$
			Helicase C	PF00271.28	372 – 490	$3.1e^{-17}$
			Dicer dimer	PF03368.11	560 – 642	$7.5e^{-25}$
			PAZ	PF02170.19	829 – 960	$1.1e^{-13}$
			Ribonuclease 3	PF00636.23	1003 – 1121	$3.1e^{-22}$
			Ribonuclease 3	PF00636.23	1192 - 1304	$2.4e^{-20}$
	SpeDCL2.3	Sopen11g004330	DEAD	PF00270.26	24 – 190	$9.9e^{-13}$

			Helicase C	PF00271.28	371 – 490	$1.5e^{-18}$
			Dicer dimer	PF03368.11	560 – 640	$7.8e^{-25}$
			PAZ	PF02170.19	830 – 960	$4e^{-14}$
			Ribonuclease 3	PF00636.23	1003 – 1121	$5.2e^{-23}$
			Ribonuclease 3	PF00636.23	1193 - 1304	$6.7e^{-20}$
	SpeDCL2.4	Sopen11g004320	DEAD	PF00270.26	24 – 190	$4e^{-13}$
			Helicase C	PF00271.28	360 – 473	$2.3e^{-21}$
			Dicer dimer	PF03368.11	542 – 587	$7.4e^{-10}$
			PAZ	PF02170.19	799 – 909	$2.7e^{-12}$
			Ribonuclease 3	PF00636.23	952 – 1070	$1.3e^{-21}$
			Ribonuclease 3	PF00636.23	1143 - 1210	$1.5e^{-11}$
	SpeDCL2.5	Sopen11g017590	Helicase C	PF00271.28	186 – 305	$3.1e^{-18}$
	SpeDCL2.6	Sopen06g015290	DEAD	PF00270.26	24 – 190	$8.7e^{-13}$
			Helicase C	PF00271.28	371 – 490	$2.6e^{-17}$
			Dicer dimer	PF03368.11	560 – 642	$6.3e^{-25}$
			PAZ	PF02170.19	829 – 960	$9e^{-14}$
			Ribonuclease 3	PF00636.23	1003 - 1121	$2.6e^{-22}$
	Ortólogo em *Malus domestica*	XP_008370841.1	DEAD	PF00270.26	20 – 163	$4.9e^{-14}$
			Helicase C	PF00271.28	368 – 486	$6.8e^{-17}$
			Dicer dimer	PF03368.11	556 – 631	$6.3e^{-22}$
			PAZ	PF02170.19	826 – 952	$5.2e^{-14}$
			Ribonuclease 3	PF00636.23	995 – 1113	$7.3e^{-24}$
			Ribonuclease 3	PF00636.23	1185 – 1296	$3e^{-22}$
			dsrm	PF00035.23	1323 - 1387	$1.5e^{-04}$
	Ortólogo em *Theobroma cacao*	XP_007029209.1	Helicase C	PF00271.28	285 – 399	$6e^{-18}$
			Dicer dimer	PF03368.11	469 – 548	$1.1e^{-22}$
			PAZ	PF02170.19	738 – 862	$1.1e^{-15}$
			Ribonuclease 3	PF00636.23	905 – 1020	$9e^{-24}$
			Ribonuclease 3	PF00636.23	1095 – 1206	$1.8e^{-21}$
			dsrm	PF00035.23	1233 - 1297	$1.7e^{-06}$
	Ortólogo em *Solanum tuberosum*	XP_015166742.1	DEAD	PF00270.26	24 – 190	$8.9e^{-13}$
			Helicase C	PF00271.28	371 – 490	$4.7e^{-19}$
			Dicer dimer	PF03368.11	560 – 640	$7.8e^{-25}$
			PAZ	PF02170.19	836 – 960	$1.1e^{-14}$
			Ribonuclease 3	PF00636.23	1003 – 1121	$1.8e^{-22}$
			Ribonuclease 3	PF00636.23	1193 - 1304	$4.1e^{-20}$
DCL3	**SlyDCL3.1**	Solyc08g067210	Helicase C	PF00271.28	161 – 277	$1.2e^{-17}$
			Dicer dimer	PF03368.11	348 – 432	$8.1e^{-23}$
			PAZ	PF02170.19	662 – 798	$1e^{-10}$

			Ribonuclease 3	PF00636.23	840 – 974	$1.2e^{-25}$
			Ribonuclease 3	PF00636.23	1052 - 1156	$8.6e^{-21}$
	SlyDCL3.2	Solyc08g067200	DEAD	PF00270.26	38 - 199	$9.9e^{-19}$
	SpeDCL3	Sopen08g021150	DEAD	PF00270.26	38 - 199	$3e^{-17}$
			Helicase C	PF00271.28	394 – 505	$2e^{-18}$
			Dicer dimer	PF03368.11	576 – 662	$1.6e^{-25}$
			PAZ	PF02170.19	890 – 1026	$7.1e^{-10}$
			Ribonuclease 3	PF00636.23	1068 – 1201	$2.2e^{-25}$
			Ribonuclease 3	PF00636.23	1280 - 1384	$1.5e^{-20}$
	Ortólogo em *Citrus sinensis*	XP_006474520.1	ResIII	PF00270.26	57 – 210	$2e^{-16}$
			Helicase C	PF00271.28	401 – 515	$2.5e^{-18}$
			Dicer dimer	PF03368.11	586 – 672	$6.9e^{-28}$
			PAZ	PF02170.19	904 – 1036	$8.8e^{-16}$
			Ribonuclease 3	PF00636.23	1078 – 1211	$5.8e^{-24}$
			Ribonuclease 3	PF00636.23	1287 - 1395	$2.7e-^{20}$
	Ortólogo em *Solanum tuberosum*	XP_006361520.1	DEAD	PF00270.26	39 – 200	$5.3e^{-17}$
			Helicase C	PF00271.28	391 – 506	$1.8e^{-18}$
			Dicer dimer	PF03368.11	577 – 663	$4.5e^{-25}$
			PAZ	PF02170.19	892 – 1027	$8.6e^{-11}$
			Ribonuclease 3	PF00636.23	1069 – 1202	$3.8e^{-25}$
			Ribonuclease 3	PF00636.23	1282 - 1385	$3.7e^{-20}$
DCL4	**SlyDCL4**	Solyc07g005030	DEAD	PF00270.26	7 – 128	$2.4e^{-08}$
			Helicase C	PF00271.28	300 – 419	$4.6e^{-19}$
			Dicer dimer	PF03368.11	485 – 568	$2.7e^{-23}$
			Ribonuclease 3	PF00636.23	937 – 1067	$1.1e^{-22}$
			Ribonuclease 3	PF00636.23	1143 – 1252	$5.9e^{-21}$
			DND1 DSRM	PF14709.4	1454 - 1528	$4.4e^{-15}$
	SpeDCL4.1	Sopen07g001140	zf-RVT	PF13966.3	9 – 64	$2.2e^{-07}$
			DEAD	PF00270.26	122 – 282	$6.2e^{-15}$
			Helicase C	PF00271.28	467 – 572	$1.6e^{-18}$
			Dicer dimer	PF03368.11	639 – 724	$2.2e^{-26}$
			PAZ	PF02170.19	929 – 1048	$1.2e^{-06}$
			Ribonuclease 3	PF00636.23	1091 – 1221	$3.8e^{-22}$
			Ribonuclease 3	PF00636.23	1297 – 1406	$7.5e^{-21}$
			DND1 DSRM	PF14709.4	1608 - 1608	$1.5e^{-15}$
	SpeDCL4.2	Sopen07g001140	DEAD	PF00270.26	106 – 268	$3.5e^{-15}$
			Helicase C	PF00271.28	453 – 558	$1.6e^{-18}$
			Dicer dimer	PF03368.11	625 – 710	$2.2e^{-26}$
			PAZ	PF02170.19	916 – 1035	$1.2e^{-06}$

			Ribonuclease 3	PF00636.23	1078 – 1208	$3.8e^{-22}$
			Ribonuclease 3	PF00636.23	1284 – 1393	$7.5e-^{21}$
			DND1 DSRM	PF14709.4	1595 - 1669	$1.5e^{-15}$
	SpeDCL4.3	Sopen07g001140	DEAD	PF00270.26	106 – 268	$3.5e^{-15}$
			Helicase C	PF00271.28	453 – 558	$1.6e^{-18}$
			Dicer dimer	PF03368.11	625 – 710	$2.2e^{-26}$
			PAZ	PF02170.19	915 – 1034	$1.2e^{-06}$
			Ribonuclease 3	PF00636.23	1077 – 1207	$3.8e^{-22}$
			Ribonuclease 3	PF00636.23	1283 – 1392	$7.5e^{-21}$
			DND1 DSRM	PF14709.4	1594 - 1668	$1.5e^{-15}$
	Ortólogo em *Phaseolus vulgaris*	XP_007155126.1	ResIII	PF04851.12	55 – 212	$1.3e^{-13}$
			Helicase C	PF00271.28	404 – 509	$2e^{-18}$
			Dicer dimer	PF03368.11	576 – 660	$2.1e^{-24}$
			PAZ	PF02170.19	868 – 989	$2.5e^{-12}$
			Ribonuclease 3	PF00636.23	1033 – 1164	$3.1e^{-21}$
			Ribonuclease 3	PF00636.23	1240 - 1349	$1e^{-21}$
	Ortólogo em *Solanum indicum*	XP_011078684.1	DEAD	PF00270.26	51 – 192	$2.7e^{-14}$
			Helicase C	PF00271.28	401 – 504	$7.3e^{-19}$
			Dicer dimer	PF03368.11	571 – 656	$4.6e^{-28}$
			PAZ	PF02170.19	866 – 982	$8.3e^{-07}$
			Ribonuclease 3	PF00636.23	1025 – 1155	$3.7e^{-21}$
			Ribonuclease 3	PF00636.23	1231 – 1340	$3.8e^{-21}$
			DND1 DSRM	PF14709.4	1552 - 1627	$2.4e^{-21}$

414 **Supplementary Table S5.** Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum*
415 *lycopersicum*.

Family	Pre-miRNA	Size of pre-miRNA	Mature miRNA	Mature miRNA sequence	Size of mature miRNA	Localization of mature in precursor	Ortholog mature miRNA	Number of mismatches with ortholog miRNA	Number of gaps with ortholog miRNA
Sly-MIR1128	sly-miR1128	269	sly-miR1128	uacuacucccuccgucccaaa	21	1-21	ssp-miR1128	0	0
Sly-MIR1446	sly-miR1446-1	113	sly-miR1446-1	ugaacucucucccucaauggcu	22	21-42	nta-miR1446	0	0
	sly-miR1446-2	108	sly-miR1446-2-5p	ugaacucucucccucaauggcu	22	11-32	nta-miR1446	0	0
Sly-MIR156/157	sly-miR156a-1	92	sly-miR156a-1	ugacagaagagagugagcaca	21	4-24	bna-miR156a	0	0
	sly-miR156a-2	93	sly-miR156a-2-3p	gcucacuucucauucugucaga	22	70-91	aly-miR156a-3p	2	0
			sly-miR156a-2-5p	ugacagaagagagugagcaca	21	4-24	bna-miR156a	0	0
	sly-miR156c	99	sly-miR156c-3p	ugcuuacucucuaucugucacc	22	77-98	mtr-miR156c-3p	0	0
			sly-miR156c-5p	ugauagaagagagugagcaca	21	4-24	rco-miR156c	1	0
	sly-miR156f	164	sly-miR156f	uugacagaagagagagaguaca	22	42-63	gma-miR156f	1	0
	sly-miR156i-1	155	sly-miR156i-1-3p	gcucacugcucuaucuuucauc	22	98-119	zma-miR156i-3p	1	0
			sly-miR156i-1-5p	ugacagaagagcgugagcac	20	33-52	zma-miR156i-5p	1	0
	sly-miR156i-2	104	sly-miR156i-2-3p	ugcucacuucucuaucugucauc	23	61-83	mtr-miR156i-3p	1	0
			sly-miR156i-2-5p	ugacagaagagagugggcac	20	7-26	zma-miR156i-5p	1	0
	sly-miR156l-1	110	sly-miR156l-1-3p	gcucacugcucuaucugucacc	22	79-100	zma-miR156l-3p	0	0
			sly-miR156l-1-5p	ugacagaagagagugagcac	20	12-31	zma-miR156l-5p	0	0
	sly-miR156l-2	112	sly-miR156l-2-3p	gcucacugcucuaucugucacc	22	84-105	zma-miR156l-3p	0	0
			sly-miR156l-2-5p	ugacagaagagagugagcac	20	10-29	zma-miR156l-5p	0	0
	sly-miR157a-1	146	sly-miR157a-1-3p	gcucuuuauucuucugucauca	22	96-117	aly-miR157a-3p	3	0
			sly-miR157a-1-5p	uugacagaagauagagagcac	21	31-51	ath-miR157a-5p	0	0
	sly-miR157a-2	202	sly-miR157a-2-3p	gcucucuauucuucugucauca	22	125-146	aly-miR157a-3p	2	0
			sly-miR157a-2-5p	uugacagaagauagagagcac	21	61-81	ath-miR157a-5p	0	0
	sly-miR157a-3	101	sly-miR157a-3-3p	gcucucuaugcuucugucauc	21	81-101	aly-miR157a-3p	2	0
			sly-miR157a-3-5p	uugacagaagauagagagcac	21	1-21	ath-miR157a-5p	0	0
	sly-miR157a-4	246	sly-miR157a-4-5p	uugacagaagauagagagcac	21	63-83	ath-miR157a-5p	0	0
Sly-MIR159	sly-miR159a	178	sly-miR159a-3p	uuuggauugaagggagcucua	21	157-177	ath-miR159a	0	0
			sly-miR159a-5p	gagcuccuugaaguccaa	18	2-19	gma-miR159a-5p	0	0
			sly-miR159b-3p	auuggaaugaagggagcucua	21	22-242	gma-miR159b-3p	2	0
	sly-miR159b	259	sly-miR159b-5p	uugcauauaucaggagcuuca	21	181-201	hbr-miR159b	1	0
Sly-MIR160	sly-miR160	95	sly-miR160	uggcauacagggagccaggca	21	67-87	aau-miR160	0	0
			sly-miR160a-3p	gcguauaaggagccaagcaua	21	65-85	gma-miR160a-3p	1	0
	sly-miR160a	86	sly-miR160a-5p	ugccuggcucccuguaugcca	21	4-24	ath-miR160a-5p	0	0
	sly-miR160g	87	sly-miR160g-5p	ugccuggcucccuggaugcca	21	2-22	ptc-miR160g	0	0

	sly-miR160h-1	95	sly-miR160h-1	ugccuggcucccuguaugccauu	23	7-29	mes-miR160h	0	0
	sly-miR160h-2	85	sly-miR160h-2	ugccuggcuccuuguaugccauu	23	4-26	mes-miR160h	1	0
Sly-MIR162	sly-miR162-1	128	sly-miR162-1-3p	ucgauaaaccucugcauccag	21	94-104	csi-miR162-3p	0	0
			sly-miR162-1-5p	uggaggcagcgguucaucgauc	22	18-39	csi-miR162-5p	0	0
	sly-miR162-2	110	sly-miR162-2-3p	ucgauaaaccucugcauccag	21	77-97	csi-miR162-3p	0	0
			sly-miR162-2-5p	uggaggcagcgguucaucgauc	22	16-37	csi-miR162-5p	0	0
Sly-MIR164	sly-miR164a	165	sly-miR164a-3p	caugugccuguuuuccccauc	21	145-165	sly-miR164a-3p	0	0
			sly-miR164a-5p	uggagaagcagggcacgugca	21	4-24	ath-miR164a	0	0
	sly-miR164e	97	sly-miR164e-5p	uggagaagcagggcacgugcaa	22	4-25	bra-miR164e-5p	0	0
			sly-miR164e-3p	cacguguucuccuucuccaac	21	77-97	bra-miR164e-3p	3	0
	sly-miR164f	88	sly-miR164f	uggagaagcagggcacaugcu	21	8-28	ptc-miR164f	0	0
Sly-MIR166	sly-miR166-1	146	sly-miR166-1	ucggaccaggcuucauuccccc	22	103-124	ctr-miR166	0	0
	sly-miR166-2	158	sly-miR166-2	ucggaccaggcuucauuccccc	22	128-149	ctr-miR166	0	0
	sly-miR166-3	166	sly-miR166-3	ucggaccaggcuucauuccccc	22	132-153	ctr-miR166	0	0
	sly-miR166a-1	120	sly-miR166a-1-3p	ucggaccaggcuucauuccccc	21	91-111	ath-miR166a-3p	0	0
	sly-miR166a-2	107	sly-miR166a-2-3p	ucggaccaggcuucauuccccc	21	77-97	ath-miR166a-3p	0	0
			sly-miR166a-2-5p	ggaauguuguuuggcucgagg	21	13-33	stu-miR166a-5p	1	0
	sly-miR166a-3	93	sly-miR166a-3-3p	ucggaccaggcuucauuccccc	21	69-89	ath-miR166a-3p	0	0
	sly-miR166a-4	158	sly-miR166a-4-3p	ucggaccaggcuucauuccccc	21	115-135	ath-miR166a-3p	0	0
			sly-miR166a-4-5p	ggaauguugucuggcucgagg	21	25-45	aly-miR166a-5p	0	0
	sly-miR166g	187	sly-miR166g-3p	ucggaccaggcuucauuccuc	21	145-165	osa-miR166g-3p	0	0
Sly-MIR167	sly-miR167a-1	122	sly-miR167a-1-3p	gaucauguggcagccuuacc	20	83-102	stu-miR167a-3p	1	0
			sly-miR167a-1-5p	ugaagcugccagcaugaucuaa	22	21-43	bna-miR167a	0	0
	sly-miR167a-2	86	sly-miR167a-2-3p	gaucauguggguugcuucacc	20	62-81	stu-miR167a-3p	3	0
			sly-miR167a-2-5p	ugaagcugccagcaugaucuaa	22	7-28	bna-miR167a	0	0
	sly-miR167c	84	sly-miR167c-3p	ggucaugcucggacagccucacu	23	62-84	stu-miR167c-3p	0	0
			sly-miR167c-5p	ugaagcugccagcaugaucua	21	2-22	osa-miR167c-5p	0	0
	sly-miR167h-1	122	sly-miR167h-1	aucaugcuggcagcuucaacugcu	24	84-107	gma-miR167h	1	0
	sly-miR167h-2	113	sly-miR167h-2	aucaugcuggcagcuucaacugcu	24	76-99	gma-miR167h	1	0
			sly-miR167h-3-3p	agaucauguggcagcaucacc	21	60-80	ptc-miR167h-3p	2	0
	sly-miR167h-3	85	sly-miR167h-3-5p	agcaguugaagcugccagcaugau	24	24...1	gma-miR167h	1	0
Sly-MIR168	sly-miR168	154	sly-miR168	auucaguugaugcaaggcgggacc	24	10-33	aau-miR168	1	0
	sly-miR168a-1	154	sly-miR168a-1-3p	cccgccuugcaucaacugaau	21	125-145	aly-miR168a-3p	0	0
			sly-miR168a-1-5p	ucgcuuggugcaggucgggac	21	10-30	sly-miR168a-5p	0	0
	sly-miR168a-2	160	sly-miR168a-2-5p	ucgcuuggugcaggucgggac	21	9-29	nta-miR168a	0	0
			sly-miR168a-2-3p	ccugccuugcaucaacugaau	21	135-155	sly-miR168a-3p	0	0
Sly-MIR169	sly-miR169a-1	315	sly-miR169a-1-3p	ggcaaguuguucuuggcuaua	21	13-33	zma-miR169a-3p	1	0
	sly-miR169a-2	158	sly-miR169a-2-5p	cagccaaggaugacuugccga	21	42-62	ath-miR169a-5p	0	0
	sly-miR169b-1	202	sly-miR169b-1-5p	cagccaaggaugacuugccgg	21	68-88	ath-miR169b-5p	0	0

	sly-miR169b-2	147	sly-miR169b-2-5p	cagccaaggaugacuugccgg	21	42-62	ath-miR169b-5p	0	0
			sly-miR169b-2-3p	ggcaaguuguucuuggcuaua	21	92-102	zma-miR169b-3p	1	0
	sly-miR169b-3	184	sly-miR169b-3-5p	cagccaaggaugacuugccgg	21	63-83	ath-miR169b-5p	0	0
	sly-miR169d	164	sly-miR169d-3p	gcaggucaucuuuagcuaacu	21	103-123	stu-miR169d-3p	0	0
			sly-miR169d-5p	uagccaaggaugacuugucu	20	43-62	sbi-miR169d-5p	1	0
			sly-miR169e-3p	uggcaagcaucuuuggcgacu	21	133-153	sly-miR169e-3p	0	0
	sly-miR169e	193	sly-miR169e-5p	uagccaaggaugacuugccuuu	22	48-69	sly-miR169e-5p	0	0
	sly-miR169f	188	sly-miR169f	uagccaaggaugacuugccua	21	45-65	osa-miR169f.1	0	0
	sly-miR169g	208	sly-miR169g	uagccaaggaugacuugccugc	22	45-66	bna-miR169g	0	0
	sly-miR169m	184	sly-miR169m	uagccaaaaaugacuugccag	21	55-75	cme-miR169m	1	0
Sly-MIR170/171	sly-miR170-1	112	sly-miR170-1-3p	ugauugagccgugucaauauc	21	72-92	ath-miR170-3p	0	0
			sly-miR170-1-5p	uauuggccugguucacucaga	21	23-43	aly-miR170-5p	0	0
			sly-miR170-2-3p	ugauugagccgugccaauau	20	70-89	ath-miR170-3p	1	0
	sly-miR170-2	89	sly-miR170-2-5p	uauuggccugguucacucaga	21	1-21	aly-miR170-5p	0	0
	sly-miR171b-1	92	sly-miR171b-1-3p	uugagccgugccaauaucacg	21	68-88	ath-miR171b-3p	0	0
			sly-miR171b-1-5p	agauauuggugcgguucaau	20	7-26	aly-miR171b-5p	1	0
	sly-miR171b-2	159	sly-miR171b-2-3p	uugagccgugccaauaucacg	21	105-125	ath-miR171b-3p	0	0
	sly-miR171b-3	110	sly-miR171b-3	ugauugagccgugccaauauc	21	72-92	osa-miR171b	0	0
			sly-miR171c-1-3p	ugauugagccgcgccaauau	20	57-76	osa-miR171c-3p	1	0
	sly-miR171c-1	76	sly-miR171c-1-5p	uauuggugcgguucaaugaga	21	1-21	sly-miR171c	0	0
	sly-miR171c-2	99	sly-miR171c-2	agauugagccgcgccaauauc	21	70-90	ptc-miR171c	0	0
	sly-miR171c-3	100	sly-miR171c-3-3p	agauugagccgcgccaauauc	21	71-91	ptc-miR171c	0	0
			sly-miR171c-3-5p	gauguuggugagguucaauc	20	10-29	aly-miR171c-5p	2	0
	sly-miR171c-4	92	sly-miR171c-4	uaauugaaccgcaccaauauc	21	65-85	aqc-miR171c	1	0
	sly-miR171f	112	sly-miR171f	augagccgaaccaauaucacu	21	72-92	sbi-miR171f	0	0
	sly-miR171i	86	sly-miR171i-3p	ggauugagccgcgucaauauc	21	63-83	osa-miR171i-3p	0	0
Sly-MIR172	sly-miR172d-1	111	sly-miR172d-1	ugugaaucuugaugaugcugcau	23	71-93	vvi-miR172d	1	0
	sly-miR172d-2	274	sly-miR172d-2	gagaaucuugaugaugcugcau	22	12-33	vvi-miR172d	0	0
	sly-miR172d-3	93	sly-miR172d-2-3p	ugagaaucuugaugaugcugcau	23	67-89	vvi-miR172d	0	0
			sly-miR172d-5p	gcagcaccauuaagauucaca	21	6-26	bra-miR172d-5p	1	0
	sly-miR172d-4	142	sly-miR172d-4-3p	gagaaucuugaugaugcugcau	22	103-124	vvi-miR172d	0	0
			sly-miR172d-4-5p	gcauaaucaagauucac	17	24-40	stu-miR172d-5p	1	0
	sly-miR172d-5	164	sly-miR172d-5-3p	ugggaaucuugaugaugcugcau	23	122-144	vvi-miR172d	1	0
			sly-miR172d-5-5p	ugcaacaucaucaagauucaca	22	14-35	mtr-miR172d-5p	2	0
	sly-miR172d-6	248	sly-miR172d-6-3p	ugagaaucuugaugaugcugcau	23	128-150	vvi-miR172d	0	0
			sly-miR172d-6-5p	ugcagcaucaucaagauucaca	22	30-51	mtr-miR172d-5p	1	0
	sly-miR172d-7	166	sly-miR172d-7-3p	ugagaaucuugaugaugcugca	22	130-151	vvi-miR172d	0	0
			sly-miR172d-7-5p	ugcagcaucuucaagauucaca	22	7-28	mtr-miR172d-5p	2	0
	sly-miR172d-8	126	sly-miR172d-8-5p	guggagcaucaucaagauucaca	23	17-39	mtr-miR172d-5p	0	0

			sly-miR172d-8-3p	ggaaucuugaugaugcugcag	21	91-111	stu-miR172d-3p	0	0
	sly-miR172d-9	111	sly-miR172d-9-5p	aaugcagcaucaucaagauucaca	24	18-41	mtr-miR172d-5p	2	0
			sly-miR172d-9-3p	agaaucuuaauagugcugcau	21	73-93	osa-miR172d-3p	3	0
	sly-miR172d-10	188	sly-miR172d-10-5p	augcagcaucaucaagauucuca	23	70-48	vvi-miR172d	0	0
			sly-miR172d-10-3p	ugcagcaucaucaagauucu	20	68-49	ath-miR172d-3p	0	0
	sly-miR172j-1	109	sly-miR172j-1-5p	gcagcaucaucaagauuccca	21	10-30	lus-miR172j	0	0
			sly-miR172j-1-3p	gaaucuugaugaugcucca	19	83-101	nta-miR172j	1	0
	sly-miR172j-2	169	sly-miR172j-2-5p	gcagcaucaucaagauuccca	21	22-42	lus-miR172j	0	0
			sly-miR172j-2-3p	gaaucuugaugauguugcau	20	132-151	nta-miR172j	1	0
Sly-MIR1886	sly-miR1886a	187	sly-miR1886a	augguaucgugagaugaaaucagc	24	64-87	stu-miR1886a	0	0
	sly-miR1886h-1	71	sly-miR1886h-1	auuuuacguugauuucaucucaug	24	39-62	stu-miR1886h	0	0
	sly-miR1886h-2	174	sly-miR1886h-2	auuuuacguugauuucaucucaug	24	89-112	stu-miR1886h	0	0
Sly-MIR1917	sly-miR1917-1	148	sly-miR1917-1	auuaauaaagagugcuaaagu	21	33-53	sly-miR1917	0	0
	sly-miR1917-2	191	sly-miR1917-2	auuaauaaagagugcuaaagu	21	43-63	sly-miR1917	0	0
Sly-MIR1918	sly-miR1918	166	sly-miR1918	uguuggugagaguucgauucuc	22	37-58	sly-miR1918	0	0
Sly-MIR1919	sly-miR1919a-1	177	sly-miR1919a-1	acgagagucaucugugacagg	21	113-133	sly-miR1919a	0	0
	sly-miR1919a-2	160	sly-miR1919a-2	acgagagucaucugugacagg	21	110-130	sly-miR1919a	0	0
	sly-miR1919a-3	164	sly-miR1919a-3	acgagagucaucugugacagg	21	111-131	sly-miR1919a	0	0
Sly-MIR2101	sly-miR2101	82	sly-miR2101-3p	auuuaacucaagugagcau	19	53-71	osa-miR2101-3p	0	0
			sly-miR2111a-3p	ccuugggaugcagauuauc	19	53-71	mtr-miR2111a-3p	1	0
Sly-MIR2111	sly-miR2111a	71	sly-miR2111a-5p	uaaucugcauccugagguuua	21	4-24	ath-miR2111a-5p	0	0
Sly-MIR2604	sly-miR2604	199	sly-miR2604	uaauuuuuauguggaaguguu	21	49-69	mtr-miR2604	1	0
Sly-MIR319	sly-miR319-1	197	sly-miR319-3p-1	uuggacugaaggguuuccuuc	21	167-187	stu-miR319-3p	1	0
			sly-miR319-5p-1	gcugcugaaucauugguuca	20	61-80	ata-miR319-5p	4	0
	sly-miR319-2	179	sly-miR319-5p-2	aggaaacuguuuaguccaacc	21	2-22	stu-miR319-5p	0	0
			sly-miR319-3p-2	uuggacugaaggguuuccuuc	21	159-179	stu-miR319-3p	1	0
	sly-miR319a-1	187	sly-miR319a-1-3p	uuggacugaagggagcucccu	21	161-181	ath-miR319a	0	0
			sly-miR319a-1-5p	gagcucucuccgguccaguc	20	10-29	zma-miR319a-5p	3	0
	sly-miR319a-2	189	sly-miR319a-2-3p	uuggacugaagggagcucccu	21	160-180	ath-miR319a	0	0
			sly-miR319a-2-5p	agagcuuccuuuaguccacuc	21	11-31	mtr-miR319a-5p	1	0
	sly-miR319c-1	177	sly-miR319c-1	uuggacugaagggagcuccu	20	158-177	ath-miR319c	0	0
	sly-miR319c-2	177	sly-miR319c-2-3p	uuggacugaagggagcuccuu	21	157-177	ath-miR319c	0	0
			sly-miR319c-2-5p	agagcuuccuucagcccacuc	21	5-25	sly-miR319c-5p	0	0

	sly-miR319c-3	171	sly-miR319c-3-3p	cuuggacugaagggagcuccc	21	151-171	ppt-miR319c	0	0
			sly-miR319c-3-5p	gagcuuucuuuaguccacac	20	2-21	zma-miR319c-5p	3	0
Sly-MIR3627	sly-miR3627	125	sly-miR3627-3p	aagugccucugucuuucgaca	21	85-105	stu-miR3627-3p	0	0
			sly-miR3627-5p	uugucgcaggagagauggcacu	22	20-41	vvi-miR3627-5p	1	0
Sly-MIR390	sly-miR390a	110	sly-miR390a-3p	cgcuauccauccugaguuuca	21	76-96	aly-miR390a-3p	0	0
			sly-miR390a-5p	aagcucaggagggauagcgcc	21	18-38	ath-miR390a-5p	0	0
	sly-miR390b	103	sly-miR390b-3p	cgcuauccauccugaguuuua	21	67-87	lja-miR390b-3p	1	0
			sly-miR390b-5p	aagcucaggagggauagcacc	21	18-38	gma-miR390b-5p	0	0
Sly-MIR393	sly-miR393a	78	sly-miR393a-3p	aucaugcgaucucuucggaau	21	58-78	aly-miR393a-3p	3	0
			sly-miR393a-5p	uccaaagggaucgcauugaucc	22	2-23	ath-miR393a-5p	0	0
Sly-MIR394	sly-miR394a	81	sly-miR394a	uuggcauucuguccaccucc	20	12-31	ath-miR394a	0	0
	sly-miR394b	235	sly-miR394b-3p	aggugggcauacugccaauag	21	146-166	ath-miR394b-3p	0	0
			sly-miR394b-5p	uuggcauucuguccaccucc	20	72-91	ath-miR394b-5p	0	0
Sly-MIR395	sly-miR395a-1	151	sly-miR395a-1	cugaaguguuuggggaacuc	21	3-23	ath-miR395a	0	0
	sly-miR395a-2	170	sly-miR395a-2	cugaaguguuuggggaacucc	22	10-31	sly-miR395a	0	0
	sly-miR395a-3	107	sly-miR395a-3	cugaaguguuuggggaacuc	21	69-89	ath-miR395a	0	0
			sly-miR395a-4-3p	cugaaguguuugagggaac	19	259-277	ath-miR395a	1	0
	sly-miR395a-4	302	sly-miR395a-4-5p	cugaaguguuuggggaacucc	22	76-97	sly-miR395a	0	0
	sly-miR395g	163	sly-miR395g	uugaaguguuuggggaacuc	21	9-29	mtr-miR395g	0	0
Sly-MIR396	sly-miR396a	144	sly-miR396a-3p	guucaauaaagcugugggaag	21	103-123	aly-miR396a-3p	0	0
			sly-miR396a-5p	uuccacagcuuucuugaacug	21	24-44	ath-miR396a-5p	0	0
	sly-miR396b	120	sly-miR396b-3p	caagaaagcugugggaaa	18	96-113	aly-miR396b-3p	0	0
			sly-miR396b-5p	uuccacagcuuucuugaacuu	21	11-31	ath-miR396b-5p	0	0
	sly-miR396g-1	144	sly-miR396g-1-3p	guucaagaaagcuguggaaaa	21	104-124	zma-miR396g-3p	1	0
			sly-miR396g-1-5p	ucccacagcuuucuuggacu	20	22-41	zma-miR396g-5p	2	0
	sly-miR396g-2	130	sly-miR396g-2-5p	ucccacagcuuuauugaaccg	21	17-37	zma-miR396g-5p	1	0
			sly-miR396g-2-3p	guucaagaaagcuguggaaaa	21	96-116	zma-miR396g-3p	1	0
Sly-MIR397	sly-miR397-1	127	sly-miR397-1-3p	caucaacgcuaaacucgauca	21	86-106	stu-miR397-3p	2	0
			sly-miR397-1-5p	auugagugcagcguugaugac	21	26-46	stu-miR397-5p	0	0
	sly-miR397-2	127	sly-miR397-2-3p	caucaacgcugcacucaauca	21	84-104	stu-miR397-3p	1	0
			sly-miR397-2-5p	aucgaguuuagcguugauga	20	24-43	stu-miR397-5p	3	0
Sly-MIR398	sly-miR398a	90	sly-miR398a-3p	uauguucucaggucgccccu	20	71-90	stu-miR398a-3p	0	0
			sly-miR398a-5p	ggguugauuugagaacauaug	21	1-21	stu-miR398a-5p	0	0
	sly-miR398b	111	sly-miR398b-3p	uguguucucagguuaccccug	21	82-102	ath-miR398b-3p	1	0
Sly-MIR399	sly-miR399a-1	140	sly-miR399a-1	ugccaaaggagaauugcccug	21	105-125	osa-miR399a	0	0
	sly-miR399a-2	140	sly-miR399a-2	ugccaaaggagaauugcacug	21	103-123	osa-miR399a	1	0
	sly-miR399a-3	103	sly-miR399a-3-3p	cgccaaaggagagcugcccug	21	64-84	nta-miR399a	0	0
			sly-miR399a-3-5p	gggcuacucucuauuggcaug	21	21-41	stu-miR399a-5p	0	0
	sly-miR399a-4	323	sly-miR399a-4-3p	cgccaaaggagagcugcccug	21	102-122	nta-miR399a	0	0

			sly-miR399a-4-5p	gggcuacucucuauuggcaug	21	59-79	stu-miR399a-5p	0	0
	sly-miR399a-5	217	sly-miR399a-5-3p	cgccaaaggagagcugcccug	21	138-158	nta-miR399a	0	0
			sly-miR399a-5-5p	gggcuacucucuauuggcaug	21	63-83	stu-miR399a-5p	0	0
	sly-miR399d-1	123	sly-miR399d-1	ugccaaagaagauuugccccg	21	82-102	ptc-miR399d	0	0
	sly-miR399d-2	171	sly-miR399d-2	ugccaaagaagauuugccccg	21	109-129	ptc-miR399d	0	0
	sly-miR399d-3	89	sly-miR399d-3-3p	gccaaaggagagcugcccua	20	61-80	mtr-miR399d	0	0
			sly-miR399d-3-5p	gggcuacucucuauaggcau	20	11-30	stu-miR399d-5p	1	0
	sly-miR399i-1	103	sly-miR399i-1	ugccaaaggagagcugcccug	21	64-84	osa-miR399i	0	0
	sly-miR399j-2	146	sly-miR399j-2	ugccaaaggagaguugcccua	21	100-120	osa-miR399j	0	0
	sly-miR399j-3	70	sly-miR399j-3-3p	ugccaaaggagaguugcccua	21	50-70	osa-miR399j	0	0
			sly-miR399j-3-5p	gggcuacacucuauuggcau	20	2-21	stu-miR399j-5p	1	0
Sly-MIR403	sly-miR403	112	sly-miR403-3p	cuagauucacgcacaagcucg	21	74-94	sly-miR403-3p	0	0
			sly-miR403-5p	cguuugugcgugaaucuaaca	21	21-41	sly-miR403-5p	0	0
	sly-miR403a	112	sly-miR403a-3p	uuagauucacgcacaaacgug	21	74-94	gma-miR403a	1	0
			sly-miR403a-5p	uugugcgugaaucua	15	24-38	aly-miR403a-5p	1	0
Sly-MIR408	sly-miR408-1	128	sly-miR408-1	cagggaagaggcagugcaugg	21	30-50	lja-miR408	1	0
	sly-miR408-2	88	sly-miR408-2-3p	augcacugccucuucccuggc	21	60-80	ath-miR408-3p	0	0
			sly-miR408-2-5p	cggggacgagccagagcaug	20	11-30	osa-miR408-5p	3	0
			sly-miR408a-3p	augcacagccucuucccuggc	21	52-72	gma-miR408a-3p	1	0
	sly-miR408a	72	sly-miR408a-5p	acagggacgaggcagcgcaug	21	1-21	stu-miR408a-5p	0	0
Sly-MIR437	sly-miR437	233	sly-miR437	aaaguuagagauguuugacuu	21	65-85	osa-miR437	1	0
Sly-MIR4376	sly-miR4376	96	sly-miR4376-3p	gcaucauacuccugcauauu	20	68-87	stu-miR4376-3p	0	0
			sly-miR4376-5p	acgcaggagagaugaugcugga	22	13-34	sly-miR4376	0	0
Sly-MIR477	sly-miR477	114	sly-miR477-3p	aguucuuguagggugagacaac	22	79-100	sly-miR477-3p	0	0
			sly-miR477-5p	ugucucucccucaagggcucc	21	18-38	sly-miR477-5p	0	0
	sly-miR477a	70	sly-miR477a-3p	gaagcucuagcagggagagcca	22	49-70	stu-miR477a-3p	0	0
			sly-miR477a-5p	ccucucccucaagggcuucuc	21	2-22	stu-miR477a-5p	0	0
	sly-miR477b	72	sly-miR477b-3p	gaggucuuucgagugagaguga	22	51-72	stu-miR477b-3p	0	0
			sly-miR477b-5p	acucucccucaaaggcuucug	21	2-22	stu-miR477b-5p	0	0
Sly-MIR482	sly-miR482a-1	136	sly-miR482a-1	ucuuuccuacucccucccauacc	22	85-106	ghr-miR482a	0	0
			sly-miR482a-2-5p	gggauuggugaguuggaaagc	21	12-32	stu-miR482a-5p	3	0
	sly-miR482a-2	91	sly-miR482a-2-3p	uuuccaauuccacccauuccua	22	60-81	sly-miR482a	0	0
	sly-miR482c	145	sly-miR482c	uuuccuauuccacccaugccaa	22	98-112	stu-miR482c	0	0
	sly-miR482d	111	sly-miR482d-3p	ucuugccuacaccgcccaugcc	22	71-92	stu-miR482d-3p	0	0
			sly-miR482d-5p	cgugagcgguggggaaagaua	21	21-41	stu-miR482d-5p	2	0
	sly-miR482e	149	sly-miR482e-3p	ucuugccaauaccgcccauucc	22	91-112	stu-miR482e-3p	0	0
			sly-miR482e-5p	aguggguggugugguaagauu	21	42-62	stu-miR482e-5p	0	0
Sly-MIR5014	sly-miR5014a	223	sly-miR5014a-3p	uuguacaaauuuaagugua	19	171-189	ath-miR5014a-3p	0	0
Sly-MIR5162	sly-miR5162	139	sly-miR5162	aaaugaccaaaauaccccuaaa	22	77-98	osa-miR5162	1	0

Sly-MIR5174	sly-miR5174d	248	sly-miR5174d-5p	ucccuccguuucaaaaagauuggc	24	1-24	bdi-miR5174d-5p	1	0
Sly-MIR5282	sly-miR5282	128	sly-miR5282-3p	gacggaauuagagagggauuuua	23	73-95	mtr-miR5282	1	0
			sly-miR5282-5p	augaaauuccuuacaaauuccuu	23	34-56	mtr-miR5282	5	0
Sly-MIR530	sly-miR530	82	sly-miR530	ucugcauuugcaccugcaccu	21	2-22	stu-miR530	0	0
Sly-MIR5300	sly-miR5300	266	sly-miR5300-5p	uccccaguccaggcauuccaac	22	18-39	sly-miR5300	0	0
Sly-MIR5303	sly-miR5303	126	sly-miR5303	uuuuugaagaguucgagcaac	21	99-119	sly-miR5303	0	0
	sly-miR5303c	136	sly-miR5303c	uuuuggagaauccgacacgcaccc	24	73-96	stu-miR5303c	0	0
	sly-miR5303f	126	sly-miR5303f	auuuuuggagaaucugacacgggu	24	67-90	stu-miR5303f	0	0
	sly-miR5303g	128	sly-miR5303g	auauuuuugaagagucugagcaac	24	92-115	stu-miR5303g	0	0
	sly-miR5303h-1	131	sly-miR5303h-1	aacauuuuugaagagucugagcaa	24	98-121	stu-miR5303h	0	0
	sly-miR5303h-2	124	sly-miR5303h-2	aacauuuuugaagagucugagcaa	24	93-116	stu-miR5303h	0	0
	sly-miR5303j-1	107	sly-miR5303j-1	aauauuuuugaagagucugagcaa	24	64-87	stu-miR5303j	0	0
	sly-miR5303j-2	128	sly-miR5303j-2	aauauuuuugaagagucugagcaa	24	98-121	stu-miR5303j	0	0
Sly-MIR5304	sly-miR5304	142	sly-miR5304-3p	agaugaguauggugcauugga	21	93-113	stu-miR5304-3p	0	0
			sly-miR5304-5p	ucaaugcuacauacucauccc	21	33-53	sly-miR5304	0	0
Sly-MIR5368	sly-miR5368	83	sly-miR5368	ggacagucucagguagaca	19	31-49	gma-miR5368	0	0
Sly-MIR5532	sly-miR5532-1	163	sly-miR5532-1	augaaauauaugacaaaggugg	22	36-57	osa-miR5532	1	0
	sly-miR5532-2	263	sly-miR5532-2	auggaauauaugacaaaggugg	22	169-190	osa-miR5532	0	0
Sly-MIR6024	sly-miR6024	116	sly-miR6024-3p	uuuuagcaagaguuguuuuacc	22	76-97	sly-miR6024	0	0
			sly-miR6024-5p	agaaacaacacuugcuaaagga	22	21-42	stu-miR6024-5p	1	0
Sly-MIR6027	sly-miR6027	153	sly-miR6027-3p	ugaauccuucggcuauccauaa	22	118-139	sly-miR6027-3p	0	0
			sly-miR6027-5p	auggguagcacaaggauuaaug	22	17-38	sly-miR6027-5p	0	0
Sly-MIR7122	sly-miR7122	79	sly-miR7122-3p	acagcguuuuucuguauaacc	21	59-79	stu-miR7122-3p	1	0
			sly-miR7122-5p	uauacagagaaaccgcugucg	21	4-24	stu-miR7122-5p	0	0
Sly-MIR7696	sly-miR7696c	246	sly-miR7696c-3p	uuuugaauuauuagaacuuga	21	5-25	mtr-miR7696c-3p	1	0
Sly-MIR7805	sly-miR7805	339	sly-miR7805-5p	aaauuugguguagugaauacu	21	238-258	rgl-miR7805-5p	1	0
Sly-MIR7980	sly-miR7980b-1	111	sly-miR7980b-3p-1	gagauggaaucaguguuuggacau	24	33-56	stu-miR7980b-3p	0	0
			sly-miR7980b-2-3p	gagauggaaucaacgu	16	32-47	stu-miR7980b-3p	2	0
	sly-miR7980b-2	111	sly-miR7980b-2-5p	guccaaacacugauuccaucuca	23	58-80	stu-miR7980b-5p	0	0
Sly-MIR7981	sly-miR7981	210	sly-miR7981-3p	auaggacuuuaguuuaguuaaggu	24	163-186	stu-miR7981-3p	0	0
			sly-miR7981-5p	uuaacuuaacuaagguucuauua	23	28-50	stu-miR7981-5p	4	0
Sly-MIR7983	sly-miR7983-1	173	sly-miR7983-1-3p	acuaaugccgguaaagacuuuaac	24	113-136	stu-miR7983-3p	0	0
			sly-miR7983-1-5p	uaaagcuuuuagcgauauuuguuc	24	77-100	stu-miR7983-5p	4	0
	sly-miR7983-2	222	sly-miR7983-2-3p	acuaaugccgguaaagacuuuaac	24	138-161	stu-miR7983-3p	0	0
			sly-miR7983-2-5p	uaaagcuuuuagcgaaauugauuc	24	102-124	stu-miR7983-5p	4	0

	sly-miR7983-3	182	sly-miR7983-3-3p	acuaaugccgguaaagacuuuaac	24	98-121	stu-miR7983-3p	0	0
			sly-miR7983-3-5p	uaacggcuuuagcaacauuggauc	24	62-85	stu-miR7983-5p	4	0
	sly-miR7983-4	137	sly-miR7983-4-5p	uaaagucuuuagcgacauugguuc	24	40-63	stu-miR7983-5p	0	0
			sly-miR7983-4-3p	acuaauuucgguaaagacuuuagc	24	76-99	stu-miR7983-3p	3	0
	sly-miR7983-5	73	sly-miR7983-5-5p	uaaagucuuuagcgacauugguuc	24	9-32	stu-miR7983-5p	0	0
			sly-miR7983-5-3p	acuaaugcugguaaagacuuuagc	24	45-68	stu-miR7983-3p	2	0
	sly-miR7983-6	100	sly-miR7983-6-5p	uaaagucuuuagcgacauugguuc	24	23-46	stu-miR7983-5p	0	0
			sly-miR7983-6-3p	acuaaugacggu-aagacuuuagc	24	59-81	stu-miR7983-3p	3	1
Sly-MIR7984	sly-miR7984c	202	sly-miR7984c-3p	uacgauaccaaacuuuauggagg	23	1-23	stu-miR7984c-3p	1	0
			sly-miR7984c-5p	acgauaccaaacuuuauggagga	23	2-24	stu-miR7984c-5p	1	0
	sly-miR7984d	216	sly-miR7984d-3p	caauuucggucaaaguucggauau	24	193-216	stu-miR7984d-3p	0	0
Sly-MIR7985	sly-miR7985	178	sly-miR7985	cgggcuugccuagugcgggguacc	24	85-108	stu-miR7985	2	0
Sly-MIR7987	sly-miR7987	208	sly-miR7987-3p	acacuaguugaucuuauugaugac	24	130-153	stu-miR7987	0	0
			sly-miR7987-5p	acacuagcugaugcuauugaugac	24	12-35	stu-miR7987	3	0
Sly-MIR7990	sly-miR7990a-1	102	sly-miR7990a-1	uucaaaugaucguaacuuuggccu	24	79-102	stu-miR7990a	0	0
	sly-miR7990a-2	211	sly-miR7990a-2	uucaaaugaucguaacuuuggccu	24	133-156	stu-miR7990a	0	0
	sly-miR7990a-3	219	sly-miR7990a-3	uucaaaugaucguaacuuuugccu	24	128-151	stu-miR7990a	1	0
Sly-MIR7992	sly-miR7992	208	sly-miR7992-3p	ugucuagaugugcacuccaaagu	23	172-194	stu-miR7992-3p	2	0
			sly-miR7992-5p	aguacacauccagacacu	18	24-41	stu-miR7992-5p	3	0
Sly-MIR7993	sly-miR7993a	218	sly-miR7993a	auauuuuauguuguuaacuuaacu	24	156-179	stu-miR7993a	1	0
Sly-MIR7997	sly-miR7997a	128	sly-miR7997a	augcugcucggacucuucaaa	21	6-26	stu-miR7997a	0	0
Sly-MIR8001	sly-miR8001a	139	sly-miR8001a	uccuggggauuaguaugaaaauuc	24	34-57	stu-miR8001a	0	0
	sly-miR8001b-1	132	sly-miR8001b-1-3p	acuuuuauacuaauucccagga	22	73-94	stu-miR8001b-3p	4	0
			sly-miR8001b-1-5p	augggauuaguaugaaaauuugc	24	28-51	stu-miR8001b-5p	0	0
	sly-miR8001b-2	90	sly-miR8001b-2-5p	augggauuaguaugaaaauuugc	24	28-51	stu-miR8001b-5p	1	0
Sly-MIR8006	sly-miR8006-1	243	sly-miR8006-1-3p	ugcccugccguccaaaaacuaga	23	211-233	stu-miR8006-3p	1	0
			sly-miR8006-1-5p	uaguuuuuggauuacagagacacc	24	14-37	stu-miR8006-5p	4	0
	sly-miR8006-2	184	sly-miR8006-2-5p	uaguuuuugaacgacaggggcacc	24	38-61	stu-miR8006-5p	1	0
Sly-MIR8007	sly-miR8007a	149	sly-miR8007a-5p	auguggcacuuuucggauuucgag	24	75-98	stu-miR8007a-5p	1	0
	sly-miR8007b	270	sly-miR8007b-5p	augugacacuuuuuggauuucgag	24	24-47	stu-miR8007b-5p	1	0
			sly-miR8007b-3p	aaaaacgaaaagugcca	17	227-243	stu-miR8007b-3p	2	0
Sly-MIR8008	sly-miR8008a-1	54	sly-miR8008a-1	auuuccagaaaagcgacggacag	23	1-23	stu-miR8008a	0	0
			sly-miR8008a-2-3p	auuuacagaaaagcgacgga	20	166-185	stu-miR8008a	1	0

	sly-miR8008a-2	188	sly-miR8008a-2-5p	auuuccagaaaagugacggacagu	24	101-124	stu-miR8008a	1	0
			sly-miR8008b-1-3p	caaggaaagcgacagacauu	20	155-174	stu-miR8008b	4	0
	sly-miR8008b-1	223	sly-miR8008b-1-5p	aaacccagaaaagcgacggaca	22	86-107	stu-miR8008b	0	0
	sly-miR8008b-2	192	sly-miR8008b-2-3p	aaacccagaaaagcgacagacag	23	72-94	stu-miR8008b	1	0
			sly-miR8008b-2-5p	aaaaaaucgacggacag	17	14-30	stu-miR8008b	2	0
	sly-miR8008b-3	193	sly-miR8008b-3-3p	aaacccagaaaagcgacggaca	22	136-157	stu-miR8008b	0	0
			sly-miR8008b-3-5p	aaucccagaaaagcgacugaca	22	5-26	stu-miR8008b	2	0
Sly-MIR8011	sly-miR8011a-1	100	sly-miR8011a-1-3p	acaaaaagaagccucacacaacu	24	72-94	stu-miR8011a-3p	1	0
	sly-miR8011a-2	168	sly-miR8011a-2-5p	uugugugaggucucuuuuguuu	23	40-62	stu-miR8011a-5p	1	0
			sly-miR8011a-2-3p	aauaaaaagaagucucacgcaacu	24	107-130	stu-miR8011a-3p	2	0
Sly-MIR8013	sly-miR8013	216	sly-miR8013	agaagaaaaucacaccgucagaag	24	44-67	stu-miR8013	2	0
Sly-MIR8019	sly-miR8019-1	283	sly-miR8019-1-3p	aaaagaaugaccugguuugacuug	24	33-56	stu-miR8019-3p	0	0
			sly-miR8019-1-5p	aggaaaggagguuauucuuuuug	23	233-255	stu-miR8019-5p	4	0
	sly-miR8019-2	262	sly-miR8019-2-3p	aaaagaaugaccugguuugacuug	24	22-45	stu-miR8019-3p	0	0
			sly-miR8019-2-5p	gaaagaggucauucuuuuu	19	188-206	stu-miR8019-5p	3	0
Sly-MIR8020	sly-miR8020	123	sly-miR8020	aauuucauugaguauguuguuguu	24	20-43	stu-miR8020	0	0
Sly-MIR8021	sly-miR8021-1	219	sly-miR8021-1	auucaaggcucaaacucgagaccu	24	1-24	stu-miR8021	0	0
	sly-miR8021-2	233	sly-miR8021-2	auucaaggcucaaacucgagaccu	24	4-27	stu-miR8021	0	0
	sly-miR8021-3	232	sly-miR8021-3	auucaaggcucaaacucgagaccu	24	8-31	stu-miR8021	0	0
Sly-MIR8025	sly-miR8025	137	sly-miR8025-3p	uuuaauugcaugccgacugugug	23	115-137	stu-miR8025-3p	2	0
			sly-miR8025-5p	acacacuacacaugcaauuaaauu	24	28-51	stu-miR8025-5p	3	0
Sly-MIR8032	sly-miR8032d	311	sly-miR8032d-3p	agugugaguuggugcgauuagg	22	117-138	stu-miR8032d-3p	0	0
Sly-MIR8033	sly-miR8033	108	sly-miR8033-3p	auuucugcagcuuuggaauu	20	71-90	stu-miR8033-3p	4	0
			sly-miR8033-5p	uuccaaagcugcagaaaugagu	22	21-42	stu-miR8033-5p	0	0
Sly-MIR8038	sly-miR8038a	136	sly-miR8038a-3p	uucagcuuacucacuugga	19	94-112	stu-miR8038a-3p	2	0
			sly-miR8038a-5p	ccuugugaguaaguugaaucuc	22	26-47	stu-miR8038a-5p	0	0
Sly-MIR8039	sly-miR8039-1	181	sly-miR8039-1	uuuccuaucugaacuaugacc	21	72-92	stu-miR8039	1	0
	sly-miR8039-2	159	sly-miR8039-2	uuuccuaucggaacuaucacc	21	57-77	stu-miR8039	1	0
Sly-MIR8045	sly-miR8045-1	95	sly-miR8045-1	auugauaguugaggugugguu	21	75-95	stu-miR8045	0	0
	sly-miR8045-2	186	sly-miR8045-2-3p	ugauaguuuagguuug	16	139-154	stu-miR8045	2	0

			sly-miR8045-2-5p	auugauaguugaggugugguu	21	76-96	stu-miR8045	0	0
Sly-MIR8051	sly-miR8051	257	sly-miR8051-5p	uaguaugguagaaagauuca	20	122-141	stu-miR8051-5p	0	0
Sly-MIR8172	sly-miR8172	92	sly-miR8172	auggaucaucuagauggagau	21	11-31	ath-miR8172	0	0
Sly-MIR8175	sly-miR8175	170	sly-miR8175	gaucccggcaacggcgcca	20	27-46	ath-miR8175	0	0
Sly-MIR827	sly-miR827	108	sly-miR827-3p	uuagaugaacaucaacaaaca	21	78-98	nta-miR827	0	0
			sly-miR827-5p	uuuguugauggucaucuauuc	21	12-32	stu-miR827-5p	0	0
Sly-MIR828	sly-miR828a	119	sly-miR828a	ucuugcucaaaugaguauucca	22	28-49	vvi-miR828a	0	0
Sly-MIR845	sly-miR845b	285	sly-miR845b-5p	ucaauugguaucagagcaa	19	206-224	aly-miR845b-5p	0	0
Sly-MIR9471	sly-miR9471a	180	sly-miR9471a-3p	uuggcugagugagcaucacgg	21	130-150	sly-miR9471a-3p	0	0
			sly-miR9471a-5p	caggugcucacucagcuaaua	21	43-63	sly-miR9471a-5p	0	0
	sly-miR9471b	147	sly-miR9471b-3p	uuggcugagugagcaucacug	21	108-128	sly-miR9471b-3p	0	0
			sly-miR9471b-5p	gaggugcucacucagcuaaua	21	21-41	sly-miR9471b-5p	0	0
Sly-MIR9472	sly-miR9472	180	sly-miR9472-3p	uucacaaucucugcugaaaaa	21	141-161	sly-miR9472-3p	0	0
			sly-miR9472-5p	uuucaguagacguugugaaua	21	23-43	sly-miR9472-5p	0	0
Sly-MIR9473	sly-miR9473-1	120	sly-miR9473-1-5p	uggcuguaaaucuaaacucgu	21	12-32	sly-miR9473-5p	0	0
			sly-miR9473-1-3p	aaacgaguucagauuuacagc	21	90-100	sly-miR9473-3p	0	0
	sly-miR9473-2	118	sly-miR9473-2-5p	acgaguuuagauuuacagcca	21	111-91	sly-miR9473-5p	0	0
			sly-miR9473-2-3p	gcuguaaaucugaacucguuu	21	33-13	sly-miR9473-3p	0	0
Sly-MIR9476	sly-miR9476-1	94	sly-miR9476-1-3p	aaaaagaugcaggacuagacc	21	63-83	sly-miR9476-3p	0	0
			sly-miR9476-1-5p	ucuaguccugcaucuuuuuuu	21	14-34	sly-miR9476-5p	0	0
	sly-miR9476-2	94	sly-miR9476-2-3p	aaaaagaugcaggacuagacc	21	63-83	sly-miR9476-3p	0	0
			sly-miR9476-2-5p	ucuaguccugcaucuuuuuuu	21	14-34	sly-miR9476-5p	0	0
Sly-MIR9478	sly-miR9478	211	sly-miR9478-3p	uucgaugacauauuugagccu	21	174-194	sly-miR9478-3p	0	0
			sly-miR9478-5p	gcuuaaauauguagaucgaacu	22	20-41	sly-miR9478-5p	0	0

418 **Supplementary Table S6.** Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum pennellii.*

Family	Pre-miRNA	Size of pre-miRNA	Mature miRNA	Mature miRNA sequence	Size of mature miRNA	Localization of mature in precursor	Ortholog mature miRNA	Number of mismatches with ortholog miRNA	Number of gaps with ortholog miRNA
Spe-MIR1128	spe-miR1128	301	spe-miR1128-5p	uacuacucccuccgucccaaa	21	91-111	ssp-miR1128	0	0
Spe-MIR1446	spe-miR1446	139	spe-miR1446-5p	ugaacucucucccucaauggcu	22	26-47	nta-miR1446	0	0
	spe-miR1446a	96	spe-miR1446a-5p	uucugaacucucucccucaa	20	8-27	ptc-miR1446a	0	0
Spe-MIR156/157	spe-miR156-1	149	spe-miR156-1-5p	uugacagaagauagagagcac	21	22-42	sly-miR156a	0	0
			spe-miR156-1-3p	gcucucuaugcuuccgucauc	21	111-131	stu-miR156d-3p	1	0
	spe-miR156-10	108	spe-miR156-10-5p	ugacagaagagagugagcaca	21	10-30	rco-miR156a	0	0
			spe-miR156-10-3p	gcucacugcucuaucugucacc	22	80-101	sly-miR156d-3p	0	0
	spe-miR156-11	157	spe-miR156-11-5p	ugacagaagggcgugagcaca	21	35-55	rco-miR156a	2	0
			spe-miR156-11-3p	gcucacugcucuaucuuucauc	22	100-121	sly-miR156d-3p	2	0
	spe-miR156-12	91	spe-miR156-12-5p	ugacagaagagagugagcaca	21	3-23	rco-miR156a	0	0
			spe-miR156-12-3p	gcucacuucucauucugucagc	22	69-90	zma-miR156d-3p	1	0
	spe-miR156-2	101	spe-miR156-2-5p	uugacagaagauagagagcac	21	1-21	sly-miR156a	0	0
			spe-miR156-2-3p	gcucucuaugcuuccugucauc	21	81-101	stu-miR156d-3p	0	0
	spe-miR156-3	188	spe-miR156-3-5p	uugacagaagauagagagcac	21	52-72	sly-miR156a	0	0
			spe-miR156-3-3p	gcucuuuauucuucugucauc	21	117-137	mtr-miR156h-3p	0	0
	spe-miR156-4	86	spe-miR156-4-5p	uugacagaagauagagagcac	21	2-22	sly-miR156a	0	0
			spe-miR156-4-3p	gcucuuuauucuucugucau	20	6-86	mtr-miR156h-3p	1	0
	spe-miR156-5	86	spe-miR156-5-5p	uugacagaagauagagagcac	21	2-22	sly-miR156a	0	0
			spe-miR156-5-3p	gcucuuuauucuucugucac	20	6-86	mtr-miR156h-3p	2	0
	spe-miR156-6	108	spe-miR156-6-5p	uugacagaagauagagagcac	21	14-34	sly-miR156a	0	0
			spe-miR156-6-3p	gcucucuauucuucugucauca	22	78-99	stu-miR156d-3p	1	0
	spe-miR156-7	97	spe-miR156-7-5p	ugacagaagagagugagcaca	21	4-24	rco-miR156a	0	0
			spe-miR156-7-3p	gcuuacucucuaucugucacc	21	76-96	sly-miR156e-3p	0	0
	spe-miR156-8	92	spe-miR156-8-5p	ugacagaagagagugagcaca	21	4-24	rco-miR156a	0	0
			spe-miR156-8-3p	gcucacuucucuaucugucacc	22	70-91	sly-miR156d-3p	1	0
	spe-miR156-9	101	spe-miR156-9-5p	ugacagaagagagugagcaca	21	9-29	rco-miR156a	0	0
			spe-miR156-9-3p	gcucacugcucuaucugucacc	22	75-96	sly-miR156d-3p	0	0
Spe-MIR160	spe-miR160-1	88	spe-miR160-1-5p	ugccuggcucccuguaugccauu	23	4-26	mes-miR160h	0	0
			spe-miR160-1-3p	gcguaugaggagccaagcaua	21	68-88	stu-miR160a-3p	0	0
	spe-miR160-2	116	spe-miR160-2-5p	ugccuggcuccuuguaugccauu	23	19-41	mes-miR160h	1	0
			spe-miR160-2-3p	gcauucuaggagcuaagcaug	21	80-100	zma-miR160b-3p	4	0
	spe-miR160a	103	spe-miR160a-5p	ugccuggcucccuguaugcca	21	12-32	sly-miR160a	0	0
			spe-miR160a-3p	gcguauaaggagccaagcaua	21	73-93	stu-miR160a-3p	1	0
	spe-miR160c	87	spe-miR160c-5p	ugccuggcucccuggaugcca	21	2-22	tcc-miR160c	0	0

	spe-miR160g-1	95	spe-miR160g-1-5p	ugcuuggcuccucauacgcca	21	7-27	ppt-miR160g	4	0
			spe-miR160g-1-3p	uggcauacagggagccaggca	21	69-89	aau-miR160	0	0
	spe-miR160g-2	95	spe-miR160g-2-5p	ugcuuggcuccuuauacgcca	21	8-28	ppt-miR160g	3	0
			spe-miR160g-2-3p	uggcauacagggagccaggca	21	67-87	aau-miR160	0	0
Spe-MIR162	spe-miR162a-1	110	spe-miR162a-1-5p	ggaggcagcgguucaucgauc	21	17-37	stu-miR162a-5p	0	0
			spe-miR162a-1-3p	ucgauaaaccucugcauccag	21	77-97	sly-miR162	0	0
	spe-miR162a-2	130	spe-miR162a-2-5p	ggaggcagcgguucaucgauc	21	19-39	stu-miR162a-5p	0	0
			spe-miR162a-2-3p	ucgauaaaccucugcauccag	21	96-116	sly-miR162	0	0
Spe-MIR164	spe-miR164	98	spe-miR164-5p	uggagaagcagggcacaugcu	21	12-32	stu-miR164-5p	0	0
			spe-miR164-3p	caugugcucuagcucuccagc	21	68-88	stu-miR164-3p	0	0
	spe-miR164a	165	spe-miR164a-5p	uggagaagcagggcacgugca	21	4-24	sly-miR164a-5p	0	0
			spe-miR164a-3p	caugugccuguuuuccccauc	21	143-163	sly-miR164a-3p	0	0
	spe-miR164b	112	spe-miR164b-5p	uggagaagcagggcacgugca	21	19-39	sly-miR164b-5p	0	0
			spe-miR164b-3p	cacguguucuccuucuccaac	21	92-112	sly-miR164b-3p	0	0
Spe-MIR166	spe-miR166-1	117	spe-miR166-1-5p	agaaugucgucugguucgaga	21	11-31	stu-miR166d-5p	0	0
			spe-miR166-1-3p	ucggaccaggcuucauucccc	21	89-109	sly-miR166a	0	0
	spe-miR166-2	107	spe-miR166-2-5p	ggaauguuguuuggcucgagg	21	13-33	stu-miR166c-5p	0	0
			spe-miR166-2-3p	ucggaccaggcuucauucccc	21	77-97	sly-miR166a	0	0
	spe-miR166a-1	146	spe-miR166a-1-3p	ucggaccaggcuucauucccc	21	103-123	sly-miR166a	0	0
	spe-miR166a-2	93	spe-miR166a-2-3p	ucggaccaggcuucauucccc	21	69-89	sly-miR166a	0	0
	spe-miR166a-3	174	spe-miR166a-3-5p	ggaauguugucuggcucgaag	21	18-38	stu-miR166a-5p	1	0
			spe-miR166a-3-3p	ucggaccaggcuucauucccc	21	140-160	sly-miR166a	0	0
	spe-miR166c	187	spe-miR166c-5p	gggauguugucuggcucgaca	21	21-41	sly-miR166c-5p	0	0
			spe-miR166c-3p	ucggaccaggcuucauuccuc	21	145-165	sly-miR166c-3p	0	0
Spe-MIR167	spe-miR167-1	85	spe-miR167-1-5p	ugaagcugccagcaugaucua	21	7-27	sly-miR167a	0	0
			spe-miR167-1-3p	gaucauguggcagcaucacc	20	61-80	stu-miR167b-3p	0	0
	spe-miR167-2	86	spe-miR167-2-5p	ugaagcugccagcaugaucua	21	7-27	sly-miR167a	0	0
			spe-miR167-2-3p	gaucaugugguugcuucacc	20	62-81	stu-miR167d-3p	0	0
	spe-miR167-3	84	spe-miR167-3-5p	ugaagcugccagcaugaucua	21	2-22	sly-miR167a	0	0
			spe-miR167-3-3p	ggucaugcucggacagccucacu	23	62-84	stu-miR167c-3p	0	0
	spe-miR167a	93	spe-miR167a-5p	ugaagcugccagcaugaucua	21	8-28	sly-miR167a	0	0
			spe-miR167a-3p	gaucauguggcagccucacc	20	69-88	stu-miR167a-3p	0	0
	spe-miR167h	196	spe-miR167h-3p	aucaugcuggcagcuucaacugau	24	117-140	gma-miR167h	1	0
Spe-MIR168	spe-miR168a	186	spe-miR168a-5p	ucgcuuggugcaggucgggac	21	22-42	sly-miR168a-5p	0	0
			spe-miR168a-3p	ccugccuugcaucaacugaau	21	147-167	sly-miR168a-3p	0	0
	spe-miR168b	170	spe-miR168b-5p	ucgcuuggugcaggucgggac	21	16-36	sly-miR168b-5p	0	0
			spe-miR168b-3p	cccgccuugcaucaacugaau	21	131-151	sly-miR168b-3p	0	0
Spe-MIR169	spe-miR169-1	155	spe-miR169-1-5p	cagccaaggaugacuugccgg	21	44-64	sly-miR169a	0	0
			spe-miR169-1-3p	ccggcaaguuguuuuuggcuau	22	92-113	gma-miR169l-3p	2	0

	spe-miR169-2	190	spe-miR169-2-5p	uagccaaggaugacuugccua	21	46-66	sly-miR169d	0	0
			spe-miR169-2-3p	gcaaguuauccuggcuauc	19	126-144	stu-miR169e-3p	0	0
	spe-miR169-3	164	spe-miR169-3-5p	uagccaagaaugacuugccug	21	43-63	sly-miR169b	1	0
			spe-miR169-3-3p	gcaggucaucuuuagcuaacu	21	103-123	stu-miR169d-3p	0	0
	spe-miR169-4	192	spe-miR169-4-5p	uagccaaggaugacuugccug	21	51-71	sly-miR169b	0	0
			spe-miR169-4-3p	gcaggucaucuuuagcuaacu	21	121-141	stu-miR169d-3p	0	0
	spe-miR169-5	224	spe-miR169-5-5p	cagccaaggaugacuugccga	21	58-78	sly-miR169c	0	0
			spe-miR169-5-3p	ggcaaguggccuuggcuaca	21	153-173	ata-miR169d-3p	1	0
	spe-miR169a-1	147	spe-miR169a-1-5p	cagccaaggaugacuugccgg	21	41-61	sly-miR169a	0	0
			spe-miR169a-1-3p	ggcaaguuguucuuggcuaua	21	91-111	zma-miR169a-3p	1	0
	spe-miR169a-2	161	spe-miR169a-2-5p	cagccaaggaugacuugccgg	21	49-69	sly-miR169a	0	0
	spe-miR169c	98	spe-miR169c-5p	cagccaaggaugacuugccga	21	20-40	sly-miR169c	0	0
	spe-miR169e	179	spe-miR169e-5p	uagccaaggaugacuugccuuu	22	48-69	sly-miR169e-5p	0	0
			spe-miR169e-3p	uggcaagcaucuuuggcgacu	21	119-139	sly-miR169e-3p	0	0
Spe-MIR170/171	spe-miR171	110	spe-miR171-5p	ugggauguuggugugguucaa	21	10-30	mdm-miR171o	1	0
			spe-miR171-3p	ugauugagccgugccaauauc	21	72-92	sly-miR171a	0	0
	spe-miR171-1	81	spe-miR171-1-5p	agauauuggugcgguucaauu	21	1-21	stu-miR171d-5p	0	0
			spe-miR171-1-3p	uaauugagccgugccaauauc	21	59-79	aqc-miR171f	0	0
	spe-miR171-2	75	spe-miR171-2-5p	uauuggugcgguucaaugaga	21	1-21	sly-miR171c	0	0
			spe-miR171-2-3p	ugauugagccgcgccaauau	20	56-75	ath-miR171a-3p	0	0
	spe-miR171-3	92	spe-miR171-3-5p	gauauuggcacggcucaauu	21	8-27	zma-miR171b-5p	3	0
			spe-miR171-3-3p	uaauugaaccgcaccaauauc	21	65-85	aqc-miR171c	1	0
	spe-miR171-4	86	spe-miR171-4-5p	agauauugaugcgguucaauc	21	2-22	ath-miR171c-5p	1	0
			spe-miR171-4-3p	uugagccgcgucaauaucucu	21	66-86	sly-miR171e	0	0
	spe-miR171-5	112	spe-miR171-5-5p	uguuggaauggcucaaucaaa	21	21-41	ata-miR171b-5p	1	0
			spe-miR171-5-3p	ugauugagccgugccaauauc	21	74-94	sly-miR171a	0	0
	spe-miR171-6	134	spe-miR171-6-5p	uauuggccugguucacucaga	21	37-57	stu-miR171a-5p	0	0
			spe-miR171-6-3p	ugauugagccgugucaauauc	21	86-106	stu-miR171c-3p	0	0
	spe-miR171-7	112	spe-miR171-7-5p	agugauauugguucggcucauc	22	21-42	ptc-miR171l-5p	2	0
			spe-miR171-7-3p	gugagccgaaccaauaucacg	21	71-91	osa-miR171h	1	0
	spe-miR171a	89	spe-miR171a-5p	uauuggccugguucacucaga	21	1-21	stu-miR171a-5p	0	0
			spe-miR171a-3p	ugauugagccgugccaauau	20	70-89	sly-miR171a	1	0
	spe-miR171e-1	127	spe-miR171e-1-5p	cgauguuggugagguucaauc	21	24-44	mtr-miR171e-5p	0	0
			spe-miR171e-1-3p	agauugagccgcgccaauauc	21	85-105	mtr-miR171e-3p	0	0
	spe-miR171e-2	100	spe-miR171e-2-5p	cgauguuggugagguucaauc	21	9-29	mtr-miR171e-5p	0	0
			spe-miR171e-2-3p	agauugagccgcgccaauauc	21	71-91	mtr-miR171e-3p	0	0
Spe-MIR172	spe-miR172-1	159	spe-miR172-1-5p	guagcaucaucaagauucaua	21	8-28	mtr-miR172c-5p	1	0
			spe-miR172-1-3p	agaaucuugaugaugcugcau	21	120-140	sly-miR172a	0	0
	spe-miR172-2	186	spe-miR172-2-5p	gcagcaucaucaagauucuca	21	29-49	lus-miR172j	1	0

			spe-miR172-2-3p	ugaaucuugaugaugcuacau	21	141-161	vvi-miR172a	0	0
	spe-miR172-3	169	spe-miR172-3-5p	gcaacaucaucaagauucaca	21	21-41	stu-miR172e-5p	0	0
			spe-miR172-3-3p	ggaaucuugaugaugcugcau	21	130-150	nta-miR172j	0	0
	spe-miR172-4	169	spe-miR172-4-5p	gcagcaucaucaagauuccca	21	22-42	lus-miR172j	0	0
			spe-miR172-4-3p	ugugaaucuugaugauguugcau	23	129-151	vvi-miR172d	2	0
	spe-miR172-5	132	spe-miR172-5-5p	gcagcaucaucaagauuccca	21	21-41	lus-miR172j	0	0
			spe-miR172-5-3p	ugaaucuugaugaugcuccac	21	93-113	osa-miR172c	1	0
	spe-miR172-6	105	spe-miR172-6-5p	gcagcaccauuaagauucaca	21	12-32	bra-miR172b-5p	0	0
			spe-miR172-6-3p	agaaucuugaugaugcugcau	21	75-95	sly-miR172a	0	0
	spe-miR172-7	105	spe-miR172-7-5p	gcagcacuauuaagauucuca	21	19-39	bra-miR172b-5p	2	0
			spe-miR172-7-3p	ugaaucuugaugaugcugcau	21	70-90	gma-miR172k	0	0
	spe-miR172-8	110	spe-miR172-8-5p	gcagcaucaucaagauucaca	21	21-41	stu-miR172b-5p	1	0
			spe-miR172-8-3p	ugagaaucuuaauagugcugcau	23	70-92	vvi-miR172d	3	0
	spe-miR172a	142	spe-miR172a-5p	guagcauaaucaagauucaca	21	21-41	stu-miR172a-5p	0	0
			spe-miR172a-3p	agaaucuugaugaugcugcau	21	104-124	sly-miR172a	0	0
	spe-miR172d	94	spe-miR172d-5p	ggagcaucaucaagauucaca	21	2-22	mtr-miR172d-5p	0	0
			spe-miR172d-3p	ggaaucuugaugaugcugcag	21	74-94	stu-miR172d-3p	0	0
Spe-MIR1886	spe-miR1886-1	131	spe-miR1886-1-5p	augagauggaauuaggguuuggac	24	39-62	stu-miR1886i-5p	3	0
			spe-miR1886-1-3p	auuuuacguugauuucaucucaug	24	68-91	stu-miR1886h	0	0
	spe-miR1886-2	116	spe-miR1886-2-5p	augguaucgugagaugaaaucagc	24	24-47	stu-miR1886f	0	0
			spe-miR1886-2-3p	auuuuacgcugauuccaucucaug	24	61-84	stu-miR1886h	2	0
	spe-miR1886h-1	173	spe-miR1886h-1-3p	auuuuacguugauuucaucucaug	24	89-112	stu-miR1886h	3	0
	spe-miR1886h-2	97	spe-miR1886h-2-5p	auuuuacguugauuucaucucaug	24	12-35	stu-miR1886h	0	0
Spe-MIR1917	spe-miR1917-1	214	spe-miR1917-1-5p	auuaauaaagagugcuaaagu	21	45-65	sly-miR1917	0	0
	spe-miR1917-2	136	spe-miR1917-2-5p	auuaauaaagagugcuaaagu	21	27-47	sly-miR1917	0	0
	spe-miR1917-3	201	spe-miR1917-3-5p	auuaauaaagagugcuaaagu	21	44-64	sly-miR1917	0	0
	spe-miR1917-4	240	spe-miR1917-4-5p	auuaauaaagagugcuaaagu	21	22-42	sly-miR1917	0	0
Spe-MIR1918	spe-miR1918	197	spe-miR1918-5p	uguuggugagaguucgauucuc	22	51-72	sly-miR1918	0	0
Spe-MIR1919	spe-miR1919	177	spe-miR1919-5p	ugucgcagaugacuuucgccc	21	47-67	stu-miR1919-5p	0	0
			spe-miR1919-3p	acgagagucaucugugacagg	21	113-133	stu-miR1919-3p	0	0
	spe-miR1919c	160	spe-miR1919c-5p	ugucgcagaugacuuucgccc	21	34-54	stu-miR1919-5p	0	0
			spe-miR1919c-3p	acgagagucaucugugacagg	21	110-130	sly-miR1919c-3p	0	0
Spe-MIR2111	spe-miR2111a	71	spe-miR2111a-5p	uaaucugcauccugagguuua	21	4-24	ath-miR2111a-5p	0	0
			spe-miR2111a-3p	guccuuaggaugcagauuauc	21	51-71	lja-miR2111-3p	1	0
Spe-MIR319	spe-miR319-1	187	spe-miR319-1-5p	gagcucucuccgguccaguc	20	10-29	zma-miR319a-5p	3	0
			spe-miR319-1-3p	uuggacugaagggagcucccu	21	161-181	sly-miR319b	0	0
	spe-miR319-2	185	spe-miR319-2-5p	agagcuuccuuuaguccacuc	21	10-30	mtr-miR319a-5p	1	0
			spe-miR319-2-3p	uuggacugaagggagcucccu	21	159-179	sly-miR319b	0	0

	spe-miR319-3	179	spe-miR319-3-5p	aggaaacuguuuaguccaacc	21	2-22	stu-miR319-5p	0	0
			spe-miR319-3-3p	uuggacugaaggguucccuuc	21	159-179	stu-miR319-3p	0	0
	spe-miR319-4	197	spe-miR319-4-3p	uuggacugaaggguuuccuuc	21	167-187	stu-miR319-3p	1	0
	spe-miR319a	170	spe-miR319a-5p.1	agagcuuucuucaguccacac	21	1-21	stu-miR319a-5p	1	0
			spe-miR319a-5p.2	uugcugccgacucauucaucca	22	44-65	ppe-miR319b	2	0
			spe-miR319a-3p	cuuggacugaagggagcucc	20	151-170	sly-miR319a	0	0
	spe-miR319c-1	177	spe-miR319c-1-3p	uuggacugaagggagcuccu	20	158-177	sly-miR319c-3p	1	0
	spe-miR319c-2	178	spe-miR319c-2-5p.1	agagcuuccuucagcccacuc	21	5-25	sly-miR319c-5p	0	0
			spe-miR319c-2-5p.2	uagcugccgacucauucaucca	22	49-70	ppe-miR319b	1	0
			spe-miR319c-2-3p	uuggacugaagggagcuccuu	21	157-177	sly-miR319c-3p	0	0
	spe-miR319c-3	179	spe-miR319c-3-5p	aggaaacuguuuaguccaacc	21	2-22	stu-miR319-5p	0	0
			spe-miR319c-3-3p	cuccaaugaugcaggagcuga	21	115-135	mdm-miR319c	3	0
Spe-MIR3627	spe-miR3627-1	83	spe-miR3627-1-5p	ucgcaggagagauggcacuuac	22	2-23	stu-miR3627-5p	1	0
			spe-miR3627-1-3p	aagugccucugucuuucgaca	21	63-83	stu-miR3627-3p	0	0
	spe-miR3627-2	148	spe-miR3627-2-5p	uugucgcaggagagauggcacu	22	34-55	vvi-miR3627-5p	1	0
			spe-miR3627-2-3p	aagugccucugucuuucgaca	21	98-118	stu-miR3627-3p	0	0
Spe-MIR390	spe-miR390	110	spe-miR390-5p	aagcucaggagggauagcgcc	21	18-38	sly-miR390b-5p	0	0
			spe-miR390-3p	cgcuauccauccugaguuuua	21	76-96	sly-miR390a-3p	0	0
	spe-miR390a	103	spe-miR390a-5p	aagcucaggagggauagcacc	21	18-38	sly-miR390a-5p	0	0
			spe-miR390a-3p	cgcuauccauccugaguuuua	21	67-87	sly-miR390a-3p	0	0
Spe-MIR393	spe-miR393	78	spe-miR393-5p	uccaaagggaucgcauugaucc	22	2-23	stu-miR393-5p	0	0
			spe-miR393-3p	aucaugugaucucuucggaau	21	58-78	stu-miR393-3p	1	0
Spe-MIR394	spe-miR394-1	203	spe-miR394-1-5p	uuggcauucuguccaccucc	20	51-70	sly-miR394-5p	0	0
			spe-miR394-1-3p	agguggcauacugucaaca	20	139-158	sly-miR394-3p	0	0
	spe-miR394-2	196	spe-miR394-2-5p	uuggcauucuguccaccucc	20	51-70	sly-miR394-5p	0	0
			spe-miR394-2-3p	agguggcauacugccaauag	21	124-144	ath-miR394b-3p	0	0
	spe-miR394-3	61	spe-miR394-3-5p	uuggcauucuguccaccucc	20	2-21	sly-miR394-5p	0	0
			spe-miR394-3-3p	agggggccaaagugccaaac	20	42-61	stu-miR384-3p	0	0
Spe-MIR395	spe-miR395a	103	spe-miR395a-3p	cugaaguguuuggggaacuuc	22	69-90	sly-miR395a	1	0
	spe-miR395d	100	spe-miR395d-3p	ugaaguguuuggggaacuuu	21	66-86	gma-miR395d	0	0
	spe-miR395g	154	spe-miR395g-3p	uugaaguguuuggggaacuc	21	93-113	mtr-miR395g	0	0
	spe-miR395i	174	spe-miR395i-5p	cugaaguguuuggaggaacuc	21	15-35	aly-miR395i	0	0
Spe-MIR396	spe-miR396-1	122	spe-miR396-1-5p	uuccacagcuuucuugaacuu	21	11-31	stu-miR396-5p	0	0
			spe-miR396-1-3p	guccaagaaagcugugggaaa	21	93-113	stu-miR396-3p	0	0
	spe-miR396-2	131	spe-miR396-2-5p	ucccacagcuuucuuggacuu	21	16-36	ath-miR396b-5p	2	0
			spe-miR396-2-3p	guucaagaaagcuguggaaaa	21	98-118	zma-miR396g-3p	1	0
	spe-miR396a	107	spe-miR396a-5p	uuccacagcuuucuugaacug	21	12-32	sly-miR396a-5p	0	0
			spe-miR396a-3p	guucaauaaagcugugggaag	21	81-101	sly-miR396a-3p	0	0
Spe-MIR397	spe-miR397	116	spe-miR397-5p	auugagugcagcguugaugac	21	19-39	stu-miR397-5p	0	0

			spe-miR397-3p	caucaacgcuacacucgauca	21	79-99	stu-miR397-3p	1	0
Spe-MIR398	spe-miR398	93	spe-miR398-5p	agggcaacuugagaucacaug	21	3-23	hbr-miR398	4	0
			spe-miR398-3p	uguguucucaggucgccccug	21	73-93	stu-miR398a-3p	1	0
	spe-miR398a	90	spe-miR398a-5p	ggguugauuugagaacauaug	21	1-21	stu-miR398a-5p	0	0
			spe-miR398a-3p	uauguucucaggucgccccu	20	71-90	stu-miR398a-3p	0	0
	spe-miR398b-1	82	spe-miR398b-1-5p	gagugugccuaagaacacaggu	22	2-23	stu-miR398b-5p	1	0
			spe-miR398b-1-3p	uuguguucucaggucaccccu	21	62-82	stu-miR398b-3p	0	0
	spe-miR398b-2	218	spe-miR398b-2-5p	gagugugccuggaaacacaggu	22	67-88	stu-miR398b-5p	3	0
			spe-miR398b-2-3p	uuguguucucaggucaccccu	21	133-153	stu-miR398b-3p	0	0
Spe-MIR399	spe-miR399-1	175	spe-miR399-1-5p	gggcuacgcucuauuggcaug	21	42-62	stu-miR399a-5p	1	0
			spe-miR399-1-3p	ugccaaaggagaguugcccug	21	115-135	ath-miR399b	0	0
	spe-miR399-2	107	spe-miR399-2-3p	ugccaaaggagaguugcccua	21	66-86	sly-miR399	0	0
	spe-miR399-3	103	spe-miR399-3-5p	gggcuacucucuauuggcaug	21	21-41	stu-miR399a-5p	0	0
			spe-miR399-3-3p	cgccaaaggagagcugcccug	21	64-84	nta-miR399g	0	0
	spe-miR399-4	103	spe-miR399-4-5p	gggcuacucucuauuggcaug	21	21-41	stu-miR399a-5p	0	0
			spe-miR399-4-3p	cgccaaaggagagcugcccug	21	64-84	nta-miR399g	0	0
	spe-miR399-5	103	spe-miR399-5-5p	gggcuacucucuauuggcaug	21	21-41	stu-miR399a-5p	0	0
			spe-miR399-5-3p	cgccaaaggagagcugcccug	21	64-84	nta-miR399g	0	0
	spe-miR399-6	103	spe-miR399-6-5p	gggcuacucucuauuggcaug	21	21-41	stu-miR399a-5p	0	0
			spe-miR399-6-3p	cgccaaaggagagcugcccug	21	64-84	nta-miR399g	0	0
	spe-miR399-7	258	spe-miR399-7-5p.1	ggacuacucucuauuggcaug	21	28-48	stu-miR399a-5p	1	0
			spe-miR399-7-5p.2	cgccaaaggaaugcugcacug	21	71-91	stu-miR399j-3p	3	0
			spe-miR399-7-3p	ugccaaaggagaguugcccug	21	210-230	ath-miR399b	0	0
	spe-miR399-8	216	spe-miR399-8-5p	cagggcaauucuccuuuggca	21	59-79	ata-miR399b-5p	1	0
			spe-miR399-8-3p	ugccaaaggagaauugcacug	21	134-154	osa-miR399a	1	0
	spe-miR399-9	90	spe-miR399-9-3p	ugccaaaggagauuugcccua	21	63-83	sly-miR399	1	0
	spe-miR399a-1	92	spe-miR399a-1-5p	gggcuacucucuguuggcaug	21	16-36	stu-miR399a-5p	1	0
			spe-miR399a-1-3p	ugccaaaggagagcugcccug	21	59-79	stu-miR399a-3p	0	0
	spe-miR399a-2	103	spe-miR399a-2-5p	gggcuacucucuauuggcaug	21	21-41	stu-miR399a-5p	0	0
			spe-miR399a-2-3p	ugccaaaggagagcugcccug	21	64-84	stu-miR399a-3p	0	0
	spe-miR399d	187	spe-miR399d-3p	ugccaaagaagauuugccccg	21	116-136	ptc-miR399d	0	0
	spe-miR399r-1	123	spe-miR399r-1-3p	ugccaaagaagauuugccccg	21	82-102	mtr-miR399r	0	0
	spe-miR399r-2	126	spe-miR399r-2-3p	ugccaaagaagauuugccccg	21	86-106	mtr-miR399r	0	0
Spe-MIR403	spe-miR403-1	112	spe-miR403-1-5p	cguuugugcgugaaucuaacg	21	21-41	sly-miR403-5p	1	0
			spe-miR403-1-3p	cuagauucacgcacaaacucg	21	74-94	sly-miR403-3p	1	0
	spe-miR403-2	112	spe-miR403-2-5p	aguuugugcgugaaucuagca	21	21-41	sly-miR403-5p	1	0
			spe-miR403-2-3p	uuagauucacgcacaaacgcg	21	74-94	ath-miR403-3p	1	0
Spe-MIR408	spe-miR408	128	spe-miR408-5p	cagggaagaggcagugcaugg	21	30-50	lja-miR408	1	0
			spe-miR408-3p	ugcucuggcucgcccccgucu	21	80-100	aqc-miR408	4	0

	spe-miR408b	88	spe-miR408b-5p	acggggacgagccagagcaug	21	10-30	stu-miR408b-5p	1	0
			spe-miR408b-3p	ugcacugccucuucccuggcu	21	61-81	stu-miR408b-3p	0	0
Spe-MIR4376	spe-miR4376	96	spe-miR4376-5p	uacgcaggagagaugaugcug	21	12-32	stu-miR4376-5p	0	0
			spe-miR4376-3p	gcaucauacuccugcauauu	20	68-87	stu-miR4376-3p	0	0
Spe-MIR477	spe-miR477	114	spe-miR477-5p	ugucucucccucaagggcucc	21	18-38	sly-miR477-5p	0	0
			spe-miR477-3p	aguucuuguagggugagacauc	22	79-100	sly-miR477-3p	1	0
	spe-miR477a	70	spe-miR477a-5p	ccucucccucaagggcuucuc	21	2-22	stu-miR477a-5p	0	0
			spe-miR477a-3p	gaagcucuagcagggagagcca	22	49-70	stu-miR477a-3p	0	0
	spe-miR477b	72	spe-miR477b-5p	acucucccucaaaggcuucug	21	2-22	stu-miR477b-5p	0	0
			spe-miR477b-3p	gaggucuuucgagugagaguga	22	51-72	stu-miR477b-3p	0	0
Spe-MIR479	spe-miR479	112	spe-miR479-5p	cgugauauugguucggcucacu	22	22-43	ghr-miR479	2	0
			spe-miR479-3p	ugagccgaaccaauaucacuc	21	73-93	stu-miR479	0	0
Spe-MIR482	spe-miR482-1	159	spe-miR482-1-5p	cgugaguggugggaaagaua	21	45-65	stu-miR482d-5p	1	0
			spe-miR482-1-3p	ucuugccuacaccgcccaugcc	22	95-117	sly-miR482b	0	0
	spe-miR482-2	110	spe-miR482-2-5p	ggaguggguggguaugguaaga	21	19-39	stu-miR482b-5p	1	0
			spe-miR482-2-3p	ucuugccaauaccgcccauucc	22	70-91	sly-miR482c	0	0
	spe-miR482a	91	spe-miR482a-5p	ggaauuggugaguuggaaagc	21	12-32	stu-miR482a-5p	2	0
			spe-miR482a-3p	uuuccaauuccacccauuccua	22	60-81	sly-miR482a	0	0
	spe-miR482b	119	spe-miR482b-5p	ggaguggguggcaugguaaga	21	19-39	stu-miR482b-5p	0	0
			spe-miR482b-3p	uuaccgauucccccccauuccaa	22	81-102	stu-miR482b-3p	0	0
	spe-miR482d	113	spe-miR482d-5p	ggaguggguggguggauggaaaaa	21	4-24	sly-miR482d-5p	0	0
			spe-miR482d-3p	uuuccuauuccacccaugccaa	22	75-96	sly-miR482d-3p	0	0
	spe-miR482e	162	spe-miR482e-5p	ugugggugggguggaaagauu	21	36-56	sly-miR482e-5p	0	0
			spe-miR482e-3p	ucuuuccuacuccucccauacc	22	111-132	sly-miR482e-3p	0	0
Spe-MIR5014	spe-miR5014a	260	spe-miR5014a-3p	uuguacaaauuuaaguguaua	21	101-121	ath-miR5014a-3p	2	0
Spe-MIR5174	spe-miR5174d-1	255	spe-miR5174d-1-5p	ucccuccguuucaaaaagauuggc	24	5-28	bdi-miR5174d-5p	1	0
	spe-miR5174d-2	266	spe-miR5174d-2-5p	ucccuccguuucaaaaagauuggc	24	10-33	bdi-miR5174d-5p	1	0
			spe-miR5174d-2-p	cauucuuuuugaaacggaaggagu	24	235-258	bdi-miR5174d-3p	5	0
	spe-miR5174d-3	268	spe-miR5174d-3-5p	ucccuccguuucaaaaagauuggc	24	14-37	bdi-miR5174d-5p	1	0
			spe-miR5174d-3-3p	cauucuuuuuuaaacggagggagu	24	235-158	bdi-miR5174d-3p	5	0
Spe-MIR530	spe-miR530	93	spe-miR530-5p	ucugcauuugcaccugcaccu	21	8-28	stu-miR530	0	0
Spe-MIR5300	spe-miR5300	265	spe-miR5300-5p	uccccaguccaggcauuccaac	22	18-39	sly-miR5300	0	0
Spe-MIR5303	spe-miR5303	202	spe-miR5303-5p	uuuuugaagaguucgagcaac	21	2-22	sly-miR5303	0	0
	spe-miR5303-1	126	spe-miR5303-1-5p	uuuuggaggauccgagucguaccc	24	68-91	stu-miR5303c	4	0
			spe-miR5303-1-3p	uuuuugaagaguucgagcaac	21	99-119	sly-miR5303	0	0
	spe-miR5303-2	118	spe-miR5303-2-5p	uuuuggaggauccaacacguaccc	24	64-87	stu-miR5303c	3	0
			spe-miR5303-2-3p	uuuuugaagaguucgagcaac	21	95-115	sly-miR5303	0	0
	spe-miR5303-3	119	spe-miR5303-3-5p	uuuugaaggauccggcacacaccc	24	65-88	stu-miR5303c	4	0

			spe-miR5303-3-3p	uuuuugaagaguucgagcaac	21	96-116	sly-miR5303	0	0
	spe-miR5303c-1	126	spe-miR5303c-1-3p	acgggugcggcuacauuuuug	21	85-105	nta-miR5303c	1	0
	spe-miR5303c-2	119	spe-miR5303c-2-3p	uuuuggagaauccgacacgcaccc	24	65-88	stu-miR5303c	0	0
	spe-miR5303e	129	spe-miR5303e-3p	uuuuggagaaucugacacgggugc	24	70-93	stu-miR5303e	1	0
	spe-miR5303f-1	310	spe-miR5303f-1-5p	auuuuuggagaaucugacacgggu	24	99-122	stu-miR5303f	0	0
	spe-miR5303f-2	133	spe-miR5303f-2-3p	auuuuuggagaaucugacacgggu	24	70-93	stu-miR5303f	0	0
	spe-miR5303f-3	147	spe-miR5303f-3-3p	auuuuuggagaaucugacacgggu	24	77-100	stu-miR5303f	0	0
	spe-miR5303h	341	spe-miR5303h-5p	aacauuuuugaagagucugagcaa	21	1-24	stu-miR5303h	0	0
Spe-MIR5368	spe-miR5368	83	spe-miR5368-5p	ggacagucucagguagaca	19	31-49	gma-miR5368	0	0
Spe-MIR6024	spe-miR6024	102	spe-miR6024-5p	agaaacaacacuugcuaaagga	22	15-36	stu-miR6024-5p	1	0
			spe-miR6024-3p	uuuuagcaagaguuguuuuccc	22	70-91	stu-miR6024-3p	0	0
Spe-MIR6027	spe-miR6027	164	spe-miR6027-5p	auggguagcacaaggauuaaug	22	22-43	sly-miR6027-5p	0	0
			spe-miR6027-3p	ugaauccuucggcuauccauaa	22	123-144	sly-miR6027-3p	0	0
Spe-MIR6144	spe-miR6144	188	spe-miR6144-5p	uggcaacuucuucaucauguu	21	18-38	nta-miR6144	2	0
Spe-MIR6440	spe-miR6440b	197	spe-miR6440b-5p	gaguuugaucaauuucgaguu	21	49-69	ptc-miR6440b	1	0
Spe-MIR6478	spe-miR6478	309	spe-miR6478-5p	ccgaccuuagcucaguuggua	21	113-133	ptc-miR6478	1	0
Spe-MIR7696	spe-miR7696c	239	spe-miR7696c-3p	uuuugaauuaugaguacuuga	21	169-189	mtr-miR7696c-3p	1	0
Spe-MIR7980	spe-miR7980b-1	149	spe-miR7980b-1-5p	gagauggaaucaguguuuggacau	24	36-59	stu-miR7980b-3p	0	0
	spe-miR7980b-2	80	spe-miR7980b-2-5p	gagauggaaucaguguuuggacau	24	16-39	stu-miR7980b-3p	0	0
	spe-miR7980b-3	114	spe-miR7980b-3-3p	guccaaacacugauuccaucucac	24	60-83	stu-miR7980b-5p	1	0
	spe-miR7980b-4	116	spe-miR7980b-4-3p	guccaaacacugauuccaucucac	24	61-84	stu-miR7980b-5p	1	0
	spe-miR7980b-5	157	spe-miR7980b-5-5p	guccaaacacugauuccaucucag	24	107-130	stu-miR7980b-5p	1	0
	spe-miR7980b-6	159	spe-miR7980b-6-3p	gagauggaaucaguguuuggacau	24	52-75	stu-miR7980b-3p	0	0
Spe-MIR7981	spe-miR7981	214	spe-miR7981-5p	cuuaacuaaacuaagguccuauua	24	9-32	stu-miR7981-5p	3	0
			spe-miR7981-3p	auaggacuuuaguuuaguuaaggc	24	185-208	stu-miR7981-3p	1	0
Spe-MIR7983	spe-miR7983-1	137	spe-miR7983-1-5p	uaaagccuuuagcgacauugguuc	24	39-62	stu-miR7983-5p	1	0
			spe-miR7983-1-3p	acuaaugccgguaaagacuuuaac	24	75-98	stu-miR7983-3p	0	0
	spe-miR7983-2	196	spe-miR7983-2-5p	uaaagccuuuagcgacauugguuc	24	89-112	stu-miR7983-5p	1	0

			spe-miR7983-2-3p	acuaaugccgguaaagacuuuaac	24	125-148	stu-miR7983-3p	0	0
	spe-miR7983-3	221	spe-miR7983-3-5p	uaaagccuuuagcgaaauugguug	24	101-124	stu-miR7983-5p	2	0
			spe-miR7983-3-3p	acuaaugccgguaaagacuuuaac	24	137-160	stu-miR7983-3p	0	0
	spe-miR7983-4	140	spe-miR7983-4-5p	uaaagucuuuagcgacauugguuc	24	41-64	stu-miR7983-5p	0	0
			spe-miR7983-4-3p	acuaaugccgauaaagacuuuaac	24	77-100	stu-miR7983-3p	1	0
	spe-miR7983-5	141	spe-miR7983-5-5p	uaaagucuuuagcgacauugguuc	24	41-64	stu-miR7983-5p	0	0
			spe-miR7983-5-3p	acuaaugccgauaaagacuuuaac	24	77-100	stu-miR7983-3p	2	0
	spe-miR7983-6	216	spe-miR7983-6-5p	uaaagucuuuagcgacauugguuc	24	99-122	stu-miR7983-5p	0	0
			spe-miR7983-6-3p	acuaaugccgguaaagacuuuagu	24	135-158	stu-miR7983-3p	2	0
	spe-miR7983-7	213	spe-miR7983-7-5p	uaaagccuuuagcgacauugguuc	24	98-121	stu-miR7983-5p	1	0
			spe-miR7983-7-3p	acuaaugccgguaaagacuuuaac	24	134-157	stu-miR7983-3p	0	0
Spe-MIR7984	spe-miR7984	230	spe-miR7984-5p	aucccaaacuuuggaaaugacucu	24	47-70	stu-miR7984b-5p	5	0
			spe-miR7984-3p	caauuucggucaaaguucagauau	24	186-209	stu-miR7984d-3p	1	0
	spe-miR7984b	205	spe-miR7984b-5p	auaucaaacuuuggaaaugaccuu	24	5-28	stu-miR7984b-5p	2	0
			spe-miR7984b-3p	ggucuuucauaaaauuugguauug	24	159-182	stu-miR7984b-3p	1	0
	spe-miR7984c	319	spe-miR7984c-3p	ccuucauaaaguuugguaucguaa	24	192-215	stu-miR7984c-3p	0	0
Spe-MIR7987	spe-miR7987	98	spe-miR7987-5p	acacuaguugaucuuauugaugac	24	17-40	stu-miR7987	0	0
Spe-MIR7990	spe-miR7990a-1	110	spe-miR7990a-1-3p	uucaaaugaucguaacuuuggccu	24	84-107	stu-miR7990a	0	0
	spe-miR7990a-2	119	spe-miR7990a-2-3p	uucaaaugaucguaacuuuggccu	24	88-111	stu-miR7990a	0	0
Spe-MIR7992	spe-miR7992	248	spe-miR7992-3p	ugucuagaugugcacuccaaagu	23	191-213	stu-miR7992-3p	2	0
Spe-MIR7993	spe-miR7993a	177	spe-miR7993a-3p	auauuuuauguggguuaacuuaaau	24	137-160	stu-miR7993a	1	0
	spe-miR7993b-1	276	spe-miR7993b-1-5p	uuaaguuaaccacauacaguaugu	24	91-114	stu-miR7993b-5p	2	0
			spe-miR7993b-1-3p	uuaauuuacguggguuaaauuaacu	24	205-228	stu-miR7993b-3p	4	0
	spe-miR7993b-2	239	spe-miR7993b-2-5p	auauuuuauguggguuaacguaauu	24	88-111	stu-miR7993b-3p	2	0
Spe-MIR7997	spe-miR7997a	184	spe-miR7997a-5p	augcugcucggacucuucaaa	21	36-56	stu-miR7997a	0	0
	spe-miR7997a-1	129	spe-miR7997a-1-5p	augcugcucggacucuucaaa	21	7-27	stu-miR7997a	0	0
	spe-miR7997a-2	128	spe-miR7997a-2-5p	augcugcucggacucuucaaa	21	6-26	stu-miR7997a	0	0
Spe-MIR7998	spe-miR7998	231	spe-miR7998-5p	acggaccguagaucaauccacggu	24	95-118	stu-miR7998	1	0
Spe-MIR8001	spe-miR8001a	144	spe-miR8001a-5p	uccuggggauuaguaugaaaauuc	24	38-61	stu-miR8001a	0	0
	spe-miR8001b-1	341	spe-miR8001b-1-3p	ggauuuucauacuaauuccuagga	24	189-212	stu-miR8001b-3p	1	0
	spe-miR8001b-	90	spe-miR8001b-2-5p	augggauuaguaugaaaauuugc	24	28-51	stu-miR8001b-5p	0	0

	2								
Spe-MIR8005	spe-miR8005	170	spe-miR8005-5p	uuuagaguuuaggauuuaguguuu	24	31-54	stu-miR8005a	3	0
			spe-miR8005-3p.1	uuuagaguuuaggguuuaggguuu	24	80-103	stu-miR8005a	2	0
			spe-miR8005-3p.2	uuuaggguuuaaggauuaggcuua	24	115-138	stu-miR8005b-3p	5	0
Spe-MIR8006	spe-miR8006	256	spe-miR8006-3p	uaguuuuuggacggcaggggcacc	24	190-213	stu-miR8006-5p	1	0
Spe-MIR8007	spe-miR8007a	268	spe-miR8007a-5p	augugacacuuuucggauuucgag	24	24-47	stu-miR8007a-5p	2	0
			spe-miR8007a-3p	cgaaaaaugaaaagugccacauaa	24	224-247	stu-miR8007a-3p	0	0
Spe-MIR8008	spe-miR8008-1	127	spe-miR8008-1-5p	aaacccagaaaagcgacggacaag	24	38-61	stu-miR8008b	2	0
			spe-miR8008-1-3p	auuucaaggaaagcgacagacauu	24	103-126	stu-miR8008a	4	0
	spe-miR8008-2	154	spe-miR8008-2-5p	aaacucagaaaagcgacggacaga	24	20-43	stu-miR8008b	2	0
			spe-miR8008-2-3p	auuuccagaaaagugacggacagu	24	85-108	stu-miR8008a	1	0
	spe-miR8008a-1	130	spe-miR8008a-1-3p	auuuccagaaaagcgacgaacagu	24	72-95	stu-miR8008a	1	0
	spe-miR8008a-2	206	spe-miR8008a-2-5p	auuuccagaaaagcgacgaacagu	24	3-26	stu-miR8008a	1	0
	spe-miR8008b-1	54	spe-miR8008b-1-5p	aaacccagaaaagcgacggacagg	24	1-24	stu-miR8008b	1	0
	spe-miR8008b-2	194	spe-miR8008b-2-5p	aaacccagaaaagcgacagacuua	24	71-94	stu-miR8008b	4	0
	spe-miR8008b-3	115	spe-miR8008b-3-5p	aaacccagaaaagcgacggacauu	24	32-55	stu-miR8008b	1	0
Spe-MIR8011	spe-miR8011	101	spe-miR8011-5p	acucauuuuugucucacaaaaa	22	18-39	stu-miR8011b-5p	0	0
			spe-miR8011-3p	acaaaaagaagucucacacaacu	24	72-95	stu-miR8011a-3p	3	0
	spe-miR8011a-1	168	spe-miR8011a-1-5p	uugugugaggucucuuuuuguuuu	24	40-63	stu-miR8011a-5p	2	0
			spe-miR8011a-1-3p	aauaaaaagaagucucacgcaacu	24	107-130	stu-miR8011a-3p	2	0
	spe-miR8011a-2	122	spe-miR8011a-2-3p	aauaaaaagaagccucacagaacu	24	88-111	stu-miR8011a-3p	1	0
Spe-MIR8013	spe-miR8013	287	spe-miR8013-3p	agaagaaaaucgcuucgucaggag	24	246-269	stu-miR8013	2	0
Spe-MIR8016	spe-miR8016	172	spe-miR8016-3p	auuuuugaauggaaggcccaugug	24	104-127	stu-miR8016	0	0
Spe-MIR8019	spe-miR8019	270	spe-miR8019	uaaagaaugaccugguuugaguug	24	24-47	stu-miR8019-3p	2	0
Spe-MIR8020	spe-miR8020	88	spe-miR8020-5p	aauuucauugaguauguuguuguu	24	2-25	stu-miR8020	0	0
Spe-MIR8021	spe-miR8021	226	spe-miR8021-5p	auucaaggcucaaacucgagaccu	24	1-24	stu-miR8021	0	0
Spe-MIR8024	spe-miR8024	85	spe-miR8024-5p.1	uuggaguauuugaagacuuuagcu	24	2-25	stu-miR8024b	4	0
			spe-miR8024-5p.2	uuggaggauuuaaagacuucagcu	24	31-54	stu-miR8024a-5p	3	0
			spe-miR8024-3p	uuggaggauuugaagacuucaacu	24	62-85	stu-miR8024a-3p	1	0
	spe-miR8024a	243	spe-miR8024a-5p.1	uuaaagaauuugaagacuucagcu	24	1-24	stu-miR8024a-5p	3	0
			spe-miR8024a-5p.2	uuaaaguauuugaagacuucaacu	24	91-114	stu-miR8024a-5p	3	0
			spe-miR8024a-3p.1		24	122-145	stu-miR8024a-3p	4	0

				uugaaugauuugaagacuucaucu					
			spe-miR8024a-3p.2	uuggaggauuugaagauuucaacu	24	184-207	stu-miR8024a-3p	0	0
Spe-MIR8025	spe-miR8025	137	spe-miR8025-5p	acacacuacacaugcaauuaaauu	24	28-51	stu-miR8025-5p	3	0
			spe-miR8025-3p	uuuaauugcaugccgagugucug	23	115-137	stu-miR8025-3p	2	0
Spe-MIR8026	spe-miR8026	124	spe-miR8026-3p	auguagagaauaugugguaacccu	24	69-92	stu-miR8026	0	0
Spe-MIR8032	spe-miR8032a	283	spe-miR8032a-5p	uugucgacaugacucccgaagu	22	86-107	stu-miR8032a-5p	3	0
			spe-miR8032a-3p	agugugaguuggugugauuagg	22	112-133	stu-miR8032a-3p	1	0
Spe-MIR8036	spe-miR8036	86	spe-miR8036-3p	uaugucuuuccgaugccuccca	22	65-86	stu-miR8036-3p	0	0
Spe-MIR8038	spe-miR8038a	136	spe-miR8038a-5p	ccuugugaguaaguuggaucuc	22	26-47	stu-miR8038a-5p	1	0
Spe-MIR8039	spe-miR8039	142	spe-miR8039-5p	uuuccuaucugaacuaucacc	21	22-42	stu-miR8039	0	0
Spe-MIR8042	spe-miR8042	158	spe-miR8042-3p	auuagacugaaaugcugaucu	21	110-130	stu-miR8042	1	0
Spe-MIR8045	spe-miR8045	262	spe-miR8045-3p	auugauaguugaggugugguu	21	206-226	stu-miR8045	0	0
Spe-MIR8047	spe-miR8047	208	spe-miR8047-5p	ccauuuuuucgaaauuagacc	21	50-70	stu-miR8047	0	0
Spe-MIR8051	spe-miR8051	334	spe-miR8051-5p	uaguaugguagaaagauuca	20	285-304	stu-miR8051-5p	0	0
Spe-MIR8175	spe-miR8175-1	237	spe-miR8175-1-5p	gaucccggcaacggcgcca	20	58-77	ath-miR8175	0	0
	spe-miR8175-2	173	spe-miR8175-2-3p	gaucccggcaacggcgcca	20	101-120	ath-miR8175	0	0
Spe-MIR827	spe-miR827	88	spe-miR827-5p	uuuguugauggucaucuauuc	21	2-22	stu-miR827-5p	0	0
			spe-miR827-3p	uuagaugaacaucaacaaaca	21	68-88	nta-miR827	0	0
Spe-MIR828	spe-miR828a	119	spe-miR828a-5p	ucuugcucaaaugaguauucca	22	28-49	gma-miR828a	0	0
			spe-miR828a-3p	agauacucauuuggguaagaag	22	76-97	aly-miR828-3p	1	0
Spe-MIR9469	spe-miR9469	141	spe-miR9469-5p	ccauauaaggagaccaaauuc	21	36-56	sly-miR9469-5p	3	0
			spe-miR9469-3p	auucggucuucuuauauggac	21	90-110	sly-miR9469-3p	1	0
Spe-MIR9471	spe-miR9471b	147	spe-miR9471b-5p	gaggugcucacucagcuaaua	21	21-41	sly-miR9471b-5p	0	0
			spe-miR9471b-3p	uuggcugagugagcaucacug	21	108-128	sly-miR9471b-3p	0	0
Spe-MIR9473	spe-miR9473-1	118	spe-miR9473-1-5p	uggcuguaaaucugaacucgu	21	11-31	sly-miR9473-5p	1	0
	spe-miR9473-2	178	spe-miR9473-2-5p	uggcuguaaaccuaaacucgu	21	29-49	sly-miR9473-5p	1	0
			spe-miR9473-2-3p	aaacgaguucagauuuacagc	21	128-148	sly-miR9473-3p	0	0
Spe-MIR9476	spe-miR9476-1	108	spe-miR9476-1-5p	ucuaguccugcaucucuuuuu	21	22-42	sly-miR9476-5p	1	0
			spe-miR9476-1-3p	aaaaaaaugcaggacuagacc	21	71-91	sly-miR9476-3p	1	0
	spe-miR9476-2	110	spe-miR9476-2-5p	ucuaguccugcauuuuuuuuu	21	23-43	sly-miR9476-5p	1	0
			spe-miR9476-2-3p	aaagagaugcaggacuagacc	21	72-92	sly-miR9476-3p	1	0
Spe-MIR9477	spe-miR9477	154	spe-miR9477-5p	uaucaguuguucucuuuuccuacc	24	45-68	sly-miR9477-5p	2	0
			spe-miR9477-3p	uugggaaagggaacaacugauagu	24	91-114	sly-miR9477-3p	0	0

421 **Supplementary Table S7.** Distribution and clustering of miRNAs in the *S lycopersicum* and *S. pennellii* genome.

Pre-miRNAs	Genome				Distribution in genome	Clustering
	Chromosome	Start	End	Strad		
sly-miR2604	Chr00	10392430	10392232	-	Intergenic	Cluster sly-miR2604 / miR5282
sly-miR5282	Chr00	10399847	10399974	+	Intergenic	Cluster sly-miR2604 / miR5282
sly-miR396a	Chr00	11583835	11583978	+	Intergenic	Cluster sly-miR396a / miR396g-2
sly-miR396g-2	Chr00	11583971	11583842	-	Intergenic	Cluster sly-miR396a / miR396g-2
sly-miR395a-1	Chr00	16085186	16085036	-	Intergenic	-
sly-miR8172	Chr00	20702851	20702942	+	Intergenic	-
sly-miR7997a	Chr01	596768	596641	-	Intergenic	-
sly-miR8011a-2	Chr01	830540	830707	+	Solyc01g006200	-
sly-miR5532-1	Chr01	1891134	1891296	+	Solyc01g007800	-
sly-miR8045-1	Chr01	2063203	2063109	-	Solyc01g007940	-
sly-miR8001a	Chr01	3719274	3719412	+	Solyc01g009530	-
sly-miR7987	Chr01	6065440	6065647	+	Intergenic	-
sly-miR8021-2	Chr01	7037876	7038108	+	Intergenic	-
sly-miR8021-3	Chr01	7517602	7517833	+	Intergenic	-
sly-miR5532-2	Chr01	23803019	23803281	+	Intergenic	-
sly-miR8008a-2	Chr01	66053158	66052971	-	Intergenic	-
sly-miR403	Chr01	78229507	78229618	+	Solyc01g079280	Cluster sly-miR403 / miR403a
sly-miR403a	Chr01	78229618	78229507	-	Intergenic	Cluster sly-miR403 / miR403a
sly-miR6024	Chr01	83111141	83111026	-	Intergenic	-
sly-miR8019-2	Chr01	85581263	85581002	-	Intergenic	-
sly-miR477a	Chr01	86753327	86753396	+	Intergenic	Cluster sly-miR477a / miR477b
sly-miR477b	Chr01	86753443	86753514	+	Intergenic	Cluster sly-miR477a / miR477b
sly-miR166a-4	Chr01	87281383	87281540	+	Solyc01g096330	-
sly-miR9476-2	Chr01	87985683	87985776	+	Solyc01g097160	Cluster sly-miR9476-1 / miR9476-2
sly-miR9476-1	Chr01	87985776	87985683	-	Intergenic	Cluster sly-miR9476-1 / miR9476-2
sly-miR164e	Chr01	89848683	89848779	+	Intergenic	-
sly-miR8033	Chr01	90484839	90484946	+	Intergenic	-
sly-miR408a	Chr01	90909531	90909460	-	Intergenic	Cluster sly-miR408a / miR408-1 / miR408-2
sly-miR408-1	Chr01	90917954	90918081	+	Intergenic	Cluster sly-miR408a / miR408-1 / miR408-2
sly-miR408-2	Chr01	90918060	90917973	-	Intergenic	Cluster sly-miR408a / miR408-1 / miR408-2
sly-miR166g	Chr01	92515524	92515338	-	Solyc01g104150	-
sly-miR394a	Chr01	92656431	92656511	+	Intergenic	-
sly-miR5304	Chr01	97117726	97117867	+	Solyc01g110540	-
sly-miR5303f	Chr02	25198110	25197985	-	Intergenic	-
sly-miR160	Chr02	26294352	26294446	+	Intergenic	Cluster sly-miR160 / miR160a
sly-miR160a	Chr02	26294441	26294356	-	Intergenic	Cluster sly-miR160 / miR160a

sly-miR395a-4	Chr02	33474379	33474078	-	Intergenic	-
sly-miR395a-3	Chr02	33492524	33492418	-	Intergenic	Cluster sly-miR395a-3 / miR395a-2
sly-miR395a-2	Chr02	33498879	33498710	-	Intergenic	Cluster sly-miR395a-3 / miR395a-2
sly-miR395g	Chr02	33515391	33515229	-	Intergenic	-
sly-miR170-1	Chr02	33887708	33887597	-	Intergenic	-
sly-miR157a-1	Chr02	35865182	35865327	+	Intergenic	-
sly-miR171c-4	Chr02	45338751	45338842	+	Intergenic	Cluster sly-miR171b-1 / miR171c-4
sly-miR171b-1	Chr02	45338842	45338751	-	Intergenic	Cluster sly-miR171b-1 / miR171c-4
sly-miR170-2	Chr02	47308145	47308057	-	Intergenic	-
sly-miR3627	Chr02	50592654	50592778	+	Intergenic	-
sly-miR169b-3	Chr02	50950663	50950846	+	Intergenic	Cluster sly-miR169b-3 / miR169m
sly-miR169m	Chr02	50950846	50950663	-	Intergenic	Cluster sly-miR169b-3 / miR169m
sly-miR1917-2	Chr02	51732657	51732467	-	Solyc02g089220	-
sly-miR157a-2	Chr02	53114883	53115084	+	Intergenic	-
sly-miR7983-4	Chr02	53246775	53246639	-	Intergenic	-
sly-miR166a-3	Chr03	293081	292989	-	Intergenic	-
sly-miR399d-1	Chr03	731281	731403	+	Intergenic	Cluster sly-miR399d-1 / miR399d-2 / miR399a-1 / miR399a-2
sly-miR399d-2	Chr03	736844	737014	+	Intergenic	Cluster sly-miR399d-1 / miR399d-2 / miR399a-1 / miR399a-2
sly-miR399a-1	Chr03	740620	740759	+	Intergenic	Cluster sly-miR399d-1 / miR399d-2 / miR399a-1 / miR399a-2
sly-miR399a-2	Chr03	740759	740620	-	Intergenic	Cluster sly-miR399d-1 / miR399d-2 / miR399a-1 / miR399a-2
sly-miR7984c	Chr03	1702291	1702492	+	Intergenic	-
sly-miR393a	Chr03	3107529	3107606	+	Intergenic	-
sly-miR8032d	Chr03	3781351	3781661	+	Intergenic	-
sly-miR399d-3	Chr03	3840855	3840767	-	Intergenic	Cluster sly-miR399d-3 / miR399a-3 / miR399a-4
sly-miR399a-3	Chr03	3842813	3842711	-	Intergenic	Cluster sly-miR399d-3 / miR399a-3 / miR399a-4
sly-miR399a-4	Chr03	3846902	3846580	-	Intergenic	Cluster sly-miR399d-3 / miR399a-3 / miR399a-4 e Cluster sly-miR399a-4 / miR399i-1
sly-miR399i-1	Chr03	3852999	3853101	+	Intergenic	Cluster sly-miR399a-4 / miR399i-1
sly-miR399a-5	Chr03	3990643	3990427	-	Intergenic	Cluster sly-miR399a-5 / miR399j-3
sly-miR399j-3	Chr03	3991756	3991825	+	Intergenic	Cluster sly-miR399a-5 / miR399j-3
sly-miR169g	Chr03	5345203	5344996	-	Intergenic	-
sly-miR8008b-3	Chr03	9579858	9579666	-	Intergenic	-
sly-miR437	Chr03	40452559	40452791	+	Intergenic	-
sly-miR7980b-2	Chr03	53079975	53080085	+	Intergenic	Cluster sly-miR7980b-1 / miR7980b-2
sly-miR7980b-1	Chr03	53080085	53079975	-	Intergenic	Cluster sly-miR7980b-1 / miR7980b-2
sly-miR166-3	Chr03	53905241	53905076	-	Intergenic	-
sly-miR171f	Chr03	54024635	54024746	+	Intergenic	-
sly-miR8011a-1	Chr03	56174770	56174671	-	Intergenic	-
sly-miR319c-2	Chr03	57879149	57879325	+	Intergenic	-
sly-miR8006-1	Chr03	58948635	58948393	-	Intergenic	-

sly-miR162-2	Chr03	65922672	65922781	+	Intergenic	-
sly-miR482a-2	Chr03	66250457	66250547	+	Intergenic	-
sly-miR1446-2	Chr03	68514759	68514652	-	Intergenic	Cluster sly-miR1446-2 / miR1446-1
sly-miR1446-1	Chr03	68519548	68519436	-	Intergenic	Cluster sly-miR1446-2 / miR1446-1
sly-miR157a-4	Chr03	69151187	69151432	+	Intergenic	-
sly-miR159a	Chr03	69217276	69217453	+	Intergenic	Cluster sly-miR159a / miR319-2
sly-miR319-2	Chr03	69225768	69225946	+	Solyc03g119020	Cluster sly-miR159a / miR319-2
sly-miR7992	Chr03	69348792	69348585	-	Intergenic	-
sly-miR319c-1	Chr03	69596922	69596746	-	Intergenic	-
sly-miR5300	Chr04	423122	423387	+	Intergenic	-
sly-miR8038a	Chr04	2889715	2889850	+	Intergenic	-
sly-miR172d-7	Chr04	4094135	4093970	-	Intergenic	-
sly-miR7983-6	Chr04	8230179	8230080	-	Intergenic	-
sly-miR8019-1	Chr04	39173419	39173701	+	Intergenic	-
sly-miR5162	Chr04	55927142	55927004	-	Intergenic	-
sly-miR482a-1	Chr04	56034622	56034757	+	Intergenic	-
sly-miR319a-1	Chr05	2724015	2723829	-	Intergenic	-
sly-miR5303h-2	Chr05	4271473	4271350	-	Intergenic	-
sly-miR7983-3	Chr05	5360758	5360939	+	Intergenic	-
sly-miR7696c	Chr05	20829006	20829251	+	Intergenic	-
sly-miR8008b-1	Chr05	40036707	40036485	-	Intergenic	-
sly-miR1128	Chr05	63296465	63296733	+	Intergenic	-
sly-miR172d-8	Chr05	64052575	64052700	+	Intergenic	Cluster sly-miR172d-8 / miR172j-1
sly-miR172j-1	Chr05	64052692	64052584	-	Intergenic	Cluster sly-miR172d-8 / miR172j-1
sly-miR172d-3	Chr05	66041801	66041893	+	Intergenic	-
sly-miR160h-1	Chr05	66284905	66284811	-	Intergenic	-
sly-miR172j-2	Chr06	654336	654168	-	Intergenic	Cluster sly-miR172j-2 / miR172d-5
sly-miR172d-5	Chr06	654174	654337	+	Intergenic	Cluster sly-miR172j-2 / miR172d-5
sly-miR319a-2	Chr06	1550348	1550536	+	Intergenic	-
sly-miR166a-1	Chr06	2515043	2514924	-	Intergenic	-
sly-miR4376	Chr06	4540537	4540632	+	Intergenic	-
sly-miR166-1	Chr06	36731233	36731378	+	Intergenic	-
sly-miR482c	Chr06	37496713	37496569	-	Intergenic	Cluster sly-miR482c / miR482d / miR482e
sly-miR482d	Chr06	37497001	37496891	-	Intergenic	Cluster sly-miR482c / miR482d / miR482e
sly-miR482e	Chr06	37504779	37504631	-	Intergenic	Cluster sly-miR482c / miR482d / miR482e
sly-miR5303c	Chr06	37747396	37747531	+	Solyc06g059750	-
sly-miR8013	Chr06	39018927	39018712	-	Intergenic	-
sly-miR164f	Chr06	39920932	39921019	+	Intergenic	-
sly-miR171b-3	Chr06	42878734	42878843	+	Intergenic	-

sly-miR157a-3	Chr06	42968571	42968471	-	Intergenic	-
sly-miR162-1	Chr06	43189917	43190044	+	Intergenic	-
sly-miR8007a	Chr06	46075067	46075215	+	Intergenic	-
sly-miR172d-4	Chr06	46670326	46670467	+	Intergenic	Cluster sly-miR172d-4 / miR172d-2
sly-miR172d-2	Chr06	46670417	46670690	+	Intergenic	Cluster sly-miR172d-4 / miR172d-2
sly-miR167h-1	Chr06	49384165	49384286	+	Intergenic	Cluster sly-miR167a-1 / miR167h-1
sly-miR167a-1	Chr06	49384286	49384165	-	Intergenic	Cluster sly-miR167a-1 / miR167h-1
sly-miR156a-2	Chr07	324086	324178	+	Solyc07g005420	-
sly-miR8001b-2	Chr07	1372053	1371964	-	Intergenic	-
sly-miR169f	Chr07	2171868	2171681	-	Intergenic	Cluster sly-miR169f / miR169d
sly-miR169d	Chr07	2181237	2181400	+	Intergenic	Cluster sly-miR169f / miR169d
sly-miR396g-1	Chr07	2628863	2629006	+	Intergenic	Cluster sly-miR396g-1 / miR396b
sly-miR396b	Chr07	2628994	2628875	-	Intergenic	Cluster sly-miR396g-1 / miR396b
sly-miR171c-3	Chr07	2683304	2683403	+	Intergenic	-
sly-miR9473-1	Chr07	3076462	3076581	+	Solyc07g008300	Cluster sly-miR9473-1 / miR9473-2
sly-miR9473-2	Chr07	3076583	3076466	-	Solyc07g008320	Cluster sly-miR9473-1 / miR9473-2
sly-miR169a-2	Chr07	4211008	4211165	+	Intergenic	-
sly-miR169b-1	Chr07	4225552	4225753	+	Intergenic	-
sly-miR169a-1	Chr07	4249896	4249582	-	Intergenic	Cluster sly-miR169a-1 / miR169b-2
sly-miR169b-2	Chr07	4249975	4249829	-	Intergenic	Cluster sly-miR169a-1 / miR169b-2
sly-miR1886h-2	Chr07	8045819	8045646	-	Intergenic	-
sly-miR171i	Chr07	60893281	60893366	+	Intergenic	-
sly-miR171b-2	Chr07	60941168	60941326	+	Intergenic	-
sly-miR156f	Chr07	61637954	61637791	-	Intergenic	-
sly-miR397-2	Chr07	66189772	66189898	+	Intergenic	Cluster sly-miR397-1 / miR397-2
sly-miR397-1	Chr07	66189898	66189772	-	Intergenic	Cluster sly-miR397-1 / miR397-2
sly-miR168a-2	Chr08	558775	558934	+	Intergenic	-
sly-miR5303	Chr08	1444437	1444312	-	Solyc08g006880	-
sly-miR8045-2	Chr08	2128401	2128216	-	Solyc08g007580	-
sly-miR1917-1	Chr08	2462200	2462053	-	Intergenic	-
sly-miR166a-2	Chr08	2974009	2974115	+	Intergenic	-
sly-miR8008b-2	Chr08	9135529	9135338	-	Intergenic	-
sly-miR2101	Chr08	13018487	13018568	+	Intergenic	-
sly-miR8008a-1	Chr08	14337669	14337722	+	Intergenic	-
sly-miR7805	Chr08	35020520	35020182	-	Intergenic	-
sly-miR5368	Chr08	47023226	47023308	+	Intergenic	-
sly-miR156l-2	Chr08	51977523	51977412	-	Intergenic	-
sly-miR156i-1	Chr08	51997251	51997097	-	Intergenic	Cluster sly-miR156i-1 / miR156i-2 / miR156a-1
sly-miR156i-2	Chr08	51997449	51997346	-	Intergenic	Cluster sly-miR156i-1 / miR156i-2 / miR156a-1

sly-miR156a-1	Chr08	51998427	51998336	-	Intergenic	Cluster sly-miR156i-1 / miR156i-2 / miR156a-1
sly-miR156c	Chr08	52009032	52008934	-	Intergenic	-
sly-miR156l-1	Chr08	52130735	52130844	+	Intergenic	-
sly-miR7983-5	Chr08	55537713	55537641	-	Intergenic	-
sly-miR1919a-1	Chr08	56630989	56631165	+	Intergenic	-
sly-miR1919a-3	Chr08	56676089	56676252	+	Intergenic	-
sly-miR169e	Chr08	57649222	57649414	+	Intergenic	-
sly-miR9472	Chr08	59087177	59087356	+	Intergenic	-
sly-miR7984d	Chr08	62451568	62451783	+	Intergenic	-
sly-miR399j-2	Chr08	63632084	63631939	-	Intergenic	-
sly-miR159b	Chr08	64458113	64457855	-	Intergenic	-
sly-miR319c-3	Chr08	64904468	64904298	-	Intergenic	-
sly-miR1918	Chr08	65545478	65545313	-	Intergenic	-
sly-miR166-2	Chr08	65815402	65815559	+	Solyc08g083150	-
sly-miR5014a	Chr09	959048	958826	-	Intergenic	-
sly-miR160h-2	Chr09	1279300	1279216	-	Intergenic	-
sly-miR530	Chr09	1677600	1677681	+	Intergenic	-
sly-miR5303h-1	Chr09	2021295	2021165	-	Solyc09g008530	-
sly-miR2111a	Chr09	4693037	4692967	-	Intergenic	-
sly-miR7981	Chr09	5247319	5247110	-	Intergenic	-
sly-miR164a	Chr09	7198221	7198385	+	Intergenic	-
sly-miR1886a	Chr09	7214468	7214282	-	Intergenic	-
sly-miR390a	Chr09	8388438	8388547	+	Intergenic	-
sly-miR7990a-2	Chr09	25942449	25942659	+	Intergenic	-
sly-miR7990a-1	Chr09	25956494	25956595	+	Intergenic	-
sly-miR8007b	Chr09	62444440	62444171	-	Solyc09g064810	-
sly-miR167c	Chr09	64211054	64211137	+	Intergenic	Cluster sly-miR167c / miR167h-2 / miR167h-3
sly-miR167h-2	Chr09	64219925	64219813	-	Intergenic	Cluster sly-miR167c / miR167h-2 / miR167h-3
sly-miR167h-3	Chr09	64219827	64219911	+	Intergenic	Cluster sly-miR167c / miR167h-2 / miR167h-3
sly-miR7990a-3	Chr09	65545808	65545590	-	Intergenic	-
sly-miR8020	Chr09	66734620	66734742	+	Solyc09g074510	-
sly-miR167a-2	Chr09	68911051	68911136	+	Solyc09g082820	-
sly-miR7983-1	Chr09	68941071	68941243	+	Intergenic	-
sly-miR1886h-1	Chr09	71247906	71247976	+	Intergenic	-
sly-miR828a	Chr10	3426299	3426181	-	Intergenic	-
sly-miR477	Chr10	3630151	3630038	-	Intergenic	-
sly-miR390b	Chr10	59448159	59448057	-	Intergenic	-
sly-miR6027	Chr10	62982445	62982597	+	Intergenic	-
sly-miR172d-1	Chr10	63860890	63861000	+	Intergenic	Cluster sly-miR172d-1 / miR172d-9

sly-miR172d-9	Chr10	63861000	63860890	-	Intergenic	Cluster sly-miR172d-1 / miR172d-9
sly-miR5303j-2	Chr10	64085507	64085380	-	Solyc10g084410	-
sly-miR7983-2	Chr11	391983	391762	-	Intergenic	-
sly-miR8006-2	Chr11	1086356	1086173	-	Intergenic	-
sly-miR172d-6	Chr11	2634582	2634829	+	Intergenic	Cluster sly-miR172d-6 / miR172d-10
sly-miR172d-10	Chr11	2634778	2634591	-	Intergenic	Cluster sly-miR172d-6 / miR172d-10
sly-miR5174d	Chr11	9333365	9333118	-	Intergenic	-
sly-miR8021-1	Chr11	10831183	10830965	-	Intergenic	-
sly-miR7122	Chr11	11649311	11649389	+	Intergenic	-
sly-miR8051	Chr11	13849248	13849504	+	Intergenic	-
sly-miR8175	Chr11	18397967	18398136	+	Intergenic	-
sly-miR398a	Chr11	50593867	50593778	-	Solyc11g064980	-
sly-miR9478	Chr11	53291082	53291292	+	Solyc11g067255	-
sly-miR8039-2	Chr11	55278501	55278343	-	Intergenic	-
sly-miR8039-1	Chr11	56044284	56044104	-	Intergenic	-
sly-miR171c-1	Chr12	519893	519818	-	Intergenic	-
sly-miR9471a	Chr12	1977913	1977734	-	Solyc12g008590	Cluster sly-miR9471a / miR9471b
sly-miR9471b	Chr12	1979536	1979390	-	Solyc12g008590	Cluster sly-miR9471a / miR9471b
sly-miR171c-2	Chr12	2882830	2882928	+	Intergenic	-
sly-miR160g	Chr12	3988728	3988814	+	Intergenic	-
sly-miR5303g	Chr12	4949950	4949823	-	Intergenic	-
sly-miR845b	Chr12	6245740	6245456	-	Intergenic	-
sly-miR1919a-2	Chr12	6989107	6988948	-	Intergenic	-
sly-miR7985	Chr12	9940295	9940118	-	Intergenic	-
sly-miR5303j-1	Chr12	40017048	40016942	-	Intergenic	-
sly-miR319-1	Chr12	54934650	54934846	+	Solyc12g040470	-
sly-miR8025	Chr12	62369237	62369101	-	Intergenic	-
sly-miR7993a	Chr12	64548759	64548976	+	Solyc12g088090	-
sly-miR394b	Chr12	65642831	65643065	+	Intergenic	-
sly-miR168a-1	Chr12	66208896	66209049	+	Solyc12g096210	Cluster sly-miR168 / miR168a-1
sly-miR168	Chr12	66209049	66208896	-	Intergenic	Cluster sly-miR168 / miR168a-1
sly-miR827	Chr12	66434453	66434560	+	Intergenic	-
sly-miR8001b-1	Chr12	66838709	66838578	-	Intergenic	-
sly-miR398b	Chr12	67765199	67765309	+	Intergenic	-
spe-miR169-1	Chr00	58746994	58746840	-	Intergenic	-
spe-miR7997a-2	Chr01	763775	763648	-	Intergenic	-
spe-miR7983-6	Chr01	777092	776877	-	Intergenic	-
spe-miR8011a-1	Chr01	993461	993628	+	Intergenic	-
spe-miR1917-4	Chr01	1337502	1337263	-	Intergenic	-

spe-miR7993a	Chr01	6222559	6222383	-	Intergenic	-
spe-miR8019	Chr01	42041349	42041618	+	Intergenic	-
spe-miR7983-2	Chr01	53590579	53590384	-	Intergenic	-
spe-miR169-5	Chr01	54778784	54778561	-	Intergenic	-
spe-miR5303h	Chr01	60381783	60381443	-	Sopen01g020360	-
spe-miR6440b	Chr01	62433325	62433521	+	Intergenic	-
spe-miR8008-2	Chr01	72794320	72794167	-	Sopen01g023900	-
spe-miR5174d-1	Chr01	87185812	87185558	-	Intergenic	-
spe-miR403-1	Chr01	88519607	88519718	+	Intergenic	Cluster spe-miR403-1 / miR403-2
spe-miR403-2	Chr01	88519718	88519607	-	Intergenic	Cluster spe-miR403-1 / miR403-2
spe-miR8006	Chr01	89260875	89260620	-	Intergenic	-
spe-miR8021	Chr01	91805432	91805657	+	Intergenic	-
spe-miR6024	Chr01	93356622	93356521	-	Intergenic	-
spe-miR477a	Chr01	97142596	97142665	+	Intergenic	Cluster spe-miR477a / miR477b
spe-miR477b	Chr01	97142710	97142781	+	Intergenic	Cluster spe-miR477a / miR477b
spe-miR9476-2	Chr01	98437025	98437134	+	Sopen01g040830	Cluster spe-miR9476-2 / miR9476-1
spe-miR9476-1	Chr01	98437135	98437028	-	Intergenic	Cluster spe-miR9476-2 / miR9476-1
spe-miR164b	Chr01	100449370	100449481	+	Intergenic	-
spe-miR408	Chr01	101515027	101515154	+	Intergenic	Cluster spe-miR408 / miR408b
spe-miR408b	Chr01	101515133	101515046	-	Sopen01g044680	Cluster spe-miR408 / miR408b
spe-miR166c	Chr01	103235260	103235074	-	Sopen01g046580	-
spe-miR394-3	Chr01	103370640	103370700	+	Sopen01g046800	-
spe-miR8032a	Chr01	104953608	104953326	-	Intergenic	-
spe-miR7983-3	Chr01	105741430	105741210	-	Intergenic	-
spe-miR8011a-2	Chr01	106347857	106347978	+	Sopen01g050440	-
spe-miR7696c	Chr01	108167656	108167418	-	Sopen01g052820	-
spe-miR7980b-6	Chr02	17944152	17944310	+	Intergenic	-
spe-miR5303f-2	Chr02	18561249	18561117	-	Sopen02g006710	-
spe-miR7997a-1	Chr02	22075994	22075866	-	Intergenic	-
spe-miR160a	Chr02	29221649	29221751	+	Intergenic	Cluster spe-miR160a / miR160g-2
spe-miR160g-2	Chr02	29221746	29221652	-	Intergenic	Cluster spe-miR160a / miR160g-2
spe-miR171-6	Chr02	35982853	35982720	-	Intergenic	-
spe-miR156-3	Chr02	38183917	38184104	+	Intergenic	Cluster spe-miR156-3 / miR156-4 / miR156-5
spe-miR156-4	Chr02	38183967	38184052	+	Intergenic	Cluster spe-miR156-3 / miR156-4 / miR156-5
spe-miR156-5	Chr02	38185080	38185165	+	Intergenic	Cluster spe-miR156-3 / miR156-4 / miR156-5
spe-miR7983-1	Chr02	38806566	38806430	-	Intergenic	-
spe-miR399-9	Chr02	46563807	46563718	-	Intergenic	-
spe-miR8042	Chr02	47269929	47269772	-	Sopen02g023840	-
spe-miR171-3	Chr02	48456158	48456249	+	Intergenic	Cluster spe-miR171-3 / miR171-1

spe-miR171-1	Chr02	48456243	48456163	-	Intergenic	Cluster spe-miR171-3 / miR171-1
spe-miR171a	Chr02	50680595	50680507	-	Intergenic	-
spe-miR3627-2	Chr02	54121220	54121367	+	Intergenic	Cluster spe-miR3627-2 / miR3627-1
spe-miR3627-1	Chr02	54121255	54121337	+	Intergenic	Cluster spe-miR3627-2 / miR3627-1
spe-miR169a-2	Chr02	54491741	54491901	+	Intergenic	-
spe-miR1917-1	Chr02	55369968	55369755	-	Sopen02g034010	-
spe-miR156-6	Chr02	56825404	56825511	+	Intergenic	-
spe-miR5174d-2	Chr02	59770711	59770446	-	Intergenic	-
spe-miR166a-2	Chr03	294780	294688	-	Intergenic	-
spe-miR399r-1	Chr03	760858	760980	+	Intergenic	Cluster spe-miR399r-1 / miR399r-2 / miR399d / miR399-8
spe-miR399r-2	Chr03	765358	765483	+	Intergenic	Cluster spe-miR399r-1 / miR399r-2 / miR399d / miR399-8
spe-miR399d	Chr03	768200	768014	-	Intergenic	Cluster spe-miR399r-1 / miR399r-2 / miR399d / miR399-8
spe-miR399-8	Chr03	770033	769818	-	Intergenic	Cluster spe-miR399r-1 / miR399r-2 / miR399d / miR399-8
spe-miR393	Chr03	3264505	3264582	+	Intergenic	-
spe-miR399-4	Chr03	4068417	4068315	-	Intergenic	Cluster spe-miR399-4 / miR399-5 / miR399a-1 / miR399-3
spe-miR399-5	Chr03	4072891	4072789	-	Intergenic	Cluster spe-miR399-4 / miR399-5 / miR399a-1 / miR399-3 e Cluster spe- miR399-5 / miR399a-1 / miR399-3 / miR399a-2
spe-miR399a-1	Chr03	4074164	4074255	+	Intergenic	Cluster spe-miR399-4 / miR399-5 / miR399a-1 / miR399-3 e Cluster spe- miR399-5 / miR399a-1 / miR399-3 / miR399a-2
spe-miR399-3	Chr03	4078343	4078241	-	Intergenic	Cluster spe-miR399-4 / miR399-5 / miR399a-1 / miR399-3 e Cluster spe- miR399-5 / miR399a-1 / miR399-3 / miR399a-2
spe-miR399a-2	Chr03	4080459	4080561	+	Intergenic	Cluster spe- miR399-5 / miR399a-1 / miR399-3 / miR399a-2 e Cluster spe- miR399a-2 / miR399-6
spe-miR399-6	Chr03	4089611	4089509	-	Intergenic	Cluster spe- miR399a-2 / miR399-6
spe-miR399-1	Chr03	4140329	4140503	+	Intergenic	-
spe-miR7983-4	Chr03	4924248	4924109	-	Intergenic	-
spe-miR395i	Chr03	31337654	31337827	+	Intergenic	-
spe-miR8001a	Chr03	33496434	33496291	-	Intergenic	-
spe-miR8175-1	Chr03	41122625	41122861	+	Intergenic	-
spe-miR166a-3	Chr03	53852958	53852785	-	Intergenic	-
spe-miR479	Chr03	53981867	53981978	+	Intergenic	Cluster spe-miR171-7 / miR479
spe-miR171-7	Chr03	53981978	53981867	-	Intergenic	Cluster spe-miR171-7 / miR479
spe-miR398b-1	Chr03	56677168	56677249	+	Sopen03g024140	-
spe-miR8011	Chr03	56824159	56824059	-	Sopen03g024290	-
spe-miR319c-2	Chr03	58587777	58587954	+	Intergenic	-
spe-miR8047	Chr03	63861049	63861256	+	Intergenic	-
spe-miR8007a	Chr03	64725491	64725758	+	Sopen03g028930	-
spe-miR171-5	Chr03	65647332	65647221	-	Intergenic	-
spe-miR162a-1	Chr03	68777282	68777391	+	Intergenic	-
spe-miR482a	Chr03	69139850	69139940	+	Sopen03g033970	-

spe-miR1446	Chr03	71566898	71566760	-	Intergenic	Cluster spe-miR1446 / miR1446a
spe-miR1446a	Chr03	71572186	71572091	-	Intergenic	Cluster spe-miR1446 / miR1446a
spe-miR156-1	Chr03	72241872	72242020	+	Intergenic	-
spe-miR319c-3	Chr03	72316257	72316435	+	Intergenic	Cluster spe-miR319c-3 / miR319-3
spe-miR319-3	Chr03	72316430	72316608	+	Intergenic	Cluster spe-miR319c-3 / miR319-3
spe-miR7992	Chr03	72436289	72436042	-	Intergenic	-
spe-miR319c-1	Chr03	72682859	72682683	-	Sopen03g038370	-
spe-miR5300	Chr04	532618	532882	+	Sopen04g001700	-
spe-miR1886-1	Chr04	2218162	2218292	+	Intergenic	-
spe-miR8038a	Chr04	3062868	3063003	+	Intergenic	-
spe-miR7997a	Chr04	5436561	5436378	-	Intergenic	-
spe-miR7998	Chr04	29817707	29817477	-	Intergenic	-
spe-miR5303f-3	Chr04	67270180	67270034	-	Intergenic	-
spe-miR482e	Chr04	67878952	67879113	+	Intergenic	Cluster spe-miR482e / miR8036
spe-miR8036	Chr04	67883283	67883368	+	Intergenic	Cluster spe-miR482e / miR8036
spe-miR394-1	Chr04	76575040	76575242	+	Intergenic	-
spe-miR395g	Chr05	1860758	1860911	+	Intergenic	-
spe-miR395d	Chr05	1873904	1873805	-	Intergenic	-
spe-miR395a	Chr05	1887692	1887590	-	Intergenic	-
spe-miR319-1	Chr05	2968193	2968007	-	Intergenic	-
spe-miR398b-2	Chr05	6357522	6357739	+	Intergenic	-
spe-miR5174d-3	Chr05	52039016	52038749	-	Intergenic	-
spe-miR8008-1	Chr05	52060990	52060864	-	Intergenic	-
spe-miR7980b-1	Chr05	69649910	69649762	-	Intergenic	Cluster spe-miR7980b-1 / miR7980b-3
spe-miR7980b-3	Chr05	69649795	69649908	+	Intergenic	Cluster spe-miR7980b-1 / miR7980b-3
spe-miR6144	Chr05	73651677	73651864	+	Sopen05g029890	-
spe-miR1128	Chr05	74342704	74343004	+	Intergenic	-
spe-miR172-5	Chr05	75143190	75143059	-	Intergenic	Cluster spe-miR172-5 / miR172d
spe-miR172d	Chr05	75143079	75143172	+	Intergenic	Cluster spe-miR172-5 / miR172d
spe-miR5303f-1	Chr05	76336809	76337118	+	Intergenic	-
spe-miR172-6	Chr05	77261541	77261645	+	Intergenic	-
spe-miR160g-1	Chr05	77521943	77522037	+	Intergenic	Cluster spe-miR160g-1 / miR160-1
spe-miR160-1	Chr05	77522034	77521947	-	Intergenic	Cluster spe-miR160g-1 / miR160-1
spe-miR172-3	Chr06	717771	717939	+	Intergenic	Cluster spe-miR172-3 / miR172-4
spe-miR172-4	Chr06	717939	717771	-	Intergenic	Cluster spe-miR172-3 / miR172-4
spe-miR8039	Chr06	810350	810209	-	Sopen06g001640	-
spe-miR319-2	Chr06	1727636	1727820	+	Intergenic	-
spe-miR166-1	Chr06	2799201	2799085	-	Intergenic	-
spe-miR4376	Chr06	4599649	4599744	+	Intergenic	-

spe-miR8024	Chr06	16538507	16538591	+	Intergenic	-
spe-miR5368	Chr06	39225149	39225231	+	Intergenic	-
spe-miR5303-2	Chr06	45062996	45062879	-	Intergenic	-
spe-miR166a-1	Chr06	46235742	46235887	+	Intergenic	-
spe-miR1917-3	Chr06	46649012	46648812	-	Intergenic	-
spe-miR482d	Chr06	47145257	47145145	-	Intergenic	Cluster spe-miR482d / miR482-1/ miR482b / miR482-2
spe-miR482-1	Chr06	47145601	47145443	-	Intergenic	Cluster spe-miR482d / miR482-1/ miR482b / miR482-2
spe-miR482b	Chr06	47148941	47148823	-	Intergenic	Cluster spe-miR482d / miR482-1/ miR482b / miR482-2
spe-miR482-2	Chr06	47153519	47153410	-	Intergenic	Cluster spe-miR482d / miR482-1/ miR482b / miR482-2
spe-miR164	Chr06	50067065	50067162	+	Intergenic	-
spe-miR7987	Chr06	51830956	51830859	-	Intergenic	-
spe-miR171	Chr06	53312500	53312609	+	Intergenic	-
spe-miR156-2	Chr06	53412503	53412403	-	Intergenic	-
spe-miR162a-2	Chr06	53636765	53636894	+	Intergenic	-
spe-miR9477	Chr06	54350260	54350413	+	Sopen06g027450	-
spe-miR172a	Chr06	57403102	57403243	+	Intergenic	-
spe-miR167a	Chr06	60329098	60329006	-	Intergenic	-
spe-miR156-12	Chr07	389395	389305	-	Intergenic	-
spe-miR8001b-2	Chr07	1638098	1638009	-	Intergenic	-
spe-miR169-2	Chr07	2514047	2513858	-	Intergenic	Cluster spe-miR169-2 / miR169-4
spe-miR169-4	Chr07	2516932	2517123	+	Intergenic	Cluster spe-miR169-2 / miR169-4
spe-miR169-3	Chr07	2533839	2534002	+	Intergenic	-
spe-miR396a	Chr07	2869277	2869383	+	Intergenic	Cluster spe-miR396a / miR396-2 / miR396-1
spe-miR396-2	Chr07	2878850	2878980	+	Intergenic	Cluster spe-miR396a / miR396-2 / miR396-1
spe-miR396-1	Chr07	2878975	2878854	-	Intergenic	Cluster spe-miR396a / miR396-2 / miR396-1
spe-miR171e-2	Chr07	2946958	2947057	+	Intergenic	-
spe-miR9473-2	Chr07	3372042	3372219	+	Sopen07g004200	Cluster spe-miR9473-2 / miR9473-1
spe-miR9473-1	Chr07	3372201	3372084	-	Intergenic	Cluster spe-miR9473-2 / miR9473-1
spe-miR1886h-1	Chr07	8373788	8373616	-	Intergenic	-
spe-miR8005	Chr07	18793709	18793540	-	Intergenic	-
spe-miR5368	Chr07	24084719	24084801	+	Intergenic	-
spe-miR8008b-3	Chr07	40677213	40677099	-	Intergenic	-
spe-miR169c	Chr07	49698756	49698853	+	Intergenic	Cluster spe-miR169c / miR169-1
spe-miR169-1	Chr07	49700826	49700980	+	Intergenic	Cluster spe-miR169c / miR169-1
spe-miR169a-1	Chr07	49721651	49721505	-	Intergenic	-
spe-miR9469	Chr07	69192575	69192435	-	Intergenic	-
spe-miR171-4	Chr07	71701400	71701485	+	Intergenic	-
spe-miR7984	Chr07	71807970	71808199	+	Sopen07g026000	-
spe-miR5303e	Chr07	73490593	73490465	-	Sopen07g027820	-

spe-miR397	Chr07	77142577	77142462	-	Sopen07g031830	-
spe-miR5303-3	Chr08	289190	289072	-	Sopen08g001310	-
spe-miR168a	Chr08	633373	633558	+	Intergenic	-
spe-miR5303-1	Chr08	1624244	1624119	-	Sopen08g002840	-
spe-miR7983-5	Chr08	1925458	1925318	-	Intergenic	-
spe-miR8045	Chr08	2182211	2181950	-	Intergenic	-
spe-miR8013	Chr08	2664770	2664484	-	Intergenic	-
spe-miR1917-2	Chr08	2694471	2694336	-	Intergenic	-
spe-miR166-2	Chr08	3223120	3223226	+	Intergenic	-
spe-miR8008b-2	Chr08	10372996	10373189	+	Intergenic	Cluster spe-miR8008b-2 / miR8008b-1
spe-miR8008b-1	Chr08	10373118	10373065	-	Intergenic	Cluster spe-miR8008b-2 / miR8008b-1
spe-miR7984c	Chr08	53205515	53205833	+	Intergenic	-
spe-miR156-10	Chr08	55832557	55832450	-	Intergenic	-
spe-miR156-11	Chr08	55860599	55860443	-	Intergenic	Cluster spe-miR156-11 / miR156-9 / miR156-8
spe-miR156-9	Chr08	55861041	55860941	-	Intergenic	Cluster spe-miR156-11 / miR156-9 / miR156-8
spe-miR156-8	Chr08	55861290	55861199	-	Intergenic	Cluster spe-miR156-11 / miR156-9 / miR156-8
spe-miR156-7	Chr08	55884801	55884705	-	Intergenic	-
spe-miR5303	Chr08	58662426	58662225	-	Intergenic	-
spe-miR1919	Chr08	60775494	60775670	+	Intergenic	-
spe-miR1919	Chr08	60800793	60800969	+	Sopen08g021530	-
spe-miR169e	Chr08	61831591	61831769	+	Sopen08g022320	-
spe-miR1886-2	Chr08	65611577	65611692	+	Intergenic	-
spe-miR399-2	Chr08	68047824	68047718	-	Sopen08g028540	-
spe-miR319a	Chr08	69369928	69369759	-	Intergenic	-
spe-miR1918	Chr08	70028312	70028116	-	Intergenic	-
spe-miR5014a	Chr09	995440	995181	-	Sopen09g002260	-
spe-miR7984b	Chr09	1178022	1178226	+	Intergenic	-
spe-miR160-2	Chr09	1305565	1305450	-	Intergenic	-
spe-miR530	Chr09	1716007	1716099	+	Sopen09g003040	-
spe-miR7980b-4	Chr09	2750347	2750232	-	Intergenic	-
spe-miR2111a	Chr09	4970364	4970294	-	Intergenic	-
spe-miR164a	Chr09	7469784	7469948	+	Intergenic	-
spe-miR390	Chr09	11503984	11504093	+	Intergenic	-
spe-miR7990a-1	Chr09	36111556	36111665	+	Intergenic	Cluster spe-miR7990a-1 / miR7990a-2
spe-miR7990a-2	Chr09	36121579	36121697	+	Intergenic	Cluster spe-miR7990a-1 / miR7990a-2
spe-miR399-7	Chr09	37782817	37782560	-	Intergenic	-
spe-miR8008a-2	Chr09	54478670	54478465	-	Intergenic	Cluster spe-miR8008a-2 / miR8008a-1
spe-miR8008a-1	Chr09	54478739	54478610	-	Intergenic	Cluster spe-miR8008a-2 / miR8008a-1
spe-miR5368	Chr09	57270515	57270433	-	Sopen09g020810	-

spe-miR8051	Chr09	58910569	58910902	+	Intergenic	-
spe-miR8175-2	Chr09	59756881	59757050	-	Intergenic	-
spe-miR8016	Chr09	62946671	62946500	-	Sopen09g022460	-
spe-miR5368	Chr09	74641434	74641352	-	Sopen09g027020	-
spe-miR167-3	Chr09	75312701	75312784	+	Intergenic	-
spe-miR167-1	Chr09	75320778	75320862	+	Intergenic	-
spe-miR8020	Chr09	77715051	77715138	+	Sopen09g029350	-
spe-miR7993b-2	Chr09	78450264	78450026	-	Sopen09g030040	-
spe-miR167h	Chr09	80024697	80024502	-	Intergenic	Cluster spe-miR167h / miR167-2
spe-miR167-2	Chr09	80024558	80024643	+	Intergenic	Cluster spe-miR167h / miR167-2
spe-miR828a	Chr10	3597458	3597340	-	Intergenic	-
spe-miR477	Chr10	3891051	3890938	-	Intergenic	-
spe-miR7981	Chr10	46960184	46959971	-	Intergenic	-
spe-miR5303c-2	Chr10	63014715	63014597	-	Sopen10g022810	-
spe-miR390a	Chr10	75977120	75977018	-	Intergenic	-
spe-miR6027	Chr10	79748661	79748824	+	Sopen10g032420	-
spe-miR172-8	Chr10	80668644	80668535	-	Intergenic	Cluster spe-miR172-8 / miR172-7
spe-miR172-7	Chr10	80668537	80668641	+	Intergenic	Cluster spe-miR172-8 / miR172-7
spe-miR7983-7	Chr10	80735644	80735432	-	Intergenic	-
spe-miR8001b-1	Chr11	1226731	1227071	+	Intergenic	-
spe-miR1886h-2	Chr11	5485202	5485298	+	Intergenic	-
spe-miR6478	Chr11	7210748	7210440	-	Intergenic	-
spe-miR7980b-5	Chr11	49545167	49545323	+	Intergenic	Cluster spe-miR7980b-5 / miR7980b-2
spe-miR7980b-2	Chr11	49545309	49545230	-	Intergenic	Cluster spe-miR7980b-5 / miR7980b-2
spe-miR398a	Chr11	59950863	59950774	-	Sopen11g024750	-
spe-miR172-2	Chr11	64255940	64256125	+	Intergenic	Cluster spe-miR172-2 / miR172-1
spe-miR172-1	Chr11	64256105	64255947	-	Sopen11g028510	Cluster spe-miR172-2 / miR172-1
spe-miR171-2	Chr12	614776	614702	-	Intergenic	-
spe-miR9471b	Chr12	2195979	2195833	-	Sopen12g003530	-
spe-miR171e-1	Chr12	3162612	3162738	+	Sopen12g004610	-
spe-miR5303c-1	Chr12	3259804	3259679	-	Intergenic	-
spe-miR160c	Chr12	5032210	5032296	+	Intergenic	-
spe-miR1919c	Chr12	7326346	7326187	-	Sopen12g008360	-
spe-miR319-4	Chr12	53120856	53121052	+	Intergenic	-
spe-miR7993b-1	Chr12	60349716	60349441	-	Intergenic	-
spe-miR8025	Chr12	61214239	61214103	-	Intergenic	-
spe-miR8024a	Chr12	66067345	66067103	-	Intergenic	-
spe-miR8026	Chr12	72433822	72433699	-	Intergenic	-
spe-miR394-2	Chr12	80462369	80462564	+	Intergenic	-

spe-miR168b	Chr12	81073196	81073365	+	Sopen12g032070	-
spe-miR827	Chr12	81335316	81335403	+	Intergenic	-
spe-miR398	Chr12	82730667	82730759	+	Intergenic	-

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Supplementary Table S8. Thermodynamic and structural characterization of *S. lycopersicum* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Pre-miRNA	Sequence	Size	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
sly-miR1128	uacuacucccuccgu cccaaaauaaguguc acuuuagcaauaau cauacucacuaagaa aaauaauaaauaga aagguauaguucac caaguuaccccuauu uauuaguuguuucu ugacaauugagcau gauugauaaguagu ucuuuaguacaaag guauacuuggaaaa acauacuaauuucu gucuuaaguuccua uggugacacuuauu uuggaaaaaaauuu auugcuaaagugac acuuauuuugggac ggauggaguauuu	269	1.561.338	3.420.074	1.561.338	3.457.249	3.122.677	6.877.323	101.087	1	-98.1	-96.7	0.003476	31.09	-364.684	-116.786
sly-miR1446-1	aauggaaauccagu guuuucugaacucuc ucccucaauggcuuc uccaauauauaaau uaauuuaaaagagc agccaugagagauu gaguucagaaaacu auggcuuuccuag	113	1.681.416	3.274.336	1.946.903	3.097.345	3.628.319	6.371.681	0.945946	0.863636	-46.8	-44.4	0.109489	4.46	-414.159	-114.146
sly-miR1446-2	cagaguuuucugaa cucucucccucaaug gcuguucauauaau auaugcugcuacuu ugcagcuuaauuaa auaacagcuuuggg gguuugaguccaga aaacucuug	108	1.851.852	2.592.593	2.037.037	3.518.519	3.888.889	6.111.111	1.357.14 3	0.909091	-51.1	-51.1	0.163176	3.74	-473.148	-121.667
sly-miR156a-1	cggugacagaagag agugagcacauaug gucuuuucaagcau gauguuuacaugcu ugaagcuaugcgug	92	2.282.609	2.391.304	2.282.609	3.043.478	4.565.217	5.434.783	1.272.72 7	1	-55.6	-55.6	0.317684	2.7	-604.348	-132.381

	cucacuucucuaucu gucaccc															
sly-miR156a-2	gacugacagaagag agugagcacacgau gucaaauuguauaa auauauauacaauu gucauuugcgugug cucacuucucauucu gucagaau	93	1.935.484	3.225.806	172.043	311.828	3.655.914	6.344.086	0.966667	1.125	-48.7	-45.7	0.094595	4.25	-523.656	-143.235
sly-miR156c	uggugauagaagag agugagcacacaug guguuuucuugcau gauguuuauauaua uauaugcuugaaac uaugugugcuuacu cucuaucugucaccc	99	2.121.212	2.525.253	1.616.162	3.737.374	3.737.374	6.262.626	1.48	13.125	-56.8	-56.8	0.39483	4.69	-573.737	-153.514
sly-miR156f	acauaugagauuug guugaggauucaaa gugagaaauucuau ugacagaagagaga gaguacaaucuguc aucagcaaaaugau auuguuguuuguug gaaugugcucucucu gcuucugccaaugga aacuauaaaaaugg auccucaacaaagau uauacau	164	2.073.171	347.561	1.402.439	304.878	347.561	652.439	0.877193	1.478.261	-67	-67	0.08395	6.09	-408.537	-117.544
sly-miR156i-1	ucuaauuaagugua aaguaagacaaaaa gaggugacagaaga gcgugagcacaugu guguuuucuagcau gauguuuauaugcu ugaaucuaugcgug cucacugcucuaucu uucauccucaucgcu uuuccucucucucua gauuuaauuuuc	155	1.806.452	2.580.645	1.935.484	3.677.419	3.741.935	6.258.065	1.425	0.933333	-50.4	-50.4	0.102397	8.43	-325.161	-0.86897
sly-miR156i-2	gggaggugacagaa gagagugggcacau augguauuuucucg caugcuugaaacua ugucugcucacuucu cuaucugucaucccu accauuuucuccguu ucu	104	2.115.385	2.019.231	2.403.846	3.461.538	4.519.231	5.480.769	1.714.28 6	0.88	-40.8	-40.8	0.169001	5.92	-392.308	-0.86809
sly-miR156l-1	aaaaggggcgguga	110	2.454.545	2.454.545	2.272.727	2.818.182	4.727.273	5.272.727	1.148.14	1.08	-67.3	-67.3	0.50298	2.24	-611.818	-129.423

	cagaagagagugag cacacauggugguu ucuagcaugauguu uuacaugcuugaaa cuaugugugcucacu gcucuaucugucacc ccccaucgcu								8							
sly-miR156l-2	aaggggcggugaca gaagagagugagca cacauggcguuuucu ggcaugauguuuau auauauauaugcuu gaaacuaugugugc ucacugcucuaucug ucaccucccacc	112	2.410.714	25	2.142.857	2.946.429	4.553.571	5.446.429	1.178.57 1	1.125	-64.1	-64.1	0.313	7.58	-572.321	-125.686
sly-miR157a-1	uguuaaaagaggag gugguaggagaugu uguugacagaagau agagagcacagaug auaaagugcaugga aauugucugcaccuu acuccuuugugcucu uuauucuucuguca ucaucauuaauccca ccuuuuuuuuugau auu	146	2.123.288	2.671.233	1.575.342	3.630.137	369.863	630.137	1.358.97 4	1.347.826	-67.1	-66.7	0.030551	8.03	-459.589	-124.259
sly-miR157a-2	cucacaacuguaagu auaaauuauuucaa agagagcaggaaag uauugggugagaua uuguugacagaaga uagagagcacgaau aaugaggugcuaau uggaagcugcaccuu aauucuuugugcuc ucuauucuucuguca ucaucuucagucccu ccccgacccucucua ccuuaauuuauuuc uacguuuauuguau u	202	1.782.178	2.772.277	1.980.198	3.465.347	3.762.376	6.237.624	1.25	0.9	-69	-65.8	0.004479	23.11	-341.584	-0.90789
sly-miR157a-3	uugacagaagauag agagcacuaaugau gauaugcuaauuuc auucaauuugggca gcaaaagcaucucaa uucauuugugcucuc uaugcuucugucauc	101	1.782.178	2.970.297	1.881.188	3.366.337	3.663.366	6.336.634	1.133.33 3	0.947368	-43.2	-41.9	0.123911	6.62	-427.723	-116.757

sly-miR157a-4	auugauuuguguaa aauguagggaggaa aaaaaaagagggga aaauggaaugggug auauuguugacaga agauagagagcaca uaugauggaaugcu gcugcugcugcugcu aaaucuggagaguc uuaacaauaaaaaa aagcauuucacuuca uuugugcucucuau gcuuccgucaucccu uucauccucuucucc uucuauuuuucucu ucucucucccuaaau cuauacaauaacucg uu	246	1.869.919	296.748	1.869.919	3.292.683	3.739.837	6.260.163	1.109.589	1	-81.6	-72.1	0.001928	29.98	-331.707	-0.88696
sly-miR159a	ggagcuccuugaag uccaacagaagaucu aacagguuagauug agcugcugaccuaug gauuccucagcccua ucuauuuaugauuu caaacauauagaua gguuugugggguuug cauaugucaggagc uuuauuuuacccuu uguuugaucauuuu uuggauugaaggga gcucuac	178	2.191.011	247.191	1.741.573	3.595.506	3.932.584	6.067.416	1.454.545	1.258.065	-79	-76.4	0.018008	12.25	-44.382	-112.857
sly-miR159b	cuguuuguggauua cacugauauucaua uaguugauuuuaac uuguucgaggaaga uuagaguucugaau guagagcuuuucug aauuucaaagagga ucugagagggaaaa ucgagcugcuaaucu auggaucccucaaac cuaucuauucucaaa auaauuuuagauag guuugugguuugca uauaucaggagcuu cauuuacucuucuag gauccuuauuggaa ugaagggagcucua	259	2.046.332	2.857.143	1.467.181	3.629.344	3.513.514	6.486.486	127.027	1.394.737	-89.5	-86.4	0.000123	25.78	-34.556	-0.98352

	cguuugauaaccua auu															
sly-miR160	gguguaugcuugg cuccuuauacgccac ccacugaucagucaa ucaaagaauuggug aaugugugguggcau acagggagccaggca cauccuuc	95	2.631.579	2.421.053	2.421.053	2.526.316	5.052.632	4.947.368	1.043.47 8	1.086.957	-42.6	-41.9	0.100259	11.91	-448.421	-0.8875
sly-miR160a	augugccuggcuccc uguaugccacacaca uucaccaauucuuug auugacugaucagu gggugggcguauaag gagccaagcauac	86	2.325.581	244.186	255.814	2.674.419	4.883.721	5.116.279	1.095.23 8	0.909091	-42	-42	0.436629	2.58	-488.372	-1
sly-miR160g	cugccuggcucccug gaugccaacuaaga acaguauugucaaa aaaauugacacucu uccuaguugguacca gaggagacaggcag a	87	2.298.851	3.103.448	2.413.793	2.183.908	4.712.644	5.287.356	0.703704	0.952381	-47.9	-47.9	0.312156	2.19	-550.575	-116.829
sly-miR160h-1	cguauaugccuggcu cccuguaugccauuu gcaaagcucaccgua auauaucgaugggc cuuguugaauggcg uaugaggagccaag cauauucc	95	2.421.053	2.315.789	2.421.053	2.842.105	4.842.105	5.157.895	1.227.27 3	1	-47.4	-47.4	0.144332	2.94	-498.947	-103.043
sly-miR160h-2	acaugccuggcuccu uguaugccauuugc auuguuccaccaaga auugauggccuuuu cagauggcauucua ggagcuaagcaug	85	2.235.294	2.235.294	2.352.941	3.176.471	4.588.235	5.411.765	1.421.05 3	0.95	-36.9	-36.7	0.38696	3.21	-434.118	-0.94615
sly-miR162-1	uaguugguugaaga cacuggaggcagcgg uucaucgauccguuc ccuggaagcugaau auauauauacgcaa aaauacagcaaaag gaaucggucgauaa accucugcauccagu gcuuaaccccuaa	128	21.875	3.203.125	2.265.625	234.375	4.453.125	5.546.875	0.731707	0.965517	-48.4	-47.7	0.011282	12.44	-378.125	-0.84912
sly-miR162-2	guugggugagaaca cuggaggcagcggu ucaucgaucuguucc cugaaaagcgauaa	110	2.545.455	2.909.091	2.545.455	20	5.090.909	4.909.091	0.6875	1	-49	-49	0.057198	7.88	-445.455	-0.875

	auacagcaacagga agcgaucgauaaacc ucugcauccagugcu uaacccgcc															
sly-miR164a	agauggagaagcag ggcacgugcauuacu aacucauacgcaaga uuuaucgauguuuc gaaaauucugcuau cauaguacuguauu uuacagcaaauagu guuuguacuuuaca uguaugugauaaaa ugaugaguuaguua uucaugugccuguu uuccccauc	165	1.939.394	2.909.091	1.636.364	3.515.152	3.575.758	6.424.242	1.208.33 3	1.185.185	-58.2	-56.1	0.002523	17.78	-352.727	-0.98644
sly-miR164e	ugggugggguaacuc auguuggagaagca gggcacgugcaaau ucuuguauucgaca auauaugcauuacu aaugguaaugcaug aauuuugcacgugu ucuccuucuccaac	112	2.321.429	2.589.286	18.75	3.214.286	4.196.429	5.803.571	1.241.37 9	1.238.095	-50.8	-50.6	0.021401	11.6	-453.571	-108.085
sly-miR164f	uuuaagcuggagaa gcagggcacaugcug aauuacuugaaacu uugaccuuucaaga auuuugcaugugcu cuagcucuccagcuu aa	88	2.045.455	2.727.273	2.045.455	3.181.818	4.090.909	5.909.091	1.166.66 7	1	-50.5	-47.5	0.215526	2.29	-573.864	-140.278
sly-miR166-1	acaaaagaaagaaa acauuuguugaggg gaauguuguuuggu ucgaaaucauucaa acaaauuaaaauuc augcaucucgauga ucgaugaauugaau aauuucggaccaggc uucauuccccccaac ucaaguuuuuguuu uaau	146	1.712.329	3.424.658	1.643.836	3.219.178	3.356.164	6.643.836	0.94	1.041.667	-54.2	-53.5	0.065467	8.11	-371.233	-110.612
sly-miR166-2	ucucaguugagggg aauguugucuggcu cgaggucaccaauua gauccauaaucccua uauauaccaugcuu uucaaaaaaaagau	158	2.025.316	2.911.392	1.835.443	3.227.848	3.860.759	6.139.241	1.108.69 6	1.103.448	-59	-58.7	0.120311	9.82	-373.418	-0.96721

	uuauaauaugaaaa gggguuaugaauca uguguuaguguugu cggaccaggcuucau ucccccccaauuguua															
sly-miR166-3	agcuuccagauuug aggggaauguuguu uggcucgaagucau uaucucauuauaga ucgaaccaauccaau uuuauauauucaau cuaguuuaaaauau augugaauuacgau gaugaugagauagu gucuucggaccaggc uucauuccccccaau uuggaaaca	166	186.747	3.012.048	1.746.988	3.373.494	3.614.458	6.385.542	1.12	1.068.966	-66	-60.6	0.034522	17.96	-39.759	-1.1
sly-miR166a-1	auauuguugaggag aaugucgucugguu cgagaucuuucaua agaaagguaaauga augacaaguuuuca uauauguaucguga augauuucggacca ggcuucauuccccuc aacucug	120	2.166.667	2.833.333	1.666.667	3.333.333	3.833.333	6.166.667	1.176.471	1.3	-52.2	-51	0.291748	5.74	-43.5	-113.478
sly-miR166a-2	uuaauuuugagggg aauguuguuuggcu cgaggccaccaacuu caucuaaugugagc aaacucuuuguuag ugucgucggaccagg cuucauuccccucaa aaucuc	107	2.149.533	2.242.991	2.336.449	3.271.028	4.485.981	5.514.019	1.458.333	0.92	-44.5	-40.1	0.039483	13.55	-415.888	-0.92708
sly-miR166a-3	aaacaagaucaugu uaaggagaauguug ucugguucgugacca uauaucuuucuucac auaaaugaucucgg accaggcuucauucc ccucaa	93	172.043	2.903.226	2.258.065	311.828	3.978.495	6.021.505	1.074.074	0.761905	-30.6	-30.6	0.192826	4.67	-329.032	-0.82703
sly-miR166a-4	ggagagagagcuuu uguauugcggggaa uguugucuggcucg aggaaucaaaaauu guuucuuauagaua gaucuguauauuuu guuuauagaucuau	158	221.519	2.531.646	1.582.278	3.670.886	3.797.468	6.202.532	1.45	1.4	-71.2	-71.2	0.176528	5.62	-450.633	-118.667

	aauguuuugaugu cgucggaccaggcuu cauuccccacaauga auauugcucucucac a															
sly-miR166g	ugugugguggugagu uugagggggauguu gucuggcucgacaca auuacucuauugua uguauuuaguuauu cguuaucaagauug augucgauaacgaa uaaauuaaacacau auauacaagaugua aaaagggaguaaag gcgucggaccaggcu ucauuccucucaaac aauauucuacuuuu ac	187	2.139.037	3.048.128	1.497.326	3.315.508	3.636.364	6.363.636	1.087.719	1.428.571	-71.3	-68.3	0.00768	17.68	-381.283	-104.853
sly-miR167a-1	acaucgugcagcacu agcaguugaagcug ccagcaugaucuaaa cuuuccuuuuaguuc aaauauaauucgag gaaagaucagauca uguggcagccuuacc ugucaaugccaucac gaauu	122	1.885.246	3.032.787	2.295.082	2.786.885	4.180.328	5.819.672	0.918919	0.821429	-47.3	-47.1	0.127815	5.41	-387.705	-0.92745
sly-miR167a-2	aucaguugaagcug ccagcaugaucuaaa cuuaccuauaaauu uauauuaaggcaag aucagaucaugugg uugcuucaccuguua	86	1.744.186	3.139.535	1.860.465	3.255.814	3.604.651	6.395.349	1.037.037	0.9375	-31.7	-31.7	0.074858	5.62	-368.605	-102.258
sly-miR167c	gugaagcugccagca ugaucuaaacuugg ccauuuauaaagaa aaugggugacuaag guuaggucaugcuc ggacagccucacu	84	25	297.619	202.381	25	452.381	547.619	0.84	1.235.294	-41.1	-41.1	0.469922	3.19	-489.286	-108.158
sly-miR167h-1	aauucgugauggca uugacagguaaggc ugccacaugaucuga ucuuuccucgaauua uauuugaacuaaaa ggaaaguuuagauc augcuggcagcuuca acugcuagugcugca	122	2.295.082	2.786.885	1.885.246	3.032.787	4.180.328	5.819.672	1.088.235	1.217.391	-57.4	-57.4	0.173226	4.72	-470.492	-112.549

	cgaugu															
sly-miR167h-2	uuccgcgaaaccauc aacaggugaugcug ccacaugaucugauc uuuccucguacggag caauagaaaaguuu agaucaugcuggca gcuucaacugcuagu gguucacgauc	113	2.212.389	2.654.867	2.477.876	2.654.867	4.690.265	5.309.735	1	0.892857	-45.6	-45.6	0.023733	9.57	-40.354	-0.86038
sly-miR167h-3	agcaguugaagcug ccagcaugaucuaaa cuuuucuauugcucc guacgaggaaagau cagaucauguggca gcaucaccuguug	85	2.352.941	2.705.882	2.235.294	2.705.882	4.588.235	5.411.765	1	1.052.632	-39.8	-39.8	0.299069	2.42	-468.235	-102.051
sly-miR168	cagucuccuauucag uugaugcaaggcgg gacccaaacuacgca acaacauguaaaaa uaagauucuuuuuu accgguacgcugccg ucgccgucagcuacc gccauuguugccggc gagguaggucccgac cugcaccaagcgaau gagaaac	154	2.337.662	2.662.338	2.857.143	2.142.857	5.194.805	4.805.195	0.804878	0.818182	-56	-53.3	0.081527	15.07	-363.636	-0.7
sly-miR168a-1	guuucucauucgcuu ggugcaggucggga ccuaccucgccggca acaauggcgguagc ugacggcgacggcag cguaccgguaaaaa agaaucuuauuuuu acauguuguugcgu aguuuggguccccgcc uugcaucaacugaa uaggagacug	154	2.857.143	2.142.857	2.337.662	2.662.338	5.194.805	4.805.195	1.242.424	1.222.222	-70.3	-69	0.01763	13.49	-456.494	-0.87875
sly-miR168a-2	ccucuuauucgcuug gugcaggucgggacc ucauucgccggcgcc gggaauaaugccgg acgaacgacggcggu guuaauucuacuaa agcugucaccgacgg auagauguuugauu agcggcgaaauuug gguccugccuugcau caacugaauuggag	160	29.375	21.25	23.75	25.625	53.125	46.875	1.205.882	1.236.842	-66	-63.5	0.016082	21.23	-41.25	-0.77647

sly-miR169a-1	uuuuauaguuucgg caaguuguucuugg cuauaguuugcucuc uucuucucaugucau ccucguuagaccuau uuuuuccuacuucuc gagaagaauuuuca auuuugagagagug uuauuugauacgaa ggauuuuuaaaauc acuuuuuaaauagu ucauacguauuauc uaaaaauuguuugu guauaacauaggaa aacacuauaggagu ugaaggugggugua ggggguguuaugaug gggugagaucagag auguauugaagggc ggggaagagacaac cauguuaaauacga cuugugaaauuuua gug	315	2.285.714	2.793.651	1.206.349	3.714.286	3.492.063	6.507.937	1.329.545	1.894.737	-81.8	-75.6	2.12E-05	58.58	-259.683	-0.74364
sly-miR169a-2	ugucuagagaguua uuguaugaagaggu agggaguggagugc agccaaggaugacu ugccgagauguugu agccuaaugcaaug acauaucggcagguc aucuuuggcuacau uuuauucucuccuau ucauguaaaacuuu auagacguauaugu au	158	2.468.354	2.721.519	1.518.987	3.291.139	3.987.342	6.012.658	1.209.302	1.625	-81.6	-81.6	0.06643	4.17	-516.456	-129.524
sly-miR169b-1	cauuugauagacaa aucuaaaauuuuug gucuauaagguuug caugaaguugaaga gagucaaguugcag ccaaggaugacuugc cggaccaaaaguug ugaccauuuucuag uuccggcaaguugu uuuuggcuauaagu uugcucucuucuucu cauguuauccucguu agaccuauuuuuucc	202	1.930.693	2.524.752	1.881.188	3.663.366	3.811.881	6.188.119	145.098	1.026.316	-73.3	-73.24	0.00086	21.53	-362.871	-0.95195

	cuauucucuacaaagag															
sly-miR169b-2	uagucuaugagguuugcaugaagaugugagagugaaguugcagccaaggaugacuugccggaccauaaauugcuaggguuuuauaguuucggcaaguuguucuuggcuauaguuugcucucuucucucaugucauccucguuaga	147	2.517.007	2.244.898	170.068	3.537.415	4.217.687	5.782.313	1.575.758	1.48	-66.5	-63.7	0.007425	12.67	-452.381	-107.258
sly-miR169b-3	uugaauagacaugucuuuauucauguuaaagucuugcaugaggaacaaggucauugaauugcagccaaggaugacuugccggcaagcucgaucaauucugcuucaugucuggcaagucauuuuuggcuacauaucugccucauuuucucaugccagauuuuuaugaaacagcuguuguuguu	184	2.065.217	2.445.652	1.902.174	3.586.957	3.967.391	6.032.609	1.466.667	1.085.714	-73.5	-68.6	0.013016	17.26	-399.457	-100.685
sly-miR169d	augagaagaggagucuaguaugaugaaaagagucuuauuugguagccaaggaugacuugucugcaccauuuccgaaauguguccuuucguucaugggguccaggcaggucaucuuuagcuaacuugacaagcucuucucuuucaugcaagacuuucucuucuucc	164	2.195.122	2.378.049	2.073.171	3.353.659	4.268.293	5.731.707	1.410.256	1.058.824	-71.9	-71.9	0.007556	9.02	-438.415	-102.714
sly-miR169e	uaggaggagaggccuuacaugaauuagaagaguuucuauuuguuuaguagccaaggaugacuugccuuucaucaaugccuuuuguaaaauggaaauugauuacaacacuuucauggauuugggaaaaugaguggcaagcau	193	2.072.539	2.694.301	1.709.845	3.523.316	3.782.383	6.217.617	1.307.692	1.212.121	-78.9	-78	0.009237	15.47	-408.808	-108.082

	cuuuggcgacuugac aaacucuucuuuguc auguuaguccaucu ucuuccu															
sly-miR169f	auuauugaagaggg guuuuauaugaagu ugagaguauuauuu aguagccaaggaug acuugccuacuucau uugauauauaguuu aaaauaauaauauu gacaauauuuguca uuuggucguaggca aguuauccuggcua ucuugacaugcucgu aauuuuucauguaa gaccuuaucuucuau ggc	188	1.914.894	287.234	1.276.596	393.617	3.191.489	6.808.511	137.037	1.5	-76.8	-74.1	0.003635	16.1	-408.511	-1.28
sly-miR169g	gguaaaagaagagu gucuuacaugaagg guaagugccuauuu gauagccaaggaug acuugccugcaucau uaauuaauucuuga ggcuagcuugugau auauaucauguaua ugacauguauacaa gcauucuucuuuga uggccaggcagucuc cuuuggcuacucgaa uagguuccucucauu caugcuagacucuuc ucuucuu	208	2.019.231	2.548.077	1.923.077	3.509.615	3.942.308	6.057.692	1.377.35 8	1.05	-82.7	-82.4	0.004952	20.96	-397.596	-100.854
sly-miR169m	aacaacaacagcugu uucauaaaaaaucu ggcaugagaaaaug aggcagauauguag ccaaaaaugacuugc cagacaugaagcag aauugaucgagcuu gccggcaagucaucc uuggcugcaauuca augaccuuguucccu caugcaagacuuua acaugaauaaagac augucuauucaa	184	1.902.174	3.586.957	2.065.217	2.445.652	3.967.391	6.032.609	0.681818	0.921053	-60.1	-55.1	0.006681	20.24	-32.663	-0.82329
sly-miR170-1	cucuaugaaauagu aacucugauauugg	112	1.428.571	25	1.964.286	4.107.143	3.392.857	6.607.143	1.642.85 7	0.727273	-31.7	-31.7	0.238476	5.81	-283.036	-0.83421

	ccugguucacucaga cacauauauuuug auugauuuuacuuu ugauugagccgugu caauaucucaguucc uuuucacuauac															
sly-miR170-2	uauuggccugguuc acucagacaacaaaa uguaaacuauauuu gaaugguugaguuu ucguuuuucguuug auugagccgugccaa uau	89	2.022.472	258.427	1.573.034	3.820.225	3.595.506	6.404.494	1.478.261	1.285.714	-32.7	-32.7	0.24661	6.11	-367.416	-102.187
sly-miR171b-1	cuaacgagauauug gugcgguucaauua gaaagcgcacuucuu uauauauagaacuu cguuauuuaauuga gccgugccaauauca cguauu	92	1.847.826	2.934.783	173.913	3.478.261	3.586.957	6.413.043	1.185.185	10.625	-42	-42	0.591447	1	-456.522	-127.273
sly-miR171b-2	gucaaaaaggauau guuugaaguugcaa agguauaucauacg agauguuggugcgg uucaaugagaaaga aguuguugaauaag uuuuugacccuacuu uuugauugagccgu gccaauaucacgugu cacuauucuguaaa uucucuuccuuuuuu uu	159	2.075.472	2.704.403	1.446.541	3.773.585	3.522.013	6.477.987	1.395.349	1.434.783	-55.1	-54	0.063395	8.77	-346.541	-0.98393
sly-miR171b-3	ugaucaacuugcga uguuggugugguuc aauuagauaacaau cuccacguaaaauua uagaguuuguuauu ugauugagccgugcc aauaucacauguaa agaaaauaac	110	1.909.091	3.363.636	1.454.545	3.272.727	3.363.636	6.636.364	0.972973	13.125	-42.6	-42.6	0.138369	4.04	-387.273	-115.135
sly-miR171c-1	uauuggugcgguuc aaugagaaagcagu acuuaagaacauuu uugagucuacuuuu ugauugagccgcgcc aauau	76	2.236.842	2.763.158	1.578.947	3.421.053	3.815.789	6.184.211	1.238.095	1.416.667	-41.2	-41.2	0.523609	1.25	-542.105	-142.069
sly-miR171c-2	ggaagaagcgaugu uggugagguucaau	99	2.323.232	2.929.293	1.818.182	2.929.293	4.141.414	5.858.586	1	1.277.778	-42.7	-39.7	0.259445	4.15	-431.313	-104.146

	ccgaagacgaauuu augcuuauuuucgu aaagaacgaucuca gauugagccgcgcca auaucacuucuuau															
sly-miR171c-3	uagagaagcgaugu uggugagguucaau cugaagacgaguuu acguuuuauuucag uaaagaacgaucuc agauugagccgcgcc aauaucauuucuuu u	100	23	28	16	33	39	61	1.178.571	14.375	-45.7	-45.7	0.228617	3.56	-45.7	-117.179
sly-miR171c-4	aauacgugauauug gcacggcucaauuaa auaacgaaguucua uauauaaagaagug cgcuuucuaauuga accgcaccaauaucu cguuag	92	173.913	3.478.261	1.847.826	2.934.783	3.586.957	6.413.043	0.84375	0.941176	-28.5	-28.1	0.473593	1.92	-309.783	-0.86364
sly-miR171f	augaugaagaagaa gacauggcgugaua uugguuuggcucac uaauuucugauucg cgaaacagauaaga gaugagccgaaccaa uaucacucuuguau ucuucuucauacc	112	2.053.571	31.25	18.75	2.946.429	3.928.571	6.071.429	0.942857	1.095.238	-54	-52.8	0.077162	7.88	-482.143	-122.727
sly-miR171i	uagauauugaugcg guucaaucugaaag acaugguuagauau guaauuagccuugu aauuuuggauugag ccgcgucaauaucuc u	86	2.209.302	2.790.698	1.395.349	3.604.651	3.604.651	6.395.349	1.291.667	1.583.333	-46	-46	0.461871	1.81	-534.884	-148.387
sly-miR172d-1	cacagucguuguuu guaaaugcagcacu auuaagauucucaa auauucugacauuu aaaaagcaauuaaa ugugaaucuugaug augcugcauuagca auaaacgacuaaa	111	1.531.532	3.783.784	1.531.532	3.153.153	3.063.063	6.936.937	0.833333	1	-42.9	-42.9	0.375882	3.68	-386.486	-126.176
sly-miR172d-10	ucauccugaauucuu uuaauucgagggga aaaagucauaauuu gucgaugcagcauca ucaagauucucauu	188	1.489.362	3.244.681	1.542.553	3.723.404	3.031.915	6.968.085	1.147.541	0.965517	-58.3	-49.7	0.002117	19.87	-310.106	-102.281

	uuugaaaaaaaaua auaauauggaauuu agaagcaacuugau uuuuuuuccuacucc auauuauuucuauu uuaugugaaucuug augaugcugcagcu gcaaauaacgacug uac															
sly-miR172d-2	uugaaacucacgag aaucuugaugaugc ugcaucagcaauaa acgacuauugcaau uagagcauugcaac gauacagaaaaaau uaauacgacaugaa uuaaggaaugaucu auauauuucuuaga ucgggaacuuguaa guauacuuccuaguc cuuuauucguauga aucuauauuuucug gaacuuuuucaugu ucuuguagcugaau uucauuguuguuaa ucuguuuuuucaag auagagcuacugaa uuuagauucucuua guuuuau	274	1.605.839	310.219	1.459.854	3.832.117	3.065.693	6.934.307	1.235.294	1.1	-61.4	-50	0.00035	49.29	-224.088	-0.73095
sly-miR172d-3	cuagugcagcaccau uaagauucacauag aaaauauggaacga aauuugcucaauuu uucaauauaugaga aucuugaugaugcu gcauuggc	93	1.827.957	344.086	1.612.903	311.828	344.086	655.914	0.90625	1.133.333	-35.8	-35.8	0.22104	6.87	-384.946	-111.875
sly-miR172d-4	uacagucguguuu gcauauguggcaua aucaagauucacgu gaaaaguugcaaau ugguuauauaauug augaaauuaauggc uggcuauuugaaac ucacgagaaucuug augaugcugcauca gcaauaaacgacua uu	142	2.042.254	3.309.859	1.408.451	3.239.437	3.450.704	6.549.296	0.978723	1.45	-55.2	-54.3	0.020854	15.42	-388.732	-112.653
sly-miR172d-5	caauguuugaggau	164	1.707.317	3.292.683	1.341.463	3.658.537	304.878	695.122	1.111.11	1.272.727	-53.3	-45.37	0.013514	22.31	-32.5	-1.066

	gcaacaucaucaaga uucacaaaacuuga agggagaaguauuu aauuauauauuuag ggugaauauuggau auauaauauaguuc aaagucucuuauuu ucucucuuugggaa ucuugaugaugcug caucaucuaacauau gacucuau								1							
sly-miR172d-6	uugacacauguaca gucguuauuugcag cugcagcaucaucaa gauucacauaaaau agaaauaauaugga guaggaaaaaaaau caaguugcuucuaa auuccauauuauua uuuuuuuucaaaaa ugagaaucuugaug augcugcaucgacaa auuaugacuuuuuc cccucgaauuaaaag aauucaggaugauc ucgacuuuacuauu uauuuuugguaagu augcaauuuggacu uugacuu	248	1.532.258	3.387.097	1.491.935	358.871	3.024.194	6.975.806	1.059.524	1.027.027	-68.2	-57.3	0.000181	36.09	-27.5	-0.90933
sly-miR172d-7	ugcagaugcagcauc uucaagauucacau agauuuauauaaaa uauagaguuccaug uuuggggugaaagu aauuaauuaauuaa uuaauuuucuccua uauauuggcucuau ugauuauuauuugu ugugagaaucuuga ugaugcugcagcggc aaugaauggc	166	1.927.711	3.072.289	1.204.819	3.795.181	313.253	686.747	1.235.294	1.6	-58.8	-58	0.014706	14.43	-354.217	-113.077
sly-miR172d-8	agucaauuuuuugc gggugagcaucau caagauucacauagc uauauuagggcuuu uauaauuuuuaaaa acccuacgggcgaug ugugggaaucuuga	126	2.380.952	2.857.143	1.587.302	3.174.603	3.968.254	6.031.746	1.111.111	1.5	-57	-50	0.01173	10.97	-452.381	-1.14

	ugaugcugcagcggc aaauaaugacu															
sly-miR172d-9	uuuagucguuuauu gcuaaugcagcauca ucaagauucacauu uaauugcuuuuuaa augucagaauauuu gagaaucuuaauag ugcugcauuuacaa acaacgacugug	111	1.531.532	3.153.153	1.531.532	3.783.784	3.063.063	6.936.937	1.2	1	-37.7	-37.7	0.147351	5.22	-33.964	-110.882
sly-miR172j-1	uuugccgcugcagca ucaucaagauuccca cacaucgcccguagg guuuuuaaaaauua uaaaagcccuaaua uagcuaugugaauc uugaugaugcuccac ccgcaaa	109	1.651.376	3.027.523	2.568.807	2.752.294	4.220.183	5.779.817	0.909091	0.642857	-46.1	-45.1	0.173853	3.7	-422.936	-100.217
sly-miR172j-2	uagagucauauguu agaugaugcagcau caucaagauucccaa agagagaaaauaag agacuuugaacuau auuauauauccaau auucacccuaaauau auaauuaaauacuu cucccuucaaguuuu gugaaucuugauga uguugcauccucaaa cauugacugau	169	1.360.947	3.609.467	1.715.976	3.313.609	3.076.923	6.923.077	0.918033	0.793103	-54	-54	0.111992	14.01	-319.527	-103.846
sly-miR1886a	acguugucuucaauc uucucacugacugag uaggcguuugacca ugggauaucauauc acgauaugguaucg ugagaugaaaucag cguuuggacauuug auuucacguugauu ccaucucaugauucc augaguugagagca uuccaacucgcauac ucagacauucaaug uacugaugucaauu g	187	2.032.086	2.620.321	2.032.086	3.315.508	4.064.171	5.935.829	1.265.30 6	1	-57.2	-38.6	0.001123	49	-305.882	-0.75263
sly-miR1886h-1	uaugguaucgugag auggaaucagcguu uggacauguaauuu uacguugauuucau	71	2.112.676	2.535.211	1.267.606	4.084.507	3.380.282	6.619.718	1.611.11 1	1.666.667	-33.4	-33.4	0.266164	3.37	-470.423	-139.167

	cucaugauuucaua u															
sly-miR1886h-2	gccaugagauaccgu aucguggccuuuggc caugagauaucaua ucacgauaugaaau cgugagauugaauu cguguuuggacaua uaauuuuacguuga uuucaucucaugau uucauauaaugaga ugugauuucguauu cuccaaaaaucauga uaugagaauuucau auc	174	183.908	2.988.506	1.551.724	362.069	3.390.805	6.609.195	1.211.538	1.185.185	-58.6	-50.17	0.005782	41.96	-336.782	-0.99322
sly-miR1917-1	aaaauuaacuuuua gcggcauuaaauau ugacauuaauaaag agugcuaaagucuu uaccgacauuaguu agugucauuagaac caaugucgcuaaag gcuuuauggacaua uacaaagagugaca agugccgcuaaaaa uucauauu	148	1.689.189	3.783.784	1.486.486	3.040.541	3.175.676	6.824.324	0.803571	1.136.364	-41	-39.8	0.019519	12.11	-277.027	-0.87234
sly-miR1917-2	ucucuacaauaaaa auaacuuuuagcgg caauaaauagauac auuaauaaagagug cuaaagucuuuaccg gcauuaguuaagug ucauuagauccaau gucgcuaaagccuuu agugacacauacaa agagugcuuauuua gcggcaauugcuaa uuaauugccgcuaa agcucauuuuuaau guagugu	191	1.675.393	3.455.497	1.623.037	3.246.073	3.298.429	6.701.571	0.939394	1.032.258	-53.1	-50.8	0.001477	31.8	-27.801	-0.84286
sly-miR1918	guagcucaguuggu uuaauuaguugaau ugucauuuuguugg ugagaguucgauuc uccauuacgcaaucu ccucuucaauuuaag agaaaaagauaugc uacaagguggagaa	166	1.927.711	3.253.012	1.626.506	3.192.771	3.554.217	6.445.783	0.981481	1.185.185	-69.6	-68.9	0.033946	9.15	-419.277	-117.966

	ucgaacuaccgcuaacagaauggaaguucaaauacuuaaucaauuaagcuac															
sly-miR1919a-1	uccgaaucgcuccgacgccuuugauguucacaucuuccgguagucugucgcagaugacuuucgcccauuuauagaaccacacuuucuuuaauuugaauucuaugugguaggacgagagucaucugugacaggauaauggaagaucgaguuaucaaaggcuuauugggcguuuccuu	177	220.339	2.316.384	220.339	3.276.836	440.678	559.322	1.414.634	1	-82.8	-78.1	0.030296	16.5	-467.797	-106.154
sly-miR1919a-2	gacgccuuugauguucacaucuucgguaguccugucgcagaugacuuucgcccuucuaaggaaccacacuuucuguaaaucuaauuaauuugaauucaaugugcaggacgagagucaucugugacaggauaauggaagaucuaguuaucaaaggcuua	160	21.25	27.5	20	31.25	41.25	58.75	1.136.364	10.625	-68.6	-67.7	0.03108	12.76	-42.875	-103.939
sly-miR1919a-3	ccgacgccuuugauguucacaucuuccgguaguccugucgcagaugacucucgaucuuguccauuaagccccuuucucuaagucuaauuaauuugaauucaaugugguaggacgagagucaucugugacaggauuauggaagaucgaguuaucaaagggcguuuu	164	2.256.098	2.378.049	2.073.171	3.292.683	4.329.268	5.670.732	1.384.615	1.088.235	-76.5	-76.02	0.005935	14.58	-466.463	-107.746
sly-miR2101	uucauuucauuaugugcaucacuugaggcuggccucauucuuucauugguaaauuuaacucaagugagcaucaugaaaucca	82	1.585.366	2.682.927	2.073.171	3.658.537	3.658.537	6.341.463	1.363.636	0.764706	-23.6	-23.6	0.482662	3.51	-287.805	-0.78667
sly-miR2111a	ugguaaucugcaucc	71	2.112.676	2.535.211	1.690.141	3.661.972	3.802.817	6.197.183	1.444.44	1.25	-36.5	-36.5	0.228867	2.13	-514.085	-135.185

	ugagguuuagauca auuuauaacuuacu ggaucuaguccuug ggaugcagauuauc								4							
sly-miR2604	ugugugugugauaa uauauauauauugg guuugcuagaacac acccacuaauuuuua uguggaaguguuuu agcaaagcuacaccu uaaggugauuuaa cuacuuuuuaguua uucacuugcuaaaa uacucuuucuaaaa aauaaguggugua uccuagcaaaugccu auaggauuugcuag aauucacccacuug	199	1.708.543	2.964.824	1.557.789	3.768.844	3.266.332	6.733.668	1.271.18 6	1.096.774	-69.4	-66.3	0.0076	28.58	-348.744	-106.769
sly-miR319-1	gaugggauaaggaa ggaaauucaucagu ccaaacaagguggu auauuugggcugau cuuugcugcugaauc auugguucaucaac auauuauacacaua caaggauauauaca uauguuguugcauc aaugaugcaggagc ugaguucaguuuug gcuaccuuuucuugg acugaaggguuucc uucucaaccccaa	197	2.182.741	284.264	177.665	319.797	3.959.391	6.040.609	1.125	1.228.571	-87	-85.3	0.069127	7.08	-441.624	-111.538
sly-miR319-2	aaggaaacuguuua guccaacccaaggug ggguauuggaacug aucuuugcugcuga aucauuggcucaug agcaugucaaagaa gaugauugaacauu cuggacauguucuu gcuccaaugaugcag gagcugagcucggu uuuucaccgccuuuu cuuggacugaaggg uuuccuuc	179	2.513.966	2.346.369	2.011.173	3.128.492	452.514	547.486	1.333.33 3	1.25	-87.2	-86.4	0.039016	6.34	-487.151	-107.654
sly-miR319a-1	gaaaauaaggagcu cucuccgguccaguc cgaggcacucaaagg	187	2.352.941	2.887.701	2.032.086	2.727.273	4.385.027	5.614.973	0.944444	1.157.895	-82.3	-77.1	0.035147	22.95	-440.107	-100.366

	cuaaaaacacagcug acgacucguugauuc ucaaacauaucaag aagcauuuuuugaa auuggugugguuuaa gauucaacgaugcg ugagcuauguuugg cuagcguugucacgu cuuggacugaaggg agcucccuauuaaa															
sly-miR319a-2	augguauaagagag cuuccuuuaguccac ucauagguagacga aggauuugaauuau cucccgacucauuca uucaaacgcaauag gaaguauguaaucu uauacuauugugaa ugugugaaugaugc gggagauaaauucu cuccuuuuuaucugu gcuuggacugaagg gagcucccuuuuacc uuc	189	2.063.492	2.698.413	1.851.852	3.386.243	3.915.344	6.084.656	1.254.902	1.114.286	-93	-92.3	0.016253	9.9	-492.063	-125.676
sly-miR319c-1	uaggagcuccuuuca agccaagaccgaggg acgaggagcggcaa gagcugccuagucau gcauauugguuaac cuuaacaaacaaau uauguauaguguua agauuaaccaguug cauggcaagggagc aacuacuuccgcuaa cuugucucacuuauu ggacugaagggagc uccu	177	2.429.379	2.937.853	2.146.893	2.485.876	4.576.271	5.423.729	0.846154	1.131.579	-88.9	-88.9	0.077301	5.76	-50.226	-109.753
sly-miR319c-2	caagagagcuuccuu cagcccacucacgga ggagaaaugggguu gaauuagcugccgac ucauucauccaacca cucaguagaaagga uagguuuugugcua cugugauugaguga augaugcgggagau aguuuucuaucccuc ucuuuccuugcuugg	177	2.542.373	2.372.881	220.339	2.881.356	4.745.763	5.254.237	1.214.286	1.153.846	-76.6	-65.4	0.013492	17.41	-432.768	-0.9119

	acugaagggagcucc uu															
sly-miR319c-3	agagcuuucuuuag uccacacauggggaa cgauaggguucaau uugcugccgacucau ucauccaaauguug aggucuugauaauc gagugccaccucagc aacugagugaauga agcgggaguacaag uugagucuugagcu uccuguacuuggacu gaagggagcuccc	171	2.631.579	251.462	2.163.743	2.690.058	4.795.322	5.204.678	1.069.767	1.216.216	-81.6	-75.1	0.053658	11.65	-477.193	-0.99512
sly-miR3627	gagagagauugagg gaaucuugucgcag gagagauggcacuu gccauuccuuuuaau ugguacaaugccua aauggaaccaauua agugccucugucuuu cgacacgaugcucac aauuucuauu	125	22.4	27.2	20	30.4	42.4	57.6	1.117.647	1.12	-47.3	-47.3	0.120122	5.38	-37.84	-0.89245
sly-miR390a	ugcauggagaaucu guaaagcucaggag ggauagcgccaugg augacucaauucga uuuuuguacacauc uuuagcgcuauccau ccugaguuucacggc uuuuucaugc	110	2.272.727	2.363.636	2.181.818	3.181.818	4.454.545	5.545.455	1.346.154	1.041.667	-55.8	-55.8	0.573051	1.42	-507.273	-113.878
sly-miR390b	ggcauggggaaucu auaaagcucaggag ggauagcaccauga auacaucuuaaugg cuaucuauagcgcua uccauccugaguuu auggcuucuucaugc uc	103	223.301	2.621.359	2.135.922	3.009.709	4.368.932	5.631.068	1.148.148	1.045.455	-50.9	-50.4	0.094194	7.05	-494.175	-113.111
sly-miR393a	uuccaaagggaucgc auugauccuguguu ccaaauuaauuaacc augggacuauggga ucaugcgaucucuuc ggaau	78	2.179.487	2.692.308	2.051.282	3.076.923	4.230.769	5.769.231	1.142.857	10.625	-39.4	-39.4	0.178529	2.76	-505.128	-119.394
sly-miR394a	guagagccauuuug gcauucuguccaccu cccagcuugcugagg	81	2.839.506	2.222.222	2.716.049	2.222.222	5.555.556	4.444.444	1	1.045.455	-43.1	-42.8	0.246535	3.22	-532.099	-0.95778

	acugaggagggggc caaagugccaaacua gcucugca															
sly-miR394b	agaugaagaaaaaa aauaugaagauuaa uuaguuucacggag guuugacaaagggu uucuuacagaguuc auuggcauucugucc accucccucguucuu uuuucgagaaaaaa agaagaagggggga agcaagauuuagug uggaggugggcaua cugccaauagagcug uguuggguuucucuu uguaaaacccucgug auacacgucaagua agauagagagugau uugaucg	235	2.553.191	3.106.383	1.446.809	2.893.617	40	60	0.931507	1.764.706	-81.4	-75.77	0.005067	29.15	-346.383	-0.86596
sly-miR395a-1	ugcugaaguguuug ggggaacucuugga cucacuuugaaauu uuacacaaacaaau agaaguguaggagu ccuggcuauggaug augaacaugauagu ucauguauaaaucu auuaaggugauccc uagaguucacuuga ccacuucauga	151	2.251.656	3.046.358	1.589.404	3.112.583	384.106	615.894	1.021.73 9	1.416.667	-49.2	-48.9	0.072932	12.8	-325.828	-0.84828
sly-miR395a-2	gaugcucugcugaa guguuuggggaac uccugggcucacucu gaaauuuuaugcaa auuaaaccaauaga aguguuggagugcu gguuguggaugaua aacaugauaguuca cguauaaaucuauc gagguguuccguag aguuuccuugaacac uucaugagggcuua	170	2.588.235	2.647.059	1.588.235	3.176.471	4.176.471	5.823.529	1.2	162.963	-60.7	-60.7	0.098269	12.98	-357.059	-0.85493
sly-miR395a-3	cuaucaagguguucc cuagaguucccuuga ccgcuucauuugggc uuacuucauuguuu gaugcccugcugaag	107	2.336.449	1.775.701	2.242.991	364.486	4.579.439	5.420.561	2.052.63 2	1.041.667	-50.1	-50.1	0.20452	5.59	-468.224	-102.245

	uguuuggggaacu cuuggacucacuuug aaau															
sly-miR395a-4	auaaaucuaucaag guuguucccuagag uuuacuugaucacu ucaugagggcuuac uuugauauuagaag ucuugcugaagugu uuggggaacuccu ggguuuacuuugaa aauuacgcaaacaa guauauauaaaugc augaugaguacgua uuagcuagagauga ugaauacaauauug auucacguauaaaa cuaccucuggaguuu ccuugaccacuuuau gagagcuuaauauu ucauuguuugaagu ccugcugaagugu ugagggaacauucg aauccacuuugaaa auuaca	302	1.986.755	3.046.358	1.523.179	3.443.709	3.509.934	6.490.066	1.130.435	1.304.348	-80.6	-80.3	0.000406	54.7	-266.887	-0.76038
sly-miR395g	augcccuguugaag uguuuggggaacu cuuggacucacuuug aaauuuuacacaaa caaauagaagugua ugaauccuggcugu ggaugaugaacaua auaguucacguaua aaucuauuaaggug uucccuagaguuccc uugaccacuucauga gggcuu	163	2.208.589	2.822.086	1.779.141	3.190.184	398.773	601.227	1.130.435	1.241.379	-61.5	-61.5	0.089717	14.41	-377.301	-0.94615
sly-miR396a	aagaaaugguccuu uuuguguuuuucca cagcuuucuugaacu gcaucuacaauuuca auucauuauugaaa aagaaaaaauugau ucauauuguuguug cgguucaauaaagc ugugggaagauaca gauagggucaaaua ga	144	18.75	3.333.333	1.319.444	3.472.222	3.194.444	6.805.556	1.041.667	1.421.053	-57.4	-54.21	0.041265	14.37	-398.611	-124.783

sly-miR396b	agucaugcuuuucca cagcuuucuugaacu ucuucuugcuaaau uuugaucucuaaau ugauaauuuugaga ugagauuugaagcu augaaaguccaaga aagcugugggaaaa gauggcaa	122	1.967.213	3.114.754	147.541	3.442.623	3.442.623	6.557.377	1.105.26 3	1.333.333	-49	-45.6	0.008986	16.78	-401.639	-116.667
sly-miR396g-1	aguccaaagcuugcc aucuuuucccacagc uuucuuggacuuuc auagcuucaaaucuc aucucaaaauuauc aauuuagagaucaa aauuuagcaagaag aaguucaagaaagc uguggaaaagcaug acuaggacuuggguc a	144	1.666.667	3.402.778	2.013.889	2.916.667	3.680.556	6.319.444	0.857143	0.827586	-51.2	-50.7	0.03314	10.36	-355.556	-0.96604
sly-miR396g-2	gacccuaucuguauc uucccacagcuuuau ugaaccgcaacaaca auaugaaucaauuu uuucuuuuucaaua augaauugaaauug uagaugcaguucaa gaaagcuguggaaa aacacaaaaaggacc	130	1.461.538	3.692.308	1.923.077	2.923.077	3.384.615	6.615.385	0.791667	0.76	-35.3	-34.3	0.027803	16.13	-271.538	-0.80227
sly-miR397-1	uuauugcagaguac uuagaaacaugauu gagugcagcguuga ugacauauuugaga aguccugcauuugg gccuuccucauuuuu caucaacgcuaaacu cgaucauguuuuua auucucugaaggg	127	2.047.244	2.598.425	1.811.024	3.543.307	3.858.268	6.141.732	1.363.63 6	1.130.435	-56.5	-56.1	0.067727	7.06	-444.882	-115.306
sly-miR397-2	cccuucagagaauua aaaacaugaucgag uuuagcguugauga aaaaugaggaaggc ccaaaugcaggacuu cucaaauaugucauc aacgcugcacucaau cauguuucuaagua cucugcaauaa	127	1.811.024	3.543.307	2.047.244	2.598.425	3.858.268	6.141.732	0.733333	0.884615	-48.9	-48.9	0.06417	8.93	-385.039	-0.99796
sly-miR398a	ggguugauuugaga	90	1.888.889	2.666.667	1.555.556	3.888.889	3.444.444	6.555.556	1.458.33	1.214.286	-34.2	-32.3	0.030062	15.31	-38	-110.323

	acauauguaugugc auauuuuguuugua acaauuuaccguuu auaaauaugacaca uauguucucagguc gccccu								3							
sly-miR398b	gguauucaacaggg gcaacuugagaucac auguugucauuuuu uucuuuuugauuug auucgaugaaucag uaucucaacaugug uucucagguuacccc uguugaauuag	111	1.981.982	2.342.342	1.711.712	3.963.964	3.693.694	6.306.306	1.692.30 8	1.157.895	-50.6	-48.5	0.160171	11.42	-455.856	-123.415
sly-miR399a-1	uggggaguaagaaa uaacagugcaauuc uccuuuggcaaaug aauaugcaaacccua uauauauauauaua uauauauguuuugc auacacauuauauu aucuuugccaaagg agaauugcccuguca uucuucuccucg	140	15	3.214.286	1.785.714	35	3.285.714	6.714.286	1.088.88 9	0.84	-62.6	-53.3	0.018557	19.05	-447.143	-136.087
sly-miR399a-2	cgaggagaagaaug acagggcaauucucc uuuggcaaagauaa uauaauguguaugc aaaacauauauaua uauauauauauaua ggguuugcauauuc auuugccaaaggag aauugcacuguuau uucuuacucccca	140	1.785.714	35	15	3.214.286	3.285.714	6.714.286	0.918367	1.190.476	-66.5	-66.5	0.050702	8.41	-47.5	-144.565
sly-miR399a-3	uuauaagcgaaaca gugauagggcuacu cucuauuggcaugca auuguauauuucag cugacacgccaaagg agagcugcccuguua cugucucugcuuaau c	103	2.135.922	2.621.359	223.301	3.009.709	4.368.932	5.631.068	1.148.14 8	0.956522	-50.3	-50.3	0.501836	1.86	-48.835	-111.778
sly-miR399a-4	gaaaacuagauuuu guaaaugaaaauau auucuugaauuugu aagggaaacaguga uagggcuacucucua uuggcaugcaauug	323	1.795.666	2.910.217	1.733.746	3.560.372	3.529.412	6.470.588	1.223.40 4	1.035.714	-83.1	-77.9	6.37E-05	57.13	-257.276	-0.72895

	uauauuucagcuga cacgccaaaggagag cugcccuguuacugu cucugcuuaaucuac augcccuucggguac ucuuaauacagugu gauguccugaagcu auuauuccacuuuuc guagugaaucguug ugucucauguuauu ccaaauacuaagucu guuuacuuuguugu gaacccaccaauuca uuugaaugugaaua uucaaauguacauu uaaauuuaaagagc aguuaua															
sly-miR399a-5	ugaugaagcggaag caugagaaaggaag ucguuggugaauga aaauaagggaaaua gugauagggcuacu cucuauuggcaugcg uuaauauauguaca gugacuccaauucac uguaucgcauauuu uaaccgauacgccaa aggagagcugcccug cuacugucucugcuu aauauaauaacuca aagauccguucuua auacuccgaugcaga a	217	2.211.982	3.225.806	1.843.318	2.718.894	40.553	59.447	0.842857	1.2	-71.1	-70.7	0.001599	15.72	-32.765	-0.80795
sly-miR399d-1	aguuauguguggau gcauuacugggcua aucuucuuuggcaa auaauuucacuauu auuuggugcaaauu uggucauuuauugc caaagaagauuugc cccguaaaucauuca uacaauauua	123	1.707.317	2.926.829	1.544.715	3.821.138	3.252.033	6.747.967	1.305.556	1.105.263	-50.4	-48.7	0.072031	15.36	-409.756	-1.26
sly-miR399d-2	aaaaucaauugguc aagugagacuucaa guuauguguggaug cauuacugggcuaa ucuucuuuggcaaa uaauuucacuauga	171	1.871.345	3.040.936	1.520.468	3.567.251	3.391.813	6.608.187	1.173.077	1.230.769	-56.8	-56.8	0.018955	16.14	-332.164	-0.97931

	uuuggugcaaauuu ggucaucuauugcca aagaagauuugcccc guaaaucacucauac auuuuaagaguauc uuugaauugauaug															
sly-miR399d-3	aacagugauagggc uacucucuauaggca uaugccguuuaucac acauuacagcugaca cgccaaaggagagcu gcccuauuacugucu	89	2.022.472	2.808.989	258.427	258.427	4.606.742	5.393.258	0.92	0.782609	-36.9	-36.9	0.514396	4.21	-414.607	-0.9
sly-miR399i-1	uuauaagagaaaca gugguagggcuacu cucuauuggcaugca cuuauauauuuaaa cugacaugccaaagg agagcugcccuguua cugucucugcuuaau g	103	2.135.922	2.815.534	1.941.748	3.106.796	407.767	592.233	1.103.44 8	1.1	-47.8	-47.8	0.232477	5.51	-464.078	-11.381
sly-miR399j-2	ggaaaauuauacua aauauguuauuauu ggugugcuuauuaa gugaaacaguugua gggcaauucuccguu uggcagauauauga uuaugaauguaauc ugccaaaggagagu ugcccuaugauugcc ucugcuuaauuaug uuua	146	2.123.288	2.945.205	1.232.877	369.863	3.356.164	6.643.836	1.255.81 4	1.722.222	-60.2	-57.9	0.029245	7.56	-412.329	-122.857
sly-miR399j-3	agggcuacacucuau uggcaugcaacuug aucaaauauuugag cugaaaugccaaag gagaguugcccua	70	2.285.714	3.142.857	20	2.571.429	4.285.714	5.714.286	0.818182	1.142.857	-29.2	-29.2	0.482753	2.04	-417.143	-0.97333
sly-miR403	ucaggaagaggcau auuucacguuugug cgugaaucuaacaac ucuuuucaucugaa aaacuguuauuguu ugcuagauucacgca caagcucguaauau ggcuuuuccaau	112	1.785.714	2.767.857	1.964.286	3.482.143	37.5	62.5	1.258.06 5	0.909091	-44.5	-41.8	0.050983	8.89	-397.321	-105.952
sly-miR403a	auuggaaaagccau auuacgagcuugug cgugaaucuagcaa acaauaacaguuuu	112	1.964.286	3.482.143	1.785.714	2.767.857	37.5	62.5	0.794872	1.1	-42.5	-41.2	0.093861	9.01	-379.464	-10.119

	ucagaugaaaagag uuguuagauucacg cacaaacgugaaau augccucuuccuga															
sly-miR408-1	aaaaggaaggauug uggggagaggagag ccagggaagaggca gugcauggaauagg caaagcaaaaauug cacaucucaugcucu ggcucgucccgucu auccauaccacacca auuuuuaccucaa	128	2.578.125	3.203.125	2.265.625	1.953.125	484.375	515.625	0.609756	1.137.931	-46.9	-41.7	0.028077	9.09	-366.406	-0.75645
sly-miR408-2	uauggauagacggg gacgagccagagcau gagaugugcaauuu uugcuuugccuauuc caugcacugccucuu cccuggcucuccucu	88	2.386.364	1.818.182	2.727.273	3.068.182	5.113.636	4.886.364	16.875	0.875	-36.5	-36.5	0.528477	1.94	-414.773	-0.81111
sly-miR408a	acagggacgaggca gcgcaugagaugua caauuuuauuaguu guccauuccaugcac agccucuucccuggc	72	2.361.111	2.361.111	2.638.889	2.638.889	50	50	1.117.647	0.894737	-37.3	-35.8	0.71327	0.93	-518.056	-103.611
sly-miR437	uauaguguucuuuu ccaaacaagacauua uuuacaauggaacu aagguauuuggaaa cacauguaaaguua gagauguuugacuu ucuauuaccaaguu ggauccccaaggcauu gaagugugcucuuu ugggauauucuugc uuuaaaaaggggua ucgauguuguuaua cuaaacuuggaaaa uauaugguaucaca ugauguggguauuuc auguuuggggcaga cacugga	233	2.188.841	3.004.292	1.287.554	3.519.313	3.476.395	6.523.605	1.171.429	1.7	-57.4	-46.45	2.47E-05	48.13	-246.352	-0.70864
sly-miR4376	aaaaggcuugcuac gcaggagagaugau gcuggacgauagag aaaaugggauuuaa uuuauuggccagca ucauacuccugcaua uuaagccuaaa	96	2.395.833	34.375	1.666.667	25	40.625	59.375	0.727273	14.375	-46.5	-46.5	0.293278	3.56	-484.375	-119.231

sly-miR477	agcuaggcauugcu uguugucucucccuc aagggcuccucuuca agauccuuauaaac aagaaagcaugagg gggaggaguucuug uagggugagacaac aagaaauuccuugc	114	254.386	2.719.298	2.105.263	2.631.579	4.649.123	5.350.877	0.967742	1.208.333	-57	-56.5	0.1357	7.35	-50	-107.547
sly-miR477a	gccucucccucaagg gcuucucuccugcau gcuuuuuauguugg gaaagaagcucuag cagggagagcca	70	2.571.429	20	2.714.286	2.714.286	5.285.714	4.714.286	1.357.143	0.947368	-35.8	-34.4	0.125649	3.54	-511.429	-0.96757
sly-miR477b	cacucucccucaaag gcuucuggcuuaaa augccuuuugugcu aaugcuagaggucu uucgagugagagug a	72	2.361.111	2.222.222	2.222.222	3.194.444	4.583.333	5.416.667	14.375	10.625	-35	-29.8	0.189934	4.51	-486.111	-106.061
sly-miR482a-1	guugaaagggauga gaguauugggaagu uguugguugugggu gggguggaaagauu ugauaaaucuaauu uuaaagagauuaaa ucuuuccuacuccuc ccauacccaugacuu ccacuagcuucuccc uuucuuc	136	2.279.412	25	1.764.706	3.455.882	4.044.118	5.955.882	1.382.353	1.291.667	-62.7	-62.6	0.019361	10.29	-461.029	-1.14
sly-miR482a-2	gaaaaucuaugggg auuggugaguugga aagcuuuucuuuuu cuucucuugugauu agcuuuccaauucca cccauuccuaugguu uuucg	91	1.978.022	1.868.132	1.868.132	4.285.714	3.846.154	6.153.846	2.294.118	1.058.824	-42	-42	0.361411	1.97	-461.538	-1.2
sly-miR482c	ggaaagggaggagg gauuugggaaucuu uuggaugggugggg auggaaaaauauug uauuuuuuuuucua acggaaaaaaagau gagaauugagauuu uuccuauuccaccca ugccaauggcuucca gucauuuacuccuuu uc	145	2.482.759	2.758.621	137.931	337.931	3.862.069	6.137.931	1.225	1.8	-59.1	-54.5	0.008533	15.09	-407.586	-105.536
sly-miR482d	gauuuuugggaagc	111	2.432.432	2.522.523	1.891.892	3.153.153	4.324.324	5.675.676	1.25	1.285.714	-50.8	-50.4	0.040436	8.57	-457.658	-105.833

	uuuuggcgugagcg gugggaaagauag aucuaucauauuag uaugauaugauaaa ucuugccuacaccgc ccaugcccauggcuu ccaaugauuuc															
sly-miR482e	uaggaaauagaaag gggaugaguguuuc gaggaggugugga gugggugguguggu aagauuucauauuu auuuuccauaaaaa uugagaucuugcca auaccgcccauuccu auggcuucugauca uuucucucuuuccuu uuucuuc	149	2.348.993	2.281.879	1.610.738	3.758.389	3.959.732	6.040.268	1.647.059	1.458.333	-67.6	-64.9	0.011285	24.78	-453.691	-114.576
sly-miR5014a	gauuaugaccuuua acuuuagaugugua caaguagacaguua aacuuguauaaaau ugagcaaaugaaca cauuugucauacau gauacugcuacaug auaacuuugucuccu acaugacauucuacg uguauuaugucauu uaggacacuugugu cuacuuuuucaaucu uguacaaauuuaag uguauacuugugua cauucaaaguugaa ggacauaguu	223	1.569.507	3.183.857	1.524.664	3.721.973	309.417	690.583	1.169.014	1.029.412	-79.1	-76.9	0.005739	10.21	-354.709	-114.638
sly-miR5174d	ucccuccguuucaaa aagauuggccuagu uugacuuggaacgg agcuuaagaaaaga aagaggacuuuuua aucuuaugguucua auuuaaaguuaugu uuaauguaccaaau uacccuuuaaucuug uggucuuaaacaug ccacguggaaaguu aaaguuaaaguguu accaaaaaaggaaa gggucauucuuuu	248	1.975.806	3.467.742	1.370.968	3.185.484	3.346.774	6.653.226	0.918605	1.441.176	-64.5	-58.15	0.000128	45.76	-260.081	-0.77711

	ugaaacaaacuaaa aaggaaauaggguc auucuuuuugaaac gggaguau															
sly-miR5282	caaaauuagcgagg gaaauuagugacgg aaaaaaugaaauuc cuuacaaauuccuug gucgcaaaauuuaa ugacggaauuagag agggauuuuacguu uuccuucacuauauu ucccucacuaaauu	128	171.875	3.515.625	1.640.625	31.25	3.359.375	6.640.625	0.888889	1.047.619	-50.9	-50.3	0.200969	3.29	-397.656	-118.372
sly-miR530	aucugcauuugcacc ugcaccuuagugaac gaauuaguucgcgu auaauucgugcaga aagguguaggugu u caugcagaca	82	2.439.024	2.682.927	195.122	2.926.829	4.390.244	5.609.756	1.090.90 9	1.25	-42.9	-42.9	0.530459	1.33	-523.171	-119.167
sly-miR5300	uugaccaaaauucu ucuuccccaguccag gcauuccaacaguug auaacaucuagauc ugccaauacuuugu auuuuuguucuucu auuuuucacaugac aucuucaaaaucuac uaugagcuucauca uaagcuaagaaaug gugaguuuugauga ugugaugccuaaaa uaggauuaaaugaa aguacuaguaaaaa gguguucagaucug gagguuauguuaag cuggugguaugcuu ugauugggaaagau gacuuagguca	266	1.954.887	3.007.519	1.578.947	3.458.647	3.533.835	6.466.165	1.15	1.238.095	-98.2	-95.8	0.003226	14.73	-369.173	-104.468
sly-miR5303	uugcuaaguugcuc gaacucuccaaaaau gucgcugcaccugug ugggauccucaaaa auacacuauuuuug gaggauccgacucgu acccgucgacauuuu ugaagaguucgagc aacauagauu	126	2.063.492	2.698.413	2.301.587	2.936.508	4.365.079	5.634.921	1.088.23 5	0.896552	-63.6	-63.6	0.099102	5.84	-504.762	-115.636
sly-miR5303c	ucauaaguuuaagu	136	2.058.824	2.794.118	2.426.471	2.720.588	4.485.294	5.514.706	0.973684	0.848485	-45.6	-43.9	0.005348	19.78	-335.294	-0.74754

	ugcgcggacucuuca auguagaugccgcac ucgugccugaucucc aaaaauaugcuacu uuuggagaauccga cacgcacccacugac auuuuugaagaguc cgagcaacauaacug uaggu															
sly-miR5303f	gaauuauguugcuc ggacucuucaaaaa ugucaaagggugug ugucggauucgccaa aaguaguguauuuu uggagaaucugaca cgggugcggcaucaa aagugaagaguccg cgcaacuaagcu	126	2.777.778	2.857.143	1.746.032	2.619.048	452.381	547.619	0.916667	1.590.909	-58.2	-56.4	0.085032	5.31	-461.905	-102.105
sly-miR5303g	auggaaugacuaug uugcucagacucuau aaaucaugucagau ccuuuauaaguccgc aacuuuuagagggg auuagacacucauuc auugauauuuuuga agagucugagcaac guaacauaucagg	128	1.953.125	31.25	171.875	3.203.125	3.671.875	6.328.125	1.025	1.136.364	-43.6	-40.7	0.039985	19.96	-340.625	-0.92766
sly-miR5303h-1	aagcaguaugcugc ucagacucuccaaaa auguugccacaccug uaucguauccuucgg acaggcacuacuuuu ggaggaucgaacaa gcaccugacaacauu uuugaagagucuga gcaacauagugaag	131	2.137.405	3.053.435	2.366.412	2.442.748	4.503.817	5.496.183	0.8	0.903226	-58.3	-55.6	0.13419	4.35	-445.038	-0.98814
sly-miR5303h-2	ggccuuuguugcucg gacuauccaaacaug uuguccccaccagugu uagauccuccaaaaa uguguaauuggaag auucgucacacaccu ucaaacauuuuuga agagucugagcaac auagacu	124	1.854.839	2.903.226	233.871	2.903.226	4.193.548	5.806.452	1	0.793103	-39	-38.9	0.08486	8.42	-314.516	-0.75
sly-miR5303j-1	acacagcagcaauuu uuguguuuuuuaaa aaaauuaacaaguc	216	1.574.074	337.963	1.666.667	337.963	3.240.741	6.759.259	1	0.944444	-53.9	-47.1	0.00238	36.67	-249.537	-0.77

	agaagaaaaucaca ccgucagaagcgauu uagcccuuuugauu aaaaaaauaauuau agcagcuauuugcu uuuuccuuaaaaaa guuaacagaggcag gcauuuugguccua acauuuggucugccc agcaacauuuguua auuuuuuuuuuuga caaaaucgcugcugg aa															
sly-miR5303j-1	gaaauaguugaaau cuauguugcuugaa uucuuguaaaaugu ucagauuaguuagg cacgaucaauauuu uugaagagucugag caacauagguugaa acucaugug	107	2.149.533	3.271.028	1.121.495	3.457.944	3.271.028	6.728.972	1.057.14 3	1.916.667	-33.5	-33.4	0.080134	4.62	-313.084	-0.95714
sly-miR5303j-2	acguauguugcucg gacuacgcaaaaugc ucccgaacuagagcg uuggauuuuccaaa aaaauaugcugcuu uuggaggauccacca cgcaccugacaauau uuuugaagagucug agcaacauaauc	128	203.125	3.046.875	2.265.625	265.625	4.296.875	5.703.125	0.871795	0.896552	-47.3	-47.3	0.144975	9.02	-369.531	-0.86
sly-miR5304	gucuaauuuagauc cauggugcaguugc ucauucaaugcuaca uacucauccccacaa cuuucaucucacguu caaaagaugaaagu uauagagaugagua uggugcauuggaug uguggccauaccaug ggugauguuaga	142	2.183.099	2.816.901	1.901.408	3.098.592	4.084.507	5.915.493	1.1	1.148.148	-66.3	-66.1	0.536117	1.27	-466.901	-11.431
sly-miR5368	cuaaccuugugucag gaccuaugggccaag ggacagucucaggu agacaguuucuaug gggcguaggccuccc aaaagguaac	83	2.891.566	253.012	2.409.639	2.168.675	5.301.205	4.698.795	0.857143	1.2	-31	-31	0.400362	2.09	-373.494	-0.70455
sly-miR5532-1	uauuccaugaauau gauaucuaucuagu	163	2.147.239	3.251.534	1.472.393	3.128.834	3.619.632	6.380.368	0.962264	1.458.333	-45.9	-45.7	0.028719	10.51	-281.595	-0.77797

	gugauguaugaaau auaugacaaaggug gaucuauugaucgg ucaugucauauagg cccgaguuggacauc caauugcuucuauu ugaauuauccggag aaugcaaugccuga uauauaucaaaaag auggacaa															
sly-miR5532-2	cugcuaccgaauuuc uucaaauuccagga gaauuguccuuuga agaggacucgaaccu caacgcucuuuagca cgagauuuuaaguc ucgcgugucuacaau uucacaaccaaggca ucuugaaagugaau cguauuccaugaau auuauaucuauuua guaugauguaugga auauaugacaaagg uggaucuauugauc cgucaugucauaaa ggcccuaguuggaca uccaauugcuucgau uugaauuauucgga gaau	263	1.901.141	2.965.779	1.901.141	3.231.939	3.802.281	6.197.719	1.089.74 4	1	-75.9	-63.5	0.000425	31.7	-288.593	-0.759
sly-miR6024	aacuggaaaugggg aaguggagaaacaa cacuugcuaaagga aguucaccagucauc ucuuuucuuuugga guuuuuuuagcaag aguuguuuuaccuc uucucaauuccgucu cu	116	1.982.759	2.586.207	1.896.552	3.534.483	387.931	612.069	1.366.66 7	1.045.455	-42.7	-42.4	0.072273	7.12	-368.103	-0.94889
sly-miR6027	guaauuuuacauga uuauggguagcaca aggauuaaugugaa acagaaaagugaua ugcaaagaagaugg agauucaauuguuu auuguuacgaagaa aacacuuuuguguu ucucgugaauccuuc ggcuauccauaauca	153	2.156.863	3.333.333	1.176.471	3.333.333	3.333.333	6.666.667	1	1.833.333	-57.4	-51.7	0.046025	16.06	-375.163	-112.549

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sly-miR7122	auauauacagagaa accgcugucgauuau aaugagaaauucgg uguuucucauacucc acagcguuuuucug uauaacc	79	164.557	3.037.975	2.025.316	3.291.139	3.670.886	6.329.114	1.083.33 3	0.8125	-31.7	-31.7	0.163599	3.57	-401.266	-10.931
sly-miR7696c	cucauuuugaauua uuagaacuugauau ggucuauuuugaug ucauuuuggggaug gauugguugcauga uuguuuugcuucca uugauuguagaacu agaauugucaaauu caauuuccaaauga acccguucuagagug gaacagggacauuc uauuccuagagguc auauuaucucuugu cuuaagguuuguag aaugaucucaaaag gguguuuauaucac auuguaagauucaa agauugg	246	2.073.171	2.764.228	1.300.813	3.861.789	3.373.984	6.626.016	1.397.05 9	159.375	-59.7	-49.5	0.000145	46.66	-242.683	-0.71928
sly-miR7805	uucaaaaauagcac acuuaaaagugugg ucauauauauaaau aauuguugccaauu auucuaauaauugg caacacuuauaacgu guagccuauaauua caaaaaggacacuu uaaaaguguuguca aaguuuucguggcc auaaaccugguuca aaagucgcgccuuca aaguauugccuuag gugucuuuggcaac acuuuuuaagcauu gucaaaauuucgug uagccuugaccaaau uuggguagugaau acuaauacuuaguu guuuucuugagaua ugucaccauacaauu ucuaauauacucucu uuuaggagauguuc	339	159.292	3.185.841	159.292	3.628.319	3.185.841	6.814.159	1.138.88 9	1	-83.3	-72.5	5.93E-05	56.54	-245.723	-0.7713

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sly-miR7980b-1	ucaugcgauaucau aucaugauauggua ucgugagauggaau caguguuuggacau gcgauuuuacguug auuccaucucacagu uccauauuaugaga ugugauccaaua	111	2.072.072	2.792.793	1.621.622	3.513.514	3.693.694	6.306.306	1.258.065	1.277.778	-46.8	-46.8	0.166089	6.29	-421.622	-114.146
sly-miR7980b-2	uauuggaucacauc ucauaauauggaac ugugagauggaauc aacguaaaaucgca uguccaaacacugau uccaucucacgauac cauaucaugauaug auaucgcauga	111	1.621.622	3.513.514	2.072.072	2.792.793	3.693.694	6.306.306	0.794872	0.782609	-36.8	-35.4	0.0911	7.86	-331.532	-0.89756
sly-miR7981	cuaugaccgaaaucu cagagacacaccuua acuuaacuaagguu cuauuaaucucaacu cauuuguuuuguaa uuuuguaaugguac acuccgugacuugag gcgcgugagagaug uuugaaugucagug uacagaauuacaaa aaaauggauucggg gguaauaggacuuu aguuuaguuaaggu cugucgcucgaauuu cggucauac	210	2.142.857	2.904.762	1.666.667	3.285.714	3.809.524	6.190.476	1.131.148	1.285.714	-86	-82.5	0.005812	25.97	-409.524	-1.075
sly-miR7983-1	ucauuagcggcaau uaauucuuaauugc cacuaaauauguau uuuuagcggcauug acacucuuuguaua ugacccuaaagcuuu uagcgauauuuguu ccagugacauuuaac uaaugccgguaaag acuuuaacacucuuu auuaaugucaauau uuaaugcugcuaaa ag	173	1.445.087	3.063.584	1.734.104	3.757.225	3.179.191	6.820.809	1.226.415	0.833333	-40.7	-29.89	0.005368	42.5	-23.526	-0.74
sly-miR7983-2	gaauagucacuaca ucaaaaaugaucau uagcggcaguuaau	222	1.486.486	3.198.198	1.576.577	3.738.739	3.063.063	6.936.937	1.169.014	0.942857	-58.4	-51.6	0.00128	39.84	-263.063	-0.85882

	uuuuaauugcugca aaauauauauuuuu agcgccaauuaacac ucuuuguauauguu ccuaaagcuuuuagc gaaauugauucuaa uggcacuuaacuaa ugccgguaaagacu uuaacacucuuuau uaaugucaauuuuu aaugccgcuaaaag uuguuuuuguugua gugaguacac															
sly-miR7983-3	aucauauacacuaca ucaaaaaugagcuu uagcggcuauuaac acuuucuguaugug ucccuaacggcuuua gcaacauuggaucu ugugacaguuaacu aaugccgguaaaga cuuuaacaauuuuu auuaauguaucuau uuauugccgcuaaa gauuauuuuuguug uagugacaucaa	182	1.538.462	3.076.923	1.703.297	3.681.319	3.241.758	6.758.242	1.196.429	0.903226	-50	-46.71	0.028504	20.43	-274.725	-0.84746
sly-miR7983-4	auauuuucagcggu aauuaucacucuuu guauauguccccuaa agucuuuagcgaca uugguucuaaugac acuuaacuaauuuc gguaaagacuuuag cacucuucauuagug uuaauauuuaaugc cgcaaaaagu	137	1.459.854	2.992.701	1.751.825	379.562	3.211.679	6.788.321	1.268.293	0.833333	-36.8	-36.8	0.076737	10.09	-268.613	-0.83636
sly-miR7983-5	uauguccuuaaagu cuuuagcgacauug guucuaauggcagu uaacuaaugcuggu aaagacuuuagcac ucu	73	1.917.808	2.739.726	1.780.822	3.561.644	369.863	630.137	1.3	1.076.923	-21.8	-20.1	0.071875	6.71	-29.863	-0.80741
sly-miR7983-6	uaacacuuuuugua uauguuccuaaagu cuuuagcgacauug guucgaauggagcu uaacuaaugacggu aagacuuuagcaau	100	17	31	14	38	31	69	1.225.806	1.214.286	-23.7	-22.8	0.017871	11.04	-23.7	-0.76452

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sly-miR7984c	uacgauaccaaacuu uauggaggaucuuu uacccuugcccuauu caauaguguauuuu uaagguauauacgu auccacauugacacg uuacuauuuauaau uaugcaauauuuau gauguucacaugac acauauauauguuu aaaauacacuacua aacagugcaagggu aaaagguccuuuuc aaaguuuaguaucg uua	202	1.386.139	3.316.832	1.633.663	3.663.366	3.019.802	6.980.198	1.104.478	0.848485	-72.2	-72.2	0.023131	18.36	-357.426	-118.361
sly-miR7984d	acuuugaaaaggac cuuuuaccccagcau uauuuaauagugua uuuaaaagguauau auguacccacgugga caucauaauuauug caucauuauaaaua guaacauguccacgu ggcacauauaccuuu agauuagacuauua aauagugcaggggc aaaagguccuuucca aaguucgguauuau uccaccaauuucggu caaaguucggauau	216	1.666.667	3.287.037	1.805.556	3.240.741	3.472.222	6.527.778	0.985915	0.923077	-92.1	-88.3	0.010609	31.24	-426.389	-1.228
sly-miR7985	ggacuuccauguug gaggucucaaguuu gaaaccccuugucag ugaaagcaaagugu uugccuucugggucg agcuugucgcaccgg gcuugccuagugcgg guuaccacuccuaug ugguugugaguuau ugcauaggagcggg gguuuuacccugugc gcauccaaagggua gcgg	178	3.146.067	1.797.753	2.191.011	2.865.169	5.337.079	4.662.921	159.375	1.435.897	-69.3	-64.1	0.005165	45.23	-389.326	-0.72947
sly-miR7987	cacaaguaccaacac uagcugaugcuauu gaugacaaaaauug	208	1.923.077	3.028.846	1.394.231	3.653.846	3.317.308	6.682.692	1.206.349	137.931	-58.4	-36.37	0.001648	57.03	-280.769	-0.84638

	guuuucuugcaaga ucaauuugugucaa ucuaguguugauac uuaguuuuaguuua ggaauaaauguuug uugauuguaaggac caacacuaguugauc uuauugaugacaaa aauuaauguucuug caagaucgaguugu guccaucuaguguu gauacuuagc															
sly-miR7990a-1	ugcaaaaguuauga ccauuugaaguguc acaaauuuacaacu acuuuuuuugaguu auacucuuuaauuu ggugaaacuucaaa ugaucguaacuuug gccu	102	1.470.588	3.039.216	1.568.627	3.921.569	3.039.216	6.960.784	1.290.323	0.9375	-32.8	-32.8	0.100838	7.57	-321.569	-105.806
sly-miR7990a-2	aagaucucgaaaaa uuaucagauugaaa aagauugccucaauc acacauccaaggcaa aaaaauuuaccauu ugaaguuucacaaa uuuacaacuacuuu uucugaguugcacuc uuuauuuuuuguga aucuucaaaugauc guaacuuuggccucg aauauccguuugag gcgauuucuuuuuc aauugcacuauuuu cucgagauaua	211	1.327.014	3.175.355	1.848.341	3.649.289	3.175.355	6.824.645	1.149.254	0.717949	-61.8	-60.4	0.009229	19.82	-292.891	-0.92239
sly-miR7990a-3	uguuuuuccgcgua gaacaugaaaaaau aacuagguugaaau aaaauauugccuca aucggacauucgag gcaagauuuaugac cguuugaauuucac aaauuuacaacuac uucauuuggugaaa cuucaaaugaucgu aacuuuugccucgaa uauacguuggaggc gauucuuuuuuuaa	219	1.598.174	3.105.023	1.598.174	369.863	3.196.347	6.803.653	1.191.176	1	-82.9	-81.6	0.011402	13.71	-378.539	-118.429

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sly-miR7992	uccaaucauuacucc aacuuuggaguaca cauccagacacuuca aaucauguccacuau aucaauugaacacuc aacaguccaacuuac aaaaugaacgugua gacaccaccaaaauu uacgugucacgucaa cguugaguucccaca agaucaguggacu gaguugagaugucu agaugugcacuccaa aguuggagaguauu auc	208	1.682.692	3.317.308	2.403.846	2.596.154	4.086.538	5.913.462	0.782609	0.7	-72.3	-70.6	0.004029	15.21	-347.596	-0.85059
sly-miR7993a	aacuuuuugcgugu guuuucauucgucu auuaguuagugaag uuaacuacaugaaa uguaucaucuuuuu uaaccguacacauua acuucaaguaaaaa augcuugagguuuu aaggcguauugagg cgcaagcguauaau uaaaggagauagag auauuuuauguugu uaacuuaacuacauc guagauaaaugagu gagcacaaaccagaa aaaaa	218	1.834.862	353.211	1.284.404	3.348.624	3.119.266	6.880.734	0.948052	1.428.571	-70.1	-69.2	0.013783	15.05	-32.156	-103.088
sly-miR7997a	auggcaugcugcucg gacucuucaaaaau guugcuaggucugu guuggauccuccaaa aguagugcauauuu gaaggauccgacau gagugcggcaacau uguuggagagucug agcaacauagcaga	128	2.734.375	2.734.375	18.75	265.625	4.609.375	5.390.625	0.971429	1.458.333	-66.6	-64	0.025577	10.04	-520.313	-112.881
sly-miR8001a	ugcuacaaagaaac ugugaauuacauag gauuuuccugggga uuaguaugaaaauu caaaagaaacuuau	139	1.438.849	352.518	1.582.734	3.453.237	3.021.583	6.978.417	0.979592	0.909091	-61.1	-60.3	0.072781	7.6	-439.568	-145.476

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sly-miR8001b-1	cuucacuacaagaaa acuaugaauuacau ggggauuaguauga aaauuugcgaaaag uuuauuuuccuaca aacuuuuauacuaa uucccaggaaaauuc cauguaauuuacac gguuuucuuguagu gcuu	132	1.439.394	3.333.333	1.590.909	3.636.364	3.030.303	6.969.697	1.090.909	0.904762	-54.8	-54.8	0.332404	3.19	-415.152	-1.37
sly-miR8001b-2	aaacacuacaagaa aaggguaaauuaaa uggggauuaguaug aaaauuugcaggga uuacccuguaguuca cacuuuucuuguag ugaaa	90	2.111.111	3.777.778	1.222.222	2.888.889	3.333.333	6.666.667	0.764706	1.727.273	-29.2	-27.04	0.033037	15.88	-324.444	-0.97333
sly-miR8006-1	cauauauauacucu aguuuuuggauuac agagacaccaauguc ccaaaaauaugaca gagaguauuuaccu aucauuuaccauaa ugacaauuuuuuug guaaaacaauaaac ucuacaaaauguau auuuuuaaggaaaa aggacaaauauauc ucaagcuaucguaa augguaugcagaua cccuccgccauauuu uuggaacauuagug cccugccguccaaaa acuagagcaauaug cc	243	1.399.177	3.703.704	1.893.004	3.004.115	3.292.181	6.707.819	0.811111	0.73913	-68.7	-59.51	0.001284	35.97	-282.716	-0.85875
sly-miR8006-2	acguguauguaugu uaguguaaagggua uauauacuauaguu uuugaacgacaggg gcaccaacgucccaa agguaugauggagg guauuugcauacca uuuacgauaguuug	184	1.956.522	298.913	1.413.043	3.641.304	3.369.565	6.630.435	1.218.182	1.384.615	-45.2	-40.9	0.01532	20.42	-245.652	-0.72903

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sly-miR8007a	auguauuuauacua aguuuauggucacu gucacaaguaucaac caguguaaugguac ucccucugugccauu uuauguggcacuuu ucggauuucgagua aacauuuugaauua uuaauuauugugac caauacuuuuuaua aauaguu	149	1.543.624	2.818.792	1.543.624	409.396	3.087.248	6.912.752	1.452.381	1	-36.1	-27.8	0.012973	23.82	-242.282	-0.78478
sly-miR8007b	caauacucccuccgu cccauuucaugugac acuuuuuggauuuc gagauucaaacaag ucuaauuuugaccg gaaauuuuucauag aucuuuuaaacauu uugaauuaucaaau guugugacuuauag uacuuuuuauguag uuuacaaauauaua aauuucacuuaaag aaguugaagauuuc augcgcaaauucccg guuaaacuuaaacu guuuaacucucgaa aaaacgaaaagugc caacauaaauuggg ucagagggaguaau a	270	1.481.481	3.407.407	162.963	3.481.481	3.111.111	6.888.889	1.021.739	0.909091	-83.2	-74.5	7.37E-05	31.02	-308.148	-0.99048
sly-miR8008a-1	auuuccagaaaagc gacggacagggucu uuaaucugucgcua uucugggauuu	54	2.407.407	2.407.407	2.037.037	3.148.148	4.444.444	5.555.556	1.307.692	1.181.818	-23.7	-23.4	0.163152	4.28	-438.889	-0.9875
sly-miR8008a-2	uuuuccaucacuuuu uuacauuacuuuuu ucaacuaaacucaga aaagcgacgaacau aaaccuuuuguccgu cucuuuuccggcuac uuuaaaaaauucau uuccagaaaaguga	188	143.617	3.031.915	2.074.468	3.457.447	3.510.638	6.489.362	1.140.351	0.692308	-49.3	-51.44	0.00226	17.7	-262.234	-0.74697

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sly-miR8008b-1	uugauuuauauuug cagguauugcagaa aaaaaugaggagca gaguggguuuugucc gucgcuuuuuugcu uuauuuauuucaaa uaaacccagaaaagc gacggacaagguuc uuugguccgucacuu cucuagguauuuua aaaaauuaauuuca aggaaagcgacaga cauuguccuuuaguc gucccucgcuuuucu ggaauuuucaaaau auaaauuua	223	1.838.565	2.959.641	161.435	3.587.444	3.452.915	6.547.085	1.212.121	1.138.889	-72.7	-71.5	0.000473	21.5	-326.009	-0.94416
sly-miR8008b-2	uaaaaaaugcaaaa aaaaaucgacggac aggugguuuuuuc caucacuuuuuugca uaauucuuucaaau aaacccagaaaagcg acagacagggguccuu uagugcgucgcguu ucuggguuuuucaa aaaaaaaaauuuca gaaaagauggauag gguccuuuaguccgu cacuuuucuacgauu uucaa	192	1.822.917	3.333.333	1.770.833	3.072.917	359.375	640.625	0.921875	1.029.412	-51.6	-52	0.000727	36.36	-26.875	-0.74783
sly-miR8008b-3	ugcaaaucccagaaa agcgacugacaaaa gaacacuauccaucg cuuuucuggaaauu auuuuuucaaaaag ucaaaaaaaaaagu gaaggacuaaaaca cacuaacugucacuu uucuugguuuuaaa aaauaaaaacccag aaaagcgacggaca aaaccauguugucu gucgcuuugucugca	193	1.450.777	388.601	1.917.098	2.746.114	3.367.876	6.632.124	0.706667	0.756757	-57.2	-52.8	0.014367	21.97	-296.373	-0.88

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sly-miR8011a-1	gacacuagucaagu gagacucauuuuug ccucacaaaaaauua agcccauuugagucu acuuuuaugugaga caaaaagaagccuca cacaacuaguauu	100	15	36	21	28	36	64	0.777778	0.714286	-29.1	-29	0.285749	3.88	-29.1	-0.80833
sly-miR8011a-2	acaugaacuuuguu uugugucucacacaa cugauguaaguugu gugaggucucuuuu uguuuuacaaguca gugcgacccaaaucg uuggacucaccaacu cgugaaauaaaaag aagucucacgcaacu ugcguuaauucugu gagucgcaaaguaa auuuucaaau	168	1.904.762	2.916.667	1.904.762	327.381	3.809.524	6.190.476	1.122.449	1	-70.2	-69.8	0.030845	9.95	-417.857	-109.687
sly-miR8019-1	uuuuacguauuaau aguacucccuccguu ucaaaaagaaugac cugguuugacuuga cacgaaguuuaaga guguaaagaagacu uuuguaucuugugg uccuaaauuaaacu uagguuaaauguac aaaauuucccuuug aucuuguggccuua aacaugccaugugg aaaacugauuuuga aagguuaccaaaaa aagaaagaggccau ucuuuuugaaauag acuaaaaaggaaag gagguuauucuuuu ugaaauggagggag uaauauauauguau uc	283	1.943.463	3.427.562	130.742	3.321.555	3.250.883	6.749.117	0.969072	1.486.486	-88.9	-86.7	0.001369	42.13	-314.134	-0.9663
sly-miR8019-2	acuaauacuccucca uuuuaaaaaagaau gaccugguuugacu uggcacgaaguuua agaaaauaaagaag acuuuggaucuugu gguacuaaauuaaa	262	1.679.389	4.160.305	1.412.214	2.748.092	3.091.603	6.908.397	0.66055	1.189.189	-58	-50.74	0.000361	47.22	-221.374	-0.71605

	guuaugugaaauac acaaaacugcccuuu aaucuuguggccuu aaacauaccacaugg aaaguugaaauaaa aauguaaccaaaaa aagaaagaggucau ucuuuuuaaaacag acuaaaaagaaaag aaagucauccauuu ugaaacggagggag uauuuau															
sly-miR8020	cucagaccccacuua guggaauuucauug aguauguuguugu guaaagcauucuga auuaaugcaaguac acaaguuacaacaac aacauacuuacuga aaugccacaaaaag gggucuagg	123	1.869.919	3.495.935	1.869.919	2.764.228	3.739.837	6.260.163	0.790698	1	-53.9	-53.9	0.093084	7.72	-438.211	-117.174
sly-miR8021-1	auucaaggcucaaac ucgagaccucugguu aagaauggaugugu cauauacaucccuuu auaacuauuuugaa ucuaauaauaacuu aauucacucucuccu gcauauucuucaau augcuagaauuaag uuauugagaucuac gaacaauauugugu uggagaagaagcuu auauuacuucauuc uuaaccagaagugu caaguuugagucuu gacga	219	1.552.511	3.196.347	173.516	3.515.982	3.287.671	6.712.329	1.1	0.894737	-76.4	-71.7	0.005823	25.94	-348.858	-106.111
sly-miR8021-2	cauauucaaggcuca aacucgagaccucug auuaaggaugaaua uuucauauacauccc cucauaaauauugu ugguucuaaacuua uaauaacaacauaa uucacacucuuuugc auauuacgcaauau guugaguuaaguua uugaguucuaccaa	233	1.459.227	3.347.639	167.382	3.519.313	3.133.047	6.866.953	1.051.282	0.871795	-65.1	-57.1	0.000512	28.41	-279.399	-0.89178

	uaauauuguguugg agaagaaguuaaua uuacuucauccuuaa ccagaagugucaaa uuugagucuuugca ugga															
sly-miR8021-3	ucuucauauucaag gcucaaacucgagac cucugguuaaggau agauggaucauaua caacccaccacaacu uuuaugguacuaau aaugacuugauuua cuuucucuuaaaua uuugacaauauguu ggauuuauuuguug uauucuaccaacaaa uauuuugauugagu gaaaguuaguauuu auuuauccuuaguc agaagugucagguu cgaaucuuagacau gaguu	232	1.594.828	3.060.345	1.551.724	3.793.103	3.146.552	6.853.448	1.239.437	1.027.778	-55.7	-55	0.001188	29.39	-240.086	-0.76301
sly-miR8025	ucaaacaucauaaa gaaauauuuuacca cacacuacacaugca auuaaauuaguaua agucgccauuaugu uuuucuuaaccaagc ugaaucauauaaug gugacuuauacuaa uuuaauugcaugcc gacugugug	137	1.240.876	3.576.642	1.824.818	3.357.664	3.065.693	6.934.307	0.938776	0.68	-56.7	-56.7	0.538141	3.17	-413.869	-1.35
sly-miR8032d	gaucauuuucgauc aaaaguucaagaag augacaucggaaucc aauucugacgauucc aucaguuccggaag ggucauuuuaggcu aguaucauggucga caccccugaaguuuu cagugugaguuggu gcgauuaggcguuu uaacuuuaaguuaa aggcuaaguuugac uuuaguuaacauuc ugaguaaaugcgcu cggaugagaaguuu	311	2.282.958	2.411.576	1.639.871	3.665.595	392.283	607.717	1.52	1.392.157	-85.6	-59.4	0.000242	71.72	-275.241	-0.70164

	cggaaugucgaguu uggucuaguuuuua cccuucuuucguguu augagguuuuugau auuuuuccgagcccu uuuguaguuuuuga cuuaaaauggcc															
sly-miR8033	gcauuagcuggagu acaagcuuccaaagc ugcagaaaugaguu uuuuuuuuuaacug aaaaagaaaaacua uuucugcagcuuug gaauuuuuuacucc agcuaaguu	108	1.759.259	3.148.148	1.574.074	3.518.519	3.333.333	6.666.667	1.117.64 7	1.117.647	-60.6	-60.6	0.145417	5.18	-561.111	-168.333
sly-miR8038a	uauuuuucaaguca aaacaguuucuccuu gugaguaaguugaa ucucgugcucguuaa accgcaagagacgua gaaugcgucccaaca ugagauucagcuua cucacuuggaaaaa uuguuuuugcuuga gaagca	136	1.985.294	2.941.176	1.911.765	3.161.765	3.897.059	6.102.941	1.075	1.038.462	-64	-61.8	0.115401	6.01	-470.588	-120.755
sly-miR8039-1	uuaauagucaaaaa cacauuugaacugu uacuuuuucgguag uuucacacuuuaacu accgguuauuccuuu uuccuaucugaacua ugaccaucguucagg uaggaaaaggaaac aacugauaguugaa augugaaacugacg agagaacaauaguu cauuugaguuuuug agcuaugcu	181	1.767.956	3.149.171	1.657.459	3.425.414	3.425.414	6.574.586	1.087.71 9	1.066.667	-81.6	-81.6	0.014355	8.82	-450.829	-131.613
sly-miR8039-2	ucaaaaagacaccug aacuaucaauuuuu cacacccccaacuau cacuuguucucuuuu ccuaucggaacuauc accaucguucaagua agaaaagggaacaa cugauaguuggggu gugaaacucgcgaa gaaaugauagauca	159	1.761.006	3.207.547	2.201.258	2.830.189	3.962.264	6.037.736	0.882353	0.8	-72.9	-68.8	0.010535	12.47	-458.491	-115.714

	ggugugcuuuuauc															
sly-miR8045-1	uaacauaccucaacu aacaauuuuucccuu uuccuaccuaaacga uagugauauuucag guaugaaaagggaa aauugauaguugag guguguuu	95	1.684.211	3.263.158	1.578.947	3.473.684	3.263.158	6.736.842	1.064.51 6	1.066.667	-46.9	-46.9	0.052742	7.75	-493.684	-15.129
sly-miR8045-2	acacaccuaggauau acccauuuuuugag uuucauauaggaaa uaucaucaucguuca gguaggaaaaguaa acaauugauaguug agguguguuuugau gaauaacggugaua guuuagguaggaaa uucgcacacaugaua guuuagguuugaaa cucgaaaaaucgga guacuuuaggugug u	186	2.311.828	327.957	1.182.796	3.225.806	3.494.624	6.505.376	0.983607	1.954.545	-48.5	-40.6	0.000396	39.21	-260.753	-0.74615
sly-miR8051	gaauugaauccucac caacaaggugggag uuagguaggauacc aacuaagcaauuga aauuccccuuguauu ucacaugaaaacucu gugaacuagaauaa acaaaaugcuagua uauggauaguaugg uagaaagauucauc ucauguguucuu uuaaugaccaugau aaaaaguuauuggu aagaacaaaaauaa ucaguucuuacaau uccuacaauaacuaa uucaagacacuuuu ggugaaauucaaaa u	257	1.634.241	385.214	151.751	2.996.109	3.151.751	6.848.249	0.777778	1.076.923	-56.8	-41	0.000408	68.07	-221.012	-0.70123
sly-miR8172	cuccauccagaugga ucaucuagauggag auaaaaaaugaugu uuguuuuugacaaa uuaauauaucauuu ggauguuccaucug aaugacu	92	173.913	326.087	1.413.043	3.586.957	3.152.174	6.847.826	1.1	1.230.769	-29.3	-28.8	0.098043	27.99	-318.478	-101.034

sly-miR8175	aaguucaaguuaau cuaaaaucuaugau ccccggcaacggcgc caaaauuugauaca cucaaacuuacuucu caaauaagaaguaa agcggucgugucaa guaaauaacccaacu agugagguugggau cguucccacgaggaa aauagucuagacuu aacuucaacgug	170	1.871.345	3.508.772	2.105.263	245.614	3.976.608	5.964.912	0.7	0.888889	-48.7	-48.7	0.087229	8.77	-284.795	-0.71618
sly-miR827	uuaugaauuuguuu guugauggucaucu auucaucauaucau uuggcauaguuuuu ggaaccauuaauau gccaugauuagaug aacaucaacaaacau cuucaucac	108	1.388.889	3.055.556	1.666.667	3.888.889	3.055.556	6.944.444	1.272.727	0.833333	-40.6	-40.6	0.076968	6.42	-375.926	-12.303
sly-miR828a	auuuacauucacuuc uuugggaaagccuc uugcucaaaugagu auuccaacaaauguc uaauugacauacuu uugagauacucauu uggguaagaaguuu uaccaggaagguug uacuu	119	1.764.706	2.941.176	1.680.672	3.613.445	3.445.378	6.554.622	1.228.571	1.05	-48.1	-48.1	0.090023	5.43	-404.202	-117.317
sly-miR845b	gaaguagucgguua uaguuaauugagag uuuuuguaguggug aguuuuugauuauu aaguuguaaucaua aaaucaucuaguug aauuaauaaaacga gguuauuccuuccuu gauugaggaagguu uuaauuuaacaagu guuuguguucugac uuaaaaccaacuuac aagaacuugguucu uguucuaggggaua gguuucuucaauug guaucagagcaagu cuuuucgauaaaag auucacaccuugaaa agacucaauggcacu	285	1.929.825	3.087.719	1.473.684	3.508.772	3.403.509	6.596.491	1.136.364	1.309.524	-72.9	-69.2	0.000971	46.05	-255.789	-0.75155

	accacccaccacaca															
sly-miR9471a	gaucauugacggauuuggguucugagauucaguugauuucucaggugcucacucagcuaauaguuauuauuuaagaaacucaauaauauuggcagcaaggagaauggugacuuucaggaugauaacuauuggcugagugagcaucacggaaaucgacgugauucugagaggaaaaugau	180	2.555.556	3.055.556	1.388.889	30	3.944.444	6.055.556	0.981818	1.84	-74.1	-74.1	0.099251	11.72	-411.667	-104.366
sly-miR9471b	uugagauucaguugauuucugaggugcucacucagcuaauaguuauuguuuaagaaacucaauaauauuggcagcaaggagaaugugacuuucaggaugauaacuauuggcugagugagcaucacugaaaucgacaugauucugag	147	2.380.952	3.061.224	1.428.571	3.129.252	3.809.524	6.190.476	1.022.222	1.666.667	-64.9	-64.8	0.098094	7.91	-441.497	-115.893
sly-miR9472	ccauagaucuacucgauuuauuuuucaguagacguugugaauaauugauaaauacagguauacagaggucuuaauauagucagaaccuagaaauaugguaacuagauucagaccuuuguacacuugauuucuguugcuauucacaaucucugcugaaaaugauugacuagaucuacga	180	1.666.667	3.277.778	1.611.111	3.444.444	3.277.778	6.722.222	1.050.847	1.034.483	-73.2	-73.2	0.021458	8.16	-406.667	-124.068
sly-miR9473-1	cuagcagauauuggcuguaaaucuaaacucguucuacuccacuagucaucauauaaugacauuuacuagaagaagagacuauuggggguaaaacgaguucagauuuacagccaauauuguu	120	17.5	3.416.667	17.5	3.083.333	35	65	0.902439	1	-53.2	-53.2	0.041358	8.37	-443.333	-126.667
sly-miR9473-2	aaaacaauauuggc	118	1.694.915	3.220.339	1.694.915	3.389.831	3.389.831	6.610.169	1.052.63	1	-56.2	-55.3	0.152958	7.56	-476.271	-1.405

	uguaaaucugaacu cguuuuaccccaaua gucucuucuucuagu aaaugucauuauau gaugacuaguggag uagaacgaguuuag auuuacagccaaua ucug								2							
sly-miR9476-1	aaacugcuauuggu cuaguccugcaucuu uuuuuacauuuuuu ccguuaucaaaaaa uauaaaaaaagaug caggacuagaccaau agcaggau	94	1.489.362	3.510.638	1.702.128	3.297.872	3.191.489	6.808.511	0.939394	0.875	-58.1	-58.1	0.76197	0.61	-618.085	-193.667
sly-miR9476-2	auccugcuauugguc uaguccugcaucuuu uuuuauauuuuuug auaacggaaaaaau guaaaaaaagaugc aggacuagaccaau agcaguuu	94	1.702.128	3.297.872	1.489.362	3.510.638	3.191.489	6.808.511	1.064.51 6	1.142.857	-63.2	-63.2	0.878756	0.55	-67.234	-210.667
sly-miR9478	ugcuuauaaaaggg auaaggcuuaaaua uguagaucgaacuu ugagaaaagacuca ucuaugucaucugg uaaaguuuggugug uaaugguuugaaug agccuuuucucgaac gaaaaugguguaga ugaguuaaauuuuu aacggauuacauaa uugagccuuuucuca uaguucgaugacau auuugagccuuuuu ccaauuauaaaug	211	2.037.915	3.127.962	1.232.227	3.601.896	3.270.142	6.729.858	1.151.51 5	1.653.846	-76.1	-68.73	0.011277	27.36	-360.664	-11.029

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Supplementary Table S9. Thermodynamic and structural characterization of *S. pennellii* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Pre-miRNA	Sequence	Size	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
spe-miR1128	agcaugucauuaguug uuuuucucacaacaau gacugcuaauugauua acuccuagaaaagaag auuucacaaggauuuc ugcauaaaauuacuac ucccuccgucccaaaa uaagugucacuuuagc aauaaucacacucauu aagaaaaauaauaaa uagaaagguaucuacc ccuauuuauuagaugu uucuugacaauugagc augauugauaaguag uuaguucuuuaguaca aagguauacuuggaaa aacauacuaauuuccg ucuuaaguuccuaugg ugacacuuauuuugg	301	1.428.571	3.455.150	1.727.575	3.388.704	3.156.146	6.843.854	0.98077	0.82692	-74	-68.6	0.00149	28.91	-2.458.472	-0.77895
spe-miR1446	auauuaauggaaaucc agaguuuucugaacuc ucucccucaauggcug uucauauaauauaugc ugcuacuuugcagcuu aauuaaauaacagcuu ugggguuuugagucca gaaaacucuugcuuuc cuaguuaagca	139	1.654.676	2.805.755	1.942.446	3.597.122	3.597.122	6.402.878	128.205	0.85185	-53.3	-50.5	0.03526	12.23	-3.834.532	-106.600
spe-miR1446a	caguguuuucugaacu cucucccucaauggcu ucuucaauauaauuaa auuaauuaaaaagagc agccaugagagauuga guucagaaaacucugg	96	1.666.667	3.333.333	1.875.000	3.125.000	3.541.667	6.458.333	0.93750	0.88889	-40.4	-38	0.17718	5.50	-4.208.333	-118.824
spe-miR156-1	aaaauggaaugggug auauuguugacagaag auagagagcacauaug auggaaugcugcugcu aaaucuggagagucuu aacaauaaaaaaagca uuucacuucauuugug	149	1.879.195	2.953.020	1.946.309	3.221.477	3.825.503	6.174.497	109.091	0.96552	-52.9	-51.47	0.03732	12.70	-3.550.336	-0.92807

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spe-miR156-10	aaggggcggugacaga agagagugagcacaca uggcguuuucuggcau gauguuuauaugguu gcuugaaacuaugugu gcucacugcucuaucu gucaccucccacc	108	2.685.185	2.222.222	2.222.222	2.870.370	4.907.407	5.092.593	129.167	120.833	-60.2	-60.2	0.09793	7.82	-5.574.074	-113.585
spe-miR156-11	ucuaauuaagugugaa guaugacaaaaaagaa ggugacagaagggcgu gagcacauguguguuu ucuagcaugauguuca uaugcuugaaucuaug ugugcucacugcucua ucuuucauccucaucg cuuuuccucucucucu agauuuaauuuug	157	1.974.522	2.484.076	1.847.134	3.694.268	3.821.656	6.178.344	148.718	106.897	-47.4	-47.3	0.02245	16.37	-3.019.108	-0.79000
spe-miR156-12	acugacagaagagagu gagcacacgcugucga auuguauaaauauau auacaauugucauuug cgugugcucacuucuc auucugucagcu	91	1.978.022	2.857.143	1.978.022	3.186.813	3.956.044	6.043.956	111.538	100.000	-50.6	-47.6	0.06892	4.78	-5.560.440	-140.556
spe-miR156-2	uugacagaagauagag agcacuaaugaugaua ugcuaauuucauucaa uuugggcagcaaaagc aucucaauucauuugu gcucucuaugcuucug ucauc	101	1.782.178	2.970.297	1.881.188	3.366.337	3.663.366	6.336.634	113.333	0.94737	-43.5	-42.2	0.11945	6.96	-4.306.931	-117.568
spe-miR156-3	ucuuucuaugauagua uauauguuaaaaaga ggaggugguaggaga uguuguugacagaaga uagagagcacagauga uaaagugcauagaaau ugucugcaccuuacuc cuuugugcucuuuauu cuucugucaucaucgu uaauaccaccucuuuu uuuuuaacguuuuugu auuguuauauaaau	188	1.861.702	2.819.149	1.382.979	3.936.170	3.244.681	6.755.319	139.623	134.615	-82.1	-80.2	0.00197	14.34	-4.367.021	-134.590
spe-miR156-4	guugacagaagauaga gagcacagaugauaaa gugcauagaaauuguc	86	1.976.744	2.790.698	1.860.465	3.372.093	3.837.209	6.162.791	120.833	106.250	-40.8	-40.8	0.07046	5.33	-4.744.186	-123.636

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spe-miR156-5	guugacagaagauaga gagcacagaugauuaa gugcaugaaaauugua ugcacauuacuccuuu gugcucuuuauucuuc ugucac	86	1.976.744	2.906.977	1.744.186	3.372.093	3.720.930	6.279.070	116.000	113.333	-43.7	-43.7	0.25302	2.44	-5.081.395	-136.562
spe-miR156-6	gggugagauauuguu gacagaagauagagag cacaaauaaugaggug cuaauuggaagcugca ccuuaauucuuugugc ucucuauucuucuguc aucaucuucaguc	108	2.222.222	2.685.185	1.759.259	3.333.333	3.981.481	6.018.519	124.138	126.316	-51.7	-51.6	0.01925	8.32	-4.787.037	-120.233
spe-miR156-7	uggugacagaagagag ugagcacacauggugu uuucuugcaugauguu uauauauauaugcuug aaacuaugugugcuua cucucuaucugucacc c	97	2.164.948	2.474.227	1.752.577	3.608.247	3.917.526	6.082.474	145.833	123.529	-58.3	-58.3	0.35058	5.07	-6.010.309	-153.421
spe-miR156-8	cggugacagaagagag ugagcacauaugguc uuucaagcaugauguu uacaugcuugaagcua ugcgugcucacuucuc uaucugucaccc	92	2.282.609	2.391.304	2.282.609	3.043.478	4.565.217	5.434.783	127.273	100.000	-56	-56	0.32224	2.67	-6.086.957	-133.333
spe-miR156-9	aagggaggugacagaa gagagugagcacacau gauguuuucucgcaug auguuuacaugcuuga aacuaugugugcucac ugcucuaucugucacc ccacc	101	2.376.238	2.574.257	2.277.228	2.772.277	4.653.465	5.346.535	107.692	104.348	-55	-55	0.10487	4.96	-5.445.545	-117.021
spe-miR160-1	auaugccuggcucccu guaugccauuugcaaa gcucaccguaauauau cgaugggccuuguuga auggcguaugaggagc caagcaua	88	2.500.000	2.500.000	2.272.727	2.727.273	4.772.727	5.227.273	109.091	110.000	-45.8	-45.8	0.13353	3.03	-5.204.545	-109.048
spe-miR160-2	gugaucgauaacacaa caugccuggcuccuug uaugccauuugcauug uuccaccaagaauuga uggccuuuucagaugg cauucuaggagcuaag	116	2.155.172	2.500.000	2.155.172	3.189.655	4.310.345	5.689.655	127.586	100.000	-41	-40.8	0.21669	7.36	-3.534.483	-0.82000

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spe-miR160a	uaagaaggaugugccu ggcucccuguaugcca cacgcauucaccaauu uuuugauugacugauc aguggguggcguauaa ggagccaagcauacca cccguuu	103	2.427.184	2.427.184	2.427.184	2.718.447	4.854.369	5.145.631	112.000	100.000	-45.4	-45.4	0.54332	2.55	-4.407.767	-0.90800
spe-miR160c	cugccuggcucccugg augccaacuaagaaca guauugucaaaaaaau ugacacucuuccuagu ugguaccagaggagac aggcaga	87	2.298.851	3.103.448	2.413.793	2.183.908	4.712.644	5.287.356	0.70370	0.95238	-47.3	-47.3	0.30868	2.21	-5.436.782	-115.366
spe-miR160g-1	ggaauaugcuuggcuc cucauacgccauucaa caaggcccaucgauau auuacggugagcuuug caaauggcauacaggg agccaggcauauacg	95	2.421.053	2.842.105	2.421.053	2.315.789	4.842.105	5.157.895	0.81481	100.000	-47.8	-47.8	0.35883	2.11	-5.031.579	-103.913
spe-miR160g-2	ggugguaugcuuggcu ccuuauacgccaccca cugaucagucaaucaa aaaauuggugaaugcg uguggcauacagggag ccaggcacauccuuc	95	2.526.316	2.526.316	2.526.316	2.421.053	5.052.632	4.947.368	0.95833	100.000	-39.5	-32.9	0.01176	15.55	-4.157.895	-0.82292
spe-miR162a-1	guugggugagaacacu ggaggcagcgguucau cgaucuguucccugaa aagcgauaaauacagc aacaggaagcgaucga uaaaccucugcaucca gugcuuaacccgcc	110	2.545.455	2.909.091	2.545.455	2.000.000	5.090.909	4.909.091	0.68750	100.000	-49.1	-49.1	0.04505	7.98	-4.463.636	-0.87679
spe-miR162a-2	uaguugguugaagaca cuggaggcagcgguuc aucgaucuguucccug gaagcugaauauauau auauaugcaaaaauac agcaaaaggaaucggu cgauaaaccucugcau ccagugcuuaaccccu ua	130	2.153.846	3.153.846	2.076.923	2.615.385	4.230.769	5.769.231	0.82927	103.704	-48.1	-48.1	0.00997	13.93	-3.700.000	-0.87455
spe-miR164	auuauuuaagcuggag aagcagggcacaugcu gaauuacuugaaacuu ugaucuuucaagaauu uugcaugugcucuagc	98	1.836.735	2.653.061	2.040.816	3.469.388	3.877.551	6.122.449	130.769	0.90000	-51.1	-48.1	0.24991	2.23	-5.214.286	-134.474

	ucuccagcuuaauucc uc															
spe-miR164a	agauggagaagcaggg cacgugcauuacuaac ucauacgcaagauuua ucgauguuucgaaaau ucugcuaucauaguac uguauuuacagcaaau aguguuuguacuuaca uguauguaguaaagu gaugaguuaguuauuc augugccuguuuuccc caucau	165	2.000.000	2.909.091	1.636.364	3.454.545	3.636.364	6.363.636	118.750	122.222	-59.3	-54.6	0.00230	22.51	-3.593.939	-0.98833
spe-miR164b	uguuggagaagcaggg cacgugcaaauuuuug uauucgacgauauaug cauuacuaaugguaau gcaucaauuuugcacg uguucuccuucuccaa c	97	2.061.856	2.577.320	1.958.763	3.402.062	4.020.619	5.979.381	132.000	105.263	-46.2	-45.3	0.04651	8.87	-4.762.887	-118.462
spe-miR166-1	uuuguugaggagaau gucgucugguucgaga ucuuucauaagaaagg uaaaugaaugacaagu uuucauauauguaucu ugaaugauuucggacc aggcuucauucccccuc aacucu	117	2.051.282	2.735.043	1.709.402	3.504.274	3.760.684	6.239.316	128.125	120.000	-52.9	-51.7	0.33112	6.15	-4.521.368	-120.227
spe-miR166-2	uuaauuuugagggga auguuguuuggcucga ggccaccaacuucauc uaaugugagcgaacuc uuuguuagugucgucg gaccaggcuucauucc ccucaaaaucuc	107	2.242.991	2.149.533	2.336.449	3.271.028	4.579.439	5.420.561	152.174	0.96000	-44.4	-41	0.04316	13.05	-4.149.533	-0.90612
spe-miR166a-1	ccaaaagaaagaaaac auuuguugaggggaa uguguuuggguucgaa aucauucaaacaaauu aaaauccaugcaucuc gaugaucgaugaauug aauaauuucggaccag gcuucauuccccccaa cucaaguuuuuguuuu aau	146	1.712.329	3.356.164	1.780.822	3.150.685	3.493.151	6.506.849	0.93878	0.96154	-50.3	-46.21	0.02766	17.23	-3.445.205	-0.98627
spe-miR166a-2	aaacaagaucauguua aggagaauguugucug guucgugaccauauau	93	1.720.430	2.903.226	2.150.538	3.225.806	3.870.968	6.129.032	111.111	0.80000	-30.9	-30.7	0.13229	6.62	-3.322.581	-0.85833

	cuuucuucauauaaau gaucucggaccaggcu ucauuccccucaa															
spe-miR166a-3	agcuuccagauuugag gggaauguugucuggc ucgaagucauuaucuc uucucgaucauuauag aucgaaccaauccaau uuuauauauucaaucu aguuuaaaauauaug ugauuacgaugaugau gagauagugucuucgg accaggcuucauuccc cccaauuuggaaaca	174	1.839.080	2.873.563	1.896.552	3.390.805	3.735.632	6.264.368	118.000	0.96970	-69.5	-69.2	0.01724	12.73	-3.994.253	-106.923
spe-miR166c	ugugugugugugcguuu gagggggauguugucu ggcucgacacaauuac ucucuuguauguauuu aguuauucguuaucaa gauugauguugauaac gaauaaauuaaacaca uauauacaagauguaa aaagggaguaaaggcg ucggaccaggcuucau uccucucaaauaauau ucuacuucuac	187	2.139.037	2.941.176	1.550.802	3.368.984	3.689.840	6.310.160	114.545	137.931	-76.5	-72.4	0.01243	17.61	-4.090.909	-110.870
spe-miR167-1	agcagcugaagcugcc agcaugaucuaaacuu uucuauugcuccguac gaggaaagaucagauc auguggcagcaucacc uguug	85	2.352.941	2.705.882	2.352.941	2.588.235	4.705.882	5.294.118	0.95652	100.000	-39.7	-39.7	0.33457	2.34	-4.670.588	-0.99250
spe-miR167-2	aucaguugaagcugcc agcaugaucuaaacuu accuauaaauuuauau uaaggcaagaucagau caugugguugcuucac cuguua	86	1.744.186	3.139.535	1.860.465	3.255.814	3.604.651	6.395.349	103.704	0.93750	-31.2	-31.2	0.07012	5.73	-3.627.907	-100.645
spe-miR167-3	gugaagcugccagcau gaucuaaacuuggcca uuuguaaagaaaaug ggugacuaagguuagg ucaugcucggacagcc ucacu	84	2.619.048	2.857.143	2.023.810	2.500.000	4.642.857	5.357.143	0.87500	129.412	-41.3	-41.3	0.37350	6.31	-4.916.667	-105.897
spe-miR167a	uagcaguugaagcugc cagcaugaucuaaacu uuccuuuuaguucaaa uauaauaugaggaaa	93	1.935.484	3.118.280	2.043.011	2.903.226	3.978.495	6.021.505	0.93103	0.94737	-41.6	-41.6	0.21117	3.68	-4.473.118	-112.432

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spe-miR167h	aauuucuuucuuucuc gacgaaguaggguuaa gauuauuuuucguagu acgaacuaacagguga agcaaccacaugaucu gaucuugccuuaauau aaauuuauagguaag uuuagaucaugcuggc agcuucaacugauagu agucuacgcuaucaau augacaaaacccuaau auuguugaagaagaa gaagaa	196	1.836.735	3.418.367	1.581.633	3.163.265	3.418.367	6.581.633	0.92537	116.129	-71.1	-67.3	0.00191	18.71	-3.627.551	-106.119
spe-miR168a	uuuuuugcggccgccu cuuauucgcuuggugc aggucgggaccucauu cgccggcgccgggaau aauggcggacgaacga cggcgguuuuaauucu acuaagcugucaccga cgaauauauguuugau uagcggcgaaauuugg guccugccuugcauca acugaauuggagacag cuguaaaucg	186	2.795.699	2.096.774	2.311.828	2.795.699	5.107.527	4.892.473	133.333	120.930	-75.1	-73.4	0.02437	20.06	-4.037.634	-0.79053
spe-miR168b	gcgguguuucucauu cgcuuggugcaggucg ggaccuaccucgccgg caacaauggcgguggc ugacggcgacggcagc guaccgguaaaaaaaa aucuuauuuuuacaug uuguugcguaguuugg gucccgccuugcauca acugaauaggagacug cggugaauuu	170	3.000.000	2.058.824	2.235.294	2.705.882	5.235.294	4.764.706	131.429	134.211	-77.2	-71.9	0.01712	15.15	-4.541.176	-0.86742
spe-miR169-1	uuuggucuauaagguu ugcaugaagaugaaga gagugaaguugcagcc aaggaugacuugccgg accaaaaguugugacc auuuucuaguuccggc aaguuguuuuuggcua uaaguuugcucucuuc uucucauguuauccuc guuagaccuuu	155	2.322.581	2.258.065	1.806.452	3.612.903	4.129.032	5.870.968	160.000	128.571	-74.7	-73.9	0.01499	9.78	-4.819.355	-116.719

spe-miR169-2	auuaauugaagaggg guuuuacaugaaguug agaguauuguuuagu agccaaggaugacuug ccuacuucauuugaua uauaguuuaaaauaa uaauauugacaauauu ugucauuuggucguag gcaaguuauccuggcu aucuugacaugcucgu aauuuuucauguaaaa ccuuaucuucuauugc u	190	1.842.105	2.894.737	1.315.789	3.947.368	3.157.895	6.842.105	136.364	140.000	-82	-79.3	0.00271	15.74	-4.315.789	-136.667
spe-miR169-3	augagaagaggagucu ugcaugaugaaaagag ucuuauuugguagcca agaaugacuugccugc accauuuccgaaaugu guccuuucguucaugg ggucaggcaggucauc uuuagcuaacuugaca agcucuucucuuucau gcaagacuuucucuuc uucc	164	2.134.146	2.378.049	2.195.122	3.292.683	4.329.268	5.670.732	138.462	0.97222	-74.3	-74.3	0.00246	12.25	-4.530.488	-104.648
spe-miR169-4	ggguacaaaaaagaag agaagucuagcaugau gagaagagucuauuu gguagccaaggaugac uugccugcaccauacu ugaaaaggucuuucau auguccuuucguuauu ggggucaagcagguca ucuuuagcuaacuuga caagcucuucuuuuuc augcaaggcuuucucu ucuuucguuuuuaauu	192	2.083.333	2.604.167	1.822.917	3.489.583	3.906.250	6.093.750	134.000	114.286	-77.4	-75.1	0.00095	15.36	-4.031.250	-103.200
spe-miR169-5	gcguaaaaaucaggau caugaaauggccuugc auguugguucaggaag aaagaguugcagccaa ggaugacuugccgacu uuuguauuacucuuca uauauauauauauau auguauauauggaaa uuacauuaaacuugga agagaaaguuggcaag ugguccuuggcuacau cuuucuuucugccccu	224	1.964.286	2.901.786	1.741.071	3.392.857	3.705.357	6.294.643	116.923	112.821	-89.3	-86.84	0.00254	26.07	-3.986.607	-107.590

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spe-miR169a-1	agucuaugagguuugc augaagauguagaga gugaaguugcagccaa ggaugacuugccggac cauaaauugcuaggau uuucgaguuucggcaa guuguucuuggcuaua guuugcucucuucuuc ucaugucauccucguu agac	147	2.517.007	2.244.898	1.836.735	3.401.361	4.353.741	5.646.259	151.515	137.037	-68.9	-67.9	0.01564	9.65	-4.687.075	-107.656
spe-miR169a-2	cuuuauucauguuaaa gucuugcaugagggaa uaagguauugaauu gcagccaaggaugacu ugccggcaagcucgau caauucugcuucaugu cuggcaagucauuuuu ggcuacauaucugccu cauuuucucaugccag auuuuuuaugaaaua gcu	161	1.987.578	2.484.472	1.925.466	3.602.484	3.913.043	6.086.957	145.000	103.226	-69.6	-69.6	0.03588	9.63	-4.322.981	-110.476
spe-miR169c	agagguagggagugg agugcagccaaggaug acuugccgagauguuu guagccuaaugcaaug acauaucggcagguca ucuuuggcuacauuuu auu	98	2.959.184	2.551.020	1.632.653	2.857.143	4.591.837	5.408.163	112.000	181.250	-51	-51	0.17474	3.02	-5.204.082	-113.333
spe-miR169e	uaggaggagaggccuu acaugaauuagaagag uuucuauuuguuuagu agccaaggaugacuug ccuuucaucaauggaa aaugauuacaacacuu uucaugguauugggaa aaugaguggcaagcau cuuuggcgacuugaca aacucuucuuugucau guuaguccaucuucuu ccu	179	2.122.905	2.737.430	1.731.844	3.407.821	3.854.749	6.145.251	124.490	122.581	-71.8	-68.1	0.00796	17.71	-4.011.173	-104.058
spe-miR171	ugaucaacuugggaug uuggugugguucaauu agauaacaaucuccac guaagauuguagaguc uguuauuugauugagc	110	2.181.818	3.181.818	1.454.545	3.181.818	3.636.364	6.363.636	100.000	150.000	-44.2	-44.2	0.22601	2.80	-4.018.182	-110.500

	cgugccaauaucacau guaaagaaaauaac															
spe-miR171-1	agauauuggugcgguu caauuagaaagcgcac uucuuuauaaauagaa cuucguuauuuaauug agccgugccaauauca c	81	1.851.852	3.086.420	1.728.395	3.333.333	3.580.247	6.419.753	108.000	107.143	-39.5	-39.5	0.72921	0.63	-4.876.543	-136.207
spe-miR171-2	uauuggugcgguucaa ugagaaagcaguacuu aagaacauuuugaguc uacuuuuugauugagc cgcgccaauau	75	2.266.667	2.800.000	1.600.000	3.333.333	3.866.667	6.133.333	119.048	141.667	-40.9	-40.9	0.48906	1.27	-5.453.333	-141.034
spe-miR171-3	aauacgugauauuggc acggcucaauuaaaua acgaaguucuauuuau aaagaagugcgcuuuc uaauugaaccgcacca auaucucguuag	92	1.739.130	3.369.565	1.847.826	3.043.478	3.586.957	6.413.043	0.90323	0.94118	-28.2	-27.8	0.40775	5.55	-3.065.217	-0.85455
spe-miR171-4	uagauauugaugcggu ucaaucugaaagacau ggcuagauauguaauu agccuuguaauuuugg auugagccgcgucaau aucucu	86	2.209.302	2.790.698	1.511.628	3.488.372	3.720.930	6.279.070	125.000	146.154	-48.1	-48.1	0.49140	1.70	-5.593.023	-150.313
spe-miR171-5	uuaauaguauaguaa aaugauguuggaaug gcucaaucaaaucaaa uuccucaaaguauugg gucauuucauuugauu gagccgugccaauauc aucuuacuuauauaug cu	112	1.607.143	3.214.286	1.517.857	3.660.714	3.125.000	6.875.000	113.889	105.882	-46.5	-46.5	0.06547	9.06	-4.151.786	-132.857
spe-miR171-6	acaagagaagauuucu cuaugaaauaguaacc cugauauuggccuggu ucacucagacacauau uauuuugauugauuu uacuuuugauugagcc gugucaauaucucagu uccuuuuuacuauauu ucaucau	134	1.417.910	2.761.194	1.791.045	4.029.851	3.208.955	6.791.045	145.946	0.79167	-33.5	-33.3	0.01749	12.57	-2.500.000	-0.77907
spe-miR171-7	gguaugaagaagaau acaagagugauauugg uucggcucaucucuua ucuguuucacgaauca gaaauuagugagccga accaauaucacgccau	112	1.964.286	2.946.429	2.142.857	2.946.429	4.107.143	5.892.857	100.000	0.91667	-46.2	-44.7	0.04037	12.41	-4.125.000	-100.435

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spe-miR171a	uauuggccugguucac ucagacaacaaaauga aaacuauauuugaaug guugaguuuucguuuu ucguuugauugagccg ugccaauau	89	2.022.472	2.696.629	1.573.034	3.707.865	3.595.506	6.404.494	137.500	128.571	-37.7	-37.7	0.47333	1.88	-4.235.955	-117.812
spe-miR171e-1	uuuugggauuaaaau ggaagaagcgauguug gugagguucaauccga agacgaauuuacgcuu auuuucguaaagaacg aucucagauugagccg cgccaauaucacuucu uauuuucauuccauuu	127	2.047.244	2.834.646	1.732.283	3.385.827	3.779.528	6.220.472	119.444	118.182	-52	-51.1	0.09527	4.07	-4.094.488	-108.333
spe-miR171e-2	uagagaagcgauguug gugagguucaauccga agacgaguuuacguuu uauuuuaguaaagaac gaucucagauugagcc gcgccaauaucauuuc uuuu	100	2.300.000	2.800.000	1.600.000	3.300.000	3.900.000	6.100.000	117.857	143.750	-40.7	-37.7	0.21389	3.86	-4.070.000	-104.359
spe-miR172-1	ugcagauguagcauca ucaagauucauacaug aaaauuaagaggcaag guuaaauauguagcuu uaauuugaaauggaa aauauaauacaucaug accaugucuauuuauu ucaaagugagaaucuu gaugaugcugcaucag caauaaauaacuaucg	159	1.698.113	3.899.371	1.320.755	3.081.761	3.018.868	6.981.132	0.79032	128.571	-57.3	-54.1	0.02713	11.52	-3.603.774	-119.375
spe-miR172-2	cugucaccgauaguua uuuauugcugaugcag caucaucaagauucuc acuuugaaauaaauag acauggucaugaugua uuauauuuuccauuuc aaauuaaagcuacaua uuuaaccuugccucuu aauuuucauguaugaa ucuugaugaugcuaca ucugcaaacaacaacu guguugauua	186	1.344.086	3.118.280	1.774.194	3.763.441	3.118.280	6.881.720	120.690	0.75758	-51.8	-49.7	0.00264	18.81	-2.784.946	-0.89310
spe-miR172-3	aucagucaauguuuga ggaugcaacaucauca agauucacaaaacuug	169	1.597.633	3.372.781	1.420.118	3.609.467	3.017.751	6.982.249	107.018	112.500	-58.7	-55.7	0.03741	12.68	-3.473.373	-115.098

	aaggaagaacuauuua auuauauguuuaggg ugaauauuggauaua uaauauaguucaaaau cucuuauuuucucucu uugggaaucuugauga ugcugcaucaucuaac auaugacucua															
spe-miR172-4	uagagucauauguuag augaugcagcaucauc aagauucccaaagaga gaaaauaagagauuu ugaacuauauuauaua uccaauauucacccua aacauauaauuaaaua guucuuccuucaaguu uugugaaucuugauga uguugcauccucaaac auugacugau	169	1.420.118	3.609.467	1.597.633	3.372.781	3.017.751	6.982.249	0.93443	0.88889	-55	-53.8	0.03580	13.26	-3.254.438	-107.843
spe-miR172-5	aauagccauuauuugc cgcugcagcaucauca agauucccacacaucg cccauaggguuuuuaa aaauaauaaaaucccu aauguagcuaugugaa ucuugaugaugcucca cccgcaaaaaauugac uuga	132	1.515.152	3.333.333	2.348.485	2.803.030	3.863.636	6.136.364	0.84091	0.64516	-43.6	-38.2	0.01507	8.78	-3.303.030	-0.85490
spe-miR172-6	uauuugcuagugcagc accauuaagauucaca uagaaaauaugaaacu aaauuugcccaauuuu ucaauacaugagaauc uugaugaugcugcauc ggcaaaugg	105	1.714.286	3.523.810	1.714.286	3.047.619	3.428.571	6.571.429	0.86486	100.000	-37.3	-36.8	0.16611	10.58	-3.552.381	-103.611
spe-miR172-7	cagucguuguuugcaa augcagcacuauuaag auucucaaauauucga cauuuaaaaugcaauu aaaugugaaucuugau gaugcugcauuagcaa uaaacgacu	105	1.619.048	3.523.810	1.619.048	3.238.095	3.238.095	6.761.905	0.91892	100.000	-44.3	-44.3	0.39910	4.45	-4.219.048	-130.294
spe-miR172-8	uuuagucguuuauugc uaaugcagcaucauca agauucacauuuaauu gcauuuuaaaugucga auauuugagaaucuua auagugcugcauuugc	110	1.636.364	3.090.909	1.545.455	3.727.273	3.181.818	6.818.182	120.588	105.882	-41.9	-41.9	0.11238	8.38	-3.809.091	-119.714

	aaacaacgacugug															
spe-miR172a	uacagucguuguuugc guauguagcauaauca agauucacaugaaaag uugcaaauugguuaua uaauuaaugaaauua auggcuggcuacuuga aacucaugagaaucuu gaugaugcugcaucug caauaaacgacuauu	142	1.901.408	3.380.282	1.408.451	3.309.859	3.309.859	6.690.141	0.97917	135.000	-54.4	-54.4	0.03828	15.79	-3.830.986	-115.745
spe-miR172d	uggagcaucaucaaga uucacauagcuacauu agggauuuuauuauu uuuaaaaacccuaugg gcgaugugugggaauc uugaugaugcugcag	94	2.340.426	2.872.340	1.489.362	3.297.872	3.829.787	6.170.213	114.815	157.143	-43.1	-39.6	0.02696	10.06	-4.585.106	-119.722
spe-miR1886-1	gcguuuggccauguaa uaccauaucacgauau gguauuaugagaugg aauuaggguuuggaca ugucauuuuacguuga uuucaucucaugauuc cacaucaugagaugug auaucauauucuccaa aaau	131	1.908.397	2.900.763	1.603.053	3.587.786	3.511.450	6.488.550	123.684	119.048	-43.1	-42.9	0.10851	6.71	-3.290.076	-0.93696
spe-miR1886-2	gccaugugauaucaua ucacaauaugguaucg ugagaugaaaucagca uuuggacauaucauuu uacgcugauuccaucu caugauuucauaucau gagaugugauaccaua uuuu	116	1.637.931	3.017.241	1.724.138	3.620.690	3.362.069	6.637.931	120.000	0.95000	-44	-43.8	0.11604	8.37	-3.793.103	-112.821
spe-miR1886h-1	gccaugagauaccaua ucguggccuuuggcca ugagauaucauaucac gauaugaaaucgugag auugaauucguguuug gacauauaauuuuacg uugauuucaucucaug auuucauauaaugaga ugugauuucguauucu ccaaaaaucaugauau ggaauuucauauc	173	1.791.908	3.005.780	1.560.694	3.641.618	3.352.601	6.647.399	121.154	114.815	-63	-58.97	0.01164	22.27	-3.641.618	-108.621
spe-miR1886h-2	uuggacaugcgauuuu acguugauuucaucuc augauaugugacucca uauucuccaaaaauca	97	1.443.299	3.298.969	1.649.485	3.608.247	3.092.784	6.907.216	109.375	0.87500	-23.9	-23.9	0.24274	9.68	-2.463.918	-0.79667

	ugauaugaaaucauau gagaauaucauaucau g															
spe-miR1917-1	ucucacuacaauaaaa auaacuuuuagcggca auaaauagauacauua auaaagagugcuaaag ucuuuaccggcauuag uuaagugucauuagau ccaaugucgcuaaagc cuuuagugacacauac aaagagugcuaauugc cacuaaaaauauauau uuagcggcaauugcua auuaauugccgcuaaa gcucauuuuuaaugua gugucu	214	1.542.056	3.598.131	1.682.243	3.177.570	3.224.299	6.775.701	0.88312	0.91667	-65.2	-62.3	0.00325	31.94	-3.046.729	-0.94493
spe-miR1917-2	aacuuuuagcggcauc aaauauugauauuaa uaaagagugcuaaagu cuuuaccgguauuagu uagugcuauuagaacu aaugucgcuaaaggcu uuacggacauauacaa agagugacaauugccg cuaaaaaua	136	1.838.235	3.676.471	1.470.588	3.014.706	3.308.824	6.691.176	0.82000	125.000	-39.1	-30.94	0.02995	19.27	-2.875.000	-0.86889
spe-miR1917-3	aaccacuguaacaaaa auaacuuuuagcggca aaaauagacacauuaa uaaagagugcuaaagu uuuuaccugcauuagu uaagugccauuagauu caacgucagaacauua uagaaagagugcuaau ugcaguuaaaaauaca cauuuagcggcaaugg cuaauaaauugccgcu aaaguucaguuuugau auagugagc	201	1.741.294	3.880.597	1.542.289	2.835.821	3.283.582	6.716.418	0.73077	112.903	-48	-43.94	0.00063	39.12	-2.388.060	-0.72727
spe-miR1917-4	uuagcugcauuaaaua uugacauuaauaaaga gugcuaaagucuuacc ggcauuaguuagaugu cauuagaaccaauguc ggucaagacuuuaggg acauauacaaagagug uugauugccgcuaaau aaaaauacauauuuag	240	1.708.333	3.500.000	1.416.667	3.375.000	3.125.000	6.875.000	0.96429	120.588	-85.3	-82.8	0.00616	21.22	-3.554.167	-113.733

	cagcaauuaagaauaa auugccgcuaauaauc auuuuugauguagug auccaaugacauauca cucuuuguuaaugugu auauuuauugcugcua a															
spe-miR1918	gucagauaauuauggu agcucaguugguuuaa cuaguuggauugucau ucuguuggugagaguu cgauucuccauuacgu aaucuccucuucaauu uaagagaaaaaaaua ugcuacaagguggaga aucggacuaucgcuaa caggauggaaguucaa auacuuaaucaauuaa gcuacuaauauuuuac ucuaug	197	1.928.934	3.147.208	1.522.843	3.401.015	3.451.777	6.548.223	108.065	126.667	-71.4	-70.4	0.00241	22.32	-3.624.365	-105.000
spe-miR1919	uccgaaucgcuccgac gccuuugauguucaca ucuuccgguaguccug ucgcagaugacuuucg cccuuuuauggaacca cacuuucucuaauuug aauucuauguggguagg acgagagucaucugug acaggauaauggaaga ucgaguuaucaaaggc uuauugggcguuuccu u	177	2.259.887	2.203.390	2.259.887	3.276.836	4.519.774	5.480.226	148.718	100.000	-85.8	-85.8	0.12075	8.43	-4.847.458	-107.250
spe-miR1919c	gacgccuuugauguuc acaucuucugguaguc cugucgcagaugacuu ucgcccuucuaaggaa ccacacuuucuguaaa ucuaauuaauuugaau ucaauguggcaggacg agagucaucugugaca ggauaauggaagaucu aguuaucaaaggcuua	160	2.125.000	2.750.000	2.000.000	3.125.000	4.125.000	5.875.000	113.636	106.250	-69.2	-69.2	0.04832	12.84	-4.325.000	-104.848
spe-miR2111a	ugguaaucugcauccu gagguuuagaucaauu ucuaauuuacuggauc uaguccuuaggaugca gauuauc	71	1.971.831	2.535.211	1.690.141	3.802.817	3.661.972	6.338.028	150.000	116.667	-37.7	-37.7	0.36708	1.82	-5.309.859	-145.000
spe-miR319-1	gaaaauaaggagcucu	187	2.245.989	2.941.176	2.139.037	2.673.797	4.385.027	5.614.973	0.90909	105.000	-79.6	-74.9	0.01428	25.65	-4.256.684	-0.97073

	cuccgguccaguccgaggcacucaaaggcuaaaaacacagcugacgacucguugauucucaaacacaucaagaagcauuuuuugaauuugacgugguuaagauucaacgaugcgugagcuauguuuagcuagcguugucacgucuuggacugaagggagcucccuauuaaa															
spe-miR319-2	ugguauaagagagcuuccuuuaguccacucauagguagacgaaggauuugaauuaucucccgaccucauucauucaaacgcaauagaaaguauguaaucuuauacuauugugaaugugugaaugaugcgggagauaaauucucuccuuuuuaucugugcuuggacugaagggagcucccuuuuacc	185	2.054.054	2.756.757	1.837.838	3.351.351	3.891.892	6.108.108	121.569	111.765	-92.3	-90.5	0.02231	10.30	-4.989.189	-128.194
spe-miR319-3	aaggaaacuguuuaguccaacccaaggugggguacuggaacugaucuuugcugcugaaucauuggcucaugagcaugucaaagaagaugauugaacauucuggacauguucuugcuccaaugauacagagagcugagcucgguuuuucaccgccuuuucuuggacugaaggguucccuuc	179	2.402.235	2.402.235	2.122.905	3.072.626	4.525.140	5.474.860	127.907	113.158	-82.3	-81.5	0.06410	6.73	-4.597.765	-101.605
spe-miR319-4	gaugggauaaggaaggaaauucaucaguccaaacaaggugguauauuugggcugaucuuugcugcugaaucauugguucaucaacauauuauacacauacaaggauauauacauauguuguugcaucaaugaugcaggagcugaguucaguuuuggcuaccuuuucuuggacugaaggguuuccuucucaaccccaa	197	2.182.741	2.842.640	1.776.650	3.197.970	3.959.391	6.040.609	112.500	122.857	-86.8	-85.1	0.06124	7.18	-4.406.091	-111.282

spe-miR319a	agagcuuucuucaguc cacacaugggagcga uaggguucaauuugcu gccgacucauucaucc aaauguugaggucuug auaaucgaaugucacc ucagcaacugagugaa ugaagcgggaguacaa guugagucuugagcuu ccuguacuuggacuga agggagcucc	170	2.647.059	2.529.412	2.117.647	2.705.882	4.764.706	5.235.294	106.977	125.000	-88.8	-88.2	0.08093	6.12	-5.223.529	-109.630
spe-miR319c-1	uaggagcuccuuucag gccaagaccgagggac gaggagcggcaagagc ugccuagucaugcaua uugguuaaccuuaaua aacaaauuauguauag uguuaagauuaaccag uugcauggcaagggag caacuacuuccgcuaa cuugucucacuuauug gacugaagggagcucc u	177	2.485.876	2.881.356	2.090.395	2.542.373	4.576.271	5.423.729	0.88235	118.919	-89.2	-89.2	0.09586	5.72	-5.039.548	-110.123
spe-miR319c-2	caagagagcuuccuuc agcccacucacggagg agaaauggguugaa uuagcugccgacucau ucauccaaccacucag uagaaaggauagguu uugugcuacugugauu gagugaaugaugcggg agauaguuuucuaucc cucucuuuccuugcuu ggacugaagggagcuc cuuu	178	2.528.090	2.359.551	2.191.011	2.921.348	4.719.101	5.280.899	123.810	115.385	-77.1	-65.9	0.02388	17.43	-4.331.461	-0.91786
spe-miR319c-3	aaggaaacuguuuagu ccaacccaaggugggc uauuggaacugaucuu ugcuguugaaucauug gcucaugagcaugcua aagaagaugauuuaac auucuggacauguucu ugcuccaaugaugcag gagcugagcuuncgga guauagguacuugaga aagcagaggagagaag gaa	179	2.737.430	3.016.760	1.564.246	2.625.698	4.301.676	5.642.458	0.87037	175.000	-54.3	-46.5	0.00367	29.81	-3.033.520	-0.70519
spe-miR3627-	gucgcaggagagaugg	83	2.048.193	2.650.602	2.289.157	3.012.048	4.337.349	5.662.651	113.636	0.89474	-33.4	-33.4	0.34502	2.22	-4.024.096	-0.92778

1	cacuuaccauuccuuuaauugguacaaugccuaaauggaaccauuaagugccucugucuuucgaca															
spe-miR3627-2	uaaaucauucaaauaggagagauugagggaaucuugucgcaggagagauggcacuuaccauuccuuuuaauugguacaaugccuaaauggaaccauuaagugccucugucuuucgacacgaugcccacaauuucuauugcauuauaca	148	1.891.892	3.040.541	2.027.027	3.040.541	3.918.919	6.081.081	100.000	0.93333	-51.7	-51.7	0.09725	6.04	-3.493.243	-0.89138
spe-miR390	ugcauggagaaucguaaagcucaggagggauagcgccauggaugacucaauucgauuuuuuuacacaucucuagcgcuauccauccugaguuuucagcuuuuucaugc	110	2.090.909	2.454.545	2.181.818	3.272.727	4.272.727	5.727.273	133.333	0.95833	-57.1	-57.1	0.38371	2.45	-5.190.909	-121.489
spe-miR390a	ggcauggggaaucuauaaagcucaggagggauagcaccaugaauacaucuuaauggcuaucuauagcgcuauccauccugaguuuuauggcuucuucaugcuu	103	2.233.010	2.621.359	2.038.835	3.106.796	4.271.845	5.728.155	118.519	109.524	-51.1	-48.4	0.11196	6.15	-4.961.165	-116.136
spe-miR393	uuccaaagggaucgcauugauccuguguccaaauuaauuaaccaugggacuaugggaucaugugaucucuucggaau	78	2.179.487	2.692.308	2.051.282	3.076.923	4.230.769	5.769.231	114.286	106.250	-40.9	-40.9	0.20082	2.59	-5.243.590	-123.939
spe-miR394-1	acgaucuugauuuucaugaagauuucucaaaggguuccuuacacaguucuuuggcauucugucccaccuccuuugucuucauauuccucuauuuuuuagaaaaauaauuuuuauuaaauuuuuuguaaaaaaaauggagguggcauacugucaacagauuuguguugguucucuuugugaaaucucuugauguuaauug	203	1.576.355	2.561.576	1.527.094	4.334.975	3.103.448	6.896.552	169.231	103.226	-67.2	-61.15	0.00574	28.79	-3.310.345	-106.667
spe-miR394-2	agauuaauuaguuuca	196	2.500.000	2.704.082	1.632.653	3.163.265	4.132.653	5.867.347	116.981	153.125	-78.6	-78.5	0.00364	13.84	-4.010.204	-0.97037

	uggagguuugacaaag ggguuucuuacagaguu cauuggcauucugucc accucccucguucuuu uuucgaaaaagaagaa gaagggggaagcaag auuuauuguggaggu gggcauacugccaaua gagcuguguugguuuc ucuuuguaaaacccuc gugauacacgucaagu aagau															
spe-miR394-3	uuuggcauucugucca ccucccagcuugcuga ggacugaggagggggc caaagugccaaac	61	2.950.820	2.131.148	2.786.885	2.131.148	5.737.705	4.262.295	100.000	105.882	-31.2	-30.9	0.17506	3.56	-5.114.754	-0.89143
spe-miR395a	ugcagugauucccgag aguuuccuugaccacu ucaugagggcuuaauu acuuguuguuuaucc cuugcugaaguguuug ggggaacuucuggguu cacuuua	103	2.427.184	1.747.573	1.941.748	3.883.495	4.368.932	5.631.068	222.222	125.000	-42	-40.1	0.06330	10.38	-4.077.670	-0.93333
spe-miR395d	ucaagguguucccuag aguucccuugaccucu ucauuaggguuuacuc auuguuugauguccug cugaaguguuuggggg aacuuuuggacucaca uuga	100	2.400.000	1.800.000	2.000.000	3.800.000	4.400.000	5.600.000	211.111	120.000	-36.3	-34.1	0.02113	11.82	-3.630.000	-0.82500
spe-miR395g	agaaugauucauuucu auauauaucaagguau ucucgagaguacccuu ugaccacuucaugagg gauuaauguuuuuau uuuugaugcucuguug aaguguuuggggaac ucucgggguucaguuug aaguauacacaaacua guaaacaugca	154	2.077.922	2.792.208	1.493.506	3.636.364	3.571.429	6.428.571	130.233	139.130	-45.8	-45.6	0.03056	13.04	-2.974.026	-0.83273
spe-miR395i	uguuugauccccuacu gaaguguuuggagga acucucgggguuuacuu agaaauuuacacaaaa aguagaaaugcaagau aaauggaagaugaug aauuuucauugauaau acuuauaucuguauau	174	1.896.552	3.275.862	1.379.310	3.448.276	3.275.862	6.724.138	105.263	137.500	-54.5	-47.5	0.00665	27.98	-3.132.184	-0.95614

	caagguguucucgaga guucccuugaacacuu cauuaaggauuaauuu															
spe-miR396-1	agucaugcuuuuccac agcuuucuugaacuuc uucuugcuaaaauuuug aucucuaaauugauaa uuuugagaugagauu ugaagcuaugaaaguc caagaaagcuguggga aaagauggcaa	122	1.967.213	3.114.754	1.475.410	3.442.623	3.442.623	6.557.377	110.526	133.333	-49.4	-46	0.00901	16.78	-4.049.180	-117.619
spe-miR396-2	aagcuugccaucuuuu cccacagcuuucuugg acuuucauagcuucaa aucucaucucaaaauu aucaauuuagagauca aaauuuagcaagaaga aguucaagaaagcugu ggaaaagcaugacuag gac	131	1.603.053	3.511.450	1.984.733	2.900.763	3.587.786	6.412.214	0.82609	0.80769	-45.1	-45.1	0.02604	10.18	-3.442.748	-0.95957
spe-miR396a	uuuuuguguuuuucca cagcuuucuugaacug caucuacaauuuauga aaaagaaaaaauuga uucauauuguuguugc gguucaauaaagcugu gggaagauacag	107	1.869.159	3.084.112	1.308.411	3.738.318	3.177.570	6.822.430	121.212	142.857	-48.2	-47.9	0.02778	8.77	-4.504.673	-141.765
spe-miR397	ugaguacuuagaaaca ucauugagugcagcgu ugaugacauauuugag aauuccugcauuuggg ccuuccucauuuuuca ucaacgcuacacucga ucauguuuuuaauucu cuga	116	1.724.138	2.500.000	2.068.966	3.706.897	3.793.103	6.206.897	148.276	0.83333	-45	-44.8	0.12429	4.97	-3.879.310	-102.273
spe-miR398	guagggcaacuugaga ucacauguugcauuu uuuucuuuuuggguuug auuugaugaaucagua ucucaacauguguucu caggucgccccug	93	2.150.538	1.935.484	1.827.957	4.086.022	3.978.495	6.021.505	211.111	117.647	-34.6	-31.27	0.09493	13.39	-3.720.430	-0.93514
spe-miR398a	gggugauuugagaac auauguaugugcauau uuuguuuguagcaauu uaucguuuauaaaugu gacacauauguucuca ggucgccccu	90	2.111.111	2.444.444	1.444.444	4.000.000	3.555.556	6.444.444	163.636	146.154	-33.8	-27.6	0.01674	17.34	-3.755.556	-105.625
spe-miR398b-	cagaggagugugccua	89	2.471.910	2.022.472	2.134.831	3.370.787	4.606.742	5.393.258	166.667	115.789	-45.1	-45.1	0.69707	1.24	-5.067.416	-110.000

1	agaacacagguguauu uuggucuucuccuguu uuggacacaaaguaug cuuguguucucagguc accccuuug															
spe-miR398b-2	ccaauuuauguugaua uauucacauuauuaau augaaucaugaugaac aauggugaauccccag aggagugugccuggaa acacaggugcauuuug guccuuuuuuuuggca auuguuggaccaaaau auauuuguguucucag gucaccccuuugggau caccuuguuuuuuuau cguauuuuaauuuugu agaauaauaguuauu acuuaaauaca	218	1.743.119	2.798.165	1.513.761	3.944.954	3.256.881	6.743.119	140.984	115.152	-75.1	-63	0.00120	41.81	-3.444.954	-105.775
spe-miR399-1	aaaguucgugaaugau gguaauuauaaggga aacagugauagggcua cgcucuauuggcaugc agcuuuuuuggucgcu ccaaguagcaacuuga ucuaauauuugagcug aaaugccaaaggagag uugcccuguuacuguc ucuacuuaauguaaug uaauuacacgcacauc	175	2.228.571	2.914.286	1.771.429	3.085.714	4.000.000	6.000.000	105.882	125.806	-62.4	-59.4	0.00681	26.21	-3.565.714	-0.89143
spe-miR399-2	cuuauuaagugaagca guuguagggcaguucu ccguuuggcagauaua ugauuaugaauguaa ucugccaaaggagagu ugcccuacgauugcgu cugcuuaauuau	107	2.429.907	2.616.822	1.588.785	3.364.486	4.018.692	5.981.308	128.571	152.941	-59.2	-56.9	0.14690	3.67	-5.532.710	-137.674
spe-miR399-3	uuauaagggaaacagu gauagggcuacucucu auuggcaugcaauugu auauuucagcugacac gccaaaggagagcugc ccuguuacugucucag cuuaauc	103	2.233.010	2.718.447	2.135.922	2.912.621	4.368.932	5.631.068	107.143	104.545	-47	-47	0.46407	2.91	-4.563.107	-104.444
spe-miR399-4	uuauaagcgaaacagu gauagggcuacucucu auuggcaugcaauugu auauuucagcugacac	103	2.233.010	2.621.359	2.233.010	2.912.621	4.466.019	5.533.981	111.111	100.000	-50.1	-50.1	0.25282	2.67	-4.864.078	-108.913

	gccaaaggagagcugc ccuguuacugucucgg cuuaauc															
spe-miR399-5	uuguaagggaaacagu gauagggcuacucucu auuggcaugcaauugu auauuucagcugacac gccaaaggagagcugc ccuguuacugucucug cuuaauc	103	2.330.097	2.524.272	2.135.922	3.009.709	4.466.019	5.533.981	119.231	109.091	-47.9	-47.9	0.29698	6.84	-4.650.485	-104.130
spe-miR399-6	uuguaaggggaacagu gauagggcuacucucu auuggcaugcaauugu auauuucagcugacac gccaaaggagagcugc ccuguuacugucucgg cuuaguc	103	2.621.359	2.330.097	2.135.922	2.912.621	4.757.282	5.242.718	125.000	122.727	-47	-45.7	0.11127	6.28	-4.563.107	-0.95918
spe-miR399-7	uuugaauuuauaagcg aaacacugauaggacu acucucuauuggcaug caguuguguaguuuag cugacacgccaaagga augcugcacuguuacc aucucuuauuaauauu cuaacaaaaagaaaga aguguagguggauga uaauaaggggaacagu gguaggacuacugauc ucuauugguaugcaac uauauauuuaagcuga caugccaaaggagagu ugcccugguacugucu cugcuuacuguaauuc uga	258	2.209.302	3.062.016	1.666.667	3.062.016	3.875.969	6.124.031	100.000	132.558	-78.2	-74.4	0.00165	44.49	-3.031.008	-0.78200
spe-miR399-8	ucuaaauucgaaucua uaaauuuuaaauucug aaucuugugauugagg agaagaacgacagggc aauucuccuuuggcaa agauaauauaaugug uaugcaaaacauauau auaggguuugcauaua uucauuugccaaagga gaauugcacuguuauu ucuuacuccccauuuu ucuucuucuaugaacu uucacauuuuauguuu gauuuucca	216	1.481.481	3.055.556	1.574.074	3.888.889	3.055.556	6.944.444	127.273	0.94118	-63.4	-56.79	0.00143	35.30	-2.935.185	-0.96061

spe-miR399-9	agaucuuuaggucaau cuguuuuuuaaacaga gaccaagauaguaucu ccaaaaggagauaaug ccaaaggagauuugcc cuaaagacaa	90	1.888.889	3.888.889	1.666.667	2.555.556	3.555.556	6.444.444	0.65714	113.333	-23.8	-21.3	0.05100	17.83	-2.644.444	-0.74375
spe-miR399a-1	agggaaacaguggua ggcuacucucuguugg caugcagugauauagu uaagcugauaugccaa aggagagcugcccugu uacugucucugc	92	2.934.783	2.391.304	1.956.522	2.717.391	4.891.304	5.108.696	113.636	150.000	-47.3	-47	0.06341	6.87	-5.141.304	-105.111
spe-miR399a-2	uuauaagagaaacagu gguagggcuacucucu auuggcaugcacuuau acauuuaaacugacau gccaaaggagagcugc ccuguuacugucucug cuuaaug	103	2.135.922	2.815.534	2.038.835	3.009.709	4.174.757	5.825.243	106.897	104.762	-47.6	-47.6	0.22637	6.15	-4.621.359	-110.698
spe-miR399d	aaaacaauuggugaag auacaauucaaacuau guauggaugcauuacu gggcuaaucuucuuug gcaaauagccacauuu ucacuauauuauuuag ugcaaguuuguucauu uuuugccaaagaagau uugccccguaaaucac caauacaauauauuau aacaugagucacuuca auacuuguaau	187	1.390.374	3.422.460	1.711.230	3.475.936	3.101.604	6.898.396	101.563	0.81250	-51.1	-42.18	0.00081	38.12	-2.732.620	-0.88103
spe-miR399r-1	aguuauguguggaugc auuacugggcuaaucu ucuuuggcaaauaauu ucacuauuauuuggug caaauuuggucauuua uugccaaagaagauuu gccccguaaaucauuc auacaauauua	123	1.707.317	2.926.829	1.544.715	3.821.138	3.252.033	6.747.967	130.556	110.526	-50.2	-48.5	0.06268	15.68	-4.081.301	-125.500
spe-miR399r-2	uucaaguuaugugugg augcauuacugggcua aucuucuuuggcaaau aauuucacuauuauuu ggugcaaauuugguca uuuauugccaaagaag auuugccccguaaauc acucauaccuuuua	126	1.666.667	2.698.413	1.746.032	3.888.889	3.412.698	6.587.302	144.118	0.95455	-44.3	-41.4	0.04785	23.82	-3.515.873	-103.023
spe-miR403-1	ucaggaagaggcauau	112	1.964.286	2.678.571	1.964.286	3.392.857	3.928.571	6.071.429	126.667	100.000	-52.3	-52.3	0.15872	8.61	-4.669.643	-118.864

	uucgcguuugugcgug aaucuaacgacucuuu ucaucagaaaaacugu uguuguuugcuagauu cacgcacaaacucgua auauggcuuuuccaau															
spe-miR403-2	auuggaaaagccauau uacgaguuugugcgug aaucuagcaaacaaca acaguuuuucugauga aaagagucguuagauu cacgcacaaacgcgaa auaugccucuuccuga	112	1.964.286	3.392.857	1.964.286	2.678.571	3.928.571	6.071.429	0.78947	100.000	-45.4	-42.8	0.10161	9.61	-4.053.571	-103.182
spe-miR408	aaaaggaaggauugu ggggagaggaaagcca gggaagaggcagugca uggaauaggcaaagca aaaauugcacaucuca ugcucuggcucguccc cgucuauccauaccac accaauuuuuaccuca a	128	2.500.000	3.281.250	2.265.625	1.953.125	4.765.625	5.234.375	0.59524	110.345	-46.6	-41.4	0.04794	8.00	-3.640.625	-0.76393
spe-miR408b	uauggauagacgggga cgagccagagcaugag augugcaauuuuugcu uugccuauuccaugca cugccucuucccuggc uuuccucu	88	2.386.364	1.818.182	2.613.636	3.181.818	5.000.000	5.000.000	175.000	0.91304	-37.4	-37.4	0.50523	1.93	-4.250.000	-0.85000
spe-miR4376	aaaaggcuugcuacgc aggagagaugaugcug gacgauagagaaaaug ggauuuaauuuauug gccagcaucauacucc ugcauauuaagccuaa a	96	2.395.833	3.437.500	1.666.667	2.500.000	4.062.500	5.937.500	0.72727	143.750	-46.7	-46.7	0.33648	3.38	-4.864.583	-119.744
spe-miR477	agcuaggcauugcuug uugucucucccucaag ggcuccucuucaagau ccuuauaaacaagaaa gcaugagggggaggag uucuuguagggugaga caucaagaaauuccuu gc	114	2.543.860	2.631.579	2.105.263	2.719.298	4.649.123	5.350.877	103.333	120.833	-52.8	-52.3	0.13027	7.43	-4.631.579	-0.99623
spe-miR477a	gccucucccucaaggg cuucucuccugcaugc uuuuuauguugggaa agaagcucuagcaggg agagcca	70	2.571.429	2.000.000	2.714.286	2.714.286	5.285.714	4.714.286	135.714	0.94737	-35.9	-34.5	0.04982	3.89	-5.128.571	-0.97027

spe-miR477b	cacucucccucaaagg cuucuggcuuaaaaug ccauuugugcuaaugc uagaggucuuucgagu gagaguga	72	2.361.111	2.361.111	2.222.222	3.055.556	4.583.333	5.416.667	129.412	106.250	-33.8	-33	0.18313	4.64	-4.694.444	-102.424
spe-miR479	augauggagaagcaga cauggcgugauauugg uucggcucacuaauuu cugauucgugaaacag auaagagaugagccga accaauaucacucuug uauucuucuucauacc	112	2.142.857	2.946.429	1.964.286	2.946.429	4.107.143	5.892.857	100.000	109.091	-52.6	-51.4	0.10829	8.75	-4.696.429	-114.348
spe-miR482-1	uucagaaauugggaaa gggaugaagauuuuu gggaagcuuuuggcgu gagugguggggaaag auagaucuauucauau uuguaugauaugaua aaucuugccuacaccg cccaugcccauggcuu ccaauuauuucucccu uuccauacaauuucuu ca	159	2.138.365	2.641.509	1.823.899	3.396.226	3.962.264	6.037.736	128.571	117.241	-69.2	-69	0.00845	10.26	-4.352.201	-109.841
spe-miR482-2	guguuucgaggaggug uuggaguggguggua ugguaagauuucauau uuauuuuucauaaaaa uugaaaucuugccaau accgcccauuccuaug gcuucugaucauuuc	110	2.272.727	2.363.636	1.545.455	3.818.182	3.818.182	6.181.818	161.538	147.059	-50.9	-47.8	0.03203	12.21	-4.627.273	-121.190
spe-miR482a	gaaaaucuaugggaau uggugaguuggaaagc uuuucuuuuucuucuc uugugauuagcuuucc aauuccacccauuccu augguuuuucg	91	1.868.132	1.978.022	1.868.132	4.285.714	3.736.264	6.263.736	216.667	100.000	-42.9	-42.9	0.36593	1.78	-4.714.286	-126.176
spe-miR482b	auuuuucaggaagcuu uuggaguggguggcau gguaagauaucauauu uuauuuuucauaaaga aaaugaaauuaaaauc uuaccgauuccccccca uuccaauggcuuccag uuauuuc	119	1.680.672	2.941.176	1.680.672	3.697.479	3.361.345	6.638.655	125.714	100.000	-49	-48.6	0.13980	6.03	-4.117.647	-122.500
spe-miR482d	uuuggaguggguggg auggaaaaauauugu auuuguuuuuuuuuuc ugaagggaaaaagau	113	2.123.894	2.743.363	1.238.938	3.893.805	3.362.832	6.637.168	141.935	171.429	-42.9	-41.8	0.05820	16.47	-3.796.460	-112.895

	gaauauugagauuuu uccuauuccacccaug ccaauggcuuccaauc auuua															
spe-miR482e	guugaaagggaugag aguauugggaaguug uugguuguggguggg guggaaagauuugau aaaucuaauuuuuuuu ucuaauugaaaaaaaa aauggaaaagagauu aaaucuuuccuacucc ucccauacccaugacu uccacuagcuucuccc uuucuuc	162	2.098.765	2.901.235	1.543.210	3.456.790	3.641.975	6.358.025	119.149	136.000	-72.2	-72.1	0.02813	10.02	-4.456.790	-122.373
spe-miR5014a	cauuugucauacauga uacaucuacaugacaa cuuugucuccuacaug auauucuacguguauu augucauguaggacac uuguguguacuuguuc aauuuuguacaaauuu aaguguauacuugugc auauucaaaguugaag gacauaguuguuuguu gaagccaaauuaagcg ucauguauuaugccag cuaucuauauguuacg ucuuagauauugaaaa uuguugguuuucaucu caauauauguaaugca auuu	260	1.653.846	2.884.615	1.461.538	4.000.000	3.115.385	6.884.615	138.667	113.158	-62.4	-47.1	0.00072	59.25	-2.400.000	-0.77037
spe-miR5174d-1	uuacucccuccguuuc aaaaagauuggcuuag uuugacuuggaacgga guuuaagaaaagaaa gaaaacuuuuuaaucu ugugguucuaauuuaa aauuaugucaaaugua ccaaaauacccuuuaa ucuugugaucuuaaac augucauguggaaagu uaaaguuaaaguguu gccaaaaaaggaaauu ggucauucuuuuugaa acagacuaaaaaggaa auaggaccauucuuuu uuaaacaaagggagua	255	1.725.490	3.686.275	1.294.118	3.294.118	3.019.608	6.980.392	0.89362	133.333	-59.9	-54.7	0.00041	56.97	-2.349.020	-0.77792

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spe-miR5174d-2	auuuauuacucccucc guuucaaaaagauugg ccuacuuugacuugaa acggaguuuaagaaaa gaaagaagacuuuuua aucuugugguucuaau uuaaaguuaugucaaa uuuaccagaauacccu uuaaucuuugugcuu aaacaugccacgugga aaguuaaaguuaaag uguugccaaaaaagga aaggggucauucuuuu uuaaacagacuaaaaa ggaaaugggucauuc uuuuugaaacggaagg aguauauauuu	266	1.879.699	3.458.647	1.353.383	3.308.271	3.233.083	6.766.917	0.95652	138.889	-73.7	-56.95	0.00006	63.57	-2.770.677	-0.85698
spe-miR5174d-3	acuaauuuacuacucc cuccguuucaaaaaga uuggccuaguuugacu uagaauggaguuuaa gaaaagaaagaagacu uucuuuugugguucua aauuaaaguuauguca aauguaccaaaauucc cuuuaaucuuugugguc uuaaacaugccacgug gaaaguuaaaguuaa aguguugccaaaaaag gaaaggaucauucuuu uuugagcaaacuaaaa aggaaauagggacauu cuuuuuuaaacggagg gaguauauauuuuu	268	1.828.358	3.507.463	1.343.284	3.320.896	3.171.642	6.828.358	0.94681	136.111	-76.9	-58.4	0.00254	51.01	-2.869.403	-0.90471
spe-miR530	auuuuuaucugcauuu gcaccugcaccuuagu gaacgaauuuguucgc guaugauucgugcaga aagguguaggugguuca ugcagacaaaaau	93	2.258.065	2.688.172	1.720.430	3.333.333	3.978.495	6.021.505	124.000	131.250	-43.5	-43.5	0.15759	9.04	-4.677.419	-117.568
spe-miR5300	uugaccaaaauucuuc uuccccaguccaggca uuccaacaguugauaa caucuagaucugccaa uccuuuguauuuuugu ucuucuauuuuucaca ugacaucuucaaaauc	265	2.000.000	2.905.660	1.660.377	3.433.962	3.660.377	6.339.623	118.182	120.455	-91.8	-89.4	0.00145	16.00	-3.464.151	-0.94639

	cacugugagcuucauc auaagcuaagaaaugg ugaguuuugaugaug ugaugccuaaaauagg auuaaugaaaguacug guaaaaagguguucaa aucuggagguuauguu aagcuggugguaugcu uugauugggaaagau gacuuagguca															
spe-miR5303	auuuuugaagaguucg agcaacauagccuuca aguacaguuuucuuua uuuuaauaguuuugca uuaccuauugcuuuac gugaaauugcuuucuc uaguaaugaccuagcu ucgauauuguauuuuc augcaaaugaggagcu agaaaacacuauggaa agaggaugguuuaau uugauguugcuugaag aguucaaacac	202	1.881.188	2.970.297	1.435.644	3.712.871	3.316.832	6.683.168	125.000	131.034	-52	-50.1	0.00570	37.44	-2.574.257	-0.77612
spe-miR5303-1	uugcuaaguugcucgg acucuccaaaaauguc gcugcacccguguggg auccuaaaaaauacac uauuuuuggaggaucc gagucguacccguuga cauuuuugaagaguuc gagcaacauagauu	126	2.222.222	2.698.413	2.142.857	2.936.508	4.365.079	5.634.921	108.824	103.704	-56.8	-52.7	0.17151	8.89	-4.507.937	-103.273
spe-miR5303-2	uaaguugcucgaacuc uccaaaauuguugucg caccccugucagaucc uccaaaaaugcauacu uuuggaggauccaaca cguacccgucuacauu uuugaagaguucgagc aacaca	118	1.694.915	2.881.356	2.711.864	2.711.864	4.406.780	5.593.220	0.94118	0.62500	-53.8	-52.9	0.40031	2.06	-4.559.322	-103.462
spe-miR5303-3	ugaguugcucggacuc ucuagaaauguuguug cacccaucucggaucc uucaaacaugcacuac uuuugaaggauccggc acacacccaaaaacau uuuugaagaguucgag caacaua	119	1.848.739	2.941.176	2.521.008	2.689.076	4.369.748	5.630.252	0.91429	0.73333	-54.4	-54.4	0.17029	3.55	-4.571.429	-104.615
spe-	aaguauguuguucgga	126	2.936.508	2.698.413	1.825.397	2.539.683	4.761.905	5.238.095	0.94118	160.870	-55.2	-53.8	0.02783	8.01	-4.380.952	-0.92000

miR5303c-1	uucuucaaaaaauguc gacgggugcgugccag auacuccaaaaguagu gcaauguuggagaauc cgacacgggugcggcu acauuuuuggagaguc cgggcaacauaugg															
spe-miR5303c-2	ucuaaguugcggacuc uucaguuucaaugcgg cacccgugucugauuc uccaaaaauacacuac uuuuggagaauccgac acgcacccauugacaa uuuugaagaguccagc aauugca	119	1.848.739	2.773.109	2.605.042	2.773.109	4.453.782	5.546.218	100.000	0.70968	-55.9	-55.9	0.17403	4.28	-4.697.479	-105.472
spe-miR5303e	agggcuauguugcucg aacucuuccaaaaugu caacgggugagugucg gacucuucaaaauuag uguacuuuuggagaau cugacacgggugcaac aucgaaagugaagagu ccgggcaacuuagcau g	129	2.713.178	2.790.698	1.937.984	2.558.140	4.651.163	5.348.837	0.91667	140.000	-49.1	-48.91	0.06095	9.77	-3.806.202	-0.81833
spe-miR5303f-1	aagagauuaucucucu uuuuauggaaacucuu uaccuauguugcucgg acucuucaaaaauguu aaggggcgcgugccgg auucgccaaaaguagu guauuuuuggagaauc ugacacgggguuuggca ucgaaagugaagaguc cacgcaacauagcucu uuacuucuaguuuucu acacgguauguuagaa guaccaacuuucuuga auuuguuuuuuugua acggaccuuauuuguc uuuaacaaaaagcaaa aagaauuccacaaucu aaucacagguuugcga caaauugaaaugcaua aucugac	310	1.903.226	2.967.742	1.838.710	3.290.323	3.741.935	6.258.065	110.870	103.509	-93	-89.5	0.00004	27.38	-3.000.000	-0.80172
spe-miR5303f-2	ccugacuuauguugcu cggacucuucaaaaau gucaaagggugcgugu cggauucaccaaaagu	133	2.556.391	2.781.955	2.105.263	2.556.391	4.661.654	5.338.346	0.91892	121.429	-56.3	-54.5	0.07538	5.70	-4.233.083	-0.90806

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spe-miR5303f-3	gguugauuaaagcuau guugcuuggaaucuuc aaaauugucaaggggu gugcgugucggauucg caaaaguaguguauuu uuggagaaucugacac gggugcggcaucaaaa guaaagaguccgcgca acuuaggauuuaagca caa	147	2.789.116	2.925.170	1.496.599	2.789.116	4.285.714	5.714.286	0.95349	186.364	-45.7	-42.9	0.01030	24.09	-3.108.844	-0.72540
spe-miR5303h	aacauuuuugaagagu cugagcaacauagcug cuuaugguuuaggacu ucuauccaaacauaac ugcuuauucauaaaac cagcuucaauacuuaa augguucauacaaug uauuguaugaauuucu aucaaguuaacuugcc aauuuuaaaaaaagu aaaucacgguaaagcc cuuguuuaaauuguac uauaaauaccaaacgu aguuugagggaauaa ucaaguuuguccuucu caugaucuuucccaua uuagcagucuagcuua cauuuucuuuugcuug auaugauugagucaaa uauuuuaaaccuuugu ugcucggacucuucaa agauauc	341	1.407.625	3.196.481	1.759.531	3.636.364	3.167.155	6.832.845	113.761	0.80000	-79.9	-55	0.00002	89.56	-2.343.109	-0.73981
spe-miR5368	cuaaccuugugucagg accuacgggccaaggg acagucucagguagac aguuucuaggggcgu aggccucccaaaaggu aac	83	2.891.566	2.530.120	2.530.120	2.048.193	5.421.687	4.578.313	0.80952	114.286	-33	-33	0.44866	1.92	-3.975.904	-0.73333
spe-miR6024	agaugaggaagugga gaaacaacacuugcua aaggaacuucaccagu caucucuuuucuuuug gaguuuuuuuagcaag	102	1.862.745	2.647.059	1.862.745	3.627.451	3.725.490	6.274.510	137.037	100.000	-41	-41	0.07024	12.97	-4.019.608	-107.895

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spe-miR6027	uuuccauaauuuuaca ugauuauggguagcac aaggauuaaugugaa acaaauaagugauaug caaagaagauggagau ucaauuguuuauuguu acgaagaaaacacuuu uguguuucucgugaau ccuucggcuauccaua aucauguugaaugugu gacuu	164	1.951.220	3.231.707	1.280.488	3.536.585	3.231.707	6.768.293	109.434	152.381	-55.7	-45.9	0.01300	27.23	-3.396.341	-105.094
spe-miR6144	uaauucaacaacaaua auggcaacuucuucau cauguucuuuaucuuc cucuaaaucuucuacc acuuugguucuccac guggacaucgucggau caauuccgauguuugug gggcccuucucuuuca ucgggaccggugccgg aggagguuugaagaa gaguagauccauagcu uuuguugcaagau	188	2.127.660	2.287.234	2.287.234	3.297.872	4.414.894	5.585.106	144.186	0.93023	-58.4	-44.07	0.03128	29.81	-3.106.383	-0.70361
spe-miR6440b	cuacaagauaccauag gaaauauuauugaau uaucuuucaacgucgc cgaguuugaucaauuu cgaguuuguacgaggg agauaugcuuuuuuga aguugggaugucuaga uaaagaaagucaaaac cggauuuuagaaggga auuugggucuuuucac aacccaauuaauuaaa uuucuuugugguaauu uugaug	197	2.081.218	3.096.447	1.269.036	3.553.299	3.350.254	6.649.746	114.754	164.000	-47.2	-47.2	0.00377	22.18	-2.395.939	-0.71515
spe-miR6478	aaauggagaaaauaa aauauacauagcuuac acuauuagccuacuca uaaggauuacucauaa agagaguaauuauua guuaaacauuuuuguu ugacuaauaaagcagc aaccgaccuuagcuca guugguagagcggaag acuguaguuggugaaa	309	1.812.298	3.203.883	1.488.673	3.495.146	3.300.971	6.699.029	109.091	121.739	-73.8	-63.1	0.00007	65.34	-2.388.350	-0.72353

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spe-miR7696c	uuuugaugguuuaag gcuuucaaguuucguu gugugcaucgucuccu aagguccauuuuaugu uuuaauuggguugau uuauagcaagugaauu augaauugugacuucc aaggaaggaacuuuuu uuguuguaauaccaua caagucaaugguagag guucucucuuuuuuga auuaugaguacuugaa acucaaauagcuucca acggaauuuggaaaac uauuuauaacaucauu c	239	1.882.845	2.761.506	1.380.753	3.974.895	3.263.598	6.736.402	143.939	136.364	-54.9	-54.4	0.00225	32.44	-2.297.071	-0.70385
spe-miR7980b-1	ugaccaugugauauca uaucaugauauuguau ugugagauggaaucag uguuuggacauacgau uuuacgcugauuacau cucaugauuucauauc augagaugugauacca uuuccuccaaaaauca ugauauggaaucauau gggau	149	1.879.195	3.087.248	1.476.510	3.557.047	3.355.705	6.644.295	115.217	127.273	-61.5	-58.6	0.04587	9.11	-4.127.517	-123.000
spe-miR7980b-2	aagauacagaauccug agauggaaucaguguu uggacauacaauuuca cguugauuccaucuca uguuucaugucaugag	80	2.000.000	3.000.000	1.750.000	3.250.000	3.750.000	6.250.000	108.333	114.286	-27.4	-26.6	0.11557	11.26	-3.425.000	-0.91333
spe-miR7980b-3	gaaaugguaucacauc ucaugauaugaaauca ugagauguaaucagcg uaaaaucguaugucca aacacugauuccaucu cacaauacaauaucau gauaugauaucacaug	114	1.491.228	3.771.930	1.842.105	2.894.737	3.333.333	6.666.667	0.76744	0.80952	-33.4	-33.4	0.11747	5.54	-2.929.825	-0.87895

	gu															
spe-miR7980b-4	aaauauggcaucacau cucaugauauggaauc augagauggaauuagc guaaaaucgcuugucc aaacacugauuccauc ucacuauaccauaucg ugauauaauaucgcau agcu	116	1.551.724	3.448.276	2.068.966	2.931.034	3.620.690	6.379.310	0.85000	0.75000	-38.5	-38.5	0.10087	8.72	-3.318.966	-0.91667
spe-miR7980b-5	uaaaaucucaaaucau gauauagaauucucau aucaugauuuuuggag aaaaugguauuccauc ucaugacaugaaacau gagauggaaucaacgu gaaauuguauguccaa acacugauuccaucuc aggauucuguaucuug auaugauauugca	157	1.592.357	3.503.185	1.592.357	3.312.102	3.184.713	6.815.287	0.94545	100.000	-52.4	-52.3	0.06990	9.06	-3.337.580	-104.800
spe-miR7980b-6	uuuaauuugcuuugua acuccaugugauacca uaucacaauaugguau cgugagauggaaucag uguuuggacaugcgau uuuacgcugguuucau cuaaugagaugugauu ccauauucucgaagaa aucauuaugagaauuc ccuaucauaauuuga	159	1.823.899	2.893.082	1.572.327	3.710.692	3.396.226	6.603.774	128.261	116.000	-42.7	-38.1	0.00359	27.12	-2.685.535	-0.79074
spe-miR7981	agacacgccuuaacua aacuaagguccuauua ccccgaauccauuuuu cuguaauuuuuuguac aauuuuucggcuuaua uggcauccaaacgucu cgcacgcgcuucaucu auguagagucacggag ugugccacauaagcua aaauguguauaaacua acaaaaaaaaugauuu uggagguaauaggacu uuaguuuaguuaaggc augucu	214	1.775.701	3.084.112	1.915.888	3.224.299	3.691.589	6.308.411	104.545	0.92683	-92.5	-92	0.02437	18.17	-4.322.430	-117.089
spe-miR7983-1	uauuuuuagcggcaau ugucacucuuuguaua uguccccuaaagccuuu agcgacauugguucua aggacacuuaacuaau	137	1.605.839	2.919.708	1.824.818	3.649.635	3.430.657	6.569.343	125.000	0.88000	-45.9	-45.8	0.11629	4.48	-3.350.365	-0.97660

	gccgguaaagacuuua acauucuuuaauagug ucaauauuuaaugccg cuaaaaguu															
spe-miR7983-2	uacaaaaaugaccauu agcggcauuuaaaucu uauuugccgcuaaaua uguauuuuuagcggca auugucacucuuugua uauuucccuaaagccu uuagcgacauugguuc uaaugacacuuaacua augccgguaaagacuu uaacacucuuuauuag ugucaauaucuaaugc cgcuaaaaguuauuuu uguu	196	1.428.571	2.959.184	1.836.735	3.775.510	3.265.306	6.734.694	127.586	0.77778	-64	-60.1	0.02231	15.33	-3.265.306	-100.000
spe-miR7983-3	ucccaucacaacaaca aaaaagaccauuagcg gcauuuaauucuuaau ugccgcuaaauauaua uuuuuagcggcaauug ucacucuuuguauaug ucccuaaagccuuuag cgaaauugguuguaau gacaguuaacuaaugc cgguaaagacuuuaac acucuuuauuaguguc aauauuuaaugccgcu aaauguuauuuuuau uguagugcauguuu	221	1.493.213	3.076.923	1.764.706	3.665.158	3.257.919	6.742.081	119.118	0.84615	-67.2	-65.4	0.01364	17.74	-3.040.724	-0.93333
spe-miR7983-4	uguauuuuuagcggca auugucacucuuugua gauguccuuaaagucu uuagcgacauugguuc uaauggcacuuaacua augccgauaaagacuu uaacaccuuuauuagu gucaauauuuaaugcc gauaaaaauugu	140	1.642.857	2.928.571	1.642.857	3.785.714	3.285.714	6.714.286	129.268	100.000	-38.6	-38.6	0.05872	10.75	-2.757.143	-0.83913
spe-miR7983-5	uguauuuuuagcggca auugucacucuuuaua uauguccuuaaagucu uuagcgacauugguuc uaaugacacuuaacua augccgguaaagacau uaucacucuuuauuag uguuaauauuuaaugc	141	1.418.440	2.978.723	1.631.206	3.971.631	3.049.645	6.950.355	133.333	0.86957	-37.8	-36.5	0.02909	17.76	-2.680.851	-0.87907

	cgcuaaaaauuau															
spe-miR7983-6	uugacacuacaacaaa aaugaccauuagcggc acuuaauucuuaauug ccgcuaaauauguauu uuuagcggucauuguc acucuuuguguauguc ccuaaagucuuuagcg acauugguucuaauga cacuuaacuaaugccg guaaagacuuuaguac ucuuuauuaguguuaa uauuuaaugccgcuaa aaguuauuuuuguua uagugugac	216	1.620.370	2.870.370	1.712.963	3.796.296	3.333.333	6.666.667	132.258	0.94595	-76.1	-74	0.00652	18.79	-3.523.148	-105.694
spe-miR7983-7	ccacacuacgauaaaa auggucauuagcggca uuuaauucuuaauuau cguuaauuauguauuu uuagcgauaauuguca cucuuuguauauauuc cuaaagccuuuagcga cauugguucuaaugac acuuaacuaaugccgg uaaagacuuuaacacu cuuuauuagugcaaaa uuuaaugucgcuaaaa guuacuuuuguuguag ugcac	213	1.455.399	3.051.643	1.690.141	3.802.817	3.145.540	6.854.460	124.615	0.86111	-58.9	-58.9	0.01200	13.43	-2.765.258	-0.87910
spe-miR7984	caaaggaaaaaaaauc ugaaauauauccuaac gcugacuuguaauaau cccaaacuuuggaaau gacucuuugcccuugc acuauuuaauagaucu uguccauguggucaca uauauaccuuuaaaau acacuauuaaauagug cugagguaauagaucc uaaucacaguuugaaa uuguugcagcaauuuc ggucaaaguucagaua uauuucgaaccuuuuu ccuaaa	230	1.391.304	3.478.261	1.826.087	3.304.348	3.217.391	6.782.609	0.95000	0.76190	-66.5	-65.7	0.02502	15.80	-2.891.304	-0.89865
spe-miR7984b	uacgauaucaaacuuu ggaaaugaccuuuuaa ccucuacaucauuuaa uaguguauuccacgug	205	1.414.634	3.560.976	1.609.756	3.414.634	3.024.390	6.975.610	0.95890	0.87879	-67.3	-62.7	0.00723	17.82	-3.282.927	-108.548

	gacauuauauauauug cauauuacaaauagua auguguccacgucggc acauauauaccuuuaa aauacacuauaaauag ugcagaggguaaaagg ucuuucauaaaauuug guauuguaauaacacu uucgaucaaaguu															
spe-miR7984c	aaaucugaaaaauacu ucaauuugagcugaca uuguugccaaacuuua agaaugacauuuuacc cccugcacuuuuuaac aauauauuuuaaaag uauauauguguccacg uggacacaacacuauu uaaaaugaugcaauau uuaugauguccuaaaa uacauuauuaaauagu gcagggguaaaaaagu ccuucauaaaguuugg uaucguaacaacaauu ucgaucaaaauucgaa uauauuucucauuuuc aaccuaaauuuuacga guuaauaccucagaug gucacucaacuuugca cuauucucucagaaag	319	1.253.918	3.605.016	1.755.486	3.385.580	3.009.404	6.990.596	0.93913	0.71429	-79.9	-71.3	0.00003	52.62	-2.504.702	-0.83229
spe-miR7987	uuuagcguaaguacca acacuaguugaucuua uugaugacaaaguuaa uuuucuugcaaaaucg auuuguguccaucuag uguugauauuaagcuu ua	98	1.632.653	2.959.184	1.428.571	3.979.592	3.061.224	6.938.776	134.483	114.286	-23.3	-22.2	0.05915	17.14	-2.377.551	-0.77667
spe-miR7990a-1	ccaaggcaaaaaguuu uuaccauuugaaguuu cacaaauuuacaacug cuuuuucugaguuaca cucuuuguuuuuguga aacuucaaaugaucgu aacuuuggccucaa	110	1.363.636	2.909.091	1.909.091	3.818.182	3.272.727	6.727.273	131.250	0.71429	-34.9	-34.9	0.19711	7.37	-3.172.727	-0.96944
spe-miR7990a-2	aacauuuggggaaaaa aguaugaccguaugaa guuucaaaaauuuaca acuacuuuuauugagu aacacucuuuaauuug	119	1.512.605	3.613.445	1.512.605	3.361.345	3.025.210	6.974.790	0.93023	100.000	-32.3	-23.3	0.05367	16.03	-2.714.286	-0.89722

	gugaaacuucaaauga ucguaacuuuggccuc aaauauc															
spe-miR7992	acacuauuggccucaa uuuccaaucaauacuc caacuuuggagugcac auccagauacuucaaa ucauguccacuauauc aauugaacacuccaac aguccaacuuacaaaa agaacuuguagacacc accaaaauuuacgugu cacgucaacgucgagu guccacaagaucagug ggacagaguugagaug ucuagaugugcacucc aaaguuggagaguau uaucuaaguguuaugc caaaagaaa	248	1.693.548	3.467.742	2.298.387	2.540.323	3.991.935	6.008.065	0.73256	0.73684	-83.6	-77.7	0.00161	22.87	-3.370.968	-0.84444
spe-miR7993a	cuuauguaucaaguag auaaguuaaacacuua aaaugucaaccuucuu gauaauaugcauuugu cucaauaagccguaaa acuucaccccuauggc aauugaggcugaugug uguccuuaaaggagag gagaugacauauuuua ugugguuaacuuaaau cuaucuucuaucaugc u	177	1.694.915	3.163.842	1.694.915	3.446.328	3.389.831	6.610.169	108.929	100.000	-51.8	-45.2	0.00151	18.51	-2.926.554	-0.86333
spe-miR7993b-1	caccucaaccccuaau acaguguuccaauuag acacuuuugguucaaa uguuggggaaauuuu gaguggucuuguacgu cuauuugguaguuaag uuaaccacauacagua ugucauuucauuuuau uuuacacauucaccuc gauaagccguaaacca caugcauuuuccacuu gagguugauguguau aauuaauggacagcuu aauuuacgugguuaaa uuaacuaccuggguca aaaguguuuaccucaa acacuuuauaggaguu	276	1.811.594	2.862.319	1.811.594	3.514.493	3.623.188	6.376.812	122.785	100.000	-87.2	-81.42	0.00014	33.99	-3.159.420	-0.87200

	gaggug															
spe-miR7993b-2	uccuuuaauuauaugc aucaaccucaaguagg aaaugccugagguuua ugacuuucugaggcaa guguuauaauuaaag uaaaugacauauuuua ugugguuaacguaauu accuaauaaacgacag agaaugccaaauuaag uucaaaauuuaaauug aaagugucuaauggga acucuuuauuaggagu ugagguguucaauugg aagagacuuaguuuga guaucuaaauaaaaau	239	1.882.845	3.640.167	1.129.707	3.347.280	3.012.552	6.987.448	0.91954	166.667	-51.3	-43.2	0.00101	62.74	-2.146.444	-0.71250
spe-miR7997a	aauuuguuaguauau auaugguaauugaacc cuauaugcugcucgga cucuucaaaaaugucg uuacguccgugucgga uccuccaaaaguagug cauuuuuuuaaggauc ugacacaucaacauuu uugggaaauccggauc uauugcuuuugguaua aaccauguauaaacac auacaaagg	184	1.793.478	3.043.478	1.793.478	3.369.565	3.586.957	6.413.043	110.714	100.000	-48.6	-44.8	0.00508	31.25	-2.641.304	-0.73636
spe-miR7997a-1	caaucuaugcugcucg gacucuucaaaaaugu cgauaggugcauguaa gauacuucaaaaauua ugcauuuucaaagaau ucgacacgggugaugc aacauuuuuggagagu cugagcaacauagacg a	129	2.093.023	3.333.333	1.782.946	2.790.698	3.875.969	6.124.031	0.83721	117.391	-48.2	-48.2	0.09329	8.88	-3.736.434	-0.96400
spe-miR7997a-2	auggcaugcugcucgg acucuucaaauauguu gcuaggucuuuguugg auccuccaaaaguagu gcauauuugaaggauc cgacaugagugcggua acauuguuggagaguc cgagcaacauagcaga	128	2.656.250	2.656.250	1.875.000	2.812.500	4.531.250	5.468.750	105.882	141.667	-65	-63.7	0.03423	9.28	-5.078.125	-112.069
spe-miR7998	uauagacgguaggucc agucacgguccauuag uggguagaccuagauu	231	2.380.952	2.813.853	2.121.212	2.683.983	4.502.165	5.497.835	0.95385	112.245	-75.1	-67.6	0.00164	45.87	-3.251.082	-0.72212

	ucucaucuaggauguu ugaguaugugucuaac uaccgaggcuagugac ggaccguagaucaauc cacgguccauacugca cguuuaucaaugauca cuuagaguuaaauuua aaagucuggaugaaaa auucuaaguguggacc cacggaggacccaugg accauggaucgacccg uacuuca															
spe-miR8001a	cugacacuauaacaau uugugaauuaaaugg ggauuuuccuggggau uaguaugaaaauucgc ggggaacuuauuuuuc ugcauauuuucauacu aauccccacggaaauc uccauauaauuuacac uuuucuuguaguguga a	144	1.736.111	2.916.667	1.666.667	3.680.556	3.402.778	6.597.222	126.190	104.167	-72.8	-72	0.13632	6.44	-5.055.556	-148.571
spe-miR8001b-1	gcauucaacaguaaaa uucauagucaguguua cuaauauagaggauua caaaaguggcuuauua ugaaugaaauauaau ugaaaggaacaggcua auuacuagacgcguga acacuauaagaagagg gugaucuauauggaga uuuuccuggggguuaa guaagaaaauuugcag gaaaauuucgugugga uuuucauacuaauucc uaggaaaaucccaugu aauucacaguuugaau gcauuaaaaagggaca aauuuuagcggauggu gcugcuacguggaaag acagaaaacagaaaac agaaaacaagcacuac ucagaauuuuuacuua gaaucu	341	2.082.111	3.841.642	1.319.648	2.756.598	3.401.760	6.598.240	0.71756	157.778	-87.2	-85.2	0.00014	28.98	-2.557.185	-0.75172
spe-miR8001b-2	aaacacuacaagaaaa gggguaaauuacauggg gauuaguaugaaaau uugcagggauuacccu	90	2.000.000	3.777.778	1.333.333	2.888.889	3.333.333	6.666.667	0.76471	150.000	-34.1	-34.1	0.32729	5.28	-3.788.889	-113.667

	guaauucacacuuuuc uuguagugaaa															
spe-miR8005	guuuuagggucuacga ccuaagauuuaugguu uagaguuuaggauuu aguguuuugauuuua gggucuaggccuugag guuuagaguuuaggg uuuaggguuuaugccg uaaggguuuaggguuu aaggauuaggcuuaag auuuagauuuugggg uuuagacccuaaggu	170	3.000.000	2.176.471	764.706	4.058.824	3.764.706	6.235.294	186.486	392.308	-61.2	-61.1	0.01259	35.46	-3.600.000	-0.95625
spe-miR8006	guaaaugguaugcaaa uuaucccauuauauuu uugagacgcugguguc ucuaccguucaaaaac uagagcauauacaaua uguccuucacucuaac ggaagacuaaauaggg acacgugacacaaucu uaucugucgauaaaug uuuaagauuauaccau guccguuaguauaaau gauauauauguucuag uuuuuggacggcaggg gcaccaauguccccaua aauaugacgaaauaua uuuacauaucauuuau	256	1.679.688	3.320.313	1.718.750	3.281.250	3.398.438	6.601.563	0.98824	0.97727	-90.9	-88.3	0.00127	24.68	-3.550.781	-104.483
spe-miR8007a	accuacucccuccguc ccauuuuaugugacac uuuucggauuucgaga uucaaacaaguguauc uuugaccauaaauuuu ucauagauauuuuaaa cauuuugaauuaucac cuauugugacuuauag uacuuuuuacguaguu uguaaauauauaaau uucguuuaaaaaaauu gaagauuucaugcgca aauucucggucaaauu uaaacgguuugacucu cgaaaaaugaaaagug ccacauaaauugggau agagcaaguauua	268	1.417.910	3.320.896	1.604.478	3.656.716	3.022.388	6.977.612	110.112	0.88372	-80.1	-75.4	0.00092	29.31	-2.988.806	-0.98889
spe-miR8008-1	uuuuguccgucgcuuu uuugcuuuauuuuuuu	127	1.732.283	2.834.646	1.811.024	3.622.047	3.543.307	6.456.693	127.778	0.95652	-42.6	-40.8	0.01050	19.08	-3.354.331	-0.94667

	caaauaaacccagaaa agcgacggacaagguu cuuugguccgucacuu cucuagguauuuuaaa aaauuaauuucaagga aagcgacagacauug															
spe-miR8008-2	uccaucucuuuuuuca acuaaacucagaaaag cgacggacagaaaccu uuaguccgucgcuuuu ccggcuacuuuaaaaa auucauuuccagaaaa gugacggacagugucc uuuaguccgucgauuu ucugagauuuucaaaa uauaaauuua	154	1.493.506	3.051.948	2.142.857	3.311.688	3.636.364	6.363.636	108.511	0.69697	-49.7	-45.7	0.02256	11.33	-3.227.273	-0.88750
spe-miR8008a-1	caaaaaaauugcagaa aaagcaauggacagcg uggucuaguccguugc uuuucuugguuuuuu aaaaauaauuuccaga aaagcgacgaacagug uccuuuuguccgucgc uuuuuugggauuuuuc aa	130	2.000.000	2.846.154	1.692.308	3.461.538	3.692.308	6.307.692	121.622	118.182	-49.6	-49.6	0.01602	11.71	-3.815.385	-103.333
spe-miR8008a-2	uaauuuccagaaaagc gacgaacaguguccuu uuguccgucgcuuuuu ugggauuuuucaaaaa ugaaauuucuacaaaa gugauaaacggcgucg cauuucgggaauuaaa aaaaaacauaucggcg gaguaugucgcuuaug uuuaaaaaauuaaaa aauaauaauaauaag uucacgacagugucug ucgcuuugggaaaagc	206	1.941.748	3.543.689	1.504.854	3.009.709	3.446.602	6.553.398	0.84932	129.032	-55	-28.8	0.00236	78.49	-2.669.903	-0.77465
spe-miR8008b-1	aaacccagaaaagcga cggacagggguccuuaa gucugucgcuuuucug gguuuu	54	2.592.593	2.407.407	2.222.222	2.777.778	4.814.815	5.185.185	115.385	116.667	-35	-35	0.29561	2.40	-6.481.481	-134.615
spe-miR8008b-2	uugaaaauugcagaaa agugacguacuaaagg acccuauccaucacuu uucugaaaauuauuuu uuugaaaaacccagaa aagcgacagacuuaag	194	1.752.577	3.144.330	1.907.216	3.195.876	3.659.794	6.340.206	101.639	0.91892	-73.9	-73.9	0.02030	12.64	-3.809.278	-104.085

	gacccuguccgucgcu uuucuggguuuauuug aaugaauuaugcaaaa aagugauggacaaaac gacccuguccgucgau uuuuucugcauuuuuu ac															
spe-miR8008b-3	uugucacuuuucuggg uuuuauuuuuuuaaa aaacccagaaaagcga cggacauuguucuuua guccaucgcuuuucaa gaguuccaaaaaauga aacuuccagaaaagcg augg	115	1.739.130	3.130.435	1.826.087	3.304.348	3.565.217	6.434.783	105.556	0.95238	-45.1	-42.7	0.04896	10.47	-3.921.739	-110.000
spe-miR8011	gacacuagucgaguga gacucauuuuugucuc acaaaaauuaagccca uuugagucuacacuuu uaugugagacaaaaag aagucucacacaacua guauu	101	1.584.158	3.465.347	1.980.198	2.970.297	3.564.356	6.435.644	0.85714	0.80000	-37.4	-35.67	0.08846	8.95	-3.702.970	-103.889
spe-miR8011a-1	ugaugaacuuuguuuu gugucucacacaacug auguaaguuguguga ggucucuuuuguuuu aaaagucagugcgacc caaaucguuggacuca ccaacucgugaaauaa aaagaagucucacgca acuugcguuaauucug ugagccgcaaaguaaa uuuucaaau	168	1.964.286	2.916.667	1.845.238	3.273.810	3.809.524	6.190.476	112.245	106.452	-66.1	-65.7	0.01854	12.98	-3.934.524	-103.281
spe-miR8011a-2	cagcugacacuaauua ugugggcuucuuuuu gucccacaaguuggug aacccaaaucauuaca cuucuggguccaccga cuuguaaaauaaaaag aagccucacagaacug guguuaguug	122	2.049.180	2.868.852	2.213.115	2.868.852	4.262.295	5.737.705	100.000	0.92593	-66.4	-66.1	0.22206	2.25	-5.442.623	-127.692
spe-miR8013	uuaaaaaaaacaaaau cgaugcuguggcagca acuucguccaaaaaau uuuuuuucuuaaaauc gcugccauugucaaaa aaaauuuugacauaag agggaggcaaacaagc	287	1.672.474	3.763.066	1.463.415	3.101.045	3.135.889	6.864.111	0.82407	114.286	-80.5	-79.5	0.00093	36.98	-2.804.878	-0.89444

	uagcagccucuauugc uggcuugcugcaaaga uaggaaaaagaaaucg cugcuauaguaacaau uuaauuuuuuuaaaa aaaauauuguacaugc aacgauauuaauagaa aaguuaugguauuaa uuuuuucagaagaaaa ucgcuucgucaggagc gauuuugcucuuuuaa u															
spe-miR8016	agcaaacgcuugcuug ccuaugcuagaaaaag uauaauuuucaugaua gcaguaugcaugguc uuucuuucaaaaauau auaauuacaccuagua auuauauauuuuuga auggaaggcccaugug uauuucauucuugaaa cuuuuucucauaggua augaacauuucca	172	1.453.488	3.197.674	1.569.767	3.779.070	3.023.256	6.976.744	118.182	0.92593	-63.9	-62.8	0.07146	6.87	-3.715.116	-122.885
spe-miR8019	auuauuauacucccuc uguuucauaaagaaug accugguuugaguuga cacgguguuaaagagu auaaagaagacuuuuu gaaucagguuguccua aauuaauguuaggug aaauguacaaaauugu ccuuugaucuuguggg cuuaaacaugcugcau ggagaguuuaaauua aaaucuuaccaaaaaa aaaagaaagagauua uuauuuuugaaacaca cuaaaaagaaaaggag gucauccuuuuagaaa cggagggaguucauga a	270	1.962.963	3.703.704	1.222.222	3.111.111	3.185.185	6.814.815	0.84000	160.606	-65.1	-58	0.00012	48.19	-2.411.111	-0.75698
spe-miR8020	gaauuucauugaguau guuguuguuguaaagc auacugaauuaaugca aguacaaaaguuacaa caacaacauacuugcu gaaauacc	88	1.590.909	3.863.636	1.477.273	3.068.182	3.068.182	6.931.818	0.79412	107.692	-32	-32	0.23198	3.42	-3.636.364	-118.519
spe-miR8021	auucaaggcucaaacu	226	1.504.425	3.185.841	1.637.168	3.672.566	3.141.593	6.858.407	115.278	0.91892	-71.9	-65.97	0.00231	33.09	-3.181.416	-101.268

	cgagaccucugauuaa ggauggauauuucaua uacauccccucguaau uauuguugguucuuaa cuuauaauaauaacau uauucacacucacuug cauauuaugcaauaug uugaauuaaguuauu gaguucuaccaauaau auuguguuggagaag aaguuaauauuacuuc auccuuaaccagaagu uucaaguuugagucuu ggca															
spe-miR8024	cuuggaguauuugaag acuuuagcuugcacuu ggaggauuuaaagacu ucagcuugcaaacuug gaggauuugaagacuu caacu	85	2.352.941	2.823.529	1.529.412	3.294.118	3.882.353	6.117.647	116.667	153.846	-24	-24	0.07273	5.16	-2.823.529	-0.72727
spe-miR8024a	uuaaagaauuugaag acuucagcuugcagaa aagaauuugaagacuu caaguugcagaguuaa agaaucugaagacuuc caccuggagacuuaaa guauuugaagacuuca acuugcauuguugaau gauuugaagacuucau cucgcauacucgggga auuugaagacuuuagc uugcauacuuggagga uuugaagauuucaacu ugcauacuccgggaau uugaaaacuucaaucu uaaa	243	1.975.309	3.333.333	1.563.786	3.127.572	3.539.095	6.460.905	0.93827	126.316	-62	-55.2	0.00064	53.56	-2.551.440	-0.72093
spe-miR8025	ucauacaucauaaaga aauauuuuaccacaca cuacacaugcaauuaa auuaguauaagucgcc auuauguuuuucuuaa ccaagcugaaucauau aauggugacuuauacu aauuuaauugcaugcc gagugucug	137	1.240.876	3.503.650	1.824.818	3.430.657	3.065.693	6.934.307	0.97917	0.68000	-56.1	-56.1	0.34591	3.73	-4.094.891	-133.571
spe-miR8026	uagucguaaauugguu ucuaccuccuugcccu aacuuuauauuaccac	124	2.338.710	2.903.226	1.774.194	2.983.871	4.112.903	5.887.097	102.778	131.818	-39.4	-38.2	0.01056	19.12	-3.177.419	-0.77255

	aaccguuagcgaugga auuaauguagagaau augugguaacccuaau gggugggaggaggacc aauuuacagaggu															
spe-miR8032a	ucgaucaaaaguucaa gaagaugacaucaaaa uccaauucugaugauu ccaucaguuccggaag ggucauuuuaggcuag uagcauugucgacaug acucccgaaguuuuca gugugaguuggugug auuaggcguuuuaacu uuaaguuaaagcuaac uuugacuuuagucaac auucugaguaaacgcg cucggaugagaauucc gucagcgcugcuagcu ccggaaugucgaguuu ggucuaguuugacccu ucuuucauguucugag guuuuugauauu	283	2.261.484	2.508.834	1.837.456	3.392.226	4.098.940	5.901.060	135.211	123.077	-89	-80.4	0.00018	50.88	-3.144.876	-0.76724
spe-miR8036	gggagggaucgaaagg uaauaaggauuuaua uauuuuuucgauuuga uugggaaaaaaaaga auuaugucuuuccgau gccuccca	86	2.325.581	3.255.814	1.162.791	3.255.814	3.488.372	6.511.628	100.000	200.000	-28	-25.9	0.06799	15.77	-3.255.814	-0.93333
spe-miR8038a	uauuuuucaagucaaa acaguuucuccuugug aguaaguuggaucuca ugcucguuaaaccaca agauauguagaaugcg uccuaacaugagauuc aguuuacucacaagga aaaauuguuuuugcuu gagaagca	136	1.838.235	3.161.765	1.691.176	3.308.824	3.529.412	6.470.588	104.651	108.696	-58.3	-58.3	0.11703	9.15	-4.286.765	-121.458
spe-miR8039	uagaacuaucagaagu uacguuuuccuaucug aacuaucaccaucguu cagguaggaagaggaa acaauugacaguugag uuguguuuuaauacau ggauggugauaguuca gguaagaaaagggaac aacugauaguugga	142	2.464.789	3.380.282	1.267.606	2.887.324	3.732.394	6.267.606	0.85417	194.444	-56.8	-53.1	0.06216	9.51	-4.000.000	-107.170
spe-miR8042	uaccuauauaguaugu	158	1.772.152	3.417.722	1.708.861	3.101.266	3.481.013	6.518.987	0.90741	103.704	-52.2	-52.2	0.05278	13.07	-3.303.797	-0.94909

	uaaaccaccagauaag cacuuccaucuaauuu cuaaaagguggucaag ggaacgaggugugaa acacaugugacuugac acaacuuucagaaauu agacugaaaugcugau cugguuucuuauauac auuauacauaguuu															
spe-miR8045	auuuuuccuaacugaa cuauaucaacuuauca aauauuguucucuuuu uucuaccugaucuacu cugcugggccgacacu gacacugagagacuaa agcuaggggagcuaau gggauucauuaacuau uuaucaauuauacauc agcugucaguuguuuc cuuuuacuagaugaaa uaucaucacuguucau uuaggauaaggaaau ugauaguugaggugu guuucgauaaacauuu gauaauaguuuaccug ggaaacua	262	1.717.557	2.977.099	1.679.389	3.625.954	3.396.947	6.603.053	121.795	102.273	-67.4	-52.8	0.00008	47.26	-2.572.519	-0.75730
spe-miR8047	cauauuuacaccaggu agucaauuuugugccc uuguaucaacaauuug accauuuuuucgaaau uagacccauggucuga auaccaguuuugaacu uugaaauacagaccag guggccacuuucgaac uucagaucacugggcu aauuuugaaaaagug gucaacuucuaaauac aaagccacaaaugagg uuauuuguguaaauca g	208	1.730.769	3.173.077	1.923.077	3.173.077	3.653.846	6.346.154	100.000	0.90000	-69.3	-62.1	0.00101	23.38	-3.331.731	-0.91184
spe-miR8051	aaccaggucauauaau aaaucacacaaacaga uauauaauaguuguuc uauucuuaguucucuc caauugcaauggccuc uucaaaauaguuuaua uuucacauuauaaaaa aaaauuggguggag	334	1.916.168	3.443.114	1.526.946	3.113.772	3.443.114	6.556.886	0.90435	125.490	-83.3	-58.45	0.00003	85.19	-2.494.012	-0.72435

	ggagaauuagagggggguuagauuacaguuuugggaauugaauccucaccaacaagguggaguucaauuggccuaccgacuaagcaauuaaaauuccccuucuauuucacaugaaaacuugguga acuagaaucggcgaaauucuaauagauagauaguaugguagaaagauucaucucaugugaguuuuuuaugaccaugaua														
spe-miR8175-1	aaucaagaaaauauuaacuaaacuauagugauaaguucaaguuaaucuaaaagcuaugaucccggcaacggcgccaaaauuuauuacgcucaaacuuacuucucaaauaagaaguaaagcggucgugucaaguaaauaacccaacuaguaagguuggaucguucccacgaggaaaauagucuagacuuaacuucaacuuguuauuacuauuguuugguuaaugacuuccuuggaa	237	1.687.764	3.586.498	1.814.346	2.911.392	3.502.110	6.497.890	0.81176	0.93023	-69.3	-67	0.00042	27.82	-2.924.051	-0.83494
spe-miR8175-2	nnnacgaccgcuuuacuucuuauuugagaaguaaguuugagcguaucaaauuuuguauagugguacguauucccgccugucacgcgggugacccggguuggauccccggcaacggcgccaaaauuugauauacucaaacuuacuucucaaauaagaaguaaugcggucguuuc	173	2.196.532	2.485.549	2.196.532	2.947.977	4.393.064	5.433.526	118.605	100.000	-93.7	-91.6	0.13394	20.41	-5.416.185	-123.289
spe-miR827	guuuguugauggucaucuauucaucauaucauuuggcauaguuuaugcaaccauuaauauguca ugauuagaugaacaucaacaaaca	88	1.477.273	3.295.455	1.590.909	3.636.364	3.068.182	6.931.818	110.345	0.92857	-33.5	-33.5	0.10637	10.78	-3.806.818	-124.074
spe-miR828a	auuuacauucacuucuuugggaaagccucuug	119	1.764.706	2.941.176	1.680.672	3.613.445	3.445.378	6.554.622	122.857	105.000	-48.2	-48.2	0.09018	5.37	-4.050.420	-117.561

	cucaaaugaguauucc aacaaaugucuaauug acauacuuuugagaua cucauuuggguaagaa guuuuaccaggaaggu uguacuu															
spe-miR9469	ccaaagcuaacucaug aggagagguuugucca aguccauauaaggaga ccaaauuccuuaagau gucccacagcgguaga gguaugggaauucggu cuucuuauauggacuu gacaaaccuauccuca ugagcuagcuuug	141	2.269.504	2.907.801	2.127.660	2.695.035	4.397.163	5.602.837	0.92683	106.667	-85.1	-85.1	0.19186	4.69	-6.035.461	-137.258
spe-miR9471b	uugagauucaguugau uucugaggugcucacu cagcuaauaguuauug uuuaagaaacucgaua auauuggcagcaagga gaauggugacuuucag gaugauaacuauuggc ugagugagcaucacug aaaucgacaugauucu gag	147	2.448.980	2.993.197	1.428.571	3.129.252	3.877.551	6.122.449	104.545	171.429	-64.5	-64.4	0.05632	9.57	-4.387.755	-113.158
spe-miR9473-1	aaaacaauauuggcug uaaaucugaacucguu uuacuccacuagucuc uucuucuaguaaauga cauuacaugaugacua gugugugaaacgagu uuagguuggugugaa acgaguu	118	2.118.644	2.966.102	1.525.424	3.389.831	3.644.068	6.355.932	114.286	138.889	-42.5	-41.6	0.04516	9.82	-3.601.695	-0.98837
spe-miR9473-2	cggaaaaugugaguga acuagcagauauuggc uguaaaccuaaacucg uuucacaccaaccuaa acucguuucacaccac uagucaucauguaaug ucauuuacuagaagaa gagacuaguggaguaa aacgaguucagauuua cagccaauauuguuuu gcuugcacgcauuuug gu	178	1.910.112	3.202.247	1.966.292	2.921.348	3.876.404	6.123.596	0.91228	0.97143	-56.8	-47.8	0.00379	33.80	-3.191.011	-0.82319
spe-miR9476-1	ccuguccaaaacugcu auuggucuaguccugc aucucuuuuuauauuu	108	1.574.074	3.333.333	1.759.259	3.333.333	3.333.333	6.666.667	100.000	0.89474	-58.4	-58.4	0.42957	1.75	-5.407.407	-162.222

	uuuucguuaucaaaaa auauaaaaaaaaaugc aggacuagaccaauag caggauggauug															
spe-miR9476-2	agccaauccauccugc uauuggucuaguccug cauuuuuuuuuauauu uuuugauaacgaaaaa aauauaaaaagagau gcaggacuagaccaau agcaguuuuggacag	110	1.727.273	3.363.636	1.636.364	3.272.727	3.363.636	6.636.364	0.97297	105.556	-64.8	-64.8	0.64210	1.56	-5.890.909	-175.135
spe-miR9477	uaucugaacuaucacu aaacguuuaucgacac acacaccucaacuauc aguuguucucuuuucc uaccugaaugauggug auauuccagguuggga aagggaacaacugaua guugagguauguuucg auaaacauuuggugau aguucagnaa	154	1.948.052	2.987.013	1.818.182	3.181.818	3.766.234	6.168.831	106.522	107.143	-92.3	-86.7	0.07699	9.40	-5.993.506	-159.138

Supplementary Table S10. Statistical analysis of the thermodynamic and structural characteristics of *S. lycopersicum* and *S. pennellii* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Characteristics	*Solanum pennellii*		*Solanum lycopersicum*		t-Test	
	Mean	Median	Mean	Median	*p-value*	Conclusion
Size	150.27	132.50	150.41	139.50	0.981>0.05	Same
G	20.00	19.64	19.96	19.84	0.889>0.05	Same
A	29.35	29.15	29.47	29.67	0.778>0.05	Same
C	18.11	17.74	18.11	17.48	0.993>0.05	Same
U	32.52	32.98	32.46	32.91	0.896>0.05	Same
GC	38.12	37.13	38.07	37.18	0.924>0.05	Same
AU	61.87	62.87	61.93	62.82	0.909>0.05	Same
AU ratio	1.14	1.12	1.13	1.12	0.740>0.05	Same
GC ratio	1.13	1.07	1.13	1.08	0.936>0.05	Same
MFE	-55.59	-52.00	-56.38	-55.80	0.613>0.05	Same
MFEE	-52.98	-49.35	-53.91	-51.70	0.532>0.05	Same
Freq	0.1040	0.0469	0.1181	0.0491	0.324>0.05	Same
Div	15.75	10.43	14.82	9.81	0.505>0.05	Same
AMFE	-39.12	-38.57	-39.42	-39.91	0.715>0.05	Same
MFEI	-1.027	-1.033	-1.040	-1.040	0.498>0.05	Same

Supplementary Table S11. Statistical analysis of the thermodynamic characteristics of *S. lycopersicum* and *S. pennellii* pre-miRNAs with the *Solanaceae*, *Fabaceae* and *Brassicaceae* pre-miRNAs (Minimum Free Energy (MFE) and Minimal Free Energy of the thermodynamic ensemble (MFEE)).

Characteristics	***Solanacea* family**		***Solanum lycopersicum***		**t-Test**	
	Mean	**Median**	**Mean**	**Median**	***p-value***	**Conclusion**
MFE	-52.89	-45.80	-56.48	-55.80	0.076>0.05	Same
MFEE	-51.32	-44.80	-53.91	-51.70	0.172>0.05	Same
	***Solanacea* family**		***Solanum pennellii***			
MFE	-52.89	-45.80	-55.59	-52.00	0.162>0.05	Same
MFEE	-51.32	-44.80	-52.98	-49.35	0.310>0.05	Same
	***Fabaceae* family**		***Solanum lycopersicum***			
MFE	-72.57	-54.50	-56.38	-55.80	0.000<0.05	Different
MFEE	-70.60	-52.30	-53.91	-51.70	0.000<0.05	Different
	***Fabaceae* family**		***Solanum pennellii***			
MFE	-72.57	-54.50	-55.59	-52.00	0.000<0.05	Different
MFEE	-70.60	-52.30	-52.98	-49.35	0.000<0.05	Different
	***Brassicaceae* family**		***Solanum lycopersicum***			
MFE	-69.76	-57.00	-56.38	-55.80	0.000<0.05	Different
MFEE	-67.45	-55.00	-53.91	-51.70	0.000<0.05	Different
	***Brassicaceae* family**		***Solanum pennellii***			
MFE	-69.76	-57.00	-55.59	-52.00	0.000<0.05	Different
MFEE	-67.45	-55.00	-52.98	-49.35	0.000<0.05	Different

Supplementary Table S12. Characterization of *S. lycopersicum* miRNA target genes using psRNAtarget. Expectation (Exp), maximum energy to unpair (UPE).

Mature miRNA	Target	Exp	UPE	Star miRNA	End miRNA	Star target	End target	miRNA aligned fragment	Target aligned fragment	Inhibition
sly-miR1128	Solyc09g074860.3.1	2.0	-1.0	1	21	53	73	UACUACUCCCUCCGUCCCAAA	AAUGAGACGGAGGGAGUAGUC	Cleavage
sly-miR1128	Solyc07g018140.3.1	2.0	-1.0	1	21	1400	1420	UACUACUCCCUCCGUCCCAAA	GGUGGGGGGGAGGGGGUAGUA	Cleavage
sly-miR1128	Solyc08g082560.3.1	2.5	-1.0	1	21	309	329	UACUACUCCCUCCGUCCCAAA	UUUUGAACGGAGGGAGUAGUG	Cleavage
sly-miR1128	Solyc12g006690.2.1	2.5	-1.0	1	21	18	38	UACUACUCCCUCCGUCCCAAA	AUUAGGACGGAGGGACUAGUA	Cleavage
sly-miR1128	Solyc12g088240.2.1	2.5	-1.0	1	21	8	28	UACUACUCCCUCCGUCCCAAA	AAAGGGACGGAGGGAGUAUUA	Cleavage
sly-miR1128	Solyc08g006530.3.1	2.5	-1.0	1	21	75	95	UACUACUCCCUCCGUCCCAAA	AAUGAGACGGAUGGAGUAGUA	Translation
sly-miR1128	Solyc06g068700.3.1	3.0	-1.0	1	21	2835	2855	UACUACUCCCUCCGUCCCAAA	AUUGGGACUGAGGGAGUAUUA	Cleavage
sly-miR1128	Solyc11g011980.3.1	3.0	-1.0	1	21	566	586	UACUACUCCCUCCGUCCCAAA	GCUGGGACGGAGGUGGUGGUG	Cleavage
sly-miR1128	Solyc06g005590.3.1	3.0	-1.0	1	21	1659	1679	UACUACUCCCUCCGUCCCAAA	AUUCCGAUGGAGGGAGUAGUG	Cleavage
sly-miR1128	Solyc03g025790.3.1	3.0	-1.0	1	21	200	220	UACUACUCCCUCCGUCCCAAA	AACAGGAGGGAGGGAGUAGUA	Cleavage
sly-miR1446-1	Solyc09g008200.3.1	1.0	-1.0	1	22	1267	1288	UGAACUCUCUCCCUCAAUGGCU	CAAUGUUGAGGGAGAGAGUUCA	Cleavage
sly-miR1446-1	Solyc03g110950.1.1	2.5	-1.0	1	22	789	810	UGAACUCUCUCCCUCAAUGGCU	AGCCUUUGAGGGAGAGAGUUUC	Cleavage
sly-miR1446-1	Solyc08g007560.2.1	3.0	-1.0	1	22	47	68	UGAACUCUCUCCCUCAAUGGCU	AGCCAUAGAGAGGGAGAGUUCA	Cleavage
sly-miR1446-1	Solyc10g044910.2.1	3.0	-1.0	1	22	69	90	UGAACUCUCUCCCUCAAUGGCU	GCCCAUUAGUGGAGAGAGUUCA	Cleavage
sly-miR1446-1	Solyc03g116000.1.1	3.0	-1.0	1	22	794	815	UGAACUCUCUCCCUCAAUGGCU	UGGCAUUUGGUGAGAGAGUUCA	Cleavage
sly-miR1446-1	Solyc02g091260.1.1	3.0	-1.0	1	22	155	176	UGAACUCUCUCCCUCAAUGGCU	UUAUAUUAAGGAAGAGAGUUCA	Translation
sly-miR1446-1	Solyc12g094440.2.1	3.0	-1.0	1	22	976	997	UGAACUCUCUCCCUCAAUGGCU	CCACAUAGAGAGAGGGAGUUCA	Cleavage
sly-miR1446-1	Solyc02g080370.3.1	3.0	-1.0	1	22	105	126	UGAACUCUCUCCCUCAAUGGCU	AUUUUUUAAGGGGGAGAGUUCA	Cleavage
sly-miR1446-2-5p	Solyc09g008200.3.1	1.0	-1.0	1	22	1267	1288	UGAACUCUCUCCCUCAAUGGCU	CAAUGUUGAGGGAGAGAGUUCA	Cleavage
sly-miR1446-2-5p	Solyc03g110950.1.1	2.5	-1.0	1	22	789	810	UGAACUCUCUCCCUCAAUGGCU	AGCCUUUGAGGGAGAGAGUUUC	Cleavage
sly-miR1446-2-5p	Solyc08g007560.2.1	3.0	-1.0	1	22	47	68	UGAACUCUCUCCCUCAAUGGCU	AGCCAUAGAGAGGGAGAGUUCA	Cleavage
sly-miR1446-2-5p	Solyc10g044910.2.1	3.0	-1.0	1	22	69	90	UGAACUCUCUCCCUCAAUGGCU	GCCCAUUAGUGGAGAGAGUUCA	Cleavage
sly-miR1446-2-5p	Solyc03g116000.1.1	3.0	-1.0	1	22	794	815	UGAACUCUCUCCCUCAAUGGCU	UGGCAUUUGGUGAGAGAGUUCA	Cleavage
sly-miR1446-2-5p	Solyc02g091260.1.1	3.0	-1.0	1	22	155	176	UGAACUCUCUCCCUCAAUGGCU	UUAUAUUAAGGAAGAGAGUUCA	Translation
sly-miR1446-2-5p	Solyc12g094440.2.1	3.0	-1.0	1	22	976	997	UGAACUCUCUCCCUCAAUGGCU	CCACAUAGAGAGAGGGAGUUCA	Cleavage
sly-miR1446-2-5p	Solyc02g080370.3.1	3.0	-1.0	1	22	105	126	UGAACUCUCUCCCUCAAUGGCU	AUUUUUUAAGGGGGAGAGUUCA	Cleavage
sly-miR156a-1	Solyc07g062980.3.1	0.5	-1.0	1	21	442	462	UGACAGAAGAGAGUGAGCACA	AAUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc05g012040.3.1	1.0	-1.0	1	21	1458	1478	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc12g038520.2.1	1.0	-1.0	1	21	1430	1450	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc04g045560.3.1	1.0	-1.0	1	21	938	958	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc05g015840.3.1	1.0	-1.0	1	21	899	919	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc05g015510.3.1	1.0	-1.0	1	21	2554	2574	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc10g078700.2.1	1.0	-1.0	1	21	3613	3633	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc07g053810.3.1	1.0	-1.0	1	21	728	748	UGACAGAAGAGAGUGAGCACA	UUUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc03g114850.3.1	1.0	-1.0	1	21	1731	1751	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc10g009080.3.1	2.0	-1.0	1	21	501	521	UGACAGAAGAGAGUGAGCACA	CACGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc07g005640.3.1	2.0	-1.0	1	21	390	410	UGACAGAAGAGAGUGAGCACA	CUUCUUCACUUUCUUCUGUCA	Cleavage
sly-miR156a-1	Solyc09g055250.3.1	2.5	-1.0	1	21	1070	1090	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
sly-miR156a-1	Solyc01g005600.3.1	2.5	-1.0	1	21	1047	1067	UGACAGAAGAGAGUGAGCACA	AAUGCUUACUCUUUUCUUUCA	Cleavage
sly-miR156a-1	Solyc09g097880.3.1	3.0	-1.0	1	21	908	929	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
sly-miR156a-1	Solyc09g063030.3.1	3.0	-1.0	1	21	220	240	UGACAGAAGAGAGUGAGCACA	ACAGUUCACUCUCCUCUGUCA	Cleavage
sly-miR156a-1	Solyc04g025260.3.1	3.0	-1.0	1	21	2320	2340	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
sly-miR156a-1	Solyc01g106200.2.1	3.0	-1.0	1	21	1638	1658	UGACAGAAGAGAGUGAGCACA	GUUGUUUACUCUCUUUUCUCA	Cleavage
sly-miR156a-1	Solyc01g010370.3.1	3.0	-1.0	1	21	88	108	UGACAGAAGAGAGUGAGCACA	UUUGGUCGUUUUUUUCUGUCA	Cleavage
sly-miR156a-1	Solyc02g070280.3.1	3.0	-1.0	1	21	648	668	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation

sly-miR156a-1	Solyc03g117547.1.1	3.0	-1.0	1	21	579	599	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
sly-miR156a-1	Solyc07g039635.1.1	3.0	-1.0	1	21	1022	1042	UGACAGAAGAGAGUGAGCACA	ACUGCUACUUCUUUUCUGUCA	Cleavage
sly-miR156a-1	Solyc09g011750.3.1	3.0	-1.0	1	21	116	136	UGACAGAAGAGAGUGAGCACA	CCUUCUUCUUCUCUUCUGUCA	Cleavage
sly-miR156a-2-3p	Solyc09g019970.3.1	3.0	-1.0	1	22	2771	2792	GCUCACUUCUCAUUCUGUCAGA	UAUGGUGGGAUGGGAAGUGGGC	Cleavage
sly-miR156a-2-3p	Solyc03g097690.3.1	3.0	-1.0	1	22	3191	3212	GCUCACUUCUCAUUCUGUCAGA	AAAGACAGGAUGAGAAGUGAAA	Cleavage
sly-miR156a-2-3p	Solyc08g023280.3.1	3.0	-1.0	1	22	200	221	GCUCACUUCUCAUUCUGUCAGA	CUUGAAAGAAUGGGAAGAGAGC	Cleavage
sly-miR156a-2-3p	Solyc10g083690.3.1	3.0	-1.0	1	22	2	23	GCUCACUUCUCAUUCUGUCAGA	AAAGAUGGAAUGGGAAUUGAGC	Cleavage
sly-miR156a-2-3p	Solyc06g035580.3.1	3.0	-1.0	1	22	543	564	GCUCACUUCUCAUUCUGUCAGA	UGGGAUGGAAUGAGAAGUUAGU	Cleavage
sly-miR156a-2-3p	Solyc02g090515.1.1	3.0	-1.0	1	22	127	148	GCUCACUUCUCAUUCUGUCAGA	CUGGAGAGGAUGAGAGGUGAGA	Cleavage
sly-miR156a-2-3p	Solyc07g025210.2.1	3.0	-1.0	1	22	468	489	GCUCACUUCUCAUUCUGUCAGA	GAAGACAGUGUGGGAGGUGAGU	Cleavage
sly-miR156a-2-5p	Solyc07g062980.3.1	0.5	-1.0	1	21	442	462	UGACAGAAGAGAGUGAGCACA	AAUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc05g012040.3.1	1.0	-1.0	1	21	1458	1478	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc12g038520.2.1	1.0	-1.0	1	21	1430	1450	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc04g045560.3.1	1.0	-1.0	1	21	938	958	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc05g015840.3.1	1.0	-1.0	1	21	899	919	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc05g015510.3.1	1.0	-1.0	1	21	2554	2574	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc10g078700.2.1	1.0	-1.0	1	21	3613	3633	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc07g053810.3.1	1.0	-1.0	1	21	728	748	UGACAGAAGAGAGUGAGCACA	UUUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc03g114850.3.1	1.0	-1.0	1	21	1731	1751	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc10g009080.3.1	2.0	-1.0	1	21	501	521	UGACAGAAGAGAGUGAGCACA	CACGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc07g005640.3.1	2.0	-1.0	1	21	390	410	UGACAGAAGAGAGUGAGCACA	CUUCUUCACUUUCUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc09g055250.3.1	2.5	-1.0	1	21	1070	1090	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
sly-miR156a-2-5p	Solyc01g005600.3.1	2.5	-1.0	1	21	1047	1067	UGACAGAAGAGAGUGAGCACA	AAUGCUUACUCUUUUCUUUCA	Cleavage
sly-miR156a-2-5p	Solyc09g097880.3.1	3.0	-1.0	1	21	908	929	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
sly-miR156a-2-5p	Solyc09g063030.3.1	3.0	-1.0	1	21	220	240	UGACAGAAGAGAGUGAGCACA	ACAGUUCACUCUCCUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc04g025260.3.1	3.0	-1.0	1	21	2320	2340	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
sly-miR156a-2-5p	Solyc01g106200.2.1	3.0	-1.0	1	21	1638	1658	UGACAGAAGAGAGUGAGCACA	GUUGUUUACUCUCUUUUCUCA	Cleavage
sly-miR156a-2-5p	Solyc01g010370.3.1	3.0	-1.0	1	21	88	108	UGACAGAAGAGAGUGAGCACA	UUUGGUCGUUUUUUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc02g070280.3.1	3.0	-1.0	1	21	648	668	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation
sly-miR156a-2-5p	Solyc03g117547.1.1	3.0	-1.0	1	21	579	599	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
sly-miR156a-2-5p	Solyc07g039635.1.1	3.0	-1.0	1	21	1022	1042	UGACAGAAGAGAGUGAGCACA	ACUGCUACUUCUUUUCUGUCA	Cleavage
sly-miR156a-2-5p	Solyc09g011750.3.1	3.0	-1.0	1	21	116	136	UGACAGAAGAGAGUGAGCACA	CCUUCUUCUUCUCUUCUGUCA	Cleavage
sly-miR156c-3p	Solyc06g010040.3.1	2.5	-1.0	1	22	754	775	UGCUUACUCUCUAUCUGUCACC	AAAGAGAGAUAAAGAGUAAGCA	Translation
sly-miR156c-3p	Solyc07g062970.3.1	3.0	-1.0	1	22	1247	1267	UGCUUACUCUCUAUCUGUCACC	GCUGACAGA-AGAGAGUAAGCA	Cleavage
sly-miR156c-3p	Solyc07g006160.3.1	3.0	-1.0	1	22	796	817	UGCUUACUCUCUAUCUGUCACC	UCAGACAGAUAGAGAGAGAGUG	Cleavage
sly-miR156c-5p	Solyc07g062980.3.1	1.0	-1.0	1	21	442	462	UGAUAGAAGAGAGUGAGCACA	AAUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc05g012040.3.1	1.5	-1.0	1	21	1458	1478	UGAUAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc12g038520.2.1	1.5	-1.0	1	21	1430	1450	UGAUAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc04g045560.3.1	1.5	-1.0	1	21	938	958	UGAUAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc05g015840.3.1	1.5	-1.0	1	21	899	919	UGAUAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc05g015510.3.1	1.5	-1.0	1	21	2554	2574	UGAUAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc10g078700.2.1	1.5	-1.0	1	21	3613	3633	UGAUAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc07g053810.3.1	1.5	-1.0	1	21	728	748	UGAUAGAAGAGAGUGAGCACA	UUUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc03g114850.3.1	1.5	-1.0	1	21	1731	1751	UGAUAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc01g105270.3.1	2.0	-1.0	1	21	882	902	UGAUAGAAGAGAGUGAGCACA	AGUUCUCAUUCUCUUCUAUUA	Cleavage
sly-miR156c-5p	Solyc10g005450.2.1	2.5	-1.0	1	21	493	513	UGAUAGAAGAGAGUGAGCACA	GGUGCUUACUCUCGUUUAUCA	Cleavage
sly-miR156c-5p	Solyc04g009020.3.1	2.5	-1.0	1	21	513	533	UGAUAGAAGAGAGUGAGCACA	UAAUUUCACUCUCUUCUAUCA	Cleavage
sly-miR156c-5p	Solyc01g005600.3.1	2.5	-1.0	1	21	1047	1067	UGAUAGAAGAGAGUGAGCACA	AAUGCUUACUCUUUUCUUUCA	Cleavage
sly-miR156c-5p	Solyc02g079040.3.1	2.5	-1.0	1	21	145	165	UGAUAGAAGAGAGUGAGCACA	UUUUCUCACUUUCUUCUAUCC	Cleavage
sly-miR156c-5p	Solyc10g009080.3.1	2.5	-1.0	1	21	501	521	UGAUAGAAGAGAGUGAGCACA	CACGCUCUCUCUCUUCUGUCA	Cleavage

sly-miR156c-5p	Solyc07g005640.3.1	2.5	-1.0	1	21	390	410	UGAUAGAAGAGAGUGAGCACA	CUUCUUCACUUUCUUCUGUCA	Cleavage
sly-miR156c-5p	Solyc03g112830.3.1	2.5	-1.0	1	21	3364	3384	UGAUAGAAGAGAGUGAGCACA	CAUGAUCAUUUUCUUCUAUUA	Cleavage
sly-miR156c-5p	Solyc11g007960.2.1	3.0	-1.0	1	21	1850	1870	UGAUAGAAGAGAGUGAGCACA	UGUACUUGCUUUCUUUUAUCA	Cleavage
sly-miR156c-5p	Solyc05g013340.3.1	3.0	-1.0	1	21	1638	1658	UGAUAGAAGAGAGUGAGCACA	AGUGUUCAUUUUCUUGUAUCA	Cleavage
sly-miR156c-5p	Solyc03g121670.3.1	3.0	-1.0	1	21	146	166	UGAUAGAAGAGAGUGAGCACA	CCCAUUCACUCUUUUCUAUCA	Cleavage
sly-miR156c-5p	Solyc09g055250.3.1	3.0	-1.0	1	21	1070	1090	UGAUAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
sly-miR156c-5p	Solyc05g051880.3.1	3.0	-1.0	1	21	52	72	UGAUAGAAGAGAGUGAGCACA	CAUGUUCAAUCUUUUCUAUUA	Cleavage
sly-miR156c-5p	Solyc01g106200.2.1	3.0	-1.0	1	21	1638	1658	UGAUAGAAGAGAGUGAGCACA	GUUGUUUACUCUCUUUUCUCA	Cleavage
sly-miR156c-5p	Solyc09g018840.3.1	3.0	-1.0	1	21	1198	1218	UGAUAGAAGAGAGUGAGCACA	UAUGAUCACUUUCUUUUAUCC	Cleavage
sly-miR156c-5p	Solyc02g087980.3.1	3.0	-1.0	1	21	3933	3953	UGAUAGAAGAGAGUGAGCACA	UCUGAUCACUUUCUUUUAUCU	Cleavage
sly-miR156c-5p	Solyc06g035790.3.1	3.0	-1.0	1	21	15	35	UGAUAGAAGAGAGUGAGCACA	CUUCCUCACUUUCUUCUAUAA	Cleavage
sly-miR156c-5p	Solyc11g013180.2.1	3.0	-1.0	1	21	119	139	UGAUAGAAGAGAGUGAGCACA	CUUUCUCUCUCUCUUCUAUCU	Cleavage
sly-miR156c-5p	Solyc06g065640.3.1	3.0	-1.0	1	21	152	172	UGAUAGAAGAGAGUGAGCACA	CUUUCUCUCUCUUUUUUAUCA	Cleavage
sly-miR156f	Solyc04g045560.3.1	0.5	-1.0	1	22	938	959	UUGACAGAAGAGAGAGAGUACA	CGUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc05g015510.3.1	0.5	-1.0	1	22	2554	2575	UUGACAGAAGAGAGAGAGUACA	CGUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc10g078700.2.1	0.5	-1.0	1	22	3613	3634	UUGACAGAAGAGAGAGAGUACA	GGUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc05g012040.3.1	1.0	-1.0	1	22	1458	1479	UUGACAGAAGAGAGAGAGUACA	UGUGCUCUCUCUCUUCUGUCAG	Cleavage
sly-miR156f	Solyc12g038520.2.1	1.5	-1.0	1	22	1430	1451	UUGACAGAAGAGAGAGAGUACA	UGUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR156f	Solyc05g015840.3.1	1.5	-1.0	1	22	899	920	UUGACAGAAGAGAGAGAGUACA	CGUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR156f	Solyc07g053810.3.1	1.5	-1.0	1	22	728	749	UUGACAGAAGAGAGAGAGUACA	UUUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR156f	Solyc03g114850.3.1	1.5	-1.0	1	22	1731	1752	UUGACAGAAGAGAGAGAGUACA	AAUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR156f	Solyc10g009180.3.1	1.5	-1.0	1	22	108	129	UUGACAGAAGAGAGAGAGUACA	AAUAAUCUCUCUCUUUUGUCAA	Cleavage
sly-miR156f	Solyc10g009080.3.1	1.5	-1.0	1	22	501	522	UUGACAGAAGAGAGAGAGUACA	CACGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR156f	Solyc02g071220.3.1	1.5	-1.0	1	22	295	316	UUGACAGAAGAGAGAGAGUACA	AUCUCUCUUUCUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc03g117547.1.1	2.5	-1.0	1	22	579	600	UUGACAGAAGAGAGAGAGUACA	UAUACUCUCUCUCUUCUGUCUG	Cleavage
sly-miR156f	Solyc04g008455.1.1	2.5	-1.0	1	22	78	99	UUGACAGAAGAGAGAGAGUACA	UUUACUCUCUCUCUUCAGUCAU	Cleavage
sly-miR156f	Solyc07g062980.3.1	2.5	-1.0	1	22	442	463	UUGACAGAAGAGAGAGAGUACA	AAUGCUUACUCUCUUCUGUCAG	Cleavage
sly-miR156f	Solyc02g068420.3.1	2.5	-1.0	1	22	368	389	UUGACAGAAGAGAGAGAGUACA	GUGACUCUCUCUUUUAUGUCGA	Cleavage
sly-miR156f	Solyc07g064190.3.1	2.5	-1.0	1	22	28	49	UUGACAGAAGAGAGAGAGUACA	UCAAUUCUCCCUCUUUUGUCAA	Cleavage
sly-miR156f	Solyc04g012060.3.1	2.5	-1.0	1	22	3408	3429	UUGACAGAAGAGAGAGAGUACA	AUAAUUCUUUUUUUUUUGUCAA	Cleavage
sly-miR156f	Solyc08g067270.3.1	2.5	-1.0	1	22	859	880	UUGACAGAAGAGAGAGAGUACA	CCCAGUUUUUCUUUUCUGUCAA	Cleavage
sly-miR156f	Solyc08g081270.3.1	2.5	-1.0	1	22	785	806	UUGACAGAAGAGAGAGAGUACA	AUAGUUCUAUUUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc02g064540.2.1	2.5	-1.0	1	22	788	809	UUGACAGAAGAGAGAGAGUACA	CAAAUUCACUUUCUUUUGUCAA	Cleavage
sly-miR156f	Solyc04g072630.3.1	2.5	-1.0	1	22	7026	7047	UUGACAGAAGAGAGAGAGUACA	UACAAUCUCUUUCUUCUGUUAG	Cleavage
sly-miR156f	Solyc11g065090.2.1	2.5	-1.0	1	22	806	827	UUGACAGAAGAGAGAGAGUACA	AGCAUCCUAUCUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc04g077850.3.1	3.0	-1.0	1	22	2620	2641	UUGACAGAAGAGAGAGAGUACA	UGUACUCUCUCUGUUCUGUGAA	Translation
sly-miR156f	Solyc11g072480.2.1	3.0	-1.0	1	22	2663	2684	UUGACAGAAGAGAGAGAGUACA	GGUACUUUCUCUUUUCUCUCGA	Cleavage
sly-miR156f	Solyc08g062040.1.1	3.0	-1.0	1	22	9	30	UUGACAGAAGAGAGAGAGUACA	UAUAUUCUCUCUCAUUUGUCAG	Cleavage
sly-miR156f	Solyc09g015830.2.1	3.0	-1.0	1	22	101	122	UUGACAGAAGAGAGAGAGUACA	CCUAUUCUCUCUCUUCUUUCAU	Cleavage
sly-miR156f	Solyc11g007020.2.1	3.0	-1.0	1	22	1912	1933	UUGACAGAAGAGAGAGAGUACA	UUUGUUCUUUCUCUACUGUCAA	Cleavage
sly-miR156f	Solyc03g006010.3.1	3.0	-1.0	1	22	140	161	UUGACAGAAGAGAGAGAGUACA	CUUGUUCUUUCUCUUCUUUCAA	Cleavage
sly-miR156f	Solyc02g089150.3.1	3.0	-1.0	1	22	72	93	UUGACAGAAGAGAGAGAGUACA	CCUAUGCUUUUUCUUCUGUCAG	Cleavage
sly-miR156f	Solyc03g098020.3.1	3.0	-1.0	1	22	57	78	UUGACAGAAGAGAGAGAGUACA	ACUUUUCUCUCUCUUCUCUCAA	Cleavage
sly-miR156f	Solyc10g076350.2.1	3.0	-1.0	1	22	1139	1160	UUGACAGAAGAGAGAGAGUACA	CAACCUUUUUUUUUUCUGUCAA	Cleavage
sly-miR156f	Solyc01g006630.3.1	3.0	-1.0	1	22	1434	1455	UUGACAGAAGAGAGAGAGUACA	CUCUCUCUCUCUCUUCUGUGAG	Cleavage
sly-miR156f	Solyc03g115180.2.1	3.0	-1.0	1	22	2242	2263	UUGACAGAAGAGAGAGAGUACA	ACUUUUUUCUCUCUUUUGUUAA	Cleavage
sly-miR156f	Solyc07g041930.3.1	3.0	-1.0	1	22	2594	2615	UUGACAGAAGAGAGAGAGUACA	AGAACUCUUUCUUUUCUUUUAA	Cleavage
sly-miR156f	Solyc03g114410.3.1	3.0	-1.0	1	22	3249	3270	UUGACAGAAGAGAGAGAGUACA	AGAGCUCUUUCUCUUUGGUCAA	Cleavage
sly-miR156f	Solyc08g065970.3.1	3.0	-1.0	1	22	98	119	UUGACAGAAGAGAGAGAGUACA	UUAACUUUUUUUCUUCUGCCAA	Cleavage
sly-miR156f	Solyc07g063850.3.1	3.0	-1.0	1	22	130	151	UUGACAGAAGAGAGAGAGUACA	CAAACUCUCUCUUUUUUGUUCA	Cleavage

sly-miR156f	Solyc03g120360.1.1	3.0	-1.0	1	22	761	782	UUGACAGAAGAGAGAGAGUACA	AUAGCUCUUUCUCUUCUGUGAG	Cleavage
sly-miR156f	Solyc07g005640.3.1	3.0	-1.0	1	22	390	411	UUGACAGAAGAGAGAGAGUACA	CUUCUUCACUUUCUUCUGUCAA	Cleavage
sly-miR156f	Solyc08g041980.3.1	3.0	-1.0	1	22	910	931	UUGACAGAAGAGAGAGAGUACA	AAUCCUUUGUCUCUUCUGUUAA	Cleavage
sly-miR156f	Solyc11g007700.2.1	3.0	-1.0	1	22	1688	1709	UUGACAGAAGAGAGAGAGUACA	AACUUUCGCUCUCUUUUGUCAA	Cleavage
sly-miR156i-1-3p	Solyc05g054365.1.1	2.5	-1.0	1	22	646	667	GCUCACUGCUCUAUCUUUCAUC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
sly-miR156i-1-3p	Solyc04g079120.3.1	3.0	-1.0	1	22	1616	1637	GCUCACUGCUCUAUCUUUCAUC	GAUGGAAGAUACAGUAGUGAGU	Translation
sly-miR156i-1-3p	Solyc12g027880.2.1	3.0	-1.0	1	22	793	814	GCUCACUGCUCUAUCUUUCAUC	UAUUGAAGGUAGGGUAGUGAGC	Cleavage
sly-miR156i-1-5p	Solyc07g062980.3.1	2.0	-1.0	1	20	443	462	UGACAGAAGAGCGUGAGCAC	AUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc01g099500.1.1	2.5	-1.0	1	20	695	714	UGACAGAAGAGCGUGAGCAC	GUGCUUGUGCUUUUCUGUUA	Cleavage
sly-miR156i-1-5p	Solyc11g040340.2.1	2.5	-1.0	1	20	871	890	UGACAGAAGAGCGUGAGCAC	GUGCUCAUGUUCUUAUGUCA	Cleavage
sly-miR156i-1-5p	Solyc04g045560.3.1	2.5	-1.0	1	20	939	958	UGACAGAAGAGCGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc05g015840.3.1	2.5	-1.0	1	20	900	919	UGACAGAAGAGCGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc05g012040.3.1	2.5	-1.0	1	20	1459	1478	UGACAGAAGAGCGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc12g038520.2.1	2.5	-1.0	1	20	1431	1450	UGACAGAAGAGCGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc05g015510.3.1	2.5	-1.0	1	20	2555	2574	UGACAGAAGAGCGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc10g078700.2.1	2.5	-1.0	1	20	3614	3633	UGACAGAAGAGCGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc03g025617.1.1	2.5	-1.0	1	20	101	120	UGACAGAAGAGCGUGAGCAC	AUGCUGAAGCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc07g053810.3.1	2.5	-1.0	1	20	729	748	UGACAGAAGAGCGUGAGCAC	UUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc03g025585.1.1	2.5	-1.0	1	20	1702	1721	UGACAGAAGAGCGUGAGCAC	AUGCUGAAGCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc05g012270.3.1	2.5	-1.0	1	20	149	168	UGACAGAAGAGCGUGAGCAC	UUCUUCAUGUUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc03g114850.3.1	2.5	-1.0	1	20	1732	1751	UGACAGAAGAGCGUGAGCAC	AUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-1-5p	Solyc11g013090.2.1	3.0	-1.0	1	20	541	560	UGACAGAAGAGCGUGAGCAC	UUGCUCGUGCUGUUUUGUCA	Cleavage
sly-miR156i-1-5p	Solyc11g013083.1.1	3.0	-1.0	1	20	541	560	UGACAGAAGAGCGUGAGCAC	UUGCUCGUGCUGUUUUGUCA	Cleavage
sly-miR156i-1-5p	Solyc07g064500.3.1	3.0	-1.0	1	20	4152	4171	UGACAGAAGAGCGUGAGCAC	AUUUUCAUGCUUUUCUGUUA	Cleavage
sly-miR156i-1-5p	Solyc12g008420.2.1	3.0	-1.0	1	20	446	465	UGACAGAAGAGCGUGAGCAC	UUCCUCUUGUUCUUCUGUCA	Cleavage
sly-miR156i-2-3p	Solyc05g032750.3.1	2.5	-1.0	1	23	88	110	UGCUCACUUCUCUAUCUGUCAUC	AUUCAUAGGUAGAGGAGUGAGUG	Cleavage
sly-miR156i-2-3p	Solyc06g008960.3.1	3.0	-1.0	1	23	4216	4238	UGCUCACUUCUCUAUCUGUCAUC	GAGGACAGAUAUAGAAGUUAGCA	Cleavage
sly-miR156i-2-3p	Solyc06g071140.3.1	3.0	-1.0	1	23	773	795	UGCUCACUUCUCUAUCUGUCAUC	GAAGAAGGUUAGAGAAGUGGGCA	Cleavage
sly-miR156i-2-3p	Solyc01g068210.3.1	3.0	-1.0	1	23	673	695	UGCUCACUUCUCUAUCUGUCAUC	AAAGAUGGAGAGAGGAGUGGGCA	Cleavage
sly-miR156i-2-3p	Solyc01g104430.2.1	3.0	-1.0	1	23	2012	2034	UGCUCACUUCUCUAUCUGUCAUC	GUGGACAUAUGGAGAAGUGAGAA	Cleavage
sly-miR156i-2-3p	Solyc08g074280.3.1	3.0	-1.0	1	23	1730	1752	UGCUCACUUCUCUAUCUGUCAUC	CUACAAAGAUGGAGAAGUGAUCA	Cleavage
sly-miR156i-2-5p	Solyc07g062980.3.1	1.0	-1.0	1	20	443	462	UGACAGAAGAGAGUGGGCAC	AUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc04g045560.3.1	1.5	-1.0	1	20	939	958	UGACAGAAGAGAGUGGGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc05g015840.3.1	1.5	-1.0	1	20	900	919	UGACAGAAGAGAGUGGGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc05g012040.3.1	1.5	-1.0	1	20	1459	1478	UGACAGAAGAGAGUGGGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc12g038520.2.1	1.5	-1.0	1	20	1431	1450	UGACAGAAGAGAGUGGGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc05g015510.3.1	1.5	-1.0	1	20	2555	2574	UGACAGAAGAGAGUGGGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc10g078700.2.1	1.5	-1.0	1	20	3614	3633	UGACAGAAGAGAGUGGGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc07g053810.3.1	1.5	-1.0	1	20	729	748	UGACAGAAGAGAGUGGGCAC	UUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc03g114850.3.1	1.5	-1.0	1	20	1732	1751	UGACAGAAGAGAGUGGGCAC	AUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc06g073090.3.1	2.5	-1.0	1	20	466	485	UGACAGAAGAGAGUGGGCAC	UGGUCCACUUUCUUCUGUUA	Cleavage
sly-miR156i-2-5p	Solyc09g075130.3.1	2.5	-1.0	1	20	57	76	UGACAGAAGAGAGUGGGCAC	UUGCCCACUUUUUUUUGUUG	Cleavage
sly-miR156i-2-5p	Solyc10g009080.3.1	2.5	-1.0	1	20	502	521	UGACAGAAGAGAGUGGGCAC	ACGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc07g005640.3.1	2.5	-1.0	1	20	391	410	UGACAGAAGAGAGUGGGCAC	UUCUUCACUUUCUUCUGUCA	Cleavage
sly-miR156i-2-5p	Solyc12g006870.2.1	3.0	-1.0	1	20	662	681	UGACAGAAGAGAGUGGGCAC	UUGCCCAUUCUUCUUUGUCA	Cleavage
sly-miR156i-2-5p	Solyc09g055250.3.1	3.0	-1.0	1	20	1071	1090	UGACAGAAGAGAGUGGGCAC	UUGCUCACUUUCAUUUGUCA	Cleavage
sly-miR156i-2-5p	Solyc01g005600.3.1	3.0	-1.0	1	20	1048	1067	UGACAGAAGAGAGUGGGCAC	AUGCUUACUCUUUUCUUUCA	Cleavage
sly-miR156l-1-3p	Solyc05g054365.1.1	1.5	-1.0	1	22	646	667	GCUCACUGCUCUAUCUGUCACC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
sly-miR156l-1-3p	Solyc06g073680.3.1	2.5	-1.0	1	22	2623	2644	GCUCACUGCUCUAUCUGUCACC	CAACACAGAUGGAGCAGUGGGU	Cleavage
sly-miR156l-1-3p	Solyc05g055980.3.1	3.0	-1.0	1	22	1493	1514	GCUCACUGCUCUAUCUGUCACC	AAGGAUAGAUAGAGGAGUGAGG	Cleavage

sly-miR156l-1-5p	Solyc07g062980.3.1	0.5	-1.0	1	20	443	462	UGACAGAAGAGAGUGAGCAC	AUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc04g045560.3.1	1.0	-1.0	1	20	939	958	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc05g015840.3.1	1.0	-1.0	1	20	900	919	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc05g012040.3.1	1.0	-1.0	1	20	1459	1478	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc12g038520.2.1	1.0	-1.0	1	20	1431	1450	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc05g015510.3.1	1.0	-1.0	1	20	2555	2574	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc10g078700.2.1	1.0	-1.0	1	20	3614	3633	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc07g053810.3.1	1.0	-1.0	1	20	729	748	UGACAGAAGAGAGUGAGCAC	UUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc03g114850.3.1	1.0	-1.0	1	20	1732	1751	UGACAGAAGAGAGUGAGCAC	AUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc10g009080.3.1	2.0	-1.0	1	20	502	521	UGACAGAAGAGAGUGAGCAC	ACGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc07g005640.3.1	2.0	-1.0	1	20	391	410	UGACAGAAGAGAGUGAGCAC	UUCUUCACUUUCUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc09g055250.3.1	2.5	-1.0	1	20	1071	1090	UGACAGAAGAGAGUGAGCAC	UUGCUCACUUUCAUUUGUCA	Cleavage
sly-miR156l-1-5p	Solyc01g005600.3.1	2.5	-1.0	1	20	1048	1067	UGACAGAAGAGAGUGAGCAC	AUGCUUACUCUUUUCUUUCA	Cleavage
sly-miR156l-1-5p	Solyc09g097880.3.1	3.0	-1.0	1	20	909	929	UGACAGAAGAGAGU-GAGCAC	GUGCUCGAUUCUCUUCUGUUA	Cleavage
sly-miR156l-1-5p	Solyc09g063030.3.1	3.0	-1.0	1	20	221	240	UGACAGAAGAGAGUGAGCAC	CAGUUCACUCUCCUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc04g025260.3.1	3.0	-1.0	1	20	2321	2340	UGACAGAAGAGAGUGAGCAC	UUGCUUGCUUUCUUCUGGCA	Cleavage
sly-miR156l-1-5p	Solyc01g106200.2.1	3.0	-1.0	1	20	1639	1658	UGACAGAAGAGAGUGAGCAC	UUGUUUACUCUCUUUUCUCA	Cleavage
sly-miR156l-1-5p	Solyc02g070280.3.1	3.0	-1.0	1	20	649	668	UGACAGAAGAGAGUGAGCAC	UUGCUCUCUGUCUUCUGUUA	Translation
sly-miR156l-1-5p	Solyc01g010370.3.1	3.0	-1.0	1	20	89	108	UGACAGAAGAGAGUGAGCAC	UUGGUCGUUUUUUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc03g117547.1.1	3.0	-1.0	1	20	580	599	UGACAGAAGAGAGUGAGCAC	AUACUCUCUCUCUUCUGUCU	Cleavage
sly-miR156l-1-5p	Solyc07g039635.1.1	3.0	-1.0	1	20	1023	1042	UGACAGAAGAGAGUGAGCAC	CUGCUACUUCUUUUCUGUCA	Cleavage
sly-miR156l-1-5p	Solyc09g011750.3.1	3.0	-1.0	1	20	117	136	UGACAGAAGAGAGUGAGCAC	CUUCUUCUUCUCUUCUGUCA	Cleavage
sly-miR156l-2-3p	Solyc05g054365.1.1	1.5	-1.0	1	22	646	667	GCUCACUGCUCUAUCUGUCACC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
sly-miR156l-2-3p	Solyc06g073680.3.1	2.5	-1.0	1	22	2623	2644	GCUCACUGCUCUAUCUGUCACC	CAACACAGAUGGAGCAGUGGGU	Cleavage
sly-miR156l-2-3p	Solyc05g055980.3.1	3.0	-1.0	1	22	1493	1514	GCUCACUGCUCUAUCUGUCACC	AAGGAUAGAUAGAGGAGUGAGG	Cleavage
sly-miR156l-2-5p	Solyc07g062980.3.1	0.5	-1.0	1	20	443	462	UGACAGAAGAGAGUGAGCAC	AUGCUUACUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc04g045560.3.1	1.0	-1.0	1	20	939	958	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc05g015840.3.1	1.0	-1.0	1	20	900	919	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc05g012040.3.1	1.0	-1.0	1	20	1459	1478	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc12g038520.2.1	1.0	-1.0	1	20	1431	1450	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc05g015510.3.1	1.0	-1.0	1	20	2555	2574	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc10g078700.2.1	1.0	-1.0	1	20	3614	3633	UGACAGAAGAGAGUGAGCAC	GUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc07g053810.3.1	1.0	-1.0	1	20	729	748	UGACAGAAGAGAGUGAGCAC	UUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc03g114850.3.1	1.0	-1.0	1	20	1732	1751	UGACAGAAGAGAGUGAGCAC	AUGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc10g009080.3.1	2.0	-1.0	1	20	502	521	UGACAGAAGAGAGUGAGCAC	ACGCUCUCUCUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc07g005640.3.1	2.0	-1.0	1	20	391	410	UGACAGAAGAGAGUGAGCAC	UUCUUCACUUUCUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc09g055250.3.1	2.5	-1.0	1	20	1071	1090	UGACAGAAGAGAGUGAGCAC	UUGCUCACUUUCAUUUGUCA	Cleavage
sly-miR156l-2-5p	Solyc01g005600.3.1	2.5	-1.0	1	20	1048	1067	UGACAGAAGAGAGUGAGCAC	AUGCUUACUCUUUUCUUUCA	Cleavage
sly-miR156l-2-5p	Solyc09g097880.3.1	3.0	-1.0	1	20	909	929	UGACAGAAGAGAGU-GAGCAC	GUGCUCGAUUCUCUUCUGUUA	Cleavage
sly-miR156l-2-5p	Solyc09g063030.3.1	3.0	-1.0	1	20	221	240	UGACAGAAGAGAGUGAGCAC	CAGUUCACUCUCCUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc04g025260.3.1	3.0	-1.0	1	20	2321	2340	UGACAGAAGAGAGUGAGCAC	UUGCUUGCUUUCUUCUGGCA	Cleavage
sly-miR156l-2-5p	Solyc01g106200.2.1	3.0	-1.0	1	20	1639	1658	UGACAGAAGAGAGUGAGCAC	UUGUUUACUCUCUUUUCUCA	Cleavage
sly-miR156l-2-5p	Solyc02g070280.3.1	3.0	-1.0	1	20	649	668	UGACAGAAGAGAGUGAGCAC	UUGCUCUCUGUCUUCUGUUA	Translation
sly-miR156l-2-5p	Solyc01g010370.3.1	3.0	-1.0	1	20	89	108	UGACAGAAGAGAGUGAGCAC	UUGGUCGUUUUUUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc03g117547.1.1	3.0	-1.0	1	20	580	599	UGACAGAAGAGAGUGAGCAC	AUACUCUCUCUCUUCUGUCU	Cleavage
sly-miR156l-2-5p	Solyc07g039635.1.1	3.0	-1.0	1	20	1023	1042	UGACAGAAGAGAGUGAGCAC	CUGCUACUUCUUUUCUGUCA	Cleavage
sly-miR156l-2-5p	Solyc09g011750.3.1	3.0	-1.0	1	20	117	136	UGACAGAAGAGAGUGAGCAC	CUUCUUCUUCUCUUCUGUCA	Cleavage
sly-miR157a-1-3p	Solyc01g081050.4.1	2.5	-1.0	1	22	3788	3809	GCUCUUUAUUCUUCUGUCAUCA	GCACGACAGAAGAAUCAAGAGC	Cleavage
sly-miR157a-1-3p	Solyc07g047980.2.1	2.5	-1.0	1	22	767	788	GCUCUUUAUUCUUCUGUCAUCA	CCUUGACUGAAGAAGAAAGAGC	Cleavage
sly-miR157a-1-3p	Solyc01g095320.3.1	3.0	-1.0	1	22	534	556	GCUCUUUAUUCUUC-UGUCAUCA	UGAUGACAUGAAGAAUAGGGAGC	Cleavage

sly-miR157a-1-3p	Solyc11g032100.2.1	3.0	-1.0	1	22	35	56	GCUCUUUAUUCUUCUGUCAUCA	UGUUGAUAGAAGAAGGAAGAGU	Cleavage
sly-miR157a-1-3p	Solyc02g091350.3.1	3.0	-1.0	1	22	175	196	GCUCUUUAUUCUUCUGUCAUCA	AUAUGAUAGAAGAAUAUAGAGA	Cleavage
sly-miR157a-1-3p	Solyc01g109470.3.1	3.0	-1.0	1	22	17	38	GCUCUUUAUUCUUCUGUCAUCA	AUAUGACAGAAGAAAAAAGAAC	Cleavage
sly-miR157a-1-3p	Solyc01g094790.3.1	3.0	-1.0	1	22	487	508	GCUCUUUAUUCUUCUGUCAUCA	AAGUGACAGAAGGAUGUGGAGC	Cleavage
sly-miR157a-1-3p	Solyc10g079170.2.1	3.0	-1.0	1	22	6676	6697	GCUCUUUAUUCUUCUGUCAUCA	UAGUGGCACAAGCAUAAAGAGC	Translation
sly-miR157a-1-3p	Solyc01g094750.3.1	3.0	-1.0	1	22	1230	1251	GCUCUUUAUUCUUCUGUCAUCA	CUCAGCCGGAAGAAUGAAGAGC	Cleavage
sly-miR157a-1-5p	Solyc04g045560.3.1	1.5	-1.0	1	21	939	959	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc05g015510.3.1	1.5	-1.0	1	21	2555	2575	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc10g078700.2.1	1.5	-1.0	1	21	3614	3634	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc11g005660.2.1	1.5	-1.0	1	21	295	315	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
sly-miR157a-1-5p	Solyc05g012040.3.1	2.0	-1.0	1	21	1459	1479	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
sly-miR157a-1-5p	Solyc02g070280.3.1	2.0	-1.0	1	21	649	669	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
sly-miR157a-1-5p	Solyc04g082845.1.1	2.0	-1.0	1	21	28	48	UUGACAGAAGAUAGAGAGCAC	AAGCUCUCUAUUUUCUGUAAA	Cleavage
sly-miR157a-1-5p	Solyc01g106780.3.1	2.0	-1.0	1	21	1169	1189	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc05g015840.3.1	2.5	-1.0	1	21	900	920	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-1-5p	Solyc12g038520.2.1	2.5	-1.0	1	21	1431	1451	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-1-5p	Solyc07g053810.3.1	2.5	-1.0	1	21	729	749	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-1-5p	Solyc03g114850.3.1	2.5	-1.0	1	21	1732	1752	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-1-5p	Solyc10g009080.3.1	2.5	-1.0	1	21	502	522	UUGACAGAAGAUAGAGAGCAC	ACGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-1-5p	Solyc03g119360.3.1	2.5	-1.0	1	21	25	45	UUGACAGAAGAUAGAGAGCAC	AGGGUUUUUAUCUUCUGUCAG	Cleavage
sly-miR157a-1-5p	Solyc07g045150.3.1	3.0	-1.0	1	21	1185	1205	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUAUUUUCUGCUGA	Cleavage
sly-miR157a-1-5p	Solyc11g065490.2.1	3.0	-1.0	1	21	1535	1555	UUGACAGAAGAUAGAGAGCAC	UUGCUUUAUAUUUUCUGUCAU	Cleavage
sly-miR157a-1-5p	Solyc09g092420.2.1	3.0	-1.0	1	21	708	728	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc01g097150.3.1	3.0	-1.0	1	21	697	717	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc10g047680.2.1	3.0	-1.0	1	21	12	32	UUGACAGAAGAUAGAGAGCAC	UGCCUCUUUAUCUUCUCUCAA	Cleavage
sly-miR157a-1-5p	Solyc02g071220.3.1	3.0	-1.0	1	21	296	316	UUGACAGAAGAUAGAGAGCAC	UCUCUCUUUCUCUUCUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc07g063510.3.1	3.0	-1.0	1	21	1317	1337	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
sly-miR157a-1-5p	Solyc06g068280.3.1	3.0	-1.0	1	21	4793	4813	UUGACAGAAGAUAGAGAGCAC	UUGAUCCUUAUCUUCUGUUAA	Cleavage
sly-miR157a-1-5p	Solyc02g064690.3.1	3.0	-1.0	1	21	262	282	UUGACAGAAGAUAGAGAGCAC	AAUCUAUUUAUCUUUUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc08g081270.3.1	3.0	-1.0	1	21	786	806	UUGACAGAAGAUAGAGAGCAC	UAGUUCUAUUUCUUCUGUCAA	Cleavage
sly-miR157a-1-5p	Solyc04g079020.3.1	3.0	-1.0	1	21	170	190	UUGACAGAAGAUAGAGAGCAC	CAGUUGUUUAUCUUCUGUUGA	Cleavage
sly-miR157a-1-5p	Solyc01g096440.3.1	3.0	-1.0	1	21	628	648	UUGACAGAAGAUAGAGAGCAC	UCGUAUUCUGUUUUCUGUCAA	Cleavage
sly-miR157a-2-3p	Solyc01g095320.3.1	2.5	-1.0	1	22	534	556	GCUCUCUAUUCUUC-UGUCAUCA	UGAUGACAUGAAGAAUAGGGAGC	Cleavage
sly-miR157a-2-3p	Solyc02g080410.3.1	2.5	-1.0	1	22	973	994	GCUCUCUAUUCUUCUGUCAUCA	UUGUCACAAAAGAAUGGAGAGC	Cleavage
sly-miR157a-2-3p	Solyc02g091350.3.1	3.0	-1.0	1	22	175	196	GCUCUCUAUUCUUCUGUCAUCA	AUAUGAUAGAAGAAUAUAGAGA	Cleavage
sly-miR157a-2-3p	Solyc01g091850.3.1	3.0	-1.0	1	22	3953	3974	GCUCUCUAUUCUUCUGUCAUCA	ACAUGAAAGAAGAAUAGGGGGA	Cleavage
sly-miR157a-2-3p	Solyc01g094790.3.1	3.0	-1.0	1	22	487	508	GCUCUCUAUUCUUCUGUCAUCA	AAGUGACAGAAGGAUGUGGAGC	Cleavage
sly-miR157a-2-3p	Solyc03g117600.3.1	3.0	-1.0	1	22	3631	3652	GCUCUCUAUUCUUCUGUCAUCA	AGUUGACAGAGAGAUGGAGAGC	Translation
sly-miR157a-2-3p	Solyc10g081650.2.1	3.0	-1.0	1	22	707	728	GCUCUCUAUUCUUCUGUCAUCA	UGUAGACAAAAGAGUGGAGAGC	Cleavage
sly-miR157a-2-3p	Solyc12g013580.2.1	3.0	-1.0	1	22	1169	1190	GCUCUCUAUUCUUCUGUCAUCA	UCGUUACGGAAGGAUGGGGAGC	Cleavage
sly-miR157a-2-5p	Solyc04g045560.3.1	1.5	-1.0	1	21	939	959	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc05g015510.3.1	1.5	-1.0	1	21	2555	2575	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc10g078700.2.1	1.5	-1.0	1	21	3614	3634	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc11g005660.2.1	1.5	-1.0	1	21	295	315	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
sly-miR157a-2-5p	Solyc05g012040.3.1	2.0	-1.0	1	21	1459	1479	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
sly-miR157a-2-5p	Solyc02g070280.3.1	2.0	-1.0	1	21	649	669	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
sly-miR157a-2-5p	Solyc04g082845.1.1	2.0	-1.0	1	21	28	48	UUGACAGAAGAUAGAGAGCAC	AAGCUCUCUAUUUUCUGUAAA	Cleavage
sly-miR157a-2-5p	Solyc01g106780.3.1	2.0	-1.0	1	21	1169	1189	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc05g015840.3.1	2.5	-1.0	1	21	900	920	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-2-5p	Solyc12g038520.2.1	2.5	-1.0	1	21	1431	1451	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage

sly-miR157a-2-5p	Solyc07g053810.3.1	2.5	-1.0	1	21	729	749	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-2-5p	Solyc03g114850.3.1	2.5	-1.0	1	21	1732	1752	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-2-5p	Solyc10g009080.3.1	2.5	-1.0	1	21	502	522	UUGACAGAAGAUAGAGAGCAC	ACGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-2-5p	Solyc03g119360.3.1	2.5	-1.0	1	21	25	45	UUGACAGAAGAUAGAGAGCAC	AGGGUUUUUAUCUUCUGUCAG	Cleavage
sly-miR157a-2-5p	Solyc07g045150.3.1	3.0	-1.0	1	21	1185	1205	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUAUUUUCUGCUGA	Cleavage
sly-miR157a-2-5p	Solyc11g065490.2.1	3.0	-1.0	1	21	1535	1555	UUGACAGAAGAUAGAGAGCAC	UUGCUUUAUAUUUUCUGUCAU	Cleavage
sly-miR157a-2-5p	Solyc09g092420.2.1	3.0	-1.0	1	21	708	728	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc01g097150.3.1	3.0	-1.0	1	21	697	717	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc10g047680.2.1	3.0	-1.0	1	21	12	32	UUGACAGAAGAUAGAGAGCAC	UGCCUCUUUAUCUUCUCUCAA	Cleavage
sly-miR157a-2-5p	Solyc02g071220.3.1	3.0	-1.0	1	21	296	316	UUGACAGAAGAUAGAGAGCAC	UCUCUCUUUCUCUUCUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc07g063510.3.1	3.0	-1.0	1	21	1317	1337	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
sly-miR157a-2-5p	Solyc06g068280.3.1	3.0	-1.0	1	21	4793	4813	UUGACAGAAGAUAGAGAGCAC	UUGAUCCUUAUCUUCUGUUAA	Cleavage
sly-miR157a-2-5p	Solyc02g064690.3.1	3.0	-1.0	1	21	262	282	UUGACAGAAGAUAGAGAGCAC	AAUCUAUUUAUCUUUUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc08g081270.3.1	3.0	-1.0	1	21	786	806	UUGACAGAAGAUAGAGAGCAC	UAGUUCUAUUUCUUCUGUCAA	Cleavage
sly-miR157a-2-5p	Solyc04g079020.3.1	3.0	-1.0	1	21	170	190	UUGACAGAAGAUAGAGAGCAC	CAGUUGUUUAUCUUCUGUUGA	Cleavage
sly-miR157a-2-5p	Solyc01g096440.3.1	3.0	-1.0	1	21	628	648	UUGACAGAAGAUAGAGAGCAC	UCGUAUUCUGUUUUCUGUCAA	Cleavage
sly-miR157a-3-3p	Solyc05g051690.3.1	2.5	-1.0	1	21	718	738	GCUCUCUAUGCUUCUGUCAUC	UGUGCCAGGAGCAUAGAGAGA	Cleavage
sly-miR157a-3-3p	Solyc09g090200.3.1	2.5	-1.0	1	21	698	718	GCUCUCUAUGCUUCUGUCAUC	GCUUGCAGGAGCGUAGAGAGC	Cleavage
sly-miR157a-3-3p	Solyc12g006180.2.1	3.0	-1.0	1	21	642	662	GCUCUCUAUGCUUCUGUCAUC	GAUGGUAGAAGCAAAGAGGGC	Cleavage
sly-miR157a-3-3p	Solyc06g016800.2.1	3.0	-1.0	1	21	262	282	GCUCUCUAUGCUUCUGUCAUC	GGUGACAGAGGUGUGGAGGGU	Cleavage
sly-miR157a-3-3p	Solyc04g008100.2.1	3.0	-1.0	1	21	657	677	GCUCUCUAUGCUUCUGUCAUC	GAUGGAAGAAGUAUGGAGAGU	Cleavage
sly-miR157a-3-3p	Solyc01g056850.3.1	3.0	-1.0	1	21	1399	1419	GCUCUCUAUGCUUCUGUCAUC	GGUGACAGAGGUGUGGAGGGU	Cleavage
sly-miR157a-3-3p	Solyc03g079865.1.1	3.0	-1.0	1	20	1	21	GCUCUCUAUGCUUCUGU-CAU	AUGUACAGAAGUGUAGAGAGC	Cleavage
sly-miR157a-3-3p	Solyc05g052590.1.1	3.0	-1.0	1	21	2205	2225	GCUCUCUAUGCUUCUGUCAUC	GUUGACGGAAGCAGAGGGAGU	Cleavage
sly-miR157a-3-3p	Solyc10g079170.2.1	3.0	-1.0	1	21	6677	6697	GCUCUCUAUGCUUCUGUCAUC	AGUGGCACAAGCAUAAAGAGC	Cleavage
sly-miR157a-3-3p	Solyc01g109700.3.1	3.0	-1.0	1	21	746	766	GCUCUCUAUGCUUCUGUCAUC	UCUAACAGAGGCAGAGAGAGC	Cleavage
sly-miR157a-3-5p	Solyc04g045560.3.1	1.5	-1.0	1	21	939	959	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc05g015510.3.1	1.5	-1.0	1	21	2555	2575	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc10g078700.2.1	1.5	-1.0	1	21	3614	3634	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc11g005660.2.1	1.5	-1.0	1	21	295	315	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
sly-miR157a-3-5p	Solyc05g012040.3.1	2.0	-1.0	1	21	1459	1479	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
sly-miR157a-3-5p	Solyc02g070280.3.1	2.0	-1.0	1	21	649	669	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
sly-miR157a-3-5p	Solyc04g082845.1.1	2.0	-1.0	1	21	28	48	UUGACAGAAGAUAGAGAGCAC	AAGCUCUCUAUUUUCUGUAAA	Cleavage
sly-miR157a-3-5p	Solyc01g106780.3.1	2.0	-1.0	1	21	1169	1189	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc05g015840.3.1	2.5	-1.0	1	21	900	920	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-3-5p	Solyc12g038520.2.1	2.5	-1.0	1	21	1431	1451	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-3-5p	Solyc07g053810.3.1	2.5	-1.0	1	21	729	749	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-3-5p	Solyc03g114850.3.1	2.5	-1.0	1	21	1732	1752	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-3-5p	Solyc10g009080.3.1	2.5	-1.0	1	21	502	522	UUGACAGAAGAUAGAGAGCAC	ACGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-3-5p	Solyc03g119360.3.1	2.5	-1.0	1	21	25	45	UUGACAGAAGAUAGAGAGCAC	AGGGUUUUUAUCUUCUGUCAG	Cleavage
sly-miR157a-3-5p	Solyc07g045150.3.1	3.0	-1.0	1	21	1185	1205	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUAUUUUCUGCUGA	Cleavage
sly-miR157a-3-5p	Solyc11g065490.2.1	3.0	-1.0	1	21	1535	1555	UUGACAGAAGAUAGAGAGCAC	UUGCUUUAUAUUUUCUGUCAU	Cleavage
sly-miR157a-3-5p	Solyc09g092420.2.1	3.0	-1.0	1	21	708	728	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc01g097150.3.1	3.0	-1.0	1	21	697	717	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc10g047680.2.1	3.0	-1.0	1	21	12	32	UUGACAGAAGAUAGAGAGCAC	UGCCUCUUUAUCUUCUCUCAA	Cleavage
sly-miR157a-3-5p	Solyc02g071220.3.1	3.0	-1.0	1	21	296	316	UUGACAGAAGAUAGAGAGCAC	UCUCUCUUUCUCUUCUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc07g063510.3.1	3.0	-1.0	1	21	1317	1337	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
sly-miR157a-3-5p	Solyc06g068280.3.1	3.0	-1.0	1	21	4793	4813	UUGACAGAAGAUAGAGAGCAC	UUGAUCCUUAUCUUCUGUUAA	Cleavage
sly-miR157a-3-5p	Solyc02g064690.3.1	3.0	-1.0	1	21	262	282	UUGACAGAAGAUAGAGAGCAC	AAUCUAUUUAUCUUUUGUCAA	Cleavage
sly-miR157a-3-5p	Solyc08g081270.3.1	3.0	-1.0	1	21	786	806	UUGACAGAAGAUAGAGAGCAC	UAGUUCUAUUUCUUCUGUCAA	Cleavage

sly-miR157a-3-5p	Solyc04g079020.3.1	3.0	-1.0	1	21	170	190	UUGACAGAAGAUAGAGAGCAC	CAGUUGUUUAUCUUCUGUUGA	Cleavage
sly-miR157a-3-5p	Solyc01g096440.3.1	3.0	-1.0	1	21	628	648	UUGACAGAAGAUAGAGAGCAC	UCGUAUUCUGUUUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc04g045560.3.1	1.5	-1.0	1	21	939	959	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc05g015510.3.1	1.5	-1.0	1	21	2555	2575	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc10g078700.2.1	1.5	-1.0	1	21	3614	3634	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc11g005660.2.1	1.5	-1.0	1	21	295	315	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
sly-miR157a-4-5p	Solyc05g012040.3.1	2.0	-1.0	1	21	1459	1479	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
sly-miR157a-4-5p	Solyc02g070280.3.1	2.0	-1.0	1	21	649	669	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
sly-miR157a-4-5p	Solyc04g082845.1.1	2.0	-1.0	1	21	28	48	UUGACAGAAGAUAGAGAGCAC	AAGCUCUCUAUUUUCUGUAAA	Cleavage
sly-miR157a-4-5p	Solyc01g106780.3.1	2.0	-1.0	1	21	1169	1189	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc05g015840.3.1	2.5	-1.0	1	21	900	920	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-4-5p	Solyc12g038520.2.1	2.5	-1.0	1	21	1431	1451	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-4-5p	Solyc07g053810.3.1	2.5	-1.0	1	21	729	749	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-4-5p	Solyc03g114850.3.1	2.5	-1.0	1	21	1732	1752	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-4-5p	Solyc10g009080.3.1	2.5	-1.0	1	21	502	522	UUGACAGAAGAUAGAGAGCAC	ACGCUCUCUCUCUUCUGUCAU	Cleavage
sly-miR157a-4-5p	Solyc03g119360.3.1	2.5	-1.0	1	21	25	45	UUGACAGAAGAUAGAGAGCAC	AGGGUUUUUAUCUUCUGUCAG	Cleavage
sly-miR157a-4-5p	Solyc07g045150.3.1	3.0	-1.0	1	21	1185	1205	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUAUUUUCUGCUGA	Cleavage
sly-miR157a-4-5p	Solyc11g065490.2.1	3.0	-1.0	1	21	1535	1555	UUGACAGAAGAUAGAGAGCAC	UUGCUUUAUAUUUUCUGUCAU	Cleavage
sly-miR157a-4-5p	Solyc09g092420.2.1	3.0	-1.0	1	21	708	728	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc01g097150.3.1	3.0	-1.0	1	21	697	717	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc10g047680.2.1	3.0	-1.0	1	21	12	32	UUGACAGAAGAUAGAGAGCAC	UGCCUCUUUAUCUUCUCUCAA	Cleavage
sly-miR157a-4-5p	Solyc02g071220.3.1	3.0	-1.0	1	21	296	316	UUGACAGAAGAUAGAGAGCAC	UCUCUCUUUCUCUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc07g063510.3.1	3.0	-1.0	1	21	1317	1337	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
sly-miR157a-4-5p	Solyc06g068280.3.1	3.0	-1.0	1	21	4793	4813	UUGACAGAAGAUAGAGAGCAC	UUGAUCCUUAUCUUCUGUUAA	Cleavage
sly-miR157a-4-5p	Solyc02g064690.3.1	3.0	-1.0	1	21	262	282	UUGACAGAAGAUAGAGAGCAC	AAUCUAUUUAUCUUUUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc08g081270.3.1	3.0	-1.0	1	21	786	806	UUGACAGAAGAUAGAGAGCAC	UAGUUCUAUUUCUUCUGUCAA	Cleavage
sly-miR157a-4-5p	Solyc04g079020.3.1	3.0	-1.0	1	21	170	190	UUGACAGAAGAUAGAGAGCAC	CAGUUGUUUAUCUUCUGUUGA	Cleavage
sly-miR157a-4-5p	Solyc01g096440.3.1	3.0	-1.0	1	21	628	648	UUGACAGAAGAUAGAGAGCAC	UCGUAUUCUGUUUUCUGUCAA	Cleavage
sly-miR159a-3p	Solyc01g009070.3.1	1.5	-1.0	1	21	1836	1856	UUUGGAUUGAAGGGAGCUCUA	UGGAGCUCCCUUCACUCCAAA	Cleavage
sly-miR159a-3p	Solyc03g119530.3.1	1.5	-1.0	1	21	2506	2526	UUUGGAUUGAAGGGAGCUCUA	AGGAGCUCCCUUCAGUCCAAU	Cleavage
sly-miR159a-3p	Solyc06g073640.3.1	1.5	-1.0	1	21	1758	1778	UUUGGAUUGAAGGGAGCUCUA	UCGAGCUCCCUUCACUCCAAA	Cleavage
sly-miR159a-3p	Solyc07g062750.3.1	2.0	-1.0	1	21	1814	1834	UUUGGAUUGAAGGGAGCUCUA	UAGAGUUCCUUUUAAUCCAAG	Cleavage
sly-miR159a-3p	Solyc10g019260.2.1	2.0	-1.0	1	21	187	207	UUUGGAUUGAAGGGAGCUCUA	UGGAGCUCCAUUCGAUCCAAA	Cleavage
sly-miR159a-3p	Solyc01g090530.2.1	2.0	-1.0	1	21	1104	1124	UUUGGAUUGAAGGGAGCUCUA	UGGAGCUCCAUUCGAUCCAAA	Cleavage
sly-miR159a-3p	Solyc06g008320.3.1	2.0	-1.0	1	21	2008	2028	UUUGGAUUGAAGGGAGCUCUA	UCGAGUUUCUUUCAAUCCGAA	Cleavage
sly-miR159a-3p	Solyc07g062685.1.1	2.5	-1.0	1	21	476	496	UUUGGAUUGAAGGGAGCUCUA	UGGAGCCCCCUUCAAACCAAA	Cleavage
sly-miR159a-3p	Solyc12g014120.2.1	2.5	-1.0	1	21	1070	1090	UUUGGAUUGAAGGGAGCUCUA	UGGAGCCCCCUUCAAACCAAA	Cleavage
sly-miR159a-3p	Solyc02g079010.3.1	2.5	-1.0	1	21	819	839	UUUGGAUUGAAGGGAGCUCUA	CGGAGCUUCAUUCAGUCCAAA	Cleavage
sly-miR159a-3p	Solyc05g006830.3.1	2.5	-1.0	1	21	1935	1955	UUUGGAUUGAAGGGAGCUCUA	GUGAGUUCCCUUCCGUCCAAA	Cleavage
sly-miR159a-3p	Solyc01g068260.3.1	2.5	-1.0	1	21	1750	1770	UUUGGAUUGAAGGGAGCUCUA	AAGAGUAGCCUUCAAUCCAAA	Cleavage
sly-miR159a-3p	Solyc07g052640.3.1	2.5	-1.0	1	21	403	423	UUUGGAUUGAAGGGAGCUCUA	CAAAACUUCCUUCAAUCCAAA	Cleavage
sly-miR159a-3p	Solyc08g076885.1.1	3.0	-1.0	1	21	786	806	UUUGGAUUGAAGGGAGCUCUA	UAGAGCUCUCCUCAAUCUAGA	Translation
sly-miR159a-3p	Solyc11g072060.2.1	3.0	-1.0	1	21	914	934	UUUGGAUUGAAGGGAGCUCUA	UGGAGCUCCCUUCUUUCCAAA	Cleavage
sly-miR159a-3p	Solyc02g078670.3.1	3.0	-1.0	1	21	542	562	UUUGGAUUGAAGGGAGCUCUA	GAGAGUUCCAUUCAAUCCAAU	Cleavage
sly-miR159a-3p	Solyc09g082890.2.1	3.0	-1.0	1	21	159	179	UUUGGAUUGAAGGGAGCUCUA	UGGAGCUGCCUACAAUCCAAG	Translation
sly-miR159a-3p	Solyc03g043890.3.1	3.0	-1.0	1	21	526	546	UUUGGAUUGAAGGGAGCUCUA	UAAAGUUACCUUUAAUCCAAA	Cleavage
sly-miR159a-3p	Solyc01g106680.3.1	3.0	-1.0	1	21	298	318	UUUGGAUUGAAGGGAGCUCUA	AAGGACUCCCUUCAAUUCAAU	Cleavage
sly-miR159a-3p	Solyc03g114330.3.1	3.0	-1.0	1	21	1594	1614	UUUGGAUUGAAGGGAGCUCUA	AGGAGUUUCUUUCAAUCCCAA	Cleavage
sly-miR159a-3p	Solyc09g013080.3.1	3.0	-1.0	1	21	1687	1707	UUUGGAUUGAAGGGAGCUCUA	GGGAGUUCCCAUUGAUCCAAA	Translation
sly-miR159a-3p	Solyc06g073520.3.1	3.0	-1.0	1	21	3885	3905	UUUGGAUUGAAGGGAGCUCUA	CAAAGCUUUCUUUGAUCCAAA	Cleavage

sly-miR159a-3p	Solyc06g075630.3.1	3.0	-1.0	1	21	81	101	UUUGGAUUGAAGGGAGCUCUA	UCGAGCUCUUUUCAAAUCAAA	Cleavage
sly-miR159a-3p	Solyc11g066590.2.1	3.0	-1.0	1	21	1184	1204	UUUGGAUUGAAGGGAGCUCUA	UUCAGCUCCUUUCAAUUUGAA	Cleavage
sly-miR159a-3p	Solyc12g042530.2.1	3.0	-1.0	1	21	1313	1333	UUUGGAUUGAAGGGAGCUCUA	UUGAGUUCCUUUCAAGCCAGA	Cleavage
sly-miR159a-3p	Solyc10g076240.2.1	3.0	-1.0	1	21	1950	1970	UUUGGAUUGAAGGGAGCUCUA	ACCAGCUCUUUUCGAUUCAAA	Cleavage
sly-miR159a-3p	Solyc06g074210.3.1	3.0	-1.0	1	21	210	230	UUUGGAUUGAAGGGAGCUCUA	CUGGGCUUCCUUCAAUUUGGA	Cleavage
sly-miR159a-3p	Solyc10g078390.2.1	3.0	-1.0	1	21	2245	2265	UUUGGAUUGAAGGGAGCUCUA	GUGAGUUCUCUUCAAUACAGA	Cleavage
sly-miR159a-3p	Solyc12g038490.2.1	3.0	-1.0	1	21	2293	2313	UUUGGAUUGAAGGGAGCUCUA	AUGGGCUUUCUUCUAUCCAAA	Cleavage
sly-miR159a-3p	Solyc07g043580.3.1	3.0	-1.0	1	21	2497	2517	UUUGGAUUGAAGGGAGCUCUA	UUGAUCUUCUUUCAAUCCAAU	Cleavage
sly-miR159a-3p	Solyc02g021430.1.1	3.0	-1.0	1	21	292	312	UUUGGAUUGAAGGGAGCUCUA	AUCACUUUCCUUCAAUCCAAA	Cleavage
sly-miR159a-3p	Solyc01g106440.3.1	3.0	-1.0	1	21	4361	4381	UUUGGAUUGAAGGGAGCUCUA	AGAAACUCCCUUCAAUCUGAA	Cleavage
sly-miR159a-3p	Solyc12g008940.2.1	3.0	-1.0	1	21	75	95	UUUGGAUUGAAGGGAGCUCUA	AUGAUCUCCUUUGAAUCCAAA	Cleavage
sly-miR159b-3p	Solyc03g119530.3.1	1.5	-1.0	1	21	2506	2526	AUUGGAAUGAAGGGAGCUCUA	AGGAGCUCCCUUCAGUCCAAU	Cleavage
sly-miR159b-3p	Solyc02g079290.3.1	2.0	-1.0	1	21	321	341	AUUGGAAUGAAGGGAGCUCUA	AAGGGUUCUCUUCAUUCUAAU	Cleavage
sly-miR159b-3p	Solyc01g080720.3.1	2.5	-1.0	1	21	3964	3984	AUUGGAAUGAAGGGAGCUCUA	UAGAGUUCCCUUCAUUCUGAG	Cleavage
sly-miR159b-3p	Solyc11g072060.2.1	2.5	-1.0	1	21	914	934	AUUGGAAUGAAGGGAGCUCUA	UGGAGCUCCCUUCUUUCCAAA	Cleavage
sly-miR159b-3p	Solyc01g009070.3.1	2.5	-1.0	1	21	1836	1856	AUUGGAAUGAAGGGAGCUCUA	UGGAGCUCCCUUCACUCCAAA	Cleavage
sly-miR159b-3p	Solyc06g073640.3.1	2.5	-1.0	1	21	1758	1778	AUUGGAAUGAAGGGAGCUCUA	UCGAGCUCCCUUCACUCCAAA	Cleavage
sly-miR159b-3p	Solyc06g009550.3.1	2.5	-1.0	1	21	2392	2412	AUUGGAAUGAAGGGAGCUCUA	UGUAACUCUCUUCAUUCCAAU	Cleavage
sly-miR159b-3p	Solyc07g039620.2.1	2.5	-1.0	1	21	3	23	AUUGGAAUGAAGGGAGCUCUA	AUGAGUUCCGUUCAUUCCGAU	Cleavage
sly-miR159b-3p	Solyc04g026210.3.1	2.5	-1.0	1	21	37	57	AUUGGAAUGAAGGGAGCUCUA	UUGAGUUACCUUCAUUCCAAG	Cleavage
sly-miR159b-3p	Solyc08g006060.3.1	2.5	-1.0	1	21	2528	2548	AUUGGAAUGAAGGGAGCUCUA	AAGUACUCCCUUCAUUUCAAU	Cleavage
sly-miR159b-3p	Solyc06g050550.3.1	3.0	-1.0	1	21	811	831	AUUGGAAUGAAGGGAGCUCUA	UAGAGGUUUUUUCAUUCCGAU	Cleavage
sly-miR159b-3p	Solyc08g066740.3.1	3.0	-1.0	1	21	3466	3486	AUUGGAAUGAAGGGAGCUCUA	UGGAUUUCCCUUUAUUCCAAC	Cleavage
sly-miR159b-3p	Solyc09g082280.3.1	3.0	-1.0	1	21	1050	1070	AUUGGAAUGAAGGGAGCUCUA	AAGAACUUCCUUCAUUUUGAU	Cleavage
sly-miR159b-3p	Solyc12g013890.2.1	3.0	-1.0	1	21	1485	1505	AUUGGAAUGAAGGGAGCUCUA	AACAGUUCCUUUCAUUCUAGU	Cleavage
sly-miR159b-3p	Solyc03g112960.1.1	3.0	-1.0	1	21	81	101	AUUGGAAUGAAGGGAGCUCUA	GUUAGCUCUCUUCAUUCCCAU	Cleavage
sly-miR159b-3p	Solyc11g065890.2.1	3.0	-1.0	1	21	208	228	AUUGGAAUGAAGGGAGCUCUA	GGUAGUUCUCUUCAUUCUAGU	Cleavage
sly-miR159b-3p	Solyc06g035970.3.1	3.0	-1.0	1	21	2473	2493	AUUGGAAUGAAGGGAGCUCUA	UUGAGUUUAUUUCAUUCCAAU	Cleavage
sly-miR159b-3p	Solyc04g026235.1.1	3.0	-1.0	1	21	202	222	AUUGGAAUGAAGGGAGCUCUA	UUGAGUUACCUUCAUUCUAAG	Cleavage
sly-miR159b-3p	Solyc10g080340.2.1	3.0	-1.0	1	21	1692	1712	AUUGGAAUGAAGGGAGCUCUA	AAGUACUCCCUUCGUUUCAAU	Cleavage
sly-miR159b-3p	Solyc08g076290.3.1	3.0	-1.0	1	21	1638	1658	AUUGGAAUGAAGGGAGCUCUA	UUCAUCUUUCUUCAUUCCAAU	Cleavage
sly-miR159b-3p	Solyc09g010160.2.1	3.0	-1.0	1	21	38	58	AUUGGAAUGAAGGGAGCUCUA	AUGGUUUUUCUUCAUUCCAAU	Cleavage
sly-miR159b-5p	Solyc09g072660.3.1	2.0	-1.0	1	21	1946	1966	UUGCAUAUAUCAGGAGCUUCA	CGAAGUUCAUGAUAUAUGCAA	Cleavage
sly-miR159b-5p	Solyc01g098640.3.1	2.0	-1.0	1	21	2120	2140	UUGCAUAUAUCAGGAGCUUCA	AGAGGAUUCUGAUAUAUGCAA	Cleavage
sly-miR159b-5p	Solyc08g068010.2.1	2.5	-1.0	1	21	3447	3467	UUGCAUAUAUCAGGAGCUUCA	UCCAGUUCUUGAUAUGUGCAA	Cleavage
sly-miR159b-5p	Solyc08g079080.4.1	3.0	-1.0	1	21	1259	1279	UUGCAUAUAUCAGGAGCUUCA	UGAAGCUGCUGAUAUUUGCAG	Cleavage
sly-miR159b-5p	Solyc01g009190.2.1	3.0	-1.0	1	21	478	498	UUGCAUAUAUCAGGAGCUUCA	AGAAGCUGCAGAUGUAUGCAA	Cleavage
sly-miR159b-5p	Solyc12g098860.2.1	3.0	-1.0	1	21	1774	1794	UUGCAUAUAUCAGGAGCUUCA	GCAAGUUCCUGAUAUUUGCAC	Cleavage
sly-miR159b-5p	Solyc01g104660.3.1	3.0	-1.0	1	21	577	597	UUGCAUAUAUCAGGAGCUUCA	AAAAGCACUUGAUAUUUGCAA	Cleavage
sly-miR159b-5p	Solyc04g005030.3.1	3.0	-1.0	1	21	159	179	UUGCAUAUAUCAGGAGCUUCA	GCGAGCUGCUGAUAUAUACAA	Cleavage
sly-miR159b-5p	Solyc06g065680.3.1	3.0	-1.0	1	21	1081	1101	UUGCAUAUAUCAGGAGCUUCA	GUAUGCUCCUGAUAUAUAUAA	Cleavage
sly-miR159b-5p	Solyc06g062780.3.1	3.0	-1.0	1	21	1293	1313	UUGCAUAUAUCAGGAGCUUCA	CCAAGCUGGUGGUAUAUGCAA	Cleavage
sly-miR159b-5p	Solyc06g065240.3.1	3.0	-1.0	1	21	2728	2748	UUGCAUAUAUCAGGAGCUUCA	AUAUGUUCCUGAUAUAUUCAA	Cleavage
sly-miR159b-5p	Solyc11g005090.2.1	3.0	-1.0	1	21	1383	1403	UUGCAUAUAUCAGGAGCUUCA	CGCAGCAGCUGAUAUAUGCAA	Cleavage
sly-miR160	Solyc06g075120.1.1	3.0	-1.0	1	21	170	190	UGGCAUACAGGGAGCCAGGCA	UCACUCGCUCUCUGUAUGCUA	Cleavage
sly-miR160	Solyc04g076910.3.1	3.0	-1.0	1	21	933	953	UGGCAUACAGGGAGCCAGGCA	GUCCUGGGUUCCUGUAUCCCA	Cleavage
sly-miR160a-3p	Solyc05g012080.3.1	2.5	-1.0	1	21	541	561	GCGUAUAAGGAGCCAAGCAUA	GGUGCUUGGCUUCUUGUACAC	Cleavage
sly-miR160a-3p	Solyc02g032140.2.1	3.0	-1.0	1	21	1042	1062	GCGUAUAAGGAGCCAAGCAUA	AAUGCUUGACUUCUUAUAUGU	Cleavage
sly-miR160a-3p	Solyc02g089770.3.1	3.0	-1.0	1	21	395	415	GCGUAUAAGGAGCCAAGCAUA	UUUAUUUGGUUUCUUAUAUGC	Cleavage
sly-miR160a-3p	Solyc06g051060.3.1	3.0	-1.0	1	21	75	95	GCGUAUAAGGAGCCAAGCAUA	AUUGUUUUGUUCUUUAUAUGC	Cleavage

sly-miR160a-5p	Solyc06g075150.3.1	0.0	-1.0	1	21	1544	1564	UGCCUGGCUCCCUGUAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160a-5p	Solyc11g069500.2.1	0.0	-1.0	1	21	1837	1857	UGCCUGGCUCCCUGUAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160a-5p	Solyc09g007810.3.1	0.5	-1.0	1	21	2031	2051	UGCCUGGCUCCCUGUAUGCCA	UGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160a-5p	Solyc11g013480.2.1	0.5	-1.0	1	21	1447	1467	UGCCUGGCUCCCUGUAUGCCA	GGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160a-5p	Solyc10g086130.2.1	1.0	-1.0	1	21	1347	1367	UGCCUGGCUCCCUGUAUGCCA	UGGUAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160a-5p	Solyc01g011350.3.1	3.0	-1.0	1	21	1020	1040	UGCCUGGCUCCCUGUAUGCCA	GUGGAUAUAGGGAGUUAGGUA	Cleavage
sly-miR160g-5p	Solyc09g007810.3.1	1.0	-1.0	1	21	2031	2051	UGCCUGGCUCCCUGGAUGCCA	UGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160g-5p	Solyc11g013480.2.1	1.0	-1.0	1	21	1447	1467	UGCCUGGCUCCCUGGAUGCCA	GGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160g-5p	Solyc06g075150.3.1	1.0	-1.0	1	21	1544	1564	UGCCUGGCUCCCUGGAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160g-5p	Solyc11g069500.2.1	1.0	-1.0	1	21	1837	1857	UGCCUGGCUCCCUGGAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160g-5p	Solyc10g086130.2.1	1.5	-1.0	1	21	1347	1367	UGCCUGGCUCCCUGGAUGCCA	UGGUAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160g-5p	Solyc01g091630.3.1	2.5	-1.0	1	21	1697	1717	UGCCUGGCUCCCUGGAUGCCA	AGGCUUCCAGGGAGACAGGCA	Cleavage
sly-miR160g-5p	Solyc07g066550.3.1	3.0	-1.0	1	21	2340	2360	UGCCUGGCUCCCUGGAUGCCA	CUGCAUCGAGGGAGACAGGCG	Cleavage
sly-miR160h-1	Solyc06g075150.3.1	0.0	-1.0	1	23	1542	1564	UGCCUGGCUCCCUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160h-1	Solyc11g069500.2.1	0.0	-1.0	1	23	1835	1857	UGCCUGGCUCCCUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160h-1	Solyc09g007810.3.1	0.5	-1.0	1	23	2029	2051	UGCCUGGCUCCCUGUAUGCCAUU	GCUGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160h-1	Solyc11g013480.2.1	0.5	-1.0	1	23	1445	1467	UGCCUGGCUCCCUGUAUGCCAUU	GCGGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160h-1	Solyc10g086130.2.1	1.0	-1.0	1	23	1345	1367	UGCCUGGCUCCCUGUAUGCCAUU	GUUGGUAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160h-2	Solyc06g075150.3.1	0.5	-1.0	1	23	1542	1564	UGCCUGGCUCCUUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160h-2	Solyc11g069500.2.1	0.5	-1.0	1	23	1835	1857	UGCCUGGCUCCUUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
sly-miR160h-2	Solyc09g007810.3.1	1.0	-1.0	1	23	2029	2051	UGCCUGGCUCCUUGUAUGCCAUU	GCUGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160h-2	Solyc11g013480.2.1	1.0	-1.0	1	23	1445	1467	UGCCUGGCUCCUUGUAUGCCAUU	GCGGGCAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160h-2	Solyc10g086130.2.1	1.5	-1.0	1	23	1345	1367	UGCCUGGCUCCUUGUAUGCCAUU	GUUGGUAUGCAGGGAGCCAGGCA	Cleavage
sly-miR160h-2	Solyc11g068950.2.1	2.5	-1.0	1	23	1671	1693	UGCCUGGCUCCUUGUAUGCCAUU	CAGGGCUAACAAGGAGCCAGGUA	Cleavage
sly-miR160h-2	Solyc06g066670.3.1	2.5	-1.0	1	23	2293	2315	UGCCUGGCUCCUUGUAUGCCAUU	UGAUGCAUGGAAGGAGUCGGGCA	Cleavage
sly-miR160h-2	Solyc04g072130.2.1	3.0	-1.0	1	23	2477	2498	UGCCUGGCUCCUUGUAUGCCAUU	AGAUGCAUA-AAGGAGUUAGGCA	Cleavage
sly-miR162-1-3p	Solyc04g016510.3.1	2.5	-1.0	1	21	910	930	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUUGAUUGG	Cleavage
sly-miR162-1-3p	Solyc03g113740.3.1	2.5	-1.0	1	21	2846	2866	UCGAUAAACCUCUGCAUCCAG	GAAGAUGCAGAGGUUUAUUGC	Cleavage
sly-miR162-1-3p	Solyc10g005130.3.1	3.0	-1.0	1	21	3432	3453	UCGAUAA-ACCUCUGCAUCCAG	CUGGAUGCAGAGGUAUUAUCGA	Cleavage
sly-miR162-1-3p	Solyc01g080500.2.1	3.0	-1.0	1	21	1161	1181	UCGAUAAACCUCUGCAUCCAG	AUGGAUGGAGGGGUUUAUUGU	Cleavage
sly-miR162-1-5p	Solyc07g063870.3.1	2.5	-1.0	1	22	562	583	UGGAGGCAGCGGUUCAUCGAUC	UCCUGGUGAACCGCUGCCUCGA	Cleavage
sly-miR162-1-5p	Solyc11g010650.3.1	3.0	-1.0	1	22	184	205	UGGAGGCAGCGGUUCAUCGAUC	GGAAGAUGAACCGCUGCUUCUC	Cleavage
sly-miR162-1-5p	Solyc07g054180.3.1	3.0	-1.0	1	22	417	438	UGGAGGCAGCGGUUCAUCGAUC	UACUGAUGGACCGUUGCUUCCU	Cleavage
sly-miR162-1-5p	Solyc10g006860.3.1	3.0	-1.0	1	22	1702	1723	UGGAGGCAGCGGUUCAUCGAUC	UCUCCGUGAGCUGCUGCCUCCG	Cleavage
sly-miR162-1-5p	Solyc10g081460.2.1	3.0	-1.0	1	22	1300	1321	UGGAGGCAGCGGUUCAUCGAUC	UCGGGAUGGAUUGCUGCCUUCA	Cleavage
sly-miR162-1-5p	Solyc03g095680.2.1	3.0	-1.0	1	22	2312	2333	UGGAGGCAGCGGUUCAUCGAUC	UGCUGAUGAACUGCAGCUUCCA	Cleavage
sly-miR162-1-5p	Solyc04g078590.3.1	3.0	-1.0	1	22	1977	1998	UGGAGGCAGCGGUUCAUCGAUC	AGUCCAUCCACCGCUGCCUCCA	Cleavage
sly-miR162-1-5p	Solyc06g063020.3.1	3.0	-1.0	1	22	823	844	UGGAGGCAGCGGUUCAUCGAUC	AGGGGAAAAACCGCUGCCUCCA	Cleavage
sly-miR162-2-3p	Solyc04g016510.3.1	2.5	-1.0	1	21	910	930	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUUGAUUGG	Cleavage
sly-miR162-2-3p	Solyc03g113740.3.1	2.5	-1.0	1	21	2846	2866	UCGAUAAACCUCUGCAUCCAG	GAAGAUGCAGAGGUUUAUUGC	Cleavage
sly-miR162-2-3p	Solyc10g005130.3.1	3.0	-1.0	1	21	3432	3453	UCGAUAA-ACCUCUGCAUCCAG	CUGGAUGCAGAGGUAUUAUCGA	Cleavage
sly-miR162-2-3p	Solyc01g080500.2.1	3.0	-1.0	1	21	1161	1181	UCGAUAAACCUCUGCAUCCAG	AUGGAUGGAGGGGUUUAUUGU	Cleavage
sly-miR162-2-5p	Solyc07g063870.3.1	2.5	-1.0	1	22	562	583	UGGAGGCAGCGGUUCAUCGAUC	UCCUGGUGAACCGCUGCCUCGA	Cleavage
sly-miR162-2-5p	Solyc11g010650.3.1	3.0	-1.0	1	22	184	205	UGGAGGCAGCGGUUCAUCGAUC	GGAAGAUGAACCGCUGCUUCUC	Cleavage
sly-miR162-2-5p	Solyc07g054180.3.1	3.0	-1.0	1	22	417	438	UGGAGGCAGCGGUUCAUCGAUC	UACUGAUGGACCGUUGCUUCCU	Cleavage
sly-miR162-2-5p	Solyc10g006860.3.1	3.0	-1.0	1	22	1702	1723	UGGAGGCAGCGGUUCAUCGAUC	UCUCCGUGAGCUGCUGCCUCCG	Cleavage
sly-miR162-2-5p	Solyc10g081460.2.1	3.0	-1.0	1	22	1300	1321	UGGAGGCAGCGGUUCAUCGAUC	UCGGGAUGGAUUGCUGCCUUCA	Cleavage
sly-miR162-2-5p	Solyc03g095680.2.1	3.0	-1.0	1	22	2312	2333	UGGAGGCAGCGGUUCAUCGAUC	UGCUGAUGAACUGCAGCUUCCA	Cleavage
sly-miR162-2-5p	Solyc04g078590.3.1	3.0	-1.0	1	22	1977	1998	UGGAGGCAGCGGUUCAUCGAUC	AGUCCAUCCACCGCUGCCUCCA	Cleavage
sly-miR162-2-5p	Solyc06g063020.3.1	3.0	-1.0	1	22	823	844	UGGAGGCAGCGGUUCAUCGAUC	AGGGGAAAAACCGCUGCCUCCA	Cleavage

sly-miR164a-3p	Solyc09g082560.3.1	2.0	-1.0	1	20	1	20	CAUGUGCCUGUUUUCCCCAU	AUGGGGAAAACAGGUAGAUG	Cleavage
sly-miR164a-3p	Solyc01g081140.1.1	3.0	-1.0	1	21	1605	1625	CAUGUGCCUGUUUUCCCCAUC	AAAGGGGAAAACAAGCAUAUG	Cleavage
sly-miR164a-3p	Solyc01g009040.3.1	3.0	-1.0	1	21	309	329	CAUGUGCCUGUUUUCCCCAUC	GCUGGGAAAAAUAGGCGUGUG	Cleavage
sly-miR164a-3p	Solyc10g005740.2.1	3.0	-1.0	1	21	1837	1857	CAUGUGCCUGUUUUCCCCAUC	AUUGGAGGAAACAGGCAAAUG	Cleavage
sly-miR164a-3p	Solyc12g010820.2.1	3.0	-1.0	1	21	1555	1575	CAUGUGCCUGUUUUCCCCAUC	ACUGUGAAAAGCAGGUACAUG	Cleavage
sly-miR164a-5p	Solyc07g062840.3.1	0.5	-1.0	1	21	1361	1381	UGGAGAAGCAGGGCACGUGCA	AGCACGUGCCCUGUUUCUCCA	Cleavage
sly-miR164a-5p	Solyc07g066330.3.1	1.0	-1.0	1	21	909	929	UGGAGAAGCAGGGCACGUGCA	AGCAAGUGCCCUGCUUCUCCA	Cleavage
sly-miR164a-5p	Solyc03g115850.3.1	1.5	-1.0	1	21	1236	1256	UGGAGAAGCAGGGCACGUGCA	GCCACGUGCACUGCUUCUCCA	Cleavage
sly-miR164a-5p	Solyc06g069710.3.1	1.5	-1.0	1	21	873	893	UGGAGAAGCAGGGCACGUGCA	GCCACGUGCACUGCUUCUCCA	Cleavage
sly-miR164a-5p	Solyc11g066150.2.1	1.5	-1.0	1	21	433	453	UGGAGAAGCAGGGCACGUGCA	CUCGCAUGCCCUGCUUCUCCA	Cleavage
sly-miR164a-5p	Solyc01g066710.3.1	2.0	-1.0	1	21	418	438	UGGAGAAGCAGGGCACGUGCA	UUGGCGUGCCCUGCUUCUCCG	Cleavage
sly-miR164a-5p	Solyc01g090590.3.1	2.5	-1.0	1	21	1539	1559	UGGAGAAGCAGGGCACGUGCA	UGCAUGUGCCCAGCUUCUUCA	Translation
sly-miR164a-5p	Solyc09g075120.3.1	2.5	-1.0	1	21	652	672	UGGAGAAGCAGGGCACGUGCA	CUCGCUUGCCCUGCUUCUCCC	Cleavage
sly-miR164a-5p	Solyc01g080840.3.1	3.0	-1.0	1	21	4926	4946	UGGAGAAGCAGGGCACGUGCA	AGCACGGGCUUUGCUUUUCUA	Cleavage
sly-miR164a-5p	Solyc03g111840.3.1	3.0	-1.0	1	21	5694	5714	UGGAGAAGCAGGGCACGUGCA	CCCACGUGUCCUUUUUUUCCA	Cleavage
sly-miR164a-5p	Solyc06g084350.3.1	3.0	-1.0	1	21	88	108	UGGAGAAGCAGGGCACGUGCA	UUCACUUGCCCUACUUUUCCA	Cleavage
sly-miR164a-5p	Solyc09g005810.3.1	3.0	-1.0	1	21	571	591	UGGAGAAGCAGGGCACGUGCA	UUGGCUUGUCCUGCUUCUCCA	Cleavage
sly-miR164a-5p	Solyc01g086750.3.1	3.0	-1.0	1	21	3471	3491	UGGAGAAGCAGGGCACGUGCA	GUCACGGGCCUUGCUUCUUCU	Cleavage
sly-miR164a-5p	Solyc08g013720.3.1	3.0	-1.0	1	21	286	306	UGGAGAAGCAGGGCACGUGCA	AUCACGAGUCCUGCUUCUCGA	Cleavage
sly-miR164a-5p	Solyc02g069580.3.1	3.0	-1.0	1	21	4461	4481	UGGAGAAGCAGGGCACGUGCA	AACAUUUGCUUUGCUUCUUCA	Cleavage
sly-miR164a-5p	Solyc06g076970.3.1	3.0	-1.0	1	21	1002	1022	UGGAGAAGCAGGGCACGUGCA	AUCGCAUACCUUGCUUCUCCA	Cleavage
sly-miR164e-3p	Solyc03g111785.1.1	2.5	-1.0	1	21	111	131	CACGUGUUCUCCUUCUCCAAC	AAUGGAGAAGGAGAACACCUU	Cleavage
sly-miR164e-3p	Solyc06g072160.3.1	3.0	-1.0	1	21	400	420	CACGUGUUCUCCUUCUCCAAC	UUUGUAGAAGGGGACCACGUG	Cleavage
sly-miR164e-3p	Solyc07g065960.1.1	3.0	-1.0	1	21	122	142	CACGUGUUCUCCUUCUCCAAC	AUCGGAGGGGGAGAAUAUGUG	Cleavage
sly-miR164e-3p	Solyc01g101070.3.1	3.0	-1.0	1	21	1192	1212	CACGUGUUCUCCUUCUCCAAC	UGUGGAUGAGGAGAACAUGUU	Cleavage
sly-miR164e-3p	Solyc00g154980.1.1	3.0	-1.0	1	21	159	179	CACGUGUUCUCCUUCUCCAAC	AGUAGAGGAGGAGAACAUGUU	Cleavage
sly-miR164e-3p	Solyc03g115680.3.1	3.0	-1.0	1	21	184	204	CACGUGUUCUCCUUCUCCAAC	UAUGUGGAAGGAGAACAAGUG	Cleavage
sly-miR164e-3p	Solyc01g090640.3.1	3.0	-1.0	1	21	1458	1478	CACGUGUUCUCCUUCUCCAAC	UAUGAAGAGGGAGAACACCUG	Cleavage
sly-miR164e-3p	Solyc03g115660.3.1	3.0	-1.0	1	21	813	833	CACGUGUUCUCCUUCUCCAAC	UAUGUGGAAGGAGAACAAGUG	Cleavage
sly-miR164e-3p	Solyc01g090645.1.1	3.0	-1.0	1	21	1534	1554	CACGUGUUCUCCUUCUCCAAC	UAUGAAGAGGGAGAACACCUG	Cleavage
sly-miR164e-5p	Solyc07g062840.3.1	0.5	-1.0	1	22	1360	1381	UGGAGAAGCAGGGCACGUGCAA	GAGCACGUGCCCUGUUUCUCCA	Cleavage
sly-miR164e-5p	Solyc07g066330.3.1	1.0	-1.0	1	22	908	929	UGGAGAAGCAGGGCACGUGCAA	GAGCAAGUGCCCUGCUUCUCCA	Cleavage
sly-miR164e-5p	Solyc03g115850.3.1	1.5	-1.0	1	22	1235	1256	UGGAGAAGCAGGGCACGUGCAA	AGCCACGUGCACUGCUUCUCCA	Cleavage
sly-miR164e-5p	Solyc06g069710.3.1	1.5	-1.0	1	22	872	893	UGGAGAAGCAGGGCACGUGCAA	AGCCACGUGCACUGCUUCUCCA	Cleavage
sly-miR164e-5p	Solyc11g066150.2.1	1.5	-1.0	1	22	432	453	UGGAGAAGCAGGGCACGUGCAA	UCUCGCAUGCCCUGCUUCUCCA	Cleavage
sly-miR164e-5p	Solyc01g066710.3.1	2.0	-1.0	1	22	417	438	UGGAGAAGCAGGGCACGUGCAA	UUUGGCGUGCCCUGCUUCUCCG	Cleavage
sly-miR164e-5p	Solyc01g090590.3.1	2.5	-1.0	1	22	1538	1559	UGGAGAAGCAGGGCACGUGCAA	CUGCAUGUGCCCAGCUUCUUCA	Translation
sly-miR164e-5p	Solyc09g075120.3.1	2.5	-1.0	1	22	651	672	UGGAGAAGCAGGGCACGUGCAA	UCUCGCUUGCCCUGCUUCUCCC	Cleavage
sly-miR164e-5p	Solyc01g080840.3.1	3.0	-1.0	1	22	4925	4946	UGGAGAAGCAGGGCACGUGCAA	GAGCACGGGCUUUGCUUUUCUA	Cleavage
sly-miR164e-5p	Solyc09g005810.3.1	3.0	-1.0	1	22	570	591	UGGAGAAGCAGGGCACGUGCAA	UUUGGCUUGUCCUGCUUCUCCA	Cleavage
sly-miR164e-5p	Solyc03g111840.3.1	3.0	-1.0	1	22	5693	5714	UGGAGAAGCAGGGCACGUGCAA	UCCCACGUGUCCUUUUUUUCCA	Cleavage
sly-miR164e-5p	Solyc06g084350.3.1	3.0	-1.0	1	22	87	108	UGGAGAAGCAGGGCACGUGCAA	GUUCACUUGCCCUACUUUUCCA	Cleavage
sly-miR164e-5p	Solyc01g086750.3.1	3.0	-1.0	1	22	3470	3491	UGGAGAAGCAGGGCACGUGCAA	UGUCACGGGCCUUGCUUCUUCU	Cleavage
sly-miR164e-5p	Solyc08g013720.3.1	3.0	-1.0	1	22	285	306	UGGAGAAGCAGGGCACGUGCAA	AAUCACGAGUCCUGCUUCUCGA	Cleavage
sly-miR164e-5p	Solyc02g069580.3.1	3.0	-1.0	1	22	4460	4481	UGGAGAAGCAGGGCACGUGCAA	AAACAUUUGCUUUGCUUCUUCA	Cleavage
sly-miR164e-5p	Solyc06g076970.3.1	3.0	-1.0	1	22	1001	1022	UGGAGAAGCAGGGCACGUGCAA	UAUCGCAUACCUUGCUUCUCCA	Cleavage
sly-miR164f	Solyc07g066330.3.1	1.0	-1.0	1	21	909	929	UGGAGAAGCAGGGCACAUGCU	AGCAAGUGCCCUGCUUCUCCA	Cleavage
sly-miR164f	Solyc07g062840.3.1	1.5	-1.0	1	21	1361	1381	UGGAGAAGCAGGGCACAUGCU	AGCACGUGCCCUGUUUCUCCA	Cleavage
sly-miR164f	Solyc01g090590.3.1	2.0	-1.0	1	21	1539	1559	UGGAGAAGCAGGGCACAUGCU	UGCAUGUGCCCAGCUUCUUCA	Translation
sly-miR164f	Solyc02g069580.3.1	2.5	-1.0	1	21	4461	4481	UGGAGAAGCAGGGCACAUGCU	AACAUUUGCUUUGCUUCUUCA	Cleavage

sly-miR164f	Solyc03g115850.3.1	2.5	-1.0	1	21	1236	1256	UGGAGAAGCAGGGCACAUGCU	GCCACGUGCACUGCUUCUCCA	Cleavage
sly-miR164f	Solyc06g069710.3.1	2.5	-1.0	1	21	873	893	UGGAGAAGCAGGGCACAUGCU	GCCACGUGCACUGCUUCUCCA	Cleavage
sly-miR164f	Solyc04g081440.3.1	3.0	-1.0	1	21	1442	1462	UGGAGAAGCAGGGCACAUGCU	AAGAUGUGCCUUGUUUCUCCU	Cleavage
sly-miR164f	Solyc07g044750.3.1	3.0	-1.0	1	21	1423	1443	UGGAGAAGCAGGGCACAUGCU	AAUAUGUGUUUUGUUUUUCCA	Cleavage
sly-miR164f	Solyc01g079590.3.1	3.0	-1.0	1	21	295	315	UGGAGAAGCAGGGCACAUGCU	CUCAUCUCCUCUGCUUUUCCA	Cleavage
sly-miR164f	Solyc11g072590.2.1	3.0	-1.0	1	21	1516	1536	UGGAGAAGCAGGGCACAUGCU	GCCAUACGUCCUGCUUCUUCA	Cleavage
sly-miR166-1	Solyc12g044410.2.1	0.5	-1.0	1	22	1032	1053	UCGGACCAGGCUUCAUUCCCCC	CCUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-1	Solyc03g120910.3.1	0.5	-1.0	1	22	1218	1239	UCGGACCAGGCUUCAUUCCCCC	CCUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-1	Solyc02g069830.3.1	1.0	-1.0	1	22	747	768	UCGGACCAGGCUUCAUUCCCCC	AUUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-1	Solyc08g066500.3.1	1.0	-1.0	1	22	1447	1468	UCGGACCAGGCUUCAUUCCCCC	CCUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-1	Solyc02g024070.3.1	1.0	-1.0	1	22	1228	1249	UCGGACCAGGCUUCAUUCCCCC	AUUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-1	Solyc11g069470.2.1	1.0	-1.0	1	22	1604	1625	UCGGACCAGGCUUCAUUCCCCC	CCUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-1	Solyc05g008940.3.1	2.5	-1.0	1	22	838	859	UCGGACCAGGCUUCAUUCCCCC	AAGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166-1	Solyc07g045410.2.1	2.5	-1.0	1	22	1248	1269	UCGGACCAGGCUUCAUUCCCCC	AAAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166-1	Solyc08g005050.3.1	3.0	-1.0	1	22	610	631	UCGGACCAGGCUUCAUUCCCCC	GGUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166-1	Solyc06g054000.1.1	3.0	-1.0	1	22	118	139	UCGGACCAGGCUUCAUUCCCCC	AAUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166-2	Solyc12g044410.2.1	0.5	-1.0	1	22	1032	1053	UCGGACCAGGCUUCAUUCCCCC	CCUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-2	Solyc03g120910.3.1	0.5	-1.0	1	22	1218	1239	UCGGACCAGGCUUCAUUCCCCC	CCUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-2	Solyc02g069830.3.1	1.0	-1.0	1	22	747	768	UCGGACCAGGCUUCAUUCCCCC	AUUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-2	Solyc08g066500.3.1	1.0	-1.0	1	22	1447	1468	UCGGACCAGGCUUCAUUCCCCC	CCUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-2	Solyc02g024070.3.1	1.0	-1.0	1	22	1228	1249	UCGGACCAGGCUUCAUUCCCCC	AUUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-2	Solyc11g069470.2.1	1.0	-1.0	1	22	1604	1625	UCGGACCAGGCUUCAUUCCCCC	CCUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-2	Solyc05g008940.3.1	2.5	-1.0	1	22	838	859	UCGGACCAGGCUUCAUUCCCCC	AAGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166-2	Solyc07g045410.2.1	2.5	-1.0	1	22	1248	1269	UCGGACCAGGCUUCAUUCCCCC	AAAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166-2	Solyc08g005050.3.1	3.0	-1.0	1	22	610	631	UCGGACCAGGCUUCAUUCCCCC	GGUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166-2	Solyc06g054000.1.1	3.0	-1.0	1	22	118	139	UCGGACCAGGCUUCAUUCCCCC	AAUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166-3	Solyc12g044410.2.1	0.5	-1.0	1	22	1032	1053	UCGGACCAGGCUUCAUUCCCCC	CCUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-3	Solyc03g120910.3.1	0.5	-1.0	1	22	1218	1239	UCGGACCAGGCUUCAUUCCCCC	CCUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-3	Solyc02g069830.3.1	1.0	-1.0	1	22	747	768	UCGGACCAGGCUUCAUUCCCCC	AUUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-3	Solyc08g066500.3.1	1.0	-1.0	1	22	1447	1468	UCGGACCAGGCUUCAUUCCCCC	CCUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-3	Solyc02g024070.3.1	1.0	-1.0	1	22	1228	1249	UCGGACCAGGCUUCAUUCCCCC	AUUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-3	Solyc11g069470.2.1	1.0	-1.0	1	22	1604	1625	UCGGACCAGGCUUCAUUCCCCC	CCUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166-3	Solyc05g008940.3.1	2.5	-1.0	1	22	838	859	UCGGACCAGGCUUCAUUCCCCC	AAGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166-3	Solyc07g045410.2.1	2.5	-1.0	1	22	1248	1269	UCGGACCAGGCUUCAUUCCCCC	AAAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166-3	Solyc08g005050.3.1	3.0	-1.0	1	22	610	631	UCGGACCAGGCUUCAUUCCCCC	GGUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166-3	Solyc06g054000.1.1	3.0	-1.0	1	22	118	139	UCGGACCAGGCUUCAUUCCCCC	AAUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166a-1-3p	Solyc12g044410.2.1	0.5	-1.0	1	21	1033	1053	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-1-3p	Solyc03g120910.3.1	0.5	-1.0	1	21	1219	1239	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-1-3p	Solyc02g069830.3.1	1.0	-1.0	1	21	748	768	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-1-3p	Solyc08g066500.3.1	1.0	-1.0	1	21	1448	1468	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-1-3p	Solyc02g024070.3.1	1.0	-1.0	1	21	1229	1249	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-1-3p	Solyc11g069470.2.1	1.0	-1.0	1	21	1605	1625	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-1-3p	Solyc05g008940.3.1	2.5	-1.0	1	21	839	859	UCGGACCAGGCUUCAUUCCCC	AGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166a-1-3p	Solyc07g045410.2.1	2.5	-1.0	1	21	1249	1269	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166a-1-3p	Solyc08g005050.3.1	3.0	-1.0	1	21	611	631	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166a-1-3p	Solyc06g054000.1.1	3.0	-1.0	1	21	119	139	UCGGACCAGGCUUCAUUCCCC	AUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166a-2-3p	Solyc12g044410.2.1	0.5	-1.0	1	21	1033	1053	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-2-3p	Solyc03g120910.3.1	0.5	-1.0	1	21	1219	1239	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-2-3p	Solyc02g069830.3.1	1.0	-1.0	1	21	748	768	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-2-3p	Solyc08g066500.3.1	1.0	-1.0	1	21	1448	1468	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage

sly-miR166a-2-3p	Solyc02g024070.3.1	1.0	-1.0	1	21	1229	1249	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-2-3p	Solyc11g069470.2.1	1.0	-1.0	1	21	1605	1625	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-2-3p	Solyc05g008940.3.1	2.5	-1.0	1	21	839	859	UCGGACCAGGCUUCAUUCCCC	AGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166a-2-3p	Solyc07g045410.2.1	2.5	-1.0	1	21	1249	1269	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166a-2-3p	Solyc08g005050.3.1	3.0	-1.0	1	21	611	631	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166a-2-3p	Solyc06g054000.1.1	3.0	-1.0	1	21	119	139	UCGGACCAGGCUUCAUUCCCC	AUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166a-2-5p	Solyc04g009040.3.1	2.0	-1.0	1	21	2535	2555	GGAAUGUUGUUUGGCUCGAGG	UCUCAAGCCAAGCAACAUUCU	Cleavage
sly-miR166a-2-5p	Solyc08g006420.3.1	2.0	-1.0	1	21	892	912	GGAAUGUUGUUUGGCUCGAGG	UAGCGAGCCAAACAAUGUUCC	Cleavage
sly-miR166a-2-5p	Solyc04g050170.3.1	2.0	-1.0	1	21	2523	2543	GGAAUGUUGUUUGGCUCGAGG	CGUCAAGUCAAACAACAUUCU	Cleavage
sly-miR166a-2-5p	Solyc06g076910.2.1	2.5	-1.0	1	21	3342	3362	GGAAUGUUGUUUGGCUCGAGG	UCUUAAGCCAAGCAACAUUCU	Cleavage
sly-miR166a-2-5p	Solyc07g065860.3.1	2.5	-1.0	1	21	4683	4703	GGAAUGUUGUUUGGCUCGAGG	GCUCGAUCCAAAUGACAUUCU	Cleavage
sly-miR166a-2-5p	Solyc06g066790.3.1	2.5	-1.0	1	21	2565	2585	GGAAUGUUGUUUGGCUCGAGG	AAUUGAGGCAAACAACAUUUU	Cleavage
sly-miR166a-2-5p	Solyc03g120020.3.1	2.5	-1.0	1	21	1636	1656	GGAAUGUUGUUUGGCUCGAGG	UAUCGUGCCAAGCAAUGUUCC	Cleavage
sly-miR166a-2-5p	Solyc08g005010.3.1	2.5	-1.0	1	21	1415	1435	GGAAUGUUGUUUGGCUCGAGG	GAUCCAGACAAACAACAUUCU	Cleavage
sly-miR166a-2-5p	Solyc10g076845.1.1	3.0	-1.0	1	21	451	471	GGAAUGUUGUUUGGCUCGAGG	CUUCGAGUCAAACAACAUGCG	Cleavage
sly-miR166a-2-5p	Solyc10g083980.1.1	3.0	-1.0	1	21	366	386	GGAAUGUUGUUUGGCUCGAGG	CUUCGAGCCAUAUGACAUUCU	Translation
sly-miR166a-2-5p	Solyc06g036180.3.1	3.0	-1.0	1	21	2316	2336	GGAAUGUUGUUUGGCUCGAGG	ACUCGAGCCAAAUAAUAUAUC	Cleavage
sly-miR166a-2-5p	Solyc09g060080.3.1	3.0	-1.0	1	21	6694	6714	GGAAUGUUGUUUGGCUCGAGG	UCUCAAGCUGAACAACGUUCU	Cleavage
sly-miR166a-2-5p	Solyc08g006920.2.1	3.0	-1.0	1	21	357	377	GGAAUGUUGUUUGGCUCGAGG	AUUUGAGUUGAACAACAUUUU	Cleavage
sly-miR166a-2-5p	Solyc06g065570.3.1	3.0	-1.0	1	21	1058	1078	GGAAUGUUGUUUGGCUCGAGG	AGUCGAGCCAAGCACUAUUCU	Cleavage
sly-miR166a-2-5p	Solyc03g095450.3.1	3.0	-1.0	1	21	949	969	GGAAUGUUGUUUGGCUCGAGG	GUUCAAGUCAAAUGACAUUCU	Cleavage
sly-miR166a-2-5p	Solyc02g081470.3.1	3.0	-1.0	1	21	324	344	GGAAUGUUGUUUGGCUCGAGG	CAUCAAGCCACACAACAUUCU	Translation
sly-miR166a-2-5p	Solyc02g081510.2.1	3.0	-1.0	1	21	153	173	GGAAUGUUGUUUGGCUCGAGG	CAUCAAGCCACACAACAUUCU	Translation
sly-miR166a-2-5p	Solyc05g005900.3.1	3.0	-1.0	1	21	1287	1307	GGAAUGUUGUUUGGCUCGAGG	UGUUGAGACAGACAACAUUUU	Cleavage
sly-miR166a-2-5p	Solyc06g066200.2.1	3.0	-1.0	1	20	1	20	GGAAUGUUGUUUGGCUCGAG	AUGGAACCAAACAACAUUCA	Cleavage
sly-miR166a-3-3p	Solyc12g044410.2.1	0.5	-1.0	1	21	1033	1053	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-3-3p	Solyc03g120910.3.1	0.5	-1.0	1	21	1219	1239	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-3-3p	Solyc02g069830.3.1	1.0	-1.0	1	21	748	768	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-3-3p	Solyc08g066500.3.1	1.0	-1.0	1	21	1448	1468	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-3-3p	Solyc02g024070.3.1	1.0	-1.0	1	21	1229	1249	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-3-3p	Solyc11g069470.2.1	1.0	-1.0	1	21	1605	1625	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-3-3p	Solyc05g008940.3.1	2.5	-1.0	1	21	839	859	UCGGACCAGGCUUCAUUCCCC	AGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166a-3-3p	Solyc07g045410.2.1	2.5	-1.0	1	21	1249	1269	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166a-3-3p	Solyc08g005050.3.1	3.0	-1.0	1	21	611	631	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166a-3-3p	Solyc06g054000.1.1	3.0	-1.0	1	21	119	139	UCGGACCAGGCUUCAUUCCCC	AUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166a-4-3p	Solyc12g044410.2.1	0.5	-1.0	1	21	1033	1053	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-4-3p	Solyc03g120910.3.1	0.5	-1.0	1	21	1219	1239	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-4-3p	Solyc02g069830.3.1	1.0	-1.0	1	21	748	768	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-4-3p	Solyc08g066500.3.1	1.0	-1.0	1	21	1448	1468	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-4-3p	Solyc02g024070.3.1	1.0	-1.0	1	21	1229	1249	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-4-3p	Solyc11g069470.2.1	1.0	-1.0	1	21	1605	1625	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166a-4-3p	Solyc05g008940.3.1	2.5	-1.0	1	21	839	859	UCGGACCAGGCUUCAUUCCCC	AGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166a-4-3p	Solyc07g045410.2.1	2.5	-1.0	1	21	1249	1269	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166a-4-3p	Solyc08g005050.3.1	3.0	-1.0	1	21	611	631	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166a-4-3p	Solyc06g054000.1.1	3.0	-1.0	1	21	119	139	UCGGACCAGGCUUCAUUCCCC	AUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR166a-4-5p	Solyc05g005900.3.1	2.5	-1.0	1	21	1287	1307	GGAAUGUUGUCUGGCUCGAGG	UGUUGAGACAGACAACAUUUU	Cleavage
sly-miR166a-4-5p	Solyc10g083980.1.1	3.0	-1.0	1	21	366	386	GGAAUGUUGUCUGGCUCGAGG	CUUCGAGCCAUAUGACAUUCU	Translation
sly-miR166a-4-5p	Solyc04g012110.2.1	3.0	-1.0	1	21	1755	1775	GGAAUGUUGUCUGGCUCGAGG	CCUAAAGCCAGACAACGUUCU	Cleavage
sly-miR166a-4-5p	Solyc01g010506.1.1	3.0	-1.0	1	21	168	188	GGAAUGUUGUCUGGCUCGAGG	UGUCGGGCUAGAUGACAUUCA	Cleavage
sly-miR166a-4-5p	Solyc07g024070.2.1	3.0	-1.0	1	21	1982	2002	GGAAUGUUGUCUGGCUCGAGG	UCUCAAUCUGGACAACAUUCC	Cleavage

sly-miR166a-4-5p	Solyc01g066840.3.1	3.0	-1.0	1	21	539	559	GGAAUGUUGUCUGGCUCGAGG	AGUUGAGUUAGACAAUGUUCU	Cleavage
sly-miR166a-4-5p	Solyc05g012253.1.1	3.0	-1.0	1	21	172	192	GGAAUGUUGUCUGGCUCGAGG	ACUGCAGCUAGACAAUAUUCC	Cleavage
sly-miR166a-4-5p	Solyc02g081470.3.1	3.0	-1.0	1	21	324	344	GGAAUGUUGUCUGGCUCGAGG	CAUCAAGCCACACAACAUUCU	Translation
sly-miR166a-4-5p	Solyc02g081510.2.1	3.0	-1.0	1	21	153	173	GGAAUGUUGUCUGGCUCGAGG	CAUCAAGCCACACAACAUUCU	Translation
sly-miR166a-4-5p	Solyc01g110430.3.1	3.0	-1.0	1	21	743	763	GGAAUGUUGUCUGGCUCGAGG	CGUCAGGUCAGACAGUAUUCC	Cleavage
sly-miR166a-4-5p	Solyc04g064750.2.1	3.0	-1.0	1	21	876	896	GGAAUGUUGUCUGGCUCGAGG	GGUGGAGCCGGACAAUGUUUC	Cleavage
sly-miR166g-3p	Solyc12g044410.2.1	0.5	-1.0	1	21	1033	1053	UCGGACCAGGCUUCAUUCCUC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166g-3p	Solyc03g120910.3.1	0.5	-1.0	1	21	1219	1239	UCGGACCAGGCUUCAUUCCUC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
sly-miR166g-3p	Solyc02g069830.3.1	1.0	-1.0	1	21	748	768	UCGGACCAGGCUUCAUUCCUC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166g-3p	Solyc08g066500.3.1	1.0	-1.0	1	21	1448	1468	UCGGACCAGGCUUCAUUCCUC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166g-3p	Solyc02g024070.3.1	1.0	-1.0	1	21	1229	1249	UCGGACCAGGCUUCAUUCCUC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166g-3p	Solyc11g069470.2.1	1.0	-1.0	1	21	1605	1625	UCGGACCAGGCUUCAUUCCUC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
sly-miR166g-3p	Solyc07g045410.2.1	2.5	-1.0	1	21	1249	1269	UCGGACCAGGCUUCAUUCCUC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
sly-miR166g-3p	Solyc05g008940.3.1	2.5	-1.0	1	21	839	859	UCGGACCAGGCUUCAUUCCUC	AGAGAAGGAAGCCUGGUUCGA	Cleavage
sly-miR166g-3p	Solyc08g005050.3.1	3.0	-1.0	1	21	611	631	UCGGACCAGGCUUCAUUCCUC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
sly-miR166g-3p	Solyc06g054000.1.1	3.0	-1.0	1	21	119	139	UCGGACCAGGCUUCAUUCCUC	AUGGCAUGAAGCUUGGUGCGA	Cleavage
sly-miR167a-1-3p	Solyc10g080440.2.1	2.5	-1.0	1	20	1093	1112	GAUCAUGUGGCAGCCUUACC	UGUAAGGCUGCCAAAUGAUA	Cleavage
sly-miR167a-1-3p	Solyc06g062887.1.1	3.0	-1.0	1	20	454	473	GAUCAUGUGGCAGCCUUACC	GGAAAGGCUGCUUCAUGAUC	Cleavage
sly-miR167a-1-3p	Solyc01g109640.3.1	3.0	-1.0	1	20	4890	4909	GAUCAUGUGGCAGCCUUACC	AGUAAGGUUGCUGCAUGAAC	Cleavage
sly-miR167a-1-3p	Solyc06g076340.3.1	3.0	-1.0	1	20	2643	2662	GAUCAUGUGGCAGCCUUACC	UGUACGGUUGCCGCGUGAUU	Cleavage
sly-miR167a-1-5p	Solyc06g036780.3.1	2.0	-1.0	1	22	971	992	UGAAGCUGCCAGCAUGAUCUAA	UGUGAUUCUGCUGGUAGCUUCA	Cleavage
sly-miR167a-1-5p	Solyc03g117700.2.1	2.5	-1.0	1	22	526	547	UGAAGCUGCCAGCAUGAUCUAA	AUUGAUCAUGUUGGCAGUCUCA	Cleavage
sly-miR167a-1-5p	Solyc06g035710.1.1	3.0	-1.0	1	22	1060	1081	UGAAGCUGCCAGCAUGAUCUAA	GUAGGGCUUGCUGGCAGCUUCG	Cleavage
sly-miR167a-1-5p	Solyc04g073990.3.1	3.0	-1.0	1	22	1100	1121	UGAAGCUGCCAGCAUGAUCUAA	UGAGAAUAUGCUGGUGGCUUUA	Cleavage
sly-miR167a-1-5p	Solyc04g009940.3.1	3.0	-1.0	1	22	836	857	UGAAGCUGCCAGCAUGAUCUAA	AUCGAGUAUGCUGGUGGUUUCA	Cleavage
sly-miR167a-1-5p	Solyc01g099790.3.1	3.0	-1.0	1	22	1417	1438	UGAAGCUGCCAGCAUGAUCUAA	UCUGAUCAGGCUGGUGGCUUCU	Cleavage
sly-miR167a-1-5p	Solyc09g074840.3.1	3.0	-1.0	1	22	474	495	UGAAGCUGCCAGCAUGAUCUAA	AAUGAUCAGGAUGGUAGCUUCA	Cleavage
sly-miR167a-2-3p	Solyc01g110480.3.1	2.5	-1.0	1	20	1675	1694	GAUCAUGUGGUUGCUUCACC	ACUGAAGCAACCACAUUAUC	Cleavage
sly-miR167a-2-3p	Solyc03g111180.3.1	2.5	-1.0	1	20	1368	1387	GAUCAUGUGGUUGCUUCACC	UGUGAAGCAUUCAUAUGAUC	Translation
sly-miR167a-2-3p	Solyc04g082510.3.1	2.5	-1.0	1	20	2154	2173	GAUCAUGUGGUUGCUUCACC	UGUAAAGCAAACACAUGAUC	Translation
sly-miR167a-2-3p	Solyc05g009970.3.1	3.0	-1.0	1	20	1021	1040	GAUCAUGUGGUUGCUUCACC	CAUGAAGCAAUCAUAUGAUA	Cleavage
sly-miR167a-2-3p	Solyc11g069530.2.1	3.0	-1.0	1	20	1716	1735	GAUCAUGUGGUUGCUUCACC	CGUGAAGAGACUGCAUGAUC	Cleavage
sly-miR167a-2-3p	Solyc01g106100.2.1	3.0	-1.0	1	20	833	852	GAUCAUGUGGUUGCUUCACC	AGAGAAGCAACUACAUGACC	Cleavage
sly-miR167a-2-3p	Solyc01g088680.3.1	3.0	-1.0	1	20	2173	2192	GAUCAUGUGGUUGCUUCACC	UGGGCAGCAAUUACAUGAUC	Cleavage
sly-miR167a-2-5p	Solyc06g036780.3.1	2.0	-1.0	1	22	971	992	UGAAGCUGCCAGCAUGAUCUAA	UGUGAUUCUGCUGGUAGCUUCA	Cleavage
sly-miR167a-2-5p	Solyc03g117700.2.1	2.5	-1.0	1	22	526	547	UGAAGCUGCCAGCAUGAUCUAA	AUUGAUCAUGUUGGCAGUCUCA	Cleavage
sly-miR167a-2-5p	Solyc06g035710.1.1	3.0	-1.0	1	22	1060	1081	UGAAGCUGCCAGCAUGAUCUAA	GUAGGGCUUGCUGGCAGCUUCG	Cleavage
sly-miR167a-2-5p	Solyc04g073990.3.1	3.0	-1.0	1	22	1100	1121	UGAAGCUGCCAGCAUGAUCUAA	UGAGAAUAUGCUGGUGGCUUUA	Cleavage
sly-miR167a-2-5p	Solyc04g009940.3.1	3.0	-1.0	1	22	836	857	UGAAGCUGCCAGCAUGAUCUAA	AUCGAGUAUGCUGGUGGUUUCA	Cleavage
sly-miR167a-2-5p	Solyc01g099790.3.1	3.0	-1.0	1	22	1417	1438	UGAAGCUGCCAGCAUGAUCUAA	UCUGAUCAGGCUGGUGGCUUCU	Cleavage
sly-miR167a-2-5p	Solyc09g074840.3.1	3.0	-1.0	1	22	474	495	UGAAGCUGCCAGCAUGAUCUAA	AAUGAUCAGGAUGGUAGCUUCA	Cleavage
sly-miR167c-5p	Solyc06g036780.3.1	2.0	-1.0	1	21	972	992	UGAAGCUGCCAGCAUGAUCUA	GUGAUUCUGCUGGUAGCUUCA	Cleavage
sly-miR167c-5p	Solyc03g117700.2.1	2.5	-1.0	1	21	527	547	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
sly-miR167c-5p	Solyc06g035710.1.1	3.0	-1.0	1	21	1061	1081	UGAAGCUGCCAGCAUGAUCUA	UAGGGCUUGCUGGCAGCUUCG	Cleavage
sly-miR167c-5p	Solyc04g073990.3.1	3.0	-1.0	1	21	1101	1121	UGAAGCUGCCAGCAUGAUCUA	GAGAAUAUGCUGGUGGCUUUA	Cleavage
sly-miR167c-5p	Solyc04g009940.3.1	3.0	-1.0	1	21	837	857	UGAAGCUGCCAGCAUGAUCUA	UCGAGUAUGCUGGUGGUUUCA	Cleavage
sly-miR167c-5p	Solyc01g099790.3.1	3.0	-1.0	1	21	1418	1438	UGAAGCUGCCAGCAUGAUCUA	CUGAUCAGGCUGGUGGCUUCU	Cleavage
sly-miR167c-5p	Solyc09g074840.3.1	3.0	-1.0	1	21	475	495	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
sly-miR167h-1	Solyc09g082820.3.1	0.0	-1.0	1	24	264	287	AUCAUGCUGGCAGCUUCAACUGCU	AUCAGUUGAAGCUGCCAGCAUGAU	Cleavage
sly-miR167h-1	Solyc09g089640.2.1	3.0	-1.0	1	24	461	484	AUCAUGCUGGCAGCUUCAACUGCU	GUCAUUUGAAGUUGCUAAUAUGAU	Cleavage

sly-miR167h-1	Solyc12g096860.2.1	3.0	-1.0	1	24	17	40	AUCAUGCUGGCAGCUUCAACUGCU	GCCAUUUGAAGUUGUAAGCAUGGU	Cleavage
sly-miR167h-1	Solyc01g107130.3.1	3.0	-1.0	1	24	1928	1951	AUCAUGCUGGCAGCUUCAACUGCU	AACAAUGGAGGCUGUUGGCAUGAU	Cleavage
sly-miR167h-1	Solyc08g079850.3.1	3.0	-1.0	1	24	198	221	AUCAUGCUGGCAGCUUCAACUGCU	AGAUGAAGAGGCUGCUAGCAUGAU	Cleavage
sly-miR167h-1	Solyc10g047050.2.1	3.0	-1.0	1	24	3026	3049	AUCAUGCUGGCAGCUUCAACUGCU	CAUGAUUGAAGCUUUUAGUAUGAU	Translation
sly-miR167h-1	Solyc01g005385.1.1	3.0	-1.0	1	24	999	1022	AUCAUGCUGGCAGCUUCAACUGCU	UCUUCUUGAUGCUGCCAGUAUGGC	Cleavage
sly-miR167h-1	Solyc01g005380.2.1	3.0	-1.0	1	24	1054	1077	AUCAUGCUGGCAGCUUCAACUGCU	UCUUCUUGAUGCUGCCAGUAUGGC	Cleavage
sly-miR167h-2	Solyc09g082820.3.1	0.0	-1.0	1	24	264	287	AUCAUGCUGGCAGCUUCAACUGCU	AUCAGUUGAAGCUGCCAGCAUGAU	Cleavage
sly-miR167h-2	Solyc09g089640.2.1	3.0	-1.0	1	24	461	484	AUCAUGCUGGCAGCUUCAACUGCU	GUCAUUUGAAGUUGCUAAUAUGAU	Cleavage
sly-miR167h-2	Solyc12g096860.2.1	3.0	-1.0	1	24	17	40	AUCAUGCUGGCAGCUUCAACUGCU	GCCAUUUGAAGUUGUAAGCAUGGU	Cleavage
sly-miR167h-2	Solyc01g107130.3.1	3.0	-1.0	1	24	1928	1951	AUCAUGCUGGCAGCUUCAACUGCU	AACAAUGGAGGCUGUUGGCAUGAU	Cleavage
sly-miR167h-2	Solyc08g079850.3.1	3.0	-1.0	1	24	198	221	AUCAUGCUGGCAGCUUCAACUGCU	AGAUGAAGAGGCUGCUAGCAUGAU	Cleavage
sly-miR167h-2	Solyc10g047050.2.1	3.0	-1.0	1	24	3026	3049	AUCAUGCUGGCAGCUUCAACUGCU	CAUGAUUGAAGCUUUUAGUAUGAU	Translation
sly-miR167h-2	Solyc01g005385.1.1	3.0	-1.0	1	24	999	1022	AUCAUGCUGGCAGCUUCAACUGCU	UCUUCUUGAUGCUGCCAGUAUGGC	Cleavage
sly-miR167h-2	Solyc01g005380.2.1	3.0	-1.0	1	24	1054	1077	AUCAUGCUGGCAGCUUCAACUGCU	UCUUCUUGAUGCUGCCAGUAUGGC	Cleavage
sly-miR167h-3-3p	Solyc02g072470.3.1	3.0	-1.0	1	21	1111	1131	AGAUCAUGUGGCAGCAUCACC	CAAGAUGCUGUCACAUGAUUA	Cleavage
sly-miR167h-3-3p	Solyc02g069040.3.1	3.0	-1.0	1	21	2006	2026	AGAUCAUGUGGCAGCAUCACC	UUUGAUGCUGCCAAAUGCUCU	Cleavage
sly-miR167h-3-3p	Solyc03g078240.2.1	3.0	-1.0	1	21	599	619	AGAUCAUGUGGCAGCAUCACC	CCUGGUGCUGCUGCAUGUUCU	Cleavage
sly-miR167h-3-3p	Solyc05g018875.1.1	3.0	-1.0	1	21	71	91	AGAUCAUGUGGCAGCAUCACC	GUUGAUGGUGUCAUAUGGUUU	Cleavage
sly-miR167h-3-3p	Solyc01g068620.3.1	3.0	-1.0	1	21	327	347	AGAUCAUGUGGCAGCAUCACC	CUUGAUACUGUCACAUGUUCU	Cleavage
sly-miR167h-3-3p	Solyc06g076930.2.1	3.0	-1.0	1	21	2314	2334	AGAUCAUGUGGCAGCAUCACC	AUUGAAGCUGUCGUAUGGUCU	Cleavage
sly-miR167h-3-3p	Solyc01g068590.3.1	3.0	-1.0	1	21	5022	5042	AGAUCAUGUGGCAGCAUCACC	CUUGAUACUGUCACAUGUUCU	Cleavage
sly-miR167h-3-5p	Solyc01g088380.2.1	1.5	-1.0	1	24	1499	1522	AGCAGUUGAAGCUGCCAGCAUGAU	GGGUUGCUGGCAGCUUCAGUUGUU	Cleavage
sly-miR167h-3-5p	Solyc03g063900.1.1	2.0	-1.0	1	24	170	193	AGCAGUUGAAGCUGCCAGCAUGAU	CCAAUGUUGGCAGUUUCAAUUGUU	Cleavage
sly-miR167h-3-5p	Solyc11g007910.2.1	3.0	-1.0	1	24	2677	2700	AGCAGUUGAAGCUGCCAGCAUGAU	GUCAGGCAGGAAGUUUCAGCUGCU	Cleavage
sly-miR167h-3-5p	Solyc01g096200.3.1	3.0	-1.0	1	24	786	809	AGCAGUUGAAGCUGCCAGCAUGAU	AACAAGUUGUUAGUUUCAAUUGCU	Cleavage
sly-miR167h-3-5p	Solyc05g013860.3.1	3.0	-1.0	1	24	670	693	AGCAGUUGAAGCUGCCAGCAUGAU	AACUCUUUGGCAGCUUUAACUGCA	Cleavage
sly-miR167h-3-5p	Solyc09g005340.3.1	3.0	-1.0	1	24	193	216	AGCAGUUGAAGCUGCCAGCAUGAU	AUGUUGAUGUCAGUUUCAACUGUU	Cleavage
sly-miR168	Solyc09g074390.2.1	3.0	-1.0	1	24	281	304	AUUCAGUUGAUGCAAGGCGGGACC	CAACUUGCCUUGCAUCAACUCAAG	Cleavage
sly-miR168	Solyc01g110090.1.1	3.0	-1.0	1	24	129	152	AUUCAGUUGAUGCAAGGCGGGACC	UCAUCCGUUUUGCAUCGACUGUAU	Cleavage
sly-miR168	Solyc10g085650.2.1	3.0	-1.0	1	24	2545	2568	AUUCAGUUGAUGCAAGGCGGGACC	UUUCUCGAUCUGCAUCAACUGGAU	Cleavage
sly-miR168	Solyc01g101050.3.1	3.0	-1.0	1	24	2549	2572	AUUCAGUUGAUGCAAGGCGGGACC	GAGUGUGUAUUGCAUCAAUUGGAU	Cleavage
sly-miR168a-1-3p	Solyc06g076700.1.1	3.0	-1.0	1	21	872	892	CCCGCCUUGCAUCAACUGAAU	UUUCAGUUGAUGCAGGGCGAU	Cleavage
sly-miR168a-1-3p	Solyc01g102510.3.1	3.0	-1.0	1	21	3881	3901	CCCGCCUUGCAUCAACUGAAU	UAUCAGUUGGUGCGGGACGGG	Cleavage
sly-miR168a-1-3p	Solyc01g108250.3.1	3.0	-1.0	1	21	816	836	CCCGCCUUGCAUCAACUGAAU	AAUCAGAUGAUGCAAUGUGGG	Cleavage
sly-miR168a-1-3p	Solyc07g066650.3.1	3.0	-1.0	1	21	347	367	CCCGCCUUGCAUCAACUGAAU	CAUCUGCUGAUGCAAGGCGGU	Cleavage
sly-miR168a-1-5p	Solyc08g005690.1.1	0.0	-1.0	1	21	118	138	UCGCUUGGUGCAGGUCGGGAC	GUCCCGACCUGCACCAAGCGA	Cleavage
sly-miR168a-1-5p	Solyc03g098280.3.1	2.5	-1.0	1	21	770	790	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
sly-miR168a-1-5p	Solyc06g072300.3.1	2.5	-1.0	1	21	528	548	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
sly-miR168a-1-5p	Solyc05g053230.3.1	2.5	-1.0	1	21	1414	1434	UCGCUUGGUGCAGGUCGGGAC	CGCUCGACCUGCACCUAGUGA	Cleavage
sly-miR168a-1-5p	Solyc00g030110.2.1	3.0	-1.0	1	21	909	929	UCGCUUGGUGCAGGUCGGGAC	UGGCCGACCUGCACAAAGCGG	Cleavage
sly-miR168a-1-5p	Solyc12g098980.2.1	3.0	-1.0	1	21	1312	1332	UCGCUUGGUGCAGGUCGGGAC	GCCUCGACCUGUACCAAGUUA	Cleavage
sly-miR168a-1-5p	Solyc01g103295.1.1	3.0	-1.0	1	21	158	178	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-1-5p	Solyc01g103300.2.1	3.0	-1.0	1	21	338	358	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-1-5p	Solyc01g103335.1.1	3.0	-1.0	1	21	954	974	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-1-5p	Solyc01g103310.3.1	3.0	-1.0	1	21	2498	2518	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-2-5p	Solyc08g005690.1.1	0.0	-1.0	1	21	118	138	UCGCUUGGUGCAGGUCGGGAC	GUCCCGACCUGCACCAAGCGA	Cleavage
sly-miR168a-2-5p	Solyc03g098280.3.1	2.5	-1.0	1	21	770	790	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
sly-miR168a-2-5p	Solyc06g072300.3.1	2.5	-1.0	1	21	528	548	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
sly-miR168a-2-5p	Solyc05g053230.3.1	2.5	-1.0	1	21	1414	1434	UCGCUUGGUGCAGGUCGGGAC	CGCUCGACCUGCACCUAGUGA	Cleavage
sly-miR168a-2-5p	Solyc00g030110.2.1	3.0	-1.0	1	21	909	929	UCGCUUGGUGCAGGUCGGGAC	UGGCCGACCUGCACAAAGCGG	Cleavage

sly-miR168a-2-5p	Solyc12g098980.2.1	3.0	-1.0	1	21	1312	1332	UCGCUUGGUGCAGGUCGGGAC	GCCUCGACCUGUACCAAGUUA	Cleavage
sly-miR168a-2-5p	Solyc01g103295.1.1	3.0	-1.0	1	21	158	178	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-2-5p	Solyc01g103300.2.1	3.0	-1.0	1	21	338	358	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-2-5p	Solyc01g103335.1.1	3.0	-1.0	1	21	954	974	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR168a-2-5p	Solyc01g103310.3.1	3.0	-1.0	1	21	2498	2518	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
sly-miR169a-1-3p	Solyc04g009330.3.1	2.0	-1.0	1	21	2516	2536	GGCAAGUUGUUCUUGGCUAUA	UAUAGCCAAGAGCAAUUUGUU	Cleavage
sly-miR169a-1-3p	Solyc02g088120.3.1	2.5	-1.0	1	21	2850	2870	GGCAAGUUGUUCUUGGCUAUA	UGCAGCCAAGGAUGACUUGCC	Cleavage
sly-miR169a-1-3p	Solyc09g090150.3.1	2.5	-1.0	1	21	570	590	GGCAAGUUGUUCUUGGCUAUA	AAUGGACAAGAACAACUUGUU	Cleavage
sly-miR169a-1-3p	Solyc09g009970.3.1	3.0	-1.0	1	21	1461	1481	GGCAAGUUGUUCUUGGCUAUA	AAUGGCCAAGAAGAAUUUGUC	Cleavage
sly-miR169a-1-3p	Solyc05g053000.1.1	3.0	-1.0	1	21	595	615	GGCAAGUUGUUCUUGGCUAUA	GGUAGCCAAGGACAAGUUGUU	Cleavage
sly-miR169a-1-3p	Solyc06g075250.3.1	3.0	-1.0	1	21	1605	1625	GGCAAGUUGUUCUUGGCUAUA	AAUGGACAAGGACAAUUUGCU	Cleavage
sly-miR169a-1-3p	Solyc05g025687.1.1	3.0	-1.0	1	21	423	443	GGCAAGUUGUUCUUGGCUAUA	UUUGGCCAAGAAUGGUUUGCU	Cleavage
sly-miR169a-1-3p	Solyc08g080860.3.1	3.0	-1.0	1	21	594	614	GGCAAGUUGUUCUUGGCUAUA	ACUAGCCAAGAACAAGUUGUG	Cleavage
sly-miR169a-1-3p	Solyc05g007130.3.1	3.0	-1.0	1	21	1416	1436	GGCAAGUUGUUCUUGGCUAUA	UCUAGUCAGGAAUGGCUUGUC	Cleavage
sly-miR169a-1-3p	Solyc02g085810.3.1	3.0	-1.0	1	21	4080	4100	GGCAAGUUGUUCUUGGCUAUA	GUUAGUCGAGAUCAACUUGCU	Translation
sly-miR169a-1-3p	Solyc10g074520.2.1	3.0	-1.0	1	21	42	62	GGCAAGUUGUUCUUGGCUAUA	GUUGGCGAAGAACAAUUUGUU	Cleavage
sly-miR169a-1-3p	Solyc09g083390.2.1	3.0	-1.0	1	21	2975	2995	GGCAAGUUGUUCUUGGCUAUA	GCUACACAAGAACAACUUGUU	Cleavage
sly-miR169a-2-5p	Solyc07g007480.2.1	1.0	-1.0	1	21	1533	1553	CAGCCAAGGAUGACUUGCCGA	CAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169a-2-5p	Solyc07g007480.2.1	2.0	-1.0	1	21	1070	1090	CAGCCAAGGAUGACUUGCCGA	CAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169a-2-5p	Solyc02g088120.3.1	2.0	-1.0	1	21	2899	2919	CAGCCAAGGAUGACUUGCCGA	CUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169a-2-5p	Solyc01g008490.3.1	2.0	-1.0	1	21	610	630	CAGCCAAGGAUGACUUGCCGA	GUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169a-2-5p	Solyc03g121940.3.1	2.0	-1.0	1	21	1276	1296	CAGCCAAGGAUGACUUGCCGA	GUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169a-2-5p	Solyc12g009050.2.1	2.0	-1.0	1	21	1409	1429	CAGCCAAGGAUGACUUGCCGA	CAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169a-2-5p	Solyc08g062210.3.1	2.5	-1.0	1	21	1637	1657	CAGCCAAGGAUGACUUGCCGA	UCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169a-2-5p	Solyc01g006930.3.1	2.5	-1.0	1	21	2833	2853	CAGCCAAGGAUGACUUGCCGA	UGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169a-2-5p	Solyc01g087240.3.1	2.5	-1.0	1	21	2573	2593	CAGCCAAGGAUGACUUGCCGA	CAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169a-2-5p	Solyc03g079850.3.1	3.0	-1.0	1	21	664	684	CAGCCAAGGAUGACUUGCCGA	AAAUUAAGUCAUUCUUGGCUG	Cleavage
sly-miR169a-2-5p	Solyc04g079550.3.1	3.0	-1.0	1	21	1635	1655	CAGCCAAGGAUGACUUGCCGA	UGUUUAAGUCAUCUUUGGCUG	Cleavage
sly-miR169a-2-5p	Solyc04g016540.2.1	3.0	-1.0	1	21	1838	1858	CAGCCAAGGAUGACUUGCCGA	GUGGAAAUUUAUCUUUGGCUG	Cleavage
sly-miR169a-2-5p	Solyc08g006830.3.1	3.0	-1.0	1	21	598	618	CAGCCAAGGAUGACUUGCCGA	CUGGAUAUUCAUCCUUGGCUG	Cleavage
sly-miR169b-1-5p	Solyc07g007480.2.1	1.0	-1.0	1	21	1533	1553	CAGCCAAGGAUGACUUGCCGG	CAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-1-5p	Solyc07g007480.2.1	2.0	-1.0	1	21	1070	1090	CAGCCAAGGAUGACUUGCCGG	CAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-1-5p	Solyc02g088120.3.1	2.0	-1.0	1	21	2899	2919	CAGCCAAGGAUGACUUGCCGG	CUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169b-1-5p	Solyc01g008490.3.1	2.0	-1.0	1	21	610	630	CAGCCAAGGAUGACUUGCCGG	GUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169b-1-5p	Solyc03g121940.3.1	2.0	-1.0	1	21	1276	1296	CAGCCAAGGAUGACUUGCCGG	GUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-1-5p	Solyc12g009050.2.1	2.0	-1.0	1	21	1409	1429	CAGCCAAGGAUGACUUGCCGG	CAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169b-1-5p	Solyc08g062210.3.1	2.5	-1.0	1	21	1637	1657	CAGCCAAGGAUGACUUGCCGG	UCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169b-1-5p	Solyc01g087240.3.1	2.5	-1.0	1	21	2573	2593	CAGCCAAGGAUGACUUGCCGG	CAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169b-1-5p	Solyc01g006930.3.1	2.5	-1.0	1	21	2833	2853	CAGCCAAGGAUGACUUGCCGG	UGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169b-1-5p	Solyc03g079850.3.1	3.0	-1.0	1	21	664	684	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
sly-miR169b-1-5p	Solyc04g079550.3.1	3.0	-1.0	1	21	1635	1655	CAGCCAAGGAUGACUUGCCGG	UGUUUAAGUCAUCUUUGGCUG	Cleavage
sly-miR169b-1-5p	Solyc08g006830.3.1	3.0	-1.0	1	21	598	618	CAGCCAAGGAUGACUUGCCGG	CUGGAUAUUCAUCCUUGGCUG	Cleavage
sly-miR169b-1-5p	Solyc04g016540.2.1	3.0	-1.0	1	21	1838	1858	CAGCCAAGGAUGACUUGCCGG	GUGGAAAUUUAUCUUUGGCUG	Cleavage
sly-miR169b-2-3p	Solyc04g009330.3.1	2.0	-1.0	1	21	2516	2536	GGCAAGUUGUUCUUGGCUAUA	UAUAGCCAAGAGCAAUUUGUU	Cleavage
sly-miR169b-2-3p	Solyc02g088120.3.1	2.5	-1.0	1	21	2850	2870	GGCAAGUUGUUCUUGGCUAUA	UGCAGCCAAGGAUGACUUGCC	Cleavage
sly-miR169b-2-3p	Solyc09g090150.3.1	2.5	-1.0	1	21	570	590	GGCAAGUUGUUCUUGGCUAUA	AAUGGACAAGAACAACUUGUU	Cleavage
sly-miR169b-2-3p	Solyc09g009970.3.1	3.0	-1.0	1	21	1461	1481	GGCAAGUUGUUCUUGGCUAUA	AAUGGCCAAGAAGAAUUUGUC	Cleavage
sly-miR169b-2-3p	Solyc05g053000.1.1	3.0	-1.0	1	21	595	615	GGCAAGUUGUUCUUGGCUAUA	GGUAGCCAAGGACAAGUUGUU	Cleavage
sly-miR169b-2-3p	Solyc06g075250.3.1	3.0	-1.0	1	21	1605	1625	GGCAAGUUGUUCUUGGCUAUA	AAUGGACAAGGACAAUUUGCU	Cleavage
sly-miR169b-2-3p	Solyc05g025687.1.1	3.0	-1.0	1	21	423	443	GGCAAGUUGUUCUUGGCUAUA	UUUGGCCAAGAAUGGUUUGCU	Cleavage

sly-miR169b-2-3p	Solyc08g080860.3.1	3.0	-1.0	1	21	594	614	GGCAAGUUGUUCUUGGCUAUA	ACUAGCCAAGAACAAGUUGUG	Cleavage
sly-miR169b-2-3p	Solyc05g007130.3.1	3.0	-1.0	1	21	1416	1436	GGCAAGUUGUUCUUGGCUAUA	UCUAGUCAGGAAUGGCUUGUC	Cleavage
sly-miR169b-2-3p	Solyc02g085810.3.1	3.0	-1.0	1	21	4080	4100	GGCAAGUUGUUCUUGGCUAUA	GUUAGUCGAGAUCAACUUGCU	Translation
sly-miR169b-2-3p	Solyc10g074520.2.1	3.0	-1.0	1	21	42	62	GGCAAGUUGUUCUUGGCUAUA	GUUGGCGAAGAACAAUUUGUU	Cleavage
sly-miR169b-2-3p	Solyc09g083390.2.1	3.0	-1.0	1	21	2975	2995	GGCAAGUUGUUCUUGGCUAUA	GCUACACAAGAACAACUUGUU	Cleavage
sly-miR169b-2-5p	Solyc07g007480.2.1	1.0	-1.0	1	21	1533	1553	CAGCCAAGGAUGACUUGCCGG	CAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-2-5p	Solyc07g007480.2.1	2.0	-1.0	1	21	1070	1090	CAGCCAAGGAUGACUUGCCGG	CAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-2-5p	Solyc02g088120.3.1	2.0	-1.0	1	21	2899	2919	CAGCCAAGGAUGACUUGCCGG	CUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169b-2-5p	Solyc01g008490.3.1	2.0	-1.0	1	21	610	630	CAGCCAAGGAUGACUUGCCGG	GUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169b-2-5p	Solyc03g121940.3.1	2.0	-1.0	1	21	1276	1296	CAGCCAAGGAUGACUUGCCGG	GUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-2-5p	Solyc12g009050.2.1	2.0	-1.0	1	21	1409	1429	CAGCCAAGGAUGACUUGCCGG	CAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169b-2-5p	Solyc08g062210.3.1	2.5	-1.0	1	21	1637	1657	CAGCCAAGGAUGACUUGCCGG	UCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169b-2-5p	Solyc01g087240.3.1	2.5	-1.0	1	21	2573	2593	CAGCCAAGGAUGACUUGCCGG	CAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169b-2-5p	Solyc01g006930.3.1	2.5	-1.0	1	21	2833	2853	CAGCCAAGGAUGACUUGCCGG	UGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169b-2-5p	Solyc03g079850.3.1	3.0	-1.0	1	21	664	684	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
sly-miR169b-2-5p	Solyc04g079550.3.1	3.0	-1.0	1	21	1635	1655	CAGCCAAGGAUGACUUGCCGG	UGUUUAAGUCAUCUUUGGCUG	Cleavage
sly-miR169b-2-5p	Solyc08g006830.3.1	3.0	-1.0	1	21	598	618	CAGCCAAGGAUGACUUGCCGG	CUGGAUAUUCAUCCUUGGCUG	Cleavage
sly-miR169b-2-5p	Solyc04g016540.2.1	3.0	-1.0	1	21	1838	1858	CAGCCAAGGAUGACUUGCCGG	GUGGAAAUUUAUCUUUGGCUG	Cleavage
sly-miR169b-3-5p	Solyc07g007480.2.1	1.0	-1.0	1	21	1533	1553	CAGCCAAGGAUGACUUGCCGG	CAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-3-5p	Solyc07g007480.2.1	2.0	-1.0	1	21	1070	1090	CAGCCAAGGAUGACUUGCCGG	CAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-3-5p	Solyc02g088120.3.1	2.0	-1.0	1	21	2899	2919	CAGCCAAGGAUGACUUGCCGG	CUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169b-3-5p	Solyc01g008490.3.1	2.0	-1.0	1	21	610	630	CAGCCAAGGAUGACUUGCCGG	GUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169b-3-5p	Solyc03g121940.3.1	2.0	-1.0	1	21	1276	1296	CAGCCAAGGAUGACUUGCCGG	GUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169b-3-5p	Solyc12g009050.2.1	2.0	-1.0	1	21	1409	1429	CAGCCAAGGAUGACUUGCCGG	CAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169b-3-5p	Solyc08g062210.3.1	2.5	-1.0	1	21	1637	1657	CAGCCAAGGAUGACUUGCCGG	UCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169b-3-5p	Solyc01g087240.3.1	2.5	-1.0	1	21	2573	2593	CAGCCAAGGAUGACUUGCCGG	CAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169b-3-5p	Solyc01g006930.3.1	2.5	-1.0	1	21	2833	2853	CAGCCAAGGAUGACUUGCCGG	UGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169b-3-5p	Solyc03g079850.3.1	3.0	-1.0	1	21	664	684	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
sly-miR169b-3-5p	Solyc04g079550.3.1	3.0	-1.0	1	21	1635	1655	CAGCCAAGGAUGACUUGCCGG	UGUUUAAGUCAUCUUUGGCUG	Cleavage
sly-miR169b-3-5p	Solyc08g006830.3.1	3.0	-1.0	1	21	598	618	CAGCCAAGGAUGACUUGCCGG	CUGGAUAUUCAUCCUUGGCUG	Cleavage
sly-miR169b-3-5p	Solyc04g016540.2.1	3.0	-1.0	1	21	1838	1858	CAGCCAAGGAUGACUUGCCGG	GUGGAAAUUUAUCUUUGGCUG	Cleavage
sly-miR169d-3p	Solyc07g007480.2.1	0.0	-1.0	1	21	1010	1030	GCAGGUCAUCUUUAGCUAACU	AGUUAGCUAAAGAUGACCUGC	Cleavage
sly-miR169d-3p	Solyc09g015880.3.1	2.5	-1.0	1	21	1613	1633	GCAGGUCAUCUUUAGCUAACU	ACUUCGCUAAAGAUGGUCUGU	Cleavage
sly-miR169d-3p	Solyc09g057710.3.1	3.0	-1.0	1	21	1652	1672	GCAGGUCAUCUUUAGCUAACU	AGUUCCCUGAGGAUGACCUGC	Cleavage
sly-miR169d-3p	Solyc09g072810.3.1	3.0	-1.0	1	21	1028	1048	GCAGGUCAUCUUUAGCUAACU	CUCUAGCUGAAAAUGACCUGC	Translation
sly-miR169d-3p	Solyc09g065040.1.1	3.0	-1.0	1	21	311	331	GCAGGUCAUCUUUAGCUAACU	AUUCAGCUAAAGAUAACUUGC	Cleavage
sly-miR169d-3p	Solyc03g013030.3.1	3.0	-1.0	1	21	486	506	GCAGGUCAUCUUUAGCUAACU	AAUCAGCUAAGGAUGAGCUGC	Cleavage
sly-miR169d-3p	Solyc05g006323.1.1	3.0	-1.0	1	21	509	529	GCAGGUCAUCUUUAGCUAACU	GGCUUGGUAAAGAUGACCUGC	Cleavage
sly-miR169d-3p	Solyc07g056650.3.1	3.0	-1.0	1	21	903	923	GCAGGUCAUCUUUAGCUAACU	CCUUUGCUGAAGAUGACUUGA	Cleavage
sly-miR169d-5p	Solyc07g007480.2.1	0.0	-1.0	1	20	1071	1090	UAGCCAAGGAUGACUUGUCU	AGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169d-5p	Solyc07g007480.2.1	0.5	-1.0	1	20	1534	1553	UAGCCAAGGAUGACUUGUCU	AGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169d-5p	Solyc02g088120.3.1	1.5	-1.0	1	20	2900	2919	UAGCCAAGGAUGACUUGUCU	UGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169d-5p	Solyc03g121940.3.1	1.5	-1.0	1	20	1277	1296	UAGCCAAGGAUGACUUGUCU	UGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169d-5p	Solyc08g062210.3.1	2.0	-1.0	1	20	1638	1657	UAGCCAAGGAUGACUUGUCU	CGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169d-5p	Solyc12g009050.2.1	2.5	-1.0	1	20	1410	1429	UAGCCAAGGAUGACUUGUCU	AGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169d-5p	Solyc01g088060.3.1	2.5	-1.0	1	20	3596	3615	UAGCCAAGGAUGACUUGUCU	UGACAGGUUAUCCUUGACUA	Cleavage
sly-miR169d-5p	Solyc01g008490.3.1	2.5	-1.0	1	20	611	630	UAGCCAAGGAUGACUUGUCU	UGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169d-5p	Solyc01g087240.3.1	3.0	-1.0	1	20	2574	2593	UAGCCAAGGAUGACUUGUCU	AGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169d-5p	Solyc10g012030.3.1	3.0	-1.0	1	20	3226	3245	UAGCCAAGGAUGACUUGUCU	ACACAAGUCAUCCUUGCCUG	Cleavage
sly-miR169d-5p	Solyc06g068930.2.1	3.0	-1.0	1	20	596	615	UAGCCAAGGAUGACUUGUCU	UCGCAAGGCAUCCUUGGCUA	Cleavage

sly-miR169d-5p	Solyc01g006930.3.1	3.0	-1.0	1	20	2834	2853	UAGCCAAGGAUGACUUGUCU	GGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169e-3p	Solyc06g082560.2.1	2.5	-1.0	1	21	2456	2476	UGGCAAGCAUCUUUGGCGACU	AGUUAUCAAAGAUGCUUGUCA	Cleavage
sly-miR169e-3p	Solyc00g016470.1.1	2.5	-1.0	1	21	59	79	UGGCAAGCAUCUUUGGCGACU	UGUUGUCAAAGAUGCUUGCUU	Cleavage
sly-miR169e-3p	Solyc01g087830.1.1	2.5	-1.0	1	21	21	41	UGGCAAGCAUCUUUGGCGACU	UUUCGCCAAAGGUGUUUCCCA	Cleavage
sly-miR169e-3p	Solyc01g087800.2.1	2.5	-1.0	1	21	723	743	UGGCAAGCAUCUUUGGCGACU	UUUCGCCAAAGGUGUUUCCCA	Cleavage
sly-miR169e-3p	Solyc01g087820.2.1	2.5	-1.0	1	21	762	782	UGGCAAGCAUCUUUGGCGACU	CUUUGCUAAAGAUGCUUCCCA	Cleavage
sly-miR169e-3p	Solyc08g075860.3.1	2.5	-1.0	1	21	842	862	UGGCAAGCAUCUUUGGCGACU	UAUCUUCAAAGAUGCUUGUUA	Cleavage
sly-miR169e-3p	Solyc03g124010.3.1	3.0	-1.0	1	21	1647	1667	UGGCAAGCAUCUUUGGCGACU	AGUGGUGAAAGAUGCUUGCCG	Cleavage
sly-miR169e-3p	Solyc06g074150.3.1	3.0	-1.0	1	21	1038	1058	UGGCAAGCAUCUUUGGCGACU	GAUUGCCAAAGAUUUUUGUCA	Cleavage
sly-miR169e-3p	Solyc07g049165.1.1	3.0	-1.0	1	21	745	765	UGGCAAGCAUCUUUGGCGACU	AUGCUCCAAAGAUGCUUGCUG	Cleavage
sly-miR169e-3p	Solyc03g119540.3.1	3.0	-1.0	1	21	656	676	UGGCAAGCAUCUUUGGCGACU	GAACACUGAAGAUGCUUGCCA	Cleavage
sly-miR169e-3p	Solyc04g024420.3.1	3.0	-1.0	1	21	1154	1174	UGGCAAGCAUCUUUGGCGACU	GUUCCGCAGAGAUGUUUGCCA	Cleavage
sly-miR169e-5p	Solyc07g007480.2.1	0.0	-1.0	1	22	1532	1553	UAGCCAAGGAUGACUUGCCUUU	GCAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169e-5p	Solyc07g007480.2.1	1.0	-1.0	1	22	1069	1090	UAGCCAAGGAUGACUUGCCUUU	GCAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169e-5p	Solyc02g088120.3.1	1.0	-1.0	1	22	2898	2919	UAGCCAAGGAUGACUUGCCUUU	UCUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169e-5p	Solyc03g121940.3.1	1.0	-1.0	1	22	1275	1296	UAGCCAAGGAUGACUUGCCUUU	UGUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169e-5p	Solyc08g062210.3.1	1.5	-1.0	1	22	1636	1657	UAGCCAAGGAUGACUUGCCUUU	AUCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169e-5p	Solyc12g009050.2.1	2.0	-1.0	1	22	1408	1429	UAGCCAAGGAUGACUUGCCUUU	GCAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169e-5p	Solyc01g008490.3.1	2.0	-1.0	1	22	609	630	UAGCCAAGGAUGACUUGCCUUU	GGUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169e-5p	Solyc01g087240.3.1	2.5	-1.0	1	22	2572	2593	UAGCCAAGGAUGACUUGCCUUU	UCAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169e-5p	Solyc06g068930.2.1	2.5	-1.0	1	22	594	615	UAGCCAAGGAUGACUUGCCUUU	GCUCGCAAGGCAUCCUUGGCUA	Cleavage
sly-miR169e-5p	Solyc01g006930.3.1	2.5	-1.0	1	22	2832	2853	UAGCCAAGGAUGACUUGCCUUU	AUGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169e-5p	Solyc03g124050.3.1	3.0	-1.0	1	22	1240	1261	UAGCCAAGGAUGACUUGCCUUU	GUGGGUAAGUUAUCCUUCGUUA	Cleavage
sly-miR169f	Solyc07g007480.2.1	0.0	-1.0	1	21	1533	1553	UAGCCAAGGAUGACUUGCCUA	CAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169f	Solyc07g007480.2.1	1.0	-1.0	1	21	1070	1090	UAGCCAAGGAUGACUUGCCUA	CAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169f	Solyc02g088120.3.1	1.0	-1.0	1	21	2899	2919	UAGCCAAGGAUGACUUGCCUA	CUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169f	Solyc03g121940.3.1	1.0	-1.0	1	21	1276	1296	UAGCCAAGGAUGACUUGCCUA	GUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169f	Solyc08g062210.3.1	1.5	-1.0	1	21	1637	1657	UAGCCAAGGAUGACUUGCCUA	UCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169f	Solyc12g009050.2.1	2.0	-1.0	1	21	1409	1429	UAGCCAAGGAUGACUUGCCUA	CAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169f	Solyc01g008490.3.1	2.0	-1.0	1	21	610	630	UAGCCAAGGAUGACUUGCCUA	GUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169f	Solyc01g006930.3.1	2.5	-1.0	1	21	2833	2853	UAGCCAAGGAUGACUUGCCUA	UGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169f	Solyc01g087240.3.1	2.5	-1.0	1	21	2573	2593	UAGCCAAGGAUGACUUGCCUA	CAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169f	Solyc06g068930.2.1	2.5	-1.0	1	21	595	615	UAGCCAAGGAUGACUUGCCUA	CUCGCAAGGCAUCCUUGGCUA	Cleavage
sly-miR169f	Solyc03g124050.3.1	3.0	-1.0	1	21	1241	1261	UAGCCAAGGAUGACUUGCCUA	UGGGUAAGUUAUCCUUCGUUA	Cleavage
sly-miR169g	Solyc07g007480.2.1	0.0	-1.0	1	22	1532	1553	UAGCCAAGGAUGACUUGCCUGC	GCAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169g	Solyc07g007480.2.1	1.0	-1.0	1	22	1069	1090	UAGCCAAGGAUGACUUGCCUGC	GCAGACAAGUCAUCCUUGGCUA	Cleavage
sly-miR169g	Solyc02g088120.3.1	1.0	-1.0	1	22	2898	2919	UAGCCAAGGAUGACUUGCCUGC	UCUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169g	Solyc03g121940.3.1	1.0	-1.0	1	22	1275	1296	UAGCCAAGGAUGACUUGCCUGC	UGUGGGAAGUCAUCCUUGGCUA	Cleavage
sly-miR169g	Solyc08g062210.3.1	1.5	-1.0	1	22	1636	1657	UAGCCAAGGAUGACUUGCCUGC	AUCGGCAGUUCAUCCUUGGCUA	Cleavage
sly-miR169g	Solyc12g009050.2.1	2.0	-1.0	1	22	1408	1429	UAGCCAAGGAUGACUUGCCUGC	GCAGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169g	Solyc01g008490.3.1	2.0	-1.0	1	22	609	630	UAGCCAAGGAUGACUUGCCUGC	GGUGGCAAUUCAUCCUUGGCUU	Cleavage
sly-miR169g	Solyc01g087240.3.1	2.5	-1.0	1	22	2572	2593	UAGCCAAGGAUGACUUGCCUGC	UCAGGCAAUUCAUUCUUGGCUU	Cleavage
sly-miR169g	Solyc06g068930.2.1	2.5	-1.0	1	22	594	615	UAGCCAAGGAUGACUUGCCUGC	GCUCGCAAGGCAUCCUUGGCUA	Cleavage
sly-miR169g	Solyc01g006930.3.1	2.5	-1.0	1	22	2832	2853	UAGCCAAGGAUGACUUGCCUGC	AUGGGCAGUUCAUCCUUGGCUU	Cleavage
sly-miR169g	Solyc03g124050.3.1	3.0	-1.0	1	22	1240	1261	UAGCCAAGGAUGACUUGCCUGC	GUGGGUAAGUUAUCCUUCGUUA	Cleavage
sly-miR169m	Solyc02g088120.3.1	0.0	-1.0	1	21	2899	2919	UAGCCAAAAAUGACUUGCCAG	CUGGCAAGUCAUUUUUGGCUA	Cleavage
sly-miR169m	Solyc10g074530.2.1	3.0	-1.0	1	21	20	40	UAGCCAAAAAUGACUUGCCAG	CUACCUAGUCAUUUUUGGCUA	Cleavage
sly-miR169m	Solyc07g007480.2.1	3.0	-1.0	1	21	1533	1553	UAGCCAAAAAUGACUUGCCAG	CAGGCAAGUCAUCCUUGGCUA	Cleavage
sly-miR169m	Solyc03g119570.2.1	3.0	-1.0	1	21	819	839	UAGCCAAAAAUGACUUGCCAG	UUUGCUCGUCAUUUUUGGCUA	Cleavage
sly-miR169m	Solyc02g067860.3.1	3.0	-1.0	1	21	948	968	UAGCCAAAAAUGACUUGCCAG	UAGGAAAGUUAUUUAUGGCUA	Cleavage

sly-miR170-1-3p	Solyc08g078800.1.1	1.0	-1.0	1	21	396	416	UGAUUGAGCCGUGUCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR170-1-3p	Solyc01g090950.3.1	1.0	-1.0	1	21	972	992	UGAUUGAGCCGUGUCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR170-1-3p	Solyc08g081890.3.1	3.0	-1.0	1	21	3719	3739	UGAUUGAGCCGUGUCAAUAUC	GAUAUUGGCAUGGCUCUAUCG	Cleavage
sly-miR170-1-3p	Solyc02g085600.1.1	3.0	-1.0	1	21	585	605	UGAUUGAGCCGUGUCAAUAUC	GAUACUGGCACGCCUCAAUCA	Cleavage
sly-miR170-1-3p	Solyc07g020910.2.1	3.0	-1.0	1	21	1378	1398	UGAUUGAGCCGUGUCAAUAUC	GUAUUUGACAUGGUUCAAUCA	Cleavage
sly-miR170-1-3p	Solyc06g051930.3.1	3.0	-1.0	1	21	4988	5008	UGAUUGAGCCGUGUCAAUAUC	UUUAUUUUCAUGGCUCGAUCA	Cleavage
sly-miR170-2-3p	Solyc08g078800.1.1	0.5	-1.0	1	20	397	416	UGAUUGAGCCGUGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR170-2-3p	Solyc01g090950.3.1	0.5	-1.0	1	20	973	992	UGAUUGAGCCGUGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR170-2-3p	Solyc08g081890.3.1	2.5	-1.0	1	20	3720	3739	UGAUUGAGCCGUGCCAAUAU	AUAUUGGCAUGGCUCUAUCG	Cleavage
sly-miR170-2-3p	Solyc02g085600.1.1	2.5	-1.0	1	20	586	605	UGAUUGAGCCGUGCCAAUAU	AUACUGGCACGCCUCAAUCA	Cleavage
sly-miR170-2-3p	Solyc03g111640.3.1	3.0	-1.0	1	20	1904	1923	UGAUUGAGCCGUGCCAAUAU	CUGUCUGCAUGGCUCAAUCA	Cleavage
sly-miR170-2-3p	Solyc06g051930.3.1	3.0	-1.0	1	20	4989	5008	UGAUUGAGCCGUGCCAAUAU	UUAUUUUCAUGGCUCGAUCA	Cleavage
sly-miR171b-1-3p	Solyc08g078800.1.1	0.5	-1.0	1	21	393	413	UUGAGCCGUGCCAAUAUCACG	AAUGAUAUUGGCGCGGCUCAA	Cleavage
sly-miR171b-1-3p	Solyc01g090950.3.1	1.5	-1.0	1	21	969	989	UUGAGCCGUGCCAAUAUCACG	AGGGAUAUUGGCGCGGCUCAA	Cleavage
sly-miR171b-1-3p	Solyc11g013150.1.1	2.0	-1.0	1	21	378	398	UUGAGCCGUGCCAAUAUCACG	AGUGAUAUUGGUUCGGCUCAA	Cleavage
sly-miR171b-1-3p	Solyc02g085600.1.1	2.5	-1.0	1	21	582	602	UUGAGCCGUGCCAAUAUCACG	UGUGAUACUGGCACGCCUCAA	Cleavage
sly-miR171b-1-3p	Solyc08g081890.3.1	3.0	-1.0	1	21	3716	3736	UUGAGCCGUGCCAAUAUCACG	UCAGAUAUUGGCAUGGCUCUA	Cleavage
sly-miR171b-1-3p	Solyc04g080050.3.1	3.0	-1.0	1	21	366	386	UUGAGCCGUGCCAAUAUCACG	UCUGAUAUUGGUACGGUUGAG	Cleavage
sly-miR171b-1-3p	Solyc09g090090.2.1	3.0	-1.0	1	21	523	543	UUGAGCCGUGCCAAUAUCACG	GCUGAUUUUGGCUCGGCUCAG	Cleavage
sly-miR171b-1-3p	Solyc03g113470.2.1	3.0	-1.0	1	21	906	926	UUGAGCCGUGCCAAUAUCACG	UCUUAUAUUGGCAUGGCUCCA	Cleavage
sly-miR171b-1-3p	Solyc03g111130.1.1	3.0	-1.0	1	21	901	921	UUGAGCCGUGCCAAUAUCACG	GUUCAAGUUGGCAUGGCUCAA	Cleavage
sly-miR171b-1-5p	Solyc03g025730.3.1	3.0	-1.0	1	20	200	219	AGAUAUUGGUGCGGUUCAAU	AUUGGAGCGCGUCAAUGUCU	Cleavage
sly-miR171b-1-5p	Solyc05g008610.3.1	3.0	-1.0	1	20	140	159	AGAUAUUGGUGCGGUUCAAU	GUUGAACUGAAUCAAUGUCU	Translation
sly-miR171b-1-5p	Solyc11g062440.2.1	3.0	-1.0	1	20	498	517	AGAUAUUGGUGCGGUUCAAU	AUGGAACUGCAGCAAUAUCU	Cleavage
sly-miR171b-1-5p	Solyc07g007870.3.1	3.0	-1.0	1	20	909	928	AGAUAUUGGUGCGGUUCAAU	CUGGAGCUGCACCAAUAUCA	Cleavage
sly-miR171b-1-5p	Solyc02g071090.3.1	3.0	-1.0	1	20	1081	1100	AGAUAUUGGUGCGGUUCAAU	CUUCAAUUGUACCAAUAUUU	Cleavage
sly-miR171b-2-3p	Solyc08g078800.1.1	0.5	-1.0	1	21	393	413	UUGAGCCGUGCCAAUAUCACG	AAUGAUAUUGGCGCGGCUCAA	Cleavage
sly-miR171b-2-3p	Solyc01g090950.3.1	1.5	-1.0	1	21	969	989	UUGAGCCGUGCCAAUAUCACG	AGGGAUAUUGGCGCGGCUCAA	Cleavage
sly-miR171b-2-3p	Solyc11g013150.1.1	2.0	-1.0	1	21	378	398	UUGAGCCGUGCCAAUAUCACG	AGUGAUAUUGGUUCGGCUCAA	Cleavage
sly-miR171b-2-3p	Solyc02g085600.1.1	2.5	-1.0	1	21	582	602	UUGAGCCGUGCCAAUAUCACG	UGUGAUACUGGCACGCCUCAA	Cleavage
sly-miR171b-2-3p	Solyc08g081890.3.1	3.0	-1.0	1	21	3716	3736	UUGAGCCGUGCCAAUAUCACG	UCAGAUAUUGGCAUGGCUCUA	Cleavage
sly-miR171b-2-3p	Solyc04g080050.3.1	3.0	-1.0	1	21	366	386	UUGAGCCGUGCCAAUAUCACG	UCUGAUAUUGGUACGGUUGAG	Cleavage
sly-miR171b-2-3p	Solyc09g090090.2.1	3.0	-1.0	1	21	523	543	UUGAGCCGUGCCAAUAUCACG	GCUGAUUUUGGCUCGGCUCAG	Cleavage
sly-miR171b-2-3p	Solyc03g113470.2.1	3.0	-1.0	1	21	906	926	UUGAGCCGUGCCAAUAUCACG	UCUUAUAUUGGCAUGGCUCCA	Cleavage
sly-miR171b-2-3p	Solyc03g111130.1.1	3.0	-1.0	1	21	901	921	UUGAGCCGUGCCAAUAUCACG	GUUCAAGUUGGCAUGGCUCAA	Cleavage
sly-miR171b-3	Solyc08g078800.1.1	0.5	-1.0	1	21	396	416	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171b-3	Solyc01g090950.3.1	0.5	-1.0	1	21	972	992	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171b-3	Solyc08g081890.3.1	2.5	-1.0	1	21	3719	3739	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCAUGGCUCUAUCG	Cleavage
sly-miR171b-3	Solyc02g085600.1.1	2.5	-1.0	1	21	585	605	UGAUUGAGCCGUGCCAAUAUC	GAUACUGGCACGCCUCAAUCA	Cleavage
sly-miR171b-3	Solyc03g111640.3.1	3.0	-1.0	1	21	1903	1923	UGAUUGAGCCGUGCCAAUAUC	ACUGUCUGCAUGGCUCAAUCA	Cleavage
sly-miR171b-3	Solyc06g051930.3.1	3.0	-1.0	1	21	4988	5008	UGAUUGAGCCGUGCCAAUAUC	UUUAUUUUCAUGGCUCGAUCA	Cleavage
sly-miR171c-1-3p	Solyc08g078800.1.1	0.0	-1.0	1	20	397	416	UGAUUGAGCCGCGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171c-1-3p	Solyc01g090950.3.1	0.0	-1.0	1	20	973	992	UGAUUGAGCCGCGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171c-1-5p	Solyc03g121740.2.1	2.0	-1.0	1	21	245	265	UAUUGGUGCGGUUCAAUGAGA	UUUCAUUGAAUUGCACUAAUG	Cleavage
sly-miR171c-1-5p	Solyc03g081220.1.1	3.0	-1.0	1	21	453	473	UAUUGGUGCGGUUCAAUGAGA	CCUUGUUGAAUCGCACCAAGA	Cleavage
sly-miR171c-1-5p	Solyc10g052815.1.1	3.0	-1.0	1	21	468	488	UAUUGGUGCGGUUCAAUGAGA	AUUUGUGGAACUGUACCAAUA	Cleavage
sly-miR171c-1-5p	Solyc08g006640.3.1	3.0	-1.0	1	21	164	184	UAUUGGUGCGGUUCAAUGAGA	AUUUUUUGAAUUGCAUCAAUA	Cleavage
sly-miR171c-1-5p	Solyc08g068840.3.1	3.0	-1.0	1	21	3460	3480	UAUUGGUGCGGUUCAAUGAGA	GAUCAAUGAACUGCACCAAAA	Cleavage
sly-miR171c-1-5p	Solyc12g088700.1.1	3.0	-1.0	1	21	1129	1149	UAUUGGUGCGGUUCAAUGAGA	AAUCAUCUAACUGCACUAAUA	Cleavage
sly-miR171c-2	Solyc08g078800.1.1	1.0	-1.0	1	21	396	416	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage

sly-miR171c-2	Solyc01g090950.3.1	1.0	-1.0	1	21	972	992	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171c-3-3p	Solyc08g078800.1.1	1.0	-1.0	1	21	396	416	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171c-3-3p	Solyc01g090950.3.1	1.0	-1.0	1	21	972	992	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171c-3-5p	Solyc06g054150.1.1	2.5	-1.0	1	20	59	78	GAUGUUGGUGAGGUUCAAUC	UUUUGAAUCUUAUCAACAUC	Cleavage
sly-miR171c-3-5p	Solyc04g007910.3.1	2.5	-1.0	1	20	1053	1072	GAUGUUGGUGAGGUUCAAUC	ACUUGAACUUCACUAACAUU	Cleavage
sly-miR171c-3-5p	Solyc01g006550.3.1	2.5	-1.0	1	20	912	931	GAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUCACCAACAUA	Cleavage
sly-miR171c-3-5p	Solyc08g066660.1.1	2.5	-1.0	1	20	406	425	GAUGUUGGUGAGGUUCAAUC	AAUUCAACUUCGUCAACAUC	Cleavage
sly-miR171c-3-5p	Solyc02g061940.3.1	2.5	-1.0	1	20	1645	1664	GAUGUUGGUGAGGUUCAAUC	UAUUGCACCUCAUCAGUAUC	Cleavage
sly-miR171c-3-5p	Solyc11g005280.1.1	3.0	-1.0	1	20	588	607	GAUGUUGGUGAGGUUCAAUC	GAUUGAACCUCUCCAACGUG	Cleavage
sly-miR171c-3-5p	Solyc11g005300.2.1	3.0	-1.0	1	20	1890	1909	GAUGUUGGUGAGGUUCAAUC	GAUUGAACCUCUCCAACGUG	Cleavage
sly-miR171c-3-5p	Solyc01g014150.1.1	3.0	-1.0	1	20	305	324	GAUGUUGGUGAGGUUCAAUC	GAUGGAAUCUUACCAACAUA	Cleavage
sly-miR171c-3-5p	Solyc05g054493.1.1	3.0	-1.0	1	20	138	157	GAUGUUGGUGAGGUUCAAUC	GAGUGAGUCUCAUCAACGUC	Cleavage
sly-miR171c-3-5p	Solyc02g081980.3.1	3.0	-1.0	1	20	463	482	GAUGUUGGUGAGGUUCAAUC	AUUUGGAUCUCAUCAAUAUC	Cleavage
sly-miR171c-3-5p	Solyc10g006600.3.1	3.0	-1.0	1	20	3029	3048	GAUGUUGGUGAGGUUCAAUC	UUUUGGACCUCAUCAACGUU	Cleavage
sly-miR171c-3-5p	Solyc01g098020.2.1	3.0	-1.0	1	20	204	223	GAUGUUGGUGAGGUUCAAUC	CGUUGAACUUCAUCAACAAC	Cleavage
sly-miR171c-3-5p	Solyc09g082260.1.1	3.0	-1.0	1	20	251	270	GAUGUUGGUGAGGUUCAAUC	CAUUGGACCUCACUGAUGUU	Cleavage
sly-miR171c-3-5p	Solyc03g110960.3.1	3.0	-1.0	1	20	1565	1584	GAUGUUGGUGAGGUUCAAUC	AAUUGAAUUUCAACAAUAUC	Cleavage
sly-miR171c-3-5p	Solyc03g043910.3.1	3.0	-1.0	1	20	349	368	GAUGUUGGUGAGGUUCAAUC	GAUUCAUCUUCACCGACAUC	Cleavage
sly-miR171c-3-5p	Solyc01g014940.1.1	3.0	-1.0	1	20	149	168	GAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUUACCAACAUA	Cleavage
sly-miR171c-3-5p	Solyc01g005730.3.1	3.0	-1.0	1	20	915	934	GAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUCACCAGCAUA	Cleavage
sly-miR171c-3-5p	Solyc02g087340.3.1	3.0	-1.0	1	20	169	188	GAUGUUGGUGAGGUUCAAUC	ACUUAAGCCUCAUCAACAUC	Cleavage
sly-miR171c-3-5p	Solyc08g005530.2.1	3.0	-1.0	1	20	22	41	GAUGUUGGUGAGGUUCAAUC	AAUGGAAUGUCACCAACAUC	Cleavage
sly-miR171c-3-5p	Solyc03g020030.3.1	3.0	-1.0	1	20	660	679	GAUGUUGGUGAGGUUCAAUC	UGUUAAACCUCAUUAACAUU	Cleavage
sly-miR171c-3-5p	Solyc08g077070.3.1	3.0	-1.0	1	20	426	445	GAUGUUGGUGAGGUUCAAUC	CAUUGACUUUUAUCAACAUC	Cleavage
sly-miR171c-3-5p	Solyc08g007660.2.1	3.0	-1.0	1	20	542	561	GAUGUUGGUGAGGUUCAAUC	CACUGAACCUCGCCAAUGUU	Cleavage
sly-miR171c-3-5p	Solyc05g006710.3.1	3.0	-1.0	1	20	1282	1301	GAUGUUGGUGAGGUUCAAUC	CAAUGAACCUGGCCAACAUC	Translation
sly-miR171c-3-5p	Solyc01g104790.3.1	3.0	-1.0	1	20	867	886	GAUGUUGGUGAGGUUCAAUC	AAUUCAACCUCAUCAUCAUC	Cleavage
sly-miR171c-3-5p	Solyc08g007620.2.1	3.0	-1.0	1	20	1682	1701	GAUGUUGGUGAGGUUCAAUC	CACUGAACCUCGCCAAUGUU	Cleavage
sly-miR171c-3-5p	Solyc12g009230.2.1	3.0	-1.0	1	20	3762	3781	GAUGUUGGUGAGGUUCAAUC	AAUUGGUUUUCACCAACAUU	Cleavage
sly-miR171c-3-5p	Solyc02g081540.2.1	3.0	-1.0	1	20	452	471	GAUGUUGGUGAGGUUCAAUC	UAAUGAUCUUCACCAAUAUC	Cleavage
sly-miR171c-4	Solyc09g091860.3.1	3.0	-1.0	1	21	2771	2791	UAAUUGAACCGCACCAAUAUC	GUUUUUGGUGCAGUUCAAUUG	Translation
sly-miR171c-4	Solyc01g009930.2.1	3.0	-1.0	1	21	808	828	UAAUUGAACCGCACCAAUAUC	GUUAUGGUUGUGGUUUAAUUA	Cleavage
sly-miR171f	Solyc07g063860.3.1	0.5	-1.0	1	21	320	340	AUGAGCCGAACCAAUAUCACU	UUUGAUAUUGGUUUGGCUCAU	Cleavage
sly-miR171f	Solyc11g013150.1.1	1.0	-1.0	1	21	378	398	AUGAGCCGAACCAAUAUCACU	AGUGAUAUUGGUUCGGCUCAA	Cleavage
sly-miR171f	Solyc07g054200.3.1	2.0	-1.0	1	21	340	360	AUGAGCCGAACCAAUAUCACU	UCUGAUAUUGGUCCGGCUCGU	Cleavage
sly-miR171f	Solyc08g069180.3.1	2.5	-1.0	1	21	2469	2489	AUGAGCCGAACCAAUAUCACU	AGUGAUGUUGGUUUGGCUCGG	Cleavage
sly-miR171f	Solyc05g008840.2.1	2.5	-1.0	1	21	785	805	AUGAGCCGAACCAAUAUCACU	CCUGGUAUUGGUUCUGCUUAU	Cleavage
sly-miR171f	Solyc01g017140.1.1	2.5	-1.0	1	21	208	228	AUGAGCCGAACCAAUAUCACU	CUUGUUAUUGCUUCGGCUCAU	Translation
sly-miR171f	Solyc01g014390.3.1	2.5	-1.0	1	21	1548	1567	AUGAGCCGAACCAAUAUCACU	UAUGA-AUUGGUUCGGCUUAU	Cleavage
sly-miR171f	Solyc12g042177.1.1	3.0	-1.0	1	21	595	615	AUGAGCCGAACCAAUAUCACU	AGUGAUAUUGGUUUGGCUAAG	Cleavage
sly-miR171f	Solyc09g015520.3.1	3.0	-1.0	1	21	2811	2831	AUGAGCCGAACCAAUAUCACU	GGAGAUUUUGGUUUGGCUCGU	Cleavage
sly-miR171f	Solyc03g114410.3.1	3.0	-1.0	1	21	3334	3354	AUGAGCCGAACCAAUAUCACU	UAUGAUAUUGGUUCGGUCUGU	Cleavage
sly-miR171i-3p	Solyc08g078800.1.1	1.5	-1.0	1	21	396	416	GGAUUGAGCCGCGUCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171i-3p	Solyc01g090950.3.1	1.5	-1.0	1	21	972	992	GGAUUGAGCCGCGUCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
sly-miR171i-3p	Solyc06g054420.3.1	2.5	-1.0	1	21	719	739	GGAUUGAGCCGCGUCAAUAUC	UUUAUUUAUGUGGUUCAAUCC	Cleavage
sly-miR171i-3p	Solyc11g007610.2.1	3.0	-1.0	1	21	841	861	GGAUUGAGCCGCGUCAAUAUC	UAUGUUGAUGCGGUUGAAUCC	Cleavage
sly-miR171i-3p	Solyc08g077350.3.1	3.0	-1.0	1	21	6165	6185	GGAUUGAGCCGCGUCAAUAUC	CUUGUUGACCUGGCUCAAUCU	Cleavage
sly-miR171i-3p	Solyc10g080500.2.1	3.0	-1.0	1	21	369	389	GGAUUGAGCCGCGUCAAUAUC	GUUGGUGACGAGGCUCAAUCC	Translation
sly-miR172d-1	Solyc09g007260.3.1	2.0	-1.0	1	23	1624	1646	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
sly-miR172d-1	Solyc11g072600.2.1	2.0	-1.0	1	23	1274	1296	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCA	Cleavage

sly-miR172d-1	Solyc05g052560.1.1	2.0	-1.0	1	23	99	121	UGUGAAUCUUGAUGAUGCUGCAU	CGAAAACAUCAUCAAGAUUCGUA	Cleavage
sly-miR172d-1	Solyc10g084340.2.1	2.5	-1.0	1	23	2182	2204	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGGA	Cleavage
sly-miR172d-1	Solyc05g012280.3.1	2.5	-1.0	1	23	325	347	UGUGAAUCUUGAUGAUGCUGCAU	AUCCAGCAUUUUCAAGAUUCAUA	Cleavage
sly-miR172d-1	Solyc04g050862.1.1	2.5	-1.0	1	23	54	76	UGUGAAUCUUGAUGAUGCUGCAU	GUUCAGUACUAUCAAGGUUCACA	Cleavage
sly-miR172d-1	Solyc04g050860.2.1	2.5	-1.0	1	23	2000	2022	UGUGAAUCUUGAUGAUGCUGCAU	GUUCAGUACUAUCAAGGUUCACA	Cleavage
sly-miR172d-1	Solyc04g050820.2.1	2.5	-1.0	1	23	2601	2623	UGUGAAUCUUGAUGAUGCUGCAU	GUUCAGUACUAUCAAGGUUCACA	Cleavage
sly-miR172d-1	Solyc09g059570.3.1	2.5	-1.0	1	23	584	606	UGUGAAUCUUGAUGAUGCUGCAU	CAUUAGUAUUAUCAAGAUUCAGA	Cleavage
sly-miR172d-1	Solyc04g016330.3.1	2.5	-1.0	1	23	283	305	UGUGAAUCUUGAUGAUGCUGCAU	UGUCAGCAAAAUCAAGAUUUACA	Cleavage
sly-miR172d-1	Solyc04g049800.3.1	3.0	-1.0	1	23	1106	1128	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCU	Cleavage
sly-miR172d-1	Solyc03g044300.3.1	3.0	-1.0	1	23	1366	1388	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCC	Cleavage
sly-miR172d-1	Solyc02g093150.3.1	3.0	-1.0	1	23	1560	1582	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-1	Solyc02g064960.3.1	3.0	-1.0	1	23	1764	1786	UGUGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-1	Solyc09g018840.3.1	3.0	-1.0	1	23	592	614	UGUGAAUCUUGAUGAUGCUGCAU	AAGUAGCAUAAUCAAGAUUUGUG	Cleavage
sly-miR172d-1	Solyc07g063780.2.1	3.0	-1.0	1	23	2016	2038	UGUGAAUCUUGAUGAUGCUGCAU	GUGUAUCUGCAUCAAGAUUCACA	Cleavage
sly-miR172d-1	Solyc07g063735.1.1	3.0	-1.0	1	23	5401	5423	UGUGAAUCUUGAUGAUGCUGCAU	GUGUAUCUGCAUCAAGAUUCACA	Cleavage
sly-miR172d-1	Solyc02g078410.1.1	3.0	-1.0	1	23	392	414	UGUGAAUCUUGAUGAUGCUGCAU	UGUUAGCAUCAUCAAGAGUUACU	Cleavage
sly-miR172d-1	Solyc01g068460.3.1	3.0	-1.0	1	23	2260	2281	UGUGAAUCUUGAUGAUGCUGCAU	GCGCAGCG-CAUCAGGAUUCACA	Cleavage
sly-miR172d-1	Solyc02g011860.1.1	3.0	-1.0	1	23	274	296	UGUGAAUCUUGAUGAUGCUGCAU	AUUUAUGAUUAUCAAGAUUCAUA	Cleavage
sly-miR172d-1	Solyc03g117530.1.1	3.0	-1.0	1	23	192	214	UGUGAAUCUUGAUGAUGCUGCAU	UCAUAGCAUCAUUAGUAUUUACA	Cleavage
sly-miR172d-1	Solyc06g053820.3.1	3.0	-1.0	1	23	468	490	UGUGAAUCUUGAUGAUGCUGCAU	UGGGAGUGUCAUUGGGAUUUACA	Cleavage
sly-miR172d-1	Solyc01g106090.3.1	3.0	-1.0	1	23	1910	1932	UGUGAAUCUUGAUGAUGCUGCAU	GAAAAGCAUCAUCAAGAUUGGUG	Cleavage
sly-miR172d-1	Solyc01g097030.3.1	3.0	-1.0	1	23	166	188	UGUGAAUCUUGAUGAUGCUGCAU	UUCAAGUAUCAUCAAUAUUUAUA	Cleavage
sly-miR172d-1	Solyc04g082250.3.1	3.0	-1.0	1	23	2625	2647	UGUGAAUCUUGAUGAUGCUGCAU	AGAGAGUAUUAUCAAGAUGCACG	Cleavage
sly-miR172d-1	Solyc03g095710.3.1	3.0	-1.0	1	23	558	580	UGUGAAUCUUGAUGAUGCUGCAU	ACCUAACAUCACCAAGAUUUACA	Cleavage
sly-miR172d-1	Solyc08g082830.3.1	3.0	-1.0	1	23	4434	4456	UGUGAAUCUUGAUGAUGCUGCAU	CAACUGCUUCAUCAGGAUUUACA	Cleavage
sly-miR172d-1	Solyc11g069010.2.1	3.0	-1.0	1	23	241	263	UGUGAAUCUUGAUGAUGCUGCAU	AAUAAUCAUCGUCAAGAUUUAUG	Cleavage
sly-miR172d-10-3p	Solyc02g077380.2.1	2.5	-1.0	1	20	1046	1065	UGCAGCAUCAUCAAGAUUCU	AGAGUUUUGAUGAUGUUGCU	Cleavage
sly-miR172d-10-3p	Solyc02g078640.3.1	2.5	-1.0	1	20	844	863	UGCAGCAUCAUCAAGAUUCU	AGAAUCUUGAAGAUGCUGCC	Translation
sly-miR172d-10-3p	Solyc12g088640.2.1	2.5	-1.0	1	20	540	559	UGCAGCAUCAUCAAGAUUCU	UCAAUCUUGAUGAUGCUGAA	Cleavage
sly-miR172d-10-3p	Solyc09g089865.1.1	2.5	-1.0	1	20	89	108	UGCAGCAUCAUCAAGAUUCU	GGAUUCUUUAUGAUGCUGCA	Cleavage
sly-miR172d-10-3p	Solyc09g074950.3.1	2.5	-1.0	1	20	1354	1373	UGCAGCAUCAUCAAGAUUCU	UGAAUCUUGAUAAUGUUGUA	Cleavage
sly-miR172d-10-3p	Solyc03g083470.3.1	2.5	-1.0	1	20	1553	1572	UGCAGCAUCAUCAAGAUUCU	ACAAAUUUGAUGAUGCUGCA	Cleavage
sly-miR172d-10-3p	Solyc01g074030.3.1	2.5	-1.0	1	20	1424	1443	UGCAGCAUCAUCAAGAUUCU	CCAAUAUUGAUGAUGUUGCA	Cleavage
sly-miR172d-10-3p	Solyc09g011020.3.1	3.0	-1.0	1	20	984	1003	UGCAGCAUCAUCAAGAUUCU	GGAAUUUUGAUGAUGCUGAG	Cleavage
sly-miR172d-10-3p	Solyc02g032173.1.1	3.0	-1.0	1	20	302	321	UGCAGCAUCAUCAAGAUUCU	AGAAUUUUGAUAAUGUUGUA	Cleavage
sly-miR172d-10-3p	Solyc12g015890.1.1	3.0	-1.0	1	20	29	48	UGCAGCAUCAUCAAGAUUCU	AGAGUAUUGUUGAUGCUGCA	Translation
sly-miR172d-10-3p	Solyc02g014355.1.1	3.0	-1.0	1	20	176	195	UGCAGCAUCAUCAAGAUUCU	UUGAUCUUGAUGAUGCUGUU	Cleavage
sly-miR172d-10-3p	Solyc05g013253.1.1	3.0	-1.0	1	20	1247	1266	UGCAGCAUCAUCAAGAUUCU	CUCAUUUUGAUGAUGCUGUA	Cleavage
sly-miR172d-10-	Solyc08g082980.2.1	3.0	-1.0	1	20	1490	1509	UGCAGCAUCAUCAAGAUUCU	GGAGUCUAGGUGAUGCUGUA	Cleavage

3p										
sly-miR172d-10-3p	Solyc11g009080.2.1	3.0	-1.0	1	20	434	453	UGCAGCAUCAUCAAGAUUCU	AGAAGCUUGGUGAGGCUGCA	Cleavage
sly-miR172d-10-3p	Solyc02g069670.3.1	3.0	-1.0	1	20	1015	1034	UGCAGCAUCAUCAAGAUUCU	AGAAUAUUGAUGAUGUUGAA	Cleavage
sly-miR172d-10-3p	Solyc02g069750.2.1	3.0	-1.0	1	20	369	388	UGCAGCAUCAUCAAGAUUCU	AGAAUUAUGAUGAUGAUGCA	Cleavage
sly-miR172d-10-3p	Solyc07g056030.3.1	3.0	-1.0	1	20	1388	1407	UGCAGCAUCAUCAAGAUUCU	AGGACCUUGAUGAGGCUGCA	Cleavage
sly-miR172d-10-3p	Solyc08g061650.3.1	3.0	-1.0	1	20	2026	2045	UGCAGCAUCAUCAAGAUUCU	AGAAACUUGAUGGUGCUUCA	Cleavage
sly-miR172d-10-3p	Solyc08g061635.1.1	3.0	-1.0	1	20	2422	2441	UGCAGCAUCAUCAAGAUUCU	AGAAACUUGAUGGUGCUUCA	Cleavage
sly-miR172d-10-3p	Solyc02g090710.3.1	3.0	-1.0	1	20	359	378	UGCAGCAUCAUCAAGAUUCU	AGUAUCUUGAUGAUUCUGUA	Cleavage
sly-miR172d-10-3p	Solyc07g056260.3.1	3.0	-1.0	1	20	1866	1885	UGCAGCAUCAUCAAGAUUCU	AGAGUGUUGAUGAUGAUGCA	Cleavage
sly-miR172d-10-3p	Solyc12g013580.2.1	3.0	-1.0	1	20	1869	1888	UGCAGCAUCAUCAAGAUUCU	GAAAUCUUGGUGAUGCUGGA	Cleavage
sly-miR172d-10-3p	Solyc06g008730.3.1	3.0	-1.0	1	20	364	383	UGCAGCAUCAUCAAGAUUCU	UUAAUUUUGAUGAUUCUGCA	Cleavage
sly-miR172d-10-3p	Solyc06g084530.3.1	3.0	-1.0	1	20	1168	1187	UGCAGCAUCAUCAAGAUUCU	UGAAUCUUGAUAAUGGUGCA	Cleavage
sly-miR172d-10-3p	Solyc06g068855.1.1	3.0	-1.0	1	20	311	330	UGCAGCAUCAUCAAGAUUCU	AAAAUAUUGGUGAUGCUGUA	Cleavage
sly-miR172d-10-3p	Solyc11g013050.1.1	3.0	-1.0	1	20	721	740	UGCAGCAUCAUCAAGAUUCU	GGGAUGUUGAUGAUGAUGCA	Cleavage
sly-miR172d-10-3p	Solyc02g061810.3.1	3.0	-1.0	1	20	240	259	UGCAGCAUCAUCAAGAUUCU	AUAGUGUUGGUGAUGCUGCA	Cleavage
sly-miR172d-10-3p	Solyc00g017870.1.1	3.0	-1.0	1	20	113	132	UGCAGCAUCAUCAAGAUUCU	UGAAGCUUGAUGAUGUUGUU	Cleavage
sly-miR172d-10-3p	Solyc01g081177.1.1	3.0	-1.0	1	20	225	244	UGCAGCAUCAUCAAGAUUCU	UGAGAUUUGGUGGUGCUGCA	Cleavage
sly-miR172d-10-3p	Solyc01g005820.3.1	3.0	-1.0	1	20	512	531	UGCAGCAUCAUCAAGAUUCU	UGGAUCCUGCUGAUGCUGCA	Translation
sly-miR172d-10-3p	Solyc02g063490.3.1	3.0	-1.0	1	20	1212	1231	UGCAGCAUCAUCAAGAUUCU	UGCAUCUUUAUGAUGUUGCA	Cleavage
sly-miR172d-10-5p	Solyc12g088640.2.1	1.5	-1.0	1	23	538	560	AUGCAGCAUCAUCAAGAUUCUCA	UCUCAAUCUUGAUGAUGCUGAAU	Cleavage
sly-miR172d-10-5p	Solyc06g008730.3.1	2.0	-1.0	1	23	362	384	AUGCAGCAUCAUCAAGAUUCUCA	UGUUAAUUUUGAUGAUUCUGCAU	Cleavage
sly-miR172d-10-5p	Solyc05g013253.1.1	2.0	-1.0	1	23	1245	1267	AUGCAGCAUCAUCAAGAUUCUCA	UUCUCAUUUUGAUGAUGCUGUAU	Cleavage
sly-miR172d-10-5p	Solyc02g061810.3.1	2.0	-1.0	1	23	238	260	AUGCAGCAUCAUCAAGAUUCUCA	AAAUAGUGUUGGUGAUGCUGCAU	Cleavage
sly-miR172d-10-5p	Solyc08g069010.3.1	2.5	-1.0	1	23	3351	3373	AUGCAGCAUCAUCAAGAUUCUCA	UAGAGAUUUUGAUGAUGCUACAU	Cleavage
sly-miR172d-10-5p	Solyc03g083470.3.1	2.5	-1.0	1	23	1551	1573	AUGCAGCAUCAUCAAGAUUCUCA	GAACAAAUUUGAUGAUGCUGCAA	Cleavage
sly-miR172d-10-5p	Solyc01g016455.1.1	2.5	-1.0	1	23	943	965	AUGCAGCAUCAUCAAGAUUCUCA	AUAAAAUGUUGAUGGUGUUGCGU	Cleavage
sly-miR172d-10-	Solyc01g074030.3.1	2.5	-1.0	1	23	1422	1444	AUGCAGCAUCAUCAAGAUUCUCA	AUCCAAUAUUGAUGAUGUUGCAA	Cleavage

5p										
sly-miR172d-10-5p	Solyc11g009080.2.1	3.0	-1.0	1	23	432	454	AUGCAGCAUCAUCAAGAUUCUCA	AGAGAAGCUUGGUGAGGCUGCAU	Cleavage
sly-miR172d-10-5p	Solyc02g078640.3.1	3.0	-1.0	1	23	842	864	AUGCAGCAUCAUCAAGAUUCUCA	AAAGAAUCUUGAAGAUGCUGCCU	Translation
sly-miR172d-10-5p	Solyc05g012770.3.1	3.0	-1.0	1	23	2237	2259	AUGCAGCAUCAUCAAGAUUCUCA	UGUGAAUCUGAAUGAUGUUGCAU	Cleavage
sly-miR172d-10-5p	Solyc01g006850.1.1	3.0	-1.0	1	23	2345	2367	AUGCAGCAUCAUCAAGAUUCUCA	GGACAAUCAUGAUAAUGCUGUAU	Translation
sly-miR172d-10-5p	Solyc12g013580.2.1	3.0	-1.0	1	23	1868	1889	AUGCAGCAUCAUCAAGAUUCUCA	UGA-AAUCUUGGUGAUGCUGGAA	Cleavage
sly-miR172d-10-5p	Solyc12g042920.2.1	3.0	-1.0	1	23	636	658	AUGCAGCAUCAUCAAGAUUCUCA	CCGUGAUCUUGUUGGUGUUGCAU	Cleavage
sly-miR172d-10-5p	Solyc09g009950.3.1	3.0	-1.0	1	23	1314	1336	AUGCAGCAUCAUCAAGAUUCUCA	AGAUAAGCCUGAUGGUGCUGUAU	Cleavage
sly-miR172d-10-5p	Solyc07g039570.3.1	3.0	-1.0	1	23	1024	1045	AUGCAGCAUCAUCAAGAUUCUCA	GUAGAAACU-GAUGAUGCUGCAU	Cleavage
sly-miR172d-2	Solyc11g072600.2.1	0.5	-1.0	1	22	1274	1295	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUC	Cleavage
sly-miR172d-2	Solyc04g049800.3.1	0.5	-1.0	1	22	1106	1127	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUC	Cleavage
sly-miR172d-2	Solyc06g075510.3.1	1.0	-1.0	1	22	1348	1369	GAGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCUU	Cleavage
sly-miR172d-2	Solyc03g044300.3.1	2.0	-1.0	1	22	1366	1387	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCC	Cleavage
sly-miR172d-2	Solyc09g007260.3.1	2.0	-1.0	1	22	1624	1645	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGC	Cleavage
sly-miR172d-2	Solyc02g093150.3.1	2.0	-1.0	1	22	1560	1581	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCC	Cleavage
sly-miR172d-2	Solyc02g064960.3.1	2.0	-1.0	1	22	1764	1785	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCC	Cleavage
sly-miR172d-2	Solyc12g095890.2.1	2.0	-1.0	1	22	2474	2495	GAGAAUCUUGAUGAUGCUGCAU	GCACAGCAUAAUCAAGAUUUUC	Cleavage
sly-miR172d-2	Solyc09g072830.3.1	2.0	-1.0	1	22	988	1009	GAGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUUC	Cleavage
sly-miR172d-2	Solyc02g087620.3.1	2.5	-1.0	1	22	96	117	GAGAAUCUUGAUGAUGCUGCAU	GUAAAGCCUUAUCAAGAUUCUC	Cleavage
sly-miR172d-2	Solyc02g081690.1.1	2.5	-1.0	1	22	769	790	GAGAAUCUUGAUGAUGCUGCAU	GCUCAGUGGCAUCAAGAUUCUU	Cleavage
sly-miR172d-2	Solyc01g096240.3.1	2.5	-1.0	1	22	1392	1413	GAGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCUU	Cleavage
sly-miR172d-2	Solyc03g045060.3.1	2.5	-1.0	1	22	1147	1168	GAGAAUCUUGAUGAUGCUGCAU	ACUCGAUAUUAUCAAGAUUCUC	Cleavage
sly-miR172d-2	Solyc04g077360.3.1	2.5	-1.0	1	22	2514	2535	GAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUC	Cleavage
sly-miR172d-2	Solyc04g077330.3.1	2.5	-1.0	1	22	9082	9103	GAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUC	Cleavage
sly-miR172d-2	Solyc10g084340.2.1	3.0	-1.0	1	22	2182	2203	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGG	Cleavage
sly-miR172d-2	Solyc01g090460.3.1	3.0	-1.0	1	22	385	406	GAGAAUCUUGAUGAUGCUGCAU	AUGCAUCAUCAUCAAGUUUCUU	Cleavage
sly-miR172d-2	Solyc09g075970.3.1	3.0	-1.0	1	22	936	957	GAGAAUCUUGAUGAUGCUGCAU	CAUGUUCAUCAUCAAGAUUCUC	Cleavage
sly-miR172d-2	Solyc07g064740.3.1	3.0	-1.0	1	22	10	31	GAGAAUCUUGAUGAUGCUGCAU	GAUAAGCAUUAUCAAUAUUCUC	Cleavage
sly-miR172d-2	Solyc03g113680.3.1	3.0	-1.0	1	22	447	468	GAGAAUCUUGAUGAUGCUGCAU	UCUGAGCAUCAUGGAGAUUCUC	Translation
sly-miR172d-2	Solyc05g055030.2.1	3.0	-1.0	1	22	448	469	GAGAAUCUUGAUGAUGCUGCAU	UCAAAUUAUUAUCAAGAUUCUC	Cleavage
sly-miR172d-2-3p	Solyc11g072600.2.1	0.5	-1.0	1	23	1274	1296	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc04g049800.3.1	1.5	-1.0	1	23	1106	1128	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCU	Cleavage
sly-miR172d-2-3p	Solyc06g075510.3.1	2.0	-1.0	1	23	1348	1370	UGAGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCUUC	Cleavage
sly-miR172d-2-3p	Solyc09g075970.3.1	2.0	-1.0	1	23	936	958	UGAGAAUCUUGAUGAUGCUGCAU	CAUGUUCAUCAUCAAGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc05g055030.2.1	2.0	-1.0	1	23	448	470	UGAGAAUCUUGAUGAUGCUGCAU	UCAAAUUAUUAUCAAGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc01g006950.3.1	2.0	-1.0	1	23	532	554	UGAGAAUCUUGAUGAUGCUGCAU	AACGAUCAUGAUCAAGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc02g023950.3.1	2.5	-1.0	1	23	3928	3950	UGAGAAUCUUGAUGAUGCUGCAU	CUGAGGCAUCAUCAACAUUCUUA	Cleavage
sly-miR172d-2-3p	Solyc12g095890.2.1	2.5	-1.0	1	23	2474	2496	UGAGAAUCUUGAUGAUGCUGCAU	GCACAGCAUAAUCAAGAUUUUCC	Cleavage
sly-miR172d-2-3p	Solyc10g083090.1.1	2.5	-1.0	1	23	386	408	UGAGAAUCUUGAUGAUGCUGCAU	AAGGAUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-2-3p	Solyc01g096240.3.1	2.5	-1.0	1	23	1392	1414	UGAGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCUUA	Cleavage
sly-miR172d-2-3p	Solyc11g071940.1.1	2.5	-1.0	1	23	15	37	UGAGAAUCUUGAUGAUGCUGCAU	UGUAAGCAUUAUCAAGAAUUUCA	Cleavage
sly-miR172d-2-3p	Solyc02g087620.3.1	2.5	-1.0	1	23	96	118	UGAGAAUCUUGAUGAUGCUGCAU	GUAAAGCCUUAUCAAGAUUCUCU	Cleavage

sly-miR172d-2-3p	Solyc04g081950.3.1	2.5	-1.0	1	23	812	834	UGAGAAUCUUGAUGAUGCUGCAU	UAAGAGCUUCAUCACGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc04g077360.3.1	2.5	-1.0	1	23	2514	2536	UGAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-2-3p	Solyc04g077330.3.1	2.5	-1.0	1	23	9082	9104	UGAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-2-3p	Solyc03g044300.3.1	3.0	-1.0	1	23	1366	1388	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCC	Cleavage
sly-miR172d-2-3p	Solyc09g007260.3.1	3.0	-1.0	1	23	1624	1646	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
sly-miR172d-2-3p	Solyc02g093150.3.1	3.0	-1.0	1	23	1560	1582	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-2-3p	Solyc02g064960.3.1	3.0	-1.0	1	23	1764	1786	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-2-3p	Solyc10g083070.1.1	3.0	-1.0	1	23	248	270	UGAGAAUCUUGAUGAUGCUGCAU	AUAUGUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-2-3p	Solyc10g083090.1.1	3.0	-1.0	1	23	248	270	UGAGAAUCUUGAUGAUGCUGCAU	AUAUGUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-2-3p	Solyc12g005290.2.1	3.0	-1.0	1	23	2105	2127	UGAGAAUCUUGAUGAUGCUGCAU	GUGUAUCUGCAUCAAGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc02g043870.2.1	3.0	-1.0	1	23	536	558	UGAGAAUCUUGAUGAUGCUGCAU	UAGUUGCAUUACCAAGAUUCUCA	Cleavage
sly-miR172d-2-3p	Solyc10g005080.3.1	3.0	-1.0	1	23	44	66	UGAGAAUCUUGAUGAUGCUGCAU	UGGUAGCGGCAUCAGGGUUCUUA	Cleavage
sly-miR172d-2-3p	Solyc09g072830.3.1	3.0	-1.0	1	23	988	1010	UGAGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUUCC	Cleavage
sly-miR172d-2-3p	Solyc02g081690.1.1	3.0	-1.0	1	23	769	791	UGAGAAUCUUGAUGAUGCUGCAU	GCUCAGUGGCAUCAAGAUUCUUG	Cleavage
sly-miR172d-2-3p	Solyc03g007360.3.1	3.0	-1.0	1	23	3356	3378	UGAGAAUCUUGAUGAUGCUGCAU	ACAUAGCAUCAUCAAGAACCUCA	Cleavage
sly-miR172d-2-3p	Solyc02g076840.3.1	3.0	-1.0	1	23	2817	2839	UGAGAAUCUUGAUGAUGCUGCAU	AGAACAUAUCAUCAAGAUUUUCA	Cleavage
sly-miR172d-2-3p	Solyc07g064740.3.1	3.0	-1.0	1	23	10	32	UGAGAAUCUUGAUGAUGCUGCAU	GAUAAGCAUUAUCAAUAUUCUCU	Cleavage
sly-miR172d-2-3p	Solyc03g113680.3.1	3.0	-1.0	1	23	447	469	UGAGAAUCUUGAUGAUGCUGCAU	UCUGAGCAUCAUGGAGAUUCUCU	Translation
sly-miR172d-2-3p	Solyc03g118840.3.1	3.0	-1.0	1	23	1116	1138	UGAGAAUCUUGAUGAUGCUGCAU	UCUAGGCAUCAUCGACAUUCUCG	Cleavage
sly-miR172d-2-3p	Solyc11g012790.2.1	3.0	-1.0	1	23	2684	2706	UGAGAAUCUUGAUGAUGCUGCAU	CACAAGUGUCAUCAUGAUUCUUA	Cleavage
sly-miR172d-2-3p	Solyc04g009050.3.1	3.0	-1.0	1	23	2850	2871	UGAGAAUCUUGAUGAUGCUGCAU	AUG-AGAAUUAUCAAGAAUCUCA	Cleavage
sly-miR172d-2-3p	Solyc02g078560.3.1	3.0	-1.0	1	23	1632	1654	UGAGAAUCUUGAUGAUGCUGCAU	CUUAAGUGUGAUCAAGAUUCUCU	Cleavage
sly-miR172d-2-3p	Solyc05g052560.1.1	3.0	-1.0	1	23	99	121	UGAGAAUCUUGAUGAUGCUGCAU	CGAAAACAUCAUCAAGAUUCGUA	Cleavage
sly-miR172d-4-3p	Solyc11g072600.2.1	0.5	-1.0	1	22	1274	1295	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc04g049800.3.1	0.5	-1.0	1	22	1106	1127	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc06g075510.3.1	1.0	-1.0	1	22	1348	1369	GAGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCUU	Cleavage
sly-miR172d-4-3p	Solyc03g044300.3.1	2.0	-1.0	1	22	1366	1387	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCC	Cleavage
sly-miR172d-4-3p	Solyc09g007260.3.1	2.0	-1.0	1	22	1624	1645	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGC	Cleavage
sly-miR172d-4-3p	Solyc02g093150.3.1	2.0	-1.0	1	22	1560	1581	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCC	Cleavage
sly-miR172d-4-3p	Solyc02g064960.3.1	2.0	-1.0	1	22	1764	1785	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCC	Cleavage
sly-miR172d-4-3p	Solyc12g095890.2.1	2.0	-1.0	1	22	2474	2495	GAGAAUCUUGAUGAUGCUGCAU	GCACAGCAUAAUCAAGAUUUUC	Cleavage
sly-miR172d-4-3p	Solyc09g072830.3.1	2.0	-1.0	1	22	988	1009	GAGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUUC	Cleavage
sly-miR172d-4-3p	Solyc02g087620.3.1	2.5	-1.0	1	22	96	117	GAGAAUCUUGAUGAUGCUGCAU	GUAAAGCCUUAUCAAGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc02g081690.1.1	2.5	-1.0	1	22	769	790	GAGAAUCUUGAUGAUGCUGCAU	GCUCAGUGGCAUCAAGAUUCUU	Cleavage
sly-miR172d-4-3p	Solyc01g096240.3.1	2.5	-1.0	1	22	1392	1413	GAGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCUU	Cleavage
sly-miR172d-4-3p	Solyc03g045060.3.1	2.5	-1.0	1	22	1147	1168	GAGAAUCUUGAUGAUGCUGCAU	ACUCGAUAUUAUCAAGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc04g077360.3.1	2.5	-1.0	1	22	2514	2535	GAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc04g077330.3.1	2.5	-1.0	1	22	9082	9103	GAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc10g084340.2.1	3.0	-1.0	1	22	2182	2203	GAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGG	Cleavage
sly-miR172d-4-3p	Solyc01g090460.3.1	3.0	-1.0	1	22	385	406	GAGAAUCUUGAUGAUGCUGCAU	AUGCAUCAUCAUCAAGUUUCUU	Cleavage
sly-miR172d-4-3p	Solyc09g075970.3.1	3.0	-1.0	1	22	936	957	GAGAAUCUUGAUGAUGCUGCAU	CAUGUUCAUCAUCAAGAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc07g064740.3.1	3.0	-1.0	1	22	10	31	GAGAAUCUUGAUGAUGCUGCAU	GAUAAGCAUUAUCAAUAUUCUC	Cleavage
sly-miR172d-4-3p	Solyc03g113680.3.1	3.0	-1.0	1	22	447	468	GAGAAUCUUGAUGAUGCUGCAU	UCUGAGCAUCAUGGAGAUUCUC	Translation
sly-miR172d-4-3p	Solyc05g055030.2.1	3.0	-1.0	1	22	448	469	GAGAAUCUUGAUGAUGCUGCAU	UCAAAUUAUUAUCAAGAUUCUC	Cleavage
sly-miR172d-5-3p	Solyc11g072600.2.1	1.0	-1.0	1	23	1274	1296	UGGGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCA	Cleavage
sly-miR172d-5-3p	Solyc03g044300.3.1	1.5	-1.0	1	23	1366	1388	UGGGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCC	Cleavage
sly-miR172d-5-3p	Solyc02g093150.3.1	1.5	-1.0	1	23	1560	1582	UGGGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-5-3p	Solyc02g064960.3.1	1.5	-1.0	1	23	1764	1786	UGGGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-5-3p	Solyc04g049800.3.1	2.0	-1.0	1	23	1106	1128	UGGGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCU	Cleavage
sly-miR172d-5-3p	Solyc06g075510.3.1	2.5	-1.0	1	23	1348	1370	UGGGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCUUC	Cleavage

sly-miR172d-5-3p	Solyc09g007700.3.1	2.5	-1.0	1	23	47	69	UGGGAAUCUUGAUGAUGCUGCAU	CAUCAUCAUCAUCAAGAUUCCUC	Cleavage
sly-miR172d-5-3p	Solyc09g075970.3.1	2.5	-1.0	1	23	936	958	UGGGAAUCUUGAUGAUGCUGCAU	CAUGUUCAUCAUCAAGAUUCUCA	Cleavage
sly-miR172d-5-3p	Solyc03g007360.3.1	2.5	-1.0	1	23	2774	2796	UGGGAAUCUUGAUGAUGCUGCAU	UUUGAGCAUCAUUAAGGCUCCCA	Cleavage
sly-miR172d-5-3p	Solyc03g115247.1.1	2.5	-1.0	1	23	963	984	UGGGAAUCUUGAUGAUGCUGCAU	AUG-AGCAUGAUCAAGGUUUCUA	Cleavage
sly-miR172d-5-3p	Solyc05g055030.2.1	2.5	-1.0	1	23	448	470	UGGGAAUCUUGAUGAUGCUGCAU	UCAAAUUAUUAUCAAGAUUCUCA	Cleavage
sly-miR172d-5-3p	Solyc01g006950.3.1	2.5	-1.0	1	23	532	554	UGGGAAUCUUGAUGAUGCUGCAU	AACGAUCAUGAUCAAGAUUCUCA	Cleavage
sly-miR172d-5-3p	Solyc09g007260.3.1	3.0	-1.0	1	23	1624	1646	UGGGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
sly-miR172d-5-3p	Solyc03g006550.3.1	3.0	-1.0	1	23	809	831	UGGGAAUCUUGAUGAUGCUGCAU	AUGGAGUGUCUUCAAGAUUUCCA	Cleavage
sly-miR172d-5-3p	Solyc02g023950.3.1	3.0	-1.0	1	23	3928	3950	UGGGAAUCUUGAUGAUGCUGCAU	CUGAGGCAUCAUCAACAUUCUUA	Cleavage
sly-miR172d-5-3p	Solyc01g091910.4.1	3.0	-1.0	1	23	1298	1320	UGGGAAUCUUGAUGAUGCUGCAU	CCUCAGCAUUAUCAACAUUCCUG	Cleavage
sly-miR172d-5-3p	Solyc12g095890.2.1	3.0	-1.0	1	23	2474	2496	UGGGAAUCUUGAUGAUGCUGCAU	GCACAGCAUAAUCAAGAUUUUCC	Cleavage
sly-miR172d-5-3p	Solyc10g083090.1.1	3.0	-1.0	1	23	386	408	UGGGAAUCUUGAUGAUGCUGCAU	AAGGAUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-5-3p	Solyc01g096240.3.1	3.0	-1.0	1	23	1392	1414	UGGGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCUUA	Cleavage
sly-miR172d-5-3p	Solyc06g069650.3.1	3.0	-1.0	1	23	998	1020	UGGGAAUCUUGAUGAUGCUGCAU	GCAUAGUAUCAUCAGGAAUUCCA	Cleavage
sly-miR172d-5-3p	Solyc04g081550.3.1	3.0	-1.0	1	23	92	114	UGGGAAUCUUGAUGAUGCUGCAU	CUUUUGCAUCAUUAAUAUUCCCA	Cleavage
sly-miR172d-5-3p	Solyc11g071940.1.1	3.0	-1.0	1	23	15	37	UGGGAAUCUUGAUGAUGCUGCAU	UGUAAGCAUUAUCAAGAAUUUCA	Cleavage
sly-miR172d-5-3p	Solyc08g007330.3.1	3.0	-1.0	1	23	1285	1307	UGGGAAUCUUGAUGAUGCUGCAU	AAUAAGUAUCGUCAAGAUUUCAA	Cleavage
sly-miR172d-5-3p	Solyc02g087620.3.1	3.0	-1.0	1	23	96	118	UGGGAAUCUUGAUGAUGCUGCAU	GUAAAGCCUUAUCAAGAUUCUCU	Cleavage
sly-miR172d-5-3p	Solyc05g052560.1.1	3.0	-1.0	1	23	99	121	UGGGAAUCUUGAUGAUGCUGCAU	CGAAAACAUCAUCAAGAUUCGUA	Cleavage
sly-miR172d-5-3p	Solyc04g081950.3.1	3.0	-1.0	1	23	812	834	UGGGAAUCUUGAUGAUGCUGCAU	UAAGAGCUUCAUCACGAUUCUCA	Cleavage
sly-miR172d-5-3p	Solyc04g077360.3.1	3.0	-1.0	1	23	2514	2536	UGGGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-5-5p	Solyc09g074950.3.1	2.0	-1.0	1	22	1352	1373	UGCAACAUCAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGUA	Cleavage
sly-miR172d-5-5p	Solyc02g077380.2.1	2.0	-1.0	1	22	1044	1065	UGCAACAUCAUCAAGAUUCACA	UAAGAGUUUUGAUGAUGUUGCU	Cleavage
sly-miR172d-5-5p	Solyc00g017870.1.1	2.5	-1.0	1	22	111	132	UGCAACAUCAUCAAGAUUCACA	GAUGAAGCUUGAUGAUGUUGUU	Cleavage
sly-miR172d-5-5p	Solyc02g063490.3.1	2.5	-1.0	1	22	1210	1231	UGCAACAUCAUCAAGAUUCACA	UCUGCAUCUUUAUGAUGUUGCA	Cleavage
sly-miR172d-5-5p	Solyc02g032173.1.1	2.5	-1.0	1	22	300	321	UGCAACAUCAUCAAGAUUCACA	UAAGAAUUUUGAUAAUGUUGUA	Cleavage
sly-miR172d-5-5p	Solyc02g069670.3.1	2.5	-1.0	1	22	1013	1034	UGCAACAUCAUCAAGAUUCACA	CAAGAAUAUUGAUGAUGUUGAA	Cleavage
sly-miR172d-5-5p	Solyc05g012770.3.1	3.0	-1.0	1	22	2237	2258	UGCAACAUCAUCAAGAUUCACA	UGUGAAUCUGAAUGAUGUUGCA	Cleavage
sly-miR172d-5-5p	Solyc04g009730.3.1	3.0	-1.0	1	22	730	751	UGCAACAUCAUCAAGAUUCACA	AGUGGAUUUUGAUGGUGUUGAA	Cleavage
sly-miR172d-5-5p	Solyc11g070170.2.1	3.0	-1.0	1	22	264	285	UGCAACAUCAUCAAGAUUCACA	UGUGAAUAGUGAUGAUGUUGUG	Cleavage
sly-miR172d-5-5p	Solyc03g083835.1.1	3.0	-1.0	1	22	18	39	UGCAACAUCAUCAAGAUUCACA	UGAGAAUCUUGAUGAAGUUGUU	Cleavage
sly-miR172d-5-5p	Solyc06g084530.3.1	3.0	-1.0	1	22	1166	1187	UGCAACAUCAUCAAGAUUCACA	GUUGAAUCUUGAUAAUGGUGCA	Cleavage
sly-miR172d-5-5p	Solyc02g091120.3.1	3.0	-1.0	1	22	2854	2875	UGCAACAUCAUCAAGAUUCACA	CGGUGAUCUUGGUGAUGUUGCU	Cleavage
sly-miR172d-5-5p	Solyc01g060490.3.1	3.0	-1.0	1	22	412	433	UGCAACAUCAUCAAGAUUCACA	GACUGAUCUUGAUGAUGUUGAA	Cleavage
sly-miR172d-5-5p	Solyc12g089280.2.1	3.0	-1.0	1	22	404	425	UGCAACAUCAUCAAGAUUCACA	UAUGGCUAUUGAUGGUGUUGCA	Cleavage
sly-miR172d-5-5p	Solyc04g081280.3.1	3.0	-1.0	1	22	529	550	UGCAACAUCAUCAAGAUUCACA	UAUGGCUAUUGAUGGUGUUGCA	Cleavage
sly-miR172d-5-5p	Solyc01g016455.1.1	3.0	-1.0	1	22	943	964	UGCAACAUCAUCAAGAUUCACA	AUAAAAUGUUGAUGGUGUUGCG	Cleavage
sly-miR172d-5-5p	Solyc05g026510.3.1	3.0	-1.0	1	22	583	604	UGCAACAUCAUCAAGAUUCACA	AACUGAUGUUGAUGAUGUUGUA	Cleavage
sly-miR172d-5-5p	Solyc02g076730.2.1	3.0	-1.0	1	22	231	252	UGCAACAUCAUCAAGAUUCACA	CAAGAGGUUUGAUGAUGUUGUG	Cleavage
sly-miR172d-5-5p	Solyc11g013050.1.1	3.0	-1.0	1	22	719	740	UGCAACAUCAUCAAGAUUCACA	GAGGGAUGUUGAUGAUGAUGCA	Cleavage
sly-miR172d-5-5p	Solyc02g069750.2.1	3.0	-1.0	1	22	367	388	UGCAACAUCAUCAAGAUUCACA	AAAGAAUUAUGAUGAUGAUGCA	Cleavage
sly-miR172d-5-5p	Solyc07g056260.3.1	3.0	-1.0	1	22	1864	1885	UGCAACAUCAUCAAGAUUCACA	CAAGAGUGUUGAUGAUGAUGCA	Cleavage
sly-miR172d-5p	Solyc06g071770.3.1	2.5	-1.0	1	21	2801	2821	GCAGCACCAUUAAGAUUCACA	CUUGAAUCUUAAUGGUUCUGA	Cleavage
sly-miR172d-5p	Solyc05g012270.3.1	2.5	-1.0	1	21	270	289	GCAGCACCAUUAAGAUUCACA	AGUGAAU-UUAAUGGUGUUGC	Cleavage
sly-miR172d-5p	Solyc12g099900.1.1	3.0	-1.0	1	21	474	494	GCAGCACCAUUAAGAUUCACA	UGUGGAUCUUAAUGCUGCUGA	Cleavage
sly-miR172d-5p	Solyc04g010070.3.1	3.0	-1.0	1	21	335	355	GCAGCACCAUUAAGAUUCACA	UGUGGAUUUUAAUGGUGAUGU	Cleavage
sly-miR172d-5p	Solyc09g072587.1.1	3.0	-1.0	1	21	417	437	GCAGCACCAUUAAGAUUCACA	UGUGGAACUUGAUGGUGCUGA	Cleavage
sly-miR172d-5p	Solyc04g009730.3.1	3.0	-1.0	1	21	730	750	GCAGCACCAUUAAGAUUCACA	AGUGGAUUUUGAUGGUGUUGA	Cleavage
sly-miR172d-5p	Solyc10g084680.1.1	3.0	-1.0	1	21	573	593	GCAGCACCAUUAAGAUUCACA	UGUGAUUGUUAAUGGUGCUGG	Cleavage
sly-miR172d-5p	Solyc07g063220.3.1	3.0	-1.0	1	21	509	529	GCAGCACCAUUAAGAUUCACA	UUUGGAUCUUAUUGGUGUUGU	Translation

sly-miR172d-5p	Solyc01g081177.1.1	3.0	-1.0	1	21	223	243	GCAGCACCAUUAAGAUUCACA	CAUGAGAUUUGGUGGUGCUGC	Cleavage
sly-miR172d-5p	Solyc09g074950.3.1	3.0	-1.0	1	21	659	679	GCAGCACCAUUAAGAUUCACA	GCUGAAAUCUAAUGGUGCUGC	Cleavage
sly-miR172d-5p	Solyc06g073640.3.1	3.0	-1.0	1	21	234	254	GCAGCACCAUUAAGAUUCACA	UUUUAUUCUUAAUGGUGUUGU	Cleavage
sly-miR172d-5p	Solyc07g064900.3.1	3.0	-1.0	1	21	536	556	GCAGCACCAUUAAGAUUCACA	GUUGUCUCUUAGUGGUGUUGC	Cleavage
sly-miR172d-6-3p	Solyc11g072600.2.1	0.5	-1.0	1	23	1274	1296	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc04g049800.3.1	1.5	-1.0	1	23	1106	1128	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCUCU	Cleavage
sly-miR172d-6-3p	Solyc06g075510.3.1	2.0	-1.0	1	23	1348	1370	UGAGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCUUC	Cleavage
sly-miR172d-6-3p	Solyc09g075970.3.1	2.0	-1.0	1	23	936	958	UGAGAAUCUUGAUGAUGCUGCAU	CAUGUUCAUCAUCAAGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc05g055030.2.1	2.0	-1.0	1	23	448	470	UGAGAAUCUUGAUGAUGCUGCAU	UCAAAUUAUUAUCAAGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc01g006950.3.1	2.0	-1.0	1	23	532	554	UGAGAAUCUUGAUGAUGCUGCAU	AACGAUCAUGAUCAAGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc02g023950.3.1	2.5	-1.0	1	23	3928	3950	UGAGAAUCUUGAUGAUGCUGCAU	CUGAGGCAUCAUCAACAUUCUUA	Cleavage
sly-miR172d-6-3p	Solyc12g095890.2.1	2.5	-1.0	1	23	2474	2496	UGAGAAUCUUGAUGAUGCUGCAU	GCACAGCAUAAUCAAGAUUUUCC	Cleavage
sly-miR172d-6-3p	Solyc10g083090.1.1	2.5	-1.0	1	23	386	408	UGAGAAUCUUGAUGAUGCUGCAU	AAGGAUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-6-3p	Solyc01g096240.3.1	2.5	-1.0	1	23	1392	1414	UGAGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCUUA	Cleavage
sly-miR172d-6-3p	Solyc11g071940.1.1	2.5	-1.0	1	23	15	37	UGAGAAUCUUGAUGAUGCUGCAU	UGUAAGCAUUAUCAAGAAUUUCA	Cleavage
sly-miR172d-6-3p	Solyc02g087620.3.1	2.5	-1.0	1	23	96	118	UGAGAAUCUUGAUGAUGCUGCAU	GUAAAGCCUUAUCAAGAUUCUCU	Cleavage
sly-miR172d-6-3p	Solyc04g081950.3.1	2.5	-1.0	1	23	812	834	UGAGAAUCUUGAUGAUGCUGCAU	UAAGAGCUUCAUCACGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc04g077360.3.1	2.5	-1.0	1	23	2514	2536	UGAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-6-3p	Solyc04g077330.3.1	2.5	-1.0	1	23	9082	9104	UGAGAAUCUUGAUGAUGCUGCAU	UUAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-6-3p	Solyc03g044300.3.1	3.0	-1.0	1	23	1366	1388	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCC	Cleavage
sly-miR172d-6-3p	Solyc09g007260.3.1	3.0	-1.0	1	23	1624	1646	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
sly-miR172d-6-3p	Solyc02g093150.3.1	3.0	-1.0	1	23	1560	1582	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-6-3p	Solyc02g064960.3.1	3.0	-1.0	1	23	1764	1786	UGAGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-6-3p	Solyc10g083070.1.1	3.0	-1.0	1	23	248	270	UGAGAAUCUUGAUGAUGCUGCAU	AUAUGUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-6-3p	Solyc10g083090.1.1	3.0	-1.0	1	23	248	270	UGAGAAUCUUGAUGAUGCUGCAU	AUAUGUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-6-3p	Solyc12g005290.2.1	3.0	-1.0	1	23	2105	2127	UGAGAAUCUUGAUGAUGCUGCAU	GUGUAUCUGCAUCAAGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc02g043870.2.1	3.0	-1.0	1	23	536	558	UGAGAAUCUUGAUGAUGCUGCAU	UAGUUGCAUUACCAAGAUUCUCA	Cleavage
sly-miR172d-6-3p	Solyc10g005080.3.1	3.0	-1.0	1	23	44	66	UGAGAAUCUUGAUGAUGCUGCAU	UGGUAGCGGCAUCAGGGUUCUUA	Cleavage
sly-miR172d-6-3p	Solyc09g072830.3.1	3.0	-1.0	1	23	988	1010	UGAGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUUCC	Cleavage
sly-miR172d-6-3p	Solyc02g081690.1.1	3.0	-1.0	1	23	769	791	UGAGAAUCUUGAUGAUGCUGCAU	GCUCAGUGGCAUCAAGAUUCUUG	Cleavage
sly-miR172d-6-3p	Solyc03g007360.3.1	3.0	-1.0	1	23	3356	3378	UGAGAAUCUUGAUGAUGCUGCAU	ACAUAGCAUCAUCAAGAACCUCA	Cleavage
sly-miR172d-6-3p	Solyc02g076840.3.1	3.0	-1.0	1	23	2817	2839	UGAGAAUCUUGAUGAUGCUGCAU	AGAACAUAUCAUCAAGAUUUUCA	Cleavage
sly-miR172d-6-3p	Solyc07g064740.3.1	3.0	-1.0	1	23	10	32	UGAGAAUCUUGAUGAUGCUGCAU	GAUAAGCAUUAUCAAUAUUCUCU	Cleavage
sly-miR172d-6-3p	Solyc03g113680.3.1	3.0	-1.0	1	23	447	469	UGAGAAUCUUGAUGAUGCUGCAU	UCUGAGCAUCAUGGAGAUUCUCU	Translation
sly-miR172d-6-3p	Solyc03g118840.3.1	3.0	-1.0	1	23	1116	1138	UGAGAAUCUUGAUGAUGCUGCAU	UCUAGGCAUCAUCGACAUUCUCG	Cleavage
sly-miR172d-6-3p	Solyc11g012790.2.1	3.0	-1.0	1	23	2684	2706	UGAGAAUCUUGAUGAUGCUGCAU	CACAAGUGUCAUCAUGAUUCUUA	Cleavage
sly-miR172d-6-3p	Solyc04g009050.3.1	3.0	-1.0	1	23	2850	2871	UGAGAAUCUUGAUGAUGCUGCAU	AUG-AGAAUUAUCAAGAAUCUCA	Cleavage
sly-miR172d-6-3p	Solyc02g078560.3.1	3.0	-1.0	1	23	1632	1654	UGAGAAUCUUGAUGAUGCUGCAU	CUUAAGUGUGAUCAAGAUUCUCU	Cleavage
sly-miR172d-6-3p	Solyc05g052560.1.1	3.0	-1.0	1	23	99	121	UGAGAAUCUUGAUGAUGCUGCAU	CGAAAACAUCAUCAAGAUUCGUA	Cleavage
sly-miR172d-6-5p	Solyc09g074950.3.1	2.5	-1.0	1	22	1352	1373	UGCAGCAUCAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGUA	Cleavage
sly-miR172d-6-5p	Solyc12g088640.2.1	2.5	-1.0	1	22	538	559	UGCAGCAUCAUCAAGAUUCACA	UCUCAAUCUUGAUGAUGCUGAA	Cleavage
sly-miR172d-6-5p	Solyc02g077380.2.1	2.5	-1.0	1	22	1044	1065	UGCAGCAUCAUCAAGAUUCACA	UAAGAGUUUUGAUGAUGUUGCU	Cleavage
sly-miR172d-6-5p	Solyc02g078640.3.1	2.5	-1.0	1	22	842	863	UGCAGCAUCAUCAAGAUUCACA	AAAGAAUCUUGAAGAUGCUGCC	Translation
sly-miR172d-6-5p	Solyc03g083470.3.1	2.5	-1.0	1	22	1551	1572	UGCAGCAUCAUCAAGAUUCACA	GAACAAAUUUGAUGAUGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc09g089865.1.1	2.5	-1.0	1	22	87	108	UGCAGCAUCAUCAAGAUUCACA	AUGGAUUCUUUAUGAUGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc01g005820.3.1	3.0	-1.0	1	22	510	531	UGCAGCAUCAUCAAGAUUCACA	UGUGGAUCCUGCUGAUGCUGCA	Translation
sly-miR172d-6-5p	Solyc06g008730.3.1	3.0	-1.0	1	22	362	383	UGCAGCAUCAUCAAGAUUCACA	UGUUAAUUUUGAUGAUUCUGCA	Cleavage
sly-miR172d-6-5p	Solyc09g011020.3.1	3.0	-1.0	1	22	982	1003	UGCAGCAUCAUCAAGAUUCACA	GGGGAAUUUUGAUGAUGCUGAG	Cleavage
sly-miR172d-6-5p	Solyc06g084530.3.1	3.0	-1.0	1	22	1166	1187	UGCAGCAUCAUCAAGAUUCACA	GUUGAAUCUUGAUAAUGGUGCA	Cleavage
sly-miR172d-6-5p	Solyc02g014355.1.1	3.0	-1.0	1	22	174	195	UGCAGCAUCAUCAAGAUUCACA	CUUUGAUCUUGAUGAUGCUGUU	Cleavage

sly-miR172d-6-5p	Solyc00g017870.1.1	3.0	-1.0	1	22	111	132	UGCAGCAUCAUCAAGAUUCACA	GAUGAAGCUUGAUGAUGUUGUU	Cleavage
sly-miR172d-6-5p	Solyc02g063490.3.1	3.0	-1.0	1	22	1210	1231	UGCAGCAUCAUCAAGAUUCACA	UCUGCAUCUUUAUGAUGUUGCA	Cleavage
sly-miR172d-6-5p	Solyc01g081177.1.1	3.0	-1.0	1	22	223	244	UGCAGCAUCAUCAAGAUUCACA	CAUGAGAUUUGGUGGUGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc05g013253.1.1	3.0	-1.0	1	22	1245	1266	UGCAGCAUCAUCAAGAUUCACA	UUCUCAUUUUGAUGAUGCUGUA	Cleavage
sly-miR172d-6-5p	Solyc08g082980.2.1	3.0	-1.0	1	22	1488	1509	UGCAGCAUCAUCAAGAUUCACA	GGGGAGUCUAGGUGAUGCUGUA	Cleavage
sly-miR172d-6-5p	Solyc12g013580.2.1	3.0	-1.0	1	22	1867	1888	UGCAGCAUCAUCAAGAUUCACA	UUGAAAUCUUGGUGAUGCUGGA	Cleavage
sly-miR172d-6-5p	Solyc02g032173.1.1	3.0	-1.0	1	22	300	321	UGCAGCAUCAUCAAGAUUCACA	UAAGAAUUUUGAUAAUGUUGUA	Cleavage
sly-miR172d-6-5p	Solyc07g006640.3.1	3.0	-1.0	1	22	585	605	UGCAGCAUCAUCAAGAUUCACA	GGUGCA-CUUGAUGAUGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc12g015890.1.1	3.0	-1.0	1	22	27	48	UGCAGCAUCAUCAAGAUUCACA	CGAGAGUAUUGUUGAUGCUGCA	Translation
sly-miR172d-6-5p	Solyc06g068855.1.1	3.0	-1.0	1	22	309	330	UGCAGCAUCAUCAAGAUUCACA	GCAAAAUAUUGGUGAUGCUGUA	Cleavage
sly-miR172d-6-5p	Solyc02g061810.3.1	3.0	-1.0	1	22	238	259	UGCAGCAUCAUCAAGAUUCACA	AAAUAGUGUUGGUGAUGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc11g009080.2.1	3.0	-1.0	1	22	432	453	UGCAGCAUCAUCAAGAUUCACA	AGAGAAGCUUGGUGAGGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc07g056030.3.1	3.0	-1.0	1	22	1386	1407	UGCAGCAUCAUCAAGAUUCACA	AGAGGACCUUGAUGAGGCUGCA	Cleavage
sly-miR172d-6-5p	Solyc02g090710.3.1	3.0	-1.0	1	22	357	378	UGCAGCAUCAUCAAGAUUCACA	AAAGUAUCUUGAUGAUUCUGUA	Cleavage
sly-miR172d-6-5p	Solyc11g013050.1.1	3.0	-1.0	1	22	719	740	UGCAGCAUCAUCAAGAUUCACA	GAGGGAUGUUGAUGAUGAUGCA	Cleavage
sly-miR172d-6-5p	Solyc02g069670.3.1	3.0	-1.0	1	22	1013	1034	UGCAGCAUCAUCAAGAUUCACA	CAAGAAUAUUGAUGAUGUUGAA	Cleavage
sly-miR172d-6-5p	Solyc02g069750.2.1	3.0	-1.0	1	22	367	388	UGCAGCAUCAUCAAGAUUCACA	AAAGAAUUAUGAUGAUGAUGCA	Cleavage
sly-miR172d-6-5p	Solyc08g061650.3.1	3.0	-1.0	1	22	2024	2045	UGCAGCAUCAUCAAGAUUCACA	GAAGAAACUUGAUGGUGCUUCA	Cleavage
sly-miR172d-6-5p	Solyc08g061635.1.1	3.0	-1.0	1	22	2420	2441	UGCAGCAUCAUCAAGAUUCACA	GAAGAAACUUGAUGGUGCUUCA	Cleavage
sly-miR172d-7-3p	Solyc11g072600.2.1	0.5	-1.0	1	22	1275	1296	UGAGAAUCUUGAUGAUGCUGCA	UGCAGCAUCAUCAGGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc04g049800.3.1	1.5	-1.0	1	22	1107	1128	UGAGAAUCUUGAUGAUGCUGCA	UGCAGCAUCAUCAGGAUUCUCU	Cleavage
sly-miR172d-7-3p	Solyc06g075510.3.1	2.0	-1.0	1	22	1349	1370	UGAGAAUCUUGAUGAUGCUGCA	GGCAGCAUCAUCAGGAUUCUUC	Cleavage
sly-miR172d-7-3p	Solyc09g075970.3.1	2.0	-1.0	1	22	937	958	UGAGAAUCUUGAUGAUGCUGCA	AUGUUCAUCAUCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc05g055030.2.1	2.0	-1.0	1	22	449	470	UGAGAAUCUUGAUGAUGCUGCA	CAAAUUAUUAUCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc11g012540.2.1	2.0	-1.0	1	22	377	398	UGAGAAUCUUGAUGAUGCUGCA	CCAAGAAUGAUCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc01g006950.3.1	2.0	-1.0	1	22	533	554	UGAGAAUCUUGAUGAUGCUGCA	ACGAUCAUGAUCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc11g012550.2.1	2.0	-1.0	1	22	266	287	UGAGAAUCUUGAUGAUGCUGCA	CCAAGAAUGAUCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc02g023950.3.1	2.5	-1.0	1	22	3929	3950	UGAGAAUCUUGAUGAUGCUGCA	UGAGGCAUCAUCAACAUUCUUA	Cleavage
sly-miR172d-7-3p	Solyc12g095890.2.1	2.5	-1.0	1	22	2475	2496	UGAGAAUCUUGAUGAUGCUGCA	CACAGCAUAAUCAAGAUUUUCC	Cleavage
sly-miR172d-7-3p	Solyc01g096240.3.1	2.5	-1.0	1	22	1393	1414	UGAGAAUCUUGAUGAUGCUGCA	AACAAUGUCAUCAAGAUUCUUA	Cleavage
sly-miR172d-7-3p	Solyc11g071940.1.1	2.5	-1.0	1	22	16	37	UGAGAAUCUUGAUGAUGCUGCA	GUAAGCAUUAUCAAGAAUUUCA	Cleavage
sly-miR172d-7-3p	Solyc10g083090.1.1	2.5	-1.0	1	22	387	408	UGAGAAUCUUGAUGAUGCUGCA	AGGAUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-7-3p	Solyc02g087620.3.1	2.5	-1.0	1	22	97	118	UGAGAAUCUUGAUGAUGCUGCA	UAAAGCCUUAUCAAGAUUCUCU	Cleavage
sly-miR172d-7-3p	Solyc04g081950.3.1	2.5	-1.0	1	22	813	834	UGAGAAUCUUGAUGAUGCUGCA	AAGAGCUUCAUCACGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc04g077360.3.1	2.5	-1.0	1	22	2515	2536	UGAGAAUCUUGAUGAUGCUGCA	UAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-7-3p	Solyc04g077330.3.1	2.5	-1.0	1	22	9083	9104	UGAGAAUCUUGAUGAUGCUGCA	UAUAUCUUCAUCAAGAUUCUCG	Cleavage
sly-miR172d-7-3p	Solyc03g044300.3.1	3.0	-1.0	1	22	1367	1388	UGAGAAUCUUGAUGAUGCUGCA	UGCAGCAUCAUCAGGAUUCCCC	Cleavage
sly-miR172d-7-3p	Solyc09g007260.3.1	3.0	-1.0	1	22	1625	1646	UGAGAAUCUUGAUGAUGCUGCA	UGCAGCAUCAUCAGGAUUCGCU	Cleavage
sly-miR172d-7-3p	Solyc02g093150.3.1	3.0	-1.0	1	22	1561	1582	UGAGAAUCUUGAUGAUGCUGCA	UGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-7-3p	Solyc02g064960.3.1	3.0	-1.0	1	22	1765	1786	UGAGAAUCUUGAUGAUGCUGCA	UGCAGCAUCAUCAGGAUUCCCU	Cleavage
sly-miR172d-7-3p	Solyc02g043870.2.1	3.0	-1.0	1	22	537	558	UGAGAAUCUUGAUGAUGCUGCA	AGUUGCAUUACCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc10g005080.3.1	3.0	-1.0	1	22	45	66	UGAGAAUCUUGAUGAUGCUGCA	GGUAGCGGCAUCAGGGUUCUUA	Cleavage
sly-miR172d-7-3p	Solyc09g072830.3.1	3.0	-1.0	1	22	989	1010	UGAGAAUCUUGAUGAUGCUGCA	CUCAUCAUCAUCAGGAUUUUCC	Cleavage
sly-miR172d-7-3p	Solyc12g005290.2.1	3.0	-1.0	1	22	2106	2127	UGAGAAUCUUGAUGAUGCUGCA	UGUAUCUGCAUCAAGAUUCUCA	Cleavage
sly-miR172d-7-3p	Solyc02g081690.1.1	3.0	-1.0	1	22	770	791	UGAGAAUCUUGAUGAUGCUGCA	CUCAGUGGCAUCAAGAUUCUUG	Cleavage
sly-miR172d-7-3p	Solyc03g007360.3.1	3.0	-1.0	1	22	3357	3378	UGAGAAUCUUGAUGAUGCUGCA	CAUAGCAUCAUCAAGAACCUCA	Cleavage
sly-miR172d-7-3p	Solyc02g076840.3.1	3.0	-1.0	1	22	2818	2839	UGAGAAUCUUGAUGAUGCUGCA	GAACAUAUCAUCAAGAUUUUCA	Cleavage
sly-miR172d-7-3p	Solyc10g083090.1.1	3.0	-1.0	1	22	249	270	UGAGAAUCUUGAUGAUGCUGCA	UAUGUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-7-3p	Solyc07g064740.3.1	3.0	-1.0	1	22	11	32	UGAGAAUCUUGAUGAUGCUGCA	AUAAGCAUUAUCAAUAUUCUCU	Cleavage
sly-miR172d-7-3p	Solyc03g113680.3.1	3.0	-1.0	1	22	448	469	UGAGAAUCUUGAUGAUGCUGCA	CUGAGCAUCAUGGAGAUUCUCU	Translation

sly-miR172d-7-3p	Solyc10g083070.1.1	3.0	-1.0	1	22	249	270	UGAGAAUCUUGAUGAUGCUGCA	UAUGUCAUCAUCAAGAUUGUCA	Cleavage
sly-miR172d-7-3p	Solyc03g118840.3.1	3.0	-1.0	1	22	1117	1138	UGAGAAUCUUGAUGAUGCUGCA	CUAGGCAUCAUCGACAUUCUCG	Cleavage
sly-miR172d-7-3p	Solyc11g012790.2.1	3.0	-1.0	1	22	2685	2706	UGAGAAUCUUGAUGAUGCUGCA	ACAAGUGUCAUCAUGAUUCUUA	Cleavage
sly-miR172d-7-3p	Solyc02g078560.3.1	3.0	-1.0	1	22	1633	1654	UGAGAAUCUUGAUGAUGCUGCA	UUAAGUGUGAUCAAGAUUCUCU	Cleavage
sly-miR172d-7-3p	Solyc05g052560.1.1	3.0	-1.0	1	22	100	121	UGAGAAUCUUGAUGAUGCUGCA	GAAAACAUCAUCAAGAUUCGUA	Cleavage
sly-miR172d-7-3p	Solyc04g009050.3.1	3.0	-1.0	1	22	2850	2871	UGAGAAUCUUGAUGAUGCUGCA	AUGAGAAUUAUCAAGAAUCUCA	Cleavage
sly-miR172d-7-5p	Solyc02g078640.3.1	1.0	-1.0	1	22	842	863	UGCAGCAUCUUCAAGAUUCACA	AAAGAAUCUUGAAGAUGCUGCC	Cleavage
sly-miR172d-7-5p	Solyc10g006530.3.1	2.0	-1.0	1	22	586	607	UGCAGCAUCUUCAAGAUUCACA	UGAGAAGCUUGAAGAUGCUGUG	Cleavage
sly-miR172d-7-5p	Solyc08g065420.3.1	2.0	-1.0	1	22	1311	1332	UGCAGCAUCUUCAAGAUUCACA	GAGGAAUUUUGAAGAAGCUGCA	Cleavage
sly-miR172d-7-5p	Solyc02g087250.3.1	2.5	-1.0	1	22	3164	3185	UGCAGCAUCUUCAAGAUUCACA	UGAGGAUUCUGGAGAUGCUGCA	Cleavage
sly-miR172d-7-5p	Solyc02g093140.3.1	2.5	-1.0	1	22	738	759	UGCAGCAUCUUCAAGAUUCACA	UACCAAUCUUGAAGAUGCAGCA	Cleavage
sly-miR172d-7-5p	Solyc11g017460.2.1	2.5	-1.0	1	22	1158	1179	UGCAGCAUCUUCAAGAUUCACA	GAUGAUUAUUGAAGAUGUUGCA	Cleavage
sly-miR172d-7-5p	Solyc02g072570.2.1	2.5	-1.0	1	22	84	105	UGCAGCAUCUUCAAGAUUCACA	AACCGAACUUGAAGAUGCUGCA	Cleavage
sly-miR172d-7-5p	Solyc01g107860.3.1	2.5	-1.0	1	22	736	757	UGCAGCAUCUUCAAGAUUCACA	CACCAACCUUGAAGAUGCUGCG	Cleavage
sly-miR172d-7-5p	Solyc06g051990.3.1	2.5	-1.0	1	22	423	444	UGCAGCAUCUUCAAGAUUCACA	AAAGAAACUUGAGGAUGCUGUG	Cleavage
sly-miR172d-7-5p	Solyc04g071270.1.1	3.0	-1.0	1	22	858	879	UGCAGCAUCUUCAAGAUUCACA	AGUGAAUGUUGAAGAUGUUGUU	Cleavage
sly-miR172d-7-5p	Solyc09g057790.3.1	3.0	-1.0	1	22	446	467	UGCAGCAUCUUCAAGAUUCACA	GGACAAUUUUGAAGAUGCUGUU	Cleavage
sly-miR172d-7-5p	Solyc01g087420.3.1	3.0	-1.0	1	22	1955	1976	UGCAGCAUCUUCAAGAUUCACA	GAGAAAUCUUGAGGAUGCUGUU	Cleavage
sly-miR172d-7-5p	Solyc07g042600.2.1	3.0	-1.0	1	22	891	912	UGCAGCAUCUUCAAGAUUCACA	CAAGAAUUUUGGAGAUGUUGUC	Cleavage
sly-miR172d-7-5p	Solyc03g115070.1.1	3.0	-1.0	1	22	1104	1125	UGCAGCAUCUUCAAGAUUCACA	GAAAAAUCUUGGAGAUUCUGCA	Cleavage
sly-miR172d-7-5p	Solyc06g082320.3.1	3.0	-1.0	1	22	803	824	UGCAGCAUCUUCAAGAUUCACA	UAAGAAUCUUAAAGAUGUUGCU	Cleavage
sly-miR172d-7-5p	Solyc01g110070.2.1	3.0	-1.0	1	22	705	726	UGCAGCAUCUUCAAGAUUCACA	CAAGAAUUUUGGAGAUGUUGUC	Cleavage
sly-miR172d-7-5p	Solyc02g083640.3.1	3.0	-1.0	1	22	1430	1451	UGCAGCAUCUUCAAGAUUCACA	CAAGGAUUUUGAAGAUGCUAUA	Cleavage
sly-miR172d-7-5p	Solyc08g008480.3.1	3.0	-1.0	1	22	602	623	UGCAGCAUCUUCAAGAUUCACA	UUCUAGUGUUGAAGAUGUUGCA	Cleavage
sly-miR172d-7-5p	Solyc01g096400.3.1	3.0	-1.0	1	22	620	641	UGCAGCAUCUUCAAGAUUCACA	CAGAGAUAUUGAAGAUGCUGCG	Cleavage
sly-miR172d-7-5p	Solyc11g064880.2.1	3.0	-1.0	1	22	1068	1089	UGCAGCAUCUUCAAGAUUCACA	AGAGAAUUCUGAAGAUGAUGCA	Cleavage
sly-miR172d-8-3p	Solyc03g044300.3.1	0.5	-1.0	1	21	1366	1386	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
sly-miR172d-8-3p	Solyc02g093150.3.1	0.5	-1.0	1	21	1560	1580	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
sly-miR172d-8-3p	Solyc02g064960.3.1	0.5	-1.0	1	21	1764	1784	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
sly-miR172d-8-3p	Solyc11g072600.2.1	1.0	-1.0	1	21	1274	1294	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCU	Cleavage
sly-miR172d-8-3p	Solyc04g049800.3.1	1.0	-1.0	1	21	1106	1126	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCU	Cleavage
sly-miR172d-8-3p	Solyc06g075510.3.1	1.0	-1.0	1	21	1348	1368	GGAAUCUUGAUGAUGCUGCAG	CGGCAGCAUCAUCAGGAUUCU	Cleavage
sly-miR172d-8-3p	Solyc09g007260.3.1	1.5	-1.0	1	21	1624	1644	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCG	Cleavage
sly-miR172d-8-3p	Solyc10g084340.2.1	1.5	-1.0	1	21	2182	2202	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCG	Cleavage
sly-miR172d-8-3p	Solyc09g007700.3.1	2.0	-1.0	1	21	47	67	GGAAUCUUGAUGAUGCUGCAG	CAUCAUCAUCAUCAAGAUUCC	Cleavage
sly-miR172d-8-3p	Solyc02g089263.1.1	2.5	-1.0	1	21	3455	3475	GGAAUCUUGAUGAUGCUGCAG	UGGCUAUAUCAUCAAGAUUCC	Cleavage
sly-miR172d-8-3p	Solyc01g090460.3.1	3.0	-1.0	1	21	385	405	GGAAUCUUGAUGAUGCUGCAG	AUGCAUCAUCAUCAAGUUUCU	Cleavage
sly-miR172d-8-3p	Solyc01g091910.4.1	3.0	-1.0	1	21	1298	1318	GGAAUCUUGAUGAUGCUGCAG	CCUCAGCAUUAUCAACAUUCC	Cleavage
sly-miR172d-8-3p	Solyc12g010650.1.1	3.0	-1.0	1	21	26	46	GGAAUCUUGAUGAUGCUGCAG	GUGAAGCUUUAUCAAGAUUUC	Cleavage
sly-miR172d-8-3p	Solyc07g063770.3.1	3.0	-1.0	1	21	2065	2085	GGAAUCUUGAUGAUGCUGCAG	AUGUAUCUUCAUCAAGAUUCU	Cleavage
sly-miR172d-8-3p	Solyc10g006710.3.1	3.0	-1.0	1	21	1980	2000	GGAAUCUUGAUGAUGCUGCAG	AUGUACCUUCAUCAAGAUUCU	Cleavage
sly-miR172d-8-3p	Solyc11g071540.2.1	3.0	-1.0	1	21	346	366	GGAAUCUUGAUGAUGCUGCAG	AACCAUCAUCAUCAGGAUUUC	Cleavage
sly-miR172d-8-5p	Solyc05g006640.3.1	2.5	-1.0	1	23	870	892	GUGGAGCAUCAUCAAGAUUCACA	UUUCAAUUUUGAUGAUGCUCGGC	Cleavage
sly-miR172d-8-5p	Solyc10g047000.2.1	2.5	-1.0	1	23	865	887	GUGGAGCAUCAUCAAGAUUCACA	UCAUCAUCUUGAUGAUGCUCAAC	Cleavage
sly-miR172d-8-5p	Solyc01g106100.2.1	2.5	-1.0	1	23	1022	1044	GUGGAGCAUCAUCAAGAUUCACA	CACCAAUCUUGAUGAUGCUUUUC	Cleavage
sly-miR172d-8-5p	Solyc09g010560.2.1	2.5	-1.0	1	23	165	187	GUGGAGCAUCAUCAAGAUUCACA	UUCUAAUUAUGAUGAUGCUCCAG	Cleavage
sly-miR172d-8-5p	Solyc11g016970.2.1	2.5	-1.0	1	23	1741	1763	GUGGAGCAUCAUCAAGAUUCACA	AGACAAGUUUGAUGAUGUUCCAU	Cleavage
sly-miR172d-8-5p	Solyc09g005160.2.1	3.0	-1.0	1	23	1009	1031	GUGGAGCAUCAUCAAGAUUCACA	UGUGAGUGUUGAUGAUGCUUUAU	Cleavage
sly-miR172d-8-5p	Solyc10g084340.2.1	3.0	-1.0	1	23	956	978	GUGGAGCAUCAUCAAGAUUCACA	UCUUAGUUUUGAUGAUGUUUCAG	Cleavage
sly-miR172d-8-5p	Solyc08g061650.3.1	3.0	-1.0	1	23	2024	2046	GUGGAGCAUCAUCAAGAUUCACA	GAAGAAACUUGAUGGUGCUUCAA	Cleavage

sly-miR172d-8-5p	Solyc08g061635.1.1	3.0	-1.0	1	23	2420	2442	GUGGAGCAUCAUCAAGAUUCACA	GAAGAAACUUGAUGGUGCUUCAA	Cleavage
sly-miR172d-8-5p	Solyc09g090320.2.1	3.0	-1.0	1	23	993	1015	GUGGAGCAUCAUCAAGAUUCACA	UUUUAGUCUUGAUGGUGUUUCGU	Cleavage
sly-miR172d-8-5p	Solyc01g091350.3.1	3.0	-1.0	1	23	237	259	GUGGAGCAUCAUCAAGAUUCACA	UGAAGAUCUUGUUGAUGCUCUGC	Cleavage
sly-miR172d-8-5p	Solyc08g041668.1.1	3.0	-1.0	1	23	393	415	GUGGAGCAUCAUCAAGAUUCACA	UUCAAGUCUUGAUUAUGUUCCAU	Translation
sly-miR172d-8-5p	Solyc08g069010.3.1	3.0	-1.0	1	23	3351	3373	GUGGAGCAUCAUCAAGAUUCACA	UAGAGAUUUUGAUGAUGCUACAU	Cleavage
sly-miR172d-8-5p	Solyc12g056990.1.1	3.0	-1.0	1	23	633	655	GUGGAGCAUCAUCAAGAUUCACA	UUUUAGUCAUAAUGAUGCUCCAC	Cleavage
sly-miR172d-8-5p	Solyc01g050070.3.1	3.0	-1.0	1	23	792	814	GUGGAGCAUCAUCAAGAUUCACA	AUCCAAUUCUGAUGAUGCUCUAG	Cleavage
sly-miR172d-9-3p	Solyc01g105130.3.1	2.5	-1.0	1	21	214	234	AGAAUCUUAAUAGUGCUGCAU	AGCCCGCACUAUUAAGGUUCU	Cleavage
sly-miR172d-9-3p	Solyc02g088560.3.1	3.0	-1.0	1	21	1436	1456	AGAAUCUUAAUAGUGCUGCAU	AUCCGUCACUGUUAAGAUUCU	Cleavage
sly-miR172d-9-3p	Solyc11g013880.1.1	3.0	-1.0	1	21	613	632	AGAAUCUUAAUAGUGCUGCAU	AUGCAGC-CUAUUGGGAUUCU	Cleavage
sly-miR172d-9-3p	Solyc01g099760.3.1	3.0	-1.0	1	21	324	344	AGAAUCUUAAUAGUGCUGCAU	CGGCAACAUUGUUGAGAUUUU	Cleavage
sly-miR172d-9-5p	Solyc06g008730.3.1	2.0	-1.0	1	24	362	385	AAUGCAGCAUCAUCAAGAUUCACA	UGUUAAUUUUGAUGAUUCUGCAUU	Cleavage
sly-miR172d-9-5p	Solyc08g069010.3.1	2.0	-1.0	1	24	3351	3374	AAUGCAGCAUCAUCAAGAUUCACA	UAGAGAUUUUGAUGAUGCUACAUU	Cleavage
sly-miR172d-9-5p	Solyc05g013253.1.1	2.0	-1.0	1	24	1245	1268	AAUGCAGCAUCAUCAAGAUUCACA	UUCUCAUUUUGAUGAUGCUGUAUC	Cleavage
sly-miR172d-9-5p	Solyc04g015450.3.1	2.0	-1.0	1	24	2113	2136	AAUGCAGCAUCAUCAAGAUUCACA	AUUGCAACUUAAUGAUGCUGCAUU	Cleavage
sly-miR172d-9-5p	Solyc05g012770.3.1	2.5	-1.0	1	24	2237	2260	AAUGCAGCAUCAUCAAGAUUCACA	UGUGAAUCUGAAUGAUGUUGCAUU	Cleavage
sly-miR172d-9-5p	Solyc12g088640.2.1	2.5	-1.0	1	24	538	561	AAUGCAGCAUCAUCAAGAUUCACA	UCUCAAUCUUGAUGAUGCUGAAUC	Cleavage
sly-miR172d-9-5p	Solyc04g009730.3.1	3.0	-1.0	1	24	730	753	AAUGCAGCAUCAUCAAGAUUCACA	AGUGGAUUUUGAUGGUGUUGAAUU	Cleavage
sly-miR172d-9-5p	Solyc11g009080.2.1	3.0	-1.0	1	24	432	455	AAUGCAGCAUCAUCAAGAUUCACA	AGAGAAGCUUGGUGAGGCUGCAUU	Cleavage
sly-miR172d-9-5p	Solyc03g013308.1.1	3.0	-1.0	1	24	210	232	AAUGCAGCAUCAUCAAGAUUCACA	UCUAGAUCUUGAUG-UGCUGCAUU	Translation
sly-miR172d-9-5p	Solyc02g061810.3.1	3.0	-1.0	1	24	238	261	AAUGCAGCAUCAUCAAGAUUCACA	AAAUAGUGUUGGUGAUGCUGCAUC	Cleavage
sly-miR172d-9-5p	Solyc01g079060.3.1	3.0	-1.0	1	24	877	899	AAUGCAGCAUCAUCAAGAUUCACA	UCUAGAUCUUGAUG-UGCUGCAUU	Translation
sly-miR172d-9-5p	Solyc07g045380.3.1	3.0	-1.0	1	24	1788	1811	AAUGCAGCAUCAUCAAGAUUCACA	CCCAAAUGUUGAUGAUGCUAUAUU	Cleavage
sly-miR172d-9-5p	Solyc01g008740.2.1	3.0	-1.0	1	24	2343	2366	AAUGCAGCAUCAUCAAGAUUCACA	CACACCUCUUGAUAAUGCUGUAUU	Translation
sly-miR172d-9-5p	Solyc07g039570.3.1	3.0	-1.0	1	24	1024	1046	AAUGCAGCAUCAUCAAGAUUCACA	GUAGAAACU-GAUGAUGCUGCAUU	Cleavage
sly-miR172j-1-3p	Solyc11g072600.2.1	1.5	-1.0	1	19	1275	1293	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc04g049800.3.1	1.5	-1.0	1	19	1107	1125	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc03g044300.3.1	1.5	-1.0	1	19	1367	1385	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc09g007260.3.1	1.5	-1.0	1	19	1625	1643	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc02g093150.3.1	1.5	-1.0	1	19	1561	1579	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc02g064960.3.1	1.5	-1.0	1	19	1765	1783	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc10g084340.2.1	1.5	-1.0	1	19	2183	2201	GAAUCUUGAUGAUGCUCCA	UGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc11g065625.1.1	2.5	-1.0	1	19	1028	1046	GAAUCUUGAUGAUGCUCCA	UGGGGCAUCAUUAAGAAUC	Cleavage
sly-miR172j-1-3p	Solyc06g075510.3.1	2.5	-1.0	1	19	1349	1367	GAAUCUUGAUGAUGCUCCA	GGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-1-3p	Solyc03g113620.3.1	2.5	-1.0	1	19	862	880	GAAUCUUGAUGAUGCUCCA	UGGAUCAUCAUCAAUAUUC	Cleavage
sly-miR172j-1-3p	Solyc05g051050.3.1	2.5	-1.0	1	19	1340	1357	GAAUCUUGAUGAUGCUCCA	UGGAG-AUCAUCAAGAUUU	Cleavage
sly-miR172j-1-3p	Solyc03g026020.3.1	3.0	-1.0	1	19	1488	1506	GAAUCUUGAUGAUGCUCCA	UGGAGCAUUGUCAUGAUUU	Cleavage
sly-miR172j-1-3p	Solyc01g104310.3.1	3.0	-1.0	1	19	1770	1788	GAAUCUUGAUGAUGCUCCA	UGGAGUAUUAUUGGGGUUC	Cleavage
sly-miR172j-1-3p	Solyc03g006550.3.1	3.0	-1.0	1	19	810	828	GAAUCUUGAUGAUGCUCCA	UGGAGUGUCUUCAAGAUUU	Translation
sly-miR172j-1-3p	Solyc10g083090.1.1	3.0	-1.0	1	19	387	405	GAAUCUUGAUGAUGCUCCA	AGGAUCAUCAUCAAGAUUG	Cleavage
sly-miR172j-1-3p	Solyc12g088460.2.1	3.0	-1.0	1	19	1140	1158	GAAUCUUGAUGAUGCUCCA	UGGAGAGUCAUCAAGGUUA	Cleavage
sly-miR172j-1-3p	Solyc10g081170.2.1	3.0	-1.0	1	19	1434	1452	GAAUCUUGAUGAUGCUCCA	AGGGGAAUCAUCAAGAUUU	Cleavage
sly-miR172j-1-3p	Solyc03g046240.1.1	3.0	-1.0	1	19	31	49	GAAUCUUGAUGAUGCUCCA	UGGGAUAUCAUCGAGGUUC	Cleavage
sly-miR172j-1-3p	Solyc05g044540.2.1	3.0	-1.0	1	19	266	284	GAAUCUUGAUGAUGCUCCA	UGGAGAAUCACCAAGAUUU	Cleavage
sly-miR172j-1-3p	Solyc12g006240.2.1	3.0	-1.0	1	19	2012	2030	GAAUCUUGAUGAUGCUCCA	UGGAGAGUGAUCAAGAUUC	Translation
sly-miR172j-1-3p	Solyc02g023950.3.1	3.0	-1.0	1	19	3929	3947	GAAUCUUGAUGAUGCUCCA	UGAGGCAUCAUCAACAUUC	Cleavage
sly-miR172j-1-3p	Solyc05g008450.3.1	3.0	-1.0	1	19	1299	1317	GAAUCUUGAUGAUGCUCCA	UGAAGGAUCAUUAAGGUUC	Cleavage
sly-miR172j-1-3p	Solyc01g106460.3.1	3.0	-1.0	1	19	1066	1084	GAAUCUUGAUGAUGCUCCA	UGGUUUGUCAUCAAGAUUC	Cleavage
sly-miR172j-1-3p	Solyc04g015600.3.1	3.0	-1.0	1	19	658	676	GAAUCUUGAUGAUGCUCCA	UGGUUUGUCAUCAAGAUUC	Cleavage
sly-miR172j-1-5p	Solyc09g011020.3.1	1.5	-1.0	1	21	982	1002	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUUUUGAUGAUGCUGA	Cleavage

sly-miR172j-1-5p	Solyc05g047420.3.1	2.5	-1.0	1	21	608	628	GCAGCAUCAUCAAGAUUCCCA	AGGUAAUCUUGUUGAUGCUGC	Translation
sly-miR172j-1-5p	Solyc02g091120.3.1	2.5	-1.0	1	21	2854	2874	GCAGCAUCAUCAAGAUUCCCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
sly-miR172j-1-5p	Solyc02g077380.2.1	2.5	-1.0	1	21	1044	1064	GCAGCAUCAUCAAGAUUCCCA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
sly-miR172j-1-5p	Solyc02g078640.3.1	2.5	-1.0	1	21	842	862	GCAGCAUCAUCAAGAUUCCCA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
sly-miR172j-1-5p	Solyc12g013580.2.1	2.5	-1.0	1	21	1867	1887	GCAGCAUCAUCAAGAUUCCCA	UUGAAAUCUUGGUGAUGCUGG	Cleavage
sly-miR172j-1-5p	Solyc04g009990.3.1	2.5	-1.0	1	21	1464	1484	GCAGCAUCAUCAAGAUUCCCA	UAGGAACCUUGGUGAUGCUGA	Cleavage
sly-miR172j-1-5p	Solyc09g089865.1.1	2.5	-1.0	1	21	87	107	GCAGCAUCAUCAAGAUUCCCA	AUGGAUUCUUUAUGAUGCUGC	Translation
sly-miR172j-1-5p	Solyc10g081240.2.1	3.0	-1.0	1	21	36	56	GCAGCAUCAUCAAGAUUCCCA	GGGGAGUUUAGAUGGUGCUGC	Cleavage
sly-miR172j-1-5p	Solyc08g082980.2.1	3.0	-1.0	1	21	1488	1508	GCAGCAUCAUCAAGAUUCCCA	GGGGAGUCUAGGUGAUGCUGU	Cleavage
sly-miR172j-1-5p	Solyc12g088640.2.1	3.0	-1.0	1	21	538	558	GCAGCAUCAUCAAGAUUCCCA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
sly-miR172j-1-5p	Solyc02g014355.1.1	3.0	-1.0	1	21	174	194	GCAGCAUCAUCAAGAUUCCCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
sly-miR172j-1-5p	Solyc01g105510.3.1	3.0	-1.0	1	21	1675	1695	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUAUUGAUGAUGCAGU	Cleavage
sly-miR172j-1-5p	Solyc04g082610.3.1	3.0	-1.0	1	21	2713	2733	GCAGCAUCAUCAAGAUUCCCA	CGGGAAAUUUGAUGGUGUUGU	Cleavage
sly-miR172j-1-5p	Solyc11g040120.2.1	3.0	-1.0	1	21	560	580	GCAGCAUCAUCAAGAUUCCCA	AAGGAAUUUUGAUGAUACUGA	Cleavage
sly-miR172j-1-5p	Solyc08g080670.1.1	3.0	-1.0	1	21	216	236	GCAGCAUCAUCAAGAUUCCCA	UUGCAAUUUUGAUGGUGCUGG	Cleavage
sly-miR172j-1-5p	Solyc05g010810.1.1	3.0	-1.0	1	21	966	986	GCAGCAUCAUCAAGAUUCCCA	UAGGAAGCUUGAUGGUGUUGG	Cleavage
sly-miR172j-1-5p	Solyc00g017870.1.1	3.0	-1.0	1	21	111	131	GCAGCAUCAUCAAGAUUCCCA	GAUGAAGCUUGAUGAUGUUGU	Cleavage
sly-miR172j-1-5p	Solyc11g013050.1.1	3.0	-1.0	1	21	719	739	GCAGCAUCAUCAAGAUUCCCA	GAGGGAUGUUGAUGAUGAUGC	Cleavage
sly-miR172j-1-5p	Solyc01g087420.3.1	3.0	-1.0	1	21	1955	1975	GCAGCAUCAUCAAGAUUCCCA	GAGAAAUCUUGAGGAUGCUGU	Cleavage
sly-miR172j-1-5p	Solyc03g007780.1.1	3.0	-1.0	1	21	29	49	GCAGCAUCAUCAAGAUUCCCA	UAGCAAUGUUGAUGAUGCUGA	Cleavage
sly-miR172j-1-5p	Solyc06g084410.3.1	3.0	-1.0	1	21	374	394	GCAGCAUCAUCAAGAUUCCCA	UUGAAACCUUGAUGAUGCUGG	Cleavage
sly-miR172j-2-3p	Solyc11g072600.2.1	1.0	-1.0	1	20	1274	1293	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc04g049800.3.1	1.0	-1.0	1	20	1106	1125	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc03g044300.3.1	1.0	-1.0	1	20	1366	1385	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc09g007260.3.1	1.0	-1.0	1	20	1624	1643	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc02g093150.3.1	1.0	-1.0	1	20	1560	1579	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc02g064960.3.1	1.0	-1.0	1	20	1764	1783	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc10g084340.2.1	1.0	-1.0	1	20	2182	2201	GAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc06g075510.3.1	2.0	-1.0	1	20	1348	1367	GAAUCUUGAUGAUGUUGCAU	CGGCAGCAUCAUCAGGAUUC	Cleavage
sly-miR172j-2-3p	Solyc01g096175.1.1	2.0	-1.0	1	20	306	325	GAAUCUUGAUGAUGUUGCAU	GUACAACAUCAUCAAGGUUU	Cleavage
sly-miR172j-2-3p	Solyc01g090460.3.1	2.5	-1.0	1	20	385	404	GAAUCUUGAUGAUGUUGCAU	AUGCAUCAUCAUCAAGUUUC	Cleavage
sly-miR172j-2-3p	Solyc02g089263.1.1	2.5	-1.0	1	20	3455	3474	GAAUCUUGAUGAUGUUGCAU	UGGCUAUAUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc12g044220.2.1	2.5	-1.0	1	20	101	120	GAAUCUUGAUGAUGUUGCAU	UUGCAAAAUCAUCAAAAUUC	Cleavage
sly-miR172j-2-3p	Solyc11g050907.1.1	3.0	-1.0	1	20	276	295	GAAUCUUGAUGAUGUUGCAU	AUGCAACGUCAUUAAUAUUU	Cleavage
sly-miR172j-2-3p	Solyc05g052560.1.1	3.0	-1.0	1	20	99	118	GAAUCUUGAUGAUGUUGCAU	CGAAAACAUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc01g044520.2.1	3.0	-1.0	1	20	570	589	GAAUCUUGAUGAUGUUGCAU	AAGCAACAUCAUCAAGGUGC	Cleavage
sly-miR172j-2-3p	Solyc12g014140.2.1	3.0	-1.0	1	20	254	273	GAAUCUUGAUGAUGUUGCAU	GUGUAACAUCGUCAAAAUUU	Cleavage
sly-miR172j-2-3p	Solyc01g096240.3.1	3.0	-1.0	1	20	1392	1411	GAAUCUUGAUGAUGUUGCAU	CAACAAUGUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc07g063770.3.1	3.0	-1.0	1	20	2065	2084	GAAUCUUGAUGAUGUUGCAU	AUGUAUCUUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc10g006710.3.1	3.0	-1.0	1	20	1980	1999	GAAUCUUGAUGAUGUUGCAU	AUGUACCUUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc07g018130.2.1	3.0	-1.0	1	20	2993	3012	GAAUCUUGAUGAUGUUGCAU	GUGCAAUAUCAUCAGUGUUC	Cleavage
sly-miR172j-2-3p	Solyc02g092920.3.1	3.0	-1.0	1	20	1367	1386	GAAUCUUGAUGAUGUUGCAU	UUGCAACAUUAUCGAGCUUU	Cleavage
sly-miR172j-2-3p	Solyc09g007700.3.1	3.0	-1.0	1	20	47	66	GAAUCUUGAUGAUGUUGCAU	CAUCAUCAUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc03g046240.1.1	3.0	-1.0	1	20	30	49	GAAUCUUGAUGAUGUUGCAU	UUGGGAUAUCAUCGAGGUUC	Cleavage
sly-miR172j-2-3p	Solyc03g006660.3.1	3.0	-1.0	1	20	1291	1310	GAAUCUUGAUGAUGUUGCAU	UUGCAAAAUUGUCAGGGUUC	Cleavage
sly-miR172j-2-3p	Solyc06g074640.2.1	3.0	-1.0	1	20	4460	4479	GAAUCUUGAUGAUGUUGCAU	UUGAAAUAUCAUCAGGGUUU	Cleavage
sly-miR172j-2-3p	Solyc03g006770.3.1	3.0	-1.0	1	20	2165	2184	GAAUCUUGAUGAUGUUGCAU	CUGUAUCUUCAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc07g062200.2.1	3.0	-1.0	1	20	622	641	GAAUCUUGAUGAUGUUGCAU	CUUCAAAGUUAUCAAGAUUC	Cleavage
sly-miR172j-2-3p	Solyc03g122230.2.1	3.0	-1.0	1	20	1604	1623	GAAUCUUGAUGAUGUUGCAU	CUGUUUCAUUAUCAAGAUUC	Cleavage
sly-miR172j-2-5p	Solyc09g011020.3.1	1.5	-1.0	1	21	982	1002	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUUUUGAUGAUGCUGA	Cleavage

sly-miR172j-2-5p	Solyc05g047420.3.1	2.5	-1.0	1	21	608	628	GCAGCAUCAUCAAGAUUCCCA	AGGUAAUCUUGUUGAUGCUGC	Translation
sly-miR172j-2-5p	Solyc02g091120.3.1	2.5	-1.0	1	21	2854	2874	GCAGCAUCAUCAAGAUUCCCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
sly-miR172j-2-5p	Solyc02g077380.2.1	2.5	-1.0	1	21	1044	1064	GCAGCAUCAUCAAGAUUCCCA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
sly-miR172j-2-5p	Solyc02g078640.3.1	2.5	-1.0	1	21	842	862	GCAGCAUCAUCAAGAUUCCCA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
sly-miR172j-2-5p	Solyc12g013580.2.1	2.5	-1.0	1	21	1867	1887	GCAGCAUCAUCAAGAUUCCCA	UUGAAAUCUUGGUGAUGCUGG	Cleavage
sly-miR172j-2-5p	Solyc04g009990.3.1	2.5	-1.0	1	21	1464	1484	GCAGCAUCAUCAAGAUUCCCA	UAGGAACCUUGGUGAUGCUGA	Cleavage
sly-miR172j-2-5p	Solyc09g089865.1.1	2.5	-1.0	1	21	87	107	GCAGCAUCAUCAAGAUUCCCA	AUGGAUUCUUUAUGAUGCUGC	Translation
sly-miR172j-2-5p	Solyc10g081240.2.1	3.0	-1.0	1	21	36	56	GCAGCAUCAUCAAGAUUCCCA	GGGGAGUUUAGAUGGUGCUGC	Cleavage
sly-miR172j-2-5p	Solyc08g082980.2.1	3.0	-1.0	1	21	1488	1508	GCAGCAUCAUCAAGAUUCCCA	GGGGAGUCUAGGUGAUGCUGU	Cleavage
sly-miR172j-2-5p	Solyc12g088640.2.1	3.0	-1.0	1	21	538	558	GCAGCAUCAUCAAGAUUCCCA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
sly-miR172j-2-5p	Solyc02g014355.1.1	3.0	-1.0	1	21	174	194	GCAGCAUCAUCAAGAUUCCCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
sly-miR172j-2-5p	Solyc01g105510.3.1	3.0	-1.0	1	21	1675	1695	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUAUUGAUGAUGCAGU	Cleavage
sly-miR172j-2-5p	Solyc04g082610.3.1	3.0	-1.0	1	21	2713	2733	GCAGCAUCAUCAAGAUUCCCA	CGGGAAAUUUGAUGGUGUUGU	Cleavage
sly-miR172j-2-5p	Solyc11g040120.2.1	3.0	-1.0	1	21	560	580	GCAGCAUCAUCAAGAUUCCCA	AAGGAAUUUUGAUGAUACUGA	Cleavage
sly-miR172j-2-5p	Solyc08g080670.1.1	3.0	-1.0	1	21	216	236	GCAGCAUCAUCAAGAUUCCCA	UUGCAAUUUUGAUGGUGCUGG	Cleavage
sly-miR172j-2-5p	Solyc05g010810.1.1	3.0	-1.0	1	21	966	986	GCAGCAUCAUCAAGAUUCCCA	UAGGAAGCUUGAUGGUGUUGG	Cleavage
sly-miR172j-2-5p	Solyc00g017870.1.1	3.0	-1.0	1	21	111	131	GCAGCAUCAUCAAGAUUCCCA	GAUGAAGCUUGAUGAUGUUGU	Cleavage
sly-miR172j-2-5p	Solyc11g013050.1.1	3.0	-1.0	1	21	719	739	GCAGCAUCAUCAAGAUUCCCA	GAGGGAUGUUGAUGAUGAUGC	Cleavage
sly-miR172j-2-5p	Solyc01g087420.3.1	3.0	-1.0	1	21	1955	1975	GCAGCAUCAUCAAGAUUCCCA	GAGAAAUCUUGAGGAUGCUGU	Cleavage
sly-miR172j-2-5p	Solyc03g007780.1.1	3.0	-1.0	1	21	29	49	GCAGCAUCAUCAAGAUUCCCA	UAGCAAUGUUGAUGAUGCUGA	Cleavage
sly-miR172j-2-5p	Solyc06g084410.3.1	3.0	-1.0	1	21	374	394	GCAGCAUCAUCAAGAUUCCCA	UUGAAACCUUGAUGAUGCUGG	Cleavage
sly-miR1886a	Solyc07g055625.1.1	2.5	-1.0	1	24	80	103	AUGGUAUCGUGAGAUGAAAUCAGC	AUAGCAUUCAUUUCACGGUACUAU	Cleavage
sly-miR1886a	Solyc08g077060.3.1	3.0	-1.0	1	24	847	870	AUGGUAUCGUGAGAUGAAAUCAGC	AUUGUUUUCAUCUUGGGAUGCCAU	Cleavage
sly-miR1886a	Solyc01g011350.3.1	3.0	-1.0	1	24	3375	3398	AUGGUAUCGUGAGAUGAAAUCAGC	UUUAAUUUUGUAUCAUGAUACCAU	Cleavage
sly-miR1886a	Solyc07g039210.3.1	3.0	-1.0	1	24	184	206	AUGGUAUCGUGAGAUGAAAUCAGC	GCUG-UUUCAUCUCAAGAUGCCAA	Cleavage
sly-miR1886a	Solyc07g007775.1.1	3.0	-1.0	1	24	1210	1233	AUGGUAUCGUGAGAUGAAAUCAGC	GAUGUUUUCAUUUUACAAUACUAU	Cleavage
sly-miR1886a	Solyc07g007770.2.1	3.0	-1.0	1	24	1648	1671	AUGGUAUCGUGAGAUGAAAUCAGC	GAUGUUUUCAUUUUACAAUACUAU	Cleavage
sly-miR1886a	Solyc11g005080.1.1	3.0	-1.0	1	24	45	68	AUGGUAUCGUGAGAUGAAAUCAGC	CUUUGUUUCAUCCCAUGAUACCAG	Cleavage
sly-miR1886a	Solyc06g083580.3.1	3.0	-1.0	1	24	2436	2459	AUGGUAUCGUGAGAUGAAAUCAGC	CAAAAUUUUAUCUCAUGGUAUCAG	Cleavage
sly-miR1886a	Solyc01g073750.3.1	3.0	-1.0	1	24	145	168	AUGGUAUCGUGAGAUGAAAUCAGC	AAGAAUUUCAUUUCUCGGUAUCAU	Translation
sly-miR1886a	Solyc01g028805.1.1	3.0	-1.0	1	24	542	565	AUGGUAUCGUGAGAUGAAAUCAGC	GCUUUUCUCAUCUCACGAUCUCAU	Cleavage
sly-miR1886a	Solyc04g074090.3.1	3.0	-1.0	1	24	3700	3723	AUGGUAUCGUGAGAUGAAAUCAGC	UUACAAAUCAUUUCAUGAUACCAU	Cleavage
sly-miR1886a	Solyc05g012920.2.1	3.0	-1.0	1	24	5	28	AUGGUAUCGUGAGAUGAAAUCAGC	GUGAAUUUGAUCUCAUGAUACAAU	Cleavage
sly-miR1886a	Solyc06g053653.1.1	3.0	-1.0	1	24	796	819	AUGGUAUCGUGAGAUGAAAUCAGC	GCAUCUUUCGUCUUAUGAUAUCAC	Cleavage
sly-miR1886a	Solyc08g067150.3.1	3.0	-1.0	1	24	287	310	AUGGUAUCGUGAGAUGAAAUCAGC	GUUUUUUUUUUAUCACGAUACCAU	Cleavage
sly-miR1886a	Solyc07g009520.2.1	3.0	-1.0	1	24	1480	1503	AUGGUAUCGUGAGAUGAAAUCAGC	UAAAAUGUGAUCUCACGAUACCAG	Cleavage
sly-miR1886h-1	Solyc12g094670.1.1	1.5	-1.0	1	24	202	225	AUUUUACGUUGAUUUCAUCUCAUG	GUAUUGAUGAAAUCAACGGAAAAU	Cleavage
sly-miR1886h-1	Solyc02g092350.3.1	1.5	-1.0	1	24	2793	2816	AUUUUACGUUGAUUUCAUCUCAUG	GAAAUGUUGAAAUCAAUGUAAAAU	Cleavage
sly-miR1886h-1	Solyc02g092350.3.1	1.5	-1.0	1	24	2860	2883	AUUUUACGUUGAUUUCAUCUCAUG	GAAAUGUUGAAAUCAAUGUAAAAU	Cleavage
sly-miR1886h-1	Solyc10g047240.2.1	2.5	-1.0	1	24	503	526	AUUUUACGUUGAUUUCAUCUCAUG	CAGGCGAUGAAAUCGAUGUAAAGC	Cleavage
sly-miR1886h-1	Solyc03g120805.1.1	2.5	-1.0	1	24	71	94	AUUUUACGUUGAUUUCAUCUCAUG	ACGUUGAUGAUAUCAAUGUGAAGU	Cleavage
sly-miR1886h-1	Solyc02g082340.3.1	2.5	-1.0	1	24	82	105	AUUUUACGUUGAUUUCAUCUCAUG	UCCCCGACGAAAUCAAAGUAAAAU	Cleavage
sly-miR1886h-1	Solyc03g119740.3.1	3.0	-1.0	1	24	944	967	AUUUUACGUUGAUUUCAUCUCAUG	UAAGAGAUGAGAUAGAUGUAAAAU	Translation
sly-miR1886h-1	Solyc07g066420.3.1	3.0	-1.0	1	24	1634	1658	AUUUUACGUUGAUUUCAUCU-CAUG	CAUGCAGAUGAAGUUAGGGUAAAAU	Cleavage
sly-miR1886h-1	Solyc12g088240.2.1	3.0	-1.0	1	24	739	762	AUUUUACGUUGAUUUCAUCUCAUG	UUUGAGCUAAAAUCGACGUAAAGU	Cleavage
sly-miR1886h-1	Solyc12g063050.2.1	3.0	-1.0	1	24	2676	2699	AUUUUACGUUGAUUUCAUCUCAUG	CGUUGGAUUAGAUCAAUGUAAAAC	Cleavage
sly-miR1886h-1	Solyc06g064840.3.1	3.0	-1.0	1	24	1843	1866	AUUUUACGUUGAUUUCAUCUCAUG	GUAGAGAUGAUAUCAUCGUGAAAU	Cleavage
sly-miR1886h-1	Solyc02g067640.3.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
sly-miR1886h-1	Solyc02g067650.3.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
sly-miR1886h-1	Solyc02g067630.3.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation

sly-miR1886h-1	Solyc11g020660.1.1	3.0	-1.0	1	24	284	307	AUUUUACGUUGAUUUCAUCUCAUG	AGGCUGAUGCAAUCAAUGUAGAAA	Cleavage
sly-miR1886h-1	Solyc10g054870.2.1	3.0	-1.0	1	24	1443	1466	AUUUUACGUUGAUUUCAUCUCAUG	UCACGGGUGAAAUCAGCGUGGAAC	Cleavage
sly-miR1886h-1	Solyc04g054880.3.1	3.0	-1.0	1	24	216	239	AUUUUACGUUGAUUUCAUCUCAUG	AUAAAGAGGAAAUGAACGUAAAGU	Translation
sly-miR1886h-1	Solyc01g111120.3.1	3.0	-1.0	1	24	519	542	AUUUUACGUUGAUUUCAUCUCAUG	UCACUGGUGAAAUCAGUGUAGAAC	Cleavage
sly-miR1886h-1	Solyc03g111260.3.1	3.0	-1.0	1	24	2162	2185	AUUUUACGUUGAUUUCAUCUCAUG	UGGCUGAUGAAAUCAAUGGAAAAC	Cleavage
sly-miR1886h-1	Solyc11g008570.2.1	3.0	-1.0	1	24	516	539	AUUUUACGUUGAUUUCAUCUCAUG	AACACUAUGAAAUCAAUAUAAAAU	Cleavage
sly-miR1886h-1	Solyc08g067620.2.1	3.0	-1.0	1	24	850	873	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUUAUGAAGUCAGCGUGGAAU	Cleavage
sly-miR1886h-1	Solyc08g067610.3.1	3.0	-1.0	1	24	890	913	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUCAUGAAGUCAGCGUGGAAU	Cleavage
sly-miR1886h-1	Solyc01g091660.3.1	3.0	-1.0	1	24	1034	1057	AUUUUACGUUGAUUUCAUCUCAUG	UCUAUGAUGAAGUUAAUGUAAACU	Cleavage
sly-miR1886h-2	Solyc12g094670.1.1	1.5	-1.0	1	24	202	225	AUUUUACGUUGAUUUCAUCUCAUG	GUAUUGAUGAAAUCAACGGAAAAU	Cleavage
sly-miR1886h-2	Solyc02g092350.3.1	1.5	-1.0	1	24	2793	2816	AUUUUACGUUGAUUUCAUCUCAUG	GAAAUGUUGAAAUCAAUGUAAAAU	Cleavage
sly-miR1886h-2	Solyc02g092350.3.1	1.5	-1.0	1	24	2860	2883	AUUUUACGUUGAUUUCAUCUCAUG	GAAAUGUUGAAAUCAAUGUAAAAU	Cleavage
sly-miR1886h-2	Solyc10g047240.2.1	2.5	-1.0	1	24	503	526	AUUUUACGUUGAUUUCAUCUCAUG	CAGGCGAUGAAAUCGAUGUAAAGC	Cleavage
sly-miR1886h-2	Solyc03g120805.1.1	2.5	-1.0	1	24	71	94	AUUUUACGUUGAUUUCAUCUCAUG	ACGUUGAUGAUAUCAAUGUGAAGU	Cleavage
sly-miR1886h-2	Solyc02g082340.3.1	2.5	-1.0	1	24	82	105	AUUUUACGUUGAUUUCAUCUCAUG	UCCCCGACGAAAUCAAAGUAAAAU	Cleavage
sly-miR1886h-2	Solyc03g119740.3.1	3.0	-1.0	1	24	944	967	AUUUUACGUUGAUUUCAUCUCAUG	UAAGAGAUGAGAUAGAUGUAAAAU	Translation
sly-miR1886h-2	Solyc07g066420.3.1	3.0	-1.0	1	24	1634	1658	AUUUUACGUUGAUUUCAUCU-CAUG	CAUGCAGAUGAAGUUAGGGUAAAAU	Cleavage
sly-miR1886h-2	Solyc12g088240.2.1	3.0	-1.0	1	24	739	762	AUUUUACGUUGAUUUCAUCUCAUG	UUUGAGCUAAAAUCGACGUAAAGU	Cleavage
sly-miR1886h-2	Solyc12g063050.2.1	3.0	-1.0	1	24	2676	2699	AUUUUACGUUGAUUUCAUCUCAUG	CGUUGGAUUAGAUCAAUGUAAAAC	Cleavage
sly-miR1886h-2	Solyc06g064840.3.1	3.0	-1.0	1	24	1843	1866	AUUUUACGUUGAUUUCAUCUCAUG	GUAGAGAUGAUAUCAUCGUGAAAU	Cleavage
sly-miR1886h-2	Solyc02g067640.3.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
sly-miR1886h-2	Solyc02g067650.3.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
sly-miR1886h-2	Solyc02g067630.3.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
sly-miR1886h-2	Solyc11g020660.1.1	3.0	-1.0	1	24	284	307	AUUUUACGUUGAUUUCAUCUCAUG	AGGCUGAUGCAAUCAAUGUAGAAA	Cleavage
sly-miR1886h-2	Solyc10g054870.2.1	3.0	-1.0	1	24	1443	1466	AUUUUACGUUGAUUUCAUCUCAUG	UCACGGGUGAAAUCAGCGUGGAAC	Cleavage
sly-miR1886h-2	Solyc04g054880.3.1	3.0	-1.0	1	24	216	239	AUUUUACGUUGAUUUCAUCUCAUG	AUAAAGAGGAAAUGAACGUAAAGU	Translation
sly-miR1886h-2	Solyc01g111120.3.1	3.0	-1.0	1	24	519	542	AUUUUACGUUGAUUUCAUCUCAUG	UCACUGGUGAAAUCAGUGUAGAAC	Cleavage
sly-miR1886h-2	Solyc03g111260.3.1	3.0	-1.0	1	24	2162	2185	AUUUUACGUUGAUUUCAUCUCAUG	UGGCUGAUGAAAUCAAUGGAAAAC	Cleavage
sly-miR1886h-2	Solyc11g008570.2.1	3.0	-1.0	1	24	516	539	AUUUUACGUUGAUUUCAUCUCAUG	AACACUAUGAAAUCAAUAUAAAAU	Cleavage
sly-miR1886h-2	Solyc08g067620.2.1	3.0	-1.0	1	24	850	873	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUUAUGAAGUCAGCGUGGAAU	Cleavage
sly-miR1886h-2	Solyc08g067610.3.1	3.0	-1.0	1	24	890	913	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUCAUGAAGUCAGCGUGGAAU	Cleavage
sly-miR1886h-2	Solyc01g091660.3.1	3.0	-1.0	1	24	1034	1057	AUUUUACGUUGAUUUCAUCUCAUG	UCUAUGAUGAAGUUAAUGUAAACU	Cleavage
sly-miR1917-1	Solyc02g071710.2.1	0.0	-1.0	1	21	1564	1584	AUUAAUAAAGAGUGCUAAAGU	AUUUUAGCACUCUUUAUUAAU	Cleavage
sly-miR1917-1	Solyc10g085570.3.1	1.0	-1.0	1	21	2789	2809	AUUAAUAAAGAGUGCUAAAGU	UCUUUGGCAUUCUUUAUUAAU	Cleavage
sly-miR1917-1	Solyc09g009090.3.1	1.5	-1.0	1	21	2728	2748	AUUAAUAAAGAGUGCUAAAGU	UAUUUGGCAUUCUUUGUUAAU	Cleavage
sly-miR1917-1	Solyc12g035555.1.1	2.5	-1.0	1	21	2395	2415	AUUAAUAAAGAGUGCUAAAGU	AUUUUGGGGCUUUUUAUUAAU	Cleavage
sly-miR1917-1	Solyc07g054930.3.1	2.5	-1.0	1	21	1395	1415	AUUAAUAAAGAGUGCUAAAGU	UUUUUAGCAGUUUUUGUUAAU	Cleavage
sly-miR1917-1	Solyc04g005680.3.1	2.5	-1.0	1	21	473	493	AUUAAUAAAGAGUGCUAAAGU	UUUUAGGGACUCUUUAUUAAU	Cleavage
sly-miR1917-1	Solyc04g009435.1.1	3.0	-1.0	1	21	20	40	AUUAAUAAAGAGUGCUAAAGU	AUUUUAGUAUUUUUUAUAAAU	Cleavage
sly-miR1917-1	Solyc07g018250.1.1	3.0	-1.0	1	21	757	777	AUUAAUAAAGAGUGCUAAAGU	CUUUUAGUGCUCUUUCUUGAU	Cleavage
sly-miR1917-1	Solyc10g038130.2.1	3.0	-1.0	1	21	241	261	AUUAAUAAAGAGUGCUAAAGU	UUUUUAGUAUUGUUUGUUAAU	Translation
sly-miR1917-1	Solyc11g010550.2.1	3.0	-1.0	1	21	1319	1339	AUUAAUAAAGAGUGCUAAAGU	UCGUUGGCACUUUUUAUUGGU	Cleavage
sly-miR1917-1	Solyc06g063085.1.1	3.0	-1.0	1	21	744	764	AUUAAUAAAGAGUGCUAAAGU	AAUUUAGUAUUUUUUUUUAAU	Cleavage
sly-miR1917-1	Solyc11g008130.2.1	3.0	-1.0	1	21	793	812	AUUAAUAAAGAGUGCUAAAGU	GCUUUAG-GCUUUUUAUUAAU	Cleavage
sly-miR1917-1	Solyc11g020180.2.1	3.0	-1.0	1	21	2788	2807	AUUAAUAAAGAGUGCUAAAGU	GCUUUAG-GCUUUUUAUUAAU	Cleavage
sly-miR1917-1	Solyc03g116930.3.1	3.0	-1.0	1	21	2198	2218	AUUAAUAAAGAGUGCUAAAGU	UCGUUAACAUUCUUUGUUAAU	Cleavage
sly-miR1917-1	Solyc07g061960.3.1	3.0	-1.0	1	21	36	56	AUUAAUAAAGAGUGCUAAAGU	UUUUUAAAAUUUUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc02g071710.2.1	0.0	-1.0	1	21	1564	1584	AUUAAUAAAGAGUGCUAAAGU	AUUUUAGCACUCUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc10g085570.3.1	1.0	-1.0	1	21	2789	2809	AUUAAUAAAGAGUGCUAAAGU	UCUUUGGCAUUCUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc09g009090.3.1	1.5	-1.0	1	21	2728	2748	AUUAAUAAAGAGUGCUAAAGU	UAUUUGGCAUUCUUUGUUAAU	Cleavage

sly-miR1917-2	Solyc12g035555.1.1	2.5	-1.0	1	21	2395	2415	AUUAAUAAAGAGUGCUAAAGU	AUUUUGGGGCUUUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc07g054930.3.1	2.5	-1.0	1	21	1395	1415	AUUAAUAAAGAGUGCUAAAGU	UUUUUAGCAGUUUUUGUUAAU	Cleavage
sly-miR1917-2	Solyc04g005680.3.1	2.5	-1.0	1	21	473	493	AUUAAUAAAGAGUGCUAAAGU	UUUUAGGGACUCUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc04g009435.1.1	3.0	-1.0	1	21	20	40	AUUAAUAAAGAGUGCUAAAGU	AUUUUAGUAUUUUUUAUAAAU	Cleavage
sly-miR1917-2	Solyc07g018250.1.1	3.0	-1.0	1	21	757	777	AUUAAUAAAGAGUGCUAAAGU	CUUUUAGUGCUCUUUCUUGAU	Cleavage
sly-miR1917-2	Solyc10g038130.2.1	3.0	-1.0	1	21	241	261	AUUAAUAAAGAGUGCUAAAGU	UUUUUAGUAUUGUUUGUUAAU	Translation
sly-miR1917-2	Solyc11g010550.2.1	3.0	-1.0	1	21	1319	1339	AUUAAUAAAGAGUGCUAAAGU	UCGUUGGCACUUUUUAUUGGU	Cleavage
sly-miR1917-2	Solyc06g063085.1.1	3.0	-1.0	1	21	744	764	AUUAAUAAAGAGUGCUAAAGU	AAUUUAGUAUUUUUUUUUAAU	Cleavage
sly-miR1917-2	Solyc11g008130.2.1	3.0	-1.0	1	21	793	812	AUUAAUAAAGAGUGCUAAAGU	GCUUUAG-GCUUUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc11g020180.2.1	3.0	-1.0	1	21	2788	2807	AUUAAUAAAGAGUGCUAAAGU	GCUUUAG-GCUUUUUAUUAAU	Cleavage
sly-miR1917-2	Solyc03g116930.3.1	3.0	-1.0	1	21	2198	2218	AUUAAUAAAGAGUGCUAAAGU	UCGUUAACAUUCUUUGUUAAU	Cleavage
sly-miR1917-2	Solyc07g061960.3.1	3.0	-1.0	1	21	36	56	AUUAAUAAAGAGUGCUAAAGU	UUUUUAAAAUUUUUUAUUAAU	Cleavage
sly-miR1918	Solyc09g065430.3.1	1.5	-1.0	1	22	702	723	UGUUGGUGAGAGUUCGAUUCUC	GAGAAUCGAACUCUCACAAACA	Cleavage
sly-miR1918	Solyc01g095820.2.1	1.5	-1.0	1	22	553	574	UGUUGGUGAGAGUUCGAUUCUC	AGGAAUCGAACUCUCACGAACA	Cleavage
sly-miR1918	Solyc11g012700.2.1	1.5	-1.0	1	22	430	451	UGUUGGUGAGAGUUCGAUUCUC	AACAGUGGAACUCUCACCAACA	Cleavage
sly-miR1918	Solyc10g045620.2.1	2.0	-1.0	1	22	23	44	UGUUGGUGAGAGUUCGAUUCUC	GGGAAUCGAAUCCUCACCAACA	Translation
sly-miR1918	Solyc01g104620.3.1	2.0	-1.0	1	22	67	88	UGUUGGUGAGAGUUCGAUUCUC	UGGAAUCAAACUCUUAUCAACA	Cleavage
sly-miR1918	Solyc01g044520.2.1	2.0	-1.0	1	22	987	1008	UGUUGGUGAGAGUUCGAUUCUC	GAAAAUUAAACUCUCAUCAACA	Cleavage
sly-miR1918	Solyc06g068090.3.1	2.0	-1.0	1	22	285	306	UGUUGGUGAGAGUUCGAUUCUC	GUAGAUCGAACUCUCGUUAACA	Cleavage
sly-miR1918	Solyc09g066500.3.1	2.0	-1.0	1	22	272	293	UGUUGGUGAGAGUUCGAUUCUC	GGUAAGUGAAUUCUCACCAACA	Cleavage
sly-miR1918	Solyc12g013710.2.1	2.5	-1.0	1	22	1445	1466	UGUUGGUGAGAGUUCGAUUCUC	UAGAAUCGAGCGCUUACCAACA	Translation
sly-miR1918	Solyc10g054100.2.1	2.5	-1.0	1	22	329	350	UGUUGGUGAGAGUUCGAUUCUC	CGGAAUCGAACUCUUGUCAAUG	Cleavage
sly-miR1918	Solyc01g105180.3.1	2.5	-1.0	1	22	1915	1936	UGUUGGUGAGAGUUCGAUUCUC	GGCAAUUGAACCCUCAUCAACA	Translation
sly-miR1918	Solyc02g063460.1.1	2.5	-1.0	1	22	148	169	UGUUGGUGAGAGUUCGAUUCUC	ACCCAUCGAACUUUUACCAAUA	Cleavage
sly-miR1918	Solyc01g090820.2.1	2.5	-1.0	1	22	561	582	UGUUGGUGAGAGUUCGAUUCUC	UUUAGUCGAAUUUUUACCAGCA	Cleavage
sly-miR1918	Solyc03g123760.3.1	2.5	-1.0	1	22	1642	1663	UGUUGGUGAGAGUUCGAUUCUC	UGCAAUUGGACUCUUGCCAGCA	Cleavage
sly-miR1918	Solyc04g077260.3.1	3.0	-1.0	1	22	95	116	UGUUGGUGAGAGUUCGAUUCUC	AGGAAUCAAACUCUCAGCAAUA	Cleavage
sly-miR1918	Solyc04g079870.2.1	3.0	-1.0	1	22	390	411	UGUUGGUGAGAGUUCGAUUCUC	AUUUAUUGAACUUUCACUAAUA	Cleavage
sly-miR1918	Solyc03g062890.3.1	3.0	-1.0	1	22	1025	1046	UGUUGGUGAGAGUUCGAUUCUC	AUAAAUUGAACUCUUAUCUACA	Cleavage
sly-miR1918	Solyc03g006920.2.1	3.0	-1.0	1	22	2216	2237	UGUUGGUGAGAGUUCGAUUCUC	ACCAGUUGAACUUUCACCAUCA	Cleavage
sly-miR1918	Solyc10g006720.3.1	3.0	-1.0	1	22	2562	2582	UGUUGGUGAGAGUUCGAUUCUC	GACAAUC-AACUUUCACUAACA	Cleavage
sly-miR1918	Solyc01g106210.3.1	3.0	-1.0	1	22	1087	1108	UGUUGGUGAGAGUUCGAUUCUC	UAAGAUAGAGCUUUCAUCAACA	Cleavage
sly-miR1918	Solyc01g106260.3.1	3.0	-1.0	1	22	1036	1057	UGUUGGUGAGAGUUCGAUUCUC	UAAGAUAGAGCUUUCAUCAACA	Cleavage
sly-miR1918	Solyc11g065820.2.1	3.0	-1.0	1	22	6525	6546	UGUUGGUGAGAGUUCGAUUCUC	ACAAAUUCAAUUCUCACCAACC	Cleavage
sly-miR1918	Solyc09g090500.3.1	3.0	-1.0	1	22	131	152	UGUUGGUGAGAGUUCGAUUCUC	UCAAAUGGAAUUGUCACCAACA	Translation
sly-miR1919a-1	Solyc04g056560.3.1	3.0	-1.0	1	21	5586	5606	ACGAGAGUCAUCUGUGACAGG	CUUGUCGUAGAUGGCUCUUGC	Cleavage
sly-miR1919a-1	Solyc12g015860.2.1	3.0	-1.0	1	21	238	258	ACGAGAGUCAUCUGUGACAGG	GAAUUUACAGAUGAUUCUCGU	Cleavage
sly-miR1919a-2	Solyc04g056560.3.1	3.0	-1.0	1	21	5586	5606	ACGAGAGUCAUCUGUGACAGG	CUUGUCGUAGAUGGCUCUUGC	Cleavage
sly-miR1919a-2	Solyc12g015860.2.1	3.0	-1.0	1	21	238	258	ACGAGAGUCAUCUGUGACAGG	GAAUUUACAGAUGAUUCUCGU	Cleavage
sly-miR1919a-3	Solyc04g056560.3.1	3.0	-1.0	1	21	5586	5606	ACGAGAGUCAUCUGUGACAGG	CUUGUCGUAGAUGGCUCUUGC	Cleavage
sly-miR1919a-3	Solyc12g015860.2.1	3.0	-1.0	1	21	238	258	ACGAGAGUCAUCUGUGACAGG	GAAUUUACAGAUGAUUCUCGU	Cleavage
sly-miR2101-3p	Solyc11g066710.2.1	2.0	-1.0	1	19	280	298	AUUUAACUCAAGUGAGCAU	AUGUUGAUUUGAGUUAAAU	Cleavage
sly-miR2101-3p	Solyc12g088820.2.1	2.5	-1.0	1	19	2207	2225	AUUUAACUCAAGUGAGCAU	AUGUUCAUUUGAGGUAAAU	Cleavage
sly-miR2101-3p	Solyc06g051040.3.1	3.0	-1.0	1	19	2210	2228	AUUUAACUCAAGUGAGCAU	AAGUUCAUUUGAGUUAGGU	Cleavage
sly-miR2101-3p	Solyc11g007770.2.1	3.0	-1.0	1	19	1859	1877	AUUUAACUCAAGUGAGCAU	AUGUGCACUGGAGUUAAAU	Translation
sly-miR2101-3p	Solyc09g007080.3.1	3.0	-1.0	1	19	4448	4466	AUUUAACUCAAGUGAGCAU	AUCCUCAUAUGAGUUAAAU	Translation
sly-miR2101-3p	Solyc08g022030.3.1	3.0	-1.0	1	19	1895	1912	AUUUAACUCAAGUGAGCAU	AUGCA-ACUUGAGUUAAAU	Cleavage
sly-miR2111a-3p	Solyc11g005790.2.1	3.0	-1.0	1	19	60	78	CCUUGGGAUGCAGAUUAUC	GAUAGUCUGCAUCCCACGU	Cleavage
sly-miR2111a-3p	Solyc01g101030.3.1	3.0	-1.0	1	19	1435	1453	CCUUGGGAUGCAGAUUAUC	GAUACCCUGUAUUCCAAGG	Cleavage
sly-miR2111a-3p	Solyc08g042040.3.1	3.0	-1.0	1	19	928	945	CCUUGGGAUGCAGAUUAUC	GAUAA-CUGCAUUCUAAGG	Cleavage

sly-miR2111a-5p	Solyc07g009410.3.1	0.0	-1.0	1	21	688	708	UAAUCUGCAUCCUGAGGUUUA	ACAACCUCAGGAUGCAGAUUA	Cleavage
sly-miR2111a-5p	Solyc09g010997.1.1	3.0	-1.0	1	21	569	589	UAAUCUGCAUCCUGAGGUUUA	GAGACUUUAGGAUGGAGAUUA	Cleavage
sly-miR2111a-5p	Solyc02g091920.3.1	3.0	-1.0	1	21	441	461	UAAUCUGCAUCCUGAGGUUUA	CAAAACUCAGGAUGUGGAUUU	Cleavage
sly-miR2111a-5p	Solyc07g049650.1.1	3.0	-1.0	1	21	18	38	UAAUCUGCAUCCUGAGGUUUA	GUCAUCUCAGGAUGCAGAUGA	Cleavage
sly-miR2111a-5p	Solyc03g121880.3.1	3.0	-1.0	1	21	1145	1165	UAAUCUGCAUCCUGAGGUUUA	AGGAUCUCAGGUUGCGGAUUA	Translation
sly-miR2111a-5p	Solyc11g008770.2.1	3.0	-1.0	1	21	150	170	UAAUCUGCAUCCUGAGGUUUA	UCAACCUCAGAAUGCAGAUAA	Translation
sly-miR2604	Solyc06g064480.3.1	1.5	-1.0	1	21	873	893	UAAUUUUUAUGUGGAAGUGUU	GGCACUUCCAUAUGAGAAUUA	Cleavage
sly-miR2604	Solyc10g005020.3.1	1.5	-1.0	1	21	872	892	UAAUUUUUAUGUGGAAGUGUU	CUCGCUUUCAUAUAAAAAUUA	Cleavage
sly-miR2604	Solyc12g013670.2.1	2.0	-1.0	1	21	97	117	UAAUUUUUAUGUGGAAGUGUU	AACACAUCCAUAUAGAAAUUA	Cleavage
sly-miR2604	Solyc10g007170.2.1	2.0	-1.0	1	21	894	914	UAAUUUUUAUGUGGAAGUGUU	UACAUUUUCACAUAAAAAUUU	Cleavage
sly-miR2604	Solyc01g096470.3.1	2.0	-1.0	1	21	192	212	UAAUUUUUAUGUGGAAGUGUU	GGGAUUUUCACAUAAAAAUUA	Cleavage
sly-miR2604	Solyc05g013440.3.1	2.5	-1.0	1	21	3814	3834	UAAUUUUUAUGUGGAAGUGUU	AACACUUCCACUUGAAGAUUA	Translation
sly-miR2604	Solyc08g062860.3.1	2.5	-1.0	1	21	1676	1696	UAAUUUUUAUGUGGAAGUGUU	CAUACUUCUGUAUAGAAAUUA	Cleavage
sly-miR2604	Solyc12g098700.1.1	2.5	-1.0	1	21	1388	1408	UAAUUUUUAUGUGGAAGUGUU	AGAACUUCUACAUAGAAGUUA	Cleavage
sly-miR2604	Solyc02g067900.3.1	2.5	-1.0	1	21	149	169	UAAUUUUUAUGUGGAAGUGUU	UCAAAUUUCACAUAAAAAUUA	Cleavage
sly-miR2604	Solyc06g011370.3.1	2.5	-1.0	1	21	141	161	UAAUUUUUAUGUGGAAGUGUU	CCCAUUUGCACAUAAGAAUUG	Cleavage
sly-miR2604	Solyc11g044570.2.1	3.0	-1.0	1	21	284	304	UAAUUUUUAUGUGGAAGUGUU	GAUGCUUCCAUAUAGAAAUUC	Cleavage
sly-miR2604	Solyc09g010780.3.1	3.0	-1.0	1	21	209	229	UAAUUUUUAUGUGGAAGUGUU	CACAUUUCUUCAUAAAAAUUG	Cleavage
sly-miR2604	Solyc01g103500.3.1	3.0	-1.0	1	21	3329	3349	UAAUUUUUAUGUGGAAGUGUU	CACACUUCCAUAUAAAGGUGA	Cleavage
sly-miR2604	Solyc03g123700.3.1	3.0	-1.0	1	21	124	144	UAAUUUUUAUGUGGAAGUGUU	GAUAAUUUUAUAUAAAAAUUA	Cleavage
sly-miR2604	Solyc06g005580.3.1	3.0	-1.0	1	21	746	766	UAAUUUUUAUGUGGAAGUGUU	CACUUUUUCACAUAAAAAUUC	Cleavage
sly-miR2604	Solyc06g060580.2.1	3.0	-1.0	1	21	1180	1200	UAAUUUUUAUGUGGAAGUGUU	UACCUUUCUAUAUGAAAAUUA	Cleavage
sly-miR2604	Solyc05g006550.3.1	3.0	-1.0	1	21	1157	1177	UAAUUUUUAUGUGGAAGUGUU	CAAGUUUCCACAUAAAGAUUG	Cleavage
sly-miR2604	Solyc11g007060.2.1	3.0	-1.0	1	21	757	777	UAAUUUUUAUGUGGAAGUGUU	AUCACUUCCAAAUAAAGAUUC	Translation
sly-miR2604	Solyc05g009540.3.1	3.0	-1.0	1	21	4796	4816	UAAUUUUUAUGUGGAAGUGUU	AUCAUUUCCUCAUAAAAAUUC	Cleavage
sly-miR2604	Solyc09g090550.3.1	3.0	-1.0	1	21	1703	1723	UAAUUUUUAUGUGGAAGUGUU	AUUAUUUUUGCGUAAAAAUUA	Cleavage
sly-miR2604	Solyc06g051200.3.1	3.0	-1.0	1	21	1489	1509	UAAUUUUUAUGUGGAAGUGUU	UUUAUUUUUACAUAAGAAUUG	Cleavage
sly-miR2604	Solyc00g090115.1.1	3.0	-1.0	1	21	2777	2797	UAAUUUUUAUGUGGAAGUGUU	UCGACGUCCACAUAAAGAUUG	Cleavage
sly-miR319-3p-1	Solyc08g048370.3.1	1.5	-1.0	1	21	908	928	UUGGACUGAAGGGUUUCCUUC	CAGGGGGACCCUUCAGUCCAA	Cleavage
sly-miR319-3p-1	Solyc07g053410.3.1	1.5	-1.0	1	21	1141	1161	UUGGACUGAAGGGUUUCCUUC	AAGGGAACCCCUUCAGUCCAA	Cleavage
sly-miR319-3p-1	Solyc01g100650.3.1	2.0	-1.0	1	21	1861	1881	UUGGACUGAAGGGUUUCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
sly-miR319-3p-1	Solyc05g012840.1.1	2.0	-1.0	1	21	615	635	UUGGACUGAAGGGUUUCCUUC	UAGGGAACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-1	Solyc02g077250.2.1	2.0	-1.0	1	21	897	917	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-1	Solyc03g119020.2.1	2.5	-1.0	1	21	56	76	UUGGACUGAAGGGUUUCCUUC	GAAGGAAACUGUUUAGUCCAA	Translation
sly-miR319-3p-1	Solyc12g040470.2.1	2.5	-1.0	1	21	134	154	UUGGACUGAAGGGUUUCCUUC	GAAGGAAAUUCAUCAGUCCAA	Translation
sly-miR319-3p-1	Solyc10g008780.1.1	2.5	-1.0	1	21	1575	1595	UUGGACUGAAGGGUUUCCUUC	GAGGGAACCCCUUCAGUCCAC	Cleavage
sly-miR319-3p-1	Solyc07g062680.2.1	2.5	-1.0	1	21	1197	1217	UUGGACUGAAGGGUUUCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-1	Solyc12g014140.2.1	2.5	-1.0	1	21	1050	1070	UUGGACUGAAGGGUUUCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-1	Solyc01g088160.3.1	2.5	-1.0	1	21	1527	1547	UUGGACUGAAGGGUUUCCUUC	GGAGGAAACACUUUGGUCCAA	Cleavage
sly-miR319-3p-1	Solyc08g007712.1.1	3.0	-1.0	1	21	1029	1049	UUGGACUGAAGGGUUUCCUUC	CGAGCAUACCCUUCAGUUCGA	Cleavage
sly-miR319-3p-2	Solyc08g048370.3.1	1.5	-1.0	1	21	908	928	UUGGACUGAAGGGUUUCCUUC	CAGGGGGACCCUUCAGUCCAA	Cleavage
sly-miR319-3p-2	Solyc07g053410.3.1	1.5	-1.0	1	21	1141	1161	UUGGACUGAAGGGUUUCCUUC	AAGGGAACCCCUUCAGUCCAA	Cleavage
sly-miR319-3p-2	Solyc01g100650.3.1	2.0	-1.0	1	21	1861	1881	UUGGACUGAAGGGUUUCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
sly-miR319-3p-2	Solyc05g012840.1.1	2.0	-1.0	1	21	615	635	UUGGACUGAAGGGUUUCCUUC	UAGGGAACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-2	Solyc02g077250.2.1	2.0	-1.0	1	21	897	917	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-2	Solyc03g119020.2.1	2.5	-1.0	1	21	56	76	UUGGACUGAAGGGUUUCCUUC	GAAGGAAACUGUUUAGUCCAA	Translation
sly-miR319-3p-2	Solyc12g040470.2.1	2.5	-1.0	1	21	134	154	UUGGACUGAAGGGUUUCCUUC	GAAGGAAAUUCAUCAGUCCAA	Translation
sly-miR319-3p-2	Solyc10g008780.1.1	2.5	-1.0	1	21	1575	1595	UUGGACUGAAGGGUUUCCUUC	GAGGGAACCCCUUCAGUCCAC	Cleavage
sly-miR319-3p-2	Solyc07g062680.2.1	2.5	-1.0	1	21	1197	1217	UUGGACUGAAGGGUUUCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319-3p-2	Solyc12g014140.2.1	2.5	-1.0	1	21	1050	1070	UUGGACUGAAGGGUUUCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage

sly-miR319-3p-2	Solyc01g088160.3.1	2.5	-1.0	1	21	1527	1547	UUGGACUGAAGGGUUUCCUUC	GGAGGAAACACUUUGGUCCAA	Cleavage
sly-miR319-3p-2	Solyc08g007712.1.1	3.0	-1.0	1	21	1029	1049	UUGGACUGAAGGGUUUCCUUC	CGAGCAUACCCUUCAGUUCGA	Cleavage
sly-miR319-5p-1	Solyc06g054380.3.1	1.5	-1.0	1	20	734	753	GCUGCUGAAUCAUUGGUUCA	UGAAUCCAUGAUUCAGCAGC	Cleavage
sly-miR319-5p-1	Solyc07g063300.3.1	1.5	-1.0	1	20	542	561	GCUGCUGAAUCAUUGGUUCA	CUAAUCAAUGAUUCAGCAGC	Cleavage
sly-miR319-5p-1	Solyc12g088470.2.1	1.5	-1.0	1	20	252	271	GCUGCUGAAUCAUUGGUUCA	AGAAGCAAUGGUUCAGCAGC	Cleavage
sly-miR319-5p-1	Solyc12g088500.2.1	1.5	-1.0	1	20	384	403	GCUGCUGAAUCAUUGGUUCA	AGAAGCAAUGGUUCAGCAGC	Cleavage
sly-miR319-5p-1	Solyc12g088520.2.1	1.5	-1.0	1	20	380	399	GCUGCUGAAUCAUUGGUUCA	AGAAGCAAUGGUUCAGCAGC	Cleavage
sly-miR319-5p-1	Solyc12g088530.2.1	2.0	-1.0	1	20	93	112	GCUGCUGAAUCAUUGGUUCA	AGAAGCAAUGGUUCAGCAGU	Cleavage
sly-miR319-5p-1	Solyc07g041900.3.1	2.5	-1.0	1	20	1158	1177	GCUGCUGAAUCAUUGGUUCA	CCAGUUAAUGAUUCAGCAGC	Cleavage
sly-miR319-5p-1	Solyc06g063240.3.1	3.0	-1.0	1	20	5151	5170	GCUGCUGAAUCAUUGGUUCA	GCAACCAAUGAUGCGGCAGC	Cleavage
sly-miR319-5p-1	Solyc12g044840.2.1	3.0	-1.0	1	20	294	313	GCUGCUGAAUCAUUGGUUCA	AGGGUCAGUGAUUCAGUAGU	Cleavage
sly-miR319-5p-1	Solyc01g108670.3.1	3.0	-1.0	1	20	7235	7254	GCUGCUGAAUCAUUGGUUCA	AGAAUCAAUGUUUUGGCAGC	Translation
sly-miR319-5p-1	Solyc07g045070.3.1	3.0	-1.0	1	20	1860	1879	GCUGCUGAAUCAUUGGUUCA	GGAACAGGUGAUUCGGCAGU	Cleavage
sly-miR319-5p-2	Solyc12g099250.2.1	2.0	-1.0	1	21	721	741	AGGAAACUGUUUAGUCCAACC	AGUUGGACUGGACAGUUUCCA	Cleavage
sly-miR319-5p-2	Solyc05g054910.3.1	2.5	-1.0	1	21	1901	1921	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
sly-miR319-5p-2	Solyc06g048520.3.1	2.5	-1.0	1	21	648	668	AGGAAACUGUUUAGUCCAACC	AGGUGGAUUGAACAGUUUCUU	Cleavage
sly-miR319-5p-2	Solyc03g119020.2.1	2.5	-1.0	1	21	213	233	AGGAAACUGUUUAGUCCAACC	UCUUGGACUGAAGGGUUUCCU	Cleavage
sly-miR319-5p-2	Solyc12g040470.2.1	2.5	-1.0	1	21	287	307	AGGAAACUGUUUAGUCCAACC	UCUUGGACUGAAGGGUUUCCU	Cleavage
sly-miR319-5p-2	Solyc01g059860.3.1	2.5	-1.0	1	21	961	981	AGGAAACUGUUUAGUCCAACC	AAUUGGACUGGACAAUUUCCU	Cleavage
sly-miR319-5p-2	Solyc11g005990.2.1	2.5	-1.0	1	21	8085	8105	AGGAAACUGUUUAGUCCAACC	CUUUUGAGUAGACAGUUUCCU	Cleavage
sly-miR319-5p-2	Solyc06g051260.3.1	3.0	-1.0	1	21	114	134	AGGAAACUGUUUAGUCCAACC	UGUUGGUCUCAACAGUUUUCU	Cleavage
sly-miR319-5p-2	Solyc02g021000.3.1	3.0	-1.0	1	21	614	634	AGGAAACUGUUUAGUCCAACC	GUUUGGAUUAGUUAGUUUCCU	Translation
sly-miR319-5p-2	Solyc04g008390.2.1	3.0	-1.0	1	21	60	80	AGGAAACUGUUUAGUCCAACC	UUUUGGGUUAAACAAUUUUCU	Cleavage
sly-miR319-5p-2	Solyc03g117210.3.1	3.0	-1.0	1	21	1131	1151	AGGAAACUGUUUAGUCCAACC	AGUUGCAGUAGACAGUUUCUU	Cleavage
sly-miR319a-1-3p	Solyc03g119530.3.1	0.0	-1.0	1	21	2505	2525	UUGGACUGAAGGGAGCUCCCU	UAGGAGCUCCCUUCAGUCCAA	Cleavage
sly-miR319a-1-3p	Solyc01g009070.3.1	1.5	-1.0	1	21	1835	1855	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319a-1-3p	Solyc02g079010.3.1	2.0	-1.0	1	21	818	838	UUGGACUGAAGGGAGCUCCCU	UCGGAGCUUCAUUCAGUCCAA	Translation
sly-miR319a-1-3p	Solyc06g073640.3.1	2.5	-1.0	1	21	1757	1777	UUGGACUGAAGGGAGCUCCCU	CUCGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319a-1-3p	Solyc08g048370.3.1	2.5	-1.0	1	21	908	928	UUGGACUGAAGGGAGCUCCCU	CAGGGGGACCCUUCAGUCCAA	Cleavage
sly-miR319a-1-3p	Solyc03g113840.2.1	3.0	-1.0	1	21	75	95	UUGGACUGAAGGGAGCUCCCU	UGGGAGAUUUCUUCAGUCCAU	Cleavage
sly-miR319a-1-3p	Solyc05g006830.3.1	3.0	-1.0	1	21	1934	1954	UUGGACUGAAGGGAGCUCCCU	UGUGAGUUCCCUUCCGUCCAA	Cleavage
sly-miR319a-1-3p	Solyc11g072060.2.1	3.0	-1.0	1	21	913	933	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCUUUCCAA	Cleavage
sly-miR319a-1-3p	Solyc07g053410.3.1	3.0	-1.0	1	21	1142	1161	UUGGACUGAAGGGAGCUCCCU	AGGGAAC-CCCUUCAGUCCAA	Cleavage
sly-miR319a-1-3p	Solyc06g071200.3.1	3.0	-1.0	1	21	3688	3708	UUGGACUGAAGGGAGCUCCCU	GUGCAGUUUCUUUCAGUUCAA	Cleavage
sly-miR319a-1-3p	Solyc06g061240.3.1	3.0	-1.0	1	21	560	580	UUGGACUGAAGGGAGCUCCCU	UUGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319a-1-3p	Solyc07g062680.2.1	3.0	-1.0	1	21	1197	1217	UUGGACUGAAGGGAGCUCCCU	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319a-1-3p	Solyc12g014140.2.1	3.0	-1.0	1	21	1050	1070	UUGGACUGAAGGGAGCUCCCU	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319a-1-3p	Solyc06g061250.2.1	3.0	-1.0	1	21	346	366	UUGGACUGAAGGGAGCUCCCU	UUGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319a-1-5p	Solyc03g083250.3.1	3.0	-1.0	1	20	498	517	GAGCUCUCUCCGGUCCAGUC	AAUUGGACAGGAGAGAGCUA	Cleavage
sly-miR319a-1-5p	Solyc03g082840.3.1	3.0	-1.0	1	20	346	365	GAGCUCUCUCCGGUCCAGUC	UACUGGACUGAAGGGGGCUC	Translation
sly-miR319a-1-5p	Solyc04g005540.3.1	3.0	-1.0	1	20	2592	2611	GAGCUCUCUCCGGUCCAGUC	GAUUCAACCGGAGAGGGCUC	Cleavage
sly-miR319a-1-5p	Solyc01g058320.3.1	3.0	-1.0	1	20	749	768	GAGCUCUCUCCGGUCCAGUC	CCCUUGAUCGGAGAGAGUUC	Cleavage
sly-miR319a-1-5p	Solyc11g066440.2.1	3.0	-1.0	1	20	749	768	GAGCUCUCUCCGGUCCAGUC	AAAUGGAUGGGAGAGAGCUC	Cleavage
sly-miR319a-2-3p	Solyc03g119530.3.1	0.0	-1.0	1	21	2505	2525	UUGGACUGAAGGGAGCUCCCU	UAGGAGCUCCCUUCAGUCCAA	Cleavage
sly-miR319a-2-3p	Solyc01g009070.3.1	1.5	-1.0	1	21	1835	1855	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319a-2-3p	Solyc02g079010.3.1	2.0	-1.0	1	21	818	838	UUGGACUGAAGGGAGCUCCCU	UCGGAGCUUCAUUCAGUCCAA	Translation
sly-miR319a-2-3p	Solyc06g073640.3.1	2.5	-1.0	1	21	1757	1777	UUGGACUGAAGGGAGCUCCCU	CUCGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319a-2-3p	Solyc08g048370.3.1	2.5	-1.0	1	21	908	928	UUGGACUGAAGGGAGCUCCCU	CAGGGGGACCCUUCAGUCCAA	Cleavage
sly-miR319a-2-3p	Solyc03g113840.2.1	3.0	-1.0	1	21	75	95	UUGGACUGAAGGGAGCUCCCU	UGGGAGAUUUCUUCAGUCCAU	Cleavage
sly-miR319a-2-3p	Solyc05g006830.3.1	3.0	-1.0	1	21	1934	1954	UUGGACUGAAGGGAGCUCCCU	UGUGAGUUCCCUUCCGUCCAA	Cleavage

sly-miR319a-2-3p	Solyc11g072060.2.1	3.0	-1.0	1	21	913	933	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCUUUCCAA	Cleavage
sly-miR319a-2-3p	Solyc07g053410.3.1	3.0	-1.0	1	21	1142	1161	UUGGACUGAAGGGAGCUCCCU	AGGGAAC-CCCUUCAGUCCAA	Cleavage
sly-miR319a-2-3p	Solyc06g071200.3.1	3.0	-1.0	1	21	3688	3708	UUGGACUGAAGGGAGCUCCCU	GUGCAGUUUCUUUCAGUUCAA	Cleavage
sly-miR319a-2-3p	Solyc06g061240.3.1	3.0	-1.0	1	21	560	580	UUGGACUGAAGGGAGCUCCCU	UUGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319a-2-3p	Solyc07g062680.2.1	3.0	-1.0	1	21	1197	1217	UUGGACUGAAGGGAGCUCCCU	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319a-2-3p	Solyc12g014140.2.1	3.0	-1.0	1	21	1050	1070	UUGGACUGAAGGGAGCUCCCU	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319a-2-3p	Solyc06g061250.2.1	3.0	-1.0	1	21	346	366	UUGGACUGAAGGGAGCUCCCU	UUGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319a-2-5p	Solyc04g080060.3.1	2.5	-1.0	1	21	478	498	AGAGCUUCCUUUAGUCCACUC	GAGUGGAUUAGAGGAAGCUUG	Cleavage
sly-miR319a-2-5p	Solyc03g082840.3.1	2.5	-1.0	1	21	346	366	AGAGCUUCCUUUAGUCCACUC	UACUGGACUGAAGGGGGCUCU	Cleavage
sly-miR319a-2-5p	Solyc03g113080.3.1	2.5	-1.0	1	21	776	795	AGAGCUUCCUUUAGUCCACUC	AAGUGG-CUGAAGGAAGCUCU	Cleavage
sly-miR319a-2-5p	Solyc08g080200.3.1	2.5	-1.0	1	21	4139	4159	AGAGCUUCCUUUAGUCCACUC	CUGUGUGUUGAAGGAAGCUCU	Cleavage
sly-miR319a-2-5p	Solyc01g109080.3.1	3.0	-1.0	1	21	9384	9404	AGAGCUUCCUUUAGUCCACUC	GAGUGAGUUGAAGGAGGCUCU	Cleavage
sly-miR319a-2-5p	Solyc12g010115.1.1	3.0	-1.0	1	21	40	60	AGAGCUUCCUUUAGUCCACUC	CAAUGGACUGAAGCAAGCUCU	Cleavage
sly-miR319a-2-5p	Solyc08g075390.3.1	3.0	-1.0	1	21	2159	2179	AGAGCUUCCUUUAGUCCACUC	CUUUGGAUUAGAGGAAGCUCA	Cleavage
sly-miR319a-2-5p	Solyc03g005620.3.1	3.0	-1.0	1	21	978	998	AGAGCUUCCUUUAGUCCACUC	GGAUGGUCUAAAGGGAGUUCU	Cleavage
sly-miR319a-2-5p	Solyc01g079060.3.1	3.0	-1.0	1	21	723	743	AGAGCUUCCUUUAGUCCACUC	UGGCGGAUUGAAGGAAGCUCA	Cleavage
sly-miR319a-2-5p	Solyc08g008660.3.1	3.0	-1.0	1	21	372	392	AGAGCUUCCUUUAGUCCACUC	UGGUGGUUUGAAGGGAGCUUU	Cleavage
sly-miR319a-2-5p	Solyc08g081050.3.1	3.0	-1.0	1	21	1179	1199	AGAGCUUCCUUUAGUCCACUC	CAAUGAGCUAAAGGAAGCUUU	Cleavage
sly-miR319a-2-5p	Solyc09g010830.3.1	3.0	-1.0	1	21	5979	5999	AGAGCUUCCUUUAGUCCACUC	UCGUGGUCUAAAGGGUGCUCU	Cleavage
sly-miR319c-1	Solyc03g119530.3.1	0.0	-1.0	1	20	2506	2525	UUGGACUGAAGGGAGCUCCU	AGGAGCUCCCUUCAGUCCAA	Cleavage
sly-miR319c-1	Solyc01g009070.3.1	1.5	-1.0	1	20	1836	1855	UUGGACUGAAGGGAGCUCCU	UGGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319c-1	Solyc02g079010.3.1	2.0	-1.0	1	20	819	838	UUGGACUGAAGGGAGCUCCU	CGGAGCUUCAUUCAGUCCAA	Translation
sly-miR319c-1	Solyc06g073640.3.1	2.5	-1.0	1	20	1758	1777	UUGGACUGAAGGGAGCUCCU	UCGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319c-1	Solyc08g048370.3.1	2.5	-1.0	1	20	909	928	UUGGACUGAAGGGAGCUCCU	AGGGGGACCCUUCAGUCCAA	Cleavage
sly-miR319c-1	Solyc05g006830.3.1	3.0	-1.0	1	20	1935	1954	UUGGACUGAAGGGAGCUCCU	GUGAGUUCCCUUCCGUCCAA	Cleavage
sly-miR319c-1	Solyc11g072060.2.1	3.0	-1.0	1	20	914	933	UUGGACUGAAGGGAGCUCCU	UGGAGCUCCCUUCUUUCCAA	Cleavage
sly-miR319c-1	Solyc03g113840.2.1	3.0	-1.0	1	20	76	95	UUGGACUGAAGGGAGCUCCU	GGGAGAUUUCUUCAGUCCAU	Cleavage
sly-miR319c-1	Solyc07g062680.2.1	3.0	-1.0	1	20	1198	1217	UUGGACUGAAGGGAGCUCCU	AGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319c-1	Solyc12g014140.2.1	3.0	-1.0	1	20	1051	1070	UUGGACUGAAGGGAGCUCCU	AGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319c-1	Solyc06g071200.3.1	3.0	-1.0	1	20	3689	3708	UUGGACUGAAGGGAGCUCCU	UGCAGUUUCUUUCAGUUCAA	Cleavage
sly-miR319c-1	Solyc06g061240.3.1	3.0	-1.0	1	20	561	580	UUGGACUGAAGGGAGCUCCU	UGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319c-1	Solyc06g061250.2.1	3.0	-1.0	1	20	347	366	UUGGACUGAAGGGAGCUCCU	UGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319c-2-3p	Solyc03g119530.3.1	0.0	-1.0	1	21	2505	2525	UUGGACUGAAGGGAGCUCCUU	UAGGAGCUCCCUUCAGUCCAA	Cleavage
sly-miR319c-2-3p	Solyc01g009070.3.1	1.5	-1.0	1	21	1835	1855	UUGGACUGAAGGGAGCUCCUU	CUGGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319c-2-3p	Solyc02g079010.3.1	2.0	-1.0	1	21	818	838	UUGGACUGAAGGGAGCUCCUU	UCGGAGCUUCAUUCAGUCCAA	Translation
sly-miR319c-2-3p	Solyc06g073640.3.1	2.5	-1.0	1	21	1757	1777	UUGGACUGAAGGGAGCUCCUU	CUCGAGCUCCCUUCACUCCAA	Cleavage
sly-miR319c-2-3p	Solyc08g048370.3.1	2.5	-1.0	1	21	908	928	UUGGACUGAAGGGAGCUCCUU	CAGGGGGACCCUUCAGUCCAA	Cleavage
sly-miR319c-2-3p	Solyc07g062680.2.1	3.0	-1.0	1	21	1197	1217	UUGGACUGAAGGGAGCUCCUU	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319c-2-3p	Solyc12g014140.2.1	3.0	-1.0	1	21	1050	1070	UUGGACUGAAGGGAGCUCCUU	GAGGGGACCCCUUCAGUCCAG	Cleavage
sly-miR319c-2-3p	Solyc05g006830.3.1	3.0	-1.0	1	21	1934	1954	UUGGACUGAAGGGAGCUCCUU	UGUGAGUUCCCUUCCGUCCAA	Cleavage
sly-miR319c-2-3p	Solyc11g072060.2.1	3.0	-1.0	1	21	913	933	UUGGACUGAAGGGAGCUCCUU	CUGGAGCUCCCUUCUUUCCAA	Cleavage
sly-miR319c-2-3p	Solyc03g113840.2.1	3.0	-1.0	1	21	75	95	UUGGACUGAAGGGAGCUCCUU	UGGGAGAUUUCUUCAGUCCAU	Cleavage
sly-miR319c-2-3p	Solyc06g071200.3.1	3.0	-1.0	1	21	3688	3708	UUGGACUGAAGGGAGCUCCUU	GUGCAGUUUCUUUCAGUUCAA	Cleavage
sly-miR319c-2-3p	Solyc06g061240.3.1	3.0	-1.0	1	21	560	580	UUGGACUGAAGGGAGCUCCUU	UUGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319c-2-3p	Solyc06g061250.2.1	3.0	-1.0	1	21	346	366	UUGGACUGAAGGGAGCUCCUU	UUGGACAUUUCUUCAGUCCAA	Cleavage
sly-miR319c-2-5p	Solyc08g080200.3.1	1.5	-1.0	1	21	4139	4159	AGAGCUUCCUUCAGCCCACUC	CUGUGUGUUGAAGGAAGCUCU	Cleavage
sly-miR319c-2-5p	Solyc01g109080.3.1	2.0	-1.0	1	21	9384	9404	AGAGCUUCCUUCAGCCCACUC	GAGUGAGUUGAAGGAGGCUCU	Cleavage
sly-miR319c-2-5p	Solyc03g113080.3.1	2.0	-1.0	1	21	776	795	AGAGCUUCCUUCAGCCCACUC	AAGUGG-CUGAAGGAAGCUCU	Cleavage
sly-miR319c-2-5p	Solyc08g008660.3.1	2.5	-1.0	1	21	372	392	AGAGCUUCCUUCAGCCCACUC	UGGUGGUUUGAAGGGAGCUUU	Cleavage
sly-miR319c-2-5p	Solyc02g093800.3.1	2.5	-1.0	1	21	1655	1675	AGAGCUUCCUUCAGCCCACUC	AGGUGAGCUGGAGGAGGUUCU	Cleavage

sly-miR319c-2-5p	Solyc06g051760.3.1	3.0	-1.0	1	21	2019	2039	AGAGCUUCCUUCAGCCCACUC	GAUUGGGUUGAAGGAAGUUCG	Cleavage
sly-miR319c-2-5p	Solyc02g069490.3.1	3.0	-1.0	1	21	631	651	AGAGCUUCCUUCAGCCCACUC	UUCGGGGUUGAAGGAAGUUCU	Cleavage
sly-miR319c-2-5p	Solyc01g094050.1.1	3.0	-1.0	1	21	1828	1848	AGAGCUUCCUUCAGCCCACUC	AAGUUGGCUGAAGAAAGUUCU	Cleavage
sly-miR319c-2-5p	Solyc03g082840.3.1	3.0	-1.0	1	21	346	366	AGAGCUUCCUUCAGCCCACUC	UACUGGACUGAAGGGGGCUCU	Cleavage
sly-miR319c-2-5p	Solyc07g049220.3.1	3.0	-1.0	1	21	1527	1547	AGAGCUUCCUUCAGCCCACUC	UGGUGAGUUGGAGGAGGUUCU	Cleavage
sly-miR319c-3-3p	Solyc03g119530.3.1	1.0	-1.0	1	21	2506	2526	CUUGGACUGAAGGGAGCUCCC	AGGAGCUCCCUUCAGUCCAAU	Cleavage
sly-miR319c-3-3p	Solyc01g009070.3.1	2.5	-1.0	1	21	1836	1856	CUUGGACUGAAGGGAGCUCCC	UGGAGCUCCCUUCACUCCAAA	Cleavage
sly-miR319c-3-3p	Solyc06g073640.3.1	2.5	-1.0	1	21	1758	1778	CUUGGACUGAAGGGAGCUCCC	UCGAGCUCCCUUCACUCCAAA	Cleavage
sly-miR319c-3-3p	Solyc09g009340.2.1	2.5	-1.0	1	21	1286	1306	CUUGGACUGAAGGGAGCUCCC	UAAAGCUCCCUUUAGUUCGAG	Cleavage
sly-miR319c-3-3p	Solyc03g078610.3.1	2.5	-1.0	1	21	1713	1733	CUUGGACUGAAGGGAGCUCCC	AUGAGCUCCUUUUAGUGCAAG	Cleavage
sly-miR319c-3-3p	Solyc02g079010.3.1	3.0	-1.0	1	21	819	839	CUUGGACUGAAGGGAGCUCCC	CGGAGCUUCAUUCAGUCCAAA	Cleavage
sly-miR319c-3-3p	Solyc05g006830.3.1	3.0	-1.0	1	21	1935	1955	CUUGGACUGAAGGGAGCUCCC	GUGAGUUCCCUUCCGUCCAAA	Cleavage
sly-miR319c-3-3p	Solyc02g065360.3.1	3.0	-1.0	1	21	1510	1530	CUUGGACUGAAGGGAGCUCCC	AUCAGUUCUCUUCAGUUUAAG	Cleavage
sly-miR319c-3-3p	Solyc07g062750.3.1	3.0	-1.0	1	21	1814	1834	CUUGGACUGAAGGGAGCUCCC	UAGAGUUCCUUUUAAUCCAAG	Cleavage
sly-miR319c-3-3p	Solyc01g080720.3.1	3.0	-1.0	1	21	3872	3892	CUUGGACUGAAGGGAGCUCCC	UAGAGUUCCCUUCACUCUGAG	Cleavage
sly-miR319c-3-3p	Solyc01g080720.3.1	3.0	-1.0	1	21	3964	3984	CUUGGACUGAAGGGAGCUCCC	UAGAGUUCCCUUCAUUCUGAG	Cleavage
sly-miR319c-3-3p	Solyc04g026210.3.1	3.0	-1.0	1	21	37	57	CUUGGACUGAAGGGAGCUCCC	UUGAGUUACCUUCAUUCCAAG	Cleavage
sly-miR319c-3-3p	Solyc03g007460.2.1	3.0	-1.0	1	21	731	751	CUUGGACUGAAGGGAGCUCCC	AAGAGUGUCCUUCGGUUCAAG	Cleavage
sly-miR319c-3-5p	Solyc05g007640.3.1	2.5	-1.0	1	20	2413	2432	GAGCUUUCUUUAGUCCACAC	UUGUGGAUUGGAGAAGGCUU	Cleavage
sly-miR319c-3-5p	Solyc08g075390.3.1	2.5	-1.0	1	20	2159	2178	GAGCUUUCUUUAGUCCACAC	CUUUGGAUUAGAGGAAGCUC	Cleavage
sly-miR319c-3-5p	Solyc04g080060.3.1	3.0	-1.0	1	20	478	497	GAGCUUUCUUUAGUCCACAC	GAGUGGAUUAGAGGAAGCUU	Cleavage
sly-miR319c-3-5p	Solyc09g009800.3.1	3.0	-1.0	1	20	3398	3417	GAGCUUUCUUUAGUCCACAC	GUGUAGACUGGGGAAAGCUU	Cleavage
sly-miR319c-3-5p	Solyc01g106230.3.1	3.0	-1.0	1	20	5201	5220	GAGCUUUCUUUAGUCCACAC	GUGUUUGCUAAAGAAGGCUC	Cleavage
sly-miR319c-3-5p	Solyc07g024000.3.1	3.0	-1.0	1	20	738	757	GAGCUUUCUUUAGUCCACAC	AAGGGGACUAGGGAAAGCUC	Cleavage
sly-miR319c-3-5p	Solyc07g066390.1.1	3.0	-1.0	1	20	1231	1250	GAGCUUUCUUUAGUCCACAC	UUGAGGAUUAAACAAAGCUC	Cleavage
sly-miR319c-3-5p	Solyc08g080200.3.1	3.0	-1.0	1	20	4139	4158	GAGCUUUCUUUAGUCCACAC	CUGUGUGUUGAAGGAAGCUC	Cleavage
sly-miR319c-3-5p	Solyc12g088460.2.1	3.0	-1.0	1	20	1097	1117	GAGCUUUCUUUAGU-CCACAC	CUGAGGCACUAAAGAAAGCUC	Cleavage
sly-miR3627-3p	Solyc07g008290.3.1	2.5	-1.0	1	21	1143	1163	AAGUGCCUCUGUCUUUCGACA	UCUGGUAAGACAGAGGUACUU	Cleavage
sly-miR3627-3p	Solyc07g042660.1.1	3.0	-1.0	1	21	350	370	AAGUGCCUCUGUCUUUCGACA	UCUUGAAAGAUGGAGGCAUUG	Cleavage
sly-miR3627-5p	Solyc09g075090.1.1	3.0	-1.0	1	22	631	652	UUGUCGCAGGAGAGAUGGCACU	AAUGCCUUUUCUCGUGCGACAA	Cleavage
sly-miR3627-5p	Solyc09g075760.3.1	3.0	-1.0	1	22	958	979	UUGUCGCAGGAGAGAUGGCACU	GCUGCUCUCUUUCUUGCGGCAA	Cleavage
sly-miR3627-5p	Solyc01g101140.3.1	3.0	-1.0	1	22	142	163	UUGUCGCAGGAGAGAUGGCACU	UGCGCCAUUUCUUCUCCGGCAA	Cleavage
sly-miR3627-5p	Solyc01g010180.3.1	3.0	-1.0	1	22	244	265	UUGUCGCAGGAGAGAUGGCACU	GUAGCCAAUUCUCUUGCGACGG	Cleavage
sly-miR390a-3p	Solyc08g066500.3.1	2.0	-1.0	1	21	920	940	CGCUAUCCAUCCUGAGUUUCA	ACAAAUUUGGGAUGGAUAGUG	Cleavage
sly-miR390a-3p	Solyc08g007210.3.1	2.5	-1.0	1	21	302	322	CGCUAUCCAUCCUGAGUUUCA	ACAGAUUCAGGAUGGAUAGUC	Cleavage
sly-miR390a-3p	Solyc08g066810.3.1	2.5	-1.0	1	21	262	282	CGCUAUCCAUCCUGAGUUUCA	ACAAAUUCAAGAUGGAUAGUG	Cleavage
sly-miR390a-3p	Solyc11g045185.1.1	3.0	-1.0	1	21	842	862	CGCUAUCCAUCCUGAGUUUCA	CAGAAAUUGGGAUGGAUAGUG	Cleavage
sly-miR390a-3p	Solyc03g121760.3.1	3.0	-1.0	1	21	1190	1210	CGCUAUCCAUCCUGAGUUUCA	GCAAGCUGAGGGUGGAUGGUG	Cleavage
sly-miR390a-5p	Solyc09g091900.3.1	2.0	-1.0	1	21	576	596	AAGCUCAGGAGGGAUAGCGCC	GUCGCUAUCCUUCCUCAGCUU	Cleavage
sly-miR390a-5p	Solyc04g005390.2.1	2.5	-1.0	1	21	796	816	AAGCUCAGGAGGGAUAGCGCC	GGUGUGAUCCCUUCUGAGCUU	Cleavage
sly-miR390a-5p	Solyc04g079120.3.1	2.5	-1.0	1	21	620	640	AAGCUCAGGAGGGAUAGCGCC	AGUGCUAUUCCUCCUGAUCUU	Cleavage
sly-miR390a-5p	Solyc01g011040.3.1	2.5	-1.0	1	21	779	799	AAGCUCAGGAGGGAUAGCGCC	CUUGCUAAUCUUCCUGAGCUU	Cleavage
sly-miR390a-5p	Solyc01g010930.3.1	2.5	-1.0	1	21	1565	1585	AAGCUCAGGAGGGAUAGCGCC	AACGGGAUCCCUCUUGAGCUU	Cleavage
sly-miR390a-5p	Solyc01g091230.3.1	3.0	-1.0	1	21	538	558	AAGCUCAGGAGGGAUAGCGCC	GGUGUUAUUCCUCCUGAGGUU	Cleavage
sly-miR390a-5p	Solyc04g015600.3.1	3.0	-1.0	1	21	1577	1597	AAGCUCAGGAGGGAUAGCGCC	GGAACUAUUCCUCCUGAGUUU	Cleavage
sly-miR390a-5p	Solyc01g058100.2.1	3.0	-1.0	1	21	137	157	AAGCUCAGGAGGGAUAGCGCC	UUGUCUAUCCCUCCUGAGCUG	Cleavage
sly-miR390a-5p	Solyc09g072810.3.1	3.0	-1.0	1	21	979	999	AAGCUCAGGAGGGAUAGCGCC	UCAACUAUUCCUUCUGAGCUU	Cleavage
sly-miR390a-5p	Solyc03g025230.3.1	3.0	-1.0	1	21	1979	1999	AAGCUCAGGAGGGAUAGCGCC	UUUGUUAUCUCUUUUGAGUUU	Cleavage
sly-miR390b-3p	Solyc08g066500.3.1	2.0	-1.0	1	21	920	940	CGCUAUCCAUCCUGAGUUUUA	ACAAAUUUGGGAUGGAUAGUG	Cleavage
sly-miR390b-3p	Solyc08g007210.3.1	2.5	-1.0	1	21	302	322	CGCUAUCCAUCCUGAGUUUUA	ACAGAUUCAGGAUGGAUAGUC	Cleavage

sly-miR390b-3p	Solyc08g066810.3.1	2.5	-1.0	1	21	262	282	CGCUAUCCAUCCUGAGUUUUA	ACAAAUUCAAGAUGGAUAGUG	Cleavage
sly-miR390b-3p	Solyc11g045185.1.1	3.0	-1.0	1	21	842	862	CGCUAUCCAUCCUGAGUUUUA	CAGAAAUUGGGAUGGAUAGUG	Cleavage
sly-miR390b-3p	Solyc03g121760.3.1	3.0	-1.0	1	21	1190	1210	CGCUAUCCAUCCUGAGUUUUA	GCAAGCUGAGGGUGGAUGGUG	Cleavage
sly-miR390b-5p	Solyc04g005390.2.1	2.0	-1.0	1	21	796	816	AAGCUCAGGAGGGAUAGCACC	GGUGUGAUCCCUUCUGAGCUU	Cleavage
sly-miR390b-5p	Solyc04g079120.3.1	2.0	-1.0	1	21	620	640	AAGCUCAGGAGGGAUAGCACC	AGUGCUAUUCCUCCUGAUCUU	Cleavage
sly-miR390b-5p	Solyc01g011040.3.1	2.0	-1.0	1	21	779	799	AAGCUCAGGAGGGAUAGCACC	CUUGCUAAUCUUCCUGAGCUU	Cleavage
sly-miR390b-5p	Solyc01g091230.3.1	2.5	-1.0	1	21	538	558	AAGCUCAGGAGGGAUAGCACC	GGUGUUAUUCCUCCUGAGGUU	Cleavage
sly-miR390b-5p	Solyc03g025230.3.1	2.5	-1.0	1	21	1979	1999	AAGCUCAGGAGGGAUAGCACC	UUUGUUAUCUCUUUUGAGUUU	Cleavage
sly-miR390b-5p	Solyc07g056410.3.1	3.0	-1.0	1	21	5141	5161	AAGCUCAGGAGGGAUAGCACC	GGUGCAAUUCCUCCUGAGAUU	Cleavage
sly-miR390b-5p	Solyc04g015600.3.1	3.0	-1.0	1	21	1577	1597	AAGCUCAGGAGGGAUAGCACC	GGAACUAUUCCUCCUGAGUUU	Cleavage
sly-miR390b-5p	Solyc01g058100.2.1	3.0	-1.0	1	21	137	157	AAGCUCAGGAGGGAUAGCACC	UUGUCUAUCCCUCCUGAGCUG	Cleavage
sly-miR390b-5p	Solyc09g072810.3.1	3.0	-1.0	1	21	979	999	AAGCUCAGGAGGGAUAGCACC	UCAACUAUUCCUUCUGAGCUU	Cleavage
sly-miR390b-5p	Solyc09g091900.3.1	3.0	-1.0	1	21	576	596	AAGCUCAGGAGGGAUAGCACC	GUCGCUAUCCUUCCUCAGCUU	Cleavage
sly-miR390b-5p	Solyc09g076050.3.1	3.0	-1.0	1	21	947	967	AAGCUCAGGAGGGAUAGCACC	CUUGCUAUCUCUCUUGGCCUU	Cleavage
sly-miR390b-5p	Solyc02g090505.1.1	3.0	-1.0	1	21	1764	1784	AAGCUCAGGAGGGAUAGCACC	AAUGUUAUCCCUAUUGAGUUU	Cleavage
sly-miR390b-5p	Solyc02g090500.3.1	3.0	-1.0	1	21	2745	2765	AAGCUCAGGAGGGAUAGCACC	AAUGUUAUCCCUAUUGAGUUU	Cleavage
sly-miR390b-5p	Solyc04g079300.3.1	3.0	-1.0	1	21	842	862	AAGCUCAGGAGGGAUAGCACC	CAUGUUAUUUUUCUUGGGCUU	Cleavage
sly-miR390b-5p	Solyc02g064595.1.1	3.0	-1.0	1	21	202	222	AAGCUCAGGAGGGAUAGCACC	AAUGCUAUCCUUCUUAGGCUU	Cleavage
sly-miR390b-5p	Solyc02g064590.2.1	3.0	-1.0	1	21	247	267	AAGCUCAGGAGGGAUAGCACC	AAUGCUAUCCUUCUUAGGCUU	Cleavage
sly-miR390b-5p	Solyc02g064590.2.1	3.0	-1.0	1	21	4769	4789	AAGCUCAGGAGGGAUAGCACC	AAUGCUAUCCUUCUUAGGCUU	Cleavage
sly-miR390b-5p	Solyc11g006180.2.1	3.0	-1.0	1	21	494	514	AAGCUCAGGAGGGAUAGCACC	UUUUCUAUCCCUCUUGAGUUG	Cleavage
sly-miR390b-5p	Solyc05g013140.3.1	3.0	-1.0	1	21	1346	1366	AAGCUCAGGAGGGAUAGCACC	AAUGGGAUUCCUCUUGAGCUU	Cleavage
sly-miR393a-3p	Solyc02g093810.3.1	3.0	-1.0	1	21	2648	2668	AUCAUGCGAUCUCUUCGGAAU	GCUUUGAAGAGAUUGCAUGGA	Cleavage
sly-miR393a-3p	Solyc02g093000.3.1	3.0	-1.0	1	21	904	924	AUCAUGCGAUCUCUUCGGAAU	UGUUCAGAGAGAUUGUAUGAU	Cleavage
sly-miR393a-3p	Solyc04g077060.3.1	3.0	-1.0	1	21	219	239	AUCAUGCGAUCUCUUCGGAAU	CCUUCCAAGAGAUCACAUGAU	Cleavage
sly-miR393a-5p	Solyc06g008780.2.1	1.0	-1.0	1	22	1156	1177	UCCAAAGGGAUCGCAUUGAUCC	GAGACAAUGCGAUCCCUUUGGA	Cleavage
sly-miR393a-5p	Solyc09g074520.3.1	1.0	-1.0	1	22	1643	1664	UCCAAAGGGAUCGCAUUGAUCC	GAGACAAUGCGAUCCCUUUGGA	Cleavage
sly-miR393a-5p	Solyc06g008470.2.1	2.0	-1.0	1	22	242	263	UCCAAAGGGAUCGCAUUGAUCC	GAGACCAUGCGAUCCCUUUGGA	Cleavage
sly-miR393a-5p	Solyc02g079190.3.1	2.5	-1.0	1	22	2591	2612	UCCAAAGGGAUCGCAUUGAUCC	GAAUCAAUGCGGUGUCUUUGGA	Cleavage
sly-miR393a-5p	Solyc05g015070.3.1	2.5	-1.0	1	22	1395	1416	UCCAAAGGGAUCGCAUUGAUCC	GUGUCAAGGUGGUUCCUUUGGA	Cleavage
sly-miR393a-5p	Solyc03g007140.3.1	2.5	-1.0	1	22	867	888	UCCAAAGGGAUCGCAUUGAUCC	CAGUAGAUGUGGUCCCUUUGGA	Cleavage
sly-miR393a-5p	Solyc04g076910.3.1	3.0	-1.0	1	22	6761	6782	UCCAAAGGGAUCGCAUUGAUCC	UGGUCGAUGCCAUUUCUUUGGA	Cleavage
sly-miR393a-5p	Solyc10g055670.2.1	3.0	-1.0	1	22	1783	1804	UCCAAAGGGAUCGCAUUGAUCC	AAGUCAAUGCUAUUUCUUUGGG	Cleavage
sly-miR393a-5p	Solyc12g038130.1.1	3.0	-1.0	1	22	63	84	UCCAAAGGGAUCGCAUUGAUCC	CCUUCAGUGUGAUCCUUUUGAA	Cleavage
sly-miR393a-5p	Solyc03g121230.3.1	3.0	-1.0	1	22	2703	2724	UCCAAAGGGAUCGCAUUGAUCC	GUUUCGGUGUGGUUCUUUUGGA	Cleavage
sly-miR394a	Solyc05g015520.3.1	1.0	-1.0	1	20	1248	1267	UUGGCAUUCUGUCCACCUCC	GGAGGUUGACAGAAUGCCAA	Cleavage
sly-miR394a	Solyc04g071000.1.1	2.5	-1.0	1	20	1788	1807	UUGGCAUUCUGUCCACCUCC	CGAGAUGGAUAGAAUGCUGA	Cleavage
sly-miR394a	Solyc06g084530.3.1	3.0	-1.0	1	20	3251	3270	UUGGCAUUCUGUCCACCUCC	CGAGGUGGAUAGCAUGCUAG	Cleavage
sly-miR394a	Solyc08g042140.3.1	3.0	-1.0	1	20	891	910	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
sly-miR394a	Solyc01g096960.3.1	3.0	-1.0	1	20	7143	7162	UUGGCAUUCUGUCCACCUCC	CAGGGUUGACAGGAUGCCAA	Cleavage
sly-miR394b-3p	Solyc09g074113.1.1	3.0	-1.0	1	21	4429	4449	AGGUGGGCAUACUGCCAAUAG	CCAUUGACAGAAUGUCCACCU	Translation
sly-miR394b-3p	Solyc03g051790.3.1	3.0	-1.0	1	21	2244	2264	AGGUGGGCAUACUGCCAAUAG	AGAAUGGAGGUAUGCCCAUCU	Cleavage
sly-miR394b-5p	Solyc05g015520.3.1	1.0	-1.0	1	20	1248	1267	UUGGCAUUCUGUCCACCUCC	GGAGGUUGACAGAAUGCCAA	Cleavage
sly-miR394b-5p	Solyc04g071000.1.1	2.5	-1.0	1	20	1788	1807	UUGGCAUUCUGUCCACCUCC	CGAGAUGGAUAGAAUGCUGA	Cleavage
sly-miR394b-5p	Solyc06g084530.3.1	3.0	-1.0	1	20	3251	3270	UUGGCAUUCUGUCCACCUCC	CGAGGUGGAUAGCAUGCUAG	Cleavage
sly-miR394b-5p	Solyc08g042140.3.1	3.0	-1.0	1	20	891	910	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
sly-miR394b-5p	Solyc01g096960.3.1	3.0	-1.0	1	20	7143	7162	UUGGCAUUCUGUCCACCUCC	CAGGGUUGACAGGAUGCCAA	Cleavage
sly-miR395a-1	Solyc11g066140.2.1	1.5	-1.0	1	21	2829	2849	CUGAAGUGUUUGGGGGAACUC	AAGUUCCUCCAAACACUUCAA	Cleavage
sly-miR395a-1	Solyc04g054730.3.1	1.5	-1.0	1	21	262	282	CUGAAGUGUUUGGGGGAACUC	GUGUUCUCCCAAACACUUCAA	Cleavage
sly-miR395a-1	Solyc10g081660.2.1	2.0	-1.0	1	21	162	182	CUGAAGUGUUUGGGGGAACUC	GGGUUCCUCCAAAGACUUCAG	Cleavage

sly-miR395a-1	Solyc06g075970.3.1	2.0	-1.0	1	21	979	999	CUGAAGUGUUUGGGGGAACUC	AUGUUCUUCCAAACACUUCAA	Cleavage
sly-miR395a-1	Solyc04g054730.3.1	2.5	-1.0	1	21	208	228	CUGAAGUGUUUGGGGGAACUC	GAGUUCUCCGGAACACUUCAG	Cleavage
sly-miR395a-1	Solyc09g056270.2.1	2.5	-1.0	1	21	41	61	CUGAAGUGUUUGGGGGAACUC	GUUUUUCCUCAAACACUUCGG	Cleavage
sly-miR395a-1	Solyc03g005260.3.1	3.0	-1.0	1	21	1267	1287	CUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-1	Solyc09g082860.3.1	3.0	-1.0	1	21	382	402	CUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-1	Solyc06g082560.2.1	3.0	-1.0	1	21	251	271	CUGAAGUGUUUGGGGGAACUC	AAGUUCCACCAAGUACUUCAC	Cleavage
sly-miR395a-1	Solyc01g068450.3.1	3.0	-1.0	1	21	2959	2979	CUGAAGUGUUUGGGGGAACUC	UAGUGCCCUCAGACACUUCAA	Cleavage
sly-miR395a-1	Solyc06g008800.2.1	3.0	-1.0	1	21	1016	1036	CUGAAGUGUUUGGGGGAACUC	UUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-1	Solyc00g102400.3.1	3.0	-1.0	1	21	849	869	CUGAAGUGUUUGGGGGAACUC	UUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-1	Solyc12g088330.1.1	3.0	-1.0	1	21	302	322	CUGAAGUGUUUGGGGGAACUC	AGGUUUCAUCAAAUAUUUCAG	Cleavage
sly-miR395a-1	Solyc08g076370.3.1	3.0	-1.0	1	21	120	140	CUGAAGUGUUUGGGGGAACUC	UUGUUCACUCAAACAUUUCAU	Cleavage
sly-miR395a-1	Solyc11g067010.2.1	3.0	-1.0	1	21	469	489	CUGAAGUGUUUGGGGGAACUC	UCGUGUCCCCAAACACCUCAG	Cleavage
sly-miR395a-1	Solyc11g065820.2.1	3.0	-1.0	1	21	3358	3378	CUGAAGUGUUUGGGGGAACUC	AUGUUCUGGCAAACACUUCAG	Cleavage
sly-miR395a-2	Solyc11g066140.2.1	1.5	-1.0	1	22	2828	2849	CUGAAGUGUUUGGGGGAACUCC	AAAGUUCCUCCAAACACUUCAA	Cleavage
sly-miR395a-2	Solyc04g054730.3.1	1.5	-1.0	1	22	261	282	CUGAAGUGUUUGGGGGAACUCC	UGUGUUCUCCCAAACACUUCAA	Cleavage
sly-miR395a-2	Solyc10g081660.2.1	2.0	-1.0	1	22	161	182	CUGAAGUGUUUGGGGGAACUCC	UGGGUUCCUCCAAAGACUUCAG	Cleavage
sly-miR395a-2	Solyc06g075970.3.1	2.0	-1.0	1	22	978	999	CUGAAGUGUUUGGGGGAACUCC	AAUGUUCUUCCAAACACUUCAA	Cleavage
sly-miR395a-2	Solyc04g054730.3.1	2.5	-1.0	1	22	207	228	CUGAAGUGUUUGGGGGAACUCC	AGAGUUCUCCGGAACACUUCAG	Cleavage
sly-miR395a-2	Solyc09g056270.2.1	2.5	-1.0	1	22	40	61	CUGAAGUGUUUGGGGGAACUCC	CGUUUUUCCUCAAACACUUCGG	Cleavage
sly-miR395a-2	Solyc03g005260.3.1	3.0	-1.0	1	22	1266	1287	CUGAAGUGUUUGGGGGAACUCC	UGAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-2	Solyc09g082860.3.1	3.0	-1.0	1	22	381	402	CUGAAGUGUUUGGGGGAACUCC	CGAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-2	Solyc01g068450.3.1	3.0	-1.0	1	22	2958	2979	CUGAAGUGUUUGGGGGAACUCC	GUAGUGCCCUCAGACACUUCAA	Cleavage
sly-miR395a-2	Solyc06g082560.2.1	3.0	-1.0	1	22	250	271	CUGAAGUGUUUGGGGGAACUCC	CAAGUUCCACCAAGUACUUCAC	Cleavage
sly-miR395a-2	Solyc06g008800.2.1	3.0	-1.0	1	22	1015	1036	CUGAAGUGUUUGGGGGAACUCC	GUUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-2	Solyc00g102400.3.1	3.0	-1.0	1	22	848	869	CUGAAGUGUUUGGGGGAACUCC	GUUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-2	Solyc12g088330.1.1	3.0	-1.0	1	22	301	322	CUGAAGUGUUUGGGGGAACUCC	GAGGUUUCAUCAAAUAUUUCAG	Cleavage
sly-miR395a-2	Solyc08g076370.3.1	3.0	-1.0	1	22	119	140	CUGAAGUGUUUGGGGGAACUCC	CUUGUUCACUCAAACAUUUCAU	Cleavage
sly-miR395a-2	Solyc11g067010.2.1	3.0	-1.0	1	22	468	489	CUGAAGUGUUUGGGGGAACUCC	GUCGUGUCCCCAAACACCUCAG	Cleavage
sly-miR395a-2	Solyc11g065820.2.1	3.0	-1.0	1	22	3357	3378	CUGAAGUGUUUGGGGGAACUCC	UAUGUUCUGGCAAACACUUCAG	Cleavage
sly-miR395a-3	Solyc11g066140.2.1	1.5	-1.0	1	21	2829	2849	CUGAAGUGUUUGGGGGAACUC	AAGUUCCUCCAAACACUUCAA	Cleavage
sly-miR395a-3	Solyc04g054730.3.1	1.5	-1.0	1	21	262	282	CUGAAGUGUUUGGGGGAACUC	GUGUUCUCCCAAACACUUCAA	Cleavage
sly-miR395a-3	Solyc10g081660.2.1	2.0	-1.0	1	21	162	182	CUGAAGUGUUUGGGGGAACUC	GGGUUCCUCCAAAGACUUCAG	Cleavage
sly-miR395a-3	Solyc06g075970.3.1	2.0	-1.0	1	21	979	999	CUGAAGUGUUUGGGGGAACUC	AUGUUCUUCCAAACACUUCAA	Cleavage
sly-miR395a-3	Solyc04g054730.3.1	2.5	-1.0	1	21	208	228	CUGAAGUGUUUGGGGGAACUC	GAGUUCUCCGGAACACUUCAG	Cleavage
sly-miR395a-3	Solyc09g056270.2.1	2.5	-1.0	1	21	41	61	CUGAAGUGUUUGGGGGAACUC	GUUUUUCCUCAAACACUUCGG	Cleavage
sly-miR395a-3	Solyc03g005260.3.1	3.0	-1.0	1	21	1267	1287	CUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-3	Solyc09g082860.3.1	3.0	-1.0	1	21	382	402	CUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-3	Solyc06g082560.2.1	3.0	-1.0	1	21	251	271	CUGAAGUGUUUGGGGGAACUC	AAGUUCCACCAAGUACUUCAC	Cleavage
sly-miR395a-3	Solyc01g068450.3.1	3.0	-1.0	1	21	2959	2979	CUGAAGUGUUUGGGGGAACUC	UAGUGCCCUCAGACACUUCAA	Cleavage
sly-miR395a-3	Solyc06g008800.2.1	3.0	-1.0	1	21	1016	1036	CUGAAGUGUUUGGGGGAACUC	UUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-3	Solyc00g102400.3.1	3.0	-1.0	1	21	849	869	CUGAAGUGUUUGGGGGAACUC	UUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-3	Solyc12g088330.1.1	3.0	-1.0	1	21	302	322	CUGAAGUGUUUGGGGGAACUC	AGGUUUCAUCAAAUAUUUCAG	Cleavage
sly-miR395a-3	Solyc08g076370.3.1	3.0	-1.0	1	21	120	140	CUGAAGUGUUUGGGGGAACUC	UUGUUCACUCAAACAUUUCAU	Cleavage
sly-miR395a-3	Solyc11g067010.2.1	3.0	-1.0	1	21	469	489	CUGAAGUGUUUGGGGGAACUC	UCGUGUCCCCAAACACCUCAG	Cleavage
sly-miR395a-3	Solyc11g065820.2.1	3.0	-1.0	1	21	3358	3378	CUGAAGUGUUUGGGGGAACUC	AUGUUCUGGCAAACACUUCAG	Cleavage
sly-miR395a-4-3p	Solyc09g056270.2.1	2.0	-1.0	1	19	43	61	CUGAAGUGUUUGAGGGAAC	UUUUCCUCAAACACUUCGG	Cleavage
sly-miR395a-4-3p	Solyc08g076370.3.1	2.5	-1.0	1	19	122	140	CUGAAGUGUUUGAGGGAAC	GUUCACUCAAACAUUUCAU	Cleavage
sly-miR395a-4-3p	Solyc01g068450.3.1	2.5	-1.0	1	19	2961	2979	CUGAAGUGUUUGAGGGAAC	GUGCCCUCAGACACUUCAA	Cleavage
sly-miR395a-4-3p	Solyc12g088330.1.1	2.5	-1.0	1	19	304	322	CUGAAGUGUUUGAGGGAAC	GUUUCAUCAAAUAUUUCAG	Cleavage
sly-miR395a-4-3p	Solyc00g030000.1.1	3.0	-1.0	1	19	276	294	CUGAAGUGUUUGAGGGAAC	AUUCCCUCAAACAUUUUAU	Cleavage

sly-miR395a-4-3p	Solyc02g089200.3.1	3.0	-1.0	1	19	762	780	CUGAAGUGUUUGAGGGAAC	CUUCCCUCAAACACAUUAG	Cleavage
sly-miR395a-4-3p	Solyc04g054730.3.1	3.0	-1.0	1	19	264	282	CUGAAGUGUUUGAGGGAAC	GUUCUCCCAAACACUUCAA	Cleavage
sly-miR395a-4-3p	Solyc11g066140.2.1	3.0	-1.0	1	19	2831	2849	CUGAAGUGUUUGAGGGAAC	GUUCCUCCAAACACUUCAA	Cleavage
sly-miR395a-4-3p	Solyc12g042200.2.1	3.0	-1.0	1	19	311	329	CUGAAGUGUUUGAGGGAAC	GUUCCCUCAAACAUUUAAC	Cleavage
sly-miR395a-4-3p	Solyc01g094060.3.1	3.0	-1.0	1	19	967	985	CUGAAGUGUUUGAGGGAAC	CUUCCCUCAAACACCUCGG	Cleavage
sly-miR395a-4-3p	Solyc06g008450.3.1	3.0	-1.0	1	19	5835	5853	CUGAAGUGUUUGAGGGAAC	GUUCUCUCAAUCACUUCAU	Cleavage
sly-miR395a-4-3p	Solyc01g106040.3.1	3.0	-1.0	1	19	2126	2144	CUGAAGUGUUUGAGGGAAC	GUUCUCUUAAAUACUUUAA	Cleavage
sly-miR395a-4-3p	Solyc10g005690.3.1	3.0	-1.0	1	19	2112	2130	CUGAAGUGUUUGAGGGAAC	GUUCUCUAAAGCAUUUCAG	Cleavage
sly-miR395a-4-3p	Solyc08g082680.3.1	3.0	-1.0	1	19	36	54	CUGAAGUGUUUGAGGGAAC	GUAUCCUCAAGCACUUCAA	Cleavage
sly-miR395a-4-3p	Solyc08g063080.3.1	3.0	-1.0	1	19	2369	2387	CUGAAGUGUUUGAGGGAAC	GGUCCUUCAAAUACUUCAU	Cleavage
sly-miR395a-4-3p	Solyc06g073940.3.1	3.0	-1.0	1	19	745	763	CUGAAGUGUUUGAGGGAAC	GUCCCCUCAAACAUUUGAG	Cleavage
sly-miR395a-4-3p	Solyc04g015750.3.1	3.0	-1.0	1	19	3776	3794	CUGAAGUGUUUGAGGGAAC	GUCUUCUCAAACGCUUCGG	Cleavage
sly-miR395a-4-3p	Solyc11g065820.2.1	3.0	-1.0	1	19	3360	3378	CUGAAGUGUUUGAGGGAAC	GUUCUGGCAAACACUUCAG	Cleavage
sly-miR395a-4-3p	Solyc06g068550.3.1	3.0	-1.0	1	19	683	701	CUGAAGUGUUUGAGGGAAC	GGUUUGUCAAACACUUCAG	Cleavage
sly-miR395a-4-3p	Solyc11g044340.2.1	3.0	-1.0	1	19	2693	2711	CUGAAGUGUUUGAGGGAAC	GUCUCAUCAAAUACUUCAG	Cleavage
sly-miR395a-4-5p	Solyc11g066140.2.1	1.5	-1.0	1	22	2828	2849	CUGAAGUGUUUGGGGGAACUCC	AAAGUUCCUCCAAACACUUCAA	Cleavage
sly-miR395a-4-5p	Solyc04g054730.3.1	1.5	-1.0	1	22	261	282	CUGAAGUGUUUGGGGGAACUCC	UGUGUUCUCCCAAACACUUCAA	Cleavage
sly-miR395a-4-5p	Solyc10g081660.2.1	2.0	-1.0	1	22	161	182	CUGAAGUGUUUGGGGGAACUCC	UGGGUUCCUCCAAAGACUUCAG	Cleavage
sly-miR395a-4-5p	Solyc06g075970.3.1	2.0	-1.0	1	22	978	999	CUGAAGUGUUUGGGGGAACUCC	AAUGUUCUUCCAAACACUUCAA	Cleavage
sly-miR395a-4-5p	Solyc04g054730.3.1	2.5	-1.0	1	22	207	228	CUGAAGUGUUUGGGGGAACUCC	AGAGUUCUCCGGAACACUUCAG	Cleavage
sly-miR395a-4-5p	Solyc09g056270.2.1	2.5	-1.0	1	22	40	61	CUGAAGUGUUUGGGGGAACUCC	CGUUUUUCCUCAAACACUUCGG	Cleavage
sly-miR395a-4-5p	Solyc03g005260.3.1	3.0	-1.0	1	22	1266	1287	CUGAAGUGUUUGGGGGAACUCC	UGAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-4-5p	Solyc09g082860.3.1	3.0	-1.0	1	22	381	402	CUGAAGUGUUUGGGGGAACUCC	CGAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395a-4-5p	Solyc01g068450.3.1	3.0	-1.0	1	22	2958	2979	CUGAAGUGUUUGGGGGAACUCC	GUAGUGCCCUCAGACACUUCAA	Cleavage
sly-miR395a-4-5p	Solyc06g082560.2.1	3.0	-1.0	1	22	250	271	CUGAAGUGUUUGGGGGAACUCC	CAAGUUCCACCAAGUACUUCAC	Cleavage
sly-miR395a-4-5p	Solyc06g008800.2.1	3.0	-1.0	1	22	1015	1036	CUGAAGUGUUUGGGGGAACUCC	GUUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-4-5p	Solyc00g102400.3.1	3.0	-1.0	1	22	848	869	CUGAAGUGUUUGGGGGAACUCC	GUUAUUCCCCCUAGCACUUCAG	Translation
sly-miR395a-4-5p	Solyc12g088330.1.1	3.0	-1.0	1	22	301	322	CUGAAGUGUUUGGGGGAACUCC	GAGGUUUCAUCAAAUAUUUCAG	Cleavage
sly-miR395a-4-5p	Solyc08g076370.3.1	3.0	-1.0	1	22	119	140	CUGAAGUGUUUGGGGGAACUCC	CUUGUUCACUCAAACAUUUCAU	Cleavage
sly-miR395a-4-5p	Solyc11g067010.2.1	3.0	-1.0	1	22	468	489	CUGAAGUGUUUGGGGGAACUCC	GUCGUGUCCCCAAACACCUCAG	Cleavage
sly-miR395a-4-5p	Solyc11g065820.2.1	3.0	-1.0	1	22	3357	3378	CUGAAGUGUUUGGGGGAACUCC	UAUGUUCUGGCAAACACUUCAG	Cleavage
sly-miR395g	Solyc11g066140.2.1	0.5	-1.0	1	21	2829	2849	UUGAAGUGUUUGGGGGAACUC	AAGUUCCUCCAAACACUUCAA	Cleavage
sly-miR395g	Solyc04g054730.3.1	0.5	-1.0	1	21	262	282	UUGAAGUGUUUGGGGGAACUC	GUGUUCUCCCAAACACUUCAA	Cleavage
sly-miR395g	Solyc06g075970.3.1	1.0	-1.0	1	21	979	999	UUGAAGUGUUUGGGGGAACUC	AUGUUCUUCCAAACACUUCAA	Cleavage
sly-miR395g	Solyc01g068450.3.1	2.0	-1.0	1	21	2959	2979	UUGAAGUGUUUGGGGGAACUC	UAGUGCCCUCAGACACUUCAA	Cleavage
sly-miR395g	Solyc10g081660.2.1	2.5	-1.0	1	21	162	182	UUGAAGUGUUUGGGGGAACUC	GGGUUCCUCCAAAGACUUCAG	Cleavage
sly-miR395g	Solyc01g106040.3.1	2.5	-1.0	1	21	2124	2144	UUGAAGUGUUUGGGGGAACUC	CUGUUCUCUUAAAUACUUUAA	Cleavage
sly-miR395g	Solyc08g082680.3.1	2.5	-1.0	1	21	34	54	UUGAAGUGUUUGGGGGAACUC	UUGUAUCCUCAAGCACUUCAA	Cleavage
sly-miR395g	Solyc04g054730.3.1	3.0	-1.0	1	21	208	228	UUGAAGUGUUUGGGGGAACUC	GAGUUCUCCGGAACACUUCAG	Cleavage
sly-miR395g	Solyc03g005260.3.1	3.0	-1.0	1	21	1267	1287	UUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395g	Solyc09g082860.3.1	3.0	-1.0	1	21	382	402	UUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
sly-miR395g	Solyc08g080050.3.1	3.0	-1.0	1	21	413	433	UUGAAGUGUUUGGGGGAACUC	GAGUUUCUCCAAGCACUACAA	Cleavage
sly-miR395g	Solyc06g050930.3.1	3.0	-1.0	1	21	2185	2205	UUGAAGUGUUUGGGGGAACUC	UAGUUCCCUCUGGCACUUCAA	Translation
sly-miR395g	Solyc10g080350.2.1	3.0	-1.0	1	21	3384	3404	UUGAAGUGUUUGGGGGAACUC	UAGUUUUCUCAAAAACUUCAA	Cleavage
sly-miR395g	Solyc12g040640.2.1	3.0	-1.0	1	21	503	523	UUGAAGUGUUUGGGGGAACUC	GAUUUACCUCAAGCACUUCAA	Cleavage
sly-miR395g	Solyc03g115070.1.1	3.0	-1.0	1	21	1154	1174	UUGAAGUGUUUGGGGGAACUC	GAAUUGCUUCAAACACUUCAA	Cleavage
sly-miR395g	Solyc06g082560.2.1	3.0	-1.0	1	21	251	271	UUGAAGUGUUUGGGGGAACUC	AAGUUCCACCAAGUACUUCAC	Cleavage
sly-miR395g	Solyc09g056270.2.1	3.0	-1.0	1	21	41	61	UUGAAGUGUUUGGGGGAACUC	GUUUUUCCUCAAACACUUCGG	Cleavage
sly-miR395g	Solyc03g119070.2.1	3.0	-1.0	1	21	642	662	UUGAAGUGUUUGGGGGAACUC	UCCUUCCUUCAGACAUUUCAA	Cleavage
sly-miR395g	Solyc12g056350.2.1	3.0	-1.0	1	21	52	72	UUGAAGUGUUUGGGGGAACUC	UUCUUCCCCUAAACCCUUCAA	Cleavage

sly-miR395g	Solyc12g062595.1.1	3.0	-1.0	1	21	193	213	UUGAAGUGUUUGGGGGAACUC	CCGUUCUCGCAAAUAUUUCAA	Cleavage
sly-miR395g	Solyc05g006570.1.1	3.0	-1.0	1	21	1764	1784	UUGAAGUGUUUGGGGGAACUC	UUGUUUCUCUGAACACUUUGA	Cleavage
sly-miR395g	Solyc02g083070.2.1	3.0	-1.0	1	21	412	432	UUGAAGUGUUUGGGGGAACUC	AACUUGCCUCAAAUACUUCAA	Cleavage
sly-miR395g	Solyc08g067450.1.1	3.0	-1.0	1	21	313	333	UUGAAGUGUUUGGGGGAACUC	UGGUGCUUCCAAAUAUUUCAA	Cleavage
sly-miR395g	Solyc08g005470.3.1	3.0	-1.0	1	21	313	333	UUGAAGUGUUUGGGGGAACUC	UGGUGCUUCCAAAUAUUUCAA	Cleavage
sly-miR395g	Solyc09g089640.2.1	3.0	-1.0	1	21	215	235	UUGAAGUGUUUGGGGGAACUC	UUUUACCCUUAAACACUUCAA	Cleavage
sly-miR395g	Solyc08g076370.3.1	3.0	-1.0	1	21	120	140	UUGAAGUGUUUGGGGGAACUC	UUGUUCACUCAAACAUUUCAU	Cleavage
sly-miR395g	Solyc04g040120.1.1	3.0	-1.0	1	21	474	494	UUGAAGUGUUUGGGGGAACUC	AUGGUUCUCCAAAUAUUUCAA	Cleavage
sly-miR395g	Solyc01g107640.3.1	3.0	-1.0	1	21	3377	3397	UUGAAGUGUUUGGGGGAACUC	CCGAUCCUUCAGAUACUUCAA	Cleavage
sly-miR396a-3p	Solyc06g063080.1.1	2.5	-1.0	1	21	197	217	GUUCAAUAAAGCUGUGGGAAG	AUUCCUGCAGCUUUGUUGAAA	Cleavage
sly-miR396a-3p	Solyc06g053210.3.1	3.0	-1.0	1	21	1541	1561	GUUCAAUAAAGCUGUGGGAAG	ACUUCCAUAACUUUAUUGAAU	Cleavage
sly-miR396a-3p	Solyc01g105090.3.1	3.0	-1.0	1	21	2070	2090	GUUCAAUAAAGCUGUGGGAAG	UCUCUUGCAGUUUUAUUGAGU	Cleavage
sly-miR396a-5p	Solyc12g088670.2.1	2.0	-1.0	1	21	615	635	UUCCACAGCUUUCUUGAACUG	AGGAUCAAGGAAGCUGUGGGA	Cleavage
sly-miR396a-5p	Solyc02g062740.3.1	2.0	-1.0	1	21	1381	1401	UUCCACAGCUUUCUUGAACUG	AGGAUCAGGAAAGCUGUGGAG	Cleavage
sly-miR396a-5p	Solyc02g050283.1.1	2.5	-1.0	1	21	196	216	UUCCACAGCUUUCUUGAACUG	UGGUUCAAGAGGUCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc07g056470.3.1	2.5	-1.0	1	21	487	507	UUCCACAGCUUUCUUGAACUG	GGCUUCAAGGAAGCUGUGGAC	Cleavage
sly-miR396a-5p	Solyc01g066730.3.1	2.5	-1.0	1	21	88	108	UUCCACAGCUUUCUUGAACUG	CUUUUCAAGAAAGCUGUGCAA	Cleavage
sly-miR396a-5p	Solyc02g071240.3.1	2.5	-1.0	1	21	432	452	UUCCACAGCUUUCUUGAACUG	AUCUUUGAGAGAGCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc12g088700.1.1	2.5	-1.0	1	21	1090	1110	UUCCACAGCUUUCUUGAACUG	AUGAUUAAGAGAGCUGUGGAG	Cleavage
sly-miR396a-5p	Solyc04g014970.2.1	2.5	-1.0	1	21	997	1017	UUCCACAGCUUUCUUGAACUG	UUGUCCGAGGAAGUUGUGGAA	Cleavage
sly-miR396a-5p	Solyc01g112320.3.1	2.5	-1.0	1	21	2145	2165	UUCCACAGCUUUCUUGAACUG	UUGUAUGAGAAAGCUGUGGAG	Cleavage
sly-miR396a-5p	Solyc03g045080.2.1	3.0	-1.0	1	21	419	439	UUCCACAGCUUUCUUGAACUG	CAGUUUCAGGAGGUUGUGGAA	Cleavage
sly-miR396a-5p	Solyc04g054840.1.1	3.0	-1.0	1	21	408	428	UUCCACAGCUUUCUUGAACUG	UAGUUUAAGAGAGUGGUGGAA	Cleavage
sly-miR396a-5p	Solyc12g056995.1.1	3.0	-1.0	1	21	1746	1766	UUCCACAGCUUUCUUGAACUG	CAAUUCGAAAAAGCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc03g082430.1.1	3.0	-1.0	1	21	456	477	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCAUGUGGAA	Cleavage
sly-miR396a-5p	Solyc10g083510.2.1	3.0	-1.0	1	21	852	873	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc12g096070.2.1	3.0	-1.0	1	21	630	651	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCAUGUGGAA	Cleavage
sly-miR396a-5p	Solyc07g041640.3.1	3.0	-1.0	1	21	1136	1157	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc08g005430.3.1	3.0	-1.0	1	21	880	901	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc08g083230.2.1	3.0	-1.0	1	21	498	519	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc06g065030.3.1	3.0	-1.0	1	21	383	403	UUCCACAGCUUUCUUGAACUG	AAGUUUAAGAGAGAUGUGGAG	Cleavage
sly-miR396a-5p	Solyc08g075950.2.1	3.0	-1.0	1	21	619	640	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc01g091540.2.1	3.0	-1.0	1	21	767	788	UUCCACA-GCUUUCUUGAACUG	ACGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc04g077510.3.1	3.0	-1.0	1	21	1062	1083	UUCCACA-GCUUUCUUGAACUG	UCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc02g092070.3.1	3.0	-1.0	1	21	960	981	UUCCACA-GCUUUCUUGAACUG	UCGUUCAAGAAAGCAUGUGGAA	Cleavage
sly-miR396a-5p	Solyc06g007320.3.1	3.0	-1.0	1	21	2657	2677	UUCCACAGCUUUCUUGAACUG	UAGAUCGAGAAAGCUGUGAAA	Cleavage
sly-miR396a-5p	Solyc02g093040.3.1	3.0	-1.0	1	21	473	493	UUCCACAGCUUUCUUGAACUG	AAAAUCAAGGGAGCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc02g062750.3.1	3.0	-1.0	1	21	862	882	UUCCACAGCUUUCUUGAACUG	GAGAUCAAGAAAUCUGUGGGA	Cleavage
sly-miR396a-5p	Solyc08g066140.3.1	3.0	-1.0	1	21	141	161	UUCCACAGCUUUCUUGAACUG	CCCUUCAAGAGAGCUGUCGAA	Cleavage
sly-miR396a-5p	Solyc01g108340.3.1	3.0	-1.0	1	21	1169	1189	UUCCACAGCUUUCUUGAACUG	AGUUUCAAGAAAGCUUUGGAG	Cleavage
sly-miR396a-5p	Solyc08g066120.3.1	3.0	-1.0	1	21	2530	2550	UUCCACAGCUUUCUUGAACUG	CCCUUCAAGAGAGCUGUCGAA	Cleavage
sly-miR396a-5p	Solyc11g045120.2.1	3.0	-1.0	1	21	152	172	UUCCACAGCUUUCUUGAACUG	AUGUUCAAGAAGGCAGUGGAC	Cleavage
sly-miR396a-5p	Solyc10g079660.2.1	3.0	-1.0	1	21	1326	1346	UUCCACAGCUUUCUUGAACUG	UCGUUCAAGAAGGUUGAGGGA	Cleavage
sly-miR396a-5p	Solyc11g013260.2.1	3.0	-1.0	1	21	601	621	UUCCACAGCUUUCUUGAACUG	GAGUUUUCGAAAGCUGUGGAG	Cleavage
sly-miR396a-5p	Solyc08g068013.1.1	3.0	-1.0	1	21	1618	1638	UUCCACAGCUUUCUUGAACUG	CCAUAUGAGAAAGCUGUGGAA	Cleavage
sly-miR396a-5p	Solyc01g059960.1.1	3.0	-1.0	1	21	348	368	UUCCACAGCUUUCUUGAACUG	UUGUGCAAGAAAGUUGUUGAA	Cleavage
sly-miR396a-5p	Solyc02g065560.1.1	3.0	-1.0	1	21	598	618	UUCCACAGCUUUCUUGAACUG	AUGGUUAAGGAGGCUGUGGGA	Cleavage
sly-miR396a-5p	Solyc04g056640.1.1	3.0	-1.0	1	21	408	428	UUCCACAGCUUUCUUGAACUG	UUGUUUAUGGAAGUUGUGGAG	Cleavage
sly-miR396a-5p	Solyc02g069080.3.1	3.0	-1.0	1	21	1339	1359	UUCCACAGCUUUCUUGAACUG	UUGUCUGAGGAAGUUGUGGAA	Cleavage
sly-miR396b-5p	Solyc12g088670.2.1	2.0	-1.0	1	21	615	635	UUCCACAGCUUUCUUGAACUU	AGGAUCAAGGAAGCUGUGGGA	Cleavage

sly-miR396b-5p	Solyc02g062740.3.1	2.0	-1.0	1	21	1381	1401	UUCCACAGCUUUCUUGAACUU	AGGAUCAGGAAAGCUGUGGAG	Cleavage
sly-miR396b-5p	Solyc02g050283.1.1	2.5	-1.0	1	21	196	216	UUCCACAGCUUUCUUGAACUU	UGGUUCAAGAGGUCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc07g056470.3.1	2.5	-1.0	1	21	487	507	UUCCACAGCUUUCUUGAACUU	GGCUUCAAGGAAGCUGUGGAC	Cleavage
sly-miR396b-5p	Solyc01g066730.3.1	2.5	-1.0	1	21	88	108	UUCCACAGCUUUCUUGAACUU	CUUUUCAAGAAAGCUGUGCAA	Cleavage
sly-miR396b-5p	Solyc02g071240.3.1	2.5	-1.0	1	21	432	452	UUCCACAGCUUUCUUGAACUU	AUCUUUGAGAGAGCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc12g088700.1.1	2.5	-1.0	1	21	1090	1110	UUCCACAGCUUUCUUGAACUU	AUGAUUAAGAGAGCUGUGGAG	Cleavage
sly-miR396b-5p	Solyc04g014970.2.1	2.5	-1.0	1	21	997	1017	UUCCACAGCUUUCUUGAACUU	UUGUCCGAGGAAGUUGUGGAA	Cleavage
sly-miR396b-5p	Solyc01g112320.3.1	2.5	-1.0	1	21	2145	2165	UUCCACAGCUUUCUUGAACUU	UUGUAUGAGAAAGCUGUGGAG	Cleavage
sly-miR396b-5p	Solyc06g065030.3.1	3.0	-1.0	1	21	383	403	UUCCACAGCUUUCUUGAACUU	AAGUUUAAGAGAGAUGUGGAG	Cleavage
sly-miR396b-5p	Solyc04g054840.1.1	3.0	-1.0	1	21	408	428	UUCCACAGCUUUCUUGAACUU	UAGUUUAAGAGAGUGGUGGAA	Cleavage
sly-miR396b-5p	Solyc01g091540.2.1	3.0	-1.0	1	21	767	788	UUCCACA-GCUUUCUUGAACUU	ACGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc03g082430.1.1	3.0	-1.0	1	21	456	477	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCAUGUGGAA	Cleavage
sly-miR396b-5p	Solyc10g083510.2.1	3.0	-1.0	1	21	852	873	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc01g108340.3.1	3.0	-1.0	1	21	1169	1189	UUCCACAGCUUUCUUGAACUU	AGUUUCAAGAAAGCUUUGGAG	Cleavage
sly-miR396b-5p	Solyc12g096070.2.1	3.0	-1.0	1	21	630	651	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCAUGUGGAA	Cleavage
sly-miR396b-5p	Solyc07g041640.3.1	3.0	-1.0	1	21	1136	1157	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc02g093040.3.1	3.0	-1.0	1	21	473	493	UUCCACAGCUUUCUUGAACUU	AAAAUCAAGGGAGCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc08g005430.3.1	3.0	-1.0	1	21	880	901	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc02g062750.3.1	3.0	-1.0	1	21	862	882	UUCCACAGCUUUCUUGAACUU	GAGAUCAAGAAAUCUGUGGGA	Cleavage
sly-miR396b-5p	Solyc08g083230.2.1	3.0	-1.0	1	21	498	519	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc04g077510.3.1	3.0	-1.0	1	21	1062	1083	UUCCACA-GCUUUCUUGAACUU	UCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc08g075950.2.1	3.0	-1.0	1	21	619	640	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc02g092070.3.1	3.0	-1.0	1	21	960	981	UUCCACA-GCUUUCUUGAACUU	UCGUUCAAGAAAGCAUGUGGAA	Cleavage
sly-miR396b-5p	Solyc03g045080.2.1	3.0	-1.0	1	21	419	439	UUCCACAGCUUUCUUGAACUU	CAGUUUCAGGAGGUUGUGGAA	Cleavage
sly-miR396b-5p	Solyc12g056995.1.1	3.0	-1.0	1	21	1746	1766	UUCCACAGCUUUCUUGAACUU	CAAUUCGAAAAAGCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc11g045120.2.1	3.0	-1.0	1	21	152	172	UUCCACAGCUUUCUUGAACUU	AUGUUCAAGAAGGCAGUGGAC	Cleavage
sly-miR396b-5p	Solyc06g007320.3.1	3.0	-1.0	1	21	2657	2677	UUCCACAGCUUUCUUGAACUU	UAGAUCGAGAAAGCUGUGAAA	Cleavage
sly-miR396b-5p	Solyc08g066140.3.1	3.0	-1.0	1	21	141	161	UUCCACAGCUUUCUUGAACUU	CCCUUCAAGAGAGCUGUCGAA	Cleavage
sly-miR396b-5p	Solyc11g013260.2.1	3.0	-1.0	1	21	601	621	UUCCACAGCUUUCUUGAACUU	GAGUUUUCGAAAGCUGUGGAG	Cleavage
sly-miR396b-5p	Solyc08g066120.3.1	3.0	-1.0	1	21	2530	2550	UUCCACAGCUUUCUUGAACUU	CCCUUCAAGAGAGCUGUCGAA	Cleavage
sly-miR396b-5p	Solyc10g079660.2.1	3.0	-1.0	1	21	1326	1346	UUCCACAGCUUUCUUGAACUU	UCGUUCAAGAAGGUUGAGGGA	Cleavage
sly-miR396b-5p	Solyc08g068013.1.1	3.0	-1.0	1	21	1618	1638	UUCCACAGCUUUCUUGAACUU	CCAUAUGAGAAAGCUGUGGAA	Cleavage
sly-miR396b-5p	Solyc02g065560.1.1	3.0	-1.0	1	21	598	618	UUCCACAGCUUUCUUGAACUU	AUGGUUAAGGAGGCUGUGGGA	Cleavage
sly-miR396b-5p	Solyc01g059960.1.1	3.0	-1.0	1	21	348	368	UUCCACAGCUUUCUUGAACUU	UUGUGCAAGAAAGUUGUUGAA	Cleavage
sly-miR396b-5p	Solyc04g056640.1.1	3.0	-1.0	1	21	408	428	UUCCACAGCUUUCUUGAACUU	UUGUUUAUGGAAGUUGUGGAG	Cleavage
sly-miR396b-5p	Solyc02g069080.3.1	3.0	-1.0	1	21	1339	1359	UUCCACAGCUUUCUUGAACUU	UUGUCUGAGGAAGUUGUGGAA	Cleavage
sly-miR396g-1-3p	Solyc06g068700.3.1	2.0	-1.0	1	21	1791	1811	GUUCAAGAAAGCUGUGGAAAA	AUUUUCACAGUUUUCUUGAAG	Cleavage
sly-miR396g-1-3p	Solyc01g066740.3.1	2.0	-1.0	1	21	6085	6105	GUUCAAGAAAGCUGUGGAAAA	AGUUGCACAGCUUUCUUGAAA	Cleavage
sly-miR396g-1-3p	Solyc10g083310.2.1	2.5	-1.0	1	21	1759	1779	GUUCAAGAAAGCUGUGGAAAA	UCUGUCACGGCUUUCUUGAAU	Cleavage
sly-miR396g-1-3p	Solyc05g017930.2.1	3.0	-1.0	1	21	142	162	GUUCAAGAAAGCUGUGGAAAA	UUCUUCGUAGCUUUCUUGGAC	Cleavage
sly-miR396g-1-3p	Solyc02g078210.3.1	3.0	-1.0	1	21	4202	4222	GUUCAAGAAAGCUGUGGAAAA	UGUUCUACAGUUGUUUUGAAC	Cleavage
sly-miR396g-1-3p	Solyc11g011560.2.1	3.0	-1.0	1	21	44	64	GUUCAAGAAAGCUGUGGAAAA	AGUUUCAUAGUUUUCUUGAUC	Cleavage
sly-miR396g-1-3p	Solyc12g057040.2.1	3.0	-1.0	1	21	1253	1273	GUUCAAGAAAGCUGUGGAAAA	GGUUCUGCAGCUUCCUUGGAC	Cleavage
sly-miR396g-1-3p	Solyc01g068280.3.1	3.0	-1.0	1	21	2334	2354	GUUCAAGAAAGCUGUGGAAAA	CUCUACACAGCUUUCUUGAAG	Cleavage
sly-miR396g-1-3p	Solyc02g081420.3.1	3.0	-1.0	1	21	2060	2082	GUUCAAGAAAGCUGU--GGAAAA	CCUUCCUAACAGCUUUUUUGAAC	Cleavage
sly-miR396g-1-3p	Solyc11g039840.2.1	3.0	-1.0	1	21	853	873	GUUCAAGAAAGCUGUGGAAAA	UCUUGCGUAGCUUUCUUGAGU	Cleavage
sly-miR396g-1-3p	Solyc01g095720.3.1	3.0	-1.0	1	21	2555	2575	GUUCAAGAAAGCUGUGGAAAA	GCUUUCAGAGUUUUUUUGAAU	Cleavage
sly-miR396g-1-5p	Solyc12g088670.2.1	2.0	-1.0	1	20	616	635	UCCCACAGCUUUCUUGGACU	GGAUCAAGGAAGCUGUGGGA	Cleavage
sly-miR396g-1-5p	Solyc02g062750.3.1	3.0	-1.0	1	20	863	882	UCCCACAGCUUUCUUGGACU	AGAUCAAGAAAUCUGUGGGA	Cleavage
sly-miR396g-1-5p	Solyc04g014970.2.1	3.0	-1.0	1	20	998	1017	UCCCACAGCUUUCUUGGACU	UGUCCGAGGAAGUUGUGGAA	Cleavage

sly-miR396g-1-5p	Solyc10g079660.2.1	3.0	-1.0	1	20	1327	1346	UCCCACAGCUUUCUUGGACU	CGUUCAAGAAGGUUGAGGGA	Cleavage
sly-miR396g-1-5p	Solyc10g076270.2.1	3.0	-1.0	1	20	277	296	UCCCACAGCUUUCUUGGACU	UGUCUGGGAAAGCUCUGGGA	Cleavage
sly-miR396g-1-5p	Solyc09g014780.3.1	3.0	-1.0	1	20	2319	2338	UCCCACAGCUUUCUUGGACU	UGUCUGGGAAAACUGUGGGA	Cleavage
sly-miR396g-1-5p	Solyc02g079095.1.1	3.0	-1.0	1	20	308	327	UCCCACAGCUUUCUUGGACU	GCUCAAAGAAAGCUGUGGGU	Cleavage
sly-miR396g-1-5p	Solyc02g065560.1.1	3.0	-1.0	1	20	599	618	UCCCACAGCUUUCUUGGACU	UGGUUAAGGAGGCUGUGGGA	Cleavage
sly-miR396g-2-3p	Solyc06g068700.3.1	2.0	-1.0	1	21	1791	1811	GUUCAAGAAAGCUGUGGAAAA	AUUUUCACAGUUUUCUUGAAG	Cleavage
sly-miR396g-2-3p	Solyc01g066740.3.1	2.0	-1.0	1	21	6085	6105	GUUCAAGAAAGCUGUGGAAAA	AGUUGCACAGCUUUCUUGAAA	Cleavage
sly-miR396g-2-3p	Solyc10g083310.2.1	2.5	-1.0	1	21	1759	1779	GUUCAAGAAAGCUGUGGAAAA	UCUGUCACGGCUUUCUUGAAU	Cleavage
sly-miR396g-2-3p	Solyc05g017930.2.1	3.0	-1.0	1	21	142	162	GUUCAAGAAAGCUGUGGAAAA	UUCUUCGUAGCUUUCUUGGAC	Cleavage
sly-miR396g-2-3p	Solyc02g078210.3.1	3.0	-1.0	1	21	4202	4222	GUUCAAGAAAGCUGUGGAAAA	UGUUCUACAGUUGUUUUGAAC	Cleavage
sly-miR396g-2-3p	Solyc11g011560.2.1	3.0	-1.0	1	21	44	64	GUUCAAGAAAGCUGUGGAAAA	AGUUUCAUAGUUUUCUUGAUC	Cleavage
sly-miR396g-2-3p	Solyc12g057040.2.1	3.0	-1.0	1	21	1253	1273	GUUCAAGAAAGCUGUGGAAAA	GGUUCUGCAGCUUCCUUGGAC	Cleavage
sly-miR396g-2-3p	Solyc01g068280.3.1	3.0	-1.0	1	21	2334	2354	GUUCAAGAAAGCUGUGGAAAA	CUCUACACAGCUUUCUUGAAG	Cleavage
sly-miR396g-2-3p	Solyc02g081420.3.1	3.0	-1.0	1	21	2060	2082	GUUCAAGAAAGCUGU--GGAAAA	CCUUCCUAACAGCUUUUUUGAAC	Cleavage
sly-miR396g-2-3p	Solyc11g039840.2.1	3.0	-1.0	1	21	853	873	GUUCAAGAAAGCUGUGGAAAA	UCUUGCGUAGCUUUCUUGAGU	Cleavage
sly-miR396g-2-3p	Solyc01g095720.3.1	3.0	-1.0	1	21	2555	2575	GUUCAAGAAAGCUGUGGAAAA	GCUUUCAGAGUUUUUUUGAAU	Cleavage
sly-miR396g-2-5p	Solyc12g013840.2.1	2.0	-1.0	1	21	2568	2588	UCCCACAGCUUUAUUGAACCG	CAAUACAAUAAAGCUGUGGGA	Cleavage
sly-miR396g-2-5p	Solyc02g031980.3.1	2.0	-1.0	1	21	238	258	UCCCACAGCUUUAUUGAACCG	AAGGUCUAUAAAGCUGUGGGA	Cleavage
sly-miR396g-2-5p	Solyc01g109350.3.1	2.5	-1.0	1	21	806	826	UCCCACAGCUUUAUUGAACCG	UGGUACCAUAAGGCUGUGGGA	Cleavage
sly-miR396g-2-5p	Solyc01g059870.4.1	2.5	-1.0	1	21	1324	1344	UCCCACAGCUUUAUUGAACCG	AAAUUCAAUGAGGCUGUGGGG	Cleavage
sly-miR396g-2-5p	Solyc05g010396.1.1	3.0	-1.0	1	21	45	65	UCCCACAGCUUUAUUGAACCG	UGGUUUGCUGAAGUUGUGGGA	Cleavage
sly-miR396g-2-5p	Solyc04g049485.1.1	3.0	-1.0	1	21	458	478	UCCCACAGCUUUAUUGAACCG	GGAUUCAAUAAUGUUGUGGGA	Translation
sly-miR396g-2-5p	Solyc02g078800.3.1	3.0	-1.0	1	21	502	522	UCCCACAGCUUUAUUGAACCG	AGGUGUAAUAAAGCUAUGGGA	Cleavage
sly-miR396g-2-5p	Solyc12g088670.2.1	3.0	-1.0	1	21	615	635	UCCCACAGCUUUAUUGAACCG	AGGAUCAAGGAAGCUGUGGGA	Cleavage
sly-miR396g-2-5p	Solyc12g006570.2.1	3.0	-1.0	1	21	1837	1857	UCCCACAGCUUUAUUGAACCG	UCGUUCAAUAAAACUAUGGGA	Cleavage
sly-miR396g-2-5p	Solyc11g007030.2.1	3.0	-1.0	1	21	274	294	UCCCACAGCUUUAUUGAACCG	UAAUACAAUGAAGUUGUGGGA	Cleavage
sly-miR397-1-3p	Solyc11g010730.2.1	2.5	-1.0	1	21	1185	1205	CAUCAACGCUAAACUCGAUCA	UAAUUGGUUUUAGUGUUGAUG	Cleavage
sly-miR397-1-3p	Solyc02g084680.2.1	3.0	-1.0	1	21	334	354	CAUCAACGCUAAACUCGAUCA	GGAUCGGGUUUGGUGAUGAUG	Cleavage
sly-miR397-1-3p	Solyc07g056390.3.1	3.0	-1.0	1	21	332	352	CAUCAACGCUAAACUCGAUCA	GCAGCGAUUUUGGUGUUGAUG	Cleavage
sly-miR397-1-5p	Solyc07g049460.3.1	0.5	-1.0	1	21	837	857	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAACGCUGCGCUCAAU	Cleavage
sly-miR397-1-5p	Solyc10g076830.2.1	1.0	-1.0	1	21	1014	1034	AUUGAGUGCAGCGUUGAUGAC	GUAAUCAACGCUGCACUCAAU	Cleavage
sly-miR397-1-5p	Solyc06g082260.3.1	1.0	-1.0	1	21	719	739	AUUGAGUGCAGCGUUGAUGAC	GUGAUCAACGCUGCACUCAAU	Cleavage
sly-miR397-1-5p	Solyc05g043360.2.1	1.0	-1.0	1	21	950	970	AUUGAGUGCAGCGUUGAUGAC	AUAAUCAACGCUGCACUCAAU	Cleavage
sly-miR397-1-5p	Solyc02g062650.3.1	1.5	-1.0	1	21	969	989	AUUGAGUGCAGCGUUGAUGAC	AUUGUCAAUGCUGCACUCAAU	Cleavage
sly-miR397-1-5p	Solyc09g011045.1.1	1.5	-1.0	1	21	726	746	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAACGCUGCACUUAAU	Cleavage
sly-miR397-1-5p	Solyc09g010993.1.1	1.5	-1.0	1	21	1195	1215	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAACGCUGCACUUAAU	Cleavage
sly-miR397-1-5p	Solyc06g076330.3.1	1.5	-1.0	1	21	2612	2632	AUUGAGUGCAGCGUUGAUGAC	AUAAUCAAUGCUGCACUCAAU	Cleavage
sly-miR397-1-5p	Solyc06g048860.2.1	2.0	-1.0	1	21	619	639	AUUGAGUGCAGCGUUGAUGAC	GUUAUCAAUGCUGCACUCAAC	Cleavage
sly-miR397-1-5p	Solyc09g014240.3.1	2.0	-1.0	1	21	797	817	AUUGAGUGCAGCGUUGAUGAC	GUAAUCAACGCUGCACUCAAC	Cleavage
sly-miR397-1-5p	Solyc06g076760.2.1	2.0	-1.0	1	21	679	699	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAAUGCUGCACUAAAU	Cleavage
sly-miR397-1-5p	Solyc07g063920.3.1	2.0	-1.0	1	21	1105	1125	AUUGAGUGCAGCGUUGAUGAC	UACCUCAACGUUGCACUUAAU	Cleavage
sly-miR397-1-5p	Solyc02g085120.3.1	2.5	-1.0	1	21	733	753	AUUGAGUGCAGCGUUGAUGAC	AUUAUCAAUGCUGCUCUCAAU	Cleavage
sly-miR397-1-5p	Solyc09g010990.3.1	2.5	-1.0	1	21	689	709	AUUGAGUGCAGCGUUGAUGAC	UUAAUCAACGCUGCACUAAAU	Cleavage
sly-miR397-1-5p	Solyc04g079100.3.1	2.5	-1.0	1	21	367	387	AUUGAGUGCAGCGUUGAUGAC	AAAAUUAACGUUGUACUCAAU	Cleavage
sly-miR397-1-5p	Solyc01g104280.2.1	2.5	-1.0	1	21	823	843	AUUGAGUGCAGCGUUGAUGAC	UGCUUCAAUGCUGUAUUCAAU	Cleavage
sly-miR397-1-5p	Solyc02g078690.2.1	3.0	-1.0	1	21	1592	1612	AUUGAGUGCAGCGUUGAUGAC	CUCAUCAAUGCUGGACUCAAG	Cleavage
sly-miR397-1-5p	Solyc01g108920.3.1	3.0	-1.0	1	21	2660	2680	AUUGAGUGCAGCGUUGAUGAC	UUCAUCAGCGUUGCAUUCAGC	Cleavage
sly-miR397-1-5p	Solyc01g108940.2.1	3.0	-1.0	1	21	2577	2597	AUUGAGUGCAGCGUUGAUGAC	UUCAUCAGCGUUGCAUUCAGC	Cleavage
sly-miR397-1-5p	Solyc06g074350.3.1	3.0	-1.0	1	21	814	834	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAAUGUUUCACUUAAU	Cleavage
sly-miR397-1-5p	Solyc03g095220.3.1	3.0	-1.0	1	21	330	350	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAACGGUGAACUCAAU	Translation

sly-miR397-1-5p	Solyc10g076710.2.1	3.0	-1.0	1	21	1545	1565	AUUGAGUGCAGCGUUGAUGAC	CUCAUUAAUGUUGCCCUCAAU	Cleavage
sly-miR397-1-5p	Solyc02g085110.3.1	3.0	-1.0	1	21	1565	1585	AUUGAGUGCAGCGUUGAUGAC	AUUGUCAAUGCUGCUCUCAAU	Cleavage
sly-miR397-1-5p	Solyc09g011960.2.1	3.0	-1.0	1	21	1110	1130	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAAUGCUGCACUUAAC	Cleavage
sly-miR397-1-5p	Solyc02g062700.3.1	3.0	-1.0	1	21	33	53	AUUGAGUGCAGCGUUGAUGAC	CACGUCAAUGUUGUAUUCGAU	Cleavage
sly-miR397-1-5p	Solyc07g043160.1.1	3.0	-1.0	1	21	601	621	AUUGAGUGCAGCGUUGAUGAC	CCCAUUCAUGCUGUAUUCAAU	Cleavage
sly-miR397-1-5p	Solyc09g018030.3.1	3.0	-1.0	1	21	407	427	AUUGAGUGCAGCGUUGAUGAC	AGCUUCAAUGUUGCAUUCAGU	Cleavage
sly-miR397-1-5p	Solyc10g082000.2.1	3.0	-1.0	1	21	1225	1245	AUUGAGUGCAGCGUUGAUGAC	UGCUUCAACGUGGCACUCAAU	Translation
sly-miR397-2-3p	Solyc07g063650.3.1	0.0	-1.0	1	21	3613	3633	CAUCAACGCUGCACUCAAUCA	UGAUUGAGUGCAGCGUUGAUG	Cleavage
sly-miR397-2-3p	Solyc06g082270.2.1	1.0	-1.0	1	21	2382	2402	CAUCAACGCUGCACUCAAUCA	UGAUUGAGUGCAGCGUUGAUC	Cleavage
sly-miR397-2-3p	Solyc12g042740.2.1	2.5	-1.0	1	21	1327	1347	CAUCAACGCUGCACUCAAUCA	GGAUUCAGUGCAGAGUUGAUG	Cleavage
sly-miR397-2-3p	Solyc08g080470.3.1	3.0	-1.0	1	21	372	392	CAUCAACGCUGCACUCAAUCA	CUGUUGGGUGUAGUGUUGAUU	Cleavage
sly-miR397-2-5p	Solyc07g063650.3.1	0.0	-1.0	1	20	3674	3693	AUCGAGUUUAGCGUUGAUGA	UCAUCAACGCUAAACUCGAU	Cleavage
sly-miR397-2-5p	Solyc06g073530.2.1	2.5	-1.0	1	20	1880	1899	AUCGAGUUUAGCGUUGAUGA	AGAUCAAUGCUAAGCUCGGU	Cleavage
sly-miR397-2-5p	Solyc02g077630.3.1	3.0	-1.0	1	20	2928	2947	AUCGAGUUUAGCGUUGAUGA	UCAUUGACCCUAAACUUGAU	Cleavage
sly-miR397-2-5p	Solyc03g122140.3.1	3.0	-1.0	1	20	1993	2012	AUCGAGUUUAGCGUUGAUGA	UUAUUAGCGCUAAACUCCAU	Cleavage
sly-miR397-2-5p	Solyc02g091090.3.1	3.0	-1.0	1	20	482	501	AUCGAGUUUAGCGUUGAUGA	UAAUUAAUGUUAAACUUGAU	Cleavage
sly-miR397-2-5p	Solyc08g068230.3.1	3.0	-1.0	1	20	349	368	AUCGAGUUUAGCGUUGAUGA	UCAGCAAUGCUAAAUUUGGU	Cleavage
sly-miR397-2-5p	Solyc06g073540.3.1	3.0	-1.0	1	20	1841	1860	AUCGAGUUUAGCGUUGAUGA	AGAUCAAUGCUAAGCUUGGU	Cleavage
sly-miR397-2-5p	Solyc05g053230.3.1	3.0	-1.0	1	20	1272	1291	AUCGAGUUUAGCGUUGAUGA	GUGUUGACGCUAGACUCGGU	Cleavage
sly-miR397-2-5p	Solyc12g089140.2.1	3.0	-1.0	1	20	3229	3248	AUCGAGUUUAGCGUUGAUGA	ACAUUAACGCCAAAUUUGAU	Translation
sly-miR397-2-5p	Solyc03g117870.3.1	3.0	-1.0	1	20	1089	1108	AUCGAGUUUAGCGUUGAUGA	UCCCUAACGCUAAACUCGGU	Cleavage
sly-miR397-2-5p	Solyc03g121470.3.1	3.0	-1.0	1	20	4480	4499	AUCGAGUUUAGCGUUGAUGA	GCAUAAAAGUUAAACUCGAU	Cleavage
sly-miR398a-3p	Solyc11g064980.1.1	2.5	-1.0	1	20	34	53	UAUGUUCUCAGGUCGCCCCU	AGGGUUGAUUUGAGAACAUA	Cleavage
sly-miR398a-3p	Solyc08g081220.1.1	3.0	-1.0	1	20	611	630	UAUGUUCUCAGGUCGCCCCU	CGGGGUUACCUGAGAAUAUU	Cleavage
sly-miR398a-3p	Solyc08g083210.3.1	3.0	-1.0	1	20	1669	1688	UAUGUUCUCAGGUCGCCCCU	GGGAGAGACCUGAGGACAUG	Cleavage
sly-miR398a-5p	Solyc10g005150.2.1	2.0	-1.0	1	21	149	169	GGGUUGAUUUGAGAACAUAUG	UUUAUGUGUUCAAAUCAACUC	Cleavage
sly-miR398a-5p	Solyc10g005160.1.1	2.5	-1.0	1	21	227	247	GGGUUGAUUUGAGAACAUAUG	UUUAUGUUUUUAAAUCAACUA	Cleavage
sly-miR398a-5p	Solyc07g045290.3.1	2.5	-1.0	1	21	3668	3688	GGGUUGAUUUGAGAACAUAUG	GUUAUAUUCUCGAAUCAACUU	Cleavage
sly-miR398a-5p	Solyc11g064980.1.1	3.0	-1.0	1	21	103	123	GGGUUGAUUUGAGAACAUAUG	CAUAUGUUCUCAGGUCGCCCC	Cleavage
sly-miR398a-5p	Solyc12g005670.2.1	3.0	-1.0	1	21	3089	3109	GGGUUGAUUUGAGAACAUAUG	AAUGUGUUAUUAAAUCAACCU	Cleavage
sly-miR398a-5p	Solyc09g083400.3.1	3.0	-1.0	1	21	2046	2066	GGGUUGAUUUGAGAACAUAUG	UGUAUGUUCUUCAAUUAACUC	Translation
sly-miR398a-5p	Solyc12g049380.2.1	3.0	-1.0	1	21	294	314	GGGUUGAUUUGAGAACAUAUG	AAUAUAUUUUUAAAUCAACCA	Cleavage
sly-miR398a-5p	Solyc06g052100.2.1	3.0	-1.0	1	21	93	113	GGGUUGAUUUGAGAACAUAUG	AAUAUGGUAUCAAAUCAACUC	Cleavage
sly-miR398a-5p	Solyc11g005550.2.1	3.0	-1.0	1	21	1075	1095	GGGUUGAUUUGAGAACAUAUG	GAUGUGUACUCAAAUCAAACC	Cleavage
sly-miR398a-5p	Solyc06g072407.1.1	3.0	-1.0	1	21	155	175	GGGUUGAUUUGAGAACAUAUG	UUUAUGUUCUCGGGUCAACUA	Cleavage
sly-miR398a-5p	Solyc11g028340.2.1	3.0	-1.0	1	21	1624	1644	GGGUUGAUUUGAGAACAUAUG	UAUCUUUUCUCGAGUCAACCC	Cleavage
sly-miR398a-5p	Solyc01g091000.3.1	3.0	-1.0	1	21	198	218	GGGUUGAUUUGAGAACAUAUG	UGUGUUUUUUCAAAUUAACCU	Cleavage
sly-miR398a-5p	Solyc03g095250.3.1	3.0	-1.0	1	21	229	249	GGGUUGAUUUGAGAACAUAUG	UUUAUGUUCUUGAAUCGAACC	Cleavage
sly-miR398a-5p	Solyc12g017480.2.1	3.0	-1.0	1	21	52	72	GGGUUGAUUUGAGAACAUAUG	GAUAUGCACUCAAAUCAGCUC	Cleavage
sly-miR398a-5p	Solyc08g066670.3.1	3.0	-1.0	1	21	1482	1502	GGGUUGAUUUGAGAACAUAUG	AAGAGGUUCUCAAGUCAACUC	Cleavage
sly-miR398a-5p	Solyc08g066690.3.1	3.0	-1.0	1	21	3763	3783	GGGUUGAUUUGAGAACAUAUG	AAGAGGUUCUCAAGUCAACUC	Cleavage
sly-miR398a-5p	Solyc12g017830.2.1	3.0	-1.0	1	21	232	252	GGGUUGAUUUGAGAACAUAUG	UUGAUGCUUUCAAAUCGACCC	Cleavage
sly-miR398a-5p	Solyc12g056440.2.1	3.0	-1.0	1	21	1117	1137	GGGUUGAUUUGAGAACAUAUG	CCUAUGAUCUCAAAUCAAUAC	Cleavage
sly-miR398a-5p	Solyc06g082190.3.1	3.0	-1.0	1	21	891	911	GGGUUGAUUUGAGAACAUAUG	AGAAUUUUCUUAAAUCAGCCC	Cleavage
sly-miR398a-5p	Solyc02g082100.3.1	3.0	-1.0	1	21	1706	1726	GGGUUGAUUUGAGAACAUAUG	UGUAUUUCUUCAAGUCAACCC	Cleavage
sly-miR398a-5p	Solyc12g017835.1.1	3.0	-1.0	1	21	252	272	GGGUUGAUUUGAGAACAUAUG	UUGAUGCUUUCAAAUCGACCC	Cleavage
sly-miR398a-5p	Solyc09g009770.3.1	3.0	-1.0	1	21	2002	2022	GGGUUGAUUUGAGAACAUAUG	AUUGUUUUUUCAAAUUAAUCC	Cleavage
sly-miR398b-3p	Solyc06g073140.2.1	3.0	-1.0	1	21	176	196	UGUGUUCUCAGGUUACCCCUG	AAGGGGUAAAAUGAGAACACA	Translation
sly-miR398b-3p	Solyc11g064980.1.1	3.0	-1.0	1	21	33	53	UGUGUUCUCAGGUUACCCCUG	UAGGGUUGAUUUGAGAACAUA	Cleavage
sly-miR398b-3p	Solyc01g067740.3.1	3.0	-1.0	1	21	317	337	UGUGUUCUCAGGUUACCCCUG	UAAGGGUGACCUGAGAUCACA	Cleavage

sly-miR398b-3p	Solyc08g081220.1.1	3.0	-1.0	1	21	610	630	UGUGUUCUCAGGUUACCCCUG	CCGGGGUUACCUGAGAAUAUU	Cleavage
sly-miR398b-3p	Solyc03g093140.3.1	3.0	-1.0	1	21	1531	1551	UGUGUUCUCAGGUUACCCCUG	UUCGGCUGACCUGGGAACACA	Cleavage
sly-miR399a-1	Solyc02g078210.3.1	1.5	-1.0	1	21	956	976	UGCCAAAGGAGAAUUGCCCUG	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399a-1	Solyc02g078210.3.1	1.5	-1.0	1	21	899	919	UGCCAAAGGAGAAUUGCCCUG	CUGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399a-1	Solyc01g103910.1.1	2.5	-1.0	1	21	1821	1841	UGCCAAAGGAGAAUUGCCCUG	GCAGGAAAUUCUCUUUUGGCA	Cleavage
sly-miR399a-1	Solyc02g088290.3.1	3.0	-1.0	1	21	3041	3061	UGCCAAAGGAGAAUUGCCCUG	UAGGAUAAUGCUCCUUUGGCA	Cleavage
sly-miR399a-1	Solyc03g071720.3.1	3.0	-1.0	1	21	985	1005	UGCCAAAGGAGAAUUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
sly-miR399a-1	Solyc06g054410.3.1	3.0	-1.0	1	21	8071	8091	UGCCAAAGGAGAAUUGCCCUG	UCUGCCAAUUUUCCUUUGGUA	Cleavage
sly-miR399a-1	Solyc02g094190.3.1	3.0	-1.0	1	21	1862	1882	UGCCAAAGGAGAAUUGCCCUG	UCGGGCAUUUCUUCUUUGCCA	Cleavage
sly-miR399a-1	Solyc05g007570.3.1	3.0	-1.0	1	21	2056	2076	UGCCAAAGGAGAAUUGCCCUG	AUGGGAAAUUCUCUAUUGGCA	Cleavage
sly-miR399a-2	Solyc03g071720.3.1	2.0	-1.0	1	21	985	1005	UGCCAAAGGAGAAUUGCACUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
sly-miR399a-2	Solyc05g053740.3.1	2.5	-1.0	1	21	1456	1476	UGCCAAAGGAGAAUUGCACUG	UGGUGCAAUUGUCUUUUGGUA	Translation
sly-miR399a-2	Solyc02g078210.3.1	2.5	-1.0	1	21	956	976	UGCCAAAGGAGAAUUGCACUG	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399a-2	Solyc02g078210.3.1	2.5	-1.0	1	21	899	919	UGCCAAAGGAGAAUUGCACUG	CUGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399a-2	Solyc08g006840.3.1	2.5	-1.0	1	21	1009	1029	UGCCAAAGGAGAAUUGCACUG	GAAUGCAGUUUUUCUUUGGCA	Cleavage
sly-miR399a-2	Solyc01g095590.3.1	3.0	-1.0	1	21	64	84	UGCCAAAGGAGAAUUGCACUG	UGGUGCAAUUUUUGUUUGGUA	Cleavage
sly-miR399a-2	Solyc08g075780.3.1	3.0	-1.0	1	21	548	568	UGCCAAAGGAGAAUUGCACUG	UUCUGCAAUUUUCUUUUGGCU	Cleavage
sly-miR399a-2	Solyc04g018063.1.1	3.0	-1.0	1	21	1729	1749	UGCCAAAGGAGAAUUGCACUG	CUGUGCAGUGUUCUUUUGGCA	Cleavage
sly-miR399a-2	Solyc03g025200.3.1	3.0	-1.0	1	21	745	765	UGCCAAAGGAGAAUUGCACUG	CCAUGCUAUUCUCCUUUGGCU	Cleavage
sly-miR399a-2	Solyc01g104915.1.1	3.0	-1.0	1	21	242	262	UGCCAAAGGAGAAUUGCACUG	AUCUGCUAUUCUCUUUUGGUA	Cleavage
sly-miR399a-2	Solyc01g104910.3.1	3.0	-1.0	1	21	442	462	UGCCAAAGGAGAAUUGCACUG	AUCUGCUAUUCUCUUUUGGUA	Cleavage
sly-miR399a-2	Solyc12g042830.2.1	3.0	-1.0	1	21	845	865	UGCCAAAGGAGAAUUGCACUG	UUGUGAGGUUUUUCUUUGGCA	Cleavage
sly-miR399a-3-3p	Solyc03g071720.3.1	2.5	-1.0	1	21	985	1005	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
sly-miR399a-3-5p	Solyc03g031410.1.1	1.5	-1.0	1	20	1	20	GGGCUACUCUCUAUUGGCAU	AUGCCAAUAGAGUGUAGCCC	Cleavage
sly-miR399a-3-5p	Solyc06g050590.3.1	3.0	-1.0	1	21	493	513	GGGCUACUCUCUAUUGGCAUG	AGUUCCAACAGAGAGUAGUCC	Cleavage
sly-miR399a-4-3p	Solyc03g071720.3.1	2.5	-1.0	1	21	985	1005	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
sly-miR399a-4-5p	Solyc03g031410.1.1	1.5	-1.0	1	20	1	20	GGGCUACUCUCUAUUGGCAU	AUGCCAAUAGAGUGUAGCCC	Cleavage
sly-miR399a-4-5p	Solyc06g050590.3.1	3.0	-1.0	1	21	493	513	GGGCUACUCUCUAUUGGCAUG	AGUUCCAACAGAGAGUAGUCC	Cleavage
sly-miR399a-5-3p	Solyc03g071720.3.1	2.5	-1.0	1	21	985	1005	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
sly-miR399a-5-5p	Solyc03g031410.1.1	1.5	-1.0	1	20	1	20	GGGCUACUCUCUAUUGGCAU	AUGCCAAUAGAGUGUAGCCC	Cleavage
sly-miR399a-5-5p	Solyc06g050590.3.1	3.0	-1.0	1	21	493	513	GGGCUACUCUCUAUUGGCAUG	AGUUCCAACAGAGAGUAGUCC	Cleavage
sly-miR399d-1	Solyc02g078210.3.1	1.5	-1.0	1	21	899	919	UGCCAAAGAAGAUUUGCCCCG	CUGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399d-1	Solyc02g078210.3.1	1.5	-1.0	1	21	956	976	UGCCAAAGAAGAUUUGCCCCG	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399d-1	Solyc02g065580.3.1	3.0	-1.0	1	21	751	771	UGCCAAAGAAGAUUUGCCCCG	CAUGGCAUGUCUUUUUUGGCA	Cleavage
sly-miR399d-1	Solyc05g016410.3.1	3.0	-1.0	1	21	802	822	UGCCAAAGAAGAUUUGCCCCG	AAGGGGAAGUCUUCCUUGGCA	Cleavage
sly-miR399d-1	Solyc04g081730.3.1	3.0	-1.0	1	21	2012	2032	UGCCAAAGAAGAUUUGCCCCG	AAGUGUCAAUUUUCUUUGGCA	Cleavage
sly-miR399d-2	Solyc02g078210.3.1	1.5	-1.0	1	21	899	919	UGCCAAAGAAGAUUUGCCCCG	CUGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399d-2	Solyc02g078210.3.1	1.5	-1.0	1	21	956	976	UGCCAAAGAAGAUUUGCCCCG	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399d-2	Solyc02g065580.3.1	3.0	-1.0	1	21	751	771	UGCCAAAGAAGAUUUGCCCCG	CAUGGCAUGUCUUUUUUGGCA	Cleavage
sly-miR399d-2	Solyc05g016410.3.1	3.0	-1.0	1	21	802	822	UGCCAAAGAAGAUUUGCCCCG	AAGGGGAAGUCUUCCUUGGCA	Cleavage
sly-miR399d-2	Solyc04g081730.3.1	3.0	-1.0	1	21	2012	2032	UGCCAAAGAAGAUUUGCCCCG	AAGUGUCAAUUUUCUUUGGCA	Cleavage
sly-miR399d-3-3p	Solyc03g071720.3.1	2.5	-1.0	1	20	985	1004	GCCAAAGGAGAGCUGCCCUA	GAGUGCGGUUCUCUUUUGGC	Cleavage
sly-miR399d-3-3p	Solyc01g096930.3.1	3.0	-1.0	1	20	3001	3020	GCCAAAGGAGAGCUGCCCUA	UAGGGCAGCUCUUCUUCGGA	Cleavage
sly-miR399d-3-3p	Solyc02g078210.3.1	3.0	-1.0	1	20	956	975	GCCAAAGGAGAGCUGCCCUA	UAGGGCAAAUCUCCUUUGGC	Cleavage
sly-miR399d-3-5p	Solyc03g031410.1.1	2.5	-1.0	1	20	1	20	GGGCUACUCUCUAUAGGCAU	AUGCCAAUAGAGUGUAGCCC	Cleavage
sly-miR399i-1	Solyc02g078210.3.1	2.5	-1.0	1	21	956	976	UGCCAAAGGAGAGCUGCCCUG	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399i-1	Solyc02g078210.3.1	2.5	-1.0	1	21	899	919	UGCCAAAGGAGAGCUGCCCUG	CUGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399i-1	Solyc03g071720.3.1	3.0	-1.0	1	21	985	1005	UGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
sly-miR399j-2	Solyc02g078210.3.1	1.5	-1.0	1	21	956	976	UGCCAAAGGAGAGUUGCCCUA	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399j-2	Solyc02g078210.3.1	1.5	-1.0	1	21	899	919	UGCCAAAGGAGAGUUGCCCUA	CUGGGCAAAUCUCCUUUGGCA	Cleavage

sly-miR399j-2	Solyc09g066410.2.1	3.0	-1.0	1	21	245	265	UGCCAAAGGAGAGUUGCCCUA	CGGGGCAACUCUUCUUUGGAU	Cleavage
sly-miR399j-2	Solyc11g061700.2.1	3.0	-1.0	1	21	3464	3484	UGCCAAAGGAGAGUUGCCCUA	AAGAGAAACUUUCUUUUGGCA	Cleavage
sly-miR399j-2	Solyc01g103910.1.1	3.0	-1.0	1	21	1821	1841	UGCCAAAGGAGAGUUGCCCUA	GCAGGAAAUUCUCUUUUGGCA	Cleavage
sly-miR399j-2	Solyc01g100810.3.1	3.0	-1.0	1	21	1910	1930	UGCCAAAGGAGAGUUGCCCUA	UUGGCCAACUCUUCUCUGGCA	Cleavage
sly-miR399j-3-3p	Solyc02g078210.3.1	1.5	-1.0	1	21	956	976	UGCCAAAGGAGAGUUGCCCUA	UAGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399j-3-3p	Solyc02g078210.3.1	1.5	-1.0	1	21	899	919	UGCCAAAGGAGAGUUGCCCUA	CUGGGCAAAUCUCCUUUGGCA	Cleavage
sly-miR399j-3-3p	Solyc09g066410.2.1	3.0	-1.0	1	21	245	265	UGCCAAAGGAGAGUUGCCCUA	CGGGGCAACUCUUCUUUGGAU	Cleavage
sly-miR399j-3-3p	Solyc11g061700.2.1	3.0	-1.0	1	21	3464	3484	UGCCAAAGGAGAGUUGCCCUA	AAGAGAAACUUUCUUUUGGCA	Cleavage
sly-miR399j-3-3p	Solyc01g103910.1.1	3.0	-1.0	1	21	1821	1841	UGCCAAAGGAGAGUUGCCCUA	GCAGGAAAUUCUCUUUUGGCA	Cleavage
sly-miR399j-3-3p	Solyc01g100810.3.1	3.0	-1.0	1	21	1910	1930	UGCCAAAGGAGAGUUGCCCUA	UUGGCCAACUCUUCUCUGGCA	Cleavage
sly-miR399j-3-5p	Solyc03g031410.1.1	0.0	-1.0	1	20	1	20	GGGCUACACUCUAUUGGCAU	AUGCCAAUAGAGUGUAGCCC	Cleavage
sly-miR403-3p	Solyc02g069260.3.1	1.5	-1.0	1	21	3356	3376	CUAGAUUCACGCACAAGCUCG	GGAGUUUGUGCGUGAAUCUAA	Cleavage
sly-miR403-3p	Solyc01g079280.1.1	2.5	-1.0	1	21	128	148	CUAGAUUCACGCACAAGCUCG	CACGUUUGUGCGUGAAUCUAA	Cleavage
sly-miR403-3p	Solyc10g075050.2.1	3.0	-1.0	1	21	489	509	CUAGAUUCACGCACAAGCUCG	CCUGUUUAUGCGUGGAUCUAG	Cleavage
sly-miR403-5p	Solyc12g042780.2.1	2.0	-1.0	1	21	845	865	CGUUUGUGCGUGAAUCUAACA	CAUUAGAUUCAUGAACAAACG	Cleavage
sly-miR403-5p	Solyc09g018955.1.1	3.0	-1.0	1	21	4045	4065	CGUUUGUGCGUGAAUCUAACA	CAAAGGAUUCACGCACAAAUG	Cleavage
sly-miR403-5p	Solyc07g007810.3.1	3.0	-1.0	1	21	488	508	CGUUUGUGCGUGAAUCUAACA	UCUCAGAUACACGCACAAAUG	Cleavage
sly-miR403a-3p	Solyc01g079280.1.1	0.0	-1.0	1	21	128	148	UUAGAUUCACGCACAAACGUG	CACGUUUGUGCGUGAAUCUAA	Cleavage
sly-miR403a-3p	Solyc02g069260.3.1	1.0	-1.0	1	21	3356	3376	UUAGAUUCACGCACAAACGUG	GGAGUUUGUGCGUGAAUCUAA	Cleavage
sly-miR403a-3p	Solyc11g012330.2.1	2.5	-1.0	1	21	2152	2172	UUAGAUUCACGCACAAACGUG	AACAUUUGUGUGUGAAUUUGA	Cleavage
sly-miR403a-3p	Solyc10g075050.2.1	2.5	-1.0	1	21	489	509	UUAGAUUCACGCACAAACGUG	CCUGUUUAUGCGUGGAUCUAG	Cleavage
sly-miR403a-3p	Solyc08g075370.3.1	2.5	-1.0	1	21	993	1013	UUAGAUUCACGCACAAACGUG	UUUGUUUCUGUGUGAAUUUAA	Cleavage
sly-miR408-1	Solyc01g080080.3.1	2.0	-1.0	1	21	1544	1564	CAGGGAAGAGGCAGUGCAUGG	AUAUGCACUGCCUUUUCUCUU	Cleavage
sly-miR408-1	Solyc06g060670.3.1	2.5	-1.0	1	21	285	305	CAGGGAAGAGGCAGUGCAUGG	CUAUGCAGUGCCUUUUCCCUA	Cleavage
sly-miR408-1	Solyc11g033270.2.1	2.5	-1.0	1	21	3936	3956	CAGGGAAGAGGCAGUGCAUGG	AUAUGCAUUGCCUCUUCUAUG	Cleavage
sly-miR408-1	Solyc01g060010.2.1	2.5	-1.0	1	21	792	813	CAGGGAAGAGGCAGUG-CAUGG	UAAUGUCACUGCUUCUUCCCUG	Cleavage
sly-miR408-1	Solyc01g111900.3.1	2.5	-1.0	1	21	510	530	CAGGGAAGAGGCAGUGCAUGG	GGCUGCUCUGCUUCUUCCCUG	Cleavage
sly-miR408-1	Solyc05g013345.1.1	3.0	-1.0	1	21	2870	2890	CAGGGAAGAGGCAGUGCAUGG	UCAUGCACUGCCUUUGCCCUU	Cleavage
sly-miR408-1	Solyc10g052860.1.1	3.0	-1.0	1	21	131	151	CAGGGAAGAGGCAGUGCAUGG	UCAUGUCAUGCUUCUUCCCUG	Cleavage
sly-miR408-1	Solyc10g005000.3.1	3.0	-1.0	1	21	1414	1434	CAGGGAAGAGGCAGUGCAUGG	AACUGUACUGCCUUUUUCUUG	Cleavage
sly-miR408-1	Solyc02g084410.3.1	3.0	-1.0	1	21	916	936	CAGGGAAGAGGCAGUGCAUGG	CGAAGCACUGCCUCUUCUUUC	Cleavage
sly-miR408-1	Solyc11g065490.2.1	3.0	-1.0	1	21	965	985	CAGGGAAGAGGCAGUGCAUGG	GUUGGAACUGCCUCUUCCCUG	Cleavage
sly-miR408-1	Solyc06g008310.3.1	3.0	-1.0	1	21	127	147	CAGGGAAGAGGCAGUGCAUGG	UAGUGAAUUGCUUCUUCUCUG	Cleavage
sly-miR408-2-3p	Solyc07g005740.1.1	2.5	-1.0	1	21	898	918	AUGCACUGCCUCUUCCCUGGC	AGCGGGGAGGAGGCAGUGCGA	Cleavage
sly-miR408-2-3p	Solyc05g054910.3.1	3.0	-1.0	1	21	2011	2031	AUGCACUGCCUCUUCCCUGGC	GCCAGCUAAGAGGCAGUGUGU	Cleavage
sly-miR408-2-3p	Solyc10g049360.2.1	3.0	-1.0	1	21	903	923	AUGCACUGCCUCUUCCCUGGC	ACCAGAGAAGAGGUAGUGAAU	Cleavage
sly-miR408-2-3p	Solyc04g072930.1.1	3.0	-1.0	1	21	940	960	AUGCACUGCCUCUUCCCUGGC	UUUGGGGAAGAUGCAGUGUAU	Translation
sly-miR408-2-3p	Solyc11g013290.2.1	3.0	-1.0	1	21	127	147	AUGCACUGCCUCUUCCCUGGC	GAAGGGGAAGAGGCAGAGCAU	Cleavage
sly-miR408-2-3p	Solyc03g082430.1.1	3.0	-1.0	1	21	796	816	AUGCACUGCCUCUUCCCUGGC	UACAGGGAAGAGGCAUUGAAU	Cleavage
sly-miR408-2-3p	Solyc04g014460.3.1	3.0	-1.0	1	21	551	571	AUGCACUGCCUCUUCCCUGGC	UUCGUGGAAGGGGUGGUGCAU	Cleavage
sly-miR408-2-3p	Solyc01g107350.3.1	3.0	-1.0	1	21	1029	1049	AUGCACUGCCUCUUCCCUGGC	UUAAAGGAAGAGGUAGUGCGU	Cleavage
sly-miR408-2-5p	Solyc03g119730.3.1	3.0	-1.0	1	20	1309	1328	CGGGGACGAGCCAGAGCAUG	UUUGCUCUGGUUCGUCCUCC	Cleavage
sly-miR408a-3p	Solyc05g052360.2.1	2.0	-1.0	1	21	473	493	AUGCACAGCCUCUUCCCUGGC	ACCAGUGAAGAGGCUGUGCAA	Cleavage
sly-miR408a-3p	Solyc05g052400.3.1	2.0	-1.0	1	21	540	560	AUGCACAGCCUCUUCCCUGGC	ACCAGUGAAGAGGCUGUGCAA	Cleavage
sly-miR408a-3p	Solyc04g080850.3.1	2.5	-1.0	1	21	5	25	AUGCACAGCCUCUUCCCUGGC	CAAAGGGAAGAUGCUGUGCAU	Translation
sly-miR408a-3p	Solyc01g090980.1.1	3.0	-1.0	1	21	5	25	AUGCACAGCCUCUUCCCUGGC	GCCGUGGAAGAGGCUUUGCAU	Cleavage
sly-miR408a-3p	Solyc06g050530.3.1	3.0	-1.0	1	21	188	208	AUGCACAGCCUCUUCCCUGGC	GCCCGUGAAGAGGCUGUGCAA	Cleavage
sly-miR408a-3p	Solyc06g048860.2.1	3.0	-1.0	1	21	21	41	AUGCACAGCCUCUUCCCUGGC	ACCAGUAAAGAGGCUGUGCAA	Cleavage
sly-miR408a-3p	Solyc08g081570.3.1	3.0	-1.0	1	21	563	583	AUGCACAGCCUCUUCCCUGGC	UUCAUGGAAGAAGCUGUGCGU	Translation
sly-miR408a-3p	Solyc05g051570.3.1	3.0	-1.0	1	21	672	692	AUGCACAGCCUCUUCCCUGGC	AGCAAGGUGGAGGUUGUGCAU	Cleavage

sly-miR408a-3p	Solyc03g078570.3.1	3.0	-1.0	1	21	835	855	AUGCACAGCCUCUUCCCUGGC	AGCAAGGUGGAGGUUGUGCAU	Cleavage
sly-miR408a-5p	Solyc09g091560.3.1	3.0	-1.0	1	21	2205	2225	ACAGGGACGAGGCAGCGCAUG	GCUGCGUUGCCUCGGCUUUGU	Cleavage
sly-miR408a-5p	Solyc10g077070.2.1	3.0	-1.0	1	21	371	391	ACAGGGACGAGGCAGCGCAUG	UUUGAGAUGUCUUGUCCCUGU	Cleavage
sly-miR437	Solyc06g063100.3.1	2.0	-1.0	1	21	2020	2040	AAAGUUAGAGAUGUUUGACUU	UUGUCAUAUAUCUCUAGCUUU	Cleavage
sly-miR437	Solyc10g008460.3.1	2.5	-1.0	1	21	1519	1539	AAAGUUAGAGAUGUUUGACUU	AAGCCAGAUAUUUCUAACUUU	Cleavage
sly-miR437	Solyc03g034090.3.1	2.5	-1.0	1	21	835	855	AAAGUUAGAGAUGUUUGACUU	GGGAUAAGCAUUUCUAACUUU	Cleavage
sly-miR437	Solyc06g082420.3.1	2.5	-1.0	1	21	40	60	AAAGUUAGAGAUGUUUGACUU	ACUUUAAACAUCUCUAGUUUU	Cleavage
sly-miR437	Solyc11g010790.1.1	3.0	-1.0	1	21	263	283	AAAGUUAGAGAUGUUUGACUU	AAGUCAAGCAUCUCAAACUUG	Cleavage
sly-miR437	Solyc10g079620.2.1	3.0	-1.0	1	21	2213	2233	AAAGUUAGAGAUGUUUGACUU	AAGUUAUGCAUCUUUAAUUUU	Cleavage
sly-miR437	Solyc10g006710.3.1	3.0	-1.0	1	21	2193	2213	AAAGUUAGAGAUGUUUGACUU	AAAUCAGACGUCUUUAGCUUU	Cleavage
sly-miR437	Solyc09g018955.1.1	3.0	-1.0	1	21	4425	4445	AAAGUUAGAGAUGUUUGACUU	AAGACGCACAUCUUUAACUUU	Cleavage
sly-miR437	Solyc12g011010.2.1	3.0	-1.0	1	21	91	110	AAAGUUAGAGAUGUUUGACUU	AAG-CAAAUAUCUCUAAUUUU	Cleavage
sly-miR437	Solyc08g069125.1.1	3.0	-1.0	1	21	304	324	AAAGUUAGAGAUGUUUGACUU	GGGUCAAUCAUUUCCAACUUU	Cleavage
sly-miR437	Solyc03g116620.3.1	3.0	-1.0	1	21	420	440	AAAGUUAGAGAUGUUUGACUU	ACAGCAAACAUCUUUAAUUUU	Cleavage
sly-miR437	Solyc10g086020.2.1	3.0	-1.0	1	21	726	746	AAAGUUAGAGAUGUUUGACUU	ACGUUGAAGGUCUCUAACUUU	Cleavage
sly-miR437	Solyc02g083670.3.1	3.0	-1.0	1	21	2516	2536	AAAGUUAGAGAUGUUUGACUU	GAUUCAGUCAUCUCUAAUUUU	Cleavage
sly-miR437	Solyc03g111840.3.1	3.0	-1.0	1	21	962	982	AAAGUUAGAGAUGUUUGACUU	UCAUCAGACGUCUUUAAUUUU	Cleavage
sly-miR437	Solyc01g009510.2.1	3.0	-1.0	1	21	1484	1504	AAAGUUAGAGAUGUUUGACUU	AUGGUGAACAUCUCUAGUUUU	Cleavage
sly-miR437	Solyc05g012950.2.1	3.0	-1.0	1	21	820	840	AAAGUUAGAGAUGUUUGACUU	GGAUCAAUCGUCUCUAAUUUU	Cleavage
sly-miR437	Solyc02g080620.3.1	3.0	-1.0	1	21	1996	2016	AAAGUUAGAGAUGUUUGACUU	GUGUUAUACAUCUUUAACUUC	Cleavage
sly-miR4376-3p	Solyc11g072810.2.1	2.0	-1.0	1	20	7958	7977	GCAUCAUACUCCUGCAUAUU	AGUAUGCAGGAGUUUGAUGC	Cleavage
sly-miR4376-3p	Solyc08g077730.3.1	3.0	-1.0	1	20	1253	1272	GCAUCAUACUCCUGCAUAUU	UAUAUGCAGGGGAAUGGUGU	Cleavage
sly-miR4376-3p	Solyc03g019930.3.1	3.0	-1.0	1	20	2670	2689	GCAUCAUACUCCUGCAUAUU	GAUGAGUAGGAGUAUGAUGA	Cleavage
sly-miR4376-3p	Solyc02g069045.1.1	3.0	-1.0	1	20	1054	1073	GCAUCAUACUCCUGCAUAUU	UAUAUACAGGAGUUUGAUGU	Cleavage
sly-miR4376-3p	Solyc03g058380.3.1	3.0	-1.0	1	20	2745	2764	GCAUCAUACUCCUGCAUAUU	CAUAUUCAGGGGUAUGAUCC	Cleavage
sly-miR4376-3p	Solyc12g019295.1.1	3.0	-1.0	1	20	169	188	GCAUCAUACUCCUGCAUAUU	GAUAAGGAGGAGUGUGAUGU	Cleavage
sly-miR4376-3p	Solyc06g008560.2.1	3.0	-1.0	1	20	1560	1579	GCAUCAUACUCCUGCAUAUU	AAAAUUGAGGAGUAUGAUGC	Cleavage
sly-miR4376-5p	Solyc01g102480.3.1	3.0	-1.0	1	22	2862	2883	ACGCAGGAGAGAUGAUGCUGGA	AAAACUAUUAUUUCUUCUGCGU	Cleavage
sly-miR477-3p	Solyc10g079160.1.1	2.0	-1.0	1	22	793	814	AGUUCUUGUAGGGUGAGACAAC	UAUGUUUCACCCUACGAGGAUU	Cleavage
sly-miR477-3p	Solyc09g005250.3.1	2.5	-1.0	1	22	310	331	AGUUCUUGUAGGGUGAGACAAC	AGGGUUUCAUCCUACAACAACU	Cleavage
sly-miR477-3p	Solyc09g083400.3.1	3.0	-1.0	1	22	1864	1885	AGUUCUUGUAGGGUGAGACAAC	UCUGUCUGGCCCUAAAAGAACU	Cleavage
sly-miR477-3p	Solyc01g105040.3.1	3.0	-1.0	1	22	778	799	AGUUCUUGUAGGGUGAGACAAC	UACAUCUCACCUUACGAGGAUU	Cleavage
sly-miR477-3p	Solyc01g057520.3.1	3.0	-1.0	1	22	2303	2324	AGUUCUUGUAGGGUGAGACAAC	UUGGUUUCAUUUUGCAAGGACU	Cleavage
sly-miR477-3p	Solyc05g055240.3.1	3.0	-1.0	1	22	2231	2252	AGUUCUUGUAGGGUGAGACAAC	GAGUUCUCGUCCUAUGAGAACU	Cleavage
sly-miR477-3p	Solyc09g091360.1.1	3.0	-1.0	1	22	188	209	AGUUCUUGUAGGGUGAGACAAC	GAGGUCGUGCCCUACAAGAACG	Cleavage
sly-miR477-3p	Solyc09g007040.1.1	3.0	-1.0	1	22	933	954	AGUUCUUGUAGGGUGAGACAAC	AUGGUUGCAUUCUGCAAGAACU	Cleavage
sly-miR477-3p	Solyc07g054120.2.1	3.0	-1.0	1	22	248	269	AGUUCUUGUAGGGUGAGACAAC	UAAGUCCUGCCUUACAAGAAUU	Cleavage
sly-miR477-3p	Solyc08g083070.3.1	3.0	-1.0	1	22	1068	1089	AGUUCUUGUAGGGUGAGACAAC	GGGGACUUGCCCUGCAGGAACU	Cleavage
sly-miR477-3p	Solyc05g020020.3.1	3.0	-1.0	1	22	546	567	AGUUCUUGUAGGGUGAGACAAC	AAGGUUUCUCUUUGCAAGAACU	Cleavage
sly-miR477-5p	Solyc03g110950.1.1	3.0	-1.0	1	21	787	807	UGUCUCUCCCUCAAGGGCUCC	GAAGCCUUUGAGGGAGAGAGU	Cleavage
sly-miR477-5p	Solyc01g081080.2.1	3.0	-1.0	1	21	591	611	UGUCUCUCCCUCAAGGGCUCC	GAAGCCUUUGAGGGAGAGAGC	Cleavage
sly-miR477-5p	Solyc01g103410.3.1	3.0	-1.0	1	21	288	308	UGUCUCUCCCUCAAGGGCUCC	AGAGUUAUUGGGGGAGAGGCA	Cleavage
sly-miR477-5p	Solyc06g060600.2.1	3.0	-1.0	1	21	1806	1826	UGUCUCUCCCUCAAGGGCUCC	CAAGGUUUUGAGGGGGAGAUA	Cleavage
sly-miR477a-3p	Solyc06g005190.3.1	1.5	-1.0	1	22	1301	1322	GAAGCUCUAGCAGGGAGAGCCA	CGGCUCUUCCUGCUGGAGCUUU	Cleavage
sly-miR477a-3p	Solyc10g085555.1.1	2.0	-1.0	1	22	47	68	GAAGCUCUAGCAGGGAGAGCCA	UGAUUCUUCCUGUUGGAGCUUC	Cleavage
sly-miR477a-3p	Solyc03g082620.3.1	2.5	-1.0	1	22	2798	2819	GAAGCUCUAGCAGGGAGAGCCA	UGCCUUUCCUUGUUGGGGCUUC	Cleavage
sly-miR477a-3p	Solyc07g065880.3.1	2.5	-1.0	1	22	3416	3437	GAAGCUCUAGCAGGGAGAGCCA	UGCCUUUUCCUGCUAGAGCUCC	Cleavage
sly-miR477a-3p	Solyc06g084250.3.1	2.5	-1.0	1	22	878	899	GAAGCUCUAGCAGGGAGAGCCA	ACGUUCUUCUUGCUGGAGCUUU	Cleavage
sly-miR477a-3p	Solyc03g119755.1.1	2.5	-1.0	1	22	2191	2212	GAAGCUCUAGCAGGGAGAGCCA	UUCCAUUUUCUGCUAGAGCUUC	Cleavage
sly-miR477a-3p	Solyc11g072590.2.1	3.0	-1.0	1	22	1079	1100	GAAGCUCUAGCAGGGAGAGCCA	CUGCUCUUCCUGCUGGCGCUUU	Cleavage

sly-miR477a-3p	Solyc05g054010.3.1	3.0	-1.0	1	22	1198	1219	GAAGCUCUAGCAGGGAGAGCCA	AUGCUCUUACUCCUAGAGCUUC	Translation
sly-miR477a-3p	Solyc05g010050.3.1	3.0	-1.0	1	22	2555	2576	GAAGCUCUAGCAGGGAGAGCCA	AGCCUCUUCUUACUAGAGCUUU	Translation
sly-miR477a-3p	Solyc02g078060.1.1	3.0	-1.0	1	22	89	110	GAAGCUCUAGCAGGGAGAGCCA	CUCCUCUUCUUGCAGGAGCUUC	Cleavage
sly-miR477a-3p	Solyc11g065380.2.1	3.0	-1.0	1	22	378	399	GAAGCUCUAGCAGGGAGAGCCA	ACUUUCUUCCUCCUGGAGCUUC	Translation
sly-miR477a-3p	Solyc09g082550.3.1	3.0	-1.0	1	22	644	665	GAAGCUCUAGCAGGGAGAGCCA	CUACUUUCUUUGCUGGAGUUUU	Cleavage
sly-miR477a-3p	Solyc01g102850.2.1	3.0	-1.0	1	22	2632	2653	GAAGCUCUAGCAGGGAGAGCCA	CUCCUAUCUCUGCCAGAGCUUC	Cleavage
sly-miR477a-5p	Solyc01g081080.2.1	1.5	-1.0	1	21	589	609	CCUCUCCCUCAAGGGCUUCUC	GGGAAGCCUUUGAGGGAGAGA	Cleavage
sly-miR477a-5p	Solyc03g110950.1.1	1.5	-1.0	1	21	785	805	CCUCUCCCUCAAGGGCUUCUC	UGGAAGCCUUUGAGGGAGAGA	Cleavage
sly-miR477a-5p	Solyc02g082910.3.1	2.5	-1.0	1	21	1445	1465	CCUCUCCCUCAAGGGCUUCUC	AAGAAGCUUUUGAGGGAGGGU	Cleavage
sly-miR477a-5p	Solyc11g028100.2.1	2.5	-1.0	1	21	1452	1472	CCUCUCCCUCAAGGGCUUCUC	ACGAGCCUUUUGAGGGAGAGG	Cleavage
sly-miR477a-5p	Solyc02g085000.3.1	3.0	-1.0	1	21	784	804	CCUCUCCCUCAAGGGCUUCUC	AAGAAGCUCUUGAUGGAGAGA	Cleavage
sly-miR477a-5p	Solyc09g020155.1.1	3.0	-1.0	1	21	605	625	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
sly-miR477a-5p	Solyc00g165195.1.1	3.0	-1.0	1	21	838	858	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
sly-miR477a-5p	Solyc00g026905.1.1	3.0	-1.0	1	21	901	921	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
sly-miR477a-5p	Solyc08g044332.1.1	3.0	-1.0	1	21	2550	2570	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
sly-miR477a-5p	Solyc01g056485.1.1	3.0	-1.0	1	21	2698	2718	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
sly-miR477a-5p	Solyc02g068110.3.1	3.0	-1.0	1	21	121	141	CCUCUCCCUCAAGGGCUUCUC	AUGGAGCUUUUGAGGGAAAGG	Cleavage
sly-miR477b-3p	Solyc03g083440.3.1	2.0	-1.0	1	22	2414	2435	GAGGUCUUUCGAGUGAGAGUGA	CGGCUCUCACUCAAAGGACCUC	Translation
sly-miR477b-3p	Solyc10g083740.2.1	2.5	-1.0	1	22	3593	3614	GAGGUCUUUCGAGUGAGAGUGA	AUACUCUUCUUCGAAAGACCUU	Cleavage
sly-miR477b-3p	Solyc00g268310.2.1	2.5	-1.0	1	22	1072	1093	GAGGUCUUUCGAGUGAGAGUGA	AAUGUCUCACUCGAAGGACCUA	Cleavage
sly-miR477b-3p	Solyc12g013550.2.1	3.0	-1.0	1	22	18	39	GAGGUCUUUCGAGUGAGAGUGA	UCACUCUCAUUCAGAAGAUCUC	Translation
sly-miR477b-3p	Solyc12g027880.2.1	3.0	-1.0	1	22	1070	1091	GAGGUCUUUCGAGUGAGAGUGA	UUGCUUUCACUCGAAAAACCUA	Cleavage
sly-miR477b-3p	Solyc09g064200.3.1	3.0	-1.0	1	22	1121	1142	GAGGUCUUUCGAGUGAGAGUGA	ACAUAUUUACUCGAAAGAUCUC	Cleavage
sly-miR477b-3p	Solyc01g091840.3.1	3.0	-1.0	1	22	1044	1065	GAGGUCUUUCGAGUGAGAGUGA	GUGUUUUCACUUGAAGGGCCUU	Cleavage
sly-miR477b-3p	Solyc01g099040.3.1	3.0	-1.0	1	22	2048	2069	GAGGUCUUUCGAGUGAGAGUGA	CCUUUCUCGCUCGAAGGAUCUA	Cleavage
sly-miR477b-3p	Solyc06g008130.3.1	3.0	-1.0	1	22	115	136	GAGGUCUUUCGAGUGAGAGUGA	AUUUUCUCUCUUGAAGGACUUC	Cleavage
sly-miR477b-5p	Solyc03g110950.1.1	1.0	-1.0	1	21	785	805	ACUCUCCCUCAAAGGCUUCUG	UGGAAGCCUUUGAGGGAGAGA	Cleavage
sly-miR477b-5p	Solyc02g082910.3.1	1.0	-1.0	1	21	1445	1465	ACUCUCCCUCAAAGGCUUCUG	AAGAAGCUUUUGAGGGAGGGU	Cleavage
sly-miR477b-5p	Solyc01g081080.2.1	1.0	-1.0	1	21	589	609	ACUCUCCCUCAAAGGCUUCUG	GGGAAGCCUUUGAGGGAGAGA	Cleavage
sly-miR477b-5p	Solyc02g089750.4.1	3.0	-1.0	1	21	488	508	ACUCUCCCUCAAAGGCUUCUG	UGGGAACCUUUGGGGGAGAGA	Cleavage
sly-miR477b-5p	Solyc03g113450.3.1	3.0	-1.0	1	21	1848	1868	ACUCUCCCUCAAAGGCUUCUG	AUCAAGUCUUUGAGAGAGAGU	Cleavage
sly-miR477b-5p	Solyc11g028100.2.1	3.0	-1.0	1	21	1452	1472	ACUCUCCCUCAAAGGCUUCUG	ACGAGCCUUUUGAGGGAGAGG	Cleavage
sly-miR482a-1	Solyc08g076000.3.1	2.0	-1.0	1	22	853	874	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGACUAGGAAAGA	Translation
sly-miR482a-1	Solyc08g075630.3.1	2.0	-1.0	1	22	745	766	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGAUUAGGAAAGA	Translation
sly-miR482a-1	Solyc05g006630.3.1	2.0	-1.0	1	22	1034	1055	UCUUUCCUACUCCUCCCAUACC	GGAAUGGGAGGAGUGGGCAAGA	Cleavage
sly-miR482a-1	Solyc04g080590.3.1	2.5	-1.0	1	22	749	770	UCUUUCCUACUCCUCCCAUACC	GCUGUGGUAGGAGUAGGAGAGG	Cleavage
sly-miR482a-1	Solyc08g067760.3.1	2.5	-1.0	1	22	933	954	UCUUUCCUACUCCUCCCAUACC	UGAGUGGAAGGAGUGGGAAAGG	Cleavage
sly-miR482a-1	Solyc06g083540.3.1	2.5	-1.0	1	22	1028	1049	UCUUUCCUACUCCUCCCAUACC	UUCAGGAGAGGAGUGGGAAAGA	Cleavage
sly-miR482a-1	Solyc04g009150.1.1	3.0	-1.0	1	22	565	586	UCUUUCCUACUCCUCCCAUACC	GGAAUGGGAGGAUUAGGCAAGA	Translation
sly-miR482a-1	Solyc04g009110.1.1	3.0	-1.0	1	22	574	595	UCUUUCCUACUCCUCCCAUACC	GGCAUGGGCGGAUUAGGGAAGA	Translation
sly-miR482a-1	Solyc06g076350.3.1	3.0	-1.0	1	22	392	413	UCUUUCCUACUCCUCCCAUACC	GCUAUGAGAGGAGUAGAGAAGA	Cleavage
sly-miR482a-1	Solyc10g007200.3.1	3.0	-1.0	1	22	503	524	UCUUUCCUACUCCUCCCAUACC	GGAAUGUGAUGAGUAGGGAAGA	Cleavage
sly-miR482a-1	Solyc04g026110.3.1	3.0	-1.0	1	22	493	514	UCUUUCCUACUCCUCCCAUACC	GGCAUGGGCGGAUUGGGAAAGA	Translation
sly-miR482a-1	Solyc11g017370.2.1	3.0	-1.0	1	22	1910	1931	UCUUUCCUACUCCUCCCAUACC	AGCAUGGGAUGGGUAGGAAAGC	Cleavage
sly-miR482a-1	Solyc07g055380.1.1	3.0	-1.0	1	22	130	151	UCUUUCCUACUCCUCCCAUACC	GGAAUGAGCGGAGUGGGGAAGA	Cleavage
sly-miR482a-1	Solyc07g055610.2.1	3.0	-1.0	1	22	553	574	UCUUUCCUACUCCUCCCAUACC	GGAAUGAGCGGAGUGGGGAAGA	Cleavage
sly-miR482a-1	Solyc00g030000.1.1	3.0	-1.0	1	22	358	379	UCUUUCCUACUCCUCCCAUACC	GGGAUGGAUGGAGUAGGAGGGA	Cleavage
sly-miR482a-1	Solyc01g090950.3.1	3.0	-1.0	1	22	196	216	UCUUUCCUACUCCUCCCAUACC	GCUAUGG-AGGAGUGGGAAGGA	Cleavage
sly-miR482a-1	Solyc09g010920.1.1	3.0	-1.0	1	22	2046	2067	UCUUUCCUACUCCUCCCAUACC	AGCUUGUGAGGGGUGGGAAAGA	Cleavage
sly-miR482a-1	Solyc04g009950.3.1	3.0	-1.0	1	22	272	293	UCUUUCCUACUCCUCCCAUACC	AUAAAGGGAGGAGUAUGGAAGA	Cleavage

sly-miR482a-2-3p	Solyc11g008140.2.1	1.0	-1.0	1	22	1224	1245	UUUCCAAUUCCACCCAUUCCUA	GUGGAGUGGGUGGAAUUGGAGA	Cleavage
sly-miR482a-2-3p	Solyc04g007320.2.1	2.0	-1.0	1	22	1110	1131	UUUCCAAUUCCACCCAUUCCUA	UUGGAAUGAGUGGAGUUGGGAA	Cleavage
sly-miR482a-2-3p	Solyc01g090860.3.1	2.0	-1.0	1	22	782	803	UUUCCAAUUCCACCCAUUCCUA	UCAGAAUGGGUGGAAUUGGGGU	Cleavage
sly-miR482a-2-3p	Solyc01g102920.2.1	2.0	-1.0	1	22	473	494	UUUCCAAUUCCACCCAUUCCUA	GUGGUAUUGGUGGAAUUGGAAA	Cleavage
sly-miR482a-2-3p	Solyc06g062440.3.1	3.0	-1.0	1	22	593	614	UUUCCAAUUCCACCCAUUCCUA	UAGGAAUGGGGGGAAUAGGAAA	Cleavage
sly-miR482a-2-3p	Solyc01g087200.3.1	3.0	-1.0	1	22	515	536	UUUCCAAUUCCACCCAUUCCUA	CAGGUAUGGGUGGGAUUGGCAA	Cleavage
sly-miR482a-2-3p	Solyc02g091890.2.1	3.0	-1.0	1	22	4704	4725	UUUCCAAUUCCACCCAUUCCUA	AAGAAGUCGGUGGAAUUGGAAG	Cleavage
sly-miR482a-2-3p	Solyc11g011350.2.1	3.0	-1.0	1	22	1381	1402	UUUCCAAUUCCACCCAUUCCUA	GGGGAAUAGGUGGAGUUGGUAA	Cleavage
sly-miR482a-2-3p	Solyc08g005510.2.1	3.0	-1.0	1	22	1512	1533	UUUCCAAUUCCACCCAUUCCUA	GGGGAAUAGGUGGAGUUGGUAA	Cleavage
sly-miR482a-2-3p	Solyc06g009550.3.1	3.0	-1.0	1	22	1187	1208	UUUCCAAUUCCACCCAUUCCUA	UUGGAGUUGGUGGAUUUGGAAA	Cleavage
sly-miR482a-2-3p	Solyc06g009533.1.1	3.0	-1.0	1	22	77	98	UUUCCAAUUCCACCCAUUCCUA	UUGGAGUUGGUGGAUUUGGAAA	Cleavage
sly-miR482a-2-3p	Solyc04g005540.3.1	3.0	-1.0	1	22	850	871	UUUCCAAUUCCACCCAUUCCUA	GUGGUAUGGGUGGAGUUGGUAA	Cleavage
sly-miR482a-2-3p	Solyc03g116360.2.1	3.0	-1.0	1	22	2405	2426	UUUCCAAUUCCACCCAUUCCUA	GUGGGAUGUGUGGACUUGGAAA	Cleavage
sly-miR482a-2-3p	Solyc12g099740.2.1	3.0	-1.0	1	22	493	514	UUUCCAAUUCCACCCAUUCCUA	AAUGAAUGGGAGGAAUUGGAGC	Cleavage
sly-miR482a-2-3p	Solyc01g088060.3.1	3.0	-1.0	1	22	863	884	UUUCCAAUUCCACCCAUUCCUA	CUGGAAUUGGAGGAAUUGGGAA	Cleavage
sly-miR482a-2-3p	Solyc07g008950.3.1	3.0	-1.0	1	22	2523	2544	UUUCCAAUUCCACCCAUUCCUA	UAUGAUUGAGUGGAGUUGGAAG	Cleavage
sly-miR482a-2-3p	Solyc08g080850.3.1	3.0	-1.0	1	22	1776	1797	UUUCCAAUUCCACCCAUUCCUA	GAAGAAUUGGAGGAAUUGGAAG	Cleavage
sly-miR482a-2-5p	Solyc01g008410.2.1	2.0	-1.0	1	21	160	180	GGGAUUGGUGAGUUGGAAAGC	CUCUUUCAACUCACCAAUCUC	Cleavage
sly-miR482a-2-5p	Solyc01g006810.3.1	2.5	-1.0	1	21	1328	1348	GGGAUUGGUGAGUUGGAAAGC	GUUUUUCAGCUCAUCAAUCUU	Cleavage
sly-miR482a-2-5p	Solyc04g079550.3.1	2.5	-1.0	1	21	870	890	GGGAUUGGUGAGUUGGAAAGC	ACUUUUCAAUUCACCGAUUUC	Cleavage
sly-miR482a-2-5p	Solyc08g068520.3.1	2.5	-1.0	1	21	249	269	GGGAUUGGUGAGUUGGAAAGC	UCUUUCAACCUCACCAAUCCC	Cleavage
sly-miR482a-2-5p	Solyc09g009630.3.1	2.5	-1.0	1	21	1000	1020	GGGAUUGGUGAGUUGGAAAGC	CUUUUUCCACUCACCAGUCCU	Cleavage
sly-miR482a-2-5p	Solyc09g066290.3.1	2.5	-1.0	1	21	3553	3573	GGGAUUGGUGAGUUGGAAAGC	UGUAUCCAACUUAUCAAUCCU	Cleavage
sly-miR482a-2-5p	Solyc02g079640.3.1	2.5	-1.0	1	21	4343	4363	GGGAUUGGUGAGUUGGAAAGC	AGUUUUGAACUCACUAAUUCC	Cleavage
sly-miR482a-2-5p	Solyc01g058670.3.1	3.0	-1.0	1	21	221	241	GGGAUUGGUGAGUUGGAAAGC	UCUCUCCGAUUCAUCAAUCUC	Cleavage
sly-miR482a-2-5p	Solyc06g072730.3.1	3.0	-1.0	1	21	2544	2564	GGGAUUGGUGAGUUGGAAAGC	AAUUUUCAACUUAUCAAUCUG	Cleavage
sly-miR482a-2-5p	Solyc01g110110.3.1	3.0	-1.0	1	21	1239	1259	GGGAUUGGUGAGUUGGAAAGC	UAUUUCCAAUUCAACAAUUCU	Cleavage
sly-miR482a-2-5p	Solyc01g096570.3.1	3.0	-1.0	1	21	1218	1238	GGGAUUGGUGAGUUGGAAAGC	CAUUUCCAACUUAUCAACCUC	Cleavage
sly-miR482a-2-5p	Solyc02g093520.3.1	3.0	-1.0	1	21	1999	2019	GGGAUUGGUGAGUUGGAAAGC	AAUUUCCAGUUCGUCAAUUUC	Cleavage
sly-miR482a-2-5p	Solyc02g090580.3.1	3.0	-1.0	1	21	986	1006	GGGAUUGGUGAGUUGGAAAGC	UGUUUCUAGUUCCCCAAUCCC	Cleavage
sly-miR482a-2-5p	Solyc09g075750.1.1	3.0	-1.0	1	21	76	96	GGGAUUGGUGAGUUGGAAAGC	GAUUUCGAAUUCACCAUUCCC	Cleavage
sly-miR482a-2-5p	Solyc03g124050.3.1	3.0	-1.0	1	21	855	875	GGGAUUGGUGAGUUGGAAAGC	AGUUUGCAACUCCCCAAUUCC	Cleavage
sly-miR482a-2-5p	Solyc06g071980.3.1	3.0	-1.0	1	21	3109	3129	GGGAUUGGUGAGUUGGAAAGC	CGUUUUGAACUCAUCAAUCUU	Cleavage
sly-miR482c	Solyc06g005410.3.1	1.0	-1.0	1	22	592	613	UUUCCUAUUCCACCCAUGCCAA	UUGGCAUUGGUGGAAUAGGAAA	Cleavage
sly-miR482c	Solyc06g005410.3.1	1.0	-1.0	1	22	1639	1660	UUUCCUAUUCCACCCAUGCCAA	AUGGCAUUGGUGGAAUAGGAAA	Cleavage
sly-miR482c	Solyc02g079310.2.1	2.0	-1.0	1	22	389	410	UUUCCUAUUCCACCCAUGCCAA	CCGGUAGGGGUGGGAUAGGAAA	Cleavage
sly-miR482c	Solyc02g079330.3.1	2.0	-1.0	1	22	1263	1284	UUUCCUAUUCCACCCAUGCCAA	CCGGUAGGGGUGGGAUAGGAAA	Cleavage
sly-miR482c	Solyc02g079350.3.1	2.0	-1.0	1	22	584	605	UUUCCUAUUCCACCCAUGCCAA	CCGGUAGGGGUGGGAUAGGAAA	Cleavage
sly-miR482c	Solyc02g032650.3.1	2.5	-1.0	1	22	796	817	UUUCCUAUUCCACCCAUGCCAA	GUGGUAUGGGUGGUAUAGGGAA	Cleavage
sly-miR482c	Solyc01g113620.2.1	2.5	-1.0	1	22	806	827	UUUCCUAUUCCACCCAUGCCAA	GUGGCAUUGGUGGAAUAGGCAA	Cleavage
sly-miR482c	Solyc02g079310.2.1	2.5	-1.0	1	22	1526	1547	UUUCCUAUUCCACCCAUGCCAA	CUGUUAGGGGUGGAAUAGGAAA	Cleavage
sly-miR482c	Solyc06g062440.3.1	2.5	-1.0	1	22	593	614	UUUCCUAUUCCACCCAUGCCAA	UAGGAAUGGGGGGAAUAGGAAA	Cleavage
sly-miR482c	Solyc10g078670.2.1	2.5	-1.0	1	22	696	717	UUUCCUAUUCCACCCAUGCCAA	UAAGCGAGAGUGGAAUAGGAAA	Cleavage
sly-miR482c	Solyc05g009750.1.1	3.0	-1.0	1	22	164	185	UUUCCUAUUCCACCCAUGCCAA	UUGGAAUGGCUGGAAUAGGGAA	Cleavage
sly-miR482c	Solyc02g037540.2.1	3.0	-1.0	1	22	479	500	UUUCCUAUUCCACCCAUGCCAA	AUGGCAUGGGUGGGGUGGGUAA	Cleavage
sly-miR482c	Solyc04g009290.1.1	3.0	-1.0	1	22	572	593	UUUCCUAUUCCACCCAUGCCAA	AUGGCAUGGGUGGAUUAGGCAA	Cleavage
sly-miR482c	Solyc04g009130.3.1	3.0	-1.0	1	22	584	605	UUUCCUAUUCCACCCAUGCCAA	AUGGCAUGGGUGGAUUAGGCAA	Cleavage
sly-miR482c	Solyc01g105340.3.1	3.0	-1.0	1	22	810	831	UUUCCUAUUCCACCCAUGCCAA	GUGGCAUGGGUGGUAUGGGAGG	Cleavage
sly-miR482c	Solyc09g075010.3.1	3.0	-1.0	1	22	611	632	UUUCCUAUUCCACCCAUGCCAA	GUGAUAUGGGUGGAAUGGGAGG	Cleavage
sly-miR482c	Solyc01g102920.2.1	3.0	-1.0	1	22	473	494	UUUCCUAUUCCACCCAUGCCAA	GUGGUAUUGGUGGAAUUGGAAA	Cleavage

sly-miR482c	Solyc11g013750.2.1	3.0	-1.0	1	22	796	817	UUUCCUAUUCCACCCAUGCCAA	GCGGGAUGGGUGGCAUAGGGAA	Cleavage
sly-miR482c	Solyc08g080360.3.1	3.0	-1.0	1	22	719	740	UUUCCUAUUCCACCCAUGCCAA	UGUUCAUGGUUGGGAUAGGAAA	Cleavage
sly-miR482c	Solyc07g022840.1.1	3.0	-1.0	1	22	353	374	UUUCCUAUUCCACCCAUGCCAA	AUAGCAUGUGUGCAGUAGGAAA	Translation
sly-miR482d-3p	Solyc04g009070.1.1	0.0	-1.0	1	22	211	232	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGUGUAGGCAAGA	Cleavage
sly-miR482d-3p	Solyc02g036270.3.1	1.0	-1.0	1	22	681	702	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUAGGUAAGA	Cleavage
sly-miR482d-3p	Solyc11g065780.2.1	1.5	-1.0	1	22	786	807	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGGGGUGUAGGUAAGA	Cleavage
sly-miR482d-3p	Solyc05g008070.3.1	2.0	-1.0	1	22	532	553	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGUAUAGGUAAGA	Translation
sly-miR482d-3p	Solyc04g009120.2.1	2.0	-1.0	1	22	601	622	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGUGGUUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc12g017800.2.1	2.0	-1.0	1	22	1104	1125	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUAUAGGUAAGA	Translation
sly-miR482d-3p	Solyc11g006530.2.1	2.0	-1.0	1	22	526	547	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUAUAGGUAAGA	Translation
sly-miR482d-3p	Solyc01g067165.1.1	2.5	-1.0	1	22	529	550	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482d-3p	Solyc10g054990.2.1	2.5	-1.0	1	22	520	541	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482d-3p	Solyc10g054940.1.1	2.5	-1.0	1	22	46	67	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482d-3p	Solyc10g055170.1.1	2.5	-1.0	1	22	46	67	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482d-3p	Solyc10g054970.1.1	2.5	-1.0	1	22	538	559	UCUUGCCUACACCGCCCAUGCC	UGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482d-3p	Solyc11g069925.1.1	2.5	-1.0	1	22	622	643	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUGCGGGUAAGA	Cleavage
sly-miR482d-3p	Solyc04g009690.2.1	2.5	-1.0	1	22	562	583	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGGGGUUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc04g009250.1.1	2.5	-1.0	1	22	577	598	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGGGGUUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc04g009660.2.1	2.5	-1.0	1	22	550	571	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGGGGUUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc04g025820.1.1	3.0	-1.0	1	22	314	335	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGAUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc07g039420.1.1	3.0	-1.0	1	22	568	589	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGAUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc04g025840.2.1	3.0	-1.0	1	22	493	514	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGAUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc07g005770.2.1	3.0	-1.0	1	22	541	562	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUAUAGGCAAAA	Translation
sly-miR482d-3p	Solyc11g069620.2.1	3.0	-1.0	1	22	706	727	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGUGGUGCGGGUAAGA	Cleavage
sly-miR482d-3p	Solyc11g068360.1.1	3.0	-1.0	1	22	622	643	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUGCGGGUGAGA	Cleavage
sly-miR482d-3p	Solyc04g009240.2.1	3.0	-1.0	1	22	565	586	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGAUUAGGCAAGA	Translation
sly-miR482d-3p	Solyc05g006630.3.1	3.0	-1.0	1	22	1034	1055	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGAGGAGUGGGCAAGA	Translation
sly-miR482d-3p	Solyc11g006640.2.1	3.0	-1.0	1	22	532	553	UCUUGCCUACACCGCCCAUGCC	GGGAUGGGAGGUAUAGGUAAGA	Translation
sly-miR482d-3p	Solyc12g005520.1.1	3.0	-1.0	1	22	121	142	UCUUGCCUACACCGCCCAUGCC	GGAAAGGGGGGUGUGGGUAAGA	Cleavage
sly-miR482d-5p	Solyc07g007040.3.1	2.5	-1.0	1	21	2233	2253	CGUGAGCGGUGGGGAAAGAUA	CAUCUGUCUCCGCCGUUCACG	Cleavage
sly-miR482d-5p	Solyc01g111780.3.1	3.0	-1.0	1	21	1856	1876	CGUGAGCGGUGGGGAAAGAUA	GAUCUUUUCCCACUGCUCGAG	Cleavage
sly-miR482d-5p	Solyc03g020030.3.1	3.0	-1.0	1	21	744	764	CGUGAGCGGUGGGGAAAGAUA	GAGCUUUUUCCACCGCUUGCG	Cleavage
sly-miR482e-3p	Solyc11g006630.1.1	0.5	-1.0	1	22	532	553	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGCGGUAUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc07g049700.1.1	1.0	-1.0	1	22	544	565	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUAUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc01g067165.1.1	1.5	-1.0	1	22	529	550	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc10g054990.2.1	1.5	-1.0	1	22	520	541	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc10g054940.1.1	1.5	-1.0	1	22	46	67	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc10g055170.1.1	1.5	-1.0	1	22	46	67	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc10g054970.1.1	1.5	-1.0	1	22	538	559	UCUUGCCAAUACCGCCCAUUCC	UGUAUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc11g006530.2.1	2.0	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGAAUGGGCGGUAUAGGUAAGA	Cleavage
sly-miR482e-3p	Solyc11g020100.2.1	2.0	-1.0	1	22	1110	1131	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUCGGUAAGA	Cleavage
sly-miR482e-3p	Solyc05g008070.3.1	2.0	-1.0	1	22	532	553	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGCGGUAUAGGUAAGA	Cleavage
sly-miR482e-3p	Solyc12g017800.2.1	2.0	-1.0	1	22	1104	1125	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUAGGUAAGA	Cleavage
sly-miR482e-3p	Solyc04g009070.1.1	2.0	-1.0	1	22	211	232	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGCGGUGUAGGCAAGA	Cleavage
sly-miR482e-3p	Solyc12g009450.2.1	2.5	-1.0	1	22	729	750	UCUUGCCAAUACCGCCCAUUCC	GGGAUGGGUGGCAUUGGUAAGA	Translation
sly-miR482e-3p	Solyc04g005550.2.1	2.5	-1.0	1	22	870	891	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGGAAGA	Cleavage
sly-miR482e-3p	Solyc11g006520.2.1	2.5	-1.0	1	22	819	840	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUAUCGGUAAGA	Cleavage
sly-miR482e-3p	Solyc07g044790.3.1	2.5	-1.0	1	22	1223	1244	UCUUGCCAAUACCGCCCAUUCC	GGUCUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc12g044200.2.1	2.5	-1.0	1	22	1186	1207	UCUUGCCAAUACCGCCCAUUCC	GGUCUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc02g032200.3.1	2.5	-1.0	1	22	769	790	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGAGGUAUUGGCAAAA	Cleavage

sly-miR482e-3p	Solyc12g044180.2.1	2.5	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGUCUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc12g044190.2.1	2.5	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGUCUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc07g044797.1.1	2.5	-1.0	1	22	286	307	UCUUGCCAAUACCGCCCAUUCC	GGUCUGGGUGGUGUUGGUAAGA	Cleavage
sly-miR482e-3p	Solyc11g069320.1.1	2.5	-1.0	1	22	408	429	UCUUGCCAAUACCGCCCAUUCC	CUCAUGGGAGGUAUUGGGAAGA	Cleavage
sly-miR482e-3p	Solyc01g014840.3.1	3.0	-1.0	1	22	649	670	UCUUGCCAAUACCGCCCAUUCC	GGGAUGGGAGGCAUUGGUAAGA	Translation
sly-miR482e-3p	Solyc11g006640.2.1	3.0	-1.0	1	22	532	553	UCUUGCCAAUACCGCCCAUUCC	GGGAUGGGAGGUAUAGGUAAGA	Cleavage
sly-miR482e-3p	Solyc02g036270.3.1	3.0	-1.0	1	22	681	702	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUAGGUAAGA	Cleavage
sly-miR482e-3p	Solyc04g005540.3.1	3.0	-1.0	1	22	852	873	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGAGUUGGUAAGA	Translation
sly-miR482e-3p	Solyc07g005770.2.1	3.0	-1.0	1	22	541	562	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUAGGCAAAA	Cleavage
sly-miR482e-3p	Solyc04g048920.1.1	3.0	-1.0	1	22	46	67	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGUUAAGA	Cleavage
sly-miR482e-3p	Solyc01g008800.2.1	3.0	-1.0	1	22	1564	1585	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGGGGAAUUGGUAAGA	Translation
sly-miR482e-3p	Solyc03g046207.1.1	3.0	-1.0	1	22	703	724	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGGGGCAUUGGUAAGA	Translation
sly-miR482e-3p	Solyc10g055050.2.1	3.0	-1.0	1	22	379	400	UCUUGCCAAUACCGCCCAUUCC	UGUAUGGGUGGUGUUGGUAAAA	Cleavage
sly-miR482e-5p	Solyc07g062450.3.1	2.5	-1.0	1	21	192	212	AGUGGGUGGUGUGGUAAGAUU	GCUUUUACCACAUCAUCCACA	Cleavage
sly-miR482e-5p	Solyc01g107340.3.1	2.5	-1.0	1	21	198	218	AGUGGGUGGUGUGGUAAGAUU	GCUCCUGCCACGUCACCCACU	Cleavage
sly-miR482e-5p	Solyc03g098750.3.1	3.0	-1.0	1	21	607	627	AGUGGGUGGUGUGGUAAGAUU	AAUCUUACCAUAUCAAUCACU	Cleavage
sly-miR482e-5p	Solyc01g087540.3.1	3.0	-1.0	1	21	1280	1300	AGUGGGUGGUGUGGUAAGAUU	GGUCUUAUCAUACUCCCCACU	Cleavage
sly-miR482e-5p	Solyc04g063345.1.1	3.0	-1.0	1	21	88	108	AGUGGGUGGUGUGGUAAGAUU	ACUCUUACAGCAUUACCCACU	Cleavage
sly-miR482e-5p	Solyc03g096810.3.1	3.0	-1.0	1	21	689	709	AGUGGGUGGUGUGGUAAGAUU	UCUUUUACCACCCCACCCACC	Translation
sly-miR482e-5p	Solyc06g071510.3.1	3.0	-1.0	1	21	322	342	AGUGGGUGGUGUGGUAAGAUU	GUUCUUGCUGCAUCACCUAUU	Cleavage
sly-miR482e-5p	Solyc01g105150.3.1	3.0	-1.0	1	21	2671	2691	AGUGGGUGGUGUGGUAAGAUU	UUUCUUACCACUCUACCUGCU	Translation
sly-miR482e-5p	Solyc10g009210.3.1	3.0	-1.0	1	21	2797	2817	AGUGGGUGGUGUGGUAAGAUU	ACACUUCUCACACCAUCCACU	Cleavage
sly-miR482e-5p	Solyc08g065980.3.1	3.0	-1.0	1	21	4885	4905	AGUGGGUGGUGUGGUAAGAUU	AUUUUUUCUGCAUCACCCACU	Cleavage
sly-miR482e-5p	Solyc11g071390.1.1	3.0	-1.0	1	21	325	345	AGUGGGUGGUGUGGUAAGAUU	CCUUUUAGCAUACUGCCCACU	Cleavage
sly-miR482e-5p	Solyc11g068360.1.1	3.0	-1.0	1	21	2551	2571	AGUGGGUGGUGUGGUAAGAUU	CCUUUUAGCAUACUGCCCACU	Cleavage
sly-miR5014a-3p	Solyc05g018710.2.1	1.0	-1.0	1	19	1982	2000	UUGUACAAAUUUAAGUGUA	UAAACUUAAAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc12g087810.2.1	2.0	-1.0	1	19	1254	1272	UUGUACAAAUUUAAGUGUA	AACAUUUAGAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc07g021405.1.1	2.0	-1.0	1	19	1242	1260	UUGUACAAAUUUAAGUGUA	AACACCUAAAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc05g015150.3.1	2.5	-1.0	1	19	375	393	UUGUACAAAUUUAAGUGUA	UACACUUAAAUUUUUAUAG	Cleavage
sly-miR5014a-3p	Solyc06g068090.3.1	2.5	-1.0	1	19	3216	3234	UUGUACAAAUUUAAGUGUA	UGCACUUGAGUUUGUAUGA	Cleavage
sly-miR5014a-3p	Solyc04g082310.3.1	2.5	-1.0	1	19	3340	3358	UUGUACAAAUUUAAGUGUA	UAGGCUUAAGUUUGUGCAA	Cleavage
sly-miR5014a-3p	Solyc01g107550.3.1	2.5	-1.0	1	19	2014	2032	UUGUACAAAUUUAAGUGUA	UAGCCUUGAAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc04g015520.3.1	3.0	-1.0	1	19	1329	1347	UUGUACAAAUUUAAGUGUA	UAUACUUAAAUUUAUACAU	Cleavage
sly-miR5014a-3p	Solyc01g009030.3.1	3.0	-1.0	1	19	2055	2073	UUGUACAAAUUUAAGUGUA	GACAUUUUAAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc05g005940.3.1	3.0	-1.0	1	19	145	163	UUGUACAAAUUUAAGUGUA	GACACUUAAACUUGUAUAA	Cleavage
sly-miR5014a-3p	Solyc05g005130.2.1	3.0	-1.0	1	19	3347	3365	UUGUACAAAUUUAAGUGUA	AAUACUUAAAUUUGGACAA	Cleavage
sly-miR5014a-3p	Solyc09g008600.3.1	3.0	-1.0	1	19	154	172	UUGUACAAAUUUAAGUGUA	UGUACUUAUAUUUGUAUAA	Translation
sly-miR5014a-3p	Solyc06g082000.3.1	3.0	-1.0	1	19	262	280	UUGUACAAAUUUAAGUGUA	UGUACUUAAAUUUGUGAAA	Cleavage
sly-miR5014a-3p	Solyc06g072590.3.1	3.0	-1.0	1	19	1695	1713	UUGUACAAAUUUAAGUGUA	UACACUUAAAUUUACACAA	Cleavage
sly-miR5014a-3p	Solyc10g080090.2.1	3.0	-1.0	1	19	1715	1733	UUGUACAAAUUUAAGUGUA	UGCAUUUAAAGUUGUGCAA	Cleavage
sly-miR5014a-3p	Solyc02g071880.3.1	3.0	-1.0	1	19	1394	1412	UUGUACAAAUUUAAGUGUA	UGUAUUUAAACUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc01g105140.3.1	3.0	-1.0	1	19	2352	2371	UUGUACAAAUUUAAG-UGUA	UACAGCUUAAAUUUGUGUAA	Cleavage
sly-miR5014a-3p	Solyc01g011093.1.1	3.0	-1.0	1	19	549	567	UUGUACAAAUUUAAGUGUA	GAUGAUUAAAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc01g011091.1.1	3.0	-1.0	1	19	5192	5210	UUGUACAAAUUUAAGUGUA	GAUGAUUAAAUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc06g005600.3.1	3.0	-1.0	1	19	962	980	UUGUACAAAUUUAAGUGUA	UAUAAUUAAACUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc03g044690.1.1	3.0	-1.0	1	19	585	603	UUGUACAAAUUUAAGUGUA	UGCACAUAAAUUCGUACAA	Cleavage
sly-miR5014a-3p	Solyc06g067990.3.1	3.0	-1.0	1	19	1587	1605	UUGUACAAAUUUAAGUGUA	UAUUUUUGAGUUUGUACAA	Cleavage
sly-miR5014a-3p	Solyc01g057520.3.1	3.0	-1.0	1	19	486	504	UUGUACAAAUUUAAGUGUA	UGCAGUUGAGUUUGUGCAA	Cleavage
sly-miR5014a-3p	Solyc04g076525.1.1	3.0	-1.0	1	19	3258	3276	UUGUACAAAUUUAAGUGUA	UAAAUUUAGGUUUGUGCAA	Cleavage
sly-miR5014a-3p	Solyc07g062230.3.1	3.0	-1.0	1	19	6	24	UUGUACAAAUUUAAGUGUA	UAAACUUGAAUUUCUACAA	Cleavage

sly-miR5014a-3p	Solyc07g063260.3.1	3.0	-1.0	1	19	1095	1113	UUGUACAAAUUUAAGUGUA	UAAAUUUAAAUUUGUGUGA	Cleavage
sly-miR5014a-3p	Solyc01g111610.3.1	3.0	-1.0	1	19	1287	1305	UUGUACAAAUUUAAGUGUA	UAAUUUUAAAUUUGUAUAA	Cleavage
sly-miR5014a-3p	Solyc08g078440.3.1	3.0	-1.0	1	19	5178	5196	UUGUACAAAUUUAAGUGUA	UAAACGUAAAUUUGUAUAG	Cleavage
sly-miR5162	Solyc05g006430.2.1	0.0	-1.0	1	22	447	468	AAAUGACCAAAAUACCCCUAAA	GUAAGGGGUAUUUUGGUCAUUU	Cleavage
sly-miR5162	Solyc12g013820.2.1	1.5	-1.0	1	22	254	275	AAAUGACCAAAAUACCCCUAAA	UUAAGGGGUAUUUUAGUCAUUU	Cleavage
sly-miR5162	Solyc12g013820.2.1	1.5	-1.0	1	22	902	923	AAAUGACCAAAAUACCCCUAAA	AUAAGGGGUAUUUUAGUCAUUU	Cleavage
sly-miR5162	Solyc12g013820.2.1	1.5	-1.0	1	22	1105	1126	AAAUGACCAAAAUACCCCUAAA	AUAAGGGGUAUUUUAGUCAUUU	Cleavage
sly-miR5162	Solyc12g013820.2.1	1.5	-1.0	1	22	458	479	AAAUGACCAAAAUACCCCUAAA	ACAAGGGGUAUUUUAGUCAUUU	Cleavage
sly-miR5162	Solyc10g009380.3.1	1.5	-1.0	1	22	662	683	AAAUGACCAAAAUACCCCUAAA	GGUAGGGGUAAUUUGGUCAUUU	Cleavage
sly-miR5162	Solyc08g044400.2.1	2.0	-1.0	1	22	18	39	AAAUGACCAAAAUACCCCUAAA	CUUAGAGGUAUUUUGGUCAUUC	Cleavage
sly-miR5162	Solyc08g076460.3.1	2.0	-1.0	1	22	51	72	AAAUGACCAAAAUACCCCUAAA	CCGAGGGCAAUUUUGGUCAUUU	Cleavage
sly-miR5162	Solyc11g066970.2.1	2.5	-1.0	1	22	2090	2113	AAAUGACCAAAAUACC--CCUAAA	UUUAGGAGGGUAUUUUGGUCAUUU	Cleavage
sly-miR5162	Solyc02g081650.3.1	2.5	-1.0	1	22	221	242	AAAUGACCAAAAUACCCCUAAA	UUUGGGGGGGUUUUGGUUAUUU	Cleavage
sly-miR5162	Solyc10g084990.2.1	2.5	-1.0	1	22	1845	1866	AAAUGACCAAAAUACCCCUAAA	AUUUGGGGUAUUUUUGUCAUUU	Cleavage
sly-miR5162	Solyc02g037495.1.1	2.5	-1.0	1	22	607	628	AAAUGACCAAAAUACCCCUAAA	CAUAGGGGUAUUUUCGUUGUUU	Cleavage
sly-miR5162	Solyc11g064780.2.1	2.5	-1.0	1	22	76	97	AAAUGACCAAAAUACCCCUAAA	AUAAGGGGCAUUUUGGUGAUUU	Cleavage
sly-miR5162	Solyc08g014110.1.1	2.5	-1.0	1	22	462	483	AAAUGACCAAAAUACCCCUAAA	GAAAGGGAUAUUAUGGUCAUUU	Translation
sly-miR5162	Solyc11g065840.2.1	2.5	-1.0	1	22	1212	1233	AAAUGACCAAAAUACCCCUAAA	GAAAAGGGUAAUUUGGUCAUUU	Cleavage
sly-miR5162	Solyc03g083580.3.1	2.5	-1.0	1	22	338	359	AAAUGACCAAAAUACCCCUAAA	AAAAGGGGCAUUUUUGUCAUUU	Cleavage
sly-miR5162	Solyc01g005590.2.1	3.0	-1.0	1	22	285	306	AAAUGACCAAAAUACCCCUAAA	GUUGAGGGUAUUUUCGUCAUUU	Cleavage
sly-miR5162	Solyc06g007380.1.1	3.0	-1.0	1	22	523	544	AAAUGACCAAAAUACCCCUAAA	CCUGGGGGUAUUUUCGUCAUUC	Cleavage
sly-miR5162	Solyc12g089230.2.1	3.0	-1.0	1	22	2061	2082	AAAUGACCAAAAUACCCCUAAA	GUUGAGCGUAUUUUGGUUAUUU	Cleavage
sly-miR5162	Solyc03g031800.3.1	3.0	-1.0	1	22	1038	1059	AAAUGACCAAAAUACCCCUAAA	UUAAGGAGUAUUUUGAUUAUUU	Cleavage
sly-miR5162	Solyc01g080550.2.1	3.0	-1.0	1	21	1	21	AAAUGACCAAAAUACCCCUAA	UGAGGGGUAUUUUGGCCACUU	Cleavage
sly-miR5162	Solyc00g143770.2.1	3.0	-1.0	1	21	1	21	AAAUGACCAAAAUACCCCUAA	AUGGUGGAAUUUUGGUUAUUU	Cleavage
sly-miR5162	Solyc07g026810.3.1	3.0	-1.0	1	22	728	749	AAAUGACCAAAAUACCCCUAAA	CAAAGGGAUGUUUUGGUCACUU	Cleavage
sly-miR5174d-5p	Solyc02g078970.3.1	1.0	-1.0	1	24	2666	2689	UCCCUCCGUUUCAAAAAGAUUGGC	GUCAUUCUUUGUGAAACGGAGGGA	Cleavage
sly-miR5174d-5p	Solyc07g008560.3.1	1.5	-1.0	1	24	4	27	UCCCUCCGUUUCAAAAAGAUUGGC	AUCAUUCUUUUUGAAACGGAAGGA	Cleavage
sly-miR5174d-5p	Solyc01g067490.3.1	2.0	-1.0	1	24	579	602	UCCCUCCGUUUCAAAAAGAUUGGC	GCAGCUCUUGUUGAGAUGGAGGGA	Cleavage
sly-miR5174d-5p	Solyc12g018990.2.1	2.0	-1.0	1	24	1458	1481	UCCCUCCGUUUCAAAAAGAUUGGC	UAUCUUCUUUUUGAGACGGAGGAA	Cleavage
sly-miR5174d-5p	Solyc02g067210.3.1	3.0	-1.0	1	24	1473	1496	UCCCUCCGUUUCAAAAAGAUUGGC	GCUAAUCUUUUUGAAAAAGAGGGA	Cleavage
sly-miR5174d-5p	Solyc11g007600.2.1	3.0	-1.0	1	24	1660	1683	UCCCUCCGUUUCAAAAAGAUUGGC	AUUGGUCUUUUUGAAUCGGAGAGA	Cleavage
sly-miR5174d-5p	Solyc05g007680.1.1	3.0	-1.0	1	24	1164	1188	UCCCUCCGUUUCAAAAAGAU-UGGC	ACCAUAUCUUGUUGAAAUGGAUGGA	Cleavage
sly-miR5174d-5p	Solyc01g108470.2.1	3.0	-1.0	1	24	426	449	UCCCUCCGUUUCAAAAAGAUUGGC	GCUCUUCAUUUGGAAAUGGAGGGA	Cleavage
sly-miR5174d-5p	Solyc08g067245.1.1	3.0	-1.0	1	24	96	119	UCCCUCCGUUUCAAAAAGAUUGGC	UUUCCUCUUUUUGAAAUGGGUGGG	Cleavage
sly-miR5174d-5p	Solyc03g117940.3.1	3.0	-1.0	1	24	1030	1053	UCCCUCCGUUUCAAAAAGAUUGGC	GCGCUUCUUUUUGAAGUGAGGGGA	Cleavage
sly-miR5174d-5p	Solyc07g052390.3.1	3.0	-1.0	1	24	533	556	UCCCUCCGUUUCAAAAAGAUUGGC	GAGUUUUUUUUUGAAGUGGUGGGA	Cleavage
sly-miR5282-3p	Solyc06g066040.2.1	2.5	-1.0	1	23	2259	2281	GACGGAAUUAGAGAGGGAUUUUA	UGUGAUCCUUCUCUAGUUCCUUC	Cleavage
sly-miR5282-3p	Solyc05g012900.3.1	3.0	-1.0	1	23	1338	1360	GACGGAAUUAGAGAGGGAUUUUA	UGAAUUUCCUCUCUAGUUUUGUC	Cleavage
sly-miR5282-3p	Solyc05g012910.3.1	3.0	-1.0	1	23	1235	1257	GACGGAAUUAGAGAGGGAUUUUA	UGGAUUUCCUCUCUAGUUUUGUC	Cleavage
sly-miR5282-3p	Solyc05g013580.3.1	3.0	-1.0	1	23	271	293	GACGGAAUUAGAGAGGGAUUUUA	ACAAAUUCCUCUCUAAUUUCAUU	Cleavage
sly-miR5282-3p	Solyc02g094485.1.1	3.0	-1.0	1	23	651	673	GACGGAAUUAGAGAGGGAUUUUA	GAACAUUCUCCUCUGAUUCUGUC	Cleavage
sly-miR5282-3p	Solyc02g094150.3.1	3.0	-1.0	1	23	66	88	GACGGAAUUAGAGAGGGAUUUUA	AGCAGUGCCUCUCUCAUUCCGUC	Cleavage
sly-miR5282-3p	Solyc09g007100.3.1	3.0	-1.0	1	23	67	89	GACGGAAUUAGAGAGGGAUUUUA	UACCAUUCCUUUCUUAUUCUGUC	Cleavage
sly-miR5282-3p	Solyc09g066100.3.1	3.0	-1.0	1	23	1138	1160	GACGGAAUUAGAGAGGGAUUUUA	UUUUUUCUCUUUUUAAUUCCGUU	Cleavage
sly-miR5282-3p	Solyc08g062250.2.1	3.0	-1.0	1	23	809	831	GACGGAAUUAGAGAGGGAUUUUA	UUCUUUUCCUCUCUGAUUCUGUU	Cleavage
sly-miR5282-3p	Solyc06g051080.3.1	3.0	-1.0	1	23	128	150	GACGGAAUUAGAGAGGGAUUUUA	CUCUAUCCCUCUCUAAUGGCGUC	Cleavage
sly-miR5282-5p	Solyc07g054640.1.1	1.5	-1.0	1	23	991	1013	AUGAAAUUCCUUACAAAUUCCUU	CGCCCAUUUGUGAGGAAUUUCAU	Cleavage
sly-miR5282-5p	Solyc12g095830.2.1	1.5	-1.0	1	23	2269	2291	AUGAAAUUCCUUACAAAUUCCUU	UAAUAAUUUGUAAGGGAUUUCAA	Cleavage
sly-miR5282-5p	Solyc04g056590.3.1	1.5	-1.0	1	23	1005	1027	AUGAAAUUCCUUACAAAUUCCUU	GGAUACUUUGUAAGGGAUUUCAU	Cleavage

sly-miR5282-5p	Solyc02g061940.3.1	2.0	-1.0	1	23	398	420	AUGAAAUUCCUUACAAAUUCCUU	AAUGUAUUUGUGAGGAGUUUCAU	Cleavage
sly-miR5282-5p	Solyc12g056600.3.1	2.5	-1.0	1	23	725	747	AUGAAAUUCCUUACAAAUUCCUU	GGGGAAUUUGAAAGGAGUUUUAU	Cleavage
sly-miR5282-5p	Solyc12g096200.2.1	2.5	-1.0	1	23	779	801	AUGAAAUUCCUUACAAAUUCCUU	AUGAAAUUUGUAAGAAAUUUCAA	Cleavage
sly-miR5282-5p	Solyc03g083240.3.1	2.5	-1.0	1	23	2487	2509	AUGAAAUUCCUUACAAAUUCCUU	UUAUGAUUUGUAUGGAAUUUUAU	Translation
sly-miR5282-5p	Solyc05g005330.3.1	2.5	-1.0	1	23	4262	4284	AUGAAAUUCCUUACAAAUUCCUU	UUACAGUUUUUAAGGAGUUUUAU	Cleavage
sly-miR5282-5p	Solyc01g091010.3.1	3.0	-1.0	1	23	345	367	AUGAAAUUCCUUACAAAUUCCUU	CAGGAAUUAGUAAGGAAUCUUAU	Cleavage
sly-miR5282-5p	Solyc02g014860.3.1	3.0	-1.0	1	23	1721	1743	AUGAAAUUCCUUACAAAUUCCUU	CAGAAAAUUGUGAGAAAUUUCAU	Cleavage
sly-miR5282-5p	Solyc04g014430.2.1	3.0	-1.0	1	23	3	25	AUGAAAUUCCUUACAAAUUCCUU	GGGAAAGUUGAAAGGAAUUUUAU	Cleavage
sly-miR5282-5p	Solyc04g008730.3.1	3.0	-1.0	1	23	1733	1755	AUGAAAUUCCUUACAAAUUCCUU	ACAAAAUUUGUAGGGAAUUUGAC	Cleavage
sly-miR5282-5p	Solyc11g011400.2.1	3.0	-1.0	1	23	544	566	AUGAAAUUCCUUACAAAUUCCUU	GAUAAAUUUGUAACGUAUUUCAU	Translation
sly-miR5282-5p	Solyc02g091900.3.1	3.0	-1.0	1	23	650	672	AUGAAAUUCCUUACAAAUUCCUU	GGAAAAUUUGCAAGGAAUUUAAU	Cleavage
sly-miR5282-5p	Solyc02g069810.2.1	3.0	-1.0	1	23	2545	2567	AUGAAAUUCCUUACAAAUUCCUU	AGUCAAUUUGUAAAUAAUUUCAU	Translation
sly-miR5282-5p	Solyc11g065470.2.1	3.0	-1.0	1	23	2158	2180	AUGAAAUUCCUUACAAAUUCCUU	CCAUGAUUUAUGAGGAAUUUCAA	Cleavage
sly-miR530	Solyc04g009450.1.1	2.5	-1.0	1	21	6	26	UCUGCAUUUGCACCUGCACCU	AUCUGCAGGAGCAAAUGCAGA	Cleavage
sly-miR530	Solyc07g053650.3.1	2.5	-1.0	1	21	1377	1397	UCUGCAUUUGCACCUGCACCU	UAGUGCAGGGGCAAGUGUAGA	Cleavage
sly-miR530	Solyc09g082620.3.1	2.5	-1.0	1	21	283	303	UCUGCAUUUGCACCUGCACCU	GCGUGGAGGUGCAAGUGUGGA	Cleavage
sly-miR530	Solyc06g068190.2.1	2.5	-1.0	1	21	75	95	UCUGCAUUUGCACCUGCACCU	UAGUGCUAGUGCAAGUGCAGA	Cleavage
sly-miR530	Solyc09g083390.2.1	3.0	-1.0	1	21	990	1010	UCUGCAUUUGCACCUGCACCU	AGGUGCAGGUGUAAAUGCAAG	Cleavage
sly-miR530	Solyc08g022100.1.1	3.0	-1.0	1	21	56	76	UCUGCAUUUGCACCUGCACCU	GGGUGCGGGUGCGGGUGCGGG	Cleavage
sly-miR530	Solyc07g053260.3.1	3.0	-1.0	1	21	988	1008	UCUGCAUUUGCACCUGCACCU	UGGUGGAGGUGAAGAUGCAGA	Translation
sly-miR530	Solyc10g049610.1.1	3.0	-1.0	1	21	189	209	UCUGCAUUUGCACCUGCACCU	AAGUGUAGGUCUAAGUGCAGA	Translation
sly-miR530	Solyc10g049610.1.1	3.0	-1.0	1	21	321	341	UCUGCAUUUGCACCUGCACCU	AUGUGUAGGUUCAAGUGCAGG	Translation
sly-miR530	Solyc08g061698.1.1	3.0	-1.0	1	21	366	386	UCUGCAUUUGCACCUGCACCU	CAUUGCAGAUGCAGAUGCAGA	Cleavage
sly-miR530	Solyc08g069170.2.1	3.0	-1.0	1	21	1941	1961	UCUGCAUUUGCACCUGCACCU	AGGCAAAGGUGCAAAUGCAGA	Cleavage
sly-miR530	Solyc04g015260.1.1	3.0	-1.0	1	21	186	206	UCUGCAUUUGCACCUGCACCU	AAGUAUAGGUCCAAAUGCAGA	Translation
sly-miR530	Solyc11g071700.2.1	3.0	-1.0	1	21	3243	3263	UCUGCAUUUGCACCUGCACCU	AAGUGAAGGUGCGAAUACAGA	Cleavage
sly-miR530	Solyc03g119895.1.1	3.0	-1.0	1	21	1472	1492	UCUGCAUUUGCACCUGCACCU	CAUUACAAGUGCAAAUGCAGA	Cleavage
sly-miR530	Solyc03g025810.3.1	3.0	-1.0	1	21	1372	1392	UCUGCAUUUGCACCUGCACCU	CAGGGGAGGUGUAGAUGCAGA	Cleavage
sly-miR530	Solyc03g078120.3.1	3.0	-1.0	1	21	1863	1883	UCUGCAUUUGCACCUGCACCU	UCGUGCUAGUGUGAAUGCAGA	Cleavage
sly-miR5300-5p	Solyc04g005650.2.1	0.0	-1.0	1	22	355	376	UCCCCAGUCCAGGCAUUCCAAC	GUUGGAAUGCCUGGACUGGGGA	Cleavage
sly-miR5300-5p	Solyc03g116550.3.1	2.5	-1.0	1	22	1101	1122	UCCCCAGUCCAGGCAUUCCAAC	ACAGGAAACCUUGGACUGGGGA	Cleavage
sly-miR5300-5p	Solyc05g008650.1.1	3.0	-1.0	1	22	1282	1303	UCCCCAGUCCAGGCAUUCCAAC	GUUGGAAUGCCUGGACUUGGCA	Cleavage
sly-miR5300-5p	Solyc06g064780.1.1	3.0	-1.0	1	22	175	196	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUUGGUA	Cleavage
sly-miR5300-5p	Solyc06g064690.1.1	3.0	-1.0	1	22	49	70	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUUGGUA	Cleavage
sly-miR5300-5p	Solyc06g064760.1.1	3.0	-1.0	1	22	175	196	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUCGGUA	Cleavage
sly-miR5300-5p	Solyc03g123960.3.1	3.0	-1.0	1	22	1121	1142	UCCCCAGUCCAGGCAUUCCAAC	GCCUCAAUGCCUGGACUGGGGC	Cleavage
sly-miR5300-5p	Solyc02g062110.3.1	3.0	-1.0	1	22	1319	1340	UCCCCAGUCCAGGCAUUCCAAC	ACUGCAUUGCUUGGAUUGGGGA	Cleavage
sly-miR5300-5p	Solyc02g062110.3.1	3.0	-1.0	1	22	1445	1466	UCCCCAGUCCAGGCAUUCCAAC	ACUGCAUUGCUUGGAUUGGGGA	Cleavage
sly-miR5300-5p	Solyc12g062410.1.1	3.0	-1.0	1	22	188	209	UCCCCAGUCCAGGCAUUCCAAC	CUCGGAAUCGCUGGAUUGGGGA	Cleavage
sly-miR5303	Solyc03g097670.3.1	0.5	-1.0	1	21	6696	6716	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc01g094210.2.1	1.0	-1.0	1	21	1076	1096	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUUUUCAAAAA	Cleavage
sly-miR5303	Solyc10g006640.3.1	1.0	-1.0	1	21	1483	1503	UUUUUGAAGAGUUCGAGCAAC	GUUGUUUGAACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc11g012890.2.1	1.0	-1.0	1	21	2700	2720	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUUCAGAAA	Cleavage
sly-miR5303	Solyc10g085210.2.1	1.0	-1.0	1	21	968	988	UUUUUGAAGAGUUCGAGCAAC	CUUGUUCGAAUUCUUCAAAAA	Cleavage
sly-miR5303	Solyc11g066940.2.1	1.0	-1.0	1	21	1067	1087	UUUUUGAAGAGUUCGAGCAAC	CUUGCUCGGACUCUUUAAAAA	Cleavage
sly-miR5303	Solyc10g085210.2.1	1.5	-1.0	1	21	1029	1049	UUUUUGAAGAGUUCGAGCAAC	GUUGUUUGAACUCUUUAAAAA	Cleavage
sly-miR5303	Solyc11g007360.1.1	1.5	-1.0	1	21	705	725	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc11g066260.2.1	1.5	-1.0	1	21	2196	2216	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCCGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc07g018290.3.1	1.5	-1.0	1	21	1547	1567	UUUUUGAAGAGUUCGAGCAAC	AUUACUCGAAUUCUUCAAAAA	Cleavage
sly-miR5303	Solyc12g096370.2.1	1.5	-1.0	1	21	2802	2822	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUGGACUCUUCGAAAA	Cleavage

sly-miR5303	Solyc10g006360.2.1	2.0	-1.0	1	21	1237	1257	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUCCAAAAA	Cleavage
sly-miR5303	Solyc05g055480.3.1	2.0	-1.0	1	21	1627	1647	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGAAUUUUUCGAAAA	Cleavage
sly-miR5303	Solyc06g054480.3.1	2.0	-1.0	1	21	2015	2035	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAACUUCUCAAAAA	Cleavage
sly-miR5303	Solyc03g097450.3.1	2.0	-1.0	1	21	1952	1972	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGUCUCUUCAAAAA	Cleavage
sly-miR5303	Solyc06g052080.3.1	2.0	-1.0	1	21	848	868	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACCCUUCAAAAA	Translation
sly-miR5303	Solyc12g010440.2.1	2.0	-1.0	1	21	2351	2371	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUCUCCAAAAA	Cleavage
sly-miR5303	Solyc04g080330.3.1	2.0	-1.0	1	21	4474	4494	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUUCAAACA	Cleavage
sly-miR5303	Solyc04g007830.3.1	2.0	-1.0	1	21	549	569	UUUUUGAAGAGUUCGAGCAAC	AUUGUUUGGACUCUUUAAAAA	Cleavage
sly-miR5303	Solyc04g051870.2.1	2.0	-1.0	1	21	1880	1900	UUUUUGAAGAGUUCGAGCAAC	AUUGCUCGUACUUUUCAAAAA	Cleavage
sly-miR5303	Solyc07g052300.3.1	2.0	-1.0	1	21	1734	1754	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGAAUUUUUUAGAAA	Cleavage
sly-miR5303	Solyc01g006520.3.1	2.0	-1.0	1	21	2647	2667	UUUUUGAAGAGUUCGAGCAAC	AUUGCUCAGACUCUUCGAAAA	Cleavage
sly-miR5303	Solyc11g072380.2.1	2.0	-1.0	1	21	2182	2202	UUUUUGAAGAGUUCGAGCAAC	CUGGCUCGAAUUUUUCAAAAA	Cleavage
sly-miR5303	Solyc06g005140.3.1	2.0	-1.0	1	21	1484	1504	UUUUUGAAGAGUUCGAGCAAC	AGUUCUCGAAUUUUUCAAAAA	Cleavage
sly-miR5303	Solyc05g051340.2.1	2.0	-1.0	1	21	2361	2381	UUUUUGAAGAGUUCGAGCAAC	UGUGGUUGGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc09g098340.3.1	2.0	-1.0	1	21	4472	4492	UUUUUGAAGAGUUCGAGCAAC	AAUAUUCGGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc07g066670.3.1	2.5	-1.0	1	21	3139	3159	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAACUCUUCAAAUG	Cleavage
sly-miR5303	Solyc10g051170.2.1	2.5	-1.0	1	21	923	943	UUUUUGAAGAGUUCGAGCAAC	GUUGCUUGAGUUUUUUAAAAA	Cleavage
sly-miR5303	Solyc12g007100.2.1	2.5	-1.0	1	21	1045	1065	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUCUUGGAAAA	Cleavage
sly-miR5303	Solyc03g005420.2.1	2.5	-1.0	1	21	876	896	UUUUUGAAGAGUUCGAGCAAC	GUUGCUUGAAUUCUUCAGGAG	Cleavage
sly-miR5303	Solyc05g053750.2.1	2.5	-1.0	1	21	674	694	UUUUUGAAGAGUUCGAGCAAC	GUUGUGUGAACUCUUCAAGAA	Cleavage
sly-miR5303	Solyc05g054720.3.1	2.5	-1.0	1	21	1111	1131	UUUUUGAAGAGUUCGAGCAAC	GUUACUCGAACUCUCCAAAAA	Cleavage
sly-miR5303	Solyc05g051580.3.1	2.5	-1.0	1	21	3343	3363	UUUUUGAAGAGUUCGAGCAAC	GUUGGUCGGACUUUUCAAAAG	Cleavage
sly-miR5303	Solyc10g008470.3.1	2.5	-1.0	1	21	2073	2093	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGAUUCUUCAAUAA	Cleavage
sly-miR5303	Solyc09g091910.2.1	2.5	-1.0	1	21	3545	3565	UUUUUGAAGAGUUCGAGCAAC	GUUACUCAAACUUUUCAAAAA	Cleavage
sly-miR5303	Solyc03g005740.2.1	2.5	-1.0	1	21	1104	1124	UUUUUGAAGAGUUCGAGCAAC	AUUUCUCGAACUCUCCAAAAA	Cleavage
sly-miR5303	Solyc03g095310.3.1	2.5	-1.0	1	21	858	878	UUUUUGAAGAGUUCGAGCAAC	AAGCUUCGAACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc03g117700.2.1	2.5	-1.0	1	21	3988	4008	UUUUUGAAGAGUUCGAGCAAC	CUUGGUCGGGUUCUUCAAAAA	Cleavage
sly-miR5303	Solyc05g056420.3.1	2.5	-1.0	1	21	5245	5265	UUUUUGAAGAGUUCGAGCAAC	UUUGUUCCGACUCUUUAAAAA	Cleavage
sly-miR5303	Solyc05g056400.3.1	2.5	-1.0	1	21	1743	1763	UUUUUGAAGAGUUCGAGCAAC	AUUGUUCAAACUCUUUGAAAA	Cleavage
sly-miR5303	Solyc12g033080.1.1	2.5	-1.0	1	21	453	473	UUUUUGAAGAGUUCGAGCAAC	AAUGUUUGGAUUUUUCAAAAA	Cleavage
sly-miR5303	Solyc02g089930.3.1	2.5	-1.0	1	21	2063	2083	UUUUUGAAGAGUUCGAGCAAC	AGUGCUUGGACUCUUCAAUAA	Cleavage
sly-miR5303	Solyc01g008050.3.1	2.5	-1.0	1	21	366	386	UUUUUGAAGAGUUCGAGCAAC	AUUUCUUCAACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc10g078700.2.1	2.5	-1.0	1	21	2470	2491	UUUUUGAAGAGUUCG-AGCAAC	GCUGCUGUGAACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc08g023600.1.1	2.5	-1.0	1	21	87	107	UUUUUGAAGAGUUCGAGCAAC	GGUGCUCUUACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc04g009710.2.1	2.5	-1.0	1	21	679	699	UUUUUGAAGAGUUCGAGCAAC	UGUGUUCAGACUCUUCAAAAG	Cleavage
sly-miR5303	Solyc11g043160.2.1	2.5	-1.0	1	21	852	872	UUUUUGAAGAGUUCGAGCAAC	CAUGUUCCAAUUCUUCAAGAA	Cleavage
sly-miR5303	Solyc05g008910.3.1	2.5	-1.0	1	21	2443	2463	UUUUUGAAGAGUUCGAGCAAC	UCUGUUCAGACUCUUCAGAAA	Cleavage
sly-miR5303	Solyc01g008100.3.1	3.0	-1.0	1	21	971	991	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAACUGUUCAUAAA	Cleavage
sly-miR5303	Solyc03g033340.3.1	3.0	-1.0	1	21	2024	2044	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGUUUCUUCAAAAA	Cleavage
sly-miR5303	Solyc01g007750.3.1	3.0	-1.0	1	21	3041	3061	UUUUUGAAGAGUUCGAGCAAC	GUUGCUUGGACUCUUUUAAAA	Cleavage
sly-miR5303	Solyc07g065860.3.1	3.0	-1.0	1	21	1048	1068	UUUUUGAAGAGUUCGAGCAAC	GUUGAUCGGAUUUUUUAAAAA	Cleavage
sly-miR5303	Solyc03g096020.2.1	3.0	-1.0	1	21	510	530	UUUUUGAAGAGUUCGAGCAAC	GGUGCUCGAACUCUUCGAAUG	Cleavage
sly-miR5303	Solyc04g005230.3.1	3.0	-1.0	1	21	1523	1543	UUUUUGAAGAGUUCGAGCAAC	GUUACUCAAACUCUUCAAAAC	Cleavage
sly-miR5303	Solyc05g005100.3.1	3.0	-1.0	1	21	2301	2321	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGACUCUCCAGAGA	Cleavage
sly-miR5303	Solyc11g065110.2.1	3.0	-1.0	1	21	698	718	UUUUUGAAGAGUUCGAGCAAC	CUUGUUUGAAUUAUUCAAAAA	Cleavage
sly-miR5303	Solyc09g009510.3.1	3.0	-1.0	1	21	1266	1286	UUUUUGAAGAGUUCGAGCAAC	GUCGUUGGGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc04g072530.2.1	3.0	-1.0	1	21	1082	1102	UUUUUGAAGAGUUCGAGCAAC	GUUGUAUAAACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc05g008980.2.1	3.0	-1.0	1	21	1938	1958	UUUUUGAAGAGUUCGAGCAAC	GUAGCUCCGACUCUUCGAAAA	Cleavage
sly-miR5303	Solyc03g005190.3.1	3.0	-1.0	1	21	24	45	UUUUUGAAGAGUUCGA-GCAAC	UUUGCAUUGAAUUCUUCAAAAA	Cleavage
sly-miR5303	Solyc06g005620.3.1	3.0	-1.0	1	21	1283	1303	UUUUUGAAGAGUUCGAGCAAC	CUUGUUCAGACUCUUCAAAAU	Cleavage

sly-miR5303	Solyc02g094030.3.1	3.0	-1.0	1	21	685	705	UUUUUGAAGAGUUCGAGCAAC	UUUACUUGAGCUUUUCAAAGA	Cleavage
sly-miR5303	Solyc08g023493.1.1	3.0	-1.0	1	21	1083	1103	UUUUUGAAGAGUUCGAGCAAC	AUGGCUCGAGCUCUCCAAAAA	Cleavage
sly-miR5303	Solyc01g010410.3.1	3.0	-1.0	1	21	726	746	UUUUUGAAGAGUUCGAGCAAC	AUUGGUCGGACUCUCCAAAAA	Cleavage
sly-miR5303	Solyc09g090550.3.1	3.0	-1.0	1	21	2012	2032	UUUUUGAAGAGUUCGAGCAAC	AUUGUAUGAACUCUUCAAGAG	Cleavage
sly-miR5303	Solyc01g090900.3.1	3.0	-1.0	1	21	1112	1132	UUUUUGAAGAGUUCGAGCAAC	ACUGCUCGGGCUCAUCAGAAA	Cleavage
sly-miR5303	Solyc06g065800.3.1	3.0	-1.0	1	21	2033	2053	UUUUUGAAGAGUUCGAGCAAC	CGUGCUCGGAUUCUUCACAAG	Cleavage
sly-miR5303	Solyc06g066120.3.1	3.0	-1.0	1	21	2805	2825	UUUUUGAAGAGUUCGAGCAAC	CGUGCUCGGAUUCUUCACAAG	Cleavage
sly-miR5303	Solyc11g066970.2.1	3.0	-1.0	1	21	1476	1496	UUUUUGAAGAGUUCGAGCAAC	AUUUUUCAAACUUUUCAAAAA	Cleavage
sly-miR5303	Solyc12g008800.2.1	3.0	-1.0	1	21	1175	1195	UUUUUGAAGAGUUCGAGCAAC	AGAGUUCCGACUCUUCAAAAA	Cleavage
sly-miR5303	Solyc02g092215.1.1	3.0	-1.0	1	21	417	437	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUAGAUUCUUCAAGAA	Cleavage
sly-miR5303	Solyc07g006740.3.1	3.0	-1.0	1	21	1932	1952	UUUUUGAAGAGUUCGAGCAAC	GGUGCUUAAACUCUCCAAAAA	Cleavage
sly-miR5303	Solyc07g006790.3.1	3.0	-1.0	1	21	1276	1296	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUUGGCUCUUCGAAAA	Cleavage
sly-miR5303	Solyc07g049680.3.1	3.0	-1.0	1	21	445	465	UUUUUGAAGAGUUCGAGCAAC	GAUUCUCGAACUCUUCCAGAA	Cleavage
sly-miR5303	Solyc03g120980.3.1	3.0	-1.0	1	21	1503	1523	UUUUUGAAGAGUUCGAGCAAC	UGUACUCGAAUUCUUCGAAAC	Cleavage
sly-miR5303	Solyc05g010450.1.1	3.0	-1.0	1	21	554	574	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCCGACUCUCCAAAAA	Cleavage
sly-miR5303	Solyc11g012690.2.1	3.0	-1.0	1	21	633	653	UUUUUGAAGAGUUCGAGCAAC	UGUGCUCAAGUUCUUCAGAAG	Cleavage
sly-miR5303	Solyc03g034000.3.1	3.0	-1.0	1	21	637	657	UUUUUGAAGAGUUCGAGCAAC	UAUGUUCAAUCUCUUCAAAAA	Cleavage
sly-miR5303	Solyc09g014400.3.1	3.0	-1.0	1	21	609	629	UUUUUGAAGAGUUCGAGCAAC	CCUGAUCGAAUUCUUCAAACA	Cleavage
sly-miR5303c	Solyc06g052080.3.1	0.0	-1.0	1	24	876	899	UUUUGGAGAAUCCGACACGCACCC	UGGUGCGUGUCGGAUUCUCCAAAA	Cleavage
sly-miR5303c	Solyc11g069350.2.1	0.5	-1.0	1	24	1907	1930	UUUUGGAGAAUCCGACACGCACCC	ACACCCGUGUUGGAUUCUCCAAAA	Cleavage
sly-miR5303c	Solyc02g087770.3.1	1.0	-1.0	1	24	2068	2091	UUUUGGAGAAUCCGACACGCACCC	UCACCUGUGUCGGAUUCUUCAAAA	Cleavage
sly-miR5303c	Solyc12g099530.2.1	1.5	-1.0	1	24	2132	2155	UUUUGGAGAAUCCGACACGCACCC	GCAGCCGUGUCAGAUUCUCCAAAA	Cleavage
sly-miR5303c	Solyc01g099210.3.1	1.5	-1.0	1	24	3752	3775	UUUUGGAGAAUCCGACACGCACCC	ACACCCGUGUUGGAUUCUCUGAAA	Cleavage
sly-miR5303c	Solyc04g076610.2.1	1.5	-1.0	1	24	498	521	UUUUGGAGAAUCCGACACGCACCC	GCACCCGCGUCGGGUUCUCCAAAA	Cleavage
sly-miR5303c	Solyc09g091725.1.1	2.0	-1.0	1	24	374	397	UUUUGGAGAAUCCGACACGCACCC	UCUACUGUGUUGGAUUUUCUAAAA	Cleavage
sly-miR5303c	Solyc12g099360.2.1	2.0	-1.0	1	24	1971	1994	UUUUGGAGAAUCCGACACGCACCC	GCAUUCGUAUCGGAUUUUCUAAAA	Cleavage
sly-miR5303c	Solyc02g068580.1.1	2.0	-1.0	1	24	53	76	UUUUGGAGAAUCCGACACGCACCC	GCCGUCGCGUCGGAUUCUCUAAGA	Cleavage
sly-miR5303c	Solyc11g072290.2.1	2.5	-1.0	1	24	1082	1105	UUUUGGAGAAUCCGACACGCACCC	UAAUGUGUGUCGGAUACUCUAAAA	Cleavage
sly-miR5303c	Solyc12g007150.2.1	2.5	-1.0	1	24	1614	1637	UUUUGGAGAAUCCGACACGCACCC	UCUAGUGUGUUGGAUCCUCCAAAA	Cleavage
sly-miR5303c	Solyc09g065660.3.1	2.5	-1.0	1	24	2219	2242	UUUUGGAGAAUCCGACACGCACCC	UAAUACGUGUUAGAUUCUUCAAAA	Cleavage
sly-miR5303c	Solyc12g008330.2.1	2.5	-1.0	1	24	1560	1583	UUUUGGAGAAUCCGACACGCACCC	UCAUCCAUGUCGGAUCCUCCAAAA	Cleavage
sly-miR5303c	Solyc03g117700.2.1	3.0	-1.0	1	24	4016	4039	UUUUGGAGAAUCCGACACGCACCC	AUGUUCGUGUUGGAUCCUUCAGAA	Cleavage
sly-miR5303c	Solyc04g082510.3.1	3.0	-1.0	1	24	2424	2447	UUUUGGAGAAUCCGACACGCACCC	UUAAGUGUGUUGGAUUCGCCAAAG	Cleavage
sly-miR5303c	Solyc05g007640.3.1	3.0	-1.0	1	24	3202	3225	UUUUGGAGAAUCCGACACGCACCC	UUCAGUGUGUUGGAUUUUCCAACA	Cleavage
sly-miR5303c	Solyc05g046390.3.1	3.0	-1.0	1	24	729	752	UUUUGGAGAAUCCGACACGCACCC	UUCUUAGUGUUGCAUUCUCCAAAA	Cleavage
sly-miR5303c	Solyc07g041920.3.1	3.0	-1.0	1	24	1631	1654	UUUUGGAGAAUCCGACACGCACCC	CCGUCUCUCUCGGAUUCUUCAAAA	Cleavage
sly-miR5303c	Solyc03g006350.3.1	3.0	-1.0	1	24	2250	2273	UUUUGGAGAAUCCGACACGCACCC	GCAUCCUUGUCGGAUCCUUCAAAA	Cleavage
sly-miR5303c	Solyc09g091720.1.1	3.0	-1.0	1	24	1046	1069	UUUUGGAGAAUCCGACACGCACCC	UCUACUGUGCUGGAUUUUCUAAAA	Cleavage
sly-miR5303c	Solyc12g010510.2.1	3.0	-1.0	1	24	2385	2408	UUUUGGAGAAUCCGACACGCACCC	GUUGCCGUGCCAGAUUCUCCGAAA	Cleavage
sly-miR5303c	Solyc05g041740.2.1	3.0	-1.0	1	24	523	546	UUUUGGAGAAUCCGACACGCACCC	UAUUACCUGUAGGAUUUUUCAAAA	Cleavage
sly-miR5303c	Solyc10g080920.2.1	3.0	-1.0	1	24	531	554	UUUUGGAGAAUCCGACACGCACCC	GUUCACAUAUCGGAUUCUUUAAAA	Cleavage
sly-miR5303f	Solyc11g069350.2.1	1.0	-1.0	1	24	1909	1932	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUGUUGGAUUCUCCAAAAAU	Cleavage
sly-miR5303f	Solyc06g052080.3.1	1.0	-1.0	1	24	878	901	AUUUUUGGAGAAUCUGACACGGGU	GUGCGUGUCGGAUUCUCCAAAAGU	Cleavage
sly-miR5303f	Solyc12g008670.2.1	1.5	-1.0	1	24	748	771	AUUUUUGGAGAAUCUGACACGGGU	AUUCGUGUCAAAUUCUCCAGAAAU	Cleavage
sly-miR5303f	Solyc09g065660.3.1	1.5	-1.0	1	24	2221	2244	AUUUUUGGAGAAUCUGACACGGGU	AUACGUGUUAGAUUCUUCAAAAGU	Cleavage
sly-miR5303f	Solyc12g010510.2.1	1.5	-1.0	1	24	2387	2410	AUUUUUGGAGAAUCUGACACGGGU	UGCCGUGCCAGAUUCUCCGAAAAU	Cleavage
sly-miR5303f	Solyc02g086440.3.1	1.5	-1.0	1	24	2229	2252	AUUUUUGGAGAAUCUGACACGGGU	CCGAGUGUCAGAUCCUCCAAAAAU	Translation
sly-miR5303f	Solyc01g099210.3.1	2.0	-1.0	1	24	3754	3777	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUGUUGGAUUCUCUGAAAAU	Cleavage
sly-miR5303f	Solyc04g076610.2.1	2.0	-1.0	1	24	500	523	AUUUUUGGAGAAUCUGACACGGGU	ACCCGCGUCGGGUUCUCCAAAAAU	Cleavage
sly-miR5303f	Solyc12g008330.2.1	2.0	-1.0	1	24	1562	1585	AUUUUUGGAGAAUCUGACACGGGU	AUCCAUGUCGGAUCCUCCAAAAAU	Translation

sly-miR5303f	Solyc12g009660.2.1	2.0	-1.0	1	24	1569	1592	AUUUUUGGAGAAUCUGACACGGGU	AUAUAUGUCAGAUUCUUCAAAACU	Cleavage
sly-miR5303f	Solyc08g067560.2.1	2.0	-1.0	1	24	742	765	AUUUUUGGAGAAUCUGACACGGGU	GCUGAUUUCAUAUUCUCCAAAAAU	Cleavage
sly-miR5303f	Solyc05g055200.3.1	2.5	-1.0	1	24	1785	1808	AUUUUUGGAGAAUCUGACACGGGU	ACUCGUGUCAGAUCCUUCAGAAAU	Translation
sly-miR5303f	Solyc12g099530.2.1	2.5	-1.0	1	24	2134	2157	AUUUUUGGAGAAUCUGACACGGGU	AGCCGUGUCAGAUUCUCCAAAAUA	Cleavage
sly-miR5303f	Solyc11g066940.2.1	2.5	-1.0	1	24	1097	1120	AUUUUUGGAGAAUCUGACACGGGU	AUGUGUGUCAGAUCCUCCAAAAAG	Translation
sly-miR5303f	Solyc06g009000.1.1	2.5	-1.0	1	24	69	92	AUUUUUGGAGAAUCUGACACGGGU	AUCCUUCUUAGGUUCUCCAAGAAU	Cleavage
sly-miR5303f	Solyc03g119920.1.1	2.5	-1.0	1	24	932	955	AUUUUUGGAGAAUCUGACACGGGU	ACUUCUGUUAUAUUCUUCAAAGAU	Cleavage
sly-miR5303f	Solyc07g041920.3.1	2.5	-1.0	1	24	1633	1656	AUUUUUGGAGAAUCUGACACGGGU	GUCUCUCUCGGAUUCUUCAAAAGU	Cleavage
sly-miR5303f	Solyc12g049180.1.1	2.5	-1.0	1	24	699	722	AUUUUUGGAGAAUCUGACACGGGU	AAAGGUGUCAUAUUUUCCAAAGGU	Cleavage
sly-miR5303f	Solyc05g053200.2.1	2.5	-1.0	1	24	12	35	AUUUUUGGAGAAUCUGACACGGGU	AUUUUUCUCAAAUUCUCUAAAAAU	Cleavage
sly-miR5303f	Solyc01g081310.3.1	2.5	-1.0	1	24	6761	6784	AUUUUUGGAGAAUCUGACACGGGU	UACUUUGUCAAAUUCUCCAGAAAG	Cleavage
sly-miR5303f	Solyc01g005830.3.1	2.5	-1.0	1	24	225	248	AUUUUUGGAGAAUCUGACACGGGU	AAAUCUGUCACAUUUUUCAAGAAU	Cleavage
sly-miR5303f	Solyc04g079025.1.1	3.0	-1.0	1	24	1956	1979	AUUUUUGGAGAAUCUGACACGGGU	GCUUGUGUUACAUUUUCUAGAAAU	Cleavage
sly-miR5303f	Solyc04g079030.2.1	3.0	-1.0	1	24	1275	1298	AUUUUUGGAGAAUCUGACACGGGU	GCUUGUGUUACAUUUUCUAGAAAU	Cleavage
sly-miR5303f	Solyc11g072290.2.1	3.0	-1.0	1	24	1084	1107	AUUUUUGGAGAAUCUGACACGGGU	AUGUGUGUCGGAUACUCUAAAAGU	Translation
sly-miR5303f	Solyc11g069580.2.1	3.0	-1.0	1	24	874	897	AUUUUUGGAGAAUCUGACACGGGU	GCUUGUUAUAGAUUCUUCAAAAAU	Cleavage
sly-miR5303f	Solyc02g080220.3.1	3.0	-1.0	1	24	65	88	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCCAAAAC	Cleavage
sly-miR5303f	Solyc02g080200.3.1	3.0	-1.0	1	24	121	144	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCCAAAAC	Cleavage
sly-miR5303f	Solyc02g080210.3.1	3.0	-1.0	1	24	8058	8081	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCCAAAAC	Cleavage
sly-miR5303f	Solyc05g007740.2.1	3.0	-1.0	1	23	1	23	AUUUUUGGAGAAUCUGACACGGG	CUCAUGUUGUAUUUUCCAAAAGU	Cleavage
sly-miR5303f	Solyc09g059410.1.1	3.0	-1.0	1	24	158	181	AUUUUUGGAGAAUCUGACACGGGU	GUAAGUCUCAGAUUCUUCGAAAAA	Cleavage
sly-miR5303f	Solyc11g069770.2.1	3.0	-1.0	1	24	67	90	AUUUUUGGAGAAUCUGACACGGGU	AGGAGUGUCACAUUCUCUAAAAGG	Cleavage
sly-miR5303f	Solyc05g046390.3.1	3.0	-1.0	1	24	731	754	AUUUUUGGAGAAUCUGACACGGGU	CUUAGUGUUGCAUUCUCCAAAAAG	Cleavage
sly-miR5303f	Solyc04g080520.1.1	3.0	-1.0	1	24	948	971	AUUUUUGGAGAAUCUGACACGGGU	AAAACCUUCAGAUUCUUCAAGAAU	Cleavage
sly-miR5303f	Solyc10g081620.2.1	3.0	-1.0	1	24	1961	1984	AUUUUUGGAGAAUCUGACACGGGU	UUUCAUCUCAGAUUCUCCAAGAUU	Cleavage
sly-miR5303f	Solyc12g014393.1.1	3.0	-1.0	1	24	461	484	AUUUUUGGAGAAUCUGACACGGGU	AUCGAUUUCAGAUUCUUCAAACAU	Cleavage
sly-miR5303f	Solyc08g079480.3.1	3.0	-1.0	1	24	326	349	AUUUUUGGAGAAUCUGACACGGGU	AAUCUUGUGAGAUUUUUCGAGAAU	Cleavage
sly-miR5303f	Solyc08g068590.3.1	3.0	-1.0	1	24	389	412	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
sly-miR5303f	Solyc01g010410.3.1	3.0	-1.0	1	24	724	747	AUUUUUGGAGAAUCUGACACGGGU	AUAUUGGUCGGACUCUCCAAAAAU	Cleavage
sly-miR5303f	Solyc05g055730.3.1	3.0	-1.0	1	24	439	462	AUUUUUGGAGAAUCUGACACGGGU	AUCAAUGUCAAAUUCUCUAAACAU	Cleavage
sly-miR5303f	Solyc06g073110.3.1	3.0	-1.0	1	24	79	102	AUUUUUGGAGAAUCUGACACGGGU	GGCUCUGUCAUAUUCUCUGAAAAA	Cleavage
sly-miR5303f	Solyc08g021920.3.1	3.0	-1.0	1	24	8957	8980	AUUUUUGGAGAAUCUGACACGGGU	GUCUUUUUUACAUUCUCCAAGAAU	Cleavage
sly-miR5303f	Solyc07g006720.3.1	3.0	-1.0	1	24	924	947	AUUUUUGGAGAAUCUGACACGGGU	UUUUAUGUCACAUUUUCCAAAAGG	Cleavage
sly-miR5303f	Solyc09g082720.3.1	3.0	-1.0	1	24	64	87	AUUUUUGGAGAAUCUGACACGGGU	AGAAAUGUCGGUUUCUUUAAAAAU	Cleavage
sly-miR5303f	Solyc04g082490.3.1	3.0	-1.0	1	24	3526	3549	AUUUUUGGAGAAUCUGACACGGGU	AAGGGUUUCUGAUUCUCUAAAGAU	Cleavage
sly-miR5303g	Solyc11g007360.1.1	0.5	-1.0	1	24	705	728	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUCAGACUCUUCAAAAAUGU	Cleavage
sly-miR5303g	Solyc03g097670.3.1	0.5	-1.0	1	24	6696	6719	AUAUUUUUGAAGAGUCUGAGCAAC	UUUGCUCGGACUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc12g006910.2.1	0.5	-1.0	1	24	172	195	AUAUUUUUGAAGAGUCUGAGCAAC	GUUAUUCAGACUCUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc11g067080.2.1	0.5	-1.0	1	24	1422	1445	AUAUUUUUGAAGAGUCUGAGCAAC	AUCCCUCAGACUCUUCAGAAAUAU	Cleavage
sly-miR5303g	Solyc09g098340.3.1	0.5	-1.0	1	24	4472	4495	AUAUUUUUGAAGAGUCUGAGCAAC	AAUAUUCGGACUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc11g011900.1.1	0.5	-1.0	1	24	439	462	AUAUUUUUGAAGAGUCUGAGCAAC	GAUCAUCAGACUCUUCAAGAAUAU	Cleavage
sly-miR5303g	Solyc01g006520.3.1	1.0	-1.0	1	24	2647	2670	AUAUUUUUGAAGAGUCUGAGCAAC	AUUGCUCAGACUCUUCGAAAAUGU	Cleavage
sly-miR5303g	Solyc11g071300.2.1	1.0	-1.0	1	24	3343	3366	AUAUUUUUGAAGAGUCUGAGCAAC	GUUACUCAGACUUUUCAAAAGUAU	Cleavage
sly-miR5303g	Solyc04g009710.2.1	1.0	-1.0	1	24	679	702	AUAUUUUUGAAGAGUCUGAGCAAC	UGUGUUCAGACUCUUCAAAAGUGU	Cleavage
sly-miR5303g	Solyc05g008910.3.1	1.0	-1.0	1	24	2443	2466	AUAUUUUUGAAGAGUCUGAGCAAC	UCUGUUCAGACUCUUCAGAAAUGU	Cleavage
sly-miR5303g	Solyc05g051340.2.1	1.0	-1.0	1	24	2361	2384	AUAUUUUUGAAGAGUCUGAGCAAC	UGUGGUUGGACUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc11g066260.2.1	1.5	-1.0	1	24	2196	2219	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUCCGACUCUUCAAAAAUGU	Cleavage
sly-miR5303g	Solyc05g056420.3.1	1.5	-1.0	1	24	5245	5268	AUAUUUUUGAAGAGUCUGAGCAAC	UUUGUUCCGACUCUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc05g008980.2.1	1.5	-1.0	1	24	1938	1961	AUAUUUUUGAAGAGUCUGAGCAAC	GUAGCUCCGACUCUUCGAAAAUAU	Cleavage
sly-miR5303g	Solyc09g091910.2.1	1.5	-1.0	1	24	3545	3568	AUAUUUUUGAAGAGUCUGAGCAAC	GUUACUCAAACUUUUCAAAAAUAU	Cleavage

sly-miR5303g	Solyc03g117700.2.1	1.5	-1.0	1	24	3988	4011	AUAUUUUUGAAGAGUCUGAGCAAC	CUUGGUCGGGUUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc09g009510.3.1	1.5	-1.0	1	24	1266	1289	AUAUUUUUGAAGAGUCUGAGCAAC	GUCGUUGGGACUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc11g066970.2.1	1.5	-1.0	1	24	1476	1499	AUAUUUUUGAAGAGUCUGAGCAAC	AUUUUUCAAACUUUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc04g040220.3.1	2.0	-1.0	1	24	1846	1869	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUUAGAUUCUUCGAGAAUAU	Cleavage
sly-miR5303g	Solyc11g066940.2.1	2.0	-1.0	1	24	1067	1090	AUAUUUUUGAAGAGUCUGAGCAAC	CUUGCUCGGACUCUUUAAAAAUAC	Cleavage
sly-miR5303g	Solyc10g006640.3.1	2.0	-1.0	1	24	1483	1506	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGUUUGAACUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc05g008910.3.1	2.0	-1.0	1	24	2353	2376	AUAUUUUUGAAGAGUCUGAGCAAC	AAGAUUCAAACUCUUCAGAAAUGU	Cleavage
sly-miR5303g	Solyc04g007830.3.1	2.0	-1.0	1	24	549	572	AUAUUUUUGAAGAGUCUGAGCAAC	AUUGUUUGGACUCUUUAAAAAUGU	Cleavage
sly-miR5303g	Solyc10g085210.2.1	2.0	-1.0	1	24	968	991	AUAUUUUUGAAGAGUCUGAGCAAC	CUUGUUCGAAUUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc12g096370.2.1	2.0	-1.0	1	24	2802	2825	AUAUUUUUGAAGAGUCUGAGCAAC	GCUGCUUGGACUCUUCGAAAAUGU	Cleavage
sly-miR5303g	Solyc07g065860.3.1	2.0	-1.0	1	24	1048	1071	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGAUCGGAUUUUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc07g018290.3.1	2.0	-1.0	1	24	1547	1570	AUAUUUUUGAAGAGUCUGAGCAAC	AUUACUCGAAUUCUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc04g025600.2.1	2.0	-1.0	1	24	558	581	AUAUUUUUGAAGAGUCUGAGCAAC	AUAGUUUAGACUCUUUGAAAAUGU	Cleavage
sly-miR5303g	Solyc11g018470.2.1	2.0	-1.0	1	24	894	917	AUAUUUUUGAAGAGUCUGAGCAAC	GGUUCUUAGACUCUUCAAAAAUCU	Cleavage
sly-miR5303g	Solyc07g006860.3.1	2.0	-1.0	1	24	1051	1074	AUAUUUUUGAAGAGUCUGAGCAAC	GGUUUUCAGACUCUUUUAAAAUAU	Cleavage
sly-miR5303g	Solyc05g014240.3.1	2.0	-1.0	1	24	743	766	AUAUUUUUGAAGAGUCUGAGCAAC	CCAUUUCAGAAUCUUCAAGGAUAU	Cleavage
sly-miR5303g	Solyc06g052080.3.1	2.5	-1.0	1	24	848	871	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUCGGACCCUUCAAAAAUGU	Cleavage
sly-miR5303g	Solyc09g005500.3.1	2.5	-1.0	1	24	542	565	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGUUCAGACUCUUUAAAUAUGU	Cleavage
sly-miR5303g	Solyc03g034060.3.1	2.5	-1.0	1	24	1985	2008	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGUUCAGACUCUAUAAAAAUGU	Translation
sly-miR5303g	Solyc10g085210.2.1	2.5	-1.0	1	24	1029	1052	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGUUUGAACUCUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc01g103360.3.1	2.5	-1.0	1	24	866	889	AUAUUUUUGAAGAGUCUGAGCAAC	GUUACUCAGGCUCUUGAAAAAUGU	Cleavage
sly-miR5303g	Solyc08g007520.3.1	2.5	-1.0	1	24	1937	1960	AUAUUUUUGAAGAGUCUGAGCAAC	GUCGCUUGGACUCUGCAAAAAUAU	Translation
sly-miR5303g	Solyc05g056400.3.1	2.5	-1.0	1	24	1743	1766	AUAUUUUUGAAGAGUCUGAGCAAC	AUUGUUCAAACUCUUUGAAAAUGU	Cleavage
sly-miR5303g	Solyc04g005230.3.1	2.5	-1.0	1	24	1523	1546	AUAUUUUUGAAGAGUCUGAGCAAC	GUUACUCAAACUCUUCAAAACUAU	Cleavage
sly-miR5303g	Solyc05g041520.1.1	2.5	-1.0	1	24	43	66	AUAUUUUUGAAGAGUCUGAGCAAC	UGUGCUCAUAUUCUUCAAGGAUAU	Cleavage
sly-miR5303g	Solyc11g011310.2.1	2.5	-1.0	1	24	2357	2380	AUAUUUUUGAAGAGUCUGAGCAAC	GUCGUACAGAUUUUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc07g006860.3.1	2.5	-1.0	1	24	940	963	AUAUUUUUGAAGAGUCUGAGCAAC	GGUUUUCAGACUCUUUUAAAAUGU	Cleavage
sly-miR5303g	Solyc07g006860.3.1	2.5	-1.0	1	24	1162	1185	AUAUUUUUGAAGAGUCUGAGCAAC	GGUUUUCAGACUCUUUUAAAAUGU	Cleavage
sly-miR5303g	Solyc07g041920.3.1	2.5	-1.0	1	24	1635	1658	AUAUUUUUGAAGAGUCUGAGCAAC	CUCUCUCGGAUUCUUCAAAAGUAC	Cleavage
sly-miR5303g	Solyc08g074270.3.1	2.5	-1.0	1	24	440	463	AUAUUUUUGAAGAGUCUGAGCAAC	UGUGAACAGACUUUUCAGAGAUAU	Cleavage
sly-miR5303g	Solyc04g049940.2.1	2.5	-1.0	1	24	650	673	AUAUUUUUGAAGAGUCUGAGCAAC	AGAAUUCAGAUUCUUCGAUAAUAU	Cleavage
sly-miR5303g	Solyc09g091980.3.1	2.5	-1.0	1	24	744	767	AUAUUUUUGAAGAGUCUGAGCAAC	AUAUUCUGGACUCUUCAAAAAUGU	Cleavage
sly-miR5303g	Solyc09g065660.3.1	2.5	-1.0	1	24	2223	2246	AUAUUUUUGAAGAGUCUGAGCAAC	ACGUGUUAGAUUCUUCAAAAGUAA	Cleavage
sly-miR5303g	Solyc06g065630.3.1	2.5	-1.0	1	24	1529	1552	AUAUUUUUGAAGAGUCUGAGCAAC	AAUUUUCUGAUUUUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc10g006360.2.1	3.0	-1.0	1	24	1237	1260	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUCGGACUCUCCAAAAAUAC	Translation
sly-miR5303g	Solyc04g080330.3.1	3.0	-1.0	1	24	4474	4497	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUCGGACUCUUCAAACAUAG	Cleavage
sly-miR5303g	Solyc11g012890.2.1	3.0	-1.0	1	24	2700	2723	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGCUCGGACUCUUCAGAAACGU	Cleavage
sly-miR5303g	Solyc10g008470.3.1	3.0	-1.0	1	24	2073	2096	AUAUUUUUGAAGAGUCUGAGCAAC	UUUGCUCGGAUUCUUCAAUAAUGU	Cleavage
sly-miR5303g	Solyc05g055480.3.1	3.0	-1.0	1	24	1627	1650	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGUUCGAAUUUUUCGAAAAUAU	Cleavage
sly-miR5303g	Solyc09g098100.3.1	3.0	-1.0	1	24	4535	4558	AUAUUUUUGAAGAGUCUGAGCAAC	AUUGUUCCGACUCUUAAAAAAUGU	Cleavage
sly-miR5303g	Solyc07g006740.3.1	3.0	-1.0	1	24	1932	1955	AUAUUUUUGAAGAGUCUGAGCAAC	GGUGCUUAAACUCUCCAAAAAUAU	Translation
sly-miR5303g	Solyc01g010410.3.1	3.0	-1.0	1	24	726	749	AUAUUUUUGAAGAGUCUGAGCAAC	AUUGGUCGGACUCUCCAAAAAUAA	Translation
sly-miR5303g	Solyc08g023600.1.1	3.0	-1.0	1	24	87	110	AUAUUUUUGAAGAGUCUGAGCAAC	GGUGCUCUUACUCUUCAAAAAUAC	Cleavage
sly-miR5303g	Solyc11g071195.1.1	3.0	-1.0	1	24	427	450	AUAUUUUUGAAGAGUCUGAGCAAC	GUUAUGCAGACCUUUCAAAAAUAU	Cleavage
sly-miR5303g	Solyc11g072850.2.1	3.0	-1.0	1	24	411	434	AUAUUUUUGAAGAGUCUGAGCAAC	GUUGAUCAAAAUUUUUAAAAAUAU	Cleavage
sly-miR5303g	Solyc03g005740.2.1	3.0	-1.0	1	24	1104	1127	AUAUUUUUGAAGAGUCUGAGCAAC	AUUUCUCGAACUCUCCAAAAAUAU	Translation
sly-miR5303g	Solyc11g072380.2.1	3.0	-1.0	1	24	2182	2205	AUAUUUUUGAAGAGUCUGAGCAAC	CUGGCUCGAAUUUUUCAAAAAUGU	Cleavage
sly-miR5303g	Solyc10g081170.2.1	3.0	-1.0	1	24	628	651	AUAUUUUUGAAGAGUCUGAGCAAC	GAAGUUUAGACUUGUCAAAAAUGU	Translation
sly-miR5303g	Solyc03g070390.3.1	3.0	-1.0	1	24	160	183	AUAUUUUUGAAGAGUCUGAGCAAC	GAAACUUAGAUUUUUUAGAAAUGU	Cleavage
sly-miR5303g	Solyc09g005180.3.1	3.0	-1.0	1	24	1498	1521	AUAUUUUUGAAGAGUCUGAGCAAC	GUCCCCUAGACUCUUUGAAGAUAU	Cleavage

sly-miR5303g	Solyc02g084590.3.1	3.0	-1.0	1	24	2085	2108	AUAUUUUUGAAGAGUCUGAGCAAC	CCGGUUCAGAGUUUUUGAAGAUAU	Cleavage
sly-miR5303g	Solyc02g067160.3.1	3.0	-1.0	1	24	3545	3568	AUAUUUUUGAAGAGUCUGAGCAAC	UGUUUUUAGAUUUUUUAAAAAUAG	Cleavage
sly-miR5303g	Solyc08g082280.3.1	3.0	-1.0	1	24	2524	2546	AUAUUUUUGAAGAGUCUGAGCAAC	GUUG-UCACGUUCUUCAAGGAUAU	Cleavage
sly-miR5303h-1	Solyc11g007360.1.1	1.0	-1.0	1	24	706	729	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303h-1	Solyc01g006520.3.1	1.5	-1.0	1	24	2648	2671	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCGAAAAUGUC	Cleavage
sly-miR5303h-1	Solyc12g096370.2.1	1.5	-1.0	1	24	2803	2826	AACAUUUUUGAAGAGUCUGAGCAA	CUGCUUGGACUCUUCGAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc04g009710.2.1	1.5	-1.0	1	24	680	703	AACAUUUUUGAAGAGUCUGAGCAA	GUGUUCAGACUCUUCAAAAGUGUA	Cleavage
sly-miR5303h-1	Solyc05g008910.3.1	1.5	-1.0	1	24	2444	2467	AACAUUUUUGAAGAGUCUGAGCAA	CUGUUCAGACUCUUCAGAAAUGUC	Cleavage
sly-miR5303h-1	Solyc04g025600.2.1	1.5	-1.0	1	24	559	582	AACAUUUUUGAAGAGUCUGAGCAA	UAGUUUAGACUCUUUGAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc11g066260.2.1	2.0	-1.0	1	24	2197	2220	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCCGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303h-1	Solyc03g034060.3.1	2.0	-1.0	1	24	1986	2009	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUAUAAAAAUGUU	Translation
sly-miR5303h-1	Solyc05g056400.3.1	2.0	-1.0	1	24	1744	1767	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAAACUCUUUGAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc12g006910.2.1	2.0	-1.0	1	24	173	196	AACAUUUUUGAAGAGUCUGAGCAA	UUAUUCAGACUCUUUAAAAAUAUU	Cleavage
sly-miR5303h-1	Solyc11g067080.2.1	2.0	-1.0	1	24	1423	1446	AACAUUUUUGAAGAGUCUGAGCAA	UCCCUCAGACUCUUCAGAAAUAUU	Cleavage
sly-miR5303h-1	Solyc07g006860.3.1	2.0	-1.0	1	24	941	964	AACAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc07g006860.3.1	2.0	-1.0	1	24	1163	1186	AACAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc09g091980.3.1	2.0	-1.0	1	24	745	768	AACAUUUUUGAAGAGUCUGAGCAA	UAUUCUGGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303h-1	Solyc10g008470.3.1	2.5	-1.0	1	24	2074	2097	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGAUUCUUCAAUAAUGUU	Cleavage
sly-miR5303h-1	Solyc05g008910.3.1	2.5	-1.0	1	24	2354	2377	AACAUUUUUGAAGAGUCUGAGCAA	AGAUUCAAACUCUUCAGAAAUGUC	Cleavage
sly-miR5303h-1	Solyc04g007830.3.1	2.5	-1.0	1	24	550	573	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUUGGACUCUUUAAAAAUGUC	Cleavage
sly-miR5303h-1	Solyc06g052080.3.1	2.5	-1.0	1	24	849	872	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACCCUUCAAAAAUGUC	Cleavage
sly-miR5303h-1	Solyc11g071300.2.1	2.5	-1.0	1	24	3344	3367	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCAGACUUUUCAAAAGUAUU	Cleavage
sly-miR5303h-1	Solyc06g070920.3.1	2.5	-1.0	1	24	424	447	AACAUUUUUGAAGAGUCUGAGCAA	CUGGCUGGAUUUUUCAAAGAUGUU	Cleavage
sly-miR5303h-1	Solyc03g097670.3.1	3.0	-1.0	1	24	6697	6720	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUUCAAAAAUAUA	Cleavage
sly-miR5303h-1	Solyc05g005100.3.1	3.0	-1.0	1	24	2302	2325	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUCCAGAGAUGUU	Translation
sly-miR5303h-1	Solyc09g005500.3.1	3.0	-1.0	1	24	543	566	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUUUAAAUAUGUG	Cleavage
sly-miR5303h-1	Solyc01g103360.3.1	3.0	-1.0	1	24	867	890	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCAGGCUCUUGAAAAAUGUC	Translation
sly-miR5303h-1	Solyc03g117700.2.1	3.0	-1.0	1	24	3989	4012	AACAUUUUUGAAGAGUCUGAGCAA	UUGGUCGGGUUCUUCAAAAAUAUU	Cleavage
sly-miR5303h-1	Solyc05g054720.3.1	3.0	-1.0	1	24	1112	1135	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCGAACUCUCCAAAAAUGUU	Translation
sly-miR5303h-1	Solyc05g008980.2.1	3.0	-1.0	1	24	1939	1962	AACAUUUUUGAAGAGUCUGAGCAA	UAGCUCCGACUCUUCGAAAAUAUU	Cleavage
sly-miR5303h-1	Solyc10g086540.2.1	3.0	-1.0	1	24	963	986	AACAUUUUUGAAGAGUCUGAGCAA	UGGUUCAGAUUUUUUGGAGAUGUU	Cleavage
sly-miR5303h-1	Solyc09g091910.2.1	3.0	-1.0	1	24	3546	3569	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCAAACUUUUCAAAAAUAUU	Cleavage
sly-miR5303h-1	Solyc11g018470.2.1	3.0	-1.0	1	24	895	918	AACAUUUUUGAAGAGUCUGAGCAA	GUUCUUAGACUCUUCAAAAAUCUC	Cleavage
sly-miR5303h-1	Solyc09g009510.3.1	3.0	-1.0	1	24	1267	1290	AACAUUUUUGAAGAGUCUGAGCAA	UCGUUGGGACUCUUCAAAAAUAUU	Cleavage
sly-miR5303h-1	Solyc07g062950.3.1	3.0	-1.0	1	24	1941	1964	AACAUUUUUGAAGAGUCUGAGCAA	UUGUCUGGAUAUUUCAAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc09g098340.3.1	3.0	-1.0	1	24	4473	4496	AACAUUUUUGAAGAGUCUGAGCAA	AUAUUCGGACUCUUCAAAAAUAUG	Cleavage
sly-miR5303h-1	Solyc00g021530.2.1	3.0	-1.0	1	24	324	347	AACAUUUUUGAAGAGUCUGAGCAA	UUUCGCAGAUUUUUCAAGAACGUU	Cleavage
sly-miR5303h-1	Solyc11g011900.1.1	3.0	-1.0	1	24	440	463	AACAUUUUUGAAGAGUCUGAGCAA	AUCAUCAGACUCUUCAAGAAUAUG	Cleavage
sly-miR5303h-1	Solyc03g043920.3.1	3.0	-1.0	1	24	764	787	AACAUUUUUGAAGAGUCUGAGCAA	AUGAUCUAACACUUCAAAAAUGUU	Cleavage
sly-miR5303h-1	Solyc11g071720.2.1	3.0	-1.0	1	24	1212	1235	AACAUUUUUGAAGAGUCUGAGCAA	UAAUUCAGAAUCUUCAAAGAAGUU	Cleavage
sly-miR5303h-1	Solyc11g011310.2.1	3.0	-1.0	1	24	2358	2381	AACAUUUUUGAAGAGUCUGAGCAA	UCGUACAGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303h-1	Solyc01g097670.3.1	3.0	-1.0	1	24	2314	2337	AACAUUUUUGAAGAGUCUGAGCAA	CCCAUCAGAAUUUUCAAAAAUCUU	Cleavage
sly-miR5303h-1	Solyc02g068020.1.1	3.0	-1.0	1	24	34	57	AACAUUUUUGAAGAGUCUGAGCAA	UCGAUAAAACUUUUUAAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc11g007360.1.1	1.0	-1.0	1	24	706	729	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303h-2	Solyc01g006520.3.1	1.5	-1.0	1	24	2648	2671	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCGAAAAUGUC	Cleavage
sly-miR5303h-2	Solyc12g096370.2.1	1.5	-1.0	1	24	2803	2826	AACAUUUUUGAAGAGUCUGAGCAA	CUGCUUGGACUCUUCGAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc04g009710.2.1	1.5	-1.0	1	24	680	703	AACAUUUUUGAAGAGUCUGAGCAA	GUGUUCAGACUCUUCAAAAGUGUA	Cleavage
sly-miR5303h-2	Solyc05g008910.3.1	1.5	-1.0	1	24	2444	2467	AACAUUUUUGAAGAGUCUGAGCAA	CUGUUCAGACUCUUCAGAAAUGUC	Cleavage
sly-miR5303h-2	Solyc04g025600.2.1	1.5	-1.0	1	24	559	582	AACAUUUUUGAAGAGUCUGAGCAA	UAGUUUAGACUCUUUGAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc11g066260.2.1	2.0	-1.0	1	24	2197	2220	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCCGACUCUUCAAAAAUGUC	Cleavage

sly-miR5303h-2	Solyc03g034060.3.1	2.0	-1.0	1	24	1986	2009	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUAUAAAAAUGUU	Translation
sly-miR5303h-2	Solyc05g056400.3.1	2.0	-1.0	1	24	1744	1767	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAAACUCUUUGAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc12g006910.2.1	2.0	-1.0	1	24	173	196	AACAUUUUUGAAGAGUCUGAGCAA	UUAUUCAGACUCUUUAAAAAUAUU	Cleavage
sly-miR5303h-2	Solyc11g067080.2.1	2.0	-1.0	1	24	1423	1446	AACAUUUUUGAAGAGUCUGAGCAA	UCCCUCAGACUCUUCAGAAAUAUU	Cleavage
sly-miR5303h-2	Solyc07g006860.3.1	2.0	-1.0	1	24	941	964	AACAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc07g006860.3.1	2.0	-1.0	1	24	1163	1186	AACAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc09g091980.3.1	2.0	-1.0	1	24	745	768	AACAUUUUUGAAGAGUCUGAGCAA	UAUUCUGGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303h-2	Solyc10g008470.3.1	2.5	-1.0	1	24	2074	2097	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGAUUCUUCAAUAAUGUU	Cleavage
sly-miR5303h-2	Solyc05g008910.3.1	2.5	-1.0	1	24	2354	2377	AACAUUUUUGAAGAGUCUGAGCAA	AGAUUCAAACUCUUCAGAAAUGUC	Cleavage
sly-miR5303h-2	Solyc04g007830.3.1	2.5	-1.0	1	24	550	573	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUUGGACUCUUUAAAAAUGUC	Cleavage
sly-miR5303h-2	Solyc06g052080.3.1	2.5	-1.0	1	24	849	872	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACCCUUCAAAAAUGUC	Cleavage
sly-miR5303h-2	Solyc11g071300.2.1	2.5	-1.0	1	24	3344	3367	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCAGACUUUUCAAAAGUAUU	Cleavage
sly-miR5303h-2	Solyc06g070920.3.1	2.5	-1.0	1	24	424	447	AACAUUUUUGAAGAGUCUGAGCAA	CUGGCUGGAUUUUUCAAAGAUGUU	Cleavage
sly-miR5303h-2	Solyc03g097670.3.1	3.0	-1.0	1	24	6697	6720	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUUCAAAAAUAUA	Cleavage
sly-miR5303h-2	Solyc05g005100.3.1	3.0	-1.0	1	24	2302	2325	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUCCAGAGAUGUU	Translation
sly-miR5303h-2	Solyc09g005500.3.1	3.0	-1.0	1	24	543	566	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUUUAAAUAUGUG	Cleavage
sly-miR5303h-2	Solyc01g103360.3.1	3.0	-1.0	1	24	867	890	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCAGGCUCUUGAAAAAUGUC	Translation
sly-miR5303h-2	Solyc03g117700.2.1	3.0	-1.0	1	24	3989	4012	AACAUUUUUGAAGAGUCUGAGCAA	UUGGUCGGGUUCUUCAAAAAUAUU	Cleavage
sly-miR5303h-2	Solyc05g054720.3.1	3.0	-1.0	1	24	1112	1135	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCGAACUCUCCAAAAAUGUU	Translation
sly-miR5303h-2	Solyc05g008980.2.1	3.0	-1.0	1	24	1939	1962	AACAUUUUUGAAGAGUCUGAGCAA	UAGCUCCGACUCUUCGAAAAUAUU	Cleavage
sly-miR5303h-2	Solyc10g086540.2.1	3.0	-1.0	1	24	963	986	AACAUUUUUGAAGAGUCUGAGCAA	UGGUUCAGAUUUUUUGGAGAUGUU	Cleavage
sly-miR5303h-2	Solyc09g091910.2.1	3.0	-1.0	1	24	3546	3569	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCAAACUUUUCAAAAAUAUU	Cleavage
sly-miR5303h-2	Solyc11g018470.2.1	3.0	-1.0	1	24	895	918	AACAUUUUUGAAGAGUCUGAGCAA	GUUCUUAGACUCUUCAAAAAUCUC	Cleavage
sly-miR5303h-2	Solyc09g009510.3.1	3.0	-1.0	1	24	1267	1290	AACAUUUUUGAAGAGUCUGAGCAA	UCGUUGGGACUCUUCAAAAAUAUU	Cleavage
sly-miR5303h-2	Solyc07g062950.3.1	3.0	-1.0	1	24	1941	1964	AACAUUUUUGAAGAGUCUGAGCAA	UUGUCUGGAUAUUUCAAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc09g098340.3.1	3.0	-1.0	1	24	4473	4496	AACAUUUUUGAAGAGUCUGAGCAA	AUAUUCGGACUCUUCAAAAAUAUG	Cleavage
sly-miR5303h-2	Solyc00g021530.2.1	3.0	-1.0	1	24	324	347	AACAUUUUUGAAGAGUCUGAGCAA	UUUCGCAGAUUUUUCAAGAACGUU	Cleavage
sly-miR5303h-2	Solyc11g011900.1.1	3.0	-1.0	1	24	440	463	AACAUUUUUGAAGAGUCUGAGCAA	AUCAUCAGACUCUUCAAGAAUAUG	Cleavage
sly-miR5303h-2	Solyc03g043920.3.1	3.0	-1.0	1	24	764	787	AACAUUUUUGAAGAGUCUGAGCAA	AUGAUCUAACACUUCAAAAAUGUU	Cleavage
sly-miR5303h-2	Solyc11g071720.2.1	3.0	-1.0	1	24	1212	1235	AACAUUUUUGAAGAGUCUGAGCAA	UAAUUCAGAAUCUUCAAAGAAGUU	Cleavage
sly-miR5303h-2	Solyc11g011310.2.1	3.0	-1.0	1	24	2358	2381	AACAUUUUUGAAGAGUCUGAGCAA	UCGUACAGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303h-2	Solyc01g097670.3.1	3.0	-1.0	1	24	2314	2337	AACAUUUUUGAAGAGUCUGAGCAA	CCCAUCAGAAUUUUCAAAAAUCUU	Cleavage
sly-miR5303h-2	Solyc02g068020.1.1	3.0	-1.0	1	24	34	57	AACAUUUUUGAAGAGUCUGAGCAA	UCGAUAAAACUUUUUAAAAAUGUU	Cleavage
sly-miR5303j-1	Solyc12g006910.2.1	0.5	-1.0	1	24	173	196	AAUAUUUUUGAAGAGUCUGAGCAA	UUAUUCAGACUCUUUAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc11g067080.2.1	0.5	-1.0	1	24	1423	1446	AAUAUUUUUGAAGAGUCUGAGCAA	UCCCUCAGACUCUUCAGAAAUAUU	Cleavage
sly-miR5303j-1	Solyc11g071300.2.1	1.0	-1.0	1	24	3344	3367	AAUAUUUUUGAAGAGUCUGAGCAA	UUACUCAGACUUUUCAAAAGUAUU	Cleavage
sly-miR5303j-1	Solyc11g007360.1.1	1.5	-1.0	1	24	706	729	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303j-1	Solyc03g097670.3.1	1.5	-1.0	1	24	6697	6720	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUUCAAAAAUAUA	Cleavage
sly-miR5303j-1	Solyc03g117700.2.1	1.5	-1.0	1	24	3989	4012	AAUAUUUUUGAAGAGUCUGAGCAA	UUGGUCGGGUUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc05g008980.2.1	1.5	-1.0	1	24	1939	1962	AAUAUUUUUGAAGAGUCUGAGCAA	UAGCUCCGACUCUUCGAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc09g091910.2.1	1.5	-1.0	1	24	3546	3569	AAUAUUUUUGAAGAGUCUGAGCAA	UUACUCAAACUUUUCAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc09g009510.3.1	1.5	-1.0	1	24	1267	1290	AAUAUUUUUGAAGAGUCUGAGCAA	UCGUUGGGACUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc09g098340.3.1	1.5	-1.0	1	24	4473	4496	AAUAUUUUUGAAGAGUCUGAGCAA	AUAUUCGGACUCUUCAAAAAUAUG	Cleavage
sly-miR5303j-1	Solyc11g011900.1.1	1.5	-1.0	1	24	440	463	AAUAUUUUUGAAGAGUCUGAGCAA	AUCAUCAGACUCUUCAAGAAUAUG	Cleavage
sly-miR5303j-1	Solyc11g011310.2.1	1.5	-1.0	1	24	2358	2381	AAUAUUUUUGAAGAGUCUGAGCAA	UCGUACAGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc01g006520.3.1	2.0	-1.0	1	24	2648	2671	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCGAAAAUGUC	Cleavage
sly-miR5303j-1	Solyc04g040220.3.1	2.0	-1.0	1	24	1847	1870	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUUAGAUUCUUCGAGAAUAUU	Cleavage
sly-miR5303j-1	Solyc12g096370.2.1	2.0	-1.0	1	24	2803	2826	AAUAUUUUUGAAGAGUCUGAGCAA	CUGCUUGGACUCUUCGAAAAUGUU	Cleavage
sly-miR5303j-1	Solyc10g006640.3.1	2.0	-1.0	1	24	1484	1507	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUUGAACUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc04g009710.2.1	2.0	-1.0	1	24	680	703	AAUAUUUUUGAAGAGUCUGAGCAA	GUGUUCAGACUCUUCAAAAGUGUA	Cleavage

sly-miR5303j-1	Solyc05g008910.3.1	2.0	-1.0	1	24	2444	2467	AAUAUUUUUGAAGAGUCUGAGCAA	CUGUUCAGACUCUUCAGAAAUGUC	Cleavage
sly-miR5303j-1	Solyc07g065860.3.1	2.0	-1.0	1	24	1049	1072	AAUAUUUUUGAAGAGUCUGAGCAA	UUGAUCGGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc07g018290.3.1	2.0	-1.0	1	24	1548	1571	AAUAUUUUUGAAGAGUCUGAGCAA	UUACUCGAAUUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc04g025600.2.1	2.0	-1.0	1	24	559	582	AAUAUUUUUGAAGAGUCUGAGCAA	UAGUUUAGACUCUUUGAAAAUGUU	Cleavage
sly-miR5303j-1	Solyc05g051340.2.1	2.0	-1.0	1	24	2362	2385	AAUAUUUUUGAAGAGUCUGAGCAA	GUGGUUGGACUCUUCAAAAAUAUC	Cleavage
sly-miR5303j-1	Solyc07g006860.3.1	2.0	-1.0	1	24	1052	1075	AAUAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc09g005180.3.1	2.0	-1.0	1	24	1499	1522	AAUAUUUUUGAAGAGUCUGAGCAA	UCCCCUAGACUCUUUGAAGAUAUU	Cleavage
sly-miR5303j-1	Solyc06g053320.3.1	2.0	-1.0	1	24	3247	3270	AAUAUUUUUGAAGAGUCUGAGCAA	UUUUGUAGUCUCUUCGAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc11g066260.2.1	2.5	-1.0	1	24	2197	2220	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCCGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303j-1	Solyc03g034060.3.1	2.5	-1.0	1	24	1986	2009	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUAUAAAAAUGUU	Translation
sly-miR5303j-1	Solyc05g056420.3.1	2.5	-1.0	1	24	5246	5269	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCCGACUCUUUAAAAAUAUC	Cleavage
sly-miR5303j-1	Solyc05g056400.3.1	2.5	-1.0	1	24	1744	1767	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCAAACUCUUUGAAAAUGUU	Cleavage
sly-miR5303j-1	Solyc08g007520.3.1	2.5	-1.0	1	24	1938	1961	AAUAUUUUUGAAGAGUCUGAGCAA	UCGCUUGGACUCUGCAAAAAUAUU	Translation
sly-miR5303j-1	Solyc07g006860.3.1	2.5	-1.0	1	24	941	964	AAUAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303j-1	Solyc07g006860.3.1	2.5	-1.0	1	24	1163	1186	AAUAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303j-1	Solyc11g066970.2.1	2.5	-1.0	1	24	1477	1500	AAUAUUUUUGAAGAGUCUGAGCAA	UUUUUCAAACUUUUCAAAAAUAUC	Cleavage
sly-miR5303j-1	Solyc04g049940.2.1	2.5	-1.0	1	24	651	674	AAUAUUUUUGAAGAGUCUGAGCAA	GAAUUCAGAUUCUUCGAUAAUAUU	Cleavage
sly-miR5303j-1	Solyc06g065630.3.1	2.5	-1.0	1	24	1530	1553	AAUAUUUUUGAAGAGUCUGAGCAA	AUUUUCUGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc08g074270.3.1	2.5	-1.0	1	24	441	464	AAUAUUUUUGAAGAGUCUGAGCAA	GUGAACAGACUUUUCAGAGAUAUG	Cleavage
sly-miR5303j-1	Solyc11g071195.1.1	2.5	-1.0	1	24	428	451	AAUAUUUUUGAAGAGUCUGAGCAA	UUAUGCAGACCUUUCAAAAAUAUC	Cleavage
sly-miR5303j-1	Solyc09g091980.3.1	2.5	-1.0	1	24	745	768	AAUAUUUUUGAAGAGUCUGAGCAA	UAUUCUGGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303j-1	Solyc10g008470.3.1	3.0	-1.0	1	24	2074	2097	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGAUUCUUCAAUAAUGUU	Cleavage
sly-miR5303j-1	Solyc05g008910.3.1	3.0	-1.0	1	24	2354	2377	AAUAUUUUUGAAGAGUCUGAGCAA	AGAUUCAAACUCUUCAGAAAUGUC	Cleavage
sly-miR5303j-1	Solyc04g007830.3.1	3.0	-1.0	1	24	550	573	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUUGGACUCUUUAAAAAUGUC	Cleavage
sly-miR5303j-1	Solyc06g052080.3.1	3.0	-1.0	1	24	849	872	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACCCUUCAAAAAUGUC	Cleavage
sly-miR5303j-1	Solyc10g085210.2.1	3.0	-1.0	1	24	969	992	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCGAAUUCUUCAAAAAUAUG	Cleavage
sly-miR5303j-1	Solyc07g006740.3.1	3.0	-1.0	1	24	1933	1956	AAUAUUUUUGAAGAGUCUGAGCAA	GUGCUUAAACUCUCCAAAAAUAUU	Translation
sly-miR5303j-1	Solyc11g018470.2.1	3.0	-1.0	1	24	895	918	AAUAUUUUUGAAGAGUCUGAGCAA	GUUCUUAGACUCUUCAAAAAUCUC	Cleavage
sly-miR5303j-1	Solyc11g072850.2.1	3.0	-1.0	1	24	412	435	AAUAUUUUUGAAGAGUCUGAGCAA	UUGAUCAAAAUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc02g084590.3.1	3.0	-1.0	1	24	2086	2109	AAUAUUUUUGAAGAGUCUGAGCAA	CGGUUCAGAGUUUUUGAAGAUAUU	Cleavage
sly-miR5303j-1	Solyc03g006220.3.1	3.0	-1.0	1	24	1203	1226	AAUAUUUUUGAAGAGUCUGAGCAA	UCAUUCGGGCUCUUUUAAAAUAUU	Cleavage
sly-miR5303j-1	Solyc09g065660.3.1	3.0	-1.0	1	24	2224	2247	AAUAUUUUUGAAGAGUCUGAGCAA	CGUGUUAGAUUCUUCAAAAGUAAU	Cleavage
sly-miR5303j-1	Solyc05g014240.3.1	3.0	-1.0	1	24	744	767	AAUAUUUUUGAAGAGUCUGAGCAA	CAUUUCAGAAUCUUCAAGGAUAUA	Cleavage
sly-miR5303j-2	Solyc12g006910.2.1	0.5	-1.0	1	24	173	196	AAUAUUUUUGAAGAGUCUGAGCAA	UUAUUCAGACUCUUUAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc11g067080.2.1	0.5	-1.0	1	24	1423	1446	AAUAUUUUUGAAGAGUCUGAGCAA	UCCCUCAGACUCUUCAGAAAUAUU	Cleavage
sly-miR5303j-2	Solyc11g071300.2.1	1.0	-1.0	1	24	3344	3367	AAUAUUUUUGAAGAGUCUGAGCAA	UUACUCAGACUUUUCAAAAGUAUU	Cleavage
sly-miR5303j-2	Solyc11g007360.1.1	1.5	-1.0	1	24	706	729	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303j-2	Solyc03g097670.3.1	1.5	-1.0	1	24	6697	6720	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUUCAAAAAUAUA	Cleavage
sly-miR5303j-2	Solyc03g117700.2.1	1.5	-1.0	1	24	3989	4012	AAUAUUUUUGAAGAGUCUGAGCAA	UUGGUCGGGUUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc05g008980.2.1	1.5	-1.0	1	24	1939	1962	AAUAUUUUUGAAGAGUCUGAGCAA	UAGCUCCGACUCUUCGAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc09g091910.2.1	1.5	-1.0	1	24	3546	3569	AAUAUUUUUGAAGAGUCUGAGCAA	UUACUCAAACUUUUCAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc09g009510.3.1	1.5	-1.0	1	24	1267	1290	AAUAUUUUUGAAGAGUCUGAGCAA	UCGUUGGGACUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc09g098340.3.1	1.5	-1.0	1	24	4473	4496	AAUAUUUUUGAAGAGUCUGAGCAA	AUAUUCGGACUCUUCAAAAAUAUG	Cleavage
sly-miR5303j-2	Solyc11g011900.1.1	1.5	-1.0	1	24	440	463	AAUAUUUUUGAAGAGUCUGAGCAA	AUCAUCAGACUCUUCAAGAAUAUG	Cleavage
sly-miR5303j-2	Solyc11g011310.2.1	1.5	-1.0	1	24	2358	2381	AAUAUUUUUGAAGAGUCUGAGCAA	UCGUACAGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc01g006520.3.1	2.0	-1.0	1	24	2648	2671	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCGAAAAUGUC	Cleavage
sly-miR5303j-2	Solyc04g040220.3.1	2.0	-1.0	1	24	1847	1870	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUUAGAUUCUUCGAGAAUAUU	Cleavage
sly-miR5303j-2	Solyc12g096370.2.1	2.0	-1.0	1	24	2803	2826	AAUAUUUUUGAAGAGUCUGAGCAA	CUGCUUGGACUCUUCGAAAAUGUU	Cleavage
sly-miR5303j-2	Solyc10g006640.3.1	2.0	-1.0	1	24	1484	1507	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUUGAACUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc04g009710.2.1	2.0	-1.0	1	24	680	703	AAUAUUUUUGAAGAGUCUGAGCAA	GUGUUCAGACUCUUCAAAAGUGUA	Cleavage

sly-miR5303j-2	Solyc05g008910.3.1	2.0	-1.0	1	24	2444	2467	AAUAUUUUUGAAGAGUCUGAGCAA	CUGUUCAGACUCUUCAGAAAUGUC	Cleavage
sly-miR5303j-2	Solyc07g065860.3.1	2.0	-1.0	1	24	1049	1072	AAUAUUUUUGAAGAGUCUGAGCAA	UUGAUCGGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc07g018290.3.1	2.0	-1.0	1	24	1548	1571	AAUAUUUUUGAAGAGUCUGAGCAA	UUACUCGAAUUCUUCAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc04g025600.2.1	2.0	-1.0	1	24	559	582	AAUAUUUUUGAAGAGUCUGAGCAA	UAGUUUAGACUCUUUGAAAAUGUU	Cleavage
sly-miR5303j-2	Solyc05g051340.2.1	2.0	-1.0	1	24	2362	2385	AAUAUUUUUGAAGAGUCUGAGCAA	GUGGUUGGACUCUUCAAAAAUAUC	Cleavage
sly-miR5303j-2	Solyc07g006860.3.1	2.0	-1.0	1	24	1052	1075	AAUAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc09g005180.3.1	2.0	-1.0	1	24	1499	1522	AAUAUUUUUGAAGAGUCUGAGCAA	UCCCCUAGACUCUUUGAAGAUAUU	Cleavage
sly-miR5303j-2	Solyc06g053320.3.1	2.0	-1.0	1	24	3247	3270	AAUAUUUUUGAAGAGUCUGAGCAA	UUUUGUAGUCUCUUCGAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc11g066260.2.1	2.5	-1.0	1	24	2197	2220	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCCGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303j-2	Solyc03g034060.3.1	2.5	-1.0	1	24	1986	2009	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUAUAAAAAUGUU	Translation
sly-miR5303j-2	Solyc05g056420.3.1	2.5	-1.0	1	24	5246	5269	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCCGACUCUUUAAAAAUAUC	Cleavage
sly-miR5303j-2	Solyc05g056400.3.1	2.5	-1.0	1	24	1744	1767	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCAAACUCUUUGAAAAUGUU	Cleavage
sly-miR5303j-2	Solyc08g007520.3.1	2.5	-1.0	1	24	1938	1961	AAUAUUUUUGAAGAGUCUGAGCAA	UCGCUUGGACUCUGCAAAAAUAUU	Translation
sly-miR5303j-2	Solyc07g006860.3.1	2.5	-1.0	1	24	941	964	AAUAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303j-2	Solyc07g006860.3.1	2.5	-1.0	1	24	1163	1186	AAUAUUUUUGAAGAGUCUGAGCAA	GUUUUCAGACUCUUUUAAAAUGUU	Cleavage
sly-miR5303j-2	Solyc11g066970.2.1	2.5	-1.0	1	24	1477	1500	AAUAUUUUUGAAGAGUCUGAGCAA	UUUUUCAAACUUUUCAAAAAUAUC	Cleavage
sly-miR5303j-2	Solyc04g049940.2.1	2.5	-1.0	1	24	651	674	AAUAUUUUUGAAGAGUCUGAGCAA	GAAUUCAGAUUCUUCGAUAAUAUU	Cleavage
sly-miR5303j-2	Solyc06g065630.3.1	2.5	-1.0	1	24	1530	1553	AAUAUUUUUGAAGAGUCUGAGCAA	AUUUUCUGAUUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc08g074270.3.1	2.5	-1.0	1	24	441	464	AAUAUUUUUGAAGAGUCUGAGCAA	GUGAACAGACUUUUCAGAGAUAUG	Cleavage
sly-miR5303j-2	Solyc11g071195.1.1	2.5	-1.0	1	24	428	451	AAUAUUUUUGAAGAGUCUGAGCAA	UUAUGCAGACCUUUCAAAAAUAUC	Cleavage
sly-miR5303j-2	Solyc09g091980.3.1	2.5	-1.0	1	24	745	768	AAUAUUUUUGAAGAGUCUGAGCAA	UAUUCUGGACUCUUCAAAAAUGUC	Cleavage
sly-miR5303j-2	Solyc10g008470.3.1	3.0	-1.0	1	24	2074	2097	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGAUUCUUCAAUAAUGUU	Cleavage
sly-miR5303j-2	Solyc05g008910.3.1	3.0	-1.0	1	24	2354	2377	AAUAUUUUUGAAGAGUCUGAGCAA	AGAUUCAAACUCUUCAGAAAUGUC	Cleavage
sly-miR5303j-2	Solyc04g007830.3.1	3.0	-1.0	1	24	550	573	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUUGGACUCUUUAAAAAUGUC	Cleavage
sly-miR5303j-2	Solyc06g052080.3.1	3.0	-1.0	1	24	849	872	AAUAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACCCUUCAAAAAUGUC	Cleavage
sly-miR5303j-2	Solyc10g085210.2.1	3.0	-1.0	1	24	969	992	AAUAUUUUUGAAGAGUCUGAGCAA	UUGUUCGAAUUCUUCAAAAAUAUG	Cleavage
sly-miR5303j-2	Solyc07g006740.3.1	3.0	-1.0	1	24	1933	1956	AAUAUUUUUGAAGAGUCUGAGCAA	GUGCUUAAACUCUCCAAAAAUAUU	Translation
sly-miR5303j-2	Solyc11g018470.2.1	3.0	-1.0	1	24	895	918	AAUAUUUUUGAAGAGUCUGAGCAA	GUUCUUAGACUCUUCAAAAAUCUC	Cleavage
sly-miR5303j-2	Solyc11g072850.2.1	3.0	-1.0	1	24	412	435	AAUAUUUUUGAAGAGUCUGAGCAA	UUGAUCAAAAUUUUUAAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc02g084590.3.1	3.0	-1.0	1	24	2086	2109	AAUAUUUUUGAAGAGUCUGAGCAA	CGGUUCAGAGUUUUUGAAGAUAUU	Cleavage
sly-miR5303j-2	Solyc03g006220.3.1	3.0	-1.0	1	24	1203	1226	AAUAUUUUUGAAGAGUCUGAGCAA	UCAUUCGGGCUCUUUUAAAAUAUU	Cleavage
sly-miR5303j-2	Solyc09g065660.3.1	3.0	-1.0	1	24	2224	2247	AAUAUUUUUGAAGAGUCUGAGCAA	CGUGUUAGAUUCUUCAAAAGUAAU	Cleavage
sly-miR5303j-2	Solyc05g014240.3.1	3.0	-1.0	1	24	744	767	AAUAUUUUUGAAGAGUCUGAGCAA	CAUUUCAGAAUCUUCAAGGAUAUA	Cleavage
sly-miR5304-3p	Solyc06g053790.3.1	2.0	-1.0	1	21	964	984	AGAUGAGUAUGGUGCAUUGGA	AAGAGUGUACCAUACUCAUCU	Cleavage
sly-miR5304-3p	Solyc09g090980.3.1	2.5	-1.0	1	21	15	35	AGAUGAGUAUGGUGCAUUGGA	UUCAAAGCAUUAUAUUCAUCU	Cleavage
sly-miR5304-3p	Solyc06g074580.1.1	3.0	-1.0	1	21	94	114	AGAUGAGUAUGGUGCAUUGGA	UCCAAUGCACUGGGCUCAUCU	Cleavage
sly-miR5304-3p	Solyc01g102360.2.1	3.0	-1.0	1	21	1200	1220	AGAUGAGUAUGGUGCAUUGGA	UCCAUUGCACCCUAUUCAUCU	Translation
sly-miR5304-3p	Solyc09g008040.3.1	3.0	-1.0	1	21	292	312	AGAUGAGUAUGGUGCAUUGGA	UUCAGUGCCCCAUACUUAUUU	Cleavage
sly-miR5304-3p	Solyc01g097170.3.1	3.0	-1.0	1	21	129	149	AGAUGAGUAUGGUGCAUUGGA	CCCAAUUCACCAUCUUCAUCU	Cleavage
sly-miR5304-3p	Solyc10g080420.2.1	3.0	-1.0	1	21	1539	1559	AGAUGAGUAUGGUGCAUUGGA	CAAAAUGCACUAUAUUCAUCC	Cleavage
sly-miR5304-3p	Solyc10g083900.2.1	3.0	-1.0	1	21	255	275	AGAUGAGUAUGGUGCAUUGGA	UGCAAUGCCUCAUGCUUAUCU	Cleavage
sly-miR5304-3p	Solyc12g010470.2.1	3.0	-1.0	1	21	1887	1907	AGAUGAGUAUGGUGCAUUGGA	UGUAAUGCACAAUAUUCAUUU	Translation
sly-miR5304-3p	Solyc06g017970.3.1	3.0	-1.0	1	21	2396	2416	AGAUGAGUAUGGUGCAUUGGA	UGGAAUGCACCAUAAUCGUCU	Cleavage
sly-miR5304-3p	Solyc06g010033.1.1	3.0	-1.0	1	21	1194	1214	AGAUGAGUAUGGUGCAUUGGA	CUCAUUGCACCAUAUUCAACU	Cleavage
sly-miR5304-3p	Solyc02g092150.3.1	3.0	-1.0	1	21	5821	5841	AGAUGAGUAUGGUGCAUUGGA	GGCAAUGAAUCAUCCUCAUCU	Cleavage
sly-miR5304-5p	Solyc04g076150.3.1	2.0	-1.0	1	21	1137	1157	UCAAUGCUACAUACUCAUCCC	AAGAUGAGUAUGUAGUAAUGA	Cleavage
sly-miR5304-5p	Solyc01g091910.4.1	3.0	-1.0	1	21	3744	3764	UCAAUGCUACAUACUCAUCCC	AUGAUGAGUAUGUGAUAUUGG	Cleavage
sly-miR5368	Solyc12g062870.2.1	2.5	-1.0	1	19	876	894	GGACAGUCUCAGGUAGACA	UAUGUACCUGAGACUGUCU	Cleavage
sly-miR5368	Solyc09g091260.3.1	3.0	-1.0	1	19	1829	1847	GGACAGUCUCAGGUAGACA	GGUCUAACUGAGACUGUCU	Cleavage
sly-miR5368	Solyc01g088060.3.1	3.0	-1.0	1	19	3479	3497	GGACAGUCUCAGGUAGACA	UGUCUAUAUGGGGCUGUCC	Cleavage

sly-miR5532-1	Solyc09g075760.3.1	2.0	-1.0	1	22	1745	1766	AUGAAAUAUAUGACAAAGGUGG	ACAUGUUUGUUAUAUAUUUCAU	Cleavage
sly-miR5532-1	Solyc02g021260.2.1	2.0	-1.0	1	22	3427	3448	AUGAAAUAUAUGACAAAGGUGG	AUCCAUUUGUUAUAUAUUUUAU	Cleavage
sly-miR5532-1	Solyc04g007760.3.1	2.5	-1.0	1	22	39	60	AUGAAAUAUAUGACAAAGGUGG	AAUCUUUUGUUAUAUAUUUUAA	Cleavage
sly-miR5532-1	Solyc09g059510.3.1	2.5	-1.0	1	22	1370	1391	AUGAAAUAUAUGACAAAGGUGG	GACCUUUUGUCAUAUGUUUGAU	Cleavage
sly-miR5532-1	Solyc06g084150.3.1	2.5	-1.0	1	22	1615	1636	AUGAAAUAUAUGACAAAGGUGG	UAGCCGUUGUCAUAUAUUUCGA	Cleavage
sly-miR5532-1	Solyc07g053870.3.1	2.5	-1.0	1	22	69	90	AUGAAAUAUAUGACAAAGGUGG	CGUCCUUUAUCGUGUAUUUCGU	Cleavage
sly-miR5532-1	Solyc04g082210.3.1	3.0	-1.0	1	22	971	992	AUGAAAUAUAUGACAAAGGUGG	UCAUUUUUGUUAUAUACUUCAU	Cleavage
sly-miR5532-1	Solyc01g016800.1.1	3.0	-1.0	1	22	486	507	AUGAAAUAUAUGACAAAGGUGG	CCUCUUUUGUUGUCUAUUUCAU	Cleavage
sly-miR5532-1	Solyc09g007060.2.1	3.0	-1.0	1	22	970	991	AUGAAAUAUAUGACAAAGGUGG	CUACAUUUAUCAUAUGUUUUAU	Cleavage
sly-miR5532-1	Solyc06g048600.3.1	3.0	-1.0	1	22	1092	1113	AUGAAAUAUAUGACAAAGGUGG	CUAGCUUUUUCAUAUAUUUUGU	Cleavage
sly-miR5532-1	Solyc02g087880.3.1	3.0	-1.0	1	22	596	617	AUGAAAUAUAUGACAAAGGUGG	UUACUCUUGUCAUAAAUUUCAU	Cleavage
sly-miR5532-1	Solyc03g005300.3.1	3.0	-1.0	1	22	18	39	AUGAAAUAUAUGACAAAGGUGG	UCUACUUUGUCGUGUGUUUUAU	Cleavage
sly-miR5532-1	Solyc03g065205.1.1	3.0	-1.0	1	22	404	425	AUGAAAUAUAUGACAAAGGUGG	UGAGCCUUGUCAUAUAUUUCAA	Cleavage
sly-miR5532-1	Solyc05g007010.2.1	3.0	-1.0	1	22	53	74	AUGAAAUAUAUGACAAAGGUGG	CUCCCUUUUUCAUGUAAUUCAU	Cleavage
sly-miR5532-1	Solyc03g006240.3.1	3.0	-1.0	1	22	525	546	AUGAAAUAUAUGACAAAGGUGG	AAAUAUUUUUUAUAUAUUUCAU	Cleavage
sly-miR5532-1	Solyc03g097220.1.1	3.0	-1.0	1	22	126	147	AUGAAAUAUAUGACAAAGGUGG	UAUUUUUUAUCAUAUAUUUUGU	Cleavage
sly-miR5532-1	Solyc08g083200.3.1	3.0	-1.0	1	22	370	391	AUGAAAUAUAUGACAAAGGUGG	AUUCCAUUGUGAUGUAUUUCAU	Cleavage
sly-miR5532-1	Solyc02g032450.3.1	3.0	-1.0	1	22	2529	2550	AUGAAAUAUAUGACAAAGGUGG	CAUUCUUUCUUGUGUAUUUCAU	Cleavage
sly-miR5532-2	Solyc09g075760.3.1	2.5	-1.0	1	22	1745	1766	AUGGAAUAUAUGACAAAGGUGG	ACAUGUUUGUUAUAUAUUUCAU	Cleavage
sly-miR5532-2	Solyc01g103500.3.1	2.5	-1.0	1	22	2329	2350	AUGGAAUAUAUGACAAAGGUGG	UGACUUUUGUUUUAUAUUCCAU	Translation
sly-miR5532-2	Solyc02g021260.2.1	2.5	-1.0	1	22	3427	3448	AUGGAAUAUAUGACAAAGGUGG	AUCCAUUUGUUAUAUAUUUUAU	Cleavage
sly-miR5532-2	Solyc04g039750.2.1	3.0	-1.0	1	22	157	178	AUGGAAUAUAUGACAAAGGUGG	UUAUUUUUAUUAUAUAUUCUAU	Cleavage
sly-miR5532-2	Solyc04g007760.3.1	3.0	-1.0	1	22	39	60	AUGGAAUAUAUGACAAAGGUGG	AAUCUUUUGUUAUAUAUUUUAA	Cleavage
sly-miR5532-2	Solyc09g059510.3.1	3.0	-1.0	1	22	1370	1391	AUGGAAUAUAUGACAAAGGUGG	GACCUUUUGUCAUAUGUUUGAU	Cleavage
sly-miR5532-2	Solyc06g084150.3.1	3.0	-1.0	1	22	1615	1636	AUGGAAUAUAUGACAAAGGUGG	UAGCCGUUGUCAUAUAUUUCGA	Cleavage
sly-miR5532-2	Solyc07g053870.3.1	3.0	-1.0	1	22	69	90	AUGGAAUAUAUGACAAAGGUGG	CGUCCUUUAUCGUGUAUUUCGU	Cleavage
sly-miR6024-3p	Solyc01g088430.3.1	0.0	-1.0	1	22	3498	3519	UUUUAGCAAGAGUUGUUUUACC	GGUAAAACAACUCUUGCUAAAA	Cleavage
sly-miR6024-3p	Solyc05g008070.3.1	1.0	-1.0	1	22	547	568	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCUAGAA	Cleavage
sly-miR6024-3p	Solyc10g051050.2.1	1.0	-1.0	1	22	944	965	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCUAGAA	Cleavage
sly-miR6024-3p	Solyc10g008230.2.1	1.0	-1.0	1	22	565	586	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACGACUCUUGCUAGAA	Cleavage
sly-miR6024-3p	Solyc10g008240.3.1	1.0	-1.0	1	22	511	532	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACGACUCUUGCUAGAA	Cleavage
sly-miR6024-3p	Solyc11g069020.2.1	1.5	-1.0	1	22	514	535	UUUUAGCAAGAGUUGUUUUACC	GGUAAAACCACUCUUGCUAAGA	Cleavage
sly-miR6024-3p	Solyc06g062440.3.1	1.5	-1.0	1	22	610	631	UUUUAGCAAGAGUUGUUUUACC	GGAAAAACCACUCUUGCUAGAA	Cleavage
sly-miR6024-3p	Solyc03g046470.3.1	1.5	-1.0	1	22	2658	2679	UUUUAGCAAGAGUUGUUUUACC	GAAAGAACAACUCUUGCUAAAC	Cleavage
sly-miR6024-3p	Solyc07g063240.3.1	1.5	-1.0	1	22	1685	1706	UUUUAGCAAGAGUUGUUUUACC	CGGAAAAUGACUUUUGCUAAAA	Cleavage
sly-miR6024-3p	Solyc07g065080.4.1	1.5	-1.0	1	22	1043	1064	UUUUAGCAAGAGUUGUUUUACC	UCCAGAAAAACUCUUGCUAAAA	Cleavage
sly-miR6024-3p	Solyc12g005970.1.1	2.0	-1.0	1	22	508	529	UUUUAGCAAGAGUUGUUUUACC	GGUAAAACAACUCUUGCGAAGA	Cleavage
sly-miR6024-3p	Solyc11g006520.2.1	2.0	-1.0	1	22	834	855	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAAAA	Cleavage
sly-miR6024-3p	Solyc02g070410.2.1	2.0	-1.0	1	22	841	862	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAAAA	Cleavage
sly-miR6024-3p	Solyc11g020100.2.1	2.0	-1.0	1	22	1125	1146	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAAAA	Cleavage
sly-miR6024-3p	Solyc09g092290.1.1	2.0	-1.0	1	22	574	595	UUUUAGCAAGAGUUGUUUUACC	GGAAAAACAACUCUUGCCAAGA	Cleavage
sly-miR6024-3p	Solyc09g018220.2.1	2.0	-1.0	1	22	569	590	UUUUAGCAAGAGUUGUUUUACC	GGGAAAACAACUCUUGCCAAGA	Cleavage
sly-miR6024-3p	Solyc04g011960.2.1	2.0	-1.0	1	22	538	559	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACAACACUUGCUAGAA	Translation
sly-miR6024-3p	Solyc01g087200.3.1	2.0	-1.0	1	22	532	553	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACGACUCUCGCUAAAA	Cleavage
sly-miR6024-3p	Solyc01g006000.3.1	2.0	-1.0	1	22	1782	1803	UUUUAGCAAGAGUUGUUUUACC	UACAAAACAGCUUUUGUUAGAA	Cleavage
sly-miR6024-3p	Solyc05g012190.3.1	2.0	-1.0	1	22	4671	4692	UUUUAGCAAGAGUUGUUUUACC	UCCAAAACAACCCUUGCUAAAG	Translation
sly-miR6024-3p	Solyc11g070020.2.1	2.5	-1.0	1	22	2005	2026	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACACUUGCUAAAG	Translation
sly-miR6024-3p	Solyc11g006630.1.1	2.5	-1.0	1	22	547	568	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAGAA	Cleavage
sly-miR6024-3p	Solyc11g006530.2.1	2.5	-1.0	1	22	541	562	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAGAA	Cleavage
sly-miR6024-3p	Solyc04g015220.3.1	2.5	-1.0	1	22	635	656	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUUUUGCCAAAA	Cleavage

sly-miR6024-3p	Solyc11g006640.2.1	2.5	-1.0	1	22	547	568	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAGAA	Cleavage
sly-miR6024-3p	Solyc11g071995.1.1	2.5	-1.0	1	22	637	658	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACACUUGCUAAAG	Translation
sly-miR6024-3p	Solyc11g069990.2.1	2.5	-1.0	1	22	1233	1254	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACACUUGCUAAAG	Translation
sly-miR6024-3p	Solyc05g006620.3.1	2.5	-1.0	1	22	952	973	UUUUAGCAAGAGUUGUUUUACC	GGUAAAACAACUCUUUCUAAGG	Cleavage
sly-miR6024-3p	Solyc05g006620.3.1	2.5	-1.0	1	22	4692	4713	UUUUAGCAAGAGUUGUUUUACC	UAGAAGUUAACUCUUGUUAAAA	Cleavage
sly-miR6024-3p	Solyc03g006750.1.1	2.5	-1.0	1	22	13	34	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUCUUGCUCAGA	Cleavage
sly-miR6024-3p	Solyc02g079950.3.1	2.5	-1.0	1	22	302	323	UUUUAGCAAGAGUUGUUUUACC	GCUAAAGCAGCUUUUGCUGAAG	Cleavage
sly-miR6024-3p	Solyc05g009750.1.1	2.5	-1.0	1	22	181	202	UUUUAGCAAGAGUUGUUUUACC	GGGAAAACAGCUCUGGCUAGAA	Cleavage
sly-miR6024-3p	Solyc05g009740.1.1	2.5	-1.0	1	22	148	169	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACAACUUUGGCUAGAA	Cleavage
sly-miR6024-3p	Solyc03g006760.3.1	2.5	-1.0	1	22	13	34	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUCUUGCUCAGA	Cleavage
sly-miR6024-3p	Solyc05g009760.2.1	2.5	-1.0	1	22	417	438	UUUUAGCAAGAGUUGUUUUACC	GGGAAAACAGCUCUGGCUAGAA	Cleavage
sly-miR6024-3p	Solyc10g008220.3.1	2.5	-1.0	1	22	604	625	UUUUAGCAAGAGUUGUUUUACC	GGAAAGACAACUUUAGCUAAAA	Cleavage
sly-miR6024-3p	Solyc08g007630.1.1	2.5	-1.0	1	22	637	658	UUUUAGCAAGAGUUGUUUUACC	GGCAAGACAACACUUGCUAAAG	Translation
sly-miR6024-3p	Solyc02g085290.3.1	2.5	-1.0	1	22	1046	1067	UUUUAGCAAGAGUUGUUUUACC	AAUAAAACAUUUCUUGUUAAAA	Cleavage
sly-miR6024-3p	Solyc03g025540.3.1	2.5	-1.0	1	22	1462	1483	UUUUAGCAAGAGUUGUUUUACC	CUCAAAGCUACUCUUGUUAAAG	Cleavage
sly-miR6024-3p	Solyc03g121050.3.1	2.5	-1.0	1	22	2317	2338	UUUUAGCAAGAGUUGUUUUACC	UGGGAAGCAACUCUUGCUGGGA	Cleavage
sly-miR6024-3p	Solyc03g077890.1.1	2.5	-1.0	1	22	307	328	UUUUAGCAAGAGUUGUUUUACC	ACCAAGACAACUUUUGUUAAGG	Cleavage
sly-miR6024-3p	Solyc04g025260.3.1	2.5	-1.0	1	22	3122	3143	UUUUAGCAAGAGUUGUUUUACC	CACAAAGCAACCUUUGCUAAAA	Translation
sly-miR6024-3p	Solyc03g007940.3.1	2.5	-1.0	1	22	3899	3920	UUUUAGCAAGAGUUGUUUUACC	ACCAAAACAACUAUUGUUAAAG	Translation
sly-miR6024-3p	Solyc12g017800.2.1	3.0	-1.0	1	22	1119	1140	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACUCUUGCCAGGA	Cleavage
sly-miR6024-3p	Solyc11g071423.1.1	3.0	-1.0	1	22	244	265	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACACUUGCUAAGG	Translation
sly-miR6024-3p	Solyc01g067165.1.1	3.0	-1.0	1	22	544	565	UUUUAGCAAGAGUUGUUUUACC	GGUAAGACAACACUUGCUGAGA	Translation
sly-miR6024-3p	Solyc07g042180.3.1	3.0	-1.0	1	22	60	81	UUUUAGCAAGAGUUGUUUUACC	GGUGUAGCAAUUUUUGCUAAAA	Cleavage
sly-miR6024-3p	Solyc02g084890.2.1	3.0	-1.0	1	22	658	679	UUUUAGCAAGAGUUGUUUUACC	GGUAAAACCACUCUUGCUCAGA	Cleavage
sly-miR6024-3p	Solyc11g068370.2.1	3.0	-1.0	1	22	1421	1442	UUUUAGCAAGAGUUGUUUUACC	AGUAAAAUGAUUUUUGCUAAAU	Cleavage
sly-miR6024-3p	Solyc09g065100.2.1	3.0	-1.0	1	22	1244	1265	UUUUAGCAAGAGUUGUUUUACC	UGUAGAGCUAUUCUUGCUAAGA	Cleavage
sly-miR6024-3p	Solyc12g038900.1.1	3.0	-1.0	1	22	196	217	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACGACUAUUGCUAGAA	Translation
sly-miR6024-3p	Solyc01g104700.3.1	3.0	-1.0	1	22	73	94	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUUUUGUCAAAA	Cleavage
sly-miR6024-3p	Solyc07g009200.1.1	3.0	-1.0	1	22	527	548	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACAACCCUUGCAAAAA	Translation
sly-miR6024-3p	Solyc01g104685.1.1	3.0	-1.0	1	22	307	328	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUUUUGUCAAAA	Cleavage
sly-miR6024-3p	Solyc07g055610.2.1	3.0	-1.0	1	22	568	589	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUCUUGCAAGAG	Cleavage
sly-miR6024-3p	Solyc07g055380.1.1	3.0	-1.0	1	22	145	166	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUCUUGCAAGAG	Cleavage
sly-miR6024-3p	Solyc04g012010.3.1	3.0	-1.0	1	22	558	579	UUUUAGCAAGAGUUGUUUUACC	GGCAAAACAACGCUCGCUAAAA	Translation
sly-miR6024-3p	Solyc04g007320.2.1	3.0	-1.0	1	22	1127	1148	UUUUAGCAAGAGUUGUUUUACC	GGGAAGACAACUCUAGCUAGAG	Cleavage
sly-miR6024-3p	Solyc01g067490.3.1	3.0	-1.0	1	22	573	594	UUUUAGCAAGAGUUGUUUUACC	AAUAGAGCAGCUCUUGUUGAGA	Cleavage
sly-miR6024-3p	Solyc03g025540.3.1	3.0	-1.0	1	22	2224	2245	UUUUAGCAAGAGUUGUUUUACC	CAUAAAACAGUUCUUGUUGGAG	Cleavage
sly-miR6024-3p	Solyc07g032510.3.1	3.0	-1.0	1	22	2053	2074	UUUUAGCAAGAGUUGUUUUACC	AAUGAAACGACACUUGCUGAAA	Translation
sly-miR6024-3p	Solyc04g016420.3.1	3.0	-1.0	1	22	111	132	UUUUAGCAAGAGUUGUUUUACC	AUUGGGGCAACUUUUGCUAGAA	Cleavage
sly-miR6024-3p	Solyc04g009420.3.1	3.0	-1.0	1	22	502	523	UUUUAGCAAGAGUUGUUUUACC	GAUAAGCUAAUUCUUGCUGAAA	Cleavage
sly-miR6024-3p	Solyc02g068795.1.1	3.0	-1.0	1	22	308	329	UUUUAGCAAGAGUUGUUUUACC	GAUACAACGGCUCUUGUUAAAG	Cleavage
sly-miR6024-3p	Solyc12g049460.2.1	3.0	-1.0	1	22	298	319	UUUUAGCAAGAGUUGUUUUACC	GCUAAUAUAAUUCUUGUUAAAG	Cleavage
sly-miR6024-3p	Solyc09g092280.1.1	3.0	-1.0	1	22	574	595	UUUUAGCAAGAGUUGUUUUACC	GGAAAAACUACUCUUGCCAAGA	Cleavage
sly-miR6024-3p	Solyc09g092310.1.1	3.0	-1.0	1	22	571	592	UUUUAGCAAGAGUUGUUUUACC	GGAAAAACUACUCUUGCCAAGA	Cleavage
sly-miR6024-3p	Solyc09g092300.3.1	3.0	-1.0	1	22	898	919	UUUUAGCAAGAGUUGUUUUACC	GGAAAAACUACUCUUGCCAAGA	Cleavage
sly-miR6024-3p	Solyc01g005110.3.1	3.0	-1.0	1	22	68	89	UUUUAGCAAGAGUUGUUUUACC	CUUAAAUUAAUUUUUGUUAAAA	Cleavage
sly-miR6024-3p	Solyc02g079030.3.1	3.0	-1.0	1	22	880	901	UUUUAGCAAGAGUUGUUUUACC	UUUAAUGCAACUCUUGCUAUAA	Cleavage
sly-miR6024-3p	Solyc09g060090.3.1	3.0	-1.0	1	22	1048	1069	UUUUAGCAAGAGUUGUUUUACC	UUUGAAAGGACUUUUGCUGAAA	Cleavage
sly-miR6024-3p	Solyc02g037595.1.1	3.0	-1.0	1	22	178	199	UUUUAGCAAGAGUUGUUUUACC	AGGAGAACAACUCUUGAUGGAA	Cleavage
sly-miR6024-3p	Solyc05g026370.2.1	3.0	-1.0	1	22	359	380	UUUUAGCAAGAGUUGUUUUACC	AGGAGAACAACUCUUGAUGGAA	Cleavage
sly-miR6024-3p	Solyc03g062930.2.1	3.0	-1.0	1	22	1004	1025	UUUUAGCAAGAGUUGUUUUACC	AGGAAAAUGACUCUUACUGAAA	Cleavage

sly-miR6024-3p	Solyc02g093720.3.1	3.0	-1.0	1	22	1674	1695	UUUUAGCAAGAGUUGUUUUACC	UGAAAAAUGACUCUUGCAAGAA	Cleavage
sly-miR6024-3p	Solyc05g041770.2.1	3.0	-1.0	1	22	1662	1683	UUUUAGCAAGAGUUGUUUUACC	AGGAGAACAACUCUUGAUGGAA	Cleavage
sly-miR6024-3p	Solyc04g053120.3.1	3.0	-1.0	1	22	1099	1120	UUUUAGCAAGAGUUGUUUUACC	CAAGAAACAAUUUUUGCUGAAU	Cleavage
sly-miR6024-3p	Solyc00g010750.2.1	3.0	-1.0	1	22	1790	1811	UUUUAGCAAGAGUUGUUUUACC	AGGAGAACAACUCUUGAUGGAA	Cleavage
sly-miR6024-3p	Solyc08g062250.2.1	3.0	-1.0	1	22	1639	1660	UUUUAGCAAGAGUUGUUUUACC	AGGAGAACAACUCUUGAUGGAA	Cleavage
sly-miR6024-3p	Solyc02g062270.3.1	3.0	-1.0	1	22	2500	2521	UUUUAGCAAGAGUUGUUUUACC	GCCAAAAUAGCUUUUGCUGAAC	Cleavage
sly-miR6024-3p	Solyc07g062290.3.1	3.0	-1.0	1	22	82	103	UUUUAGCAAGAGUUGUUUUACC	CUCAAAACAAUUUUUGAUAAAG	Cleavage
sly-miR6024-3p	Solyc01g049960.3.1	3.0	-1.0	1	22	617	638	UUUUAGCAAGAGUUGUUUUACC	GAGAGAGCAUCUCUUGCUGAAA	Cleavage
sly-miR6024-5p	Solyc01g088430.3.1	0.0	-1.0	1	22	3553	3574	AGAAACAACACUUGCUAAAGGA	UCCUUUAGCAAGUGUUGUUUCU	Cleavage
sly-miR6024-5p	Solyc08g081100.3.1	1.5	-1.0	1	22	2298	2319	AGAAACAACACUUGCUAAAGGA	AAGUUUAACAAGUGUUGUUUUU	Cleavage
sly-miR6024-5p	Solyc06g072320.3.1	2.5	-1.0	1	22	2322	2343	AGAAACAACACUUGCUAAAGGA	AGUUUUAGUAGGUCUUGUUUCU	Cleavage
sly-miR6024-5p	Solyc02g069220.2.1	2.5	-1.0	1	22	1096	1117	AGAAACAACACUUGCUAAAGGA	CAGUUUUGGGAGUGUUGUUUCU	Cleavage
sly-miR6024-5p	Solyc11g065820.2.1	3.0	-1.0	1	22	5686	5707	AGAAACAACACUUGCUAAAGGA	ACCUUUAGCAAGUGUUGUCUUA	Cleavage
sly-miR6024-5p	Solyc11g064750.2.1	3.0	-1.0	1	22	4905	4926	AGAAACAACACUUGCUAAAGGA	GGCUUUAGCAAGUGUUGUCUUA	Cleavage
sly-miR6024-5p	Solyc03g005930.3.1	3.0	-1.0	1	22	1164	1185	AGAAACAACACUUGCUAAAGGA	CUCUUUAACCAGUGUUGUUUUU	Cleavage
sly-miR6024-5p	Solyc10g083300.2.1	3.0	-1.0	1	22	48	69	AGAAACAACACUUGCUAAAGGA	AUUUUUAAUAAUUGUUGUUUCU	Translation
sly-miR6024-5p	Solyc02g079850.3.1	3.0	-1.0	1	22	13	34	AGAAACAACACUUGCUAAAGGA	AAUGUUAGCAGAUGUUGUUUCU	Translation
sly-miR6024-5p	Solyc11g005760.2.1	3.0	-1.0	1	22	2355	2376	AGAAACAACACUUGCUAAAGGA	AAUCAUAGAAAGUGUUGUUUCU	Cleavage
sly-miR6024-5p	Solyc12g098450.2.1	3.0	-1.0	1	22	2766	2787	AGAAACAACACUUGCUAAAGGA	GGAUUUAGAAAGUGUAGUUUUU	Cleavage
sly-miR6024-5p	Solyc12g088410.2.1	3.0	-1.0	1	22	518	539	AGAAACAACACUUGCUAAAGGA	AAGUUGGUCAAGUGUUGUUUUU	Cleavage
sly-miR6027-3p	Solyc04g008190.1.1	2.0	-1.0	1	22	106	127	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAAGGGUUUG	Cleavage
sly-miR6027-3p	Solyc11g069020.2.1	2.0	-1.0	1	22	1252	1273	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUUGCUGAAGGAUUUA	Cleavage
sly-miR6027-3p	Solyc04g008140.2.1	2.0	-1.0	1	22	2328	2349	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAAGGGUUUG	Cleavage
sly-miR6027-3p	Solyc09g098130.2.1	2.0	-1.0	1	22	2563	2584	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUUGCUGAAGGAUUCG	Cleavage
sly-miR6027-3p	Solyc04g008120.2.1	2.0	-1.0	1	22	2519	2540	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAAGGGUUUG	Cleavage
sly-miR6027-3p	Solyc04g009155.1.1	2.5	-1.0	1	22	285	306	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCUGAAGGGUUUG	Cleavage
sly-miR6027-3p	Solyc04g009090.1.1	2.5	-1.0	1	22	187	208	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAGGGUUUCA	Cleavage
sly-miR6027-3p	Solyc04g026110.3.1	2.5	-1.0	1	22	1117	1138	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAGGGUUUCA	Cleavage
sly-miR6027-3p	Solyc04g009150.1.1	2.5	-1.0	1	22	1312	1333	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAGGGUUUCA	Cleavage
sly-miR6027-3p	Solyc05g009630.3.1	2.5	-1.0	1	22	1431	1452	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUCGCGGAAGGAUUCA	Translation
sly-miR6027-3p	Solyc04g007070.3.1	2.5	-1.0	1	22	1532	1553	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUAGCCGAGGGGUUGA	Cleavage
sly-miR6027-3p	Solyc05g013280.3.1	2.5	-1.0	1	22	4344	4365	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGGUAGCUGAAGGGUUUG	Cleavage
sly-miR6027-3p	Solyc10g047320.2.1	2.5	-1.0	1	22	1522	1543	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUUGCGGAAGGAUUCA	Translation
sly-miR6027-3p	Solyc02g027080.2.1	3.0	-1.0	1	22	1429	1450	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUGGCUGAGGGGUUCC	Cleavage
sly-miR6027-3p	Solyc04g009250.1.1	3.0	-1.0	1	22	1324	1345	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCUGAGGGUUUCA	Cleavage
sly-miR6027-3p	Solyc05g012910.3.1	3.0	-1.0	1	22	3127	3148	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUAGCGGAAGGCUUCA	Translation
sly-miR6027-3p	Solyc05g012900.3.1	3.0	-1.0	1	22	3218	3239	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUAGCGGAAGGCUUCA	Translation
sly-miR6027-3p	Solyc01g088060.3.1	3.0	-1.0	1	22	1603	1624	UGAAUCCUUCGGCUAUCCAUAA	CUAUGGAUGGCAGAAGGAUUUG	Translation
sly-miR6027-3p	Solyc03g005660.3.1	3.0	-1.0	1	22	1449	1470	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUCGCGGAAGGGUUCA	Translation
sly-miR6027-3p	Solyc02g070393.1.1	3.0	-1.0	1	22	640	661	UGAAUCCUUCGGCUAUCCAUAA	AUGUGGGUGGCCGAGGGGUUUG	Cleavage
sly-miR6027-3p	Solyc04g009120.2.1	3.0	-1.0	1	22	1312	1333	UGAAUCCUUCGGCUAUCCAUAA	CUGUGGAUGGCUGAGGGUUUCA	Cleavage
sly-miR6027-3p	Solyc02g070390.3.1	3.0	-1.0	1	22	3751	3772	UGAAUCCUUCGGCUAUCCAUAA	AUGUGGGUGGCCGAGGGGUUUG	Cleavage
sly-miR6027-3p	Solyc01g108890.3.1	3.0	-1.0	1	22	1410	1432	UGAAUCCUUCGGCUA-UCCAUAA	AAAUGGAAUGGCCGGAGGAUUCA	Cleavage
sly-miR6027-3p	Solyc02g069940.3.1	3.0	-1.0	1	22	1542	1563	UGAAUCCUUCGGCUAUCCAUAA	AAAUGGAAAGCUGGAGGAUUCU	Cleavage
sly-miR6027-3p	Solyc07g053020.2.1	3.0	-1.0	1	22	1909	1930	UGAAUCCUUCGGCUAUCCAUAA	UGGUGGAUAGGAGAAGGAUUCA	Translation
sly-miR6027-3p	Solyc04g015200.3.1	3.0	-1.0	1	22	643	664	UGAAUCCUUCGGCUAUCCAUAA	ACUUCGAUAUUCGAAGGAUUCA	Cleavage
sly-miR6027-5p	Solyc07g047990.1.1	2.0	-1.0	1	22	435	456	AUGGGUAGCACAAGGAUUAAUG	UCAUGAUCCUUGUGUUAUUCAU	Cleavage
sly-miR6027-5p	Solyc01g097250.3.1	2.5	-1.0	1	22	1907	1928	AUGGGUAGCACAAGGAUUAAUG	CUAUGAUCCUUGUGUUGCUUAU	Cleavage
sly-miR6027-5p	Solyc10g049340.1.1	3.0	-1.0	1	22	297	318	AUGGGUAGCACAAGGAUUAAUG	UAUUGAUUCUAGUGCUACUCAU	Cleavage
sly-miR6027-5p	Solyc03g007010.3.1	3.0	-1.0	1	22	490	511	AUGGGUAGCACAAGGAUUAAUG	CAUUAGCCUUUGUGUUGCCCAU	Cleavage

sly-miR6027-5p	Solyc01g079110.3.1	3.0	-1.0	1	22	321	342	AUGGGUAGCACAAGGAUUAAUG	CACUAAUCUGUGUGCUAUUCAU	Cleavage
sly-miR6027-5p	Solyc03g005960.3.1	3.0	-1.0	1	22	3276	3297	AUGGGUAGCACAAGGAUUAAUG	UCUUGAUCCUUGUGUUAUCUAC	Cleavage
sly-miR6027-5p	Solyc02g068680.1.1	3.0	-1.0	1	22	1189	1210	AUGGGUAGCACAAGGAUUAAUG	GAUUUAACUUUGUGCUACUCAU	Cleavage
sly-miR6027-5p	Solyc01g080600.3.1	3.0	-1.0	1	22	321	342	AUGGGUAGCACAAGGAUUAAUG	UACUAAUCUUUGUGCAAUUCAU	Cleavage
sly-miR6027-5p	Solyc08g080360.3.1	3.0	-1.0	1	22	1159	1180	AUGGGUAGCACAAGGAUUAAUG	UUGUAGUUCUAGUGCUAUCCAU	Cleavage
sly-miR6027-5p	Solyc09g064270.3.1	3.0	-1.0	1	22	1785	1806	AUGGGUAGCACAAGGAUUAAUG	UUCUAAUCCUCGUGUUAUUCAU	Cleavage
sly-miR6027-5p	Solyc09g018730.3.1	3.0	-1.0	1	22	234	255	AUGGGUAGCACAAGGAUUAAUG	AAACAAUGCUUGUGCUACCCAA	Cleavage
sly-miR6027-5p	Solyc03g013225.1.1	3.0	-1.0	1	22	261	282	AUGGGUAGCACAAGGAUUAAUG	GGAUGGUAUUUGUGCUACUCAU	Cleavage
sly-miR6027-5p	Solyc02g070100.3.1	3.0	-1.0	1	22	840	861	AUGGGUAGCACAAGGAUUAAUG	UUAUAUUUCUUGUGCUGCUCGU	Cleavage
sly-miR7122-3p	Solyc03g093150.2.1	2.0	-1.0	1	21	1193	1213	ACAGCGUUUUUCUGUAUAACC	ACUUAUACAGGAAGAUGUUGU	Cleavage
sly-miR7122-3p	Solyc09g007050.1.1	2.5	-1.0	1	21	638	658	ACAGCGUUUUUCUGUAUAACC	GAUUAUAUAGAGAAAUGCUGC	Cleavage
sly-miR7122-3p	Solyc11g045180.2.1	2.5	-1.0	1	21	207	227	ACAGCGUUUUUCUGUAUAACC	UCUUGUACAGAGAAACGUUGG	Cleavage
sly-miR7122-3p	Solyc12g100000.2.1	2.5	-1.0	1	21	1332	1352	ACAGCGUUUUUCUGUAUAACC	GAAUGUACAGGAAAAUGCUGU	Cleavage
sly-miR7122-3p	Solyc12g099310.2.1	2.5	-1.0	1	21	1151	1171	ACAGCGUUUUUCUGUAUAACC	ACUUAUGCAGAAAAAUGCAGU	Cleavage
sly-miR7122-3p	Solyc06g053300.3.1	2.5	-1.0	1	21	455	475	ACAGCGUUUUUCUGUAUAACC	AAUUGUACAGAAGGAUGUUGU	Cleavage
sly-miR7122-3p	Solyc01g087140.3.1	2.5	-1.0	1	21	385	405	ACAGCGUUUUUCUGUAUAACC	AUUUGUCCAGAGAAACGUUGU	Cleavage
sly-miR7122-3p	Solyc01g104600.3.1	3.0	-1.0	1	21	317	337	ACAGCGUUUUUCUGUAUAACC	AAUUAUACAGAAAAAGGAUGU	Cleavage
sly-miR7122-3p	Solyc06g076750.3.1	3.0	-1.0	1	21	2136	2156	ACAGCGUUUUUCUGUAUAACC	UAUUAUACAUAGAAAUGUUGU	Cleavage
sly-miR7122-3p	Solyc08g075610.2.1	3.0	-1.0	1	21	4486	4506	ACAGCGUUUUUCUGUAUAACC	AAUUAUACAGAGGAUUGCUGU	Cleavage
sly-miR7122-3p	Solyc05g012060.3.1	3.0	-1.0	1	21	4028	4048	ACAGCGUUUUUCUGUAUAACC	GCGGAGACAGAAAAACGCUGU	Cleavage
sly-miR7122-3p	Solyc10g006000.3.1	3.0	-1.0	1	21	271	291	ACAGCGUUUUUCUGUAUAACC	CUUUAUAGAGAAGAAUGCUGA	Cleavage
sly-miR7122-3p	Solyc08g068960.3.1	3.0	-1.0	1	21	1354	1374	ACAGCGUUUUUCUGUAUAACC	AUAUAAACAGGAAAAUGCUGU	Cleavage
sly-miR7122-3p	Solyc01g108670.3.1	3.0	-1.0	1	21	2521	2541	ACAGCGUUUUUCUGUAUAACC	ACUUAUUCAGAACAAUGCUGU	Cleavage
sly-miR7122-5p	Solyc11g012560.2.1	2.5	-1.0	1	21	1485	1505	UAUACAGAGAAACCGCUGUCG	GAACAGAGGUUUCUCUGUACA	Cleavage
sly-miR7122-5p	Solyc07g025140.3.1	2.5	-1.0	1	21	240	260	UAUACAGAGAAACCGCUGUCG	ACACAGCAGUUUCUCUGCAUA	Cleavage
sly-miR7122-5p	Solyc08g076190.3.1	2.5	-1.0	1	21	2543	2563	UAUACAGAGAAACCGCUGUCG	UUGUAUCGGUUUUUCUGUAUA	Cleavage
sly-miR7122-5p	Solyc12g096280.2.1	2.5	-1.0	1	21	977	997	UAUACAGAGAAACCGCUGUCG	ACACAAUCGUUUCUCUGUAUA	Cleavage
sly-miR7122-5p	Solyc07g008450.3.1	3.0	-1.0	1	21	3908	3928	UAUACAGAGAAACCGCUGUCG	AAGUGGUGGUUUCUUUGUAUG	Cleavage
sly-miR7122-5p	Solyc02g093800.3.1	3.0	-1.0	1	21	790	810	UAUACAGAGAAACCGCUGUCG	GUGCAGCAGUUUUUCUGUGUG	Cleavage
sly-miR7696c-3p	Solyc07g014650.3.1	1.5	-1.0	1	21	274	294	UUUUGAAUUAUUAGAACUUGA	CGAAGUUCUAGUAAUUCAGGA	Cleavage
sly-miR7696c-3p	Solyc08g079770.3.1	2.5	-1.0	1	21	2318	2338	UUUUGAAUUAUUAGAACUUGA	ACAAGUUCUAAUAAAUCAAAU	Cleavage
sly-miR7696c-3p	Solyc10g049450.2.1	2.5	-1.0	1	21	157	177	UUUUGAAUUAUUAGAACUUGA	UUGAGUUGUGAUAAUUCAAAG	Cleavage
sly-miR7696c-3p	Solyc01g011040.3.1	2.5	-1.0	1	21	740	760	UUUUGAAUUAUUAGAACUUGA	CUAAGUUUUAAUAAUUUCAAA	Cleavage
sly-miR7696c-3p	Solyc10g051170.2.1	2.5	-1.0	1	21	677	697	UUUUGAAUUAUUAGAACUUGA	CAAACUUCUAAUGGUUCAAAG	Cleavage
sly-miR7696c-3p	Solyc01g104110.3.1	2.5	-1.0	1	21	345	365	UUUUGAAUUAUUAGAACUUGA	AGAAGUUGUAAAAAUUCAAAA	Translation
sly-miR7696c-3p	Solyc08g076530.3.1	2.5	-1.0	1	21	539	559	UUUUGAAUUAUUAGAACUUGA	AAAAGUGCUGGUAAUUCAGAA	Cleavage
sly-miR7696c-3p	Solyc01g081410.3.1	2.5	-1.0	1	21	1036	1056	UUUUGAAUUAUUAGAACUUGA	GAAAAUUCUGAUGGUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc03g044200.3.1	3.0	-1.0	1	21	1259	1279	UUUUGAAUUAUUAGAACUUGA	UCAAGUUCUAAUAAAUUAAAC	Cleavage
sly-miR7696c-3p	Solyc12g042760.1.1	3.0	-1.0	1	21	1099	1119	UUUUGAAUUAUUAGAACUUGA	UCGAGUUUUGGUAAUUUAAGA	Cleavage
sly-miR7696c-3p	Solyc06g071000.3.1	3.0	-1.0	1	21	2065	2085	UUUUGAAUUAUUAGAACUUGA	UCAAGUUCUUAAAAUUCAAAA	Translation
sly-miR7696c-3p	Solyc01g109640.3.1	3.0	-1.0	1	21	4816	4836	UUUUGAAUUAUUAGAACUUGA	UCAAGUUUUCAUAAUUUAGAA	Cleavage
sly-miR7696c-3p	Solyc09g018905.1.1	3.0	-1.0	1	21	623	643	UUUUGAAUUAUUAGAACUUGA	UUAAGUUUUAAUAAUUUUAGA	Cleavage
sly-miR7696c-3p	Solyc03g044600.2.1	3.0	-1.0	1	21	744	764	UUUUGAAUUAUUAGAACUUGA	UUAAGUUUUAAUAAUUUUAGA	Cleavage
sly-miR7696c-3p	Solyc06g007970.3.1	3.0	-1.0	1	21	934	954	UUUUGAAUUAUUAGAACUUGA	UUAGGUUCUGAUGAUACAAAA	Cleavage
sly-miR7696c-3p	Solyc07g052340.3.1	3.0	-1.0	1	21	1197	1217	UUUUGAAUUAUUAGAACUUGA	UUAAGUUCUGAUGAGUCAAAG	Cleavage
sly-miR7696c-3p	Solyc02g081010.2.1	3.0	-1.0	1	21	323	343	UUUUGAAUUAUUAGAACUUGA	UCUAGUUUUAAUAAUCCAAAA	Cleavage
sly-miR7696c-3p	Solyc11g072930.2.1	3.0	-1.0	1	21	308	328	UUUUGAAUUAUUAGAACUUGA	ACAAGUUUUAAUAAUAUAAAG	Cleavage
sly-miR7696c-3p	Solyc09g011110.1.1	3.0	-1.0	1	21	493	513	UUUUGAAUUAUUAGAACUUGA	UUGAGUGUUGAUGAUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc06g066820.3.1	3.0	-1.0	1	21	833	853	UUUUGAAUUAUUAGAACUUGA	UUAACUUUUAAUUAUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc04g058200.3.1	3.0	-1.0	1	21	2880	2900	UUUUGAAUUAUUAGAACUUGA	UUGAAUUCUAAUAAUUAAAAA	Cleavage

sly-miR7696c-3p	Solyc09g007300.2.1	3.0	-1.0	1	21	25	45	UUUUGAAUUAUUAGAACUUGA	UCAACUUAUAAUAAUUUAAGA	Cleavage
sly-miR7696c-3p	Solyc06g063110.2.1	3.0	-1.0	1	21	589	609	UUUUGAAUUAUUAGAACUUGA	AUGGGUUCUAAUAAUUUGGAG	Cleavage
sly-miR7696c-3p	Solyc04g015660.2.1	3.0	-1.0	1	21	2548	2568	UUUUGAAUUAUUAGAACUUGA	GCAAGUACAAAUGAUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc01g094050.1.1	3.0	-1.0	1	21	184	204	UUUUGAAUUAUUAGAACUUGA	CCAGGAUCUGAUAAUUUAAGA	Cleavage
sly-miR7696c-3p	Solyc03g025150.3.1	3.0	-1.0	1	21	511	531	UUUUGAAUUAUUAGAACUUGA	ACAUGUCCUGAUAAUUUAAAA	Cleavage
sly-miR7696c-3p	Solyc02g093365.1.1	3.0	-1.0	1	21	3647	3667	UUUUGAAUUAUUAGAACUUGA	GUAAGUUCUGAUAGUUAAAGA	Cleavage
sly-miR7696c-3p	Solyc02g093360.3.1	3.0	-1.0	1	21	6765	6785	UUUUGAAUUAUUAGAACUUGA	GUAAGUUCUGAUAGUUAAAGA	Cleavage
sly-miR7696c-3p	Solyc05g015950.3.1	3.0	-1.0	1	21	2197	2217	UUUUGAAUUAUUAGAACUUGA	UUAGAAUCUAAUAAUUCGAAA	Cleavage
sly-miR7696c-3p	Solyc01g068540.3.1	3.0	-1.0	1	21	225	245	UUUUGAAUUAUUAGAACUUGA	UUAGGUAAUAAUAAUUUAAAA	Cleavage
sly-miR7696c-3p	Solyc01g087610.3.1	3.0	-1.0	1	21	4308	4328	UUUUGAAUUAUUAGAACUUGA	GAAGGUUCCAGUAGUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc11g020470.1.1	3.0	-1.0	1	21	85	105	UUUUGAAUUAUUAGAACUUGA	GCAAGGCCUAGUAGUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc02g078380.3.1	3.0	-1.0	1	21	575	595	UUUUGAAUUAUUAGAACUUGA	GUAUGUUCUGAUGAUUCAGAG	Cleavage
sly-miR7696c-3p	Solyc08g080250.3.1	3.0	-1.0	1	21	1989	2009	UUUUGAAUUAUUAGAACUUGA	AUAAGUCCAAAUGAUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc08g068420.3.1	3.0	-1.0	1	21	1002	1022	UUUUGAAUUAUUAGAACUUGA	GCAUGUCCUAGUAAUUCGAAA	Cleavage
sly-miR7696c-3p	Solyc02g087360.3.1	3.0	-1.0	1	21	631	651	UUUUGAAUUAUUAGAACUUGA	GCUAGUGCUAGUAAUUCAAAG	Cleavage
sly-miR7696c-3p	Solyc03g116650.2.1	3.0	-1.0	1	21	435	454	UUUUGAAUUAUUAGAACUUGA	GCAAGU-CUAGUGAUUCAAAA	Cleavage
sly-miR7696c-3p	Solyc07g042590.3.1	3.0	-1.0	1	21	1272	1292	UUUUGAAUUAUUAGAACUUGA	UAAAGUUGUAAUGAUGCAAAA	Cleavage
sly-miR7805-5p	Solyc01g079950.3.1	2.0	-1.0	1	21	730	750	AAAUUUGGUGUAGUGAAUACU	AAUAUUCUCUACACCAAAUUA	Cleavage
sly-miR7805-5p	Solyc07g014700.3.1	2.0	-1.0	1	21	1516	1536	AAAUUUGGUGUAGUGAAUACU	GAUGUUAACUACACCAGAUUU	Cleavage
sly-miR7805-5p	Solyc04g080220.3.1	2.5	-1.0	1	21	2422	2442	AAAUUUGGUGUAGUGAAUACU	AGUGUUUAUUGCAUCAAAUUU	Cleavage
sly-miR7805-5p	Solyc05g015630.3.1	2.5	-1.0	1	21	1806	1826	AAAUUUGGUGUAGUGAAUACU	GGUAUUCAUUAUGCUGAAUUU	Cleavage
sly-miR7805-5p	Solyc09g005070.1.1	2.5	-1.0	1	21	187	207	AAAUUUGGUGUAGUGAAUACU	GCAAUUCACUAUGUCAAAUUU	Cleavage
sly-miR7805-5p	Solyc07g063990.1.1	2.5	-1.0	1	21	957	977	AAAUUUGGUGUAGUGAAUACU	GGUACCCAUUACACCAAAUUU	Cleavage
sly-miR7805-5p	Solyc01g079940.3.1	2.5	-1.0	1	21	741	761	AAAUUUGGUGUAGUGAAUACU	GAUAUUCUCUACACCAAACUU	Cleavage
sly-miR7805-5p	Solyc02g062430.3.1	2.5	-1.0	1	21	2235	2255	AAAUUUGGUGUAGUGAAUACU	CCUGUUCUUUACAUCAAAUUU	Cleavage
sly-miR7805-5p	Solyc07g045380.3.1	2.5	-1.0	1	21	1991	2011	AAAUUUGGUGUAGUGAAUACU	UAUCUACACUACACCAGAUUU	Cleavage
sly-miR7805-5p	Solyc01g087230.3.1	3.0	-1.0	1	21	1647	1667	AAAUUUGGUGUAGUGAAUACU	UGUAUUUGUUACACCAAACUU	Cleavage
sly-miR7805-5p	Solyc01g079160.3.1	3.0	-1.0	1	21	889	909	AAAUUUGGUGUAGUGAAUACU	GGAGUUCACUACACUGAGUUU	Cleavage
sly-miR7805-5p	Solyc12g049617.1.1	3.0	-1.0	1	21	434	454	AAAUUUGGUGUAGUGAAUACU	UGUAUUUUCUAUGCUAAAUUU	Cleavage
sly-miR7805-5p	Solyc12g049617.1.1	3.0	-1.0	1	21	223	243	AAAUUUGGUGUAGUGAAUACU	UGUAUUAUCUAUGCCAAAUUU	Cleavage
sly-miR7805-5p	Solyc03g097780.3.1	3.0	-1.0	1	21	1624	1644	AAAUUUGGUGUAGUGAAUACU	CGAAUUCAUUACACCAAACUU	Cleavage
sly-miR7805-5p	Solyc09g090670.3.1	3.0	-1.0	1	21	853	873	AAAUUUGGUGUAGUGAAUACU	UGUUUUCAUUACUCCAAAUUU	Cleavage
sly-miR7805-5p	Solyc01g081200.3.1	3.0	-1.0	1	21	722	742	AAAUUUGGUGUAGUGAAUACU	UUCAUUUACUAUAUCAAGUUU	Cleavage
sly-miR7805-5p	Solyc08g006860.3.1	3.0	-1.0	1	21	524	544	AAAUUUGGUGUAGUGAAUACU	AAUAUUCACUAAGUCAAGUUU	Translation
sly-miR7805-5p	Solyc11g013520.2.1	3.0	-1.0	1	21	319	339	AAAUUUGGUGUAGUGAAUACU	UAUGUUCAUUACACUGAAUUC	Cleavage
sly-miR7805-5p	Solyc04g064740.3.1	3.0	-1.0	1	21	2072	2092	AAAUUUGGUGUAGUGAAUACU	GGUUUUGAUUAUACCAAAUUU	Cleavage
sly-miR7805-5p	Solyc02g086850.2.1	3.0	-1.0	1	21	2804	2824	AAAUUUGGUGUAGUGAAUACU	UUUAUUCAUUAUGCCGAAUUG	Cleavage
sly-miR7805-5p	Solyc04g054280.2.1	3.0	-1.0	1	21	987	1007	AAAUUUGGUGUAGUGAAUACU	UUUAUACACUAUACUAAAUUA	Cleavage
sly-miR7805-5p	Solyc04g080710.3.1	3.0	-1.0	1	21	202	222	AAAUUUGGUGUAGUGAAUACU	GCUAUUGGUUAUAUCAAAUUU	Cleavage
sly-miR7805-5p	Solyc03g026300.3.1	3.0	-1.0	1	21	1561	1581	AAAUUUGGUGUAGUGAAUACU	CAUGUUCUCUAUAUCAAGUUU	Cleavage
sly-miR7980b-2-5p	Solyc01g111080.3.1	1.5	-1.0	1	23	17785	17807	GUCCAAACACUGAUUCCAUCUCA	ACACAUGAAAUCAGUGUUUGGAU	Cleavage
sly-miR7980b-2-5p	Solyc10g080610.1.1	2.0	-1.0	1	23	437	459	GUCCAAACACUGAUUCCAUCUCA	GGAGAUGGAAUCAGUGUAUGGAU	Cleavage
sly-miR7980b-2-5p	Solyc01g094350.3.1	2.0	-1.0	1	23	2121	2143	GUCCAAACACUGAUUCCAUCUCA	GCACAUGGGUUCAGUGUUUGGGC	Cleavage
sly-miR7980b-2-5p	Solyc12g010100.1.1	2.5	-1.0	1	23	709	731	GUCCAAACACUGAUUCCAUCUCA	AAACAUGGGAUCGGUGUUUGGGA	Cleavage
sly-miR7980b-2-5p	Solyc01g087150.3.1	3.0	-1.0	1	23	1352	1374	GUCCAAACACUGAUUCCAUCUCA	GCAGAUGGGAUUAGUGUUGGGAU	Cleavage

sly-miR7980b-2-5p	Solyc10g079330.1.1	3.0	-1.0	1	23	980	1002	GUCCAAACACUGAUUCCAUCUCA	GUGGAUGGAAUUCGUGUUUGGAA	Translation
sly-miR7980b-2-5p	Solyc05g046120.3.1	3.0	-1.0	1	23	2045	2067	GUCCAAACACUGAUUCCAUCUCA	GAUGAUGGAAUCGUUGUUUGGGU	Translation
sly-miR7980b-2-5p	Solyc03g044910.1.1	3.0	-1.0	1	23	730	752	GUCCAAACACUGAUUCCAUCUCA	UGUAAUGGAAUUGGUGCUUGGAU	Cleavage
sly-miR7980b-2-5p	Solyc01g108450.3.1	3.0	-1.0	1	23	1297	1319	GUCCAAACACUGAUUCCAUCUCA	AAAAGUGGAAUUAGGGUUUGGAU	Cleavage
sly-miR7980b-2-5p	Solyc07g005110.3.1	3.0	-1.0	1	23	1857	1879	GUCCAAACACUGAUUCCAUCUCA	GAUUAUGGGAUUAAUGUUUGGAU	Translation
sly-miR7980b-2-5p	Solyc06g074960.3.1	3.0	-1.0	1	23	3970	3992	GUCCAAACACUGAUUCCAUCUCA	UACAAUGGCAUCAGUGGUUGGAU	Cleavage
sly-miR7980b-3p-1	Solyc07g043590.3.1	1.5	-1.0	1	24	982	1005	GAGAUGGAAUCAGUGUUUGGACAU	UGCUGCAGAUGCUGAUUCCAUCUC	Cleavage
sly-miR7980b-3p-1	Solyc01g096060.3.1	2.5	-1.0	1	24	2461	2485	GAGAUGGAAUCAGUGU-UUGGACAU	AUUUUCAAUACACUGAUUUCAUCUC	Cleavage
sly-miR7980b-3p-1	Solyc06g008200.3.1	2.5	-1.0	1	24	444	467	GAGAUGGAAUCAGUGUUUGGACAU	UUCUCUGAACUCUGAUUUCAUCUC	Cleavage
sly-miR7980b-3p-1	Solyc05g026360.3.1	2.5	-1.0	1	24	330	353	GAGAUGGAAUCAGUGUUUGGACAU	UGAUUCAAGCAGUGAUUCCAUUUC	Cleavage
sly-miR7980b-3p-1	Solyc05g010140.3.1	2.5	-1.0	1	24	1584	1607	GAGAUGGAAUCAGUGUUUGGACAU	CACCCCAAAUUCUGAUUCCGUCUU	Cleavage
sly-miR7980b-3p-1	Solyc09g064530.3.1	2.5	-1.0	1	24	1107	1130	GAGAUGGAAUCAGUGUUUGGACAU	UAAGAGAAACGCUGAUUCUAUUUC	Cleavage
sly-miR7980b-3p-1	Solyc11g072600.2.1	2.5	-1.0	1	24	1474	1497	GAGAUGGAAUCAGUGUUUGGACAU	UAACUCAAAAACUGAUUCCAUUUG	Cleavage
sly-miR7980b-3p-1	Solyc02g077720.3.1	3.0	-1.0	1	24	515	538	GAGAUGGAAUCAGUGUUUGGACAU	UCACCUAAAAACUGAUUUUAUUUC	Cleavage
sly-miR7980b-3p-1	Solyc03g013310.3.1	3.0	-1.0	1	24	1060	1083	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
sly-miR7980b-3p-1	Solyc01g086730.3.1	3.0	-1.0	1	24	482	505	GAGAUGGAAUCAGUGUUUGGACAU	AAGGGCAAAUGCUGGUUCCGUUUU	Cleavage
sly-miR7981-3p	Solyc12g005050.2.1	1.0	-1.0	1	24	2439	2462	AUAGGACUUUAGUUUAGUUAAGGU	ACCAUAACUAAACUAAGGUCUUAU	Cleavage
sly-miR7981-3p	Solyc09g098620.2.1	1.5	-1.0	1	24	2141	2164	AUAGGACUUUAGUUUAGUUAAGGU	GAAUUAACUAAAUUAAGGUUCUAU	Cleavage
sly-miR7981-3p	Solyc01g111080.3.1	2.5	-1.0	1	24	10265	10288	AUAGGACUUUAGUUUAGUUAAGGU	AUCUUAAUUAAUCUAAGGUCCUAU	Cleavage
sly-miR7981-3p	Solyc10g005950.3.1	2.5	-1.0	1	24	315	338	AUAGGACUUUAGUUUAGUUAAGGU	AUUUGGACUAAGUUGAGGUCCUAU	Cleavage
sly-miR7981-3p	Solyc02g090710.3.1	2.5	-1.0	1	24	693	716	AUAGGACUUUAGUUUAGUUAAGGU	CACUAACCUAAAAUAAAGUCCUAU	Cleavage
sly-miR7981-3p	Solyc02g079710.3.1	2.5	-1.0	1	24	324	347	AUAGGACUUUAGUUUAGUUAAGGU	AGUAUAACCAAACAAAAGUCCUAU	Translation
sly-miR7981-3p	Solyc05g015640.3.1	3.0	-1.0	1	24	1615	1638	AUAGGACUUUAGUUUAGUUAAGGU	ACCCUAACAAAGCUAAAGUCCAAU	Cleavage
sly-miR7981-3p	Solyc06g062690.3.1	3.0	-1.0	1	24	1752	1775	AUAGGACUUUAGUUUAGUUAAGGU	UGGUUGACUGCAUUGAAGUCCUAU	Cleavage
sly-miR7981-3p	Solyc05g012330.3.1	3.0	-1.0	1	24	581	604	AUAGGACUUUAGUUUAGUUAAGGU	AAAUUAACAAAGCUGAAGUUCUGU	Cleavage
sly-miR7981-3p	Solyc02g027080.2.1	3.0	-1.0	1	24	3046	3069	AUAGGACUUUAGUUUAGUUAAGGU	ACUUAUAUUAUACUAAGGUCCUAU	Cleavage
sly-miR7981-3p	Solyc11g045230.2.1	3.0	-1.0	1	24	289	312	AUAGGACUUUAGUUUAGUUAAGGU	AUAGAAGCUAAAUUAUAGUUCUAU	Cleavage
sly-miR7981-5p	Solyc01g068400.3.1	2.5	-1.0	1	23	413	435	UUAACUUAACUAAGGUUCUAUUA	UAAAGGAACUUUGGUUGAGUUAG	Cleavage
sly-miR7981-5p	Solyc02g021010.2.1	2.5	-1.0	1	23	1464	1486	UUAACUUAACUAAGGUUCUAUUA	AUAUAGUGUUUUAGUUAAGUUAA	Cleavage
sly-miR7981-5p	Solyc02g021010.2.1	2.5	-1.0	1	23	2353	2375	UUAACUUAACUAAGGUUCUAUUA	AUAUAGUGUUUUAGUUAAGUUAA	Cleavage
sly-miR7981-5p	Solyc02g021010.2.1	2.5	-1.0	1	23	3602	3624	UUAACUUAACUAAGGUUCUAUUA	AUAUAGUGUUUUAGUUAAGUUAA	Cleavage
sly-miR7981-5p	Solyc03g122340.3.1	2.5	-1.0	1	23	3504	3526	UUAACUUAACUAAGGUUCUAUUA	UGUAAGAACAUUAAUUAAGUUAA	Translation
sly-miR7981-5p	Solyc03g098230.3.1	3.0	-1.0	1	22	1	22	UUAACUUAACUAAGGUUCUAUU	AAAAGAACUUUAGUUAAGUGAU	Cleavage
sly-miR7981-5p	Solyc06g073160.3.1	3.0	-1.0	1	23	3480	3502	UUAACUUAACUAAGGUUCUAUUA	UGAAAGAAGAUUAGUUGAGUUAG	Cleavage
sly-miR7981-5p	Solyc11g012760.2.1	3.0	-1.0	1	23	1863	1885	UUAACUUAACUAAGGUUCUAUUA	AUUCAGAAUCUUGGUUAAGAUGA	Cleavage

sly-miR7981-5p	Solyc06g073140.2.1	3.0	-1.0	1	23	914	936	UUAACUUAACUAAGGUUCUAUUA	AGAAAGAAGAUUAGUUGAGUUAG	Cleavage
sly-miR7981-5p	Solyc11g065340.2.1	3.0	-1.0	1	23	268	290	UUAACUUAACUAAGGUUCUAUUA	GAUGAGAUCUUUAGUAAAGUUAA	Cleavage
sly-miR7983-1-3p	Solyc09g011580.2.1	1.0	-1.0	1	24	822	845	ACUAAUGCCGGUAAAGACUUUAAC	GAUAAAGUUUUUAUCGGCAUUAGU	Cleavage
sly-miR7983-1-5p	Solyc06g065340.1.1	1.5	-1.0	1	24	428	451	UAAAGCUUUUAGCGAUAUUUGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
sly-miR7983-1-5p	Solyc08g008610.3.1	2.0	-1.0	1	24	1707	1730	UAAAGCUUUUAGCGAUAUUUGUUC	AUUUGGAUAUAGUUAAAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc12g010530.2.1	2.5	-1.0	1	24	424	447	UAAAGCUUUUAGCGAUAUUUGUUC	UGGCAAGUUGCGCUAAAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc04g011980.1.1	2.5	-1.0	1	24	637	660	UAAAGCUUUUAGCGAUAUUUGUUC	AGAAAUGUAUUGCUAGAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc11g045350.2.1	2.5	-1.0	1	24	3464	3487	UAAAGCUUUUAGCGAUAUUUGUUC	AUGAGGAUAUUGCUAAAAGGUUUA	Cleavage
sly-miR7983-1-5p	Solyc00g026903.1.1	2.5	-1.0	1	24	746	769	UAAAGCUUUUAGCGAUAUUUGUUC	UCGUCAACAUCGCUGAAGGCUUUG	Cleavage
sly-miR7983-1-5p	Solyc05g056140.3.1	3.0	-1.0	1	24	1755	1778	UAAAGCUUUUAGCGAUAUUUGUUC	GGACAAAUAUUGCUGAAGGCUUGA	Cleavage
sly-miR7983-1-5p	Solyc09g014890.3.1	3.0	-1.0	1	24	716	739	UAAAGCUUUUAGCGAUAUUUGUUC	GGACUACUGAUGCUAAAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc08g065500.2.1	3.0	-1.0	1	24	1651	1674	UAAAGCUUUUAGCGAUAUUUGUUC	UUUUAAUUAUUGCUAAAAGUUUUC	Cleavage
sly-miR7983-1-5p	Solyc04g011960.2.1	3.0	-1.0	1	24	637	660	UAAAGCUUUUAGCGAUAUUUGUUC	AGAAAUGUAUUGUUAGAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc04g012010.3.1	3.0	-1.0	1	24	657	680	UAAAGCUUUUAGCGAUAUUUGUUC	AGAAAUGUAUUGUUAGAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc04g011900.3.1	3.0	-1.0	1	24	1539	1562	UAAAGCUUUUAGCGAUAUUUGUUC	AGAAAUGUAUUGUUAGAAGCUUUA	Cleavage
sly-miR7983-1-5p	Solyc10g083200.2.1	3.0	-1.0	1	24	620	643	UAAAGCUUUUAGCGAUAUUUGUUC	UUAUUACUAUCGCUAUAAGCUUUG	Cleavage
sly-miR7983-2-3p	Solyc09g011580.2.1	1.0	-1.0	1	24	822	845	ACUAAUGCCGGUAAAGACUUUAAC	GAUAAAGUUUUUAUCGGCAUUAGU	Cleavage
sly-miR7983-2-5p	Solyc12g010530.2.1	1.5	-1.0	1	24	424	447	UAAAGCUUUUAGCGAAAUUGAUUC	UGGCAAGUUGCGCUAAAAGCUUUA	Cleavage
sly-miR7983-2-5p	Solyc06g065340.1.1	2.0	-1.0	1	24	428	451	UAAAGCUUUUAGCGAAAUUGAUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
sly-miR7983-2-5p	Solyc04g074190.3.1	2.5	-1.0	1	24	1355	1378	UAAAGCUUUUAGCGAAAUUGAUUC	CGGUUGAUUUAGCUAGAGGCUUUA	Cleavage
sly-miR7983-2-5p	Solyc03g006460.3.1	2.5	-1.0	1	24	1813	1836	UAAAGCUUUUAGCGAAAUUGAUUC	GAGACAUUUUAGCUAAAAGCUUUG	Cleavage
sly-miR7983-2-5p	Solyc09g065170.2.1	2.5	-1.0	1	24	2077	2100	UAAAGCUUUUAGCGAAAUUGAUUC	CUAGAGAUUUUGUUAAAAGCUUUU	Cleavage
sly-miR7983-2-5p	Solyc01g058540.3.1	2.5	-1.0	1	24	2725	2748	UAAAGCUUUUAGCGAAAUUGAUUC	CUUCAGAUUUUGUUAAAGGUUUUA	Cleavage
sly-miR7983-2-5p	Solyc04g051500.3.1	2.5	-1.0	1	24	1847	1870	UAAAGCUUUUAGCGAAAUUGAUUC	UUUGCAUUUUGGCUAAAAGCUUUG	Cleavage
sly-miR7983-2-5p	Solyc03g121630.3.1	3.0	-1.0	1	24	3540	3563	UAAAGCUUUUAGCGAAAUUGAUUC	GCGUUAAUUUCGUUGAAAAUUUUA	Cleavage
sly-miR7983-2-5p	Solyc07g053430.3.1	3.0	-1.0	1	24	1616	1639	UAAAGCUUUUAGCGAAAUUGAUUC	AAGGCAAUUUUGUUAAGAGCUCUA	Cleavage
sly-miR7983-2-5p	Solyc01g111690.3.1	3.0	-1.0	1	24	1157	1180	UAAAGCUUUUAGCGAAAUUGAUUC	AUUUUGAUUCUGUUAAAAGCUUUG	Cleavage
sly-miR7983-2-5p	Solyc01g088080.3.1	3.0	-1.0	1	24	1487	1510	UAAAGCUUUUAGCGAAAUUGAUUC	UAGCUAAGUUUGCUGAAAGUUUUG	Cleavage
sly-miR7983-2-5p	Solyc04g076560.3.1	3.0	-1.0	1	24	1699	1722	UAAAGCUUUUAGCGAAAUUGAUUC	AAAAAAGUUUUGCUGAAAGCAUUA	Cleavage
sly-miR7983-2-5p	Solyc02g086810.1.1	3.0	-1.0	1	24	316	339	UAAAGCUUUUAGCGAAAUUGAUUC	GUUCAAGUUUCGUUAAAGGAUUUA	Cleavage
sly-miR7983-3-3p	Solyc09g011580.2.1	1.0	-1.0	1	24	822	845	ACUAAUGCCGGUAAAGACUUUAAC	GAUAAAGUUUUUAUCGGCAUUAGU	Cleavage
sly-miR7983-3-5p	Solyc10g052470.1.1	2.0	-1.0	1	24	110	133	UAACGGCUUUAGCAACAUUGGAUC	GGUCCAAUGUUGCUAAAGCAGUUG	Cleavage
sly-miR7983-3-5p	Solyc01g099120.3.1	2.0	-1.0	1	24	1029	1052	UAACGGCUUUAGCAACAUUGGAUC	AAAGAAAUGUUGUUAAGGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc01g109670.3.1	2.5	-1.0	1	24	110	133	UAACGGCUUUAGCAACAUUGGAUC	GGUCUAACGUUGCUAGAGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc01g109655.1.1	2.5	-1.0	1	24	373	396	UAACGGCUUUAGCAACAUUGGAUC	GGUCUAACGUUGCUAGAGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc04g005200.3.1	2.5	-1.0	1	24	3554	3577	UAACGGCUUUAGCAACAUUGGAUC	AUUACAAGGUUGCUGGAGCUGUUA	Cleavage
sly-miR7983-3-5p	Solyc02g071710.2.1	2.5	-1.0	1	24	1499	1522	UAACGGCUUUAGCAACAUUGGAUC	UUGUAUAUGUUGCUAAAGCCUUUA	Cleavage
sly-miR7983-3-5p	Solyc01g102510.3.1	2.5	-1.0	1	24	3644	3667	UAACGGCUUUAGCAACAUUGGAUC	AGGAAAAUGUUGUUGAAGCUGUUC	Cleavage
sly-miR7983-3-5p	Solyc08g060940.1.1	2.5	-1.0	1	24	788	811	UAACGGCUUUAGCAACAUUGGAUC	CUAUGAAUGUUGCUGGGGUUGUUA	Cleavage
sly-miR7983-3-5p	Solyc05g005460.3.1	3.0	-1.0	1	24	1382	1405	UAACGGCUUUAGCAACAUUGGAUC	AUUCUAAUGUUGCUGAAGCCGUCG	Cleavage
sly-miR7983-3-5p	Solyc06g062990.2.1	3.0	-1.0	1	24	770	793	UAACGGCUUUAGCAACAUUGGAUC	UAUUCAAUUUUGCUGAAGCCAUUA	Cleavage
sly-miR7983-3-5p	Solyc05g021500.2.1	3.0	-1.0	1	24	28	51	UAACGGCUUUAGCAACAUUGGAUC	UAUUUAAUUUUGUUAAGGUUGUUA	Cleavage
sly-miR7983-3-5p	Solyc04g082560.3.1	3.0	-1.0	1	24	3035	3058	UAACGGCUUUAGCAACAUUGGAUC	GAAUCAGUGGUGUUGAAGCCGUUG	Cleavage
sly-miR7983-3-5p	Solyc01g066980.3.1	3.0	-1.0	1	24	525	548	UAACGGCUUUAGCAACAUUGGAUC	UUCACAAUGUUGCUAAGGUUGUAA	Cleavage
sly-miR7983-3-5p	Solyc11g012870.2.1	3.0	-1.0	1	24	675	698	UAACGGCUUUAGCAACAUUGGAUC	UGUCAUAUGUUGUUAGAGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc12g044880.2.1	3.0	-1.0	1	24	351	374	UAACGGCUUUAGCAACAUUGGAUC	AUGGCAAUGUUGCUGAUGUUGUUA	Cleavage
sly-miR7983-3-5p	Solyc09g092410.3.1	3.0	-1.0	1	24	782	805	UAACGGCUUUAGCAACAUUGGAUC	UUGAUAGUGUUGCUGAAGGUGUUA	Cleavage
sly-miR7983-3-5p	Solyc04g079430.3.1	3.0	-1.0	1	24	3448	3471	UAACGGCUUUAGCAACAUUGGAUC	CAAUUAGUGAUGCUAAGGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc06g075990.3.1	3.0	-1.0	1	24	47	70	UAACGGCUUUAGCAACAUUGGAUC	GUAAAGAUGUUGCUAAAUCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc04g074780.3.1	3.0	-1.0	1	24	714	737	UAACGGCUUUAGCAACAUUGGAUC	UCAAAAAUGUUAUUAAAGCUGUUG	Cleavage

sly-miR7983-3-5p	Solyc03g113540.3.1	3.0	-1.0	1	24	943	966	UAACGGCUUUAGCAACAUUGGAUC	ACAAGGAUGUUGAUAAAGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc06g062650.1.1	3.0	-1.0	1	24	74	97	UAACGGCUUUAGCAACAUUGGAUC	UCAGUAGUGCUGUUAAAGCUGUUG	Cleavage
sly-miR7983-3-5p	Solyc05g053540.3.1	3.0	-1.0	1	24	373	396	UAACGGCUUUAGCAACAUUGGAUC	UGUUGAAACUUGCUGAAGCUGUUA	Cleavage
sly-miR7983-3-5p	Solyc11g020230.1.1	3.0	-1.0	1	24	2014	2037	UAACGGCUUUAGCAACAUUGGAUC	GGAGUAAUGAUGCUAGAGUUGUUG	Cleavage
sly-miR7983-3-5p	Solyc12g043020.2.1	3.0	-1.0	1	24	512	535	UAACGGCUUUAGCAACAUUGGAUC	UGUUAAAGCUUGCUGAAGCUGUUA	Cleavage
sly-miR7983-3-5p	Solyc12g088720.2.1	3.0	-1.0	1	24	1111	1134	UAACGGCUUUAGCAACAUUGGAUC	CAGAUGAUGCUGCUAAGGCUGUUG	Cleavage
sly-miR7983-4-3p	Solyc03g025550.3.1	2.5	-1.0	1	24	477	500	ACUAAUUUCGGUAAAGACUUUAGC	AAUGGAGUCUUUAUGGAAGUUAGU	Translation
sly-miR7983-4-3p	Solyc07g054160.3.1	2.5	-1.0	1	24	418	441	ACUAAUUUCGGUAAAGACUUUAGC	UAUGCAGUCAUUGUUGAAAUUAGU	Cleavage
sly-miR7983-4-3p	Solyc09g011580.2.1	3.0	-1.0	1	24	822	845	ACUAAUUUCGGUAAAGACUUUAGC	GAUAAAGUUUUUAUCGGCAUUAGU	Cleavage
sly-miR7983-4-3p	Solyc11g020210.2.1	3.0	-1.0	1	24	690	713	ACUAAUUUCGGUAAAGACUUUAGC	CUCAAAGUUUUUUCCGAAGUUGGU	Cleavage
sly-miR7983-4-3p	Solyc03g121410.3.1	3.0	-1.0	1	24	2569	2592	ACUAAUUUCGGUAAAGACUUUAGC	AAUGUAGUUUUUACUGAAAAUGGU	Cleavage
sly-miR7983-4-3p	Solyc11g008400.2.1	3.0	-1.0	1	24	1110	1133	ACUAAUUUCGGUAAAGACUUUAGC	GAAUUAGUCUUUACGGAAAUUCGU	Translation
sly-miR7983-4-5p	Solyc07g054940.2.1	1.5	-1.0	1	24	1312	1335	UAAAGUCUUUAGCGACAUUGGUUC	GAGAUAAUGUCGAUAAAGACUUUA	Cleavage
sly-miR7983-4-5p	Solyc06g060690.2.1	1.5	-1.0	1	24	1536	1559	UAAAGUCUUUAGCGACAUUGGUUC	CAUCUACUGUCGCUAAAGAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc08g079440.1.1	2.5	-1.0	1	24	956	979	UAAAGUCUUUAGCGACAUUGGUUC	AAGGUAGUGUUGCUAGGGAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc05g007950.3.1	2.5	-1.0	1	24	87	110	UAAAGUCUUUAGCGACAUUGGUUC	UCCUCAAUGCUGCUAAAGAUUUUG	Cleavage
sly-miR7983-4-5p	Solyc09g056290.2.1	2.5	-1.0	1	24	254	277	UAAAGUCUUUAGCGACAUUGGUUC	UAUAUAGUGUCGUUGGAGACUUUG	Cleavage
sly-miR7983-4-5p	Solyc03g083550.1.1	2.5	-1.0	1	24	839	862	UAAAGUCUUUAGCGACAUUGGUUC	ACAAAAGUGUAGCUAGAGAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc10g018260.1.1	2.5	-1.0	1	24	926	949	UAAAGUCUUUAGCGACAUUGGUUC	AUGGGACUGUUGCUAGGGACUUUA	Cleavage
sly-miR7983-4-5p	Solyc06g065340.1.1	3.0	-1.0	1	24	428	451	UAAAGUCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
sly-miR7983-4-5p	Solyc00g033990.2.1	3.0	-1.0	1	24	598	621	UAAAGUCUUUAGCGACAUUGGUUC	UUUUCGAUGUUGCUGAAGGUUUUG	Cleavage
sly-miR7983-4-5p	Solyc09g048980.3.1	3.0	-1.0	1	24	593	616	UAAAGUCUUUAGCGACAUUGGUUC	UCUCUGAUGUUGCUGGGGAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc00g202560.2.1	3.0	-1.0	1	24	406	429	UAAAGUCUUUAGCGACAUUGGUUC	ACAGCAAUGUCGUUACAGGUUUUA	Cleavage
sly-miR7983-4-5p	Solyc02g071710.2.1	3.0	-1.0	1	24	1499	1522	UAAAGUCUUUAGCGACAUUGGUUC	UUGUAUAUGUUGCUAAAGCCUUUA	Cleavage
sly-miR7983-4-5p	Solyc11g010980.2.1	3.0	-1.0	1	24	1627	1650	UAAAGUCUUUAGCGACAUUGGUUC	AAUUUGAUGUUGCUCAAGAUUUUA	Translation
sly-miR7983-4-5p	Solyc08g016750.3.1	3.0	-1.0	1	24	1582	1605	UAAAGUCUUUAGCGACAUUGGUUC	UGUCUGAUUUUGCUAGAGAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc07g049430.3.1	3.0	-1.0	1	24	1358	1381	UAAAGUCUUUAGCGACAUUGGUUC	AUAAUAAUGUUGCUAAGCAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc09g059330.2.1	3.0	-1.0	1	24	789	812	UAAAGUCUUUAGCGACAUUGGUUC	AAGUGAAGGUUGUUGAAGAUUUUA	Cleavage
sly-miR7983-4-5p	Solyc02g062220.2.1	3.0	-1.0	1	24	367	390	UAAAGUCUUUAGCGACAUUGGUUC	GGGAAAAUGUUGUUAAGGACUUAA	Cleavage
sly-miR7983-4-5p	Solyc01g109320.3.1	3.0	-1.0	1	24	125	148	UAAAGUCUUUAGCGACAUUGGUUC	UUCAGAAUGUUGUUGAAGGUUUUG	Cleavage
sly-miR7983-4-5p	Solyc02g090890.3.1	3.0	-1.0	1	24	761	784	UAAAGUCUUUAGCGACAUUGGUUC	AUUUGGAUGUUGCUGAAGACAUUA	Cleavage
sly-miR7983-5-3p	Solyc09g011580.2.1	1.5	-1.0	1	24	822	845	ACUAAUGCUGGUAAAGACUUUAGC	GAUAAAGUUUUUAUCGGCAUUAGU	Cleavage
sly-miR7983-5-3p	Solyc06g060150.3.1	2.5	-1.0	1	24	3091	3114	ACUAAUGCUGGUAAAGACUUUAGC	GGGCUAGUUUUUAUCAGCAUUUGU	Cleavage
sly-miR7983-5-3p	Solyc07g065730.1.1	3.0	-1.0	1	24	1123	1146	ACUAAUGCUGGUAAAGACUUUAGC	CGAGAAUUCUUUACUAGCAUGAGU	Cleavage
sly-miR7983-5-3p	Solyc01g006370.3.1	3.0	-1.0	1	24	589	612	ACUAAUGCUGGUAAAGACUUUAGC	UGCAGAGCUUUUACCAGCAUUACU	Cleavage
sly-miR7983-5-3p	Solyc01g073750.3.1	3.0	-1.0	1	24	826	849	ACUAAUGCUGGUAAAGACUUUAGC	UGCAGAGUUUCUACCAGCAUUACU	Cleavage
sly-miR7983-5-3p	Solyc07g065880.3.1	3.0	-1.0	1	24	2745	2768	ACUAAUGCUGGUAAAGACUUUAGC	AAACAAAUCUUUGUCAGCAUUAGG	Cleavage
sly-miR7983-5-3p	Solyc07g063930.3.1	3.0	-1.0	1	24	1286	1309	ACUAAUGCUGGUAAAGACUUUAGC	UGCCUAUUUUUUAACAGCAUUAGU	Translation
sly-miR7983-5-5p	Solyc07g054940.2.1	1.5	-1.0	1	24	1312	1335	UAAAGUCUUUAGCGACAUUGGUUC	GAGAUAAUGUCGAUAAAGACUUUA	Cleavage
sly-miR7983-5-5p	Solyc06g060690.2.1	1.5	-1.0	1	24	1536	1559	UAAAGUCUUUAGCGACAUUGGUUC	CAUCUACUGUCGCUAAAGAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc08g079440.1.1	2.5	-1.0	1	24	956	979	UAAAGUCUUUAGCGACAUUGGUUC	AAGGUAGUGUUGCUAGGGAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc05g007950.3.1	2.5	-1.0	1	24	87	110	UAAAGUCUUUAGCGACAUUGGUUC	UCCUCAAUGCUGCUAAAGAUUUUG	Cleavage
sly-miR7983-5-5p	Solyc09g056290.2.1	2.5	-1.0	1	24	254	277	UAAAGUCUUUAGCGACAUUGGUUC	UAUAUAGUGUCGUUGGAGACUUUG	Cleavage
sly-miR7983-5-5p	Solyc03g083550.1.1	2.5	-1.0	1	24	839	862	UAAAGUCUUUAGCGACAUUGGUUC	ACAAAAGUGUAGCUAGAGAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc10g018260.1.1	2.5	-1.0	1	24	926	949	UAAAGUCUUUAGCGACAUUGGUUC	AUGGGACUGUUGCUAGGGACUUUA	Cleavage
sly-miR7983-5-5p	Solyc06g065340.1.1	3.0	-1.0	1	24	428	451	UAAAGUCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
sly-miR7983-5-5p	Solyc00g033990.2.1	3.0	-1.0	1	24	598	621	UAAAGUCUUUAGCGACAUUGGUUC	UUUUCGAUGUUGCUGAAGGUUUUG	Cleavage
sly-miR7983-5-5p	Solyc09g048980.3.1	3.0	-1.0	1	24	593	616	UAAAGUCUUUAGCGACAUUGGUUC	UCUCUGAUGUUGCUGGGGAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc00g202560.2.1	3.0	-1.0	1	24	406	429	UAAAGUCUUUAGCGACAUUGGUUC	ACAGCAAUGUCGUUACAGGUUUUA	Cleavage
sly-miR7983-5-5p	Solyc02g071710.2.1	3.0	-1.0	1	24	1499	1522	UAAAGUCUUUAGCGACAUUGGUUC	UUGUAUAUGUUGCUAAAGCCUUUA	Cleavage

sly-miR7983-5-5p	Solyc11g010980.2.1	3.0	-1.0	1	24	1627	1650	UAAAGUCUUUAGCGACAUUGGUUC	AAUUUGAUGUUGCUCAAGAUUUUA	Translation
sly-miR7983-5-5p	Solyc08g016750.3.1	3.0	-1.0	1	24	1582	1605	UAAAGUCUUUAGCGACAUUGGUUC	UGUCUGAUUUUGCUAGAGAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc07g049430.3.1	3.0	-1.0	1	24	1358	1381	UAAAGUCUUUAGCGACAUUGGUUC	AUAAUAAUGUUGCUAAGCAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc09g059330.2.1	3.0	-1.0	1	24	789	812	UAAAGUCUUUAGCGACAUUGGUUC	AAGUGAAGGUUGUUGAAGAUUUUA	Cleavage
sly-miR7983-5-5p	Solyc02g062220.2.1	3.0	-1.0	1	24	367	390	UAAAGUCUUUAGCGACAUUGGUUC	GGGAAAAUGUUGUUAAGGACUUAA	Cleavage
sly-miR7983-5-5p	Solyc01g109320.3.1	3.0	-1.0	1	24	125	148	UAAAGUCUUUAGCGACAUUGGUUC	UUCAGAAUGUUGUUGAAGGUUUUG	Cleavage
sly-miR7983-5-5p	Solyc02g090890.3.1	3.0	-1.0	1	24	761	784	UAAAGUCUUUAGCGACAUUGGUUC	AUUUGGAUGUUGCUGAAGACAUUA	Cleavage
sly-miR7983-6-3p	Solyc05g008830.3.1	3.0	-1.0	1	23	2114	2136	ACUAAUGACGGUAAGACUUUAGC	UUUGAAUUCUUAUUGUUAUUGGU	Cleavage
sly-miR7983-6-3p	Solyc02g080340.3.1	3.0	-1.0	1	23	1699	1721	ACUAAUGACGGUAAGACUUUAGC	GGAAGAGUGUUACUGUUGUUAGU	Cleavage
sly-miR7983-6-5p	Solyc07g054940.2.1	1.5	-1.0	1	24	1312	1335	UAAAGUCUUUAGCGACAUUGGUUC	GAGAUAAUGUCGAUAAAGACUUUA	Cleavage
sly-miR7983-6-5p	Solyc06g060690.2.1	1.5	-1.0	1	24	1536	1559	UAAAGUCUUUAGCGACAUUGGUUC	CAUCUACUGUCGCUAAAGAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc08g079440.1.1	2.5	-1.0	1	24	956	979	UAAAGUCUUUAGCGACAUUGGUUC	AAGGUAGUGUUGCUAGGGAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc05g007950.3.1	2.5	-1.0	1	24	87	110	UAAAGUCUUUAGCGACAUUGGUUC	UCCUCAAUGCUGCUAAAGAUUUUG	Cleavage
sly-miR7983-6-5p	Solyc09g056290.2.1	2.5	-1.0	1	24	254	277	UAAAGUCUUUAGCGACAUUGGUUC	UAUAUAGUGUCGUUGGAGACUUUG	Cleavage
sly-miR7983-6-5p	Solyc03g083550.1.1	2.5	-1.0	1	24	839	862	UAAAGUCUUUAGCGACAUUGGUUC	ACAAAAGUGUAGCUAGAGAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc10g018260.1.1	2.5	-1.0	1	24	926	949	UAAAGUCUUUAGCGACAUUGGUUC	AUGGGACUGUUGCUAGGGACUUUA	Cleavage
sly-miR7983-6-5p	Solyc06g065340.1.1	3.0	-1.0	1	24	428	451	UAAAGUCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
sly-miR7983-6-5p	Solyc00g033990.2.1	3.0	-1.0	1	24	598	621	UAAAGUCUUUAGCGACAUUGGUUC	UUUUCGAUGUUGCUGAAGGUUUUG	Cleavage
sly-miR7983-6-5p	Solyc09g048980.3.1	3.0	-1.0	1	24	593	616	UAAAGUCUUUAGCGACAUUGGUUC	UCUCUGAUGUUGCUGGGGAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc00g202560.2.1	3.0	-1.0	1	24	406	429	UAAAGUCUUUAGCGACAUUGGUUC	ACAGCAAUGUCGUUACAGGUUUUA	Cleavage
sly-miR7983-6-5p	Solyc02g071710.2.1	3.0	-1.0	1	24	1499	1522	UAAAGUCUUUAGCGACAUUGGUUC	UUGUAUAUGUUGCUAAAGCCUUUA	Cleavage
sly-miR7983-6-5p	Solyc11g010980.2.1	3.0	-1.0	1	24	1627	1650	UAAAGUCUUUAGCGACAUUGGUUC	AAUUUGAUGUUGCUCAAGAUUUUA	Translation
sly-miR7983-6-5p	Solyc08g016750.3.1	3.0	-1.0	1	24	1582	1605	UAAAGUCUUUAGCGACAUUGGUUC	UGUCUGAUUUUGCUAGAGAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc07g049430.3.1	3.0	-1.0	1	24	1358	1381	UAAAGUCUUUAGCGACAUUGGUUC	AUAAUAAUGUUGCUAAGCAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc09g059330.2.1	3.0	-1.0	1	24	789	812	UAAAGUCUUUAGCGACAUUGGUUC	AAGUGAAGGUUGUUGAAGAUUUUA	Cleavage
sly-miR7983-6-5p	Solyc02g062220.2.1	3.0	-1.0	1	24	367	390	UAAAGUCUUUAGCGACAUUGGUUC	GGGAAAAUGUUGUUAAGGACUUAA	Cleavage
sly-miR7983-6-5p	Solyc01g109320.3.1	3.0	-1.0	1	24	125	148	UAAAGUCUUUAGCGACAUUGGUUC	UUCAGAAUGUUGUUGAAGGUUUUG	Cleavage
sly-miR7983-6-5p	Solyc02g090890.3.1	3.0	-1.0	1	24	761	784	UAAAGUCUUUAGCGACAUUGGUUC	AUUUGGAUGUUGCUGAAGACAUUA	Cleavage
sly-miR7984c-3p	Solyc08g068320.3.1	2.5	-1.0	1	23	501	523	UACGAUACCAAACUUUAUGGAGG	UAGACAUAAAAUUUGGUAUCGUU	Cleavage
sly-miR7984c-3p	Solyc06g075970.3.1	3.0	-1.0	1	23	1791	1813	UACGAUACCAAACUUUAUGGAGG	AUUUCAUAGCGUUUGUUAUCGUA	Cleavage
sly-miR7984c-3p	Solyc02g086500.3.1	3.0	-1.0	1	23	771	793	UACGAUACCAAACUUUAUGGAGG	UUUAUAAGAAGUUUGGUAUCGUC	Cleavage
sly-miR7984c-3p	Solyc12g098460.2.1	3.0	-1.0	1	23	971	993	UACGAUACCAAACUUUAUGGAGG	UUAUUAUGAAGUUUGGUAUUGGA	Cleavage
sly-miR7984c-3p	Solyc04g008410.2.1	3.0	-1.0	1	23	1351	1373	UACGAUACCAAACUUUAUGGAGG	GAAUCAGGAAGUUUGGUAUCAUA	Cleavage
sly-miR7984c-5p	Solyc06g053200.3.1	2.5	-1.0	1	23	1118	1140	ACGAUACCAAACUUUAUGGAGGA	UAUUCUAUAAGGUUUGGUAACGU	Cleavage
sly-miR7984c-5p	Solyc08g068320.3.1	2.5	-1.0	1	23	500	522	ACGAUACCAAACUUUAUGGAGGA	AUAGACAUAAAAUUUGGUAUCGU	Cleavage
sly-miR7984c-5p	Solyc09g097980.3.1	2.5	-1.0	1	23	259	281	ACGAUACCAAACUUUAUGGAGGA	UUAGCAACAAAGUUUGGUAUUGU	Cleavage
sly-miR7984c-5p	Solyc12g098460.2.1	3.0	-1.0	1	23	970	992	ACGAUACCAAACUUUAUGGAGGA	UUUAUUAUGAAGUUUGGUAUUGG	Cleavage
sly-miR7984c-5p	Solyc04g077460.3.1	3.0	-1.0	1	23	1391	1413	ACGAUACCAAACUUUAUGGAGGA	AGCGCCAUAGAGUUUGGUUUCGG	Cleavage
sly-miR7984d-3p	Solyc05g055690.2.1	2.0	-1.0	1	24	965	988	CAAUUUCGGUCAAAGUUCGGAUAU	GUCCUCGAACAUUGAUCGGAAUUG	Cleavage
sly-miR7984d-3p	Solyc03g114380.3.1	3.0	-1.0	1	24	65	88	CAAUUUCGGUCAAAGUUCGGAUAU	AUCUUUGAAUUUUUACUGAAAUUG	Translation
sly-miR7984d-3p	Solyc03g119780.3.1	3.0	-1.0	1	24	2627	2650	CAAUUUCGGUCAAAGUUCGGAUAU	GCAUCCGGUCUUUGACCCAAAUUG	Cleavage
sly-miR7984d-3p	Solyc05g008637.1.1	3.0	-1.0	1	24	356	378	CAAUUUCGGUCAAAGUUCGGAUAU	GAAUCC-AAUUUUGACUGAAAUUG	Cleavage
sly-miR7984d-3p	Solyc08g079670.3.1	3.0	-1.0	1	24	185	208	CAAUUUCGGUCAAAGUUCGGAUAU	GGUUUUGGAUUUUGAUUGGAAUUG	Cleavage
sly-miR7984d-3p	Solyc05g025640.1.1	3.0	-1.0	1	23	1	23	CAAUUUCGGUCAAAGUUCGGAUA	AUGCAUGACUUUGAUCGAAAUUG	Cleavage
sly-miR7984d-3p	Solyc08g006860.3.1	3.0	-1.0	1	24	463	486	CAAUUUCGGUCAAAGUUCGGAUAU	UGAAUCAAACUUUGACAGAAGUUG	Cleavage
sly-miR7984d-3p	Solyc02g069740.3.1	3.0	-1.0	1	24	1703	1726	CAAUUUCGGUCAAAGUUCGGAUAU	UUUAAUGAAUUUUGACUGAAUUUG	Cleavage
sly-miR7985	Solyc01g009850.3.1	1.0	-1.0	1	24	1319	1342	CGGGCUUGCCUAGUGCGGGUUACC	GGUAACCCGCACUAGGCAAGCUUG	Cleavage
sly-miR7985	Solyc09g075980.3.1	2.5	-1.0	1	24	336	359	CGGGCUUGCCUAGUGCGGGUUACC	AGUAACCCGCACUAGACAAGCCCA	Cleavage
sly-miR7985	Solyc11g068610.2.1	2.5	-1.0	1	24	631	654	CGGGCUUGCCUAGUGCGGGUUACC	UUCCUUCCGAUCUAGGCAAGCCCG	Cleavage
sly-miR7987-3p	Solyc05g007330.2.1	0.5	-1.0	1	24	287	310	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage

sly-miR7987-3p	Solyc12g062737.1.1	0.5	-1.0	1	24	167	190	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc12g062737.1.1	0.5	-1.0	1	24	287	310	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc07g043207.1.1	0.5	-1.0	1	24	141	164	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc07g041260.2.1	0.5	-1.0	1	24	72	95	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc07g041260.2.1	0.5	-1.0	1	24	192	215	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc05g007330.2.1	1.0	-1.0	1	24	47	70	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAUGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc07g043207.1.1	1.0	-1.0	1	24	21	44	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUUAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc12g062737.1.1	1.5	-1.0	1	24	47	70	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUAAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-3p	Solyc05g007330.2.1	2.0	-1.0	1	24	167	190	ACACUAGUUGAUCUUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAAUGU	Cleavage
sly-miR7987-3p	Solyc06g072340.3.1	2.0	-1.0	1	24	2294	2317	ACACUAGUUGAUCUUAUUGAUGAC	UGGUUCAGUAAGGUCAAUUGGUGU	Cleavage
sly-miR7987-3p	Solyc02g081730.3.1	2.5	-1.0	1	24	99	122	ACACUAGUUGAUCUUAUUGAUGAC	UAAAUCAAAGAGAUUAAUUAGUGU	Cleavage
sly-miR7987-3p	Solyc12g006670.2.1	2.5	-1.0	1	24	1154	1177	ACACUAGUUGAUCUUAUUGAUGAC	CUAUAUAAUAGGAUCAACUAGUAU	Cleavage
sly-miR7987-3p	Solyc09g090940.3.1	3.0	-1.0	1	24	2980	3003	ACACUAGUUGAUCUUAUUGAUGAC	UCCAUCAGUAGGAUCAGCUAGUAU	Cleavage
sly-miR7987-3p	Solyc12g056170.2.1	3.0	-1.0	1	24	2258	2281	ACACUAGUUGAUCUUAUUGAUGAC	UGAAUCAAUAAGAUCAACUCCUGU	Cleavage
sly-miR7987-3p	Solyc05g007870.2.1	3.0	-1.0	1	24	1783	1806	ACACUAGUUGAUCUUAUUGAUGAC	UUUAGUAGUGAGAUCAAAUAGUGU	Cleavage
sly-miR7987-3p	Solyc09g092680.3.1	3.0	-1.0	1	24	4247	4270	ACACUAGUUGAUCUUAUUGAUGAC	CUCCAAAGUGAGAUCAAUUGGUGU	Cleavage
sly-miR7987-3p	Solyc08g013700.1.1	3.0	-1.0	1	24	705	728	ACACUAGUUGAUCUUAUUGAUGAC	UAAUCUGAUGAAAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc11g068570.1.1	2.5	-1.0	1	24	60	83	ACACUAGCUGAUGCUAUUGAUGAC	UUUCCAAAUAGCAUCAGCUGGUGA	Cleavage
sly-miR7987-5p	Solyc05g056570.3.1	2.5	-1.0	1	24	5431	5454	ACACUAGCUGAUGCUAUUGAUGAC	CUAAGCAAUGGCAUAAGUUAGUGU	Translation
sly-miR7987-5p	Solyc05g007330.2.1	3.0	-1.0	1	24	287	310	ACACUAGCUGAUGCUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc12g062737.1.1	3.0	-1.0	1	24	167	190	ACACUAGCUGAUGCUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc12g062737.1.1	3.0	-1.0	1	24	287	310	ACACUAGCUGAUGCUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc07g043207.1.1	3.0	-1.0	1	24	141	164	ACACUAGCUGAUGCUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc07g041260.2.1	3.0	-1.0	1	24	72	95	ACACUAGCUGAUGCUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc07g041260.2.1	3.0	-1.0	1	24	192	215	ACACUAGCUGAUGCUAUUGAUGAC	GUCAUCAAUAGGAUCAACUAGUGU	Cleavage
sly-miR7987-5p	Solyc11g030770.1.1	3.0	-1.0	1	24	141	164	ACACUAGCUGAUGCUAUUGAUGAC	CAAAUGGAAAGCAUCAGUUAGUGU	Cleavage
sly-miR7987-5p	Solyc07g006390.2.1	3.0	-1.0	1	24	403	426	ACACUAGCUGAUGCUAUUGAUGAC	UUCUAUAAUAGCAGCAGCUAGUGA	Translation
sly-miR7987-5p	Solyc02g032840.1.1	3.0	-1.0	1	24	69	92	ACACUAGCUGAUGCUAUUGAUGAC	UAAAGCAGUGGCAUUGGCUAGUGC	Cleavage
sly-miR7990a-1	Solyc09g030370.3.1	2.0	-1.0	1	24	1664	1687	UUCAAAUGAUCGUAACUUUGGCCU	AACCCAAAGUUAUGUUCAUUUGAA	Translation
sly-miR7990a-1	Solyc04g056550.1.1	2.5	-1.0	1	24	465	488	UUCAAAUGAUCGUAACUUUGGCCU	UUUCAAAAUUUGCGAUCGUUUGAG	Cleavage
sly-miR7990a-1	Solyc01g059990.3.1	3.0	-1.0	1	24	1008	1031	UUCAAAUGAUCGUAACUUUGGCCU	AGAUCAAGGUUCCGAUUGUUUGAA	Cleavage
sly-miR7990a-1	Solyc11g010690.2.1	3.0	-1.0	1	24	1600	1623	UUCAAAUGAUCGUAACUUUGGCCU	CUGUUAGUGUUAUGAUCAUUUGGG	Cleavage
sly-miR7990a-1	Solyc12g056280.2.1	3.0	-1.0	1	24	1043	1066	UUCAAAUGAUCGUAACUUUGGCCU	UUGUAAAACUUAUGAUUAUUUGAU	Cleavage
sly-miR7990a-1	Solyc08g081990.3.1	3.0	-1.0	1	24	2878	2901	UUCAAAUGAUCGUAACUUUGGCCU	CAGUGGAAGUGACGAUCAUUUGGU	Cleavage
sly-miR7990a-1	Solyc11g011060.2.1	3.0	-1.0	1	24	7192	7215	UUCAAAUGAUCGUAACUUUGGCCU	GAUGAAGGGUUACGGUCAUUGGAA	Cleavage
sly-miR7990a-1	Solyc12g036380.1.1	3.0	-1.0	1	24	212	234	UUCAAAUGAUCGUAACUUUGGCCU	UGAAAAAAGUUACGA-CAUUUGAA	Cleavage
sly-miR7990a-1	Solyc12g006480.2.1	3.0	-1.0	1	24	550	573	UUCAAAUGAUCGUAACUUUGGCCU	GAAAGUAAUUUACGAUUGUUUGAA	Cleavage
sly-miR7990a-1	Solyc02g078340.3.1	3.0	-1.0	1	24	246	269	UUCAAAUGAUCGUAACUUUGGCCU	AUCGAAAACUUACGAUCUUUUGGA	Cleavage
sly-miR7990a-1	Solyc06g050820.2.1	3.0	-1.0	1	24	1279	1302	UUCAAAUGAUCGUAACUUUGGCCU	AGAGAAAACUUAUGAUCACUUGAA	Cleavage
sly-miR7990a-2	Solyc09g030370.3.1	2.0	-1.0	1	24	1664	1687	UUCAAAUGAUCGUAACUUUGGCCU	AACCCAAAGUUAUGUUCAUUUGAA	Translation
sly-miR7990a-2	Solyc04g056550.1.1	2.5	-1.0	1	24	465	488	UUCAAAUGAUCGUAACUUUGGCCU	UUUCAAAAUUUGCGAUCGUUUGAG	Cleavage
sly-miR7990a-2	Solyc01g059990.3.1	3.0	-1.0	1	24	1008	1031	UUCAAAUGAUCGUAACUUUGGCCU	AGAUCAAGGUUCCGAUUGUUUGAA	Cleavage
sly-miR7990a-2	Solyc11g010690.2.1	3.0	-1.0	1	24	1600	1623	UUCAAAUGAUCGUAACUUUGGCCU	CUGUUAGUGUUAUGAUCAUUUGGG	Cleavage
sly-miR7990a-2	Solyc12g056280.2.1	3.0	-1.0	1	24	1043	1066	UUCAAAUGAUCGUAACUUUGGCCU	UUGUAAAACUUAUGAUUAUUUGAU	Cleavage
sly-miR7990a-2	Solyc08g081990.3.1	3.0	-1.0	1	24	2878	2901	UUCAAAUGAUCGUAACUUUGGCCU	CAGUGGAAGUGACGAUCAUUUGGU	Cleavage
sly-miR7990a-2	Solyc11g011060.2.1	3.0	-1.0	1	24	7192	7215	UUCAAAUGAUCGUAACUUUGGCCU	GAUGAAGGGUUACGGUCAUUGGAA	Cleavage
sly-miR7990a-2	Solyc12g036380.1.1	3.0	-1.0	1	24	212	234	UUCAAAUGAUCGUAACUUUGGCCU	UGAAAAAAGUUACGA-CAUUUGAA	Cleavage
sly-miR7990a-2	Solyc12g006480.2.1	3.0	-1.0	1	24	550	573	UUCAAAUGAUCGUAACUUUGGCCU	GAAAGUAAUUUACGAUUGUUUGAA	Cleavage
sly-miR7990a-2	Solyc02g078340.3.1	3.0	-1.0	1	24	246	269	UUCAAAUGAUCGUAACUUUGGCCU	AUCGAAAACUUACGAUCUUUUGGA	Cleavage
sly-miR7990a-2	Solyc06g050820.2.1	3.0	-1.0	1	24	1279	1302	UUCAAAUGAUCGUAACUUUGGCCU	AGAGAAAACUUAUGAUCACUUGAA	Cleavage

sly-miR7990a-3	Solyc09g030370.3.1	2.0	-1.0	1	24	1664	1687	UUCAAAUGAUCGUAACUUUUGCCU	AACCCAAAGUUAUGUUCAUUUGAA	Translation
sly-miR7990a-3	Solyc04g056550.1.1	2.5	-1.0	1	24	465	488	UUCAAAUGAUCGUAACUUUUGCCU	UUUCAAAAUUUGCGAUCGUUUGAG	Cleavage
sly-miR7990a-3	Solyc12g056280.2.1	3.0	-1.0	1	24	1043	1066	UUCAAAUGAUCGUAACUUUUGCCU	UUGUAAAACUUAUGAUUAUUUGAU	Cleavage
sly-miR7990a-3	Solyc08g081990.3.1	3.0	-1.0	1	24	2878	2901	UUCAAAUGAUCGUAACUUUUGCCU	CAGUGGAAGUGACGAUCAUUUGGU	Cleavage
sly-miR7990a-3	Solyc11g011060.2.1	3.0	-1.0	1	24	7192	7215	UUCAAAUGAUCGUAACUUUUGCCU	GAUGAAGGGUUACGGUCAUUGGAA	Cleavage
sly-miR7990a-3	Solyc12g036380.1.1	3.0	-1.0	1	24	212	234	UUCAAAUGAUCGUAACUUUUGCCU	UGAAAAAAGUUACGA-CAUUUGAA	Cleavage
sly-miR7990a-3	Solyc06g050820.2.1	3.0	-1.0	1	24	1279	1302	UUCAAAUGAUCGUAACUUUUGCCU	AGAGAAAACUUAUGAUCACUUGAA	Cleavage
sly-miR7990a-3	Solyc09g092410.3.1	3.0	-1.0	1	24	331	354	UUCAAAUGAUCGUAACUUUUGCCU	AAACAAAAGCAACGAUUAUUUGGA	Cleavage
sly-miR7990a-3	Solyc01g059990.3.1	3.0	-1.0	1	24	1008	1031	UUCAAAUGAUCGUAACUUUUGCCU	AGAUCAAGGUUCCGAUUGUUUGAA	Cleavage
sly-miR7990a-3	Solyc02g078340.3.1	3.0	-1.0	1	24	246	269	UUCAAAUGAUCGUAACUUUUGCCU	AUCGAAAACUUACGAUCUUUUGGA	Cleavage
sly-miR7990a-3	Solyc06g072520.2.1	3.0	-1.0	1	24	1608	1631	UUCAAAUGAUCGUAACUUUUGCCU	AAAUAAAAUUAAUGAUUAUUUGAA	Cleavage
sly-miR7990a-3	Solyc11g010690.2.1	3.0	-1.0	1	24	1600	1623	UUCAAAUGAUCGUAACUUUUGCCU	CUGUUAGUGUUAUGAUCAUUUGGG	Cleavage
sly-miR7990a-3	Solyc09g066460.3.1	3.0	-1.0	1	24	1181	1204	UUCAAAUGAUCGUAACUUUUGCCU	GCUUGAUAGAUACGGUCAUUUGAG	Cleavage
sly-miR7992-3p	Solyc03g046450.3.1	0.0	-1.0	1	23	5083	5105	UGUCUAGAUGUGCACUCCAAAGU	GCCAUGGAGUGCACAUCUAGACA	Cleavage
sly-miR7992-3p	Solyc02g089390.2.1	2.5	-1.0	1	23	5536	5558	UGUCUAGAUGUGCACUCCAAAGU	GCUAUGGAAUGCACAUCAAGACA	Cleavage
sly-miR7992-3p	Solyc04g056590.3.1	3.0	-1.0	1	23	1083	1105	UGUCUAGAUGUGCACUCCAAAGU	GCAUUUGGGUGCUCAUCUAGACA	Translation
sly-miR7992-3p	Solyc05g055800.3.1	3.0	-1.0	1	23	1695	1717	UGUCUAGAUGUGCACUCCAAAGU	UCAUUUGGGUGCUCAUCUAGACA	Translation
sly-miR7992-3p	Solyc02g030120.2.1	3.0	-1.0	1	23	901	923	UGUCUAGAUGUGCACUCCAAAGU	GACAUGAAGAGCACAUCUGGAUA	Cleavage
sly-miR7993a	Solyc08g078520.3.1	1.5	-1.0	1	24	1079	1102	AUAUUUUAUGUUGUUAACUUAACU	UAUAAGGUUGACAACAUAGAAUAU	Cleavage
sly-miR7993a	Solyc04g078600.3.1	2.0	-1.0	1	24	5140	5163	AUAUUUUAUGUUGUUAACUUAACU	UUGUUGGUUAACAACAUAAAGUAG	Cleavage
sly-miR7993a	Solyc05g010240.3.1	2.0	-1.0	1	24	2179	2202	AUAUUUUAUGUUGUUAACUUAACU	UUGUCAGUUGAUGACAUGAAAUAU	Cleavage
sly-miR7993a	Solyc09g098190.3.1	2.5	-1.0	1	24	2120	2143	AUAUUUUAUGUUGUUAACUUAACU	GCGGAAGAUAACAAUAUGAAGUAU	Cleavage
sly-miR7993a	Solyc05g005200.3.1	2.5	-1.0	1	24	213	236	AUAUUUUAUGUUGUUAACUUAACU	ACGGCAGUUAGCAACUUGAAAUAU	Cleavage
sly-miR7993a	Solyc01g107370.3.1	2.5	-1.0	1	24	1998	2021	AUAUUUUAUGUUGUUAACUUAACU	AAAUCAAUUAACAACAUAAGAUAG	Cleavage
sly-miR7993a	Solyc04g007630.2.1	2.5	-1.0	1	24	22	45	AUAUUUUAUGUUGUUAACUUAACU	ACCACAAUUAACAACUUAAAAUAU	Cleavage
sly-miR7993a	Solyc01g057460.3.1	2.5	-1.0	1	24	93	116	AUAUUUUAUGUUGUUAACUUAACU	AUAAUAGUUUACAACUUAAAAUAU	Cleavage
sly-miR7993a	Solyc06g082260.3.1	3.0	-1.0	1	24	3517	3540	AUAUUUUAUGUUGUUAACUUAACU	AGAUAUGUUAACAGCAUCAAAUAU	Cleavage
sly-miR7993a	Solyc02g086690.3.1	3.0	-1.0	1	24	1199	1222	AUAUUUUAUGUUGUUAACUUAACU	AAUUGAGCUGAUAAUGUAAAAUAU	Cleavage
sly-miR7993a	Solyc06g071840.2.1	3.0	-1.0	1	24	734	757	AUAUUUUAUGUUGUUAACUUAACU	AAAUAAGUUUGCAACAUAAAGUAA	Cleavage
sly-miR7993a	Solyc02g089650.3.1	3.0	-1.0	1	24	1198	1221	AUAUUUUAUGUUGUUAACUUAACU	UCAUAAGUAAACAUUAUAAAAUAU	Translation
sly-miR7993a	Solyc04g011350.3.1	3.0	-1.0	1	24	3342	3365	AUAUUUUAUGUUGUUAACUUAACU	GGUAACGUAGACGACAUAAAAUAU	Cleavage
sly-miR7993a	Solyc04g080300.3.1	3.0	-1.0	1	24	753	776	AUAUUUUAUGUUGUUAACUUAACU	CUUGAAGUUAAUGGUAUAAGAUGU	Cleavage
sly-miR7993a	Solyc01g099970.3.1	3.0	-1.0	1	24	2824	2847	AUAUUUUAUGUUGUUAACUUAACU	UCUAAAGUUAACGGCAGAGAAUAU	Cleavage
sly-miR7993a	Solyc01g090920.3.1	3.0	-1.0	1	24	1136	1159	AUAUUUUAUGUUGUUAACUUAACU	CAAGAAGUUGACAGCGUGAAAUAG	Cleavage
sly-miR7993a	Solyc10g055460.2.1	3.0	-1.0	1	24	1276	1299	AUAUUUUAUGUUGUUAACUUAACU	GCAAAAGUUAAUAGCAUGAUAUAU	Cleavage
sly-miR7993a	Solyc03g006120.3.1	3.0	-1.0	1	24	75	98	AUAUUUUAUGUUGUUAACUUAACU	UUUUCAAUUAAUAAAAUAAAAUAU	Translation
sly-miR7993a	Solyc06g054590.3.1	3.0	-1.0	1	24	869	892	AUAUUUUAUGUUGUUAACUUAACU	CCCUUGGUUAACAACAUAACAUAC	Cleavage
sly-miR7993a	Solyc02g021230.3.1	3.0	-1.0	1	24	837	860	AUAUUUUAUGUUGUUAACUUAACU	GAUGUUCUUAACAAUAUAAAGUAU	Cleavage
sly-miR7993a	Solyc02g068830.2.1	3.0	-1.0	1	24	1666	1689	AUAUUUUAUGUUGUUAACUUAACU	GGAAAAGUUACCAGUAUGAGAUAU	Cleavage
sly-miR7993a	Solyc01g065560.3.1	3.0	-1.0	1	24	4074	4097	AUAUUUUAUGUUGUUAACUUAACU	UGACAAGCUAGUAGCAUAAAGUAU	Cleavage
sly-miR7993a	Solyc06g048670.3.1	3.0	-1.0	1	24	1192	1215	AUAUUUUAUGUUGUUAACUUAACU	UUCAUUGUUAACAAUACAAAAUAU	Cleavage
sly-miR7997a	Solyc01g044480.3.1	1.5	-1.0	1	21	1230	1250	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
sly-miR7997a	Solyc06g068760.3.1	1.5	-1.0	1	21	4268	4288	AUGCUGCUCGGACUCUUCAAA	AUUGAAGAGUCCGAGCAACAU	Cleavage
sly-miR7997a	Solyc02g069450.3.1	2.0	-1.0	1	21	1097	1117	AUGCUGCUCGGACUCUUCAAA	UUGGAGGAGUCUGAGCAGCAU	Cleavage
sly-miR7997a	Solyc04g078590.3.1	2.0	-1.0	1	21	2526	2546	AUGCUGCUCGGACUCUUCAAA	CAAGAAGAGUUUGAGCAGCAU	Cleavage
sly-miR7997a	Solyc07g007460.2.1	2.5	-1.0	1	21	957	977	AUGCUGCUCGGACUCUUCAAA	GAUGAAGAGUCCGAGUGUCAU	Cleavage
sly-miR7997a	Solyc02g087770.3.1	3.0	-1.0	1	21	2134	2154	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCUGAGCAUCAG	Cleavage
sly-miR7997a	Solyc12g099360.2.1	3.0	-1.0	1	21	2018	2038	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCUGAGCAACAG	Cleavage
sly-miR7997a	Solyc10g006120.2.1	3.0	-1.0	1	21	1762	1782	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCUAGCAACAU	Cleavage
sly-miR7997a	Solyc12g014490.2.1	3.0	-1.0	1	21	785	805	AUGCUGCUCGGACUCUUCAAA	UUUGGAGAGUUGGAGCAGUAU	Translation

sly-miR7997a	Solyc03g005630.3.1	3.0	-1.0	1	21	3297	3317	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCAGAGCAACAU	Translation
sly-miR7997a	Solyc05g007290.2.1	3.0	-1.0	1	21	1397	1417	AUGCUGCUCGGACUCUUCAAA	UUUGGAGGGUUCGAGCAACAU	Cleavage
sly-miR7997a	Solyc08g008480.3.1	3.0	-1.0	1	21	725	745	AUGCUGCUCGGACUCUUCAAA	UUUGAAAAGUUCGAGCAACAU	Cleavage
sly-miR7997a	Solyc10g044780.2.1	3.0	-1.0	1	21	714	734	AUGCUGCUCGGACUCUUCAAA	ACUGAAGAGUUUGUGCAGUAU	Cleavage
sly-miR7997a	Solyc04g058200.3.1	3.0	-1.0	1	21	2000	2020	AUGCUGCUCGGACUCUUCAAA	AGUUGAGAGUUUGGGCAGCAU	Cleavage
sly-miR8001a	Solyc01g108410.2.1	2.0	-1.0	1	24	3572	3595	UCCUGGGGAUUAGUAUGAAAAUUC	GCAACUUCAUACUAAUCUACAGGA	Cleavage
sly-miR8001a	Solyc12g017310.2.1	3.0	-1.0	1	24	663	686	UCCUGGGGAUUAGUAUGAAAAUUC	UGAUCUUCAGGUUGAUCCUCAGGA	Cleavage
sly-miR8001a	Solyc08g076040.2.1	3.0	-1.0	1	24	2290	2313	UCCUGGGGAUUAGUAUGAAAAUUC	GAAAAAUCAUACUAAUCUUUGGGA	Cleavage
sly-miR8001a	Solyc05g009540.3.1	3.0	-1.0	1	24	2569	2592	UCCUGGGGAUUAGUAUGAAAAUUC	GUCUCUUCAUAUGAAUCUCCGGGA	Cleavage
sly-miR8001a	Solyc08g079450.3.1	3.0	-1.0	1	24	652	675	UCCUGGGGAUUAGUAUGAAAAUUC	UGGAAUUCGUGAUAGUCCCCAGGA	Cleavage
sly-miR8001b-1-3p	Solyc03g006790.2.1	2.5	-1.0	1	22	353	374	ACUUUUAUACUAAUUCCCAGGA	AUUAGGGGAUUGGUAUGAAAGU	Cleavage
sly-miR8001b-1-3p	Solyc11g006220.2.1	3.0	-1.0	1	22	1276	1297	ACUUUUAUACUAAUUCCCAGGA	UUGUGGGAAUUAGUAAAAAGGA	Cleavage
sly-miR8001b-1-3p	Solyc03g031530.3.1	3.0	-1.0	1	22	560	581	ACUUUUAUACUAAUUCCCAGGA	UAUUGGGAGUUAGUAUUGGAGU	Cleavage
sly-miR8001b-1-3p	Solyc12g042460.2.1	3.0	-1.0	1	22	1068	1089	ACUUUUAUACUAAUUCCCAGGA	UGCUUGGAAUUGGUACAAAAGU	Cleavage
sly-miR8001b-1-5p	Solyc04g006990.3.1	1.0	-1.0	1	24	1255	1278	AUGGGGAUUAGUAUGAAAAUUUGC	GUAAAUUUUUAUACUAAUCUCCAU	Cleavage
sly-miR8001b-1-5p	Solyc04g083010.3.1	1.5	-1.0	1	24	1465	1488	AUGGGGAUUAGUAUGAAAAUUUGC	GGUUAUUUUCAUGCUGAUCCUCAU	Cleavage
sly-miR8001b-1-5p	Solyc03g110960.3.1	2.0	-1.0	1	24	1130	1153	AUGGGGAUUAGUAUGAAAAUUUGC	AACUAUUUACAUGCUAAUUCCCAU	Cleavage
sly-miR8001b-1-5p	Solyc02g084810.3.1	2.5	-1.0	1	24	1732	1755	AUGGGGAUUAGUAUGAAAAUUUGC	AGCAAUUUUGGUAUUAAUUCCCAU	Cleavage
sly-miR8001b-1-5p	Solyc03g031780.3.1	2.5	-1.0	1	24	329	352	AUGGGGAUUAGUAUGAAAAUUUGC	UGUUGUUUUCGUACUAAUUCCAAU	Cleavage
sly-miR8001b-1-5p	Solyc09g090680.3.1	2.5	-1.0	1	24	1153	1176	AUGGGGAUUAGUAUGAAAAUUUGC	CAUCAUCUUCAUACUGGUCUCCAU	Cleavage
sly-miR8001b-1-5p	Solyc02g031930.2.1	2.5	-1.0	1	24	112	135	AUGGGGAUUAGUAUGAAAAUUUGC	CUCAUUUUUCAUAAUAAUCCUUAU	Translation
sly-miR8001b-1-5p	Solyc03g117550.1.1	2.5	-1.0	1	24	139	162	AUGGGGAUUAGUAUGAAAAUUUGC	CAUCGUUCUCGUACUAAUCCUUAU	Cleavage
sly-miR8001b-1-5p	Solyc10g011960.2.1	2.5	-1.0	1	24	280	303	AUGGGGAUUAGUAUGAAAAUUUGC	AUUUUUCUUCAUAUUAAUUCUCAU	Cleavage
sly-miR8001b-1-5p	Solyc08g068920.3.1	2.5	-1.0	1	24	427	450	AUGGGGAUUAGUAUGAAAAUUUGC	GGGUUUUUCCAUGCUGAUCCUCAU	Cleavage
sly-miR8001b-1-5p	Solyc10g074960.2.1	3.0	-1.0	1	24	1383	1406	AUGGGGAUUAGUAUGAAAAUUUGC	UGCAAUUUUUGUGCUGAUUUCCAU	Cleavage
sly-miR8001b-1-5p	Solyc10g081760.2.1	3.0	-1.0	1	24	973	996	AUGGGGAUUAGUAUGAAAAUUUGC	CUUGAUUUUGAUACUGAUCCACAU	Cleavage
sly-miR8001b-1-5p	Solyc10g007860.3.1	3.0	-1.0	1	24	1933	1956	AUGGGGAUUAGUAUGAAAAUUUGC	CCUAUUUUUCAUAUUACUCCUUAU	Cleavage
sly-miR8001b-2-5p	Solyc04g006990.3.1	1.0	-1.0	1	24	1255	1278	AUGGGGAUUAGUAUGAAAAUUUGC	GUAAAUUUUUAUACUAAUCUCCAU	Cleavage
sly-miR8001b-2-5p	Solyc04g083010.3.1	1.5	-1.0	1	24	1465	1488	AUGGGGAUUAGUAUGAAAAUUUGC	GGUUAUUUUCAUGCUGAUCCUCAU	Cleavage
sly-miR8001b-2-5p	Solyc03g110960.3.1	2.0	-1.0	1	24	1130	1153	AUGGGGAUUAGUAUGAAAAUUUGC	AACUAUUUACAUGCUAAUUCCCAU	Cleavage
sly-miR8001b-2-5p	Solyc02g084810.3.1	2.5	-1.0	1	24	1732	1755	AUGGGGAUUAGUAUGAAAAUUUGC	AGCAAUUUUGGUAUUAAUUCCCAU	Cleavage

sly-miR8001b-2-5p	Solyc03g031780.3.1	2.5	-1.0	1	24	329	352	AUGGGGAUUAGUAUGAAAAUUUGC	UGUUGUUUUCGUACUAAUUCCAAU	Cleavage
sly-miR8001b-2-5p	Solyc09g090680.3.1	2.5	-1.0	1	24	1153	1176	AUGGGGAUUAGUAUGAAAAUUUGC	CAUCAUCUUCAUACUGGUCUCCAU	Cleavage
sly-miR8001b-2-5p	Solyc02g031930.2.1	2.5	-1.0	1	24	112	135	AUGGGGAUUAGUAUGAAAAUUUGC	CUCAUUUUUCAUAAUAAUCCUUAU	Translation
sly-miR8001b-2-5p	Solyc03g117550.1.1	2.5	-1.0	1	24	139	162	AUGGGGAUUAGUAUGAAAAUUUGC	CAUCGUUCUCGUACUAAUCCUUAU	Cleavage
sly-miR8001b-2-5p	Solyc10g011960.2.1	2.5	-1.0	1	24	280	303	AUGGGGAUUAGUAUGAAAAUUUGC	AUUUUUCUUCAUAUUAAUUCUCAU	Cleavage
sly-miR8001b-2-5p	Solyc08g068920.3.1	2.5	-1.0	1	24	427	450	AUGGGGAUUAGUAUGAAAAUUUGC	GGGUUUUUCCAUGCUGAUCCUCAU	Cleavage
sly-miR8001b-2-5p	Solyc10g074960.2.1	3.0	-1.0	1	24	1383	1406	AUGGGGAUUAGUAUGAAAAUUUGC	UGCAAUUUUUGUGCUGAUUUCCAU	Cleavage
sly-miR8001b-2-5p	Solyc10g081760.2.1	3.0	-1.0	1	24	973	996	AUGGGGAUUAGUAUGAAAAUUUGC	CUUGAUUUUGAUACUGAUCCACAU	Cleavage
sly-miR8001b-2-5p	Solyc10g007860.3.1	3.0	-1.0	1	24	1933	1956	AUGGGGAUUAGUAUGAAAAUUUGC	CCUAUUUUUCAUAUUACUCCUUAU	Cleavage
sly-miR8006-1-3p	Solyc09g011210.3.1	3.0	-1.0	1	23	782	804	UGCCCUGCCGUCCAAAAACUAGA	AAUUAUUUCUGGAUGGCAGGGUA	Cleavage
sly-miR8006-1-5p	Solyc11g008960.2.1	1.5	-1.0	1	24	1962	1985	UAGUUUUUGGAUUACAGAGACACC	AUGAACACUGUAAUCCAAAAAUUA	Cleavage
sly-miR8006-1-5p	Solyc01g057760.3.1	2.0	-1.0	1	24	249	272	UAGUUUUUGGAUUACAGAGACACC	UGUACUUCUGGAAUCCAGAAACUA	Cleavage
sly-miR8006-1-5p	Solyc03g078520.3.1	2.0	-1.0	1	24	2021	2044	UAGUUUUUGGAUUACAGAGACACC	AUGAACACUGUAAUCCAAAGAUUA	Cleavage
sly-miR8006-1-5p	Solyc02g085810.3.1	2.5	-1.0	1	24	5658	5681	UAGUUUUUGGAUUACAGAGACACC	CUUGGAUCUGUAAUCCAGAAACUC	Cleavage
sly-miR8006-1-5p	Solyc03g080190.3.1	2.5	-1.0	1	24	40	63	UAGUUUUUGGAUUACAGAGACACC	CUUUCAUUUGUAAUUCAAAAAUUA	Cleavage
sly-miR8006-1-5p	Solyc09g075330.3.1	2.5	-1.0	1	24	1776	1799	UAGUUUUUGGAUUACAGAGACACC	AACUGUUUUGUAGUCCAAAAGUUA	Cleavage
sly-miR8006-1-5p	Solyc07g045540.3.1	2.5	-1.0	1	24	741	764	UAGUUUUUGGAUUACAGAGACACC	UGAGCCUCUUUGGUCCAGAAACUA	Cleavage
sly-miR8006-1-5p	Solyc04g082580.3.1	2.5	-1.0	1	24	4939	4962	UAGUUUUUGGAUUACAGAGACACC	AGUUGCUUAGUAGUCUAAAAACUA	Cleavage
sly-miR8006-1-5p	Solyc11g020850.2.1	2.5	-1.0	1	24	1683	1706	UAGUUUUUGGAUUACAGAGACACC	AUGCACUCUGAAAUCCAAAGAUUG	Cleavage
sly-miR8006-1-5p	Solyc02g089810.3.1	2.5	-1.0	1	24	1932	1955	UAGUUUUUGGAUUACAGAGACACC	AUGAACUUGGUGAUCCAGAAACUA	Cleavage
sly-miR8006-1-5p	Solyc04g077450.3.1	3.0	-1.0	1	24	877	900	UAGUUUUUGGAUUACAGAGACACC	UUUCUCUUUGUAAUCUAUAAGCUA	Cleavage
sly-miR8006-1-5p	Solyc05g050020.3.1	3.0	-1.0	1	24	1849	1872	UAGUUUUUGGAUUACAGAGACACC	CAAAUUUCUGCAAUCCAAAAAUUC	Cleavage
sly-miR8006-1-5p	Solyc03g082660.3.1	3.0	-1.0	1	24	3231	3254	UAGUUUUUGGAUUACAGAGACACC	AUUAUGUUUGUAAUGCAAAAACUA	Translation
sly-miR8006-1-5p	Solyc05g054010.3.1	3.0	-1.0	1	24	3103	3126	UAGUUUUUGGAUUACAGAGACACC	CAAAUCUCUGCAAUCUAGAAACUC	Cleavage
sly-miR8006-1-5p	Solyc12g042730.1.1	3.0	-1.0	1	24	112	135	UAGUUUUUGGAUUACAGAGACACC	UUCCGUUCUGUGGUUCAAAAACUC	Cleavage
sly-miR8006-1-5p	Solyc12g057130.2.1	3.0	-1.0	1	24	662	685	UAGUUUUUGGAUUACAGAGACACC	UUGUUCUUUUUAAUCCGGAAAUUA	Cleavage
sly-miR8006-1-5p	Solyc03g118800.3.1	3.0	-1.0	1	24	62	85	UAGUUUUUGGAUUACAGAGACACC	UACAAUUUUGUGAUUCAGAAACUG	Cleavage
sly-miR8006-1-5p	Solyc04g064570.3.1	3.0	-1.0	1	24	2571	2594	UAGUUUUUGGAUUACAGAGACACC	CUUUGCUUUGUAGUCUAACAACUA	Cleavage
sly-miR8006-1-5p	Solyc01g101020.3.1	3.0	-1.0	1	24	2037	2060	UAGUUUUUGGAUUACAGAGACACC	AAGCACUUUGUAGUCCCAAAGCUA	Cleavage
sly-miR8006-2-5p	Solyc12g044670.1.1	2.5	-1.0	1	24	43	66	UAGUUUUUGAACGACAGGGGCACC	CAACCGCCUGUCGUCCAAAAACUA	Translation
sly-miR8006-2-5p	Solyc08g077170.3.1	2.5	-1.0	1	24	163	186	UAGUUUUUGAACGACAGGGGCACC	UGAAUACCUUUCGUUCAAAAAUUA	Cleavage
sly-miR8006-2-5p	Solyc05g055070.3.1	2.5	-1.0	1	24	371	394	UAGUUUUUGAACGACAGGGGCACC	UUCUACCCUUUUGUUCAAAGAUUA	Cleavage
sly-miR8006-2-5p	Solyc06g051830.2.1	2.5	-1.0	1	24	1228	1250	UAGUUUUUGAACGACAGGGGCACC	AAGUUCUCUG-CGUUCAAAAACUA	Cleavage
sly-miR8006-2-5p	Solyc11g066760.2.1	3.0	-1.0	1	24	1204	1227	UAGUUUUUGAACGACAGGGGCACC	CUAGCUCCUGAUGUUCAAAAGUUA	Cleavage
sly-miR8006-2-5p	Solyc10g075040.2.1	3.0	-1.0	1	24	3161	3184	UAGUUUUUGAACGACAGGGGCACC	AGCUCCCUUGUUGCUCAGAAACUA	Translation
sly-miR8006-2-5p	Solyc08g016500.3.1	3.0	-1.0	1	24	367	390	UAGUUUUUGAACGACAGGGGCACC	GUUACUUUUUUUGUUCAAAAACUA	Cleavage
sly-miR8006-2-5p	Solyc12g035710.2.1	3.0	-1.0	1	24	513	536	UAGUUUUUGAACGACAGGGGCACC	AUCCUUCCUGUUGUUCAGAAACAA	Cleavage
sly-miR8006-2-5p	Solyc04g072265.1.1	3.0	-1.0	1	24	2046	2069	UAGUUUUUGAACGACAGGGGCACC	AAUAGGCCUGUUGUUCAGGAACUG	Cleavage
sly-miR8006-2-5p	Solyc02g067060.3.1	3.0	-1.0	1	24	2790	2813	UAGUUUUUGAACGACAGGGGCACC	UAUCUUCCUGAUGUUCAGAAAUUA	Cleavage
sly-miR8006-2-5p	Solyc02g061820.3.1	3.0	-1.0	1	24	308	331	UAGUUUUUGAACGACAGGGGCACC	GACGACCCUUUUGUUCAAAAACCA	Cleavage
sly-miR8007a-5p	Solyc04g082810.3.1	2.0	-1.0	1	24	9036	9059	AUGUGGCACUUUUCGGAUUUCGAG	UUAUUAAUGUGAAAAGUGCCAUAU	Cleavage
sly-miR8007a-5p	Solyc08g076400.3.1	3.0	-1.0	1	24	408	431	AUGUGGCACUUUUCGGAUUUCGAG	CUCGAAAUUUGAACAGUGCCACGU	Translation

sly-miR8007a-5p	Solyc02g077670.3.1	3.0	-1.0	1	24	17	40	AUGUGGCACUUUUCGGAUUUCGAG	ACUGAAGUCCGGAAAGUUCUACAU	Cleavage
sly-miR8007a-5p	Solyc03g095970.3.1	3.0	-1.0	1	24	723	746	AUGUGGCACUUUUCGGAUUUCGAG	AUGCAAAUUUGAAAGGUGUUACGU	Cleavage
sly-miR8007a-5p	Solyc01g098600.3.1	3.0	-1.0	1	24	863	886	AUGUGGCACUUUUCGGAUUUCGAG	AAAAGAAUCAGAGAAGUGCAACAU	Cleavage
sly-miR8007b-5p	Solyc07g006035.1.1	2.0	-1.0	1	24	4823	4846	AUGUGACACUUUUUGGAUUUCGAG	CUGGUGAUCUAGGAAGUGUCACAU	Cleavage
sly-miR8007b-5p	Solyc09g092450.3.1	2.5	-1.0	1	24	980	1003	AUGUGACACUUUUUGGAUUUCGAG	CUGGUAAUCCAAAAGGUGUCAUGC	Cleavage
sly-miR8007b-5p	Solyc04g071490.3.1	2.5	-1.0	1	24	282	305	AUGUGACACUUUUUGGAUUUCGAG	UACUAAACUUAAAAAGUGUUACAU	Cleavage
sly-miR8007b-5p	Solyc07g045170.3.1	2.5	-1.0	1	24	4725	4748	AUGUGACACUUUUUGGAUUUCGAG	AAAUGAAUCUAAAAAGUGUCGUAA	Cleavage
sly-miR8007b-5p	Solyc06g071490.2.1	2.5	-1.0	1	24	75	98	AUGUGACACUUUUUGGAUUUCGAG	GUCCCAAUUCAAGAAGUGUCACUU	Cleavage
sly-miR8007b-5p	Solyc02g085870.3.1	2.5	-1.0	1	24	353	376	AUGUGACACUUUUUGGAUUUCGAG	AAGAUAAUCCAAAAAGUGUUGAAU	Cleavage
sly-miR8007b-5p	Solyc02g088290.3.1	2.5	-1.0	1	24	1673	1696	AUGUGACACUUUUUGGAUUUCGAG	AACUUGAUCCAAAAAGUGUAGCAU	Cleavage
sly-miR8007b-5p	Solyc01g056850.3.1	3.0	-1.0	1	24	1088	1111	AUGUGACACUUUUUGGAUUUCGAG	UUCUGAAUCUAAAAGGUGUUGCAC	Cleavage
sly-miR8007b-5p	Solyc02g082900.3.1	3.0	-1.0	1	24	955	978	AUGUGACACUUUUUGGAUUUCGAG	GAGGAAAUGCAAAAAGUAUCAUAU	Cleavage
sly-miR8007b-5p	Solyc10g037877.1.1	3.0	-1.0	1	24	362	385	AUGUGACACUUUUUGGAUUUCGAG	ACCCAAAUCUAAAGAGUGUCAAGU	Cleavage
sly-miR8007b-5p	Solyc01g105150.3.1	3.0	-1.0	1	24	239	262	AUGUGACACUUUUUGGAUUUCGAG	UCUGACUUCUAAGAAGUGUCACAU	Cleavage
sly-miR8007b-5p	Solyc03g095970.3.1	3.0	-1.0	1	24	723	746	AUGUGACACUUUUUGGAUUUCGAG	AUGCAAAUUUGAAAGGUGUUACGU	Cleavage
sly-miR8007b-5p	Solyc12g032933.1.1	3.0	-1.0	1	24	284	307	AUGUGACACUUUUUGGAUUUCGAG	CUGAGAAUCCAAAAACUGUUACAG	Cleavage
sly-miR8007b-5p	Solyc09g008913.1.1	3.0	-1.0	1	24	822	845	AUGUGACACUUUUUGGAUUUCGAG	UAAAAAGUUCAAAGAGCGUCACAU	Cleavage
sly-miR8007b-5p	Solyc02g079950.3.1	3.0	-1.0	1	24	1432	1455	AUGUGACACUUUUUGGAUUUCGAG	AUAAAAAUUCAAGAAAUGUUACAU	Cleavage
sly-miR8007b-5p	Solyc12g006450.2.1	3.0	-1.0	1	24	50	73	AUGUGACACUUUUUGGAUUUCGAG	UAUAAAAUUUAAACAGUGUCACGU	Translation
sly-miR8007b-5p	Solyc04g078430.2.1	3.0	-1.0	1	24	376	399	AUGUGACACUUUUUGGAUUUCGAG	UAAUGAGUCCAAAAAGUGUGACAA	Cleavage
sly-miR8007b-5p	Solyc06g008920.3.1	3.0	-1.0	1	24	754	777	AUGUGACACUUUUUGGAUUUCGAG	CGUCGAGUCCAAAGGGUGUCGUGU	Cleavage
sly-miR8008a-1	Solyc03g097675.1.1	2.5	-1.0	1	23	958	980	AUUUCCAGAAAAGCGACGGACAG	GAUCCUGUUGUUUUUCUGGAAAA	Cleavage
sly-miR8008a-1	Solyc01g014180.3.1	2.5	-1.0	1	23	152	174	AUUUCCAGAAAAGCGACGGACAG	ACAACUGUGGCUUUUUUGGAAGU	Cleavage
sly-miR8008a-1	Solyc03g122130.3.1	3.0	-1.0	1	23	1087	1109	AUUUCCAGAAAAGCGACGGACAG	UGAUCCGUCGCUUUGCUGGAAGG	Cleavage
sly-miR8008a-1	Solyc08g005493.1.1	3.0	-1.0	1	23	154	176	AUUUCCAGAAAAGCGACGGACAG	UCUAUUGUUGUUUUUCUGGAAAC	Cleavage
sly-miR8008a-1	Solyc06g068600.3.1	3.0	-1.0	1	23	2833	2855	AUUUCCAGAAAAGCGACGGACAG	CAUGCUGUUGCUCUUUUGGAAAU	Translation
sly-miR8008a-2-3p	Solyc03g032020.3.1	3.0	-1.0	1	20	806	825	AUUUACAGAAAAGCGACGGA	UCCGUUUCUUCUCUGUAAAU	Translation
sly-miR8008a-2-3p	Solyc01g058720.3.1	3.0	-1.0	1	20	579	598	AUUUACAGAAAAGCGACGGA	UUCGCCUUUUUUCUGUAAAU	Cleavage
sly-miR8008a-2-3p	Solyc06g008810.3.1	3.0	-1.0	1	20	53	72	AUUUACAGAAAAGCGACGGA	GCCGUUUUUUUUUUGUAGAU	Cleavage
sly-miR8008a-2-5p	Solyc02g036470.3.1	3.0	-1.0	1	24	3746	3769	AUUUCCAGAAAAGUGACGGACAGU	UCUCACCGUCACUUUUCUUGGAAA	Cleavage
sly-miR8008a-2-5p	Solyc03g097675.1.1	3.0	-1.0	1	24	957	980	AUUUCCAGAAAAGUGACGGACAGU	AGAUCCUGUUGUUUUUCUGGAAAA	Cleavage
sly-miR8008a-2-5p	Solyc04g073960.3.1	3.0	-1.0	1	24	826	849	AUUUCCAGAAAAGUGACGGACAGU	AGCGCCCGUUACUCUUUUGGGAAU	Translation
sly-miR8008a-2-5p	Solyc07g021630.3.1	3.0	-1.0	1	24	2228	2250	AUUUCCAGAAAAGUGACGGACAGU	UCUG-CUGUCACCUUUUUGGAAGU	Cleavage
sly-miR8008a-2-5p	Solyc01g014180.3.1	3.0	-1.0	1	24	151	174	AUUUCCAGAAAAGUGACGGACAGU	AACAACUGUGGCUUUUUUGGAAGU	Cleavage
sly-miR8008b-1-3p	Solyc06g083380.3.1	2.5	-1.0	1	20	1456	1475	CAAGGAAAGCGACAGACAUU	CGUGUCUGUCUCUUUUCUUG	Translation
sly-miR8008b-1-3p	Solyc01g098350.3.1	2.5	-1.0	1	20	3732	3750	CAAGGAAAGCGACAGACAUU	GAUGU-UGUUGCUUUCCUUG	Cleavage
sly-miR8008b-1-3p	Solyc03g112320.3.1	3.0	-1.0	1	20	1647	1666	CAAGGAAAGCGACAGACAUU	GGUGUCUGUUGUUUUCCUAG	Cleavage
sly-miR8008b-1-3p	Solyc08g075390.3.1	3.0	-1.0	1	20	2117	2136	CAAGGAAAGCGACAGACAUU	AAUGUAUGUCUCUUUUCUUG	Translation
sly-miR8008b-1-	Solyc09g064450.3.1	3.0	-1.0	1	20	2654	2673	CAAGGAAAGCGACAGACAUU	GGUUUCUGUCUCUUUCCUUG	Translation

3p										
sly-miR8008b-1-3p	Solyc01g080150.3.1	3.0	-1.0	1	20	916	935	CAAGGAAAGCGACAGACAUU	UAUGAGUGUUGCUUUCUUUG	Cleavage
sly-miR8008b-1-5p	Solyc02g032970.3.1	2.5	-1.0	1	22	108	129	AAACCCAGAAAAGCGACGGACA	UCGCCGUCUCUUCUCUGGGUUU	Translation
sly-miR8008b-1-5p	Solyc02g079580.3.1	3.0	-1.0	1	22	1311	1332	AAACCCAGAAAAGCGACGGACA	UUCCUGUCUCUUUUCUGGUUUU	Cleavage
sly-miR8008b-1-5p	Solyc02g073574.1.1	3.0	-1.0	1	22	652	673	AAACCCAGAAAAGCGACGGACA	UUCCCAUUGCUUUUAUGGGUUU	Cleavage
sly-miR8008b-1-5p	Solyc02g084450.3.1	3.0	-1.0	1	22	2179	2200	AAACCCAGAAAAGCGACGGACA	UUCCCAUUGCUUUUAUGGGUUU	Cleavage
sly-miR8008b-2-3p	Solyc02g079580.3.1	2.5	-1.0	1	23	1310	1332	AAACCCAGAAAAGCGACAGACAG	UUUCCUGUCUCUUUUCUGGUUUU	Cleavage
sly-miR8008b-2-3p	Solyc02g082590.3.1	3.0	-1.0	1	23	96	118	AAACCCAGAAAAGCGACAGACAG	UUUUCUGUCGCUUUUCUGCGAUU	Cleavage
sly-miR8008b-2-3p	Solyc02g078560.3.1	3.0	-1.0	1	23	2566	2588	AAACCCAGAAAAGCGACAGACAG	UUUCUUGUUGCUAUUUUGGGUUU	Translation
sly-miR8008b-2-3p	Solyc09g061250.3.1	3.0	-1.0	1	23	4320	4342	AAACCCAGAAAAGCGACAGACAG	CUUAUUGUGUCUUUUUUGGGUUU	Cleavage
sly-miR8008b-2-3p	Solyc02g064690.3.1	3.0	-1.0	1	23	1782	1804	AAACCCAGAAAAGCGACAGACAG	CAACUUUUCACUUUUUUGGGUUU	Cleavage
sly-miR8008b-3-3p	Solyc02g032970.3.1	2.5	-1.0	1	22	108	129	AAACCCAGAAAAGCGACGGACA	UCGCCGUCUCUUCUCUGGGUUU	Translation
sly-miR8008b-3-3p	Solyc02g079580.3.1	3.0	-1.0	1	22	1311	1332	AAACCCAGAAAAGCGACGGACA	UUCCUGUCUCUUUUCUGGUUUU	Cleavage
sly-miR8008b-3-3p	Solyc02g073574.1.1	3.0	-1.0	1	22	652	673	AAACCCAGAAAAGCGACGGACA	UUCCCAUUGCUUUUAUGGGUUU	Cleavage
sly-miR8008b-3-3p	Solyc02g084450.3.1	3.0	-1.0	1	22	2179	2200	AAACCCAGAAAAGCGACGGACA	UUCCCAUUGCUUUUAUGGGUUU	Cleavage
sly-miR8008b-3-5p	Solyc02g082590.3.1	2.5	-1.0	1	22	97	118	AAUCCCAGAAAAGCGACUGACA	UUUCUGUCGCUUUUCUGCGAUU	Cleavage
sly-miR8008b-3-5p	Solyc07g009490.3.1	2.5	-1.0	1	22	216	237	AAUCCCAGAAAAGCGACUGACA	UUAUAUUCGUUUUUUUGGGAUU	Cleavage
sly-miR8008b-3-5p	Solyc06g054110.2.1	3.0	-1.0	1	22	49	70	AAUCCCAGAAAAGCGACUGACA	CUUCAGUCACUUUGCUGGGGUU	Cleavage
sly-miR8008b-3-5p	Solyc06g054120.2.1	3.0	-1.0	1	22	778	799	AAUCCCAGAAAAGCGACUGACA	CUUCAGUCACUUUGCUGGGGUU	Cleavage
sly-miR8008b-3-5p	Solyc11g071730.2.1	3.0	-1.0	1	22	1567	1588	AAUCCCAGAAAAGCGACUGACA	GGACAGUUGCUUUUCCGGGAUC	Cleavage
sly-miR8008b-3-5p	Solyc08g077960.3.1	3.0	-1.0	1	22	180	201	AAUCCCAGAAAAGCGACUGACA	AUUCAGUGGUUUUUCUGGGACU	Cleavage
sly-miR8008b-3-5p	Solyc09g015473.1.1	3.0	-1.0	1	22	61	81	AAUCCCAGAAAAGCGACUGACA	AGGCAGUU-CUUUUUUGGGAUU	Cleavage
sly-miR8011a-1-3p	Solyc01g105150.3.1	1.0	-1.0	1	23	3342	3364	ACAAAAAGAAGCCUCACACAACU	UAUGGUGUGAGGUUUUUUUUUGU	Cleavage
sly-miR8011a-1-3p	Solyc10g079310.2.1	1.5	-1.0	1	23	1509	1531	ACAAAAAGAAGCCUCACACAACU	UAUUGUGUGAGGCUCCUUUUUGU	Cleavage
sly-miR8011a-1-3p	Solyc09g009260.3.1	2.5	-1.0	1	23	1261	1283	ACAAAAAGAAGCCUCACACAACU	UAAUGUGUAAGGCUUCUUUUUUU	Cleavage
sly-miR8011a-1-3p	Solyc09g011260.2.1	3.0	-1.0	1	23	1027	1049	ACAAAAAGAAGCCUCACACAACU	UGUUGUGUAAAGUUUCUUUUUGU	Cleavage
sly-miR8011a-1-	Solyc09g082200.2.1	3.0	-1.0	1	23	911	933	ACAAAAAGAAGCCUCACACAACU	UAUGGUGUGAGGUUUGUUUUUGG	Cleavage

3p										
sly-miR8011a-2-3p	Solyc01g094590.3.1	3.0	-1.0	1	24	1445	1468	AAUAAAAAGAAGUCUCACGCAACU	GUUUGUGUGAAACUUUUUUUUAUA	Cleavage
sly-miR8011a-2-3p	Solyc11g011080.2.1	3.0	-1.0	1	24	569	592	AAUAAAAAGAAGUCUCACGCAACU	AAUUACGUGAGACUUCUUUAUCUU	Cleavage
sly-miR8011a-2-3p	Solyc08g023493.1.1	3.0	-1.0	1	24	477	501	AAUAAAAAGAAGUCUCACGCA-ACU	AGUGUACGUGGGGUUUAUUUUUAUU	Cleavage
sly-miR8011a-2-3p	Solyc10g045623.1.1	3.0	-1.0	1	24	926	949	AAUAAAAAGAAGUCUCACGCAACU	AAAUUUGUGAGGUUUCUUGUUAUU	Cleavage
sly-miR8011a-2-3p	Solyc07g040750.2.1	3.0	-1.0	1	24	865	888	AAUAAAAAGAAGUCUCACGCAACU	CAUGGCAUGAAAUUUUUUUUUAUU	Cleavage
sly-miR8011a-2-5p	Solyc05g012560.2.1	1.0	-1.0	1	23	3	25	UUGUGUGAGGUCUCUUUUUGUUU	GGAAAAAGAGAGACCUUACACAA	Cleavage
sly-miR8011a-2-5p	Solyc03g093460.3.1	2.0	-1.0	1	23	1710	1732	UUGUGUGAGGUCUCUUUUUGUUU	AGACAAAAAGAAGCCUCACACAA	Cleavage
sly-miR8011a-2-5p	Solyc02g078050.3.1	2.0	-1.0	1	23	1553	1575	UUGUGUGAGGUCUCUUUUUGUUU	UAGGAAAAAGAGGUCUCAUAUAA	Cleavage
sly-miR8011a-2-5p	Solyc03g098560.2.1	2.0	-1.0	1	23	603	625	UUGUGUGAGGUCUCUUUUUGUUU	GGGGAAAAAGAGACUACACACAA	Cleavage
sly-miR8011a-2-5p	Solyc03g122370.3.1	2.5	-1.0	1	23	384	406	UUGUGUGAGGUCUCUUUUUGUUU	AUAUAAAGAGAGAUCUCACAAAA	Cleavage
sly-miR8011a-2-5p	Solyc11g071820.2.1	2.5	-1.0	1	23	824	846	UUGUGUGAGGUCUCUUUUUGUUU	GAAAAGAAAGAGACCUUACAAAA	Cleavage
sly-miR8011a-2-5p	Solyc06g082040.2.1	2.5	-1.0	1	23	2559	2581	UUGUGUGAGGUCUCUUUUUGUUU	UUGCAGAGGGAGACCUCGUACAA	Cleavage
sly-miR8011a-2-5p	Solyc01g105600.3.1	2.5	-1.0	1	23	711	733	UUGUGUGAGGUCUCUUUUUGUUU	AUAAAAAAAGAGGCCUUAUAUGA	Cleavage
sly-miR8011a-2-5p	Solyc05g053250.3.1	2.5	-1.0	1	23	471	493	UUGUGUGAGGUCUCUUUUUGUUU	AUCAAGAAAGAGACCACAUACAA	Cleavage
sly-miR8011a-2-5p	Solyc02g020910.3.1	3.0	-1.0	1	23	456	478	UUGUGUGAGGUCUCUUUUUGUUU	AAAUAAAUAGAGACCUCAUAAAA	Cleavage
sly-miR8011a-2-5p	Solyc10g006360.2.1	3.0	-1.0	1	23	1097	1119	UUGUGUGAGGUCUCUUUUUGUUU	UGACAGAAAGGGACCUUACAUGG	Cleavage
sly-miR8011a-2-5p	Solyc02g072100.3.1	3.0	-1.0	1	23	768	790	UUGUGUGAGGUCUCUUUUUGUUU	AGGCAGAAAUAGGCCUUGCACAA	Cleavage
sly-miR8011a-2-5p	Solyc06g082040.2.1	3.0	-1.0	1	23	1923	1945	UUGUGUGAGGUCUCUUUUUGUUU	UUGCAGAGGGAGAUCUCGUACAA	Cleavage
sly-miR8011a-2-5p	Solyc09g010460.3.1	3.0	-1.0	1	23	2677	2699	UUGUGUGAGGUCUCUUUUUGUUU	GAAAAAGAAGAGAUCUUGCGCAG	Cleavage
sly-miR8011a-2-5p	Solyc01g096920.3.1	3.0	-1.0	1	23	1257	1279	UUGUGUGAGGUCUCUUUUUGUUU	GGAGAAAAAGAGACCUCUCAUGG	Cleavage
sly-miR8011a-2-5p	Solyc07g049360.3.1	3.0	-1.0	1	23	2452	2474	UUGUGUGAGGUCUCUUUUUGUUU	CAGAAAAAAGAAGUCUCACACAG	Cleavage
sly-miR8011a-2-5p	Solyc03g098520.1.1	3.0	-1.0	1	23	369	391	UUGUGUGAGGUCUCUUUUUGUUU	GGGGAAGAAGAGACUACGCACAA	Cleavage
sly-miR8011a-2-5p	Solyc03g098530.1.1	3.0	-1.0	1	23	541	563	UUGUGUGAGGUCUCUUUUUGUUU	GGGGAAGAAGAGACUACGCACAA	Cleavage
sly-miR8011a-2-5p	Solyc04g081230.3.1	3.0	-1.0	1	23	1609	1631	UUGUGUGAGGUCUCUUUUUGUUU	UCCCUAGAAGAGAUUUCACACGA	Cleavage
sly-miR8011a-2-5p	Solyc04g081510.3.1	3.0	-1.0	1	23	1970	1992	UUGUGUGAGGUCUCUUUUUGUUU	UGCUAAAGAGAGAUCUCAAGCAA	Cleavage
sly-miR8011a-2-	Solyc06g069450.3.1	3.0	-1.0	1	23	1270	1292	UUGUGUGAGGUCUCUUUUUGUUU	CUUUCUAAAGAGACUUCACAUAA	Cleavage

5p										
sly-miR8013	Solyc01g009770.3.1	2.5	-1.0	1	24	1521	1544	AGAAGAAAAUCACACCGUCAGAAG	AUAUUUAUCGUGUGAUUUUCUUCU	Cleavage
sly-miR8013	Solyc07g042460.2.1	2.5	-1.0	1	24	2239	2262	AGAAGAAAAUCACACCGUCAGAAG	GAACGAACCGUGUGAUUUUCUUUU	Cleavage
sly-miR8013	Solyc05g012190.3.1	3.0	-1.0	1	24	3513	3536	AGAAGAAAAUCACACCGUCAGAAG	UUGCUGACAGAGUGAUUUUCUUCA	Cleavage
sly-miR8019-1-3p	Solyc12g011040.2.1	2.0	-1.0	1	24	2856	2879	AAAAGAAUGACCUGGUUUGACUUG	CAAGUCAAACUAGGUCAUUCUGUU	Cleavage
sly-miR8019-1-3p	Solyc07g009410.3.1	2.5	-1.0	1	24	1706	1729	AAAAGAAUGACCUGGUUUGACUUG	UUCUUCAAACCAGGUAAUUCUUUC	Cleavage
sly-miR8019-1-3p	Solyc01g044480.3.1	3.0	-1.0	1	24	2674	2697	AAAAGAAUGACCUGGUUUGACUUG	CAAGUUAAACUAUGUCAUUUUUUU	Cleavage
sly-miR8019-1-3p	Solyc01g081450.3.1	3.0	-1.0	1	24	5	28	AAAAGAAUGACCUGGUUUGACUUG	UAAAUCAAAUUAGGACAUUUUUUU	Translation
sly-miR8019-1-3p	Solyc09g065710.1.1	3.0	-1.0	1	24	865	888	AAAAGAAUGACCUGGUUUGACUUG	GUUAUGAAAUUGGGUUAUUCUUUU	Cleavage
sly-miR8019-1-5p	Solyc06g076670.3.1	1.5	-1.0	1	23	2099	2121	AGGAAAGGAGGUUAUUCUUUUUG	GUUCCAGAAUAACCUCCUUUCUU	Cleavage
sly-miR8019-1-5p	Solyc06g082710.3.1	2.5	-1.0	1	23	1934	1956	AGGAAAGGAGGUUAUUCUUUUUG	UAACAAGGGUGAUUUCCUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc01g103335.1.1	2.5	-1.0	1	23	15	37	AGGAAAGGAGGUUAUUCUUUUUG	AGACAAGAAUAUCCUUUUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc07g062660.3.1	2.5	-1.0	1	23	1581	1603	AGGAAAGGAGGUUAUUCUUUUUG	CCUCAAGAAUGACCUCUUAUCCU	Cleavage
sly-miR8019-1-5p	Solyc01g101100.3.1	2.5	-1.0	1	23	2685	2707	AGGAAAGGAGGUUAUUCUUUUUG	UUUCAAGAGUGACCUUUUUUUCU	Cleavage
sly-miR8019-1-5p	Solyc09g090670.3.1	3.0	-1.0	1	23	7078	7100	AGGAAAGGAGGUUAUUCUUUUUG	AAAAAAGAAUUACCUCUUUUCCC	Cleavage
sly-miR8019-1-5p	Solyc01g096420.3.1	3.0	-1.0	1	22	1	22	AGGAAAGGAGGUUAUUCUUUUU	AAGAAGAAUAAUUUUUUUUUUU	Cleavage
sly-miR8019-1-5p	Solyc08g066290.3.1	3.0	-1.0	1	23	1909	1931	AGGAAAGGAGGUUAUUCUUUUUG	AAAAAAGACUAAUUUUUUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc02g084350.3.1	3.0	-1.0	1	23	21	43	AGGAAAGGAGGUUAUUCUUUUUG	CUAAAAGAAUAAUGUCCUUUUUU	Translation
sly-miR8019-1-5p	Solyc02g067930.3.1	3.0	-1.0	1	23	4226	4248	AGGAAAGGAGGUUAUUCUUUUUG	CCAAAAGGGUAACCUUUUUUUUU	Cleavage
sly-miR8019-1-5p	Solyc04g074110.3.1	3.0	-1.0	1	23	221	243	AGGAAAGGAGGUUAUUCUUUUUG	AGAAAACAAUGAUUUCCUUUCUU	Cleavage
sly-miR8019-1-5p	Solyc01g090210.3.1	3.0	-1.0	1	23	4529	4551	AGGAAAGGAGGUUAUUCUUUUUG	AAGAAACAAUGGCUUUCUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc08g082320.3.1	3.0	-1.0	1	23	1916	1938	AGGAAAGGAGGUUAUUCUUUUUG	CCAAAUGAAUAGCUUUUUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc05g014790.3.1	3.0	-1.0	1	23	1236	1258	AGGAAAGGAGGUUAUUCUUUUUG	ACAGAAGAAUAAUUUUCUUUCUG	Cleavage
sly-miR8019-1-5p	Solyc12g087960.2.1	3.0	-1.0	1	23	105	127	AGGAAAGGAGGUUAUUCUUUUUG	GUAAAAAAAUAAUCUCUUUUUUU	Cleavage
sly-miR8019-1-5p	Solyc12g016220.2.1	3.0	-1.0	1	23	755	777	AGGAAAGGAGGUUAUUCUUUUUG	AAGGAAUGAUAACCUUCUUUCCC	Cleavage
sly-miR8019-1-5p	Solyc04g011910.3.1	3.0	-1.0	1	23	406	428	AGGAAAGGAGGUUAUUCUUUUUG	AAAUGAGAAUGACCUCAUUUUCU	Cleavage
sly-miR8019-1-5p	Solyc11g007700.2.1	3.0	-1.0	1	23	688	710	AGGAAAGGAGGUUAUUCUUUUUG	GAGGAAGAAAAGUUUCCUUUCUU	Cleavage
sly-miR8019-1-5p	Solyc03g059350.3.1	3.0	-1.0	1	23	1185	1207	AGGAAAGGAGGUUAUUCUUUUUG	CUGAAGUAAUAGCUUCUUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc04g082900.3.1	3.0	-1.0	1	23	1892	1914	AGGAAAGGAGGUUAUUCUUUUUG	UUUAAGGAAUGAUUUCUUUUUCU	Cleavage
sly-miR8019-1-5p	Solyc11g008860.2.1	3.0	-1.0	1	23	369	391	AGGAAAGGAGGUUAUUCUUUUUG	AAUAAAUAAUAAUUUCCUUUUUU	Cleavage
sly-miR8019-1-5p	Solyc02g036240.1.1	3.0	-1.0	1	23	116	138	AGGAAAGGAGGUUAUUCUUUUUG	CGCGAGGAAAGACCUCUUUUCUU	Cleavage
sly-miR8019-1-5p	Solyc01g010150.3.1	3.0	-1.0	1	23	19	41	AGGAAAGGAGGUUAUUCUUUUUG	AAAUAAAAAUAAUUUUUUUUCCU	Cleavage
sly-miR8019-1-5p	Solyc07g017740.3.1	3.0	-1.0	1	23	948	970	AGGAAAGGAGGUUAUUCUUUUUG	CUUGAAGAGUAGCCUCUUAUCCU	Cleavage
sly-miR8019-2-3p	Solyc12g011040.2.1	2.0	-1.0	1	24	2856	2879	AAAAGAAUGACCUGGUUUGACUUG	CAAGUCAAACUAGGUCAUUCUGUU	Cleavage
sly-miR8019-2-3p	Solyc07g009410.3.1	2.5	-1.0	1	24	1706	1729	AAAAGAAUGACCUGGUUUGACUUG	UUCUUCAAACCAGGUAAUUCUUUC	Cleavage
sly-miR8019-2-3p	Solyc01g044480.3.1	3.0	-1.0	1	24	2674	2697	AAAAGAAUGACCUGGUUUGACUUG	CAAGUUAAACUAUGUCAUUUUUUU	Cleavage
sly-miR8019-2-3p	Solyc01g081450.3.1	3.0	-1.0	1	24	5	28	AAAAGAAUGACCUGGUUUGACUUG	UAAAUCAAAUUAGGACAUUUUUUU	Translation
sly-miR8019-2-3p	Solyc09g065710.1.1	3.0	-1.0	1	24	865	888	AAAAGAAUGACCUGGUUUGACUUG	GUUAUGAAAUUGGGUUAUUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc10g085080.2.1	1.0	-1.0	1	19	42	60	GAAAGAGGUCAUUCUUUUU	AAAAAUAAUGACCUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc05g052260.3.1	1.5	-1.0	1	19	1566	1584	GAAAGAGGUCAUUCUUUUU	AGAAAGAAUGACCUCUUUA	Cleavage
sly-miR8019-2-5p	Solyc09g090670.3.1	2.0	-1.0	1	19	7079	7097	GAAAGAGGUCAUUCUUUUU	AAAAAGAAUUACCUCUUUU	Translation
sly-miR8019-2-5p	Solyc04g076140.3.1	2.0	-1.0	1	19	69	87	GAAAGAGGUCAUUCUUUUU	ACAAAGAAUGACUUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc03g098260.2.1	2.5	-1.0	1	19	511	529	GAAAGAGGUCAUUCUUUUU	AAGAAGAAAGACUUCUUUC	Translation
sly-miR8019-2-5p	Solyc09g098280.3.1	2.5	-1.0	1	19	1285	1303	GAAAGAGGUCAUUCUUUUU	AAAGAGAAUGACCUUUAUC	Cleavage
sly-miR8019-2-5p	Solyc04g074640.3.1	2.5	-1.0	1	19	113	131	GAAAGAGGUCAUUCUUUUU	AGAAGGAAUGGUCUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc01g100880.3.1	2.5	-1.0	1	19	3735	3753	GAAAGAGGUCAUUCUUUUU	AAAUAUAAUGACCUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc04g064590.2.1	2.5	-1.0	1	19	4502	4520	GAAAGAGGUCAUUCUUUUU	AAAUAAAAUGACUUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc02g082160.2.1	3.0	-1.0	1	19	479	497	GAAAGAGGUCAUUCUUUUU	GCAAAGAAUGGCCUUUUUC	Cleavage
sly-miR8019-2-5p	Solyc06g066473.1.1	3.0	-1.0	1	19	133	151	GAAAGAGGUCAUUCUUUUU	CGAGAGAAUGACUUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc06g010005.1.1	3.0	-1.0	1	19	1298	1316	GAAAGAGGUCAUUCUUUUU	CAGAGGGAUGACUUCUUUC	Cleavage

sly-miR8019-2-5p	Solyc01g098080.3.1	3.0	-1.0	1	19	3385	3403	GAAAGAGGUCAUUCUUUUU	AGAAAGAAUGGUUUCUUUA	Cleavage
sly-miR8019-2-5p	Solyc02g071340.2.1	3.0	-1.0	1	19	509	527	GAAAGAGGUCAUUCUUUUU	CAAAGGGAUGGCUUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc00g237680.2.1	3.0	-1.0	1	19	266	284	GAAAGAGGUCAUUCUUUUU	AAAAAGGAUGGUUUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc11g066090.1.1	3.0	-1.0	1	19	985	1003	GAAAGAGGUCAUUCUUUUU	AAAAGGAAAGACUUCUUUU	Translation
sly-miR8019-2-5p	Solyc11g072130.2.1	3.0	-1.0	1	19	285	303	GAAAGAGGUCAUUCUUUUU	AGAAGGAAUGAUUUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc07g008100.3.1	3.0	-1.0	1	19	185	203	GAAAGAGGUCAUUCUUUUU	AAAAAGAAUUGCUUUUUUC	Translation
sly-miR8019-2-5p	Solyc09g092670.3.1	3.0	-1.0	1	19	1450	1468	GAAAGAGGUCAUUCUUUUU	AAGAAGAAUGAUCUUUGUC	Cleavage
sly-miR8019-2-5p	Solyc10g084050.2.1	3.0	-1.0	1	19	454	472	GAAAGAGGUCAUUCUUUUU	AGGAAGGGUGAUCUUUUUC	Cleavage
sly-miR8019-2-5p	Solyc07g062080.3.1	3.0	-1.0	1	19	238	256	GAAAGAGGUCAUUCUUUUU	AAAAAGGGUUACUUCUUUC	Translation
sly-miR8019-2-5p	Solyc06g065450.3.1	3.0	-1.0	1	19	2163	2181	GAAAGAGGUCAUUCUUUUU	GAGGAGAAUGACAUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc06g075590.3.1	3.0	-1.0	1	19	4997	5015	GAAAGAGGUCAUUCUUUUU	AAAAAGAGUAACUUUUUUC	Translation
sly-miR8019-2-5p	Solyc10g081750.1.1	3.0	-1.0	1	19	424	442	GAAAGAGGUCAUUCUUUUU	AUAAAGAAUGGCUUCUUUG	Cleavage
sly-miR8019-2-5p	Solyc04g064910.1.1	3.0	-1.0	1	19	193	211	GAAAGAGGUCAUUCUUUUU	AAUAAGGAUGACUUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc11g072150.2.1	3.0	-1.0	1	19	411	429	GAAAGAGGUCAUUCUUUUU	AAAAACAAUGAAUUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc01g006950.3.1	3.0	-1.0	1	19	487	505	GAAAGAGGUCAUUCUUUUU	AAGAUGAAUGAUCUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc05g055770.3.1	3.0	-1.0	1	19	1649	1667	GAAAGAGGUCAUUCUUUUU	AAAAUGAUUGACCUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc04g009920.3.1	3.0	-1.0	1	19	215	233	GAAAGAGGUCAUUCUUUUU	AAAAAAAGUGAUCUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc06g069380.3.1	3.0	-1.0	1	19	477	495	GAAAGAGGUCAUUCUUUUU	AAAAAAAGUGACUUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc07g052480.3.1	3.0	-1.0	1	19	1850	1868	GAAAGAGGUCAUUCUUUUU	AAAAAAAGUGAUUUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc04g005100.3.1	3.0	-1.0	1	19	1576	1594	GAAAGAGGUCAUUCUUUUU	AAAAAAAAUGAUUUUUUUU	Cleavage
sly-miR8019-2-5p	Solyc11g072140.2.1	3.0	-1.0	1	19	525	543	GAAAGAGGUCAUUCUUUUU	AAAAACAAUGAAUUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc03g112830.3.1	3.0	-1.0	1	19	2637	2655	GAAAGAGGUCAUUCUUUUU	GAAAGCAAUGACUUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc03g117580.3.1	3.0	-1.0	1	19	4071	4089	GAAAGAGGUCAUUCUUUUU	AAAAUGAAUAGCCUCUUUC	Translation
sly-miR8019-2-5p	Solyc09g072880.3.1	3.0	-1.0	1	19	266	284	GAAAGAGGUCAUUCUUUUU	AACAACAAUGGCUUCUUUC	Cleavage
sly-miR8019-2-5p	Solyc06g009550.3.1	3.0	-1.0	1	19	2149	2167	GAAAGAGGUCAUUCUUUUU	AACAAAAAUGAUCUCUUUU	Cleavage
sly-miR8019-2-5p	Solyc12g056300.2.1	3.0	-1.0	1	19	94	112	GAAAGAGGUCAUUCUUUUU	AUAUGGAAUGACCUUUUUC	Cleavage
sly-miR8020	Solyc10g008540.3.1	2.0	-1.0	1	24	1936	1959	AAUUUCAUUGAGUAUGUUGUUGUU	AACAACAACAUACUCUAUGAAGUU	Cleavage
sly-miR8020	Solyc06g065260.3.1	2.0	-1.0	1	24	1480	1503	AAUUUCAUUGAGUAUGUUGUUGUU	AACAAUAAUAUAUUUAAUGAAAUU	Cleavage
sly-miR8020	Solyc08g082910.2.1	2.0	-1.0	1	24	1646	1669	AAUUUCAUUGAGUAUGUUGUUGUU	AAUAAUAACAUACUCAAUAAAAUU	Cleavage
sly-miR8020	Solyc12g095890.2.1	2.0	-1.0	1	24	132	155	AAUUUCAUUGAGUAUGUUGUUGUU	AGUAACAACAUACUCGGUGAAAUC	Cleavage
sly-miR8020	Solyc12g006300.2.1	2.0	-1.0	1	24	849	872	AAUUUCAUUGAGUAUGUUGUUGUU	CGAGAUAAUAUACUUAGUGAAAUU	Cleavage
sly-miR8020	Solyc03g115810.3.1	2.0	-1.0	1	24	1839	1862	AAUUUCAUUGAGUAUGUUGUUGUU	GAGUCCAAUGUACUUAAUGAAGUU	Cleavage
sly-miR8020	Solyc07g063430.3.1	2.5	-1.0	1	24	1865	1888	AAUUUCAUUGAGUAUGUUGUUGUU	AACAAUAACAUACUCGAUGUAAUU	Cleavage
sly-miR8020	Solyc07g063260.3.1	2.5	-1.0	1	24	6083	6106	AAUUUCAUUGAGUAUGUUGUUGUU	AACAACAACAUACCCGGUGAAAUU	Translation
sly-miR8020	Solyc06g066740.2.1	2.5	-1.0	1	24	1798	1821	AAUUUCAUUGAGUAUGUUGUUGUU	UACAACAAUGUACCCAAUGAAAUU	Translation
sly-miR8020	Solyc08g007295.1.1	2.5	-1.0	1	24	862	885	AAUUUCAUUGAGUAUGUUGUUGUU	AAGAACAACAUAUUCAGUGGAAUC	Cleavage
sly-miR8020	Solyc08g077170.3.1	2.5	-1.0	1	24	3014	3038	AAUUUCAUUGAGUAUG-UUGUUGUU	AUCAACAAACAUACUCAGUGAAAUU	Cleavage
sly-miR8020	Solyc02g069230.3.1	2.5	-1.0	1	24	24	47	AAUUUCAUUGAGUAUGUUGUUGUU	AAACAUAACGUACUUAAUGAAAUA	Cleavage
sly-miR8020	Solyc09g059100.1.1	2.5	-1.0	1	24	109	132	AAUUUCAUUGAGUAUGUUGUUGUU	UCAUAUGAUAUAUUCAAUGAGAUU	Cleavage
sly-miR8020	Solyc09g066070.3.1	2.5	-1.0	1	24	391	414	AAUUUCAUUGAGUAUGUUGUUGUU	UCAUAUGAUAUAUUCAAUGAGAUU	Cleavage
sly-miR8020	Solyc09g066030.2.1	2.5	-1.0	1	24	1277	1300	AAUUUCAUUGAGUAUGUUGUUGUU	UCAUAUGAUAUAUUCAAUGAGAUU	Cleavage
sly-miR8020	Solyc05g024180.3.1	3.0	-1.0	1	24	1899	1922	AAUUUCAUUGAGUAUGUUGUUGUU	AACAACAACAUACUCAGUGUAAUC	Cleavage
sly-miR8020	Solyc12g009180.2.1	3.0	-1.0	1	24	1245	1268	AAUUUCAUUGAGUAUGUUGUUGUU	AACAAUAGCAUAUUCAAUGAACUU	Cleavage
sly-miR8020	Solyc05g050510.3.1	3.0	-1.0	1	24	823	846	AAUUUCAUUGAGUAUGUUGUUGUU	AACGAUAACAUAUUUAAUGUAAUU	Cleavage
sly-miR8020	Solyc08g081060.3.1	3.0	-1.0	1	24	1015	1038	AAUUUCAUUGAGUAUGUUGUUGUU	UACAACAGCAUACUCAAUGUAAUC	Cleavage
sly-miR8020	Solyc02g068700.3.1	3.0	-1.0	1	24	393	416	AAUUUCAUUGAGUAUGUUGUUGUU	CACAAUAACAUACCCAGUGGAAUU	Translation
sly-miR8020	Solyc01g099470.3.1	3.0	-1.0	1	24	723	746	AAUUUCAUUGAGUAUGUUGUUGUU	CACGACAACAUACUUAAUCAAAUA	Cleavage
sly-miR8020	Solyc01g099460.2.1	3.0	-1.0	1	24	2869	2892	AAUUUCAUUGAGUAUGUUGUUGUU	CACGACAACAUACUUAAUCAAAUA	Cleavage
sly-miR8020	Solyc01g096940.3.1	3.0	-1.0	1	24	3717	3740	AAUUUCAUUGAGUAUGUUGUUGUU	CGUAACAACAUACCCAGUGAAAUC	Translation
sly-miR8020	Solyc01g008270.3.1	3.0	-1.0	1	24	840	863	AAUUUCAUUGAGUAUGUUGUUGUU	AAUUAUAACAUAUUCAGUGUAAUU	Cleavage

sly-miR8020	Solyc01g008270.3.1	3.0	-1.0	1	24	951	974	AAUUUCAUUGAGUAUGUUGUUGUU	AAUUAUAACAUAUUCAGUGUAAUU	Cleavage
sly-miR8020	Solyc12g049400.2.1	3.0	-1.0	1	24	1283	1306	AAUUUCAUUGAGUAUGUUGUUGUU	ACUAUCAACAUACUCGAUGUAAUA	Cleavage
sly-miR8020	Solyc10g076640.1.1	3.0	-1.0	1	24	55	78	AAUUUCAUUGAGUAUGUUGUUGUU	AAUUGUAACAUACCCAAUGAAAUG	Translation
sly-miR8020	Solyc05g014390.3.1	3.0	-1.0	1	24	745	768	AAUUUCAUUGAGUAUGUUGUUGUU	UAUGACAACAAAUACAAUGAAAUU	Translation
sly-miR8020	Solyc12g014060.2.1	3.0	-1.0	1	24	1437	1460	AAUUUCAUUGAGUAUGUUGUUGUU	GGUGAUAGUCUACUUAAUGAAAUU	Cleavage
sly-miR8020	Solyc07g019490.1.1	3.0	-1.0	1	24	29	52	AAUUUCAUUGAGUAUGUUGUUGUU	CAAGACAACAUAUUCAAUCAAAUC	Cleavage
sly-miR8020	Solyc03g121210.3.1	3.0	-1.0	1	24	320	343	AAUUUCAUUGAGUAUGUUGUUGUU	UACAUAAAUAUACACAAUGAAAUU	Translation
sly-miR8020	Solyc10g005390.3.1	3.0	-1.0	1	24	1000	1023	AAUUUCAUUGAGUAUGUUGUUGUU	GGUGAAUACAUACUUGAUGAAAUU	Cleavage
sly-miR8020	Solyc10g005410.3.1	3.0	-1.0	1	24	1650	1673	AAUUUCAUUGAGUAUGUUGUUGUU	GGUGAAUACAUACUUGAUGAAAUU	Cleavage
sly-miR8020	Solyc05g010363.1.1	3.0	-1.0	1	24	162	185	AAUUUCAUUGAGUAUGUUGUUGUU	CCUGAGAAUGUACUUGAUGAAAUU	Cleavage
sly-miR8020	Solyc05g010363.1.1	3.0	-1.0	1	24	1143	1166	AAUUUCAUUGAGUAUGUUGUUGUU	CCUGAGAAUGUACUUGAUGAAAUU	Cleavage
sly-miR8021-1	Solyc09g066140.3.1	1.5	-1.0	1	24	124	147	AUUCAAGGCUCAAACUCGAGACCU	AGAUUUUGAGUUUGAGUUUUGAAU	Cleavage
sly-miR8021-1	Solyc09g091590.3.1	1.5	-1.0	1	24	1212	1235	AUUCAAGGCUCAAACUCGAGACCU	UAAUUUCGAGUUUGAGCCUUGAGA	Cleavage
sly-miR8021-1	Solyc12g096590.2.1	2.5	-1.0	1	24	1014	1037	AUUCAAGGCUCAAACUCGAGACCU	UUGUUUCAAGUUUGAGUUUUGGAU	Cleavage
sly-miR8021-1	Solyc05g007140.3.1	2.5	-1.0	1	24	811	834	AUUCAAGGCUCAAACUCGAGACCU	AUAUUUCAAGUUUGAGCUUUGGGU	Cleavage
sly-miR8021-1	Solyc03g119140.3.1	2.5	-1.0	1	24	806	829	AUUCAAGGCUCAAACUCGAGACCU	UUUUUUCGAAUUUGAGUUUUGGAU	Cleavage
sly-miR8021-1	Solyc06g075260.3.1	2.5	-1.0	1	24	1654	1677	AUUCAAGGCUCAAACUCGAGACCU	GUCAUUCGAGUGUGAGUUUUGAAU	Cleavage
sly-miR8021-1	Solyc04g077560.3.1	3.0	-1.0	1	24	58	81	AUUCAAGGCUCAAACUCGAGACCU	AAGUCUCAAAUUUGAGUUUUGAAU	Cleavage
sly-miR8021-1	Solyc06g075400.3.1	3.0	-1.0	1	24	2431	2454	AUUCAAGGCUCAAACUCGAGACCU	UACCUUCGGCUUUGGGCUUUGAGU	Cleavage
sly-miR8021-2	Solyc09g066140.3.1	1.5	-1.0	1	24	124	147	AUUCAAGGCUCAAACUCGAGACCU	AGAUUUUGAGUUUGAGUUUUGAAU	Cleavage
sly-miR8021-2	Solyc09g091590.3.1	1.5	-1.0	1	24	1212	1235	AUUCAAGGCUCAAACUCGAGACCU	UAAUUUCGAGUUUGAGCCUUGAGA	Cleavage
sly-miR8021-2	Solyc12g096590.2.1	2.5	-1.0	1	24	1014	1037	AUUCAAGGCUCAAACUCGAGACCU	UUGUUUCAAGUUUGAGUUUUGGAU	Cleavage
sly-miR8021-2	Solyc05g007140.3.1	2.5	-1.0	1	24	811	834	AUUCAAGGCUCAAACUCGAGACCU	AUAUUUCAAGUUUGAGCUUUGGGU	Cleavage
sly-miR8021-2	Solyc03g119140.3.1	2.5	-1.0	1	24	806	829	AUUCAAGGCUCAAACUCGAGACCU	UUUUUUCGAAUUUGAGUUUUGGAU	Cleavage
sly-miR8021-2	Solyc06g075260.3.1	2.5	-1.0	1	24	1654	1677	AUUCAAGGCUCAAACUCGAGACCU	GUCAUUCGAGUGUGAGUUUUGAAU	Cleavage
sly-miR8021-2	Solyc04g077560.3.1	3.0	-1.0	1	24	58	81	AUUCAAGGCUCAAACUCGAGACCU	AAGUCUCAAAUUUGAGUUUUGAAU	Cleavage
sly-miR8021-2	Solyc06g075400.3.1	3.0	-1.0	1	24	2431	2454	AUUCAAGGCUCAAACUCGAGACCU	UACCUUCGGCUUUGGGCUUUGAGU	Cleavage
sly-miR8021-3	Solyc09g066140.3.1	1.5	-1.0	1	24	124	147	AUUCAAGGCUCAAACUCGAGACCU	AGAUUUUGAGUUUGAGUUUUGAAU	Cleavage
sly-miR8021-3	Solyc09g091590.3.1	1.5	-1.0	1	24	1212	1235	AUUCAAGGCUCAAACUCGAGACCU	UAAUUUCGAGUUUGAGCCUUGAGA	Cleavage
sly-miR8021-3	Solyc12g096590.2.1	2.5	-1.0	1	24	1014	1037	AUUCAAGGCUCAAACUCGAGACCU	UUGUUUCAAGUUUGAGUUUUGGAU	Cleavage
sly-miR8021-3	Solyc05g007140.3.1	2.5	-1.0	1	24	811	834	AUUCAAGGCUCAAACUCGAGACCU	AUAUUUCAAGUUUGAGCUUUGGGU	Cleavage
sly-miR8021-3	Solyc03g119140.3.1	2.5	-1.0	1	24	806	829	AUUCAAGGCUCAAACUCGAGACCU	UUUUUUCGAAUUUGAGUUUUGGAU	Cleavage
sly-miR8021-3	Solyc06g075260.3.1	2.5	-1.0	1	24	1654	1677	AUUCAAGGCUCAAACUCGAGACCU	GUCAUUCGAGUGUGAGUUUUGAAU	Cleavage
sly-miR8021-3	Solyc04g077560.3.1	3.0	-1.0	1	24	58	81	AUUCAAGGCUCAAACUCGAGACCU	AAGUCUCAAAUUUGAGUUUUGAAU	Cleavage
sly-miR8021-3	Solyc06g075400.3.1	3.0	-1.0	1	24	2431	2454	AUUCAAGGCUCAAACUCGAGACCU	UACCUUCGGCUUUGGGCUUUGAGU	Cleavage
sly-miR8025-3p	Solyc08g082630.3.1	2.5	-1.0	1	23	2049	2071	UUUAAUUGCAUGCCGACUGUGUG	UAUGCAGUUGGCAUGCGAUUCAA	Cleavage
sly-miR8025-3p	Solyc03g096640.3.1	2.5	-1.0	1	23	2980	3002	UUUAAUUGCAUGCCGACUGUGUG	UAUCCAUUUGGUAUGCAAUUGAA	Cleavage
sly-miR8025-3p	Solyc03g096645.1.1	2.5	-1.0	1	23	3023	3045	UUUAAUUGCAUGCCGACUGUGUG	UAUCCAUUUGGUAUGCAAUUGAA	Cleavage
sly-miR8025-3p	Solyc08g006050.2.1	3.0	-1.0	1	23	579	601	UUUAAUUGCAUGCCGACUGUGUG	CAUCCGGUUGGCAUGCAGUUACA	Cleavage
sly-miR8025-5p	Solyc12g019960.2.1	3.0	-1.0	1	24	2267	2290	ACACACUACACAUGCAAUUAAAUU	GCAACAAUUGUAUGUGGAGUGUGA	Cleavage
sly-miR8032d-3p	Solyc08g076690.2.1	3.0	-1.0	1	22	1570	1591	AGUGUGAGUUGGUGCGAUUAGG	GAUGAUAGCACCAACUCACAUG	Cleavage
sly-miR8032d-3p	Solyc05g015510.3.1	3.0	-1.0	1	22	902	923	AGUGUGAGUUGGUGCGAUUAGG	UCCGUUCGCACCAGCUCACACA	Cleavage
sly-miR8032d-3p	Solyc06g060150.3.1	3.0	-1.0	1	22	6350	6371	AGUGUGAGUUGGUGCGAUUAGG	UGCAGUCGAACCAACUCUCACU	Cleavage
sly-miR8033-3p	Solyc06g050730.3.1	2.0	-1.0	1	20	2599	2618	AUUUCUGCAGCUUUGGAAUU	GAUUUCAAAGUUGUAGAGAU	Cleavage
sly-miR8033-3p	Solyc10g081240.2.1	2.0	-1.0	1	20	163	182	AUUUCUGCAGCUUUGGAAUU	GAUUCAAAAGUUGCAGAGAU	Cleavage
sly-miR8033-3p	Solyc08g079710.3.1	2.5	-1.0	1	20	1738	1757	AUUUCUGCAGCUUUGGAAUU	GAUUUUAAAGCUGCGGAAAA	Cleavage
sly-miR8033-3p	Solyc01g096920.3.1	2.5	-1.0	1	20	1459	1478	AUUUCUGCAGCUUUGGAAUU	GGUUUUGAAGUUGCAGAAAU	Cleavage
sly-miR8033-3p	Solyc10g050540.2.1	2.5	-1.0	1	20	343	362	AUUUCUGCAGCUUUGGAAUU	AAUGUUGAAGCUGCAGAAAU	Cleavage
sly-miR8033-3p	Solyc02g069400.3.1	2.5	-1.0	1	20	1758	1777	AUUUCUGCAGCUUUGGAAUU	UAUUCCAAAGUUGUAGGAAA	Cleavage
sly-miR8033-3p	Solyc09g072820.3.1	2.5	-1.0	1	20	5966	5985	AUUUCUGCAGCUUUGGAAUU	UGUUUUGAAGCUGCAGAGAU	Cleavage

sly-miR8033-3p	Solyc03g095290.3.1	2.5	-1.0	1	20	1898	1917	AUUUCUGCAGCUUUGGAAUU	UAUUACAAAGCUGCUGAAAU	Cleavage
sly-miR8033-3p	Solyc01g091860.3.1	3.0	-1.0	1	20	899	918	AUUUCUGCAGCUUUGGAAUU	GAUUUCAAAGCUGCAGCAAC	Cleavage
sly-miR8033-3p	Solyc04g076980.3.1	3.0	-1.0	1	20	850	869	AUUUCUGCAGCUUUGGAAUU	AAUUACGAAGCUGAAGAAAU	Cleavage
sly-miR8033-3p	Solyc03g007800.3.1	3.0	-1.0	1	20	4143	4162	AUUUCUGCAGCUUUGGAAUU	UAUUCUAAAGCUGGAGAAAC	Cleavage
sly-miR8033-3p	Solyc10g083850.2.1	3.0	-1.0	1	20	253	272	AUUUCUGCAGCUUUGGAAUU	UGUUUCAAAGCUGCAAGAAU	Cleavage
sly-miR8033-3p	Solyc02g089210.3.1	3.0	-1.0	1	20	494	513	AUUUCUGCAGCUUUGGAAUU	CAUUUCUGAGCUGCAGAAAA	Cleavage
sly-miR8033-3p	Solyc10g049820.2.1	3.0	-1.0	1	20	469	488	AUUUCUGCAGCUUUGGAAUU	UAUUGUAAAGUUGCAGGGAU	Cleavage
sly-miR8033-3p	Solyc12g014120.2.1	3.0	-1.0	1	20	1648	1667	AUUUCUGCAGCUUUGGAAUU	CAAUCUGAAGCUGUAGAAGU	Cleavage
sly-miR8033-3p	Solyc06g009280.1.1	3.0	-1.0	1	20	715	734	AUUUCUGCAGCUUUGGAAUU	UAUGCCAAGGCUGCAGGGGU	Cleavage
sly-miR8033-3p	Solyc02g090160.3.1	3.0	-1.0	1	20	2226	2245	AUUUCUGCAGCUUUGGAAUU	UAUUGCAGAGCUGCAUAAAU	Cleavage
sly-miR8033-3p	Solyc05g053240.3.1	3.0	-1.0	1	20	1932	1951	AUUUCUGCAGCUUUGGAAUU	CAUUCAAAAGUUGCAGAAUU	Cleavage
sly-miR8033-5p	Solyc04g015940.3.1	2.5	-1.0	1	22	1815	1836	UUCCAAAGCUGCAGAAAUGAGU	GAAUAUUUCUGCAGCUUUGCAG	Cleavage
sly-miR8033-5p	Solyc07g066620.3.1	2.5	-1.0	1	22	748	769	UUCCAAAGCUGCAGAAAUGAGU	UAACAUUGCUGCAGUUUUGGGG	Cleavage
sly-miR8033-5p	Solyc05g051220.3.1	3.0	-1.0	1	22	3120	3141	UUCCAAAGCUGCAGAAAUGAGU	GCUCGUUACUGCAGCUUCGGAA	Cleavage
sly-miR8033-5p	Solyc01g095290.3.1	3.0	-1.0	1	22	447	468	UUCCAAAGCUGCAGAAAUGAGU	GAUCAUUCCUCCAGUUUUGGAA	Cleavage
sly-miR8033-5p	Solyc08g061000.3.1	3.0	-1.0	1	22	248	269	UUCCAAAGCUGCAGAAAUGAGU	CAUUUUUUCUGCAGCUUCGGAA	Cleavage
sly-miR8033-5p	Solyc03g025370.3.1	3.0	-1.0	1	22	213	234	UUCCAAAGCUGCAGAAAUGAGU	UUGAGUUUUUGUAGCUUUGGGA	Cleavage
sly-miR8033-5p	Solyc02g087760.3.1	3.0	-1.0	1	22	1380	1401	UUCCAAAGCUGCAGAAAUGAGU	AAAGGUUUCUGCAGCUUUGGCA	Cleavage
sly-miR8033-5p	Solyc08g066840.3.1	3.0	-1.0	1	22	941	962	UUCCAAAGCUGCAGAAAUGAGU	AUCUAUUCUUGUAGUUUUGGAA	Cleavage
sly-miR8033-5p	Solyc01g008820.3.1	3.0	-1.0	1	22	888	909	UUCCAAAGCUGCAGAAAUGAGU	UGGCAUUUUUGUGGCUUUGGCA	Cleavage
sly-miR8033-5p	Solyc09g075450.3.1	3.0	-1.0	1	22	775	796	UUCCAAAGCUGCAGAAAUGAGU	GCACAUUGCUGCAGCUAUGGAG	Cleavage
sly-miR8033-5p	Solyc07g018350.2.1	3.0	-1.0	1	22	404	426	UUCCAAAGCUGCAGAA-AUGAGU	AUGCAUCUUGUGCAGCUUUGGAA	Cleavage
sly-miR8033-5p	Solyc10g076450.2.1	3.0	-1.0	1	22	6373	6394	UUCCAAAGCUGCAGAAAUGAGU	AAACACUUUUGUAGCUUUGGAU	Cleavage
sly-miR8038a-3p	Solyc02g069560.3.1	2.5	-1.0	1	19	1100	1118	UUCAGCUUACUCACUUGGA	UUCAAAUGAGUAGGUUGAA	Cleavage
sly-miR8038a-3p	Solyc05g012800.1.1	2.5	-1.0	1	19	914	932	UUCAGCUUACUCACUUGGA	UACAAUUGAGUGAGCUGAA	Cleavage
sly-miR8038a-3p	Solyc03g123700.3.1	3.0	-1.0	1	19	1117	1135	UUCAGCUUACUCACUUGGA	GCCAAGUGAGGAAGCUGAG	Cleavage
sly-miR8038a-3p	Solyc11g045100.2.1	3.0	-1.0	1	19	570	588	UUCAGCUUACUCACUUGGA	ACCAGAUGAGUGAGCUGAA	Cleavage
sly-miR8038a-3p	Solyc00g024570.2.1	3.0	-1.0	1	19	1286	1304	UUCAGCUUACUCACUUGGA	UCCUAGUGAGUGAGCUUAA	Cleavage
sly-miR8038a-3p	Solyc01g100390.3.1	3.0	-1.0	1	19	2623	2641	UUCAGCUUACUCACUUGGA	UGUAGGUGAGUAAGUUGAG	Cleavage
sly-miR8038a-5p	Solyc04g009475.1.1	0.5	-1.0	1	22	112	133	CCUUGUGAGUAAGUUGAAUCUC	GAAAUUCAACUUAUUCACAAGG	Cleavage
sly-miR8038a-5p	Solyc04g009477.1.1	1.5	-1.0	1	22	46	67	CCUUGUGAGUAAGUUGAAUCUC	GAGAUUCAACUUCCUCACAAGG	Translation
sly-miR8038a-5p	Solyc04g009500.3.1	1.5	-1.0	1	22	1888	1909	CCUUGUGAGUAAGUUGAAUCUC	GAUAUUCAACUUUCUCACAAGG	Translation
sly-miR8038a-5p	Solyc03g118950.2.1	2.5	-1.0	1	22	244	265	CCUUGUGAGUAAGUUGAAUCUC	GAUAUUUCACUUAUUUACAAGG	Cleavage
sly-miR8038a-5p	Solyc03g118943.1.1	2.5	-1.0	1	22	1269	1290	CCUUGUGAGUAAGUUGAAUCUC	GAUAUUUCACUUAUUUACAAGG	Cleavage
sly-miR8038a-5p	Solyc09g009770.3.1	2.5	-1.0	1	22	2087	2108	CCUUGUGAGUAAGUUGAAUCUC	GGAAUUCAACUUACUUGCAAAG	Cleavage
sly-miR8038a-5p	Solyc06g064430.1.1	2.5	-1.0	1	22	320	341	CCUUGUGAGUAAGUUGAAUCUC	UAAAUUCGAUUUGUUUACAAGG	Cleavage
sly-miR8038a-5p	Solyc09g074280.1.1	2.5	-1.0	1	22	746	767	CCUUGUGAGUAAGUUGAAUCUC	UGAAUUCAAUUGAUUCACAAGG	Translation
sly-miR8038a-5p	Solyc03g005380.3.1	2.5	-1.0	1	22	2534	2555	CCUUGUGAGUAAGUUGAAUCUC	ACAACUCAACUUACACACAAGG	Cleavage
sly-miR8038a-5p	Solyc04g079770.3.1	3.0	-1.0	1	22	714	735	CCUUGUGAGUAAGUUGAAUCUC	AAGAUUUAAUUUAUUCACAGGA	Cleavage
sly-miR8038a-5p	Solyc10g054080.2.1	3.0	-1.0	1	22	581	602	CCUUGUGAGUAAGUUGAAUCUC	CCGAUUCGGUGUACUCACAAGG	Cleavage
sly-miR8038a-5p	Solyc03g062650.3.1	3.0	-1.0	1	22	1523	1544	CCUUGUGAGUAAGUUGAAUCUC	UACAUUCAAUUUGUUCACGAGA	Cleavage
sly-miR8038a-5p	Solyc04g082350.1.1	3.0	-1.0	1	22	66	87	CCUUGUGAGUAAGUUGAAUCUC	AUUAUUCAACUUUUUCACAAGC	Translation
sly-miR8038a-5p	Solyc06g007670.3.1	3.0	-1.0	1	22	247	268	CCUUGUGAGUAAGUUGAAUCUC	GUUGUUCGAUUUACUAACAAGG	Cleavage
sly-miR8038a-5p	Solyc05g008070.3.1	3.0	-1.0	1	22	1484	1505	CCUUGUGAGUAAGUUGAAUCUC	UUGUUUCUACUUACUCACAAGA	Cleavage
sly-miR8038a-5p	Solyc05g054970.3.1	3.0	-1.0	1	22	1209	1230	CCUUGUGAGUAAGUUGAAUCUC	UUGAUUGUGCUUGCUCACAAGG	Cleavage
sly-miR8038a-5p	Solyc09g074610.3.1	3.0	-1.0	1	22	107	128	CCUUGUGAGUAAGUUGAAUCUC	UCCAUUCACCUUUCUUACAAGG	Translation
sly-miR8038a-5p	Solyc04g005790.3.1	3.0	-1.0	1	22	1512	1533	CCUUGUGAGUAAGUUGAAUCUC	AUCAUUCCAUUUGCUCGUAAGG	Cleavage
sly-miR8039-1	Solyc08g080360.3.1	2.5	-1.0	1	21	720	740	UUUCCUAUCUGAACUAUGACC	GUUCAUGGUUGGGAUAGGAAA	Translation
sly-miR8039-1	Solyc00g114550.1.1	3.0	-1.0	1	21	165	185	UUUCCUAUCUGAACUAUGACC	CUCUAUAGUUCAGAUAGGCAA	Cleavage
sly-miR8039-1	Solyc10g008450.1.1	3.0	-1.0	1	21	142	162	UUUCCUAUCUGAACUAUGACC	GUUUAUGGUUCAGGUAGAAAA	Cleavage

sly-miR8039-1	Solyc04g079390.3.1	3.0	-1.0	1	21	1496	1516	UUUCCUAUCUGAACUAUGACC	UACCAUGGUUCAGAAAGGAAA	Cleavage
sly-miR8039-1	Solyc01g106580.2.1	3.0	-1.0	1	21	346	366	UUUCCUAUCUGAACUAUGACC	UAUCAUAGUUCAGGUGGAAGA	Cleavage
sly-miR8039-1	Solyc11g067090.2.1	3.0	-1.0	1	21	1674	1694	UUUCCUAUCUGAACUAUGACC	CUUUAUGGUUCAGACAGGAGA	Cleavage
sly-miR8039-1	Solyc03g045090.3.1	3.0	-1.0	1	21	1217	1237	UUUCCUAUCUGAACUAUGACC	GAUGGUGGUUCAGGUAGGAGA	Cleavage
sly-miR8039-1	Solyc08g014380.2.1	3.0	-1.0	1	21	2200	2220	UUUCCUAUCUGAACUAUGACC	UUCUGUACUUCAGAUAGGAAA	Cleavage
sly-miR8039-1	Solyc07g021120.2.1	3.0	-1.0	1	21	2868	2888	UUUCCUAUCUGAACUAUGACC	GUUCAUUGUUCAGAUGGAAAA	Cleavage
sly-miR8039-1	Solyc12g062480.2.1	3.0	-1.0	1	21	2983	3003	UUUCCUAUCUGAACUAUGACC	GUUCAUUGUUCAGAUGGAAAA	Cleavage
sly-miR8039-1	Solyc05g010100.3.1	3.0	-1.0	1	21	2091	2111	UUUCCUAUCUGAACUAUGACC	AAUCAUGUUUCACAUAGGAAA	Cleavage
sly-miR8039-1	Solyc02g093080.3.1	3.0	-1.0	1	21	1701	1721	UUUCCUAUCUGAACUAUGACC	GAUCAAAUUUUGGAUAGGAAA	Cleavage
sly-miR8039-1	Solyc05g047690.3.1	3.0	-1.0	1	21	554	574	UUUCCUAUCUGAACUAUGACC	ACUUAAAUUUCAGAUAGGAGA	Cleavage
sly-miR8039-1	Solyc03g095190.3.1	3.0	-1.0	1	21	2947	2967	UUUCCUAUCUGAACUAUGACC	UAUCAUUCUUCAGAUGGGGAA	Cleavage
sly-miR8039-2	Solyc01g109660.2.1	2.5	-1.0	1	21	558	578	UUUCCUAUCGGAACUAUCACC	GGUGGUGGUUCCGAUGGGAAC	Cleavage
sly-miR8039-2	Solyc01g095670.3.1	2.5	-1.0	1	21	183	203	UUUCCUAUCGGAACUAUCACC	UCUGUUCGUUCUGAUAGGAAA	Cleavage
sly-miR8039-2	Solyc01g111530.3.1	3.0	-1.0	1	21	743	763	UUUCCUAUCGGAACUAUCACC	AGUCAUGGUUCCGAUAGGGAU	Cleavage
sly-miR8039-2	Solyc10g005490.3.1	3.0	-1.0	1	21	3036	3056	UUUCCUAUCGGAACUAUCACC	UACGAUAGUUCCUAUGGGAAA	Cleavage
sly-miR8039-2	Solyc05g006680.3.1	3.0	-1.0	1	21	489	509	UUUCCUAUCGGAACUAUCACC	UUUGAUAGUUUUGAUAAGGAA	Cleavage
sly-miR8039-2	Solyc11g008800.2.1	3.0	-1.0	1	21	2268	2288	UUUCCUAUCGGAACUAUCACC	GUCGGAAGUUCCGGUAGGAAA	Cleavage
sly-miR8039-2	Solyc12g049520.2.1	3.0	-1.0	1	21	520	540	UUUCCUAUCGGAACUAUCACC	UUUGAAGGUUCUGAUAGGAGG	Cleavage
sly-miR8039-2	Solyc01g095590.3.1	3.0	-1.0	1	21	2875	2895	UUUCCUAUCGGAACUAUCACC	UCUGAUUCUUCCGAUGGGGAA	Cleavage
sly-miR8045-1	Solyc10g055710.2.1	2.0	-1.0	1	21	4487	4507	AUUGAUAGUUGAGGUGUGUUU	CGACAUGCUUCAACUAUUAAU	Cleavage
sly-miR8045-1	Solyc12g099800.2.1	2.5	-1.0	1	21	1194	1214	AUUGAUAGUUGAGGUGUGUUU	CAACAUGCCUCAAUUAUCAAA	Cleavage
sly-miR8045-1	Solyc07g005650.3.1	2.5	-1.0	1	21	658	678	AUUGAUAGUUGAGGUGUGUUU	GAAAACACCUCAACUAUCAUU	Cleavage
sly-miR8045-1	Solyc03g123990.3.1	2.5	-1.0	1	21	205	225	AUUGAUAGUUGAGGUGUGUUU	CGGCACACCUCAACUACUAAU	Cleavage
sly-miR8045-1	Solyc05g052430.2.1	2.5	-1.0	1	21	3417	3437	AUUGAUAGUUGAGGUGUGUUU	CAACAUAACUCAAUUGUCAAU	Cleavage
sly-miR8045-1	Solyc05g051740.3.1	2.5	-1.0	1	21	360	380	AUUGAUAGUUGAGGUGUGUUU	UGAAACACCUCUACUAUCAAU	Translation
sly-miR8045-1	Solyc00g237680.2.1	3.0	-1.0	1	21	562	582	AUUGAUAGUUGAGGUGUGUUU	AAACACCCCUCAACUUUCGAU	Cleavage
sly-miR8045-1	Solyc10g049570.2.1	3.0	-1.0	1	21	1117	1137	AUUGAUAGUUGAGGUGUGUUU	ACAUAUACCUCAGUUAUCAAG	Cleavage
sly-miR8045-1	Solyc09g089610.3.1	3.0	-1.0	1	21	2623	2643	AUUGAUAGUUGAGGUGUGUUU	GUACACACCUUGACUGUUAAA	Cleavage
sly-miR8045-1	Solyc11g010690.2.1	3.0	-1.0	1	21	2788	2808	AUUGAUAGUUGAGGUGUGUUU	AUAUAUAUUUCAACUGUUAAU	Cleavage
sly-miR8045-1	Solyc06g082980.3.1	3.0	-1.0	1	21	574	594	AUUGAUAGUUGAGGUGUGUUU	GCACGUACUUCAACUAUCCAU	Cleavage
sly-miR8045-1	Solyc02g077240.3.1	3.0	-1.0	1	21	2108	2128	AUUGAUAGUUGAGGUGUGUUU	CCACACGUCUCUAUUAUCAAU	Translation
sly-miR8045-1	Solyc09g010360.3.1	3.0	-1.0	1	21	392	412	AUUGAUAGUUGAGGUGUGUUU	CCACGCACCUUGGUUGUCAAU	Cleavage
sly-miR8045-1	Solyc03g116060.3.1	3.0	-1.0	1	21	3757	3777	AUUGAUAGUUGAGGUGUGUUU	UCAAACACCCCAACUAUUAAU	Cleavage
sly-miR8045-2-5p	Solyc10g055710.2.1	2.0	-1.0	1	21	4487	4507	AUUGAUAGUUGAGGUGUGUUU	CGACAUGCUUCAACUAUUAAU	Cleavage
sly-miR8045-2-5p	Solyc12g099800.2.1	2.5	-1.0	1	21	1194	1214	AUUGAUAGUUGAGGUGUGUUU	CAACAUGCCUCAAUUAUCAAA	Cleavage
sly-miR8045-2-5p	Solyc07g005650.3.1	2.5	-1.0	1	21	658	678	AUUGAUAGUUGAGGUGUGUUU	GAAAACACCUCAACUAUCAUU	Cleavage
sly-miR8045-2-5p	Solyc03g123990.3.1	2.5	-1.0	1	21	205	225	AUUGAUAGUUGAGGUGUGUUU	CGGCACACCUCAACUACUAAU	Cleavage
sly-miR8045-2-5p	Solyc05g052430.2.1	2.5	-1.0	1	21	3417	3437	AUUGAUAGUUGAGGUGUGUUU	CAACAUAACUCAAUUGUCAAU	Cleavage
sly-miR8045-2-5p	Solyc05g051740.3.1	2.5	-1.0	1	21	360	380	AUUGAUAGUUGAGGUGUGUUU	UGAAACACCUCUACUAUCAAU	Translation
sly-miR8045-2-5p	Solyc00g237680.2.1	3.0	-1.0	1	21	562	582	AUUGAUAGUUGAGGUGUGUUU	AAACACCCCUCAACUUUCGAU	Cleavage
sly-miR8045-2-5p	Solyc10g049570.2.1	3.0	-1.0	1	21	1117	1137	AUUGAUAGUUGAGGUGUGUUU	ACAUAUACCUCAGUUAUCAAG	Cleavage
sly-miR8045-2-5p	Solyc09g089610.3.1	3.0	-1.0	1	21	2623	2643	AUUGAUAGUUGAGGUGUGUUU	GUACACACCUUGACUGUUAAA	Cleavage
sly-miR8045-2-5p	Solyc11g010690.2.1	3.0	-1.0	1	21	2788	2808	AUUGAUAGUUGAGGUGUGUUU	AUAUAUAUUUCAACUGUUAAU	Cleavage
sly-miR8045-2-5p	Solyc06g082980.3.1	3.0	-1.0	1	21	574	594	AUUGAUAGUUGAGGUGUGUUU	GCACGUACUUCAACUAUCCAU	Cleavage
sly-miR8045-2-5p	Solyc02g077240.3.1	3.0	-1.0	1	21	2108	2128	AUUGAUAGUUGAGGUGUGUUU	CCACACGUCUCUAUUAUCAAU	Translation
sly-miR8045-2-5p	Solyc09g010360.3.1	3.0	-1.0	1	21	392	412	AUUGAUAGUUGAGGUGUGUUU	CCACGCACCUUGGUUGUCAAU	Cleavage
sly-miR8045-2-5p	Solyc03g116060.3.1	3.0	-1.0	1	21	3757	3777	AUUGAUAGUUGAGGUGUGUUU	UCAAACACCCCAACUAUUAAU	Cleavage
sly-miR8051-5p	Solyc04g008520.3.1	1.5	-1.0	1	20	1422	1441	UAGUAUGGUAGAAAGAUUCA	UGAAUCUUUCUACCAUAUUC	Cleavage
sly-miR8051-5p	Solyc10g051310.2.1	2.0	-1.0	1	20	391	410	UAGUAUGGUAGAAAGAUUCA	UGGAUCUUUCUACCGUGUUA	Cleavage
sly-miR8051-5p	Solyc03g097280.3.1	2.5	-1.0	1	20	1858	1877	UAGUAUGGUAGAAAGAUUCA	UGGAUGUUUCUACCAUAUUG	Cleavage

sly-miR8051-5p	Solyc04g018060.1.1	2.5	-1.0	1	20	126	145	UAGUAUGGUAGAAAGAUUCA	CGAAUUUUUCUACCGAACUA	Cleavage
sly-miR8051-5p	Solyc06g072300.3.1	2.5	-1.0	1	20	3992	4011	UAGUAUGGUAGAAAGAUUCA	GCAAUCUUUUUAUUAUACUA	Cleavage
sly-miR8051-5p	Solyc02g091350.3.1	3.0	-1.0	1	20	283	302	UAGUAUGGUAGAAAGAUUCA	UGAGUCUUUUUAUCAUUCUA	Cleavage
sly-miR8051-5p	Solyc12g011120.2.1	3.0	-1.0	1	20	1494	1513	UAGUAUGGUAGAAAGAUUCA	UGAAGCUUUCUACAAUGCUA	Cleavage
sly-miR8051-5p	Solyc06g060100.3.1	3.0	-1.0	1	20	2415	2434	UAGUAUGGUAGAAAGAUUCA	UGAGAUUUUCUAUUAUACUA	Cleavage
sly-miR8051-5p	Solyc11g012530.2.1	3.0	-1.0	1	20	295	314	UAGUAUGGUAGAAAGAUUCA	ACAAUUUUUCUGCUAUAUUA	Cleavage
sly-miR8051-5p	Solyc01g005450.3.1	3.0	-1.0	1	20	152	171	UAGUAUGGUAGAAAGAUUCA	ACAAUUUUUUUAUCAUAUUA	Cleavage
sly-miR8051-5p	Solyc02g083730.3.1	3.0	-1.0	1	20	100	119	UAGUAUGGUAGAAAGAUUCA	AAAAUCUUUUUAUCAUGUUA	Cleavage
sly-miR8051-5p	Solyc02g086830.3.1	3.0	-1.0	1	20	1502	1521	UAGUAUGGUAGAAAGAUUCA	UAAAUAUUUCUACUAUAUUA	Cleavage
sly-miR8051-5p	Solyc07g065890.3.1	3.0	-1.0	1	20	391	410	UAGUAUGGUAGAAAGAUUCA	GGAUUCUUUUUAUCAUACUU	Cleavage
sly-miR8051-5p	Solyc08g005010.3.1	3.0	-1.0	1	20	1061	1080	UAGUAUGGUAGAAAGAUUCA	GGAACUUUUCUACCGUGCUG	Cleavage
sly-miR8051-5p	Solyc03g032040.3.1	3.0	-1.0	1	20	430	449	UAGUAUGGUAGAAAGAUUCA	GGAAUGUUUUUGUCAUACUG	Cleavage
sly-miR8172	Solyc08g016070.2.1	2.5	-1.0	1	21	913	933	AUGGAUCAUCUAGAUGGAGAU	UUUUUCAUCUAGAUGCUCCAU	Cleavage
sly-miR8172	Solyc01g100190.3.1	2.5	-1.0	1	21	1545	1565	AUGGAUCAUCUAGAUGGAGAU	UUCUUCAUCUAGGGGAUCCAU	Cleavage
sly-miR8172	Solyc08g082410.3.1	2.5	-1.0	1	21	3076	3095	AUGGAUCAUCUAGAUGGAGAU	AACUCCA-CUAGAUGAUUCAU	Cleavage
sly-miR8172	Solyc08g013680.3.1	3.0	-1.0	1	21	187	207	AUGGAUCAUCUAGAUGGAGAU	AUCUUUAUCUAGACGAUCCGU	Cleavage
sly-miR8172	Solyc05g055090.3.1	3.0	-1.0	1	21	2708	2728	AUGGAUCAUCUAGAUGGAGAU	AUCUUCGCUUGGAUGAUCCAU	Cleavage
sly-miR8172	Solyc11g006420.2.1	3.0	-1.0	1	21	1079	1099	AUGGAUCAUCUAGAUGGAGAU	UUCUCUAUCUGAAUGAUUCAU	Translation
sly-miR8172	Solyc01g109620.3.1	3.0	-1.0	1	21	1154	1174	AUGGAUCAUCUAGAUGGAGAU	AUUUGGAUCUGGAUGAUCCAU	Cleavage
sly-miR8172	Solyc03g122070.2.1	3.0	-1.0	1	21	2366	2386	AUGGAUCAUCUAGAUGGAGAU	CUUCCCAUCUGGAUGGUCUAU	Cleavage
sly-miR8172	Solyc05g008990.3.1	3.0	-1.0	1	21	2383	2403	AUGGAUCAUCUAGAUGGAGAU	ACCUCUAUUUAUAUGGUCCAU	Translation
sly-miR8172	Solyc01g097110.2.1	3.0	-1.0	1	21	1564	1584	AUGGAUCAUCUAGAUGGAGAU	ACCUCCAUCUGGAUGAUAUGU	Cleavage
sly-miR8175	Solyc05g052880.3.1	2.0	-1.0	1	20	581	600	GAUCCCCGGCAACGGCGCCA	AUACGCCGUUGCCGGGGAUC	Cleavage
sly-miR827-3p	Solyc08g007800.3.1	1.0	-1.0	1	21	245	265	UUAGAUGAACAUCAACAAACA	UGAUUGUUGAUGUUCAUCUAA	Cleavage
sly-miR827-3p	Solyc08g080200.3.1	2.0	-1.0	1	21	477	497	UUAGAUGAACAUCAACAAACA	UGUUUGUUGAUGCUUAUCUAA	Cleavage
sly-miR827-3p	Solyc03g063650.1.1	3.0	-1.0	1	21	906	926	UUAGAUGAACAUCAACAAACA	UGUUUGUUGGUGUCCAUUUAG	Cleavage
sly-miR827-3p	Solyc01g096410.3.1	3.0	-1.0	1	21	431	451	UUAGAUGAACAUCAACAAACA	UGAUUGUUGAUGUUCAUGUGA	Cleavage
sly-miR827-3p	Solyc08g060810.3.1	3.0	-1.0	1	21	1636	1656	UUAGAUGAACAUCAACAAACA	GGUUUGUUGGUGUUCUUUUGA	Cleavage
sly-miR827-3p	Solyc04g025280.3.1	3.0	-1.0	1	21	1599	1619	UUAGAUGAACAUCAACAAACA	UAUUUGUUGAUUUUUAUUUGA	Translation
sly-miR827-3p	Solyc06g060110.3.1	3.0	-1.0	1	21	1943	1963	UUAGAUGAACAUCAACAAACA	UUAUUGUUGAUGUUCAUUAAA	Cleavage
sly-miR827-3p	Solyc10g085360.2.1	3.0	-1.0	1	21	2063	2083	UUAGAUGAACAUCAACAAACA	GAUUUGUUGAUGUUGAUUUAU	Cleavage
sly-miR827-3p	Solyc10g039367.1.1	3.0	-1.0	1	21	132	152	UUAGAUGAACAUCAACAAACA	CAUUUGUUGGUGUUUGUAUAA	Cleavage
sly-miR827-3p	Solyc09g010090.4.1	3.0	-1.0	1	21	1630	1650	UUAGAUGAACAUCAACAAACA	GAUUUGUUGAUGUUGAUUUGG	Cleavage
sly-miR827-3p	Solyc12g039180.2.1	3.0	-1.0	1	21	196	216	UUAGAUGAACAUCAACAAACA	AUUUUGUUCAUGUUCAUUUGG	Cleavage
sly-miR827-3p	Solyc12g087893.1.1	3.0	-1.0	1	21	113	133	UUAGAUGAACAUCAACAAACA	UAUCUGUUGAUGUUUAUCGAA	Cleavage
sly-miR827-3p	Solyc10g037965.1.1	3.0	-1.0	1	21	1053	1073	UUAGAUGAACAUCAACAAACA	UUUUUGUGGAUGUUCAUCAAG	Cleavage
sly-miR827-3p	Solyc06g059995.1.1	3.0	-1.0	1	21	809	829	UUAGAUGAACAUCAACAAACA	AUUUGGUUGAUGUUUUUCUAA	Cleavage
sly-miR827-3p	Solyc06g066230.3.1	3.0	-1.0	1	21	1600	1620	UUAGAUGAACAUCAACAAACA	AUUUGGUUGAUGUUUUUCUAA	Cleavage
sly-miR827-3p	Solyc01g090640.3.1	3.0	-1.0	1	21	2636	2656	UUAGAUGAACAUCAACAAACA	AAUUUGGUGAUCUUCAUCUAG	Translation
sly-miR827-3p	Solyc02g093980.3.1	3.0	-1.0	1	21	3718	3738	UUAGAUGAACAUCAACAAACA	GAUUUCUUGGUUUUCAUCUAA	Translation
sly-miR827-3p	Solyc03g062880.2.1	3.0	-1.0	1	21	6003	6023	UUAGAUGAACAUCAACAAACA	ACUUUGAUGAUGUUCAUUUUA	Cleavage
sly-miR827-3p	Solyc07g008450.3.1	3.0	-1.0	1	21	314	334	UUAGAUGAACAUCAACAAACA	GCUCUUUUGAUGUUUAUUUAA	Cleavage
sly-miR827-5p	Solyc08g080030.3.1	2.0	-1.0	1	21	1289	1309	UUUGUUGAUGGUCAUCUAUUC	AAAUAGGGGAUCAUCAACAAA	Cleavage
sly-miR827-5p	Solyc09g090100.3.1	2.5	-1.0	1	21	2722	2742	UUUGUUGAUGGUCAUCUAUUC	AAACAGAUGACCGUCAGCAGA	Cleavage
sly-miR827-5p	Solyc05g051580.3.1	2.5	-1.0	1	21	2971	2991	UUUGUUGAUGGUCAUCUAUUC	AAACAGAUGGUCAUCAACGAA	Cleavage
sly-miR827-5p	Solyc12g041890.2.1	2.5	-1.0	1	21	1273	1293	UUUGUUGAUGGUCAUCUAUUC	CGAUGGAUGAUUGUCAACGAA	Cleavage
sly-miR827-5p	Solyc09g060110.3.1	2.5	-1.0	1	21	3227	3247	UUUGUUGAUGGUCAUCUAUUC	UCAUGGAUGAUUGUUAACAAA	Cleavage
sly-miR827-5p	Solyc03g006160.1.1	2.5	-1.0	1	21	173	193	UUUGUUGAUGGUCAUCUAUUC	CAAAUGAUGAUCAUCAACAAA	Cleavage
sly-miR827-5p	Solyc04g079710.3.1	2.5	-1.0	1	21	75	95	UUUGUUGAUGGUCAUCUAUUC	AGGUAAAUGAUCAUUAACAAA	Cleavage
sly-miR827-5p	Solyc06g071780.3.1	2.5	-1.0	1	21	2408	2428	UUUGUUGAUGGUCAUCUAUUC	UCAUAAAUGAUCGUCAAUAAA	Cleavage

sly-miR827-5p	Solyc07g039190.3.1	3.0	-1.0	1	21	1211	1231	UUUGUUGAUGGUCAUCUAUUC	GAGUAGAUGAUCAUCAAAGAA	Cleavage
sly-miR827-5p	Solyc05g007740.2.1	3.0	-1.0	1	21	1061	1081	UUUGUUGAUGGUCAUCUAUUC	GAAUAGUUGGCCAUCAAGAAA	Cleavage
sly-miR827-5p	Solyc04g050225.1.1	3.0	-1.0	1	21	242	262	UUUGUUGAUGGUCAUCUAUUC	AGGAAGAUGAUCAUCAACAGA	Cleavage
sly-miR827-5p	Solyc12g049320.2.1	3.0	-1.0	1	21	932	952	UUUGUUGAUGGUCAUCUAUUC	CAAUAGAAGAUGAUCAACAAA	Translation
sly-miR827-5p	Solyc04g079710.3.1	3.0	-1.0	1	21	133	153	UUUGUUGAUGGUCAUCUAUUC	AGGUAAAUGAUUAUUAACAAA	Cleavage
sly-miR827-5p	Solyc01g112320.3.1	3.0	-1.0	1	21	2974	2994	UUUGUUGAUGGUCAUCUAUUC	AUAUAGAUGACCAUAAGCAAC	Cleavage
sly-miR827-5p	Solyc04g077260.3.1	3.0	-1.0	1	21	1410	1430	UUUGUUGAUGGUCAUCUAUUC	UGAUAAAUAAUCAUCAACAAA	Cleavage
sly-miR827-5p	Solyc04g050010.2.1	3.0	-1.0	1	21	691	710	UUUGUUGAUGGUCAUCUAUUC	AAAUA-AUGAUCAUCAACAAG	Cleavage
sly-miR827-5p	Solyc09g011080.3.1	3.0	-1.0	1	21	1262	1282	UUUGUUGAUGGUCAUCUAUUC	CCAAAGAUGACUAUCGAUAAG	Cleavage
sly-miR827-5p	Solyc09g075480.3.1	3.0	-1.0	1	21	1518	1538	UUUGUUGAUGGUCAUCUAUUC	CCAUAGUUGACCAACAGCAAA	Cleavage
sly-miR828a	Solyc02g077250.2.1	2.0	-1.0	1	22	578	599	UCUUGCUCAAAUGAGUAUUCCA	UGCAAUAUUCAUUUGAUCAAGA	Cleavage
sly-miR828a	Solyc06g048770.3.1	2.0	-1.0	1	22	143	164	UCUUGCUCAAAUGAGUAUUCCA	ACAAAUAUACAUUUGAGUAAGA	Cleavage
sly-miR828a	Solyc08g082890.3.1	2.5	-1.0	1	22	490	511	UCUUGCUCAAAUGAGUAUUCCA	UGGAAUACGCAUUUGACCAAGA	Cleavage
sly-miR828a	Solyc12g010730.2.1	2.5	-1.0	1	22	1706	1727	UCUUGCUCAAAUGAGUAUUCCA	AGGAAGGUUUAUUUGAGCAAGA	Cleavage
sly-miR828a	Solyc10g018710.1.1	2.5	-1.0	1	22	380	401	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
sly-miR828a	Solyc05g032780.1.1	2.5	-1.0	1	22	503	524	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
sly-miR828a	Solyc11g045640.1.1	2.5	-1.0	1	22	524	545	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
sly-miR828a	Solyc05g012840.1.1	2.5	-1.0	1	22	296	317	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
sly-miR828a	Solyc11g031960.2.1	2.5	-1.0	1	22	460	481	UCUUGCUCAAAUGAGUAUUCCA	CUAAAUGCACAUUUGAGCAAGU	Cleavage
sly-miR828a	Solyc10g005550.2.1	3.0	-1.0	1	22	328	349	UCUUGCUCAAAUGAGUAUUCCA	UGGAAUACUCAUUUGAAGAAGA	Cleavage
sly-miR828a	Solyc01g087730.3.1	3.0	-1.0	1	22	1077	1098	UCUUGCUCAAAUGAGUAUUCCA	CCGAAUGCUUAAUUGAGCGAGA	Translation
sly-miR828a	Solyc02g093040.3.1	3.0	-1.0	1	22	1018	1039	UCUUGCUCAAAUGAGUAUUCCA	AAGAAUGGUCAUUUGGGCAAGU	Cleavage
sly-miR828a	Solyc10g011900.3.1	3.0	-1.0	1	22	187	208	UCUUGCUCAAAUGAGUAUUCCA	UAAAAUAUUUAUUUGAGAAGGA	Cleavage
sly-miR828a	Solyc01g098080.3.1	3.0	-1.0	1	22	980	1000	UCUUGCUCAAAUGAGUAUUCCA	UGUAGUG-UCAUUUGAGCAAGA	Cleavage
sly-miR828a	Solyc10g062020.1.1	3.0	-1.0	1	22	643	665	UCUUGCUCAAAUGAG-UAUUCCA	CCAAAUAAUUCAUUUGGGCAAGA	Cleavage
sly-miR828a	Solyc03g013240.3.1	3.0	-1.0	1	22	314	335	UCUUGCUCAAAUGAGUAUUCCA	CCAUAUGGUUAUUUGAGCAAGA	Cleavage
sly-miR828a	Solyc09g074190.2.1	3.0	-1.0	1	22	2136	2157	UCUUGCUCAAAUGAGUAUUCCA	AGAAACACUCAUUUGAGAAGGA	Cleavage
sly-miR828a	Solyc09g074200.2.1	3.0	-1.0	1	22	1937	1958	UCUUGCUCAAAUGAGUAUUCCA	AGAAACACUCAUUUGAGAAGGA	Cleavage
sly-miR828a	Solyc10g085505.1.1	3.0	-1.0	1	22	531	552	UCUUGCUCAAAUGAGUAUUCCA	CAAAAAGCUCAUUGGAGCAAGA	Cleavage
sly-miR828a	Solyc04g071000.1.1	3.0	-1.0	1	22	2008	2029	UCUUGCUCAAAUGAGUAUUCCA	CCAAGAACUCAUUUUAGCAAGA	Cleavage
sly-miR828a	Solyc02g063180.3.1	3.0	-1.0	1	22	366	387	UCUUGCUCAAAUGAGUAUUCCA	UAAAAUCCACAUUUGAGCAAGU	Cleavage
sly-miR845b-5p	Solyc09g091260.3.1	2.0	-1.0	1	19	5101	5119	UCAAUUGGUAUCAGAGCAA	UUGUUCUGAUGCUGAUUGA	Cleavage
sly-miR845b-5p	Solyc03g097355.1.1	2.0	-1.0	1	19	1582	1600	UCAAUUGGUAUCAGAGCAA	CUUCUCUGAUACCAAUUGA	Cleavage
sly-miR845b-5p	Solyc01g111660.3.1	2.5	-1.0	1	19	41	59	UCAAUUGGUAUCAGAGCAA	UUCCUCUGAUACAAAUUGA	Cleavage
sly-miR845b-5p	Solyc01g080550.2.1	2.5	-1.0	1	19	419	437	UCAAUUGGUAUCAGAGCAA	UGGCUUUGAUACUAGUUGA	Cleavage
sly-miR845b-5p	Solyc05g012080.3.1	2.5	-1.0	1	19	897	915	UCAAUUGGUAUCAGAGCAA	UUUUUAUGAUACCAAUUGA	Cleavage
sly-miR845b-5p	Solyc01g108390.3.1	3.0	-1.0	1	19	321	339	UCAAUUGGUAUCAGAGCAA	UUGCUCUGGUACCUAUUGU	Cleavage
sly-miR845b-5p	Solyc04g057990.3.1	3.0	-1.0	1	19	5175	5193	UCAAUUGGUAUCAGAGCAA	UUGCUCUGAUACUAACUGU	Cleavage
sly-miR845b-5p	Solyc05g020043.1.1	3.0	-1.0	1	19	467	485	UCAAUUGGUAUCAGAGCAA	UUGUUCUGGUAUUGAUUGG	Cleavage
sly-miR845b-5p	Solyc09g092690.3.1	3.0	-1.0	1	19	2363	2381	UCAAUUGGUAUCAGAGCAA	UUGCUCUGAUAACAAUUCA	Cleavage
sly-miR845b-5p	Solyc02g086580.3.1	3.0	-1.0	1	19	1072	1090	UCAAUUGGUAUCAGAGCAA	UUGCAUUGGUGCUAAUUGA	Cleavage
sly-miR845b-5p	Solyc08g077930.3.1	3.0	-1.0	1	19	327	345	UCAAUUGGUAUCAGAGCAA	UUGCUGAGGUACCAAUUGA	Cleavage
sly-miR845b-5p	Solyc08g077920.3.1	3.0	-1.0	1	19	339	357	UCAAUUGGUAUCAGAGCAA	UUGCUGAGGUACCAAUUGA	Cleavage
sly-miR845b-5p	Solyc10g080260.2.1	3.0	-1.0	1	19	2452	2470	UCAAUUGGUAUCAGAGCAA	UUGUACUGAAACCAAUUGA	Translation
sly-miR845b-5p	Solyc03g083350.3.1	3.0	-1.0	1	19	1559	1577	UCAAUUGGUAUCAGAGCAA	UUGUGCUUAUACCAAUUGA	Cleavage
sly-miR845b-5p	Solyc07g063260.3.1	3.0	-1.0	1	19	1201	1219	UCAAUUGGUAUCAGAGCAA	UUGCUACGAUACUAAUUGA	Cleavage
sly-miR845b-5p	Solyc06g051550.3.1	3.0	-1.0	1	19	1861	1879	UCAAUUGGUAUCAGAGCAA	UUUAUUUGAUAUCAAUUGA	Cleavage
sly-miR845b-5p	Solyc03g097320.3.1	3.0	-1.0	1	19	2393	2411	UCAAUUGGUAUCAGAGCAA	UUGAUGUGAUACUGAUUGA	Cleavage
sly-miR845b-5p	Solyc11g066370.2.1	3.0	-1.0	1	19	2157	2175	UCAAUUGGUAUCAGAGCAA	UGGAUCUGGUACCAAUUGG	Cleavage
sly-miR845b-5p	Solyc07g022790.3.1	3.0	-1.0	1	19	3142	3160	UCAAUUGGUAUCAGAGCAA	UUCCUGUGAUAUUAAUUGA	Cleavage

sly-miR845b-5p	Solyc10g050350.1.1	3.0	-1.0	1	19	119	137	UCAAUUGGUAUCAGAGCAA	UUGACAUGAUACCAAUUGA	Cleavage
sly-miR845b-5p	Solyc10g050400.1.1	3.0	-1.0	1	19	119	137	UCAAUUGGUAUCAGAGCAA	UUGACAUGAUACCAAUUGA	Cleavage
sly-miR9471a-3p	Solyc02g089260.3.1	2.5	-1.0	1	21	1571	1591	UUGGCUGAGUGAGCAUCACGG	AUGUCAGGUUCACUCAGCCAA	Cleavage
sly-miR9471a-3p	Solyc03g111100.1.1	3.0	-1.0	1	21	512	532	UUGGCUGAGUGAGCAUCACGG	UUGUGAUGUUUCCUCAGCCAG	Translation
sly-miR9471a-3p	Solyc10g005690.3.1	3.0	-1.0	1	21	2084	2104	UUGGCUGAGUGAGCAUCACGG	GUGUGGUGUUUACUCGGCUAG	Cleavage
sly-miR9471a-3p	Solyc07g017320.1.1	3.0	-1.0	1	21	63	83	UUGGCUGAGUGAGCAUCACGG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471a-3p	Solyc00g040290.2.1	3.0	-1.0	1	21	328	348	UUGGCUGAGUGAGCAUCACGG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471a-3p	Solyc00g040390.2.1	3.0	-1.0	1	21	329	349	UUGGCUGAGUGAGCAUCACGG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471a-3p	Solyc07g014580.3.1	3.0	-1.0	1	21	543	563	UUGGCUGAGUGAGCAUCACGG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471a-3p	Solyc08g082850.3.1	3.0	-1.0	1	21	1176	1196	UUGGCUGAGUGAGCAUCACGG	CAUUGAUGCUUACUCGGCUGA	Cleavage
sly-miR9471a-3p	Solyc09g061750.2.1	3.0	-1.0	1	21	1310	1330	UUGGCUGAGUGAGCAUCACGG	CAGUGCUGUUCGCUCAGCCAU	Cleavage
sly-miR9471a-3p	Solyc05g013253.1.1	3.0	-1.0	1	21	1302	1322	UUGGCUGAGUGAGCAUCACGG	GGAUGUUGCUCAUUCAGCCGA	Cleavage
sly-miR9471a-5p	Solyc12g009620.2.1	3.0	-1.0	1	21	855	875	CAGGUGCUCACUCAGCUAAUA	AGUUGGUUGAGAGAGCACUUG	Translation
sly-miR9471a-5p	Solyc12g019110.2.1	3.0	-1.0	1	21	914	934	CAGGUGCUCACUCAGCUAAUA	CUUUGGCUGAGAGGGCACUUG	Translation
sly-miR9471b-3p	Solyc02g089260.3.1	2.5	-1.0	1	21	1571	1591	UUGGCUGAGUGAGCAUCACUG	AUGUCAGGUUCACUCAGCCAA	Cleavage
sly-miR9471b-3p	Solyc09g061750.2.1	3.0	-1.0	1	21	1310	1330	UUGGCUGAGUGAGCAUCACUG	CAGUGCUGUUCGCUCAGCCAU	Cleavage
sly-miR9471b-3p	Solyc08g082850.3.1	3.0	-1.0	1	21	1176	1196	UUGGCUGAGUGAGCAUCACUG	CAUUGAUGCUUACUCGGCUGA	Cleavage
sly-miR9471b-3p	Solyc07g017320.1.1	3.0	-1.0	1	21	63	83	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471b-3p	Solyc00g040290.2.1	3.0	-1.0	1	21	328	348	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471b-3p	Solyc00g040390.2.1	3.0	-1.0	1	21	329	349	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471b-3p	Solyc07g014580.3.1	3.0	-1.0	1	21	543	563	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
sly-miR9471b-3p	Solyc03g111100.1.1	3.0	-1.0	1	21	512	532	UUGGCUGAGUGAGCAUCACUG	UUGUGAUGUUUCCUCAGCCAG	Translation
sly-miR9471b-3p	Solyc10g005690.3.1	3.0	-1.0	1	21	2084	2104	UUGGCUGAGUGAGCAUCACUG	GUGUGGUGUUUACUCGGCUAG	Cleavage
sly-miR9471b-3p	Solyc05g013253.1.1	3.0	-1.0	1	21	1302	1322	UUGGCUGAGUGAGCAUCACUG	GGAUGUUGCUCAUUCAGCCGA	Cleavage
sly-miR9471b-3p	Solyc11g071310.1.1	3.0	-1.0	1	21	467	487	UUGGCUGAGUGAGCAUCACUG	UGGCUGUGCUCAUUCAGCCAA	Cleavage
sly-miR9472-3p	Solyc01g080150.3.1	0.5	-1.0	1	21	639	659	UUCACAAUCUCUGCUGAAAAA	GUUUUCAGCAGAGGUUGUGAA	Cleavage
sly-miR9472-3p	Solyc11g040080.1.1	0.5	-1.0	1	21	88	108	UUCACAAUCUCUGCUGAAAAA	CAUUUCAGCAGGGAUUGUGAA	Cleavage
sly-miR9472-3p	Solyc05g007250.3.1	2.5	-1.0	1	21	818	838	UUCACAAUCUCUGCUGAAAAA	GUUCUUAGCGGAGAUUGUGAG	Cleavage
sly-miR9472-3p	Solyc03g113215.1.1	2.5	-1.0	1	21	21	41	UUCACAAUCUCUGCUGAAAAA	GAUUUUGUUAGAGAUUGUGAA	Cleavage
sly-miR9472-3p	Solyc03g113220.3.1	2.5	-1.0	1	21	1358	1378	UUCACAAUCUCUGCUGAAAAA	GAUUUUGUUAGAGAUUGUGAA	Cleavage
sly-miR9472-3p	Solyc08g067260.3.1	2.5	-1.0	1	21	86	106	UUCACAAUCUCUGCUGAAAAA	UCUAUCAACGGAGAUUGUGAA	Cleavage
sly-miR9472-3p	Solyc04g079140.3.1	3.0	-1.0	1	21	508	528	UUCACAAUCUCUGCUGAAAAA	ACUGGCAGCAGAGAUUGUGAA	Cleavage
sly-miR9472-3p	Solyc04g072050.3.1	3.0	-1.0	1	21	1385	1405	UUCACAAUCUCUGCUGAAAAA	CUUUUGAGCGGAGAAUGUGAA	Cleavage
sly-miR9472-3p	Solyc04g078270.3.1	3.0	-1.0	1	21	3203	3223	UUCACAAUCUCUGCUGAAAAA	UCCUUCAGCAGAGGUUGUGGC	Cleavage
sly-miR9472-3p	Solyc04g078290.3.1	3.0	-1.0	1	21	2300	2320	UUCACAAUCUCUGCUGAAAAA	UCCUUCAGCAGAGGUUGUGGC	Cleavage
sly-miR9472-3p	Solyc07g042170.3.1	3.0	-1.0	1	21	152	172	UUCACAAUCUCUGCUGAAAAA	GGCUUCAUCGGAGAUUGUGGA	Cleavage
sly-miR9472-3p	Solyc01g057270.3.1	3.0	-1.0	1	21	1735	1755	UUCACAAUCUCUGCUGAAAAA	UGUUCCAGUAGAGAGUGUGAA	Cleavage
sly-miR9472-3p	Solyc01g007025.1.1	3.0	-1.0	1	21	39	59	UUCACAAUCUCUGCUGAAAAA	AAUUUCACUAGAGAUUAUGAA	Cleavage
sly-miR9472-3p	Solyc01g007000.3.1	3.0	-1.0	1	21	108	128	UUCACAAUCUCUGCUGAAAAA	AAUUUCACUAGAGAUUAUGAA	Cleavage
sly-miR9472-3p	Solyc08g075840.3.1	3.0	-1.0	1	21	2361	2381	UUCACAAUCUCUGCUGAAAAA	CAUAUCAGCAGAGAUAGUGGA	Cleavage
sly-miR9472-3p	Solyc01g111680.3.1	3.0	-1.0	1	21	3104	3124	UUCACAAUCUCUGCUGAAAAA	AAUUGUAGCAGAGAUUUUGAA	Cleavage
sly-miR9472-5p	Solyc02g085400.3.1	1.5	-1.0	1	21	954	974	UUUCAGUAGACGUUGUGAAUA	GCUUCGCAACGUUUACUGGAA	Cleavage
sly-miR9472-5p	Solyc08g076200.3.1	2.5	-1.0	1	21	826	846	UUUCAGUAGACGUUGUGAAUA	CGUUUACAAUGUUUGCUGGAA	Cleavage
sly-miR9472-5p	Solyc07g006300.3.1	2.5	-1.0	1	21	1652	1672	UUUCAGUAGACGUUGUGAAUA	UGUUAACUAUGUCUACUGAAA	Cleavage
sly-miR9472-5p	Solyc02g093860.3.1	2.5	-1.0	1	21	1421	1441	UUUCAGUAGACGUUGUGAAUA	CUUUCACAAUGUUUGUUGGAA	Cleavage
sly-miR9472-5p	Solyc10g008170.3.1	2.5	-1.0	1	21	697	717	UUUCAGUAGACGUUGUGAAUA	CUUUGACAAUGUCUGCUGAAG	Cleavage
sly-miR9472-5p	Solyc01g080670.3.1	2.5	-1.0	1	21	1052	1072	UUUCAGUAGACGUUGUGAAUA	CGUCCAAAACGUCUGCUGAAA	Cleavage
sly-miR9472-5p	Solyc03g053100.3.1	3.0	-1.0	1	21	1411	1432	UUUCAG-UAGACGUUGUGAAUA	CAUUCACAACGUCUAUCUGAAA	Cleavage
sly-miR9472-5p	Solyc01g066380.3.1	3.0	-1.0	1	21	216	236	UUUCAGUAGACGUUGUGAAUA	UGUUAAUAACGUCUCCUGAAA	Cleavage
sly-miR9472-5p	Solyc03g097990.3.1	3.0	-1.0	1	21	378	398	UUUCAGUAGACGUUGUGAAUA	GAGUCACAUUGUCUACUGAAA	Cleavage

sly-miR9472-5p	Solyc12g006000.1.1	3.0	-1.0	1	21	1940	1960	UUUCAGUAGACGUUGUGAAUA	CAUUUCCAACGUCUACUGACA	Cleavage
sly-miR9472-5p	Solyc06g082780.3.1	3.0	-1.0	1	21	847	867	UUUCAGUAGACGUUGUGAAUA	UUUUUACAACUUCUGCUGGAA	Translation
sly-miR9472-5p	Solyc06g069000.3.1	3.0	-1.0	1	21	383	403	UUUCAGUAGACGUUGUGAAUA	AAUACUCAAUGUCUGCUGAAA	Cleavage
sly-miR9473-1-3p	Solyc07g008320.3.1	0.0	-1.0	1	21	7863	7883	AAACGAGUUCAGAUUUACAGC	GCUGUAAAUCUGAACUCGUUU	Cleavage
sly-miR9473-1-3p	Solyc04g082600.3.1	2.5	-1.0	1	21	2713	2733	AAACGAGUUCAGAUUUACAGC	UUUGUAAAUUUGAAUUUGUUG	Cleavage
sly-miR9473-1-3p	Solyc09g090650.3.1	2.5	-1.0	1	21	359	379	AAACGAGUUCAGAUUUACAGC	UUUGUGAAUCUGAACUUUUUU	Cleavage
sly-miR9473-1-3p	Solyc11g071250.2.1	2.5	-1.0	1	21	223	243	AAACGAGUUCAGAUUUACAGC	UUAGCAAAUCUGGACUCGUUU	Cleavage
sly-miR9473-1-3p	Solyc08g074260.3.1	3.0	-1.0	1	21	963	983	AAACGAGUUCAGAUUUACAGC	GCAGUAAUUCUGGACUUGUUU	Cleavage
sly-miR9473-1-3p	Solyc07g054490.3.1	3.0	-1.0	1	21	240	260	AAACGAGUUCAGAUUUACAGC	AUUUUAGAUUUGAGCUUGUUU	Cleavage
sly-miR9473-1-3p	Solyc10g079300.2.1	3.0	-1.0	1	21	397	417	AAACGAGUUCAGAUUUACAGC	UUUGAAAAUUUUAACUCGUUU	Translation
sly-miR9473-1-3p	Solyc08g066210.3.1	3.0	-1.0	1	21	814	834	AAACGAGUUCAGAUUUACAGC	UGUAUGGAUUUGAACUUGUUU	Cleavage
sly-miR9473-1-5p	Solyc07g008320.3.1	0.0	-1.0	1	21	7941	7961	UGGCUGUAAAUCUAAACUCGU	ACGAGUUUAGAUUUACAGCCA	Cleavage
sly-miR9473-1-5p	Solyc10g006330.3.1	2.0	-1.0	1	21	894	914	UGGCUGUAAAUCUAAACUCGU	UGGAGUUGGGAUUUAUAGCCA	Cleavage
sly-miR9473-1-5p	Solyc03g026190.3.1	2.5	-1.0	1	21	1716	1736	UGGCUGUAAAUCUAAACUCGU	AAGAGUUUGGAGUUACAGUCA	Translation
sly-miR9473-1-5p	Solyc10g078970.1.1	3.0	-1.0	1	21	595	615	UGGCUGUAAAUCUAAACUCGU	GUGAGUUUAGAUUUGCACUUA	Cleavage
sly-miR9473-1-5p	Solyc12g015660.2.1	3.0	-1.0	1	21	2295	2315	UGGCUGUAAAUCUAAACUCGU	GAGAGUUUAGAUUUAUGAUCA	Cleavage
sly-miR9473-2-3p	Solyc07g008320.3.1	0.5	-1.0	1	21	7939	7959	GCUGUAAAUCUGAACUCGUUU	GAACGAGUUUAGAUUUACAGC	Cleavage
sly-miR9473-2-3p	Solyc12g096290.2.1	3.0	-1.0	1	21	992	1012	GCUGUAAAUCUGAACUCGUUU	AGCUGAGUUCAGAUUUGCAGA	Cleavage
sly-miR9473-2-3p	Solyc07g062110.3.1	3.0	-1.0	1	21	723	743	GCUGUAAAUCUGAACUCGUUU	GAAUGACUGCAGAUUUACAGC	Cleavage
sly-miR9473-2-3p	Solyc05g054560.3.1	3.0	-1.0	1	21	536	556	GCUGUAAAUCUGAACUCGUUU	CGAUGCGUUCAGAUUUGUGGC	Cleavage
sly-miR9473-2-5p	Solyc07g008320.3.1	0.5	-1.0	1	21	7861	7881	ACGAGUUUAGAUUUACAGCCA	UGGCUGUAAAUCUGAACUCGU	Cleavage
sly-miR9473-2-5p	Solyc04g008280.2.1	2.5	-1.0	1	21	884	904	ACGAGUUUAGAUUUACAGCCA	AUGUUGUAAGUCAAAACUCGU	Cleavage
sly-miR9473-2-5p	Solyc06g051790.3.1	3.0	-1.0	1	21	1549	1569	ACGAGUUUAGAUUUACAGCCA	GGGGUGUGAAUUUGAACUUGU	Cleavage
sly-miR9473-2-5p	Solyc04g005425.1.1	3.0	-1.0	1	21	219	239	ACGAGUUUAGAUUUACAGCCA	UCUUUGUAGAUCUAAGCUUGU	Cleavage
sly-miR9473-2-5p	Solyc02g063040.3.1	3.0	-1.0	1	21	1116	1136	ACGAGUUUAGAUUUACAGCCA	AGACUAUAAAUUUAAGCUCGU	Cleavage
sly-miR9473-2-5p	Solyc01g099880.3.1	3.0	-1.0	1	21	1267	1287	ACGAGUUUAGAUUUACAGCCA	AAGCUCUAAAUCUGAGCUCGC	Cleavage
sly-miR9476-1-3p	Solyc04g058140.3.1	2.0	-1.0	1	21	1611	1631	AAAAAGAUGCAGGACUAGACC	UAUCUAGUCUUGUAUCUUUUC	Cleavage
sly-miR9476-1-3p	Solyc01g090350.3.1	2.5	-1.0	1	21	542	562	AAAAAGAUGCAGGACUAGACC	UGUUUAAUUCUGCAUUUUUUU	Cleavage
sly-miR9476-1-3p	Solyc02g083900.3.1	2.5	-1.0	1	21	2384	2404	AAAAAGAUGCAGGACUAGACC	AAGCUGGUUUUGCAUCUUUUU	Cleavage
sly-miR9476-1-3p	Solyc07g025170.3.1	2.5	-1.0	1	21	3467	3487	AAAAAGAUGCAGGACUAGACC	ACUCUAGUUUUGCUUCUUUUU	Cleavage
sly-miR9476-1-3p	Solyc07g062450.3.1	2.5	-1.0	1	21	1271	1291	AAAAAGAUGCAGGACUAGACC	GUUCUGAUUCUGCAUUUUUUU	Cleavage
sly-miR9476-1-3p	Solyc02g069370.3.1	3.0	-1.0	1	21	275	295	AAAAAGAUGCAGGACUAGACC	AGUCUAGUUCUGCGUUUUGUU	Cleavage
sly-miR9476-1-3p	Solyc00g009050.2.1	3.0	-1.0	1	21	1338	1358	AAAAAGAUGCAGGACUAGACC	GAUUUAGUGUUGUAUCUUUUU	Cleavage
sly-miR9476-1-3p	Solyc04g007440.1.1	3.0	-1.0	1	21	21	41	AAAAAGAUGCAGGACUAGACC	CCUCUUGUUCUUCAUCUUUUU	Translation
sly-miR9476-1-3p	Solyc04g014820.3.1	3.0	-1.0	1	21	233	253	AAAAAGAUGCAGGACUAGACC	AAUCUGGGCCUUCAUCUUUUU	Translation
sly-miR9476-1-3p	Solyc07g041330.2.1	3.0	-1.0	1	21	5	25	AAAAAGAUGCAGGACUAGACC	AUUCAAGUUCAGCAUCUUUUU	Translation
sly-miR9476-1-3p	Solyc09g098540.3.1	3.0	-1.0	1	21	1407	1427	AAAAAGAUGCAGGACUAGACC	UUUUUGGACUUGCAUUUUUUU	Cleavage
sly-miR9476-1-3p	Solyc02g022870.3.1	3.0	-1.0	1	21	1733	1753	AAAAAGAUGCAGGACUAGACC	AUUCCAGUUCAGCAUCUUUUU	Translation
sly-miR9476-1-3p	Solyc04g050570.3.1	3.0	-1.0	1	21	1342	1362	AAAAAGAUGCAGGACUAGACC	CUUGUAUUCCUGCAUCUUUUC	Cleavage
sly-miR9476-1-5p	Solyc06g054540.3.1	2.0	-1.0	1	21	272	292	UCUAGUCCUGCAUCUUUUUUU	AGGAGAAGAUGCAGGAUUAGG	Cleavage
sly-miR9476-1-5p	Solyc09g007120.3.1	2.0	-1.0	1	21	120	140	UCUAGUCCUGCAUCUUUUUUU	AAAACAAGAUGUAGGGCUAGA	Cleavage
sly-miR9476-1-5p	Solyc09g031970.3.1	2.0	-1.0	1	21	798	818	UCUAGUCCUGCAUCUUUUUUU	GGAAAAAGAUGCAGCACUAGG	Cleavage
sly-miR9476-1-5p	Solyc05g006950.3.1	2.5	-1.0	1	21	1616	1636	UCUAGUCCUGCAUCUUUUUUU	AAAGAAAGAUGCAGGAUCAGA	Cleavage
sly-miR9476-1-5p	Solyc11g005640.2.1	2.5	-1.0	1	21	1367	1387	UCUAGUCCUGCAUCUUUUUUU	UAAAAAAGAAGUAGGACUAGG	Cleavage
sly-miR9476-1-5p	Solyc03g044273.1.1	2.5	-1.0	1	21	3100	3120	UCUAGUCCUGCAUCUUUUUUU	AGAAAAUGAUGCAUGACUAGA	Cleavage
sly-miR9476-1-5p	Solyc03g119730.3.1	3.0	-1.0	1	21	2065	2085	UCUAGUCCUGCAUCUUUUUUU	AAAAAAAGACGCAGGACUGGU	Cleavage
sly-miR9476-1-5p	Solyc01g067360.3.1	3.0	-1.0	1	21	250	270	UCUAGUCCUGCAUCUUUUUUU	AGGAGAAGAUGCAAGAUUAGA	Cleavage
sly-miR9476-1-5p	Solyc07g006650.3.1	3.0	-1.0	1	21	433	453	UCUAGUCCUGCAUCUUUUUUU	GAGAAAAGAUGAAGGAUUGGA	Translation
sly-miR9476-1-5p	Solyc12g019080.2.1	3.0	-1.0	1	21	2094	2114	UCUAGUCCUGCAUCUUUUUUU	AAAAGAAAGUGUAGGACUGGA	Cleavage
sly-miR9476-1-5p	Solyc01g111310.3.1	3.0	-1.0	1	21	1563	1583	UCUAGUCCUGCAUCUUUUUUU	UAAAAAAGAUGCAUGACUGGU	Cleavage

sly-miR9476-1-5p	Solyc02g065220.3.1	3.0	-1.0	1	21	928	948	UCUAGUCCUGCAUCUUUUUUU	CAAAAAAGAUGCAGGAGUUGA	Cleavage
sly-miR9476-1-5p	Solyc07g055270.1.1	3.0	-1.0	1	21	566	586	UCUAGUCCUGCAUCUUUUUUU	AGAAAAAAAUGGAGGACUGGA	Translation
sly-miR9476-1-5p	Solyc01g100455.1.1	3.0	-1.0	1	21	469	489	UCUAGUCCUGCAUCUUUUUUU	CAAAGAAAGUGCAGGAUUAGG	Cleavage
sly-miR9476-1-5p	Solyc06g073780.3.1	3.0	-1.0	1	21	3562	3582	UCUAGUCCUGCAUCUUUUUUU	UGAGAUAGAUGCAGCACUAGA	Cleavage
sly-miR9476-1-5p	Solyc09g015530.3.1	3.0	-1.0	1	21	1010	1030	UCUAGUCCUGCAUCUUUUUUU	ACAAAAAUGUGCAGGAUUGGG	Cleavage
sly-miR9476-2-3p	Solyc04g058140.3.1	2.0	-1.0	1	21	1611	1631	AAAAAGAUGCAGGACUAGACC	UAUCUAGUCUUGUAUCUUUUC	Cleavage
sly-miR9476-2-3p	Solyc01g090350.3.1	2.5	-1.0	1	21	542	562	AAAAAGAUGCAGGACUAGACC	UGUUUAAUUCUGCAUUUUUUU	Cleavage
sly-miR9476-2-3p	Solyc02g083900.3.1	2.5	-1.0	1	21	2384	2404	AAAAAGAUGCAGGACUAGACC	AAGCUGGUUUUGCAUCUUUUU	Cleavage
sly-miR9476-2-3p	Solyc07g025170.3.1	2.5	-1.0	1	21	3467	3487	AAAAAGAUGCAGGACUAGACC	ACUCUAGUUUUGCUUCUUUUU	Cleavage
sly-miR9476-2-3p	Solyc07g062450.3.1	2.5	-1.0	1	21	1271	1291	AAAAAGAUGCAGGACUAGACC	GUUCUGAUUCUGCAUUUUUUU	Cleavage
sly-miR9476-2-3p	Solyc02g069370.3.1	3.0	-1.0	1	21	275	295	AAAAAGAUGCAGGACUAGACC	AGUCUAGUUCUGCGUUUUGUU	Cleavage
sly-miR9476-2-3p	Solyc00g009050.2.1	3.0	-1.0	1	21	1338	1358	AAAAAGAUGCAGGACUAGACC	GAUUUAGUGUUGUAUCUUUUU	Cleavage
sly-miR9476-2-3p	Solyc04g007440.1.1	3.0	-1.0	1	21	21	41	AAAAAGAUGCAGGACUAGACC	CCUCUUGUUCUUCAUCUUUUU	Translation
sly-miR9476-2-3p	Solyc04g014820.3.1	3.0	-1.0	1	21	233	253	AAAAAGAUGCAGGACUAGACC	AAUCUGGGCCUUCAUCUUUUU	Translation
sly-miR9476-2-3p	Solyc07g041330.2.1	3.0	-1.0	1	21	5	25	AAAAAGAUGCAGGACUAGACC	AUUCAAGUUCAGCAUCUUUUU	Translation
sly-miR9476-2-3p	Solyc09g098540.3.1	3.0	-1.0	1	21	1407	1427	AAAAAGAUGCAGGACUAGACC	UUUUUGGACUUGCAUUUUUUU	Cleavage
sly-miR9476-2-3p	Solyc02g022870.3.1	3.0	-1.0	1	21	1733	1753	AAAAAGAUGCAGGACUAGACC	AUUCCAGUUCAGCAUCUUUUU	Translation
sly-miR9476-2-3p	Solyc04g050570.3.1	3.0	-1.0	1	21	1342	1362	AAAAAGAUGCAGGACUAGACC	CUUGUAUUCCUGCAUCUUUUC	Cleavage
sly-miR9476-2-5p	Solyc06g054540.3.1	2.0	-1.0	1	21	272	292	UCUAGUCCUGCAUCUUUUUUU	AGGAGAAGAUGCAGGAUUAGG	Cleavage
sly-miR9476-2-5p	Solyc09g007120.3.1	2.0	-1.0	1	21	120	140	UCUAGUCCUGCAUCUUUUUUU	AAAACAAGAUGUAGGGCUAGA	Cleavage
sly-miR9476-2-5p	Solyc09g031970.3.1	2.0	-1.0	1	21	798	818	UCUAGUCCUGCAUCUUUUUUU	GGAAAAAGAUGCAGCACUAGG	Cleavage
sly-miR9476-2-5p	Solyc05g006950.3.1	2.5	-1.0	1	21	1616	1636	UCUAGUCCUGCAUCUUUUUUU	AAAGAAAGAUGCAGGAUCAGA	Cleavage
sly-miR9476-2-5p	Solyc11g005640.2.1	2.5	-1.0	1	21	1367	1387	UCUAGUCCUGCAUCUUUUUUU	UAAAAAAGAAGUAGGACUAGG	Cleavage
sly-miR9476-2-5p	Solyc03g044273.1.1	2.5	-1.0	1	21	3100	3120	UCUAGUCCUGCAUCUUUUUUU	AGAAAAUGAUGCAUGACUAGA	Cleavage
sly-miR9476-2-5p	Solyc03g119730.3.1	3.0	-1.0	1	21	2065	2085	UCUAGUCCUGCAUCUUUUUUU	AAAAAAAGACGCAGGACUGGU	Cleavage
sly-miR9476-2-5p	Solyc01g067360.3.1	3.0	-1.0	1	21	250	270	UCUAGUCCUGCAUCUUUUUUU	AGGAGAAGAUGCAAGAUUAGA	Cleavage
sly-miR9476-2-5p	Solyc07g006650.3.1	3.0	-1.0	1	21	433	453	UCUAGUCCUGCAUCUUUUUUU	GAGAAAAGAUGAAGGAUUGGA	Translation
sly-miR9476-2-5p	Solyc12g019080.2.1	3.0	-1.0	1	21	2094	2114	UCUAGUCCUGCAUCUUUUUUU	AAAAGAAAGUGUAGGACUGGA	Cleavage
sly-miR9476-2-5p	Solyc01g111310.3.1	3.0	-1.0	1	21	1563	1583	UCUAGUCCUGCAUCUUUUUUU	UAAAAAAGAUGCAUGACUGGU	Cleavage
sly-miR9476-2-5p	Solyc02g065220.3.1	3.0	-1.0	1	21	928	948	UCUAGUCCUGCAUCUUUUUUU	CAAAAAAGAUGCAGGAGUUGA	Cleavage
sly-miR9476-2-5p	Solyc07g055270.1.1	3.0	-1.0	1	21	566	586	UCUAGUCCUGCAUCUUUUUUU	AGAAAAAAAUGGAGGACUGGA	Translation
sly-miR9476-2-5p	Solyc01g100455.1.1	3.0	-1.0	1	21	469	489	UCUAGUCCUGCAUCUUUUUUU	CAAAGAAAGUGCAGGAUUAGG	Cleavage
sly-miR9476-2-5p	Solyc06g073780.3.1	3.0	-1.0	1	21	3562	3582	UCUAGUCCUGCAUCUUUUUUU	UGAGAUAGAUGCAGCACUAGA	Cleavage
sly-miR9476-2-5p	Solyc09g015530.3.1	3.0	-1.0	1	21	1010	1030	UCUAGUCCUGCAUCUUUUUUU	ACAAAAAUGUGCAGGAUUGGG	Cleavage
sly-miR9478-3p	Solyc10g085690.2.1	1.0	-1.0	1	21	3260	3280	UUCGAUGACAUAUUUGAGCCU	AAGUUCAGAUAUGUCAUCGAA	Cleavage
sly-miR9478-3p	Solyc04g054190.3.1	2.0	-1.0	1	21	3607	3627	UUCGAUGACAUAUUUGAGCCU	GGGAUCAAAUAUGUCAUUGAG	Cleavage
sly-miR9478-3p	Solyc01g006620.3.1	2.0	-1.0	1	21	1748	1768	UUCGAUGACAUAUUUGAGCCU	UUGAUCAAAUAUGUCAUUGGA	Cleavage
sly-miR9478-3p	Solyc08g067420.3.1	2.5	-1.0	1	21	1053	1073	UUCGAUGACAUAUUUGAGCCU	UUGUUCAGAUGUGUCAUCGAC	Cleavage
sly-miR9478-3p	Solyc04g072380.3.1	2.5	-1.0	1	21	3256	3276	UUCGAUGACAUAUUUGAGCCU	GAGUUCAAAUAUGUCAUUGGU	Cleavage
sly-miR9478-3p	Solyc01g068350.3.1	2.5	-1.0	1	21	157	177	UUCGAUGACAUAUUUGAGCCU	AAGCUGAUAUAUGUCAUUGAA	Cleavage
sly-miR9478-3p	Solyc11g020478.1.1	3.0	-1.0	1	21	52	72	UUCGAUGACAUAUUUGAGCCU	CGGCUCAAGUAUGUUGUUGAU	Cleavage
sly-miR9478-3p	Solyc03g116100.3.1	3.0	-1.0	1	21	1568	1588	UUCGAUGACAUAUUUGAGCCU	GUGCUCAAAUAUUUUAUUGAG	Cleavage
sly-miR9478-3p	Solyc02g091390.3.1	3.0	-1.0	1	21	1604	1624	UUCGAUGACAUAUUUGAGCCU	UAGCUUAAAGAUGUUAUCGAG	Cleavage
sly-miR9478-3p	Solyc10g055640.2.1	3.0	-1.0	1	21	21	41	UUCGAUGACAUAUUUGAGCCU	UAGCUCAAAUAUGUCAUAUAA	Cleavage
sly-miR9478-3p	Solyc01g088550.3.1	3.0	-1.0	1	21	547	567	UUCGAUGACAUAUUUGAGCCU	AAGUCUAAAUAUGUCAUUGGA	Cleavage
sly-miR9478-3p	Solyc12g008890.2.1	3.0	-1.0	1	21	2291	2311	UUCGAUGACAUAUUUGAGCCU	AAGCUCUAAUAGGUUAUCGAA	Translation
sly-miR9478-3p	Solyc12g100140.2.1	3.0	-1.0	1	21	365	385	UUCGAUGACAUAUUUGAGCCU	UAGGUCAAAUAUGUCGUCUAA	Cleavage
sly-miR9478-5p	Solyc05g007970.3.1	2.0	-1.0	1	22	471	492	GCUUAAAUAUGUAGAUCGAACU	CAAUCAAUGUACAUAUUUAAGC	Cleavage
sly-miR9478-5p	Solyc02g070580.1.1	2.5	-1.0	1	22	364	385	GCUUAAAUAUGUAGAUCGAACU	AACUUGAUUUACAUGUUUGGGC	Cleavage
sly-miR9478-5p	Solyc09g005910.3.1	3.0	-1.0	1	22	503	524	GCUUAAAUAUGUAGAUCGAACU	UCUUCCAUUUGCAUAUUUAAGG	Cleavage

sly-miR9478-5p	Solyc01g008250.3.1	3.0	-1.0	1	22	904	925	GCUUAAAUAUGUAGAUCGAACU	GUUUGGAUUUGUAUAUUUGAGC	Cleavage
sly-miR9478-5p	Solyc07g043510.3.1	3.0	-1.0	1	22	1725	1746	GCUUAAAUAUGUAGAUCGAACU	UCUUCGGGCUAUAUGUUUGAGC	Cleavage
sly-miR9478-5p	Solyc03g007870.3.1	3.0	-1.0	1	22	794	815	GCUUAAAUAUGUAGAUCGAACU	UUAUUGAUCUAUAUAUUUGAAC	Cleavage

454 **Supplementary Table S13.** Characterization of *S. pennellii* miRNA target genes using psRNAtarget. Expectation (Exp),
455 maximum energy to unpair (UPE).

Mature miRNA	Target	Exp	UPE	Star miRNA	End miRNA	Star target	End target	miRNA aligned fragment	Target aligned fragment	Inhibition
spe-miR1128-5p	Sopen08g030810.1	2.5	-1.0	1	21	176	196	UACUACUCCCUCCGUCCCAAA	UUUUGAACGGAGGGAGUAGUG	Cleavage
spe-miR1128-5p	Sopen11g016530.3	2.5	-1.0	1	21	3688	3708	UACUACUCCCUCCGUCCCAAA	CGUGGGACAGAGGGAGUAGUU	Cleavage
spe-miR1128-5p	Sopen11g016530.2	2.5	-1.0	1	21	3688	3708	UACUACUCCCUCCGUCCCAAA	CGUGGGACAGAGGGAGUAGUU	Cleavage
spe-miR1128-5p	Sopen06g004850.1	2.5	-1.0	1	21	562	582	UACUACUCCCUCCGUCCCAAA	CCUAGGCCGGAGGGAGUGGUA	Cleavage
spe-miR1128-5p	Sopen11g006790.1	3.0	-1.0	1	21	85	105	UACUACUCCCUCCGUCCCAAA	GCUGGGACGGAGGUGGUGGUG	Cleavage
spe-miR1128-5p	Sopen06g001550.1	3.0	-1.0	1	21	1034	1054	UACUACUCCCUCCGUCCCAAA	AUUCCGAUGGAGGGAGUAGUG	Cleavage
spe-miR1128-5p	Sopen06g001550.2	3.0	-1.0	1	21	1034	1054	UACUACUCCCUCCGUCCCAAA	AUUCCGAUGGAGGGAGUAGUG	Cleavage
spe-miR1446-5p	Sopen00g005310.1	2.0	-1.0	1	22	2169	2190	UGAACUCUCUCCCUCAAUGGCU	ACCCAUUGAGGGAGAGGGUUUU	Cleavage
spe-miR1446-5p	Sopen06g028960.1	2.0	-1.0	1	22	926	947	UGAACUCUCUCCCUCAAUGGCU	ACAGAUUCAGGGAGAGAGUUCA	Cleavage
spe-miR1446-5p	Sopen03g030140.1	2.5	-1.0	1	22	789	810	UGAACUCUCUCCCUCAAUGGCU	AGCCUUUGAGGGAGAGAGUUUC	Cleavage
spe-miR1446-5p	Sopen05g016560.1	2.5	-1.0	1	22	1980	2001	UGAACUCUCUCCCUCAAUGGCU	ACCCGUUGAGGGAGAGGGUUUU	Cleavage
spe-miR1446-5p	Sopen08g003520.1	3.0	-1.0	1	22	292	313	UGAACUCUCUCCCUCAAUGGCU	AGCCAUAGAGAGGGAGAGUUCA	Cleavage
spe-miR1446-5p	Sopen04g009650.1	3.0	-1.0	1	22	2397	2418	UGAACUCUCUCCCUCAAUGGCU	GUCCAUUGAGGGAGAGGGUGCU	Cleavage
spe-miR1446-5p	Sopen00g013010.1	3.0	-1.0	1	22	1780	1801	UGAACUCUCUCCCUCAAUGGCU	ACCCAUGGAGGGAGAGGGUUUU	Cleavage
spe-miR1446-5p	Sopen12g025890.1	3.0	-1.0	1	22	273	294	UGAACUCUCUCCCUCAAUGGCU	UCCGAUUGAGGGAGAGGGUUUC	Cleavage
spe-miR1446-5p	Sopen10g013910.1	3.0	-1.0	1	22	5	26	UGAACUCUCUCCCUCAAUGGCU	GCCCAUUAGUGGAGAGAGUUCA	Cleavage
spe-miR1446-5p	Sopen03g034990.1	3.0	-1.0	1	22	794	815	UGAACUCUCUCCCUCAAUGGCU	UGGCAUUUGGUGAGAGAGUUCA	Cleavage
spe-miR1446-5p	Sopen02g035880.1	3.0	-1.0	1	22	155	176	UGAACUCUCUCCCUCAAUGGCU	UUAUAUUAAGGAAGAGAGUUCA	Translation
spe-miR1446a-5p	Sopen12g016490.1	2.5	-1.0	1	20	20	39	UUCUGAACUCUCUCCCUCAA	AUGAGGGAGAGAAUUUGGAA	Cleavage
spe-miR1446a-5p	Sopen07g010080.1	2.5	-1.0	1	20	4787	4806	UUCUGAACUCUCUCCCUCAA	AUGAGGUUGAGAGUUCAGAA	Cleavage
spe-miR1446a-5p	Sopen12g017330.1	3.0	-1.0	1	20	3164	3183	UUCUGAACUCUCUCCCUCAA	AUGAGGGUGACAGUUCAGAA	Translation
spe-miR1446a-5p	Sopen06g028960.1	1.5	-1.0	1	20	931	950	UUCUGAACUCUCUCCCUCAA	UUCAGGGAGAGAGUUCAGAG	Cleavage
spe-miR1446a-5p	Sopen06g014290.1	2.5	-1.0	1	20	7118	7137	UUCUGAACUCUCUCCCUCAA	AUGAGGCUGAGAGUUCAGAA	Cleavage
spe-miR1446a-5p	Sopen09g021610.1	3.0	-1.0	1	20	2039	2058	UUCUGAACUCUCUCCCUCAA	UUGAUGGAGAGGGUUCCGAA	Cleavage
spe-miR1446a-5p	Sopen05g018560.1	3.0	-1.0	1	20	2001	2020	UUCUGAACUCUCUCCCUCAA	UGGAGGGAAAGGGUUCAGAA	Cleavage
spe-miR1446a-5p	Sopen06g008160.1	3.0	-1.0	1	20	3514	3533	UUCUGAACUCUCUCCCUCAA	UUGAAGGAGGAAGUUCAGAA	Translation
spe-miR1446a-5p	Sopen05g005930.1	3.0	-1.0	1	20	763	782	UUCUGAACUCUCUCCCUCAA	GCGAGGGAGGGAGUUUGGGA	Cleavage
spe-miR1446a-5p	Sopen12g032410.1	3.0	-1.0	1	20	23	42	UUCUGAACUCUCUCCCUCAA	AUGAGGGAGAUAGUUUGGAG	Translation
spe-miR1446a-5p	Sopen09g036500.1	3.0	-1.0	1	20	34	53	UUCUGAACUCUCUCCCUCAA	AUGAGAGAGAGAGUUGAGGA	Cleavage
spe-miR1446a-5p	Sopen03g012350.1	3.0	-1.0	1	20	2477	2496	UUCUGAACUCUCUCCCUCAA	AUGAGGCUGAGAGUUCGGAA	Cleavage
spe-miR1446a-5p	Sopen08g006610.1	3.0	-1.0	1	20	2264	2283	UUCUGAACUCUCUCCCUCAA	AUGAGGCUGAGAGUUCGGAA	Cleavage
spe-miR1446a-5p	Sopen02g009050.1	3.0	-1.0	1	20	6439	6458	UUCUGAACUCUCUCCCUCAA	AUGAGGCAGACAGUUCGGAA	Translation
spe-miR156-10-3p	Sopen09g009280.1	1.5	-1.0	1	22	177	198	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGCAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen11g017850.1	1.5	-1.0	1	22	696	717	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGCAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen05g032860.1	1.5	-1.0	1	22	536	557	GCUCACUGCUCUAUCUGUCACC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
spe-miR156-10-3p	Sopen01g018450.1	2.5	-1.0	1	22	726	747	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen05g021610.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen07g007550.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen12g012420.1	2.5	-1.0	1	22	108	129	GCUCACUGCUCUAUCUGUCACC	UUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen03g011830.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	AUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen05g016080.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	UUUGACGGAUGGAGUAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen06g030090.1	2.5	-1.0	1	22	2171	2192	GCUCACUGCUCUAUCUGUCACC	CAACACAGAUGGAGCAGUGGGU	Cleavage
spe-miR156-10-3p	Sopen01g009890.1	3.0	-1.0	1	22	111	132	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen02g005260.1	3.0	-1.0	1	22	1896	1917	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen01g026210.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage

spe-miR156-10-3p	Sopen07g013640.1	3.0	-1.0	1	22	1584	1605	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen04g014930.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen01g026620.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen04g017490.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GCUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen04g018070.1	3.0	-1.0	1	22	27	48	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen11g015420.1	3.0	-1.0	1	22	498	519	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen10g007760.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen05g012810.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGAUAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen10g015900.1	3.0	-1.0	1	22	21	42	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen01g019370.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen03g017480.1	3.0	-1.0	1	22	192	213	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen10g021890.1	3.0	-1.0	1	22	159	180	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen11g022550.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen07g021080.1	3.0	-1.0	1	22	150	171	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen03g016910.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen01g025760.1	3.0	-1.0	1	22	27	48	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen08g007980.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen10g018420.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-10-3p	Sopen04g016790.1	3.0	-1.0	1	22	243	264	GCUCACUGCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen09g013220.1	3.0	-1.0	1	22	1122	1143	GCUCACUGCUCUAUCUGUCACC	AUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen06g010360.1	3.0	-1.0	1	22	96	117	GCUCACUGCUCUAUCUGUCACC	CUUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-10-3p	Sopen05g034390.1	3.0	-1.0	1	22	1017	1038	GCUCACUGCUCUAUCUGUCACC	AAGGAUAGAUAGAGGAGUGAGG	Cleavage
spe-miR156-10-5p	Sopen05g006830.1	1.0	-1.0	1	21	1240	1260	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen12g018830.1	1.0	-1.0	1	21	970	990	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen05g010900.1	1.0	-1.0	1	21	1117	1137	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen10g029320.1	1.0	-1.0	1	21	763	783	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen04g017460.1	1.0	-1.0	1	21	790	810	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen05g011450.1	1.0	-1.0	1	21	655	675	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen03g033930.1	1.0	-1.0	1	21	1156	1176	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-10-5p	Sopen09g017280.1	2.5	-1.0	1	21	1851	1871	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
spe-miR156-10-5p	Sopen11g017850.1	2.5	-1.0	1	21	172	192	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-10-5p	Sopen03g012590.1	2.5	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-10-5p	Sopen07g013960.1	2.5	-1.0	1	21	148	168	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-10-5p	Sopen05g024090.1	2.5	-1.0	1	21	445	465	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-10-5p	Sopen04g012860.1	3.0	-1.0	1	21	275	295	UGACAGAAGAGAGUGAGCACA	UGGGCUUAUUUUCUUCUGUUA	Cleavage
spe-miR156-10-5p	Sopen09g035820.2	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-10-5p	Sopen09g035820.1	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-10-5p	Sopen04g011710.1	3.0	-1.0	1	21	1715	1735	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
spe-miR156-10-5p	Sopen09g013010.1	3.0	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGUUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-10-5p	Sopen02g019370.1	3.0	-1.0	1	21	366	386	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation
spe-miR156-10-5p	Sopen03g016770.1	3.0	-1.0	1	21	205	225	UGACAGAAGAGAGUGAGCACA	GAUGCUCCUUCUCUUGUGUCA	Cleavage
spe-miR156-10-5p	Sopen03g036450.2	3.0	-1.0	1	21	2280	2300	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
spe-miR156-11-3p	Sopen05g023590.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUUUCAUC	GUUGAAAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-11-3p	Sopen09g009280.1	2.5	-1.0	1	22	177	198	GCUCACUGCUCUAUCUUUCAUC	GUUGACAGAUGGAGCAGUGAGA	Cleavage
spe-miR156-11-3p	Sopen11g017850.1	2.5	-1.0	1	22	696	717	GCUCACUGCUCUAUCUUUCAUC	GUUGACAGAUGGAGCAGUGAGG	Cleavage
spe-miR156-11-3p	Sopen05g032860.1	2.5	-1.0	1	22	536	557	GCUCACUGCUCUAUCUUUCAUC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
spe-miR156-11-3p	Sopen04g032730.1	3.0	-1.0	1	22	1264	1285	GCUCACUGCUCUAUCUUUCAUC	GAUGGAAGAUACAGUAGUGAGU	Translation
spe-miR156-11-3p	Sopen12g013380.1	3.0	-1.0	1	22	606	627	GCUCACUGCUCUAUCUUUCAUC	UAUUGAAGGUAGGGUAGUGAGC	Cleavage
spe-miR156-11-5p	Sopen01g050530.1	2.0	-1.0	1	21	499	519	UGACAGAAGGGCGUGAGCACA	CUUGCUCAUGCCCUCCUGUCA	Cleavage
spe-miR156-11-5p	Sopen12g013740.1	2.5	-1.0	1	21	96	116	UGACAGAAGGGCGUGAGCACA	UAUGCUCAAGCCUUUUUGUCA	Cleavage

spe-miR156-11-5p	Sopen11g017950.1	2.5	-1.0	1	21	652	672	UGACAGAAGGGCGUGAGCACA	GCUGUUCAAGCCCUUUUGUCA	Cleavage
spe-miR156-11-5p	Sopen05g006830.1	3.0	-1.0	1	21	1240	1260	UGACAGAAGGGCGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen12g018830.1	3.0	-1.0	1	21	970	990	UGACAGAAGGGCGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen11g018340.1	3.0	-1.0	1	21	811	831	UGACAGAAGGGCGUGAGCACA	GGUGCUCAUGUUCUUAUGUCA	Cleavage
spe-miR156-11-5p	Sopen05g010900.1	3.0	-1.0	1	21	1117	1137	UGACAGAAGGGCGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen10g029320.1	3.0	-1.0	1	21	763	783	UGACAGAAGGGCGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen04g017460.1	3.0	-1.0	1	21	790	810	UGACAGAAGGGCGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen05g011450.1	3.0	-1.0	1	21	655	675	UGACAGAAGGGCGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen05g007100.1	3.0	-1.0	1	21	20	40	UGACAGAAGGGCGUGAGCACA	UUUCUUCAUGUUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen04g004380.1	3.0	-1.0	1	21	1	21	UGACAGAAGGGCGUGAGCACA	AUGGCUGAUGCCUUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen06g015580.1	3.0	-1.0	1	21	556	576	UGACAGAAGGGCGUGAGCACA	UAUGCUCCCGCUCUUGUGUCA	Cleavage
spe-miR156-11-5p	Sopen03g004440.1	3.0	-1.0	1	21	3805	3825	UGACAGAAGGGCGUGAGCACA	GAUGCUGAAGCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen03g004450.1	3.0	-1.0	1	21	2539	2559	UGACAGAAGGGCGUGAGCACA	GAUGCUGAAGCUCUUCUGUCA	Cleavage
spe-miR156-11-5p	Sopen03g033930.1	3.0	-1.0	1	21	1156	1176	UGACAGAAGGGCGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-3p	Sopen03g020680.1	2.5	-1.0	1	22	27	48	GCUCACUUCUCAUUCUGUCAGC	GUUGACAGAAGGAGAAGUGAGG	Cleavage
spe-miR156-12-3p	Sopen01g017900.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCAUUCUGUCAGC	GUUGACGGAAGGAGAAGUGAGA	Cleavage
spe-miR156-12-3p	Sopen01g049520.1	3.0	-1.0	1	22	160	181	GCUCACUUCUCAUUCUGUCAGC	CCUGACAGAUUGGGAAGUGAGA	Cleavage
spe-miR156-12-3p	Sopen09g012740.1	3.0	-1.0	1	22	2587	2608	GCUCACUUCUCAUUCUGUCAGC	UAUGGUGGGAUGGGAAGUGGGC	Cleavage
spe-miR156-12-3p	Sopen08g008190.1	3.0	-1.0	1	22	19	40	GCUCACUUCUCAUUCUGUCAGC	CUUGAAAGAAUGGGAAGAGAGC	Cleavage
spe-miR156-12-3p	Sopen04g004220.1	3.0	-1.0	1	22	2599	2620	GCUCACUUCUCAUUCUGUCAGC	GAAUAUGGGAUGGGAAGUGAGC	Cleavage
spe-miR156-12-3p	Sopen07g010200.1	3.0	-1.0	1	22	235	256	GCUCACUUCUCAUUCUGUCAGC	GAGGAGAGGAUGAGGAGUGAGG	Cleavage
spe-miR156-12-3p	Sopen07g013020.1	3.0	-1.0	1	22	462	483	GCUCACUUCUCAUUCUGUCAGC	GAAGACAGUGUGGGAGGUGAGU	Cleavage
spe-miR156-12-3p	Sopen07g013050.1	3.0	-1.0	1	22	483	504	GCUCACUUCUCAUUCUGUCAGC	GAAGACAGUGUGGGAGGUGAGU	Cleavage
spe-miR156-12-5p	Sopen05g006830.1	1.0	-1.0	1	21	1240	1260	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen12g018830.1	1.0	-1.0	1	21	970	990	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen05g010900.1	1.0	-1.0	1	21	1117	1137	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen10g029320.1	1.0	-1.0	1	21	763	783	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen04g017460.1	1.0	-1.0	1	21	790	810	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen05g011450.1	1.0	-1.0	1	21	655	675	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen03g033930.1	1.0	-1.0	1	21	1156	1176	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-12-5p	Sopen09g017280.1	2.5	-1.0	1	21	1851	1871	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
spe-miR156-12-5p	Sopen11g017850.1	2.5	-1.0	1	21	172	192	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-12-5p	Sopen03g012590.1	2.5	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-12-5p	Sopen07g013960.1	2.5	-1.0	1	21	148	168	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-12-5p	Sopen05g024090.1	2.5	-1.0	1	21	445	465	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-12-5p	Sopen04g012860.1	3.0	-1.0	1	21	275	295	UGACAGAAGAGAGUGAGCACA	UGGGCUUAUUUUCUUCUGUUA	Cleavage
spe-miR156-12-5p	Sopen09g035820.2	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-12-5p	Sopen09g035820.1	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-12-5p	Sopen04g011710.1	3.0	-1.0	1	21	1715	1735	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
spe-miR156-12-5p	Sopen09g013010.1	3.0	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGUUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-12-5p	Sopen02g019370.1	3.0	-1.0	1	21	366	386	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation
spe-miR156-12-5p	Sopen03g016770.1	3.0	-1.0	1	21	205	225	UGACAGAAGAGAGUGAGCACA	GAUGCUCCUUCUCUUGUGUCA	Cleavage
spe-miR156-12-5p	Sopen03g036450.2	3.0	-1.0	1	21	2280	2300	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
spe-miR156-1-3p	Sopen07g005330.1	1.5	-1.0	1	21	922	942	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGAAGUAUAGAGAGU	Cleavage
spe-miR156-1-3p	Sopen11g005950.1	2.0	-1.0	1	21	460	480	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGAAGUAUAGAGAGA	Cleavage
spe-miR156-1-3p	Sopen10g016840.1	2.0	-1.0	1	21	2263	2283	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGGAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen05g028940.1	2.5	-1.0	1	21	184	204	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGAAGUGUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen05g028940.2	2.5	-1.0	1	21	1381	1401	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGAAGUGUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen12g022690.1	2.5	-1.0	1	21	1597	1617	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGGAGUAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen05g031120.1	2.5	-1.0	1	21	2205	2225	GCUCUCUAUGCUUCCGUCAUC	GUUGACGGAAGCAGAGGGAGU	Cleavage

spe-miR156-1-3p	Sopen01g009030.1	3.0	-1.0	1	21	445	465	GCUCUCUAUGCUUCCGUCAUC	CAUGAUGGAAGUGUGGAGAGA	Cleavage
spe-miR156-1-3p	Sopen08g014040.1	3.0	-1.0	1	21	689	709	GCUCUCUAUGCUUCCGUCAUC	UAUGGUGGAAGCAUAAAGAGU	Cleavage
spe-miR156-1-3p	Sopen06g011730.1	3.0	-1.0	1	21	433	453	GCUCUCUAUGCUUCCGUCAUC	GCCGAUGGAAGUAUAGAGAGA	Cleavage
spe-miR156-1-3p	Sopen01g009520.1	3.0	-1.0	1	21	709	729	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGUAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen09g028050.1	3.0	-1.0	1	21	2365	2385	GCUCUCUAUGCUUCCGUCAUC	GCAGAUGGGAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen02g013440.1	3.0	-1.0	1	21	1447	1467	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGGAGUGUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen03g033260.1	3.0	-1.0	1	21	1429	1449	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGUAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen07g004340.1	3.0	-1.0	1	21	1495	1515	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGGAGUGUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen05g001080.1	3.0	-1.0	1	21	1744	1764	GCUCUCUAUGCUUCCGUCAUC	GCAGAUGGGAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen06g011980.1	3.0	-1.0	1	21	1645	1665	GCUCUCUAUGCUUCCGUCAUC	GCUGAUGGUAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen09g028050.2	3.0	-1.0	1	21	2365	2385	GCUCUCUAUGCUUCCGUCAUC	GCAGAUGGGAGCAUAGAGAGG	Cleavage
spe-miR156-1-3p	Sopen03g024190.1	3.0	-1.0	1	21	2953	2973	GCUCUCUAUGCUUCCGUCAUC	GCAGAUGGGAGCAUAGAGAGG	Cleavage
spe-miR156-1-5p	Sopen05g010900.1	1.5	-1.0	1	21	1118	1138	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-1-5p	Sopen10g029320.1	1.5	-1.0	1	21	764	784	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-1-5p	Sopen04g017460.1	1.5	-1.0	1	21	791	811	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-1-5p	Sopen11g001610.2	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-1-5p	Sopen11g001610.1	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-1-5p	Sopen05g006830.1	2.0	-1.0	1	21	1241	1261	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
spe-miR156-1-5p	Sopen02g019370.1	2.0	-1.0	1	21	367	387	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
spe-miR156-1-5p	Sopen01g049090.1	2.0	-1.0	1	21	495	515	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
spe-miR156-1-5p	Sopen12g018830.1	2.5	-1.0	1	21	971	991	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-1-5p	Sopen05g011450.1	2.5	-1.0	1	21	656	676	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-1-5p	Sopen03g033930.1	2.5	-1.0	1	21	1157	1177	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-1-5p	Sopen01g053840.1	3.0	-1.0	1	21	1089	1109	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
spe-miR156-1-5p	Sopen07g031690.1	3.0	-1.0	1	21	1270	1290	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
spe-miR156-1-5p	Sopen03g021270.1	3.0	-1.0	1	21	1155	1175	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-1-5p	Sopen08g008590.1	3.0	-1.0	1	21	922	942	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-1-5p	Sopen04g017690.1	3.0	-1.0	1	21	703	723	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-1-5p	Sopen03g038230.1	3.0	-1.0	1	21	2	22	UUGACAGAAGAUAGAGAGCAC	UGGGUUUUUAUCUUCUGUUAG	Cleavage
spe-miR156-2-3p	Sopen07g005330.1	2.0	-1.0	1	21	922	942	GCUCUCUAUGCUUCUGUCAUC	GCUGAUGGAAGUAUAGAGAGU	Cleavage
spe-miR156-2-3p	Sopen08g007190.1	2.5	-1.0	1	21	351	371	GCUCUCUAUGCUUCUGUCAUC	CGUGGCAGAAGCAUGGAGGGA	Cleavage
spe-miR156-2-3p	Sopen11g005950.1	2.5	-1.0	1	21	460	480	GCUCUCUAUGCUUCUGUCAUC	GCUGAUGGAAGUAUAGAGAGA	Cleavage
spe-miR156-2-3p	Sopen10g016840.1	2.5	-1.0	1	21	2263	2283	GCUCUCUAUGCUUCUGUCAUC	GCUGAUGGGAGCAUAGAGAGG	Cleavage
spe-miR156-2-3p	Sopen05g030160.1	2.5	-1.0	1	21	545	565	GCUCUCUAUGCUUCUGUCAUC	UGUGCCAGGAGCAUAGAGAGA	Cleavage
spe-miR156-2-3p	Sopen09g033110.1	2.5	-1.0	1	21	200	220	GCUCUCUAUGCUUCUGUCAUC	GCUUGCAGGAGCGUAGAGAGC	Cleavage
spe-miR156-2-3p	Sopen12g002130.1	3.0	-1.0	1	21	219	239	GCUCUCUAUGCUUCUGUCAUC	GAUGGUAGAAGCAAAGAGGGC	Cleavage
spe-miR156-2-3p	Sopen01g025830.1	3.0	-1.0	1	21	1117	1137	GCUCUCUAUGCUUCUGUCAUC	GGUGACAGAGGUGUGGAGGGU	Cleavage
spe-miR156-2-3p	Sopen05g028940.1	3.0	-1.0	1	21	184	204	GCUCUCUAUGCUUCUGUCAUC	GCUGAUGGAAGUGUAGAGAGG	Cleavage
spe-miR156-2-3p	Sopen05g028940.2	3.0	-1.0	1	21	1381	1401	GCUCUCUAUGCUUCUGUCAUC	GCUGAUGGAAGUGUAGAGAGG	Cleavage
spe-miR156-2-3p	Sopen12g022690.1	3.0	-1.0	1	21	1597	1617	GCUCUCUAUGCUUCUGUCAUC	GCUGAUGGGAGUAUAGAGAGG	Cleavage
spe-miR156-2-3p	Sopen05g031120.1	3.0	-1.0	1	21	2205	2225	GCUCUCUAUGCUUCUGUCAUC	GUUGACGGAAGCAGAGGGAGU	Cleavage
spe-miR156-2-3p	Sopen01g051890.1	3.0	-1.0	1	21	442	462	GCUCUCUAUGCUUCUGUCAUC	UCUAACAGAGGCAGAGAGAGC	Cleavage
spe-miR156-2-5p	Sopen05g010900.1	1.5	-1.0	1	21	1118	1138	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-2-5p	Sopen10g029320.1	1.5	-1.0	1	21	764	784	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-2-5p	Sopen04g017460.1	1.5	-1.0	1	21	791	811	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-2-5p	Sopen11g001610.2	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-2-5p	Sopen11g001610.1	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-2-5p	Sopen05g006830.1	2.0	-1.0	1	21	1241	1261	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
spe-miR156-2-5p	Sopen02g019370.1	2.0	-1.0	1	21	367	387	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
spe-miR156-2-5p	Sopen01g049090.1	2.0	-1.0	1	21	495	515	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage

spe-miR156-2-5p	Sopen12g018830.1	2.5	-1.0	1	21	971	991	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-2-5p	Sopen05g011450.1	2.5	-1.0	1	21	656	676	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-2-5p	Sopen03g033930.1	2.5	-1.0	1	21	1157	1177	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-2-5p	Sopen01g053840.1	3.0	-1.0	1	21	1089	1109	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
spe-miR156-2-5p	Sopen07g031690.1	3.0	-1.0	1	21	1270	1290	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
spe-miR156-2-5p	Sopen03g021270.1	3.0	-1.0	1	21	1155	1175	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-2-5p	Sopen08g008590.1	3.0	-1.0	1	21	922	942	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-2-5p	Sopen04g017690.1	3.0	-1.0	1	21	703	723	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-2-5p	Sopen03g038230.1	3.0	-1.0	1	21	2	22	UUGACAGAAGAUAGAGAGCAC	UGGGUUUUUAUCUUCUGUUAG	Cleavage
spe-miR156-3-3p	Sopen05g023480.1	3.0	-1.0	1	21	346	366	GCUCUUUAUUCUUCUGUCAUC	AGCGAAAGAAGAGUAAAGGGC	Cleavage
spe-miR156-3-3p	Sopen07g024410.1	2.5	-1.0	1	21	768	788	GCUCUUUAUUCUUCUGUCAUC	UUUGACUGAAGAAGAAAGAGC	Cleavage
spe-miR156-3-3p	Sopen10g032270.1	3.0	-1.0	1	21	2191	2211	GCUCUUUAUUCUUCUGUCAUC	GAUGACAUGAGAGUAGAGAGU	Cleavage
spe-miR156-3-3p	Sopen07g009400.1	3.0	-1.0	1	21	398	418	GCUCUUUAUUCUUCUGUCAUC	CAUGGUGGAGGAGUAAAGAGU	Cleavage
spe-miR156-3-3p	Sopen01g038560.1	3.0	-1.0	1	21	168	188	GCUCUUUAUUCUUCUGUCAUC	AGUGACAGAAGGAUGUGGAGC	Cleavage
spe-miR156-3-3p	Sopen01g038530.1	3.0	-1.0	1	21	1087	1107	GCUCUUUAUUCUUCUGUCAUC	UCAGCCGGAAGAAUGAAGAGC	Cleavage
spe-miR156-3-5p	Sopen05g010900.1	1.5	-1.0	1	21	1118	1138	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-3-5p	Sopen10g029320.1	1.5	-1.0	1	21	764	784	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-3-5p	Sopen04g017460.1	1.5	-1.0	1	21	791	811	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-3-5p	Sopen11g001610.2	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-3-5p	Sopen11g001610.1	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-3-5p	Sopen05g006830.1	2.0	-1.0	1	21	1241	1261	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
spe-miR156-3-5p	Sopen02g019370.1	2.0	-1.0	1	21	367	387	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
spe-miR156-3-5p	Sopen01g049090.1	2.0	-1.0	1	21	495	515	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
spe-miR156-3-5p	Sopen12g018830.1	2.5	-1.0	1	21	971	991	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-3-5p	Sopen05g011450.1	2.5	-1.0	1	21	656	676	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-3-5p	Sopen03g033930.1	2.5	-1.0	1	21	1157	1177	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-3-5p	Sopen01g053840.1	3.0	-1.0	1	21	1089	1109	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
spe-miR156-3-5p	Sopen07g031690.1	3.0	-1.0	1	21	1270	1290	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
spe-miR156-3-5p	Sopen03g021270.1	3.0	-1.0	1	21	1155	1175	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-3-5p	Sopen08g008590.1	3.0	-1.0	1	21	922	942	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-3-5p	Sopen04g017690.1	3.0	-1.0	1	21	703	723	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-3-5p	Sopen03g038230.1	3.0	-1.0	1	21	2	22	UUGACAGAAGAUAGAGAGCAC	UGGGUUUUUAUCUUCUGUUAG	Cleavage
spe-miR156-4-3p	Sopen05g023480.1	3.0	-1.0	1	20	347	366	GCUCUUUAUUCUUCUGUCAU	GCGAAAGAAGAGUAAAGGGC	Cleavage
spe-miR156-4-3p	Sopen07g024410.1	2.5	-1.0	1	20	769	788	GCUCUUUAUUCUUCUGUCAU	UUGACUGAAGAAGAAAGAGC	Cleavage
spe-miR156-4-3p	Sopen07g009400.1	3.0	-1.0	1	20	399	418	GCUCUUUAUUCUUCUGUCAU	AUGGUGGAGGAGUAAAGAGU	Cleavage
spe-miR156-4-3p	Sopen10g032270.1	3.0	-1.0	1	20	2192	2211	GCUCUUUAUUCUUCUGUCAU	AUGACAUGAGAGUAGAGAGU	Cleavage
spe-miR156-4-3p	Sopen01g038560.1	3.0	-1.0	1	20	169	188	GCUCUUUAUUCUUCUGUCAU	GUGACAGAAGGAUGUGGAGC	Cleavage
spe-miR156-4-3p	Sopen01g038530.1	3.0	-1.0	1	20	1088	1107	GCUCUUUAUUCUUCUGUCAU	CAGCCGGAAGAAUGAAGAGC	Cleavage
spe-miR156-4-5p	Sopen05g010900.1	1.5	-1.0	1	21	1118	1138	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-4-5p	Sopen10g029320.1	1.5	-1.0	1	21	764	784	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-4-5p	Sopen04g017460.1	1.5	-1.0	1	21	791	811	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-4-5p	Sopen11g001610.2	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-4-5p	Sopen11g001610.1	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-4-5p	Sopen05g006830.1	2.0	-1.0	1	21	1241	1261	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
spe-miR156-4-5p	Sopen02g019370.1	2.0	-1.0	1	21	367	387	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
spe-miR156-4-5p	Sopen01g049090.1	2.0	-1.0	1	21	495	515	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
spe-miR156-4-5p	Sopen12g018830.1	2.5	-1.0	1	21	971	991	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-4-5p	Sopen05g011450.1	2.5	-1.0	1	21	656	676	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-4-5p	Sopen03g033930.1	2.5	-1.0	1	21	1157	1177	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-4-5p	Sopen01g053840.1	3.0	-1.0	1	21	1089	1109	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage

spe-miR156-4-5p	Sopen07g031690.1	3.0	-1.0	1	21	1270	1290	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
spe-miR156-4-5p	Sopen03g021270.1	3.0	-1.0	1	21	1155	1175	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-4-5p	Sopen08g008590.1	3.0	-1.0	1	21	922	942	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-4-5p	Sopen04g017690.1	3.0	-1.0	1	21	703	723	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-4-5p	Sopen03g038230.1	3.0	-1.0	1	21	2	22	UUGACAGAAGAUAGAGAGCAC	UGGGUUUUUAUCUUCUGUUAG	Cleavage
spe-miR156-5-3p	Sopen05g023480.1	3.0	-1.0	1	20	347	366	GCUCUUUAUUCUUCUGUCAC	GCGAAAGAAGAGUAAAGGGC	Cleavage
spe-miR156-5-3p	Sopen07g024410.1	2.5	-1.0	1	20	769	788	GCUCUUUAUUCUUCUGUCAC	UUGACUGAAGAAGAAAGAGC	Cleavage
spe-miR156-5-3p	Sopen01g038560.1	3.0	-1.0	1	20	169	188	GCUCUUUAUUCUUCUGUCAC	GUGACAGAAGGAUGUGGAGC	Cleavage
spe-miR156-5-3p	Sopen07g009400.1	3.0	-1.0	1	20	399	418	GCUCUUUAUUCUUCUGUCAC	AUGGUGGAGGAGUAAAGAGU	Cleavage
spe-miR156-5-3p	Sopen01g038530.1	3.0	-1.0	1	20	1088	1107	GCUCUUUAUUCUUCUGUCAC	CAGCCGGAAGAAUGAAGAGC	Cleavage
spe-miR156-5-3p	Sopen10g032270.1	3.0	-1.0	1	20	2192	2211	GCUCUUUAUUCUUCUGUCAC	AUGACAUGAGAGUAGAGAGU	Cleavage
spe-miR156-5-5p	Sopen05g010900.1	1.5	-1.0	1	21	1118	1138	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-5-5p	Sopen10g029320.1	1.5	-1.0	1	21	764	784	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-5-5p	Sopen04g017460.1	1.5	-1.0	1	21	791	811	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-5-5p	Sopen11g001610.2	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-5-5p	Sopen11g001610.1	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-5-5p	Sopen05g006830.1	2.0	-1.0	1	21	1241	1261	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
spe-miR156-5-5p	Sopen02g019370.1	2.0	-1.0	1	21	367	387	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
spe-miR156-5-5p	Sopen01g049090.1	2.0	-1.0	1	21	495	515	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
spe-miR156-5-5p	Sopen12g018830.1	2.5	-1.0	1	21	971	991	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-5-5p	Sopen05g011450.1	2.5	-1.0	1	21	656	676	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-5-5p	Sopen03g033930.1	2.5	-1.0	1	21	1157	1177	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-5-5p	Sopen01g053840.1	3.0	-1.0	1	21	1089	1109	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
spe-miR156-5-5p	Sopen07g031690.1	3.0	-1.0	1	21	1270	1290	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
spe-miR156-5-5p	Sopen03g021270.1	3.0	-1.0	1	21	1155	1175	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-5-5p	Sopen08g008590.1	3.0	-1.0	1	21	922	942	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-5-5p	Sopen04g017690.1	3.0	-1.0	1	21	703	723	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-5-5p	Sopen03g038230.1	3.0	-1.0	1	21	2	22	UUGACAGAAGAUAGAGAGCAC	UGGGUUUUUAUCUUCUGUUAG	Cleavage
spe-miR156-6-3p	Sopen10g032270.1	2.5	-1.0	1	22	2190	2211	GCUCUCUAUUCUUCUGUCAUCA	CGAUGACAUGAGAGUAGAGAGU	Cleavage
spe-miR156-6-3p	Sopen01g039110.1	3.0	-1.0	1	22	534	556	GCUCUCUAUUCUUC-UGUCAUCA	UGAUGACAUGGAGAAUAGGGAGC	Cleavage
spe-miR156-6-3p	Sopen05g016520.1	3.0	-1.0	1	22	414	435	GCUCUCUAUUCUUCUGUCAUCA	UGAGGAUAGAGGAAUAGAGGGU	Cleavage
spe-miR156-6-3p	Sopen06g006710.1	3.0	-1.0	1	22	462	483	GCUCUCUAUUCUUCUGUCAUCA	UGUUGCUAGAGGAAUAGAGGGU	Cleavage
spe-miR156-6-3p	Sopen05g025470.1	3.0	-1.0	1	22	18	39	GCUCUCUAUUCUUCUGUCAUCA	UAAUGCUAGAAGAAUGGAGGGU	Cleavage
spe-miR156-6-3p	Sopen01g038560.1	3.0	-1.0	1	22	167	188	GCUCUCUAUUCUUCUGUCAUCA	AAGUGACAGAAGGAUGUGGAGC	Cleavage
spe-miR156-6-3p	Sopen07g005330.1	3.0	-1.0	1	22	921	942	GCUCUCUAUUCUUCUGUCAUCA	AGCUGAUGGAAGUAUAGAGAGU	Translation
spe-miR156-6-3p	Sopen09g018690.1	3.0	-1.0	1	22	34	55	GCUCUCUAUUCUUCUGUCAUCA	UUAAGGAGGAAGAAUAGAGAGC	Cleavage
spe-miR156-6-5p	Sopen05g010900.1	1.5	-1.0	1	21	1118	1138	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-6-5p	Sopen10g029320.1	1.5	-1.0	1	21	764	784	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-6-5p	Sopen04g017460.1	1.5	-1.0	1	21	791	811	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAA	Cleavage
spe-miR156-6-5p	Sopen11g001610.2	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-6-5p	Sopen11g001610.1	1.5	-1.0	1	21	177	197	UUGACAGAAGAUAGAGAGCAC	CAGCUUUUUAUCUUCUGUUAA	Cleavage
spe-miR156-6-5p	Sopen05g006830.1	2.0	-1.0	1	21	1241	1261	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAG	Cleavage
spe-miR156-6-5p	Sopen02g019370.1	2.0	-1.0	1	21	367	387	UUGACAGAAGAUAGAGAGCAC	UUGCUCUCUGUCUUCUGUUAC	Cleavage
spe-miR156-6-5p	Sopen01g049090.1	2.0	-1.0	1	21	495	515	UUGACAGAAGAUAGAGAGCAC	UGGCUCUUCAUCUUCUGUCAA	Cleavage
spe-miR156-6-5p	Sopen12g018830.1	2.5	-1.0	1	21	971	991	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-6-5p	Sopen05g011450.1	2.5	-1.0	1	21	656	676	UUGACAGAAGAUAGAGAGCAC	GUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-6-5p	Sopen03g033930.1	2.5	-1.0	1	21	1157	1177	UUGACAGAAGAUAGAGAGCAC	AUGCUCUCUCUCUUCUGUCAU	Cleavage
spe-miR156-6-5p	Sopen01g053840.1	3.0	-1.0	1	21	1089	1109	UUGACAGAAGAUAGAGAGCAC	GGAAUUUCUAUCUUUUGUCAA	Cleavage
spe-miR156-6-5p	Sopen07g031690.1	3.0	-1.0	1	21	1270	1290	UUGACAGAAGAUAGAGAGCAC	CCUUUCUCUGUUUUCUGUCAG	Cleavage
spe-miR156-6-5p	Sopen03g021270.1	3.0	-1.0	1	21	1155	1175	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage

spe-miR156-6-5p	Sopen08g008590.1	3.0	-1.0	1	21	922	942	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-6-5p	Sopen04g017690.1	3.0	-1.0	1	21	703	723	UUGACAGAAGAUAGAGAGCAC	AAGUUCUCUUUCUUUUGUUAA	Cleavage
spe-miR156-6-5p	Sopen03g038230.1	3.0	-1.0	1	21	2	22	UUGACAGAAGAUAGAGAGCAC	UGGGUUUUUAUCUUCUGUUAG	Cleavage
spe-miR156-7-3p	Sopen11g023160.1	2.5	-1.0	1	21	397	417	GCUUACUCUCUAUCUGUCACC	AUUGACGGAUGGAGAGUGAGA	Cleavage
spe-miR156-7-3p	Sopen05g023150.1	3.0	-1.0	1	21	153	173	GCUUACUCUCUAUCUGUCACC	AGUGACAUAUAGGGAGAAAGC	Cleavage
spe-miR156-7-3p	Sopen08g008400.1	3.0	-1.0	1	21	336	356	GCUUACUCUCUAUCUGUCACC	AGUGACAUAUAGAGAGAAGGC	Cleavage
spe-miR156-7-3p	Sopen06g026790.1	3.0	-1.0	1	21	4638	4658	GCUUACUCUCUAUCUGUCACC	CCUGGCAGAAAGAGAGUGGGC	Cleavage
spe-miR156-7-5p	Sopen05g006830.1	1.0	-1.0	1	21	1240	1260	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen12g018830.1	1.0	-1.0	1	21	970	990	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen05g010900.1	1.0	-1.0	1	21	1117	1137	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen10g029320.1	1.0	-1.0	1	21	763	783	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen04g017460.1	1.0	-1.0	1	21	790	810	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen05g011450.1	1.0	-1.0	1	21	655	675	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen03g033930.1	1.0	-1.0	1	21	1156	1176	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-7-5p	Sopen09g017280.1	2.5	-1.0	1	21	1851	1871	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
spe-miR156-7-5p	Sopen11g017850.1	2.5	-1.0	1	21	172	192	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-7-5p	Sopen03g012590.1	2.5	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-7-5p	Sopen07g013960.1	2.5	-1.0	1	21	148	168	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-7-5p	Sopen05g024090.1	2.5	-1.0	1	21	445	465	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-7-5p	Sopen04g012860.1	3.0	-1.0	1	21	275	295	UGACAGAAGAGAGUGAGCACA	UGGGCUUAUUUUCUUCUGUUA	Cleavage
spe-miR156-7-5p	Sopen09g035820.2	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-7-5p	Sopen09g035820.1	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-7-5p	Sopen04g011710.1	3.0	-1.0	1	21	1715	1735	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
spe-miR156-7-5p	Sopen09g013010.1	3.0	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGUUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-7-5p	Sopen02g019370.1	3.0	-1.0	1	21	366	386	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation
spe-miR156-7-5p	Sopen03g016770.1	3.0	-1.0	1	21	205	225	UGACAGAAGAGAGUGAGCACA	GAUGCUCCUUCUCUUGUGUCA	Cleavage
spe-miR156-7-5p	Sopen03g036450.2	3.0	-1.0	1	21	2280	2300	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
spe-miR156-8-3p	Sopen01g018660.1	2.5	-1.0	1	22	102	123	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGU	Cleavage
spe-miR156-8-3p	Sopen01g018660.1	3.0	-1.0	1	22	474	495	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen05g015100.1	3.0	-1.0	1	22	1668	1689	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen05g015100.1	3.0	-1.0	1	22	2118	2139	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen05g024620.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen05g024620.1	3.0	-1.0	1	22	339	360	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen01g018450.1	1.0	-1.0	1	22	726	747	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen05g021610.1	1.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen07g007550.1	1.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen12g012420.1	1.0	-1.0	1	22	108	129	GCUCACUUCUCUAUCUGUCACC	UUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen03g011830.1	1.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen01g009890.1	1.5	-1.0	1	22	111	132	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen02g005260.1	1.5	-1.0	1	22	1896	1917	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen01g026210.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen07g013640.1	1.5	-1.0	1	22	1584	1605	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen04g014930.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen01g026620.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen04g017490.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GCUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen04g018070.1	1.5	-1.0	1	22	27	48	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen11g015420.1	1.5	-1.0	1	22	498	519	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen10g007760.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen05g012810.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGAUAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen10g015900.1	1.5	-1.0	1	22	21	42	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage

spe-miR156-8-3p	Sopen01g019370.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen03g017480.1	1.5	-1.0	1	22	192	213	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen10g021890.1	1.5	-1.0	1	22	159	180	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen11g022550.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen07g021080.1	1.5	-1.0	1	22	150	171	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen03g016910.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen01g025760.1	1.5	-1.0	1	22	27	48	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen08g007980.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen10g018420.1	1.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen04g016790.1	1.5	-1.0	1	22	243	264	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen09g013220.1	1.5	-1.0	1	22	1122	1143	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen06g010360.1	1.5	-1.0	1	22	96	117	GCUCACUUCUCUAUCUGUCACC	CUUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen05g017830.1	2.0	-1.0	1	22	744	765	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen12g014150.1	2.0	-1.0	1	22	735	756	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen10g026080.1	2.0	-1.0	1	22	1650	1671	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen01g022420.1	2.0	-1.0	1	22	102	123	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen07g010090.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen12g011820.1	2.0	-1.0	1	22	48	69	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen04g019970.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen02g001170.1	2.0	-1.0	1	22	1188	1209	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen01g017270.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen03g020600.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen09g017650.1	2.0	-1.0	1	22	219	240	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen08g016940.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen03g019520.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGGCAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen07g018880.1	2.0	-1.0	1	22	4947	4968	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen04g013680.1	2.0	-1.0	1	22	111	132	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen03g016380.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen04g014110.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen09g020350.1	2.0	-1.0	1	22	108	129	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUCAGC	Cleavage
spe-miR156-8-3p	Sopen03g012430.1	2.0	-1.0	1	22	438	459	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen07g013370.1	2.0	-1.0	1	22	753	774	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen05g013320.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen12g013480.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen05g023590.1	2.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGAAAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen05g034390.1	2.0	-1.0	1	22	1017	1038	GCUCACUUCUCUAUCUGUCACC	AAGGAUAGAUAGAGGAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen06g008810.1	2.5	-1.0	1	22	1071	1092	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUCAGG	Cleavage
spe-miR156-8-3p	Sopen03g016590.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUAGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen04g014360.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGAUGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen05g016290.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGGUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen11g017650.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGAUGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen06g007370.1	2.5	-1.0	1	22	99	120	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUUAGA	Cleavage
spe-miR156-8-3p	Sopen10g013250.1	2.5	-1.0	1	22	687	708	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUGGAGAAGUAAGC	Cleavage
spe-miR156-8-3p	Sopen04g010720.1	2.5	-1.0	1	22	2742	2763	GCUCACUUCUCUAUCUGUCACC	GUUGACAAAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen12g011810.1	2.5	-1.0	1	22	75	96	GCUCACUUCUCUAUCUGUCACC	GUUGACCGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen09g015080.1	2.5	-1.0	1	22	27	48	GCUCACUUCUCUAUCUGUCACC	GUUGACCGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen09g014870.1	2.5	-1.0	1	22	255	276	GCUCACUUCUCUAUCUGUCACC	GUUGACCGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen08g007210.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUCACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen02g004230.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACAUAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen09g014050.1	2.5	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACUGAUGGAGAAGUGAGA	Cleavage

spe-miR156-8-3p	Sopen03g012270.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAUG	Cleavage
spe-miR156-8-3p	Sopen11g017930.1	3.0	-1.0	1	22	111	132	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAUA	Cleavage
spe-miR156-8-3p	Sopen07g015170.1	3.0	-1.0	1	22	102	123	GCUCACUUCUCUAUCUGUCACC	AGUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen09g014030.1	3.0	-1.0	1	22	6333	6354	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGAGAGA	Cleavage
spe-miR156-8-3p	Sopen10g014570.1	3.0	-1.0	1	22	2269	2290	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen09g019120.1	3.0	-1.0	1	22	312	333	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen09g017190.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAAUGAGG	Cleavage
spe-miR156-8-3p	Sopen04g018110.1	3.0	-1.0	1	22	2151	2172	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen09g009280.1	3.0	-1.0	1	22	177	198	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGCAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen08g008920.1	3.0	-1.0	1	22	2172	2193	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen02g005700.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen09g012530.1	3.0	-1.0	1	22	426	447	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen01g020550.1	3.0	-1.0	1	22	27	48	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGCGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen03g020680.1	3.0	-1.0	1	22	27	48	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAAGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen10g008980.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen11g017850.1	3.0	-1.0	1	22	696	717	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGCAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen05g015280.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACGGAUAAAGAAGUGAGA	Translation
spe-miR156-8-3p	Sopen02g004810.1	3.0	-1.0	1	22	105	126	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen07g012120.1	3.0	-1.0	1	22	798	819	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen06g010580.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen12g008980.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen01g018670.1	3.0	-1.0	1	22	102	123	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen01g017980.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAAUGAGA	Cleavage
spe-miR156-8-3p	Sopen04g014410.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGUGG	Cleavage
spe-miR156-8-3p	Sopen06g013360.1	3.0	-1.0	1	22	102	123	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUUAGA	Cleavage
spe-miR156-8-3p	Sopen09g015900.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen05g023180.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen11g022380.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGAGAGG	Cleavage
spe-miR156-8-3p	Sopen06g013370.1	3.0	-1.0	1	22	102	123	GCUCACUUCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUUAGA	Cleavage
spe-miR156-8-3p	Sopen08g013910.1	3.0	-1.0	1	22	1287	1308	GCUCACUUCUCUAUCUGUCACC	AUUGACAGAUGGUGAAGUGAGG	Translation
spe-miR156-8-3p	Sopen01g049520.1	3.0	-1.0	1	22	160	181	GCUCACUUCUCUAUCUGUCACC	CCUGACAGAUUGGGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen09g010440.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACAGAUGGAGAAGUAAGA	Cleavage
spe-miR156-8-3p	Sopen09g014390.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACAGAUGGUGAAGUGAGA	Translation
spe-miR156-8-3p	Sopen09g015680.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	AUUGACAGAUGGAGAAGUAAGG	Cleavage
spe-miR156-8-3p	Sopen08g007070.1	3.0	-1.0	1	22	1764	1785	GCUCACUUCUCUAUCUGUCACC	GUUGAAGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen07g024020.1	3.0	-1.0	1	22	672	693	GCUCACUUCUCUAUCUGUCACC	UGUGUUAGUUAGAGAAGUGAGU	Cleavage
spe-miR156-8-3p	Sopen11g017500.1	3.0	-1.0	1	22	111	132	GCUCACUUCUCUAUCUGUCACC	GUUAACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen11g015430.1	3.0	-1.0	1	22	21	42	GCUCACUUCUCUAUCUGUCACC	GAUGACGAAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen12g014680.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUCACGGAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen08g013250.1	3.0	-1.0	1	22	114	135	GCUCACUUCUCUAUCUGUCACC	GUUAACGGAUGGAGAAGUGAGG	Cleavage
spe-miR156-8-3p	Sopen01g014190.1	3.0	-1.0	1	22	108	129	GCUCACUUCUCUAUCUGUCACC	AUUGACGAAUGGAGAAGUGAGA	Cleavage
spe-miR156-8-3p	Sopen05g032860.1	3.0	-1.0	1	22	536	557	GCUCACUUCUCUAUCUGUCACC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
spe-miR156-8-5p	Sopen05g006830.1	1.0	-1.0	1	21	1240	1260	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen12g018830.1	1.0	-1.0	1	21	970	990	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen05g010900.1	1.0	-1.0	1	21	1117	1137	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen10g029320.1	1.0	-1.0	1	21	763	783	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen04g017460.1	1.0	-1.0	1	21	790	810	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen05g011450.1	1.0	-1.0	1	21	655	675	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen03g033930.1	1.0	-1.0	1	21	1156	1176	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-8-5p	Sopen09g017280.1	2.5	-1.0	1	21	1851	1871	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage

spe-miR156-8-5p	Sopen11g017850.1	2.5	-1.0	1	21	172	192	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-8-5p	Sopen03g012590.1	2.5	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-8-5p	Sopen07g013960.1	2.5	-1.0	1	21	148	168	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-8-5p	Sopen05g024090.1	2.5	-1.0	1	21	445	465	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-8-5p	Sopen04g012860.1	3.0	-1.0	1	21	275	295	UGACAGAAGAGAGUGAGCACA	UGGGCUUAUUUUCUUCUGUUA	Cleavage
spe-miR156-8-5p	Sopen09g035820.2	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-8-5p	Sopen09g035820.1	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-8-5p	Sopen04g011710.1	3.0	-1.0	1	21	1715	1735	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
spe-miR156-8-5p	Sopen09g013010.1	3.0	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGUUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-8-5p	Sopen02g019370.1	3.0	-1.0	1	21	366	386	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation
spe-miR156-8-5p	Sopen03g016770.1	3.0	-1.0	1	21	205	225	UGACAGAAGAGAGUGAGCACA	GAUGCUCCUUCUCUUGUGUCA	Cleavage
spe-miR156-8-5p	Sopen03g036450.2	3.0	-1.0	1	21	2280	2300	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
spe-miR156-9-3p	Sopen09g009280.1	1.5	-1.0	1	22	177	198	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGCAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen11g017850.1	1.5	-1.0	1	22	696	717	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGCAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen05g032860.1	1.5	-1.0	1	22	536	557	GCUCACUGCUCUAUCUGUCACC	AGAGACAGGUAGAGCGGUGGGC	Cleavage
spe-miR156-9-3p	Sopen01g018450.1	2.5	-1.0	1	22	726	747	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen05g021610.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen07g007550.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen12g012420.1	2.5	-1.0	1	22	108	129	GCUCACUGCUCUAUCUGUCACC	UUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen03g011830.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	AUUGACAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen05g016080.1	2.5	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	UUUGACGGAUGGAGUAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen06g030090.1	2.5	-1.0	1	22	2171	2192	GCUCACUGCUCUAUCUGUCACC	CAACACAGAUGGAGCAGUGGGU	Cleavage
spe-miR156-9-3p	Sopen01g009890.1	3.0	-1.0	1	22	111	132	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen02g005260.1	3.0	-1.0	1	22	1896	1917	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen01g026210.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen07g013640.1	3.0	-1.0	1	22	1584	1605	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen04g014930.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen01g026620.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen04g017490.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GCUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen04g018070.1	3.0	-1.0	1	22	27	48	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen11g015420.1	3.0	-1.0	1	22	498	519	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen10g007760.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen05g012810.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGAUAGAUAGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen10g015900.1	3.0	-1.0	1	22	21	42	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen01g019370.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen03g017480.1	3.0	-1.0	1	22	192	213	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen10g021890.1	3.0	-1.0	1	22	159	180	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen11g022550.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen07g021080.1	3.0	-1.0	1	22	150	171	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen03g016910.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen01g025760.1	3.0	-1.0	1	22	27	48	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen08g007980.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen10g018420.1	3.0	-1.0	1	22	114	135	GCUCACUGCUCUAUCUGUCACC	GUUGACAGAUGGAGAAGUGAGG	Cleavage
spe-miR156-9-3p	Sopen04g016790.1	3.0	-1.0	1	22	243	264	GCUCACUGCUCUAUCUGUCACC	GUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen09g013220.1	3.0	-1.0	1	22	1122	1143	GCUCACUGCUCUAUCUGUCACC	AUUGACGGAUAGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen06g010360.1	3.0	-1.0	1	22	96	117	GCUCACUGCUCUAUCUGUCACC	CUUGACAGAUGGAGAAGUGAGA	Cleavage
spe-miR156-9-3p	Sopen05g034390.1	3.0	-1.0	1	22	1017	1038	GCUCACUGCUCUAUCUGUCACC	AAGGAUAGAUAGAGGAGUGAGG	Cleavage
spe-miR156-9-5p	Sopen05g006830.1	1.0	-1.0	1	21	1240	1260	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-9-5p	Sopen12g018830.1	1.0	-1.0	1	21	970	990	UGACAGAAGAGAGUGAGCACA	UGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-9-5p	Sopen05g010900.1	1.0	-1.0	1	21	1117	1137	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage

spe-miR156-9-5p	Sopen10g029320.1	1.0	-1.0	1	21	763	783	UGACAGAAGAGAGUGAGCACA	GGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-9-5p	Sopen04g017460.1	1.0	-1.0	1	21	790	810	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-9-5p	Sopen05g011450.1	1.0	-1.0	1	21	655	675	UGACAGAAGAGAGUGAGCACA	CGUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-9-5p	Sopen03g033930.1	1.0	-1.0	1	21	1156	1176	UGACAGAAGAGAGUGAGCACA	AAUGCUCUCUCUCUUCUGUCA	Cleavage
spe-miR156-9-5p	Sopen09g017280.1	2.5	-1.0	1	21	1851	1871	UGACAGAAGAGAGUGAGCACA	UUUGCUCACUUUCAUUUGUCA	Cleavage
spe-miR156-9-5p	Sopen11g017850.1	2.5	-1.0	1	21	172	192	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-9-5p	Sopen03g012590.1	2.5	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-9-5p	Sopen07g013960.1	2.5	-1.0	1	21	148	168	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-9-5p	Sopen05g024090.1	2.5	-1.0	1	21	445	465	UGACAGAAGAGAGUGAGCACA	UAUGCUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-9-5p	Sopen04g012860.1	3.0	-1.0	1	21	275	295	UGACAGAAGAGAGUGAGCACA	UGGGCUUAUUUUCUUCUGUUA	Cleavage
spe-miR156-9-5p	Sopen09g035820.2	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-9-5p	Sopen09g035820.1	3.0	-1.0	1	21	424	445	UGACAGAAGAGAGU-GAGCACA	CGUGCUCGAUUCUCUUCUGUUA	Cleavage
spe-miR156-9-5p	Sopen04g011710.1	3.0	-1.0	1	21	1715	1735	UGACAGAAGAGAGUGAGCACA	CUUGCUUGCUUUCUUCUGGCA	Cleavage
spe-miR156-9-5p	Sopen09g013010.1	3.0	-1.0	1	21	46	66	UGACAGAAGAGAGUGAGCACA	UAUGUUCCCUCUCUUGUGUCA	Cleavage
spe-miR156-9-5p	Sopen02g019370.1	3.0	-1.0	1	21	366	386	UGACAGAAGAGAGUGAGCACA	CUUGCUCUCUGUCUUCUGUUA	Translation
spe-miR156-9-5p	Sopen03g016770.1	3.0	-1.0	1	21	205	225	UGACAGAAGAGAGUGAGCACA	GAUGCUCCUUCUCUUGUGUCA	Cleavage
spe-miR156-9-5p	Sopen03g036450.2	3.0	-1.0	1	21	2280	2300	UGACAGAAGAGAGUGAGCACA	UAUACUCUCUCUCUUCUGUCU	Cleavage
spe-miR160-1-3p	Sopen09g004010.1	3.0	-1.0	1	21	61	81	GCGUAUGAGGAGCCAAGCAUA	UAUCCUUGGCUUCUUAUAUGU	Cleavage
spe-miR160-1-3p	Sopen02g003520.1	3.0	-1.0	1	21	3650	3670	GCGUAUGAGGAGCCAAGCAUA	UACACUUGGCUCCUUAUAUGC	Cleavage
spe-miR160-1-5p	Sopen06g031560.1	0.0	-1.0	1	23	1267	1289	UGCCUGGCUCCCUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160-1-5p	Sopen11g028210.1	0.0	-1.0	1	23	1300	1322	UGCCUGGCUCCCUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160-1-5p	Sopen09g002650.1	0.5	-1.0	1	23	1351	1373	UGCCUGGCUCCCUGUAUGCCAUU	GCUGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160-1-5p	Sopen11g008490.1	0.5	-1.0	1	23	1390	1412	UGCCUGGCUCCCUGUAUGCCAUU	GCGGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160-1-5p	Sopen10g035510.1	1.0	-1.0	1	23	1342	1364	UGCCUGGCUCCCUGUAUGCCAUU	GUUGGUAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160-2-3p	Sopen03g041640.1	2.0	-1.0	1	21	869	889	GCAUUCUAGGAGCUAAGCAUG	CAUGCUUUGCUCCUGGAAUGU	Cleavage
spe-miR160-2-3p	Sopen09g001230.1	2.5	-1.0	1	21	846	866	GCAUUCUAGGAGCUAAGCAUG	AGUGCUUAGUUUUUGGAGUGC	Cleavage
spe-miR160-2-3p	Sopen08g025830.1	3.0	-1.0	1	21	739	759	GCAUUCUAGGAGCUAAGCAUG	UGUGCAUUGCUCCUGGGAUGC	Cleavage
spe-miR160-2-5p	Sopen06g031560.1	0.5	-1.0	1	23	1267	1289	UGCCUGGCUCCUUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160-2-5p	Sopen11g028210.1	0.5	-1.0	1	23	1300	1322	UGCCUGGCUCCUUGUAUGCCAUU	GCAGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160-2-5p	Sopen09g002650.1	1.0	-1.0	1	23	1351	1373	UGCCUGGCUCCUUGUAUGCCAUU	GCUGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160-2-5p	Sopen11g008490.1	1.0	-1.0	1	23	1390	1412	UGCCUGGCUCCUUGUAUGCCAUU	GCGGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160-2-5p	Sopen10g035510.1	1.5	-1.0	1	23	1342	1364	UGCCUGGCUCCUUGUAUGCCAUU	GUUGGUAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160-2-5p	Sopen06g024940.2	2.5	-1.0	1	23	1980	2002	UGCCUGGCUCCUUGUAUGCCAUU	UGAUGCAUGGAAGGAGUCGGGCA	Cleavage
spe-miR160-2-5p	Sopen06g024940.1	2.5	-1.0	1	23	2073	2095	UGCCUGGCUCCUUGUAUGCCAUU	UGAUGCAUGGAAGGAGUCGGGCA	Cleavage
spe-miR160-2-5p	Sopen06g024940.3	2.5	-1.0	1	23	2082	2104	UGCCUGGCUCCUUGUAUGCCAUU	UGAUGCAUGGAAGGAGUCGGGCA	Cleavage
spe-miR160-2-5p	Sopen11g027660.1	3.0	-1.0	1	23	1373	1395	UGCCUGGCUCCUUGUAUGCCAUU	CGGGGCUAACAAGGAGUCAGGUA	Cleavage
spe-miR160a-3p	Sopen09g004010.1	2.5	-1.0	1	21	61	81	GCGUAUAAGGAGCCAAGCAUA	UAUCCUUGGCUUCUUAUAUGU	Cleavage
spe-miR160a-3p	Sopen02g003520.1	2.5	-1.0	1	21	3650	3670	GCGUAUAAGGAGCCAAGCAUA	UACACUUGGCUCCUUAUAUGC	Cleavage
spe-miR160a-5p	Sopen06g031560.1	0.0	-1.0	1	21	1269	1289	UGCCUGGCUCCCUGUAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160a-5p	Sopen11g028210.1	0.0	-1.0	1	21	1302	1322	UGCCUGGCUCCCUGUAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160a-5p	Sopen09g002650.1	0.5	-1.0	1	21	1353	1373	UGCCUGGCUCCCUGUAUGCCA	UGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160a-5p	Sopen11g008490.1	0.5	-1.0	1	21	1392	1412	UGCCUGGCUCCCUGUAUGCCA	GGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160a-5p	Sopen10g035510.1	1.0	-1.0	1	21	1344	1364	UGCCUGGCUCCCUGUAUGCCA	UGGUAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160c-5p	Sopen09g002650.1	1.0	-1.0	1	21	1353	1373	UGCCUGGCUCCCUGGAUGCCA	UGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160c-5p	Sopen11g008490.1	1.0	-1.0	1	21	1392	1412	UGCCUGGCUCCCUGGAUGCCA	GGGCAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160c-5p	Sopen06g031560.1	1.0	-1.0	1	21	1269	1289	UGCCUGGCUCCCUGGAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160c-5p	Sopen11g028210.1	1.0	-1.0	1	21	1302	1322	UGCCUGGCUCCCUGGAUGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160c-5p	Sopen10g035510.1	1.5	-1.0	1	21	1344	1364	UGCCUGGCUCCCUGGAUGCCA	UGGUAUGCAGGGAGCCAGGCA	Cleavage
spe-miR160c-5p	Sopen01g037400.1	2.5	-1.0	1	21	1160	1180	UGCCUGGCUCCCUGGAUGCCA	AGGCUUCCAGGGAGACAGGCA	Cleavage
spe-miR160c-5p	Sopen07g034710.1	3.0	-1.0	1	21	2259	2279	UGCCUGGCUCCCUGGAUGCCA	CUGCAUCGAGGGAGACAGGCG	Cleavage

spe-miR160g-1-3p	Sopen05g014680.1	2.5	-1.0	1	21	1888	1908	UGGCAUACAGGGAGCCAGGCA	AACCUCCCUCCUUGUAUGCCA	Cleavage
spe-miR160g-1-3p	Sopen08g009050.1	3.0	-1.0	1	21	1128	1148	UGGCAUACAGGGAGCCAGGCA	CUCAUGGCUCCCUGUAUUUCA	Cleavage
spe-miR160g-1-3p	Sopen07g015050.1	3.0	-1.0	1	21	283	303	UGGCAUACAGGGAGCCAGGCA	AACUUCCUUCCCUGUAUGCCA	Cleavage
spe-miR160g-1-3p	Sopen05g017380.1	3.0	-1.0	1	21	139	159	UGGCAUACAGGGAGCCAGGCA	AACUUACCUCCUUGUAUGCCA	Cleavage
spe-miR160g-1-3p	Sopen11g015530.1	3.0	-1.0	1	21	2278	2298	UGGCAUACAGGGAGCCAGGCA	ACCUUUCCUCCUUGUAUGCCA	Cleavage
spe-miR160g-2-3p	Sopen05g014680.1	2.5	-1.0	1	21	1888	1908	UGGCAUACAGGGAGCCAGGCA	AACCUCCCUCCUUGUAUGCCA	Cleavage
spe-miR160g-2-3p	Sopen08g009050.1	3.0	-1.0	1	21	1128	1148	UGGCAUACAGGGAGCCAGGCA	CUCAUGGCUCCCUGUAUUUCA	Cleavage
spe-miR160g-2-3p	Sopen07g015050.1	3.0	-1.0	1	21	283	303	UGGCAUACAGGGAGCCAGGCA	AACUUCCUUCCCUGUAUGCCA	Cleavage
spe-miR160g-2-3p	Sopen05g017380.1	3.0	-1.0	1	21	139	159	UGGCAUACAGGGAGCCAGGCA	AACUUACCUCCUUGUAUGCCA	Cleavage
spe-miR160g-2-3p	Sopen11g015530.1	3.0	-1.0	1	21	2278	2298	UGGCAUACAGGGAGCCAGGCA	ACCUUUCCUCCUUGUAUGCCA	Cleavage
spe-miR160g-2-5p	Sopen09g004290.1	3.0	-1.0	1	21	149	169	UGCUUGGCUCCUUAUACGCCA	UGGCGUAUAAGGAGCAAGGUG	Cleavage
spe-miR160g-2-5p	Sopen06g003000.1	3.0	-1.0	1	21	1433	1453	UGCUUGGCUCCUUAUACGCCA	UGGUUUAUAAGGAGUUGAGCA	Cleavage
spe-miR160g-2-5p	Sopen06g002900.1	3.0	-1.0	1	21	5111	5131	UGCUUGGCUCCUUAUACGCCA	UGGUUUAUAAGGAGUUGAGCA	Cleavage
spe-miR160g-2-5p	Sopen06g031560.1	3.0	-1.0	1	21	1269	1289	UGCUUGGCUCCUUAUACGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR160g-2-5p	Sopen11g028210.1	3.0	-1.0	1	21	1302	1322	UGCUUGGCUCCUUAUACGCCA	AGGCAUACAGGGAGCCAGGCA	Cleavage
spe-miR162a-1-3p	Sopen11g007970.1	3.0	-1.0	1	21	3075	3095	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g007970.1	3.0	-1.0	1	21	3852	3872	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g015770.1	1.5	-1.0	1	21	4874	4894	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g015850.1	3.0	-1.0	1	21	2409	2429	UCGAUAAACCUCUGCAUCCAG	CUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g018400.1	3.0	-1.0	1	21	1749	1769	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g012630.1	3.0	-1.0	1	21	3096	3116	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g014370.1	3.0	-1.0	1	21	3522	3542	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g015370.1	3.0	-1.0	1	21	2952	2972	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g015370.1	3.0	-1.0	1	21	5238	5258	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g014680.1	3.0	-1.0	1	21	1611	1631	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g014680.1	3.0	-1.0	1	21	5412	5432	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g016030.1	3.0	-1.0	1	21	1725	1745	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g033540.1	0.0	-1.0	1	21	462	482	UCGAUAAACCUCUGCAUCCAG	CUGGAUGCAGAGGUUUAUCGA	Cleavage
spe-miR162a-1-3p	Sopen04g015920.1	1.5	-1.0	1	21	1776	1796	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g009220.1	1.5	-1.0	1	21	2977	2997	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen11g022160.1	1.5	-1.0	1	21	4152	4172	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g018960.1	1.5	-1.0	1	21	1206	1226	UCGAUAAACCUCUGCAUCCAG	UAGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g022790.1	2.0	-1.0	1	21	189	209	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-3p	Sopen05g025280.1	2.0	-1.0	1	21	1824	1844	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-3p	Sopen11g011420.1	2.0	-1.0	1	21	2022	2042	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-3p	Sopen12g027200.1	2.0	-1.0	1	21	3621	3641	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-3p	Sopen07g013870.1	2.0	-1.0	1	21	3762	3782	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-3p	Sopen08g014940.1	2.0	-1.0	1	21	3978	3998	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-3p	Sopen08g006930.1	2.5	-1.0	1	21	1929	1949	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUCGC	Cleavage
spe-miR162a-1-3p	Sopen04g008580.1	2.5	-1.0	1	21	787	807	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUUGAUUGG	Cleavage
spe-miR162a-1-3p	Sopen03g032790.1	2.5	-1.0	1	21	1612	1632	UCGAUAAACCUCUGCAUCCAG	GAAGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g014030.1	2.5	-1.0	1	21	5446	5466	UCGAUAAACCUCUGCAUCCAG	CAGGGUGUAGAGGUUUAUCCA	Cleavage
spe-miR162a-1-3p	Sopen10g001150.1	3.0	-1.0	1	21	3073	3094	UCGAUAA-ACCUCUGCAUCCAG	CUGGAUGCAGAGGUAUUAUCGA	Cleavage
spe-miR162a-1-3p	Sopen04g016610.1	3.0	-1.0	1	21	3378	3398	UCGAUAAACCUCUGCAUCCAG	CUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g015700.1	3.0	-1.0	1	21	2865	2885	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUUUAUUAC	Cleavage
spe-miR162a-1-3p	Sopen09g025870.5	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g019170.1	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen06g017400.1	3.0	-1.0	1	21	288	308	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g027840.1	3.0	-1.0	1	21	642	662	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g013160.1	3.0	-1.0	1	21	882	902	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-1-3p	Sopen10g020850.1	3.0	-1.0	1	21	894	914	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g010440.1	3.0	-1.0	1	21	1020	1040	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g018610.2	3.0	-1.0	1	21	1008	1028	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g012090.1	3.0	-1.0	1	21	795	815	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g011360.1	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g025870.4	3.0	-1.0	1	21	1080	1100	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g009510.1	3.0	-1.0	1	21	1287	1307	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g024850.1	3.0	-1.0	1	21	1251	1271	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g012080.1	3.0	-1.0	1	21	1689	1709	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g011520.1	3.0	-1.0	1	21	1278	1298	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen09g010030.1	3.0	-1.0	1	21	1537	1557	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g025870.3	3.0	-1.0	1	21	1332	1352	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g019070.1	3.0	-1.0	1	21	1578	1598	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g020430.1	3.0	-1.0	1	21	1137	1157	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g022310.1	3.0	-1.0	1	21	1755	1775	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g021250.1	3.0	-1.0	1	21	1533	1553	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g008510.1	3.0	-1.0	1	21	2061	2081	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g020870.1	3.0	-1.0	1	21	1524	1544	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g018670.1	3.0	-1.0	1	21	1248	1268	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g016300.1	3.0	-1.0	1	21	2094	2114	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g018310.1	3.0	-1.0	1	21	1860	1880	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g016300.2	3.0	-1.0	1	21	2094	2114	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g013510.1	3.0	-1.0	1	21	1716	1736	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g025870.2	3.0	-1.0	1	21	1935	1955	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g014920.1	3.0	-1.0	1	21	2292	2312	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g010270.1	3.0	-1.0	1	21	2463	2483	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g019300.1	3.0	-1.0	1	21	2316	2336	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g013350.1	3.0	-1.0	1	21	2214	2234	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g019050.1	3.0	-1.0	1	21	2268	2288	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g009290.1	3.0	-1.0	1	21	2484	2504	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g017190.1	3.0	-1.0	1	21	2427	2447	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUGUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g010320.1	3.0	-1.0	1	21	1914	1934	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen02g009480.1	3.0	-1.0	1	21	2190	2210	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g013690.1	3.0	-1.0	1	21	2473	2493	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g021750.1	3.0	-1.0	1	21	2277	2297	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g018980.1	3.0	-1.0	1	21	2279	2299	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g010430.1	3.0	-1.0	1	21	2220	2240	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g015900.1	3.0	-1.0	1	21	2397	2417	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g012670.1	3.0	-1.0	1	21	2505	2525	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g025580.1	3.0	-1.0	1	21	2427	2447	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g019730.1	3.0	-1.0	1	21	792	812	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g011530.1	3.0	-1.0	1	21	2649	2669	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g021040.1	3.0	-1.0	1	21	2673	2693	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g018110.1	3.0	-1.0	1	21	1758	1778	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g015300.1	3.0	-1.0	1	21	2610	2630	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g019640.1	3.0	-1.0	1	21	2457	2477	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g018950.1	3.0	-1.0	1	21	2658	2678	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g010300.1	3.0	-1.0	1	21	2052	2072	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g006190.1	3.0	-1.0	1	21	2505	2525	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g016500.1	3.0	-1.0	1	21	2553	2573	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-1-3p	Sopen01g023620.1	3.0	-1.0	1	21	2781	2801	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUAUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g014360.1	3.0	-1.0	1	21	2799	2819	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g011300.1	3.0	-1.0	1	21	2805	2825	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g014120.1	3.0	-1.0	1	21	2259	2279	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g015880.1	3.0	-1.0	1	21	2190	2210	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g017700.1	3.0	-1.0	1	21	2829	2849	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGUUUUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g011520.1	3.0	-1.0	1	21	2673	2693	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen03g012400.1	3.0	-1.0	1	21	2391	2411	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g016160.1	3.0	-1.0	1	21	741	761	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g021530.1	3.0	-1.0	1	21	2856	2876	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g025540.1	3.0	-1.0	1	21	2829	2849	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g015570.1	3.0	-1.0	1	21	2880	2900	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g022360.1	3.0	-1.0	1	21	2781	2801	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g021690.1	3.0	-1.0	1	21	2802	2822	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g008030.2	3.0	-1.0	1	21	2940	2960	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen02g004730.1	3.0	-1.0	1	21	2892	2912	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g021320.1	3.0	-1.0	1	21	2844	2864	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g018150.1	3.0	-1.0	1	21	3102	3122	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g011010.1	3.0	-1.0	1	21	2934	2954	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g014520.1	3.0	-1.0	1	21	1449	1469	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g014210.1	3.0	-1.0	1	21	3208	3228	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g017290.1	3.0	-1.0	1	21	2910	2930	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g013390.1	3.0	-1.0	1	21	3009	3029	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g013170.1	3.0	-1.0	1	21	3279	3299	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g027080.1	3.0	-1.0	1	21	2856	2876	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g015490.1	3.0	-1.0	1	21	2997	3017	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g026400.1	3.0	-1.0	1	21	3000	3020	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g016670.1	3.0	-1.0	1	21	3078	3098	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g016760.1	3.0	-1.0	1	21	2970	2990	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen02g004670.1	3.0	-1.0	1	21	2976	2996	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g007720.1	3.0	-1.0	1	21	2988	3008	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen02g002060.1	3.0	-1.0	1	21	3039	3059	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g008440.1	3.0	-1.0	1	21	2880	2900	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g008300.2	3.0	-1.0	1	21	3045	3065	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g026590.1	3.0	-1.0	1	21	3051	3071	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g006370.1	3.0	-1.0	1	21	3177	3197	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g013940.1	3.0	-1.0	1	21	591	611	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g006790.1	3.0	-1.0	1	21	3201	3221	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen03g020440.1	3.0	-1.0	1	21	3192	3212	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g011450.1	3.0	-1.0	1	21	3150	3170	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g015490.1	3.0	-1.0	1	21	3363	3383	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g012110.1	3.0	-1.0	1	21	3309	3329	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g015410.1	3.0	-1.0	1	21	3243	3263	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g016060.1	3.0	-1.0	1	21	3243	3263	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g007380.1	3.0	-1.0	1	21	3261	3281	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g009570.1	3.0	-1.0	1	21	3567	3587	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g009910.1	3.0	-1.0	1	21	2862	2882	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen02g007340.1	3.0	-1.0	1	21	2343	2363	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g021270.1	3.0	-1.0	1	21	3375	3395	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen01g026340.3	3.0	-1.0	1	21	2538	2558	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-1-3p	Sopen09g012910.1	3.0	-1.0	1	21	3501	3521	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g014960.1	3.0	-1.0	1	21	3225	3245	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g018760.1	3.0	-1.0	1	21	3609	3629	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g018780.1	3.0	-1.0	1	21	3288	3308	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g016970.1	3.0	-1.0	1	21	3510	3530	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g020990.1	3.0	-1.0	1	21	3210	3230	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g008950.1	3.0	-1.0	1	21	3453	3473	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g027520.1	3.0	-1.0	1	21	1804	1824	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g019810.1	3.0	-1.0	1	21	3798	3818	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g022250.1	3.0	-1.0	1	21	3708	3728	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAAGUUUAUUGC	Translation
spe-miR162a-1-3p	Sopen01g019350.1	3.0	-1.0	1	21	1914	1934	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen01g018610.1	3.0	-1.0	1	21	3696	3716	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g027810.1	3.0	-1.0	1	21	3462	3482	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g008570.1	3.0	-1.0	1	21	3735	3755	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g011720.1	3.0	-1.0	1	21	3444	3464	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g010410.1	3.0	-1.0	1	21	2931	2951	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g016170.1	3.0	-1.0	1	21	3891	3911	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g026340.2	3.0	-1.0	1	21	2538	2558	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g016340.1	3.0	-1.0	1	21	4194	4214	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g012390.1	3.0	-1.0	1	21	3960	3980	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen02g004530.1	3.0	-1.0	1	21	3189	3209	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g026340.1	3.0	-1.0	1	21	2538	2558	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g008790.1	3.0	-1.0	1	21	4053	4073	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g014250.1	3.0	-1.0	1	21	4059	4079	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g009450.1	3.0	-1.0	1	21	4194	4214	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen10g015130.1	3.0	-1.0	1	21	4191	4211	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g011600.1	3.0	-1.0	1	21	4581	4601	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g018060.1	3.0	-1.0	1	21	3852	3872	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g014910.1	3.0	-1.0	1	21	4512	4532	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen12g020370.1	3.0	-1.0	1	21	4851	4871	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g016580.1	3.0	-1.0	1	21	4830	4850	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g011210.1	3.0	-1.0	1	21	4770	4790	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g025870.1	3.0	-1.0	1	21	4689	4709	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g020910.1	3.0	-1.0	1	21	4890	4910	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g014690.1	3.0	-1.0	1	21	4587	4607	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g010070.1	3.0	-1.0	1	21	4545	4565	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-1-3p	Sopen04g017480.1	3.0	-1.0	1	21	4740	4760	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g009180.1	3.0	-1.0	1	21	3543	3563	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g018700.1	3.0	-1.0	1	21	2523	2543	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g012500.1	3.0	-1.0	1	21	3171	3191	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g011120.1	3.0	-1.0	1	21	4656	4676	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen07g008130.1	3.0	-1.0	1	21	3948	3968	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g009850.1	3.0	-1.0	1	21	4848	4868	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen09g026290.1	3.0	-1.0	1	21	5682	5702	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g012230.1	3.0	-1.0	1	21	6018	6038	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g009510.2	3.0	-1.0	1	21	5868	5888	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g020610.1	3.0	-1.0	1	21	5139	5159	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g013200.1	3.0	-1.0	1	21	5961	5981	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUAUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g013570.1	3.0	-1.0	1	21	5979	5999	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g007670.1	3.0	-1.0	1	21	5649	5669	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-1-3p	Sopen06g012610.1	3.0	-1.0	1	21	3219	3239	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g008140.1	3.0	-1.0	1	21	2670	2690	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g011080.1	3.0	-1.0	1	21	3333	3353	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g017160.1	3.0	-1.0	1	21	7125	7145	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen03g013510.1	3.0	-1.0	1	21	7779	7799	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g017780.1	3.0	-1.0	1	21	6588	6608	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g020870.2	3.0	-1.0	1	21	7158	7178	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen08g012200.1	3.0	-1.0	1	21	7680	7700	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g011520.2	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	AUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen11g018370.1	3.0	-1.0	1	21	1968	1988	UCGAUAAACCUCUGCAUCCAG	AUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g018280.1	3.0	-1.0	1	21	2238	2258	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen05g015010.1	3.0	-1.0	1	21	2727	2747	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g011520.1	3.0	-1.0	1	21	2718	2738	UCGAUAAACCUCUGCAUCCAG	AUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen06g011650.1	3.0	-1.0	1	21	3636	3656	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen04g017510.1	3.0	-1.0	1	21	2700	2720	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-1-3p	Sopen01g022920.1	3.0	-1.0	1	21	669	689	UCGAUAAACCUCUGCAUCCAG	UUGGAUGAAGAGGUCUAUUGA	Cleavage
spe-miR162a-1-5p	Sopen05g007330.1	3.0	-1.0	1	21	2441	2461	GGAGGCAGCGGUUCAUCGAUC	UUUCAAUGAAUGGCUGCCUCC	Translation
spe-miR162a-1-5p	Sopen03g033540.1	0.0	-1.0	1	21	522	542	GGAGGCAGCGGUUCAUCGAUC	GAUCGAUGAACCGCUGCCUCC	Cleavage
spe-miR162a-1-5p	Sopen11g015090.1	2.5	-1.0	1	21	1833	1853	GGAGGCAGCGGUUCAUCGAUC	CAGCGAUGGAUCGUUGCCUCC	Cleavage
spe-miR162a-1-5p	Sopen07g028110.1	3.0	-1.0	1	21	372	392	GGAGGCAGCGGUUCAUCGAUC	UACUGAUGGACCGUUGCUUCC	Cleavage
spe-miR162a-1-5p	Sopen07g032000.1	3.0	-1.0	1	21	285	305	GGAGGCAGCGGUUCAUCGAUC	UCCUGGUGAACCGCUGCCUCG	Cleavage
spe-miR162a-1-5p	Sopen07g032000.2	3.0	-1.0	1	21	285	305	GGAGGCAGCGGUUCAUCGAUC	UCCUGGUGAACCGCUGCCUCG	Cleavage
spe-miR162a-1-5p	Sopen09g018100.1	3.0	-1.0	1	21	3786	3806	GGAGGCAGCGGUUCAUCGAUC	UCUCGAUGGACCGUUAUCUCC	Cleavage
spe-miR162a-2-3p	Sopen11g007970.1	3.0	-1.0	1	21	3075	3095	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g007970.1	3.0	-1.0	1	21	3852	3872	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g015770.1	1.5	-1.0	1	21	4874	4894	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g015850.1	3.0	-1.0	1	21	2409	2429	UCGAUAAACCUCUGCAUCCAG	CUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g018400.1	3.0	-1.0	1	21	1749	1769	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g012630.1	3.0	-1.0	1	21	3096	3116	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g014370.1	3.0	-1.0	1	21	3522	3542	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g015370.1	3.0	-1.0	1	21	2952	2972	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g015370.1	3.0	-1.0	1	21	5238	5258	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g014680.1	3.0	-1.0	1	21	1611	1631	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g014680.1	3.0	-1.0	1	21	5412	5432	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g016030.1	3.0	-1.0	1	21	1725	1745	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g033540.1	0.0	-1.0	1	21	462	482	UCGAUAAACCUCUGCAUCCAG	CUGGAUGCAGAGGUUUAUCGA	Cleavage
spe-miR162a-2-3p	Sopen04g015920.1	1.5	-1.0	1	21	1776	1796	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g009220.1	1.5	-1.0	1	21	2977	2997	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen11g022160.1	1.5	-1.0	1	21	4152	4172	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g018960.1	1.5	-1.0	1	21	1206	1226	UCGAUAAACCUCUGCAUCCAG	UAGGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g022790.1	2.0	-1.0	1	21	189	209	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-3p	Sopen05g025280.1	2.0	-1.0	1	21	1824	1844	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-3p	Sopen11g011420.1	2.0	-1.0	1	21	2022	2042	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-3p	Sopen12g027200.1	2.0	-1.0	1	21	3621	3641	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-3p	Sopen07g013870.1	2.0	-1.0	1	21	3762	3782	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-3p	Sopen08g014940.1	2.0	-1.0	1	21	3978	3998	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-3p	Sopen08g006930.1	2.5	-1.0	1	21	1929	1949	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUCGC	Cleavage
spe-miR162a-2-3p	Sopen04g008580.1	2.5	-1.0	1	21	787	807	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUUGAUUGG	Cleavage
spe-miR162a-2-3p	Sopen03g032790.1	2.5	-1.0	1	21	1612	1632	UCGAUAAACCUCUGCAUCCAG	GAAGAUGCAGAGGUUUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g014030.1	2.5	-1.0	1	21	5446	5466	UCGAUAAACCUCUGCAUCCAG	CAGGGUGUAGAGGUUUAUCCA	Cleavage

spe-miR162a-2-3p	Sopen10g001150.1	3.0	-1.0	1	21	3073	3094	UCGAUAA-ACCUCUGCAUCCAG	CUGGAUGCAGAGGUAUUAUCGA	Cleavage
spe-miR162a-2-3p	Sopen04g016610.1	3.0	-1.0	1	21	3378	3398	UCGAUAAACCUCUGCAUCCAG	CUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g015700.1	3.0	-1.0	1	21	2865	2885	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUUUAUUAC	Cleavage
spe-miR162a-2-3p	Sopen09g025870.5	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g019170.1	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen06g017400.1	3.0	-1.0	1	21	288	308	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g027840.1	3.0	-1.0	1	21	642	662	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g013160.1	3.0	-1.0	1	21	882	902	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g020850.1	3.0	-1.0	1	21	894	914	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g010440.1	3.0	-1.0	1	21	1020	1040	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g018610.2	3.0	-1.0	1	21	1008	1028	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g012090.1	3.0	-1.0	1	21	795	815	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g011360.1	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g025870.4	3.0	-1.0	1	21	1080	1100	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g009510.1	3.0	-1.0	1	21	1287	1307	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g024850.1	3.0	-1.0	1	21	1251	1271	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g012080.1	3.0	-1.0	1	21	1689	1709	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g011520.1	3.0	-1.0	1	21	1278	1298	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen09g010030.1	3.0	-1.0	1	21	1537	1557	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g025870.3	3.0	-1.0	1	21	1332	1352	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g019070.1	3.0	-1.0	1	21	1578	1598	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g020430.1	3.0	-1.0	1	21	1137	1157	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g022310.1	3.0	-1.0	1	21	1755	1775	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g021250.1	3.0	-1.0	1	21	1533	1553	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g008510.1	3.0	-1.0	1	21	2061	2081	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g020870.1	3.0	-1.0	1	21	1524	1544	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g018670.1	3.0	-1.0	1	21	1248	1268	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g016300.1	3.0	-1.0	1	21	2094	2114	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g018310.1	3.0	-1.0	1	21	1860	1880	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g016300.2	3.0	-1.0	1	21	2094	2114	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g013510.1	3.0	-1.0	1	21	1716	1736	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g025870.2	3.0	-1.0	1	21	1935	1955	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g014920.1	3.0	-1.0	1	21	2292	2312	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g010270.1	3.0	-1.0	1	21	2463	2483	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g019300.1	3.0	-1.0	1	21	2316	2336	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g013350.1	3.0	-1.0	1	21	2214	2234	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g019050.1	3.0	-1.0	1	21	2268	2288	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g009290.1	3.0	-1.0	1	21	2484	2504	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g017190.1	3.0	-1.0	1	21	2427	2447	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUGUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g010320.1	3.0	-1.0	1	21	1914	1934	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen02g009480.1	3.0	-1.0	1	21	2190	2210	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g013690.1	3.0	-1.0	1	21	2473	2493	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g021750.1	3.0	-1.0	1	21	2277	2297	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g018980.1	3.0	-1.0	1	21	2279	2299	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g010430.1	3.0	-1.0	1	21	2220	2240	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g015900.1	3.0	-1.0	1	21	2397	2417	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g012670.1	3.0	-1.0	1	21	2505	2525	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g025580.1	3.0	-1.0	1	21	2427	2447	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g019730.1	3.0	-1.0	1	21	792	812	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g011530.1	3.0	-1.0	1	21	2649	2669	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-2-3p	Sopen10g021040.1	3.0	-1.0	1	21	2673	2693	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g018110.1	3.0	-1.0	1	21	1758	1778	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g015300.1	3.0	-1.0	1	21	2610	2630	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g019640.1	3.0	-1.0	1	21	2457	2477	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g018950.1	3.0	-1.0	1	21	2658	2678	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g010300.1	3.0	-1.0	1	21	2052	2072	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g006190.1	3.0	-1.0	1	21	2505	2525	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g016500.1	3.0	-1.0	1	21	2553	2573	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g023620.1	3.0	-1.0	1	21	2781	2801	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUAUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g014360.1	3.0	-1.0	1	21	2799	2819	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g011300.1	3.0	-1.0	1	21	2805	2825	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g014120.1	3.0	-1.0	1	21	2259	2279	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g015880.1	3.0	-1.0	1	21	2190	2210	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g017700.1	3.0	-1.0	1	21	2829	2849	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGUUUUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g011520.1	3.0	-1.0	1	21	2673	2693	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen03g012400.1	3.0	-1.0	1	21	2391	2411	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g016160.1	3.0	-1.0	1	21	741	761	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g021530.1	3.0	-1.0	1	21	2856	2876	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g025540.1	3.0	-1.0	1	21	2829	2849	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g015570.1	3.0	-1.0	1	21	2880	2900	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g022360.1	3.0	-1.0	1	21	2781	2801	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g021690.1	3.0	-1.0	1	21	2802	2822	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g008030.2	3.0	-1.0	1	21	2940	2960	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen02g004730.1	3.0	-1.0	1	21	2892	2912	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g021320.1	3.0	-1.0	1	21	2844	2864	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g018150.1	3.0	-1.0	1	21	3102	3122	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g011010.1	3.0	-1.0	1	21	2934	2954	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g014520.1	3.0	-1.0	1	21	1449	1469	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g014210.1	3.0	-1.0	1	21	3208	3228	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g017290.1	3.0	-1.0	1	21	2910	2930	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g013390.1	3.0	-1.0	1	21	3009	3029	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g013170.1	3.0	-1.0	1	21	3279	3299	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g027080.1	3.0	-1.0	1	21	2856	2876	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g015490.1	3.0	-1.0	1	21	2997	3017	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g026400.1	3.0	-1.0	1	21	3000	3020	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g016670.1	3.0	-1.0	1	21	3078	3098	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g016760.1	3.0	-1.0	1	21	2970	2990	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen02g004670.1	3.0	-1.0	1	21	2976	2996	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g007720.1	3.0	-1.0	1	21	2988	3008	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen02g002060.1	3.0	-1.0	1	21	3039	3059	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g008440.1	3.0	-1.0	1	21	2880	2900	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g008300.2	3.0	-1.0	1	21	3045	3065	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g026590.1	3.0	-1.0	1	21	3051	3071	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g006370.1	3.0	-1.0	1	21	3177	3197	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g013940.1	3.0	-1.0	1	21	591	611	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g006790.1	3.0	-1.0	1	21	3201	3221	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen03g020440.1	3.0	-1.0	1	21	3192	3212	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g011450.1	3.0	-1.0	1	21	3150	3170	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g015490.1	3.0	-1.0	1	21	3363	3383	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g012110.1	3.0	-1.0	1	21	3309	3329	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-2-3p	Sopen12g015410.1	3.0	-1.0	1	21	3243	3263	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g016060.1	3.0	-1.0	1	21	3243	3263	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g007380.1	3.0	-1.0	1	21	3261	3281	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g009570.1	3.0	-1.0	1	21	3567	3587	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g009910.1	3.0	-1.0	1	21	2862	2882	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen02g007340.1	3.0	-1.0	1	21	2343	2363	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g021270.1	3.0	-1.0	1	21	3375	3395	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen01g026340.3	3.0	-1.0	1	21	2538	2558	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g012910.1	3.0	-1.0	1	21	3501	3521	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g014960.1	3.0	-1.0	1	21	3225	3245	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g018760.1	3.0	-1.0	1	21	3609	3629	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g018780.1	3.0	-1.0	1	21	3288	3308	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g016970.1	3.0	-1.0	1	21	3510	3530	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g020990.1	3.0	-1.0	1	21	3210	3230	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g008950.1	3.0	-1.0	1	21	3453	3473	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g027520.1	3.0	-1.0	1	21	1804	1824	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g019810.1	3.0	-1.0	1	21	3798	3818	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g022250.1	3.0	-1.0	1	21	3708	3728	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAAGUUUAUUGC	Translation
spe-miR162a-2-3p	Sopen01g019350.1	3.0	-1.0	1	21	1914	1934	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen01g018610.1	3.0	-1.0	1	21	3696	3716	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g027810.1	3.0	-1.0	1	21	3462	3482	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g008570.1	3.0	-1.0	1	21	3735	3755	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g011720.1	3.0	-1.0	1	21	3444	3464	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g010410.1	3.0	-1.0	1	21	2931	2951	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g016170.1	3.0	-1.0	1	21	3891	3911	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g026340.2	3.0	-1.0	1	21	2538	2558	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g016340.1	3.0	-1.0	1	21	4194	4214	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g012390.1	3.0	-1.0	1	21	3960	3980	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen02g004530.1	3.0	-1.0	1	21	3189	3209	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g026340.1	3.0	-1.0	1	21	2538	2558	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g008790.1	3.0	-1.0	1	21	4053	4073	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g014250.1	3.0	-1.0	1	21	4059	4079	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g009450.1	3.0	-1.0	1	21	4194	4214	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen10g015130.1	3.0	-1.0	1	21	4191	4211	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g011600.1	3.0	-1.0	1	21	4581	4601	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g018060.1	3.0	-1.0	1	21	3852	3872	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g014910.1	3.0	-1.0	1	21	4512	4532	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen12g020370.1	3.0	-1.0	1	21	4851	4871	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g016580.1	3.0	-1.0	1	21	4830	4850	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g011210.1	3.0	-1.0	1	21	4770	4790	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g025870.1	3.0	-1.0	1	21	4689	4709	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g020910.1	3.0	-1.0	1	21	4890	4910	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g014690.1	3.0	-1.0	1	21	4587	4607	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g010070.1	3.0	-1.0	1	21	4545	4565	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGU	Cleavage
spe-miR162a-2-3p	Sopen04g017480.1	3.0	-1.0	1	21	4740	4760	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g009180.1	3.0	-1.0	1	21	3543	3563	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g018700.1	3.0	-1.0	1	21	2523	2543	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g012500.1	3.0	-1.0	1	21	3171	3191	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g011120.1	3.0	-1.0	1	21	4656	4676	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen07g008130.1	3.0	-1.0	1	21	3948	3968	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage

spe-miR162a-2-3p	Sopen01g009850.1	3.0	-1.0	1	21	4848	4868	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen09g026290.1	3.0	-1.0	1	21	5682	5702	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g012230.1	3.0	-1.0	1	21	6018	6038	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g009510.2	3.0	-1.0	1	21	5868	5888	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g020610.1	3.0	-1.0	1	21	5139	5159	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g013200.1	3.0	-1.0	1	21	5961	5981	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUAUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g013570.1	3.0	-1.0	1	21	5979	5999	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g007670.1	3.0	-1.0	1	21	5649	5669	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g012610.1	3.0	-1.0	1	21	3219	3239	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g008140.1	3.0	-1.0	1	21	2670	2690	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g011080.1	3.0	-1.0	1	21	3333	3353	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g017160.1	3.0	-1.0	1	21	7125	7145	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen03g013510.1	3.0	-1.0	1	21	7779	7799	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g017780.1	3.0	-1.0	1	21	6588	6608	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g020870.2	3.0	-1.0	1	21	7158	7178	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen08g012200.1	3.0	-1.0	1	21	7680	7700	UCGAUAAACCUCUGCAUCCAG	UUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g011520.2	3.0	-1.0	1	21	30	50	UCGAUAAACCUCUGCAUCCAG	AUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen11g018370.1	3.0	-1.0	1	21	1968	1988	UCGAUAAACCUCUGCAUCCAG	AUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g018280.1	3.0	-1.0	1	21	2238	2258	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen05g015010.1	3.0	-1.0	1	21	2727	2747	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g011520.1	3.0	-1.0	1	21	2718	2738	UCGAUAAACCUCUGCAUCCAG	AUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen06g011650.1	3.0	-1.0	1	21	3636	3656	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen04g017510.1	3.0	-1.0	1	21	2700	2720	UCGAUAAACCUCUGCAUCCAG	GUGGAUGCAGAGGUCUAUUGC	Cleavage
spe-miR162a-2-3p	Sopen01g022920.1	3.0	-1.0	1	21	669	689	UCGAUAAACCUCUGCAUCCAG	UUGGAUGAAGAGGUCUAUUGA	Cleavage
spe-miR162a-2-5p	Sopen05g007330.1	3.0	-1.0	1	21	2441	2461	GGAGGCAGCGGUUCAUCGAUC	UUUCAAUGAAUGGCUGCCUCC	Translation
spe-miR162a-2-5p	Sopen03g033540.1	0.0	-1.0	1	21	522	542	GGAGGCAGCGGUUCAUCGAUC	GAUCGAUGAACCGCUGCCUCC	Cleavage
spe-miR162a-2-5p	Sopen11g015090.1	2.5	-1.0	1	21	1833	1853	GGAGGCAGCGGUUCAUCGAUC	CAGCGAUGGAUCGUUGCCUCC	Cleavage
spe-miR162a-2-5p	Sopen07g028110.1	3.0	-1.0	1	21	372	392	GGAGGCAGCGGUUCAUCGAUC	UACUGAUGGACCGUUGCUUCC	Cleavage
spe-miR162a-2-5p	Sopen07g032000.1	3.0	-1.0	1	21	285	305	GGAGGCAGCGGUUCAUCGAUC	UCCUGGUGAACCGCUGCCUCG	Cleavage
spe-miR162a-2-5p	Sopen07g032000.2	3.0	-1.0	1	21	285	305	GGAGGCAGCGGUUCAUCGAUC	UCCUGGUGAACCGCUGCCUCG	Cleavage
spe-miR162a-2-5p	Sopen09g018100.1	3.0	-1.0	1	21	3786	3806	GGAGGCAGCGGUUCAUCGAUC	UCUCGAUGGACCGUUAUCUCC	Cleavage
spe-miR164-3p	Sopen07g014240.1	3.0	-1.0	1	21	109	129	CAUGUGCUCUAGCUCUCCAGC	AGUGGGGAGCAAGAGCAUGUG	Translation
spe-miR164-3p	Sopen07g014240.1	3.0	-1.0	1	21	397	417	CAUGUGCUCUAGCUCUCCAGC	AGUGGGGAGCAAGAGCAUGUG	Translation
spe-miR164-3p	Sopen05g022910.1	2.5	-1.0	1	21	2143	2163	CAUGUGCUCUAGCUCUCCAGC	AGUGGAGAGCAAGAGUGCAUG	Translation
spe-miR164-3p	Sopen01g047190.1	3.0	-1.0	1	21	204	224	CAUGUGCUCUAGCUCUCCAGC	AGAGGAGAGUGAGAGCACAUG	Translation
spe-miR164-5p	Sopen07g034510.1	1.0	-1.0	1	21	656	676	UGGAGAAGCAGGGCACAUGCU	AGCAAGUGCCCUGCUUCUCCA	Cleavage
spe-miR164-5p	Sopen07g031040.1	1.5	-1.0	1	21	713	733	UGGAGAAGCAGGGCACAUGCU	AGCACGUGCCCUGUUUCUCCA	Cleavage
spe-miR164-5p	Sopen01g036340.1	2.0	-1.0	1	21	1275	1295	UGGAGAAGCAGGGCACAUGCU	UGCAUGUGCCCAGCUUCUUCA	Translation
spe-miR164-5p	Sopen01g036340.2	2.0	-1.0	1	21	1272	1292	UGGAGAAGCAGGGCACAUGCU	UGCAUGUGCCCAGCUUCUUCA	Translation
spe-miR164-5p	Sopen06g008090.2	2.5	-1.0	1	21	796	816	UGGAGAAGCAGGGCACAUGCU	AUUAUGAGCCCUGUUUUUCCA	Cleavage
spe-miR164-5p	Sopen06g008090.1	2.5	-1.0	1	21	796	816	UGGAGAAGCAGGGCACAUGCU	AUUAUGAGCCCUGUUUUUCCA	Cleavage
spe-miR164-5p	Sopen06g027010.1	2.5	-1.0	1	21	623	643	UGGAGAAGCAGGGCACAUGCU	GCCACGUGCACUGCUUCUCCA	Cleavage
spe-miR164-5p	Sopen03g034840.1	2.5	-1.0	1	21	614	634	UGGAGAAGCAGGGCACAUGCU	GCCACGUGCACUGCUUCUCCA	Cleavage
spe-miR164-5p	Sopen04g035050.1	3.0	-1.0	1	21	909	929	UGGAGAAGCAGGGCACAUGCU	AAGAUGUGCCUUGUUUCUCCU	Cleavage
spe-miR164-5p	Sopen01g046980.1	3.0	-1.0	1	21	160	180	UGGAGAAGCAGGGCACAUGCU	UGGAGGUGUCCUGCUUCUUCA	Cleavage
spe-miR164-5p	Sopen10g011370.1	3.0	-1.0	1	21	1031	1051	UGGAGAAGCAGGGCACAUGCU	CCCAUGCGUCCUGCUACUCCA	Cleavage
spe-miR164-5p	Sopen11g030240.1	3.0	-1.0	1	21	1333	1353	UGGAGAAGCAGGGCACAUGCU	GCCAUACGUCCUGCUUCUUCA	Cleavage
spe-miR164-5p	Sopen10g036150.1	3.0	-1.0	1	21	211	231	UGGAGAAGCAGGGCACAUGCU	UACAUAUUUCCUGCUUCUUCA	Cleavage
spe-miR164-5p	Sopen01g031370.1	3.0	-1.0	1	21	131	151	UGGAGAAGCAGGGCACAUGCU	CUCAUCUCCUCUGCUUUUCCA	Cleavage
spe-miR164a-3p	Sopen09g031420.1	2.0	-1.0	1	20	1	20	CAUGUGCCUGUUUUCCCCAU	AUGGGGAAAACAGGUAGAUG	Cleavage

spe-miR164a-3p	Sopen06g026770.1	3.0	-1.0	1	21	307	327	CAUGUGCCUGUUUUCCCCAUC	GGUGAGGAAAACAGGCGUAUU	Cleavage
spe-miR164a-3p	Sopen05g013480.1	3.0	-1.0	1	21	1246	1266	CAUGUGCCUGUUUUCCCCAUC	GAUCAGGAGAGCAGGCACAUG	Cleavage
spe-miR164a-3p	Sopen01g048320.1	3.0	-1.0	1	21	325	345	CAUGUGCCUGUUUUCCCCAUC	UAUGAGGGAGACAGGUAUAUG	Cleavage
spe-miR164a-3p	Sopen01g032750.1	3.0	-1.0	1	21	1563	1583	CAUGUGCCUGUUUUCCCCAUC	AAAGGGGAAAACAAGCAUAUG	Cleavage
spe-miR164a-3p	Sopen01g048290.1	3.0	-1.0	1	21	169	189	CAUGUGCCUGUUUUCCCCAUC	UAUGCGGGAGACAGGUAUAUG	Cleavage
spe-miR164a-3p	Sopen01g004530.1	3.0	-1.0	1	21	31	51	CAUGUGCCUGUUUUCCCCAUC	GCUGGGAAAAAUAGGCGUGUG	Cleavage
spe-miR164a-3p	Sopen10g001710.2	3.0	-1.0	1	21	1505	1525	CAUGUGCCUGUUUUCCCCAUC	GUUGGAGGAAACAGGCAAAUG	Cleavage
spe-miR164a-3p	Sopen10g001710.1	3.0	-1.0	1	21	1508	1528	CAUGUGCCUGUUUUCCCCAUC	GUUGGAGGAAACAGGCAAAUG	Cleavage
spe-miR164a-3p	Sopen06g014990.1	3.0	-1.0	1	21	646	666	CAUGUGCCUGUUUUCCCCAUC	AGUGUGGUAAGCAGGUACAUG	Cleavage
spe-miR164a-3p	Sopen03g014270.1	3.0	-1.0	1	21	1126	1146	CAUGUGCCUGUUUUCCCCAUC	AGUGUGGUAAGCAGGUACAUG	Cleavage
spe-miR164a-3p	Sopen09g026030.1	3.0	-1.0	1	21	841	861	CAUGUGCCUGUUUUCCCCAUC	AGUGUGGUAAGCAGGUACAUG	Cleavage
spe-miR164a-3p	Sopen08g018100.1	3.0	-1.0	1	21	1978	1998	CAUGUGCCUGUUUUCCCCAUC	AGUGUGGUAAGCAGGUACAUG	Cleavage
spe-miR164a-3p	Sopen01g016920.1	3.0	-1.0	1	21	3616	3636	CAUGUGCCUGUUUUCCCCAUC	AGUGUGGUAAGCAGGUACAUG	Cleavage
spe-miR164a-5p	Sopen01g036340.1	2.5	-1.0	1	21	1275	1295	UGGAGAAGCAGGGCACGUGCA	UGCAUGUGCCCAGCUUCUUCA	Translation
spe-miR164a-5p	Sopen01g036340.2	2.5	-1.0	1	21	1272	1292	UGGAGAAGCAGGGCACGUGCA	UGCAUGUGCCCAGCUUCUUCA	Translation
spe-miR164a-5p	Sopen07g031040.1	0.5	-1.0	1	21	713	733	UGGAGAAGCAGGGCACGUGCA	AGCACGUGCCCUGUUUCUCCA	Cleavage
spe-miR164a-5p	Sopen07g034510.1	1.0	-1.0	1	21	656	676	UGGAGAAGCAGGGCACGUGCA	AGCAAGUGCCCUGCUUCUCCA	Cleavage
spe-miR164a-5p	Sopen06g027010.1	1.5	-1.0	1	21	623	643	UGGAGAAGCAGGGCACGUGCA	GCCACGUGCACUGCUUCUCCA	Cleavage
spe-miR164a-5p	Sopen03g034840.1	1.5	-1.0	1	21	614	634	UGGAGAAGCAGGGCACGUGCA	GCCACGUGCACUGCUUCUCCA	Cleavage
spe-miR164a-5p	Sopen11g025920.1	1.5	-1.0	1	21	310	330	UGGAGAAGCAGGGCACGUGCA	CUCGCAUGCCCUGCUUCUCCA	Cleavage
spe-miR164a-5p	Sopen01g028320.1	2.5	-1.0	1	21	487	507	UGGAGAAGCAGGGCACGUGCA	UUGGCGUGCCCUGCUUCUCCU	Cleavage
spe-miR164a-5p	Sopen09g029930.1	2.5	-1.0	1	21	568	588	UGGAGAAGCAGGGCACGUGCA	CUCGCUUGCCCUGCUUCUCCU	Cleavage
spe-miR164a-5p	Sopen01g046980.1	3.0	-1.0	1	21	160	180	UGGAGAAGCAGGGCACGUGCA	UGGAGGUGUCCUGCUUCUUCA	Cleavage
spe-miR164a-5p	Sopen01g033750.1	3.0	-1.0	1	21	3354	3374	UGGAGAAGCAGGGCACGUGCA	GUCACGGGCCUUGCUUCUUCU	Cleavage
spe-miR164a-5p	Sopen06g008090.2	3.0	-1.0	1	21	796	816	UGGAGAAGCAGGGCACGUGCA	AUUAUGAGCCCUGUUUUUCCA	Cleavage
spe-miR164a-5p	Sopen06g008090.1	3.0	-1.0	1	21	796	816	UGGAGAAGCAGGGCACGUGCA	AUUAUGAGCCCUGUUUUUCCA	Cleavage
spe-miR164a-5p	Sopen08g004560.1	3.0	-1.0	1	21	204	224	UGGAGAAGCAGGGCACGUGCA	AUCACGGGUCCUGCUUCUCGA	Cleavage
spe-miR164b-3p	Sopen03g030890.1	2.5	-1.0	1	20	1	20	CACGUGUUCUCCUUCUCCAA	AUGGAGAAGGAGAACACCUU	Cleavage
spe-miR164b-3p	Sopen06g028460.1	3.0	-1.0	1	21	274	294	CACGUGUUCUCCUUCUCCAAC	UUUGUAGAAGGGGACCACGUG	Cleavage
spe-miR164b-3p	Sopen07g034160.1	3.0	-1.0	1	21	122	142	CACGUGUUCUCCUUCUCCAAC	AUCGGAGGGGGAGAAUAUGUG	Cleavage
spe-miR164b-3p	Sopen06g019720.1	3.0	-1.0	1	21	205	225	CACGUGUUCUCCUUCUCCAAC	CAUGGAGAAGGGGAGAGCGUG	Cleavage
spe-miR164b-3p	Sopen01g044530.1	3.0	-1.0	1	21	147	167	CACGUGUUCUCCUUCUCCAAC	UGUGGAUGAGGAGAACAUGUU	Cleavage
spe-miR164b-3p	Sopen05g030400.1	3.0	-1.0	1	21	159	179	CACGUGUUCUCCUUCUCCAAC	AGUAGAGGAGGAGAACAUGUU	Cleavage
spe-miR164b-3p	Sopen01g036380.2	3.0	-1.0	1	21	1051	1071	CACGUGUUCUCCUUCUCCAAC	UAUGAAGAGGGAGAACACCUG	Cleavage
spe-miR164b-3p	Sopen03g034650.1	3.0	-1.0	1	21	271	291	CACGUGUUCUCCUUCUCCAAC	UAUGUGGAAGGAGAACAAGUG	Cleavage
spe-miR164b-3p	Sopen01g036380.4	3.0	-1.0	1	21	1084	1104	CACGUGUUCUCCUUCUCCAAC	UAUGAAGAGGGAGAACACCUG	Cleavage
spe-miR164b-3p	Sopen01g036380.3	3.0	-1.0	1	21	1051	1071	CACGUGUUCUCCUUCUCCAAC	UAUGAAGAGGGAGAACACCUG	Cleavage
spe-miR164b-5p	Sopen01g036340.1	2.5	-1.0	1	21	1275	1295	UGGAGAAGCAGGGCACGUGCA	UGCAUGUGCCCAGCUUCUUCA	Translation
spe-miR164b-5p	Sopen01g036340.2	2.5	-1.0	1	21	1272	1292	UGGAGAAGCAGGGCACGUGCA	UGCAUGUGCCCAGCUUCUUCA	Translation
spe-miR164b-5p	Sopen07g031040.1	0.5	-1.0	1	21	713	733	UGGAGAAGCAGGGCACGUGCA	AGCACGUGCCCUGUUUCUCCA	Cleavage
spe-miR164b-5p	Sopen07g034510.1	1.0	-1.0	1	21	656	676	UGGAGAAGCAGGGCACGUGCA	AGCAAGUGCCCUGCUUCUCCA	Cleavage
spe-miR164b-5p	Sopen06g027010.1	1.5	-1.0	1	21	623	643	UGGAGAAGCAGGGCACGUGCA	GCCACGUGCACUGCUUCUCCA	Cleavage
spe-miR164b-5p	Sopen03g034840.1	1.5	-1.0	1	21	614	634	UGGAGAAGCAGGGCACGUGCA	GCCACGUGCACUGCUUCUCCA	Cleavage
spe-miR164b-5p	Sopen11g025920.1	1.5	-1.0	1	21	310	330	UGGAGAAGCAGGGCACGUGCA	CUCGCAUGCCCUGCUUCUCCA	Cleavage
spe-miR164b-5p	Sopen01g028320.1	2.5	-1.0	1	21	487	507	UGGAGAAGCAGGGCACGUGCA	UUGGCGUGCCCUGCUUCUCCU	Cleavage
spe-miR164b-5p	Sopen09g029930.1	2.5	-1.0	1	21	568	588	UGGAGAAGCAGGGCACGUGCA	CUCGCUUGCCCUGCUUCUCCU	Cleavage
spe-miR164b-5p	Sopen01g046980.1	3.0	-1.0	1	21	160	180	UGGAGAAGCAGGGCACGUGCA	UGGAGGUGUCCUGCUUCUUCA	Cleavage
spe-miR164b-5p	Sopen01g033750.1	3.0	-1.0	1	21	3354	3374	UGGAGAAGCAGGGCACGUGCA	GUCACGGGCCUUGCUUCUUCU	Cleavage
spe-miR164b-5p	Sopen06g008090.2	3.0	-1.0	1	21	796	816	UGGAGAAGCAGGGCACGUGCA	AUUAUGAGCCCUGUUUUUCCA	Cleavage
spe-miR164b-5p	Sopen06g008090.1	3.0	-1.0	1	21	796	816	UGGAGAAGCAGGGCACGUGCA	AUUAUGAGCCCUGUUUUUCCA	Cleavage

spe-miR164b-5p	Sopen08g004560.1	3.0	-1.0	1	21	204	224	UGGAGAAGCAGGGCACGUGCA	AUCACGGGUCCUGCUUCUCGA	Cleavage
spe-miR166-1-3p	Sopen11g028190.1	1.0	-1.0	1	21	560	580	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen03g039740.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen12g022680.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen02g018990.1	1.0	-1.0	1	21	530	550	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen02g018990.2	1.0	-1.0	1	21	533	553	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen08g020320.1	1.0	-1.0	1	21	557	577	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen02g006800.1	1.0	-1.0	1	21	572	592	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-1-3p	Sopen07g023950.1	2.5	-1.0	1	21	1163	1183	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
spe-miR166-1-3p	Sopen09g033010.1	3.0	-1.0	1	21	1571	1591	UCGGACCAGGCUUCAUUCCCC	AGGGAAAGGAGCCUUGUCCGA	Cleavage
spe-miR166-1-3p	Sopen08g001070.1	3.0	-1.0	1	21	671	691	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
spe-miR166-1-5p	Sopen09g019910.1	2.0	-1.0	1	21	1242	1262	AGAAUGUCGUCUGGUUCGAGA	GUUGGAAUCAGACGAUAUUCU	Cleavage
spe-miR166-1-5p	Sopen04g034200.1	3.0	-1.0	1	21	426	446	AGAAUGUCGUCUGGUUCGAGA	CCUGGGACCAGAUGACAUUCA	Cleavage
spe-miR166-1-5p	Sopen07g034050.1	3.0	-1.0	1	21	2943	2963	AGAAUGUCGUCUGGUUCGAGA	GCUCGAUCCAAAUGACAUUCU	Translation
spe-miR166-1-5p	Sopen11g022340.1	3.0	-1.0	1	21	2289	2309	AGAAUGUCGUCUGGUUCGAGA	GGUCGAGCCAGCUGGCAUUCU	Translation
spe-miR166-2-3p	Sopen11g028190.1	1.0	-1.0	1	21	560	580	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen03g039740.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen12g022680.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen02g018990.1	1.0	-1.0	1	21	530	550	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen02g018990.2	1.0	-1.0	1	21	533	553	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen08g020320.1	1.0	-1.0	1	21	557	577	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen02g006800.1	1.0	-1.0	1	21	572	592	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166-2-3p	Sopen07g023950.1	2.5	-1.0	1	21	1163	1183	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
spe-miR166-2-3p	Sopen09g033010.1	3.0	-1.0	1	21	1571	1591	UCGGACCAGGCUUCAUUCCCC	AGGGAAAGGAGCCUUGUCCGA	Cleavage
spe-miR166-2-3p	Sopen08g001070.1	3.0	-1.0	1	21	671	691	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
spe-miR166-2-5p	Sopen04g004220.1	2.0	-1.0	1	21	2445	2465	GGAAUGUUGUUUGGCUCGAGG	UCUCAAGCCAAGCAACAUUCU	Cleavage
spe-miR166-2-5p	Sopen08g002360.2	2.0	-1.0	1	21	762	782	GGAAUGUUGUUUGGCUCGAGG	CAGCGAGCCAAACAAUGUUCC	Cleavage
spe-miR166-2-5p	Sopen08g002360.1	2.0	-1.0	1	21	777	797	GGAAUGUUGUUUGGCUCGAGG	CAGCGAGCCAAACAAUGUUCC	Cleavage
spe-miR166-2-5p	Sopen04g020890.1	2.0	-1.0	1	21	2379	2399	GGAAUGUUGUUUGGCUCGAGG	CGUCAAGUCAAACAACAUUCU	Cleavage
spe-miR166-2-5p	Sopen06g033300.1	2.5	-1.0	1	21	2478	2498	GGAAUGUUGUUUGGCUCGAGG	UCUUAAGCCAAGCAACAUUCU	Cleavage
spe-miR166-2-5p	Sopen07g034050.1	2.5	-1.0	1	21	2943	2963	GGAAUGUUGUUUGGCUCGAGG	GCUCGAUCCAAAUGACAUUCU	Cleavage
spe-miR166-2-5p	Sopen12g018730.1	2.5	-1.0	1	21	4041	4061	GGAAUGUUGUUUGGCUCGAGG	UCUCAAACCAAAUAACAUUCC	Cleavage
spe-miR166-2-5p	Sopen03g038900.1	2.5	-1.0	1	21	759	779	GGAAUGUUGUUUGGCUCGAGG	UAUCGUGCCAAGCAAUGUUCC	Cleavage
spe-miR166-2-5p	Sopen06g025070.1	2.5	-1.0	1	21	2253	2273	GGAAUGUUGUUUGGCUCGAGG	AAUUGAGGCAAACAACAUUUU	Cleavage
spe-miR166-2-5p	Sopen08g001030.1	2.5	-1.0	1	21	972	992	GGAAUGUUGUUUGGCUCGAGG	GAUCCAGACAAACAACAUUCU	Cleavage
spe-miR166-2-5p	Sopen09g025580.1	3.0	-1.0	1	21	825	845	GGAAUGUUGUUUGGCUCGAGG	UCUUGAGCUAAAAGACAUUCC	Cleavage
spe-miR166-2-5p	Sopen09g023690.1	3.0	-1.0	1	21	5440	5460	GGAAUGUUGUUUGGCUCGAGG	UCUCAAGCUGAACAACGUUCU	Cleavage
spe-miR166-2-5p	Sopen03g025430.1	3.0	-1.0	1	21	561	581	GGAAUGUUGUUUGGCUCGAGG	GUUCAAGUCAAAUGACAUUCU	Cleavage
spe-miR166-2-5p	Sopen02g026130.1	3.0	-1.0	1	21	1329	1349	GGAAUGUUGUUUGGCUCGAGG	CAUCAAGCCACACAACAUUCU	Translation
spe-miR166-2-5p	Sopen02g026140.1	3.0	-1.0	1	21	1707	1727	GGAAUGUUGUUUGGCUCGAGG	CAUCAAGCCACACAACAUUCU	Translation
spe-miR166-2-5p	Sopen05g001920.1	3.0	-1.0	1	21	810	830	GGAAUGUUGUUUGGCUCGAGG	UGUUGAGACAGACAACAUUUU	Cleavage
spe-miR166a-1-3p	Sopen11g028190.1	1.0	-1.0	1	21	560	580	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen03g039740.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen12g022680.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen02g018990.1	1.0	-1.0	1	21	530	550	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen02g018990.2	1.0	-1.0	1	21	533	553	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen08g020320.1	1.0	-1.0	1	21	557	577	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen02g006800.1	1.0	-1.0	1	21	572	592	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-1-3p	Sopen07g023950.1	2.5	-1.0	1	21	1163	1183	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
spe-miR166a-1-3p	Sopen09g033010.1	3.0	-1.0	1	21	1571	1591	UCGGACCAGGCUUCAUUCCCC	AGGGAAAGGAGCCUUGUCCGA	Cleavage

spe-miR166a-1-3p	Sopen08g001070.1	3.0	-1.0	1	21	671	691	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
spe-miR166a-2-3p	Sopen11g028190.1	1.0	-1.0	1	21	560	580	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen03g039740.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen12g022680.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen02g018990.1	1.0	-1.0	1	21	530	550	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen02g018990.2	1.0	-1.0	1	21	533	553	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen08g020320.1	1.0	-1.0	1	21	557	577	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen02g006800.1	1.0	-1.0	1	21	572	592	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-2-3p	Sopen07g023950.1	2.5	-1.0	1	21	1163	1183	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
spe-miR166a-2-3p	Sopen09g033010.1	3.0	-1.0	1	21	1571	1591	UCGGACCAGGCUUCAUUCCCC	AGGGAAAGGAGCCUUGUCCGA	Cleavage
spe-miR166a-2-3p	Sopen08g001070.1	3.0	-1.0	1	21	671	691	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
spe-miR166a-3-3p	Sopen11g028190.1	1.0	-1.0	1	21	560	580	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen03g039740.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen12g022680.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCCC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen02g018990.1	1.0	-1.0	1	21	530	550	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen02g018990.2	1.0	-1.0	1	21	533	553	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen08g020320.1	1.0	-1.0	1	21	557	577	UCGGACCAGGCUUCAUUCCCC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen02g006800.1	1.0	-1.0	1	21	572	592	UCGGACCAGGCUUCAUUCCCC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166a-3-3p	Sopen07g023950.1	2.5	-1.0	1	21	1163	1183	UCGGACCAGGCUUCAUUCCCC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
spe-miR166a-3-3p	Sopen09g033010.1	3.0	-1.0	1	21	1571	1591	UCGGACCAGGCUUCAUUCCCC	AGGGAAAGGAGCCUUGUCCGA	Cleavage
spe-miR166a-3-3p	Sopen08g001070.1	3.0	-1.0	1	21	671	691	UCGGACCAGGCUUCAUUCCCC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
spe-miR166a-3-5p	Sopen05g001920.1	2.5	-1.0	1	21	810	830	GGAAUGUUGUCUGGCUCGAAG	UGUUGAGACAGACAACAUUUU	Cleavage
spe-miR166a-3-5p	Sopen07g017540.1	3.0	-1.0	1	21	585	605	GGAAUGUUGUCUGGCUCGAAG	UUUGGAUUCAGACAACAUUUC	Cleavage
spe-miR166a-3-5p	Sopen07g017540.2	3.0	-1.0	1	21	1026	1046	GGAAUGUUGUCUGGCUCGAAG	UUUGGAUUCAGACAACAUUUC	Cleavage
spe-miR166a-3-5p	Sopen02g026130.1	3.0	-1.0	1	21	1329	1349	GGAAUGUUGUCUGGCUCGAAG	CAUCAAGCCACACAACAUUCU	Translation
spe-miR166a-3-5p	Sopen02g026140.1	3.0	-1.0	1	21	1707	1727	GGAAUGUUGUCUGGCUCGAAG	CAUCAAGCCACACAACAUUCU	Translation
spe-miR166a-3-5p	Sopen04g026710.1	3.0	-1.0	1	21	669	689	GGAAUGUUGUCUGGCUCGAAG	GGUGGAGCCGGACAAUGUUUC	Cleavage
spe-miR166a-3-5p	Sopen07g012480.1	3.0	-1.0	1	21	1504	1524	GGAAUGUUGUCUGGCUCGAAG	UCUCAAUCUGGACAACAUUCC	Cleavage
spe-miR166c-3p	Sopen11g028190.1	1.0	-1.0	1	21	560	580	UCGGACCAGGCUUCAUUCCUC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen03g039740.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCUC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen12g022680.1	0.5	-1.0	1	21	548	568	UCGGACCAGGCUUCAUUCCUC	CUGGAAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen02g018990.1	1.0	-1.0	1	21	530	550	UCGGACCAGGCUUCAUUCCUC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen02g018990.2	1.0	-1.0	1	21	533	553	UCGGACCAGGCUUCAUUCCUC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen08g020320.1	1.0	-1.0	1	21	557	577	UCGGACCAGGCUUCAUUCCUC	CUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen02g006800.1	1.0	-1.0	1	21	572	592	UCGGACCAGGCUUCAUUCCUC	UUGGGAUGAAGCCUGGUCCGG	Cleavage
spe-miR166c-3p	Sopen07g023950.1	2.5	-1.0	1	21	1163	1183	UCGGACCAGGCUUCAUUCCUC	AAGGUAUCAAGCCUGGUUCGA	Cleavage
spe-miR166c-3p	Sopen09g033010.1	3.0	-1.0	1	21	1571	1591	UCGGACCAGGCUUCAUUCCUC	AGGGAAAGGAGCCUUGUCCGA	Cleavage
spe-miR166c-3p	Sopen08g001070.1	3.0	-1.0	1	21	671	691	UCGGACCAGGCUUCAUUCCUC	GUGUAGUGGAGCUUGGUUCGA	Cleavage
spe-miR166c-5p	Sopen02g017630.1	2.5	-1.0	1	21	1601	1621	GGGAUGUUGUCUGGCUCGACA	UUUUGAGUCAGAUAAUAUCUC	Cleavage
spe-miR166c-5p	Sopen09g004830.1	2.5	-1.0	1	21	510	530	GGGAUGUUGUCUGGCUCGACA	GAUCAAGCCAGACAACAACCC	Cleavage
spe-miR166c-5p	Sopen12g019630.1	3.0	-1.0	1	21	930	950	GGGAUGUUGUCUGGCUCGACA	UGUUGGGCCAGAUGAUAUCCU	Cleavage
spe-miR166c-5p	Sopen05g001920.1	3.0	-1.0	1	21	810	830	GGGAUGUUGUCUGGCUCGACA	UGUUGAGACAGACAACAUUUU	Cleavage
spe-miR166c-5p	Sopen03g018670.1	3.0	-1.0	1	21	1520	1540	GGGAUGUUGUCUGGCUCGACA	CGUCGUGCCAGGUAAUAUCUC	Cleavage
spe-miR166c-5p	Sopen08g014940.1	3.0	-1.0	1	21	3023	3043	GGGAUGUUGUCUGGCUCGACA	CGUCGUGCCAGGUAAUAUCUC	Cleavage
spe-miR166c-5p	Sopen09g034520.1	3.0	-1.0	1	21	817	837	GGGAUGUUGUCUGGCUCGACA	UUUCGAUCCAGACGACUUCCC	Cleavage
spe-miR166c-5p	Sopen07g028990.1	3.0	-1.0	1	21	1917	1937	GGGAUGUUGUCUGGCUCGACA	CAUCAAGCCACACAACAUCCU	Translation
spe-miR166c-5p	Sopen03g001660.1	3.0	-1.0	1	21	688	708	GGGAUGUUGUCUGGCUCGACA	AAUUGUGUCAGACAACAUCUU	Cleavage
spe-miR167-1-3p	Sopen05g016190.1	2.5	-1.0	1	20	175	194	GAUCAUGUGGCAGCAUCACC	CGAGAUGCUGCCAUAUGGUU	Cleavage
spe-miR167-1-3p	Sopen06g008510.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCAUCACC	GGAGAUGCUGCUAUAUGGUU	Cleavage
spe-miR167-1-3p	Sopen02g004310.1	2.0	-1.0	1	20	2100	2119	GAUCAUGUGGCAGCAUCACC	UGAGAUGUUGCCACAUGAUU	Cleavage

spe-miR167-1-3p	Sopen07g010340.1	2.5	-1.0	1	20	43	62	GAUCAUGUGGCAGCAUCACC	GGAGAUGCUGCCAUAUGGUU	Cleavage
spe-miR167-1-3p	Sopen09g007530.1	2.5	-1.0	1	20	678	697	GAUCAUGUGGCAGCAUCACC	UGAGAUGUUGCCAUAUGAUU	Cleavage
spe-miR167-1-3p	Sopen12g019610.1	3.0	-1.0	1	20	385	404	GAUCAUGUGGCAGCAUCACC	GGAGAUGCUGCUAUAUGGUU	Cleavage
spe-miR167-1-3p	Sopen08g016090.1	3.0	-1.0	1	20	337	356	GAUCAUGUGGCAGCAUCACC	GGAGAUGCUGCUAUAUGGUU	Cleavage
spe-miR167-1-3p	Sopen01g011810.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCAUCACC	GGAGAUGCUGCUAUAUGGUU	Cleavage
spe-miR167-1-3p	Sopen09g005560.2	3.0	-1.0	1	20	2329	2348	GAUCAUGUGGCAGCAUCACC	GUUGAUGCUGCCAUAUUAUC	Cleavage
spe-miR167-1-3p	Sopen09g005560.1	3.0	-1.0	1	20	2356	2375	GAUCAUGUGGCAGCAUCACC	GUUGAUGCUGCCAUAUUAUC	Cleavage
spe-miR167-1-3p	Sopen11g030750.1	3.0	-1.0	1	20	640	659	GAUCAUGUGGCAGCAUCACC	CGUGAUGUUGUCACAGGAUU	Cleavage
spe-miR167-1-3p	Sopen07g018800.1	3.0	-1.0	1	20	1980	1999	GAUCAUGUGGCAGCAUCACC	UGUGAUGCUGCUGAAUGAUU	Cleavage
spe-miR167-1-3p	Sopen05g020090.1	3.0	-1.0	1	20	4642	4661	GAUCAUGUGGCAGCAUCACC	AGUGCUGUUGCCACAAGAUC	Cleavage
spe-miR167-1-3p	Sopen07g001760.1	3.0	-1.0	1	20	939	958	GAUCAUGUGGCAGCAUCACC	UGUGAUAUUGUUGCAUGAUC	Cleavage
spe-miR167-1-5p	Sopen06g012940.1	2.0	-1.0	1	21	835	855	UGAAGCUGCCAGCAUGAUCUA	GUGAUUCUGCUGGUAGCUUCA	Cleavage
spe-miR167-1-5p	Sopen03g036620.2	2.5	-1.0	1	21	368	388	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-1-5p	Sopen03g036620.1	2.5	-1.0	1	21	446	466	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-1-5p	Sopen03g036620.3	2.5	-1.0	1	21	722	742	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-1-5p	Sopen04g029200.1	3.0	-1.0	1	21	904	924	UGAAGCUGCCAGCAUGAUCUA	GAGAAUAUGCUGGUGGCUUUA	Cleavage
spe-miR167-1-5p	Sopen07g027610.1	3.0	-1.0	1	21	1298	1318	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAUGCUAGCAGCUACA	Translation
spe-miR167-1-5p	Sopen04g005070.1	3.0	-1.0	1	21	776	796	UGAAGCUGCCAGCAUGAUCUA	UCGAGUAUGCUGGUGGUUUCA	Cleavage
spe-miR167-1-5p	Sopen01g043310.1	3.0	-1.0	1	21	1016	1036	UGAAGCUGCCAGCAUGAUCUA	CUGAUCAGGCUGGUGGCUUCU	Cleavage
spe-miR167-1-5p	Sopen09g029680.2	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-1-5p	Sopen09g029680.1	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-1-5p	Sopen09g029680.3	3.0	-1.0	1	21	308	328	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-1-5p	Sopen08g023310.1	3.0	-1.0	1	21	1544	1564	UGAAGCUGCCAGCAUGAUCUA	CUGAGUAUGUUGGUAGCUUCG	Cleavage
spe-miR167-2-3p	Sopen03g030330.1	2.5	-1.0	1	20	1368	1387	GAUCAUGUGGUUGCUUCACC	UGUGAAGCAUUCAUAUGAUC	Translation
spe-miR167-2-3p	Sopen04g036130.1	2.5	-1.0	1	20	1080	1099	GAUCAUGUGGUUGCUUCACC	UGUAAAGCAAACACAUGAUC	Translation
spe-miR167-2-3p	Sopen11g028240.1	3.0	-1.0	1	20	1404	1423	GAUCAUGUGGUUGCUUCACC	CGUGAAGAGACUGCAUGAUC	Cleavage
spe-miR167-2-3p	Sopen12g008750.1	3.0	-1.0	1	20	945	964	GAUCAUGUGGUUGCUUCACC	UGUGGAGCAACCACCUGGUU	Cleavage
spe-miR167-2-3p	Sopen01g013360.1	3.0	-1.0	1	20	867	886	GAUCAUGUGGUUGCUUCACC	GAUGGACCAACUACAUGAUC	Cleavage
spe-miR167-2-3p	Sopen04g029880.1	3.0	-1.0	1	20	1380	1399	GAUCAUGUGGUUGCUUCACC	AGCGAAGCAACAACAUGAUU	Cleavage
spe-miR167-2-3p	Sopen01g048490.1	3.0	-1.0	1	20	576	595	GAUCAUGUGGUUGCUUCACC	AGAGAAGCAACUACAUGACC	Cleavage
spe-miR167-2-5p	Sopen06g012940.1	2.0	-1.0	1	21	835	855	UGAAGCUGCCAGCAUGAUCUA	GUGAUUCUGCUGGUAGCUUCA	Cleavage
spe-miR167-2-5p	Sopen03g036620.2	2.5	-1.0	1	21	368	388	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-2-5p	Sopen03g036620.1	2.5	-1.0	1	21	446	466	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-2-5p	Sopen03g036620.3	2.5	-1.0	1	21	722	742	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-2-5p	Sopen04g029200.1	3.0	-1.0	1	21	904	924	UGAAGCUGCCAGCAUGAUCUA	GAGAAUAUGCUGGUGGCUUUA	Cleavage
spe-miR167-2-5p	Sopen07g027610.1	3.0	-1.0	1	21	1298	1318	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAUGCUAGCAGCUACA	Translation
spe-miR167-2-5p	Sopen04g005070.1	3.0	-1.0	1	21	776	796	UGAAGCUGCCAGCAUGAUCUA	UCGAGUAUGCUGGUGGUUUCA	Cleavage
spe-miR167-2-5p	Sopen01g043310.1	3.0	-1.0	1	21	1016	1036	UGAAGCUGCCAGCAUGAUCUA	CUGAUCAGGCUGGUGGCUUCU	Cleavage
spe-miR167-2-5p	Sopen09g029680.2	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-2-5p	Sopen09g029680.1	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-2-5p	Sopen09g029680.3	3.0	-1.0	1	21	308	328	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-2-5p	Sopen08g023310.1	3.0	-1.0	1	21	1544	1564	UGAAGCUGCCAGCAUGAUCUA	CUGAGUAUGUUGGUAGCUUCG	Cleavage
spe-miR167-3-3p	Sopen02g002680.1	2.5	-1.0	1	23	5469	5491	GGUCAUGCUCGGACAGCCUCACU	CUCGACGUUGUCCGAGCGUGACU	Cleavage
spe-miR167-3-3p	Sopen02g002680.1	2.5	-1.0	1	23	9312	9334	GGUCAUGCUCGGACAGCCUCACU	CUCGACGUUGUCCGAGCGUGACU	Cleavage
spe-miR167-3-5p	Sopen06g012940.1	2.0	-1.0	1	21	835	855	UGAAGCUGCCAGCAUGAUCUA	GUGAUUCUGCUGGUAGCUUCA	Cleavage
spe-miR167-3-5p	Sopen03g036620.2	2.5	-1.0	1	21	368	388	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-3-5p	Sopen03g036620.1	2.5	-1.0	1	21	446	466	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-3-5p	Sopen03g036620.3	2.5	-1.0	1	21	722	742	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167-3-5p	Sopen04g029200.1	3.0	-1.0	1	21	904	924	UGAAGCUGCCAGCAUGAUCUA	GAGAAUAUGCUGGUGGCUUUA	Cleavage
spe-miR167-3-5p	Sopen07g027610.1	3.0	-1.0	1	21	1298	1318	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAUGCUAGCAGCUACA	Translation

spe-miR167-3-5p	Sopen04g005070.1	3.0	-1.0	1	21	776	796	UGAAGCUGCCAGCAUGAUCUA	UCGAGUAUGCUGGUGGUUUCA	Cleavage
spe-miR167-3-5p	Sopen01g043310.1	3.0	-1.0	1	21	1016	1036	UGAAGCUGCCAGCAUGAUCUA	CUGAUCAGGCUGGUGGCUUCU	Cleavage
spe-miR167-3-5p	Sopen09g029680.2	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-3-5p	Sopen09g029680.1	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-3-5p	Sopen09g029680.3	3.0	-1.0	1	21	308	328	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167-3-5p	Sopen08g023310.1	3.0	-1.0	1	21	1544	1564	UGAAGCUGCCAGCAUGAUCUA	CUGAGUAUGUUGGUAGCUUCG	Cleavage
spe-miR167a-3p	Sopen07g009170.1	3.0	-1.0	1	20	529	548	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g009080.1	3.0	-1.0	1	20	361	380	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g012500.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g013470.1	3.0	-1.0	1	20	958	977	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g027520.1	3.0	-1.0	1	20	160	179	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g013760.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g020660.1	3.0	-1.0	1	20	253	272	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g010670.1	3.0	-1.0	1	20	1786	1805	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g009090.1	2.5	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUACAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g016060.1	2.5	-1.0	1	20	460	479	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUACAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g009740.1	2.5	-1.0	1	20	1927	1946	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCCAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g015120.1	3.0	-1.0	1	20	490	509	GAUCAUGUGGCAGCCUCACC	GGGGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g015210.1	3.0	-1.0	1	20	349	368	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g008460.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g021080.1	3.0	-1.0	1	20	553	572	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g011560.1	3.0	-1.0	1	20	385	404	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g014110.1	3.0	-1.0	1	20	262	281	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g012850.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g014650.1	3.0	-1.0	1	20	718	737	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g006930.1	3.0	-1.0	1	20	370	389	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g016710.1	3.0	-1.0	1	20	292	311	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g014780.1	3.0	-1.0	1	20	370	389	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g014610.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g014530.1	3.0	-1.0	1	20	403	422	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen00g014220.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g013200.1	3.0	-1.0	1	20	265	284	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g004720.1	3.0	-1.0	1	20	649	668	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g013130.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g015240.1	3.0	-1.0	1	20	217	236	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g018330.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g014790.1	3.0	-1.0	1	20	523	542	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g020910.1	3.0	-1.0	1	20	370	389	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g018440.1	3.0	-1.0	1	20	1036	1055	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g005670.1	3.0	-1.0	1	20	370	389	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g023120.1	3.0	-1.0	1	20	901	920	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g017220.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g028390.1	3.0	-1.0	1	20	370	389	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g017970.1	3.0	-1.0	1	20	160	179	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g014600.1	3.0	-1.0	1	20	361	380	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g019990.1	3.0	-1.0	1	20	1216	1235	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g014210.1	3.0	-1.0	1	20	712	731	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g018860.1	3.0	-1.0	1	20	205	224	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g012920.1	3.0	-1.0	1	20	478	497	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g012100.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage

spe-miR167a-3p	Sopen03g020650.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g020600.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g025900.1	3.0	-1.0	1	20	541	560	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g022450.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g012490.1	3.0	-1.0	1	20	160	179	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g012460.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g010960.1	3.0	-1.0	1	20	1297	1316	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g007890.1	3.0	-1.0	1	20	181	200	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g020980.1	3.0	-1.0	1	20	661	680	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g014480.1	3.0	-1.0	1	20	502	521	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g020430.1	3.0	-1.0	1	20	1729	1748	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g022370.1	3.0	-1.0	1	20	160	179	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g023040.1	3.0	-1.0	1	20	394	413	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g010290.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g010240.1	3.0	-1.0	1	20	361	380	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g028280.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g010270.1	3.0	-1.0	1	20	361	380	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g008170.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g015560.1	3.0	-1.0	1	20	562	581	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g011410.1	3.0	-1.0	1	20	154	173	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g021490.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g014060.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g011550.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g018590.1	3.0	-1.0	1	20	268	287	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g016570.1	3.0	-1.0	1	20	466	485	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g007230.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g011550.1	3.0	-1.0	1	20	361	380	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g033770.1	3.0	-1.0	1	20	178	197	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g015860.1	3.0	-1.0	1	20	688	707	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g021960.1	3.0	-1.0	1	20	403	422	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g010690.1	3.0	-1.0	1	20	475	494	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g019780.1	3.0	-1.0	1	20	610	629	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g017180.1	3.0	-1.0	1	20	331	350	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g011770.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g025580.1	3.0	-1.0	1	20	160	179	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g010110.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g016260.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g021790.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g026860.1	3.0	-1.0	1	20	886	905	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g006150.1	3.0	-1.0	1	20	1303	1322	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g020210.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g013450.1	3.0	-1.0	1	20	268	287	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g015660.1	3.0	-1.0	1	20	556	575	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g024170.1	3.0	-1.0	1	20	250	269	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g018470.1	3.0	-1.0	1	20	421	440	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g015030.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g015900.1	3.0	-1.0	1	20	4	23	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g013680.1	3.0	-1.0	1	20	235	254	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g018990.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g015950.1	3.0	-1.0	1	20	349	368	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage

spe-miR167a-3p	Sopen08g018360.1	3.0	-1.0	1	20	715	734	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g027980.1	3.0	-1.0	1	20	427	446	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g010100.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g014840.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g014240.1	3.0	-1.0	1	20	631	650	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g022520.1	3.0	-1.0	1	20	619	638	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g018360.1	3.0	-1.0	1	20	553	572	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g017930.1	3.0	-1.0	1	20	1264	1283	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g021610.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g019220.1	3.0	-1.0	1	20	361	380	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g013090.1	3.0	-1.0	1	20	259	278	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g008820.1	3.0	-1.0	1	20	535	554	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g008950.1	3.0	-1.0	1	20	1339	1358	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g011420.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g026820.1	3.0	-1.0	1	20	583	602	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g012570.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g011220.2	3.0	-1.0	1	20	223	242	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g018340.1	3.0	-1.0	1	20	322	341	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g002230.1	3.0	-1.0	1	20	220	239	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g006380.1	3.0	-1.0	1	20	439	458	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g012650.1	3.0	-1.0	1	20	1285	1304	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUACGUGGUU	Cleavage
spe-miR167a-3p	Sopen11g021890.1	3.0	-1.0	1	20	844	863	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g017830.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g021320.1	3.0	-1.0	1	20	238	257	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g010230.1	3.0	-1.0	1	20	655	674	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g025950.1	3.0	-1.0	1	20	664	683	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g017430.1	3.0	-1.0	1	20	880	899	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g015090.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g005260.1	3.0	-1.0	1	20	514	533	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g013960.1	3.0	-1.0	1	20	223	242	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g022410.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g015490.1	3.0	-1.0	1	20	268	287	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g008620.1	3.0	-1.0	1	20	622	641	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g010810.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g015720.1	3.0	-1.0	1	20	640	659	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g004670.1	3.0	-1.0	1	20	541	560	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g007350.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g011720.1	3.0	-1.0	1	20	463	482	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g014390.1	3.0	-1.0	1	20	394	413	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g019780.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g013010.1	3.0	-1.0	1	20	265	284	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g010650.1	3.0	-1.0	1	20	682	701	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g016050.1	3.0	-1.0	1	20	631	650	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g021570.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g015580.1	3.0	-1.0	1	20	187	206	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g014490.1	3.0	-1.0	1	20	2644	2663	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g013420.1	3.0	-1.0	1	20	82	101	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g013880.1	3.0	-1.0	1	20	529	548	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g013070.1	3.0	-1.0	1	20	394	413	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g022410.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage

spe-miR167a-3p	Sopen05g012110.1	3.0	-1.0	1	20	220	239	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g014940.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g008250.1	3.0	-1.0	1	20	391	410	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g015410.1	3.0	-1.0	1	20	454	473	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g011350.1	3.0	-1.0	1	20	763	782	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g017420.1	3.0	-1.0	1	20	1804	1823	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g007340.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g019450.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g013550.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g016140.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g006540.1	3.0	-1.0	1	20	619	638	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g010650.1	3.0	-1.0	1	20	370	389	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g018390.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g014490.1	3.0	-1.0	1	20	1147	1166	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g018760.1	3.0	-1.0	1	20	391	410	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g005370.1	3.0	-1.0	1	20	631	650	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g016530.1	3.0	-1.0	1	20	661	680	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g027200.1	3.0	-1.0	1	20	682	701	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g010100.1	3.0	-1.0	1	20	2806	2825	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g022250.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g012490.2	3.0	-1.0	1	20	160	179	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g017240.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g027810.1	3.0	-1.0	1	20	1753	1772	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g019160.1	3.0	-1.0	1	20	463	482	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g018700.1	3.0	-1.0	1	20	694	713	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g016450.1	3.0	-1.0	1	20	355	374	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g010140.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g005860.1	3.0	-1.0	1	20	763	782	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g016340.1	3.0	-1.0	1	20	856	875	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g012110.1	3.0	-1.0	1	20	622	641	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen09g009210.1	3.0	-1.0	1	20	487	506	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen10g007000.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g016480.1	3.0	-1.0	1	20	445	464	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g014250.1	3.0	-1.0	1	20	1105	1124	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g005270.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g013780.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g011220.1	3.0	-1.0	1	20	223	242	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g014900.1	3.0	-1.0	1	20	154	173	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g006590.1	3.0	-1.0	1	20	328	347	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen07g008300.1	3.0	-1.0	1	20	778	797	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g009370.1	3.0	-1.0	1	20	442	461	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen12g020370.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g018380.1	3.0	-1.0	1	20	1186	1205	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g014680.1	3.0	-1.0	1	20	562	581	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g014060.1	3.0	-1.0	1	20	694	713	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g015750.1	3.0	-1.0	1	20	2023	2042	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen11g015010.1	3.0	-1.0	1	20	715	734	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen01g011260.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g009060.1	3.0	-1.0	1	20	2890	2909	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen08g008620.1	3.0	-1.0	1	20	469	488	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage

spe-miR167a-3p	Sopen05g013340.1	3.0	-1.0	1	20	742	761	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen03g018600.1	3.0	-1.0	1	20	397	416	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen06g012560.1	3.0	-1.0	1	20	430	449	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen02g009000.1	3.0	-1.0	1	20	235	254	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen04g017480.1	3.0	-1.0	1	20	2104	2123	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-3p	Sopen05g024770.1	3.0	-1.0	1	20	922	941	GAUCAUGUGGCAGCCUCACC	GGAGAGGCUGCUAUAUGGUU	Cleavage
spe-miR167a-5p	Sopen06g012940.1	2.0	-1.0	1	21	835	855	UGAAGCUGCCAGCAUGAUCUA	GUGAUUCUGCUGGUAGCUUCA	Cleavage
spe-miR167a-5p	Sopen03g036620.2	2.5	-1.0	1	21	368	388	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167a-5p	Sopen03g036620.1	2.5	-1.0	1	21	446	466	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167a-5p	Sopen03g036620.3	2.5	-1.0	1	21	722	742	UGAAGCUGCCAGCAUGAUCUA	UUGAUCAUGUUGGCAGUCUCA	Cleavage
spe-miR167a-5p	Sopen04g029200.1	3.0	-1.0	1	21	904	924	UGAAGCUGCCAGCAUGAUCUA	GAGAAUAUGCUGGUGGCUUUA	Cleavage
spe-miR167a-5p	Sopen07g027610.1	3.0	-1.0	1	21	1298	1318	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAUGCUAGCAGCUACA	Translation
spe-miR167a-5p	Sopen04g005070.1	3.0	-1.0	1	21	776	796	UGAAGCUGCCAGCAUGAUCUA	UCGAGUAUGCUGGUGGUUUCA	Cleavage
spe-miR167a-5p	Sopen01g043310.1	3.0	-1.0	1	21	1016	1036	UGAAGCUGCCAGCAUGAUCUA	CUGAUCAGGCUGGUGGCUUCU	Cleavage
spe-miR167a-5p	Sopen09g029680.2	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167a-5p	Sopen09g029680.1	3.0	-1.0	1	21	305	325	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167a-5p	Sopen09g029680.3	3.0	-1.0	1	21	308	328	UGAAGCUGCCAGCAUGAUCUA	AUGAUCAGGAUGGUAGCUUCA	Cleavage
spe-miR167a-5p	Sopen08g023310.1	3.0	-1.0	1	21	1544	1564	UGAAGCUGCCAGCAUGAUCUA	CUGAGUAUGUUGGUAGCUUCG	Cleavage
spe-miR167h-3p	Sopen08g028220.1	3.0	-1.0	1	24	198	221	AUCAUGCUGGCAGCUUCAACUGAU	AGAUGAAGAGGCUGCUAGCAUGAU	Cleavage
spe-miR167h-3p	Sopen09g032580.1	3.0	-1.0	1	24	141	164	AUCAUGCUGGCAGCUUCAACUGAU	GUCAUUUGAAGUUGCUAAUAUGAU	Cleavage
spe-miR167h-3p	Sopen04g002640.1	3.0	-1.0	1	24	2010	2033	AUCAUGCUGGCAGCUUCAACUGAU	GCAAAUUGAAGCUGCCAUUAUGAA	Cleavage
spe-miR168a-3p	Sopen01g035540.1	2.0	-1.0	1	21	2375	2395	CCUGCCUUGCAUCAACUGAAU	AGUCGGUUGAUGCAAGUCAGG	Cleavage
spe-miR168a-5p	Sopen03g028990.1	2.5	-1.0	1	21	611	631	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
spe-miR168a-5p	Sopen06g028670.1	2.5	-1.0	1	21	335	355	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
spe-miR168a-5p	Sopen01g045690.1	3.0	-1.0	1	21	63	83	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168a-5p	Sopen01g045690.1	3.0	-1.0	1	21	1449	1469	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168a-5p	Sopen05g031740.1	2.5	-1.0	1	21	1047	1067	UCGCUUGGUGCAGGUCGGGAC	CGCUCGACCUGCACCUAGUGA	Cleavage
spe-miR168a-5p	Sopen03g011340.1	3.0	-1.0	1	21	465	485	UCGCUUGGUGCAGGUCGGGAC	CCUCCGGCCUGCGCCAAGUGU	Cleavage
spe-miR168a-5p	Sopen12g033720.1	3.0	-1.0	1	21	1044	1064	UCGCUUGGUGCAGGUCGGGAC	GCCUCGACCUGUACCAAGUUA	Cleavage
spe-miR168a-5p	Sopen01g045700.2	3.0	-1.0	1	21	1989	2009	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168a-5p	Sopen01g045700.3	3.0	-1.0	1	21	1989	2009	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168a-5p	Sopen01g045710.1	3.0	-1.0	1	21	1794	1814	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168a-5p	Sopen01g045700.1	3.0	-1.0	1	21	1521	1541	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168a-5p	Sopen03g015640.1	3.0	-1.0	1	21	469	489	UCGCUUGGUGCAGGUCGGGAC	CCUCCUACCUGCACCAAGUGU	Cleavage
spe-miR168b-3p	Sopen06g033090.1	3.0	-1.0	1	21	872	892	CCCGCCUUGCAUCAACUGAAU	UUUCAGUUGAUGCAGGGCGAU	Cleavage
spe-miR168b-3p	Sopen01g044950.1	3.0	-1.0	1	21	3239	3259	CCCGCCUUGCAUCAACUGAAU	UAUCAGUUGGUGCGGGACGGG	Cleavage
spe-miR168b-3p	Sopen01g050470.1	3.0	-1.0	1	21	650	670	CCCGCCUUGCAUCAACUGAAU	AAUCAGAUGAUGCAAUGUGGG	Cleavage
spe-miR168b-5p	Sopen03g028990.1	2.5	-1.0	1	21	611	631	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
spe-miR168b-5p	Sopen06g028670.1	2.5	-1.0	1	21	335	355	UCGCUUGGUGCAGGUCGGGAC	UUCCCGAGCUGCACCAAGCAA	Cleavage
spe-miR168b-5p	Sopen01g045690.1	3.0	-1.0	1	21	63	83	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168b-5p	Sopen01g045690.1	3.0	-1.0	1	21	1449	1469	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168b-5p	Sopen05g031740.1	2.5	-1.0	1	21	1047	1067	UCGCUUGGUGCAGGUCGGGAC	CGCUCGACCUGCACCUAGUGA	Cleavage
spe-miR168b-5p	Sopen03g011340.1	3.0	-1.0	1	21	465	485	UCGCUUGGUGCAGGUCGGGAC	CCUCCGGCCUGCGCCAAGUGU	Cleavage
spe-miR168b-5p	Sopen12g033720.1	3.0	-1.0	1	21	1044	1064	UCGCUUGGUGCAGGUCGGGAC	GCCUCGACCUGUACCAAGUUA	Cleavage
spe-miR168b-5p	Sopen01g045700.2	3.0	-1.0	1	21	1989	2009	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168b-5p	Sopen01g045700.3	3.0	-1.0	1	21	1989	2009	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168b-5p	Sopen01g045710.1	3.0	-1.0	1	21	1794	1814	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168b-5p	Sopen01g045700.1	3.0	-1.0	1	21	1521	1541	UCGCUUGGUGCAGGUCGGGAC	GAUCCAGCCUGUAUCAAGCGA	Cleavage
spe-miR168b-5p	Sopen03g015640.1	3.0	-1.0	1	21	469	489	UCGCUUGGUGCAGGUCGGGAC	CCUCCUACCUGCACCAAGUGU	Cleavage
spe-miR169-1-3p	Sopen12g017580.1	2.0	-1.0	1	22	382	403	CCGGCAAGUUGUUUUUGGCUAU	AACGCCGAAAACAACUUGCCAG	Cleavage

spe-miR169-1-3p	Sopen01g037810.1	3.0	-1.0	1	22	7	28	CCGGCAAGUUGUUUUUGGCUAU	GAAGCUAAAAGCGAAUUGCCGG	Cleavage
spe-miR169-1-3p	Sopen11g011450.1	3.0	-1.0	1	22	2316	2337	CCGGCAAGUUGUUUUUGGCUAU	UGUGCCAAAGACAGCUUUUCGG	Cleavage
spe-miR169-1-3p	Sopen12g001900.2	3.0	-1.0	1	22	1297	1318	CCGGCAAGUUGUUUUUGGCUAU	GAUGUAAAAGAUAAUUUGCCGG	Cleavage
spe-miR169-1-3p	Sopen12g001900.1	3.0	-1.0	1	22	1732	1753	CCGGCAAGUUGUUUUUGGCUAU	GAUGUAAAAGAUAAUUUGCCGG	Cleavage
spe-miR169-1-5p	Sopen02g010830.1	3.0	-1.0	1	21	2893	2913	CAGCCAAGGAUGACUUGCCGG	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169-1-5p	Sopen03g027310.3	3.0	-1.0	1	21	115	135	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169-1-5p	Sopen03g027310.2	3.0	-1.0	1	21	547	567	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169-1-5p	Sopen04g033130.1	3.0	-1.0	1	21	614	634	CAGCCAAGGAUGACUUGCCGG	UGUUUAAGUCAUCUUUGGCUG	Cleavage
spe-miR169-1-5p	Sopen02g010310.1	3.0	-1.0	1	21	3053	3073	CAGCCAAGGAUGACUUGCCGG	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169-1-5p	Sopen08g002780.1	3.0	-1.0	1	21	416	436	CAGCCAAGGAUGACUUGCCGG	CUGGAUAUUCAUCCUUGGCUG	Cleavage
spe-miR169-1-5p	Sopen04g008620.1	3.0	-1.0	1	21	1397	1417	CAGCCAAGGAUGACUUGCCGG	GUGGAAAUUUAUCUUUGGCUG	Cleavage
spe-miR169-2-3p	Sopen08g021590.1	2.5	-1.0	1	19	391	409	GCAAGUUAUCCUGGCUAUC	GAUAGCUAUGGUAACUUGC	Translation
spe-miR169-2-3p	Sopen07g001470.1	3.0	-1.0	1	19	673	691	GCAAGUUAUCCUGGCUAUC	GAUAGUGAGGAUGAUUUGC	Cleavage
spe-miR169-2-3p	Sopen05g015600.1	3.0	-1.0	1	19	232	250	GCAAGUUAUCCUGGCUAUC	GAUAAUUGGGAUAACUUGU	Cleavage
spe-miR169-2-5p	Sopen06g026220.1	2.5	-1.0	1	21	644	664	UAGCCAAGGAUGACUUGCCUA	CUCGCAAGGCAUCCUUGGCUA	Cleavage
spe-miR169-2-5p	Sopen03g041780.1	3.0	-1.0	1	21	1208	1228	UAGCCAAGGAUGACUUGCCUA	UGGGUAAGUUAUCCUUCGUUA	Cleavage
spe-miR169-3-3p	Sopen09g021180.1	3.0	-1.0	1	21	1295	1315	GCAGGUCAUCUUUAGCUAACU	AGUUCCCUGAGGAUGACCUGC	Cleavage
spe-miR169-3-3p	Sopen10g017840.1	3.0	-1.0	1	21	1520	1540	GCAGGUCAUCUUUAGCUAACU	AAGAAGCUAAAGAUGACCUGG	Cleavage
spe-miR169-3-3p	Sopen08g023410.1	3.0	-1.0	1	21	113	133	GCAGGUCAUCUUUAGCUAACU	UAAUGGUUGAAGAUGAUCUGC	Cleavage
spe-miR169-3-3p	Sopen02g010780.1	3.0	-1.0	1	21	185	205	GCAGGUCAUCUUUAGCUAACU	UAAUGGUUGAAGAUGAUCUGC	Cleavage
spe-miR169-3-3p	Sopen09g026780.1	3.0	-1.0	1	21	311	331	GCAGGUCAUCUUUAGCUAACU	AUUCAGCUAAAGAUAACUUGC	Cleavage
spe-miR169-3-3p	Sopen03g020360.1	3.0	-1.0	1	21	323	343	GCAGGUCAUCUUUAGCUAACU	AAUCAGCUAAGGAUGAGCUGC	Cleavage
spe-miR169-3-3p	Sopen07g029990.1	3.0	-1.0	1	21	455	475	GCAGGUCAUCUUUAGCUAACU	CCUUUGCUGAAGAUGACUUGA	Cleavage
spe-miR169-3-3p	Sopen05g002290.1	3.0	-1.0	1	21	236	256	GCAGGUCAUCUUUAGCUAACU	GGCUUGGUAAAGAUGACCUGC	Cleavage
spe-miR169-3-5p	Sopen03g027310.3	3.0	-1.0	1	21	115	135	UAGCCAAGAAUGACUUGCCUG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169-3-5p	Sopen03g027310.2	3.0	-1.0	1	21	547	567	UAGCCAAGAAUGACUUGCCUG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169-4-3p	Sopen09g021180.1	3.0	-1.0	1	21	1295	1315	GCAGGUCAUCUUUAGCUAACU	AGUUCCCUGAGGAUGACCUGC	Cleavage
spe-miR169-4-3p	Sopen10g017840.1	3.0	-1.0	1	21	1520	1540	GCAGGUCAUCUUUAGCUAACU	AAGAAGCUAAAGAUGACCUGG	Cleavage
spe-miR169-4-3p	Sopen08g023410.1	3.0	-1.0	1	21	113	133	GCAGGUCAUCUUUAGCUAACU	UAAUGGUUGAAGAUGAUCUGC	Cleavage
spe-miR169-4-3p	Sopen02g010780.1	3.0	-1.0	1	21	185	205	GCAGGUCAUCUUUAGCUAACU	UAAUGGUUGAAGAUGAUCUGC	Cleavage
spe-miR169-4-3p	Sopen09g026780.1	3.0	-1.0	1	21	311	331	GCAGGUCAUCUUUAGCUAACU	AUUCAGCUAAAGAUAACUUGC	Cleavage
spe-miR169-4-3p	Sopen03g020360.1	3.0	-1.0	1	21	323	343	GCAGGUCAUCUUUAGCUAACU	AAUCAGCUAAGGAUGAGCUGC	Cleavage
spe-miR169-4-3p	Sopen07g029990.1	3.0	-1.0	1	21	455	475	GCAGGUCAUCUUUAGCUAACU	CCUUUGCUGAAGAUGACUUGA	Cleavage
spe-miR169-4-3p	Sopen05g002290.1	3.0	-1.0	1	21	236	256	GCAGGUCAUCUUUAGCUAACU	GGCUUGGUAAAGAUGACCUGC	Cleavage
spe-miR169-4-5p	Sopen06g026220.1	2.5	-1.0	1	21	644	664	UAGCCAAGGAUGACUUGCCUG	CUCGCAAGGCAUCCUUGGCUA	Cleavage
spe-miR169-4-5p	Sopen03g041780.1	3.0	-1.0	1	21	1208	1228	UAGCCAAGGAUGACUUGCCUG	UGGGUAAGUUAUCCUUCGUUA	Cleavage
spe-miR169-5-3p	Sopen01g040400.1	3.0	-1.0	1	21	580	600	GGCAAGUGGUCCUUGGCUACA	AGUAGACAAGGAUCCCUUGCC	Cleavage
spe-miR169-5-3p	Sopen01g040400.2	3.0	-1.0	1	21	2500	2520	GGCAAGUGGUCCUUGGCUACA	AGUAGACAAGGAUCCCUUGCC	Cleavage
spe-miR169-5-3p	Sopen02g020320.2	3.0	-1.0	1	21	3175	3195	GGCAAGUGGUCCUUGGCUACA	CCUGGCCAAGGACUACCUGCU	Cleavage
spe-miR169-5-3p	Sopen02g020320.1	3.0	-1.0	1	21	3178	3198	GGCAAGUGGUCCUUGGCUACA	CCUGGCCAAGGACUACCUGCU	Cleavage
spe-miR169-5-5p	Sopen02g010830.1	3.0	-1.0	1	21	2893	2913	CAGCCAAGGAUGACUUGCCGA	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169-5-5p	Sopen03g027310.3	3.0	-1.0	1	21	115	135	CAGCCAAGGAUGACUUGCCGA	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169-5-5p	Sopen03g027310.2	3.0	-1.0	1	21	547	567	CAGCCAAGGAUGACUUGCCGA	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169-5-5p	Sopen04g033130.1	3.0	-1.0	1	21	614	634	CAGCCAAGGAUGACUUGCCGA	UGUUUAAGUCAUCUUUGGCUG	Cleavage
spe-miR169-5-5p	Sopen02g010310.1	3.0	-1.0	1	21	3053	3073	CAGCCAAGGAUGACUUGCCGA	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169-5-5p	Sopen04g008620.1	3.0	-1.0	1	21	1397	1417	CAGCCAAGGAUGACUUGCCGA	GUGGAAAUUUAUCUUUGGCUG	Cleavage
spe-miR169-5-5p	Sopen08g002780.1	3.0	-1.0	1	21	416	436	CAGCCAAGGAUGACUUGCCGA	CUGGAUAUUCAUCCUUGGCUG	Cleavage
spe-miR169a-1-3p	Sopen09g004720.1	3.0	-1.0	1	21	673	693	GGCAAGUUGUUCUUGGCUAUA	AAUGGCCAAGAAGAAUUUGUC	Cleavage
spe-miR169a-1-3p	Sopen02g035530.1	3.0	-1.0	1	21	303	323	GGCAAGUUGUUCUUGGCUAUA	UGAAGCCAAGAACAGUUUGCA	Cleavage
spe-miR169a-1-3p	Sopen06g031640.1	3.0	-1.0	1	21	1228	1248	GGCAAGUUGUUCUUGGCUAUA	AAUGGACAAGGACAAUUUGCU	Cleavage

spe-miR169a-1-3p	Sopen09g033070.1	3.0	-1.0	1	21	541	561	GGCAAGUUGUUCUUGGCUAUA	AAUGGACAAGAACGACUUGUU	Cleavage
spe-miR169a-1-3p	Sopen05g031520.1	3.0	-1.0	1	21	529	549	GGCAAGUUGUUCUUGGCUAUA	GGUAGCCAAGGACAAGUUGUU	Cleavage
spe-miR169a-1-3p	Sopen04g030460.1	3.0	-1.0	1	21	153	173	GGCAAGUUGUUCUUGGCUAUA	GAAGGCUAAGAACAAUUUGUC	Cleavage
spe-miR169a-1-3p	Sopen05g021750.1	3.0	-1.0	1	21	414	434	GGCAAGUUGUUCUUGGCUAUA	UUUGGCCAAGAAUGGUUUGCU	Cleavage
spe-miR169a-1-3p	Sopen02g002110.1	3.0	-1.0	1	21	339	359	GGCAAGUUGUUCUUGGCUAUA	UUUGGCUAAGAAAAACUUGCU	Cleavage
spe-miR169a-1-3p	Sopen05g003090.1	3.0	-1.0	1	21	310	330	GGCAAGUUGUUCUUGGCUAUA	UCUAGUCAGGAAUGGCUUGUC	Cleavage
spe-miR169a-1-3p	Sopen08g029160.1	3.0	-1.0	1	21	418	438	GGCAAGUUGUUCUUGGCUAUA	ACUAGCCAAGAACAAGUUGUG	Cleavage
spe-miR169a-1-3p	Sopen02g030490.1	3.0	-1.0	1	21	3961	3981	GGCAAGUUGUUCUUGGCUAUA	GUUAGUCGAGAUCAACUUGCU	Translation
spe-miR169a-1-3p	Sopen03g023320.1	3.0	-1.0	1	21	1233	1253	GGCAAGUUGUUCUUGGCUAUA	AUUGGCCAAGAGCAACUUUUC	Cleavage
spe-miR169a-1-5p	Sopen02g010830.1	3.0	-1.0	1	21	2893	2913	CAGCCAAGGAUGACUUGCCGG	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169a-1-5p	Sopen03g027310.3	3.0	-1.0	1	21	115	135	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169a-1-5p	Sopen03g027310.2	3.0	-1.0	1	21	547	567	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169a-1-5p	Sopen04g033130.1	3.0	-1.0	1	21	614	634	CAGCCAAGGAUGACUUGCCGG	UGUUUAAGUCAUCUUUGGCUG	Cleavage
spe-miR169a-1-5p	Sopen02g010310.1	3.0	-1.0	1	21	3053	3073	CAGCCAAGGAUGACUUGCCGG	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169a-1-5p	Sopen08g002780.1	3.0	-1.0	1	21	416	436	CAGCCAAGGAUGACUUGCCGG	CUGGAUAUUCAUCCUUGGCUG	Cleavage
spe-miR169a-1-5p	Sopen04g008620.1	3.0	-1.0	1	21	1397	1417	CAGCCAAGGAUGACUUGCCGG	GUGGAAAUUUAUCUUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen02g010830.1	3.0	-1.0	1	21	2893	2913	CAGCCAAGGAUGACUUGCCGG	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen03g027310.3	3.0	-1.0	1	21	115	135	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen03g027310.2	3.0	-1.0	1	21	547	567	CAGCCAAGGAUGACUUGCCGG	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen04g033130.1	3.0	-1.0	1	21	614	634	CAGCCAAGGAUGACUUGCCGG	UGUUUAAGUCAUCUUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen02g010310.1	3.0	-1.0	1	21	3053	3073	CAGCCAAGGAUGACUUGCCGG	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen08g002780.1	3.0	-1.0	1	21	416	436	CAGCCAAGGAUGACUUGCCGG	CUGGAUAUUCAUCCUUGGCUG	Cleavage
spe-miR169a-2-5p	Sopen04g008620.1	3.0	-1.0	1	21	1397	1417	CAGCCAAGGAUGACUUGCCGG	GUGGAAAUUUAUCUUUGGCUG	Cleavage
spe-miR169c-5p	Sopen02g010830.1	3.0	-1.0	1	21	2893	2913	CAGCCAAGGAUGACUUGCCGA	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169c-5p	Sopen03g027310.3	3.0	-1.0	1	21	115	135	CAGCCAAGGAUGACUUGCCGA	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169c-5p	Sopen03g027310.2	3.0	-1.0	1	21	547	567	CAGCCAAGGAUGACUUGCCGA	AAAUUAAGUCAUUCUUGGCUG	Cleavage
spe-miR169c-5p	Sopen04g033130.1	3.0	-1.0	1	21	614	634	CAGCCAAGGAUGACUUGCCGA	UGUUUAAGUCAUCUUUGGCUG	Cleavage
spe-miR169c-5p	Sopen02g010310.1	3.0	-1.0	1	21	3053	3073	CAGCCAAGGAUGACUUGCCGA	GCCGCAAGACAUCUUUGGCUG	Cleavage
spe-miR169c-5p	Sopen04g008620.1	3.0	-1.0	1	21	1397	1417	CAGCCAAGGAUGACUUGCCGA	GUGGAAAUUUAUCUUUGGCUG	Cleavage
spe-miR169c-5p	Sopen08g002780.1	3.0	-1.0	1	21	416	436	CAGCCAAGGAUGACUUGCCGA	CUGGAUAUUCAUCCUUGGCUG	Cleavage
spe-miR169e-3p	Sopen01g034760.1	2.5	-1.0	1	21	213	233	UGGCAAGCAUCUUUGGCGACU	UUUCGCCAAAGGUGUUUCCCA	Cleavage
spe-miR169e-3p	Sopen06g033960.1	2.5	-1.0	1	21	2459	2479	UGGCAAGCAUCUUUGGCGACU	AGUUAUCAAAGAUGCUUGUCA	Cleavage
spe-miR169e-3p	Sopen12g019050.1	2.5	-1.0	1	21	1011	1031	UGGCAAGCAUCUUUGGCGACU	UGUUGCUGAAGGUGCUUGCCG	Cleavage
spe-miR169e-3p	Sopen01g034730.1	2.5	-1.0	1	21	618	638	UGGCAAGCAUCUUUGGCGACU	CUUCGCCAAAGGUGUUUCCCA	Cleavage
spe-miR169e-3p	Sopen10g035210.1	2.5	-1.0	1	21	264	284	UGGCAAGCAUCUUUGGCGACU	UUUUGACAAGGAUGCUUGUCA	Cleavage
spe-miR169e-3p	Sopen12g010190.1	3.0	-1.0	1	21	903	923	UGGCAAGCAUCUUUGGCGACU	GGUUGCCAAGGAUGGUUGCUA	Cleavage
spe-miR169e-3p	Sopen03g041740.1	3.0	-1.0	1	21	1519	1539	UGGCAAGCAUCUUUGGCGACU	AGUGGUGAAAGAUGCUUGCCG	Cleavage
spe-miR169e-3p	Sopen12g007870.1	3.0	-1.0	1	21	407	427	UGGCAAGCAUCUUUGGCGACU	GUUUGCUAAAGGUGUUUGCUG	Cleavage
spe-miR169e-3p	Sopen01g034750.1	3.0	-1.0	1	21	636	656	UGGCAAGCAUCUUUGGCGACU	CUUUGCUAAAGGUGCUUCCCA	Cleavage
spe-miR169e-3p	Sopen01g034780.1	3.0	-1.0	1	21	678	698	UGGCAAGCAUCUUUGGCGACU	CUUUGCCAAAGGUGUUUCCCA	Cleavage
spe-miR169e-3p	Sopen10g010620.1	3.0	-1.0	1	21	861	881	UGGCAAGCAUCUUUGGCGACU	AUUGGCCAAGGUUGCUUGCCA	Translation
spe-miR169e-3p	Sopen08g024500.1	3.0	-1.0	1	21	659	679	UGGCAAGCAUCUUUGGCGACU	UAUCUUCGAAGAUGCUUGUUA	Cleavage
spe-miR169e-3p	Sopen11g020800.1	3.0	-1.0	1	21	291	311	UGGCAAGCAUCUUUGGCGACU	UCUUCCCAAGGGUGCUUGUCA	Cleavage
spe-miR169e-5p	Sopen06g026220.1	2.5	-1.0	1	22	643	664	UAGCCAAGGAUGACUUGCCUUU	GCUCGCAAGGCAUCCUUGGCUA	Cleavage
spe-miR169e-5p	Sopen03g041780.1	3.0	-1.0	1	22	1207	1228	UAGCCAAGGAUGACUUGCCUUU	GUGGGUAAGUUAUCCUUCGUUA	Cleavage
spe-miR171-1-3p	Sopen08g027270.1	2.0	-1.0	1	21	1077	1097	UAAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-1-3p	Sopen01g036680.1	2.0	-1.0	1	21	1287	1307	UAAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-1-3p	Sopen09g005820.1	3.0	-1.0	1	21	582	602	UAAUUGAGCCGUGCCAAUAUC	UAUAUUGGCAUGGGUUGAUUA	Cleavage
spe-miR171-1-3p	Sopen02g013860.1	3.0	-1.0	1	21	164	183	UAAUUGAGCCGUGCCAAUAUC	GGUAUUG-UACGGCUCGAUUA	Cleavage
spe-miR171-1-3p	Sopen02g013850.1	3.0	-1.0	1	21	164	183	UAAUUGAGCCGUGCCAAUAUC	GGUAUUG-UACGGCUCGAUUA	Cleavage

spe-miR171-1-3p	Sopen11g015160.1	3.0	-1.0	1	21	4171	4191	UAAUUGAGCCGUGCCAAUAUC	AGUAUUGAUAUGGCUCAAUUU	Cleavage
spe-miR171-1-5p	Sopen03g004550.1	3.0	-1.0	1	21	128	148	AGAUAUUGGUGCGGUUCAAUU	AAUUGGAGCGCGUCAAUGUCU	Cleavage
spe-miR171-1-5p	Sopen11g024620.1	3.0	-1.0	1	21	238	258	AGAUAUUGGUGCGGUUCAAUU	GAUGGAACUGCAGCAAUAUCU	Cleavage
spe-miR171-1-5p	Sopen09g013940.3	3.0	-1.0	1	21	2648	2668	AGAUAUUGGUGCGGUUCAAUU	UGUUGACCUGCACCAGUAUCC	Cleavage
spe-miR171-1-5p	Sopen07g003770.1	3.0	-1.0	1	21	361	381	AGAUAUUGGUGCGGUUCAAUU	GCUGGAGCUGCACCAAUAUCA	Cleavage
spe-miR171-1-5p	Sopen08g029390.1	3.0	-1.0	1	21	1246	1266	AGAUAUUGGUGCGGUUCAAUU	GCUUCGUCUGCACCAAUAUCU	Cleavage
spe-miR171-2-3p	Sopen01g036680.1	0.0	-1.0	1	20	1288	1307	UGAUUGAGCCGCGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-2-3p	Sopen08g027270.1	0.0	-1.0	1	20	1078	1097	UGAUUGAGCCGCGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-2-3p	Sopen05g023420.1	3.0	-1.0	1	20	35	54	UGAUUGAGCCGCGCCAAUAU	AUAUUGGCGUGGCUAAAUCU	Cleavage
spe-miR171-2-5p	Sopen03g040550.1	2.0	-1.0	1	21	731	751	UAUUGGUGCGGUUCAAUGAGA	UUUCAUUGAAUUGCACUAAUG	Cleavage
spe-miR171-2-5p	Sopen10g015270.1	2.5	-1.0	1	21	794	814	UAUUGGUGCGGUUCAAUGAGA	CUUUAUUGGACUGUACCAAUG	Cleavage
spe-miR171-2-5p	Sopen03g021950.1	3.0	-1.0	1	21	459	479	UAUUGGUGCGGUUCAAUGAGA	CCUUGUUGAAUCGCACCAAGA	Cleavage
spe-miR171-2-5p	Sopen10g009270.1	3.0	-1.0	1	21	323	343	UAUUGGUGCGGUUCAAUGAGA	GGUCAUUGAGCUGCACUAGUU	Cleavage
spe-miR171-2-5p	Sopen08g002590.1	3.0	-1.0	1	21	164	184	UAUUGGUGCGGUUCAAUGAGA	AUUUUUUGAAUUGCAUCAAUA	Cleavage
spe-miR171-3-3p	Sopen08g003030.1	2.5	-1.0	1	21	535	555	UAAUUGAACCGCACCAAUAUC	GAUAUUUCUGCGGUUCAAUUG	Cleavage
spe-miR171-3p	Sopen08g027270.1	0.5	-1.0	1	21	1077	1097	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-3p	Sopen01g036680.1	0.5	-1.0	1	21	1287	1307	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-3p	Sopen02g030270.1	2.5	-1.0	1	21	585	605	UGAUUGAGCCGUGCCAAUAUC	GAUACUGGCACGCCUCAAUCA	Cleavage
spe-miR171-3p	Sopen08g030180.1	2.5	-1.0	1	21	3463	3483	UGAUUGAGCCGUGCCAAUAUC	UAUAUUGGCAUGGCUCUAUCG	Cleavage
spe-miR171-3p	Sopen01g029300.1	2.5	-1.0	1	21	595	615	UGAUUGAGCCGUGCCAAUAUC	AUUCUUGACAUGGCUCAAUCA	Cleavage
spe-miR171-3p	Sopen08g015500.1	3.0	-1.0	1	21	379	399	UGAUUGAGCCGUGCCAAUAUC	CUUGUGGGCACGGCUCAAGCA	Cleavage
spe-miR171-3p	Sopen03g030760.1	3.0	-1.0	1	21	1693	1713	UGAUUGAGCCGUGCCAAUAUC	ACUGUCUGCAUGGCUCAAUCA	Cleavage
spe-miR171-4-3p	Sopen01g036680.1	1.0	-1.0	1	21	1284	1304	UUGAGCCGCGUCAAUAUCUCU	AGGGAUAUUGGCGCGGCUCAA	Cleavage
spe-miR171-4-3p	Sopen08g027270.1	1.5	-1.0	1	21	1074	1094	UUGAGCCGCGUCAAUAUCUCU	AAUGAUAUUGGCGCGGCUCAA	Cleavage
spe-miR171-4-5p	Sopen03g004550.1	2.5	-1.0	1	21	128	148	AGAUAUUGAUGCGGUUCAAUC	AAUUGGAGCGCGUCAAUGUCU	Cleavage
spe-miR171-4-5p	Sopen11g024620.1	3.0	-1.0	1	21	238	258	AGAUAUUGAUGCGGUUCAAUC	GAUGGAACUGCAGCAAUAUCU	Cleavage
spe-miR171-4-5p	Sopen01g033110.1	3.0	-1.0	1	21	2200	2220	AGAUAUUGAUGCGGUUCAAUC	UCUUGGAAUGUAUUAAUAUCU	Cleavage
spe-miR171-4-5p	Sopen04g008660.1	3.0	-1.0	1	21	2911	2931	AGAUAUUGAUGCGGUUCAAUC	AUUGGAGCCGUAUUGAUAUCU	Cleavage
spe-miR171-4-5p	Sopen01g052390.1	3.0	-1.0	1	21	177	197	AGAUAUUGAUGCGGUUCAAUC	GCUUCCACCGCAUCAAUAUCC	Cleavage
spe-miR171-5-3p	Sopen08g027270.1	0.5	-1.0	1	21	1077	1097	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-5-3p	Sopen01g036680.1	0.5	-1.0	1	21	1287	1307	UGAUUGAGCCGUGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-5-3p	Sopen02g030270.1	2.5	-1.0	1	21	585	605	UGAUUGAGCCGUGCCAAUAUC	GAUACUGGCACGCCUCAAUCA	Cleavage
spe-miR171-5-3p	Sopen08g030180.1	2.5	-1.0	1	21	3463	3483	UGAUUGAGCCGUGCCAAUAUC	UAUAUUGGCAUGGCUCUAUCG	Cleavage
spe-miR171-5-3p	Sopen01g029300.1	2.5	-1.0	1	21	595	615	UGAUUGAGCCGUGCCAAUAUC	AUUCUUGACAUGGCUCAAUCA	Cleavage
spe-miR171-5-3p	Sopen08g015500.1	3.0	-1.0	1	21	379	399	UGAUUGAGCCGUGCCAAUAUC	CUUGUGGGCACGGCUCAAGCA	Cleavage
spe-miR171-5-3p	Sopen03g030760.1	3.0	-1.0	1	21	1693	1713	UGAUUGAGCCGUGCCAAUAUC	ACUGUCUGCAUGGCUCAAUCA	Cleavage
spe-miR171-5-5p	Sopen08g027080.1	3.0	-1.0	1	21	121	141	UGUUGGAAUGGCUCAAUCAAA	UCUGAUUCAGCCAUUUCGACU	Cleavage
spe-miR171-5-5p	Sopen10g001500.1	3.0	-1.0	1	21	1072	1092	UGUUGGAAUGGCUCAAUCAAA	CGUGGUUUAGACAUUCCAACA	Translation
spe-miR171-5-5p	Sopen03g006830.1	3.0	-1.0	1	21	160	180	UGUUGGAAUGGCUCAAUCAAA	GAUGAUGAGGCCAUUCCAAUA	Cleavage
spe-miR171-5-5p	Sopen04g010630.1	3.0	-1.0	1	21	439	459	UGUUGGAAUGGCUCAAUCAAA	AAUGACAGAGCUAUUCCAGCA	Cleavage
spe-miR171-5p	Sopen10g005440.1	3.0	-1.0	1	21	3634	3654	UGGGAUGUUGGUGUGGUUCAA	ACCAGCCAUGCCAACAUCUCA	Cleavage
spe-miR171-5p	Sopen08g016830.1	2.0	-1.0	1	21	430	450	UGGGAUGUUGGUGUGGUUCAA	AAGAACCACACUGGCAUCUCA	Cleavage
spe-miR171-5p	Sopen01g032170.1	2.5	-1.0	1	21	820	840	UGGGAUGUUGGUGUGGUUCAA	CUUAACUACACCAACAUUUCA	Cleavage
spe-miR171-5p	Sopen06g031830.2	2.5	-1.0	1	21	291	311	UGGGAUGUUGGUGUGGUUCAA	CGGAAACGCAUCAACAUUCCA	Cleavage
spe-miR171-5p	Sopen06g031830.1	2.5	-1.0	1	21	291	311	UGGGAUGUUGGUGUGGUUCAA	CGGAAACGCAUCAACAUUCCA	Cleavage
spe-miR171-5p	Sopen05g001140.1	3.0	-1.0	1	21	4792	4812	UGGGAUGUUGGUGUGGUUCAA	UUGGACAACAUCAACAUUUCA	Cleavage
spe-miR171-5p	Sopen10g013210.1	3.0	-1.0	1	21	1840	1860	UGGGAUGUUGGUGUGGUUCAA	CUGAACAACACUAGCAUCCCU	Cleavage
spe-miR171-5p	Sopen06g014910.1	3.0	-1.0	1	21	1444	1464	UGGGAUGUUGGUGUGGUUCAA	ACCAGCCAUGCCAACAUCUCA	Cleavage
spe-miR171-5p	Sopen07g014320.1	3.0	-1.0	1	21	1327	1347	UGGGAUGUUGGUGUGGUUCAA	UGGAAUCACAUCGAUAUCUUA	Cleavage
spe-miR171-5p	Sopen10g005400.1	3.0	-1.0	1	21	3301	3321	UGGGAUGUUGGUGUGGUUCAA	ACCAGCCAUGCCAACAUCUCA	Cleavage

spe-miR171-5p	Sopen00g001230.1	3.0	-1.0	1	21	3236	3256	UGGGAUGUUGGUGUGGUUCAA	UCGAACCACAUCAAUGUCGCA	Cleavage
spe-miR171-5p	Sopen10g019610.1	3.0	-1.0	1	21	1000	1020	UGGGAUGUUGGUGUGGUUCAA	UGGAUUCCCACCAAUAUCCCA	Cleavage
spe-miR171-6-3p	Sopen08g027270.1	1.0	-1.0	1	21	1077	1097	UGAUUGAGCCGUGUCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-6-3p	Sopen01g036680.1	1.0	-1.0	1	21	1287	1307	UGAUUGAGCCGUGUCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171-6-3p	Sopen01g029300.1	1.5	-1.0	1	21	595	615	UGAUUGAGCCGUGUCAAUAUC	AUUCUUGACAUGGCUCAAUCA	Cleavage
spe-miR171-6-3p	Sopen11g015160.1	2.5	-1.0	1	21	4171	4191	UGAUUGAGCCGUGUCAAUAUC	AGUAUUGAUAUGGCUCAAUUU	Cleavage
spe-miR171-6-3p	Sopen02g030270.1	3.0	-1.0	1	21	585	605	UGAUUGAGCCGUGUCAAUAUC	GAUACUGGCACGCCUCAAUCA	Cleavage
spe-miR171-6-3p	Sopen08g030180.1	3.0	-1.0	1	21	3463	3483	UGAUUGAGCCGUGUCAAUAUC	UAUAUUGGCAUGGCUCUAUCG	Cleavage
spe-miR171-7-3p	Sopen11g008200.1	1.0	-1.0	1	21	381	401	GUGAGCCGAACCAAUAUCACG	AGUGAUAUUGGUUCGGCUCAA	Cleavage
spe-miR171-7-3p	Sopen11g016480.1	1.5	-1.0	1	21	328	348	GUGAGCCGAACCAAUAUCACG	GAUGAUGUUGGUUCGGUUCAU	Cleavage
spe-miR171-7-3p	Sopen07g031990.1	2.0	-1.0	1	21	283	303	GUGAGCCGAACCAAUAUCACG	UUCGAUAUUGGUUUGGCUCAU	Cleavage
spe-miR171-7-3p	Sopen08g022810.1	2.5	-1.0	1	21	1816	1836	GUGAGCCGAACCAAUAUCACG	AGUGAUGUUGGUUUGGCUCGG	Cleavage
spe-miR171-7-3p	Sopen07g028130.1	2.5	-1.0	1	21	340	360	GUGAGCCGAACCAAUAUCACG	UCUGAUAUUGGUCCGGCUCGU	Cleavage
spe-miR171-7-3p	Sopen05g004600.1	3.0	-1.0	1	21	193	213	GUGAGCCGAACCAAUAUCACG	CCUGGUAUUGGUUCUGCUUAU	Cleavage
spe-miR171-7-3p	Sopen04g036010.3	3.0	-1.0	1	21	2251	2271	GUGAGCCGAACCAAUAUCACG	GUUGAUAUUGGUCCGGAUCAC	Cleavage
spe-miR171-7-3p	Sopen04g036010.2	3.0	-1.0	1	21	2164	2184	GUGAGCCGAACCAAUAUCACG	GUUGAUAUUGGUCCGGAUCAC	Cleavage
spe-miR171-7-3p	Sopen04g036010.1	3.0	-1.0	1	21	2104	2124	GUGAGCCGAACCAAUAUCACG	GUUGAUAUUGGUCCGGAUCAC	Cleavage
spe-miR171-7-3p	Sopen12g007250.1	3.0	-1.0	1	21	520	540	GUGAGCCGAACCAAUAUCACG	GAUGAUGUUGGUUUGGAUUAC	Cleavage
spe-miR171-7-3p	Sopen05g018610.1	3.0	-1.0	1	21	1996	2016	GUGAGCCGAACCAAUAUCACG	AGUGAAUUUGGUUCGGUUCAU	Cleavage
spe-miR171-7-5p	Sopen01g051050.1	3.0	-1.0	1	22	521	542	AGUGAUAUUGGUUCGGCUCAUC	AGUUAGCAGAACUGAUAUCACU	Cleavage
spe-miR171-7-5p	Sopen01g020540.1	3.0	-1.0	1	22	1225	1246	AGUGAUAUUGGUUCGGCUCAUC	UUAGAGUUGAAUCAAAAUCACU	Cleavage
spe-miR171-7-5p	Sopen06g004100.1	3.0	-1.0	1	22	1862	1883	AGUGAUAUUGGUUCGGCUCAUC	UAACAGCAGAACCAGUGUCACU	Cleavage
spe-miR171-7-5p	Sopen02g033560.1	3.0	-1.0	1	22	2266	2287	AGUGAUAUUGGUUCGGCUCAUC	GGCGAUCCUAACCAAUAUCACA	Cleavage
spe-miR171a-3p	Sopen08g027270.1	0.5	-1.0	1	20	1078	1097	UGAUUGAGCCGUGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171a-3p	Sopen01g036680.1	0.5	-1.0	1	20	1288	1307	UGAUUGAGCCGUGCCAAUAU	AUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171a-3p	Sopen08g030180.1	2.5	-1.0	1	20	3464	3483	UGAUUGAGCCGUGCCAAUAU	AUAUUGGCAUGGCUCUAUCG	Cleavage
spe-miR171a-3p	Sopen02g030270.1	2.5	-1.0	1	20	586	605	UGAUUGAGCCGUGCCAAUAU	AUACUGGCACGCCUCAAUCA	Cleavage
spe-miR171a-3p	Sopen01g029300.1	2.5	-1.0	1	20	596	615	UGAUUGAGCCGUGCCAAUAU	UUCUUGACAUGGCUCAAUCA	Cleavage
spe-miR171a-3p	Sopen08g015500.1	3.0	-1.0	1	20	380	399	UGAUUGAGCCGUGCCAAUAU	UUGUGGGCACGGCUCAAGCA	Cleavage
spe-miR171a-3p	Sopen03g030760.1	3.0	-1.0	1	20	1694	1713	UGAUUGAGCCGUGCCAAUAU	CUGUCUGCAUGGCUCAAUCA	Cleavage
spe-miR171e-1-3p	Sopen01g036680.1	1.0	-1.0	1	21	1287	1307	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171e-1-3p	Sopen08g027270.1	1.0	-1.0	1	21	1077	1097	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171e-1-3p	Sopen05g023420.1	2.0	-1.0	1	21	34	54	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGUGGCUAAAUCU	Cleavage
spe-miR171e-1-3p	Sopen07g034070.1	3.0	-1.0	1	21	2398	2418	AGAUUGAGCCGCGCCAAUAUC	GAUCUUGGCGCAGCUCGAUCU	Translation
spe-miR171e-1-5p	Sopen01g001730.1	3.0	-1.0	1	21	923	943	CGAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUCACCAACAUAG	Cleavage
spe-miR171e-1-5p	Sopen01g001870.1	2.0	-1.0	1	21	902	922	CGAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUCACCAACAUUG	Cleavage
spe-miR171e-1-5p	Sopen09g031140.1	2.5	-1.0	1	21	230	250	CGAUGUUGGUGAGGUUCAAUC	UAUUGGACCUCACCGAUGUUG	Cleavage
spe-miR171e-1-5p	Sopen04g003050.2	2.5	-1.0	1	21	773	793	CGAUGUUGGUGAGGUUCAAUC	ACUUGAACUUCACUAACAUUC	Cleavage
spe-miR171e-1-5p	Sopen04g003050.1	2.5	-1.0	1	21	698	718	CGAUGUUGGUGAGGUUCAAUC	ACUUGAACUUCACUAACAUUC	Cleavage
spe-miR171e-1-5p	Sopen06g019300.1	2.5	-1.0	1	21	59	79	CGAUGUUGGUGAGGUUCAAUC	UUUUGAAUCUUAUCAACAUCU	Cleavage
spe-miR171e-1-5p	Sopen07g002070.1	2.5	-1.0	1	21	646	666	CGAUGUUGGUGAGGUUCAAUC	CCUUUAAUUUCACCAGCAUCG	Cleavage
spe-miR171e-1-5p	Sopen02g026610.1	2.5	-1.0	1	21	179	199	CGAUGUUGGUGAGGUUCAAUC	AUUUGGAACUCAUCAAUAUCG	Cleavage
spe-miR171e-1-5p	Sopen03g007730.1	3.0	-1.0	1	21	130	150	CGAUGUUGGUGAGGUUCAAUC	GAUUCAUCUUCACCGACAUCG	Cleavage
spe-miR171e-1-5p	Sopen08g020590.1	3.0	-1.0	1	21	406	426	CGAUGUUGGUGAGGUUCAAUC	AAUUCAACUUCAUCAACAUCA	Cleavage
spe-miR171e-1-5p	Sopen10g005400.1	3.0	-1.0	1	21	3699	3719	CGAUGUUGGUGAGGUUCAAUC	CAUUGAAGCUCACCAAAAUUG	Cleavage
spe-miR171e-1-5p	Sopen01g044650.1	3.0	-1.0	1	21	209	229	CGAUGUUGGUGAGGUUCAAUC	AGUUGAAUCUCAUUGAUAUUG	Cleavage
spe-miR171e-1-5p	Sopen10g006220.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen10g012180.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen10g023760.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen05g015480.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation

spe-miR171e-1-5p	Sopen10g017430.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen06g024970.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen09g031250.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen07g025420.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g036790.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen01g028400.1	3.0	-1.0	1	21	3896	3916	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g010750.1	3.0	-1.0	1	21	3728	3748	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g013160.1	3.0	-1.0	1	21	3611	3631	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen07g007680.1	3.0	-1.0	1	21	3260	3280	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g005190.1	3.0	-1.0	1	21	3158	3178	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g023570.1	3.0	-1.0	1	21	2783	2803	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen07g015600.1	3.0	-1.0	1	21	2720	2740	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen08g021040.2	3.0	-1.0	1	21	2489	2509	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen08g020140.1	3.0	-1.0	1	21	2333	2353	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen04g013370.1	3.0	-1.0	1	21	2240	2260	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g009870.1	3.0	-1.0	1	21	2174	2194	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen03g023570.2	3.0	-1.0	1	21	1928	1948	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen10g013190.1	3.0	-1.0	1	21	1139	1159	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen05g027270.1	3.0	-1.0	1	21	863	883	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen06g027280.1	3.0	-1.0	1	21	860	880	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen01g012130.1	3.0	-1.0	1	21	740	760	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen08g021040.1	3.0	-1.0	1	21	578	598	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-1-5p	Sopen12g029320.1	3.0	-1.0	1	21	283	303	CGAUGUUGGUGAGGUUCAAUC	GUUGGAGUCUUACCAGCAUCG	Cleavage
spe-miR171e-1-5p	Sopen12g029320.2	3.0	-1.0	1	21	283	303	CGAUGUUGGUGAGGUUCAAUC	GUUGGAGUCUUACCAGCAUCG	Cleavage
spe-miR171e-2-3p	Sopen01g036680.1	1.0	-1.0	1	21	1287	1307	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171e-2-3p	Sopen08g027270.1	1.0	-1.0	1	21	1077	1097	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGCGGCUCAAUCA	Cleavage
spe-miR171e-2-3p	Sopen05g023420.1	2.0	-1.0	1	21	34	54	AGAUUGAGCCGCGCCAAUAUC	GAUAUUGGCGUGGCUAAAUCU	Cleavage
spe-miR171e-2-3p	Sopen07g034070.1	3.0	-1.0	1	21	2398	2418	AGAUUGAGCCGCGCCAAUAUC	GAUCUUGGCGCAGCUCGAUCU	Translation
spe-miR171e-2-5p	Sopen01g001730.1	3.0	-1.0	1	21	923	943	CGAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUCACCAACAUAG	Cleavage
spe-miR171e-2-5p	Sopen01g001870.1	2.0	-1.0	1	21	902	922	CGAUGUUGGUGAGGUUCAAUC	UAUGGAAUCUCACCAACAUUG	Cleavage
spe-miR171e-2-5p	Sopen09g031140.1	2.5	-1.0	1	21	230	250	CGAUGUUGGUGAGGUUCAAUC	UAUUGGACCUCACCGAUGUUG	Cleavage
spe-miR171e-2-5p	Sopen04g003050.2	2.5	-1.0	1	21	773	793	CGAUGUUGGUGAGGUUCAAUC	ACUUGAACUUCACUAACAUUC	Cleavage
spe-miR171e-2-5p	Sopen04g003050.1	2.5	-1.0	1	21	698	718	CGAUGUUGGUGAGGUUCAAUC	ACUUGAACUUCACUAACAUUC	Cleavage
spe-miR171e-2-5p	Sopen06g019300.1	2.5	-1.0	1	21	59	79	CGAUGUUGGUGAGGUUCAAUC	UUUUGAAUCUUAUCAACAUCU	Cleavage
spe-miR171e-2-5p	Sopen07g002070.1	2.5	-1.0	1	21	646	666	CGAUGUUGGUGAGGUUCAAUC	CCUUUAAUUUCACCAGCAUCG	Cleavage
spe-miR171e-2-5p	Sopen02g026610.1	2.5	-1.0	1	21	179	199	CGAUGUUGGUGAGGUUCAAUC	AUUUGGAACUCAUCAAUAUCG	Cleavage
spe-miR171e-2-5p	Sopen03g007730.1	3.0	-1.0	1	21	130	150	CGAUGUUGGUGAGGUUCAAUC	GAUUCAUCUUCACCGACAUCG	Cleavage
spe-miR171e-2-5p	Sopen08g020590.1	3.0	-1.0	1	21	406	426	CGAUGUUGGUGAGGUUCAAUC	AAUUCAACUUCAUCAACAUCA	Cleavage
spe-miR171e-2-5p	Sopen10g005400.1	3.0	-1.0	1	21	3699	3719	CGAUGUUGGUGAGGUUCAAUC	CAUUGAAGCUCACCAAAAUUG	Cleavage
spe-miR171e-2-5p	Sopen01g044650.1	3.0	-1.0	1	21	209	229	CGAUGUUGGUGAGGUUCAAUC	AGUUGAAUCUCAUUGAUAUUG	Cleavage
spe-miR171e-2-5p	Sopen10g006220.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen10g012180.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen10g023760.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen05g015480.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen10g017430.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen06g024970.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen09g031250.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen07g025420.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen03g036790.1	3.0	-1.0	1	21	3986	4006	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen01g028400.1	3.0	-1.0	1	21	3896	3916	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation

spe-miR171e-2-5p	Sopen03g010750.1	3.0	-1.0	1	21	3728	3748	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen03g013160.1	3.0	-1.0	1	21	3611	3631	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen07g007680.1	3.0	-1.0	1	21	3260	3280	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen03g005190.1	3.0	-1.0	1	21	3158	3178	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen03g023570.1	3.0	-1.0	1	21	2783	2803	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen07g015600.1	3.0	-1.0	1	21	2720	2740	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen08g021040.2	3.0	-1.0	1	21	2489	2509	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen08g020140.1	3.0	-1.0	1	21	2333	2353	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen04g013370.1	3.0	-1.0	1	21	2240	2260	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen03g009870.1	3.0	-1.0	1	21	2174	2194	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen03g023570.2	3.0	-1.0	1	21	1928	1948	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen10g013190.1	3.0	-1.0	1	21	1139	1159	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen05g027270.1	3.0	-1.0	1	21	863	883	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen06g027280.1	3.0	-1.0	1	21	860	880	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen01g012130.1	3.0	-1.0	1	21	740	760	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen08g021040.1	3.0	-1.0	1	21	578	598	CGAUGUUGGUGAGGUUCAAUC	GUUUGAACUUGAUCAACAUUG	Translation
spe-miR171e-2-5p	Sopen12g029320.1	3.0	-1.0	1	21	283	303	CGAUGUUGGUGAGGUUCAAUC	GUUGGAGUCUUACCAGCAUCG	Cleavage
spe-miR171e-2-5p	Sopen12g029320.2	3.0	-1.0	1	21	283	303	CGAUGUUGGUGAGGUUCAAUC	GUUGGAGUCUUACCAGCAUCG	Cleavage
spe-miR172-1-3p	Sopen11g030250.1	0.5	-1.0	1	21	1331	1351	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-1-3p	Sopen11g030250.2	0.5	-1.0	1	21	1286	1306	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-1-3p	Sopen04g020090.1	0.5	-1.0	1	21	1103	1123	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-1-3p	Sopen06g031890.1	0.5	-1.0	1	21	1298	1318	AGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-1-3p	Sopen06g031890.2	0.5	-1.0	1	21	1253	1273	AGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-1-3p	Sopen02g037720.1	1.5	-1.0	1	21	1439	1459	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-1-3p	Sopen02g015090.1	1.5	-1.0	1	21	1430	1450	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-1-3p	Sopen03g008400.3	1.5	-1.0	1	21	1343	1363	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-1-3p	Sopen09g002150.1	1.5	-1.0	1	21	1277	1297	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-1-3p	Sopen03g008400.2	1.5	-1.0	1	21	1331	1351	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-1-3p	Sopen09g002130.1	1.5	-1.0	1	21	1274	1294	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-1-3p	Sopen10g033790.1	1.5	-1.0	1	21	1241	1261	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-1-3p	Sopen09g002130.2	1.5	-1.0	1	21	1229	1249	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-1-3p	Sopen03g008400.1	1.5	-1.0	1	21	1127	1147	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-1-3p	Sopen10g002630.2	2.5	-1.0	1	21	1864	1884	AGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-1-3p	Sopen07g031900.1	2.5	-1.0	1	21	1816	1836	AGAAUCUUGAUGAUGCUGCAU	AUGUAUCUUCAUCAAGAUUCU	Cleavage
spe-miR172-1-3p	Sopen10g002630.3	2.5	-1.0	1	21	1258	1278	AGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-1-3p	Sopen11g006420.1	3.0	-1.0	1	21	1126	1145	AGAAUCUUGAUGAUGCUGCAU	AUGCAGC-UUAUCAAGAUUUU	Cleavage
spe-miR172-1-3p	Sopen04g020260.1	3.0	-1.0	1	21	256	275	AGAAUCUUGAUGAUGCUGCAU	AUGCAGC-UUAUCAAGGUUCU	Cleavage
spe-miR172-1-3p	Sopen06g034240.1	3.0	-1.0	1	21	1403	1422	AGAAUCUUGAUGAUGCUGCAU	GUGCAGC-UCGUCAAGAUUUU	Cleavage
spe-miR172-1-3p	Sopen01g027180.1	3.0	-1.0	1	21	93	113	AGAAUCUUGAUGAUGCUGCAU	GGUGAGGAUCAUCAAGAUUCU	Cleavage
spe-miR172-1-3p	Sopen09g028620.2	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172-1-3p	Sopen01g018650.1	3.0	-1.0	1	21	807	827	AGAAUCUUGAUGAUGCUGCAU	AAGCAACAUCAUCAAGGUGCU	Cleavage
spe-miR172-1-3p	Sopen01g048830.1	3.0	-1.0	1	21	379	399	AGAAUCUUGAUGAUGCUGCAU	GAUCAUUGUCAUCAAGAUUCU	Cleavage
spe-miR172-1-3p	Sopen01g005710.1	3.0	-1.0	1	21	820	840	AGAAUCUUGAUGAUGCUGCAU	AGGCAGAAUCAUCAAGGUACU	Cleavage
spe-miR172-1-3p	Sopen09g028620.4	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172-1-3p	Sopen09g028620.3	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172-1-3p	Sopen01g040000.1	3.0	-1.0	1	21	106	126	AGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCU	Cleavage
spe-miR172-1-3p	Sopen08g014470.1	3.0	-1.0	1	21	2104	2124	AGAAUCUUGAUGAUGCUGCAU	AGGAGGCUUCAUCAGGAUUCU	Cleavage
spe-miR172-1-5p	Sopen09g029230.1	3.0	-1.0	1	21	783	803	GUAGCAUCAUCAAGAUUCAUA	GAUGAAUCUUGGUGAUGAUGU	Cleavage
spe-miR172-1-5p	Sopen10g032510.1	1.0	-1.0	1	21	1923	1943	GUAGCAUCAUCAAGAUUCAUA	AGUGAGUCUUGAUGAUGCUAU	Cleavage
spe-miR172-1-5p	Sopen07g019560.1	2.0	-1.0	1	21	771	791	GUAGCAUCAUCAAGAUUCAUA	AAUGAAUUUUGAUGAUGUUGU	Cleavage

spe-miR172-1-5p	Sopen10g017470.1	2.5	-1.0	1	21	876	896	GUAGCAUCAUCAAGAUUCAUA	UGUGAGUCUUGAUCAUGCUAU	Cleavage
spe-miR172-1-5p	Sopen00g003020.1	2.5	-1.0	1	20	1	20	GUAGCAUCAUCAAGAUUCAU	AUGAAUUUUGAUGAAGCUAU	Cleavage
spe-miR172-1-5p	Sopen07g022010.1	2.5	-1.0	1	21	2868	2888	GUAGCAUCAUCAAGAUUCAUA	UGUGAAAUUUGGUGAUGCUAU	Cleavage
spe-miR172-1-5p	Sopen12g030540.1	2.5	-1.0	1	21	375	395	GUAGCAUCAUCAAGAUUCAUA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
spe-miR172-1-5p	Sopen12g001960.2	2.5	-1.0	1	21	375	395	GUAGCAUCAUCAAGAUUCAUA	UUUGGCUUUUGAUGAUGCUAU	Cleavage
spe-miR172-1-5p	Sopen12g001960.1	2.5	-1.0	1	21	309	329	GUAGCAUCAUCAAGAUUCAUA	UUUGGCUUUUGAUGAUGCUAU	Cleavage
spe-miR172-1-5p	Sopen02g022280.1	3.0	-1.0	1	21	228	248	GUAGCAUCAUCAAGAUUCAUA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
spe-miR172-1-5p	Sopen11g011480.1	3.0	-1.0	1	21	582	602	GUAGCAUCAUCAAGAUUCAUA	UAUGUAUCUUGGUAAUGCUAC	Cleavage
spe-miR172-1-5p	Sopen08g026540.1	3.0	-1.0	1	21	375	395	GUAGCAUCAUCAAGAUUCAUA	AAUGAAUUUUGAUGAUUUUAU	Cleavage
spe-miR172-1-5p	Sopen08g019040.1	3.0	-1.0	1	21	273	293	GUAGCAUCAUCAAGAUUCAUA	CAUGAGUCUUGAUGAUCCUGU	Cleavage
spe-miR172-1-5p	Sopen11g030420.1	3.0	-1.0	1	21	324	344	GUAGCAUCAUCAAGAUUCAUA	AAUGAGUCUUGGUGGUGAUAC	Cleavage
spe-miR172-1-5p	Sopen05g014030.1	3.0	-1.0	1	21	597	617	GUAGCAUCAUCAAGAUUCAUA	AAUGAAUUUUGAUGAAGCUGU	Cleavage
spe-miR172-1-5p	Sopen10g023950.1	3.0	-1.0	1	21	225	245	GUAGCAUCAUCAAGAUUCAUA	AAUGAAUUUUGAUGAAGCUGU	Cleavage
spe-miR172-1-5p	Sopen04g006670.1	3.0	-1.0	1	21	3738	3758	GUAGCAUCAUCAAGAUUCAUA	UGUGAAAUUUGGUGAUGCUGU	Cleavage
spe-miR172-1-5p	Sopen00g013390.1	3.0	-1.0	1	21	1416	1436	GUAGCAUCAUCAAGAUUCAUA	UGUGAAAUUUGGUGAUGCUGU	Cleavage
spe-miR172-1-5p	Sopen06g021350.1	3.0	-1.0	1	21	738	758	GUAGCAUCAUCAAGAUUCAUA	UAUUGAACUUGAUGAUGUUAC	Cleavage
spe-miR172-1-5p	Sopen08g002930.1	3.0	-1.0	1	21	735	755	GUAGCAUCAUCAAGAUUCAUA	UAUUGAGCUUGAUGAUGUUAC	Cleavage
spe-miR172-1-5p	Sopen06g021350.2	3.0	-1.0	1	21	735	755	GUAGCAUCAUCAAGAUUCAUA	UAUUGAACUUGAUGAUGUUAC	Cleavage
spe-miR172-1-5p	Sopen02g018230.2	3.0	-1.0	1	21	1050	1070	GUAGCAUCAUCAAGAUUCAUA	UGUGGAACUUGGUGAUGCUGU	Cleavage
spe-miR172-1-5p	Sopen01g051050.1	3.0	-1.0	1	21	777	797	GUAGCAUCAUCAAGAUUCAUA	UGUAAAUCUUGGUGACGCUAC	Cleavage
spe-miR172-1-5p	Sopen02g018230.1	3.0	-1.0	1	21	294	314	GUAGCAUCAUCAAGAUUCAUA	UGUGGAACUUGGUGAUGCUGU	Cleavage
spe-miR172-1-5p	Sopen07g017110.1	3.0	-1.0	1	21	111	131	GUAGCAUCAUCAAGAUUCAUA	CAAGAAUCUUGAUGGUGUUAG	Cleavage
spe-miR172-1-5p	Sopen02g034360.1	3.0	-1.0	1	21	180	200	GUAGCAUCAUCAAGAUUCAUA	AAUCAAUUUUGAUGAUGUUAA	Cleavage
spe-miR172-1-5p	Sopen02g023500.1	3.0	-1.0	1	21	500	520	GUAGCAUCAUCAAGAUUCAUA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
spe-miR172-1-5p	Sopen09g005740.1	3.0	-1.0	1	21	819	839	GUAGCAUCAUCAAGAUUCAUA	GGGGAAUUUUGAUGAUGCUGA	Cleavage
spe-miR172-1-5p	Sopen06g004300.1	3.0	-1.0	1	21	471	491	GUAGCAUCAUCAAGAUUCAUA	GGUGAAUCUUGCUGAUUCUAC	Translation
spe-miR172-1-5p	Sopen01g025210.1	3.0	-1.0	1	21	849	869	GUAGCAUCAUCAAGAUUCAUA	UGGGAGGCUUGAUGAUGCUAU	Cleavage
spe-miR172-2-3p	Sopen09g002150.1	2.0	-1.0	1	21	1277	1297	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-2-3p	Sopen09g002130.1	2.0	-1.0	1	21	1274	1294	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-2-3p	Sopen10g033790.1	2.0	-1.0	1	21	1241	1261	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-2-3p	Sopen09g002130.2	2.0	-1.0	1	21	1229	1249	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-2-3p	Sopen09g022750.1	2.0	-1.0	1	21	177	197	UGAAUCUUGAUGAUGCUACAU	CAUUAGUAUUAUCAAGAUUCA	Cleavage
spe-miR172-2-3p	Sopen03g030690.1	2.0	-1.0	1	21	2798	2818	UGAAUCUUGAUGAUGCUACAU	CAGUAGUGUUAUCAAGAUUUA	Cleavage
spe-miR172-2-3p	Sopen03g002770.1	2.0	-1.0	1	21	1957	1977	UGAAUCUUGAUGAUGCUACAU	CUGUAUCUUCAUCAAGAUUCA	Cleavage
spe-miR172-2-3p	Sopen11g011780.1	2.0	-1.0	1	21	314	334	UGAAUCUUGAUGAUGCUACAU	CAGUAGCUUCAUUAAGGUUCA	Cleavage
spe-miR172-2-3p	Sopen02g037720.1	2.5	-1.0	1	21	1439	1459	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-2-3p	Sopen02g015090.1	2.5	-1.0	1	21	1430	1450	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-2-3p	Sopen11g030250.1	2.5	-1.0	1	21	1331	1351	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-2-3p	Sopen11g030250.2	2.5	-1.0	1	21	1286	1306	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-2-3p	Sopen03g008400.3	2.5	-1.0	1	21	1343	1363	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-2-3p	Sopen03g008400.2	2.5	-1.0	1	21	1331	1351	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-2-3p	Sopen03g008400.1	2.5	-1.0	1	21	1127	1147	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-2-3p	Sopen04g020090.1	2.5	-1.0	1	21	1103	1123	UGAAUCUUGAUGAUGCUACAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-2-3p	Sopen04g021710.1	2.5	-1.0	1	21	1840	1860	UGAAUCUUGAUGAUGCUACAU	CAGUGGCAUCAUCGACAUUCA	Cleavage
spe-miR172-2-3p	Sopen06g031890.1	2.5	-1.0	1	21	1298	1318	UGAAUCUUGAUGAUGCUACAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-2-3p	Sopen06g031890.2	2.5	-1.0	1	21	1253	1273	UGAAUCUUGAUGAUGCUACAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-2-3p	Sopen10g002630.2	3.0	-1.0	1	21	1864	1884	UGAAUCUUGAUGAUGCUACAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-2-3p	Sopen07g031900.1	3.0	-1.0	1	21	1816	1836	UGAAUCUUGAUGAUGCUACAU	AUGUAUCUUCAUCAAGAUUCU	Cleavage
spe-miR172-2-3p	Sopen10g002630.3	3.0	-1.0	1	21	1258	1278	UGAAUCUUGAUGAUGCUACAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-2-3p	Sopen07g020390.1	3.0	-1.0	1	21	2270	2290	UGAAUCUUGAUGAUGCUACAU	UUGGAGUAUCAUCAAGAUCCA	Cleavage

spe-miR172-2-3p	Sopen09g012590.1	3.0	-1.0	1	21	237	257	UGAAUCUUGAUGAUGCUACAU	AAGUAGCAUAGUCAAGAUUUG	Cleavage
spe-miR172-2-3p	Sopen02g023270.1	3.0	-1.0	1	21	383	403	UGAAUCUUGAUGAUGCUACAU	UGUUAGCAUCAUCAAGAGUUA	Cleavage
spe-miR172-2-3p	Sopen03g040970.1	3.0	-1.0	1	21	548	568	UGAAUCUUGAUGAUGCUACAU	CUGUUUCGUUAUCAAGAUUCA	Cleavage
spe-miR172-2-3p	Sopen02g024410.1	3.0	-1.0	1	21	1945	1965	UGAAUCUUGAUGAUGCUACAU	CUAUACCUUCAUCAAGAUUCA	Cleavage
spe-miR172-2-5p	Sopen04g005270.1	2.5	-1.0	1	21	399	419	GCAGCAUCAUCAAGAUUCUCA	GGAGGGUCUUGGUGAUGUUGU	Cleavage
spe-miR172-2-5p	Sopen11g025370.1	3.0	-1.0	1	21	1251	1271	GCAGCAUCAUCAAGAUUCUCA	UGAUGAGCUUGAUGAUGUUGC	Cleavage
spe-miR172-2-5p	Sopen02g022280.1	1.5	-1.0	1	21	228	248	GCAGCAUCAUCAAGAUUCUCA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
spe-miR172-2-5p	Sopen02g023500.1	1.5	-1.0	1	21	500	520	GCAGCAUCAUCAAGAUUCUCA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
spe-miR172-2-5p	Sopen09g003390.1	2.0	-1.0	1	21	450	470	GCAGCAUCAUCAAGAUUCUCA	UGAGAAUCUCGAUGAUGUUGC	Cleavage
spe-miR172-2-5p	Sopen09g023370.1	2.0	-1.0	1	21	4383	4403	GCAGCAUCAUCAAGAUUCUCA	UGAGAGUGUUGAUGAUGUUGC	Cleavage
spe-miR172-2-5p	Sopen09g005740.1	2.0	-1.0	1	21	819	839	GCAGCAUCAUCAAGAUUCUCA	GGGGAAUUUUGAUGAUGCUGA	Cleavage
spe-miR172-2-5p	Sopen08g006720.1	2.0	-1.0	1	21	162	182	GCAGCAUCAUCAAGAUUCUCA	GGAGAAUCUUGGUGAUGGUGC	Cleavage
spe-miR172-2-5p	Sopen07g019560.1	2.5	-1.0	1	21	771	791	GCAGCAUCAUCAAGAUUCUCA	AAUGAAUUUUGAUGAUGUUGU	Cleavage
spe-miR172-2-5p	Sopen09g015100.1	3.0	-1.0	1	21	663	683	GCAGCAUCAUCAAGAUUCUCA	UGAGAUUCUUGAUGCUGUUGC	Cleavage
spe-miR172-2-5p	Sopen07g010610.1	3.0	-1.0	1	21	597	617	GCAGCAUCAUCAAGAUUCUCA	UGAGAUUCUUGAUGCUGUUGC	Cleavage
spe-miR172-2-5p	Sopen10g010360.1	3.0	-1.0	1	21	690	710	GCAGCAUCAUCAAGAUUCUCA	UGAGAACCCUGGUGAUGCUGC	Cleavage
spe-miR172-2-5p	Sopen10g002480.1	3.0	-1.0	1	21	555	575	GCAGCAUCAUCAAGAUUCUCA	UGAGAAGCUUGAAGAUGCUGU	Cleavage
spe-miR172-2-5p	Sopen03g014410.1	3.0	-1.0	1	21	6783	6803	GCAGCAUCAUCAAGAUUCUCA	AAGGAAUCUUGAUGAUGCUCU	Cleavage
spe-miR172-2-5p	Sopen01g002960.1	3.0	-1.0	1	21	1008	1028	GCAGCAUCAUCAAGAUUCUCA	AGAGAGUCUUGGUGAUACUGU	Cleavage
spe-miR172-2-5p	Sopen07g022890.1	3.0	-1.0	1	21	192	212	GCAGCAUCAUCAAGAUUCUCA	GGAGAAUCUCGAUGAAGCUGC	Cleavage
spe-miR172-2-5p	Sopen10g031740.3	3.0	-1.0	1	21	303	323	GCAGCAUCAUCAAGAUUCUCA	GGAGAGUUUAGAUGGUGCUGC	Cleavage
spe-miR172-2-5p	Sopen10g031740.1	3.0	-1.0	1	21	303	323	GCAGCAUCAUCAAGAUUCUCA	GGAGAGUUUAGAUGGUGCUGC	Cleavage
spe-miR172-2-5p	Sopen10g031740.2	3.0	-1.0	1	21	282	302	GCAGCAUCAUCAAGAUUCUCA	GGAGAGUUUAGAUGGUGCUGC	Cleavage
spe-miR172-2-5p	Sopen06g013970.1	3.0	-1.0	1	21	2625	2645	GCAGCAUCAUCAAGAUUCUCA	GGAGAAUAUUGGUAAUGCUGC	Cleavage
spe-miR172-2-5p	Sopen12g030540.1	3.0	-1.0	1	21	375	395	GCAGCAUCAUCAAGAUUCUCA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
spe-miR172-2-5p	Sopen02g035770.2	3.0	-1.0	1	21	2709	2729	GCAGCAUCAUCAAGAUUCUCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-2-5p	Sopen02g035770.1	3.0	-1.0	1	21	2709	2729	GCAGCAUCAUCAAGAUUCUCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-2-5p	Sopen02g003380.2	3.0	-1.0	1	21	2661	2681	GCAGCAUCAUCAAGAUUCUCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-2-5p	Sopen02g003380.1	3.0	-1.0	1	21	2595	2615	GCAGCAUCAUCAAGAUUCUCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-2-5p	Sopen07g029380.1	3.0	-1.0	1	21	1041	1061	GCAGCAUCAUCAAGAUUCUCA	AGAGGACCUUGAUGAGGCUGC	Cleavage
spe-miR172-2-5p	Sopen05g020750.1	3.0	-1.0	1	21	567	587	GCAGCAUCAUCAAGAUUCUCA	AGAGAACCUUGAUGAGGCUGU	Cleavage
spe-miR172-2-5p	Sopen11g004870.1	3.0	-1.0	1	21	321	341	GCAGCAUCAUCAAGAUUCUCA	AGAGAAGCUUGGUGAGGCUGC	Cleavage
spe-miR172-2-5p	Sopen05g027750.1	3.0	-1.0	1	21	441	461	GCAGCAUCAUCAAGAUUCUCA	AGGUAAUCUUGUUGAUGCUGC	Translation
spe-miR172-2-5p	Sopen02g010480.1	3.0	-1.0	1	21	168	188	GCAGCAUCAUCAAGAUUCUCA	UAAGAAUUUUGAUAAUGUUGU	Cleavage
spe-miR172-3-3p	Sopen02g037720.1	0.5	-1.0	1	21	1439	1459	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-3-3p	Sopen02g015090.1	0.5	-1.0	1	21	1430	1450	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-3-3p	Sopen03g008400.3	0.5	-1.0	1	21	1343	1363	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-3-3p	Sopen03g008400.2	0.5	-1.0	1	21	1331	1351	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-3-3p	Sopen03g008400.1	0.5	-1.0	1	21	1127	1147	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-3-3p	Sopen11g030250.1	1.0	-1.0	1	21	1331	1351	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-3-3p	Sopen11g030250.2	1.0	-1.0	1	21	1286	1306	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-3-3p	Sopen04g020090.1	1.0	-1.0	1	21	1103	1123	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-3-3p	Sopen06g031890.1	1.0	-1.0	1	21	1298	1318	GGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-3-3p	Sopen06g031890.2	1.0	-1.0	1	21	1253	1273	GGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-3-3p	Sopen09g002150.1	1.5	-1.0	1	21	1277	1297	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-3-3p	Sopen09g002130.1	1.5	-1.0	1	21	1274	1294	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-3-3p	Sopen10g033790.1	1.5	-1.0	1	21	1241	1261	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-3-3p	Sopen09g002130.2	1.5	-1.0	1	21	1229	1249	GGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-3-3p	Sopen02g034050.1	2.5	-1.0	1	21	7640	7660	GGAAUCUUGAUGAUGCUGCAU	UGGCUAUAUCAUCAAGAUUCC	Cleavage
spe-miR172-3-3p	Sopen10g002630.2	3.0	-1.0	1	21	1864	1884	GGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage

spe-miR172-3-3p	Sopen07g031900.1	3.0	-1.0	1	21	1816	1836	GGAAUCUUGAUGAUGCUGCAU	AUGUAUCUUCAUCAAGAUUCU	Cleavage
spe-miR172-3-3p	Sopen10g002630.3	3.0	-1.0	1	21	1258	1278	GGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-3-3p	Sopen01g037690.1	3.0	-1.0	1	21	445	465	GGAAUCUUGAUGAUGCUGCAU	CCUCAGCAUUAUCAACAUUCC	Cleavage
spe-miR172-3-3p	Sopen10g019280.1	3.0	-1.0	1	21	179	199	GGAAUCUUGAUGAUGCUGCAU	GAUCAGCAUCAUCAAGGGUCC	Cleavage
spe-miR172-3-3p	Sopen12g005650.1	3.0	-1.0	1	21	26	46	GGAAUCUUGAUGAUGCUGCAU	GUGAAGCUUUAUCAAGAUUUC	Cleavage
spe-miR172-3-3p	Sopen04g019810.1	3.0	-1.0	1	21	1199	1219	GGAAUCUUGAUGAUGCUGCAU	AAGUAACAUCAUCAAGAUUAC	Cleavage
spe-miR172-3-5p	Sopen07g019560.1	1.0	-1.0	1	21	771	791	GCAACAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAUGUUGU	Cleavage
spe-miR172-3-5p	Sopen02g022280.1	2.0	-1.0	1	21	228	248	GCAACAUCAUCAAGAUUCACA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen09g029770.2	2.0	-1.0	1	21	1086	1106	GCAACAUCAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGU	Cleavage
spe-miR172-3-5p	Sopen09g029770.1	2.0	-1.0	1	21	1035	1055	GCAACAUCAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGU	Cleavage
spe-miR172-3-5p	Sopen09g003390.1	2.5	-1.0	1	21	450	470	GCAACAUCAUCAAGAUUCACA	UGAGAAUCUCGAUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen04g004840.1	2.5	-1.0	1	21	519	539	GCAACAUCAUCAAGAUUCACA	AGUGGAUUUUGAUGGUGUUGA	Cleavage
spe-miR172-3-5p	Sopen09g023370.1	2.5	-1.0	1	21	4383	4403	GCAACAUCAUCAAGAUUCACA	UGAGAGUGUUGAUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen07g026900.1	2.5	-1.0	1	21	681	701	GCAACAUCAUCAAGAUUCACA	UGUGACAUUUGAUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen04g012630.1	2.5	-1.0	1	21	4524	4544	GCAACAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-3-5p	Sopen04g008870.1	2.5	-1.0	1	21	312	332	GCAACAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-3-5p	Sopen09g029230.1	2.5	-1.0	1	21	783	803	GCAACAUCAUCAAGAUUCACA	GAUGAAUCUUGGUGAUGAUGU	Cleavage
spe-miR172-3-5p	Sopen08g008020.1	2.5	-1.0	1	21	360	380	GCAACAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-3-5p	Sopen11g014800.1	2.5	-1.0	1	21	153	173	GCAACAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-3-5p	Sopen02g014570.1	2.5	-1.0	1	21	204	224	GCAACAUCAUCAAGAUUCACA	UCUGCAUCUUUAUGAUGUUGC	Translation
spe-miR172-3-5p	Sopen02g014570.2	2.5	-1.0	1	21	135	155	GCAACAUCAUCAAGAUUCACA	UCUGCAUCUUUAUGAUGUUGC	Translation
spe-miR172-3-5p	Sopen06g006330.1	3.0	-1.0	1	21	21	41	GCAACAUCAUCAAGAUUCACA	AGUGAGUCUUAGUGAUGUUGU	Translation
spe-miR172-3-5p	Sopen04g005270.1	3.0	-1.0	1	21	399	419	GCAACAUCAUCAAGAUUCACA	GGAGGGUCUUGGUGAUGUUGU	Cleavage
spe-miR172-3-5p	Sopen03g019160.1	3.0	-1.0	1	21	441	461	GCAACAUCAUCAAGAUUCACA	AGUGAUUCUUGCUGAUGUUGU	Translation
spe-miR172-3-5p	Sopen02g035770.2	3.0	-1.0	1	21	2709	2729	GCAACAUCAUCAAGAUUCACA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen02g035770.1	3.0	-1.0	1	21	2709	2729	GCAACAUCAUCAAGAUUCACA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen04g027220.1	3.0	-1.0	1	21	858	878	GCAACAUCAUCAAGAUUCACA	AGUGAAUGUUGAAGAUGUUGU	Cleavage
spe-miR172-3-5p	Sopen04g035870.1	3.0	-1.0	1	21	750	770	GCAACAUCAUCAAGAUUCACA	AGUGACUUUUGCUGAUGUUGC	Translation
spe-miR172-3-5p	Sopen08g006720.1	3.0	-1.0	1	21	162	182	GCAACAUCAUCAAGAUUCACA	GGAGAAUCUUGGUGAUGGUGC	Cleavage
spe-miR172-3-5p	Sopen04g006250.1	3.0	-1.0	1	21	957	977	GCAACAUCAUCAAGAUUCACA	UAUGGAUCUUGAUGAUUUUGA	Cleavage
spe-miR172-3-5p	Sopen01g023190.1	3.0	-1.0	1	21	675	695	GCAACAUCAUCAAGAUUCACA	UGUAACUGUUGAUGAUGUUGC	Cleavage
spe-miR172-3-5p	Sopen06g035910.1	3.0	-1.0	1	21	1065	1085	GCAACAUCAUCAAGAUUCACA	GUUGAAUCUUGAUAAUGGUGC	Cleavage
spe-miR172-3-5p	Sopen02g018790.1	3.0	-1.0	1	21	915	935	GCAACAUCAUCAAGAUUCACA	CAAGAAUAUUGAUGAUGUUGA	Cleavage
spe-miR172-3-5p	Sopen07g002790.1	3.0	-1.0	1	21	435	455	GCAACAUCAUCAAGAUUCACA	GUUGACUUUUGAUGGUGUUGA	Cleavage
spe-miR172-3-5p	Sopen01g024140.1	3.0	-1.0	1	21	732	752	GCAACAUCAUCAAGAUUCACA	UCUUGGUCUUGGUGGUGUUGC	Cleavage
spe-miR172-3-5p	Sopen01g024140.2	3.0	-1.0	1	21	732	752	GCAACAUCAUCAAGAUUCACA	UCUUGGUCUUGGUGGUGUUGC	Cleavage
spe-miR172-4-3p	Sopen03g030690.1	2.5	-1.0	1	23	2798	2820	UGUGAAUCUUGAUGAUGUUGCAU	CAGUAGUGUUAUCAAGAUUUACA	Cleavage
spe-miR172-4-3p	Sopen03g025640.1	2.0	-1.0	1	23	570	592	UGUGAAUCUUGAUGAUGUUGCAU	ACCUAACAUCACCAAGAUUUACA	Cleavage
spe-miR172-4-3p	Sopen03g025640.2	2.0	-1.0	1	23	570	592	UGUGAAUCUUGAUGAUGUUGCAU	ACCUAACAUCACCAAGAUUUACA	Cleavage
spe-miR172-4-3p	Sopen09g002150.1	2.5	-1.0	1	23	1277	1299	UGUGAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
spe-miR172-4-3p	Sopen09g002130.1	2.5	-1.0	1	23	1274	1296	UGUGAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
spe-miR172-4-3p	Sopen09g002130.2	2.5	-1.0	1	23	1229	1251	UGUGAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUCGCU	Cleavage
spe-miR172-4-3p	Sopen11g030250.1	2.5	-1.0	1	23	1331	1353	UGUGAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUCUCA	Cleavage
spe-miR172-4-3p	Sopen11g030250.2	2.5	-1.0	1	23	1286	1308	UGUGAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUCUCA	Cleavage
spe-miR172-4-3p	Sopen04g030810.1	2.5	-1.0	1	23	122	144	UGUGAAUCUUGAUGAUGUUGCAU	UAUCAACAUCAUCAGAGUUCACA	Cleavage
spe-miR172-4-3p	Sopen10g033790.1	3.0	-1.0	1	23	1241	1263	UGUGAAUCUUGAUGAUGUUGCAU	CUGCAGCAUCAUCAGGAUUCGGA	Cleavage
spe-miR172-4-3p	Sopen06g023340.1	3.0	-1.0	1	23	514	536	UGUGAAUCUUGAUGAUGUUGCAU	UGGCAACAACAUCAAGGUUUACU	Cleavage
spe-miR172-4-3p	Sopen08g003820.1	3.0	-1.0	1	23	497	519	UGUGAAUCUUGAUGAUGUUGCAU	CUACAACAUCAUCAAGAUGUACU	Cleavage
spe-miR172-4-3p	Sopen07g026000.1	3.0	-1.0	1	23	729	751	UGUGAAUCUUGAUGAUGUUGCAU	GGACAACAUUAUCAAUGUUCAUA	Cleavage
spe-miR172-4-3p	Sopen10g031820.1	3.0	-1.0	1	23	870	892	UGUGAAUCUUGAUGAUGUUGCAU	GACCAAUAUUGUCAAGAUUUAUG	Cleavage

spe-miR172-4-3p	Sopen01g040000.1	3.0	-1.0	1	23	106	128	UGUGAAUCUUGAUGAUGUUGCAU	CAACAAUGUCAUCAAGAUUCUUA	Cleavage
spe-miR172-4-3p	Sopen06g024260.1	3.0	-1.0	1	23	3598	3620	UGUGAAUCUUGAUGAUGUUGCAU	ACCCAACUUCAUCAAGAUUCGUC	Cleavage
spe-miR172-4-3p	Sopen01g030420.1	3.0	-1.0	1	23	2145	2166	UGUGAAUCUUGAUGAUGUUGCAU	GCGCAGCA-CAUCAGGAUUCACA	Cleavage
spe-miR172-4-3p	Sopen11g026060.1	3.0	-1.0	1	23	202	224	UGUGAAUCUUGAUGAUGUUGCAU	ACUCAACACCAUCGAGAUUCAUU	Cleavage
spe-miR172-4-3p	Sopen03g006600.1	3.0	-1.0	1	23	558	580	UGUGAAUCUUGAUGAUGUUGCAU	AAGCAAGACAAUCAAGAUUCACA	Cleavage
spe-miR172-4-3p	Sopen11g024480.1	3.0	-1.0	1	23	945	967	UGUGAAUCUUGAUGAUGUUGCAU	AGGGAAUAUCAUCAAGAUUGAUG	Cleavage
spe-miR172-4-3p	Sopen12g006560.1	3.0	-1.0	1	23	913	935	UGUGAAUCUUGAUGAUGUUGCAU	CAACAACAACAUCAAGGUUCAGA	Cleavage
spe-miR172-4-3p	Sopen09g022750.1	3.0	-1.0	1	23	177	199	UGUGAAUCUUGAUGAUGUUGCAU	CAUUAGUAUUAUCAAGAUUCAGA	Cleavage
spe-miR172-4-3p	Sopen05g005350.1	3.0	-1.0	1	23	1686	1708	UGUGAAUCUUGAUGAUGUUGCAU	UGGGGACGUUGUUGAGAUUCACA	Cleavage
spe-miR172-4-3p	Sopen11g006420.1	3.0	-1.0	1	23	19	41	UGUGAAUCUUGAUGAUGUUGCAU	AGAGAACAUUGUCAAGGUUUACC	Cleavage
spe-miR172-4-3p	Sopen12g002270.1	3.0	-1.0	1	23	409	431	UGUGAAUCUUGAUGAUGUUGCAU	AAAGAACAUCAUGAAGAUUCAGA	Translation
spe-miR172-4-5p	Sopen04g005120.1	2.5	-1.0	1	21	723	743	GCAGCAUCAUCAAGAUUCCCA	UAGGAACCUUGGUGAUGCUGA	Cleavage
spe-miR172-4-5p	Sopen09g005740.1	1.5	-1.0	1	21	819	839	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUUUUGAUGAUGCUGA	Cleavage
spe-miR172-4-5p	Sopen03g014410.1	2.5	-1.0	1	21	6783	6803	GCAGCAUCAUCAAGAUUCCCA	AAGGAAUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen02g035770.2	2.5	-1.0	1	21	2709	2729	GCAGCAUCAUCAAGAUUCCCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-4-5p	Sopen02g035770.1	2.5	-1.0	1	21	2709	2729	GCAGCAUCAUCAAGAUUCCCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-4-5p	Sopen05g027750.1	2.5	-1.0	1	21	441	461	GCAGCAUCAUCAAGAUUCCCA	AGGUAAUCUUGUUGAUGCUGC	Translation
spe-miR172-4-5p	Sopen02g023500.1	2.5	-1.0	1	21	500	520	GCAGCAUCAUCAAGAUUCCCA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
spe-miR172-4-5p	Sopen07g019560.1	2.5	-1.0	1	21	771	791	GCAGCAUCAUCAAGAUUCCCA	AAUGAAUUUUGAUGAUGUUGU	Cleavage
spe-miR172-4-5p	Sopen02g022280.1	2.5	-1.0	1	21	228	248	GCAGCAUCAUCAAGAUUCCCA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
spe-miR172-4-5p	Sopen12g028920.1	2.5	-1.0	1	21	177	197	GCAGCAUCAUCAAGAUUCCCA	AUGGAGUUUUGAUGAUGAUGC	Cleavage
spe-miR172-4-5p	Sopen12g028920.2	2.5	-1.0	1	21	177	197	GCAGCAUCAUCAAGAUUCCCA	AUGGAGUUUUGAUGAUGAUGC	Cleavage
spe-miR172-4-5p	Sopen02g002770.1	3.0	-1.0	1	21	4113	4133	GCAGCAUCAUCAAGAUUCCCA	UGGGAUUCUUGAUGUUGUUGC	Cleavage
spe-miR172-4-5p	Sopen04g036240.1	3.0	-1.0	1	21	1605	1625	GCAGCAUCAUCAAGAUUCCCA	UGGGAAAUUUGAUGGUGUUGU	Cleavage
spe-miR172-4-5p	Sopen09g003390.1	3.0	-1.0	1	21	450	470	GCAGCAUCAUCAAGAUUCCCA	UGAGAAUCUCGAUGAUGUUGC	Cleavage
spe-miR172-4-5p	Sopen05g018970.1	3.0	-1.0	1	21	1689	1709	GCAGCAUCAUCAAGAUUCCCA	UAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen05g020090.1	3.0	-1.0	1	21	2796	2816	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen01g014860.1	3.0	-1.0	1	21	5808	5828	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen04g022460.1	3.0	-1.0	1	21	4038	4058	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen05g025370.1	3.0	-1.0	1	21	2400	2420	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen01g014920.1	3.0	-1.0	1	21	873	893	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen11g016140.1	3.0	-1.0	1	21	1890	1910	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen07g018280.1	3.0	-1.0	1	21	750	770	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen08g031200.1	3.0	-1.0	1	21	1488	1508	GCAGCAUCAUCAAGAUUCCCA	GGGGAGUCUAGGUGAUGCUGU	Cleavage
spe-miR172-4-5p	Sopen11g023070.1	3.0	-1.0	1	21	30	50	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-4-5p	Sopen09g023370.1	3.0	-1.0	1	21	4383	4403	GCAGCAUCAUCAAGAUUCCCA	UGAGAGUGUUGAUGAUGUUGC	Cleavage
spe-miR172-4-5p	Sopen02g003340.1	3.0	-1.0	1	21	114	134	GCAGCAUCAUCAAGAUUCCCA	UGGUGAUGUUGAUGAUGUUGC	Cleavage
spe-miR172-4-5p	Sopen12g030540.1	3.0	-1.0	1	21	375	395	GCAGCAUCAUCAAGAUUCCCA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
spe-miR172-4-5p	Sopen02g003380.2	3.0	-1.0	1	21	2661	2681	GCAGCAUCAUCAAGAUUCCCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-4-5p	Sopen02g003380.1	3.0	-1.0	1	21	2595	2615	GCAGCAUCAUCAAGAUUCCCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-4-5p	Sopen01g047980.2	3.0	-1.0	1	21	1392	1412	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUAUUGAUGAUGCAGU	Cleavage
spe-miR172-4-5p	Sopen08g006720.1	3.0	-1.0	1	21	162	182	GCAGCAUCAUCAAGAUUCCCA	GGAGAAUCUUGGUGAUGGUGC	Cleavage
spe-miR172-4-5p	Sopen01g047980.3	3.0	-1.0	1	21	159	179	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUAUUGAUGAUGCAGU	Cleavage
spe-miR172-4-5p	Sopen11g017320.1	3.0	-1.0	1	21	504	524	GCAGCAUCAUCAAGAUUCCCA	AAGGAAUUUUGAUGAUACUGA	Cleavage
spe-miR172-4-5p	Sopen00g002420.1	3.0	-1.0	1	21	930	950	GCAGCAUCAUCAAGAUUCCCA	UAGGAAGCUUGAUGGUGUUGG	Cleavage
spe-miR172-4-5p	Sopen08g028970.1	3.0	-1.0	1	21	216	236	GCAGCAUCAUCAAGAUUCCCA	UUGCAAUUUUGAUGGUGCUGG	Cleavage
spe-miR172-4-5p	Sopen09g016560.1	3.0	-1.0	1	21	3012	3032	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-4-5p	Sopen12g027960.1	3.0	-1.0	1	21	1446	1466	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-4-5p	Sopen01g034360.1	3.0	-1.0	1	21	1191	1211	GCAGCAUCAUCAAGAUUCCCA	GAGAAAUCUUGAGGAUGCUGU	Cleavage
spe-miR172-4-5p	Sopen11g018440.1	3.0	-1.0	1	21	12	32	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage

spe-miR172-4-5p	Sopen12g015630.1	3.0	-1.0	1	21	891	911	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-5-3p	Sopen07g020390.1	2.0	-1.0	1	21	2270	2290	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUCAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen09g002150.1	2.0	-1.0	1	21	1277	1297	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-5-3p	Sopen09g002130.1	2.0	-1.0	1	21	1274	1294	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-5-3p	Sopen10g033790.1	2.0	-1.0	1	21	1241	1261	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-5-3p	Sopen09g002130.2	2.0	-1.0	1	21	1229	1249	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-5-3p	Sopen12g025840.1	2.5	-1.0	1	21	3830	3850	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen05g004820.1	2.5	-1.0	1	21	3434	3454	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen04g015180.1	2.5	-1.0	1	21	2693	2713	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen02g014660.1	2.5	-1.0	1	21	2270	2290	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen08g008550.1	2.5	-1.0	1	21	1967	1987	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen05g016400.1	2.5	-1.0	1	21	1988	2008	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen05g002620.1	2.5	-1.0	1	21	1670	1690	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen04g022370.1	2.5	-1.0	1	21	1640	1660	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen09g011110.1	2.5	-1.0	1	21	752	772	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUCCA	Cleavage
spe-miR172-5-3p	Sopen02g037720.1	2.5	-1.0	1	21	1439	1459	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-5-3p	Sopen02g015090.1	2.5	-1.0	1	21	1430	1450	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-5-3p	Sopen11g030250.1	2.5	-1.0	1	21	1331	1351	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-5-3p	Sopen11g030250.2	2.5	-1.0	1	21	1286	1306	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-5-3p	Sopen03g008400.3	2.5	-1.0	1	21	1343	1363	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-5-3p	Sopen03g008400.2	2.5	-1.0	1	21	1331	1351	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-5-3p	Sopen03g008400.1	2.5	-1.0	1	21	1127	1147	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-5-3p	Sopen04g020090.1	2.5	-1.0	1	21	1103	1123	UGAAUCUUGAUGAUGCUCCAC	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-5-3p	Sopen06g031890.1	2.5	-1.0	1	21	1298	1318	UGAAUCUUGAUGAUGCUCCAC	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-5-3p	Sopen06g031890.2	2.5	-1.0	1	21	1253	1273	UGAAUCUUGAUGAUGCUCCAC	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-5-3p	Sopen05g009530.1	3.0	-1.0	1	21	334	354	UGAAUCUUGAUGAUGCUCCAC	GUUGAGCAUUAUCAAGAAUCA	Cleavage
spe-miR172-5-3p	Sopen08g005960.1	3.0	-1.0	1	21	1430	1450	UGAAUCUUGAUGAUGCUCCAC	UUGGAGUAUUAUCAAGAUGUA	Cleavage
spe-miR172-5-3p	Sopen09g022750.1	3.0	-1.0	1	21	177	197	UGAAUCUUGAUGAUGCUCCAC	CAUUAGUAUUAUCAAGAUUCA	Cleavage
spe-miR172-5-3p	Sopen06g015620.1	3.0	-1.0	1	21	556	576	UGAAUCUUGAUGAUGCUCCAC	CGGGAGCAUCAUCAAUAUGCA	Cleavage
spe-miR172-5-3p	Sopen12g023300.1	3.0	-1.0	1	21	8	28	UGAAUCUUGAUGAUGCUCCAC	CCGGAGCAUCAUCGGGAAUCG	Cleavage
spe-miR172-5-3p	Sopen06g018940.1	3.0	-1.0	1	21	288	308	UGAAUCUUGAUGAUGCUCCAC	UGGGAGUGUCAUUGGGAUUUA	Cleavage
spe-miR172-5-3p	Sopen01g027180.1	3.0	-1.0	1	21	93	113	UGAAUCUUGAUGAUGCUCCAC	GGUGAGGAUCAUCAAGAUUCU	Cleavage
spe-miR172-5-3p	Sopen01g030350.1	3.0	-1.0	1	21	1897	1917	UGAAUCUUGAUGAUGCUCCAC	GCGGAAUAUCGUCAAGGUUUA	Cleavage
spe-miR172-5-3p	Sopen03g030690.1	3.0	-1.0	1	21	2798	2818	UGAAUCUUGAUGAUGCUCCAC	CAGUAGUGUUAUCAAGAUUUA	Cleavage
spe-miR172-5-3p	Sopen11g024480.1	3.0	-1.0	1	21	945	965	UGAAUCUUGAUGAUGCUCCAC	AGGGAAUAUCAUCAAGAUUGA	Cleavage
spe-miR172-5-3p	Sopen03g002770.1	3.0	-1.0	1	21	1957	1977	UGAAUCUUGAUGAUGCUCCAC	CUGUAUCUUCAUCAAGAUUCA	Cleavage
spe-miR172-5-3p	Sopen02g007340.1	3.0	-1.0	1	21	2409	2429	UGAAUCUUGAUGAUGCUCCAC	GCGGAAGAUCAUUGAGAUUCA	Cleavage
spe-miR172-5-3p	Sopen04g032210.1	3.0	-1.0	1	21	358	378	UGAAUCUUGAUGAUGCUCCAC	UGGGAGAUUUGUCAAGAUUCA	Cleavage
spe-miR172-5-3p	Sopen11g011780.1	3.0	-1.0	1	21	314	334	UGAAUCUUGAUGAUGCUCCAC	CAGUAGCUUCAUUAAGGUUCA	Cleavage
spe-miR172-5-5p	Sopen04g005120.1	2.5	-1.0	1	21	723	743	GCAGCAUCAUCAAGAUUCCCA	UAGGAACCUUGGUGAUGCUGA	Cleavage
spe-miR172-5-5p	Sopen09g005740.1	1.5	-1.0	1	21	819	839	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUUUUGAUGAUGCUGA	Cleavage
spe-miR172-5-5p	Sopen03g014410.1	2.5	-1.0	1	21	6783	6803	GCAGCAUCAUCAAGAUUCCCA	AAGGAAUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen02g035770.2	2.5	-1.0	1	21	2709	2729	GCAGCAUCAUCAAGAUUCCCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-5-5p	Sopen02g035770.1	2.5	-1.0	1	21	2709	2729	GCAGCAUCAUCAAGAUUCCCA	CGGUGAUCUUGGUGAUGUUGC	Cleavage
spe-miR172-5-5p	Sopen05g027750.1	2.5	-1.0	1	21	441	461	GCAGCAUCAUCAAGAUUCCCA	AGGUAAUCUUGUUGAUGCUGC	Translation
spe-miR172-5-5p	Sopen02g023500.1	2.5	-1.0	1	21	500	520	GCAGCAUCAUCAAGAUUCCCA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
spe-miR172-5-5p	Sopen07g019560.1	2.5	-1.0	1	21	771	791	GCAGCAUCAUCAAGAUUCCCA	AAUGAAUUUUGAUGAUGUUGU	Cleavage
spe-miR172-5-5p	Sopen02g022280.1	2.5	-1.0	1	21	228	248	GCAGCAUCAUCAAGAUUCCCA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
spe-miR172-5-5p	Sopen12g028920.1	2.5	-1.0	1	21	177	197	GCAGCAUCAUCAAGAUUCCCA	AUGGAGUUUUGAUGAUGAUGC	Cleavage
spe-miR172-5-5p	Sopen12g028920.2	2.5	-1.0	1	21	177	197	GCAGCAUCAUCAAGAUUCCCA	AUGGAGUUUUGAUGAUGAUGC	Cleavage

spe-miR172-5-5p	Sopen02g002770.1	3.0	-1.0	1	21	4113	4133	GCAGCAUCAUCAAGAUUCCCA	UGGGAUUCUUGAUGUUGUUGC	Cleavage
spe-miR172-5-5p	Sopen04g036240.1	3.0	-1.0	1	21	1605	1625	GCAGCAUCAUCAAGAUUCCCA	UGGGAAAUUUGAUGGUGUUGU	Cleavage
spe-miR172-5-5p	Sopen09g003390.1	3.0	-1.0	1	21	450	470	GCAGCAUCAUCAAGAUUCCCA	UGAGAAUCUCGAUGAUGUUGC	Cleavage
spe-miR172-5-5p	Sopen05g018970.1	3.0	-1.0	1	21	1689	1709	GCAGCAUCAUCAAGAUUCCCA	UAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen05g020090.1	3.0	-1.0	1	21	2796	2816	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen01g014860.1	3.0	-1.0	1	21	5808	5828	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen04g022460.1	3.0	-1.0	1	21	4038	4058	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen05g025370.1	3.0	-1.0	1	21	2400	2420	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen01g014920.1	3.0	-1.0	1	21	873	893	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen11g016140.1	3.0	-1.0	1	21	1890	1910	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen07g018280.1	3.0	-1.0	1	21	750	770	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen08g031200.1	3.0	-1.0	1	21	1488	1508	GCAGCAUCAUCAAGAUUCCCA	GGGGAGUCUAGGUGAUGCUGU	Cleavage
spe-miR172-5-5p	Sopen11g023070.1	3.0	-1.0	1	21	30	50	GCAGCAUCAUCAAGAUUCCCA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172-5-5p	Sopen09g023370.1	3.0	-1.0	1	21	4383	4403	GCAGCAUCAUCAAGAUUCCCA	UGAGAGUGUUGAUGAUGUUGC	Cleavage
spe-miR172-5-5p	Sopen02g003340.1	3.0	-1.0	1	21	114	134	GCAGCAUCAUCAAGAUUCCCA	UGGUGAUGUUGAUGAUGUUGC	Cleavage
spe-miR172-5-5p	Sopen12g030540.1	3.0	-1.0	1	21	375	395	GCAGCAUCAUCAAGAUUCCCA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
spe-miR172-5-5p	Sopen02g003380.2	3.0	-1.0	1	21	2661	2681	GCAGCAUCAUCAAGAUUCCCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-5-5p	Sopen02g003380.1	3.0	-1.0	1	21	2595	2615	GCAGCAUCAUCAAGAUUCCCA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-5-5p	Sopen01g047980.2	3.0	-1.0	1	21	1392	1412	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUAUUGAUGAUGCAGU	Cleavage
spe-miR172-5-5p	Sopen08g006720.1	3.0	-1.0	1	21	162	182	GCAGCAUCAUCAAGAUUCCCA	GGAGAAUCUUGGUGAUGGUGC	Cleavage
spe-miR172-5-5p	Sopen01g047980.3	3.0	-1.0	1	21	159	179	GCAGCAUCAUCAAGAUUCCCA	GGGGAAUAUUGAUGAUGCAGU	Cleavage
spe-miR172-5-5p	Sopen11g017320.1	3.0	-1.0	1	21	504	524	GCAGCAUCAUCAAGAUUCCCA	AAGGAAUUUUGAUGAUACUGA	Cleavage
spe-miR172-5-5p	Sopen00g002420.1	3.0	-1.0	1	21	930	950	GCAGCAUCAUCAAGAUUCCCA	UAGGAAGCUUGAUGGUGUUGG	Cleavage
spe-miR172-5-5p	Sopen08g028970.1	3.0	-1.0	1	21	216	236	GCAGCAUCAUCAAGAUUCCCA	UUGCAAUUUUGAUGGUGCUGG	Cleavage
spe-miR172-5-5p	Sopen09g016560.1	3.0	-1.0	1	21	3012	3032	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-5-5p	Sopen12g027960.1	3.0	-1.0	1	21	1446	1466	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-5-5p	Sopen01g034360.1	3.0	-1.0	1	21	1191	1211	GCAGCAUCAUCAAGAUUCCCA	GAGAAAUCUUGAGGAUGCUGU	Cleavage
spe-miR172-5-5p	Sopen11g018440.1	3.0	-1.0	1	21	12	32	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-5-5p	Sopen12g015630.1	3.0	-1.0	1	21	891	911	GCAGCAUCAUCAAGAUUCCCA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172-6-3p	Sopen11g030250.1	0.5	-1.0	1	21	1331	1351	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-6-3p	Sopen11g030250.2	0.5	-1.0	1	21	1286	1306	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-6-3p	Sopen04g020090.1	0.5	-1.0	1	21	1103	1123	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-6-3p	Sopen06g031890.1	0.5	-1.0	1	21	1298	1318	AGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-6-3p	Sopen06g031890.2	0.5	-1.0	1	21	1253	1273	AGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-6-3p	Sopen02g037720.1	1.5	-1.0	1	21	1439	1459	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-6-3p	Sopen02g015090.1	1.5	-1.0	1	21	1430	1450	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-6-3p	Sopen03g008400.3	1.5	-1.0	1	21	1343	1363	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-6-3p	Sopen09g002150.1	1.5	-1.0	1	21	1277	1297	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-6-3p	Sopen03g008400.2	1.5	-1.0	1	21	1331	1351	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-6-3p	Sopen09g002130.1	1.5	-1.0	1	21	1274	1294	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-6-3p	Sopen10g033790.1	1.5	-1.0	1	21	1241	1261	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-6-3p	Sopen09g002130.2	1.5	-1.0	1	21	1229	1249	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-6-3p	Sopen03g008400.1	1.5	-1.0	1	21	1127	1147	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-6-3p	Sopen10g002630.2	2.5	-1.0	1	21	1864	1884	AGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-6-3p	Sopen07g031900.1	2.5	-1.0	1	21	1816	1836	AGAAUCUUGAUGAUGCUGCAU	AUGUAUCUUCAUCAAGAUUCU	Cleavage
spe-miR172-6-3p	Sopen10g002630.3	2.5	-1.0	1	21	1258	1278	AGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172-6-3p	Sopen11g006420.1	3.0	-1.0	1	21	1126	1145	AGAAUCUUGAUGAUGCUGCAU	AUGCAGC-UUAUCAAGAUUUU	Cleavage
spe-miR172-6-3p	Sopen04g020260.1	3.0	-1.0	1	21	256	275	AGAAUCUUGAUGAUGCUGCAU	AUGCAGC-UUAUCAAGGUUCU	Cleavage
spe-miR172-6-3p	Sopen06g034240.1	3.0	-1.0	1	21	1403	1422	AGAAUCUUGAUGAUGCUGCAU	GUGCAGC-UCGUCAAGAUUUU	Cleavage
spe-miR172-6-3p	Sopen01g027180.1	3.0	-1.0	1	21	93	113	AGAAUCUUGAUGAUGCUGCAU	GGUGAGGAUCAUCAAGAUUCU	Cleavage

spe-miR172-6-3p	Sopen09g028620.2	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172-6-3p	Sopen01g018650.1	3.0	-1.0	1	21	807	827	AGAAUCUUGAUGAUGCUGCAU	AAGCAACAUCAUCAAGGUGCU	Cleavage
spe-miR172-6-3p	Sopen01g048830.1	3.0	-1.0	1	21	379	399	AGAAUCUUGAUGAUGCUGCAU	GAUCAUUGUCAUCAAGAUUCU	Cleavage
spe-miR172-6-3p	Sopen01g005710.1	3.0	-1.0	1	21	820	840	AGAAUCUUGAUGAUGCUGCAU	AGGCAGAAUCAUCAAGGUACU	Cleavage
spe-miR172-6-3p	Sopen09g028620.4	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172-6-3p	Sopen09g028620.3	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172-6-3p	Sopen01g040000.1	3.0	-1.0	1	21	106	126	AGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCU	Cleavage
spe-miR172-6-3p	Sopen08g014470.1	3.0	-1.0	1	21	2104	2124	AGAAUCUUGAUGAUGCUGCAU	AGGAGGCUUCAUCAGGAUUCU	Cleavage
spe-miR172-6-5p	Sopen09g029770.2	3.0	-1.0	1	21	393	413	GCAGCACCAUUAAGAUUCACA	GCUGAAAUCUAAUGGUGCUGC	Cleavage
spe-miR172-6-5p	Sopen09g029770.1	3.0	-1.0	1	21	342	362	GCAGCACCAUUAAGAUUCACA	GCUGAAAUCUAAUGGUGCUGC	Cleavage
spe-miR172-6-5p	Sopen01g025830.1	2.0	-1.0	1	21	807	827	GCAGCACCAUUAAGAUUCACA	UCUGAAUCUUAAAGGUGUUGC	Cleavage
spe-miR172-6-5p	Sopen12g027800.1	2.5	-1.0	1	21	504	524	GCAGCACCAUUAAGAUUCACA	GAUGGAUCUUAAUGGUGCGGU	Cleavage
spe-miR172-6-5p	Sopen05g007100.1	2.5	-1.0	1	21	142	161	GCAGCACCAUUAAGAUUCACA	AGUGAAU-UUAAUGGUGUUGC	Cleavage
spe-miR172-6-5p	Sopen12g034520.1	3.0	-1.0	1	21	474	494	GCAGCACCAUUAAGAUUCACA	UGUGGAUCUUAAUGCUGCUGA	Cleavage
spe-miR172-6-5p	Sopen04g005210.1	3.0	-1.0	1	21	6	26	GCAGCACCAUUAAGAUUCACA	UGUGGAUUUUAAUGGUGAUGU	Cleavage
spe-miR172-6-5p	Sopen04g004840.1	3.0	-1.0	1	21	519	539	GCAGCACCAUUAAGAUUCACA	AGUGGAUUUUGAUGGUGUUGA	Cleavage
spe-miR172-6-5p	Sopen10g034120.1	3.0	-1.0	1	21	513	533	GCAGCACCAUUAAGAUUCACA	UGUGAUUGUUAAUGGUGCUGG	Cleavage
spe-miR172-6-5p	Sopen11g023560.1	3.0	-1.0	1	21	693	713	GCAGCACCAUUAAGAUUCACA	AGUAAAUCUUAAUGGUUCUGU	Cleavage
spe-miR172-6-5p	Sopen07g031410.1	3.0	-1.0	1	21	393	413	GCAGCACCAUUAAGAUUCACA	UUUGGAUCUUAUUGGUGUUGU	Translation
spe-miR172-6-5p	Sopen07g033100.1	3.0	-1.0	1	21	273	293	GCAGCACCAUUAAGAUUCACA	GUUGUCUCUUAGUGGUGUUGC	Cleavage
spe-miR172-7-3p	Sopen09g002150.1	1.0	-1.0	1	21	1277	1297	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-7-3p	Sopen09g002130.1	1.0	-1.0	1	21	1274	1294	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-7-3p	Sopen10g033790.1	1.0	-1.0	1	21	1241	1261	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-7-3p	Sopen09g002130.2	1.0	-1.0	1	21	1229	1249	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172-7-3p	Sopen02g037720.1	1.5	-1.0	1	21	1439	1459	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-7-3p	Sopen02g015090.1	1.5	-1.0	1	21	1430	1450	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-7-3p	Sopen11g030250.1	1.5	-1.0	1	21	1331	1351	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-7-3p	Sopen11g030250.2	1.5	-1.0	1	21	1286	1306	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-7-3p	Sopen03g008400.3	1.5	-1.0	1	21	1343	1363	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-7-3p	Sopen03g008400.2	1.5	-1.0	1	21	1331	1351	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-7-3p	Sopen03g008400.1	1.5	-1.0	1	21	1127	1147	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172-7-3p	Sopen04g020090.1	1.5	-1.0	1	21	1103	1123	UGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-7-3p	Sopen06g031890.1	1.5	-1.0	1	21	1298	1318	UGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-7-3p	Sopen06g031890.2	1.5	-1.0	1	21	1253	1273	UGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172-7-3p	Sopen09g022750.1	2.5	-1.0	1	21	177	197	UGAAUCUUGAUGAUGCUGCAU	CAUUAGUAUUAUCAAGAUUCA	Cleavage
spe-miR172-7-3p	Sopen03g030690.1	2.5	-1.0	1	21	2798	2818	UGAAUCUUGAUGAUGCUGCAU	CAGUAGUGUUAUCAAGAUUUA	Cleavage
spe-miR172-7-3p	Sopen03g002770.1	2.5	-1.0	1	21	1957	1977	UGAAUCUUGAUGAUGCUGCAU	CUGUAUCUUCAUCAAGAUUCA	Cleavage
spe-miR172-7-3p	Sopen11g011780.1	2.5	-1.0	1	21	314	334	UGAAUCUUGAUGAUGCUGCAU	CAGUAGCUUCAUUAAGGUUCA	Cleavage
spe-miR172-7-3p	Sopen07g020390.1	3.0	-1.0	1	21	2270	2290	UGAAUCUUGAUGAUGCUGCAU	UUGGAGUAUCAUCAAGAUCCA	Cleavage
spe-miR172-7-3p	Sopen01g039920.1	3.0	-1.0	1	21	306	326	UGAAUCUUGAUGAUGCUGCAU	GUACAACAUCAUCAAGGUUUA	Cleavage
spe-miR172-7-3p	Sopen04g021710.1	3.0	-1.0	1	21	1840	1860	UGAAUCUUGAUGAUGCUGCAU	CAGUGGCAUCAUCGACAUUCA	Cleavage
spe-miR172-7-3p	Sopen01g037320.1	3.0	-1.0	1	21	174	194	UGAAUCUUGAUGAUGCUGCAU	CCGCAGCUUCCUCAAGGUUCA	Translation
spe-miR172-7-5p	Sopen12g006260.1	3.0	-1.0	1	21	1359	1379	GCAGCACUAUUAAGAUUCUCA	UGAAAAUCUUAAUGGUGUUGA	Cleavage
spe-miR172-7-5p	Sopen09g002210.1	2.5	-1.0	1	21	2277	2297	GCAGCACUAUUAAGAUUCUCA	GGAUAAUCUUAAUAGUGUUGG	Cleavage
spe-miR172-7-5p	Sopen02g037170.1	2.5	-1.0	1	21	393	413	GCAGCACUAUUAAGAUUCUCA	UAAGAGCCUUGAUAGUGCUGU	Cleavage
spe-miR172-7-5p	Sopen07g029640.1	2.5	-1.0	1	21	285	305	GCAGCACUAUUAAGAUUCUCA	AAAGAAUAUUAAUAGUGUUGA	Cleavage
spe-miR172-7-5p	Sopen12g002420.1	3.0	-1.0	1	21	2217	2237	GCAGCACUAUUAAGAUUCUCA	UGAGGAUAUUGAUAGUGUUGU	Cleavage
spe-miR172-7-5p	Sopen02g017020.1	3.0	-1.0	1	21	834	854	GCAGCACUAUUAAGAUUCUCA	UAAGAAUCUUGAUCGUGUUGU	Cleavage
spe-miR172-7-5p	Sopen01g050050.1	3.0	-1.0	1	21	1934	1954	GCAGCACUAUUAAGAUUCUCA	AUGGAAGCUUAAUAGUGAUGC	Cleavage
spe-miR172-7-5p	Sopen02g033340.1	3.0	-1.0	1	21	1713	1733	GCAGCACUAUUAAGAUUCUCA	AUAUGAUCUUAAUCGUGCUGC	Cleavage

spe-miR172-8-3p	Sopen01g047660.1	2.5	-1.0	1	23	162	184	UGAGAAUCUUAAUAGUGCUGCAU	AGCCCGCACUAUUAAGGUUCUUG	Cleavage
spe-miR172-8-3p	Sopen06g012370.1	2.5	-1.0	1	23	2541	2563	UGAGAAUCUUAAUAGUGCUGCAU	GGAGGGCACUAUUGAGGUUUUUA	Cleavage
spe-miR172-8-3p	Sopen07g002210.1	3.0	-1.0	1	23	1356	1378	UGAGAAUCUUAAUAGUGCUGCAU	AAAUAGCAUUAUGAGGAUUCUUA	Translation
spe-miR172-8-3p	Sopen04g031850.1	3.0	-1.0	1	23	534	556	UGAGAAUCUUAAUAGUGCUGCAU	UGCCAUUGCAAUUAAGAUUCUCA	Cleavage
spe-miR172-8-3p	Sopen05g001280.1	3.0	-1.0	1	23	823	845	UGAGAAUCUUAAUAGUGCUGCAU	ACAAAGAACUAUGAAGAUUUUCA	Translation
spe-miR172-8-5p	Sopen02g023500.1	2.5	-1.0	1	21	500	520	GCAGCAUCAUCAAGAUUCACA	AAAGAAUCUUGAAGAUGCUGC	Cleavage
spe-miR172-8-5p	Sopen09g029230.1	2.5	-1.0	1	21	783	803	GCAGCAUCAUCAAGAUUCACA	GAUGAAUCUUGGUGAUGAUGU	Cleavage
spe-miR172-8-5p	Sopen07g019560.1	1.5	-1.0	1	21	771	791	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAUGUUGU	Cleavage
spe-miR172-8-5p	Sopen12g030540.1	2.0	-1.0	1	21	375	395	GCAGCAUCAUCAAGAUUCACA	UCUCAAUCUUGAUGAUGCUGA	Cleavage
spe-miR172-8-5p	Sopen02g003380.2	2.0	-1.0	1	21	2661	2681	GCAGCAUCAUCAAGAUUCACA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-8-5p	Sopen02g003380.1	2.0	-1.0	1	21	2595	2615	GCAGCAUCAUCAAGAUUCACA	CUUUGAUCUUGAUGAUGCUGU	Cleavage
spe-miR172-8-5p	Sopen04g006670.1	2.5	-1.0	1	21	3738	3758	GCAGCAUCAUCAAGAUUCACA	UGUGAAAUUUGGUGAUGCUGU	Cleavage
spe-miR172-8-5p	Sopen00g013390.1	2.5	-1.0	1	21	1416	1436	GCAGCAUCAUCAAGAUUCACA	UGUGAAAUUUGGUGAUGCUGU	Cleavage
spe-miR172-8-5p	Sopen02g018230.2	2.5	-1.0	1	21	1050	1070	GCAGCAUCAUCAAGAUUCACA	UGUGGAACUUGGUGAUGCUGU	Cleavage
spe-miR172-8-5p	Sopen02g018230.1	2.5	-1.0	1	21	294	314	GCAGCAUCAUCAAGAUUCACA	UGUGGAACUUGGUGAUGCUGU	Cleavage
spe-miR172-8-5p	Sopen09g005740.1	2.5	-1.0	1	21	819	839	GCAGCAUCAUCAAGAUUCACA	GGGGAAUUUUGAUGAUGCUGA	Cleavage
spe-miR172-8-5p	Sopen02g022280.1	2.5	-1.0	1	21	228	248	GCAGCAUCAUCAAGAUUCACA	UAAGAGUUUUGAUGAUGUUGC	Cleavage
spe-miR172-8-5p	Sopen09g029770.2	2.5	-1.0	1	21	1086	1106	GCAGCAUCAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGU	Cleavage
spe-miR172-8-5p	Sopen09g029770.1	2.5	-1.0	1	21	1035	1055	GCAGCAUCAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGU	Cleavage
spe-miR172-8-5p	Sopen08g019040.1	2.5	-1.0	1	21	273	293	GCAGCAUCAUCAAGAUUCACA	CAUGAGUCUUGAUGAUCCUGU	Cleavage
spe-miR172-8-5p	Sopen05g014030.1	2.5	-1.0	1	21	597	617	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGCUGU	Cleavage
spe-miR172-8-5p	Sopen10g023950.1	2.5	-1.0	1	21	225	245	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGCUGU	Cleavage
spe-miR172-8-5p	Sopen11g015280.1	2.5	-1.0	1	21	2367	2387	GCAGCAUCAUCAAGAUUCACA	UUUCAAUUUUGAUGAUGCUGA	Cleavage
spe-miR172-8-5p	Sopen10g032510.1	3.0	-1.0	1	21	1923	1943	GCAGCAUCAUCAAGAUUCACA	AGUGAGUCUUGAUGAUGCUAU	Cleavage
spe-miR172-8-5p	Sopen06g003520.1	3.0	-1.0	1	21	168	188	GCAGCAUCAUCAAGAUUCACA	UGUUAAUUUUGAUGAUUCUGC	Cleavage
spe-miR172-8-5p	Sopen09g003390.1	3.0	-1.0	1	21	450	470	GCAGCAUCAUCAAGAUUCACA	UGAGAAUCUCGAUGAUGUUGC	Cleavage
spe-miR172-8-5p	Sopen04g004840.1	3.0	-1.0	1	21	519	539	GCAGCAUCAUCAAGAUUCACA	AGUGGAUUUUGAUGGUGUUGA	Cleavage
spe-miR172-8-5p	Sopen09g023370.1	3.0	-1.0	1	21	4383	4403	GCAGCAUCAUCAAGAUUCACA	UGAGAGUGUUGAUGAUGUUGC	Cleavage
spe-miR172-8-5p	Sopen07g026900.1	3.0	-1.0	1	21	681	701	GCAGCAUCAUCAAGAUUCACA	UGUGACAUUUGAUGAUGUUGC	Cleavage
spe-miR172-8-5p	Sopen08g006720.1	3.0	-1.0	1	21	162	182	GCAGCAUCAUCAAGAUUCACA	GGAGAAUCUUGGUGAUGGUGC	Cleavage
spe-miR172-8-5p	Sopen04g012630.1	3.0	-1.0	1	21	4524	4544	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-8-5p	Sopen06g035910.1	3.0	-1.0	1	21	1065	1085	GCAGCAUCAUCAAGAUUCACA	GUUGAAUCUUGAUAAUGGUGC	Cleavage
spe-miR172-8-5p	Sopen04g008870.1	3.0	-1.0	1	21	312	332	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-8-5p	Sopen01g010730.1	3.0	-1.0	1	21	117	137	GCAGCAUCAUCAAGAUUCACA	AGUCACUCUUGAUGAUGCUGA	Cleavage
spe-miR172-8-5p	Sopen08g008020.1	3.0	-1.0	1	21	360	380	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-8-5p	Sopen11g014800.1	3.0	-1.0	1	21	153	173	GCAGCAUCAUCAAGAUUCACA	AAUGAAUUUUGAUGAAGUUGU	Cleavage
spe-miR172-8-5p	Sopen02g014570.1	3.0	-1.0	1	21	204	224	GCAGCAUCAUCAAGAUUCACA	UCUGCAUCUUUAUGAUGUUGC	Translation
spe-miR172-8-5p	Sopen02g014570.2	3.0	-1.0	1	21	135	155	GCAGCAUCAUCAAGAUUCACA	UCUGCAUCUUUAUGAUGUUGC	Translation
spe-miR172a-3p	Sopen11g030250.1	0.5	-1.0	1	21	1331	1351	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172a-3p	Sopen11g030250.2	0.5	-1.0	1	21	1286	1306	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172a-3p	Sopen04g020090.1	0.5	-1.0	1	21	1103	1123	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172a-3p	Sopen06g031890.1	0.5	-1.0	1	21	1298	1318	AGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172a-3p	Sopen06g031890.2	0.5	-1.0	1	21	1253	1273	AGAAUCUUGAUGAUGCUGCAU	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172a-3p	Sopen02g037720.1	1.5	-1.0	1	21	1439	1459	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172a-3p	Sopen02g015090.1	1.5	-1.0	1	21	1430	1450	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172a-3p	Sopen03g008400.3	1.5	-1.0	1	21	1343	1363	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172a-3p	Sopen09g002150.1	1.5	-1.0	1	21	1277	1297	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172a-3p	Sopen03g008400.2	1.5	-1.0	1	21	1331	1351	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172a-3p	Sopen09g002130.1	1.5	-1.0	1	21	1274	1294	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172a-3p	Sopen10g033790.1	1.5	-1.0	1	21	1241	1261	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage

spe-miR172a-3p	Sopen09g002130.2	1.5	-1.0	1	21	1229	1249	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172a-3p	Sopen03g008400.1	1.5	-1.0	1	21	1127	1147	AGAAUCUUGAUGAUGCUGCAU	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172a-3p	Sopen10g002630.2	2.5	-1.0	1	21	1864	1884	AGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172a-3p	Sopen07g031900.1	2.5	-1.0	1	21	1816	1836	AGAAUCUUGAUGAUGCUGCAU	AUGUAUCUUCAUCAAGAUUCU	Cleavage
spe-miR172a-3p	Sopen10g002630.3	2.5	-1.0	1	21	1258	1278	AGAAUCUUGAUGAUGCUGCAU	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172a-3p	Sopen11g006420.1	3.0	-1.0	1	21	1126	1145	AGAAUCUUGAUGAUGCUGCAU	AUGCAGC-UUAUCAAGAUUUU	Cleavage
spe-miR172a-3p	Sopen04g020260.1	3.0	-1.0	1	21	256	275	AGAAUCUUGAUGAUGCUGCAU	AUGCAGC-UUAUCAAGGUUCU	Cleavage
spe-miR172a-3p	Sopen06g034240.1	3.0	-1.0	1	21	1403	1422	AGAAUCUUGAUGAUGCUGCAU	GUGCAGC-UCGUCAAGAUUUU	Cleavage
spe-miR172a-3p	Sopen01g027180.1	3.0	-1.0	1	21	93	113	AGAAUCUUGAUGAUGCUGCAU	GGUGAGGAUCAUCAAGAUUCU	Cleavage
spe-miR172a-3p	Sopen09g028620.2	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172a-3p	Sopen01g018650.1	3.0	-1.0	1	21	807	827	AGAAUCUUGAUGAUGCUGCAU	AAGCAACAUCAUCAAGGUGCU	Cleavage
spe-miR172a-3p	Sopen01g048830.1	3.0	-1.0	1	21	379	399	AGAAUCUUGAUGAUGCUGCAU	GAUCAUUGUCAUCAAGAUUCU	Cleavage
spe-miR172a-3p	Sopen01g005710.1	3.0	-1.0	1	21	820	840	AGAAUCUUGAUGAUGCUGCAU	AGGCAGAAUCAUCAAGGUACU	Cleavage
spe-miR172a-3p	Sopen09g028620.4	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172a-3p	Sopen09g028620.3	3.0	-1.0	1	21	233	253	AGAAUCUUGAUGAUGCUGCAU	UCUCAUCAUCAUCAGGAUUUU	Cleavage
spe-miR172a-3p	Sopen01g040000.1	3.0	-1.0	1	21	106	126	AGAAUCUUGAUGAUGCUGCAU	CAACAAUGUCAUCAAGAUUCU	Cleavage
spe-miR172a-3p	Sopen08g014470.1	3.0	-1.0	1	21	2104	2124	AGAAUCUUGAUGAUGCUGCAU	AGGAGGCUUCAUCAGGAUUCU	Cleavage
spe-miR172a-5p	Sopen11g011620.1	2.0	-1.0	1	21	99	119	GUAGCAUAAUCAAGAUUCACA	UAUGGAUAUUGAUUAUGCUAU	Cleavage
spe-miR172a-5p	Sopen09g024810.1	2.0	-1.0	1	21	99	119	GUAGCAUAAUCAAGAUUCACA	UAUGGAUAUUGAUUAUGCUAU	Cleavage
spe-miR172a-5p	Sopen10g017470.1	2.5	-1.0	1	21	876	896	GUAGCAUAAUCAAGAUUCACA	UGUGAGUCUUGAUCAUGCUAU	Cleavage
spe-miR172a-5p	Sopen12g027430.1	2.5	-1.0	1	21	506	526	GUAGCAUAAUCAAGAUUCACA	UGCGAAUCUUGGUUGUGCUAU	Cleavage
spe-miR172a-5p	Sopen10g032510.1	2.5	-1.0	1	21	1923	1943	GUAGCAUAAUCAAGAUUCACA	AGUGAGUCUUGAUGAUGCUAU	Cleavage
spe-miR172a-5p	Sopen06g022340.1	2.5	-1.0	1	21	642	662	GUAGCAUAAUCAAGAUUCACA	CUUGAAGCUUGAUUAUGCUGA	Cleavage
spe-miR172a-5p	Sopen09g029770.1	3.0	-1.0	1	21	1035	1055	GUAGCAUAAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGU	Cleavage
spe-miR172a-5p	Sopen09g029770.2	3.0	-1.0	1	21	1086	1106	GUAGCAUAAUCAAGAUUCACA	CUUGAAUCUUGAUAAUGUUGU	Cleavage
spe-miR172a-5p	Sopen11g011480.1	3.0	-1.0	1	21	582	602	GUAGCAUAAUCAAGAUUCACA	UAUGUAUCUUGGUAAUGCUAC	Cleavage
spe-miR172a-5p	Sopen00g009370.1	3.0	-1.0	1	21	3303	3323	GUAGCAUAAUCAAGAUUCACA	UAUGAAACUUGAAUAUGCUAU	Cleavage
spe-miR172a-5p	Sopen00g007260.1	3.0	-1.0	1	21	3306	3326	GUAGCAUAAUCAAGAUUCACA	UAUGAAACUUGAAUAUGCUAU	Cleavage
spe-miR172a-5p	Sopen02g039300.1	3.0	-1.0	1	21	3669	3689	GUAGCAUAAUCAAGAUUCACA	UUUGAAACUUGAAUAUGCUAU	Cleavage
spe-miR172d-3p	Sopen03g008400.1	0.5	-1.0	1	21	1127	1147	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172d-3p	Sopen03g008400.2	0.5	-1.0	1	21	1331	1351	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172d-3p	Sopen03g008400.3	0.5	-1.0	1	21	1343	1363	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172d-3p	Sopen02g015090.1	0.5	-1.0	1	21	1430	1450	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172d-3p	Sopen02g037720.1	0.5	-1.0	1	21	1439	1459	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCC	Cleavage
spe-miR172d-3p	Sopen04g020090.1	1.0	-1.0	1	21	1103	1123	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172d-3p	Sopen11g030250.2	1.0	-1.0	1	21	1286	1306	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172d-3p	Sopen11g030250.1	1.0	-1.0	1	21	1331	1351	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172d-3p	Sopen06g031890.2	1.0	-1.0	1	21	1253	1273	GGAAUCUUGAUGAUGCUGCAG	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172d-3p	Sopen06g031890.1	1.0	-1.0	1	21	1298	1318	GGAAUCUUGAUGAUGCUGCAG	CGGCAGCAUCAUCAGGAUUCU	Cleavage
spe-miR172d-3p	Sopen09g002130.2	1.5	-1.0	1	21	1229	1249	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172d-3p	Sopen10g033790.1	1.5	-1.0	1	21	1241	1261	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172d-3p	Sopen09g002130.1	1.5	-1.0	1	21	1274	1294	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172d-3p	Sopen09g002150.1	1.5	-1.0	1	21	1277	1297	GGAAUCUUGAUGAUGCUGCAG	CUGCAGCAUCAUCAGGAUUCG	Cleavage
spe-miR172d-3p	Sopen02g034050.1	2.5	-1.0	1	21	7640	7660	GGAAUCUUGAUGAUGCUGCAG	UGGCUAUAUCAUCAAGAUUCC	Cleavage
spe-miR172d-3p	Sopen10g019280.1	3.0	-1.0	1	21	179	199	GGAAUCUUGAUGAUGCUGCAG	GAUCAGCAUCAUCAAGGGUCC	Cleavage
spe-miR172d-3p	Sopen01g037690.1	3.0	-1.0	1	21	445	465	GGAAUCUUGAUGAUGCUGCAG	CCUCAGCAUUAUCAACAUUCC	Cleavage
spe-miR172d-3p	Sopen12g005650.1	3.0	-1.0	1	21	26	46	GGAAUCUUGAUGAUGCUGCAG	GUGAAGCUUUAUCAAGAUUUC	Cleavage
spe-miR172d-3p	Sopen10g002630.3	3.0	-1.0	1	21	1258	1278	GGAAUCUUGAUGAUGCUGCAG	AUGUACCUUCAUCAAGAUUCU	Cleavage
spe-miR172d-3p	Sopen07g031900.1	3.0	-1.0	1	21	1816	1836	GGAAUCUUGAUGAUGCUGCAG	AUGUAUCUUCAUCAAGAUUCU	Cleavage
spe-miR172d-3p	Sopen10g002630.2	3.0	-1.0	1	21	1864	1884	GGAAUCUUGAUGAUGCUGCAG	AUGUACCUUCAUCAAGAUUCU	Cleavage

spe-miR172d-3p	Sopen04g019810.1	3.0	-1.0	1	21	1199	1219	GGAAUCUUGAUGAUGCUGCAG	AAGUAACAUCAUCAAGAUUAC	Cleavage
spe-miR172d-5p	Sopen05g013530.1	3.0	-1.0	1	21	2862	2882	GGAGCAUCAUCAAGAUUCACA	AAGGAGACUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g013530.1	3.0	-1.0	1	21	10050	10070	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g013530.1	3.0	-1.0	1	21	13611	13631	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g013530.1	3.0	-1.0	1	21	16287	16307	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g009840.1	3.0	-1.0	1	21	4878	4898	GGAGCAUCAUCAAGAUUCACA	GAGGAAUCUUGAUGAUACUCU	Cleavage
spe-miR172d-5p	Sopen12g010580.1	3.0	-1.0	1	21	1953	1973	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g010580.1	3.0	-1.0	1	21	7815	7835	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g005910.1	3.0	-1.0	1	21	4278	4298	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g005910.1	3.0	-1.0	1	21	11487	11507	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g012430.1	3.0	-1.0	1	21	5091	5111	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g012430.1	3.0	-1.0	1	21	7722	7742	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g017090.1	3.0	-1.0	1	21	2886	2906	GGAGCAUCAUCAAGAUUCACA	AAGGAGACUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g014410.1	1.5	-1.0	1	21	6783	6803	GGAGCAUCAUCAAGAUUCACA	AAGGAAUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g020090.1	2.0	-1.0	1	21	2796	2816	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen01g014860.1	2.0	-1.0	1	21	5808	5828	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g022460.1	2.0	-1.0	1	21	4038	4058	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g025370.1	2.0	-1.0	1	21	2400	2420	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g018970.1	2.0	-1.0	1	21	1689	1709	GGAGCAUCAUCAAGAUUCACA	UAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen01g014920.1	2.0	-1.0	1	21	873	893	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g016140.1	2.0	-1.0	1	21	1890	1910	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen07g018280.1	2.0	-1.0	1	21	750	770	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g023070.1	2.0	-1.0	1	21	30	50	GGAGCAUCAUCAAGAUUCACA	AAGGAGUCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g011780.1	2.0	-1.0	1	21	948	968	GGAGCAUCAUCAAGAUUCACA	AAUGAAUCUUGAUGAUUCUCU	Cleavage
spe-miR172d-5p	Sopen06g007450.1	2.0	-1.0	1	21	6267	6287	GGAGCAUCAUCAAGAUUCACA	AAUGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g009220.1	2.0	-1.0	1	21	1479	1499	GGAGCAUCAUCAAGAUUCACA	AAUGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g031090.1	2.5	-1.0	1	21	1362	1382	GGAGCAUCAUCAAGAUUCACA	UACGAAUCUUGAUGAUGUUUU	Cleavage
spe-miR172d-5p	Sopen02g035340.1	2.5	-1.0	1	21	177	197	GGAGCAUCAUCAAGAUUCACA	UUUGAGUCUUGUUGAUGCUUC	Translation
spe-miR172d-5p	Sopen05g031560.1	2.5	-1.0	1	21	435	455	GGAGCAUCAUCAAGAUUCACA	ACUGGAUUCUGAUGAUGCUCC	Cleavage
spe-miR172d-5p	Sopen05g002580.1	2.5	-1.0	1	21	1425	1445	GGAGCAUCAUCAAGAUUCACA	UUUCAAUUUUGAUGAUGCUCG	Cleavage
spe-miR172d-5p	Sopen12g026590.1	2.5	-1.0	1	21	1140	1160	GGAGCAUCAUCAAGAUUCACA	AAGGAAGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g016560.1	2.5	-1.0	1	21	3012	3032	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172d-5p	Sopen12g027960.1	2.5	-1.0	1	21	1446	1466	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172d-5p	Sopen01g021120.1	2.5	-1.0	1	21	1032	1052	GGAGCAUCAUCAAGAUUCACA	AAGGAAGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g011300.1	2.5	-1.0	1	21	1128	1148	GGAGCAUCAUCAAGAUUCACA	AAGGAAGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g018440.1	2.5	-1.0	1	21	12	32	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172d-5p	Sopen12g015630.1	2.5	-1.0	1	21	891	911	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCC	Cleavage
spe-miR172d-5p	Sopen06g013530.1	2.5	-1.0	1	21	1224	1244	GGAGCAUCAUCAAGAUUCACA	CAGGAAGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g002950.1	2.5	-1.0	1	21	888	908	GGAGCAUCAUCAAGAUUCACA	AAUUGAUUUUGAUGAUGUUCC	Cleavage
spe-miR172d-5p	Sopen06g027350.1	2.5	-1.0	1	21	333	353	GGAGCAUCAUCAAGAUUCACA	ACUCAAUCUUGAUGAUGUUUU	Cleavage
spe-miR172d-5p	Sopen10g032510.1	3.0	-1.0	1	21	1923	1943	GGAGCAUCAUCAAGAUUCACA	AGUGAGUCUUGAUGAUGCUAU	Cleavage
spe-miR172d-5p	Sopen01g021680.1	3.0	-1.0	1	21	3120	3140	GGAGCAUCAUCAAGAUUCACA	UGGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g039840.1	3.0	-1.0	1	21	57	77	GGAGCAUCAUCAAGAUUCACA	UGCGACUUUUGAUGGUGCUCC	Cleavage
spe-miR172d-5p	Sopen03g026140.1	3.0	-1.0	1	21	1809	1829	GGAGCAUCAUCAAGAUUCACA	AGUGAGGUUUGGUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g013640.1	3.0	-1.0	1	21	828	848	GGAGCAUCAUCAAGAUUCACA	AGUUAAUCAUGAUGAUGUUCC	Cleavage
spe-miR172d-5p	Sopen01g048490.1	3.0	-1.0	1	21	765	785	GGAGCAUCAUCAAGAUUCACA	CACCAAUCUUGAUGAUGCUUU	Cleavage
spe-miR172d-5p	Sopen01g047980.2	3.0	-1.0	1	21	573	593	GGAGCAUCAUCAAGAUUCACA	CGUCAAACUUGAUGAUGCUCA	Cleavage
spe-miR172d-5p	Sopen01g047980.1	3.0	-1.0	1	21	573	593	GGAGCAUCAUCAAGAUUCACA	CGUCAAACUUGAUGAUGCUCA	Cleavage
spe-miR172d-5p	Sopen10g018610.1	3.0	-1.0	1	21	91971	91991	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g012400.1	3.0	-1.0	1	21	2292	2312	GGAGCAUCAUCAAGAUUCACA	AGGGAGGCUUGAUGAUGCUCU	Cleavage

spe-miR172d-5p	Sopen07g025480.1	3.0	-1.0	1	21	1593	1613	GGAGCAUCAUCAAGAUUCACA	AGUGUAUGUUGAUGAUGUUCU	Cleavage
spe-miR172d-5p	Sopen05g022640.1	3.0	-1.0	1	21	837	857	GGAGCAUCAUCAAGAUUCACA	AGGGAGCCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g017770.1	3.0	-1.0	1	21	2793	2813	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g010970.1	3.0	-1.0	1	21	5835	5855	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen07g014000.1	3.0	-1.0	1	21	5784	5804	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g019830.2	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen07g014790.1	3.0	-1.0	1	21	6594	6614	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g026200.1	3.0	-1.0	1	21	6948	6968	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g009630.1	3.0	-1.0	1	21	5727	5747	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g018900.1	3.0	-1.0	1	21	3864	3884	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g016700.1	3.0	-1.0	1	21	4752	4772	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g013650.1	3.0	-1.0	1	21	4245	4265	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g013510.1	3.0	-1.0	1	21	6216	6236	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen02g004980.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g026100.1	3.0	-1.0	1	21	4803	4823	GGAGCAUCAUCAAGAUUCACA	GAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g013180.1	3.0	-1.0	1	21	4908	4928	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g018890.1	3.0	-1.0	1	21	5787	5807	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen10g010280.1	3.0	-1.0	1	21	4920	4940	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g009900.1	3.0	-1.0	1	21	5220	5240	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g017390.1	3.0	-1.0	1	21	6684	6704	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g017320.1	3.0	-1.0	1	21	4989	5009	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g024920.1	3.0	-1.0	1	21	1887	1907	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g022810.1	3.0	-1.0	1	21	5646	5666	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g026930.1	3.0	-1.0	1	21	5166	5186	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g021580.1	3.0	-1.0	1	21	4620	4640	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen08g007390.1	3.0	-1.0	1	21	4878	4898	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g013570.1	3.0	-1.0	1	21	4413	4433	GGAGCAUCAUCAAGAUUCACA	AAAGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g013200.1	3.0	-1.0	1	21	4251	4271	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g009770.1	3.0	-1.0	1	21	4179	4199	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen08g016490.1	3.0	-1.0	1	21	6180	6200	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g018920.1	3.0	-1.0	1	21	3714	3734	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g009820.1	3.0	-1.0	1	21	4761	4781	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g014260.1	3.0	-1.0	1	21	5424	5444	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g014020.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g016950.1	3.0	-1.0	1	21	4230	4250	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen01g023120.1	3.0	-1.0	1	21	3648	3668	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen08g015720.1	3.0	-1.0	1	21	4911	4931	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen01g009850.1	3.0	-1.0	1	21	3186	3206	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g018670.1	3.0	-1.0	1	21	4904	4924	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen10g011720.1	3.0	-1.0	1	21	3822	3842	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g012180.1	3.0	-1.0	1	21	3513	3533	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g026780.1	3.0	-1.0	1	21	4428	4448	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g014480.1	3.0	-1.0	1	21	4761	4781	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g015680.1	3.0	-1.0	1	21	2883	2903	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g024770.1	3.0	-1.0	1	21	3900	3920	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g012150.1	3.0	-1.0	1	21	3627	3647	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g012560.1	3.0	-1.0	1	21	2868	2888	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g024250.1	3.0	-1.0	1	21	5055	5075	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen10g016750.1	3.0	-1.0	1	21	4014	4034	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen10g017130.1	3.0	-1.0	1	21	882	902	GGAGCAUCAUCAAGAUUCACA	AAGGAGCCUUGAUGAUGCUCU	Cleavage

spe-miR172d-5p	Sopen08g008620.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen08g006580.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g014720.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen11g019830.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g026030.1	3.0	-1.0	1	21	4998	5018	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g014690.1	3.0	-1.0	1	21	3162	3182	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen10g016150.1	3.0	-1.0	1	21	3363	3383	GGAGCAUCAUCAAGAUUCACA	AAAGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g014870.1	3.0	-1.0	1	21	2934	2954	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen07g012820.1	3.0	-1.0	1	21	4878	4898	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g020910.1	3.0	-1.0	1	21	3453	3473	GGAGCAUCAUCAAGAUUCACA	AAGGAGACUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g020240.1	3.0	-1.0	1	21	3810	3830	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g021270.1	3.0	-1.0	1	21	1794	1814	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g015770.1	3.0	-1.0	1	21	3543	3563	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g006200.1	3.0	-1.0	1	21	2580	2600	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen09g025870.1	3.0	-1.0	1	21	3048	3068	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen03g011210.1	3.0	-1.0	1	21	3369	3389	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen06g016150.1	3.0	-1.0	1	21	3567	3587	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g011970.1	3.0	-1.0	1	21	4071	4091	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen10g011940.1	3.0	-1.0	1	21	3051	3071	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen12g015150.1	3.0	-1.0	1	21	4530	4550	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g014900.1	3.0	-1.0	1	21	2970	2990	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen04g013650.1	3.0	-1.0	1	21	4053	4073	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR172d-5p	Sopen05g016320.1	3.0	-1.0	1	21	4293	4313	GGAGCAUCAUCAAGAUUCACA	AAGGAGGCUUGAUGAUGCUCU	Cleavage
spe-miR1886-1-3p	Sopen10g017470.1	2.5	-1.0	1	24	476	499	AUUUUACGUUGAUUUCAUCUCAUG	CAGGCGAUGAAAUCGAUGUAAAGC	Cleavage
spe-miR1886-1-3p	Sopen03g039620.1	2.5	-1.0	1	24	71	94	AUUUUACGUUGAUUUCAUCUCAUG	ACGUUGAUGAUAUCAAUGUGAAGU	Cleavage
spe-miR1886-1-3p	Sopen12g013920.1	3.0	-1.0	1	24	2223	2246	AUUUUACGUUGAUUUCAUCUCAUG	CGUUGGAUCAGAUCAAUGUAAAAC	Cleavage
spe-miR1886-1-3p	Sopen02g016750.1	3.0	-1.0	1	24	467	490	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
spe-miR1886-1-3p	Sopen02g016740.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
spe-miR1886-1-3p	Sopen10g024790.1	3.0	-1.0	1	24	392	415	AUUUUACGUUGAUUUCAUCUCAUG	UCACGGGUGAAAUCAGCGUGGAAC	Cleavage
spe-miR1886-1-3p	Sopen10g028230.3	3.0	-1.0	1	24	650	673	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886-1-3p	Sopen10g028230.1	3.0	-1.0	1	24	1439	1462	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886-1-3p	Sopen10g028230.2	3.0	-1.0	1	24	1439	1462	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886-1-3p	Sopen12g020640.4	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886-1-3p	Sopen01g053180.1	3.0	-1.0	1	24	434	457	AUUUUACGUUGAUUUCAUCUCAUG	UCACUGGUGAAAUCAGUGUAGAAC	Cleavage
spe-miR1886-1-3p	Sopen12g020640.2	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886-1-3p	Sopen12g020640.3	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886-1-3p	Sopen12g020640.1	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886-1-3p	Sopen03g030390.1	3.0	-1.0	1	24	1925	1948	AUUUUACGUUGAUUUCAUCUCAUG	UGGCUGAUGAAAUCAAUGGAAAAC	Cleavage
spe-miR1886-1-3p	Sopen08g021570.1	3.0	-1.0	1	24	850	873	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUUAUGAAGUCAGCGUGGAAU	Cleavage
spe-miR1886-1-3p	Sopen08g021560.1	3.0	-1.0	1	24	853	876	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUCAUGAAGUCAGCGUGGAAU	Cleavage
spe-miR1886-1-3p	Sopen12g031570.1	3.0	-1.0	1	24	538	561	AUUUUACGUUGAUUUCAUCUCAUG	AUAUUGAUGAAAUCAACAGAAAAU	Cleavage
spe-miR1886-1-5p	Sopen09g032540.1	2.5	-1.0	1	24	287	310	AUGAGAUGGAAUUAGGGUUUGGAC	ACCCUAACCCUAGUUUUGUUUCAU	Cleavage
spe-miR1886-1-5p	Sopen07g014840.1	1.5	-1.0	1	24	368	391	AUGAGAUGGAAUUAGGGUUUGGAC	GCUCCAGCCAUAAUUCCAUCUCAU	Cleavage
spe-miR1886-1-5p	Sopen03g020830.1	2.0	-1.0	1	24	101	124	AUGAGAUGGAAUUAGGGUUUGGAC	UUUCGAAUCCUAAUUCCUUCUCAU	Cleavage
spe-miR1886-1-5p	Sopen01g002530.1	2.0	-1.0	1	24	28	51	AUGAGAUGGAAUUAGGGUUUGGAC	ACAAAAACCCUAAUUCCAUCUUGG	Cleavage
spe-miR1886-1-5p	Sopen01g045460.1	2.0	-1.0	1	24	770	793	AUGAGAUGGAAUUAGGGUUUGGAC	ACAAAAACCCUAAUUUCAUCUCUU	Cleavage
spe-miR1886-1-5p	Sopen05g005910.1	2.5	-1.0	1	24	1082	1105	AUGAGAUGGAAUUAGGGUUUGGAC	CCCCAAAUUCUGAUUCCGUCUUAU	Cleavage
spe-miR1886-1-5p	Sopen09g007670.1	2.5	-1.0	1	24	1996	2019	AUGAGAUGGAAUUAGGGUUUGGAC	CAAAAAACCUUCAUUCCAUCUUAU	Cleavage
spe-miR1886-1-5p	Sopen08g022040.1	2.5	-1.0	1	24	83	106	AUGAGAUGGAAUUAGGGUUUGGAC	CUAAAAACCCUAAUUCCUUUUCGU	Cleavage
spe-miR1886-1-5p	Sopen03g026660.1	2.5	-1.0	1	24	18	41	AUGAGAUGGAAUUAGGGUUUGGAC	UAACCAAUUCUGGUUCUAUCUCAU	Cleavage

spe-miR1886-1-5p	Sopen04g033400.1	3.0	-1.0	1	24	968	991	AUGAGAUGGAAUUAGGGUUUGGAC	AUCAAAACCCUAAUUCCAACUCGG	Cleavage
spe-miR1886-1-5p	Sopen03g023670.1	3.0	-1.0	1	24	961	984	AUGAGAUGGAAUUAGGGUUUGGAC	UACCAAAUCCCAAUCCCAUCUCAU	Translation
spe-miR1886-1-5p	Sopen09g002940.1	3.0	-1.0	1	24	28	51	AUGAGAUGGAAUUAGGGUUUGGAC	AUCGGCGUUCUAAUUCUAUCUCAU	Cleavage
spe-miR1886-1-5p	Sopen08g018260.1	3.0	-1.0	1	24	370	393	AUGAGAUGGAAUUAGGGUUUGGAC	ACUAGAGCUCUGAUUCCAUCUCCU	Cleavage
spe-miR1886-1-5p	Sopen07g020840.1	3.0	-1.0	1	24	412	435	AUGAGAUGGAAUUAGGGUUUGGAC	AAACCAAUCUUAAUUCCACCUUAU	Cleavage
spe-miR1886-2-3p	Sopen04g005360.1	3.0	-1.0	1	24	1888	1911	AUUUUACGCUGAUUCCAUCUCAUG	GAGGGGAUGGAAUCAGAGAAAAAU	Cleavage
spe-miR1886-2-3p	Sopen06g009720.1	3.0	-1.0	1	24	513	536	AUUUUACGCUGAUUCCAUCUCAUG	UGAGAGAGAGAGUCAGCGUAAGAU	Cleavage
spe-miR1886-2-3p	Sopen01g042380.1	3.0	-1.0	1	24	1112	1135	AUUUUACGCUGAUUCCAUCUCAUG	GAAUUGGUGGAAACGGCGUAGAAU	Cleavage
spe-miR1886-2-3p	Sopen04g023030.1	3.0	-1.0	1	24	2957	2980	AUUUUACGCUGAUUCCAUCUCAUG	CUGGUGGUGUAGUUAGUGUAAAAU	Cleavage
spe-miR1886-2-5p	Sopen07g017560.1	3.0	-1.0	1	24	73	95	AUGGUAUCGUGAGAUGAAAUCAGC	GCUG-UUUCAUCUCAAGAUGCCAA	Cleavage
spe-miR1886-2-5p	Sopen11g001080.1	3.0	-1.0	1	24	45	68	AUGGUAUCGUGAGAUGAAAUCAGC	CUUUGUUUCAUCCCAUGAUACCAG	Cleavage
spe-miR1886h-1-3p	Sopen10g017470.1	2.5	-1.0	1	24	476	499	AUUUUACGUUGAUUUCAUCUCAUG	CAGGCGAUGAAAUCGAUGUAAAGC	Cleavage
spe-miR1886h-1-3p	Sopen03g039620.1	2.5	-1.0	1	24	71	94	AUUUUACGUUGAUUUCAUCUCAUG	ACGUUGAUGAUAUCAAUGUGAAGU	Cleavage
spe-miR1886h-1-3p	Sopen12g013920.1	3.0	-1.0	1	24	2223	2246	AUUUUACGUUGAUUUCAUCUCAUG	CGUUGGAUCAGAUCAAUGUAAAAC	Cleavage
spe-miR1886h-1-3p	Sopen02g016750.1	3.0	-1.0	1	24	467	490	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
spe-miR1886h-1-3p	Sopen02g016740.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
spe-miR1886h-1-3p	Sopen10g024790.1	3.0	-1.0	1	24	392	415	AUUUUACGUUGAUUUCAUCUCAUG	UCACGGGUGAAAUCAGCGUGGAAC	Cleavage
spe-miR1886h-1-3p	Sopen10g028230.3	3.0	-1.0	1	24	650	673	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886h-1-3p	Sopen10g028230.1	3.0	-1.0	1	24	1439	1462	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886h-1-3p	Sopen10g028230.2	3.0	-1.0	1	24	1439	1462	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886h-1-3p	Sopen12g020640.4	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-1-3p	Sopen01g053180.1	3.0	-1.0	1	24	434	457	AUUUUACGUUGAUUUCAUCUCAUG	UCACUGGUGAAAUCAGUGUAGAAC	Cleavage
spe-miR1886h-1-3p	Sopen12g020640.2	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-1-3p	Sopen12g020640.3	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-1-3p	Sopen12g020640.1	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-1-3p	Sopen03g030390.1	3.0	-1.0	1	24	1925	1948	AUUUUACGUUGAUUUCAUCUCAUG	UGGCUGAUGAAAUCAAUGGAAAAC	Cleavage
spe-miR1886h-1-3p	Sopen08g021570.1	3.0	-1.0	1	24	850	873	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUUAUGAAGUCAGCGUGGAAU	Cleavage
spe-miR1886h-1-3p	Sopen08g021560.1	3.0	-1.0	1	24	853	876	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUCAUGAAGUCAGCGUGGAAU	Cleavage
spe-miR1886h-1-3p	Sopen12g031570.1	3.0	-1.0	1	24	538	561	AUUUUACGUUGAUUUCAUCUCAUG	AUAUUGAUGAAAUCAACAGAAAAU	Cleavage
spe-miR1886h-2-5p	Sopen10g017470.1	2.5	-1.0	1	24	476	499	AUUUUACGUUGAUUUCAUCUCAUG	CAGGCGAUGAAAUCGAUGUAAAGC	Cleavage
spe-miR1886h-2-5p	Sopen03g039620.1	2.5	-1.0	1	24	71	94	AUUUUACGUUGAUUUCAUCUCAUG	ACGUUGAUGAUAUCAAUGUGAAGU	Cleavage
spe-miR1886h-2-	Sopen12g013920.1	3.0	-1.0	1	24	2223	2246	AUUUUACGUUGAUUUCAUCUCAUG	CGUUGGAUCAGAUCAAUGUAAAAC	Cleavage

5p										
spe-miR1886h-2-5p	Sopen02g016750.1	3.0	-1.0	1	24	467	490	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
spe-miR1886h-2-5p	Sopen02g016740.1	3.0	-1.0	1	24	575	598	AUUUUACGUUGAUUUCAUCUCAUG	ACACAGAUGGAAUUCAUGUAAAAU	Translation
spe-miR1886h-2-5p	Sopen10g024790.1	3.0	-1.0	1	24	392	415	AUUUUACGUUGAUUUCAUCUCAUG	UCACGGGUGAAAUCAGCGUGGAAC	Cleavage
spe-miR1886h-2-5p	Sopen10g028230.3	3.0	-1.0	1	24	650	673	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886h-2-5p	Sopen10g028230.1	3.0	-1.0	1	24	1439	1462	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886h-2-5p	Sopen10g028230.2	3.0	-1.0	1	24	1439	1462	AUUUUACGUUGAUUUCAUCUCAUG	AAGGUGAUGAAAUCAGCCUGGAAU	Cleavage
spe-miR1886h-2-5p	Sopen12g020640.4	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-2-5p	Sopen01g053180.1	3.0	-1.0	1	24	434	457	AUUUUACGUUGAUUUCAUCUCAUG	UCACUGGUGAAAUCAGUGUAGAAC	Cleavage
spe-miR1886h-2-5p	Sopen12g020640.2	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-2-5p	Sopen12g020640.3	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-2-5p	Sopen12g020640.1	3.0	-1.0	1	24	563	586	AUUUUACGUUGAUUUCAUCUCAUG	ACAUUGGUGGAAUCAAUGUAGAAG	Cleavage
spe-miR1886h-2-5p	Sopen03g030390.1	3.0	-1.0	1	24	1925	1948	AUUUUACGUUGAUUUCAUCUCAUG	UGGCUGAUGAAAUCAAUGGAAAAC	Cleavage
spe-miR1886h-2-5p	Sopen08g021570.1	3.0	-1.0	1	24	850	873	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUUAUGAAGUCAGCGUGGAAU	Cleavage
spe-miR1886h-2-5p	Sopen08g021560.1	3.0	-1.0	1	24	853	876	AUUUUACGUUGAUUUCAUCUCAUG	AUCUUCAUGAAGUCAGCGUGGAAU	Cleavage
spe-miR1886h-2-5p	Sopen12g031570.1	3.0	-1.0	1	24	538	561	AUUUUACGUUGAUUUCAUCUCAUG	AUAUUGAUGAAAUCAACAGAAAAU	Cleavage
spe-miR1917-1-5p	Sopen11g005350.1	3.0	-1.0	1	21	937	957	AUUAAUAAAGAGUGCUAAAGU	UCGUUGGCACUUUUUAUUGGU	Cleavage
spe-miR1917-2-5p	Sopen11g005350.1	3.0	-1.0	1	21	937	957	AUUAAUAAAGAGUGCUAAAGU	UCGUUGGCACUUUUUAUUGGU	Cleavage
spe-miR1917-3-5p	Sopen11g005350.1	3.0	-1.0	1	21	937	957	AUUAAUAAAGAGUGCUAAAGU	UCGUUGGCACUUUUUAUUGGU	Cleavage
spe-miR1917-4-5p	Sopen11g005350.1	3.0	-1.0	1	21	937	957	AUUAAUAAAGAGUGCUAAAGU	UCGUUGGCACUUUUUAUUGGU	Cleavage
spe-miR1918-5p	Sopen07g022010.1	2.0	-1.0	1	22	989	1010	UGUUGGUGAGAGUUCGAUUCUC	AGCAGUUGCACUCUCACCAACA	Cleavage
spe-miR1918-5p	Sopen10g023960.1	2.5	-1.0	1	22	70	91	UGUUGGUGAGAGUUCGAUUCUC	CGGAAUCGAACUCUUGUCAAUG	Cleavage
spe-miR1918-5p	Sopen02g014550.1	2.5	-1.0	1	22	148	169	UGUUGGUGAGAGUUCGAUUCUC	ACCCAUCGAACUUUUACCAAUA	Cleavage
spe-miR1918-5p	Sopen01g036550.1	2.5	-1.0	1	22	561	582	UGUUGGUGAGAGUUCGAUUCUC	UUUAGUCGAAUUUUUACCAGCA	Cleavage
spe-miR1918-5p	Sopen03g041530.1	2.5	-1.0	1	22	708	729	UGUUGGUGAGAGUUCGAUUCUC	UGCAAUUGGACUCUUGCCAGCA	Cleavage
spe-miR1918-5p	Sopen09g033270.1	3.0	-1.0	1	22	4	25	UGUUGGUGAGAGUUCGAUUCUC	AAGAAUCAAAGUUUCACCAACA	Cleavage
spe-miR1918-5p	Sopen01g022820.1	3.0	-1.0	1	22	190	211	UGUUGGUGAGAGUUCGAUUCUC	AUGAAUAGAACUCUUAUUGACA	Cleavage
spe-miR1918-5p	Sopen00g001680.1	3.0	-1.0	1	22	227	248	UGUUGGUGAGAGUUCGAUUCUC	CGCUAUCGGACUCUCGCCAGUA	Cleavage
spe-miR1918-5p	Sopen07g011570.3	3.0	-1.0	1	22	34	55	UGUUGGUGAGAGUUCGAUUCUC	UUUGAUCGGACUCUCAUUGACG	Cleavage
spe-miR1918-5p	Sopen07g011570.2	3.0	-1.0	1	22	34	55	UGUUGGUGAGAGUUCGAUUCUC	UUUGAUCGGACUCUCAUUGACG	Cleavage
spe-miR1918-5p	Sopen07g011570.1	3.0	-1.0	1	22	34	55	UGUUGGUGAGAGUUCGAUUCUC	UUUGAUCGGACUCUCAUUGACG	Cleavage
spe-miR1918-5p	Sopen10g002640.1	3.0	-1.0	1	22	2146	2166	UGUUGGUGAGAGUUCGAUUCUC	GACAAU-GAACUUUCACUAACA	Cleavage
spe-miR1918-5p	Sopen06g013670.1	3.0	-1.0	1	22	434	455	UGUUGGUGAGAGUUCGAUUCUC	AGAAAUCUAACUUUUACCAACC	Cleavage
spe-miR1918-5p	Sopen01g048650.1	3.0	-1.0	1	22	924	945	UGUUGGUGAGAGUUCGAUUCUC	UAAGAUAGAGCUUUCAUCAACA	Cleavage
spe-miR1918-5p	Sopen01g048620.1	3.0	-1.0	1	22	954	975	UGUUGGUGAGAGUUCGAUUCUC	UAAGAUAGAGCUUUCAUCAACA	Cleavage
spe-miR1919-3p	Sopen12g007740.1	3.0	-1.0	1	21	76	96	ACGAGAGUCAUCUGUGACAGG	GAAUUUACAGAUGAUUCUCGU	Cleavage

spe-miR1919-5p	Sopen08g021530.1	0.0	-1.0	1	21	284	304	UGUCGCAGAUGACUUUCGCCC	ACGCGAAAGUCAUCUGCGACA	Cleavage
spe-miR1919-5p	Sopen08g021530.1	2.0	-1.0	1	21	463	483	UGUCGCAGAUGACUUUCGCCC	GGACGAGAGUCAUCUGUGACA	Cleavage
spe-miR1919-5p	Sopen08g021500.1	0.0	-1.0	1	21	287	307	UGUCGCAGAUGACUUUCGCCC	ACGCGAAAGUCAUCUGCGACA	Cleavage
spe-miR1919-5p	Sopen12g008360.1	2.0	-1.0	1	21	176	196	UGUCGCAGAUGACUUUCGCCC	GGACGAGAGUCAUCUGUGACA	Cleavage
spe-miR1919-5p	Sopen01g002930.1	3.0	-1.0	1	21	764	784	UGUCGCAGAUGACUUUCGCCC	GUGCAAAAGUCAUCUAUGACA	Cleavage
spe-miR1919-5p	Sopen04g014770.1	3.0	-1.0	1	21	3097	3117	UGUCGCAGAUGACUUUCGCCC	CUGCAAAAGUCGUCUGCAACA	Cleavage
spe-miR1919c-3p	Sopen12g007740.1	3.0	-1.0	1	21	76	96	ACGAGAGUCAUCUGUGACAGG	GAAUUUACAGAUGAUUCUCGU	Cleavage
spe-miR1919c-5p	Sopen08g021530.1	0.0	-1.0	1	21	284	304	UGUCGCAGAUGACUUUCGCCC	ACGCGAAAGUCAUCUGCGACA	Cleavage
spe-miR1919c-5p	Sopen08g021530.1	2.0	-1.0	1	21	463	483	UGUCGCAGAUGACUUUCGCCC	GGACGAGAGUCAUCUGUGACA	Cleavage
spe-miR1919c-5p	Sopen08g021500.1	0.0	-1.0	1	21	287	307	UGUCGCAGAUGACUUUCGCCC	ACGCGAAAGUCAUCUGCGACA	Cleavage
spe-miR1919c-5p	Sopen12g008360.1	2.0	-1.0	1	21	176	196	UGUCGCAGAUGACUUUCGCCC	GGACGAGAGUCAUCUGUGACA	Cleavage
spe-miR1919c-5p	Sopen01g002930.1	3.0	-1.0	1	21	764	784	UGUCGCAGAUGACUUUCGCCC	GUGCAAAAGUCAUCUAUGACA	Cleavage
spe-miR1919c-5p	Sopen04g014770.1	3.0	-1.0	1	21	3097	3117	UGUCGCAGAUGACUUUCGCCC	CUGCAAAAGUCGUCUGCAACA	Cleavage
spe-miR2111a-3p	Sopen05g027760.2	3.0	-1.0	1	21	148	168	GUCCUUAGGAUGCAGAUUAUC	UCUAAUCAGAAUCCUAAGGAU	Cleavage
spe-miR2111a-3p	Sopen05g027760.1	3.0	-1.0	1	21	4297	4317	GUCCUUAGGAUGCAGAUUAUC	UCUAAUCAGAAUCCUAAGGAU	Cleavage
spe-miR2111a-5p	Sopen07g005160.1	0.0	-1.0	1	21	186	206	UAAUCUGCAUCCUGAGGUUUA	ACAACCUCAGGAUGCAGAUUA	Cleavage
spe-miR2111a-5p	Sopen03g040700.1	2.5	-1.0	1	21	636	656	UAAUCUGCAUCCUGAGGUUUA	AGGAUCUCAGGUUGCAGAUUA	Translation
spe-miR2111a-5p	Sopen03g040700.2	2.5	-1.0	1	21	828	848	UAAUCUGCAUCCUGAGGUUUA	AGGAUCUCAGGUUGCAGAUUA	Translation
spe-miR2111a-5p	Sopen02g036490.1	3.0	-1.0	1	21	190	210	UAAUCUGCAUCCUGAGGUUUA	CAAAACUCAGGAUGUGGAUUU	Cleavage
spe-miR2111a-5p	Sopen11g004550.1	3.0	-1.0	1	21	150	170	UAAUCUGCAUCCUGAGGUUUA	UCAACCUCAGAAUGCAGAUAA	Translation
spe-miR319-1-3p	Sopen01g004560.1	1.5	-1.0	1	21	925	945	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319-1-3p	Sopen01g004560.2	1.5	-1.0	1	21	955	975	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319-1-3p	Sopen02g023820.1	2.0	-1.0	1	21	304	324	UUGGACUGAAGGGAGCUCCCU	UCGGAGCUUCAUUCAGUCCAA	Translation
spe-miR319-1-3p	Sopen06g030050.1	2.5	-1.0	1	21	979	999	UUGGACUGAAGGGAGCUCCCU	CUCGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319-1-3p	Sopen08g015840.1	2.5	-1.0	1	21	867	887	UUGGACUGAAGGGAGCUCCCU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen08g010620.1	2.5	-1.0	1	21	1020	1040	UUGGACUGAAGGGAGCUCCCU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen08g010620.2	2.5	-1.0	1	21	1080	1100	UUGGACUGAAGGGAGCUCCCU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen02g007680.1	3.0	-1.0	1	21	1700	1720	UUGGACUGAAGGGAGCUCCCU	GAGGAGCUCCAUUCAGUUCAU	Translation
spe-miR319-1-3p	Sopen07g027370.1	3.0	-1.0	1	21	736	755	UUGGACUGAAGGGAGCUCCCU	AGGGAAC-CCCUUCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen01g006470.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen11g029710.1	3.0	-1.0	1	21	913	933	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCUUUCCAA	Cleavage
spe-miR319-1-3p	Sopen09g017170.1	3.0	-1.0	1	21	392	412	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen12g016000.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen04g017170.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen07g025660.2	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen01g007850.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-3p	Sopen03g012270.1	3.0	-1.0	1	21	3113	3133	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-1-5p	Sopen09g012310.1	2.0	-1.0	1	20	1573	1592	GAGCUCUCUCCGGUCCAGUC	AACUGGAUUGGAGAGGGUUC	Cleavage
spe-miR319-1-5p	Sopen03g023000.1	3.0	-1.0	1	20	504	523	GAGCUCUCUCCGGUCCAGUC	AAUUGGACAGGAGAGAGCUA	Cleavage
spe-miR319-1-5p	Sopen03g022580.1	3.0	-1.0	1	20	202	221	GAGCUCUCUCCGGUCCAGUC	UACUGGACUGAAGGGGGCUC	Translation
spe-miR319-1-5p	Sopen04g001560.1	3.0	-1.0	1	20	2260	2279	GAGCUCUCUCCGGUCCAGUC	GAUUCAACCGGAGAGGGCUC	Cleavage
spe-miR319-1-5p	Sopen11g026190.1	3.0	-1.0	1	20	615	634	GAGCUCUCUCCGGUCCAGUC	AAAUGGAUGGGAGAGAGCUC	Cleavage
spe-miR319-2-3p	Sopen01g004560.1	1.5	-1.0	1	21	925	945	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319-2-3p	Sopen01g004560.2	1.5	-1.0	1	21	955	975	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319-2-3p	Sopen02g023820.1	2.0	-1.0	1	21	304	324	UUGGACUGAAGGGAGCUCCCU	UCGGAGCUUCAUUCAGUCCAA	Translation
spe-miR319-2-3p	Sopen06g030050.1	2.5	-1.0	1	21	979	999	UUGGACUGAAGGGAGCUCCCU	CUCGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319-2-3p	Sopen08g015840.1	2.5	-1.0	1	21	867	887	UUGGACUGAAGGGAGCUCCCU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen08g010620.1	2.5	-1.0	1	21	1020	1040	UUGGACUGAAGGGAGCUCCCU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen08g010620.2	2.5	-1.0	1	21	1080	1100	UUGGACUGAAGGGAGCUCCCU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen02g007680.1	3.0	-1.0	1	21	1700	1720	UUGGACUGAAGGGAGCUCCCU	GAGGAGCUCCAUUCAGUUCAU	Translation

spe-miR319-2-3p	Sopen07g027370.1	3.0	-1.0	1	21	736	755	UUGGACUGAAGGGAGCUCCCU	AGGGAAC-CCCUUCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen01g006470.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen11g029710.1	3.0	-1.0	1	21	913	933	UUGGACUGAAGGGAGCUCCCU	CUGGAGCUCCCUUCUUUCCAA	Cleavage
spe-miR319-2-3p	Sopen09g017170.1	3.0	-1.0	1	21	392	412	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen12g016000.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen04g017170.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen07g025660.2	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen01g007850.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-3p	Sopen03g012270.1	3.0	-1.0	1	21	3113	3133	UUGGACUGAAGGGAGCUCCCU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319-2-5p	Sopen04g033650.1	2.5	-1.0	1	21	406	426	AGAGCUUCCUUUAGUCCACUC	GAGUGGAUUAGAGGAAGCUUG	Cleavage
spe-miR319-2-5p	Sopen03g022580.1	2.5	-1.0	1	21	202	222	AGAGCUUCCUUUAGUCCACUC	UACUGGACUGAAGGGGGCUCU	Cleavage
spe-miR319-2-5p	Sopen03g032150.1	2.5	-1.0	1	21	2573	2592	AGAGCUUCCUUUAGUCCACUC	AAGUGG-CUGAAGGAAGCUCU	Cleavage
spe-miR319-2-5p	Sopen01g051280.1	3.0	-1.0	1	21	9279	9299	AGAGCUUCCUUUAGUCCACUC	GAGUGAGUUGAAGGAGGCUCU	Cleavage
spe-miR319-2-5p	Sopen07g029050.1	3.0	-1.0	1	21	604	624	AGAGCUUCCUUUAGUCCACUC	AACUGGACUAAAGGAGGCUUG	Cleavage
spe-miR319-2-5p	Sopen08g024020.1	3.0	-1.0	1	21	2028	2048	AGAGCUUCCUUUAGUCCACUC	CUUUGGAUUAGAGGAAGCUCA	Cleavage
spe-miR319-2-5p	Sopen03g001620.1	3.0	-1.0	1	21	628	648	AGAGCUUCCUUUAGUCCACUC	GGAUGGUCUAAAGGGAGUUCU	Cleavage
spe-miR319-2-5p	Sopen07g006170.1	3.0	-1.0	1	21	1629	1649	AGAGCUUCCUUUAGUCCACUC	GCUUGAACUAAAGGAAGCUCA	Cleavage
spe-miR319-2-5p	Sopen03g036860.1	3.0	-1.0	1	21	492	512	AGAGCUUCCUUUAGUCCACUC	UAUUGGAAUAGAGGAAGCUUU	Cleavage
spe-miR319-2-5p	Sopen08g029370.1	3.0	-1.0	1	21	1461	1481	AGAGCUUCCUUUAGUCCACUC	CAAUGAGCUAAAGGAAGCUUU	Cleavage
spe-miR319-2-5p	Sopen04g029080.1	3.0	-1.0	1	21	72	92	AGAGCUUCCUUUAGUCCACUC	UGGUGAAUUAAUGGAAGCUCU	Translation
spe-miR319-2-5p	Sopen09g005560.1	3.0	-1.0	1	21	5664	5684	AGAGCUUCCUUUAGUCCACUC	UCGUGGUCUAAAGGGUGCUCU	Cleavage
spe-miR319-2-5p	Sopen09g005560.2	3.0	-1.0	1	21	5637	5657	AGAGCUUCCUUUAGUCCACUC	UCGUGGUCUAAAGGGUGCUCU	Cleavage
spe-miR319-2-5p	Sopen00g002540.1	3.0	-1.0	1	21	204	224	AGAGCUUCCUUUAGUCCACUC	CUGUGAACAAGAGGAAGCUCU	Cleavage
spe-miR319-3-3p	Sopen08g015840.1	1.0	-1.0	1	21	867	887	UUGGACUGAAGGGUUCCCUUC	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen08g010620.1	1.0	-1.0	1	21	1020	1040	UUGGACUGAAGGGUUCCCUUC	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen08g010620.2	1.0	-1.0	1	21	1080	1100	UUGGACUGAAGGGUUCCCUUC	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen01g044170.4	1.5	-1.0	1	21	319	339	UUGGACUGAAGGGUUCCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen01g044170.5	1.5	-1.0	1	21	856	876	UUGGACUGAAGGGUUCCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen01g044170.3	1.5	-1.0	1	21	913	933	UUGGACUGAAGGGUUCCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen01g044170.6	1.5	-1.0	1	21	913	933	UUGGACUGAAGGGUUCCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen12g005920.1	2.0	-1.0	1	21	915	935	UUGGACUGAAGGGUUCCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319-3-3p	Sopen07g030910.1	2.0	-1.0	1	21	936	956	UUGGACUGAAGGGUUCCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319-3-3p	Sopen07g027370.1	3.0	-1.0	1	21	734	755	UUGGACUGAA-GGGUUCCCUUC	AAAGGGAACCCCUUCAGUCCAA	Translation
spe-miR319-3-3p	Sopen05g026990.1	3.0	-1.0	1	21	217	237	UUGGACUGAAGGGUUCCCUUC	UCUAGGGACCCUUUAGUCCAA	Cleavage
spe-miR319-3-3p	Sopen06g027780.1	3.0	-1.0	1	21	2052	2072	UUGGACUGAAGGGUUCCCUUC	UCCGGGAACUUUUCAGUCUGA	Cleavage
spe-miR319-3-3p	Sopen12g007190.1	3.0	-1.0	1	21	463	483	UUGGACUGAAGGGUUCCCUUC	UCAGGGAACUUUUCAUUUCAA	Cleavage
spe-miR319-3-5p	Sopen12g033930.1	2.0	-1.0	1	21	568	588	AGGAAACUGUUUAGUCCAACC	AGUUGGACUGGACAGUUUCCA	Cleavage
spe-miR319-3-5p	Sopen05g033370.3	2.5	-1.0	1	21	1351	1371	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
spe-miR319-3-5p	Sopen05g033370.1	2.5	-1.0	1	21	1693	1713	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
spe-miR319-3-5p	Sopen05g033370.4	2.5	-1.0	1	21	1750	1770	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
spe-miR319-3-5p	Sopen06g014680.1	2.5	-1.0	1	21	448	468	AGGAAACUGUUUAGUCCAACC	AGGUGGAUUGAACAGUUUCUU	Cleavage
spe-miR319-3-5p	Sopen01g025170.1	2.5	-1.0	1	21	526	546	AGGAAACUGUUUAGUCCAACC	AAUUGGACUGGACAAUUUCCU	Cleavage
spe-miR319-3-5p	Sopen02g005300.1	3.0	-1.0	1	21	471	491	AGGAAACUGUUUAGUCCAACC	GUUUGGAUUAGUUAGUUUCCU	Translation
spe-miR319-3-5p	Sopen02g014300.1	3.0	-1.0	1	21	723	743	AGGAAACUGUUUAGUCCAACC	GUUUGGAUUAAGCACUUUCUU	Cleavage
spe-miR319-3-5p	Sopen05g031160.1	3.0	-1.0	1	21	542	562	AGGAAACUGUUUAGUCCAACC	CUCUGGACUCAACAGUUUUCU	Cleavage
spe-miR319-3-5p	Sopen05g031160.2	3.0	-1.0	1	21	1187	1207	AGGAAACUGUUUAGUCCAACC	CUCUGGACUCAACAGUUUUCU	Cleavage
spe-miR319-3-5p	Sopen06g017200.1	3.0	-1.0	1	21	100	120	AGGAAACUGUUUAGUCCAACC	UAUUGGUCUCAACAGUUUUCU	Cleavage
spe-miR319-3-5p	Sopen10g010800.1	3.0	-1.0	1	21	619	639	AGGAAACUGUUUAGUCCAACC	AAUUGGAAUAAGCAUUUUCCU	Cleavage
spe-miR319-3-5p	Sopen07g014820.1	3.0	-1.0	1	21	1303	1323	AGGAAACUGUUUAGUCCAACC	AAUUGGGAUAAACAUUUUCCU	Cleavage
spe-miR319-3-5p	Sopen10g010800.2	3.0	-1.0	1	21	4588	4608	AGGAAACUGUUUAGUCCAACC	AAUUGGAAUAAGCAUUUUCCU	Cleavage

spe-miR319-4-3p	Sopen08g015840.1	1.5	-1.0	1	21	867	887	UUGGACUGAAGGGUUUCCUUC	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen08g010620.1	1.5	-1.0	1	21	1020	1040	UUGGACUGAAGGGUUUCCUUC	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen08g010620.2	1.5	-1.0	1	21	1080	1100	UUGGACUGAAGGGUUUCCUUC	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen07g027370.1	1.5	-1.0	1	21	735	755	UUGGACUGAAGGGUUUCCUUC	AAGGGAACCCCUUCAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen01g044170.4	2.0	-1.0	1	21	319	339	UUGGACUGAAGGGUUUCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen01g044170.5	2.0	-1.0	1	21	856	876	UUGGACUGAAGGGUUUCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen01g044170.3	2.0	-1.0	1	21	913	933	UUGGACUGAAGGGUUUCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen01g044170.6	2.0	-1.0	1	21	913	933	UUGGACUGAAGGGUUUCCUUC	GAAGGGAACUUUUUAGUCCAA	Cleavage
spe-miR319-4-3p	Sopen01g007840.1	2.0	-1.0	1	21	749	769	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen06g007580.1	2.0	-1.0	1	21	749	769	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen07g025650.1	2.0	-1.0	1	21	749	769	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen04g017180.1	2.0	-1.0	1	21	821	841	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen02g022170.1	2.0	-1.0	1	21	687	707	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen03g012280.1	2.0	-1.0	1	21	822	842	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen12g015990.1	2.0	-1.0	1	21	6749	6769	UUGGACUGAAGGGUUUCCUUC	CAGGGAACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen12g005920.1	2.5	-1.0	1	21	915	935	UUGGACUGAAGGGUUUCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen07g030910.1	2.5	-1.0	1	21	936	956	UUGGACUGAAGGGUUUCCUUC	GAGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319-4-3p	Sopen01g035040.1	2.5	-1.0	1	21	1484	1504	UUGGACUGAAGGGUUUCCUUC	GGAGGAAACACUUUGGUCCAA	Cleavage
spe-miR319a-3p	Sopen01g004560.1	2.5	-1.0	1	20	927	946	CUUGGACUGAAGGGAGCUCC	GGAGCUCCCUUCACUCCAAA	Cleavage
spe-miR319a-3p	Sopen01g004560.2	2.5	-1.0	1	20	957	976	CUUGGACUGAAGGGAGCUCC	GGAGCUCCCUUCACUCCAAA	Cleavage
spe-miR319a-3p	Sopen06g030050.1	2.5	-1.0	1	20	981	1000	CUUGGACUGAAGGGAGCUCC	CGAGCUCCCUUCACUCCAAA	Cleavage
spe-miR319a-3p	Sopen09g004090.2	2.5	-1.0	1	20	1083	1102	CUUGGACUGAAGGGAGCUCC	AAAGCUCCCUUUAGUUCGAG	Cleavage
spe-miR319a-3p	Sopen09g004090.1	2.5	-1.0	1	20	1083	1102	CUUGGACUGAAGGGAGCUCC	AAAGCUCCCUUUAGUUCGAG	Cleavage
spe-miR319a-3p	Sopen02g023820.1	3.0	-1.0	1	20	306	325	CUUGGACUGAAGGGAGCUCC	GGAGCUUCAUUCAGUCCAAA	Cleavage
spe-miR319a-3p	Sopen10g015400.1	3.0	-1.0	1	20	3	22	CUUGGACUGAAGGGAGCUCC	GGAGUUGCUUUUAGUUCAAG	Cleavage
spe-miR319a-3p	Sopen02g015570.1	3.0	-1.0	1	20	649	668	CUUGGACUGAAGGGAGCUCC	UCAGUUCUCUUCAGUUUAAG	Cleavage
spe-miR319a-3p	Sopen08g002940.1	3.0	-1.0	1	20	1468	1487	CUUGGACUGAAGGGAGCUCC	AGAGCUUUCUUUUGUCCAAG	Cleavage
spe-miR319a-3p	Sopen01g031330.1	3.0	-1.0	1	20	1804	1823	CUUGGACUGAAGGGAGCUCC	AGAUUUCCUUUCAGUUUAAG	Cleavage
spe-miR319a-5p.1	Sopen03g016090.1	2.5	-1.0	1	21	1272	1292	AGAGCUUUCUUCAGUCCACAC	GAGUGAAAUGGAGAAAGCUCU	Cleavage
spe-miR319a-5p.1	Sopen05g003530.1	2.0	-1.0	1	21	2254	2274	AGAGCUUUCUUCAGUCCACAC	UUGUGGAUUGGAGAAGGCUUU	Cleavage
spe-miR319a-5p.1	Sopen01g037870.1	2.0	-1.0	1	21	1828	1848	AGAGCUUUCUUCAGUCCACAC	AAGUUGGCUGAAGAAAGUUCU	Cleavage
spe-miR319a-5p.1	Sopen03g022580.1	2.5	-1.0	1	21	202	222	AGAGCUUUCUUCAGUCCACAC	UACUGGACUGAAGGGGGCUCU	Cleavage
spe-miR319a-5p.1	Sopen05g003520.2	3.0	-1.0	1	21	2224	2244	AGAGCUUUCUUCAGUCCACAC	AUGUGGAUUGCAGAAGGCUUU	Translation
spe-miR319a-5p.1	Sopen05g003520.1	3.0	-1.0	1	21	2224	2244	AGAGCUUUCUUCAGUCCACAC	AUGUGGAUUGCAGAAGGCUUU	Translation
spe-miR319a-5p.1	Sopen01g051280.1	3.0	-1.0	1	21	9279	9299	AGAGCUUUCUUCAGUCCACAC	GAGUGAGUUGAAGGAGGCUCU	Cleavage
spe-miR319a-5p.1	Sopen05g027870.1	3.0	-1.0	1	21	1143	1163	AGAGCUUUCUUCAGUCCACAC	AAGUGAAUUGAAGAGAGUUUU	Cleavage
spe-miR319a-5p.1	Sopen04g002630.1	3.0	-1.0	1	21	1362	1382	AGAGCUUUCUUCAGUCCACAC	CCGUGGAGUGCAGAAAGUUCU	Translation
spe-miR319a-5p.1	Sopen01g011080.1	3.0	-1.0	1	21	285	305	AGAGCUUUCUUCAGUCCACAC	CUAUGUAGUGAAGAAAGCUCU	Cleavage
spe-miR319a-5p.1	Sopen12g018410.1	3.0	-1.0	1	21	102	122	AGAGCUUUCUUCAGUCCACAC	CUAUGUAGUGAAGAAAGCUCU	Cleavage
spe-miR319a-5p.2	Sopen01g031030.2	3.0	-1.0	1	22	40	61	UUGCUGCCGACUCAUUCAUCCA	GUGGUGGAUGACUCGGCAGCGA	Translation
spe-miR319a-5p.2	Sopen01g031030.1	3.0	-1.0	1	22	40	61	UUGCUGCCGACUCAUUCAUCCA	GUGGUGGAUGACUCGGCAGCGA	Translation
spe-miR319a-5p.2	Sopen06g028860.1	3.0	-1.0	1	22	538	559	UUGCUGCCGACUCAUUCAUCCA	GACCUGAAGGAGUUGGUAGCAA	Cleavage
spe-miR319a-5p.2	Sopen03g041030.1	3.0	-1.0	1	22	13	34	UUGCUGCCGACUCAUUCAUCCA	GUAAUCAGUGAGUCGGCGGUAG	Cleavage
spe-miR319a-5p.2	Sopen04g035740.1	3.0	-1.0	1	22	1415	1435	UUGCUGCCGACUCAUUCAUCCA	CAGCUGAA-GAGUCGGCAGCAA	Cleavage
spe-miR319c-1-3p	Sopen01g004560.1	1.5	-1.0	1	20	926	945	UUGGACUGAAGGGAGCUCCU	UGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319c-1-3p	Sopen01g004560.2	1.5	-1.0	1	20	956	975	UUGGACUGAAGGGAGCUCCU	UGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319c-1-3p	Sopen02g023820.1	2.0	-1.0	1	20	305	324	UUGGACUGAAGGGAGCUCCU	CGGAGCUUCAUUCAGUCCAA	Translation
spe-miR319c-1-3p	Sopen06g030050.1	2.5	-1.0	1	20	980	999	UUGGACUGAAGGGAGCUCCU	UCGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319c-1-3p	Sopen08g015840.1	2.5	-1.0	1	20	868	887	UUGGACUGAAGGGAGCUCCU	AGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen08g010620.1	2.5	-1.0	1	20	1021	1040	UUGGACUGAAGGGAGCUCCU	AGGGGGACCCUUCAGUCCAA	Cleavage

spe-miR319c-1-3p	Sopen08g010620.2	2.5	-1.0	1	20	1081	1100	UUGGACUGAAGGGAGCUCCU	AGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen02g007680.1	3.0	-1.0	1	20	1701	1720	UUGGACUGAAGGGAGCUCCU	AGGAGCUCCAUUCAGUUCAU	Translation
spe-miR319c-1-3p	Sopen01g006470.1	3.0	-1.0	1	20	405	424	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen11g029710.1	3.0	-1.0	1	20	914	933	UUGGACUGAAGGGAGCUCCU	UGGAGCUCCCUUCUUUCCAA	Cleavage
spe-miR319c-1-3p	Sopen09g017170.1	3.0	-1.0	1	20	393	412	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen01g007850.1	3.0	-1.0	1	20	405	424	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen12g016000.1	3.0	-1.0	1	20	405	424	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen04g017170.1	3.0	-1.0	1	20	405	424	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen07g025660.2	3.0	-1.0	1	20	405	424	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen03g012270.1	3.0	-1.0	1	20	3114	3133	UUGGACUGAAGGGAGCUCCU	UGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-1-3p	Sopen12g005920.1	3.0	-1.0	1	20	916	935	UUGGACUGAAGGGAGCUCCU	AGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319c-1-3p	Sopen07g030910.1	3.0	-1.0	1	20	937	956	UUGGACUGAAGGGAGCUCCU	AGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319c-1-3p	Sopen06g021440.1	3.0	-1.0	1	20	248	267	UUGGACUGAAGGGAGCUCCU	UGGACAUUUCUUCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen01g004560.1	1.5	-1.0	1	21	925	945	UUGGACUGAAGGGAGCUCCUU	CUGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319c-2-3p	Sopen01g004560.2	1.5	-1.0	1	21	955	975	UUGGACUGAAGGGAGCUCCUU	CUGGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319c-2-3p	Sopen02g023820.1	2.0	-1.0	1	21	304	324	UUGGACUGAAGGGAGCUCCUU	UCGGAGCUUCAUUCAGUCCAA	Translation
spe-miR319c-2-3p	Sopen06g030050.1	2.5	-1.0	1	21	979	999	UUGGACUGAAGGGAGCUCCUU	CUCGAGCUCCCUUCACUCCAA	Cleavage
spe-miR319c-2-3p	Sopen08g015840.1	2.5	-1.0	1	21	867	887	UUGGACUGAAGGGAGCUCCUU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen08g010620.1	2.5	-1.0	1	21	1020	1040	UUGGACUGAAGGGAGCUCCUU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen08g010620.2	2.5	-1.0	1	21	1080	1100	UUGGACUGAAGGGAGCUCCUU	UAGGGGGACCCUUCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen02g007680.1	3.0	-1.0	1	21	1700	1720	UUGGACUGAAGGGAGCUCCUU	GAGGAGCUCCAUUCAGUUCAU	Translation
spe-miR319c-2-3p	Sopen12g005920.1	3.0	-1.0	1	21	915	935	UUGGACUGAAGGGAGCUCCUU	GAGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319c-2-3p	Sopen07g030910.1	3.0	-1.0	1	21	936	956	UUGGACUGAAGGGAGCUCCUU	GAGGGGACCCCUUCAGUCCAG	Cleavage
spe-miR319c-2-3p	Sopen01g006470.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen11g029710.1	3.0	-1.0	1	21	913	933	UUGGACUGAAGGGAGCUCCUU	CUGGAGCUCCCUUCUUUCCAA	Cleavage
spe-miR319c-2-3p	Sopen09g017170.1	3.0	-1.0	1	21	392	412	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen04g017170.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen07g025660.2	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen12g016000.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen01g007850.1	3.0	-1.0	1	21	404	424	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-3p	Sopen03g012270.1	3.0	-1.0	1	21	3113	3133	UUGGACUGAAGGGAGCUCCUU	CUGGAGUUCUUUCCAGUCCAA	Cleavage
spe-miR319c-2-5p.1	Sopen02g038440.1	2.5	-1.0	1	21	1104	1124	AGAGCUUCCUUCAGCCCACUC	AGGUGAGCUGGAGGAGGUUCU	Cleavage
spe-miR319c-2-5p.1	Sopen01g051280.1	2.0	-1.0	1	21	9279	9299	AGAGCUUCCUUCAGCCCACUC	GAGUGAGUUGAAGGAGGCUCU	Cleavage
spe-miR319c-2-5p.1	Sopen03g032150.1	2.0	-1.0	1	21	2573	2592	AGAGCUUCCUUCAGCCCACUC	AAGUGG-CUGAAGGAAGCUCU	Cleavage
spe-miR319c-2-5p.1	Sopen01g030580.1	2.5	-1.0	1	21	543	563	AGAGCUUCCUUCAGCCCACUC	UGGCGGGUUGAAGGAAGCUCA	Cleavage
spe-miR319c-2-5p.1	Sopen06g021180.1	2.5	-1.0	1	21	721	741	AGAGCUUCCUUCAGCCCACUC	AUGUUUGCUGAAGGAAGUUCU	Cleavage
spe-miR319c-2-5p.1	Sopen03g004130.1	2.5	-1.0	1	21	721	741	AGAGCUUCCUUCAGCCCACUC	AUGUUCGCUGAAGGAAGUUCU	Cleavage
spe-miR319c-2-5p.1	Sopen06g017720.1	3.0	-1.0	1	21	1764	1784	AGAGCUUCCUUCAGCCCACUC	GAUUGGGUUGAAGGAAGUUCG	Cleavage
spe-miR319c-2-5p.1	Sopen02g018630.1	3.0	-1.0	1	21	508	528	AGAGCUUCCUUCAGCCCACUC	UUCGGGGUUGAAGGAAGUUCU	Cleavage
spe-miR319c-2-5p.1	Sopen01g037870.1	3.0	-1.0	1	21	1828	1848	AGAGCUUCCUUCAGCCCACUC	AAGUUGGCUGAAGAAAGUUCU	Cleavage
spe-miR319c-2-5p.1	Sopen12g027970.1	3.0	-1.0	1	21	189	209	AGAGCUUCCUUCAGCCCACUC	UGGUGAGCUGAGGGAAGCCCU	Cleavage

spe-miR319c-2-5p.1	Sopen03g022580.1	3.0	-1.0	1	21	202	222	AGAGCUUCCUUCAGCCCACUC	UACUGGACUGAAGGGGGCUCU	Cleavage
spe-miR319c-2-5p.1	Sopen07g025230.1	3.0	-1.0	1	21	1161	1181	AGAGCUUCCUUCAGCCCACUC	UGGUGAGUUGGAGGAGGUUCU	Cleavage
spe-miR319c-2-5p.2	Sopen02g002620.1	3.0	-1.0	1	22	661	682	UAGCUGCCGACUCAUUCAUCCA	AGUGUGAAUGACUUGGCAGCUG	Translation
spe-miR319c-3-3p	Sopen07g001280.3	2.5	-1.0	1	21	1126	1146	CUCCAAUGAUGCAGGAGCUGA	GGCAUUCCUGCAUCAUUGGAG	Cleavage
spe-miR319c-3-3p	Sopen07g001280.2	2.5	-1.0	1	21	1126	1146	CUCCAAUGAUGCAGGAGCUGA	GGCAUUCCUGCAUCAUUGGAG	Cleavage
spe-miR319c-3-3p	Sopen07g001280.1	2.5	-1.0	1	21	1126	1146	CUCCAAUGAUGCAGGAGCUGA	GGCAUUCCUGCAUCAUUGGAG	Cleavage
spe-miR319c-3-3p	Sopen01g034920.1	2.5	-1.0	1	21	499	519	CUCCAAUGAUGCAGGAGCUGA	GGAGCUCUUGCAUUAUUGCAG	Cleavage
spe-miR319c-3-3p	Sopen07g004840.1	3.0	-1.0	1	21	469	489	CUCCAAUGAUGCAGGAGCUGA	ACAGCACCUUUAUCAUUGGAG	Cleavage
spe-miR319c-3-5p	Sopen12g033930.1	2.0	-1.0	1	21	568	588	AGGAAACUGUUUAGUCCAACC	AGUUGGACUGGACAGUUUCCA	Cleavage
spe-miR319c-3-5p	Sopen05g033370.3	2.5	-1.0	1	21	1351	1371	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
spe-miR319c-3-5p	Sopen05g033370.1	2.5	-1.0	1	21	1693	1713	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
spe-miR319c-3-5p	Sopen05g033370.4	2.5	-1.0	1	21	1750	1770	AGGAAACUGUUUAGUCCAACC	AGUUGGAAUAAACAGUUUUCA	Cleavage
spe-miR319c-3-5p	Sopen06g014680.1	2.5	-1.0	1	21	448	468	AGGAAACUGUUUAGUCCAACC	AGGUGGAUUGAACAGUUUCUU	Cleavage
spe-miR319c-3-5p	Sopen01g025170.1	2.5	-1.0	1	21	526	546	AGGAAACUGUUUAGUCCAACC	AAUUGGACUGGACAAUUUCCU	Cleavage
spe-miR319c-3-5p	Sopen02g005300.1	3.0	-1.0	1	21	471	491	AGGAAACUGUUUAGUCCAACC	GUUUGGAUUAGUUAGUUUCCU	Translation
spe-miR319c-3-5p	Sopen02g014300.1	3.0	-1.0	1	21	723	743	AGGAAACUGUUUAGUCCAACC	GUUUGGAUUAAGCACUUUCUU	Cleavage
spe-miR319c-3-5p	Sopen05g031160.1	3.0	-1.0	1	21	542	562	AGGAAACUGUUUAGUCCAACC	CUCUGGACUCAACAGUUUUCU	Cleavage
spe-miR319c-3-5p	Sopen05g031160.2	3.0	-1.0	1	21	1187	1207	AGGAAACUGUUUAGUCCAACC	CUCUGGACUCAACAGUUUUCU	Cleavage
spe-miR319c-3-5p	Sopen06g017200.1	3.0	-1.0	1	21	100	120	AGGAAACUGUUUAGUCCAACC	UAUUGGUCUCAACAGUUUUCU	Cleavage
spe-miR319c-3-5p	Sopen10g010800.1	3.0	-1.0	1	21	619	639	AGGAAACUGUUUAGUCCAACC	AAUUGGAAUAAGCAUUUUCCU	Cleavage
spe-miR319c-3-5p	Sopen07g014820.1	3.0	-1.0	1	21	1303	1323	AGGAAACUGUUUAGUCCAACC	AAUUGGGAUAAACAUUUUCCU	Cleavage
spe-miR319c-3-5p	Sopen10g010800.2	3.0	-1.0	1	21	4588	4608	AGGAAACUGUUUAGUCCAACC	AAUUGGAAUAAGCAUUUUCCU	Cleavage
spe-miR3627-1-3p	Sopen07g004180.1	2.5	-1.0	1	21	1141	1161	AAGUGCCUCUGUCUUUCGACA	UCUGGUAAGACAGAGGUACUU	Cleavage
spe-miR3627-1-3p	Sopen07g022360.1	3.0	-1.0	1	21	1109	1129	AAGUGCCUCUGUCUUUCGACA	GCUUGAAAGAUGGAGGCAUUG	Cleavage
spe-miR3627-2-3p	Sopen07g004180.1	2.5	-1.0	1	21	1141	1161	AAGUGCCUCUGUCUUUCGACA	UCUGGUAAGACAGAGGUACUU	Cleavage
spe-miR3627-2-3p	Sopen07g022360.1	3.0	-1.0	1	21	1109	1129	AAGUGCCUCUGUCUUUCGACA	GCUUGAAAGAUGGAGGCAUUG	Cleavage
spe-miR3627-2-5p	Sopen08g010640.1	2.5	-1.0	1	22	2822	2843	UUGUCGCAGGAGAGAUGGCACU	CGGACCAUUUCUCCUGCGACGG	Cleavage
spe-miR3627-2-5p	Sopen09g029910.1	3.0	-1.0	1	22	526	547	UUGUCGCAGGAGAGAUGGCACU	AAUGCCUUUUCUCGUGCGACAA	Cleavage
spe-miR3627-2-5p	Sopen09g029910.2	3.0	-1.0	1	22	526	547	UUGUCGCAGGAGAGAUGGCACU	AAUGCCUUUUCUCGUGCGACAA	Cleavage
spe-miR3627-2-5p	Sopen09g030570.1	3.0	-1.0	1	22	718	739	UUGUCGCAGGAGAGAUGGCACU	GCUGCUCUCUUUCUUGCGGCAA	Cleavage
spe-miR3627-2-5p	Sopen09g030570.2	3.0	-1.0	1	22	718	739	UUGUCGCAGGAGAGAUGGCACU	GCUGCUCUCUUUCUUGCGGCAA	Cleavage
spe-miR3627-2-5p	Sopen09g035690.1	3.0	-1.0	1	22	31	52	UUGUCGCAGGAGAGAUGGCACU	UUGGCUAUUUUUCUUGUGAUAA	Cleavage
spe-miR3627-2-5p	Sopen05g012110.1	3.0	-1.0	1	22	2171	2192	UUGUCGCAGGAGAGAUGGCACU	CGGACCUUUUCUCCUGCGACAG	Cleavage
spe-miR3627-2-5p	Sopen01g005770.1	3.0	-1.0	1	22	13	34	UUGUCGCAGGAGAGAUGGCACU	GUAGCCAAUUCUCUUGCGACGG	Cleavage
spe-miR390-3p	Sopen08g020320.1	2.0	-1.0	1	21	29	49	CGCUAUCCAUCCUGAGUUUUA	ACAAAUUUGGGAUGGAUAGUG	Cleavage
spe-miR390-3p	Sopen08g003160.1	2.5	-1.0	1	21	115	135	CGCUAUCCAUCCUGAGUUUUA	ACAGAUUCAGGAUGGAUAGUC	Cleavage
spe-miR390-3p	Sopen11g020620.2	3.0	-1.0	1	21	10154	10174	CGCUAUCCAUCCUGAGUUUUA	CAGAAAUUGGGAUGGAUAGUG	Cleavage
spe-miR390-3p	Sopen11g020620.1	3.0	-1.0	1	21	10148	10168	CGCUAUCCAUCCUGAGUUUUA	CAGAAAUUGGGAUGGAUAGUG	Cleavage
spe-miR390-3p	Sopen01g007670.1	3.0	-1.0	1	21	38	58	CGCUAUCCAUCCUGAGUUUUA	CAAUAAUCAGGAUGGAUGGUG	Cleavage
spe-miR390-3p	Sopen01g007660.1	3.0	-1.0	1	21	38	58	CGCUAUCCAUCCUGAGUUUUA	CAACAAUCAGGAUGGAUGGUG	Cleavage
spe-miR390-3p	Sopen03g040570.1	3.0	-1.0	1	21	534	554	CGCUAUCCAUCCUGAGUUUUA	GCAAGCUGAGGGUGGAUGGUG	Cleavage
spe-miR390-3p	Sopen12g009120.1	3.0	-1.0	1	21	416	436	CGCUAUCCAUCCUGAGUUUUA	CCAACAUUAGGAUGGAUAGUG	Cleavage
spe-miR390-3p	Sopen12g009010.1	3.0	-1.0	1	21	38	58	CGCUAUCCAUCCUGAGUUUUA	CCAACAUUAGGAUGGAUAGUG	Cleavage
spe-miR390-5p	Sopen09g028600.1	3.0	-1.0	1	21	979	999	AAGCUCAGGAGGGAUAGCGCC	UCAACUAUUCCUUCUGAGCUU	Cleavage
spe-miR390-5p	Sopen04g007680.1	3.0	-1.0	1	21	961	981	AAGCUCAGGAGGGAUAGCGCC	GGAACUAUUCCUCCUGAGUUU	Cleavage
spe-miR390-5p	Sopen09g034800.1	2.0	-1.0	1	21	391	411	AAGCUCAGGAGGGAUAGCGCC	GUCGCUAUCCUUCCUCAGCUU	Cleavage
spe-miR390-5p	Sopen04g032730.1	2.5	-1.0	1	21	268	288	AAGCUCAGGAGGGAUAGCGCC	AGUGCUAUUCCUCCUGAUCUU	Cleavage

spe-miR390-5p	Sopen07g003410.1	2.5	-1.0	1	21	1140	1160	AAGCUCAGGAGGGAUAGCGCC	CCUGCUAUCCCUCUUCAGCUU	Cleavage
spe-miR390-5p	Sopen01g044390.1	2.5	-1.0	1	21	340	360	AAGCUCAGGAGGGAUAGCGCC	CUUGCUGUCCUUUCUGGGCUU	Cleavage
spe-miR390-5p	Sopen01g044390.2	2.5	-1.0	1	21	340	360	AAGCUCAGGAGGGAUAGCGCC	CUUGCUGUCCUUUCUGGGCUU	Cleavage
spe-miR390-5p	Sopen01g034040.1	2.5	-1.0	1	21	508	528	AAGCUCAGGAGGGAUAGCGCC	CUUGCUAAUCUUCCUGAGCUU	Cleavage
spe-miR390-5p	Sopen01g006760.1	2.5	-1.0	1	21	472	492	AAGCUCAGGAGGGAUAGCGCC	AACGGGAUCCCUCUUGAGCUU	Cleavage
spe-miR390-5p	Sopen01g036980.1	3.0	-1.0	1	21	418	438	AAGCUCAGGAGGGAUAGCGCC	GGUGUUAUUCCUCCUGAGGUU	Cleavage
spe-miR390-5p	Sopen03g031640.1	3.0	-1.0	1	21	895	915	AAGCUCAGGAGGGAUAGCGCC	GGAACAAUCCCUCCUGAGCUU	Cleavage
spe-miR390a-3p	Sopen08g020320.1	2.0	-1.0	1	21	29	49	CGCUAUCCAUCCUGAGUUUUA	ACAAAUUUGGGAUGGAUAGUG	Cleavage
spe-miR390a-3p	Sopen08g003160.1	2.5	-1.0	1	21	115	135	CGCUAUCCAUCCUGAGUUUUA	ACAGAUUCAGGAUGGAUAGUC	Cleavage
spe-miR390a-3p	Sopen11g020620.2	3.0	-1.0	1	21	10154	10174	CGCUAUCCAUCCUGAGUUUUA	CAGAAAUUGGGAUGGAUAGUG	Cleavage
spe-miR390a-3p	Sopen11g020620.1	3.0	-1.0	1	21	10148	10168	CGCUAUCCAUCCUGAGUUUUA	CAGAAAUUGGGAUGGAUAGUG	Cleavage
spe-miR390a-3p	Sopen01g007670.1	3.0	-1.0	1	21	38	58	CGCUAUCCAUCCUGAGUUUUA	CAAUAAUCAGGAUGGAUGGUG	Cleavage
spe-miR390a-3p	Sopen01g007660.1	3.0	-1.0	1	21	38	58	CGCUAUCCAUCCUGAGUUUUA	CAACAAUCAGGAUGGAUGGUG	Cleavage
spe-miR390a-3p	Sopen03g040570.1	3.0	-1.0	1	21	534	554	CGCUAUCCAUCCUGAGUUUUA	GCAAGCUGAGGGUGGAUGGUG	Cleavage
spe-miR390a-3p	Sopen12g009120.1	3.0	-1.0	1	21	416	436	CGCUAUCCAUCCUGAGUUUUA	CCAACAUUAGGAUGGAUAGUG	Cleavage
spe-miR390a-3p	Sopen12g009010.1	3.0	-1.0	1	21	38	58	CGCUAUCCAUCCUGAGUUUUA	CCAACAUUAGGAUGGAUAGUG	Cleavage
spe-miR390a-5p	Sopen09g028600.1	3.0	-1.0	1	21	979	999	AAGCUCAGGAGGGAUAGCACC	UCAACUAUUCCUUCUGAGCUU	Cleavage
spe-miR390a-5p	Sopen07g029780.1	3.0	-1.0	1	21	763	783	AAGCUCAGGAGGGAUAGCACC	GGUGCAAUUCCUCCUGAGGUU	Cleavage
spe-miR390a-5p	Sopen04g007680.1	3.0	-1.0	1	21	961	981	AAGCUCAGGAGGGAUAGCACC	GGAACUAUUCCUCCUGAGUUU	Cleavage
spe-miR390a-5p	Sopen04g032730.1	2.0	-1.0	1	21	268	288	AAGCUCAGGAGGGAUAGCACC	AGUGCUAUUCCUCCUGAUCUU	Cleavage
spe-miR390a-5p	Sopen07g003410.1	2.0	-1.0	1	21	1140	1160	AAGCUCAGGAGGGAUAGCACC	CCUGCUAUCCCUCUUCAGCUU	Cleavage
spe-miR390a-5p	Sopen01g044390.1	2.0	-1.0	1	21	340	360	AAGCUCAGGAGGGAUAGCACC	CUUGCUGUCCUUUCUGGGCUU	Cleavage
spe-miR390a-5p	Sopen01g044390.2	2.0	-1.0	1	21	340	360	AAGCUCAGGAGGGAUAGCACC	CUUGCUGUCCUUUCUGGGCUU	Cleavage
spe-miR390a-5p	Sopen01g034040.1	2.0	-1.0	1	21	508	528	AAGCUCAGGAGGGAUAGCACC	CUUGCUAAUCUUCCUGAGCUU	Cleavage
spe-miR390a-5p	Sopen01g036980.1	2.5	-1.0	1	21	418	438	AAGCUCAGGAGGGAUAGCACC	GGUGUUAUUCCUCCUGAGGUU	Cleavage
spe-miR390a-5p	Sopen09g003850.1	2.5	-1.0	1	21	2191	2211	AAGCUCAGGAGGGAUAGCACC	AUUCCUGUUCUUCCUGAGCUU	Cleavage
spe-miR390a-5p	Sopen04g001380.1	3.0	-1.0	1	21	751	771	AAGCUCAGGAGGGAUAGCACC	GGUGUGAUCCCUUCUGAGCUA	Cleavage
spe-miR390a-5p	Sopen03g031640.1	3.0	-1.0	1	21	895	915	AAGCUCAGGAGGGAUAGCACC	GGAACAAUCCCUCCUGAGCUU	Cleavage
spe-miR390a-5p	Sopen09g034800.1	3.0	-1.0	1	21	391	411	AAGCUCAGGAGGGAUAGCACC	GUCGCUAUCCUUCCUCAGCUU	Cleavage
spe-miR390a-5p	Sopen04g032890.1	3.0	-1.0	1	21	433	453	AAGCUCAGGAGGGAUAGCACC	CAUGUUAUUUUUCUUGGGCUU	Cleavage
spe-miR390a-5p	Sopen09g030890.2	3.0	-1.0	1	21	868	888	AAGCUCAGGAGGGAUAGCACC	CUUGCUAUCUCUCUUGGCCUU	Cleavage
spe-miR390a-5p	Sopen09g030890.1	3.0	-1.0	1	21	868	888	AAGCUCAGGAGGGAUAGCACC	CUUGCUAUCUCUCUUGGCCUU	Cleavage
spe-miR390a-5p	Sopen11g002110.1	3.0	-1.0	1	21	175	195	AAGCUCAGGAGGGAUAGCACC	UUUUCUAUCCCUCUUGAGUUG	Cleavage
spe-miR390a-5p	Sopen05g007880.1	3.0	-1.0	1	21	652	672	AAGCUCAGGAGGGAUAGCACC	AAUGGGAUUCCUCUUGAGCUU	Cleavage
spe-miR393-3p	Sopen04g030710.1	1.5	-1.0	1	21	19	39	AUCAUGUGAUCUCUUCGGAAU	CCUUCCAAGAGAUCACAUGAU	Cleavage
spe-miR393-3p	Sopen06g003990.1	2.5	-1.0	1	21	883	902	AUCAUGUGAUCUCUUCGGAAU	AAUCCGA-GAGAUCAUAUGAU	Cleavage
spe-miR393-3p	Sopen10g016150.1	3.0	-1.0	1	21	2832	2852	AUCAUGUGAUCUCUUCGGAAU	UAUCCGAACAGCUCACAUGAU	Translation
spe-miR393-3p	Sopen01g039820.1	3.0	-1.0	1	21	694	714	AUCAUGUGAUCUCUUCGGAAU	GUUGCACAGAGAUCACAUGAU	Cleavage
spe-miR393-3p	Sopen07g016470.1	3.0	-1.0	1	21	249	269	AUCAUGUGAUCUCUUCGGAAU	CGUCAAAAGAGGUCAUAUGAU	Cleavage
spe-miR393-5p	Sopen09g029360.1	1.0	-1.0	1	22	1504	1525	UCCAAAGGGAUCGCAUUGAUCC	GAGACAAUGCGAUCCCUUUGGA	Cleavage
spe-miR393-5p	Sopen02g023990.1	2.5	-1.0	1	22	1573	1594	UCCAAAGGGAUCGCAUUGAUCC	GAAUCAAUGCGGUGUCUUUGGA	Cleavage
spe-miR393-5p	Sopen05g010300.1	2.5	-1.0	1	22	1181	1202	UCCAAAGGGAUCGCAUUGAUCC	GUGUCAAAGUGGUUCCUUUGGA	Cleavage
spe-miR393-5p	Sopen03g003130.1	2.5	-1.0	1	22	695	716	UCCAAAGGGAUCGCAUUGAUCC	CAGUAGAUGUGGUCCCUUUGGA	Cleavage
spe-miR393-5p	Sopen00g005130.1	3.0	-1.0	1	22	797	818	UCCAAAGGGAUCGCAUUGAUCC	UUGUUGAUGCUAUUCCUUUGGA	Cleavage
spe-miR393-5p	Sopen01g042720.1	3.0	-1.0	1	22	974	995	UCCAAAGGGAUCGCAUUGAUCC	UUGUUGAUGCUAUUCCUUUGGA	Cleavage
spe-miR393-5p	Sopen03g040040.1	3.0	-1.0	1	22	2366	2387	UCCAAAGGGAUCGCAUUGAUCC	GUUUCGGUGUGGUUCUUUUGGA	Cleavage
spe-miR394-1-3p	Sopen01g036230.1	2.5	-1.0	1	20	1230	1249	AGGUGGGCAUACUGUCAACA	AUUUGAGAGUAUGCCCAUCU	Cleavage
spe-miR394-1-3p	Sopen09g028930.1	3.0	-1.0	1	20	5639	5658	AGGUGGGCAUACUGUCAACA	CAUUGACAGAAUGUCCACCU	Translation
spe-miR394-1-5p	Sopen12g034970.1	1.0	-1.0	1	20	1152	1171	UUGGCAUUCUGUCCACCUCC	GGAGGUUGACAGAAUGCCAA	Cleavage
spe-miR394-1-5p	Sopen09g013340.1	2.5	-1.0	1	20	913	932	UUGGCAUUCUGUCCACCUCC	GGAGGUGUACAGAGUGUCAA	Cleavage

spe-miR394-1-5p	Sopen03g018350.1	2.5	-1.0	1	20	254	273	UUGGCAUUCUGUCCACCUCC	AGAUGUGGGUAGAAUGCCGA	Cleavage
spe-miR394-1-5p	Sopen04g026950.1	2.5	-1.0	1	20	1788	1807	UUGGCAUUCUGUCCACCUCC	CGAGAUGGAUAGAAUGCUGA	Cleavage
spe-miR394-1-5p	Sopen06g020390.1	3.0	-1.0	1	20	1683	1702	UUGGCAUUCUGUCCACCUCC	UGAGGUGGAUGAAAUGUCAA	Cleavage
spe-miR394-1-5p	Sopen06g035910.1	3.0	-1.0	1	20	3150	3169	UUGGCAUUCUGUCCACCUCC	CGAGGUGGAUAGCAUGCUAG	Cleavage
spe-miR394-1-5p	Sopen04g023830.1	3.0	-1.0	1	20	919	938	UUGGCAUUCUGUCCACCUCC	GAAGGAGGACAGAAUGCUAG	Cleavage
spe-miR394-1-5p	Sopen08g013650.1	3.0	-1.0	1	20	709	728	UUGGCAUUCUGUCCACCUCC	GAAGGAGGACAGAAUGCUAG	Cleavage
spe-miR394-1-5p	Sopen08g012750.1	3.0	-1.0	1	20	1225	1244	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
spe-miR394-1-5p	Sopen08g012750.2	3.0	-1.0	1	20	1416	1435	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
spe-miR394-1-5p	Sopen11g003350.1	3.0	-1.0	1	20	375	394	UUGGCAUUCUGUCCACCUCC	UGACGUGGACACAAUGUCAA	Cleavage
spe-miR394-1-5p	Sopen11g013460.1	3.0	-1.0	1	20	1461	1480	UUGGCAUUCUGUCCACCUCC	UGAGAUUGAUGGAAUGCCAA	Cleavage
spe-miR394-2-3p	Sopen09g028930.1	3.0	-1.0	1	21	5638	5658	AGGUGGGCAUACUGCCAAUAG	CCAUUGACAGAAUGUCCACCU	Translation
spe-miR394-2-3p	Sopen03g011160.1	3.0	-1.0	1	21	1963	1983	AGGUGGGCAUACUGCCAAUAG	AGAAUGGAGGUAUGCCCAUCU	Cleavage
spe-miR394-2-5p	Sopen12g034970.1	1.0	-1.0	1	20	1152	1171	UUGGCAUUCUGUCCACCUCC	GGAGGUUGACAGAAUGCCAA	Cleavage
spe-miR394-2-5p	Sopen09g013340.1	2.5	-1.0	1	20	913	932	UUGGCAUUCUGUCCACCUCC	GGAGGUGUACAGAGUGUCAA	Cleavage
spe-miR394-2-5p	Sopen03g018350.1	2.5	-1.0	1	20	254	273	UUGGCAUUCUGUCCACCUCC	AGAUGUGGGUAGAAUGCCGA	Cleavage
spe-miR394-2-5p	Sopen04g026950.1	2.5	-1.0	1	20	1788	1807	UUGGCAUUCUGUCCACCUCC	CGAGAUGGAUAGAAUGCUGA	Cleavage
spe-miR394-2-5p	Sopen06g020390.1	3.0	-1.0	1	20	1683	1702	UUGGCAUUCUGUCCACCUCC	UGAGGUGGAUGAAAUGUCAA	Cleavage
spe-miR394-2-5p	Sopen06g035910.1	3.0	-1.0	1	20	3150	3169	UUGGCAUUCUGUCCACCUCC	CGAGGUGGAUAGCAUGCUAG	Cleavage
spe-miR394-2-5p	Sopen04g023830.1	3.0	-1.0	1	20	919	938	UUGGCAUUCUGUCCACCUCC	GAAGGAGGACAGAAUGCUAG	Cleavage
spe-miR394-2-5p	Sopen08g013650.1	3.0	-1.0	1	20	709	728	UUGGCAUUCUGUCCACCUCC	GAAGGAGGACAGAAUGCUAG	Cleavage
spe-miR394-2-5p	Sopen08g012750.1	3.0	-1.0	1	20	1225	1244	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
spe-miR394-2-5p	Sopen08g012750.2	3.0	-1.0	1	20	1416	1435	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
spe-miR394-2-5p	Sopen11g003350.1	3.0	-1.0	1	20	375	394	UUGGCAUUCUGUCCACCUCC	UGACGUGGACACAAUGUCAA	Cleavage
spe-miR394-2-5p	Sopen11g013460.1	3.0	-1.0	1	20	1461	1480	UUGGCAUUCUGUCCACCUCC	UGAGAUUGAUGGAAUGCCAA	Cleavage
spe-miR394-3-3p	Sopen04g026220.1	3.0	-1.0	1	20	530	549	AGGGGGCCAAAGUGCCAAAC	CCUUGGCGCUUUGGCUUUCU	Cleavage
spe-miR394-3-5p	Sopen12g034970.1	1.0	-1.0	1	20	1152	1171	UUGGCAUUCUGUCCACCUCC	GGAGGUUGACAGAAUGCCAA	Cleavage
spe-miR394-3-5p	Sopen09g013340.1	2.5	-1.0	1	20	913	932	UUGGCAUUCUGUCCACCUCC	GGAGGUGUACAGAGUGUCAA	Cleavage
spe-miR394-3-5p	Sopen03g018350.1	2.5	-1.0	1	20	254	273	UUGGCAUUCUGUCCACCUCC	AGAUGUGGGUAGAAUGCCGA	Cleavage
spe-miR394-3-5p	Sopen04g026950.1	2.5	-1.0	1	20	1788	1807	UUGGCAUUCUGUCCACCUCC	CGAGAUGGAUAGAAUGCUGA	Cleavage
spe-miR394-3-5p	Sopen06g020390.1	3.0	-1.0	1	20	1683	1702	UUGGCAUUCUGUCCACCUCC	UGAGGUGGAUGAAAUGUCAA	Cleavage
spe-miR394-3-5p	Sopen06g035910.1	3.0	-1.0	1	20	3150	3169	UUGGCAUUCUGUCCACCUCC	CGAGGUGGAUAGCAUGCUAG	Cleavage
spe-miR394-3-5p	Sopen04g023830.1	3.0	-1.0	1	20	919	938	UUGGCAUUCUGUCCACCUCC	GAAGGAGGACAGAAUGCUAG	Cleavage
spe-miR394-3-5p	Sopen08g013650.1	3.0	-1.0	1	20	709	728	UUGGCAUUCUGUCCACCUCC	GAAGGAGGACAGAAUGCUAG	Cleavage
spe-miR394-3-5p	Sopen08g012750.1	3.0	-1.0	1	20	1225	1244	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
spe-miR394-3-5p	Sopen08g012750.2	3.0	-1.0	1	20	1416	1435	UUGGCAUUCUGUCCACCUCC	AAAGUUGGACAGAGUGCUAA	Cleavage
spe-miR394-3-5p	Sopen11g003350.1	3.0	-1.0	1	20	375	394	UUGGCAUUCUGUCCACCUCC	UGACGUGGACACAAUGUCAA	Cleavage
spe-miR394-3-5p	Sopen11g013460.1	3.0	-1.0	1	20	1461	1480	UUGGCAUUCUGUCCACCUCC	UGAGAUUGAUGGAAUGCCAA	Cleavage
spe-miR395a-3p	Sopen04g024490.1	1.5	-1.0	1	22	126	147	CUGAAGUGUUUGGGGGAACUUC	UGUGUUCUCCCAAACACUUCAA	Cleavage
spe-miR395a-3p	Sopen11g025910.1	1.5	-1.0	1	22	987	1008	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCCUCCAAACACUUCAA	Cleavage
spe-miR395a-3p	Sopen06g032390.1	2.0	-1.0	1	22	978	999	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCUUCCAAACACUUCAA	Cleavage
spe-miR395a-3p	Sopen11g016060.1	2.0	-1.0	1	22	2026	2047	CUGAAGUGUUUGGGGGAACUUC	UACGUUCCCCCAGGCACUUCAA	Cleavage
spe-miR395a-3p	Sopen04g017250.1	3.0	-1.0	1	22	367	388	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395a-3p	Sopen06g005780.1	3.0	-1.0	1	22	538	559	CUGAAGUGUUUGGGGGAACUUC	CAAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395a-3p	Sopen07g011680.1	3.0	-1.0	1	22	478	499	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395a-3p	Sopen06g005350.1	3.0	-1.0	1	22	910	931	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395a-3p	Sopen06g005350.2	3.0	-1.0	1	22	910	931	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395a-3p	Sopen11g017420.1	3.0	-1.0	1	22	1537	1558	CUGAAGUGUUUGGGGGAACUUC	AAAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395a-3p	Sopen09g031690.1	3.0	-1.0	1	22	339	360	CUGAAGUGUUUGGGGGAACUUC	CGAGUUCCUCCAAACUCUUCAU	Cleavage
spe-miR395a-3p	Sopen03g001290.1	3.0	-1.0	1	22	339	360	CUGAAGUGUUUGGGGGAACUUC	UGAGUUCCUCCAAACUCUUCAU	Cleavage
spe-miR395a-3p	Sopen08g030880.1	3.0	-1.0	1	22	417	438	CUGAAGUGUUUGGGGGAACUUC	UCAGUUUCCUCAAACGUUUCAU	Cleavage

spe-miR395a-3p	Sopen06g003240.1	3.0	-1.0	1	22	838	859	CUGAAGUGUUUGGGGGAACUUC	GUUAUUCCCCCUAGCACUUCAG	Translation
spe-miR395a-3p	Sopen10g021110.1	3.0	-1.0	1	22	1536	1557	CUGAAGUGUUUGGGGGAACUUC	UGGGUUGCCCAAAACACUUCGG	Cleavage
spe-miR395a-3p	Sopen01g021570.1	3.0	-1.0	1	22	2479	2500	CUGAAGUGUUUGGGGGAACUUC	UAUGUACCCCCAGGCACUUCAA	Cleavage
spe-miR395d-3p	Sopen04g024490.1	1.5	-1.0	1	21	126	146	UGAAGUGUUUGGGGGAACUUU	UGUGUUCUCCCAAACACUUCA	Cleavage
spe-miR395d-3p	Sopen04g024490.1	2.5	-1.0	1	21	72	92	UGAAGUGUUUGGGGGAACUUU	AGAGUUCUCCGGAACACUUCA	Translation
spe-miR395d-3p	Sopen12g026590.1	3.0	-1.0	1	21	4819	4839	UGAAGUGUUUGGGGGAACUUU	UAUGUUCCCCCAGGCACUUCC	Cleavage
spe-miR395d-3p	Sopen01g025420.1	3.0	-1.0	1	21	3373	3393	UGAAGUGUUUGGGGGAACUUU	UACGUUCCCCCAGGCACUUCC	Cleavage
spe-miR395d-3p	Sopen08g030890.1	3.0	-1.0	1	21	417	437	UGAAGUGUUUGGGGGAACUUU	UCAGUUUCCUCAAACUUUUCA	Cleavage
spe-miR395d-3p	Sopen06g016660.1	3.0	-1.0	1	21	2065	2085	UGAAGUGUUUGGGGGAACUUU	GUAGUUCCCUCUGGCACUUCA	Translation
spe-miR395d-3p	Sopen11g025910.1	0.5	-1.0	1	21	987	1007	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAACACUUCA	Cleavage
spe-miR395d-3p	Sopen06g032390.1	1.0	-1.0	1	21	978	998	UGAAGUGUUUGGGGGAACUUU	AAAGUUCUUCCAAACACUUCA	Cleavage
spe-miR395d-3p	Sopen03g001290.1	2.0	-1.0	1	21	339	359	UGAAGUGUUUGGGGGAACUUU	UGAGUUCCUCCAAACUCUUCA	Cleavage
spe-miR395d-3p	Sopen09g031690.1	2.0	-1.0	1	21	339	359	UGAAGUGUUUGGGGGAACUUU	CGAGUUCCUCCAAACUCUUCA	Cleavage
spe-miR395d-3p	Sopen11g016060.1	2.0	-1.0	1	21	2026	2046	UGAAGUGUUUGGGGGAACUUU	UACGUUCCCCCAGGCACUUCA	Cleavage
spe-miR395d-3p	Sopen08g030880.1	2.0	-1.0	1	21	417	437	UGAAGUGUUUGGGGGAACUUU	UCAGUUUCCUCAAACGUUUCA	Cleavage
spe-miR395d-3p	Sopen02g035660.3	2.5	-1.0	1	21	1657	1677	UGAAGUGUUUGGGGGAACUUU	AUAUUUCCCCCAAACACAUCA	Cleavage
spe-miR395d-3p	Sopen02g035660.2	2.5	-1.0	1	21	1807	1827	UGAAGUGUUUGGGGGAACUUU	AUAUUUCCCCCAAACACAUCA	Cleavage
spe-miR395d-3p	Sopen02g035660.1	2.5	-1.0	1	21	1810	1830	UGAAGUGUUUGGGGGAACUUU	AUAUUUCCCCCAAACACAUCA	Cleavage
spe-miR395d-3p	Sopen07g028150.1	2.5	-1.0	1	21	701	721	UGAAGUGUUUGGGGGAACUUU	UCAAUUUCCCCGAACACUUUA	Cleavage
spe-miR395d-3p	Sopen04g017250.1	3.0	-1.0	1	21	367	387	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen03g019180.1	3.0	-1.0	1	21	625	645	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen07g011680.1	3.0	-1.0	1	21	478	498	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen06g005350.1	3.0	-1.0	1	21	910	930	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen06g005350.2	3.0	-1.0	1	21	910	930	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen11g017420.1	3.0	-1.0	1	21	1537	1557	UGAAGUGUUUGGGGGAACUUU	AAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen08g028400.1	3.0	-1.0	1	21	279	299	UGAAGUGUUUGGGGGAACUUU	AGAGUUUCUCCAAGCACUACA	Cleavage
spe-miR395d-3p	Sopen06g005780.1	3.0	-1.0	1	21	538	558	UGAAGUGUUUGGGGGAACUUU	CAAGUUCCUCCAAGUGUUUCG	Cleavage
spe-miR395d-3p	Sopen07g016920.1	3.0	-1.0	1	21	1693	1713	UGAAGUGUUUGGGGGAACUUU	UACGUUCCCCCAGGCACUUCC	Cleavage
spe-miR395d-3p	Sopen08g013490.1	3.0	-1.0	1	21	1006	1026	UGAAGUGUUUGGGGGAACUUU	UACGUUCCCCCAGGCACUUCC	Cleavage
spe-miR395d-3p	Sopen01g015750.1	3.0	-1.0	1	21	103	123	UGAAGUGUUUGGGGGAACUUU	UACGUUCCCCCAGGCACUUCC	Cleavage
spe-miR395d-3p	Sopen12g012780.1	3.0	-1.0	1	21	121	141	UGAAGUGUUUGGGGGAACUUU	CAAGUUGCUCCAAAUGUUUCA	Cleavage
spe-miR395d-3p	Sopen03g001280.1	3.0	-1.0	1	21	210	230	UGAAGUGUUUGGGGGAACUUU	UGAGUUUCUUCAAACUCUUCA	Cleavage
spe-miR395d-3p	Sopen09g013790.1	3.0	-1.0	1	21	925	945	UGAAGUGUUUGGGGGAACUUU	AUAGUUCCCCCAGAUUUUUCA	Cleavage
spe-miR395d-3p	Sopen10g030910.1	3.0	-1.0	1	21	3191	3211	UGAAGUGUUUGGGGGAACUUU	CUAGUUUUCUCAAAAACUUCA	Cleavage
spe-miR395d-3p	Sopen02g015860.1	3.0	-1.0	1	21	667	687	UGAAGUGUUUGGGGGAACUUU	UCAGUUUCUUCAGAUAUUUCA	Cleavage
spe-miR395d-3p	Sopen03g001480.1	3.0	-1.0	1	21	966	986	UGAAGUGUUUGGGGGAACUUU	UCAGUUCCCUCAAAGAUUUCG	Cleavage
spe-miR395d-3p	Sopen01g021570.1	3.0	-1.0	1	21	2479	2499	UGAAGUGUUUGGGGGAACUUU	UAUGUACCCCCAGGCACUUCA	Cleavage
spe-miR395d-3p	Sopen02g027840.1	3.0	-1.0	1	21	192	212	UGAAGUGUUUGGGGGAACUUU	CAACUUGCCUCAAAUACUUCA	Cleavage
spe-miR395g-3p	Sopen04g024490.1	0.5	-1.0	1	21	127	147	UUGAAGUGUUUGGGGGAACUC	GUGUUCUCCCAAACACUUCAA	Cleavage
spe-miR395g-3p	Sopen04g024490.1	2.5	-1.0	1	21	73	93	UUGAAGUGUUUGGGGGAACUC	GAGUUCUCCGGAACACUUCAA	Cleavage
spe-miR395g-3p	Sopen01g025420.1	2.5	-1.0	1	21	3374	3394	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCCCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen12g026590.1	2.5	-1.0	1	21	4820	4840	UUGAAGUGUUUGGGGGAACUC	AUGUUCCCCCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen11g025910.1	0.5	-1.0	1	21	988	1008	UUGAAGUGUUUGGGGGAACUC	AAGUUCCUCCAAACACUUCAA	Cleavage
spe-miR395g-3p	Sopen06g032390.1	1.0	-1.0	1	21	979	999	UUGAAGUGUUUGGGGGAACUC	AAGUUCUUCCAAACACUUCAA	Cleavage
spe-miR395g-3p	Sopen11g016060.1	1.0	-1.0	1	21	2027	2047	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCCCAGGCACUUCAA	Cleavage
spe-miR395g-3p	Sopen01g021570.1	2.0	-1.0	1	21	2480	2500	UUGAAGUGUUUGGGGGAACUC	AUGUACCCCCAGGCACUUCAA	Cleavage
spe-miR395g-3p	Sopen07g016920.1	2.5	-1.0	1	21	1694	1714	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCCCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen08g013490.1	2.5	-1.0	1	21	1007	1027	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCCCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen01g015750.1	2.5	-1.0	1	21	104	124	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCCCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen08g030900.1	2.5	-1.0	1	21	34	54	UUGAAGUGUUUGGGGGAACUC	UUGUAUCCUCAAGCACUUCAA	Cleavage

spe-miR395g-3p	Sopen09g031690.1	3.0	-1.0	1	21	340	360	UUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
spe-miR395g-3p	Sopen03g001290.1	3.0	-1.0	1	21	340	360	UUGAAGUGUUUGGGGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
spe-miR395g-3p	Sopen08g028400.1	3.0	-1.0	1	21	280	300	UUGAAGUGUUUGGGGGAACUC	GAGUUUCUCCAAGCACUACAA	Cleavage
spe-miR395g-3p	Sopen08g030880.1	3.0	-1.0	1	21	418	438	UUGAAGUGUUUGGGGGAACUC	CAGUUUCCUCAAACGUUUCAU	Cleavage
spe-miR395g-3p	Sopen06g016660.1	3.0	-1.0	1	21	2066	2086	UUGAAGUGUUUGGGGGAACUC	UAGUUCCCUCUGGCACUUCAA	Translation
spe-miR395g-3p	Sopen10g030910.1	3.0	-1.0	1	21	3192	3212	UUGAAGUGUUUGGGGGAACUC	UAGUUUUCUCAAAAACUUCAA	Cleavage
spe-miR395g-3p	Sopen12g020190.1	3.0	-1.0	1	21	460	480	UUGAAGUGUUUGGGGGAACUC	GAUUUACCUCAAGCACUUCAA	Cleavage
spe-miR395g-3p	Sopen03g034140.1	3.0	-1.0	1	21	1154	1174	UUGAAGUGUUUGGGGGAACUC	GAAUUGCUUCAAACACUUCAA	Cleavage
spe-miR395g-3p	Sopen12g012780.1	3.0	-1.0	1	21	122	142	UUGAAGUGUUUGGGGGAACUC	AAGUUGCUCCAAAUGUUUCAA	Cleavage
spe-miR395g-3p	Sopen03g027250.1	3.0	-1.0	1	21	1497	1517	UUGAAGUGUUUGGGGGAACUC	UGGUUUUCCCAAAAAUUUCAA	Cleavage
spe-miR395g-3p	Sopen12g028920.2	3.0	-1.0	1	21	30	50	UUGAAGUGUUUGGGGGAACUC	UUCUUCCCCUAAACCCUUCAA	Cleavage
spe-miR395g-3p	Sopen12g028920.1	3.0	-1.0	1	21	30	50	UUGAAGUGUUUGGGGGAACUC	UUCUUCCCCUAAACCCUUCAA	Cleavage
spe-miR395g-3p	Sopen03g037960.1	3.0	-1.0	1	21	642	662	UUGAAGUGUUUGGGGGAACUC	UCCUUCCUUCAGACAUUUCAA	Cleavage
spe-miR395g-3p	Sopen05g002520.1	3.0	-1.0	1	21	1764	1784	UUGAAGUGUUUGGGGGAACUC	UUGUUUCUCUGAACACUUUGA	Cleavage
spe-miR395g-3p	Sopen12g011720.1	3.0	-1.0	1	21	2354	2374	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCCCAAAAACUUCCA	Cleavage
spe-miR395g-3p	Sopen00g003520.1	3.0	-1.0	1	21	2462	2482	UUGAAGUGUUUGGGGGAACUC	AUGUUCCUCCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen03g014120.1	3.0	-1.0	1	21	6395	6415	UUGAAGUGUUUGGGGGAACUC	ACGUUCCCUCAGGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen02g027840.1	3.0	-1.0	1	21	193	213	UUGAAGUGUUUGGGGGAACUC	AACUUGCCUCAAAUACUUCAA	Cleavage
spe-miR395g-3p	Sopen08g021380.1	3.0	-1.0	1	21	313	333	UUGAAGUGUUUGGGGGAACUC	UGGUGCUUCCAAAUAUUUCAA	Cleavage
spe-miR395g-3p	Sopen08g001510.1	3.0	-1.0	1	21	313	333	UUGAAGUGUUUGGGGGAACUC	UGGUGCUUCCAAAUAUUUCAA	Cleavage
spe-miR395g-3p	Sopen08g001510.2	3.0	-1.0	1	21	313	333	UUGAAGUGUUUGGGGGAACUC	UGGUGCUUCCAAAUAUUUCAA	Cleavage
spe-miR395g-3p	Sopen02g012790.1	3.0	-1.0	1	21	1280	1300	UUGAAGUGUUUGGGGGAACUC	AGGAUCUCCCAAAAACUUCAA	Cleavage
spe-miR395g-3p	Sopen06g001630.1	3.0	-1.0	1	21	1064	1084	UUGAAGUGUUUGGGGGAACUC	GUGUAUCUUCAAGCACUUCAA	Cleavage
spe-miR395g-3p	Sopen04g016340.1	3.0	-1.0	1	21	474	494	UUGAAGUGUUUGGGGGAACUC	AUGGUUCUCCAAAUAUUUCAA	Cleavage
spe-miR395g-3p	Sopen10g014050.1	3.0	-1.0	1	21	170	190	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen10g015030.1	3.0	-1.0	1	21	893	913	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen05g021020.1	3.0	-1.0	1	21	1016	1036	UUGAAGUGUUUGGGGGAACUC	AUGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen07g010740.1	3.0	-1.0	1	21	170	190	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen05g015900.1	3.0	-1.0	1	21	1799	1819	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen06g012290.1	3.0	-1.0	1	21	983	1003	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen08g013390.1	3.0	-1.0	1	21	2138	2158	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen10g016760.1	3.0	-1.0	1	21	1931	1951	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen05g021120.1	3.0	-1.0	1	21	2819	2839	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen05g020870.1	3.0	-1.0	1	21	2468	2488	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUGCAA	Cleavage
spe-miR395g-3p	Sopen12g021830.1	3.0	-1.0	1	21	2891	2911	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen02g002260.1	3.0	-1.0	1	21	2264	2284	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen04g018390.1	3.0	-1.0	1	21	2135	2155	UUGAAGUGUUUGGGGGAACUC	AUGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen11g022890.1	3.0	-1.0	1	21	2843	2863	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen06g010410.1	3.0	-1.0	1	21	2087	2107	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen05g018700.1	3.0	-1.0	1	21	2837	2857	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen07g019300.1	3.0	-1.0	1	21	2852	2872	UUGAAGUGUUUGGGGGAACUC	AUGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen04g011220.1	3.0	-1.0	1	21	3572	3592	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen10g007670.1	3.0	-1.0	1	21	3902	3922	UUGAAGUGUUUGGGGGAACUC	AUGUUCUACCAAAUGUUUCAA	Cleavage
spe-miR395g-3p	Sopen07g014640.1	3.0	-1.0	1	21	104	124	UUGAAGUGUUUGGGGGAACUC	AUGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395g-3p	Sopen07g010080.1	3.0	-1.0	1	21	1820	1840	UUGAAGUGUUUGGGGGAACUC	AUGUGCCCCCAGACACUUCCA	Cleavage
spe-miR395g-3p	Sopen05g026200.1	3.0	-1.0	1	21	7547	7567	UUGAAGUGUUUGGGGGAACUC	ACGUGCCCCCAAGCACUUCCA	Cleavage
spe-miR395i-5p	Sopen04g024490.1	2.5	-1.0	1	21	127	147	CUGAAGUGUUUGGAGGAACUC	GUGUUCUCCCAAACACUUCAA	Cleavage
spe-miR395i-5p	Sopen11g025910.1	1.0	-1.0	1	21	988	1008	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAACACUUCAA	Cleavage
spe-miR395i-5p	Sopen06g032390.1	1.5	-1.0	1	21	979	999	CUGAAGUGUUUGGAGGAACUC	AAGUUCUUCCAAACACUUCAA	Cleavage
spe-miR395i-5p	Sopen09g031690.1	2.5	-1.0	1	21	340	360	CUGAAGUGUUUGGAGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage

spe-miR395i-5p	Sopen03g001290.1	2.5	-1.0	1	21	340	360	CUGAAGUGUUUGGAGGAACUC	GAGUUCCUCCAAACUCUUCAU	Cleavage
spe-miR395i-5p	Sopen04g017250.1	2.5	-1.0	1	21	368	388	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395i-5p	Sopen06g005780.1	2.5	-1.0	1	21	539	559	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395i-5p	Sopen07g011680.1	2.5	-1.0	1	21	479	499	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395i-5p	Sopen06g005350.1	2.5	-1.0	1	21	911	931	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395i-5p	Sopen06g005350.2	2.5	-1.0	1	21	911	931	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395i-5p	Sopen11g017420.1	2.5	-1.0	1	21	1538	1558	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUCGG	Cleavage
spe-miR395i-5p	Sopen10g011650.1	3.0	-1.0	1	21	212	232	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUAUUCCAG	Cleavage
spe-miR395i-5p	Sopen06g007750.1	3.0	-1.0	1	21	551	571	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAGUGUUUUGG	Cleavage
spe-miR395i-5p	Sopen08g022280.1	3.0	-1.0	1	21	46	66	CUGAAGUGUUUGGAGGAACUC	CAGUUCCUCCAAGUCCUUCGG	Cleavage
spe-miR395i-5p	Sopen05g023820.1	3.0	-1.0	1	21	719	739	CUGAAGUGUUUGGAGGAACUC	AAGUUUCUCCAAAAACUUUGG	Cleavage
spe-miR395i-5p	Sopen08g014910.1	3.0	-1.0	1	21	1400	1420	CUGAAGUGUUUGGAGGAACUC	AAGUUCCUCCAAAUGCUCCGG	Cleavage
spe-miR395i-5p	Sopen08g007180.1	3.0	-1.0	1	21	314	334	CUGAAGUGUUUGGAGGAACUC	AAGUUACUCCAAGUAUUUCGG	Cleavage
spe-miR395i-5p	Sopen02g024400.1	3.0	-1.0	1	21	755	775	CUGAAGUGUUUGGAGGAACUC	CCUUUCUUCCAAAUACUUCAU	Cleavage
spe-miR395i-5p	Sopen05g002180.1	3.0	-1.0	1	21	230	250	CUGAAGUGUUUGGAGGAACUC	GUGUUCCUCCAGGCACUUUUG	Cleavage
spe-miR395i-5p	Sopen10g034670.1	3.0	-1.0	1	21	86	106	CUGAAGUGUUUGGAGGAACUC	UCUUUCCUCCAUGCACUUCAG	Translation
spe-miR395i-5p	Sopen11g016060.1	3.0	-1.0	1	21	2027	2047	CUGAAGUGUUUGGAGGAACUC	ACGUUCCCCCAGGCACUUCAA	Cleavage
spe-miR395i-5p	Sopen01g035210.1	3.0	-1.0	1	21	1466	1486	CUGAAGUGUUUGGAGGAACUC	UUGUUCAUCCAGAUAUUUUAG	Cleavage
spe-miR396-1-3p	Sopen04g011340.1	1.5	-1.0	1	21	484	504	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g020850.1	2.0	-1.0	1	21	481	501	GUCCAAGAAAGCUGUGGGAAA	GCUCCUUCAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen03g004080.1	2.5	-1.0	1	21	2002	2022	GUCCAAGAAAGCUGUGGGAAA	UCUCCUACUGUUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen12g022440.2	2.5	-1.0	1	21	1018	1038	GUCCAAGAAAGCUGUGGGAAA	UCUCCUACUGUUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen00g014240.1	2.5	-1.0	1	21	289	309	GUCCAAGAAAGCUGUGGGAAA	UCUCCUACUGUUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen02g009220.1	2.5	-1.0	1	21	364	384	GUCCAAGAAAGCUGUGGGAAA	GCUCCUACAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen02g009220.2	2.5	-1.0	1	21	364	384	GUCCAAGAAAGCUGUGGGAAA	GCUCCUACAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen10g018020.1	2.5	-1.0	1	21	319	339	GUCCAAGAAAGCUGUGGGAAA	UAUCCCCAAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g012870.1	2.5	-1.0	1	21	358	378	GUCCAAGAAAGCUGUGGGAAA	GAUCCCCAAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen08g014910.1	2.5	-1.0	1	21	808	828	GUCCAAGAAAGCUGUGGGAAA	GAUCCCCAAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g019860.1	2.5	-1.0	1	21	169	189	GUCCAAGAAAGCUGUGGGAAA	GAUCCCCAAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen05g023500.1	2.5	-1.0	1	21	40	60	GUCCAAGAAAGCUGUGGGAAA	GAUCCCCAAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen08g006710.1	2.5	-1.0	1	21	295	315	GUCCAAGAAAGCUGUGGGAAA	GAUCCCCAAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen12g002820.1	3.0	-1.0	1	21	301	321	GUCCAAGAAAGCUGUGGGAAA	UUCUUCGUAGCUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen02g009730.1	3.0	-1.0	1	21	364	384	GUCCAAGAAAGCUGUGGGAAA	GUUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g014510.1	3.0	-1.0	1	21	1070	1090	GUCCAAGAAAGCUGUGGGAAA	AUAUCCGUAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g008160.1	3.0	-1.0	1	21	2710	2730	GUCCAAGAAAGCUGUGGGAAA	UCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen12g009100.1	3.0	-1.0	1	21	1106	1126	GUCCAAGAAAGCUGUGGGAAA	ACAUCCGUAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen12g026690.1	3.0	-1.0	1	21	196	216	GUCCAAGAAAGCUGUGGGAAA	UCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen10g031100.2	3.0	-1.0	1	21	247	267	GUCCAAGAAAGCUGUGGGAAA	ACCCUUAUAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen10g031100.1	3.0	-1.0	1	21	247	267	GUCCAAGAAAGCUGUGGGAAA	ACCCUUAUAGCUUUCUUGGAU	Cleavage
spe-miR396-1-3p	Sopen03g007020.1	3.0	-1.0	1	21	360	380	GUCCAAGAAAGCUGUGGGAAA	UCUCUUAUACCUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen10g021510.1	3.0	-1.0	1	21	235	255	GUCCAAGAAAGCUGUGGGAAA	CAGCCUAUAGCUUUUUUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g015880.1	3.0	-1.0	1	21	1411	1431	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g012970.1	3.0	-1.0	1	21	976	996	GUCCAAGAAAGCUGUGGGAAA	ACUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen08g018050.1	3.0	-1.0	1	21	3073	3093	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen08g012280.1	3.0	-1.0	1	21	394	414	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g021470.1	3.0	-1.0	1	21	1840	1860	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g019350.1	3.0	-1.0	1	21	2500	2520	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g016280.1	3.0	-1.0	1	21	2701	2721	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g020510.1	3.0	-1.0	1	21	1837	1857	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen05g023720.1	3.0	-1.0	1	21	1429	1449	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage

spe-miR396-1-3p	Sopen07g006980.1	3.0	-1.0	1	21	1651	1671	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen05g021310.1	3.0	-1.0	1	21	1519	1539	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g026010.1	3.0	-1.0	1	21	916	936	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g008020.1	3.0	-1.0	1	21	1909	1929	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g006960.1	3.0	-1.0	1	21	1285	1305	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g006960.2	3.0	-1.0	1	21	1249	1269	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen03g020900.1	3.0	-1.0	1	21	1723	1743	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g014660.2	3.0	-1.0	1	21	955	975	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g013840.1	3.0	-1.0	1	21	592	612	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g023320.1	3.0	-1.0	1	21	1273	1293	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen05g023440.1	3.0	-1.0	1	21	697	717	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen11g020690.1	3.0	-1.0	1	21	1123	1143	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g008850.1	3.0	-1.0	1	21	1426	1446	GUCCAAGAAAGCUGUGGGAAA	GCUCCUACAGUUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g010520.1	3.0	-1.0	1	21	661	681	GUCCAAGAAAGCUGUGGGAAA	GAUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen08g009810.1	3.0	-1.0	1	21	796	816	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen08g006760.1	3.0	-1.0	1	21	430	450	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen10g021290.1	3.0	-1.0	1	21	1060	1080	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g010870.1	3.0	-1.0	1	21	1150	1170	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen05g016800.1	3.0	-1.0	1	21	769	789	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g015330.1	3.0	-1.0	1	21	1285	1305	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g015590.1	3.0	-1.0	1	21	694	714	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen11g023780.1	3.0	-1.0	1	21	994	1014	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen00g013010.1	3.0	-1.0	1	21	1567	1587	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUUAUGGAC	Cleavage
spe-miR396-1-3p	Sopen07g007470.1	3.0	-1.0	1	21	256	276	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen10g011470.1	3.0	-1.0	1	21	232	252	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen12g029700.1	3.0	-1.0	1	21	1092	1112	GUCCAAGAAAGCUGUGGGAAA	GGUUCUGCAGCUUCCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen07g020960.1	3.0	-1.0	1	21	868	888	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen05g026160.1	3.0	-1.0	1	21	826	846	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen11g021260.1	3.0	-1.0	1	21	289	309	GUCCAAGAAAGCUGUGGGAAA	GGUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen10g021940.1	3.0	-1.0	1	21	205	225	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen07g007070.1	3.0	-1.0	1	21	22	42	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen09g023450.1	3.0	-1.0	1	21	1417	1437	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen12g026790.1	3.0	-1.0	1	21	628	648	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen01g009670.1	3.0	-1.0	1	21	856	876	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen06g013100.1	3.0	-1.0	1	21	22	42	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen12g016890.1	3.0	-1.0	1	21	364	384	GUCCAAGAAAGCUGUGGGAAA	GCUCCUGCAGCUUUCAUGGAU	Cleavage
spe-miR396-1-3p	Sopen04g005180.1	3.0	-1.0	1	21	643	663	GUCCAAGAAAGCUGUGGGAAA	UCUGCCAUUGCUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen09g013040.1	3.0	-1.0	1	21	787	807	GUCCAAGAAAGCUGUGGGAAA	GAUCUAAUGGUUUUCUUGGAC	Cleavage
spe-miR396-1-3p	Sopen09g013040.2	3.0	-1.0	1	21	787	807	GUCCAAGAAAGCUGUGGGAAA	GAUCUAAUGGUUUUCUUGGAC	Cleavage
spe-miR396-1-5p	Sopen02g016540.1	3.0	-1.0	1	21	728	748	UUCCACAGCUUUCUUGAACUU	GAGUUUGUGAAGGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen02g013760.2	2.0	-1.0	1	21	1150	1170	UUCCACAGCUUUCUUGAACUU	AGGAUCAGGAAAGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen02g013760.1	2.0	-1.0	1	21	1150	1170	UUCCACAGCUUUCUUGAACUU	AGGAUCAGGAAAGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen12g030570.1	2.0	-1.0	1	21	461	481	UUCCACAGCUUUCUUGAACUU	AGGAUCAAGGAAGCUGUGGGA	Cleavage
spe-miR396-1-5p	Sopen01g049740.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen01g047890.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen05g007960.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen12g009510.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen07g018530.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen05g025680.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen02g006210.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAAAGAGUUGUGGAA	Cleavage

spe-miR396-1-5p	Sopen02g020300.2	2.5	-1.0	1	21	391	411	UUCCACAGCUUUCUUGAACUU	AUCUUUGAGAGAGCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen02g020300.1	2.5	-1.0	1	21	271	291	UUCCACAGCUUUCUUGAACUU	AUCUUUGAGAGAGCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen01g044760.1	2.5	-1.0	1	21	475	495	UUCCACAGCUUUCUUGAACUU	GAGGUGAAGAAAGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen01g028340.1	2.5	-1.0	1	21	88	108	UUCCACAGCUUUCUUGAACUU	CUUUUCAAGAAAGCUGUGCAA	Cleavage
spe-miR396-1-5p	Sopen12g030600.1	2.5	-1.0	1	21	1369	1389	UUCCACAGCUUUCUUGAACUU	AUGAUUAAGAGAGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen01g054420.1	2.5	-1.0	1	21	1444	1464	UUCCACAGCUUUCUUGAACUU	UUGUAUGAGAAAGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen03g012400.1	3.0	-1.0	1	21	1129	1149	UUCCACAGCUUUCUUGAACUU	AAGUUUAAGAAAGAUGUGGAU	Cleavage
spe-miR396-1-5p	Sopen09g016510.1	3.0	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUU	AAGUUCAAUAGAGUUGUGGGA	Cleavage
spe-miR396-1-5p	Sopen12g011470.1	3.0	-1.0	1	21	737	757	UUCCACAGCUUUCUUGAACUU	GAGUUCAGGGAGGAUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen04g024640.1	3.0	-1.0	1	21	408	428	UUCCACAGCUUUCUUGAACUU	UAGUUUAAGAGAGUGGUGGAA	Cleavage
spe-miR396-1-5p	Sopen01g037310.1	3.0	-1.0	1	21	468	489	UUCCACA-GCUUUCUUGAACUU	ACGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen02g036640.1	3.0	-1.0	1	21	753	774	UUCCACA-GCUUUCUUGAACUU	UCGUUCAAGAAAGCAUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen02g036640.2	3.0	-1.0	1	21	744	765	UUCCACA-GCUUUCUUGAACUU	UCGUUCAAGAAAGCAUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen04g031110.1	3.0	-1.0	1	21	720	741	UUCCACA-GCUUUCUUGAACUU	UCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen02g013780.1	3.0	-1.0	1	21	862	882	UUCCACAGCUUUCUUGAACUU	GAGAUCAAGAAAUCUGUGGGA	Cleavage
spe-miR396-1-5p	Sopen02g013780.2	3.0	-1.0	1	21	814	834	UUCCACAGCUUUCUUGAACUU	GAGAUCAAGAAAUCUGUGGGA	Cleavage
spe-miR396-1-5p	Sopen03g022150.1	3.0	-1.0	1	21	462	483	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCAUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen10g032980.1	3.0	-1.0	1	21	576	597	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen08g031420.1	3.0	-1.0	1	21	465	486	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen08g024600.1	3.0	-1.0	1	21	375	396	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen08g001470.1	3.0	-1.0	1	21	384	405	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen07g021120.1	3.0	-1.0	1	21	342	363	UUCCACA-GCUUUCUUGAACUU	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen07g027420.1	3.0	-1.0	1	21	101	121	UUCCACAGCUUUCUUGAACUU	AGGAUCAAAAAAGUUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen06g002240.1	3.0	-1.0	1	21	2189	2209	UUCCACAGCUUUCUUGAACUU	UAGAUCGAGAAAGCUGUGAAA	Cleavage
spe-miR396-1-5p	Sopen11g020570.1	3.0	-1.0	1	21	1	21	UUCCACAGCUUUCUUGAACUU	AUGUUCAAGAAGGCAGUGGAC	Cleavage
spe-miR396-1-5p	Sopen12g029640.1	3.0	-1.0	1	21	418	438	UUCCACAGCUUUCUUGAACUU	CAAUUCGAAAAAGCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen09g023800.1	3.0	-1.0	1	21	4231	4251	UUCCACAGCUUUCUUGAACUU	UGCUUCAAGGAAGCUGUAGAA	Cleavage
spe-miR396-1-5p	Sopen01g016080.1	3.0	-1.0	1	21	3482	3502	UUCCACAGCUUUCUUGAACUU	GAGGUCAUGGAGGCUGUGGAA	Cleavage
spe-miR396-1-5p	Sopen08g019820.1	3.0	-1.0	1	21	2052	2072	UUCCACAGCUUUCUUGAACUU	CCCUUCAAGAGAGCUGUCGAA	Cleavage
spe-miR396-1-5p	Sopen11g008280.1	3.0	-1.0	1	21	544	564	UUCCACAGCUUUCUUGAACUU	GAGUUUUCGAAAGCUGUGGAG	Cleavage
spe-miR396-1-5p	Sopen10g030300.1	3.0	-1.0	1	21	1029	1049	UUCCACAGCUUUCUUGAACUU	UCGUUCAAGAAGGUUGAGGGA	Cleavage
spe-miR396-1-5p	Sopen10g030300.2	3.0	-1.0	1	21	1029	1049	UUCCACAGCUUUCUUGAACUU	UCGUUCAAGAAGGUUGAGGGA	Cleavage
spe-miR396-2-3p	Sopen06g025980.1	2.5	-1.0	1	21	1429	1449	GUUCAAGAAAGCUGUGGAAAA	AUUUUUACAGUUUUCUUGAAG	Cleavage
spe-miR396-2-3p	Sopen10g032790.1	2.5	-1.0	1	21	1718	1738	GUUCAAGAAAGCUGUGGAAAA	UCUGUCACGGCUUUCUUGAAU	Cleavage
spe-miR396-2-3p	Sopen12g002820.1	3.0	-1.0	1	21	301	321	GUUCAAGAAAGCUGUGGAAAA	UUCUUCGUAGCUUUCUUGGAC	Cleavage
spe-miR396-2-3p	Sopen09g014510.1	3.0	-1.0	1	21	1070	1090	GUUCAAGAAAGCUGUGGAAAA	AUAUCCGUAGCUUUCUUGGAU	Cleavage
spe-miR396-2-3p	Sopen07g011490.1	3.0	-1.0	1	21	2845	2865	GUUCAAGAAAGCUGUGGAAAA	AGUUUCACCGCUUUCUUGAAA	Cleavage
spe-miR396-2-3p	Sopen12g009100.1	3.0	-1.0	1	21	1106	1126	GUUCAAGAAAGCUGUGGAAAA	ACAUCCGUAGCUUUCUUGGAU	Cleavage
spe-miR396-2-3p	Sopen01g030220.2	3.0	-1.0	1	21	2320	2340	GUUCAAGAAAGCUGUGGAAAA	CUCUACACAGCUUUCUUGAAG	Cleavage
spe-miR396-2-3p	Sopen01g030220.1	3.0	-1.0	1	21	2320	2340	GUUCAAGAAAGCUGUGGAAAA	CUCUACACAGCUUUCUUGAAG	Cleavage
spe-miR396-2-3p	Sopen11g006430.1	3.0	-1.0	1	21	50	70	GUUCAAGAAAGCUGUGGAAAA	AGUUUCAUAGUUUUCUUGAUC	Cleavage
spe-miR396-2-3p	Sopen12g029700.1	3.0	-1.0	1	21	1092	1112	GUUCAAGAAAGCUGUGGAAAA	GGUUCUGCAGCUUCCUUGGAC	Cleavage
spe-miR396-2-3p	Sopen02g026050.1	3.0	-1.0	1	21	1815	1837	GUUCAAGAAAGCUGU--GGAAAA	CCUUCCUAACAGCUUUUUUGAAC	Cleavage
spe-miR396-2-3p	Sopen04g011340.1	3.0	-1.0	1	21	484	504	GUUCAAGAAAGCUGUGGAAAA	GCUCCUGCAGCUUUCUUGGAU	Cleavage
spe-miR396-2-3p	Sopen01g039460.1	3.0	-1.0	1	21	1795	1815	GUUCAAGAAAGCUGUGGAAAA	GCUUUCAGAGUUUUUUUGAAU	Cleavage
spe-miR396-2-5p	Sopen12g030570.1	2.0	-1.0	1	21	461	481	UCCCACAGCUUUCUUGGACUU	AGGAUCAAGGAAGCUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen10g015040.1	2.5	-1.0	1	21	240	260	UCCCACAGCUUUCUUGGACUU	AAGACUAAGAGAGUUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen00g008240.1	2.5	-1.0	1	21	925	945	UCCCACAGCUUUCUUGGACUU	GUUUGCAAGGAAGCUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen06g019510.1	2.5	-1.0	1	21	691	711	UCCCACAGCUUUCUUGGACUU	ACGUCCUUGGAAGCUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen09g016510.1	3.0	-1.0	1	21	306	326	UCCCACAGCUUUCUUGGACUU	AAGUUCAAUAGAGUUGUGGGA	Cleavage

spe-miR396-2-5p	Sopen12g025180.1	3.0	-1.0	1	21	219	239	UCCCACAGCUUUCUUGGACUU	AAGGCUAAGAAAGCUUUGGGA	Cleavage
spe-miR396-2-5p	Sopen02g013780.1	3.0	-1.0	1	21	862	882	UCCCACAGCUUUCUUGGACUU	GAGAUCAAGAAAUCUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen02g013780.2	3.0	-1.0	1	21	814	834	UCCCACAGCUUUCUUGGACUU	GAGAUCAAGAAAUCUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen10g030300.1	3.0	-1.0	1	21	1029	1049	UCCCACAGCUUUCUUGGACUU	UCGUUCAAGAAGGUUGAGGGA	Cleavage
spe-miR396-2-5p	Sopen10g030300.2	3.0	-1.0	1	21	1029	1049	UCCCACAGCUUUCUUGGACUU	UCGUUCAAGAAGGUUGAGGGA	Cleavage
spe-miR396-2-5p	Sopen09g007660.1	3.0	-1.0	1	21	1833	1853	UCCCACAGCUUUCUUGGACUU	UUGUCUGGGAAAACUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen10g027940.1	3.0	-1.0	1	21	285	305	UCCCACAGCUUUCUUGGACUU	UUGUCUGGGAAAGCUCUGGGA	Cleavage
spe-miR396-2-5p	Sopen10g027940.2	3.0	-1.0	1	21	285	305	UCCCACAGCUUUCUUGGACUU	UUGUCUGGGAAAGCUCUGGGA	Cleavage
spe-miR396-2-5p	Sopen02g015760.1	3.0	-1.0	1	21	598	618	UCCCACAGCUUUCUUGGACUU	AUGGUUAAGGAGGCUGUGGGA	Cleavage
spe-miR396-2-5p	Sopen07g014510.1	3.0	-1.0	1	21	355	375	UCCCACAGCUUUCUUGGACUU	GUGUGCAAGGAAGCUGCGGGA	Cleavage
spe-miR396-2-5p	Sopen11g021700.1	3.0	-1.0	1	21	19	39	UCCCACAGCUUUCUUGGACUU	CCGACUAAGAGAGUUGUGGGG	Cleavage
spe-miR396a-3p	Sopen06g022530.1	2.5	-1.0	1	21	197	217	GUUCAAUAAAGCUGUGGGAAG	AUUCCUGCAGCUUUGUUGAAA	Cleavage
spe-miR396a-3p	Sopen07g005380.1	2.5	-1.0	1	21	1259	1279	GUUCAAUAAAGCUGUGGGAAG	AUUCUCACAAUUUUAUUGAAC	Cleavage
spe-miR396a-3p	Sopen01g010380.1	2.5	-1.0	1	21	695	715	GUUCAAUAAAGCUGUGGGAAG	GUUCUCACAAUUUUAUUGAAC	Cleavage
spe-miR396a-3p	Sopen06g015970.1	2.5	-1.0	1	21	2736	2756	GUUCAAUAAAGCUGUGGGAAG	ACUACCACAGUUUUAUUGGGC	Cleavage
spe-miR396a-5p	Sopen02g013760.2	2.0	-1.0	1	21	1150	1170	UUCCACAGCUUUCUUGAACUG	AGGAUCAGGAAAGCUGUGGAG	Cleavage
spe-miR396a-5p	Sopen02g013760.1	2.0	-1.0	1	21	1150	1170	UUCCACAGCUUUCUUGAACUG	AGGAUCAGGAAAGCUGUGGAG	Cleavage
spe-miR396a-5p	Sopen12g030570.1	2.0	-1.0	1	21	461	481	UUCCACAGCUUUCUUGAACUG	AGGAUCAAGGAAGCUGUGGGA	Cleavage
spe-miR396a-5p	Sopen01g049740.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen01g047890.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen05g007960.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen12g009510.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen07g018530.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen05g025680.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen02g006210.1	2.5	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAAAGAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen02g020300.2	2.5	-1.0	1	21	391	411	UUCCACAGCUUUCUUGAACUG	AUCUUUGAGAGAGCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen02g020300.1	2.5	-1.0	1	21	271	291	UUCCACAGCUUUCUUGAACUG	AUCUUUGAGAGAGCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen01g028340.1	2.5	-1.0	1	21	88	108	UUCCACAGCUUUCUUGAACUG	CUUUUCAAGAAAGCUGUGCAA	Cleavage
spe-miR396a-5p	Sopen01g044760.1	2.5	-1.0	1	21	475	495	UUCCACAGCUUUCUUGAACUG	GAGGUGAAGAAAGCUGUGGAG	Cleavage
spe-miR396a-5p	Sopen01g054420.1	2.5	-1.0	1	21	1444	1464	UUCCACAGCUUUCUUGAACUG	UUGUAUGAGAAAGCUGUGGAG	Cleavage
spe-miR396a-5p	Sopen12g030600.1	2.5	-1.0	1	21	1369	1389	UUCCACAGCUUUCUUGAACUG	AUGAUUAAGAGAGCUGUGGAG	Cleavage
spe-miR396a-5p	Sopen04g024640.1	3.0	-1.0	1	21	408	428	UUCCACAGCUUUCUUGAACUG	UAGUUUAAGAGAGUGGUGGAA	Cleavage
spe-miR396a-5p	Sopen12g029640.1	3.0	-1.0	1	21	418	438	UUCCACAGCUUUCUUGAACUG	CAAUUCGAAAAAGCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen03g012400.1	3.0	-1.0	1	21	1129	1149	UUCCACAGCUUUCUUGAACUG	AAGUUUAAGAAAGAUGUGGAU	Cleavage
spe-miR396a-5p	Sopen03g022150.1	3.0	-1.0	1	21	462	483	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCAUGUGGAA	Cleavage
spe-miR396a-5p	Sopen10g032980.1	3.0	-1.0	1	21	576	597	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen08g031420.1	3.0	-1.0	1	21	465	486	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen08g024600.1	3.0	-1.0	1	21	375	396	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen08g001470.1	3.0	-1.0	1	21	384	405	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen07g021120.1	3.0	-1.0	1	21	342	363	UUCCACA-GCUUUCUUGAACUG	CCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen12g011470.1	3.0	-1.0	1	21	737	757	UUCCACAGCUUUCUUGAACUG	GAGUUCAGGGAGGAUGUGGAA	Cleavage
spe-miR396a-5p	Sopen09g016510.1	3.0	-1.0	1	21	306	326	UUCCACAGCUUUCUUGAACUG	AAGUUCAAUAGAGUUGUGGGA	Cleavage
spe-miR396a-5p	Sopen06g002240.1	3.0	-1.0	1	21	2189	2209	UUCCACAGCUUUCUUGAACUG	UAGAUCGAGAAAGCUGUGAAA	Cleavage
spe-miR396a-5p	Sopen02g036640.1	3.0	-1.0	1	21	753	774	UUCCACA-GCUUUCUUGAACUG	UCGUUCAAGAAAGCAUGUGGAA	Cleavage
spe-miR396a-5p	Sopen02g036640.2	3.0	-1.0	1	21	744	765	UUCCACA-GCUUUCUUGAACUG	UCGUUCAAGAAAGCAUGUGGAA	Cleavage
spe-miR396a-5p	Sopen04g031110.1	3.0	-1.0	1	21	720	741	UUCCACA-GCUUUCUUGAACUG	UCGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen01g037310.1	3.0	-1.0	1	21	468	489	UUCCACA-GCUUUCUUGAACUG	ACGUUCAAGAAAGCCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen02g013780.1	3.0	-1.0	1	21	862	882	UUCCACAGCUUUCUUGAACUG	GAGAUCAAGAAAUCUGUGGGA	Cleavage
spe-miR396a-5p	Sopen02g013780.2	3.0	-1.0	1	21	814	834	UUCCACAGCUUUCUUGAACUG	GAGAUCAAGAAAUCUGUGGGA	Cleavage
spe-miR396a-5p	Sopen02g016540.1	3.0	-1.0	1	21	728	748	UUCCACAGCUUUCUUGAACUG	GAGUUUGUGAAGGCUGUGGAG	Cleavage

spe-miR396a-5p	Sopen09g023800.1	3.0	-1.0	1	21	4231	4251	UUCCACAGCUUUCUUGAACUG	UGCUUCAAGGAAGCUGUAGAA	Cleavage
spe-miR396a-5p	Sopen08g019820.1	3.0	-1.0	1	21	2052	2072	UUCCACAGCUUUCUUGAACUG	CCCUUCAAGAGAGCUGUCGAA	Cleavage
spe-miR396a-5p	Sopen11g020570.1	3.0	-1.0	1	21	1	21	UUCCACAGCUUUCUUGAACUG	AUGUUCAAGAAGGCAGUGGAC	Cleavage
spe-miR396a-5p	Sopen10g030300.1	3.0	-1.0	1	21	1029	1049	UUCCACAGCUUUCUUGAACUG	UCGUUCAAGAAGGUUGAGGGA	Cleavage
spe-miR396a-5p	Sopen10g030300.2	3.0	-1.0	1	21	1029	1049	UUCCACAGCUUUCUUGAACUG	UCGUUCAAGAAGGUUGAGGGA	Cleavage
spe-miR396a-5p	Sopen01g016080.1	3.0	-1.0	1	21	3482	3502	UUCCACAGCUUUCUUGAACUG	GAGGUCAUGGAGGCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen11g008280.1	3.0	-1.0	1	21	544	564	UUCCACAGCUUUCUUGAACUG	GAGUUUUCGAAAGCUGUGGAG	Cleavage
spe-miR396a-5p	Sopen07g027420.1	3.0	-1.0	1	21	101	121	UUCCACAGCUUUCUUGAACUG	AGGAUCAAAAAAGUUGUGGAA	Cleavage
spe-miR396a-5p	Sopen08g021930.1	3.0	-1.0	1	21	4096	4116	UUCCACAGCUUUCUUGAACUG	CCAUAUGAGAAAGCUGUGGAA	Cleavage
spe-miR396a-5p	Sopen00g008240.1	3.0	-1.0	1	21	925	945	UUCCACAGCUUUCUUGAACUG	GUUUGCAAGGAAGCUGUGGGA	Cleavage
spe-miR397-3p	Sopen11g024230.1	3.0	-1.0	1	21	190	210	CAUCAACGCUACACUCGAUCA	AGAUCGAGGGAAGCGUUGAUG	Translation
spe-miR397-3p	Sopen11g016530.1	3.0	-1.0	1	21	1927	1947	CAUCAACGCUACACUCGAUCA	UGCUCUGGUGUGGCGUUGAUG	Cleavage
spe-miR397-3p	Sopen11g016530.2	3.0	-1.0	1	21	1927	1947	CAUCAACGCUACACUCGAUCA	UGCUCUGGUGUGGCGUUGAUG	Cleavage
spe-miR397-3p	Sopen11g016530.3	3.0	-1.0	1	21	1927	1947	CAUCAACGCUACACUCGAUCA	UGCUCUGGUGUGGCGUUGAUG	Cleavage
spe-miR397-3p	Sopen08g028790.1	3.0	-1.0	1	21	209	229	CAUCAACGCUACACUCGAUCA	CCGUUGGGUGUAGUGUUGAUU	Cleavage
spe-miR397-3p	Sopen08g027850.1	3.0	-1.0	1	21	76	96	CAUCAACGCUACACUCGAUCA	GAAUCGAGUGUAGCGGAGAUG	Cleavage
spe-miR397-5p	Sopen07g024810.1	0.5	-1.0	1	21	661	681	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAACGCUGCGCUCAAU	Cleavage
spe-miR397-5p	Sopen06g033620.1	1.0	-1.0	1	21	682	702	AUUGAGUGCAGCGUUGAUGAC	GUGAUCAACGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen06g033640.1	1.0	-1.0	1	21	664	684	AUUGAGUGCAGCGUUGAUGAC	GUGAUCAACGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen06g033630.1	1.0	-1.0	1	21	664	684	AUUGAGUGCAGCGUUGAUGAC	GUGAUCAACGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen10g028490.1	1.0	-1.0	1	21	661	681	AUUGAGUGCAGCGUUGAUGAC	GUAAUCAACGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen06g032740.1	1.0	-1.0	1	21	691	711	AUUGAGUGCAGCGUUGAUGAC	AUAAUCAACGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen02g013680.1	1.5	-1.0	1	21	532	552	AUUGAGUGCAGCGUUGAUGAC	AUUGUCAAUGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen09g005780.1	1.5	-1.0	1	21	667	687	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAACGCUGCACUUAAU	Cleavage
spe-miR397-5p	Sopen09g005720.1	1.5	-1.0	1	21	667	687	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAACGCUGCACUUAAU	Cleavage
spe-miR397-5p	Sopen05g026580.1	1.5	-1.0	1	21	454	474	AUUGAGUGCAGCGUUGAUGAC	AUAAUCAAUGCUGCACUCAAU	Cleavage
spe-miR397-5p	Sopen06g015180.1	2.0	-1.0	1	21	685	705	AUUGAGUGCAGCGUUGAUGAC	GUUAUCAAUGCUGCACUCAAC	Cleavage
spe-miR397-5p	Sopen09g007120.1	2.0	-1.0	1	21	664	684	AUUGAGUGCAGCGUUGAUGAC	GUAAUCAACGCUGCACUCAAC	Cleavage
spe-miR397-5p	Sopen07g032060.2	2.0	-1.0	1	21	1102	1122	AUUGAGUGCAGCGUUGAUGAC	UACCUCAACGUUGCACUUAAU	Cleavage
spe-miR397-5p	Sopen07g032060.1	2.0	-1.0	1	21	1102	1122	AUUGAGUGCAGCGUUGAUGAC	UACCUCAACGUUGCACUUAAU	Cleavage
spe-miR397-5p	Sopen02g029810.1	2.5	-1.0	1	21	673	693	AUUGAGUGCAGCGUUGAUGAC	AUUAUCAAUGCUGCUCUCAAU	Cleavage
spe-miR397-5p	Sopen06g033140.1	2.5	-1.0	1	21	679	699	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAAUGCUGCAUUAAAU	Cleavage
spe-miR397-5p	Sopen09g005710.1	2.5	-1.0	1	21	781	801	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAACGCUGCACUAAAU	Cleavage
spe-miR397-5p	Sopen05g030930.1	3.0	-1.0	1	21	673	693	AUUGAGUGCAGCGUUGAUGAC	GUUAUCAACGCUGCACUGAAC	Cleavage
spe-miR397-5p	Sopen01g051120.1	3.0	-1.0	1	21	1871	1891	AUUGAGUGCAGCGUUGAUGAC	UUCAUCAGCGUUGCAUUCAGC	Cleavage
spe-miR397-5p	Sopen02g023540.1	3.0	-1.0	1	21	1171	1191	AUUGAGUGCAGCGUUGAUGAC	CUCAUCAAUGCUGGACUCAAG	Cleavage
spe-miR397-5p	Sopen02g029800.1	3.0	-1.0	1	21	673	693	AUUGAGUGCAGCGUUGAUGAC	AUUGUCAAUGCUGCUCUCAAU	Cleavage
spe-miR397-5p	Sopen03g025230.1	3.0	-1.0	1	21	150	170	AUUGAGUGCAGCGUUGAUGAC	AUCAUCAACGGUGAACUCAAU	Translation
spe-miR397-5p	Sopen09g006750.1	3.0	-1.0	1	21	385	405	AUUGAGUGCAGCGUUGAUGAC	UUGAUCAAUGCUGCACUUAAC	Cleavage
spe-miR397-5p	Sopen12g015390.1	3.0	-1.0	1	21	505	525	AUUGAGUGCAGCGUUGAUGAC	GGUGUCAACGCUGCACUAGAU	Cleavage
spe-miR397-5p	Sopen10g032510.1	3.0	-1.0	1	21	214	234	AUUGAGUGCAGCGUUGAUGAC	UGCUUCAACGUGGCACUCAAU	Translation
spe-miR397-5p	Sopen09g010490.1	3.0	-1.0	1	21	310	330	AUUGAGUGCAGCGUUGAUGAC	AGCUUCAAUGUUGCAUUCAGU	Cleavage
spe-miR397-5p	Sopen09g010490.2	3.0	-1.0	1	21	310	330	AUUGAGUGCAGCGUUGAUGAC	AGCUUCAAUGUUGCAUUCAGU	Cleavage
spe-miR398-3p	Sopen02g014920.1	2.5	-1.0	1	21	403	423	UGUGUUCUCAGGUCGCCCCUG	AGGGGGUGGCCUGGGGGCACA	Cleavage
spe-miR398-3p	Sopen03g023930.1	3.0	-1.0	1	21	1275	1295	UGUGUUCUCAGGUCGCCCCUG	UUCGGCUGACCUGGGAACACA	Cleavage
spe-miR398-3p	Sopen08g011100.1	3.0	-1.0	1	21	310	330	UGUGUUCUCAGGUCGCCCCUG	AUGGCGCGACUUGAGGACAUG	Cleavage
spe-miR398-5p	Sopen06g001460.1	2.5	-1.0	1	21	571	591	AGGGCAACUUGAGAUCACAUG	AAUGUGGUCUUGAGUUGUCUU	Cleavage
spe-miR398-5p	Sopen11g003660.1	3.0	-1.0	1	21	1553	1573	AGGGCAACUUGAGAUCACAUG	CUUGUGAUCUUGGGUUGCCAU	Cleavage
spe-miR398-5p	Sopen01g030340.1	3.0	-1.0	1	21	19	39	AGGGCAACUUGAGAUCACAUG	UCUGACACCUCAAGUUGCCCU	Cleavage
spe-miR398a-3p	Sopen08g011100.1	2.5	-1.0	1	20	311	330	UAUGUUCUCAGGUCGCCCCU	UGGCGCGACUUGAGGACAUG	Cleavage

spe-miR398a-3p	Sopen03g027080.1	3.0	-1.0	1	20	884	903	UAUGUUCUCAGGUCGCCCCU	UGGGGCGAGUUGAGAAUAUG	Cleavage
spe-miR398a-3p	Sopen04g014020.1	3.0	-1.0	1	20	968	987	UAUGUUCUCAGGUCGCCCCU	UGGUGCGAUUUGAGGACAUG	Cleavage
spe-miR398a-3p	Sopen12g028280.1	3.0	-1.0	1	20	1139	1158	UAUGUUCUCAGGUCGCCCCU	UGGCGCGACUUGAGGAUAUG	Cleavage
spe-miR398a-3p	Sopen03g013720.1	3.0	-1.0	1	20	902	921	UAUGUUCUCAGGUCGCCCCU	UGGCGCGACUUGAGGAUAUG	Cleavage
spe-miR398a-3p	Sopen11g011670.1	3.0	-1.0	1	20	1475	1494	UAUGUUCUCAGGUCGCCCCU	UGGCGCGAUUUGAGAAUAUG	Cleavage
spe-miR398a-3p	Sopen03g026930.1	3.0	-1.0	1	20	3104	3123	UAUGUUCUCAGGUCGCCCCU	UGGCGCGACUUGAGGAUAUG	Cleavage
spe-miR398a-3p	Sopen08g031400.1	3.0	-1.0	1	20	434	453	UAUGUUCUCAGGUCGCCCCU	GGGAGAGACCUGAGGACAUG	Cleavage
spe-miR398a-5p	Sopen06g033570.1	2.0	-1.0	1	21	719	739	GGGUUGAUUUGAGAACAUAUG	AGAAUGUUCUUAAAUCAGCCC	Cleavage
spe-miR398a-5p	Sopen03g009140.1	3.0	-1.0	1	21	2037	2057	GGGUUGAUUUGAGAACAUAUG	CAUAAGUUCUCAAAAUAACCC	Cleavage
spe-miR398a-5p	Sopen06g011340.1	3.0	-1.0	1	21	904	924	GGGUUGAUUUGAGAACAUAUG	UCUGUGUUAUUAGAUCAACCC	Cleavage
spe-miR398a-5p	Sopen12g008270.1	3.0	-1.0	1	21	307	327	GGGUUGAUUUGAGAACAUAUG	GAUAUGCACUCAAAUCAGCUC	Cleavage
spe-miR398a-5p	Sopen08g020630.1	3.0	-1.0	1	21	1320	1340	GGGUUGAUUUGAGAACAUAUG	AAGAGGUUCUCAAGUCAACUC	Cleavage
spe-miR398a-5p	Sopen11g018470.1	3.0	-1.0	1	21	910	930	GGGUUGAUUUGAGAACAUAUG	AAGAUAUUCUCAAAUCAACUU	Cleavage
spe-miR398a-5p	Sopen09g018880.1	3.0	-1.0	1	21	1295	1315	GGGUUGAUUUGAGAACAUAUG	UGUAUUCUCUUAAAUUAACCC	Cleavage
spe-miR398a-5p	Sopen12g029030.2	3.0	-1.0	1	21	995	1015	GGGUUGAUUUGAGAACAUAUG	CCUAUGAUCUCAAAUCAAUAC	Cleavage
spe-miR398a-5p	Sopen12g029030.1	3.0	-1.0	1	21	995	1015	GGGUUGAUUUGAGAACAUAUG	CCUAUGAUCUCAAAUCAAUAC	Cleavage
spe-miR398a-5p	Sopen02g026760.1	3.0	-1.0	1	21	148	168	GGGUUGAUUUGAGAACAUAUG	UGUAUUUCUUCAAGUCAACCC	Cleavage
spe-miR398a-5p	Sopen03g027670.1	3.0	-1.0	1	21	689	709	GGGUUGAUUUGAGAACAUAUG	GCUAUAUUUUUGAAUCAACUC	Cleavage
spe-miR398b-1-3p	Sopen02g014920.1	2.0	-1.0	1	21	404	424	UUGUGUUCUCAGGUCACCCCU	GGGGGUGGCCUGGGGGCACAA	Cleavage
spe-miR398b-1-3p	Sopen03g023930.1	2.5	-1.0	1	21	1276	1296	UUGUGUUCUCAGGUCACCCCU	UCGGCUGACCUGGGAACACAU	Cleavage
spe-miR398b-1-3p	Sopen01g013350.1	3.0	-1.0	1	21	388	408	UUGUGUUCUCAGGUCACCCCU	AGUGGUGAUUUGAGGAUACAA	Cleavage
spe-miR398b-1-3p	Sopen07g033090.1	3.0	-1.0	1	21	66	86	UUGUGUUCUCAGGUCACCCCU	ACCGGUGGCCGGAGAACACAA	Translation
spe-miR398b-1-3p	Sopen02g037330.1	3.0	-1.0	1	21	994	1014	UUGUGUUCUCAGGUCACCCCU	AUGGGUGACAUGAUAACACAA	Cleavage
spe-miR398b-1-3p	Sopen06g031830.2	3.0	-1.0	1	21	1427	1447	UUGUGUUCUCAGGUCACCCCU	GAUGGUUGCCUGAGAACAUAA	Cleavage
spe-miR398b-1-3p	Sopen06g031830.1	3.0	-1.0	1	21	1427	1447	UUGUGUUCUCAGGUCACCCCU	GAUGGUUGCCUGAGAACAUAA	Cleavage
spe-miR398b-1-3p	Sopen10g035120.1	3.0	-1.0	1	21	718	738	UUGUGUUCUCAGGUCACCCCU	UUGGCUGACCUGAAAACACGA	Cleavage
spe-miR398b-1-5p	Sopen09g033390.1	2.5	-1.0	1	22	459	480	GAGUGUGCCUAAGAACACAGGU	AGCUGUGUUCUUUGGUGCACUC	Translation
spe-miR398b-1-5p	Sopen06g026460.1	2.5	-1.0	1	22	1503	1524	GAGUGUGCCUAAGAACACAGGU	UAAUGUGUGCUUAGGUAUACUU	Cleavage
spe-miR398b-1-5p	Sopen10g022080.1	3.0	-1.0	1	22	348	369	GAGUGUGCCUAAGAACACAGGU	AUAUGGGAUCUUAGGCAUACUU	Cleavage
spe-miR398b-2-3p	Sopen02g014920.1	2.0	-1.0	1	21	404	424	UUGUGUUCUCAGGUCACCCCU	GGGGGUGGCCUGGGGGCACAA	Cleavage
spe-miR398b-2-3p	Sopen03g023930.1	2.5	-1.0	1	21	1276	1296	UUGUGUUCUCAGGUCACCCCU	UCGGCUGACCUGGGAACACAU	Cleavage
spe-miR398b-2-3p	Sopen01g013350.1	3.0	-1.0	1	21	388	408	UUGUGUUCUCAGGUCACCCCU	AGUGGUGAUUUGAGGAUACAA	Cleavage
spe-miR398b-2-3p	Sopen07g033090.1	3.0	-1.0	1	21	66	86	UUGUGUUCUCAGGUCACCCCU	ACCGGUGGCCGGAGAACACAA	Translation
spe-miR398b-2-3p	Sopen02g037330.1	3.0	-1.0	1	21	994	1014	UUGUGUUCUCAGGUCACCCCU	AUGGGUGACAUGAUAACACAA	Cleavage
spe-miR398b-2-3p	Sopen06g031830.2	3.0	-1.0	1	21	1427	1447	UUGUGUUCUCAGGUCACCCCU	GAUGGUUGCCUGAGAACAUAA	Cleavage
spe-miR398b-2-3p	Sopen06g031830.1	3.0	-1.0	1	21	1427	1447	UUGUGUUCUCAGGUCACCCCU	GAUGGUUGCCUGAGAACAUAA	Cleavage
spe-miR398b-2-3p	Sopen10g035120.1	3.0	-1.0	1	21	718	738	UUGUGUUCUCAGGUCACCCCU	UUGGCUGACCUGAAAACACGA	Cleavage
spe-miR398b-2-5p	Sopen12g005660.1	2.5	-1.0	1	22	2223	2244	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen08g010040.1	2.5	-1.0	1	22	2934	2955	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen01g007960.1	2.5	-1.0	1	22	3495	3516	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen04g011970.1	2.5	-1.0	1	22	4401	4422	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen07g012820.1	2.5	-1.0	1	22	5208	5229	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen08g006580.1	2.5	-1.0	1	22	5328	5349	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen11g019830.1	2.5	-1.0	1	22	5328	5349	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen03g026030.1	2.5	-1.0	1	22	5328	5349	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen11g014720.1	2.5	-1.0	1	22	5328	5349	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen05g014260.1	2.5	-1.0	1	22	5754	5775	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen05g016700.1	2.5	-1.0	1	22	5082	5103	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen11g009630.1	2.5	-1.0	1	22	6057	6078	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen11g019830.2	2.5	-1.0	1	22	5328	5349	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage

spe-miR398b-2-5p	Sopen07g014000.1	2.5	-1.0	1	22	6114	6135	GAGUGUGCCUGGAAACACAGGU	GCGCGUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen01g054390.1	2.5	-1.0	1	22	30	51	GAGUGUGCCUGGAAACACAGGU	GUGUGUGUUUCUGGUCACACUC	Cleavage
spe-miR398b-2-5p	Sopen02g003760.1	2.5	-1.0	1	22	2745	2766	GAGUGUGCCUGGAAACACAGGU	GCGUUUGUUUCCAGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen12g015760.1	3.0	-1.0	1	22	207	228	GAGUGUGCCUGGAAACACAGGU	GCGCUUGUUUCCAGGCAUGCUC	Cleavage
spe-miR398b-2-5p	Sopen05g018550.1	3.0	-1.0	1	22	198	219	GAGUGUGCCUGGAAACACAGGU	GCAUUUGUUUCCGGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen08g015590.1	3.0	-1.0	1	22	1176	1197	GAGUGUGCCUGGAAACACAGGU	GCGUUUGUUUCCGGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen02g005160.1	3.0	-1.0	1	22	2454	2475	GAGUGUGCCUGGAAACACAGGU	GCGUUUGUUUCCGGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen05g014210.1	3.0	-1.0	1	22	2079	2100	GAGUGUGCCUGGAAACACAGGU	GCGUUUGUUUCCGGGCAUGCUU	Cleavage
spe-miR398b-2-5p	Sopen06g012550.1	3.0	-1.0	1	22	2151	2172	GAGUGUGCCUGGAAACACAGGU	GCGUUUGUUUCCGGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen03g013000.1	3.0	-1.0	1	22	2961	2982	GAGUGUGCCUGGAAACACAGGU	GCGUUUGUUUCCGGGCAAACUC	Cleavage
spe-miR398b-2-5p	Sopen04g027650.5	3.0	-1.0	1	22	1897	1918	GAGUGUGCCUGGAAACACAGGU	AGGAGUGCUUCUAGGCAUACUC	Cleavage
spe-miR398b-2-5p	Sopen04g027650.4	3.0	-1.0	1	22	1897	1918	GAGUGUGCCUGGAAACACAGGU	AGGAGUGCUUCUAGGCAUACUC	Cleavage
spe-miR398b-2-5p	Sopen04g027650.1	3.0	-1.0	1	22	1897	1918	GAGUGUGCCUGGAAACACAGGU	AGGAGUGCUUCUAGGCAUACUC	Cleavage
spe-miR398b-2-5p	Sopen04g027650.3	3.0	-1.0	1	22	1897	1918	GAGUGUGCCUGGAAACACAGGU	AGGAGUGCUUCUAGGCAUACUC	Cleavage
spe-miR398b-2-5p	Sopen04g027650.2	3.0	-1.0	1	22	1897	1918	GAGUGUGCCUGGAAACACAGGU	AGGAGUGCUUCUAGGCAUACUC	Cleavage
spe-miR398b-2-5p	Sopen10g031200.1	3.0	-1.0	1	22	145	166	GAGUGUGCCUGGAAACACAGGU	AAGUUUGUUUUCUGGCACACUC	Translation
spe-miR399-1-3p	Sopen07g026190.1	3.0	-1.0	1	21	481	501	UGCCAAAGGAGAGUUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399-1-3p	Sopen07g026190.2	3.0	-1.0	1	21	391	411	UGCCAAAGGAGAGUUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399-1-3p	Sopen11g023540.1	3.0	-1.0	1	21	2473	2493	UGCCAAAGGAGAGUUGCCCUG	AAGAGAAACUUUCUUUUGGCA	Cleavage
spe-miR399-1-3p	Sopen01g046300.1	3.0	-1.0	1	21	1887	1907	UGCCAAAGGAGAGUUGCCCUG	GCAGGAAAUUCUCUUUUGGCA	Cleavage
spe-miR399-1-3p	Sopen12g003070.1	3.0	-1.0	1	21	1271	1291	UGCCAAAGGAGAGUUGCCCUG	UUUGGGAACUCUUCUUUGGUA	Cleavage
spe-miR399-1-3p	Sopen01g044310.1	3.0	-1.0	1	21	1413	1433	UGCCAAAGGAGAGUUGCCCUG	UUGGCCAACUCUUCUCUGGCA	Cleavage
spe-miR399-1-5p	Sopen07g010120.1	3.0	-1.0	1	21	2001	2021	GGGCUACGCUCUAUUGGCAUG	GGUGUUAAUAGAAUGUAGCCC	Cleavage
spe-miR399-1-5p	Sopen11g010710.1	3.0	-1.0	1	21	532	552	GGGCUACGCUCUAUUGGCAUG	UUUGCUAAUAGAGCGUAUCCA	Cleavage
spe-miR399-1-5p	Sopen06g016130.1	3.0	-1.0	1	21	258	278	GGGCUACGCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399-2-3p	Sopen07g026190.1	3.0	-1.0	1	21	481	501	UGCCAAAGGAGAGUUGCCCUA	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399-2-3p	Sopen07g026190.2	3.0	-1.0	1	21	391	411	UGCCAAAGGAGAGUUGCCCUA	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399-2-3p	Sopen11g023540.1	3.0	-1.0	1	21	2473	2493	UGCCAAAGGAGAGUUGCCCUA	AAGAGAAACUUUCUUUUGGCA	Cleavage
spe-miR399-2-3p	Sopen01g046300.1	3.0	-1.0	1	21	1887	1907	UGCCAAAGGAGAGUUGCCCUA	GCAGGAAAUUCUCUUUUGGCA	Cleavage
spe-miR399-2-3p	Sopen01g044310.1	3.0	-1.0	1	21	1413	1433	UGCCAAAGGAGAGUUGCCCUA	UUGGCCAACUCUUCUCUGGCA	Cleavage
spe-miR399-2-3p	Sopen12g003070.1	3.0	-1.0	1	21	1271	1291	UGCCAAAGGAGAGUUGCCCUA	UUUGGGAACUCUUCUUUGGUA	Cleavage
spe-miR399-3-3p	Sopen03g020000.1	2.5	-1.0	1	21	591	611	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
spe-miR399-3-5p	Sopen06g016130.1	1.5	-1.0	1	21	258	278	GGGCUACUCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399-3-5p	Sopen03g012230.1	2.0	-1.0	1	21	171	191	GGGCUACUCUCUAUUGGCAUG	AUUGCUAAUAGAAAGUAGCCC	Cleavage
spe-miR399-3-5p	Sopen03g011650.1	2.5	-1.0	1	21	804	824	GGGCUACUCUCUAUUGGCAUG	ACUGACAAUAGAAAGUAGCCC	Cleavage
spe-miR399-3-5p	Sopen01g036990.1	3.0	-1.0	1	21	1020	1040	GGGCUACUCUCUAUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399-3-5p	Sopen12g018160.1	3.0	-1.0	1	21	1223	1243	GGGCUACUCUCUAUUGGCAUG	AUUGCCAACAGAAAGUAGCCC	Cleavage
spe-miR399-4-3p	Sopen03g020000.1	2.5	-1.0	1	21	591	611	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
spe-miR399-4-5p	Sopen06g016130.1	1.5	-1.0	1	21	258	278	GGGCUACUCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399-4-5p	Sopen03g012230.1	2.0	-1.0	1	21	171	191	GGGCUACUCUCUAUUGGCAUG	AUUGCUAAUAGAAAGUAGCCC	Cleavage
spe-miR399-4-5p	Sopen03g011650.1	2.5	-1.0	1	21	804	824	GGGCUACUCUCUAUUGGCAUG	ACUGACAAUAGAAAGUAGCCC	Cleavage
spe-miR399-4-5p	Sopen01g036990.1	3.0	-1.0	1	21	1020	1040	GGGCUACUCUCUAUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399-4-5p	Sopen12g018160.1	3.0	-1.0	1	21	1223	1243	GGGCUACUCUCUAUUGGCAUG	AUUGCCAACAGAAAGUAGCCC	Cleavage
spe-miR399-5-3p	Sopen03g020000.1	2.5	-1.0	1	21	591	611	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
spe-miR399-5-5p	Sopen06g016130.1	1.5	-1.0	1	21	258	278	GGGCUACUCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399-5-5p	Sopen03g012230.1	2.0	-1.0	1	21	171	191	GGGCUACUCUCUAUUGGCAUG	AUUGCUAAUAGAAAGUAGCCC	Cleavage
spe-miR399-5-5p	Sopen03g011650.1	2.5	-1.0	1	21	804	824	GGGCUACUCUCUAUUGGCAUG	ACUGACAAUAGAAAGUAGCCC	Cleavage
spe-miR399-5-5p	Sopen01g036990.1	3.0	-1.0	1	21	1020	1040	GGGCUACUCUCUAUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399-5-5p	Sopen12g018160.1	3.0	-1.0	1	21	1223	1243	GGGCUACUCUCUAUUGGCAUG	AUUGCCAACAGAAAGUAGCCC	Cleavage
spe-miR399-6-3p	Sopen03g020000.1	2.5	-1.0	1	21	591	611	CGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage

spe-miR399-6-5p	Sopen06g016130.1	1.5	-1.0	1	21	258	278	GGGCUACUCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399-6-5p	Sopen03g012230.1	2.0	-1.0	1	21	171	191	GGGCUACUCUCUAUUGGCAUG	AUUGCUAAUAGAAAGUAGCCC	Cleavage
spe-miR399-6-5p	Sopen03g011650.1	2.5	-1.0	1	21	804	824	GGGCUACUCUCUAUUGGCAUG	ACUGACAAUAGAAAGUAGCCC	Cleavage
spe-miR399-6-5p	Sopen01g036990.1	3.0	-1.0	1	21	1020	1040	GGGCUACUCUCUAUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399-6-5p	Sopen12g018160.1	3.0	-1.0	1	21	1223	1243	GGGCUACUCUCUAUUGGCAUG	AUUGCCAACAGAAAGUAGCCC	Cleavage
spe-miR399-7-3p	Sopen07g026190.1	3.0	-1.0	1	21	481	501	UGCCAAAGGAGAGUUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399-7-3p	Sopen07g026190.2	3.0	-1.0	1	21	391	411	UGCCAAAGGAGAGUUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399-7-3p	Sopen11g023540.1	3.0	-1.0	1	21	2473	2493	UGCCAAAGGAGAGUUGCCCUG	AAGAGAAACUUUCUUUUGGCA	Cleavage
spe-miR399-7-3p	Sopen01g046300.1	3.0	-1.0	1	21	1887	1907	UGCCAAAGGAGAGUUGCCCUG	GCAGGAAAUUCUCUUUUGGCA	Cleavage
spe-miR399-7-3p	Sopen12g003070.1	3.0	-1.0	1	21	1271	1291	UGCCAAAGGAGAGUUGCCCUG	UUUGGGAACUCUUCUUUGGUA	Cleavage
spe-miR399-7-3p	Sopen01g044310.1	3.0	-1.0	1	21	1413	1433	UGCCAAAGGAGAGUUGCCCUG	UUGGCCAACUCUUCUCUGGCA	Cleavage
spe-miR399-7-5p.1	Sopen06g016130.1	1.0	-1.0	1	21	258	278	GGACUACUCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399-7-5p.1	Sopen01g036990.1	2.5	-1.0	1	21	1020	1040	GGACUACUCUCUAUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399-8-3p	Sopen03g020000.1	2.0	-1.0	1	21	591	611	UGCCAAAGGAGAAUUGCACUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
spe-miR399-8-3p	Sopen01g018940.1	2.0	-1.0	1	21	346	366	UGCCAAAGGAGAAUUGCACUG	AAGUCCAAUUUUCUUUUGGCA	Cleavage
spe-miR399-8-3p	Sopen03g004040.1	3.0	-1.0	1	21	615	635	UGCCAAAGGAGAAUUGCACUG	CCAUGCUAUUCUCCUUUGGCU	Cleavage
spe-miR399-8-5p	Sopen11g002240.1	1.5	-1.0	1	21	224	244	CAGGGCAAUUCUCCUUUGGCA	AUCCAAUGGAGAAUUGUCCUG	Cleavage
spe-miR399-8-5p	Sopen11g030020.1	2.5	-1.0	1	21	588	608	CAGGGCAAUUCUCCUUUGGCA	UCCUGAAGGAGGAUUGCCCUU	Cleavage
spe-miR399-8-5p	Sopen03g012120.1	2.5	-1.0	1	21	1592	1612	CAGGGCAAUUCUCCUUUGGCA	GUCUAGAGGAGAACUGCCCUG	Cleavage
spe-miR399-8-5p	Sopen12g024300.1	2.5	-1.0	1	21	14	34	CAGGGCAAUUCUCCUUUGGCA	GUGCAAACGAGAAUUGCCUUG	Cleavage
spe-miR399-8-5p	Sopen02g039050.1	3.0	-1.0	1	21	263	283	CAGGGCAAUUCUCCUUUGGCA	UGACAAAGGAUGAUUGCCCUG	Translation
spe-miR399-8-5p	Sopen02g032040.1	3.0	-1.0	1	21	432	452	CAGGGCAAUUCUCCUUUGGCA	UGACGAAGAAGAAUUGCCCUG	Cleavage
spe-miR399-8-5p	Sopen10g022400.1	3.0	-1.0	1	21	726	746	CAGGGCAAUUCUCCUUUGGCA	GUCCAAAGGGGAAUUGUUUUU	Cleavage
spe-miR399-8-5p	Sopen03g022340.1	3.0	-1.0	1	21	906	926	CAGGGCAAUUCUCCUUUGGCA	ACCCGAAGGAGAAUUGGUUUG	Cleavage
spe-miR399-8-5p	Sopen11g028330.1	3.0	-1.0	1	21	3021	3041	CAGGGCAAUUCUCCUUUGGCA	UCCUCAAGGAGGAUUGCCCUU	Cleavage
spe-miR399-9-3p	Sopen10g006610.1	3.0	-1.0	1	21	3627	3648	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen03g013860.1	3.0	-1.0	1	21	3909	3930	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen06g008270.1	3.0	-1.0	1	21	1542	1562	UGCCAAAGGAGAUUUGCCCUA	UAGGAGAGAUUUCCUUUGGCA	Cleavage
spe-miR399-9-3p	Sopen03g016120.1	2.0	-1.0	1	21	489	509	UGCCAAAGGAGAUUUGCCCUA	UAGGGAGAAUUUCCUUUGGCA	Cleavage
spe-miR399-9-3p	Sopen09g010430.1	2.5	-1.0	1	21	1296	1317	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUCCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen06g006220.1	2.5	-1.0	1	21	160	180	UGCCAAAGGAGAUUUGCCCUA	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g010440.1	2.5	-1.0	1	21	673	693	UGCCAAAGGAGAUUUGCCCUA	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g025730.1	3.0	-1.0	1	21	552	573	UGCCAAAGGAGAUU-UGCCCUA	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen11g022310.1	3.0	-1.0	1	21	1608	1629	UGCCAAAGGAGAUU-UGCCCUA	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen03g011270.1	3.0	-1.0	1	21	825	846	UGCCAAAGGAGAUU-UGCCCUA	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen02g009680.1	3.0	-1.0	1	21	1725	1746	UGCCAAAGGAGAUU-UGCCCUA	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen07g006960.2	3.0	-1.0	1	21	2106	2127	UGCCAAAGGAGAUU-UGCCCUA	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen07g006960.1	3.0	-1.0	1	21	2142	2163	UGCCAAAGGAGAUU-UGCCCUA	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g026610.1	3.0	-1.0	1	21	183	204	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g010170.1	3.0	-1.0	1	21	120	141	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g020080.1	3.0	-1.0	1	21	267	288	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g022420.1	3.0	-1.0	1	21	684	705	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen10g007910.1	3.0	-1.0	1	21	618	639	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g021320.1	3.0	-1.0	1	21	252	273	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen11g021760.1	3.0	-1.0	1	21	120	141	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g021160.1	3.0	-1.0	1	21	885	906	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen02g009810.1	3.0	-1.0	1	21	603	624	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g010970.1	3.0	-1.0	1	21	696	717	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g021630.1	3.0	-1.0	1	21	825	846	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen12g017450.1	3.0	-1.0	1	21	492	513	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage

spe-miR399-9-3p	Sopen01g007180.1	3.0	-1.0	1	21	915	936	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen01g018260.1	3.0	-1.0	1	21	969	990	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen11g011980.1	3.0	-1.0	1	21	1530	1551	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen01g025130.1	3.0	-1.0	1	21	1416	1437	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen07g019040.1	3.0	-1.0	1	21	768	789	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen01g020400.1	3.0	-1.0	1	21	1617	1638	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen03g023850.1	3.0	-1.0	1	21	1446	1467	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen01g021590.1	3.0	-1.0	1	21	1854	1875	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen10g020260.1	3.0	-1.0	1	21	1461	1482	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g023140.1	3.0	-1.0	1	21	1596	1617	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g025320.1	3.0	-1.0	1	21	351	372	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g010200.1	3.0	-1.0	1	21	1596	1617	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen04g011480.1	3.0	-1.0	1	21	3486	3507	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen06g006250.1	3.0	-1.0	1	21	351	372	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen12g016700.1	3.0	-1.0	1	21	882	903	UGCCAAAGGAGAUU-UGCCCUA	UGGGGUAGAAUCUUCUUUGGCA	Cleavage
spe-miR399-9-3p	Sopen07g021860.1	3.0	-1.0	1	21	7239	7260	UGCCAAAGGAGAUU-UGCCCUA	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen10g026120.1	3.0	-1.0	1	21	1254	1275	UGCCAAAGGAGAUU-UGCCCUA	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen10g024040.1	3.0	-1.0	1	21	1584	1605	UGCCAAAGGAGAUU-UGCCCUA	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen05g029300.1	3.0	-1.0	1	21	576	596	UGCCAAAGGAGAUUUGCCCUA	GGUGGAGAAUUUCCUUUGGCA	Cleavage
spe-miR399-9-3p	Sopen01g015130.1	3.0	-1.0	1	21	916	936	UGCCAAAGGAGAUUUGCCCUA	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399-9-3p	Sopen11g014130.1	3.0	-1.0	1	21	2329	2349	UGCCAAAGGAGAUUUGCCCUA	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399a-1-3p	Sopen07g026190.1	2.5	-1.0	1	21	481	501	UGCCAAAGGAGAGCUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399a-1-3p	Sopen07g026190.2	2.5	-1.0	1	21	391	411	UGCCAAAGGAGAGCUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399a-1-3p	Sopen03g020000.1	3.0	-1.0	1	21	591	611	UGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
spe-miR399a-1-5p	Sopen12g018160.1	1.5	-1.0	1	21	1223	1243	GGGCUACUCUCUGUUGGCAUG	AUUGCCAACAGAAAGUAGCCC	Cleavage
spe-miR399a-1-5p	Sopen08g012110.1	2.0	-1.0	1	21	4260	4280	GGGCUACUCUCUGUUGGCAUG	AUUGCUAACAGAAAGUAGCCC	Cleavage
spe-miR399a-1-5p	Sopen03g014410.1	2.0	-1.0	1	21	3615	3635	GGGCUACUCUCUGUUGGCAUG	AUUGCUAACAGAAAGUAGCCC	Cleavage
spe-miR399a-1-5p	Sopen06g016130.1	2.0	-1.0	1	21	258	278	GGGCUACUCUCUGUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399a-1-5p	Sopen08g003690.1	2.5	-1.0	1	21	966	986	GGGCUACUCUCUGUUGGCAUG	CUUGCCGGCAGAGAGGAGCCC	Cleavage
spe-miR399a-1-5p	Sopen03g012230.1	2.5	-1.0	1	21	171	191	GGGCUACUCUCUGUUGGCAUG	AUUGCUAAUAGAAAGUAGCCC	Cleavage
spe-miR399a-1-5p	Sopen01g036990.1	3.0	-1.0	1	21	1020	1040	GGGCUACUCUCUGUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399a-1-5p	Sopen01g040990.1	3.0	-1.0	1	21	4910	4930	GGGCUACUCUCUGUUGGCAUG	GAUGCAAACAAAGAGUAGCUC	Translation
spe-miR399a-1-5p	Sopen08g007770.1	3.0	-1.0	1	21	2718	2738	GGGCUACUCUCUGUUGGCAUG	AUUGCUAACAGAAAGUAGCCA	Cleavage
spe-miR399a-1-5p	Sopen10g009510.1	3.0	-1.0	1	21	1596	1616	GGGCUACUCUCUGUUGGCAUG	AUUGCUAACGGAAAGUAGCUC	Cleavage
spe-miR399a-1-5p	Sopen03g011650.1	3.0	-1.0	1	21	804	824	GGGCUACUCUCUGUUGGCAUG	ACUGACAAUAGAAAGUAGCCC	Cleavage
spe-miR399a-2-3p	Sopen07g026190.1	2.5	-1.0	1	21	481	501	UGCCAAAGGAGAGCUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399a-2-3p	Sopen07g026190.2	2.5	-1.0	1	21	391	411	UGCCAAAGGAGAGCUGCCCUG	GAAGGCAGCUAUCCUUUGGCA	Translation
spe-miR399a-2-3p	Sopen03g020000.1	3.0	-1.0	1	21	591	611	UGCCAAAGGAGAGCUGCCCUG	GAGUGCGGUUCUCUUUUGGCG	Cleavage
spe-miR399a-2-5p	Sopen06g016130.1	1.5	-1.0	1	21	258	278	GGGCUACUCUCUAUUGGCAUG	AGUUCCAAUAGAGAGUAGUCC	Cleavage
spe-miR399a-2-5p	Sopen03g012230.1	2.0	-1.0	1	21	171	191	GGGCUACUCUCUAUUGGCAUG	AUUGCUAAUAGAAAGUAGCCC	Cleavage
spe-miR399a-2-5p	Sopen03g011650.1	2.5	-1.0	1	21	804	824	GGGCUACUCUCUAUUGGCAUG	ACUGACAAUAGAAAGUAGCCC	Cleavage
spe-miR399a-2-5p	Sopen01g036990.1	3.0	-1.0	1	21	1020	1040	GGGCUACUCUCUAUUGGCAUG	UAUGUUAAGAGAGAGUAGUCC	Cleavage
spe-miR399a-2-5p	Sopen12g018160.1	3.0	-1.0	1	21	1223	1243	GGGCUACUCUCUAUUGGCAUG	AUUGCCAACAGAAAGUAGCCC	Cleavage
spe-miR399d-3p	Sopen03g013860.1	2.5	-1.0	1	21	3909	3930	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g006610.1	2.5	-1.0	1	21	3627	3648	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g006610.1	3.0	-1.0	1	21	4012	4032	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g010440.1	2.0	-1.0	1	21	673	693	UGCCAAAGAAGAUUUGCCCCG	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen06g006220.1	2.0	-1.0	1	21	160	180	UGCCAAAGAAGAUUUGCCCCG	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g021860.1	2.5	-1.0	1	21	7239	7260	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen12g016700.1	2.5	-1.0	1	21	882	903	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGCA	Cleavage

spe-miR399d-3p	Sopen06g006250.1	2.5	-1.0	1	21	351	372	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g011480.1	2.5	-1.0	1	21	3486	3507	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g010200.1	2.5	-1.0	1	21	1596	1617	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g025320.1	2.5	-1.0	1	21	351	372	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g023140.1	2.5	-1.0	1	21	1596	1617	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g020260.1	2.5	-1.0	1	21	1461	1482	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g021590.1	2.5	-1.0	1	21	1854	1875	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen03g023850.1	2.5	-1.0	1	21	1446	1467	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g020400.1	2.5	-1.0	1	21	1617	1638	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g019040.1	2.5	-1.0	1	21	768	789	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g025130.1	2.5	-1.0	1	21	1416	1437	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen11g011980.1	2.5	-1.0	1	21	1530	1551	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g018260.1	2.5	-1.0	1	21	969	990	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g007180.1	2.5	-1.0	1	21	915	936	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen12g017450.1	2.5	-1.0	1	21	492	513	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g021630.1	2.5	-1.0	1	21	825	846	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g010970.1	2.5	-1.0	1	21	696	717	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen02g009810.1	2.5	-1.0	1	21	603	624	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g021160.1	2.5	-1.0	1	21	885	906	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen11g021760.1	2.5	-1.0	1	21	120	141	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g021320.1	2.5	-1.0	1	21	252	273	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g007910.1	2.5	-1.0	1	21	618	639	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g022420.1	2.5	-1.0	1	21	684	705	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g020080.1	2.5	-1.0	1	21	267	288	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g010170.1	2.5	-1.0	1	21	120	141	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g026610.1	2.5	-1.0	1	21	183	204	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g027000.1	2.5	-1.0	1	21	931	951	UGCCAAAGAAGAUUUGCCCCG	AGGGCUGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g018880.1	2.5	-1.0	1	21	4558	4578	UGCCAAAGAAGAUUUGCCCCG	AGGGUAAAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen11g014130.1	2.5	-1.0	1	21	2329	2349	UGCCAAAGAAGAUUUGCCCCG	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g015130.1	2.5	-1.0	1	21	916	936	UGCCAAAGAAGAUUUGCCCCG	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g006960.1	2.5	-1.0	1	21	2142	2163	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g006960.2	2.5	-1.0	1	21	2106	2127	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen02g009680.1	2.5	-1.0	1	21	1725	1746	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g024040.1	2.5	-1.0	1	21	1584	1605	UGCCAAAGAAGAUU-UGCCCCG	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen03g011270.1	2.5	-1.0	1	21	825	846	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen11g022310.1	2.5	-1.0	1	21	1608	1629	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g026120.1	2.5	-1.0	1	21	1254	1275	UGCCAAAGAAGAUU-UGCCCCG	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g025730.1	2.5	-1.0	1	21	552	573	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g011500.1	3.0	-1.0	1	21	330	351	UGCCAAAGAAGAUU-UGCCCCG	CGGGGCAGAAUCUUUUUUGGUA	Cleavage
spe-miR399d-3p	Sopen12g026780.1	3.0	-1.0	1	21	969	990	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCGGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g008020.1	3.0	-1.0	1	21	2553	2574	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUUUUUGGUA	Cleavage
spe-miR399d-3p	Sopen03g016530.1	3.0	-1.0	1	21	1791	1812	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g017750.1	3.0	-1.0	1	21	966	987	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUG	Cleavage
spe-miR399d-3p	Sopen03g017240.1	3.0	-1.0	1	21	456	477	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen11g021550.1	3.0	-1.0	1	21	4276	4296	UGCCAAAGAAGAUUUGCCCCG	GGGGCUGAAUCUUCUUUGGUG	Cleavage
spe-miR399d-3p	Sopen12g025590.1	3.0	-1.0	1	21	1048	1068	UGCCAAAGAAGAUUUGCCCCG	GGGGCCAAAUCAUCUUUGGUA	Translation
spe-miR399d-3p	Sopen12g025560.1	3.0	-1.0	1	21	1661	1681	UGCCAAAGAAGAUUUGCCCCG	GGGGCCAAAUCGUCUUUGGUA	Translation
spe-miR399d-3p	Sopen08g010920.1	3.0	-1.0	1	21	820	841	UGCCAAAGAAGAUU-UGCCCCG	UGGAGCAGAAUCUUCUUUGGCA	Cleavage
spe-miR399d-3p	Sopen05g025230.1	3.0	-1.0	1	21	2370	2390	UGCCAAAGAAGAUUUGCCCCG	UGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen10g024160.1	3.0	-1.0	1	21	1036	1056	UGCCAAAGAAGAUUUGCCCCG	UUGGGCAGAAUUUCUUUGGUA	Cleavage

spe-miR399d-3p	Sopen01g008750.1	3.0	-1.0	1	21	2311	2331	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen08g006150.1	3.0	-1.0	1	21	37	57	UGCCAAAGAAGAUUUGCCCCG	AGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen04g009280.1	3.0	-1.0	1	21	985	1005	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen01g009020.1	3.0	-1.0	1	21	1414	1434	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen02g006260.1	3.0	-1.0	1	21	1216	1236	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g025260.1	3.0	-1.0	1	21	961	981	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen07g017620.1	3.0	-1.0	1	21	1087	1107	UGCCAAAGAAGAUUUGCCCCG	AGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g021640.1	3.0	-1.0	1	21	976	996	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen09g012130.1	3.0	-1.0	1	21	940	960	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399d-3p	Sopen05g024970.1	3.0	-1.0	1	21	556	576	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen03g013860.1	2.5	-1.0	1	21	3909	3930	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen10g006610.1	2.5	-1.0	1	21	3627	3648	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen10g006610.1	3.0	-1.0	1	21	4012	4032	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g010440.1	2.0	-1.0	1	21	673	693	UGCCAAAGAAGAUUUGCCCCG	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen06g006220.1	2.0	-1.0	1	21	160	180	UGCCAAAGAAGAUUUGCCCCG	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g021860.1	2.5	-1.0	1	21	7239	7260	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen12g016700.1	2.5	-1.0	1	21	882	903	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGCA	Cleavage
spe-miR399r-1-3p	Sopen06g006250.1	2.5	-1.0	1	21	351	372	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g011480.1	2.5	-1.0	1	21	3486	3507	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g010200.1	2.5	-1.0	1	21	1596	1617	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g025320.1	2.5	-1.0	1	21	351	372	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g023140.1	2.5	-1.0	1	21	1596	1617	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen10g020260.1	2.5	-1.0	1	21	1461	1482	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g021590.1	2.5	-1.0	1	21	1854	1875	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen03g023850.1	2.5	-1.0	1	21	1446	1467	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g020400.1	2.5	-1.0	1	21	1617	1638	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g019040.1	2.5	-1.0	1	21	768	789	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g025130.1	2.5	-1.0	1	21	1416	1437	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen11g011980.1	2.5	-1.0	1	21	1530	1551	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g018260.1	2.5	-1.0	1	21	969	990	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g007180.1	2.5	-1.0	1	21	915	936	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen12g017450.1	2.5	-1.0	1	21	492	513	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g021630.1	2.5	-1.0	1	21	825	846	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g010970.1	2.5	-1.0	1	21	696	717	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen02g009810.1	2.5	-1.0	1	21	603	624	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g021160.1	2.5	-1.0	1	21	885	906	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen11g021760.1	2.5	-1.0	1	21	120	141	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g021320.1	2.5	-1.0	1	21	252	273	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen10g007910.1	2.5	-1.0	1	21	618	639	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g022420.1	2.5	-1.0	1	21	684	705	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g020080.1	2.5	-1.0	1	21	267	288	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g010170.1	2.5	-1.0	1	21	120	141	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g026610.1	2.5	-1.0	1	21	183	204	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g027000.1	2.5	-1.0	1	21	931	951	UGCCAAAGAAGAUUUGCCCCG	AGGGCUGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g018880.1	2.5	-1.0	1	21	4558	4578	UGCCAAAGAAGAUUUGCCCCG	AGGGUAAAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen11g014130.1	2.5	-1.0	1	21	2329	2349	UGCCAAAGAAGAUUUGCCCCG	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g015130.1	2.5	-1.0	1	21	916	936	UGCCAAAGAAGAUUUGCCCCG	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g006960.1	2.5	-1.0	1	21	2142	2163	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g006960.2	2.5	-1.0	1	21	2106	2127	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen02g009680.1	2.5	-1.0	1	21	1725	1746	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage

spe-miR399r-1-3p	Sopen10g024040.1	2.5	-1.0	1	21	1584	1605	UGCCAAAGAAGAUU-UGCCCCG	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen03g011270.1	2.5	-1.0	1	21	825	846	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen11g022310.1	2.5	-1.0	1	21	1608	1629	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen10g026120.1	2.5	-1.0	1	21	1254	1275	UGCCAAAGAAGAUU-UGCCCCG	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g025730.1	2.5	-1.0	1	21	552	573	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g011500.1	3.0	-1.0	1	21	330	351	UGCCAAAGAAGAUU-UGCCCCG	CGGGGCAGAAUCUUUUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen12g026780.1	3.0	-1.0	1	21	969	990	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCGGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g008020.1	3.0	-1.0	1	21	2553	2574	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUUUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen03g016530.1	3.0	-1.0	1	21	1791	1812	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g017750.1	3.0	-1.0	1	21	966	987	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUG	Cleavage
spe-miR399r-1-3p	Sopen03g017240.1	3.0	-1.0	1	21	456	477	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen11g021550.1	3.0	-1.0	1	21	4276	4296	UGCCAAAGAAGAUUUGCCCCG	GGGGCUGAAUCUUCUUUGGUG	Cleavage
spe-miR399r-1-3p	Sopen12g025590.1	3.0	-1.0	1	21	1048	1068	UGCCAAAGAAGAUUUGCCCCG	GGGGCCAAAUCAUCUUUGGUA	Translation
spe-miR399r-1-3p	Sopen12g025560.1	3.0	-1.0	1	21	1661	1681	UGCCAAAGAAGAUUUGCCCCG	GGGGCCAAAUCGUCUUUGGUA	Translation
spe-miR399r-1-3p	Sopen08g010920.1	3.0	-1.0	1	21	820	841	UGCCAAAGAAGAUU-UGCCCCG	UGGAGCAGAAUCUUCUUUGGCA	Cleavage
spe-miR399r-1-3p	Sopen05g025230.1	3.0	-1.0	1	21	2370	2390	UGCCAAAGAAGAUUUGCCCCG	UGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen10g024160.1	3.0	-1.0	1	21	1036	1056	UGCCAAAGAAGAUUUGCCCCG	UUGGGCAGAAUUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g008750.1	3.0	-1.0	1	21	2311	2331	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen08g006150.1	3.0	-1.0	1	21	37	57	UGCCAAAGAAGAUUUGCCCCG	AGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen04g009280.1	3.0	-1.0	1	21	985	1005	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen01g009020.1	3.0	-1.0	1	21	1414	1434	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen02g006260.1	3.0	-1.0	1	21	1216	1236	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g025260.1	3.0	-1.0	1	21	961	981	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen07g017620.1	3.0	-1.0	1	21	1087	1107	UGCCAAAGAAGAUUUGCCCCG	AGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g021640.1	3.0	-1.0	1	21	976	996	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen09g012130.1	3.0	-1.0	1	21	940	960	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-1-3p	Sopen05g024970.1	3.0	-1.0	1	21	556	576	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen03g013860.1	2.5	-1.0	1	21	3909	3930	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g006610.1	2.5	-1.0	1	21	3627	3648	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g006610.1	3.0	-1.0	1	21	4012	4032	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g010440.1	2.0	-1.0	1	21	673	693	UGCCAAAGAAGAUUUGCCCCG	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen06g006220.1	2.0	-1.0	1	21	160	180	UGCCAAAGAAGAUUUGCCCCG	GGGGCCGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g021860.1	2.5	-1.0	1	21	7239	7260	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen12g016700.1	2.5	-1.0	1	21	882	903	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGCA	Cleavage
spe-miR399r-2-3p	Sopen06g006250.1	2.5	-1.0	1	21	351	372	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g011480.1	2.5	-1.0	1	21	3486	3507	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g010200.1	2.5	-1.0	1	21	1596	1617	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g025320.1	2.5	-1.0	1	21	351	372	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g023140.1	2.5	-1.0	1	21	1596	1617	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g020260.1	2.5	-1.0	1	21	1461	1482	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g021590.1	2.5	-1.0	1	21	1854	1875	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen03g023850.1	2.5	-1.0	1	21	1446	1467	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g020400.1	2.5	-1.0	1	21	1617	1638	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g019040.1	2.5	-1.0	1	21	768	789	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g025130.1	2.5	-1.0	1	21	1416	1437	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen11g011980.1	2.5	-1.0	1	21	1530	1551	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g018260.1	2.5	-1.0	1	21	969	990	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g007180.1	2.5	-1.0	1	21	915	936	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen12g017450.1	2.5	-1.0	1	21	492	513	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g021630.1	2.5	-1.0	1	21	825	846	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage

spe-miR399r-2-3p	Sopen05g010970.1	2.5	-1.0	1	21	696	717	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen02g009810.1	2.5	-1.0	1	21	603	624	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g021160.1	2.5	-1.0	1	21	885	906	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen11g021760.1	2.5	-1.0	1	21	120	141	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g021320.1	2.5	-1.0	1	21	252	273	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g007910.1	2.5	-1.0	1	21	618	639	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g022420.1	2.5	-1.0	1	21	684	705	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g020080.1	2.5	-1.0	1	21	267	288	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g010170.1	2.5	-1.0	1	21	120	141	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g026610.1	2.5	-1.0	1	21	183	204	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g027000.1	2.5	-1.0	1	21	931	951	UGCCAAAGAAGAUUUGCCCCG	AGGGCUGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g018880.1	2.5	-1.0	1	21	4558	4578	UGCCAAAGAAGAUUUGCCCCG	AGGGUAAAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen11g014130.1	2.5	-1.0	1	21	2329	2349	UGCCAAAGAAGAUUUGCCCCG	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g015130.1	2.5	-1.0	1	21	916	936	UGCCAAAGAAGAUUUGCCCCG	GGGGAAAAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g006960.1	2.5	-1.0	1	21	2142	2163	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g006960.2	2.5	-1.0	1	21	2106	2127	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen02g009680.1	2.5	-1.0	1	21	1725	1746	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g024040.1	2.5	-1.0	1	21	1584	1605	UGCCAAAGAAGAUU-UGCCCCG	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen03g011270.1	2.5	-1.0	1	21	825	846	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen11g022310.1	2.5	-1.0	1	21	1608	1629	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g026120.1	2.5	-1.0	1	21	1254	1275	UGCCAAAGAAGAUU-UGCCCCG	UUGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g025730.1	2.5	-1.0	1	21	552	573	UGCCAAAGAAGAUU-UGCCCCG	UAGGGCAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g011500.1	3.0	-1.0	1	21	330	351	UGCCAAAGAAGAUU-UGCCCCG	CGGGGCAGAAUCUUUUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen12g026780.1	3.0	-1.0	1	21	969	990	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCGGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g008020.1	3.0	-1.0	1	21	2553	2574	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUUUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen03g016530.1	3.0	-1.0	1	21	1791	1812	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g017750.1	3.0	-1.0	1	21	966	987	UGCCAAAGAAGAUU-UGCCCCG	UGGGGCAGAAUCUUCUUUGGUG	Cleavage
spe-miR399r-2-3p	Sopen03g017240.1	3.0	-1.0	1	21	456	477	UGCCAAAGAAGAUU-UGCCCCG	UGGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen11g021550.1	3.0	-1.0	1	21	4276	4296	UGCCAAAGAAGAUUUGCCCCG	GGGGCUGAAUCUUCUUUGGUG	Cleavage
spe-miR399r-2-3p	Sopen12g025590.1	3.0	-1.0	1	21	1048	1068	UGCCAAAGAAGAUUUGCCCCG	GGGGCCAAAUCAUCUUUGGUA	Translation
spe-miR399r-2-3p	Sopen12g025560.1	3.0	-1.0	1	21	1661	1681	UGCCAAAGAAGAUUUGCCCCG	GGGGCCAAAUCGUCUUUGGUA	Translation
spe-miR399r-2-3p	Sopen08g010920.1	3.0	-1.0	1	21	820	841	UGCCAAAGAAGAUU-UGCCCCG	UGGAGCAGAAUCUUCUUUGGCA	Cleavage
spe-miR399r-2-3p	Sopen05g025230.1	3.0	-1.0	1	21	2370	2390	UGCCAAAGAAGAUUUGCCCCG	UGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen10g024160.1	3.0	-1.0	1	21	1036	1056	UGCCAAAGAAGAUUUGCCCCG	UUGGGCAGAAUUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g008750.1	3.0	-1.0	1	21	2311	2331	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen08g006150.1	3.0	-1.0	1	21	37	57	UGCCAAAGAAGAUUUGCCCCG	AGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen04g009280.1	3.0	-1.0	1	21	985	1005	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen01g009020.1	3.0	-1.0	1	21	1414	1434	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen02g006260.1	3.0	-1.0	1	21	1216	1236	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g025260.1	3.0	-1.0	1	21	961	981	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen07g017620.1	3.0	-1.0	1	21	1087	1107	UGCCAAAGAAGAUUUGCCCCG	AGGGUAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g021640.1	3.0	-1.0	1	21	976	996	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen09g012130.1	3.0	-1.0	1	21	940	960	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR399r-2-3p	Sopen05g024970.1	3.0	-1.0	1	21	556	576	UGCCAAAGAAGAUUUGCCCCG	GGGGAAGAAUCUUCUUUGGUA	Cleavage
spe-miR403-1-5p	Sopen02g012680.1	3.0	-1.0	1	21	260	280	CGUUUGUGCGUGAAUCUAACG	UCUUAGGCUCGCGCAUGAACG	Cleavage
spe-miR403-1-5p	Sopen07g001100.1	3.0	-1.0	1	21	488	508	CGUUUGUGCGUGAAUCUAACG	UCUCAGAUACACGCACAAAUG	Cleavage
spe-miR403-2-5p	Sopen05g015450.1	3.0	-1.0	1	21	2832	2852	AGUUUGUGCGUGAAUCUAGCA	AUCCAGAUUCAUGCACGAACC	Cleavage
spe-miR408-5p	Sopen11g015750.1	2.5	-1.0	1	21	3627	3647	CAGGGAAGAGGCAGUGCAUGG	AUAUGCAUUGCCUCUUCUAUG	Cleavage
spe-miR408-5p	Sopen09g012530.1	2.5	-1.0	1	21	1510	1530	CAGGGAAGAGGCAGUGCAUGG	ACAUCCAUUGCUUCUUCUCUG	Cleavage
spe-miR408-5p	Sopen01g053940.1	2.5	-1.0	1	21	148	168	CAGGGAAGAGGCAGUGCAUGG	GGCUGCUCUGCUUCUUCCCUG	Cleavage

spe-miR408-5p	Sopen01g053950.1	2.5	-1.0	1	21	97	117	CAGGGAAGAGGCAGUGCAUGG	GGCUGCUCUGCUUCUUCCCUG	Cleavage
spe-miR408-5p	Sopen11g025240.1	3.0	-1.0	1	21	877	897	CAGGGAAGAGGCAGUGCAUGG	GUUGGAACUGCCUCUUCCCUG	Cleavage
spe-miR408-5p	Sopen05g026960.1	3.0	-1.0	1	21	84	105	CAGGGAAGAGGCAGUG-CAUGG	UAAUGUCACUGUCUCUUCCUUG	Cleavage
spe-miR408b-3p	Sopen07g001840.1	2.5	-1.0	1	21	897	917	UGCACUGCCUCUUCCCUGGCU	AAGCGGGGAGGAGGCAGUGCG	Cleavage
spe-miR408b-3p	Sopen05g030940.1	2.5	-1.0	1	21	122	142	UGCACUGCCUCUUCCCUGGCU	CACCAGUGAAGAGGCUGUGCA	Cleavage
spe-miR408b-3p	Sopen05g030920.1	2.5	-1.0	1	21	122	142	UGCACUGCCUCUUCCCUGGCU	CACCAGUGAAGAGGCUGUGCA	Cleavage
spe-miR408b-3p	Sopen10g017610.1	3.0	-1.0	1	21	28	48	UGCACUGCCUCUUCCCUGGCU	AGACAGGGAGGAGGAAGUGCA	Cleavage
spe-miR408b-3p	Sopen03g015260.1	3.0	-1.0	1	21	86	106	UGCACUGCCUCUUCCCUGGCU	AAAUAGGGAAGAGGCAUUGCA	Cleavage
spe-miR408b-3p	Sopen05g033370.3	3.0	-1.0	1	21	1460	1480	UGCACUGCCUCUUCCCUGGCU	GGCCAGCUAAGAGGCAGUGUG	Cleavage
spe-miR408b-3p	Sopen05g033370.2	3.0	-1.0	1	21	1736	1756	UGCACUGCCUCUUCCCUGGCU	GGCCAGCUAAGAGGCAGUGUG	Cleavage
spe-miR408b-3p	Sopen05g033370.1	3.0	-1.0	1	21	1802	1822	UGCACUGCCUCUUCCCUGGCU	GGCCAGCUAAGAGGCAGUGUG	Cleavage
spe-miR408b-3p	Sopen05g033370.4	3.0	-1.0	1	21	1859	1879	UGCACUGCCUCUUCCCUGGCU	GGCCAGCUAAGAGGCAGUGUG	Cleavage
spe-miR408b-3p	Sopen10g019800.1	3.0	-1.0	1	21	672	692	UGCACUGCCUCUUCCCUGGCU	CACCAGAGAAGAGGUAGUGAA	Cleavage
spe-miR408b-3p	Sopen02g003820.1	3.0	-1.0	1	21	844	864	UGCACUGCCUCUUCCCUGGCU	UCCCAAGGGGGAGGUGGUGCA	Cleavage
spe-miR408b-3p	Sopen09g010650.1	3.0	-1.0	1	21	2770	2790	UGCACUGCCUCUUCCCUGGCU	CACCAAGGAAGAGGUAGUGGA	Cleavage
spe-miR408b-3p	Sopen02g036420.1	3.0	-1.0	1	21	2856	2876	UGCACUGCCUCUUCCCUGGCU	CACCAUGCGAGAGGUAGUGCA	Cleavage
spe-miR408b-5p	Sopen03g038580.1	2.5	-1.0	1	21	961	981	ACGGGGACGAGCCAGAGCAUG	UUUGCUCUGGUUCGUCCUCCU	Cleavage
spe-miR408b-5p	Sopen07g032190.1	3.0	-1.0	1	21	141	161	ACGGGGACGAGCCAGAGCAUG	CUUGCUCCGGUUUGUCUUCGU	Cleavage
spe-miR408b-5p	Sopen04g006640.1	3.0	-1.0	1	21	77	97	ACGGGGACGAGCCAGAGCAUG	CUUUCUCUGGUUCGUCGCCGU	Cleavage
spe-miR408b-5p	Sopen06g023950.1	3.0	-1.0	1	21	1350	1370	ACGGGGACGAGCCAGAGCAUG	GCUGCAGUGGCUUGUUCCCGU	Cleavage
spe-miR4376-3p	Sopen02g023780.1	2.5	-1.0	1	20	394	413	GCAUCAUACUCCUGCAUAUU	AAAAUGAAGGAGUGUGAUGC	Cleavage
spe-miR4376-3p	Sopen08g026240.1	3.0	-1.0	1	20	1007	1026	GCAUCAUACUCCUGCAUAUU	UAUAUGCAGGGGAAUGGUGU	Cleavage
spe-miR4376-3p	Sopen06g003320.1	3.0	-1.0	1	20	1167	1186	GCAUCAUACUCCUGCAUAUU	AAAAUUGAGGAGUAUGAUGC	Cleavage
spe-miR4376-3p	Sopen06g019130.1	3.0	-1.0	1	20	496	515	GCAUCAUACUCCUGCAUAUU	UACAAGCAGGAGUAUGGUGU	Cleavage
spe-miR4376-3p	Sopen10g031560.1	3.0	-1.0	1	20	2737	2756	GCAUCAUACUCCUGCAUAUU	UACAAGCAGGAGUAUGGUGU	Cleavage
spe-miR4376-3p	Sopen10g016240.1	3.0	-1.0	1	20	2737	2756	GCAUCAUACUCCUGCAUAUU	UACAAGCAGGAGUAUGGUGU	Cleavage
spe-miR4376-3p	Sopen05g010210.1	3.0	-1.0	1	20	2737	2756	GCAUCAUACUCCUGCAUAUU	UACAAGCAGGAGUAUGGUGU	Cleavage
spe-miR4376-3p	Sopen11g010630.1	3.0	-1.0	1	20	2737	2756	GCAUCAUACUCCUGCAUAUU	UACAAGCAGGAGUAUGGUGU	Cleavage
spe-miR4376-5p	Sopen00g005400.1	3.0	-1.0	1	21	2237	2257	UACGCAGGAGAGAUGAUGCUG	UGCCAUCAUCUCCCUUGCGUA	Cleavage
spe-miR4376-5p	Sopen00g006860.1	3.0	-1.0	1	21	2	22	UACGCAGGAGAGAUGAUGCUG	UGCCAUCAUCUCUCUUGGGUA	Cleavage
spe-miR477-3p	Sopen10g029810.1	2.0	-1.0	1	22	793	814	AGUUCUUGUAGGGUGAGACAUC	UAUGUUUCACCCUACGAGGAUU	Cleavage
spe-miR477-3p	Sopen00g008420.1	2.5	-1.0	1	22	192	213	AGUUCUUGUAGGGUGAGACAUC	AGGGUUUCAUCCUACAACAACU	Cleavage
spe-miR477-3p	Sopen12g009440.1	3.0	-1.0	1	22	346	367	AGUUCUUGUAGGGUGAGACAUC	UGUGUUCCAUCCUACAAGAACG	Cleavage
spe-miR477-3p	Sopen00g009000.1	3.0	-1.0	1	22	2248	2269	AGUUCUUGUAGGGUGAGACAUC	UUUGUCUCAUUUUAUAAGAGUU	Cleavage
spe-miR477-3p	Sopen03g034540.1	3.0	-1.0	1	22	666	687	AGUUCUUGUAGGGUGAGACAUC	UAUUUCCCACUCUACAAGAAUU	Cleavage
spe-miR477-3p	Sopen01g020380.1	3.0	-1.0	1	22	1239	1260	AGUUCUUGUAGGGUGAGACAUC	GUUGUCCCACUCUACAGGGGCU	Cleavage
spe-miR477-3p	Sopen01g047570.1	3.0	-1.0	1	22	778	799	AGUUCUUGUAGGGUGAGACAUC	UGCAUCUCACCUUACGAGGAUU	Cleavage
spe-miR477-3p	Sopen03g002310.1	3.0	-1.0	1	22	274	295	AGUUCUUGUAGGGUGAGACAUC	UACGUUUCAUUCUACAAUAACU	Cleavage
spe-miR477-3p	Sopen02g001210.1	3.0	-1.0	1	22	313	334	AGUUCUUGUAGGGUGAGACAUC	CUAGUCUCACUCUAUAUGAGCU	Cleavage
spe-miR477-3p	Sopen08g031290.1	3.0	-1.0	1	22	983	1004	AGUUCUUGUAGGGUGAGACAUC	GGGGACUUGCCCUGCAGGAACU	Cleavage
spe-miR477-3p	Sopen01g022220.1	3.0	-1.0	1	22	3179	3200	AGUUCUUGUAGGGUGAGACAUC	UUGGUUUCAUUUUGCAAGGACU	Cleavage
spe-miR477-3p	Sopen05g017100.1	3.0	-1.0	1	22	190	211	AGUUCUUGUAGGGUGAGACAUC	AAGGUUUCUCUUUGCAAGAACU	Cleavage
spe-miR477-3p	Sopen04g014260.1	3.0	-1.0	1	22	1379	1400	AGUUCUUGUAGGGUGAGACAUC	CUCUUCACACUCUACAAGGACU	Cleavage
spe-miR477-5p	Sopen03g030140.1	3.0	-1.0	1	21	787	807	UGUCUCUCCCUCAAGGGCUCC	GAAGCCUUUGAGGGAGAGAGU	Cleavage
spe-miR477-5p	Sopen01g032700.1	3.0	-1.0	1	21	1656	1676	UGUCUCUCCCUCAAGGGCUCC	GAAGCCUUUGAGGGAGAGAGC	Cleavage
spe-miR477-5p	Sopen01g045760.1	3.0	-1.0	1	21	114	134	UGUCUCUCCCUCAAGGGCUCC	AGAGUUAUUGGGGGAGAGGCA	Cleavage
spe-miR477-5p	Sopen06g020730.1	3.0	-1.0	1	21	870	890	UGUCUCUCCCUCAAGGGCUCC	CAAGGUUUUGAGGGGGAGAUA	Cleavage
spe-miR477a-3p	Sopen06g001180.1	1.5	-1.0	1	22	911	932	GAAGCUCUAGCAGGGAGAGCCA	CGGCUCUUCCUGCUGGAGCUUU	Cleavage
spe-miR477a-3p	Sopen10g034960.1	2.0	-1.0	1	22	521	542	GAAGCUCUAGCAGGGAGAGCCA	UGAUUCUUCCUGUUGGAGCUUC	Cleavage
spe-miR477a-3p	Sopen07g034070.1	2.5	-1.0	1	22	2855	2876	GAAGCUCUAGCAGGGAGAGCCA	UGCCUUUUCCUGCUAGAGCUCC	Cleavage

spe-miR477a-3p	Sopen06g035640.2	2.5	-1.0	1	22	827	848	GAAGCUCUAGCAGGGAGAGCCA	ACGUUCUUCUUGCUGGAGCUUU	Cleavage
spe-miR477a-3p	Sopen06g035640.1	2.5	-1.0	1	22	827	848	GAAGCUCUAGCAGGGAGAGCCA	ACGUUCUUCUUGCUGGAGCUUU	Cleavage
spe-miR477a-3p	Sopen03g038600.1	2.5	-1.0	1	22	1121	1142	GAAGCUCUAGCAGGGAGAGCCA	UUCCAUUUUCUGCUAGAGCUUC	Cleavage
spe-miR477a-3p	Sopen03g038600.2	2.5	-1.0	1	22	1121	1142	GAAGCUCUAGCAGGGAGAGCCA	UUCCAUUUUCUGCUAGAGCUUC	Cleavage
spe-miR477a-3p	Sopen03g022380.1	3.0	-1.0	1	22	1778	1799	GAAGCUCUAGCAGGGAGAGCCA	UGCCUUUUCUUGUUGGGGCUUC	Cleavage
spe-miR477a-3p	Sopen11g030240.1	3.0	-1.0	1	22	896	917	GAAGCUCUAGCAGGGAGAGCCA	CUGCUCUUCCUGCUGGCGCUUU	Cleavage
spe-miR477a-3p	Sopen01g033470.1	3.0	-1.0	1	22	155	176	GAAGCUCUAGCAGGGAGAGCCA	AGGCUGUUACUGCUAGAGCUUU	Cleavage
spe-miR477a-3p	Sopen05g005850.1	3.0	-1.0	1	22	182	203	GAAGCUCUAGCAGGGAGAGCCA	AGCCUCUUCUUACUAGAGCUUU	Translation
spe-miR477a-3p	Sopen09g031410.1	3.0	-1.0	1	22	500	521	GAAGCUCUAGCAGGGAGAGCCA	CUACUUUCUUUGCUGGAGUUUU	Cleavage
spe-miR477a-3p	Sopen11g025160.1	3.0	-1.0	1	22	44	65	GAAGCUCUAGCAGGGAGAGCCA	ACUUUCUUCCUCCUGGAGCUUC	Translation
spe-miR477a-3p	Sopen01g045250.1	3.0	-1.0	1	22	2632	2653	GAAGCUCUAGCAGGGAGAGCCA	CUCCUAUCUCUGCCAGAGCUUC	Cleavage
spe-miR477a-5p	Sopen04g031700.1	3.0	-1.0	1	21	299	319	CCUCUCCCUCAAGGGCUUCUC	GUGAAGACUUUGAGGGGGAGA	Cleavage
spe-miR477a-5p	Sopen04g031700.2	3.0	-1.0	1	21	299	319	CCUCUCCCUCAAGGGCUUCUC	GUGAAGACUUUGAGGGGGAGA	Cleavage
spe-miR477a-5p	Sopen01g032700.1	1.5	-1.0	1	21	1654	1674	CCUCUCCCUCAAGGGCUUCUC	GGGAAGCCUUUGAGGGAGAGA	Cleavage
spe-miR477a-5p	Sopen03g030140.1	1.5	-1.0	1	21	785	805	CCUCUCCCUCAAGGGCUUCUC	UGGAAGCCUUUGAGGGAGAGA	Cleavage
spe-miR477a-5p	Sopen02g027700.1	2.5	-1.0	1	21	1244	1264	CCUCUCCCUCAAGGGCUUCUC	AAGAAGCUUUUGAGGGAGGGU	Cleavage
spe-miR477a-5p	Sopen03g021570.1	3.0	-1.0	1	21	574	594	CCUCUCCCUCAAGGGCUUCUC	GCGGAGCUUUUGAGUGAGAGG	Cleavage
spe-miR477a-5p	Sopen06g003810.1	3.0	-1.0	1	21	1225	1245	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
spe-miR477a-5p	Sopen06g003040.1	3.0	-1.0	1	21	1318	1338	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
spe-miR477a-5p	Sopen12g007430.1	3.0	-1.0	1	21	1846	1866	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
spe-miR477a-5p	Sopen09g026450.1	3.0	-1.0	1	21	3100	3120	CCUCUCCCUCAAGGGCUUCUC	GCGGAGUUCUUGAGUGAGAGG	Cleavage
spe-miR477a-5p	Sopen02g017220.1	3.0	-1.0	1	21	1	21	CCUCUCCCUCAAGGGCUUCUC	AUGGAGCUUUUGAGGGAAAGG	Cleavage
spe-miR477a-5p	Sopen11g020130.1	3.0	-1.0	1	21	4349	4369	CCUCUCCCUCAAGGGCUUCUC	AGGUAGCCUUUGUGGGAGAGG	Cleavage
spe-miR477a-5p	Sopen02g001990.1	3.0	-1.0	1	21	3242	3262	CCUCUCCCUCAAGGGCUUCUC	AGGUAGCCUUUGUGGGAGAGG	Cleavage
spe-miR477a-5p	Sopen03g016130.1	3.0	-1.0	1	21	2888	2908	CCUCUCCCUCAAGGGCUUCUC	AUGUAGCCUUUGUGGGAGAGG	Cleavage
spe-miR477b-3p	Sopen06g009480.1	2.5	-1.0	1	22	102	123	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCACUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen12g015180.1	3.0	-1.0	1	22	150	171	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen12g015180.1	3.0	-1.0	1	22	780	801	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen03g023210.1	2.0	-1.0	1	22	2056	2077	GAGGUCUUUCGAGUGAGAGUGA	CGGCUCUCACUCAAAGGACCUC	Translation
spe-miR477b-3p	Sopen03g023210.2	2.0	-1.0	1	22	2068	2089	GAGGUCUUUCGAGUGAGAGUGA	CGGCUCUCACUCAAAGGACCUC	Translation
spe-miR477b-3p	Sopen11g015790.1	2.5	-1.0	1	22	150	171	GAGGUCUUUCGAGUGAGAGUGA	GGCCUUUCAUUUGAGAGACUUC	Cleavage
spe-miR477b-3p	Sopen10g013840.1	2.5	-1.0	1	22	81	102	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCAUUUGAGAGACUUC	Cleavage
spe-miR477b-3p	Sopen10g012700.1	2.5	-1.0	1	22	291	312	GAGGUCUUUCGAGUGAGAGUGA	UGCUUCUCACUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen12g013860.1	2.5	-1.0	1	22	267	288	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCACUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen09g017280.1	2.5	-1.0	1	22	306	327	GAGGUCUUUCGAGUGAGAGUGA	GACUUCUCACUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen08g006630.1	2.5	-1.0	1	22	3132	3153	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCACUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen05g022630.1	3.0	-1.0	1	22	51	72	GAGGUCUUUCGAGUGAGAGUGA	GCACUUUCAUUCUAAAGACCUU	Translation
spe-miR477b-3p	Sopen12g013380.1	3.0	-1.0	1	22	883	904	GAGGUCUUUCGAGUGAGAGUGA	UUGCUUUCACUCGAAAAACCUA	Cleavage
spe-miR477b-3p	Sopen09g025420.1	3.0	-1.0	1	22	709	730	GAGGUCUUUCGAGUGAGAGUGA	ACAUAUUUACUCGAAAGAUCUC	Cleavage
spe-miR477b-3p	Sopen01g018720.1	3.0	-1.0	1	22	342	363	GAGGUCUUUCGAGUGAGAGUGA	GGCCUCUCGUUUGAGAGACUUU	Cleavage
spe-miR477b-3p	Sopen11g013180.1	3.0	-1.0	1	22	285	306	GAGGUCUUUCGAGUGAGAGUGA	GGCCUCUCGUUUGAGAGAUUUC	Cleavage
spe-miR477b-3p	Sopen11g015540.1	3.0	-1.0	1	22	285	306	GAGGUCUUUCGAGUGAGAGUGA	GGCCUCUCGCUUGAGGGAUUUC	Cleavage
spe-miR477b-3p	Sopen02g007990.1	3.0	-1.0	1	22	291	312	GAGGUCUUUCGAGUGAGAGUGA	GGCCUCUCGUUUGAGAGACUUU	Cleavage
spe-miR477b-3p	Sopen12g012680.1	3.0	-1.0	1	22	111	132	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen03g015810.1	3.0	-1.0	1	22	300	321	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen09g012810.1	3.0	-1.0	1	22	729	750	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCAUUUGAGAGACUUU	Cleavage
spe-miR477b-3p	Sopen04g017080.1	3.0	-1.0	1	22	102	123	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCAUUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen02g003290.1	3.0	-1.0	1	22	726	747	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen08g015680.1	3.0	-1.0	1	22	633	654	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen12g028060.1	3.0	-1.0	1	22	318	339	GAGGUCUUUCGAGUGAGAGUGA	GGCUUCUCGCUUGAGGGACUUC	Cleavage

spe-miR477b-3p	Sopen01g023230.1	3.0	-1.0	1	22	114	135	GAGGUCUUUCGAGUGAGAGUGA	GGCCUCUCGCUUGAGGGAUUUC	Cleavage
spe-miR477b-3p	Sopen03g017360.1	3.0	-1.0	1	22	210	231	GAGGUCUUUCGAGUGAGAGUGA	GUCUUCUCUCUUGAAGGACUUC	Cleavage
spe-miR477b-3p	Sopen10g010810.1	3.0	-1.0	1	22	363	384	GAGGUCUUUCGAGUGAGAGUGA	GACUUCUCUCUCGAGGGACUUC	Cleavage
spe-miR477b-3p	Sopen05g002560.1	3.0	-1.0	1	22	123	144	GAGGUCUUUCGAGUGAGAGUGA	CGCCUUAUACUCGAAAGGCCUU	Cleavage
spe-miR477b-5p	Sopen04g031700.1	2.5	-1.0	1	21	299	319	ACUCUCCCUCAAAGGCUUCUG	GUGAAGACUUUGAGGGGGAGA	Cleavage
spe-miR477b-5p	Sopen04g031700.2	2.5	-1.0	1	21	299	319	ACUCUCCCUCAAAGGCUUCUG	GUGAAGACUUUGAGGGGGAGA	Cleavage
spe-miR477b-5p	Sopen03g030140.1	1.0	-1.0	1	21	785	805	ACUCUCCCUCAAAGGCUUCUG	UGGAAGCCUUUGAGGGAGAGA	Cleavage
spe-miR477b-5p	Sopen02g027700.1	1.0	-1.0	1	21	1244	1264	ACUCUCCCUCAAAGGCUUCUG	AAGAAGCUUUUGAGGGAGGGU	Cleavage
spe-miR477b-5p	Sopen01g032700.1	1.0	-1.0	1	21	1654	1674	ACUCUCCCUCAAAGGCUUCUG	GGGAAGCCUUUGAGGGAGAGA	Cleavage
spe-miR477b-5p	Sopen00g009370.1	2.0	-1.0	1	21	2638	2658	ACUCUCCCUCAAAGGCUUCUG	AGGAGGCCUUUGUGGGAGAGU	Cleavage
spe-miR477b-5p	Sopen00g007260.1	2.0	-1.0	1	21	2641	2661	ACUCUCCCUCAAAGGCUUCUG	AGGAGGCCUUUGUGGGAGAGU	Cleavage
spe-miR477b-5p	Sopen11g012610.1	2.0	-1.0	1	21	1196	1216	ACUCUCCCUCAAAGGCUUCUG	ACGAGCCUUUUGAGGGAGAGU	Cleavage
spe-miR477b-5p	Sopen03g032500.1	3.0	-1.0	1	21	1046	1066	ACUCUCCCUCAAAGGCUUCUG	AUCAAGUCUUUGAGAGAGAGU	Cleavage
spe-miR477b-5p	Sopen08g014670.1	3.0	-1.0	1	21	910	930	ACUCUCCCUCAAAGGCUUCUG	GCGGAGUUUUUGAGUGAGAGU	Cleavage
spe-miR477b-5p	Sopen00g007930.1	3.0	-1.0	1	21	3494	3514	ACUCUCCCUCAAAGGCUUCUG	AGGUGGCCUUUGUGGGAGAGU	Cleavage
spe-miR479-3p	Sopen11g008200.1	0.0	-1.0	1	21	380	400	UGAGCCGAACCAAUAUCACUC	GAGUGAUAUUGGUUCGGCUCA	Cleavage
spe-miR479-3p	Sopen08g022810.1	1.5	-1.0	1	21	1815	1835	UGAGCCGAACCAAUAUCACUC	UAGUGAUGUUGGUUUGGCUCG	Cleavage
spe-miR479-3p	Sopen11g016480.1	2.0	-1.0	1	21	327	347	UGAGCCGAACCAAUAUCACUC	UGAUGAUGUUGGUUCGGUUCA	Cleavage
spe-miR479-3p	Sopen07g031990.1	2.5	-1.0	1	21	282	302	UGAGCCGAACCAAUAUCACUC	UUUCGAUAUUGGUUUGGCUCA	Cleavage
spe-miR479-3p	Sopen05g018610.1	2.5	-1.0	1	21	1995	2015	UGAGCCGAACCAAUAUCACUC	UAGUGAAUUUGGUUCGGUUCA	Cleavage
spe-miR479-3p	Sopen01g048640.2	3.0	-1.0	1	21	45	65	UGAGCCGAACCAAUAUCACUC	GAGUGAGACUGGUUCGGCUCG	Cleavage
spe-miR479-3p	Sopen05g018470.1	3.0	-1.0	1	21	51	71	UGAGCCGAACCAAUAUCACUC	UGGUGAUAUUGCUUUGGCUUG	Translation
spe-miR479-3p	Sopen01g022310.1	3.0	-1.0	1	21	1374	1394	UGAGCCGAACCAAUAUCACUC	UAGUGAUUUUGCUUCGGUUCA	Translation
spe-miR479-3p	Sopen07g028130.1	3.0	-1.0	1	21	339	359	UGAGCCGAACCAAUAUCACUC	UUCUGAUAUUGGUCCGGCUCG	Cleavage
spe-miR479-3p	Sopen02g029770.1	3.0	-1.0	1	21	1235	1255	UGAGCCGAACCAAUAUCACUC	UUGUGAUGUUGGGUUGGCUCG	Cleavage
spe-miR479-3p	Sopen08g008920.1	3.0	-1.0	1	21	1467	1487	UGAGCCGAACCAAUAUCACUC	UUGUGAAAUGGGUUCGGUUCA	Cleavage
spe-miR479-3p	Sopen09g009470.1	3.0	-1.0	1	21	2463	2483	UGAGCCGAACCAAUAUCACUC	UGGAGAUUUUGGUUUGGCUCG	Cleavage
spe-miR479-5p	Sopen04g011320.1	3.0	-1.0	1	22	663	684	CGUGAUAUUGGUUCGGCUCACU	UUUGAGUCGAACCGAUAUUAGG	Cleavage
spe-miR479-5p	Sopen02g033560.1	3.0	-1.0	1	22	2266	2287	CGUGAUAUUGGUUCGGCUCACU	GGCGAUCCUAACCAAUAUCACA	Cleavage
spe-miR482-1-3p	Sopen11g025550.1	0.5	-1.0	1	22	595	616	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUGUAGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen02g011670.1	1.0	-1.0	1	22	529	550	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUAGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen05g003910.1	2.0	-1.0	1	22	526	547	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen11g002560.1	2.0	-1.0	1	22	529	550	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen12g008600.1	2.0	-1.0	1	22	526	547	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen11g002430.1	2.0	-1.0	1	22	526	547	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen12g008600.2	2.0	-1.0	1	22	178	199	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen10g024900.1	2.0	-1.0	1	22	493	514	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGUGUUGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen11g028360.1	2.0	-1.0	1	22	1666	1687	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUGCAGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen11g028610.1	2.0	-1.0	1	22	622	643	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUGCAGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen01g028960.1	2.5	-1.0	1	22	838	859	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen12g008030.1	2.5	-1.0	1	22	421	442	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen11g024570.1	2.5	-1.0	1	22	427	448	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGCGGCGUGGGUAAGA	Translation
spe-miR482-1-3p	Sopen04g018240.1	2.5	-1.0	1	22	304	325	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen10g024980.1	2.5	-1.0	1	22	46	67	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen11g028330.1	2.5	-1.0	1	22	622	643	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUGCGGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen11g029090.1	2.5	-1.0	1	22	622	643	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGCGUGGGUAAGA	Translation
spe-miR482-1-3p	Sopen11g027070.1	2.5	-1.0	1	22	265	286	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGCGGUGCGGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen04g004380.1	2.5	-1.0	1	22	586	607	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGGGGUUUAGGCAAGA	Translation
spe-miR482-1-3p	Sopen03g011610.1	2.5	-1.0	1	19	1	19	UCUUGCCUACACCGCCCAU	AUGGGCGGUGCGGGUAAGA	Cleavage
spe-miR482-1-3p	Sopen11g024590.1	2.5	-1.0	1	22	1936	1957	UCUUGCCUACACCGCCCAUGCC	GCAAUGGGCGGCGUGGGUAAGA	Translation

spe-miR482-1-3p	Sopen04g013450.1	3.0	-1.0	1	22	2722	2743	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGAUUAGGCAAGA	Translation
spe-miR482-1-3p	Sopen04g004410.1	3.0	-1.0	1	22	454	475	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGAUUAGGCAAGA	Translation
spe-miR482-1-3p	Sopen10g020540.1	3.0	-1.0	1	22	386	407	UCUUGCCUACACCGCCCAUGCC	GGCAUGGGCGGAUUAGGCAAGA	Translation
spe-miR482-1-3p	Sopen10g022740.1	3.0	-1.0	1	22	529	550	UCUUGCCUACACCGCCCAUGCC	GGUAUGGGAGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen05g002570.2	3.0	-1.0	1	22	655	676	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGAGGAGUGGGCAAGA	Translation
spe-miR482-1-3p	Sopen11g002570.1	3.0	-1.0	1	22	724	745	UCUUGCCUACACCGCCCAUGCC	GGGAUGGGAGGUAUAGGUAAGA	Translation
spe-miR482-1-3p	Sopen05g002570.1	3.0	-1.0	1	22	655	676	UCUUGCCUACACCGCCCAUGCC	GGAAUGGGAGGAGUGGGCAAGA	Translation
spe-miR482-1-3p	Sopen09g024830.1	3.0	-1.0	1	22	361	382	UCUUGCCUACACCGCCCAUGCC	GAUAUGGGUGGUGUAGCUAAGG	Cleavage
spe-miR482-1-5p	Sopen09g010850.1	2.5	-1.0	1	21	1142	1162	CGUGAGUGGUGGGGAAAGAUA	GUUCUUUCCCCAACACUUAUG	Cleavage
spe-miR482-1-5p	Sopen12g016110.1	2.5	-1.0	1	21	731	751	CGUGAGUGGUGGGGAAAGAUA	UCUCUUUGCCCACCAUUCACA	Cleavage
spe-miR482-1-5p	Sopen09g031740.1	3.0	-1.0	1	21	2090	2110	CGUGAGUGGUGGGGAAAGAUA	CAUCUUUCUUCACCACUUGCA	Cleavage
spe-miR482-1-5p	Sopen05g002110.2	3.0	-1.0	1	21	995	1015	CGUGAGUGGUGGGGAAAGAUA	UUUCUUUCCGCAUCAUUCAUG	Cleavage
spe-miR482-1-5p	Sopen05g002110.1	3.0	-1.0	1	21	992	1012	CGUGAGUGGUGGGGAAAGAUA	UUUCUUUCCGCAUCAUUCAUG	Cleavage
spe-miR482-1-5p	Sopen01g003620.1	3.0	-1.0	1	21	800	820	CGUGAGUGGUGGGGAAAGAUA	UUUCUUUCCGCAUCAUUCAUG	Cleavage
spe-miR482-1-5p	Sopen09g015070.1	3.0	-1.0	1	21	3623	3643	CGUGAGUGGUGGGGAAAGAUA	UCUCUUUGCCCACCAUUCGCC	Cleavage
spe-miR482-1-5p	Sopen11g004230.1	3.0	-1.0	1	21	79	99	CGUGAGUGGUGGGGAAAGAUA	UUUCUUGCCUCAUCACUCACA	Cleavage
spe-miR482-1-5p	Sopen09g007140.1	3.0	-1.0	1	21	211	231	CGUGAGUGGUGGGGAAAGAUA	UCUCAUUUCCCACCACUCGCC	Cleavage
spe-miR482-1-5p	Sopen05g024660.1	3.0	-1.0	1	21	613	633	CGUGAGUGGUGGGGAAAGAUA	UUUCUAUCCCCAUUAUUCAUG	Cleavage
spe-miR482-1-5p	Sopen09g012300.1	3.0	-1.0	1	21	6754	6774	CGUGAGUGGUGGGGAAAGAUA	ACUCGUUUUCCACCAUUCAUG	Cleavage
spe-miR482-2-3p	Sopen01g028960.1	1.5	-1.0	1	22	838	859	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen01g028960.1	2.5	-1.0	1	22	46	67	UCUUGCCAAUACCGCCCAUUCC	GGUUUGGGAGGUAUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen07g025300.1	1.0	-1.0	1	22	547	568	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUAUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen10g024900.1	1.0	-1.0	1	22	493	514	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUGUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen12g008030.1	1.5	-1.0	1	22	421	442	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen04g018240.1	1.5	-1.0	1	22	304	325	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen10g024980.1	1.5	-1.0	1	22	46	67	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen05g003910.1	2.0	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGCGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen11g002560.1	2.0	-1.0	1	22	529	550	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen12g008600.1	2.0	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen11g002430.1	2.0	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen12g008600.2	2.0	-1.0	1	22	178	199	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen11g010240.1	2.0	-1.0	1	22	520	541	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUAUCGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen12g004450.1	2.5	-1.0	1	22	514	535	UCUUGCCAAUACCGCCCAUUCC	GGGAUGGGUGGCAUUGGUAAGA	Translation
spe-miR482-2-3p	Sopen11g002420.1	2.5	-1.0	1	22	511	532	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUAUCGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen04g001570.1	2.5	-1.0	1	22	358	379	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUUGGGAAGA	Cleavage
spe-miR482-2-3p	Sopen11g025550.1	2.5	-1.0	1	22	595	616	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGCGGUGUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen01g009410.1	2.5	-1.0	1	22	22	43	UCUUGCCAAUACCGCCCAUUCC	AGGGUGGUUGGUAUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen12g022450.1	2.5	-1.0	1	22	526	547	UCUUGCCAAUACCGCCCAUUCC	GGUCUGGGUGGUGUUGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen02g010550.1	2.5	-1.0	1	22	592	613	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGAGGUAUUGGCAAAA	Cleavage
spe-miR482-2-3p	Sopen11g028040.1	2.5	-1.0	1	22	921	942	UCUUGCCAAUACCGCCCAUUCC	CUCAUGGGAGGUAUUGGGAAGA	Cleavage
spe-miR482-2-3p	Sopen01g009830.1	3.0	-1.0	1	22	76	97	UCUUGCCAAUACCGCCCAUUCC	GGGAUGGGAGGCAUUGGUAAGA	Translation
spe-miR482-2-3p	Sopen06g023660.1	3.0	-1.0	1	22	64	85	UCUUGCCAAUACCGCCCAUUCC	GGGAUCGGUGGAAUUGGCAAGA	Translation
spe-miR482-2-3p	Sopen11g002570.1	3.0	-1.0	1	22	724	745	UCUUGCCAAUACCGCCCAUUCC	GGGAUGGGAGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen04g001560.1	3.0	-1.0	1	22	541	562	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGAGUUGGUAAGA	Translation
spe-miR482-2-3p	Sopen02g011670.1	3.0	-1.0	1	22	529	550	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGUGGUGUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen01g004310.1	3.0	-1.0	1	22	676	697	UCUUGCCAAUACCGCCCAUUCC	GGCAUGGGGGGAAUUGGUAAGA	Translation
spe-miR482-2-3p	Sopen10g022740.1	3.0	-1.0	1	22	529	550	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGAGGUAUAGGUAAGA	Cleavage
spe-miR482-2-3p	Sopen11g027730.1	3.0	-1.0	1	22	283	304	UCUUGCCAAUACCGCCCAUUCC	GGUAUGGGGGGUAUUGGUAAAA	Cleavage
spe-miR482-2-5p	Sopen03g003690.1	1.5	-1.0	1	21	234	254	GGAGUGGGUGGUAUGGUAAGA	CAUUAGCAUGCCACCCACUCC	Cleavage
spe-miR482-2-5p	Sopen11g027080.1	2.5	-1.0	1	21	843	863	GGAGUGGGUGGUAUGGUAAGA	UUUUAGCAUACUGCCCACUUC	Cleavage

spe-miR482-2-5p	Sopen03g017220.1	2.5	-1.0	1	21	1457	1477	GGAGUGGGUGGUAUGGUAAGA	GGUUACUAUGUCAUCUACUCC	Cleavage
spe-miR482-2-5p	Sopen12g029490.1	3.0	-1.0	1	21	42	62	GGAGUGGGUGGUAUGGUAAGA	GUUUACUUUACCACCUAUUCU	Cleavage
spe-miR482-2-5p	Sopen01g049390.1	3.0	-1.0	1	21	1116	1136	GGAGUGGGUGGUAUGGUAAGA	UGUCACCAUAUUACCUACUCU	Cleavage
spe-miR482a-3p	Sopen11g003950.1	1.0	-1.0	1	22	894	915	UUUCCAAUUCCACCCAUUCCUA	GUGGAGUGGGUGGAAUUGGAGA	Cleavage
spe-miR482a-3p	Sopen01g036600.2	2.0	-1.0	1	22	538	559	UUUCCAAUUCCACCCAUUCCUA	UCAGAAUGGGUGGAAUUGGGGU	Cleavage
spe-miR482a-3p	Sopen01g036600.1	2.0	-1.0	1	22	538	559	UUUCCAAUUCCACCCAUUCCUA	UCAGAAUGGGUGGAAUUGGGGU	Cleavage
spe-miR482a-3p	Sopen01g045330.1	2.0	-1.0	1	22	704	725	UUUCCAAUUCCACCCAUUCCUA	GUGGUAUUGGUGGAAUUGGAAA	Cleavage
spe-miR482a-3p	Sopen06g021930.1	3.0	-1.0	1	22	593	614	UUUCCAAUUCCACCCAUUCCUA	UAGGAAUGGGGGGAAUAGGAAA	Cleavage
spe-miR482a-3p	Sopen01g034260.1	3.0	-1.0	1	22	473	494	UUUCCAAUUCCACCCAUUCCUA	CAGGUAUGGGUGGGAUUGGCAA	Cleavage
spe-miR482a-3p	Sopen11g006130.1	3.0	-1.0	1	22	683	704	UUUCCAAUUCCACCCAUUCCUA	GGGGAAUAGGUGGAGUUGGUAA	Cleavage
spe-miR482a-3p	Sopen06g023660.1	3.0	-1.0	1	22	62	83	UUUCCAAUUCCACCCAUUCCUA	GGGGGAUCGGUGGAAUUGGCAA	Cleavage
spe-miR482a-3p	Sopen02g036460.1	3.0	-1.0	1	22	757	778	UUUCCAAUUCCACCCAUUCCUA	AAGAAGUCGGUGGAAUUGGAAG	Cleavage
spe-miR482a-3p	Sopen06g004210.1	3.0	-1.0	1	22	1661	1682	UUUCCAAUUCCACCCAUUCCUA	UUGGAGUUGGUGGAUUUGGAAA	Cleavage
spe-miR482a-3p	Sopen06g004220.1	3.0	-1.0	1	22	1634	1655	UUUCCAAUUCCACCCAUUCCUA	UUGGAGUUGGUGGAUUUGGAAA	Cleavage
spe-miR482a-3p	Sopen04g001560.1	3.0	-1.0	1	22	539	560	UUUCCAAUUCCACCCAUUCCUA	GUGGUAUGGGUGGAGUUGGUAA	Cleavage
spe-miR482a-3p	Sopen01g034940.1	3.0	-1.0	1	22	587	608	UUUCCAAUUCCACCCAUUCCUA	CUGGAAUUGGAGGAAUUGGGAA	Cleavage
spe-miR482a-3p	Sopen03g035290.1	3.0	-1.0	1	22	818	839	UUUCCAAUUCCACCCAUUCCUA	GUGGGAUGUGUGGACUUGGAAA	Cleavage
spe-miR482a-3p	Sopen08g029150.1	3.0	-1.0	1	22	58	79	UUUCCAAUUCCACCCAUUCCUA	GAAGAAUUGGAGGAAUUGGAAG	Cleavage
spe-miR482a-3p	Sopen11g016540.1	3.0	-1.0	1	22	16	37	UUUCCAAUUCCACCCAUUCCUA	AUAGAUUGGGUGAAAUUGGAAG	Translation
spe-miR482a-5p	Sopen05g001780.1	3.0	-1.0	1	21	2235	2255	GGAAUUGGUGAGUUGGAAAGC	CCCUUCCAGCUCACCAAUUGC	Cleavage
spe-miR482a-5p	Sopen12g006590.1	2.5	-1.0	1	21	125	145	GGAAUUGGUGAGUUGGAAAGC	UUUUUCCAACUCAUCAAGUUC	Cleavage
spe-miR482a-5p	Sopen02g038140.1	2.5	-1.0	1	21	940	960	GGAAUUGGUGAGUUGGAAAGC	AAUUUCCAGUUCGUCAAUUUC	Cleavage
spe-miR482a-5p	Sopen07g009150.1	3.0	-1.0	1	21	1693	1713	GGAAUUGGUGAGUUGGAAAGC	UCUUUCCAACUGACCAAUUUG	Translation
spe-miR482a-5p	Sopen11g004340.2	3.0	-1.0	1	21	948	968	GGAAUUGGUGAGUUGGAAAGC	ACCUUUCAACUUAUCAAUUCU	Cleavage
spe-miR482a-5p	Sopen11g023410.1	3.0	-1.0	1	21	141	161	GGAAUUGGUGAGUUGGAAAGC	UUUUUCCAAUUUACCAAAUUC	Cleavage
spe-miR482a-5p	Sopen11g004340.3	3.0	-1.0	1	21	627	647	GGAAUUGGUGAGUUGGAAAGC	ACCUUUCAACUUAUCAAUUCU	Cleavage
spe-miR482b-3p	Sopen12g004510.1	2.0	-1.0	1	22	369	390	UUACCGAUUCCCCCCAUUCCAA	UAGGGAUGGGGGGAAUCGGGAA	Cleavage
spe-miR482b-3p	Sopen12g004510.1	2.0	-1.0	1	22	1317	1338	UUACCGAUUCCCCCCAUUCCAA	UAGGGAUGGGGGGAAUCGGGAA	Cleavage
spe-miR482b-3p	Sopen12g004510.1	2.0	-1.0	1	22	2265	2286	UUACCGAUUCCCCCCAUUCCAA	UAGGGAUGGGGGGAAUCGGGAA	Cleavage
spe-miR482b-3p	Sopen11g005850.1	3.0	-1.0	1	22	713	734	UUACCGAUUCCCCCCAUUCCAA	GUGGAAUUGGGGGAGUCGGCAA	Cleavage
spe-miR482b-3p	Sopen11g006120.1	0.5	-1.0	1	22	35	56	UUACCGAUUCCCCCCAUUCCAA	GGGGAAUGGGGGGAGUCGGUAA	Cleavage
spe-miR482b-3p	Sopen01g004310.1	1.5	-1.0	1	22	674	695	UUACCGAUUCCCCCCAUUCCAA	GGGGCAUGGGGGGAAUUGGUAA	Cleavage
spe-miR482b-3p	Sopen11g005840.1	2.5	-1.0	1	22	674	695	UUACCGAUUCCCCCCAUUCCAA	GGGGAAUGGUGGGAGUUGGUAA	Cleavage
spe-miR482b-3p	Sopen11g027730.1	3.0	-1.0	1	22	281	302	UUACCGAUUCCCCCCAUUCCAA	UUGGUAUGGGGGGUAUUGGUAA	Cleavage
spe-miR482b-3p	Sopen06g021930.1	3.0	-1.0	1	22	593	614	UUACCGAUUCCCCCCAUUCCAA	UAGGAAUGGGGGGAAUAGGAAA	Cleavage
spe-miR482b-3p	Sopen05g003710.1	3.0	-1.0	1	22	677	698	UUACCGAUUCCCCCCAUUCCAA	GGGGAAUAGGCGGAGUCGGUAA	Cleavage
spe-miR482b-3p	Sopen05g003710.2	3.0	-1.0	1	22	389	410	UUACCGAUUCCCCCCAUUCCAA	GGGGAAUAGGCGGAGUCGGUAA	Cleavage
spe-miR482b-5p	Sopen03g003690.1	1.0	-1.0	1	21	234	254	GGAGUGGGUGGCAUGGUAAGA	CAUUAGCAUGCCACCCACUCC	Cleavage
spe-miR482b-5p	Sopen03g017220.1	2.0	-1.0	1	21	1457	1477	GGAGUGGGUGGCAUGGUAAGA	GGUUACUAUGUCAUCUACUCC	Cleavage
spe-miR482b-5p	Sopen04g022700.1	3.0	-1.0	1	21	465	485	GGAGUGGGUGGCAUGGUAAGA	AAUUACCAUGUCAUCUAUUCA	Cleavage
spe-miR482b-5p	Sopen02g024510.1	3.0	-1.0	1	21	147	167	GGAGUGGGUGGCAUGGUAAGA	GAUUACCAAGCUACCCAUUUC	Cleavage
spe-miR482b-5p	Sopen01g032610.1	3.0	-1.0	1	21	1344	1364	GGAGUGGGUGGCAUGGUAAGA	AGUUAUCAUGCUACUCUCUCC	Cleavage
spe-miR482b-5p	Sopen06g016810.1	3.0	-1.0	1	21	828	848	GGAGUGGGUGGCAUGGUAAGA	CAUUACUAUGUCAUUUGCUCC	Cleavage
spe-miR482b-5p	Sopen08g023090.1	3.0	-1.0	1	21	561	581	GGAGUGGGUGGCAUGGUAAGA	AUUCACCAUGCUGCCUACUUC	Cleavage
spe-miR482b-5p	Sopen12g004990.1	3.0	-1.0	1	21	1548	1568	GGAGUGGGUGGCAUGGUAAGA	UGUUCUCAUGUCGCCUACUCC	Cleavage
spe-miR482d-3p	Sopen09g029830.1	3.0	-1.0	1	22	338	359	UUUCCUAUUCCACCCAUGCCAA	GUGAUAUGGGUGGAAUGGGAGG	Cleavage
spe-miR482d-3p	Sopen06g001380.1	1.0	-1.0	1	22	261	282	UUUCCUAUUCCACCCAUGCCAA	UUGGCAUUGGUGGAAUAGGAAA	Cleavage
spe-miR482d-3p	Sopen02g024130.1	1.5	-1.0	1	22	308	329	UUUCCUAUUCCACCCAUGCCAA	CUGGUAGGGGUGGAAUAGGAAA	Cleavage
spe-miR482d-3p	Sopen02g024150.1	2.0	-1.0	1	22	326	347	UUUCCUAUUCCACCCAUGCCAA	CCGGUAGGGGUGGGAUAGGAAA	Cleavage
spe-miR482d-3p	Sopen02g010920.1	2.5	-1.0	1	22	701	722	UUUCCUAUUCCACCCAUGCCAA	GUGGUAUGGGUGGUAUAGGGAA	Cleavage

spe-miR482d-3p	Sopen01g044060.1	2.5	-1.0	1	22	614	635	UUUCCUAUUCCACCCAUGCCAA	GUGGCAUUGGUGGAAUAGGCAA	Cleavage
spe-miR482d-3p	Sopen06g021930.1	2.5	-1.0	1	22	593	614	UUUCCUAUUCCACCCAUGCCAA	UAGGAAUGGGGGGAAUAGGAAA	Cleavage
spe-miR482d-3p	Sopen10g029290.1	2.5	-1.0	1	22	351	372	UUUCCUAUUCCACCCAUGCCAA	UAAGCGAGAGUGGAAUAGGAAA	Cleavage
spe-miR482d-3p	Sopen05g005560.1	3.0	-1.0	1	22	164	185	UUUCCUAUUCCACCCAUGCCAA	UUGGAAUGGCUGGAAUAGGGAA	Cleavage
spe-miR482d-3p	Sopen02g011950.1	3.0	-1.0	1	22	479	500	UUUCCUAUUCCACCCAUGCCAA	AUGGCAUGGGUGGGGUGGGUAA	Cleavage
spe-miR482d-3p	Sopen01g047850.1	3.0	-1.0	1	22	539	560	UUUCCUAUUCCACCCAUGCCAA	GUGGCAUGGGUGGUAUGGGAGG	Cleavage
spe-miR482d-3p	Sopen01g045330.1	3.0	-1.0	1	22	704	725	UUUCCUAUUCCACCCAUGCCAA	GUGGUAUUGGUGGAAUUGGAAA	Cleavage
spe-miR482d-3p	Sopen11g008710.1	3.0	-1.0	1	22	584	605	UUUCCUAUUCCACCCAUGCCAA	GCGGGAUGGGUGGCAUAGGGAA	Cleavage
spe-miR482d-3p	Sopen08g028690.1	3.0	-1.0	1	22	603	624	UUUCCUAUUCCACCCAUGCCAA	UGUUCAUGGUUGGGAUAGGAAA	Cleavage
spe-miR482d-3p	Sopen05g012400.1	3.0	-1.0	1	22	358	379	UUUCCUAUUCCACCCAUGCCAA	AAUGCUUGGGGGGAAUGGGAAA	Cleavage
spe-miR482d-5p	Sopen09g032890.1	3.0	-1.0	1	21	288	308	GGAGUGGGUGGGAUGGAAAAA	AAUUUCUAUUUCACCCUCUCC	Cleavage
spe-miR482d-5p	Sopen07g005700.1	2.0	-1.0	1	21	36	56	GGAGUGGGUGGGAUGGAAAAA	UCUUUCCGUUCCAUUCACUCC	Cleavage
spe-miR482d-5p	Sopen11g028120.1	2.5	-1.0	1	21	48	68	GGAGUGGGUGGGAUGGAAAAA	CUUCUCCGUCCUACUCACUCC	Cleavage
spe-miR482d-5p	Sopen06g023870.1	3.0	-1.0	1	21	107	127	GGAGUGGGUGGGAUGGAAAAA	CUUUUCUAUCUCACUCAUUUU	Cleavage
spe-miR482d-5p	Sopen05g034710.1	3.0	-1.0	1	21	150	170	GGAGUGGGUGGGAUGGAAAAA	CUUAUCCGUUCCGCCCACUUC	Cleavage
spe-miR482d-5p	Sopen04g009670.1	3.0	-1.0	1	21	585	605	GGAGUGGGUGGGAUGGAAAAA	AUUUUCAAUCCCAGCCACUUC	Cleavage
spe-miR482d-5p	Sopen10g005750.1	3.0	-1.0	1	21	157	177	GGAGUGGGUGGGAUGGAAAAA	UCUUUCUGUCCCACCUGUUUC	Cleavage
spe-miR482d-5p	Sopen02g012560.1	3.0	-1.0	1	21	788	808	GGAGUGGGUGGGAUGGAAAAA	GAUUUCCAUCCGAUUCACUCU	Translation
spe-miR482d-5p	Sopen10g008230.1	3.0	-1.0	1	21	1904	1924	GGAGUGGGUGGGAUGGAAAAA	GCUUUCCGUUCCAUCCAUUUU	Cleavage
spe-miR482d-5p	Sopen05g007660.1	3.0	-1.0	1	21	420	440	GGAGUGGGUGGGAUGGAAAAA	CAUUUUCAUUUCAUUCACUCU	Cleavage
spe-miR482d-5p	Sopen01g046130.1	3.0	-1.0	1	21	64	84	GGAGUGGGUGGGAUGGAAAAA	GCUUUCCAUCCCUCUCGCUCU	Cleavage
spe-miR482d-5p	Sopen12g014550.1	3.0	-1.0	1	21	50	70	GGAGUGGGUGGGAUGGAAAAA	UCUCUCCAUCUUAUUCACUCC	Cleavage
spe-miR482d-5p	Sopen10g030620.1	3.0	-1.0	1	21	141	161	GGAGUGGGUGGGAUGGAAAAA	UCUUUUCUUCCCAUCUGCUCC	Cleavage
spe-miR482e-3p	Sopen08g024300.1	2.0	-1.0	1	22	1267	1288	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGACUAGGAAAGA	Translation
spe-miR482e-3p	Sopen08g024300.1	2.0	-1.0	1	22	3979	4000	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGACUAGGAAAGA	Translation
spe-miR482e-3p	Sopen00g003430.1	2.0	-1.0	1	22	1267	1288	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGACUAGGAAAGA	Translation
spe-miR482e-3p	Sopen08g024640.1	2.0	-1.0	1	22	550	571	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGACUAGGAAAGA	Translation
spe-miR482e-3p	Sopen09g025780.1	2.0	-1.0	1	22	334	355	UCUUUCCUACUCCUCCCAUACC	GGUAUGGGGGGACUAGGAAAGA	Translation
spe-miR482e-3p	Sopen05g002570.2	2.0	-1.0	1	22	655	676	UCUUUCCUACUCCUCCCAUACC	GGAAUGGGAGGAGUGGGCAAGA	Cleavage
spe-miR482e-3p	Sopen05g002570.1	2.0	-1.0	1	22	655	676	UCUUUCCUACUCCUCCCAUACC	GGAAUGGGAGGAGUGGGCAAGA	Cleavage
spe-miR482e-3p	Sopen04g034180.1	2.0	-1.0	1	22	634	655	UCUUUCCUACUCCUCCCAUACC	GCUGUGGUAGGAGUAGGAGAGA	Cleavage
spe-miR482e-3p	Sopen11g008730.1	2.5	-1.0	1	22	269	290	UCUUUCCUACUCCUCCCAUACC	GGUAUGGAAGGAAUAGGAAAGA	Translation
spe-miR482e-3p	Sopen08g021650.1	2.5	-1.0	1	22	570	591	UCUUUCCUACUCCUCCCAUACC	UGAGUGGAAGGAGUGGGAAAGG	Cleavage
spe-miR482e-3p	Sopen07g002190.1	2.5	-1.0	1	22	710	731	UCUUUCCUACUCCUCCCAUACC	UUAAUGUGGGGAGUGGGAAGGA	Cleavage
spe-miR482e-3p	Sopen06g034920.1	2.5	-1.0	1	22	119	140	UCUUUCCUACUCCUCCCAUACC	UUCAGGAGAGGAGUGGGAAAGA	Cleavage
spe-miR482e-3p	Sopen04g004250.1	3.0	-1.0	1	22	583	604	UCUUUCCUACUCCUCCCAUACC	GGCAUGGGCGGAUUAGGGAAGA	Translation
spe-miR482e-3p	Sopen06g032760.1	3.0	-1.0	1	22	506	527	UCUUUCCUACUCCUCCCAUACC	GCUAUGAGAGGAGUAGAGAAGA	Cleavage
spe-miR482e-3p	Sopen10g003280.1	3.0	-1.0	1	22	200	221	UCUUUCCUACUCCUCCCAUACC	GGAAUGUGAUGAGUAGGGAAGA	Cleavage
spe-miR482e-3p	Sopen07g028980.1	3.0	-1.0	1	22	379	400	UCUUUCCUACUCCUCCCAUACC	GGAAUGAGCGGAGUGGGGAAGA	Cleavage
spe-miR482e-3p	Sopen07g005680.2	3.0	-1.0	1	19	1	19	UCUUUCCUACUCCUCCCAU	AUGGGAAGAGUUGGAAAGA	Cleavage
spe-miR482e-3p	Sopen07g005680.1	3.0	-1.0	1	19	1	19	UCUUUCCUACUCCUCCCAU	AUGGGAAGAGUUGGAAAGA	Cleavage
spe-miR482e-3p	Sopen01g036680.1	3.0	-1.0	1	22	436	456	UCUUUCCUACUCCUCCCAUACC	GCUAUGG-AGGAGUGGGAAGGA	Cleavage
spe-miR482e-3p	Sopen00g010390.1	3.0	-1.0	1	19	1	19	UCUUUCCUACUCCUCCCAU	AUGGGAAGAGUUGGAAAGA	Cleavage
spe-miR482e-3p	Sopen07g015650.1	3.0	-1.0	1	22	220	241	UCUUUCCUACUCCUCCCAUACC	AGAACGGGAGGAGAAGGAGAGA	Cleavage
spe-miR482e-3p	Sopen09g005640.1	3.0	-1.0	1	22	2046	2067	UCUUUCCUACUCCUCCCAUACC	AGCUUGUGAGGGGUGGGAAAGA	Cleavage
spe-miR482e-3p	Sopen04g005080.1	3.0	-1.0	1	22	13	34	UCUUUCCUACUCCUCCCAUACC	AUAAAGGGAGGAGUAUGGAAGA	Cleavage
spe-miR482e-3p	Sopen04g005080.2	3.0	-1.0	1	22	13	34	UCUUUCCUACUCCUCCCAUACC	AUAAAGGGAGGAGUAUGGAAGA	Cleavage
spe-miR482e-5p	Sopen01g028490.1	2.5	-1.0	1	21	2189	2209	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g028490.1	2.5	-1.0	1	21	3989	4009	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g031910.2	2.5	-1.0	1	21	2510	2530	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation

spe-miR482e-5p	Sopen07g031910.1	2.5	-1.0	1	21	2504	2524	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g028800.1	3.0	-1.0	1	21	145	165	UGUGGGUGGGGUGGAAAGAUU	AAUCUAUCCAUCCCACUCACU	Cleavage
spe-miR482e-5p	Sopen05g026520.1	2.5	-1.0	1	21	986	1006	UGUGGGUGGGGUGGAAAGAUU	AUUCUUUCCAUCUCACCCAAA	Cleavage
spe-miR482e-5p	Sopen11g014040.1	2.5	-1.0	1	21	4259	4279	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g007280.1	2.5	-1.0	1	21	1505	1525	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g006610.1	2.5	-1.0	1	21	1646	1666	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g005070.1	2.5	-1.0	1	21	4034	4054	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g017650.1	2.5	-1.0	1	21	3866	3886	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g001870.1	2.5	-1.0	1	21	2486	2506	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g026650.1	2.5	-1.0	1	21	2315	2335	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g048190.1	2.5	-1.0	1	21	1412	1432	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g002610.1	2.5	-1.0	1	21	1241	1261	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g003070.1	2.5	-1.0	1	21	3137	3157	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g024810.1	2.5	-1.0	1	21	3089	3109	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g027170.1	2.5	-1.0	1	21	3014	3034	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g048190.2	2.5	-1.0	1	21	1412	1432	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g006100.1	2.5	-1.0	1	21	2882	2902	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g028780.1	2.5	-1.0	1	21	1076	1096	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g020050.1	2.5	-1.0	1	21	2522	2542	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g029550.1	2.5	-1.0	1	21	1721	1741	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g008990.1	2.5	-1.0	1	21	2219	2239	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g014330.1	2.5	-1.0	1	21	2117	2137	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g014330.2	2.5	-1.0	1	21	2048	2068	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g017710.1	2.5	-1.0	1	21	2006	2026	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g052250.1	2.5	-1.0	1	21	1961	1981	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g010150.1	2.5	-1.0	1	21	1943	1963	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g026390.1	2.5	-1.0	1	21	1931	1951	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g028860.1	2.5	-1.0	1	21	1919	1939	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g033580.1	2.5	-1.0	1	21	1916	1936	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g017330.1	2.5	-1.0	1	21	1829	1849	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g022760.1	2.5	-1.0	1	21	1817	1837	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g050140.1	2.5	-1.0	1	21	1781	1801	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g011600.1	2.5	-1.0	1	21	1769	1789	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g027700.1	2.5	-1.0	1	21	1751	1771	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g016540.1	2.5	-1.0	1	21	1622	1642	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g008260.1	2.5	-1.0	1	21	1658	1678	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g030640.1	2.5	-1.0	1	21	1418	1438	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g005470.1	2.5	-1.0	1	21	1085	1105	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g023370.1	2.5	-1.0	1	21	1547	1567	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g003510.1	2.5	-1.0	1	21	1526	1546	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g030640.2	2.5	-1.0	1	21	1352	1372	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g012550.1	2.5	-1.0	1	21	1490	1510	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g011330.1	2.5	-1.0	1	21	1484	1504	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g010190.1	2.5	-1.0	1	21	1481	1501	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g033970.1	2.5	-1.0	1	21	1463	1483	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g002540.1	2.5	-1.0	1	21	1421	1441	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g021090.1	2.5	-1.0	1	21	1367	1387	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g015560.1	2.5	-1.0	1	21	1340	1360	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g021970.2	2.5	-1.0	1	21	1310	1330	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g007530.1	2.5	-1.0	1	21	1310	1330	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation

spe-miR482e-5p	Sopen01g006500.1	2.5	-1.0	1	21	1274	1294	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g012100.1	2.5	-1.0	1	21	1247	1267	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g021970.1	2.5	-1.0	1	21	1229	1249	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g021970.1	2.5	-1.0	1	21	1217	1237	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g024960.1	2.5	-1.0	1	21	1208	1228	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g012760.1	2.5	-1.0	1	21	1205	1225	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g024460.1	2.5	-1.0	1	21	1202	1222	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g033680.1	2.5	-1.0	1	21	1184	1204	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g001720.1	2.5	-1.0	1	21	1169	1189	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g001790.1	2.5	-1.0	1	21	1169	1189	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g022950.1	2.5	-1.0	1	21	1163	1183	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g006630.1	2.5	-1.0	1	21	1157	1177	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g012070.1	2.5	-1.0	1	21	1151	1171	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g030270.1	2.5	-1.0	1	21	1148	1168	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g019120.1	2.5	-1.0	1	21	1145	1165	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g021450.1	2.5	-1.0	1	21	1136	1156	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g015290.1	2.5	-1.0	1	21	1127	1147	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g006820.1	2.5	-1.0	1	21	1121	1141	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g017530.1	2.5	-1.0	1	21	1118	1138	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g018760.1	2.5	-1.0	1	21	1118	1138	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g024300.1	2.5	-1.0	1	21	1115	1135	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g019480.1	2.5	-1.0	1	21	1109	1129	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g020160.1	2.5	-1.0	1	21	1103	1123	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g009850.2	2.5	-1.0	1	21	1094	1114	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g034320.1	2.5	-1.0	1	21	1082	1102	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g002520.1	2.5	-1.0	1	21	1073	1093	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g033850.1	2.5	-1.0	1	21	1067	1087	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g026760.2	2.5	-1.0	1	21	1061	1081	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g010540.1	2.5	-1.0	1	21	1055	1075	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g010200.1	2.5	-1.0	1	21	1052	1072	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g026760.1	2.5	-1.0	1	21	1052	1072	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g035060.1	2.5	-1.0	1	21	1043	1063	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g047600.1	2.5	-1.0	1	21	1040	1060	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g032680.1	2.5	-1.0	1	21	1037	1057	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g035280.1	2.5	-1.0	1	21	1034	1054	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g015400.1	2.5	-1.0	1	21	1031	1051	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g011670.1	2.5	-1.0	1	21	1031	1051	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g027810.1	2.5	-1.0	1	21	1028	1048	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g020670.1	2.5	-1.0	1	21	1028	1048	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g014230.1	2.5	-1.0	1	21	1025	1045	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g015780.1	2.5	-1.0	1	21	1025	1045	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g013750.1	2.5	-1.0	1	21	1022	1042	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g029050.1	2.5	-1.0	1	21	1019	1039	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g006330.1	2.5	-1.0	1	21	1019	1039	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g034530.1	2.5	-1.0	1	21	1019	1039	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g024500.2	2.5	-1.0	1	21	1016	1036	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g010100.1	2.5	-1.0	1	21	1013	1033	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g019370.1	2.5	-1.0	1	21	1004	1024	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g009990.1	2.5	-1.0	1	21	995	1015	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g009190.1	2.5	-1.0	1	21	992	1012	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation

spe-miR482e-5p	Sopen05g011730.1	2.5	-1.0	1	21	992	1012	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g040560.1	2.5	-1.0	1	21	986	1006	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g013250.1	2.5	-1.0	1	21	986	1006	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g005520.2	2.5	-1.0	1	21	986	1006	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g031280.1	2.5	-1.0	1	21	983	1003	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g004570.1	2.5	-1.0	1	21	983	1003	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g027020.1	2.5	-1.0	1	21	980	1000	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g028440.1	2.5	-1.0	1	21	977	997	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g024630.1	2.5	-1.0	1	21	950	970	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g025500.1	2.5	-1.0	1	21	929	949	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g031440.1	2.5	-1.0	1	21	914	934	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g011090.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g011880.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g023250.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g023230.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g032960.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g006440.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g018970.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g030530.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g026790.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g017880.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g031490.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g013430.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g015220.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g017600.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g034900.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g028340.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g017050.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g015810.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g005110.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g022310.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g043200.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g003580.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g022980.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g036820.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g014860.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g011370.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g013150.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g002070.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g029020.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g009600.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen08g013550.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g009370.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g015390.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g025140.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g020540.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g001850.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g020480.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g005410.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g008060.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation

spe-miR482e-5p	Sopen05g005160.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g028650.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g002460.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g051440.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g027120.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g027260.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g009800.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g032610.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen05g006820.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g030280.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g007370.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g013110.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g007780.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g016510.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen02g031460.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen06g033920.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g002280.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen01g004150.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g024110.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g024510.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g005610.2	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g012010.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen09g020710.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen10g027730.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g012800.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen03g022000.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen12g019970.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g006620.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g024990.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen07g021580.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g011010.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen11g029070.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR482e-5p	Sopen04g025750.1	2.5	-1.0	1	21	827	847	UGUGGGUGGGGUGGAAAGAUU	CUUCUUUUCACGCUACCCACA	Translation
spe-miR5014a-3p	Sopen06g005020.1	2.5	-1.0	1	21	1770	1790	UUGUACAAAUUUAAGUGUAUA	AGUACACUUAGAUUUGUGUGG	Cleavage
spe-miR5014a-3p	Sopen02g024260.1	3.0	-1.0	1	21	530	550	UUGUACAAAUUUAAGUGUAUA	UGUAUGCUCAAGUUUGUACAA	Cleavage
spe-miR5014a-3p	Sopen10g030700.1	3.0	-1.0	1	21	1225	1245	UUGUACAAAUUUAAGUGUAUA	GAUGCAUUUAAAGUUGUGCAA	Cleavage
spe-miR5014a-3p	Sopen05g001140.1	3.0	-1.0	1	21	4779	4799	UUGUACAAAUUUAAGUGUAUA	CAAAUACUUAAAUUUGGACAA	Cleavage
spe-miR5014a-3p	Sopen02g020870.1	3.0	-1.0	1	21	1092	1112	UUGUACAAAUUUAAGUGUAUA	CCUGUAUUUAAACUUGUACAA	Cleavage
spe-miR5014a-3p	Sopen01g007030.1	3.0	-1.0	1	21	1132	1152	UUGUACAAAUUUAAGUGUAUA	GAGAUGAUUAAAUUUGUACAA	Cleavage
spe-miR5174d-1-5p	Sopen01g029400.1	2.0	-1.0	1	24	376	399	UCCCUCCGUUUCAAAAAGAUUGGC	GCAGCUCUUGUUGAGAUGGAGGGA	Cleavage
spe-miR5174d-1-5p	Sopen02g016390.1	3.0	-1.0	1	24	1324	1347	UCCCUCCGUUUCAAAAAGAUUGGC	GCUAAUCUUUUUGAAAAAGAGGGA	Cleavage
spe-miR5174d-1-5p	Sopen11g003450.1	3.0	-1.0	1	24	1309	1332	UCCCUCCGUUUCAAAAAGAUUGGC	AUUGGUCUUUUUGAAUCGGAGAGA	Cleavage
spe-miR5174d-1-5p	Sopen05g003560.1	3.0	-1.0	1	24	1164	1188	UCCCUCCGUUUCAAAAAGAU-UGGC	ACCAUAUCUUGUUGAAAUGGAUGGA	Cleavage
spe-miR5174d-1-5p	Sopen01g016010.1	3.0	-1.0	1	24	2976	2999	UCCCUCCGUUUCAAAAAGAUUGGC	UUAUUUCUUUUGGGGAUGGAGGGA	Cleavage
spe-miR5174d-2-	Sopen01g029400.1	2.0	-1.0	1	24	376	399	UCCCUCCGUUUCAAAAAGAUUGGC	GCAGCUCUUGUUGAGAUGGAGGGA	Cleavage

5p										
spe-miR5174d-2-5p	Sopen02g016390.1	3.0	-1.0	1	24	1324	1347	UCCCUCCGUUUCAAAAAGAUUGGC	GCUAAUCUUUUUGAAAAAGAGGGA	Cleavage
spe-miR5174d-2-5p	Sopen11g003450.1	3.0	-1.0	1	24	1309	1332	UCCCUCCGUUUCAAAAAGAUUGGC	AUUGGUCUUUUUGAAUCGGAGAGA	Cleavage
spe-miR5174d-2-5p	Sopen05g003560.1	3.0	-1.0	1	24	1164	1188	UCCCUCCGUUUCAAAAAGAU-UGGC	ACCAUAUCUUGUUGAAAUGGAUGGA	Cleavage
spe-miR5174d-2-5p	Sopen01g016010.1	3.0	-1.0	1	24	2976	2999	UCCCUCCGUUUCAAAAAGAUUGGC	UUAUUUCUUUUGGGGAUGGAGGGA	Cleavage
spe-miR5174d-2-p	Sopen04g026870.1	2.5	-1.0	1	24	554	577	CAUUCUUUUUGAAACGGAAGGAGU	AAUUUUUCCUAUUCAAAAAGGAUG	Cleavage
spe-miR5174d-2-p	Sopen09g016150.1	2.5	-1.0	1	24	78	101	CAUUCUUUUUGAAACGGAAGGAGU	AACUCUUUUGGUUCAAAAAGGAUG	Cleavage
spe-miR5174d-2-p	Sopen03g040680.1	2.5	-1.0	1	24	129	152	CAUUCUUUUUGAAACGGAAGGAGU	UGAGUUUCUGUUUCAGGAAGAAUC	Cleavage
spe-miR5174d-2-p	Sopen08g029000.1	2.5	-1.0	1	24	3788	3811	CAUUCUUUUUGAAACGGAAGGAGU	AUGUAUUUCGUUCCAAAAAGGAUG	Cleavage
spe-miR5174d-2-p	Sopen07g029280.1	2.5	-1.0	1	24	488	511	CAUUCUUUUUGAAACGGAAGGAGU	GUAGAGUCCGUUCCAAAAAGAAUG	Cleavage
spe-miR5174d-2-p	Sopen11g029410.1	2.5	-1.0	1	24	68	91	CAUUCUUUUUGAAACGGAAGGAGU	AUAUGUUUCAUUUCAGAAGGAAUG	Cleavage
spe-miR5174d-2-p	Sopen03g037500.1	3.0	-1.0	1	24	782	805	CAUUCUUUUUGAAACGGAAGGAGU	CAUCUUUCUUUUUCAUAAAGAAUG	Cleavage
spe-miR5174d-2-p	Sopen06g023470.1	3.0	-1.0	1	24	575	600	CAUUCUUUUUGAAACGGAAG--GAGU	ACUUGACUUCUGUUUUAAAGGGAAUU	Cleavage
spe-miR5174d-2-p	Sopen06g023480.1	3.0	-1.0	1	24	446	471	CAUUCUUUUUGAAACGGAAG--GAGU	ACUUAACUUCUGUUUUAAAGGGAAUU	Cleavage
spe-miR5174d-2-p	Sopen02g033360.1	3.0	-1.0	1	24	382	405	CAUUCUUUUUGAAACGGAAGGAGU	UUUGCUUUGGUUUUAAAGGGAAUG	Cleavage
spe-miR5174d-2-p	Sopen09g006190.1	3.0	-1.0	1	24	9	32	CAUUCUUUUUGAAACGGAAGGAGU	CAAUUUUUCAUUUCAAGAAGAAUC	Cleavage
spe-miR5174d-2-p	Sopen07g005100.1	3.0	-1.0	1	24	4009	4032	CAUUCUUUUUGAAACGGAAGGAGU	GGUACUGCUGCUUCAAAAAGGAUG	Cleavage
spe-miR5174d-3-3p	Sopen03g015780.1	2.5	-1.0	1	24	2200	2224	CAUUCUUUUUUAAACGGAGG-GAGU	AUUCUCCGCCGUUUGAAAAGGGAUG	Cleavage
spe-miR5174d-3-3p	Sopen01g020870.1	3.0	-1.0	1	24	2396	2419	CAUUCUUUUUUAAACGGAGGGAGU	UAACUCUUCGUUUGGAAAAGGAUC	Cleavage
spe-miR5174d-3-3p	Sopen01g013030.1	3.0	-1.0	1	24	374	397	CAUUCUUUUUUAAACGGAGGGAGU	AAGAAUUCCGUUUAGAAAAGGGUA	Cleavage
spe-miR5174d-3-3p	Sopen06g022280.2	3.0	-1.0	1	24	80	103	CAUUCUUUUUUAAACGGAGGGAGU	AUAAUCUCCCUGUAAAGAAGAAUG	Cleavage
spe-miR5174d-3-3p	Sopen06g022280.1	3.0	-1.0	1	24	80	103	CAUUCUUUUUUAAACGGAGGGAGU	AUAAUCUCCCUGUAAAGAAGAAUG	Cleavage
spe-miR5174d-3-5p	Sopen01g029400.1	2.0	-1.0	1	24	376	399	UCCCUCCGUUUCAAAAAGAUUGGC	GCAGCUCUUGUUGAGAUGGAGGGA	Cleavage
spe-miR5174d-3-5p	Sopen02g016390.1	3.0	-1.0	1	24	1324	1347	UCCCUCCGUUUCAAAAAGAUUGGC	GCUAAUCUUUUUGAAAAAGAGGGA	Cleavage
spe-miR5174d-3-5p	Sopen11g003450.1	3.0	-1.0	1	24	1309	1332	UCCCUCCGUUUCAAAAAGAUUGGC	AUUGGUCUUUUUGAAUCGGAGAGA	Cleavage
spe-miR5174d-3-5p	Sopen05g003560.1	3.0	-1.0	1	24	1164	1188	UCCCUCCGUUUCAAAAAGAU-UGGC	ACCAUAUCUUGUUGAAAUGGAUGGA	Cleavage
spe-miR5174d-3-5p	Sopen01g016010.1	3.0	-1.0	1	24	2976	2999	UCCCUCCGUUUCAAAAAGAUUGGC	UUAUUUCUUUUGGGGAUGGAGGGA	Cleavage
spe-miR5300-5p	Sopen03g035460.1	2.5	-1.0	1	22	545	566	UCCCCAGUCCAGGCAUUCCAAC	ACAGGAAACCUUGGACUGGGGA	Cleavage
spe-miR5300-5p	Sopen03g035460.2	2.5	-1.0	1	22	818	839	UCCCCAGUCCAGGCAUUCCAAC	ACAGGAAACCUUGGACUGGGGA	Cleavage
spe-miR5300-5p	Sopen06g023170.1	3.0	-1.0	1	22	49	70	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUUGGUA	Cleavage
spe-miR5300-5p	Sopen06g023300.1	3.0	-1.0	1	22	136	157	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUCGGUA	Cleavage
spe-miR5300-5p	Sopen06g023160.1	3.0	-1.0	1	22	175	196	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUCGGUA	Cleavage
spe-miR5300-5p	Sopen06g023200.1	3.0	-1.0	1	22	178	199	UCCCCAGUCCAGGCAUUCCAAC	UAUGGAAUGCCUGGACUCGGUA	Cleavage
spe-miR5300-5p	Sopen03g041690.1	3.0	-1.0	1	22	1063	1084	UCCCCAGUCCAGGCAUUCCAAC	GCCUCAAUGCCUGGACUGGGGC	Cleavage
spe-miR5300-5p	Sopen03g041690.2	3.0	-1.0	1	22	1066	1087	UCCCCAGUCCAGGCAUUCCAAC	GCCUCAAUGCCUGGACUGGGGC	Cleavage
spe-miR5300-5p	Sopen03g041690.3	3.0	-1.0	1	22	1171	1192	UCCCCAGUCCAGGCAUUCCAAC	GCCUCAAUGCCUGGACUGGGGC	Cleavage
spe-miR5303-1-3p	Sopen09g004210.1	2.5	-1.0	1	21	215	235	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUCCAGAAA	Cleavage

spe-miR5303-1-3p	Sopen09g004210.1	3.0	-1.0	1	21	83	103	UUUUUGAAGAGUUCGAGCAAC	AUUGUUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-1-3p	Sopen09g025700.2	1.0	-1.0	1	21	132	152	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen01g034820.1	1.5	-1.0	1	21	1631	1651	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAG	Cleavage
spe-miR5303-1-3p	Sopen07g012560.1	1.5	-1.0	1	21	61	81	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen08g028160.1	2.0	-1.0	1	21	482	502	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen00g008820.1	2.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGCUGAAACUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen06g014130.1	2.0	-1.0	1	21	8	28	UUUUUGAAGAGUUCGAGCAAC	AUUGCUUCAAUUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen06g001130.1	2.0	-1.0	1	21	1236	1256	UUUUUGAAGAGUUCGAGCAAC	AGUUCUCGAAUUUUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen12g003080.1	2.5	-1.0	1	21	775	795	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUCUUGGAAAA	Cleavage
spe-miR5303-1-3p	Sopen07g003140.1	2.5	-1.0	1	21	125	145	UUUUUGAAGAGUUCGAGCAAC	GUUACUCGGAUUUUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen03g025330.1	2.5	-1.0	1	21	640	660	UUUUUGAAGAGUUCGAGCAAC	AAGCUUCGAACUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen02g034620.1	2.5	-1.0	1	21	812	832	UUUUUGAAGAGUUCGAGCAAC	AGUGCUUGGACUCUUCAAUAA	Cleavage
spe-miR5303-1-3p	Sopen01g003610.1	2.5	-1.0	1	21	381	401	UUUUUGAAGAGUUCGAGCAAC	AUUUCUUCAACUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen11g019610.1	2.5	-1.0	1	21	990	1010	UUUUUGAAGAGUUCGAGCAAC	CAUGUUCCAAUUCUUCAAGAA	Cleavage
spe-miR5303-1-3p	Sopen05g028590.1	2.5	-1.0	1	21	307	327	UUUUUGAAGAGUUCGAGCAAC	UAUGAUCCAACUUUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen12g002770.1	3.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGAUUCUUCAGAAA	Cleavage
spe-miR5303-1-3p	Sopen10g001690.1	3.0	-1.0	1	21	51	71	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGAGUCUUCAAAAA	Translation
spe-miR5303-1-3p	Sopen04g034150.1	3.0	-1.0	1	21	224	244	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGAUAUUUCAAAAA	Translation
spe-miR5303-1-3p	Sopen02g038670.1	3.0	-1.0	1	21	438	458	UUUUUGAAGAGUUCGAGCAAC	UUUACUUGAGCUUUUCAAAGA	Cleavage
spe-miR5303-1-3p	Sopen01g036640.1	3.0	-1.0	1	21	952	972	UUUUUGAAGAGUUCGAGCAAC	ACUGCUCGGGCUCAUCAGAAA	Cleavage
spe-miR5303-1-3p	Sopen03g039810.1	3.0	-1.0	1	21	1305	1325	UUUUUGAAGAGUUCGAGCAAC	UGUACUCGAAUUCUUCGAAAC	Cleavage
spe-miR5303-1-3p	Sopen07g025100.1	3.0	-1.0	1	21	195	215	UUUUUGAAGAGUUCGAGCAAC	GAUUCUCGAACUCUUCCAGAA	Cleavage
spe-miR5303-1-3p	Sopen07g002890.1	3.0	-1.0	1	21	1165	1185	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUUGGCUCUUCGAAAA	Cleavage
spe-miR5303-1-3p	Sopen02g036790.1	3.0	-1.0	1	21	462	482	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUAGAUUCUUCAAGAA	Cleavage
spe-miR5303-1-3p	Sopen09g018940.1	3.0	-1.0	1	21	480	500	UUUUUGAAGAGUUCGAGCAAC	UCAGCAUGAACUUUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen01g047970.1	3.0	-1.0	1	21	846	866	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCAAAUUCUUUGAAGA	Cleavage
spe-miR5303-1-3p	Sopen01g038710.1	3.0	-1.0	1	21	756	776	UUUUUGAAGAGUUCGAGCAAC	CAUGUACGGAUUCUUCAAGAA	Cleavage
spe-miR5303-1-3p	Sopen09g007230.1	3.0	-1.0	1	21	475	495	UUUUUGAAGAGUUCGAGCAAC	CCUGAUCGAAUUCUUCAAACA	Cleavage
spe-miR5303-1-3p	Sopen05g006240.1	3.0	-1.0	1	21	554	574	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCCGACUCUCCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen01g033510.1	3.0	-1.0	1	21	779	799	UUUUUGAAGAGUUCGAGCAAC	UGUGUGCGAAUUUUUCAAAAG	Cleavage
spe-miR5303-1-3p	Sopen11g007420.1	3.0	-1.0	1	21	361	381	UUUUUGAAGAGUUCGAGCAAC	UGUGCUCAAGUUCUUCAGAAG	Cleavage
spe-miR5303-1-3p	Sopen03g006760.1	3.0	-1.0	1	21	364	384	UUUUUGAAGAGUUCGAGCAAC	UAUGUUCAAUCUCUUCAAAAA	Cleavage
spe-miR5303-1-3p	Sopen10g005630.1	3.0	-1.0	1	21	110	130	UUUUUGAAGAGUUCGAGCAAC	CAUUCUUGAAUUUUUCAAAGA	Cleavage
spe-miR5303-1-5p	Sopen09g025700.2	3.0	-1.0	1	24	160	183	UUUUGGAGGAUCCGAGUCGUACCC	GGGUGCGUGUUGGAUUCUCCAAAA	Cleavage
spe-miR5303-1-5p	Sopen01g019870.1	2.0	-1.0	1	24	2821	2844	UUUUGGAGGAUCCGAGUCGUACCC	GGGAUCGAGUUGGAUCCUUCAAAA	Cleavage
spe-miR5303-1-5p	Sopen06g004440.1	3.0	-1.0	1	24	1985	2008	UUUUGGAGGAUCCGAGUCGUACCC	AGGCACGCCUUGGAUCUUUCAAAG	Cleavage
spe-miR5303-1-5p	Sopen07g029270.1	3.0	-1.0	1	24	3161	3184	UUUUGGAGGAUCCGAGUCGUACCC	AGGCACGCCUUGGAUCUUUCAAAG	Cleavage
spe-miR5303-2-3p	Sopen09g004210.1	2.5	-1.0	1	21	215	235	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-2-3p	Sopen09g004210.1	3.0	-1.0	1	21	83	103	UUUUUGAAGAGUUCGAGCAAC	AUUGUUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-2-3p	Sopen09g025700.2	1.0	-1.0	1	21	132	152	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen01g034820.1	1.5	-1.0	1	21	1631	1651	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAG	Cleavage
spe-miR5303-2-3p	Sopen07g012560.1	1.5	-1.0	1	21	61	81	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen08g028160.1	2.0	-1.0	1	21	482	502	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen00g008820.1	2.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGCUGAAACUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen06g014130.1	2.0	-1.0	1	21	8	28	UUUUUGAAGAGUUCGAGCAAC	AUUGCUUCAAUUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen06g001130.1	2.0	-1.0	1	21	1236	1256	UUUUUGAAGAGUUCGAGCAAC	AGUUCUCGAAUUUUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen12g003080.1	2.5	-1.0	1	21	775	795	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUCUUGGAAAA	Cleavage
spe-miR5303-2-3p	Sopen07g003140.1	2.5	-1.0	1	21	125	145	UUUUUGAAGAGUUCGAGCAAC	GUUACUCGGAUUUUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen03g025330.1	2.5	-1.0	1	21	640	660	UUUUUGAAGAGUUCGAGCAAC	AAGCUUCGAACUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen02g034620.1	2.5	-1.0	1	21	812	832	UUUUUGAAGAGUUCGAGCAAC	AGUGCUUGGACUCUUCAAUAA	Cleavage

spe-miR5303-2-3p	Sopen01g003610.1	2.5	-1.0	1	21	381	401	UUUUUGAAGAGUUCGAGCAAC	AUUUCUUCAACUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen11g019610.1	2.5	-1.0	1	21	990	1010	UUUUUGAAGAGUUCGAGCAAC	CAUGUUCCAAUUCUUCAAGAA	Cleavage
spe-miR5303-2-3p	Sopen05g028590.1	2.5	-1.0	1	21	307	327	UUUUUGAAGAGUUCGAGCAAC	UAUGAUCCAACUUUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen12g002770.1	3.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGAUUCUUCAGAAA	Cleavage
spe-miR5303-2-3p	Sopen10g001690.1	3.0	-1.0	1	21	51	71	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGAGUCUUCAAAAA	Translation
spe-miR5303-2-3p	Sopen04g034150.1	3.0	-1.0	1	21	224	244	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGAUAUUUCAAAAA	Translation
spe-miR5303-2-3p	Sopen02g038670.1	3.0	-1.0	1	21	438	458	UUUUUGAAGAGUUCGAGCAAC	UUUACUUGAGCUUUUCAAAGA	Cleavage
spe-miR5303-2-3p	Sopen01g036640.1	3.0	-1.0	1	21	952	972	UUUUUGAAGAGUUCGAGCAAC	ACUGCUCGGGCUCAUCAGAAA	Cleavage
spe-miR5303-2-3p	Sopen03g039810.1	3.0	-1.0	1	21	1305	1325	UUUUUGAAGAGUUCGAGCAAC	UGUACUCGAAUUCUUCGAAAC	Cleavage
spe-miR5303-2-3p	Sopen07g025100.1	3.0	-1.0	1	21	195	215	UUUUUGAAGAGUUCGAGCAAC	GAUUCUCGAACUCUUCCAGAA	Cleavage
spe-miR5303-2-3p	Sopen07g002890.1	3.0	-1.0	1	21	1165	1185	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUUGGCUCUUCGAAAA	Cleavage
spe-miR5303-2-3p	Sopen02g036790.1	3.0	-1.0	1	21	462	482	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUAGAUUCUUCAAGAA	Cleavage
spe-miR5303-2-3p	Sopen09g018940.1	3.0	-1.0	1	21	480	500	UUUUUGAAGAGUUCGAGCAAC	UCAGCAUGAACUUUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen01g047970.1	3.0	-1.0	1	21	846	866	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCAAAUUCUUUGAAGA	Cleavage
spe-miR5303-2-3p	Sopen01g038710.1	3.0	-1.0	1	21	756	776	UUUUUGAAGAGUUCGAGCAAC	CAUGUACGGAUUCUUCAAGAA	Cleavage
spe-miR5303-2-3p	Sopen09g007230.1	3.0	-1.0	1	21	475	495	UUUUUGAAGAGUUCGAGCAAC	CCUGAUCGAAUUCUUCAAACA	Cleavage
spe-miR5303-2-3p	Sopen05g006240.1	3.0	-1.0	1	21	554	574	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCCGACUCUCCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen01g033510.1	3.0	-1.0	1	21	779	799	UUUUUGAAGAGUUCGAGCAAC	UGUGUGCGAAUUUUUCAAAAG	Cleavage
spe-miR5303-2-3p	Sopen11g007420.1	3.0	-1.0	1	21	361	381	UUUUUGAAGAGUUCGAGCAAC	UGUGCUCAAGUUCUUCAGAAG	Cleavage
spe-miR5303-2-3p	Sopen03g006760.1	3.0	-1.0	1	21	364	384	UUUUUGAAGAGUUCGAGCAAC	UAUGUUCAAUCUCUUCAAAAA	Cleavage
spe-miR5303-2-3p	Sopen10g005630.1	3.0	-1.0	1	21	110	130	UUUUUGAAGAGUUCGAGCAAC	CAUUCUUGAAUUUUUCAAAGA	Cleavage
spe-miR5303-2-5p	Sopen09g004210.1	0.5	-1.0	1	24	9	32	UUUUGGAGGAUCCAACACGUACCC	GUACCCGUGUUGGAUCCUCCAGAA	Cleavage
spe-miR5303-2-5p	Sopen09g004210.1	2.0	-1.0	1	24	243	266	UUUUGGAGGAUCCAACACGUACCC	GCACACUUGUCGGAUCCUCCAAAA	Cleavage
spe-miR5303-2-5p	Sopen01g010260.1	1.5	-1.0	1	24	3166	3189	UUUUGGAGGAUCCAACACGUACCC	GGAAUCGAGUUGGAUCCUUCAAAA	Cleavage
spe-miR5303-2-5p	Sopen04g001200.1	2.0	-1.0	1	24	190	213	UUUUGGAGGAUCCAACACGUACCC	GCAAUUGUGUUGGAUCCUCCGGGA	Cleavage
spe-miR5303-2-5p	Sopen09g025700.2	0.5	-1.0	1	24	160	183	UUUUGGAGGAUCCAACACGUACCC	GGGUGCGUGUUGGAUUCUCCAAAA	Cleavage
spe-miR5303-2-5p	Sopen01g019870.1	1.5	-1.0	1	24	2821	2844	UUUUGGAGGAUCCAACACGUACCC	GGGAUCGAGUUGGAUCCUUCAAAA	Cleavage
spe-miR5303-2-5p	Sopen06g029330.1	2.0	-1.0	1	24	1373	1396	UUUUGGAGGAUCCAACACGUACCC	CACCACGUGUUGGAUUUUCUAGAA	Cleavage
spe-miR5303-2-5p	Sopen07g016340.1	2.5	-1.0	1	24	832	855	UUUUGGAGGAUCCAACACGUACCC	AAAAGUGUGUUGGGUUUUCUAAAA	Cleavage
spe-miR5303-2-5p	Sopen02g003900.1	2.5	-1.0	1	24	1789	1812	UUUUGGAGGAUCCAACACGUACCC	GAGGACGAGAUGGAUCCUCCAAAG	Cleavage
spe-miR5303-2-5p	Sopen01g007130.1	2.5	-1.0	1	24	2911	2934	UUUUGGAGGAUCCAACACGUACCC	GACUUCGUGGUGGGUCUUCCAAAG	Cleavage
spe-miR5303-2-5p	Sopen04g020300.1	2.5	-1.0	1	24	3862	3885	UUUUGGAGGAUCCAACACGUACCC	GAUUUCGUGGUGGGUCUUCCAAAG	Cleavage
spe-miR5303-2-5p	Sopen07g012250.1	3.0	-1.0	1	24	1148	1171	UUUUGGAGGAUCCAACACGUACCC	CAAUACAUGUUGGGUCCUCCAAUA	Cleavage
spe-miR5303-2-5p	Sopen06g035470.2	3.0	-1.0	1	24	1067	1090	UUUUGGAGGAUCCAACACGUACCC	GAGAAUGUGUUGGACCUUCUAAAA	Translation
spe-miR5303-2-5p	Sopen06g035470.1	3.0	-1.0	1	24	1346	1369	UUUUGGAGGAUCCAACACGUACCC	GAGAAUGUGUUGGACCUUCUAAAA	Translation
spe-miR5303-2-5p	Sopen01g024940.1	3.0	-1.0	1	24	37	60	UUUUGGAGGAUCCAACACGUACCC	ACUCAUGUGUUUGAUCCUCCAAAU	Cleavage
spe-miR5303-2-5p	Sopen02g011050.1	3.0	-1.0	1	24	667	690	UUUUGGAGGAUCCAACACGUACCC	ACUCAUGUGUUUGAUCCUCCAAAU	Cleavage
spe-miR5303-2-5p	Sopen01g048110.1	3.0	-1.0	1	24	352	375	UUUUGGAGGAUCCAACACGUACCC	AAGCAUGUGUUGGAUCCUAUAAGA	Cleavage
spe-miR5303-2-5p	Sopen06g018590.2	3.0	-1.0	1	24	367	390	UUUUGGAGGAUCCAACACGUACCC	AAGUUUGUGUUGGAUCUUCUCAAA	Cleavage
spe-miR5303-2-5p	Sopen05g010560.1	3.0	-1.0	1	24	478	501	UUUUGGAGGAUCCAACACGUACCC	AAGUUUGUGUUGGAUCUUCUCAAA	Cleavage
spe-miR5303-2-5p	Sopen06g018590.1	3.0	-1.0	1	24	3796	3819	UUUUGGAGGAUCCAACACGUACCC	AAGUUUGUGUUGGAUCUUCUCAAA	Cleavage
spe-miR5303-2-5p	Sopen06g021680.1	3.0	-1.0	1	24	3796	3819	UUUUGGAGGAUCCAACACGUACCC	AAGUUUGUGUUGGAUCUUCUCAAA	Cleavage
spe-miR5303-2-5p	Sopen04g035530.1	3.0	-1.0	1	24	3796	3819	UUUUGGAGGAUCCAACACGUACCC	AAGUUUGUGUUGGAUCUUCUCAAA	Cleavage
spe-miR5303-2-5p	Sopen04g032870.1	3.0	-1.0	1	24	2858	2881	UUUUGGAGGAUCCAACACGUACCC	GCUUGCGUGGUGGACCCUUCAAAA	Translation
spe-miR5303-2-5p	Sopen02g027600.1	3.0	-1.0	1	24	131	154	UUUUGGAGGAUCCAACACGUACCC	ACUCAAGUGUUGGAUCCUUCAAGU	Cleavage
spe-miR5303-2-5p	Sopen03g005710.1	3.0	-1.0	1	24	31	54	UUUUGGAGGAUCCAACACGUACCC	ACACCAGUGUUGGGUCCUCAAAAA	Cleavage
spe-miR5303-2-5p	Sopen03g025850.1	3.0	-1.0	1	24	1924	1947	UUUUGGAGGAUCCAACACGUACCC	AAACGUGUGUUGGAUUAUCUAAAA	Cleavage
spe-miR5303-2-5p	Sopen11g014430.1	3.0	-1.0	1	24	2143	2166	UUUUGGAGGAUCCAACACGUACCC	AAACGUGUGUUGGGUCAUCUAAAA	Cleavage
spe-miR5303-2-5p	Sopen05g003530.1	3.0	-1.0	1	24	3043	3066	UUUUGGAGGAUCCAACACGUACCC	UUCAGUGUGUUGGAUUUUCCAACA	Cleavage
spe-miR5303-2-5p	Sopen11g013210.2	3.0	-1.0	1	24	535	558	UUUUGGAGGAUCCAACACGUACCC	CAGCUAGUGUUGCAUCCUCCAAGA	Cleavage

spe-miR5303-2-5p	Sopen11g013210.1	3.0	-1.0	1	24	535	558	UUUUGGAGGAUCCAACACGUACCC	CAGCUAGUGUUGCAUCCUCCAAGA	Cleavage
spe-miR5303-2-5p	Sopen11g010830.1	3.0	-1.0	1	24	545	568	UUUUGGAGGAUCCAACACGUACCC	CAACUAGUGUUGCAUCCUCCAAGA	Cleavage
spe-miR5303-2-5p	Sopen09g018520.1	3.0	-1.0	1	24	3691	3714	UUUUGGAGGAUCCAACACGUACCC	GAUUUCGUGUUUGGUCUUCCAAAG	Cleavage
spe-miR5303-2-5p	Sopen07g022670.1	3.0	-1.0	1	24	1276	1299	UUUUGGAGGAUCCAACACGUACCC	UGUAGUGUGAUGGAUCCUUUGAAA	Cleavage
spe-miR5303-2-5p	Sopen02g039190.1	3.0	-1.0	1	24	152	175	UUUUGGAGGAUCCAACACGUACCC	CUACUUCUGGUGGAUCCUCCAAAA	Cleavage
spe-miR5303-2-5p	Sopen12g006980.1	3.0	-1.0	1	24	2590	2613	UUUUGGAGGAUCCAACACGUACCC	GACUUCUUGUUGGAUCUUUCAAAU	Cleavage
spe-miR5303-3-3p	Sopen09g004210.1	2.5	-1.0	1	21	215	235	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-3-3p	Sopen09g004210.1	3.0	-1.0	1	21	83	103	UUUUUGAAGAGUUCGAGCAAC	AUUGUUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-3-3p	Sopen09g025700.2	1.0	-1.0	1	21	132	152	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen01g034820.1	1.5	-1.0	1	21	1631	1651	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAG	Cleavage
spe-miR5303-3-3p	Sopen07g012560.1	1.5	-1.0	1	21	61	81	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen08g028160.1	2.0	-1.0	1	21	482	502	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen00g008820.1	2.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGCUGAAACUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen06g014130.1	2.0	-1.0	1	21	8	28	UUUUUGAAGAGUUCGAGCAAC	AUUGCUUCAAUUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen06g001130.1	2.0	-1.0	1	21	1236	1256	UUUUUGAAGAGUUCGAGCAAC	AGUUCUCGAAUUUUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen12g003080.1	2.5	-1.0	1	21	775	795	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUCUUGGAAAA	Cleavage
spe-miR5303-3-3p	Sopen07g003140.1	2.5	-1.0	1	21	125	145	UUUUUGAAGAGUUCGAGCAAC	GUUACUCGGAUUUUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen03g025330.1	2.5	-1.0	1	21	640	660	UUUUUGAAGAGUUCGAGCAAC	AAGCUUCGAACUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen02g034620.1	2.5	-1.0	1	21	812	832	UUUUUGAAGAGUUCGAGCAAC	AGUGCUUGGACUCUUCAAUAA	Cleavage
spe-miR5303-3-3p	Sopen01g003610.1	2.5	-1.0	1	21	381	401	UUUUUGAAGAGUUCGAGCAAC	AUUUCUUCAACUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen11g019610.1	2.5	-1.0	1	21	990	1010	UUUUUGAAGAGUUCGAGCAAC	CAUGUUCCAAUUCUUCAAGAA	Cleavage
spe-miR5303-3-3p	Sopen05g028590.1	2.5	-1.0	1	21	307	327	UUUUUGAAGAGUUCGAGCAAC	UAUGAUCCAACUUUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen12g002770.1	3.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGAUUCUUCAGAAA	Cleavage
spe-miR5303-3-3p	Sopen10g001690.1	3.0	-1.0	1	21	51	71	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGAGUCUUCAAAAA	Translation
spe-miR5303-3-3p	Sopen04g034150.1	3.0	-1.0	1	21	224	244	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGAUAUUUCAAAAA	Translation
spe-miR5303-3-3p	Sopen02g038670.1	3.0	-1.0	1	21	438	458	UUUUUGAAGAGUUCGAGCAAC	UUUACUUGAGCUUUUCAAAGA	Cleavage
spe-miR5303-3-3p	Sopen01g036640.1	3.0	-1.0	1	21	952	972	UUUUUGAAGAGUUCGAGCAAC	ACUGCUCGGGCUCAUCAGAAA	Cleavage
spe-miR5303-3-3p	Sopen03g039810.1	3.0	-1.0	1	21	1305	1325	UUUUUGAAGAGUUCGAGCAAC	UGUACUCGAAUUCUUCGAAAC	Cleavage
spe-miR5303-3-3p	Sopen07g025100.1	3.0	-1.0	1	21	195	215	UUUUUGAAGAGUUCGAGCAAC	GAUUCUCGAACUCUUCCAGAA	Cleavage
spe-miR5303-3-3p	Sopen07g002890.1	3.0	-1.0	1	21	1165	1185	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUUGGCUCUUCGAAAA	Cleavage
spe-miR5303-3-3p	Sopen02g036790.1	3.0	-1.0	1	21	462	482	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUAGAUUCUUCAAGAA	Cleavage
spe-miR5303-3-3p	Sopen09g018940.1	3.0	-1.0	1	21	480	500	UUUUUGAAGAGUUCGAGCAAC	UCAGCAUGAACUUUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen01g047970.1	3.0	-1.0	1	21	846	866	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCAAAUUCUUUGAAGA	Cleavage
spe-miR5303-3-3p	Sopen01g038710.1	3.0	-1.0	1	21	756	776	UUUUUGAAGAGUUCGAGCAAC	CAUGUACGGAUUCUUCAAGAA	Cleavage
spe-miR5303-3-3p	Sopen09g007230.1	3.0	-1.0	1	21	475	495	UUUUUGAAGAGUUCGAGCAAC	CCUGAUCGAAUUCUUCAAACA	Cleavage
spe-miR5303-3-3p	Sopen05g006240.1	3.0	-1.0	1	21	554	574	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCCGACUCUCCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen01g033510.1	3.0	-1.0	1	21	779	799	UUUUUGAAGAGUUCGAGCAAC	UGUGUGCGAAUUUUUCAAAAG	Cleavage
spe-miR5303-3-3p	Sopen11g007420.1	3.0	-1.0	1	21	361	381	UUUUUGAAGAGUUCGAGCAAC	UGUGCUCAAGUUCUUCAGAAG	Cleavage
spe-miR5303-3-3p	Sopen03g006760.1	3.0	-1.0	1	21	364	384	UUUUUGAAGAGUUCGAGCAAC	UAUGUUCAAUCUCUUCAAAAA	Cleavage
spe-miR5303-3-3p	Sopen10g005630.1	3.0	-1.0	1	21	110	130	UUUUUGAAGAGUUCGAGCAAC	CAUUCUUGAAUUUUUCAAAGA	Cleavage
spe-miR5303-3-5p	Sopen05g012590.1	2.5	-1.0	1	24	1232	1255	UUUUGAAGGAUCCGGCACACACCC	CCAUGGGUGCAGGAUCCUUCGAAA	Cleavage
spe-miR5303-3-5p	Sopen07g022670.1	2.5	-1.0	1	24	1276	1299	UUUUGAAGGAUCCGGCACACACCC	UGUAGUGUGAUGGAUCCUUUGAAA	Cleavage
spe-miR5303-3-5p	Sopen12g006300.1	3.0	-1.0	1	24	180	203	UUUUGAAGGAUCCGGCACACACCC	AGAUGUAUGUCGGAUCAUUCAAAA	Cleavage
spe-miR5303-3-5p	Sopen09g023600.1	3.0	-1.0	1	24	118	141	UUUUGAAGGAUCCGGCACACACCC	UAUGGAGUGUCGGAUUUUUUAAAA	Cleavage
spe-miR5303-3-5p	Sopen11g030380.1	3.0	-1.0	1	24	653	676	UUUUGAAGGAUCCGGCACACACCC	AUGCAAGUGCUGGAUUUUUCAAGA	Cleavage
spe-miR5303-3-5p	Sopen01g019870.1	3.0	-1.0	1	24	2821	2844	UUUUGAAGGAUCCGGCACACACCC	GGGAUCGAGUUGGAUCCUUCAAAA	Cleavage
spe-miR5303-3-5p	Sopen01g010260.1	3.0	-1.0	1	24	3166	3189	UUUUGAAGGAUCCGGCACACACCC	GGAAUCGAGUUGGAUCCUUCAAAA	Cleavage
spe-miR5303-5p	Sopen09g004210.1	2.5	-1.0	1	21	215	235	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-5p	Sopen09g004210.1	3.0	-1.0	1	21	83	103	UUUUUGAAGAGUUCGAGCAAC	AUUGUUCGGACUCUCCAGAAA	Cleavage
spe-miR5303-5p	Sopen09g025700.2	1.0	-1.0	1	21	132	152	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAA	Cleavage

spe-miR5303-5p	Sopen01g034820.1	1.5	-1.0	1	21	1631	1651	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCGGACUCUUCAAAAG	Cleavage
spe-miR5303-5p	Sopen07g012560.1	1.5	-1.0	1	21	61	81	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen08g028160.1	2.0	-1.0	1	21	482	502	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGACUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen00g008820.1	2.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGCUGAAACUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen06g014130.1	2.0	-1.0	1	21	8	28	UUUUUGAAGAGUUCGAGCAAC	AUUGCUUCAAUUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen06g001130.1	2.0	-1.0	1	21	1236	1256	UUUUUGAAGAGUUCGAGCAAC	AGUUCUCGAAUUUUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen12g003080.1	2.5	-1.0	1	21	775	795	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCGAAUUCUUGGAAAA	Cleavage
spe-miR5303-5p	Sopen07g003140.1	2.5	-1.0	1	21	125	145	UUUUUGAAGAGUUCGAGCAAC	GUUACUCGGAUUUUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen03g025330.1	2.5	-1.0	1	21	640	660	UUUUUGAAGAGUUCGAGCAAC	AAGCUUCGAACUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen02g034620.1	2.5	-1.0	1	21	812	832	UUUUUGAAGAGUUCGAGCAAC	AGUGCUUGGACUCUUCAAUAA	Cleavage
spe-miR5303-5p	Sopen01g003610.1	2.5	-1.0	1	21	381	401	UUUUUGAAGAGUUCGAGCAAC	AUUUCUUCAACUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen11g019610.1	2.5	-1.0	1	21	990	1010	UUUUUGAAGAGUUCGAGCAAC	CAUGUUCCAAUUCUUCAAGAA	Cleavage
spe-miR5303-5p	Sopen05g028590.1	2.5	-1.0	1	21	307	327	UUUUUGAAGAGUUCGAGCAAC	UAUGAUCCAACUUUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen12g002770.1	3.0	-1.0	1	21	3	23	UUUUUGAAGAGUUCGAGCAAC	GUUGUUCAGAUUCUUCAGAAA	Cleavage
spe-miR5303-5p	Sopen10g001690.1	3.0	-1.0	1	21	51	71	UUUUUGAAGAGUUCGAGCAAC	GUUGCUCAGAGUCUUCAAAAA	Translation
spe-miR5303-5p	Sopen04g034150.1	3.0	-1.0	1	21	224	244	UUUUUGAAGAGUUCGAGCAAC	UUUGCUCGGAUAUUUCAAAAA	Translation
spe-miR5303-5p	Sopen02g038670.1	3.0	-1.0	1	21	438	458	UUUUUGAAGAGUUCGAGCAAC	UUUACUUGAGCUUUUCAAAGA	Cleavage
spe-miR5303-5p	Sopen01g036640.1	3.0	-1.0	1	21	952	972	UUUUUGAAGAGUUCGAGCAAC	ACUGCUCGGGCUCAUCAGAAA	Cleavage
spe-miR5303-5p	Sopen03g039810.1	3.0	-1.0	1	21	1305	1325	UUUUUGAAGAGUUCGAGCAAC	UGUACUCGAAUUCUUCGAAAC	Cleavage
spe-miR5303-5p	Sopen07g025100.1	3.0	-1.0	1	21	195	215	UUUUUGAAGAGUUCGAGCAAC	GAUUCUCGAACUCUUCCAGAA	Cleavage
spe-miR5303-5p	Sopen07g002890.1	3.0	-1.0	1	21	1165	1185	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUUGGCUCUUCGAAAA	Cleavage
spe-miR5303-5p	Sopen02g036790.1	3.0	-1.0	1	21	462	482	UUUUUGAAGAGUUCGAGCAAC	GCUGCUUAGAUUCUUCAAGAA	Cleavage
spe-miR5303-5p	Sopen09g018940.1	3.0	-1.0	1	21	480	500	UUUUUGAAGAGUUCGAGCAAC	UCAGCAUGAACUUUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen01g047970.1	3.0	-1.0	1	21	846	866	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCAAAUUCUUUGAAGA	Cleavage
spe-miR5303-5p	Sopen01g038710.1	3.0	-1.0	1	21	756	776	UUUUUGAAGAGUUCGAGCAAC	CAUGUACGGAUUCUUCAAGAA	Cleavage
spe-miR5303-5p	Sopen09g007230.1	3.0	-1.0	1	21	475	495	UUUUUGAAGAGUUCGAGCAAC	CCUGAUCGAAUUCUUCAAACA	Cleavage
spe-miR5303-5p	Sopen05g006240.1	3.0	-1.0	1	21	554	574	UUUUUGAAGAGUUCGAGCAAC	AAUGCUCCGACUCUCCAAAAA	Cleavage
spe-miR5303-5p	Sopen01g033510.1	3.0	-1.0	1	21	779	799	UUUUUGAAGAGUUCGAGCAAC	UGUGUGCGAAUUUUUCAAAAG	Cleavage
spe-miR5303-5p	Sopen11g007420.1	3.0	-1.0	1	21	361	381	UUUUUGAAGAGUUCGAGCAAC	UGUGCUCAAGUUCUUCAGAAG	Cleavage
spe-miR5303-5p	Sopen03g006760.1	3.0	-1.0	1	21	364	384	UUUUUGAAGAGUUCGAGCAAC	UAUGUUCAAUCUCUUCAAAAA	Cleavage
spe-miR5303-5p	Sopen10g005630.1	3.0	-1.0	1	21	110	130	UUUUUGAAGAGUUCGAGCAAC	CAUUCUUGAAUUUUUCAAAGA	Cleavage
spe-miR5303c-1-3p	Sopen08g001380.1	2.0	-1.0	1	21	753	773	ACGGGUGCGGCUACAUUUUUG	GGAAAAUGUGGCUGCACUUGU	Cleavage
spe-miR5303c-1-3p	Sopen08g001380.2	2.0	-1.0	1	21	753	773	ACGGGUGCGGCUACAUUUUUG	GGAAAAUGUGGCUGCACUUGU	Cleavage
spe-miR5303c-1-3p	Sopen02g019920.1	2.5	-1.0	1	21	5664	5684	ACGGGUGCGGCUACAUUUUUG	ACCAAGUGUAGCUGCACCUGU	Cleavage
spe-miR5303c-1-3p	Sopen12g030040.1	3.0	-1.0	1	21	6876	6896	ACGGGUGCGGCUACAUUUUUG	AGAAAAUGUAGCUGAAUCUGU	Cleavage
spe-miR5303c-1-3p	Sopen09g031730.1	3.0	-1.0	1	21	2466	2486	ACGGGUGCGGCUACAUUUUUG	AGUAAAUGUGGCUGCGCUCGU	Cleavage
spe-miR5303c-2-3p	Sopen09g004210.1	2.5	-1.0	1	24	9	32	UUUUGGAGAAUCCGACACGCACCC	GUACCCGUGUUGGAUCCUCCAGAA	Cleavage
spe-miR5303c-2-3p	Sopen09g004210.1	2.5	-1.0	1	24	243	266	UUUUGGAGAAUCCGACACGCACCC	GCACACUUGUCGGAUCCUCCAAAA	Cleavage
spe-miR5303c-2-3p	Sopen09g025700.2	0.5	-1.0	1	24	160	183	UUUUGGAGAAUCCGACACGCACCC	GGGUGCGUGUUGGAUUCUCCAAAA	Cleavage
spe-miR5303c-2-3p	Sopen00g012160.1	1.5	-1.0	1	24	45	68	UUUUGGAGAAUCCGACACGCACCC	GCGCCCGCGUCGGGUUCUCCAAAA	Cleavage
spe-miR5303c-2-3p	Sopen12g003610.1	2.0	-1.0	1	24	582	605	UUUUGGAGAAUCCGACACGCACCC	CGAUUCGUGUCAGAUUCUCCAGAA	Cleavage

spe-miR5303c-2-3p	Sopen06g029330.1	2.0	-1.0	1	24	1373	1396	UUUUGGAGAAUCCGACACGCACCC	CACCACGUGUUGGAUUUUCUAGAA	Cleavage
spe-miR5303c-2-3p	Sopen04g001920.1	2.0	-1.0	1	24	244	267	UUUUGGAGAAUCCGACACGCACCC	GCACCCGUCUCGGAUUCUUCAAAG	Cleavage
spe-miR5303c-2-3p	Sopen02g017740.1	2.0	-1.0	1	24	53	76	UUUUGGAGAAUCCGACACGCACCC	GCCGUCGCGUCGGAUUCUCUAAGA	Cleavage
spe-miR5303c-2-3p	Sopen07g016340.1	2.5	-1.0	1	24	832	855	UUUUGGAGAAUCCGACACGCACCC	AAAAGUGUGUUGGGUUUUCUAAAA	Cleavage
spe-miR5303c-2-3p	Sopen09g023600.1	2.5	-1.0	1	24	118	141	UUUUGGAGAAUCCGACACGCACCC	UAUGGAGUGUCGGAUUUUUUAAAA	Cleavage
spe-miR5303c-2-3p	Sopen09g027430.3	3.0	-1.0	1	24	1931	1954	UUUUGGAGAAUCCGACACGCACCC	UGGUGCGUUUCGGAUUAUCCGAAA	Cleavage
spe-miR5303c-2-3p	Sopen06g012190.1	3.0	-1.0	1	24	1510	1533	UUUUGGAGAAUCCGACACGCACCC	AAACGUGUGUCGGGUUAUCUAAAA	Cleavage
spe-miR5303c-2-3p	Sopen03g025850.1	3.0	-1.0	1	24	1924	1947	UUUUGGAGAAUCCGACACGCACCC	AAACGUGUGUUGGAUUAUCUAAAA	Cleavage
spe-miR5303c-2-3p	Sopen05g003530.1	3.0	-1.0	1	24	3043	3066	UUUUGGAGAAUCCGACACGCACCC	UUCAGUGUGUUGGAUUUUCCAACA	Cleavage
spe-miR5303c-2-3p	Sopen01g049130.1	3.0	-1.0	1	24	1436	1459	UUUUGGAGAAUCCGACACGCACCC	ACCCACUUGUGGGAUUCUUUAAAA	Cleavage
spe-miR5303c-2-3p	Sopen01g023560.1	3.0	-1.0	1	24	997	1020	UUUUGGAGAAUCCGACACGCACCC	AUGAUCGUUUCGGAUGCUCCAGAA	Cleavage
spe-miR5303c-2-3p	Sopen02g011520.1	3.0	-1.0	1	24	1864	1887	UUUUGGAGAAUCCGACACGCACCC	AUGACCGUUUCGGAUGCUCCAGAA	Cleavage
spe-miR5303c-2-3p	Sopen09g024450.1	3.0	-1.0	1	24	1723	1746	UUUUGGAGAAUCCGACACGCACCC	AUGACCGUUUCGGAUGCUCCAGAA	Cleavage
spe-miR5303e-3p	Sopen09g004210.1	3.0	-1.0	1	24	9	32	UUUUGGAGAAUCUGACACGGGUGC	GUACCCGUGUUGGAUCCUCCAGAA	Cleavage
spe-miR5303e-3p	Sopen09g004210.1	3.0	-1.0	1	24	243	266	UUUUGGAGAAUCUGACACGGGUGC	GCACACUUGUCGGAUCCUCCAAAA	Cleavage
spe-miR5303e-3p	Sopen12g003610.1	0.5	-1.0	1	24	582	605	UUUUGGAGAAUCUGACACGGGUGC	CGAUUCGUGUCAGAUUCUCCAGAA	Cleavage
spe-miR5303e-3p	Sopen09g025700.2	1.0	-1.0	1	24	160	183	UUUUGGAGAAUCUGACACGGGUGC	GGGUGCGUGUUGGAUUCUCCAAAA	Cleavage
spe-miR5303e-3p	Sopen00g012160.1	2.0	-1.0	1	24	45	68	UUUUGGAGAAUCUGACACGGGUGC	GCGCCCGCGUCGGGUUCUCCAAAA	Cleavage
spe-miR5303e-3p	Sopen04g001920.1	2.5	-1.0	1	24	244	267	UUUUGGAGAAUCUGACACGGGUGC	GCACCCGUCUCGGAUUCUUCAAAG	Cleavage
spe-miR5303e-3p	Sopen05g033640.1	2.5	-1.0	1	24	4791	4814	UUUUGGAGAAUCUGACACGGGUGC	GCACUCGUGUCAGAUCCUUCAGAA	Cleavage
spe-miR5303e-3p	Sopen11g010700.1	2.5	-1.0	1	24	691	714	UUUUGGAGAAUCUGACACGGGUGC	AAACCCGGUUCAGAUUCUUCAAAA	Cleavage
spe-miR5303e-3p	Sopen08g028160.1	2.5	-1.0	1	24	510	533	UUUUGGAGAAUCUGACACGGGUGC	ACAAUUGUGUCAGAUUCAUCAAAA	Cleavage
spe-miR5303e-3p	Sopen03g027630.1	2.5	-1.0	1	24	1168	1191	UUUUGGAGAAUCUGACACGGGUGC	UCAACCGAGUCAGAUUCUCUGGAA	Cleavage
spe-miR5303e-3p	Sopen10g032130.1	2.5	-1.0	1	24	931	954	UUUUGGAGAAUCUGACACGGGUGC	GAUUUCAUCUCAGAUUCUCCAAGA	Cleavage
spe-miR5303e-3p	Sopen02g024920.1	3.0	-1.0	1	24	16	39	UUUUGGAGAAUCUGACACGGGUGC	CAACCAUUGUUAGAUUCUCCGAAA	Cleavage
spe-miR5303e-3p	Sopen02g024930.1	3.0	-1.0	1	24	16	39	UUUUGGAGAAUCUGACACGGGUGC	CAACCAUUGUUAGAUUCUCCGAAA	Cleavage
spe-miR5303e-3p	Sopen04g003960.1	3.0	-1.0	1	24	968	991	UUUUGGAGAAUCUGACACGGGUGC	AUGAUUGUGUCACAUUCUUCAAAG	Cleavage
spe-miR5303e-3p	Sopen11g028510.1	3.0	-1.0	1	24	56	79	UUUUGGAGAAUCUGACACGGGUGC	AGAGGAGUGUCACAUUCUCUAAAA	Cleavage
spe-miR5303e-3p	Sopen09g023600.1	3.0	-1.0	1	24	118	141	UUUUGGAGAAUCUGACACGGGUGC	UAUGGAGUGUCGGAUUUUUUAAAA	Cleavage
spe-miR5303e-3p	Sopen07g016340.1	3.0	-1.0	1	24	832	855	UUUUGGAGAAUCUGACACGGGUGC	AAAAGUGUGUUGGGUUUUCUAAAA	Cleavage
spe-miR5303f-1-5p	Sopen09g004210.1	2.0	-1.0	1	24	245	268	AUUUUUGGAGAAUCUGACACGGGU	ACACUUGUCGGAUCCUCCAAAAAU	Translation
spe-miR5303f-1-5p	Sopen09g004210.1	3.0	-1.0	1	24	11	34	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUGUUGGAUCCUCCAGAAAU	Translation
spe-miR5303f-1-5p	Sopen09g025700.2	1.5	-1.0	1	24	162	185	AUUUUUGGAGAAUCUGACACGGGU	GUGCGUGUUGGAUUCUCCAAAAGU	Cleavage
spe-miR5303f-1-5p	Sopen08g028160.1	2.0	-1.0	1	24	512	535	AUUUUUGGAGAAUCUGACACGGGU	AAUUGUGUCAGAUUCAUCAAAAAU	Cleavage
spe-miR5303f-1-5p	Sopen04g003960.1	3.0	-1.0	1	24	970	993	AUUUUUGGAGAAUCUGACACGGGU	GAUUGUGUCACAUUCUUCAAAGAG	Cleavage
spe-miR5303f-1-5p	Sopen12g003610.1	0.5	-1.0	1	24	584	607	AUUUUUGGAGAAUCUGACACGGGU	AUUCGUGUCAGAUUCUCCAGAAAU	Cleavage
spe-miR5303f-1-5p	Sopen00g012160.1	2.0	-1.0	1	24	47	70	AUUUUUGGAGAAUCUGACACGGGU	GCCCGCGUCGGGUUCUCCAAAAAU	Cleavage
spe-miR5303f-1-5p	Sopen02g024930.1	2.0	-1.0	1	24	18	41	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCGAAAAC	Cleavage

spe-miR5303f-1-5p	Sopen02g024920.1	2.0	-1.0	1	24	18	41	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCGAAAAC	Cleavage
spe-miR5303f-1-5p	Sopen04g001920.1	2.5	-1.0	1	24	246	269	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUCUCGGAUUCUUCAAAGAU	Cleavage
spe-miR5303f-1-5p	Sopen05g033640.1	2.5	-1.0	1	24	4793	4816	AUUUUUGGAGAAUCUGACACGGGU	ACUCGUGUCAGAUCCUUCAGAAAU	Translation
spe-miR5303f-1-5p	Sopen03g038800.1	2.5	-1.0	1	24	932	955	AUUUUUGGAGAAUCUGACACGGGU	ACUUCUGUUAUAUUCUUCAAAGAU	Cleavage
spe-miR5303f-1-5p	Sopen08g023050.1	2.5	-1.0	1	20	1	20	AUUUUUGGAGAAUCUGACAC	AUGUCAGAUCCUCCAAAAAA	Translation
spe-miR5303f-1-5p	Sopen10g018860.1	2.5	-1.0	1	24	2587	2610	AUUUUUGGAGAAUCUGACACGGGU	CUUUAUGUCAAAUUCUCCAAGGGU	Cleavage
spe-miR5303f-1-5p	Sopen01g001200.1	3.0	-1.0	1	24	1044	1067	AUUUUUGGAGAAUCUGACACGGGU	AUCUGUGUCAGAUAAUCCAAAAAU	Translation
spe-miR5303f-1-5p	Sopen06g029330.1	3.0	-1.0	1	24	1375	1398	AUUUUUGGAGAAUCUGACACGGGU	CCACGUGUUGGAUUUUCUAGAAGU	Cleavage
spe-miR5303f-1-5p	Sopen11g028290.1	3.0	-1.0	1	24	495	518	AUUUUUGGAGAAUCUGACACGGGU	GCUUGUUAUAGAUUCUUCAAAAAU	Cleavage
spe-miR5303f-1-5p	Sopen02g024940.1	3.0	-1.0	1	24	24	47	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCCAAAAC	Cleavage
spe-miR5303f-1-5p	Sopen01g011000.1	3.0	-1.0	1	24	363	386	AUUUUUGGAGAAUCUGACACGGGU	UGGAGUGUCAGAUUUUGUGAAAAU	Cleavage
spe-miR5303f-1-5p	Sopen12g009130.1	3.0	-1.0	1	24	388	411	AUUUUUGGAGAAUCUGACACGGGU	GCUAGUGUUCCAUUCUCCAAGAAU	Cleavage
spe-miR5303f-1-5p	Sopen11g028510.1	3.0	-1.0	1	24	58	81	AUUUUUGGAGAAUCUGACACGGGU	AGGAGUGUCACAUUCUCUAAAAGG	Cleavage
spe-miR5303f-1-5p	Sopen12g002770.1	3.0	-1.0	1	24	1	24	AUUUUUGGAGAAUCUGACACGGGU	AUGUUGUUCAGAUUCUUCAGAAAU	Cleavage
spe-miR5303f-1-5p	Sopen10g032130.1	3.0	-1.0	1	24	933	956	AUUUUUGGAGAAUCUGACACGGGU	UUUCAUCUCAGAUUCUCCAAGAUU	Cleavage
spe-miR5303f-1-5p	Sopen08g027850.1	3.0	-1.0	1	24	56	79	AUUUUUGGAGAAUCUGACACGGGU	AAUCUUGUGAGAUUUUUCGAGAAU	Cleavage
spe-miR5303f-1-5p	Sopen08g022350.2	3.0	-1.0	1	24	386	409	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
spe-miR5303f-1-5p	Sopen08g022350.1	3.0	-1.0	1	24	389	412	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
spe-miR5303f-1-5p	Sopen11g003650.1	3.0	-1.0	1	24	1600	1622	AUUUUUGGAGAAUCUGACACGGGU	CCUCUUGUU-GAUUCUUCAAAAAU	Cleavage
spe-miR5303f-1-5p	Sopen01g006020.1	3.0	-1.0	1	24	243	266	AUUUUUGGAGAAUCUGACACGGGU	AUAUUGGUCGGAAUCUCCAAAAAU	Cleavage
spe-miR5303f-1-5p	Sopen11g016830.1	3.0	-1.0	1	24	267	290	AUUUUUGGAGAAUCUGACACGGGU	CAUAAUGUCAGAUUUUCUCGAAAU	Cleavage
spe-miR5303f-1-5p	Sopen07g002820.1	3.0	-1.0	1	24	924	947	AUUUUUGGAGAAUCUGACACGGGU	UUUUAUGUCACAUUUUCCAAAAGG	Cleavage
spe-miR5303f-2-3p	Sopen09g004210.1	2.0	-1.0	1	24	245	268	AUUUUUGGAGAAUCUGACACGGGU	ACACUUGUCGGAUCCUCCAAAAAU	Translation
spe-miR5303f-2-3p	Sopen09g004210.1	3.0	-1.0	1	24	11	34	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUGUUGGAUCCUCCAGAAAU	Translation
spe-miR5303f-2-3p	Sopen09g025700.2	1.5	-1.0	1	24	162	185	AUUUUUGGAGAAUCUGACACGGGU	GUGCGUGUUGGAUUCUCCAAAAGU	Cleavage
spe-miR5303f-2-3p	Sopen08g028160.1	2.0	-1.0	1	24	512	535	AUUUUUGGAGAAUCUGACACGGGU	AAUUGUGUCAGAUUCAUCAAAAAU	Cleavage
spe-miR5303f-2-3p	Sopen04g003960.1	3.0	-1.0	1	24	970	993	AUUUUUGGAGAAUCUGACACGGGU	GAUUGUGUCACAUUCUUCAAAGAG	Cleavage
spe-miR5303f-2-3p	Sopen12g003610.1	0.5	-1.0	1	24	584	607	AUUUUUGGAGAAUCUGACACGGGU	AUUCGUGUCAGAUUCUCCAGAAAU	Cleavage
spe-miR5303f-2-3p	Sopen00g012160.1	2.0	-1.0	1	24	47	70	AUUUUUGGAGAAUCUGACACGGGU	GCCCGCGUCGGGUUCUCCAAAAAU	Cleavage
spe-miR5303f-2-3p	Sopen02g024930.1	2.0	-1.0	1	24	18	41	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCGAAAAC	Cleavage
spe-miR5303f-2-3p	Sopen02g024920.1	2.0	-1.0	1	24	18	41	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCGAAAAC	Cleavage
spe-miR5303f-2-3p	Sopen04g001920.1	2.5	-1.0	1	24	246	269	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUCUCGGAUUCUUCAAAGAU	Cleavage
spe-miR5303f-2-3p	Sopen05g033640.1	2.5	-1.0	1	24	4793	4816	AUUUUUGGAGAAUCUGACACGGGU	ACUCGUGUCAGAUCCUUCAGAAAU	Translation
spe-miR5303f-2-3p	Sopen03g038800.1	2.5	-1.0	1	24	932	955	AUUUUUGGAGAAUCUGACACGGGU	ACUUCUGUUAUAUUCUUCAAAGAU	Cleavage
spe-miR5303f-2-3p	Sopen08g023050.1	2.5	-1.0	1	20	1	20	AUUUUUGGAGAAUCUGACAC	AUGUCAGAUCCUCCAAAAAA	Translation
spe-miR5303f-2-3p	Sopen10g018860.1	2.5	-1.0	1	24	2587	2610	AUUUUUGGAGAAUCUGACACGGGU	CUUUAUGUCAAAUUCUCCAAGGGU	Cleavage
spe-miR5303f-2-3p	Sopen01g001200.1	3.0	-1.0	1	24	1044	1067	AUUUUUGGAGAAUCUGACACGGGU	AUCUGUGUCAGAUAAUCCAAAAAU	Translation
spe-miR5303f-2-3p	Sopen06g029330.1	3.0	-1.0	1	24	1375	1398	AUUUUUGGAGAAUCUGACACGGGU	CCACGUGUUGGAUUUUCUAGAAGU	Cleavage
spe-miR5303f-2-3p	Sopen11g028290.1	3.0	-1.0	1	24	495	518	AUUUUUGGAGAAUCUGACACGGGU	GCUUGUUAUAGAUUCUUCAAAAAU	Cleavage
spe-miR5303f-2-3p	Sopen02g024940.1	3.0	-1.0	1	24	24	47	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCCAAAAC	Cleavage
spe-miR5303f-2-3p	Sopen01g011000.1	3.0	-1.0	1	24	363	386	AUUUUUGGAGAAUCUGACACGGGU	UGGAGUGUCAGAUUUUGUGAAAAU	Cleavage
spe-miR5303f-2-3p	Sopen12g009130.1	3.0	-1.0	1	24	388	411	AUUUUUGGAGAAUCUGACACGGGU	GCUAGUGUUCCAUUCUCCAAGAAU	Cleavage
spe-miR5303f-2-3p	Sopen11g028510.1	3.0	-1.0	1	24	58	81	AUUUUUGGAGAAUCUGACACGGGU	AGGAGUGUCACAUUCUCUAAAAGG	Cleavage
spe-miR5303f-2-3p	Sopen12g002770.1	3.0	-1.0	1	24	1	24	AUUUUUGGAGAAUCUGACACGGGU	AUGUUGUUCAGAUUCUUCAGAAAU	Cleavage
spe-miR5303f-2-3p	Sopen10g032130.1	3.0	-1.0	1	24	933	956	AUUUUUGGAGAAUCUGACACGGGU	UUUCAUCUCAGAUUCUCCAAGAUU	Cleavage
spe-miR5303f-2-3p	Sopen08g027850.1	3.0	-1.0	1	24	56	79	AUUUUUGGAGAAUCUGACACGGGU	AAUCUUGUGAGAUUUUUCGAGAAU	Cleavage
spe-miR5303f-2-3p	Sopen08g022350.2	3.0	-1.0	1	24	386	409	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
spe-miR5303f-2-3p	Sopen08g022350.1	3.0	-1.0	1	24	389	412	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
spe-miR5303f-2-3p	Sopen11g003650.1	3.0	-1.0	1	24	1600	1622	AUUUUUGGAGAAUCUGACACGGGU	CCUCUUGUU-GAUUCUUCAAAAAU	Cleavage
spe-miR5303f-2-3p	Sopen01g006020.1	3.0	-1.0	1	24	243	266	AUUUUUGGAGAAUCUGACACGGGU	AUAUUGGUCGGAAUCUCCAAAAAU	Cleavage

spe-miR5303f-2-3p	Sopen11g016830.1	3.0	-1.0	1	24	267	290	AUUUUUGGAGAAUCUGACACGGGU	CAUAAUGUCAGAUUUUCUCGAAAU	Cleavage
spe-miR5303f-2-3p	Sopen07g002820.1	3.0	-1.0	1	24	924	947	AUUUUUGGAGAAUCUGACACGGGU	UUUUAUGUCACAUUUUCCAAAAGG	Cleavage
spe-miR5303f-3-3p	Sopen09g004210.1	2.0	-1.0	1	24	245	268	AUUUUUGGAGAAUCUGACACGGGU	ACACUUGUCGGAUCCUCCAAAAAU	Translation
spe-miR5303f-3-3p	Sopen09g004210.1	3.0	-1.0	1	24	11	34	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUGUUGGAUCCUCCAGAAAU	Translation
spe-miR5303f-3-3p	Sopen09g025700.2	1.5	-1.0	1	24	162	185	AUUUUUGGAGAAUCUGACACGGGU	GUGCGUGUUGGAUUCUCCAAAAGU	Cleavage
spe-miR5303f-3-3p	Sopen08g028160.1	2.0	-1.0	1	24	512	535	AUUUUUGGAGAAUCUGACACGGGU	AAUUGUGUCAGAUUCAUCAAAAAU	Cleavage
spe-miR5303f-3-3p	Sopen04g003960.1	3.0	-1.0	1	24	970	993	AUUUUUGGAGAAUCUGACACGGGU	GAUUGUGUCACAUUCUUCAAAGAG	Cleavage
spe-miR5303f-3-3p	Sopen12g003610.1	0.5	-1.0	1	24	584	607	AUUUUUGGAGAAUCUGACACGGGU	AUUCGUGUCAGAUUCUCCAGAAAU	Cleavage
spe-miR5303f-3-3p	Sopen00g012160.1	2.0	-1.0	1	24	47	70	AUUUUUGGAGAAUCUGACACGGGU	GCCCGCGUCGGGUUCUCCAAAAAU	Cleavage
spe-miR5303f-3-3p	Sopen02g024930.1	2.0	-1.0	1	24	18	41	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCGAAAAC	Cleavage
spe-miR5303f-3-3p	Sopen02g024920.1	2.0	-1.0	1	24	18	41	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCGAAAAC	Cleavage
spe-miR5303f-3-3p	Sopen04g001920.1	2.5	-1.0	1	24	246	269	AUUUUUGGAGAAUCUGACACGGGU	ACCCGUCUCGGAUUCUUCAAAGAU	Cleavage
spe-miR5303f-3-3p	Sopen05g033640.1	2.5	-1.0	1	24	4793	4816	AUUUUUGGAGAAUCUGACACGGGU	ACUCGUGUCAGAUCCUUCAGAAAU	Translation
spe-miR5303f-3-3p	Sopen03g038800.1	2.5	-1.0	1	24	932	955	AUUUUUGGAGAAUCUGACACGGGU	ACUUCUGUUAUAUUCUUCAAAGAU	Cleavage
spe-miR5303f-3-3p	Sopen08g023050.1	2.5	-1.0	1	20	1	20	AUUUUUGGAGAAUCUGACAC	AUGUCAGAUCCUCCAAAAAA	Translation
spe-miR5303f-3-3p	Sopen10g018860.1	2.5	-1.0	1	24	2587	2610	AUUUUUGGAGAAUCUGACACGGGU	CUUUAUGUCAAAUUCUCCAAGGGU	Cleavage
spe-miR5303f-3-3p	Sopen01g001200.1	3.0	-1.0	1	24	1044	1067	AUUUUUGGAGAAUCUGACACGGGU	AUCUGUGUCAGAUAAUCCAAAAAU	Translation
spe-miR5303f-3-3p	Sopen06g029330.1	3.0	-1.0	1	24	1375	1398	AUUUUUGGAGAAUCUGACACGGGU	CCACGUGUUGGAUUUUCUAGAAGU	Cleavage
spe-miR5303f-3-3p	Sopen11g028290.1	3.0	-1.0	1	24	495	518	AUUUUUGGAGAAUCUGACACGGGU	GCUUGUUAUAGAUUCUUCAAAAAU	Cleavage
spe-miR5303f-3-3p	Sopen02g024940.1	3.0	-1.0	1	24	24	47	AUUUUUGGAGAAUCUGACACGGGU	ACCAUUGUUAGAUUCUCCCAAAAC	Cleavage
spe-miR5303f-3-3p	Sopen01g011000.1	3.0	-1.0	1	24	363	386	AUUUUUGGAGAAUCUGACACGGGU	UGGAGUGUCAGAUUUUGUGAAAAU	Cleavage
spe-miR5303f-3-3p	Sopen12g009130.1	3.0	-1.0	1	24	388	411	AUUUUUGGAGAAUCUGACACGGGU	GCUAGUGUUCCAUUCUCCAAGAAU	Cleavage
spe-miR5303f-3-3p	Sopen11g028510.1	3.0	-1.0	1	24	58	81	AUUUUUGGAGAAUCUGACACGGGU	AGGAGUGUCACAUUCUCUAAAAGG	Cleavage
spe-miR5303f-3-3p	Sopen12g002770.1	3.0	-1.0	1	24	1	24	AUUUUUGGAGAAUCUGACACGGGU	AUGUUGUUCAGAUUCUUCAGAAAU	Cleavage
spe-miR5303f-3-3p	Sopen10g032130.1	3.0	-1.0	1	24	933	956	AUUUUUGGAGAAUCUGACACGGGU	UUUCAUCUCAGAUUCUCCAAGAUU	Cleavage
spe-miR5303f-3-3p	Sopen08g027850.1	3.0	-1.0	1	24	56	79	AUUUUUGGAGAAUCUGACACGGGU	AAUCUUGUGAGAUUUUUCGAGAAU	Cleavage
spe-miR5303f-3-3p	Sopen08g022350.2	3.0	-1.0	1	24	386	409	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
spe-miR5303f-3-3p	Sopen08g022350.1	3.0	-1.0	1	24	389	412	AUUUUUGGAGAAUCUGACACGGGU	AGGUGGGUCAAAUUUUCCAGAAAU	Cleavage
spe-miR5303f-3-3p	Sopen11g003650.1	3.0	-1.0	1	24	1600	1622	AUUUUUGGAGAAUCUGACACGGGU	CCUCUUGUU-GAUUCUUCAAAAAU	Cleavage
spe-miR5303f-3-3p	Sopen01g006020.1	3.0	-1.0	1	24	243	266	AUUUUUGGAGAAUCUGACACGGGU	AUAUUGGUCGGAAUCUCCAAAAAU	Cleavage
spe-miR5303f-3-3p	Sopen11g016830.1	3.0	-1.0	1	24	267	290	AUUUUUGGAGAAUCUGACACGGGU	CAUAAUGUCAGAUUUUCUCGAAAU	Cleavage
spe-miR5303f-3-3p	Sopen07g002820.1	3.0	-1.0	1	24	924	947	AUUUUUGGAGAAUCUGACACGGGU	UUUUAUGUCACAUUUUCCAAAAGG	Cleavage
spe-miR5303h-5p	Sopen05g004670.1	2.5	-1.0	1	24	594	617	AACAUUUUUGAAGAGUCUGAGCAA	AGAUUCAAACUCUUCAGAAAUGUC	Cleavage
spe-miR5303h-5p	Sopen09g004210.1	2.5	-1.0	1	24	216	239	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCGGACUCUCCAGAAAUGUU	Translation
spe-miR5303h-5p	Sopen09g004210.1	2.5	-1.0	1	24	84	107	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCGGACUCUCCAGAAAUGUU	Translation
spe-miR5303h-5p	Sopen08g028160.1	1.5	-1.0	1	24	483	506	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGACUCUUCAAAAAUAUU	Cleavage
spe-miR5303h-5p	Sopen10g029660.1	3.0	-1.0	1	24	592	615	AACAUUUUUGAAGAGUCUGAGCAA	CAACAAGGGUUCUUCAAAGAUGUU	Cleavage
spe-miR5303h-5p	Sopen10g029660.1	3.0	-1.0	1	24	1093	1116	AACAUUUUUGAAGAGUCUGAGCAA	CAACAAGGGUUCUUCAAAGAUGUU	Cleavage
spe-miR5303h-5p	Sopen12g002770.1	1.0	-1.0	1	24	4	27	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCAGAUUCUUCAGAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen10g001690.1	1.0	-1.0	1	24	52	75	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGAGUCUUCAAAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen09g025700.2	1.5	-1.0	1	24	133	156	AACAUUUUUGAAGAGUCUGAGCAA	UUGUUCGGACUCUUCAAAAAUGUC	Cleavage
spe-miR5303h-5p	Sopen00g013020.1	2.0	-1.0	1	24	485	508	AACAUUUUUGAAGAGUCUGAGCAA	CUAUUAAGGCUCUUCAGAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen03g005640.1	2.5	-1.0	1	24	766	789	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUGAGACGUUUCAAAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen07g003140.1	2.5	-1.0	1	24	126	149	AACAUUUUUGAAGAGUCUGAGCAA	UUACUCGGAUUUUUCAAAAAUGUC	Cleavage
spe-miR5303h-5p	Sopen06g027200.1	2.5	-1.0	1	24	1315	1338	AACAUUUUUGAAGAGUCUGAGCAA	CUGGCUGGAUUUUUCAAAGAUGUU	Cleavage
spe-miR5303h-5p	Sopen00g010630.1	2.5	-1.0	1	24	1166	1189	AACAUUUUUGAAGAGUCUGAGCAA	CUAUUAAGGCACUUCAAAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen09g017330.1	2.5	-1.0	1	24	1385	1408	AACAUUUUUGAAGAGUCUGAGCAA	CCAUCAAGGCUCUUCAAGGAUGUU	Cleavage
spe-miR5303h-5p	Sopen07g017340.1	2.5	-1.0	1	24	3128	3151	AACAUUUUUGAAGAGUCUGAGCAA	CCAUCAAGGCUCUUCAAGGAUGUU	Cleavage
spe-miR5303h-5p	Sopen04g034840.2	2.5	-1.0	1	24	137	160	AACAUUUUUGAAGAGUCUGAGCAA	CCAUUCAUUCUCUUCAGAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen04g034840.1	2.5	-1.0	1	24	137	160	AACAUUUUUGAAGAGUCUGAGCAA	CCAUUCAUUCUCUUCAGAAAUGUU	Cleavage

spe-miR5303h-5p	Sopen09g017320.1	2.5	-1.0	1	24	866	889	AACAUUUUUGAAGAGUCUGAGCAA	CCAUCAAGGCUCUUCAAGGAUGUU	Cleavage
spe-miR5303h-5p	Sopen03g016020.1	2.5	-1.0	1	24	812	835	AACAUUUUUGAAGAGUCUGAGCAA	CCAUUAAGGCACUUCAAAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen12g026810.1	2.5	-1.0	1	24	368	391	AACAUUUUUGAAGAGUCUGAGCAA	CCAUCAAGGCUCUUCAAAGGUGUU	Cleavage
spe-miR5303h-5p	Sopen07g012560.1	3.0	-1.0	1	24	62	85	AACAUUUUUGAAGAGUCUGAGCAA	UUGCUCAGACUCUUCAAAAAAAUU	Cleavage
spe-miR5303h-5p	Sopen10g035920.1	3.0	-1.0	1	24	774	797	AACAUUUUUGAAGAGUCUGAGCAA	UGGUUCAGAUUUUUUGGAGAUGUU	Cleavage
spe-miR5303h-5p	Sopen04g018890.1	3.0	-1.0	1	24	1406	1429	AACAUUUUUGAAGAGUCUGAGCAA	AUGAUCCGAUUCUUCAAAAGUGUG	Cleavage
spe-miR5303h-5p	Sopen00g010500.1	3.0	-1.0	1	24	1262	1285	AACAUUUUUGAAGAGUCUGAGCAA	CUAUUAAGGCUCUUCAUAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen00g009380.1	3.0	-1.0	1	24	1337	1360	AACAUUUUUGAAGAGUCUGAGCAA	CUAUUAAGGCUCUUCAUAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen00g008350.1	3.0	-1.0	1	24	2882	2905	AACAUUUUUGAAGAGUCUGAGCAA	CCAUUAAGGCUCUUCAAAAUUGUU	Cleavage
spe-miR5303h-5p	Sopen11g029390.1	3.0	-1.0	1	24	903	926	AACAUUUUUGAAGAGUCUGAGCAA	UAAUUCAGAAUCUUCAAAGAAGUU	Cleavage
spe-miR5303h-5p	Sopen12g019260.1	3.0	-1.0	1	24	595	618	AACAUUUUUGAAGAGUCUGAGCAA	CAGCAUAAACUUUUCAAGAGUGUU	Cleavage
spe-miR5303h-5p	Sopen09g027430.3	3.0	-1.0	1	24	1904	1927	AACAUUUUUGAAGAGUCUGAGCAA	AGGAAAUGACUCUUCAAAAAUGUC	Cleavage
spe-miR5303h-5p	Sopen07g020960.1	3.0	-1.0	1	24	1319	1342	AACAUUUUUGAAGAGUCUGAGCAA	CAGCCCAGAGUCUUCAGAAAUCUU	Cleavage
spe-miR5303h-5p	Sopen01g041280.1	3.0	-1.0	1	24	2389	2412	AACAUUUUUGAAGAGUCUGAGCAA	CCCAUCAGAAUUUUCAAAAAUCUU	Cleavage
spe-miR5303h-5p	Sopen02g012370.1	3.0	-1.0	1	24	1419	1442	AACAUUUUUGAAGAGUCUGAGCAA	AUGGAGAGAUUCGUCAAAAAUGUU	Cleavage
spe-miR5303h-5p	Sopen10g029640.1	3.0	-1.0	1	24	103	126	AACAUUUUUGAAGAGUCUGAGCAA	CAACAAGGGUUCUUCAAAGAUGUU	Cleavage
spe-miR5303h-5p	Sopen02g021140.1	3.0	-1.0	1	24	880	903	AACAUUUUUGAAGAGUCUGAGCAA	CCAACAGGACUUUUCAAAGGUGUU	Cleavage
spe-miR5303h-5p	Sopen02g021140.2	3.0	-1.0	1	24	763	786	AACAUUUUUGAAGAGUCUGAGCAA	CCAACAGGACUUUUCAAAGGUGUU	Cleavage
spe-miR530-5p	Sopen05g026950.1	2.5	-1.0	1	21	600	620	UCUGCAUUUGCACCUGCACCU	AUGUGCAGGUCCAAGUGCAGG	Translation
spe-miR530-5p	Sopen04g021240.1	2.5	-1.0	1	21	342	362	UCUGCAUUUGCACCUGCACCU	AUGUGCAGGUCCAAGUGCAGG	Translation
spe-miR530-5p	Sopen10g024270.1	2.5	-1.0	1	21	852	872	UCUGCAUUUGCACCUGCACCU	AUGUGCAGGUCCAAGUGCAGG	Translation
spe-miR530-5p	Sopen04g021240.1	3.0	-1.0	1	21	522	542	UCUGCAUUUGCACCUGCACCU	AUGUGCAGGUCCAAGUGCAGC	Translation
spe-miR530-5p	Sopen09g031470.1	2.5	-1.0	1	21	283	303	UCUGCAUUUGCACCUGCACCU	GCGUGGAGGUGCAAGUGUGGA	Cleavage
spe-miR530-5p	Sopen03g027930.1	2.5	-1.0	1	21	520	540	UCUGCAUUUGCACCUGCACCU	UGGUGCGGGUGCGGGUGCAGG	Cleavage
spe-miR530-5p	Sopen04g004580.1	2.5	-1.0	1	21	6	26	UCUGCAUUUGCACCUGCACCU	AUCUGCAGGAGCAAAUGCAGA	Cleavage
spe-miR530-5p	Sopen07g027620.1	2.5	-1.0	1	21	1080	1100	UCUGCAUUUGCACCUGCACCU	UAGUGCAGGGGCAAGUGUAGA	Cleavage
spe-miR530-5p	Sopen09g032310.1	3.0	-1.0	1	21	93	113	UCUGCAUUUGCACCUGCACCU	AGGUGCAGGUGUAAAUGCAAG	Cleavage
spe-miR530-5p	Sopen07g027220.1	3.0	-1.0	1	21	762	782	UCUGCAUUUGCACCUGCACCU	UGGUGGAGGUGAAGAUGCAGA	Translation
spe-miR530-5p	Sopen05g002150.1	3.0	-1.0	1	21	852	872	UCUGCAUUUGCACCUGCACCU	UGGUGAAGAUGCAGAUGCAGA	Cleavage
spe-miR530-5p	Sopen08g022800.1	3.0	-1.0	1	21	3585	3605	UCUGCAUUUGCACCUGCACCU	AGGCAAAGGUGCAAAUGCAGA	Cleavage
spe-miR530-5p	Sopen04g007340.1	3.0	-1.0	1	21	117	137	UCUGCAUUUGCACCUGCACCU	AAGUAUAGGUCCAAAUGCAGA	Translation
spe-miR530-5p	Sopen04g018460.1	3.0	-1.0	1	21	270	290	UCUGCAUUUGCACCUGCACCU	GAAUGGGGGUGUAAAUGCAGA	Cleavage
spe-miR530-5p	Sopen11g029370.1	3.0	-1.0	1	21	3077	3097	UCUGCAUUUGCACCUGCACCU	AAGUGAAGGUGCGAAUACAGA	Cleavage
spe-miR530-5p	Sopen11g029370.2	3.0	-1.0	1	21	3080	3100	UCUGCAUUUGCACCUGCACCU	AAGUGAAGGUGCGAAUACAGA	Cleavage
spe-miR530-5p	Sopen11g029370.3	3.0	-1.0	1	21	3080	3100	UCUGCAUUUGCACCUGCACCU	AAGUGAAGGUGCGAAUACAGA	Cleavage
spe-miR530-5p	Sopen11g029370.4	3.0	-1.0	1	21	3086	3106	UCUGCAUUUGCACCUGCACCU	AAGUGAAGGUGCGAAUACAGA	Cleavage
spe-miR530-5p	Sopen01g044060.1	3.0	-1.0	1	21	3483	3503	UCUGCAUUUGCACCUGCACCU	CUGUGAAGAUGCAAGUGCAGA	Cleavage
spe-miR5368-5p	Sopen12g026630.1	2.5	-1.0	1	19	436	454	GGACAGUCUCAGGUAGACA	UAUGUACCUGAGACUGUCU	Cleavage
spe-miR5368-5p	Sopen01g034940.1	3.0	-1.0	1	19	3203	3221	GGACAGUCUCAGGUAGACA	UGUCUAUAUGGGGCUGUCC	Cleavage
spe-miR6024-3p	Sopen09g026580.1	3.0	-1.0	1	22	121	142	UUUUAGCAAGAGUUGUUUUCCC	AGGAGAACAACUCUUGAUGGAA	Cleavage
spe-miR6024-3p	Sopen10g004090.1	1.0	-1.0	1	22	511	532	UUUUAGCAAGAGUUGUUUUCCC	GGCAAAACGACUCUUGCUAGAA	Cleavage
spe-miR6024-3p	Sopen05g003910.1	1.0	-1.0	1	22	541	562	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCUAGAA	Cleavage
spe-miR6024-3p	Sopen11g002560.1	1.0	-1.0	1	22	544	565	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCUAGAA	Cleavage
spe-miR6024-3p	Sopen10g022740.1	1.0	-1.0	1	22	544	565	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCUAGAA	Cleavage
spe-miR6024-3p	Sopen07g031430.1	1.5	-1.0	1	22	1516	1537	UUUUAGCAAGAGUUGUUUUCCC	CGGAAAAUGACUUUUGCUAAAA	Cleavage
spe-miR6024-3p	Sopen08g008520.1	1.5	-1.0	1	22	619	640	UUUUAGCAAGAGUUGUUUUCCC	AUGAAAACAACUCUUGUUGAGA	Cleavage
spe-miR6024-3p	Sopen06g021930.1	1.5	-1.0	1	22	610	631	UUUUAGCAAGAGUUGUUUUCCC	GGAAAAACCACUCUUGCUAGAA	Cleavage
spe-miR6024-3p	Sopen11g027730.1	1.5	-1.0	1	22	298	319	UUUUAGCAAGAGUUGUUUUCCC	GGUAAAACCACUCUUGCUAAGA	Cleavage
spe-miR6024-3p	Sopen09g010980.1	2.0	-1.0	1	22	445	466	UUUUAGCAAGAGUUGUUUUCCC	GGGAAAACAACUCUUGCCAAGA	Cleavage
spe-miR6024-3p	Sopen05g001340.1	2.0	-1.0	1	22	1663	1684	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCUAACA	Cleavage

spe-miR6024-3p	Sopen01g034260.1	2.0	-1.0	1	22	490	511	UUUUAGCAAGAGUUGUUUUCCC	GGCAAAACGACUCUCGCUAAAA	Cleavage
spe-miR6024-3p	Sopen09g035210.1	2.0	-1.0	1	22	448	469	UUUUAGCAAGAGUUGUUUUCCC	GGAAAAACAACUCUUGCCAAGA	Cleavage
spe-miR6024-3p	Sopen12g001930.1	2.0	-1.0	1	22	556	577	UUUUAGCAAGAGUUGUUUUCCC	GGUAAAACAACUCUUGCGAAGA	Cleavage
spe-miR6024-3p	Sopen09g016280.1	2.0	-1.0	1	22	496	517	UUUUAGCAAGAGUUGUUUUCCC	GGUAAAACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen11g020860.1	2.0	-1.0	1	22	541	562	UUUUAGCAAGAGUUGUUUUCCC	GGUAAAACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen11g010240.1	2.0	-1.0	1	22	535	556	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCCAAAA	Cleavage
spe-miR6024-3p	Sopen03g002750.1	2.5	-1.0	1	22	2905	2926	UUUUAGCAAGAGUUGUUUUCCC	GGGAAGACAACUCUUGCUCAGA	Cleavage
spe-miR6024-3p	Sopen03g002750.2	2.5	-1.0	1	22	2866	2887	UUUUAGCAAGAGUUGUUUUCCC	GGGAAGACAACUCUUGCUCAGA	Cleavage
spe-miR6024-3p	Sopen07g028980.1	2.5	-1.0	1	22	394	415	UUUUAGCAAGAGUUGUUUUCCC	GGGAAGACAACUCUUGCAAAAG	Cleavage
spe-miR6024-3p	Sopen05g005560.1	2.5	-1.0	1	22	181	202	UUUUAGCAAGAGUUGUUUUCCC	GGGAAAACAGCUCUGGCUAGAA	Cleavage
spe-miR6024-3p	Sopen07g018200.1	2.5	-1.0	1	22	1704	1725	UUUUAGCAAGAGUUGUUUUCCC	GGGCGAACAACUCUUGCUGAAG	Cleavage
spe-miR6024-3p	Sopen03g039880.1	2.5	-1.0	1	22	1933	1954	UUUUAGCAAGAGUUGUUUUCCC	UGGGAAGCAACUCUUGCUGGGA	Cleavage
spe-miR6024-3p	Sopen05g002560.1	2.5	-1.0	1	22	664	685	UUUUAGCAAGAGUUGUUUUCCC	GGUAAAACAACUCUUUCUAAGG	Cleavage
spe-miR6024-3p	Sopen11g029660.1	2.5	-1.0	1	22	613	634	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen11g027060.1	2.5	-1.0	1	22	613	634	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen11g029090.1	2.5	-1.0	1	22	637	658	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen01g028960.1	2.5	-1.0	1	22	853	874	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUGAAA	Translation
spe-miR6024-3p	Sopen11g029100.2	2.5	-1.0	1	22	13	34	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen11g002570.1	2.5	-1.0	1	22	739	760	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCCAGAA	Cleavage
spe-miR6024-3p	Sopen10g004080.1	2.5	-1.0	1	22	565	586	UUUUAGCAAGAGUUGUUUUCCC	GGAAAGACAACUUUAGCUAAAA	Cleavage
spe-miR6024-3p	Sopen11g002420.1	2.5	-1.0	1	22	526	547	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCCAGAA	Cleavage
spe-miR6024-3p	Sopen11g002430.1	2.5	-1.0	1	22	541	562	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUCUUGCCAGAA	Cleavage
spe-miR6024-3p	Sopen04g007280.1	2.5	-1.0	1	22	478	499	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACUUUUGCCAAAA	Cleavage
spe-miR6024-3p	Sopen11g028680.1	2.5	-1.0	1	22	553	574	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen05g005550.1	2.5	-1.0	1	22	151	172	UUUUAGCAAGAGUUGUUUUCCC	GGCAAAACAACUUUGGCUAGAA	Cleavage
spe-miR6024-3p	Sopen11g024570.1	2.5	-1.0	1	22	442	463	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen08g003590.1	2.5	-1.0	1	22	637	658	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen11g025550.1	2.5	-1.0	1	22	610	631	UUUUAGCAAGAGUUGUUUUCCC	GGUAAGACAACACUUGCUAAAG	Translation
spe-miR6024-3p	Sopen06g008910.1	3.0	-1.0	1	22	3663	3684	UUUUAGCAAGAGUUGUUUUCCC	GGGAGAACAAGUCUUGCUGAAG	Cleavage
spe-miR6024-3p	Sopen04g002380.1	3.0	-1.0	1	22	688	709	UUUUAGCAAGAGUUGUUUUCCC	GGGAAGACAACUCUAGCUAGAG	Cleavage
spe-miR6024-3p	Sopen05g005580.1	3.0	-1.0	1	22	154	175	UUUUAGCAAGAGUUGUUUUCCC	GGGAAAACAGCUCUGGCUGGAA	Cleavage
spe-miR6024-3p	Sopen01g047200.1	3.0	-1.0	1	22	73	94	UUUUAGCAAGAGUUGUUUUCCC	GGGAAGACAACUUUUGUCAAAA	Cleavage
spe-miR6024-3p	Sopen01g047220.1	3.0	-1.0	1	22	73	94	UUUUAGCAAGAGUUGUUUUCCC	GGGAAGACAACUUUUGUCAAAA	Cleavage
spe-miR6024-3p	Sopen12g025780.1	3.0	-1.0	1	22	1764	1785	UUUUAGCAAGAGUUGUUUUCCC	GGGUGAACAAUUCUUGCUGAAG	Cleavage
spe-miR6024-3p	Sopen10g021980.1	3.0	-1.0	1	22	1950	1971	UUUUAGCAAGAGUUGUUUUCCC	GGGUGAACAAUUCUUGCUGAAG	Cleavage
spe-miR6024-5p	Sopen08g004960.1	2.5	-1.0	1	22	744	765	AGAAACAACACUUGCUAAAGGA	UACUUCACUAAGUGUUGUUUCU	Cleavage
spe-miR6024-5p	Sopen11g025280.1	2.5	-1.0	1	22	660	681	AGAAACAACACUUGCUAAAGGA	GGUUGUAGCAAGUGUUGUUGCU	Cleavage
spe-miR6024-5p	Sopen03g016180.1	3.0	-1.0	1	22	9471	9492	AGAAACAACACUUGCUAAAGGA	AAGUAUGGCAAAUGUUGUUUCU	Translation
spe-miR6024-5p	Sopen09g017750.1	3.0	-1.0	1	22	934	955	AGAAACAACACUUGCUAAAGGA	AAGUAUAGCAAGUGUGGUUUUU	Cleavage
spe-miR6027-3p	Sopen11g016230.1	2.5	-1.0	1	22	718	739	UGAAUCCUUCGGCUAUCCAUAA	AAUAGGAUAGUUGAAGGAUUUA	Cleavage
spe-miR6027-3p	Sopen04g004250.1	3.0	-1.0	1	22	2920	2941	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCUGAGGGUUUCA	Cleavage
spe-miR6027-3p	Sopen11g027730.1	2.0	-1.0	1	22	1036	1057	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUUGCUGAAGGAUUUA	Cleavage
spe-miR6027-3p	Sopen04g003320.1	2.0	-1.0	1	22	1828	1849	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAAGGGUUUG	Cleavage
spe-miR6027-3p	Sopen04g003290.1	2.0	-1.0	1	22	2413	2434	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAAGGGUUUG	Cleavage
spe-miR6027-3p	Sopen09g036080.1	2.0	-1.0	1	22	2419	2440	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUUGCUGAAGGAUUCG	Cleavage
spe-miR6027-3p	Sopen08g004640.1	2.0	-1.0	1	22	892	913	UGAAUCCUUCGGCUAUCCAUAA	UGGUGGAUAGCCGAGGGGUUUG	Cleavage
spe-miR6027-3p	Sopen04g004290.1	2.5	-1.0	1	22	657	678	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCUGAAGGGUUUG	Cleavage
spe-miR6027-3p	Sopen05g005440.1	2.5	-1.0	1	22	1102	1123	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUCGCGGAAGGAUUCA	Translation
spe-miR6027-3p	Sopen04g004270.1	2.5	-1.0	1	22	1312	1333	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAGGGUUUCA	Cleavage
spe-miR6027-3p	Sopen05g008040.1	2.5	-1.0	1	22	4084	4105	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGGUAGCUGAAGGGUUUG	Cleavage

spe-miR6027-3p	Sopen10g017600.1	2.5	-1.0	1	22	1285	1306	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUUGCGGAAGGAUUCA	Translation
spe-miR6027-3p	Sopen02g006820.1	3.0	-1.0	1	22	823	844	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUGGCUGAGGGGUUCC	Cleavage
spe-miR6027-3p	Sopen02g009360.1	3.0	-1.0	1	22	1285	1306	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUGGCUGAGGGGUUCC	Cleavage
spe-miR6027-3p	Sopen07g018790.1	3.0	-1.0	1	22	283	304	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCCGAGGGUUUCG	Cleavage
spe-miR6027-3p	Sopen04g004370.1	3.0	-1.0	1	22	277	298	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUGGCUGAGGGUUUCA	Cleavage
spe-miR6027-3p	Sopen04g002150.1	3.0	-1.0	1	22	1189	1210	UGAAUCCUUCGGCUAUCCAUAA	UUAUGGAUCGCUGAAGGUUUCA	Cleavage
spe-miR6027-3p	Sopen05g007710.1	3.0	-1.0	1	22	3226	3247	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUAGCGGAAGGCUUCA	Translation
spe-miR6027-3p	Sopen01g034940.1	3.0	-1.0	1	22	1327	1348	UGAAUCCUUCGGCUAUCCAUAA	CUAUGGAUGGCAGAAGGAUUUG	Translation
spe-miR6027-3p	Sopen03g001670.1	3.0	-1.0	1	22	1273	1294	UGAAUCCUUCGGCUAUCCAUAA	UUGUGGAUCGCGGAAGGGUUCA	Translation
spe-miR6027-3p	Sopen01g051090.1	3.0	-1.0	1	22	1235	1257	UGAAUCCUUCGGCUA-UCCAUAA	AAAUGGAAUGGCCGGAGGAUUCA	Cleavage
spe-miR6027-3p	Sopen07g026570.1	3.0	-1.0	1	22	1339	1360	UGAAUCCUUCGGCUAUCCAUAA	UGGUGGAUAGGAGAAGGAUUCA	Translation
spe-miR6027-3p	Sopen11g016660.1	3.0	-1.0	1	22	403	424	UGAAUCCUUCGGCUAUCCAUAA	AAAAGGAUAGUUGAAGGGUUUA	Cleavage
spe-miR6027-3p	Sopen03g010630.2	3.0	-1.0	1	22	99	120	UGAAUCCUUCGGCUAUCCAUAA	UAGUGGAGAGUUGGGGGAUUCA	Cleavage
spe-miR6027-3p	Sopen03g010630.1	3.0	-1.0	1	22	99	120	UGAAUCCUUCGGCUAUCCAUAA	UAGUGGAGAGUUGGGGGAUUCA	Cleavage
spe-miR6027-3p	Sopen09g009980.1	3.0	-1.0	1	22	577	598	UGAAUCCUUCGGCUAUCCAUAA	UGGAGGAUUGUCGAAGGGUUCA	Cleavage
spe-miR6027-3p	Sopen05g003260.1	3.0	-1.0	1	22	2083	2104	UGAAUCCUUCGGCUAUCCAUAA	GUUUUGGUGGCUGAAGGAUUUA	Cleavage
spe-miR6027-5p	Sopen07g024420.1	2.0	-1.0	1	22	435	456	AUGGGUAGCACAAGGAUUAAUG	UCAUGAUCCUUGUGUUAUUCAU	Cleavage
spe-miR6027-5p	Sopen03g013960.1	3.0	-1.0	1	22	1377	1398	AUGGGUAGCACAAGGAUUAAUG	UAUUGAUUCUAGUGCUACUCAU	Cleavage
spe-miR6027-5p	Sopen03g003010.1	3.0	-1.0	1	22	488	509	AUGGGUAGCACAAGGAUUAAUG	CAUUAGCCUUUGUGUUGCCCAU	Cleavage
spe-miR6027-5p	Sopen10g019830.1	3.0	-1.0	1	22	297	318	AUGGGUAGCACAAGGAUUAAUG	UAUUGAUUCUAGUGCUACUCAU	Cleavage
spe-miR6027-5p	Sopen01g009610.1	3.0	-1.0	1	22	1614	1635	AUGGGUAGCACAAGGAUUAAUG	CAAUAAUGCUGGUGCUACCUAU	Cleavage
spe-miR6027-5p	Sopen01g030790.1	3.0	-1.0	1	22	321	342	AUGGGUAGCACAAGGAUUAAUG	UACUAAUCUUUGUGCAAUUCAU	Cleavage
spe-miR6027-5p	Sopen01g032420.1	3.0	-1.0	1	22	321	342	AUGGGUAGCACAAGGAUUAAUG	UACUAAUCUUUGUGCAAUUCAU	Cleavage
spe-miR6027-5p	Sopen01g030620.1	3.0	-1.0	1	22	321	342	AUGGGUAGCACAAGGAUUAAUG	UACUAAUCUCUGUGCUAUUCAU	Cleavage
spe-miR6027-5p	Sopen09g025470.1	3.0	-1.0	1	22	1491	1512	AUGGGUAGCACAAGGAUUAAUG	UUCUAAUCCUCGUGUUAUUCAU	Cleavage
spe-miR6027-5p	Sopen09g012270.1	3.0	-1.0	1	22	234	255	AUGGGUAGCACAAGGAUUAAUG	AAACAAUGCUUGUGCUACCCAA	Cleavage
spe-miR6027-5p	Sopen02g019260.1	3.0	-1.0	1	22	741	762	AUGGGUAGCACAAGGAUUAAUG	UUAUAUUUCUUGUGCUGCUCGU	Cleavage
spe-miR6144-5p	Sopen09g005270.2	3.0	-1.0	1	21	581	601	UGGCAACUUCUUCAUCAUGUU	AGAAUGAUGGAGAAGUUGCAA	Cleavage
spe-miR6144-5p	Sopen09g005270.2	3.0	-1.0	1	21	1010	1030	UGGCAACUUCUUCAUCAUGUU	AGAAUGAUGGAGAAGUUGCAA	Cleavage
spe-miR6144-5p	Sopen09g005270.1	3.0	-1.0	1	21	524	544	UGGCAACUUCUUCAUCAUGUU	AGAAUGAUGGAGAAGUUGCAA	Cleavage
spe-miR6144-5p	Sopen09g005270.1	3.0	-1.0	1	21	953	973	UGGCAACUUCUUCAUCAUGUU	AGAAUGAUGGAGAAGUUGCAA	Cleavage
spe-miR6144-5p	Sopen04g023260.1	3.0	-1.0	1	21	2948	2968	UGGCAACUUCUUCAUCAUGUU	GUGCUGAUGAAGAAGUUGCUG	Cleavage
spe-miR6144-5p	Sopen04g023250.1	3.0	-1.0	1	21	1313	1333	UGGCAACUUCUUCAUCAUGUU	GUGCUGAUGAAGAAGUUGCUG	Cleavage
spe-miR6144-5p	Sopen09g018350.1	2.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACAUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen03g012930.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen07g015060.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen06g005710.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen05g012970.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAAGAAGUUGUUA	Cleavage
spe-miR6144-5p	Sopen03g012980.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen01g014200.1	3.0	-1.0	1	21	554	574	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen04g016950.1	3.0	-1.0	1	21	476	496	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen01g018370.1	1.5	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACAUGAGGAGGAAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen12g016080.1	1.5	-1.0	1	21	2783	2803	UGGCAACUUCUUCAUCAUGUU	AUUAUGAUGAAGAAGUUGCUG	Cleavage
spe-miR6144-5p	Sopen10g015210.1	1.5	-1.0	1	21	364	384	UGGCAACUUCUUCAUCAUGUU	GCAAUGAUGGAGAAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen06g022700.1	2.0	-1.0	1	21	1262	1282	UGGCAACUUCUUCAUCAUGUU	UCUAUGGUGAGGAAGUUGUCA	Cleavage
spe-miR6144-5p	Sopen11g016740.1	2.5	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACAUGAUGAAGAGAUUGCUA	Cleavage
spe-miR6144-5p	Sopen12g004630.1	2.5	-1.0	1	21	2294	2314	UGGCAACUUCUUCAUCAUGUU	UAUAUGGUGAAGAAGCUGCCA	Cleavage
spe-miR6144-5p	Sopen04g001510.1	2.5	-1.0	1	21	752	772	UGGCAACUUCUUCAUCAUGUU	AGCAUGAGGAGGAAGUUGCCC	Cleavage
spe-miR6144-5p	Sopen01g035540.1	2.5	-1.0	1	21	4075	4095	UGGCAACUUCUUCAUCAUGUU	GAUAUGUUGGAGAAGUUGUCA	Cleavage
spe-miR6144-5p	Sopen02g003680.1	2.5	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	AACUUGAAGAGGAAGUUGCCA	Cleavage

spe-miR6144-5p	Sopen05g007060.1	2.5	-1.0	1	21	182	202	UGGCAACUUCUUCAUCAUGUU	CAGAUGAUGAAGAAGUUUCCA	Cleavage
spe-miR6144-5p	Sopen05g007060.2	2.5	-1.0	1	21	182	202	UGGCAACUUCUUCAUCAUGUU	CAGAUGAUGAAGAAGUUUCCA	Cleavage
spe-miR6144-5p	Sopen04g028880.1	2.5	-1.0	1	21	866	886	UGGCAACUUCUUCAUCAUGUU	UGAUUGAUGAAGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen04g027970.1	2.5	-1.0	1	21	776	796	UGGCAACUUCUUCAUCAUGUU	UUUGUGAUGAAGAAGUUGCUC	Cleavage
spe-miR6144-5p	Sopen09g028160.1	2.5	-1.0	1	21	89	109	UGGCAACUUCUUCAUCAUGUU	AGAAUGGAGAAGAAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen06g003170.1	2.5	-1.0	1	21	89	109	UGGCAACUUCUUCAUCAUGUU	AGAAUGGAGAAGAAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen01g032140.1	2.5	-1.0	1	21	1247	1267	UGGCAACUUCUUCAUCAUGUU	UUGAUGAUGAAGAAGCUGCCA	Cleavage
spe-miR6144-5p	Sopen09g021340.1	2.5	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAAGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen04g028870.1	2.5	-1.0	1	21	2538	2557	UGGCAACUUCUUCAUCAUGUU	GACA-GAUGAAGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g004620.1	2.5	-1.0	1	21	107	127	UGGCAACUUCUUCAUCAUGUU	AUCUUGAUGAAGAAGUUGUUG	Cleavage
spe-miR6144-5p	Sopen12g004620.1	2.5	-1.0	1	21	461	481	UGGCAACUUCUUCAUCAUGUU	UGAAUGAAGAAGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen12g025210.1	3.0	-1.0	1	21	194	214	UGGCAACUUCUUCAUCAUGUU	AACAUGAUGAAGAAGUAGACA	Cleavage
spe-miR6144-5p	Sopen07g033530.1	3.0	-1.0	1	21	586	606	UGGCAACUUCUUCAUCAUGUU	GACCUGAUGAAGAAGUUGUUU	Cleavage
spe-miR6144-5p	Sopen12g026510.1	3.0	-1.0	1	21	184	204	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen03g037090.1	3.0	-1.0	1	21	1571	1591	UGGCAACUUCUUCAUCAUGUU	AACAAUAUGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen03g012810.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen01g019240.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen10g034460.1	3.0	-1.0	1	21	1094	1114	UGGCAACUUCUUCAUCAUGUU	AGGAUGAUGAAGGAAUUGCCA	Cleavage
spe-miR6144-5p	Sopen09g006570.1	3.0	-1.0	1	21	1094	1114	UGGCAACUUCUUCAUCAUGUU	AGGAUGAUGAAGGAAUUGCCA	Cleavage
spe-miR6144-5p	Sopen06g035240.1	3.0	-1.0	1	21	89	109	UGGCAACUUCUUCAUCAUGUU	AAAAUGGAGAAGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen05g002860.1	3.0	-1.0	1	21	968	988	UGGCAACUUCUUCAUCAUGUU	GACAUGAGGGAGAAGUUGUUG	Cleavage
spe-miR6144-5p	Sopen11g013090.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen04g011650.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen04g014180.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACAUGAAGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen12g001030.1	3.0	-1.0	1	21	469	489	UGGCAACUUCUUCAUCAUGUU	GAGGUGAUAAAGAAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen05g020270.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen07g007910.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAAAUUGCCG	Cleavage
spe-miR6144-5p	Sopen11g013180.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen10g012790.1	3.0	-1.0	1	21	2075	2095	UGGCAACUUCUUCAUCAUGUU	CACUUGAUGAAGAGAUUGCCA	Cleavage
spe-miR6144-5p	Sopen11g029090.1	3.0	-1.0	1	21	1771	1791	UGGCAACUUCUUCAUCAUGUU	UACAAGAUUAAGGAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen07g017340.1	3.0	-1.0	1	21	340	360	UGGCAACUUCUUCAUCAUGUU	UACAUGAGGAGGAAAUUGCCA	Cleavage
spe-miR6144-5p	Sopen12g001710.1	3.0	-1.0	1	21	59	79	UGGCAACUUCUUCAUCAUGUU	ACGUUGAUGGAGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen12g007960.1	3.0	-1.0	1	21	113	133	UGGCAACUUCUUCAUCAUGUU	UGUGUGAUGUGGAAGUUGCCA	Cleavage
spe-miR6144-5p	Sopen03g018500.1	3.0	-1.0	1	21	4676	4696	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen05g015100.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen10g021560.1	3.0	-1.0	1	21	605	625	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g012740.1	3.0	-1.0	1	21	1280	1300	UGGCAACUUCUUCAUCAUGUU	GACCAGAUGAAGAAGUUGCUG	Cleavage
spe-miR6144-5p	Sopen10g014810.1	3.0	-1.0	1	21	1289	1309	UGGCAACUUCUUCAUCAUGUU	CCCAUGAUGAAGAAGUUCCUC	Cleavage
spe-miR6144-5p	Sopen02g001940.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAAGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen05g023640.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAAGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen11g017670.1	3.0	-1.0	1	21	926	946	UGGCAACUUCUUCAUCAUGUU	AUGAUGAUGAGGAAAUUGCCA	Cleavage
spe-miR6144-5p	Sopen10g017730.1	3.0	-1.0	1	21	13	33	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen02g038660.1	3.0	-1.0	1	21	1885	1905	UGGCAACUUCUUCAUCAUGUU	GAAAUUGUGAAGAAGUUGUCA	Cleavage
spe-miR6144-5p	Sopen09g017300.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen11g018470.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen08g014900.1	3.0	-1.0	1	21	401	421	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen02g001250.1	3.0	-1.0	1	21	11	31	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g020480.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen01g032490.1	3.0	-1.0	1	21	61	81	UGGCAACUUCUUCAUCAUGUU	GACAAGAAGAAGAGGUUGUCA	Cleavage
spe-miR6144-5p	Sopen01g022770.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAAGAGGAAGUUGCUA	Cleavage

spe-miR6144-5p	Sopen05g018170.1	3.0	-1.0	1	21	236	256	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen11g016950.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen05g017730.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g011620.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen12g004320.1	3.0	-1.0	1	21	419	439	UGGCAACUUCUUCAUCAUGUU	AUAAUGGUGAAGAUGUUGCCA	Cleavage
spe-miR6144-5p	Sopen12g004330.1	3.0	-1.0	1	21	329	349	UGGCAACUUCUUCAUCAUGUU	AUAAUGGUGAAGAUGUUGCCA	Cleavage
spe-miR6144-5p	Sopen02g007690.1	3.0	-1.0	1	21	914	934	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen06g007310.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen07g009790.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen01g019190.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAAGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen08g010750.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g011610.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen04g016990.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g018810.1	3.0	-1.0	1	21	32	52	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6144-5p	Sopen09g016380.1	3.0	-1.0	1	21	29	49	UGGCAACUUCUUCAUCAUGUU	GACUUGAGGAGGAAGUUGCUA	Cleavage
spe-miR6440b-5p	Sopen08g013910.1	3.0	-1.0	1	21	1615	1635	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUUGUUAAACUC	Translation
spe-miR6440b-5p	Sopen05g019530.1	1.5	-1.0	1	21	667	687	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUGGUUAAACUC	Cleavage
spe-miR6440b-5p	Sopen02g032330.1	2.5	-1.0	1	21	1373	1393	GAGUUUGAUCAAUUUCGAGUU	GAGUUGAAAUUGAUCAAGUUC	Cleavage
spe-miR6440b-5p	Sopen09g031020.1	2.5	-1.0	1	21	1082	1102	GAGUUUGAUCAAUUUCGAGUU	AGGAUGAAAUUGAUCAAACUC	Cleavage
spe-miR6440b-5p	Sopen11g021920.1	2.5	-1.0	1	21	2042	2062	GAGUUUGAUCAAUUUCGAGUU	GUCUCGAAAUUGAACAAGUUC	Cleavage
spe-miR6440b-5p	Sopen03g012620.1	2.5	-1.0	1	21	442	462	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCAUUAAACUC	Translation
spe-miR6440b-5p	Sopen03g020560.1	2.5	-1.0	1	21	496	516	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCAUUAAACUC	Translation
spe-miR6440b-5p	Sopen04g014930.1	2.5	-1.0	1	21	442	462	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAGUUGGUUAAACUU	Cleavage
spe-miR6440b-5p	Sopen05g033350.1	2.5	-1.0	1	21	567	587	GAGUUUGAUCAAUUUCGAGUU	ACCACGAAAUUUAUCAAACUC	Translation
spe-miR6440b-5p	Sopen02g017830.1	2.5	-1.0	1	21	1604	1624	GAGUUUGAUCAAUUUCGAGUU	CUAUUGCAAUUGAUCAAACUC	Cleavage
spe-miR6440b-5p	Sopen11g023890.1	3.0	-1.0	1	21	3116	3136	GAGUUUGAUCAAUUUCGAGUU	GAAUUGAAAUUGAUCAAGCUA	Cleavage
spe-miR6440b-5p	Sopen11g023890.2	3.0	-1.0	1	21	3116	3136	GAGUUUGAUCAAUUUCGAGUU	GAAUUGAAAUUGAUCAAGCUA	Cleavage
spe-miR6440b-5p	Sopen06g034360.1	3.0	-1.0	1	21	491	511	GAGUUUGAUCAAUUUCGAGUU	CAUUUGAAGUUGAUCCAACUC	Cleavage
spe-miR6440b-5p	Sopen10g030380.1	3.0	-1.0	1	21	799	819	GAGUUUGAUCAAUUUCGAGUU	GACGUGGAAUUGGUCAAACUU	Cleavage
spe-miR6440b-5p	Sopen11g006170.1	3.0	-1.0	1	21	882	902	GAGUUUGAUCAAUUUCGAGUU	UACUGGAAAUAGAUCAAACUU	Translation
spe-miR6440b-5p	Sopen09g028050.2	3.0	-1.0	1	21	882	902	GAGUUUGAUCAAUUUCGAGUU	UACUGGAAAUAGAUCAAACUU	Translation
spe-miR6440b-5p	Sopen09g028050.1	3.0	-1.0	1	21	882	902	GAGUUUGAUCAAUUUCGAGUU	UACUGGAAAUAGAUCAAACUU	Translation
spe-miR6440b-5p	Sopen03g002790.1	3.0	-1.0	1	21	1001	1021	GAGUUUGAUCAAUUUCGAGUU	CCAGUGAAAUUGAUCAAACUU	Cleavage
spe-miR6440b-5p	Sopen03g011500.1	3.0	-1.0	1	21	578	598	GAGUUUGAUCAAUUUCGAGUU	CGUUUGAACUUGAUCAAAUUC	Cleavage
spe-miR6440b-5p	Sopen08g014940.1	3.0	-1.0	1	21	511	531	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCGUUAAACUC	Translation
spe-miR6440b-5p	Sopen02g006380.1	3.0	-1.0	1	21	157	177	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUUGUUAAACUC	Translation
spe-miR6440b-5p	Sopen03g016590.1	3.0	-1.0	1	21	571	591	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCGUUAAACUC	Translation
spe-miR6440b-5p	Sopen09g017380.1	3.0	-1.0	1	21	526	546	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCGUUAAACUC	Translation
spe-miR6440b-5p	Sopen09g012530.1	3.0	-1.0	1	21	883	903	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUUGUUAAACUC	Translation
spe-miR6440b-5p	Sopen03g009800.1	3.0	-1.0	1	21	568	588	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCGUUAAACUC	Translation
spe-miR6440b-5p	Sopen12g003610.1	3.0	-1.0	1	21	809	829	GAGUUUGAUCAAUUUCGAGUU	UUCUUGAAAUUGAUCAACUUU	Cleavage
spe-miR6440b-5p	Sopen09g017760.1	3.0	-1.0	1	21	355	375	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCGUUAAACUC	Translation
spe-miR6440b-5p	Sopen01g020340.1	3.0	-1.0	1	21	256	276	GAGUUUGAUCAAUUUCGAGUU	UCCUUGAAAUUCGUUAAACUC	Translation
spe-miR6440b-5p	Sopen02g011500.1	3.0	-1.0	1	21	1661	1681	GAGUUUGAUCAAUUUCGAGUU	AUCUUCAAAUUGAUCAAUCUC	Cleavage
spe-miR6440b-5p	Sopen06g015970.1	3.0	-1.0	1	21	3854	3874	GAGUUUGAUCAAUUUCGAGUU	GUCUUCAAAUUGAUCAAUCUC	Cleavage
spe-miR6478-5p	Sopen05g017220.1	2.5	-1.0	1	21	122	142	CCGACCUUAGCUCAGUUGGUA	UGACAACUGAGUUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen03g008330.1	3.0	-1.0	1	21	629	649	CCGACCUUAGCUCAGUUGGUA	UGCGAACUGAGCUUAGGUUGG	Cleavage
spe-miR6478-5p	Sopen05g018000.1	3.0	-1.0	1	21	605	625	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen02g007520.1	3.0	-1.0	1	21	860	880	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen09g013530.1	3.0	-1.0	1	21	572	592	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage

spe-miR6478-5p	Sopen08g016070.1	3.0	-1.0	1	21	209	229	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen12g011750.1	3.0	-1.0	1	21	107	127	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen07g019300.1	3.0	-1.0	1	21	932	952	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen04g017390.1	3.0	-1.0	1	21	4301	4321	CCGACCUUAGCUCAGUUGGUA	UGAGAACUGAGCUAGGGUUGG	Cleavage
spe-miR6478-5p	Sopen10g014010.1	3.0	-1.0	1	21	297	317	CCGACCUUAGCUCAGUUGGUA	CUCUAGUGGAGCUAAGGUUGG	Cleavage
spe-miR6478-5p	Sopen02g028540.1	3.0	-1.0	1	21	476	496	CCGACCUUAGCUCAGUUGGUA	GCCCGACGGAGCUAAGGGCGG	Cleavage
spe-miR7696c-3p	Sopen07g022880.1	2.0	-1.0	1	21	2314	2334	UUUUGAAUUAUGAGUACUUGA	UCAAGUGCUCGUAAUUUAGAA	Cleavage
spe-miR7696c-3p	Sopen07g022880.1	3.0	-1.0	1	21	1735	1755	UUUUGAAUUAUGAGUACUUGA	UCAACUGCUCGUAAUUUAGAA	Cleavage
spe-miR7696c-3p	Sopen05g010470.1	2.5	-1.0	1	21	1330	1350	UUUUGAAUUAUGAGUACUUGA	ACCAGUACUCGUGAUUCAAGA	Cleavage
spe-miR7696c-3p	Sopen06g034310.1	2.5	-1.0	1	21	691	711	UUUUGAAUUAUGAGUACUUGA	CGAGGUACUCAUAAUUUGAAU	Cleavage
spe-miR7696c-3p	Sopen07g012580.1	3.0	-1.0	1	21	775	795	UUUUGAAUUAUGAGUACUUGA	UUAAGUACUCAUAAGUCCAAA	Cleavage
spe-miR7696c-3p	Sopen05g033780.1	3.0	-1.0	1	21	1006	1026	UUUUGAAUUAUGAGUACUUGA	GCAAGUAUUCAUAGUUUGGAG	Cleavage
spe-miR7696c-3p	Sopen05g033780.3	3.0	-1.0	1	21	1006	1026	UUUUGAAUUAUGAGUACUUGA	GCAAGUAUUCAUAGUUUGGAG	Cleavage
spe-miR7696c-3p	Sopen05g033780.2	3.0	-1.0	1	21	1006	1026	UUUUGAAUUAUGAGUACUUGA	GCAAGUAUUCAUAGUUUGGAG	Cleavage
spe-miR7696c-3p	Sopen11g028070.1	3.0	-1.0	1	21	271	291	UUUUGAAUUAUGAGUACUUGA	CCUAGUACUUGUGAUUCAAGA	Cleavage
spe-miR7696c-3p	Sopen12g032830.1	3.0	-1.0	1	21	1644	1664	UUUUGAAUUAUGAGUACUUGA	ACAAAUACUCAUAAUUCAUGA	Cleavage
spe-miR7696c-3p	Sopen08g025110.1	3.0	-1.0	1	21	283	303	UUUUGAAUUAUGAGUACUUGA	AAAAGUGCUGGUAAUUCAGAA	Cleavage
spe-miR7696c-3p	Sopen10g032510.1	3.0	-1.0	1	21	655	675	UUUUGAAUUAUGAGUACUUGA	GAAAGUAUUGAUAAUUUAGAA	Cleavage
spe-miR7696c-3p	Sopen11g001480.1	3.0	-1.0	1	21	39	59	UUUUGAAUUAUGAGUACUUGA	CCAAUUAAUUGUAAUUCAAAA	Cleavage
spe-miR7696c-3p	Sopen04g022100.1	3.0	-1.0	1	21	436	456	UUUUGAAUUAUGAGUACUUGA	GUAACUACUUAUUAUUCAAAA	Cleavage
spe-miR7696c-3p	Sopen10g025530.1	3.0	-1.0	1	21	454	474	UUUUGAAUUAUGAGUACUUGA	GUAACUACUUAUUAUUCAAAA	Cleavage
spe-miR7696c-3p	Sopen05g030290.1	3.0	-1.0	1	21	439	459	UUUUGAAUUAUGAGUACUUGA	GUAACUACUUAUUAUUCAAAA	Cleavage
spe-miR7696c-3p	Sopen12g001410.1	3.0	-1.0	1	21	442	462	UUUUGAAUUAUGAGUACUUGA	GUAACUACUUAUUAUUCAAAA	Cleavage
spe-miR7696c-3p	Sopen04g013090.1	3.0	-1.0	1	21	187	207	UUUUGAAUUAUGAGUACUUGA	AGAUGUGCUUAUAAUUCAAAC	Cleavage
spe-miR7696c-3p	Sopen02g022020.1	3.0	-1.0	1	21	1752	1772	UUUUGAAUUAUGAGUACUUGA	AGAAGAGCUUAUAAUUCAAGG	Cleavage
spe-miR7980b-1-5p	Sopen07g023160.1	1.5	-1.0	1	24	594	617	GAGAUGGAAUCAGUGUUUGGACAU	UGCUGCAGAUGCUGAUUCCAUCUC	Cleavage
spe-miR7980b-1-5p	Sopen09g005560.1	2.0	-1.0	1	24	3794	3817	GAGAUGGAAUCAGUGUUUGGACAU	GCAGUCAAGAACUGAUUUCAUCUC	Cleavage
spe-miR7980b-1-5p	Sopen09g005560.2	2.0	-1.0	1	24	3767	3790	GAGAUGGAAUCAGUGUUUGGACAU	GCAGUCAAGAACUGAUUUCAUCUC	Cleavage
spe-miR7980b-1-5p	Sopen01g028370.1	2.0	-1.0	1	24	99	122	GAGAUGGAAUCAGUGUUUGGACAU	CGAAGCAAUUACUGAUUUCAUCUC	Cleavage
spe-miR7980b-1-5p	Sopen01g039780.1	2.5	-1.0	1	24	2221	2245	GAGAUGGAAUCAGUGU-UUGGACAU	AUUUUCAAUACACUGAUUUCAUCUC	Cleavage
spe-miR7980b-1-5p	Sopen05g022670.1	2.5	-1.0	1	24	6	29	GAGAUGGAAUCAGUGUUUGGACAU	UGAUUCAAGCAGUGAUUCCAUUUC	Cleavage
spe-miR7980b-1-5p	Sopen05g005910.1	2.5	-1.0	1	24	1080	1103	GAGAUGGAAUCAGUGUUUGGACAU	CACCCCAAAUUCUGAUUCCGUCUU	Cleavage
spe-miR7980b-1-5p	Sopen11g021390.1	2.5	-1.0	1	24	2241	2264	GAGAUGGAAUCAGUGUUUGGACAU	AUCAGUAAGCAUUGAUUUCAUUUC	Cleavage
spe-miR7980b-1-5p	Sopen03g012490.1	3.0	-1.0	1	24	714	737	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
spe-miR7980b-1-5p	Sopen03g012490.2	3.0	-1.0	1	24	450	473	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
spe-miR7980b-2-5p	Sopen07g023160.1	1.5	-1.0	1	24	594	617	GAGAUGGAAUCAGUGUUUGGACAU	UGCUGCAGAUGCUGAUUCCAUCUC	Cleavage
spe-miR7980b-2-5p	Sopen09g005560.1	2.0	-1.0	1	24	3794	3817	GAGAUGGAAUCAGUGUUUGGACAU	GCAGUCAAGAACUGAUUUCAUCUC	Cleavage
spe-miR7980b-2-5p	Sopen09g005560.2	2.0	-1.0	1	24	3767	3790	GAGAUGGAAUCAGUGUUUGGACAU	GCAGUCAAGAACUGAUUUCAUCUC	Cleavage

spe-miR7980b-2-5p	Sopen01g028370.1	2.0	-1.0	1	24	99	122	GAGAUGGAAUCAGUGUUUGGACAU	CGAAGCAAUUACUGAUUUCAUCUC	Cleavage
spe-miR7980b-2-5p	Sopen01g039780.1	2.5	-1.0	1	24	2221	2245	GAGAUGGAAUCAGUGU-UUGGACAU	AUUUUCAAUACACUGAUUUCAUCUC	Cleavage
spe-miR7980b-2-5p	Sopen05g022670.1	2.5	-1.0	1	24	6	29	GAGAUGGAAUCAGUGUUUGGACAU	UGAUUCAAGCAGUGAUUCCAUUUC	Cleavage
spe-miR7980b-2-5p	Sopen05g005910.1	2.5	-1.0	1	24	1080	1103	GAGAUGGAAUCAGUGUUUGGACAU	CACCCCAAAUUCUGAUUCCGUCUU	Cleavage
spe-miR7980b-2-5p	Sopen11g021390.1	2.5	-1.0	1	24	2241	2264	GAGAUGGAAUCAGUGUUUGGACAU	AUCAGUAAGCAUUGAUUUCAUUUC	Cleavage
spe-miR7980b-2-5p	Sopen03g012490.1	3.0	-1.0	1	24	714	737	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
spe-miR7980b-2-5p	Sopen03g012490.2	3.0	-1.0	1	24	450	473	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
spe-miR7980b-3-3p	Sopen01g050680.1	3.0	-1.0	1	24	2496	2519	GUCCAAACACUGAUUCCAUCUCAC	GAAAAGUGGAAUUAGGGUUUGGAU	Cleavage
spe-miR7980b-3-3p	Sopen12g004960.1	3.0	-1.0	1	24	564	587	GUCCAAACACUGAUUCCAUCUCAC	AAAGAACGGGAUCAGUGUUUGGGA	Cleavage
spe-miR7980b-3-3p	Sopen10g031150.1	1.5	-1.0	1	24	436	459	GUCCAAACACUGAUUCCAUCUCAC	CGGAGAUGGAAUCAGUGUAUGGAC	Cleavage
spe-miR7980b-3-3p	Sopen12g004980.1	2.0	-1.0	1	24	693	716	GUCCAAACACUGAUUCCAUCUCAC	UGGGCAUGGAAUCGGUGUUUGGGA	Cleavage
spe-miR7980b-3-3p	Sopen01g034210.1	3.0	-1.0	1	24	1184	1207	GUCCAAACACUGAUUCCAUCUCAC	UACAGAUGGGAUUAGUGUUGGGAU	Cleavage
spe-miR7980b-3-3p	Sopen05g027340.1	3.0	-1.0	1	24	1460	1483	GUCCAAACACUGAUUCCAUCUCAC	AGAUGAUGGAAUCGUUGUUUGGGU	Translation
spe-miR7980b-3-3p	Sopen03g009260.1	3.0	-1.0	1	24	729	752	GUCCAAACACUGAUUCCAUCUCAC	AUGUAAUGGAAUUGGUGCUUGGAU	Cleavage
spe-miR7980b-3-3p	Sopen12g031390.1	3.0	-1.0	1	24	977	1000	GUCCAAACACUGAUUCCAUCUCAC	CUAUCAUGGGAUCACUGUUUGGAG	Translation
spe-miR7980b-3-3p	Sopen01g034220.1	3.0	-1.0	1	24	1299	1322	GUCCAAACACUGAUUCCAUCUCAC	UCUCAAUGGGAUUAGUGUUGGGAU	Cleavage
spe-miR7980b-3-3p	Sopen06g031360.1	3.0	-1.0	1	24	770	793	GUCCAAACACUGAUUCCAUCUCAC	AUACAAUGGCAUCAGUGGUUGGAU	Cleavage
spe-miR7980b-4-3p	Sopen01g050680.1	3.0	-1.0	1	24	2496	2519	GUCCAAACACUGAUUCCAUCUCAC	GAAAAGUGGAAUUAGGGUUUGGAU	Cleavage
spe-miR7980b-4-3p	Sopen12g004960.1	3.0	-1.0	1	24	564	587	GUCCAAACACUGAUUCCAUCUCAC	AAAGAACGGGAUCAGUGUUUGGGA	Cleavage
spe-miR7980b-4-3p	Sopen10g031150.1	1.5	-1.0	1	24	436	459	GUCCAAACACUGAUUCCAUCUCAC	CGGAGAUGGAAUCAGUGUAUGGAC	Cleavage
spe-miR7980b-4-3p	Sopen12g004980.1	2.0	-1.0	1	24	693	716	GUCCAAACACUGAUUCCAUCUCAC	UGGGCAUGGAAUCGGUGUUUGGGA	Cleavage
spe-miR7980b-4-3p	Sopen01g034210.1	3.0	-1.0	1	24	1184	1207	GUCCAAACACUGAUUCCAUCUCAC	UACAGAUGGGAUUAGUGUUGGGAU	Cleavage
spe-miR7980b-4-3p	Sopen05g027340.1	3.0	-1.0	1	24	1460	1483	GUCCAAACACUGAUUCCAUCUCAC	AGAUGAUGGAAUCGUUGUUUGGGU	Translation
spe-miR7980b-4-3p	Sopen03g009260.1	3.0	-1.0	1	24	729	752	GUCCAAACACUGAUUCCAUCUCAC	AUGUAAUGGAAUUGGUGCUUGGAU	Cleavage
spe-miR7980b-4-3p	Sopen12g031390.1	3.0	-1.0	1	24	977	1000	GUCCAAACACUGAUUCCAUCUCAC	CUAUCAUGGGAUCACUGUUUGGAG	Translation
spe-miR7980b-4-3p	Sopen01g034220.1	3.0	-1.0	1	24	1299	1322	GUCCAAACACUGAUUCCAUCUCAC	UCUCAAUGGGAUUAGUGUUGGGAU	Cleavage

spe-miR7980b-4-3p	Sopen06g031360.1	3.0	-1.0	1	24	770	793	GUCCAAACACUGAUUCCAUCUCAC	AUACAAUGGCAUCAGUGGUUGGAU	Cleavage
spe-miR7980b-5-5p	Sopen01g050680.1	3.0	-1.0	1	24	2496	2519	GUCCAAACACUGAUUCCAUCUCAG	GAAAAGUGGAAUUAGGGUUUGGAU	Cleavage
spe-miR7980b-5-5p	Sopen12g004960.1	3.0	-1.0	1	24	564	587	GUCCAAACACUGAUUCCAUCUCAG	AAAGAACGGGAUCAGUGUUUGGGA	Cleavage
spe-miR7980b-5-5p	Sopen10g031150.1	1.5	-1.0	1	24	436	459	GUCCAAACACUGAUUCCAUCUCAG	CGGAGAUGGAAUCAGUGUAUGGAC	Cleavage
spe-miR7980b-5-5p	Sopen12g004980.1	2.0	-1.0	1	24	693	716	GUCCAAACACUGAUUCCAUCUCAG	UGGGCAUGGAAUCGGUGUUUGGGA	Cleavage
spe-miR7980b-5-5p	Sopen01g034210.1	3.0	-1.0	1	24	1184	1207	GUCCAAACACUGAUUCCAUCUCAG	UACAGAUGGGAUUAGUGUUGGGAU	Cleavage
spe-miR7980b-5-5p	Sopen05g027340.1	3.0	-1.0	1	24	1460	1483	GUCCAAACACUGAUUCCAUCUCAG	AGAUGAUGGAAUCGUUGUUUGGGU	Translation
spe-miR7980b-5-5p	Sopen03g009260.1	3.0	-1.0	1	24	729	752	GUCCAAACACUGAUUCCAUCUCAG	AUGUAAUGGAAUUGGUGCUUGGAU	Cleavage
spe-miR7980b-5-5p	Sopen12g031390.1	3.0	-1.0	1	24	977	1000	GUCCAAACACUGAUUCCAUCUCAG	CUAUCAUGGGAUCACUGUUUGGAG	Translation
spe-miR7980b-5-5p	Sopen01g034220.1	3.0	-1.0	1	24	1299	1322	GUCCAAACACUGAUUCCAUCUCAG	UCUCAAUGGGAUUAGUGUUGGGAU	Cleavage
spe-miR7980b-5-5p	Sopen06g031360.1	3.0	-1.0	1	24	770	793	GUCCAAACACUGAUUCCAUCUCAG	AUACAAUGGCAUCAGUGGUUGGAU	Cleavage
spe-miR7980b-6-3p	Sopen07g023160.1	1.5	-1.0	1	24	594	617	GAGAUGGAAUCAGUGUUUGGACAU	UGCUGCAGAUGCUGAUUCCAUCUC	Cleavage
spe-miR7980b-6-3p	Sopen09g005560.1	2.0	-1.0	1	24	3794	3817	GAGAUGGAAUCAGUGUUUGGACAU	GCAGUCAAGAACUGAUUUCAUCUC	Cleavage
spe-miR7980b-6-3p	Sopen09g005560.2	2.0	-1.0	1	24	3767	3790	GAGAUGGAAUCAGUGUUUGGACAU	GCAGUCAAGAACUGAUUUCAUCUC	Cleavage
spe-miR7980b-6-3p	Sopen01g028370.1	2.0	-1.0	1	24	99	122	GAGAUGGAAUCAGUGUUUGGACAU	CGAAGCAAUUACUGAUUUCAUCUC	Cleavage
spe-miR7980b-6-3p	Sopen01g039780.1	2.5	-1.0	1	24	2221	2245	GAGAUGGAAUCAGUGU-UUGGACAU	AUUUUCAAUACACUGAUUUCAUCUC	Cleavage
spe-miR7980b-6-3p	Sopen05g022670.1	2.5	-1.0	1	24	6	29	GAGAUGGAAUCAGUGUUUGGACAU	UGAUUCAAGCAGUGAUUCCAUUUC	Cleavage
spe-miR7980b-6-3p	Sopen05g005910.1	2.5	-1.0	1	24	1080	1103	GAGAUGGAAUCAGUGUUUGGACAU	CACCCCAAAUUCUGAUUCCGUCUU	Cleavage
spe-miR7980b-6-3p	Sopen11g021390.1	2.5	-1.0	1	24	2241	2264	GAGAUGGAAUCAGUGUUUGGACAU	AUCAGUAAGCAUUGAUUUCAUUUC	Cleavage
spe-miR7980b-6-3p	Sopen03g012490.1	3.0	-1.0	1	24	714	737	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
spe-miR7980b-6-3p	Sopen03g012490.2	3.0	-1.0	1	24	450	473	GAGAUGGAAUCAGUGUUUGGACAU	CACUAUAAACAUUGAGUCCAUCUU	Cleavage
spe-miR7981-3p	Sopen11g021580.1	2.5	-1.0	1	24	1273	1296	AUAGGACUUUAGUUUAGUUAAGGC	UGGGGACCAAAACUAAAGUUCUAU	Cleavage
spe-miR7981-3p	Sopen05g007160.1	3.0	-1.0	1	24	407	430	AUAGGACUUUAGUUUAGUUAAGGC	AAAUUAACAAAGCUGAAGUUCUGU	Cleavage
spe-miR7981-3p	Sopen03g020480.1	3.0	-1.0	1	24	571	594	AUAGGACUUUAGUUUAGUUAAGGC	ACUCAAACUAGGCAAAAGUCUUAU	Translation
spe-miR7981-3p	Sopen07g025250.1	3.0	-1.0	1	24	2791	2814	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen02g010330.1	3.0	-1.0	1	24	3487	3510	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen04g014160.1	3.0	-1.0	1	24	3736	3759	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen10g005990.1	3.0	-1.0	1	24	3652	3675	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen05g012140.1	3.0	-1.0	1	24	3652	3675	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen02g012390.1	3.0	-1.0	1	24	3736	3759	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen12g024530.1	3.0	-1.0	1	24	3736	3759	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage

spe-miR7981-3p	Sopen04g020730.1	3.0	-1.0	1	24	3736	3759	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen07g025250.2	3.0	-1.0	1	24	3736	3759	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen07g017800.1	3.0	-1.0	1	24	3736	3759	AUAGGACUUUAGUUUAGUUAAGGC	AUGGGAACUGAACUAAAGUUUUCU	Cleavage
spe-miR7981-3p	Sopen02g020780.1	3.0	-1.0	1	24	1177	1200	AUAGGACUUUAGUUUAGUUAAGGC	UACACAGUCAAACUAAAGUUUUAU	Cleavage
spe-miR7981-3p	Sopen02g020780.2	3.0	-1.0	1	24	1177	1200	AUAGGACUUUAGUUUAGUUAAGGC	UACACAGUCAAACUAAAGUUUUAU	Cleavage
spe-miR7981-5p	Sopen07g025370.1	3.0	-1.0	1	24	628	651	CUUAACUAAACUAAGGUCCUAUUA	CACGAGGAUCUUAGUUUGUUUGAG	Cleavage
spe-miR7981-5p	Sopen03g037860.1	3.0	-1.0	1	24	2692	2715	CUUAACUAAACUAAGGUCCUAUUA	CUCAAGGACAUUGGUUUAGUUGAU	Cleavage
spe-miR7983-1-3p	Sopen01g006360.1	0.0	-1.0	1	24	2539	2562	ACUAAUGCCGGUAAAGACUUUAAC	GCUAAAGUCUUUACCGGCAUUAGU	Cleavage
spe-miR7983-1-5p	Sopen05g021080.1	3.0	-1.0	1	24	3766	3789	UAAAGCCUUUAGCGACAUUGGUUC	GAACAAGUAUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-1-5p	Sopen06g023830.1	2.5	-1.0	1	24	443	466	UAAAGCCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
spe-miR7983-1-5p	Sopen00g001490.1	3.0	-1.0	1	24	4417	4440	UAAAGCCUUUAGCGACAUUGGUUC	GAACAAGUCUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-2-3p	Sopen01g006360.1	0.0	-1.0	1	24	2539	2562	ACUAAUGCCGGUAAAGACUUUAAC	GCUAAAGUCUUUACCGGCAUUAGU	Cleavage
spe-miR7983-2-5p	Sopen05g021080.1	3.0	-1.0	1	24	3766	3789	UAAAGCCUUUAGCGACAUUGGUUC	GAACAAGUAUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-2-5p	Sopen06g023830.1	2.5	-1.0	1	24	443	466	UAAAGCCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
spe-miR7983-2-5p	Sopen00g001490.1	3.0	-1.0	1	24	4417	4440	UAAAGCCUUUAGCGACAUUGGUUC	GAACAAGUCUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-3-3p	Sopen01g006360.1	0.0	-1.0	1	24	2539	2562	ACUAAUGCCGGUAAAGACUUUAAC	GCUAAAGUCUUUACCGGCAUUAGU	Cleavage
spe-miR7983-3-5p	Sopen05g021080.1	3.0	-1.0	1	24	3766	3789	UAAAGCCUUUAGCGAAAUUGGUUG	GAACAAGUAUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-3-5p	Sopen00g008820.1	2.0	-1.0	1	24	377	400	UAAAGCCUUUAGCGAAAUUGGUUG	CGGUUGAUUUAGCUAGAGGCUUUA	Cleavage
spe-miR7983-3-5p	Sopen03g017620.1	2.5	-1.0	1	24	730	753	UAAAGCCUUUAGCGAAAUUGGUUG	UCUCCAAUUUCUCUGAAGGUUUUA	Cleavage
spe-miR7983-3-5p	Sopen02g031580.1	2.5	-1.0	1	24	307	330	UAAAGCCUUUAGCGAAAUUGGUUG	GUUCAAGUUUCGUUAAAGGAUUUA	Cleavage
spe-miR7983-3-5p	Sopen05g013550.1	3.0	-1.0	1	24	4834	4857	UAAAGCCUUUAGCGAAAUUGGUUG	GAACAAGUUUUGCUAAAGGUUUCA	Cleavage
spe-miR7983-3-5p	Sopen00g001490.1	3.0	-1.0	1	24	4417	4440	UAAAGCCUUUAGCGAAAUUGGUUG	GAACAAGUCUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-3-5p	Sopen12g005540.1	3.0	-1.0	1	24	199	222	UAAAGCCUUUAGCGAAAUUGGUUG	UGGCAAGUUGCGCUAAAAGCUUUA	Cleavage
spe-miR7983-3-5p	Sopen01g010220.1	3.0	-1.0	1	24	119	142	UAAAGCCUUUAGCGAAAUUGGUUG	ACAUAAAUUCUGCUAGAGGUUUUG	Cleavage
spe-miR7983-4-3p	Sopen03g004080.1	3.0	-1.0	1	24	5091	5114	ACUAAUGCCGAUAAAGACUUUAAC	GGGAUGGUCUUUAUCGGCAUUAAA	Cleavage
spe-miR7983-4-3p	Sopen01g006360.1	1.5	-1.0	1	24	2539	2562	ACUAAUGCCGAUAAAGACUUUAAC	GCUAAAGUCUUUACCGGCAUUAGU	Translation
spe-miR7983-4-3p	Sopen09g013360.1	3.0	-1.0	1	24	180	203	ACUAAUGCCGAUAAAGACUUUAAC	GCCAUGGAUUUUGUUGGCAUUAGU	Cleavage
spe-miR7983-4-5p	Sopen05g003800.1	2.5	-1.0	1	24	65	88	UAAAGUCUUUAGCGACAUUGGUUC	UCCUCAAUGCUGCUAAAGAUUUUG	Cleavage
spe-miR7983-4-5p	Sopen08g027810.1	2.5	-1.0	1	24	956	979	UAAAGUCUUUAGCGACAUUGGUUC	AUGGUAGUGUUGCUAGGGAUUUUA	Cleavage
spe-miR7983-4-5p	Sopen06g023830.1	3.0	-1.0	1	24	443	466	UAAAGUCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
spe-miR7983-4-5p	Sopen09g022470.1	3.0	-1.0	1	24	533	556	UAAAGUCUUUAGCGACAUUGGUUC	AAGUGAAGGUUGUUGAAGAUUUUA	Cleavage
spe-miR7983-4-5p	Sopen07g025410.1	3.0	-1.0	1	24	647	670	UAAAGUCUUUAGCGACAUUGGUUC	CAUGUGAUGUUGCUGGAGAUUUUG	Cleavage
spe-miR7983-5-3p	Sopen03g004080.1	3.0	-1.0	1	24	5091	5114	ACUAAUGCCGAUAAAGACUUUAAC	GGGAUGGUCUUUAUCGGCAUUAAA	Cleavage
spe-miR7983-5-3p	Sopen01g006360.1	1.5	-1.0	1	24	2539	2562	ACUAAUGCCGAUAAAGACUUUAAC	GCUAAAGUCUUUACCGGCAUUAGU	Translation
spe-miR7983-5-3p	Sopen09g013360.1	3.0	-1.0	1	24	180	203	ACUAAUGCCGAUAAAGACUUUAAC	GCCAUGGAUUUUGUUGGCAUUAGU	Cleavage
spe-miR7983-5-5p	Sopen05g003800.1	2.5	-1.0	1	24	65	88	UAAAGUCUUUAGCGACAUUGGUUC	UCCUCAAUGCUGCUAAAGAUUUUG	Cleavage
spe-miR7983-5-5p	Sopen08g027810.1	2.5	-1.0	1	24	956	979	UAAAGUCUUUAGCGACAUUGGUUC	AUGGUAGUGUUGCUAGGGAUUUUA	Cleavage
spe-miR7983-5-5p	Sopen06g023830.1	3.0	-1.0	1	24	443	466	UAAAGUCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
spe-miR7983-5-5p	Sopen09g022470.1	3.0	-1.0	1	24	533	556	UAAAGUCUUUAGCGACAUUGGUUC	AAGUGAAGGUUGUUGAAGAUUUUA	Cleavage
spe-miR7983-5-5p	Sopen07g025410.1	3.0	-1.0	1	24	647	670	UAAAGUCUUUAGCGACAUUGGUUC	CAUGUGAUGUUGCUGGAGAUUUUG	Cleavage
spe-miR7983-6-3p	Sopen01g006360.1	0.0	-1.0	1	24	2539	2562	ACUAAUGCCGGUAAAGACUUUAGU	GCUAAAGUCUUUACCGGCAUUAGU	Cleavage
spe-miR7983-6-5p	Sopen05g003800.1	2.5	-1.0	1	24	65	88	UAAAGUCUUUAGCGACAUUGGUUC	UCCUCAAUGCUGCUAAAGAUUUUG	Cleavage
spe-miR7983-6-5p	Sopen08g027810.1	2.5	-1.0	1	24	956	979	UAAAGUCUUUAGCGACAUUGGUUC	AUGGUAGUGUUGCUAGGGAUUUUA	Cleavage
spe-miR7983-6-5p	Sopen06g023830.1	3.0	-1.0	1	24	443	466	UAAAGUCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
spe-miR7983-6-5p	Sopen09g022470.1	3.0	-1.0	1	24	533	556	UAAAGUCUUUAGCGACAUUGGUUC	AAGUGAAGGUUGUUGAAGAUUUUA	Cleavage
spe-miR7983-6-5p	Sopen07g025410.1	3.0	-1.0	1	24	647	670	UAAAGUCUUUAGCGACAUUGGUUC	CAUGUGAUGUUGCUGGAGAUUUUG	Cleavage
spe-miR7983-7-3p	Sopen01g006360.1	0.0	-1.0	1	24	2539	2562	ACUAAUGCCGGUAAAGACUUUAAC	GCUAAAGUCUUUACCGGCAUUAGU	Cleavage
spe-miR7983-7-5p	Sopen05g021080.1	3.0	-1.0	1	24	3766	3789	UAAAGCCUUUAGCGACAUUGGUUC	GAACAAGUAUUGCUGAAGGUUUUA	Cleavage
spe-miR7983-7-5p	Sopen06g023830.1	2.5	-1.0	1	24	443	466	UAAAGCCUUUAGCGACAUUGGUUC	GAAAAAAUGUUGCUAAAAGUUUUA	Cleavage
spe-miR7983-7-5p	Sopen00g001490.1	3.0	-1.0	1	24	4417	4440	UAAAGCCUUUAGCGACAUUGGUUC	GAACAAGUCUUGCUGAAGGUUUUA	Cleavage

spe-miR7984-3p	Sopen11g024880.1	3.0	-1.0	1	24	1695	1718	CAAUUUCGGUCAAAGUUCAGAUAU	GAAUAUGGAUUUUGAUCGGAAUUC	Cleavage
spe-miR7984-3p	Sopen08g009750.1	3.0	-1.0	1	24	2008	2031	CAAUUUCGGUCAAAGUUCAGAUAU	AAAUGUGAGUUUUGGUUGAGAUUG	Cleavage
spe-miR7984-3p	Sopen10g012650.1	3.0	-1.0	1	24	538	561	CAAUUUCGGUCAAAGUUCAGAUAU	AAUUUUGGAGUUUGGUUGAAAUUG	Cleavage
spe-miR7984-3p	Sopen01g019530.1	3.0	-1.0	1	24	2133	2156	CAAUUUCGGUCAAAGUUCAGAUAU	UGCUCUCAGCGUUGACCGAAGUUG	Cleavage
spe-miR7984-3p	Sopen12g012420.1	3.0	-1.0	1	24	5009	5032	CAAUUUCGGUCAAAGUUCAGAUAU	GUCACAGAACUUUUACUGAAAUUG	Translation
spe-miR7984-3p	Sopen08g019420.1	3.0	-1.0	1	24	627	650	CAAUUUCGGUCAAAGUUCAGAUAU	GAAGGGGAACUUUGAACGAGAUUG	Cleavage
spe-miR7984-3p	Sopen10g010700.1	3.0	-1.0	1	24	608	630	CAAUUUCGGUCAAAGUUCAGAUAU	AUGU-UGGAGUUUGGUUGAAAUUG	Cleavage
spe-miR7984-3p	Sopen08g007910.1	3.0	-1.0	1	24	860	882	CAAUUUCGGUCAAAGUUCAGAUAU	AUGU-UGGAGUUUGGUUGAAAUUG	Cleavage
spe-miR7984-3p	Sopen01g018880.1	3.0	-1.0	1	24	863	885	CAAUUUCGGUCAAAGUUCAGAUAU	AUGU-UGGAGUUUGGUUGAAAUUG	Cleavage
spe-miR7984-3p	Sopen00g014020.1	3.0	-1.0	1	24	360	383	CAAUUUCGGUCAAAGUUCAGAUAU	AAUAAUGAACUUUGAUAGGGAUUG	Cleavage
spe-miR7984-3p	Sopen02g002320.1	3.0	-1.0	1	24	1106	1128	CAAUUUCGGUCAAAGUUCAGAUAU	AUGU-UGGAGUUUGGUUGAAAUUG	Cleavage
spe-miR7984-3p	Sopen09g008760.1	3.0	-1.0	1	24	1428	1451	CAAUUUCGGUCAAAGUUCAGAUAU	GAUAAUGAAUUUUGAUAGAGAUUG	Cleavage
spe-miR7984-3p	Sopen05g031810.1	3.0	-1.0	1	24	596	619	CAAUUUCGGUCAAAGUUCAGAUAU	GAGCUUUAGCUUUGACUGAAAUUC	Cleavage
spe-miR7984-3p	Sopen03g014470.1	3.0	-1.0	1	24	1854	1877	CAAUUUCGGUCAAAGUUCAGAUAU	GAUAAUGAAUUUUGAUAGAGAUUG	Cleavage
spe-miR7984-3p	Sopen07g007700.1	3.0	-1.0	1	24	6572	6594	CAAUUUCGGUCAAAGUUCAGAUAU	AUGU-UGGAGUUUGGUUGAAAUUG	Cleavage
spe-miR7984-5p	Sopen01g013390.1	2.5	-1.0	1	24	492	515	AUCCCAAACUUUGGAAAUGACUCU	CCAUUCGUCUCCAAAGUUUGGGAA	Cleavage
spe-miR7984-5p	Sopen12g013250.1	2.5	-1.0	1	24	718	741	AUCCCAAACUUUGGAAAUGACUCU	ACUCCCAUUUCUAGAAUUUGGGAU	Cleavage
spe-miR7984-5p	Sopen01g017900.1	2.5	-1.0	1	24	1301	1324	AUCCCAAACUUUGGAAAUGACUCU	UUGAUCAGCUCCAAGGUUUGGGAU	Cleavage
spe-miR7984-5p	Sopen12g015830.1	3.0	-1.0	1	24	340	363	AUCCCAAACUUUGGAAAUGACUCU	ACUCUCGUUUCUAGAAUUUGGGAU	Cleavage
spe-miR7984-5p	Sopen01g041900.1	3.0	-1.0	1	24	1033	1056	AUCCCAAACUUUGGAAAUGACUCU	UGGGCCCUUUUCAAAGAUUGGGAU	Cleavage
spe-miR7984-5p	Sopen01g041830.1	3.0	-1.0	1	24	1801	1824	AUCCCAAACUUUGGAAAUGACUCU	UGGGCCCUUUUCAAAGAUUGGGAU	Cleavage
spe-miR7984-5p	Sopen00g008510.1	3.0	-1.0	1	24	1876	1899	AUCCCAAACUUUGGAAAUGACUCU	UGGGCCCUUUUCAAAGAUUGGGAU	Cleavage
spe-miR7984-5p	Sopen04g012680.1	3.0	-1.0	1	24	72	95	AUCCCAAACUUUGGAAAUGACUCU	AACUUCACUUCCAAGGUUUGAGAU	Cleavage
spe-miR7984-5p	Sopen09g015730.1	3.0	-1.0	1	24	985	1008	AUCCCAAACUUUGGAAAUGACUCU	CCCAGAAUUUCCGAUGUUUGGGAU	Translation
spe-miR7984-5p	Sopen09g015730.2	3.0	-1.0	1	24	985	1008	AUCCCAAACUUUGGAAAUGACUCU	CCCAGAAUUUCCGAUGUUUGGGAU	Translation
spe-miR7984-5p	Sopen11g001160.1	3.0	-1.0	1	24	397	420	AUCCCAAACUUUGGAAAUGACUCU	UUUCGUGUUUCUCAAGUUUGGGAU	Cleavage
spe-miR7984-5p	Sopen09g031960.1	3.0	-1.0	1	24	31	54	AUCCCAAACUUUGGAAAUGACUCU	UUUGCCCUUUUCAAAGUUUUGGAU	Cleavage
spe-miR7984-5p	Sopen12g006700.1	3.0	-1.0	1	24	1615	1638	AUCCCAAACUUUGGAAAUGACUCU	CAAAGAAUUCCUAAAGUUUGGGGU	Cleavage
spe-miR7984-5p	Sopen04g023280.1	3.0	-1.0	1	24	82	105	AUCCCAAACUUUGGAAAUGACUCU	UUACCCAUUACCAAGGUUGGGGAU	Cleavage
spe-miR7984b-3p	Sopen11g017830.1	2.5	-1.0	1	24	2939	2962	GGUCUUUCAUAAAAUUUGGUAUUG	GUUAUGCAAAGUUUAUGAAAGAUC	Cleavage
spe-miR7984b-3p	Sopen01g037160.1	2.5	-1.0	1	24	768	791	GGUCUUUCAUAAAAUUUGGUAUUG	AGGUGCUAAAUUUUAUGGAAUACC	Cleavage
spe-miR7984b-3p	Sopen10g006240.1	2.5	-1.0	1	24	620	643	GGUCUUUCAUAAAAUUUGGUAUUG	UGAAACUACAUUUUGUGGAAGACC	Cleavage
spe-miR7984b-3p	Sopen07g007670.1	2.5	-1.0	1	24	3384	3406	GGUCUUUCAUAAAAUUUGGUAUUG	UUAUGCCAA-UUUUAUGAAAGAUC	Cleavage
spe-miR7984b-3p	Sopen10g015010.1	2.5	-1.0	1	24	7425	7447	GGUCUUUCAUAAAAUUUGGUAUUG	UUAUGCCAA-UUUUAUGAAAGAUC	Cleavage
spe-miR7984b-3p	Sopen02g025270.1	3.0	-1.0	1	24	648	671	GGUCUUUCAUAAAAUUUGGUAUUG	GGAUACCAAAUUUUAUGAGAUAUU	Cleavage
spe-miR7984b-3p	Sopen03g003940.1	3.0	-1.0	1	24	354	377	GGUCUUUCAUAAAAUUUGGUAUUG	CUGUGAUGAAUUUUGUGAAAGACU	Cleavage
spe-miR7984b-5p	Sopen11g022870.1	2.5	-1.0	1	24	2	26	AUAUCAAACUUUGG-AAAUGACCUU	UGGAUCGUUUUCCAAAGUUUGAUAU	Cleavage
spe-miR7984b-5p	Sopen01g020130.1	2.5	-1.0	1	24	1417	1440	AUAUCAAACUUUGGAAAUGACCUU	GAGAGCAUGUCCAAAGUUUCAUAU	Cleavage
spe-miR7984b-5p	Sopen06g032740.1	2.5	-1.0	1	24	63	86	AUAUCAAACUUUGGAAAUGACCUU	UUUGCUAUUUCCAGAGUUUGUUAU	Cleavage
spe-miR7984b-5p	Sopen06g022890.1	3.0	-1.0	1	24	90	113	AUAUCAAACUUUGGAAAUGACCUU	GCUUUCAUUUCAUAAGUUUGAUAU	Cleavage
spe-miR7984b-5p	Sopen04g012680.1	3.0	-1.0	1	24	72	95	AUAUCAAACUUUGGAAAUGACCUU	AACUUCACUUCCAAGGUUUGAGAU	Cleavage
spe-miR7984b-5p	Sopen07g034450.2	3.0	-1.0	1	24	435	458	AUAUCAAACUUUGGAAAUGACCUU	GAGUGGAUUUCCAAAAUUUGAUGU	Cleavage
spe-miR7984b-5p	Sopen03g022340.1	3.0	-1.0	1	24	621	644	AUAUCAAACUUUGGAAAUGACCUU	GAGUGGAUUUCCAAAAUUUGAUGU	Cleavage
spe-miR7984b-5p	Sopen07g034450.3	3.0	-1.0	1	24	648	671	AUAUCAAACUUUGGAAAUGACCUU	GAGUGGAUUUCCAAAAUUUGAUGU	Cleavage
spe-miR7984b-5p	Sopen07g034450.1	3.0	-1.0	1	24	1071	1094	AUAUCAAACUUUGGAAAUGACCUU	GAGUGGAUUUCCAAAAUUUGAUGU	Cleavage
spe-miR7984b-5p	Sopen04g025160.1	3.0	-1.0	1	24	1563	1586	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen10g006650.1	3.0	-1.0	1	24	768	791	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen05g015150.2	3.0	-1.0	1	24	651	674	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen12g012540.1	3.0	-1.0	1	24	999	1022	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen03g005240.1	3.0	-1.0	1	24	1020	1043	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage

spe-miR7984b-5p	Sopen12g016630.1	3.0	-1.0	1	24	1179	1202	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen10g022390.1	3.0	-1.0	1	24	1269	1292	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen08g012130.1	3.0	-1.0	1	24	1302	1325	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen12g020620.1	3.0	-1.0	1	24	1473	1496	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen09g020620.1	3.0	-1.0	1	24	1413	1436	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen02g003610.1	3.0	-1.0	1	24	1473	1496	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen02g036070.1	3.0	-1.0	1	24	1473	1496	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen12g010990.1	3.0	-1.0	1	24	1599	1622	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUAUGAUAG	Cleavage
spe-miR7984b-5p	Sopen01g027250.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen12g026920.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen05g025220.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen02g013230.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen04g019600.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen10g027160.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen08g008450.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen08g030170.1	3.0	-1.0	1	24	1515	1538	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen04g025160.2	3.0	-1.0	1	24	1563	1586	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen12g021170.1	3.0	-1.0	1	24	1563	1586	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen08g021210.1	3.0	-1.0	1	24	1563	1586	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen05g015150.1	3.0	-1.0	1	24	1842	1865	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen07g022780.1	3.0	-1.0	1	24	3066	3089	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen06g011350.1	3.0	-1.0	1	24	4386	4409	AUAUCAAACUUUGGAAAUGACCUU	UCAAACAUUUUCAAAGUGUGAUAG	Cleavage
spe-miR7984b-5p	Sopen07g025410.1	3.0	-1.0	1	24	1630	1653	AUAUCAAACUUUGGAAAUGACCUU	AGAUCCAUUUUUGAAGUUUGUUAU	Cleavage
spe-miR7984c-3p	Sopen10g019210.1	2.5	-1.0	1	24	1442	1465	CCUUCAUAAAGUUUGGUAUCGUAA	GGGAUAUACCAGACUUUGUGAGGU	Cleavage
spe-miR7984c-3p	Sopen05g002430.1	2.0	-1.0	1	24	863	886	CCUUCAUAAAGUUUGGUAUCGUAA	AAAUGACACCAAAUUUUGUGAAGG	Cleavage
spe-miR7984c-3p	Sopen03g027870.1	2.5	-1.0	1	24	333	356	CCUUCAUAAAGUUUGGUAUCGUAA	UGUCAAGAUCAGGCUUUAUGAAGG	Cleavage
spe-miR7984c-3p	Sopen02g039300.1	3.0	-1.0	1	24	10800	10823	CCUUCAUAAAGUUUGGUAUCGUAA	UCACAAUACUAGGGUUUAUGAAGG	Translation
spe-miR7984c-3p	Sopen01g029510.1	3.0	-1.0	1	24	2085	2108	CCUUCAUAAAGUUUGGUAUCGUAA	ACAUUAUACUGAACUUCGUGAAGG	Cleavage
spe-miR7984c-3p	Sopen10g032250.1	3.0	-1.0	1	24	1370	1393	CCUUCAUAAAGUUUGGUAUCGUAA	CAGAGAUACGAGACUUGAUGAAGG	Cleavage
spe-miR7984c-3p	Sopen04g032190.1	3.0	-1.0	1	24	1341	1364	CCUUCAUAAAGUUUGGUAUCGUAA	GUCUGAAAUGAAACUUUAUGGAGG	Cleavage
spe-miR7984c-3p	Sopen08g024770.1	3.0	-1.0	1	24	326	349	CCUUCAUAAAGUUUGGUAUCGUAA	ACUUGAUUGUAAACUUUGUGAAGG	Cleavage
spe-miR7984c-3p	Sopen07g023630.2	3.0	-1.0	1	24	860	883	CCUUCAUAAAGUUUGGUAUCGUAA	CAGCAAUAGCAAGCCUUAUGAAGG	Translation
spe-miR7984c-3p	Sopen12g030000.1	3.0	-1.0	1	24	181	204	CCUUCAUAAAGUUUGGUAUCGUAA	AGAGAAUAUCAAAUGUUAUGGAGG	Translation
spe-miR7984c-3p	Sopen07g023630.1	3.0	-1.0	1	24	965	988	CCUUCAUAAAGUUUGGUAUCGUAA	CAGCAAUAGCAAGCCUUAUGAAGG	Translation
spe-miR7984c-3p	Sopen00g009410.1	3.0	-1.0	1	24	77	100	CCUUCAUAAAGUUUGGUAUCGUAA	CCGUCAUGUCAAAUUUUCUGAAGG	Cleavage
spe-miR7987-5p	Sopen12g028680.2	3.0	-1.0	1	24	1857	1880	ACACUAGUUGAUCUUAUUGAUGAC	UGAAUCAAUAAGAUCAACUCCUGU	Cleavage
spe-miR7987-5p	Sopen12g028680.1	3.0	-1.0	1	24	1719	1742	ACACUAGUUGAUCUUAUUGAUGAC	UGAAUCAAUAAGAUCAACUCCUGU	Cleavage
spe-miR7987-5p	Sopen02g019690.1	3.0	-1.0	1	24	330	353	ACACUAGUUGAUCUUAUUGAUGAC	UAUACCAAUAAGACCAACUGGUGC	Translation
spe-miR7987-5p	Sopen01g032380.2	3.0	-1.0	1	24	2958	2981	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen10g004960.2	3.0	-1.0	1	24	2958	2981	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen07g025180.1	3.0	-1.0	1	24	2904	2927	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen05g005590.1	3.0	-1.0	1	24	2568	2591	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen05g009390.1	3.0	-1.0	1	24	2523	2546	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen01g032380.1	3.0	-1.0	1	24	2603	2626	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen10g004960.3	3.0	-1.0	1	24	1599	1622	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen12g022070.1	3.0	-1.0	1	24	1179	1202	ACACUAGUUGAUCUUAUUGAUGAC	AGACUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen00g014010.1	3.0	-1.0	1	24	1235	1258	ACACUAGUUGAUCUUAUUGAUGAC	AGAUUCAAGAAGAUCAGUUAGUGG	Cleavage
spe-miR7987-5p	Sopen01g010260.1	3.0	-1.0	1	24	4100	4123	ACACUAGUUGAUCUUAUUGAUGAC	AUUUUGAAGAAGGUCAAUUAGUGU	Cleavage
spe-miR7987-5p	Sopen06g028710.1	3.0	-1.0	1	24	1920	1943	ACACUAGUUGAUCUUAUUGAUGAC	UGGUUCAGUUAGGUCAAUUGGUGU	Cleavage
spe-miR7987-5p	Sopen12g027530.1	3.0	-1.0	1	24	1631	1654	ACACUAGUUGAUCUUAUUGAUGAC	AUUUUGAAGAGGGUCAACUAGUGU	Cleavage

spe-miR7990a-1-3p	Sopen11g005490.1	3.0	-1.0	1	24	1271	1294	UUCAAAUGAUCGUAACUUUGGCCU	CUGUUAGUGUUAUGAUCAUUUGGG	Cleavage
spe-miR7990a-1-3p	Sopen08g030290.1	3.0	-1.0	1	24	2544	2567	UUCAAAUGAUCGUAACUUUGGCCU	CAGUGGAAGUGACGAUCAUUUGGU	Cleavage
spe-miR7990a-2-3p	Sopen11g005490.1	3.0	-1.0	1	24	1271	1294	UUCAAAUGAUCGUAACUUUGGCCU	CUGUUAGUGUUAUGAUCAUUUGGG	Cleavage
spe-miR7990a-2-3p	Sopen08g030290.1	3.0	-1.0	1	24	2544	2567	UUCAAAUGAUCGUAACUUUGGCCU	CAGUGGAAGUGACGAUCAUUUGGU	Cleavage
spe-miR7992-3p	Sopen03g010670.1	0.0	-1.0	1	23	5062	5084	UGUCUAGAUGUGCACUCCAAAGU	GCCAUGGAGUGCACAUCUAGACA	Cleavage
spe-miR7992-3p	Sopen02g034150.1	2.5	-1.0	1	23	5071	5093	UGUCUAGAUGUGCACUCCAAAGU	GCUAUGGAAUGCACAUCAAGACA	Cleavage
spe-miR7992-3p	Sopen12g031430.1	2.5	-1.0	1	23	202	224	UGUCUAGAUGUGCACUCCAAAGU	GAUCUGAAGUGCACGUUUAGACG	Cleavage
spe-miR7992-3p	Sopen11g023600.1	3.0	-1.0	1	23	552	574	UGUCUAGAUGUGCACUCCAAAGU	AGAUUGGGGUGCAUGUCUAGAAA	Cleavage
spe-miR7992-3p	Sopen04g025510.1	3.0	-1.0	1	23	592	614	UGUCUAGAUGUGCACUCCAAAGU	GCAUUUGGGUGCUCAUCUAGACA	Translation
spe-miR7992-3p	Sopen07g012580.1	3.0	-1.0	1	23	1353	1375	UGUCUAGAUGUGCACUCCAAAGU	AGAUUGGGGUGCAUGUCUAGAAA	Cleavage
spe-miR7992-3p	Sopen05g034210.1	3.0	-1.0	1	23	595	617	UGUCUAGAUGUGCACUCCAAAGU	UCAUUUGGGUGCUCAUCUAGACA	Translation
spe-miR7992-3p	Sopen08g018030.1	3.0	-1.0	1	23	1096	1118	UGUCUAGAUGUGCACUCCAAAGU	GAUAUGAAGAGCACAUCUGGAUA	Cleavage
spe-miR7992-3p	Sopen09g027810.1	3.0	-1.0	1	23	1015	1037	UGUCUAGAUGUGCACUCCAAAGU	GACAUGAAGAGCACAUCUGGAUA	Cleavage
spe-miR7993a-3p	Sopen03g017710.1	2.5	-1.0	1	24	463	486	AUAUUUUAUGUGGUUAACUUAAAU	CACAAAGUUGACCACAUGAAAUUU	Cleavage
spe-miR7993a-3p	Sopen10g034550.1	2.5	-1.0	1	24	199	222	AUAUUUUAUGUGGUUAACUUAAAU	AAAGUUGUUAAUCAUGUAAAAUAU	Cleavage
spe-miR7993a-3p	Sopen05g011160.1	2.5	-1.0	1	24	362	385	AUAUUUUAUGUGGUUAACUUAAAU	CGCAUAGUCAACCGUGUAAAAUAU	Cleavage
spe-miR7993a-3p	Sopen11g002790.1	3.0	-1.0	1	24	2854	2877	AUAUUUUAUGUGGUUAACUUAAAU	ACUGAAGCUGACCACAUUAAAUAU	Cleavage
spe-miR7993a-3p	Sopen11g020300.1	3.0	-1.0	1	24	1075	1098	AUAUUUUAUGUGGUUAACUUAAAU	AUUCUGGAGAACUACAUAAAAUAU	Cleavage
spe-miR7993b-1-3p	Sopen05g033770.1	2.5	-1.0	1	24	2629	2652	UUAAUUUACGUGGUUAAAUUAACU	CUUGCAUUUAACCACGUCAAUUAC	Cleavage
spe-miR7993b-1-3p	Sopen09g004090.1	3.0	-1.0	1	24	307	330	UUAAUUUACGUGGUUAAAUUAACU	AACCUAUUUGGUCAUGUAAAUUAU	Cleavage
spe-miR7993b-1-3p	Sopen09g004090.2	3.0	-1.0	1	24	307	330	UUAAUUUACGUGGUUAAAUUAACU	AACCUAUUUGGUCAUGUAAAUUAU	Cleavage
spe-miR7993b-1-3p	Sopen11g026710.1	3.0	-1.0	1	24	2584	2607	UUAAUUUACGUGGUUAAAUUAACU	CUAGCAUUCAACCAUGUGAAUUAU	Cleavage
spe-miR7993b-1-3p	Sopen09g025480.2	3.0	-1.0	1	24	700	723	UUAAUUUACGUGGUUAAAUUAACU	AUCCUGUCUAACCACGUAAAUGAA	Cleavage
spe-miR7993b-1-3p	Sopen09g025480.1	3.0	-1.0	1	24	649	672	UUAAUUUACGUGGUUAAAUUAACU	AUCCUGUCUAACCACGUAAAUGAA	Cleavage
spe-miR7993b-1-5p	Sopen01g049550.1	3.0	-1.0	1	24	419	442	UUAAGUUAACCACAUACAGUAUGU	GUGAAUUGUAUGUGGCUAAUUUAG	Cleavage
spe-miR7993b-1-5p	Sopen01g049550.2	3.0	-1.0	1	24	419	442	UUAAGUUAACCACAUACAGUAUGU	GUGAAUUGUAUGUGGCUAAUUUAG	Cleavage
spe-miR7993b-1-5p	Sopen02g001810.1	3.0	-1.0	1	24	1292	1315	UUAAGUUAACCACAUACAGUAUGU	AAAACAUGUAUGUGGCUAACUUAG	Cleavage
spe-miR7993b-1-5p	Sopen12g021440.1	3.0	-1.0	1	24	1331	1354	UUAAGUUAACCACAUACAGUAUGU	AAAACAUGUAUGUGGCUAACUUAG	Cleavage
spe-miR7993b-1-5p	Sopen05g011220.1	3.0	-1.0	1	24	797	820	UUAAGUUAACCACAUACAGUAUGU	AAAACAUGUAUGUGGCUAACUUAG	Cleavage
spe-miR7993b-1-5p	Sopen05g011220.2	3.0	-1.0	1	24	1109	1132	UUAAGUUAACCACAUACAGUAUGU	AAAACAUGUAUGUGGCUAACUUAG	Cleavage
spe-miR7993b-1-5p	Sopen09g016140.1	3.0	-1.0	1	24	2198	2221	UUAAGUUAACCACAUACAGUAUGU	AAAACAUGUAUGUGAUUAACUUAG	Translation
spe-miR7993b-1-5p	Sopen09g007750.1	3.0	-1.0	1	24	1862	1885	UUAAGUUAACCACAUACAGUAUGU	AAAACAUGUAUGUGGCUAACUUAG	Cleavage
spe-miR7993b-2-5p	Sopen10g034550.1	2.0	-1.0	1	24	199	222	AUAUUUUAUGUGGUUAACGUAAUU	AAAGUUGUUAAUCAUGUAAAAUAU	Cleavage

spe-miR7993b-2-5p	Sopen04g005540.1	3.0	-1.0	1	24	2923	2946	AUAUUUUAUGUGGUUAACGUAAUU	GGUAACGUAGACGACAUAAAAUAU	Cleavage
spe-miR7993b-2-5p	Sopen10g028490.1	3.0	-1.0	1	24	199	222	AUAUUUUAUGUGGUUAACGUAAUU	AAUGUUGUUAACCAUGUCAAAUAU	Cleavage
spe-miR7993b-2-5p	Sopen08g011920.1	3.0	-1.0	1	24	30	53	AUAUUUUAUGUGGUUAACGUAAUU	AGCAGCAUUAAUCACAUACAAUAU	Cleavage
spe-miR7997a-1-5p	Sopen04g001920.1	1.5	-1.0	1	21	310	330	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-1-5p	Sopen03g005640.1	1.5	-1.0	1	21	850	870	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-1-5p	Sopen01g001200.1	1.5	-1.0	1	21	1090	1110	AUGCUGCUCGGACUCUUCAAA	AGUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-1-5p	Sopen00g008820.1	2.0	-1.0	1	21	91	111	AUGCUGCUCGGACUCUUCAAA	AUUGAAGAGUCUGAGCAACAU	Cleavage
spe-miR7997a-1-5p	Sopen04g032170.1	2.0	-1.0	1	21	1261	1281	AUGCUGCUCGGACUCUUCAAA	CAAGAAGAGUUUGAGCAGCAU	Cleavage
spe-miR7997a-1-5p	Sopen08g023050.1	2.5	-1.0	1	21	64	84	AUGCUGCUCGGACUCUUCAAA	UUGGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-1-5p	Sopen09g035370.1	3.0	-1.0	1	21	118	138	AUGCUGCUCGGACUCUUCAAA	UUUGAUGAGUCUGAGCAGAAU	Cleavage
spe-miR7997a-1-5p	Sopen10g013470.1	3.0	-1.0	1	21	628	648	AUGCUGCUCGGACUCUUCAAA	ACUGAAGAGUUUGUGCAGUAU	Cleavage
spe-miR7997a-1-5p	Sopen05g016630.1	3.0	-1.0	1	21	235	255	AUGCUGCUCGGACUCUUCAAA	CGUGAGGAAUUCGAGCAGCGU	Cleavage
spe-miR7997a-1-5p	Sopen12g019930.1	3.0	-1.0	1	21	451	471	AUGCUGCUCGGACUCUUCAAA	CGUGAAGGGUCUGAGCAACGU	Cleavage
spe-miR7997a-2-5p	Sopen04g001920.1	1.5	-1.0	1	21	310	330	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-2-5p	Sopen03g005640.1	1.5	-1.0	1	21	850	870	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-2-5p	Sopen01g001200.1	1.5	-1.0	1	21	1090	1110	AUGCUGCUCGGACUCUUCAAA	AGUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-2-5p	Sopen00g008820.1	2.0	-1.0	1	21	91	111	AUGCUGCUCGGACUCUUCAAA	AUUGAAGAGUCUGAGCAACAU	Cleavage
spe-miR7997a-2-5p	Sopen04g032170.1	2.0	-1.0	1	21	1261	1281	AUGCUGCUCGGACUCUUCAAA	CAAGAAGAGUUUGAGCAGCAU	Cleavage
spe-miR7997a-2-5p	Sopen08g023050.1	2.5	-1.0	1	21	64	84	AUGCUGCUCGGACUCUUCAAA	UUGGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-2-5p	Sopen09g035370.1	3.0	-1.0	1	21	118	138	AUGCUGCUCGGACUCUUCAAA	UUUGAUGAGUCUGAGCAGAAU	Cleavage
spe-miR7997a-2-5p	Sopen10g013470.1	3.0	-1.0	1	21	628	648	AUGCUGCUCGGACUCUUCAAA	ACUGAAGAGUUUGUGCAGUAU	Cleavage
spe-miR7997a-2-5p	Sopen05g016630.1	3.0	-1.0	1	21	235	255	AUGCUGCUCGGACUCUUCAAA	CGUGAGGAAUUCGAGCAGCGU	Cleavage
spe-miR7997a-2-5p	Sopen12g019930.1	3.0	-1.0	1	21	451	471	AUGCUGCUCGGACUCUUCAAA	CGUGAAGGGUCUGAGCAACGU	Cleavage
spe-miR7997a-5p	Sopen04g001920.1	1.5	-1.0	1	21	310	330	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-5p	Sopen03g005640.1	1.5	-1.0	1	21	850	870	AUGCUGCUCGGACUCUUCAAA	UUUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-5p	Sopen01g001200.1	1.5	-1.0	1	21	1090	1110	AUGCUGCUCGGACUCUUCAAA	AGUGAAGAGUCCGAGCAACAU	Cleavage
spe-miR7997a-5p	Sopen00g008820.1	2.0	-1.0	1	21	91	111	AUGCUGCUCGGACUCUUCAAA	AUUGAAGAGUCUGAGCAACAU	Cleavage
spe-miR7997a-5p	Sopen04g032170.1	2.0	-1.0	1	21	1261	1281	AUGCUGCUCGGACUCUUCAAA	CAAGAAGAGUUUGAGCAGCAU	Cleavage
spe-miR7997a-5p	Sopen08g023050.1	2.5	-1.0	1	21	64	84	AUGCUGCUCGGACUCUUCAAA	UUGGAAGAGUCCGAGCAACAU	Cleavage

spe-miR7997a-5p	Sopen09g035370.1	3.0	-1.0	1	21	118	138	AUGCUGCUCGGACUCUUCAAA	UUUGAUGAGUCUGAGCAGAAU	Cleavage
spe-miR7997a-5p	Sopen10g013470.1	3.0	-1.0	1	21	628	648	AUGCUGCUCGGACUCUUCAAA	ACUGAAGAGUUUGUGCAGUAU	Cleavage
spe-miR7997a-5p	Sopen05g016630.1	3.0	-1.0	1	21	235	255	AUGCUGCUCGGACUCUUCAAA	CGUGAGGAAUUCGAGCAGCGU	Cleavage
spe-miR7997a-5p	Sopen12g019930.1	3.0	-1.0	1	21	451	471	AUGCUGCUCGGACUCUUCAAA	CGUGAAGGGUCUGAGCAACGU	Cleavage
spe-miR8001a-5p	Sopen04g005290.1	2.0	-1.0	1	24	1820	1843	UCCUGGGGAUUAGUAUGAAAAUUC	ACAACUUCAUACUAUUCCUCAGGA	Translation
spe-miR8001a-5p	Sopen12g008120.1	3.0	-1.0	1	24	252	275	UCCUGGGGAUUAGUAUGAAAAUUC	UGAUCUUCAGGUUGAUCCUCAGGA	Cleavage
spe-miR8001a-5p	Sopen08g024690.1	3.0	-1.0	1	24	1490	1513	UCCUGGGGAUUAGUAUGAAAAUUC	GAAAAAUCAUACUAAUCUUUGGGA	Cleavage
spe-miR8001a-5p	Sopen05g005350.1	3.0	-1.0	1	24	2319	2342	UCCUGGGGAUUAGUAUGAAAAUUC	GUCUCUUCAUAUGAAUCUCCGGGA	Cleavage
spe-miR8001a-5p	Sopen08g027820.1	3.0	-1.0	1	24	489	512	UCCUGGGGAUUAGUAUGAAAAUUC	UGGAAUUCGUGAUAGUCCCCAGGA	Cleavage
spe-miR8001b-1-3p	Sopen06g004210.1	3.0	-1.0	1	24	753	776	GGAUUUUCAUACUAAUUCCUAGGA	AAUGAGGAGUUGGUAUGAAGAUAC	Cleavage
spe-miR8001b-1-3p	Sopen06g023760.1	3.0	-1.0	1	24	2138	2161	GGAUUUUCAUACUAAUUCCUAGGA	GGAAAGGGAUUGGUGUGAAAGUUU	Cleavage
spe-miR8001b-2-5p	Sopen04g036630.1	1.5	-1.0	1	24	1135	1158	AUGGGGAUUAGUAUGAAAAUUUGC	GGUUAUUUUCAUGCUGAUCCUCAU	Cleavage
spe-miR8001b-2-5p	Sopen09g033620.1	2.5	-1.0	1	24	836	859	AUGGGGAUUAGUAUGAAAAUUUGC	CAUCAUCUUCAUACUGGUCUCCAU	Cleavage
spe-miR8001b-2-5p	Sopen03g005640.1	2.5	-1.0	1	24	16	39	AUGGGGAUUAGUAUGAAAAUUUGC	UGUUGUUUUCGUACUAAUUCCAAU	Cleavage
spe-miR8001b-2-5p	Sopen01g047170.1	2.5	-1.0	1	24	52	75	AUGGGGAUUAGUAUGAAAAUUUGC	CUCAUUUUUCGUAUUAAUUUCCGU	Cleavage
spe-miR8001b-2-5p	Sopen03g036460.1	2.5	-1.0	1	24	139	162	AUGGGGAUUAGUAUGAAAAUUUGC	CAUCGUUCUCGUACUAAUCCUUAU	Cleavage
spe-miR8001b-2-5p	Sopen08g022600.1	2.5	-1.0	1	24	1138	1161	AUGGGGAUUAGUAUGAAAAUUUGC	GGGUUUUUCCAUGCUGAUCCUCAU	Cleavage
spe-miR8001b-2-5p	Sopen10g027460.1	3.0	-1.0	1	24	1203	1226	AUGGGGAUUAGUAUGAAAAUUUGC	UGCAAUUUUUGUGCUGAUUUCCAU	Cleavage
spe-miR8001b-2-5p	Sopen07g023200.1	3.0	-1.0	1	24	564	587	AUGGGGAUUAGUAUGAAAAUUUGC	ACCAAUUCUUAUAUUAAUCCCCAA	Cleavage
spe-miR8001b-2-5p	Sopen10g032270.1	3.0	-1.0	1	24	970	993	AUGGGGAUUAGUAUGAAAAUUUGC	CUUGAUUUUGAUACUGAUCCACAU	Cleavage
spe-miR8001b-2-5p	Sopen03g012040.1	3.0	-1.0	1	24	327	350	AUGGGGAUUAGUAUGAAAAUUUGC	CUAUCUUUUCGUACUAGUUCCUAA	Cleavage
spe-miR8001b-2-5p	Sopen00g007520.1	3.0	-1.0	1	24	396	419	AUGGGGAUUAGUAUGAAAAUUUGC	CUAUCUUUUCGUACUAGUUCCUAA	Cleavage
spe-miR8005-3p.1	Sopen06g019640.1	3.0	-1.0	1	24	248	271	UUUAGAGUUUAGGGUUUAGGGUUU	GGGCCUUAAAGCCUAAACUCAAAA	Cleavage
spe-miR8005-3p.2	Sopen09g009940.1	3.0	-1.0	1	24	453	476	UUUAGGGUUUAAGGAUUAGGCUUA	CGGUCCUAAUUCUGAAGCUCUAAA	Translation
spe-miR8005-3p.2	Sopen02g024540.1	3.0	-1.0	1	24	25	48	UUUAGGGUUUAAGGAUUAGGCUUA	UUUUCCAAAACCUUAAACCCUAAU	Cleavage
spe-miR8005-5p	Sopen06g019640.1	3.0	-1.0	1	24	248	271	UUUAGAGUUUAGGAUUUAGUGUUU	GGGCCUUAAAGCCUAAACUCAAAA	Cleavage
spe-miR8006-3p	Sopen02g007050.1	3.0	-1.0	1	24	1754	1777	UAGUUUUUGGACGGCAGGGGCACC	AUCGUCUGUGCUGUCCAAGGACUA	Cleavage
spe-miR8006-3p	Sopen02g005040.1	3.0	-1.0	1	24	774	797	UAGUUUUUGGACGGCAGGGGCACC	AUCGACCGUGCUGUCCAAGGGCUA	Cleavage
spe-miR8006-3p	Sopen12g023030.1	2.5	-1.0	1	24	43	66	UAGUUUUUGGACGGCAGGGGCACC	CAACCGCCUAUCGUCCAAAAACUA	Cleavage
spe-miR8006-3p	Sopen06g035070.2	3.0	-1.0	1	24	649	672	UAGUUUUUGGACGGCAGGGGCACC	CUGUUUCUUGACGUCCAAAAACUU	Cleavage
spe-miR8006-3p	Sopen06g035070.1	3.0	-1.0	1	24	649	672	UAGUUUUUGGACGGCAGGGGCACC	CUGUUUCUUGACGUCCAAAAACUU	Cleavage
spe-miR8007a-5p	Sopen06g014220.2	2.0	-1.0	1	24	194	217	AUGUGACACUUUUCGGAUUUCGAG	AUGGAAAUCUGAAAGGUGUUGCAU	Cleavage
spe-miR8007a-5p	Sopen06g014220.1	2.0	-1.0	1	24	914	937	AUGUGACACUUUUCGGAUUUCGAG	AUGGAAAUCUGAAAGGUGUUGCAU	Cleavage
spe-miR8007a-5p	Sopen03g026000.1	2.0	-1.0	1	24	638	661	AUGUGACACUUUUCGGAUUUCGAG	AUGCAAAUUUGAAAGGUGUUACAU	Cleavage
spe-miR8007a-5p	Sopen09g008350.1	2.5	-1.0	1	24	1055	1078	AUGUGACACUUUUCGGAUUUCGAG	AUUGUAAUGCUAAAAGUGUUACAU	Cleavage
spe-miR8007a-5p	Sopen05g002780.1	2.5	-1.0	1	24	84	107	AUGUGACACUUUUCGGAUUUCGAG	ACAUGUAUCUCAAAAGUGUCACAU	Cleavage
spe-miR8007a-5p	Sopen07g025500.1	3.0	-1.0	1	24	580	603	AUGUGACACUUUUCGGAUUUCGAG	CUCGAAAUUCAAAAAGUUUCACAU	Cleavage
spe-miR8007a-5p	Sopen09g024740.1	3.0	-1.0	1	24	918	941	AUGUGACACUUUUCGGAUUUCGAG	CUCAGAAUCCCAAAAGGGUUACAU	Cleavage

spe-miR8007a-5p	Sopen10g023000.1	3.0	-1.0	1	24	4197	4220	AUGUGACACUUUUCGGAUUUCGAG	GACCAGGUCUGGAAGGUGUUACAU	Cleavage
spe-miR8007a-5p	Sopen07g002170.2	3.0	-1.0	1	24	4586	4609	AUGUGACACUUUUCGGAUUUCGAG	CUGGUGAUCUAGGAAGUGUCACAU	Cleavage
spe-miR8007a-5p	Sopen07g002170.1	3.0	-1.0	1	24	4598	4621	AUGUGACACUUUUCGGAUUUCGAG	CUGGUGAUCUAGGAAGUGUCACAU	Cleavage
spe-miR8007a-5p	Sopen05g031870.1	3.0	-1.0	1	24	205	228	AUGUGACACUUUUCGGAUUUCGAG	GGAGUAGUCCGAAAAGUAUCACAA	Cleavage
spe-miR8007a-5p	Sopen05g031870.2	3.0	-1.0	1	24	709	732	AUGUGACACUUUUCGGAUUUCGAG	GGAGUAGUCCGAAAAGUAUCACAA	Cleavage
spe-miR8008-1-3p	Sopen06g017420.1	2.0	-1.0	1	24	2295	2318	AUUUCAAGGAAAGCGACAGACAUU	CUUAUCUGUUGUUUUCCUUGAAAA	Cleavage
spe-miR8008-1-3p	Sopen02g036040.1	2.5	-1.0	1	24	319	342	AUUUCAAGGAAAGCGACAGACAUU	GUCUUCGGUCGCUUUCCUUGGAAA	Cleavage
spe-miR8008-1-3p	Sopen11g029230.1	2.5	-1.0	1	24	774	797	AUUUCAAGGAAAGCGACAGACAUU	AUAUUUUGCUGCUUUUCUUGAAAU	Cleavage
spe-miR8008-1-3p	Sopen09g001990.1	2.5	-1.0	1	24	639	662	AUUUCAAGGAAAGCGACAGACAUU	GUAUUUUGCUGCUUUUCUUGAAAU	Cleavage
spe-miR8008-1-3p	Sopen04g024980.1	3.0	-1.0	1	24	2856	2879	AUUUCAAGGAAAGCGACAGACAUU	UGAAUCUGUUGCUUUCUUUGGAGG	Cleavage
spe-miR8008-1-3p	Sopen11g028080.1	3.0	-1.0	1	24	642	665	AUUUCAAGGAAAGCGACAGACAUU	AGAGACUGUUGCUAUCCUUGAAAG	Translation
spe-miR8008-1-3p	Sopen09g034580.1	3.0	-1.0	1	24	1788	1811	AUUUCAAGGAAAGCGACAGACAUU	AAUCCCUGUAACUUUUCUUGAAGU	Cleavage
spe-miR8008-1-3p	Sopen01g020030.1	3.0	-1.0	1	24	483	506	AUUUCAAGGAAAGCGACAGACAUU	UAUCCCUGUAGCUUUUCUUGAGAA	Cleavage
spe-miR8008-1-5p	Sopen02g024400.1	1.5	-1.0	1	24	1360	1383	AAACCCAGAAAAGCGACGGACAAG	UUUUCCUGUCUCUUUUCUGGGUUU	Cleavage
spe-miR8008-1-5p	Sopen09g029330.1	2.5	-1.0	1	24	6	29	AAACCCAGAAAAGCGACGGACAAG	UUCUUCCGUCGUUUUGUUGGGUUU	Cleavage
spe-miR8008-1-5p	Sopen01g012870.1	2.5	-1.0	1	24	5448	5471	AAACCCAGAAAAGCGACGGACAAG	GGAAAUCGUUGCUUUUCUAGGUUU	Cleavage
spe-miR8008-1-5p	Sopen12g026540.1	3.0	-1.0	1	24	390	413	AAACCCAGAAAAGCGACGGACAAG	UUUCUUCUGCGUUUUUCUGGGUUU	Cleavage
spe-miR8008-2-3p	Sopen06g031040.1	2.5	-1.0	1	24	751	774	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGACAU	Cleavage
spe-miR8008-2-3p	Sopen08g021260.1	2.5	-1.0	1	24	751	774	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGACAU	Cleavage
spe-miR8008-2-3p	Sopen04g028260.1	2.5	-1.0	1	24	751	774	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGACAU	Cleavage
spe-miR8008-2-3p	Sopen04g028260.2	2.5	-1.0	1	24	751	774	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGACAU	Cleavage
spe-miR8008-2-3p	Sopen01g043380.1	2.5	-1.0	1	24	751	774	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGACAU	Cleavage
spe-miR8008-2-3p	Sopen01g023950.1	3.0	-1.0	1	24	123	146	AUUUCCAGAAAAGUGACGGACAGU	AGGGUCUGUUUUUUUUCUGGGAAU	Cleavage
spe-miR8008-2-3p	Sopen09g014070.1	3.0	-1.0	1	24	2750	2773	AUUUCCAGAAAAGUGACGGACAGU	AGUUUACGUCACAUUUCUGGAGAU	Cleavage
spe-miR8008-2-3p	Sopen05g024640.1	3.0	-1.0	1	24	1505	1528	AUUUCCAGAAAAGUGACGGACAGU	AGUUCACGUCACAUUUCUGGAGAU	Cleavage
spe-miR8008-2-3p	Sopen04g029160.1	3.0	-1.0	1	24	459	482	AUUUCCAGAAAAGUGACGGACAGU	AGCGCCCGUUACUCUUUUGGGAAU	Translation
spe-miR8008-2-3p	Sopen03g028430.1	3.0	-1.0	1	24	582	605	AUUUCCAGAAAAGUGACGGACAGU	AGAUCCUGUUGUUUUUCUGGAAAA	Cleavage
spe-miR8008-2-3p	Sopen07g022320.1	3.0	-1.0	1	24	1183	1206	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGGCAU	Cleavage
spe-miR8008-2-3p	Sopen08g007840.1	3.0	-1.0	1	24	772	795	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGGCAU	Cleavage
spe-miR8008-2-3p	Sopen07g006000.1	3.0	-1.0	1	24	772	795	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGGCAU	Cleavage
spe-miR8008-2-3p	Sopen08g029210.1	3.0	-1.0	1	24	772	795	AUUUCCAGAAAAGUGACGGACAGU	GAUUACUGUCAUUUUUCUGGGCAU	Cleavage
spe-miR8008-2-3p	Sopen11g015320.1	3.0	-1.0	1	24	1466	1489	AUUUCCAGAAAAGUGACGGACAGU	AGCACCCUUCACAUUUCUGGAGAU	Cleavage
spe-miR8008-2-3p	Sopen01g008490.1	3.0	-1.0	1	24	58	81	AUUUCCAGAAAAGUGACGGACAGU	AACAACUGUGGCUUUUUUGGAAGU	Cleavage
spe-miR8008-2-5p	Sopen01g012870.1	3.0	-1.0	1	24	5448	5471	AAACUCAGAAAAGCGACGGACAGA	GGAAAUCGUUGCUUUUCUAGGUUU	Cleavage
spe-miR8008-2-5p	Sopen02g024400.1	2.0	-1.0	1	24	1360	1383	AAACUCAGAAAAGCGACGGACAGA	UUUUCCUGUCUCUUUUCUGGGUUU	Cleavage
spe-miR8008-2-5p	Sopen12g032720.1	2.5	-1.0	1	24	30	53	AAACUCAGAAAAGCGACGGACAGA	AAAGUACGAUGCUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen07g016210.1	2.5	-1.0	1	24	1366	1389	AAACUCAGAAAAGCGACGGACAGA	CCUAGCCACCGUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen09g029330.1	3.0	-1.0	1	24	7	29	AAACUCAGAAAAGCGACGGACAGA	UCU-UCCGUCGUUUUGUUGGGUUU	Cleavage
spe-miR8008-2-5p	Sopen12g032710.1	3.0	-1.0	1	24	30	53	AAACUCAGAAAAGCGACGGACAGA	AAAGUACGAUGUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen06g011590.1	3.0	-1.0	1	24	5131	5154	AAACUCAGAAAAGCGACGGACAGA	ACCAGUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen11g019890.1	3.0	-1.0	1	24	808	831	AAACUCAGAAAAGCGACGGACAGA	ACCAGUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen09g016680.1	3.0	-1.0	1	24	3343	3366	AAACUCAGAAAAGCGACGGACAGA	CCCAGUCAUCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen08g007700.1	3.0	-1.0	1	24	511	534	AAACUCAGAAAAGCGACGGACAGA	CCCAGUCAUCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen11g015490.1	3.0	-1.0	1	24	2719	2742	AAACUCAGAAAAGCGACGGACAGA	AACAAUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen11g022820.1	3.0	-1.0	1	24	961	984	AAACUCAGAAAAGCGACGGACAGA	ACCAGUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen07g009150.1	3.0	-1.0	1	24	313	336	AAACUCAGAAAAGCGACGGACAGA	ACCAGUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen03g007080.1	3.0	-1.0	1	24	805	828	AAACUCAGAAAAGCGACGGACAGA	ACCAGUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen12g020040.1	3.0	-1.0	1	24	1065	1088	AAACUCAGAAAAGCGACGGACAGA	ACCCAUCGGCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen10g016920.1	3.0	-1.0	1	24	865	888	AAACUCAGAAAAGCGACGGACAGA	AACAGUCAUCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen07g006830.1	3.0	-1.0	1	24	136	159	AAACUCAGAAAAGCGACGGACAGA	CCCAGUCAUCCUUUUUCUGAGUUU	Cleavage

spe-miR8008-2-5p	Sopen05g016490.1	3.0	-1.0	1	24	706	729	AAACUCAGAAAAGCGACGGACAGA	CCCAGUCAUCCUUUUUCUGAGUUU	Cleavage
spe-miR8008-2-5p	Sopen06g010600.1	3.0	-1.0	1	24	742	765	AAACUCAGAAAAGCGACGGACAGA	CCCAGUCAUCCUUUUUCUGAGUUU	Cleavage
spe-miR8008b-1-5p	Sopen02g024400.1	1.5	-1.0	1	24	1360	1383	AAACCCAGAAAAGCGACGGACAGG	UUUUCCUGUCUCUUUUCUGGGUUU	Cleavage
spe-miR8008b-1-5p	Sopen09g029330.1	2.5	-1.0	1	24	6	29	AAACCCAGAAAAGCGACGGACAGG	UUCUUCCGUCGUUUUGUUGGGUUU	Cleavage
spe-miR8008b-1-5p	Sopen01g012870.1	2.5	-1.0	1	24	5448	5471	AAACCCAGAAAAGCGACGGACAGG	GGAAAUCGUUGCUUUUCUAGGUUU	Cleavage
spe-miR8008b-1-5p	Sopen12g026540.1	3.0	-1.0	1	24	390	413	AAACCCAGAAAAGCGACGGACAGG	UUUCUUCUGCGUUUUUCUGGGUUU	Cleavage
spe-miR8008b-2-5p	Sopen02g024400.1	1.0	-1.0	1	24	1360	1383	AAACCCAGAAAAGCGACAGACUUA	UUUUCCUGUCUCUUUUCUGGGUUU	Cleavage
spe-miR8008b-2-5p	Sopen12g026540.1	2.5	-1.0	1	24	391	413	AAACCCAGAAAAGCGACAGACUUA	UUCUUCUG-CGUUUUUCUGGGUUU	Cleavage
spe-miR8008b-2-5p	Sopen02g023410.1	3.0	-1.0	1	24	2379	2402	AAACCCAGAAAAGCGACAGACUUA	UUUUCUUGUUGCUAUUUUGGGUUU	Translation
spe-miR8008b-2-5p	Sopen06g008670.1	3.0	-1.0	1	24	262	285	AAACCCAGAAAAGCGACAGACUUA	GUUUUCUGGUAUUUUUCUGGGUUU	Cleavage
spe-miR8008b-3-5p	Sopen02g024400.1	1.5	-1.0	1	24	1360	1383	AAACCCAGAAAAGCGACGGACAUU	UUUUCCUGUCUCUUUUCUGGGUUU	Cleavage
spe-miR8008b-3-5p	Sopen09g029330.1	2.5	-1.0	1	24	6	29	AAACCCAGAAAAGCGACGGACAUU	UUCUUCCGUCGUUUUGUUGGGUUU	Cleavage
spe-miR8008b-3-5p	Sopen01g012870.1	2.5	-1.0	1	24	5448	5471	AAACCCAGAAAAGCGACGGACAUU	GGAAAUCGUUGCUUUUCUAGGUUU	Cleavage
spe-miR8008b-3-5p	Sopen12g026540.1	3.0	-1.0	1	24	390	413	AAACCCAGAAAAGCGACGGACAUU	UUUCUUCUGCGUUUUUCUGGGUUU	Cleavage
spe-miR8011-3p	Sopen02g031400.1	2.5	-1.0	1	23	937	959	ACAAAAAGAAGUCUCACACAACU	CUUUGUGUGAGACUUCUUUUAGC	Cleavage
spe-miR8011-3p	Sopen11g005360.1	2.5	-1.0	1	23	451	473	ACAAAAAGAAGUCUCACACAACU	UGUCGUGUGAGACCUCUUUUUGA	Translation
spe-miR8011-3p	Sopen12g002810.1	3.0	-1.0	1	23	2014	2036	ACAAAAAGAAGUCUCACACAACU	AUUCAUGUGGGACUUCUUUGUGU	Cleavage
spe-miR8011-5p	Sopen01g036050.1	2.5	-1.0	1	22	2533	2553	ACUCAUUUUUGUCUCACAAAAA	AGGUUGUG-GAUAAAAAUGAGU	Cleavage
spe-miR8011-5p	Sopen01g036050.2	2.5	-1.0	1	22	1795	1815	ACUCAUUUUUGUCUCACAAAAA	AGGUUGUG-GAUAAAAAUGAGU	Cleavage
spe-miR8011-5p	Sopen06g027730.1	3.0	-1.0	1	22	278	298	ACUCAUUUUUGUCUCACAAAAA	AUUUUGUG-GAUAAAGAUGAGU	Cleavage
spe-miR8011-5p	Sopen06g017590.2	3.0	-1.0	1	22	1507	1528	ACUCAUUUUUGUCUCACAAAAA	AAUUUGUCUGACAAGGAUGAGU	Cleavage
spe-miR8011-5p	Sopen06g017590.1	3.0	-1.0	1	22	1504	1525	ACUCAUUUUUGUCUCACAAAAA	AAUUUGUCUGACAAGGAUGAGU	Cleavage
spe-miR8011-5p	Sopen03g028960.1	3.0	-1.0	1	22	1438	1459	ACUCAUUUUUGUCUCACAAAAA	GUGUUGGGGGACAAAAGUGAGC	Cleavage
spe-miR8011-5p	Sopen05g008660.1	3.0	-1.0	1	22	1439	1460	ACUCAUUUUUGUCUCACAAAAA	AUCGUGAGAGACAGAAAUGGGU	Cleavage
spe-miR8011-5p	Sopen06g032620.1	3.0	-1.0	1	22	4078	4099	ACUCAUUUUUGUCUCACAAAAA	CAAUUGUGUGACAAAGAUGAUU	Cleavage
spe-miR8011a-1-3p	Sopen07g029080.1	2.5	-1.0	1	24	1592	1615	AAUAAAAAGAAGUCUCACGCAACU	AGUCUUGUGAGAUUUGUUUUUAUU	Cleavage
spe-miR8011a-1-3p	Sopen07g031980.1	2.5	-1.0	1	24	1592	1615	AAUAAAAAGAAGUCUCACGCAACU	AGUCUUGUGAGAUUUGUUUUUAUU	Cleavage
spe-miR8011a-1-3p	Sopen01g027350.1	2.5	-1.0	1	24	1592	1615	AAUAAAAAGAAGUCUCACGCAACU	AGUCUUGUGAGAUUUGUUUUUAUU	Cleavage
spe-miR8011a-1-3p	Sopen02g011330.1	3.0	-1.0	1	24	953	976	AAUAAAAAGAAGUCUCACGCAACU	CCUUGUUAGAGGCUUCUUUUUAUU	Cleavage
spe-miR8011a-1-3p	Sopen11g005840.1	3.0	-1.0	1	24	557	580	AAUAAAAAGAAGUCUCACGCAACU	AAUUACGUGAGACUUCUUUAUCUU	Cleavage
spe-miR8011a-1-3p	Sopen07g007410.1	3.0	-1.0	1	24	812	835	AAUAAAAAGAAGUCUCACGCAACU	AAAUUUGUGAGGUUUCUUGUUAUU	Cleavage
spe-miR8011a-1-3p	Sopen08g019750.1	3.0	-1.0	1	24	1211	1234	AAUAAAAAGAAGUCUCACGCAACU	AAAUUUGUGAGGUUUCUUGUUAUU	Cleavage
spe-miR8011a-1-	Sopen06g033490.1	3.0	-1.0	1	24	1906	1929	AAUAAAAAGAAGUCUCACGCAACU	CAGCUUGUGAAACUUCUUAUUAUU	Cleavage

3p										
spe-miR8011a-1-5p	Sopen06g033450.1	2.5	-1.0	1	24	2528	2551	UUGUGUGAGGUCUCUUUUUGUUUU	CUUGCAGAGGGAGACCUCGUACAA	Cleavage
spe-miR8011a-1-5p	Sopen06g033450.1	3.0	-1.0	1	24	1256	1279	UUGUGUGAGGUCUCUUUUUGUUUU	CUUGCAGAGGGAGAUCUCGUACAA	Cleavage
spe-miR8011a-1-5p	Sopen06g033450.1	3.0	-1.0	1	24	1892	1915	UUGUGUGAGGUCUCUUUUUGUUUU	CUUGCAGAGGGAGAUCUCGUACAA	Cleavage
spe-miR8011a-1-5p	Sopen07g009900.1	1.5	-1.0	1	24	1425	1448	UUGUGUGAGGUCUCUUUUUGUUUU	UUCUCAAGAAGAGACUUCAUACAA	Cleavage
spe-miR8011a-1-5p	Sopen06g020910.1	2.5	-1.0	1	24	995	1018	UUGUGUGAGGUCUCUUUUUGUUUU	AAGGAGAAGAGAGACCUUACAUGA	Cleavage
spe-miR8011a-1-5p	Sopen10g017620.1	2.5	-1.0	1	24	646	669	UUGUGUGAGGUCUCUUUUUGUUUU	AACGAGAAAAGAGAGCUCAUACAA	Translation
spe-miR8011a-1-5p	Sopen03g029250.1	2.5	-1.0	1	24	498	521	UUGUGUGAGGUCUCUUUUUGUUUU	GGGGGAAGAAGAGACUACACACAA	Cleavage
spe-miR8011a-1-5p	Sopen02g021060.1	3.0	-1.0	1	24	190	213	UUGUGUGAGGUCUCUUUUUGUUUU	GAGGCAGAAAUAGGCCUUGCACAA	Cleavage
spe-miR8011a-1-5p	Sopen10g002310.1	3.0	-1.0	1	24	368	391	UUGUGUGAGGUCUCUUUUUGUUUU	CUGACAGAAAGGGACCUUACAUGG	Cleavage
spe-miR8011a-1-5p	Sopen09g005200.1	3.0	-1.0	1	24	2556	2579	UUGUGUGAGGUCUCUUUUUGUUUU	GGAAAAAGAAGAGAUCUUGCGCAG	Cleavage
spe-miR8011a-1-5p	Sopen01g040630.1	3.0	-1.0	1	24	1259	1282	UUGUGUGAGGUCUCUUUUUGUUUU	UGGAGAAAAAGAGACCUCUCAUGG	Cleavage
spe-miR8011a-1-5p	Sopen01g040630.3	3.0	-1.0	1	24	1259	1282	UUGUGUGAGGUCUCUUUUUGUUUU	UGGAGAAAAAGAGACCUCUCAUGG	Cleavage
spe-miR8011a-1-5p	Sopen01g040630.2	3.0	-1.0	1	24	1250	1273	UUGUGUGAGGUCUCUUUUUGUUUU	UGGAGAAAAAGAGACCUCUCAUGG	Cleavage
spe-miR8011a-2-3p	Sopen07g007410.1	2.0	-1.0	1	24	812	835	AAUAAAAAGAAGCCUCACAGAACU	AAAUUUGUGAGGUUUCUUGUUAUU	Cleavage
spe-miR8011a-2-3p	Sopen08g019750.1	2.0	-1.0	1	24	1211	1234	AAUAAAAAGAAGCCUCACAGAACU	AAAUUUGUGAGGUUUCUUGUUAUU	Cleavage
spe-miR8011a-2-3p	Sopen02g011330.1	2.0	-1.0	1	24	953	976	AAUAAAAAGAAGCCUCACAGAACU	CCUUGUUAGAGGCUUCUUUUUAUU	Cleavage
spe-miR8013-3p	Sopen06g031860.1	3.0	-1.0	1	24	503	526	AGAAGAAAAUCGCUUCGUCAGGAG	AAAAAGAUGAAGGGAUUUUCUUCA	Cleavage
spe-miR8013-3p	Sopen03g038560.1	2.0	-1.0	1	24	511	534	AGAAGAAAAUCGCUUCGUCAGGAG	AAAGUGGUGAAGUGGUUUUCUUCU	Cleavage
spe-miR8013-3p	Sopen04g025150.2	2.5	-1.0	1	24	2793	2816	AGAAGAAAAUCGCUUCGUCAGGAG	GAAGGGAAGAAGAGAUUUUCUUCU	Cleavage
spe-miR8013-3p	Sopen04g025150.1	2.5	-1.0	1	24	2814	2837	AGAAGAAAAUCGCUUCGUCAGGAG	GAAGGGAAGAAGAGAUUUUCUUCU	Cleavage
spe-miR8013-3p	Sopen05g031930.1	3.0	-1.0	1	24	239	262	AGAAGAAAAUCGCUUCGUCAGGAG	GUCAUGGAGAAGCGGUUUUCUUCC	Cleavage
spe-miR8013-3p	Sopen04g012040.3	3.0	-1.0	1	24	2183	2206	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen06g014210.1	3.0	-1.0	1	24	2627	2650	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen02g006340.1	3.0	-1.0	1	24	3011	3034	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen06g012790.1	3.0	-1.0	1	24	3089	3112	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen01g022020.1	3.0	-1.0	1	24	3703	3726	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen07g004910.1	3.0	-1.0	1	24	3815	3838	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen04g012040.2	3.0	-1.0	1	24	3908	3931	AGAAGAAAAUCGCUUCGUCAGGAG	UUGAUGAUGAAGAGAUUUUUUUUU	Cleavage
spe-miR8013-3p	Sopen10g034410.1	3.0	-1.0	1	24	437	460	AGAAGAAAAUCGCUUCGUCAGGAG	AUGUCCACGAGGUGAUUUUCUUCC	Cleavage
spe-miR8013-3p	Sopen06g031830.2	3.0	-1.0	1	24	410	433	AGAAGAAAAUCGCUUCGUCAGGAG	CAAAUCACCAAGCGAUUUUCUUCA	Cleavage
spe-miR8013-3p	Sopen06g031830.1	3.0	-1.0	1	24	410	433	AGAAGAAAAUCGCUUCGUCAGGAG	CAAAUCACCAAGCGAUUUUCUUCA	Cleavage
spe-miR8013-3p	Sopen09g007710.1	3.0	-1.0	1	24	227	250	AGAAGAAAAUCGCUUCGUCAGGAG	UAGGAGUCGGAGCGAUUUGCUUCU	Cleavage
spe-miR8013-3p	Sopen03g003690.1	3.0	-1.0	1	24	1169	1192	AGAAGAAAAUCGCUUCGUCAGGAG	UUAAAGAAGGACCGAUUUUCUUCU	Cleavage
spe-miR8016-3p	Sopen01g053980.1	2.5	-1.0	1	24	524	547	AUUUUUGAAUGGAAGGCCCAUGUG	AGCUUGUGCCUUCCAUUCAACAAU	Cleavage

spe-miR8016-3p	Sopen06g027450.1	3.0	-1.0	1	24	1525	1548	AUUUUUGAAUGGAAGGCCCAUGUG	ACCAUGGGCCUUCCAUUUACAGGU	Cleavage
spe-miR8016-3p	Sopen04g031030.1	3.0	-1.0	1	24	469	493	AUUUUUGAAUGGAAGGCCCA-UGUG	CACAAUGGGCGUUUCAUUCAAAGAA	Cleavage
spe-miR8016-3p	Sopen01g037560.1	3.0	-1.0	1	24	655	678	AUUUUUGAAUGGAAGGCCCAUGUG	AACCUGGGACCUUUAUUCAAAAAU	Cleavage
spe-miR8016-3p	Sopen09g028930.1	3.0	-1.0	1	24	5311	5334	AUUUUUGAAUGGAAGGCCCAUGUG	AAGCUCUUCCUUCCAUUCAAAAAU	Cleavage
spe-miR8016-3p	Sopen01g026050.1	3.0	-1.0	1	24	1722	1745	AUUUUUGAAUGGAAGGCCCAUGUG	AGCAAGGAAUUUCCAUUUAAAAAU	Cleavage
spe-miR8016-3p	Sopen05g034220.1	3.0	-1.0	1	24	619	642	AUUUUUGAAUGGAAGGCCCAUGUG	CUUAAAGGCCUUCAAUUCAAGAAU	Translation
spe-miR8016-3p	Sopen05g034880.1	3.0	-1.0	1	24	566	589	AUUUUUGAAUGGAAGGCCCAUGUG	GGAGAGGGUUUACCAUUCAAGAAU	Cleavage
spe-miR8016-3p	Sopen09g028250.1	3.0	-1.0	1	24	773	796	AUUUUUGAAUGGAAGGCCCAUGUG	AUGAGAAGGCUUCCAUUCAAAAAU	Cleavage
spe-miR8019	Sopen00g003330.1	2.0	-1.0	1	24	512	535	UAAAGAAUGACCUGGUUUGAGUUG	GAAAACAAAUCAGAUCAUUCUUUA	Translation
spe-miR8019	Sopen05g022460.1	2.0	-1.0	1	24	1268	1291	UAAAGAAUGACCUGGUUUGAGUUG	AAAAACAAAUCAGAUCAUUCUUUA	Translation
spe-miR8019	Sopen05g011230.1	3.0	-1.0	1	24	3203	3226	UAAAGAAUGACCUGGUUUGAGUUG	GAAAACAAACCAGAUCAUCCUUUA	Translation
spe-miR8019	Sopen10g018640.1	3.0	-1.0	1	24	203	226	UAAAGAAUGACCUGGUUUGAGUUG	GGAAACAAACCAGAUCAUUAUUUA	Translation
spe-miR8019	Sopen07g024460.1	3.0	-1.0	1	24	529	552	UAAAGAAUGACCUGGUUUGAGUUG	AUUCCCACACCAGGCCAUUCUUUG	Translation
spe-miR8020-5p	Sopen02g018690.1	3.0	-1.0	1	24	361	384	AAUUUCAUUGAGUAUGUUGUUGUU	UCGCGUGAUCUAUUCAAUGAAAUU	Cleavage
spe-miR8020-5p	Sopen04g014310.1	2.0	-1.0	1	24	71	94	AAUUUCAUUGAGUAUGUUGUUGUU	UGGAACAACAUAUUCAAUGGAAUC	Cleavage
spe-miR8020-5p	Sopen03g034790.1	2.0	-1.0	1	24	1324	1347	AAUUUCAUUGAGUAUGUUGUUGUU	GAGUCCAAUGUACUUAAUGAAGUU	Cleavage
spe-miR8020-5p	Sopen06g016060.1	2.5	-1.0	1	24	478	501	AAUUUCAUUGAGUAUGUUGUUGUU	GAGAAUAAUAUAUUCAAUGAAAUG	Cleavage
spe-miR8020-5p	Sopen10g011800.1	2.5	-1.0	1	24	760	783	AAUUUCAUUGAGUAUGUUGUUGUU	GAGGAUAAUAUAUUCAAUGAAAUG	Cleavage
spe-miR8020-5p	Sopen09g027820.3	2.5	-1.0	1	24	1138	1161	AAUUUCAUUGAGUAUGUUGUUGUU	UCAUAUGAUAUAUUCAAUGAGAUU	Cleavage
spe-miR8020-5p	Sopen09g027790.1	2.5	-1.0	1	24	109	132	AAUUUCAUUGAGUAUGUUGUUGUU	UCAUAUGAUAUAUUCAAUGAGAUU	Cleavage
spe-miR8020-5p	Sopen02g005140.1	2.5	-1.0	1	24	994	1017	AAUUUCAUUGAGUAUGUUGUUGUU	GAGGCCAAUGUAUUCAAUGAAAUG	Cleavage
spe-miR8020-5p	Sopen04g021990.1	3.0	-1.0	1	24	808	831	AAUUUCAUUGAGUAUGUUGUUGUU	GAGAAUAAUAUAUUUAAUGAAAUG	Cleavage
spe-miR8020-5p	Sopen10g020240.1	3.0	-1.0	1	24	727	750	AAUUUCAUUGAGUAUGUUGUUGUU	GAAGAUAAUGUAUUCAAUGAAAUG	Cleavage
spe-miR8020-5p	Sopen12g018410.1	3.0	-1.0	1	24	202	225	AAUUUCAUUGAGUAUGUUGUUGUU	UACGCCAACGUGUUCAAUGGAAUG	Cleavage
spe-miR8020-5p	Sopen03g024560.1	3.0	-1.0	1	23	1	23	AAUUUCAUUGAGUAUGUUGUUGU	AUGGCAAGAUAUUCAAGGAAAUU	Cleavage
spe-miR8020-5p	Sopen10g001380.1	3.0	-1.0	1	24	262	285	AAUUUCAUUGAGUAUGUUGUUGUU	GGUGAAUACAUACUUGAUGAAAUU	Cleavage
spe-miR8020-5p	Sopen05g006140.1	3.0	-1.0	1	24	70	93	AAUUUCAUUGAGUAUGUUGUUGUU	CCUGAGAAUGUACUUGAUGAAAUU	Cleavage
spe-miR8020-5p	Sopen03g019320.1	3.0	-1.0	1	24	580	603	AAUUUCAUUGAGUAUGUUGUUGUU	GCGGAAAAUAUAUUCAAUGAAAUG	Cleavage
spe-miR8020-5p	Sopen08g001430.1	3.0	-1.0	1	24	1509	1533	AAUUUCAUUGAGUAUGUUGU-UGUU	AAUACAUAAAAUACUUGAUGAGAUU	Cleavage
spe-miR8020-5p	Sopen09g002540.1	3.0	-1.0	1	24	160	183	AAUUUCAUUGAGUAUGUUGU-UGUU	AACACACAACA-ACUCAAUGAAAUC	Cleavage
spe-miR8020-5p	Sopen01g048360.1	3.0	-1.0	1	24	199	222	AAUUUCAUUGAGUAUGUUGUUGUU	GGAUAUGACGUAUUCGAUGGAAUU	Cleavage
spe-miR8020-5p	Sopen02g029660.1	3.0	-1.0	1	24	532	558	AAUUUCAUUGAGUAUGUUGU---UGUU	AACAGAUACAACAGAUUCAGUGGAGUU	Cleavage
spe-miR8020-5p	Sopen06g017670.2	3.0	-1.0	1	24	776	799	AAUUUCAUUGAGUAUGUUGUUGUU	ACCAUCGACAAAUUCAAUGGGAUU	Cleavage
spe-miR8020-5p	Sopen06g017670.1	3.0	-1.0	1	24	746	769	AAUUUCAUUGAGUAUGUUGUUGUU	ACCAUCGACAAAUUCAAUGGGAUU	Cleavage
spe-miR8021-5p	Sopen12g020880.1	3.0	-1.0	1	24	2373	2396	AUUCAAGGCUCAAACUCGAGACCU	AGGUAUCGAGUUUGAUCCUUCAAU	Cleavage
spe-miR8021-5p	Sopen01g024850.1	3.0	-1.0	1	24	491	514	AUUCAAGGCUCAAACUCGAGACCU	UCAUAUCGAGUUUGGGCAUUGGGU	Cleavage
spe-miR8021-5p	Sopen03g022890.1	3.0	-1.0	1	24	1205	1228	AUUCAAGGCUCAAACUCGAGACCU	CACACUGUGGUUUGGGCCUUGAAU	Cleavage
spe-miR8021-5p	Sopen06g031810.1	3.0	-1.0	1	24	2170	2193	AUUCAAGGCUCAAACUCGAGACCU	UACCUUCGGCUUUGGGCUUUGAGU	Cleavage
spe-miR8024-3p	Sopen04g007800.2	2.0	-1.0	1	24	1805	1828	UUGGAGGAUUUGAAGACUUCAACU	AACCUAAGACUUCAAGUUCUCCAA	Cleavage
spe-miR8024-3p	Sopen04g007800.2	2.0	-1.0	1	24	2279	2302	UUGGAGGAUUUGAAGACUUCAACU	AACCUAAGACUUCAAGUUCUCCAA	Cleavage
spe-miR8024-3p	Sopen12g020090.1	1.5	-1.0	1	24	1218	1241	UUGGAGGAUUUGAAGACUUCAACU	CAAUGAAGUCGUCAAAUCCUUCAA	Cleavage
spe-miR8024-3p	Sopen03g006100.1	2.0	-1.0	1	24	484	507	UUGGAGGAUUUGAAGACUUCAACU	GGUGAAGGUCUUCAAAUUCUCCAU	Cleavage
spe-miR8024-3p	Sopen04g007800.1	2.0	-1.0	1	24	1805	1828	UUGGAGGAUUUGAAGACUUCAACU	AACCUAAGACUUCAAGUUCUCCAA	Cleavage
spe-miR8024-3p	Sopen11g014030.1	2.5	-1.0	1	24	456	479	UUGGAGGAUUUGAAGACUUCAACU	UUUGGAAAUCUUUAAGUUCUCCAA	Cleavage
spe-miR8024-3p	Sopen10g003050.1	2.5	-1.0	1	24	1427	1450	UUGGAGGAUUUGAAGACUUCAACU	CUGCGAAGCCUUCAGGUCCUUCAA	Cleavage
spe-miR8024-3p	Sopen08g018650.1	2.5	-1.0	1	24	507	530	UUGGAGGAUUUGAAGACUUCAACU	GGCAGAAGCCUUCAAAUCCUUUGA	Cleavage
spe-miR8024-3p	Sopen03g038480.1	2.5	-1.0	1	24	397	420	UUGGAGGAUUUGAAGACUUCAACU	UCUCCCAGUUUUCAAAUCCUUCGA	Cleavage
spe-miR8024-3p	Sopen03g038480.2	2.5	-1.0	1	24	397	420	UUGGAGGAUUUGAAGACUUCAACU	UCUCCCAGUUUUCAAAUCCUUCGA	Cleavage
spe-miR8024-3p	Sopen04g004270.1	2.5	-1.0	1	24	1936	1959	UUGGAGGAUUUGAAGACUUCAACU	CUCACUAGUCUUCAAGUUCUUCAA	Cleavage
spe-miR8024-3p	Sopen09g014590.1	2.5	-1.0	1	24	3560	3583	UUGGAGGAUUUGAAGACUUCAACU	AUGAUGAGUCUUUGGAUCCUCCGA	Cleavage

spe-miR8024-3p	Sopen12g025220.1	3.0	-1.0	1	24	3410	3433	UUGGAGGAUUUGAAGACUUCAACU	GGUUGAAGUAUUCAAAUACUCUAA	Cleavage
spe-miR8024-3p	Sopen12g013080.1	3.0	-1.0	1	24	13	36	UUGGAGGAUUUGAAGACUUCAACU	ACCAGAGGUCUUCAAGUUCUCUAU	Cleavage
spe-miR8024-3p	Sopen08g006380.1	3.0	-1.0	1	24	326	349	UUGGAGGAUUUGAAGACUUCAACU	AGCUUAAGGUUUCAAAUCCUUCAU	Cleavage
spe-miR8024-3p	Sopen05g015140.2	3.0	-1.0	1	24	719	742	UUGGAGGAUUUGAAGACUUCAACU	AAGGGAGGUUUGCAGAUCCUCCAA	Cleavage
spe-miR8024-3p	Sopen05g015140.4	3.0	-1.0	1	24	638	661	UUGGAGGAUUUGAAGACUUCAACU	AAGGGAGGUUUGCAGAUCCUCCAA	Cleavage
spe-miR8024-3p	Sopen05g015140.3	3.0	-1.0	1	24	635	658	UUGGAGGAUUUGAAGACUUCAACU	AAGGGAGGUUUGCAGAUCCUCCAA	Cleavage
spe-miR8024-3p	Sopen02g034050.1	3.0	-1.0	1	24	10831	10854	UUGGAGGAUUUGAAGACUUCAACU	AGUAAGAGUGUUCAAACCCUCCAA	Cleavage
spe-miR8024-3p	Sopen09g031730.1	3.0	-1.0	1	24	1491	1514	UUGGAGGAUUUGAAGACUUCAACU	AGGUAGUGUUUUCAAGUCCUCCGA	Cleavage
spe-miR8024-3p	Sopen09g031720.1	3.0	-1.0	1	24	1455	1478	UUGGAGGAUUUGAAGACUUCAACU	AGGUAGUGUUUUCAAGUCCUCCGA	Cleavage
spe-miR8024-3p	Sopen11g001160.1	3.0	-1.0	1	24	320	343	UUGGAGGAUUUGAAGACUUCAACU	AAUUUAAGAUUUUGAAUCCUCUAA	Cleavage
spe-miR8024-3p	Sopen07g006580.1	3.0	-1.0	1	24	206	229	UUGGAGGAUUUGAAGACUUCAACU	AUGUUUCAUCUUCAAAUCCUCCAA	Cleavage
spe-miR8024-3p	Sopen09g030530.1	3.0	-1.0	1	24	618	641	UUGGAGGAUUUGAAGACUUCAACU	CUUUAGAGAUUUCAAAUCUUCUAA	Cleavage
spe-miR8024-3p	Sopen05g008590.1	3.0	-1.0	1	24	1073	1096	UUGGAGGAUUUGAAGACUUCAACU	ACGGCUCGUUUUCAGAUCCUCCAA	Cleavage
spe-miR8024-3p	Sopen00g003220.1	3.0	-1.0	1	24	527	550	UUGGAGGAUUUGAAGACUUCAACU	AUAUUAAGUCUUCGAAUAUUCUAA	Cleavage
spe-miR8024-5p.1	Sopen05g023250.2	2.0	-1.0	1	24	960	983	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen04g025080.1	2.5	-1.0	1	24	42	65	UUGGAGUAUUUGAAGACUUUAGCU	UGUUGAGGUCAUCAAAUACUUCAG	Cleavage
spe-miR8024-5p.1	Sopen04g025080.1	2.5	-1.0	1	24	498	521	UUGGAGUAUUUGAAGACUUUAGCU	UGUUGAGGUCAUCAAAUACUUCAG	Cleavage
spe-miR8024-5p.1	Sopen08g017350.1	2.5	-1.0	1	24	6393	6416	UUGGAGUAUUUGAAGACUUUAGCU	GGAAGAAGUCAUUAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen08g017350.1	3.0	-1.0	1	24	7608	7631	UUGGAGUAUUUGAAGACUUUAGCU	GGAAGAAGUCAUUGAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen12g025220.1	1.5	-1.0	1	24	3410	3433	UUGGAGUAUUUGAAGACUUUAGCU	GGUUGAAGUAUUCAAAUACUCUAA	Cleavage
spe-miR8024-5p.1	Sopen00g003220.1	1.5	-1.0	1	24	527	550	UUGGAGUAUUUGAAGACUUUAGCU	AUAUUAAGUCUUCGAAUAUUCUAA	Cleavage
spe-miR8024-5p.1	Sopen05g011210.1	2.0	-1.0	1	24	1128	1151	UUGGAGUAUUUGAAGACUUUAGCU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen06g014220.2	2.0	-1.0	1	24	2028	2051	UUGGAGUAUUUGAAGACUUUAGCU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen06g014220.1	2.0	-1.0	1	24	2748	2771	UUGGAGUAUUUGAAGACUUUAGCU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen05g026130.2	2.0	-1.0	1	24	21	44	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen06g011480.1	2.0	-1.0	1	24	888	911	UUGGAGUAUUUGAAGACUUUAGCU	UACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen01g022390.1	2.0	-1.0	1	24	1155	1178	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen00g008330.1	2.0	-1.0	1	24	1152	1175	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen10g011960.1	2.0	-1.0	1	24	1170	1193	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen03g026040.1	2.0	-1.0	1	24	1446	1469	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen02g010050.1	2.0	-1.0	1	24	1653	1676	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen11g011880.1	2.0	-1.0	1	24	2238	2261	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen05g026130.1	2.0	-1.0	1	24	2703	2726	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen05g023250.1	2.0	-1.0	1	24	3201	3224	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen05g013910.1	2.0	-1.0	1	24	3414	3437	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen06g011460.1	2.0	-1.0	1	24	3504	3527	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen04g023980.1	2.0	-1.0	1	24	216	239	UUGGAGUAUUUGAAGACUUUAGCU	CAGUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen01g012780.1	2.0	-1.0	1	24	1230	1253	UUGGAGUAUUUGAAGACUUUAGCU	CAGUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen01g041600.1	2.0	-1.0	1	24	428	451	UUGGAGUAUUUGAAGACUUUAGCU	AUUCUAGUUCUUCAAAUGCUCCAA	Cleavage
spe-miR8024-5p.1	Sopen01g041610.1	2.0	-1.0	1	24	428	451	UUGGAGUAUUUGAAGACUUUAGCU	AUUCUAGUUCUUCAAAUGCUCCAA	Cleavage
spe-miR8024-5p.1	Sopen01g053050.1	2.5	-1.0	1	24	26	49	UUGGAGUAUUUGAAGACUUUAGCU	UCAAGAAGUCUUCAGAUAUUCCCA	Cleavage
spe-miR8024-5p.1	Sopen12g024200.1	2.5	-1.0	1	24	704	727	UUGGAGUAUUUGAAGACUUUAGCU	GGAAGAAGUCUUCAGAUGUUUCAG	Cleavage
spe-miR8024-5p.1	Sopen12g028710.1	2.5	-1.0	1	24	176	199	UUGGAGUAUUUGAAGACUUUAGCU	CAACAAUCUCUUCAAAUACUUCAA	Cleavage
spe-miR8024-5p.1	Sopen06g013860.1	3.0	-1.0	1	24	144	167	UUGGAGUAUUUGAAGACUUUAGCU	AGCCAAGGUCAUCAAAUACUGCAA	Cleavage
spe-miR8024-5p.1	Sopen03g006100.1	3.0	-1.0	1	24	484	507	UUGGAGUAUUUGAAGACUUUAGCU	GGUGAAGGUCUUCAAAUUCUCCAU	Cleavage
spe-miR8024-5p.1	Sopen04g013960.1	3.0	-1.0	1	24	1362	1385	UUGGAGUAUUUGAAGACUUUAGCU	UACUGAAGUAUUCAAACACUUCAA	Cleavage
spe-miR8024-5p.1	Sopen03g019980.1	3.0	-1.0	1	24	2733	2756	UUGGAGUAUUUGAAGACUUUAGCU	CACUAAAAUAUUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen01g012140.1	3.0	-1.0	1	24	906	929	UUGGAGUAUUUGAAGACUUUAGCU	CACUGAAGUACUCAAAUACUUUAA	Cleavage
spe-miR8024-5p.1	Sopen07g003790.1	3.0	-1.0	1	24	911	934	UUGGAGUAUUUGAAGACUUUAGCU	GCUUGAAAUCUUCAAAUGAUCCAA	Cleavage
spe-miR8024-5p.1	Sopen12g020090.1	3.0	-1.0	1	24	1218	1241	UUGGAGUAUUUGAAGACUUUAGCU	CAAUGAAGUCGUCAAAUCCUUCAA	Cleavage

spe-miR8024-5p.1	Sopen04g025090.1	3.0	-1.0	1	24	261	284	UUGGAGUAUUUGAAGACUUUAGCU	UGUCGAGGUCAUCAAAUACUUCAC	Cleavage
spe-miR8024-5p.1	Sopen03g032440.1	3.0	-1.0	1	24	950	973	UUGGAGUAUUUGAAGACUUUAGCU	CCAAAAAGGCUUCAAAUGUUCCAC	Cleavage
spe-miR8024-5p.1	Sopen07g027010.1	3.0	-1.0	1	24	38	61	UUGGAGUAUUUGAAGACUUUAGCU	CAGAGGAGUUUUCAAAUAAUCCAG	Cleavage
spe-miR8024-5p.1	Sopen05g033120.1	3.0	-1.0	1	24	1355	1378	UUGGAGUAUUUGAAGACUUUAGCU	UUGCAAAGGCUUUGGAUAUUCCAA	Cleavage
spe-miR8024-5p.1	Sopen05g034750.1	3.0	-1.0	1	24	711	734	UUGGAGUAUUUGAAGACUUUAGCU	UAGGAAAGUUCUCAGGUACUUCAA	Cleavage
spe-miR8024-5p.1	Sopen06g002000.1	3.0	-1.0	1	24	887	910	UUGGAGUAUUUGAAGACUUUAGCU	AGAACAAGUUUUCAGGUACUCUAC	Cleavage
spe-miR8024-5p.2	Sopen09g025680.1	3.0	-1.0	1	24	596	619	UUGGAGGAUUUAAAGACUUCAGCU	AAUUGAAGUUUUUAGGUCUUUCAG	Cleavage
spe-miR8024-5p.2	Sopen11g014030.1	2.0	-1.0	1	24	456	479	UUGGAGGAUUUAAAGACUUCAGCU	UUUGGAAAUCUUUAAGUUCUCCAA	Cleavage
spe-miR8024-5p.2	Sopen09g014590.1	2.0	-1.0	1	24	3560	3583	UUGGAGGAUUUAAAGACUUCAGCU	AUGAUGAGUCUUUGGAUCCUCCGA	Cleavage
spe-miR8024-5p.2	Sopen11g001160.1	2.5	-1.0	1	24	320	343	UUGGAGGAUUUAAAGACUUCAGCU	AAUUUAAGAUUUUGAAUCCUCUAA	Cleavage
spe-miR8024-5p.2	Sopen09g022470.1	3.0	-1.0	1	24	543	566	UUGGAGGAUUUAAAGACUUCAGCU	UGUUGAAGAUUUUAAGUUCUUCAA	Cleavage
spe-miR8024-5p.2	Sopen08g028750.1	3.0	-1.0	1	24	954	977	UUGGAGGAUUUAAAGACUUCAGCU	UGCCGAGGUCUUUGAAUUUUUCAG	Cleavage
spe-miR8024-5p.2	Sopen01g004760.1	3.0	-1.0	1	24	932	955	UUGGAGGAUUUAAAGACUUCAGCU	UGAUGAAGUUGUUAGAUUCUCCAG	Cleavage
spe-miR8024-5p.2	Sopen12g020090.1	3.0	-1.0	1	24	1218	1241	UUGGAGGAUUUAAAGACUUCAGCU	CAAUGAAGUCGUCAAAUCCUUCAA	Cleavage
spe-miR8024-5p.2	Sopen04g007450.1	3.0	-1.0	1	24	198	221	UUGGAGGAUUUAAAGACUUCAGCU	GCUUGCAUUCUUUAAAUCUUCUAA	Cleavage
spe-miR8024-5p.2	Sopen04g007480.1	3.0	-1.0	1	24	189	212	UUGGAGGAUUUAAAGACUUCAGCU	GCUUGCAUUCUUUAAAUCUUCUAA	Cleavage
spe-miR8024-5p.2	Sopen04g007460.1	3.0	-1.0	1	24	180	203	UUGGAGGAUUUAAAGACUUCAGCU	GAUUGCAUUCUUUAAAUCUUCUAA	Cleavage
spe-miR8024-5p.2	Sopen04g031570.1	3.0	-1.0	1	24	6	28	UUGGAGGAUUUAAAGACUUCAGCU	ACUUGAAG-CUUUGAAUUCUCCAA	Cleavage
spe-miR8024-5p.2	Sopen12g004840.1	3.0	-1.0	1	24	221	244	UUGGAGGAUUUAAAGACUUCAGCU	AAUCGAAGUCCUUAACUCCUCUAA	Cleavage
spe-miR8024-5p.2	Sopen06g031880.1	3.0	-1.0	1	24	991	1014	UUGGAGGAUUUAAAGACUUCAGCU	CAAUUAAGUUUUUCAGUCCUUCAA	Translation
spe-miR8024a-3p.1	Sopen10g002900.1	2.0	-1.0	1	24	474	497	UUGAAUGAUUUGAAGACUUCAUCU	GCCAGAGGUCUUUGGAUCAUUCAA	Cleavage
spe-miR8024a-3p.1	Sopen12g020090.1	2.5	-1.0	1	24	1218	1241	UUGAAUGAUUUGAAGACUUCAUCU	CAAUGAAGUCGUCAAAUCCUUCAA	Cleavage
spe-miR8024a-3p.2	Sopen05g032510.1	3.0	-1.0	1	24	3127	3150	UUGGAGGAUUUGAAGAUUUCAACU	UUUCCUAAUCUUAAAAUCCUUCAA	Cleavage
spe-miR8024a-3p.2	Sopen11g014030.1	1.5	-1.0	1	24	456	479	UUGGAGGAUUUGAAGAUUUCAACU	UUUGGAAAUCUUUAAGUUCUCCAA	Cleavage
spe-miR8024a-3p.2	Sopen12g020090.1	2.0	-1.0	1	24	1218	1241	UUGGAGGAUUUGAAGAUUUCAACU	CAAUGAAGUCGUCAAAUCCUUCAA	Cleavage
spe-miR8024a-3p.2	Sopen07g006580.1	2.0	-1.0	1	24	206	229	UUGGAGGAUUUGAAGAUUUCAACU	AUGUUUCAUCUUCAAAUCCUCCAA	Cleavage
spe-miR8024a-3p.2	Sopen06g024840.1	2.0	-1.0	1	24	836	859	UUGGAGGAUUUGAAGAUUUCAACU	AGGACAAAUCUUCAGAUUCUUCAG	Cleavage
spe-miR8024a-3p.2	Sopen00g008760.2	2.0	-1.0	1	24	185	208	UUGGAGGAUUUGAAGAUUUCAACU	AGGAUAAAUCUUCAGAUUCUUCAG	Cleavage
spe-miR8024a-3p.2	Sopen00g008760.1	2.0	-1.0	1	24	185	208	UUGGAGGAUUUGAAGAUUUCAACU	AGGAUAAAUCUUCAGAUUCUUCAG	Cleavage
spe-miR8024a-3p.2	Sopen04g014060.1	2.0	-1.0	1	24	328	351	UUGGAGGAUUUGAAGAUUUCAACU	AAUACAAACCUUCAAAUCCUCCAU	Cleavage
spe-miR8024a-3p.2	Sopen02g010600.1	2.5	-1.0	1	24	1337	1360	UUGGAGGAUUUGAAGAUUUCAACU	AAUUUGAAUCUUUGGAUCUUCCAA	Cleavage
spe-miR8024a-3p.2	Sopen02g010600.2	2.5	-1.0	1	24	116	139	UUGGAGGAUUUGAAGAUUUCAACU	AAUUUGAAUCUUUGGAUCUUCCAA	Cleavage
spe-miR8024a-3p.2	Sopen05g008830.1	2.5	-1.0	1	24	4183	4206	UUGGAGGAUUUGAAGAUUUCAACU	AGACGAGAUAUUCAGGUCCUCCAA	Cleavage
spe-miR8024a-3p.2	Sopen03g006100.1	2.5	-1.0	1	24	484	507	UUGGAGGAUUUGAAGAUUUCAACU	GGUGAAGGUCUUCAAAUUCUCCAU	Cleavage
spe-miR8024a-3p.2	Sopen06g032090.1	2.5	-1.0	1	24	2672	2695	UUGGAGGAUUUGAAGAUUUCAACU	CUGUUUCAUCUUCAAAUCCUCCAG	Cleavage
spe-miR8024a-	Sopen04g034110.1	2.5	-1.0	1	24	944	967	UUGGAGGAUUUGAAGAUUUCAACU	GGGUAAAACCUUCAGAUUCUUCAA	Cleavage

3p.2										
spe-miR8024a-3p.2	Sopen01g033720.1	2.5	-1.0	1	24	407	430	UUGGAGGAUUUGAAGAUUUCAACU	CUAAAAAAUCUUCUAGUCCUUCAA	Translation
spe-miR8024a-3p.2	Sopen03g010960.1	2.5	-1.0	1	24	167	190	UUGGAGGAUUUGAAGAUUUCAACU	UAAACAAAUCUUUUAGUCCUCCAA	Translation
spe-miR8024a-3p.2	Sopen09g002050.1	3.0	-1.0	1	24	248	271	UUGGAGGAUUUGAAGAUUUCAACU	AGUUGAAAUCUUCAGGUCCUUUAU	Cleavage
spe-miR8024a-3p.2	Sopen07g003790.1	3.0	-1.0	1	24	911	934	UUGGAGGAUUUGAAGAUUUCAACU	GCUUGAAAUCUUCAAAUGAUCCAA	Cleavage
spe-miR8024a-3p.2	Sopen10g031280.1	3.0	-1.0	1	24	966	989	UUGGAGGAUUUGAAGAUUUCAACU	AUCUGAAAUCUUCAAAACCUUUAG	Cleavage
spe-miR8024a-3p.2	Sopen10g033090.1	3.0	-1.0	1	24	2039	2062	UUGGAGGAUUUGAAGAUUUCAACU	AUUUAAAAUCUCCAAAUCUUCUAG	Cleavage
spe-miR8024a-3p.2	Sopen10g003050.1	3.0	-1.0	1	24	1427	1450	UUGGAGGAUUUGAAGAUUUCAACU	CUGCGAAGCCUUCAGGUCCUUCAA	Cleavage
spe-miR8024a-3p.2	Sopen08g018650.1	3.0	-1.0	1	24	507	530	UUGGAGGAUUUGAAGAUUUCAACU	GGCAGAAGCCUUCAAAUCCUUUGA	Cleavage
spe-miR8024a-3p.2	Sopen10g006860.1	3.0	-1.0	1	24	140	163	UUGGAGGAUUUGAAGAUUUCAACU	AAAAGAUAUCUUCAAUUCCUUCAA	Cleavage
spe-miR8024a-5p.1	Sopen08g017350.1	3.0	-1.0	1	24	6393	6416	UUAAAGAAUUUGAAGACUUCAGCU	GGAAGAAGUCAUUAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen06g011460.1	2.5	-1.0	1	24	3504	3527	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen05g013910.1	2.5	-1.0	1	24	3414	3437	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen05g023250.1	2.5	-1.0	1	24	3201	3224	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen05g026130.1	2.5	-1.0	1	24	2703	2726	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen11g011880.1	2.5	-1.0	1	24	2238	2261	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen02g010050.1	2.5	-1.0	1	24	1653	1676	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen03g026040.1	2.5	-1.0	1	24	1446	1469	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen10g011960.1	2.5	-1.0	1	24	1170	1193	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen00g008330.1	2.5	-1.0	1	24	1152	1175	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen01g022390.1	2.5	-1.0	1	24	1155	1178	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen05g023250.2	2.5	-1.0	1	24	960	983	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen06g011480.1	2.5	-1.0	1	24	888	911	UUAAAGAAUUUGAAGACUUCAGCU	UACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen05g026130.2	2.5	-1.0	1	24	21	44	UUAAAGAAUUUGAAGACUUCAGCU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen01g012780.1	2.5	-1.0	1	24	1230	1253	UUAAAGAAUUUGAAGACUUCAGCU	CAGUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen04g023980.1	2.5	-1.0	1	24	216	239	UUAAAGAAUUUGAAGACUUCAGCU	CAGUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-	Sopen06g014220.1	2.5	-1.0	1	24	2748	2771	UUAAAGAAUUUGAAGACUUCAGCU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage

5p.1										
spe-miR8024a-5p.1	Sopen06g014220.2	2.5	-1.0	1	24	2028	2051	UUAAAGAAUUUGAAGACUUCAGCU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen05g011210.1	2.5	-1.0	1	24	1128	1151	UUAAAGAAUUUGAAGACUUCAGCU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen04g004250.1	2.5	-1.0	1	24	1954	1977	UUAAAGAAUUUGAAGACUUCAGCU	CUCACGAGUCUUCAAGUUCUUAAA	Cleavage
spe-miR8024a-5p.1	Sopen00g008680.1	2.5	-1.0	1	24	1908	1931	UUAAAGAAUUUGAAGACUUCAGCU	CAGAGUAGGCUUUAAAUUCUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen07g004450.1	3.0	-1.0	1	24	647	670	UUAAAGAAUUUGAAGACUUCAGCU	AUGUGAAGUUUUUGGAUUUUUUGA	Cleavage
spe-miR8024a-5p.1	Sopen08g018650.1	3.0	-1.0	1	24	507	530	UUAAAGAAUUUGAAGACUUCAGCU	GGCAGAAGCCUUCAAAUCCUUUGA	Cleavage
spe-miR8024a-5p.1	Sopen02g023450.1	3.0	-1.0	1	24	122	145	UUAAAGAAUUUGAAGACUUCAGCU	CGCCGGAGAUUUCAAGUUUUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen08g007060.1	3.0	-1.0	1	24	150	173	UUAAAGAAUUUGAAGACUUCAGCU	AUGUGAAGAAUUCGGAUUCUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen09g021360.1	3.0	-1.0	1	24	5463	5486	UUAAAGAAUUUGAAGACUUCAGCU	CCAAGAUGUCUUCAGUUUCUUUAA	Cleavage
spe-miR8024a-5p.1	Sopen08g005320.1	3.0	-1.0	1	24	1252	1275	UUAAAGAAUUUGAAGACUUCAGCU	CGAGGAAGUCGUCAAGUUCUUGAA	Cleavage
spe-miR8024a-5p.1	Sopen03g016960.1	3.0	-1.0	1	24	1582	1605	UUAAAGAAUUUGAAGACUUCAGCU	GAAAGAAGCUUUCAAAUUCUUAAA	Cleavage
spe-miR8024a-5p.1	Sopen04g004270.1	3.0	-1.0	1	24	1936	1959	UUAAAGAAUUUGAAGACUUCAGCU	CUCACUAGUCUUCAAGUUCUUCAA	Cleavage
spe-miR8024a-5p.1	Sopen04g004410.1	3.0	-1.0	1	24	1702	1725	UUAAAGAAUUUGAAGACUUCAGCU	CUUACUAGUCUUCAAGUUCUUAAA	Cleavage
spe-miR8024a-5p.1	Sopen04g013420.1	3.0	-1.0	1	24	268	291	UUAAAGAAUUUGAAGACUUCAGCU	CUCACUAGUCUUCAAGUUCUUGAA	Cleavage
spe-miR8024a-5p.1	Sopen03g004870.1	3.0	-1.0	1	24	3786	3809	UUAAAGAAUUUGAAGACUUCAGCU	GCUUCACGUCUUCAAGUUCUUGAA	Cleavage
spe-miR8024a-5p.2	Sopen08g017350.1	1.5	-1.0	1	24	6393	6416	UUAAAGUAUUUGAAGACUUCAACU	GGAAGAAGUCAUUAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen08g017350.1	2.0	-1.0	1	24	7608	7631	UUAAAGUAUUUGAAGACUUCAACU	GGAAGAAGUCAUUGAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen06g011460.1	1.0	-1.0	1	24	3504	3527	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g013910.1	1.0	-1.0	1	24	3414	3437	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g023250.1	1.0	-1.0	1	24	3201	3224	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g026130.1	1.0	-1.0	1	24	2703	2726	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen11g011880.1	1.0	-1.0	1	24	2238	2261	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen02g010050.1	1.0	-1.0	1	24	1653	1676	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen03g026040.1	1.0	-1.0	1	24	1446	1469	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g012780.1	1.0	-1.0	1	24	1230	1253	UUAAAGUAUUUGAAGACUUCAACU	CAGUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-	Sopen10g011960.1	1.0	-1.0	1	24	1170	1193	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage

5p.2										
spe-miR8024a-5p.2	Sopen00g008330.1	1.0	-1.0	1	24	1152	1175	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g022390.1	1.0	-1.0	1	24	1155	1178	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g023250.2	1.0	-1.0	1	24	960	983	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen06g011480.1	1.0	-1.0	1	24	888	911	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen04g023980.1	1.0	-1.0	1	24	216	239	UUAAAGUAUUUGAAGACUUCAACU	CAGUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g026130.2	1.0	-1.0	1	24	21	44	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen06g014220.1	1.0	-1.0	1	24	2748	2771	UUAAAGUAUUUGAAGACUUCAACU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen06g014220.2	1.0	-1.0	1	24	2028	2051	UUAAAGUAUUUGAAGACUUCAACU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g011210.1	1.0	-1.0	1	24	1128	1151	UUAAAGUAUUUGAAGACUUCAACU	CACUAAAGUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g012140.1	2.0	-1.0	1	24	906	929	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUACUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen03g019980.1	2.0	-1.0	1	24	2733	2756	UUAAAGUAUUUGAAGACUUCAACU	CACUAAAAUAUUCAAAUACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen12g025220.1	2.5	-1.0	1	24	3410	3433	UUAAAGUAUUUGAAGACUUCAACU	GGUUGAAGUAUUCAAAUACUCUAA	Cleavage
spe-miR8024a-5p.2	Sopen03g016180.1	2.5	-1.0	1	24	5250	5273	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen12g016700.1	2.5	-1.0	1	24	6036	6059	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen04g019810.1	2.5	-1.0	1	24	4272	4295	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen02g010600.1	2.5	-1.0	1	24	1437	1460	UUAAAGUAUUUGAAGACUUCAACU	AACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen02g010600.2	2.5	-1.0	1	24	216	239	UUAAAGUAUUUGAAGACUUCAACU	AACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen12g025350.1	2.5	-1.0	1	24	2811	2834	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACAUUAA	Cleavage
spe-miR8024a-5p.2	Sopen12g009970.1	2.5	-1.0	1	24	1377	1400	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAAUACUUUCA	Cleavage
spe-miR8024a-5p.2	Sopen08g019790.1	2.5	-1.0	1	24	1446	1469	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen02g001800.1	2.5	-1.0	1	24	1353	1376	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCCAAUACUUUAA	Translation
spe-miR8024a-5p.2	Sopen09g016130.1	2.5	-1.0	1	24	1056	1079	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen10g011790.1	2.5	-1.0	1	24	882	905	UUAAAGUAUUUGAAGACUUCAACU	AACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g022530.1	2.5	-1.0	1	24	906	929	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen12g021450.2	2.5	-1.0	1	24	777	800	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-	Sopen08g019780.1	2.5	-1.0	1	24	216	239	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAACACUUUAA	Cleavage

5p.2										
spe-miR8024a-5p.2	Sopen05g018420.1	2.5	-1.0	1	24	1113	1136	UUAAAGUAUUUGAAGACUUCAACU	CACCGAAGUAUUCAAACACUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen00g003220.1	2.5	-1.0	1	24	527	550	UUAAAGUAUUUGAAGACUUCAACU	AUAUUAAGUCUUCGAAUAUUCUAA	Cleavage
spe-miR8024a-5p.2	Sopen02g020730.1	2.5	-1.0	1	24	833	856	UUAAAGUAUUUGAAGACUUCAACU	ACCUAGAGCCUUCAAAUAUUUUGA	Cleavage
spe-miR8024a-5p.2	Sopen08g018050.1	3.0	-1.0	1	24	1446	1469	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g022380.1	3.0	-1.0	1	24	3591	3614	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUUAAAUACUUUUA	Cleavage
spe-miR8024a-5p.2	Sopen11g019790.1	3.0	-1.0	1	24	3492	3515	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen10g013210.1	3.0	-1.0	1	24	3048	3071	UUAAAGUAUUUGAAGACUUCAACU	UACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g006350.1	3.0	-1.0	1	24	1260	1283	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen06g004600.1	3.0	-1.0	1	24	1170	1193	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen04g010040.1	3.0	-1.0	1	24	1212	1235	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen05g008270.1	3.0	-1.0	1	24	117	140	UUAAAGUAUUUGAAGACUUCAACU	CACUGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen01g030120.1	3.0	-1.0	1	24	1455	1478	UUAAAGUAUUUGAAGACUUCAACU	UUUAGAAGUCUUUGAAUAUUUGAA	Cleavage
spe-miR8024a-5p.2	Sopen01g015800.1	3.0	-1.0	1	24	5208	5231	UUAAAGUAUUUGAAGACUUCAACU	CACAGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen12g020010.1	3.0	-1.0	1	24	4602	4625	UUAAAGUAUUUGAAGACUUCAACU	CACCGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen03g021620.1	3.0	-1.0	1	24	1116	1139	UUAAAGUAUUUGAAGACUUCAACU	CACAGAAGUAUUCAAACAUUUUAA	Cleavage
spe-miR8024a-5p.2	Sopen08g018650.1	3.0	-1.0	1	24	507	530	UUAAAGUAUUUGAAGACUUCAACU	GGCAGAAGCCUUCAAAUCCUUUGA	Cleavage
spe-miR8025-3p	Sopen04g002800.2	3.0	-1.0	1	23	305	327	UUUAAUUGCAUGCCGAGUGUCUG	GUGACCUUCAGCAUGUAAUUAAA	Cleavage
spe-miR8025-3p	Sopen04g002800.1	3.0	-1.0	1	23	305	327	UUUAAUUGCAUGCCGAGUGUCUG	GUGACCUUCAGCAUGUAAUUAAA	Cleavage
spe-miR8025-3p	Sopen01g048150.1	3.0	-1.0	1	23	196	218	UUUAAUUGCAUGCCGAGUGUCUG	GGAGUACUGGGCAUGCAAUUGGG	Cleavage
spe-miR8025-3p	Sopen07g022080.1	3.0	-1.0	1	23	47	69	UUUAAUUGCAUGCCGAGUGUCUG	UUGUCUCUCGGCGUGUGAUUGAA	Cleavage
spe-miR8025-5p	Sopen12g010470.1	3.0	-1.0	1	24	1917	1940	ACACACUACACAUGCAAUUAAAUU	GCAACAAUUGUAUGUGGAGUGUGA	Cleavage
spe-miR8025-5p	Sopen10g025970.1	3.0	-1.0	1	24	435	458	ACACACUACACAUGCAAUUAAAUU	ACAAAAAUUGCAUGUUUACUGUGU	Cleavage
spe-miR8026-3p	Sopen02g010900.1	2.5	-1.0	1	24	63	86	AUGUAGAGAAUAUGUGGUAACCCU	CGCCCUACCAGCUAUUCUCUACAU	Cleavage
spe-miR8026-3p	Sopen07g012180.1	2.5	-1.0	1	24	63	86	AUGUAGAGAAUAUGUGGUAACCCU	CGCCCUACCAGCUAUUCUCUACAU	Cleavage
spe-miR8026-3p	Sopen07g022990.1	2.5	-1.0	1	24	63	86	AUGUAGAGAAUAUGUGGUAACCCU	CGCCCUACCAGCUAUUCUCUACAU	Cleavage
spe-miR8026-3p	Sopen06g032620.1	2.5	-1.0	1	24	5259	5282	AUGUAGAGAAUAUGUGGUAACCCU	CGCCCUACCAGCUAUUCUCUACAU	Cleavage
spe-miR8026-3p	Sopen08g018650.1	3.0	-1.0	1	24	13	36	AUGUAGAGAAUAUGUGGUAACCCU	CUUUCUACUACAUGUUCUUUAGAU	Cleavage
spe-miR8032a-3p	Sopen09g030770.1	3.0	-1.0	1	22	275	296	AGUGUGAGUUGGUGUGAUUAGG	GUGAGUCAUAUGAACUCACACU	Translation
spe-miR8032a-3p	Sopen00g001470.1	2.5	-1.0	1	22	1764	1785	AGUGUGAGUUGGUGUGAUUAGG	AGAAAUUGCACCAACACACACU	Cleavage
spe-miR8032a-3p	Sopen05g021130.1	3.0	-1.0	1	22	585	606	AGUGUGAGUUGGUGUGAUUAGG	AUUAAUCGUGCCAACUCAGACU	Cleavage
spe-miR8032a-3p	Sopen06g001180.1	3.0	-1.0	1	22	687	708	AGUGUGAGUUGGUGUGAUUAGG	CGAAAUCAUAUCAGCUUACACA	Cleavage
spe-miR8032a-3p	Sopen04g031670.2	3.0	-1.0	1	22	891	912	AGUGUGAGUUGGUGUGAUUAGG	UACGAUCACAUCAACUUACCCU	Cleavage
spe-miR8032a-3p	Sopen07g001070.1	3.0	-1.0	1	22	1220	1241	AGUGUGAGUUGGUGUGAUUAGG	UGAAAACAUAUCAACUCACACC	Cleavage
spe-miR8036-3p	Sopen10g032410.1	2.5	-1.0	1	22	2178	2199	UAUGUCUUUCCGAUGCCUCCCA	CAGGAGACGUCGGAAAGGCAUG	Cleavage

spe-miR8036-3p	Sopen01g009190.1	3.0	-1.0	1	22	109	130	UAUGUCUUUCCGAUGCCUCCCA	CCUGAGGAAUUGGAGAGGCGUA	Cleavage
spe-miR8036-3p	Sopen01g009190.2	3.0	-1.0	1	22	115	136	UAUGUCUUUCCGAUGCCUCCCA	CCUGAGGAAUUGGAGAGGCGUA	Cleavage
spe-miR8038a-5p	Sopen04g004650.2	1.0	-1.0	1	22	211	232	CCUUGUGAGUAAGUUGGAUCUC	GAUAUUCAACUUAUUCACAAGG	Cleavage
spe-miR8038a-5p	Sopen04g004650.1	1.0	-1.0	1	22	211	232	CCUUGUGAGUAAGUUGGAUCUC	GAUAUUCAACUUAUUCACAAGG	Cleavage
spe-miR8038a-5p	Sopen04g004650.2	2.0	-1.0	1	22	1807	1828	CCUUGUGAGUAAGUUGGAUCUC	GAGAUUCAACUUUCUCACAAGG	Translation
spe-miR8038a-5p	Sopen04g004650.1	2.0	-1.0	1	22	1816	1837	CCUUGUGAGUAAGUUGGAUCUC	GAGAUUCAACUUUCUCACAAGG	Translation
spe-miR8038a-5p	Sopen04g004640.1	2.0	-1.0	1	22	256	277	CCUUGUGAGUAAGUUGGAUCUC	GACAUUCAACUUAAUCACAAGG	Cleavage
spe-miR8038a-5p	Sopen04g031240.1	2.5	-1.0	1	22	1036	1057	CCUUGUGAGUAAGUUGGAUCUC	GAGAUCCAAUUUAUUGACAAGG	Cleavage
spe-miR8038a-5p	Sopen04g004660.2	2.5	-1.0	1	22	1984	2005	CCUUGUGAGUAAGUUGGAUCUC	GAUAUUCAACUUUCUCAUAAGG	Translation
spe-miR8038a-5p	Sopen04g004660.3	2.5	-1.0	1	22	1993	2014	CCUUGUGAGUAAGUUGGAUCUC	GAUAUUCAACUUUCUCAUAAGG	Translation
spe-miR8038a-5p	Sopen04g004660.1	2.5	-1.0	1	22	2002	2023	CCUUGUGAGUAAGUUGGAUCUC	GAUAUUCAACUUUCUCAUAAGG	Translation
spe-miR8038a-5p	Sopen01g016330.1	2.5	-1.0	1	22	2288	2309	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAAGG	Cleavage
spe-miR8038a-5p	Sopen09g010540.1	3.0	-1.0	1	22	1225	1246	CCUUGUGAGUAAGUUGGAUCUC	CAGAUUCAGCUUGCUCAUAAGU	Cleavage
spe-miR8038a-5p	Sopen06g011250.1	3.0	-1.0	1	22	1306	1327	CCUUGUGAGUAAGUUGGAUCUC	CAGAUUCAGCUUGCUCAUAAGU	Cleavage
spe-miR8038a-5p	Sopen01g006550.1	3.0	-1.0	1	22	2944	2965	CCUUGUGAGUAAGUUGGAUCUC	CAGAUUCAGCUUGCUCAUAAGU	Cleavage
spe-miR8038a-5p	Sopen05g013790.1	3.0	-1.0	1	22	271	292	CCUUGUGAGUAAGUUGGAUCUC	CAGAGCCAAUUUACUGACAAGG	Cleavage
spe-miR8038a-5p	Sopen03g037880.1	3.0	-1.0	1	22	226	247	CCUUGUGAGUAAGUUGGAUCUC	GAUAUUUCACUUAUUUACAAGG	Cleavage
spe-miR8038a-5p	Sopen08g008500.1	3.0	-1.0	1	22	1285	1306	CCUUGUGAGUAAGUUGGAUCUC	UGGUACCAAUUUGCUCACAAGG	Cleavage
spe-miR8038a-5p	Sopen09g003840.1	3.0	-1.0	1	22	86	107	CCUUGUGAGUAAGUUGGAUCUC	AUAAUCCAAUUUCCUCACAAGU	Translation
spe-miR8038a-5p	Sopen08g005620.1	3.0	-1.0	1	22	1307	1328	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g029170.1	3.0	-1.0	1	22	314	335	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g018830.1	3.0	-1.0	1	22	314	335	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g027180.2	3.0	-1.0	1	22	314	335	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g014630.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g029270.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g017860.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g029030.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g030770.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g023420.3	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g021320.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g013280.2	3.0	-1.0	1	22	1499	1520	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g029450.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g034830.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g029450.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g019560.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g020150.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g005620.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g023550.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g018480.1	3.0	-1.0	1	22	1307	1328	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g003910.3	3.0	-1.0	1	22	1307	1328	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g019440.1	3.0	-1.0	1	22	1307	1328	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g026210.1	3.0	-1.0	1	22	1313	1334	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g020570.1	3.0	-1.0	1	22	1355	1376	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g015950.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g028040.1	3.0	-1.0	1	22	1490	1511	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g009930.1	3.0	-1.0	1	22	1496	1517	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g013280.1	3.0	-1.0	1	22	1499	1520	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g028970.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g029850.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g024410.1	3.0	-1.0	1	22	1535	1556	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage

spe-miR8038a-5p	Sopen02g011420.1	3.0	-1.0	1	22	1550	1571	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g035530.1	3.0	-1.0	1	22	2309	2330	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g020730.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g036040.1	3.0	-1.0	1	22	1646	1667	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g023420.1	3.0	-1.0	1	22	1694	1715	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g020730.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g019060.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g015470.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g016210.1	3.0	-1.0	1	22	2534	2555	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g008580.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g013770.3	3.0	-1.0	1	22	1856	1877	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g027110.1	3.0	-1.0	1	22	2066	2087	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g022530.2	3.0	-1.0	1	22	1856	1877	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g030880.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g007490.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g019070.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g023990.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g024540.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g025390.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g005210.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g020420.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g023550.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g006130.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g008820.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g018600.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g025110.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g035150.1	3.0	-1.0	1	22	1940	1961	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g023450.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g011400.1	3.0	-1.0	1	22	2081	2102	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g019520.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g027040.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g015050.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g008940.1	3.0	-1.0	1	22	2225	2246	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g006800.1	3.0	-1.0	1	22	2225	2246	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g012240.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g029880.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g018800.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g014880.1	3.0	-1.0	1	22	2225	2246	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g005410.1	3.0	-1.0	1	22	2204	2225	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g028820.1	3.0	-1.0	1	22	2213	2234	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g026940.1	3.0	-1.0	1	22	2291	2312	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g014450.1	3.0	-1.0	1	22	2225	2246	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g006780.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g024200.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g015350.1	3.0	-1.0	1	22	2225	2246	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g025720.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g027780.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g016130.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g023450.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g016170.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage

spe-miR8038a-5p	Sopen04g027600.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g010130.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g010440.1	3.0	-1.0	1	22	2267	2288	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g008670.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g027770.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g026500.1	3.0	-1.0	1	22	2294	2315	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g021160.1	3.0	-1.0	1	22	2372	2393	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g025570.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g003240.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g024780.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g004710.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g013770.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g016770.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g010720.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g005860.1	3.0	-1.0	1	22	2309	2330	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g027320.1	3.0	-1.0	1	22	2321	2342	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g025720.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g010800.1	3.0	-1.0	1	22	2327	2348	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g010710.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g017310.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g022860.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g010150.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g029170.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g009230.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g005030.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g021020.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g011020.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g016490.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g023240.1	3.0	-1.0	1	22	2375	2396	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g011910.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g007880.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g007420.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g019730.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g025080.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g022510.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g004950.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g026650.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g006210.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g023340.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g014070.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g009780.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g016780.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g010750.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g005390.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g010580.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g020330.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g022330.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g020960.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g017060.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g004970.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage

spe-miR8038a-5p	Sopen02g005670.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g015950.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g009090.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g016720.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g014920.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen11g025380.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g005250.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen02g010500.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g003910.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g018600.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen01g008570.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g023420.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen09g026410.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen07g007090.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen06g010020.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g026390.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g015200.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen10g017360.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g027290.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen08g012530.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen03g003830.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g026820.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen05g022780.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen12g017700.2	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8038a-5p	Sopen04g023840.1	3.0	-1.0	1	22	2378	2399	CCUUGUGAGUAAGUUGGAUCUC	UUUUUCCAACAUACUCACAGGG	Cleavage
spe-miR8039-5p	Sopen02g020620.2	2.5	-1.0	1	21	373	393	UUUCCUAUCUGAACUAUCACC	AGUGUCAGUUCAGAUAGGGAA	Cleavage
spe-miR8039-5p	Sopen02g020620.1	2.5	-1.0	1	21	373	393	UUUCCUAUCUGAACUAUCACC	AGUGUCAGUUCAGAUAGGGAA	Cleavage
spe-miR8039-5p	Sopen10g013850.1	2.5	-1.0	1	21	475	495	UUUCCUAUCUGAACUAUCACC	GUGGAGAGUUCAGAUAGGGAA	Cleavage
spe-miR8039-5p	Sopen11g026880.1	2.5	-1.0	1	21	289	309	UUUCCUAUCUGAACUAUCACC	AUUGAUAAUUCAGAUAUGAAA	Cleavage
spe-miR8039-5p	Sopen09g026540.2	3.0	-1.0	1	21	826	846	UUUCCUAUCUGAACUAUCACC	UCAGAUGGUUUAGAUAGGAAC	Cleavage
spe-miR8039-5p	Sopen09g026540.1	3.0	-1.0	1	21	826	846	UUUCCUAUCUGAACUAUCACC	UCAGAUGGUUUAGAUAGGAAC	Cleavage
spe-miR8039-5p	Sopen04g001290.1	3.0	-1.0	1	21	694	714	UUUCCUAUCUGAACUAUCACC	GAUGAUAGUUCAGACAUGAAA	Cleavage
spe-miR8039-5p	Sopen06g011720.1	3.0	-1.0	1	21	58	78	UUUCCUAUCUGAACUAUCACC	GAUGGUAGUUCAGAAAGGAGG	Cleavage
spe-miR8039-5p	Sopen06g024150.1	3.0	-1.0	1	21	859	879	UUUCCUAUCUGAACUAUCACC	AGUGUUUGUUCAGAUAGGAAU	Cleavage
spe-miR8039-5p	Sopen04g022570.1	3.0	-1.0	1	21	686	706	UUUCCUAUCUGAACUAUCACC	AAGGAAAGUUCAGGUGGGAAA	Cleavage
spe-miR8039-5p	Sopen07g003930.1	3.0	-1.0	1	21	1366	1386	UUUCCUAUCUGAACUAUCACC	AUGGGUAUUUCAGAUGGGAAA	Cleavage
spe-miR8039-5p	Sopen12g021190.1	3.0	-1.0	1	21	327	347	UUUCCUAUCUGAACUAUCACC	AUUGAAAGUUCAAAUGGGAAA	Cleavage
spe-miR8039-5p	Sopen06g022120.2	3.0	-1.0	1	21	678	698	UUUCCUAUCUGAACUAUCACC	UAUAAUGGUUCAGAUAGAAAA	Cleavage
spe-miR8039-5p	Sopen02g008630.1	3.0	-1.0	1	21	1333	1353	UUUCCUAUCUGAACUAUCACC	GUUGCUAUUUUAGAUAGGGAA	Cleavage
spe-miR8039-5p	Sopen03g003210.1	3.0	-1.0	1	21	751	771	UUUCCUAUCUGAACUAUCACC	AUUGAAAAUUCAGGUGGGAAA	Cleavage
spe-miR8042-3p	Sopen02g023740.1	2.5	-1.0	1	21	339	359	AUUAGACUGAAAUGCUGAUCU	AGAUGAGCAUUUCAGCCUAAU	Cleavage
spe-miR8042-3p	Sopen02g016790.1	2.5	-1.0	1	21	232	252	AUUAGACUGAAAUGCUGAUCU	CCAUCAUCAUCUCAGUCUAAU	Translation
spe-miR8042-3p	Sopen02g025810.2	3.0	-1.0	1	21	717	737	AUUAGACUGAAAUGCUGAUCU	UGAUCAUCAUUUUAGUCUCAU	Cleavage
spe-miR8042-3p	Sopen12g008060.1	3.0	-1.0	1	21	160	180	AUUAGACUGAAAUGCUGAUCU	GGUUCAGGAUUUCAGUCUAAG	Cleavage
spe-miR8042-3p	Sopen04g031540.1	3.0	-1.0	1	21	2833	2853	AUUAGACUGAAAUGCUGAUCU	GGAUAUGCAUUUCAGUCUAAC	Cleavage
spe-miR8042-3p	Sopen12g023330.1	3.0	-1.0	1	21	814	834	AUUAGACUGAAAUGCUGAUCU	GAAACAGAAUUUCAGUUUGAU	Cleavage
spe-miR8042-3p	Sopen12g023350.1	3.0	-1.0	1	21	814	834	AUUAGACUGAAAUGCUGAUCU	GAAACAGAAUUUCAGUUUGAU	Cleavage
spe-miR8045-3p	Sopen01g002710.2	1.0	-1.0	1	21	555	575	AUUGAUAGUUGAGGUGUGUUU	AAACACACUUCAACUAUCAGU	Cleavage
spe-miR8045-3p	Sopen03g035030.1	3.0	-1.0	1	21	490	510	AUUGAUAGUUGAGGUGUGUUU	UCAAACACCCCAACUAUUAAU	Cleavage
spe-miR8045-3p	Sopen03g033970.1	2.0	-1.0	1	21	854	874	AUUGAUAGUUGAGGUGUGUUU	UCACAAACUUCAACUAUCGAU	Cleavage

spe-miR8045-3p	Sopen06g004790.1	2.5	-1.0	1	21	1414	1434	AUUGAUAGUUGAGGUGUGUUU	GGACAUGCCUCAACUGUUGAU	Cleavage
spe-miR8045-3p	Sopen06g004790.2	2.5	-1.0	1	21	1414	1434	AUUGAUAGUUGAGGUGUGUUU	GGACAUGCCUCAACUGUUGAU	Cleavage
spe-miR8045-3p	Sopen03g041730.1	2.5	-1.0	1	21	4	24	AUUGAUAGUUGAGGUGUGUUU	CGGCACACCUCAACUACUAAU	Cleavage
spe-miR8045-3p	Sopen10g007140.1	3.0	-1.0	1	21	454	474	AUUGAUAGUUGAGGUGUGUUU	AGGUUCACUUCAAUUAUCAAU	Cleavage
spe-miR8045-3p	Sopen03g038800.1	3.0	-1.0	1	21	3118	3138	AUUGAUAGUUGAGGUGUGUUU	GAACUUACCUCGGCUGUCAAU	Cleavage
spe-miR8045-3p	Sopen10g021030.1	3.0	-1.0	1	21	1036	1056	AUUGAUAGUUGAGGUGUGUUU	ACAUAUACCUCAGUUAUCAAG	Cleavage
spe-miR8045-3p	Sopen06g034370.1	3.0	-1.0	1	21	435	455	AUUGAUAGUUGAGGUGUGUUU	ACACGUACUUCAACUAUCCAU	Cleavage
spe-miR8045-3p	Sopen01g016130.1	3.0	-1.0	1	21	253	273	AUUGAUAGUUGAGGUGUGUUU	GCAUACACUUCAAUCAUCAAU	Cleavage
spe-miR8047-5p	Sopen06g030520.1	3.0	-1.0	1	21	683	703	CCAUUUUUUCGAAAUUAGACC	CAUCAAAUUUUGAAAAAAUUG	Cleavage
spe-miR8047-5p	Sopen06g030520.1	3.0	-1.0	1	21	2318	2338	CCAUUUUUUCGAAAUUAGACC	CAUCAAAUUUUGAAAAAAUUG	Cleavage
spe-miR8047-5p	Sopen02g035770.1	2.0	-1.0	1	21	893	913	CCAUUUUUUCGAAAUUAGACC	GGCCUAAUUUUGAGAAAAUGG	Cleavage
spe-miR8047-5p	Sopen02g035770.2	2.0	-1.0	1	21	893	913	CCAUUUUUUCGAAAUUAGACC	GGCCUAAUUUUGAGAAAAUGG	Cleavage
spe-miR8047-5p	Sopen05g021200.1	2.5	-1.0	1	21	110	130	CCAUUUUUUCGAAAUUAGACC	UGUCUAAUUUUGAGAUAAUGG	Cleavage
spe-miR8047-5p	Sopen06g023650.1	2.5	-1.0	1	21	1499	1519	CCAUUUUUUCGAAAUUAGACC	AGUCUAAUUUUGAAAAGUUGG	Cleavage
spe-miR8047-5p	Sopen06g023650.2	2.5	-1.0	1	21	1499	1519	CCAUUUUUUCGAAAUUAGACC	AGUCUAAUUUUGAAAAGUUGG	Cleavage
spe-miR8047-5p	Sopen02g023510.1	2.5	-1.0	1	21	836	856	CCAUUUUUUCGAAAUUAGACC	AAGCUAAUUUCGAAAACAUGG	Cleavage
spe-miR8047-5p	Sopen06g004000.1	2.5	-1.0	1	21	629	649	CCAUUUUUUCGAAAUUAGACC	AUUCUGAUUUUGGAAGGAUGG	Cleavage
spe-miR8047-5p	Sopen06g001180.1	2.5	-1.0	1	21	2429	2449	CCAUUUUUUCGAAAUUAGACC	CUUCUCAUUUUGAGAGAAUGG	Cleavage
spe-miR8047-5p	Sopen12g024070.1	2.5	-1.0	1	21	2783	2803	CCAUUUUUUCGAAAUUAGACC	UUUAUGGUUUCGGAAAAAUGG	Cleavage
spe-miR8047-5p	Sopen12g001830.2	3.0	-1.0	1	21	43	63	CCAUUUUUUCGAAAUUAGACC	AGUGUAGUUUCUAAAAAAUGG	Translation
spe-miR8047-5p	Sopen12g001830.1	3.0	-1.0	1	21	43	63	CCAUUUUUUCGAAAUUAGACC	AGUGUAGUUUCUAAAAAAUGG	Translation
spe-miR8047-5p	Sopen07g004180.1	3.0	-1.0	1	21	1031	1051	CCAUUUUUUCGAAAUUAGACC	GUUCUGAUUUUGAGAAAGUGA	Cleavage
spe-miR8047-5p	Sopen03g030320.1	3.0	-1.0	1	21	812	832	CCAUUUUUUCGAAAUUAGACC	GAUUUGAUUUCGAGAAGAUGU	Cleavage
spe-miR8047-5p	Sopen08g001270.2	3.0	-1.0	1	21	479	499	CCAUUUUUUCGAAAUUAGACC	UUCGUGAUUUCGAGAAAAUGG	Cleavage
spe-miR8047-5p	Sopen08g001270.1	3.0	-1.0	1	21	479	499	CCAUUUUUUCGAAAUUAGACC	UUCGUGAUUUCGAGAAAAUGG	Cleavage
spe-miR8047-5p	Sopen06g026800.1	3.0	-1.0	1	21	587	607	CCAUUUUUUCGAAAUUAGACC	UCUUUGAUUUCGAGAAACUGG	Cleavage
spe-miR8047-5p	Sopen04g020910.1	3.0	-1.0	1	21	1040	1060	CCAUUUUUUCGAAAUUAGACC	UUUCUGAUUUUGAGAAAAGGG	Cleavage
spe-miR8047-5p	Sopen09g023690.1	3.0	-1.0	1	21	3524	3544	CCAUUUUUUCGAAAUUAGACC	GAUCUCAUUUUGAGAAAAUGA	Cleavage
spe-miR8047-5p	Sopen11g001990.1	3.0	-1.0	1	21	409	429	CCAUUUUUUCGAAAUUAGACC	GUUUUAGCUUUGAAGAAAUGG	Cleavage
spe-miR8047-5p	Sopen08g006510.1	3.0	-1.0	1	21	992	1012	CCAUUUUUUCGAAAUUAGACC	GAACCAAUUUCGGAGAAAUGG	Cleavage
spe-miR8047-5p	Sopen03g040690.1	3.0	-1.0	1	21	657	677	CCAUUUUUUCGAAAUUAGACC	CUUUUACUUUCGAGGAGAUGG	Cleavage
spe-miR8051-5p	Sopen10g022990.1	2.0	-1.0	1	20	296	315	UAGUAUGGUAGAAAGAUUCA	UGGAUCUUUCUACCGUGUUA	Cleavage
spe-miR8051-5p	Sopen03g028060.1	2.5	-1.0	1	20	3209	3228	UAGUAUGGUAGAAAGAUUCA	UGGAUGUUUCUACCAUAUUG	Cleavage
spe-miR8051-5p	Sopen04g009230.1	2.5	-1.0	1	20	285	304	UAGUAUGGUAGAAAGAUUCA	CGAAUUUUUCUACCGAACUA	Cleavage
spe-miR8051-5p	Sopen12g006480.1	3.0	-1.0	1	20	1056	1075	UAGUAUGGUAGAAAGAUUCA	UGAAGCUUUCUACAAUGCUA	Cleavage
spe-miR8051-5p	Sopen07g034080.1	3.0	-1.0	1	20	240	259	UAGUAUGGUAGAAAGAUUCA	GGAUUCUUUUUAUCAUACUU	Cleavage
spe-miR8051-5p	Sopen08g001030.1	3.0	-1.0	1	20	618	637	UAGUAUGGUAGAAAGAUUCA	GGAACUUUUCUACCGUGCUG	Cleavage
spe-miR8051-5p	Sopen03g005890.1	3.0	-1.0	1	20	430	449	UAGUAUGGUAGAAAGAUUCA	GGAAUGUUUUUGUCAUACUG	Cleavage
spe-miR8175-1-5p	Sopen03g018060.1	3.0	-1.0	1	20	498	517	GAUCCCCGGCAACGGCGCCA	UGGCGCCGUUGCCGGGAACC	Cleavage
spe-miR8175-2-3p	Sopen03g018060.1	3.0	-1.0	1	20	498	517	GAUCCCCGGCAACGGCGCCA	UGGCGCCGUUGCCGGGAACC	Cleavage
spe-miR827-3p	Sopen01g011390.1	2.5	-1.0	1	21	1802	1822	UUAGAUGAACAUCAACAAACA	ACUUUGUUGUUGUUUAUCUAG	Cleavage
spe-miR827-3p	Sopen08g005660.1	2.5	-1.0	1	21	569	589	UUAGAUGAACAUCAACAAACA	GCUUAGUUGAUGUUGAUCUAA	Cleavage
spe-miR827-3p	Sopen10g034020.1	2.5	-1.0	1	21	566	586	UUAGAUGAACAUCAACAAACA	AUUUAGUUGAUGUUCUUCUAA	Cleavage
spe-miR827-3p	Sopen03g016360.1	3.0	-1.0	1	21	906	926	UUAGAUGAACAUCAACAAACA	UGUUUGUUGGUGUCCAUUUAG	Cleavage
spe-miR827-3p	Sopen08g015960.1	3.0	-1.0	1	21	1313	1333	UUAGAUGAACAUCAACAAACA	GGUUUGUUGGUGUUCUUUUGA	Cleavage
spe-miR827-3p	Sopen10g034810.1	3.0	-1.0	1	21	1310	1330	UUAGAUGAACAUCAACAAACA	GAUUUGUUGAUGUUGAUUUAU	Cleavage
spe-miR827-3p	Sopen09g004830.1	3.0	-1.0	1	21	1520	1540	UUAGAUGAACAUCAACAAACA	GAUUUGUUGAUGUUGAUUUGG	Cleavage
spe-miR827-3p	Sopen10g005990.1	3.0	-1.0	1	21	2192	2212	UUAGAUGAACAUCAACAAACA	ACUUUGUUGUUGUUUAUUUAG	Cleavage
spe-miR827-3p	Sopen12g017890.1	3.0	-1.0	1	21	2183	2203	UUAGAUGAACAUCAACAAACA	ACUUUGUUGUUGUUUAUUUAG	Cleavage
spe-miR827-3p	Sopen01g036380.1	3.0	-1.0	1	21	755	775	UUAGAUGAACAUCAACAAACA	AAUUUGGUGAUCUUCAUCUAG	Translation

spe-miR827-3p	Sopen06g021790.1	3.0	-1.0	1	21	719	739	UUAGAUGAACAUCAACAAACA	AUUUGGUUGAUGUUUUUCUAA	Cleavage
spe-miR827-3p	Sopen02g002290.1	3.0	-1.0	1	21	2000	2020	UUAGAUGAACAUCAACAAACA	GUUUUGUGGAUGUUGAUCUAG	Cleavage
spe-miR827-3p	Sopen01g036380.2	3.0	-1.0	1	21	2387	2407	UUAGAUGAACAUCAACAAACA	AAUUUGGUGAUCUUCAUCUAG	Translation
spe-miR827-5p	Sopen09g033010.1	2.5	-1.0	1	21	1777	1797	UUUGUUGAUGGUCAUCUAUUC	AAACAGAUGACCGUCAGCAGA	Cleavage
spe-miR827-5p	Sopen05g030030.1	2.5	-1.0	1	21	1608	1628	UUUGUUGAUGGUCAUCUAUUC	AAACAGAUGGUCAUCAACGAA	Cleavage
spe-miR827-5p	Sopen07g017540.2	3.0	-1.0	1	21	1652	1672	UUUGUUGAUGGUCAUCUAUUC	GAGUAGAUGAUCAUCAAAGAA	Cleavage
spe-miR827-5p	Sopen07g017540.1	3.0	-1.0	1	21	1211	1231	UUUGUUGAUGGUCAUCUAUUC	GAGUAGAUGAUCAUCAAAGAA	Cleavage
spe-miR827-5p	Sopen05g003600.1	3.0	-1.0	1	21	914	934	UUUGUUGAUGGUCAUCUAUUC	GAAUAGUUGGCCAUCAAGAAA	Cleavage
spe-miR827-5p	Sopen04g008480.1	3.0	-1.0	1	21	29	49	UUUGUUGAUGGUCAUCUAUUC	UGAUGGAUGGUCAUCGACAAC	Cleavage
spe-miR827-5p	Sopen09g006930.1	3.0	-1.0	1	21	283	303	UUUGUUGAUGGUCAUCUAUUC	AAAGGGAUGGCUGUCAACAAA	Cleavage
spe-miR827-5p	Sopen09g006930.2	3.0	-1.0	1	21	283	303	UUUGUUGAUGGUCAUCUAUUC	AAAGGGAUGGCUGUCAACAAA	Cleavage
spe-miR827-5p	Sopen01g054420.1	3.0	-1.0	1	21	2273	2293	UUUGUUGAUGGUCAUCUAUUC	AUAUAGAUGACCAUAAGCAAC	Cleavage
spe-miR827-5p	Sopen10g029870.1	3.0	-1.0	1	21	866	886	UUUGUUGAUGGUCAUCUAUUC	CUAUGGAUGAUCAUCAGCUAA	Cleavage
spe-miR827-5p	Sopen05g017840.1	3.0	-1.0	1	21	314	334	UUUGUUGAUGGUCAUCUAUUC	AAGGACAUGGCCAUCAACAAA	Cleavage
spe-miR827-5p	Sopen04g020660.1	3.0	-1.0	1	21	408	427	UUUGUUGAUGGUCAUCUAUUC	AAAUA-AUGAUCAUCAACAAG	Cleavage
spe-miR827-5p	Sopen09g030270.1	3.0	-1.0	1	21	962	982	UUUGUUGAUGGUCAUCUAUUC	CCAUAGUUGACCAACAGCAAA	Cleavage
spe-miR827-5p	Sopen09g005830.1	3.0	-1.0	1	21	1159	1179	UUUGUUGAUGGUCAUCUAUUC	CCAAAGAUGACUAUCGAUAAG	Cleavage
spe-miR828a-3p	Sopen02g001870.1	2.5	-1.0	1	22	41	62	AGAUACUCAUUUGGGUAAGAAG	UUCCCUUCCCAAAUGAGUGUCU	Cleavage
spe-miR828a-3p	Sopen03g021790.1	3.0	-1.0	1	22	683	704	AGAUACUCAUUUGGGUAAGAAG	CACCUUACUUGAAUGAGUAUAU	Cleavage
spe-miR828a-3p	Sopen03g021780.1	3.0	-1.0	1	22	683	704	AGAUACUCAUUUGGGUAAGAAG	CACCUUACUUGAAUGAGUAUAU	Cleavage
spe-miR828a-3p	Sopen04g021440.1	3.0	-1.0	1	22	2353	2374	AGAUACUCAUUUGGGUAAGAAG	GAUCCGGUCCAAAUGAGUAUCU	Cleavage
spe-miR828a-3p	Sopen09g020150.1	3.0	-1.0	1	22	986	1007	AGAUACUCAUUUGGGUAAGAAG	UGGUUUACAUGAAUGAGUAUUU	Cleavage
spe-miR828a-5p	Sopen11g015280.1	3.0	-1.0	1	22	2821	2842	UCUUGCUCAAAUGAGUAUUCCA	AGGGAUGUUGAUUUGAGCAAGA	Cleavage
spe-miR828a-5p	Sopen06g011830.1	2.0	-1.0	1	22	2066	2087	UCUUGCUCAAAUGAGUAUUCCA	AGAAAGACUUGUUUGAGCAAGA	Cleavage
spe-miR828a-5p	Sopen08g031120.1	2.5	-1.0	1	22	322	343	UCUUGCUCAAAUGAGUAUUCCA	UGGAAUACGCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen12g005270.1	2.5	-1.0	1	22	410	431	UCUUGCUCAAAUGAGUAUUCCA	AGGAAGGUUUAUUUGAGCAAGA	Cleavage
spe-miR828a-5p	Sopen06g007580.1	2.5	-1.0	1	22	431	452	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen07g025650.1	2.5	-1.0	1	22	431	452	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen01g007840.1	2.5	-1.0	1	22	431	452	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen04g017180.1	2.5	-1.0	1	22	503	524	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen02g022170.1	2.5	-1.0	1	22	416	437	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen03g012280.1	2.5	-1.0	1	22	503	524	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen12g015990.1	2.5	-1.0	1	22	6431	6452	UCUUGCUCAAAUGAGUAUUCCA	UGCAGUAUUCAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen10g001530.1	3.0	-1.0	1	22	328	349	UCUUGCUCAAAUGAGUAUUCCA	UGGAAUACUCAUUUGAAGAAGA	Cleavage
spe-miR828a-5p	Sopen11g025350.1	3.0	-1.0	1	22	164	185	UCUUGCUCAAAUGAGUAUUCCA	UGGAAUGUUUAUUUGAUCAAGA	Cleavage
spe-miR828a-5p	Sopen02g037610.1	3.0	-1.0	1	22	970	991	UCUUGCUCAAAUGAGUAUUCCA	AAGAAUGGUCAUUUGGGCAAGU	Cleavage
spe-miR828a-5p	Sopen11g014410.2	3.0	-1.0	1	22	460	481	UCUUGCUCAAAUGAGUAUUCCA	CUAAAUGCAUAUUUGAGCAAGU	Cleavage
spe-miR828a-5p	Sopen11g014410.1	3.0	-1.0	1	22	460	481	UCUUGCUCAAAUGAGUAUUCCA	CUAAAUGCAUAUUUGAGCAAGU	Cleavage
spe-miR828a-5p	Sopen03g016610.1	3.0	-1.0	1	22	284	305	UCUUGCUCAAAUGAGUAUUCCA	CCAUAUGGUUAUUUGAGCAAGA	Cleavage
spe-miR828a-5p	Sopen09g028990.1	3.0	-1.0	1	22	1832	1853	UCUUGCUCAAAUGAGUAUUCCA	AGAAACACUCAUUUGAGAAGGA	Cleavage
spe-miR828a-5p	Sopen04g026950.1	3.0	-1.0	1	22	2008	2029	UCUUGCUCAAAUGAGUAUUCCA	CCAAGAACUCAUUUUAGCAAGA	Cleavage
spe-miR828a-5p	Sopen10g010810.1	3.0	-1.0	1	22	1672	1693	UCUUGCUCAAAUGAGUAUUCCA	GAAGAUAGUCAUUUGAGGAAGA	Cleavage
spe-miR9469-3p	Sopen04g005080.2	3.0	-1.0	1	21	164	184	AUUCGGUCUUCUUAUAUGGAC	CUUCAAUUAAGAAGACUGAAU	Cleavage
spe-miR9469-3p	Sopen04g005080.1	3.0	-1.0	1	21	164	184	AUUCGGUCUUCUUAUAUGGAC	CUUCAAUUAAGAAGACUGAAU	Cleavage
spe-miR9469-3p	Sopen02g023090.1	2.0	-1.0	1	21	1901	1921	AUUCGGUCUUCUUAUAUGGAC	AGCCAUACAAGAAGAUUGAAU	Cleavage
spe-miR9469-3p	Sopen03g016390.1	2.5	-1.0	1	21	254	274	AUUCGGUCUUCUUAUAUGGAC	CAUCAUGUGAGAAGGCCGAGU	Cleavage
spe-miR9469-3p	Sopen09g027930.1	3.0	-1.0	1	21	443	463	AUUCGGUCUUCUUAUAUGGAC	AUCCAGAUGAGAAGAUUGAGU	Cleavage
spe-miR9469-3p	Sopen02g004750.1	3.0	-1.0	1	21	272	292	AUUCGGUCUUCUUAUAUGGAC	CUUCAAGUGAGAAGACCGAGU	Cleavage
spe-miR9469-3p	Sopen04g013580.1	3.0	-1.0	1	21	1253	1273	AUUCGGUCUUCUUAUAUGGAC	CUCGAUAUGAGAAGACCGCAU	Cleavage
spe-miR9469-3p	Sopen01g047990.1	3.0	-1.0	1	21	793	813	AUUCGGUCUUCUUAUAUGGAC	AACCAUGUAAGGAGAAUGAAU	Cleavage

spe-miR9469-3p	Sopen03g030520.1	3.0	-1.0	1	21	230	250	AUUCGGUCUUCUUAUAUGGAC	AUCCAUUGAAGGAGACUGAAU	Cleavage
spe-miR9469-3p	Sopen09g029320.1	3.0	-1.0	1	21	104	124	AUUCGGUCUUCUUAUAUGGAC	AACUAGAUGAGAAGACUGAGU	Cleavage
spe-miR9469-3p	Sopen01g015540.1	3.0	-1.0	1	21	440	460	AUUCGGUCUUCUUAUAUGGAC	UCCCAGAUGAGAAGAUUGGAU	Cleavage
spe-miR9469-3p	Sopen02g003880.1	3.0	-1.0	1	21	113	133	AUUCGGUCUUCUUAUAUGGAC	AGCUCUGUGAGAAGACCGAGU	Cleavage
spe-miR9469-5p	Sopen07g027790.1	2.5	-1.0	1	21	200	220	CCAUAUAAGGAGACCAAAUUC	AGAUUUGGUUUCUAUAUAUGG	Cleavage
spe-miR9469-5p	Sopen06g012450.1	3.0	-1.0	1	21	97	117	CCAUAUAAGGAGACCAAAUUC	UUGUUUGGUCUCCUAAUAUGU	Cleavage
spe-miR9469-5p	Sopen05g001300.1	3.0	-1.0	1	21	332	352	CCAUAUAAGGAGACCAAAUUC	UUAUUUGGCCUUCUUAUAUGA	Cleavage
spe-miR9469-5p	Sopen02g014710.1	3.0	-1.0	1	21	28	48	CCAUAUAAGGAGACCAAAUUC	GUAUUUGCUCUUCUUCUAUGG	Cleavage
spe-miR9471b-3p	Sopen04g024360.1	1.0	-1.0	1	21	18	38	UUGGCUGAGUGAGCAUCACUG	UAGUGAUGCUCACUCAGCCAC	Cleavage
spe-miR9471b-3p	Sopen02g034050.1	2.5	-1.0	1	21	1266	1286	UUGGCUGAGUGAGCAUCACUG	AUGUCAGGUUCACUCAGCCAA	Cleavage
spe-miR9471b-3p	Sopen09g024730.1	3.0	-1.0	1	21	765	785	UUGGCUGAGUGAGCAUCACUG	CAGUGCUGUUCGCUCAGCCAU	Cleavage
spe-miR9471b-3p	Sopen08g031080.1	3.0	-1.0	1	21	936	956	UUGGCUGAGUGAGCAUCACUG	UAUUGAUGCUUACUCGGCUGA	Cleavage
spe-miR9471b-3p	Sopen10g026410.1	3.0	-1.0	1	21	2027	2047	UUGGCUGAGUGAGCAUCACUG	AAGCGAUGCUUGUUCAGCCGA	Cleavage
spe-miR9471b-3p	Sopen07g005960.1	3.0	-1.0	1	21	315	335	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
spe-miR9471b-3p	Sopen07g005390.1	3.0	-1.0	1	21	360	380	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
spe-miR9471b-3p	Sopen01g011560.1	3.0	-1.0	1	21	342	362	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen10g016400.1	3.0	-1.0	1	21	846	866	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen05g025940.1	3.0	-1.0	1	21	174	194	UUGGCUGAGUGAGCAUCACUG	CCCUGAUGCUCACAUAGCCAA	Cleavage
spe-miR9471b-3p	Sopen00g002900.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen07g005360.1	3.0	-1.0	1	21	2442	2462	UUGGCUGAGUGAGCAUCACUG	UGCUGAUGCAUACUCAGCCAA	Cleavage
spe-miR9471b-3p	Sopen01g023070.1	3.0	-1.0	1	21	927	947	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen05g015410.1	3.0	-1.0	1	21	939	959	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen11g018910.1	3.0	-1.0	1	21	762	782	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen07g008180.1	3.0	-1.0	1	21	828	848	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen08g019200.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen06g010510.1	3.0	-1.0	1	21	852	872	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen03g012390.1	3.0	-1.0	1	21	63	83	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen11g013950.3	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen11g022600.2	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen07g025250.1	3.0	-1.0	1	21	63	83	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen01g011390.1	3.0	-1.0	1	21	726	746	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen05g026540.1	3.0	-1.0	1	21	672	692	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen05g028570.1	3.0	-1.0	1	21	711	731	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen02g010330.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen05g021280.1	3.0	-1.0	1	21	588	608	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen04g014160.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen12g017890.1	3.0	-1.0	1	21	915	935	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen05g012140.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen04g020730.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen12g024530.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen07g025250.2	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen03g033370.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen02g012390.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen07g017800.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen11g021550.1	3.0	-1.0	1	21	790	810	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen11g022600.1	3.0	-1.0	1	21	1008	1028	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen06g011350.1	3.0	-1.0	1	21	1326	1346	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen09g025530.1	3.0	-1.0	1	21	3516	3536	UUGGCUGAGUGAGCAUCACUG	UGGUGGUCCUCAUUUGGCCAA	Cleavage
spe-miR9471b-3p	Sopen03g030250.1	3.0	-1.0	1	21	509	529	UUGGCUGAGUGAGCAUCACUG	UUGUGAUGUUUCCUCAGCCAG	Translation
spe-miR9471b-3p	Sopen10g001660.1	3.0	-1.0	1	21	992	1012	UUGGCUGAGUGAGCAUCACUG	GUGUGGUGUUUACUCGGCUAG	Cleavage

spe-miR9471b-3p	Sopen10g001660.2	3.0	-1.0	1	21	1160	1180	UUGGCUGAGUGAGCAUCACUG	GUGUGGUGUUUACUCGGCUAG	Cleavage
spe-miR9471b-3p	Sopen05g007990.1	3.0	-1.0	1	21	4893	4913	UUGGCUGAGUGAGCAUCACUG	GGAUGUUGCUCAUUCAGCCGA	Cleavage
spe-miR9473-1-5p	Sopen09g023020.1	3.0	-1.0	1	21	1076	1096	UGGCUGUAAAUCUGAACUCGU	UUGAGUUCAGAUUUACUCCCA	Cleavage
spe-miR9473-1-5p	Sopen05g008970.1	2.5	-1.0	1	21	479	499	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGACAGUCA	Cleavage
spe-miR9473-1-5p	Sopen10g002280.1	2.5	-1.0	1	21	894	914	UGGCUGUAAAUCUGAACUCGU	UGGAGUUGGGAUUUAUAGUCA	Cleavage
spe-miR9473-1-5p	Sopen05g033040.1	3.0	-1.0	1	21	248	268	UGGCUGUAAAUCUGAACUCGU	AUGCGUUCAGAUUUGUGGCUA	Cleavage
spe-miR9473-1-5p	Sopen07g020390.1	3.0	-1.0	1	21	932	952	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen05g016400.1	3.0	-1.0	1	21	650	670	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen08g008550.1	3.0	-1.0	1	21	947	967	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen02g009320.1	3.0	-1.0	1	21	932	952	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen02g014660.1	3.0	-1.0	1	21	932	952	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen03g005060.1	3.0	-1.0	1	21	1534	1554	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUGGAGUUACAGUCA	Translation
spe-miR9473-1-5p	Sopen04g015180.1	3.0	-1.0	1	21	1361	1381	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen05g004820.1	3.0	-1.0	1	21	2096	2116	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen12g025840.1	3.0	-1.0	1	21	2672	2692	UGGCUGUAAAUCUGAACUCGU	AAGAGUUUAGAUUGGCAGUCA	Cleavage
spe-miR9473-1-5p	Sopen04g018550.1	3.0	-1.0	1	21	1696	1716	UGGCUGUAAAUCUGAACUCGU	AGAAGUUCAGAUUUAAAGCUA	Cleavage
spe-miR9473-1-5p	Sopen01g048470.1	3.0	-1.0	1	21	1512	1532	UGGCUGUAAAUCUGAACUCGU	UGGAGUUCAGUUUUACACCCA	Translation
spe-miR9473-1-5p	Sopen06g007270.1	3.0	-1.0	1	21	119	139	UGGCUGUAAAUCUGAACUCGU	CUGAGUUGAGAUUUACAACUA	Cleavage
spe-miR9473-2-3p	Sopen09g033590.1	2.5	-1.0	1	21	35	55	AAACGAGUUCAGAUUUACAGC	UUUGUGAAUCUGAACUUUUUU	Cleavage
spe-miR9473-2-3p	Sopen08g022910.1	3.0	-1.0	1	21	868	888	AAACGAGUUCAGAUUUACAGC	GCAGUAAUUCUGGACUUGUUU	Cleavage
spe-miR9473-2-3p	Sopen08g019890.1	3.0	-1.0	1	21	523	543	AAACGAGUUCAGAUUUACAGC	UGUAUGGAUUUGAACUUGUUU	Cleavage
spe-miR9476-1-3p	Sopen02g018520.1	2.5	-1.0	1	21	73	93	AAAAAAAUGCAGGACUAGACC	AGUCUAGUUCUGCGUUUUGUU	Cleavage
spe-miR9476-1-3p	Sopen04g004780.1	3.0	-1.0	1	21	60	80	AAAAAAAUGCAGGACUAGACC	UAUCUUGUUCUUCAUUUUUUU	Translation
spe-miR9476-1-5p	Sopen06g002350.1	3.0	-1.0	1	21	1071	1091	UCUAGUCCUGCAUCUCUUUUU	CAAAAGGGAUGCAGGACUACU	Cleavage
spe-miR9476-1-5p	Sopen06g019610.1	3.0	-1.0	1	21	64	84	UCUAGUCCUGCAUCUCUUUUU	AGGAGAAGAUGCAGGAUUAGG	Cleavage
spe-miR9476-1-5p	Sopen01g041170.1	3.0	-1.0	1	21	255	275	UCUAGUCCUGCAUCUCUUUUU	UGAAAGAGAUGCACGGCUAGC	Cleavage
spe-miR9476-1-5p	Sopen11g008560.1	3.0	-1.0	1	21	810	830	UCUAGUCCUGCAUCUCUUUUU	GGGUGGAGAUGCAGGAUUGGA	Cleavage
spe-miR9476-1-5p	Sopen09g015910.1	3.0	-1.0	1	21	384	404	UCUAGUCCUGCAUCUCUUUUU	GGAAAAAGAUGCAGCACUAGG	Cleavage
spe-miR9476-1-5p	Sopen08g003480.1	3.0	-1.0	1	21	732	752	UCUAGUCCUGCAUCUCUUUUU	ACGAGGAGGUGCAGGGUUGGA	Cleavage
spe-miR9476-1-5p	Sopen06g030170.1	3.0	-1.0	1	21	1080	1100	UCUAGUCCUGCAUCUCUUUUU	UGAGAUAGAUGCAGCACUAGA	Cleavage
spe-miR9476-1-5p	Sopen12g031790.1	3.0	-1.0	1	21	102	122	UCUAGUCCUGCAUCUCUUUUU	UCAAAGAAAUGCAGAACUGGA	Cleavage
spe-miR9476-2-3p	Sopen02g028690.2	3.0	-1.0	1	21	1975	1995	AAAGAGAUGCAGGACUAGACC	AAGCUGGUUUUGCAUCUUUUU	Cleavage
spe-miR9476-2-3p	Sopen02g028690.1	3.0	-1.0	1	21	1975	1995	AAAGAGAUGCAGGACUAGACC	AAGCUGGUUUUGCAUCUUUUU	Cleavage
spe-miR9476-2-3p	Sopen08g006390.1	2.0	-1.0	1	21	2240	2260	AAAGAGAUGCAGGACUAGACC	CCACUAAUCCUGCAUCUCUUU	Cleavage
spe-miR9476-2-3p	Sopen06g028710.1	2.5	-1.0	1	21	2420	2440	AAAGAGAUGCAGGACUAGACC	AUUCUAGCCCUUCAUCUCUUU	Translation
spe-miR9476-2-3p	Sopen05g004620.1	3.0	-1.0	1	21	248	268	AAAGAGAUGCAGGACUAGACC	CUUCUAGUCUUGGAUCUCUUA	Cleavage
spe-miR9476-2-3p	Sopen12g007130.1	3.0	-1.0	1	21	1391	1411	AAAGAGAUGCAGGACUAGACC	UUUCUGGACUUGCAUCUCUUG	Cleavage
spe-miR9476-2-3p	Sopen09g034400.1	3.0	-1.0	1	21	86	106	AAAGAGAUGCAGGACUAGACC	CAUCUAUUUCUGCAUCUGUUU	Cleavage
spe-miR9476-2-3p	Sopen01g030930.1	3.0	-1.0	1	21	895	915	AAAGAGAUGCAGGACUAGACC	CCUCUAGACUUGCAUCACUUU	Cleavage
spe-miR9476-2-5p	Sopen12g009280.1	2.0	-1.0	1	21	1902	1922	UCUAGUCCUGCAUUUUUUUUU	AAAAGAAAGUGUAGGACUGGA	Cleavage
spe-miR9476-2-5p	Sopen07g026950.1	2.0	-1.0	1	21	587	607	UCUAGUCCUGCAUUUUUUUUU	AGAAAAAAAUGGAGGACUGGA	Translation
spe-miR9476-2-5p	Sopen12g032490.1	2.5	-1.0	1	21	1941	1961	UCUAGUCCUGCAUUUUUUUUU	AAAAGAAACUGUAGGACUAGA	Cleavage
spe-miR9476-2-5p	Sopen08g016040.1	2.5	-1.0	1	21	975	995	UCUAGUCCUGCAUUUUUUUUU	AAAAGAAACUGUAGGACUAGA	Cleavage
spe-miR9476-2-5p	Sopen06g019610.1	2.5	-1.0	1	21	64	84	UCUAGUCCUGCAUUUUUUUUU	AGGAGAAGAUGCAGGAUUAGG	Cleavage
spe-miR9476-2-5p	Sopen05g019280.1	2.5	-1.0	1	21	392	412	UCUAGUCCUGCAUUUUUUUUU	GAAAAAAAAUGCAUGAUUGGA	Cleavage
spe-miR9476-2-5p	Sopen09g015910.1	2.5	-1.0	1	21	384	404	UCUAGUCCUGCAUUUUUUUUU	GGAAAAAGAUGCAGCACUAGG	Cleavage
spe-miR9476-2-5p	Sopen12g031790.1	2.5	-1.0	1	21	102	122	UCUAGUCCUGCAUUUUUUUUU	UCAAAGAAAUGCAGAACUGGA	Cleavage
spe-miR9476-2-5p	Sopen09g009460.1	2.5	-1.0	1	21	703	723	UCUAGUCCUGCAUUUUUUUUU	ACAAAAAUGUGCAGGAUUGGA	Cleavage
spe-miR9476-2-5p	Sopen02g019620.1	2.5	-1.0	1	21	1503	1523	UCUAGUCCUGCAUUUUUUUUU	CCAAACAAAUGCAGGACCAGA	Cleavage
spe-miR9476-2-5p	Sopen00g006180.1	2.5	-1.0	1	21	192	212	UCUAGUCCUGCAUUUUUUUUU	UGAACAACAUGCAGGACUGGA	Cleavage

spe-miR9476-2-5p	Sopen05g002910.1	3.0	-1.0	1	21	1533	1553	UCUAGUCCUGCAUUUUUUUUU	AAAGAAAGAUGCAGGAUCAGA	Cleavage
spe-miR9476-2-5p	Sopen06g009570.1	3.0	-1.0	1	21	442	462	UCUAGUCCUGCAUUUUUUUUU	AAGAAAAAAAGUAGGAUUAGA	Cleavage
spe-miR9476-2-5p	Sopen08g025150.1	3.0	-1.0	1	21	691	711	UCUAGUCCUGCAUUUUUUUUU	AAGAAGAAACGCAGGAUUAGA	Cleavage
spe-miR9476-2-5p	Sopen08g005570.1	3.0	-1.0	1	21	1932	1952	UCUAGUCCUGCAUUUUUUUUU	GAAAGAAACUGUAGGACUGGA	Cleavage
spe-miR9476-2-5p	Sopen04g027640.1	3.0	-1.0	1	21	662	682	UCUAGUCCUGCAUUUUUUUUU	AGGAAAGAAUGGAGGACUGGA	Translation
spe-miR9476-2-5p	Sopen11g015320.1	3.0	-1.0	1	21	9	29	UCUAGUCCUGCAUUUUUUUUU	GAGGAGAAAUGCAGGAGUAGA	Cleavage
spe-miR9476-2-5p	Sopen07g008460.1	3.0	-1.0	1	21	2169	2189	UCUAGUCCUGCAUUUUUUUUU	CAAAAAGAAUGCAGAACUGGG	Cleavage
spe-miR9476-2-5p	Sopen10g035000.1	3.0	-1.0	1	21	818	838	UCUAGUCCUGCAUUUUUUUUU	UAAAGGAAAUGCAGGAUGAGA	Cleavage
spe-miR9476-2-5p	Sopen05g031950.1	3.0	-1.0	1	21	332	352	UCUAGUCCUGCAUUUUUUUUU	UAAAGAAAAUGCAUGAUUGGA	Cleavage
spe-miR9477-3p	Sopen04g014070.1	3.0	-1.0	1	24	2599	2622	UUGGGAAAGGGAACAACUGAUAGU	CAGUUCAGUUGGUCUCUUUUUCAA	Cleavage
spe-miR9477-3p	Sopen04g014070.1	3.0	-1.0	1	24	5116	5139	UUGGGAAAGGGAACAACUGAUAGU	CAGUUCAGUUGGUCUCUUUUUCAA	Cleavage
spe-miR9477-3p	Sopen08g003550.1	2.0	-1.0	1	24	2196	2219	UUGGGAAAGGGAACAACUGAUAGU	ACACCCAAUUGUUUCUUUUCCCAA	Cleavage
spe-miR9477-3p	Sopen08g003550.2	2.0	-1.0	1	24	2196	2219	UUGGGAAAGGGAACAACUGAUAGU	ACACCCAAUUGUUUCUUUUCCCAA	Cleavage
spe-miR9477-3p	Sopen07g014230.1	3.0	-1.0	1	24	1584	1607	UUGGGAAAGGGAACAACUGAUAGU	UCUUUCAAUUGGUCCUUUUCCCAA	Cleavage
spe-miR9477-3p	Sopen12g016570.1	3.0	-1.0	1	24	3157	3180	UUGGGAAAGGGAACAACUGAUAGU	CAGUUCAGUUGGUCUCUUUUUCAA	Cleavage
spe-miR9477-3p	Sopen11g010840.1	3.0	-1.0	1	24	307	330	UUGGGAAAGGGAACAACUGAUAGU	CAGUUCAGUUGGUCUCUUUUUCAA	Cleavage
spe-miR9477-3p	Sopen03g032070.1	3.0	-1.0	1	24	45	68	UUGGGAAAGGGAACAACUGAUAGU	CGUUUCGGUCGUUUCUUUUCUCAA	Cleavage
spe-miR9477-3p	Sopen04g033000.1	3.0	-1.0	1	24	1637	1660	UUGGGAAAGGGAACAACUGAUAGU	UGGAGGAGUUGUUCCCCUUUCCAA	Cleavage
spe-miR9477-3p	Sopen02g025470.1	3.0	-1.0	1	24	157	180	UUGGGAAAGGGAACAACUGAUAGU	GUCAGCAGUUGUUCUUUUUCUUGG	Cleavage
spe-miR9477-3p	Sopen01g029630.1	3.0	-1.0	1	24	474	497	UUGGGAAAGGGAACAACUGAUAGU	UCAUUCAACUGUUUCCUUUCCUAA	Cleavage
spe-miR9477-3p	Sopen01g029630.2	3.0	-1.0	1	24	474	497	UUGGGAAAGGGAACAACUGAUAGU	UCAUUCAACUGUUUCCUUUCCUAA	Cleavage
spe-miR9477-5p	Sopen01g034420.1	3.0	-1.0	1	24	4022	4045	UAUCAGUUGUUCUCUUUUCCUACC	CCCCUGAGAAGAGAGCAGCUGCUA	Cleavage
spe-miR9477-5p	Sopen01g034420.2	3.0	-1.0	1	24	4019	4042	UAUCAGUUGUUCUCUUUUCCUACC	CCCCUGAGAAGAGAGCAGCUGCUA	Cleavage
spe-miR9477-5p	Sopen06g023990.1	2.0	-1.0	1	24	470	493	UAUCAGUUGUUCUCUUUUCCUACC	UUUGUGAAAAGGGAAUGGCUGAUA	Cleavage
spe-miR9477-5p	Sopen02g023090.1	2.0	-1.0	1	24	2464	2487	UAUCAGUUGUUCUCUUUUCCUACC	AAGAAGAGAACAGAACAACUGAUG	Cleavage
spe-miR9477-5p	Sopen11g024210.1	2.0	-1.0	1	24	2690	2713	UAUCAGUUGUUCUCUUUUCCUACC	AACUUGGCAAGAGGACAACUGAUA	Cleavage
spe-miR9477-5p	Sopen03g022800.2	2.5	-1.0	1	24	857	880	UAUCAGUUGUUCUCUUUUCCUACC	UGAAGGAAAGGAGAGUGACUGAUG	Cleavage
spe-miR9477-5p	Sopen03g022800.1	2.5	-1.0	1	24	854	877	UAUCAGUUGUUCUCUUUUCCUACC	UGAAGGAAAGGAGAGUGACUGAUG	Cleavage
spe-miR9477-5p	Sopen12g033960.1	2.5	-1.0	1	24	1397	1420	UAUCAGUUGUUCUCUUUUCCUACC	UACGGGAGAAGGGUACAACUGAUA	Translation
spe-miR9477-5p	Sopen12g005240.1	2.5	-1.0	1	24	207	230	UAUCAGUUGUUCUCUUUUCCUACC	UGCUGGAAAAGAGAAUAACAGAUG	Cleavage
spe-miR9477-5p	Sopen01g028320.1	2.5	-1.0	1	24	692	715	UAUCAGUUGUUCUCUUUUCCUACC	AUGAAGGAAAGAGAACAGCUGAGA	Cleavage
spe-miR9477-5p	Sopen05g030590.1	2.5	-1.0	1	24	799	822	UAUCAGUUGUUCUCUUUUCCUACC	GAGGUGAAAAGAGAACAAAUGGUG	Cleavage
spe-miR9477-5p	Sopen05g031940.1	2.5	-1.0	1	24	178	201	UAUCAGUUGUUCUCUUUUCCUACC	CAGCAGAAAGGAGAGCAAAUGAUA	Cleavage
spe-miR9477-5p	Sopen03g015720.2	2.5	-1.0	1	24	1952	1975	UAUCAGUUGUUCUCUUUUCCUACC	UUGGAGAUGGGGGAACAACUGAUA	Cleavage
spe-miR9477-5p	Sopen12g002660.1	3.0	-1.0	1	24	962	985	UAUCAGUUGUUCUCUUUUCCUACC	AAUGGGAAAGGAGAAAAACUGGUG	Cleavage
spe-miR9477-5p	Sopen11g005080.1	3.0	-1.0	1	24	970	993	UAUCAGUUGUUCUCUUUUCCUACC	AGAAGGAAAAGAGAGAAACUGGUG	Cleavage
spe-miR9477-5p	Sopen12g032070.1	3.0	-1.0	1	24	1052	1075	UAUCAGUUGUUCUCUUUUCCUACC	CUUGGAAAGAGAGAAUAACUGAUC	Cleavage
spe-miR9477-5p	Sopen07g016960.1	3.0	-1.0	1	24	7235	7258	UAUCAGUUGUUCUCUUUUCCUACC	GGGAAGGAAAGAGUACAGCUGAUG	Translation
spe-miR9477-5p	Sopen02g013560.1	3.0	-1.0	1	24	748	771	UAUCAGUUGUUCUCUUUUCCUACC	GCAUGGAAAAGAGGAUACCUGAUG	Cleavage
spe-miR9477-5p	Sopen02g026160.1	3.0	-1.0	1	24	848	871	UAUCAGUUGUUCUCUUUUCCUACC	AGAUGGAGAAGAGGGCAGUUGGUA	Cleavage
spe-miR9477-5p	Sopen12g002990.1	3.0	-1.0	1	24	2074	2097	UAUCAGUUGUUCUCUUUUCCUACC	UCUAAGAAAGAUGAACAACUGAUA	Cleavage
spe-miR9477-5p	Sopen04g014040.1	3.0	-1.0	1	24	4835	4858	UAUCAGUUGUUCUCUUUUCCUACC	UUGAUGAGAAGAGAAUGGUUGAUG	Cleavage
spe-miR9477-5p	Sopen01g023330.1	3.0	-1.0	1	24	1092	1115	UAUCAGUUGUUCUCUUUUCCUACC	ACAUAAGAAAGAGGACAACUGGUG	Cleavage
spe-miR9477-5p	Sopen09g001890.1	3.0	-1.0	1	24	1568	1591	UAUCAGUUGUUCUCUUUUCCUACC	AAUCUGAAAAGGAAAUGACUGAUA	Cleavage
spe-miR9477-5p	Sopen03g018410.1	3.0	-1.0	1	24	2066	2089	UAUCAGUUGUUCUCUUUUCCUACC	UUGUUGAGAGGAGAACUACUGAUG	Cleavage
spe-miR9477-5p	Sopen00g008700.2	3.0	-1.0	1	24	1031	1054	UAUCAGUUGUUCUCUUUUCCUACC	AAUCUGAAAAGGAAAUGACUGAUA	Cleavage
spe-miR9477-5p	Sopen00g008700.1	3.0	-1.0	1	24	1013	1036	UAUCAGUUGUUCUCUUUUCCUACC	AAUCUGAAAAGGAAAUGACUGAUA	Cleavage
spe-miR9477-5p	Sopen04g030380.1	3.0	-1.0	1	24	1548	1571	UAUCAGUUGUUCUCUUUUCCUACC	AAGGAGAAAAGAGGACGGCUCAUA	Cleavage

458 **Supplementary Table S14.** Expression profile values, showed in count per million (CPM), between flowers and leaves of the *Solanum*
459 *lycopersicum* (Sly) and *Solanum pennellii* (Spe).

Gene	ID	Expression values in flowers (CPM)	Expression values in leaves (CPM)
SlyABH1	Solyc10g005530.3.1	115.444852	52.1872168
SlyAGO1.1	Solyc06g072300.3.1	554.549283	236.476941
SlyAGO1.2	Solyc03g098280.3.1	983.936678	276.205843
SlyAGO10.1	Solyc09g082830.3.1	338.57108	60.7240166
SlyAGO10.2	Solyc12g006790.2.1	95.8993628	9.21962841
SlyCBP20	Solyc02g062620.3.1	129.33665	91.3615657
SlyCDC5	Solyc04g009950.3.1	166.48385	116.105279
SlyCPL1	Solyc02g078550.3.1	60.6229746	48.663535
SlyDCL1	Solyc10g005130.3.1	91.7558091	104.242512
SlyDDL	Solyc10g006390.3.1	73.2100946	37.3722361
SlyEXO.1	Solyc04g074450.1.1	5.3392198	25.2812386
SlyEXO.2	Solyc04g074410.2.1	47.0192544	21.4652852
SlyEXO.3	Solyc04g074440.1.1	1.26156435	21.0011354
SlyEXO.4	Solyc04g074400.1.1	1.71196188	1.96351561
SlyHEN	Solyc02g070030.3.1	8.44937955	9.52887989
SlyHESO1.1	Solyc06g051790.3.1	23.0835192	17.3695524
SlyHESO1.2	Solyc11g044900.2.1	17.6155718	18.360006
SlyHST	Solyc01g098170.3.1	49.5060962	37.1582806
SlyHYL1	Solyc04g076420.3.1	39.4395615	25.6856802
SlyNOT2.1	Solyc11g072940.2.1	54.087307	44.9573852
SlyNOT2.2	Solyc06g075590.3.1	79.2242882	65.6660652
SlySE	Solyc01g009090.3.1	190.729155	100.339415
SlySQN.1	Solyc01g108340.3.1	40.1230857	18.0619814
SlySQN.2	Solyc02g090480.3.1	25.8472208	4.08469482
SlySTA1	Solyc07g054200.3.1	107.87164	77.08357

SlyTGH	Solyc03g114410.3.1	56.7897735	33.0774406
SlyVCS1.1	Solyc07g065950.3.1	167.794026	147.861092
SlyVCS1.2	Solyc10g005920.3.1	28.2916594	25.5557185
SlyXRN4	Solyc04g049010.3.1	54.6603746	33.1742515
SpeABH1	Sopen10g001510.1	74.17147916	41.82168983
SpeAGO1.1	Sopen06g028670.1	561.7262007	234.6132123
SpeAGO1.2	Sopen03g028990.1	797.8744787	182.5957222
SpeAGO10	Sopen09g031660.1	272.3394847	36.99650933
SpeCBP20	Sopen02g013650.1	14.01122266	13.14750259
SpeCPL1	Sopen02g023400.1	42.96757865	39.77289285
SpeDCL1	Sopen10g001150.1	79.92114549	86.06395606
SpeDDL	Sopen10g002340.1	49.45302454	22.66397733
SpeEXO.1	Sopen04g029470.1	25.86088596	10.0061042
SpeEXO.2	Sopen04g029460.1	0.454449558	0.00000000
SpeEXO.3	Sopen01g047900.1	52.23479504	42.49424417
SpeEXO.4	Sopen04g029480.1	9.531894255	10.19669835
SpeEXO.5	Sopen10g027040.1	112.3584832	49.36014175
SpeEXO.6	Sopen03g023370.1	53.16402678	19.64904854
SpeEXO.7	Sopen02g017980.1	2.368545132	1.402463911
SpeEXO.8	Sopen06g011130.1	42.19569417	8.716362738
SpeHEN	Sopen02g019190.1	29.98277927	22.95094378
SpeHESO1.1	Sopen06g017790.1	18.248202	26.6204945
SpeHESO1.2	Sopen09g034750.1	28.5515385	11.60838765
SpeHST	Sopen01g041740.1	3.966331996	3.452130078
SpeHYL1	Sopen04g030180.1	30.57804613	17.47057378
SpeNOT2.2	Sopen06g031990.1	0.50620271	1.353570116
SpeSE	Sopen01g004580.1	190.9284597	75.39198166
SpeSQN.1	Sopen01g050560.1	26.87909008	13.2713065

SpeSQN.2	Sopen02g035160.1	13.95862105	1.787305332
SpeSTA1	Sopen07g028130.1	109.6964154	68.49296034
SpeTGH	Sopen03g033510.1	37.88674519	34.73325799
SpeVCS.1	Sopen07g034150.1	202.3288705	118.2873192
SpeVCS.2	Sopen10g001880.1	129.9715733	140.5036149
SpeXRN4	Sopen04g018450.1	37.69853894	34.35767022

Supplementary Table S15. Validation of the presence tomato mature miRNAs identified in *S. lycopersicum* small RNAs libraries available in the SRA. The accessions numbers of the libraries in the SRA: S1 (SRR039920), S2 (SRR039921), S3 (SRR039922), S4 (SRR039923), S5 (SRR039924), S6 (SRR039925), S7 (SRR039926), S8 (SRR039927), S9 (SRR039928), S10 (SRR039929), S11 (SRR065156), S12 (SRR065157), S13 (SRR627529), S14 (SRR627530), S15 (SRR627531), S16 (SRR627532), S17 (SRR627533), S18 (SRR627534), S19 (SRR627535), S20 (SRR943813), S21 (SRR943814), S22 (SRR943815), S23 (SRR943816), S24 (SRR943817), S25 (SRR943818), S26 (SRR943819), S27 (SRR943820), S28 (SRR943821), S29 (SRR943822), S30 (SRR943823).

miRNA	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15	S16	S17	S18	S19	S20	S21	S22	S23	S24	S25	S26	S27	S28	S29	S30
sly-miR1128	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR1446-1/2-5p	0	0	1	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156a-1/a-2-5p	768	205	33	54	235	1438	186	5264	227	1679	6918	5537	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156a-2-3p	0	0	0	0	0	1	0	0	0	0	0	1	2	1	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156c-5p	3	3	4	3	4	0	0	6	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156f	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156i-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156i-1-5p	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156i-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
sly-miR156i-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156l-1-3p/l-2-3p	0	0	0	0	0	1	0	2	2	0	0	3	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156l-1-5p/l-2-5p	768	205	33	54	235	1438	186	5264	227	1679	6918	5537	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR157a-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR157a-1-5p/a-2-5p/a-3-5p/a-4-5p	26799	9243	1874	1072	3406	13604	970	6063	288	1560	137345	98349	0	0	1	1	0	0	0	0	0	0	0	0	0	3	0	1	0	0
sly-miR157a-2-3p	0	0	0	0	0	0	0	0	0	0	6	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR157a-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR159a-3p	9	4	18	14	14	1	0	0	0	1	5	21	238	201	48	50	9	11	21	0	0	0	0	0	0	0	0	0	0	0
sly-miR159a-5p	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR159b-3p	0	0	0	0	0	13	6	5	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR159b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
sly-miR160a-5p	19	0	0	6	8	3	0	1	0	1	2	17	20	8	2	1	1	0	0	5	2	0	0	0	0	1	1	2	0	0
sly-miR160g-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160h-1	19	0	0	6	8	3	0	1	0	1	2	17	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160h-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR162-1-3p/2-3p	263	243	115	39	139	487	109	411	28	73	559	760	2	2	15	16	3	8	11	0	0	1	0	0	0	0	0	0	1	0

sly-miR162-1-5p/2-5p	81	215	36	51	46	95	19	63	7	49	22	107	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
sly-miR164a-3p	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR164a-5p	56824	21320	2454	2683	8608	36098	55365	648975	48506	489556	11131	10817	2	7	19	16	11	18	21	0	0	0	0	0	0	0	0	0	0	0
sly-miR164e-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR164e-5p	553	456	64	35	140	293	558	4754	425	3656	43	93	2	7	19	16	0	18	21	0	0	0	0	0	0	0	0	0	0	0
sly-miR164f	3	0	0	0	0	1	0	4	0	4	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR166-1/2/3	504	1365	79	64	164	578	112	508	36	121	339	206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR166a-1-3p/a-2-3p/a-3-3p/a-4-3p	9900	6543	1667	2016	6418	27123	5424	21115	1025	4708	9665	2029	5	3	0	2	1	0	0	1	0	0	0	0	1	1	0	0	1	1
sly-miR166a-2-5p	2	2	3	6	12	0	2	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR166a-4-5p	26	39	385	459	1028	48	55	45	7	13	33	187	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR166g-3p	12655	6902	1482	683	2143	6159	1111	4085	196	1311	4235	812	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	1	0	0
sly-miR167a-1-3p	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167a-1-5p/a-2-5p	540	1430	63	5	26	78	0	23	0	5	207	491	47	39	25	23	0	1	1	0	0	0	0	0	0	1	0	0	0	0
sly-miR167a-2-3p	8	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167c-3p	1	0	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167c-5p	540	1430	63	5	26	78	0	23	0	5	207	491	47	39	25	23	0	1	1	0	0	0	0	0	0	1	0	0	0	0
sly-miR167h-1/h-2	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167h-3-3p	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167h-3-5p	539	1426	63	5	26	77	0	23	0	5	206	487	47	39	25	23	0	1	1	0	0	0	0	0	0	0	0	0	0	0
sly-miR168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
sly-miR168a-1-3p	1	8	7	2	6	13	0	16	0	7	6	4	0	2	2	1	8	8	5	0	0	0	1	0	0	0	0	0	0	0
sly-miR168a-1-5p/a-2-5p	29	18	26	20	26	17	19	20	6	9	0	13	0	0	0	0	6	0	0	0	1	2	2	0	0	0	0	3	3	2
sly-miR168a-2-3p	2	8	1	2	15	17	5	18	0	17	11	11	0	0	0	0	1	0	0	0	0	2	0	0	0	1	1	0	0	1
sly-miR169a-1-3p/b-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169b-1-5p/b-2-5p/b-3-5p	5	2	11	8	5	0	5	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169d-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169d-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169e-3p	2	3	0	2	8	23	0	14	0	1	26	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169e-5p	3	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169f-1	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169g	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169m	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR170-1-3p	103	81	0	0	3	1	0	2	0	1	49	217	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

sly-miR170-1-5p/2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR170-2-3p	106	82	2	0	3	1	0	2	0	1	40	215	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171b-1-3p/b-2-3p	10	5	1	0	11	2	0	0	0	0	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171b-1-5p	0	1	1	0	0	0	0	0	0	0	1	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171b-3	115	86	3	0	14	3	0	2	0	1	42	215	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171c-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171c-1-5p	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171c-2/c-3-3p	1	2	0	0	0	0	0	0	0	0	3	4	0	0	0	0	1	0	0	0	0	2	1	0	0	0	1	1	2	0
sly-miR171c-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171c-4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171f	0	0	0	0	1	6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171i-3p	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-1	76	259	16	2	9	18	9	11	1	11	2	118	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-10-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
sly-miR172d-10-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
sly-miR172d-2/d-4-3p	62	103	11	4	18	22	5	28	0	12	13	97	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	3	0
sly-miR172d-2-3p/d-6-3p	62	103	11	4	18	22	5	28	0	12	13	97	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-4-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5-3p	9	0	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5-5p	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5p	2	2	0	0	1	2	0	0	0	0	1	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-6-5p	2	1	1	1	8	2	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-7-3p	62	103	11	4	18	22	5	28	0	12	13	97	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-7-5p	12	3	0	0	0	0	0	0	0	0	0	0	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-8-3p	9	5	4	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	2	9	2	13	0	1	3	5	1
sly-miR172d-8-5p	132	40	13	0	6	7	0	6	0	0	2	22	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-9-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-9-5p	2	1	1	1	7	2	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172j-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172j-1-5p/j-2-5p	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172j-2-3p	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR1886a	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR1886h-1/h-2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR1917-1/2	3	0	0	0	7	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	1
sly-miR1918	4	0	2	3	9	0	2	0	0	3	0	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

sly-miR1919a-1/a-2/a-3	12	0	2	1	5	11	16	6	3	6	1	16	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	2	1
sly-miR2101-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2111a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2111a-5p	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2604	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319-3p-1/3p-2	95	11	0	2	14	15	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0
sly-miR319-5p-1	3	5	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319-5p-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
sly-miR319a-1-3p/a-2-3p	7303	32	84	41	96	26	34	69	1	21	2929	2252	2	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
sly-miR319a-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319a-2-5p	1	3	0	0	0	0	0	0	0	0	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319c-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319c-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319c-2-5p	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	2	1	0
sly-miR319c-3-3p	7303	32	84	42	96	28	34	69	1	21	2929	2252	2	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
sly-miR319c-3-5p	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR3627-3p	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR3627-5p	156	345	17	3	7	8	0	11	1	2	22	78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR390a-3p	0	4	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR390a-5p	21	175	25	0	1	0	0	0	0	0	11	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR390b-3p	0	0	0	1	0	1	0	0	0	0	5	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR390b-5p	3	9	4	0	4	2	2	0	0	0	23	32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR393a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR393a-5p	9	1	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR394b-3p	5	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR394b-5p/a	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR395a-1/a-3	5	2	0	5	26	16	2	3	0	0	1	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR395a-2/a-4-5p	5	0	0	2	19	5	2	3	0	0	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR395a-4-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR395g	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR396a-3p	23	21	6	162	385	103	27	104	2	42	17	71	27	29	182	192	0	8	6	2	1	0	0	0	0	3	2	2	0	0
sly-miR396a-5p	1	8	0	5	8	8	3	4	1	1	2	32	0	0	0	0	0	0	0	0	1	0	0	0	0	1	2	0	1	0
sly-miR396b-3p	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	2	0	3	2	0	0	0	0	1	0	0	0	0	0	0
sly-miR396b-5p	47	42	14	10	51	60	24	19	6	13	30	119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR396g-1-3p/g-2-3p	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0

sly-miR396g-1-5p	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR396g-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
sly-miR397-1-3p	2	5	4	0	2	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR397-1-5p	0	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR397-2-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR397-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
sly-miR398a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR398a-5p	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR398b-3p	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399a-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399a-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399a-3-3p/a-4-3p/a-5-3p	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399a-3-5p/a-4-5p/a-5-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399d-1/d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399d-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399d-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399i-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399j-2/j-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399j-3-5p	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR403-3p	105	64	16	8	48	171	48	172	7	47	94	89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR403-5p	2	1	0	1	2	2	0	1	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR403a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR403a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408-1	1	0	3	3	5	3	20	3	3	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408-2-3p	0	0	1	0	0	0	0	9	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408-2-5p	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408a-5p	3	0	0	2	2	1	17	4	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR437	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR4376-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR4376-5p	1064	964	142	31	62	241	31	30	2	14	201	925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR477-3p	0	0	1	0	5	19	0	7	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR477-5p	5	0	0	1	5	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR477a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR477a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

sly-miR477b-3p	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR477b-5p	0	0	0	1	1	0	0	0	0	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR482a-1	52	33	16	14	13	30	16	51	9	2	330	834	3	1	0	0	1	0	0	0	0	1	0	0	0	1	1	0	0	0
sly-miR482a-2-3p	119	49	19	2	5	11	2	16	2	0	69	411	39	28	1	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
sly-miR482a-2-5p	0	0	0	0	0	0	0	0	0	2	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR482c	21	19	17	3	11	6	7	6	0	3	40	141	3	10	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
sly-miR482d-3p	112	78	52	55	28	42	43	50	17	13	70	146	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	1	1	0
sly-miR482d-5p	0	0	7	0	9	1	2	0	0	0	0	2	3	4	2	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
sly-miR482e-3p	29	34	9	2	4	10	3	29	0	0	8	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR482e-5p	0	2	0	2	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5014a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5174d-5p	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5282-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5282-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR530	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5300-5p	673	1538	60	23	34	113	30	94	10	14	367	769	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5303	1	5	6	2	7	2	8	3	0	1	6	6	12	8	15	24	0	10	10	13	11	6	2	0	1	6	10	6	7	6
sly-miR5303c	3	2	0	0	0	6	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2	0	2	0	1	1	0	1	0	1
sly-miR5303f	13	6	6	4	6	30	51	23	43	17	32	27	0	0	0	0	0	0	0	7	3	5	0	0	0	2	2	2	1	0
sly-miR5303g	128	51	39	23	45	26	29	28	9	22	55	147	4	4	22	24	1	28	26	17	15	9	1	0	6	11	11	11	10	2
sly-miR5303h-1/h-2	118	46	41	51	41	56	40	46	17	40	60	139	4	3	22	25	0	34	31	21	16	11	3	0	8	14	12	12	13	2
sly-miR5303j-1/j-2	127	50	40	23	43	29	32	28	9	18	56	145	4	3	22	24	0	28	26	17	13	9	1	0	6	11	11	10	9	3
sly-miR5304-3p	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
sly-miR5304-5p	3	4	0	0	0	6	0	0	0	0	2	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5368	0	0	0	0	0	5	1	0	0	1	0	2	0	0	0	1	0	3	0	6	54	88	12	2	0	63	268	10	36	102
sly-miR5532-1/2	0	0	4	0	0	6	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
sly-miR6024-3p	48	187	20	3	8	28	3	29	4	6	15	142	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR6024-5p	0	6	2	0	0	3	0	2	0	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	1
sly-miR6027-3p	2319	10070	1863	609	1423	4627	730	2998	186	808	2105	4940	4	10	5	2	0	1	1	3	1	2	1	0	0	1	1	2	2	2
sly-miR6027-5p	10	16	35	6	10	6	1	8	0	4	5	21	0	0	1	1	0	0	0	0	0	2	0	0	0	0	1	0	1	0
sly-miR7122-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7122-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7696c-3p	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7805-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7980b-2-3p	6	1	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

sly-miR7980b-2-5p	1	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
sly-miR7980b-3p-1	0	4	0	0	2	4	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7981-3p	9	5	1	3	3	2	5	0	0	0	0	9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7981-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-1-3p/2-3p/3-3p	83	76	49	14	40	59	16	24	1	18	51	113	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-3-5p	3	2	3	3	1	2	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-4-3p	4	2	2	1	1	0	0	0	0	3	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-4-5p/5-5p/6-5p	7	3	0	3	8	5	6	4	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
sly-miR7983-5-3p	10	3	3	0	1	1	3	1	0	1	5	16	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7983-6-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7984c-3p	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7984c-5p	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7984d-3p	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7985	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	1	0	0	2	3	4	5	1
sly-miR7987-3p	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
sly-miR7987-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7990a-1/a-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7990a-3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7992-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7992-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7993a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7997a	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
sly-miR8001a	0	0	1	0	4	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8001b-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8001b-1-5p/b-2-5p	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8006-1-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
sly-miR8006-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8006-2-5p	9	7	7	5	9	14	12	10	4	9	25	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8007a-5p	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8007b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8007b-5p	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008a-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008a-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

sly-miR8008a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-1-5p/b-3-3p	2	2	1	2	1	2	6	2	0	2	4	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8011a-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8011a-2-3p	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
sly-miR8011a-2-5p	2	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
sly-miR8013	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8019-1-3p/2-3p	32	16	16	8	10	16	28	17	3	12	9	40	0	0	0	0	0	0	0	3	3	0	0	0	0	2	3	1	1	0
sly-miR8019-1-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8019-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
sly-miR8020	3	1	0	0	0	0	1	0	0	0	0	4	0	0	0	0	0	0	0	1	1	0	0	0	0	1	1	1	1	0
sly-miR8021-1/2/3	1	3	0	0	0	1	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8025-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8025-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8032d-3p	3	3	4	0	1	7	10	16	8	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0
sly-miR8033-3p	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8033-5p	0	7	0	0	0	1	2	4	0	2	4	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8038a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8038a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
sly-miR8039-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8039-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8045-1/2-5p	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0
sly-miR8045-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8051-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR827-3p	0	3	3	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR827-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR828a	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR845b-5p	0	0	0	0	2	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
sly-miR9471a-3p	29	119	95	76	192	86	45	46	7	39	18	31	0	0	4	3	0	6	11	0	0	0	0	0	0	0	0	0	0
sly-miR9471a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9471b-3p	5	13	23	16	52	18	6	4	0	8	5	25	0	0	25	27	0	3	2	0	0	0	0	0	0	0	0	0	0

sly-miR9471b-5p	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
sly-miR9472-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0
sly-miR9472-5p	1	2	3	0	0	2	0	1	0	3	1	2	0	0	0	0	0	1	1	0	0	0	0	0	0	2	2	1	0	0
sly-miR9473-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-1-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9476-1-3p/2-3p	0	3	2	0	3	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9476-1-5p/2-5p	2	1	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9478-3p	2	4	2	0	0	2	0	1	0	3	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9478-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S15. (continuation) Validation of the presence tomato mature miRNAs identified in *S. lycopersicum* small RNAs libraries available in the SRA. The accessions numbers of the libraries in the SRA: S31 (SRR943824), S32 (SRR943825), S33 (SRR943826), S34 (SRR943827), S35 (SRR943828), S36 (SRR943829), S37 (SRR943830), S38 (SRR955375), S39 (SRR955376), S40 (SRR955377), S41 (SRR955378), S42 (SRR955379), S43 (SRR955380), S44 (SRR955381), S45 (SRR955382), S46 (SRR955383), S47 (SRR955384), S48 (SRR1022870), S49 (SRR1022871), S50 (SRR1022872), S51 (SRR1022873), S52 (SRR1028350), S53 (SRR1028351), S54 (SRR1028352), S55 (SRR1028353), S56 (SRR1182757), S57 (SRR1182758), S58 (SRR1223225), S59 (SRR1223226), S60 (SRR1223238).

miRNA	S31	S32	S33	S34	S35	S36	S37	S38	S39	S40	S41	S42	S43	S44	S45	S46	S47	S48	S49	S50	S51	S52	S53	S54	S55	S56	S57	S58	S59	S60
sly-miR1128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
sly-miR1446-1/2-5p	0	0	0	0	0	0	0	18	173	97	3	4	18	0	0	0	0	6	7	32	43	23	21	13	27	0	0	0	0	0
sly-miR156a-1/a-2-5p	0	0	0	0	0	0	0	13598	21798	7788	11155	11930	17721	0	0	0	0	18	17	1	6	2810	1723	1352	668	0	0	0	0	0
sly-miR156a-2-3p	0	0	0	0	0	0	0	9	14	5	6	10	15	7	123	35	58	0	3	0	0	9	6	5	1	0	0	0	0	0
sly-miR156c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	0	103	83	92	53	0	0	0	0	0
sly-miR156c-5p	0	0	0	0	0	0	0	2	3	2	2	2	2	0	0	0	0	3	5	0	1	230	143	145	129	0	0	0	0	0
sly-miR156f	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	4	1	5	3	0	0	0	0	0
sly-miR156i-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156i-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	1	1	0	0	0	0	0
sly-miR156i-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
sly-miR156i-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
sly-miR156l-1-3p/l-2-3p	0	0	0	0	0	0	0	20	48	2	11	18	21	0	0	0	5	100	176	18	16	217	131	70	55	0	0	0	0	0
sly-miR156l-1-5p/l-2-5p	0	0	0	0	0	0	0	13598	21798	7788	11155	11930	17721	0	0	0	0	18	16	1	6	2810	1723	1352	668	0	0	0	0	0
sly-miR157a-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	7	4	7	2	0	0	0	0	0
sly-miR157a-1-5p/a-2-5p/a-3-5p/a-4-5p	0	1	0	1	1	0	0	317265	524722	286818	513214	498705	528163	0	0	15	15	9112	11897	1748	1943	31206	25626	34046	18831	0	0	0	0	0
sly-miR157a-2-3p	0	0	0	0	0	0	0	2	3	4	7	2	6	0	0	0	0	87	106	7	8	151	121	136	85	0	0	0	0	0
sly-miR157a-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	15	1	0	90	69	116	45	0	0	0	0	0
sly-miR159a-3p	0	0	0	2	0	0	0	6	1	1	8	5	0	0	0	3	0	768	607	559	565	201958	205799	180573	111595	0	0	0	0	0
sly-miR159a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	6	1	0	80	75	44	31	0	0	0	0	0
sly-miR159b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	11	4	5	69	63	49	43	0	0	0	0	0

sly-miR159b-5p	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	256	0	0	0	0	0	0	8	6	0	0	0	0	0
sly-miR160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160a-3p	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	2	0	0	0	0	0
sly-miR160a-5p	0	2	2	2	1	0	0	58	122	54	55	154	55	0	0	0	0	224	337	83	111	632	494	430	245	0	0	0	0	0
sly-miR160g-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
sly-miR160h-1	0	1	0	0	0	0	0	58	122	54	55	154	55	0	0	0	0	224	337	83	111	632	494	430	245	0	0	0	0	0
sly-miR160h-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	1	0	0	0	0	0	0
sly-miR162-1-3p/2-3p	0	0	0	0	1	0	0	3569	4166	3007	4692	2862	5043	0	0	32	0	2127	2778	276	249	6857	5656	4826	2913	0	1	0	1	1
sly-miR162-1-5p/2-5p	0	1	0	0	0	1	1	111	173	491	233	147	299	0	0	0	0	1	2	0	0	4	3	1	2	0	0	1	1	1
sly-miR164a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	3	0	0	0	0	0
sly-miR164a-5p	0	0	0	0	0	0	0	2275	2371	5931	5110	5721	2673	18	16	0	0	37	54	5	7	81	72	72	54	0	0	0	0	0
sly-miR164e-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58	65	38	16	0	0	0	0	0
sly-miR164e-5p	0	0	0	0	0	0	0	5	4	18	7	13	6	18	16	0	0	1	1	0	0	75	67	66	51	0	0	0	0	0
sly-miR164f	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
sly-miR166-1/2/3	0	0	0	0	0	0	0	2117	4898	3439	1715	1709	1358	0	0	0	0	2696	2496	563	746	235665	236378	224493	139201	0	0	0	0	0
sly-miR166a-1-3p/a-2-3p/a-3-3p/a-4-3p	0	0	1	0	0	0	0	160565	221094	87724	134250	80507	87250	0	0	1	0	89867	106615	23225	26849	403026	405822	302624	189745	0	0	0	0	0
sly-miR166a-2-5p	0	0	0	0	0	0	0	2	2	11	7	2	6	0	0	0	0	1	2	0	0	11	3	1	4	0	0	0	0	0
sly-miR166a-4-5p	0	0	0	0	0	0	0	499	518	2416	846	456	1033	0	0	0	0	482	755	51	82	1845	1546	1663	1080	0	0	0	0	0
sly-miR166g-3p	0	0	1	1	4	0	1	309043	403114	129379	269312	224487	103701	0	0	0	0	36046	42888	6128	10478	87331	107950	81173	48070	0	0	0	0	0
sly-miR167a-1-3p	0	0	0	0	0	0	0	1	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167a-1-5p/a-2-5p	0	0	0	0	0	0	0	10890	8945	5162	12829	13147	13016	0	0	0	0	19	25	4	9	991	889	788	439	0	0	0	0	0
sly-miR167a-2-3p	0	0	0	0	0	0	0	32	34	27	19	30	44	0	0	0	0	13	26	9	2	330	327	313	94	0	0	0	0	0
sly-miR167c-3p	0	0	0	0	0	0	0	1	5	21	11	6	3	0	0	0	0	56	97	7	35	267	294	300	141	0	0	0	0	0
sly-miR167c-5p	0	0	0	0	0	0	0	10890	8945	5162	12829	13147	13016	0	0	0	0	19	25	4	9	991	889	788	439	0	0	0	0	0
sly-miR167h-1/h-2	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
sly-miR167h-3-3p	0	0	0	0	0	0	0	7	13	19	8	5	14	0	0	0	0	1	2	0	1	14	12	10	11	0	0	0	0	0
sly-miR167h-3-5p	0	0	0	0	0	0	0	10883	8941	5148	12811	13124	12989	0	0	0	0	18	25	4	9	986	883	780	437	0	0	0	0	0
sly-miR168	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR168a-1-3p	0	0	0	0	1	0	0	386	618	180	469	315	195	8	0	0	0	238	277	76	40	605	459	406	265	0	0	0	0	0
sly-miR168a-1-5p/a-2-5p	0	3	1	0	2	0	0	6739	6875	2058	2809	2726	2658	0	0	0	0	4926	5539	1477	2227	21249	16963	16848	8378	0	1	1	0	0
sly-miR168a-2-3p	0	0	1	1	0	0	0	844	1218	445	1411	787	493	0	0	0	0	323	367	85	55	319	185	239	147	0	0	0	0	0
sly-miR169a-1-3p/b-2-3p	0	3	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
sly-miR169a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	11	2	2	1	0	0	0	0	0
sly-miR169b-1-5p/b-2-5p/b-3-5p	1	1	1	1	0	1	0	5	5	27	34	14	3	0	0	0	0	1	0	0	0	14	10	1	0	0	0	0	0	0
sly-miR169d-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	0
sly-miR169d-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
sly-miR169e-3p	0	0	0	0	0	0	0	1096	1185	637	1526	5117	1595	0	0	0	0	101	192	6	4	1172	1288	833	282	0	0	0	0	0
sly-miR169e-5p	0	0	0	0	0	0	0	2	1	9	7	8	8	0	0	0	0	0	1	0	0	233	145	71	32	0	0	0	0	0
sly-miR169f-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	233	141	71	32	0	0	0	0	0
sly-miR169g	0	0	0	0	0	0	0	1	2	3	0	0	0	0	0	0	0	0	1	0	0	235	148	72	33	0	0	0	0	0
sly-miR169m	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR170-1-3p	0	0	0	0	0	0	0	628	749	472	620	505	252	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0
sly-miR170-1-5p/2-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3	6	1	5	270	319	171	98	0	0	0	0	0
sly-miR170-2-3p	0	0	0	0	0	0	0	628	748	473	618	510	247	0	0	0	0	4	2	0	0	147	143	105	78	0	0	0	0	0
sly-miR171b-1-3p/b-	0	0	0	0	0	0	0	7	9	6	17	4	3	0	0	0	7	57	71	12	11	142	145	108	78	0	0	0	0	0

2-3p																														
sly-miR171b-1-5p	0	0	0	0	0	0	0	31	27	26	44	63	27	0	0	0	0	1	3	0	0	13	19	12	9	0	0	0	0	0
sly-miR171b-3	0	0	0	0	0	0	0	634	756	477	635	514	250	0	0	0	1	57	71	12	11	149	146	111	78	0	0	0	0	0
sly-miR171c-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	5	1	0	0	0	0	0
sly-miR171c-1-5p	0	0	0	0	0	0	0	14	9	2	12	11	6	0	0	0	0	1	0	0	0	9	4	2	6	0	0	0	0	0
sly-miR171c-2/c-3-3p	1	0	0	0	1	1	1	32	42	47	53	29	33	0	0	0	0	26	15	0	2	145	154	131	85	0	1	0	0	0
sly-miR171c-3-5p	0	0	0	0	0	0	0	0	0	4	0	1	1	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0	0	0
sly-miR171c-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	1	4	4	1	0	0	0	0	0
sly-miR171f	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
sly-miR171i-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	230	212	222	146	0	0	0	0	0
sly-miR172d-1	0	0	0	0	0	0	0	345	473	459	850	649	137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-10-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-10-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-2/d-4-3p	2	1	0	0	1	0	1	11272	11080	6122	25286	16583	5739	0	0	0	0	3	0	1	2	7	3	6	4	0	0	0	3	3
sly-miR172d-2-3p/d-6-3p	0	0	0	0	0	0	0	11272	11080	6122	25286	16583	5739	0	0	0	0	3	0	1	2	7	3	6	4	0	0	0	3	3
sly-miR172d-4-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5-3p	0	0	0	0	0	0	0	4	1	2	5	0	2	0	0	0	0	2	0	0	1	1	3	4	1	0	0	0	0	0
sly-miR172d-5-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5p	0	0	0	0	0	0	0	14	40	21	76	88	12	34	0	0	0	0	3	3	11	11	9	26	10	0	0	0	0	0
sly-miR172d-6-5p	0	0	0	0	0	0	0	8	7	3	11	11	8	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0
sly-miR172d-7-3p	0	0	0	0	0	0	0	11272	11080	6122	25286	16583	5739	0	0	0	0	3	0	1	2	7	3	6	4	0	0	1	3	3
sly-miR172d-7-5p	0	0	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-8-3p	1	4	1	1	2	1	0	2	2	4	4	3	0	0	0	0	0	2	0	0	1	3	6	4	1	2	1	0	0	0
sly-miR172d-8-5p	0	0	0	0	0	0	0	11	21	172	59	45	21	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	0	0
sly-miR172d-9-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-9-5p	0	0	0	0	0	0	0	8	7	2	11	11	8	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0
sly-miR172j-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172j-1-5p/j-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172j-2-3p	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR1886a	0	0	0	0	0	0	0	12	15	5	8	14	3	0	0	0	0	1	5	2	3	5	2	25	20	0	0	0	0	0
sly-miR1886h-1/h-2	0	0	0	0	0	0	0	1	2	0	2	1	2	0	0	0	0	1	1	1	3	5	1	1	1	0	0	0	0	0
sly-miR1917-1/2	0	0	0	0	1	0	0	11	8	3	27	17	5	0	0	0	0	4	3	7	2	10	9	4	12	0	0	1	0	0
sly-miR1918	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	3	4	7	3	11	3	0	1	2	0	0
sly-miR1919a-1/a-2/a-3	0	0	0	3	2	1	2	41	41	13	33	34	20	0	0	0	0	30	38	8	6	247	249	320	253	1	0	1	0	0
sly-miR2101-3p	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2111a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2111a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	1	0	0	0	0	0	0
sly-miR2604	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319-3p-1/3p-2	0	0	0	0	0	0	0	21	28	19	42	34	6	0	0	0	0	2143	2307	205	385	1933	1745	1953	1579	0	0	1	0	0
sly-miR319-5p-1	0	0	0	0	0	0	0	1	0	20	10	0	0	0	0	0	0	3	5	0	1	16	11	13	9	0	0	0	0	0
sly-miR319-5p-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
sly-miR319a-1-3p/a-2-3p	0	0	0	0	0	0	0	18	11	6	94	58	1	0	10	0	0	33746	41162	8018	17547	25598	40794	31990	18479	0	0	0	0	0
sly-miR319a-1-5p	0	0	0	0	0	0	0	2	0	0	1	2	0	0	0	0	0	1	0	0	0	18	14	7	0	0	0	0	0	0
sly-miR319a-2-5p	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	22	35	3	5	83	113	101	65	0	0	0	0	0
sly-miR319c-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	167	222	64	100	1765	1895	1893	959	0	0	0	0	0

sly-miR319c-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	167	222	64	100	1765	1895	1893	959	0	0	0	0	0
sly-miR319c-2-5p	1	2	0	0	1	0	1	0	4	12	7	5	3	0	0	0	0	0	0	1	0	22	21	18	10	0	0	0	0	0
sly-miR319c-3-3p	0	0	0	0	0	0	0	18	11	6	94	58	2	0	10	0	0	33748	41164	8018	17548	25599	40796	31991	18479	0	0	0	0	0
sly-miR319c-3-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3	8	2	1	28	40	38	20	0	0	0	0	0
sly-miR3627-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
sly-miR3627-5p	0	0	0	0	0	0	0	216	879	804	267	446	1457	0	0	0	0	5	3	2	1	14	7	6	7	0	0	0	0	0
sly-miR390a-3p	0	0	0	0	0	0	0	1	0	9	1	0	2	0	0	0	0	0	14	1	0	40	34	25	11	0	0	0	0	0
sly-miR390a-5p	0	0	0	0	0	0	0	3	4	72	5	5	5	0	0	0	0	2	2	0	0	129	137	95	44	0	0	0	0	0
sly-miR390b-3p	0	0	0	1	1	0	0	47	71	68	126	84	61	0	0	0	0	14	19	1	0	80	69	79	34	0	0	0	0	0
sly-miR390b-5p	0	0	0	0	0	0	0	182	196	202	284	248	115	0	0	0	3	7	4	0	1	490	461	379	208	0	0	0	0	0
sly-miR393a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24	22	20	7	0	0	0	0	0
sly-miR393a-5p	0	0	0	0	0	0	0	8	11	3	3	21	4	0	0	0	0	14	30	8	13	129	129	85	59	0	0	0	0	0
sly-miR394b-3p	0	0	0	0	0	0	0	1	2	1	2	4	1	0	0	0	0	20	19	16	9	672	695	642	376	0	0	0	0	0
sly-miR394b-5p/a	0	0	0	0	0	0	0	9	5	3	20	13	1	0	0	0	0	3	6	3	6	12	3	0	0	0	0	0	0	0
sly-miR395a-1/a-3	0	0	0	0	0	0	0	13	7	18	5	16	31	0	0	0	0	66	24	0	5	111	72	74	57	0	0	0	0	0
sly-miR395a-2/a-4-5p	0	0	0	0	0	0	0	1	2	1	1	3	7	0	0	0	0	2	2	0	3	109	72	74	57	0	0	0	0	0
sly-miR395a-4-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	4	1	2	0	0	0	0	0	0
sly-miR395g	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0	5	6	1	3	16	3	8	9	0	0	0	0	0
sly-miR396a-3p	0	4	2	4	3	0	0	38	39	41	6	9	29	0	0	0	0	14	20	3	1	776	773	808	358	0	0	1	0	0
sly-miR396a-5p	1	5	1	2	1	0	0	8	7	10	14	22	14	0	0	0	15	754	897	123	102	27326	30271	25472	13888	0	0	0	0	0
sly-miR396b-3p	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	7	2	1	36	27	52	23	0	0	0	0	0
sly-miR396b-5p	0	0	0	1	0	1	0	294	389	109	369	386	288	0	0	0	7	486	548	98	112	10176	8614	8285	4138	0	0	0	0	0
sly-miR396g-1-3p/g-2-3p	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0
sly-miR396g-1-5p	0	0	0	0	0	0	0	1	0	0	2	0	2	0	0	0	0	3	0	0	0	1	2	1	1	0	0	0	0	0
sly-miR396g-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	1	0	0	0	0	0	0	0	0	0
sly-miR397-1-3p	0	0	0	0	0	0	0	3	10	677	179	73	751	0	0	0	0	28	27	111	152	53	37	81	42	0	0	0	0	0
sly-miR397-1-5p	0	0	0	0	0	0	0	3	15	1907	286	309	1384	0	0	0	0	12	15	64	92	56	41	139	62	0	0	0	0	0
sly-miR397-2-3p	0	0	0	0	0	0	0	1	3	3	0	3	2	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
sly-miR397-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
sly-miR398a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	38	23	59	72	37	18	115	66	0	0	0	0	0
sly-miR398a-5p	0	0	0	0	0	0	0	0	0	126	28	15	39	0	0	0	0	34	22	15	15	7	4	41	31	0	0	0	0	0
sly-miR398b-3p	0	0	0	0	0	0	0	0	0	32	11	18	32	0	0	0	0	54	50	290	247	59	53	70	36	0	0	0	0	0
sly-miR399a-1	0	0	0	0	0	0	0	21	24	51	6	24	21	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0
sly-miR399a-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399a-3-3p/a-4-3p/a-5-3p	0	0	0	0	0	0	0	76	82	221	24	94	69	0	0	0	0	1	5	0	0	1	2	1	1	0	0	0	0	0
sly-miR399a-3-5p/a-4-5p/a-5-5p	0	0	0	0	0	0	0	269	232	447	46	220	198	0	20	0	0	1	4	0	0	6	7	1	1	0	0	0	0	0
sly-miR399d-1/d-2	0	0	0	0	0	0	0	203	135	1039	17	140	191	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399d-3-3p	0	0	0	0	0	0	0	2	0	3	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
sly-miR399d-3-5p	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
sly-miR399i-1	0	0	0	0	0	0	0	81	102	293	39	202	241	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399j-2/j-3-3p	0	0	0	0	0	0	0	96	78	277	45	134	85	0	0	0	0	1	3	0	0	3	15	3	2	0	0	0	0	0
sly-miR399j-3-5p	0	0	0	0	0	0	0	104	60	46	10	36	30	0	0	0	0	0	0	0	0	9	10	2	1	0	0	0	0	0
sly-miR403-3p	0	0	0	0	0	0	0	1518	1734	1031	1163	1076	2024	0	0	0	0	1607	2171	720	686	4355	4144	3567	2037	0	0	0	0	0
sly-miR403-5p	0	0	0	0	0	0	0	2	1	0	2	1	2	0	0	0	0	0	3	0	0	124	102	74	57	0	0	0	0	0
sly-miR403a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR403a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408-1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

sly-miR408-2-3p	0	0	0	0	0	0	0	2	2	210	102	49	193	0	0	0	8	65	88	297	307	100	171	254	153	0	0	0	0	0
sly-miR408-2-5p	0	0	0	0	0	0	0	0	2	48	9	10	14	0	11	0	0	4	2	15	14	0	1	3	3	0	0	0	0	0
sly-miR408a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	6	0	1	0	1	0	0	0	0	0
sly-miR408a-5p	0	0	0	0	0	0	0	0	0	2	3	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR437	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR4376-3p	0	0	0	0	0	0	0	2	5	8	4	1	3	0	0	0	0	15	29	3	7	248	195	220	198	0	0	0	0	0
sly-miR4376-5p	0	0	0	0	0	0	0	14439	35249	16815	260	809	395	34	0	0	0	43	46	12	21	1145	674	1318	1350	0	0	0	0	0
sly-miR477-3p	0	0	0	0	0	0	0	2	2	0	6	3	1	0	0	0	0	17	30	0	0	21	31	23	5	0	0	0	0	0
sly-miR477-5p	0	0	0	0	0	0	0	1	0	0	2	1	1	0	0	0	0	28	57	1	4	30	31	41	4	0	0	0	0	0
sly-miR477a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
sly-miR477a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	7	3	8	1	0	0	0	0	0
sly-miR477b-3p	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	4	5	0	0	41	51	53	19	0	0	0	0	0
sly-miR477b-5p	0	0	0	0	0	0	0	11	8	1	12	7	5	0	0	0	0	0	4	0	0	39	41	41	11	0	0	0	0	0
sly-miR482a-1	0	1	0	0	0	0	0	422	636	5080	1414	408	2876	26	0	0	11	9684	13319	1889	2535	17493	20393	18151	14014	0	0	0	0	0
sly-miR482a-2-3p	0	0	0	0	0	0	0	307	448	1638	4020	948	796	0	14	5	0	1954	2122	126	170	5014	5570	4672	2756	0	0	0	0	0
sly-miR482a-2-5p	0	0	0	0	0	0	0	1	4	6	6	1	6	0	0	0	0	81	112	6	4	218	111	151	128	0	0	0	0	0
sly-miR482c	0	0	0	0	0	0	0	273	367	1256	847	575	821	0	52	0	7	147	214	24	31	536	505	372	191	0	0	2	0	0
sly-miR482d-3p	0	1	0	1	0	0	3	343	655	2333	1695	511	1652	24	0	0	18	1826	2284	613	803	4236	2861	3082	2073	2	0	0	0	0
sly-miR482d-5p	0	0	0	0	0	1	0	2	0	5	5	2	1	38	0	0	0	0	1	0	0	1	3	2	5	0	0	0	0	0
sly-miR482e-3p	0	1	0	0	0	0	0	44	84	441	406	61	320	0	0	0	0	509	647	103	110	510	569	475	277	0	0	0	0	0
sly-miR482e-5p	0	0	0	0	0	0	0	25	58	92	60	37	115	0	0	0	0	0	1	0	0	5	5	13	3	0	0	0	0	0
sly-miR5014a-3p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	2	2	0	0	0	0	0
sly-miR5162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5174d-5p	0	1	0	0	0	0	0	1	1	1	0	1	1	0	0	0	0	1	2	2	2	6	7	5	6	0	0	0	0	0
sly-miR5282-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5282-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR530	0	1	0	0	0	0	0	12	6	6	16	18	5	0	0	0	0	2	9	1	2	31	47	42	32	0	0	0	0	0
sly-miR5300-5p	0	0	0	0	1	0	0	3963	3200	4392	20332	12187	3957	0	0	0	0	152	110	14	16	111	158	66	35	0	0	0	0	0
sly-miR5303	3	11	5	12	13	8	9	58	36	37	43	42	21	0	0	0	0	11	19	13	13	20	38	23	6	2	1	8	12	12
sly-miR5303c	1	3	2	0	1	0	2	11	11	3	3	6	2	0	0	0	0	31	29	18	19	56	54	12	15	1	1	1	3	3
sly-miR5303f	0	4	1	2	0	0	3	26	11	9	21	22	4	0	0	0	0	15	23	2	6	39	56	31	20	1	0	5	6	6
sly-miR5303g	5	7	5	20	2	3	11	103	82	53	83	80	37	0	7	2	0	48	61	33	47	142	153	147	95	2	3	16	4	4
sly-miR5303h-1/h-2	7	10	7	21	5	5	15	154	152	80	156	144	83	0	0	2	0	67	81	45	58	223	241	175	126	4	2	23	7	7
sly-miR5303j-1/j-2	5	7	5	17	1	3	10	101	82	59	97	79	45	0	7	2	0	33	54	30	40	136	138	140	91	2	3	16	4	4
sly-miR5304-3p	0	0	0	0	0	0	1	2	5	12	3	5	2	0	0	0	0	0	2	0	0	11	6	4	3	0	0	0	0	0
sly-miR5304-5p	0	1	0	0	0	0	0	27	24	52	55	61	32	0	0	0	0	1	0	0	0	79	84	63	45	0	0	0	0	0
sly-miR5368	11	2	11	8	1	5	1	24	18	15	22	18	26	0	0	0	0	3	9	8	4	35	16	34	30	4	2	0	1	1
sly-miR5532-1/2	0	0	0	0	0	0	0	1	1	1	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR6024-3p	0	0	0	0	0	0	0	1860	1765	1371	3350	2169	1780	0	0	0	0	1083	1721	326	388	2377	2442	2076	1270	0	0	0	0	0
sly-miR6024-5p	0	1	0	1	0	0	0	15	17	20	24	19	27	0	0	0	0	12	10	3	0	48	57	169	104	0	0	0	0	0
sly-miR6027-3p	0	3	2	2	0	1	2	34934	31041	19016	37414	31609	15326	0	15	0	0	92	163	32	41	446	411	349	232	0	0	0	0	0
sly-miR6027-5p	0	0	1	2	0	0	0	765	929	1324	1285	947	1280	0	0	0	0	1383	1529	524	418	4957	3263	6134	3687	0	0	0	0	0
sly-miR7122-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7122-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7696c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
sly-miR7805-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7980b-2-3p	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7980b-2-5p	0	0	0	0	0	0	0	1	2	5	5	6	2	0	0	0	0	0	5	5	2	2	5	6	6	0	0	0	0	0
sly-miR7980b-3p-1	0	0	0	0	0	0	0	175	112	72	81	119	58	0	0	0	0	62	79	15	9	259	262	338	268	0	0	0	0	0
sly-miR7981-3p	1	0	0	0	1	0	0	219	219	50	99	114	29	0	0	0	0	39	33	39	54	110	166	50	24	0	0	0	0	0

sly-miR7981-5p	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
sly-miR7983-1-3p/2-3p/3-3p	0	1	0	1	0	0	0	255	274	137	274	283	154	0	0	0	0	275	316	306	327	990	1012	723	480	0	0	0	0	0
sly-miR7983-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
sly-miR7983-2-5p	0	0	0	0	0	0	0	1	4	1	4	6	2	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	1
sly-miR7983-3-5p	0	0	0	0	0	0	0	3	6	0	2	0	0	0	0	0	0	1	2	7	5	11	10	6	4	0	0	0	0	0
sly-miR7983-4-3p	0	0	0	0	0	0	0	5	2	0	1	2	0	0	0	0	0	17	18	16	26	50	39	134	75	0	0	0	0	0
sly-miR7983-4-5p/5-5p/6-5p	2	0	0	1	0	0	1	54	60	32	48	55	23	0	0	0	0	6	5	9	9	11	5	34	18	0	0	0	0	0
sly-miR7983-5-3p	0	0	0	0	0	0	1	76	75	28	74	65	41	0	0	0	1	52	51	41	75	195	178	234	142	0	0	0	0	0
sly-miR7983-6-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7984c-3p	0	0	0	0	0	0	0	27	17	4	19	23	3	0	0	0	0	4	6	7	7	18	14	14	7	0	0	1	0	0
sly-miR7984c-5p	0	0	0	0	0	0	0	27	18	4	20	23	3	0	0	0	0	4	6	7	7	18	14	15	7	0	0	1	0	0
sly-miR7984d-3p	0	0	0	0	0	0	0	17	12	5	6	12	1	0	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0	0
sly-miR7985	1	3	4	7	6	4	2	7	7	5	1	1	1	0	0	0	3	1	1	2	1	1	2	0	2	0	0	0	0	0
sly-miR7987-3p	0	0	0	0	0	0	0	3	1	0	5	3	0	0	0	0	0	2	1	4	2	6	2	6	2	0	0	0	0	0
sly-miR7987-5p	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7990a-1/a-2	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	1	2	7	3	2	2	2	0	0	0	0	0
sly-miR7990a-3	0	0	0	0	0	0	0	3	4	1	1	1	0	0	0	0	0	7	9	10	10	11	7	31	12	0	0	0	0	0
sly-miR7992-3p	0	0	0	0	0	0	0	4	1	1	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
sly-miR7992-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7993a	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7997a	0	0	0	0	0	0	0	1	3	0	0	4	0	0	0	0	0	7	0	2	2	38	34	35	23	0	0	0	0	0
sly-miR8001a	0	0	0	0	0	0	0	5	3	1	3	2	2	0	0	0	0	38	50	14	15	85	87	52	36	0	0	0	0	0
sly-miR8001b-1-3p	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8001b-1-5p/b-2-5p	0	0	0	0	1	0	0	13	5	10	16	23	11	0	0	0	0	17	25	17	14	52	49	51	26	0	0	0	0	0
sly-miR8006-1-3p	0	0	0	0	0	0	0	30	19	4	12	18	2	0	0	0	0	2	1	0	0	11	11	11	14	0	0	0	0	0
sly-miR8006-1-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0
sly-miR8006-2-5p	0	0	0	0	0	0	0	185	124	79	98	120	48	0	0	0	0	29	21	14	8	93	119	170	142	0	0	0	0	0
sly-miR8007a-5p	0	0	0	0	0	0	0	15	18	9	6	17	4	0	0	0	0	0	2	1	1	2	4	4	2	0	0	0	0	0
sly-miR8007b-3p	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8007b-5p	0	1	0	0	0	0	0	9	16	11	25	22	8	0	0	0	0	6	16	5	12	25	28	14	8	0	0	0	0	0
sly-miR8008a-1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
sly-miR8008a-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-1-5p/b-3-3p	0	0	0	0	0	0	0	23	14	6	14	19	3	0	0	0	0	5	9	1	3	50	66	3	3	0	0	0	0	0
sly-miR8008b-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-2-5p	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
sly-miR8011a-1-3p	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	7	7
sly-miR8011a-2-3p	0	1	0	1	0	0	0	6	3	5	11	3	3	0	0	0	0	0	0	0	1	0	2	5	1	0	0	0	0	0
sly-miR8011a-2-5p	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	16	15	21	18	23	40	1	2	0	0	0	0	0
sly-miR8013	0	0	0	0	0	0	0	1	0	0	2	1	0	0	0	0	0	0	5	1	1	0	5	2	0	0	0	0	0	0
sly-miR8019-1-3p/2-3p	1	2	1	3	3	1	2	938	689	227	580	824	233	0	0	0	0	826	1052	860	907	2006	2574	2179	1407	0	0	0	0	0
sly-miR8019-1-5p	0	1	0	0	0	0	0	3	2	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0
sly-miR8019-2-5p	0	1	1	0	1	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	1	2	4	0	0	0	0	0	0
sly-miR8020	0	1	1	1	2	0	1	19	11	15	27	20	7	0	0	0	0	5	5	7	5	9	16	9	11	0	0	0	0	0

sly-miR8021-1/2/3	0	0	0	0	0	0	0	2	1	3	8	6	1	0	0	0	0	31	27	24	40	67	72	113	71	0	0	0	0	0
sly-miR8025-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8025-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8032d-3p	0	0	0	0	0	0	0	209	201	104	136	177	134	0	0	0	0	0	1	1	0	4	9	11	2	0	0	0	0	0
sly-miR8033-3p	0	0	0	0	0	0	0	3	2	8	6	7	20	0	0	0	0	24	27	0	1	83	81	89	46	0	0	0	0	0
sly-miR8033-5p	0	0	0	0	0	0	0	9	14	14	11	11	18	0	0	0	0	10	24	0	0	72	84	93	33	0	0	0	0	0
sly-miR8038a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
sly-miR8038a-5p	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8039-1	0	0	0	0	0	0	0	0	1	1	1	2	1	0	0	0	0	1	0	0	0	3	6	3	0	0	0	0	0	0
sly-miR8039-2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	3	4	1	1	0	0	0	0	0
sly-miR8045-1/2-5p	0	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0
sly-miR8045-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	4	10	3	0	0	0	0	0
sly-miR8051-5p	0	0	0	0	0	0	0	3	0	0	2	0	0	0	0	0	0	0	0	0	0	3	3	0	1	0	0	0	0	0
sly-miR8172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR827-3p	0	0	0	0	0	0	0	239	86	155	13	33	31	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
sly-miR827-5p	0	0	0	0	0	0	0	30	9	9	0	7	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
sly-miR828a	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	10	10	8	4	0	0	0	0	0
sly-miR845b-5p	0	1	0	0	1	0	0	2	3	1	3	6	2	0	0	0	0	0	0	1	1	4	2	1	1	0	0	0	0	0
sly-miR9471a-3p	0	0	0	0	0	0	0	499	560	334	545	489	266	0	0	0	0	116	120	22	29	2122	1752	1630	1024	0	0	0	0	0
sly-miR9471a-5p	0	0	0	0	0	0	0	0	1	0	2	1	0	0	0	0	0	0	2	1	0	40	28	27	3	0	0	0	0	0
sly-miR9471b-3p	0	0	0	0	0	0	0	46	50	52	47	28	71	0	0	0	0	126	154	35	34	3914	3361	2942	1709	0	0	0	0	0
sly-miR9471b-5p	0	0	0	0	0	0	0	1	1	2	9	2	0	0	0	0	0	1	0	0	0	9	6	4	3	0	0	0	0	0
sly-miR9472-3p	0	0	0	0	0	0	0	0	2	4	2	0	1	0	0	0	0	0	1	0	0	0	0	0	0	3	1	0	0	0
sly-miR9472-5p	1	1	0	0	0	0	1	56	110	132	49	71	108	0	0	0	0	2	1	0	0	3	3	31	7	0	0	0	0	0
sly-miR9473-1-3p	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0
sly-miR9473-1-5p	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	12	18	0	4	87	68	63	35	0	0	0	0	0
sly-miR9473-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9476-1-3p/2-3p	0	0	0	0	0	0	0	142	105	85	115	155	148	0	0	0	0	17	24	2	0	1280	1176	1236	556	0	0	0	0	0
sly-miR9476-1-5p/2-5p	0	0	0	0	0	0	0	6	10	2	8	4	3	0	0	0	0	0	1	0	0	8	6	4	4	0	0	0	0	0
sly-miR9478-3p	0	0	0	0	0	0	0	28	19	12	14	27	18	0	0	0	0	71	108	8	10	171	194	196	133	0	0	0	0	0
sly-miR9478-5p	0	1	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	1	1	0	0	1	2	1	0	0	0	0	0	0

Supplementary Table S15. (continuation) Validation of the presence tomato mature miRNAs identified in *S. lycopersicum* small RNAs libraries available in the SRA. The accessions numbers of the libraries in the SRA: S62 (SRR1706544), S63 (SRR1706545), S64 (SRR1706546), S65 (SRR1706547), S66 (SRR1706548), S67 (SRR1706549), S68 (SRR1706550), S69 (SRR1706551), S70 (SRR1706552), S71 (SRR1706553), S72 (SRR1706554), S73 (SRR1706555), S74 (SRR4346447), S75 (SRR4346448), S76 (SRR4346450), S77 (SRR4346452), S78 (SRR4346454), S79 (SRR4346456), S80 (SRR4733709), S81 (SRR4733710), S82 (SRR4733711), S83 (SRR4733748), S84 (SRR4733749), S85 (SRR4733750), S86 (SRR4733751), S87 (SRR4733752), S88 (SRR4733759), S89 (SRR4733770), S90 (SRR4733781), S91 (SRR4733794), S92 (SRR4733806), S93 (SRR4733818), S94 (SRR4733829 and S95 (SRR4733840).

miRNA	S61	S62	S63	S64	S65	S66	S67	S68	S69	S70	S71	S72	S73	S74	S75	S76	S77	S78	S79	S80	S81	S82	S83	S84	S85	S86	S87	S88	S89	S90	S91	S92	S93	S94	S95
sly-miR1128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR1446-1/2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	87	34	69	79	45	25	0	2	1	1	0	0	0	0	0	1	4	3	0	0	1	0
sly-miR156a-1/a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	70	138	234	166	170	290	9	15	0	0	6	12	0	2	13	17	2	2	0	1	0	0

sly-miR156a-2-3p	0	0	0	0	0	1	6	2	1	1	0	4	0	8	11	8	16	19	13	1	1	0	0	1	1	1	1	2	1	2	0	0	0	0	1
sly-miR156c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	194	176	437	264	458	649	1	0	0	1	0	0	1	0	0	1	0	1	0	1	0	0
sly-miR156c-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	32	69	146	66	92	107	3	21	0	2	2	9	0	0	10	12	1	5	0	0	1	0
sly-miR156f	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	1
sly-miR156i-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156i-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0
sly-miR156i-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156i-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR156l-1-3p/l-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	88	70	161	93	84	131	29	35	3	4	8	5	0	5	18	14	34	20	6	5	6	2
sly-miR156l-1-5p/l-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	70	138	234	166	170	290	9	15	0	0	6	12	0	2	13	17	2	2	0	1	0	0
sly-miR157a-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	1	9	2	0	0	0	1	0	0	0	0	1	0	3	0	0	1	0	0
sly-miR157a-1-5p/a-2-5p/a-3-5p/a-4-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	473	762	1056	845	994	1462	864	2286	159	174	1486	1354	118	306	4282	3738	501	312	1955	1718	314	182
sly-miR157a-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	3	8	6	4	6	8	3	4	3	1	0	1	0	3	2	1	2	0	3	1	1	2
sly-miR157a-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	7	56	44	31	149	23	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
sly-miR159a-3p	0	0	0	0	0	0	0	0	0	0	0	1	0	10978	2978	10167	14330	7273	4262	4	5	55	90	8	2	27	107	6	5	216	130	2	5	23	32
sly-miR159a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	9	9	13	9	16	13	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
sly-miR159b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	14	7	10	5	12	11	21	56	0	0	8	3	1	0	29	30	2	1	2	1	0	0
sly-miR159b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
sly-miR160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR160a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	33	20	50	67	44	33	84	332	927	1213	138	139	1063	1436	400	365	3541	2057	144	165	766	595
sly-miR160g-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	3	4	5	5	4	4	0	3	13	12	12	5	1	1	2	1
sly-miR160h-1	0	0	0	0	0	0	0	0	0	0	0	0	0	32	20	52	64	44	27	84	331	927	1213	137	137	1060	1436	395	362	3518	2037	144	165	766	595
sly-miR160h-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	6	0	1	2	0	0	0	6	0	0	1	0	0
sly-miR162-1-3p/2-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	1057	4426	3042	2535	2239	4099	31	48	14	35	36	33	8	21	101	83	133	84	37	21	48	17
sly-miR162-1-5p/2-5p	4	0	0	0	0	0	0	0	0	0	0	0	0	1	5	11	6	3	2	58	106	19	15	22	22	12	8	67	63	36	12	31	27	25	18
sly-miR164a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	2	2	0	0	7	5	0	0	4	0	1	0	11	6	0	0
sly-miR164a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	771	106	350	211	95	77	3830	6483	578	468	5591	6988	652	521	7141	5998	724	479	14833	9374	930	791
sly-miR164e-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR164e-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	745	83	338	201	89	76	113	116	10	16	125	169	4	17	158	86	24	9	192	108	26	5
sly-miR164f	0	0	0	0	0	0	0	0	0	0	0	0	0	7	10	8	17	28	13	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0
sly-miR166-1/2/3	0	0	0	0	0	0	0	0	0	0	0	0	0	124366	226017	514210	591936	281385	831550	2066	4208	2410	3610	2421	3357	3293	3766	5174	4622	8481	5024	5255	5606	4899	3160
sly-miR166a-1-3p/a-2-3p/a-3-3p/a-4-3p	1	0	0	0	0	0	0	0	1	0	0	0	0	707946	851975	1370741	1164160	637068	1362470	2066	4208	2410	3610	2421	3357	3293	3766	5174	4622	8481	5024	5255	5606	4899	3462
sly-miR166a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	58	451	246	569	615	281	0	2	2	0	1	0	1	2	0	0	3	2	0	1	4	2
sly-miR166a-4-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	965	3688	1997	4176	4836	2696	2	4	2	3	4	2	6	6	7	3	6	3	4	4	8	5
sly-miR166g-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	10393	13665	14069	22292	21220	35608	82	225	101	253	110	209	110	240	208	177	517	277	181	226	190	88
sly-miR167a-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	2	0	0	0	0	1	0	0	0	1
sly-miR167a-1-5p/a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	147	148	228	252	181	134	990	1982	341	577	2427	2222	392	773	3291	2917	1194	743	2331	2386	225	196
sly-miR167a-2-3p	0	3	0	2	0	2	3	1	0	3	0	0	0	30	16	29	42	30	32	13	39	1	3	43	18	3	8	92	74	5	6	31	62	3	1

sly-miR167c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	34	46	38	72	43	48	0	0	0	2	0	0	0	1	0	0	0	1	1	0	1	1
sly-miR167c-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	147	148	228	252	181	134	988	1982	341	577	2427	2222	392	773	3291	2917	1194	743	2331	2386	225	196
sly-miR167h-1/h-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR167h-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	5	11	8	4	0	1	0	2	0	0	0	0	0	0	0	1	0	1	0	0
sly-miR167h-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	146	147	225	251	181	133	983	1974	341	576	2417	2216	385	773	3262	2894	1191	743	2326	2382	225	196
sly-miR168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR168a-1-3p	0	4	2	3	1	2	2	2	2	1	0	3	1	214	1169	452	1155	348	680	29	47	10	17	28	45	39	33	26	17	27	18	34	42	17	14
sly-miR168a-1-5p/a-2-5p	0	1	2	2	1	0	1	1	1	0	0	3	0	4478	3033	6431	7390	3253	5626	752	1220	345	370	590	683	515	379	616	563	511	339	746	729	370	337
sly-miR168a-2-3p	0	0	1	0	0	0	0	0	1	0	0	0	0	167	1237	414	770	351	412	9	23	6	10	14	11	9	15	20	16	12	7	10	6	11	5
sly-miR169a-1-3p/b-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	4	1	0	10	25	2	0	9	6	1	1	19	11	2	1	12	16	0	0
sly-miR169b-1-5p/b-2-5p/b-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	2	4	1	0	1	2	2	2	5	6	1	8	8	5	8	6	2	8	1	1
sly-miR169d-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169d-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR169e-3p	0	0	0	0	0	0	1	0	0	0	0	0	0	85	112	89	11	5	2	12	21	0	1	7	3	0	2	5	6	7	7	1	3	3	1
sly-miR169e-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	32	19	18	6	2	0	1	1	1	0	1	0	0	2	7	3	6	3	1	2	1	1
sly-miR169f-1	0	0	0	0	0	0	0	0	0	0	0	0	0	22	19	18	6	2	0	0	0	1	0	0	0	0	0	0	2	3	1	0	0	0	0
sly-miR169g	0	0	0	0	0	0	0	0	0	0	0	0	0	22	16	17	6	2	0	0	1	0	0	0	0	0	0	1	1	1	2	0	0	0	0
sly-miR169m	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR170-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	3	7	8	20	10	5	1	21	6	9	52	29	4	5	10	11
sly-miR170-1-5p/2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	63	225	476	65	67	362	659	205	144	1050	650	121	150	424	341
sly-miR170-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	5	3	16	12	5	11	11	13	37	90	15	6	20	82	28	8	163	115	10	16	56	62
sly-miR171b-1-3p/b-2-3p	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	4	1	1	4	8	18	21	29	29	21	18	35	25	20	45	29	24	31	30	19
sly-miR171b-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2	9	2	0	1	8	3	0	2	1	1	4	3	5	3	3	1	1	4
sly-miR171b-3	0	0	1	0	0	0	0	0	0	0	0	0	0	5	3	16	12	5	11	14	17	46	103	23	11	37	96	35	13	178	124	16	26	65	69
sly-miR171c-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR171c-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	1	2	1	2	4	2	2	3	9	4	3	18	4	1	1	2	1
sly-miR171c-2/c-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	17	26	28	41	8	21	1	3	8	7	2	2	4	5	1	5	16	7	5	4	8	11
sly-miR171c-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5	7	2	2	2	0	0	0	0	0	0	0	2	0	1	1	1	0	1	0	1
sly-miR171c-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
sly-miR171f	0	0	0	0	0	0	0	0	0	0	0	0	0	45	94	140	91	46	29	1	1	3	4	2	1	0	8	3	1	4	6	1	0	2	4
sly-miR171i-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	12	26	45	69	25	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	8	4	5	0	4	1	4	4	1	0	1	13	8	6	6	3	5	2	1
sly-miR172d-10-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	8	2	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-10-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	8	2	10	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
sly-miR172d-2/d-4-3p	1	0	0	0	0	2	0	0	0	0	1	2	0	2	4	4	16	7	9	272	593	478	733	783	528	282	425	1351	969	1291	861	1169	1566	263	247
sly-miR172d-2-3p/d-6-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	2	4	4	16	7	9	272	593	480	733	784	528	282	425	1352	970	1293	861	1169	1566	263	248
sly-miR172d-4-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5-	0	0	0	0	0	0	0	0	0	0	0	1	0	3	1	7	7	1	4	14	16	3	18	13	8	5	5	27	17	15	6	8	12	3	4

3p																																				
sly-miR172d-5-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	2	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	5	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
sly-miR172d-6-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	4	14	11	4	14	2	1	3	5	4	3	2	9	2	3	2	7	12	2	6	6	3
sly-miR172d-7-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	2	4	4	16	7	9	1161	3601	653	796	3827	3031	550	862	5761	4675	1337	900	4203	7721	539	711
sly-miR172d-7-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	0	0	4	4	0	1	3	4	0	1	7	12	0	2
sly-miR172d-8-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	4	1	1	720	1512	592	781	1059	861	540	555	2603	2122	1137	876	1025	1132	305	536
sly-miR172d-8-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	4	1	2	7	1	0	5	0	1	1	3	4	4	4	1	4	2	0
sly-miR172d-9-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR172d-9-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	3	14	11	3	14	2	1	3	5	4	3	2	9	2	3	2	7	12	2	6	6	3
sly-miR172j-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
sly-miR172j-1-5p/j-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	9	3	14	1	0	1	1	0	0	0	3	0	0	0	0	2	1	0	2	0
sly-miR172j-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	2	1	3	0	2	1	0	1	2	0	0	0	0	1	0	0	0	1	0	0
sly-miR1886a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5	7	8	5	3	4	15	5	5	9	24	12	16	49	12	7	17	24	19
sly-miR1886h-1/h-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	5	2	3	2	1	0	1	0	0	2	0	0	1	4	7	0	2	3	0
sly-miR1917-1/2	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	2	19	9	8	3	8	6	9	3	8	11	8	13	10	25	18	5	6	10	2
sly-miR1918	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	2	4	3	0	28	57	30	38	21	18	16	24	149	129	107	59	9	21	18	14
sly-miR1919a-1/a-2/a-3	0	0	0	0	0	0	0	0	0	0	0	0	0	93	654	410	334	475	896	24	38	8	24	36	35	23	35	49	43	33	33	47	50	40	20
sly-miR2101-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2111a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2111a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	3	12	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR2604	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR319-3p-1/3p-2	0	0	0	0	0	0	0	0	0	0	0	0	0	32	51	32	57	24	47	66	89	9	38	50	39	21	65	149	126	140	87	28	34	6	11
sly-miR319-5p-1	0	0	0	0	0	0	0	0	0	0	0	0	0	4	5	7	4	2	3	1	2	0	1	2	0	0	0	2	3	1	3	0	3	0	0
sly-miR319-5p-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	12	0	0	18	28	2	2	94	77	0	0	14	7	0	0
sly-miR319a-1-3p/a-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	3392	3469	5183	8128	5441	5713	350	481	530	2077	271	222	629	2457	526	439	4914	2638	38	97	745	439
sly-miR319a-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	8	11	2	0	19	11	1	0	13	10	1	3	57	30
sly-miR319a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	13	14	10	16	10	5	10	0	0	2	1	0	0	7	9	0	0	1	0	0	0
sly-miR319c-1	0	0	0	0	0	0	0	0	0	0	0	0	0	991	485	637	753	615	664	0	0	0	1	1	0	0	1	0	0	0	1	0	0	1	0
sly-miR319c-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	991	485	637	753	615	664	0	0	0	1	1	0	0	1	0	0	0	1	0	0	1	0
sly-miR319c-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	17	7	12	8	4	3	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0
sly-miR319c-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	3392	3469	5183	8128	5442	5713	350	481	530	2077	271	222	629	2457	526	439	4914	2639	38	97	745	439
sly-miR319c-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	6	6	7	18	22	17	0	0	0	3	0	1	0	1	0	0	5	4	0	0	2	1
sly-miR3627-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	5	0	2	0	3	0	5	6	3	0	2	24	12	19	7	1	0	0	0
sly-miR3627-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	8	9	9	10	22	32	8	10	30	33	8	6	92	81	13	8	34	26	27	14
sly-miR390a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	4	4	12	11	151	214	46	52	145	132	24	37	135	134	114	73	160	105	36	40
sly-miR390a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	12	9	29	22	35	26	1136	1723	536	436	941	1233	563	304	898	788	520	435	1441	741	580	751

sly-miR390b-3p	0	0	1	0	0	0	0	0	0	0	0	0	0	12	8	7	16	17	17	2	2	4	6	8	4	5	10	2	2	9	8	11	16	10	6
sly-miR390b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	17	24	36	68	36	77	39	63	96	126	105	110	131	164	74	64	126	95	156	156	181	204
sly-miR393a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR393a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	26	52	35	50	64	76	1006	1105	88	379	1570	893	47	252	1553	1274	467	322	253	566	91	68
sly-miR394b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	27	18	31	49	29	86	153	224	267	818	376	351	303	786	795	623	2221	1508	668	549	853	346
sly-miR394b-5p/a	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	2	0	0	1	1	0	0	0	1	0	2	1	0	1	0	2	0
sly-miR395a-1/a-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	197	325	43	59	17	24	18	7	177	155	86	38	16	15	7	4
sly-miR395a-2/a-4-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	197	325	43	59	17	24	18	7	177	155	86	38	16	15	7	4
sly-miR395a-4-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR395g	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	2	0	1	1	0	0	0	1	1	0	0	0	0	0	0
sly-miR396a-3p	0	0	1	0	0	0	0	0	0	1	0	0	0	147	144	206	494	362	193	657	973	71	39	824	559	90	71	927	791	66	48	1847	2084	160	140
sly-miR396a-5p	0	0	1	0	0	0	0	0	0	0	0	0	0	3363	8583	16009	21438	11251	44076	2440	9829	303	381	9578	7375	250	431	17078	13827	714	469	4504	5547	245	292
sly-miR396b-3p	0	0	0	0	0	0	0	0	1	0	0	0	0	4	1	8	9	6	6	1	0	0	0	2	3	0	0	1	1	0	0	1	2	0	0
sly-miR396b-5p	0	0	0	0	0	0	0	1	0	0	0	0	0	208	2435	983	1283	1337	2317	4139	14173	1071	1618	13247	10270	1259	2075	24837	20480	3142	2063	6864	9860	1150	963
sly-miR396g-1-3p/g-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
sly-miR396g-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR396g-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1
sly-miR397-1-3p	0	0	0	1	0	1	0	0	0	2	0	0	0	1	0	0	4	1	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0
sly-miR397-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	102	136	229	545	11	9	24	51	19	12	78	34	18	27	52	28
sly-miR397-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
sly-miR397-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR398a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	9	11	3	3	3	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR398a-5p	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	4	4	3	4	0	0	0	0	0	0	0	1	0	1	4	2
sly-miR398b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	7	6	8	53	64	78	139	3	1	3	4	6	3	15	1	3	6	5	2
sly-miR399a-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0
sly-miR399a-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
sly-miR399a-3-3p/a-4-3p/a-5-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	4	6	4	2	4	0	0	2	0	0	7	3	1	0	1	3	0	0	4	6	0	0
sly-miR399a-3-5p/a-4-5p/a-5-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	3	19	14	0	5	1	0	1	0	0	0	0	1	0	0	0	0	0	2	1	0	0
sly-miR399d-1/d-2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
sly-miR399d-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399d-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR399i-1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	5	2	0	0	0	1	0	0	0	3	0	0
sly-miR399j-2/j-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2	6	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
sly-miR399j-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	7	2	12	3	6	3	1	0	0	1	0	0	0	0	3	0	1	0	0	0	0	0
sly-miR403-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	211	716	433	400	445	575	0	1	0	1	6	2	2	3	1	2	7	1	1	2	1	1
sly-miR403-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	67	139	94	119	171	93	0	0	0	0	1	1	0	0	0	2	0	0	0	2	0	0
sly-miR403a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR403a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0
sly-miR408-2-3p	0	0	0	1	0	0	0	0	0	0	0	0	0	41	55	27	36	35	121	23	51	108	116	2	2	11	8	1	3	28	18	10	7	54	23
sly-miR408-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	3	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR408a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR437	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR4376-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	5	3	4	2	10	7	0	0

sly-miR4376-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	1	4	8	28	10	8	21	24	8	9	60	21	10	9	14	9
sly-miR477-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	27	26	22	3	4	0	228	335	7	24	92	81	27	48	101	76	52	24	84	77	50	12
sly-miR477-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	120	98	100	27	8	2	5	14	1	6	8	5	0	1	3	3	6	2	6	5	3	1
sly-miR477a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1	0
sly-miR477a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	29	20	9	2	4	1	0	1	0	1	2	0	0	0	0	0	0	0	0	1	0	0
sly-miR477b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	34	23	10	1	0	1	15	9	5	5	4	5	1	2	8	8	8	5	8	4	3	3
sly-miR477b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	114	39	30	5	0	4	7	17	2	7	12	9	2	2	17	8	14	10	11	13	3	2
sly-miR482a-1	0	0	0	0	0	0	0	0	0	0	0	0	0	11896	1633	6766	6546	3663	7071	4157	7046	7840	7522	3863	5664	8390	7418	9242	7432	19713	11987	13318	12971	17788	14766
sly-miR482a-2-3p	0	0	0	0	1	0	2	0	0	0	1	2	0	140	80	104	84	33	33	1867	3440	1941	2796	4502	5109	1678	1870	6695	5396	7868	4981	5781	5598	1648	1195
sly-miR482a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	78	189	68	52	44	35	0	1	0	0	1	0	1	0	0	0	1	1	1	3	0	0
sly-miR482c	4	0	0	0	0	0	0	0	0	0	0	0	1	148	67	152	236	123	114	205	333	339	384	253	288	309	265	683	529	1229	697	211	258	237	222
sly-miR482d-3p	0	0	0	0	0	0	0	0	0	0	0	0	1	1903	602	1945	2263	1134	2090	775	1964	1999	1238	790	1391	2889	1611	2068	1698	4246	2568	3234	4393	4134	4576
sly-miR482d-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	10	8	4	25	16	2	0	3	0	1	0	4	1	1	4	1	0	0	2	0	1	1
sly-miR482e-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	484	172	284	448	235	598	250	460	466	480	237	289	387	322	576	494	1081	746	557	586	662	519
sly-miR482e-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	7	1	3	6	2	0	2	3	3	0	2	1	6	0	2	3	5	0	2	0	2	3
sly-miR5014a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
sly-miR5174d-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	6	5	6	5	0	0	0	2	0	0	0	0	0	0	2	1	1	0	0	0
sly-miR5282-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR5282-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR530	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	12	0	0	1	4	0	0	28	14	0	0	5	0
sly-miR5300-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	197	538	335	318	195	239	1154	1796	1223	1063	827	956	1199	827	1889	1513	1954	1169	1529	1616	1209	1372
sly-miR5303	7	0	1	1	0	0	2	0	0	0	0	2	0	4	1	2	6	9	6	2	5	4	8	3	2	1	2	6	7	18	7	1	3	4	5
sly-miR5303c	5	2	0	2	0	0	0	1	3	0	0	3	1	2	8	3	8	12	8	0	2	2	3	1	0	0	4	0	1	4	2	1	4	0	3
sly-miR5303f	6	0	2	2	0	0	0	0	0	0	0	0	1	0	2	2	5	3	7	0	0	0	0	0	0	0	1	1	1	2	1	0	0	1	1
sly-miR5303g	3	1	4	4	2	1	3	2	3	0	5	7	3	11	26	26	70	48	17	7	11	18	20	6	13	9	26	30	30	61	32	9	14	16	15
sly-miR5303h-1/h-2	10	0	2	4	0	4	2	1	3	0	2	6	0	12	21	23	83	58	21	14	21	29	30	10	15	9	30	43	35	91	45	12	17	30	21
sly-miR5303j-1/j-2	3	1	4	4	1	1	2	2	3	0	5	7	2	10	21	14	70	43	15	7	12	18	20	6	13	8	26	30	28	61	29	9	14	14	15
sly-miR5304-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	5	1	4	1	0	1	0	2	1	0	0	0	4	1	0	1	1	0	0	1
sly-miR5304-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	28	22	32	26	16	45	3	4	2	5	1	1	0	2	26	10	6	7	2	3	3	0
sly-miR5368	0	26	3	3	3	7	7	4	4	8	1	0	15	9	28	12	16	11	35	1	1	8	20	7	10	20	25	4	2	44	26	34	13	33	16
sly-miR5532-1/2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
sly-miR6024-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	228	926	320	491	512	983	62	88	106	137	110	61	106	140	443	323	708	390	140	234	176	127
sly-miR6024-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	44	86	42	103	167	32	6	2	3	1	7	3	2	5	18	19	6	1	5	6	2	3
sly-miR6027-3p	1	1	1	0	0	1	1	0	0	1	0	1	1	115	78	103	166	98	82	555	918	515	720	589	512	527	520	1347	1187	1259	748	686	662	296	346
sly-miR6027-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	395	608	1166	1127	646	307	135	350	170	174	376	352	135	194	1060	829	462	252	213	154	187	130
sly-miR7122-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7122-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7696c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7805-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7980b-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	5	0	3	1	2	1
sly-miR7980b-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	2	1	1	3	11	9	14	7	1	5	7	12	15	21	16	8	7	10	12
sly-miR7980b-3p-1	0	0	0	0	0	0	0	0	0	0	0	0	0	24	82	55	93	81	56	5	15	10	19	12	15	20	23	16	21	34	17	9	24	17	9
sly-miR7981-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	7	17	11	22	21	18	11	12	12	48	18	10	21	58	51	16	115	54	11	13	16	13
sly-miR7981-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	1	1	1	0	1	1	0	0	0	1	1	0	0	0	0	2	1	1
sly-miR7983-1-3p/2-3p/3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	84	182	228	398	294	155	31	48	45	64	25	30	66	86	71	52	143	86	25	52	46	26
sly-miR7983-1-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

5p																																				
sly-miR7983-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	1	0	0	1	1	3	0	1	0	1	0	1	0
sly-miR7983-3-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4	3	3	4	1	2	0	0	0	0	0	0	2	1	0	0	0	0	1	0	1
sly-miR7983-4-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	24	54	34	93	93	35	0	0	0	3	2	0	1	1	1	2	7	4	0	0	1	0
sly-miR7983-4-5p/5-5p/6-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	18	14	17	47	34	12	4	13	13	25	10	13	13	19	23	18	42	29	8	15	16	12
sly-miR7983-5-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	31	59	94	175	122	68	8	14	10	18	7	7	19	28	25	18	50	32	9	17	10	5
sly-miR7983-6-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7984c-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	18	8	1	1	3	2	4	1	0	3	6	5	2	11	7	3	1	0	2
sly-miR7984c-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	19	10	4	1	4	2	5	1	1	3	7	6	3	11	7	3	1	0	3
sly-miR7984d-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
sly-miR7985	3	1	0	2	1	1	1	0	1	1	0	2	1	0	0	0	0	1	0	6	12	2	5	2	1	3	2	4	2	0	3	1	2	1	0
sly-miR7987-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	1	1	1	4	6	1	3	3	11	8	5	18	10	0	1	0	3
sly-miR7987-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
sly-miR7990a-1/a-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7990a-3	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	2	5	1	2	1	0	0	2	0	1	0	4	1	1	6	4	0	1	0	0
sly-miR7992-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7992-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7993a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR7997a	0	0	0	0	0	0	0	0	0	0	0	0	0	2	13	4	2	3	2	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1
sly-miR8001a	0	0	0	0	0	0	0	0	0	0	0	0	0	6	22	28	45	32	11	2	6	2	11	6	1	13	11	5	8	23	11	7	7	9	8
sly-miR8001b-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
sly-miR8001b-1-5p/b-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	6	12	14	17	9	6	0	1	3	2	2	3	2	3	4	2	4	1	5	2	9	2
sly-miR8006-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	6	5	5	7	2	8	0	2	3	3	1	2	4	1	3	1	0	0	2	0	0	0
sly-miR8006-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
sly-miR8006-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	38	102	169	131	90	209	1	4	3	1	1	1	4	4	3	4	10	0	6	3	6	4
sly-miR8007a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2	1	2	5	1	0	2	0	3	5	4	2	2	4	2	1	5	4	2
sly-miR8007b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
sly-miR8007b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	2	4	6	4	4	3	1	1	4	2	4	7	6	8	7	4	4	5	2
sly-miR8008a-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008a-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	1
sly-miR8008b-1-5p/b-3-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	4	10	5	5	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	1
sly-miR8008b-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8008b-3-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0

5p																																				
sly-miR8011a-1-3p	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8011a-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	1	0	1	2	0	2	2	1	4	3	3	5	0	0	4	0
sly-miR8011a-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	2	6	7	1	7	9	19	41	5	5	9	22	23	15	67	38	3	6	8	6
sly-miR8013	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	6	2	0	0	0	0	3	0	0	2	0	0	0	0	0	1	0	0	0
sly-miR8019-1-3p/2-3p	1	0	0	1	0	0	0	0	1	1	0	0	0	185	258	308	481	459	253	39	83	92	123	41	44	128	137	107	107	232	115	93	97	128	123
sly-miR8019-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	2	1	2	0	4	2	2	1	3	1	0	3	1
sly-miR8019-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
sly-miR8020	0	0	0	0	0	0	0	0	0	0	0	0	0	4	10	1	17	10	11	4	3	5	6	2	2	3	11	16	13	21	9	3	4	8	8
sly-miR8021-1/2/3	0	0	0	0	0	0	0	0	0	0	0	0	0	32	61	52	97	77	53	3	4	3	5	5	1	4	6	6	8	10	11	8	3	4	5
sly-miR8025-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
sly-miR8025-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8032d-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	4	5	9	9	0	2	3	5	0	1	1	5	3	7	11	8	2	7	3	8
sly-miR8033-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	12	11	11	27	20	14	2	8	0	4	1	0	0	2	3	5	5	2	1	2	0	0
sly-miR8033-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	4	11	6	7	5	6	2	4	0	1	0	0	1	1	5	2	2	2	0	0	1	0
sly-miR8038a-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8038a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8039-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	1	0	1	1	0	0	0	0	0	0	1	0	1	0	1
sly-miR8039-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8045-1/2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	1	0	0	0
sly-miR8045-2-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	3	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8051-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
sly-miR8172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR8175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR827-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	3	13	0	0	2	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR827-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	5	24	1	1	10	4	0	0	0	0	0	0	0	0	4	5	5	0	1	2	1	0
sly-miR828a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	2	0	0	2	7	0	0	0	0
sly-miR845b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	4	5	2	2	5	5	4	3	12	7	3	2	4	4	0	2
sly-miR9471a-3p	1	0	0	0	0	0	0	0	0	0	0	0	0	1031	1096	1268	1282	853	1162	8	13	5	11	4	5	4	11	15	11	38	16	6	7	13	3
sly-miR9471a-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	21	10	10	14	21	7	72	171	25	40	244	153	27	73	273	224	99	58	133	217	36	21
sly-miR9471b-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	1575	3071	2614	2632	1841	2614	48	82	20	63	50	59	28	93	88	76	140	71	41	55	42	17
sly-miR9471b-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	4	9	7	3	9	42	12	20	50	39	3	41	48	44	56	26	30	39	33	13
sly-miR9472-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
sly-miR9472-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	8	16	22	60	30	31	0	0	0	0	1	0	0	1	1	0	0	0	3	0	1	1
sly-miR9473-1-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-1-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	5	4	5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9473-2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sly-miR9476-1-3p/2-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	47	54	68	111	59	51	5	11	8	12	10	7	8	21	26	22	21	22	12	16	18	8

sly-miR9476-1-5p/2-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	2	3	5	3	10	11	4	10	2	4	11	5	2
sly-miR9478-3p	0	0	0	0	0	0	0	0	0	0	0	0	0	4	17	16	23	27	23	3	7	3	3	3	3	6	6	8	7	7	10	6	6	11	0
sly-miR9478-5p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0

Supplementary Table S16. Data sequence of the stem-loop RT primers designed according to Chen (2004).

miRNA	miRNA sequence	RT primer	Forward	Reverse
sly-miR166	ucggaccaggcuucauucccc	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGGGGAA	TTGTCGGACCAGGCTTCA	
spe-miR166	ucggaccaggcuucauuccuc	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGAGGAA	TTGTCGGACCAGGCTTCA	
sly-miR167	ugaagcugccagcaugaucuaa	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTTAGAT	CCTTGAAGCTGCCAGCATG	
spe-miR167	ugaagcugccagcaugaucua	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTAGATC	CCTTGAAGCTGCCAGCAT	
sly/spe-miR530	ucugcauuugcaccugcaccu	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAGGTGC	CGGTCTGCATTTGCACCT	
sly/spe-miR7983	acuaaugccgguaaagacuuuaac	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGTTAAA	TCGACTAATGCCGGTAAAGAC	
U6			GGACATCCGATAAAATTGG	GATTTGTGCGTGTCATCCT
Universal Primer				GTGCAGGGTCCGAGGT
5.8S			GGGCGAGTCCAAAATCCAAT	GGTGTTTTCACGTCTTACCGT

APÊNDICE II - SUPPLEMENTARY TABLES - CAPÍTULO II – Article: Computational prediction and characterisation of miRNAs and their pathway genes in human schistosomiasis caused by *Schistosoma haematobium* from Memórias do Instituto Oswaldo Cruz Journal

Table S1 – miRNAs identified in *S. haematobium* Egypt genome; sht: *S. haematobium*.

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
sht-miR-9711	GGUUGGAAAUCAUGUAGUGCCAGACAAACAUCUUACACAUUAGUUAAUGUUUCACUUGGUACUGUAUACAAGAUUAUCCACGC	83	sht-miR-9711-3p	aauguuucacuugguacugua	46-66	dvi-miR-9711-3p	3	0	21	21	1
sht-miR-2238h	CAUUUGAUAUUAGACUACUGCUGAAGAGUGUCAUAUUAAGACGAAAUGACAGUUCAGUGCUUUCAUUUUUCCAACGGUGGUCUAAUAUCAAUCG	94	sht-miR-2238h-3p	aaugacaguucagugcuuucau	45-66	ppc-miR-2238h-3p	6	0	22	22	1
sht-miR-4680	AUUAAAAGUCCUUUGAAUUGAUAUGCUUAACUUAGCUCUUAGCAUUUCACUCGGUGCAUCGCCUCUGAAUUGUAAGAGUAUAUACAGAGGCUUUUUAU	98	sht-miR-4680-3p	ucugaauuguaagaguauaua	64-84	hsa-miR-4680-3p	3	0	21	21	1
sht-miR-2340	CACGAGAAGGCAGUGUGUAGGACUUCCCUGGUGGUUGCUAUGUGAAAGCAUUUCGAGAGGGAAAGCUAACUCUUCCCAUUCUCAGC	86	sht-miR-2340-5p	ggacuucccuggugguugcuau	20-41	bta-miR-2340	6	0	22	22	1
sht-miR-2162	ACCUCUCUAGGGGAUGAGUGGGAUGGUUGCAUAUAUACAAUGCUGAUAAUGUAUUAUGCAACGUUUCACUCUACCCCAGGGACUC	85	sht-miR-2162-5p	agugggaugguugcauauauac	17-38	sma-miR-2162-5p	0	0	22	22	1
			sht-miR-2162-3p	uauuaugcaacguuucacucu	52-72	sja-miR-2162-3p	0	0	21	21	1

sht-miR-466c	CACUAGAAAUCAAGACU ACGAUCUCUAGGUCUUG UGAUGUGUGUAUGUGU GCUAUAUUUAGACCAUU UAGUUGGAAGAUAGUAG UUUGAAUUUUUAUUU	99	sht-miR-466c-5p	ugugaugugugu augugugcu	33-53	rno-miR-466c-5p	5	0	21	21	1
sht-miR-11629	UCGGAUUAGAGUACAGG UGUUAAACUUCAAGUUC CAAAUAUUCUUAGCAUU UAUUCAUUUUGGACUUU UAGUUUAAGCCCAUUAU UUUAUUCUUA	95	sht-miR-11629-3p	ucauuuuggacu uuuaguuua	55-75	tca-miR-11629-5p	5	0	21	21	1
sht-miR-138	AUGCAAACAUUAUUGGA ACUUGAGUAGAACUGCA UUGCUGAAGAGAGUCAA AAGGGCUUCUUCACAAC ACCAAUUUACCAAAAAA CUGUUUGUGA	95	sht-miR-138-3p	gcuucuucacaa caccaauuu	56-76	dre-miR-138-2-3p	3	0	21	21	1
sht-miR-545	GUCUGAGUAAAUGUUUA UGUACUCGAUUUUGAGU UGGCUUUUGGUAGGCU AAUUAUAGUAUAGAAAA CGGUUACUUGAUACGUU UACUCAUUU	93	sht-miR-545-5p	cugaguaaaugu uuauguacuc	3-24	dno-miR-545-5p	5	0	22	22	1
sht-let-7d	UUAAUGCACUUGAUUUC CAACUGUUGAGGUAGUA GGUUUAAACUCCCUACC ACCUACUUCAGCUUCAG CAACCAAGUCGCAUCAG	85	sht-let-7d-5p	ugagguaguagg uuuaaacucc	25-46	pma-let-7d	6	0	22	22	1
sht-miR-203b	GUGCUUCUUAAUAUUAA UUGAACUGUUGAGAACU AACUUGCUCGAUCACUG UUUGUUAGUUUGCCGCA GUCCAAUAGUUAUUAUG AAGUGG	91	sht-miR-203b-5p	uugaacuguuga gaacuaacuu	18-39	oni-miR-203b	4	0	22	22	1
sht-miR-61	GUUGUGGGUCCCUUUC UUGUCCAUGGUACAGCA GUUGAAGCUCACUGCUU UAGUGUGCAUCCUCUUU ACAUCACAUGACUAGAA AGUGCACUCACUUC	98	sht-miR-61-5p	ugugggucccuu ucuuguccau	3-24	sma-miR-61-5p	1	0	22	22	1
			sht-miR-61-3p	augacuagaaag ugcacucacuu	75-97	fhe-miR-61	0	0	23	23	1
sht-miR-3618	AAUAUAUGUUGAAUAUA UGGAUCAUAUGGAUUAA ACCAUAAAGGUUUCGAU GAUUUAUAAUGAUAAUU	97	sht-miR-3618-3p	ugugauuuccaa uaauugaaau	70-91	mmu-miR-3618-5p	3	0	22	22	1

	AUGUGAUUUCCAAUAAU UGAAAUCAUCUA										
sht-miR-4172	AAACCACUAAGCUGCCA GUAAAAUUAAAACCUGA CUAUUAUGUCAUAUAUU UGCCAUGCAUAUCAGAU UACUGUAUGACUGGAUA GCUAGAGGCUC	96	sht-miR-4172-3p	uauuaugucaua uauuugc	36-54	cin-miR-4172-3p	2	0	19	19	1
sht-miR-1-1	GUAUCUUUGUACUUCUU UUCAUCUCCUCCAUGUG UUUGUCGAUGAAUUUCA UCGGGUACCCACAUUGC CAUGAUGAUAAACUAAU UGAAAAGAAAU	96	sht-miR-1-1-5p	uguacuucuuuu caucuccucc	8-29	asu-miR-1-5p	6	0	22	22	2
sht-miR-4206-1	UAAACAUAAUGCCCUUU AUACACACCGCCCGUCG CUACUACCAAUUGAAUA GUUUAGUGAAAUCGUUA GAUUGGUGUCGUUGUA AUGGCUUUACUGUUCG	100	sht-miR-4206-1-3p	auugaauaguuu agugaa	44-61	cin-miR-4206-3p	1	0	18	18	1
sht-miR-10501	ACUACUUCUCACCAGCA CUCCAGGAUAUACCACU UCCAAUGGUCAAUAUCG UGGAUGCGCACUGCUG AGAAGUCAU	76	sht-miR-10501-3p	accacuuccaau ggucaaua	29-48	sfr-miR-10501-5p	4	0	20	20	1
sht-miR-10644	GAGAUGGUUGGAAGAAA GUUAGGGGCGGUCAAA CCAAAACGUGGCAUUAG UGCUUGAAGUCACUAAC UUCUAGUCCGAGCCAUG UU	86	sht-miR-10644-3p	uggcauuagugc uugaagucac	42-63	oni-miR-10644	6	0	22	22	1
sht-miR-10107	AUGGAAUAAUGUAUGAU GUAAUGGGUUAAAAUCC UUUUUGACGAUAUUUUU AUGACAUUGGAGAGGGU UUUUAACAUAGCUAUAA UAUUCCUC	93	sht-miR-10107-5p	uuaaaauccuuu uugacgauau	26-47	hpo-miR-10107-3p	4	0	22	22	1
sht-miR-559	CUAACGGUUCGUUACUU UAUGUUUGCCACUUGUU UAAAGUAAAUAAGCACU CUGAAGAAGUGGCCAGC ACGAAGUGACGAAACGU CAC	88	sht-miR-559-3p	uaaaguaaauaa gcacucuga	35-55	ppy-miR-559	4	0	21	21	1
sht-miR-3812	AAAGAAUACUUUCCAUC GUCUUCACAAUCAUUUU UCUGGGUAUUUCAUGCU AAGUGAUUUUGAUGAUG	79	sht-miR-3812-3p	uaagugauuuug augauggaaaau	51-74	tca-miR-3812-5p	7	0	24	24	1

	GAAAAUUCAUA										
sht-miR-79	AUCAUCAGUCAGUUAAA GCUAGAUUACCAUGGAA AACGUGGAAGCACUGGA CGGCCGUUUCGUCCUA UUGUGAUGGUCAAGCUU CAAUUGACUAAUGAU	99	sht-miR-79-5p	uaaagcuagauu accauggaaa	14-35	dme-miR-79-3p	4	0	22	22	1
sht-miR-7194	AGCAGUGAAAUCCAGUU UGAUGAGCAUUUCGUCU UAUUUGUGAUUCGUCAG CUAUACGUACCUGCAUC UCAGAUUCUGGAUUCCA CUAUU	90	sht-miR-7194-3p	cucagauucugg auuccacua	68-88	mml-miR-7194-3p	4	0	21	21	1
sht-miR-11181	AGUAGUGGUAGUAGUAG UAGUAGUCGUAGUAGUA GUCGUAGUAGUAGUAGU AGUAGUAGGAGGAGGA GGUCAGUUACUAUUUCU AUUAUUAACACUGUG	99	sht-miR-11181-3p	aggaggaggagg ucaguu	58-75	hsa-miR-11181-3p	2	0	18	18	1
sht-miR-141	CCUGAGGGAAACAUGUU GCUGACGUCACAUCUUC CAGUACAGUCAGCACUA AGACUUUACCCUCGAU	67	sht-miR-141-3p	caucuuccagua cagucagcac	28-49	hsa-miR-141-5p	6	0	22	22	1
sht-miR-71a	UAUGAAGAUGUGAUACU AGUGCUGUGAAAGACGA UGGUAGUGAGAUGCCAA UUGCAUCUCGCUUCCCC GCCUUUCCCGGUAAGAA UCACGAGUCGUCAGC	100	sht-miR-71a-5p	ugaaagacgaug guagugagaug	25-47	fhe-miR-71a	0	0	23	23	1
			sht-miR-71a-3p	ucucgcuucccc gccuuucccg	57-78	sma-miR-71a-3p	0	0	22	22	1
sht-miR-2a-1	UUACCUCUUGCGCCGCA GUCAAUAUUGGCUGAAG GCAUUGCUUUAUUGUCA CAGCCAGUCUUGAUGAA CGGUGUAAAAGGCGC	83	sht-miR-2a-1-5p	cagucaauauug gcugaaggca	16-37	sma-miR-2a-5p	0	0	22	22	1
			sht-miR-2a-1-3p	ucacagccaguc uugaugaacg	49-70	sja-miR-2a-3p	1	0	22	22	1
sht-miR-2b	ACUGCAGGUGGUGCGC GUCUCAAGGGACUGUGA AGCAACGUAAUUAAUUG UAUCACAGCCCUGCUUG GGACACAGCCUACCUGC UAA	87	sht-miR-2b-5p	cgucucaaggga cugugaagca	16-37	sma-miR-2b-5p	1	0	22	22	1
			sht-miR-2b-3p	uaucacagcccu gcuugggacaca	51-74	sja-miR-2b-3p	0	0	24	24	1
sht-miR-2e	GCUCUUACCAACUUCGA	74	sht-miR-2e-5p	uaccaacuucga	6-26	sja-miR-2e-5p	1	0	21	21	1

	CUGAGUUAUACUGCUCCUGCAGGCCUUGUAUAUCACAGUCCAAGCUUUGGUAAGUUU			cugaguuau							
			sht-miR-2e-3p	uaucacaguccaagcuuuggu	48-68	sja-miR-2e-3p	0	0	21	21	1
sht-miR-124c	CCGUGGAUGACAUUCACCGCGUGCCUUAAUAUUUCUGUUGCGAGUAUUAUUUGUAACAAAUCAAGGCAAUCGCGGAAAAUGGCAUACAAAA	91	sht-miR-124c-5p	cauucaccgcgugccuuaaua	11-31	gga-miR-124c-5p	1	0	21	21	1
sht-miR-10704	UUUUUUAUUUGUUGGGAUGAAUAGGGGUAUUAAUUAGAUUACGAUGUAUGUUCCUAACCUGUUAUAUAAAUAUUGCCCUUUCUGUCAACAAGUGAACUU	99	sht-miR-10704-3p	uacgauguauguuccuaaccu	40-60	oni-miR-10704	3	0	21	21	1
sht-miR-3499-1	CUUUCUGAAUCCGUGCUGAGAUUUCAUCAAACAAUAACCCAUUAGGGUUUAUCAGACUUCCAAGAUGAGUGAAAUUUCCGACGCGUUCGACUA	93	sht-miR-3499-1-5p	ucugaauccgugcugagauuuc	4-25	sja-miR-3499	1	0	22	22	1
sht-miR-6306	UCACUGAGAUGGUGGGGAAAAUUUGUAGCUAAGAUGGAUGAUUUUGAUGGAGUUUUGUUCUCUAAGCUAAAUGAACCAAACCAUCCAGCUC	91	sht-miR-6306-3p	ucuaagcuaaaugaaccaaacc	61-82	hme-miR-6306-3p	4	0	22	22	1
sht-miR-563-1	AGACUAAGUAAUUAGAAUUGGUUUGUGAUCCUUCAUCAUGAGGGUUGAAACUCAAGGGUCUAGAAGGUUGACAUACAUUUCCAUUUGUUUAGAAC	95	sht-miR-563-1-3p	agguugacauacauuucca	65-83	ppy-miR-563	1	0	19	19	1
sht-miR-7092	CGAAACGGUUAUUCUUGUAUUUAAAAAGGCAAACUCACAGAAGAGAUGGAAUCCCAUCACUUUUGAUACAAGAAAAUCCCUUAAU	85	sht-miR-7092-5p	aaaggcaaacucacagaagagau	25-47	mmu-miR-7092-5p	4	0	23	23	1
sht-miR-4106	AUUUAUAAAAUAUUGGUUUAGAAUAGAAAAUAUUAGAAAGAGGGAGAAAAAUUAUUUCCCUACUCUCUUUGAUUGCCUACUCUAACAAAUUUCAUAAUA	100	sht-miR-4106-5p	uaaaauauuggguuagaauag	6-26	cin-miR-4106-3p	4	0	21	21	1

sht-miR-3851l	CCAUACAUUCCAAUUCUGAUUGAUGUUAGAUACUACUUAUGUCUGUUGGCAUAAGUAGUGUACACCAUAACACAACUGAAUUACCC	86	sht-miR-3851l-3p	uguuggcauaaguaguguacac	44-65	tca-miR-3851l-3-5p	6	0	22	22	1
sht-miR-125c	GAUUCCGUAUCCCUGAGACCUUAGAGUUGUCCUGUUUGGAAGUAUUCUUCAAUUAUUCUAAAGAAGAUUGACACCUCUACGGUAUCAGGUCACGGAACA	99	sht-miR-125c-5p	ucccugagaccuuagaguuguc	10-31	sma-miR-125c-5p	0	0	22	22	1
			sht-miR-125c-3p	caccucuacgguaucaggucacg	72-94	sma-miR-125c-3p	0	0	23	23	1
sht-miR-6733	UGCUGAUUUUCACACAAUUUUUUUACAUUCAUUAUCAGUGUCUGGAUUUCCUUUCGAGCCAGUGAUUUAGAAGUAUAGAAAUAUGUUUCAUAUCAAUG	98	sht-miR-6733-3p	ucagugucuggauuuccuuu	35-54	hsa-miR-6733-3p	2	0	20	20	1
sht-miR-84a	AAGUCCUUCAUAAUAAUCAUCUAUCGAAUAAAUUUCAGUCUGACUAUCGCUAGUCAAGGCAAUAAAUAUUGUUUAGUAUGAGGUAGUUAAGAAUGAUAG	99	sht-miR-84a-3p	ugagguaguuaagaaugauag	79-99	ppc-miR-84a	3	0	21	21	1
sht-miR-9126	UUUGUGAAAUAAAUUUGAGUUCAUUUCAUUUAAAUUUUACUCGUUGGUGAAGUUUCGAUGAAAAUAACAAAAAUCAUUUUCACUUU	86	sht-miR-9126-3p	uuuuacucguuggugaaguuuc	35-56	eca-miR-9126	5	0	22	22	1
sht-miR-8448-1	GAUCAGUGUUGCGCGCGAAAGCUUAAACCUAUGACCAAUGACCAUGCACUCAGUAGUGUACAGGUCUAGAGGUUAAACGUUCGCGCGCAAGACUGGUC	98	sht-miR-8448-1-3p	cuagagguuaaacguucgc	66-84	sma-miR-8448-3p	1	0	19	19	1
sht-miR-12366a	AGUGACUUAUCGAUCGGAUCAAAGGAUUCAGAAUCUCGAUAGACUAUUCUGGUCCGUUGUCCCCGACUCAGCUAACUCGAU	81	sht-miR-12366a-5p	aucaaaggauucagaaucucga	18-39	mdo-miR-12366a-3p	6	0	22	22	1
sht-miR-8	AGCAAGAAUGAGUGUGACAUCUUACUAACAGUAUUUGACAAAUUAAUUUCUAAUACUGUUAGGUAAAG	88	sht-miR-8-5p	caucuuacuaacaguauuuga	18-38	sma-miR-8-5p	0	0	21	21	1

	AUGCCAGCUCAAUUCUU UGU										
			sht-miR-8-3p	uaauacuguuag guaaagaugcc	51-73	sja-miR-8-3p	0	0	23	23	1
sht-miR-466g	UGCAAAACGUGGUCGAG AGUGGCAUGUAGACUGA CCUUGUCCACAGUAGAA CCACCACUACUUAUACA GACACAUGCACUCCUUG ACUAUUUUCAA	96	sht-miR-466g-3p	auacagacacau gcacuccuu	64-84	mmu-miR-466g	4	0	21	21	1
sht-miR-2463	AAUAUCAACACAGUUCU ACUGCAUGUGGUGGAAA CUUGGAGAACUACGAAA UCCAUCAUCGAGAAGAU ACAAAUGUUGAUUAA	83	sht-miR-2463-5p	cugcauguggug gaaacuugga	19-40	bta-miR-2463	5	0	22	22	1
sht-miR-16b	UUUUUACAAUAAGUUUC AUCAUAAAUUGAUGUUC CCUAGAAAGCUGUAGAA CUACUGAAUCCCACUAG GCGACCCAGUAUUAUUG UGCUUAUUGUAAAAC	100	sht-miR-16b-3p	ccaguauuauug ugcuuauugu	74-95	xla-miR-16b-3p	4	0	22	22	1
sht-miR-3853	CUGCUUCACAUAAUAUU AUAUGCUUGUAUGAAUU UUAAUACAUUUUCAUAA AAUGUGUGUAUUUUGUG AAGUAU	74	sht-miR-3853-3p	gugugauuuug ugaaguau	55-74	tca-miR-3853-5p	3	0	20	22	1
sht-miR-7643	AUUUUUAUUCACAGGCA AUGUCAAGUAUACCACA CAGCAAAACAUUCUAUA CUAAUGUGUGACUGAGA CAUGAUAGUUGACGUUG AACGAAUAAAGGU	98	sht-miR-7643-3p	gugacugagaca ugauaguuga	59-80	tgu-miR-7643-5p	5	0	22	22	1
sht-miR-1960	UUAUCUCUGUCAAUGAA CAAGAGGAUUUCCAGUG CUGUUAGAAGUAGGUUU CCUUCUGACCACACUGU GGAAGUAUAUGUCUUCU UGAGGAGACUG	96	sht-miR-1960-3p	ccagugcuguua gaaguagguu	29-50	mmu-miR-1960	3	0	22	22	1
sht-miR-4000e	AACUGAAACAGUGAUGU AGUUUGUGAAACUUCUU CGGAAAAAAGCUUUCCG CCUUUAUCACGAAUAAU AUCAAUUUUUCAAUC	83	sht-miR-4000e-5p	ugaaacuucuuc ggaaaaaa	24-43	cin-miR-4000e-5p	3	0	20	20	1
sht-miR-4111	GCUUUAACAUUUGAUUA UUUUGUGAUUGACGGAA UAUAGUGACAGCUAAUU CCGUGGAAUAUAACUAU	83	sht-miR-4111-5p	auuugauuauuu ugugauu	9-27	cin-miR-4111-3p	2	0	19	19	1

	AUCAAAUAAUAAUAA										
sht-miR-4913	CUUAAUAUAUUUAUUCC UAAUUGUGAUUUACUGA GUUGUACUAUUGCAUGU GCUCAUGUAAUACAAUA GUGUAUUAACCAAUUCG AAUAAAUAUUUAGG	99	sht-miR-4913-3p	auuaaccaauuc gaauaaauauu	73-95	dme-miR-4913-3p	6	0	23	23	1
sht-miR-4000g	CGAUGAAACUUCUUUAG AAUGUUGGAAUCUCGAU UUCCUUUUUAGGUCAAA AGGGUAAGUCUCAGAGU AGAACAUUUUAGGAAAC GAUUCAGCC	94	sht-miR-4000g-5p	ugaaacuucuuu agaauguu	4-23	cin-miR-4000g-5p	3	0	20	20	1
sht-miR-9396	UGAACUAUCCUAGAAAA CAUUGUAAGUGAUGAAG AAAUAUUCACAAAUACA UUGUUUAAGAGGGUAGU GAA	71	sht-miR-9396-3p	guaagugaugaa gaaauauuca	22-43	gsa-miR-9396-5p	3	0	22	22	1
sht-miR-4175	CUACCAUCGGACUGCAU CUCCUAACGUUGCUCUA CUGCCUCGUGGAUUCG ACAUUCAGGUCAAAGGC UACGGGUGUAGCUCCG AUGGGGA	90	sht-miR-4175-3p	gguguagcuccg augggga	72-90	cin-miR-4175-3p	3	0	19	19	1
sht-miR-592	AGAAGAGACUGUCAGAU GACACAAGCAUUACUUU GGUUCUCAGUGGGGAC UUGUGUCAAUAUGCGAU CUCUCGA	74	sht-miR-592-3p	uugugucaauau gcgaucucuc	51-72	hsa-miR-592	5	0	22	22	1
sht-miR-9388	UGCAUUAUAUGUGUAUG UAUGUAUGUACGUGUGU CGGUGUGACAGAAUUGA AGACCCCUAUGUAUGUA UGUACAUAUACACGUAA AUACC	90	sht-miR-9388-5p	guauguauguau guacgugugguc	13-35	dme-miR-9388-5p	5	0	23	23	1
			sht-miR-9388-3p	cuauguauguau guacauauaca	58-80	dme-miR-9388-5p	4	0	23	23	2
sht-miR-4027-1	AGGUUAGUUAAAGUCGU CAGAAAGCAUACAGACU AUUAUAUAUAUGCAUAU AUUACUUUUAUGUUAAC CUGACUUUGUUAACUAA GUA	88	sht-miR-4027-1-3p	uauauuacuuuu auguuaac	49-68	cin-miR-4027-3p	2	0	20	20	1
sht-miR-1350	CUUGUGGGUGAAGGAC CUAAACAAUCAGUUUAA UGACGAUGUUUAUUUGU CAACUGGGUCUCUGUUU	89	sht-miR-1350-3p	ugucaacugggu cucuguuugu	48-69	oan-miR-1350	4	0	22	22	1

	GUACAACUCCUUGACUCACUUA										
sht-miR-43b	GUGUAUGUAUAUAUAAGAAUGUGAAUGUGUGUGGGGUAUGAUUAGUUUAUAGCUUAUCACAGUUUCCUUGUCACACUCUCUAUGUCUUCAUAUAU	95	sht-miR-43b-3p	uaucacaguuuccuugucacacu	55-77	hpo-miR-43b-3p	6	0	23	23	1
sht-miR-36b	AGGGAAUGUCUGUUCGGUUUGUGUUAUCUUGGUUACUUGUUAAGUACUACUUAAUAAUGUAACUAUUUUUCAGUACACCACCGGGUAGACAUUCAUC	97	sht-miR-36b-5p	agggaaugucguucggguuugu	1-22	sma-miR-36b-5p	0	0	22	22	1
			sht-miR-36b-3p	accaccggguagacauucauc	77-97	fhe-miR-36b	0	0	21	21	1
sht-miR-36	GGUAUAUCUUGUGAAGAGUGCCGACCCGGUUAGCCAUUAAAUUAUUGUUAAAGAAAUGAGGCCACCGGGUAGACAUUCAUUCGCAGGAUAUUUC	94	sht-miR-36-3p	ccaccggguagacauucauucgc	62-84	sja-miR-36-3p	0	0	23	23	1
sht-miR-10	UGAUUCCUCAGUAUGAACCCUGUAGACCCGAGUUUGGAUGCAGUCAAAUGCAAAUUCGAGUCUAUAAGGAAAAAUACUUUGGAAGUG	87	sht-miR-10-5p	aacccuguagaccccgaguuugg	16-37	sja-miR-10-5p	0	0	22	22	1
			sht-miR-10-3p	aaauucgagucuauaaggaaaaa	52-74	sma-miR-10-3p	0	0	23	23	1
sht-miR-10954	UGGGUCAACUGAAGCUGCACCACAAUGGAAAACCUGAAAGCAUUGGACGGCCGUUUCGUCCUACUAUGGGUUUAGCUUCAAUUAACUCA	89	sht-miR-10954-5p	caacugaagcugcaccacaau	6-26	oni-miR-10954	5	0	21	21	1
sht-miR-563-2	UCGAAUUUCAUGCAACAUGAUACAUAAUAUGUCGGUCCAAGGUUGACAUACAUUUAACAAGUAUGUCAUCUGACAAUUGUG	81	sht-miR-563-2-3p	agguugacauacauuuaac	40-58	ppy-miR-563	2	0	19	19	1
sht-miR-5594	CAAGGUUAUCAAUGUCUUUUGAAAUAAAGAACUCAUCAAACUGUGAUGCGUAUUCAGCUUCUCUCUUUGAUUGUAAUGCGAAUGAUGAUAACCAUU	96	sht-miR-5594-5p	uuuugaaauaaagaacucauca	17-38	prd-miR-5594-3p	4	0	22	22	1

sht-miR-6574	UGGUUAGAGACUUUGAAUGACAUGGCUCAAAAUCGUUUGUAAUAGCGCAGGUGCAUCCAUUCCUUGUCUUUUCUUAGUUUCUAAAUU	87	sht-miR-6574-3p	auuccuugucuuuucuuaguu	59-79	gga-miR-6574-5p	4	0	21	21	1
sht-let-7	UUCUGGGAGGUAGUUCGUUGUGUGGUUUGCUUAUCAAAAUGAAUAAAAGAAGACCAUACAACCGACUGGCUUUCCCAUUG	80	sht-let-7-5p	ggagguaguucguuguguggu	6-26	sja-let-7	0	0	21	21	1
			sht-let-7-3p	cauacaaccgacuggcuuucccau	55-78	sma-let-7-3p	0	0	24	24	1
sht-miR-510	UAGAAGUAUCAGUAACAAUAGUAGUCUACCAGUCAAGAUUUCAAAUUGAAACCUCUAAGAUUCUUCAUAAGGCUAGGCACUACUGAGCUGAUUCUUAUU	100	sht-miR-510-3p	auugaaaccucuaagauucuu	45-65	hsa-miR-510-3p	4	0	21	21	1
sht-miR-87a	CAAACCUUGAGCAAAGUUUCAAGUAGUGAGUUACACAAAAUUGGUUUGUCGUGAUUCUCGCGCUAGUGAUAAGUCGCAUGAUAUUACUCAAGGUACC	97	sht-miR-87a-5p	ugagcaaaguuucaaguagu	8-27	sme-miR-87a-3p	3	0	20	20	1
sht-miR-33a	CUCAAAUAAUAUCAAUGUGUCCACAGUGUGUGUGUUUGUGCACUUUACUCAGUCUGAGAAUUUAUUUCACUCACUAUGGACUUGAUGUCUUUUACC	96	sht-miR-33a-5p	caauguguccacagugugugu	13-33	dno-miR-33a-3p	4	0	21	21	1
sht-miR-2493	ACCAAAACGAACUGAAAGAAAUAUUGGCAAGUGUGUUGUCGAAUUUUCGCUCACACACACACACUCUAUUUAUGUAUUUUUCAUGGUUUGUUUUUAA	97	sht-miR-2493-3p	gcucacacacacacacucuau	49-69	dme-miR-2493-5p	5	0	21	21	1
sht-miR-5894b	AAGUGGAGAGUAUACAAAACUCUCGGAAGCCUAUAUCUGAUGGUAUUUUCCUAAACUUAAAGCAUUUCCAAGCAGUUUGUGUAAUUCCAUGA	92	sht-miR-5894b-5p	gccuauaucugaugguauuuu	29-49	hco-miR-5894b	4	0	21	21	1
sht-miR-10828	AGUUUCAGUAAAUCUCUGGAUGAUAUGCUUUUAGGUGUGGAAAUAAUUGCUAAAAGUAUGUAAAGUCA	88	sht-miR-10828-3p	aagucaucacagaacuaccuga	63-84	oni-miR-10828	4	0	22	22	1

	UCACAGAACUACCUGAAUAA										
sht-miR-4206-2	AUACAAUAAAACACCACCAGUCGCUACUACCGAUUGAAUAGUUUAGUGAGGUCGUUGGAUUGGUGUCGUUUUAGUGGCU	79	sht-miR-4206-2-3p	auugaauaguuuagugag	33-50	cin-miR-4206-3p	0	0	18	18	1
sht-miR-1187	UGUAUGUAUCUGUGUAUGUGUGUGUGUAUGUGGGUAUUCAUUUGUUACUUAGUAAGUAACAAUGUUCACACAUAUCAACCAACUCAUUGUUACAUGUA	98	sht-miR-1187-5p	uaugugugugguaugugggguau	15-37	mmu-miR-1187	2	0	23	23	1
sht-miR-8335	GCUUUAAUUGACUCAUGAAUUCAACUAUAUAACCAAACUAGUCAAAAUCCAGUGAUUGGAUGUUGUUGUUGUUGUUGUUUUCUUUGAUCAUAAAUGC	100	sht-miR-8335-3p	guuguuguuguuguuuucuuugauc	68-92	ppc-miR-8335-3p	7	0	25	25	1
sht-miR-281	UUUCUGAUGGAGAGAGCACUUUUAUGACGGAAACAAUUAUAUUCUUCGAAUUUAUUGAAGUUCCAUAAUGUCAUGGAGUUGCUCUCUAUAUCAGGUU	97	sht-miR-281-5p	gagagagcacuuuuaugacgga	10-31	sma-miR-281-5p	0	0	22	22	1
			sht-miR-281-3p	ugucauggaguugcucucuaua	69-90	sma-miR-281-3p	0	0	22	22	1
sht-miR-10345	UUUACUGAAGAUUAUAAAUUCUUCAUCACAGUUUCAGUGUAUGAUUAUUUCGUAAUUUAAUAUUAUACUGUUGAUUUCGAAUUCGAACUUCUUCAGUCCG	100	sht-miR-10345-3p	uuucgaauucgaacuucuucag	75-96	tcf-miR-10345	5	0	22	22	1
sht-miR-184a	UACCUACUGAAUAAUUAAUUUCUUUAACAAUUUUCGAUCCUUGGGGAACAGAUGACGUGGGUUAAGAGGUGUUAAAGUAAUUUGGAUUACCUGUAGAUU	99	sht-miR-184a-5p	ucuuuaacaauuuucgauccuug	21-43	gsa-miR-184a-5p	4	0	23	23	1
sht-miR-9814	AGUCAGCAAAAGUGAAAACAAUAAACAUUGGCAUAAGCCCGACUACCAGGUAAAUCAACUGACUUGCUAAUGUUCGGAAUGUUUUCUGAUUUCCUGUCU	99	sht-miR-9814-3p	cggaauguuuucugauuuccugu	75-97	ssc-miR-9814-3p	5	0	23	23	1
sht-miR-2023-1	UCAAAAGAAGUACAAGUGGAAAGUUUGAUUUCGA	94	sht-miR-2023-1-5p	aaagaaguacaaguggaaagu	4-24	nve-miR-2023-3p	3	0	21	21	1

	UUUAUCAUUGAAUCGCAUGAAAACAUCUAGAAGGUAAAAUUCAAAUUGUAUUUCUUUGUU										
sht-miR-1671	CUUGGACGGCCGUUCCAUCAUAGUAUGGGAAUUCUCGGAUGCGGAGUCGUGGGUGAGGACUGUUGAGUAGUCUUAUUCUAGAAUGAAACAGCCGUCCAGU	100	sht-miR-1671-3p	gugaggacuguugaguagucuua	53-75	gga-miR-1671	4	0	23	23	1
sht-miR-2023-2	UAACCAGAUUUAUUUCGUUGGCGAUCUCGUGGUAUCGAACGAAUACCAAGAUCGUGCCAAAAGAAGUACAAGUGGAAU	78	sht-miR-2023-2-3p	aaagaaguacaaguggaau	60-78	nve-miR-2023-3p	2	0	19	21	1
sht-miR-7790	CAAGCUGUUCAUUGUAUUCUGUGCUUUUCCUGAGAUGUGGAGGUCUUCCUAAUCUAGCCUGCCACUGGAAGAAAGAGGAAAGGGGAGAAUAAACAGCCUU	100	sht-miR-7790-3p	uggaagaaagaggaaagggga	66-86	hhi-miR-7790	3	0	21	21	1
sht-miR-219	AUUGUCCAUUCGCAUUUCUUGUUAAUUAUAUUUAUUAAAUAUUAUCAGUUAGUAUGAUAAUAUUUAAUUUACAAGAGGUGUUGAUGGACAUC	92	sht-miR-219-3p	agagguguugaugacauc	74-92	sma-miR-219-3p	0	0	19	19	1
sht-miR-927a	UGUAGGAGGCUCAGAAGGAGCCGAAGAUAUUCCAUCCAAUCACCUUUUGGGAGGAUAUUUUAGAAUUCCUACGUGUAGCUUCCUGAU	87	sht-miR-927a-3p	uuuuagaauucccuacguguagcu	58-80	ame-miR-927a-5p	5	0	23	23	1
sht-miR-71b	UUUGCUGUGAAAGACUUGAGUAGUGAGACGCUUAUAGCAUGGUUUUCCCUUCGGCGCCUCAUACUGAGUCUUUCCCGGCUCA	82	sht-miR-71b-5p	ugaaagacuugaguagugagacgcu	8-32	gsa-miR-71b-5p	1	0	25	25	1
			sht-miR-71b-3p	ccucauacugagucuuucccg	57-77	sma-miR-71b-3p	0	0	21	21	1
sht-miR-2a-2	CAGUUCGUCAUCAUUGGAUUGUGAUUUUCCGAAAUAAAGCUUUAUGAGUAGAAUAUCACAGUCCUGCUUAGGUGACGAAUUU	82	sht-miR-2a-2-3p	uaucacaguccugcuuaggugacga	54-78	gsa-miR-2a-3p	2	0	25	25	1
sht-miR-2c	CCAGGUUGCUGGCGCA	91	sht-miR-2c-5p	acccuuguacga	17-38	sja-miR-2c-5p	1	0	22	22	1

	ACCCUUGUACGACUGUGAUGUGUUCGAAAAUAAAAUCAUAUCACAGCCGUGCUUAAGGGCUUCGUCAAAACCGUA			cugugaugug							
			sht-miR-2c-3p	auaucacagccgugcuuaagggcu	54-77	fhe-miR-2c	0	0	24	24	1
sht-miR-3479	GGUCCAUGUUUGUGAGGGGGAUGUUUGUGCAAUUUAAUGUUGUAAAUAUAUUGCACUAACCUUCGCCUUGCAAAUAUAGGGUA	83	sht-miR-3479-3p	uauugcacuaaccuucgccuug	49-70	sma-miR-3479-3p	0	0	22	22	1
sht-miR-548b	AAACUUUGUGUUACAAGAAAUUCUUUAAGCAGGUAAGUUGGCUGAGAUACUAGCAAGAACCUCAGUUGCUAAAGGUCUUUUGAUGAACAAAGAUA	95	sht-miR-548b-3p	caagaaccucaguugcuaaagg	54-75	hsa-miR-548b-3p	4	0	22	22	1
sht-miR-124	UUUUGUAUGCCAUUUUCCGCGAUUGCCUUGAUUUGUUACAAAUAAUACUCGCAACAGAAAUAUUAAGGCACGCGGUGAAUGUCAUCCACGG	91	sht-miR-124-5p	ccauuuuccgcgauugccuugauuu	10-34	sja-miR-124-5p	0	0	25	25	1
			sht-miR-124-3p	uuaaggcacgcggugaauguca	63-84	fhe-miR-124	0	0	22	22	1
sht-miR-5934	AUGAUUUUACUCUGAUGUUUCAGCUGCUUUCAUACUAAUUAACGUUUGUUAGCUAUUUAGUCUGAUCAGAAGAAACUCAAAUGUAAAAUGGU	92	sht-miR-5934-3p	uuagucugaucagaagaaacuc	57-78	hco-miR-5934	6	0	22	22	1
sht-miR-9648	GGGGGUAGACUAACGGCCGGUUGUUCUACAGAGUCAACCCUUAAGAUUUAAACAACAGCUACGGGACUGUAGAAUUAAUGGCAGUUACGCUCCGUA	96	sht-miR-9648-3p	cuguagaauuaauggcaguua	67-87	cli-miR-9648-3p	4	0	21	21	1
sht-miR-8416	AAUGUUUUUAUGGCGUAUCUGUAUGAUUGGUCACAUAGUUCUGUGCUGUAAAGACAUAAUGAGCCUGUGAACAAGAAACAGAAGGACAAGGAAAAACAAA	100	sht-miR-8416-5p	ugauuggucacauaguucu	24-42	sma-miR-8416-3p	3	0	19	19	1
sht-miR-4260	UAUAUUUUCGUUAUUAGCAGUCCUAUAGUUUACGGACGGUAAUGUCUGGG	98	sht-miR-4260-3p	cuuggggcauggagucuau	67-85	hsa-miR-4260	3	0	19	19	1

	ACAAAGUUCAUGAAGAC UUGGGGCAUGGAGUCU AUAAUCUAAAAUGAU										
sht-miR-427	GAUAGUGGGUAACAGUG GGAAUCAGAAAGUGCUU UCUGUUUUAUCUCGGUU UCUUUUAGCUGUAUCUA CCUGUUUUCCAUUGUUC AUGCCCACUUUA	97	sht-miR-427-5p	gaaagugcuuuc uguuuuaucuc	25-47	xtr-miR-427	5	0	23	23	1
sht-miR-190	UUCUAGUGUUGACAGUG UAAAAUCCGUUCUUUAG UAGGAAGUAGAUAUGUU UGAUUUUACACCCUGUU CACGCUAAUC	78	sht-miR-190-3p	agauauguuuga uuuuacacccug	43-66	dqu-miR-190-5p	7	0	24	24	1
sht-miR-8422	UUGAAUCAUCCCAUUGA UGUUUAGGACUUUUAUU GGCAUAUGUGCAUACUC UACGUAUUACCUCGAUA UUGCAGUCCUAAACAUC AAUGGGAAGAUUCAA	100	sht-miR-8422-5p	uuaggacuuuua uuggcaua	21-40	sma-miR-8422-3p	3	0	20	20	1
sht-miR-737	CCUACUGAUUUCAACCA UCAUACAUGAAGAUUUG UUUUCUUAGGUUUUGAA AAUAGGGAAAUCGAAUC UUUCCAUACUCAUGUAA UUCAAAUUGAGUAUA	100	sht-miR-737-5p	guuuucuuaggu uuugaaaau	34-54	pbv-miR-737-5p	3	0	21	21	1
sht-miR-83	AGAGGCACCGAAAUAUA UCCGCGCCACACAAAGU AGCUAUCACUGAAUUUA UGUGUGGGCUACGAUA CUGCUCGGGUGCCCAA	83	sht-miR-83-3p	acugaauuuaug ugugggcuacg	42-64	cel-miR-83-5p	5	0	23	23	1
sht-miR-125b	AUCCCUGAGACUGAUAA UUGCUCUGUUUAUCAUG AUAAGUGUAUUUGAUGA GAACAAUUAUUAUUCUC AGGUGU	74	sht-miR-125b-5p	ucccugagacug auaauugcuc	2-23	sja-miR-125b	0	0	22	22	1
sht-miR-8485	CACACACACACACACAC ACACACGCAUACAUAUA UUUAUAUAUGUGUGCGU AUGUGUGUGUAUGUGC GUAAG	72	sht-miR-8485-5p	cacacacacaca cacacgcau	7-27	hsa-miR-8485	1	0	21	21	1
sht-miR-137	CUCAACUUCGGAAAACA ACUUUUCUCUGCAAGCG AUUAUUGCUUGAGAAUA CUGUUACUGAAGUUAUU	68	sht-miR-137-3p	uuauugcuugag aauacuguua	36-57	fru-miR-137	3	0	22	22	1
sht-miR-130a	AUAGUAACCAAGAUAGA AAUUUUGAGACAAGAAG	97	sht-miR-130a-5p	aagugcaauguu aaaagauuua	32-53	mmu-miR-130a-3p	6	0	22	22	2

	UGCAAUGUUAAAAGAUU UAAAUGUUUUUUGUUCG CUUCUUUUAAUUCAAUC UUGAGAUACACA										
sht-miR-7192	AUAGCAACAGUAUAGGA UCAGUCUUGUGUAAGGU UUCACUCAGAAUUAAAA AAACACAAUACGGUGCU UUUACUGUUUGCACA	83	sht-miR-7192-3p	ucacucagaauu aaaaaaacaca	36-58	mml-miR-7192-5p	3	0	23	23	1
sht-miR-466i-1	CUGUAGCUCUAGUGUG UGUGUGUGUGUGUGUG UUAAUAAAAUACAAAUAC ACACGCACACGAUCAAA CAUACAGAGGUAUGU	82	sht-miR-466i-1-5p	ugugugugugug ugugugug	13-32	mmu-miR-466i-5p	0	0	20	20	1
sht-miR-8357	UUAAACCGUUUUUGUUA UUGUGUUUUAGUCAGCA GUAGAUUGGAAUCAUAU UGAAGUGACUGAAAAGC AUACAUCACAAAAAGAU UAUG	89	sht-miR-8357-5p	uuuuagucagca guagauuggaa	23-45	ppc-miR-8357-5p	7	0	23	23	1
sht-miR-4919	CGAUGGCGUGUUUGUG AUCUAACUUGACUGAGU AUUAUGUGAGUCUCUAG GGGAAGUGUAUGUUUCA UAAAACGCCAAAU	80	sht-miR-4919-3p	gugagucucuag gggaagugu	39-59	dme-miR-4919-5p	4	0	21	21	1
sht-miR-7956	AGGUGUCUAAUUCAGUA CAAUGGAAGAUGGUCGC GCAAUUUCGUCGAUUGG UUGAGGUUAGACAUUA	67	sht-miR-7956-5p	gugucuaauuca guacaaug	3-22	prd-miR-7956-5p	0	0	20	20	1
sht-miR-466i-2	CAAACAAACAAAUAACAC AUAAAUAUUGGUACAAG AGGGCACCAAAUAUAUA UGCGCCACACCAUAUUU GUGUGUGUGUGUGUGU GUGGG	90	sht-miR-466i-2-3p	ugugugugugug ugugugug	69-88	mmu-miR-466i-5p	0	0	20	20	1
sht-miR-2538	CUAAUUAGGAUAAAUAA AUUAGAUUUUCUGACGU UUCGUGACUUAGUGUAA GCCACUUCUUCAGAAAA UAAAGCUUUAUUUAUAA UAAUCUA	92	sht-miR-2538-5p	uaaauuagauuu ucugacguuu	15-36	dps-miR-2538-3p	5	0	22	22	1
sht-miR-4027-2	GGUAUAUUACUUUUAUG UAUAUUAACUAGUACAU GUUCAUUGUAUCUCCAA CACAGAUACAUACGAAC AUCAGUACGUAUACACU CAGAGAUAAAUCAA	99	sht-miR-4027-2-5p	uauauuacuuuu auguauau	3-22	cin-miR-4027-3p	3	0	20	20	1

sht-miR-9197	GUUGAGAUGAAAAUUCACUUGUGAGAGAAGUAGAUCAAAGGACAUUGUGUGUUUUGAUUACGCUUUGAUUGUUUGUGUCUAACACUGAUUUUCCCUCUUU	100	sht-miR-9197-3p	uacgcuuugauuguuugugucu	59-80	efu-miR-9197	4	0	22	22	1
sht-miR-1-2	AGUAAAUGGCUUAAAGAGGUCAUCGCAACUUUUAUUCUGGUAUAUGCUGCAGAAUAGUUCACAUACUUCUUUAUGCCCAUUUUAU	85	sht-miR-1-2-3p	ucacauacuucuuuaugcccau	59-80	rno-miR-1-5p	5	0	22	22	2
sht-miR-3499-2	AAAGCCAAACGAGCUUUCUGAAUCCGUGCUGAGAUUUCGUCAGAAACCAACCUAUUAGGACUGAUCAGACUUCCAGCAUGAGUGAAGUCGUUGGCGAG	98	sht-miR-3499-2-5p	ucugaauccgugcugagauuuc	17-38	sja-miR-3499	1	0	22	22	1
sht-miR-3492-1	CUAGUCGAGCCUUCUGUAUCCGUGCUGAGAUUUCGUCACACACCAGACCACAAGGGCUGACGAAACUUUCAAGAUAAGUGAAGCGAUCGACACG	94	sht-miR-3492-1-5p	auccgugcugagauuucguca	18-38	sma-miR-3492	0	0	21	21	1
sht-miR-234	AGGAAGGUGCGGUUCGUACCACUUGGGACACGUCAGCUGGAUGCACCGGUAUUCCAGAGUUGAUGUUCCUUCCAGGAUUCGAACCAAGCACCUUUCG	97	sht-miR-234-3p	cgguauuccagaguugauguuc	47-68	cel-miR-234-5p	3	0	22	22	1
sht-miR-59	GAGUUCUGAAAACUGUUUCGUCAUCUUCACUGUGCAUUUUCAUCCAAAAACGGAAAUGAAGCAGUCUUAAGGUCUUCGAAUCGUUUAUCAGUAAAAA	97	sht-miR-59-3p	ucgaaucguuuaucaguaaaaa	76-97	cel-miR-59-3p	4	0	22	23	1
sht-miR-8437	GAUGAUUUUUUACAUUUGGCGCUUAGUAGAAUGUCACCGCAUGUACUGAACACAACGGUAACAUUUACUAAGAGCUCAGAUGUAGAAAGUCGUG	94	sht-miR-8437-5p	uggcgcuuaguagaauguc	17-35	sma-miR-8437-5p	0	0	19	19	1
			sht-miR-8437-3p	uaacauuuacuaagagcucaga	59-80	sma-miR-8437-3p	0	0	22	22	1
sht-bantam	UUUCAGAUCGGCAAGUCGGCUUUUAUUGCGCUCUGAGAAAAAUUUAUUGUCAUCUGAGAUCGCGAUU	89	sht-bantam-5p	cggcuuuuauugcgcucugaga	17-38	sma-bantam-5p	0	0	22	22	1

	AAAGCUGGUUUUCCAUU UGUGA										
			sht-bantam-3p	ugagaucgcgau uaaagcuggu	55-76	sja-bantam	0	0	22	22	1
sht-miR-944	AUGACUUUCGAACUGAG CUGAGCAAUAUAAUUAA UUUACUAAAUUUAGACA UGUAAAUUAUUGUACAU CGACUCAGUAGUCUGAA GGUUAA	91	sht-miR-944-3p	aaauuauuguac aucgacucag	55-76	hsa-miR-944	3	0	22	22	1
sht-miR-3492	AUAGACGGAUAUCUCGC CUUCGCAAAAGGUGGUG UAAGUAGGCAAAAGCCA AACGAGUUUUUCGAAUC CGUGCUGAGAUUUCGU CCGA	88	sht-miR-3492-3p	auccgugcugag auuucgucc	66-86	sja-miR-3492	1	0	21	21	1
sht-miR-8448-2	UUAAAGUUAGACAUUAA CACCGUUGGAUACUGCC UCUGUGGUCUAGAGGU UAAACGUUCGCGAGCGA GACCAAAGGUCUUAGAU UCAAUUGGU	93	sht-miR-8448-2-3p	cuagagguuaaa cguucgc	43-61	sma-miR-8448-3p	1	0	19	19	1
sht-miR-3492-2	CUAGUCGAGCCUUCUGU AUCCGUGCUGAGAUUUC GUCACACACUAGACCAC AAGGGCUGAUGAGACUC GCAAGUUAAAUGAAGCG GUCGACACG	94	sht-miR-3492-2-5p	auccgugcugag auuucguca	18-38	sma-miR-3492	0	0	21	21	1
sht-miR-2253a	GUCUGACAUGGCACUGC UGAAGAGUUAUUCCCAU UCUCAACAUGCAGCAAU GUAUCAUGGGAAACGCC AAGAAUAACGCCUUGAG UACUGAUCUCAGUC	99	sht-miR-2253a-5p	cauggcacugcu gaagaguua	7-27	ppc-miR-2253a	4	0	21	21	1
sht-miR-7	UAUCUUACCGUUGCUUA AUCAUGGAAGACUGGUG AUAUGUUGUUCAAUGAU GAAACUUUCAAAUAAAU AUGAAACGUUUCAUCAG AAUAAUUAAAAUAAGAG CAACCUAUCUCAUUCUU CCAUGUAUGCGAUCGGU UAAACAAC	144	sht-miR-7-5p	uggaagacuggu gauauguuguu	22-44	sja-miR-7-5p	0	0	23	23	1
sht-miR-7b	AUUCUAUAUUCCAGAGA AACUUGGAAGACUUGUG AUUUAGUUGUUUAAUAU UAAGUGCAAUGAACUUG	125	sht-miR-7b-5p	uggaagacuugu gauuuaguuguu	22-45	mmu-miR-7b-5p	1	0	24	24	1

	UUAAAUAUGACGAACAA CAAUCACAAAUCUCCAU GUGAUAUCUGGUUAAAC AACUGA										
sht-miR-98	UAGAGUAUUUGGUAGUG UUUCCUUGUAGCUAUUU CUACGUUUUACACAUUA ACAGUAGAGAAUGCUAU UUAAGUACGCAAUACAA CUUACUACA	94	sht-miR-98-3p	caauacaacuua cuaca	78-94	cpi-miR-98-3p	5	0	17	21	1

498 Table S2 - Distribution and clustering of miRNAs in the *S. haematobium* Egypt genome; sht: *S. haematobium*.

Pre-miRNAs	Lenght	Genome				Distribution in genome	Clustering
		Supercontig	Start	End	Strand		
sht-miR-71a	100	KL250488	743729	743828	+	Intergenic	Cluster sht-miR-71a / sht-miR-2a-1 / sht-miR-2b / sht-miR-2e
sht-miR-2a-1	83	KL250488	743830	743912	+	Intergenic	Cluster sht-miR-71a / sht-miR-2a-1 / sht-miR-2b / sht-miR-2e
sht-miR-2b	87	KL250488	743922	744008	+	Intergenic	Cluster sht-miR-71a / sht-miR-2a-1 / sht-miR-2b / sht-miR-2e
sht-miR-2e	74	KL250488	744028	744101	+	Intergenic	Cluster sht-miR-71a / sht-miR-2a-1 / sht-miR-2b / sht-miR-2e
sht-miR-59	97	KL250492	516835	516739	-	Intergenic	-
sht-miR-7192	83	KL250495	120934	120852	-	Intragenic (Intron = MS3_00312)	-
sht-miR-3492-2	94	KL250497	660631	660538	-	Intergenic	-
sht-miR-2238h	94	KL250498	217566	217659	+	Intergenic	-
sht-miR-9711	83	KL250500	664273	664355	+	Intergenic	-
sht-miR-9648	96	KL250503	139099	139004	-	Intergenic	-
sht-miR-6574	87	KL250510	255578	255492	-	Intragenic (Intron = MS3_00753)	-
sht-miR-10644	86	KL250516	139681	139766	+	Intragenic (Intron = MS3_00920)	-
sht-miR-7956	67	KL250516	553340	553274	-	Intragenic (Intron = MS3_00899)	-
sht-miR-466i-2	90	KL250516	421076	420987	-	Intragenic (Intron = MS3_00903)	-
sht-miR-3618	97	KL250522	647830	647926	+	Intergenic	-
sht-miR-737	100	KL250525	254954	254855	-	Intergenic	-
sht-miR-4206-1	100	KL250526	303362	303461	+	Intragenic (Intron = MS3_01153)	-
sht-miR-10501	76	KL250527	23753	23828	+	Intragenic (Intron = MS3_01170)	-
sht-miR-8448-1	98	KL250532	176861	176958	+	Intragenic (Intron = MS3_01254)	-
sht-miR-203b	91	KL250537	526682	526772	+	Intergenic	-
sht-miR-61	98	KL250537	563488	563585	+	Intergenic	-
sht-miR-130a	97	KL250539	419955	419859	-	Intragenic (Intron = MS3_01409)	-
sht-miR-11181	99	KL250543	123168	123266	+	Intergenic	-
sht-miR-3492-1	94	KL250543	534705	534612	-	Intragenic (Intron = MS3_01496)	-
sht-miR-219	92	KL250548	331717	331626	-	Intergenic	-
sht-miR-2463	83	KL250555	655885	655967	+	Intergenic	-
sht-miR-427	97	KL250565	110508	110412	-	Intergenic	-

sht-miR-36b	97	KL250570	64600	64696	+	Intergenic	-
sht-miR-36	94	KL250570	112933	113026	+	Intragenic (Intron = MS3_01995)	-
sht-miR-545	93	KL250573	442593	442685	+	Intergenic	-
sht-miR-1-2	85	KL250578	398179	398095	-	Intragenic (Intron = MS3_02134)	-
sht-miR-16b	100	KL250579	321731	321830	+	Intragenic (Intron = MS3_02140)	-
sht-miR-8335	100	KL250586	426435	426336	-	Intergenic	-
sht-miR-1187	98	KL250593	347993	347896	-	Intergenic	-
sht-miR-466g	96	KL250602	510686	510781	+	Intergenic	-
sht-miR-7b	125	KL250614	164830	164954	+	Intergenic	-
sht-miR-10	87	KL250619	296260	296346	+	Intergenic	-
sht-miR-98	94	KL250621	70810	70903	+	Intergenic	-
sht-miR-2023-2	78	KL250628	336131	336054	-	Intergenic	-
sht-miR-1671	100	KL250640	51931	51832	-	Intragenic (Intron = MS3_03106)	-
sht-miR-548b	95	KL250645	242978	242884	-	Intergenic	-
sht-miR-4106	100	KL250652	427888	427987	+	Intergenic	-
sht-miR-84e	99	KL250654	165406	165504	+	Intergenic	-
sht-miR-3851l	86	KL250667	262091	262176	+	Intergenic	-
sht-miR-125c	99	KL250667	300683	300781	+	Intergenic	-
sht-miR-12366a	81	KL250677	306970	307050	+	Intragenic (Intron = MS3_03591)	-
sht-miR-8	88	KL250679	385558	385645	+	Intergenic	-
sht-let-7	80	KL250686	349875	349796	-	Intergenic	-
sht-miR-87a	97	KL250689	416232	416136	-	Intergenic	-
sht-miR-3812	79	KL250690	72321	72399	+	Intergenic	-
sht-miR-79	99	KL250691	39971	40069	+	Intergenic	-
sht-miR-510	99	KL250692	119986	119888	-	Intergenic	-
sht-miR-4000e	83	KL250696	211466	211548	+	Intergenic	-
sht-miR-9388	90	KL250706	248314	248403	+	Intergenic	-
sht-miR-124c	91	KL250711	234695	234785	+	Intergenic	Cluster sht-miR-124c / sht-miR-124
sht-miR-124	91	KL250711	234785	234695	-	Intergenic	Cluster sht-miR-124c / sht-miR-124
sht-miR-944	91	KL250725	82596	82506	-	Intergenic	-
sht-bantam	89	KL250727	19688	19600	-	Intergenic	-
sht-miR-141	67	KL250729	322361	322427	+	Intragenic (Intron = MS3_04203)	-
sht-miR-466i-1	82	KL250737	183053	182972	-	Intergenic	-

sht-miR-8357	89	KL250737	86620	86532	-	Intragenic (Exon-E4 / Intron = MS3_04286)	Cluster sht-miR-8357 / sht-miR-8357
sht-miR-8357	89	KL250737	90778	90690	-	Intragenic (Intron = MS3_04286)	Cluster sht-miR-8357 / sht-miR-8357
sht-miR-7194	90	KL250739	111000	111089	+	Intragenic (Intron = MS3_04311)	-
sht-miR-4260	98	KL250753	117377	117280	-	Intergenic	-
sht-miR-8416	100	KL250754	194910	194811	-	Intergenic	-
sht-miR-563-1	81	KL250767	6219	6299	+	Intragenic (Intron = MS3_04651)	-
sht-miR-9396	71	KL250777	7325	7395	+	Intragenic (Intron = MS3_04754)	-
sht-miR-6306	91	KL250778	339016	339106	+	Intragenic (Intron = MS3_04766)	-
sht-miR-8485	72	KL250779	68626	68555	-	Intergenic	-
sht-miR-125b	74	KL250779	289530	289457	-	Intragenic (Intron = MS3_04773)	-
sht-miR-563-1	95	KL250781	198855	198949	+	Intergenic	-
sht-miR-9197	100	KL250791	175452	175353	-	Intragenic (Intron = MS3_04902)	-
sht-miR-281	97	KL250799	268121	268025	-	Intergenic	-
sht-miR-7643	98	KL250821	261174	261271	+	Intergenic	-
sht-miR-1960	96	KL250822	152398	152493	+	Intragenic (Intron = MS3_05215)	-
sht-miR-4919	80	KL250829	134241	134162	-	Intergenic	-
sht-miR-2538	92	KL250851	214237	214146	-	Intergenic	-
sht-miR-1-1	96	KL250865	139078	139173	+	Intergenic	-
sht-miR-3853	74	KL250867	179565	179638	+	Intergenic	-
sht-miR-4027-2	99	KL250872	189091	188993	-	Intergenic	-
sht-miR-10954	89	KL250887	228048	228136	+	Intergenic	-
sht-miR-137	68	KL250933	254738	254671	-	Intergenic	-
sht-miR-2493	97	KL250952	85692	85596	-	Intergenic	-
sht-miR-2340	86	KL250954	188883	188968	+	Intragenic (Intron = MS3_06342)	-
sht-miR-2162	85	KL250957	29464	29548	+	Intergenic	-
sht-miR-466c	99	KL250957	132588	132686	+	Intergenic	-
sht-miR-8422	100	KL250978	224937	224838	-	Intergenic	-
sht-miR-559	88	KL250987	68340	68427	+	Intergenic	-
sht-miR-3492-2	98	KL250996	107206	107109	-	Intergenic	-
sht-miR-6733	98	KL251003	199764	199861	+	Intergenic	-

sht-miR-8437	94	KL251005	96579	96486	-	Intergenic	-
sht-miR-190	78	KL251017	202086	202009	-	Intragenic (Intron = MS3_06804)	-
sht-miR-4175	90	KL251018	213689	213778	+	Intergenic	-
sht-miR-8448-2	93	KL251078	43246	43154	-	Intergenic	-
sht-miR-234	97	KL251107	154646	154550	-	Intergenic	-
sht-miR-5934	92	KL251138	75931	75840	-	Intragenic (Intron = MS3_07543)	Cluster sht-miR-5934 / sht-miR-5594
sht-miR-5594	96	KL251138	83414	83509	+	Intergenic	Cluster sht-miR-5934 / sht-miR-5594
sht-miR-10107	93	KL251153	78801	78893	+	Intergenic	-
sht-miR-3479	83	KL251162	13849	13767	-	Intergenic	-
sht-miR-2c	91	KL251164	31087	30997	-	Intergenic	Cluster sht-miR-2c / sht-miR-2a-2 / sht-miR-71b
sht-miR-2a-2	82	KL251164	31189	31108	-	Intergenic	Cluster sht-miR-2c / sht-miR-2a-2 / sht-miR-71b
sht-miR-71b	82	KL251164	31425	31344	-	Intergenic	Cluster sht-miR-2c / sht-miR-2a-2 / sht-miR-71b
sht-miR-10345	100	KL251176	16308	16209	-	Intergenic	-
sht-miR-4172	96	KL251220	54855	54950	+	Intergenic	-
sht-miR-10704	99	KL251231	52876	52974	+	Intragenic (Intron = MS3_07999)	-
sht-miR-4027-1	88	KL251241	75178	75265	+	Intergenic	-
sht-miR-1350	89	KL251242	75558	75646	+	Intergenic	-
sht-miR-43b	95	KL251244	103935	104029	+	Intragenic (Intron = MS3_08060)	-
sht-miR-7	144	KL251326	50920	51063	+	Intergenic	-
sht-let-7d	85	KL251382	42794	42878	+	Intragenic (Intron = MS3_08607)	-
sht-miR-3492	88	KL251430	91850	91763	-	Intergenic	-
sht-miR-7790	100	KL251451	7521	7422	-	Intergenic	-
sht-miR-83	83	KL251464	5302	5220	-	Intragenic (Intron = MS3_08899)	-
sht-miR-4111	83	KL251468	50419	50501	+	Intergenic	-
sht-miR-4206-2	79	KL251484	88461	88383	-	Intergenic	-
sht-miR-10828	88	KL251495	32275	32188	-	Intergenic	-
sht-miR-9126	86	KL251502	66483	66568	+	Intergenic	-
sht-miR-2253a	99	KL251655	10634	10536	-	Intergenic	-
sht-miR-4680	98	KL251680	15321	15418	+	Intergenic	-
sht-miR-2023-1	94	KL251690	7682	7589	-	Intragenic (Intron / Exon-E5 = MS3_09528)	-
sht-miR-9814	99	KL251702	5507	5409	-	Intergenic	-
sht-miR-138	95	KL251725	58641	58735	+	Intergenic	-
sht-miR-5894b	92	KL251905	7283	7192	-	Intergenic	-

sht-miR-184a	99	KL252131	10810	10712	-	Intergenic	-
sht-miR-4913	99	KL252163	14387	14485	+	Intragenic (Intron = MS3_10354)	-
sht-miR-4000g	94	KL252167	17653	17746	+	Intergenic	-
sht-miR-7092	85	KL252226	16119	16203	+	Intergenic	-
sht-miR-927a	87	KL252228	11451	11365	-	Intragenic (Intron = MS3_10477)	-
sht-miR-592	74	KL252387	17418	17491	+	Intergenic	-
sht-miR-3499-1	93	KL252542	8533	8625	+	Intergenic	-
sht-miR-33a	96	KL252724	7872	7777	-	Intergenic	-
sht-miR-11629	95	KL252922	1451	1545	+	Intergenic	Cluster sht-miR-11629 / sht-miR-11629
sht-miR-11629	95	KL252922	2852	2946	+	Intergenic	Cluster sht-miR-11629 / sht-miR-11629

501 Table S3 – Thermodynamic characteristics of the sequences found in the *S. haematobium* Egypt genome; sht: *S. haematobium.*

	Sequence	Len	G	A	C	U	GC	AU	UA-ratio	GC-ratio	MFE	MFE-ensemble	frequency	diversity	AMFE	MFEI
sht-miR-9711	GGUUGGAAAUCAUGUAGUGCCAGACAAACAUCUUACACAUUAGUUAAUGUUUCACUUGGUACUGUAUACAAGAUUAUCCACGC	83	18,072	31,325	19,277	31,325	37,349	62,651	1,000	0,938	-19,600	-18,900	0,019	9,530	-23,614	-0,632
sht-miR-2238h	CAUUUGAUAUUAGACUACUGCUGAAGAGUGUCAUAUUAAGACGAAAUGACAGUUCAGUGCUUUCAUUUUUCCAACGGUGGUCUAAUAUCAAUCG	94	19,149	29,787	17,021	34,043	36,170	63,830	1,143	1,125	-31,000	-28,900	0,114	17,850	-32,979	-0,912
sht-miR-4680	AUUAAAAGUCCUUUGAAUUGAUAUGCUUAACUUAGCUCUUAGCAUUUCACUCGGUGCAUCGCCUCUGAAUUGUAAGAGUAUAUACAGAGGCUUUUUAU	98	17,347	27,551	17,347	37,755	34,694	65,306	1,370	1,000	-21,300	-18,400	0,013	15,570	-21,735	-0,626
sht-miR-2340	CACGAGAAGGCAGUGUGUAGGACUUCCCUGGUGGUUGCUAUGUGAAAGCAUUUCGAGAGGGAAAGCUAACUCUUCCCAUUCUCAGC	86	27,907	24,419	22,093	25,581	50,000	50,000	1,048	1,263	-22,300	-20,600	0,036	12,270	-25,930	-0,519
sht-miR-2162	ACCUCUCUAGGGGAUGAGUGGGAUGGUUGCAUAUAUACAAUGCUGAUAAUGUAUUAUGCAACGUUUCACUCUACCCCAGGGACUC	85	23,529	25,882	21,176	29,412	44,706	55,294	1,136	1,111	-36,900	-36,900	0,077	5,140	-43,412	-0,971
sht-miR-466c	CACUAGAAAUCAAGACUACGAUCUCUAGGUCUUGUGAUGUGUGUAUGUGUGCUAUAUUUAGACCAUUUAGUUGGAAGAUAGUAGUUUGAAUUUUUAUUU	99	21,212	27,273	11,111	40,404	32,323	67,677	1,481	1,909	-24,200	-24,200	0,088	8,610	-24,444	-0,756
sht-miR-11629	UCGGAUUAGAGUACAGGUGUUAAACUUCAAGUUCCAAAUAUUCUUAGCAUUUAUUCAUUUUGGACUUUUAGUUUAAGCCCAUUAUUUUAUUCUUA	95	13,684	27,368	14,737	44,211	28,421	71,579	1,615	0,929	-22,700	-22,700	0,173	5,800	-23,895	-0,841

sht-miR-138	AUGCAAACAUUAUUGGA ACUUGAGUAGAACUGCA UUGCUGAAGAGAGUCAA AAGGGCUUCUUCACAAC ACCAAUUUACCAAAAAAC UGUUUGUGA	95	18,947	36,842	17,895	26,316	36,842	63,158	0,714	1,059	-18,500	-16,600	0,009	15,220	-19,474	-0,529
sht-miR-545	GUCUGAGUAAAUGUUUA UGUACUCGAUUUUGAGU UGGCUUUUGGUAGGCUA AUUAUAGUAUAGAAAAC GGUUACUUGAUACGUUU ACUCAUUU	93	21,505	25,806	10,753	41,935	32,258	67,742	1,625	2,000	-24,000	-22,500	0,066	9,390	-25,806	-0,800
sht-let-7d	UUAAUGCACUUGAUUUC CAACUGUUGAGGUAGUA GGUUUAAACUCCCUACC ACCUACUUCAGCUUCAG CAACCAAGUCGCAUCAG	85	16,471	27,059	27,059	29,412	43,529	56,471	1,087	0,609	-23,800	-23,800	0,241	15,410	-28,000	-0,643
sht-miR-203b	GUGCUUCUUAAUAUUAA UUGAACUGUUGAGAACU AACUUGCUCGAUCACUG UUUGUUAGUUUGCCGCA GUCCAAUAGUUAUUAUG AAGUGG	91	20,879	25,275	15,385	38,462	36,264	63,736	1,522	1,357	-26,700	-26,500	0,265	3,430	-29,341	-0,809
sht-miR-61	GUUGUGGGUCCCUUUC UUGUCCAUGGUACAGCA GUUGAAGCUCACUGCUU UAGUGUGCAUCCUCUUU ACAUCACAUGACUAGAA AGUGCACUCACUUC	98	20,408	20,408	25,510	33,673	45,918	54,082	1,650	0,800	-27,800	-26,200	0,070	14,920	-28,367	-0,618
sht-miR-3618	AAUAUAUGUUGAAUAUA UGGAUCAUAUGGAUUAA ACCAUAAAGGUUUCGAU GAUUUAUAAUGAUAAUU AUGUGAUUUCCAAUAAU UGAAAUCAUCUA	97	14,433	39,175	8,247	38,144	22,680	77,320	0,974	1,750	-18,500	-14,000	0,061	21,600	-19,072	-0,841
sht-miR-4172	AAACCACUAAGCUGCCA GUAAAAUUAAAACCUGA CUAUUAUGUCAUAUAUU UGCCAUGCAUAUCAGAU UACUGUAUGACUGGAUA GCUAGAGGCUC	96	16,667	34,375	19,792	29,167	36,458	63,542	0,848	0,842	-22,500	-14,340	0,085	16,910	-23,438	-0,643
sht-miR-1-1	GUAUCUUUGUACUUCUU UUCAUCUCCUCCAUGUG UUUGUCGAUGAAUUUCA UCGGGUACCCACAUUGC CAUGAUGAUAAACUAAU UGAAAAGAAAU	96	15,625	27,083	19,792	37,500	35,417	64,583	1,385	0,789	-18,600	-14,700	0,045	23,880	-19,375	-0,547

sht-miR-4206-1	UAAACAUAAUGCCCUUU AUACACACCGCCCGUCG CUACUACCAAUUGAAUA GUUUAGUGAAAUCGUUA GAUUGGUGUCGUUGUAA UGGCUUUACUGUUCG	100	19,000	26,000	21,000	34,000	40,000	60,000	1,308	0,905	-20,500	-19,100	0,035	10,960	-20,500	-0,513
sht-miR-10501	ACUACUUCUCACCAGCA CUCCAGGAUAUACCACU UCCAAUGGUCAAUAUCG UGGAUGCGCACUGCUGA GAAGUCAU	76	18,421	27,632	28,947	25,000	47,368	52,632	0,905	0,636	-26,900	-26,800	0,315	3,130	-35,395	-0,747
sht-miR-10644	GAGAUGGUUGGAAGAAA GUUAGGGGCGGUCAAAC CAAAACGUGGCAUUAGU GCUUGAAGUCACUAACU UCUAGUCCGAGCCAUGU U	86	29,070	29,070	17,442	24,419	46,512	53,488	0,840	1,667	-23,700	-23,700	0,014	11,380	-27,558	-0,593
sht-miR-10107	AUGGAAUAAUGUAUGAU GUAAUGGGUUAAAAUCC UUUUUGACGAUAUUUUU AUGACAUUGGAGAGGGU UUUUAACAUAGCUAUAA UAUUCCUC	93	19,355	31,183	9,677	39,785	29,032	70,968	1,276	2,000	-20,000	-15,600	0,131	16,130	-21,505	-0,741
sht-miR-559	CUAACGGUUCGUUACUU UAUGUUUGCCACUUGUU UAAAGUAAAUAAGCACU CUGAAGAAGUGGCCAGC ACGAAGUGACGAAACGU CAC	88	21,591	30,682	20,455	27,273	42,045	57,955	0,889	1,056	-37,800	-37,800	0,361	1,560	-42,955	-1,022
sht-miR-3812	AAAGAAUACUUUCCAUC GUCUUCACAAUCAUUUU UCUGGGUAUUUCAUGCU AAGUGAUUUUGAUGAUG GAAAAUUCAUA	79	15,190	30,380	15,190	39,241	30,380	69,620	1,292	1,000	-22,100	-20,800	0,164	7,160	-27,975	-0,921
sht-miR-79	AUCAUCAGUCAGUUAAA GCUAGAUUACCAUGGAA AACGUGGAAGCACUGGA CGGCCGUUUCGUCCUAU UGUGAUGGUCAAGCUUC AAUUGACUAAUGAU	99	23,232	29,293	19,192	28,283	42,424	57,576	0,966	1,211	-34,400	-33,800	0,065	6,810	-34,747	-0,819
sht-miR-7194	AGCAGUGAAAUCCAGUU UGAUGAGCAUUUCGUCU UAUUUGUGAUUCGUCAG CUAUACGUACCUGCAUC UCAGAUUCUGGAUUCCA CUAUU	90	18,889	23,333	21,111	36,667	40,000	60,000	1,571	0,895	-22,000	-22,000	0,142	8,790	-24,444	-0,611
sht-miR-11181	AGUAGUGGUAGUAGUAG UAGUAGUCGUAGUAGUA GUCGUAGUAGUAGUAGU AGUAGUAGGAGGAGGAG GUCAGUUACUAUUUCUA UUAUUAACACUGUG	99	31,313	28,283	7,071	33,333	38,384	61,616	1,179	4,429	-21,600	-20,900	0,087	19,730	-21,818	-0,568

sht-miR-141	CCUGAGGGAAACAUGUU GCUGACGUCACAUCUUC CAGUACAGUCAGCACUA AGACUUUACCCUCGAU	67	19,403	26,866	28,358	25,373	47,761	52,239	0,944	0,684	-18,900	-18,900	0,052	6,050	-28,209	-0,591
sht-miR-71a	UAUGAAGAUGUGAUACU AGUGCUGUGAAAGACGA UGGUAGUGAGAUGCCAA UUGCAUCUCGCUUCCCC GCCUUUCCCGGUAAGAA UCACGAGUCGUCAGC	100	26,000	25,000	23,000	26,000	49,000	51,000	1,040	1,130	-38,000	-38,000	0,164	5,110	-38,000	-0,776
sht-miR-2a-1	UUACCUCUUGCGCCGCA GUCAAUAUUGGCUGAAG GCAUUGCUUUAUUGUCA CAGCCAGUCUUGAUGAA CGGUGUAAAAGGCGC	83	25,301	22,892	22,892	28,916	48,193	51,807	1,263	1,105	-34,700	-34,700	0,426	2,310	-41,807	-0,867
sht-miR-2b	ACUGCAGGUGGUGCGC GUCUCAAGGGACUGUGA AGCAACGUAAUUAAUUG UAUCACAGCCCUGCUUG GGACACAGCCUACCUGC UAA	87	26,437	25,287	25,287	22,989	51,724	48,276	0,909	1,045	-41,900	-41,400	0,372	3,540	-48,161	-0,931
sht-miR-2e	GCUCUUACCAACUUCGA CUGAGUUAUACUGCUCC UGCAGGCCUUGUAUAUC ACAGUCCAAGCUUUGGU AAGUUU	74	18,919	21,622	25,676	33,784	44,595	55,405	1,563	0,737	-23,000	-21,200	0,249	8,280	-31,081	-0,697
sht-miR-124c	CCGUGGAUGACAUUCAC CGCGUGCCUUAAUAUUU CUGUUGCGAGUAUUAUU UGUAACAAAUCAAGGCA AUCGCGGAAAAUGGCAU ACAAAA	91	20,879	31,868	19,780	27,473	40,659	59,341	0,862	1,056	-28,500	-28,500	0,072	5,990	-31,319	-0,770
sht-miR-10704	UUUUUUAUUUGUUGGGA UGAAUAGGGGUAUUAAU UAGAUUACGAUGUAUGU UCCUAACCUGUUAUAUA AAUAUUGCCCUUUCUGU CAACAAGUGAACUU	99	18,182	27,273	12,121	42,424	30,303	69,697	1,556	1,500	-21,300	-19,100	0,015	11,970	-21,515	-0,710
sht-miR-3499-1	CUUUCUGAAUCCGUGCU GAGAUUUCAUCAAACAA UAACCCAUUAGGGUUUA UCAGACUUCCAAGAUGA GUGAAAUUUCCGACGCG UUCGACUA	93	18,280	29,032	22,581	30,108	40,860	59,140	1,037	0,810	-21,000	-17,800	0,103	9,740	-22,581	-0,553
sht-miR-6306	UCACUGAGAUGGUGGG GAAAAUUUGUAGCUAAG AUGGAUGAUUUUGAUGG AGUUUUGUUCUCUAAGC UAAAUGAACCAAACCAU CCAGCUC	91	24,176	29,670	15,385	30,769	39,560	60,440	1,037	1,571	-25,100	-25,100	0,039	9,280	-27,582	-0,697

sht-miR-563-1	AGACUAAGUAAUUAGAA UUGGUUUGUGAUCCUUC AUCAUGAGGGUUGAAAC UCAAGGGUCUAGAAGGU UGACAUACAUUUCCAUU UGUUUAGAAC	95	22,105	30,526	13,684	33,684	35,789	64,211	1,103	1,615	-20,700	-19,700	0,284	4,900	-21,789	-0,609
sht-miR-7092	CGAAACGGUUAUUCUUG UAUUUAAAAAGGCAAAC UCACAGAAGAGAUGGAA UCCCAUCACUUUUGAUA CAAGAAAAUCCCUUAAU	85	15,294	38,824	18,824	27,059	34,118	65,882	0,697	0,813	-20,200	-20,200	0,131	6,840	-23,765	-0,697
sht-miR-4106	AUUUAUAAAAUAUUGGU UUAGAAUAGAAAAUAUU AGAAAGAGGGAGAAAAA AUUAUUUCCCUACUCUC UUUGAUUGCCUACUCUA ACAAAUUUCAUAAUA	100	12,000	41,000	12,000	35,000	24,000	76,000	0,854	1,000	-19,900	-19,900	0,117	8,720	-19,900	-0,829
sht-miR-3851l	CCAUACAUUCCAAUUCU GAUUGAUGUUAGAUACU ACUUAUGUCUGUUGGCA UAAGUAGUGUACACCAU AACACAACUGAAUUACC C	86	13,953	31,395	22,093	32,558	36,047	63,953	1,037	0,632	-24,200	-21,500	0,186	10,270	-28,140	-0,781
sht-miR-125c	GAUUCCGUAUCCCUGAG ACCUUAGAGUUGUCCUG UUUGGAAGUAUUCUUCA AUUAUUCUAAAGAAGAU UGACACCUCUACGGUAU CAGGUCACGGAACA	99	20,202	27,273	21,212	31,313	41,414	58,586	1,148	0,952	-34,000	-34,000	0,087	5,350	-34,343	-0,829
sht-miR-6733	UGCUGAUUUUCACACAA UUUUUUUACAUUCAUUA UCAGUGUCUGGAUUUCC UUUCGAGCCAGUGAUUU AGAAGUAUAGAAAUAUG UUUCAUAUCAAUG	98	15,306	27,551	15,306	41,837	30,612	69,388	1,519	1,000	-18,800	-18,800	0,236	6,120	-19,184	-0,627
sht-miR-84a	AAGUCCUUCAUAAUAAU CAUCUAUCGAAUAAAUU UCAGUCUGACUAUCGCU AGUCAAGGCAAUAAAUA UUGUUUAGUAUGAGGUA GUUAAGAAUGAUAG	99	17,172	36,364	13,131	33,333	30,303	69,697	0,917	1,308	-18,900	-16,200	0,116	10,970	-19,091	-0,630
sht-miR-9126	UUUGUGAAAUAAAUUUG AGUUCAUUUCAUUUAAA UUUUACUCGUUGGUGAA GUUUCGAUGAAAAUAAC AAAAAUCAUUUUCACUU U	86	12,791	33,721	10,465	43,023	23,256	76,744	1,276	1,222	-22,000	-22,000	0,411	2,250	-25,581	-1,100

sht-miR-8448-1	GAUCAGUGUUGCGCGC GAAAGCUUAAACCUAUG ACCAAUGACCAUGCACU CAGUAGUGUACAGGUCU AGAGGUUAAACGUUCGC GCGCAAGACUGGUC	98	26,531	27,551	23,469	22,449	50,000	50,000	0,815	1,130	-45,200	-44,300	0,049	12,900	-46,122	-0,922
sht-miR-12366a	AGUGACUUAUCGAUCGG AUCAAAGGAUUCAGAAU CUCGAUAGACUAUUCUG GUCCGUUGUCCCCGACU CAGCUAACUCGAU	81	20,988	25,926	24,691	28,395	45,679	54,321	1,095	0,850	-18,500	-14,400	0,057	14,260	-22,840	-0,500
sht-miR-8	AGCAAGAAUGAGUGUGA CAUCUUACUAACAGUAU UUGACAAAUUAAUUUCU AAUACUGUUAGGUAAAG AUGCCAGCUCAAUUCUU UGU	88	17,045	34,091	14,773	34,091	31,818	68,182	1,000	1,154	-28,400	-27,300	0,010	9,670	-32,273	-1,014
sht-miR-466g	UGCAAAACGUGGUCGAG AGUGGCAUGUAGACUGA CCUUGUCCACAGUAGAA CCACCACUACUUAUACA GACACAUGCACUCCUUG ACUAUUUUCAA	96	18,750	30,208	26,042	25,000	44,792	55,208	0,828	0,720	-24,900	-24,900	0,043	10,520	-25,938	-0,579
sht-miR-2463	AAUAUCAACACAGUUCU ACUGCAUGUGGUGGAAA CUUGGAGAACUACGAAA UCCAUCAUCGAGAAGAU ACAAAUGUUGAUUAA	83	19,277	38,554	16,867	25,301	36,145	63,855	0,656	1,143	-18,500	-18,500	0,242	4,830	-22,289	-0,617
sht-miR-16b	UUUUUACAAUAAGUUUC AUCAUAAAUUGAUGUUC CCUAGAAAGCUGUAGAA CUACUGAAUCCCACUAG GCGACCCAGUAUUAUUG UGCUUAUUGUAAAAC	100	15,000	32,000	19,000	34,000	34,000	66,000	1,063	0,789	-23,800	-20,500	0,102	14,740	-23,800	-0,700
sht-miR-3853	CUGCUUCACAUAAUAUU AUAUGCUUGUAUGAAUU UUAAUACAUUUUCAUAA AAUGUGUGUAUUUUGUG AAGUAU	74	13,514	31,081	9,459	45,946	22,973	77,027	1,478	1,429	-18,800	-14,600	0,040	12,600	-25,405	-1,106
sht-miR-7643	AUUUUUAUUCACAGGCA AUGUCAAGUAUACCACA CAGCAAAACAUUCUAUA CUAAUGUGUGACUGAGA CAUGAUAGUUGACGUUG AACGAAUAAAGGU	98	18,367	36,735	16,327	28,571	34,694	65,306	0,778	1,125	-23,600	-23,600	0,301	5,310	-24,082	-0,694
sht-miR-1960	UUAUCUCUGUCAAUGAA CAAGAGGAUUUCCAGUG CUGUUAGAAGUAGGUUU CCUUCUGACCACACUGU GGAAGUAUAUGUCUUCU UGAGGAGACUG	96	23,958	25,000	17,708	33,333	41,667	58,333	1,333	1,353	-28,400	-24,900	0,038	21,230	-29,583	-0,710

sht-miR-4000e	AACUGAAACAGUGAUGU AGUUUGUGAAACUUCUU CGGAAAAAAGCUUUCCG CCUUUAUCACGAAUAAU AUCAAUUUUUCAAUC	83	14,458	33,735	18,072	33,735	32,530	67,470	1,000	0,800	-21,900	-21,900	0,465	1,860	-26,386	-0,811
sht-miR-4111	GCUUUAACAUUUGAUUA UUUUGUGAUUGACGGAA UAUAGUGACAGCUAAUU CCGUGGAAUAUAACUAU AUCAAAUAAUAAUAA	83	15,663	37,349	10,843	36,145	26,506	73,494	0,968	1,444	-20,700	-20,700	0,270	3,690	-24,940	-0,941
sht-miR-4913	CUUAAUAUAUUUAUUCC UAAUUGUGAUUUACUGA GUUGUACUAUUGCAUGU GCUCAUGUAAUACAAUA GUGUAUUAACCAAUUCG AAUAAAUAUUUAGG	99	14,141	32,323	12,121	41,414	26,263	73,737	1,281	1,167	-24,400	-24,200	0,062	7,280	-24,646	-0,938
sht-miR-4000g	CGAUGAAACUUCUUUAG AAUGUUGGAAUCUCGAU UUCCUUUUUAGGUCAAA AGGGUAAGUCUCAGAGU AGAACAUUUUAGGAAAC GAUUCAGCC	94	21,277	30,851	15,957	31,915	37,234	62,766	1,034	1,333	-20,800	-20,700	0,062	9,340	-22,128	-0,594
sht-miR-9396	UGAACUAUCCUAGAAAA CAUUGUAAGUGAUGAAG AAAUAUUCACAAAUACAU UGUUUAAGAGGGUAGUG AA	71	19,718	42,254	9,859	28,169	29,577	70,423	0,667	2,000	-21,900	-21,900	0,512	3,270	-30,845	-1,043
sht-miR-4175	CUACCAUCGGACUGCAU CUCCUAACGUUGCUCUA CUGCCUCGUGGAUUCGA CAUUCAGGUCAAAGGCU ACGGGUGUAGCUCCGAU GGGGA	90	26,667	20,000	27,778	25,556	54,444	45,556	1,278	0,960	-32,400	-21,530	0,072	20,000	-36,000	-0,661
sht-miR-592	AGAAGAGACUGUCAGAU GACACAAGCAUUACUUU GGUUCUCAGUGGGGAC UUGUGUCAAUAUGCGAU CUCUCGA	74	25,676	27,027	18,919	28,378	44,595	55,405	1,050	1,357	-21,500	-19,300	0,048	10,650	-29,054	-0,652
sht-miR-9388	UGCAUUAUAUGUGUAUG UAUGUAUGUACGUGUGU CGGUGUGACAGAAUUGA AGACCCCUAUGUAUGUA UGUACAUAUACACGUAA AUACC	90	22,222	28,889	14,444	34,444	36,667	63,333	1,192	1,538	-27,700	-27,100	0,185	12,080	-30,778	-0,839
sht-miR-4027-1	AGGUUAGUUAAAGUCGU CAGAAAGCAUACAGACU AUUAUAUAUAUGCAUAU AUUACUUUUAUGUUAAC CUGACUUUGUUAACUAA GUA	88	14,773	35,227	12,500	37,500	27,273	72,727	1,065	1,182	-18,600	-17,700	0,176	7,680	-21,136	-0,775

sht-miR-1350	CUUGUGGGUGAAGGACC UAAACAAUCAGUUUAAU GACGAUGUUUAUUUGUC AACUGGGUCUCUGUUUG UACAACUCCUUGACUCA CUUA	89	20,225	24,719	19,101	35,955	39,326	60,674	1,455	1,059	-24,600	-24,600	0,131	11,310	-27,640	-0,703
sht-miR-43b	GUGUAUGUAUAUAUAAG AAUGUGAAUGUGUGUGG GGUAUGAUUAGUUUAUA GCUUAUCACAGUUUCCU UGUCACACUCUCUAUGU CUUCAUAUAU	95	20,000	25,263	12,632	42,105	32,632	67,368	1,667	1,583	-23,700	-23,700	0,255	8,290	-24,947	-0,765
sht-miR-36b	AGGGAAUGUCUGUUCGG UUUGUGUUAUCUUGGUU ACUUGUUAAGUACUACU UAAUAAUGUAACUAUUU UUCAGUACACCACCGGG UAGACAUUCAUC	97	19,588	24,742	16,495	39,175	36,082	63,918	1,583	1,188	-35,000	-35,000	0,237	5,080	-36,082	-1,000
sht-miR-36	GGUAUAUCUUGUGAAGA GUGCCGACCCGGUUAGC CAUUAAAUUAUUGUUAA AGAAAUGAGGCCACCGG GUAGACAUUCAUUCGCA GGAUAUUUC	94	24,468	28,723	18,085	28,723	42,553	57,447	1,000	1,353	-36,800	-36,600	0,186	7,050	-39,149	-0,920
sht-miR-10	UGAUUCCUCAGUAUGAA CCCUGUAGACCCGAGUU UGGAUGCAGUCAAAUGC AAAUUCGAGUCUAUAAG GAAAAAUACUUUGGAAG UG	87	22,989	32,184	17,241	27,586	40,230	59,770	0,857	1,333	-31,400	-31,300	0,201	4,130	-36,092	-0,897
sht-miR-10954	UGGGUCAACUGAAGCUG CACCACAAUGGAAAACC UGAAAGCAUUGGACGGC CGUUUCGUCCUACUAUG GGUUUAGCUUCAAUUAA CUCA	89	22,472	28,090	23,596	25,843	46,067	53,933	0,920	0,952	-24,900	-21,900	0,020	11,110	-27,978	-0,607
sht-miR-563-2	UCGAAUUUCAUGCAACA UGAUACAUAAUAUGUCG GUCCAAGGUUGACAUAC AUUUAACAAGUAUGUCA UCUGACAAUUGUG	81	17,284	33,333	17,284	32,099	34,568	65,432	0,963	1,000	-19,300	-19,300	0,279	4,400	-23,827	-0,689
sht-miR-5594	CAAGGUUAUCAAUGUCU UUUGAAAUAAAGAACUC AUCAAACUGUGAUGCGU AUUCAGCUUCUCUCUUU GAUUGUAAUGCGAAUGA UGAUAACCAUU	96	16,667	31,250	16,667	35,417	33,333	66,667	1,133	1,000	-19,500	-19,500	0,075	10,880	-20,313	-0,609
sht-miR-6574	UGGUUAGAGACUUUGAA UGACAUGGCUCAAAAUC GUUUGUAAUAGCGCAGG UGCAUCCAUUCCUUGUC UUUUCUUAGUUUCUAAA	87	19,540	24,138	17,241	39,080	36,782	63,218	1,619	1,133	-20,900	-20,900	0,232	7,400	-24,023	-0,653

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sht-let-7	UUCUGGGAGGUAGUUC GUUGUGUGGUUUGCUU AUCAAAAUGAAUAAAAGA AGACCAUACAACCGACU GGCUUUCCCAUUG	80	23,750	27,500	17,500	31,250	41,250	58,750	1,136	1,357	-29,100	-24,300	0,008	10,570	-36,375	-0,882
sht-miR-510	UAGAAGUAUCAGUAACA AUAGUAGUCUACCAGUC AAGAUUUCAAAUUGAAA CCUCUAAGAUUCUUCAU AAGGCUAGGCACUACUG AGCUGAUUCUUAUU	99	16,162	34,343	18,182	31,313	34,343	65,657	0,912	0,889	-20,600	-14,400	0,089	14,490	-20,808	-0,606
sht-miR-87a	CAAACCUUGAGCAAAGU UUCAAGUAGUGAGUUAC ACAAAAUUGGUUUGUCG UGAUUCUCGCGCUAGUG AUAAGUCGCAUGAUAUU ACUCAAGGUACC	97	21,649	29,897	18,557	29,897	40,206	59,794	1,000	1,167	-25,000	-18,500	0,079	16,890	-25,773	-0,641
sht-miR-33a	CUCAAAUAAUAUCAAUG UGUCCACAGUGUGUGUG UUUGUGCACUUUACUCA GUCUGAGAAUUUAUUUC ACUCACUAUGGACUUGA UGUCUUUUACC	96	16,667	23,958	19,792	39,583	36,458	63,542	1,652	0,842	-21,700	-21,700	0,117	8,160	-22,604	-0,620
sht-miR-2493	ACCAAAACGAACUGAAA GAAAUAUUGGCAAGUGU GUUGUCGAAUUUUCGCU CACACACACACACUCUA UUUAUGUAUUUUUCAUG GUUUGUUUUUAA	97	15,464	30,928	17,526	36,082	32,990	67,010	1,167	0,882	-22,800	-19,500	0,034	18,760	-23,505	-0,712
sht-miR-5894b	AAGUGGAGAGUAUACAA AACUCUCGGAAGCCUAU AUCUGAUGGUAUUUUCC UAAACUUAAAGCAUUUC CAAGCAGUUUGUGUAAU UCCAUGA	92	18,478	32,609	17,391	31,522	35,870	64,130	0,967	1,063	-18,900	-17,700	0,018	11,220	-20,543	-0,573
sht-miR-10828	AGUUUCAGUAAAUCUCU GGAUGAUAUGCUUUUAG GUGUGGAAAUAAUUGCU AAAAGUAUGUAAAGUCA UCACAGAACUACCUGAA UAA	88	19,318	36,364	12,500	31,818	31,818	68,182	0,875	1,545	-22,500	-22,500	0,089	6,300	-25,568	-0,804
sht-miR-4206-2	AUACAAUAAAACACCACC AGUCGCUACUACCGAUU GAAUAGUUUAGUGAGGU CGUUGGAUUGGUGUCG UUUUAGUGGCU	79	24,051	26,582	17,722	31,646	41,772	58,228	1,190	1,357	-22,800	-22,200	0,250	3,480	-28,861	-0,691

sht-miR-1187	UGUAUGUAUCUGUGUAU GUGUGUGUGUAUGUGG GUAUUCAUUUGUUACUU AGUAAGUAACAAUGUUC ACACAUAUCAACCAACU CAUUGUUACAUGUA	98	19,388	26,531	13,265	40,816	32,653	67,347	1,538	1,462	-23,100	-22,800	0,032	13,560	-23,571	-0,722
sht-miR-8335	GCUUUAAUUGACUCAUG AAUUCAACUAUAUAACCA AACUAGUCAAAAUCCAG UGAUUGGAUGUUGUUGU UGUUGUUGUUGUUUUCU UUGAUCAUAAAUGC	100	17,000	28,000	14,000	41,000	31,000	69,000	1,464	1,214	-18,700	-15,500	0,020	17,770	-18,700	-0,603
sht-miR-281	UUUCUGAUGGAGAGAGC ACUUUUAUGACGGAAAC AAUUAUAUUCUUCGAAU UUAUUGAAGUUCCAUAA UGUCAUGGAGUUGCUCU CUAUAUCAGGUU	97	19,588	27,835	14,433	38,144	34,021	65,979	1,370	1,357	-34,100	-34,100	0,069	14,030	-35,155	-1,033
sht-miR-10345	UUUACUGAAGAUUAUAA AUUCUUCAUCACAGUUU CAGUGUAUGAUUAUUUC GUAAUUUAAUAUUAUAC UGUUGAUUUCGAAUUCG AACUUCUUCAGUCCG	100	13,000	28,000	15,000	44,000	28,000	72,000	1,571	0,867	-20,600	-20,600	0,064	11,280	-20,600	-0,736
sht-miR-184a	UACCUACUGAAUAAUUA AUUUCUUUAACAAUUUU CGAUCCUUGGGGAACAG AUGACGUGGGUUAAGAG GUGUUAAAGUAAUUUGG AUUACCUGUAGAUU	99	21,212	30,303	12,121	36,364	33,333	66,667	1,200	1,750	-19,500	-19,100	0,082	9,090	-19,697	-0,591
sht-miR-9814	AGUCAGCAAAAGUGAAA ACAAUAAACAUUGGCAU AAGCCCGACUACCAGGU AAAUCAACUGACUUGCU AAUGUUCGGAAUGUUUU CUGAUUUCCUGUCU	99	18,182	33,333	20,202	28,283	38,384	61,616	0,848	0,900	-19,500	-18,670	0,034	10,660	-19,697	-0,513
sht-miR-2023-1	UCAAAAGAAGUACAAGU GGAAAGUUUGAUUUCGA UUUAUCAUUGAAUCGCA UGAAAACAUCUAGAAGG UAAAAUUCAAAUUGUAU UUCUUUGUU	94	17,021	37,234	10,638	35,106	27,660	72,340	0,943	1,600	-19,800	-16,500	0,081	14,320	-21,064	-0,762
sht-miR-1671	CUUGGACGGCCGUUCCA UCAUAGUAUGGGAAUUC UCGGAUGCGGAGUCGU GGGUGAGGACUGUUGA GUAGUCUUAUUCUAGAA UGAAACAGCCGUCCAGU	100	31,000	22,000	19,000	28,000	50,000	50,000	1,273	1,632	-37,000	-30,000	0,043	11,650	-37,000	-0,740

sht-miR-2023-2	UAACCAGAUUUAUUUCG UUGGCGAUCUCGUGGUA UCGAACGAAUACCAAGA UCGUGCCAAAAGAAGUA CAAGUGGAAU	78	23,077	33,333	17,949	25,641	41,026	58,974	0,769	1,286	-24,100	-24,100	0,148	4,430	-30,897	-0,753
sht-miR-7790	CAAGCUGUUCAUUGUAU UCUGUGCUUUUCCUGAG AUGUGGAGGUCUUCCUA AUCUAGCCUGCCACUGG AAGAAAGAGGAAAGGGG AGAAUAAACAGCCUU	100	26,000	27,000	19,000	28,000	45,000	55,000	1,037	1,368	-29,000	-25,700	0,273	11,650	-29,000	-0,644
sht-miR-219	AUUGUCCAUUCGCAUUU CUUGUUAAUUAUAUUUA UUAAAUAUUAUCAGUUA GUAUGAUAAUAUUUAAU UUACAAGAGGUGUUGAU GGACAUC	92	14,130	31,522	9,783	44,565	23,913	76,087	1,414	1,444	-35,300	-35,300	0,344	4,570	-38,370	-1,605
sht-miR-927a	UGUAGGAGGCUCAGAAG GAGCCGAAGAUAUUCCA UCCAAUCACCUUUUGGG AGGAUAUUUUAGAAUUC CUACGUGUAGCUUCCUG AU	87	24,138	26,437	19,540	29,885	43,678	56,322	1,130	1,235	-30,800	-30,400	0,197	3,320	-35,402	-0,811
sht-miR-71b	UUUGCUGUGAAAGACUU GAGUAGUGAGACGCUUA UAGCAUGGUUUUCCCUU CGGCGCCUCAUACUGAG UCUUUCCCGGCUCA	82	24,390	18,293	24,390	32,927	48,780	51,220	1,800	1,000	-30,400	-30,400	0,162	4,440	-37,073	-0,760
sht-miR-2a-2	CAGUUCGUCAUCAUUGG AUUGUGAUUUUCCGAAA UAAAGCUUUAUGAGUAG AAUAUCACAGUCCUGCU UAGGUGACGAAUUU	82	20,732	28,049	15,854	35,366	36,585	63,415	1,261	1,308	-28,700	-28,700	0,292	2,940	-35,000	-0,957
sht-miR-2c	CCAGGUUGCUGGCGCAA CCCUUGUACGACUGUGA UGUGUUCGAAAAUAAAA UCAUAUCACAGCCGUGC UUAAGGGCUUCGUCAAA ACCGUA	91	23,077	27,473	24,176	25,275	47,253	52,747	0,920	0,955	-36,800	-36,800	0,281	2,290	-40,440	-0,856
sht-miR-3479	GGUCCAUGUUUGUGAG GGGGAUGUUUGUGCAAU UUAAUGUUGUAAAUAUA UUGCACUAACCUUCGCC UUGCAAAUAUAGGGUA	83	25,301	25,301	13,253	36,145	38,554	61,446	1,429	1,909	-31,300	-28,700	0,082	5,940	-37,711	-0,978
sht-miR-548b	AAACUUUGUGUUACAAG AAAUUCUUUAAGCAGGU AAGUUGGCUGAGAUACU AGCAAGAACCUCAGUUG CUAAAGGUCUUUUGAUG AACAAAGAUA	95	21,053	35,789	13,684	29,474	34,737	65,263	0,824	1,538	-19,400	-16,000	0,016	21,130	-20,421	-0,588

sht-miR-124	UUUUGUAUGCCAUUUUC CGCGAUUGCCUUGAUUU GUUACAAAUAAUACUCG CAACAGAAAUAUUAAGG CACGCGGUGAAUGUCAU CCACGG	91	19,780	27,473	20,879	31,868	40,659	59,341	1,160	0,947	-27,000	-23,400	0,110	7,030	-29,670	-0,730
sht-miR-5934	AUGAUUUUACUCUGAUG UUUCAGCUGCUUUCAUA CUAAUUAACGUUUGUUA GCUAUUUAGUCUGAUCA GAAGAAACUCAAAUGUA AAAUGGU	92	16,304	30,435	14,130	39,130	30,435	69,565	1,286	1,154	-21,300	-21,300	0,268	5,870	-23,152	-0,761
sht-miR-9648	GGGGGUAGACUAACGGC CGGUUGUUCUACAGAGU CAACCCUUAAGAUUUAA ACAACAGCUACGGGACU GUAGAAUUAAUGGCAGU UACGCUCCGUA	96	26,042	29,167	20,833	23,958	46,875	53,125	0,821	1,250	-26,100	-18,300	0,065	16,600	-27,188	-0,580
sht-miR-8416	AAUGUUUUUAUGGCGUA UCUGUAUGAUUGGUCAC AUAGUUCUGUGCUGUAA AGACAUAAUGAGCCUGU GAACAAGAAACAGAAGG ACAAGGAAAAACAAA	100	23,000	38,000	13,000	26,000	36,000	64,000	0,684	1,769	-22,200	-21,500	0,072	11,260	-22,200	-0,617
sht-miR-4260	UAUAUUUUCGUUAUUAG CAGUCCUAUAGUUUACG GACGGUAAUGUCUGGGA CAAAGUUCAUGAAGACU UGGGGCAUGGAGUCUAU AAUCUAAAAUGAU	98	23,469	29,592	13,265	33,673	36,735	63,265	1,138	1,769	-18,900	-15,700	0,025	32,800	-19,286	-0,525
sht-miR-427	GAUAGUGGGUAACAGUG GGAAUCAGAAAGUGCUU UCUGUUUUAUCUCGGUU UCUUUUAGCUGUAUCUA CCUGUUUUCCAUUGUUC AUGCCCACUUUA	97	20,619	19,588	18,557	41,237	39,175	60,825	2,105	1,111	-28,400	-27,200	0,032	13,030	-29,278	-0,747
sht-miR-190	UUCUAGUGUUGACAGUG UAAAAUCCGUUCUUUAG UAGGAAGUAGAUAUGUU UGAUUUUACACCCUGUU CACGCUAAUC	78	19,231	25,641	16,667	38,462	35,897	64,103	1,500	1,154	-20,100	-15,400	0,093	9,510	-25,769	-0,718
sht-miR-8422	UUGAAUCAUCCCAUUGA UGUUUAGGACUUUUAUU GGCAUAUGUGCAUACUC UACGUAUUACCUCGAUA UUGCAGUCCUAAACAUC AAUGGGAAGAUUCAA	100	17,000	29,000	19,000	35,000	36,000	64,000	1,207	0,895	-46,600	-45,500	0,098	5,870	-46,600	-1,294

sht-miR-737	CCUACUGAUUUCAACCA UCAUACAUGAAGAUUUG UUUUCUUAGGUUUUGAA AAUAGGGAAAUCGAAUC UUUCCAUACUCAUGUAA UUCAAAUUGAGUAUA	100	14,000	33,000	16,000	37,000	30,000	70,000	1,121	0,875	-19,000	-19,000	0,046	18,000	-19,000	-0,633
sht-miR-83	AGAGGCACCGAAAUAUA UCCGCGCCACACAAAGU AGCUAUCACUGAAUUUA UGUGUGGGCUACGAUAC UGCUCGGGUGCCCAA	83	24,096	28,916	25,301	21,687	49,398	50,602	0,750	0,952	-26,000	-21,500	0,032	8,140	-31,325	-0,634
sht-miR-125b	AUCCCUGAGACUGAUAA UUGCUCUGUUUAUCAUG AUAAGUGUAUUUGAUGA GAACAAUUAUUAUUCUC AGGUGU	74	18,919	28,378	13,514	39,189	32,432	67,568	1,381	1,400	-24,100	-24,100	0,182	5,620	-32,568	-1,004
sht-miR-8485	CACACACACACACACACA CACACGCAUACAUAUAU UUAUAUAUGUGUGCGUA UGUGUGUGUAUGUGCG UAAG	72	18,056	31,944	22,222	27,778	40,278	59,722	0,870	0,813	-38,800	-38,800	0,519	5,020	-53,889	-1,338
sht-miR-137	CUCAACUUCGGAAAACA ACUUUUCUCUGCAAGCG AUUAUUGCUUGAGAAUA CUGUUACUGAAGUUAUU	68	16,176	29,412	19,118	35,294	35,294	64,706	1,200	0,846	-18,900	-15,300	0,259	7,960	-27,794	-0,788
sht-miR-130a	AUAGUAACCAAGAUAGA AAUUUUGAGACAAGAAG UGCAAUGUUAAAAGAUU UAAAUGUUUUUUGUUCG CUUCUUUUAAUUCAAUC UUGAGAUACACA	97	15,464	37,113	11,340	36,082	26,804	73,196	0,972	1,364	-19,300	-17,700	0,063	10,330	-19,897	-0,742
sht-miR-7192	AUAGCAACAGUAUAGGA UCAGUCUUGUGUAAGGU UUCACUCAGAAUUAAAA AAACACAAUACGGUGCU UUUACUGUUUGCACA	83	18,072	34,940	16,867	30,120	34,940	65,060	0,862	1,071	-19,500	-17,900	0,060	8,800	-23,494	-0,672
sht-miR-466i-1	CUGUAGCUCUAGUGUGU GUGUGUGUGUGUGUGU UAAUAAAAUACAAAUACA CACGCACACGAUCAAAC AUACAGAGGUAUGU	82	23,171	31,707	15,854	29,268	39,024	60,976	0,923	1,462	-34,300	-34,300	0,059	20,420	-41,829	-1,072
sht-miR-8357	UUAAACCGUUUUUGUUA UUGUGUUUUAGUCAGCA GUAGAUUGGAAUCAUAU UGAAGUGACUGAAAAGC AUACAUCACAAAAAGAUU AUG	89	19,101	34,831	11,236	34,831	30,337	69,663	1,000	1,700	-18,500	-18,500	0,055	9,250	-20,787	-0,685
sht-miR-4919	CGAUGGCGUGUUUGUG AUCUAACUUGACUGAGU AUUAUGUGAGUCUCUAG GGGAAGUGUAUGUUUCA UAAAACGCCAAAU	80	26,250	26,250	13,750	33,750	40,000	60,000	1,286	1,909	-20,100	-18,200	0,092	7,000	-25,125	-0,628

sht-miR-7956	AGGUGUCUAAUUCAGUA CAAUGGAAGAUGGUCGC GCAAUUUCGUCGAUUGG UUGAGGUUAGACAUUA	67	28,358	26,866	13,433	31,343	41,791	58,209	1,167	2,111	-18,600	-18,300	0,057	7,170	-27,761	-0,664
sht-miR-466i-2	CAAACAAACAAAUAACAC AUAAAUAUUGGUACAAG AGGGCACCAAAUAUAUA UGCGCCACACCAUAUUU GUGUGUGUGUGUGUGU GUGGG	90	22,222	35,556	16,667	25,556	38,889	61,111	0,719	1,333	-22,800	-17,400	0,046	18,500	-25,333	-0,651
sht-miR-2538	CUAAUUAGGAUAAAUAA AUUAGAUUUUCUGACGU UUCGUGACUUAGUGUAA GCCACUUCUUCAGAAAA UAAAGCUUUAUUUAUAA UAAUCUA	92	13,043	35,870	13,043	38,043	26,087	73,913	1,061	1,000	-18,900	-18,300	0,197	3,960	-20,543	-0,788
sht-miR-4027-2	GGUAUAUUACUUUUAUG UAUAUUAACUAGUACAU GUUCAUUGUAUCUCCAA CACAGAUACAUACGAAC AUCAGUACGUAUACACU CAGAGAUAAAUCAA	99	12,121	37,374	18,182	32,323	30,303	69,697	0,865	0,667	-20,700	-20,700	0,235	8,110	-20,909	-0,690
sht-miR-9197	GUUGAGAUGAAAAUUCA CUUGUGAGAGAAGUAGA UCAAAGGACAUUGUGUG UUUUGAUUACGCUUUGA UUGUUUGUGUCUAACAC UGAUUUUCCCUCUUU	100	22,000	25,000	13,000	40,000	35,000	65,000	1,600	1,692	-20,100	-15,270	0,038	25,970	-20,100	-0,574
sht-miR-1-2	AGUAAAUGGCUUAAAGA GGUCAUCGCAACUUUUA UUCUGGUAUAUGCUGCA GAAUAGUUCACAUACUU CUUUAUGCCCAUUUUAU	85	16,471	28,235	17,647	37,647	34,118	65,882	1,333	0,933	-20,600	-19,600	0,020	10,490	-24,235	-0,710
sht-miR-3499-2	AAAGCCAAACGAGCUUU CUGAAUCCGUGCUGAGA UUUCGUCAGAAACCAAC CUAUUAGGACUGAUCAG ACUUCCAGCAUGAGUGA AGUCGUUGGCGAG	98	24,490	29,592	22,449	23,469	46,939	53,061	0,793	1,091	-28,700	-27,500	0,033	11,670	-29,286	-0,624
sht-miR-3492-1	CUAGUCGAGCCUUCUGU AUCCGUGCUGAGAUUUC GUCACACACCAGACCAC AAGGGCUGACGAAACUU UCAAGAUAAGUGAAGCG AUCGACACG	94	23,404	28,723	26,596	21,277	50,000	50,000	0,741	0,880	-23,900	-22,700	0,136	11,000	-25,426	-0,509
sht-miR-234	AGGAAGGUGCGGUUCG UACCACUUGGGACACGU CAGCUGGAUGCACCGGU AUUCCAGAGUUGAUGUU CCUUCCAGGAUUCGAAC CAAGCACCUUUCG	97	27,835	21,649	25,773	24,742	53,608	46,392	1,143	1,080	-45,100	-43,500	0,157	9,690	-46,495	-0,867

sht-miR-59	GAGUUCUGAAAACUGUU UCGUCAUCUUCACUGUG CAUUUUCAUCCAAAAAC GGAAAUGAAGCAGUCUU AAGGUCUUCGAAUCGUU UAUCAGUAAAAA	97	17,526	31,959	18,557	31,959	36,082	63,918	1,000	0,944	-20,900	-20,900	0,052	6,870	-21,546	-0,597
sht-miR-8437	GAUGAUUUUUUACAUUU GGCGCUUAGUAGAAUGU CACCGCAUGUACUGAAC ACAACGGUAACAUUUAC UAAGAGCUCAGAUGUAG AAAGUCGUG	94	22,340	30,851	17,021	29,787	39,362	60,638	0,966	1,313	-40,500	-40,500	0,095	6,140	-43,085	-1,095
sht-bantam	UUUCAGAUCGGCAAGUC GGCUUUUAUUGCGCUCU GAGAAAAAUUUAUUGUC AUCUGAGAUCGCGAUUA AAGCUGGUUUUCCAUUU GUGA	89	22,472	23,596	16,854	37,079	39,326	60,674	1,571	1,333	-28,500	-28,500	0,129	4,740	-32,022	-0,814
sht-miR-944	AUGACUUUCGAACUGAG CUGAGCAAUAUAAUUAA UUUACUAAAUUUAGACA UGUAAAUUAUUGUACAU CGACUCAGUAGUCUGAA GGUUAA	91	16,484	36,264	13,187	34,066	29,670	70,330	0,939	1,250	-23,700	-23,700	0,145	10,520	-26,044	-0,878
sht-miR-3492	AUAGACGGAUAUCUCGC CUUCGCAAAAGGUGGUG UAAGUAGGCAAAAGCCA AACGAGUUUUUCGAAUC CGUGCUGAGAUUUCGUC CGA	88	26,136	28,409	20,455	25,000	46,591	53,409	0,880	1,278	-23,100	-16,600	0,058	20,230	-26,250	-0,563
sht-miR-8448-2	UUAAAGUUAGACAUUAA CACCGUUGGAUACUGCC UCUGUGGUCUAGAGGUU AAACGUUCGCGAGCGAG ACCAAAGGUCUUAGAUU CAAUUGGU	93	24,731	27,957	18,280	29,032	43,011	56,989	1,038	1,353	-21,200	-20,800	0,019	10,120	-22,796	-0,530
sht-miR-3492-2	CUAGUCGAGCCUUCUGU AUCCGUGCUGAGAUUUC GUCACACACUAGACCAC AAGGGCUGAUGAGACUC GCAAGUUAAAUGAAGCG GUCGACACG	94	25,532	26,596	25,532	22,340	51,064	48,936	0,840	1,000	-29,600	-23,000	0,195	6,450	-31,489	-0,617
sht-miR-2253a	GUCUGACAUGGCACUGC UGAAGAGUUAUUCCCAU UCUCAACAUGCAGCAAU GUAUCAUGGGAAACGCC AAGAAUAACGCCUUGAG UACUGAUCUCAGUC	99	21,212	29,293	24,242	25,253	45,455	54,545	0,862	0,875	-24,000	-24,000	0,082	9,440	-24,242	-0,533

sht-miR-7	UAUCUUACCGUUGCUUA AUCAUGGAAGACUGGUG AUAUGUUGUUCAAUGAU GAAACUUUCAAAUAAAUA UGAAACGUUUCAUCAGA AUAAUUAAAAUAAGAGCA ACCUAUCUCAUUCUUCC AUGUAUGCGAUCGGUUA AACAAC	144	15,278	35,417	16,667	32,639	31,944	68,056	0,922	0,917	-48,500	-48,500	0,201	3,970	-33,681	-1,054
sht-miR-7b	AUUCUAUAUUCCAGAGA AACUUGGAAGACUUGUG AUUUAGUUGUUUAAUAU UAAGUGCAAUGAACUUG UUAAAUAUGACGAACAA CAAUCACAAAUCUCCAU GUGAUAUCUGGUUAAAC AACUGA	125	16,000	36,800	14,400	32,800	30,400	69,600	0,891	1,111	-31,400	-29,200	0,040	10,660	-25,120	-0,826
sht-miR-98	UAGAGUAUUUGGUAGUG UUUCCUUGUAGCUAUUU CUACGUUUUACACAUUA ACAGUAGAGAAUGCUAU UUAAGUACGCAAUACAA CUUACUACA	94	15,957	30,851	15,957	37,234	31,915	68,085	1,207	1,000	-20,500	-20,500	0,096	11,470	-21,809	-0,683

Table S4 - Statistical analysis of the thermodynamic and structural characteristics of *Schistosoma haematobium* Egypt pre-miRNAs with the Ecdysozoa, Cnidaria, Polifera, Platyhelminthes and *Schistosoma* pre-miRNAs (Size. G content. A content. C content. U content. GC content. AU content. AU ratio. GC ratio. Minimum Free Energy (MFE). Minimal Free Energy of the thermodynamic ensemble (MFEE). MFE structure Frequency in the ensemble (Freq). Ensemble Diversity (Div). Adjusted Minimum Free Energy (AMFE). Minimum Free Energy Index (MFEI); sht: *S. haematobium.*

	Superphylum *Ecdysozoa*		***Schistosoma haematobium***		**Mann Whitney test**	
Characteristics	**Mean**	**Median**	**Mean**	**Median**	***p-value***	**Conclusion**
Size	86.48	86.00	91.22	93.00	0.000<0.05	Different
G content	22.93	22.61	20.04	19.54	0.000<0.05	Different
A content	25.24	25.00	29.72	29.07	0.000<0.05	Different
C content	20.52	20.34	17.57	17.39	0.000<0.05	Different
U content	30.06	30.00	32.67	32.64	0.003<0.05	Different
GC content	43.46	43.18	37.61	36.59	0.000<0.05	Different
AU content	55.31	55.56	62.39	63.41	0.000<0.05	Different
UA ratio	1.24	1.19	1.13	1.06	0.003<0.05	Different
MFE	-31.61	-30.50	-25.32	-23.00	0.000<0.05	Different
MFEE	-30.47	-29.40	-23.78	-21.70	0.000<0.05	Different
Freq	0.2070	0.1540	0.1309	0.0878	0.000<0.05	Different
Div	6.77	5.17	10.02	9.39	0.000<0.05	Different
AMFE	-36.87	-36.35	-27.92	-25.77	0.000<0.05	Different
MFEI	-0.862	-0.843	-0.752	-0.710	0.000<0.05	Different
	Phylum *Cnidaria*		***Schistosoma haematobium***			
Size	76.05	69.00	91.22	93.00	0.000<0.05	Different
G content	22.71	22.47	20.04	19.54	0.000<0.05	Different
C content	19.65	20.03	17.57	17.39	0.000<0.05	Different
U content	28.25	27.96	32.67	32.64	0.000<0.05	Different
GC content	42.36	42.19	37.61	36.59	0.001<0.05	Different
AU content	56.30	56.49	62.39	63.41	0.000<0.05	Different
MFE	-30.27	-28.70	-25.32	-23.00	0.000<0.05	Different
MFEE	-29.57	-28.65	-23.78	-21.70	0.000<0.05	Different
Freq	0.3028	0.2617	0.1309	0.0878	0.000<0.05	Different
Div	4.67	3.48	10.02	9.39	0.000<0.05	Different
AMFE	-39.85	-38.39	-27.92	-25.77	0.000<0.05	Different
MFEI	-0.969	-0.919	-0.752	-0.710	0.000<0.05	Different

	Phylum *Polifera*		*Schistosoma haematobium*			
Size	117.20	115.50	91.22	93.00	0.045<0.05	Different
G content	26.80	25.16	20.04	19.54	0.003<0.05	Different
A content	22.96	23.28	29.72	29.07	0.000<0.05	Different
C content	22.99	23.19	17.57	17.39	0.020<0.05	Different
U content	26.34	26.53	32.67	32.64	0.023<0.05	Different
GC content	49.80	50.22	37.61	36.59	0.020<0.05	Different
AU content	49.30	49.03	62.39	63.41	0.003<0.05	Different
MFE	-51.03	-51.40	-25.32	-23.00	0.023<0.05	Different
MFEE	-49.03	-48.70	-23.78	-21.70	0.023<0.05	Different
AMFE	-42.30	-45.55	-27.92	-25.77	0.023<0.05	Different
MFEI	-0.859	-0.974	-0.752	-0.710	0.023<0.05	Different
	Genus Schistosoma		***Schistosoma haematobium***			
G content	20.43	20.00	20.04	19.54	0.486>0.05	Same
A content	28.43	28.13	29.72	29.07	0.135>0.05	Same
C content	17.16	17.39	17.57	17.39	0.920>0.05	Same
U content	32.95	32.99	32.67	32.64	0.816>0.05	Same
GC content	37.59	37.23	37.61	36.59	0.408>0.05	Same
AU content	61.38	61.80	62.39	63.41	0.353>0.05	Same
UA ratio	1.20	1.15	1.13	1.06	0.246>0.05	Same
GC ratio	1.27	1.20	1.21	1.13	0.154>0.05	Same
Freq	0.1087	0.0665	0.1309	0.0878	0.063>0.05	Same
Div	13.08	9.87	10.02	9.39	0.642>0.05	Same
AMFE	-27.13	-25.58	-27.92	-25.77	0.816>0.05	Same
MFEI	-0.730	-0.685	-0.752	-0.710	0.642>0.05	Same

Table S5 - Validation of the presence of mature miRNAs identified in small RNAs libraries of adult male (SRR6655496) and adult female (SRR6655494) in *S. haematobium* Egypt available in the SRA; sht: *S. haematobium.*

miRNA	SRR6655494	SRR6655496
shtbantam-3p	16517	15614
shtbantam-5p	0	2
sht-let-7-3p	42	538
sht-let-7-5p	3176	150423
sht-let-7d-5p	0	0
sht-miR-10107-5p	0	0
sht-miR-10345-3p	0	0
sht-miR-10-3p	4	44
sht-miR-10501-3p	0	0
sht-miR-10-5p	1625	29529
sht-miR-10644-3p	1	1
sht-miR-10704-3p	0	0
sht-miR-10828-3p	0	0
sht-miR-10954-5p	0	0
sht-miR-11181-3p	0	0
sht-miR-1-1-5p	0	0
sht-miR-11629-3p	0	0
sht-miR-1187-5p	0	0
sht-miR-12366a-5p	0	0
sht-miR-1-2-3p	0	0
sht-miR-124-3p	1179	17155
sht-miR-124-5p	2	29
sht-miR-124c-5p	0	0
sht-miR-125b-5p	18464	396114
sht-miR-125c-3p	1	12
sht-miR-125c-5p	199	4210
sht-miR-130a-5p	0	0
sht-miR-1350-3p	0	0
sht-miR-137-3p	0	0
sht-miR-138-3p	0	0
sht-miR-141-3p	0	0
sht-miR-1671-3p	0	0
sht-miR-16b-3p	0	0
sht-miR-184a-5p	0	0
sht-miR-190-3p	0	0

sht-miR-1960-3p	0	0
sht-miR-2023-1-5p	6	37
sht-miR-2023-2-3p	9	49
sht-miR-203b-5p	0	0
sht-miR-2162-3p	2682	19988
sht-miR-2162-5p	120	1182
sht-miR-219-3p	0	1
sht-miR-2238-h-3p	0	0
sht-miR-2253a-5p	0	0
sht-miR-2340-5p	0	0
sht-miR-234-3p	0	0
sht-miR-2463-5p	0	0
sht-miR-2493-3p	0	0
sht-miR-2538-5p	3	10
sht-miR-281-3p	0	0
sht-miR-281-5p	8	100
sht-miR-2a-1-3p	7765	60159
sht-miR-2a-2-3p	17	84
sht-miR-2a-1-5p	0	3
sht-miR-2b-3p	273	3241
sht-miR-2b-5p	54	233
sht-miR-2c-3p	13	8
sht-miR-2c-5p	200	108
sht-miR-2e-3p	123	1873
sht-miR-2e-5p	4	21
sht-miR-33a-5p	0	0
sht-miR-3479-3p	445	4582
sht-miR-3492-1-5p/2-5p	260	443
sht-miR-3492-3p	226	549
sht-miR-3499-1-5p/2-5p	245	432
sht-miR-3618-3p	0	0
sht-miR-36-3p	2039	26723
sht-miR-36b-3p	171	1987
sht-miR-36b-5p	30	163
sht-miR-3812-3p	0	0
sht-miR-3851-l-3p	0	0
sht-miR-3853-3p	0	0
sht-miR-4000e-5p	0	0
sht-miR-4000g-5p	0	0
sht-miR-4027-1-3p	0	0
sht-miR-4027-2-5p	0	0
sht-miR-4106-5p	0	0
sht-miR-4111-5p	0	0
sht-miR-4172-3p	0	0
sht-miR-4175-3p	0	0
sht-miR-4206-1-3p	0	0
sht-miR-4206-2-3p	102	919

sht-miR-4260-3p	0	0
sht-miR-427-5p	0	0
sht-miR-43b-3p	0	0
sht-miR-466c-5p	0	0
sht-miR-466g-3p	0	0
sht-miR-466i-1-5p/-2-3p	1	13
sht-miR-4680-3p	9	3
sht-miR-4913-3p	0	0
sht-miR-4919-3p	0	0
sht-miR-510-3p	0	0
sht-miR-545-5p	0	0
sht-miR-548b-3p	0	0
sht-miR-559-3p	0	0
sht-miR-5594-5p	0	0
sht-miR-563-1-3p	0	0
sht-miR-563-2-3p	0	0
sht-miR-5894b-5p	0	0
sht-miR-592-3p	0	0
sht-miR-5934-3p	0	0
sht-miR-59-3p	0	0
sht-miR-61-3p	389	4780
sht-miR-61-5p	0	3
sht-miR-6306-3p	0	0
sht-miR-6574-3p	0	0
sht-miR-6733-3p	0	0
sht-miR-7092-5p	0	0
sht-miR-7192-3p	0	0
sht-miR-7194-3p	0	0
sht-miR-71a-3p	0	3
sht-miR-71a-5p	103330	1515126
sht-miR-71b-3p	16	6
sht-miR-71b-5p	19825	47162
sht-miR-737-5p	0	0
sht-miR-7-5p	9576	244928
sht-miR-7643-3p	0	0
sht-miR-7790-3p	0	1
sht-miR-7956-5p	0	0
sht-miR-79-5p	0	1
sht-miR-7b-5p	9	96
sht-miR-8335-3p	0	2
sht-miR-83-3p	0	0
sht-miR-8357-5p	0	0
sht-miR-8-3p	104	1160
sht-miR-8416-5p	0	0
sht-miR-8422-5p	0	0
sht-miR-8437-3p	4	0
sht-miR-8437-5p	861	80

sht-miR-8448-1-3p/2-3p	1	7
sht-miR-8485-5p	0	5
sht-miR-84a-3p	0	0
sht-miR-8-5p	0	0
sht-miR-87a-5p	0	0
sht-miR-9126-3p	0	0
sht-miR-9197-3p	0	0
sht-miR-927a-3p	0	4
sht-miR-9388-3p	0	0
sht-miR-9388-5p	0	0
sht-miR-9396-3p	0	0
sht-miR-944-3p	0	0
sht-miR-9648-3p	0	0
sht-miR-9711-3p	0	0
sht-miR-9814-3p	0	0
sht-miR-98-3p	0	0

APÊNDICE III - SUPPLEMENTARY TABLES - CAPÍTULO II – Article: Genome-wide identification and characterization of genes involved in the acylsugar pathway in tomato - Manuscript Draft sob revision for Plant Gene Journal

Supplementary Table S1. Primers designed for real-time PCR from the putative genes sequences of the acylsugar pathway and reference endogenous genes.

Gene	Sense primer	Antisense primer
BCKD E2	5’ TGTTATCCACACCTGCTGTCC 3’	5’ GTATCCTTCCACCTTTCCCAG 3’
IPMSA	5’ CAACGAGGCAAATTATCTGAC 3’	5’ GTTTAGCAGTCATGGATGCAC 3’
TD	5’ AACTCCCGAAAGAGCAGTTG 3’	5’ TCGCAGCCAAGTCTCTGAG 3’
eEF-1	5’ TTGACAGGCGTTCAGGTAAGG 3’	5’ GGGCTTGGTGGGAATCATC 3’
GAPDH	5’ CTGTTGATGTGTCCGTGGTTG 3’	5’ CAGATTCCTCCTTGATGGCAG 3’

Supplementary Table S2. Proteins involved in the acylsugar pathway in *Solanum lycopersicum* (Sly) and *Solanum pennellii* (Spe) retrieved from Sol Genomics Database. Chromosome (Chr).

Protein families	Species	NCBI identification	Size (aa)	NCBI orthologs identification	Size (aa)	Blastp (e-value) with orthologous protein	Genome version	Chr	Start position	End position	Strand	Name/ID
Acetyl-CoA synthase	*Sly*	XP_004231738.1	778	*Solanum pennellii* XP_015065927.1	778	0.0	ITAG3.0	Chr02	55866386	55881323	+	Solyc02g094640
		XP_004242910.1	677	*Solanum pennellii* XP_015065927.1	778	0.0	ITAG3.0	Chr07	8194894	8200704	+	Solyc07g017860
	Spe	XP_015065927.1	778	*Solanum tuberosum* XP_006338753.1	781	0.0	Spenn_v2.0	Chr02	59748505	59763555	+	Sopen02g039280
		XP_015080763.1	677	*Solanum tuberosum* XP_006338753.1	781	0.0	Spenn_v2.0	Chr07	8454814	8460224	+	Sopen07g006650
AKR - Aldo keto reductase	*Sly*	NP_001315612	317	*Arabidopsis thaliana* NP_181315.2	314	$6e^{-176}$	ITAG3.0	Chr09	4573065	4578626	+	Solyc09g011240
		XP_010314928.1	290	*Arabidopsis thaliana* XP_002879707.1	311	0.0	ITAG3.0	Chr00	10284549	10286072	+	Solyc00g015733
		XP_004247478.1	359	*Nicotiana sylvestris* XP_009778409.1	359	0.0	ITAG3.0	Chr09	66514297	66518361	+	Solyc09g074310
		XP_004241009.1	401	*Nicotiana tomentosiformis* XP_009601408.1	415	0.0	ITAG3.0	Chr06	36496448	36508164	-	Solyc06g053585
		XP_004235169.1	315	*Solanum pennellii* XP_015069485.1	315	0.0	ITAG3.0	Chr03	55887911	55889550	+	Solyc03g093280
		XP_004235168.1	315	*Solanum pennellii* XP_015069485.1	315	0.0	ITAG3.0	Chr03	55881491	55883519	+	Solyc03g093270
		XP_004251040.1	398	*Nicotiana tomentosiformis* XP_009629477.1	405	0.0	ITAG3.0	Chr11	53188917	53192730	+	Solyc11g067160
		NP_001315616.1	346	*Solanum*	346	0.0	ITAG3.0	Chr09	68848350	68852214	-	Solyc09g082730

				tuberosum XP_006363466.1								
		NP_001333054.1	346	*Nicotiana attenuata* XP_019243755.1	346	0.0	ITAG3.0	Chr09	72418289	72419750	+	Solyc09g097960
	Spe	XP_015069444.1	315	*Solanum tuberosum* XP_006358247.1	315	0.0	Spenn_v2.0	Chr03	56495115	56496537	+	Sopen03g024070
		XP_015069485.1	315	*Solanum tuberosum* XP_006358247.1	315	0.0	Spenn_v2.0	Chr03	56489025	56491399	+	Sopen03g024060
		XP_015086033.1	317	*Solanum tuberosum* XP_006340995.1	317	0.0	Spenn_v2.0	Chr09	4837266	4842591	+	Sopen09g005990
		XP_015062400.1	344	*Solanum tuberosum* XP_006363582.1	345	0.0	Spenn_v2.0	Chr01	81446003	81449453	+	Sopen01g026810
ALS (AHAS) - Acetolactate (acetohydroxyacid) synthase	*Sly*	XP_004234664	659	*Chenopodium quinoa* XP_021737451.1	670	0.0	ITAG3.0	Chr03	8871620	8873599	-	Solyc03g044330
		XP_004242053	650	*Chenopodium quinoa* XP_021737451.1	670	0.0	ITAG3.0	Chr06	37897925	37900508	-	Solyc06g059880
		XP_004250085.1	490	*Arabidopsis thaliana* NP_197133.1	477	0.0	ITAG3.0	Chr11	2962920	2972883	+	Solyc11g008780
		XP_004251994.1	481	*Arabidopsis thaliana* NP_850172.1	491	0.0	ITAG3.0	Chr12	9942755	9954072	-	Solyc12g019310
		XP_010324415.1	657	*Solanum pennellii* XP_015081631.1	657	0.0	ITAG3.0	Chr07	64944566	64946539	-	Solyc07g061940
	Spe	XP_015061725.1	481	*Solanum tuberosum* XP_006353111.1	481	0.0	Spenn_v2.0	Chr12	11154094	11182956	-	Sopen12g009610
		XP_015058906.1	486	*Solanum tuberosum* XP_006353111.1	481	0.0	Spenn_v2.0	Chr11	3059983	3067907	+	Sopen11g004560
		XP_015081631.1	657	*Solanum tuberosum* XP_006348357.1	657	0.0	Spenn_v2.0	Chr07	75836653	75840083	-	Sopen07g030210
		XP_015069723.1	659	*Solanum tuberosum*	657	0.0	Spenn_v2.0	Chr03	8496649	8498943	-	Sopen03g008440

				XP_006348357.1								
AT2 (AT4) – Acylsugar Acyltransferase 2 (4)	*Sly*	NP_001266253.1	451	*Solanum habrochaites* gb| AUG68746.1	445	0.0	ITAG3.0	Chr01	93607124	93608446	-	Solyc01g105580
		NP_001316321.1	446	*Solanum habrochaites* gb| AUG68746.1	445	0.0	ITAG3.0	Chr04	4353166	4354506	-	Solyc04g012020
	Spe	XP_015071716.1	445	*Solanum habrochaites* gb| AUG68746.1	445	0.0	ITAG3.0	Chr04	4524972	4526516	-	Sopen04g006140
AT3 – Acylsugar Acyltransferase 3	*Sly*	XP_004251378.3	328	*Solanum pennellii* XP_015058409.1	428	0.0	ITAG3.0	Chr11	53307619	53308911	+	Solyc11g067270
		XP_004251382.2	332	*Solanum pennellii* XP_015058038.1	433	0.0	ITAG3.0	Chr11	53360820	53362121	+	Solyc11g067330
		XP_004251383.1	332	*Solanum pennellii* XP_015058038.1	433	0.0	ITAG3.0	Chr11	53364562	53365863	+	Solyc11g067340
		XP_004251384.1	234	*Solanum pennellii* XP_015058038.1	433	$3e^{-132}$	ITAG3.0	Chr11	53368437	53369141	+	Solyc11g067350
		XP_004233828.1	196	*Solanum pennellii* XP_015058038.1	433	$2e^{-30}$	ITAG3.0	Chr02	43736991	43738507	-	Solyc02g078510
		XP_004243889.2	436	*Solanum pennellii* XP_015081753.1	424	0.0	ITAG3.0	Chr07	57801353	57802893	+	Solyc07g043710
		XP_004243890.1	429	*Solanum pennellii* XP_015081753.1	424	$3e^{-114}$	ITAG3.0	Chr07	57794534	57795822	-	Solyc07g043700
		XP_004243893.1	431	*Solanum tuberosum* XP_006357897.2	392	0.0	ITAG3.0	Chr07	57763292	57764587	-	Solyc07g043670
		XP_004246214.1	424	*Solanum tuberosum* XP_006351214.1	461	0.0	ITAG3.0	Chr08	59452369	59453687	-	Solyc08g075210
		XP_004246215.2	426	*Solanum tuberosum* XP_006351214.1	461	0.0	ITAG3.0	Chr08	59440332	59441123	-	Solyc08g075180
		XP_004244824.1	436	*Solanum tuberosum* XP_006351057.1	350	0.0	ITAG3.0	Chr08	4616497	4617807	-	Solyc08g014490

		XP_004233767.1	431	*Solanum tuberosum* XP_006363207.1	430	0.0	ITAG3.0	Chr02	46169449	46170744	+	Solyc02g081800
		XP_004251404.1	474	*Solanum tuberosum* XP_015158798.1	376	0.0	ITAG3.0	Chr01 1	54592276	54593700	+	Solyc11g069680
		XP_004232633.1	438	*Solanum tuberosum* XP_006363208.1	416	0.0	ITAG3.0	Chr02	46139658	46141880	+	Solyc02g081760
		XP_004232634.1	440	*Solanum tuberosum* XP_006363208.1	416	0.0	ITAG3.0	Chr02	46132818	46136005	-	Solyc02g081745
		XP_004232635.1	437	*Solanum tuberosum* XP_006363208.1	416	0.0	ITAG3.0	Chr02	46126046	46127844	-	Solyc02g081740
		XP_010321585.1	357	*Solanum tuberosum* XP_006351057.1	350	$4e^{-108}$	ITAG3.0	Chr05	49186116	49188597	-	Solyc05g039950
		XP_010313351.2	325	*Solanum tuberosum* XP_015164920.1	427	0.0	ITAG3.0	Chr11	53323360	53324643	-	Solyc11g067290
	Spe	XP_015061012.1	427	*Solanum tuberosum* XP_015166199.1	427	0.0	Spenn_v2.0	Chr12	949573	951177	-	Sopen12g002290
		XP_015058409.1	428	*Solanum habrochaites* AJF98596.1	428	0.0	Spenn_v2.0	Chr11	62767836	62769279	+	Sopen11g026960
		XP_015058038.1	433	*Solanum habrochaites* AJF98596.1	428	$2e^{-151}$	Spenn_v2.0	Chr11	62842616	62844063	+	Sopen11g027030
		XP_015055409.1	190	*Solanum habrochaites* AJF98596.1	428	$3e^{-50}$	Spenn_v2.0	Chr10	77901614	77903044	+	Sopen10g030210
		XP_015085868.1	430	*Solanum habrochaites* AJF98596.1	428	$1e^{-95}$	Spenn_v2.0	Chr08	63608042	63609570	-	Sopen08g023820
		XP_015084674.1	436	*Solanum habrochaites* AJF98596.1	428	$9e^{-65}$	Spenn_v2.0	Chr08	5034384	5035743	-	Sopen08g005480
		XP_015084374.1	429	*Solanum tuberosum* XP_006351214.1	461	0.0	Spenn_v2.0	Chr08	63595785	63597250	-	Sopen08g023810
		XP_015081753.1	424	*Solanum*	461	$1e^{-105}$	Spenn_v2.0	Chr07	68195986	68197597	+	Sopen07g023290

				tuberosum XP_006351214.1								
		XP_015083111.1	431	*Solanum tuberosum* XP_015166199.1	427	$6e^{-108}$	Spenn_v2.0	Chr07	68100095	68101531	-	Sopen07g023230
		XP_015081727.1	429	*Solanum habrochaites* AJF98596.1	428	$3e^{-133}$	Spenn_v2.0	Chr07	68161760	68163207	-	Sopen07g023280
		XP_015075888.1	434	*Solanum tuberosum* XP_006351214.1	461	$8e^{-104}$	Spenn_v2.0	Chr05	62080016	62081411	-	Sopen05g024660
		XP_015078011.1	431	*Solanum tuberosum* XP_006351214.1	461	$1e^{-88}$	Spenn_v2.0	Chr06	56167725	56169335	-	Sopen06g030010
		XP_015065374.1	441	*Solanum tuberosum* XP_006351214.1	461	$4e^{-99}$	Spenn_v2.0	Chr02	49322805	49324435	-	Sopen02g026350
		XP_015064859.1	431	*Solanum tuberosum* XP_006351214.1	461	$6e^{-102}$	Spenn_v2.0	Chr02	49367634	49368996	+	Sopen02g026400
		XP_015057957.1	448	*Solanum habrochaites* AJF98596.1	428	$2e^{-157}$	Spenn_v2.0	Chr11	62848156	62850410	+	Sopen11g027040
BCAT - Branched-chain aminotransferase	*Sly*	XP_004230170.1	557	*Solanum tuberosum* XP_006361872.1	557	0.0	ITAG3.0	Chr01	88994535	89006516	+	Solyc01g098700
	Spe	XP_015062638.1	557	*Solanum tuberosum* XP_006361872.1	557	0.0	Spenn_v2.0	Chr01	99522786	99534162	+	Sopen01g042240
BCAT - Branched-chain aminotransferase 2	*Sly*	XP_004253486.1	189	*Solanum pennellii* XP_015072938.1	367	$5e^{-134}$	ITAG3.0	Chr00	17281850	17282980	+	Solyc00g178340
		XP_010314598.1	380	*Solanum pennellii* XP_015072938.1	367	0.0	ITAG3.0	Chr12	64644048	64650337	+	Solyc12g088220
		XP_010323427.1	383	*Solanum pennellii* XP_015072938.1	367	0.0	ITAG3.0	Chr07	20368123	20376250	-	Solyc07g021630
		XP_019069001.1	283	*Solanum pennellii* XP_015072938.1	367	$1e^{-105}$	ITAG3.0	Chr04	62274104	62276964	+	Solyc04g077240
	Spe	XP_015071937.1	378	*Solanum tuberosum*	378	0.0	Spenn_v2.0	Chr04	72615922	72618282	+	Sopen04g030820

				XP_006356815.1								
		XP_015072938.1	367	*Solanum tuberosum* XP_006356815.1	378	0.0	Spenn_v2.0	Chr04	72625012	72627442	+	Sopen04g030830
		XP_015080902.1	383	*Solanum tuberosum* XP_006356815.1	378	0.0	Spenn_v2.0	Chr07	24511250	24525459	-	Sopen07g011210
BCAT - Branched-chain aminotransferase 5	*Sly*	XP_004234645.1	418	*Solanum pennellii* XP_015068352.1	418	0.0	ITAG3.0	Chr03	7557106	7564500	-	Solyc03g043880
		XP_004231952.1	417	*Solanum pennellii* XP_015068352.1	418	0.0	ITAG3.0	Chr02	53815326	53822433	-	Solyc02g091970
	Spe	XP_015066719.1	417	*Arabidopsis thaliana* NP_201379.2	415	0.0	Spenn_v2.0	Chr02	57545620	57552285	-	Sopen02g036540
		XP_015068352.1	418	*Arabidopsis thaliana* NP_201379.2	415	0.0	Spenn_v2.0	Chr03	7170836	7176740	-	Sopen03g007690
BCKD E1a - Branched-chain keto acid dehydrogenase E1-alpha subunit	*Sly*	NP_001234066.2	456	*Solanum pennellii* XP_015077702.1	456	0.0	ITAG3.0	Chr06	37846164	37850453	-	Solyc06g059840
		XP_004239633.1	467	*Solanum pennellii* XP_015077702.1	456	0.0	ITAG3.0	Chr05	66605073	66614528	+	Solyc05g056480
		XP_004237706.1	472	*Solanum pennellii* XP_015077702.1	456	0.0	ITAG3.0	Chr04	55473351	55480565	+	Solyc04g063350
	Spe	XP_015074287.1	472	*Solanum tuberosum* XP_006356334.1	471	0.0	Spenn_v2.0	Chr04	67255062	67260948	+	Sopen04g026270
		XP_015076473.1	467	*Solanum tuberosum* XP_006345758.1	467	0.0	Spenn_v2.0	Chr05	77860897	77864993	+	Sopen05g034880
		XP_015077702.1	456	*Solanum tuberosum* XP_006356334.1	471	0.0	Spenn_v2.0	Chr06	47435728	47439986	-	Sopen06g019920
		XP_015078845.1	445	*Solanum tuberosum* XP_006356334.1	471	0.0	Spenn_v2.0	Chr06	47448127	47453236	-	Sopen06g019930
		XP_015074054.1	391	*Solanum tuberosum* XP_006363541.1	388	0.0	Spenn_v2.0	Chr04	73146	79687	-	Sopen04g001100

		XP_015076383.1	391	*Solanum tuberosum* XP_006363541.1	388	0.0	Spenn_v2.0	Chr05	1250444	1257254	-	Sopen05g002470
BCKD E1b - Branched-chain keto acid dehydrogenase E1 beta subunit	*Sly*	XP_004228950.1	358	*Arabidopsis thaliana* NP_187954.1	358	0.0	ITAG3.0	Chr01	40717765	40727649	+	Solyc01g028900
		XP_004241456.1	367	*Solanum pennellii* XP_015069743.1	377	0.0	ITAG3.0	Chr06	44902117	44909773	-	Solyc06g072580
		XP_010321111.1	372	*Solanum pennellii* XP_015069743.1	377	0.0	ITAG3.0	Chr05	30516539	30522622	-	Solyc05g024160
	Spe	XP_015062780.1	358	*Solanum tuberosum* XP_006359200.1	358	0.0	Spenn_v2.0	Chr01	48057258	48067758	-	Sopen01g017080
		XP_015079698.1	367	*Solanum tuberosum* XP_015164279.1	367	0.0	Spenn_v2.0	Chr06	55470650	55478270	-	Sopen06g028930
		XP_015074867.1	372	*Solanum tuberosum* XP_015164279.1	367	0.0	Spenn_v2.0	Chr05	38638281	38652327	-	Sopen05g018850
		XP_015069743.1	377	*Solanum tuberosum* XP_015164279.1	367	0.0	Spenn_v2.0	Chr03	64077549	64084755	+	Sopen03g028430
BCKD E2 - Branched-chain keto acid dehydrogenase E2	*Sly*	XP_004229256.1	505	*Solanum pennellii* XP_015062778.1	505	0.0	ITAG3.0	Chr01	74335277	74341774	-	Solyc01g066520
	Spe	XP_015062778.1	505	*Solanum tuberosum* NP_001305524.1	505	0.0	Spenn_v2.0	Chr01	84159159	84165579	-	Sopen01g028100
DHAD – Dihydroxyacid dehydratase	*Sly*	NP_001311413.1	615	*Arabidopsis thaliana* NP_189036.1	608	0.0	ITAG3.0	Chr12	59554960	59568451	+	Solyc12g043020
		XP_004240214.1	611	*Arabidopsis thaliana* NP_189036.1	608	0.0	ITAG3.0	Chr05	64466995	64474048	-	Solyc05g053540
	Spe	XP_015061319.1	620	*Solanum tuberosum* XP_006346583.1	619	0.0	Spenn_v2.0	Chr12	58290363	58305073	+	Sopen12g022260
		XP_015076738.1	611	*Solanum tuberosum* XP_006346583.1	619	0.0	Spenn_v2.0	Chr05	75579002	75586056	-	Sopen05g032060
Dihydrolipoyl	*Sly*	XP_004239903.1	571	*Arabidopsis*	630	0.0	ITAG3.0	Chr05	64068089	64075891	+	Solyc05g053100

dehydrogenase 1				*thaliana* NP_567487.4								
	Spe	XP_015076244.1	571	*Solanum tuberosum* XP_015167962.1	566	0.0	Spenn_v2.0	Chr05	75159371	75167210	+	Sopen05g031610
Dihydrolipoyl dehydrogenase 2	*Sly*	XP_004230295.1	570	*Arabidopsis thaliana* NP_567487.4	630	0.0	ITAG3.0	Chr01	90293964	90301497	-	Solyc01g100360
	Spe	XP_015055489.1	570	*Solanum tuberosum* XP_006344750.1	570	0.0	Spenn_v2.0	Chr01	100886646	100894000	-	Sopen01g043880
Dihydrolipoyl dehydrogenase mitochondrial	*Sly*	XP_004252936.1	504	*Solanum pennellii* XP_015061404.1	504	0.0	ITAG3.0	Chr12	67351093	67356317	+	Solyc12g099100
		NP_001234770.1	500	*Solanum pennellii* XP_015061404.1	504	0.0	ITAG3.0	Chr05	64274861	64279739	+	Solyc05g053300
	Spe	XP_015061404.1	504	*Solanum tuberosum* NP_001275339.1	504	0.0	Spenn_v2.0	Chr12	82289469	82295903	+	Sopen12g033810
		XP_015076098.1	500	*Solanum tuberosum* NP_001275339.1	504	0.0	Spenn_v2.0	Chr05	75396455	75401149	+	Sopen05g031810
IPDS - Isopropylmalate dehydratase/ IPMI - Isopropylmalate isomerase	*Sly*	XP_004234053.1	509	*Arabidopsis thaliana* NP_567405.1	509	0.0	ITAG3.0	Chr03	509215	517469	-	Solyc03g005730
		XP_004247789	505	*Arabidopsis thaliana* NP_567405.1	509	0.0	ITAG3.0	Chr09	70783641	70788642	+	Solyc09g090900
		XP_010322896	256	*Arabidopsis thaliana* NP_191458.1	253	$5e^{-97}$	ITAG3.0	Chr06	38930561	38931331	-	Solyc06g060790
	Spe	XP_015070021.1	509	*Solanum tuberosum* XP_006356071.1	509	0.0	Spenn_v2.0	Chr03	513770	522123	-	Sopen03g001740
		XP_015087737.1	505	*Solanum tuberosum* XP_006356071.1	509	0.0	Spenn_v2.0	Chr09	81926504	81931794	+	Sopen09g033880
		XP_015079863.1	255	*Solanum tuberosum* XP_006367458.1	256	$9e^{-168}$	Spenn_v2.0	Chr06	48675313	48676467	-	Sopen06g020930
IPMD - Isopropylmalate	*Sly*	XP_004238906.1	406	*Arabidopsis thaliana*	409	0.0	ITAG3.0	Chr05	3194199	3201926	-	Solyc05g009030

dehydrogenase				NP_196924.1								
		XP_004245819.1	367	*Solanum tuberosum* NP_001305547.*1*	357	0.0	ITAG3.0	Chr08	61935866	61942325	-	Solyc08g077920
		XP_004245818.1	367	*Solanum tuberosum* NP_001305547.*1*	357	0.0	ITAG3.0	Chr08	61943809	61949412	-	Solyc08g077930
	Spe	XP_015075676.1	406	*Solanum tuberosum* XP_006344159.1	405	0.0	Spenn_v2.0	Chr05	3451209	3462069	-	Sopen05g004770
		XP_015085405.1	367	*Solanum tuberosum* XP_006359219.1	367	0.0	Spenn_v2.0	Chr08	66246104	66255008	-	Sopen08g026440
IPMSA - Isopropylmalate synthase A	*Sly*	XP_010324707	414	*Solanum pennellii* XP_015083287.1	414	0.0	ITAG3.0	Chr08	3970260	3973179	-	Solyc08g014240
		NP_001306258.1	445	*Solanum pennellii* XP_015083287.1	414	0.0	ITAG3.0	Chr08	3942115	3949835	-	Solyc08g014230
		NP_001316379.1	661	*Solanum pennellii* NP_001310380.1	589	0.0	ITAG3.0	Chr08	3830314	3840086	+	Solyc08g014130
	Spe	NP_001310380.1	589	*Solanum tuberosum* XP_015168011.1	613	0.0	Spenn_v2.0	Chr08	4086948	4102498	+	Sopen08g005060
		XP_015083288.1	394	*Solanum tuberosum* XP_015168011.1	613	$3e^{-178}$	Spenn_v2.0	Chr08	4254804	4254804	-	Sopen08g005140
		XP_015089205.1	401	*Solanum tuberosum* XP_015168011.1	613	$2e^{-179}$	Spenn_v2.0	Chr10	5092585	5095247	-	Sopen10g006110
		XP_015083287.1	414	*Solanum tuberosum* XP_015168011.1	613	0.0	Spenn_v2.0	Chr08	4282152	4287132	-	Sopen08g005150
IPMSB - Isopropylmalate synthase B	*Sly*	NP_001306252.1	612	*Solanum pennellii* NP_001310373.1	612	0.0	ITAG3.0	Chr06	36255636	36265617	+	Solyc06g053400
	Spe	NP_001310373.1	612	*Solanum tuberosum* XP_006350708.1	612	0.0	Spenn_v2.0	Chr06	45714154	45724798	+	Sopen06g018460
Isovaleryl-CoA dehydrogenase 1, mitochondrial	*Sly*	XP_004241386	412	*Solanum tuberosum* NP_001275043	412	0.0	ITAG3.0	Chr06	45496443	45500954	-	Solyc06g073560

/ Methylacyl-CoA dehydrogenase		XP_004251116	412	*Solanum tuberosum* NP_001275043	412	0.0	ITAG3.0	Chr11	54103540	54111023	+	Solyc11g069180
	Spe	XP_015078656.1	412	*Solanum tuberosum* NP_001275043	412	0.0	Spenn_v2.0	Chr06	56104966	56109075	-	Sopen06g029920
		XP_015056789.1	412	*Solanum tuberosum* NP_001275043	412	0.0	Spenn_v2.0	Chr11	63586553	63593903	+	Sopen11g027920
KARI – Ketol-acid (Acetohydroxy-acid) reductoisomerase, chloroplastic	*Sly*	XP_004243410	594	*Gossypium arboreum* XP_017648797.1	585	0.0	ITAG3.0	Chr07	61875637	61881023	-	Solyc07g053280
		XP_004251800	591	*Gossypium arboreum* XP_017648797.1	585	0.0	ITAG3.0	Chr12	3772925	3778928	+	Solyc12g010840
	Spe	XP_015082094.1	594	*Solanum tuberosum* XP_006350031.1	590	0.0	Spenn_v2.0	Chr07	72943045	72948596	-	Sopen07g027240
		XP_015061020.1	591	*Solanum tuberosum* XP_006350031.1	590	0.0	Spenn_v2.0	Chr12	4816573	4822664	+	Sopen12g006200
KAS I- Ketoacyl-ACP synthase I	*Sly*	XP_004244796	468	*Solanum tuberosum* XP_006365563.1	469	0.0	ITAG3.0	Chr08	6981923	6993086	+	Solyc08g016170
		XP_004233105	469	*Solanum tuberosum* XP_006365563.1	469	0.0	ITAG3.0	Chr02	40964042	40968061	-	Solyc02g070790
		XP_004245499	485	*Solanum tuberosum* XP_006343829.1	485	0.0	ITAG3.0	Chr08	65458830	65462904	+	Solyc08g082620
	Spe	XP_015066388.1	469	*Solanum tuberosum* XP_006365563.1	469	0.0	Spenn_v2.0	Chr02	43724504	43728648	-	Sopen02g019880
		XP_015085240.1	468	*Solanum tuberosum* XP_006365563.1	469	0.0	Spenn_v2.0	Chr08	7826684	7837720	+	Sopen08g006520
		XP_015083584.1	485	*Solanum tuberosum* XP_006343829.1	485	0.0	Spenn_v2.0	Chr08	69943891	69947659	+	Sopen08g030860
KAS II- Ketoacyl-ACP synthase II	*Sly*	XP_004251704.1	526	*Solanum tuberosum* XP_006345248.1	532	0.0	ITAG3.0	Chr12	2538359	2545262	+	Solyc12g009260
		XP_010318480.1	558	*Solanum*	558	0.0	ITAG3.0	Chr03	71553937	71559774	-	Solyc03g122120

				pennellii XP_015070593.1								
	Spe	XP_015082190.1	540	*Solanum tuberosum* XP_006353782.1	540	0.0	Spenn_v2.0	Chr07	65956696	65969520	+	Sopen07g021960
		XP_015070593.1	558	*Solanum tuberosum* XP_006353782.1	540	0.0	Spenn_v2.0	Chr03	74669273	74675011	-	Sopen03g040910
KAS III-Ketoacyl-ACP synthase III	*Sly*	XP_004235286.1	431	*Arabidopsis thaliana* NP_176452.1	404	0.0	ITAG3.0	Chr03	61235534	61248899	-	Solyc03g097470
		NP_001308573.1	381	*Arabidopsis thaliana* NP_176452.1	404	0.0	ITAG3.0	Chr08	1170545	1174964	+	Solyc08g006560
	Spe	XP_015070295.1	431	*Solanum tuberosum* XP_006347624.1	431	0.0	Spenn_v2.0	Chr03	63856194	63869424	-	Sopen03g028240
		XP_015083523.1	381	*Solanum tuberosum* XP_006347624.1	431	0.0	Spenn_v2.0	Chr08	1327129	1331696	+	Sopen08g002520
KAS - Ketoacyl-ACP synthase mitochondrial	*Sly*	XP_004243502.1	465	*Solanum pennellii* XP_015083062.1	476	0.0	ITAG3.0	Chr07	60033246	60042888	+	Solyc07g049570
		XP_015083063.1	465	*Solanum tuberosum* XP_006357986.1	465	0.0	Spenn_v2.0	Chr07	70487093	70497505	+	Sopen07g024970
KCR2 - 3-ketoacyl/oxoacyl -CoA reductase 2	*Sly*	XP_004239165.1	316	*Solanum pennellii* XP_015075024.1	316	0.0	ITAG3.0	Chr05	7870548	7872027	-	Solyc05g014150
	Spe	XP_015075024.1	316	*Solanum tuberosum* XP_006341777.1	316	0.0	Spenn_v2.0	Chr05	8414586	8444408	-	Sopen05g009160
KCS3 - 3-ketoacyl-CoA synthase 3	*Sly*	XP_004251303	466	*Arabidopsis thaliana* NP_172251.1	478	0.0	ITAG3.0	Chr11	56422006	56423406	-	Solyc11g072990
		XP_004251302	464	*Arabidopsis thaliana* NP_172251.1	478	0.0	ITAG3.0	Chr11	53207039	53208433	-	Solyc11g072980
	Spe	XP_015058894.1	466	*Solanum tuberosum* XP_006363392.1	464	0.0	Spenn_v2.0	Chr11	66013470	66015325	-	Sopen11g030650
		XP_015058895.1	464	*Solanum tuberosum*	464	0.0	Spenn_v2.0	Chr11	66009234	66010755	-	Sopen11g030640

				XP_006363392.1								
KCS19 - 3-ketoacyl-CoA synthase 19	*Sly*	XP_004247624.1	513	*Nicotiana tomentosiformis* XP_009601634.1	517	0.0	ITAG3.0	Chr09	69144365	69146999	-	Solyc09g083050
		XP_004241035.1	486	*Nicotiana tomentosiformis* XP_009601634.1	517	0.0	ITAG3.0	Chr06	36851071	36852665	+	Solyc06g053870
		XP_004239114.1	493	*Nicotiana tomentosiformis* XP_009601634.1	517	0.0	ITAG3.0	Chr05	6280307	6282544	-	Solyc05g013207
TD - Threonine deaminase (dehydratase)	*Sly*	NP_001296095	595	*Nicotiana attenuata* XP_019250776.1	601	0.0	ITAG3.0	Chr09	2123903	2127996	+	Solyc09g008670
		NP_001234234	606	*Nicotiana attenuata* XP_019234171.1	607	0.0	ITAG3.0	Chr10	63636332	63642888	-	Solyc10g083760
		XP_004249785	592	*Nicotiana attenuata* XP_019234171.1	607	0.0	ITAG3.0	Chr10	63452102	63455329	-	Solyc10g083540
	Spe	XP_015086154.1	595	*Solanum tuberosum* XP_006339100.1	609	0.0	Spenn_v2.0	Chr09	2172890	2178371	+	Sopen09g003470
		XP_015055091.1	592	*Solanum tuberosum* XP_006339100.1	609	0.0	Spenn_v2.0	Chr10	80234880	80238074	-	Sopen10g033010
		XP_015055759.1	606	*Solanum tuberosum* XP_006339100.1	609	0.0	Spenn_v2.0	Chr10	80437205	80443489	-	Sopen10g033220

Supplementary Table S3. Distribution and localization of the conserved domains in the proteins involved in the acylsugar pathway in *Solanum lycopersicum* (Sly), *Solanum pennellii* (Spe) and their orthologs.

Protein families	Species	Name/ID	**Conserved domain**	**Domain ID**	**Start and End**	**E-value**
Acetyl-CoA synthase	***Sly***	Solyc02g094640	ACAS_N	PF16177	1 - 58	$4.2e^{-19}$
			AMP-binding	PF00501	59 – 507	$2.7e^{-96}$
			AMP-binding_C	PF13193	515 - 593	$1.6e^{-22}$
		Solyc07g017860	ACAS_N	PF16177	44 – 104	$5.7e^{-21}$
			AMP-binding	PF00501	106 – 553	$8.3e^{-97}$
			AMP-binding_C	PF13193	561 - 639	$1.4e^{-21}$
	Spe	Sopen02g039280	ACAS_N	PF16177	145 – 205	$1.7e^{-20}$
			AMP-binding	PF00501	206 - 579	$6.9e^{-78}$
		Sopen07g006650	ACAS_N	PF16177	44 – 104	$1.3e^{-21}$
			AMP-binding	PF00501	106 – 553	$9.1e^{-97}$
			AMP-binding_C	PF13193	561 - 639	$2e^{-22}$
	Ortholog in *Solanum tuberosum*	XP_006344535	ACAS_N	PF16177	51 – 111	$7.8e^{-22}$
			AMP-binding	PF00501	113 – 560	$7.4e^{-97}$
			AMP-binding_C	PF13193	568 - 646	$2e^{-22}$
		XP_006338753	ACAS_N	PF16177	148 – 208	$2.6e^{-20}$
			AMP-binding	PF00501	209 – 657	$1.7e^{-96}$
			AMP-binding_C	PF13193	665 - 743	$1.1e^{-22}$
AKR - Aldo keto reductase	***Sly***	Solyc00g015733	Aldo_ket_red	PF00248	20 - 286	$1.4e^{-49}$
		Solyc06g053585	Aldo_ket_red	PF00248	1 - 290	$3e^{-69}$
		Solyc09g082730	Aldo_ket_red	PF00248	4 - 291	$1.6e^{-46}$
		Solyc09g074310	Aldo_ket_red	PF00248	18 - 352	$2.3e^{-71}$
		Solyc09g011240	Aldo_ket_red	PF00248	20 - 288	$4.4e^{-51}$
		Solyc09g097960	Aldo_ket_red	PF00248	3 - 290	$3e^{-69}$

		Solyc03g093280	Aldo_ket_red	PF00248	16 - 287	$8.6e^{-80}$
		Solyc03g093270	Aldo_ket_red	PF00248	16 - 287	$1.6e^{-46}$
		Solyc11g067160	Aldo_ket_red	PF00248	74 - 379	$9.2e^{-59}$
	Spe	Sopen03g024070	Aldo_ket_red	PF00248	16 - 287	$5.2e^{-48}$
		Sopen03g024060	Aldo_ket_red	PF00248	16 - 287	$2.9e^{-46}$
		Sopen09g005990	Aldo_ket_red	PF00248	20 - 288	$4.3e^{-51}$
		Sopen01g026810	Aldo_ket_red	PF00248	1 - 288	$4.6e^{-73}$
	Ortholog in *Solanum tuberosum*	XP_006363582.1	Aldo_ket_red	PF00248	23 - 316	$3.8e^{-76}$
		XP_006363583.1	Aldo_ket_red	PF00248	6 - 252	$1.8e^{-60}$
		XP_006358247.1	Aldo_ket_red	PF00248	16 - 287	$2.1e^{-46}$
ALS (AHAS) - Acetolactate (acetohydroxyacid) synthase	***Sly***	Solyc03g044330	TPP_enzyme_N	PF02776	86 – 254	$6.7e^{-52}$
			TPP_enzyme_M	PF00205	278 – 411	$7.3e^{-44}$
			TPP_enzyme_C	PF02775	473 – 628	$5.5e^{-47}$
		Solyc06g059880	TPP_enzyme_N	PF02776	77 – 245	$3.2e^{-53}$
			TPP_enzyme_M	PF00205	269 – 402	$7.6e^{-42}$
			TPP_enzyme_C	PF02775	464 – 619	$1e^{-40}$
		Solyc07g061940	TPP_enzyme_N	PF02776	84 – 252	$2.3e^{-52}$
			TPP_enzyme_M	PF00205	276 – 409	$3.3e^{-44}$
			TPP_enzyme_C	PF02775	471 – 508	$2.1e^{-08}$
		Solyc11g008780	ACT	PF01842	90 - 154	$5.6e^{-12}$
			ALS_ss_C	PF10369	169 – 242	$1.1e^{-25}$
			ACT_5	PF13710	329 – 391	$3.2e^{-13}$
			ALS_ss_C	PF10369	402 – 475	$4.1e^{-25}$
		Solyc12g019310	ACT	PF01842	79 – 143	$1.1e^{-11}$
			ALS_ss_C	PF10369	158 – 231	$1.7e^{-26}$
			ACT_5	PF13710	320 - 381	$3.9e^{-11}$
	Spe	Sopen12g009610	ACT	PF01842	79 – 143	$1.4e^{-11}$
			ALS_ss_C	PF10369	158 –	$2.1e^{-26}$

					231	
			ACT_5	PF13710	320 – 382	$1.1e^{-11}$
			ALS_ss_C	PF10369	393 - 466	$2.1e^{-24}$
		Sopen11g004560	ACT	PF01842	86 – 150	$5.6e^{-12}$
			ALS_ss_C	PF10369	165 – 238	$7.7e^{-26}$
			ACT_5	PF13710	325 – 387	$3.2e^{-13}$
			ALS_ss_C	PF10369	398 – 471	$4e^{-25}$
		Sopen07g030210	TPP_enzyme_N	PF02776	84 – 252	$3.6e^{-52}$
			TPP_enzyme_M	PF00205	276 – 409	$9.2e^{-44}$
			TPP_enzyme_C	PF02775	471 – 626	$7.9e^{-47}$
		Sopen03g008440	TPP_enzyme_N	PF02776	86 – 254	$6.7e^{-52}$
			TPP_enzyme_M	PF00205	278 – 411	$7.3e^{-44}$
			TPP_enzyme_C	PF02775	473 - 628	$8.7e^{-47}$
	Ortholog in *Solanum tuberosum*	XP_006353111.1	ACT	PF01842	79 – 143	$1.4e^{-11}$
			ALS_ss_C	PF10369	158 – 231	$2e^{-26}$
			ACT_5	PF13710	320 – 382	$1.1e^{-11}$
			ALS_ss_C	PF10369	393 – 466	$2.1e^{-24}$
		XP_006361740.1	TPP_enzyme_N	PF02776	86 – 254	$6.7e^{-52}$
			TPP_enzyme_M	PF00205	278 – 411	$5.8e^{-43}$
			TPP_enzyme_C	PF02775	473 – 628	$5.7e^{-47}$
		XP_006348357.1	TPP_enzyme_N	PF02776	84 – 252	$3.6e^{-52}$
			TPP_enzyme_M	PF00205	276 – 409	$5.7e^{-43}$
			TPP_enzyme_C	PF02775	471 - 626	$5.3e^{-47}$
AT2 (AT4) – Acylsugar Acyltransferase 2 (4)	***Sly***	Solyc01g105580	Transferase	PF02458	1 - 428	$9.4e^{-71}$
		Solyc04g012020	Transferase	PF02458	7 - 433	$1.2e^{-64}$

	Spe	Sopen04g006140	Transferase	PF02458	7 - 433	$7.1e^{-63}$
AT3 – Acylsugar Acyltransferase 3	***Sly***	Solyc11g067270	Transferase	PF02458	2 - 419	$1.6e^{-63}$
		Solyc11g067330	Transferase	PF02458	124 - 433	$2.7e^{-34}$
		Solyc11g067340	Transferase	PF02458	113 - 433	$1.4e^{-37}$
		Solyc11g067350	Transferase	PF02458	229 - 433	$2.1e^{-21}$
		Solyc02g078510	Transferase	PF02458	189 - 331	0.00016
		Solyc07g043710	Transferase	PF02458	5 - 432	$1.6e^{-67}$
		Solyc07g043700	Transferase	PF02458	3 - 431	$7.2e^{-69}$
		Solyc07g043670	Transferase	PF02458	4 - 431	$7.6e^{-67}$
		Solyc08g075210	Transferase	PF02458	6 - 433	$5.8e^{-62}$
		Solyc08g075180	Transferase	PF02458	8 - 433	$1.6e^{-67}$
		Solyc08g014490	Transferase	PF02458	6 - 433	$6.1e^{-69}$
		Solyc02g081800	Transferase	PF02458	5 - 433	$9.7e^{-67}$
		Solyc11g069680	Transferase	PF02458	4 - 433	$6e^{-62}$
		Solyc02g081760	Transferase	PF02458	3 - 433	$2.8e^{-67}$
		Solyc02g081745	Transferase	PF02458	3 - 433	$1.9e^{-70}$
		Solyc02g081740	Transferase	PF02458	3 - 433	$4e^{-71}$
		Solyc05g039950	Transferase	PF02458	80 - 433	$8.4e^{-51}$
		Solyc11g067290	Transferase	PF02458	106 - 433	$6e^{-37}$
	Spe	Sopen12g002290	Transferase	PF02458	2 - 417	$9.9e^{-62}$
		Sopen11g026960	Transferase	PF02458	2 - 315	$1.4e^{-40}$
		Sopen11g027030	Transferase	PF02458	10 - 431	$2.1e^{-62}$
		Sopen10g030210	Transferase	PF02458	33 - 176	$3.1e^{-25}$
		Sopen08g023820	Transferase	PF02458	6 - 433	$2.4e^{-68}$
		Sopen08g005480	Transferase	PF02458	6 - 431	$5.6e^{-68}$
		Sopen08g023810	Transferase	PF02458	8 - 431	$3e^{-65}$
		Sopen07g023290	Transferase	PF02458	7 - 432	$6.2e^{-71}$
		Sopen07g023230	Transferase	PF02458	4 - 431	$4.5e^{-64}$
		Sopen07g023280	Transferase	PF02458	3 - 431	$2.7e^{-69}$
		Sopen05g024660	Transferase	PF02458	3 - 433	$7.6e^{-72}$
		Sopen06g030010	Transferase	PF02458	6 - 432	$5.6e^{-65}$
		Sopen02g026350	Transferase	PF02458	3 - 433	$2.6e^{-73}$
		Sopen02g026400	Transferase	PF02458	5 - 431	$2.1e^{-67}$
		Sopen11g027040	Transferase	PF02458	4 - 433	$2.3e^{-59}$
	Ortholog in *Solanum tuberosum*	XP_006357899.1	Transferase	PF02458	6 - 420	$1.4e^{-67}$
		XP_015164920.1	Transferase	PF02458	2 - 416	$1.2e^{-60}$
BCAT - Branched-chain aminotransferase 2	***Sly***	Solyc12g088220	Aminotran_4	PF01063	99 - 337	$2.3e^{-33}$
		Solyc07g021630	Aminotran_4	PF01063	102 - 340	$8.6e^{-34}$

		Solyc00g178340	Aminotran_4	PF01063	102 - 340	$3.9e^{-34}$
		Solyc04g077240	Aminotran_4	PF01063	207 - 240	$9.8e^{-06}$
	Spe	Sopen04g030820	Aminotran_4	PF01063	97 - 335	$9.5e^{-38}$
		Sopen04g030830	Aminotran_4	PF01063	86 - 324	$2.5e^{-37}$
		Sopen07g011210	Aminotran_4	PF01063	102 - 340	$9.8e^{-34}$
	Ortholog in *Solanum tuberosum*	XP_006356816.2	Aminotran_4	PF01063	86 - 324	$8.1e^{-38}$
		XP_006345331.1	Aminotran_4	PF01063	102 - 340	$3.9e^{-34}$
BCAT - Branched-chain aminotransferase	***Sly***	Solyc01g098700	Aminotran_4	PF01063	292 - 517	$1.8e^{-45}$
	Spe	Sopen01g042240	Aminotran_4	PF01063	292 - 519	$4.2e^{-46}$
	Ortholog in *Solanum tuberosum*	XP_006361872.1	Aminotran_4	PF01063	292 - 519	$1.1e^{-44}$
BCAT - Branched-chain aminotransferase 5	***Sly***	Solyc03g043880	Aminotran_4	PF01063	136 - 374	$5.5e^{-42}$
		Solyc02g091970	Aminotran_4	PF01063	95 - 333	$2.2e^{-42}$
	Spe	Sopen02g036540	Aminotran_4	PF01063	135 - 373	$2.9e^{-42}$
		Sopen03g007690	Aminotran_4	PF01063	136 - 374	$5.5e^{-42}$
	Ortholog in *Arabidopsis thaliana*	NP_201379.2	Aminotran_4	PF01063	133 - 371	$7e^{-41}$
BCKD E1a - Branched-chain keto acid dehydrogenase E1-alpha subunit	***Sly***	Solyc06g059840.2.1	E1_dh	PF00676	118 - 418	$3.5e^{-96}$
		Solyc05g056480.2.1	E1_dh	PF00676	129 - 429	$1.8e^{-94}$
		Solyc04g063350.2.1	E1_dh	PF00676	134 - 434	$1.4e^{-94}$
	Spe	Sopen04g026270	E1_dh	PF00676	134 - 434	$1.7e^{-94}$
		Sopen05g034880	E1_dh	PF00676	129 - 429	$6.4e^{-95}$
		Sopen06g019920	E1_dh	PF00676	104 - 404	$2.5e^{-97}$
		Sopen04g001100	E1_dh	PF00676	118 - 408	$1.5e^{-93}$
		Sopen06g019930	E1_dh	PF00676	107 - 407	$2.7e^{-95}$
		Sopen05g002470	E1_dh	PF00676	66 - 363	$2.3e^{-115}$
	Ortholog in *Solanum tuberosum*	XP_015168276.1	E1_dh	PF00676	55 - 355	$1e^{-94}$
		XP_015168276.1	E1_dh	PF00676	55 - 355	$1e^{-94}$
		XP_006356334.1	E1_dh	PF00676	133 - 433	$1.7e^{-94}$
BCKD E1b - Branched-chain keto acid dehydrogenase E1 beta subunit	***Sly***	Solyc01g028900	Transket_pyr	PF02779	36 – 214	$2.3e^{-44}$
			Transketolase_C	PF02780	228 - 348	$1.3e^{-35}$
		Solyc06g072580	Transket_pyr	PF02779	37 – 215	$2.8e^{-48}$
			Transketolase_C	PF02780	232 - 354	$1.2e^{-42}$
		Solyc05g024160	Transket_pyr	PF02779	36 – 214	$2.7e^{-46}$
			Transketolase_C	PF02780	231 - 353	$8e^{-43}$
	Spe	Sopen01g017080	Transket_pyr	PF02779	36 – 214	$1.2e^{-44}$
			Transketolase_C	PF02780	228 - 348	$1.4e^{-35}$

		Sopen06g028930	Transket_pyr	PF02779	37 – 215	$2.8e^{-48}$
			Transketolase_C	PF02780	232 - 354	$1.2e^{-42}$
		Sopen05g018850	Transket_pyr	PF02779	37 – 215	$1.2e^{-46}$
			Transketolase_C	PF02780	232 - 354	$8e^{-43}$
		Sopen03g028430	Transket_pyr	PF02779	31 – 209	$1.6e^{-47}$
			Transketolase_C	PF02780	226 - 348	$1e^{-42}$
	Ortholog in *Solanum tuberosum*	XP_006359200.1	Transket_pyr	PF02779	36 – 214	$1.5e^{-44}$
			Transketolase_C	PF02780	228 - 348	$7.8e^{-36}$
		XP_015164279.1	Transket_pyr	PF02779	37 – 215	$2.7e^{-48}$
			Transketolase_C	PF02780	232 - 354	$1.5e^{-42}$
BCKD E2 - Branched-chain keto acid dehydrogenase E2	***Sly***	Solyc01g066520	Biotin_lipoyl	PF00364	90 – 163	$1.6e^{-18}$
			E3_binding	PF02817	206 – 240	$1.3e^{-13}$
			2-oxoacid_dh	PF00198	272 - 502	$8.3e^{-78}$
	Spe	Sopen01g028100	Biotin_lipoyl	PF00364	90 – 163	$1.6e^{-18}$
			E3_binding	PF02817	206 – 240	$1.2e^{-13}$
			2-oxoacid_dh	PF00198	272 - 502	$9.5e^{-78}$
	Ortholog in *Solanum tuberosum*	NP_001305524.1	Biotin_lipoyl	PF00364	90 – 163	$1.3e^{-17}$
			E3_binding	PF02817	206 – 240	$1.9e^{-13}$
			2-oxoacid_dh	PF00198	272 - 502	$2.7e^{-77}$
DHAD – Dihydroxyacid dehydratase	***Sly***	Solyc12g043020	ILVD_EDD	PF00920	92 - 611	$4e^{-218}$
		Solyc05g053540	ILVD_EDD	PF00920	88 - 607	$6.2e^{-217}$
	Spe	Sopen12g022260	ILVD_EDD	PF00920	97 - 616	$1.2e^{-217}$
		Sopen05g032060	ILVD_EDD	PF00920	88 - 607	$8.1e^{-217}$
	Ortholog in *Solanum tuberosum*	XP_006346583.1	ILVD_EDD	PF00920	96 - 615	$6.2e^{-217}$
		XP_006349441.1	ILVD_EDD	PF00920	88 - 607	$1.e^{-217}$
Dihydrolipoyl dehydrogenase 1	***Sly***	Solyc05g053100	Pyr_redox_2	PF07992	85 - 420	$8.9e^{-60}$
			Pyr_redox_dim	PF02852	439 - 552	$6.2e^{-32}$
	Spe	Sopen05g031610	Pyr_redox_2	PF07992	85 - 420	$2.6e^{-59}$
			Pyr_redox_dim	PF02852	439 - 552	$1.5e^{-31}$
		XP_015076245.1	Pyr_redox_2	PF07992	85 - 420	$2.6e^{-59}$
			Pyr_redox_dim	PF02852	439 - 552	$1.5e^{-31}$
	Ortholog in *Solanum tuberosum*	XP_015167962.1	Pyr_redox_2	PF07992	84 – 419	$8.7e^{-60}$
			Pyr_redox_dim	PF02852	438 - 551	$1.2e^{-31}$
Dihydrolipoyl dehydrogenase 2	***Sly***	Solyc01g100360	Pyr_redox_2	PF07992	89 – 419	$2.2e^{-59}$

			Pyr_redox_dim	PF02852	438 - 551	$8.3e^{-31}$
	Spe	Sopen01g043880	Pyr_redox_2	PF07992	89 – 419	$2.2e^{-59}$
			Pyr_redox_dim	PF02852	438 - 551	$1.1e^{-30}$
	Ortholog in *Solanum tuberosum*	XP_006344750.1	Pyr_redox_2	PF07992	89 – 419	$2.2e^{-59}$
			Pyr_redox_dim	PF02852	438 - 551	$8.3e^{-31}$
Dihydrolipoyl dehydrogenase mitochondrial	***Sly***	Solyc12g099100	Pyr_redox_2	PF07992	41 – 366	$1.9e^{-69}$
			Pyr_redox_dim	PF02852	385 - 494	$3.9e^{-40}$
		Solyc05g053300	Pyr_redox_2	PF07992	37 – 362	$3.5e^{-71}$
			Pyr_redox_dim	PF02852	381 - 490	$5.8e^{-40}$
	Spe	Sopen12g033810	Pyr_redox_2	PF07992	41 – 366	$1.3e^{-69}$
			Pyr_redox_dim	PF02852	385 - 494	$3.8e^{-40}$
		Sopen05g031810	Pyr_redox_2	PF07992	37 – 362	$3.4e^{-71}$
			Pyr_redox_dim	PF02852	381 - 490	$5.7e^{-40}$
	Ortholog in *Solanum tuberosum*	NP_001275339.1	Pyr_redox_2	PF07992	41 – 366	$3e^{-70}$
			Pyr_redox_dim	PF02852	385 - 494	$3.8e^{-40}$
IPDS - Isopropylmalate dehydratase/ IPMI - Isopropylmalate isomerase	***Sly***	Solyc03g005730	Aconitase	PF00330	71 - 499	$8.2e^{-79}$
		Solyc09g090900	Aconitase	PF00330	67 - 495	$3.1e^{-78}$
		Solyc06g060790	Aconitase_C	PF00694	123 - 195	$3.9e^{-18}$
	Spe	Sopen03g001740	Aconitase	PF00330	71 - 499	$8.2e^{-79}$
		Sopen09g033880	Aconitase	PF00330	67 - 495	$8.9e^{-78}$
		Sopen06g020930	Aconitase_C	PF00694	125 - 194	$4.1e^{-18}$
	Ortholog in *Solanum tuberosum*	XP_006356071.1	Aconitase	PF00330	71 - 499	$8.2e^{-79}$
		XP_006367458.1	Aconitase_C	PF00694	130 - 195	$1.3e^{-17}$
IPMD - Isopropylmalate dehydrogenase	***Sly***	Solyc05g009030	Iso_dh	PF00180	45 - 394	$8.1e^{-136}$
		Solyc08g077920	Iso_dh	PF00180	38 - 365	$1.2e^{-104}$
		Solyc08g077930	Iso_dh	PF00180	38 - 365	$5.2e^{-105}$
	Spe	Sopen05g004770	Iso_dh	PF00180	45 - 394	$9.6e^{-136}$
		Sopen08g026440	Iso_dh	PF00180	38 - 365	$1.2e^{-104}$
	Ortholog in *Solanum tuberosum*	XP_006344159.1	Iso_dh	PF00180	44 - 393	$7.2e^{-135}$
		XP_006359219.1	Iso_dh	PF00180	38 - 365	$3.7e^{-104}$
IPMSA - Isopropylmalate synthase A	***Sly***	Solyc08g014240	HMGL-like	PF00682	15 - 295	$2.8e^{-90}$
		Solyc08g014230	HMGL-like	PF00682	15 - 331	$2e^{-91}$
		Solyc08g014130	HMGL-like	PF00682	72 – 352	$8.5e^{-94}$
			LeuA_dimer	PF08502	451 - 596	$4.2e^{-42}$
	Spe	Sopen08g005060	HMGL-like	PF00682	51 - 331	$3.1e^{-91}$
			LeuA_dimer	PF08502	426 - 571	$5.9e^{-42}$
		Sopen08g005140	HMGL-like	PF00682	51 - 331	$1.8e^{-90}$

		Sopen10g006110	HMGL-like	PF00682	51 - 331	$7.3e^{-91}$
		Sopen08g005150	HMGL-like	PF00682	15 - 295	$1.7e^{-89}$
	Ortholog in *Solanum tuberosum*	XP_015168011.1	HMGL-like	PF00682	70 - 351	$2.3e^{-92}$
			LeuA_dimer	PF08502	450 - 595	$5.9e^{-42}$
IPMSB - Isopropylmalate synthase B	***Sly***	Solyc06g053400	HMGL-like	PF00682	70 – 350	$1.7e^{-93}$
			LeuA_dimer	PF08502	449 - 595	$1.5e^{-38}$
	Spe	Sopen06g018460	HMGL-like	PF00682	70 – 350	$2.3e^{-91}$
			LeuA_dimer	PF08502	449 - 594	$9.3e^{-39}$
	Ortholog in *Solanum tuberosum*	XP_006350708.1	HMGL-like	PF00682	70 – 350	$4.8e^{-93}$
			LeuA_dimer	PF08502	449 - 593	$5.2e^{-39}$
Isovaleryl-CoA dehydrogenase 1, mitochondrial / Methylacyl-CoA dehydrogenase	***Sly***	Solyc06g073560	Acyl-CoA_dh_N	PF02771	35 – 149	$1.8e^{-35}$
			Acyl-CoA_dh_M	PF02770	153 – 248	$6.2e^{-26}$
			Acyl-CoA_dh_1	PF00441	260 - 409	$4.2e^{-44}$
		Solyc11g069180	Acyl-CoA_dh_N	PF02771	35 – 149	$2e^{-37}$
			Acyl-CoA_dh_M	PF02770	153 – 248	$1.6e^{-24}$
			Acyl-CoA_dh_1	PF00441	260 - 409	$2.9e^{-41}$
	Spe	Sopen06g029920	Acyl-CoA_dh_N	PF02771	35 – 149	$1.8e^{-35}$
			Acyl-CoA_dh_M	PF02770	153 – 248	$6.2e^{-26}$
			Acyl-CoA_dh_1	PF00441	260 - 409	$8.2e^{-44}$
		Sopen11g027920	Acyl-CoA_dh_N	PF02771	35 – 149	$1.9e^{-37}$
			Acyl-CoA_dh_M	PF02770	153 – 248	$1.6e^{-24}$
			Acyl-CoA_dh_1	PF00441	260 - 409	$8.5e^{-41}$
	Ortholog in *Solanum tuberosum*	NP_001275043.1	Acyl-CoA_dh_N	PF02771	35 – 149	$6.8e^{-35}$
			Acyl-CoA_dh_M	PF02770	153 – 248	$2.9e^{-26}$
			Acyl-CoA_dh_1	PF00441	260 - 409	$3.3e^{-44}$
KARI - Ketoacid (Acetohydroxy-acid) reductoisomerase, chloroplastic	***Sly***	Solyc07g053280	IlvN	PF07991	119 – 299	$8.5e^{-31}$
			IlvC	PF01450	305 – 451	$7.8e^{-34}$
			IlvC	PF01450	460 - 545	$3.3e^{-08}$
		Solyc12g010840	IlvN	PF07991	116 – 296	$1.1e^{-30}$
			IlvC	PF01450	302 –	$3.5e^{-34}$

					448	
			IlvC	PF01450	457 - 541	$3.7e^{-08}$
	Spe	Sopen07g027240	IlvN	PF07991	119 – 299	$8.4e^{-31}$
			IlvC	PF01450	305 – 451	$7.8e^{-34}$
			IlvC	PF01450	460 - 545	$3.2e^{-08}$
		Sopen12g006200	IlvN	PF07991	116 – 296	$1e^{-30}$
			IlvC	PF01450	302 – 448	$3.5e^{-34}$
			IlvC	PF01450	457 - 541	$3.7e^{-08}$
	Ortholog in *Solanum tuberosum*	XP_006350031.1	IlvN	PF07991	115 – 295	$1.1e^{-30}$
			IlvC	PF01450	301 – 447	$5.5e^{-34}$
			IlvC	PF01450	456 - 540	$3.7e^{-08}$
KAS I- Ketoacyl-ACP synthase I	***Sly***	Solyc08g016170	ketoacyl-synt	PF00109	55 – 302	$7.5e^{-60}$
			Ketoacyl-synt_C	PF02801	310 - 423	$2.6e^{-32}$
		Solyc02g070790	ketoacyl-synt	PF00109	56 - 303	$1.4e^{-57}$
			Ketoacyl-synt_C	PF02801	311 – 424	$4.9e^{-31}$
		Solyc08g082620	ketoacyl-synt	PF00109	72 - 319	$1.2e^{-53}$
			Ketoacyl-synt_C	PF02801	327 - 441	$3.6e^{-30}$
	Spe	Sopen02g019880	ketoacyl-synt	PF00109	56 – 303	$2.6e^{-57}$
			Ketoacyl-synt_C	PF02801	311 - 424	$4.8e^{-31}$
		Sopen08g006520	ketoacyl-synt	PF00109	55 – 302	$7.5e^{-60}$
			Ketoacyl-synt_C	PF02801	310 - 423	$2.6e^{-32}$
		Sopen08g030860	ketoacyl-synt	PF00109	72 – 319	$1.3e^{-53}$
			Ketoacyl-synt_C	PF02801	327 - 441	$6.6e^{-31}$
	Ortholog in *Solanum tuberosum*	XP_006365563.1	ketoacyl-synt	PF00109	56 – 303	$2.4e^{-57}$
			Ketoacyl-synt_C	PF02801	311 - 424	$4.8e^{-31}$
		XP_006343829.1	ketoacyl-synt	PF00109	72 – 319	$5.1e^{-54}$
			Ketoacyl-synt_C	PF02801	327 - 441	$4.8e^{-31}$
KAS II- Ketoacyl-ACP synthase II	***Sly***	Solyc12g009260	ketoacyl-synt	PF00109	67 – 313	$2.3e^{-59}$
			Ketoacyl-synt_C	PF02801	321 - 435	$2.8e^{-35}$
		Solyc03g122120	ketoacyl-synt	PF00109	144 – 390	$3.1e^{-55}$

			Ketoacyl-synt_C	PF02801	398 - 512	$1.1e^{-33}$
	Spe	Sopen07g021960	ketoacyl-synt	PF00109	128 – 374	$1.9e^{-60}$
			Ketoacyl-synt_C	PF02801	382 - 496	$7.9e^{-34}$
		Sopen03g040910	ketoacyl-synt	PF00109	144 – 390	$8.9e^{-56}$
			Ketoacyl-synt_C	PF02801	398 - 512	$1.1e^{-33}$
	Ortholog in *Solanum tuberosum*	XP_006353782.1	ketoacyl-synt	PF00109	128 – 374	$5e^{-61}$
			Ketoacyl-synt_C	PF02801	382 - 496	$3e^{-34}$
KAS III- Ketoacyl-ACP synthase III	***Sly***	Solyc03g097470	ACP_syn_III	PF08545	201 – 280	$1.6e^{-28}$
			ACP_syn_III_C	PF08541	341 - 430	$4e^{-36}$
		Solyc08g006560	ACP_syn_III	PF08545	150 – 229	$1.7e^{-27}$
			ACP_syn_III_C	PF08541	290 - 380	$3.6e^{-33}$
	Spe	Sopen03g028240	ACP_syn_III	PF08545	201 – 280	$1.6e^{-28}$
			ACP_syn_III_C	PF08541	341 - 430	$4e^{-36}$
		Sopen08g002520	ACP_syn_III	PF08545	150 – 229	$1.8e^{-27}$
			ACP_syn_III_C	PF08541	290 - 380	$4e^{-33}$
	Ortholog in *Solanum tuberosum*	XP_006347624.1	ACP_syn_III	PF08545	201 – 280	$1.6e^{-28}$
			ACP_syn_III_C	PF08541	341 - 430	$1.3e^{-35}$
KAS - Ketoacyl-ACP synthase mitochondrial	***Sly***	Solyc07g049570	ketoacyl-synt	PF00109	30 – 296	$2.5e^{-55}$
			Ketoacyl-synt_C	PF02801	304 - 421	$1.2e^{-36}$
	Spe	Sopen07g024970	ketoacyl-synt	PF00109	30 – 296	$3.7e^{-55}$
			Ketoacyl-synt_C	PF02801	304 - 421	$5.8e^{-37}$
	Ortholog in *Solanum tuberosum*	XP_006357986.1	ketoacyl-synt	PF00109	30 – 296	$1.9e^{-54}$
			Ketoacyl-synt_C	PF02801	304 - 421	$4.5e^{-36}$
		XP_006357987.1	ketoacyl-synt	PF00109	30 - 294	$2.8e^{-51}$
			Ketoacyl-synt_C	PF02801	302 - 419	$4.5e^{-36}$
KCR2 - 3-ketoacyl/oxoacyl-CoA reductase 2	***Sly***	Solyc05g014150	adh_short	PF00106	51 - 210	$2.8e^{-33}$
	Spe	Sopen05g009160	adh_short	PF00106	55 - 255	$5.9e^{-43}$
	Ortholog in *Solanum tuberosum*	XP_006341777.1	adh_short	PF00106	55 - 255	$5.6e^{-43}$
KCS3 - 3-ketoacyl-CoA	***Sly***	Solyc11g072990	FAE1_CUT1_RppA	PF08392	24 – 314	$2.4e^{-100}$

synthase			ACP_syn_III_C	PF08541	331 - 416	$2.5e^{-13}$
		Solyc11g072980	FAE1_CUT1_RppA	PF08392	24 – 314	$7.1e^{-111}$
			ACP_syn_III_C	PF08541	328 - 413	$9e^{-14}$
	Spe	Sopen11g030650	FAE1_CUT1_RppA	PF08392	1 – 268	$1.7e^{-100}$
			ACP_syn_III_C	PF08541	285 - 310	$2.1e-^{13}$
		Sopen11g030640	FAE1_CUT1_RppA	PF08392	1 – 268	$1.6e^{-98}$
			ACP_syn_III_C	PF08541	281 - 367	$8.2e^{-14}$
	Ortholog in *Solanum tuberosum*	XP_006363390.1	FAE1_CUT1_RppA	PF08392	24 – 324	$1.1e^{-110}$
			ACP_syn_III_C	PF08541	330 - 415	$8.4e-^{14}$
KCS19 - 3-ketoacyl-CoA synthase 19	***Sly***	Solyc09g083050	FAE1_CUT1_RppA	PF08392	93 – 382	$9.7e^{-143}$
			ACP_syn_III_C	PF08541	396 - 479	$6.1e^{-10}$
		Solyc06g053870	FAE1_CUT1_RppA	PF08392	73 – 359	$4.5e^{-118}$
			ACP_syn_III_C	PF08541	372 - 457	$7.6e^{-13}$
		Solyc05g013207	FAE1_CUT1_RppA	PF08392	83 – 369	$7.4e^{-118}$
			ACP_syn_III_C	PF08541	382 - 467	$6.1e^{-12}$
	Ortholog in *Nicotiana tomentosiformis*	XP_009601634.1	FAE1_CUT1_RppA	PF08392	97 – 386	$5.3e^{-144}$
			ACP_syn_III_C	PF08541	400 - 483	$7.2e^{-10}$
TD - Threonine deaminase (dehydratase)	***Sly***	Solyc09g008670	PALP	PF00291	106 – 397	$1.4e^{-76}$
			Thr_dehydrat_C	PF00585	410 – 500	$2e^{-27}$
			Thr_dehydrat_C	PF00585	504 - 593	$3.9e^{-26}$
		Solyc10g083760	PALP	PF00291	117 – 409	$2.5e^{-85}$
			Thr_dehydrat_C	PF00585	422 – 512	$1.2e^{-22}$
			Thr_dehydrat_C	PF00585	516 - 605	$1.3e^{-22}$
		Solyc10g083540	PALP	PF00291	103 – 395	$9.5e^{-80}$
			Thr_dehydrat_C	PF00585	408 – 498	$5.1e^{-21}$
			Thr_dehydrat_C	PF00585	503 - 591	$5e^{-19}$
	Spe	Sopen09g003470	PALP	PF00291	68 – 359	$1.7e^{-75}$
			Thr_dehydrat_C	PF00585	372 – 462	$1.8e^{-27}$
			Thr_dehydrat_C	PF00585	466 - 555	$1.3e^{-25}$

		Sopen10g033010	PALP	PF00291	103 – 395	$2.9e^{-80}$
			Thr_dehydrat_C	PF00585	408 – 498	$3.3e^{-21}$
			Thr_dehydrat_C	PF00585	503 - 591	$1e^{-19}$
		Sopen10g033220	PALP	PF00291	117 – 409	$2.5e^{-85}$
			Thr_dehydrat_C	PF00585	422 – 512	$1.1e^{-21}$
			Thr_dehydrat_C	PF00585	516 - 605	$4.9e^{-23}$
	Ortholog in *Solanum tuberosum*	XP_006339100.1	PALP	PF00291	120 – 412	$7.3e^{-85}$
			Thr_dehydrat_C	PF00585	425 – 515	$9.6e^{-23}$
			Thr_dehydrat_C	PF00585	519 - 608	$5.1e^{-23}$
		XP_006366786.1	PALP	PF00291	107 – 398	$3.7e^{-75}$
			Thr_dehydrat_C	PF00585	411 – 501	$4.4e^{-29}$
			Thr_dehydrat_C	PF00585	505 - 594	$2.2e^{-24}$

Supplementary Table S4. Statistical comparisons between *Solanum lycopersicum* (Sly) and *Solanum pennellii* (Spe) genotypes related to the BCKD E2, IPMSA and TD genes.

Genotypes	BCKD E2	IPMSA	TD
	p-value		
Sly x Spe	0.000*	0.000*	0.986

*$p<0.05$.

Supplementary Table S5. Statistical data of the *Solanum lycopersicum* (Sly) and *Solanum pennellii* (Spe) genotypes at 30, 60 and 90 days related to the *BCKD E2* gene.

Genotype		Sly			Spe		
Genotype	Time	30	60	90	30	60	90
Sly	30		0.340	0.222	0.014*	0.000*	0.000*
	60			0.863	0.006*	0.001*	0.004*
	90				0.040*	0.006*	0.004*
Spe	30					0.063	0.258
	60						0.730
	90						

*$p<0.05$.

Supplementary Table S6. Statistical data of the *Solanum lycopersicum* (Sly) and *Solanum pennellii* (Spe) genotypes at 30, 60 and 90 days related to the *IPMSA* gene.

Genotype		Sly			Spe		
Genotype	Time	30	60	90	30	60	90
Sly	30		0.136	0.863	0.000*	0.000*	0.000*
	60			0.094	0.000*	0.000*	0.000*
	90				0.004*	0.004*	0.004*
Spe	30					0.387	0.006*
	60						0.024*
	90						

*$p<0.05$.

Supplementary Table S7. Statistical data of the *Solanum lycopersicum* (Sly) and *Solanum pennellii* (Spe) genotypes at 30, 60 and 90 days related to the *TD* gene.

Genotype		Sly			Spe		
Genotype	Time	30	60	90	30	60	90
Sly	30		0.222	0.546	0.796	0.003*	0.490
	60			0.190	0.040*	0.222	0.063
	90				0.436	0.000*	0.113
Spe	30					0.014*	0.796
	60						0.000*
	90						

*$p<0.05$.

APÊNDICE IV - SUPPLEMENTARY TABLES - RESULTADOS COMPLEMENTARES - Article: Description of acylsugar pathway, miRNA pathway and miRNA molecules in seven tomato species for submission in Molecular Genetics and Genomics Journal

Supplementary Table S1. Putative AGO and DCL proteins predicted in *Solanum galapagense* (Sga), *Solanum peruvianum* (Spr), *Solanum chilense* (Sch), *Solanum pimpinellifolium* LA0480 (SpiLA0480), *Solanum pimpinellifolium* LA1589 (SpiLA1589).

Protein families	Protein	Species	Protein sequence	Size
Argonaute	**AGO1**	*Sly*	>NP_001266057.1_Solanum_lycopersicum_Solyc06g072300 MVRKRRTDVPGGAESSESHETGGGRGGVQRPPPQQQQGGGRGSGPQRGGYGGRGGGGAPRGGIAPQQSYGGPPEYYQQGRGTQQYQRGGGQPQRRGGIG GRGAPSGGSSRPPVPELHQATETPHQPVPYGRPAETYSEAGSSSQPPEPMTHQVTQQFQQIAVQPEAGASQAIPPVSSKSMRFPLRPGKGSNGTRCIVKANHFFA ELPDKDLHQYDVSITPEVASRGVNRAVMEQLVKLYRESHLGKRLPAYDGRKSLYTAGPLPFVQKDFKITLLDDDDGPGGARREREFKVVIKLAARADLHHLGMFLQ GRQADAPQEALQVLDIVLRELPTSRYCPVGRSFYSPDLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTAFIEPLPVIEFVSQLLNRDISSRPLSDADRVKIK KALRGVKVEVTHRGNMRRKYRISGLTSQATRELTFPVDERGTMKAVVEYFRETYGFVIQHTQLPCLQVGNTQRPNYLPMEVCKIVEGQRYSKRLNERQITALLKVTC QRPQERENDILQTVRHNAYSDDPYAREFGIKISEKLAQVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDSVARGFCSELA QMCMISGMIFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPNGRELDLLIVILPDNNGSLYGDLKRICETDLGIVSQCCLTKHVFKMSKQYLANVSLKINVKVGGR NTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYKTWQDPTRGTVTGGMIKELLISFRRATGQKPQRIIFY RDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDE NNFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAPYRGGVGAVGRSTRAPGVGAAVRPLPALKENVKRVMFYC	1054 aa
			>NP_001266261.2_Solanum_lycopersicum_Solyc03g098280 MARKRRSELPGSGESSGSQETVGGQGRGQYPPQQQQEGGYQGGGQGRGMRPPPQHQQQLGGYQGGGQGRGQRPPQQHQHEGGYQGGGQGRGMRPPPQ QSQQEGGYQGGGQGRGQRPPQQLQQEGGYQGGGRGWRPQQGGYGGRGSGGAPRGGMAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRG APSGGPSRPPIPELHQATTQTQHQAVMTTQPITCGRPADTSMEVGSSSEPPEMSALQVTQQFQQLAVQPEAAATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANH FFAELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPLPFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMF LEGRQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRV KIKKALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQHTQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKV TCQRPQERERDILETVKHNAYAEDKYAKEFGIKISDKLAQVEARILPPPWLKYHDNGREKDCLPQVGQWNMMNKKMVNGGTVANWICINFSRNVQDTVAHGFCSE LAQMCGISGMNFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPLSKELDLLVAILPDNNGSLYGDLKRICETDLGVVSQCCLTKHVFKMSKQYLANVALKINVKV GGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYTTRQDPVKGTVSGGMIKDLLISFRRATGQKPQR IIFYRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLW DENKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAGRGVGAGAAGKNTRAPGAGSAVRPLPALKDNVKRVMFYC	11522 aa
		Spe	>XP_015079116_Solanum_pennellii_Sopen06g028670 MVRKRRTDVPGGAESSESHETGGGRGGVQRPPQQQQGGGRGSGPQRGGYGGRGGGGAPRGGMAPQQSYGGSPEYYQQGRGTQQYQRGGGQPQRRGGIG GRGAPSGGSSRPPVPELHQATETPHQPVPYGRPAETYSEAGSSSQPPEPMTQQVTQQFQQLAVQPEAGASQAIPPVSSKSMRFPLRPGKGSNGTRCIVKANHFF AELPDKDLHQYDVSITPEVASRGVNRAVMEQLVKLYRESHLGKRLPAYDGRKSLYTAGPLPFVQKDFKITLLDDDDDGPGGARREREFKVVIKLAARADLHHLGMFLQ GRQADAPQEALQVLDIVLRELPTSRYCPVGRSFYSPDLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTAFIEPLPVIEFVSQLLNRDISSRPLSDADRVKIK KALRGVKVEVTHRGNMRRKYRISGLTSQATRELTFPVDERGTMKAVVEYFRETYGFVIQHTQLPCLQVGNTQRPNYLPMEVCKIVEGQRYSKRLNERQITALLKVTC QRPQERENDILQTVRHNAYSDDPYAREFGIKISEKLAQVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDSVARGFCSELA QMCMISGMIFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPNGRELDLLIVILPDNNGSLYGDLKRICETDLGIVSQCCLTKHVFKMSKQYLANVSLKINVKVGGR NTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYKTWQDPTRGTVTGGMIKELLISFRRATGQKPQRIIFY RDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDE NNFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAPYRGGVGAVGRSTRAPGAGAAVRPLPALKENVKRVMFYC	1053 aa
			>XP_015069669_Solanum_pennellii_Sopen03g028990 MVRKRRTELPGSGESSGSQETVGGQGRGQYPPQQQQQGGYQGGGQGRGMRPPPQHQQQLGGYQGGGQGRGQRPPQQHQHEGGYQGGGQGRGMGPPPQ QSQQEGGYQGGGQGRGQRPPQQLQQEGGYQGGGRGWRPQQGGYGGRGSGGAPRGGMAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRG APSGGPSRPPIPELHQATTQTQHQAVMTTQPITYGRPADTSMEVGSSSEPPEMSALQVTQQFQQLAVQPEAAATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANH FFAELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPLPFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMF LEGRQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRV KIKKALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQHTQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKV TCQRPQERERDILETVKHNAYAEDKYAKEFGIKISDKLAQVEARILPPPWLKYHDNGREKDCLPQVGQWNMMNKKMVNGGTVANWICINFSRNVQDTVAHGFCSE LAQMCGISGMNFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPLSKELDLLVAILPDNNGSLYGDLKRICETELGVVSQCCLTKHVFKMSKQYLANVALKINVKV GGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYTTKQDPVKGTVSGGMIKDLLISFRRATGQKPQR	1152 aa

			IIFYRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLW DENKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAGRGVGAGAAGRNTRAPGAGSAVRPLPALKDNVKRVMFYC	
		Sga	>Sga_Solyc06g072300_NM_001279128.1_scaffold43013_12.5_contig4_1036_aa MVRKRRTDVPGGAESSESHETGGGRGGVQRPPPQQQQGGGRGSGPQRGGYGGRGGGGAPRGGIAPQQSYGGPPEYYQQGRGTQQYQRGGGQPQRRGGIG GRGAPSGGSSRPPVPELHQATETPHQPVPYGRPAETYSEAGSSSQPPEPMTHQVTQQFQQIAVQPEAGASQAIPPVSSKSMRFPLRPGKGSNGTRCIVKANHFFA ELPDKDLHQYDVSITPEVASRGVNRAVMEQLVKLYRESHLGKRLPAYDGRKSLYTAGPLPFVQKDFKITLLDDDDGPGGARREREFKVVIKLAARADLHHLGMFLQ GRQADAPQEALQVLDIVLRELPTSRYCPVGRSFYSPDLGRRQPLGVGLESWRGFYQSIRPTQMGLSLNIDMSSTAFIEPLPVIEFVSQLLNRDISSRPLSDADRVKIK KALRGVKVEVTHRGNMRRKYRISGLTSQATRELTFPVDERGTMKAVVEYFRETYGFVIQHTQLPCLQVGNTQRPNYLPMEVCKIVEGQRYSKRLNERQITALLKVTC QRPQERENDILQTVRHNAYSDDPYAREFGIKISEKLAQVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDSVARGFCSELA QMCMISGMIFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPNGRELDLLIVILPDNNGSLYGDLKRICETDLGIVSQCCLTKHVFKMSKQYLANVSLKINVKVGGR NTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYKTWQDPTRGTVTGGMIKELLISFRRATGQKPQRIIFY RDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDE NNFSADGLQSLTNNLCYRYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAPYRGGVGAVGRSTRAPGVGAA	1036 aa
			>Sga_Solyc03g098280_NM_001279332.2_scaffold28885_12.6_contig8_1152_aa MARKRRTELPGSGESSGSQETVGGQGRGQYPPQQQQEGGYQGGGQGRGMRPPPQHQQQLGGYQGGGQGRGQRPPQQHQHEGGYQGGGQGRGMRPPPQ QSQQEGGYQGGGQGRGQRPPQQLQQEGGYQGGGRGWRPQQGGYGGRGSGGAPRGGMAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRG APSGGPSRPPIPELHQATTQTQHQAVMTTQPITYGRPADTSMEVGSSSEPPEMSALQVTQQFQQLAVQPEAAATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANH FFAELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPLPFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMF LEGRQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIGMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRV KIKKALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQHTQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKV TCQRPQERERDILETVKHNAYAEDKYAKEFGIKISDKLAQVEARILPPPWLKYHDNGREKDCLPQVGQWNMMNKKMVNGGTVANWICINFSRNVQDTVAHGFCSE LAQMCGISGMNFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPLSKELDLLVAILPDNNGSLYGDLKRICETDLGVVSQCCLTKHVFKMSKQYLANVALKINVKV GGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYTTRQDPVKGTVSGGMIKDLLISFRRATGQKPQR IIFFRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLW DENKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAGRGVGAGAAGKNTRAPGAGSAVRPLPALKDNVKRVMFYC	1152 aa
		Spr	>Spr_Solyc03g098280_NM_001279332.2_a308_1000_aa MAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRGAPSGGPSRPPIPELHQATTQTQHQAVMTTQPITYGRPADTSMEVGSSSEPPEMSALQVTQQ FQQLAVQPEAAATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANHFFAELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPL PFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMFLEGRQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIR PTQMGLSLNIDMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRVKIKKALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQH TQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKVTCQRPQERENDILQTVRHNAYSDDPYAREFGIKISEKLAQVEARILPAPWLKYHDTGREKDC LPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDSVAHGFCSELAQMCGISGMNFNPNPVLPPVSARPDQVERVLKARFHDAMTKLQPLSKELDLLVAILPDNN GSLYGDLKRICETDLGVVSQCCLTKHVFKMSKQYLANVALKINVKVGGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVS AQAHRQELIQDLYTTKQDPVKGTVSGGMIKDLLISFRRATGQKPQRIIFYRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRN AVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTS GAAGGGVGAGAAGRNTRAPGAGCAVRPLPALKDNVKRVMFYC	1000 aa
		Sch	>Sch_mRNA_Solyc06g072300_NM_001279128.1_scaffold2127_1011_aa XYGGGWLEKGGNRCTGGDFELLPWCGRGELMFLVVLRALSPMKLEGDEVVPNAHHHSSNKVEEEARDLSVEDMVAVVVEELLVVEWPLNSPMVDPPSTINRAGE LSSINEGEDNPSAVVPPEPMTHQVTQQFQQLAVQPEAGASQAIPPVSSKSMRFPLRPGKGSNGTRCIVKANHFFAELPDKDLHQYDVSITPEVASRGVNRAVMEQL VKLYRESHLGKRLPAYDGRKSLYTAGPLPFVQKDFKITLLDDDDGPGGARREREFKVVIKLAARADLHHLGMFLQGRQADAPQEALQVLDIVLRELPTSRYCPVGRS FYSPDLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTAFIEPLPVIEFVSQLLNRDISSRPLSDADRVKIKKALRGVKVEVTHRGNMRRKYRISGLTSQATRE LTFPVDERGTMKAVVEYFRETYGFVIQHTQLPCLQVGNTQRPNYLPMEVCKIVEGQRYSKRLNERQITALLKVTCQRPQERENDILQTVRHNAYSDDPYAREFGIKIS EKLAQVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDSVARGFCSELAQMCMISGMIFNPNPVLPPVSARPDQVERVLKT RFHDAMTKLQPNGRELDLLIVILPDNNGSLYGDLKRICETDLGIVSQCCLTKHVFKMSKQYLANVSLKINVKVGGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGE DSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYKTWQDPTRGTVTGGMIKELLISFRRATGQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQ PPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFSADGLQSLTNNLCYTYARCTRSVSIVPPAY YAHLAAFRARFYMEPETSDGGSVTSGAAPYRGGVGAVGRSTRAPGAGAA	1011 aa
			>Sch_mRNA_Solyc03g098280_NM_001279332.2_scaffold1227_1152_aa MARKRRTELPGSGESSGSQETVGGQGRGQYPPQQQQEGGYQGGGQGRGMRPPPQHQQQLGGYQGGGQGRGQRPPQQHQHEGGYQGGGQGRGMRPPPQ QSQQEGGYQAGGQGRGQRPPQQLQQEGGYQGGGRGWRPQQGGYGGRGSGGAPRGGMAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRG APSGGPSRPPIPELHQATTQTQHQAVMTTQPITYGRPADTSMEVGSSSEPPEMSALQVTQQFQQLAVQPEADATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANH FFAELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPLPFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMF LEGRQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRV KIKKALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQHTQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKV TCQRPQERERDILETVKHNAYAEDKYAKEFGIKISDKLAQVEARILPPPWLKYHDNGREKDCLPQVGQWNMMNKKMVNGGTVANWICINFSRNVQDTVAHGFCSE LAQMCGISGMNFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPLSKELDLLVAILPDNNGSLYGDLKRICETDLGVVSQCCLTKHVFKMSKQYLANVALKINVKV	1152 aa

			GGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYTTKQDPVKGTVSGGMIKDLLISFRRATGQKPQR IIFYRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLW DENKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAGRGVGAGAAGRNTRAPGAGCAVRPLPALKDNVKRVMFYC	
		SpiLA1589	>SpiLA1589_Solyc06g072300_NM_001279128.1_contig:385000:1:10591:1_799_aa MTHQVTQQFQQIAVQPEAGASQAIPPVSSKSMRFPLRPGKGSNGTRCIVKANHFFAELPDKDLHQYDVSITPEVASRGVNRAVMEQLVKLYRESHLGKRLPAYDGR KSLYTAGPLPFVQKDFKITLLDDDDDGPGGARREREFKVVIKLAARADLHHLGMFLQGRQADAPQEALRFLILFCMGLSLNIDMSSTAFIEPLPVIEFVSQLLNRDISSRP LSDADRVKIKKALRGVKVEVTHRGNMRRKYRISGLTSQATRELTFPVDERGTMKAVVEYFRETYGFVIQHTQLPCLQVGNTQRPNYLPMEVCKIVEGQRYSKRLNE RQITALLKVTCQRPQERENDILQTVRHNAYSDDPYAREFGIKISEKLAQVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDS VARGFCSELAQMCMISGMIFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPNGRELDLLIVILPDNNGSLYGDLKRICETDLGIVSQCCLTKHVFKMSKQYLANVS LKINVKVGGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYKTWQDPTRGTVTGGMIKELLISFRRAT GQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQAYYAHL AAFRARFYMEPETSDGGSVTSGAAPYRGGVGAVGRSTRAPGVGAA	799 aa
			>SpiLA1589_Solyc03g098280_NM_001279332.2_contig:2773654:1:3680:1_1149_aa MARKRRTELPGSGESSGSQETVGGQGRGQYPPQQQQEGGYQCGGQGRGMRPPPQHQQQLGGYQGGGQGRGQRPPQQHQHEGGYQGGGQGRGMRPPPQ QSQQEGGYQGGGQGRGQRPPQQLQQEGGYQGGGRGWRPQQGGYGGRGSGGAPRGGMAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRG APSGGPPIPELHQATTQTQHQAVMTTQPITYGRPADTSMEVGSSSEPPEMSALQVTQQFQQLAVQPEAAATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANHFFA ELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPLPFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMFLEG RQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRVKIK KALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQHTQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKVTC QRPQERERDILETVKHNAYAEDKYAKEFGIKISDKLAQVEARILPPPWLKYHDNGREKDCLPQVGQWNMMNKKMVNGGTVANWICINFSRNVQDTVAHGFCSELA QMCGISGMNFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPLSKELDLLVAILPDNNGSLYGDLKRICETDLGVVSQCCLTKHVFKMSKQYLANVALKINVKVGG RNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYTTRQDPVKGTVSGGMIKDLLISFRRATGQKPQRIIF FRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDE NKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAGRGVGAGAAGKNTRAPGAGSAVRPLPALKDNVKRVMFYC	1149 aa
			>SpiLA0480_Solyc06g072300_NM_001279128.1_Scaffold3068023_1036_aa MVRKRRTDVPGGAESSESHETGGGRGGVQRPPPQQQQGGGRGSGPQRGGYGGRGGGGAPRGGIAPQQSYGGPPEYYQQGRGTQQYQRGGGQPQRRGGIG GRGAPSGGSSRPPVPELHQATETPHQPVPYGRPAETYSEAGSSSQPPEPMTHQVTQQFQQIAVQPEAGASQAIPPVSSKSMRFPLRPGKGSNGTRCIVKANHFFA ELPDKDLHQYDVSITPEVASRGVNRAVMEQLVKLYRESHLGKRLPAYDGRKSLYTAGPLPFVQKDFKITLLDDDDDGPGGARREREFKVVIKLAARADLHHLGMFLQ GRQADAPQEALQVLDIVLRELPTSRYCPVGRSFYSPDLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTAFIEPLPVIEFVSQLLNRDISSRPLSDADRVKIK KALRGVKVEVTHRGNMRRKYRISGLTSQATRELTFPVDERGTMKAVVEYFRETYGFVIQHTQLPCLQVGNTQRPNYLPMEVCKIVEGQRYSKRLNERQITALLKVTC QRPQERENDILQTVRHNAYSDDPYAREFGIKISEKLAQVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINFSRNVQDSVARGFCSELA QMCMISGMIFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPNGRELDLLIVILPDNNGSLYGDLKRICETDLGIVSQCCLTKHVFKMSKQYLANVSLKINVKVGGR NTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYKTWQDPTRGTVTGGMIKELLISFRRATGQKPQRIIFY RDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDE NNFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAPYRGGVGAVGRSTRAPGVGAA	1036 aa
		SpiLA0480	>SpiLA0480_mRNA_Solyc03g098280_NM_001279332.2_Scaffold3008857_1152_aa MARKRRTELPGSGESSGSQETVGGQGRGQYPPQQQQEGGYQGGGQGRGMRPPPQHQQQLGGYQGGGQGRGQRPPQQHQHEGGYQGGGQGRGMRPPPQ QSQQEGGYQGGGQGRGQRPPQQLQQEGGYQGGGRGWRPQQGGYGGRGSGGAPRGGMAPQQPYGGQAEYYQQGRGTQQHQQRGGGPLQQHGGIGGRG APSGGPSRPPIPELHQATTQTQHQAVMTTQPITYGRPADTSMEVGSSSEPPEMSALQVTQQFQQLAVQPEAAATHTIPPVSSKSLRFPLRPGKGKFGQSCIVKANH FFAELPDKDLHQYDVTITPEVSSRGVNRAVMAQLVLLYQESHLGKRLPAYDGRKSLYTAGPLPFVQKEFKITLTDDEDGPGGARRDREFKVVIKFASRADLHHLGMF LEGRQADAPQEALQVLDIVLRELPTSKYCPVGRSFYSPNLGRRQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTSFIEPLLVVDFVAQLLNRDVSSRPLSDADRV KIKKALRGVKVEVTHRGNMRRKYRIANLTSQATRELTFPVDEKGTLKSVIEYFRETYGFVIQHTQWPCLQVGNQQRPNYLPMEVCKIVEGQRYSKRLNEKQITALLKV TCQRPQERERDILETVKHNAYAEDKYAKEFGIKISDKLAQVEARILPPPWLKYHDNGREKDCLPQVGQWNMMNKKMVNGGTVANWICINFSRNVQDTVAHGFCSE LAQMCGISGMNFNPNPVLPPVSARPDQVERVLKTRFHDAMTKLQPLSKELDLLVAILPDNNGSLYGDLKRICETDLGVVSQCCLTKHVFKMSKQYLANVALKINVKV GGRNTVLVDAISRRIPLVSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEITKYAGLVSAQAHRQELIQDLYTTRQDPVKGTVSGGMIKDLLISFRRATGQKPQR IIFYRDGVSEGQFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQKRHHTRLFANNHRDRNAVDRSGNIIPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLW DENKFSADGLQSLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPETSDGGSVTSGAAGRGVGAGAAGKNTRAPGAGSAVRPLPALKDNVKRVMFYC	1152 aa
	AGO2	*Sly*	>Solyc02g069260.2.1 MDRGNYRRGGGHDNAGRGGGNRGRGQGRGGGRGEPQIGGGRGGTHIGGGSQMGQPPQQWGNQPRGSGQYQIRGGAPQNQPGQNYPVNQNPGRGGTWV NQPVQRGGGGGGSAWPRPQQQGSGVPNTTWPRPPPQQQGSGSGVANAWARPPPQRSQQHGGGNQQQVVDRSPPQSSDPVQVDLGSLKITDQSPSSRQESS KEKRVPIARPDTGKIAVKSIALLANHFPVRFNPQSTIMHYDVDIQQRADGNRPVKKLTNKSVLHMIREKLCADDPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSD GEDARLRSYDITIKLVAELKLCKLKEYLSGSLSHIPRDILQGMELVMKENPTRCRTSVGRCFYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKP MPVLDFLKEYLGESNENTFRNNIRAAKGALVGLKVRVIHRRTSQKFLIKQLTDCKTREITFPLEDPEGINPPRDVLLVDYFRDKYQREIQFKDFPSLDIGKGNKKNYVP MEFCVLVEGQRYPKEDLDKDTALFLKNISLARPQDRRQAICEMVRAGDGPCGAVTRNFDIGVDRNMTRVPGRILPPPDLKLGGQNRLPVNDKCQWNLVGKSVVEG KALQRWALIDFSAQDRKPFFRLRVDEFVFRLKDRCRKLSINMEEPAVVHFTDMHVLSEVGKVHKLLDGVVNAAKREINGKLQMIVCVMTSKHNGYKYLKWVSETQIG VVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMDRLPNFGREDNVMFIGADVNHPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKM	1060 aa

			CADLVHTYKEINSVKPNKIVVFRDGVSEGQFDMVLNEELLDLAKAIYDSNYQPAITLVVAQKRHHTRLFPEGGPANVPPGTVVDTIIVHPSDFDFYLCSHFGGLGTSK PTHYHVLWDDNGFNSDSLQKLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLMEMNSPSSATSSSPTASFQQKFYDLHSDLQNVMFFV	
			>Solyc02g069280.2.1 MDRGNNNGRGGDRKRGRNSDRVPGHNEQRQGPARGYYDPSQYRARAYYEEEQGRARGQHEEEQGRARVQHEQEQGRGRGRGGRDAFQMGSSSSNQPRPS DQHQFTETVAPENQLVSQTPVATGMNWLNAARKGAGTASPPPQQQQKDAPVLLGKITLKDSKKREPMGRPDGGNTSDESVSLHANHFPVDFNDGTIILHYDVDVQ KVDGDQPGKSVTDRFDLRKIREKWLMDKPAEFPCDKTAYDGIRNIYSAVDLPAKPLTVNCSVEDDAKEYKYILTFKLVAQLQLDNVTEYLRRSLQNIIPRDVLQGMDL VMKENPRRCRISVGRCFYSNSARTSFNGGVAARKGFQQSLKLTSEGLALCLDYSELLVIPEQIPVIEFLENYYGKNIDDIFKYTRAGASDLLVGLKVKVTHRPNKQKFV IKELLPGETRTVKFKLQDTGEEVLLVDYFDKNYTPKIKNRHLPSLNIGKGDKDNYVPMEFCDLVEGQRFPKDLLKTTSLEPKTRRDLIRETVLAKDGPRMTIPDNFKIR VDDNMTQISGRILPVPVLKLGGQNPPPNLNYKTCQWNLVGKSVVEGKALQRWALIDFSSKGCRDSLKLQVDEFVVKLKDRCTQLSINMDIPAVVHLTDMNELSTVG KVENLLKVVTDAAEKKLQGKLQMILCVMTSKHNGYKYLKWVSETKIGIVTQCCLSSNANKGHNQYIVNLCMKINAKLGGSNMELMERLPNFRSDDNVMFIGADVNHP AGKDADKYPSIAAVVATINWPAANKYAARVSPQKSRTEKIIEFGKMCKDLVLTYEKRNSVKPNKIVVFRDGVSDSQFDMVLNEELTDLANAIYESNKYQPAITLVVAQK RHHTRLFPKEGNVSPGTVVDTQIVHPSGFDFYLCSHYGQLGTSKATHYHVLYDDNGFISVDLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLMEM KSPRSTTSSSEASSSSSSPIDSFAQEFYDLHHDLKDIMFFV	999 aa
			>Solyc02g069270.2.1 MDRGNYQRGGGDNTGRGRGNRGRGGRGGTHVGGGRGGPQMGSFHQPPQQWGNQPRGSGQYQFRGAPPGRGGTWVNQPVQRGGGNAWQRPQQQGSGV PITAWARPPPQQPQQQGSGGGVATAWARPPPPPQEVVDRPQSSDPVHVDMGSLKITEASSSESSKEKRVPVARPDTGKNCVKQIELLANHFVVAFDPHSTIMHYD VNIQQQQSCARDNPIRFPLDNTAYDGNKNIFSAVQLPTGCFAVNWSDGEDFKSRTYDITINLVAELQLRKLEQYLSGNLSYTPRDILQGMDLFMKDNPSRHRISVGR CFYSKNPHKDFRFGAAAYKGFQQSLKPTEAGLALCLDYSVLALRKPMSVLNYLRNYFQIPKEDIFRYNHQAAHDALKGLKVTVNHRRTSQKFVIKKLTDRKTSEITFP LEDPEGKDPPRDVLLVEYFRDKYQREIQFKDFPSLDVGKGSKINYVPMEFCVLVEGQRFPKEELDKASAMFLKNMSLAQPNERKEATCEMVKAEDGPCGAITDNFG IKVDKNMTGVVGRVLPPPDLKLGGQSPLRVNDKCQWNLVGKSVVEGKALQRWALIDFSSKERNWLRVDEFVIGLRDRCSKLSINMEGPAEVHLTDMHELSEVGKV EKLLNFVVDAAKRKINGKLQMIVCVMTSKHNGYKYLKWVSETKIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMQRLPNFRNGDNVMFIGADVNHPT SRDADKYPSIAAVVATINWPAANRYAARVCPQKHRTEKILEFGKMCADLVRTYEELNSVKPNKIVVFRDGVSGSQFDMVLNEELNDLVKDIYDRYKYKPEITLVVAQK RHHTRLFPREGNVPPGTVVDTQIVHPFDFDFYLCSHFGQLGTSKATHYHVLWDENGFNSDILQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVVMEM NASSSTTSPASFEQRFYNLQPDLQNIMFFV	977 aa
		Spe	>Sopen02g018430 MDRGNYQRGGGDNTGRGRGNRGRGGPHIGGGRGGPHVGGGRSGPQMGSFHQPPQQWGNQPRGSGQYQFRGAPPGRGGTWVNQPVQRGGGNAWQRPQQ QGSGVPITAWARPPPQQPQQQGSGGGVATAWARPPPPPQEVVDRPQSSDPVHVDMGSLKITEASSSESSKEKRVPVTRPDTGKNCVKQIELLANHFVVTFDPHS TIMHYDVNIQQQADENRPVKNLTNKSVLHMIRAKLCEDDPIRFPLDNTAYDGNKNIFSAVQLPTGCFAVNWSDGEDVKSRTYDITINLVAELQLRKLEQYLSGNLSYIP RDILQGMDLFMKDNPSRHRISVGRCFYSKNPHKDFRFGFAAYKGFQQSLKPTEAGLALCLDYSVLALRKPMSVLDYLRDYFQIRKEDIFKYNHQAAHDALKGLKVTV NHRRTSQKFVIKKLTDRKTSEITFPLEDPEGKDPPRDVLLVEYFRDKYQREIQFKDFPSLDVGKGSKINYVPMEFCVLVEGQRFPKEELDKDSAMFLKNMSLARPNE RKEAICEMVKAEDGPCGAITDNFGIKVDKNMTGVVGRVLPPPDLKLGGQSPLRVNDKCQWNLVGKSVVEGKALQRWALIDFSYKERNRLRVDEFVFGLRDRCIKLSI NMEEPAEVHFTDMHELSEVGKVEKLLNFVVDAAKRKINGKLQMIVCVMTSKHNGYKYLKWVSETKIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELM QRLPNFRNGDNVMFIGADVNHPTSRDADKYPSIAAVVATINWPAANRYAARVCPQKHRTEKILEFGKMCADLVRTYEELNSVKPNKIVVFRDGVSGSQFDMVLNEE LNDLVKDIYDRYKYKPEITLVVAQKRHHTRLFPREGNVPPGTVVDTQIVHPFDFDFYLCSHFGQLGTSKATHYHVLWDENGFNSDSLQRLIYNMCFTFARCTKPVSL VPPVYYADLVAYRGRMFQEVVMEMNASSSTTSPASFEQRFYNLQPDLQNIMFFV	1003 aa
			>Sopen02g018440 MDRGNNNGRGGDRKRGRNSDRVPGYNEQRQGPARGYYDPSQYRARAYYEEEQGRARGQHEEEQGRARVQHEQEQGRGRGRGGRDGFQMGSSSSNQPRPS DQHQFTETVAPENQLVSQTPAATRMNWLNAARKGVGTASPPPQQQQKDAPVLLGNITLKDSKKREPMGRPDGGNTSDESVSLHANHFPVDFNDGTIILHYDVDVQ KVDGNQPGKSVTDKFDLHKIREKWLMDKPAEFPCDKTAYDGIRNIYSAVDLPAKPLTVNCSVGDDAKEYKYILTFKLVAQLQLDNVTEYLRRSLQNIIPRDVLQGMDL VMKENPRRCRISVGRCFYSNNARTSFNGGVAARKGFQQSLKLTSEGLALCLDYSELLVIQEQIPVIDFLEKYYGKNIDDIFKYTRAGASDLLVGLKVKVTHRPNKQKF VIKELLPGETRTVKFKLQDTGEEVLLVDYFDKNYTPKIKNRHLPSLNIGKGDKDNYVPMEFCDLVEGQRFPKDLLKTTSLEPKTRRELIRETVLAEDGPRMTIPGNFKI RVDDNMTQISGRVLPVPVLKLGSQNPPNLNDKCQWNLVGKSVVEGKALQRWALIDFSSKGCRDSLKLQVDQFVVKLKDQCRQLSINMVIPAVVHLTDMNELSTVG KVENLLKVVTDAAEKKLQGKLQMILCVMTSKHNGYKYLKWVSETKIGIVTQCCLSSNANKGHNQYIANLCMKINAKLGGSNMELMERLPNFGSDDNVMFIGADVNHP AGKDADKYPSIAAVVATINWPAANKYAARVSPQKSRTEKIVEFGKMCKDLVLTYEKRNSVKPNKIVVFRDGVSDSQFDMVLNEELTDLANAIYESNKYQPAITLVVAQ KRHHTRLFSKVGNVSPGTVVDTQIVHPSGFDFYLCSHYGQLGTSKATHYHVLYDENGFISVDLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLME MKSPRSTTSSSEASSSSSSPIDSFAQEFYDLHHDLKDIMFFV	997 aa
			>Sopen02g018420 MDRGNYRRGGGHDNAGRGGGNRGRGQGRGGGRGEPQIGGGRGGTQIGGGSQMGQPPQQWGNQPRGSGQYQIRGGAPQNQPGQNYPVNQNPGRGGTWV NQPVQRGGGGGSAWPRPQQQGSGVPNTTWARPPPQQQGSGGGVANAWARPPPQRIQQHGGGNQQQVVDRAPPQSSDPVQVDLGSLKITDQSPSSRPESSK EKRVPIARPDTGKIAVKSIALLANHFPVRFNPQSTIMHYDVDIQQRADGNRPVKKLTNKSVLHMIREKLCADDPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSDG EDARLRSYDITIKLVAELKLCKLKEYLSGSLSHIPRDILQGMELVMKENPTRCRTSVGRCFYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKPM PVLDFLKEYLGESNENTFRNNIRAAKGALVGLKVRVIHRRTSQKFLIKQLTDCKTREITFPLEDPEGINPPRDVLLVDYFRDKYQREIQFKDYPSLDIGKGNKKNYVPM EFCVLVEGQRYPKEDLDKDTALFLKNISLARPQDRRQAICEMVRAGDGPCGAVTRNFDIGVDRNMTRVPGRILPPPDLKLGGQNRFPVNDKCQWNLVGKSVVEGK ALQRWALIDFSAHDRKPFFRLRVDEFVFRLKDRCRKLSINMEEPAVVHLTDMHELSAVGKVKELLDGVVAEAKRKINGELQMIVCVMTSKHNGYKYLKWVSETKIGV VTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMDRLPNFRNGDNVMFIGADVNHPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKMC ADLVRTYEEINLVKPNKIVVFRDGVSEGQFDMVLNEELLDLAKAIYDSDYQPAITLVVAQKRHHTRLFPEGGPANVPPGTVVDTIIVHPSDFDFYLCSHFGGLGTSKPT	1041 aa

			HYHVLWDDNGFNSDSLQKLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMYQEVLMEMNSPRSTTSSSPTASFQQTFYDLHSDLQNVMFFV	
		Sga	>Sga_Scaffold119639_10.1_Contig2_947_aa MITPAEVEVTVVEDKAVVVEGVSLRSEVEGVGPTSVVGPKWVSLHSNGGISRGDRVNTRFVVGLRKINRVKTIRLIRIRVVVVLGAWPRPQQQGSGVPNTTWARPP PQQQGSGGGVANAWARPPPQRSQQHGAGNQLQVVDRSPPQSSDPVQVDLGSLKITDQSPSSRPESSKEKRVPIARPDTGKIAVKSIALLANHFPVRFNPQSTIMH YDVDIQQRADGNRPVKKLTNKSVLHMIREKLCADDPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSDGEDARLRSYDITIKLVAELKLCKLKEYLSGSLSHIPRDIL QGMEVVMKENPTRCRTSVGRCFYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKPMPVLDFLKEYLGESNENTFRNNIRAAKGALVGLKVRVI HRRTSQKFLIKQLTDCKTHEITFPLEDPEGINPPRDVLLVDYFRDKYQREIQFKDFPSLDIGKGNKKNYVPMEFCVLVEGQRYPKEDLDKDTALFLKNISLARPQDRR QAICEMVRAGDGPCGAVTRNFDIGVDRNMTRVPGRILPPPDLKLGGQNRLPVNDKCQWNLVGKSVVEGKALQRWALIDFSAQDRKPFFRLRVDEFVFRLKDRCRK LSINMEEPAVVHFTDMHELSEVGKVHKLLDGVVNAAKREINGKLQMIVCVMTSKHNGYKYLKWVSETQIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNME LMDRLPNFGREDHVMFIGADVNHPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKMCRDLVDTYAKINYVKPNKIVVFRDGVSEGQFDMVLNE ELLDLAKAIYDSNYQPAITLVVAQKRHHTRLFPEGGPANVPPVYYADLVAYRGRMFQEVLMEMNSPSSATSSSPTASFQQKFYDLHSDLQNVMFFV	947 aa
			>Sga_Scaffold80102_13.1_Contig4_930_aa MSVVEGVGPKWVHFISLHSNGGISQGGRVNISFVELRRVVVVLGSTNRSNVVVVTLGNGHNSREVVDRPQSSDPVHVDMGSLKITEASSSESSKEKRVPVTRPDT GKNCVKQIELLANHFVVTFNPHSTIMHYDVDIQQQADENRPVKNLTNKSVLHMIRAKLCEDDPIQFPLDNTAYDGNKNIFSAVQLPTGCFAVNWSDGEDFKSRTYDIT INLVAELQLRKLEQYLSGNLSYIPRYILQGMDLFMKDNPSRHRISVGRCFYSKNPHKDFRFGAAAYKGFQQSLKPTEAGLALCLDYSVLALRKPMSVLDYLRNYFQIP KEDIFRYNHQAAHDALKGLKVAVNHRRTSQKFVIKKLTDRKTSEITFPLEDPEGKDPPRDVLLVEYFRDKYQREIQFKDFPSLDVGKGSKINYVPMEFCVLVEGQRFP KEELDKASAMFLKNMSLAQPNERKEAICEMVKAEDGPCGAITDNFGIKVDKSMTGVVGRVLPPPDLKLGGQSPLRVNDKCQWNLVGKSVVEGKALQRWALIDFSY KERNRLRVDEFVFRLRDRCIKLSINMEEPAEVHLTDMHELSEVGKVEKLLNFVVDAAKRKINGKLQMILCVMTSKHNGYKYLKWVSETKIGVVTQCCLSTNANKGQD QYLANLCMKINAKLGGSNMELMQRLPNFRNGDNVMFIGADVNHPTSRDADKYPSIAAVVATINWPAANRYAARVCPQKHRTEKILEFGKMCADLVRTYEELNSVKP NKIVVFRDGVSGSQFDMVLNEELNDLVKDIYDRYKYKPEITLVVAQKRHHTRLFPREGNVPPGTVVDTQIVHPFDFDFYLCSHFGQLGTSKATHYHVLWDENGFNSD SLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVVMEMNASSSTTSPASFEQRFYNLQPDLQNIMFFV	930 aa
			>Sga_Scaffold80102_13.1_Contig3_996_aa MDRGNNNGRGGDRKRGRNSDRVPGHNEQRQGPARGYYDPSQYRARAYYEEEQGRARGQHEEEQGRARVQHEQEQGRGRGRGGRDGFQMGSSSSNQPRPS DQHQFTETVAPENQLVSQTPVAGEKVLVLLHPCTASPPPQQQQKDAPVLLGKITLKDSKKREPMGRPDGGNTSDESVSLHANHFPVDFNDGTIILHYDVDVRKVDG DQPGKSVTDRFDLRKIREKWLMDKPAEFPCDKTAYDGIRNIYSAVDLPAKPLTVNCSVEDDAKEYKYILTFKLVAQLQLDNVTEYLRRSLQNIIPRDVLQGMDLVMKE NPRRCRISVGRCFYSNSARTSFNGGVAARKGFQQSLKLTSEGLALCLDYSELLVIPEQIPVIEFLENYYGKNIDDIFKYTRAGASDLLVGLKVKVTHRPNKQKFVIKELL PGETRTVKFKLQDTGEEVLLVDYFDKNYTPKIKNRHLPSLNIGKGDKDNYVPMEFCDLVEGQRFPKDLLKTTSLEPKTRRDLIRETVLAKDGPRMTIPGNFKIRVDDN MTQISGRILPVPVLKLGGQNPPPNLKDKTCQWNLVGKSVVEGKALQRWALIDFSSKGCRDSLKLQVDQFVMKLKDQCRQLSINMDIPAVVHLTDMNELSTVGKVEN LLKVVTDAAEKKLQGKLQMILCVMTSKHNGYKYLKWVSETKIGIVTQCCLSSNANKGHNQYIVNLCMKINAKLGGSNMELMERLPNFRSDDNVMFIGADVNHPAGK DADKYPSIAAVVATINWPAANKYAARVSPQKSRTEKIVEFGKMCKDLVLTYEKRNSVKPNKIVVFRDGVSDSQFDMVLNEELTDLANAIYESNKYQPAITLVVAQKRH HTRLFPKEGNVSPGTVVDTQIVHPSGFDFYLCSHYGQLGTSKATHYHVLYDDNGFISVDLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLMEMKS PRSTTSSSEASSSSSSPIDSFAQEFYDLHHDLKDIMFFV	996 aa
		Spr	>Spr_a8305_954_aa XWIVGTTDVVAVMITPAEVEVTVVEDKAVVVEGVSIRSEVEGVGPRLVVGPKWVRLHSNGGISRGDRVNTRFVVGLRKINRVKTIRLIRIRVVVVLGAWPRPQQQGS GVPNTTWARPPPQQQGSGGGVANAWARPPPQRSQQHGGGNQQQVVDRSPPQSSDPVQVDLGSLKITDQSPSSRQESSKEKRVPIARPDTGKIAVKSIALLANHF PVRFNPQSTIMHYDVDIQQRADGNRPVKKLTNKSVLHMIREKLCADYPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSDGEDARLRSYDITIKLVAELKLCKLKEY LSGSLSHIPRDIIQGMELVMKENPTRCRTSVGRCFYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKPMPVLDFLKEYLGESNENTFRNNIRAA KGALVGLKVRVIHRRTSQKFLIKQLTDCKTREITFPLEDPEGINPPRDVLLVDYFRDKYQREIQFKDFPSLDIGKGNKKNYVPMEFCVLVEGQRYPKEDLDKDTALFLK NISLARPQDRRQAICEMVRAGDGPCGAVTRNFDIGVDRNMTRVPGRILPPPDLKLGGQNRLPVNDKCQWNLVGKSVVEGKALQRWALIDFSAKDRKPFFRLRVDE FVFRLRDRCRKLSINMEEPAVVHFTDMHELSEVGKVEKLLNFVVDAAKRKINGKLQMIVCVMTSKHNGYKYLKWVSEIQIGVVTQCCLSTNANKGQDQYLANLCMKI NAKLGGSNMELMDRLPNFGREDNVMFIGADVNHPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKMCRDLVDTYAKINHVKPNKIVVFRDGVS EGQFDMVLNEELLDLAKAIYDSDYQPAITLVVAQKRHHTRLFPEGGPANVPPVYYADLVAYRGRMFQEVLMEMNSPSSATSSSPTASFQQKFYDLHSDLEN	954 aa
		Sch	>Sch_Scaffold1612_906_aa XWIVGTTDVVAVMITPAEVEVTVVEDKAVVVEGVSLRSEVEGVGPRSVVGPKWVRLHSNGGISRGDRVNTRFVVGLRKINRVKTIRLIRIRVVVVLGAWPRPQQQGS GVPNTTWARPPPQQQGSGGGVANAWARPPPQRSQQHGGGNQQQVVDRSPPQSSDPVQVDLGSLKITDQCSSSRQESSKEKRVPIARPDTGKIAVKSIALLANHF PVRFNPQSTIMHYDVDIQQRADGNRPVKKLTNKSVLHMIREKLCADDPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSDGEDARLRSYDITIKLVAELKLCKLKEY LSGSLSHIPRDILQGMELVMKENPTRCRTSVGRCFYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKPMPVLDFLKEYLGESNENTFRNNIRAA KGALVGLKVRVIHRRTSQKFLIKQLTDCKTREITFPLEDPEGINPPRDVLLVDYFRDKYQREIQFMDFPSLDIGKGNKKNYVPMEFCVLVEGQRYPKEDLDKDTALFLK NISLARPQDRRQAICEMVRAGDGPCGAVTRNFDIGVDRNMTRVPGRILPPPDLKLGGQNRLPVNDKCQWNLVGKSVVEGKALQRWALIDFSAQDRKPFFRLRVDE FVFRLKDRCRKLSINMEEPAVVHFTDMHELSAVGKVHKLLDGVVNAAKREINGKLQMIVCVMTSKHNGYKYLKWVSETQIGVVTQCCLSTNANKGQDQYLANLCMK INAKLGGSNMELMDRLPNFGREDNVMFIGADVNHPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKMCRDLVDTYAKINNVKPNKIVVFRDGVS EGQFDMVLNEELLDLAKAIYDSDYQPAITLVVAQKRHHTRLFPEGGPANVPPX	906 aa
			>Sch_Scaffold1612_958_aa MGSFHQPPQQWGNQPRGSGQYQFRGAPPGLGGTWVNQPVQRGGGNAWQRPQQQGSGVPINAWARPPPQQPQQQGSGGGVATAWARPPPPPQEVVDRPQ SSDPVQVDMGSLKITEASSSESSKEKRVPVTRPDTGKNCVKQIELLANHFVVTFNPHSTIMHYDVDIQQQADENRPVKNLTNKSVLHMIRAKLCEEDPIRFPLDNTAY DGNKNIFSAVQLPTGCFAVDWSDGEDVKSRTYNITINLVAELQLRKLEQYLSGNLSYIPRDILQGMDLFMKDNPSRHRISVGRCFYSKNPHKDFVFGVAAYKGFQQS	958 aa

			LKPTEAGLALCLDYSVLALRKPMSVLDYLREYFQIPNEDIFRYNHQAAHDALKGLKVTVNHRRTSQKFVIKKLTDRKTSEITFPLEDPEGKDPPRDVLLVEYFRDKYQR EIQFKDFPSLDVGKGSKINYVPMEFCVLVEGQRFPKEELDKGSAIFLKDMSLARPNERKEAICEMVKAEDGPCGAITDNFGIKVDKNMTGVVGRVLPPPDLKLGGQS PLRVNDKCQWNLVGKSVVEGKALQRWALIDFSYKERNRLRVDEFVFRLRDRCIKLSINMEEPAEVHLTDMHELSEVGKVEKLLNFVVDAAKRKINGKLQMIVCVMTS KHNGYKYLKWVSETKIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMQRLPNFKNGDNVMFIGADVNHPTSRDADKYPSIAAVVATINWPAANRYAA RVCPQKHRTEKILEFGKMCVDLIRTYEELNSVKPNKIVVFRDGVSGSQFDMVLNEELNDLVKDIYDSYKYKPEITLVVAQKRHHTRLFPREGNVPPGTVVDTQIVHPF DFDFYLCSHFGQLGTSKATHYHVLWDENGFNSDSLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVVMEMNASSSTTSPASFEQRFYNLQPDLQNV MFFV	
			>Sch_Scaffold1612_999_aa MDRGNNNGRGGDRKRGRNSDRVPGYNEQRQGPGRGYYDPSQYRARAYYEEEQGRARGQHEEEQGRARVQHEQEQGRGRGRGGRDGFQMGSSSSNQPRP SDHHQFTETVAPENQLVSQTPAATPLNWLNAARKGAGTASPPPQQQQKDAPVLLGKIILKDSKKREPMGRPDGGNTSDESVSLHANHFPVDFNDGTIILHYDVDVQ KIDGNQPWKSVTDKFDLRKIREKWLVDKPAEFPCDKTAYDGIRNIYSAVDLPAKPLTVNCSVGDDDKEYKYILTFKLVAQLQLDNVTEYLRRSLQNIIPRDVLQGMELV MKENPRRCRISVGRCFYSNSARTSFNGGVDARKGFQQSLKLTSEGLALCLDYSELLVIPEQIPVIDFLEKYYGKSIDYIFKYTRAGARDLLVGLKVKVTHRPNKQKFVI KELLPGETRTVKFKLQDTGEEVLLVDYFDKNYTTKIKNRHLPSLNIGKGDKDNYVPMEFCDLVEGQRFPKDLLKTTSLEPKTRRDLIRETVLAKDGPRMTIPDNFKIRV DDNMTQISGRILPVPVLKLGGQNPPPNLNYKTCQWNLVGKSVVEGKALQRWALIDFSSKGCRDSLKLQVDEFVVKLKDRCTQLSINMDIPAVVHLTDMNELSTVGK VENLLKVVTDAAGKKLQGKLQMILCVMTSKHNGYKYLKWVSETKIGIVTQCCLSSNANKGHNQYIVNLCMKINAKLGGSNMELMERLPNFRSDDNVMFIGADVNHP AGKDAEKYPSIAAVVATINWPAANKYAARVSPQKSRTEKIVEFGKMCKDLVLTYEKRNSVKPNKIVVFRDGVSDSQFDMVLNEELTDLANAIYESNKYQPAITLVVAQ KRHHTRLFPKEGNVSPGTVVDTQIVHPSGFDFYLCSHYGQLGTSKATHYHVLYDDNGFISVDLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLME MKSPRSTTSSSEASSSSSSPIDSFAQEFYDLHHDLKDIMFFV	999 aa
		SpiLA1589	>SpiLA1589_Contig:unspecified:6529832:1:10855:1_891_aa RSQQHGAGNQLQVVDRSPPQSSDPVQVDLGSLKITDQSPSSRPESSKEKRVPIARPDTGKIAVKSIALLANHFPVRFNPQSTIMHYDVDIQQRADGNRPVKKLTNKS VLHMIREKLCADDPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSDGEDARLRSYDITIKLVAELKLCKLKEYLSGSLSHIPRDILQGMEVVMKENPTRCRTSVGRC FYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKPMPVLDFLKEYLGESNENTFRNNIRAAKGALVGLKVRVIHRRTSQKFLIKQLTDCKTREITF PLEDPEGINPPRDVLLVDYFRDKYQREIQFKDFPSLDIGKGNKKNYVPMEFCVLVEGQRYPKEDLDKDTALFLKNISLARPQDRRQAICEMVRAGDGPCGAVTRNFD IGVDRNMTRVPGRILPPPDLKLGGQNRLPVNDKCQWNLVGKSVVEGKALQRWALIDFSAQDRKPFFRLRVDEFVFRLKDRCRKLSINMEEPAVVHFTDMHELSEVG KVHKLLDGVVNAAKREINGKLQMIVCVMTSKHNGYKYLKWVSETQIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMDRLPNFGREDHVMFIGADVN HPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKMCRDLVDTYAKINHVKPNKIVVFRDGVSEGQFDMVLNEELLDLAKAIYDSNYQPAITLVVAQ KRHHTRLFPEGGPANVPPGTVVDTIIVHPSDFDFYLCSHFGGLGTSKPTHYHVLWDDNGFNSDSLQKLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVL MEMNSPSSATSSSPTASFQQKFYDLHSDLQNVMFFV	891 aa
			>SpiLA1589_Contig:unspecified:6757462:1:3785:1_852_aa MGSLKITEASSSESSKEKRVPVTRPDTGKNCVKQIELLANHFVVTFNPHSTIMHYDVDIQQQADENRPVKNLTNKSVLHMIRAKLCEDDPIQFPLDNTAYDGNKNIFS AVQLPTGCFAVNWSDGEDFKSRTYDITINLVAELQLRKLEQYLSGNLSYIPRYILQGMDLFMKDNPSRHRISVGRCFYSKNPHKDFRFGAAAYKGFQQSLKPTEAGL ALCLDYSVLALRKPMSVLDYLRNYFQIPKEDIFTYNHQAAHDALKGLKVAVNHRRTSQKFVIKKLTDRKTSEITFPLEDPEGKDPPRDVLLVEYFRDKYQREIQFKDFP SLDVGKGSKINYVPMEFCVLVEGQRFPKEELDKASAMFLKNMSLAQPNERKEAICEMVKAEDGPCGAITDNFGIKVDKSMTGVVGRVLPPPDLKLGGQSPLRVNDK CQWNLVGKSVVEGKALQRWALIDFSYKERNRLRVDEFVFRLRDRCIKLSINMEEPAEVHLTDMHELSEVGKVEKLLNFVVDAAKRKINGKLQMILCVMTSKHNGYKY LKWVSETKIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMQRLPNFRNGDNVMFIGADVNHPTSRDADKYPSIAAVVATINWPAANRYAARVCPQKH RTEKILEFGKMCADLVRTYEELNSVKPNKIVVFRDGVSGSQFDMVLNEELNDLVKDIYDRYKYKPEITLVVAQKRHHTRLFPREGNVPPGTVVDTQIVHPFDFDFYLC SHFGQLGTSKATHYHVLWDENGFNSDSLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVVMEMNASSSTTSPASFEQRFYNLQPDLQNIMFFV	852 aa
			>SpiLA1589_Contig:unspecified:6718737:1:4619:1_983_aa LKKYSQMDRGNNNGRGGDRKRGRNSDRVPGHNEQRQGPARGYYDPSQYRARAYYEEEQGRARGQHEEEQGRARVQHEQEQGRGRGRGGRDGFQMGSSSS NQPRPSDQHQFTETVAPENQLVSQTPVAGGMNWLNAARKGACTASPPPQQQQKDAPVLLGKITLKDSKKREPMGRPDGGNTSDESVSLHANHFPVDFNDGTIILH YDVDVRKVDGDQPGKSVTDRFDLRKIREKWLMDKPAEFPCDKTAYDGIRNIYSAVDLPAKPLTVNCSVEDDAKEYKYILTFKLVAQLQLDNVTEYLRRSLQNIIPRDV LQGMDLVMKENPRRCRISVGRCFYSNSARTSFNGGVAARKGFQQSLKLTSEGLALCLDYSELLVIPEQIPVIEFLENYYGKNIDDIFKYTRAGASDLLVGLKVKVTHR PNKQKFVIKELLPGETRTVKFKLQDTGEEVLLVDYFDKNYTPKIKNRHLPSLNIGKGSFENTSLEPKTRRDLIRETVLAKDGPRMTIPGNFKIRVDDNMTQISGRILPVP VLKLGGQNPPPNLKDKTCQWNLVGKSVVEGKALQRWALIDFSSKGCRDSLKLQVDQFVMKLKDQCRQLSINMDIPAVVHLTDMNELSTVGKVENLLKVVTDAAEKK LQGKLQMILCVMTSKHNGYKYLKWVSETKIGIVTQCCLSSNANKGHNQYIVNLCMKINAKLGGSNMELMERLPNFRSDDNVMFIGADVNHPAGKDADKYPSIAAVVA TINWPAANKYAARVSPQKSRTEKIVEFGKMCKDLVLTYEKRNSVKPNKIVVFRDGVSDSQFDMVLNEELTDLANAIYESNKYQPAITLVVAQKRHHTRLFPKEGNVS PGTVVDTQIVHPSGFDFYLCSHYGQLGTSKATHYHVLYDDNGFISVDLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLMEMKSPRSTTSSSEASS SSSSPIDSFAQEFYDLHHDLKDIMFFV	983 aa
		SpiLA0480	>SpiLA0480_Scaffold3065360_935_aa XTEWIVGTTDVVAVMITPAEVEVTVVEDKAVVVEGVSLRSEVEGVGPTSVVGPKWVSLHSNGGISRGDRVNTRFVVGLRKINRVKTIRLIRIRVVVQQGSGGGVANA WARPPPQRSQQHGAGNQLQVVDRSPPQSSDPVQVDLGSLKITDQSPSSRPESSKEKRVPIARPDTGKIAVKSIALLANHFPVRFNPQSTIMHYDVDIQQRADGNRP VKKLTNKSVLHMIREKLCADDPTRFPLDKTAYDGKKNIFSAVQLPTGCFAVNWSDGEDARLRSYDITIKLVAELKLCKLKEYLSGSLSHIPRDILQGMEVVMKENPTRC RTSVGRCFYSNEHLPDHDFRFGVAAYRGFQQSLKPTKGGLALCLDYSVLALRKPMPVLDFLKEYLGESNENTFRNNIRAAKGALVGLKVRVIHRRTSQKFLIKQLTD CKTREITFPLEDPEGINPPRDVLLVDYFRDKYQREIQFKDFPSLDIGKGNKKNYVPMEFCVLVEGQRYPKEDLDKDTALFLKNISLARPQDRRQAICEMVRAGDGPC GAVTRNFDIGVDRNMTRVPGRILPPPDLKLGGQNRLPVNDKCQWNLVGKSVVEGKALQRWALIDFSAQDRKPFFRLRVDEFVFRLKDRCRKLSINMEEPAVVHFTD MHELSEVGKVHKLLDGVVNAAKREINGKLQMIVCVMTSKHNGYKYLKWVSETQIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMELMDRLPNFGREDHV	935 aa

			MFIGADVNHPAAKNVTCPSIAAVVATVNWPAANRYAARVCPQVHRTEKILEFGKMCRDLVDTYAKINHVKPNKIVVFRDGVSEGQFDMVLNEELLDLAKAIYDSNYQ PAITLVVAQKRHHTRLFPEGGPANVPPVYYADLVAYRGRMFQEVLMEMNSPSSATSSSPTASFQQKFYDLHSDLQNVMFFV	
			>SpiLA0480_Scaffold3065190_1003_aa MDRGNYQRGGGDNTGRGRGNRGRGGPHVGGGRGGPHVGGGRGGPQMGSNHQPPQQWGNQPRGSGQYQFRGAPPGRGGTWVNQPVQRGGGNAWQRPQ QQGSGVPITAWARPPPQQPQQQGSGGGVATAWARPPPPPQEVVDRPQSSDPVHVDMGSLKITEASSSESSKEKRVPVTRPDTGKNCVKQIELLANHFVVTFNPH STIMHYDVDIQQQADENRPVKNLTNKSVLHMIRAKLCEDDPIQFPLDNTAYDGNKNIFSAVQLPTGCFAVNWSDGEDFKSRTYDITINLVAELQLRKLEQYLSGNLSYI PRYILQGMDLFMKDNPSRHRISVGRCFYSKNPHKDFRFGAAAYKGFQQSLKPTEAGLALCLDYSVLALRKPMSVLDYLRNYFQIPKEDIFTYNHQAAHDALKGLKVA VNHRRTSQKFVIKKLTDRKTSEITFPLEDPEGKDPPRDVLLVEYFRDKYQREIQFKDFPSLDVGKGSKINYVPMEFCVLVEGQRFPKEELDKASAMFLKNMSLAQPN ERKEAICEMVKAEDGPCGAITDNFGIKVDKSMTGVVGRVLPPPDLKLGGQSPLRVNDKCQWNLVGKSVVEGKALQRWALIDFSYKERNRLRVDEFVFRLRDRCIKL SINMEEPAEVHLTDMHELSEVGKVEKLLNFVVDAAKRKINGKLQMILCVMTSKHNGYKYLKWVSETKIGVVTQCCLSTNANKGQDQYLANLCMKINAKLGGSNMEL MQRLPNFRNGDNVMFIGADVNHPTSRDADKYPSIAAVVATINWPAANRYAARVCPQKHRTEKILEFGKMCADLVRTYEELNSVKPNKIVVFRDGVSGSQFDMVLNE ELNDLVKDIYDRYKYKPEITLVVAQKRHHTRLFPREGNVPPGTVVDTQIVHPFDFDFYLCSHFGQLGTSKATHYHVLWDENGFNSDSLQRLIYNMCFTFARCTKPVS LVPPVYYADLVAYRGRMFQEVVMEMNASSSTTSPASFEQRFYNLQPDLQNIMFFV	1003 aa
			>SpiLA0480_Scaffold3065190_999_aa MDRGNNNGRGGDRKRGRNSDRVPGHNEQRQGPARGYYDPSQYRARAYYEEEQGRARGQHEEEQGRARVQHEQEQGRGRGRGGRDGFQMGSSSSNQPRPS DQHQFTETVAPENQLVSQTPVAGGMNWLNAARKGACTASPPPQQQQKDAPVLLGKITLKDSKKREPMGRPDGGNTSDESVSLHANHFPVDFNDGTIILHYDVDVR KVDGDQPGKSVTDRFDLRKIREKWLMDKPAEFPCDKTAYDGIRNIYSAVDLPAKPLTVNCSVEDDAKEYKYILTFKLVAQLQLDNVTEYLRRSLQNIIPRDVLQGMDL VMKENPRRCRISVGRCFYSNSARTSFNGGVAARKGFQQSLKLTSEGLALCLDYSELLVIPEQIPVIEFLENYYGKNIDDIFKYTRAGASDLLVGLKVKVTHRPNKQKFV IKELLPGETRTVKFKLQDTGEEVLLVDYFDKNYTPKIKNRHLPSLNIGKGDKDNYVPMEFCDLVEGQRFPKDLLKTTSLEPKTRRDLIRETVLAKDGPRMTIPGNFKIR VDDNMTQISGRILPVPVLKLGGQNPPPNLKDKTCQWNLVGKSVVEGKALQRWALIDFSSKGCRDSLKLQVDQFVMKLKDQCRQLSINMDIPAVVHLTDMNELSTVG KVENLLKVVTDAAEKKLQGKLQMILCVMTSKHNGYKYLKWVSETKIGIVTQCCLSSNANKGHNQYIVNLCMKINAKLGGSNMELMERLPNFRSDDNVMFIGADVNHP AGKDADKYPSIAAVVATINWPAANKYAARVSPQKSRTEKIVEFGKMCKDLVLTYEKRNSVKPNKIVVFRDGVSDSQFDMVLNEELTDLANAIYESNKYQPAITLVVAQ KRHHTRLFPKEGNVSPGTVVDTQIVHPSGFDFYLCSHYGQLGTSKATHYHVLYDDNGFISVDLQRLIYNMCFTFARCTKPVSLVPPVYYADLVAYRGRMFQEVLME MKSPRSTTSSSEASSSSSSPIDSFAQEFYDLHHDLKDIMFFV	999 aa
	AGO4	*Sly*	>AGO4.1_Solyc06g073540.2.1 MAEEENGGSTEALPPPPPVPLNFSPAQAEPEPVKKKVLRVPMARRGLGSKGQKIPILTNHFKVNVSNVDGHFFHYSVALFYEDGRPVEGKGIGRKVLDRVHETYDT ELAGKDFAYDGEKSLFTIGSLPRNKLEFTVVLDDITSNRNNGTNGNSSPGRHGSPPNETDRKRLRRPYQSKTYKVEISFAAKIPMQAIANALRGQESENSQEALRVL DIILRQHAAKQGCLLVRQSFFHNDPKNFADVGGGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTAPANQEF KITGLSEKPCREQMFTLKQKSKDEDGEVQTSEVTVYDYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILS NALKINNYDAEPLLRSSGVSISSNFTQVDGRVLPAPKLKAGNGDDLFTRNGRWNFNNKRFFEPAKVERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFE ESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAAEISPSIPMVSKVPTMI LGMDVSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNIFKKVSDTDDDGIMRELLLDFYVSSGKRKPEHIIVFRDGVSESQFNQVLNIELDQLIEA CNFLDEKWSPKFVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFSPDELQELVHNLSYVYQRSTTAISIVAPISY AHLAATQVGQWMKFEDASETSSSHGGLTNAGPVTVPQLPRLQENVASSMFFC	913 aa
			>AGO4.2_Solyc01g008960.2.1 MAEEETNGAAAEGLPPPPPVPPDFTPAKTEIEPVKKKILRVPMARRGVGNKGQKIQILTNHFKVNVNNVDGHFFHYSVALFYEDGRPVDGKGVGRKVLDTVHETYD TELAGKDFAYDGEKSLFTIGALPRNKMEFTVVLDDVISNRNNGNSSPGGHGSPNEADRKRLRRPYQSKTFKVEISFAAKIPMQAIANALRGQESENSQEALRVLDIIL RQHAAKQGCLLVRQSFFHNDPKNFVDVGAGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTTPTNQEYKIT GLSDRPCREQLFTLKQKGKDADGEVQTTEVTVFDYFVNHRNIELRYSADLPCINVGKPKRPTFFPIELCSLVSLQRYTKSLSTFQRSSLVEKSRQKPQERMQVLSNA LKINQYDAEPLLRSCGISISNNFTQIEGRVLPPPKLKTGGDDFVPRNGRWNFNNKRLVDPTKIERWAVVNFSARCNVQGLVSDLIKCGKQKGIMVEDPFDVFEESPQ VRRAPPLVRVEKMFEQVQSKLPGAPKFLLCLLPERKNCDVYGPWKRKNLAEYGIVTQCIAPTRVNDQYITNVLLKINAKLGGLNSMLTVEHSPAIPMVSKVPTIILGMD VSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNLFKRTSDTEDDGIMREALLDFYVSSGKRKPEHIIIFRDGVSESQFSQVLNVELDQIIEACKFLD EKWSPKFVVIVAQKNHHTKFFQPNDPNNVPPGTIIDNKVCHPRNYDFYLCAHAGMIGTTRPTHYHVLYDELGFSADDLQELVHNLSYVYQRSTTAISVVAPICYAHLA ATQMGQWMKFEDASETSSSHNGVTNAGPVSVPQLPKLEEKVSSSMFFC	909 aa
			>AGO4.3_Solyc06g073530.1.1 MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKMNNYDA EPLLHSCGVTINSDFTQIEGRVLSAPELKAGNGVDIFAQSGRWNFNNKRFFESAKVEKWAVVNFSTNCDIGKLVECLTGLGETKGISVEAPLKVFEESRHHRRAPPV GRVDKMFEEIQSKLPDAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSP GQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPK FVIIVAQKNHHTKFFPYGSANNVPPGTIIDNKVCHPRNNDFYLCAHGGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQ WMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKNVASSMFFC	904 aa
			>AGO4.4_Solyc01g096750.1.1 MASSKDEATATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN	881 aa

			KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGGVQEV ETTVYDYFTYHRRIPLQYSGELPCINVGKPKHPTFIPLELCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRI LPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLCMDLQRCGKMKGIFISPPFQHIFEENQQYRRNPAPVRVEKMLEELKSKLPAPPQ FLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISR YRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQVINIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNV PPGTVIDNAVCHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVL VPQLPRLHKNVRSSMFFC	
		Spe	>AGO4.1_Sopen01g004450 MAEGETNGAAAEGLPPPPPVPPDFTPAKTEIEPVKKKILRVPMARRGVGNKGQKIQILTNHFKVNVNNVDGHFFHYSVALFYEDGRPVDGKGVGRKVLDTVHETYD TELAGKDFAYDGEKSLFTIGALPRNKMEFTVVLDDVISNRNNGNSSPGGHGSPNEADRKRLRRPYQSKTFKVEISFAAKIPMQAIANALRGQESENSQEALRVLDIIL RQHAAKQGCLLVRQSFFHNDPKNFVDVGAGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTSPTNQEYKIT GLSDRPCREQLFTLKQKGKDADGEVQTTEVTVFDYFVNHRNIELRYSADLPCINVGKPKRPTFFPIELCSLVSLQRYTKSLSTFQRSSLVEKSRQKPQERMQVLSNA LKINQYDAEPLLRSCGISISNNFTQIEGRVLPPPKLKTGGDDFVPRNGRWNFNNKRLVDPTKIERWAVVNFSARCNVQGLVSDLIKCGKQKGIMVEDPFDVFEESPQ VRRAPPLVRVEKMFEQVQSKLPGAPKFLLCLLPERKNCDVYGPWKRKNLAEYGIVTQCIAPTRVNDQYITNVLLKINAKLGGLNSMLTVEHSPAIPMVSKVPTIILGMD VSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNLFKRTSDTEDDGIMREALLDFYVSSGKRKPEHIIIFRDGVSESQFSQVLNVELDQIIEACKFLD EKWSPKFVVIVAQKNHHTKFFQPNDPNNVPPGTIIDNKVCHPRNYDFYLCAHAGMIGTTRPTHYHVLYDELGFSADDLQELVHNLSYVYQRSTTAISVVAPICYAHLA ATQMGQWMKFEDASETSSSHNGVTNAGPVSVPQLPKLEEKVSSSMFFC	909 aa
			>AGO4.3_Sopen03g030870 MSENQDLKAQREAVTLRAEIKILVDRWRLQKMQDAERLNESDALYENMLDKFKTASIQNFPRLQVDDVVPRSVQNFPSTCRQRIPAHDGGCASILFEYKSSKLISGG QDQEIKIWDTRSGSLSNIFYGCLGSVLDLSITHDNKSIIAASSSNDLYVWDANSGRIRHILTGTSTRFVQLM	179 aa
			>AGO4.7_Sopen06g029900 MAEEENGGSTEALPPPPPVPLNFSPAQAEPEPVKKKVLRVPMARRGLGSKGQKIPILTNHFKVNVSNVDGHFFHYSVALFYEDSRPVEGKGIGRKVLDRVHETYDT ELAGKDFAYDGEKSLFTIGSLPRNKLEFTVVLDDITSNRNNGTNGNSSPGRHGSPPNETDRKRLRRPYQSKTYKVEISFAAKIPMQAIANALRGQESENSQEALRVL DIILRQHAAKQGCLLVRQSFFHNDPKNFADVGGGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTAPANQEF KITGLSEKPCREQMFTLKQRSKDEDGEVQTSEVTVYDYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILS NALKINNYDAEPLLRSSGVSISSNFTQVDGRVLPAPKLKAGNGDDLFTRNGRWNFNNKRFFEPAKVERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFE ESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAAEVSPSIPMVSKVPTM ILGMDVSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNIFKKVSDTDDDGIMRELLLDFYVSSGKRKPEHIIVFRDGVSESQFNQVLNIELDQLIEA CNFLDEKWSPKFVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFSPDELQELVHNLSYVYQRSTTAISIVAPISY AHLAATQVGQWMKFEDASETSSSHGGLTNAGPVTVPQLPRLQENVASSMFFC	913 aa
			>AGO4.6_Sopen06g029890 MAEQEYGGSTEALPPPPPVPLDISPVKAEPAPVEKKLLRVPMARRGLGKKGHNIRILTNHFQVNVSNVDGHFFHYSVALFYENGQPVEVKGIGRKVLDRVHETYHAE LAGKRFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISFAGKIPMQAIANAFRGQEYDNSQEALRVLDIILRQHAAKKD CLLVRQSFFHNDSNNFVDVGGGVHGWRGFHSSFRTTQSGLSLNIDMSTTMIIQPGPVLDFLIANQNARNSVSLDWAKAKRVLKNLRVKTATSNQEFKITGLSEKSCR EQTFILKRRSKDEDGEVQTSEVTVYDYFVNDRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKLNNYVAE PLLHSCGVSINSDFTQIEGRVLAAPGLKAGNGVDIFAQNGRWNFNNKRFFESAKVEQWAVVNFSTNCDIGELVERLTGLGETKGISVEAPLEVFEEYPQLRRAPPVIR VDKMFEEIHSKLHGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPAKVNNHYLTNLLLKINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSPGQ SEVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNIFKKVSDTRDDGIMRELLLDFHASSQQRKPQQIIVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPKFVII VAQKNHHTKFFQSGSPHNVPPGTIIDNKVCHPRNNDFYLCAHAGTIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQWMK SEGTSETSSSQDGLRNAGPVTVPQLPSLQKNVATSMFFC	904 aa
			>AGO4.2_Sopen01g040460 MASSKDEGTATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGVSDKPCNEQTFTLKQKNGDEGVQEV ETTVYDYFTYHRRIPLQYSGDLPCINVGKQKHPTYIPLELCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRI LPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLCMDLQRCGKMKGIFISPPFQHIFEENQQYRRNPAPVRVEKMLEELKSKLPAPPQ FLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISR YRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQVINIELNQIIEACNHLEESWSPKFTVIVAQKNHHTRFFQTNSPDNV PPGTVIDNAVCHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGTVL VPQLPRLHKNVRSSMFFC	881 aa
		Sga	>Sga_AGO4.1_Scaffold69304_13.6_Contig6_913_aa MAEEENGGSTEALPPPPPVPLNFSPAQAEPEPVKKKVLRVPMARRGLGSKGQKIPILTNHFKVNVSNVDGHFFHYSVALFYEDGRPVEGKGIGRKVLDRVHETYDT ELAGKDFAYDGEKSLFTIGSLPRNKLEFTVVLDDITSNRNNGTNGNSSPGRHGSPPNETDRKRLRRPYQSKTYKVEISFAAKIPMQAIANALRGQESENSQEALRVL DIILRQHAAKQGCLLVRQSFFHNDPKNFADVGGGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTAPANQEF KITGLSEKPCREQMFTLKQKSKDEDGEVQTSEVTVYDYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILS	913 aa

			NALKINNYDAEPLLRSSGVSISSNFTQVDGRVLPAPKLKAGNGDDLFTRNGRWNFNNKRFFEPAKVERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFE ESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAAEISPSIPMVSKVPTMI LGMDVSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNIFKKVSDTDDDGIMRELLLDFYVSSGKRKPEHIIVFRDGVSESQFNQVLNIELDQLIEA CNFLDEKWSPKFVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFSPDELQELVHNLSYVYQRSTTAISIVAPISY AHLAATQVGQWMKFEDASETSSSHGGLTNAGPVTVPQLPRLQENVASSMFFC	
			>Sga_AGO4.2_Scaffold9634_12.7_Contig2_909_aa MAEEETNGAAAEGLPPPPPVPPDFTPAKTEIEPVKKKILRVPMARRGVGNKGQKIQILTNHFKVNVNNVDGHFFHYSVALFYEDGRPVDGKGVGRKVLDTVHETYD TELAGKDFAYDGEKSLFTIGALPRNKMEFTVVLDDVISNRNNGNSSPGGHGSPNEADRKRLRRPYQSKTFKVEISFAAKIPMQAIANALRGQESENSQEALRVLDIIL RQHAAKQGCLLVRQSFFHNDPKNFVDVGAGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTTPTNQEYKIT GLSDRPCREQLFTLKQKGKDADGEVQTTEVTVFDYFVNHRNIELRYSADLPCINVGKPKRPTFFPIELCSLVSLQRYTKSLSTFQRSSLVEKSRQKPQERMQVLSNA LKINQYDAEPLLRSCGISISNNFTQIEGRVLPPPKLKTGGDDFVPRNGRWNFNNKRLVDPTKIERWAVVNFSARCNVQGLVSDLIKCGKQKGIMVEDPFDVFEESPQ VRRAPPLVRVEKMFEQVQSKLPGAPKFLLCLLPERKNCDVYGPWKRKNLAEYGIVTQCIAPTRVNDQYITNVLLKINAKLGGLNSMLTVEHSPAIPMVSKVPTIILGMD VSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNLFKRTSDTEDDGIMREALLDFYVSSGKRKPEHIIIFRDGVSESQFSQVLNVELDQIIEACKFLD EKWSPKFVVIVAQKNHHTKFFQPNDPNNVPPGTIIDNKVCHPRNYDFYLCAHAGMIGTTRPTHYHVLYDELGFSADDLQELVHNLSYVYQRSTTAISVVAPICYAHLA ATQMGQWMKFEDASETSSSHNGVTNAGPVSVPQLPKLEEKVSSSMFFC	909 aa
			>Sga_AGO4.3_Scaffold96132_14.3_Contig1_905_aa MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKMNNYDA EPLLHSCGVTINSDFTQIEGRVLSAPELKAGNGVDIFAQSGRWNFNNKRFFEPAKVERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFEESPQLRRAPPV VRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSP GQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPP KFVIIVAQKNHHTKFFQYGSANNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVG QWMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKNVASSMFFC	905 aa
			>Sga_AGO4.4_Scaffold15546_11.9_Contig4_881_aa MASSKDEGTATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGGVQEV ETTVYDYFTYHRRIPLQYSGELPCINVGKPKHPTFIPLELCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRI LPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLCMDLQRCGKMKGIFISPPFQHIFEENQQYRRNPAPVRVEKMLEELKSKLPAPPQ FLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISR YRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQVINIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNV PPGTVIDNAVCHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVL VPQLPRLHKNVRSSMFFC	881 aa
			>Sga_AGO4.2_Scaffold15546_11.9_Contig4_816_aa MASSKDEGTATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGGVQEV ETTVYDYFTYHRRIPLQYSGELPCINVGKPKHPTFIPLLCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRIL PTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVQRKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTELS PTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISRYRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQV INIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNVPPGTVIDNAVCHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRST TAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVLVPQLPRLHKNVRSSMFFC	816 aa
			>Sga_AGO4.6_Sopen06g029890.1_Scaffold96132_14.3_Contig1_821_aa MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRWNFNNKRFFEPAKVERWAVVNFSARCDVRGLVRDLTRL GETKGISVEAPFEVFEESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLA VEVSRSIPMISKVPTMILGMDVSHGSPGQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSES QFNQVLNIELDQLIEACKFLDEKWSPPKFVIIVAQKNHHTKFFQYGSANNVPPGTIIDNKVCHPRNNDFYLCVIEGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQ RSTTATSIVAPIGYAHLAAAQVGQWMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKNVASSMFFC	821 aa
			>Sga_AGO4.3_Sopen03g030870.3_Scaffold97525_11.8_Contig5_120_aa MAEHQDLKAQLEAMTLRANNAEAENKTLVDRWMLLKMQDAERLNEANALYGDMLDKVKAASIEKLARQQVDGVVRQSEDGAEFYVESSIPSTCKQRIPAHDGGCA SIVFEYNSSKLISGX	120 aa

		Spr	>Spr_AGO4.1_a8588_820_aa MNNTDGHFFHYSVAINYEDGNPVEVGHFFHYSVAINYEDGNPVEVGKDFAYDGEKSLFTIGALPGNKLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWS KAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDLGGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVID FLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGEVQEVETTVYDYFTYHRRIPLQYSGDLPCINVGKPKHPTYIPLELCTL VSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRILPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAV NFSARCDVRKLCMDLQRCGKMKGIFIDPPFQHIFEENQQYRRNPAPVRVEKMLDELKSKLPAPPQFLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYL TNVLLKINAKLGGMNSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISRYRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSS KSVKPEHIIIFRDGVSESQFNQVINIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNVPPGTVIDNAICHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIG FSADDMQELVHSLSYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAX	820 aa
			>Spr_AGO4.3_a8588_809_aa XVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGNKLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKI PMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDLGGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPY QIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGEVQEVETTVYDYFTYHRRIPLQYSGDLPCINVGKPKHPTYIPLELCTLVSLQRYTKALSN LQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRILPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLC MDLQRCGKMKGIFIDPPFQHIFEENQQYRRNPAPVRVEKMLDELKSKLPAPPQFLLCIQMLDELKSKLPAPPQFLLCILGIVTQCIAPTKINDQYLTNVLLKINAKLGGM NSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISRYRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKSVKPEHIIIFRDGV SESQFNQVINIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNVPPGTVIDNAICHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSL SYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAX	809 aa
			>Spr_AGO4.4_a8588_881_aa MASSKDEGTATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGEVQEV ETTVYDYFTYHRRIPLQYSGDLPCINVGKPKHPTYIPLELCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRI LPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLCMDLQRCGKMKGIFIDPPFQHIFEENQQYRRNPAPVRVEKMLDELKSKLPAPPQ FLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISR YRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKSVKPEHIIIFRDGVSESQFNQVINIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNV PPGTVIDNAICHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVLV PQLPRLHKNVRSSMFFC	881 aa
		Sch	>Sch_AGO4.1_Scaffold431_913_aa MAEEENGGSTEALPPPPPVPLNFSPAQAEPESVKKKVLRVPMARRGLGSKGQKIPILTNHFKVNVSNVDGHFFHYSVALFYEDGRPVEGKGIGRKVLDRVHETYDT ELAGKDFAYDGEKSLFTIGSLPRNKLEFTVVLDDITSNRNNGTNGNSSPGRHGSPPNETDRKRLRRPYQSKTYKVEISFAAKIPMQAIANALRGQESENSQEALRVL DIILRQHAAKQGCLLVRQSFFHNDPKNFADVGGGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTAPANQEF KITGLSEKPCREQMFTLKQKSKDEDGEVQTSEVTVYDYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILS NALKINNYDAEPLLRSSGVSISSNFTQVEGRVLPAPKLKAGNGDDLFTRNGRWNFNNKRFFEPAKIERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFEE SPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAAEVSPSIPMVSKVPTMI LGMDVSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNIFKKVSETDDDGIMRELLLDFYVSSGKRKPEHIIVFRDGVSESQFNQVLNIELDQLIEA CNFLDEKWSPKFVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFSPDELQELVHNLSYVYQRSTTAISIVAPISY AHLAATQVGQWMKFEDASETSSSHGGLTNAGPVTVPQLPRLQENVASSMFFC	913 aa
			>Sch_AGO4.2_Scaffold2265_909_aa MAEEETNGAAAEGLPPPPPVPPDFTPAKTEIEPVKKKILRVPMARRGVGNKGQKIQILTNHFKVNVNNVDGHFFHYSVALFYEDGRPVDGKGVGRKVLDTVHETYD TELAGKDFAYDGEKSLFTIGALPRNKMEFTVVLDDVISNRNNGNSSPGGHGSPNEADRKRLRRPYQSKTFKVEISFAAKIPMQAIANALRGQESENSQEALRVLDIIL RQHAAKQGCLLVRQSFFHNDPKNFVDVGAGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTTPTNQEYKIT GLSDRPCREQLFTLKQKGKDADGEVQTTEVTVFDYFVNHRNIELRYSADLPCINVGKPKRPTFFPIELCSLVSLQRYTKSLSTFQRSSLVEKSRQKPQERMQVLSNA LKINQYDAEPLLRSCGISISNNFTQIEGRVLPPPKLKTGGDDFVPRNGRWNFNNKRLVDPTKIERWAVVNFSARCNVQGLVSDLIKCGKQKGIMVEDPFDVFEESPQ VRRAPPLVRVEKMFEQVQSKLPGAPKFLLCLLPERKNCDVYGPWKRKNLAEYGIVTQCIAPTRVNDQYITNVLLKINAKLGGLNSMLTVEHSPAIPMVSKVPTIIIGMD VSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNLFKRTSDTEDDGIMREALLDFYVSSGKRKPEHIIIFRDGVSESQFSQVLNVELDQIIEACKFLD EKWSPKFVVIVAQKNHHTKFFQPNDPNNVPPGTIIDNKVCHPRNYDFYLCAHAGMIGTTRPTHYHVLYDELGFSADDLQELVHNLSYVYQRSTTAISVVAPICYAHLA ATQMGQWMKFEDASETSSSHNGVTNAGPVSVPQLPKLEEKVSSSMFFC	909 aa
			>Sch_AGO4.3_Scaffold431_849_aa MAEQEYGGSTEALPPPPPLPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGNNIRILTNHFQVNVSNVDGHFFHYSVALFYEDDQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISFAGKIPMQAIANAFRGEEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNARDPFSLDWVKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDGEVQTSEVTVYNYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSNALKINNYDA EPLLRSSGVSISSNFTQVEGRVLPAPKLKAGNEVDIFAQNGRWNFNNKRFFEPAKIERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFEESPQLRRAPPV VRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPVKVFNDHYLTNLLLKINAKLGGLNSTLAVEVSRSIPMISKVPTMILGMDVSHGSP GQSDVPSIAAVEASANHSIQDGVSESQFNQVLNIELDQIIEACKFLDEKWSPKFVIIVAQKNHHTKFFQSGSSNNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPT	849 aa

			HYHVLLDEVGFSPDELQELVHNLSYVYQRSTTATSIVAPIGYAHLAAAQVGQWMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKNVASSMFFC	
			>Sch_AGO4.4_Scaffold1590_881_aa MASSKDEGTATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGIGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGEVQEV ETTVYDYFTYHRRIPLQYSGDLPCINVGKPKHPTFIPLELCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRI LPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLCMDLQRCGKMKGIFIDPPFQHIFEENQQYRRNPAPVRVEKMLDELKSKLPAPPQ FLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKVNDQYLTNVLLKINAKLGGMNSFLTTELSPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISR YRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQVINIELNQIIEACNHLEESWSPKFTVIVAQKNHHTRFFQTNSPDNV PPGTVIDNAICHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRSTTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVLV PQLPRLHKNVRSSMFFC	881 aa
			>Sch_AGO4.2_Scaffold1590_peptide_1_290_aa MASSKDEGTATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGIGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKASPGKEDAKESEDQDQPFK	290 aa
			>Sch_AGO4.2_Scaffold1590_peptide_2|490_aa MRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRILPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVRKLCMDLQRCGKMKGIFIDPP FQHIFEENQQYRRNPAPVRVEKMLDELKSKLPAPPQFLLCILPERKNSDLYGPWKKRNLADLGIVTQCIAPTKVNDQYLTNVLLKINAKLGGMNSFLTTELSPTLPQIS KVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISRYRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQVINIELNQI IEACNHLEESWSPKFTVIVAQKNHHTRFFQTNSPDNVPPGTVIDNAICHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRSTTAISVVAP ICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVLVPQLPRLHKNVRSSMFFC	490 aa
			>Sch_AGO4.6_Scaffold431_867_aa MAEQEYGGSTEALPPPPPLPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGNNIRILTNHFQVNVSNVDGHFFHYSVALFYEDDQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISFAGKIPMQAIANAFRGEEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLITDMSTTMIIKPGPVLDFLIANQNARDPFSLDWVKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDGEVQTSEVTVYNYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSNALKINNYDA EPLLRSSGVSISSNFTQVEKWAVVNFSTNCDIGKLVERLTGLGETKGISVEAPFEVFEESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKR KNLADHGIVTQCLAPVKVFNDHYLTNLLLKINAKLGGLNSTLAVEVSRSIPMISKVPTMILGMDVSHGSPGQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNI FKKVSDTRDDGIMRELLLDFHASSQQRKPQQIIVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPKFVIIVAQKNHHTKFFQSGSSNNVPPGTIIDNKVCHPRNND FYLCAHAGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQWMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKNVASS MFFC	867 aa
		SpiLA1589	>SpiLA1589_AGO4.1_Contig:unspecified:6668547:1:4047:1_Contig:unspecified:6679784:1:4385:1_913_aa MAEEENGGSTEALPPPPPVPLNFSPAQAEPEPVKKKVLRVPMARRGLGSKGQKIPILTNHFKVNVSNVDGHFFHYSVALFYEDGRPVEGKGIGRKVLDRVHETYDT ELAGKDFAYDGEKSLFTIGSLPRNKLEFTVVLDDITSNRNNGTNGNSSPGRHGSPPNETDRKRLRRPYQSKTYKVEISFAAKIPMQAIANALRGQESENSQEALRVL DIILRQHAAKQGCLLVRQSFFHNDPKNFADVGGGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTAPANQEF KITGLSEKPCREQMFTLKQKSKDEDGEVQTSEVTVYDYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILS NALKMNNYDAEPLLHSCGVTINSDFTQIEGRVLSAPELKAGNGVDIFAQSGRWNFNNKRFFESAKVEKWAVVNFSTNCDIGKLVERLTGLGETKGISVEAPLKVFEE SRHHRRAPPVGRVDKMFEEIQSKLPDAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAAEISPSIPMVSKVPTMIL GMDVSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNIFKKVSDTDDDGIMRELLLDFYVSSGKRKPEHIIVFRDGVSESQFNQVLNIELDQLIEAC NFLDEKWSPKFVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFSPDELQELVHNLSYVYQRSTTAISIVAPISYA HLAATQVGQWMKFEDASETSSSHGGLTNAGPVTVPQLPRLQENVASSMFFC	913 aa
			>SpiLA1589_AGO4.2_Contig:unspecified:4637809:1:8203:1_786_aa MAEEETNGAAAEGLPPPPPVPPDFTPAKTEIEPVKKKILRVPMARRGVGNKGQKIQILTNHFKVNVNNVDGHFFHYSVALFYEDGRPVDGKGVGRKVLDTVHETYD TELAGKDFAYDGEKSLFTIGALPRNKMEFTVVLDDVISNRNNGNSSPGGHGSPNEADRKRLRRPYQSKTFKVEISFAAKIPMQAIANALRGQESENSQEALRVLDIIL RQHAAKQGCLLVRQSFFHNDPKNFVDVGAGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTTPTNQEYKIT GLSDRPCREQLFTLKQKGKDADGGDDFVPRNGRWNFNNKRLVDPTKIERWAVVNFSARCNVQGLVSDLIKCGKQKGIMVEDPFDVFEESPQVRRAPPLVRVEKM FEQVQSKLPGAPKFLLCLLPERKNCDVYGPWKRKNLAEYGIVTQCIAPTRVNDQYITNVLLKINAKLGGLNSMLTVEHSPAIPMVSKVPTIILGMDVSHGSPGQSDVP SIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNLFKRTSDTEDDGIMREALLDFYVSSGKRKPEHIIIFRDGVSESQFSQVLNVELDQIIEACKFLDEKWSPKFVVIVAQ KNHHTKFFQPNDPNNVPPGTIIDNKVCHPRNYDFYLCAHAGMIGTTRPTHYHVLYDELGFSADDLQELVHNLSYVYQRSTTAISVVAPICYAHLAATQMGQWMKFED ASETSSSHNGVTNAGPVSVPQLPKLEEKVSSSMFFC	786 aa
			>SpiLA1589_AGO4.3_Contig:unspecified:6556837:1:2234:1_904_aa MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKMNNYDA EPLLHSCGVTINSDFTQIEGRVLSAPELKAGNGVDIFAQSGRWNFNNKRFFESAKVEKWAVVNFSTNCDIGKLVERLTGLGETKGISVEAPLKVFEESRHHRRAPPV	904 aa

			GRVDKMFEEIQSKLPDAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSP GQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPK FVIIVAQKNHHTKFFPYGSANNVPPGTIIDNKVCHPRNNDFYLCAHGGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQ WMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKNVASSMFFC	
			>SpiLA1589_AGO4.4_Contig:unspecified:15014:1:12910:1_816_aa MASSKDEATATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGGVQEV ETTVYDYFTYHRRIPLQYSGELPCINVGKPKHPTFIPLLCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRIL PTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVQRKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTELS PTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISRYRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQV INIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNVPPGTVIDNAVCHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRST TAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVLVPQLPRLHKNVRSSMFFC	816 aa
			>SpiLA1589_AGO4.6_Contig:unspecified:6556837:1:2234:1_871_aa MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKMNNYDA EPLLHSCGVTINSDFTQIEGPKVEKWAVVNFSTNCDIGKLVERLTGLGETKGISVEAPFEVFEESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYG PWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSPGQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKV EIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPKFVIIVAQKNHHTKFFPYGSANNVPPGTIIDNKVCHP RNNDFYLCAHGGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQWMKSEGTSETSSSQDGLRNAGPVTVPQLPRLQKN VASSMFFC	871 aa
		SpiLA0480	>SpiLA0480_AGO4.1_Scaffold3067271_3_913_aa MAEEENGGSTEALPPPPPVPLNFSPAQAEPEPVKKKVLRVPMARRGLGSKGQKIPILTNHFKVNVSNVDGHFFHYSVALFYEDGRPVEGKGIGRKVLDRVHETYDT ELAGKDFAYDGEKSLFTIGSLPRNKLEFTVVLDDITSNRNNGTNGNSSPGRHGSPPNETDRKRLRRPYQSKTYKVEISFAAKIPMQAIANALRGQESENSQEALRVL DIILRQHAAKQGCLLVRQSFFHNDPKNFADVGGGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTAPANQEF KITGLSEKPCREQMFTLKQKSKDEDGEVQTSEVTVYDYFVNHRNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILS NALKINNYDAEPLLRSSGVSISSNFTQVDGRVLPAPKLKAGNGDDLFTRNGRWNFNNKRFFEPAKVERWAVVNFSARCDVRGLVRDLTRLGETKGISVEAPFEVFE ESPQLRRAPPVVRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAAEISPSIPMVSKVPTMI LGMDVSHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNIFKKVSDTDDDGIMRELLLDFYVSSGKRKPEHIIVFRDGVSESQFNQVLNIELDQLIEA CNFLDEKWSPKFVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFSPDELQELVHNLSYVYQRSTTAISIVAPISY AHLAATQVGQWMKFEDASETSSSHGGLTNAGPVTVPQLPRLQENVASSMFFC	913 aa
			>SpiLA0480_AGO4.2_Scaffold3067963_909_aa MAEEETNGAAAEGLPPPPPVPPDFTPAKTEIEPVKKKILRIPMARRGVGNKGQKIQILTNHFKVNVNNVDGHFFHYSVALFYEDGRPVDGKGVGRKVLDTVHETYDT ELAGKDFAYDGEKSLFTIGALPRNKMEFTVVLDDVISNRNNGNSSPGGHGSPNEADRKRLRRPYQSKTFKVEISFAAKIPMQAIANALRGQESENSQEALRVLDIILR QHAAKQGCLLVRQSFFHNDPKNFVDVGAGVLGCRGFHSSFRTTQSGLSLNIDVSTTMIIQPGPVVDFLIANQNAKDPFSLDWAKAKRVLKNLRVKTTPTNQEYKITG LSDRPCREQLFTLKQKGKDADGEVQTTEVTVFDYFVNHRNIELRYSADLPCINVGKPKRPTFFPIELCSLVSLQRYTKSLSTFQRSSLVEKSRQKPQERMQVLSNAL KINQYDAEPLLRSCGISISNNFTQIEGRVLPPPKLKTGGDDFVPRNGRWNFNNKRLVDPTKIERWAVVNFSARCNVQGLVSDLIKCGKQKGIMVEDPFDVFEESPQV RRAPPLVRVEKMFEQVQSKLPGAPKFLLCLLPERKNCDVYGPWKRKNLAEYGIVTQCIAPTRVNDQYITNVLLKINAKLGGLNSMLTVEHSPAIPMVSKVPTIILGMDV SHGSPGQSDVPSIAAVVSSRQWPSISRYRASVRTQSPKVEMIDNLFKRTSDTEDDGIMREALLDFYVSSGKRKPEHIIIFRDGVSESQFSQVLNVELDQIIEACKFLDE KWSPKFVVIVAQKNHHTKFFQPNDPNNVPPGTIIDNKVCHPRNYDFYLCAHAGMIGTTRPTHYHVLYDELGFSADDLQELVHNLSYVYQRSTTAISVVAPICYAHLAA TQMGQWMKFEDASETSSSHNGVTNAGPVSVPQLPKLEEKVSSSMFFC	909 aa
			>SpiLA0480_AGO4.3_Scaffold3067271_881_aa MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKMNNYDA EPLLHSCGVTINSDFTQIEGRVLSAPELKAGNGVDIFAQSGRWNFNNKRFFESAKVEKWAVVNFSTNCDIGKLVERLTGLGETKGISVEAPLKVLKSLDIIEGLLLLAEL TKCLKRSSQNFLTPQSFFSVFFLRGKIVTYVDHGSEKIWLIMINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSPGQSDVPSIAAVVSSRQWPSISHYRASV RTQSPKVEIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSESQFNQVLNIELDQIIEACKFLDEKWSPKFVIIVAQKNHHTKFFQYGSANNVPPGTII DNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQWMKSEDTSETSSSQDGLRNAGPVTVP QLPRLQKNVASSMFFC	881 aa
			>SpiLA0480_AGO4.4_Scaffold3060406_817_aa MASSKDEATATKLDRHPMARQGTGSKGQKIRLLTNHFKVGMNNTDGHFFHYSVAINYEDGNPVEVKGVGRKILDKVHQTYSMELAGKDFAYDGEKSLFTIGALPGN KLEFDVVLEDVSSSRTDRGSPDGSPSDVDRKRSKKQPWSKAYKVVIKYAAKIPMQAIANALRGQDSEQYQEAVRVLDIILRQHAAKRGCLIVRQSFFHNEPRNFVDL	817 aa

			GGGVSGCRGFHASFRATQGGLSLNMDVSTTMIVKPGAVIDFLLANQNAKEPYQIDWSKAKRMLKSLRIKTSPSNREYKITGLSDKPCNEQTFTLKQKNGDGGVQEV ETTVYDYFTYHRRIPLQYSGELPCINVGKPKHPTFIPLELCTLVSLQRYTKALSNLQRASLVEKSRQKPQERMRALTDALKTSNYKADPLLGSAGISISDQFTQVDGRI LPTPKLRVGDDQDLFPRNGRWNFNQKRLVEPVKLERWAAVNFSARCDVQRKNSDLYGPWKKRNLADLGIVTQCIAPTKINDQYLTNVLLKINAKLGGMNSFLTTEL SPTLPQISKVPTIIIGMDVSHGSPGRADAPSIAAVVSSRQWPFISRYRAAVCTQSPKLEMIDSLYKKVSDTVDEGLFRELLRDFYVSSKNVKPEHIIIFRDGVSESQFNQ VINIELNQIIEACNHLEETWSPKFTVIVAQKNHHTRFFQTNSPDNVPPGTVIDNAVCHPKTNDFYMCAHAGPIGTTRPTHYHILHDEIGFSADDMQELVHSLSYVYQRS TTAISVVAPICYAHLAAAQVAQFIKFDEISEATSSHGGVSTAGSVLVPQLPRLHKNVRSSMFFC	
			>SpiLA0480_AGO4.5_Scaffold3064212_759_aa QKLDFTVVLDAATSKRWKTDGNLSGDGELSEGDQKRQKIISRFKTFRIQINFVSIIPFKTMPDGKHGVKSRNNEVLIALDTILQHSNAKRNSLLLRQSYFPNEMKNFMG LTGGILGCRGFHSSFQSVQGGLYFNLDTSTTTLIQPGPLVNFLMANQNVEIPFKIDWTKAKILKNLRIKLLHSNREHKITGLSNRTCKEEKFLLRLRGSNNQNDNGQTV EITVYEYFVRRCGIELGYSSNLPCINVGSQHKPQFIPVELCSLVPLQRFKKELSLHQRSLLVNNSSQKPIELMKHLNEELKANDYNTDPMLRACGISINKSYTEVEGRV LFPPQLRVGNKEYLASRFSCWSFNGKKFADPKSIEFWAVVNFSTGHDIRAFCIEMAKLGAMRGMHIHPPSFVFEENAKHKKKPGSVRVNKMFEQIIPKFRKDPPRFL LCFLPAKFSNLYGPWKKKCLMTFGIRNQCIAKNKVDETYLANVMLKINAKVWDTNRFFTYMLITHKNSKSLVVLQLGGLNSMLSAEVSQTIPLVSKVPTMILAMGLTHA PSSRSDLPSVAAVVGSRQWPMISYYRASTCIQPPKTETIHSLFRPVSDREDTGMIRELLMDFHASSGNRKPEQIIIFRQGLGESQFNHIFSEMEEIIIGLRHHTKLFQPN SSDNIPPGTVVDTKICHPLYNNNFYICAHAARVGTSRPIHYFVLLDEIGFSSDTVQELVHCLCYVSQRCTSAISEVAPIRYARLVSAQMLEIMKTEGPELPMLHKN	759 aa
			>SpiLA0480_AGO4.6_Scaffold3067271_904_aa MAEQEYGGSTEALPPPPPVPLDFSPEKAEPAPVEKKLLRVPMARRGLGKKGRNIQILTNHFQVNVSNVDGHFFHYSVALFYEDGQPVEVKGIGRKVLDRVHETYHA ELAGKGFAYDGEKSLFTIGSLPRSRFEFTVVLNDITSNRNVGTSSPPNEADRKRLRRPYQSKTYKVKISLAGKIPMQAIANAFRGQEYENSQEALRVLDIILRQHAAKK DCLLVRQSFFHNDSNNFVDVGGGVHGLRGFHSSFRTTQSGLSLNIDMSTTMIIKPGPVLDFLIANQNSRDSVSLDWAKAKRVLKNLKVQTATSNQEFKITGLSEKSC REQTFILKRRSKDEDCEVQTSEVTVYDYFVNHCNIDLRYSADLPCLNVGKPKRPTYFPIELCTLVSLQRYTKALSTFQRASLVEKSRQKPQERMQILSHALKMNNYDA EPLLHSCGVTINSDFTQIEGRVLSAPELKAGNGVDIFAQSGRWNFNNKRFFESAKVEKWAVVNFSTNCDIGKLVERLTGLGETKGISVEAPFEVFEESPQLRRAPPV VRVDKMFEEIQSKLPGAPKFLLCLLPERKNCDIYGPWKRKNLADHGIVTQCLAPGRVNDQYLTNLLLKINAKLGGLNSMLAVEVSRSIPMISKVPTMILGMDVSHGSP GQSDVPSIAAVVSSRQWPSISHYRASVRTQSPKVEIIDNIFKEVSDTRDDGIMRELLLDFHASSQQRKPQQILVFRDGVSESQFNQVLNIELDQIIEACNFLDEKWSPK FVIIVAQKNHHTKFFQSGSPDNVPPGTIIDNKVCHPRNNDFYLCAHAGMIGTTRPTHYHVLLDEVGFKPDELQELVHNLCYVYQRSTTATSIVAPIGYAHLAAAQVGQ WMKSEDTSETSSSQDGLRNAGPVTVPQLPRLQKNVASSMFFC	904 aa
	AGO5	*Sly*	>Solyc06g074730.2.1 MSERGRGRRGGSPYGGGRGGGRTPPYGGGRGDGRTPPYGGGRGGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTREVE QKLSLQPSTSANPPARPQPAQQSSPPVQPPVATIPAHLAGPSTSTQPPRPPPVSSKSIRPPPRPDNGKLGRKCVVRANHFLVQVADRDVHHYDVTISPEVLSKKVC RLIIQQLVNNYRLSHLGGRGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGPRREKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVG RSLFHHTFAGDAGLLTGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESVFVSDYVLRHLNLRDHPQVSLSDQDHSKVRKVLKGVKVEATHQGRHYRITGLTPK SSSQMMFPVDGTDGMISVEQYFNTKYEIVLAYPRLPAIQCGNSAKPVYLPMEICKIVPGQRYTKMLNGRQVTEMLRATCQRPKERLNGIQNIVRVNKYADDDLVHEF GIGVDARLTTIEARVLNPPTLRFHASGKESRVDPRVGQWNMIDKKMINPAHVYYWTCVSFSQQIPPDRLVDGLHRMCISKGMTFDAPLVPFRQARPDHIETTLRDIH RESMQAIDRLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQCCHPKNLRPPSIAFLENLSLKINVKVGGRNSVLELAVSKNMPFLTDKTTIVFGADVTHPQP GEDSSPSIAAVVASMDWPEVTKYRGIVSAQPHRQEIIMDLYTEKEDSKRGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQFNQVLLEEMDAIRKACVALQSD YMPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICHPTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLCYTYVRCTRSVSLVPP AYYAHLAAFRARYYMENDVDVRAANEGGEGGAAAQFRQLPKIHENVSEVMFYC	1011 aa
		Spe	>Sopen06g031140 MSERGRGRRGGSPYGGGRGGGRTPPYGGGRGDGRTPPYGGGRGGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTREVE QKLSLQPSTSANPPARPQPAQQSSPPVQPPVATIPAHLAGPSTSTQPPRPPPVSSKSIRPPPRPDYGKLGRKCVVRANHFLVQVADRDVHHYDVTISPEVLSKKVC RLIIQQLVNNYRLSHLGGRGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGPRREKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVG RSLFHHTFAGDAGLLSGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESVFVSDYVLRHLNLRDHPQVSLSDQDHSKVRKVLKGVKVEATHQGRRYRITGLTPK SSSQMMFPVDGTDGMISVDQYFNKKYNIVLAYTKLPAIQCGNSAKPVYLPMEICKIVPGQRYTKMLNGRQVTEMLRATCQRPKERQNGIQNIVKVNKYADDDLVHEF GIGVDARLTTIEARVLNPPTLRFHASGKESRVDPRVGQWNMIDKKMINPAHVYYWTCVSFSQQIPPERLVDGLLRMCISKGMTFAASLVPFRQARPDHIETTLRDIHR ESMQAIDKLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQCCHPKNLRPPSIAFLENLSLKINVKVGGRNSVLEMAVSKKMPFLTDKTTIVFGADVTHPQPG EDSSPSIAAVVASMDWPEVAKYRGIVSAQPHRQEIITDLYTEKEDSKRGVVRGGMIMDLLKAFYAATKIKPERIIFYRDGVSEGQFNQVLLEEMDAIRKACVALQSDY MPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICHPTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLCYTYVRCTRSVSLVPPA YYAHLAAFRARYYMENDVDVRSANEGGEGGAAAHFRQLPKIHENVSEVMFYC	1011 aa
		Sga	>Sga_Scaffold41608_11.7_Contig4_858_aa MSERGRGRRGGSPYGGGRGGGRTPPYGGGRGDGRTPPYGGGRGGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTRER DRRLRRSRQGRHRYHLKAFGLLLDRITGSWGVADRDVHHYDVTISPEVLSKKVCRLIIQQLVNNYRLSHLGGRGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGP RREKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVGRSLFHHTFAGDAGLLTGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESV FVSDYVLRHLNLRDHPQVSLSDQDHSKVRKVLKGVKVEATHQGRRYRITGLTPKSSSQMMFPVDGTDGMISVEQYFNTKYKIVLAYPRLPAIQCGNSAKPVYLPMEI CKIVPGQRYTKMLNGRQIPPDRLVDGLHRMCISKGMTFDAPLVPFRQARPDHIETTLRDIHRESMQAIDKLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQ CCHPKNLRPPSIAFLENLSLKINVKVGGRNSVLELAVSKNMPFLTDKTTIVFGADVTHPQPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQPHRQEIIMDLYTEKEDS KRGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQFNQVLLEEMDAIRKACVALQSDYMPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICH PTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLCYTYVRCTRSVSLVPPAYYAHLAAFRARYYMENDVDVRAANEGGEGGAAAQFRQLPKIHENV SEVMFYC	858 aa

			>Sga_Sopen06g031140.1_Scaffold41608_11.7_Contig4_921_aa MSERGRGRRGGSPYGGGRGGGRTPPYGGGRGDGRTPPYGGGRGGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTRER DRRLRRSRQGRHRYHLKAFGLLLDRITGSWGVADRDVHHYDVTISPEVLSKKVCRLIIQQLVNNYRLSHLGGRGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGP RREKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVGRSLFHHTFAGDAGLLTGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESV FVSDYVLRHLNLRDHPQVSLSDQDHSKVRKVLKGVKVEATHQGRRYRITGLTPKSSSQMMFPVDGTDGMISVEQYFNTKYKIVLAYPRLPAIQCGNSAKPVYLPMEI CKIVPGQRYTKMLNGRQVTEMLRATCQRPKERLNGIQNIVRVNKYADDDLVHEFGIGVIVRVNKYADDDLVHEFGIGVAKIPPDRLVDGLHRMCISKGMTFDAPLVPF RQARPDHIETTLRDIHRESMQAIDKLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQCCHPKNLRPPSIAFLENLSLKINVKVGGRNSVLELAVSKNMPFLTD KTTIVFGADVTHPQPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQPHRQEIIMDLYTEKEDSKRGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQFNQVLLE EMDAIRKACVALQSDYMPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICHPTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLC YTYVRCTRSVSLVPPAYYAHLAAFRARYYMENDVDVRAANEGGEGGAAAQFRQLPKIHENVSEVMFYC	921 aa
		Spr	>Spr_a2745_999_aa MSERGRGRRGGSPYGGGRGDGRTPPYGGGRGGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTREVEQKLSLQPSTSANP PARPQPAQQSSPPVQPPVATIPAHLAGPSTSTQPPRPPPVSSKSIRPPPRPDLGKLGRKCLVRANHFLVQVADRDVHHYDVTISPEVLSKKVCRLIIQQLVNNYRLSH LGGMGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGPRREKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVGRSLFHHTFAGDAGL LTGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESVFVSDYVLRHLNLRDHPRVSLSDQDHSKVRKVLKGVKVEATHQGRRYRITGLTPESSSEMMFRVDGTDG MISVEQYFNKKYNIVLAYPKLPAIQCGNSAKPVYLPMEICKIVPGQRYTKMLNGRQVTEMLRATCQRPRERQNGIQNIVRVNKYADDDLVHEFGIGVDARLTTIEARVL NPPTLRFHASGKESRVDPRVGQWNMIDKKMINPAHVYYWTCVSFSQQIPPERLVDGLLRMCISKGMTFAAPLVPFRQARPDHIATTLRDIHRESMQAIDKLGEDLKI KHLQLLLVILPDSTGQYGRIKSLCEIDLGIVSQCCHPKNLRPPSIAYLENLSLKINVKVGGRNSVLELAVSKNMPFLTDKTTIVFGADVTHPQPGEDSSPSIAAVVASMD WPEVTKYRGIVSAQPHRQEIIMDLYTEKEDSKRGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQFNQVLLEEMDAIRKACVALQSDYMPRVTFVVVQKRHHT RLFPSNHDDRTLTDRSGNILPGTVVDTNICHPTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLCYTYVRCTRSVSLVPPAYYAHLAAFRARYYME NDVDVRAANEGGEGGAAAQFRQLPKIHENVSEVMFYC	999 aa
		Sch	>Sch_Scaffold7262_858_aa MSERGRGRRGGSPYGGGRGGGRTPPYGGGRGDGRTPPYGGGRSGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTRERD RRLRRSRQGRHRYHLKAFGLLLDRIPESWGVADRDVHHYDVTISPEVLSKKVCRLIIQQLVNNYRLSHLGGMGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGPR REKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVGRSLFHRTFAGDAGLLTGGLEYWRGYYQSLRPTQMGLALNIGMSARAFYESVF VSDYVLRHLNLRDHPRVSLSDQDHSKVRKVLKGVKVEATHQGRRYRITGLTPESSSQMMFPLDGTDGMISVEQYFNKKYKIVLAYPMLPAIQCGNSAKPVYLPMEIC KIVPGQRYTKMLNGRQIPPERLVDGLLRMCISKGMTFAAPLVPFRQARPDHIATTLRDIHRESMQAIDKLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQC CHPKNLRPPSIAYLENLSLKINVKVGGRNSVLELAVSKNMPFLTDKTTIVFGADVTHPQPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQPHRQEIIMDLYTEKEDSK KGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQFNQVLLEEMDAIRKACVALQSDYMPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICHP TEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLCYTYVRCTRSVSLVPPAYYAHLAAFRARYYMENDVDVRAANEGGEGGASAQFRQLPKIHENVS EVMFYC	858 aa
		SpiLA1589	>SpiLA1589_Contig:unspecified:40433:1:13665:1_804_aa VADRDVHHYDVTISPEVLSKKVCRLIIQQLVNNYRLSHLGGRGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGPRREKEFKVSIKFAAKADIHHLKQFLQSRQSDVP QETIQALDVVLRTNPSAKYEVVGRSLFHHTFAGDAGLLTGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESVFVSDYVLRHLNLRDHPQVSLSDQDHSKVRKVL KGVKVEATHQGRRYRITGLTPKSSSQMMFPVDGTDGMISVEQYFNTKYEIVLAYPRLPAIQCGNSAKPVYLPMEICKIVPGQRYTKMLNGRQVTEMLRATCQRPKE RLNGIQNIVRVNKYADDDLVHEFGIGVDARLTTIEARVLNPPTLRFHASGKESRVDPRVGQWNMIDKKMINPAHVYNWTCVSFSQQIPPDRLVDGLHRMCISKGMTF DAPLVPFRQARPDHIETTLRDIHRESMQAIDKLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQCCHPKNLRPPSIAFLENLSLKINVKVGGRNSVLELAVSK NMPFLTDKTTIVFGADVTHPQPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQPHRQEIIMDLYTEKEDSKRGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQ FNQVLLEEMDAIRKACVALQSDYMPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICHPTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQ NVTNYLCYTYVRCTRSVSLVPPAYYAHLAAFRARYYMENDVDVRAANEGX	804 aa
		SpiLA0480	>SpiLA0480_Scaffold2990443_858_aa MSERGRGRRGGSPYGGGRGGGRTPPYGGGRGDGRTPPYGGGRGGGRTSPSDGRGRGYQSPGGRGRGTYSSGGSPSYNAPPMYHHQQQSMEVSSMTRER DRQLRRSRQGRHRYHLKAFGLLLDRITGSWGVADRDVHHYDVTISPEVLSKKVCRLIIQQLVNNYRLSHLGGRGLAYDGRKSAYTAGALPFTSKEFVIIFADDNGGP RREKEFKVSIKFAAKADIHHLKQFLQSRQSDVPQETIQALDVVLRTNPSAKYEVVGRSLFHHTFAGDAGLLTGGLEYWRGYYQSLRPTQMGLALNIDMSARAFYESV FVSDYVLRHLNLRDHPQVSLSDQDHSKVRKVLKGVKVEATHQGRRYRITGLTPKSSSQMMFPVDGTDGMISVEQYFNTKYEIVLAYPRLPAIQCGNSAKPVYLPMEI CKIVPGQRYTKMLNGRQIPPDRLVDGLHRMCISKGMTFDAPLVPFRQARPDHIETTLRDIHRESMQAIDKLGEDLKIKHLQLLLVILPDGTGQYGRIKRLCEIDLGIVSQ CCHPKNLRPPSIAFLENLSLKINVKVGGRNSVLELAVSKNMPFLTDKTTIVFGADVTHPQPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQPHRQEIIMDLYTEKEDS KRGVVRGGMIMDLLKAFYAATKIKPDRIIFYRDGVSEGQFNQVLLEEMDAIRKACVALQSDYMPRVTFVVVQKRHHTRLFPSNHDDRTLTDRSGNILPGTVVDTNICH PTEFDFYLCSHAGIKGTSRPAHYHVLYDENNFTADGIQNVTNYLCYTYVRCTRSVSLVPPAYYAHLAAFRARYYMENDVDVRAANEGGEGGAAAQFRQLPKIHENV SEVMFYC	858 aa
	AGO6/ 16	*Sly*	>Solyc07g049500.2.1 MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR	903 aa

			VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNRHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIVA QKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKYE DHSETLSEQGSVKSIGTTPVTQLPRLHKNVSDSMFFC	
		Spe	>Sopen07g024850 MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGFHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSASCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVRV EQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDIP SIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKNLGEGGNPKFTLIVA QKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKYE DHSETLSEQGSVKSIGTTPVTELPRLHKNVSDSMFFC	903 aa
		Sga	>Sga_Scaffold4662_11.7_Contig9_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDKGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIV AQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKY EDHSETLSEQGSVKSIGTTPVTQLPRLHKNVSDSMFFC	903 aa
			>Sga_Sopen07g024850.1_Scaffold4662_11.7_Contig9_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDKGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIV AQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKY VAPVRYAHLAAQQFGQFDKYVTQLPRLHKNVSDSMFFC	903 aa
		Spr	>Spr_a5684_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQAGESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLL VRQSFFHDDSRNFTDVGGGIMSCRGFHSSFRLTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQ LFSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKAITDAVRDYSYDDD PLLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVV RVEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQS DIPSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLI VAQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDK YEDHSETLSEQGSVKSIGTTPVTELPRLHKNVSDSMFFC	903 aa
			>Spr_a5684_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQAGESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLL VRQSFFHDDSRNFTDVGGGIMSCRGFHSSFRLTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQ LFSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKAITDAVRDYSYDDD PLLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVV RVEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQS DIPSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLI VAQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDK YEDHSETLSEQGSVKSIGTTPVTELPRLHKNVSDSMFFC	903 aa
		Sch	>Sch_Scaffold3937_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF	903 aa

			AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAVNRGCLLV RQSFFHDDSRNFTDVGGGIMSCRGFHSSFRLTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQLF SMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDPL LVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVRV EQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDIP SIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIVA QKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKYE DHSETLSEQGSVKSIGTTPVTELPRLHKNVSDSMFFC	
			>Sch_Scaffold3937_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAVNRGCLLV RQSFFHDDSRNFTDVGGGIMSCRGFHSSFRLTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQLF SMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDPL LVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVRV EQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDIP SIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIVA QKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKYE DHSETLSEQGSVKSIGTTPVTELPRLHKNVSDSMFFC	903 aa
		SpiLA1589	>SpiLA1589_Contig:unspecified:6569105:1:31791:1_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIV AQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKY EDHSETLSEQGSVKSIGTTPVTQLPRLHKNVSDSMFFC	903 aa
			>SpiLA1589_Contig:unspecified:6569105:1:31791:1_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLEVCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIV AQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKY EDHSETLSEQGSVKSIGTTPVTQLPRLHKNVSDSMFFC	903 aa
		SpiLA0480	>SpiLA0480_Scaffold3066155_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIV AQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKY EDHSETLSEQGSVKSIGTTPVTQLPRLHKNVSDSMFFC	903 aa
			>SpiLA0480_Scaffold3066155_903_aa MENSEGRESCFSPVEEPPPVIMSNAEPERVDQPKRTIMMRAGDGTSGREISLLANHLKVSIKCPDEIFYHYSVSITSDEKRAVNSKVIRRKIVDKLHETYSSEFAGKKF AYDGEKNLYTVGPLPRNRLEFTVVVEESSARQASESPSDNGSLNHSIKRFKHSLHSKAFLVEIDYAAKIPLRSVDLALQGADPENVQDALRVLDIILRQKAANRGCLLV RQSFFHDDSRNFTDVGGGVMSCRGLHSSFRPTDGGLTLNMDVSTTMILSPGPVIDFLLANQNVKEPRYIDWARAKRMLKNMRVKAKHDNREFKIIGLTDKPCNQQL FSMKVKNGGSPDDGGETLDITVYQYFTKHRNIELSSSVYMPCLDVGKPKRPNYLPLELCYLVSLQRYTKALSSVQRASLVEKSRQKPRERIKVITDAVRDYSYDDDP LLVACGISIEKQLIQMNGRVLEAPKLKVGNGEEVTPCDGRWNFKNKHLFNPARIERWAVVNFSANCDTSHLSRELISCGRSKGIHFERPHTLIEEDPQYRRAGPVVR VEQMFEEIIARLPGHPDFLLCVLPERKNSELYGPWKKKSLTDLGIVTQCISPLKITDRYLTNVLLKINAKLGGTNSLLAMEHTSHLPLIKDTPTMILGMDVSHGSRVQSDI PSIAAVVGSLYWPLISKYKAVVRSQSPKLEIVESLYKPLPNGDDEGIMRELLLDFYRTSNGHKPAQIIVFRDGVSESQFSQVLNLELDQMIKAYKHLGEGGNPKFTLIV	903 aa

			AQKNHHTKLFQANAVDNVPPGTVVDTNIVHPRNNDFFMCAHAGMIGTTKPAHYHVLLDEIGFAPDVLQNLIHSLSYVYQRSTSATSIVAPVRYAHLAAQQFGQFDKY EDHSETLSEQGSVKSIGTTPVTQLPRLHKNVSDSMFFC	
	AGO7	*Sly*	>Solyc01g010970.2.1 MEHTENSNKCNSKSTTAKICPNNNNNNNNNHYIAFGFHHNTNNNQYHETYPPLLPLPPLLPPLQLPFPQNHNFRSRTHLHKPSFNQNHPFLATPSDFKIQQISASKV LQRQNDVSKQKYGRRVRAAATTTESVVVARRPDSGGVEGPVISLLANHFLVQFDPSQRIFHYDVEISPHPSKDIARLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIE FQNNKIEFYISLPIPSSGSNKSGEIVKLQKEGQQIKLFRVNIKLISKFDGKELNSYLNKEGDDGGSPLPQEYLHALDVVLRESPTEKCITAGRSFYSSCMGGQKDIGGG AVALRGFFQSLRPTQQGLALNVDFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTNEEKKEVEKALKNIRVFVCHRETVQRYRIYSLTEEVTENLCFQDRDGKILRI VSYFKDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTGLVGPTSGNHASDFKLQISKEMTQLYGRILQPP KLKLGDRGQVRNLIPSRHDRQWNFLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKNTVLNPQFEPLHLLNNVKNLESKLNKLHRASFN NLQLVICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFKHDGPVIFMGADVTHPHPLDDFSPSVAAVVGSV NWPAANKYVSRMRSQTHRQEIIQDLSAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRLACSRFPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNT LFNENILPGTVVDTVITHPSEFDFYLCSHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISLVPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISR AAPPKTTPLPKLTENIKRLMFYC	1000 aa
		Spe	>Sopen01g006840 MEHTENSNKCNSKSTTAKICPNNNNNNNNNHYIAFGFHHNTNNNQYHETYPPLLPLPPLLPPLQLPFPQNHNFRSRTHLHKPSFNQNHPFLATPSDFKIQQISASKVLQ RQNDVSKQKYGRRVKAAATTIESLVVARRPDSGGVEGPVISLLANHFLVQLDPSQRIFHYDVEISPHPSKDIARLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIEFQN NKIEFYISLPIPCSGSNKSGEIVKLQKEGQQIKLFRVNIKLISQFDGKELKSYLNKEGDDGGSPLPQEYLHALDVVLRESPTEKCITAGRSFYSSCMGGQKDIGGGAVA LRGFFQSLRPTQQGLALNVDFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTNEEKKEVEKALKNIRVFVCHRETVQRYRIYSLTEEITENLCFQDRDGKILRIVSYF KDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTGLVGPTSGNHASDFKLQISKEMTQLYGRILQPPKLKL GDRGQVRNLIPSRHDRQWNLLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKNTVLNPQFEPLHLLNNVKNLESKLNKLHRASFNNLQL VICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFKHDGPVIFMGADVTHPHPLDDFSPSVAAVVGSVNWP AANKYVSRMRSQTHRQEIIQDLSAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRVACSRFPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNTLFN ENILPGTVVDTVITHPSEFDFYLCSHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISLVPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISRAAP PKTTPLPKLTENIKRLMFYC	998 aa
		Sga	>Sga_Scaffold106756_9.6_Contig3_1000_aa MEHTENSNKCNSKSTTAKICPNNNNNNNNNHYIAFGFHHNTNNNQYHETYPPLLPLPPLLPPLQLPFPQNHNFRSRTHLHKPSFNQNHPFLATPSDFKIQQISASKV LQRQNDVSKQKYGRRVRAAATTTESVVVARRPDSGGVEGPVISLLANHFLVQFDPSQRIFHYDVEISPHPSKDIARLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIE FQNNKIEFYISLPIPSSGSNKSGEIVKLQKEGQQIKLFRVNIKLISKFDGKELNSYLNKEGDDGGSPLPQEYLHALDVVLRESPTEKCITAGRSFYSSCMGGQKDIGGG AVALRGFFQSLRPTQQGLALNVDFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTNEEKKEVEKALKNIRVFVCHRETVQRYRIYSLTEEVTENLCFQDRDGKILRI VSYFKDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTGLVGPTSGNHASDFKLQISKEMTQLYGRILQPP KLKLGDRGQVRNLIPSRHDRQWNFLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKNTVLNPQFEPLHLLNNVKNLESKLNKLHRASFN NLQLVICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFKHDGPVIFMGADVTHPHPLDDFSPSVAAVVGSV NWPAANKYVSRMRSQTHRQEIIQDLSAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRLACSRFPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNT LFNENILPGTVVDTVITHPSEFDFYLCSHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISLVPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISR AAPPKTTPLPKLTENIKRLMFYC	1000 aa
		Spr	>Spr_A22060_927_aa XSRTHLHKPSFNQNHPFLATPSDFKIQQISASKVLQRQNDVSKQKYGRRVKAAATTIESLVVARRPDSGGVEGPVISLLANHFLVQFDPSQRIFHYDVEISPHPSKDIA RLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIEFQNNKIEFYISLPIPSSGSNKSGEIVKLQKEGQQIKLFRVNIKLISKFDGKELNSYLNKEGDDGGSPLPQEYLHALDV VLRESPTEKCITAGRSFYSSCMGGQKDIGGGAVALRGFFQSLRPTQQGLALNVNFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTNEEKKEVEKALKNIRVFVC HRETVQRYRIYSLTEEVTENLCFQDRDGKILRIVSYFKDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTG LVGPTSGNHASDFKLQISKEMTQLYGRILQPPKLKLGDRGQVRNLIPSRHDRQWNLLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKN TVLNPQFEPLHLLNNVKNLESKLNKLHRASFNNLQLVICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFK HDGPVIFMGADVTHPHPLDDFSPSVAAVVGSVNWPAANKYVSRMRSQTHRQEIIQDLSAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRMACSR FPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNTLFNENILPGTVVDTVITHPSEFDFYLCSHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISL VPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISRAAPPKTTPLPKLTENIKRLMFYC	927 aa
		Sch	>Sch_Scaffold3477_1000_aa MEHTENSNKCNSKSTTAKICPNNNNNNNNNHYIAFGFHHNTNNNQYHETYPPLLPLPPLLPPLQLPFPQNHNFRSRTHLHKPSFNQNHPFLATPSDFKIQQISASKV LQRQNDVSKQKYGRRVKAAATTIESLVVARRPDSGGVEGPVISLLANHFLVQFDPSQRIFHYDVEISPHPSKDIARLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIEF QNNKIEFYISLPIPSSGSNKSGEIVKLQKEGQQIKLFRVNIKLISKFDGKELNSYLNKEGDDGGSPLPQEYLHALDVVLRESPTEKFPQEYLHALDVVLRESPTEKCGA VALRGFFQSLRPTQQGLALNVDFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTMEKRLDFLHDISHRKTRGLTRETVQRYRIYSLTEEVTENLCFQDRDGKILRIV SYFKDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTGLVGPTSGSHASDFKLQISKEMTQLYGRILHPPKL KLGDRGQVRNLIPSRHDRQWNLLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKNTVLNPQFEPLNLLNNVKNLESKLNKLHRASFNNL QLVICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFKHDGPVIFMGADVTHPHPLDDFSPSVAAVVGSVN WPAANKYVSRMRSQTHRQEIIQDLSAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRVACSRFPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNTL FNENILPGTVVDTVITHPSEFDFYLCSHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISLVPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISRA APPKTTPLPKLTENIKRLMFYC	1000 aa

		SpiLA1589	>SpiLA1589_Contig:unspecified:2714577:1:3182:1_974_aa MEHTENSNKCNSKSTTAKICPNNNNNNNNNHYIAFGFHHNTNNNQYHETYPPLLPLPPLLPPLQLPFPQNHNFRSRTHLHKPSFNQNHPFLATPSDFKIQQISASKV LQRQNDVSKQKYGRRVRAAATTTESVVVARRPDSGGVEGPVISLLANHFLVQFDPSQRIFHYDVEISPHPSKDIARLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIE FQNNKIEFYISLPIPSSGSNKSGEIVKLQKEGQQIKLFRVNIKLISKFDGKELNSYLNKEGDDGGSPLPQEYLHALDVVLRESPTEKCITAGRSFYSSCMGGQKDIGGG AVALRGFFQSLRPTQQGLALNVDFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTNEEKKEVEKALKNIRVFVCHRETVQRYRIYSLTEEVTENLCFQDRDGKILRI VSYFKDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTGLVGPTSGNHASDFKLQISKEMTQLYGRILQPP KLKLGDRGQVRNLIPSRHDRQWNFLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKNTVLNPQFEPLHLLNNVKNLESKLNKLHRASFN NLQLVICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFKHDVGSVNWPAANKYVSRMRSQTHRQEIIQDL SAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRLACSRFPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNTLFNENILPGTVVDTVITHPSEFDFYLC SHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISLVPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISRAAPPKTTPLPKLTENIKKLMFYC	974 aa
		SpiLA0480	>SpiLA0480_Scaffold3073856_1000_aa MEHTENSNKCNSKSTTAKICPNNNNNNNNNHYIAFGFHHNTNNNQYHETYPPLLPLPPLLPPLQLPFPQNHNFRSRTHLHKPSFNQNHPFLATPSDFKIQQISASKV LQRQNDVSKQKYGRRVRAAATTTESVVVARRPDSGGVEGPVISLLANHFLVQFDPSQRIFHYDVEISPHPSKDIARLIKKKLVEDHSVMLSGALPVYDGGRTIYSPIE FQNNKIEFYISLPIPSSGSNKSGEIVKLQKEGQQIKLFRVNIKLISKFDGKELNSYLNKEGDDGGSPLPQEYLHALDVVLRESPTEKCITAGRSFYSSCMGGQKDIGGG AVALRGFFQSLRPTQQGLALNVDFSVTAFHESIGVITYLEKRLDFLHDISHRKTRGLTNEEKKEVEKALKNIRVFVCHRETVQRYRIYSLTEEVTENLCFQDRDGKILRI VSYFKDHYNYDILYRNLPCLQISRSKPCYLPMELCMICEGQKFLGKLSDDQTARILKMGCQRPRERKAIIDRVVTGLVGPTSGNHASDFKLQISKEMTQLYGRILQPP KLKLGDRGQVRNLIPSRHDRQWNFLDSHVFESTRVERWALMSFGGTSDQKSHVPKFINQLCQRCEQLGIFLNKNTVLNPQFEPLHLLNNVKNLESKLNKLHRASFN NLQLVICVMERKHKGYADLKRIAETSIGIVTQCCLYPNLGKISSQFLANLALKINAKVGGCTVALYNSLPSQIPRLFKHDGPVIFMGADVTHPHPLDDFSPSVAAVVGSV NWPAANKYVSRMRSQTHRQEIIQDLSAMVGEIIDDFYEELLKLPERIIFFRDGVSETQFLKVLKEELQAIRLACSRFPGYKPPITFVVVQKRHHTRLFPCELDPSTTKNT LFNENILPGTVVDTVITHPSEFDFYLCSHWGVKGTSRPIHYHVLWDENQFTSDELQKLVYNLCYTFVRCTKPISLVPPVYYAHLAAYRGRLYLERSDLSTLTRSSNISR AAPPKTTPLPKLTENIKRLMFYC	1000 aa
	AGO10	*Sly*	>XP_004247613.1_Solanum_lycopersicum_Solyc09g082830 MPIRQMKESSEQHIVIKPHLQNTMNPVQKNPKTTQNGKGPPNQEPPNNKIHIQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVSG VESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADFPDKELNQYDVTVIPEVSSRTVNRAIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKEF TIKLIDEDDVINGPKREREYKVVIKFVARANLHHLSEFLAGKRADGPKEALQILDIVLRELSIKRYCPVGRSFFSPDIRKPQPLGDGLEAWCGFYQSIRPTQMGLSLNID MASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFTIKNTHLPCLQVG NQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEKDCLPQVGQWN MMNKKMINGMTVNRWACINFSRSVQESVARGFCNELTQMCQVSGMEFNPDPIIPIYMARPDQVEKALKHVYHSCVNKLKGKELELLLVILPDNNGSLYGDIKRICET DLGLITQCCLTKHVFKISKQYLANVSLKINVKMGGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLYK TWHDPARGTVSGGMIRDLLISFRKATGQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDRSGNILPGTVVD TKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFTADGIQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAFRARFYMEPDMPETNSGSPHQGSSKAIRETGVR PLPALKENVKRVMFYC	982 aa
			>NP_001266268_Solanum_lycopersicum_Solyc12g006790 MPQWQMKLELEQKHMVSRTPLQESLNQNAQCQSSGEHSRMEEVKRHNNAGKRRGRRKGKGILVEKMQDNSVCSASSSSERSLVFPRRPGYGQLGTKCLVKAN HFIAELSERNLSQYSVRITPEVKCTRLNKAIMAELVKLHKDADLGKRVPVFDGRRTLYTAGLLPFNSKEFTITLGDDDEWIGITKERKFAVTIKLISQANMLQLRELLAGK QVDNPPQALKIIDIVLRELASQRYISVGRFFYSPNIKKPQTLGNGLQSWRGFYQSIKPTQMGLSLNIDMSTTAFIEPLPVVEFVAQVLGKDVSSRPLSDADRIKVKKALR GVKVEVTHRGNIRRKYRISGLTSQPTRELIFPVDEEKNMKSVIEYFQEVYGYTIQYPHLPCLLVGSQKKVNYLPMEACKILEGQRYTKRLDEKQITSLLKSSCQRPRE QEMDILQTIRQNGYKQDPIAKEFGINIDDKLASVEARVLPAPWLKYHDAGKEKECHPQLGQWNMLNKKVINGSTVNHWACINFSCNVQENAARGFCHQLAQMCQV SGMEFNCEPVIPVYYARPDQAKKALNYVYNAAVNKLGGKELELLIAILPDNNGSLYGTLKKICETDLGMISQCCLTKHVLKISKQYLSNVSLKINVKMGGRNTVLLDAL RWKIPLVSDIPTIIFGADVTHPESGEDFSPSIAAVVASQDWPEVTKYAGLVCAQPHRQELIQDLYRTWQDPQRGTMSGGMIRELLLAFKKATGQKPLRIIFYRDGVSD GQFYQVLLYELDAIRKACASLEPGYQPPVTFIVVQKRHHTRLLPNNHNDRNHTDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFSADE MQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAYGARFYVEPDSRDNGSIRGTRATNGSVNVRPLPALKEKVKNVMFYC	938 aa
		Spe	>XP_015088227_Solanum_pennellii_Sopen09g031660 MPIRQMKESSEQHIVIKPHLQNTMNPVQKNPKTTQNGKGPPNQEPQNNKIHNQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVS GVESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADLPDKELNQYDVTVIPEVSSRTVNRAIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKE FTIKLIDEDDVINGPKREREYKVVIKFVARANLHHLSEFLAGKRADGPKEALQILDIVLRELSIKRYCPVGRSFFSPDIRKPQPLGDGLEAWCGFYQSIRPTQMGLSLNI DMASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFTIKNTHLPCLQV GNQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEKDCLPQVGQW NMMNKKMINGMTVNRWACINFSRSVQESVARGFCNELAQMCQVSGMEFNPEPIIPIYMARPDQVEKALKHVYHSCVNKLKGKELELLLVILPDNNGSLYGDIKRICE TDLGLITQCCLTKHVFKISKQYLANVSLKINVKMGGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLY KTWHDPARGTVSGGMIRDLLISFRKATGQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDRSGNILPGTVV DTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFTADGIQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAFRARFYMEPDMPENNSGSPHQGSSKAIRETGV RPLPALKENVKRVMFYC	982 aa
		Sga	>Sga_Solyc09g082830_XM_004247565.4_scaffold84584__8.7_contig9_953_aa MPIRQMKESSEQHIVIKPHLQNTMNPVQKNPKTTQNGKGPPNQEPPNNKIHIQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVSG VESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADLPDKELNQYDVTVIPEVSSRTVNRAIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKEF	953 aa

			TIKLIDEDDVINGPKREREYKVVIKFVARANLHHLSEFLAGKRADGPKEALQILDIVLRELSIKRYCPVGRSFFSPDIRKPQPLGDGLEAWCGFYQSIRPTQMGLSLNIG MASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFTIKNTHLPCLQVG NQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEKDCLPQVGQWN MMNKKMINGMTVNRWACINFSRSVQESVARGFCNELTQMCQVSGMGVQSGPNNSNIHGQARSNNNGSLYGDIKRICETDLGLITQCCLTKHVFKISKQYLANVSLK INVKMGGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLYKTWHDPARGTVSGGMIRDLLISFRKATG QKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHY HVLWDENNFTADGIQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAFRARFYMEPDMPETNSGSPHQGSSKAIRETGVRPLPALKENVKRVMFYC	
			>Sga_Solyc12g006790_NM_001279339.2_scaffold104755_11.7_contig5_913_aa MPQWQMKLELEQKHMVSRTPLQEPLNQNAQCQSSGEHSRMEEVKRHNNAGKRRGRRKGKGILVEKMQDNSVCSASSSSERSLVFPRRPGYGQLGTKCLVKAN HFIAELSERNLSQYSVRITPEVKCTRLNKAIMAELVKLHKDADLGKRVPVFDGRRTLYTAGLLPFNSKEFTITLGDDDEWIGITKERKFAVTIKLISQANMLQLRELLAGK QVDNPPQALKIIDIVLRELASQRYISVGRFFYSPNIKKPQTLDMSTTAFIEPLPVVEFVAQVLGKDVSSRPLSDADRIKVKKALRGVKVEVTHRGNIRRKYRISGLTSQP TRELIFPVDEEKNMKSVIEYFQEVYGYTIQYPHLPCLLVGSQKKVNYLPMEACKILEGQRYTKRLDEKQITSLLKSSCQRPREQEMDILQTIRQNGYKQDPIAKEFGINI DDKLASVEARVLPAPWLKYHDAGKEKECHPQLGQWNMLNKKVINGSTVNHWACINFSCNVQENAARGFCHQLAQMCQVSGMEFNCEPVIPVYYARPDQAKKALN YVYNAAANKLGGKELELLIAILPDNNGSLYGTLKKICETDLGMISQCCLTKHVLKISKQYLSNVSLKINVKMGGRNTVLLDALRWKIPLVSDIPTIIFGADVTHPESGEDF SPSIAAVVASQDWPEVTKYAGLVCAQPHRQELIQDLYRTWQDPQRGTMSGGMIRELLLAFKKATGQKPLRIIFYRYGVSDGQFYQVLLYELDAIRKACASLEPGYQP PVTFIVVQKRHHTRLLPNNHNDRNHTDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFSADEMQSLTNNLCYTYARCTRSVSVVPPAYY AHLAAYRARFYVEPDSRDNGSIRGTRATNGSVNVRPLPALKEKVKNVMFYC	913 aa
		Spr	>Spr_Solyc09g082830_XM_004247565.4_a939_982_aa MPIRQMKESSEQHIVIKPHLQSTMNPVQKNPKTTQNGKGPPNQEPQSNKIHSQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVSG VESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADLPDKELNQYDVTVIPEVSSRTVNRAIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKEF TIKLIDEDDVINGPKREREYKVVIKFVARANLHHLSEFLAGKRADGPKEALQILDIVLRELSIKRYCPVGRSFFSPDIRKPQPLGDGLEAWCGFYQSIRPTQMGLSLNID MASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFTIKNTHLPCLQVG NQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEKDCLPQVGQWN MMNKKMINGMTVNRWACINFSRSVQESVARGFCNELAQMCQVSGMEFNPEPIIPIYMARPDQVEKALKHVYHSCVNKLKGKELELLLVILPDNNGSLYGDIKRICET DLGLITQCCLTKHVFKISKQYLANVSLKINVKMGGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLYK TWHDPARGTVSGGMIRDLLISFRKATGQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDRSGNILPGTVVD TKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFTADGIQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAFRARFYMEPDMPETNSGSPHQGSSKAIRETGVR PLPALKENVKRVMFYC	982 aa
			>Spr_Solyc12g006790_NM_001279339.2_a12868_938_aa MPQWQMKLELEQKHMVSRTPLQESLNQNAQCQSSGERSRMEEVKRHNNAGKRRGRRKGKGILVEKMQDNSVCSASSSSERSLVFPRRPGYGQLGTKCLVKAN HFIAELSERNLSQYSVRITPEVKCTRLNKAIMAELVKLHKDADLGKRVPVFDGRRTLYTAGLLPFNSKEFTITLGDDDEWIGITKERKFAVTIKFISQANMLQLRELLAG KQVDNPPQALKIIDIVLRELASQRYISVGRFFYSPNIKKPQTLGNGLQSWRGFYQSIKPTQMGLSLNIDMSTTAFIEPLPVVEFVAQVLGKDVSSRPLSDADRIKVKKAL RGVKVEVTHRGNIRRKYRISGLTSQPTRELIFPVDEEKNMKSVIEYFQEVYGYTIQYPHLPCLLVGSQKKVNYLPMEACKILEGQRYTKRLDEKQITSLLKSSCQRPRE QEMDILQTIRQNGYKQDPIAKEFGINIDDKLASVEARVLPAPWLKYHDAGKEKECHPQLGQWNMLNKKVINGSTVNHWACINFSCNVQENAARGFCHQLAQMCQV SGMDFNCEPVIPVYYARPDQAKKALNYVYNAAANKLGGKELELLIAILPDNNGSLYGTLKKICETDLGMISQCCLTKHVLKISKQYLSNVSLKINVKMGGRNTVLLDAL RWKIPLVSDIPTIIFGADVTHPESGEDFSPSIAAVVASQDWPEVTKYAGLVCAQPHRQELIQDLYRTWQDPQRGTMSGGMIRELLLAFKKATGQKPLRIIFYRDGVSD GQFYQVLLYELDAIRKACASLEPGYQPPVTFIVVQKRHHTRLLPNNHNDRNHTDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFSADE MQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAYRARFYVEPDSRDNGSIRGTRATNGSVNVRPLPALKEKVKNVMFYC	938 aa
		Sch	>Sch_mRNA_Solyc09g082830_XM_004247565.4_scaffold1098_885_aa MPIRQMKESSEQHIVIKPHLQNTMNPVQKNPKTTQNGKGPPNQEPQNNKIHNQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVS GVESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADLPDKELNQYDVTVIPEVSSRTVNRDIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKE FTIKLIDEDDVINDMASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFT IKNTHLPCLQVGNQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEK DCLPQVGQWNMMNKKMINGMTVNRWACINFSRSVQESVARGFCNELAQMCQVSGMEFNPEPIIPIYMARPDQVEKALKHVYHSCVNKLKGKELELLLVILPDNNG SLYGDIKRICETDLGLITQCCLTKHVFKISKQYLANVSLKINVKMGGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQA HRQELIQDLYKTWHDPARGTVSGGMIRDLLISFRKATGQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDR SGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFTADGIQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAFRARFYMEPDMPETNSGSPHQG SSKAIRETGVRPLPALKENVKRVMFYC	885 aa
			>Sch_mRNA_Solyc12g006790_NM_001279339.2_scaffold7430_898_aa MPQWQMKLELEQKHMVSRTPLQESLNQNAQCQSSGERSRMEEFKRNNNAGKRRGRRKGKGILVEKMQDNSVCSASSSSERSLVFPRRPGYGQLGTKCLVKAN HFIAQLSERNLSQYSVRVTPEVKCTRLNKAIMAELVKLHKDADLGKRIPVFDGRRTLYTAGLLPFNSKEFTITLGDDDEWIGITKERKFAVTIKFISQANMLQLRELLAG KQVDNPPQALKIIDIVLRELASQRYISVGRFFYSPNIKKPQTLGNGLQSWRGFYQSIKPTQMGLSLNIDMSTTAFIEPLPVVEFVAQVLGKDVSSRPLSDADRIKVKKAL RGVKVEVTHRGNIRRKYRISGLTSQPTRELIFPVDEEKNMKSVIEYFQEVYGYTIQYPHLPCLLVGSQKKVNYLPMEACKILEGQRYTKRLDEKQITSLLKSSCQRPRE QEMDILQTIRQNGYKQDPIAKEFGINIDDKLASVEARVLPAPWVKYHDAGKEKECHPQLGQWNMLNKKVINGSTVNHWACINFSCNVQENAARGFCHQLAQMCQV SGMEFNCEPVIPVYYARPDQAKKALNYVYNTAANKLGGKELELLIAILPDNNGSLYGTLKKICETDLGMISQCCLTKHVLKISKQYLSNVSLKINVKMGGRNTVLLDAL RWKIPLVSDIPTIIFGADVTHPESGEDFSPSIAAVVASQDWPEVTKYAGLVCAQPHRQELIQDLYRTWQDPQRGTMSGGMIRELLLAFKKATGQKPLRIIFYRDGVSD	898 aa

			GQFYQVLLYELDAIRKACASLEPGYQPPVTFIVVQKRHHTRLLPNNHNDRNHTDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFSADE MQSLTNNLCYTYARCTRSVSVFLLHIMLIWRPIERVSM	
		SpiLA1589	>SpiLA1589_Solyc09g082830_XM_004247565.4_contig:3758907:1:8311:1_949_aa MPIRQMKESSEQHIVIKPHLQNTMNPVQKNPKTTQNGKGPPNQEPPNNKIHIQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVSG VESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADLPDKELNQYDVTVIPEVSSRTVNRAIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKEF TIKLIDEDDVINGPKREREYKVVIKFVARANLHHLSEFLAGKRADGPKEALQILDIVLRELSIKRYCPVGRSFFSPDIRKPQPLGDGLEAWCGFYQSIRPTQMGLSLNID MASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFTIKNTHLPCLQVG NQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEKDCLPQVGQWN MMNKKMINGMTVNRWACINFSRSVQESVARGFCNELTQMCQVSGMEFNPDPIIPIYMARPDQVEKALKHVYHSCVNKLKGKELELLLVILPDNNGSLYGDIKRICET DLGLITQCCLTKHVFKISKQYLANVSLKINVKMGGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLYK TWHDPARGTVSGGMIRDLLISFRKATGQKPQRIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDRSGNILPGTVVD TKICHPTEFDFYLCSHAGIQAGCTRSVSVVPPAYYAHLAAFRARFYMEPDMPETNSGSPHQGSSKAIRETGVRPLPALKENVKRVMFYC	949 aa
			>SpiLA1589_Solyc12g006790_NM_001279339.2_contig:6745152:1:10334:1_860_aa MPQWQMKLELEQKHMVSRTPLQESLNQNAQCQSSGEHSRMEEVKRHNNAGKRRGRRKGKGILIEKMQDNSVCSASSSSERSLVFPRRPGYGQLGTKCLVKANH FIAELSERNLSQYSVRITPEVKCTRLNKAIMAELVKLHKDADLGKRVPVFDGRRTLYTAGLLPFNSKEFTITLGDDDEWIGITKERKFAVTIKLISQANMLQLRELLAGK QVDNPPQALKIIDIVLRELASQRSNKVKKALRGVKVEVTHRGNIRRKYRISGLTSQPTRELIFPVDEEKNMKSVIEYFQEVYGYTIQYPHLPCLLVGSQKKVNYLPMEA CKILEGQRYTKRLDEKQITSLLKSSCQRPREQEMDILQTIRQNGYKQDPIAKEFGINIDDKLASVEARVLPAPWLKYHDAGKEKECHPQLGQWNMLNKKVINGSTVN HWACINFSCNVQENAARGFCHQLAQMCQVSGMEFNCEPVIPVYYARPDQAKKALNYVYNAAANKLGGKELELLIAILPDNNGSLYGTLKKICETDLGMISQCCLTKH VLKISKQYLSNVSLKINVKMGGRNTVLLDALRWKIPLVSDIPTIIFGADVTHPESGEDFSPSIAAVVASQDWPEVTKYAGLVCAQPHRQELIQDLYRTWQDPQRGTMS GGMIRELLLAFKKATGQKPLRIIFYRDGVSDGQFYQVLLFELDAIRKACASLEPGYQPPVTFIVVQKRHHTRLLPNNHNDRNHTDRSGNILPGTVVDTKICHPTEFDFY LCSHAGIQGTSRPAHYHVLWDENNFSADEMQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAYRARFYVEPDSRDNGSIRGTRATNGSVNVRPLPALKEKVKNVMF YC	860 aa
		SpiLA0480	>SpiLA0480_Solyc09g082830_XM_004247565.4_Scaffold3067183_950_aa MPIRQMKESSEQHIVIKPHLQNTMNPVQKNPKTTQNGKGPPNQEPPNNKIHIQTSPPSRNRGRRRGRGGKKSDQGETFMRPSSRPCTAASKPVIAASVEATNVSG VESNGTSSGFPSSSKSLCFAPRPGYGQLGTKCIVKANHFLADLPDKELNQYDVTVIPEVSSRTVNRAIMAELVKLYKESHLGMRLPAYDGRKSLYTAGELPFKWKEF TIKLIDEDDVINGPKREREYKVVIKFVARANLHHLSEFLAGKRADGPKEALQILDIVLRELSIKRYCPVGRSFFSPDIRKPQPLGDGLEAWCGFYQSIRPTQMGLSLNID MASAAFIEALPVIEFVAQLLGKDVSSRPLSDSDRVKIKKALRGVKVEVTHRGNVRRKYRVSGLTTQPTRELVFPVDDNLTMKSVVEYFQEMYGFTIKNTHLPCLQVG NQKKANYLPMEACKIVEGQRYTKRLSEKQITSLLKVTCQRPRDRENSILQTVQHNDYNEDPYAKEFGIKISEKQASVEARVLPAPWLKYHETGKEKDCLPQVGQWN MMNKKMINGMTVNRWACINFSRSVQESVARGFCNELTQMCQVSGMLKGKELELLLVILPDNNGSLYGDIKRICETDLGLITQCCLTKHVFKISKQYLANVSLKINVKM GGRNTVLLDAISCRIPLVSDIPTIIFGADVTHPENGEDSSPSIAAVVASQDWPEVTKYAGLVCAQAHRQELIQDLYKTWHDPARGTVSGGMIRDLLISFRKATGQKPQ RIIFYRDGVSEGQFYQVLLFELDAIRKACASLEPNYQPPVTFIVVQKRHHTRLFANNHKDRSSIDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLW DENNFTADGIQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAFRARFYMEPDMPETNSGSPHQGSSKAIRETGVRPLPALKENVKRVMFYC	950 aa
			>SpiLA0480_Solyc12g006790_NM_001279339.2_Scaffold3061531_938_aa MPQWQMKLELEQKHMVSRTPLQESLNQNAQCQSSGEHSRMEEVKRHNNAGKRRGRRKGKGILVEKMQDNSVCSASSSSERSLVFPRRPGYGQLGTKCLVKAN HFIAELSERNLSQYSVRITPEVKCTRLNKAIMAELVKLHKDADLGKRVPVFDGRRTLYTAGLLPFNSKEFTITLGDDDEWIGITKERKFAVTIKLISQANMLQLRELLAGK QVDNPPQALKIIDIVLRELASQRYISVGRFFYSPNIKKPQTLGNGLQSWRGFYQSIKPTQMGLSLNIDMSTTAFIEPLPVVEFVAQVLGKDVSSRPLSDADRIKVKKALR GVKVEVTHRGNIRRKYRISGLTSQPTRELIFPVDEEKNMKSVIEYFQEVYGYTIQYPHLPCLLVGSQKKVNYLPMEACKILEGQRYTKRLDEKQITSLLKSSCQRPRE QEMDILQTIRQNGYKQDPIAKEFGINIDDKLASVEARVLPAPWLKYHDAGKEKECHPQLGQWNMLNKKVINGSTVNHWACINFSCNVQENAARGFCHQLAQMCQV SGMEFNCEPVIPVYYARPDQAKKALNYVYNAAANKLGGKELELLIAILPDNNGSLYGTLKKICETDLGMISQCCLTKHVLKISKQYLSNVSLKINVKMGGRNTVLLDAL RWKIPLVSDIPTIIFGADVTHPESGEDFSPSIAAVVASQDWPEVTKYAGLVCAQPHRQELIQDLYRTWQDPQRGTMSGGMIRELLLAFKKATGQKPLRIIFYRDGVSD GQFYQVLLFELDAIRKACASLEPGYQPPVTFIVVQKRHHTRLLPNNHNDRNHTDRSGNILPGTVVDTKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENNFSADE MQSLTNNLCYTYARCTRSVSVVPPAYYAHLAAYRARFYVEPDSRDNGSIRGTRATNGSVNVRPLPALKEKVKNVMFYC	938 aa
Dicer-like	**DCL1**	*Sly*	>Solyc10g005130 MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDETLDPCFFGGIDGILEKLKNGDGSVHSVDGNNSNVHTEALAAPGICKDNGPQVKKDVD HNKGDLGKKSLQEGNGFSRHKERGCSDKEEKNGKRARLGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKEKK EMIYRVGSWEADRNREGKLPTERSREPSGAIEKKDDKLKEQAPKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLVY QQAEVIREQTGYQVGHYCGEMGQDFWDARRWQREFETKQVLVMTAQILLNILRHSIIKMEAINLLIMDECHHAVKKHPYSLVMSEFYHTTQKEKRPSVFGMTASPV NLKGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKKMESEVEEAALLSSRRSKWQFMGACDAGARGELRQVYGVSERT ESDGAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAETHKGDNPNSDRPDEMEEGELLESH VVSVGEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAEE GLDIRQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLIH FYCSQLPSDRYSILRPEFIMESHEKSGCPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGTS RHREFYPEGVADILRGDWILSGKDPLVSSKFIHLYMYAIKCVNIGPSKDPFLTDVSEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFHV RMMSIVLDVDVEPSTTPWDPAKAYLFAPVSGDESGDPIKDINWDHIKKITETGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGAI AHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAAHSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIR GRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGSLVRGAQRLPSIMRRIESMLLAVQLKEMIGYPVPALKILEALTAASCQETFCYERAELL	1888 aa

			GDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQSYIQADRFSPSRWAAPGVLPVYDEDLNEDETSIFDHETAENGTVAAKALAGDEFEDE ETEEGVYYVEGGKYAANHFMKWIGVEVDFDFNFKETEYSIRSCSIPENVLKSVEFDALQGALNISFNDKGLLLEAITHASRPSSGVSCYQRLEFVGDAVLDHLITRHLF FTYTDLPPGRLTDLRAAAVNNENFARVAVKHSLHLHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLGDIVESIAGAIFLDSGCNTKSVWEVFQPLL HPMVTPETLPMHPVRELQERCQQQAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKEREEAEAKKADDTKKKKNGNPSFTRQTLN DICLRKNWPMPLYRCVHEGGPAHAKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRYS	
		Spe	>Sopen10g001150 MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDESLDPCFFGGIDGILEKLKNGDGSVHSVDGNNSNVHTEALAAPGICKDNRPQVKKDVD HNKGDLGKKSLQEGNGFSRHKERGCNDKEEKNGKRARLGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKER KEMIYRVGSWEADKNREGKLPTERSREASGAIEKKDDKLKEQAPKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLV YQQAEVIREQTGYQVGHYCGEMGQDFWDARRWQREFETKQVLVMTAQILLNILRHSIIKMEAINLLIMDECHHAVKKHPYSLVMSEFYHTTQKEKRPSVFGMTASP VNLKGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKKMESEVEEAALLSSRRSKWQFMGACDAGARGELRQVYGVSER TESDGAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAEMHKGDNPNSDRPDEMEEGELLES HVVSVGEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAE EGLDIRQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLI HFYCSQLPSDRYSILRPEFIMESHEKSGYPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGT SRHREFYPEGVADILRGDWILSGKDPLVSSKFIHLYMYAIKCVNIGPSKDPFLTDVSEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFH VRMMSIVLDVDVEPSTTPWDPAKAYLFAPVTGDESGDPIIDINWDHIKKITETGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGA IAHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAAHSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIR GRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGSLVRGAQRLPSIMRRIESMLLAVQLKEMIGYPVPALKILEALTAASCQETFCYERAELL GDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQSYIQADRFSPSRWAAPGVLPVYDEDLNEDETSIFDHETAENGTVAAKALAGDEFEDE ETEEGELDNDSGSYRVLSSKTMADVVEALIGVYYVEGGKYAANHFMKWIGVEVDFDFNFKETEYSIRSCSIPENVLKSVDFDALQGALNISFNDKGLLLEAITHASRP SSGVSCYQRLEFVGDAVLDHLITRHLFFTYTDLPPGRLTDLRAAAVNNENFARVAVKHSLHLHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLGD IVESIAGAIFLDSGCNTKSVWEVFQPLLHPMVTPETLPMHPVRELQERCQQQAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKERE EAEAKKADDAKKKKNGNPSFTRQTLNDICLRKNWPMPLYRCVHEGGPAHAKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRYS	1914 aa
		Sga	>Sga_mRNA_Solyc10g005130_NM_001302898.1_scaffold96676_12.8_contig7_1914_aa MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDETLDPCFFGGIDGILEKLKNGDGSVHSVDGNNSNVHTEALAAPGICKDNGPQVKNDVD HNKGDLGKKSLQEGNGFSRHKERGCSDKEEKNGKRARLGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKEKK EMIYRVGSWEADRNREGKLPTERSREPSGAIEKKDDKLKEQAPKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLVY QQAEVIREQTGYQVGHYCGEMGQDFWDARRWQCEFETKQVLVMTAQILLNILRHSIIKMEAINLLIMDECHHAVKKHPYSLVMSEFYHTTQKEKRPSVFGMTASPV NLKGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKKMESEVEEAALLSSRRSKWQFMGACDAGARGELRQVYGVSERT ESDGAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAETHKGDNPNSDRPDEMEEGELLESH VVSVGEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAEE GLDIRQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLIH FYCSQLPSDRYSILRPEFIMESHEKSGCPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGTS RHREFYPEGVADILKGDWILSGKDPLVSSKFIHLYMYAIKCVNIGPSKDPFLTDVSEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFHV RMMSIVLDVDVEPSTTPWDPAKAYLFAPVSGDESGDPIKDINWDHIKKITETGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGAI AHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAAHSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIR GRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGSLVRGAQRLPSIMRRIESMLLAVQLKEMIGYPVPALKILEALTAASCQETFCYERAELL GDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQSYIQADRFSPSRWAAPGVLPVYDEDLNEDETSIFDHETAENGTVAAKALAGDEFEDE ETEEGELDNDSGSYRVLSSKTMADVVEALIGVYYVEGGKYAANHFMKWIGVEVDFDFNFKETEYSIRSCSIPENVLKSVEFDALQGALNISFNDKGLLLEAITHASRP SSGVSCYQRLEFVGDAVLDHLITRHLFFTYTDLPPGRLTDLRAAAVNNENFARVAVKHSLHLHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLGD IVESIAGAIFLDSGCNTKSVWEVFQPLLHPMVTPETLPMHPVRELQERCQQQAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKERE EAEAKKADDTKKKKNGNPSFTRQTLNDICLRKNWPMPLYRCVHEGGPAHAKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRYS	1914 aa
		Spr	>Spr_mRNA_Solyc10g005130_NM_001302898.1_a12916_1914_aa MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDESLDPCFFGGIDGILEKLKNGDGSVHSVDGNNSNVQTEALAAPGICKDNGPQVKKDVD HNKGDLGKKSLQEGNGFSRHKEWGCNDKEERNGKRARFGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKER KEMIYRVGSWEADRNREGKLPTERSHEPSGAIEKKDDKLKEQAPKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLV YQQAEVIREQTGYQVGHYCGEMGQDFWDARRWQREFETKQVLVMTAQILLNILRHSIIKMEAINLLIMDECHHAVKKHPYSLVMSEFYHTTQKEKRPSVFGMTASP VNLKGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKKMESEVEEAALLSSRRSKWQFMGACDAGARGELRQVYGVSER TESDGAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAETHKGDNPNSDRPDEMEEGELLESH VVSVGEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAEE GLDIRQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLIH FYCSQLPSDRYSILRPEFIMESHEKSGCPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGTS RHREFYPEGVADILRGDWILSGKDPLVSSKFIHLYMYAIKCVNIGPSKDPFLTDVSEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFHV RMMSIVLDVDVEPSTTPWDPAKAYLFAPVTGDESGDPIKDINWDHIKKITETGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGAI AHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAAHSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIR GRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGSLVRGAQRLPSIMRRIESMLLAVQLKEMIGYPVPALKILEALTAASCQETFCYERAELL	1914 aa

			GDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQSYIQADRFSPSRWAAPGVLPVYDEDLNEDETSMFDHETAENGTVAAKALGGDEFED EETEEGELDNDSGSYRVLSSKTMADVVEALIGVYYVEGGKYAANHFMKWIGVEVDFDFNFKETEYSIRSCSIPENVLKSVDFDALQGALNISFNDKGLLLEAITHASR PSSGVSCYQRLEFVGDAVLDHLITRHLFFTYTDLPPGRLTDLRAAAVNNENFARVAVKHSLHSHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLG DIVESIAGAIFLDSGCNTKSVWEVFQPLLHPMVTPETLPMHPVRELQERCQQQAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKER EEAEAKKADDAKKKKNGNPSFTRQTLNDICLRKNWPMPLYRCVHEGGPAHAKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRYS	
		Sch	>Sch_mRNA_Solyc10g005130_NM_001302898.1_scaffold7114_1914_aa MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDETLDPCFFGGIDGILEKLKNGDGSEHSVDGNNSNVQTEALAAPGICKDNGPQVKKDVD HNKGDLGKKSLQEGNGFSRHKEWGCNDKEERNGKRARFGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKER KEMIYRVGSWEADRNREGKLPTERSREPSGAIEKKDDKLKEQAPKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLV YQQAEVIREQTGYQVGHYCGEMGQDFWDARRWQREFETKQVLVMTAQILLNILRHSIIKMEAINLLIMDECHHAVKKHPYSLVMSEFYHTTQKEKRPSVFGMTASP VNLKGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKKMESEVEEAALLSSRRSKWQFMGACDAGARGELRQVYGVSER TESDGAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAETHKGDNPNSDRPDEMEEGELLESH VVSVGEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAEE GLDIRQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLIH FYCSQLPSDRYSILRPEFIMESHEKSGCPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGTS RHREFYPEGVADILRGDWILSGKDPLVSSKFIHLYMYAIKCVNIGPSKDPFLTDVSEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFHV RMMSIVLDVDVEPSTTPWDPAKAYLFAPVSGDESGDPIKDINWDHIKKITETGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGAI AHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAAHSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIR GRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGSLVRGAQRLPSIMRRIESMLLAVQLKEMIGYPVPALKILEALTAASCQETFCYERAELL GDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQSYIQADRFSPSRWAAPGVLPVYDEDLNEDETSMFDHETAENGTVAAKALGGDEFED EETEEGELDNDSGSYRVLSSKTMADVVEALIGVYYVEGGKYAANHFMKWIGVEVDFDFNFKETEYSIRSCSIPENVLKSVDFDALQGALNISFNDKGLLLEAITHASR PSSGVSCYQRLEFVGDAVLDHLITRHLFFTYTDLPPGRLTDLRAAAVNNENFARVAVKHSLHSHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLG DIVESIAGAIFLDSGCNTKSVWEVFQPLLHPMVTPETLPMHPVRELQERCQQQAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKER EEAEAKKADDAKKKKNGNPSFTRQTLNDICLRKNWPMPLYRCVHEGGPAHAKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRYS	1914 aa
		SpiLA1589	>SpiLA1589_mRNA_Solyc10g005130_NM_001302898.1_contig:unspecified:3391119:1:3923:1_1900_aa MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDETLDPCFFGGIDGILEKLKNGDGSVHSVDGNNSNVHTEALAAPGICKDNGPQVKKDVD HNKGDLGKKSLQEGNGFSRHKERGCSDKEEKNGKRARLGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKEKK EMIYRVGSWEADRNREGKLPTERSREPSGAIEKKDDKLKEQAPKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLVY QQAEVIREQTGYQVGHYCGEMGQDFWDARRWQREFETKQVLVMTAQILLNILRHSIIKQVLVMTAQILLNILRHSIIKYSLVMSEFYHTTQKEKRPSVFGMTASPVNL KGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKEVVVEYDKAASLWSFHEQIKFMGACDAGARGELRQVYGVSERTESD GAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAETHKGDNPNSDRPDEMEEGELLESHVVSV GEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAEEGLDI RQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLIHFYCS QLPSDRYSILRPEFIMESHEKSGCPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGTSRHR EFYPEEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFHVRMMSIVLDVDVEPSTTPWDPAKAYLFAPVSGDESGDPIKDINWDHIKKITE TGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGAIAHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAA HSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIRGRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGS LVRGVFLPPELCVLHPLPGSLVRGKEMIGYPVPALKILEALTAASCQETFCYERAELLGDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQS YIQADRFSPSRWAAPGVLPVYDEDLNEDETSIFDHETAENGTVAAKALAGDEFEDEETEEGELDNDSGSYRVLSSKTMADVVEALIGVYYVEGGKYAANHFMKWIG VEVDFDFNFKETEYSIRSCSIPENVLKSVEFDALQGALNISFNDKGLLLEAITHASRPSSGVSCYQRLEFVGDAVLDHLITRHLFFTYTDLPPGRLTDLRAAAVNNENF ARVAVKHSLHLHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLGDIVESIAGAIFLDSGCNTKSVWEVFQPLLHPMVTPETLPMHPVRELQERCQQ QAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKEREEAEAKKADDAKKKKNGNPSFTRQTLNDICLRKNWPMPLYRCVHEGGPAH AKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRFYQTLLNYATSFFSYIYGIQFFILQTFLISNYIELV	1900 aa
		SpiLA0480	>SpiLA0480_mRNA_Solyc10g005130_NM_001302898.1_Scaffold3065974_1914_aa MDGDGSGVSEKPSYWIDAYEDISCDDLIQDFVGSNTVPVAPLNQLGPDETLDPCFFGGIDGILEKLKNGDGSVHSVDGNNSNVHTEALAAPGICKDNGPQVKKDVD HNKGDLGKKSLQEGNGFSRHKERGCSDKEEKNGKRARLGDDSYQRRGCDRPLARKRLRENDEINRVGRDQRKRREYHGGRGGRDRNWREGSGFWEWDKEKK EMIYRVGSWEADRNREGKLPTERYRVGSWEADRNREGKLPTERKEEARKYQLDVLEHARKSNTIAFLETGAGKTLIAILLMKSLCSDLQKKNKKMLAVFLVPKVPLV YQQAEVIREQTGYQVGHYCGEMGQDFWDARRWQREFETKQVLVMTAQILLNILRHSIIKMEAINLLIMDECHHAVKKHPYSLVMSEFYHTTQKEKRPSVFGMTASP	1914 aa

			VNLKGVSSQVDCAIKIRNLETKLDSVVFTIKDRKELEKHVPMPSEVVVEYDKAASLWSFHEQIKKMESEVEEAALLSSRRSKWQFMGACDAGARGELRQVYGVSER TESDGAANLIQKLRAINYALGELGQWCAYKVAHSFLTALQNDERASYQLDVKFQESYLDKVVSLLQCQLSEGAVAQSNLNAETHKGDNPNSDRPDEMEEGELLESH VVSVGEHVDVILGAAVADGKVTPKVQSLIKILLKYQHTEDFRAIIFVERVVTALVLPKVFEELPSLSFINSSSLIGHNNSQEMRTGQMQDTIAKFRDGRINLLVATSVAEE GLDIRQCNVVIRFDLAKTILAYIQSRGRARKPGSDYILMVERDNSSHEAFLRNARNSEETLRKEAIERTDISHLKDASKLISAEAPTDSVYQVESTGAVVSLNSAVGLIH FYCSQLPSDRYSILRPEFIMESHEKSGCPTEYSCRLQLPCNAPFETLDGPVCSSMRLAQQAACLDACKKLHQMGAFTDMLLPDKGSGVESEKVEQDEEGDPIPGTS RHREFYPEGVADILKGDWILSGKDPLVSSKFIHLYMYAIKCVNIGPSKDPFLTDVSEFAILFGNELDAEVLSMSMDLFIARTVVTKATLVFRGPIDVTEFQLASLKSFHV RMMSIVLDVDVEPSTTPWDPAKAYLFAPVSGDESGDPIKDINWDHIKKITETGVWSNPLQRARPDVYLGTNERSLGGDRREYGFAKLRHGMAIGLKSHPTYGVRGAI AHYDLVQASGLVPNRSSLDDVEVDLNKDKIMMADCSLRAEDIVGRIVTAAHSGKRFYVDCIRSDMTAENSFPRKEGYLGPLEYSSYAAYYKQKYGVDLVYKKQPLIR GRGVSYCKNLLSPRFEHSEEHEGELEEATDKTYYVFLPPELCVLHPLPGSLVRGAQRLPSIMRRIESMLLAVQLKEMIGYPVPALKILEALTAASCQETFCYERAELL GDAYLKWVVSRYLFLKYPQKHEGQLTRMRQQMVSNMVLYQNALSKGIQSYIQADRFSPSRWAAPGVLPVYDEDLNEDETSIFDHETAENGTVAAKALAGDEFEDE ETEEGELDNDSGSYRVLSSKTMADVVEALIGVYYVEGGKYAANHFMKWIGVEVDFDFNFKETEYSIRSCSIPENVLKSVEFDALQGALNISFNDKGLLLEAITHASRP SSGVSCYQRLEFVGDAVLDHLITRHLFFTYTDLPPGRLTDLRAAAVNNENFARVAVKHSLHLHLRHGSSALEKQIRDFVNEVKNELSKPGFNSFGLGDCKAPKVLGD IVESIAGAIFLDSGCNTKSVWEVFQPLLHPMVTPETLPMHPVRELQERCQQQAQGLEYKATRSGNMATVEVYVDGVQVGMAQNPQKKMAQKLAARNALVVLKERE EAEAKKADDAKKKKNGNPSFTRQTLNDICLRKNWPMPLYRCVHEGGPAHAKRFTYGVRVNISDKGFTDECIGEPMPSVKKAKDSAAALLLELLNRRYS	
	DCL2	*Sly*	>DCL2.1_protein_Solyc11g008520 MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQQETDFFSW GELDVCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTECTAGHASVVQS QSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKRYILCNIWKRFHYIYGLIISQFDSNRSGDESTLARMQNFM ASGEMMRQESLRHASEPCSPLVDEMYDEPCYKVESTGAIITLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEA CKELHRVGALTDNLVPDIVEEEAINKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLK YSKVVTLTSEEIRRCQRFQVSVFKILLDRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCL LENSLVFTPHNGNIYCITGFLDNLDCNSLLNVRTGESITYREYYKKRQGIELCFEEPLLSGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSY VPSIMHRIESLVMASHLNSMLLNDCKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRN EAFTLQAWIIPGDSSQVHSFNEELMTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFH DPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQCAIKASLHKHILHASPDLQRQICNTIEDFKNPVSTFGWEA ETTFPKVLADVIESLAGAIFVDSGFNQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSRENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACK NVLKSLKECSYNA	1428 aa
			>DCL2.2_protein_Solyc06g048960 MLQSLKTNSSPLTLCLLLEGCYQLEALETALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDSLMMHTDLKVGKYWGEMGVDYWDAA TWQRQVDAHEVLVMTPAILLAALRHSFIQINMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRQSLQLPRVFGMTASPIKSKGSSTADSYWQKIRDLENLMNSKVYT CGSESVLAEYIPFSNPKLKIYKHVDIPCTLFLSLAHDLEQLKEMHDCSISKSNLSFMSAGTARRRLSKLYSAFLFCLSEMGAWLAFKATEFLSREEVDFLSWGELDVC AQTIVRDFSWGASKIFSARLPSGPYWSIGGDIQANVDAGYLSSKVTCLLESLLEYRDQKDLRCIIFVERIITAIVLRSLLNELLPELCGWRTEYTAGHISVVQSQSRKLQ NKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGRARMQNSDFLLMVRSGDDSTLTRMHNYMASGEIMRQESLCHASIPCSPLDDELYDEPC YKVESTGAIVTLSSSVSLLYLYCSRLPSDGYFKPNPRCVIDKETGTCTLQLPKSCPLQRIISVQGNSKISKQLACLEACKELHRVGALTDNLVPDIMEEETINKELECQI HTVEELKYFPPELVSHCGNDSEAVYYCYLVELQHDACNDFQLHGIILAVRTRLKFDDEIMAFDLDIDRRGRLQVQLNYHNVVTLTSEEIQRCRRFQSSIFRILLDRDLS KLQGALAAVQSPIGSAVSDYLLLPSLGTTPEINWKCVNSLLFPSQALEAKHMDCCSTQGRKRSVSTKTGVICSCMLENSLVFTPHNGHIYCITGFLDNLDCNSLLDTR TGEPITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRCRIQKAKDSTDSSVELPPELCSLIMSPVSISTLNTYSYVPSIMHRIESLVMALNLKRMHLDHCTLDIFIPTI KVLEAVTTKKCLEKFHLESLETLGDSFLKYASSIQLFKTYENHHEGLLTIKKNKIISNDALCRLGCARKIPGFIRNEPFDLKAWLIPGDNSQIQTFDEEFLTSSDKMYSRG KQKFRSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDIDFVDAPLPRNFPMNAEKLINVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLD YVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILHASQDLQRQILSTVEDFEKLDLLSMFGWEAETTFPKVLGDVIESLGGAIFVDSGFNKDITFQSI RPLLEPLVTPQTVKLQPVRELSELCDQKGYIKKKDVISRENGLAYITVEVEANGVIHKSTCSGRDKIMAKKVASKNVLKSLKECPSNA	1399 aa
			>DCL2.3_protein_Solyc11g008540 MLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEMGVDYWDASTWQQQVDDHEVLVMTPAILLAALRHSFLQIDMIKVIIFDECHNARGKHP YASIMVEFYHHQLTHESAQLPRIFGMTASPIKSKGASTAHSYWQKIHDLENLMNSKVYTCSSESVLAEYIPFSNPKLKIYEHEDIPCSLFNTLAHDLERLKEKHECSISK SNLSAMSAGSARRRLSKLHMAFLFCLSEMGVWLAFKAAEFLSFEENDFFSWGEFDACAQTIVRDFSLGASKIFSARLPSGPHWSIGGDIQANADAGYLSSKVNCLLE SLLEYRDQKDLRCIIFVERIVTAIVLRSLLNELLPERSGWRTEYTAGHVSVLQSQSRKSQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGR ARMQNSDFLLMVRDGDDPTLTRMQNYMASGEIMRQESLRHASIPCSPLDDELYDEPCYKVESTGAVVTLSSSVSLLYFYCSRLPSDGYFKPNPRCVIDKETETCTL QLPKSSPLQGIISVQGKRKILKQLACLEACKQLHRVGALTDNLVPDIVEEEIINKELECQIQTVEESKYFPPELVSHCSNDSEAVYYCYLVEMQHASYNDFELHGIILAV RTRLKCDDEILAFDLDVDRRGLLQVQLNYSKVVTLTAEEIRRCQRFQVSVFRILLDRDLSILQDALGAVQSPIGSAVSDYLLLPSLGSTPEINWKCVNSLLFPSQALGD KHMDWCSTQDRKRSVNTKNGLVCSCMLENSLVFTPHNGYIYCVTGFLDKLDCNSLLGMRTGESITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRSRTQKAK DSTDSSVELPPEICSLIMSPLSISTLNTYSYVPSIMHRIESLVMASNLKRMHLDHCTLNVPIPTATILEAMTTKKCLEKFHLESLETLGDSFLKYAASIKLFKTYENHHEGL LTVKKTQIISNAALCKLGCARKIPGFIRNEPFDLKAWIIPGDNSQVHSFDEVLLTSSDKMYSRVKQKIRSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDA PMSRHFPMNAEKLVNVRYLESLLHYKFNDPSLLVEALTHGSYMIPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHI LHASQDLQRQICSTVEDFDKLNLDSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFDKETTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYIRKKDVVSRENGIA YITVEVEANGVVHKSTCSGRDKLIAKKVASKNVLKSLKECPSNATEQ	1352 aa

			>DCL2.4_protein_Solyc11g008530 MLLRSYASLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYWNAATWQQLVDDHEVLVMTPAILHAALRHSFLQMGMIKVIIFDECHNARGKHP YASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHSKVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLIS QSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDACVRDFCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRK DLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIVATSILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILMVRKGDD ATLTRMQNYKASVEIMRQESLRHASIPCSTLHDELYDECYKVESTGAVVTLSSSVSLLDFYCSRLPSDGYFKPDPTYVINEETETCTLQLPKSSPLQGIISVQGKRKIL KQLACLEACKQLHRVGALTDNLVPDIVEEETINKELECKIKIVEQSLYYPSEFVSHCGNESEAVYYCYLVELPHDSYNDSQLHGIILAVRTKLKFDDEILAFDLDVDRRG RLKVQLNYRKVVIFTSEEIRRCQRFQVSVFRILRDPDLSKLQEVLAAVQSPIGSAVSDYLLLPSVGTPPEINWQYVNSLLFPSQVLGDKHMDWCSTQGRRCSVNTISE VVCSCMLENSLVCTPHNGRIYCINGFLENLDCNSLMGVRSEESITYREHYRKRYGINICSEEVPLLRGKHISKEAKDSSVALPPELCSLIMSPLFISTLNTYSYVPSIMH RIESLIMASNLKKMHLDHCTQNVVIPTAKILEAMTTKNCLEKFHLESLETLGDSFLKYAASIKLFKTYENDHQGLLTVKRKQIISNATLCRLGCARKMPGFIRNKPFVLKA WIIPGDNSQVHNFDEELLTSSVKMYSRGKQKIKSKIMADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDAPTSRHLPVNAEKLVNVRYLESLLHYKFNDPSLLVE ALSHGSCMLPDIPRCYKRLEFLGDAVLDYVVTTHLYFKYPGLTPGLITDLRSASVNNECYALSAVKAGLHDHILYDLQVLQRHISSTVEDFKKLNLVSTFGWEAETTYP KVLADVIESLAGAIFVDSGFNQDTTFLCIRPLLEPLITPQTLKVHPARELRELCHQKGYIKQKNVVFRENGIVYVTVEVEANGVIHKDSNSGRNQKMAEKVASKYLLKSL KEYPYNP	1317 aa
			>DCL2.2_protein_Sopen11g004310 MHPDNYGMSVLLQKKHLELAKDENDLVEQQRASTQLGRTYHEIFLKSDDDHDSVGNARKYFTLSLNLAKTLKKNLQSSKHSFVKDYIDAYNNIDNMSMARANDVVC GNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGVDFWDAATWKRQ VDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRQSAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLMHSKVYTCDSEAV LAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQEETDFFSWGELDVCAQTIVRD FSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASVVQSQSRKIQNKIVEEF RKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLVDEMYDEPCYKVES TGAIVTLSSSVSLLYFYCSRLPSDGYFKSNPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAINKELECQIHTVEE SKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLTSEEIRRCQRFQVSVFKILLDRDLSKLQDA LAAGQSPISSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLDCNSLLNVRTGESI TYREYYKKRQGIELCFEEPLLRGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLIDCKLNVFIPTAMVLE AVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFNLQAWIIPGDSSQVHSFNEEFMTSSDKMYSRIKQ KIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVV TAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHKHILHASPDLQRQICNTIEDFKNLNLVSTFGWEAETTFPKVLADVIESLAGAIFVDSGFNQDTTFQCIRPLL EPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSRENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	1499 aa
		Spe	>DCL2.3_protein_Sopen11g004320 MEPTNVAVFENQQVSADPLPFARSYQLEALEIALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW NASTWQQLVDDHEVLVMTPAILHAALRHHFLQMGMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHC KVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFHTLVHDLERLKEKHECLISQSNLSFMRYGSARGRLSKLHSDFLFCLSEMGAWLAFRSCEENDFLSSDDACVRD FCLGASTIFSAHLPSGPHWSIGEDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIV ATSILEEGLDVRSCNLVIRFDPPTTVCSFIQSRGRARMQNSDFLLMVRKGDDATLTRMQNYKASVEIMRQESLRHASIPCSTLHDELYDECYKVESTGAVVTLSSSVS LLDFYCSRLPSDGYFKPDPTYVINEETETCTLQLPKSSPLQGIIKLHRVGALTDNLVPDIVEEETINKELECKIKIVEQSLYYPSEFVSHCGNESEAVYYCYLVELRHDSY NDSQLHGIILAVRTKLKFDDEILAFDLDVDRRGRLKVQLNYSKVVIFTSEEIRRCQRFQVSVFRILRDPDLSKLQEVLAAVQSPIGSAVSDYLLLPSVGTPPEINWQCVN SLLFPSQVLGDKHMDWCSTQGRRRCVNTISEVVCSCMLENSLVCTPHNGRIYCINGFLENLDCNSLRDVRSEESITYREHYRKRYGINICFEEVPLLRGKHISKEAKD SSVALPPELCSLIMSPLFISTLNTYSYVPSIMHQIESLIMASNLKKMHLDHCTQNVVIPTAKILEAMTTKNCLEKFHLESLETLGDSFLKYAASIKLFKTYENDHQGLLTVK RKQIISNATLCRLGCARKMPGFIRNEPFVLKTWIIPGDNSQVHSFDEELLTSSVKMYSRGKQKIKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDAPTS RHFPVNAEKLVNVRYLESLLHYKFNDPSLLVEALSHGSCMLPDIPRCYKRLEFLGDAVLDYVVTTHLYFKYLGLTPGLITDLRSASVNNECYALSAVKAGLHDHILYDP LVLQRHISSTVENFKKLNLG	1222 aa
			>DCL2.4_protein_Sopen11g004330 MEPTDVAVSENQQLSADPLPFARSYQLEALETALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEMGVDYW DASTWQQQVDDHEVLVMTPAILLAALRHSFLQIDMIKVIIFDECHNARGKHPYASIMVEFYHHQLTHESAQLPRIFGMTASPIKSKGASTVHSYWQKIHDLENLMNSK VYTCSSESVLAEYIPFSNPKLKIYEHVDIPCSLFNTLAHDLERLKEKHECSISKSNLSAMSAGSARRRLSKLHMAFLFCLSEMGVWLAFKAAEFLSFEENDFFSWGEF DACAQTIVRDFSLGASKIFSARLPSGPHWSIGGDIQANADAGYLSSKVNCLLESLLEYRDQKDLRCIIFVERIVTAIVLRSLLNELLPERSGWRTEYTAGHVSVLQSQS RKSQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGRARMQNSDFLLMVRDGDDPTLTRMQNYMASGEIMRQESLRHASIPCSPLDDELY DEPCYKVESTGAVVTLSSSVSLLYFYCSRLPSDGYFKPNPRCVIDKETGTCTLQLPKSSPLQRIISVQGNRKILKQLACLEACEELHRVGALTDNLVPDIVEEETINKEL ECQIQTVEESKYFPPELVSHCSNDSEAVYYCYLVEMQHASYNDFELHEIILAVRTRLKCDDEILAFDLDVDRRGLLQVQLNYSKVVTLTAEEIRRCQRFQVSVFRILLD RDLSILQDALGAVQSPIGSAVSDYLLLPSLGSTPEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKNGLVCSCMLENSLVFTPHNGHIYCVTGFLDKLDCNS LLGMRTGESITYIEYYRKRHGINICFEEEPLLRGKHICKVRNYLQRSRTQKAKDSTDSSVELPPEICSLIMSPLSISTLNTYSYVPSIMHRIESLVMASNLKRMHLDHCTL NVPIPTAKILEAMTTKKCLEKFHLESLETLGDSFLKYAASKKLFKTYENHHEGLLTVKKTQIISNAALCKLGCARKIPGFIRNEPFDLKAWIIPGDNSQVHSFDEELLTSS DKMYSRVKQKIKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDAPMSRHFPMNAEKLVNVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLE FLGDAVLDYVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILHASQDLQRQICSTVEDFEKLNLDSTFGWEAETTFPKVLGDVIESLGGAIFVDSGF DKDTTFQCIRPLLEPLVTPQTLKPHPVRELTELCDQKGYIKKKDVVSRENGIAYITVEVEANGVVHTSTCSGRDKLIAKKVASKNVLKSLKECPSNASEQ	1405 aa

			>DCL2.5_protein_Sopen11g017590 MTASPIKSKGPSTPDSYWRKIHDLENLMHSKVYTCDSEAVLAEYISFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFC LSEMGVWLAFKAAEFLSQEETDFFSWGELDVCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDARYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLR SLLNELLPKLSGWRTEYTAGHASVVQSQSRKIQNKIVEEFRKGVVNIIVATSILEKGLDVQSCNLVIRFDPSATICSYIQSRGRARMQNSDFLLMVKSGDESTLARMQN FMASGEMMRQ	338 aa
		Sga	>Sga_DCL2.1_mRNA_Solyc11g008520_NM_001329412.1_scaffold2617_14.2_contig4_1402_aa MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQQETDFFSW GELDEAAEFLSQQETDFFSWGELDGLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASVVQ SQSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLV DEMYDEPCYKVESTGAIITLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAI NKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLTSEEIRRCQRFQVSVFK ILLDRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLD CNSLLNVRTGESITYREYYKKRQGIELCFEEPLLSGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLND CKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFTLQAWIIPGDSSQVHSFNEEL MTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQ RLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQCAIKASLHKHILHASPDLQRQICNTIEDFKNPVSTFGWEAETTFPKVLADVIESLAGAIFVDSGF NQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSRENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	1402 aa
			>Sga_DCL2.2_mRNA_Solyc06g048960_NM_001329410.1_scaffold18956_13.8_contig1_1399_aa MLQSLKTNSSPLTLCLLLEGCYQLEALETALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDSLMMHTDLKVGKYWGEMGVDYWDAA TWQRQVDAHEVLVMTPAILLAALRHSFIQINMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRQSLQLPRVFGMTASPIKSKGSSTADSYWQKIRDLENLMNSKVYT CGSESVLAEYIPFSNPKLKIYKHVDIPCTLFLSLAHDLEQLKEMHDCSISKSNLSFMSAGTARRRLSKLYSAFLFCLSEMGAWLAFKATEFLSREEVDFLSWGELDVC AQTIVRDFSWGASKIFSARLPSGPYWSIGGDIQANVDAGYLSSKVTCLLESLLEYRDQKDLRCIIFVERIITAIVLRSLLNELLPELCGWRTEYTAGHISVVQSQSRKLQ NKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGRARMQNSDFLLMVRSGDDSTLTRMHNYMASGEIMRQESLCHASIPCSPLDDELYDEPC YKVESTGAIVTLSSSVSLLYLYCSRLPSDGYFKPNPRCVIDKETGTCTLQLPKSCPLQRIISVQGNSKISKQLACLEACKELHRVGALTDNLVPDIMEEETINKELECQI HTVEELKYFPPELFSHCGNDSEAVYYCYLVELQHDACNNFQLHGIILAVRTRLKFDDEIMAFDLDIDRRGRLQVQLNYHNVVTLTSEEIQRCRRFQSSIFRILLDRDLS KLQGALAAVQSPIGSAVSDYLLLPSLGTTPEINWKCVNSLLFPSQALEAKHMDCCSTQGRKRSVSTKTGVICSCMLENSLVFTPHNGHIYCITGFLDNLDCNSLLDTR TGEPITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRCRIQKAKDSTDSSVELPPELCSLIMSPVSISTLNTYSYVPSIMHRIESLVMALNLKRMHLDHCTLDIFIPTI KVLEAVTTKKCLEKFHLESLETLGDSFLKYASSIQLFKTYENHHEGLLTIKKNKIISNDALCRLGCARKIPGFIRNEPFDLKAWLIPGDNSQIQTFDEEFLTSSDKMYSRG KQKFRSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDIDFVDAPLPRNFPMNAEKLINVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLD YVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILHASQDLQRQILSTVEDFEKLDLLSMFGWEAETTFPKVLGDVIESLGGAIFVDSGFNKDITFQSI RPLLEPLVTPQTVKLQPVRELSELCDQKGYIKKKDVISRENGLAYITVEVEANGVIHKSTCSGRDKIMAKKVASKNVLKSLKECPSNA	1399 aa
			>Sga_DCL2.3_mRNA_Solyc11g008540_NM_001329413.1_scaffold2617_14.2_contig12_1355_aa MLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEMGVDYWDASTWQQQVDDHEVLVMTPAILLAALRHSFLQIDMIKVIIFDECHNARGKHP YASIMVEFYHHQLTHESAQLPRIFGMTASPIKSKGASTAHSYWQKIHDLENLMNSKVYTCSSESVLAEYIPFSNPKLKIYEHEDIPCSLFNTLAHDLERLKEKHECSISK SNLSAMSAGSARRRLSKLHMAFLFCLSEMGVWLAFKAAEFLSFEENDFFSWGEFDACAQTIVRDFSLGASKIFSARLPSGPHWSIGGDIQANADAGYLSSKVNCLLE SLLEYRDQKDLRCIIFVERIVTAIVLRSLLNELLPERSGWRTEYTAGHVSVLQSQSRKSQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGR ARMQNSDFLLMVRDGDDPTLTRMQNYMASGEIMRQESLRHASIPCSPLDDELYDEPCYKVESTGAIVTLSSSVSLLYLYCSRLPSDGYFKPNPRCVIDKETETCTLQ LPKSSPLQGIISVQGKRKILKQLACLEACKQLHRVGALTDNLVPDIVEEETINIINKELECQIQTVEESKYFPPELVSHCSNDSEAVYYCYLVEMQHASYNDFELHGIILA VRTRLKCDDEILAFDLDVDRRGLLQVQLNYSKVVTLTAEEIRRCQRFQVSVFRILLDRDLSILQDALGAVQSPIGSAVSDYLLLPSLGSTPEINWKCVNSLLFPSQALG DKHMDWCSTQDRKRSVNTKNGLVCSCMLENSLVFTPHNGYIYCVTGFLDKLDCNSLLGMRTGESITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRSRTQKA KDSTDSSVELPPEICSLIMSPLSISTLNAYSYVPSIMHRIESLVMASNLKRMHLDHCTLNVPIPTATILEAMTTKKCLEKFHLESLETLGDSFLKYAASIKLFKTYENHHE GLLTVKKTQIISNAALCKLGCARKIPGFIRNEPFDLKAWIIPGDNSQVHSFDEVLLTSSDKMYSRVKQKIRSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFV DAPMSRHFPMNAEKLVNVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLH KHILHASQDLQRQICSTVEDFDKLNLDSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFDKETTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYIRKKDVVSREN GIAYITVEVEANGVVHKSTCSGRDKLIAKKVASKNVLKSLKECPSNATEQ	1355 aa
			>Sga_DCL2.4_mRNA_Solyc11g008530_NM_001329414.1_scaffold2617_14.2_contig7_scaffold32326_14.0_contig6_1158_aa MHSKVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLISQSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDAC VRDFCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGL VNIIVATSILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILMVRKGDDATLTRMQNYKASVEIMRQESLRHASIPCSTLHDELYDECYKVESTGAVVTLS SSVSLLDFYCSRLPSDGYFKPDPTYVINEETETCTLQLPKSSRLQGIISVQGKRKILKQLACLEACKQLHRVGALTDNLVPDIVEEETINKELECKIKIVEQSLYYPSEFV SHCGNESEAVYYCYLVELPHDSYNDSQLHGIILAVRTKLKFDDEILAFDLDVDRRGRLKVQLNYRKVVIFTSEEIRRCQRFQVSVFRILRDPDLSKLQEVLAAVQSPIG SAVSDYLLLPSVGTPPEINWQCVNSLLFPSQVLGDKHMDWCSTQGRRRSVNTISEVVCSCMLENSLVCTPHNGRIYCINGFLENLDCNSLMGVRSEESITYREHYR KRYGINICSEEVPLLRGKHISKEAKDSSVALPPELCSLIMSPLFISTLNTYSYVPSIMHRIESLIMASNLKKMHLDHCTQNVVIPTAKILEAMTTKNCLEKFHLESLETLGD SFLKYAASIKLFKTYENDHQGLLTVKRKQIISNATLCRLGCARKMPGFIRNKPFVLKAWIIPGDNSQVHNFDEELLTSSVKMYSRGKQKIKSKIMADVVEALIGAYLSSG	1158 aa

			GEVAALSFMKWLGVDINFVDAPTSRHLPVNAEKLVNVRYLESLLHYKFNDPSLLVEALSHGSCMLPDIPRCYKRLEFLGDAVLDYVVTTHLYFKYPGLTPGLITDLRS ASVNNECYALSAVKAGLHDHILYDLQVLQRHISSTVEDFKKLNPVSTFGWEAETTCPKVLADVIESLAGAIFVDSGFNQDTTFLCIRPLLEPLITPQTLKLHPARELREL CHQKGYIKQKNVVFRENGIVYVTVEVEANGVIHKDSNSGRNQKMAEKVASKYLLKSLKEYPYNP	
			>Sga_DCL2.2_mRNA_Sopen11g004310_XM_027913104.1_scaffold2617_14.2_contig4_1349_aa MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLRPHWSIGGDIQANTDAGYLSSKVHCL VESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASVVQSQSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRG RARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLVDEMYDEPCYKVESTGAIITLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCT LQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAINKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILA VRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLTSEEIRRCQRFQVSVFKILLDRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVL GDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLDCNSLLNVRTGESITYREYYKKRQGIELCFEEPLLSGKRISKVHNYLQRNRTQKA KDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLNDCKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHH EGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFTLQAWIIPGDSSQVHSFNEELMTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFA DAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQCAIKASLHKH ILHASPDLQRQICNTIEDFKNPVSTFGWEAETTFPKVLADVIESLAGAIFVDSGFNQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSRENGVAY ITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	1349 aa
			>Sga_DCL2.3_mRNA_Sopen11g004320_scaffold2617_14.2_contig7_scaffold2617_14.2_contig6_482_aa MESTDVAVFENQHLSADPLPFARSYQLEALEIALKQNTIVYLETGSGKTLIAIMLLRSYASLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW NAATWQQLVDDHEVLVMTPAILHAALRHSFLQMGMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHS KVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLISQSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDACVRD FCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIV ATSILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILM	482 aa
			>Sga_DCL2.5_mRNA_Sopen11g017590_scaffold2617_14.2_contig4_253_aa VYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQQETDFFSWGELD VCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASVVQSQSRK IQNKIVEEFRKGVVNIIVATSILEEGLDVQSCKS	253 aa
		Sch	>Sch_DCL2.1_mRNA_Solyc11g008520_NM_001329412.1_scaffold6549_1404_aa MSMARSNDVVCGNQLVFADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKNVDIPSTLSKSLANDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQEETDFFSWG ELDVCAQTIVRDFSSDASKVFSACLPSGPNWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASVVQSQ SRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLTRMQNFMASGEMMRQESLRHASEPCSPLVDE MYDEPCYKVESTGAIVTLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAIN KELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKFKCDDEILAFDFDVDRRRCVQVQLKYSKVVTLTSEEIRRCQRFQVSVFKI LLDRDLSKLQDALAAGQSPIGSAVSDYLLLPAVGKSSEINWKCVNSLLFPSQVLGNKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLIFTPHNGNIYCITGFLDNLDC NSLLNVRTGESITYREYYKKRQGIELCFEEPLLSGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLNDC KLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDSFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFNLQAWIIPGDSSQVHSFNEEFM TSSDKMYSRIKQNIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQR LEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHKHILHASPDLQRQICNTIEDFKNLNLVSTFGWEAETTFPKVLADVIESLAGAIFVDSG FNQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSRDNGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	1404 aa
			>Sch_DCL2.2_mRNA_Solyc06g048960_NM_001329410.1_scaffold6326_1399_aa MLQSLKSNSSPLTLCLLLEGCYQLEALETALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDSLMMHTDLKVGKYWGEMGVDYWDAA TWQRQVDAHEVLVMTPAILLAALRHSFIQINMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRQSLQLPRVFGMTASPIKSKGSSTADSYWQKIRDLENLMNSKVYT CGSESVLAEYIPFSNPKLKIYKHVDIPCTLFLSLAHDLEQLKEMHDCSISKSNLSFMSAGTARRRLSKLYSAFLFCLSEMGAWLAFKATEFLSREEVDFLSWGELDVC AQTIVRDFSWGASKIFSARLPSGPHWSIGGDIQANVDAGYLSSKVTCLLESLLEYRDQKDLRCIIFVERIITAIVLRSLLNELLPELCGWRTEYTAGHISVVQSQSRKLQ NKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGRARMQNSDFLLMVSSGDDSTLTRMHNYMASGEIMRQESLRHASIPCSPLDDELYDEPCY KVESTGAIVTLSSSVSLLYLYCSRLPSDGYFKPNPRCVIDKETGTCTLQLPKSCPLQRIISVQGNSKISKQLACLEACKELHRVGALTDNLVPDIMEEETINKELECQIHT VEESKYFPPELVSHCGNDSEAVYYCYLVELQHDACNDFQLHGIILAVRTRLKFDDEIMAFDLDIDRRGRLQVQLNYHNVVTLTSEEIQRCRRFQSSIFRILLDRDLSKL QGALAAVQSPIGSAVSDYLLLPSLGTTPEINWKCVNSLLFPSQVLGAKHMDCCSTQGRKRSVSTKTGVVCSCMLENSLVFTPHNGHIYCITGFLDNLDCNSLLDTRT GEPITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRCRIQKAKDSTDSSVELPPELCSLIMSPVSVSTLNTYSYVPSIMHRIESLVMASNLKRMHLDHCTLDIFIPTI KVLEAMTTKKCLEKFHLESLETLGDSFLKYASSIQLFKTYENHHEGLLTIKKNKIISNDALCRLGCARKIPGFIRNEPFDLKAWLIPGDNSQIHTLDEEFLTSSDKMYSRV KQKFKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDIDFVDAPLPRNFPMNAEKLINVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLD YVVTAHLFFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILHASQDLQRQILSTVEDFKKLDLLSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFNKDITFQSI RPLLEPLVTPQTVKLQPVRELSELCDQKGYIKKKDVVSHENGVAYITVEVEANGVIHKSTCSGRDKIMAKKVASKNVLKSLKECPSNA	1399 aa
			>Sch_DCL2.3_mRNA_Solyc11g008540_NM_001329413.1_scaffold6549_1353_aa	1353 aa

			MLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEMGVDYWDASTWQQQVDDHEVLVMTPAILLAALRHSFIQINMIKVIIFDECHNARGKHPY ASIMMEFYHRQLTRQSLQLPRVFGMTASPIKSKGSSTADSYWQKIRDLENLMNSKVYTCDSEAVLAEYIPFSNPKLKIYKNVDIPSTLSKSLANDMERLKEKHECSITK STLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKEAAEFLSFEENDFFSWGEFDACAQTIVRDFSLGASKIFSARLPSGPHWSIGDDIQANVDAGYLSSKVNCLL ESLLDYRDQKDLRCIIFVERIITAIVLRSLLNELLPELCGWRTEYTAGHISVVQSQSRKLQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGR ARMQNSDFLLMVSGDDPTITRMQNYMASGEIMRQESLRHASIPCSPLDDELYDEPCYKVESTGAVVTLSSSVSLLYFYCSRLPSDGYFKPNPRCVIDKETGTCTLQL PKSSPLQRIISVQGNTKILKQLACLEACEELHRVGALTDNLVPDIVEEETINKELECQIQTVEESKYFPPELVSHCGNDSEAVYYCYLVEMQHASYNDFELHGIILAVRT RLKCDDEILAFDLDVDRRGLLQVQLNYSKVVTLTAEEIRRCQRFQVSVFRILLDRDLSILQDALGAVQSPIGSAVSDYLLLPSLGSTPEINWKCVNSLLFPSQVLGDKH MDWCSTQDRKRSVNTKNGLVCSCMLENSLVFTPHNGYIYCVTGFLDELDCNSLLGMRTGESITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRSRTQNAKDS TDSSVELPPEICSLIMSPLSISTLNTYSYVPSIMHRIESLVMASNLKRMHLDHCTLNVPIPTAKILEAMTTKKCLEKFHLESLETLGDSFLKYAASIKLFKTYENHHEGLLT VKKTQIISNAALCKLGCARKIPGFIRNEPVDLKAWIIPGDNSQVHSFDEELLTSSDKMYSRVKQKIKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDAPM SRHFPVNAEKLVNVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILH ASQDLQRQICSTVEDFEKLNLDSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFDKDTTFQCIRPLLEPLVTPQTLKLHPVRELTELCDQKGYIKKKDVVSRENGIAYIT VEVEANGVVHTSTCSGRDKLIAKKVASKNVLKSLKGCPSNATTEQ	
			>Sch_DCL2.4_mRNA_Solyc11g008530_NM_001329414.1_scaffold6549_1013_aa XTQQGDALMLHTDLKVGKYWGEKGVDYWNAATWQQQVDDHEVYTCGSESVLADYIPFSNPKLKIYEHVDIPSTLFHTLVHDLEKLKEKHEWSISQSNFMRDGSAR RRLSKLHSDFLFCLSEMGAWLAFKSCEENDFFSSDDACIKGFCLGASKIFSARLPSGPHWSIGDDIQANVDAGYLSSKVNCLLESLLDYRDRKDLRCIIFVERIITAIVL RSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIVTTSILEEGLDVRSCNLVIKFDPPTTVCSYIQSLGRARMQNSNFLLMVRKGDDATLTRMQNYKASV EIMRQESLRHASIPCSTLHDELYDECYKVESTGAIVTLSSSVNCYTSIAQGYRRIGTLNPILACEELHRVGALTDNLVPDIVEEETINKELECQIHTVEESKYFPPEFVSH FGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKFKCDDEILAFDFDVDRRRCVQVQLKYSKVVTLTSEEIRRCQRFQVSVFRILLDRDLSILQDALGAVQSPIGSA VSDYLLLPSLGSTPEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKNGLILEAMTTKNCLEKFHLKSLETLGDSFLKYAASIKLFKTYENDHHGLLTVKREQII SNAALCRLGCARKMPGFICNKPFVLKAWIIPGDNSQVHSFDEELLTSSVKMYSRGKQKIISKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDAPTSRHFPV NAEKLVNVRYLESLLHYKFNDPSLLVEALSHGSCMLPDIPRCYKRLEFLGDAVLDYVVTTHLYFKYPGLTPGLITDLRSASVNNECYALSAVKAGLHDHILYNPQVLQ RHISSTVEDFKKLNLVSTFGWEAETTYPKVLADVIESLAGAIFVDSGFNQDTTFLCIRPLLEPLITPQTLKLHPARELHELCHQKGYIKQKNVVFRENGIVYVTVEVEAN GVIHKDSNSGRNKKMAEKVASKYVLKSLKEYPSV	1013 aa
			>Sch_DCL2.2_mRNA_Sopen11g004310_XM_027913104.1_scaffold6549_1335_aa MSMARSNDVVCGNQLVFADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKNVDIPSTLSKSLANDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLRPNWSIGGDIQANTDAGYLSSKVHCL VESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASVVQSQSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRG RARMQNSDFLLMVKSGDESTLTRMQNFMASGEMMRQESLRHASEPCSPLVDEMYDEPCYKVESTGAIVTLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTC TLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAINKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIIL AVRTKFKCDDEILAFDFDVDRRRCVQVQLKYSKVVTLTSEEIRRCQRFQVSVFKILLDRDLSKLQDALAAGQSPIGSAVSDYLLLPAVGKSSEINWKCVNSLLFPSQV LGNKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLIFTPHNGNIYCITGFLDNLDCNSLLNVRTGESITYREYYKKRQGIELCFEEPLLSGKRISKVHNYLQRNRTQKA KDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLNDCKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDSFLKYAVSTQLFKTHENHH EGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFNLQAWIIPGDSSQVHSFNEEFMTSSDKMYSRIKQNIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDF ADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHK HILHASPDLQRQICNTIEDFKNLNLCPRSDGRLKQLSLRYLQMLSSPLLCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSRDNGVAYITVEIDADGVTHK STCSGRDKIMAKKVACKNVLKSLKECSYNA	1335 aa
			>Sch_DCL2.3_mRNA_Sopen11g004320_scaffold2617_14.2_contig7_scaffold6549_385_aa MEPTNVAVFENQQVSADPLPFARSYQLEALEIALKQNTIVYLESYQLEALEIALKQNTIVYLERKPSPFIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW NAATWQQQVDDHEVYTCGSESVLADYIPFSNPKLKIYEHVDIPSTLFHTLVHDLEKLKEKHEWSISQSNFMRDGSARRRLSKLHSDFLFCLSEMGAWLAFKSCEEND FFSSDDACIKGFCLGASKIFSARLPSGPHWSIGDDIQANVDAGYLSSKVNCLLESLLDYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIV EEFRKGLVNIIVTTSILEEGLDVRSCNLVIKFDPPTTVCSYIQSLGRARMQNSNFLLM	385 aa
			>Sch_DCL2.5_mRNA_Sopen11g017590_scaffold6549_301_aa VYTCDSEAVLAEYIPFSNPKLKIYKNVDIPSTLSKSLANDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQEETDFFSWGELD VCAQTIVRDFSSDASKVFSACLPSGPNWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVRNLKDLRCIIFVERIITAIVAGHASVVQSQSRKIQN KIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLTRMQNFMAX	301 aa
		SpiLA1589	>SpiLA1589_DCL2.1_mRNA_Solyc11g008520_NM_001329412.1_contig:unspecified:6538610:1:8256:1_1402_aa MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQQETDFFSW GELDVCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASMVQS QSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLVD EMYDEPCYKVESTGAIVTLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAI NKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLISEEIRRCQRFQVSVFKI LLDRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLD	1402 aa

			CNSLLNVRTGESITYREYYKKRQGIELCFEEPLLRGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLND CKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFTLQAWIIPGDSSQVHSFNEEL MTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQ RLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHKHILHASPDLQRQICNTIEDFKNPVSTFGWEAETTFPKVLADVIESLAGAIFVDSGF NQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSHENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	
			>SpiLA1589_DCL2.2_mRNA_Solyc06g048960_NM_001329410.1_contig:unspecified:6489456:1:9223:1_contig:unspecified:6756388:1:2206:1_contig:unspecifie d:6713762:1:553:1_1217_aa MTASPIKSKGSSTADSYWQKIRDLENLMNSKVYTCGSESVLAEYIPFSNPKLKIYKHVDIPCTLFLSLAHDLEQLKEMHDCSISKSNLSFMSAGTARRRLSKLYSAFLF CLSEMGAWLAFKATEFLSREEVDFLSWGELDVCAQTIVRDFSWGASKIFSARLPSGPHWSIGGDIQTNVDAGYLSSKVTCLLESLLEYRDQKDLRCIIFVERIITAIVLR SLLNELLPELCGWRTEYTAGHISVVQSQSRKLQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGRARMQNSDFLLMVRSGDDSTLTRMH NYMASGEIMRQESLRHASIPCSPLDDELYDEPCYKVESTGAIVTLSSSVSLLYLYCSRLPSDGYFKPNPRCVIDKDTGTCTLQLPKSCPLQRIISVQGNSKISKQLACL EACKELHRVGALTDNLVPDIMEEETINKELECQIHTVEESKYFPPELVSHCGNDSEAVYYCYLVELQHDTCNDFQLHGIILAVRTRLKFDDEIMAFDLDIDRRGRLQVQ LNYHNVVTLTSEEIQRCRRFQSSIFRILLDRDLSKLQGALAAVQSPLGSAVSDYLLLPSLGTTPEINWKCVNSLLFPSQVLGAKHMDCCSTQGRKRSVSTKTGVVCSC MLENSLVFTPHNGHIYCITGFLDNLDCNSLLDTRIGEPITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRCRIQKAKDSTDSSVELPPELCSLIMSPVSISTLNTYS YVPSIMHRIESLVMASNLKRMHLNHCTLDIFIPTIKVLEAMTTKKCLEKFHLESLETLGDSFLKYASSIQLFKTYENHHEGLLTIKKNKIISNDALCRLGCARKIPGFIRNEP FDLKAWLIPGDNSQIHTLDEEFLTSSDKMYSRGKQKFKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDIDFVDAPLPRNFPMNAEKLINVRYLESLLHYKFNDP SLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLFFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILHASQDLQRQILSTVEDFEKLDLLSTFGWEA ETTFPKVLGDVIESLGGAIFVDSGFNKDITFQSIRPLLEPLVTPQTVKLQPVRELSELCDQKGYIKKKDVVSHENGVAYITVEVEANGVIHKSTCSGREKIMAKKVASKN VLKSLKECPSNA	1217 aa
			>SpiLA1589_DCL2.3_mRNA_Solyc11g008540_NM_001329413.1_contig:unspecified:6566908:1:4607:1_contig:unspecified:6566027:1:3553:1__contig:unspecifi ed:6681690:1:2350:1_1353_aa MLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEMGVDYWDASTWQQQVDDHEVLVMTPAILLAALRHSFLQIDMIKVIIFDECHNARGKHP YASIMVEFYHHQLTHESAQLPRIFGMTASPIKSKGASTARSYWQKIHDLENLMNSKVYTCSSESVLAEYIPFSNPKLKIYEHEDIPCSLFNTLAHDLERLKEKHECSISK SNLSAMSAGSARRRLSKLHMAFLFCLSEMGVWLAFKAAEFLSFEENDFFSWGEFDACAQTIVRDFSLGASKIFSARLPSGPHWSIGGDIQANADAGYLSSKVNCLLE SLLEYRDQKDLRCIIFVERIVTAIVLRSLLNELLPERSGWRTEYTAGHVSVLQSQSRKSQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGR ARMQNSDFLLMVRDGDDPTLTRMQNYMASGEIMRQESLRHASIPCSPLDDELYDEPCYKVESTGAVVTLSSSVSLLDFYCSRLPSDGWYFKPNPRCVIDKETGTCT LQLPKSSPLQRIISVQGNTKILKQLACLEACEELHRVGALTDNLVPDIVEEETINKELECQIQTVEESKYFPPELVSHCSNDSEAVYYCYLVEMQHASYNDFELHGIILA VRTRLKCDDEILAFDLDVDRRGLLQVQLNYSKVVTLTAEEIRRCQRFQVSVFRILLDRDLSILQDALGAVQSPIGSAVSDYLLLPSLGSTPEINWKCVNSLLFPSQALG DKHMDWCSTQDRKRSVNTKNGLVCSCMLENSLVFTPHNGYIYCVTGFLDKLDCNSLLGMRTGESITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRSRTQKA KDSTDSSVELPPEICSLIMSPLSISTLNTYSYVPSIMHRIESLVMASNLKRMHLDHCTLNVPIPTATILEAMTTKKCLEKFHLESLETLGDSFLKYAASIKLFKTYENHHEG LLTVKKTRIISNAALCKLGCARKIPGFIRNEPFDLKAWIIPGDNSQVHSFDEVLLTSSDKMYSRVKQKIKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDA PMSRHFPMNAEKLVNVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHI LHASQDLQRQICSTVEDFDKLNLDSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFDKETTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYIRKKDVVSRENGIA YITVEVEANGVVHKSTCSGRDKLIAKKVASKNVLKSLKECPSNATEQ	1353 aa
			>SpiLA1589_DCL2.4_mRNA_Solyc11g008530_NM_001329414.1_contig:unspecified:6742142:1:2591:1_contig:unspecified:6660195:1:6613:1_1370_aa MESTDVAVFENQHLSADPLPFARSYQLEALEIALKQNTIVYLETGSGKTLIAIMLLRSYASLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW NAATWQQLVDDHEVLVMTPAILHAALRHSFLQMGMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHS KVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLISQSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDACVRD FCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIV ATSILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILMVRKGDDATLTRMQNYKASVEIMRQESLRHASIPCSTLHDELYDECYKVESTGAVVTLSSSVS LLDFYCSRLPSDGYFKPDPTYVINEETETCTLQLPKSSRLQGIISVQGKRKILKQLACLEACKQLHRVGALTDNLVPDIVEEETINKELECKIKIVEQSLYYPSEFVSHCG NESEAVYYCYLVELPHDSYNDSQLHGIILAVRTKLKFDDEILAFDLDVDRRGRLKVQLNYRKVVIFTSEEIRRCQRFQVSVFRILRDPDLSKLQEVLAAVQSPIGSAVSD YLLLPSVGTPPEINWQCVNSLLFPSQVLGDKHMDWCSTQGRRRSVNTISEVVCSCMLENSLVCTPHNGRIYCINGFLENLDCNSLMGVRSEESITYREHYRKRYGIN ICSEEVPLLRGKHISKEAKDSSVALPPELCSLIMSPLFISTLNTYSYVPSIMHRIESLIMASNLKKMHLDHCTQNVVIPTAKILEAMTTKNCLEKFHLESLETLGDSFLKYA ASIKLFKTYENDHQGLLTVKRKQIISNATLCRLGCARKMPGFIRNKPFVLKAWIIPGDNSQVHNFDEELLTSSVKMYSRGKQKIKSKIMADVVEALIGAYLSSGGEVAAL SFMKWLGVDINFVDAPTSRHLPVNAEKLVNVRYLESLLHYKFNDPSLLVEALSHGSCMLPDIPRCYKRLEFLGDAVLDYVVTTHLYFKYPGLTPGLITDLRSASVNNE CYALSAVKAGLHDHILYDLQVLQRHISSTVEDFKKLNPVSTFGWEAETTCPKVLADVIESLAGAIFVDSGFNQDTTFLCIRPLLEPLITPQTLKLHPARELRELCHQKGY IKQKNVVFRENGIVYVTVEVEANGVIHKDSNSGRNQKMAEKVASKYLLKSLKEYPYNP	1370 aa
			>SpiLA1589_DCL2.2_mRNA_Sopen11g004310_XM_027913104.1_contig:unspecified:6538610:1:8256:1_1402_aa MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKKHECSITKSTLSDKSAASAKMAFKAAEFLSQQETDFFSWG ELDVCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLPKLSGWRTEYTAGHASMVQSQ SRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCKVNIIVATSILEEGLDVQSCKARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLVDEM YDEPCYKVESTGAIVTLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAINK ELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLISEEIRRCQRFQVSVFKILL	1402 aa

			DRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLDCN SLLNVRTGESITYREYYKKRQGIELCFEEPLLRGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPDSTDSSVQLPPELCFVIMSPSLVMASHLNSMLLND CKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFTLQAWIIPGDSSQVHSFNEEL MTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLDIDFADAPIQRHFPLNAEKLVEALTHGSYMLPEIPRCYQR LEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHKHILHASPDLQRQICNTIEDFKNPVSTFGWEAETTFPKVLADVIESLAGAIFVDSGFN QDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSHENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	
			>SpiLA1589_DCL2.3_mRNA_Sopen11g004320_contig:unspecified:6660195:1:6613:1_482_aa MESTDVAVFENQHLSADPLPFARSYQLEALEIALKQNTIVYLETGSGKTLIAIMLLRSYASLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW NAATWQQLVDDHEVLVMTPAILHAALRHSFLQMGMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHS KVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLISQSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDACVRD FCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIV ATSILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILM	482 aa
		SpiLA0480	>SpiLA0480_DCL2.1_mRNA_Solyc11g008520_NM_001329412.1_Scaffold3061571_1402_aa MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQQETDFFSW GELDVCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLLKLSGWRTEYTAGHASMVQS QSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLVD EMYDEPCYKVESTGAIVTLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAI NKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLTSEEIRRCQRFQVSVFK ILLDRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLD CNSLLNVRTGESITYREYYKKRQGIELCFEEPLLRGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLND CKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFTLQAWIIPGDSSQVHSFNEEL MTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQ RLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHKHILHASPDLQRQICNTIEDFKNPVSTFGWEAETTFPKVLADVIESLAGAIFVDSGF NQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSHENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	1402 aa
			>SpiLA0480_DCL2.2_mRNA_Solyc06g048960_NM_001329410.1_Scaffold3062417_contig1_1399_aa MLQSLKTNSSPLTLCLLLEGCYQLEALETALKQNTIVYLETGSGKTLIALMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDSLMMHTDLKVGKYWGEMGVDYWDAA TWQRQVDAHEVLVMTPAILLAALRHSFIQINMIKVIIFDECHNARGKHPYASIMMEFYHRHLTRQSLQLPRVFGMTASPIKSKGSSTADSYWQKIRDLENLMNSKVYT CGSESVLAEYIPFSNPKLKIYKHVDIPCTLFLSLAHDLEQLKEMHDCSISKSNLSFMSAGTARRRLSKLYSAFLFCLSEMGAWLAFKATEFLSREEVDFLSWGELDVC AQTIVRDFSWGASKIFSARLPSGPHWSIGGDIQTNVDAGYLSSKVTCLLESLLEYRDQKDLRCIIFVERIITAIVLRSLLNELLPELCGWRTEYTAGHISVVQSQSRKLQ NKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGRARMQNSDFLLMVRSGDDSTLTRMHNYMASGEIMRQESLRHASIPCSPLDDELYDEPC YKVESTGAIVTLSSSVSLLYLYCSRLPSDGYFKPNPRCVIDKDTGTCTLQLPKSCPLQRIISVQGNSKISKQLACLEACKELHRVGALTDNLVPDIMEEETINKELECQI HTVEESKYFPPELVSHCGNDSEAVYYCYLVELQHDTCNDFQLHGIILAVRTRLKFDDEIMAFDLDIDRRGRLQVQLNYHNVVTLTSEEIQRCRRFQSSIFRILLDRDLS KLQGALAAVQSPLGSAVSDYLLLPSLGTTPEINWKCVNSLLFPSQVLGAKHMDCCSTQGRKRSVSTKTGVVCSCMLENSLVFTPHNGHIYCITGFLDNLDCNSLLDT RIGEPITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRCRIQKAKDSTDSSVELPPELCSLIMSPVSISTLNTYSYVPSIMHRIESLVMASNLKRMHLNHCTLDIFIPT IKVLEAMTTKKCLEKFHLESLETLGDSFLKYASSIQLFKTYENHHEGLLTIKKNKIISNDALCRLGCARKIPGFIRNEPFDLKAWLIPGDNSQIHTLDEEFLTSSDKMYSR GKQKFKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDIDFVDAPLPRNFPMNAEKLINVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVL DYVVTAHLFFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHILHASQDLQRQILSTVEDFEKLDLLSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFNKDITFQ SIRPLLEPLVTPQTVKLQPVRELSELCDQKGYIKKKDVVSHENGVAYITVEVEANGVIHKSTCSGREKIMAKKVASKNVLKSLKECPSNA	1399 aa
			>SpiLA0480_DCL2.3_mRNA_Solyc11g008540_NM_001329413.1_Scaffold3069414_1352_aa MLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEMGVDYWDASTWQQQVDDHEVLVMTPAILLAALRHSFLQIDMIKVIIFDECHNARGKHP YASIMVEFYHHQLTHESAQLPRIFGMTASPIKSKGASTARSYWQKIHDLENLMNSKVYTCSSESVLAEYIPFSNPKLKIYEHEDIPCSLFNTLAHDLERLKEKHECSISK SNLSAMSAGSARRRLSKLHMAFLFCLSEMGVWLAFKAAEFLSFEENDFFSWGEFDACAQTIVRDFSLGASKIFSARLPSGPHWSIGGDIQANADAGYLSSKVNCLLE SLLEYRDQKDLRCIIFVERIVTAIVLRSLLNELLPERSGWRTEYTAGHVSVLQSQSRKSQNKIVEEFRKGLVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSFIQSRGR ARMQNSDFLLMVRDGDDPTLTRMQNYMASGEIMRQESLRHASIPCSPLDDELYDEPCYKVESTGAVVTLSSSVSLLYFYCSRLPSDGYFKPNPRCVIDKETGTCTL QLPKSSPLQRIISVQGNRKILKQLACLEACEELHRVGALTDNLVPDIVEEETINKELECQIQTVEESKYFPPELVSHCSNDSEAVYYCYLVEMQHASYNDFELHGIILAV RTRLKCDDEILAFDLDVDRRGLLQVQLNYSKVVTLTAEEIRRCQRFQVSVFRILLDRDLSILQDALGAVQSPIGSAVSDYLLLPSLGSTPEINWKCVNSLLFPSQALGD KHMDWCSTQDRKRSVNTKNGLVCSCMLENSLVFTPHNGYIYCVTGFLDKLDCNSLLGMRTGESITYIEYYKKRHGINICFEEEPLLRGKHICKVHNYLQRSRTQKAK DSTDSSVELPPEICSLIMSPLSISTLNTYSYVPSIMHRIESLVMASNLKRMHLDHCTLNVPIPTATILEAMTTKKCLEKFHLESLETLGDSFLKYAASIKLFKTCENHHEGL LTVKKTRIISNAALCKLGCARKIPGFIRNEPFDLKAWIIPGDNSQVHSFDEVLLTSSDKMYSRVKQKIKSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFVDAP MSRHFPMNAEKLVNVRYLESLLHYKFNDPSLLVEALTHGSYMLPEIPRCYQRLEFLGDAVLDYVVTAHLYFKYPGLTPGLITDLRSASVNNECYAQSAVKAGLHKHIL HASQDLQRQICSTVEDFDKLNLDSTFGWEAETTFPKVLGDVIESLGGAIFVDSGFDKETTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYIRKKDVVSRENGIAY ITVEVEANGVVHKSTCSGRDKLIAKKVASKNVLKSLKECPSNATEQ	1352 aa
			>SpiLA0480_DCL2.4_mRNA_Solyc11g008530_NM_001329414.1_Scaffold3061571_1370_aa MESTDVAVFENQHLSADPLPFARSYQLEALEIALKQNTIVYLETGSGKTLIAIMLLRSYASLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW	1370 aa

			NAATWQQLVDDHEVLVMTPAILHAALRHSFLQMGMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHS KVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLISQSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDACVRD FCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIVLRSLLNELFLERSGWRTEVTTGRITTFKQNKIVEEFRKGLVNIIV ATSILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILMVRKGDDATLTRMQNYKASVEIMRQESLRHASIPCSTLHDELYDECYKVESTGAVVTLSSSVS LLDFYCSRLPSDGYFKPDPTYVINEETETCTLQLPKSSRLQGIISVQGKRKILKQLACLEACKQLHRVGALTDNLVPDIVEEETINKELECKIKIVEQSLYYPSEFVSHCG NESEAVYYCYLVELPHDSYNDSQLHGIILAVRTKLKFDDEILAFDLDVDRRGRLKVQLNYRKVVIFTSEEIRRCQRFQVSVFRILRDPDLSKLQEVLAAVQSPIGSAVSD YLLLPSVGTPPEINWQCVNSLLFPSQVLGDKHMDWCSTQGRRRSVNTISEVVCSCMLENSLVCTPHNGRIYCINGFLENLDCNSLMGVRSEESITYREHYRKRYGIN ICSEEVPLLRGKHISKEAKDSSVALPPELCSLIMSPLFISTLNTYSYVPSIMHRIESLIMASNLKKMHLDHCTQNVVIPTAKILEAMTTKNCLEKFHLESLETLGDSFLKYA ASIKLFKTYENDHQGLLTVKRKQIISNATLCRLGCARKMPGFIRNKPFVLKAWIIPGDNSQVHNFDEELLTSSVKMYSRGKQKIKSKIMADVVEALIGAYLSSGGEVAAL SFMKWLGVDINFVDAPTSRHLPVNAEKLVNVRYLESLLHYKFNDPSLLVEALSHGSCMLPDIPRCYKRLEFLGDAVLDYVVTTHLYFKYPGLTPGLITDLRSASVNNE CYALSAVKAGLHDHILYDLQVLQRHISSTVEDFKKLNPVSTFGWEAETTCPKVLANVIESLAGAIFVDSGFNQDTTFLCIRPLLEPLITPQTLKLHPARELRELCHQKGY IKQKNVVFRENGIVYVTVEVEANGVIHKDSNSGRNQKMAEKVASKYLLKSLKEYPYNP	
			>SpiLA0480_DCL2.2_mRNA_Sopen11g004310_XM_027913104.1_Scaffold3061571_1402_aa MSMARANDVVCGNQLVSADPLPFARSYQLEALEAALKQNTIVYLETGSGKTLIAIMLLRSYAYLLRKPSPYIAVFLVPTVVLVTQQGDALMMQTDLKVGTYWGEMGV DFWDAATWKRQVDGHEVLVMTPAILLSALRHNFLQIDMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRESAQLPRIFGMTASPIKSKGPSTPDSYWRKIHDLENLM HSKVYTCDSEAVLAEYIPFSNPKLKIYKHVDIPSTLSKSLAHDMERLKEKHECSITKSTLSDKSAASAKRRLSKLYSAFLFCLSEMGVWLAFKAAEFLSQQETDFFSW GELDVCAQTIVRDFSSDASKVFSACLPSGPHWSIGGDIQANTDAGYLSSKVHCLVESLLEYRNLKDLRCIIFVERIITAIVLRSLLNELLLKLSGWRTEYTAGHASMVQS QSRKIQNKIVEEFRKGVVNIIVATSILEEGLDVQSCNLVIRFDPSATVCSYIQSRGRARMQNSDFLLMVKSGDESTLARMQNFMASGEMMRQESLRHASEPCSPLVD EMYDEPCYKVESTGAIVTLSSSVSLLYFYCSRLPSDGYFKSYPRCVIDKESRTCTLQLPKSCPLQRIITVQGNSTKILRQLACLEACKELHRVGALTDNLVPDIVEEEAI NKELECQIHTVEESKYFPPEFVSHFGNETEAVYYCYLVELQHETYDDFQLHGIILAVRTKLKCDDEILAFDLDVDRRRRVQVQLKYSKVVTLTSEEIRRCQRFQVSVFK ILLDRDLSKLQDALAAGQSPIGSAVSDYLLLPSVGKSSEINWKCVNSLLFPSQVLGDKHMDWCSTQDRKRSVNTKTGVVCSCLLENSLVFTPHNGNIYCITGFLDNLD CNSLLNVRTGESITYREYYKKRQGIELCFEEPLLRGKRISKVHNYLQRNRTQKAKDSTDSSVQLPPELCFVIMSPISISTLYTYSYVPSIMHRIESLVMASHLNSMLLND CKLNVFIPTAMVLEAVTTRKCLEKFHLESLETLGDAFLKYAVSTQLFKTHENHHEGLLCVKKSKIISNAALCKLGCARKIPGFIRNEAFTLQAWIIPGDSSQVHSFNEEL MTSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSLMKWLGMDIDFADAPIQRHFPLNAEKLVNVKYLESLLHYKFHDPSLLVEALTHGSYMLPEIPRCYQ RLEFLGDAVLDYVVTAHLYFKYPGLSPGLITDLRSASVNNECYAQSAIKASLHKHILHASPDLQRQICNTIEDFKNPVSTFGWEAETTFPKVLADVIESLAGAIFVDSGF NQDTTFQCIRPLLEPLVTPQTLKPHPVRELSELCDQKGYVKKKDVVSHENGVAYITVEIDADGVTHKSTCSGRDKIMAKKVACKNVLKSLKECSYNA	1402 aa
			>SpiLA0480_DCL2.3_mRNA_Sopen11g004320_Scaffold3061571_482_aa MESTDVAVFENQHLSADPLPFARSYQLEALEIALKQNTIVYLETGSGKTLIAIMLLRSYASLLRKPSPYIAVFLVPTVVLVTQQGDALMLHTDLKVGKYWGEKGVDYW NAATWQQLVDDHEVLVMTPAILHAALRHSFLQMGMIKVIIFDECHNARGKHPYASIMMEFYHRQLTRENAQLPRIFGMTASPIKSKGSSTADSYWQKIRDLENLMHS KVYTCSSESVLADYIPFSNPKLKIYEHVDIPSKLFQTLVHDLERLKEKHECLISQSNLSFMRDGSARRRLSKLHSNFLFCLSEMGAWLAFKSCEENDFLSSDDACVRD FCLGASTIFSAHLPSGPHWSIGKDIQANVDAGYLSSKVNCLLESLLEYRDRKDLRCIIFVERIITAIDRDRKDLRCIIFVERIITAIATGRITTFKQNKIVEEFRKGLVNIIVAT SILEEGLDVRSCNLVIRFDPSTTVCSFIQSRGRARMQNSDFILM	482 aa
	DCL3	*Sly*	>DCL3.1_protein_Solyc08g067210 MATSTCELIWLKQLLRELKFGEINQMELVCDNQAALYIASNLFDAALADLKLSLPSQYKDTDDIYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICLENVPNDKDENEI LRTSSLQHRYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYLTGTNTSVDALTR KAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDPDDSVVKPCLVKE TKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALNDHLLPFNEKPPRG GSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGKVHLDSQQVAKA KIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTASFVEDIDQTDLIH FANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGPKSKDSTMVVKK PLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKDISSHSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFLKYPKKHEGQLTN ERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEALIGAYYVGGGFV AALKLMKWLGFKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKDIDPGELTDLRSA SVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPFRELIELCDSLGYF FKEHCVMKGDTVNAELRLQLIDDLLIAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKRKKVYLNNKTDEAQ SVPSDCSTSSSYSNKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERADKKSSLDSAALHM LYELERQGKIAIGNQ	1430 aa
		Spe	>protein_Sopen08g021150 SNCYAKILCCLENLGIICAYEAVKICLENVPNDKDENEILRTSSLQHRYFLEEALSIIQESMPQDCESLFDVGYDLSATLLMGHISSKLQVLLEIFQLLGKATQVRCLIFVE RIITAKVIERVMKKMTWFSHFTIAYLTGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNK KQREQMFDIIRSEYSMTDTAIKRDPDDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECR SSQLSRQLVCLDACKKLHQIGALNDHLLPFNEKPPRGGSDVQDRKLGAGTTKLKELHGTACISALSGSRGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDY DVGNVEVELFLVSKFVESSVSHCGKVHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDREKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFL KKNVWLSKEKSEDKRKNSLVDRTASFVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFVVDSEATVAPFSSFADYFHKKYGIVLVYPGQP LLLLKQSHNAYNLLVDFKKEGISCGPKSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKEISSHSGDLHISSSLILEALTTLRCNES FSMERLELLGDSVLKYAVSCYLFLKYPKKHEGQLSNERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSEVPLDKKFLTEDPKEV	1358 aa

			VGKHCDRGHRWMGSKTISDCVEALIGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSY QRLEFLGDSVLDILVTWYLYQKHKDIDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLN LDEVWKIFKPLLSPIVTPDKLELPPFRELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLVAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEAGFVDVPQ SLDFDGDICIQANTSCPDTASRKKRKKVYLNNKTDEAQSVPSDCSTSSSYSNKDTQVIGPINMTRGGPRVSLFELCKKLQWPMPNFESTERTSKSLIECGEGSDKRK VYNTFASRISLTIPDYGLIELTGDERADKKSSLDSAALHMLYELERQGKIAIGNQ	
		Sga	>Sga_DCL3.1_mRNA_Solyc08g067210_NM_001302897.1_scaffold32326_14.0_contig2_scaffold32326_14.0_contig3_scaffold32326_14.0_contig5_scaffold874 05_10.5_contig3_1658_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHLG VQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYIKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKVFGMTASPVIRKGVSSSADCEEQIS ELESLLDSQVYTLESRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDIYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICLE NVPNDKDENEILRTSSLQHRYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYLT GTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDPD DSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALNDH LLPVNEKPPRGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGKV HLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTAS FVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGP KSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKDISSHSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFLK YPKKHEGQLTNERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEAL IGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKD IDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPFR ELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLIAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKRKK VYLNNKTDEAQSVPSDCSTSSSYSNKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERADK KSSLDSAALHMLYELERQGKIAIGNQ	1658 aa
			>Sga_mRNA_Sopen08g021150_XM_015230219.2_scaffold32326_14.0_contig2_scaffold32326_14.0_contig6_scaffold32326_14.0_contig3_scaffold32326_14.0 _contig5_scaffold87405_10.5_contig3_scaffold32326_14.0_contig1_scaffold67957_14.7_1591_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHLG VQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYIKFDTVCFLILDECHRASADCEEQISELESLLDSQVYTLESRVELDEFVPSAKETCKFYDPIVFS NTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDIYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICLENVPNDKDENEILRTSSLQHRYFLEEALSIVQESMPQDC ESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYLTGTNTSVDALTRKAQKETLGSFLSGKTVRSYVQSRGRA RQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDPDDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLT LPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALNDHLLPVNEKPPRGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIK EVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGKVHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYR VDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTASFVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFAD YFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGPKSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKDISSHSGDLHI SSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFLKYPKKHEGQLTNERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETS QVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEALIGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLL EAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKDIDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVL GDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPFRELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLIAEGSGQTRKNAKAQAALKLLKNLEKKGI SFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKRKKVYLNNKTDEAQSVPSDCSTSSSYSNKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTER TSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERADKKSSLDSAALHMLYELERQGKIAIGNQ	1591 aa
		Spr	>Spr_DCL3.1_mRNA_Solyc08g067210_NM_001302897.1_A21158_1658_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHLG VQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYLKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKIFGMTASPVIRKGVSSSADCEEQIS ELESLLDSQVYTLENRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDMYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICL ENVPNDKDENEILRTSSLQHKYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYL TGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDP DDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALND HLLPFNEKPPQGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGK VHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNAWLSKEKSEAKRKNSLVDRTAS FVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGP KSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKEISSQSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFLK YPKKHEGQLTNERSHAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEAL IGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKD IDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPFR ELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLVAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSVDFDGDICIQANTSCPDMASRKKRK KVYLNNKTDEAQSVPGDCSTSSSYSKKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERAD KKSSLDSAALHMLYELERQGKIAIGNQ	1658 aa

		Sch	>Sch_DCL3.1_mRNA_Solyc08g067210_NM_001302897.1_scaffold3675_scaffold11699_scaffold12663_1679_aa XLHALGIAVETLKNLFEKKDKMEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRIDDEKKLIVFLA PTVHLVHQQYEVIQHHTHLGVQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYLKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKIFGM TASPVIRKGVSSSADCEEQISELESLLDSQVYTLENRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDMYKKLRKRLSNCY AKILCCLENLGIICAYEAVKICLENVPNDKDENEILRTSSLQHKYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITA KVIERVMKKMTWFSHFTIAYLTGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQRE QMFDIIRSEYSMTDTAIKRDPDDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQL SRQLVCLDACKKLHQIGALNDHLLPFNEKPPQGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGN VEVELFLVSKFVESSVSHCGKVHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNA WLSKEKSEAKRKNSLVDRTASFVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLL KQSHNAYNLLVDFKKEGISCGPKSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKEISSQSGDLHISSSLILEALTTLRCNESFSM ERLELLGDSILKYAVSCYLFLKYPKKHEGQLTNERSHAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKH CDRGHRWMGSKTISDCVEALIGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLE FLGDSVLDILVTWYLYQKHKDIDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEV WKIFKPLLSPIVTPDKLELPPFRELIELCDSLGYFFKEHCVMKGDTVNAVLRLQLIDDLLVAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDF DGDICIQANTSCPDMASRKKRKKVYLNNKTDEAQSVPGDCSTSSSYSKKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNT FASRISLTIPDYGLIELTGDERADKKSSLDSAALHMLYELERQGKIAIGNQ	1679 aa
			>Sch_mRNA_Sopen08g021150_XM_015230219.2_scaffold3675_scaffold12663_1658_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRIDDEKKLIVFLAPTVHLVHQQYEVIQHHTHLG VQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYLKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKIFGMTASPVIRKGVSSSADCEEQIS ELESLLDSQVYTLENRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDMYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICL ENVPNDKDENEILRTSSLQHKYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYL TGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDP DDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALND HLLPFNEKPPQGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGK VHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNAWLSKEKSEAKRKNSLVDRTAS FVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGP KSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKEISSQSGDLHISSSLILEALTTLRCNESFSMERLELLGDSILKYAVSCYLFLKY PKKHEGQLTNERSHAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEALI GAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKDI DPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHNDNFAYAAVRRNLHVHLQHHLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPF RELIELCDSLGYFFKEHCVMKGDTVNAVLRLQLIDDLLVAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKR KKVYLNNKTDEAQSVPGDCSTSSSYSKKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERA DKKSSLDSAALHMLYELERQGKIAIGNQ	1658 aa
		SpiLA1589	>SpiLA1589_DCL3.1_mRNA_Solyc08g067210_NM_001302897.1_contig:unspecified:6317254:1:3688:1_contig:unspecified:6738495:1:5156:1_contig:unspecifie d:6663527:1:1192:1_contig:unspecified:6607024:1:7114:1_contig:unspecified:6511344:1:4039:1_contig:unspecified:6597567:1:2887:1_1658_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHLG VQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYIKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKVFGMTASPVIRKGVSSSADCEEQIS ELESLLDSQVYTLESRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDMYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICL ENVPNDKDENEILRTSSLQHRYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYL TGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDP DDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALND HLLPFNEKPPRGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGK VHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTA SFVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCG PKSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKDISSHSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFL KYPKKHEGQLTNERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVE ALIGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKH KDIDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPP FRELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLIAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKR KKVYLNNKTDEAQSVPGDCSTSSSYSKKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERA DKKSSLDSAALHMLYELERQGKIAIGNQ	1658 aa
			>SpiLA1589_mRNA_Sopen08g021150_XM_015230219.2_contig:unspecified:6317254:1:3688:1_contig:unspecified:5110292:1:5983:1_contig:unspecified:67384 95:1:5156:1_contig:unspecified:6663527:1:1192:1_contig:unspecified:6511345:1:4016:1_contig:unspecified:6506556:1:2830:1_1627_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHLG VQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYIKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKVFGMTASPVIRKGVSSSADCEEQIS ELESLLDSQVYTLESRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDIYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICLE	1627 aa

			NVPNDKDENEILRTSSLQHRYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGESHSTYLTGTNTSVDALTRKAQKETLGSFLSGKVNLL FATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDPDDSVVKPCLVKETKAYYVEATGASVTADSS VSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALNDHLLPFNEKPPRGGSDVQDRKLGAGTTKLK ELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGKVHLDSQQVAKAKIFQELFFNGLFGKLFIKS SCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTASFVEDIDQTDLIHFANMSISRSKIMDMVVV AIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGPKSKDSTMVVKKPLNNVHMPPELLVCFDI RLDILKSFYLLPSLMHRLASLMLASQLRKDISSHSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFLKYPKKHEGQLTNERSQAISNSALHKLGTN QHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEALIGAYYVGGGFVAALKLMKWLGVKAELE PSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKDIDPGELTDLRSASVNNDNFAYAAVRRN LHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPFRELIELCDSLGYFFKEHCVMKGDTVNAE LRLQLIDDLLIAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKRKKVYLNNKTDEAQSVPGDCSTSSSYSKK DTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERADKKSSLDSAALHMLYELERQGKIAIGNQ	
		SpiLA0480	>SpiLA0480_DCL3.1_mRNA_Solyc08g067210_NM_001302897.1_Scaffold3064143_1607_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHL GVQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYIKFDTVCFLILDECHRASADCEEQISELESLLDSQVYTLESRVELDEFVPSAKETCKFYDPIVF SNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDIYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICLENVPNDKDENEILRTSSLQHRYFLEEALSIVQESMPQD CESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYLTGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEE GIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERSEYSMTDTAIKRDPDDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKP VFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALNDHLLPFNEKPPRGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNG EVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGKVHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMY LLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTASFVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPF EVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCGPKSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLML ASQLRKDISSHSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFLKYPKKHEGQLTNERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPG QLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVEALIGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDI EDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKHKDIDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKS VSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPPFRELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLIAEGSGQTRKNA KAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKRKKVYLNNKTDEAQSVPSDCSTSSSYSNKDTQVIGPINMTRGGPRISLFEL CKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDERADKKSSLDSAALHMLYELERQGKIAIGNQ	1607 aa
			>SpiLA0480_mRNA_Sopen08g021150_XM_015230219.2_Scaffold3064143_1659_aa MEEEKQENPLKRNFEAFSSEAEKMDVEKKKKIEEFIPREYQLKVFKVAMRRNTIAVLDTGAGKTNIAVMMIREIGITLRNDDEKKLIVFLAPTVHLVHQQYEVIQHHTHL GVQEYYGAKGVDEWNAESWKKETDDNDVLVMTPQIFLDALRKGYIKFDTVCFLILDECHRASGNHPYARIMKEFYHLSRKRSKVFGMTASPVIRKGVSSSADCEEQI SELESLLDSQVYTLESRVELDEFVPSAKETCKFYDPIVFSNTELKAKLEFSWSKFDAALADLKLSLPSQYKDTDDIYKKLRKRLSNCYAKILCCLENLGIICAYEAVKICL ENVPNDKDENEILRTSSLQHRYFLEEALSIVQESMPQDCESLFDVGYDLSATLSMGHISSKLQVLLEIFQLLGKATQVRCLIFVERIITAKVIERVMKKMTWFSHFTIAYL TGTNTSVDALTRKAQKETLGSFLSGKVNLLFATDVVEEGIDVPHCSSVIRFDLPKTVRSYVQSRGRARQTESQYILMLERGNKKQREQMFDIIRSEYSMTDTAIKRDP DDSVVKPCLVKETKAYYVEATGASVTADSSVSVLTKYCEMLPGDKFFSPKPVFQYILSGELYRCKLTLPPNAALQTIVGPECRSSQLSRQLVCLDACKKLHQIGALND HLLPFNEKPPRGGSDVQDRKLGAGTTKLKELHGTACISALSGSWGNDPNGEVYQVYKMNFLCNIKEVKYSSFILLLQSELDYDVGNVEVELFLVSKFVESSVSHCGK VHLDSQQVAKAKIFQELFFNGLFGKLFIKSSCGRKFLLDTEKSLWEPSNMYLLLPLDPLDSSCEPYRVDWEAIESSVSVVEFLKKNGWLSKEKSEAKRKNSLVDRTA SFVEDIDQTDLIHFANMSISRSKIMDMVVVAIHTGRIYSVLEAVANSSAESPFEVDSEATVAPFSSFADYFHKKYGIVLVYPGQPLLLLKQSHNAYNLLVDFKKEGISCG PKSKDSTMVVKKPLNNVHMPPELLVCFDIRLDILKSFYLLPSLMHRLASLMLASQLRKDISSHSGDLHISSSLILEALTTLRCNESFSMERLELLGDSVLKYAVSCYLFL KYPKKHEGQLTNERSQAISNSALHKLGTNQHLQGYIRDGAFDPRRWTAPGQLSLWLCPCEHGVETSQVPLDKKFLTEDPKEVVGKHCDRGHRWMGSKTISDCVE ALIGAYYVGGGFVAALKLMKWLGVKAELEPSLVEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLLEAITHATVQELEAGYSYQRLEFLGDSVLDILVTWYLYQKH KDIDPGELTDLRSASVNNDNFAYAAVRRNLHVHLQHHSGCLESEISLFVKSVSNSDSLQGNKAPKVLGDLVESIAGAVLIDTKLNLDEVWKIFKPLLSPIVTPDKLELPP FRELIELCDSLGYFFKEHCVMKGDTVNAELRLQLIDDLLIAEGSGQTRKNAKAQAALKLLKNLEKKGISFKKKKEEASFVDVPQSLDFDGDICIQANTSCPDMASRKKR KKVYLNNKTDEAQSVPSDCSTSSSYSNKDTQVIGPINMTRGGPRISLFELCKKLQWPMPSFESTERTSKSLIECGEGSDKRKVYNTFASRISLTIPDYGLIELTGDETS RISLTIPDYGLIELTGDERQGKIAIGNQ	1659 aa
	DCL4	*Sly*	>protein_Solyc07g005030 MGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKSHQDWEKEMEQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKIF YKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVNVYQYGPGSSCHTKAYSQKLEEIKHQCVKELHKKAVDSTLRNTKKMLKRLHG HLIFSLENLGVLGALQASCILLKGDHHERHQMVEAEVNASDDSLCDRYLSQVDTVFTSGCAKDGMNPDLALMEVLKEPYFSKKLLRLIGILSNFGVQPDMKCIVFVNR IVTARSLSYILQHLKILSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKVGEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGNQRE LDLIEHFTRSEAQMDDEISSRKSRTMVADFQENIYKVDMTGATVSSALSISLLHHYCSKLPHDEYFCPKPQFYYFDDVDGTICKLILPSNAAMHSIDSAPQSSIEAAKK DACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGEDAREELHEMIVPASLKEPWTETDNPVCLNSYYISFFPFPNDRVYKKFGLFLKAPLPQEAERMK LDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVDSGSKFYLLLPVNLFGHDKISVDWELVRRCLSSPVFGTSVCTSNNMSKF EEQLQLANGSKSVHDVVNSLVYVPCKDAFFFISDVVKDKNAYSMYKDSKNHVEHYYDTFSVHLLYPDQPLIKAKQLFCLENLLRKKGYSELRDKEEHFVELPPEICQL KIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHESFSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNSNLY MVAIKKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLCGSGTDGIKTEVRCSKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDFKEPQLK SICSASKVFMPLADEIDVLGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGDAVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHSHILC	1536 aa

			DSSDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAWQIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFLVEA RVNGENVSAAASALNINKKSAQRMAAQIVCSSLKAQGYRPKSKSLEQVLKAAIKMEAKLIGYDETPCVLTTICDDLDKHETSESDCHLKVFPVNEELARSCNFKSKST RKLLSTEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLFECCKETGPSHLKEFTFRVLVEIEETSRVIESYGEAQAKKKDAAEHAAEGAL WFLKQEGYLLDN	
		Spe	>protein_Sopen07g001140 MNQMGSQVNFLSWKLIWKGKIPYKVVVYTWLVVKEAVLTQEDLMKRGIQMCPRCYFWRTGQALESWNTEGSGCTDKSRWQIVPAVIWWTIWKERNSRNFDNKSS PLHKIKMNCTITFCYWYQMDLCKKALEENVVVYLGTGCGKTHIAVLLIYEMGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKSHQDWEKEM EQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKIFYKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVNVY HYGPGSSCHTKAYSQKLEEIKHQCVKELHKKAVDSTLRNTKKMLKRLHGHLIFSLENLGVLGALQASCILLKGDHHERHQMVEAEVNASDDSLCDRYLSQVDTVFTS GCAKDGMNPDLALMEVLKEPYFSKKLLRLIGILSNFGVQPDMKCIVFVNRIVTARSLSYILQHLKVLSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKV GEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGNQRELDLIEHFTRSEAQMDDEISSRKSRTTVADFQENIYKVDMTGATVSSALSISLLHHYCSK LPHDEYFCPKPQFYYFDDIDGTICKLILPSNAAMHSIDSAPQSSIEAAKKDACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGEDAREELHEMIVPASL KEPWTETDNPVCLNSYYISFFPFPNDRVYKKFGLFLKAPLPQEAERMKLDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVD SGSKFYLLLPVDLFGHDKISVDWELVRRCLSSPIFGTSVCTSNNMSKFEEQLQLANGSKSVHDVVNSLVYVPCKDAFFFISDVVKDKNACSMYKDSKNYVEHYYDTF SVHLLYPDQPLIKAKQLFCLENLLRKKGYSELRDKEEHFVELPPEICQLKIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHES FSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNSNLYMVAIRKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLGGSGTYGVKTEVRC SKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDFKEPQLKSICSASKVFMPLAGEIDVHGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGD AVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHSHILCDSNDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAW QIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFLVEARVNGENVSAAASALNINKKSAQRMAAQMVCSSLKAQGYRPKSKSLEQVLKAAIKMEA KLIGYDETPCVLNTICDDLDKHETSESDCDLKVFPVNEELARSCNFKSKSTRKLLSPEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLF ECCKETGPSHLKEFTFRVVVEIEETSRVIESYGEAQAKKKDAAEHAAEGALWFLKQEGYLLDN	1690 aa
		Sga	>Sga_mRNA_Solyc07g005030_XM_010324849.3_scaffold52151_12.8_contig1_scaffold52151_12.8_contig2_scaffold10910_12.1_contig13_1536_aa MGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKSHQDWEKEMEQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKIF YKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVNVYQYGPGSSCHTKAYSQKLEEIKHQCVKELHKKAVDSTLRNTKKMLKRLHG HLIFSLENLGVLGALQASCILLKGDHHERHQMVEAEVNASDDSLCDRYLSQVDTVFTSGCAKDGMNPDLALMEVLKEPYFSKKLLRLIGILSNFGVQPDMKCIVFVNR IVTARSLSYVLQHLKILSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKVGEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGNQRE LDLIEHFTRSEAQMDDEISSRKSRTMVADFQENIYKVDMTGATVSSALSISLLHHYCSKLPHDEYFCPKPQFYYFDDVDGTICKLILPSNAAMHSIDSAPQSSIEAAKK DACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGEDAREELHEMIVPASLKEPWTETDNPVCLNSYYISFFPFPNDRVYKKFGLFLKAPLPQEAERMK LDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVDSGSKFYLLLPVNLFGHDKISVDWELVRRCLSSPVFGTSVCTSNNMSKF EEQLQLANGSKSVHDVVNSLVYVPCKDAFFFISDVVKDKNAYSMYKDSKNHVEHYYDTFSVHLLYPDQPLIKAKQLFCLENLLRKKGYSELRDKEEHFVELPPEICQL KIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHESFSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNSNLY MVAIKKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLCGSGTDGIKTEVRCSKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDFKEPQLK SICSASKVFMPLADEIDVLGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGDAVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHSHILC DSSDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAWQIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFLVEA RVNGENVSAAASALNINKKSAQRMAAQIVCSSLKAQGYRPKSKSLEQVLKAAIKMEAKLIGYDETPCVLTTICDDLDKHETSESDCHLKVFPVNEELARSCNFKSKST RKLLSTEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLFECCKETGPSHLKEFTFRVLVEIEETSRVIESYGEAQAKKKDAAEHAAEGAL WFLKQEGYLLDN	1536 aa
		Spr	>Spr_mRNA_Solyc07g005030_XM_010324849.3_ A25270_1536_aa MGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKCHQDWEKEMEQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKI FYKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVNVYHYGPGSSCHTKAYSQKLEEIKHQCVKELHKKAVDSTLRNTKKMLKRLH GHLLFSLENLGVLGALQASCILLKGDHHERHQMVEAEVYASDDSLCDRYLSQVDTVFTSGCAKDGMNPDLALMEILKEPYFSKKLLRLIGILSNFGVQPDMKCIVFVN RIVTARSLSYILQHLKVLSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKVGEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGNQ RELDLIEHFTRSEAQMNDDISSRKSCTTVADFQENIYKVDMTGATVSSALSISLLHHYCSKLPHDEYFCPKPQFYYFDDIDGTICKLILPSNAAMHSINSAPQSSIEAAK KDACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGEDVREELHEMIVPASLKEPWTETDNPVCLNSYYVSFFPFPNDRVYKKFGLFLKAPLPQEAER MKLDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVDSGSKFYLLLPVNLFEHDKISVDWELVRRCLSSPIFGTSVCTSNNMS KFEEQLQLANGSKSVHDVVNSLVYVPCKDAFFFISDVVKDINAYSMYKDSKNHVEHYYDTFSVHLLYPNQPLIKAKQLFCLENLLRKKGYSALRDKEEHFVELPPEIC QLKIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHESFSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNS NLYMVAIRKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLCGSGKDGVKTEVRCSKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDIKEP QLKSICSASKVFMPLADEIDVLGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGDAVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHS HILCDSSDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAWQIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFL VEARVNGENVSAAASALNINKKSAQRMAAQIVCSSLKAQGYRPKSKSLEQVLKTAIKMEAKLIGYDETPCVLTTICDDLDKHETSESDCDLKVFPVNEELARSCNFKS KSTRKLLSPEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLFECCKETGPSHLKEFTFRVLVEIEETSRVIESYGEAQLKKKDAAEHAAE GALWFLKQEGYLLDN	1536 aa
		Sch	>Sch_mRNA_Solyc07g005030_XM_010324849.3_scaffold1398_1536_aa MGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKCHQDWEKEMEQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKI FYKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVNVYHYGPGSSCHTKAYSQKLEEIKHQCVKELHKKAVDSTLRNTKKMLKRLH	1536 aa

			GHLLFSLENLGVLGALQASCILLKGDHHERHQMVEAEVYASDDSLCDRYLSQVDTVFTSGCAKDGMNPDLALMEVLKEPYFSKKLLRLIGILSNFGVQPDMKCIVFV NRIVTARSLSYILQHLKVLSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKVGEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGN QRELDLIEHFTRSEAQMNDDISSRKICTTVADFQENIYKVDMTGATVSSALSIQLLHRYCSKLPHDEYFCPKPQFYYFDDIDGTICKLILPSNAAMHSIDSAPQSSIEAA KKDACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGEDVREELHEMIVPASLKEPWTETDNPVCLNSYYVSFFPFPNDRVYKKFGLFLKAPLPQEAER MKLDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVDSGSKFYLLLPVNLFEHDKISVDWELVRRCLSSPIFGTSVCTSNNMS KFEEQLQLANGSKSVHDVVNSLVYVPCKDAFFFISDVVKDINAYSMYKDSKNHVEHYYDTFSVHLLYPDQPLIKAKQLFCLENLLRKKGYSALRDKEEHFVELPPEIC QIKIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHESFSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNSN LYMVAIRKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLCGSGTDGVKTEVRCSKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDFKEP QLKSICSASKVFMPLADEIDVLGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGDAVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHS HILCDSSDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAWQIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFL VEARVNGENVSAAASALNINKKSAQRMAAQIVCSSLKAQGYRPKSKSLEQVLKTAIKMEAKLIGYDETPCVLTTICDDLDKHETSESDCDLKVFPVNEELARSCNFKS KSTRKLLSPEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLFECCKETGPSHLKEFTFRVVVEIEETSRVIESYGEAQAKKKDAAEHAAE GALWFLKQEGYLLDN	
		SpiLA1589	>SpiLA1589_mRNA_Solyc07g005030_XM_010324849.3_contig:unspecified:6649770:1:14572:1_contig:unspecified:3896467:1:2199:1_contig:unspecified:6584 918:1:12556:1_1536_aa MGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKSHQDWEKEMEQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKIF YKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVKVYSVEDKDELEQFVASPKVKEIKHQCVKELHKKAVDSTLRNTKKMLKRLHG HLIFSLENLGVLGALQASCILLKGDHHERHQMVEAEVNASDDSLCDRYLSQVDTVFTSGCAKDGMNPDLALMEVLKEPYFSKKLLRLIGILSNFGVQPDMKCIVFVNR IVTARSLSYILQHLKILSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKVGEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGNQRE LDLIEHFTRSEAQMDDEISSRKSRTMVADFQENIYKVDMTGATVSSALSISLLHHYCSKLPHDEYFCPKPQFYYFDDVDGTICKLILPSNAAMHSIDSAPQSSIEAAKK DACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGKDAREELHEMIVPASLKEPWTETDNPVCLNSYYISFFPFPNDRVYKKFGLFLKAPLPQEAERMK LDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVDSGSKFYLLLPVNLFGHDKISVDWELVRRCLSSPVFGTSVCTSNNMSKF EEQLQLANGSKNVHDVVNSLVYVPCKDAFFFISDVVKDKNAHSMYKDSKNHVEHYYDTFSVHLLYPDQPLIKAKQLFCLENLLRKKGYSELRDKEEHFVELPPEICQ LKIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHESFSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNSNL YMVAIKKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLCGSGTDGIKTEVRCSKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDFKEPQL KSICSASKVFMPLADEIDVLGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGDAVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHSHIL CDSSDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAWQIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFLVE ARVNGENVSAAASALNINKKSAQRMAAQIVCSSLKAQGYRPKSKSLEQVLKAAIKMEAKLIGYDETPCVLTTICDDLDKHETSESDCHLKVFPVNEELARSCNFKSKS TRKLLSTEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLFECCKETGPSHLKEFTFRVLVEIEETSRVIESYGEAQAKKKDAAEHAAEGA LWFLKQEGYLLDN	1536 aa
		SpiLA0480	>SpiLA0480_mRNA_Solyc07g005030_XM_010324849.3_Scaffold3072084_1536_aa MGHLIKKPQKSICVFLAPTVALVQQQAKVIEESIDFKVGTYCGKSKHLKSHQDWEKEMEQYEVLVMTPQILLHNLSHCYIRIEFIALLIFDECHYAQVESDHPYAEIMKIF YKPDVVKQPRIFGMTASPISGKGATVEGLETLLRSKVYSVEDKDELEQFVASPKVNVYQYGPGSSCHTKAYSQKLEEIKHQCVKELHKKAVDSTLRNTKKMLKRLHG HLIFSLENLGVLGALQASCILLKGDHHERHQMVEAEVNASDDSLCDRYLSQVDTVFTSGCAKDGMNPDLALMEVLKEPYFSKKLLRLIGILSNFGVQPDMKCIVFVNR IVTARSLSYILQHLKILSSWKCGFLVGVHSGLKSMSRKNTNIILDKFRSGELNLLIATKVGEEGLDIQTCCLVIRFDLPETVASFIQSRGRARMPKSEYAFLVDRGNQRE LDLIEHFTRSEAQMDDEISSRKSRTMVADFQENIYKVDMTGATVSSALSISLLHHYCSKLPHDEYFCPKPQFYYFDDVDGTICKLILPSNAAMHSIDSAPQSSIEAAKK DACLRACKSLHELGALTDYLLPDQADEDKDLVPDFSDLECCEGEDAREELHEMIVPASLKEPWTETDNPVCLNSYYISFFPFPNDRVYKKFGLFLKAPLPQEAERMK LDLNLARGRSVKTELIPSGTTSFENNEIQLAEKFQRMFFKIILDRSEFISEFVSLEKKDFVDSGSKFYLLLPVNLFGHDKISVDWELVRRCLSSPVFGTSVCTSNNMSKF EEQLQLANGSKSVHDVVNSLVYVPCKDAFFFISDVVKDKNAYSMYKDSKNHVEHYYDTFSVHLLYPDQPLIKAKQLFCLENLLRKKGYSELRDKEEHFVELPPEICQL KIIGFSKDIGSSLSLLPSIMHRLESLLVAIELKGCLSASFPEGRELAIDHVLEALTTENCHESFSLERLEVLGDAFLKFAVGRHLFLLHDAFDEGQLTRKRSNAVNNSNLY MVAIKKNLQAYIRDQSFEPDHFYVVGRPCPVTCNKQTEKNIHGLCGSGTDGIKTEVRCSKYHHWLRKKTIADIVEALVGAFVVDSGFKAAIAFLKWIGIHTDFKEPQLK SICSASKVFMPLADEIDVLGIERLLGYSFIHKGLLIQAFIHPSYNRHGGGCYQRLEFLGDAVLDYLITSYLYSVYPKLKPGQLTDLRSISVNNNTFAVVAVRQSFHSHILC DSSDLRESITRYVNFIGRPDSTRRLGEEPSCPKALGDLVESCMGAILLDTGFDLNRAWQIILSFLKPVMSFTRLQLNPTRELYELCQSFGWNLKFLPSKKDGNFLVEA RVNGENVSAAASALNINKKSAQRMAAQIVCSSLKAQGYRPKSKSLEQVLKAAIKMEAKLIGYDETPCVLTTICDDLDKHETSESDCDLKVFPVNEELARSCNFKSKST RKLLSTEASVQCNSDQTIMSNGSKEDAKATGGSKTESAKSRLHEICAANCWKPPLFECCKETGPSHLKEFTFRVLVEIEETSRVVESYGEAQAKKKDAAEHAAEGAL WFLKQEGYLLDN	1536 aa

Supplementary Table S2. Distribution of conserved domains and their locations in putative AGO proteins identified in seven species of the tomato and their orthologs.

Protein families	Species	ID protein	ID protein SolGenomics	ID query	Protein Length	Conserved domain	Domain ID	Start and End	E-value
AGO1	Ortholog in *Solanum tuberosum*	XP_006347371.1	_	_	1054 aa	PIWI	PF02171	681-1000	8.0e-116
						ARGO-N	PF16486	194-328	8.5e-34
						PAZ	PF02170	394-519	2.8e-27
						GLY-RICH	PF12764	70-174	6.4e-27
						ARGO-L1	PF08699	338-387	1.9e-22
						ARGO-L2	PF16488	530-576	8.0e-16
						ARGO-MID	PF16487	587-661	7.7e-08
		XP_006364394.1	_	_	1127 aa	PIWI	PF02171	754-1073	1.0e-115
						ARGO-N	PF16486	267-401	2.3e-33
						PAZ	PF02170	135-247	9.2e-30
						GLY-RICH	PF12764	466-592	4.3e-28
						ARGO-L1	PF08699	411-460	1.1e-21
						ARGO-L2	PF16488	603-649	9.2e-15
						ARGO-MID	PF16487	660-734	1.3e-07
	Solanum lycopersicum	NP_001266057.1	Solyc06g072300	_	1054aa	PIWI	PF02171	681-1000	1.0e-115
						ARGO-N	PF16486	194-328	8.5e-34
						GLY-RICH	PF12764	70-174	1.0e-27
						PAZ	PF02170	394-519	2.8e-27
						ARGO-L1	PF08699	338-387	1.9e-22
						ARGO-L2	PF16488	530-576	3.9e-16
						ARGO-MID	PF16487	587-661	7.7e-08
		NP_001266261.2	Solyc03g098280	_	1152aa	PIWI	PF02171	779-1098	1.7e-115
						ARGO-N	PF16486	292-426	2.3e-33
						PAZ	PF02170	492-617	6.8e-28
						GLY-RICH	PF12764	160-272	7.6e-27
						ARGO-L1	PF08699	436-485	1.2e-21
						ARGO-L2	PF16488	628-674	4.3e-15
						ARGO-MID	PF16487	685-759	1.0e-07
	Solanum pennellii	XP_015079116	Sopen06g028670	_	1053aa	PIWI	PF02171	680-999	1.0e-115
						ARGO-N	PF16486	193-327	8.5e-34
						GLY-RICH	PF12764	69-173	1.7e-27
						PAZ	PF02170	393-518	2.8e-27
						ARGO-L1	PF08699	337-386	1.9e-22
						ARGO-L2	PF16488	529-575	3.9e-16
						ARGO-MID	PF16487	586-660	7.7e-08
		XP_015069669	Sopen03g028990	_	1152aa	PIWI	PF02171	779-1098	2.6e-115
						ARGO-N	PF16486	292-426	2.3e-33

						PAZ	PF02170	492-617	6.8e-28
						GLY-RICH	PF12764	160-272	1.0e-26
						ARGO-L1	PF08699	436-485	1.2e-21
						ARGO-L2	PF16488	628-674	4.3e-15
						ARGO-MID	PF16487	685-759	1.0e-07
	Solanum galapagense	scaffold43013_12.5	Solyc06g072300	NP_001266057.1	1036 aa	PIWI	PF02171	681-1000	5.0e-115
						ARGO-N	PF16486	194-328	8.3e-34
						GLY-RICH	PF12764	70-174	1.0e-27
						PAZ	PF02170	394-519	2.7e-27
						ARGO-L1	PF08699	338-387	9.7e-22
						ARGO-L2	PF16488	530-576	3.8e-16
						ARGO-MID	PF16487	587-661	7.5e-08
		scaffold28885_12.6	Solyc03g098280	NP_001266261.2	1152 aa	PIWI	PF02171	779-1098	4.4e-115
						ARGO-N	PF16486	292-426	2.3e-33
						PAZ	PF02170	492-617	6.8e-28
						GLY-RICH	PF12764	160-272	1.0e-26
						ARGO-L1	PF08699	436-485	1.8e-19
						ARGO-L2	PF16488	628-674	4.3e-15
						ARGO-MID	PF16487	685-759	1.0e-07
	Solanum peruvianum	a308	Solyc03g098280	NP_001266261.2	1000 aa	PIWI	PF02171	627-946	1.3e-115
						ARGO-N	PF16486	140-274	1.9e-33
						PAZ	PF02170	340-465	5.6e-28
						GLY-RICH	PF12764	8-120	8.5e-27
						ARGO-L1	PF08699	284-333	9.7e-22
						ARGO-L2	PF16488	476-522	3.7e-16
						ARGO-MID	PF16487	533-607	4.1e-08
	Solanum chilense	scaffold2127	Solyc06g072300	NP_001266057.1	1011 aa	PIWI	PF02171	656-975	9.7e-116
						ARGO-N	PF16486	169-303	8.0e-34
						PAZ	PF02170	369-494	2.6e-27
						ARGO-L1	PF08699	313-362	1.8e-22
						ARGO-L2	PF16488	505-551	3.7e-16
						ARGO-MID	PF16487	562-636	7.3e-08
						GLY-RICH	PF12764	115-149	6.3e-07
		scaffold1227	Solyc03g098280	NP_001266261.2	1152 aa	PIWI	PF02171	779-1098	1.7e-115
						ARGO-N	PF16486	292-426	2.3e-33
						PAZ	PF02170	492-617	6.8e-28
						GLY-RICH	PF12764	160-272	3.1e-26
						ARGO-L1	PF08699	436-485	1.2e-21
						ARGO-L2	PF16488	628-674	4.3e-15
						ARGO-MID	PF16487	685-759	1.0e-07
	Solanum pimpinellifolium	contig:385000:1:10591:1	Solyc06g072300	NP_001266057.1	799 aa	PIWI	PF02171	489-748	2.2e-85
						ARGO-N	PF16486	46-176	3.3e-30

	LA1589					PAZ	PF02170	202-327	1.9e-27
						ARGO-L2	PF16488	338-384	2.8e-16
						ARGO-MID	PF16487	395-469	5.4e-08
		contig:2773654:1:3680:1	Solyc03g098280	NP_001266261.2	1149 aa	PIWI	PF02171	776-1095	4.4e-115
						ARGO-N	PF16486	289-423	2.3e-33
						PAZ	PF02170	489-614	6.8e-28
						GLY-RICH	PF12764	160-269	1.4e-22
						ARGO-L1	PF08699	433-482	1.1e-21
						ARGO-L2	PF16488	625-671	4.3e-15
						ARGO-MID	PF16487	682-756	1.0e-07
	Solanum pimpinellifolium LA0480	Scaffold3068023	Solyc06g072300	NP_001266057.1	1036 aa	PIWI	PF02171	681-1000	1.0e-115
						ARGO-N	PF16486	194-328	8.3e-34
						GLY-RICH	PF12764	70-174	1.0e-27
						PAZ	PF02170	394-519	2.7e-27
						ARGO-L1	PF08699	338-387	1.9e-22
						ARGO-L2	PF16488	530-576	3.8e-16
						ARGO-MID	PF16487	587-661	7.5e-08
AGO2	Ortholog in *Solanum tuberosum*	XP_006353071.1	_	_	1052 aa	PIWI	PF02171	720-1010	1.4e-91
						ARGO-N	PF16486	224-361	6.9e-23
						PAZ	PF02170	426-548	1.4e-19
						ARGO-L1	PF08699	371-418	6.5e-09
						ARGO-L2	PF16488	566-611	1.3e-08
		XP_006353091.1	_	_	821 aa	PIWI	PF02171	492-783	1.4e-89
						ARGO-N	PF16486	69-176	4.4e-14
						PAZ	PF02170	202-325	2.7e-18
	Solanum lycopersicum	NP_001266235.2	Solyc02g069260.2.1	_	1042 aa	PIWI	PF02171	711-1001	1.7e-91
						ARGO-N	PF16486	215-352	1.1e-22
						PAZ	PF02170	417-539	1.0e-19
						ARGO-L1	PF08699	362-409	4.7e-09
						ARGO-L2	PF16488	558-602	2.7e-08
		NP_001274720.1	Solyc02g069280.2.1	_	999 aa	PIWI	PF02171	660-950	3.0e-86
						ARGO-N	PF16486	178-314	1.6e-19
						PAZ	PF02170	380-498	4.0e-16
						ARGO-L1	PF08699	324-366	2.4e-08
		_	Solyc02g069270.2.1	_	977 aa	PIWI	PF02171	649-939	5.6e-88
						ARGO-N	PF16486	178-295	1.4e-18
						PAZ	PF02170	362-480	6.8e-20
						ARGO-L1	PF08699	305-350	1.3e-08
						ARGO-L2	PF16488	518-543	4.1e-08
	Solanum pennellii	XP_015064393.1	Sopen02g018430.1	_	1003 aa	PIWI	PF02171	67-965	1.2e-88
						ARGO-N	PF16486	184-321	8.7e-22
						PAZ	PF02170	385-506	4.9e-20

						ARGO-L1	PF08699	524-569	2.7e-09
						ARGO-L2	PF16488	331-376	9.7e-09
		XP_015065365.1	Sopen02g018440.1	_	997 aa	PIWI	PF02171	658-948	4.7e-86
						ARGO-N	PF16486	178-314	6.3e-19
						PAZ	PF02170	379-498	2.5e-16
						ARGO-L1	PF08699	324-366	2.1e-08
		XP_015067109.1	Sopen02g018420.1	_	1041 aa	PIWI	PF02171	710-1000	1.7e-91
						ARGO-N	PF16486	214-351	1.1e-22
						PAZ	PF02170	416-538	2.0e-19
						ARGO-L1	PF08699	361-408	4.7e-09
						ARGO-L2	PF16488	557-601	2.7e-08
	Solanum galapagense	scaffold119639_10.1_contig2	Solyc02g069260.2.1	NP_001266235.2	947 aa	PIWI	PF02171	686-892	5.4e-50
						ARGO-N	PF16486	190-327	3.0e-23
						PAZ	PF02170	392-514	1.4e-19
						ARGO-L1	PF08699	337-384	4.2e-09
						ARGO-L2	PF16488	533-577	2.4e-08
		scaffold80102_13.1_contig4	Solyc02g069270.2.1	_	930 aa	PIWI	PF02171	602-892	1.4e-88
						ARGO-N	PF16486	111-248	4.6e-21
						PAZ	PF02170	312-433	7.8e-20
						ARGO-L1	PF08699	451-496	7.8e-09
						ARGO-L2	PF16488	258-303	1.2e-08
		scaffold80102_13.1_contig3	Solyc02g069280.2.1	NP_001274720.1	996 aa	PIWI	PF02171	657-947	1.6e-86
						ARGO-N	PF16486	175-311	2.0e-19
						PAZ	PF02170	377-495	4.0e-16
						ARGO-L1	PF08699	321-363	2.4e-08
	Solanum peruvianum	a8305	Sopen02g018420.1	XP_015067109.1	954 aa	PIWI	PF02171	698-905	7.5e-50
						ARGO-N	PF16486	202-339	4.3e-23
						PAZ	PF02170	404-526	9.2e-20
						ARGO-L1	PF08699	349-396	4.2e-09
						ARGO-L2	PF16488	545-589	2.4e-08
	Solanum chilense	scaffold1612	Sopen02g018420.1	XP_015067109.1	906 aa	PIWI	PF02171	698-903	1.6e-50
						ARGO-N	PF16486	202-339	9.0e-23
						PAZ	PF02170	404-526	1.8e-19
						ARGO-L1	PF08699	349-396	4.0e-09
						ARGO-L2	PF16488	545-589	2.3e-08
		scaffold1612	Sopen02g018430.1	XP_015064393.1	958 aa	PIWI	PF02171	630-920	1.3e-88
						ARGO-N	PF16486	139-276	4.3e-22
						PAZ	PF02170	340-459	3.3e-20
						ARGO-L1	PF08699	479-524	2.5e-09
						ARGO-L2	PF16488	286-331	1.0e-08
		scaffold1612	Sopen02g018440.1	XP_015065365.1	999 aa	PIWI	PF02171	660-950	2.1e-86
						ARGO-N	PF16486	178-314	1.5e-18

						PAZ	PF02170	396-498	1.5e-16
						ARGO-L1	PF08699	324-366	1.4e-08
	Solanum pimpinellifolium LA1589	contig:6529832:1:10855:1	Sopen02g018420.1	XP_015067109.1	891 aa	PIWI	PF02171	560-850	2.7e-91
						ARGO-N	PF16486	64-201	2.7e-23
						PAZ	PF02170	266-388	8.3e-20
						ARGO-L1	PF08699	211-258	3.9e-09
						ARGO-L2	PF16488	407-451	2.2e-08
		contig:6757462:1:3785:1	Sopen02g018430.1	XP_015064393.1	852 aa	PIWI	PF02171	524-814	1.1e-88
						ARGO-N	PF16486	33-170	4.0e-21
						PAZ	PF02170	234-355	1.8e-19
						ARGO-L1	PF08699	373-418	7.0e-09
						ARGO-L2	PF16488	180-225	1.1e-08
		contig:6718737:1:4619:1	Sopen02g018440.1	XP_015065365.1	983 aa	PIWI	PF02171	644-934	1.5e-86
						ARGO-N	PF16486	184-320	1.9e-19
						PAZ	PF02170	386-481	4.1e-09
						ARGO-L1	PF08699	330-372	2.3e-08
						ARGO-L2	PF16488	509-533	2.6e-05
	Solanum pimpinellifolium LA0480	Scaffold3065360	Sopen02g018420.1	XP_015067109.1	935 aa	PIWI	PF02171	674-880	2.5e-50
						ARGO-N	PF16486	178-315	2.9e-23
						PAZ	PF02170	380-502	8.9e-20
						ARGO-L1	PF08699	325-372	4.1e-09
						ARGO-L2	PF16488	521-565	2.3e-08
		Scaffold3065190	Sopen02g018430.1	XP_015064393.1	1003 aa	PIWI	PF02171	675-965	1.6e-88
						ARGO-N	PF16486	184-321	5.1e-21
						PAZ	PF02170	385-506	2.3e-19
						ARGO-L1	PF08699	524-569	8.5e-09
						ARGO-L2	PF16488	331-376	1.4e-08
		Scaffold3065190	Sopen02g018440.1	XP_015065365.1	999 aa	PIWI	PF02171	660-950	1.6e-86
						ARGO-N	PF16486	178-314	2.0e-19
						PAZ	PF02170	380-498	4.0e-16
						ARGO-L1	PF08699	324-366	2.4e-08
AGO4	Ortholog in *Solanum tuberosum*	XP_006362741.1	_	_	909 aa	PIWI	PF02171	563-869	1.1e-104
						ARGO-N	PF16486	53-214	4.8e-30
						PAZ	PF02170	281-410	1.2e-26
						ARGO-L1	PF08699	226-274	9.7e-17
						ARGO-L2	PF16488	420-465	1.4e-14
		XP_006347269.1	_	_	913 aa	PIWI	PF02171	567-873	1.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	3.1e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-14
						ARGO-MID	PF16487	478-556	4.2e-07

		XP_006347268.1	_	_	913 aa	PIWI	PF02171	567-873	1.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	3.1e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-14
						ARGO-MID	PF16487	478-556	4.2e-07
		XP_015164242.1	_	_	913 aa	PIWI	PF02171	567-873	1.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	3.1e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-14
						ARGO-MID	PF16487	478-556	4.2e-07
		XP_015165956.1	_	_	475 aa	PIWI	PF02171	145-454	8.7e-78
						ARGO-L2	PF16488	06 a 44	3.6e-08
		XP_006347690.1	_	_	881 aa	PIWI	PF02171	535-842	8.9e-105
						ARGO-N	PF16486	28-186	7.2e-29
						PAZ	PF02170	252-380	1.1e-24
						ARGO-L1	PF08699	198-246	3.4e-16
						ARGO-L2	PF16488	390-435	1.2e-12
	Solanum lycopersicum	NP_001266156.1	Solyc01g008960.2.1	_	909 aa	PIWI	PF02171	563-869	2.0e-104
						ARGO-N	PF16486	53-214	4.3e-30
						PAZ	PF02170	281-410	3.7e-27
						ARGO-L1	PF08699	226-274	4.9e-16
						ARGO-L2	PF16488	420-465	1.4e-14
		XP_025887079.1	Solyc06g073540.2.1	_	913 aa	PIWI	PF02171	567-873	2.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	5.0e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-13
						ARGO-MID	PF16487	478-556	2.0e-07
		XP_025885826.1	Solyc03g111760.2.1	_	916 aa	PIWI	PF02171	565-895	2.2e-72
						ARGO-N	PF16486	285-408	2.1e-19
						PAZ	PF02170	45-205	6.1e-13
						ARGO-L1	PF08699	427-465	1.0e-09
						ARGO-L2	PF16488	227-274	8.6e-10
		NP_001266010.1	Solyc01g096750.1.1	_	881 aa	PIWI	PF02171	535-842	1.1e-104
						ARGO-N	PF16486	28-186	9.1e-29
						PAZ	PF02170	252-380	2.2e-25
						ARGO-L1	PF08699	198-246	3.4e-16
						ARGO-L2	PF16488	390-435	9.2e-13
		XP_025887457.1	Solyc06g073530.1.1	_	904 aa	PIWI	PF02171	558-864	1.4e-101
						ARGO-N	PF16486	52-208	5.1e-29

						PAZ	PF02170	274-404	9.2e-27
						ARGO-L1	PF08699	220-269	2.8e-16
						ARGO-L2	PF16488	414-459	6.9e-11
	Solanum pennellii	XP_015079260.1	Sopen06g029900	_	913 aa	PIWI	PF02171	567-873	3.2e-103
						ARGO-N	PF16486	52-217	5.4e-30
						PAZ	PF02170	284-413	6.8e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-13
						ARGO-MID	PF16487	478-556	2.0e-07
		XP_015079262.1	Sopen06g029890.1	_	904 aa	PIWI	PF02171	558-864	6.0e-103
						ARGO-N	PF16486	53-208	2.3e-29
						PAZ	PF02170	274-404	3.4e-26
						ARGO-L1	PF08699	220-268	2.8e-17
						ARGO-L2	PF16488	414-459	2.7e-09
		XP_015056100.1	Sopen01g004450	_	909 aa	PIWI	PF02171	563-869	2.0e-104
						ARGO-N	PF16486	53-214	4.3e-30
						PAZ	PF02170	281-410	7.8e-27
						ARGO-L1	PF08699	226-274	4.9e-16
						ARGO-L2	PF16488	420-465	1.4e-14
		XP_027768416.1	Sopen01g040460	_	881 aa	PIWI	PF02171	535-842	7.1e-105
						ARGO-N	PF16486	28-186	9.1e-29
						PAZ	PF02170	252-380	2.8e-26
						ARGO-L1	PF08699	198-246	3.4e-16
						ARGO-L2	PF16488	390-435	9.2e-13
	Solanum galapagense	scaffold69304_13.6_contig6	Solyc06g073540.2.1	XP_025887079.1	913 aa	PIWI	PF02171	567-873	2.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	5.0e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-13
						ARGO-MID	PF16487	478-556	2.0e-07
		scaffold9634_12.7_contig2	Solyc01g008960.2.1	NP_001266156.1	909 aa	PIWI	PF02171	563-869	2.0e-104
						ARGO-N	PF16486	53-214	4.3e-30
						PAZ	PF02170	281-410	3.7e-27
						ARGO-L1	PF08699	226-274	4.9e-16
						ARGO-L2	PF16488	420-465	1.4e-14
		scaffold96132_14.3_contig1	Solyc06g073530.1.1	XP_025887457.1	905 aa	PIWI	PF02171	558-865	1.8e-101
						ARGO-N	PF16486	52-208	5.1e-29
						PAZ	PF02170	274-404	9.2e-27
						ARGO-L1	PF08699	220-269	2.8e-16
						ARGO-L2	PF16488	414-459	6.9e-11
						ARGO-MID	PF16487	469-547	8.9e-07
		scaffold15546_11.9_contig4	Solyc01g096750.1.1	NP_001266010.1	881 aa	PIWI	PF02171	535-842	1.1e-104

						ARGO-N	PF16486	28-186	9.1e-29
						PAZ	PF02170	252-380	2.2e-25
						ARGO-L1	PF08699	198-246	3.4e-16
						ARGO-L2	PF16488	390-435	9.2e-13
		C9872419_14.0	Solyc03g111760.2.1	XP_025885826.1	759 aa	PIWI	PF02171	434-746	1.1e-57
						PAZ	PF02170	154-277	1.6e-19
						ARGO-L1	PF08699	296-334	8.4e-10
						ARGO-L2	PF16488	96-143	6.8e-10
		scaffold15546_11.9_contig4	Sopen01g040460.1	XP_027768416.1	816 aa	PIWI	PF02171	475-777	1.7e-102
						ARGO-N	PF16486	28-186	8.1e-29
						PAZ	PF02170	252-379	9.5e-22
						ARGO-L1	PF08699	198-246	3.1e-16
						ARGO-L2	PF16488	389-434	8.4e-13
		scaffold96132_14.3_contig1	Sopen06g029890.1	XP_015079262.1	821 aa	PIWI	PF02171	477-781	2.3e-96
						ARGO-N	PF16486	52-208	4.4e-29
						PAZ	PF02170	274-394	3.8e-23
						ARGO-L1	PF08699	220-269	2.5e-16
	Solanum peruvianum	a8588	Solyc06g073540.2.1	XP_025887079.1	820 aa	PIWI	PF02171	495-802	8.1e-105
						PAZ	PF02170	212-340	4.5e-26
						ARGO-N	PF16486	5-146	1.2e-17
						ARGO-L1	PF08699	158-206	3.2e-16
						ARGO-L2	PF16488	350-395	8.4e-13
		a8588	Solyc06g073530.1.1	XP_025887457.1	809 aa	PIWI	PF02171	508-791	1.3e-96
						PAZ	PF02170	201-329	4.4e-26
						ARGO-N	PF16486	13-135	1.6e-20
						ARGO-L1	PF08699	147-195	3.1e-16
						ARGO-L2	PF16488	339-384	8.3e-13
		a8588	Solyc01g096750.1.1	NP_001266010.1	881 aa	PIWI	PF02171	535-842	9.4e-105
						ARGO-N	PF16486	28-186	9.1e-29
						PAZ	PF02170	252-380	5.0e-26
						ARGO-L1	PF08699	198-246	3.4e-16
						ARGO-L2	PF16488	390-435	9.2e-13
	Solanum chilense	scaffold431	Solyc06g073540.2.1	XP_025887079.1	913 aa	PIWI	PF02171	567-873	3.2e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	5.0e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	6.6e-13
						ARGO-MID	PF16487	478-556	1.6e-07
		scaffold2265	Solyc01g008960.2.1	NP_001266156.1	909 aa	PIWI	PF02171	563-869	1.1e-104
						ARGO-N	PF16486	53-214	4.3e-30
						PAZ	PF02170	281-410	3.7e-27
						ARGO-L1	PF08699	226-274	4.9e-16

						ARGO-L2	PF16488	420-465	1.4e-14
		scaffold431	Solyc06g073530.1.1	XP_025887457.1	849 aa	PIWI	PF02171	558-663	3.8e-23
						PIWI	PF02171	667-809	1.1e-58
						ARGO-N	PF16486	53-208	6.7e-29
						PAZ	PF02170	274-404	5.5e-26
						ARGO-L1	PF08699	220-269	2.6e-16
						ARGO-L2	PF16488	414-459	6.0e-13
						ARGO-MID	PF16487	469-547	2.0e-07
		scaffold1590	Solyc01g096750.1.1	NP_001266010.1	881 aa	PIWI	PF02171	535-842	7.0e-105
						ARGO-N	PF16486	28-186	8.6e-29
						PAZ	PF02170	252-380	1.1e-25
						ARGO-L1	PF08699	198-246	3.4e-16
						ARGO-L2	PF16488	390-435	9.2e-13
		scaffold45	Solyc03g111760.2.1	XP_025885826.1	895 aa	PIWI	PF02171	564-854	9.5e-60
						PAZ	PF02170	282-407	1.7e-17
						ARGO-N	PF16486	45-205	2.2e-12
						ARGO-L1	PF08699	426-464	2.6e-10
						ARGO-L2	PF16488	227-274	7.1e-10
		scaffold1590_peptide_1	Sopen01g040460.1	XP_027768416.1	290 aa	ARGO-N	PF16486	28-186	8.9e-30
						ARGO-L1	PF08699	198-246	7.6e-17
		scaffold1590_peptide_2	Sopen01g040460.1	XP_027768416.1	490 aa	PIWI	PF02171	144-451	1.7e-105
						ARGO-L2	PF16488	1_44	2.7e-11
		scaffold431	Sopen06g029890.1	XP_015079262.1	867 aa	PIWI	PF02171	520-827	7.6e-104
						PAZ	PF02170	53-208	6.9e-29
						ARGO-N	PF16486	274-404	5.7e-26
						ARGO-L1	PF08699	220-269	3.8e-13
	Solanum pimpinellifolium LA1589	contig:6668547:1:4047:1	Solyc06g073540.2.1	XP_025887079.1	913 aa	PIWI	PF02171	567-873	2.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	5.0e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	3.7e-11
		contig:4637809:1:8203:1	Solyc01g008960.2.1	NP_001266156.1	786 aa	PIWI	PF02171	440-746	1.5e-104
						ARGO-L1	PF08699	53-214	3.4e-30
						ARGO-N	PF16486	226-274	4.1e-16
						PAZ	PF02170	281-339	1.1e-07
		contig:6556837:1:2234:1	Solyc06g073530.1.1	XP_025887457.1	904 aa	PIWI	PF02171	558-864	1.4e-101
						ARGO-N	PF16486	52-208	5.1e-29
						PAZ	PF02170	274-404	9.2e-27
						ARGO-L1	PF08699	220-269	2.8e-16
						ARGO-L2	PF16488	414-459	6.9e-11
		contig:15014:1:12910:1	Solyc01g096750.1.1	NP_001266010.1	816 aa	PIWI	PF02171	475-777	1.7e-102
						ARGO-N	PF16486	28-186	8.1e-29

						PAZ	PF02170	252-379	9.5e-22
						ARGO-L1	PF08699	198-246	3.1e-16
						ARGO-L2	PF16488	389-434	8.4e-13
		contig:6556837:1:2234:1	Sopen06g029890.1	XP_015079262.1	871 aa	PIWI	PF02171	525-831	1.3e-101
						ARGO-L1	PF08699	52-208	4.8e-29
						ARGO-N	PF16486	274-404	8.7e-27
						PAZ	PF02170	220-269	2.7e-16
	Solanum pimpinellifolium LA0480	Scaffold3067271	Solyc06g073540.2.1	XP_025887079.1	913 aa	PIWI	PF02171	567-873	2.4e-103
						ARGO-N	PF16486	52-217	5.9e-30
						PAZ	PF02170	284-413	5.0e-28
						ARGO-L1	PF08699	229-277	1.3e-16
						ARGO-L2	PF16488	423-468	4.4e-13
						ARGO-MID	PF16487	478-556	2.0e-07
		Scaffold3067963	Solyc01g008960.2.1	NP_001266156.1	909 aa	PIWI	PF02171	563-869	2.0e-104
						ARGO-N	PF16486	53-214	4.3e-30
						PAZ	PF02170	281-410	3.7e-27
						ARGO-L1	PF08699	226-274	4.9e-16
						ARGO-L2	PF16488	420-465	1.4e-14
		Scaffold3067271	Solyc06g073530.1.1	XP_025887457.1	881 aa	PIWI	PF02171	581-841	1.3e-89
						ARGO-N	PF16486	52-208	4.9e-29
						PAZ	PF02170	274-404	8.9e-27
						ARGO-L1	PF08699	220-269	2.7e-16
						ARGO-L2	PF16488	414-459	6.7e-11
		Scaffold3060406	Solyc01g096750.1.1	NP_001266010.1	817 aa	PIWI	PF02171	476-778	1.7e-102
						ARGO-N	PF16486	28-186	8.1e-29
						PAZ	PF02170	252-380	2.0e-25
						ARGO-L1	PF08699	198-246	3.1e-16
						ARGO-L2	PF16488	390-435	8.4e-13
		Scaffold3064212	Solyc03g111760.2.1	XP_025885826.1	759 aa	PIWI	PF02171	434-746	1.1e-57
						ARGO-N	PF16486	154-277	1.6e-19
						PAZ	PF02170	296-334	8.4e-10
						ARGO-L1	PF08699	96-143	6.6e-09
		Scaffold3067271	Sopen06g029890.1	XP_015079262.1	904 aa	PIWI	PF02171	558-864	7.4e-103
						ARGO-N	PF16486	52-208	5.1e-29
						PAZ	PF02170	274-404	9.2e-27
						ARGO-L1	PF08699	220-269	2.8e-16
						ARGO-L2	PF16488	414-459	6.9e-11
AGO5	Ortholog in *Solanum tuberosum*	XP_006347212.1	_	_	1025 aa	PIWI	PF02171	663-981	1.4e-104
						ARGO-N	PF16486	178-310	2.2e-32
						PAZ	PF02170	390-502	4.2e-22
						ARGO-L1	PF08699	321-371	2.0e-18
						ARGO-L2	PF16488	511-557	2.1e-11

						ARGO-MID	PF16487	568-642	1.2e-06
	Solanum lycopersicum	NP_001265878.1	Solyc06g074730.2.1	_	1011 aa	PIWI	PF02171	655-973	1.9e-103
						ARGO-N	PF16486	170-302	1.1e-32
						PAZ	PF02170	382-494	3.5e-23
						ARGO-L1	PF08699	313-363	1.6e-17
						ARGO-L2	PF16488	503-549	2.2e-11
	Solanum pennellii	XP_015077849.1	Sopen06g031140.1	_	1011 aa	PIWI	PF02171	655-973	3.4e-104
						ARGO-N	PF16486	170-302	1.1e-32
						PAZ	PF02170	382-494	2.9e-24
						ARGO-L1	PF08699	313-363	1.0e-17
						ARGO-L2	PF16488	503-549	8.3e-12
	Solanum galapagense	scaffold41608_11.7_contig4	Sopen06g031140.1	XP_015077849.1	921 aa	PIWI	PF02171	565-883	1.6e-103
						ARGO-N	PF16486	131-249	4.3e-26
						PAZ	PF02170	329-441	1.3e-23
						ARGO-L1	PF08699	260-310	1.4e-17
		scaffold41608_11.7_contig4	Solyc06g074730.2.1	NP_001265878.1	858 aa	PIWI	PF02171	502-820	1.4e-103
						ARGO-N	PF16486	131-249	3.8e-26
						PAZ	PF02170	329-432	8.0e-23
						ARGO-L1	PF08699	260-310	1.3e-17
	Solanum peruvianum	a2745	Solyc06g074730.2.1	NP_001265878.1	999 aa	PIWI	PF02171	643-961	1.7e-104
						ARGO-N	PF16486	158-290	3.3e-32
						PAZ	PF02170	370-482	1.2e-23
						ARGO-L1	PF08699	301-351	1.5e-17
						ARGO-L2	PF16488	491-537	1.7e-11
	Solanum chilense	scaffold7262	Sopen06g031140.1	XP_015077849.1	858 aa	PIWI	PF02171	502-820	2.5e-104
						PAZ	PF02170	131-249	5.8e-26
						ARGO-N	PF16486	329-432	5.8e-23
						ARGO-L1	PF08699	260-310	1.0e-15
		scaffold7262	Solyc06g074730.2.1	NP_001265878.1	858 aa	PIWI	PF02171	502-820	2.5e-104
						ARGO-N	PF16486	131-249	5.8e-26
						PAZ	PF02170	329-432	5.8e-23
						ARGO-L1	PF08699	260-310	6.7e-18
	Solanum pimpinellifolium LA1589	contig:40433:1:13665:1	Solyc06g074730.2.1	NP_001265878.1	804 aa	PIWI	PF02171	473-791	1.2e-103
						ARGO-N	PF16486	3-120	4.3e-26
						PAZ	PF02170	200-312	2.0e-23
						ARGO-L1	PF08699	131-181	1.2e-17
						ARGO-L2	PF16488	321-367	1.7e-11
	Solanum pimpinellifolium LA0480	Scaffold2990443	Solyc06g074730.2.1	NP_001265878.1	858 aa	PIWI	PF02171	502-820	1.4e-103
						ARGO-N	PF16486	131-249	3.8e-26
						PAZ	PF02170	329-432	1.5e-22
						ARGO-L1	PF08699	260-310	1.3e-17
AGO6/16	Ortholog in	XP_015169183.1	_	_	903 aa	PIWI	PF02171	557-862	6.7e-101

	Solanum tuberosum					ARGO-N	PF16486	48-206	1.7e-27
						PAZ	PF02170	272-403	4.4e-27
						ARGO-L1	PF08699	218-265	5.0e-16
						ARGO-L2	PF16488	413 458	1.1e-12
	Solanum lycopersicum	NP_001266273.1	Solyc07g049500.2.1	_	903 aa	PIWI	PF02171	557-862	4.7e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
	Solanum pennellii	XP_015082313.1	Sopen07g024850.1	_	903 aa	PIWI	PF02171	557-862	4.3e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	5.0e-16
						ARGO-L2	PF16488	413-458	7.0e-12
	Solanum galapagense	scaffold4662_11.7_contig9	Solyc07g049500.2.1	NP_001266273.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.1e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
		scaffold4662_11.7_contig9	Sopen07g024850.1	XP_015082313.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.1e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
	Solanum peruvianum	a5684	Solyc07g049500.2.1	NP_001266273.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	2.4e-15
						ARGO-L2	PF16488	413-458	4.4e-12
		a5684	Sopen07g024850.1	XP_015082313.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	2.4e-15
						ARGO-L2	PF16488	413-458	4.4e-12
	Solanum chilense	scaffold3937	Solyc07g049500.2.1	NP_001266273.1	902 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	2.4e-15
						ARGO-L2	PF16488	413-458	7.0e-12
		scaffold3937	Sopen07g024850.1	XP_015082313.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26

						ARGO-L1	PF08699	218-265	2.4e-15
						ARGO-L2	PF16488	413-458	7.0e-12
	Solanum pimpinellifolium LA1589	contig:6569105:1:31791:1	Solyc07g049500.2.1	NP_001266273.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
		contig:6569105:1:31791:1	Sopen07g024850.1	XP_015082313.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	1.4e-25
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
	Solanum pimpinellifolium LA0480	Scaffold3066155	Solyc07g049500.2.1	NP_001266273.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
		Scaffold3066155	Sopen07g024850.1	XP_015082313.1	903 aa	PIWI	PF02171	557-862	4.9e-100
						ARGO-N	PF16486	48-206	6.4e-27
						PAZ	PF02170	272-403	5.5e-26
						ARGO-L1	PF08699	218-265	4.3e-15
						ARGO-L2	PF16488	413-458	7.0e-12
AGO7	Ortholog in *Solanum tuberosum*	XP_015159857.1	_	_	962 aa	PIWI	PF02171	655-836	1.6e-39
						PIWI	PF02171	838-921	7.6e-34
						ARGO-N	PF16486	150-297	3.3e-23
						PAZ	PF02170	369-491	7.3e-22
						ARGO-L1	PF08699	308-356	5.8e-17
						ARGO-L2	PF16488	501-547	4.1e-07
		XP_006365299.1	_	_	1002 aa	PIWI	PF02171	655-961	9.0e-91
						ARGO-N	PF16486	150-297	3.5e-23
						PAZ	PF02170	369-491	7.8e-22
						ARGO-L1	PF08699	308-356	6.1e-17
						ARGO-L2	PF16488	501-547	4.3e-07
	Solanum lycopersicum	NP_001266209.1	Solyc01g010970.2.1	_	1000 aa	PIWI	PF02171	653-959	2.1e-91
						ARGO-N	PF16486	149-295	1.6e-22
						PAZ	PF02170	367-489	1.0e-21
						ARGO-L1	PF08699	306-354	5.0e-17
						ARGO-L2	PF16488	499-545	3.2e-07
	Solanum pennellii	XP_015070360.1	Sopen01g006840	_	998 aa	PIWI	PF02171	651-957	2.9e-91
						ARGO-N	PF16486	147-293	8.5e-22
						PAZ	PF02170	365-487	1.1e-21
						ARGO-L1	PF08699	304-352	5.0e-17

						ARGO-L2	PF16488	497-543	3.2e-07
	Solanum galapagense	scaffold106756__9.6_contig3	Solyc01g010970.2.1	NP_001266209.1	1000 aa	PIWI	PF02171	653-959	2.1e-91
						ARGO-N	PF16486	149-295	1.6e-22
						PAZ	PF02170	367-489	1.0e-21
						ARGO-L1	PF08699	306-354	5.0e-17
						ARGO-L2	PF16488	499-545	3.2e-07
	Solanum peruvianum	A22060	Solyc01g010970.2.1	NP_001266209.1	927 aa	PIWI	PF02171	580-886	1.7e-91
						ARGO-N	PF16486	76-222	1.4e-22
						PAZ	PF02170	294-416	9.4e-22
						ARGO-L1	PF08699	233-281	1.2e-16
						ARGO-L2	PF16488	426-472	2.9e-07
	Solanum chilense	scaffold3477	Solyc01g010970.2.1	NP_001266209.1	1000 aa	PIWI	PF02171	653-959	2.9e-91
						ARGO-N	PF16486	149-295	1.6e-22
						PAZ	PF02170	403-489	9.0e-15
						ARGO-L1	PF08699	324-354	4.6e-12
						ARGO-L2	PF16488	499-545	2.1e-06
	Solanum pimpinellifolium LA1589	contig:2714577:1:3182:1	Solyc01g010970.2.1	NP_001266209.1	974 aa	PIWI	PF02171	653-715	3.7e-09
						PIWI	PF02171	731-933	3.9e-68
						ARGO-N	PF16486	149-295	1.5e-22
						PAZ	PF02170	367-489	1.0e-21
						ARGO-L1	PF08699	306 354	4.8e-17
						ARGO-L2	PF16488	499-545	3.1e-07
	Solanum pimpinellifolium LA0480	Scaffold3073856	Solyc01g010970.2.1	NP_001266209.1	1000 aa	PIWI	PF02171	653-959	2.1e-91
						ARGO-N	PF16486	149-295	1.6e-22
						PAZ	PF02170	367-489	1.0e-21
						ARGO-L1	PF08699	306-354	5.0e-17
						ARGO-L2	PF16488	499-545	3.2e-07
AGO10	Ortholog in *Solanum tuberosum*	XP_006363457.1	_	_	982 aa	PIWI	PF02171	621-940	6.7e-117
						ARGO-N	PF16486	136-270	1.6e-30
						PAZ	PF02170	340-462	9.8e-27
						ARGO-L1	PF08699	280-329	3.2e-21
						ARGO-L2	PF16488	472-518	2.2e-15
						ARGO-MID	PF16487	529-606	2.3e-13
	Solanum lycopersicum	NP_001266268	Solyc12g006790	_	938aa	PIWI	PF02171	580-897	4.6e-111
						ARGO-N	PF16486	303-421	8.6e-25
						PAZ	PF02170	96-229	2.4e-22
						ARGO-L1	PF08699	239-288	4.4e-20
						ARGO-L2	PF16488	433-477	2.2e-13
						ARGO-MID	PF16487	488-566	2.4e-11
		XP_004247613.1	Solyc09g082830	_	982aa	PIWI	PF02171	621-940	6.7e-117
						ARGO-N	PF16486	136-270	1.0e-30
						PAZ	PF02170	340-462	9.7e-27

					ARGO-L1	PF08699	280-329	3.2e-21
					ARGO-L2	PF16488	472-518	2.2e-15
					ARGO-MID	PF16487	529-606	2.8e-13
Solanum pennellii	XP_015088227	Sopen09g031660	_	982aa	PIWI	PF02171	621-940	6.7e-117
					ARGO-N	PF16486	136-270	1.6e-30
					PAZ	PF02170	340-462	9.7e-27
					ARGO-L1	PF08699	280-329	3.2e-21
					ARGO-L2	PF16488	472-518	2.2e-15
					ARGO-MID	PF16487	529-606	2.3e-13
Solanum galapagense	scaffold28885_12.6	Solyc09g082830	XP_004247613.1	1152 aa	PIWI	PF02171	779-1098	4.4e-115
					ARGO-N	PF16486	292-426	2.3e-33
					PAZ	PF02170	492-617	6.8e-28
					GLY-RICH	PF12764	160-272	1.0e-26
					ARGO-L1	PF08699	436-485	1.8e-19
					ARGO-L2	PF16488	628-674	4.3e-15
					ARGO-MID	PF16487	685-759	1.0e-07
	scaffold84584_8.7	Solyc12g006790	NP_001266268	953 aa	PIWI	PF02171	598-911	3.8e-114
					ARGO-N	PF16486	136-270	1.6e-30
					PAZ	PF02170	340-462	9.3e-27
					ARGO-L1	PF08699	280-329	4.7e-19
					ARGO-L2	PF16488	472-518	2.1e-15
					ARGO-MID	PF16487	529-587	1.0e-08
Solanum peruvianum	a939	Solyc09g082830	XP_004247613.1	982 aa	PIWI	PF02171	621-940	6.7e-117
					ARGO-N	PF16486	136-270	1.6e-30
					PAZ	PF02170	340-462	9.7e-27
					ARGO-L1	PF08699	280-329	3.2e-21
					ARGO-L2	PF16488	472-518	2.2e-15
					ARGO-MID	PF16487	529-606	2.3e-13
	a12868	Solyc12g006790	NP_001266268	938 aa	PIWI	PF02171	580-898	5.7e-112
					PAZ	PF02170	303-421	8.6e-25
					ARGO-N	PF16486	96-229	7.8e-23
					ARGO-L1	PF08699	239-288	4.4e-20
					ARGO-L2	PF16488	433-477	2.2e-13
					ARGO-MID	PF16487	488-566	3.3e-11
Solanum chilense	scaffold1098	Solyc09g082830	XP_004247613.1	885 aa	PIWI	PF02171	524-843	5.4e-117
					PAZ	PF02170	243-365	8.4e-27
					ARGO-N	PF16486	136-267	1.7e-17
					ARGO-L2	PF16488	375-421	2.0e-15
					ARGO-MID	PF16487	432 509	2.0e-13
	scaffold7430	Solyc12g006790	NP_001266268	898 aa	PIWI	PF02171	580-881	1.8e-104
					PAZ	PF02170	303-421	8.1e-25
					ARGO-N	PF16486	96-229	1.3e-22

					ARGO-L1	PF08699	239-288	4.2e-20
					ARGO-L2	PF16488	433-477	3.4e-13
					ARGO-MID	PF16487	488-566	1.9e-11
Solanum pimpinellifolium LA1589	contig:3758907:1:8311:1	Solyc09g082830	XP_004247613.1	949 aa	PIWI	PF02171	621-881	9.5e-87
					ARGO-N	PF16486	136-270	1.6e-30
					PAZ	PF02170	340-462	9.3e-27
					ARGO-L1	PF08699	280-329	3.1e-21
					ARGO-L2	PF16488	472-518	2.1e-15
					ARGO-MID	PF16487	529-606	2.7e-13
	contig:6745152:1:10334:1	Solyc12g006790	NP_001266268	860 aa	PIWI	PF02171	502-820	1.8e-111
					PAZ	PF02170	230-343	2.3e-24
					ARGO-N	PF16486	96-229	2.1e-22
					ARGO-L2	PF16488	355-399	2.0e-13
					ARGO-MID	PF16487	410-488	2.1e-11
Solanum pimpinellifolium LA0480	Scaffold3067183	Solyc09g082830	XP_004247613.1	950 aa	PIWI	PF02171	589-908	6.3e-117
					ARGO-N	PF16486	136-270	1.6e-30
					PAZ	PF02170	340-462	9.3e-27
					ARGO-L1	PF08699	280-329	3.1e-21
					ARGO-L2	PF16488	472-518	2.1e-15
					ARGO-MID	PF16487	529-580	1.7e-07
	Scaffold3061531	Solyc12g006790	NP_001266268	938 aa	PIWI	PF02171	580-898	2.2e-111
					ARGO-N	PF16486	303-421	8.6e-25
					PAZ	PF02170	96-229	2.4e-22
					ARGO-L1	PF08699	239-288	4.4e-20
					ARGO-L2	PF16488	433-477	2.2e-13
					ARGO-MID	PF16487	488-566	2.4e-11

Supplementary Table S3. Distribution of conserved domains and their locations in putative DCL proteins identified in seven species of the tomato and their orthologs.

Protein families	Specie	ID protein	ID protein query SolGenomics	ID query	Protein Length	Conserved domain	Domain ID	Start and End	E-value
DCL1	Ortholog in *Solanum tuberosum*	XP_006352611.1	_	_	1914 aa	Ribonuclease_3	PF00636	1386-1534	7.4e-30
						Ribonuclease_3	PF00636	1612-1725	1.5e-24
						Dicer_dimer	PF03368	848-936	3.2e-22
						PAZ	PF02170	1214-1349	4.8e-22
						dsrm	PF00035	1752-1810	0.00023
						Helicase_C	PF00271	656-773	5.9e-17
						DND1_DSRM	PF14709	1837-1909	6.4e-14
						ResIII	PF04851	260-420	4.1e-14
	Solanum lycopersicum	NP_001289827.1	Solyc10g005130	_	1888 aa	Ribonuclease_3	PF00636	1386-1468	8.3e-22
						Ribonuclease_3	PF00636	1586-1699	3.0e-24
						Dicer_dimer	PF03368	848-936	4.2e-22
						PAZ	PF02170	1214-1349	4.7e-22
						dsrm	PF00035	1726-1784	0.00011
						Helicase_C	PF00271	656-773	5.8e-17
						DND1_DSRM	PF14709	1811-1883	6.3e-14
						ResIII	PF04851	260-420	2.7e-14
	Solanum pennellii	XP_015085705.1	Sopen10g001150	_	1914 aa	Ribonuclease_3	PF00636	1386-1534	7.4e-30
						Ribonuclease_3	PF00636	1612-1725	3.1e-24
						Dicer_dimer	PF03368	848-936	1.5e-22
						PAZ	PF02170	1214-1349	4.8e-22
						dsrm	PF00035	1752-1810	0.00011
						Helicase_C	PF00271	656-773	5.9e-17
						DND1_DSRM	PF14709	1837-1909	6.4e-14
						ResIII	PF04851	256-420	2.4e-14
	Solanum galapagense	Scaffold96676_12.8_contig7	Solyc10g005130	NP_001289827.1	1914 aa	Ribonuclease_3	PF00636	1386-1534	7.4e-30
						Ribonuclease_3	PF00636	1612-1725	3.1e-24
						Dicer_dimer	PF03368	848-936	4.2e-22
						PAZ	PF02170	1214-1349	4.8e-22
						dsrm	PF00035	1752-1810	0.00011
						Helicase_C	PF00271	656-773	5.9e-17
						DND1_DSRM	PF14709	1837-1909	6.4e-14
						ResIII	PF04851	260-420	8.8e-14
	Solanum peruvianum	a12916	Solyc10g005130	NP_001289827.1	1914 aa	Ribonuclease_3	PF00636	1386-1534	6.9e-30
						Ribonuclease_3	PF00636	1612-1725	2.8e-25
						Dicer_dimer	PF03368	848-936	4.2e-22
						PAZ	PF02170	1214-1349	4.8e-22
						dsrm	PF00035	1752-1810	0.00011

						Helicase_C	PF00271	656-773	5.9e-17
						DND1_DSRM	PF14709	1837-1909	6.4e-14
						ResIII	PF04851	260-420	2.7e-14
	Solanum chilense	Scaffold7114	Solyc10g005130	NP_001289827.1	1914 aa	Ribonuclease_3	PF00636	1386-1534	6.9e-30
						Ribonuclease_3	PF00636	1612-1725	2.8e-25
						Dicer_dimer	PF03368	848-936	4.2e-22
						PAZ	PF02170	1214-1349	4.8e-22
						dsrm	PF00035	1752-1810	0.00011
						Helicase_C	PF00271	656-773	5.9e-17
						DND1_DSRM	PF14709	1837-1909	6.4e-14
						ResIII	PF04851	260-420	2.7e-14
	Solanum pimpinellifolium LA1589	contig:3391119:1:3923:1	Solyc10g005130	NP_001289827.1	1900 aa	Ribonuclease_3	PF00636	1338-1486	7.3e-30
						Ribonuclease_3	PF00636	1564-1677	3.1e-24
						Dicer_dimer	PF03368	848-936	4.2e-22
						PAZ	PF02170	1166-1286	9.0e-19
						dsrm	PF00035	1704-1762	0.00011
						Helicase_C	PF00271	656-773	5.8e-17
						DND1_DSRM	PF14709	1789-1861	6.3e-14
						ResIII	PF04851	260-369	1.9e-06
	Solanum pimpinellifolium LA0480	Scaffold3065974	Solyc10g005130	NP_001289827.1	1914 aa	Ribonuclease_3	PF00636	1386-1534	7.4e-30
						Ribonuclease_3	PF00636	1612-1725	3.1e-24
						Dicer_dimer	PF03368	848-936	4.2e-22
						PAZ	PF02170	1214-1349	4.8e-22
						dsrm	PF00035	1752-1810	0.00011
						Helicase_C	PF00271	656-773	5.9e-17
						DND1_DSRM	PF14709	1837-1909	6.4e-14
						ResIII	PF04851	261-420	3.2e-14
DCL2	Ortholog in *Solanum tuberosum*	XP_015166743.1	_	_	1371 aa	Ribonuclease_3	PF00636	972-1090	1.9e-21
						Ribonuclease_3	PF00636	1162-1273	1.2e-18
						Dicer_dimer	PF03368	360-473	3.2e-20
						Helicase_C	PF00271	543-623	5.5e-18
						DEAD	PF00270	24-191	4.1e-12
						PAZ	PF02170	818-929	6.4e-12
		XP_015169591.1	_	_	1357 aa	Ribonuclease_3	PF00636	958-1076	9.0e-23
						Ribonuclease_3	PF00636	1148-1259	1.4e-19
						Dicer_dimer	PF03368	515-597	6.5e-19
						Helicase_C	PF00271	327-445	4.8e-17
						PAZ	PF02170	786-915	5.3e-14
						DEAD	PF00270	24-88	6.2e-06
		XP_015166742.1	_	_	1402 aa	Ribonuclease_3	PF00636	1003-1121	4.0e-22
						Ribonuclease_3	PF00636	1193-1304	8.6e-20
						Dicer_dimer	PF03368	371-490	7.0e-19

						Helicase_C	PF00271	560-640	5.5e-18
						PAZ	PF02170	835-960	2.6e-14
						DEAD	PF00270	24-190	8.7e-13
	Solanum lycopersicum	NP_001316341.1	Solyc11g008520	_	1428 aa	Ribonuclease_3	PF00636	1031-1149	4.7e-22
						Ribonuclease_3	PF00636	1221-1330	5.0e-21
						Helicase_C	PF00271	374-492	6.6e-18
						Dicer_dimer	PF03368	588-669	1.1e-17
						DEAD	PF00270	26-192	1.9e-13
						PAZ	PF02170	862-988	9.0e-13
		NP_001316339.1	Solyc06g048960	_	1399 aa	Ribonuclease_3	PF00636	1000-1118	9.5e-22
						Ribonuclease_3	PF00636	1190-1301	5.1e-20
						Dicer_dimer	PF03368	557-639	6.5e-19
						Helicase_C	PF00271	369-487	5.0e-17
						PAZ	PF02170	826-957	5.0e-14
						DEAD	PF00270	22-187	8.1e-13
		NP_001316342.1	Solyc11g008540	_	1352 aa	Ribonuclease_3	PF00636	950-1068	8.2e-22
						Ribonuclease_3	PF00636	1140-1251	1.2e-19
						Helicase_C	PF00271	318-437	1.9e-18
						Dicer_dimer	PF03368	507-587	8.7e-18
						PAZ	PF02170	776-907	1.2e-13
						ResIII	PF04851	8-137	8.0e-05
		NP_001316343.1	Solyc11g008530	_	1317 aa	Ribonuclease_3	PF00636	918-1036	1.1e-21
						Ribonuclease_3	PF00636	1109-1219	6.9e-19
						Helicase_C	PF00271	307-420	1.1e-20
						Dicer_dimer	PF03368	489-569	4.0e-18
						PAZ	PF02170	764-875	1.6e-13
	Solanum pennellii	XP_027768905.1	Sopen11g004310	_	1499 aa	Ribonuclease_3	PF00636	1100-1218	6.7e-22
						Ribonuclease_3	PF00636	1290-1401	4.5e-20
						Dicer_dimer	PF03368	657-738	4.8e-18
						Helicase_C	PF00271	469-587	6.3e-18
						DEAD	PF00270	121-287	1.5e-13
						PAZ	PF02170	931-1057	8.8e-13
		_	Sopen11g004320	_	1222 aa	Ribonuclease_3	PF00636	952-1070	2.0e-21
						Ribonuclease_3	PF00636	1143-1210	1.1e-11
						Helicase_C	PF00271	360-473	1.4e-21
						DEAD	PF00270	24-190	4.1e-13
						PAZ	PF02170	798-909	1.5e-12
						Dicer_dimer	PF03368	542-588	2.6e-07
		_	Sopen11g004330	_	1405 aa	Ribonuclease_3	PF00636	1003-1121	1.0e-22
						Ribonuclease_3	PF00636	1193-1304	1.2e-19
						Helicase_C	PF00271	371-490	2.0e-18
						Dicer_dimer	PF03368	560-640	6.8e-18

						PAZ	PF02170	829-960	1.2e-13
						DEAD	PF00270	24-190	9.8e-13
	Solanum galapagense	Scaffold2617_14.2_contig4	Solyc11g008520	NP_001316341.1	1402 aa	Ribonuclease_3	PF00636	1005-1123	4.6e-22
						Ribonuclease_3	PF00636	1195-1304	4.9e-21
						Helicase_C	PF00271	374-492	5.8e-18
						Dicer_dimer	PF03368	562-643	1.1e-17
						DEAD	PF00270	26-192	1.8e-13
						PAZ	PF02170	836-962	8.7e-13
		Scaffold18956_13.8_contig1	Solyc06g048960	NP_001316339.1	1399 aa	Ribonuclease_3	PF00636	1000-1118	9.5e-22
						Ribonuclease_3	PF00636	1190-1301	5.1e-20
						Dicer_dimer	PF03368	557-639	6.5e-19
						Helicase_C	PF00271	369-487	5.0e-17
						PAZ	PF02170	826-957	5.0e-14
						DEAD	PF00270	22-187	8.1e-13
		Scaffold2617_14.2_contig12	Solyc11g008540	NP_001316342.1	1355 aa	Ribonuclease_3	PF00636	953-1071	8.2e-22
						Ribonuclease_3	PF00636	1143-1254	1.2e-19
						Helicase_C	PF00271	318-437	1.9e-18
						Dicer_dimer	PF03368	507-587	1.5e-17
						PAZ	PF02170	779-910	2.5e-13
						ResIII	PF04851	8-137	8.0e-05
		Scaffold2617_14.2_contig7	Solyc11g008530	NP_001316343.1	1158 aa	Ribonuclease_3	PF00636	759-877	9.6e-22
						Ribonuclease_3	PF00636	950-1060	4.4e-19
						Helicase_C	PF00271	148-261	9.3e-21
						Dicer_dimer	PF03368	330-410	2.1e-17
						PAZ	PF02170	601-716	9.1e-14
		Scaffold2617_14.2_contig4	Sopen11g004310	XP_027768905.1	1349 aa	Ribonuclease_3	PF00636	952-1070	4.4e-22
						Ribonuclease_3	PF00636	1142-1251	4.7e-21
						Helicase_C	PF00271	321-439	5.5e-18
						Dicer_dimer	PF03368	509-590	1.0e-17
						DEAD	PF00270	26-192	1.7e-13
						PAZ	PF02170	783-909	8.3e-13
		Scaffold2617_14.2_contig6	Sopen11g004320	_	482 aa	Helicase_C	PF00271	360-473	2.5e-21
						DEAD	PF00270	24-190	1.8e-13
		Scaffold2617_14.2_contig4	Sopen11g017590	_	253 aa	Helicase_C	PF00271	156-252	5.8e-09
	Solanum chilense	Scaffold6549	Solyc11g008520	NP_001316341.1	1404 aa	Ribonuclease_3	PF00636	1005-1123	4.9e-22
						Ribonuclease_3	PF00636	1195-1306	4.2e-20
						Helicase_C	PF00271	374-492	5.8e-18
						Dicer_dimer	PF03368	562-643	1.1e-17
						DEAD	PF00270	26-192	1.8e-13
						PAZ	PF02170	836-962	2.0e-12
		Scaffold6326	Solyc06g048960	NP_001316339.1	1399 aa	Ribonuclease_3	PF00636	1000-1118	6.2e-22
						Ribonuclease_3	PF00636	1190-1301	4.9e-20

						Dicer_dimer	PF03368	557-639	6.5e-19
						Helicase_C	PF00271	369-487	5.0e-17
						PAZ	PF02170	826-957	2.5e-14
						DEAD	PF00270	22-187	8.1e-13
		Scaffold6549	Solyc11g008540	NP_001316342.1	1353 aa	Ribonuclease_3	PF00636	950-1068	3.8e-21
						Ribonuclease_3	PF00636	1140-1251	1.1e-19
						Dicer_dimer	PF03368	507-587	6.6e-18
						Helicase_C	PF00271	319-438	3.5e-17
						PAZ	PF02170	776-907	1.5e-13
		Scaffold6549	Solyc11g008530	NP_001316343.1	1013 aa	Ribonuclease_3	PF00636	616-733	3.0e-19
						Ribonuclease_3	PF00636	806-916	1.7e-19
						Helicase_C	PF00271	183-296	2.1e-21
		Scaffold6549	Sopen11g004310	XP_027768905.1	1335 aa	Ribonuclease_3	PF00636	952-1070	4.6e-22
						Ribonuclease_3	PF00636	1142-1213	3.9e-14
						Helicase_C	PF00271	321-439	5.4e-18
						Dicer_dimer	PF03368	509-590	1.0e-17
						DEAD	PF00270	26-192	1.7e-13
						PAZ	PF02170	783-909	1.9e-12
		Scaffold2617_14.2_contig7	Sopen11g004320	_	385 aa	Helicase_C	PF00271	263-376	4.4e-22
		Scaffold6549	Sopen11g017590	_	301 aa	Helicase_C	PF00271	157-274	3.4e-18
		Scaffold12663	Sopen08g021150	XP_015085705.1	1658 aa	Ribonuclease_3	PF00636	1068-1202	6.0e-25
						Ribonuclease_3	PF00636	1280-1384	6.7e-20
						Dicer_dimer	PF03368	576-662	1.1e-22
						Helicase_C	PF00271	392-505	8.3e-19
						DEAD	PF00270	38-199	5.9e-17
						PAZ	PF02170	890-1026	5.6e-11
	Solanum pimpinellifolium LA1589	contig:6538610:1:8256:1	Solyc11g008520	NP_001316341.1	1402 aa	Ribonuclease_3	PF00636	1005-1123	4.6e-22
						Ribonuclease_3	PF00636	1195-1304	3.3e-20
						Helicase_C	PF00271	374-492	3.0e-18
						Dicer_dimer	PF03368	562-643	1.1e-17
						DEAD	PF00270	26-192	1.8e-13
						PAZ	PF02170	836-962	8.0e-13
		contig:6489456:1:9223:1	Solyc06g048960	NP_001316339.1	1217 aa	Ribonuclease_3	PF00636	818-936	5.0e-22
						Ribonuclease_3	PF00636	1008-1119	3.6e-20
						Dicer_dimer	PF03368	375-457	5.3e-19
						Helicase_C	PF00271	187-305	4.1e-17
						PAZ	PF02170	644-775	1.6e-13
		contig:6566908:1:4607:1	Solyc11g008540	NP_001316342.1	1353 aa	Ribonuclease_3	PF00636	951-1069	8.7e-22
						Ribonuclease_3	PF00636	1141-1252	1.2e-19
						Helicase_C	PF00271	318-437	1.9e-18
						Dicer_dimer	PF03368	507-588	6.6e-16
						PAZ	PF02170	777-908	1.2e-13

						ResIII	PF04851	8-137	8.0e-05
		contig:6742142:1:2591:1	Solyc11g008530	NP_001316343.1	1370 aa	Ribonuclease_3	PF00636	971-1089	1.2e-21
						Ribonuclease_3	PF00636	1162-1272	5.5e-19
						Helicase_C	PF00271	360-473	1.2e-20
						Dicer_dimer	PF03368	542-622	2.5e-17
						PAZ	PF02170	813-928	1.1e-13
						DEAD	PF00270	24-190	1.0e-12
		contig:6538610:1:8256:1	Sopen11g004310	XP_027768905.1	1402 aa	Ribonuclease_3	PF00636	1005-1123	4.6e-22
						Ribonuclease_3	PF00636	1195-1304	3.3e-20
						Dicer_dimer	PF03368	562-643	1.1e-17
						DEAD	PF00270	26-192	1.8e-13
						PAZ	PF02170	836-940	6.8e-11
						Helicase_C	PF00271	374-473	1.3e-08
		contig:6660195:1:6613:1	Sopen11g004320	_	482 aa	Helicase_C	PF00271	360-473	2.5e-21
						DEAD	PF00270	24-190	1.8e-13
	Solanum pimpinellifolium LA0480	Scaffold3061571	Solyc11g008520	NP_001316341.1	1402 aa	Ribonuclease_3	PF00636	1005-1123	4.6e-22
						Ribonuclease_3	PF00636	1195-1304	3.3e-20
						Helicase_C	PF00271	374-492	1.8e-18
						Dicer_dimer	PF03368	562-643	1.1e-17
						DEAD	PF00270	26-192	1.8e-13
						PAZ	PF02170	836-962	8.0e-13
		Scaffold3062417_contig1	Solyc06g048960	NP_001316339.1	1399 aa	Ribonuclease_3	PF00636	1000-1118	6.0e-22
						Ribonuclease_3	PF00636	1190-1301	4.4e-20
						Dicer_dimer	PF03368	557-639	6.3e-19
						Helicase_C	PF00271	369-487	5.0e-17
						DEAD	PF00270	826-957	1.9e-13
						PAZ	PF02170	22-187	8.8e-13
		Scaffold3069414	Solyc11g008540	NP_001316342.1	1352 aa	Ribonuclease_3	PF00636	950-1068	1.5e-20
						Ribonuclease_3	PF00636	1140-1251	1.2e-19
						Helicase_C	PF00271	318-437	1.9e-18
						Dicer_dimer	PF03368	507-587	6.5e-18
						PAZ	PF02170	776-907	1.2e-13
						ResIII	PF04851	8-137	8.0e-05
		Scaffold3061571	Solyc11g008530	NP_001316343.1	1370 aa	Ribonuclease_3	PF00636	971-1089	1.2e-21
						Ribonuclease_3	PF00636	1162-1272	4.7e-18
						Helicase_C	PF00271	360-473	1.2e-20
						Dicer_dimer	PF03368	542-622	2.5e-17
						PAZ	PF02170	813-928	1.1e-13
						DEAD	PF00270	24-190	1.0e-12
		Scaffold3061571	Sopen11g004310	XP_027768905.1	1402 aa	Ribonuclease_3	PF00636	1005-1123	4.6e-22
						Ribonuclease_3	PF00636	1195-1304	3.3e-20
						Helicase_C	PF00271	374-492	1.8e-18

						Dicer_dimer	PF03368	562-643	1.1e-17
						PAZ	PF02170	26-192	1.8e-13
						DEAD	PF00270	836-962	8.0e-13
		Scaffold3061571	Sopen11g004320	_	482 aa	Helicase_C	PF00271	360-473	5.3e-19
						DEAD	PF00270	24-190	1.8e-13
DCL3	Ortholog in *Solanum tuberosum*	XP_006361520.1	_	_	1659 aa	Ribonuclease_3	PF00636	1069-1203	3.3e-25
						Ribonuclease_3	PF00636	1281-1385	5.2e-20
						Dicer_dimer	PF03368	577-663	3.0e-22
						Helicase_C	PF00271	389-506	8.0e-19
						DEAD	PF00270	39-200	2.3e-17
						PAZ	PF02170	892-1027	4.1e-11
	Solanum lycopersicum	NP_001289826.1	Solyc08g067210	_	1430 aa	Ribonuclease_3	PF00636	840-974	1.3e-25
						Ribonuclease_3	PF00636	1052-1156	2.2e-20
						Dicer_dimer	PF03368	348-434	8.9e-23
						Helicase_C	PF00271	164-277	6.9e-19
						PAZ	PF02170	662-798	4.6e-11
	Solanum pennellii	XP_015085705.1	Sopen08g021150	_	1358 aa	Ribonuclease_3	PF00636	768-902	1.3e-25
						Ribonuclease_3	PF00636	980-1084	2.0e-20
						Dicer_dimer	PF03368	276-362	8.3e-23
						Helicase_C	PF00271	92-205	6.4e-19
						PAZ	PF02170	590-726	2.4e-10
	Solanum galapagense	Scaffold32326_14.0_contig2	Solyc08g067210	NP_001289826.1	1658 aa	Ribonuclease_3	PF00636	1068-1202	1.6e-25
						Ribonuclease_3	PF00636	1280-1384	2.6e-20
						Dicer_dimer	PF03368	576-662	6.5e-23
						Helicase_C	PF00271	392-505	8.3e-19
						DEAD	PF00270	38-199	2.3e-17
						PAZ	PF02170	890-1026	5.6e-11
		Scaffold32326_14.0_contig2	Sopen08g021150	XP_015085705.1	1591 aa	Ribonuclease_3	PF00636	1001-1135	1.5e-25
						Ribonuclease_3	PF00636	1213-1317	2.5e-20
						Dicer_dimer	PF03368	509-595	6.2e-23
						DEAD	PF00270	38-183	5.9e-17
						PAZ	PF02170	823-959	5.3e-11
	Solanum peruvianum	A21158	Solyc08g067210	NP_001289826.1	1658 aa	Ribonuclease_3	PF00636	1068-1202	4.8e-25
						Ribonuclease_3	PF00636	1280-1384	2.6e-20
						Dicer_dimer	PF03368	576-662	1.1e-22
						Helicase_C	PF00271	392-505	8.3e-19
						DEAD	PF00270	38-199	1.8e-17
						PAZ	PF02170	890-1026	5.6e-11
	Solanum chilense	Scaffold3675	Solyc08g067210	NP_001289826.1	1679 aa	Ribonuclease_3	PF00636	1089-1223	6.1e-25
						Ribonuclease_3	PF00636	1301-1405	2.6e-20
						Dicer_dimer	PF03368	597-683	1.1e-22
						Helicase_C	PF00271	413-526	8.4e-19

						DEAD	PF00270	59-220	6.0e-17
						PAZ	PF02170	911-1047	5.7e-11
	Solanum pimpinellifolium LA1589	contig:6317254:1:3688:1	Solyc08g067210	NP_001289826.1	1658 aa	Ribonuclease_3	PF00636	1068-1202	1.6e-25
						Ribonuclease_3	PF00636	1280-1384	2.6e-20
						Dicer_dimer	PF03368	576-662	1.1e-22
						Helicase_C	PF00271	392-505	8.3e-19
						DEAD	PF00270	38-199	2.3e-17
						PAZ	PF02170	890-1026	5.6e-11
		contig:5110292:1:5983:1	Sopen08g021150	XP_015085705.1	1627 aa	Ribonuclease_3	PF00636	1037-1171	1.6e-25
						Ribonuclease_3	PF00636	1249-1353	2.5e-20
						Dicer_dimer	PF03368	545-631	1.0e-22
						DEAD	PF00270	38-199	2.3e-17
						Helicase_C	PF00271	403-474	4.9e-15
						PAZ	PF02170	859-995	5.4e-11
	Solanum pimpinellifolium LA0480	Scaffold3064143	Solyc08g067210	NP_001289826.1	1607 aa	Ribonuclease_3	PF00636	1017-1151	1.6e-25
						Ribonuclease_3	PF00636	1229-1333	2.5e-20
						Dicer_dimer	PF03368	525-611	1.0e-22
						Helicase_C	PF00271	355-468	8.0e-19
						DEAD	PF00270	39-184	6.0e-17
						PAZ	PF02170	839-975	5.3e-11
		Scaffold3064143	Sopen08g021150	XP_015085705.1	1659 aa	Ribonuclease_3	PF00636	1069-1203	1.6e-25
						Ribonuclease_3	PF00636	1281-1385	2.6e-20
						Dicer_dimer	PF03368	577-663	1.1e-22
						Helicase_C	PF00271	393-506	8.3e-19
						DEAD	PF00270	39-200	2.3e-17
						PAZ	PF02170	891-1027	5.6e-11
DCL4	Ortholog in *Solanum tuberosum*	XP_015162544.1	_	_	1540 aa	Ribonuclease_3	PF00636	1023-1153	1.1e-20
						Ribonuclease_3	PF00636	1229-1338	3.7e-20
						Dicer_dimer	PF03368	569-654	1.8e-22
						Helicase_C	PF00271	397-503	2.2e-19
						DEAD	PF00270	50-195	3.9e-15
		XP_006343690.1	_	_	1622 aa	Ribonuclease_3	PF00636	1023-1153	1.2e-20
						Ribonuclease_3	PF00636	1229-1338	4.0e-20
						Dicer_dimer	PF03368	569-654	2.0e-22
						Helicase_C	PF00271	397-503	2.3e-19
						DND1_DSRM	PF14709	1540-1613	1.4e-15
						DEAD	PF00270	50-195	4.2e-15
		XP_006343691.1	_	_	1621 aa	Ribonuclease_3	PF00636	1022-1152	1.2e-20
						Ribonuclease_3	PF00636	1228-1337	4.0e-20
						Dicer_dimer	PF03368	569-654	2.0e-22
						Helicase_C	PF00271	397-503	2.3e-19
						DND1_DSRM	PF14709	1539-1612	1.4e-15

						DEAD	PF00270	50-195	4.2e-15
	Solanum lycopersicum	XP_010323151.1	Solyc07g005030	_	1536 aa	Ribonuclease_3	PF00636	937-1067	8.6e-22
						Ribonuclease_3	PF00636	1143-1252	2.9e-20
						Dicer_dimer	PF03368	485-570	2.2e-22
						Helicase_C	PF00271	313-419	3.4e-19
						DND1_DSRM	PF14709	1454-1527	4.4e-15
						DEAD	PF00270	7-128	2.0e-08
	Solanum pennellii	XP_015082002.1	Sopen07g001140	_	1690 aa	Ribonuclease_3	PF00636	1091-1221	2.6e-21
						Ribonuclease_3	PF00636	1297-1406	4.8e-20
						Dicer_dimer	PF03368	639-724	2.5e-22
						Helicase_C	PF00271	467-573	4.3e-19
						DND1_DSRM	PF14709	1608-1681	1.5e-15
						DEAD	PF00270	122-282	3.8e-15
						zf-RVT	PF13966	10_57	1.3e-09
						PAZ	PF02170	926-1048	2.8e-07
	Solanum galapagense	Scaffold52151_12.8_contig1	Solyc07g005030	XP_010323151.1	1536 aa	Ribonuclease_3	PF00636	937-1067	8.6e-22
						Ribonuclease_3	PF00636	1143-1252	2.9e-20
						Dicer_dimer	PF03368	485-570	2.2e-22
						Helicase_C	PF00271	313-419	4.1e-19
						DND1_DSRM	PF14709	1454-1527	4.4e-15
						DEAD	PF00270	7-128	2.0e-08
	Solanum peruvianum	A25270	Solyc07g005030	XP_010323151.1	1536 aa	Ribonuclease_3	PF00636	937-1067	1.9e-21
						Ribonuclease_3	PF00636	1143-1252	2.9e-20
						Dicer_dimer	PF03368	485-570	1.9e-22
						Helicase_C	PF00271	313-419	3.8e-19
						DND1_DSRM	PF14709	1454-1527	1.7e-14
						DEAD	PF00270	7-128	5.1e-08
	Solanum chilense	Scaffold1398	Solyc07g005030	XP_010323151.1	1536 aa	Ribonuclease_3	PF00636	937-1067	2.1e-21
						Ribonuclease_3	PF00636	1143-1252	2.9e-20
						Dicer_dimer	PF03368	485-570	4.9e-22
						Helicase_C	PF00271	313-419	3.8e-19
						DND1_DSRM	PF14709	1454-1527	1.3e-15
						DEAD	PF00270	7-128	5.1e-08
	Solanum pimpinellifolium LA1589	contig:6649770:1:14572:1	Solyc07g005030	XP_010323151.1	1536 aa	Ribonuclease_3	PF00636	937-1067	8.6e-22
						Ribonuclease_3	PF00636	1143-1252	2.9e-20
						Dicer_dimer	PF03368	485-570	2.2e-22
						Helicase_C	PF00271	313-419	3.4e-19
						DND1_DSRM	PF14709	1454-1527	4.4e-15
						DEAD	PF00270	7-128	2.0e-08
	Solanum pimpinellifolium LA0480	Scaffold3072084	Solyc07g005030	XP_010323151.1	1536 aa	Ribonuclease_3	PF00636	937-1067	8.6e-22
						Ribonuclease_3	PF00636	1143-1252	2.9e-20
						Dicer_dimer	PF03368	485-570	2.2e-22

						Helicase_C	PF00271	313-419	3.4e-19
						DND1_DSRM	PF14709	1454-1527	7.0e-15
						DEAD	PF00270	7-128	2.0e-08

Supplementary Table S4. Putative AT, BCKD and IPMS proteins predicted in *Solanum galapagense* (Sga), *Solanum peruvianum* (Spr), *Solanum chilense* (Sch), *Solanum pimpinellifolium* LA0480 (SpiLA0480), *Solanum pimpinellifolium* LA1589 (SpiLA1589).

Protein families	Protein	Species	Protein sequence	Size
Acylsugar Acyltransferase	**AT2 (AT4)**	*Sly*	>Solyc01g105580.1.1_NP_001266253.1 MVKPSAPTPDNLRRLKLSLFDQMDIGAYVPIVFNYLPNSTSSYDHDDKLEKSLSETLTKFYPFAGRFRKGIDPFSIDCNDEGIEYVRTKVNADDLAQYLRGQAHNDIES SLIDLLPVMHRLPSSPLFGVQVNVFNNGGVTIGIQILHMVSDAFTLVKFVNEWAHTTLTGTMPLDNPGFGQLPWLFPARALPFPLPDFNTTTAPNYKNVTKRFLFDAL AIENLRNTIKANDMMMKQPSRVVVVMSLIWKVLTHISSAKNNGNSRDSSLVFVVNLRGKLSCTAPSLEHVVGNCVIPATANKEGDEARRKDDELNDFVKLVRNTIRDT TCEAIGKAESVDDISSLAFNNLTKCIEKILHGDEMDFYSCSSWCGFPWYEADFGWGKPFWVSSVSFGHHGVTNLMDTKDGDGIQVTICLKENDMIEFERDPHILSST SKLAFHSLG	439 aa
		Spe	>Sopen04g006140_XP_015071716.1 MCLSHKVGDGYTFGNFMNHWATIARNPLSSEIYPISPKFDGSFYFPPTKDEDSSNVSNNNIVPQREECVSKGFSISSSKLTALKARVINESKVQNPSDTEVVSAFLYQ RAMATKKLVNSSSIRPSLLHQAVNLRPPLPKHTMGNIGCLFSILTKEEKEMDLAQVVSKLRKEKEEVKQKYKNAKIEELLPITLEQYRKANELLVNNSCYDLYRFSSLIT FPSYDVDFGWGKPEKVISPLSTSNPPIKNMFILMADKNRDGVDLTCSMKKQDMLAFERDEELLQFASPTS	288 aa
		Sga	>Sga_ scaffold79604_12.8_contig10_440_aa MVKPSAPTPDNLRRLKLSLFDQMDIGAYVPILFNYLPNSTSSYDHDDKLEKSLSETLTKFYPFAGRFRKGIDPFSIDCNDEGIEYVRTKVNADDLAQYLRGQAHNDIES SLIDLLPVMHRLPSSPLFGVQVNVFNNGGVTIGIQILHMVSDAFTLVKFVNEWAHTTLTGTMPLDNPGFGQLPWLFPARALPFPLPDFNTTTAPNYKNVTKRLLFDAL AIENLRNTIKANDTMMKQPSRVVVVMSLIWKVLTHISSAKNNGNSRDSSLVFVVNLRGKLSCTAPSLEHVVGNCVIPATANKEGDEARRKDDELNDFVKLVRNTIRDT CEAIGKAESVDDISSLAFNNLTKCIEKILHGDEMDFYSCSSWCGFPWYEADFGWGKPFWVSSVSFGHHGVTNLMDTKDGDGIQVTICLKENDMIEFERDPHILSSTS KLAFHSLG	440 aa
			>Sga_ scaffold10203_12.0_contig3_446_aa MSSSVSRLVSSVCKKIIKPYSPTPISLRCPKLSYLDQMVGGIYIPLALFYPKLSNTWSNKPNNVVSQHLEKSLSKVLTNYYPFAGKLNDNISIDCNDNGVEFFVTEINCP MSEIFNHPYFEKHNLVYPTEVINNQYTYEGSLAVFQLTHFNCGGIAISMCLSHKVGDGYTFGNFMNHWATIARNPLSSEIYPISPKFDGSFYFPPTKDEDSSNVSNNNI VPQREECVSKGFSISSSKLTALKARVINDSEVQNPSDTEVVSAFLYQRAMATKKLVNSDSIRPSLLHQAVNLRPPLPKHTMGNICSLFSILTKEEKEMDLARVVSKLRK EKEEVKQKYKNAKIEELLPITLEQHRKANDLLVNNSCYDLYRFSSLITFPSYEVDFGWGKPEKVISPISTSNPPIKNMFFLMADKNRDGVNLTCSMKKQDMLAFERDE ELLRFASPTS	446 aa
		Sch	>Sch_Scaffold3063050_432_aa MLKPSAPTPDNLRRLKLSLFDQLDVGAYVPILFNYLPNSTSSYDDDKLEKSLSETLTKFYPFAGRFRKDIDPFFIDCKDEGIEYVRTKVNADDLAQYLRGQAHNDIESS LIDLLPVMDRLPSSPLFGVQVNVFDNGGVTIGIQILHIVADAFTSVKFVNEWAYTTLTGTTPLDNPGFGQLPWLFPARALPFPLPDFNTTTAPNYKNVTKRFLFDALAIE NLRKTIKANDMMMKQPSRVVVLMSQIWKVLTHISSAKNNGNSRDSSLVFVVNLRGKLSCTAPSLEHVVGNCVIPAIANKEGDELNDFVKLVGNTIRDTCEAIGKAERV DDISSLAFNNLTKCIEKIMQGDEMDVYSSSSWCGFPWYDADFGWGKPFWVSGVSFGHHGVINLMDTKDGDGIQVTICLKENDMIEFERDPHILSSTSKLAFHSFG	432 aa
			>Sch_Scaffold3066370_442_aa MSSVSKLVSSVCKKIIKPYSPTPISLRCHKLSYLDQMVGGIYMPLALFYPNLSNTWSNKPNNVVSQHLEKSLSKVLTNYYPFAGKLSDNISIDCNDNGVEFFITKINCSM SEIFNHPYFEKHNLVYPSQVINNQYTYEGSLAVFQLTHFNCGGIAISMCLSHKVGDGYTFGNFMNHWATIARNPLSSEIYPISPKFDGSFYFPPTSSSNVSNNNIVPQR EECVSKGFSISSSKLNALKARVINESEVQNPSDTEVVSAFLYQRAMATKKLVSSSSIRPSLLHQAVNLRPPLPKHTMGNICSLFSILTKEEEEMDLARVVSKLRKEKEE VKQKYKNAKIEELLPITLEQHRKANDLLVNNSCCDLYRFSSLITFPSYDVDFGWGKPEKVISPISTSNPPIKNMFVLMADKNRDGVNLTCSMKKQDMLAFERDEELLQ FASPTS	442 aa
		SpiLA1589	>SpiLA1589_contig:unspecified:6737738:1:3270:1_440_aa MVKPSAPTPDNLRRLKLSLFDQLDIGAYVPILFNYLPNSTSSYDHDDKLEKSLSETLTKFYPFAGRFRKGIDPFSIDCNDEGIEYVRTKVNADDLAQYLRGQAHNDIES SLIDLLPVMHRLPSSPLFGVQVNVFNNGGVTIGIQILHMVSDAFTLVKFVNEWAHTTLTGTMPLDNPGFGQLPWLFPARALPFPLPDFNTTTAPNYKNVTKRFLFDAL AIENLRNTIKANDMMMKQPSRVVVVMSLIWKVLTHISSAKNNGNSRDSSLVFVVNLRGKLSCTAPSLEHVVGNCVIPAIANKEGDEARRKDDELNDFVKLVRNTIRDT CEAIGKAESVDDISSLAFNNLTKCIEKILHGDEMDFYSCSSWCGFPWYEADFGWGKPFWVSSVSFGHHGVTNLMDTKDGDGIQVTICLKENDMIEFERDPHILSSTS KLAFHSFG	440 aa
			>SpiLA1589_contig:unspecified:6764003:1:4383:1_446_aa MSSSVSRLVSSVCKKIIKPYSPTPISLRCPKLSYLDQMVGGIYIPLALFYPKLSNTWSNKPNNVVSQHLEKSLSKVLTNYYPFAGKLNDNISIDCNDNGVEFFVTEINCP	446 aa

			MSEIFNHPYFEKHNLVYPTEVINNQYTYEGSLAVFQLTHFNCGGIAISMCLSHKVGDGYTFGNFMNHWATIARNPLSSEIYPISPKFDGSFYFPPTKDEDSSNVSNNNI VPQREECVSKGFSISSSKLTALKARVINDSEVQNPSDTEVVSAFLYQRAMATKKLVNSDSIRPSLLHQAVNLRPPLPKHTMGNICSLFSILTKEEKEMDLARVVSKLRK EKEEVKQKYKNAKIEELLPITLEQHRKANDLLVNNSCYDLYRFSSLITFPSYEVDFGWGKPEKVISPISTSNPPIKNMFFLMADKNRDGVNLTCSMKKQDMLAFERDE ELLRFASPTS	
		SpiLA0480	>SpiLA0480_Scaffold3063050_440_aa MVKPSAPTPDNLRRLKLSLFDQLDIGAYVPILFNYLPNSTSSYDHDDKLEKSLSETLTKFYPFAGRFRKGIDPFSIDCNDEGIEYVRTKVNADDLAQYLRGQAHNDIES SLIDLLPVMHRLPSSPLFGVQVNVFNNGGVTIGIQILHMVSDAFTLVKFVNEWAHTTLTGTMPLDNPGFGQLPWLFPARALPFPLPDFNTTTAPNYKNVTKRFLFDAL AIENLRNTIKANDMMMKQPSRVVVVMSLIWKVLTHISSAKNNGNSRDSSLVFVVNLRGKLSCTAPSLEHVVGNCVIPAIANKEGDEARRKDDELNDFAKLVRNTIRDT CEAIGKAESVDDISSLAFNNLTKCIEKILHGDEMDFYSCSSWCGFPWYEADFGWGKPFWVSSVSFGHHGVTNLMDTKDGDGIQVTICLKENDMIEFERDPHILSSTS KLAFHSFG	440 a
			>SpiLA0480_Scaffold3066370_446_aa MSSSVSRLVSSVCKKIIKPYSPTPISLRCPKLSYLDQMVGGIYIPLALFYPKLSNTWSNKPNNVVSQHLEKSLSKVLTNYYPFAGKLNDNISIDCNDNGVEFFVTEINCP MSEIFNHPYFEKHNLVYPTEVINNQYTYEGSLAVFQLTHFNCGGIAISMCLSHKVGDGYTFGNFMNHWATIARNPLSSEIYPISPKFDGSFYFPPTKDEDSSNVSNNNI VPQREECVSKGFSISSSKLTALKARVINDSEVQNPSDTEVVSAFLYQRAMATKKLVNSDSIRPSLLHQAVNLRPPLPKHTMGNICSLFSILTKEEKEMDLARVVSKLRK EKEEVKQKYKNAKIEELLPITLEQHRKANDLLVNNSCYDLYRFSSLITFPSYEVDFGWGKPEKVISPISTSNPPIKNMFFLMADKNRDGVNLTCSMKKQDMLAFERDE ELLRFASPTS	446 aa
	AT3	*Sly*	>Solyc02g081760.1.1_XP_004232633.1 MAFALLSSPSLVSVCDKTFIKPSSLTPPTLRYHKLSYIDQFHSNMYIPLAFFYPKVQQREESTDNELSHIVHLLQTSLSKTLVSYYPYAGKLRDNAIVDCNDMGAEFLS VRINCTMSEILDHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLSHKIGDGTSVLNFVNDWSRMTYSPMTTTLAPKFVGDSVFSANNYSPIIAP QMLSNVSECVQKRIIFHKIKLDALRAKVAAESGVENPTRAEVVSAILFRCAIKAASSTTSSMVPSKFVHFLNVRSMMKCRPSAIGNILSIFSTTATKEEDIELPTLVHNLR KGVEKSYKKDQVEQNELILEVVESMRKGKKPFDEEYENVYSCSNVCRFPFYNVDFGWGKPERVGLPNGPFKNLFFLKDLKIGQGVDARVMLQKQHMSEFERDEEL LELIS	438 aa
			>Solyc11g069680.1.1_XP_004251404.1 MSSFSRLLSTISKKVVKPFSPTPSTQKIHKLSLLDQCMGNFYMPLVLFYPKHQLEQGPKQLSKLLETSFSKVLTYHQPWAGSLRDNATIHCDGTGAEFFEVEVNCPM NQIVHRPDLTFPPGLPWKNVPHVNDGGRLSVAQLSHFDCGGIAISVCMSHKVGDARSAFSFLKDWATLTREQSNDQLSCPSNSNDQLSCPSYYVQDSLMPSLPDG PLKFPVVVEPNGEESIEFEKRFFLSESNIRALKALIVDDPSSIVQNPTTTEVVSAIVYKCAAIAGANTSNGNNDSSSQMVFVSDLRKTIPPSIKSTSTIGNILTTFSTPTYN LEDLRLPKLVADIRKSKHELSTRDNFNENRWVSEMIEYANKINTGTEYELSYRRESSSHDVYRCSSVCNIPFQDLDFGWGRPTRASIASTPFNNMIYLMNTQDQNRG IEVFINLDQQQMSIFEQDKEFLQFASPVGDNNFHEDKEKLCCL	474 aa
			>Solyc02g081800.1.1_XP_004233767.1 MAIAPSQLVSPVTEKIIVKPSLPTPSPLKYHKLSFIDQSLSHLYIPLVFFYSKQQQEFDQLVANKLQNSLATTLSAYYPYAGRMRDSATIECNDRGIEFLNVRISCPMSE MMNNPHDYAEGNIFTKDLPWKNSFDGSLLVAQLSHFDCGGIAISTCLSHKVGDGGSVASFIYDWAKITRNPNQIARPKFISDTFFPTPNGPLIAPLIDSKLDKCVHKKF HFSASKLQGLRAKIAAEAGIKNPTRAEVVSALLFISATKAASKINNTSFRPSKLINYVDIRPMTTPPLSRNVIGNLLTVTSTTASHDEEMELPRLVREFRKEFEQVYKKDP VQHNSLVLKLLEIMESPYAIDEFDTYYCSNMCKFSGYSIDFGWGKPERVCAPMGPFKNFFILSADQNMDGVEAMVTLEEQHMLAFECDEELLEFASPISSF	431 aa
			>Solyc08g014490.1.1_XP_004244824.1 MASPALKILSRASKKLIKPSSPTPLTQKWHKFSLIEQAQTHTYVPFGFFYSNNQLGALSNQPSQTSKLLENSLSKNLVSYYPYAGHMKDNAVIDCNDKGVEFLNVHID APMSQVLNDKDCHVKDLIFPHGVAWENDSEYGLAVIQLTHFDCGGIAVSTCLSHKIGDACNGLQFLIDWAKLTRDPNAKITPPYYISDTIFPSPPTGPLDSPVVPSILD GCTQKRYVFSSSKVSELRSSIASVSQVKDPTPTEVLSALLFKCVAKAVTANSGSFVPSKLIQYADLRGMISPKLPPNSIGNVLSHFSTHISNEADMNLPQIVSLMREEK LLFRTRDNIKENAWALEILELAKGLPPKKKEFDEYTCSSVCKFPFYDVDFGWGKPMAATIATGPYNKLFNLMNYKDDGVEAFVVLDEQDMSVFERDEEFLEFASPYA NYF	436 aa
			>Solyc08g075180.1.1_XP_004246215.2 MANFVSDWASIAREANIIPSPTMTGSSIFPPCTNLPSTDIYTNTIVNVPIENIKKRYRFSNSKLEMLKSQVTSEAEVQNPSRVDVLSALIYKCAVTAARAQANSFKPSML TLAVNLRPILDPPLATRAIGNMVSFIKVETTSVDEITIAGVVRELRKAKDEFKKEDHVNANKLVALHSENLPISNEFETYRSHSMCNFPLNNLDFGWGKPNKVTIPPIGV GFCFILMDSPSGDGIEAIVAVPETYVTQFENNKELLQFATPIN	263 aa
			>Solyc08g075210.1.1_XP_004246214.1 MTASSFVSMAEKIIKPHSPTPFSVKRYNLCLMDEIMVPVYMPIVAFYPNPSKTPEQVSNILEDSLSKVLSSYYPFAGTLGSDNATFVDCNDRGAKSIQVRYDCPMSEIV NLPDTGPEYLPFAKGTPWSSTPEEQSLLVVQLSHFNCGGLGISARLSHKIADGCTLANFISDWASVARDDNANIPSPQLIGSSIFPPFTEMRIHTDTNVDYEFYNLPVC KKRYLFSNAKLEMLKTQVESETGVQNPTRIEVLSALIYKCAVTANSSSFRPSSLSLPVNLRPILNPPLETRTVGNIISFIKVETTSEDEMTIGRVVREIRKGKDELKQEGG VKKEKLVSLWSEWIHSIDLYRSSSVCNYPLNNLDFGWGKPNRVAIPVFGVANTCMFMDNLSGDGIEVIIALPEKDATQFENSKELLHFASPVTNL	424 aa
			>Solyc07g043670.1.1_XP_004243893.1 MAASQLALISKKIIKPSSPTPLIHRIQKLSIFDQLNPCSYMSYGLFFPKQCHPTLPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FDQKSTEAEDLVLPRDLPWTPSKENLVVAQVNHFNCGGIAIGVCVSHKVVDGSSMANFTHHWSTMARNPSAPIPSFQFVGGSHFPPVSSPIAEAILQSKTRGNNTCI SKKYLLSRSKINSLKAMIAAESGNKSSSITPSSVEAASAFVYKCIASNSTKPSIFTQSVNLRPIMKKWLPEEFQGNASFLFMAPEISDPADIKLHRLISELRKEKEMYWE TTNLMSTLLEKVKLLQNQLERDHDDEVDVYKCTSLSKFIFGQMDYGWGSPTRVCLGSVPINKKIFLTDSQTEDGIEVVVSLKQQQMSALETKSNLLEFASPL	431 aa
			>Solyc07g043700.1.1_XP_004243890.1 MVTPKSHIVSMSKKIIKPSSPTPSSLRHHNLSFLDQINSPLHNPLAFFYPKPKNSSYDINHISTLLQNSLANLLTSYYPFAGTYNDNIFIDCNDVGAEFFDVQLDIPMSEIL DHPYYNDDINLVYPQGCPWNIYDGTLVVAQLTHFDCGGIAVSVCISHKVADAYSVIKFITDWAYLTRDSSHAKPSVLFDGTSFFPPVTDTSTLPDFDAGNDRNCVTRM	429 aa

			FHFSSSGLDKLKTIAAAESGVENPSRVEVATALIHKHAMIASGSFKPSLLCHIMGLRPPLPLNSIGNACSFFLTSTQTEDEMELSNSVAVLRKSKDQLREKMKNATQS DIFFKVVEITKQGAELVEKVNKADVYKCSSLCNFGLYDMDFGWGKAIRVSSVSRAVKNQIFFMDSPTGNGMDVLISLDEKEMEIFQSDKVILEYASPVVKM	
			>Solyc07g043710.2.1_XP_004243889.2 MGSISRIVSMSRKIIKPSSATPPSHKRHNLSLLDCYANNEYASSVMFYPKPTIPSNNISQLLQKSLSKALTYYYPFAGMLKDNTYVDCNDRGAEFLNVRVDGRMSDVI NSCDNDRSGKNCVFPQGLCFGNTSDSFDGRLAMTQLTHFDCGGIAVSFCFSHKIVDGYSAGKFMSDWAAIAKDPNHHAITYPQFDGASFFPPGIHDAGTSEVNSLP EEGLVQQRFVTRRYLFSASKLNTLKAKIVDSGSGIVGNPSRIESVSALLYKSAAANRNNTSFRPSTFTLFANMRPPLPLNTIGNAPGYISTSIEEEVDMQLPRIVAELRK GKEKLRNRFNTVDPNKLVFESFELMKEVGQVYNREGFDIYRCSSLCNFPFYGIDFGWGTPQRVAFLIPPCNFFVLLDNQNRDGGVEALVTLEESEMTVFQQDQQIL QFARPI	436 aa
			>Solyc11g067350.1.1_XP_004251384.1 MAKSGAFRPTVLFHVMNLRPPIPFNTIGNATCYFSTRAMSIDKTTLPNYVGELQKAKQQIRYELKDMNTKELALHAIEKIKEIVNIANEDVFDIYFCTSLCTFGSHKIDFG WGSPLRVTQVKHPTKNKFMFLDDPSGEGINVLITLTEADMLLFQNNKELLEFASPVVESSLLGSTLSLNVELSDVKSKL	190 aa
			>Solyc11g067340.1.1_XP_004251383.1 MASSTILSRKIITPSPPTPSSHRHCNLSFRDQTANTLYLPIAALYSKPENHTITQISNILENSLSKILYFYYPFGGRIKDNKYVDCNDIGAEYFNVHINCQMSEILSNPYND AIEIVFPQNMAWGNSLSEERSSLLVVQLSHFDCGGVGISICLSHKVADGYSAFKFLGDWISMARDDHKLNFQPSPQFDGALFLPPIDNPPPMPNVVPDPQQCVSRM YNLSSSTLSKLKDSIVSTNPQIQNPSRIEVAMALIHKCGVDVSMSKSGVFRPTMLYQVMNLRPPIPLNTMGNATCLFSTIAMSIDKTTLPSYVGELQKAKQQLRHKLKQ MDTNQLASHAIEKLKEIVNIANEDVFDIYFCTSLCTFGSHKIDFGWGSPLRVTQVKHPTKNKFMFLDDPSGEGINVLITLTEADMLLFQNNKELLEFASPVVQSLE	433 aa
			>Solyc11g067330.1.1_XP_004251382.2 MASSTILSRKFIKPSPPTPSSHRHYNLSFRDQTANNLYLPIAALYSKPENHTITQISNILENSLSKILFFYYPFGGRIKDNKYVDCNDIGAEYFNVHINCQMSEILSNPYND AIEIVFPQNLAWGNSLSEERSSLLVVQLSHFDCGGVGISICLSHKVADGYSGCKFLSDWVSMARDDHKLNFQLSCQFDGASFFPPIDNPPPMPNVVPDPERCVSRM YNLSSSTLLKLKDIVVSTNPQIQNPSRIEVATALFHKCGVDVSMAKSGVFRRTVLFHVMNLRPPIPFNTIGNATCYFSTRAMSIDKTTLPNYVGELQKAKQQIRYELKD MNTKELALHAIEKIKEIVNIAKDDCFDMYFCTSLCTFGSRKIDFGWGSPLRVTHVKDPMKNKFIFMDDPSGEGINVLITLTEADMLLFESNKELLEFASPVVQSLE	433 aa
			>Solyc11g067270.1.1_XP_004251378.3 MASSTIISRKMIKLLSPTPSSLRCHKLSFMDHINFPLHSPYAFFYPKIPQNYSNKISQVLENSLSKVLSFYYPLAGKINNNYTYVDCNDTGAEYLNVRIDCPMSQILNHPY NDVVDVVFPQDLPWSSSSLTRSPLVVQLSHFDCGGVAVSACTSHTIFDGYCLSKFINDWASTARNMEFKPSPQFNASTFFPLPSETNLSSTLPATRPSQRHVSRMY NFSSSNLTRLKDIVTKESHVKNPTRVEVASALVHKCGVTMSMESSGMFKPTLMSHAMNLRPPIPLNTMGNATCIILTTAMTEDEVKLPNFVAKLQKDKQQLRDKLKD MKEDRMPLYTLELGKNAMNIIEKDTHDVYLCSGMTNTGLHKIDFGWGEPVRVTLATHPNKNNFIFMDEQSGDGLNVLITLTKDDMLKFQSNKELLEFASPVVESTK	430 aa
			>Solyc11g067290.1.1_XP_010313351.2 MASSTILSRKMIKLLSPTPSSLRHHKLSFMDCINLPQYSPFAFLYPKPKNHTKTQISQILENSLSKVLSSYYPFAGRIKDNNTYVDCNDIGVEYLNVRINHSMSDILNSRC NDVADIVYPKDLPWSSSVNRSPLVIQLSHFDCGGIGLGVCLSHKIVDGYCIAKFISDWANTARDMDFKPSIKFNASTFFPLIEGAPNIMSINSSPQSQRYVSRAYNFSS SNLKRLKRSITGVQNPTRVEVATSLIHKCGAIASMKNLGSFKPSLISQVINLRPLIPLDTMGNATCIYSIIATTENEIELPNYVAQMQNVKQQIRNELKNLDTDKIVPYTLE KVRGIVDIMEKDIFDIYLSTSVHNFGLYSKANFGWGKPIKVSNTKYPTKKSIMLFDDPSEEGIDAQITLTEDEMAIFQEDKELLEFASPMVQSTK	427 aa
			>Solyc05g039950.1.1_XP_010321585.1 MLDFSWITSPAATELEMIVLDWLTKALKLLDEFLQQIYKSGKGRLKDNTTVDCNDAGAEFIQVQIDCLISETLNWHNTAIEDLLFPQGLPWSNCASRGLVVVQLTYFNC GGIAISMCISHKIGDGCSGYNLFRDWSHITSHPNNFSIPSLHYVEQSVFPPPSSGPFLSPLFMSNKHDCVQRRYIFSNQKLLNLKNTVASESEVQNPTRTEVVSALIFK CAVRAAKANSGIFLPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKRDNVNDNMFVALLLELAKSKREYHDNGPNAYQITSLV KFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	395 aa
			>Solyc02g081740.1.1_XP_004232635.1 MAFALLSSPSLVSVCDKTFIKPFSLTPPTLRYHKLSYIDQFYSNLYIPLAFFYPKVQQREENELSHIAHLLQTSLSKTLVSYYPYAGKLRDNATIDCNDMGAEFLSVRIN CTMSEILDHPDASQAESIVFPKALPWANNYEGGNLLVAQVSKFDCGGIAISLCLAHKIGDGTSMLNFVNDWSRMTHSPMTTTLAPKFVGDSVFSSNNYSPIITPQMLS DVSECVQKRIIFPTAKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKAASSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFSTTATKEEDIELPALVRSLRKE VEEAYKKDHVEQNEFMLEVVESMRKGKKPYDDEYENVYSCSNLCRFPLYKVDFGLGKPERVSLPNGPFKNFFFLKDYKIGKGVDARVMLDKQHMSKFERDEELLD LIS	437 aa
			>Solyc02g081745.1_XP_004232634.1 MAFASLSSPSLVSVCDKTFIKPSSLTPPTLKYHKLSYIDQFYSNMYIPLAFFYPKVQQREESTDNELSQIAHLLQTSLSKTLVFYYPYAGKLRDNATIDCNDMGAEFLSV RINCTMFEILNHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLAHKIGDGTSALNFVNDWSRMTLSPMTTTLSPKFVGDSIFSSNKYSPIITPQM LSDVSECVQKRIIFPTTKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKATSSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFTTTATKEEDIELPTLVRSLR KGVEEAHKKDHVEQNEMMLEVVESMRKGKKPYDDDYENVYSCCNLCKFPLYKVDFGWGKPERVSLPNGPFKNFFFLNDYKIGEGVDARVMLDKQHMSEFERDE ELLDLIS	440 aa
		Spe	>Sopen11g027040_XP_015057957.1 MSEILSNPYNDAIEIVFPQNMAWSDSLSKERSSLVVVQLSHFDCGGVGVSLCVSHKIADGYSAFKFLGDWISMARDDHKLNFQPSPQFDGALFLPPIDNPPPMPNVV PDPQRCVSRMYNLSSSSLSKLKDIIVSTNSQIQNPSRIEVATALIHKCGVDVSMAKSGVFRPTMLYQVMNLRPLIPLNTMGNATCLFSTIAMTKDNVTLSNYVGELQKA KQQLRHELKHMDTNELASHAIEKLKEIVKIANEDVFDIYFCTSLCTFGSHKIDFGWGSPLRVTQVKHPTKNKFMLLDDPSGEGINVLITLTEADMLLFQNNKELLEFASP VVESSLLGSTLPLNVGLSDVK	347 aa
			>Sopen02g026400_XP_015064859.1 MAIAPSQLVSPVTEKIIVKPSLPTPSPLKYHKLSFIDQSLSHLYIPLVFFYSKQQQEFDQLVANKLQNSLATTLSAYYPYAGRMRDSATIECNDRGIEFLNVRINCPMSE MLNNPHDYAEGNIFMKDLPWKNSSDGSLLVAQLSHFDCGGIAISTCLSHKVGDGGSVASFIYDWAKVTRNPNQIARPKFISDTFFPTPNGPLIAPLIDSKLEKCVHKKF	431 aa

			HFSASKLQGLRAKIGAEAGIKNPTRAEVVSALLFISATKAASKINNTSFRPSKLINYVDIRPMTTPPLSRNVIGNLLTVTSTTASHDEEMELPRLVREFRKEFEQVYKKD PVQHNSLVLKLLEIMESPYAIDEFDTYYCSNMCKFSGYSIDFGWGKPERVCAPMGPFKNFFILSADQNMDGVEAMVTLEEQHMLAFECDEELLEYASPISSF	
			>Sopen02g026350_XP_015065374.1 MAFALLSSPSLVSVCDKTFIKPSSLTPPTLRYHKLSYIDQFYSNLYIPLAFFYPKVQQREESDNSHELCHIASLLQTSLSKTLVSYYPYAGKLRDNATIDCNDMGAEFLS VRINCTMSEILDHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISMCLAHKIGDGTSTLNFVNDWSRMTHSPTTTTLSPKFVGDSVFSSNNYSPIITP QMLSDVSECVQKRIIFPTAKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKAASSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFSTTATKEEDIELPELVR SLRKGVEEAYKKDHVEQNEFMLEVVESMRKGKKPYDDDDQNVYSCSNLCKFPLYKVDFGWGKPERVSLPNGPFKNFFFLKDYKIGEGVDARVMLDKQHMSEFER DEELLDLIS	441 aa
			>Sopen06g030010_XP_015078011.1 MISKKIIKPFTPTPSTQRWHKLSLLDQCLTSLYVPLVFFYTKNQVNAIPNGPKTLSNLLSNSLSKVLSYYYPWAGTLKDNATIECDDHGAEFLEVQINSPMDKVVNHPD SNVKDLTFPQGVPWANGVDRALIVAQLSHFDCGGIALSVCLSHKIADGSSAHCFLRDWAALTRNSNTDPSPYFVEDSIVPSPIGPLVSPVFGSDTDKCVQKRFVFSS TKLSALKSSIGVQNVTSNEAVNALIYKSAASSATVVNSGSLKRSQLVQFFDLREITSPPLPPNSIGNLVSIISSPIYEDKEELKLPKLVTDIKKSKNFLSARNNVEENEFAI EMLDTYRTGEEPFSKRKCDLYISSSLCKFPFLQDLDFGFGKPIRSSFAKGPLNKVIYLMRTYDGGIEAFVNLNEQEMSVFEHDKQLLEFATPINEDFCNKEKQ	431 aa
			>Sopen05g024660_XP_015075888.1 MESVAHPLVSIISEKLIKPSSPTCPTKRWHKLSLIDQAFSNTYIPFSLFYTKDNAISNTSQISQLLEESLSKILSTYYPYAGRLKDNTTIDCNDAGAEFIQVQIDCLISETLN WHNTAIEDLLFPQGLPWSNCASRGLIVVQLTYFNCGGIAISMCISHKIGDGCSGYNFFRDWSHITSHPNNFSIPSLHYVEQSVFPPPSSGPFLSPLFMSNKHDCVQRR YIFSNQKLLNLKNTVAAESEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNILTICPTSIITNNEESITISKLVSEMRKSKELVYKRDN VNDNMFVALLLELAKSKQEYHENGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAFVTLTEQDMSVFQHDTELLEFASLVPSC	464 aa
			>Sopen07g023230_XP_015083111.1 MAASQLALISKKIIKPSSPTPLIHRIQKLSIFDQLNPSSYMSYGLFFPKQGNPALPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FYQNSTEAEDLVFPRDLPWTPSKENLVVAQLNHFNCGGIAIGVCVSHKVVDGSSMANFTHHWSTMARNPNAPIPSFQFVGGSHFPPVSSPIAEAILKSKTGGNNSCI SKKYLLSRSKINSLKAMIAAESGNKSSSINPSSVEAASAFVYKCIASNSTKPSIFTQSVNLRPIMKKWLPEEFQGNASFLFMAPEISDPADIKLHRLISELRKEKEMYWE TKNLMSTLLEKVKLLQNQLERDHDDEVDVYKCTSLSKFSFRHMDYGWGSPTRVCLGSVPINKKIFLMDSQTEDGIEVLVSLKQQQISALETKSNLLEFASPL	431 aa
			>Sopen07g023280_XP_015081727.1 MVTPKSHIVSMSKKIIKPSSPTPSSLRHHNLSFLDQINSPLHNPLAFFYPKPENSSYDINHISTLLQNSLANLLTSYYPFAGTYNDNIFIDCNDVGAEFFDVQLDIPISEILD HPYYNDDVNLVYPQGCPWNIYDGTLVVAQLTHFDCGGIAVSVCISHKVADAYSVIKFITDWANLTRDSSHAKPSVLFDGTSFFPPVTDTSTLPDFDAGNDRNCVTRM FHFSSSGLDKLKTIAAAESGVENPSRVEVATALIHKHAMIASGSFKPSLLCHIMGLRPPLPLNSIGNACSFFLTSTQTEDEMELSNSVAVLRKSKDQLREKLKNATQSD IFFKVVEITKQGAELVEKVNKADVYKCSSLCNFGLYDMDFGWGKAIRVSSVSRGVKNQIFFMDSPTGNGMDVLITLDEEEMEIFQSDKVILEYASPVVKM	429 aa
			>Sopen07g023290_XP_015081753.1 MGSISRIVSMTKRMIKPSSPTLPSLKRHNLSLLDCNANNEYLPIVFFYPKPTVPVNNISQILQQSFSKALKYYYPFAGVLKDNTYVDCNDRGAEFLNVRVDCRMSDVIN SCDDSRSGEKYVFPQGLAYGKSNFFDGRLVMAQLTHFDCGGIAVSFCFSHKIADGYSSCNFMNDWAAIARDPNSAKPSPRFDGASFFPPIRNAGTSDVNNLPQEG AVQQRYVTRRYLFSASKLNTLKAKIVDSGSGIVRNPSRVESVSALLYKSAAANRNNTSFRPSTFTLFANIRPPLPLNTIGNAPGYISTSIEEEVDMQLHRIVAEIRKGKE KLRNRFNTVDTNKLVFESFELMKEVGQVFNKEGFDIYRCSSLCNFPFYNVDFGWGRPNRVSLLIPPCNIICLLDSQNLDGGVEAIVTLQESDMTFFQQDKQLLQFATP I	433 aa
			>Sopen08g023810_XP_015084374.1 MAAASRLVSFAEKIIKPNRATPLSLGRYNLSINDQIMVPFYLSIAAFYPNPSKTPEQVSNILQNSLSKVLSSYYPFAGTLRDNTFVDCNDRGAKFMNVRYDCPMSEIAN LPDTGPEYLPFAKGIHDSLLLGDEDLLVVQLSHFNCGGLAIGTSISHKIADGCTTSNFISDWASIARDDEEANIIPSPQMIGSSIFPPSTNLPSTDIYTNTIVNVPIENIKRR YLFSNSKLEMLKSQVTSETGLQNPSRVDVLSALIYKCAVTAARAQANSFKPSMLTLAVNLRPILDPPVATRAIGNMVSFIKVETTSVDEITIARVVRELRKAKDEFKKED HVNANKLVALHSENLPISNEFETYRSHSMCNFPLNNLDFGWGKPNKVTIPLIGVGFCFFLLDSPSGDGIEAIVAVPETYVTQFENNKELLQFATPMN	429 aa
			>Sopen08g005480_XP_015085868.1 MKDNAVIDCNDKGVEFLNVHIDAPMSQVLNDKDCHVKDLIFPHGVAWENDSEYGLAVIQLTHFDCGGIAVSTCLSHKIGDACNGLQFSIDWAKLARDPNAKITPPYYI SDTIFPSPPSGPLDSPVVPSILDGCTQKRYVFSSSKVSELRSSIASVSQVKDPTPTEVLSALLFKCVAKAVTANSGSFVPSKLIQYADLRGMISPKLPPNSIGNVLSHFS THISNEADMNLPQIVSLMREEKLLFRTRDNIKENAWALEILELAKGLPPKKKEFDEYTCSSVCKFPFYDVDFGWGKPMAATIATGPYNKLFNLMNYKDDGIEAFVVLN EQDMSVFERDEEFLEFASPYANYF	350 aa
			>Sopen08g023820_XP_015055409.1 MTASSFVSMAEKIIKPHSPTPFSLKRYNLCLTDEIMVPVYMPIVAFYPNPSKTPEQVSNLLQNSLSKLLSSYYPFAGTLGSDNASFVDCNDRGAKFIQVRYDCPMSEIV NLPDTGPEYLPFAKGTPWSSTPDEQSLLLVQLSHFNCGGLAVSVRLSHKIADGCTLANFISDWASIARDDNANIPSPQLIGSSIFPPFTEMPSTGIHTDTNVDYEFYNL PVCKKRYLFSNSKLEMLKTQVESETGVQNPTRIEVLSALIYKCAVTAARANSSSFKPSSLSLPVNLRPMLNPPLETRTIGNIISFIKVDTTSEDEMTMGRVAREIRKGKD ELKQEGDVKKEKLVSLWSEWIHSIELYRSSSVCNYPLNNLDFGWGKPNRVTIPVFGVANTCMFMDNLSGDGIEVIIVLPEKDVTQFENSKELLQFASPVTNL	430 aa
			>Sopen11g027030_XP_015058038.1 MASSTILSRKIIKPSPSIPSSHRHYNLSFRDQTANNLYLPIAALYSKPENHTITQISNILENSLSKLLFFYYPFGGRIKDNKYVDCNDIGAEYFNVHINCQMSEILSNPYND AIEIVFPQNMAWGNSLSEERSSLLVVQLSHFDCGGVGISICLSHKVADGYSGCKFLSDWVSMARDDHKLNFQLSCQFDGPSFFPPIDNPPPMPNVVPDPQRCVSR MYNLSSATLLKLKDVVVSTNPQILNPSRIEVATALFHKCGVDVSMAKSGVFRPTVLFHVMNLRPPIPFNTIGNATCLFSTRAMSIDSITLPNYVGELQKAKQQLRYGLK DMNTNELALHAIKKIKEIVNIAKEYCFDMYFCSSLCTFGSSKIDFGWGSPLRVTHVKDPMKNKFVFMDDPSGEGINVLITLTEADMLLFESNKELLEFASPVVQSLE	433 aa
			>Sopen11g026960_XP_015058409.1 MSQIINDPYNDAVGVVFPQDLPWSSSWNRSPLVVQLSHFDCGGIAVSACTSHTIFDGHSLSKFINDWASTARNMDFKPSPQFNASTFFPLPSETNLSSTLPTKHPSK	326 aa

			RHVSRMYNFSSSNLTRLKDMVTKESHVKNPTRIEVASALVHKCGVTMSMEKSGMFKPTLMTHAMNLRPPIPLNTMGNAVCIILTTTVTEDEVKLPNFVAKLQKDKQQ LRDKLKDMKKDMMPLYTLELGKNAMNIIEKDTHDVYVCSGMTNTGLHKIDFGWGEPVRVTLATSNKNNFIFMDEQSGDGLNVLITLTKDYMLKFQSNKELLEFASPV VESTK	
			>Sopen12g002290_XP_015061012.1 MSASRLVSLSRKIIKPSSPTPLSHRIHKLSLMDQMGTHSYMAALLFYPKQNTTTSMPEPTKISQVLEKSLSKVLTSYYPFAGQVRDNSFVECNDIGADLSQVRIDCPM SSIFDHPRTYIDNLVLPFDPWFPSTDSLVAAKLCHFECGGVALGVCLSHKVSDGYSLGKFLKDWSMVARDSEAKLSLLFNGSSIFKPSNSSSFQVVADPPLYKNESK RFHFTASNLKSLKSLISSSADSATQICPTTVEAITAFIYRCVSTPQSLLIQAVDQRGTSNDALVPADLTGNAILPFVVSATNKEEMNLERLVSELRKGKEKIQDMLKYIES EEFLCSMVSDIARELNERTSNNDIPMYRFSSLRRFPSNDINFGWGRPRQVDFSTYPMNMFILMDNQNGDGVEVIASLQDGELSALERNDEFLQFASPCLGF	427 aa
		Sga	>Sga_Sopen12g002290_XP_015061012.1_scaffold75447_13.0_contig2_426_aa MSASRLVSLSRKIIKPSSPTPLSHRIHKLSLMDQMGTHSYMAALIFYPKQNTTTSMPEPTKISRVLEKSLSKVLTSYYPFAGQVRDNSFVECNDIGADLSQVRIDCPMS SIFDHPRTYIDNLVLPFDPWFPSTDSLVAAKLCHFECGGVALGVCLSHKVSDGYSLGKFLKDWSMVARDSEAKLSLLFNGSSIFKPSNSSSFQVVADPPLYKNESKR FHFSASNLKSLKSLISSADSATQICPTTVEAITAFIYRCVSTPQSLLIQAVDQRGTSNDALVPADLTGNAILPFVVSATNKEEMNLERLVSELRKGKEKIQDMLKYIESEE FLCSKVSDIARELNERTSNNDIPMYRFSSLRRFPSNDINFGWGRPRQVDISTFPINMFILMDNQNGDGVEVIASLQDGELSALERNDDFLQFASPCLGF	426 aa
			>Sga_Solyc11g067270_XP_004251378.3_scaffold95263_13.0_contig6_356_aa XGKINNNYTYVDCNDTGAEYLNVRIDCPMSQILNHPYNDVVDVVFPQDLPWSSSSLTRSPLVVQLSHFDCGGVAVSACTSHTIFDGYCLSKFMNDWASTARNMDFK PSPQFNASTFFPLPSETNLSSTLPATRPSQRHVSRMYNFSSSNLTRLKDIVTKESHVKNPTRVEVASALVHKCGVTMSMESSGMFKPTLMSHAMNLRPPIPLNTMG NATCIILTTAMTEDEVKLPNFVAKLQKDKQQLRDKLKDMKEDRMPLYTLELGKNAMNIIEKDTHDVYLCSGMTNTGLHKIDFGWGEPVRVTLATHPNKNNFIFMDEQS GDGLNVLITLTKDDMLKFQSNKELLEFASPVVESTK	356 aa
			>Sga_Solyc11g067330_XP_004251382.2_scaffold48551_16.3_contig2_276_aa VADGYSAFKFLGDWISMARDDHKLNFQPSPQFDGALFLPPIDNPPPMPNVVPDPQQCVSRMYNLSSSTLSKLKDSIVSTNPQIQNPSRIEVATALIHKCGVDVSMAK SGAFRPTVLFHVMNLRPPIPFNTIGNATCYFSTRAMSIDKTTLPNYVGELQKAKQQIRYELKDMNTKELALHAIEKIKEIVNIAKDDCFDMYFCTSLCTFGSRKIDFGWG SPLRVTHVKDPMKNKFIFMDDPSGEGINVLITLTEDDMLLFESNKELLEFASPVVQSLE	276 aa
			>Sga_scaffold1766_10.6_contig2_419_aa MGSISRIVSMSKKIIKPSSATPPSHKRHNLSLLDCYANNEYASSVMFYPKPTIPSNNISQLLQKSLSKALTYYYPFAGMLKDNTYVDCNDRGAEFLNVRVDGRMSDCR LCFGNTSDSFDGRLAMTQLTHFDCGGIAVSFCFSHKIVDGYSAGKFMSDWAAIAKDPNHHAITYPQFDGASFFPPGIHDAGTSEVNSLPEEGLVQQRFVTRRYLFSA SKLNTLKAKIVDSGSGIVGNPSRIESVSALLYKSAAANRNNTSFRPSTFTLFANMRPPLPLNTIGNAPGYISTSIEEEVDMQLPRIVAELRKGKEKLRNRFNTVDPNKLV FESFELMKEVGQVYNREGFDIYRCSSLCNFPFYGIDFGWGTPQRVAFLIPPCNFFVLLDNQNRDGGVEALVTLEESEMTVFQQDQQILQFARPI	419 aa
			>Sga_scaffold1766_10.6_contig6_429_aa MVTPKSHIVSMSKKIIKPSSPTPSSLRHHNLSFLDQINSPLHNPLAFFYPKPKNSSYDINHISTLLQNSLANLLTSYYPFAGTYNDNIFIDCNDVGAEFFDVQLDIPMSEIL DHPYYNDDINLVYPQGCPWNIYDGTLVVAQLTHFDCGGIAVSVCISHKVADAYSVIKFITDWAYLTRDSSHAKPSVLFDGTSFFPPVTDTSTLPDFDAGNDRNCVTRM FHFSSSGLDKLKTIAAAESGVENPSRVEVATALIHKHAMIASGSFKPSLLCHIMGLRPPLPLNSIGNACSFFLTSTQTEDEMELSNSVAVLRKSKDQLREKMKNASQS DIFFKVVEITKQGAELVEKVNKADVYKCSSLCNFGLYDMDFGWGKAIRVSSVSRAVKNQIFFMDSPTGNGMDVLISLDEKEMEIFQSDKVILEYASPVVKM	429 aa
			>Sga_scaffold36606_13.5_contig3_407_aa MAASQLALISKKIIKPSSPTPLIHSIQKLSIFDQLNPCSYMSYGLFFPKQCHPTLPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FDQKSTEAEDLVLPRDLPWTPSKENLVVAQLNHFNCGGIAIGVCVSHKVVDGSSMANFTHHWSTVARNPSAPIPSFQFVGGSHFPPVSSPIAEAILKSKTRGNNTCI SKKYLLSRSKINSLKAMIAAESGNKSSSINPSSVEAASAFVYKCIASNSTKPSIFTQSVNLRPIMKKWLPEEFQGNASFLFMAPEISDPADIKLHRLINELRKEKEMYWE TTNLMSTLLEKVKLLQNQLERDHDNEVDVYKCTSLSKFIFGQMDYGWGSPRRVCLGSVPINKKIFLTDSQTEDGIEVV	407 aa
			>Sga_C9792443_12.0_421_aa MTASSLAEKIIKPHSPTPFSVKRYNLCLMDEIMVPVYMPIVAFYPNPSKTPEQVSNILEDSLSKVLSSYYPFAGTLGSDNATFVDCNDRGAKFIQVRYDCPMSEIVNLP DTGPEYLPFAKGTPWSSTPEEQSLLVVQLSHFNCGGLGVSVRLSHKIADGCTLANFISDWASVARDDNANIPSPQLIGSSIFPPFTEMRIHTDTNVDYEFYNLPVCKK RYLFSNAKLEMLKTQVESETGVQNPTRIEVLSALIYKCAVTANSSSFRPSSLSLPVNLRPILNPPLETRTVGNIISFIKVETTSEDEMTIGRVVREIRKGKDELKQEGGVK KEKLVSLWSEWIHSIELYRSSSVCNYPLNNLDFGWGKPNRVAIPVFGVANTCMFMDNLSGDGIEVIIALPEKDATQFENSKELLHFASPVTNL	421 aa
			>Sga_C9732333_11.0_391_aa MAAASRLVSFAEKIIKPHRATPLSLGRYNLSINDQIMVPFYQSIAAFYPNPSKTPEQGSLMNVRYDCPMSEIAKLPDTGPEYLPFAKGIHNSLLLGDEDLLVVQLSHFN CGGLAIGTSISHKIADGCTMANFVSDWASIAREANIIPSPTMIGSSIFPPCTNLPSTDIYTNTIVNVPIENIKKRYRFSNSKLEMLKSQVTSEAEVQNPSRVDVLSALIYKC AVTAARAQANSFKPSMLTLAVNLRPILDPPLATRAIGNMVSFIKVETTSVDEITIAGVVRELRKAKDEFKKEDHVNANKLVALHSENLPISNEFETYRSHSMCNFPLNNL DFGWGKPNKVTIPPIGVGFCFILMDSPSGDGIEAIVAVPETYVTQFENNKELLQFATPIN	391 aa
			>Sga_scaffold75298_12.0_contig2_436_aa MASPALKILSRASKKLIKPSSPTPLTQKWHKFSLIEQAQTHTYVPFGFFYSNNQLGALSNQPSQTSKLLENSLSKNLVSYYPYAGHMKDNAVIDCNDKGVEFLNVHID APMSQVLNDKDCHVKDLIFPHGVAWENDSEYGLAVIQLTHFDCGGIAVSTCLSHKIGDACNGLQFLIDWAKLTRDPNAKITPPYYISDTIFPSPPTGPLDSPVVPSILD GCTQKRYVFSSSKVSELRSSIASVSQVKDPTPTEVLSALLFKCVAKAVTENSGSFVPSKLIQYADLRGMISPKLPPNSIGNVLSHFSTHISNEADMNLPQIVSLMREEK LLFRTRDNIKENAWALEILELAKGLPPKKKEFDEYTCSSVCKFPFYDVDFGWGKPMAATIATGPYNKLFNLMNYKDDGVEAFVVLDEQDMSVFERDEEFLEFASPYA NYF	436 aa
			>Sga_scaffold102228_12.4_contig3_348_aa MRDSATIECNDRGIEFLNVRISCPMSEMLNNPHDYAEGNIFTKDLPWKNSFDGSLLVAQLSHFDCGGIAISTCLSHKVGDGGSVASFIYDWAKITRNPNQIARPKFISD TFFPTPNGPLIAPLIDSKLDKCVHKKFHFSASKLQGLRAKIAAEAGIKNPTRAEVVSALLFISATKAASKINNTSFRPSKLINYVDIRPMTTPPLSRNVIGNLLTVTSTTAS	348 aa

			HDEEMELPRLVREFRKEFEQVYKKDPVQHNSLVLKLLEIMESPYAIDEFDTYYCSNMCKFSGYSIDFGWGKPERVCAPMGPFKNFFILSADQNMDGVEAMVTLEEQ HMLAFECDEELLEFASPISSF	
			>Sga_C9690433_16.0_474_aa MSSFSRLLSTISKKVVKPFSPTPSTQKIHKLSLLDQCMGNFYMPLVLFYPKHQLEQGPKQLSKLLETSFSKVLTYHQPWAGSLRDNATIHCDGTGAEFFEVEVNCPM NQIVHRPDLTFPPELPWKNVPHVNDGGRLSVAQLSHFDCGGIAISVCMSHKVGDARSAFSFLKDWATLTREQSNDQLSCPSNSNDQLSCPSYYVQDLLMPSLPDG PLKFPVVVEPNGEESIEFEKRFFLSESNIRALKALIVDDPSSIVQNPTTTEVVSAIVYKCAAIAGANASNGNNDSSSQMVFVSDLRKTIPPSIKSTSTIGNILTTFSTPMYD LEDLRLPKLVADIRKSKHELSTRDNFNENRWVSEMIEYANKINTGTGYELSYRRESSSHDVYRCSSVCNIPFQDLDFGWGRPTRASIASTPFNNMIYLMNTQDQNRG IEVFINLDQQQMSIFEQDKEFLQFASPVGDNNFHEDKEKLCCL	474 aa
			>Sga_scaffold65521__7.7_contig2_396_aa MAFASLSSPSLVSICDKTFIKPSSLTPPTLKYHKLSYIDQFYSNMYIPLAFFYPKVQQRVENELSHIAHLLQTSLSKTLVSYYPYAGKLRDNATIDCNDMGAEFLSVRIN CTMSEILDHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLSHKIGDGTSVLNFVNDWSRMTYSPMTTTLAPKFVGDSVFSANNYSPIIAPQMLS NVSECVQKRIIFHKIKLDALRAKVAAESGVENPTRAEVVSAILFRCAIKTASSTTTSMRPSKLVHFLNVRRLMKCRLPQSAIGNILSSFSTTATKEEDIELPTLVRNLRKG VEEAYKKDHVEQNEYILEVVESMRKGKKPFDDEYKDVYFCSNLCKFPLYKVDFGWGKLRESVYQMVL	396 aa
			>Sga_scaffold65521__7.7_contig6_440_aa MAFASLSSPSLVSICDKTFIKPSSLTPPTLKYHKLSYIDQFYSNMYIPLAFFYPKVQQREESTGNELSQIAHLLQTSLSKTLVFYYPYAGKLRDNATIDCNDMGAEFLSV RINCTMSEILNHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLAHKIGDGTSALNFVNDWSRMTLSPMTTTLSPKFVGDSVFSSNKYSPIITPQ MLSDVSECVQKRIIFPTTKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKATSSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFSTTATKEEDIELPTLVRSL RKGVEEAHKKDHVEQNEMMLEVVESIRKGKKPYDDDYENVYSCCNLCKFPLYKVDFGWGKPERVSLPNGPFKNFFFLNDYKIGEGVDARVMLDKQHMSKFERDE ELLDLIS	440 aa
			>Sga_scaffold61734_12.4_contig8_249_aa MTTTLAPKFVGDSVFSANNYSPIIAPQMLSNVSECVQKRIIFPTTKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKAASSTTTSMRLSKFVHLLNVRSMLKSRLPQ STIGNILSSFSTTATKEEDIELPALVRSLRKGVEEAYKKDHVEQNEFMLEVVESMRKGKKPYDDEYENVYSCSNLCRFPLYKVDFGLGKPERVSLPNGPFKNFFFLKD YKIGKGVDARVMLDKQHMSKFERDEELLDLIS	249 aa
			>Sga_C9830397_12.0_200_aa MIVSKEEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKRDNVNDNMFVALLLE LAKSKREYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	200 aa
			>Sga_C9708165_13.0_427_aa MASSTILSRKMIKLLSPTPSSLRHHKLSFMDCINLPQYSPFAFLYPKPKNHTKTQISQILENSLSKVLSSYYPFAGRIKDNNTYVDCNDIGVEYLNVRINHSMSDILNSPC NDVADIVYPKDLPWSSSVNRSPLVIQLSHFDCGGIGLGVCLSHKIVDGYCIAKFISDWANTARDMDFKPSIKFNASTLFPLIEGAPNIMSINSSPQSQRYVSRAYNFSS SNLKRLKRSITGVQNPTRVEVATSLIHKCGAIASMKNLGSFKPSLISQVINLRPLIPLDTMGNATCIYSIIATTENEIELPNYVAQMQKVKQQIRNELKNLDTDKIVPYTLE KVRGIVDMMEKDIYDIYLSTSVHNFGLYSKANFGWGKPIKVSNTKYPTKKSFMLFDDPSEEGIDAQITLTEDEMAIFQEDKELLEFASPMVQSTK	427 aa
			>Sga_scaffold88985_12.1_contig2_251_aa XQPYTNSDHVVFPVEQPYAHMNEGNLATTQVGDGCTTSNFFNDWGILTRDINATLSLARESKVQNPTRVEVVSALLYKCALVARGVNDSGSFKPSSLFQVANMRH RLNPPLSYDTCGNILSGYFVETDNEKDVNCSKMVGEMKKGKLNLHPKESALVKSIKKGKTPFYSNDEVDNYFCSSLIEFPLYKVDFGWGRPIRVGMGAGPFDKFFIL LDNQSGDGVEVIVMLDEQNMAMFERDLELLEFASPITNL	251 aa
			>Sga_C9830397_12.0_contig6_434_aa MESVAHPLVSIISEKLIKPSSPTCPTKRWHKLSLIDQAFSNSYIPFSLFYTKDNAISNTSQISQLLEESLSKILSTYYPYAGRLKDNTTVDCNDAGAEFIQVQIDCLISETLN WHNTAIEDLLFPQGLPWSNCASRGLVVVQLTYFNCGGIAISMCISHKIGDGCSGYNLFRDWSHITSHPNNFSIPSLHYVEQSVFPPPSSGPFLSPLFMSNKHDCVQR RYIFSNQKLLNLKNTVASESEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKR DNVNDNMFVALLLELAKSKREYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	434 aa
			>Sga_scaffold104954_12.6_contig3_157_aa VSPVLGSDTDKCVQKRFFFSSTKLSALKSSVGVQNVTSNEAANALIYKCAASSAAVVNSGSFKRSQLVQFFDLREITSPNSIGNLISIFSSPIYEDKEELKLPNLVTDVK NSKNYLSATDNIVEENEFAIEMFDAYRSGEVPFYKRKCDLYISSSLX	157 aa
		Spr	>Spr_a249376_207_aa KLLNLKNTVAAESEVQSPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSILTNNEESMTISKLVTEMRKSKELVYKRDNVNDN MFVALLLELAKSKQEYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAFVTLTEQDMSVFQYDTELLEFASLVPSC	207 aa
		Sch	>Sch_Scaffold3065296_312_aa MSASRLVSLSRKIIKPSSPTPLSHRIHKLSLMDQMGTHSYMAALLFYPKQNTTTSMPEPTKISRVLEKSLSKVLTSYYPFAGQVRDNSFVECNDIGADLSQVRIDCPM SSIFDHPRTYIDNLVLPFDPWFPSTDSLVAAKLCHFECGGVALGVCLSHKVSDGYSLGKFLKDWSMVARDSEAKLSLLFNGSSIFKPSNSSSFQVVADPPLYKNESK RFHFSASNLKSLKSLISSADSATQICPTTVEAITAFIYRCVSTPQSLLIQAVDQRGTSNDALVPADLTGNAILPFVVSATNKEEMNLERLVSELRKX	312 aa
			>Sch_scaffold1315_356_aa XGKINNNYTYVDCSDTGAEYLNVRINCPMSQILNHPYNDVVDVVFPQDLPWSSSSLHRCPLVVQLSHFDCGGVAVSACTSHTIFDGYSLSKFINDWASTARNMDFK PSPQFNASTFFPLPSETNLSSTLPTTRPSQRHVSRMYNFSSSNLTRLKDIVTKESHVKNPTRIEVASALVHKCGVSMSMEKSGMFKPTLMNHTMNLRPPIPLNTMGN ATSIILTTTMTEDEVKLPNFVAKLHKNKQQLRDKLKDMKEDMMPLYTIELGKNAMNIIDKDTHDVYLCSSMTNTGLHKIDFGWGEPVRVTLATHPNKNTFIFMDEQSG DGLNVLITMTKDDMLKFQSNKELLEFASPVVESTK	356 aa
			>Sch_scaffold28625_356_aa	356 aa

			MLKDNTYVDCNDRGAEFLNVRVDGRMSDVINSCDNDRSGKNCVFPQGLCFGNTSDSFDGRLAMTQLTHFDCGGIAVSFCFSHKIVDGYSAGKFMSDWAAIAKDPN HAITYPQFDGASFFPPIHDAGASEVNNLPEEGLVQQRFVTRRYLFSASKLNTLKAKIVDSGSGIVRNPSRIESVSALLYKSAAANKNNTSFRPSTFTLFANMRPPLPLN TIGNAPGYISTSIEEEVDMQLPRIVAELRKGKEKLRNRFNTVDPNKLVFESFELMKEVGQVYNREGFDIYRCSSLCNFPFYDIDFGWGTPQRVAFLIPPCNFFVLVDN QNRDGGVEALVTLEESEMTVFQQDQQILQFAHPI	
			>Sch_scaffold5092_429_aa MVTPESHIVSMSKKIIKPSSPTPSSLRHHNLSFLDQINSPVHNPLAFFYPKPKNSSYDINHISTLLQNSLANLLTSYYPFAGTYNDNIFIDCNDVGAEFFDVQLDIPISEIL DHPYYNDDINLVYPQGCPWNIYDGTLVVAQLTHFDCGGIAVSVCISHKVADAYSVIKFITDWAYLTRDSSHAKPSVLFDGTSFFPPVTDTSTLPDFDAGNDRNCVTRM FHFSSSGLDKLKTIAAAESGVENPSRVEVATALIHKHAMIASGSFKPSLLCHIMGLRPPLPLNSIGNACSFFVTSTQTEDEMELSNSVAVLRKSKDQLREKMKNATQS DIFFKVVEITKQGAKLVENVNKADVYKCSSLCNFGLYDMDFGWGKAIRVSSVSRGVKNQIFFMDSPTGIGMDVLITLDEKEMEIFQSDKVILEYASPVVKM	429 aa
			>Sch_scaffold5170_283_aa MAASQLALISKKIIKPSSPTPLIHRIQKLSIFDQLNPCSYMSYGLFFPKQCHPTLPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FDQKSTEAEDLVLPRDLPWTPSKENLVVAQLNHFNCGGIAIVNLRPIMKKWLPEEFQGNASFLLMAPEISDPADIKLHRLISELRKEKEMYWETKNLMSTLLEKVKLLQ NQLERDHEDEVDVYKCTSLSKFIFPHMDYGWGSPTRVCLGSVPINRKIFLMDSQTEDGIEVV	283 aa
			>Sch_scaffold6055_430_aa MAASSCVSMAEKIIKPHSPTPSSLKRYNLCLTDEIMVPVYMPIVALYPFSSKTPQQVSNILENSLSKLLSSYYPFAGTLGPDNATFVDCNDRGAKFIQVRYDCTMSEIV NLPDTGPEYLPFAKGTPWSSTPDEQSLLLVQLSHFNCGGLAISVRLSHKIADGCTLANFISDWASIARDDNANIPSPQLIGSSIFPPFTETPSTGIHTDTNVDYEFYNLP VSKKRYLFSNSKLEMLKTQVESETGVQNPTRIEVLSALIYKCAVTAARANSSSYKPSSLSLPVNLRPILNPPLETRTIGNIISFIKVDTMSEDEMTIGRVVREIRKGKDEL KQEGDVKKEKLVSLWNEWIHSIELYRSSSVCNYPLNNLDFGWGKPNRVTIPVFGVANTCMFMDNLSGDGIEVIIVLPEKDVTQFENSKELLQFASPVTNL	430 aa
			>Sch_scaffold6055_377_aa MAASRLVSFAEKIIKPNCPTPLSLGRYNLSINDQIMFPIYMPIAAFYPNPSKTPQQVSNILQNSLSKVLSSYYPFAGTLRHNTFVDCNDRGAKFMNVRYDCPMSQVVN LPDTGPEYLPFPKGVPWGRTLDEESLLVVQVSHFNCGGLAISASLSHKIADGCTLANFISDWASIARDYNANIPSAQMIGSSIFPPFTNMPSTKSCTDTMVDEIDNQPL SRKRYVFSNSKLEMLKTQVESETGVQNLTRFEVLSALIYTCAGTAARANSSSYKPSMLLLAVNLRPILDPPVATRAIGNIISFIKIETMSEDEMTIARMVREIRKAKDELK KEDQVKENQLLSLWSELSSMGNELEMYRCSSVCNYPLNNLDFGWGKPNR	377 aa
			>Sch_scaffold22722_436_aa MSSPALKILSRASKKLIKPSSPTPLTQKWHKFSLIEQAQTHTYVPFGFFYSNNQLGALSNQPSQTSKLVENSLSKNLVSYYPYAGHMKDNAVIDCNDKGVEFLNVHID APMSQVLNHQDCYVKDLIFPHGVAWENDSEYGLAVIQLTHFDCGGIAVSTCLSHKIGDACNGLQFLIDWAKLTRDPNAKITPPYYISDTIFPSPPSGPLDSPVVPSILD GCTQKRYVFTSSKVSELRSSIASVSQVKDPTPTEVLSALLFKCVAKAVTANSGSFVPSKLIQYADLRGMISPKLPPNSIGNVLSHFSTHIYNETDMNLPQIVSLMREEK LLFRTRDNIKENAWALEILELAKGLPPKKKEFDEYTCSSVCKFPFYDVDFGWGKPMAATIATGPYNKLFNLMNYKDDGIEAFVVLDEQDMSVFERDEEFLEFASPYA NYF	436 aa
			>Sch_scaffold3609_348_aa MRDSATIECNDRGIEFLNVRINCPMSEMLNNPHDYAEGNIFTKDLPWKNSFDGSLLVAQLSHFDCGGIAISTCLSHKVGDGGSVASFIYDWAKITRNPNQIAHPKFISD TFFRTPNGPLIAPLIDSKLDKCVHKKFHFSASKLQGLRAKIAAEAGIKNPTRAEVVSALLFISATKAASKINNTSFRPSKLINYVDIRPMTTPPLSRNVIGNLLTVTSTTAS HGEEMKLPRLVREFRKEFEQVYKKDPVQHNSLVLKLLEIMESPYAIDEFDTYYCSNMCKFSGYSIDFGWGKPERVCAPMGPFKNFFILSADQNMDGVEAMVTLEEQ HMLAFECDEELLEFASPISSF	348 aa
			>Sch_scaffold1294_356_aa XTSFSKVLTFHQPWAGSLRDNATIHCDGTGAEFFEVEVNCSMDQIVHRPDLTFPPGLPWKNVPHVNDGGRLSVAQLSHFDCGGIAISVCMSHKDSLMPSLPDGPLK FPVVVEPNGEESIEFEKRAFKALIVDDPSSIVQNPTTTEVVSAIVYKCAAIAGANTSNGNNDSSSQMVFVSDLRKTIPPSIKSTSTIGNILTTFSTPIYNLEDLRLPKLVADI RKSKHELSTRDNFNENRWVSEMIEYANKINTGTGYELSYRRESSSHDVYRCSSVCNIPFQDLDFGWGRPTRASIASTPFNNMIYLMNTQDQNRGIEVFINLDQQQM SIFEQDKEFLQFASPVGDNNVHEDEEKLCCL	356 aa
			>Sch_scaffold9285_305_aa XSYYPYAGKLRDNAIVDCNDMGAEFLSVRINCTMSEILDHPDASQAESIVFPKDLPWANNYEGGNLLVAQVRDSIFSSNPIIAPQMLSNVSECVQKRIIFHKTKLDALR AKVAAESGVENPTRAEVVSAILFRCAIKAASSTTTSMVPSKFVHFLNVRSMMKCRPSAIGNILSIFSTTATKEEDIELPTLVRNLRKGVEESYKKDQVEQNELILEVVES MRKGKKPFDEEYENVYSCSNVCRFPFYNVDFGWGKPERVGLPNGPFKNLFFLKDLKIGQGVDARVMLQKQHMSEFERDDEIIELIS	305 aa
			>Sch_scaffold324_215_aa XRYIFSNQKLLNLKNTVAAESEVQSPTRTEVVSALIFKCAVRAAKANSGIFQLSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYK RDNVNDNMFVALLLELAKSKQEYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAYVTLTEQDMSVFQYDTELLEFASLVPSC	215 aa
			>Sch_scaffold24772_427_aa MASSTILSRKMIKLLSPTPSSLRHHKLSSMDCINLPQYSPFSFLYPKPKNHTKTQISQILENSLSKVLSSYYPFAGRIKDNNTYVDCDDTGVEYLNVKINHSMSDILNSP SNDVADIVYPKDLPWSSSVNRSPLVIQLSHFDCGGIALGVCLSHKIVDGYCIAKFISDWSNTARDMDFKPSIKFNASTFFPLIEGAPNIMSINSSPQSQRYVSRAYNFS SSNLKRLKRSITGVQNPTRVEVATSLIHKCGAIASMKNLGSFKPSLISQVINLRPLIPLDTIGNATCIYSIVAMKENEIELSNYVAQMQKVKQQIRNELKNLDTDQIVPYTL EKVKGIVDIMEKDIFDIYLSTSVHNFGLYSKANFGWGKPIKVSNTKYPTKKSIMLLDDPSEEGIDAQITLTEDEMAIFQEDKELLEFASPMVQSTK	427 aa
			>Sch_scaffold4352_136_aa MNEGNLATTQVSHFDCGGIAIGGCLSHKIGHGCTTSNFFNDWGILARDINTTLSLAHESKVQNPTRVEVVSALLYKCALVARGVNNSGSFKPSSLFQVANMRHRLSP PLSYDTCGNILSGYVVEINNEKDVNCPKM	136 aa
			>Sch_scaffold324_311_aa MESVPHPLVSIISEKLIKPSSPTCPTKRWHKLSLIDQAFSNSYIPFSLFYTKDNAISNTSQISQLLEESLSKILSTYYPYAGRLKDNTTVDCNDAGAEFIQVQIDCHISETL	311 aa

			NWHNTEVQSPTRTEVVSALIFKCAVRAAKANSGIFQLSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKRDNVNDNMFVALLLE LAKSKQEYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNNKLAILMGNQTGGIDAYVTLTEQDMSVFQYDTELLEFASLVPSC	
			>Sch_scaffold17163_331_aa MDKVVNHPDSNVKDLTFPQGVPWANGVDRALIVAQLSHFDCGGIALSVCLTHKIGDGSSAYCFLRDWAALTRSSNTNPSPYFVEDSIVPSPIGPLVSPVFGSDMDK CVQKRFVFSSTKLSALKSSIGVQDVTSNEAVNALIYKCAASSAIVANTSLFKQSQLVQPSDLRGIMSSTLPPNPIGNLVSIFSSPIYKDEEELKLPKLVTDIKKSKNYLSA RNNVEENEFAIEMLDAYRSGEVTFSKRKCDLYISSSLCKFPFSQDLDFGFGKPIRSSIAKGPLNKFIYLMRTYDGGIEAFVNLNEQEMSVFEHDDQLLEFATPINGDFC YEEEQ	331 aa
		SpiLA1589	>SpiLA1589_contig:unspecified:6668071:1:4087:1_312_aa MSASRLVSLSRKIIKPSSPTPSASRLVSLSRKIIKPSSPTPAALIFYPKQNTTTSMPEPTKISRVLEKSLSKVLTSYYPFAGQVRDNSFVECNDIGADLSQVRIDCPMSSI FDHPRTYIDNLVLPFDPWFPSTDSLVAAKLCHFECGGVALGVCLSHKVSDGYSLGKFLKDWSMVARDSEAKLSLLFNGSSIFKPSNSSSFQVVADPPLYKNESKRFH FSASNLKSLKSLISSADSATQICPTTVEAITAFIYRCVSTPQSLLIQAVDQRGTSNDALVPADLTGNAILPFVVSATNKEEMNLERLVSELRKX	312 aa
			>SpiLA1589_contig:unspecified:3409582:1:5301:1_356_aa XGKINNNYTYVDCNDTGAEYLNVRIDCPMSQILNHPYNDVVDVVFPQDLPWSSSSLTRSPLVVQLSHFDCGGVAVSACTSHTIFDGYCLSKFINDWASTARNMDFN PSPQFNASTFFPLPSETNLSSTLPATRPSQRHVSRMYNFSSSNLTRLKDIVTKESHVKNPTRIEVASALVHKCGVTMSMESSGMFKPTLMSHAMNLRPPIPLNTMGN ATCIILTTAMTEDEVKLPNFVAKLQKDKQQLRDKLKDMKEDRMPLYTLELGKNAMNIIEKDTHDVYLCSGMTNTGLHKIDFGWGEPVRVTLATHPKKNNFIFMDEQSG DGLNVFITLTKDDMLKFQSNKELLEFASPVVESTK	356 aa
			>SpiLA1589_contig:unspecified:6446698:1:8456:1_200_aa XNPPPMPNVVPDPQRCVSRMYNLSSSTLLKLKDIVVSTNPQIQNPSRIEVATALFHKCGVDVSMAKSGAFRPTVLFHVMNLRPPIPFNTIGNATCYFSTRAMSIDKTT LPNYVGELQKAKQQIRHELKDMNTKELALHAIEKIKEIVNIAKEDCFDMYFCTSLCTFGSRKIDFGWGSPLRVTHVKDPMKNKFIFMDDPSX	200 aa
			>SpiLA1589_contig:unspecified:6763618:1:5679:1_436_aa MGSISRIVSMSKKIIKPSSATPPSHKRHNLSLLDCYANNEYASSVMFYPKPTIPSNNISQLLQKSLSKALTYYYPFAGMLKDNTYVDCNDRGAEFLNVRVDGRMSDVI NSCDNDRSGKNCVFPQGLCFGNTSDSFDGRLAMTQLTHFDCGGIAVSFCFSHKIVDGYSAGKFMSDWAAIAKDPNHHAITYPQFDGASFFPPGIHDAGTSEVNSLP EEGLVQQRFVTRRYLFSASKLNTLKAKIVDSGSGIVGNPSRIESVSALLYKSAAANRNNTSFRPSTFTLFANMRPPLPLNTIGNAPGYISTSIEEEVDMQLPRIVAELRK GKEKLRNRFNTVDPNKLVFESFELMKEVGQVYNREGFDIYRCSSLCNFPFYGIDFGWGTPQRVAFLIPPCNFFVLLDNQNRDGGVEALVTLEESEMTVFQQDQQIL QFARPI	436 aa
			>SpiLA1589_contig:unspecified:6564705:1:5198:1_429_aa MVTPKSHIVSMSKKIIKPSSPTPSSLRHHNLSFLDQINSPLHNPLAFFYPKPKNSSYDINHISTLLQNSLANLLTSYYPFAGTYNDNIFIDCNDVGAEFFDVQLDIPMSEIL DHPYYNDDINLVYPQGCPWNIYDGTLVVAQLTHFDCGGIAVSVCISHKVADAYSVIKFITDWAYLTRDSSHAKPSVLFDGTSFFPPVTDTSTLPDFDAGNDRNCVTRM FHFSSSGLDKLKTIAAAESGVENPSRVEVATALIHKHAMIASGSFKPSLLCHIMGLRPPLPLNSIGNACSFFLTSTQTEDEMELSNSVAVLRKSKDQLREKMKNATQS DIFFKVVEITKQGAELVEKVNKADVYKCSSLCNFGLYDMDFGWGKAIRVSSVSRAVKNQIFFMDSPTGNGMDVLISLDEKEMEIFQSDKVILEYASPVVKM	429 aa
			>SpiLA1589_contig:unspecified:6537998:1:5095:1_377_aa MAASQLALISKKIIKPSSPTPLIHRIQKLSIFDQLNPCSYMSYGLFFPKQCHPTLPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FDQKSTEAEDLVLPRDLPWTPSKENLVVAQLNHFNCGGIAIGVCVSHKVVDGSSMANFTHHWSTMARNPSAPIPSFQFVGGSHFPPVSSPIAEAILKSKTRGNNTCI SKKYLLSRSKINSLKAMIAAESGNKSSSINPSSVEAASAFVYKCIASNSTKPSIFTQSVNLRPIMKKWLPEEFQGNASFLFMAPEISDPADIKLHRLISELRKEKEMYWE TTNLMSTLLEKVKLLQNQLERDHDDEVDVYKCTSLSKFIFGQMDYGWX	377 aa
			>SpiLA1589_contig:unspecified:6441578:1:6413:1_424_aa MTASSFVSMAEKIIKPHSPTPFSVKRYNLCLMDEIMVPVYMPIVAFYPNPSKTPEQVSNILEDSLSKVLSSYYPFAGTLGSDNATFVDCNDRGAKFIQVRYDCPMSEIV NLPDTGPEYLPFAKGTPWSSTPEEQSLLVVQLSHFNCGGLGISVRLSHKIADGCTLANFISDWASVARDDNANIPSPQLIGSSIFPPFTEMRIHTDTNVDYEFYNLPVC KKRYLFSNAKLEMLKTQVESETGVQNPTRIEVLSALIYKCAVTANSSSFKPSSLSLPVNLRPILNPPLETRTVGNIISFIKVETTSEDEMTIGRVVREIRKGKDELKQEGG VKKEKLVSLWSEWIHSIDLYRSSSVCNYPLNNLDFGWGKPNRVAIPVFGVANTCMFMDNLSGDGIEVIIALPEKDATQFENSKELLHFASPVTNL	424 aa
			>SpiLA1589_contig:unspecified:2218516:1:4030:1_358_aa XLSSYYPFAGTLRDNTFVDCNDRGAKFMNVRYDCPMSEIAKLPDTGPEYLPFAKGIHNSLLLGDEDLLVVQLSHFNCGGLAIGTSISHKIADGCTMANFVSDWASIAR EANIIPSPTMIGSSIFPPCTNLPSTDIYTNTIVNVPIENIKKRYRFSNSKLEMLKSQVTSEAEVQNPSRVDVLSALIYKCAVTAARAQANSFKPSMLTLAVNLRPILDPPLA TRAIGNMVSFIKVETTSVDEITIAGVVRELRKAKDEFKKEDHVNANKLVALHSENLPISNEFETYRSHSMCNFPLNNLDFGWGKPNKVTIPPIGVGFCFILMDSPSGDGI EAIVAVPETYVTQFENNKELLQFATPIN	358 aa
			>SpiLA1589_contig:unspecified:6756412:1:6109:1_436_aa MASPALKILSRASKKLIKPSSPTPLTQKWHKFSLIEQAQTHTYVPFGFFYSNNQLGALSNQPSQTSKLLENSLSKNLVSYYPYAGHMKDNAVIDCNDKGVEFLNVHID APMSQVLNDKDCHVKDLIFPHGVAWENDSEYGLAVIQLTHFDCGGIAVSTCLSHKIGDACNGLQFLIDWAKLTRDPNAKITPPYYISDTIFPSPPTGPLDSPVVPSILD GCTQKRYVFSSSKVSELRSSIASVSQVKDPTPTEVLSALLFKCVAKAVTANSGSFVPSKLIQYADLRGMISPKLPPNSIGNVLSHFSTHISNEADMNLPQIVSLMREEK LLFRTRDNIKENAWALEILELAKGLPPKKKEFDEYTCSSVCKFPFYDVDFGWGKPMAATIATGPYNKLFNLMNYKDDGVEAFVVLDEQDMSVFERDEEFLEFASPYA NYL	436 aa
			>SpiLA1589_contig:unspecified:6506105:1:2513:1_164_aa MRDSATIECNDRGIEFLNVRISCPMSEMLNNPHDYAEGNIFTKDLPWKNSFDGSLLVAQLSHFDCGGIAISTCLSHKVGDGGSVASFIYDWAKITRNPNQIARPKFISD TFFPTPNGPLIAPLIDSKLDKCVHKKFHFSASKLQGLRAKIAAEAGIKNPTRAEV	164 aa
			>SpiLA1589_contig:unspecified:3170230:1:3669:1_contig:unspecified:6613364:1:4416:1_345_aa DSLMPSLPDGPLKFPVVVEPNGEESIEFEKRFFLSESNIRALKALIVDDPSSIVQNPTTTEVVSAIVYKCAAIAGANASNGNNDSSSQMVFVSDLRKTIPPSIKSTSTIGN	345 aa

			lLTTFSTPTYNLEDLRLPKLVADIRKSKHELSTRDNFNENRWVSEMIEYANKINTGTGYELSYRRESSSHDVYRCSSVSPVLGSDTDKCVQKRFFFSSTKLSALKSSV GVQNVTSNEAANALIYKCAASSAAVVNSGSFKRSQLVQFFDLREITSPNSIGNLISIFSSPIYEDKEELKLPNLVTDVKNSKNYLSATDNIVEENEFAIEMFDAYRSGEV PFYKRKCDLYISSSLX	
			>SpiLA1589_contig:unspecified:6737245:1:3002:1_contig:unspecified:6547528:1:2079:1_145_aa MKCRPSAIGNILSIFSTTATKEEDIELPTLVHNLRKGVEKSYKKDQVEQNELILEVVESMRKGKKPFDEEYENVYSCSNVCRFPFYNVDFGWGKPERVGLPNGPFKN LFFLKDLKIGQGVDARVMLQKQHMSEFERDEELLELIS	145 aa
			>SpiLA1589_contig:unspecified:6547528:1:2079:1_contig:unspecified:6507090:1:2101:1_440_aa MAFASLSSPSLVSVCDKTFIKPSSLTPPTLKYHKLSYIDQFYSNMYIPLAFFYPKVQQREESTDNELSQIAHLLQTSLSKTLVFYYPYAGKLRDNATIDCNDMGAEFLSV RINCTMSEILNHPNASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLAHKIGDGTSALNFVNDWSRMTLSPMTTTLSPKFVGDSVFSSNKYSPIITPQ MLSDVSECVQKRIIFPTTKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKATSSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFTTTATKEEDIELPTLVSSL RKGVEEAHKKDHVEQNEMMLEVVESMRKGKKPYDDDYENVYSCCNLCKFPLYKVDFGWGKPERVSLPNGPFKNFFFLNDYKIGEGVDARVMLDKQHMSEFERD EELLDLIS	440 aa
			>SpiLA1589_contig:unspecified:6507090:1:2101:1_222_aa MLSDVSECVQKRIIFPTAKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKATSSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFTTTATKEEDIELPTLVSSL RKGVEEAHKKDHVEQNEMMLEVVESMRKGKKPYDDDYENVYSCCNLCKFPLYKVDFGWGKPERVSLPNGPFKNFFFLNDYKIGEGVDARVMLDKQHMSEFERD EELLDLIS	222 aa
			>SpiLA1589_contig:unspecified:6650000:1:7877:1_200_aa MIVSKEEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKRDNVNDNMFVALLLE LAKSKREYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNSKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	200 aa
			>SpiLA1589_contig:unspecified:6671100:1:5917:1_427_aa MASSTILSRKMIKLLSPTPSSLRHHKLSFMDCINLPQYSPFAFLYPKPKNHTKTQISHILENSLSKVLSSYYPFAGRIKDNNTYVDCNDTGVEYLNVRINHSMSDILNSP SNDVEDIVFQKDLPWSSSVNRSPLVIQLSHFDCGGIALGVCLSHKIVDGYCIAKFISDWANTARDMDFKPSIKFNASTFFPLIEGAPNIMSINSSPQSQRYVSRAYNFS SSNLKRLKRSITGVQNPTRVEVATSLIHKCGAIASMKNLGSFKPSLISQVINLRPLIPLDTMGNATCIYSIIATTENEIELSNYVAQMQKVKQQIRNELKNLDTDKIVPYTL EKVRGIVDMMEKDIYDIYLSTSVHNFGLYSKANFGWGKPIKVSNTKYPTKKSFMLFDDPSEEGIDAQITLTEDEMAIFQEDKELLEFASPMVQSTK	427 aa
			>SpiLA1589_contig:unspecified:6656419:1:8388:1_138_aa XQPYTNSDHVVFPVEQPYAHMNEGNLATTQVGDGCTTSNFFNDWGILTLDINATLSLARESKVQNPTRVEVVSALLYKCALVARGVNDSGSFKPSSLFQVANMRHR LNPPLSYDTCGNILSGYFMETNNEKNVNYSKM	138 aa
			>SpiLA1589_contig:unspecified:6537998:1:5095:1_407_aa MAASQLALISKKIIKPSSPTPLIHRIQKLSIFDQLNPCSYMSYGLFFPKQCHPTLPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FDQKSTEAEDLVLPRDLPWTPSKENLVVAQLNHFNCGGIAIGVCVSHKVVDGSSMANFTHHWSTMARNPSAPIPSFQFVGGSHFPPVSSPIAEAILKSKTRGNNTCI SKKYLLSRSKINSLKAMIAAESGNKSSSINPSSVEAASAFVYKCIASNSTKPSIFTQSVNLRPIMKKWLPEEFQGNASFLFMAPEISDPADIKLHRLISELRKEKEMYWE TTNLMSTLLEKVKLLQNQLERDHDDEVDVYKCTSLSKFIFGQMDYGWGSPTRVCLGSVPINKKIFLTDSQTEDGIEVV	407 aa
			>SpiLA1589_contig:unspecified:6650000:1:7877:1_434_aa MESVAHPLVSIISEKLIKPSSPTCPTKRWHKLSLIDQAFSNSYIPFSLFYTKDNAISNTSQISQLLEESLSKILSTYYPYAGRLKDNTTVDCNDAGAEFIQVQIDCLISETLN WHNTAIEDLLFPQGLPWSNCASRGLVVVQLTYFNCGGIAISMCISHKIGDGCSGYNLFRDWSHITSHPNNFSIPSLHYVEQSVFPPPSSGPFLSPLFMSNKHDCVQR RYIFSNQKLLNLKNTVASESEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKR DNVNDNMFVALLLELAKSKREYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNSKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	434 aa
		SpiLA0480	>SpiLA0480_Scaffold3065296_312_aa MSASRLVSLSRKIIKPSSPTPLSHRIHKLSLMDQMGTHSYMAALIFYPKQNTTTSMPEPTKISRVLEKSLSKVLTSYYPFAGQVRDNSFVECNDIGADLSQVRIDCPMS SIFDHPRTYIDNLVLPFDPWFPSTDSLVAAKLCHFECGGVALGVCLSHKVSDGYSLGKFLKDWSMVARDSEAKLSLLFNGSSIFKPSNSSSFQVVADPPLYKNESKR FHFSASNLKSLKSLISSADSATQICPTTVEAITAFIYRCVSTPQSLLIQAVDQRGTSNDALVPADLTGNAILPFVVSATNKEEMNLERLVSELRKX	312 aa
			>SpiLA0480_Scaffold3071141_356_aa XGKINNNYTYVDCNDTGAEYLNVRIDCPMSQILNHPYNDVVDVVFPQDLPWSSSSLTRSPLVVQLSHFDCGGVAVSACTSHTIFDGYCLSKFINDWASTARNMDFN PSPQFNASTFFPLPSETNLSSTLPATRPSQRHVSRMYNFSSSNLTRLKDIVTKESHVKNPTRIEVASALVHKCGVTMSMESSGMFKPTLMSHAMNLRPPIPLNTMGN ATCIILTTAMTEDEVKLPNFVAKLQKDKQQLRDKLKDMKEDRMPLYTLELGKNAMNIIEKDTHDVYLCSGMTNTGLHKIDFGWGEPVRVTLATHPKKNNFIFMDEQSG DGLNVFITLTKDDMLKFQSNKELLEFASPVVESTK	356 aa
			>SpiLA0480_Scaffold3065973_433_aa MASSTILSRKFIKPSPPTPSSHRHYNLSFRDQTANNLYLPIAALYSKPENHTITQISNILENSLSKILYFYYPFGGRIKDNKYVDCNDIGAEYLNVHINCQMSEILSNPYND AIEIVFPQNLAWGNSLSEERSSLVVVQLSHFDCGGVGISICLSHKVADGYSGCKFLSDWVSMARDDHKLNFQLSCQFDGASFFPPIDNPPPMPNVVPDPERCVSRM YNLSSSTLLKLKDIVVSTNPQIQNPSRIEVATALFHKCGVDVSMAKSGVFRPTMLFHVMNLRPPIPFNTIGNATCYFSTRAMSIDKTTLPNYVGELQKAKQQIRHELKD MNTKELALHAIEKIKEIVNIAKEDCFDMYFCTSLCTFGSRKIDFGWGSPLRVTHVKDPMKNKFIFMDDPSGEGINVLITLTEADMLLFESNKELLEFASPVVQSLE	433 aa
			>SpiLA0480_Scaffold3071140_436_aa MGSISRIVSMSKKIIKPSSATPPSHKRHNLSLLDCYANNEYASSVMFYPKPTIPSNNISQLLQKSLSKALTYYYPFAGMLKDNTYVDCNDRGAEFLNVRVDGRMSDVI NSCDNDTSGKNCVFPQGLCFGNTSDSFDGRLAMTQLTHFDCGGIAVSFCFSHKIVDGYSAGKFMSDWAAIAKDPNHHAITYPQFDGASFFPPGIHDAGTSEVNSLP EEGLVQQRFVTRRYLFSASKLNTLKAKIVDSGSGIVGNPSRIESVSALLYKSAAANRNNTSFRPSTFTLFANMRPPLPLNTIGNAPGYISTSIEEEVDMQLPRIVAELRK GKEKLRNRFNTVDPNKLVFESFELMKEVGQVYNREGFDIYRCSSLCNFPFYGIDFGWGTPQRVAFLIPPCNFFVLLDNQNRDGGVEALVTLEESEMTVFQQDQQIL	436 aa

			QFARPI	
			>SpiLA0480_Scaffold3074328_429_aa MVTPKSHIVSMSKKIIKPSSPTPSSLRHHNLSFLDQINSPLHNPLAFFYPKPKNSSYDINHISTLLQNSLANLLTSYYPFAGTYNDNIFIDCNDVGAEFFDVQLDIPMSEIL DHPYYNDDINLVYPQGCPWNIYDGTLVVAQLTHFDCGGIAVSVCISHKVADAYSVIKFITDWAYLTRDSSHAKPSVLFDGTSFFPPVTDTSTLPDFDAGNDRNCVTRM FHFSSSGLDKLKTIAAAESGVENPSRVEVATALIHKHAMIASGSFKPSLLCHIMGLRPPLPLNSIGNACSFFLTSTQTEDEMELSNSVAVLRKSKDQLREKMKNATQS DIFFKVVEITKQGAELVEKVNKADVYKCSSLCNFGLYDMDFGWGKAIRVSSVSRAVKNQIFFMDSPTGNGMDVLISLDEKEMEIFQSDKVILEYASPVVKM	429 aa
			>SpiLA0480_Scaffold3074328_407_aa MAASQLALISKKIIKPSSPTPLIHRIQKLSIFDQLNPCSYMSYGLFFPKQCHPTLPDDPTHISTILENSLSRALTSYYPLAGTIRDEGLHVECNDVGAKFLQVKIDCPMSQI FDQKSTEAEDLVLPRDLPWTPSKENLVVAQLNHFNCGGIAIGVCVSHKVVDGSSMANFTHHWSTMARNPSAPIPSFQFVGGSHFPPVSSPIAEAILQSKTRGNNTCI SKKYLLSRSKINSLKAMIAAESGNKSSSINPSSVEAASAFVYKCIASNSTKPSIFTQSVNLRPIMKKWLPEEFQGNASFLFMAPEISDPADIKLHRLISELRKEKEMYWE TTNLMSTLLEKVKLLQNQLERDHDDEVDVYKCTSLSKFIFGQMDYGWGSPTRVCLGSVPINKKIFLTDSQTEDGIEVV	407 aa
			>SpiLA0480_Scaffold3063131_424_aa MTASSFVSMAEKIIKPHSPTPSSLKRYNLCLTDEIMVPVYMPIVAFYPNPSKTPQQVSNILEDSLSKVLSSYYPFAGTLGSDNATFVDCNDRGAKFIQVRYDCPMSEIV NLPDTGPEYLPFAKGTPWSSTPEEQSLLVVQLSHFNCGGLGISVRLSHKIADGCTLANFISDWASVARDDNANIPSPQLIGSSIFPPFTEMRIHTDTNVDYEFYNLPVC KKRYLFSNAKLEMLKTQVETETGVQNPTRIEVLSALIYKCAVTANSSSFKPSSLSLPVNLRPILNPPLETRTVGNIISFIKVETTSEDEMTIGRVVREIRKGKDELKQEGG VKKEKLVSLWSEWIHSIDLYRSSSVCNYPLNNLDFGWGKPNRVAIPVFGVANTCMFMDNLSGDGIEVIIVLPEKDVTQFENSKELLHFASPVTNL	424 aa
			>SpiLA0480_Scaffold3063131_426_aa MAAASRLVSFAEKIIKPHRATPLSLGRYNLSINDQIMVPFYQSIAAFYPNPSKTPEQVSNILENSLSKVLSSYYPFAGTLRDNTFVDCNDRGAKFMNVRYDCPMSEIAK LPDTGPEYLPFAKGIHNSLLLGDEDLLVVQLSHFNCGGLAIGTSISHKIADGCTMANFVSDWASIAREANIIPSPTMIGSSIFPPCTNLPSTDIYTNTIVNVPIENIKKRYRF SNSKLEMLKSQVTSEAEVQNPSRVDVLSALIYKCAVTAARAQANSFKPSMLTLAVNLRPILDPPLATRAIGNMVSFIKVETTSVDEITIAGVVRELRKAKDEFKKEDHV NANKLVALHSENLPISNEFETYRSHSMCNFPLNNLDFGWGKPNKVTIPPIGVGFCFILMDSPSGDGIEAIVAVPETYVTQFENNKELLQFATPIN	426 aa
			>SpiLA0480_Scaffold3062588_436_aa MASPALKILSRASKKLIKPSSPTPLTQKWHKFSLIEQAQTHTYVPFGFFYSNNQLGALSNQPSQTSKLLENSLSKNLVSYYPYAGHMKDNAVIDCNDKGVEFLNVHID APMSQVLNDKDCHVKDLIFPHGVAWENDSEYGLAVIQLTHFDCGGIAVSTCLSHKIGDACNGLQFLIDWAKLTRDPNAKITPPYYISDTIFPSPPTGPLDSPVVPSILD GCTQKRYVFSSSKVSELRSSIASVSQVKDPTPTEVLSALLFKCVAKAVTANSGSFVPSKLIQYADLRGMISPKLPPNSIGNVLSHFSTHISNEADMNLPQIVSLMREEK LLFRTRDNIKENAWALEILELAKGLPPKKKEFDEYTCSSVCKFPFYDVDFGWGKPMAATIATGPYNKLFNLMNYKDDGVEAFVVLDEQDMSVFERDEEFLEFASPYA NYL	436 aa
			>SpiLA0480_Scaffold3071251_348_aa MRDSATIECNDRGIEFLNVRISCPMSEMLNNPHDYAEGNIFTKDLPWKNSFDGSLLVAQLSHFDCGGIAISTCLSHKVGDGGSVASFIYDWAKITRNPNQIARPKFISD TFFPTPNGPLIAPLIDSKLDKCVHKKFHFSASKLQGLRAKIAAEAGIKNPTRAEVVSALLFISATKAASKINNTSFRPSKLINYVDIRPMTTPPLSRNVIGNLLTVTSTTAS HDEEMELPRLVREFRKEFEQVYKKDPVQHNSLVLKLLEIMESPYAIDEFDTYYCSNMCKFSGYSIDFGWGKPERVCAPMGPFKNFFILSADQNMDGVEAMVTLEEQ HMLAFECDEELLEFASPISSF	348 aa
			>SpiLA0480_Scaffold3061625_474_aa MSSFSRLLSTISKKVVKPFSPTPSTQKIHKLSLLDQCMGNFYMPLVLFYPKHQLEQGPKQLSKLLETSFSKVLTYHQPWAGSLRDNATIHCDGTGAEFFEVEVNCPM NQIVHRPDLTFPPGLPWKNVPHVNDGGRLSVAQLSHFDCGGIAISVCMSHKVGDARSAFSFLKDWATLTREQSNDQLSCPSNSNDQLSCPSYYVQDSLMPSLPDG PLKFPVVVEPNGEESIEFEKRFFLSESNIRALKALIVDDPSSIVQNPTTTEVVSAIVYKCAAIAGANTSNGNNDSSSQMVFVSDLRKTIPPSIKSTSTIGNILTTFSTPTYN LEDLRLPKLVADIRKSKHELSTRDNFNENRWVSEMIEYANKINTGTEYELSYRRESSSHDVYRCSSVCNIPFQDLDFGWGRPTRASIASTPFNNMIYLMNTQDQNRG IEVFINLDQQQMSIFEQDKEFLQFASPVGDNNFHEDKEKLCCL	474 aa
			>SpiLA0480_Scaffold2964846_438_aa MAFALLSSPSLVSVCDKTFIKPSSLTPPTLRYHKLSYIDQFHSNMYIPLAFFYPKVQQREESTDNELSHIVHLLQTSLSKTLVSYYPYAGKLRDNAIVDCNDMGAEFLS VRINCTMSEILDHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLSHKIGDGTSVLNFVNDWSRMTYSPMTTTLAPKFVGDSVFSANNYSPIIAP QMLSNVSECVQKRIIFHKIKLDALRAKVAAESGVENPTRAEVVSAILFRCAIKAASSTTSSMVPSKFVHFLNVRSMMKCRPSAIGNILSIFSTTATKEEDIELPTLVHNLR KGVEKSYKKDQVEQNELILEVVESMRKGKKPFDEEYENVYSCSNVCRFPFYNVDFGWGKPERVGLPNGPFKNLFFLKDLKIGQGVDARVMLQKQHMSEFERDEEL LELIS	438 aa
			>SpiLA0480_Scaffold3062767_440_aa MAFASLSSPSLVSVCDKTFIKPSSLTPPTLKYHKLSYIDQFYSNMYIPLAFFYPKVQQREESTDNELSQIAHLLQTSLSKTLVFYYPYAGKLRDNATIDCNDMGAEFLSV RINCTMSEILNHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISVCLAHKIGDGTSMLNFVNDWSRMTLSPMTTTLSPKFVGDSVFSSNKYSPIITPQ MLSDVSECVQKRIIFPTTKLDALRAKVAAESGVENPTRAEVVSALLFKCAIKATSSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFTTTAIKEEDIELPTLVRSL RKGVEEAHKKDHVEQNEMMLEVVESMRKGKKPYDDDYENVYSCCNLCKFPLYKVDFGWGKPERVSLPNGPFKNFFFLNDYKIGEGVDARVMLDKQHMSEFERD EELLDLIS	440 aa
			>SpiLA0480_Scaffold3062767_439_aa MAFALLSSPSLVSVCDKTFIKPFSLTPPTLRYHKLSYIDQFYSNLYIPLAFFYPKVQQREENELSHIAHLLQTSLSKTLVSYYPYAGKLRDNATIDCNDMGAEFLSVRIN CTMSEILDHPDASQAESIVFPKDLPWANNYEGGNLLVAQVSKFDCGGIAISLCLAHKIGDGTSMLNFVNDWSRMTHSPMTTTLAPKFVGDSVFSSNNYSPIITPQMLS DVSECVQKRIIFPTAKLDALRAKVKVAAESGVENPTRAEVVSALLFKCAIKAASSTTTSMRPSKFVHLLNVRSMLKSRLPQSTIGNILSSFSTTATKEEDIELPALVSSLR KGVEEAYKKDHVEQNEFMLEVVESMRKGKKPYDDEYENVYSCSNLCRFPLYKVDFGLGKPERVSLPNGPFKNFFFLKDYKIGKGVDARVMLNKQHMSEFERDEEL LDLIS	439 aa

			>SpiLA0480_Scaffold3070359_200_aa MIVSKEEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKRDNVNDNMFVALLLE LAKSKREYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNSKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	200 aa
			>SpiLA0480_Scaffold3060154_427_aa MASSTILSRKMIKLLSPTPSSLRHHKLSFMDCINLPQYSPFAFLYPKPKNHTKTQISHILENSLSKVLSSYYPFAGRIKDNNTYVDCNDTGVEYLNVRINHSMSDILNSP SNDVEDIVFQKDLPWSSSVNRSPLVIQLSHFDCGGIALGVCLSHKIVDGYCIAKFISDWANTARDMDFKPSIKFNASTFFPLIEGAPNIMSINSSPPSQRYVSRAYNFSS SNLKRLKRSITGVQNPTRVEVATSLIHKCGAIASMKNLGSFKPSLISQVINLRPLIPLDTMGNATCIYSIIATTENEIELSNYVAQMQKVKQQIRNELKNLDTDKIVPYTLE KVRGIVDMMEKDIYDIYLSTSVHNFGLYSKANFGWGKPIKVSNTKYPTKKSFMLFDDPSEEGIDAQITLTEDEMAIFQEDKELLEFASPMVQSTK	427 aa
			>SpiLA0480_Scaffold3072289_217_aa XQPYTNDEHVVFPVEQPYGHMNEGNLATTQFKILLEVVSALLYKCALVARGVNDSGSFKPSSLFQVANMRHRLNPPLSYDTCGNILSGYFVETNNEKDVNCSKMVG EMKKGKLNLHPKESALVKSIKKGKTPFYSNDEVDNYFCSSLIEFPLYKVDFGWGRPIRVGMGAGPFDKFFILLDNQSGDGVEVIVMLDEQNMAIFERDLELLEFASPIT NL	217 aa
			>SpiLA0480_Scaffold3070359_434_aa MESVAHPLVSIISEKLIKPSSPTCPTKRWHKLSLIDQAFSNSYIPFSLFYTKDNAISNTSQISQLLEESLSKILSTYYPYAGRLKDNTTVDCNDAGAEFIQVQIDCLISETLN WHNTAIEDLLFPQGLPWSNCASRGLVVVQLTYFNCGGIAISMCISHKIGDGCSGYNLFRDWSHITSHPNNFSIPSLHYVEQSVFPPPSSGPFLSPLFMSNKHDCVQR RYIFSNQKLLNLKNTVASESEVQNPTRTEVVSALIFKCAVRAAKANSGIFQPSSMVQAVDLRAQVGLPPNAIGNLLTICPTSIITNNEESMTISKLVSEMRKSKELVYKR DNVNDNMFVALLLELAKSKREYHDNGPNAYQITSLVKFALHEIDFGWGKPTKVSIANGLNSKLAILMGNQTGGIDAFVTLTEQDMSVLQYDTELLEFASLVPSC	434 aa
			>SpiLA0480_Scaffold3067271_157_aa VSPVLGSDTDKCVQKRFFFSSTKLSALKSSVGVQNVTSNEAANALIYKCAASSAAVVNSGSFKRSQLVQFFDLREITSPNSIGNLISIFSSPIYEDKEELKLPNLVTDIKK SKNYLSATDNIVEENEFAIEMLDAYRSGEVPFYKRKCDLYISSSLX	157 aa
Branched-chain keto acid dehydrogenase	BCKD E1a	*Sly*	>Solyc06g059840_BCKDE1a_NP_001234066.2 MATWFLRRLNNHGVMQKLSMAFSGKSTTAIGRRYFVSMEVGQKLDPYSCDDDYRENIDHQNQDLDFPGGKIPLTSQMKFISEASEKRLPCYRVLNDDGSLISNSIH DQLGEEVAVNMYSAMVTLKTMDTYLYEAQRQGRISFYMTTFGEEAINIASAAALSPHDFVLPQYREAGVLLWRGFTVQECTNQCFGNKDDKGKGRQMPVHYGSNK HNVITISSPLATQISQAAGVAYSLKMDKTGACAVAYTGEGATSEGDFHAGLNFAAVLEAPVIFLCRNNGWAISTPVHEQFRSDGIVSKGLGYGIRSIRVDGNDVIAVYN AVRAARTMAISEERPILVEAMTYRVGHHSTSDDSTKYRPTNEIEYWKTARCPINLFRKHIQRNGWWSDVQESELYTHVKNQVLEAIKTAEGMEKPALTELFSDVYEK MTPNLQEQERCIRDAIHKYPKDYPTDFQV	442 aa
			>Solyc05g056480_BCKDE1a_XP_004239633.1 MALLLSKSRKLICLKPKIGFLSSVYHNHTLISPNLRTPFRILGLNQSHFAYFRFGSTKAQTQLNPMHSIHNDSQVLDFPGGEVKFTSHLNFIPETREERVHCYRVLDDD GYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTDDFIFPQYRESGVLLWRGFTIQEFANQLFGNKNDYGKGRQMPIHYG SNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLDAPVIFFCRNNGFAISTPVSDQFRSDGVVTKGQGYGIRSIRVDGNDA LAVFTAVHEARKMAVNECKPILVEALTYRAGHHSTSDDSTKYRPAKEIEWWRRERDPVSRFKKWIEREGWLNPQVESDLRSNIRKQVLQAIQVAEKQEKPPIKDVFT DVYDVSPANLQEQEVSIRETVRKHPQDYPTDVPV	467 aa
			>Solyc04g063350_BCKDE1a_XP_004237706.1 MANLISKSTKFNHFLQNTRVCFLRSFTTSAAGAGAGGYIQPAGSFSGESAAIFRPERYQSGKAGEQLDTIDYEEDENQVMDFPGGKVPITPQMKFISESSEKRLPCY RVLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTIFYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYREVGVILWRGYPLEQVANQLFGNKFDYGK GRQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICRNNGWAISTPINQQFRSDGIASRGQAYGV RSIRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGWWNDENESELRGDIRKQVLQAIQAAEKVD KPSLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	472 aa
		Spe	>Sopen04g026270_BCKDE1a_XP_015074287.1 MANLISKSTKFNHFLLNTRVCFLRSFTTSAAGAGAGGYIKPAGSFSGESAAIFRPERYQSGKAGEQLDTIDYEEDENQVMDFPGGKVPITPQMKFISESSEKRLPCYR VLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTIFYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYREVGVILWRGYPLEQVANQLFGNKFDYGKG RQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICRNNGWAISTPINQQFRSDGIASRGQAYGVRS IRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGWWNDEDESELRGDIRKQVLQAIQAAEKVDKP SLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	472 aa
			>Sopen05g034880_BCKDE1a_XP_015076473.1 MALLLSKSRKLICLKPKIGFLSSVYHNHTLISPNLRTPFRILGLNQPHFAYFRFGSTKAQTQLNPMHSIDNDSQVLDFPGGEVKFTSHLNFIPETREERVHCYRVLDDD GYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTDDFIFPQYRESGVLLWRGFTIQEFANQLFGNKNDYGKGRQMPIHYG SNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLDAPVIFFCRNNGFAISTPVSDQFRSDGVVTKGQGYGIRSIRVDGNDA LAVFTAVHEARKMAVNERKPILVEALTYRAGHHSTSDDSTKYRPAKEIEWWRRERDPVSRFKKWIEREGWLNPQVESDLRSNIRKQVLQAIQVAEKQEKPPIKDIFT DVYDVSPANLQEQEVSIRETVRKHPQDYPTDVPV	467 aa
			>Sopen06g019920_BCKDE1a_XP_015077702 MQKLSMAFSGKSTTAIARRYFVSMEVGQKSDPYSCDDDYSENIDHQNQDLDFPGGKIPLTSQMKFISEASEKRLPCYRVLNDDGSLISNSIHDQLGEEVAVNMYSA MVTLKTMDTYLYEAQRQGRISFYMTTFGEEAINIASAAALSPHDFVLPQYREAGVLLWRGFTVQECTNQCFGNKDDKGKGRQMPVHYGSNKHNVITISSPLATQISQ AAGVAYSLKMDKTGACAVAYTGEGATSEGDFHAGLNFAAVLEAPVIFLCRNNGWAISTPVHEQFRSDGIVSKGLGYGIRSIRVDGNDVIAVYNAVRAARTMAISEER PILVEAMTYRVGHHSTSDDSTKYRATNEIEYWKTARCPITIFRKHIHRNGWWSDDQESELYRHVKNQVLEAIKRAEGMEKPALTELFSDVYEKMTPNLQEQERCIRD AIHKYPKDYPTDFHV	442 aa

			>Sopen06g019930_BCKDE1a_XP_015078845.1 MKMLFSKSRSLTHSLQYYTRKYAVISIQQRCFESIKAGELQLDNYNEDDQQTLNFPGGRIPITTRMKFISESFEKRLPCYRVLDDDGDLIPGSIFEQVKKGLAVNMYST MVALQIMDTIFYEAQRQGRLSFYLTSTGEEAINIASAAALTSDDIVLPQYREPGVLLWRGFTLEEFADQLFGNKNDYGKGRQMPIHYGSNKLNYFTVSSPLATQLPQA AGVAYSLKMDKKEACVVVYFGDGSTSEGDFHAGLNFAAVMESPVIFLCRNNGWAISTPVTEQFRSDGIAIKGQAYGIRSIRVDGNDALAVYSAIRAARQMAIKEQRPI LVEAMTYRVSHHSTSDDSTKYRCVKEIEQWRTEKNPITRFRKWIQRNDWWDDQNETELRGNIRKQVVEAIQTAEKVEKPPLKDLFGDVYDKIPSNLQEQERFIRDSI RRYPKEYPFDVPV	445 aa
			>Sopen04g001100_BCKDE1a_XP_015074054.1 MALSTIRTVNHLLKPFTAAISATRRLSSDSNATISVEISKPYTAHNIDPPSSIVETTPNELMTFFADMVEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAIGMEAAITKK DCIITAYRDHCIFLARGGGLVESFAELMGRKDGCSKGKGGSMHFYKKDSGFYGGHGIVGAQVPLGIGISFAQKYNKEDHVTFAMYGDGAANQGQLFEALNMAALW DLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLKVDGMDALAVKQACKFAKDHVLKKGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRGERDPVERI RNLILDHNIATEQELKDIEKGKRKVVDEAIAKAKESPMPDPSDLFTNVYVKGFGVEVFGADRKELRATLP	391 aa
			>Sopen05g002470_BCKDE1a_XP_015076383.1 MALSTSRAINHIMKPLSAAVCATRRLLSDSTATITVETSLPFTSHNVDPPSRSVETSPKELMTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAVGMEAAIT KKDCIITAYRDHCIFLGRGGTLVESFAELMGRRDGCSRGKGGSMHFYKKESGFYGGHGIVGAQVPLGIGLAFAQKYKKEDYVTFAMYGDGAANQGQLFEALNMAA LWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLRVDGMDVFAVKQACAFAKQHALKNGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPV ERIRSLILAHNIATEAELKDIEKENRKVVDEAIAKAKESPMPDPSELFTNVYVKGFGVEAYGADRKELRATLP	391 aa
			>Sga_BCKDE1a_protein_Solyc06g059840_NM_001247137.2_NP_001234066.2_scaffold115541_10.3_C9451447_10.0_442_aa MQKLSMAFSGKSTTAIGRRYFVSMEVGQKLDPYSCDDDYRENIDHQNQDLDFPGGKIPLTSQMKFISEASEKRLPCYRVLNDDGSLISNSIHDQLGEEVAVNMYSA MVTLKTMDTYLYEAQRQGRISFYMTTFGEEAINIASAAALSPHDFVLPQYREAGVLLWRGFTVQECTNQCFGNKDDKGKGRQMPVHYGSNKHNVITISSPLATQISQ AAGVAYSLKMDKTGACAVAYTGEGATSEGDFHAGLNFAAVLEAPVIFLCRNNGWAISTPVHEQFRSDGIVSKGLGYGIRSIRVDGNDVIAVYNAVRAARTMAISEER PILVEAMTYRVGHHSTSDDSTKYRPTNEIEYWKTARCPINLFRKHIQRNGWWSHDQESELYTHVKNQVLEAIKTAEGMEKPALTELFSDVYEKMTPNLQEQERCIRD AIHKYPKDYPDDFHV	442 aa
			>Sga_BCKDE1a_protein_Solyc05g056480_XM_004239585.4_XP_004239633.1_scaffold81122_13.5_contig1_467_aa MALLLSKSRKLICLKPKIGFLSSVYRNHTLISPNLRTPFRILGLNQSHFAYFRFGSTKAQTQLNPMHSIHNDSQVLDFPGGEVKFTSHLNFIPETREERVHCYRVLDDD GYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTDDFIFPQYRESGVLLWRGFTIQEFANQLFGNKNDYGKGRQMPIHYG SNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLDAPVIFFCRNNGFAISTPVSDQFRSDGVVTKGQGYGIRSIRVDGNDA LAVFTAVHEARKMAVNECKPILVEALTYRAGHHSTSDDSTKYRPAKEIEWWRRERDPVSRFKKWIEREGWLNPQVESDLRSNIRKQVLQAIQVAEKQEKPPIKDVFT DVYDVSPANLQEQEVSIRETVRKHPQDYPTDVPV	467 aa
			>Sga_BCKDE1a_protein_Solyc04g063350_XM_004237658.4_XP_004237706.1_scaffold83116_11.2_contig2_374_aa MDFPGGKVPITPQMKFISESSEKRLPCYRVLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTISYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYR EVGVILWRGYPLEQVANQLFGNKFDYGKGRQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICR NNGWAISTPINQQFRSDGIASRGQAYGVRSIRVDGNDALATYSAIRAARQMAIKEQRPILYRPVEEIEHWKTAKSPISKFRKYIQRNGWWNDENESELRGDIRKQVLQ AIQAAEKVDKPSLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	374 aa
		Sga	>Sga_BCKDE1a_protein_Sopen04g026270_XM_015218801.2_XP_015074287.1_scaffold83116_11.2_contig2_393_aa MDFPGGKVPITPQMKFISESSEKRLPCYRVLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTISYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYR EVGVILWRGYPLEQVANQLFGNKFDYGKGRQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICR NNGWAISTPINQQFRSDGIASRGQAYGVRSIRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGW WNDENESELRGDIRKQVLQAIQAAEKVDKPSLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	393 aa
			>Sga_BCKDE1a_protein_Sopen06g019930_XM_015223359.2_XP_015078845.1_C9794957_10.0_scaffold105084_6.4_contig3_380_aa MKFISESFEKRLPCYRVLDDDGDLIPGSIFEQVKKGLAVNMYSTMVALQIMDTIFYEAQRQGRLSFYLTSTGEEAINIASAAALTSDDIVLPQYREPGVLLWRGFTLEEF ADQLFGNKNDYGKGRQMPIHYGSNKLNYFTVSSPLATQLPQAAGVAYSLKMDKKEACVVVYFGDGSTSEGDFHAGLNFAAVMESPVIFLCRNNGWAISTPVTEQF RSDGIAIKGQAYGIRSIRVDGNDALAVYSAIRAARQMAIKEQRPILVEAMTYRVSHHSTSDDSTKYRCVKEIEQWRTEKNPITRFRKWIQRNDWWDDQNETELRGNIR KQVVEAIQTAEKVEKPPLRDLFGDVYDKIPSNLQEQERFIRDSTKRYPKEYPFDVPV	380 aa
			>Sga_BCKDE1a_protein_Sopen04g001100_XM_015218568.1_XP_015074054.1_scaffold99439_13.8_contig1_391_aa MALSTIRTVNHLLKPFTAAISATRRLSSDSNATISVEISKPYTAHNIDPPSSIVETTPNELMTFFADMVEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAIGMEAAITKK DCIITAYRDHCIFLARGGGLVESFAELMGRKDGCSKGKGGSMHFYKKDSGFYGGHGIVGAQVPLGIGISFAQKYNKEDHVTFAMYGDGAANQGQLFEALNMAALW DLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLKVDGMDALAVKQACKFAKDHVLKKGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRGERDPVERI RNLILDHNIATEQELKDIEKGKRKVVDEAIAKAKVSPMPDPSDLFTNVYVKGFGVEVFGADRKELRATLP	391 aa
			>Sga_BCKDE1a_protein_Sopen05g002470_XM_015220897.2_XP_015076383.1_scaffold110240_12.2_contig5_349_aa MTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAVGMEAAITKKDCIITAYRDHCIFLGRGGTLVESFAELMGRRDGCSRGKGGSMHFYKKESGFYGGHG IVGAQVPLGIGLAFAQKYKKEDYVTFAMYGDGAANQGQLFEALNMAALWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLRVDGMDVFAVKQACAFA KQHALKNGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPVERIRSLILAHNIATEAELKDIEKENRKVVDEAIAKAKGLELRLMEQIGRNSELHFPEETMFA FFDRLFIRTRDKAISTTNNYDGKIIVLHQA	349 aa
		Spr	>Spr_BCKDE1a_protein_Solyc06g059840_NM_001247137.2_NP_001234066.2_a194813_361_aa MKFISESFEKRLPCYRVLDDDGDLIPGSIFEQVKKGLAVNMYSTMVALQIMDTIFYEAQRQGRLSFYLTSTGEEAINIASAAALTSDDIVLPQYREPGVLLWRGFTLEEF ADQLFGNKNDYGKGRQMPIHYGSNKLNYFTVSSPLATQLPQAAGVAYSLKMDKKEACVVVYFGDGSTSEGDFHAGLNFAAVMESPVIFLCRNNGWAISTPVTEQF	361 aa

			RSDGIAIKGQAYGIRSIRVDGNDALAVYSAIRAARQMAIKEQRPILVEAMTYRVSHHSTSDDSTKYRCVKEIEQWRTEKNPITRFRKWIQRNDWWDDQNETELRRNIR KQVVEAIQTAEKVEKPPLRDLFGDVYDKIPSNLQEQEX	
			>Spr_BCKDE1a_protein_Solyc05g056480_XM_004239585.4_XP_004239633.1_a142361_402_aa MHSSHNDSQVLDFPGGEVKFTSHLNFIPETREERVHCYRVLDDDGYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTD DFIFPQYRESGVLLWRGFTIQEFANQLFGNKNDYGKGRQMPIHYGSNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLD APVIFFCRNNGFAISTPVSDQFRSDGVVTKGQGYGIRSIRVDGNDALAVFTAVHEARKMAVNERKPILVEALTYRAGHHSTSDDSTKYRPAEEIEWWRRERDPVSRF KKWIEREGWLNPQVESDLRSNIRKQVLQAIQVAEKQEKPPIKDVFTDVYDVSPANLQEQEESIRETVRKHPQDYPTDVPV	402 aa
			>Spr_BCKDE1a_protein_Solyc04g063350_XM_004237658.4_XP_004237706.1_A17497_472_aa MANLISKSTKFNHFLLNTRVCFLRSFTTSAAGAGAGGYIKPAGSFSGESAAIFRPERYQSGKAGEQLDTIDYEEDENQVMDFPGGKVPITPQMKFISESSEKRLPCYR VLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTIFYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYREVGVILWRGYPLEQVANQLFGNKFDYGKG RQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICRNNGWAISTPINQQFRSDGIASRGQAYGVRS IRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGWWNDENESELRGDIRKQVLQAIQAAEKVDKP SLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	472 aa
			>Spr_BCKDE1a_protein_Sopen04g001100_XM_015218568.1_XP_015074054.1_a9028_373_aa MALSTSRAINHIMKPLSAAVCATRRLSSDSTATITVETSLPFTSHNVDPPSRSVETSPKELMTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAVGMEAAIT KKDCIITAYRDHCIFLGRGGTLVESFAELMGRRDGCSRGKGGSMHFYKKESGFYGGHGIVGAQVPLGIGLAFAQKYKKEDYVTFAMYGDGAANQGQLFEALNMAA LWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLRVDGMDVFAVKQACAFAKQHALKNGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPV ERIRSLILAHNIATEAELKDIEKANRKVVDEAIAKAKESPMPDPSELFTNVYVKX	373 aa
		Sch	>Sch_BCKDE1a_protein_Solyc06g059840_NM_001247137.2_NP_001234066.2_scaffold18074_442_aa MQKVSMAFSGKSTTAIGRRYFVSMEVGQKLDPYSCDDDYRENIDHQNQDLDFPGGKIPLTSQMKFISEASEKRLPCYRVLNDDGSLISNSIHDQLGEEVAVNIYSAM VTLKTMDTYLYEAQRQGRISFYMTTFGEEAINIASAAALSPHDFVLPQYREAGVLLWRGFTVQECTNQCFGNKDDKGKGRQMPVHYGSNKHNVITISSPLATQISQA AGVAYSLKMDKTGACAVAYTGEGATSEGDFHAGLNFAAVLEAPVIFLCRNNGWAISTPVHEQFRSDGIVSKGLGYGIRSIRVDGNDVIAVYNAVRAARTMAISEERPI LVEAMTYRVGHHSTSDDSTKYRPTNEIEYWKTARCPINLFRKHIHRNGWWSDDQESELYRHVKNQVLEAIKTAEGMEKPALTELFSDVYEKMTPNLQEQERCIRDAI HKYPKDYPTDFHV	442 aa
			>Sch_BCKDE1a_protein_Solyc05g056480_XM_004239585.4_XP_004239633.1_scaffold418_467_aa MALLLSKSRKLICLKPKIGFLSSVYHNHTLISPNLRTPFRILGLNQPHFAYFRFGSTKAQTQLNPMHSIHNDSQVLDFPGGEVKFTSHLNFIPETREERVHCYRVLDDD GYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTDDFIFPQYRESGVLLWRGFTIQEFANQLFGNKNDYGKGRQMPIHYG SNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLDAPVIFFCRNNGFAISTPVSDQFRSDGVVTKGQGYGIRSIRVDGNDA LAVFTAVHEARKMAVNERKPILVEALTYRAGHHSTSDDSTKYRPAEEIEWWRRERDPVSRFKKWIEREGWLNPQVESDLCSNIRKQVLQAIQVAEKQEKPPIKDVFT DVYDVSPANLQEQEVSIRETVRKHPQDYPTDVPV	467 aa
			>Sch_BCKDE1a_protein_Solyc04g063350_XM_004237658.4_XP_004237706.1_ scaffold4382_472_aa MANLISKSTKFNHFLLNTRVCFLRSFTTSAAGAGAGGYIKPAGSFSGESAAIFRPERYQSGKAGEQLDTIEYEEDENQVMDFPGGKVPITPQMKFISESSEKRLPCYR VLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTIFYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYREVGVILWRGYPLEQVANQLFGNKFDYGKG RQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICRNNGWAISTPINQQFRSDGIASKGQAYGVRS IRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGWWNDENESELRGDIRKQVLQAIQAAEKVDKP SLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	472 aa
			>Sch_BCKDE1a_protein_Sopen06g019930_XM_015223359.2_XP_015078845.1_scaffold10778_scaffold13244_443_aa MLFSKSRSLTHFLQYYTKKYAVISIQQRCFESIKAGELQLDNYNEDDQQTLNFPGGRIPITTRMKFISESSEKRLPCYRVLDDDGDLIPGSIFEQVKKGLAVNMYSTMV ALQIMDTIFYEAQRQGRLSFYLTSTGEEAINIASAAALTSDDIVLPQYREPGVLLWRGFTLEEFADQLFGNKNDYGKGRQMPIHYGSNKLNYFTVSSPLATQLPQAAG VAYSLKMDKKEACVVVYFGDGSTSEGDFHAGLNFAAVMESPVIFLCRNNGWAISTPVTEQFRSDGVAIKGQAYGIRSIRVDGNDALAVYSAIRAARQMAIKEQRPILV EAMTYRVSHHSTSDDSTKYRCVKEIDQWRTEKNPITRFRKWIQRNDWWDDQNETELRGNIRKQVVEAIQTAEKVEKPPLRDLFGDVYDKIPSNLQEQERFIRDSIKR YPKEYPFDVPV	443 aa
			>Sch_BCKDE1a_protein_Sopen04g001100_XM_015218568.1_XP_015074054.1_scaffold123_378_aa MALSTIRTVNHLLKPFTAAISATRRLSSDSNATISVEISKPYTAHNIDPPSSIVETTPNELMTFFADMVEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAIGMEAAITKK DCIITAYRDHCIFLARGGGLVESFAELMGRKDGCSKGKGGSMHFYKKDSGFYGGHGIVGAQVPLGIGISFAQKYNKEDHVTFAMYGDGAANQGQLFEALNMAALW DLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLKVDGMDALAVKQACKFAKDHVLKKGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRGERDPVERI RNLILDHNIATEQELKDIEKGKRKVVDEAIAKAKVSPMPDPSDLFTNVYVKGFGVEV	378 aa
			>Sch_BCKDE1a_protein_Sopen05g002470_XM_015220897.2_XP_015076383.1_scaffold3266_438_aa XSLNTDRKMALSTSRAINHIMKPLSAAVCATRRLSSDSTATITVETSLPFTSHNVDPPSRSVETSPKELMTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAV AVGMEAAITKKDCIITAYRDHCIFLGRGGTLVESFAELMGRRDGCSRGKGGSMHFYKKESGFYGGHGIVGAQVPLGIGLAFAQKYKKEDYVTFAMYGDGAANQGQL FEALNMAALWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLRVDGMDVFAVKQACAFAKQHALKNGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGV RQERDPVERIRSLILAHNIATEAELKDIEKENRKVVDEAIAKAKESPMPDPSELFTNVYVKGFGVEAMEQTGRNSELHFPEETMFAFFDRLFIRTRDKSYKYNKIIMMV KSLRFIRHSN	438 aa
		SpiLA1589	>SpiLA1589_BCKDE1a_protein_Solyc06g059840_NM_001247137.2_NP_001234066.2_contig:unspecified:6683921:1:4011:1_442_aa MQKLSMAFSGKSTTAIGRRYFVSMEVGQKLDPYSCDDDYRENIDHQNQDLDFPGGKIPLTSQMKFISEASEKRLPCYRVLNDDGSLISNSIHDQLGEEVAVNMYSA MVTLKTMDTYLYEAQRQGRISFYMTTFGEEAINIASAAALSPHDFVLPQYREAGVLLWRGFTVQECTNQCFGNKDDKGKGRQMPVHYGSNKHNVITISSPLATQISQ	442 aa

			AAGVAYSLKMDKTGACAVAYTGEGATSEGDFHAGLNFAAVLEAPVIFLCRNNGWAISTPVHEQFRSDGIVSKGLGYGIRSIRVDGNDVIAVYNAVRAARTMAISEER PILVEAMTYRVGHHSTSDDSTKYRPTNEIEYWKTARCPINLFRKHIQRNGWWSDVQESELYTHVKNQVLEAIKTAEGMEKPALTELFSDVYEKMTPNLQEQERCIRD AIHKYPKDYPDDFHV	
			>SpiLA1589_BCKDE1a_protein_Solyc05g056480_XM_004239585.4_XP_004239633.1_contig:unspecified:6644818:1:18043:1_372_aa XEERVHCYRVLDDDGYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTDDFIFPQYRESGVLLWRGFTIQEFANQLFGNK NDYGKGRQMPIHYGSNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLDAPVIFFCRNNGFAISTPVSDQFRSDGVVTKG QGYGIRSIRVDGNDALAVFTAVHEARKMAVNECKPILVEALTYRAGHHSTSDDSTKYRPAKEIEWWRRERDPVSRFKKWIEREGWLNPQVESDLRSNIRKQVLQAI QVAEKQEKPPIKDVFTDVYDVSPANLQEQEVSIRETVRKHPQDYPTDVPV	372 aa
			>SpiLA1589_BCKDE1a_protein_Solyc04g063350_XM_004237658.4_XP_004237706.1_contig:unspecified:6595385:1:3779:1_393_aa MDFPGGKVPITPQMKFISESSEKRLPCYRVLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTIFYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYRE VGVILWRGYPLEQVANQLFGNKFDYGKGRQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICRN NGWAISTPINQQFRSDGIASRGQAYGVRSIRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGW WNDENESELRGDIRKQVLQAIQAAEKVDKPSLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	393 aa
			>SpiLA1589_BCKDE1a_protein_Sopen06g019930_XM_015223359.2_XP_015078845.1_contig:unspecified:1263451:1:6634:1_443_aa MLFSKSRSLTHFLQYYTKKYAVISIQQRCFESIKAGELQLDNYNEDDQQTLNFPGGRIPITTRMKFISESFEKRLPCYRVLDDDGDLIPGSIFEQVKKGLAVNMYSTMV ALQIMDTIFYEAQRQGRLSFYLTSTGEEAINIASAAALTSDDIVLPQYREPGVLLWRGFTLEEFADQLFGNKNDYGKGRQMPIHYGSNKLNYFTVSSPLATQLPQAAG VAYSLKMDKKEACVVVYFGDGSTSEGDFHAGLNFAAVMESPVIFLCRNNGWAISTPVTEQFRSDGIAIKGQAYGIRSIRVDGNDALAVYSAIRAARQMAIKEQRPILV EAMTYRVSHHSTSDDSTKYRRVKEIEQWRTEKNPITRFRKWIQRNDWWDDQNETELRGNIRKQVVEAIQTAEKVEKPPLRDLFDDVYDKIPSNLQEQERFIRDSTKR YPKEYPFNVPV	443 aa
			>SpiLA1589_BCKDE1a_protein_Sopen04g001100_XM_015218568.1_XP_015074054.1_contig:unspecified:2579139:1:3053:1_contig:unspecified:5976261:1:32 20:1_324_aa MVEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAIGMEAAITKKDCIITAYRDHCIFLARGGGLVESFAELMGRKDGCSKGKGGSMHFYKKDSGFYGGHGIVGAQVP LGIGISFAQKYNKEDHVTFAMYGDGAANQGQLFEALNMAALWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLKVDGMDALAVKQACKFAKDHVLKK GPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRGERDPVERIRNLILDHNIATEQELKDIEKGKRKVVDEAIAKAKESPMPDPSDLFTNVYVKGFGVEVFGADRKEL RATLP	324 aa
			>SpiLA1589_BCKDE1a_protein_Sopen05g002470_XM_015220897.2_XP_015076383.1_contig:unspecified:4584595:1:7163:1_324_aa MTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAVGMEAAITKKDCIITAYRDHCIFLGRGGTLVESFAELMGRRDGCSRGKGGSMHFYKKESGFYGGHGIVGAQV PLGIGLAFAQKYKKEDYVTFAMYGDGAANQGQLFEALNMAALWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLRVDGMDVFAVKQACAFAKQHALK NGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPVERIRSLILAHNIATEAELKDIEKENRKVVDEAIAKAKESPMPDPSELFTNVYVKGFGVEAYGADRKEL RATLP	324 aa
		SpiLA0480	>SpiLA0480_BCKDE1a_protein_Solyc06g059840_NM_001247137.2_NP_001234066.2_Scaffold3066199_380_aa MKFISEASEKRLPCYRVLNDDGSLISNSIHDQLGEEVAVNMYSAMVTLKTMDTYLYEAQRQGRISFYMTTFGEEAINIASAAALSPHDFVLPQYREAGVLLWRGFTVQ ECTNQCFGNKDDKGKGRQMPVHYGSNKHNVITISSPLATQISQAAGVAYSLKMDKTGACAVAYTGEGATSEGDFHAGLNFAAVLEAPVIFLCRNNGWAISTPVHEQ FRSDGIVSKGLGYGIRSIRVDGNDVIAVYNAVRAARTMAISEERPILVEAMTYRVGHHSTSDDSTKYRPTNEIEYWKTARCPINLFRKHIQRNGWWSDVQESELYTHV KNQVLEAIKTAEGMEKPALTELFSDVYEKMTPNLQEQERCIRDAIHKYPKDYPDDFHV	380 aa
			>SpiLA0480_BCKDE1a_protein_Solyc05g056480_XM_004239585.4_XP_004239633.1_Scaffold3061128_467_aa MALLLSKSRKLICLKPKIGFLSPVYHNHTLISPNLRTPFRILGLNQSHFAYFRFGSTKAQTQLNPMHSIHNDSQVLDFPGGEVKFTSHLNFIPETREERVHCYRVLDDD GYPITNDFAQIEKEVALKIYTDMVTLQTMDTIFYEAQRQGRISFYLTTVGEEAINIASAAALKTDDFIFPQYRESGVLLWRGFTIQEFANQLFGNKNDYGKGRQMPIHYG SNKHNYITVASTVATQLPHAVGAAYALKMDAKNACTIVYFGDGGSSTGDFHAALNFAAVLDAPVIFFCRNNGFAISTPVSDQFRSDGVVTKGQGYGIRSIRVDGNDA LAVFTAVHEARKMAVNECKPILVEALTYRAGHHSTSDDSTKYRPAKEIEWWRRERDPVSRFKKWIEREGWLNPQVESDLRSNIRKQVLQAIQVAEKQEKPPIKDVFT DVYDVSPANLQEQEVSIRETVRKHPQDYPTDVPV	467 aa
			>SpiLA0480_BCKDE1a_protein_Solyc04g063350_XM_004237658.4_XP_004237706.1_Scaffold3071394_393_aa MDFPGGKVPITPQMKFISESSEKRLPCYRVLDDDGYPLPGTIFEEVSKELAIKMYSSMVTLQTMDTIFYEAQRQGRLSFYLTTAGEEAINVASAAALSLDDFVLPQYRE VGVILWRGYPLEQVANQLFGNKFDYGKGRQMPCHYGSNELNYLTVSSPIATQIPQAVGVAYSLKMEKKEACAVTYFGDGSTSEGDFHAALNFAAVLDAPVVFICRN NGWAISTPINQQFRSDGIASRGQAYGVRSIRVDGNDALATYSAIRAARQMAIKEQRPILVEAMTYRVAHHSTSDDSTKYRPVEEIEHWKTAKSPISKFRKYIQRNGW WNDENESELRGDIRKQVLQAIQAAEKVDKPSLKDLFTDVYDKMPLNLQDQEKFVKDAVKRSPKEYPSDVPI	393 aa
			>SpiLA0480_BCKDE1a_protein_Sopen06g019930_XM_015223359.2_XP_015078845.1_Scaffold3066199_440_aa MLFSKSRSLTHFLQYYTKKYAVQQRCFESIKAGELQLDNYNEDDQQTLNFPGGRIPITTRMKFISESFEKRLPCYRVLDDDGDLIPGSIFEQVKKGLAVNMYSTMVAL QIMDTIFYEAQRQGRLSFYLTSTGEEAINIASAAALTSDDIVLPQYREPGVLLWRGFTLEEFADQLFGNKNDYGKGRQMPIHYGSNKLNYFTVSSPLATQLPQAAGVA YSLKMDKKEACVVVYFGDGSTSEGDFHAGLNFAAVMESPVIFLCRNNGWAISTPVTEQFRSDGIAIKGQAYGIRSIRVDGNDALAVYSAIRAARQMAIKEQRPILVEA MTYRVSHHSTSDDSTKYRRVKEIEQWRTEKNPITRFRKWIQRNDWWDDQNETELRGNIRKQVVEAIQTAEKVEKPPLRDLFGDVYDKIPSNLQEQERFIRDSTKRY PKEYPFDVPV	440 aa
			>SpiLA0480_BCKDE1a_protein_Sopen04g001100_XM_015218568.1_XP_015074054.1_Scaffold3069794_391_aa MALSTIRTVNHLLKPFTAAISATRRLSSDSNATISVEISKPYTAHNIDPPSSIVETTPNELMTFFADMVEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVAIGMEAAITKK DCIITAYRDHCIFLARGGGLVESFAELMGRKDGCSKGKGGSMHFYKKDSGFYGGHGIVGAQVPLGIGISFAQKYNKEDHVTFAMYGDGAANQGQLFEALNMAALW DLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLKVDGMDALAVKQACKFAKDHVLKKGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRGERDPVERI	391 aa

			RNLILDHNIATEQELKDIEKGKRKVVDEAIAKAKVSPMPDPSDLFTNVYVKGFGVEVFGADRKELRATLP	
			>SpiLA0480_BCKDE1a_protein_Sopen05g002470_XM_015220897.2_XP_015076383.1_Scaffold3065109_399_aa XSLNTDRKMALSTSRAINHIMKPLSAAVCATRRLSSDSTATITVETSLPFTSHNVDPPSRSVETSPKELMTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAV AVGMEAAITKKDCIITAYRDHCIFLGRGGTLVESFAELMGRRDGCSRGKGGSMHFYKKESGFYGGHGIVGAQVPLGIGLAFAQKYKKEDYVTFAMYGDGAANQGQL FEALNMAALWDLPAILVCENNHYGMGTAEWRAAKSPAYYKRGDYVPGLRVDGMDVFAVKQACAFAKQHALKNGPIILEMDTYRYHGHSMSDPGSTYRTRDEISGV RQERDPVERIRSLILAHNIATEAELKDIEKENRKVVDEAIAKAKVSPMPDPSELFTNVYVKGFGVEAYGADRKELRATLP	399 aa
	BCKD E1b	*Sly*	>Solyc05g024160_BCKDE1b_XP_010321111.1 MLRIAKPKVSIRILTHLIFGAPTLTRRSYSSGVKVKQMMVREALNSALDEEMAADPRIFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYG LRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNISVPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESF RVSEEVLDPNFTLPIGKAKIEKEGTDVTITAFSRMVGYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPV ERITGADVPMPYAANLERMALPQVEDIVRAAKRVCYKSISMAAAV	371 aa
			>Solyc01g028900_BCKDE1b_XP_004228950.1 MGSNFRRIGKLAAISSKNQSCMGFSSTVNKNDTSTKSVNLFSAINQALHIALDSDPRSYVFGEDVGFGGVFRCTTGLADRFGKQRVFNTPLCEQGIVGFAIGLAAMD NRAVAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSPESFFCHVPGIKVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMAV EEVPKDDYMLPLSEAEVLREGTDITLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVAR VCGLDTPFPLVFEPFYLPTTNKILDAIKSTVSY	358 aa
			>Solyc06g072580_BCKDE1b_XP_004241456.1 MSGIIGRTMANRRISDLNKFLVGSRLFASRTYSSAVKEMTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYH GLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQISVPIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESF PISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMVGYAIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVE RISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYRSSK	367 aa
		Spe	>Sopen01g017080_BCKDE1b_XP_015062780.1 MGSNFKRIGKLAAISSKNQSCMGFSSTVNKNDTSTKSVNLFSAINQALHIALDSDPRSYVFGEDVGFGGVFRCTTGLVDRFGKQRVFNTPLCEQGIVGFAIGLAAMD NRAIAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSPESFFCHVPGIKVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMAVE EVPKDDYMLPLSEAEVLREGTDITLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVARV CGLDTPFPLVFEPFYLPTTNKILDAIKSTVSY	358 aa
			>Sopen03g028430_BCKDE1b_XP_015069743.1 MATRGISALNMNQFLLGSRAFASRNFSSATKEMTVRDALNSALDEEMSADPKVFIMGEEVGEYQGAYKITKGLLNKYGPQRVLDTPITEAGFTGMGVGAAYHGLKP VIEFMTFNFSMQAIDHIINSAAKSNYMSAGQIAVPIVFRGPNGAAAGVGAQHSQCYAAWFGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFPVSA EVLDSSFALPIGKAKIEREGKDITITAFSKMVGSALKAAEILAKEGISAEVINLRSIRPLDRSTINASVRKTNRLLTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISG ADVPMPYAANLERMAVPQIEDIVRGAKRACYRAAKSVPMAATA	396 aa
			>Sopen05g018850_BCKDE1b_XP_015074867.1 MMLRIAKPKVSIRILTHSIFGAPTLTRRSYSSGVKVKQMMVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAY YGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNISVPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGE SFRVSEEVLDPNFTLPIGKAKIEKEGTDVTITAFSRMVGYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAP VERITGADVPMPYAANLERMALPQVEDIVRAAKRVCYKSISMAAAV	372 aa
			>Sopen06g028930_BCKDE1b_XP_015079698.1 MSGIIGRIMANRRISDLNKFLVGSRVFASRTYSSAVKEMTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYH GLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQISVPIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESF PISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMVGYAIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVE RISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYRSSK	367 aa
		Sga	>Sga_BCKDE1b_protein_Solyc01g028900_XM_004228902.4_XP_004228950.1_scaffold10693_14.0_contig4_scaffold10693_14.0_contig3_scaffold62230_11.3 _contig9_336_aa IPTFLRESSKKMGSNFRRIGKLAAISSKNQSCMGFSSTVNKNDTSTKSVNLFSAINQALHIALDSDPRSYVFGEDVGFGGVFRCTTGLADRFGKQRVFNTPLCEQGIV GFAIGLAAMDNRAVAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCEVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMAVEEVPKDDYMLPLSEAEVLREGTDI TLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKEMVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVARVCGLDTPFPLVFEPFYLPTTNKIL DAIKSTVSY	336 aa
			>Sga_BCKDE1b_protein_Solyc06g072580_XM_004241408.4_XP_004241456.1_scaffold62230_11.3_contig8_329_aa MTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYHGLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQISV PIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFPISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMVGY AIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYR SSK	329 aa
			>Sga_BCKDE1b_protein_Solyc05g024160_XM_010322809.3_XP_010321111.1_C9838877_14.0_scaffold64088_12.4_contig1_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGRDVTITAFSRMV GYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYAANLERMALPQVEDIVRAAKRVC	333 aa

			YKSISMAAAV	
			>Sga_BCKDE1b_protein_Sopen06g028930_XM_015224212.2_XP_015079698.1scaffold62230_11.3_contig8_332_aa XKEVTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYHGLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQI SVPIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFPISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMV GYAIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERLAVPQVEDIVRAVKRVC YRSSK	332 aa
			>Sga_BCKDE1b_protein_Sopen05g018850_XM_015219381.2_XP_015074867.1_scaffold64088_12.4_contig1_C9838877_14.0_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGRDVTITAFSRMV GYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYAANLERMALPQVEDIVRAAKRVC YKSISMAAAV	333 aa
			>Sga_BCKDE1b_protein_Sopen03g028430_XM_015214257.2_XP_015069743.1_scaffold26312_11.3_contig3_278_aa MTVRDALNSALDEEMSADPKVFIMGEEAIDHIINSAAKSNYMSAGQIAVPIVFRGPNGAAAGVGAQHSQCYAAWFGACPGLKVLAPYSSEDARGLLKAAIRDPDPVV FLENELLYGESFPVSAEVLDSSFALPIGKAKIEREGKDITITAFSKMVGSALKAAEILAKEGISAEVINLRSIRPLDRSTINASVRKTNRLLTVEEGFPQHGVGAEICASVV EESFEYLDAPVERISGADVPMPYAANLERMAVPQIEDIVRGAKRACYRAAKSVPMAATA	278 aa
		Spr	>Spr_BCKDE1b_protein_Solyc01g028900_XM_004228902.4_XP_004228950.1_A11557_358_aa MGSNFRRIGKLAAISSKNQSCMGFSSTVNKNDTSTKSVNLFSAINQALHIALDSDPRSYVFGEDVGFGGVFRCTTGLADRFGKQRVFNTPLCEQGIVGFAIGLAAMD NRAIAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSPESFFCHVPGIKVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMAVE EVPKDDYMLPLSEAEVLREGTDITLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVARV CGLDTPFPLVFEPFYLPTTNKILDAIKSTVSY	358 aa
			>Spr_BCKDE1b_protein_Solyc06g072580_XM_004241408.4_XP_004241456.1_a3335_367_aa MSGIIGRTMANRRISDLNKFLVGSRVFASRTYSSAVKEMTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYH GLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQIAVPIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESF PISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMVGYAIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVE RISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYRSSK	367 aa
			>Spr_BCKDE1b_protein_Solyc05g024160_XM_010322809.3_XP_010321111.1_a150581_238_aa MQAIDHLINSAAKTHYMSGGNISVPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTL PIGKAKIEKEGTDVTITAFSRMVGYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYA ANLERMALPQVEDIVRAAKR	238 aa
		Sch	>Sch_BCKDE1b_protein_Solyc01g028900_XM_004228902.4_XP_004228950.1_scaffold1500_358_aa MGSNFRRIGKLAAISSKNQSCMGFSSTVNKNDTSTKSVNLFSAINQALHIALDSDPRSYVFGEDVGFGGVFRCTTGLADRFGKQRVFNTPLCEQGIVGFAIGLAAMD NRAIAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSPESFFCHVPGIKVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMAVE EVPKDDYMLPLSEAEVLREGTDITLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVARV CGLDTPFPLVFEPFYLPTTNKILDAIKSTVSY	358 aa
			>Sch_BCKDE1b_protein_Solyc06g072580_XM_004241408.4_XP_004241456.1_scaffold58468_scaffold4835_305_aa MTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYHGLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGVLMV LQLVSVPNTLSAMRHGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYALDSSFSLPIGKAKIEREGKDVTITAFSKMVGYAIKAAELLAKEGISAEVINLRSIRPLD RPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYRSSK	305 aa
			>Sch_BCKDE1b_protein_Solyc05g024160_XM_010322809.3_XP_010321111.1_scaffold2304_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGTDVTITAFSRMVG YALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVLMPYAANLERMALPQVEDIVRAAKRVCY KSISMAAAV	333 aa
			>Sch_BCKDE1b_protein_Sopen05g018850_XM_015219381.2_XP_015074867.1_scaffold2304_372_aa MMLRIAKPKVSIRILTHSIFGAPTLTRRSYSSGVKVKQMMVREALNSALDEEMAADPRVFLMGEEVGHYGGSYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAY YGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNISVPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGE SFRVSEEVLDPNFTLPIGKAKIEKEGTDVTITAFSRMVGYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAP VERITGADVLMPYAANLERMALPQVEDIVRAAKRVCYKSISMAAAV	372 aa
			>Sch_BCKDE1b_protein_Sopen03g028430_XM_015214257.2_XP_015069743.1_scaffold319_315_aa XEFDSYKEADMSGIINRKMATRGISALNMNQFLLGSRVFASRNFSSATKEMTVRDALNSALDEEMSADPKVFIMGEEAIDHIINSAAKSNYMSAGQIAVPIVFRGPNG AAAGVGAQHSQCYAAWFGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYVSLFPLEKLRLNVKERISQLLLSQRWLVLLLRAAEILAKEGISAEVINLRSIR PLDRSTINASVRKTNRLLTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERMAVPQIEDIVRGAKRACYRAAKSVPMAATA	315 aa
		SpiLA1589	>SpiLA1589_BCKDE1b_protein_Solyc01g028900_XM_004228902.4_XP_004228950.1_contig:unspecified:2587342:1:4186:1_contig:unspecified:6610764:1:678 5:1_358_aa MGSNFRRIGKLAAISSKNQSCMGFSSRIGKLAAISSKNQSCMGFSSTLHIALDSDPRSYVFGEDVGFGGVFRCTTGLADRFGKQRVFNTPLCEQGIVGFAIGLAAMD NRAVAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSPESFFCHVPGIKVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMAV	358 aa

			EEVPKDDYMLPLSEAEVLREGTDITLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVAR VCGLDTPFPLVFEPFYLPTTNKILDAIKSTVSY	
			>SpiLA1589_BCKDE1b_protein_Solyc06g072580_XM_004241408.4_XP_004241456.1_contig:unspecified:3862692:1:10449:1_contig:unspecified:4688340:1:28 34:1_274_aa MTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYHGLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQISV PIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYDGWLCDQGAELLAKEGISAEVINLRSIRPLDRPAINASVRKT NRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERLAVPQ	274 aa
			>SpiLA1589_BCKDE1b_protein_Solyc05g024160_XM_010322809.3_XP_010321111.1_contig:unspecified:6423638:1:21070:1_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGRDVTITAFSRMV GYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYAANLERMALPQVEDIVRAAKRVC YKSISMAAAV	333 aa
			>SpiLA1589_BCKDE1b_protein_Sopen06g028930_XM_015224212.2_XP_015079698.1_contig:unspecified:3862692:1:10449:1_contig:unspecified:4688340:1:2 834:1_329_aa MTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYHGLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQISV PIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFPISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMVGY AIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYR SSK	329 aa
			>SpiLA1589_BCKDE1b_protein_Sopen05g018850_XM_015219381.2_XP_015074867.1_contig:unspecified:6423638:1:21070:1_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGRDVTITAFSRMV GYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYAANLERMALPQVEDIVRAAKRVC YKSISMAAAV	333 aa
			>SpiLA1589_BCKDE1b_protein_Sopen03g028430_XM_015214257.2_XP_015069743.1_contig:unspecified:5524304:1:6948:1_contig:unspecified:5775481:1:42 06:1_328_aa XEFDSYKEADMSGIINRKMATRGISALNMNQFLLGSRVFASRNFSSATKEMTVRDALNSALDEEMSADPKVFIMGEEAIDHIINSAAKSNYMSAGQIAVPIVFRGPNG AAAGVGAQHSQCYAAWFGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFPVSAEVLDSSFALPIGKAKIEREGKDITITAFSKMVGSALKAAEILAK EGISAEVINLRSIRPLDRSTINASVRKTNRLLTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERMAVPQIEDIVRGAKRACYRAAKSVPMAA TA	328 aa
		SpiLA0480	>SpiLA0480_BCKDE1b_protein_Solyc01g028900_XM_004228902.4_XP_004228950.1_Scaffold3065941_358_aa MGSNFRRIGKLAAISSKNQSCMGFSSTVNKKAAISSKNQSCMGFSSTVNKNLDSDPRSYVFGEDVGFGGVFRCTTGLADRFGKQRVFNTPLCEQGIVGFAIGLAAM DNRAVAEIQFADYIFPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSPESFFCHVPGIKVVIPRSPQQAKGLLLSSIRDPNPVVFFEPKLLYRMA VEEVPKDDYMLPLSEAEVLREGTDITLVGWGAQLSIMEQACVEAAKEGISCELIDLKTLIPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISASIVERCFTRLEAPVA RVCGLDTPFPLVFEPFYLPTTNKILDAIKSTVSY	358 aa
			>SpiLA0480_BCKDE1b_protein_Solyc06g072580_XM_004241408.4_XP_004241456.1_Scaffold3066858_329_aa MTVRDALNSALDEEMSADPKVFVMGEEVGEYQGAYKITKGLLAKYGPQRVIDTPITEAGFTGIGVGAAYHGLRPVIEFMTFNFSMQAIDHIINSAAKSNYMSAGQISV PIVFRGPNGAAAGVGAQHSQCYAAWYGACPGLKVLAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFPISAEALDSSFSLPIGKAKIEREGKDVTITAFSKMVGY AIKAAELLAKEGISAEVINLRSIRPLDRPAINASVRKTNRLVTVEEGFPQHGVGAEICASVVEESFEYLDAPVERISGADVPMPYAANLERLAVPQVEDIVRAVKRVCYR SSK	329 aa
			>SpiLA0480_BCKDE1b_protein_Solyc05g024160_XM_010322809.3_XP_010321111.1_Scaffold3070794_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGRDVTITAFSRMV GYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYAANLERMALPQVEDIVRAAKRVC YKSISMAAAV	333 aa
			>SpiLA0480_BCKDE1b_protein_Sopen05g018850_XM_015219381.2_XP_015074867.1_Scaffold3070794_333_aa MVREALNSALDEEMAADPRVFLMGEEVGEYQGAYKVSKGLLHKYGPDRVVDTPITEAGFTGLATGAAYYGLRPVLEFMTFNFAMQAIDHLINSAAKTHYMSGGNIS VPIVFRGPNGAALGVGAQHSQCYAPWYGSVPGLKVVAPYSSEDARGLLKAAIRDPDPVVFLENELLYGESFRVSEEVLDPNFTLPIGKAKIEKEGRDVTITAFSRMV GYALKAAETLAKEDINAEVINIRSIRPLDRSSINASVRKTNRLVTVEEGFPQHGVGAEICASVVEEIFEYLDAPVERITGADVPMPYAANLERMALPQVEDIVRAAKRVC YKSISMAAAV	333 aa
			>SpiLA0480_BCKDE1b_protein_Sopen03g028430_XM_015214257.2_XP_015069743.1_Scaffold3063753_278_aa MTVRDALNSALDEEMSADPKVFIMGEEAIDHIINSAAKSNYMSAGQIAVPIVFRGPNGAAAGVGAQHSQCYAAWFGACPGLKVLAPYSSEDARGLLKAAIRDPDPVV FLENELLYGESFPVSAEVLDSSFALPIGKAKIEREGKDITITAFSKMVGSALKAAEILAKEGISAEVINLRSIRPLDRSTINASVRKTNRLLTVEEGFPQHGVGAEICASVV EESFEYLDAPVERISGADVPMPYAANLERMAVPQIEDIVRGAKRACYRAAKSVPMAATA	278 aa
	BCKD E2	*Sly*	>Solyc01g066520_BCKDE2_protein_XM_004229208.4 MICRKIYQGKLPNSVLRQTIFRWFQSSVETPVTPVTSTVSSGKRIQSQLHFLRIYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVDGIIDIPLAQTGEGIAECELIKWFV QEGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDPTETSDASEKMISLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYSL	505 aa

			DINDVPATGKGGRILKEDVINYAMQKGLINGAPACEQQNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHTF LPVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDVSGGTITLSNIGGIGGKFGSPLVNSPEVAI IAMGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	
		Spe	>Sopen01g028100_BCKDE2_protein_XM_015207292.2 MICRKIYQGKLPNSVLRQTIFRWFQSSVETPVTPVTSTVSSGKRIQSQLHCLRNYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVGGIIDIPLAQTGEGIAECELIKWF VQEGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDPTETSDASEKMTSLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYS LDINDVPATGKGGRILKEDVINYAMQKGLINGAPACEQQNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHT FLPVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDISGGTITLSNIGGIGGKFGSPLVNSPEVA IIAMGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	505 aa
		Sga	>Sga_BCKDE2_protein_Sopen01g028100_XM_015207292.2_scaffold6421_10.7_contig15_505_aa MICRKIYQGKLPNSVLRQTIFRWFQSSVETPVTPVTSTVSSGKRIQSQLHFLRIYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVDGIIDIPLAQTGEGIAECELIKWFV QEGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDPTETSDASEKMISLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYSL DINDVPATGKGGRILKEDVINYAMQKGLINGAPACEQQNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHTF LPVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDVSGGTITLSNIGGIGGKFGSPLVNSPEVAI IAMGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	505 aa
		Spr	>Spr_BCKDE2_protein_Sopen01g028100_XM_015207292.2_a38204_505_aa MICRKIYQGKLPNSVLRQTIFRWFQSSVETPVTPVTSTVSSGKRIQSQLHFLRNYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVGGIIDIPLAQTGEGIAECELIKWF VQEGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDPTETSDASEKMISLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYS LDINDVPATGKGGRILKEDVINYAMQKGLINGAPACEQQNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHT FLPVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDISGGTITLSNIGGIGGKFGSPLVNSPEVA IIAMGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	505 aa
		Sch	>Sch_BCKDE2_protein_Sopen01g028100_XM_015207292.2_scaffold7233_503_aa MICRKIYQGKLPNSVLRQTIFRWFQSSVETPVTTSTVSSGKRIQSQLHFLRNYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVGGIIDIPLAQTGEGIAECELIKWFVQ EGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDLTETSDASEKMTSLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYSLDI NDVLATGKGGRILKEDVINYAMQKGLINGAPACEQHNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHTFL PVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDISGGTITLSNIGGIGGKFGSPLVNSPEVAIIA MGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	503 aa
		SpiLA1589	>SpiLA1589_BCKDE2_protein_Sopen01g028100_XM_015207292.2_contig:unspecified:3749617:1:11322:1_505_aa MICRKIYQGKLPNSVLRQTIFRWFQSSVETPVTPVTSTVSSGKRIQSQLHFLRIYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVDGIIDIPLAQTGEGIAECELIKWFV QEGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDPTETSDASEKMISLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYSL DINDVPATGKGGRILKEDVINYAMQKGLINGAPACEQQNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHTF LPVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDVSGGTITLSNIGGIGGKFGSPLVNSPEVAI IAMGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	505 aa
		SpiLA0480	>SpiLA0480_BCKDE2_protein_Sopen01g028100_XM_015207292.2_Scaffold3067685_505_aa MICRKTYQGKLPNSVLRQTIFRWFQSSVETPVTPVTSTVSSGKRIQSQLHFLRIYTPPFCSYTKSNASFTLRGCGFSTQAALDIPVDGIIDIPLAQTGEGIAECELIKWF VQEGDQVEEFQPLCEVQSDKATIEITSRYKGKISQILHVPGSIVKVGETLLKIGVDEILDPTETSDASEKMILLESDFSGTSDISSVPAETKMGGVLSTPAVRNLAKQYS LDINDVPATGKGGRILKEDVINYAMQKGLINGAPACEQQNLSEVSPPIGGGYEDKTLQLRGYQRAMVKSMTLAAKIPHFHYVEEINCDALVELKTSFKNETSDPEIKHT FLPVLIKSLSMALTTHPMLNSRFSEESYEVILKGSHNIGIAMATPNGLVVPNIKNVQSLSILEITKELSRLLNCAKINKLSSDDVSGGTITLSNIGGIGGKFGSPLVNSPEV AIIAMGRIQKIPHFAEDGNVCPASVMTINIGADHRVLDGATVARFCNDWKKFVEKPDLLLLHTR	505 aa
Isopropylmalate synthase	**IPMSA**	*Sly*	>IPMSA-1_Solyc08g014240.3.1_XP_010324707.1_Length=414 MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIARQLVKLGVDVIEAGFPASSEVEFELVKSIAHEIGNSIDEEGYVPMICGAARCTKKEIERCWEALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARTLGCEHVRFAIEDATRSDKEFLCHIIGEIIKAGATCICLADTVGCNLPNEFGQLVAHVKVNTPGIQNVIL AVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMAIKCRGEEVLGGVHTGINTKHIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGILK NRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFDDKVLEDLFWRFKSMAGNKKNITDDDLRALVSNEDIQTQIA	414 aa
			>IPMSA2_Solyc08g014130.3.1_ NP_001316379.1_Length=661 MTWYPLGSNNLEYTFFFLLYKSPHFVSIKTPLFLFSSVFDPFLHIFRMSSSSSLCSNSVFSYRNNFSIFQSKNVLLPPISSTNNFSFSIKKHYYSTFIRCSISNRRPEYVP SKISDPKYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEAGFPASSEADFESVKLIAEEIGNNTDENGFVPVICGLSRCNKSDIDKAWEAVKYAKKPRVH TFIATSEIHMKYKLKMSREQVVEKARSMVAYARSLGCEDVEFSPEDAGRSDREFLYDILGEVIKAGATTLNIPDTVGYTVPSEFGQLIADIKANTPGIENVIISTHCQND LGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQVLGGLYTGINTQHIVPSSKMVEEYSGLQVQPHKAIVGANAFAHESGIHQDGMLKHKDTY EIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELEDLFWRFKSVAEKKKKITDDDLIALMSDEVLQPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQ EHIACSVGTGPVDAAYKAVDLIVKVPITLLEYSMNAVTEGIDAIASTRVSICSIDRHTIMNGSTGQTIHRTFSGTGADMDVVISSVRAYIGALNKMLSYEKLVSRYSKPED SVVV	661 aa
			>IPMSA3_Solyc08g014230.3.1_NP_001306258.1_Length=445 MTSLCANYSFGNYISLHSKNNSVPPIKRNFQSSYDIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMKIACQLAKLGVDVIEVGFPAASHAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKA GATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVVLAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGGEVLGGVYTGINTKYIFTTS	445 aa

			NMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGMLKNRGTYEFISAEDVGFIRATKHGIKLGKLSGRHALKNKMLELGYSFEEKQLGDLFWRFKSLAEGKKNITDDD LRALILDETI	
		Spe	>Sopen08g005140 MTSLCANYSFGNYISLHSKNNSVPPIKRNFHSSYGIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMEIACQLAKLGVDVIEVGFPAASQAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWEGLKYAKTPMIHMFIATSDMHMKYKLNMGREEVVERARSMVAYATSPGFEHVRFSLEDATRSDKDFVYHIIEEVIK AGATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVILAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEEVLGGVYTGINTKYIFTT SNMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGMLKNRGTYEFISAEDVGFIRATEHGIKLGKLRI*	394 aa
			>Sopen10g006110 MTSLCANYSFGNYISLHSKNNSVPPIKRNFHSSYGIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMEIACQLAKLGVDVIEVGFPAASQAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWEGLKYAKTPMIHMFIATSDMHMKYKLNMGREEVVERARSMVAYATSPGFEHVRFSLEDATRSDKEFVYHIIEEVIK AGATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVILAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEEVLGGVYTGINTKYIFTT SNMVEEYSGLKLQPNKAIVGANAFSHESGIHQVNFI*	363 aa
			>IPMSA-1_Sopen08g005150_XP_015083287.1_Length=414 MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIAHQLVKLGVDVIEAGFPASSEVEFELVKSIAHEIGNSVDEEGYVPMICGAARCTKKEIERCWDALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARSLGCEHVRFAIEDATRSDKEFLCHIIGEIIKAGATCICLADTVGCNLPNEFGQLVAHVKANTPGIQNVIL AVHCHNDLGLATANTLAGICSGVRQVDVTINGIGERAGNASLEEIVMAIKCRGEEVLGGVYTGINTKHIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGILK NRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFEDKVLEDLFWRFKSMAGNKKNITDDDLRALVSNEDIQTQIA	414 aa
			>IPMSA2_Sopen08g005060_NP_001310380.1_Length=589 MSSSSLCSNSVFSHRNNFSIFQSKNVLLPPISNTNNFSFSIKKHHYCTFIRCSISNRRPEYIPSKISDPKYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIE AGFPASSEADFESVKLIAEEIGNNTDENGFVPVICGLSRCNKSDIDKAWEAVKYAKKPRVHTFIATSEIHMKYKLKMSREQVVEKAKSMVAYARSLGCEDVEFSPEDA GRSDREFLYDILGEVIKAGATTLNIPDTVGYTVPSEFGQLIADIKANTPGIENVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGE QVLGGLYTGINTQHIVPSSKMVEEYTGLQVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELEDL FWRFKSVAEKKKKITDDDLIALMSDEVLQPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQEHIACLVGTGPVDAAYKAVDLIVKVPITLLEYSMNAVTEGIDAIASTRV SICSDDRHTIMNGSTGQTIHRTFSGTGADMDVVISSVRAYIGALNKMLSFEKLVSRYSKPEDSVVV	589 aa
		Sga	>Sga_IPMSA2_mRNA_Solyc08g014130_NM_001329450.1_scaffold90874_8.2_contig_22470nt_614_aa MSSSSSLCSNSVFSYRNNFSIFQSKNVLLPPISSTNNFSFSIKKHYYSTFIRCSISNRRPEYVPSKISDPKYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDII EAGFPASSEADFESVKLIAEEIGNNTDENGFVPVICGLSRCNKSDIDKAWEAVKYAKKPRVHTFIATSEIHMKYKLKMSREQVVEKARSMVAYARSLGCEDVEFSPED AGRSDREFLYDILGEVIKAGATTLNIPDTVGYTVPSEFGQLIADIKANTPGIENVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRG EQVLGGLYTGINTQHIVPSSKMVEEYSGLQVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELED LFWRFKSVAEKKKKITDDDLIALMSDEVLQPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQEHIACSVGTGPVDAAYKAVDLIVKVPITLLEYSMNAVTEGIDAIASTR VSICSIDRHTIMNGSTGQTIHRTFSGTGADMDVVISSVRAYIGALNKMLSYEKLVSRYSKPEDSVVV	614 aa
			>Sga_IPMSA2_mRNA_Sopen08g005060_NM_001323451.1_scaffold90874_8.2_contig_22127nt_586_aa XNNFSIFQSKNVLLPPISSTNNFSFSIKKHYYSTFIRCSISNRRPEYVPSKISDPKYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEAGFPASSEADFESV KLIAEEIGNNTDENGFVPVICGLSRCNKSDIDKAWEAVKYAKKPRVHTFIATSEIHMKYKLKMSREQVVEKARSMVAYARSLGCEDVEFSPEDAEVIKAGATTLNIPDT VGYTVPSEFGQLIADIKANTPGIENVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQVLGGLYTGINTQHIVPSSKMVEEYSG LQVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELEDLFWRFKSVAEKKKKITDDDLIALMSDEVL QPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQEHIACSVGTGPVDAAYKAVDLIVKVPITLLEYSMNAVTEGIDAIASTRVSICSIDRHTIMNGSTGQTIHRTFSGTGA DMDVVISSVRAYIGALNKMLSYEKLVSRYSKPEDSVVV	586 aa
			>Sga_IPMSA3_mRNA_Solyc08g014230_NM_001319329.1_C9561637_9.0_1566nt_445_aa MTSLCANYSFGNYISLHSKNNSVPPIKRNFQSSYDIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMKIACQLAKLGVDVIEVGFPAASQAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKA GATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVVLAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEVVMALKCRGEEVLGGVHTGINTKHIFT TSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGMLKNRGTYEFISAEDVGFIRATKHGIKLGKLSGRHALKNKMLELGYSFEEKQLGDLFWRFKSLAEKKKNITDD DLRALILDETI	445 aa
			>Sga_IPMSA1_mRNA_Solyc08g014240_XM_010326405.3_scaffold104176_10.7_contig2_1595nt_414_aa MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIAHQLVKLGVDVIEAGFPASSEVEFELVKSIAHEIGNSIDEEGYVPMICGAARCTKKEIERCWEALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARTLGCEHVRFAIEDATRSDKEFLCHIIGEIIKAGATCICLADTVGCNLPNEFGQLVAHVKANTPRIQNVIL AVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEVVMALKCRGEEVLGGVHTGINTKHIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGIL KNRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFDDKVLEDLFWRFKSMAGNKKNITDDDLRALVSNEDIQTQIA	414 aa
			>Sga_IPMSA1_mRNA_Sopen08g005150_XM_015227801.2_scaffold104176_10.7_contig2_1471nt_414_aa MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIAHQLVKLGVDVIEAGFPASSEVEFELVKSIAHEIGNSIDEEGYVPMICGAARCTKKEIERCWEALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARTLGCEHVRFAIEDATRSDKEFLCHIIGEIIKAGATCICLADTVGCNLPNEFGQLVAHVKANTPRIQNVIL AVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEVVMALKCRGEEVLGGVHTGINTKHIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGIL KNRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFDDKVLEDLFWRFKSMAGNKKNITDDDLRALVSNEDIQTQIA	414 aa
			>Sga_mRNA_Sopen10g006110_NM_001323473.1_C9561637_9.0_1178nt_386_aa MTSLCANYSFGNYISLHSKNNSVPPIKRNFQSSYDIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMKIACQLAKLGVDVIEVGFPAASQAEFDLVKLV	386 aa

			AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKA GATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVVLAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEVVMALKCRGEEVLGGVHTGINTKHIFT TSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGILKNRSTYEFISAEDIGFIRSTEHX	
			>Sga_mRNA_Sopen08g005140_NM_001323449.1_C9561637__9.0_1178nt_386_aa MTSLCANYSFGNYISLHSKNNSVPPIKRNFQSSYDIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMKIACQLAKLGVDVIEVGFPAASQAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKA GATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVVLAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEVVMALKCRGEQVLGGLYTGINTQHILM SSKMVEEYSGLQVQPHKAIVGANAFAHESGIHQDGMLKNRGTYEFISAEDVGFIRATKHX	386 aa
		Sch	>Sch_mRNA_Sopen10g006110_NM_001323473.1_scaffold6177_1187nt_389_aa MTSLCANSTIYSFGNYISLHSKNNSVPPIKRNFHASYGIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTTKQKMEIACQLAKLGVDVIEVGFPAASQAEFDLVK LVAQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVI KAGATCICVADTVGCNLPNEFAQLIVDIKANILGIQNVILAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEEVLGGVYIGINTKNIFTT SNMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGILKNRGTYEFISAEDVGFIRATEHX	389 aa
			>Sch_mRNA_Sopen08g005140_NM_001323449.1_scaffold6177_1187nt_389_aa MTSLCANSTIYSFGNYISLHSKNNSVPPIKRNFHASYGIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTTKQKMEIACQLAKLGVDVIEVGFPAASQAEFDLVK LVAQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVI KAGATCICVADTVGCNLPNEFAQLIVDIKANILGIQNVILAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEEVLGGVYTGINTKYIFTT SNMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGMLKNRGTYEFISAEDVGFIHATKHX	389 aa
			>Sch_IPMSA2_mRNA_Solyc08g014130_NM_001329450.1_scaffold7114_2472nt_594_aa XNNFSIFQSKNVLLPPISNTNNFSFSIKKHHYSTFIRCSISNRRPEYIPSKISDPKYVRIFDTTLRDGATMTTKEKLDVARQLAKLGVDIIEAGFPASSEADFESVKLIAEEI GNNTDEIGFVPVICGLSRCNKSDIDKAWAAVKYAKKPRVHTFIATSEIHMKYKLKMSREQVVEKARSMVAYARSLGCEDVEFSPEDAGRSDREFLYDILGEVIKAGAT TLNIPDTVGYTVPSEFGQLIADIKANTPGIENVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQVLGGLYTGINTQHIVPSSKM VEEYTGLQVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELEDLFWRFKSVAEKKKKITDDDLIAL MSDEVLQPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQEQIACSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTEGIDAIASTRVLICSDDRHTIMNGSTGQTIHR TFSGTGADMDVVISSVRAYIGALNKMLSFEKLVSRYSKPEDSVVV	594 aa
			>Sch_IPMSA3_mRNA_Solyc08g014230_NM_001319329.1_scaffold21581_1565nt_376_aa MTTKQKMEIACQLAKLGVDVIEVGFPAASQAEFDLVKLVAQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERA RSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKAGATCICVADTVGCNLPNEFAQLIVDIKANILGIQNVILAVHCHNDLGLATANTLAGICAGVRQVDVTINGIG ERAGNASLEEIVMTIKYRGEEVLGGVYTGINTKYIFTTSNMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGMLKNRGTYEFISAEDVGFIHATKHGIKLGKLSGRHAL KIKMLELGYNFEEKQLGDLFWRFKSLSEGKKNITDDDLRALILDETI	376 aa
			>Sch_IPMSA1_mRNA_Solyc08g014240_XM_010326405.3_scaffold7732_1592nt_327_aa MICGAARCTKKEIERCWDALKYAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARSLGCEHVRFAIEDATRSDKEFLCHIIGEIIKAGATCICLADTVGCNLPN EFGQLVAHVKANTPGIQNVILAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMAIKYRGEEVLGGVYTGINTKHIFTTSNMVEEYSGLKLQPHK AIVGVNAFSHESGIHQDGILKNRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFEDKVLEDLFWRFKSMAGNKKNITNDDLRALVSNEDIQTQIA	327 aa
			>Sch_IPMSA1_mRNA_Sopen08g005150_XM_015227801.2_scaffold7732_1470nt_414_aa MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIAHQLVKLGVDVIEAGFPSSSEVEFELVKSIAHEIGNSVDEEGYVPMICGAARCTKKEIERCWDALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARSLGCEHVRFAIEDATRSDKEFLCHIIGEIIKAGATCICLADTVGCNLPNEFGQLVAHVKANTPGIQNVIL AVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMAIKYRGEEVLGGVYTGINTKHIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGILK NRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFEDKVLEDLFWRFKSMAGNKKNITNDDLRALVSNEDIQTQIA	414 aa
		SpiLA1589	>SpiLA1589_IPMSA2_mRNA_Solyc08g014130_NM_001329450.1_contig:unspecified:921951:1:3418:1_2471nt_614_aa MSSSSSLCSNSVFSYRNNFSIFQSKNVLLPPISSTNNFSFSIKKHHYSTFIRCSISNRRPEYVPSKISDPKYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDII EAGFPASSEADFESVKLIAEEIGNNTDENGFVPVICGLSRCNKSDIDKAWEAVKYAKKPRVHTFIATSEIHMKYKLKMSREQVVEKARSMVAYARSLGCEDVEFSPED AGRSDREFLYDILGEVIKAGATTLNIPDTVGYTVPSEFGQLIADIKANTPGIENVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRG EQVLGGLYTGINTQHIVPSSKMVEEYSGLQVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELED LFWRFKSVAEKKKKITDDDLIALMSDEVLQPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQEHIACSVGTGPVDAAYKAVDLIVKVPITLLEYSMNAVTEGIDAIASTR VSICSIDRHTIMNGSTGQTIHRTFSGTGADMDVVISSVRAYIGALNKMLSYEKLVSRYSKPEDSVVV	614 aa
			>SpiLA1589_IPMSA3_mRNA_Solyc08g014230_NM_001319329.1_contig:unspecified:6495264:1:3291:1_1544nt_423_aa MTSLCANYSFGNYISLHSKNNSVPPIKRNFQSSYDIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMKIACQLAKLGVDVIEVGFPAASQAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKA GATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVVLAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEKVLGGVYTGINTKYIFTTS NMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGMLKNRGTYEFISAEDVGFIRATKHGIKLGKLSGRHALKNKMLELGYSFEEKQLGDLFWRFRI	423 aa
			>SpiLA1589_IPMSA1_mRNA_Solyc08g014240_XM_010326405.3_contig:unspecified:6445387:1:16869:1_1601nt_414_aa MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIARQLVKLGVDVIEAGFPASSEVEFELVKSIANEIGNSVDEEGYVPMICGAARCTKKEIERCWEALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARTLGCEHVRFAIEDATRSDKEFLCHIIGGIIKAGATCICLADTVGCNLPNEFGQLVAHVKANTPGIQNVIL AVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMAIKCRGEEVLGGVHTGINTKHIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGILK NRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFDDKVLEDLFWRFKSMAGNKKNITDDDLRALVSNEDIQTQIA	414 aa

		SpiLA0480	>SpiLA0480_IPMSA2_mRNA_Solyc08g014130_NM_001329450.1_Scaffold2425123_2472nt_614_aa MSSSSSLCSNSVFSYRNNFSIFQSKNVLLPPISSTNNFSFSIKKHHYSTFIRCSISNRRPEYVPSKISDPKYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDII EAGFPASSEADFESVKLIAEEIGNNTDENGFVPVICGLSRCNKSDIDKAWEAVKYAKKPRVHTFIATSEIHMKYKLKMSREQVVEKARSMVAYARSLGCEDVEFSPED AGRSDREFLYDILGEVIKAGATTLNIPDTVGYTVPSEFGQLIADIKANTPGIENVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRG EQVLGGLYTGINTQHIVPSSKMVEEYSGLQVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPDDVGLSRSNEAGIVLGKLSGRHALKSKMLELGYDIDGKELED LFWRFKSVAEKKKKITDDDLIALMSDEVLQPNVYWKLGDVQIMCGSLGLSTATVKLINTDGQEHIACSVGTGPVDAAYKAVDLIVKVPITLLEYSMNAVTEGIDAIASTR VSICSIDRHTIMNGSTGQTIHRTFSGTGADMDVVISSVRAYIGALNKMLSYEKLVSRYSKPEDSVVV	614 aa
			>SpiLA0480_IPMSA3_mRNA_Solyc08g014230_NM_001319329.1_Scaffold3066246_1566nt_445_aa MTSLCANYSFGNYISLHSKNNSVPPIKRNFQSSYDIRCSNIQRGKLSDPNYVTIFDTTLRDGEQAPGASMTAKQKMKIACQLAKLGVDVIEVGFPAASQAEFDLVKLV AQKIGNNIDEEGYVPMICGLARSTKEDIDRAWESLKYAKTPMIHMFIATSDMHMKYKLNMSREEVVERARSMVAYATSLGFEHVRFSLEDATRSDKEFVYHIIEEVIKA GATCICVADTVGCNLPNEFAQLIVDIKANTLGIQNVVLAVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEKVLGGVYTGINTKYIFTTS NMVEEYSGLKLQPNKAIVGANAFSHESGIHQDGMLKNRGTYEFISAEDVGFIRATKHGIKLGKLSGRHALKNKMLELGYSFEEKQLGDLFWRFKSLAEGKKNITDDD LRALILDETV	445 aa
			>SpiLA0480_IPMSA1_mRNA_Solyc08g014240_XM_010326405.3_Scaffold3063254_1601nt_414_aa MTLVNGLNKFSNPNYVSIFDTTLRDGEQAPGAAMTAKQKMDIARQLVKLGVDVIEAGFPASSEVEFELVKSIANEIGNSVDEEGYVPMICGAARCTKKEIERCWEALK YAKIPMICTFIATSDIHMKYKLNMSREQVVEKATSMVAYARTLGCEHVRFAIEDATRSDKEFLCHIIGGIIKAGATCICLADTVGCNLPNEFGQLVAHVKANTPGIQNVIL AVHCHNDLGLATANTLAGICAGVRQVDVTINGIGERAGNASLEEIVMTIKYRGEKVLGGVYTGINTKYIFTTSNMVEEYSGLKLQPHKAIVGVNAFSHESGIHQDGILK NRSTYEFISAEDIGFIRSTEHGIKLGKLSGRHALKAKMLLLGYNFDDKVLEDLFWRFKSMAGNKKNITDDDLRALVSNEDIQTQIA	414 aa
	IPMSB	*Sly*	>Solyc06g053400.3.1_NP_001306252.1_Length=612aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFW RFKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRV LIRGENGHTSTHAVTGETIHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	612 aa
		Spe	>Sopen06g018460_NP_001310373.1_Length=612 MASITANNPISGNPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPIVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEAG FPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAGR SDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQV LGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFWR FKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTCGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLI RGENGHTSTHALTGETVHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	612 aa
		Sga	>Sga_mRNA_Solyc06g053400_NM_001319323.1_2218nt_scaffold78620_12.4_contig_6_612_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFW RFKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRV LIRGENGHTSTHAVTGETIHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	612 aa
			>Sga_mRNA_Sopen06g018460_NM_001323444.1_scaffold78620_12.4_contig_6_2150nt_594_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESELGYEIEGKELDDLFWRFKSVAEKKKKITDDDLV ALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLIRGENGHTSTHAVTGET IHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	594 aa
		Spr	>Spr_mRNA_Solyc06g053400_NM_001319323.1_a5613_2202nt_612_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPIVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEAG FPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAGR SDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGELIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQV LGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKNTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFWR FKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLI RGENGHTSTHALTGETVHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVI	612 aa
		Sch	>Sch_mRNA_Solyc06g053400_NM_001319323.1_scaffold3988_2209nt_612_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPIVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEAG FPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAGR	612 aa

			SDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQV LGGLYTGINTKHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFWR FKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTCGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLI RGENGHTSTHALTGETVHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVI	
			>Sch_mRNA_Sopen06g018460_NM_001323444.1_scaffold3988_2149nt_594_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPIVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEAG FPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAGR SDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQV LGGLYTGINTKHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESELGYEIEGKELDDLFWRFKSVAEKKKKITDDDLVA LMSDEVFQPQFVWQLQNVQVTCGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLIRGENGHTSTHALTGETV HRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVI	594 aa
		SpiLA1589	>SpiLA1589_mRNA_Sopen06g018460_NM_001323444.1_contig:unspecified:6617565:1:10356:1_2150nt_594_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSLSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESELGYEIEGKELDDLFWRFKSVAEKKKKITDDDLV ALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLIRGENGHTSTHAVTGET IHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	594 aa
			>SpiLA1589_mRNA_Solyc06g053400_NM_001319323.1_contig:unspecified:6617565:1:10356:1_2218nt_612_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSLSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFW RFKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRV LIRGENGHTSTHAVTGETIHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	612 aa
		SpiLA0480	>SpiLA0480_mRNA_Solyc06g053400_NM_001319323.1_Scaffold3065567_2209nt_612_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESGIVLGKLSGRHALQAKMLELGYEIEGKELDDLFW RFKSVAEKKKKITDDDLVALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRV LIRGENGHTSTHAVTGETIHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	612 aa
			>SpiLA0480_mRNA_Sopen06g018460_NM_001323444.1_Scaffold3065567_2149nt_594_aa MASITANHPISGKPLISFRPKNPLLQTQTLFNFKPSISKHSNSSFSIPVVRCSIRRRPEYTPSHIPDPNYVRIFDTTLRDGEQSPGATMTTKEKLDVARQLAKLGVDIIEA GFPASSEADLEAVKLIAKEVGNGVYEEGYVPVICGLARCNKKDIDKAWEAVKYAKKPRIHTFIATSEIHMNYKLKMSRDQVVEKARSMVAYARSIGCEDVEFSPEDAG RSDPEFLYHILGEVIKAGATTLNIPDTVGYTVPEEFGQLIAKIKANTPGVEDVIISTHCQNDLGLSTANTLAGACAGARQLEVTINGIGERAGNASLEEVVMALKCRGEQ VLGGLYTGINTQHILMSSKMVEEYSGLHVQPHKAIVGANAFAHESGIHQDGMLKHKDTYEIISPEDIGLNRANESELGYEIEGKELDDLFWRFKSVAEKKKKITDDDLV ALMSDEVFQPQFVWQLQNVQVTSGSLGLSTATVKLIDADGREHISCSVGTGPVDAAYKAVDLIVKVPVTLLEYSMNAVTQGIDAIASTRVLIRGENGHTSTHAVTGET IHRTFSGTGADMDIVISSVRAYVGALNKMMSFRKLMAKNNKPESSAVV	594 aa

Supplementary Table S5. Distribution of conserved domains and their locations in putative BCKD proteins identified in seven species of the tomato and their orthologous.

Protein families	Specie	ID protein	ID protein query SolGenomics	ID query	Protein Length	Conserved domain	Domain ID	Start and End	E-value
BCKD-E2	*Ortholog in Solanum tuberosum*	NP_001305524.1	_	_	505 aa	2-oxoacid_dh	(PF00198)	274-502	2.1e-77
						Biotin_lipoyl	(PF00364)	92-163	1.5e-17
						E3_binding	(PF02817)	206-240	2.3e-13
	Arabidopsis thaliana	NP_187341.1 2	_	_	483 aa	2-oxoacid_dh	(PF00198)	251-480	1.8e-77
						Biotin_lipoyl	(PF00364)	78-149	2.0e-18
						E3_binding	(PF02817)	184-217	1.7e-14
	Solanum lycopersicum	XP_004229256.1	Solyc01g066520	_	505 aa	2-oxoacid_dh	(PF00198)	274-502	6.4e-78
						Biotin_lipoyl	(PF00364)	92-163	1.8e-18
						E3_binding	(PF02817)	206-240	1.5e-13
	Solanum penneellii	XP_015062778.1	Sopen01g028100	_	505 aa	2-oxoacid_dh	(PF00198)	274-502	7.3e-78
						Biotin_lipoyl	(PF00364)	92-163	1.8e-18
						E3_binding	(PF02817)	206-240	1.5e-13
	Solanum galapagense	scaffold6421_10.7_contig15	Sopen01g028100	XP_015062778.1	505 aa	2-oxoacid_dh	(PF00198)	274-502	6.4e-78
						Biotin_lipoyl	(PF00364)	92-163	1.8e-18
						E3_binding	(PF02817)	206-240	1.5e-13
	Solanum peruvianum	a38204	Sopen01g028100	XP_015062778.1	505 aa	2-oxoacid_dh	(PF00198)	274-502	7.3e-78
						Biotin_lipoyl	(PF00364)	92-163	1.8e-18
						E3_binding	(PF02817)	206-240	1.5e-13
	Solanum pimpinellifolium LA1589	contig:3749617:1:11322:1	Sopen01g028100	XP_015062778.1	505 aa	2-oxoacid_dh	(PF00198)	274-502	6.4e-78
						Biotin_lipoyl	(PF00364)	92-163	1.8e-18
						E3_binding	(PF02817)	206-240	1.5e-13
	Solanum pimpinellifolium LA0480	Scaffold3067685	Sopen01g028100	XP_015062778.1	505 aa	2-oxoacid_dh	(PF00198)	274-502	6.4e-78
						Biotin_lipoyl	(PF00364)	92-163	1.8e-18
						E3_binding	(PF02817)	206-240	1.5e-13
	Solanum chilense	scaffold7233	Sopen01g028100	XP_015062778.1	503 aa	2-oxoacid_dh	(PF00198)	272-500	7.2e-78
						Biotin_lipoyl	(PF00364)	90-161	1.8e-18
						E3_binding	(PF02817)	204-238	1.9e-12

BCKD-E1a	*Ortholog in Solanum tuberosum*	NP_001275386.1	_	_	391 aa	E1_dh	(PF00676)	67-362	8.6e-115
		XP_006363541.1	_	_	388 aa	E1_dh	(PF00676)	64-359	5.6e-113
	Solanum lycopersicum	NP_001234066.2	Solyc06g059840	_	456 aa	E1_dh	(PF00676)	119-415	3.8e-97
		XP_004239633.1	Solyc05g056480	_	467 aa	E1_dh	(PF00676)	132-428	3.1e-95
		XP_004237706.1	Solyc04g063350	_	472 aa	E1_dh	(PF00676)	135-432	2.9e-95
	Solanum penneellii	XP_015074287.1	Sopen04g026270	_	472 aa	E1_dh	(PF00676)	135-432	3.7e-95
		XP_015076473.1	Sopen05g034880	_	467 aa	E1_dh	(PF00676)	132-428	1.1e-95
		XP_015077702	Sopen06g019920	_	442 aa	E1_dh	(PF00676)	105-401	4.3e-98
		XP_015078845.1	Sopen06g019930	_	445 aa	E1_dh	(PF00676)	108-405	4.8e-96
		XP_015074054.1	Sopen04g001100	_	391 aa	E1_dh	(PF00676)	67-362	1.4e-113
		XP_015076383.1	Sopen05g002470	_	391 aa	E1_dh	(PF00676)	67-362	1.6e-114
	Solanum galapagense	scaffold115541_10.3_C9451447_10.0	Solyc06g059840	NP_001234066.2	442 aa	E1_dh	(PF00676)	105-401	1.7e-97
		scaffold81122_13.5_contig1	Solyc05g056480	XP_004239633.1	467 aa	E1_dh	(PF00676)	132-428	3.1e-95
		scaffold83116_11.2_contig2_374	Solyc04g063350	XP_004237706.1	374 aa	E1_dh	(PF00676)	56-274	4.9e-67
		scaffold83116_11.2_contig2	Sopen04g026270	XP_015074287.1	393 aa	E1_dh	(PF00676)	56-353	5.5e-96
		scaffold105084_6.4_contig3	Sopen06g019930	XP_015078845.1	380 aa	E1_dh	(PF00676)	43-339	3.4e-96
		scaffold99439_13.8_contig1	Sopen04g001100	XP_015074054.1	391 aa	E1_dh	(PF00676)	67-362	7.0e-113
		scaffold110240_12.2_contig5	Sopen05g002470	XP_015076383.1	349 aa	E1_dh	(PF00676)	6-294	1.7e-112
	Solanum chilense	scaffold18074	Solyc06g059840	NP_001234066.2	442 aa	E1_dh	(PF00676)	105-401	1.2e-97
		scaffold418	Solyc05g056480	XP_004239633.1	467 aa	E1_dh	(PF00676)	132-428	3.3e-95
		scaffold4382	Solyc04g063350	XP_004237706.1	472 aa	E1_dh	(PF00676)	135-432	4.2e-95
		scaffold10778	Sopen06g019930	XP_015078845.1	443 aa	E1_dh	(PF00676)	106-402	9.5e-96
		scaffold123	Sopen04g001100	XP_015074054.1	378 aa	E1_dh	(PF00676)	67-362	6.2e-113
		scaffold3266	Sopen05g002470	XP_015076383.1	438 aa	E1_dh	(PF00676)	75-370	2.4e-114
	Solanum peruvianum	a194813	Solyc06g059840	NP_001234066.2	361 aa	E1_dh	(PF00676)	43-339	8.9e-97
		a142361	Solyc05g056480	XP_004239633.1	402 aa	E1_dh	(PF00676)	67-363	6.3e-96
		A17497	Solyc04g063350	XP_004237706.1	472 aa	E1_dh	(PF00676)	135-432	2.9e-95
		a9028	Sopen04g001100	XP_015074054.1	373 aa	E1_dh	(PF00676)	67-362	6.4e-114
	Solanum pimpinellifolium	contig::6683921:1:4011:1	Solyc06g059840	NP_001234066.2	442 aa	E1_dh	(PF00676)	105-401	3.4e-97
		contig:6644818:1:18043:1	Solyc05g056480	XP_004239633.1	372 aa	E1_dh	(PF00676)	37-333	1.5e-95

	LA1589	contig:6595385:1:3779:1	Solyc04g063350	XP_004237706.1	393 aa	E1_dh	(PF00676)	56-353	1.7e-95
		contig:1263451:1:6634:1	Sopen06g019930	XP_015078845.1	443 aa	E1_dh	(PF00676)	106-402	6.8e-96
		contig:2579139:1:3053:1	Sopen04g001100	XP_015074054.1	324 aa	E1_dh	(PF00676)	1-295	2.1e-113
		contig:4584595:1:7163:1	Sopen05g002470	XP_015076383.1	324 aa	E1_dh	(PF00676)	2-295	2.3e-114
	Solanum pimpinellifolium LA0480	Scaffold3066199	Solyc06g059840	NP_001234066.2	380 aa	E1_dh	(PF00676)	43-339	2.1e-97
		Scaffold3061128	Solyc05g056480	XP_004239633.1	467 aa	E1_dh	(PF00676)	132-428	3.1e-95
		Scaffold3071394	Solyc04g063350	XP_004237706.1	393 aa	E1_dh	(PF00676)	56-353	1.7e-95
		Scaffold3066199	Sopen06g019930	XP_015078845.1	440 aa	E1_dh	(PF00676)	103-399	6.6e-96
		Scaffold3069794	Sopen04g001100	XP_015074054.1	391 aa	E1_dh	(PF00676)	67-362	7.0e-113
		Scaffold3065109	Sopen05g002470	XP_015076383.1	399 aa	E1_dh	(PF00676)	75-370	8.5e-114
BCKD-E1b	*Ortholog in Solanum tuberosum*	XP_015164279.1	_	_	367 aa	Transket_pyr	(PF02779)	38-213	1.3e-46
						Transketolase_C	(PF02780)	232-354	1.7e-42
		XP_015158846.1	_	_	401 aa	Transketolase_C	(PF02780)	261-383	2.0e-42
						Transket_pyr	(PF02779)	38-168	1.5e-30
						Transket_pyr	(PF02779)	199-242	2.8e-07
		XP_006363263.1	_	_	372 aa	Transket_pyr	(PF02779)	38-213	4.8e-45
						Transketolase_C	(PF02780)	232-354	1.7e-42
		XP_006366909.1	_	_	377 aa	Transket_pyr	(PF02779)	40-215	5.3e-46
						Transketolase_C	(PF02780)	234-356	1.4e-42
	Solanum lycopersicum	XP_010321111.1	Solyc05g024160	_	371 aa	Transket_pyr	(PF02779)	37-212	6.9e-45
						Transketolase_C	(PF02780)	231-353	8.8e-43
		XP_004228950.1	Solyc01g028900	_	358 aa	Transket_pyr	(PF02779)	38-213	3.1e-44
						Transketolase_C	(PF02780)	229-348	1.4e-35
		XP_004241456.1	Solyc06g072580	_	367 aa	Transket_pyr	(PF02779)	38-213	1.3e-46
						Transketolase_C	(PF02780)	232-354	1.4e-42
	Solanum penneellii	XP_015062780.1	Sopen01g017080	_	358 aa	Transket_pyr	(PF02779)	38-213	1.6e-44
						Transketolase_C	(PF02780)	229-348	1.4e-35
		XP_015069743.1	Sopen03g028430	_	369 aa	Transket_pyr	(PF02779)	32-207	6.6e-46
						Transketolase_C	(PF02780)	226-348	1.1e-42
		XP_015074867.1	Sopen05g018850	_	372 aa	Transket_pyr	(PF02779)	38-213	3.0e-45

						Transketolase_C	(PF02780)	232-354	8.8e-43
		XP_015079698.1	Sopen06g028930	_	367 aa	Transket_pyr	(PF02779)	38-213	1.3e-46
						Transketolase_C	(PF02780)	232-354	1.4e-42
	Solanum galapagense	scaffold10693_14.0_contig4	Solyc01g028900	XP_004228950.1	336 aa	Transket_pyr	(PF02779)	49-158	6.3e-22
						Transketolase_C	(PF02780)	207-326	1.3e-35
		scaffold62230	Solyc06g072580	XP_004241456.1	329 aa	Transket_pyr	(PF02779)	1-175	2.9e-46
						Transketolase_C	(PF02780)	194-316	1.1e-42
		scaffold64088_12.4_contig1	Solyc05g024160	XP_010321111.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	8.0e-43
		scaffold62230_11.3_contig8	Sopen06g028930	XP_015079698.1	332 aa	Transket_pyr	(PF02779)	3-178	1.2e-46
						Transketolase_C	(PF02780)	197-319	1.1e-42
		scaffold64088_12.4_contig1	Sopen05g018850	XP_015074867.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	8.0e-43
		scaffold26312_11.3_contig3	Sopen03g028430	XP_015069743.1	278 aa	Transket_pyr	(PF02779)	31-116	5.2e-19
						Transketolase_C	(PF02780)	135-257	6.1e-43
	Solanum chilense	scaffold1500	Solyc01g028900	XP_004228950.1	358 aa	Transket_pyr	(PF02779)	38-213	2.0e-44
						Transketolase_C	(PF02780)	229-348	1.4e-35
		scaffold58468	Solyc06g072580	XP_004241456.1	305 aa	Transket_pyr	(PF02779)	1-159	4.1e-30
						Transketolase_C	(PF02780)	170-292	9.2e-43
		scaffold2304	Solyc05g024160	XP_010321111.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	2.8e-42
		scaffold2304	Sopen05g018850	XP_015074867.1	372 aa	Transket_pyr	(PF02779)	38-213	1.6e-45
						Transketolase_C	(PF02780)	232-354	3.6e-42
		scaffold31	Sopen03g028430	XP_015069743.1	315 aa	Transket_pyr	(PF02779)	81-165	1.2e-18
						Transketolase_C	(PF02780)	194-294	1.2e-32
	Solanum peruvianum	A11557	Solyc01g028900	XP_004228950.1	358 aa	Transket_pyr	(PF02779)	38-213	2.0e-44
						Transketolase_C	(PF02780)	229-348	1.4e-35
		a3335	Solyc06g072580	XP_004241456.1	367 aa	Transket_pyr	(PF02779)	38-213	1.6e-46
						Transketolase_C	(PF02780)	232-354	1.4e-42
		a150581	Solyc05g024160	XP_010321111.1	238 aa	Transket_pyr	(PF02779)	3_91	2.5e-18

						Transketolase_C	(PF02780)	110-232	3.2e-43
	Solanum pimpinellifolium LA1589	a150581	Solyc05g024160	XP_010321111.1	238 aa	Transket_pyr	(PF02779)	3_91	2.5e-18
						Transketolase_C	(PF02780)	110-232	3.2e-43
		contig:6610764:1:6785:1	Solyc01g028900	XP_004228950.1	358 aa	Transket_pyr	(PF02779)	44-213	1.5e-42
						Transketolase_C	(PF02780)	229-348	1.4e-35
		contig:4688340:1:2834:1	Solyc06g072580	XP_004241456.1	274 aa	Transket_pyr	(PF02779)	1-175	2.3e-46
						Transketolase_C	(PF02780)	182-273	1.1e-29
		contig:6423638:1:21070:1	Solyc05g024160	XP_010321111.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	8.0e-43
		contig:3862692:1:10449:1	Sopen06g028930	XP_015079698.1	329 aa	Transket_pyr	(PF02779)	1-175	2.9e-46
						Transketolase_C	(PF02780)	194-316	1.1e-42
		contig:6423638:1:21070:1	Sopen05g018850	XP_015074867.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	8.0e-43
		contig:5524304:1:6948:1	Sopen03g028430	XP_015069743.1	328 aa	Transket_pyr	(PF02779)	81-166	8.8e-43
						Transketolase_C	(PF02780)	185-307	8.2e-19
	Solanum pimpinellifolium LA0480	Scaffold3065941	Solyc01g028900	XP_004228950.1	358 aa	Transket_pyr	(PF02779)	43-213	8.5e-43
						Transketolase_C	(PF02780)	229-348	1.4e-35
		Scaffold3066858	Solyc06g072580	XP_004241456.1	329 aa	Transket_pyr	(PF02779)	1-175	2.9e-46
						Transketolase_C	(PF02780)	194-316	1.1e-42
		Scaffold3070794	Solyc05g024160	XP_010321111.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	8.0e-43
		Scaffold3070794	Sopen05g018850	XP_015074867.1	333 aa	Transket_pyr	(PF02779)	2-174	1.3e-44
						Transketolase_C	(PF02780)	193-315	8.0e-43
		Scaffold3063753	Sopen03g028430	XP_015069743.1	278 aa	Transket_pyr	(PF02779)	31-116	5.2e-19
						Transketolase_C	(PF02780)	135-257	6.1e-43

Supplementary Table S6. Distribution of conserved domains and their locations in putative IPMS proteins identified in seven species of the tomato and their orthologous.

Protein families	Species	ID protein	ID protein query SolGenomics	ID query	Protein Length	Conserved domain	Domain ID	Start and End	E-value
IPMSA	Ortholog in *Solanum tuberosum*	XP_015168011.1	_	_	613 aa	HMGL-like	PF00682	71-350	2.5e-92
						LeuA_dimer	PF08502	450-595	6.5e-42
		XP_006366146.2	_	_	463 aa	HMGL-like	PF00682	58-337	6.7e-92
	Solanum lycopersicum	XP_006367400.1	_	_	382 aa	HMGL-like	PF00682	25-304	1.2e-90
		XP_010324707.1	Solyc08g014240	_	329 aa	HMGL-like	PF00682	122-240	2.6e-37
		NP_001316379.1	Solyc08g014130	_	661 aa	HMGL-like	PF00682	120-398	1.1e-93
						LeuA_dimer	PF08502	498-643	5.2e-42
	Solanum pennellii	NP_001306258.1	Solyc08g014230	_	445 aa	HMGL-like	PF00682	52-331	2.1e-91
		NP_001310378.1	Sopen08g005140	_	394 aa	HMGL-like	PF00682	52-331	2.0e-90
		NP_001310402.1	Sopen10g006110	_	363 aa	HMGL-like	PF00682	52-331	8.0e-91
		XP_015083287.1	Sopen08g005150	_	414 aa	HMGL-like	PF00682	16-295	1.8e-89
		NP_001310380.1	Sopen08g005060	_	613 aa	HMGL-like	PF00682	72-350	8.4e-94
						LeuA_dimer	PF08502	450-595	8.1e-42
	Solanum galapagense	C9561637_9.0	Sopen10g006110	NP_001310402.1	386 aa	HMGL-like	PF00682	52-331	1.5e-93
		C9561637__9.0	Sopen08g005140	NP_001310378.1	386 aa	HMGL-like	PF00682	52-331	6.3e-92
		scaffold104176_10.7_contig2	Solyc08g014240	XP_010324707.1	414 aa	HMGL-like	PF00682	16-295	4.5e-91
		scaffold104176_10.7_contig2	Sopen08g005150	XP_015083287.1	414 aa	HMGL-like	PF00682	16-295	4.5e-91
		scaffold90874_8.2_contig_2	Solyc08g014130	NP_001316379.1	614 aa	HMGL-like	PF00682	73-351	9.3e-94
						LeuA_dimer	PF08502	451-596	4.6e-42
		scaffold90874_8.2_contig_2	Sopen08g005060	NP_001310380.1	586 aa	HMGL-like	PF00682	58-323	3.4e-82
						LeuA_dimer	PF08502	423-568	4.2e-42
	Solanum chilense	C9561637_9.0	Solyc08g014230	NP_001306258.1	445 aa	HMGL-like	PF00682	52-331	2.3e-93
		scaffold6177	Sopen10g006110	NP_001310402.1	389 aa	HMGL-like	PF00682	55-334	2.6e-92
		scaffold6177	Sopen08g005140	NP_001310378.1	389 aa	HMGL-like	PF00682	55-334	6.4e-93
		scaffold7732	Solyc08g014240	XP_010324707.1	327 aa	HMGL-like	PF00682	2-208	4.5e-64
		scaffold7732	Sopen08g005150	XP_015083287.1	414 aa	HMGL-like	PF00682	16-295	5.1e-90
		scaffold7114	Solyc08g014130	NP_001316379.1	594 aa	HMGL-like	PF00682	58-331	6.9e-87
						LeuA_dimer	PF08502	431-576	9.6e-42
	Solanum pimpinellifolium LA1589	scaffold21581	Solyc08g014230	NP_001306258.1	376 aa	HMGL-like	PF00682	1-262	1.1e-81
		contig:6445387:1:16869:1	Solyc08g014240	XP_010324707.1	414 aa	HMGL-like	PF00682	16-295	2.0e-90
		contig:921951:1:3418:1	Solyc08g014130	NP_001316379.1	614 aa	HMGL-like	PF00682	73-351	9.3e-94
						LeuA_dimer	PF08502	451-596	4.6e-42
	Solanum pimpinellifolium LA0480	contig:6495264:1:3291:1	Solyc08g014230	NP_001306258.1	423 aa	HMGL-like	PF00682	52-331	6.3e-92
		Scaffold3063254	Solyc08g014240	XP_010324707.1	414 aa	HMGL-like	PF00682	16-295	2.1e-89
		Scaffold2425123	Solyc08g014130	NP_001316379.1	614 aa	HMGL-like	PF00682	73-351	9.3e-94
						LeuA_dimer	PF08502	451-596	4.6e-42

		Scaffold3066246	Solyc08g014230	NP_001306258.1	445 aa	HMGL-like	PF00682	52-331	7.3e-92
IPMSB	Ortholog in *Solanum tuberosum*	XP_006350708.1	–	–	612 aa	HMGL-like	PF00682	71-350	5.3e-93
						LeuA_dimer	PF08502	449-593	5.8e-39
	Solanum lycopersicum	NP_001306252.1	Solyc06g053400	–	612 aa	HMGL-like	PF00682	71-350	5.3e-93
						LeuA_dimer	PF08502	449-593	1.6e-38
	Solanum pennellii	NP_001310373.1	Sopen06g018460	–	612 aa	HMGL-like	PF00682	71-350	5.3e-93
						LeuA_dimer	PF08502	449-593	1.6e-38
	Solanum galapagense	scaffold78620_12.4_contig_6	Solyc06g053400	NP_001306252.1	612 aa	HMGL-like	PF00682	71-350	1.9e-93
						LeuA_dimer	PF08502	449-593	1.6e-38
		scaffold78620_12.4_contig_6	Sopen06g018460	NP_001310373.1	594 aa	HMGL-like	PF00682	71-350	1.8e-93
						LeuA_dimer	PF08502	431 575	1.6e-38
	Solanum peruvianum	a5613	Solyc06g053400	NP_001306252.1	612 aa	HMGL-like	PF00682	71-350	1.1e-93
						LeuA_dimer	PF08502	449-593	1.5e-38
	Solanum chilense	scaffold3988	Solyc06g053400	NP_001306252.1	612 aa	HMGL-like	PF00682	71-350	3.1e-93
						LeuA_dimer	PF08502	449-593	1.0e-38
		scaffold3988	Sopen06g018460	NP_001310373.1	594 aa	HMGL-like	PF00682	71-350	2.8e-93
						LeuA_dimer	PF08502	431 575	9.7e-39
	Solanum pimpinellifolium LA1589	contig:6617565:1:10356:1	Sopen06g018460	NP_001310373.1	594 aa	HMGL-like	PF00682	71-350	1.8e-93
						LeuA_dimer	PF08502	431 575	1.6e-38
		contig:6617565:1:10356:1	Solyc06g053400	NP_001306252.1	612 aa	HMGL-like	PF00682	71-350	1.9e-93
						LeuA_dimer	PF08502	449-593	1.6e-38
	Solanum pimpinellifolium LA0480	Scaffold3065567	Solyc06g053400	NP_001306252.1	612 aa	HMGL-like	PF00682	71-350	1.9e-93
						LeuA_dimer	PF08502	449-593	1.6e-38
		Scaffold3065567	Sopen06g018460	NP_001310373.1	594 aa	HMGL-like	PF00682	71-350	1.8e-93
						LeuA_dimer	PF08502	431 575	1.6e-38

Supplementary Table S7. Characterization of families, mature sequences and pre-miRNAs of miRNAs in Solanum lycopersicum (sly).

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
sly-MIR319b	UUAGAUGUAAGUAGGAGCUCCUUUCAAGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAUUACUAUACUCUUAGAGGUCUGUAGUCAUUAUGUGGGUUGUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUGUUUU	198	sly-miR319b-3p	AUUGGACUGAAGGGAGCUCCU	168-188	aof-miR319b	1	0	21	21	2
sly-MIR169n	GGAUAAUGGUCUGGACAUGGUUUGUUUUGGAUGUCCGCUUGUACAGGGGCAGGCCUUGUUGGCUGUGUACAUCAUUAUAUAUUGUUAGU	171	sly-miR169n-3p	GGCAGGCCUUGUUGGCUGUG	129-148	zma-miR169n-3p	3	0	20	20	1
sly-MIR159b-1	UGGAUACUCUGUUUGUGGAUUACACUGAUAUUCAUAUAGUUGAUUUUAACUUGUUCGAGGAAGAUUAGAGUUCUGAAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACGUU	254	sly-miR159b-1-3p	AGCUGCUAAUCUAUGGAUCCC	124-144	cas-miR159b-5p	1	0	21	21	1
sly-MIR159b-2	UUGCAUACUCUGCUUGUUGAUUAUACUAAUAUUCAUAUAGUUGAUUUUAACUGUUCGAAAAAGACCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAAAGGAUCUGAGAGGGAAAAUUGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUACAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACU	254	sly-miR159b-2-3p	UUGGAAAGAAGGGAGCUCUAC	231-251	sly-miR159b	0	0	21	21	1
sly-MIR390a-1	GGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGCUC	103	sly-miR390a-1-5p	AAGCUCAGGAGGGAUAGCACC	18-38	sly-miR390a-5p	0	0	21	21	1
			sly-miR390a-1-3p	CGCUAUCCAUCCUGAGUUUUA	67-87	sly-miR390a-3p	0	0	21	21	1
sly-MIR171c-1	UCUUCUAACGAGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCACGUAUUACUAU	101	sly-miR171c-1-5p	AGAUAUUGGUGCGGUUCAAUU	11-31	cas-miR171c-5p	1	0	21	21	1
			sly-miR171c-1-3p	UUGAGCCGUGCCAAUAUCACG	72-92	cas-miR171c-3p	0	0	21	21	1
sly-MIR395b-1	GUUCCCUAGAGUUCCCUUGAUCACUUCAUUAGGGAUAACUUCGUUAUUUGAUGCCCUGCUGAAGUGUUUGGGGAAACUCCUGGGCUCA	88	sly-miR395b-1-3p	CUGAAGUGUUUGGGGAAACUCC	59-80	sly-miR395b	1	0	22	22	1
sly-MIR395a-1	GUUCCCUAGAGUUCCCUUGACCGCUUUAUUAGGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUAGGGGAACUCUUGAACUCA	88	sly-miR395a-1-3p	UGAAGUGUUUAGGGGAACUCU	60-80	aof-miR395a	1	0	21	21	1
sly-MIR395b-2	GUUCCAUAGAGUUCCCUUGACCACUUCAUGAGGGCUUACUUUGAUGUUAGAAGCAUUGCGGAAGUGUUUGGGGGAACUCCCUGGGUUGA	88	sly-miR395b-2-3p	CGGAAGUGUUUGGGGGAACUCC	59-80	sly-miR395b	1	0	22	22	1
sly-MIR395b-3	UUCCCUAGAGUUCCCUUGACCGCUUCAUUAGGGCUUACUUUGAUGUUAGAAGCAUUGCGGAAGUGUUUGGGGGAACUCCUGGGUUGAC	88	sly-miR395b-3-3p	CGGAAGUGUUUGGGGGAACUCC	58-79	sly-miR395b	1	0	22	22	1
sly-MIR395b-4	UUCCCUAGAGUUCCCUUGACCGCUUUAUUAGGGCUUACUUUAUUGUUUGAUGCCCUGUUGAAGUGUAUGGGGGAACUCUUGGACUCAC	88	sly-miR395b-4-3p	UUGAAGUGUAUGGGGGAACUC	58-78	aof-miR395b	1	0	21	21	2
sly-MIR395a-2	UUCCCUAGAGUUCCCUUGACCGCUUUAUUAGGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUAGGGGAACUCUUGAACUCAC	88	sly-miR395a-2-3p	UGAAGUGUUUAGGGGAACUCU	59-79	aof-miR395a	1	0	21	21	1
sly-MIR479-1	GAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUU	92	sly-miR479-1-5p	CGUGAUAUUGGUUUGGCUCACU	11-32	ghr-miR479	3	0	22	22	1
			sly-miR479-1-3p	UGAGCCGAACCAAUAUCACUC	62-82	aof-miR479	0	0	21	21	1
sly-MIR1917-1	UUUUAGCGGCAAUAAACAUGCACAUUAACAAAGAGUGCUA	130	sly-miR1917-	AUUAACAAAGAGUGCUAAAGC	24-44	sly-miR1917	2	0	21	21	1

	AAGCCGUUACAAGCAUUAGUUAAUUGUCAUUGGAUCCUAUGUCUCAAUAGGCUUUAGAGACAUUUACAAAGAAUGUUAAUUGCCUCUAAG		1-5p								
sly-MIR1919-1	CAUCUUCCGGUAGUCCUGUCGCAGAUGACUCUCGAUCUUGUCAUUAAGCCCCUUUCUCUAAGUCUAAUUAAUUUGAAUUCAAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUUAUGGAAGAU	124	sly-miR1919-1-5p	UGUCGCAGAUGACUCUCGAUC	17-37	stu-miR1919-5p	3	0	21	21	1
			sly-miR1919-1-3p	ACGAGAGUCAUCUGUGACAGG	92-112	stu-miR1919-3p	0	0	21	21	1
sly-MIR395b-5	AUCAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUUACUUUGAUGUUAGAAGCCUUGCUGAAGUGUUUGUGGGAACUCCUGUAUUGACUUUGA	102	sly-miR395b-5-3p	CUGAAGUGUUUGUGGGAACUCC	67-88	sly-miR395b	1	0	22	22	1
sly-MIR397-1	CAGAGUACUUAGAAACAUGAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAGUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUAAACUCGAUCAUGUUUUUAAUUCUCU	115	sly-miR397-1-5p	AUUGAGUGCAGCGUUGAUGAC	20-40	stu-miR397-5p	0	0	21	21	1
			sly-miR397-1-3p	UCAACGCUAAACUCGAUCAUG	82-102	sly-miR397-3p	0	0	21	21	1
sly-MIR2604-1	GAACAUUUACGACAAAGAAGUUUCGGAAAUGACAUUUAUCUCCUAAUUUUAUUUAUCACACUAUUGACCGCAAUCAAAAUUUUUUCCAGACUCGAUAAAAUUCCUCCGCCACUCUGUGUGUGUGUGUGUAUAUAUAUAUAUAUUGGGUUUGCUAGAACACACCCACUAAUUUUUAUGUGGAAGUGUUUUAGCAAAGCUACACCUUAAGGUGUAUUUAACUACUUUUUAGUUAUUCACUUGCUAAAAUACUCUUUCUAAAAAAUAAGUGGGUGUAUCCUAGCAAAU	287	sly-miR2604-1-3p	UAAUUUUUAUGUGGAAGUGUU	169-189	mtr-miR2604	1	0	21	21	1
sly-MIR160h-1	UGCCUGGCUCCUUGUAUGCCAUUUGCAUUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAUGGCAUUCUAGGAGCUAAGCAU	81	sly-miR160h-1-5p	UGCCUGGCUCCUUGUAUGCCAUU	1-23	mes-miR160h	1	0	23	23	1
sly-MIR319a-1	AAUAAGGAGCUCUCUCCGGUCCAGUCCGAGGCACUCAAAGGCUAAAAACACAGCUGACGACUCGUUGAUUCUCAAACAUAUCAAGAAGCAUUUUUUGAAAUUGGUGUGUUUAAGAUUCAACGAUGCGUGAGCUAUGUUUGGCUAGCGUUGUCACGUCUUGGACUGAAGGGAGCUCCCUAUUA	182	sly-miR319a-1-3p	UUGGACUGAAGGGAGCUCCCU	158-178	aof-miR319a	0	0	21	21	1
sly-MIR395b-6	UCAUGGUUUUCCCUAGAGUUCCCUUGACCACUUCAUUAGGGAUUACUUCGUUGUUUGAUGCUCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCACUCUG	100	sly-miR395b-6-3p	CUGAAGUGUUUGGGGGAACUCC	66-87	sly-miR395b	0	0	22	22	1
sly-MIR395b-7	AUCAAGGUGUUCCUAGAGUUCCCUUGACCACUUCAUUAGGGAUUACUUCGUUGUUUGAUGCUCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCACUCUG	100	sly-miR395b-7-3p	CUGAAGUGUUUGGGGGAACUCC	66-87	sly-miR395b	0	0	22	22	1
sly-MIR172-1	AUCAUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUA	164	sly-miR172-1-3p	UGGGAAUCUUGAUGAUGCUGCAU	131-153	aau-miR172	1	0	23	23	1
sly-MIR172-2	CAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAU	164	sly-miR172-2-3p	UGGGAAUCUUGAUGAUGCUGCAU	122-144	aau-miR172	1	0	23	23	1
sly-MIR172e	UCAUCCUGAAUUCUUUUAAUUCGAGGGGAAAAAGUCAUAAUUUGUCGAUGCAGCAUCAUCAAGAUUCUCAUUUUUGAAAAAAAAUAAUAAUGGAAUUUAGAAGCAACUUGAUUUUUUUUCCUACUCCAUAUUAUUUCUAUUUUAUGUGAAUCUUGAUGAUGCUGCAGCUGCAAAUAACGACUGUAC	188	sly-miR172e-5p	GCAGCAUCAUCAAGAUUCUCA	50-70	stu-miR172e-5p	2	0	21	21	1
			sly-miR172e-3p	UGAAUCUUGAUGAUGCUGCAGCUG	149-172	gma-miR172e	2	0	24	24	2
sly-MIR171a-1	GCGAUGUUGGUGUGGUUCAAUUAGAUAACAAUCUCCACGUAAAAUUAUAGAGUUUGUUAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAA	91	sly-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	62-82	aof-miR171a	0	0	21	21	1
sly-MIR5282	CAAAAUUAGCGAGGGAAAUUAGUGACGGAAAAAAUGAAAUUCCUUACAAAUUCCUUGGUCGCAAAAUUUAAUGACGGAAUUAGAGAGGGAUUUUACGUUUUCCUUCACUAUAUUUCCCUCACUAAAUU	128	sly-miR5282-3p	GACGGAAUUAGAGAGGGAUUUUAC	73-96	mtr-miR5282	2	0	24	24	1
sly-MIR5300	UUGACCAAAAUUCUUCUUCCCCAGUCCAGGCAUUCCAACAGUUGAUAACAUCUAGAUCUGCCAAUACUUUGUAUUUUUGUUCUUCUAUUUUUCACAUGACAUCUUCAAAAUCUACUAUGA	266	sly-miR5300-5p	UCCCCAGUCCAGGCAUUCCAAC	18-39	sly-miR5300	0	0	22	22	1

sly-MIR482e	GCUUCAUCAUAAGCUAAGAAAUGGUGAGUUUUGAUGAUGUGAUGCCUAAAAUAGGAUUAAAUGAAAGUACUAGUAAAAAGGUGUUCAGAUCUGGAGGUUAUGUUAAGCUGGUGGUAUGCUUUGAUUGGGAAAGAUGACUUAGGUCAAGAUCUGUGCUAUGGAAAUAUUGAUGGCGUUGAAAGGGAUGAGAGUAUUGGGAAGUUGUUGGUUGUGGGUGGGGUGGAAAGAUUUGAUAAAUCUAAUUUUAAAGAGAUUAAAUCUUUCCUACUCCUCCCAUACCCAUGACUUCCACUAGCUUCUCCCUUUCUUCAUUUGUCAUCUCCUUUGCUAAGUUC	189	sly-miR482e-5p	UGUGGGUGGGGUGGAAAGAUU	64-84	sly-miR482e-5p	0	0	21	21	1
			sly-miR482e-3p	UCUUUCCUACUCCUCCCAUACC	113-134	sly-miR482e-3p	0	0	22	22	1
sly-MIR482c-1	ACAAAAACUUUUGGGAAUGGGUGGGUCGGUAAGCUUUUCUUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUCCUAUGGGUUUUUG	97	sly-miR482c-1-3p	UUACCAAUUCCACCCAUUCCUA	66-87	nta-miR482c	1	0	22	22	1
sly-MIR5368-1	CACUGUUCCCUGGGAUUGGCUUUGGGCCUUUCUUGCGUAGCUUAGGUGUAAGGCGAAGAAGGCCUCCUUCCGGGGGGGCCCGAGCCAUCAGUGAGAUACCACUCUGGAAGGGCUAGAAUUCUAACCUUGUGUCAGGACCUAUGGGCCAAGGGACAGUCUCAGGUAGACAGU	171	sly-miR5368-1-3p	GGACAGUCUCAGGUAGACA	151-169	gma-miR5368	0	0	19	19	1
sly-MIR319a-2	UGGUAUAAGAGAGCUUCCUUUAGUCCACUCAUAGGUAGACGAAGGAUUUGAAUUAUCUCCCGACUCAUUCAUUCAAACGCAAUAGGAAGUAUGUAAUCUUAUACUAUUGUGAAUGUGUGAAUGAUGCGGGAGAUAAAUUCUCUCCUUUUUAUCUGUGCUUGGACUGAAGGGAGCUCCCUUUUACC	185	sly-miR319a-2-5p	AGAGCUUCCUUUAGUCCACUC	10-30	mtr-miR319a-5p	1	0	21	21	1
			sly-miR319a-2-3p	UUGGACUGAAGGGAGCUCCCU	159-179	aof-miR319a	0	0	21	21	1
sly-MIR396b-1	AUGGUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAUAGGGUCA	133	sly-miR396b-1-5p	UUCCACAGCUUUCUUGAACUG	19-39	aof-miR396b	0	0	21	21	1
			sly-miR396b-1-3p	GUUCAAUAAAGCUGUGGGAAG	98-118	csi-miR396b-3p	0	0	21	21	1
sly-MIR156i-1	CAAAAAGAGGUGACAGAAGAGCGUGAGCACAUGUGUGUUUUCUAGCAUGAUGUUUAUAUGCUUGAAUCUAUGCGUGCUCACUGCUCUAUCUUUCAUCCUCAUCG	104	sly-miR156i-1-5p	UGACAGAAGAGCGUGAGCAC	11-30	stu-miR156i-5p	1	0	20	20	1
			sly-miR156i-1-3p	GCUCACUGCUCUAUCUUUCAUC	76-97	zma-miR156i-3p	1	0	22	22	1
sly-MIR6022	AUACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAGUUAUUUAGACCGAGUUUUAACCAAUUGCACGGUCCUCUACCCAAGAUUGAGGUUUCGUAAAAUGUAACUUAAGAUCAAGUCGCGUUAGGUUCAUGAAGUUUUGAAUUGACUUAGGAAGAGUACCUUGCAACUUAAAACUUUGAGCCGAAAUAAGUUAGUGAUGGAAAGGAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGG	236	sly-miR6022-3p	UGGAAAGGAUAAUAUCCAGGA	197-217	sly-miR6022	2	0	21	21	1
sly-MIR6024	AACUGGAAAUGGGGAAGUGGAGAAACAACACUUGCUAAAGGAAGUUCACCAGUCAUCUCUUUUCUUUUGGAGUUUUUUUAGCAAGAGUUGUUUUACCUCUUCUCAAUUCCGUCUCU	116	sly-miR6024-5p	AGAAACAACACUUGCUAAAGGA	21-42	stu-miR6024-5p	1	0	22	22	1
			sly-miR6024-3p	UUUUAGCAAGAGUUGUUUUACC	76-97	sly-miR6024	0	0	22	22	1
sly-MIR482c-2	AAAAACUUUUGGGAAUGGGUGGGUCGGUAAGCUUUUCUUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUCCUAUGGGUUUUUGGGCUUUUAUC	105	sly-miR482c-2-3p	UUACCAAUUCCACCCAUUCCUA	64-85	nta-miR482c	1	0	22	22	1
sly-MIR6025b-1	UGUAUAGUUAUUUCAUGUACACUUGCACAAAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACUAUUGGGAUGGCAUCUCGGUUUGUUA	162	sly-miR6025b-1-3p	UGCCAACUAUUGGGAUGGCAUC	130-151	nta-miR6025b	2	0	22	22	1
sly-MIR6025b-2	AAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACUAUUGGGAUGGCAUCUCGGUUUGUUAGUUGCUGUGCAGUAUGAUCACUGUGGCAG	162	sly-miR6025b-2-3p	UGCCAACUAUUGGGAUGGCAUC	101-122	nta-miR6025b	2	0	22	22	1
sly-MIR169c-1	AGGAAGAGAGAUCUUACAUGAAAAGAAAAGCCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGCACCUACUAUUUUCCUCCAUUUUUUUUUAUGGAGUACUUAAUAGUAUACUAGGCAGUCAUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUU	170	sly-miR169c-1-5p	UAGCCAAGGAUGACUUGCCUA	42-62	ata-miR169c-5p	0	0	21	21	1

sly-MIR172-3	UUGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUUCAAAAAUGAGAAUCUUGAUGAUGCUGCAUCGACAAAUUAUGACUUUUUCCCCUCGAAUUAAAAGAAUUCAGGAUGAUCUCGACUUUACUAUUUAUUUUUGGUAAGUAUGCAAUUUGGACUUUGACUU	248	sly-miR172-3-3p	UGAGAAUCUUGAUGAUGCUGCAU	128-150	aau-miR172	0	0	23	23	1
sly-MIR394-1	GUAGAGCCAUUUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAACUAGCUCUGCA	81	sly-miR394-1-5p	UUUGGCAUUCUGUCCACCUCC	11-31	cas-miR394	0	0	21	21	1
sly-MIR397-2	UAGAAACAUGAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAGUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUAAACUCGAUCAUGUUUUUAAUUCUCUGAAGGGACAUUUUA	120	sly-miR397-2-5p	AUUGAGUGCAGCGUUGAUGAC	11-31	stu-miR397-5p	0	0	21	21	1
			sly-miR397-2-3p	UCAACGCUAAACUCGAUCAUG	73-93	sly-miR397-3p	0	0	21	21	1
sly-MIR398-1	UAUUCAACAGGGGCAACUUGAGAUCACAUGUUGUCAUUUUUUUCUUUUUGAUUUGAUUCGAUGAAUCAGUAUCUCAACAUGUGUUCUCAGGUUACCCCUGUUGAAUUA	108	sly-miR398-1-5p	GGGGCAACUUGAGAUCACAUG	10-30	hbr-miR398	3	0	21	21	1
			sly-miR398-1-3p	UGUGUUCUCAGGUUACCCCUG	80-100	bra-miR398-3p	1	0	21	21	1
sly-MIR399o	AACAGUGAUAGGGCUACUCUCUAUAGGCAUAUGCCGUUUAUCACACAUUACAGCUGACACGCCAAAGGAGAGCUGCCCUAUUACUGUCU	89	sly-miR399o-5p	GGGCUACUCUCUAUAGGCAUA	11-31	stu-miR399o-5p	2	0	21	21	1
			sly-miR399o-3p	CGCCAAAGGAGAGCUGCCCUA	60-80	stu-miR399o-3p	1	0	21	21	1
sly-MIR477-1	CAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAACAAGAAAUUCCUUGCUCACUUCACAUGGCAAACAUACUUA	132	sly-miR477-1-5p	UGUCUCUCCCUCAAGGGCUCC	11-31	sly-miR477-5p	0	0	21	21	1
			sly-miR477-1-3p	AGUUCUUGUAGGGUGAGACAAC	72-93	sly-miR477-3p	0	0	22	22	1
sly-MIR1919-2	UCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUAUGGAACCACACUUUCUUUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUUUUUCAUC	149	sly-miR1919-2-5p	UGUCGCAGAUGACUUUCGCCC	12-32	stu-miR1919-5p	0	0	21	21	1
			sly-miR1919-2-3p	ACGAGAGUCAUCUGUGACAGG	78-98	stu-miR1919-3p	0	0	21	21	1
sly-MIR482c-3	GAAAAUCUAUGGGGAUUGGUGAGUUGGAAAGCUUUUCUUUUUCUUCUCUUGUGAUUAGCUUUCCAAUUCCACCCAUUCCUAUGGUUUUUCG	91	sly-miR482c-3-3p	UUUCCAAUUCCACCCAUUCCUA	60-81	nta-miR482c	0	0	22	22	1
sly-MIR156k	GGUGGUGAUAGAAGAGAGUGAGCACACAUGGUGUUUUCUGCAUGAUGUUUAUAUAUAUAUAUGCUUGAAACUAUGUGUGCUUACUCUCUAUCUGUCACCC	101	sly-miR156k-5p	UGAUAGAAGAGAGUGAGCAC	6-25	cas-miR156k-5p	1	0	20	20	1
sly-MIR156k			sly-miR156k-3p	UGCUUACUCUCUAUCUGUCACC	79-100	cas-miR156k-3p	0	0	22	22	1
sly-MIR164-1	AGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUC	165	sly-miR164-1-5p	UGGAGAAGCAGGGCACGUGCA	4-24	aof-miR164	0	0	21	21	1
sly-MIR390a-2	UGGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGC	102	sly-miR390a-2-5p	AAGCUCAGGAGGGAUAGCACC	19-39	sly-miR390a-5p	0	0	21	21	1
			sly-miR390a-2-3p	CGCUAUCCAUCCUGAGUUUUA	68-88	sly-miR390a-3p	0	0	21	21	1
sly-MIR394b	AGAUGAAGAAAAAAAAAUAUGAAGAUUAAUUAGUUUCACGGAGGUUUGACAAAGGGUUUCUUACAGAGUUCAUUGGCAUUCUGUCCACCUCCCUCGUUCUUUUUUCGAGAAAAAAAGAAGAAGGGGGGAAGCAAGAUUUAGUGUGGAGGUGGGCAUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUUGUAAAACCCUCGUGAUACACGUCAAGUAAGAUAGAGAGUGAUUUGAUCG	235	sly-miR394b-5p	UUGGCAUUCUGUCCACCUCC	72-91	csi-miR394b-5p	0	0	20	20	1
			sly-miR394b-3p	AGGUGGGCAUACUGCCAAUAG	146-166	ath-miR394b-3p	0	0	21	21	1
sly-MIR166-1	AUAUUGUUGAGGAGAAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUGUAUCGUGAAUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUG	120	sly-miR166-1-3p	AUUUCGGACCAGGCUUCAUUCCCC	88-111	lja-miR166-3p	0	0	24	24	1

sly-MIR171a-2	UCAUACGAGAUGUUGGUGCGGUUCAAUGAGAAAGAAGUUGUUGAAUAAGUUUUUGACCCUACUUUUUGAUUGAGCCGUGCCAAUAUCACGUGUCACUAU	99	sly-miR171a-2-5p	UGUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	1	0	21	21	1
			sly-miR171a-2-3p	UGAUUGAGCCGUGCCAAUAUC	67-87	aof-miR171a	0	0	21	21	1
sly-MIR160g	AAUUGUUCUGCCUGGCUCCCUGGAUGCCAACUAAGAACAGUAUUGUCAAAAAAAUUGACACUCUUCCUAGUUGGUACCAGAGGAGACAGGCAGAUCCAU	99	sly-miR160g-5p	UGCCUGGCUCCCUGGAUGCCA	9-29	lus-miR160g	0	0	21	21	1
sly-MIR164c	UUUAAGCUGGAGAAGCAGGGCACAUGCUGAAUUACUUGAAACUUUGACCUUUCAAGAAUUUUGCAUGUGCUCUAGCUCUCCAGCUUAA	88	sly-miR164c-5p	UGGAGAAGCAGGGCACAUGCU	8-28	fve-miR164c	0	0	21	21	1
			sly-miR164c-3p	CAUGUGCUCUAGCUCUCCAGC	64-84	bdi-miR164c-3p	4	0	21	21	1
sly-MIR171f-1	AUGAAAUAGUAACUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAGUUCCUUUUCACUAUACUUCAUCAUAUUAAGCUCCCAUAU	131	sly-miR171f-1-5p	UAUUGGCCUGGUUCACUCAGA	19-39	csi-miR171f-5p	0	0	21	21	1
			sly-miR171f-1-3p	UGAUUGAGCCGUGUCAAUAUC	68-88	csi-miR171f-3p	1	0	21	21	1
sly-MIR168c	CCUCUUAUUCGCUUGGUGCAGGUCGGGACCUCAUUCGCCGGCGCCGGGAAUAAUGCCGGACGAACGACGGCGGUGUUAAUUCUACUAAAGCUGUCACCGACGGAUAGAUGUUUGAUUAGCGGCGAAAUUUGGGUCCUGCCUUGCAUCAACUGAAUUGGAG	160	sly-miR168c-5p	UCGCUUGGUGCAGGUCGGGAC	9-29	bra-miR168c-5p	0	0	21	21	1
			sly-miR168c-3p	CCUGCCUUGCAUCAACUGAAU	135-155	bra-miR168c-3p	1	0	21	21	1
sly-MIR7984b-1	CUUUGGAAAAAACUUUUACCCCAUGUACCCCAUGUGCUACUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGUUCAUGUGGAUAUCAUAAAUAUUGCAUCAUUAUAAAUAGUAAUGUGUCCACAUUGACAAAUAUAUACCCUUACAAUACACUAUUAAAUAGUUAAGGGGCGUAAAAGAUCUUCGAUAAAGUUUGAUAUCG	199	sly-miR7984b-1-3p	GAUCUUCGAUAAAGUUUGAUAUCG	176-199	stu-miR7984b-3p	5	0	24	24	1
sly-MIR7984c-1	ACGAUAUCAAACUUUAUGGAGGACCUGUUACCCCCUGCACUAUUUAAUAAUGUAUUUUAAAAGUAUAUAUGUGUCCACAUGGACACAUUACUAUUUAUAAUGAUGCAAUGUGUAUGAUGUCCACGUGGACACAUAUAUACCUUUAAAAUACACUAUUAAAUAUUGCAUGGGGAUAAAAGGUCCUUUUCAAAAUUUGAUAUUCUC	204	sly-miR7984c-1-5p	ACGAUAUCAAACUUUAUGGAGGAC	1-24	stu-miR7984c-5p	2	0	24	24	1
sly-MIR7990a-1	UGCAAAAGUUAUGACCAUUUGAAGUGUCACAAAUUUACAACUACUUUUUUUGAGUUAUACUCUUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCCU	102	sly-miR7990a-1-3p	UUCAAAUGAUCGUAACUUUGGCCU	79-102	stu-miR7990a	0	0	24	24	1
sly-MIR1886h-1	UAUGGUAUCGUGAGAUGGAAUCAGCGUUUGGACAUGUAAUUUUACGUUGAUUUCAUCUCAUGAUUUCAUAU	71	sly-miR1886h-1-3p	AUUUUACGUUGAUUUCAUCUCAUG	39-62	stu-miR1886h	0	0	24	24	1
sly-MIR8020	GAAUUUCAUUGAGUAUGUUGUUGUUGUAAAGCAUUCUGAAUUAAUGCAAGUACACAAGUUACAACAACAACAUACUUACUGAAAUGCC	88	sly-miR8020-5p	AAUUUCAUUGAGUAUGUUGUUGUU	2-25	stu-miR8020	0	0	24	24	1
sly-MIR8025	UCAAACAUCAUAAAGAAAUAUUUUACCACACACUACACAUGCAAUUAAAUUAGUAUAAGUCGCCAUUAUGUUUUUCUUAACCAAGCUGAAUCAUAUAAUGGUGACUUAUACUAAUUUAAUUGCAUGCCGACUGUGUG	137	sly-miR8025-5p	ACACACUACACAUGCAAUUAAAUU	28-51	stu-miR8025-5p	3	0	24	24	1
			sly-miR8025-3p	UUUAAUUGCAUGCCGACUGUGUG	115-137	stu-miR8025-3p	2	0	23	24	1
sly-MIR7984d-1	ACUUUGAAAAGGACCUUUUACCCCAGCAUUAUUUAAUAGUGUAUUUAAAAGGUAUAUAUGUACCCACGUGGACAUCAUAAUUAUUGCAUCAUUAUAAAUAGUAACAUGUCCACGUGGCACAUAUACCUUUAGAUUAGACUAUUAAAUAGUGCAGGGGCAAAAGGUCCUUUCCAAAGUUCGGUAUUAUUCCACCAAUUUCGGUCAAAGUUCGGAUAU	216	sly-miR7984d-1-3p	CAAUUUCGGUCAAAGUUCGGAUAU	193-216	stu-miR7984d-3p	0	0	24	24	1
sly-MIR319d	AAGGAAACUGUUUAGUCCAACCCAAGGUGGGGUAUUGGAACUGAUCUUUGCUGCUGAAUCAUUGGCUCAUGAGCAUGUCAAAGAAGAUGAUUGAACAUUCUGGACAUGUUCUUGCUCCAAUGAUGCAGGAGCUGAGCUCGGUUUUUCACCGCCUUUUCUUGGACUGAAGGGUUUCCUUC	179	sly-miR319d-5p	AGGAAACUGUUUAGUCCAACC	2-22	sly-miR319d	0	0	21	21	1
			sly-miR319d-3p	UUGGACUGAAGGGUUUCCUU	159-178	zma-miR319d-3p	5	0	20	20	1
sly-MIR7122	UAUAUACAGAGAAACCGCUGUCGAUUAUAAUGAGAAAUUC	78	sly-miR7122-	AUAUACAGAGAAACCGCUGUCG	2-23	stu-	1	0	22	22	2

	GGUGUUUCUCAUACUCCACAGCGUUUUUCUGUAUAACC		5p			miR7122-5p					
			sly-miR7122-3p	ACAGCGUUUUUCUGUAUAACC	58-78	stu-miR7122-3p	1	0	21	21	1
	UCAAUGCUACAUACUCAUCCCCACAACUUUCAUCUCACGU										
	UCAAAAGAUGAAAGUUAUAGAGAUGAGUAUGGUGCAUUGG		sly-miR5304-5p	UCAAUGCUACAUACUCAUCCC	1-21	sly-miR5304	0	0	21	21	1
sly-MIR5304	A	81	sly-miR5304-3p	AGAUGAGUAUGGUGCAUUGGA	61-81	stu-miR5304-3p	0	0	21	21	1
	UAGAUAUUGAUGCGGUUCAAUCUGAAAGACAUGGUUAGAU										
	AUGUAAUUAGCCUUGUAAUUUUGGAUUGAGCCGCGUCAAU										
sly-MIR171e	AUCUCU	86	sly-miR171e-3p	UUGAGCCGCGUCAAUAUCUCU	66-86	sly-miR171e	0	0	21	21	1
	GGGAAUGUUGUUUGGUUCGAAAUCAUUCAAACAAAUUAAA										
	AUUCAUGCAUCUCGAUGAUCGAUGAAUUGAAUAAUUUCGG										
sly-MIR166-2	ACCAGGCUUCAUUCCCC	97	sly-miR166-2-3p	AUUUCGGACCAGGCUUCAUUCCCC	74-97	lja-miR166-3p	0	0	24	24	1
	GUUUGUUGAUGGUCAUCUAUUCAUCAUAUCAUUUGGCAUA										
	GUUUUUGGAACCAUUAAUAUGCCAUGAUUAGAUGAACAUC										
sly-MIR827-1	AACAAACA	88	sly-miR827-1-5p	UUUGUUGAUGGUCAUCUAUUC	2-22	stu-miR827-5p	0	0	21	21	1
			sly-miR827-1-3p	UUAGAUGAACAUCAACAAACA	68-88	sly-miR827	0	0	21	21	1
	UGCCUGGCUCCCUGUAUGCCACACACAUUCACCAAUUCUU										
	UGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGC		sly-miR160c-5p	UGCCUGGCUCCCUGUAUGCCA	1-21	aof-miR160c	0	0	21	21	1
sly-MIR160c	AU	81	sly-miR160c-3p	GCGUAUAAGGAGCCAAGCAU	62-81	aly-miR160c-3p	1	0	20	21	1
	UGGAGCAUCAUCAAGAUUCACAUAGCUAUAUUAGGGCUUU										
	UAUAAUUUUUAAAAACCCUACGGGCGAUGUGUGGGAAUCU										
sly-MIR172c	UGAUGAUGCUGCAG	94	sly-miR172c-5p	GGAGCAUCAUCAAGAUUCACA	2-22	cas-miR172c	0	0	21	21	1
			sly-miR172c-3p	GGGAAUCUUGAUGAUGCUGCAG	73-94	csi-miR172c-3p	1	0	22	22	2
	UUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUU										
	UCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGU										
sly-MIR156b-1	GCUCUCUAUGCUUCUGUCAUC	101	sly-miR156b-1-5p	UUGACAGAAGAUAGAGAGCAC	1-21	aof-miR156b	0	0	21	21	1
			sly-miR156b-1-3p	GCUCUCUAUGCUUCUGUCAUC	81-101	vca-miR156b-3p	0	0	21	21	1
	AGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAU										
	AUAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCA										
sly-MIR171d	C	81	sly-miR171d-5p	AGAUAUUGGUGCGGUUCAAUU	1-21	stu-miR171d-5p	0	0	21	21	1
			sly-miR171d-3p	UUGAGCCGUGCCAAUAUCAC	62-81	stu-miR171d-3p	0	0	20	21	1
	GUGAAGCUGCCAGCAUGAUCUAAACUUGGCCAUUUAUAAA										
	GAAAAUGGGUGACUAAGGUUAGGUCAUGCUCGGACAGCCU										
sly-MIR167c-1	CACU	84	sly-miR167c-1-5p	UGAAGCUGCCAGCAUGAUCUA	2-22	ata-miR167c-5p	0	0	21	21	1
			sly-miR167c-1-3p	GGUCAUGCUCGGACAGCCUCACU	62-84	stu-miR167c-3p	0	0	23	23	1
	UUCCAAAGGGAUCGCAUUGAUCCUGUGUUCCAAAUUAAUU										
	AACCAUGGGACUAUGGGAUCAUGCGAUCUCUUCGGAAU		sly-miR393b-5p	UUCCAAAGGGAUCGCAUUGAUC	1-22	csi-miR393b-5p	0	0	22	22	1
sly-MIR393b		78	sly-miR393b-3p	UCAUGCGAUCUCUUCGGAAU	59-78	csi-miR393b-3p	1	0	20	21	1
	GCCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUAU										
	GUUGGGAAAGAAGCUCUAGCAGGGAGAGCCA		sly-miR477a-5p	CCUCUCCCUCAAGGGCUUCUC	2-22	stu-miR477a-5p	0	0	21	21	1
sly-MIR477a		70	sly-miR477a-3p	GAAGCUCUAGCAGGGAGAGCCA	49-70	stu-miR477a-3p	0	0	22	22	1
	CACUCUCCCUCAAAGGCUUCUGGCUUAAAAUGCCUUUUGU										
	GCUAAUGCUAGAGGUCUUUCGAGUGAGAGUGA		sly-miR477b-5p	ACUCUCCCUCAAAGGCUUCUG	2-22	stu-miR477b-5p	0	0	21	21	1
sly-MIR477b		72	sly-miR477b-3p	GAGGUCUUUCGAGUGAGAGUGA	51-72	stu-miR477b-3p	0	0	22	22	1
	ACAGGGACGAGGCAGCGCAUGAGAUGUACAAUUUUAUUAG										
	UUGUCCAUUCCAUGCACAGCCUCUUCCCUGGC		sly-miR408a-5p	ACAGGGACGAGGCAGCGCAUG	1-21	stu-miR408a-5p	0	0	21	21	1
sly-MIR408a		72	sly-miR408a-3p	AUGCACAGCCUCUUCCCUGGC	52-72	mdm-miR408a	1	0	21	21	1
	ACGGGGACGAGCCAGAGCAUGAGAUGUGCAAUUUUUGCU										
	UUGCCUAUUCCAUGCACUGCCUCUUCCCUGGC		sly-miR408-1-5p	ACGGGGACGAGCCAGAGCAUG	1-21	sly-miR408	0	0	21	21	1
sly-MIR408-1		71	sly-miR408-1-3p	AUGCACUGCCUCUUCCCUGGC	51-71	cas-miR408	0	0	21	21	1
	GUGACAGAAGAGAGUGAGCACACAUGGUUCUUUCAUGGAU										
	UAUUCCCCAUGUUUAAAAGCUCUGCGUGCUCACGCUCUAU		sly-miR156b-2-5p	UGACAGAAGAGAGUGAGCACA	2-22	hvu-miR156b	0	0	21	21	1
sly-MIR156b-2		88									

	CUGUCACA										
			sly-miR156b-2-3p	UGCUCACGCUCUAUCUGUCACA	67-88	mtr-miR156b-3p	2	0	22	22	1
sly-MIR394-2	UUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAAC UACAUCGUGCAGCACUAGCAGUUGAAGCUGCCAGCAUGAU	61	sly-miR394-2-5p	UUUGGCAUUCUGUCCACCUCC	1-21	cas-miR394	0	0	21	21	1
sly-MIR167b-1	CUAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAUCAGAUCAUGUGGCAGCCUUACCUGUCAAU	110	sly-miR167b-1-5p	UGAAGCUGCCAGCAUGAUCUAA	23-44	bna-miR167b	0	0	22	22	1
			sly-miR167b-1-3p	GAUCAUGUGGCAGCCUUACC	84-103	stu-miR167b-3p	2	0	20	20	1
sly-MIR168	GCGGUGGUUUCUCAUUCGCUUGGUGCAGGUCGGGACCUA CCUCGCCGGCAACAAUGGCGGUAGCUGACGGCGACGGCA GCGUACCGGUAAAAAAGAAUCUUAUUUUUACAUGUUGUUG CGUAGUUUGGGUCCCGCCUUGCAUCAACUGAAUAGGAGAC UGCGGUGAAUUU	170	sly-miR168-5p	UCGCUUGGUGCAGGUCGGGACC	16-37	lja-miR168-5p	1	0	22	22	1
			sly-miR168-3p	UCCCGCCUUGCAUCAACUGAAU	130-151	lja-miR168-3p	0	0	22	22	1
sly-MIR169a-1	UGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGAGUGGAG UGCAGCCAAGGAUGACUUGCCGAGAUGUUGUAGCCUAAUG CAAUGACAUAUCGGCAGGUCAUCUUUGGCUACAUUUUAUU CUCUCCUAUUCAUGUAAAACUUUAUAGACGUAUAUGUAU AGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAA	158	sly-miR169a-1-5p	CAGCCAAGGAUGACUUGCCGA	42-62	cas-miR169a	0	0	21	21	1
sly-MIR169c-2	UUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUU UUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGG CAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAU GCUAGUUCUCUUUCUUCCCAUUUAUAUUAAUCUCAUCUCG GAUUU	205	sly-miR169c-2-5p	UAGCCAAGGAUGACUUGCCUA	42-62	ata-miR169c-5p	0	0	21	21	1
sly-MIR172-4	UCUUACAGUCGUUGUUUGCAUAUGUGGCAUAAUCAAGAUU CACGUGAAAAGUUGCAAAUUGGUUAUAUAAUUGAUGAAAU UAAUGGCUGGCUAUUUGAAACUCACGAGAAUCUUGAUGAU GCUGCAUCAGCAAUAAACGACU	142	sly-miR172-4-3p	CGAGAAUCUUGAUGAUGCUGCAU	105-127	aau-miR172	1	0	23	23	2
sly-MIR395a-3	AUAUAUCAAGGUAUUCUCGAGAGUUCCCUUGACCACUUCA UGAGGGAUUAAUAUCUUUAUUUUUGAUGCCCUACUAAAGU GUUUGGGGGAACUCUUGGGUUCACUUUGAAGUAUA	115	sly-miR395a-3-3p	UAAAGUGUUUGGGGGAACUCU	75-95	aof-miR395a	1	0	21	21	1
sly-MIR2111d	UGGUAAUCUGCAUCCUGAGGUUUAGAUCAAUUUAUAACUU ACUGGAUCUAGUCCUUGGGAUGCAGAUUAUC	71	sly-miR2111d-5p	UAAUCUGCAUCCUGAGGUUUA	4-24	ppe-miR2111d	0	0	21	21	1
			sly-miR2111d-3p	GUCCUUGGGAUGCAGAUUAUC	51-71	gma-miR2111d	2	0	21	21	1
sly-MIR319c	CAAGAGAGCUUCCUUCAGCCCACUCACGGAGGAGAAAUGG GGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGU AGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGA UGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCCUUGCUUG GACUGAAGGGAGCUCCUUU	178	sly-miR319c-5p	AGAGCUUCCUUCAGCCCACUC	5-25	sly-miR319c-5p	0	0	21	21	1
			sly-miR319c-3p	UUGGACUGAAGGGAGCUCCUU	157-177	sly-miR319c-3p	0	0	21	21	1
sly-MIR164-2	AUCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAU ACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUA GUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUG UAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUU UUCCCCAUCAUGA	173	sly-miR164-2-5p	UGGAGAAGCAGGGCACGUGCA	8-28	aof-miR164	0	0	21	21	1
sly-MIR164e	UGUUGGAGAAGCAGGGCACGUGCAAAUUCUUGUAUUCGAC AAUAUAUGCAUUACUAAUGGUAAUGCAUGAAUUUUGCACG UGUUCUCCUUCUCCAAC	97	sly-miR164e-5p	UGGAGAAGCAGGGCACGUGCAA	4-25	bra-miR164e-5p	0	0	22	22	1
			sly-miR164e-3p	CACGUGUUCUCCUUCUCCAAC	77-97	bra-miR164e-3p	3	0	21	21	1
sly-MIR166c	UGUGUGUGGUGAGUUUGAGGGGGAUGUUGUCUGGCUCGA CACAAUUACUCUAUUGUAUGUAUUUAGUUAUUCGUUAUCA AGAUUGAUGUCGAUAACGAAUAAAUUAAACACAUAUAUACA AGAUGUAAAAAGGGAGUAAAGGCGUCGGACCAGGCUUCAU UCCUCUCAAACAAUAUUCUACUUUUAC	187	sly-miR166c-5p	GGGAUGUUGUCUGGCUCGACA	21-41	sly-miR166c-5p	0	0	21	21	1
			sly-miR166c-3p	UCGGACCAGGCUUCAUUCCUC	145-165	sly-miR166c-3p	0	0	21	21	1
sly-MIR9471a-1	GAUCAUUGACGGAUUUGGGGUUCUGAGAUUCAGUUGAUU UCUCAGGUGCUCACUCAGCUAAUAGUUAUUAUUUAAGAAA	180	sly-miR9471a-1-	CAGGUGCUCACUCAGCUAAUA	43-63	sly-miR9471a-	0	0	21	21	1

	CUCAAUAAUAUUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUGAGUGAGCAUCACGGAAAUCGACGUGAUUCUGAGAGGAAAAUGAU		5p			5p					
			sly-miR9471a-1-3p	UUGGCUGAGUGAGCAUCACGG	130-150	sly-miR9471a-3p	0	0	21	21	1
sly-MIR9472	UAUGGGUUUCAAUUAUAGCUACAGAUCUUCCCAUAGAUCUACUCGAUUUAUUUUUCAGUAGACGUUGUGAAUAAUUGAUAAAUACAGGUAUACAGAGGUCUUAAUAUAGUCAGAACCUAGAAAUAUGUGUAACUAGAUUCAGACCUUUGUACACUUGUAUUCUGUUGCUAUUCACAAUCUCUGCUGAAAAAUGAUUGACUAGAUCUACGAAUAAUCUAGAUUAUUAAUGCCCGU	234	sly-miR9472-5p	UUUCAGUAGACGUUGUGAAUA	53-73	sly-miR9472-5p	0	0	21	21	1
			sly-miR9472-3p	UUCACAAUCUCUGCUGAAAAA	171-191	sly-miR9472-3p	0	0	21	21	1
sly-MIR9473-1	CUAGCAGAUAUUGGCUGUAAAUCUAAACUCGUUCUACUCCACUAGUCAUCAUAUAAUGACAUUUACUAGAAGAAGAGACUAUUGGGGUAAAACGAGUUCAGAUUUACAGCCAAUAUUGUU	120	sly-miR9473-1-5p	UGGCUGUAAAUCUAAACUCGU	12-32	sly-miR9473-5p	0	0	21	21	1
			sly-miR9473-1-3p	AAACGAGUUCAGAUUUACAGC	90-110	sly-miR9473-3p	0	0	21	21	1
sly-MIR9473-2	AAAACAAUAUUGGCUGUAAAUCUGAACUCGUUUUACCCCAAUAGUCUCUUCUUCUAGUAAAUGUCAUUAUAUGAUGACUAGUGGAGUAGAACGAGUUUAGAUUUACAGCCAAUAUCUG	118	sly-miR9473-2-5p	UGGCUGUAAAUCUGAACUCGU	11-31	sly-miR9473-5p	1	0	21	21	1
			sly-miR9473-2-3p	GAACGAGUUUAGAUUUACAGC	89-109	sly-miR9473-3p	2	0	21	21	2
sly-MIR9478-1	CUUAUAAAAGGGAUAAGGCUUAAAUAUGUAGAUCGAACUUUGAGAAAAGACUCAUCUAUGUCAUCUGGUAAAGUUUGGUGUGUAAUGGUUUGAAUGAGCCUUUUCUCGAACGAAAAUGGUGUAGAUGAGUUAAAUUUUUAACGGAUUACAUAAUUGAGCCUUUUCUCAUAGUUCGAUGACAUAUUUGAGCCUUUUUCCAAUUAUAA	206	sly-miR9478-1-5p	GCUUAAAUAUGUAGAUCGAACU	18-39	sly-miR9478-5p	0	0	22	22	1
			sly-miR9478-1-3p	UUCGAUGACAUAUUUGAGCCU	172-192	sly-miR9478-3p	0	0	21	21	1
sly-MIR9478-2	UUUAAUUAAAAAAAUUGAUGACGUGGCCGAAUUAUAAUUGGUCACGUGUCAAAAAUGGUUUUGAAAACUACUAUUAAAAAAUAAUGGCAUGAAUGAACCUUUUCUUUAAAGGUAAUGGCAUAAAUGAGCCAAACUUUAACUGAUGGCAUAAAUGAGCCUUUUCUGAAAGUUCGAUGGCAUAUUUGAGUCUUUUGUACCAGAUU	204	sly-miR9478-2-3p	UUCGAUGGCAUAUUUGAGUCU	171-191	sly-miR9478-3p	2	0	21	21	1
sly-MIR169e-1	UAGGAGGAGAGGCCUUACAUGAAUUAGAAGAGUUUCUAUUUGUUUAGUAGCCAAGGAUGACUUGCCUUUCAUCAAUGCCUUUUGUAAAAUGGAAAUUGAUUACAACACUUUCUAUGGUAUUGGGAAAAUGAGUGGCAAGCAUCUUUGGCGACUUGACAAACUCUUCUUUGUCAUGUUAGUCCAUCUUCUUCCU	193	sly-miR169e-1-5p	UAGCCAAGGAUGACUUGCCUUU	48-69	sly-miR169e-5p	0	0	22	22	1
			sly-miR169e-1-3p	UGGCAAGCAUCUUUGGCGACU	133-153	sly-miR169e-3p	0	0	21	21	1
sly-MIR171a-3	AAAGGUAUAUCAUACGAGAUGUUGGUGCGGUUCAAUGAGAAAGAAGUUGUUGAAUAAGUUUUUGACCCUACUUUUUGAUUGAGCCGUGCCAAUAUCACGUGUCACU	106	sly-miR171a-3-5p	UGUUGGUGCGGUUCAAUGAGA	20-40	nta-miR171a	1	0	21	21	1
			sly-miR171a-3-3p	UGAUUGAGCCGUGCCAAUAUC	76-96	aof-miR171a	0	0	21	21	1
sly-MIR477-2	AGCUAGGCAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAACAAGAAAUUCCUUGC	114	sly-miR477-2-5p	UGUCUCUCCCUCAAGGGCUCC	18-38	sly-miR477-5p	0	0	21	21	1
			sly-miR477-2-3p	AGUUCUUGUAGGGUGAGACAAC	79-100	sly-miR477-3p	0	0	22	22	1
sly-MIR396b-2	GUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAUAGGGUCAAAUAGAAUUGCUACAAUUGAAUUGAAGUUUA	161	sly-miR396b-2-5p	UUCCACAGCUUUCUUGAACUG	16-36	aof-miR396b	0	0	21	21	1
			sly-miR396b-2-3p	GUUCAAUAAAGCUGUGGGAAG	95-115	csi-miR396b-3p	0	0	21	21	1
sly-MIR172-5	CAGAUGCAGCAUCUUCAAGAUUCACAUAGAUUUAUAUAAAAUAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUAAUUUUCUCCUAUAUAUUGGCUCUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGC	154	sly-miR172-5-3p	UGAGAAUCUUGAUGAUGCUGCAG	128-150	aau-miR172	1	0	23	23	1
sly-MIR10528	AUAAUGAAUGCAAUGUCAUAUACCAUCAACACUUGGAAACU	97	sly-	AAUGCAAUGUCAUAUACCAUC	7-27	sly-	0	0	21	21	1

	CAAAUUGAGGUUAAAUCUCGGAGUGAUGAUGGUAUAUGAC CUUGCAAUUCACUAUG		miR10528-5p			miR10528					
sly-MIR10529	AAACAUAACGAGUGAGACUUGCUCAGUUGGUAAAACACCU CCACGGUCUAACCAAUUAUCUUGGUCGAGGGUUCAAGUCA UGUUGGAAGCAAUGUGAGGGCGUCCAGCUUAGCAAGCCU CAUCCGUUUUGCUUC	134	sly-miR10529-5p	AACGAGUGAGACUUGCUCAGUUGG	7-30	sly-miR10529	0	0	24	24	1
sly-MIR530	UUUAUCUGCAUUUGCACCUGCACCUUAGUGAACGAAUUAG UUCGCGUAUAAUUCGUGCAGAAAGGUGUAGGUGUUCAUG CAGACAAAA	88	sly-miR530-5p	UCUGCAUUUGCACCUGCACCU	5-25	eun-miR530-5p	0	0	21	21	1
			sly-miR530-3p	AGGUGUAGGUGUUCAUGCAGA	63-83	sly-miR530	0	0	21	21	1
sly-MIR398a	CAAUAGGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUU GUUUGUAACAAUUUACCGUUUAUAAAUAUGACACAUAUGU UCUCAGGUCGCCCCUGUAGA	100	sly-miR398a-5p	GGGUUGAUUUGAGAACAUAUG	6-26	stu-miR398a-5p	0	0	21	21	1
			sly-miR398a-3p	UAUGUUCUCAGGUCGCCCCUG	76-96	sly-miR398a	0	0	21	21	1
sly-MIR399i-1	GUGAUAGGGCUACACUCUAUUGGCAUGCAACUUGAUCAAA UAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUAUUACU	80	sly-miR399i-1-5p	GGGCUACACUCUAUUGGCAUG	7-27	stu-miR399i-5p	0	0	21	21	1
			sly-miR399i-1-3p	UGCCAAAGGAGAGUUGCCCUA	55-75	stu-miR399i-3p	0	0	21	21	1
sly-MIR10531	GAUAUCUGGGGUCCUAGUAGAGUCGGUUCUACAUUGGGU GUUAAGUGUUUUGAGUAAUCAUCAUUGAAAGUAACAUACU UAAAACCCAAUGUUGAACUGACUCUACUCGGAUUCCAAAU AUCG	123	sly-miR10531-5p	UGGGGUCCUAGUAGAGUCGGUUC	7-29	sly-miR10531	0	0	23	23	1
sly-MIR10534	GGCUCCAAAAUACCCUUGUCAUCCACCUUUUUGUUCAAAA UGGACCGUUAAAUAAGUGGUCAAUUUUGAAUCCAAUGUUG GAUGACAAGGGUAUUUUGGAGUCA	104	sly-miR10534-5p	CAAAAUACCCUUGUCAUCCAC	6-26	sly-miR10534	1	0	21	21	1
sly-MIR10532-1	AUAUGCUUGAAAUUUCAGAGACACACUUAUAUUAUAAUAAG AUCUUAUUGCCCCCUGACCUUAUUUUAUAAAUAAUUUCGA CCCCUUUUUGGCCUACAUGACACUAGCUUGAAAAAAUGUG AACAGUCGUUGGGCAUAGAUUAGGGGGUAAUAGGACCUUA GUAUAGUAUAUGUGUGUCUCUGAGAUUUCGGGCAUAGGU UGAGGGAGUACUUGUGUAUUUUCCCUAAAAAUAAUUUUAA CCAUAU	246	sly-miR10532-1-3p	AUGUGUGUCUCUGAGAUUUCGGGC	171-194	sly-miR10532	1	0	24	24	1
sly-MIR10532-2	AACAUUUACUAUGUAUAUAUAAAAAUAACGAAAAAUGCAUA AGUAUCCUCCAACAUAUGCUUGAAAUUUCAGAGACACACU UAUAUUAUAAUAAGAUCUUAUUGCCCCCUGACCUUAUUUU AUAAAUAAUUUCGACCCCUUUUUGGCCUACAUGACACUAG CUUGAAAAAAUGUGAACAGUCGUUGGGCAUAGAUUAGGGG GUAAUAGGACCUUAGUAUAGUAUAUGUGUGUCUCUGAGAU UUCGGGCAUAGG	253	sly-miR10532-2-3p	AUGUGUGUCUCUGAGAUUUCGGGC	225-248	sly-miR10532	1	0	24	24	1
sly-MIR10535a	AAGGGUUGGCAUAAGUUUGUGAAAGCCGGAGAUUUAGGA GUAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGC UCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUU	119	sly-miR10535a-5p	UUGGCAUAAGUUUGUGAAAGCCGG	6-29	sly-miR10535a	0	0	24	24	1
sly-MIR10535b-1	AAGGGUUGGCAUGAGUUUGUGAAAGCCGGAGGUUUAGGA GCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGC UCUUAAACCUUUAGCUUUAACAAAUUUGUGUCAACCCUUU	119	sly-miR10535b-1-5p	UUGGCAUGAGUUUGUGAAAGCCGG	6-29	sly-miR10535b	0	0	24	24	1
sly-MIR10535b-2	AAGGGUUGGCAUGAGUUUGUGAAAGCCGGAGGUUUAGGA GCAAAGUACAAUUAUUUUCGCAAAUAAUUAUAUCUUUUGC UCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUU	119	sly-miR10535b-2-5p	UUGGCAUGAGUUUGUGAAAGCCGG	6-29	sly-miR10535b	0	0	24	24	1
sly-MIR10536-1	AAGGAAGCUGACGAUUAGAACAUGUCAAAGGAAUCGGUCC AAUGCAGCUGACUAACGUGCUUAUAUCAAGUGUUGUAAAC UCGUUAGUUAACUUUGUUAGACAUGUUCUAAUCGUCAGCU UCCUUC	126	sly-miR10536-1-3p	AGACAUGUUCUAAUCGUCAGCUUC	99-122	sly-miR10536	0	0	24	24	1
sly-MIR10537	GUUCUACAACGUACGUAGGGUAAGUGGAUGGCUGAAAUUC GUUAGCCUAGCCGUGGCCCUGGAAAUACUUCUCUGCAGG ACAAGCUUCAUUUCCAUUACCGGAUAUCAACAGAAAGGUU GAAAAAGACAACAAUGUAGAGGAUUUGGUGGAGUGUGGAA AGAUUUGAAUGCAAACUUAUCGAAGAUUGAUCAUCAUGGA UUUAAGCCAUCCAUUUACCCCAAGUUCGUUGUCAAACG	237	sly-miR10537-3p	AUUUACCCCAAGUUCGUUGUC	212-232	sly-miR10537	0	0	21	21	1
sly-MIR7986-1	ACGUUUCACUCCUAAAACCUUACUGUGAGUAACGUUUUAA GAGUAAGACGUUACUGUGAGUAACGUUUUACUCCUAAAAC GUU	83	sly-miR7986-1-3p	AGAGUAAGACGUUACUGUGAGUAA	40-63	stu-miR7986	5	0	24	24	1
sly-MIR159b-3	AAGGUAGAGCUCUUCUGAAUUCCAAAAAGGAUCUGAGAGG GAAAAUUGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUC UAUUCUCAAAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUA	180	sly-miR159b-3-5p	AGCUGCUAAUCUAUGGAUCCC	49-69	cas-miR159b-5p	1	0	21	21	1

	UAUCAGGAGCUACAUUUACUCUUCUAGGAUCCUUAUUGGA AAGAAGGGAGCUCUACACUU		sly-miR159b-3-3p	UUGGAAAGAAGGGAGCUCUAC	156-176	sly-miR159b	0	0	21	21	1
sly-MIR159b-4	AAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAGAGG GAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUC UAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUA UAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGA AUGAAGGGAGCUCUACGUUU	180	sly-miR159b-4-5p	AGCUGCUAAUCUAUGGAUCCC	49-69	cas-miR159b-5p	1	0	21	21	1
			sly-miR159b-4-3p	UUGGAAUGAAGGGAGCUCUAC	156-176	sly-miR159b	1	0	21	21	1
sly-MIR171f-2	UCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUG AUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAG	79	sly-miR171f-2-5p	UAUUGGCCUGGUUCACUCAGA	6-26	csi-miR171f-5p	0	0	21	21	1
			sly-miR171f-2-3p	UGAUUGAGCCGUGUCAAUAUC	55-75	csi-miR171f-3p	1	0	21	21	1
sly-MIR169r-1	CAUCCAAUGAGCUUCUCACAAGUUGUGUUUUGUUAGAUGA AGUAGGAAACUGCUAAUUCUAUUUGCCAUAGGGAAUGUUG GAUUUUCUUCUUCAGGAAACUACACUUCCCUAUAAUUGAA UAGACAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGA ACAAGGUCAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCA AGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUU GGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUA UGAAA	285	sly-miR169r-1-3p	CAGCCAAGGAUGACUUGCCGG	178-198	csi-miR169r-5p	0	0	21	21	1
sly-MIR11155e-1	GUUAAUUGUCAAAUUAGUCCCUGAGUUUGUAAGCGUGUUU GAUUUUAGUCCCUCUGGAGAUAAAUGACGUUUAGUGACAG UCAAAAACUGCUAGUGAUUGUAAAAAUGACUACCACUAAAC GUAAUUUUUCUUCAAAGGGACUAAAAUCAAACUCGCUUAC AAACUCAGUUACUAAUUUGAUCAUUAA	188	sly-miR11155e-1-5p	UUUGUAAGCGUGUUUGAUUUUAGU	26-49	lja-miR11155e-5p	1	0	24	24	1
sly-MIR11155e-2	AUUAGUAACUGAGUUUGUAAGCGAGUUUGAUUUUAGUCCC UUUGAAGAAAAAUUACGUUUAGUGGUAGUCAUUUUUACAA UCACUAGCAGUUUUUGACUGUCACUAAACGUCAUUUAUCU CCAGAGGGACUAAAAUCAAACACGCUUACAAACUCAGGGA CUAA	164	sly-miR11155e-2-5p	UUUGUAAGCGAGUUUGAUUUUAGU	14-37	lja-miR11155e-5p	0	0	24	24	1
sly-MIR156c-1	GGCGGUGACAGAAGAGAGUGAGCACACAUGGCGUUUUCU GGCAUGAUGUUUAUAUAUAUAUAUGCUUGAAACUAUGUGU GCUCACUGCUCUAUCUGUCACCU	102	sly-miR156c-1-5p	UGACAGAAGAGAGUGAGCACA	6-26	rco-miR156c	0	0	21	21	1
			sly-miR156c-1-3p	GCUCACUGCUCUAUCUGUCACC	80-101	ata-miR156c-3p	0	0	22	22	1
sly-MIR160h-2	UAUAUGCCUGGCUCCCUGUAUGCCAUUUGCAAAGCUCACC GUAAUAUAUCGAUGGGCCUUGUUGAAUGGCGUAUGAGGA GCCAAGCAUAU	90	sly-miR160h-2-5p	UGCCUGGCUCCCUGUAUGCCAUU	5-27	mes-miR160h	0	0	23	23	1
sly-MIR166k	AGGAAGUUCUCUCAGUUGAGGGGAAUGUUGUCUGGCUCG AGGUCACCAAUUAGAUCCAUAAUCCCUAUAUAUACCAUGC UUUUCAAAAAAAAGAUUUAUAAUAUGAAAAGGGGUUAUGAA UCAUGUGUUAGUGUUGUCGGACCAGGCUUCAUUCCCCCC AAUUGU	165	sly-miR166k-3p	UCGGACCAGGCUUCAUUCCCCC	137-158	lus-miR166k	0	0	22	22	1
sly-MIR166-3	UCCAGAUUUGAGGGGAAUGUUGUUUGGCUCGAAGUCAUU AUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAA UCUAGUUUAAAAUAUAUGUGAAUUACGAUGAUGAUGAGAU AGUGUCUUCGGACCAGGCUUCAUUCCCCCCA	151	sly-miR166-3-3p	UCUUCGGACCAGGCUUCAUUCCCC	125-148	lja-miR166-3p	2	0	24	24	3
sly-MIR169d	GUAUGAUGAAAAGAGUCUUAUUUGGUAGCCAAGGAUGACU UGUCUGCACCAUUUCCGAAAUGUGUCCUUUCGUUCAUGG GGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUC UCUUUCAUGCAAGACUU	136	sly-miR169d-5p	UAGCCAAGGAUGACUUGUCU	26-45	csi-miR169d-5p	1	0	20	20	1
			sly-miR169d-3p	GCAGGUCAUCUUUAGCUAACU	86-106	stu-miR169d-3p	0	0	21	21	1
sly-MIR171b-1	AUUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUU CAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACG AUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAU	115	sly-miR171b-1-3p	UUGAGCCGCGCCAAUAUCACU	89-109	aof-miR171b	0	0	21	21	1
sly-MIR390-1	UAUGCAUGGAGAAUCUGUAAAGCUCAGGAGGGAUAGCGCC AUGGAUGACUCAAUUCGAUUUUUGUACACAUCUUUAGCGC UAUCCAUCCUGAGUUUCACGGCUUUUUCAUGCU	113	sly-miR390-1-5p	AAGCUCAGGAGGGAUAGCGCC	20-40	aof-miR390	0	0	21	21	1
			sly-miR390-1-3p	CGCUAUCCAUCCUGAGUUUC	78-97	mes-miR390	0	0	20	20	1
sly-MIR396f	AAGUCCUAGUCAUGCUUUUCCACAGCUUUCUUGAACUUCU UCUUGCUAAAUUUUGAUCUCUAAAUUGAUAAUUUUGAGAU	134	sly-miR396f-5p	UUCCACAGCUUUCUUGAACUU	18-38	csi-miR396f-5p	0	0	21	21	1

sly-MIR166f-1	GAGAUUUGAAGCUAUGAAAGUCCAAGAAAGCUGUGGGAAA AGAUGGCAAGCUUU UUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUU CAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACC AGGCUUCAUUCCCCUCAAA	98	sly-miR166f-1-5p	GGAAUGUUGUUUGGCUCGAGG	9-29	cas-miR166f-5p	0	0	21	21	1
			sly-miR166f-1-3p	UCGGACCAGGCUUCAUUCCCCU	73-94	cas-miR166f-3p	0	0	22	22	1
sly-MIR171a-4	AUUGAUCAACUUGCGAUGUUGGUGUGGUUCAAUUAGAUAA CAAUCUCCACGUAAAAUUAUAGAGUUUGUUAUUUGAUUGA GCCGUGCCAAUAUCACAUGUAAAGAAAAUA	110	sly-miR171a-4-3p	UGAUUGAGCCGUGCCAAUAUC	74-94	aof-miR171a	0	0	21	21	1
sly-MIR169a-2	GUUGCAGCCAAGGAUGACUUGCCGACUUUUGUAUUACUCU UCAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA UAUAUAUAUAUAUGGAAAUUACAUUAAACUUGGAAGAGAAA GUUGGCAAGUGGUCCUUGGCUACAUCUUUCUUUCUGCCC CUCAUGCCAGGUCUUUCCUG	181	sly-miR169a-2-5p	CAGCCAAGGAUGACUUGCCGA	5-25	cas-miR169a	0	0	21	21	1
			sly-miR169a-2-3p	GGCAAGUGGUCCUUGGCUACA	126-146	aly-miR169a-3p	1	0	21	21	1
sly-MIR156b-3	CAAGACUGACAGAAGAGAGUGAGCACACGAUGUCAAAUUG UAUAAAUAUAUAUACAAUUGUCAUUUGCGUGUGCUCACUU CUCAUUCUGUCAGAAUCU	98	sly-miR156b-3-5p	UGACAGAAGAGAGUGAGCACA	7-27	hvu-miR156b	0	0	21	21	1
sly-MIR156i-2	GGUGACAGAAGAGAGUGGGCACAUAUGGUAUUUUCUCGCA UGCUUGAAACUAUGUCUGCUCACUUCUCUAUCUGUCAUCC CUACCAUUUUCUCCGUUUCU	100	sly-miR156i-2-5p	UGACAGAAGAGAGUGGGCAC	3-22	pab-miR156i	0	0	20	20	1
			sly-miR156i-2-3p	UGCUCACUUCUCUAUCUGUCAUC	57-79	mtr-miR156i-3p	1	0	23	23	1
sly-MIR156f-1	UCUGUUGACAGAAGAGAGAAAGCACAGUCUGUCAUCAACA AAAUGGUAUUUGUUGUUUGUUUGGAAUGUGCUCUCUCUG CUUCUGCCAAUAG	92	sly-miR156f-1-5p	UUGACAGAAGAGAGAAAGCACA	5-26	gma-miR156f	1	0	22	22	1
sly-MIR156b-4	AGGGCGGUGACAGAAGAGAGUGAGCACAUAUGGUCUUUU CAAGCAUGAUGUUUACAUGCUUGAAGCUAUGCGUGCUCAC UUCUCUAUCUGUCACCCCCCAA	101	sly-miR156b-4-5p	UGACAGAAGAGAGUGAGCACA	8-28	hvu-miR156b	0	0	21	21	1
			sly-miR156b-4-3p	GCUCACUUCUCUAUCUGUCACC	74-95	bdi-miR156b-3p	1	0	22	22	1
sly-MIR156c-2	AGGGAGGUGACAGAAGAGAGUGAGCGCACAUGAUGUUUU CUCGCAUGAUGUUUACAUGCUUGAAACUAUGCGUGCUCAC UGCUCUAUCUGUCACCCCACCU	101	sly-miR156c-2-5p	UGACAGAAGAGAGUGAGCGCA	8-28	rco-miR156c	1	0	21	21	1
			sly-miR156c-2-3p	GCUCACUGCUCUAUCUGUCACC	74-95	ata-miR156c-3p	0	0	22	22	1
sly-MIR156d	UAUAAUUGAAAUUGAUAGGAAGAAAGAGUGAUUAUUGUUG ACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCA UUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCU CUCUAUGCUUCUGUCAUCAC	140	sly-miR156d-5p	UUGACAGAAGAUAGAGAGCAC	38-58	stu-miR156d-5p	0	0	21	21	1
			sly-miR156d-3p	GCUCUCUAUGCUUCUGUCAUCA	118-139	stu-miR156d-3p	0	0	22	22	1
sly-MIR166f-2	AUGAAGAAAAACAAGAAAAGUGAUGCUAGAAGGGAAGGAA GAAUAAACAUUUUUUGUUUAAUUUUGAGGGGAAUGUUGUU UGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUC UUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAA	158	sly-miR166f-2-3p	UCGGACCAGGCUUCAUUCCCCU	134-155	cas-miR166f-3p	0	0	22	22	1
sly-MIR167c-2	UGGAACAAGUGAAGCUGCCAGCAUGAUCUAAACUUGGCCA UUUAUAAAGAAAAUGGGUGACUAAGGUUAGGUCAUGCUCG GACAGCCUCACUCCUUCCUUUCUUGAUAAC	110	sly-miR167c-2-5p	UGAAGCUGCCAGCAUGAUCUA	10-30	ata-miR167c-5p	0	0	21	21	1
			sly-miR167c-2-3p	GGUCAUGCUCGGACAGCCUCACU	70-92	stu-miR167c-3p	0	0	23	23	1
sly-MIR171f-3	CUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUU GAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCA	79	sly-miR171f-3-5p	UAUUGGCCUGGUUCACUCAGA	7-27	csi-miR171f-5p	0	0	21	21	1
			sly-miR171f-3-3p	UGAUUGAGCCGUGUCAAUAUC	56-76	csi-miR171f-3p	1	0	21	21	1
sly-MIR171a-5	UACACGAGAUAUUGGUGCGGUUCAAUGAGAAAGCAGUACU UAAGAACAUUUUUGAGUCUACUUUUUGAUUGAGCCGCGCC AAUAUCACGUGU	92	sly-miR171a-5-5p	UAUUGGUGCGGUUCAAUGAGA	10-30	nta-miR171a	0	0	21	21	1
			sly-miR171a-5-3p	UGAUUGAGCCGCGCCAAUAUCA	66-87	cas-miR171a-3p	1	0	22	22	1
sly-MIR162b-1	GAAAAGAAAAAAAAAUCCUUAGGGGUUAAGCACUGGAUGC AGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCG UAUAUAUAUAUUCAGCUUCCAGGGAACGGAUCGAUGAACC GCUGCCUCCAGUGUCUUC	137	sly-miR162b-1-5p	UGGAUGCAGAGGUUUAUCGACC	34-55	ath-miR162b-5p	4	0	22	22	1

			sly-miR162b-1-3p	AUCGAUGAACCGCUGCCUCC	109-128	cas-miR162b	0	0	20	20	1
sly-MIR156f-2	UUGGUUGAGGAUUCAAAGUGAGAAAUUCUAUUGACAGAAGAGAGAGUACAAUCUGUCAUCAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUGGAAACUAUAAAAAUGGAUCCUCAACAAAG	144	sly-miR156f-2-5p	UUGACAGAAGAGAGAGAGUACA	31-52	gma-miR156f	1	0	22	22	1
sly-MIR156b-5	AUGUUAAAAGAGGAGGUGGUAGGAGAUGUUGUUGACAGAAGAUAGAGAGCACAGAUGAUAAAGUGCAUGGAAAUUGUCUGCACCUUACUCCUUUGUGCUCUUUAUUCUUCUGUCAUCAUCAUUAAUCCCACCUUUUUUUUUGAUAUU	147	sly-miR156b-5-5p	UUGACAGAAGAUAGAGAGCAC	32-52	aof-miR156b	0	0	21	21	1
			sly-miR156b-5-3p	GCUCUUUAUUCUUCUGUCAUC	97-117	vca-miR156b-3p	2	0	21	21	1
sly-MIR167b-2	CUACUAUCAGUUGAAGCUGCCAGCAUGAUCUAAACUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGAUCAUGUGGUUGCUUCACCUGUUAGUU	94	sly-miR167b-2-5p	UGAAGCUGCCAGCAUGAUCUAA	12-33	bna-miR167b	0	0	22	22	1
			sly-miR167b-2-3p	GAUCAUGUGGUUGCUUCACC	67-86	stu-miR167b-3p	3	0	20	20	1
sly-MIR169j-1	UGCCUAAUUUGAUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGCUAGCUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUCCUUGGCUACUCUAAUAGACUCUU	163	sly-miR169j-1-5p	UAGCCAAGGAUGACUUGCCUGC	13-34	ppe-miR169j	0	0	22	22	1
sly-MIR169j-2	UGUCUUACAUGAAGGGAAGUGCCUAAUUUGAUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGCUAGCUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUCUUUGAUGGCCAGGCAGUCUCCUUGGCUACUCUAAUAGGUUCCUC	163	sly-miR169j-2-5p	UAGCCAAGGAUGACUUGCCUGC	32-53	ppe-miR169j	0	0	22	22	1
sly-MIR169r-2	AAAGUCUUGCAUGAGGGAACAAGGUCAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAACAGCUGUUGUUGUUAAUUGUCAAAUCAGGAAUUGUGGACAA	184	sly-miR169r-2-5p	CAGCCAAGGAUGACUUGCCGG	36-56	csi-miR169r-5p	0	0	21	21	1
sly-MIR169j-3	UAUUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAAUAUUACUUAUAAGGUUUUUAAUUUUAUCAUUAUUAAUAUAAUGGUGACCUUUUAUUGGUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUCCUCUUUCAUGCAAGAAC	156	sly-miR169j-3-5p	UAGCCAAGGAUGACUUGCCUGC	14-35	ppe-miR169j	0	0	22	22	1
sly-MIR169a-3	GAGUUGCAGCCAAGGAUGACUUGCCGACUUUUGUAUUACUCUUCAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUGGAAAUUACAUUAAACUUGGAAGAGAAAGUUGGCAAGUGGUCCUUGGCUACAUCUUUCUUUCUGCCCCUCAUGCCAGGUC	176	sly-miR169a-3-5p	CAGCCAAGGAUGACUUGCCGA	7-27	cas-miR169a	0	0	21	21	1
			sly-miR169a-3-3p	GGCAAGUGGUCCUUGGCUACA	128-148	aly-miR169a-3p	1	0	21	21	1
sly-MIR171a-6	GUAUAGUAAAAUGAUGUUGGAAUGGCUCAAUCAAAUCAAAUUUCUCAAAGUAUUGGGUCAUUUCAUUUGAUUGAGCCGUGCCAAUAUCAUCUUACUU	97	sly-miR171a-6-3p	UGAUUGAGCCGUGCCAAUAUC	68-88	aof-miR171a	0	0	21	21	1
sly-MIR172-6	GCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAUCCUUGUAAACAAAAGGGAGGUGACAGAAGAGAGUGGGCACAUAUGGUAUU	160	sly-miR172-6-3p	UGGGAAUCUUGAUGAUGCUGCAU	108-130	aau-miR172	1	0	23	23	1
sly-MIR156i-3	UUCUCGCAUGCUUGAAACUAUGUCUGCUCACUUCUCUAUCUGUCAUCCCUACCA	94	sly-miR156i-3-5p	UGACAGAAGAGAGUGGGCAC	11-30	pab-miR156i	0	0	20	20	1
			sly-miR156i-3-3p	UGCUCACUUCUCUAUCUGUCAUC	65-87	mtr-miR156i-3p	1	0	23	23	1
sly-MIR159b-5	AUACUCUGCUUGUUGAUUAUACUAAUAUUCAUAUAGUUGAUUUUAACUGUUCGAAAAAGACCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAAAGGAUCUGAGAGGGAAAAUUGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUACAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUAGUUUUUUUUC	270	sly-miR159b-5-3p	UUGGAAAGAAGGGAGCUCUAC	227-247	sly-miR159b	0	0	21	21	1
sly-MIR159b-6	UACUCUGCUUGUGGAUUAUACUGAUAUUCAUAUAGUUGAUUUUAACUUGUUCGGGGAAGACCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAA	270	sly-miR159b-6-3p	UUGGAAAGAAGGGAGCUCUAC	227-247	sly-miR159b	0	0	21	21	1

sly-MIR166-4	AAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAG CUGUAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGA GCUCUACACUUGAUAACUUUUUUUUUUCUA	119	sly-miR166-4-3p	AUCUCGGACCAGGCUUCAUUCCCC	72-95	lja-miR166-3p	1	0	24	24	1
sly-MIR171b-2	UAAACUAAACAAGAUCAUGUUAAGGAGAAUGUUGUCUGGU UCGUGACCAUAUAUCUUUCUUCACAUAAAUGAUCUCGGAC CAGGCUUCAUUCCCCUCAACUCAUCAAGGUUAUGUCAUG UUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUU CAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACG AUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAUUUUC AAAAAGAAAUGGUCCUUUUUGUGUUUUUCCACAGCUUUCU UGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAA AAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUG GGAAGAUACAGAUA	118	sly-miR171b-2-3p	UUGAGCCGCGCCAAUAUCACU	88-108	aof-miR171b	0	0	21	21	1
sly-MIR396b-3		135	sly-miR396b-3-5p	UUCCACAGCUUUCUUGAACUG	27-47	aof-miR396b	0	0	21	21	1
			sly-miR396b-3-3p	GUUCAAUAAAGCUGUGGGAAG	106-126	csi-miR396b-3p	0	0	21	21	1
sly-MIR7997c-1	GGAUCCUAUGUUGCUCGGACUCUUCAAAAAAGUCGAGGGG UGUUUGUCAGGUCCUCCGAAAGCAGUGUGCUUUUGAAGG AUCUGACACGGGUGGGGCAACAUACUUGGAGAGUCCGAG CAACAUAGGAGGG	131	sly-miR7997c-1-5p	AUGUUGCUCGGACUCUUCAAAAAA	8-31	stu-miR7997c	2	0	24	24	1
sly-MIR168b	AUGCUUGGCCCGCAAGGCUUGGGCCAGGUGGGGCUGGAC CAACCCUUUUUGACAACUCUAGAUACAUCAAAAGUAGAGU UGUCAAAACGUGUCGAUCCAGUCUCACCCGGCCCAAGCCU GGUGGGCCAAGGAA	133	sly-miR168b-5p	AGGCUUGGGCCAGGUGGGG	15-33	gma-miR168b	5	0	19	19	3
sly-MIR10405d	AAAAUGAAAUCGCUGCUUAGGCAGCGAUUUCAAAAUUUUG UUUCUUAGAGAUCGCUGUCUUGGCAGCGAUUUCAUUUUUU UUUAAUUAUAUUUUUUUUUGAAAAAAAUAAUGUAUAUCGCU GCCCAGGCAGCGACUUUAUGAAAAACAAUUUGUUUUUUAU AAAACGCUGCACAGGCAGCGACUUUAUGAA	191	sly-miR10405d-3p	UUGUUUUUUAUAAAACGCUGC	151-171	gma-miR10405d	5	0	21	21	1
sly-MIR11416-1	CCAGUUUCUCAAAGGCAUAACACAUACAUAGACACUCAAGU UUGGCCUCGAUUGGCAAGUAGACAAUCCAAUUUUGGGAGU GGACACACGAUGAUGCUGACUUGACACAUAAAUUUUGGAU GCGUCCAGAUGAUUAUUUCUUUAAGCUGAGUGUUCAACUG ACACAAUGGAGACGAGUUGAAAUUAGUAGAUGUGCAUCGU CCUUGGAGCGUUUUGUCAGUUGAGACCAAGUUUGAGUGU CUAUCUUUAUAUUAUAUACCUUUCUCAAACACC	273	sly-miR11416-1-5p	ACAUAAAUUUUGGAUGCGUCC	107-127	pab-miR11416	5	0	21	21	1
sly-MIR156b-6	AUUGAUUUGUGUAAAAUGUAGGGAGGAAAAAAAAAGAGGG GAAAAUGGAAUGGGUGAUAUUGUUGACAGAAGAUAGAGAG CACAUAUGAUGGAAUGCUGCUGCUGCUGCUGCUAAAUCUG GAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUCAUUUGU GCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUCUCCU UCUAUUUUUCUCUUCUCUCUCCCUAAAUCUAUACAAUAAC UCGUU	246	sly-miR156b-6-5p	UUGACAGAAGAUAGAGAGCAC	63-83	aof-miR156b	0	0	21	21	1
			sly-miR156b-6-3p	GCUCUCUAUGCUUCCGUCAUC	162-182	vca-miR156b-3p	1	0	21	21	1
sly-MIR159a	GAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAU UGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUA UGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUG UCAGGAGCUUUAUUUUACCCUUUGUUUGAUCAUUUUUUGG AUUGAAGGGAGCUC	174	sly-miR159a-5p	GAGCUCCUUGAAGUCCAACAG	1-21	fve-miR159a-5p	1	0	21	21	1
			sly-miR159a-3p	UUUGGAUUGAAGGGAGCUC	156-174	cas-miR159a	0	0	19	21	1
sly-MIR1863	CGUCAAAGUCAAUACCCUUUCUUUGACCGAAUUUCUUAUU AAGGUCAGUAGUCGAUUGCAACAAAGGUGUGCCCAAUUUG CUGCAAAUCUUGCCAAAAAGAUUUUCUUCCUUUAAAGAUG GGAUUUGGACCCCAUAACUUGAAGCUCAGGUACAAAGUUA GAUUGGUUGUUAAGCUAUUUGGCCGAAGGAAGGGUAUUG ACUUUGAAG	208	sly-miR1863-3p	AGCUCAGGUACAAAGUUAGAUU	143-164	pab-miR1863	3	0	22	22	1
sly-MIR167c-3	CCAUAGGCCUAAAAAAGUUUUGAGAAUGUGAAGAACUAAC UGAAUUCUAGUAAACUAAUGGGUGAAAGGAAACCCACUAG UGAACUCCCACAUACAUGGUGACAAAAUAUACGAAGAAAUC CUUUUAAAUUUAGGACUAAAAUUUGAAGAACACUUCUUCU UAUUCUUGAGAGGACAUGUUGAUAGUUUCCUCUUGUAUUU GGUCAAAGUAGGAUUAUUUUUCGAGAAUGAGGGAGUUGG GUAGAUUUUUACUAUAUUGUUAGGCUUAGAC	271	sly-miR167c-3-3p	AGGACAUGUUGAUAGUUUCCU	172-192	aly-miR167c-3p	5	0	21	21	1
sly-MIR6232b	GAGCUCUACAGUGCAACUUCAGCAUAGUAAAGAGUAGAGA CUAAUUAAUGCCUACAUAUGUAGGGAUUAAUGAGUCUACU	112	sly-miR6232b-	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-	5	0	21	21	1

	CUUUGCUAUACUGAAGUUGCACUGUAGAGAUA		3p			5p					
sly-MIR5035	UUUACCAAAUGCCUAGAUAAGCCAAAAAAUUGCUUAUAAGC UAGUUUGACCAGCUUAUAAGCUUAGAGGGUGUUUGACUAA GCUUAUAAGCUGGUCAAAUUGGCUUAUUAACACUUUUUAG CUUAUCUACUCAUUUGGUAAA	142	sly-miR5035-3p	CUUAUUAACACUUUUUAGCUUA	104-125	gma-miR5035-5p	5	0	22	22	1
sly-MIR169f	GUUGAAGAGAGGUAUUGCAUGAAGAUAAAGUGCCUGCUCU GAUAGCCAAGGAUGACUUGCCUAAAAUCAUUUUUAUGAAG GGUCUUAACUAAUUAAACUUUAGUUACUAAAAUUAAAGUUU AUAUUAUAUGAUCUUAAAAUUGGAAUUUUAGGCGUUGUCU GAGGCUAACUGAGAGACACUUAUCUUUCAUGUAACACCUU CAUUCUCU	209	sly-miR169f-5p	UAGCCAAGGAUGACUUGCCUA	43-63	bna-miR169f	0	0	21	21	1
			sly-miR169f-3p	UAGGCGUUGUCUGAGGCUAAC	150-170	sly-miR169f	0	0	21	21	1
sly-MIR12142-1	GCAUUUCUCUUUCAUGAAAAGUUGUGACUUUUAUGAACAG UUGUGACUUUUACGAAGAGUUGCGACUUUUUUAAAAAGUU GUGACUUUUACAAAAAAUAAUUGCAACUUUAAUGAAUAUCU AUAACUUUUAUGAAAGAUUGUGACAUUUCCUAAGGGUUGC AACUUUUCCAAAUAGUUGUGACCUUUUCGAAGGGUUGCAA CUUUUCCAAAUAGUUGUAACCUUUCUGAUAAGACACAAGA A	242	sly-miR12142-1-3p	ACUUUUCCAAAUAGUUGUAAC	201-221	aof-miR12142	5	0	21	21	3
sly-MIR3447	GCGUGAGGAAGAUAACGAAGCGUGGCUUUAUGCCGCUGU UUGGGUACAUAAUUUCUUUAAAAAAAAGGUAUUGAUUAGU CAAAUCUCUUUUGUUUUAAUUGUUCAUGACUAUGGGUUCU UUAAAACCCAUGAGUUGUCCCUAGUUUUUGAAGUCUUCGU CUUUCCACGAGGUAGACAUUGUUUGGGCCAGCUGUUCUU AUUCUUCUUCAUUU	212	sly-miR3447-5p	CGUGAGGAAGAUAACGAAGCG	2-22	aly-miR3447-5p	5	0	21	21	1
sly-MIR10211a	UGUCUUCACAAUAUGGAGCUUCGAGUGAAGAACAGGAAGC CACUUGCUUGUUCUUCUCAUAAUGCUCCAGAUAUUUGAAG CCU	83	sly-miR10211a-3p	CUCCAGAUAUUUGAAGCCU	65-83	eun-miR10211a-3p	5	0	19	21	2
sly-MIR1865	UAAAACUUCGGUUCUUCGGUGCACUGAAGUUUCGGGACCC UUGCACUGAACUUCAAACCGAAGAAUCGAAGUUCCG	76	sly-miR1865-3p	CGAAGAAUCGAAGUUCCG	59-76	osa-miR1865-3p	4	0	18	24	1
sly-MIR5658	UGCGGUGCGGUAAAGAUGUUGAUGAUGAAGAGAUUUUUU UUUGAGAAUGUAUUUUUUGGAUGACGGAAUCAGUCUCCAA AUCGGAGAAUUGUUAGGUAGUGGAUCCUGAUUAAUAGUUG AUGUACUUUAACAAAAAAUACUCUGAUUUAUUAAUAUAUGU ACCCAACCUCC	171	sly-miR5658-5p	AAGAUGUUGAUGAUGAAGAGA	13-33	ath-miR5658	4	0	21	21	1
sly-MIR7502c-1	CUUAUCACACUUUCAAGAAGACUUAUUUAAGUCAUCCGUC AAAAGUUUAGUCAUCUAUGUUAUUUCUGUUUGAGAAAAGU CUCAUCCAUGUCAUUAUUUGUAAAUUGAAAUGACAUAGAU GAUCCAAACUAUUAACGGAUGACAUAGAUGAACCUUUUCU CAAUGUUCGAUGAC	174	sly-miR7502c-1-3p	UUGAGAAAAGUCUCAUCCAUG	70-90	gra-miR7502c	4	0	21	21	1
sly-MIR7504j	AAAGCCCCCUAACCUAUAUCCGGAUUUCCAACAACUUCAC UUGAGUCUUAUCACCCUGUGAACUAUUUAAAACUGAAAUU CCAUCUCCCUGGAGGUGAUAGGACUCAAGUGAAGUUGAAG AGUGUGGUUGAAAAUCCGGAUAUAAGUUAGGGGGCUUU	158	sly-miR7504j-3p	AUUUAAAACUGAAAUUCCAUC	65-85	gra-miR7504j	5	0	21	21	1
sly-MIR8002	AAUCAUUUAUUAUAAAGAAAAAGGCUCAAAUAUGCCAUCGA AUCUAAAGUUUGGCUCAACUAUGCCAUUUCAGUGAACAAA UAAUGUUUUAAUGGCAUGGAUGAGCCUUUACUCAAAACGG AAAUGGCAUAUAUGAGCAAACUUUUAACGGAUGACAUAAAU GAGCCUUUUCUCAAUGUUAAAUGGCA	188	sly-miR8002-5p	AAUCAUUUAUUAUAAAGAAAAAGG	1-24	stu-miR8002-3p	5	0	24	24	1
sly-MIR156a	AGCAACGAAAAUAUAUGUAUAUAUACAAUUUUCUCUAGCUU UAUACAAACACAAACACAUUUUAUACAAUUUCAUUUUUGUA UAAAGUGAGAGAUGCGAGUGAGCAAGCAAGAUCUGGGAGA AGGGGUGAGAGGAAAAUGAAAAGAUAGGUAUAUACAGAAU UUUCUCUUGCUUUAUACAAACACAAACAUAUUUUAUAUAAU UUCGUUUUUGUAUAAAGUUAGAGAGAUGAGUGAGCGACCG AAACCUGGGAGAGAGGAGAGAGGAAAAAGAAAAUAUCUGU AUAUAUACAAUUUUCUCUCGUUUUA	308	sly-miR156a-5p	UGAGAGAUGCGAGUGAGCAA	88-107	aof-miR156a	4	0	20	20	1
sly-MIR1525	UGAAAAAAUCGAACCGACUGAUAAAUCGAAUCGAAAAAAAU GUUAUUGGGUUAUUGGGUUUUCAAUGGGUUUAUAAAUUUU UUUAUUGGGUUAUGGGUUCGGUAUCGGUUUUUACU	116	sly-miR1525-3p	UGGGUUUAUAAAUUUUUUUAU	66-86	gma-miR1525	5	0	21	21	1
sly-MIR7740	UAUAGUCUGUAUGUAAAAUGAAUGAUAUGAAAUAAACAGUU GGUUUUUAUAUCCUUCUUCUUAAAACUCCAUUAAUAGUCA UAAGUGAAGGUUGCGAUCUUCCGCCUCAGGGAGGAACAG UAACAGAGUAGCCAAAGACUGAGGUCGUUAGGGUGAAACA CUGUUCAUGGCCUAAAGGGAGAACUACUGAGGUAGUGAUA	282	sly-miR7740-3p	AAGACUGAGGUCGUUAGGGUG	135-155	bdi-miR7740-3p	5	0	21	21	2

sly-MIR9565	AAGAGUAUUCAUCGACAAAAGAGAAAAAAGGUAUACACGCAAACUUUUUAUUAAAUGUUAUUAAUUUUACAAAUAUACUAUAAACACAAGAGAAAACAAAGAGUGAAAGAGUUAGUCUAAAAGAGAUUCUUAUUAGUUGAAGGGAGGUGUUUUUUUUUGUGAUGCUUUGGACUCAAUUCUUGUCCAGAGUUGUUGAGUUAUAUUUUGUGAAGACUGUUGUAUCCUGGAUGGGACAAGUCAAAGAGGACUACUGCUGGACCGGUGAAAACAUUUGCUAUAGUGGGCUUGAAUCUCCUUAAAGAGAGAGAGAUAUCCACGCCUUAGCCUGGAGAGAUUGAUUUCUUCAUUUUAUUUUCACUUGUAAU	284	sly-miR9565-3p	UUGAAUCUCCUUAAAGAGAGA	205-225	bra-miR9565-3p	5	0	21	21	2
sly-MIR9556	GUAAUGAUCUUGACCUAAUAUCUUUUAUUGACGUUGUGAAUGAGUACACCAAUAAGUUAGGUUUUGUUGGUGUGCAAGAAUGUAUUUUACUUGCUCCAACUGGAAAACAUUUUGAAAUAAUAGGUGAUGAGGGAGUUAGGACCUUAAUAUUUUUUAUCUCUGCCGAGUAUUAUCUAUUCACUUGUUUGCUAUAGAAGAUUGUGAAUUGUCUCUUGAUGUAACUGAUAUUGUCAUGCAUGAUGGGUCAUUUCUACUUUCACCAACUGUUAAUGACUGCACUGACUGUAGUUAAAGUGAAGAUGAAAAUAAUAACGAUAUAGUGUUUAGUUCAUAUU	335	sly-miR9556-3p	UCUACUUUCACCAACUGUUAA	250-270	bra-miR9556-3p	5	0	21	21	1
sly-MIR7980b-1	UCUCAUGAUAUGAAAUCAUGAGAUGGAAUUAACGUGAAAUUAUAUGUCCAAACGCUGAUUUCAUCUCAUGAUUUCAUAUUGCAUGUCC	88	sly-miR7980b-1-3p	GUCCAAACGCUGAUUUCAUCUCAU	46-69	stu-miR7980b-5p	2	0	24	24	1
sly-MIR2872	UCAUUAAUGAGUGAAAUUUAUGAUCGUUUGAAGUUGACCCAAAACUUAAAAAAACUAAGAAAUGACUUGAAAUGAAUUCUAUGUAAUUCUUUUUGAAACUCAAAAUGCUAUAUCUAGUGAUAUUAAUAUUUGAGAAAUUUCAAAUUCCUUGGUAAAAUCCUAUUCACAACGAAGGAUUGCUCGAGUCUUUGGUCAAAAACUUUUUGGGGUGCUACAACUUCAACUUUCACCCCUUUUAACUUUUUAAGGCUUGGGCUCCACUUUUUAACUCAUGCAUAUUACUUUUAACGC	291	sly-miR2872-3p	UGGGGUGCUACAACUUCAACU	205-225	osa-miR2872	5	0	21	21	1
sly-MIR171c-2	AAUACGUGAUAUUGGCACGGCUCAAUUAAAUAACGAAGUUCUAUAUAUAAAGAAGUGCGCUUUCUAAUUGAACCGCACCAAUAUCUCGUUAG	92	sly-miR171c-2-5p	UAUUGGCACGGCUCAAUUAAA	10-30	csi-miR171c-5p	3	0	21	21	1
			sly-miR171c-2-3p	UAAUUGAACCGCACCAAUAUC	65-85	aqc-miR171c	1	0	21	21	1
sly-MIR171t	AAUCCGGGCUCUGCAACUAUGUUGAACUGCGUGACUAUCUCAUUUAAAAGGUUUAGAUGAGAUAGUCAGACACUUCAACAUUGUAUCAAGCCAGGCCC	98	sly-miR171t-5p	UUGAACUGCGUGACUAUCUCA	22-42	gma-miR171t	4	0	21	21	1
sly-MIR837	UAUCUCUCUCUCUCUCUCCCUCGCUUUAUACAAACAUAAAAUAUGCAAUGUAUUUUGUAUAAUUUGUAUUUGUAUAAAGCGAGAAAGAAAGAACGGAAAAGAGAACUGGGCAAGGGUAUAUUUGUAUUGUAUAAUUACGAGUAUAUAAGACGAAGAUAUAUGUAUUUGCAUGUGUCUAUACAAUUUUUUCUCGUUUUAUACAAAUAAAGCCGCAAUUUAUACUGAUUGUAUAAAGUGAGAGAGGCGAGCGACAGAGGGA	261	sly-miR837-3p	AAUUUUUUCUCGUUUUAUACA	184-204	aly-miR837-5p	5	0	21	21	2
sly-MIR169j-4	AAAGAAGAGAAGUCUUACAUGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAUAGUCUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUUUUCUUUUAUGCAAGAUAUCUUUUCAAA	169	sly-miR169j-4-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1
sly-MIR396a-1	AGUCCAAAGCUUGCCAUCUUUUCCCACAGCUUUCUUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAAAUUAUCAAUUUAGAGAUCAAAAUUUAGCAAGAAGAAGUUCAAGAAAGCUGUGGAAAAGCAUGACUAGGACUUGGUCA	144	sly-miR396a-1-5p	CACAGCUUUCUUGGACUUUCA	25-45	hbr-miR396a	2	0	21	21	1
			sly-miR396a-1-3p	GUUCAAGAAAGCUGUGGAAAA	104-124	csi-miR396a-3p	1	0	21	21	2
sly-MIR171f-4	UAGAGAAGCGAUGUUGGUGAGGUUCAAUCUGAAGACGAGUUUACGUUUUAUUUCAGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCAUUUCUUUU	100	sly-miR171f-4-5p	CGAUGUUGGUGAGGUUCAAUC	9-29	fve-miR171f-5p	0	0	21	21	1
			sly-miR171f-4-3p	AGAUUGAGCCGCGCCAAUAUC	71-91	mes-miR171f	0	0	21	21	1
sly-MIR11115	UAAAAAGAUAUGUAGGACUACUAGACAACUCAAGCUUUAACACUCUAACUUGUCUACCAGUUGAUUCAGUCCCCUUUGGUUAGGGACUGUCUUCAUUGGUUAUGGUGGUCAACUGGUAGGCAAGUUAGAGUUUUUAAGCUUGAGCUGUCUAGUAGUCUUAUAUACCGUUAAC	172	sly-miR11115-3p	UGGUAGGCAAGUUAGAGUUUU	114-134	lja-miR11115-5p	5	0	21	21	1

sly-MIR10532-3	CCCAACCAAACAUGAGAAGAUUGGAAAACAUUUUCCAGAAAAUGUUUUCCUUUAUACCAAACACAAACAGACUCUCAAUGUGUCUCUGAGAUUUCGAGCAUAGGUUGAGGGGCUACUUGUGCAUUAUCUCUUUUGAUAAUGUGUUUUAAGAAUUGAAGGUUUUCUAGUCUUGAAUAUGUUAGAGUUUGA	189	sly-miR10532-3-3p	CAAUGUGUCUCUGAGAUUUCGAGC	76-99	sly-miR10532	3	0	24	24	2
sly-MIR5628-1	CUGGAGAAAUAUGGAAGAGAUGAUCGGAGAAAUAUUAUGUUCUCAUGAGCUAAUGCCACAAGAAAAGUAAUGAUGUCUAUAACUUUAAAGCUCUGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGA	135	sly-miR5628-1-5p	GAAAUAUGGAAGAGAUGAUCG	6-26	ath-miR5628	5	0	21	21	1
sly-MIR5628-2	UGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGAAUAGGUUGCUAAUUCAAGCAUUAGAGAAAUAUGGAAGAGGUGAUUGGAGAAAUAUUUCUAGG	103	sly-miR5628-2-3p	GAAAUAUGGAAGAGGUGAUUG	67-87	ath-miR5628	5	0	21	21	1
sly-MIR8001a-1	UCCUGGGGAUUAGUAUGAAAAUUCAAAAGAAACUUAUUUUCCUGCAAAUUUUCACACUAAUUCCCAUGA	69	sly-miR8001a-1-5p	UCCUGGGGAUUAGUAUGAAAAUUC	1-24	stu-miR8001a	0	0	24	24	1
sly-MIR8001b-1	UUUAAGUUGGUAAAUGUAGAGUAUAAUUGCACUAGCAACUUCUUUUUGGUGGCAAUUGGUUCGAAUUUGCCACGCGAUAUAUCUAGUAUACAUGGUAUAUUCAAACUAAUUCCCACAAAAAAUCGUUUGCACUUAAGGCAAUAUGAGUAUAAUUGCACUAGCAACUU	171	sly-miR8001b-1-3p	GUAUAUUCAAACUAAUUCCCACAA	95-118	stu-miR8001b-3p	5	0	24	24	1
sly-MIR1918-1	AUUUGAACUUCCAUUCUGUUAGCGGUAGUUCGAUUCUCCACCUUGUAGCAUAUCUUUUUCUCUUAAAUUGAAGAGGAGAUUGCGUAAUGGAGAAUCGAACUCUCACCAACAAAAUGACAAUUCAACU	127	sly-miR1918-1-5p	UGUUAGCGGUAGUUCGAUUCUC	17-38	sly-miR1918	4	0	22	22	1
sly-MIR7980b-2	AUAUGGUAUCACAUCUCAUUAUAUGAAAUCAUGAGACGGAAUUAACGUAAAAUCGAAUGUCCAAACGCUGAUUUCAUUUCAUGAUAUCAUAUCGUGAUAUGGUAUCACAA	110	sly-miR7980b-2-3p	GUCCAAACGCUGAUUUCAUUUCAU	59-82	stu-miR7980b-5p	3	0	24	24	1
sly-MIR160-1	GACAUGAAACUCUAUACAUGCUUAGCUCCUAGAAUGCCAUCUGAAAAGGCCAUCAAUUCUUGGUGGAACAAUGCAAAUGGCAUACAAGGAGCCAGGCAUGUUGUGUUAUCGAUCAC	116	sly-miR160-1-5p	UGCUUAGCUCCUAGAAUGCCA	19-39	vca-miR160-5p	4	0	21	21	1
			sly-miR160-1-3p	UGGCAUACAAGGAGCCAGGCA	78-98	aau-miR160	1	0	21	21	1
sly-MIR7997c-2	CGACUAUAUUGCUCGUACUUUUCAAAAAUGUUGUCAGACCUGUAUGUAUGUACUUUUGGACGAUCUGACACACACCUGACAGUACUUUUGAAGAGCUCGAGCAACAUAGAAA	112	sly-miR7997c-2-5p	AUAUUGCUCGUACUUUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
sly-MIR7984b-2	UUUUCCAGAAGUUCAGGAUGAAGCACGUUCCACAUGUAGAACAAAUUUAUCUACACGUUGAAUGUGCUUCAUCCUGAACUUUGGACGU	88	sly-miR7984b-2-3p	AUCCUGAACUUUGGACGU	71-88	stu-miR7984b-5p	4	0	18	24	1
sly-MIR11039	UUCUCUACUUGUUAUGAGGAUAUGCAUGGUAUGUGUCUAUAUGAUGUAAUCUUAUUCUUAUGUGAACUAUGUGAGUCUUAGUGACUAUAGGAUGGAAAUUGUUGAUAGUAAUUGAGUUGUACUUAUGCAUUAUGUUGAUGUAUGAAGUGUUAAGAUUUGUGGUGUCGUGAAGGGUUUACAGAAUGUAUGGAGUUAUGGGGCUUCAUAUGUUCAUUGAACUAGUAGACUA	229	sly-miR11039-3p	UGGAAAUUGUUGAUAGUAAUUGA	93-115	seu-miR11039	2	0	23	23	1
sly-MIR10186e	UUUAAAAUCUGACGUGGAUGACGACAUGUCACUUUUGUUGAGCGAUUGAAGUUCAACAAAGCCAAUGGGAUUUAAAAUGUUAAGUUUCAUUGAGUCUAAGGGCUUAGUUGAUAAAUAGUUAAGUAGAAGGGUUUAGAAUACAAACUGAUACAAGUAUAAGGGUCUACCAGACCAUUCUGUCAAUAAUAAUUAACUAAAUAGUCCUAAAAAUGACGCAUGUCUUGAUCCUAGCCUAGAUUUUCUU	244	sly-miR10186e-5p	AUGGGAUUUAAAAUGUUAAGUU	65-86	gma-miR10186e	4	0	22	22	2
sly-MIR812o	GUUCUAGUUUGCCUUUCGGGGAAGAAAUUUGAUUUUCCAUCUUGAAGGUUUACCAUGAAAUAGUCAUUCUUGUCUUGAAUGUUUGACUGACCUCUGCUUAUUUCAUGGGCAAACUUUCAAGACGAAAAAACAAGUUUCUUUUCCAAGAGGCAAACAAGGUC	161	sly-miR812o-3p	UGUCUUGAAUGUUUGACUGAC	71-91	osa-miR812o-5p	5	0	21	21	2
sly-MIR6021	UCACAUUACAUAUUUUUUUUUAUUUUUCUGCCAAUGUUAUUUUUAUAAUUAUCUUACUUAAUUAUUUUUUAUAGUUUAUUUGGCAACCUUAUUCGGAAGAUGUUAUUAUUGGAUUGUCUGAGUGGUGUCGGUUAGGACAACAUGUCUGGAUGACACAGGUGCCACUUAUUUAUGAAAUUUAUCGUGAGUGGCACAUGGUUAAUCAUGUUGUGAGACAGUUUGGUUAUUUACAACAUAUUCUUAGAUCGUGUACCCAAUUUUUCGAAUAUCAUUUUAAACGUGAUAAACGAGCCAAAAUAAAACAAGAAGAUAUAGAUGCAU	321	sly-miR6021-5p	UCGGAAGAUGUUAUUAUUGGA	93-113	nta-miR6021	5	0	21	21	1
sly-MIR5049c-	UGGUAAUUUAUGCAUUGACUCCCUCUGUCCCUUUUUACUU	295	sly-	GGACAAAUACUUAGGGACGGAGG	251-273	hvu-	4	0	23	23	2

1	GUCCACUUUUGAAUUGGCACACCUAUUAAGAAAAUAAUUAA UGACGUAGAAGUUUACCAUUUUAUCCCUAUUAAUUAUGAA GUGGAUGAAAAGUUUUACAUUUUUCAAAGUAAUUAGUCAU UUAAUUGUGGGUAUAAUAGGCAAAAAAAUUGUCAUUUCUU GAUUUGUCAAAAUGGACGAGUAAAUAGGGACUACUAUAAA AAGAAAAGUGGACAAAUACUUAGGGACGGAGGUAGUAUUA UGGAUCAACUAUUU		miR5049c-1-3p			miR5049c					
sly-MIR5021-1	UUCAGAAAGACGAGAGAGUCACGAUCGGAGUUGAGAAGGA AGAUAAGAUAAUGAGAAAGAAUAUUUGUUUUGAUAGUCGA ACUUUUAGAUUUUCUAAAGAGGAAGAAUAAGAGAAGAGAG AACAUUGAGAGAAGAAGAAGAGAAAUACCUAUCUUCAUUUA CUUUUUUUUUAAAAAAAAAGAAUGGUUUGAAAAGAAUUAUA AAAGUUGAAAUAAAACAUCAACUUUUUUCUCUUUCUAUUUC GCUUUCUUUUUCAACUUCUCCUUCUCCAUCUCUAGGUCCU UCUCCU	289	sly-miR5021-1-3p	AGAGAAGAAGAAGAGAAAUA	128-147	ath-miR5021	4	0	20	20	2
sly-MIR7987-1	CACAAGUACCAACACUAGCUGAUGCUAUUGAUGACAAAAAU UGGUUUUCUUGCAAGAUCAAUUUGUGUCAAUCUAGUGUUG AUACUUAGUUUUAGUUUAGGAAUAAAUGUUUGUUGAUUGU AAGGACCAACACUAGUUGAUCUUAUUGAUGACAAAAAUUAA UGUUCUUGCAAGAUCGAGUUGUGUCCAUCUAGUGUUGAUA CUUAGC	208	sly-miR7987-1-3p	ACACUAGUUGAUCUUAUUGAUGAC	130-153	stu-miR7987	0	0	24	24	1
sly-MIR7987-2	AAGAUCAAUUUGUGUCAAUCUAGUGUUGAUACUUAGUUUU AGUUUAGGAAUAAAUGUUUGUUGAUUGUAAGGACCAACAC UAGUUGAUCUUAUUGAUGACAAAAAUUAAUGUUCUUGCAA GAUCGAGUUGUGUCCAUCUAGUGUUGAUACUUAGCUUUAA UUUAGUAAUAAUGGUGUUUGUUAGGCAUAAGUACCAACAC UAGUUGAUCCUAUUGAUGAA	220	sly-miR7987-2-5p	ACACUAGUUGAUCUUAUUGAUGAC	77-100	stu-miR7987	0	0	24	24	1
sly-MIR7992-1	UUUAUACAAAUUUAAGUGUCUACCAACUUUGGAAAUGCAC AAGUAGACACUUAAACAUGUAUAAAGUUGAAUAAGUAGACG CAUGAGUCCUAUGUGACAAAAUACACGUAGGACAAAAAAAU GAUAUGUAGGACAUGUGUGUUUAUUUGUUCAACUUUAUAC AACUAUAAGUGAGCAAAUCCAAAGUUGAAAAACAUAAAUGU GAUUUG	209	sly-miR7992-1-5p	UUUGGAAAUGCACAAGUAGACACU	28-51	stu-miR7992-5p	4	0	24	24	1
sly-MIR10540-1	CGUAUGGCUCUUGAAUUGUCGGAGUUGAUUUCUCAUAUAG UCACUUAAUUAACUGUUAUUAUCUUGUAAAAUUACUUUUC UUUAUUGACUUUCUAAGCUAAUAACUGUUAGUUGAGUGAU CAUUUGAGAAAUCAACCUGAAUUGAUGGCAAUCUU	155	sly-miR10540-1-3p	CUAAUAACUGUUAGUUGAGUG	98-118	sly-miR10540	3	0	21	21	2
sly-MIR2101	UUUCAUUCAUUAUGUGCAUCACUUGAGGCUGGCCUCAUUC UUUCAUUGGUAAAUUUAACUCAAGUGAGCAUCAUGAAAUC CA	82	sly-miR2101-3p	AUUUAACUCAAGUGAGCAUCAU	53-74	osa-miR2101-3p	2	0	22	22	1
sly-MIR8006-1	UCGUAGUGGUAUCCCUGUUGUCGAAAAAUUAGAGUGUGUA UACCUUUCACUCUAAAGGAAUGCUAAAUAGGGACAUGUGG CUGUAGUCUCAUUCGUCGAUCUGAUGUUGGGUCGGUGGA UAAGAUAAUGACGCGUGUAUAUCCGUUAGUGUAAAGAUAU AUAUGCUUUAAUUUUUGGAGCGACAGGGGCACCAAUAUGU	199	sly-miR8006-1-3p	AAUUUUUGGAGCGACAGGGGCACC	169-192	stu-miR8006-5p	5	0	24	24	2
sly-MIR5205a-1	ACUCUAAAAAUAGAAAACAUGACAAACAAUUCCGGACGGAG GGAGUAGCAAGGAUAAAAUAAGUGCAAAAUACUACCUCCG UCCUUAAUUACUUGUCCACUUUUCCUUUAUAGUUG	116	sly-miR5205a-1-5p	CAAACAAUUCCGGACGGAGGGAG	23-45	mtr-miR5205a	3	0	23	23	1
sly-MIR6299	UAGAUAAGUAUUUUUUAGUUUGUAUGUAAAAUUAUUAAUA UGAAAUAAAAAGUGAGUUUUUAUAUCAUUCUUCUUAAAACU CCAUAUAUAGUCGAAAGUGAAGGUUGCGAUCUUCAGCCUU AAGGAGGAACAGUAACAAAGUAGCCAAAGACUGCGGUCGC CAGGGUGAAACACUGUUCAUGGCCUGAAAGGAGAAAUACU GCGGCAUUGAUAGAGACUAUUCAUCGACAAAAGAGAAGAA AGGUAUACACACAAACUUUUUAUUACAUACUAUAUAAUUUU ACAGAUAUACUAUAUACACUUAUUUU	308	sly-miR6299-5p	AUGUAAAAUUAUUAAUAUGAAA	24-45	gma-miR6299	5	0	22	22	1
sly-MIR8172	GUUUCUCCAUCCAGAUGGAUCAUCUAGAUGGAGAUAAAAA AUGAUGUUUGUUUUUGACAAAUUAAUAUAUCAUUUGGAUG UUCCAUCUGAAUGACUUUGUAAAUUUAAGCUAAUUUGUGA AACUCAUUUGGAUGGACUUGGAAGAACCAUUUGGAUGGAG AUGA	164	sly-miR8172-5p	AUGGAUCAUCUAGAUGGAGAU	15-35	ath-miR8172	0	0	21	21	1
sly-MIR8011a-1	ACAUGAACUUUGUUUUGUGUCUCACACAACUGAUGUAAGU UGUGUGAGGUCUCUUUUUGUUUUACAAGUCAGUGCGACC CAAAUCGUUGGACUCACCAACUCGUGAAAUAAAAAGAAGU CUCACGCAACUUGCGUUAAUUCUGUGAGUCGCAAAGUAAA UUUUCAAAU	168	sly-miR8011a-1-5p	UUGUGUGAGGUCUCUUUUUGUUUU	40-63	stu-miR8011a-5p	2	0	24	24	1

			sly-miR8011a-1-3p	AAUAAAAAGAAGUCUCACGCAACU	107-130	stu-miR8011a-3p	2	0	24	24	1
sly-MIR5161	CCAUUUAAAAAAGACCAACAAGUCUUUUUCAAUUUAAGGACCCUAAAAACUACACUAUUUCUGGUUCAAUUUGUUUGCCCUACUUUACUUUUAAAGUAAAGUAAAGUGAGACGAACAAAUUGAAUCAGAGAGAGUAUAGUUUUUAGUUCGGUUCAAAAAAAGUAUCUCCUUCCUUUUUGACAACUA	186	sly-miR5161-3p	AUUGAAUCAGAGAGAGUAUA	119-138	osa-miR5161	4	0	20	20	3
sly-MIR9479	CAAGUCCAGUCCUCUACCCUUCUCCACUUAAAAGACCAAGCUUGUCUACAACAAGGUUCCAACUCAUGACAAACAUAUGAUGUGUGAGUUAGGCACGUGUCACGGGUUCAAAUGCUACCACCGACAAAAGUAUGGUAUUUAAGUGGAGAAUGGUAGAGGGUCGGACCCA	169	sly-miR9479-5p	UCCAGUCCUCUACCCUUCUCCA	5-26	sly-miR9479-5p	0	0	22	22	1
			sly-miR9479-3p	GAGAAUGGUAGAGGGUCGGACC	146-167	sly-miR9479-3p	0	0	22	22	1
sly-MIR172-7	UACUUGCUAGUGCAGCACCAUUAAGAUUCACAUAGAAAAUAUGGAACGAAAUUUGCUCAAUUUUUCAAUAUAUGAGAAUCUUGAUGAUGCUGCAUUGGCAAAUC	104	sly-miR172-7-3p	UGAGAAUCUUGAUGAUGCUGCAU	73-95	aau-miR172	0	0	23	23	1
sly-MIR160-2	GGUAACUUUAUAUGACGAGAUGGUUACAUAUUUCAACAUCAUAUACACGAUAUCGGAAUAUGCUUGGCUCCUCAUACGCCAUUCAACAAGGCCCAUCGAUAUAUUACGGUGAGCUUUGCAAAUGGCAUACAGGGAGCCAGGCAUAUACGUGUACACGACUUGUAUCAGUACAUAUAUACACACUCAUAUGUAUAUAUAAAAUUUUU	206	sly-miR160-2-5p	UGCUUGGCUCCUCAUACGCCA	61-81	dpr-miR160	4	0	21	21	1
			sly-miR160-2-3p	UGGCAUACAGGGAGCCAGGCA	123-143	aau-miR160	0	0	21	21	1
sly-MIR160-3	UCUUAAAAUUGUAUAAAGUAAUUGAACAAGUAGACAUAUGAGUCUUACAUGACGCAAUACAAGUAAGAUACGACGUAGAACAUAAAUUCUCAUGUAGGGUGUCACGUAAGAUGCAUGUUUACUUUUUCAACUUUAUAAAAGCUUAGUG	148	sly-miR160-3-3p	UCAUGUAGGGUGUCACGUAAG	90-110	ahy-miR160-3p	5	0	21	21	2
sly-MIR391	AAAAGGCUUGCUACGCAGGAGAGAUGAUGCUGGACGAUAGAGAAAAUGGGAUUUAAUUUAUUGGCCAGCAUCAUACUCCUGCAUAUUAAGCCUAAA	96	sly-miR391-5p	ACGCAGGAGAGAUGAUGCUGGA	13-34	sly-miR391	0	0	22	22	1
			sly-miR391-3p	GCAUCAUACUCCUGCAUAUU	68-87	stu-miR391-3p	0	0	20	20	1
sly-MIR477e-1	GAGACAUUAUGUGGUGAAAAUCAAGAUAGCAAGAUUGAUAUCAAGAAUGGUCUCUUUUAAUGAAUCUUUCAUGAUACGUUGAGCCCUUUGUGGGUGAUUGGAAACUUUCAUAUCCAAGAUGGACCACAACCCCAUUCUUGAUAUCAAUCUUGCUAUCUUGAUUUGCACCACAUAUGUGUU	180	sly-miR477e-1-3p	UGAGCCCUUUGUGGGUGAUUGG	80-101	ptc-miR477e-3p	4	0	22	22	1
sly-MIR399r-1	AGUUAUGUGUGGAUGCAUUACUGGGCUAAUCUUCUUUGGCAAAUAAUUUCACUAUUAUUUGGUGCAAAUUUGGUCAUUUAUUGCCAAAGAAGAUUUGCCCCGUAAAUCAUUCAUACAAUAUUA	123	sly-miR399r-1-3p	UGCCAAAGAAGAUUUGCCCCG	82-102	mtr-miR399r	0	0	21	21	1
sly-MIR399a-1	UGGGGAGUAAGAAAUAACAGUGCAAUUCUCCUUUGGCAAAUGAAUAUGCAAACCCUAUAUAUAUAUAUAUAUAUAUGUUUUGCAUACACAUUAUAUUAUCUUUGCCAAAGGAGAAUUGCCCUGUCAUUCUUCUCCUCG	140	sly-miR399a-1-3p	UGCCAAAGGAGAAUUGCCCUG	105-125	ata-miR399a-3p	0	0	21	21	1
sly-MIR2673b	CCCAUAUCCAAAUCGACCUCUUCCUCUUCCUCUUCCACUUCCACUUUCACUAGUAUGGUAAAAUGAAUUAUGAACAUUGAAAUUUGUUCGAGGUAUAUUGGGAGGAGAAAAGCUGUAGUGGGAGAGAAGAAAUGCUUUGCCACUCAUAGCACCACCAGACAGCUGUAGUGGAAGGGGAUUGAUUGGUUGAUAUUUC	196	sly-miR2673b-5p	CCUCUUCCUCUUCCUCUUCCAC	17-38	mtr-miR2673b	0	0	22	22	1
sly-MIR5174e	AACUGUAUGGUACUCCCUCUGUUUCAAUUUGUUUGUCUGGCUUUGACAUGACACAAAGUUUAGGAAAGUAAAAAAUACUUUUGAAUCUUGUGAUCUUAAACAUGUCACGUGAAAAGUUGAAAUUAAAGAGUUGCAAAAAAGGAAAGUAAGACAAGCAAAUUGAAACGGACUGGAUGUAUCAUGCAAAG	188	sly-miR5174e-5p	UACUCCCUCUGUUUCAAUUUG	11-31	bdi-miR5174e-5p-2	5	0	21	21	1
sly-MIR6020a	AAAUGGAGUUUAAUGGCGAAAAUACUCGUAAAACAUUUACGGAUCACUUCUAGGUAGGAUUGAAUAUCAGAGCAAUAUCAUAUAUUGUAGAUCUGUAAAUGUUUUCCGAGUAUCUUUUGCCCAUAACCUUCAAAA	135	sly-miR6020a-3p	AAAUGUUUUCCGAGUAUCUUU	97-117	nta-miR6020a-5p	2	0	21	21	1
sly-MIR7992-2	AGUAAGCACUCAAACUUUGAGAGUGCACAUCUAGAUACCUCAACUUGGUCAUAACCGACUACUAAACAAUCCACGACCACUCGUCUCCACUUUGUCUCAUGCACACUAGACUCUGACAUGACACAUAAAUUUUGGAGGUGUCUAGAUGAUCAUUUUGUAAG	209	sly-miR7992-2-5p	UUUGAGAGUGCACAUCUAGAUACC	16-39	stu-miR7992-5p	4	0	24	24	1

sly-MIR156b-7	UUGAAGUGUUCUGUCUAGAUAUACAUUCUCAAAGUUGGAG CGCUUGAG UAUUGUUGACAGAAGAUAGAGAGCACGAAUAAUGAGGUGC UAAUUGGAAGCUGCACCUUAAUUCUUUGUGCUCUCUAUUC UUCUGUCAUCAUCU	94	sly-miR156b-7-5p	UUGACAGAAGAUAGAGAGCAC	6-26	aof-miR156b	0	0	21	21	1
			sly-miR156b-7-3p	GCUCUCUAUUCUUCUGUCAUC	70-90	vca-miR156b-3p	1	0	21	21	1
sly-MIR823-1	CAUCUCCUCAUUAGGUAUUAUGUUCAUCCUCUUGUAACCA GAUGAUUCAAUACAAAGUGUAUAUGUAUAAUUCUGAAUGU ACGUACAAUACUUUUAGCUUAAAGACAUUUCCUUGAGGAA AUGCAGAUAUUGAAGUAGAUGUGUGAUCAUAUAGCAACAA UAUGAUUAGAAAUGAAGAUAUCUGAAAUAAGGUGGGACUG AUCUCCACGUUGGAGUGAGACUGAGAUGAUUUGGACAUGU GAAUAGGAGAUGCAUAGACGCACCAAUGAGGAGGUG	276	sly-miR823-1-3p	UAGAUGUGUGAUCAUAUAGCAA	136-157	aly-miR823-3p	5	0	22	22	1
sly-MIR2864	GUUUUUGGUGCCCCUGUCAUUCAUAAACUAGAGCAUAUAU GUCCUUCACUCUAACGGAAGGCUAAAUAGGGACACAUAGC GCAAUCUUAUUCGUCGAUAAGUGUCGAAUCGGUGGAUAAG AUUAUGAUACGUGUAUGUCGUGUUAGUACGAAGGAUAUAU AUGCUCUAGUUUUUGAACUGUAGGAACACCAAAGUU	196	sly-miR2864-5p	UUUUGGUGCCCCUGUCAUUCA	3-23	osa-miR2864-1	5	0	21	21	1
sly-MIR8001b-2	UUGCAGGAAAAUAAGUUACUUGCAGAUUUUCAUACUAAUC CCUAGGAAAAUCUCCAUGUAAUUCAUACUUUUCUUGUAG	79	sly-miR8001b-2-3p	AGAUUUUCAUACUAAUCCCUAGGA	24-47	stu-miR8001b-3p	3	0	24	24	2
sly-MIR830	AAGUUGUUUGGAAUUGACUUUUCCAUAGUAUUGGGAGAGU GAUAUUGCUUCUUGGUGGUGGCCAACUUUUAUUUUACUUU GACUUUUAGUUAUGGAAAUUUUCAUAAUUUCUUGGAGGAA CUAAUAUGAGAAGUAGGGUGGUAUAUCGGCCGGUUUGGU UUGGUUUUGAAGUUUAUCGGGUUGGCUUAUUGGUUAUCG AUUUGUAGAGAUGCUAAAUCGUUAUAGAACCAUUAAGAUA UUAGUUUAUCGGUUAUUGAUCGUUAUCGGUUCGGUUAUC GAUUUAAUCGUUAAGAUUUGACAAAAAAAAAACAUUAAAAA UCAAUUAGAAACAAGGG	335	sly-miR830-5p	GAACUAAUAUGAGAAGUAGGG	118-138	ath-miR830-3p	5	0	21	21	2
sly-MIR8739-1	CAUAUACCCUCCGUCAUACUUUUAGGACAGUGGUGAACAU AUAUGUCCUUCACUCUAACGAAAGACUAAAUAGGGACACG UGACACAAUCUUAUUCAUCGAUAAUAUUUAAUAAAUGUCG GGUCAGUCGAUGAGAUUAUGUCAUGUAUAUGUCCGUAUUC AUAAAGGGUAUAUAUGCUCUAAUUUUUGGACGGCAUGAGC ACCAAUGUCUCAAAAGUAUGACGGCAGAUAUUUU	234	sly-miR8739-1-5p	AGACUAAAUAGGGACACGUGACAC	63-86	gra-miR8739	5	0	24	24	3
sly-MIR7997c-3	CUUCUAUGUUGCUCAGACUCUUCAAAAAUGUCGCCAUGUG CAUGUUGGAUCCUUCAAAAGCAGUACGUCUUUUUAUGGAU ACCACAGGUGUGGCGACAUUAUUGGAGAGUCCGAGCAACA UAGCUG	126	sly-miR7997c-3-5p	AUGUUGCUCAGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
sly-MIR169r-3	UUGCAUGAAGUUGAAGAGAGUCAAGUUGCAGCCAAGGAUG ACUUGCCGGACCAAAAGUUGUGACCAUUUUCUAGUUCCGG CAAGUUGUUUUUGGCUAUAAGUUUGCUCUCUUCUUCUCAU GUUA	124	sly-miR169r-3-5p	CAGCCAAGGAUGACUUGCCGG	29-49	csi-miR169r-5p	0	0	21	21	1
sly-MIR10532-4	AGGGAAAAUGCACAAGUAGCCCCUCAAUCUAUGUCCGAAA UCCCAAAAACACACAAGAUAGUGCCACGUAGGCUAAAAAG GGGUAAAAAAUUAUUAAUAAAAUAAAUUCAGGGGUAACAGG ACCUUAAUAUAGUAUAACUGUGUCUCUGAGAUUUCGGGCA UAGGUUGAGGGAUACUUGGGCAUUAUCUCA	191	sly-miR10532-4-3p	AACUGUGUCUCUGAGAUUUCGGGC	137-160	sly-miR10532	1	0	24	24	1
sly-MIR161	UGGUGGCUGCCGAAAAGCAGCAAGAGAAGGCUGCAACGCA AACCGGAAGUUCUGCCGGGGAGCAACGAGGGCAGAAUAG CGGGACGGACAAGGGCAAGAACGUUGCUGUUGGCAUGUU CAAUUACAUGGCGUUGAUCAACCAUAUUUCUAUUGCUGCU UUGGCUGCCAAAC	171	sly-miR161-3p	UUCAAUUACAUGGCGUUGAUC	117-137	bra-miR161-3p	5	0	21	21	2
sly-MIR8573-1	GACAUACAGCUAGAUAUCACAUACCCUUUGAACUUCCAAAC AGACCAUAGAGUGAUUUACGUAAUUAACAUACAAGGCUAC UAAACAACCCCAAGAAACAAAAUUAGGUGGUUGCUCAGGG GUAGUCUUGUAUGUCGUUUAUGUAUGUAUGGUCUGGAAC AAUCUUUGCACGCUUGGGUUGGGAAGUUCAACACUGUAAU UUUAUUAGUGUAUUUU	216	sly-miR8573-1-3p	AUGGUCUGGAACAAUCUUUGC	149-169	atr-miR8573	5	0	21	21	3
sly-MIR8011a-2	AAAUUAAUUAUCAAUCCGUAACUGUCAAUUGAAUGAGGUC UCUUUUUAUUUCACAAGUAGUUAGAAACUUAAAUCUUACAA AAAGUCCACAUUACUUUGUGUCCUGUCCACUUGUGAGAUA AAAAAGAGGUUCUGACAAAUAUUGUUAGCUUGUGGCACAU GUCAUCAAGGGCGGAGUCACUUUGUAGGUAGGGGUUCAU	238	sly-miR8011a-2-5p	UUGAAUGAGGUCUCUUUUUAUUUC	29-52	stu-miR8011a-5p	4	0	24	24	1

sly-MIR859-1	CUGAACCUCAUUCAACGGAAAAUUAUAUUAUUUAAACA AGAUUUCAUUGAUUUUACAAAAAAUAGGAUUGAAUUUCUCA AAUGUUCUCCAGUUUAUACUUUCCAUUAUGUUGGUGGUAG AUACGGCAGAGUGGCAUGGAUCAUGUGAGAAUCAAGUUAC UCUUAAACUUGUAUUGGAAUGUGGUUUGCAUGUGUGCAUU GUUGCAAUUAUGAAAUGUUUAGUGCAUGGGAGCUGGGGA CCAUAUGGAAAUUGAUAUGUAGUGAUGUCCAAUUGCAGUA ACUAAGGUUUUCUGAGAAAACAAAUAGUUUUUUUUUCUUC UUUUUAAAGUCAAUAAAAAAA	301	sly-miR859-1-5p	UGAUUUUACAAAAAAUAGGAU	10-30	aly-miR859-3p	5	0	21	21	1
sly-MIR839	CAUUGCACCUAUGGACGUGUUCGAUAUCAUUUUAGGGCUG GAGUUUUGGUACGAGGUUAACGCGUUUAUUUCACCGCAUC ACAACCAGAUGCACAUCAGCGACACCGGAGGUUCAUGCGU GGUACCCCUUAUUCAGGUACCACAAAACGGGAUGCACUUA UCGGUGAUGCAAAUUGUUAAGGUUUUUAAGAGAGGUGAAC CAACCUUUCUUGCUGCCCUUGUUGCUUUUCUGAGGCAGU UCCAUUUUCUCAUUGCAUUGAGCACGUCCUUAGUGACAAU A	280	sly-miR839-3p	AACCAACCUUUCUUGCUGCCC	198-218	ath-miR839-5p	5	0	21	21	2
sly-MIR8656	GGAACCUUAAUGAAGAGUUGUGACUUUAUGAAAAGUUAUG ACUUUUAUGAAAGCUUGUGAACUUUUAAAAAGGUUGCAAC UUUUCCAAAUAGUUGCAACAGUUCUAAUAAGGUGCA	116	sly-miR8656-3p	UGCAACAGUUCUAAUAAGGUG	94-114	gra-miR8656	5	0	21	21	1
sly-MIR1106-1	UUACCCCAGCAUUAUUUAAUAGUGUAUUUUAAAGGUAUAU AUGUGCGCAUGUGGACAUCAAAGAUAUUGCAUAAUUAUGA AUAGUAAUGUGUCCACGUGGACACAUAUAUACCUUUAAAA UACAGUUUUAAAUAGUUCAGGGGGUG	146	sly-miR1106-1-5p	UUUAAAGGUAUAUAUGUGCGC	28-48	smo-miR1106	5	0	21	21	1
sly-MIR10532-5	CCCUCUAAACUUAUUUUACAAGUAAUUUUUUUAUCCCUUU UUGGCCUACGUGACACUAGUUUGAAAGAAAAGUCAACCAG CGUUGGGCCCACAAGAUAGUAUCACGUAGACCAAAAAGAA GUAGAAAUUUUUUAAUUAAAUAAGUUCAGGGGGUAAUAGG ACUUUAAUAUAGUAUAAGUGUGUUUCUGAGAUUUCGGGCA UAGGUUGAGGGGUACUUGUGUAUUAUCCCAAAUAAGAAAG AAUAACCAAUAAAUUAAAAUUUUCAAAAGAAAGUCUAGUGG A	282	sly-miR10532-5-3p	AAGUGUGUUUCUGAGAUUUCGGGC	176-199	sly-miR10532	1	0	24	24	1
sly-MIR10542-1	AACUUUGAUAGAAGAAUCAUAUAUACUCCUAAAUAUAUUUU UUUUUAAAAAUAGAACUAAUAAAUAUAAAUUUAAAACUAAU UUUUUAACUUCCGUUAAAUGAAGGGUAUAUGUGUGCCAUU UUGUAACGGCAGUGGUAUAUGUGAGCCGUUUGUAUAACG GUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGUGGUAUA UCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCACACCCU UUUCCCUUCUUUUUGUACCCUUUUCUUCCUUGGUUAUUUC AAUCUAUGUUAGGAUUCUUGAAGCUUUAUUAAAAAA	317	sly-miR10542-1-5p	UAGAAGAAUCAUAUAUACUCCUA	9-31	sly-miR10542	1	0	23	23	1
sly-MIR5185l	AAUUGAAUUCAGAGGCGGAGCUAGGUAGGGAUUUUGUGG GUUCGGAAGAACUCAGUAAAAUUUUCGUAGAUCGUACUUG AAAAUUAAUUAAAUAUAUAUGUGCAUUUAUUUAAGAAUCCU UAACAAAAUUGAUUGACAAUUCUAAAAGAAAUUUGAAAUCU CCAAACUCUUUAUUCUAGUUCCACCUCUAAUUCACCG	198	sly-miR5185l-3p	UUCUAGUUCCACCUCUAAUUC	174-194	bdi-miR5185l-5p	5	0	21	21	1
sly-MIR8668-1	AGUUUGAUUUCUCAGAUGAUCACUCGACUAAUUGUUAUCA UCUCAGGAAGUCACUUUCUUUGUUGAAAGUUUUGGAAUCA AGAAGAAAGGGGACUUUCGAGAUAAUAACUAUUAAUCAAG UGACUAUAUGAGAAAUCAACCG	142	sly-miR8668-1-3p	UUUUGGAAUCAAGAAGAAAG	70-89	gra-miR8668	4	0	20	20	1
sly-MIR7993d-1	AACUUUUUGCGUGUGUUUUCAUUCGUCUAUUAGUUAGUGA AGUUAACUACAUGAAAUGUAUCAUCUUUUUUAACCGUACA CAUUAACUUCAAGUAAAAAAUGCUUGAGGUUUUAAGGCGU AUUGAGGCGCAAGCGUAUAAUUAAAGGAGAUAGAGAUAUU UUAUGUUGUUAACUUAACUACAUCGUAGAUAAAUGAGUGA GCACAAACCAGAAAAAAA	218	sly-miR7993d-1-3p	AUAUUUUAUGUUGUUAACUUAACU	156-179	stu-miR7993d	1	0	24	24	1
sly-MIR11592	GAUGUACCGGUACCGGUCCAGUACCUUCCGAUUUGUUUC GGUUCGUCCCGAUUCGGUUGCCUACGAGACGAAAUGGGA CAUCCUGAAUCGGGACACGGAACGGAACGAAACCGAAGUU UGGUACCGGUGUACUGGUACCGA	141	sly-miR11592-3p	GAACGGAACGAAACCGAAG	98-116	cas-miR11592	4	0	19	19	1
sly-MIR8033	GCAUUAGCUGGAGUACAAGCUUCCAAAGCUGCAGAAAUGA GUUUUUUUUUUUAACUGAAAAAGAAAAACUAUUUCUGCAG CUUUGGAAUUUUUUACUCCAGCUAAGUU	108	sly-miR8033-5p	UUCCAAAGCUGCAGAAAUGAGU	21-42	stu-miR8033-5p	0	0	22	22	1
sly-MIR408-2	AAAAGGAAGGAUUGUGGGGAGAGGAGAGCCAGGGAAGAG GCAGUGCAUGGAAUAGGCAAAGCAAAAAUUGCACAUCUCA UGCUCUGGCUCGUCCCCGUCUAUCCAUACCACACCAAUUU UUACCUCAA	128	sly-miR408-2-5p	GAGAGCCAGGGAAGAGGCAGU	24-44	bra-miR408-5p	1	0	21	21	1

			sly-miR408-2-3p	AUGCUCUGGCUCGUCCCCGUC	79-99	cas-miR408	5	0	21	21	1
sly-MIR419	CAUAACACAUGCCUAAAUAAUUAAUUGUUCAGCUCUUCCUCCACAUCCAUUCAAAUGGUUUGAAUGGCCAUGGAGGAAGAGCUGAGUAAUUAAUUAUUAAUGUUGUUGUUGUUAACAGCAUUAGGUUGAUAUACGUUACUGUAAGUAAUGUUU	113	sly-miR419-3p	UUAUUAAUGUUGUUGUUGUU	94-113	ath-miR419	5	0	20	21	1
sly-MIR10538-1	UACUCCUAAAACAUUAUUUUCAGUAACGUUUUACUCCUAAAACGUUACUAUGAGUAACGUUUUAGGAGUAAAAUGUUACUGUGAGUAACGUAUAUCAAUCUGACGCUAUC	150	sly-miR10538-1-5p	AGGUUGAUAUACGUUACUGUAAGU	10-33	sly-miR10538	4	0	24	24	1
sly-MIR7983-1	UAAUAAAUAGCAAAUCACAUUACAACAAAAAUAACUUUUAGCGUCAUUAAAUAUUGACACUAAUAAAGAGUGCUAAAGUCUUUACCGACAUUAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUACAAAGAGUAACAACUGCCGCUAAAAAUACAUAUUUAGCGGCAAUUAAGAAUUAAAUAUCGCUAAUGGUCAUUUUUGUUGUAGUGUCAUGGUAUGUAAUC	240	sly-miR7983-1-5p	UAAAGUCUUUACCGACAUUAGUUA	74-97	stu-miR7983-5p	3	0	24	24	1
sly-MIR7504f	UCUUUACAUUUUUCUUUUUCAUUCUCCAUUCAACUUUCUUUUUGGAGAGGCACCAACAACGGAGAAUGAGAAAAAAAUGUAAGUG	85	sly-miR7504f-3p	AUGAGAAAAAAAUGUAAGUG	66-85	gra-miR7504f	5	0	20	24	1
sly-MIR162-1	UGUUUAGUUGGUUGAAGACACUGGAGGCAGCGGUUCAUCGAUCCGUUCCCUGGAAGCUGAAUAUAUAUAUACGCAAAAAUACAGCAAAAGGAAUCGGUCGAUAAACCUCUGCAUCCAGUGCUUAACCCCUAAGGA	135	sly-miR162-1-5p	UGGAGGCAGCGGUUCAUCGAUC	22-43	csi-miR162-5p	0	0	22	22	1
			sly-miR162-1-3p	UCGAUAAACCUCUGCAUCCAG	98-118	fve-miR162-3p	0	0	21	21	1
sly-MIR7983-2	GUAAUUGUCACCUUUUGUAUAUGUCCCUAAAGUCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGUCAAUAAAGACGUUAGCACUAUUUAUUAGUGUCAAUAUU	109	sly-miR7983-2-5p	UAAAGUCUUUAGCGACAUUGGUUC	28-51	stu-miR7983-5p	0	0	24	24	1
			sly-miR7983-2-3p	ACUAAUGUCAAUAAAGACGUUAGC	64-87	stu-miR7983-3p	5	0	24	24	1
sly-MIR171a-7	GUGUGAUGUUGGAAUGGCUCAAUCUAAUGAAAGUUUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAUAU	86	sly-miR171a-7-3p	UGAUUGAGCCGUGCCAAUAUC	62-82	aof-miR171a	0	0	21	21	1
sly-MIR7984c-2	UAAAAUUGUUGUUACGAUACCAAAUUUUGGCAAGGACCUUUUUACCUUUGCGCUAUUUAAUAGUGUAUUUUAAAGGUAUAUGUGCGCACGUGGACAUAAAAAAUAUUGCAAAAUCAUAAAUAAUAGUGUGUCCACAUGGACACAUAUAUACUUUUAAAUUAUACUGUUAAAUAGUUCAGGGGCUAAAAGAUCCUCCAUAAAAUUUGCAUCGUAACAUUAAUUCCG	225	sly-miR7984c-2-5p	ACGAUACCAAAUUUUGGCAAGGAC	14-37	stu-miR7984c-5p	4	0	24	24	1
sly-MIR399b-1	UUAUAAGAGAAACAGUGGUAGGGCUACUCUCUAUUGGCAUGCACUUAUAUAUUUAAACUGACAUGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUG	103	sly-miR399b-1-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			sly-miR399b-1-3p	UGCCAAAGGAGAGCUGCCCUG	64-84	stu-miR399b-3p	0	0	21	21	1
sly-MIR11114	CCCUCUGUCCCUAUUUAGUUGUCCGCUUUAGAAGUGACACACAUAUUAAGGCACCAAUUAUCAUCAUAGGUUAGCUACAAUUUUAUCCUUAACUUAAAAGAUUAUGCAUAUCCACAAGUAUAAUAAAUGUAUUUCUGGUUCCAAAAAGCAUGCAUUACAACUUAGUAGUACUAGAAAUUUUCUAGAAUUAAAUAAGGGCAUAUUAGGAAAAAAAAUGUUGUCCUUCCUUGAUUUGUUAAAAUGAACAAGUAAAUAGGGACAGAUAU	266	sly-miR11114-5p	UGUCCCUAUUUAGUUGUCCGCUU	6-28	lja-miR11114-5p	5	0	23	23	1
			sly-miR11114-3p	UGAACAAGUAAAUAGGGACAG	242-262	lja-miR11114-3p	5	0	21	21	1
sly-MIR156c-3	AGAUAAUUGAAUCGAAGAGGUAAAAUAAAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUAGCAUGAUGUUUUACAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCCCCCAUCGCUUUCUAUAUCUCUCUCUAGAUUUUAUUAGAG	166	sly-miR156c-3-5p	UGACAGAAGAGAGUGAGCACA	38-58	rco-miR156c	0	0	21	21	1
			sly-miR156c-3-3p	GCUCACUGCUCUAUCUGUCACC	105-126	ata-miR156c-3p	0	0	22	22	1
sly-MIR9470-1	CAUAAACACAAUACUUAACUUGACAUCAGCUGACAACCAUGACCUUUAACUUCUGAUAUUCCAUGUAUUAUGUCAUGUAGGACACGUGUUUCUACUUGUUCAAUUUUUAUAUAAGUUUAAGUUUUUAUUUGUACAGACUCAAAGUUGGAGGGCACAGCCGUUGGCUGAAAGCAAGUUAAGAUCAUGUUUGCG	192	sly-miR9470-1-5p	UGACAACCAUGACCUUUAACU	31-51	sly-miR9470-5p	5	0	21	21	1
sly-MIR10538-	UUAUUGUUUAAAAGUUGACGACGUUAGAUUGAUAUACAUU	162	sly-	AGAUUGAUAUACAUUACUCACAGU	26-49	sly-	1	0	24	24	1

2	ACUCACAGUAACGUUGUACUCACAUUUUAGUAGUAAAACG GUACUCAAAAUAACGUUUUAGGAGUAAAACGCUACUUACA GUAAUGUAUAUCAACCUAACGCUGUUCGUUUUUUAAAAAU GA		miR10538-2-5p			miR10538					
sly-MIR171b-3	AGCUACACGUGAUAUUGGCGCGGCUCAAUCAAAAAGUAGA CUCAAAAAUGUUCUUAAGUACUGCUUUCUCAUUGAACCGC ACCAAUAUCUCGUGUAUUC	99	sly-miR171b-3-5p	GAUAUUGGCGCGGCUCAAUC	11-30	zma-miR171b-5p	1	0	20	20	1
			sly-miR171b-3-3p	UCAUUGAACCGCACCAAUAUC	69-89	tcc-miR171b	4	0	21	21	3
sly-MIR10215-1	AAUUAGUAACGUAAUAGAAAUAACAUUGUAAUAAUCAAAAA GUAAAAUAGAGAUGUGAAUCAUAGUUCUCCAAAUUGGAGA ACUACUAUCCACCUCUUUAUAAUUGCAGAAUAGAGAGUUA AAUAGAGAGUGGUCUAUUUUACUUUCCAAAUAUAGAGAAU GGAGAGUAAAAUAGAGAUGGAUUGAAGAUGGUCUAAGGGG UACGAGAGCCACUCAUACUAUGUCACUUACUCAUAACUCA UGCCCAAGAGCUCGUCACAUAGCUACAGUUUCUAUAAUGA UAGAUGAAGCUUUGGGUACUUACAUUAUUUUUCUUGUUAC UAGGC	326	sly-miR10215-1-3p	GAGAAUGGAGAGUAAAAUAGA	156-176	eun-miR10215-3p	4	0	21	21	1
sly-MIR8714	AUCACAUUCGACGAGAUGAACAUAGAGGUAACUGAGUUAC AAUAUAUGACUUGCUUUACUAUGUUUAUCAUGUCAAGGUA AC	82	sly-miR8714-5p	UUCGACGAGAUGAACAUAGAG	7-27	gra-miR8714	5	0	21	21	2
sly-MIR7840	GGCAAUGGAAUAGGUGGUCACUAGAAUGCAUUAAUUGCAC UCCAAUUAUAGGAGUAAUUAAUGUCAUUGGAAUUGUCUAA ACAAUUAAUUGACUUUUUAAAAAAAUGAAAACAAAUGGUCG UAUAUGUGUUUUAAAAUUGGGUCGGAUAAUUAGGGCAUAA GUGACCCCUUUCUCUUUUAA	181	sly-miR7840-5p	AUAGGAGUAAUUAAUGUCAUU	48-68	ptc-miR7840	5	0	21	21	3
sly-MIR1530-1	AAUGGAGUUUGAGUGGUUAGGAGGAAGGUUGAUGGUGGA UGCUUUGAGAAGAUGGUGGUUUCACUAUUUUGAAAUAAAU UAAUAUUUUAUUUUAAAAUAGAUAAUACAUAAUUAUGACGU GGUAUUAAUGUGAGUGACAUGGAUUUGACUUGUCAUCUAU GCAAGAGAGAGUGAGGUACUCACAUGGUUAGAGUGGUUUA GCAAUCAUUUUUUUAUUGAGUUCAGGGGUCUAGAUGACAA AAGGGUAAGUAGAAGGAUUCACACUACAAACGCAUACAAG UACAAGGGUCCACCAGACCAUUCCACCUAAAUUCUAAUCC UGA	323	sly-miR1530-1-5p	UUUUGAAAUAAAUUAAUAUUU	67-87	gma-miR1530	4	0	21	21	1
sly-MIR8668-2	UGGUCGCCUUGGCUUACAGAAACAUUUUGGAAUGAUGACU AUAAUGAGUGGGAUAAUCUGAGAAAUGUUUUUGUACAAGG AGAUAU	86	sly-miR8668-2-5p	UUUUGGAAUGAUGACUAUAA	25-44	gra-miR8668	4	0	20	20	1
sly-MIR414	UUCAUUACAAAGUUUUAUCAUCCUGAUCCUCCUUCUCCUU UCAUGCCUCCUCUUCUCUAGUUAAAUCUUCUGAUCGUACU UAUUAACAAUCUAGAGCUUCUAAAAUUGUUAGCAGGAUCG AAAAAUUUAACUAAAGAGAGGAAUCCAUGAAGGAAGAACGG GGAUUUGGAUUAGAGAACUUUAUAAUUUU	190	sly-miR414-5p	UCAUCCUGAUCCUCCUUCUCC	18-38	ppt-miR414	4	0	21	21	1
sly-MIR477-3	CAUUAUCAAUGUAAAUGGUACAGAGUUAUAUUUUGACUUA AAAGAGUUAGUUGUUGUAACCGGUCUAAAAUCUGGACCAA UUUCUGAUUUUGUUUCUGAUCCAUCUGUUCCCAAUAGAUU AAUUGCAGAAAAUUUCAGAGAUUUUGACAAAGUCCCCAAG UCAAAUUUUUACCACAAGUUUAAAUUGGAAAACUUUUGGG AAGAAGAUGACCGUUUAUAAUCAGUUCAUAUAAUUGAUACA C	242	sly-miR477-3-3p	AUUGGAAAACUUUUGGGAAGA	184-204	cpa-miR477	5	0	21	21	1
sly-MIR8011a-3	UUCUUUAUGACAACACGAAUACUAGUUGUGUGAGGCUUCU UUUUGUCUCACAUAAAAGUAGACUCAAAUGGGCUUAAUUU UUUGUGAGGCAAAAAUGAGUCUCACUUGACUAGUGUCAGA UGUGUGAGUCACAAAAUU	138	sly-miR8011a-3-5p	UUGUGUGAGGCUUCUUUUUGUCUC	26-49	stu-miR8011a-5p	2	0	24	24	1
sly-MIR1070	AUUUUUUGUAGCUCAUCGAGCAUCUAGGGUGGCAAGUUG UACUAUGAACUGCUCAUAUCUUGAUAUACCUUUUAAGCAC CUCCAUACCUUUUCAGAAUAAGCAGUUCAUAGUACAACUU GCCACCCUAGAUGCUAGAUGAGCUACAAAAUCA	152	sly-miR1070-3p	GCAGUUCAUAGUACAACUUGC	101-121	ppt-miR1070	5	0	21	21	2
sly-MIR8050-1	AUAAUAAGGGUGCUAAUUCCUCAAAAAUUUCCCUCCUCUU GAAAAAAAAGGAAACAAAGUCAAAUAUCUUAUUACCUUUAU UUUCCUUUUCCAGAAGAGGGAAAUUUUUGAGGAUUUGACC CCCUUAUGUU	131	sly-miR8050-1-5p	AAAAAGGAAACAAAGUCAAA	45-64	stu-miR8050-5p	5	0	20	20	1
sly-MIR8050-2	AUAAUAAGGAUGCUAAUUCCUCAAAAAUUUCCCUCCUCUU GAAAAAAAAGGAAACAAAGUCAAAUAUCUUAUUACCUUUAU UUUCCUUUUCUAGAAGAGGGAAUUUUUUGAGGAUUUGACC CCCUUAUGUU	131	sly-miR8050-2-5p	AAAAAGGAAACAAAGUCAAA	45-64	stu-miR8050-5p	5	0	20	20	1

sly-MIR169r-4	UUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAACAAGGUCAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAACAGCUGUUGUUGUU	184	sly-miR169r-4-5p	CAGCCAAGGAUGACUUGCCGG	63-83	csi-miR169r-5p	0	0	21	21	1
sly-MIR5014a-1	UGCACAAACAGACACUUUAACUAUCCAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGGAACAAUACACCUACGACACCAUGUAGGACAAAAAAUGACAUGUAUGAUGAUAUGUGGGACAUGUGUGUCGAUUUGUUCAACUUAUACAAGUUUAAGUGUCUAUUUGUGCA	172	sly-miR5014a-1-3p	UUAUACAAGUUUAAGUGUCUA	144-164	ath-miR5014a-3p	5	0	21	21	1
sly-MIR167h-1	AAUUCGUGAUGGCAUUGACAGGUAAGGCUGCCACAUGAUCUGAUCUUUCCUCGAAUUAUAUUUGAACUAAAAGGAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGCUGCACGAUGU	122	sly-miR167h-1-3p	AUCAUGCUGGCAGCUUCAACUGCU	84-107	gma-miR167h	1	0	24	24	1
sly-MIR6271-1	GAAAUCCAUGUAGAAAUCUCACAUUUAAGAUUGAGAGAAAUCAAGGAUUGUAUUGAUGUAUUGAAAAUAUUGAUCAAUAUUCAUAUAUUGAUACUAUCAACACAUCAAUACAAUCCUUGAUUUUUCUACAGAGGACUGCAAAUCCUUUUUCCCCGUCCAAAUUCGGGUGUCGCCUGAUCAAAAAUCCUUGAUUUCACUAUGAGAGAUUUCUACAUGGUAUCAG	223	sly-miR6271-1-5p	UUAAGAUUGAGAGAAAUCAAG	25-45	ppe-miR6271	4	0	21	21	1
sly-MIR6474	ACCCUCCGUCAUACUUUUGGGAUACUAUUAUUCUUGCCGUUCAAAAACUAGAGCAUAUGACCUUCACUCUAACGGAAGACUAAAUAGGGAUACGUGACACAAUCUUAUCCAUCGAUAUAAUGUGCGGAUCAGUGGAUAAGAUUAUGAGACGUGUAUGGCCAUUAAUAUCAAAGGUAUAUAUGCUUUAAUUUUUUAAACAACAAAGACACCAAUGUCCGAAAAACGUGACGAAGAUA	236	sly-miR6474-3p	UGUGCGGAUCAGUGGAUAAGA	121-141	ptc-miR6474	5	0	21	21	1
sly-MIR166d-1	UGUAUUGCGGGGAAUGUUGUCUGGCUCGAGGAAUCAAAAAUUGUUUCUUAUAGAUAGAUCUGUAUAUUUUGUUUAUAGAUCUAUAAUGUUUUUGAUGUCGUCGGACCAGGCUUCAUUCCCCACAAUGAA	129	sly-miR166d-1-5p	GGAAUGUUGUCUGGCUCGAGG	11-31	aly-miR166d-5p	0	0	21	21	1
			sly-miR166d-1-3p	UCGGACCAGGCUUCAUUCCCC	101-121	aof-miR166d	0	0	21	21	1
sly-MIR2863b	AAAUUUCUCUCGAAGAUUUGCUAUUUUGUUAACAGUCUCCGGGGUUUUUAGAAUUUGCUCAAUUUUCUUAAUACGGAUUUCAUCCUUUAAAAAGGUGAGAUGUUGAGAAAGUUUGUUUAUUUUGAAAACAGUUUUUUCUCUGACAAAAUCACUUUCUUCUUGAGAAAGAG	170	sly-miR2863b-3p	UUUGUUUAUUUUGAAAACAGU	112-132	osa-miR2863b	5	0	21	21	1
sly-MIR10532-6	UAAAAUAAGUUCAGGGGGGUAAUAGUACCUUAGUAUAGUAUAAGUGUGUUUCUGAGAUUUCGAGCAUAGGUUGAGGGGGUACUUGGGCUUUAUCCCUAAGAACAACUAUAAAUGAGUAAAGACAAAAUUCCCUCUUAAACUUGUACCGAAAAGUUAGUUACACGCUUAAACUAUCACAGUAACAUAUUACACACCUAUAUUAUUCAG	207	sly-miR10532-6-5p	AAGUGUGUUUCUGAGAUUUCGAGC	42-65	sly-miR10532	2	0	24	24	1
sly-MIR156t	UCAACUAAGGGGUACUUUAGUAAUUUUUCUAGGUUACCUAAUUAAUUUAUGUAGCAAAUUAAUUAAUUAAUUUAAAGGGCUAAAACCAAAACUACAAAGGAAAUUUUUAGAUUUUGGUUAAGACAAGAAAGGGACAACCUAGAACCUAACCUACGAUGGUCCAAAGAGUUAGUUAAGGUCCUAACAACAUAGAGAUACUUUAGUAAGUACCCUAUUAGUAAU	222	sly-miR156t-3p	UUAAGACAAGAAAGGGACAAC	118-138	gma-miR156t	5	0	21	21	1
sly-MIR846	GCCAUUGGUUUCCGCAACCAGUGGCUUAAUUUUAAGUUACUAUUCACCAUCAUCAUAUAAGUAGAGUUUUAGUAUAUUGUGAUAGGUAAUUAAAUAUUUGUAGUAUUGAAUUACUUAAAUUUCAUUAAAAUUAUGCUAAUUGGAAGAACUAAGGCUUACCCUUAGGUUUAAACUUUAAGAAAGUGAUUAUAGGAUUAGGUGAAUUGAUGGGUAUAGACUAGAUACAGAAUAAUCGGAAUGUUUAUGGCCUUGUGAACAUACACCUUGUGUGAUAUAUACUUGAUAGAUUGGAAGGGUUCGGAAGCAAUAAG	311	sly-miR846-5p	UAGUAUUGAAUUACUUAAAUU	101-121	aly-miR846-3p	5	0	21	21	1
sly-MIR8013-1	GCGUUUUUUAAAAAAGAAGAAGUUGAAAUCGCUGCUUUUCAUUAAAAAAGUUAAUAGAGACAGACAACAUUUUGGUCCAACAUUCGGUUUGCCCCUACAUCAUUUGUUAAAAAAAAAAAUUGACAAGUCACUGCUAUGGCAACGAUUUAAGGAAAAAGAAUUAGUUUUUCAAUGAAAUCGCUGCCAUAAUAGCGAUUUUUGUGUUUUUUUAAAAAAAAUUAACACGUUAAAUUUGUCAGAAGAAAAUCGCUCUGUCAGGAGCGAUUUUGCCCUUUUGAUUAAAAAAAA	289	sly-miR8013-1-3p	AGAAGAAAAUCGCUCUGUCAGGAG	238-261	stu-miR8013	2	0	24	24	1
sly-MIR5532	CUGCUACCGAAUUUCUUCAAAUUCCAGGAGAAUUGUCCUU	263	sly-miR5532-	AUGGAAUAUAUGACAAAGGUGG	169-190	osa-	0	0	22	22	1

	UGAAGAGGACUCGAACCUCAACGCUCUUUAGCACGAGAUU		3p			miR5532					
	UUAAGUCUCGCGUGUCUACAAUUUCACAACCAAGGCAUCU										
	UGAAAGUGAAUCGUAUUCCAUGAAUAUUAUAUCUAUUUAG										
	UAUGAUGUAUGGAAUAUAUGACAAAGGUGGAUCUAUUGAU										
	CCGUCAUGUCAUAAAGGCCCUAGUUGGACAUCCAAUUGCU										
	UCGAUUUGAAUUAUUCGGAGAAU										
	ACCCCUGAACUUAUUUUAUAAAUAAUUUUUAACUCCUUUUU										
	GACCUAUGUAACACUAGUUUGAAAAAAAAUGUCAACACAUG										
	UUGGACCCACAAGAUAGUGUCACGUAGGCGGAAAAGGGAU		sly-miR5026-								
sly-MIR5026-1	AGAAAAUCAUUUAUAAAAUAAGUUUAGGAUA	153	1-3p	ACCCACAAGAUAGUGUCACGU	87-107	ath-miR5026	4	0	21	21	1
	GUAUAACUAAUACCCACAUAACUUAUUUCACUUUCUACCCU										
	GCAUAACUUUAUACAUAGAUUCCCUCAUAAGUUAUGUUGG		sly-miR8766-								
sly-MIR8766	UAUUAGUUAGGU	93	3p	UUAUGUUGGUAUUAGUUAGGU	73-93	gra-miR8766	5	0	21	24	1
	AUUCUCUCUCUCUCUCUCUCUCGCUUUACACAAACCUAAA										
	UUAUACAUUGUAUUUUGUAUAAUUUGUGUUUGUAUAAAAC										
	GAGAAAGAGAGAAAGACAAAAGAGAACUGGGAAGGGGUAU										
	GUUUGUAUUGUAUAAUUAUAAGGAUAUCGGACGAAAAUAU										
	AUGUAUUUGCAUGUUUGUAAUAAUUUUCUCCUCGCUUUAUA										
	CAAACAGAAACACAAUUUAUAAAUUUCUGAUUGUAUAAAGC		sly-miR7539-								
sly-MIR7539	GAGAGAGACAGCGACAAAGGGA	263	3p	GCGAGAGAGACAGCGACAAAG	240-260	lja-miR7539	4	0	21	21	2
	UCCUUCUAUAAAUAGAGCAUUGUUGCUCAUUUGGUAAGAU										
	UUACAACCAUUUUUGACUUUGCUAUAUUUACCUAUGUCAU										
	UAGUGACAUAAGCAUGAUUUUAUCCUUCUAUAAAUAGAGC		sly-miR9726-			gma-					
sly-MIR9726-1	AUUCUUGCUCAUUUGUAGAACAC	143	1-3p	CAUAAGCAUGAUUUUAUCCUUC	87-108	miR9726	5	0	22	22	2
	AAAAACGACUUCACUCUUUCUCCCUCAUUUCGUGGCUAGG										
	AGUUUCACAGUUUUCUUCGUCGGUUUCAAAGUGGAUAUUC										
	CUGAUUGUAGGUUAGUAAAUAUUUUUUUUUUAUUUUAUUA										
	UGUUUACAACCACGAAUGUCCACUUUGAAACUCAACCCCG										
	AAGAAAGCUAUGAAGCCCUAAUCGAAAAAUGAGGGGAAAG		sly-miR9773-								
sly-MIR9773	UUGUGAAAUCUUAAC	215	3p	UUUUUUUUUAUUUUAUUAUGUUUA	103-126	tae-miR9773	5	0	24	24	1
	UGGACAUACCCAUUUAAGGGAAAAUUACAUGGGAUGUCAA		sly-miR2607-								
sly-MIR2607-1	ACAUCCCCAUGUAAUUAGUUAAUAAGGGUAUAGUUUA	77	1-3p	AUGUAAUUAGUUAAUAAGGGU	49-69	mtr-miR2607	5	0	21	21	1
	CAGAGACACACCGUAACUAAACUAAGGUCCUAUUACCCCC										
	AUAAACGUAUUUUUUUAAAAUUUUGUGAACCUUUUGUCUU										
	ACUUGAAAUAUUGCGUGACUCCACGCAAUUGAGGCGCGUG										
	AGAGAUAUUUGGAUGCCACAUAUGCCAAAAAGGUGCACAA										
	AAUUACAAAAAAAAAAAAAAGUUUAGGGGGUAAUAAAAUCUU		sly-miR7981-			stu-					
sly-MIR7981-5	AGUUUAGUUAAGGUGUAUCUAAU	224	5-5p	CGUAACUAAACUAAGGUCCUAUUA	12-35	miR7981-5p	4	0	24	24	3
			sly-miR7981-			stu-					
			5-3p	AUAAAAUCUUAGUUUAGUUAAGGU	192-215	miR7981-3p	4	0	24	24	1
	UUAUACUCCCUCCGUCCCAAUUUAAGUGUCCUAGUUUAAC										
	UGUGCACUAAGUUUAUGAAAGGGGAGACACUGACUCUUUU										
	GGUCUUAAAUUAAAGAUGCAUGUGUGUAUCCCUUUGAUUU										
	UUGGUCUUAGACCUGCCAUGUAGAAUGUUGGAACUGGAAA										
	GGUUACUAAAUAUAGAAAGAGACGCUUUUUUUGGGACAGA										
	UCAAAAGGAAAAUAAGACAACUUAAACUUGGGACGGAGGG		sly-miR5049-			tae-					
sly-MIR5049	AGUACCA	247	3p	AACUUGGGACGGAGGGAGUAC	225-245	miR5049-3p	4	0	21	21	1
	UUUUAUGUAAGACUAUUAAUAGUGUUGGACUUGUUCGUCC										
	UCAUGCCUUUCGUCUAAAUUCAGUCAACAAUAGUUAUGCU										
	UAGUCAACAAUAUGGUUCAUGUGACUUUUUUAGGAUAAAA										
	CCCUAAACAUAACUUUUGUCGGCUAAAUUUAGAUGUAGGG										
	CGUAAGUACGAACUAGUCCAACACUAUGAAUAGCCUUACA		sly-miR8763-								
sly-MIR8763	UACCU	205	5p	UUAAUAGUGUUGGACUUGUUCGU	16-38	gra-miR8763	5	0	23	23	1
	GCGAAUUAUUAGAUUCAUUUUUGAAUCAUUGACAGCCUUA										
	AAAAUAUCACUUUACAUGACUAUUUAAGCUAAAAACACCCU										
	UGAUCUUGCAACAUUAGUAAAAUACACUCCUAAAUUCUCG										
	UUAAGUUUAGGGAUGUUUUUAAUACUUCUCUCAAUUUUUA										
	UUAACAAUUUCAUGCUCCUACAAGAGUUUGAAACCACUUG										
	UCAUCGUGUUGCAUGUCGGGAGCAUACAUAGGAUGUAUCU		sly-			lja-					
	AGGUUUAGUUAGUCAAGUAGAGAGAUAUUUUUAACGUUAU		miR11077d-			miR11077d-					
sly-MIR11077d	CAAUAAUUCAGAGAUAAAACUUGUAAUUUAC	312	5p	AAAUACACUCCUAAAUUCUCGUU	101-123	3p	5	0	23	23	1
	AACUACUCCCUCCGUCCCAUUUUAUAUGGCUCCGUUUCCU										
	UUUUGGUCAGUCCCAAAAAGAAUGUCACAUUUCCUUAUAU										
	GGUAAAUAUUUAAAGGUACAAUUCCUCUUUUAUCCUUGUU										
	GGUCCCACUUAAUUUUAAAAAUAGUACUCUUAAACAUUUAU		sly-miR1127-								
sly-MIR1127-1	GAGGAGAGAAAAGUAAGUCUACUUUUGAAGGGUAAUUUGG	258	1-5p	AACUACUCCCUCCGUCCCAUU	1-21	bdi-miR1127	2	0	21	21	1

sly-MIR7502f	UAAACAUUUCAAAGUCGGUCAAAUGUUGCCACAUAAAAUG GGACGGAGGGAGUAUAA UAACUUCGUCUAGCUCGCCUUCUAACUUACUCUGGACUUU UACUCAUUAAAAAUUAUCGUAACCACCUCUGCACCACUACA UUAAUAACUGAAAUGUCAGUAGUUAGUUAGAAGGGGAGAU AGAUGAAGUUA	132	sly-miR7502f-3p	GUUAGAAGGGGAGAUAGAUGA	107-127	gra-miR7502f	5	0	21	21	2
sly-MIR1518	GAUGGUGUAUAUUUCUACUUAUUUAAUAUCCUAUUUGAAG GACAUGAGUAUCAGUUGAUGACAAAUCAUCACUACGUUUA AUACAUAAACGUGCUUCUUAACUUAAUAUUCAUAUCCUAUC UGGCAUCCUAUGUGACCAUUCUAUGUCAUGGAGACAUAUU AUGUCACGUAGGACGAUGUAUAUUUCUACUUACUUAAUAU CCUAUUUUGAAGGACAUGAAUAUCAGUUGACGACAAAUCA UGUAUUUGUAGGAGGAACAAGAGGAUAUUGUAAAGAGAAG AUCAUCACCAAA	293	sly-miR1518-3p	GAUAUUGUAAAGAGAAGAUCA	265-285	gma-miR1518	5	0	21	21	3
sly-MIR7984d-2	AGGAAGAGUCUGAAAAAUACUUUAAUUUUGGUCGGUAUUG CAGUUACGAUACCAAACUUUAUAAAAGACCUUUUACCGCU GCACUUUUAAAAAGUGUAUUUUAAAGGUAUAUAUGUGUCC ACGUGACACAUUACUAUUUAAAAAGAUGCAAUAUUUUUUAU GUCCACGUGAGCACAAUACGCUAUUAAAUAGUGCAAGGGG GUAAAAAGGUCUUCCAUAAAAUUUAGUAUCGUAACACAAUU UCGAUCAAAGUUCAGAUAUAUUUCAAACUUUUUUC	277	sly-miR7984d-2-3p	CAAUUUCGAUCAAAGUUCAGAUAU	238-261	stu-miR7984d-3p	2	0	24	24	1
sly-MIR7992-3	AACCUUAACUUGGACUCAAUUGACAGCUAGCCAACCUAAC UCUGAAAAUGCACAUCUAGACCCCUUAACUUGAUCUAACU UUCCCCCUUUAAGACCUCAACUUUGAGAAUGCACAUCUAG AAUUCACAAUUUGAGAAUGCACAUCCGGAAAAGUGUAUUU AGGGGGCCAACUUACACCAGGUUAAGAUGUCUAGAUGUGU CUUUUCAAAGUUGGGGUGUCCAAUUGUCAGUUGAGACCAA GUUAAGAUG	249	sly-miR7992-3-5p	UUUGAGAAUGCACAUCUAGAAUUC	102-125	stu-miR7992-5p	5	0	24	24	1
			sly-miR7992-3-3p	UGUCUAGAUGUGUCUUUUCAAAGU	188-211	stu-miR7992-3p	2	1	24	23	1
sly-MIR1128-1	UAUUACUCCCUCCGUCCCAAUUUAUAUGAGUUAGUUUGAC UUGUCAUGGAGUGUAUGAAAGAAGAAAAGACUUUUGAAAC UUGUGGUCUAAAAUAAGUCCUAUAUAUUUGUAAGGCUAGA GCCUAGAAAUAAUUUCAUUAAGGGUAACAUGAACAUUUUAA AGUUAAAUCGUUAUUAAUUAUAGAAAUAUGUCAUUCUUUU UGGGACUGAGUAAAAAGGAAAGUAAGUCAUAUAAAGUGGG ACAGAGGGAGUAGUU	256	sly-miR1128-1-5p	UAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1
sly-MIR7981-6	CGCCUUAAUUAAACUAAGGUCCUAUUAUUCCCUGUUCCCC CUCUCCCCGAACCCUUUUUUUAUAAUUUUGUGCACCUUUU AGCUUACGUGGCAUCCAAAUAUUUCCUAUGCACCUCAUUG UGUGGAGUCACGGAGUGUGCCACAUAAGACAAAAGGUCUA CAAAAUGACCAAAAUAAAUUUCGAAGGUAAUAGAACUAUAG UUUAGUUAAGAUA	214	sly-miR7981-6-5p	CUUAAUUAAACUAAGGUCCUAUUA	4-27	stu-miR7981-5p	2	0	24	24	2
			sly-miR7981-6-3p	AUAGAACUAUAGUUUAGUUAAGAU	190-213	stu-miR7981-3p	3	0	24	24	1
sly-MIR7990a-2	AAGAUCUCGAAAAAUUAUCAGAUUGAAAAAGAUUGCCUCAA UCACACAUCCAAGGCAAAAAAAUUUACCAUUUGAAGUUUCA CAAAUUUACAACUACUUUUUCUGAGUUGCACUCUUUAUUU UUUGUGAAUCUUCAAAUGAUCGUAACUUUGGCCUCGAAUA UCCGUUUGAGGCGAUUUCUUUUUCAAUUGCACUAUUUUCU CGAGAUAUA	211	sly-miR7990a-2-3p	UUCAAAUGAUCGUAACUUUGGCCU	133-156	stu-miR7990a	0	0	24	24	1
sly-MIR8009-1	CAUGGUGAUUUUGUUCGUCGCUUUUCUGGGUUUUAUUUU UUUAAAACCCAAAAAAGAGACGAGCAAUGUCCUUUAGUCC GUCGCUCUUCUGGAUUUCUCACAAAAAUAAUUUCCAGAAA AGCGACGGACAGGGUCCUUUAAUCUGUCGCUAUUCUGGG AUUUUCAAAUAUUAAAUAACCAGAAAAGUGAUGGACUAUAU CGCCUUU	206	sly-miR8009-1-3p	AUUUCCAGAAAAGCGACGGACAGG	109-132	stu-miR8009	1	0	24	24	1
sly-MIR5274b-1	ACCCCCAAAUUAUCGUAAAUGGUAGCAUAUAUAUUCCGUC AUUUUUUUGGGACAUUGGUGUCCCUGUCGUUCGUAAAUUA AAGCAUACAUGCCCUUUCACUCUAACAAAGUGGCAUGGGC ACCAAAUGUCCCAAAAAUAUGACGGCAGGAACAUCAAUGU CCCAAAAGUAUGACGAACAGUAUUUGCAUACCACUUAUAAU AGUUCGGGAUA	212	sly-miR5274b-1-5p	CAUAUAUAUUCCGUCAUUUUU	26-46	mtr-miR5274b-3p	5	0	21	21	1
sly-MIR1088	UACGAAAGAGGUGAAGGUGAUGACAGAAGCAUAGAGAGCA CAAAUGAAUUGAGAUGCUUUUGCUGCCCAAAUUGAAUGAA AUUAGCAUAUCAUCAUUAGUGCUCUCUAUCUUCUGUCAAC	138	sly-miR1088-3p	UAGUGCUCUCUAUCUUCUGUC	97-117	smo-miR1088-3p	4	0	21	21	3

sly-MIR159e	AAUAAUCACUCUUUCUUC AAUAGGUCUUUAAGAAUGUGUAUUGGUUAUAAAUAUGCAU UCCAAUGUCCAGUAUAUAGAAAUAUUGGGCAUUGUAUAGA CAAUUUGCGAAGGGUAGUAGAAAAUUUCUAUAUAAUACCC ACUAAGCAAAAUAUUAGGUACAUUAGAAAAUAUUGGUUUGA AGGGUGUUAGCCAUAUAUCUAAGUAUUAAUGAGCAUGUAU AGGAAAUAUACCAUGCAAUGAAGACCCUAAGCGAAAAUUCA GAUAUUGAUCAAUUUCAAACACAUUAGUUACUAGACCUUC G	283	sly-miR159e-3p	AUUGGUUUGAAGGGUGUUAGC	152-172	zma-miR159e-3p	5	0	21	21	1
sly-MIR172-8	AUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCAC AAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGU GAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUU CUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAU AUGACUCUA	169	sly-miR172-8-3p	UGGGAAUCUUGAUGAUGCUGCAU	128-150	aau-miR172	1	0	23	23	1
sly-MIR7984b-3	AAUAUAUUCGAAUUUAGACCGAAAUUGUUGUAACAAUACC GAACUUUGGAAAGGACCUUUUACCUCCCUAAUCUAUUUAA UAGCAUAUUUUAAAGACAUAUAUGAUAUAUAUGUUCACCU GGACAUCAUAAAUAUUGCAUCACUAUAACUAGUAAUGUGU CCACACGGACAUAUAUAUACCUUUAAAAUACGUUAUUAAAU AGUGCAGGGGAAAAUGUCCUCCAUAAAGUUUGGUAUCGCA ACAGUAAUUUUGACCAAAAAUGAAGUAUUUU	272	sly-miR7984b-3-5p	AUACCGAACUUUGGAAAGGACCUU	36-59	stu-miR7984b-5p	1	0	24	24	1
			sly-miR7984b-3-3p	UGUCCUCCAUAAAGUUUGGUAUCG	216-239	stu-miR7984b-3p	4	0	24	24	2
sly-MIR8038b	UAUUUUUCAAGUCAAAACAGUUUCUCCUUGUGAGUAAGUU GAAUCUCGUGCUCGUUAAACCGCAAGAGACGUAGAAUGCG UCCCAACAUGAGAUUCAGCUUACUCACUUGGAAAAAUUGU UUUUGCUUGAGAAGCA	136	sly-miR8038b-5p	CCUUGUGAGUAAGUUGAAUCUC	26-47	stu-miR8038b-5p	0	0	22	22	1
			sly-miR8038b-3p	AUUCAGCUUACUCACUUGGAA	93-113	stu-miR8038b-3p	4	0	21	21	2
sly-MIR7525	GUGAUCCACCCGCAUAGUAUGUCUACUCUGCUGAUUGGGA GAGCUCCACUGUUCCGGAGCCCAGUCGUUUUGGUACAUAA CUUUUUGUGCAAUCUUUUGCUUGUCUAUGGGUAUGGCGG GGCCCUUUCCCGUCGAGUUUCACUACUAUACUCUUAGAGG UCUGUAGACAUUAUGUGGGUUGUAUAUA	187	sly-miR7525-5p	CAGUCGUUUUGGUACAUAACU	62-82	lja-miR7525	4	0	21	21	3
sly-MIR3513	GGCGCCACAUCCAUCAUUGCUCUUGCAUACAUCUCCUAGA GAAGAUAGAAAUGAUAUGUAAUUGAAGGGAUACCUGGUGC AUCCACCUAUCUUCUCUAAGAGAUGUAUGCAAGAGCAAUG AUGGAUGUGGCACA	134	sly-miR3513-5p	UAGAGAAGAUAGAAAUGAUAU	37-57	ahy-miR3513-3p	4	0	21	21	1
sly-MIR5014a-2	ACCCUUUAAUUUUUAAAUGUGCACAAAUAGACACUUAAACU AUUAUAAAAUUGAACAAGUAAACACAAUUAUCCUACAUGAC AUAAUACAUGUAAGAUGCCAUAUAGGAUACAAAAUUGCCAU GCAGGGUGCCACGUAGGACAAUGUGUUUAUUUGUUUAAUU UUGUACAAAUUUAAGUGUCUACUUGUGCACACUCAAAAUA AAGCAU	209	sly-miR5014a-2-3p	UUGUACAAAUUUAAGUGUCUA	164-184	ath-miR5014a-3p	3	0	21	21	1
sly-MIR6149	ACACUUAAAAACAUUCCGUUACUUUACUAACUGAAGUGUG AAAUACAUCCCUAAUUUCUCGCCAGAUUUAGGUGUGUUUU CAAACUUCAUGUUCCUCCAAUAGUUUGAGAUCACUUGUUA UGUCACGUGUCAGAUCUGACGUGUAUUGGGAUGUAUCUG AGUUUAGUUAGUCAAGUAGAGAGGUACUUUUAAGGCU	196	sly-miR6149-5p	AGAUUUAGGUGUGUUUUCAAAC	64-85	stu-miR6149-3p	5	0	22	22	2
sly-MIR403	UCAGGAAGAGGCAUAUUUCACGUUUGUGCGUGAAUCUAAC AACUCUUUUCAUCUGAAAAACUGUUAUUGUUUGCUAGAUU CACGCACAAGCUCGUAAUAUGGCUUUUCCAAU	112	sly-miR403-5p	CGUUUGUGCGUGAAUCUAACA	21-41	sly-miR403-5p	0	0	21	21	1
			sly-miR403-3p	CUAGAUUCACGCACAAGCUCG	74-94	sly-miR403-3p	0	0	21	21	1
sly-MIR11085	ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAAUUCCCUA CCAUAUUGCCAAAUAUUUGCCUUUAUCUUUGUGUUCAUCU AGCUAAAGACAAAUGUUUGGCAAUAUGGUAGGGGAUCUG GUCUUCUGUACACAGGGAAAAGUUGACUUCU	151	sly-miR11085-5p	AGUGAACUUCAUCUUUGUAA	4-23	lja-miR11085-3p	5	0	20	20	1
sly-MIR8006-2	ACUUCCGUUAUAUUUUUGGGAUAUUGGUAAUCAUGCCAUC UAAAAACUAGAGUGUAUAUCUAUCCCUUUAUACUAGCAGA UCUAUCCGACACAAUAUUUAUUAAAUAUCGGAUCGAUGAA UGAGAAUGCGAUACGUUUCCCUAUUUAGUCUUUUGUUAGA GUGAAGGGCAUAUAUACUCUAGUUUUUGGAUGACAGGUGC ACCAGUGUUCCAAAAGUAUGACAGAGGU	228	sly-miR8006-2-3p	UAGUUUUUGGAUGACAGGUGCACC	180-203	stu-miR8006-5p	2	0	24	24	1

sly-MIR868	CAGAUAUCUUCGUCAUACUUUUGGGACAUUUAGUGCCCCUGCCGUAAAAAACUAGAGCAUAUAUACCCUUUAUAUUAACGGAUAUAUGCGUGUCGUAAUCUUAUUCACUAAUCGAACAUUUAUUAAAUAUCAGAUCAACGGAUAAGAUUGCACCAUGUAUCCCAAUUUAGGUUUCUCUUAGAGUGAAAGACAUAUAUGCUCUAACACGAUAACACAUAUAUCCCAAAAAUAUGACGGAGGAUAUAUC	247	sly-miR868-5p	GCGUGUCGUAAUCUUAUUCAC	88-108	ath-miR868-5p	5	0	21	21	2
sly-MIR7992-4	GGACCCUAUACUUGGCUUUAAAUUUUAACUUUGACCUCCAACUUUCAUAAUGCACAAUUAGGCACUUUAACUAUUCAGCUUUUAAAUAAAUAAACACGAGUCCUACAUGGUAAUACCACGUAGGACAAAAAAUGACAUGUGUGUCUAUUUGUUUAACUUUAUACAAGUUUAAGUGCAUAUUUGUGCACAUCCAAAGUUGAAGGGCAUAAAUGUGAUUUGAAGCCAAGUUAAAGGGCAC	238	sly-miR7992-4-5p	UUUCAUAAUGCACAAUUAGGCACU	43-66	stu-miR7992-5p	5	0	24	24	1
sly-MIR5165	UAAGACUAUAAAUAUGAGAUUAGGUCCCUCUCCUAGCUUAAGAAAAAGAUGUAUUCCCAUAAGGUGGAUACGUCAUAAGCUAAAGGAGAGGAAGACUCAGCCUAGCUUAUAUUCAGU	117	sly-miR5165-5p	CCUAGCUUAAGAAAAAGAUGU	32-52	bdi-miR5165-3p	5	0	21	21	1
sly-MIR9726-2	UUUAUCAUUAUAAGUGUAAUUUUUUUCUUCAAUUGAUUUAAGUAAGUUAGGCCAAGGGUCCGCUCGAGGCCAGUAAUGGUCAUCGAGUAUCAGUCUCAUCCAGGAUGUAGGAUCGCGAUGUGAAAUUUUUAGCGUCAAACUAUAAAAACUUUGACCAAUAUUUUACGAUGUAUAUUUUCAUCAUAUUGAUAUGAAAAAAGAUUACAAUUUAUAGUAUUUU	220	sly-miR9726-2-5p	UAUAAGUGUAAUUUUUUUCUUC	9-30	gma-miR9726	4	0	22	22	1
sly-MIR7981-7	AAUAUCCCCUAGGAUAUGACCGAAUUCCAAGAGAUACAUUUUAACUAAACAAAGGUCUUAUUACCACUAAACUUAAGUUUUUGGUAAUUUUAUACAUCUUUUGUCUUACGUGAUACAUUCCGUUUCUCCACGUAAUUCAGGUGCAUGAGAGAUAUUUUGGUGCUAUGUAAGUAAAAAAGGUGCAGCAAAAAAAUAGAAAAAUGGUUUCAAGGGGUAAUAUGAUAUUAGUUUAGUUAAGAUGUGUCUUUGAGAUUUUGGAUAUAGUUUAGGUGAUACU	277	sly-miR7981-7-5p	UUUAACUAAACAAAGGUCUUAUUA	40-63	stu-miR7981-5p	5	0	24	24	2
			sly-miR7981-7-3p	AUAUGAUAUUAGUUUAGUUAAGAU	217-240	stu-miR7981-3p	4	0	24	24	1
sly-MIR11288d	UAUUCAUACUUUUGAGACACAUGUGUUUUUGUCGUUUAAAAAUAAGAGCAUAUAUAUCCUUUAUAUUAACGGAAUCUUAUUCAUCGACUCGACAUCGAAUCAAUAGAUAAGAUUGUGUCACCGUGUCCCUAUUUAAUCUUCCGUUAGUGUGAAGGGGCAUAUACGCUCUAGCUUUGGAUGGACAGGGACACCAAUGUCUCAAAAGUAUGACGG	213	sly-miR11288d-5p	UUCAUACUUUUGAGACACAUG	3-23	fve-miR11288d	4	0	21	21	1
sly-MIR164a	UGGUUGAAUUUGAAUAUUAUAUUGACCGCUAGAUUUGUAGAUUCAAGACGUUCAUUGAUAGGGAGUACACGUGUACUCCUUAUCAAUGAAUUUCCUGAUUUCUACAACUCUCACGACCACUAUAAGAUCGAAAGUAAUUU	140	sly-miR164a-3p	CACGUGUACUCCUUAUCAAUG	68-88	zma-miR164a-3p	4	0	21	21	1
sly-MIR7997c-4	AUUAUUUUAGUCUAUAUUGCUCGGACUCUUCAAAAAUGCCAAUGGUAGUGUAUUUUUGAAGAAUCUCAGACGGGUGCGGCAUCAAAAGUGAAGAGUCCGUGCAACUAAGAUUUUAAUUGC	120	sly-miR7997c-4-5p	AUAUUGCUCGGACUCUUCAAAAAU	14-37	stu-miR7997c	0	0	24	24	1
sly-MIR10419	UUUUUAAAUAAAUAAACAUGUGAGUUCUACAUGACAAAAUACACAUAGGACACCAUGUAGACAAAAAUGACAUGUAGGACACGUGUGUCUAUUUGUUCAACUU	103	sly-miR10419-3p	CAAAAUACACAUAGGACACCA	35-55	gma-miR10419	5	0	21	21	1
sly-MIR7748a	AUAUCUACUUUUGAGACAUUAGUGUCCCUGUCGUCAAAGAAUUAAAGCAUAUAUAUCCUAUAUACUAACGGAUAUACAUGUGUCAUAAUUUUAUCUAUCUAUCCGACAUUUAUACCAUUUAUACUAACAAACAUACACAUGUCAUAUUCUUAUCUACCGAUCCGACAUUUAUCGACGGAUAAGAUUAUGCCACGUGUCCCUAUUUAGUACUUCGUUAGAGUGAAGGGAAUAUAUGCUCUAUUUUUGGACGGCAGGAGCGUCAGGAUCACAAAAGUACGACGAUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAUUUUCAUUCCGUA	282	sly-miR7748a-3p	AAUAUAUGCUCUAUUUUUGGACGG	228-251	bdi-miR7748a-3p	4	0	24	24	1
sly-MIR171b-4	AGCGCACAUCGAGACACCUCAACUUGGUAUCAAAUGAACACUAAACACUUCAACUAGACCCCACUGUGUUUCAUGGACACCCUGCGUUGACAUGGCACAUAAAUUUUGGAGAUGUCUAGAUGAUCAUAUUUGUAAGUUGGAGUGUUCAUCCGAUACAGUGGAGACAAGUUGAGGUGUCUAGAUGUGCAUU	125	sly-miR171b-4-3p	UUGAGCCGCGCCAAUAUCACU	87-107	aof-miR171b	0	0	21	21	1
sly-MIR6230-1	UCUGAUAUGUUUUAAUAGUGUUGGUAAUUUGAUCCAGUAG	190	sly-miR6230-1-3p	AGACAAGUUGAGGUGUCUAGA	162-182	sbi-miR6230-3p	5	0	21	21	3
sly-MIR6140b	UUCUUGCCCAUAUAACUAUCCAGUUGCUGGAUCUUGUCUG	244	sly-miR6140b-	AAAGUUUGUAAAAUAUUUUCGGUA	95-118	pgi-miR6140b	5	0	24	24	1

	UUUAACUUCUCCCAAAAGUUUGUAAAAUAUUUUCGGUACA		5p								
	AACAAGGGACGUUUUCAAUUGGGGUAUAACCCACUUCUGG										
	AAUCCAUUUAUGGAUCCAAGGAAUAGAAAAUUCUAUAAAGA										
	AAUACAUUUGAUCAAUUUUCUCAAUAUUUGAGACAUGAUC										
	UUG										
	AUAAAGAAAAUAUCAACUAAACUAUAGUAAAAAGUUCAAGU										
	UAAUCUAAAAUCUAUGAUCCCCGGCAACGGCGCCAAAAUU										
	UGAUACACUCAAACUUACUUCUCAAAUAAGAAGUAAAGCGG										
	UCGUGUCAAGUAAAUAACCCAACUAGUGAGGUUGGGAUCG										
	UUCCCACGAGGAAAAUAGUCUAGACUUAACUUCAACGUGU		sly-miR8175-								
sly-MIR8175	UAUUACUAUUAUUUGGUCAAUGACUUCCUUGGA	235	5p	GAUCCCCGGCAACGGCGCCA	57-76	ath-miR8175	0	0	20	20	1
	UUUGGCUUACGUGGCAUUAGCUUGAAAAAAAAAGUCAAUC		sly-miR5026-								
sly-MIR5026-2	ACCGUUGAGCCCACAAGAUAGUGUCACGUAGGCCUAA	77	2-3p	GCCCACAAGAUAGUGUCACGU	49-69	ath-miR5026	5	0	21	21	2
	CGAGCAUGAAGAAGCCAUAAAACUCAGGAUGGAUAGCGCU										
	AUAGAUAGCCAUUAAGAUGUAUUCAUGGUGCUAUCCCUCC		sly-miR390-								
sly-MIR390-2	UGAGCUUUAUAGAUUCCCCAUGCCAU	106	2-5p	UAAAACUCAGGAUGGAUAGCG	18-38	atr-miR390-1	2	0	21	21	1
			sly-miR390-			stu-miR390-					
			2-3p	UGCUAUCCCUCCUGAGCUUUA	69-89	3p	4	0	21	21	2
	AAGCCAACUAUCCGUUGUUCACUUUUCCUACCUAAACACU										
	CUGUGUUUUCUAUAUAGAUGGUGAUAGUUCAGGUACAAGA		sly-miR9477-			sly-miR9477-					
sly-MIR9477	GGGAACAACAAAUAGUUGGGAU	102	5p	UAUCCGUUGUUCACUUUUCCUACC	9-32	5p	1	0	24	24	1
	GGGACAUGUGGCACAAUCUUAUCCAUCGAUCCGAUGUCGA		sly-miR5725-								
sly-MIR5725-1	GUCGGUGGAUAAGAUUAUGACACGUGUAUG	70	1-5p	AUGUGGCACAAUCUUAUCCAU	6-26	bra-miR5725	5	0	21	21	1
	GGCUAAUAAUGUACUACUCCCUCCGUCCCAUUUUAUGUGG										
	CACCAUUUCCUUUUUGGUCAGUCCCAAAAAGAAUGUCACA										
	UUUUCUUAUAUGGUAAGUAUUUAAAGGUACAAUUCCUCUU										
	UUACCCUUGUUGGUCCCACUUAAGUACUCUAAUACAUUUA										
	UGAGGAGAGAGAAAGGCGAGUUUACUUUUUUGAAGGGCAA										
	UUUGGUAAACAUUUCAAAGUCUUCAUUAUUUCUUAAACUC										
	CGUGCCGGGUCAAAUGUUGCCACAUAAAAUGGGACAGAGG		sly-miR1128-								
sly-MIR1128-2	GAGUAUUAUUUUAUCUAUUA	300	2-5p	UACUACUCCCUCCGUCCCAUU	12-32	ssp-miR1128	2	0	21	21	1
	UGAAACCUAAGUUGCUUGGACUCUUCAAAAAUGUUGUCUC										
	ACCCGUGUCGGAUCCUUCAAAAUACACUAUUUUUUGGAGG										
	AUCUAUACACCCGUCAAUAUUUUUGAAGACUUCGAGCAAC		sly-miR5303-								
sly-MIR5303-7	AAAGCUUGAA	130	7-3p	UUUUUGAAGACUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
	UAUUAUGCAUGAUUCCGGUGGAGCUUACAACAGCAAGAAA										
	AUGAGAGAGAGCAAAAAUCUCUCUCACUGUCUUGCUGUUG		sly-miR535f-			csi-miR535f-					
sly-MIR535f	UAAGCUCCACCGAAAUUAUGCAUAGGG	107	3p	AGAAAAUGAGAGAGAGCAAAA	36-56	5p	4	0	21	21	2
	UGAUUUUCGUGUGCUAUAGUCCAUGGAUUUUUUGUGAUU										
	CAGGAUUACAGAUUUUCUUUUGUCAAAAUUUUUCAUGAUA										
	GAUUGGCUCCUAAAUAUAAAAAAUGGACUCUCGAAUUGGU										
	GACUGUACAUAUUACUCCUCCAACUCCCUACAGAGAGUUC										
	UCUAAUGGUUUCAAAUUGAAAUCGUUUGAAAGCAAUAUGA		sly-miR1435-			osa-					
sly-MIR1435	CCAAAAUAUUCAUGGGCUAACACACACAAAAAAUU	234	5p	UUUCUUUUGUCAAAAUUUUU	53-72	miR1435	3	0	20	20	1
	UCGCCUCAAUCGGACAUCUGAGGUAAAAGUUAUGACCGUU										
	UGUAGUUUCACAAUUUUACAACUACUUUUUUCAAUUACAC										
	UCUUUAAUUUGGUGAAAUUUCAAAUAAUCAUAAUGUUGAC										
	CUUGACUAUGCGAUUGCUUGUUCGCGUAUAUCUCGAAAAA										
	CUAACUAAUUUGAAAUAAAAAAUAGCCUCAAUCGUACACCU										
	GAGACAAAAGUAUUGUCCAUUUGAAGGUUCACAAAUUUAC										
	AACUAUUUUUUUGAGUUUUACUCUUUAAUUUGGUUAAAAU										
sly-MIR7990a-3	UCAAAUGAUCGUAACUUUGGCCUCAAAUAUCUGUUUGAGG		sly-			stu-					
	UGA	324	miR7990a-3-3p	UUCAAAUGAUCGUAACUUUGGCCU	281-304	miR7990a	0	0	24	24	1
	GGAGGAGAAGAAGAAGAAGAAUAAUCGAGGUCAAAAUUCA										
	CCAUUGAAUCAAGGUUUCUUUAGAGCUUUGAAUAAAGGUA										
sly-MIR5021-2	UGUUUAUAUUAUUCAUCUAUGGGUUCUUCUCCCAU	115	sly-miR5021- 2-5p	GGAGAAGAAGAAGAAGAAUA	4-23	ath-miR5021	2	0	20	20	2
	GUAAUUUUACAUGAUUAUGGGUAGCACAAGGAUUAAUGUG										
	AAACAGAAAAGUGAUAUGCAAAGAAGAUGGAGAUUCAAUU										
	GUUUAUUGUUACGAAGAAAACACUUUUGUGUUUCUCGUGA		sly-miR6027-			sly-miR6027-					
sly-MIR6027	AUCCUUCGGCUAUCCAUAAUCAUGUUGAAUGUG	153	5p	AUGGGUAGCACAAGGAUUAAUG	17-38	5p	0	0	22	22	1
			sly-miR6027-								
			3p	UGAAUCCUUCGGCUAUCCAUAA	118-139	stu-miR6027	0	0	22	22	1
	UUUUACGUAUUAAUAGUACUCCCUCCGUUUCAAAAAGAAU										
	GACCUGGUUUGACUUGACACGAAGUUUAAGAGUGUAAAGA										
	AGACUUUUGUAUCUUGUGGUCCUAAAUUAAACUUAGGUUA		sly-miR8019-			stu-					
sly-MIR8019-1	AAUGUACAAAAUUUCCCUUUGAUCUUGUGGCCUUAAACAU	283	1-5p	AAAAGAAUGACCUGGUUUGACUUG	33-56	miR8019-3p	0	0	24	24	1

	GCCAUGUGGAAAACUGAUUUUGAAAGGUUACCAAAAAAAG AAAGAGGCCAUUCUUUUUGAAAUAGACUAAAAAGGAAAGG AGGUUAUUCUUUUUGAAAUGGAGGGAGUAAUAUAUGUA UUC		sly-miR8019-1-3p	AGGAAAGGAGGUUAUUCUUUUUG	233-255	stu-miR8019-5p	4	0	23	23	1
sly-MIR7997c-5	UGGACUAUAUUGCUUAUACUCUUCAAAAAUAACGACGGAU GCAUAUCGGAUACUCCAAAAAUAGUGUACUUUUGGAGAAU UCGAUAUGGAUGUGACAACACUUUUGGAGAGUUCGAGCAA CAUAGUUUU	129	sly-miR7997c-5-5p	AUAUUGCUUAUACUCUUCAAAAAU	7-30	stu-miR7997c	3	0	24	24	1
sly-MIR5368-2	CUAACCUUGUGUCAGGACCUAUGGGCCAAGGGACAGUCUC AGGUAGACAGUUUCUAUGGGGCGUAGGCCUCCCAAAAGG UAAC	83	sly-miR5368-2-3p	GGACAGUCUCAGGUAGACA	31-49	gma-miR5368	0	0	19	19	1
sly-MIR11317	CGGACUAUUUGCCAUGUCUGAAAUCAUCUUAAGCUAUUCU UUUUAUUUCUCAAAAAAUGAAUAGGUGAUGAUGAUUCCAG AUAUGGAAAAUAGUAUC	97	sly-miR11317-5p	UCUGAAAUCAUCUUAAGCUAU	17-37	ppt-miR11317	5	0	21	21	1
sly-MIR11575	UUGGGUGGUCGUCUUAUGUAGCACCUUUAUAUCCUGCAG GUUUCUGAUCUUCACAUUGUCAUAUUUGAAUCUUACUCCC CAGCAGUCCCGAAAUCUGUGUUAGGGAGUAUGAUUCAAAU CUGACAACGUGAACAGCUGAAACCCUACAGGGUACAACAG GUGCUUCAUAAGACGAUGACCUGU	183	sly-miR11575-5p	UUGUCAUAUUUGAAUCUUACU	56-76	pab-miR11575	5	0	21	21	1
sly-MIR2118a	CAUCCAAUUUUCUUCAUUUUCCGUAGAAUUUAGAAACGAU UUCACUGAAUUACAUAGAACCCCUUUUCCUCAUUUCUCCA UUUCCUUAGAACGAUUUCACAAAAUACAUAAGUUCUAAGG GAAAGGGGUUUUAUGUUCUUCAGUGAAGUCGUUUCUAAAU UCUAAGGGAAAGAGGAAAUUGGGGG	185	sly-miR2118a-5p	UUCCUCAUUUCUCCAUUUCCUU	66-87	ata-miR2118a-5p	5	0	22	22	1
sly-MIR6463-1	UAGUUUAUUUGGCAUCCUUAUUCGGAAGAUGUUAUUAAUG GAUUGCCUGAGUGGUGUCGGUCAGGACAACGUGUCUGGA UGGCACAGGUGCCACUGAUUUAUGGAAUUUAUCGUGAGU GGCACAUGGUUGAUCAUGUUGUGAGACAGUUCGGUUAUU UACAACAUAUUUCUGGACCGUGUACCCAAUUUUCCGAAUA UCAUUUUAAGCGUGAUAAACGAUCCAAAAUAAAACA	233	sly-miR6463-1-3p	UGGUUGAUCAUGUUGUGAGAC	125-145	ptc-miR6463	5	0	21	21	1
sly-MIR5303-8	ACCUAAGUUGCUCGAACUCUCCAAAAUUGUUGCCCCACCC CCGUCGGAUCCUCCAAAAAUGCACUACUUUUGGAGGAUCU GACACACACAUGUCGAUAUCUUUGAAGAGUUCGAGCAACA UAACU	125	sly-miR5303-8-3p	UCUUUGAAGAGUUCGAGCAAC	99-119	sly-miR5303	1	0	21	21	1
sly-MIR2118	UUUUCAUUUCCGUUUAAGGAAAAGGGUAUAUGUGAGUCAU UUGUUUAUAAGUAGGGAUAUAUAUGAGUCACUUUCAUAAC AAGGGAUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAU AUCAUACCCUUUUUCCUUUAAAAUUAAAUGAUUA	154	sly-miR2118-5p	GAAAAGGGUAUAUGUGAGUCA	19-39	hbr-miR2118	5	0	21	21	1
sly-MIR7984d-3	UUUGGGAAAAAGUGUGAAAUAUAUUUGAAUUUUGAUCGAA AUUGCCGUUACGAUACCAAACUUUGGGAAUGACACGUGGA CAUAAAUUUUUUUGCCGAAUUAUCAAUAAUAAUGUCCUCCA UAAAGUUUGAUACGUAACAACAAUUUCGGUCAAAGUUUGA GUAUUUUUUUAGACCCUUUUCCCUAU	187	sly-miR7984d-3-5p	AUUUGAAUUUUGAUCGAAAUUGCC	23-46	stu-miR7984d-5p	5	0	24	24	1
			sly-miR7984d-3-3p	CAAUUUCGGUCAAAGUUUGAGUAU	142-165	stu-miR7984d-3p	3	0	24	24	1
sly-MIR7543	GGGACACGUGUCACAAUCUUAUCCAUCGAUCUAAUGUCUG GUCGGUGAAUAAGAUUAUGACACAUGUAUG	70	sly-miR7543-3p	AUUAUGACACAUGUAUG	54-70	lja-miR7543	4	0	17	20	2
sly-MIR5570	UAUAUUUGUUUUUUUAAACAAAUAAGAUAUAACGCUGCCA GGGCAGCAACUUUAUGAUUUUUUUUUAUAUAUAUAACGCU GCCCAGGCAGCGACUUUAUGGAAAAAAAAAUUUCAUAAAG UGGUCCAUUAGUAUGCUGCAGGAGACAAUUUAUUUUAUAA AAAGAAAAAUCAUAAUGUCGCUGCCUGGGCAGCGUUUAGA AAAAAAAAUUCUAUAAAUCGCUGCCUUGGCAGCGAUUUAU UUUAUAAAAAAAAAAUUUU	259	sly-miR5570-3p	AAAAGAAAAAUCAUAAUGUCG	160-180	sbi-miR5570	4	0	21	21	1
sly-MIR9476-1	AUCCUGCUAUUGGUCUAGUCCUGCAUCUUUUUUUAUAUUU UUUGAUAACGGAAAAAAUGUAAAAAAAGAUGCAGGACUAGA CCAAUAGCAGUUU	94	sly-miR9476-1-5p	UCUAGUCCUGCAUCUUUUUUU	14-34	sly-miR9476-5p	0	0	21	21	1
			sly-miR9476-1-3p	AAAAAGAUGCAGGACUAGACC	63-83	sly-miR9476-3p	0	0	21	21	1
sly-MIR162-2	GAGAACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUG AAAAGCGAUAAAUACAGCAACAGGAAGCGAUCGAUAAACCU CUGCAUCCAGUGCUUAAC	98	sly-miR162-2-5p	UGGAGGCAGCGGUUCAUCGAUC	9-30	csi-miR162-5p	0	0	22	22	1
			sly-miR162-	UCGAUAAACCUCUGCAUCCAG	70-90	fve-miR162-	0	0	21	21	1

			2-3p			3p					
sly-MIR10992	GUCAAAAAUUCAAAAAAAAUUAUUCGUCAUUCAAGUUUAGCCAGUUCCAUAUAGCAUUGCAGGUAUGAUUUUAUGAGUGUUGUCAUCCAUUAGACAACACAGUUGCUAUCCAUGCUUGAGAUCACACACGCGUAUCUUGAACUGGAAGACAACAAAUGACGUUAUUUUUUUUUUGAUGAUUUGAAGAAAAUGAUUUUCAGAACACAUGGCAAUCAGGUAAAUUUUUAUUGAAUAUAAUUAAACUAAAGUGUUUGGGGGAACUCUUGGGUUCACUUUGAAGU	242	sly-miR10992-5p	CAAAAAAAAUUAUUCGUCAUU	11-31	mdm-miR10992	5	0	21	21	1
sly-MIR395a-4	AUACACAAACUAGUAAACAUGCAAGAGAACUAGAGUUAGAUGAUGAAUGCAAUGCUUCAUUACUACAUCUAUCAAGGUGUUCCCGAGAGUUCCUUUAACCACUUCGU	146	sly-miR395a-4-5p	UAAAGUGUUUGGGGGAACUCU	2-22	aof-miR395a	1	0	21	21	1
sly-MIR395a-5	CUAUCAAGGUGUUCCCUGGAGUUCCCUUGACCGCUUCAUUAGGGUUUACUUCAUCGUUUCAUGCCCUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAU	107	sly-miR395a-5-3p	UGAAGUGUUUGGGGGAACUCU	70-90	aof-miR395a	0	0	21	21	1
sly-MIR395a-6	UGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACUCAAACAAAUAAAAUUGUUGGAGUGCUGGUUGUGGAUGAUGAACGAAAUAGUUCACGUAUAAAUCUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGA	151	sly-miR395a-6-5p	UGAAGUGUUUGGGGGAACUCU	4-24	aof-miR395a	0	0	21	21	1
sly-MIR7980b-3	UAUUGGAUCACAUCUCAUAAUAUGGAACUGUGAGAUGGAAUCAACGUAAAAUCGCAUGUCCAAACACUGAUUCCAUCUCACGAUACCAUAUCAUGAUAUGAUAUCGCAUGA	111	sly-miR7980b-3-3p	GUCCAAACACUGAUUCCAUCUCAC	58-81	stu-miR7980b-5p	1	0	24	24	1
sly-MIR479-2	AUGAUGAAGAAGAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUUCUUCAUACC	112	sly-miR479-2-5p	CGUGAUAUUGGUUUGGCUCACU	22-43	ghr-miR479	3	0	22	22	1
			sly-miR479-2-3p	UGAGCCGAACCAAUAUCACUC	73-93	aof-miR479	0	0	21	21	1
sly-MIR7695	AGAUCGGACACGUCACUUGACGAUGUAUCAAGACAUUACUUUACACAAUGUAACGGUCAGGUACAUUACUUUAAUUAUGCGAUAUAUCGGGAUGCAUGUGAUGUAUCAGGACGUUGAGUGAUGUAUUCGAAAUCGAGACGUGAUGUAUCACGACGU	156	sly-miR7695-3p	ACGUGAUGUAUCACGACGU	138-156	osa-miR7695-3p	5	0	19	21	1
sly-MIR8739-2	UCCUGUCGUCCAAAAUUAAGAGCAUAUAUGCCCUUCACUCUAACAAAAUACUAAAUAGGGACACGUGGCGCAUGUAAUCUUAGCCGUCGAUCCGAUAUUUAAUAAAUAUCAUGUCGGUAGAUAAGAUUAUGACACGUGUAUAUUCGUUAGUAUAAAAGAUAUACAUACUCUUAAUUUUUGAAUGACAAAG	190	sly-miR8739-2-5p	AUACUAAAUAGGGACACGUGGCGC	48-71	gra-miR8739	5	0	24	24	3
sly-MIR7988	UUUUAAGGGAAAAGGGACAAACAUACUUCGAUACUAACAUAAAUGGUACGCAGAUAAUCUUUCGUCAUACUUUUGAGAUAUUAGUACCACCGUCGUCCAAAAACUAGAGUAUAUAUAUCCUUUGUACUAACGGACAUACACGUGUCAUAAUUUUAUCCACCGAUUGUAUAUCGAAUACGGAUAAAAUUGUGUCAUGAUGGAGAGUAUUUGCAUAUCAUUUACUAAUAUUAUAGAGAUAUAUUUAUAGUUUUCCCUAUAUUU	261	sly-miR7988-5p	AAGGGAAAAGGGACAAACAUACUU	5-28	stu-miR7988	5	0	24	24	1
sly-MIR11413a	ACAUAUAAUUAAAGACCCAAGCCCAAUUCGAAGCCAGAGAAGUAGUCCAGAUAACUCAGAAAACUAAAGACAUAGAAUUGCAUUGUUUCUAAGAAAUCUUGUGAGUUAUCUCGACUUCUUCUCUGGCUUGGAAUUGGGCUUGGGUCUCUAAUUAUAAUG	159	sly-miR11413a-5p	AAGCCCAAUUCGAAGCCAGAG	19-39	pab-miR11413a	5	0	21	21	1
sly-MIR10540-2	UGCGGGGUUGAAUUCUCAAAUGGUUACUCAACUUAUAGUUAUUAUCUCAGAAAAUCUCUUUUCGUUCUUGAUUCUGAUGCAAAGAAAGUCACUUUGUUAGAUAUAAACUAUUAGUUGAGUGACCAUCUGUGAAAUCAACUCCUGU	145	sly-miR10540-2-3p	AUAUAAACUAUUAGUUGAGUG	101-121	sly-miR10540	3	0	21	21	1
sly-MIR5014a-3	UAUCUUUAGUUUGUCUUAUUUUAUAUUUAUGCUCUUUAAUUUUAGGUAUGCAUAAGCAGAUACUUAAAUUUAUAUAAACUUGAACAAGUAGACACAUGAGUCUUACGUAGGACAACACAUGUAGGAGAUCAUAUAGGACAAAAAAUAACAGGUAAGAUGUCAUGCGGGACAUGUGUGUCUACUUGUUCAACUUUAUACAAAUUUAAGUGUCUAUUUAUGCACACCCAAAGUUGAAGAACAUAAACAUAAUUUGAAGCCAAGUUAAAGGAC	270	sly-miR5014a-3-3p	UUAUACAAAUUUAAGUGUCUA	193-213	ath-miR5014a-3p	4	0	21	21	1
sly-MIR8019-2	UAAUACUCACCCCGUUUAAAAAAGAUUGACCUAGUUUGACUUGAAAUGGAGUUUAAGAAAAGAAAGAAAACUUUUUAAUGUUGUGGUUCUAAAUUAAAGUUAUUUCAAAUGUACCAAAAUGCCCUUUAAUCUCGUGGUCUUAAACAUGCCAUGUGGAAAGUUAAAGUUAAAGUGUUGCCAAAAAAGGAAAGAGUCAUUCUUUUUGAAACGGAGGGAGUAACA	258	sly-miR8019-2-5p	AAAAGAUUGACCUAGUUUGACUUG	20-43	stu-miR8019-3p	2	0	24	24	1
sly-MIR2676f	ACACCAUUUAGACUCUUGCAAUGUACUCAAAUCGUUAUCUAAGCAUAUCUUUUGUGAGUAAUACCUUCUCUUUGGGGUCU	135	sly-miR2676f-3p	UACUGUUUAGAUAACAAUUUC	88-108	mtr-miR2676f	5	0	21	21	2

sly-MIR7722	CAAUAUCUACUGUUUAGAUAACAAUUUCAGUUCAUUGCAAGAGUCUAAAUGGCUCACAAAAAAGAAAAAAAGGAUACGUGUGAGGAGGAUCAAAUAUACCCACUAUAUGGAUUUUUAUUUUUUCACGUCCGUUGGAGGAAAAAGGUAUAUAUGAGCCAUUUGUAUAAUAGUUGGGGUAUAUAUGAACCACUUUCAUAACGAGAGAUAUAUCAACUCUAAAUGACAAAGUGGAGGGGAAUGUUAGGCCCUUUUCCCUAUUAAUUAUACUUAAUAAAAUAUUUCAGUUCGAUUGAUUCGGUUGUAUUGCCUCCUCCCCGUACUUUUCUUGGUUUUCAC	281	sly-miR7722-3p	CCUCCUCCCCGUACUUUUCUU	252-272	bdi-miR7722-5p	4	0	21	21	2
sly-MIR319h	UUGUGUCGCUUCUUCAUCUGAAGCGAGCGCCUUUUUCAGAUCGCAUCGCCUCAGGAGAAAGAAGCGCAGUG	71	sly-miR319h-5p	CUUCAUCUGAAGCGAGCGCCU	12-32	mes-miR319h	5	0	21	21	1
sly-MIR319n	AGAGGCGGAGUCAGAAUUUUCAAUAAGGGGUUCAAAAUCUGUAGAUAUAGAUAGUCAAAGAGGGUUCGACAUCUACUAUAAACUUAUUUUAACCAUGUACAAUUAAUAUAAUUUUCCUCCGAAGGGAACCCCUUGUAUGAAGGUAGCUCCUCCGCCCCU	159	sly-miR319n-3p	UUUCCUCCGAAGGGAACCCCU	113-133	gma-miR319n	4	0	21	21	1
sly-MIR1919-3	UCCGAAUCGCUCCGACGCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUAUAGAACCACACUUUCUUUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUU	177	sly-miR1919-3-5p	UGUCGCAGAUGACUUUCGCCC	47-67	stu-miR1919-5p	0	0	21	21	1
			sly-miR1919-3-3p	ACGAGAGUCAUCUGUGACAGG	113-133	stu-miR1919-3p	0	0	21	21	1
sly-MIR1919-4	UCCGAAUCGCUCCGACGCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUAUGGAACCACACUUUCUUUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUU	177	sly-miR1919-4-5p	UGUCGCAGAUGACUUUCGCCC	47-67	stu-miR1919-5p	0	0	21	21	1
			sly-miR1919-4-3p	ACGAGAGUCAUCUGUGACAGG	113-133	stu-miR1919-3p	0	0	21	21	1
sly-MIR8644-1	ACAUUGUACAAAAACCAAAAAAACCAAAAAAACCCGAAAUCAAACCGAAUUACCGAACCUUAAACCCUAAAACUAGGGGUGGGCAUUCGGUAAUUCAGUUCGAUUUCGUAUAGUUUUUGAAUAUAUAUUUUUUAAAAAAA	142	sly-miR8644-1-3p	UUAAACCCUAAAACUAGGGGU	60-80	gra-miR8644	5	0	21	21	1
sly-MIR169c-3	UUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUUCUUCCCAU	183	sly-miR169c-3-5p	UAGCCAAGGAUGACUUGCCUA	44-64	ata-miR169c-5p	0	0	21	21	1
sly-MIR5303-9	GUUUGUGUUGUUCGGAUUCUACAAAAAUGUUGCAGUGUUCGUGUCAGAUCCUCCAUAAAUGCGUUCUUUCUGAAAGUUCUGACACAUUUUUUAAGAGUUCGAGCAACACAGAU	113	sly-miR5303-9-3p	UUUUUUAAGAGUUCGAGCAAC	87-107	sly-miR5303	1	0	21	21	1
sly-MIR7997b-1	AAGAAACUAUGCUGCUCGGACUCUUCAAAGAUAUUGGUGGGUUUGUGUAGCAUCAGCUAUACAUUUUUGGAGAUCUAACACAGGUGCAGCAACAUCUUUAGAGAGUUCGAGCAACAUAGGUUAGC	125	sly-miR7997b-1-5p	AUGCUGCUCGGACUCUUCAAA	9-29	stu-miR7997b	0	0	21	21	1
sly-MIR5021-3	UGUCUCGUGCUAAGGGAAAUGGUGAACGAAUGUCAGAAGAGGGAUGGGGUGGGAUGUUCUGGGAAGAAGAAGAAGAAAAGGGGAACGAAAUAUUUUUUUUUAAUUAUUUUUUUAGUGAAAACAUAAUUUUUGUUUAUUUUAUUUUUUUAAUUUAUGUUUUAAGUGUGUUUAUGGGCCCAAUGCCACAUGUCUCUUUUUAUUAGCUAUUAUUUCACGUUAGCAGCGAGUGU	232	sly-miR5021-3-5p	UGGGAAGAAGAAGAAGAAAA	60-79	ath-miR5021	1	0	20	20	1
sly-MIR857	CACUACUUAAUAGUGUGUCUUUUGAAGGUAUAUAUGUGUCCACGUGGACAUCAUAAAUAUUUCAUAAUUAUAAAUAGUAGUGUGUCCACGUGGGCACAUAUAUACCUUUAAAAUACACUAUUAAAUAGUG	130	sly-miR857-5p	GUGUGUCUUUUGAAGGUAUAU	13-33	aly-miR857-3p	5	0	21	21	2
sly-MIR397b	CCCUUCAGAGAAUUAAAAACAUGAUCGAGUUUAGCGUUGAUGAAAAAUGAGGAAGGCCCAAAUGCAGGACUUCUCAAAUAUGUCAUCAACGCUGCACUCAAUCAUGUUUCUAAGUACUCUGCAAUAA	127	sly-miR397b-5p	AUCGAGUUUAGCGUUGAUGAA	24-44	bdi-miR397b-5p	3	0	21	21	1
			sly-miR397b-3p	UCAACGCUGCACUCAAUCAUG	86-106	eun-miR397b-3p	1	0	21	21	1
sly-MIR398-2	CCAAUUUUGGUUGAUAUAUUCACAUUAUUAAUAUGAAUGAUGAUGAGCAAUGGUGAAUCCCCAGAGGAGUGUGCCUGGAAACACAGGUGCAUUUUGGUCUUUUUUUAAAAAAAAUUGCGGACCAAAGUACACUUGUGUUCUCAGGUCACCCCUUUGGGAUCACCUUGUUUUUUUUUUAAUAUUAUAGAAUGAUAGUUAU	211	sly-miR398-2-3p	UUGUGUUCUCAGGUCACCCCU	133-153	lja-miR398-3p	0	0	21	21	1

sly-MIR10532-7	UACUUAAAUACA UUAAUAUAGUAUAACUGUGUCUCUGAGAUUUUGGGUAUAU GUUGAGGGGGUUGGUACUUGUGCAUUAUCCCUUAAAAUAA CCCAAAUCAUGAUAUGAUAUUCUCAUAUGAU	111	sly-miR10532-7-5p	AACUGUGUCUCUGAGAUUUUGGGU	13-36	sly-miR10532	3	0	24	24	1
sly-MIR11288c-1	ACUACAGGAAUCUAUUGAUUUAGGAUUUGUCAAACUAUAC CGUUAUCAAGAACAGAGGAGAUGUGACCAUUACUCAUCUC CUCUGUUCUUGAUAACUGUAUAGUUUGACAAAUCCUAAAU CAAUAGAUUCCUGUGAA	137	sly-miR11288c-1-5p	UGAUUUAGGAUUUGUCAAACU	16-36	fve-miR11288c-3p	4	0	21	21	1
sly-MIR9679-1	GACUUAUAAAACCCUCUAAAUCUCAUGGUCUUGUACUGCA UUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUC CCAGGUUUGUAAUAAAUU	98	sly-miR9679-1-3p	CAGAACAAGAAAGAGGUGUUC	60-80	tae-miR9679-5p	5	0	21	21	1
sly-MIR6231-1	CCCCCCCCUACAAUUUUUAGUACUGUAUGUUAAACGUAUA UGUGUGUCCACAUGGACAUAAAAAGUCCACGUGGGCACAU AUAUAUCUUUAAAAUACAGUUUUAAAUAGUUCAGGGGGCA U	121	sly-miR6231-1-5p	UAUGUGUGUCCACAUGGACAU	39-59	sbi-miR6231-3p	4	0	21	21	1
sly-MIR7984c-3	GAUCAAAAUUGAUGUUACGAUACCAAACUUUGUAAAUGACA UUUUACCCCCCCCCCCUACAAUUUUUAGUAGUGUAAGUUA AACGUAUAUGUAUGUCCACAUGGACAUAAAAAGUCCACGU GAGCACAUAUAUAUCUUUAAAAUACAGUUUUAAAUAGUUUC GGGGGCAUAAAUACACUAUUUAAUAGUUCAAGAGGUAAAA GGUCCUUCAUAAAGUUUGAUAUCGUAACAACAAUUUUGGU C	243	sly-miR7984c-3-5p	ACGAUACCAAACUUUGUAAAUGAC	17-40	stu-miR7984c-5p	3	0	24	24	1
			sly-miR7984c-3-3p	CCUUCAUAAAGUUUGAUAUCGUAA	206-229	stu-miR7984c-3p	1	0	24	24	1
sly-MIR7981-10	UUCAGAGACAUACCUUAACUAAACUAAGGUCCUAUUGCCC CCCUGAACUUAUUUUUUUUGUAAUUAUAUACACCUUUCGU CUUACGUGGCAUACUCCAUGACUCCAUGUAAUUGAAGGAC GUUGGAGAUAUUAUGUAAGCUAAAAAGGUGCACAGAAUUA CAAAAAAAUAAGUUCGAGGUUGGGGGAAAAGGACCUUAAU UUGAUUAAGGUGUCUCUGGG	220	sly-miR7981-10-5p	CUUAACUAAACUAAGGUCCUAUUG	14-37	stu-miR7981-5p	4	0	24	24	2
			sly-miR7981-10-3p	AAAGGACCUUAAUUUGAUUAAGGU	188-211	stu-miR7981-3p	5	0	24	24	1
sly-MIR8046-1	AUGUUUAGCAAGUAUAAUUAAAGAAUAGAAAAAAAAUUCAA AUUUUCGGCUAAAAAUUAACCUAUGUAAAGUAAGAAUGAC GUAAGUAGGCUUGUUUGCGACCUCUGAGAGGUCAAUGAU GCCGGUCUCGUCUGGGGUCUAGAUUCCAGUCGUGACAAC AUUGGUAUCAGAGCGCUAGGUUAAAUUUCGAGAAUAAUGA GUUCACAUCAACCACAUUGAGUAGUUUCUAAGUCAUGGUA GUGAAGUGCACCAAUAUCCUGGAUUAGAGACUGCAUGAUG CGUAGAAAAAAAUUUUCCUUCUUCUAAUCUUAUCGUGCUU AAGCU	324	sly-miR8046-1-3p	AGGUUAAAUUUCGAGAAUAAU	177-197	stu-miR8046-3p	5	0	21	21	2
sly-MIR1046-1	UGGCACUACAAGAAAACUGUGAAUUACAUGGGAUUUUCCU AGGAUUAGUAUGAAAAUACGUAGGAAACUUAUUUUCCUGC AAAAAUUCAUCCUGAUUUUCAGGAAAAUCUCAAUGUAAUUC AUACUUUUCUUGUAGUGUGG	141	sly-miR1046-1-3p	UGUAAUUCAUACUUUUCUUG	114-133	ppt-miR1046-5p	5	0	20	20	1
sly-MIR10215-2	GAGAACCUAUUCUCUAUUUUACUCUCCAAAUAUAGAGAAU GGAGAGUAAAAUAGAGAUGGGUUGGA	66	sly-miR10215-2-3p	GAGAAUGGAGAGUAAAAUAGA	35-55	eun-miR10215-3p	4	0	21	21	1
sly-MIR3627	GAGAGAGAUUGAGGGAAUCUUGUCGCAGGAGAGAUGGCA CUUGCCAUUCCUUUUAAUUGGUACAAUGCCUAAAUGGAAC CAAUUAAGUGCCUCUGUCUUUCGACACGAUGCUCACAAUU UCUAUU	125	sly-miR3627-5p	UUGUCGCAGGAGAGAUGGCACU	20-41	vvi-miR3627-5p	1	0	22	22	1
			sly-miR3627-3p	AAGUGCCUCUGUCUUUCGACA	85-105	stu-miR3627-3p	0	0	21	21	1
sly-MIR1533-1	AACAUAUUCAGUAUUUGGGCUGUUGGUUUGUAGUGUGACA CUACAUGUCAGACGUCUCCGGUUCGAACCGAAGGUCCAAA AUGGACAGUGAAAUAAAAAUAAUGUUGUCACUCAUGCUCG AACUGGAGACCCGUGAUAUGUAGUGUCAAGCUCCAACCAA CAGCCCAAGUAGCUAAAUAUACA	183	sly-miR1533-1-3p	GAAAUAAAAAUAAUGUUGU	90-108	gma-miR1533	5	0	19	19	3
sly-MIR8007b-1	AAACACAUGUGUCCUAAAUGACACAAUACACGUAGAAAACC ACGUAGGACGAAAAAUGACAUGUAGGACAUAUGUGUCU	79	sly-miR8007b-1-3p	CGAAAAAUGACAUGUAGGACAUAU	50-73	stu-miR8007b-3p	5	0	24	24	1
sly-MIR5303d-1	UCAUAAGUUUAAGUUGCGCGGACUCUUCAAUGUAGAUGCC GCACUCGUGCCUGAUCUCCAAAAAUAUGCUACUUUUGGAG AAUCCGACACGCACCCACUGACAUUUUUGAAGAGUCCGAG	136	sly-miR5303d-1-3p	UUUUGGAGAAUCCGACACGCACCC	73-96	stu-miR5303d	0	0	24	24	1

sly-MIR10420-1	CAACAUAACUGUAGGUGUUAAGUGUGCCAAUCUGACACAUCACUUUUUUUUUUCACUUUACCCGCUCAAAAGGCGUGCCUAAACGACAGGUGACAAGUCAGUCAGGUGUGUUUGAUAGGUACACUUGUU	113	sly-miR10420-1-5p	UCUGACACAUCACUUUUUU	15-33	gma-miR10420	4	0	19	19	2
sly-MIR1043-1	UUUCUGAAUUUCUUCAAAUCACAUUUAUGCCCUUCAACUUUAGGUGUGCACAAGUAGACACUUAAACUUGUAUAAAACUAAACAAAUAGACACACAUGUCCUACAUGUCAUUUUUUGUCCUACAUGGUGUCCUACAUGUAUUUUGCCAUGCAGGACUAAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUGGAGGUCAAAGUUAAAAUUUGAAGCCAAGUUUAGGGU	255	sly-miR1043-1-5p	CCUUCAACUUUAGGUGUGCA	31-50	ppt-miR1043-5p	3	0	20	20	1
sly-MIR1133	UAAAGAUAUACUACCUCCGUCCCUACUUGUUUGUCCAUUUUUCCUUUUAUAGUUGUCCCUAAUACUUGUCCAUUUUGACAAAUCAAGAAAGGACAAUUUUUUUACCUAUUAUACCCACAAUUAAAUGACUAAUUACUUUGAAAAAUGUAGAACUUUUCACCCACUUCAUAAUUAAUAGGGGUAAAAUGGUAAACUCACUAUGUCAUUAUUUAUUUUCUUAAUAGGUGUGUCAAUUCAAAAGUGGACAAGUAAAAAGGGACAGAGGGAGUCCUAUCUAGCACCACCGACAGACCGUAGGGUGACCUACGGUCCAUAGGUAGGGUCUAUAGAUGGUCACCUGCAACUCUCCCCGGAAAAGUCCAAAAAAUUGUUCACGGUCGAACCCACGGACCGUAGGUCAAUCCACGGUUGUGGUCCU	279	sly-miR1133-5p	GAUAUACUACCUCCGUCCCUAC	5-26	tae-miR1133	5	0	22	22	2
sly-MIR7998-1	UCGAGCGACAGACCUUAACUAAACUAAAGUCCUAUUACCCCCGAAUCCAUUUUUUUGUAAUUCUGUACACUGACAUUCAAACACUCUCACGCGCCUCAAGUCACGGAGUGUACCAUUACAAAAUUACAAAACAAAUGAGUUGAGAUUAAUAGAACCUUAGUUAAGUUAAGGUGUGUCUCUGAG	139	sly-miR7998-1-3p	ACGGACCGUAGGUCAAUCCACGGU	107-130	stu-miR7998	2	0	24	24	1
sly-MIR7981-11		184	sly-miR7981-11-5p	CUUAACUAAACUAAAGUCCUAUUA	14-37	stu-miR7981-5p	4	0	24	24	2
			sly-miR7981-11-3p	AUAGAACCUUAGUUAAGUUAAGGU	150-173	stu-miR7981-3p	3	0	24	24	1
sly-MIR167c-4	GAUCGUGAACCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUUCUAUUGCUCCGUACGAGGAAAGAUCAGAUCAUGUGGCAGCAUCACCUGUUGAUGGUUUCGCGGAA	113	sly-miR167c-4-5p	UGAAGCUGCCAGCAUGAUCUA	21-41	ata-miR167c-5p	0	0	21	21	1
			sly-miR167c-4-3p	AUCAGAUCAUGUGGCAGCAUCACC	71-94	eun-miR167c-3p	1	0	24	24	1
sly-MIR11891	AUGUUAGUACUUUAGUUCAUAUAUGCCCUUACCGUCAAAUACUUGGUCUAAAUACUAUGCGCAAUUGAGCAGAAUAAGGGCGUAUUUGGAUCAAGUAUUUGAUGCUAAGGGCUUAAGUAAAUUGAAGUAUAAACG	135	sly-miR11891-3p	AGUAAAUUGAAGUAUAAACG	116-135	mes-miR11891	5	0	20	20	3
sly-MIR160-4	GGUGGUAUGCUUGGCUCCUUAUACGCCACCCACUGAUCAGUCAAUCAAAGAAUUGGUGAAUGUGUGUGGCAUACAGGGAGCCAGGCACAUCCUUC	95	sly-miR160-4-5p	UGCUUGGCUCCUUAUACGCCA	8-28	dpr-miR160	3	0	21	21	1
			sly-miR160-4-3p	UGGCAUACAGGGAGCCAGGCA	67-87	aau-miR160	0	0	21	21	1
sly-MIR6169	UUUAAUUAUCAAAUUUUAGAAUAUCGACCUCCGGAAGUUGGUAUUUUUAUUUUCUAUUUUUUAGAUUUUGACCUCUGGAGGUCGGUAUUUUCAUUUCUUAUUUUUUUGAUUCUGAUCUCUGGAGGUCGGUAUUUCUAUUUCUUAUUUUUUAGAUUCCGACCUCCAGAGGUCGGUAUUUCUAUUUCUUAAUUCUUUAGAUUCCGACUUUCGGAGGUCGGUAUUUAUAUUUCCUAUUUUUUGGCAAUUGUGAAGUCAGUCUGCCCCGUCCAAUCUCCUAAGUCAAUUGGAACUUCAGUCGCAAAGCCAUGGACGGUAGUCGGAGUGGGGUUGACUGUCUUCAAUUUUGU	239	sly-miR6169-5p	UGGUAUUUUUAUUUUCUAUUU	39-59	hbr-miR6169	5	0	21	21	1
sly-MIR158b		108	sly-miR158b-3p	ACUGUCUUCAAUUUUGU	92-108	aly-miR158b-5p	4	0	17	20	3
sly-MIR6149b	UUAUAGCCUUUGUAUGUCAAAGUUUCGAUACGCACCUGAAUCGACAAAUACAUAUAUUAUUCAGACUUUUUAAGAAUAUCACGCGUUUAUUAUUUUUAUAAGUCUGAAUAACAUAAAUCAUAUAUAACAUAUAUGUCGAUUCGGGUUCGUAUGAAAACUAUGGCAUACCUCAAAGGGUAACG	182	sly-miR6149b-5p	UCGAUACGCACCUGAAUCGAC	25-45	nta-miR6149b	2	0	21	21	1
sly-MIR5303d-2	AACCUAUGUUGCUCAUACUCUCCAAAAAUGUUGCUGCACCCCUGUCGGAUUCUCCAAAAGUGCAGUACUUUUGGAGAAUCCGACACGCACCCGCCGACAUUUCUGAAGAGUCCAAGCAACAAGACU	126	sly-miR5303d-2-3p	UUUUGGAGAAUCCGACACGCACCC	69-92	stu-miR5303d	0	0	24	24	1
sly-MIR11066-1	CCUUGGAAAUAGGUGGUCUUGAACUUUUGCUACAUGGUUAAACCUUUGACGCCAAAAGUCGAUACUUGAUGUUCUGUUCAUGGGGCGCAAGAUUAAAAGUUCAAGAUCAUCCACCUCCAAAG	122	sly-miR11066-1-5p	GAAAUAGGUGGUCUUGAAC	6-24	lja-miR11066-3p	5	0	19	19	2
sly-MIR8771f-1	UUUUAUAACUUGGCUUCAAAUUACGUUUAUGCUCUUCAAC	256	sly-	UUGGAGGUCAAAGUUAAAAUUUA	219-241	gra-	5	0	23	23	1

	UUUGGAUGUGCACAAAUAGACACUUAAACUUGUAUAAAGU UGAACAAAUAGACACACAUGUCCUACAUGACAUUUUUUGU CCUACGUGGUGUCUUACGUGUAUUGUGUCAUAUAGGAGU CAUGUGUUUAUUUAUUUAAAAGUUGAAUAACUAAAGUGAC GGUUUGUGCAUUAUGAAAGUUGGAGGUCAAAGUUAAAAUU UAAAGCAAAAUUUAGGG		miR8771f-1-3p			miR8771f					
sly-MIR9476-2	AAACUGCUAUUGGUCUAGUCCUGCAUCUUUUUUUACAUUU UUUCCGUUAUCAAAAAAUAUAAAAAAAGAUGCAGGACUAGA CCAAUAGCAGGAU	94	sly-miR9476-2-5p	UCUAGUCCUGCAUCUUUUUUU	14-34	sly-miR9476-5p	0	0	21	21	1
			sly-miR9476-2-3p	AAAAAGAUGCAGGACUAGACC	63-83	sly-miR9476-3p	0	0	21	21	1
sly-MIR10536-2	CACUGUUGAAUAAGAAGGAAAUUGAAGAUUAAAACAUGUCA AAGGAACUGGUCCGACGUAGUAGAUUGACUUGUCUACAAC AAGUAUUGAUGAAGAAGGAAGCUGAGGAUCAUAACAUGUU GUUGGACCUUUCUUCAUCAUCACUCGUUAUAGAUAAGUCA AUUAACUGCGUUGUCCUUUGACAUGUUCCAAUCGUUAGUU UUCUUUUUUUUUUAACAAAA	221	sly-miR10536-2-3p	UGACAUGUUCCAAUCGUUAGUUUU	180-203	sly-miR10536	5	0	24	24	2
sly-MIR5168	GGUUUCCAUGGUCAGUUUAUGCUUAUCCAGAAGGUGCAG GGGUUGGUUUCUGGUAGAACGAGCUUAUCUUAUACAUGU UUUGUUGAAGAAGCUAUGGUUUCGAUCUGAUUUGCCUGCA CCUUAUGUUUGAGCAUGCGCUACCAUGAACUA	150	sly-miR5168-5p	GGGUUGGUUUCUGGUAGAACG	40-60	ata-miR5168-5p	5	0	21	21	1
sly-MIR417	AACAAAAACACUUAAAUUGUUCCAAUUUGUUGAGUUUCAUA GCUAAACUAUCAAGUGUGUGUGAGUUUUCUGUCUGUACUA GUAUCAAAUGCUUCGCGAAGCAAACCUGAUUGUUCAGGUA GGAAAAGUGAACAACUUGUAGUUCAUUUGUGUUUCCGUAA ACAUUUGGUGAUAGUACAGGUAGGAAACUCACACACCUGA UAGUUCAUGUAUGAAACUCAAAAAUGAAAAAAUGUAAUGAA UUUGUU	248	sly-miR417-3p	AAAUGUAAUGAAUUUGUU	231-248	osa-miR417	2	0	18	21	2
sly-MIR7984b-4	AAUUUUGAUCGAAAUUAUUAUGAUAAUAUCAAACUCUAGAA AGGACCUUUUACUUCCUAUACUAUUUAAAGGUAUAUAUGU ACCCACGUGGAUGCAACAUUAUAAAUGGCAAUAUGUCCAC GUGGGCACAUAUAUAUCUUUAGAAUACAUUAUUAUAUAGU GCACGGGUAAAAGGUCCUUCAAUAAAGUUUGGUAUCGUAA CAACAAUUUUGGCAAAUAU	220	sly-miR7984b-4-5p	AUAUCAAACUCUAGAAAGGACCUU	26-49	stu-miR7984b-5p	5	0	24	24	1
sly-MIR2931-1	AGGAACAAUACCUUUCAUGAUGCAGUUUCUAUCAGCACCG CUAUCAAGCAAAACAACUUUGUUAAUAACAAAAUGUUUGUU AAUCACUAUUUUGAUAGGGAUAUGAUGGCUCUGAGGUCUG AUAGAGGAGAUUACUGUUAAACCUGGUGUUGCAGAAGUGG AAGCAUUGUUAUUGGUUUGUGUAAAAACUUCUGGUUCAAC CAGAUGGUUAUUGUUGAUGUCAGGUUGAUUGAUAUCAUCC UCAUUAUCCGAAUUGUUUUU	261	sly-miR2931-1-3p	GGUUAUUGUUGAUGUCAGGU	207-226	osa-miR2931	5	0	20	20	3
sly-MIR482c-4	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGUCCAUGG CUUUGCUCCUUAAGUCCCCAUUGAUUUAGGAGAGUGGACG GGGCAGACUGACUUCACGA	99	sly-miR482c-4-5p	CUCCCACUUCCGUCCAUGGCU	22-42	gma-miR482c-3p	5	0	21	21	2
sly-MIR8008b-1	UGCAAAUCCCAGAAAAGCGACUGACAAAAGAACACUAUCCA UCGCUUUUCUGGAAAUUAUUUUUUCAAAAAGUCAAAAAAAA AAGUGAAGGACUAAAACACACUAACUGUCACUUUUCUUGG UUUUAAAAAAUAAAAACCCAGAAAAGCGACGGACAAAACCA UGUUGUCUGUCGCUUUGUCUGCAAUUUUUU	193	sly-miR8008b-1-3p	AAACCCAGAAAAGCGACGGACAAA	136-159	stu-miR8008b	2	0	24	24	1
sly-MIR2275a-1	UCAUGCCUUGGGCCACGACCGUUUCUAUGACAAACUUGGG UUUGGCAAGAGUCUUCGAGGGCACCAAGGCAACA	74	sly-miR2275a-1-3p	AGAGUCUUCGAGGGCACCAA	48-67	ata-miR2275a-5p	5	0	20	20	2
sly-MIR5780c	UUAUUUUAAGUUUUAAAAAAUAAAAUAUAUCCUAAAACGUU UCUGUGGAAUACAUUUUAGAAAGACUUAGUUUGGUUAAAA CCUCUGGAACACAAUGGCAACCAGAACUCCAUACUAAGUC UUACAUAUUUAAUAUAUGUGAGAUUUGGCUCCAAGUCUGG AACAUACCACUACAUUGAAUAUCGUAAGGAGUAGGCAGUA ACACUUACAUAGGUGAUUUCUAAAUGUGUUAUCCCAUAGA UACACCAUUUGAUAUUCCUUGUAUCAAACUUAGAAACCA AAAACGCCCUUUGAUAACUCGAUCUUCCAUAAUCCUGUCA CAGAUGACUCUCGUCCUACCACAUUGAAUUCAAAUUAAUU AGACUUAGAGAAAGGGGCUUAAUGACAAGAUCGAGAGUCA UCUGCGACAGGACUACCGGAAGAUGUGAACAUCAAAGGCG UCGG	280	sly-miR5780c-3p	UUUAAUAUAUGUGAGAUUUGGC	129-150	gma-miR5780c	5	0	22	22	1
sly-MIR1919-5		164	sly-miR1919-5-5p	UGUCACAGAUGACUCUCGUCC	36-56	stu-miR1919-5p	3	0	21	21	1
			sly-miR1919-5-3p	UCGAGAGUCAUCUGCGACAGG	111-131	stu-miR1919-3p	2	0	21	21	2

sly-MIR156c-4	AAGGGAGGUGACAGAAGAGAGUGAGCACACAUGAUGUUUUCUCGCAUGAUGUUUACAUGCUUGAAACUAUGCGUGCUCACUGCUCUAUCUGUCACCCCACC	101	sly-miR156c-4-5p	UGACAGAAGAGAGUGAGCACA	9-29	rco-miR156c	0	0	21	21	1
			sly-miR156c-4-3p	GCUCACUGCUCUAUCUGUCACC	75-96	ata-miR156c-3p	0	0	22	22	1
sly-MIR390a-3	AGCAGAUUAAAAAUAAAAAUAAUAUAUUUAAAAAAAAGCAUGAAAAAGCCGUGAAACUCAGGAUGGAUAGCGCUAAAGAUGUGUACAAAAAUCGAAUUGAGUCAUCCAUGGCGCUAUCCCUCCUGAGCUUUACAGAUUCUCCAUGCAUAUCCACUAGAAAUUAUUUGUUUUUUCACUAUA	181	sly-miR390a-3-5p	AAACUCAGGAUGGAUAGCGCU	54-74	cas-miR390a-5p	3	0	21	21	1
			sly-miR390a-3-3p	CGCUAUCCCUCCUGAGCUUUA	112-132	sly-miR390a-3p	2	0	21	21	1
sly-MIR5140	CGACUGACUUGUCUACUUCAAGUGUUGAUGAAGAAGGAAGCUGAGUAUUGGAGCAUGUCGAAGGAACAUGUUCAACGAAGCUGACUGACGAGUUACAACACUGUUGAAGAUUUAGAGUCAGAUU	124	sly-miR5140-3p	ACUGUUGAAGAUUUAGAG	100-117	rgl-miR5140	4	0	18	18	2
sly-MIR908	CAAAAAAGAAAUUGAUAAUUUAUUAGCAAAGGGACUUAUAAAACCCUCUAAAUCUCCAUGGUCUUGUACUGCAUUUUAUGUUAAUAAAGCAGCAGAACAAGAAACAGGUGUUCCCAGGUUGGUAAUAAAUUACAAACCUUUUAAC	145	sly-miR908-3p	UUUAUGUUAAUAAAGCAGC	75-93	cre-miR908-3	5	0	19	19	3
sly-MIR11066-2	AUGUCUUACUUUAAAGUUGCGAUAGAUUGUGCUAUAGAACUCCAAAUUGGGCGAUUCAAAAAGCUAAAAUUUGCGAUUUUUUGAGGGCAACACAUUGGUGAUCUUGAAAUCUGAUUUGGGGUCCCGAUUUGAGGUAAAGUUUGUGUUUUAGCUGCUGCUAUAGCUCAUUUUCGAGCUCAACUUUUGUAAGAUUU	194	sly-miR11066-2-3p	CACAUUGGUGAUCUUGAAA	91-109	lja-miR11066-3p	4	0	19	19	2
sly-MIR10430	GUCAAUGGGUUGACCCACCCCAACCCAAUCUAACCCUAACGGGCUAGAGAGUUAAAUGGGUUGGGACGGGCUGACCCUUUUAG	83	sly-miR10430-3p	ACGGGCUGACCCUUUUAG	66-83	gma-miR10430	4	0	18	24	2
sly-MIR160-5	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAACUAGGAAGAGUGUCAAUUUUUUUGACAAUACUGUUCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACAAUUUC	104	sly-miR160-5-3p	UGGCAUCCAGGGAGCCAGGCA	74-94	aau-miR160	1	0	21	21	1
sly-MIR156f-3	UGGAAGAGAGGGACUGGCAGAAGAGAGUGAGCAUACACAUAUAAUUAUAUAAACAUGUUUACAUAAUUCUUUUGAUAUAUAUAUAUAUAUAAUUUUGCGUGUGCUCACUUCUCUUUCUGUCAAUCUCUCUUAGA	132	sly-miR156f-3-5p	CUGGCAGAAGAGAGUGAGCA	14-33	stu-miR156f-5p	1	0	20	20	1
			sly-miR156f-3-3p	CUCACUUCUCUUUCUGUCAAUC	102-123	stu-miR156f-3p	0	0	22	22	1
sly-MIR2607-2	UUUUUAAUCCUCGAGAGUAGUAUAUAAGAAUCUUGUUCAAUUUCUAAAUACGUGCAAUUUUUUUUUUAACUGAGAUUACCUUUUGAUGCAAUAUAUGUUUUUGUUAACGAGAGAAAGGAGACUGAGAUGUAGUUUGGACAUGUGAAUAGGAGAUAUGUGGAUGUACUACUAAGGAGGUGUAAGAG	185	sly-miR2607-2-3p	AUGUGAAUAGGAGAUAUGUGG	140-160	mtr-miR2607	5	0	21	21	1
sly-MIR171b-5	AUAAGAAGUGAUAUUGGCGCGGCUCAAUCUGAGAUCGUUCUUUACGAAAAUAAGCAUAAAUUCGUCUUCGGAUUGAACCUCACCAACAUCGCUUCUUCC	99	sly-miR171b-5-5p	GAUAUUGGCGCGGCUCAAUC	10-29	zma-miR171b-5p	1	0	20	20	1
			sly-miR171b-5-3p	GGAUUGAACCUCACCAACAUC	70-90	tcc-miR171b	5	0	21	21	2
sly-MIR5752b	UAGAAUGUAUUAGUAAUGUUUGCAUUAAUUAAACAUAUAUGAUUUCUUAUGCAUUGUUUGGUUUGGUGUAUUUUAUAUUUUUUUUAGUUUCCCACCCUGUGUCUGGAGCCCAUGUUGGAGCUCCGUCUAAAUCCGAAUCGCGCUCUGCAGGGGCACAUUCGGGGGUGACACUCCCAAAAGGUUUUCUCCAUAUCGAGGGACCUCUGAUUAAGGAUGAAACACUCCACCAAUGCACCACAACCCAUGUUGGUGGUUUGGUGAAUUAUUAAUAGCAUACAUUGCAUAAAAUAUUUAC	295	sly-miR5752b-5p	CAUUGUUUGGUUUGGUGUAUU	52-72	mtr-miR5752b	5	0	21	21	1
sly-MIR7997c-6	AUUCUAUGUUGCUCGGACUCUUCAAAAAUGUGAUCGUUAGGUACGUGUUGGAUCGUUCAAAAGCAAUAGUACUUCAUUACAUUUUUGGAAAGUUCGAGCAAUUUAGUGA	109	sly-miR7997c-6-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
sly-MIR8001b-3	CACUACAAGAAAAGGGUAAAUUAAAUGGGGAUUAGUAUGAAAAUUUGCAGGGAUUACCCUGUAGUUCACACUUUUCUUGUAGUG	84	sly-miR8001b-3-3p	AUGGGGAUUAGUAUGAAAAUUUGC	25-48	stu-miR8001b-5p	0	0	24	24	1
sly-MIR7997c-7	UGGAAAAUUUCUAUGUUGCUCGGACUCUUCAAAAAUGUUGAUGGGUGUGUGUUGGAUACUCCAAAAGUAGUGCAUUUUGGAGGAUACGACACGGGUGUGGUGAUAAUUUUGAGAGUUUGAGUAACGUAGGCAAAAUUUAUU	141	sly-miR7997c-7-5p	AUGUUGCUCGGACUCUUCAAAAAU	13-36	stu-miR7997c	1	0	24	24	1
sly-MIR1512a	AAAAGUUCAUGGGUUAUCACACACGUAAAUCGAUAAAAGUA	195	sly-	CCAUAAAAAAUUUCAGUUAUU	136-156	gma-	5	0	21	21	2

	GCAUUCGCCUGAUUUGGGAUUCGUUUGAACUUGAAGAUG CACCAUUUUUCUUCACGGAACGAACUGGUUUCAUUUUUAA UCUCUUAACGGACAUCCAUAAAAAAUUUCAGUUAUUUUAUU UUGGAUUUCCGAAUGAAAAAACUCAUGAACUAUA		miR1512a-3p			miR1512a-3p					
sly-MIR7493	GGUAUUUCAUCCUUUUUGAGGAUUUUUUGGUUUCUAUAUA AAUCCACUUCAUUCACUAUUUUUAGAGGAGGAUUUUUGAG GGGAAGACCAAAGAGUACCCAUAAAAUUUUGAGAAUUCU	119	sly-miR7493-3p	AAAAUUUUGAGAAUUCU	103-119	ghr-miR7493	4	0	17	24	1
sly-MIR6224c	GCUCCAUCCUAAAAUAAAUGUCUCAAACGACAGGUGACAA GUCAGUCACGUGUGUUUGAUAGAUACACUUUUUAAGUGGU UU	82	sly-miR6224c-5p	CUCCAUCCUAAAAUAAAUGUC	2-22	sbi-miR6224c-5p	5	0	21	21	1
sly-MIR4415b	AACACAUAUGUGGUGCAAAUCAAGAUAGCAAGAUUGAUAU CAAGAAUGGGGUUGUGGUCCAUCUUGGAUAUGAAAGUUUC CAAUCACCCACAAAGGGCUCAACGUAUCAUGAAAGAUUCA UUAAAAGAGACCAUUCUUGAUAUCAAUCUUGCUAUCUUGA UUUUCACCACAUAAUGUCUC	180	sly-miR4415b-3p	UUGAUUUUCACCACAUAAUGU	157-177	gma-miR4415b-3p	5	0	21	21	1
sly-MIR8013-2	AUCAAAUCGCUGCCCUGGCAGCGAUUUGUAAGAAGAAAAA UUUUGAAAUCACUGCUUGAGCAGCGAUUUCAUUUUUUUAU UAAACAAUUUUUUUUUUGGCAAAAUCGCUGCCUCAGCAGC GAUUUUACUUUUUAGUUGAAGUAAAUCGCUGCGUCGGCAG CGAUUUUAC	169	sly-miR8013-2-3p	UGAAGUAAAUCGCUGCGUCGGCAG	137-160	stu-miR8013	5	0	24	24	2
sly-MIR7981-12	AAAAAAGCACAAGUACCUCUUAGACUAUGAUCGAAAAAUUA GAGACAUGCCUUAACUGAACUAAGGUUCUAUUACAACCCA CCUACCUCUCCUUCCAAACCCAUUUUUUUUUGUAAUUUUG UGCAAAUUUUUGGCUUACGUGACAUCCAAAUAUCUCUCAC GCAUGAGUGUGCCUCAUAAGACAAAAGGUGUACAAAAUUU UAAAAAGAAUAAGUAAUGGGGUAAUAAGACAUUAGUUUAG UUAAGACGUGUUACUGAAAUAUCGGUCAUAAUCUAGAAGU AUUUGUACCUUAUC	295	sly-miR7981-12-5p	CUUAACUGAACUAAGGUUCUAUUA	51-74	stu-miR7981-5p	5	0	24	24	2
			sly-miR7981-12-3p	AUAAGACAUUAGUUUAGUUAAGAC	225-248	stu-miR7981-3p	4	0	24	24	1
sly-MIR1888b-1	ACUAAAUUAUAUUCACAAUGAUUAAUCAUUAAUCAAUAAAU UUUAUUUGGUAUAUUUAGAGCCGUCAAUAUGGGCUAGGCC CGUUGGGCCGGCCUGGCCUAACCCGGGAUUUAAUAGGGU UGGGCUAAAAUUUUUGGAGCCCAUUUAAGAAAAGACUUUU UAGCCCGCCCUGAAUAAGUCUGUUGAUUUGAUGGGCUUG AGAAAUAUAGAUAGGGCCGGCUCGUGGGCCAAUAAUAAUU AAUUAAAAAUAUAAUAUAAUAUUAAAUUUUAA	271	sly-miR1888b-1-3p	UUGGGCUAAAAUUUUUGGAGC	120-140	ath-miR1888b	5	0	21	21	1
sly-MIR169j-5	GGUAAAAGAAGAGUGUCUUACAUGAAGGGUAAGUGCCUAU UUGAUAGCCAAGGAUGACUUGCCUGCAUCAUUAAUUAAUU CUUGAGGCUAGCUUGUGAUAUAUAUCAUGUAUAUGACAUG UAUACAAGCAUUCUUCUUUGAUGGCCAGGCAGUCUCCUUU GGCUACUCGAAUAGGUUCCUCUCAUUCAUGCUAGACUCUU CUCUUCUU	208	sly-miR169j-5-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1
sly-MIR7493b	AUAAAAUCUUGAACAAUAGACUCAAAAUCCUAGCUCCACUU UUAAUUUAAUGUAUUAUGUAUUUCAUUUACAUCAACGUGG ACGUGCCGGAGUGGUUAUCGGGCAUGACUAGAAAUCAUG UGGGCUCUGCCCGCGCAGGUUCGAAUCCUGCCGUCUACG AUUUUGAUUGUUAAAGAUUUAAA	182	sly-miR7493b-3p	UUUGAUUGUUAAAGAUUUAAA	162-182	gra-miR7493b	5	0	21	24	1
sly-MIR399b-2	UGAUGAAGCGGAAGCAUGAGAAAGGAAGUCGUUGGUGAAU GAAAAUAAGGGAAAUAGUGAUAGGGCUACUCUCUAUUGGC AUGCGUUAAUAUAUGUACAGUGACUCCAAUUCACUGUAUC GCAUAUUUUAACCGAUACGCCAAAGGAGAGCUGCCCUGCU ACUGUCUCUGCUUAAUAUAAUAACUCAAAGAUCCGUUCUU AAUACUCCGAUGCAGAA	217	sly-miR399b-2-5p	GGGCUACUCUCUAUUGGCAUG	63-83	sly-miR399b	0	0	21	21	1
			sly-miR399b-2-3p	CGCCAAAGGAGAGCUGCCCUG	138-158	nta-miR399b	0	0	21	21	1
sly-MIR399b-3	GAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGU AUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUAC UGUCUC	86	sly-miR399b-3-5p	GGGCUACUCUCUAUUGGCAUG	13-33	sly-miR399b	0	0	21	21	1
			sly-miR399b-3-3p	CGCCAAAGGAGAGCUGCCCUG	56-76	nta-miR399b	0	0	21	21	1
sly-MIR399b-4	UUAUAAGCGAAACAGUGAUAGGGCUACUCUCUAUUGGCAU GCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGC CCUGUUACUGUCUCUGCUUAAUC	103	sly-miR399b-4-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			sly-miR399b-4-3p	CGCCAAAGGAGAGCUGCCCUG	64-84	nta-miR399b	0	0	21	21	1

sly-MIR11048	UAUUUGUUAUAUCUUUGCAGAAUGGCAGGCAGAGAUGAGCCUCCGCCAUGGUCGCAUAUUCGUAGUCGUGGAGGAAAAACUAGAGGAAGAGGAAGAUCAUCCUCUUCACAGAACAGAAGAUCGUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGAAAAACUUUAAUCAAUUCAAAGAUUGGGGAAGCUUCUUCAUCAGCUUCAUCUUCUGUGAAUCUAAAAGAUAUCCCAAAGG	241	sly-miR11048-5p	AAAAACUAGAGGAAGAGGAAG	75-95	seu-miR11048	5	0	21	21	3
sly-MIR9679-2	GAAAUUGAUAAUUUAUUAUCAAAGGGACUUAUAAAACCCUCUAAAUCUCCAUGGUCUUGUACUACAUUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGUUUGGUAAUAAAUUACAAUACC	132	sly-miR9679-2-3p	CAGAACAAGAAAGAGGUGUUC	86-106	tae-miR9679-5p	5	0	21	21	1
sly-MIR1888b-2	GAUAUUAUUUAUGUAUGAGAUAUUCUAAAGUCAAGUAUAAUAAAAUAUAUUUGUUUGAUUUUAACAGUUAUGGUUUGUUCAUAUUUUGGGGUAGAACCAUCAAUAUAGGCUAGGCCCGUUGGGCUGGGGUGGCCUAACCCGGAUUUAAUAGGGUUGGGCUAAGAUUUUUGGAGCCCAUUUAAGAAAAGGAUUUUUUAUCCCGGCCUGAAUAAGCAUGUUGAUUUGAUGGGCUUGAGAAAUAUAGGUUGUGCCAGCCCGUGGGCCAAAAAUAAUUAAUUAAAAAUAUAAUAUAAUAUUAAAAUUUAAAAUUAGAGAGAGUCCAAAUUCAAAAAAAAUAGG	340	sly-miR1888b-2-3p	UUGGGCUAAGAUUUUUGGAGC	154-174	ath-miR1888b	4	0	21	21	1
sly-MIR5568e	CCCUCUAGUGCCCAAUUUAACUAGAACUCAGAAUCUUAUUUUCUAGUAGAAGAUGGAAAAGUAGCGUGUAUUUUUUCUUUCAAGAAGAAACGUGUGUUUUAGGUUUUCUUGAGGAAAAAGAAUUUGUGUUCUCUUCUCCUCUUUGGAUUAGGAAGACAUCUCUAAAAGUAGGGAUUAUUUUAACCUAGAGAAAAAGAAUUCAUUUAUUCUAUACAAUACUUGCCCACCCAAGUCUAUAGAGAGUUCAAUUGUUAAUUGGGAUCACUGGAAAA	272	sly-miR5568e-5p	UGUGUUUUAGGUUUUCUUGAG	93-113	sbi-miR5568e-5p	5	0	21	21	3
sly-MIR5237	UAGUAUGUUCCAAAAGGUUAGUUAUGGUCCUAAAAACUUAGGGGUACUUUAGUAAUUCUUUUAGGUUACAUAAUUAAUUAAUUAAAGGGACAACAGAGAACCUAACCUAAGAUGGUCCAAAGAGUUAGUUAAGAUCCUAAUGACUUAAGGGUAAUUUAGUAAUAACCCUUGGAUACAUAAUU	182	sly-miR5237-3p	GUCCAAAGAGUUAGUUAAGAU	115-135	mtr-miR5237	5	0	21	21	2
sly-MIR5542	AUGUAUUGAGUGAUAUUUUAAGGUCUCCUAUGUACUUGAUUGUGUGGUUGUAGGUUUUGAUUGUGUGAUUUGUGGUUGGCCUAAAAUUAUUAGACUAUUGAAUUUCUAAUCUUUAACCCUGUCUAUUAAAAUGACGCCUUUAAUAAAGAAGGCUUGAUGAAAUAAAAUAAUGAGAUAAUUGGAUCGGAGUGUCACGUUCUGACACGGUAUUAUUGGAUCGGUGUGUCACGUUUUGACACAGUAUUAUGAGAUCGUAGUGUCACGUUCCGACACAAUAACAUUAAGAGAAAGGAAACUUGAAGUAACUUAAUAUAC	315	sly-miR5542-3p	UUUGACACAGUAUUAUGAGAU	232-252	osa-miR5542	4	0	21	21	1
sly-MIR169a-4	GAGUUUACAUGAUAGAAAUGGAGAGUGGAUUGCAGCCAGGGAUGACUUGCCGAUGAUUUCUUUCCUAGUUUUCCUAUUAAAGAUUAUGUAUCGGCAAGUUGUCCCUGGCUACCUUUCGCUCUCUUCUUCUCAUGCAAAUUU	141	sly-miR169a-4-5p	CAGCCAGGGAUGACUUGCCGA	33-53	cas-miR169a	1	0	21	21	1
			sly-miR169a-4-3p	GGCAAGUUGUCCCUGGCUACC	93-113	aly-miR169a-3p	2	0	21	21	1
sly-MIR1106-2	AUAUCAAACUUCAUGGAGGACCUUAUACCCCUUACACUUUUUAAAAGUGCAUUUUAAAGGUAUAUAUGUGUCCACGUGGACACAUUACUAUUUAAAAUGUUUAUGAUGUCCACGUGAAUACAUAUAUCUUUAAAAUACAUUAUUUAAUAGCACAGGGGCAUGAAAGGUCCUACAUAAACUUCGAGAU	189	sly-miR1106-2-5p	UUUAAAGGUAUAUAUGUGUCC	53-73	smo-miR1106	5	0	21	21	1
sly-MIR5812	AAUAAUAUCAAAUCGCUGCCAUGGCAGCGAUUUGUAAGAAGAAAAAUUUUGAAAUCGCUGUUUGGGCAGCGAUUUCAUUUUUUUAUUAAAUUUUCUUUUUUUGCAAAAUCGCUGCCUCAACAGCGAUUUUACUUUUUCAGGUAAAGUAAAUCGCUGCACCGGCAGCGAUUUUAUCAUUUUG	181	sly-miR5812-3p	GGCAGCGAUUUUAUCAUUUUG	161-181	osa-miR5812	5	0	21	24	2
sly-MIR9476-3	GUUAACGGUAUAUAAGACUACUAGACAGCUCAAGCUUAAAAACUCUAACUUGCCUACCAGUUGACCACCAUAACCAAUGAAGACAGUCCCUAACCAAAGGGGACUGAAUCAACUGGUAGACAAGUUAGAGUGUUAAAGCUUGAGUUGUCUAGUAGUCCUACAUAUCUUUUUA	172	sly-miR9476-3-3p	AGUAGUCCUACAUAUCUUUUU	151-171	sly-miR9476-5p	5	0	21	21	3
sly-MIR171b-6	ACUAGUAAAUGAAUUGGUAAAAAGAAAUGAUAUUGGCGCGGCUCAAUCUGAGAUCGUUCUUUACUGAAAUAAAACGUAAACUCGUCUUCAGAUUGAACCUCACCAACAUCGCUUCUCUAAUUCAAUAUAUACUCAC	136	sly-miR171b-6-5p	GAUAUUGGCGCGGCUCAAUC	29-48	zma-miR171b-5p	1	0	20	20	1
			sly-miR171b-	AGAUUGAACCUCACCAACAUC	90-110	tcc-miR171b	4	0	21	21	1

			6-3p								
sly-MIR5171b	CCAAAAAUCAAAUCAAACUGCAAAUCGAGUCAACCCGGAAAAAAACCCGACUAGUGAUUUGGUUUGACUUGAUUUGGUAUUGAAGAAAAAAACUCGACUAUAUUUGAGUUAGUUUGAUUUUGAC	124	sly-miR5171b-3p	ACUUGAUUUGGUAUUGAAGAA	67-87	bdi-miR5171b	5	0	21	21	1
sly-MIR169e-2	CUAAAAAAACGAAAGAGGAGUUCUUGCAUGAAAGAGGAGAGCAUGUCAAGGUAGCCAAGGAGACUGCCUGAAACCAACCAAUAAAAGGUCACCAUUAUAUUAAUAAUGAUAAAAUUAAAAACCUUAUAAGUAAUAUUGGAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUAAUAUAACUCUCCUCUUCAUGUAAGACAUCUCUUCUUUUUCAU	215	sly-miR169e-2-5p	UAGCCAAGGAGACUGCCUGAA	52-72	zma-miR169e	3	0	21	21	1
sly-MIR169e-3	UUUGAAAAGAUAUCUUGCAUAAAAGAAAAGAGCAUGUCAAGGUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAUUAAACACAUUUUAGACUAUGGAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUAUGACUCUCCUCUUCAUGUAAGACUUCUCUUCUUU	169	sly-miR169e-3-5p	UAGCCAAGGAGACUGCCUGAA	43-63	zma-miR169e	3	0	21	21	1
sly-MIR169c-4	AUUAUUGAAGAGGGGUUUUAUAUGAAGUUGAGAGUAUUAUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAGACCUUAUCUUCUAUGGC	188	sly-miR169c-4-5p	UAGCCAAGGAUGACUUGCCUA	45-65	ata-miR169c-5p	0	0	21	21	1
sly-MIR5049c-2	GGCAGUAGCUUGAUACUCCCUUUGUCCAACAAUAGUUGUCCACUAUUGACUUGCCACACCUUAAAAAACAAUAAAUAAUAGGGGUAAUAUUACUAUAUUAUCAUUUGAAUUUAUUAAAUUUUAUGCUUUGAGAAAUGUGUAGAUGAUAAAUAGUAUUUAAUAGCAAGUUUAAAAUAGACACAAAAAGGUAAAUUAUUUCUUGGUUUUCCAAAAGGACAAGUAUUGUUGGACAACUAUUUUUAGUAGAGUGGACAACUAUUGUUGGACAGAGGAGCAUAGAAGCUACUUAC	290	sly-miR5049c-2-3p	GGACAACUAUUGUUGGACAGAGG	250-272	hvu-miR5049c	5	0	23	23	2
sly-MIR8001b-4	CCACACUACAAGAAAAGUAUGAAUUACAUUGAGAUUUUCCUGAAAAUCAGGAUGAAUUUUUGCAGGAAAAUAAGUUUCCUACGUAUUUUCAUACUAAUCCUAGGAAAAUCCCAUGUAAUUCACAGUUUUCUUGUAGUGCCA	141	sly-miR8001b-4-3p	GUAUUUUCAUACUAAUCCUAGGAA	83-106	stu-miR8001b-3p	5	0	24	24	1
sly-MIR8138-1	GACAUAAGAUAGGUGGACUCCUUGUAAGGUUUGGGCAAUCCUCCUCCCACCUUUUGGGUGUGAGUUAAGUCUAAGACCUAAUUACACAUGGUAUCAAAGGAUUGUACAAGCUUUAUAAGGAGUCCACUAUCUCAUUAA	138	sly-miR8138-1-3p	UACACAUGGUAUCAAAGGAUUG	83-104	cpa-miR8138	5	0	22	22	1
sly-MIR2929	CCUCACUUCACGCACUCAAAAGGUGUGCCUCAAACGACAGGUGACAAGUCAGUCAAGUGUGUUUGGUAGAUACACUUUUUGAAUGGUUAAGUGUUC	96	sly-miR2929-3p	GUCAAGUGUGUUUGGUAGAUA	52-72	osa-miR2929	5	0	21	21	2
sly-MIR482j	UUUAAGAGGUGAGGGUUACCCAUGCAAUAUAAAGAGACCACCCAUCUCUUAACCAACCGAUGUUGGUCUCUUUUACAACCCCUCGCCUGCCUAGGAUUGGACGUAUAAUACGGGGUCUAAACAUUGAGAAACCAAGAAUUGGGAUGAGUCCUACUUUGCUACCAUGUUAAAGUGUGUCAGUUUUUAUGCUGUUAGAGGGAUAACACAUUUUAAUUAUUUAAUUAUAUUAUGUCUCGACAGUUGAGAAGUCUCACAUUAGUUGGUCAAGGGAUGUGCGGUAUUCUCAUAUGGGUUGAGCAAUCUUCACCUCUUGAG	315	sly-miR482j-5p	UUUACAACCCCUCGCCUGCCUA	72-93	pab-miR482j	4	0	22	22	1
sly-MIR8578	AAGUGGCUAACAAAAUUCACUAUUGAUGUCUUCUUUGUUAGCUUCAUAAACGUACUCAAUAAAAUCUAACACCAUUUCUCCUACGUUCUCUAACAAAACUUUACUAUUUUCUCUUUUCUAAAAUAUUAUUCUACUUGCCUAGUAUUCAUUUCUGUUUUCUCUAAAAGUUACAAAAGGGAUCCAAACAAAAAAAAAUUCAAGUCUGAUCUUUUCAAUGUGUACAUGCGCAUUUUAGAGCUAACAAAGAAGACAACAAUGGUGGACAUUGUUAACCAUAU	278	sly-miR8578-3p	UUCAAGUCUGAUCUUUUCAAU	196-216	atr-miR8578-1	5	0	21	21	1
sly-MIR5303f-6	GAAUUAUGUUGCUCGGACUCUUCAAAAAUGUCAAAGGGUGUGUGUCGGAUUCGCCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCAAAAGUGAAGAGUCCGCGCAACUAAGCU	126	sly-miR5303f-6-3p	AUUUUUGGAGAAUCUGACACGGGU	67-90	stu-miR5303f	0	0	24	24	1
sly-MIR829	AUGAGAUGGCUCUGAGGUUGAGUUUGAUCCACAUUCAUUUCAUUACACGAUAGUAUAGCAAAAUCUAUGUAUGUACUACCUUGUAGUGAAAUGGAUGUUGAAUCUAAUUUAACUUUAGAGCUUUCUUUU	129	sly-miR829-3p	ACUUUAGAGCUUUCUUUU	112-129	ath-miR829-5p	4	0	18	21	1
sly-MIR11409d	CUGAACUUUAUUCACUAUAACAGUAUGGUCACAAAACUAUCUUUUGUUGCGUUAAAGUACGUGUUAAUUGCUCAAAUGAUGACUAGAAGGUUAAAUAUUCUUUUAAUAUUAUUUUGAGCCA	237	sly-miR11409d-3p	CAUUUGUCUCAUUUGAGCAAU	140-160	pab-miR11409d	4	0	21	21	1

sly-MIR9736-1	GAAAUUUAACCUUUGGGCCAUUUGUCUCAUUUGAGCAAUCCACACCCCUAGUUCAGUUACUUUAAUGUGACAAAAAUUAGUUCUGUGAUUCUACCGUUACCGCGGAUAAAAUUAAAUGAUCCACCCACCUAACCUGGCCCAUUAAAAAAAUAUGAUGACCCAUUUUAUUUUGUCUUUAAUCCUAAAUCAAUUCCUCUCUUUAAACCUUGAAUUAGGAUUAAAGACAAAAUAAAAUGGGUUAUAUCAUAUUUUUUAAUGGAUCGGGUUAGGUGGGUGGAUCA	165	sly-miR9736-1-3p	UUAAAGACAAAAUAAAAUGGG	102-122	gma-miR9736	5	0	21	21	1
sly-MIR5014a-4	CUCCAAUUUUGAAUGUGUACAAGUGGACACCUAACUUGUAAAAAAUUGAACAAGUAGACACAUCUUACGUGGCAUAAUACACAUAGGACACAAAAUUGUCAUGACAGAUGCCAUAUAGAAUAAAUGAUUUUAUUUGUUUAAUUUUGUACAAAUUUAAGUGUCUACGUACGCAUACUCAAAAUUGAAA	187	sly-miR5014a-4-3p	UUGUACAAAUUUAAGUGUCUA	144-164	ath-miR5014a-3p	3	0	21	21	1
sly-MIR319a-3	AUAUAUGAAGAGAGCUUUCUUUAGUCCACACAUGGGGAACGAUAGGGUUCAAUUUGCUGCCGACUCAUUCAUCCAAAUGUUGAGGUCUUGAUAAUCGAGUGCCACCUCAGCAACUGAGUGAAUGAAGCGGGAGUACAAGUUGAGUCUUGAGCUUCCUGUACUUGGACUGAAGGGAGCUCCCUCUUACCU	189	sly-miR319a-3-5p	AGAGCUUUCUUUAGUCCACAC	11-31	stu-miR319a-5p	2	0	21	21	1
			sly-miR319a-3-3p	UUGGACUGAAGGGAGCUCCCU	162-182	aof-miR319a	0	0	21	21	1
sly-MIR2875	CGUUAAUUUUAGGUAUGGACAAGUAAACAUUUAAACUUGUAUAAAAUUAAACAAAUAGACACAUUUGUCCUACAUGACACCCUACAUGAAAAUUGUGUCCUACGCGGCGUCCGAUACAUAUUAUGUCAUGUAGAACACGUGUGUUUACAUGUUCAGUUAUAUACAGUUUUAAGUGCCUACUUGUGUACACUCAAAGUUAGAA	202	sly-miR2875-3p	AUGUUCAGUUAUAUACAGUUUUAA	149-172	osa-miR2875	5	0	24	24	1
sly-MIR159b-7	AGAGUUUUGAAUGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUG	198	sly-miR159b-7-5p	AGCUGCUAAUCUAUGGAUCCC	58-78	cas-miR159b-5p	1	0	21	21	1
			sly-miR159b-7-3p	UUGGAAAGAAGGGAGCUCUAC	165-185	sly-miR159b	0	0	21	21	1
sly-MIR159b-8	AGGAAGAUCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAGCUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUAUUUUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCUUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUGGUUUUUUU	215	sly-miR159b-8-5p	AGCUGCUGAUCUAUGGAUCCC	67-87	cas-miR159b-5p	2	0	21	21	1
			sly-miR159b-8-3p	UUGGAAAGAAGGGAGCUCUAC	174-194	sly-miR159b	0	0	21	21	1
sly-MIR399i-2	CUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCCUCUGCUUAAUUAU	107	sly-miR399i-2-3p	UGCCAAAGGAGAGUUGCCCUA	66-86	stu-miR399i-3p	0	0	21	21	1
sly-MIR11404	CCGCAUUGUUUUUACUAUUUAUGAUUGAUUUACUGGUAAAUGUUGGGGUUUAGAUUUGUUGGUUCGCUCACCUAGUAGGUUAAGGGUGAGUGUCACUCACGACUCGUUUGGGUCGUGACAGGGAUUCAUUUAAUAAAAAUGAAAUAUAUAUAUGUUAUUAUUGAAAUGGGUUUUCAUGUCUUCCUUCUAUUAAUUUGUGCAUAUAUGUGGAGUUUUAAAGAUUUCAAAAUGUUAAUAUAGAAAUACAAUGAUU	253	sly-miR11404-3p	UCGUGACAGGGAUUCAUUUAA	113-133	pab-miR11404	5	0	21	21	1
sly-MIR1217	UUUAUGUUAGUUAUUAUACACUAGAAAUAUUUGAAUCAUGAAUUCUAGUUUGCUAGUAACGGGAAACAGGGAAAAAACUGCUAGACUAUUCCAUCCCACAGUGGAAACCGGUAGGCGAGGGAUGCCGUUAGGGGAGUACACAAGGUUAAGGCGCUGAUAAGCAGUAAUUAUCCGCUAAAGUACUAUGCUAGUAGUGACCGGAAAACAUGAUAACGAUACUCUAGUUUAUAAUAAACUAAUAUGAA	245	sly-miR1217-5p	UAUUUGAAUCAUGAAUUCUAG	28-48	ppt-miR1217-3p	5	0	21	21	2
sly-MIR11553	UGACAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUACCCAACAUGGCAACUAAUGCUCAUUAGGGCAUAUUUGGACCAAAAGUUGGACGGCGAGGACAUGAGUGAACCAAUCUUUAAACGGAGAAUAUAUCUAAACUUUUUCGAAUAGUUUAGAGGCAUAUUUGACUCUUUUCCUUUCUUUAAAUGAAA	188	sly-miR11553-5p	GAAAAAUGAGUUGGAUAUACC	17-37	pab-miR11553	5	0	21	21	3
sly-MIR8005b	GACAUUGGAAUUUUGUGAAACUCUACAAGACGUGUUCAAUUUGAGUUGGGACUCUACAAAUUGUGAUAAACUCAAAUUAGGAUUCUCUCUUAAAUCAAAUAUAAAAAUCUAAAGCAGCAAA	323	sly-miR8005b-3p	ACUCUAAAUUCUAAUUUA	306-323	stu-miR8005b-5p	3	0	18	24	1

	GAUGGAAGAAUGAGUACUUCAAUUCUCGUCUUUGAGUUUUAUCAAGUCUAUGCUCCGACAAGCCUUGAAGCAGGGGGCAUUUGUAGACAUUGAAAUUUUGUGAAACUCUACAAGACGUGUUCAAUUUGAGUUGGGGCUCUACAAAUUGUGAUCAACUCAAAUUAGGAUUCUUGGAGGCUACUCAACUCUAAAUUCUAAUUUA										
sly-MIR10424d	CAGUGGACAUUUCUAGACAUUGAAAUUUUGCAGGACUCUACAAGAUAUUUUCUAUUUGAGUUGGGACUUUACAAGGUGUGUUCUAUUCAAAUAGGAUUCUUGGAGGCUACUCAAUCCUAACCCUAGUUCACACUUCUACAAAGGGUAUGAAAUUCCCUUAAAACACAUCUCAAAUAUCACAUAAACUCUUGGGUAUUUUUUAAAGAUCAAUGUCUCAAAAAUUCCAUAA	229	sly-miR10424d-5p	UUUUCUAUUUGAGUUGGGACU	48-68	gma-miR10424d	4	0	21	21	1
sly-MIR10536-3	UAAUGUUGAAGAAGAAGGAAGCUGACGAUUGAAACACGUCAAAGAAAUAUGUUUCAAUCGUCAGCUUCCUUCUUCAUCAACACAU	85	sly-miR10536-3-3p	AAAUAUGUUUCAAUCGUCAGCUUC	45-68	sly-miR10536	4	0	24	24	1
sly-MIR8050-3	AUAAUAAGGGUGCUAAUUCCUCAAAAAUUUCCCUCCUCUUGAAAAAAAAGGAAACAAAGUCAAAUAUCUUAUUACCUUUAUUUUCCUUUUCCAGAAGAGGGAAAUUUUUGAGGAUUUUACCCCCUUAUGUU	131	sly-miR8050-3-5p	AAAAAGGAAACAAAGUCAAA	45-64	stu-miR8050-5p	5	0	20	20	1
sly-MIR7806	UGUGCCACAUCCAUCAUUGCUCUUGCAUACAUCUCUUAGAGAAGAUAGGUGGAUGCACCAGGUAUCCCUUCAAUUACAUAUCAUUUCUAUCUUCUCUAGGAGAUGUAUGCAAGAGCAAUGAUGGAUGUGGCGCC	134	sly-miR7806-3p	UAGGAGAUGUAUGCAAGAGCA	97-117	rgl-miR7806	5	0	21	21	1
sly-MIR5205a-2	AAUUACUCCCUUUGCCCCAUUUUAUGUGCCACCAUUUCCUUUUUGGUCAAUCCCAAAAAGAAUGUCACAUUUUCUUAUAUGGGUAAGUAUUUAAAGGUAUAACUUCUCUUUUACCCUUGUUGGUCACAGUUAAUUUUAAACAUAGUACUCUAAUAUAUUUAUGAGGAGAGUGAAAAGUGAGUUUAAUUUUUUGAAGGGAAAUUUGGUAAAACAUUUCAAAGUCUUCUUUUUUUCUUACACUCCGUGUCCGGUCAAAUAUUGCUACAUAAAAUGGGACGGAGGGAGUAUAA	290	sly-miR5205a-2-3p	UACAUAAAAUGGGACGGAGGGAG	263-285	mtr-miR5205a	5	0	23	23	2
sly-MIR396a-2	GACCCUAUCUGUAUCUUCCCACAGCUUUAUUGAACCGCAACAACAAUAUGAAUCAAUUUUUUCUUUUUCAAUAAUGAAUUGAAAUUGUAGAUGCAGUUCAAGAAAGCUGUGGAAAAACACAAAAAGGACC	130	sly-miR396a-2-5p	UCCCACAGCUUUAUUGAACCG	17-37	cas-miR396a	3	0	21	21	1
			sly-miR396a-2-3p	GUUCAAGAAAGCUGUGGAAAA	96-116	csi-miR396a-3p	1	0	21	21	2
sly-MIR2089	UCUGAUCUGUAUAGCAUGCAUUAAGGUUUGAUCGUACUUCUGCAAUAAGUAAAGAAAUGCUCAAAACCAAUAUCUUUUCUUUUUUGAGAUAAAAAAAAAAGUUAUAUUGGUUUUGAGCAUUUCUUUACCUAUUGCACAAGUACGAUCACAAUUUAGUAUGACGCUAUAAAGGUCUUC	177	sly-miR2089-3p	UUACCUAUUGCACAAGUACGAU	125-146	mtr-miR2089-5p	5	0	22	22	1
sly-MIR7997c-8	UGACAUAUAUGUUAUGUUGCUCGGACUCUUCAAAAAUGUUGUAACAUUCAUGUUAGAUCCUCUGAAAAUGCACAACUUUUGAAGAAUCUGACAUGUAUUGACGAUAUUUUUGAAGAGCUCGAGCAACAUAGCAUAGAGUGAAA	143	sly-miR7997c-8-5p	AUGUUGCUCGGACUCUUCAAAAAU	14-37	stu-miR7997c	1	0	24	24	1
sly-MIR5725-2	AACCGUCCAAAAACUAGAGCGUAUAUGCCCUUCAUUCUAACGGAAAGUUGUAUAGGGACAUGUGGCGCAAUCUUAUCUAUUGAUUCGAUGUCGGGUCUGUGGAUAAGAUUAUGACACAUGUAUAUCCAUUAGUAUAAAGGGUAUAUAUGCUCUAAUUUUUGGACGACA	168	sly-miR5725-2-5p	AUGUGGCGCAAUCUUAUCUAU	60-80	bra-miR5725	5	0	21	21	1
sly-MIR5558	UUCUAGAUUAUGAAAUAGAUAAGGGGUGUCAAAUAGGCGGGUGAACUGAAAAUUGAAAAUAUUAAAUCGAGUUGAGAUAGAAGUCGGGUUGGGUAUUGACCCACCCAAGUUUAAUUUGGGCUCGAAUGGACUUAAAAACGGGUUGGAUCUUGACCCGUCAAUUUGAUCCGAUUAAUCUCACUAAUCUAACA	191	sly-miR5558-5p	UAGAUUAUGAAAUAGAUAAGG	4-24	mtr-miR5558-3p	5	0	21	21	1
sly-MIR172j	UUUGCCGCUGCAGCAUCAUCAAGAUUCCCACACAUCGCCCGUAGGGUUUUUAAAAAUUAUAAAAGCCCUAAUAUAGCUAUGUGAAUCUUGAUGAUGCUCCACCCGCAAA	109	sly-miR172j-5p	GCAGCAUCAUCAAGAUUCCCA	10-30	lus-miR172j	0	0	21	21	1
			sly-miR172j-3p	UGAAUCUUGAUGAUGCUCCAC	82-102	mdm-miR172j	3	0	21	21	2
sly-MIR8034	CUAAGAGUCCGUUUGGAUUGGCUUAAAAAAGUAGACUUCCUUAAAUCAAAAAUAAAAAAUCAAACUUAAAUGACUUUUAAGCCAAAAAAAAAAAGAAGGUUGGUAGGGGAGACCUACUUUUGGUUUUUGGCUUAUUUUAAGUCAAUUUGUUACCUUGCCAAACACUUCCGAAUGAAUUUUAAGUCAUUUUUUUUACUUAUUG	289	sly-miR8034-3p	UUUGCCAAACACUUCCAAAACU	218-239	stu-miR8034	4	0	22	22	1

sly-MIR415	UAAGUUAUGUUUUAUAUUUGCCAAACACUUCCAAAACUUA GAAGUAGGUUUGAUGACAACUUUUAAGUCGAUCCGAACAC CCUCUAAG	273	sly-miR415-5p	UACAAAACAGAAACAGAAUAU	77-97	ath-miR415	4	0	21	21	2
sly-MIR3932b	UGUAAAUUGUAUAAUUAAGUGUAUAACAUGAAGAUAAAUGU UUUUGUAUGUGUAUAUACAAUUUUCUCUAGCUUUAUACAA AACAGAAACAGAAUAUAUACACUUCUGUGUAUAAAGCGAGA GAGGCGAGCAGAAGGAGGGUGGCGAGCGAGAUUUUUGAG AAAGAGGCGCCUGACAAACUUUGGCUAACGUUUGUUAUGG AGCAUAAUUAAAUCAAAUCUUAGCUACUCCAUUUAUUUUAG GUUAUUAAUUUGCUAUUAUUUACAAUUUUCU	179	sly-miR3932b-3p	UUUGACGUGCUUAAUCUGAAU	115-135	ath-miR3932b-5p	5	0	21	21	1
sly-MIR167b-3	UUAAAAAUGGGUUGAAUAGAAAUUAGGUUGGGUCAUGAUC CACCCAAGUUUACUUCAGGCUCAAAUAGGUUGGACUCGAA UGGGCUAAAUUUGGUUGGGUCAUGACCCACCCAAUUUGAC GUGCUUAAUCUGAAUAAUUUUAACAUAUUGUUAUCUAAUU UCUAUAACCACAAUUUGCA	122	sly-miR167b-3-5p	UGAAGCUGCCAGCAUGAUCUAA	22-43	bna-miR167b	0	0	22	22	1
	ACAUCGUGCAGCACUAGCAGUUGAAGCUGCCAGCAUGAUC UAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAU CAGAUCAUGUGGCAGCCUUACCUGUCAAUGCCAUCACGAA UU		sly-miR167b-3-3p	GAUCAUGUGGCAGCCUUACC	83-102	stu-miR167b-3p	2	0	20	20	1
sly-MIR11492	UAAGUCAGUCCACCUAAUUAAUAUAUAAUGUUAGUCGCGA GUGAAAAUUAUAGCAAACUAUAGCUAUGAUAAGUAAUUAAA UAGUAUAAAUUUGUUUUGUUGCGUAAUUUUUCCUCUAAUU UUGGGUCUGCUAAUUUUUGGGCCUUGUCCAUUAUUGGCC CAAAUAUGUUUUCCUUUUCCUAAUACAUUGGUUGGAGAUU UUUGGAAGAUAUUUUAGGGGAAAUCUUAAUAUCUUCUCAU UAAUUAUGGUGUCGUGACCAC	261	sly-miR11492-5p	UAGUAUAAAUUUGUUUUGUUG	82-102	pab-miR11492	5	0	21	21	1
sly-MIR11416-2	UUGCAAGUAAGCACUCCAACUUUAAAGGGUGCACAUCCAG ACAUCUCAACUGCCAACUAAACACUCCAACUUGUCUCACUU UGUCUCGUAGACACCUGAUGCUGAUGUGACACAAAUUUUG GAGGUGUCGAGAUGAUCAUUUUUGUCAGCUGGAGUGUUC AACUACCACAAUGGAGAUGAGUUGAGGUGUCUAGAUGUGC AUACUCAAAAGUUGGAGUGUUUUUUGUUU	229	sly-miR11416-2-3p	ACACAAAUUUUGGAGGUGUCG	110-130	pab-miR11416	5	0	21	21	1
sly-MIR5185k	AUCUUUAUUUGAAUGAGAUCUAGAAAUAGUCUAGUUCAUU UUUUAUUUUCAAAUUGAGAGCAAAAAGUAAAAGUGAAAGG GAAAAGUAUAUUGAGAGAAGGAGAGGUGGUCCUCCUAGAC UGGCUAGAUUUCAUCAAAUUAAUAC	145	sly-miR5185k-5p	GUCUAGUUCAUUUUUUAUUUU	29-49	bdi-miR5185k-5p	5	0	21	21	2
sly-MIR6447	UAUGAAGAGUUCUGACUUUUAUGAAAGGUUGUGACUUUUA UGAAAGGUUGCGACUUUUAUGAAAAGUUGCGACUUUUAUG AAAAGUUGUGACUUUUAUGGAAAGUUGUAACUUUUAUGAA AGAUGACGACUAUUCCGAAAGAAUUUAUGGACUUCUUCUU C	161	sly-miR6447-3p	UUUAUGAAAGAUGACGACUAU	113-133	ptc-miR6447	5	0	21	21	1
sly-MIR11314-1	GAAAUGAAGAGUUGCGACUUUUAUGAAGAGUUGUGACUUU UAUGAAAUGUUGCGACUUUUAUGAAAAGUUGUGACUUUUA UGAAAAGUUGUGACUUUUAUGAAAAGUUGCGACUUUUAUG AAAAGUUGUGACAUUUAUGAAAAGUUGCGACUUUUAUGAA AAGUUGUGACUUUUAUGGA	179	sly-miR11314-1-5p	AGAGUUGUGACUUUUAUGAAA	27-47	fve-miR11314	5	0	21	21	1
sly-MIR6440a	UAUUUCCAAAGUCCAUUGAGUUUGAUCGAUUUUGAGUUCU UAUGAGUGAGUUAUGCCCAUUGGAAGUUGGGUUGUUCGA UUAAGGAAAGUCCAAUUUGGAUUUUGGAAGGA	111	sly-miR6440a-5p	GAGUUUGAUCGAUUUUGAGUU	18-38	ptc-miR6440a	1	0	21	21	1
sly-MIR6451	ACCAUAUGUUCCCUAAAUAUGCAUGUAGACAUUGAAAUUU UGUGGGACUUUAUAAGAUGUCAAUUCAAGUUAGGACUAUA CAAAUUGUGUUCAACUCAAAUUAGGAUUCUUGGAGGCUAC UCAACCCUAAAUCCUAGUUUAUGCGUAUAUAAAUGGUACU AAAUUCUCUUAAAGACAUCUCAAAAGUUCCAUAAAGAGAUC AACAAUGUCUCAAAAUAUUCCACAAAAGUCAUGGAAUAUUC AUAUAGAGGUCAAAUAUAAA	262	sly-miR6451-5p	AUGUCAAUUCAAGUUAGGACU	57-77	ptc-miR6451	5	0	21	21	1
sly-MIR7983-3	AUAUUUUCAGCGGUAAUUAUCACUCUUUGUAUAUGUCCCU AAAGUCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAA UUUCGGUAAAGACUUUAGCACUCUUCAUUAGUGUUAAUAU UUAAUGCCGCAAAAAGU	137	sly-miR7983-3-5p	UAAAGUCUUUAGCGACAUUGGUUC	40-63	stu-miR7983-5p	0	0	24	24	1
			sly-miR7983-3-3p	ACUAAUUUCGGUAAAGACUUUAGC	76-99	stu-miR7983-3p	3	0	24	24	1
sly-MIR821b-1	UUCAAAUAGGAGCUUAAUGUUUGUAGUUUGAUUGAUCCGG UUUCAACCACUCAAAUUUUUAAGUUUCAAAUAGGAGCUUAA	282	sly-miR821b-1-5p	UACUUAUGAACAUCAAAGUUG	109-129	sbi-miR821b	3	0	21	21	2

sly-MIR1917-2	UGUUUGUAGUUUGAUUGAUCCGGUGUUUACUUAUGAACAUCAAAGUUGCGUAUUAAGCUAGCGUUUGGCCAUAGAUUUCCAAAUAUUCUUGGCAAAUAUUAUUUGAGUGAAAAUUUGGGUGAAAUUUCACCUGUGUUUGGCCAUAAAAUUUGGAGUGAGUGCAACAAGAAUUAUUCACUAAAUAUUUCAUCACUAUUUUGGUCUCUACAAUAAAAAUAACUUUUAGCGGCAAUAAAUAGAUACAUUAAUAAAGAGUGCUAAAGUCUUUACCGGCAUUAGUUAAGUGUCAUUAGAUCCAAUGUCGCUAAAGCCUUUAGUGACACAUACAAAGAGUGCUUAUUUAGCGGCAAUUGCUAAUUAAUUGCCGCUAAAGCUCAUUUUUAAUGUAGUGU	191	sly-miR1917-2-5p	AUUAAUAAAGAGUGCUAAAGU	43-63	sly-miR1917	0	0	21	21	1
sly-MIR12162	UGAUGAUGAAGAGAUUUCUUUUGAAAAUGUAUUUUUGGAUGACUGAGUCAGUCUCCAAGUGGGAGAACUGUUAGGUAGUGGAGCCUGAUUAAUUUUAGGUUUUCCUAUUUAUUCUCUAUUUUAGGCUUUCCUAUUUAUUCUCUAUUUUAGGUUUUCCUAUUUUAUUAUCUGUAACCAAAAAUACUCUGAUUUAUUAAUAUAAAUAUAUCUCACCACCG	217	sly-miR12162-3p	AAUACUCUGAUUUAUUAAUAU	179-199	aof-miR12162	5	0	21	21	3
sly-MIR7985	GGACUUCCAUGUUGGAGGUCUCAAGUUUGAAACCCCUUGUCAGUGAAAGCAAAGUGUUUGCCUUCUGGGUCGAGCUUGUCGCACCGGGCUUGCCUAGUGCGGGUUACCACUCCUAUGUGGUUGUGAGUUAUUGCAUAGGAGCGGGGGUUUUACCCUGUGCGCAUCCAAAGGGUAGCGG	178	sly-miR7985-3p	CGGGCUUGCCUAGUGCGGGUUACC	85-108	stu-miR7985	2	0	24	24	1
sly-MIR7805-1	AUUAUAAGUGUAUAGGAUGAAAAUAUAUGUACUUGUAUUUAUAUGUACAGUUUUCUCUCGCCUUAUACAAACACAAACAUAUUUUAUACAUUUGUGUUUGUGUAAAGUGAGAGAGGCGAGGGAGAGACCGGCAAGCGAGAAAUCUAGGGAGAGAGGCGAAUGACAAUUGUUUGGUACGGGUUACUAAAUCAAACUUUGAUUAUAACAUUUAAGUGAUUUGUUAUUUUAUACAUUUUCACCUUAUUUU	247	sly-miR7805-1-3p	UAUACAUUUUCACCUUAUUUU	227-247	rgl-miR7805-3p	5	0	21	22	1
sly-MIR8006-3	CUAAACAAAUGUGAACACAUCAUUGGUCCGAUGUCGGGUCGGUGGAUAAGAUUAUGACACGUGUAUAUCCGUUAGUAUAAAGGGUAUAUAUGCUCUAGUUUUUGGAUGACAGGGGCACCUAUGUCACAAAAGCAUGAUGGAGGGUAUUAUAAUACCAUUAAUGAUAGUUCGGGGGUAUAUUUGUCCUUUUUCCCUAUUUAUAACGAGUGAGUGCUCUUUACAUUUGUUACG	231	sly-miR8006-3-3p	UAGUUUUUGGAUGACAGGGGCACC	96-119	stu-miR8006-5p	1	0	24	24	1
sly-MIR11131	UACUUACGUCCAACAAAUGACCUAUUUGUUGCAAUAAAUAGGUCAUUUGUUGAACGAAAACUCAAUCAUUUGCUAUUGAUUUACUUACGUUCAACAAAUGAUCUAUUUGUUGCAACAAAUAGAUCAUUUGUUGGACGAAAUCU	143	sly-miR11131-3p	CUUACGUUCAACAAAUGAUC	84-103	lja-miR11131-3p	3	0	20	20	1
sly-MIR5014a-5	GACUUCAACUGACAAUUAUGAUAUUUAACUUUGAGUGUGUACAAGUAGACAAUUAAACUUGUAUAAAAUUGAACAAAUAGACACAUUCAUCCUACAUAGCACCCUACACGACAAUUGUGUAACCUACAUGGCAUCAUCCAUGUAUUAUGUCACGUAGAAUAUGUGUAUCUACUUGUUUAAUUUUGUACAAAUUUAAAUGUUUAAUUGUGCAUGCAUUUCCAAAGUUUAAGGACAUAGUUGUCAAUUGAAACC	252	sly-miR5014a-5-3p	UUGUACAAAUUUAAAUGUUUA	183-203	ath-miR5014a-3p	4	0	21	21	1
sly-MIR1053	GUCGUUAAAGAUAUGAGUGGACUCCUUAUAAGGCUUGGUCAAUUCUCUUCCUUUUGAGCUAGCUUUUGGAGUGUGAGUUAGACAUAAGAUCUAAUUUCACAUAGUCCACCCAUCUCUUUAACCAC	125	sly-miR1053-3p	AUCUAAUUUCACAUAGUCCACC	89-110	ppt-miR1053-3p	5	0	22	22	2
sly-MIR8006-4	CAUAUAUAUACUCUAGUUUUUGGAUUACAGAGACACCAAUGUCCCAAAAAUAUGACAGAGAGUAUUUACCUAUCAUUUACCAUAAUGACAAUUUUUUUGGUAAAACAAUAAACUCUACAAAAUGUAUAUUUUUAAGGAAAAAGGACAAAUAUAUCUCAAGCUAUCGUAAAUGGUAUGCAGAUACCCUCCGCCAUAUUUUUGGAACAUUAGUGCCCUGCCGUCCAAAAACUAGAGCAAUAUGCC	243	sly-miR8006-4-5p	UAGUUUUUGGAUUACAGAGACACC	14-37	stu-miR8006-5p	4	0	24	24	1
			sly-miR8006-4-3p	UGCCCUGCCGUCCAAAAACUAGA	211-233	stu-miR8006-3p	1	0	23	23	1
sly-MIR1533-2	UCUGUUUAUUAUGUUUGAAAUGUUGGGGUUUAGAUUGGUUGGUUCGCUCACAUAGUAGGAUAAGUGUGGGUGCCACUCGCGGCUCGUUUUGGGUCGUGACAGGUUGGUACUUGAAAAUUAUGGUAACAUAUCAUACUUUAUUUAGUGCAUUGUAUAAAUAAUAAUAACAAUAAAAUUAAAAAAUUAAUACAAACAUGCAGCUAGAAAUUGACAUAAAGUGUAGUCAUUUCUAGUAAAUAACAUAUUUAUAACUAAUAAACUUC	263	sly-miR1533-2-3p	AUAAUAAUAACAAUAAAAU	158-176	gma-miR1533	5	0	19	19	1
sly-MIR395a-7	UGUUUGAUGCCUUGCUGAAGUGUUUGGGGGAACUCUUGG	174	sly-miR395a-	UGAAGUGUUUGGGGGAACUCU	16-36	aof-miR395a	0	0	21	21	1

	ACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAGGA GUCCUGGCUAUGGAUGAUGAACAUGAUAGUUCAUGUAUAA AUCUAUUAAGGUGAUCCCUAGAGUUCACUUGACCACUUCA UGAGGGCUUAAUUU		7-5p							
sly-MIR482c-5	UAGGAAAUAGAAAGGGGAUGAGUGUUUCGAGGAGGUGUU GGAGUGGGUGGUGUGGUAAGAUUUCAUAUUUAUUUUCCA UAAAAAUUGAGAUCUUGCCAAUACCGCCCAUUCCUAUGGC UUCUGAUCAUUUCUCUCUUUCCUUUUUCUUC	149	sly-miR482c-5-3p	UCUUGCCAAUACCGCCCAUUCC	91-112	sly-miR482c	0	0	22	22	1
sly-MIR482b-1	UUUGGCGUGAGCGGUGGGGAAAGAUAGAUCUAUCAUAUUA GUAUGAUAUGAUAAAUCUUGCCUACACCGCCCAUGCCCAU UUGGGAAUCUUUUGGAGUGGGUGGGAUGGAAAAAUAUUG	80	sly-miR482b-1-3p	UCUUGCCUACACCGCCCAUGCC	56-77	sly-miR482b	0	0	22	22	1
sly-MIR482d-1	UAUUUUUUUUUCUAACGGAAAAAAAGAUGAGAAUUGAGAU UUUUCCUAUUCCACCCAUGCCAAUGGCUUCCAGU	113	sly-miR482d-1-5p	GGAGUGGGUGGGAUGGAAAAA	14-34	sly-miR482d-5p	0	0	21	21	1
			sly-miR482d-1-3p	UUUCCUAUUCCACCCAUGCCAA	81-102	sly-miR482d-3p	0	0	22	22	1
sly-MIR169r-5	UGCAGCCAAGGAUGACUUGCCGGACCAUAAAUUGCUAGGG UUUUAUAGUUUCGGCAAGUUGUUCUUGGCUAUA	73	sly-miR169r-5-5p	CAGCCAAGGAUGACUUGCCGG	3-23	csi-miR169r-5p	0	0	21	21	1
sly-MIR1044-1	UAUUUAACUUGGUCUCCAUUCACAUUUACACCCUCGAACU CUGGGUGUGGAUAAGUAGACAAUAGAACUUAGACACAUGA GUUCUACUUGACAUGGUACACAUAGGUCUCAAAUUGUUAU GUAGGACGUGUGUGUCUAUUUGUUCAACUUUAAAAAAAAA UUGAAGUGCCUACUUGUAUAAAUUCAAAAUUGGCGGGUGU AAGUGUUAAUUGAGUCCAAGUUAAAAG	227	sly-miR1044-1-3p	UUGAAGUGCCUACUUGUAUA	161-180	ppt-miR1044-3p	5	0	20	20	1
sly-MIR8001a-2	GUUCACUACAAGAAAACUGUGAAUUACAUGGGGAUUUUUC UGGGGAUUAGUAUGAAAAUUCGCAGAAAACUUAUAUUCCU GCAACUUUUCAUACUAAUUCCUAGAAAAAUCCCCAUGUAAU ACACAAUUUUCUUGUAGUGGUA	143	sly-miR8001a-2-5p	UUCUGGGGAUUAGUAUGAAAAUUC	38-61	stu-miR8001a	1	0	24	24	1
sly-MIR8001b-5	UCCCACUACAAGAAAACUGUGAAUUACAUGGGGAUUUUUC GAGGAAUUAGUAUGAAAAUUUGCAGGAAUAUAAGUUUUCU GCGAAUUUUCAUACUAAUCCCCAGAAAAAUGCCCAUAUAAU UCAUAGUUUUCUUGUAGUGCAC	143	sly-miR8001b-5-3p	GAAUUUUCAUACUAAUCCCCAGAA	83-106	stu-miR8001b-3p	3	0	24	24	1
sly-MIR6025c	GUUGAUGUUUGAACCAAGUGAUGUUGAAAAAUCAACGGAU AAGUUGUGGUUAGGGGUGAAAUGUCACUCUAACCCAGAGC UAGCUAGUUCUCCCUGAAAUGCUUUGUGGCACAUCAUUUG ACUAGACAUCUAG	133	sly-miR6025c-3p	UCAUUUGACUAGACAUCUAG	114-133	nta-miR6025c	4	0	20	21	1
sly-MIR4221-1	AUUAACAGUAAGUACCCCAAUGACACAUCCGAUUUCAACAA GAGAAGUUUGAAGGACAUGCAUUUAGUGUAAUCCAACUAU CCCUUGCACCUAACCUUCUUUGUGAAGUGAGUAAAAGUAC UGAAGAGGUGACCAAAUAACUUUGGGAAGGGAUGGAAGGA CUUUACUGGGACUAAUUGGUGACAAGAAGGAUGUUGUUUC AACAACGUCUUUACACAUUUAAGAUGUAGUCGGGUACUUU GUUGCA	247	sly-miR4221-1-3p	AAGUGAGUAAAAGUACUGAAGA	106-127	aly-miR4221	5	0	22	22	1
sly-MIR816	ACAUAUACAAUUGUAUGAUUCGCUGGCCUAAAUUAUAUAA UUCGCUGGUCUAUUUCGCUGCAAUUGUAUAAUUCGCUGAC CUAUUUCACUGCAAUUGUAUAAU	104	sly-miR816-3p	CUGACCUAUUUCACUGCAAU	76-95	osa-miR816	5	0	20	20	2
sly-MIR6218	UUGUUUCUAGGAAAAUCAGGAGACUUGUGUCCAGACUUUC CACAAGUCCAACAUUUAACUUCGUUAGAUGUGUUGUGAGA AAUUUUCUUACUUCUCUUUCCUUUUGAAAAUCCUUUUUCU UUUGAGGAUCUUCUCUUAGUUGUGGAUUUUCCAGAUUGU UCUUUCUUUGAAACCCUUUUUGCAGAAGGGGGUUUUAGAC UUGGGAAACCAAAGUCUUGAAAGAAUCUACCAAGUUCGUU ACUUGAAAAUU	250	sly-miR6218-5p	GGAAAAUCAGGAGACUUGUGU	10-30	sbi-miR6218-5p	5	0	21	21	2
sly-MIR9760	UCUUUCUCUCAUGAAAUUGAUGAGAAAUUGGAGGAUUUAG UAUUGACUGUUGAGGAUGAUUUGGGGAUGAAGAUGGUUG GAUGGGUCAUCCUCUCAUGAAAUUCAUGAGAAAUUG	115	sly-miR9760-5p	UGGAGGAUUUAGUAUUGACUG	29-49	gma-miR9760	4	0	21	21	1
sly-MIR6116	CGCCUCUGUGUGCAUUCAACAUUAGAGGAUUCAUCAUUAU UGUUAGAAAAUGAUGGAUCCUCUAAUACUAAAUUCACAUCA GAGAUU	87	sly-miR6116-3p	CAUUAUUGUUAGAAAAUGAUG	35-55	cca-miR6116-5p	5	0	21	21	1
sly-MIR10532-8	GCUCUAUACCCGAAAUUUCAGAGACACACUUAUAUUAUAC UAAGGUCACUUUUUUCGGUCUACGUGACACUAGCUUGAAA AAAUGUCAAAACGCGCUGAGCCCAGAAAAUAGUGUCACGU GGCCAAAAACGGGUAGAAAAUUCUUUUUAUAAAAUAAGUUA UGGAGAGUAAUAAGACCUUAGUAUAAUAUAAGUGUGUCUC UGAGAUUUCGAGCAUAGCUU	221	sly-miR10532-8-3p	AAGUGUGUCUCUGAGAUUUCGAGC	191-214	sly-miR10532	1	0	24	24	1
sly-MIR11078d	AAGUGCUAUUCUUAUUUUUGCUUAUCUGGAGUUACAAGUU GAGGAUCUUAUUGGUUAACGAUAGUUAUUAUCCCACUGUA	147	sly-miR11078d-	GGAUCUUAUUGGUUAACGAU	43-62	lja-miR11078d-	5	0	20	20	3

	AUAAAUACUUCUAACCAUGAAGAUCCUCAACUUGUCGCUU		5p			3p					
sly-MIR7983-4	CAGAUAAGAAAAUUAGUCAUUGCAUGG GAAUAGUCACUACAUCAAAAAUGAUCAUUAGCGGCAGUUA AUUUUUAAUUGCUGCAAAAUAUAUAUUUUUAGCGCCAAUU AACACUCUUUGUAUAUGUUCCUAAAGCUUUUAGCGAAAUU GAUUCUAAUGGCACUUAACUAAUGCCGGUAAAGACUUUAA CACUCUUUAUUAAUGUCAAUUUUUAAUGCCGCUAAAAGUU GUUUUUGUUGUAGUGAGUACAC	222	sly-miR7983-4-3p	ACUAAUGCCGGUAAAGACUUUAAC	138-161	stu-miR7983-3p	0	0	24	24	1
sly-MIR5083	UCACAAGGAUAUCAACAAUUACUGCAAUUCUCUGAUCAAG CAACGUGGAGAAAAAACUUAUCAAGCAACGUGGAUACAACA UCCAUCCAACAGAUUAGUUUUUCUCCACGUUGCUUGAUCA GAGAAUUGCAAUAAUUUUUGAUAUCCUUGUGA	153	sly-miR5083-5p	UUACUGCAAUUCUCUGAUCA	19-38	osa-miR5083	4	0	20	20	3
sly-MIR5670b	UACUAUAAAACUCUCUCAGACCGUCCUCUAAGCAUAUAAU GUCAUAUUGGCUUCAAAGAGACCACUGAAAAUCUUUUGCA ACCAUAAAGAGAAAUAUAUAUAUAUAUAUAUAUACGCUU AGAGGACGGUCUGAGAGAGUUUUAUACAA	150	sly-miR5670b-5p	CAUAUAAUGUCAUAUUGGCUUC	33-54	gma-miR5670b	5	0	22	22	1
sly-MIR171a-8	CUAUGAAACAGUAACUUUGAUAUUGGCCUGGUUCACUCAG ACAACAAAAUGUAAACUAUAUUUGAAUGGUUGAGUUUUCG UUUUUCGUUUGAUUGAGCCGUGCCAAUAUCUCAGUUUCUC UUUCACUU	128	sly-miR171a-8-5p	UAUUGGCCUGGUUCACUCAGA	21-41	cas-miR171a-5p	0	0	21	21	1
			sly-miR171a-8-3p	UGAUUGAGCCGUGCCAAUAUC	90-110	aof-miR171a	0	0	21	21	1
sly-MIR162b-2	UCCUUAGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGAC CGAUUCCUUUUGCUGUAUUUUUGCGUAUAUAUAUUCAG CUUCCAGGGAACGGAUCGAUGAACCGCUGCCUCCAGUGU CUUCAACCAACUAAACA	135	sly-miR162b-2-5p	UGGAUGCAGAGGUUUAUCGACC	19-40	ath-miR162b-5p	4	0	22	22	1
			sly-miR162b-2-3p	AUCGAUGAACCGCUGCCUCC	94-113	cas-miR162b	0	0	20	20	1
sly-MIR6281-1	UGUGUUUGUACUCCCUCUAUCCCUACUUACUUGUCCAUAU UUUCUCUUUUAAAUGUCCCCAUUUGCUUGUCCAUUUUGAC AAAUUAAGAAAGGAAAAAAUUGUUUUUCCUAUUAUACCCUC AUUUAAACUUAUUGAAAAUUUCUAAGUUUUAAUUCAUCCUU UCUGAAACCAUAUUUAAUAAAGGUAAAACUGUAAUUACUAU GUUAAUUAUUGUUAUCUUAAGAUGUGUCCCUUUUCUAAAG UGGACAACUAAAUAGGGACAGAUGGAGUAUUAAGUGAGAG AGAGAGAGAGUGACGAACAAG	304	sly-miR6281-1-3p	GUGAGAGAGAGAGAGAGUGAC	277-297	ppe-miR6281	3	0	21	21	1
sly-MIR5026-3	AUGCCAUCCAAAAACUAGAGCAUAUAUAUCUUUUAUACUAA CAAGCAUACACGUGCCAUAAUCUUAUCCACCGAUUCGAUA UUUAUCGAUUGAUAAAAUUGUGUCACGUGUCCGUAUUUAG UCUUCCGUUAGAGUGAAGGGCAUAUAUACUCUAGUUUAUG AAUGGAAA	169	sly-miR5026-3-3p	AUUGAUAAAAUUGUGUCACGU	89-109	ath-miR5026	5	0	21	21	1
sly-MIR8001b-6	CAUGGGGAUUAGUAUGAAAAUUCGCAGGGAACUUAUUUUU CUGCAAAUUUUCAUACUAAUCCCCGAA	67	sly-miR8001b-6-5p	AUGGGGAUUAGUAUGAAAAUUCGC	2-25	stu-miR8001b-5p	1	0	24	24	1
sly-MIR10538-3	ACUAGUAUAAACGUAUUUCACAGUAACGUUUUAGUGUAUA UUUCAUUUUUUAGAAGUUGACCGCGUUAGAUUGAUAUACG UUACUGUGAGCAACGUUUUACUCUU	105	sly-miR10538-3-3p	AGAUUGAUAUACGUUACUGUGAGC	68-91	sly-miR10538	4	0	24	24	1
sly-MIR5543	UUUUUGGGUGUCCCUGCUGUUAAAAAAUUAGAGCAUAUAU GUUCUUCACUCUACGGGAGACUAAAUAGGAACAUGUGGCA CAAUCUUAUUCGUUGAUCCGAUAUUUAAUAAAUGUCAGGU CGGUGGAUAAGAUUAUGAUACGUGUAUGUCCGUUAGUAUA AAUGGUAUAUUUGCUCUAGUUUUUUUUUACGGUAGGAUCA CCAAUGU	207	sly-miR5543-3p	UAUAAAUGGUAUAUUUGCUCU	157-177	osa-miR5543	4	0	21	21	1
sly-MIR2680e	UUCGGAAACAAAAAAAAUUGAAAAAUAAGUUACCUUGUCGA AAUGACUGGGAUCAGAUUUUUGCUUGAGGCUGUUCAUUCC CUCGAUGACAAUGUUGAUCUCAGUCAUUUCGACAAGGUAA CUUAUUUUUCGAAUUUUUUUUGUUUCCGAA	151	sly-miR2680e-3p	CCCUCGAUGACAAUGUUGAU	80-99	mtr-miR2680e	5	0	20	20	2
sly-MIR7508	GUAAGAUUAUAUAUAUGAAAUAAAAGUUUGUUUAUAUAUCA AUAUUUUUCAAACUUGAUAAGUAGUUCAAAGUGGAAGUUG CGAUUUCCAGCCUUUAGGAGGAAUAGCGAGAAAAGUAGCC GUAAGAGUGAAGAAGGCGAAAAAAGCUAUUCAUGGCCUAA GAGGAGAAAUGCUGAGGCAUUGAUAAGACUAAUUAUCAAC UAGAGGAAGAAGGUAUAAAAAACUAUCUUUUAUUAAGUAUA UUAUAAUCUUAU	254	sly-miR7508-3p	CGAGAAAAGUAGCCGUAAGAG	108-128	ghr-miR7508	5	0	21	21	1
sly-MIR7981-14	AAUUCUAGAGACACCUUAAUUAUUCUAAGGUCCUAUUACC CCCCCCCUCCUUAACUCUUUUUUUUAAAAUUUUGUGCACC	239	sly-miR7981-14-5p	CUUAAUUAUUCUAAGGUCCUAUUA	15-38	stu-miR7981-5p	4	0	24	24	2

	UUUUUGGCUUACGUGGCAUCCAAAUAUCUCCCACGCGCCU CAAUUGUGUGGAGUCACAAAGUGUGUCAUGUAAGACAAAA GGUGUAAAAUUACAAAAAAAAAUUAAUAAGUUCAGGGGGU UAAUAGGACCUUAGUUUAGUUAAGGUAUGUCUCUGAUAU		sly-miR7981-14-3p	AUAGGACCUUAGUUUAGUUAAGGU	203-226	stu-miR7981-3p	1	0	24	24	1
sly-MIR1106-3	CACCCCCUGAACUAUUUAAAACUGUAUUUUAAAGGUAUAUA UGUGUCCACGUGGACACAUUACUAUUCAUAAUUAUGCAAU AUCUUUGAUGUCCACAUGCGCACAUAUAUACCUUUAAAAU ACACUAUUAAAUAAUGCUGGGGUAA	146	sly-miR1106-3-5p	UUUAAAGGUAUAUAUGUGUCC	28-48	smo-miR1106	5	0	21	21	1
sly-MIR7993d-2	GUGUAUUCUCAAGUGCUCAUACGUAGAUAAGCUAACCACA UAGAUUAUGUACUUUAAUUAUUCACAUCAGACUAAACUGG AACAUGCUUGAGCCUUUACUUGAUGUGUAUAACUAAAGGA GGUGACAUAUUUUUAGUGGUUAACUUAUCUAGGUAACGGA UACUUGAGAAUAUGU	175	sly-miR7993d-2-3p	AUAUUUUUAGUGGUUAACUUAUCU	127-150	stu-miR7993d	3	0	24	24	1
sly-MIR5049b	AACAUUUCAGUUGAUCUUGAUCCCAUUUACUCCCUCUCCC UUUGCCGGACAAUAGUUGUCCACUAUUGACUUGGUACAGG GAUUAAGAAGCAGUAAAUGAUAGGGGUAAUUUUACCAAAU CACCCUUAUUAAAAGUAAGUCACAUAAACAUCGAAAAAUAA AUAGUAUUUAAUAGCAAGGUAAAAACGACACAACAUGCUAA AUGACUCAUUGAUUUAAUAAACUGGACAAGUAUUGUUGGA CGUCUCAAAAUAGUAUAGUGGACAAGUAAAGAUGGACAGA GGGAGAGGGAGUAGCUUAGACUCAUAGCAGCAAAGAAAUU AU	324	sly-miR5049b-3p	AGUAAAGAUGGACAGAGGGAG	267-287	hvu-miR5049b	5	0	21	21	1
sly-MIR7502c-2	UCCUAAUAUGAUAAUAACCUUGAAUCAAUAAUUCAAAUUCA AGUUAGAUUGAAGAGUUAAAUUUUGAGAAUUCUUUCCAAA AUUCUAAGAAAGUCCCUUUUGACACAUUCGAGAGUUCGAG UUAGCUAUGGUGAGUCUCCUUGCUUCCAUAGGAUUUCAUU UACUUUUCAGUUUAGUCAGGAUCUCAUGGGUCGUAUCCCG ACUUCCAUAUUUCUCUGUUAGAGGCUUCAUCGAUUGUUAG UAUAGUUGAGGAGUUUGUAUUAAUCUUUUAAUUUAUUAAA UGUUAUAA	289	sly-miR7502c-2-3p	CUGUUAGAGGCUUCAUCGAUU	216-236	gra-miR7502c	5	0	21	21	2
sly-MIR7997b-2	AUGGCAUGCUGCUCGGACUCUUCAAAAAUGUUGCUAGGUC UGUGUUGGAUCCUCCAAAAGUAGUGCAUAUUUGAAGGAUC CGACAUGAGUGCGGCAACAUUGUUGGAGAGUCUGAGCAAC AUAGCAGA	128	sly-miR7997b-2-5p	AUGCUGCUCGGACUCUUCAAA	6-26	stu-miR7997b	0	0	21	21	1
sly-MIR10532-9	UACGUUCGGAGGUGUAAUAGGACCUUAGUAUAGUAUAAGU GUGUCUCUAAGAUUUCGGGCAUUAGAUUGAGGGGUUACU UGUGCAUUAUCCCUAAAAAUUAAUAGAGAAAAUGCACAAAU ACUCCCCUACAAUAUGAUCAAAAUCCCAGAGACACACCUUA ACUAAAGUAAGGUCCUAUUACCCCCAUGAACUUU	195	sly-miR10532-9-5p	AAGUGUGUCUCUAAGAUUUCGGGC	37-60	sly-miR10532	1	0	24	24	1
sly-MIR7984c-4	CCCACUCACCAUUUAAAGGUAUAUAUGUGUCCACGUGGAC AUAUAGAAUAUUUCAUAAUUAUAAAUAGUAAUGUUUCCAUG UGGGCACAUAAAAUACAUUAUUAAAUAGUUCAAGGGGAGG GGGUAAAAGGUUCUCCGUAAAGUCUGAUAUCGUAACAACA AUUUCGGCUAAAGUUAAAAUAUUUCUCAAGACUUUUUUUC CUUUUAUUUUUAUAUUCUUCAAAUUUGUUGUAUGGGACAA AGUGUUAGACAGUCAAGACUCUAAGUGGUGAAGUACU	278	sly-miR7984c-4-3p	UCUCCGUAAAGUCUGAUAUCGUAA	133-156	stu-miR7984c-3p	5	0	24	24	2
sly-MIR7992-5	GCAUAAUAUAUAGAUAGACACCUUAAAUUGGCCUUAACGA GCAAGUAAAGACCCAAACUAACACGGGGCCAACUUAAACCA AGUUCAUGUGUCUAGAUGUGCAUUCUCAAAGUGUAGGUCU UUACAUGUCAGUUAAGUCCAAGUUAAGGUGUCUAUCUACG UGUUACAA	169	sly-miR7992-5-3p	UGUCUAGAUGUGCAUUCUCAAAG	90-112	stu-miR7992-3p	5	0	23	23	1
sly-MIR8005c	UGUACCUUACAAAUCAAAAUCUUCUUUUUAAACUCAUUCAA AUUCUCAUCCUCAAAUUGGUUGGCCUUGAUCUCUUUAAUG AAUUUGGCCCUCAAUUCAAUACUAGAUAGUUUUAGGUUUA GGGUUUAGGAUUUAGGGUUUGGAUAUAGGGUUUAGAGUU UAGGGUUUUGAGUUUAGGGUUUU	183	sly-miR8005c-3p	UUUAGAGUUUAGGGUUUUGAGUUU	152-175	stu-miR8005c	2	0	24	24	1
sly-MIR6235	AAAUAUAAGUAUGUAGUUGAAAAUCAUAUAAUUAAAGCUGU UAAAAUGGGUCGGUCCAACUCAACCCAAUCCUAACGGGCU AGAGAGUUAAAUGGGUUGGGACGGGCUGAUCCUUUUAAU UAAAGGACCUGUAAAAUAGCAAUCCAACCAAGCCCUAAGC GGGCCACGGGUUGGGAUGGGUUGACCCUUCAACGAAAAA CGGACAACAUUUUUCUCUUUGAAAGAACACGAACGUUGAU GAAUUACACAUACUUUAGUGAAUAUUUACAAAAUAAAUACA UAAUAGCC	288	sly-miR6235-3p	AACGGACAACAUUUUUCUCUUUGA	198-221	sbi-miR6235-3p	5	0	24	24	1

sly-MIR8007b-2	AUGCUAACAUGAUACUCCCUCUGUCCCAUUUUAUGUGACACUUUUUGUUUUUCGAGAGUCAAACGAUUUAACUUUGAUCAGACAUUUGCGCAUGGAAUCUUCAAUUUUUUUUUUGAAAUGAAAUUUAUAUAUUUGUAACUACGUAAAGAGUUACUAAUGAGUCACAGUAAUUGAUAAUUCAAAAUGUUAAAAGGAUCUAUGAAAAACUUACGGUCAAAAAUAGACUUAUUUAAAUCUCGAAAUGCGAAAAGUGCAACGUAAAAUGGGACGGAGGGAGUAUUUAUUUAGUCG	291	sly-miR8007b-2-5p	AUGUGACACUUUUUGUUUUUCGAG	33-56	stu-miR8007b-5p	2	0	24	24	1
sly-MIR156g	GUGUCAAUAACAGCUGUGAAGGAAUAUCUGGGCCCAAAGAUGUAUUGACAUAGCUUUCUCUUUUUUUGUGUCAGUACAUCUUUGGGCCCAGACAUAUUCCUUCAUAGCUGUCAUGAUUAAAUUACUCCCUCCGUCCCAAUUUAAGUGUUUUAGUUCGAU	119	sly-miR156g-3p	GCUUUCUCUUUUUUUGUGUCA	53-73	aly-miR156g-3p	5	0	21	21	1
sly-MIR1128-3	UGGACACAAAGUUUAAGAAAUAAAGGGAGACUUUGAAUCUUGUGGUCUUCAAUUAAAGAUGUGUGUAGUCCUUUAAAUCUUGUGGUCUCAAAACUUUCCAUGUAUAAUGUUGGAAUUGGAGAACUUAUUAAAUAUUGAAAGAGGCAGUCUUGCUGGGACAGACUAAAUGGGAAGACACUUAAAUUGGGAUGGAGGGAGUAGUA	243	sly-miR1128-3-5p	AAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	3	0	21	21	2
sly-MIR9471b	UUGAGAUUCAGUUGAUUUCUGAGGUGCUCACUCAGCUAAUAGUUAUUGUUUAAGAAACUCAAUAAUAUUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUGAGUGAGCAUCACUGAAAUCGACAUGAUUCUGAG	147	sly-miR9471b-5p	GAGGUGCUCACUCAGCUAAUA	21-41	sly-miR9471b-5p	0	0	21	21	1
			sly-miR9471b-3p	UUGGCUGAGUGAGCAUCACUG	108-128	sly-miR9471b-3p	0	0	21	21	1
sly-MIR9471a-2	GGUUCUGAGAUUUAGUUGAUUUCUCUGGUGCUUACUCAACUAAUAGUUAUUAUUUAAGAAAAUCAAUAAUAUUGGAAGCAAGGAGAAUGGAGACUAUCAGGAUGAUAACUAUUGGUUGAGCAGCAUUAGAGAAAUUGACAUGAUUCUGAGAGGA	154	sly-miR9471a-2-5p	CUGGUGCUUACUCAACUAAUA	25-45	sly-miR9471a-5p	3	0	21	21	1
sly-MIR773b-1	UGCUUAACCUCAAGUCAGUUUUCUUUUCUCCUAUAGCCUGUUUGACCAAACUUCUAAAAUCAGCUUAUUUUGAAGAGUGCUUCUGGAAAAAAGAAGUAACACUUUUGGCCUUCCAAAACUUGGGCAAACAGGCUGUUAAAGUGUUUUCACAGCAUUUUGCUCUUGUGUGAUAUGGAAAUCACUUGGGUUAAAUC	194	sly-miR773b-1-3p	UUCCAAAACUUGGGCAAACA	111-130	ath-miR773b-5p	5	0	20	20	3
sly-MIR3951b-1	UAAGUACAAUGUCUCGCUAUUUCUUUUAUUUUUUAUCUAACAAUAAUUAGUUUCACCCCAGGGGAUCUUGUUGUCCCUAUAAAGGGGUAGUAGUUAUUGUUGUUGUGGUGUAUGAGCAUGAAAUCUUUAUAUCAACCUUAAGUAGGAAAGCUUAAAGAACUCAAGUGAGCAUUGUGACAUG	181	sly-miR3951b-1-5p	UUUCUUUUAUUUUUUAUCUAAC	20-41	csi-miR3951b-3p	5	0	22	22	1
sly-MIR2928	GGCGAAUGAGUGUUUUAAUUUAACACUUAAAGUGUGCAAUCAGAAGUUGAAAAAUAAUUCUUCGUCAUUUAAGUUCAGCUAGUUUCAUAUAGCAUUACAGGUAUGAUUUUAUGAGUGUUGUCAUCCACUUGACAUUACAAUUGCUAUCCAUGAUUCAGAUCGCACACUGCGUAUUCUGAACUGGAAGACAAAAAAUGACGUUAUUUUGUUGACGAUUUGAAGAAAAUGAUUUUCAGAACACAUGGAAAUCACGUAGUUUUUUAUUGAAUUUUAUUUAAGUAACUAUAAAUUAUAACACAUUCUCA	305	sly-miR2928-3p	AAAAUGACGUUAUUUUGUUG	192-211	osa-miR2928	4	0	20	20	1
sly-MIR8051	AAUGCAAAUUUCUUCUGCCAUACUAUUGGGGCAAUGAUACCCCUGCUAUAUAAAAGCUAGAGCAUAUACACCCUCUACUUUAACAGAAGACUAAUAGGGAUACAUAACACAAUCUUAUCUGUCAUCAGAUAUUUAAUUAGUGGAUAAAAUUACGACAAUAUAUAUCCGUUAGUAUAAAGGACGUAUAUGCUUUAGUUUUUGGACGGCAUGAACAUCAAUGUUCAAAAAAUAUGACGAAAAAUAUUUGCUCA	251	sly-miR8051-5p	AAUUUCUUCUGCCAUACUAUU	7-27	stu-miR8051-3p	2	0	21	21	2
sly-MIR11314-2	GAGUUGUGACUCUUAUGAAAUGUUACGACUUUUAUGAAAAGUUGUGAAUUUUAUGAAAAUUUGCGACUUUUAUGAAAAGUUGUGUCUUUUAUGGAAAGUUCUGACUUUUAUGAAAGGUGAUGACCUUUCCGAAAGAUUGUGACUUUUCCAAAGGUUUGUGACAUUUCCGGUAAGGCACAAUAA	183	sly-miR11314-2-5p	AAAGUUGUGAAUUUUAUGAAA	38-58	fve-miR11314	5	0	21	21	1
sly-MIR8030-1	AACUGAUUUGUGGUUUGGUUUGACUUGAUUUGGUAUUGAAAUAGAACCCAAGUAUGCCUUGUUGAUUUUGUUUCAACUAAAAAAGAAGUCAAAAUGAGACCAAAUCAACC	110	sly-miR8030-1-3p	AUGAGACCAAAUCAACC	94-110	stu-miR8030-3p	3	0	17	22	2
sly-MIR9555b	GUGCCCUUUCACUUGACUUUAAAUCACAUUUAUGCUCUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACUUAUAUAAAGUUGAAAAAAUAGACACAUCUGUCCUAAAUUUUUUUUUGUCCUACGUGGUGUCCUACAUUUAUUGUGCCAUGUAGUGCU	260	sly-miR9555b-5p	AUAGACACUUAAACUUAUAUA	59-79	bra-miR9555b-3p	5	0	21	21	2

sly-MIR167h-2	CAUGUGUAUAUUUAUUUAAAAGUUAGAUAGUUGAAGUGUUUCUCUGUGCAUUAAUAAGGUUGGAGGUUAAGGUUAAAAUUUGAAGCCAAGUGUAGGGUAA	113	sly-miR167h-2-3p	AUCAUGCUGGCAGCUUCAACUGCU	76-99	gma-miR167h	1	0	24	24	1
sly-MIR167h-3	UUCCGCGAAACCAUCAACAGGUGAUGCUGCCACAUGAUCUGAUCUUUCCUCGUACGGAGCAAUAGAAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGGUUCACGAUC	119	sly-miR167h-3-3p	AUCAUGCUGGCAGCUUCACUUGUU	83-106	gma-miR167h	3	0	24	24	1
sly-MIR7711	UUAUCAAGAAAGGAAGGAGUGAGGCUGUCCGAGCAUGACCUAACCUUAGUCACCCAUUUUCUUUAUAAAUGGCCAAGUUUAGAUCAUGCUGGCAGCUUCACUUGUUCCACUCUAGACCC	109	sly-miR7711-3p	UAGAUAGAGUAUCUAAAUA	91-109	bdi-miR7711-5p-2	5	0	19	24	3
sly-MIR5569	AAAUUAGACACUCCCAACUAGGCUUUAUUUAUUUUAGUGUCAAUGAUACAACGGAACAUGACCUGAGGUGUUUAAAAUGAACAAAAAGUCUAGAUAGAGUAUCUAAAUA	99	sly-miR5569-3p	UAUUGCAUGCUUGAAUUAUGGAGG	57-80	sbi-miR5569	4	0	24	24	1
sly-MIR7983-5	CCUAUGGACCGUAGGUGGCCUCCGUAGUUUGUGAUUGAGGCUGAGUUUUGCCUUCCUAUUGCAUGCUUGAAUUAUGGAGGGAAGACCUAAGGUGCAUCAU	265	sly-miR7983-5-5p	UAAAGUCUUUAUCGGCAUCAGUUA	87-110	stu-miR7983-5p	5	0	24	24	1
sly-MIR11472	AAACAUGUGUUCGUCAUUAAAGGAUAAAAUCACUACAAUAAAAACAAUUUUUAGCGGCAUUAAAUAUUGACACUAACAAAGAAUGCUAAAGUCUUUAUCGGCAUCAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUACAAAGAGUGACAAUUGCUGCUAAAAAUAAAUAUUUAGCAGCAAUUAAGAAUUAAAUGCCGCUAAUUAUCACUUUUGUUGUAGUGAAUGAGUCAUAAUCGAGAAAGAUGAAU	70	sly-miR11472-3p	CUCUUGUCACGUUUCUUGGUA	44-64	pab-miR11472	5	0	21	21	1
sly-MIR11074	UCUACCAACAAGAGAAGGGUUACAAGAAGGUUCUCUUACCUUGCUCUUGUCACGUUUCUUGGUAGGUUCC	121	sly-miR11074-3p	GGGUUGGGUUGAUUUCAA	104-121	lja-miR11074-5p	3	0	18	19	1
sly-MIR7990a-4	CGAAAAUUAAACUAAACCGCAAAUCUAGUCAAAUAAAAAAAACCCUGACUAGUGGUUUGGUUUGACUUGAUUUGGUGUUGGAAAAAAAAAUCCGACUAUAUUUGGGUUGGGUUGAUUUCAA	219	sly-miR7990a-4-3p	UUCAAAUGAUCGUAACUUUUGCCU	128-151	stu-miR7990a	1	0	24	24	1
sly-MIR6273-1	UGUUUUUCCGCGUAGAACAUGAAAAAAUAACUAGGUUGAAAUAAAAUAUUGCCUCAAUCGGACAUUCGAGGCAAGAUUUAUGACCGUUUGAAUUUCACAAAUUUACAACUACUUCAUUUGGUGAAACUUCAAAUGAUCGUAACUUUUGCCUCGAAUAUACGUUGGAGGCGAUUCUUUUUUUAAACUUUCUUAUUUUUUUAAGAUCUACGUGGUAAACUU	178	sly-miR6273-1-3p	AAUGUAGCAGGAUUUUAUUCU	73-93	ppe-miR6273	4	0	21	21	1
sly-MIR8007a	UGUCGUAAUUGAUAGUCACGAUUUAAUGCAGAAAUGUGAUCAGCGAUAACGUUUUAUGAUCUGUAAGAUUCCAAUGUAGCAGGAUUUUAUUCUUAAUCUGGUGCCCCGUGAUUAAAUAAACAUAAAACGUGAUUGACAGUUAUGUUUUAUAUAAUAAACGUGAUUGUCAGUUACGGUU	146	sly-miR8007a-5p	CGAAAAAUGAAAAGUGACACAUAA	1-24	stu-miR8007a-3p	1	0	24	24	1
sly-MIR8006-5	CGAAAAAUGAAAAGUGACACAUAAAAUGGGACAGAGGGAGUAACAAUUUACUCCCUCCAAUUGAAAAGGAAUGUCCCUAUUUCGUUUUUAGUUCGUUCAAAAAAGAAUGACCUCUUUCCUUUUUAGGCAAUACUUUUAACUUUAAU	232	sly-miR8006-5-5p	CCCCCUGUCGUCCAAAAACUAGA	28-50	stu-miR8006-3p	4	0	23	23	3
	CCUCUAUCAUACUUUUGAGACAUUGAUCCCCCUGUCGUCCAAAAACUAGAGUAUAUAUAUACCCUUUAUAAUAACGGACAUAAAUGUAUCAUAAUAUUAUCCACUGAUCCGAUAUUUAUUGACGCAUAAGAUUGUGUCACGUGUCCCUAGUUAGUGUUUCGUUAGACUGAAGGGCAUAUCUGCUUUAGUUUUUGGACGGCAGGGGCACCAAUAUCCCAAAAGUAUGAAGCAU		sly-miR8006-5-3p	UAGUUUUUGGACGGCAGGGGCACC	186-209	stu-miR8006-5p	1	0	24	24	1
sly-MIR5174d-1	UCCCUCCGUUUCAAAAAGAUUGGCCUAGUUUGACUUGGAACGGAGCUUAAGAAAAGAAAGAGGACUUUUUAAUCUUAUGGUUCUAAUUUAAAGUUAUGUUUAAUGUACCAAAUUACCCUUUAAUCUUGUGGUCUUAAACAUGCCACGUGGAAAGUUAAAGUUAAAGUGUUACCAAAAAAGGAAAGGGGUCAUUCUUUUUGAAACAAACUAAAAAGGAAAUAGGGUCAUUCUUUUUGAAACGGGAGUAU	248	sly-miR5174d-1-5p	UCCCUCCGUUUCAAAAAGAUUGGC	1-24	bdi-miR5174d-5p	1	0	24	24	1
sly-MIR7842	CCGGUGUCACAAAUACAUGUAAAUCAAUCCAGAUACAUGUACCUAGUGUAUAUCUGGUGUGAUUCACAUGUAUUCGAGAUACAAA	85	sly-miR7842-5p	UAAAUCAAUCCAGAUACAUGU	20-40	ptc-miR7842	5	0	21	21	1
sly-MIR9470-2	CGGAAUCGAUAAGCCGAACCGAUAAAAAAGUUAUUGGUUUAUAGUAUUGGGUUAUUGAUUUAGUGGUUUUGAUAAUGGUUUUGACUUUUUUUUUGUUAUCGGCUUAUCGAUUUUU	115	sly-miR9470-2-3p	AUCGGCUUAUCGAUUUUU	98-115	sly-miR9470-3p	5	0	18	20	2
sly-MIR8021-1	AUUCAAGGCUCAAACUCGAGACCUCUGGUUAAGGAUAGAU	218	sly-miR8021-	AUUCAAGGCUCAAACUCGAGACCU	1-24	stu-miR8021	0	0	24	24	1

	AUGUCAUAUACAUCCCUUCAUAACUAUUGUUGGUUCUAAU		1-5p								
	AAUAACUUAAUUCACUCUCUCUUGUAUAUACGCAAUAUGAU										
	AGAAUUAAGUUAUUGAGUUCUACCAACAAUAUUGUUUUGG										
	AGAAGAAGUUAAUAUUACUUUAUCCUUAAUCAGAAGUGUC										
	AAGUUUGAGUCUUGGGU										
	UUGCAUUUGAAAGAUAUAGUUUUUAUGAUAUUGGAUACUU										
	GAAUCAUCUUCGUACCUUUGGUUCUGAUUCUUAUGAAAAC										
	AAAAAUGGAACCAGUGUUGAAGAUGGAACUAGUGUUGAAG										
	AUGAAACUAGUGUUGAAGAUGGAACUACUGCAAAUAUUCU		sly-miR11068e-3p			lja-miR11068e-3p					
sly-MIR11068e	UUCAAGUGUUG	171		AUGAAACUAGUGUUGAAGAUG	121-141		5	0	21	21	1
	AAUGAACUAUCUUUAGGAAUAUCCUUAAGAUUUAUAGAAGA										
	UGAAGCUGAUGAAGAAGCUUCGCCAAUCUUUGAAUUAAUU										
	AGAGUUUUACUUCCUAACUGUAUAACAGGAAAGGAAGAGU										
	CGUAUGACGACCUUUUUUGUGGUGAAGAAGAGGAUGAUCU										
	UCCUCUUCCGCGGUUUCUUCCUCCAUGACCACGCACUUGU										
	GACCAUGGUGGAGGGUCAGUACCUCCCAUGCUGCAAAAUU										
	GGAACAAAGAUUAGUAUAAAUCCGAAAAAUAUCCGGAAAUA		sly-miR3448-1-5p			aly-miR3448-3p					
sly-MIR3448-1	UCCAGUUCCCA	293		UAUGACGACCUUUUUUGUGGUG	124-145		5	0	22	22	1
	UUCUGCUUAAGUUGGUGUCUUAACUUGUAAUUCACUUCUA										
	UCGUGGAUCGCUUCUGCUUUUGAAGUACCAUAGAAGUGAA		sly-miR482b-2-3p			stu-miR482b-5p					
sly-MIR482b-2	UUGCAAGGUAAGACACCAACUUAAGCAGAA	110		GAAGUGAAUUGCAAGGUAAGA	73-93		5	0	21	21	1
	AGGUAGGUUCUUCAUUAUUUCGAUAUACAAAUGGGUCCUG										
	UAUUUUUUUCGGUAUACAAUGGAUCCUGCAUUUGUAUAUU										
	UCAGUAUAUAAACGGGUUCUGCAUUUGAAUAUUUCGGUCU										
	AAUUGUAUAUUUUGAUAUACAAAUGGGUCCUACAUUUGUA										
	UAUUUCGGUAUACAAAUGGGAUGACAAAAAAUAUGGAAUG		sly-miR8003-3p								
sly-MIR8003	UUUGCUACGAAUUACAAAUAGAAGAAACUAUGG	233		AUUUCGGUAUACAAAUGGGAUGAC	162-185	stu-miR8003	0	0	24	24	1
	CGGAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAA		sly-miR9668-3p			tae-miR9668-5p					
sly-MIR9668	UUGUAUCUUUUGCUCUUAAACCUUUA	66		CAAAGUACAAUUAUUUUCGCA	15-35		5	0	21	21	1
	AGCACAUGAUACAUGUGUGUUACGUUACCCAAAAUAUACA										
	UUUGUGUUUUGAAUUAAAAGCACAUGAUACAUUGGCUAAA		sly-miR7696d-3p			mtr-miR7696d-3p					
sly-MIR7696d	GCAUAUGUAUCAUGUACG	98		UUUUGAAUUAAAAGCACAUGA	47-67		4	0	21	21	1
	UAGAUAUGCUACAACAAAAAUGAUCAUUAGCGGCAUUUAAU										
	UCUUAAUUGCCGCUAAAUAUGUAUUUUUUUGCGGCAAUUG		sly-miR7492f-5p			gra-miR7492f					
sly-MIR7492f	U	82		AAAUGAUCAUUAGCGGCAUUU	18-38		4	0	21	21	3
	ACACAAAAUUAGAAUUUAACAUUAAAAACUUUUAGUGAUGA										
	UUUUUUGGGCUUUUGUGGCGAUUAUUGUCGUCGCUAAAG										
	GUCUAGUUCUUUUUGUAGUGAAUCCUAGUUGGCAACGCUU										
	AGGUGGAGGGAUUAGUCCCAUGUGGCAUGCCACGUCACU										
	AAAAAAUUGGGGUGUUAACUCUUGAGGGUAUUUGUGGUCU										
	CCUAGGAUAACAACGGGGGUAUUUUUGCUCCAAAAAUGUA										
	AUGAAGGAUAUAAAUGGUCUAUUUCGCUUAGUUCAAAUAU										
	UGAAAAAUUAUAUAAAAAGUGAUUAACUCUUUAAAUUCUAU		sly-miR9761-5p			gma-miR9761					
sly-MIR9761	UUUGCCA	327		UAAAGGUCUAGUUCUUUUUGU	76-96		5	0	21	21	1
	CUGGCAAGUAAGCGCUCCAACUUUGUGUAUGCACAUCUAG										
	ACGCCAAGUUGAGGUGUCUAGAUGUGCACUCUCAAAGUUG		sly-miR7992-6-5p			stu-miR7992-5p					
sly-MIR7992-6	GAGUGCGUACUUGCUAG	97		UUUGUGUAUGCACAUCUAGACGCC	22-45		5	0	24	24	1
	ACACACCUAGGAUAUACCCAUUUUUUGAGUUUCAUAUAGG										
	AAAUAUCAUCAUCGUUCAGGUAGGAAAAGUAAACAAUUGAU										
	AGUUGAGGUGUGUUUUGAUGAAUAACGGUGAUAGUUUAG										
	GUAGGAAAUUCGCACACAUGAUAGUUUAGGUUUGAAACUC		sly-miR8045-3p								
sly-MIR8045	GAAAAAUCGGAGUACUUUAGGUGUGU	186		AUUGAUAGUUGAGGUGUGUUU	76-96	stu-miR8045	0	0	21	21	1
	UUUGAAAGAAGUAUCAUAAUAUACCCCUAAAUAAUUUUUUA										
	CAAAAAUUAAAAGUAAAAAAUAUAAAUUUUAAACUAAUUUU										
	UUGAAUUCCGUUAAAUGGAGGGUAUAUGUGAGCUCAUUUU										
	GUAACGGUAGGGAUAUAUGGGAACCAUUUGUAUAAUGGUA										
	AGGGCAUAUAUGUGCCACUUUCAUAACGAGGGGUAUAUCA										
	GCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUU		sly-miR1530-2-5p			gma-miR1530					
sly-MIR1530-2	UCCUU	247		UUUUUACAAAAAUUAAAAGUA	36-56		5	0	21	21	1
	AGUCGGAUCCAAGUUGGACGAGGGAAAGUACAUCGACGGU										
	CUUGCGUCAACAAAAUUGGGGCCGAAUCCGGGUGGAGGC										
	GUGUCCUGCCUUCGCUGCAUCCCAACUCUCAUAUCAGCUA										
	UCUGCUGCAUCAGUUGCGCAAUUAGCUCAUUUUGUUCUGC										
	CACGGUGGGCUGAGCCACCACAACAUCUGUGAGGCUAACU										
	UCAUCAUUGUUGUCUCCCAUGGCUGUAUUUCCUCUGUCU		sly-miR171l-3p			ptc-miR171l-5p					
sly-MIR171l	GAGUUUGGUCCGGCG	253		UCUGAGUUUGGUCCGGCG	236-253		4	0	18	22	1

sly-MIR7822-1	UUUGUAUAAAAUUGAACAAAUAGACACACGCGUCUUACAUGGCAUAAUACACGUAGGAUACCAUGUAAGACACAAAAUAGUCAUGUAGUAGGAUGUGUGUGUCUAUUUGUUCAACUUUAUACAAG	125	sly-miR7822-1-5p	UAUAAAAUUGAACAAAUAGAC	5-25	ptc-miR7822	5	0	21	21	1
sly-MIR6151i	UUUAAAAUUUUAUUUUUAUGGAAAACGGGCUAAAAUGCCCUUAAAUUAUGAGAUUUGGUACACUAUUACCCUCCAACCACCUAAUGAGUGUGAUACGUUGGACAUAAGGGGUUUUUUUUAGUACAAAUUCAAAUACUUGAGGGGCAUGUUUGGCCCUUCUUUGUAAUUUAAAUUUUCUU	179	sly-miR6151i-3p	UGAGUGUGAUACGUUGGACAUA	85-106	nta-miR6151i	5	0	22	22	1
sly-MIR2654	UUUAUGUUAAGGAGUCAAGAUCGAACCAUACAUGUUUUAUUCAGGCAAGAAGUUUGUGUGGUUCGGGUAUUGACUUCUACACAUGAU	87	sly-miR2654-3p	AUUCAGGCAAGAAGUUUGUG	39-58	mtr-miR2654	5	0	20	20	1
sly-MIR3511	UUUAUUGAGUUACCCACGCAUGAUUUUGAUAUUAUUCUUGGCAUGGACUGGCUUCACAGUUAUUAUGCUUUCUUGGACUGUCGUAGUAGAGUGGUGAGAUUUCACUUCCCUCAUGAAGAAGAGUUAGUUUGGGAGGGGUAUGAUUCGAGUCGUCCUCAUCCCUUGAUUUUAAAUCUUAAGGCCAAUGAAAUGAUGUCCAAGGGGUAACUAUGUCAUCUUGUGAGUGUUAAUGAUUUAGAUCAUGACAUCAUGUGCAUAGACUCAAUGCC	269	sly-miR3511-3p	GGUAACUAUGUCAUCUUGUGA	203-223	ahy-miR3511-3p	5	0	21	21	2
sly-MIR7980b-4	ACCAUGCGAUACUAUAUCACGAUAUGAUAUCGUGAGAUGGAAUCAGCGUUUGGAUAUGCGAUUUCACGCUGAUUCAAUCUCAUGAUUCCGUAUCCUGAGAUGUGAUUCCAUAUU	114	sly-miR7980b-4-5p	GAGAUGGAAUCAGCGUUUGGAUAU	34-57	stu-miR7980b-3p	2	0	24	24	1
sly-MIR11003	UUAAACUUGGCUUCAAAUUUUAACUUUGACCUCAAACUUUCAUGAUGUUCAAACUAGACACUUUAACUAUCCAACUUUUAAAUAAAUAAACACGUGAGUCUUACAUGGCACAAUACACGUAGAACAAAAAAUUAUAUGUAAGAUUACAUGUAGGACAUUUGUGUCUAUUUGUUCAACUCGAUACAAGUUUAAGUAUCUACUUGUGCACACUCGAAGUUGAAGGGCAUAAAUGUGAUUUAAAACCAAGUUAAAGGACACAUUUAUGUGUUAAGUCAAAAAAUAAAGGUGUUAUGAGUUAUGAGUGAAAUGGUUAAAUAUCGC	251	sly-miR11003-3p	GCACAAUACACGUAGAACAAA	107-127	mdm-miR11003	5	0	21	21	2
sly-MIR1529	UCCCUCCGUUUCAAUUUGUUUGUUUUACUUUUCUUGUUGGUCUGUUUCAAAAAGAAUGUUUUUUCCCCUUUUUGACGAUACAUAGAGCAUAAUAUCAUAAGAUUCAAAUGUUUUAUAUACUUUCUCAAACUCUGUGUCAAGUCAAAACCAGACAAACAAAUUGAAAUGGAGUGU	307	sly-miR1529-3p	UUAAAGGACACAUUUAUGUGUUA	234-256	gma-miR1529	5	0	23	23	1
sly-MIR6164b	GUAUAAAUGUGUCUCUGAGAUUUCGAGCAUAGAUUAAGGGGGUACUUGGGCAUUAUCCCAACAUAAUAAUUAGUUUCUAUAUUCCGAUCAUGUAAGGAAAAAUAAUAUUACACACGGAAUGGAACGGAGUAUAUAUAUUUGGUAACAUUCUAAAAUUUAGAGAUACAAUUAAAU	174	sly-miR6164b-3p	ACAAACAAAUUGAAAUGGAGU	152-172	nta-miR6164b	5	0	21	21	2
sly-MIR10532-10	UAAAUUGAGCUAAUCAUUGAUAGUCUGGUAAUGAGAUUUUGCAAGCACAUGUAAGACUUAUGAGAUGAGACUACCACCAAAGUGGAUAAUGGUCUCAAAAUUACAGGAAAAUUAUUCCCCGGACUACCUAGUGAGAUAGUAAAUACA	174	sly-miR10532-10-5p	AAAUGUGUCUCUGAGAUUUCGAGC	5-28	sly-miR10532	2	0	24	24	1
sly-MIR9772b	UUUCUGCAAAAAAGAAAUUGAUAAUUUAUUAUCAAAGGGACUUAUAAAACCCUCUAAAUAUCCAUGGUCUUGUACUGCAUUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGGUUGGUAAUAAAUUACAAGCCUUUGAACAAAGUUUUAA	147	sly-miR9772b-3p	UGAGAUGAGACUACCACCAAA	61-81	ata-miR9772b-5p	5	0	21	21	1
sly-MIR2120	AGUGGAUAAGAUAUCCCAUUCCUAAUAAAAAAGAUCUUCUUUCCAGGUU	210	sly-miR2120-3p	AAAGAUCUUCUUUCCAGGUU	191-210	osa-miR2120	4	0	20	24	1
sly-MIR823-2	UUAGAUAGAAUAAUUGAGGAUCUUUUUAUGCACUUCUUUUUACAAGGAUCAAAAUUUUCUGAUCUUUCCCUAGCUGAUGAUAAUUGGGAACUAGAUAUUGAAGGAUAUUUGUAUGAUUACUAAUCUAUUUGUUAUAUCUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUCCGUGGUCGUGGGGGAAGAAGUAGAGGAAGUGGAAGAUCAUCCUCUUCACAGUCUAGAAGAUCGUCAUAUGAUUCUUCCUU	263	sly-miR823-2-5p	UUUGUAUGAUUACUAAUCUA	108-127	aly-miR823-5p	5	0	20	20	2
sly-MIR408-3	AAGGAUAUUUGUAUGAUUACUAAUCUAUUUGUUAUAUCUUUUGUAGUAUGGAAGGCGACGAUCCUCCGCCAUGGUCACAU	291	sly-miR408-3-5p	GGGGGAAGAGGUAGAGGAAGG	93-113	lja-miR408	5	0	21	21	3

sly-MIR9674b	AUUUGUGGUCGUGGGGGAAGAGGUAGAGGAAGGGGAAGA UCAUCCUCUUCACAGUCUAGAAGAUUGUCAUACGAUUCUU CCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAA AUCAACGAUUGGCGAAGCCUCCUCAUCAGCUUCAUCCUCU GUAAAUUUAAAAGAUAUUCCUAAGGACAGUUCAUUAUAUGA ACAAAUUCAAA UAAAUCAGCUUCUCUGGCUAAAGAGGUAUAGGUAUUACCU UGCUCUUUUUUCUGCAAAUAUGUUUGAAUUUGUUCAUAUA AUGAACUGUCCUUAGGUUUAUCUUUUAAAUUUACAGAGGA UGAAGCUUAUGAGGAGGCUUCGCUAAUCUUUGAUUUGAUU AAUGUUUUACUUCCUAACUGUAUAACAGGAAAGGAAGAAU CGUAUGACGAUCUUCUAGACUGUGAAGAGGAUGAU CAUAGAUAAGGCACUAGUACUACAUUCGACUAUGACCAAAA UUUCAGAGACGCAUCUUAACUAAACUAAGGUCAUAUUAUU CCACUCAACUUGUUUUGUUUUAUUUUUGUAAUUUUGUAAA CCUGUUUGUCCUACGUGGUAUCAAAACAUCUCUCACCCGU CUCACUUAAAUGGUGUGCCACAUAAGCCAAAAGGUGUAUA AGAUUACACAAAAAAUUAGUUUAAGUGUGUCUCUGAGAUU UUGAUCAUAACUAGGGGAUACUUGUGUCUUAUCUCUA GACACUAGUCAAGUGAGACUCAUUUUUGCCUCACAAAAAA UUAAGCCCAUUUGAGUCUACUUUUAUGUGAGACAAAAAGA AGCCUCACACAACUAGUAUU UAAUACUCCCUCCGUCCCAUUUUAUGAGGCAAAAUUUGAC CAGGCACGGAGUUUAAGAAAUAAUGAAGACUUUGAAAUGU UUAUCAAAUUGUCCUUCAAAAAAGUAAAUUCACUUUUCUCU CUCCUCAUAAAUGUAUUAGAGUACUAUGUUUAAAAUUAAG UGGGACCAACAAGAGUAAAAGAGGAAUUGUACCUUUAAAU ACUUACCAUAUAAGGAAAUAUGACAUUCUUAUUGAGACUG ACCAAAAAGGAAAUGGUGCCACAUAAAAUGGAAGGGGGGG AGUAGUA CUUCACUACAAGAAAACUAUGAAUUACAUGGGGAUUAGUA UGAAAAUUUGCGAAAAGUUUAUUUUCCUACAAACUUUUAUA CUAAUUCCCAGGAAAAUUCCAUGUAAUUUACACGGUUUUC UUGUAGUGCUU ACAUGAAGUGAUGAAGAUGUUUGUUGAUGUUCAUCUAAUC AUGGCAUAUUAAUGGUUCCAAAAACUAUGCCAAAUGAUAU GAUGAAUAGAUGACCAUCAACAAACAAAUUCAUAACUACAC AA	235	sly-miR9674b-5p	UGAAUUUGUUCAUAUAAUGAA	65-85	ata-miR9674b-3p	5	0	21	21	1
sly-MIR10532-11		278	sly-miR10532-11-3p	AAGUGUGUCUCUGAGAUUUUGAUC	224-247	sly-miR10532	3	0	24	24	1
sly-MIR8011a-4		100	sly-miR8011a-4-3p	GACAAAAAGAAGCCUCACACAACU	71-94	stu-miR8011a-3p	2	0	24	24	2
sly-MIR1128-4		288	sly-miR1128-4-5p	UAAUACUCCCUCCGUCCCAUU	1-21	ssp-miR1128	3	0	21	21	1
sly-MIR8001b-7		132	sly-miR8001b-7-5p	AUGGGGAUUAGUAUGAAAAUUUGC	28-51	stu-miR8001b-5p	0	0	24	24	1
sly-MIR827-2		123	sly-miR827-2-5p	GUUUGUUGAUGUUCAUCUAAUC	19-40	eun-miR827-5p	3	0	22	22	2
			sly-miR827-2-3p	AUAGAUGACCAUCAACAAACA	86-106	aof-miR827	1	0	21	21	2
sly-MIR444b	UAGUUGUAAGCCUGUAAAUGUAAGUCUGGGUAUACCUGAA AGUUUUUAAGGAAGUAGUUACAUUUGUAACGACACACAUU AAGGAUACAAGAAGACUUUAAGUAACGUCACAUUUUCCCU UUUUAAUUCAUUAACUUGAUGUGUCUUUCUUGGAAAUUUU ACUUGUUGAUGACUGUCUGUACAUUUAAUUGCUUAUAAAU G AUGUGGAACCAUAACAAGUCAGAAUCCCUUUAAAUUUAUU	201	sly-miR444b-3p	AUGUGUCUUUCUUGGAAAUUU	139-159	ssp-miR444b-1	5	0	21	21	2
sly-MIR11425f	CAUUUCCAAGAUUAGCUAUCUCUUUUCAUGAAAAGUUGUG ACAUUUAUGAAAAGUUGAUUUUAGUAUGAUGCUAUUCAUG UUGAUAUGAACUUAUGUUGAUAAUAUGCAUGUGAAAAUGC CUUUAUGAUGAUGGUGGUCUUGUGUUGAAUAUGGACUUG UCUCAAGUAAUGUUAUGUCUAUUGGCUUGUAUGCAUUCCU AAUUUGAGCAUAAAGGCUUUUUAAGUGACUUAGCAUAGUU UUGAACAAAUAGUCCUUUUUUAGCAUGAUUUCAAUGGUUU UACUUGUAUAUGUUUUCAUAC	340	sly-miR11425f-3p	UUUACUUGUAUAUGUUUUCAU	318-338	pab-miR11425f	4	0	21	21	1
sly-MIR8009-2	UUGCAGAAAAAGUGUCGAAUAAGGUGAGUUUUCCAUCACU UUUUUACAUUACUUUUUUCAACUAAACUCAGAAAAGCGAC GAACAUAAACCUUUUGUCCGUCUCUUUUCCGGCUACUUUA AAAAAUUCAUUUCCAGAAAAGUGACGGACAGUGUCCUUUA GUCCGUCGAUUUUCUGAGC	179	sly-miR8009-2-3p	AUUUCCAGAAAAGUGACGGACAGU	129-152	stu-miR8009	1	0	24	24	1
sly-MIR1069	GUGUGUUAAUGGCCUUCAUAAUCCCAAAUAAGCUGAGUUA AUUCAAAGUGCUUAUUUGAUUCAUGGGAGGCCUAAAUCAA UU	82	sly-miR1069-3p	AGUUAAUUCAAAGUGCUUAUU	36-56	ppt-miR1069-3p	5	0	21	21	2
sly-MIR482d-2	AUGAACUAUUUGUUGCCUCUUUUAUUCCCUCCUAUUUUUU UUUAGUAACUAGCAAAAAUGAAAAAGUUGGUGAGUAGUUG GGAAAGAAGAAAUGGACGGGAAGGAGCAAAGGGCACCAGA	128	sly-miR482d-2-3p	AAUGGACGGGAAGGAGCAAAG	91-111	mdm-miR482d	5	0	21	21	1

sly-MIR8011b	GGGUUUGG CCUUCACACAACUAACACCAGUUCUUUGAGGCUUCUUUUU AUUUUACAAGUCGGUGGACCCAGAAGUGUAAUAAUUUGGG UUCAUUAACUUGUGGGACAAAAAGAAGCCUACAUAAUUAG UGUCAGCUGUGUGAGAC GAAAAUACAUCCUAUUACCCCUUUGGUCUACGUGGCACUA	137	sly-miR8011b-3p	CUUGUGGGACAAAAAGAAGCCU	89-110	stu-miR8011b-3p	3	0	22	22	2
sly-MIR773b-2	GCUUGAAAAAAAAGUCAAUUAGCGUUGGACUUACAGGAUA GUGUCACGUAGGCAGAAAAGGGGUAGAAAAUUAUUAAU CACGUAGGCACGCAAGGGGUGAUAAAUUAGUUAAAAAAAA AGAUGGAGGGGGUAAUAGGACCUCAUCAAAGAUAAGGUGU GUCGUAGGGAUUUUGGGUAUAGGCUAGGGGGUAAUUGAG UAUUAUCCUUUUUUUUUCCAAAUAAAAGUAUAAAUAUUAAA AUUGUUUUGAGUUUGAACUCUAUUUAAUUUUAUAUUUUAA UAUCAUAUUAUAUUUUUUAAUUAAUUGUUAUUGGCCCACG UGUCAGUCCUACCGA	118	sly-miR773b-2-5p	GGCACUAGCUUGAAAAAAAA	34-53	ath-miR773b-5p	5	0	20	20	1
sly-MIR2923	AUGCAAGUUUAGAUCUAAUUUUCAACGAUUUAUCUCUAUU UGUUGGAUCAUAUUUCUUCUUCGCUCGUGAAAAUGUUUAA CUAGAAUAAAAUUUGAUCGCUCUUAUUGAAUUUCUCUAUU GAGAAGUUCGUUUUUAUCUUCUAUUUGAAGAAAUUGUUGC UCGAAAAUGAUGGGUUGUUGUGGUGAACAAAUCUACGUGA AUUGAUAAAGGUGAAAUGGAGAUGAAGAGUUAAUAUUUGG UGAAAAUGGUGGGUCAACUUGAGU	255	sly-miR2923-3p	AAAUAAAAGUAUAAAUAUUAAA	139-160	osa-miR2923	5	0	22	22	1
sly-MIR11295	UGGAUUGGAUUUGGAUGGAUUGGAUAUGGAUUGAAAAAAA AUGGUUUGGAUUUCAAUCCAUCCAAAUAGAAUAUG AACAGCAUUAGGUUGAUAUACGUUACUGUAAGUAACAUUU UACUCCUAAAACGUUACUAUGAGUAAUGUUUUAGGAGUAA AACGUUACUACUGUGAGUAACGUAUAUCAAUCUGACGCUA UC	264	sly-miR11295-5p	CUUAUUGAAUUUCUCUAUUGAG	102-123	fve-miR11295	5	0	22	22	1
sly-MIR11118	UAGUCCUGUCGCAGAUGACUUUCGCCCUUCUAAGGAACCA CACUUUCUGUAAAUCUAAUUAAUUUGAAUUCAAUGUGGCA GGACGAGAGUCAUCUGUGACAGGAUAA	75	sly-miR11118-3p	CAUCCAAAUAGAAUAUG	59-75	lja-miR11118-5p	3	0	17	23	1
sly-MIR10538-4	UACCCCCCUGAACUUAUUUUAUUAGUAAUUUUUUUACCCG UUUUAGCCUAUGUGACACUAUCUGGUGGGCCCAACGAUG GUUGACUUCUUUUUUUUCAAACUAGUGCCACGUAGGCCAA AAAGGGGUAGAAAAUUACUUAUAAAAUAGGUUCAGGGGGU AA	122	sly-miR10538-4-5p	AGGUUGAUAUACGUUACUGUAAGU	10-33	sly-miR10538	4	0	24	24	1
sly-MIR1919-6	AAGCAUAUCAUGUUCUUCAAUUUUGAGUGUCAACAAGUAG ACAAUUGAACUUGUAUGAAAUUGAACAAGUAGACACAUGU GUUCUACAUAGUAUAAUGCACAUAAGAUGCCACGUAGUAC ACAAAAUUAUCAUGCAGGACUAAUAUGUCUAUUUGUUCAA CUUUAUACAAGUUUAAAUGUCUACUUGUUGACACCUAAAG UUAAAGAUCAUAAUUGUCA	219	sly-miR7822-2-5p	UAUGAAAUUGAACAAGUAGAC	54-74	ptc-miR7822	5	0	21	21	1
sly-MIR11077b	GAUCAAGGCUUACUUCGAGCGAAUAUCAACCAGAUCUUGA UGAUGAGGCUAUAGUAGCAAAUAUCGAAAACAUUUUAACA UUAGAUUGUCUUGGUAAUUAACAAGAACAUGAACAACAAUA AUAUGUAAUUUUAUUUCUCAAGUUUAAUUGAUGAAUUAAG AAUAUGUAAAGGCCUACAAGACACUAUUACAAACUUCACUU UGUUAUAUUAAUCAAGCAAUACAUUGAUGAAAUGUAAGAUC UUUGCUUCAUUUUGCCUCUUUCAUCAUGAGGACUAUAGUU UCAUCUAGUCGAGUUAGCUUGCAC	307	sly-miR11077b-3p	UAAUUGAUGAAUUAAGAAUAU	146-166	lja-miR11077b-5p	5	0	21	21	3
sly-MIR7997c-9	GUUAUAUUGCUCCGACUCUUCAAAAGUGGUCACACCCAUG UUGAAUCCUCCAAAAAGGCAAUACUUUUGGUGGAUCCAAC AUGCACCUGUUGACAUUUCUGAAGAGUUCGAGCAACAUAG U	121	sly-miR7997c-9-5p	AUAUUGCUCCGACUCUUCAAAAGU	4-27	stu-miR7997c	2	0	24	24	1
sly-MIR7992-7	UCCAACUUUGAGAAUGCACAUGUAGACACCUCAACUGAAC CCAUUGUGUCUCGUGGACACCCCAUGCUGAUGUGGCAUA UGCACCUUGGAGGUGCCGAGAUGACCAUUUUCUAAUUCG GGAGUGUUCAAUUAACACAGUGGAGACUAGUUGAGGUGUC UAGAUGUGCAUUCUCAAGGUUUUU	182	sly-miR7992-7-5p	UUUGAGAAUGCACAUGUAGACACC	7-30	stu-miR7992-5p	3	0	24	24	1
			sly-miR7992-7-3p	UGUCUAGAUGUGCAUUCUCAAGG	155-177	stu-miR7992-3p	4	0	23	23	1
sly-MIR1127-2	CGGGACAAGUAUCGUUGGACAACUACUUUUAGUGUAGUGG ACAAGUAAAGGUGGAUGGAAGAAUUACUUCCUCCGUCCAC	131	sly-miR1127-2-3p	AAUUACUUCCUCCGUCCACUU	62-82	bdi-miR1127	5	0	21	21	1

sly-MIR7823	UUUUAUUUGUUCGCUAUACUAAAAUUAGAUAUCCACUUUUACUUUGUCAUC	122	sly-miR7823-5p	AUGCAUGCAUUAGCUUGAUGU	26-46	ptc-miR7823	5	0	21	21	2
sly-MIR10532-12	UUGAUAGAGUGUAUUAGAGAAAAUAAUGCAUGCAUUAGCUUGAUGUAUUAGUAGUACCUUCUUUGGUACACUUUUCUAACCUAUGCAUCACUAAUGCUUGUAUUAGUAAUACACUCUAUUGUCCUGAAAACGAGUAGAAAAUUAUUUAUAAAGUAAGUUCAGGACGAUAAUCGGACCUUAUUAUAGUAUAAGUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGAUAGUUGUGAAUUAUCCCUUUAUCAUAUGAUAAAAUAAUUCUCUUUCUCUUAUUCUUUCAACUAUAAAGGAAAAGUGGACAAGUAAUUAAGGACGGAG	161	sly-miR10532-12-3p	AAGUGUGUCUCUGAGAUUUCGGGC	68-91	sly-miR10532	0	0	24	24	1
sly-MIR478f	GUAGUAUUUUGCACUUAUUUUAUCCUUGCUACUCCCUCCGUCCGGAAUUGUUUGUCAUGUUUUCUAUUUUUAGAGUUGGUUUUGAAUCUUCAAAACUUGUUCAUCAAGCAUCCUCU	116	sly-miR478f-3p	UGUCAUGUUUUCUAUUUUUAGAGU	93-116	ptc-miR478f	4	0	24	24	1
sly-MIR10995	UCAUCCUCGUCGUCCUCAUCAUCAUCGUCUUCUUCUUCUUCGAGUAUGUUAGGUACUAAUAAUAAAAAAGAAGAAGAAGAGAGUGAAAAACAAGAACAAGAGUGUGUUUUGUUCCAUGAAGAUGGUAAGAAGCAAGGUUCAGAUUCAACAAAUG	194	sly-miR10995-5p	CAAGCAUCCUCUUCAUCCUCGU	29-50	mdm-miR10995	2	0	22	22	1
sly-MIR9736-2	UGAUCCACCCACCUAACCCGACCCAUUGAAAAAAUUAUAUGACCCAUUUUAUUUUGUCUUUAAUCCUAAUUCAAGGUUUAAAGAGAGGGAUUAGUUUAGGAUUAAAGACAAAAUAAAAUGGGUCAAAUCAUAUUUUUUAAUGGAUCGGGUUAGGUGGAUGGAUCA	165	sly-miR9736-2-3p	UUAAAGACAAAAUAAAAUGGG	102-122	gma-miR9736	5	0	21	21	1
sly-MIR1886f-1	ACGUUGUCUUCAAUCUUCUCACUGACUGAGUAGGCGUUUGACCAUGGGAUAUCAUAUCACGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGGACAUUUGAUUUCACGUUGAUUCCAUCUCAUGAUUCCAUGAGUUGAGAGCAUUCCAACUCGCAUACUCAGACAUUCAAUGUACUGAUGUCAAUUG	187	sly-miR1886f-1-5p	AUGGUAUCGUGAGAUGAAAUCAGC	64-87	stu-miR1886f	0	0	24	24	1
sly-MIR1521a	UUGUUCUAACUCUCCAAAGAUGCAUCACUACUUUUGAAGGAUCUGACAUGCAUCUGUCGUCAUUAUUGAAGACACAGAUGUGUUGUGUCAAUGCUAAUAGAAAUUGUUGUGUCUUUAGAGUGAAGUUAAAUUU	133	sly-miR1521a-3p	AUGCUAAUAGAAAUUGUUGU	91-110	gma-miR1521a	5	0	20	20	2
sly-MIR8764	ACGGGUAAAACUUAUCUGCACAUGGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUCAAAUUUAUAGUUCAUUUUACUUCUUUAAAUAUCGUAAUAAUAUUUUUUGCAUUUACUUGAUGUAAACACCCGGUACGAAUAAGUUUUUCCUUU	155	sly-miR8764-3p	UUAUAGUUCAUUUUACUUCUU	67-87	gra-miR8764	5	0	21	21	1
sly-MIR7992-8	UGGUAAGUAAGUAAUACCACGUAACUUUGAGAGUGCACAUCUAGAUACCUCAACUAGACCCUCCAACUCGUGCCCGCUGUGUCUUGUAGACACUUGACAUUAAAGUAGCAGAUAAACUUUAGAGGUGUCUCAAUGAUGAUUUUGUAGAUGUUGGAGUAUUUAACUAACACAUUGGAGACGAGUUGAGGUGUCUAGAUGUGCAUACUCAAAGUUUAAGUGUUUGUUUCUGUAUUAUGC	237	sly-miR7992-8-5p	UUUGAGAGUGCACAUCUAGAUACC	26-49	stu-miR7992-5p	4	0	24	24	1
sly-MIR7981-15	CUAUGACCGAAAUCUCAGAGACACACCUUAACUUAACUAAGGUUCUAUUAAUCUCAACUCAUUUGUUUUGUAAUUUUGUAAUGGUACACUCCGUGACUUGAGGCGCGUGAGAGAUGUUUGAAUGUCAGUGUACAGAAUUACAAAAAAAUGGAUUCGGGGGUAAUAGGACUUUAGUUUAGUUAAGGUCUGUCGCUCGAAUUUCGGUCAUAC	210	sly-miR7981-15-5p	CUUAACUUAACUAAGGUUCUAUUA	27-50	stu-miR7981-5p	5	0	24	24	2
			sly-miR7981-15-3p	AUAGGACUUUAGUUUAGUUAAGGU	163-186	stu-miR7981-3p	0	0	24	24	1
sly-MIR5014a-6	CAAUUUGAGUUUGUAUAAAACGAGAAAGAUAGAAAGACAAAGAGACUUGGGCAGAGAAAUAUUUGCAUUGUAUAAUUAAAGUGUAUAGGACGGAGAUAUAUGUAUUUGCAUGUGUAUAUACAAUUUUCUCUCGCUUUUAUACAAACGGAAACAC	155	sly-miR5014a-6-3p	UUGUAUAAUUAUAAGUGUAUA	68-88	ath-miR5014a-3p	5	0	21	21	1
sly-MIR4348c	GACCUUGUUUGCCUCUUGGAAAAGAAACUUGUUUUUUCGUCUUGAAAGUUUGCCCAUGAAAUAAGCAGAGGUCAGUCAAACAUUCAAGACAAGAAUGACUAUUUCAUGGUAAACCUUCAAGAUGGAAAAUCAAAUUUCUUCCCCGAAAGGCAAACUAGAAC	161	sly-miR4348c-3p	UGGUAAACCUUCAAGAUGGAA	107-127	gma-miR4348c	5	0	21	21	1
sly-MIR8039	CUUGUUUCAUAUCUCUACUAUCCAUGGUUCUAUUUACCUAUCUAAACUAUCACUCCCUUUGUAUUAAAGACAAAUGAGCGCUGAGCUAGCCAAUAUGUAUUUGACCAACUCAGCUUCGAGGUUCCUUUUAAUAAAAACUGAGUGAUAGUUUAGCUAAGUACAGAGAACAAUAGAUAGUUGAGGUAAGAAACUAU	194	sly-miR8039-5p	UUACCUAUCUAAACUAUCACU	34-54	stu-miR8039	3	0	21	21	1
sly-MIR1917-3	AAAUUUAGCGGCAUUAAGUAUUGACAUUAAUAAAGAGUGC	94	sly-miR1917-	AUUAAUAAAGAGUGCUAAAGU	26-46	sly-miR1917	0	0	21	21	1

	UAAAGUCUUUAUCGGCAUUAUUUAAGUGUCAUUAGAACGA AUGUGGCUAAAAAC		3-5p								
sly-MIR7992-9	UCUCGCAAACAUCUUAACUUUGAUAAUGCACACUUUUGAG AACGUGUCUAGAUGUGCAUUUUCAAAGUUAGGCUGUUUAC GGGG	84	sly-miR7992-9-3p	UGUCUAGAUGUGCAUUUUCAAAG	45-67	stu-miR7992-3p	4	0	23	23	1
sly-MIR828b	AUUUACAUUCACUUCUUUGGGAAAGCCUCUUGCUCAAAUG AGUAUUCCAACAAAUGUCUAAUUGACAUACUUUUGAGAUA CUCAUUUGGGUAAGAAGUUUUACCAGGAAGGUUGUACUU	119	sly-miR828b-5p	UCUUGCUCAAAUGAGUAUUCCA	28-49	mes-miR828b	0	0	22	22	1
			sly-miR828b-3p	UCAUUUGGGUAAGAAGUUUUA	82-102	ptc-miR828b-3p	5	0	21	21	1
sly-MIR5725-3	CGCAAAUUGUAUGUAAAUAUCCCCAUCAUACUUUUGAGAU AUUGUUGUCCCUGCCGUCAGAAAGCUAGAGCACGUACUUC CUUCACUCUAACGGAAGACUAAAUAGGGACAUGUGGCGCA AUCUUAUCGGUCGAUAUGAUAUUUAAUAAGUUGUUGUUAG UGGAUAAGAUUAUGACACGUAUAUGUCCGUUAGUAUAAAC GGUAUGUAUAUUCUAGUUUUUGAAUGGCAUGGCACCAAUG UUUUAAAAGUAUAACGGAAGAUAUCCGCAUAUACCAUUUAC A	282	sly-miR5725-3-5p	AUGUGGCGCAAUCUUAUCGGU	111-131	bra-miR5725	5	0	21	21	1
sly-MIR8672	UGGAAAUGGAAAUAAUGUUAAAAUAACUAUAACUAUAAUUA AAAAGAAUGUUGAAAUAAAUAAAGAAUGAAAAAGGAAUCUU AAAGCAACUCAAGAAUGAGAAAUAAUUAGAUGAAAAAGGGG UCUGACAGCACCUGUAAGGCGCAGAAUAUCAGGCACCUUU UUUUUUAAUGCAAGGCAAAAGCCAUCAUGUGCCUUCCUCU UUUCAUCGGUUGACGCCGUUAACGGCGUAUAGGGGAAGG CACGUGGGCCCCUGUGCCUUUAGCGUUUUGGUUUCCUGA AUAAAUUGUUUGCCCUUUUUGGAACUUUUAGACAAUUAUG UUGCCCUUUUGG	333	sly-miR8672-5p	AUGAGAAAUAAUUAGAUGAAAAAG	97-120	gra-miR8672	5	0	24	24	1
sly-MIR1128-5	UAAUUUGUUGACUUCCAAGAAAGCUAUUACUCCCUCCGUC CAACAAUACUUGUCCACUUCAUGAAAUCCAUGAAUAAUUUU ACACUUAGUUCCUAAUUUACCCUUAUCAUAAAUUAUAGUCA UUUCACUCAUUUCCCUAUUUCCCUAUUAUAUUUUUCAAGA CAUUGUAUUUAUUAUAUUCAAAGGGUGAUAUAAUAAAAUUA CCCAUCUAUAAGAAGUGUGCCAAGUCAAUAGUGGACAACU AUUGUUGGACAGAGGGAGUAUAAAAGUUUUGAAAGACACC AAAAUG	289	sly-miR1128-5-5p	UAUUACUCCCUCCGUCCAACA	25-45	ssp-miR1128	3	0	21	21	1
sly-MIR8019-3	ACUAAUACUCCUCCAUUUUAAAAAAGAAUGACCUGGUUUG ACUUGGCACGAAGUUUAAGAAAAUAAAGAAGACUUUGGAU CUUGUGGUACUAAAUUAAAGUUAUGUGAAAUACACAAAACU GCCCUUUAAUCUUGUGGCCUUAAACAUACCACAUGGAAAG UUGAAAUAAAAAUGUAACCAAAAAAAGAAAGAGGUCAUUCU UUUUAAAACAGACUAAAAAGAAAAGAAAGUCAUCCAUUUUG AAACGGAGGGAGUAUUUAU	262	sly-miR8019-3-5p	AAAAGAAUGACCUGGUUUGACUUG	22-45	stu-miR8019-3p	0	0	24	24	1
sly-MIR3509	GAUCGGAGACUCAUGUAACGACUCACUAGUAAUCUUUUUU AAAGGGGUUCUAUCCAUGUUUUUCUUUCACUUUUGCUUGA GCUGCUUGAGGUGGGAUGCUGAAUCCCUUCAAAAACAAUU ACUUGUGAGCCGUGACAUGGGUCUCCGGUC	150	sly-miR3509-3p	UUACUUGUGAGCCGUGACAUGG	119-140	ahy-miR3509-5p	5	0	22	22	2
sly-MIR7122a	CCUCUCUCACUUUAUAUACAGACACAAAUGUAUAAAAUGUG UUUGUGUUUGUAUAAAGUGAGAGAAAAUUGUAUUUAUACA UCUCUUUUCGUUUGCCUAUCUACCCAGAAAAUCUCGCUCG UUACUCUCACUCGUCUCUCUCACUUUAUACAAACACAAAU GUAUAAAAUUACGUUUAUGUUUGUAUAAAGCGAGAGUAA	200	sly-miR7122a-3p	UACGUUUAUGUUUGUAUAAAG	171-191	ppe-miR7122a-3p	5	0	21	21	3
sly-MIR7997c-10	AUGUUAUGUUGCUCGGGCUCUUCAAAAAUGAUUUAUAAGA UCACCCUCAACAAUGAGAUACUCACUUUUGAAGAACCUUU UCAUACGUUGUUCAGACUCUCCAAAAAUAUACUCUCACCAA GUCUAAUCCUCAACAACCGCACUAACUGUUGUAGGAUCAG CAUAAGCACGUCAACACUUUUGAAGAGUUCGAGCAACAUA AAAC	205	sly-miR7997c-10-5p	AUGUUGCUCGGGCUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
sly-MIR9563a	AUUUUGUUUUUUGUGUCGGCUGAAUAUCAGCCAUAUGCAC AAAGUAAUAGUCUUUUAUUUUUAUCGUGUUGUGUCGGCUG UAAAAAGCCAAUUAUAAAAGUCGUAAAGUAAAUAGUAAGAG UCAAGUUACUGUGUAAAUAGUAAGAGUCAAGUAACUGUGU AAAUAGUAAAGGUCAAUCGUCUUAUAGUAAGGAUGAAAGG UCAUUAUGUAUGUGUAUAUAAGAGGCAUUUGCCCUCAUAA AUAAAACAAGCC	253	sly-miR9563a-3p	UAAAUAGUAAGAGUCAAGUUA	109-129	bra-miR9563a-3p	4	0	21	21	1
sly-MIR3448-2	UAAAAGAAGGAGUCAAGAACGCACCAUACAGGAAAACAUCU UGAUAAGAAGUGUUACUAUGUUUAGACAAUUGUAUGGUUC	104	sly-miR3448-2-5p	ACAGGAAAACAUCUUGAUAAG	28-48	aly-miR3448-5p	5	0	21	21	2

sly-MIR11011a	GGGUAUUGACUUCUGUACUUGGA AAGUGUUAAUAAGCCAAUUUGACCAGCUUAUAAGCUUAGU CAAACACCCUCUAAGCUUAUAAGCUGGUCAAACUAGCUUA UAAGCAAUU	89	sly-miR11011a-3p	AAGCUUAGUCAAACACCCUCU	32-52	mdm-miR11011a	5	0	21	21	1
sly-MIR7805-2	ACUUAAAAGUGUGGUCAUAUAUAUAAAUAAUUGUUGCCAA UUAUUCUAAUAAUUGGCAACACUUAUAACGUGUAGCCUAU AAUUACAAAAAGGACACUUUAAAAGUGUUGUCAAAGUUUUC GUGGCCAUAAACCUGGUUCAAAAGUCGCGCCUUCAAAGUA UUGCCUUAGGUGUCUUUGGCAACACUUUUUAAGCAUUGUC AAAAUUUCGUGUAGCCUUGACCAAAUUUGGUGUAGUGAAU ACUAAUACUUAGUUGUUUUCUUGAGAUAUGUCACCAUACA AUUUCUAAUAUACUCUCUUUUAGGA	306	sly-miR7805-2-3p	AAAUUUGGUGUAGUGAAUACU	224-244	rgl-miR7805-5p	1	0	21	21	1
sly-MIR1023e	ACAAUAUGUUUGGUGUAAUCUCACAAAUGAAGUCGGGGAG AGUGCAUACUUUUAUUUCUACUUUUAGAAGGUAGAGAGAU UGUUUCUGAUAGACCAUCCGCAUUUAUAAAGUUCUUGGAU UCACAUCCACUCCCUGUAUGCUGAAUUCAUUUCUGGGAAU GAAAGAAGUUAGCAAGUUUCUUAGACACAGAUUGCUGAGA UUCAUCAAACAAAUCCU	217	sly-miR1023e-5p	AUGAAGUCGGGGAGAGUGCAU	27-47	ppt-miR1023e-3p	5	0	21	21	1
sly-MIR7981-16	AUAUAUAAUAUUAGGGGUAAGAUAUAAGUACCUCUUAGAU UAUGAUCGAAAUUUGAGAUAUCUUAAUUAAACUAAAUUCAU AUUAUCUCCUCACACAGUUGAGGCGCGUGAGAGAUAUUUU GAUGCCAUGUAAAAGCCAAAAAGGUCUACGAAAUAACAAAA CAAAUUGGUUCGGAUAAUAGAACCUUAAUAUAGUUAAGGU GUGUCUCUAAGUUUCAGUCAUAGUCUAGAGGAUAUUUACA CCUUAUCCCUAUAAUAUUGUAGAC	266	sly-miR7981-16-5p	CUUAAUUAAACUAAAUUCAUAUUA	62-85	stu-miR7981-5p	5	0	24	24	2
			sly-miR7981-16-3p	AUAGAACCUUAAUAUAGUUAAGGU	179-202	stu-miR7981-3p	4	0	24	24	1
sly-MIR395a-8	GAUGCCCUGUUGAAGUGUUUGGGGGAACUCUUGGACUCA CUUUGAAAUUUUACACAAACAAAUAGAAGUGUAUGAAUCCU GGCUGUGGAUGAUGAACAUAAUAGUUCACGUAUAAAUCUA UUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGG GCUUA	165	sly-miR395a-8-5p	UGAAGUGUUUGGGGGAACUCU	11-31	aof-miR395a	0	0	21	21	1
sly-MIR395b-8	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCGCUUCAUU AGGGCUUACUUUAUUGUUUGAUGCCCUGUUGAAGUGUAU GGGGGAACUCUUGGACUCACUUUGAAAU	107	sly-miR395b-8-3p	UUGAAGUGUAUGGGGGAACUC	69-89	aof-miR395b	1	0	21	21	2
sly-MIR395b-9	GAUGCUCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCA CUCUGAAAUUUUAUGCAAAUUAAACCAAUAGAAGUGUUGG AGUGCUGGUUGUGGAUGAUAAACAUGAUAGUUCACGUAUA AAUCUAUCGAGGUGUUCCGUAGAGUUUCCUUGAACACUUC AUGAGGGCUUA	170	sly-miR395b-9-5p	CUGAAGUGUUUGGGGGAACUCC	10-31	sly-miR395b	0	0	22	22	1
sly-MIR395a-9	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCGCUUCAUU UGGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUU GGGGGAACUCUUGGACUCACUUUGAAAU	107	sly-miR395a-9-3p	UGAAGUGUUUGGGGGAACUCU	70-90	aof-miR395a	0	0	21	21	1
sly-MIR395a-10	GAUGCCCUGCUGAAGUGUUUAGGGGAACUCUUGAACUCAC UUUGAAAUUUUACACAAACAAAUAGAAGUGUAAGAGUCCU GGCUGUGGUUGAUGAACAUGAUAGUUCAUGUAUAAAUCUA UUAAGGUGUUCCAUAGAGUUCCCUUGACCACUUCAUGAGG GCUUA	165	sly-miR395a-10-5p	UGAAGUGUUUAGGGGAACUCU	11-31	aof-miR395a	1	0	21	21	1
sly-MIR9764	CCAUCUCACUUUUAUACAAGCACAAAUGUAUAAAAUGUGUU UGUGUUUGUGUAAAGCAAGAAAAAAUUGUAUAUGUACAUA UAUUUUCGUUACCCUCUCCCUUUCUCAAUCUCGCGCGCCA CCUUCACUUAUACAAAAAGAAACGGAAUGUAUAAAUUGUGU UUCUGAUUGUAUAAAGCGAGAGAA	186	sly-miR9764-3p	UCGUUACCCUCUCCCUUUCUC	87-107	gma-miR9764	5	0	21	21	1
sly-MIR7984c-5	UGUUGUUACGAUAUCAAACUUUAUGAAGGACUUUUUACCU CUUGAACUAUUAAAUAGUGUAUUUAUGCCCCCUGAACUAU UUAAAACUGUAUUUUAAAGAUAUAUAUGUGCCCACGUGGA CUUUUUAUGUCCAUGUGGACACACAUAUACGUUUAACAUA CAGUACUAAAAAUUGUAGGGGGGGGGAGGUAAAAUGUCAU UUACAAAGUUUGGUAUCGUAACAUCA	226	sly-miR7984c-5-5p	ACGAUAUCAAACUUUAUGAAGGAC	8-31	stu-miR7984c-5p	1	0	24	24	1
			sly-miR7984c-5-3p	CAUUUACAAAGUUUGGUAUCGUAA	198-221	stu-miR7984c-3p	3	0	24	24	1
sly-MIR773b-3	GAUAAAAUCAUUGAUGAUCUUCUCAUGAAUUACUUUCUGC AAGGAUCACAAUUUGCUGAUCUUUCCCUAGCUGAUGAUAG UUGGCAAUUGGAUAUUGAAGGAUAUUUGUAUGAUUACUAA UCUAUUUGUUAUAUCUUUGCAGAAUGGCAGGAGGAGAUGA	261	sly-miR773b-3-5p	AAUUGGAUAUUGAAGGAUAUU	86-106	aly-miR773b-3p	4	0	21	21	1

sly-MIR11288c-2	GCCUCCGCCAUGGUCGCAUAUUCGUGGCCGUGGAGGAAAAACUAGAGGAAGAGGAAGAUCAUCCUCUUCACAGACCAGAAGAUCGUCAUACGAUUCUUCCUUUCACAGGAAUCUAUUGAUUUAGGAUUUGUCAAACUAUACAGUUAUCAAGAACAGAGGAGAUGAGUAAUGGUCACAUCUCCUCUGUUCUUGAUAACGGUAUAGUUUGACAAAUCCUAAAUCAAUAGAUUCCUGUAGU	137	sly-miR11288c-2-5p	UGAUUUAGGAUUUGUCAAACU	16-36	fve-miR11288c-3p	4	0	21	21	1
sly-MIR162b-3	GGCGGGUUAAGCACUGGAUGCAGAGGUUUAUCGAUCGCUUCCUGUUGCUGUAUUUAUCGCUUUUCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUUCUCACCCAAC	110	sly-miR162b-3-5p	UGGAUGCAGAGGUUUAUCGAUC	15-36	ath-miR162b-5p	3	0	22	22	1
			sly-miR162b-3-3p	AUCGAUGAACCGCUGCCUCC	75-94	cas-miR162b	0	0	20	20	1
sly-MIR2931-2	AAGGGGGUAAAACUUACCUGCAUCGGGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUUAAGUUUAUUGUUCAUGUCAUGUUACUUCAUUAAAUCACAUAAUAAUGAAAAUUGUAUUGACUUGGUGUAAACACAAAGUGUAGGUAGUUUUUUCCCAAG	163	sly-miR2931-2-3p	GUUUAUUGUUCAUGUCAUGU	67-86	osa-miR2931	5	0	20	20	2
sly-MIR7981-18	UUUUAAUUAAAUGUCAGAGAGGCACACCUUAAUUAAACUAAGGUCAUAUUACCACCUAAAUCUUUUUUUGGUAAUUUUGUGCACCUUUAUCUUAUGUGGCACGCUCCGUGACUUUAUGUAAUUGAGGCGCGUGAGAUAUUUUGAUAUCACGUAAGUAAAAAAGGUACACAAAAUGGCAAAAAAAAAAGUUCAGGGGAUAAUAGGACCUUAGUAUGGUUAAGGUGUCUCUGGAAUUUCGAUUAUAG	245	sly-miR7981-18-5p	CUUAAUUAAACUAAGGUCAUAUUA	28-51	stu-miR7981-5p	3	0	24	24	2
			sly-miR7981-18-3p	AUAGGACCUUAGUAUGGUUAAGGU	200-223	stu-miR7981-3p	3	0	24	24	1
sly-MIR407	AUAACUUGUAAGAAAUCAUUAUGUUUAGAUGUUCCUACUAGGUGGAACUCUACAUAUUCGAUGCUUGAUAUAGCACAACAUUUUGAGCUUGCAUUUAAAAGAUAUAGUUUUUAUGAUAUUGGAUACUUGAAUCAUCUUCGUACCUUUGGUUCUGAUUCUUCUGAAAACAAAGAUGAAACUAGUGUUGAUGAUGGAACUAGUGUUGAAGAUGAAUUUAGUGUUGAAGAUGGAACUAUUGCAAAUAUCUUUCAAGUGGU	258	sly-miR407-5p	UUUAAAAGAUAUAGUUUUUAU	94-114	ath-miR407	5	0	21	21	1
sly-MIR10532-13	GAAAAUUAUUAAUAAAAUAAGUUAAGGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUCAGGCAUAGUUUGAGGGGGGUACUUGUGCAUUAUCCCUUGAAUUUAUGUCUUAAUCUACUUUUCUUAAAAAGUGUG	148	sly-miR10532-13-3p	AAGUGUGUCUCUGAGAUUUCAGGC	54-77	sly-miR10532	1	0	24	24	1
sly-MIR8573-2	GAGUUGUGACUUUUAUGAAAUGUUGCGAUUUUUAUGAAAAGUUGCGACUUUUAUGAAAAGUUGUGACUUUUAUGGAAAGUUAUGAUAUGAAAGGUGACGAUCUUUCUGAAAGAUUGUGACUUUUCCAAAGGUUUGUGACAUUUCCGGUAAGGCACAAUAAUAAACUAUGACCGAAAUCUCAAAGACAAAUCUUAAUUAAACUAAGGUCCUAUUACCUCCUAAACCUAUUGUUUUGUAAUUUUGUGUACAUUUUUGGCUUAUGUAGAUUUAAAAUAUCUCUCACGUGUCUCAAUUAUGUGGAGACACGGAGUGUGCUAUGUAUGACAAAAGGUGUAUAAAAUUACCAAAAAAAAGUUAAGGGGGGUAAGGACUUCAUUUUAGUUAAGGUGUGUCUUCUGAAUUUCGGUCAUAGUCUG	160	sly-miR8573-2-3p	CCGGUAAGGCACAAUAA	144-160	atr-miR8573	4	0	17	21	1
sly-MIR7981-19		256	sly-miR7981-19-5p	CUUAAUUAAACUAAGGUCCUAUUA	31-54	stu-miR7981-5p	2	0	24	24	2
			sly-miR7981-19-3p	UAAGGACUUCAUUUUAGUUAAGGU	205-228	stu-miR7981-3p	4	0	24	24	3
sly-MIR1078	GUUCGAACCAAGAACAAGAAAUGGAAGAAUGAAAGUCUUAUAGGUUCAGAAAGACUCUGUGGCAAAAAAAUAAAAAAGAUAUAUCGAAGUUGUUUUGAUGAUUCAAGAAUGUUAUUACUUAAAUCCAAUGUUCUUAGUUACUUCGACUGGAUGAGUCCUAGUGAGGGAAUAACUAAGUCCUAAUUCAUUGGUUUGAUUGUAUCAUUAACCAUUUCUUUUUUUGGUACGGGG	231	sly-miR1078-5p	UUUUGAUGAUUCAAGAAUGUU	93-113	ppt-miR1078	5	0	21	21	1
sly-MIR8046-2	CAUAAGUAUCUUCUAGACUAUGAUCGAAAUCUCAAAGACAUGCCUUAAUUAAGUUAAUUCUAUAAUAAUUAACUCCUCCCCCCCCCCCUCCCCCUUCCCCCCUCCUCAAACUUUUUUUAAAAAUAUAAUUUUGUAUAUGUCUUGGCUUAUGUGGCACACUUCGUGACUCCACGCAGUUGAGACGCAUGAGAGAUAUUUAGAUGCCAUAUAAGCCUAAAUACAAAAUUACAAAAAAAAAAUAAAAAAAGUUUGAGUAAGAAAAGAUAAUAGAACUUUAAUUUAGUAAGGAAUGUGAAUCUUAACAUUUCGAUGAUAUUCUAGGAGUACUUCUA	332	sly-miR8046-2-5p	UAUGAUCGAAAUCUCAAAGAC	19-39	stu-miR8046-5p	3	0	21	21	1
sly-MIR2107-1	UACAAUAAGGAGGUUGUGGGUUCGAACACUCACAACCUCC	189	sly-miR2107-	CAAACCCCCAUAGCCCGUCUA	90-110	gma-	5	0	21	21	1

	UUAUUUUUCUUUUAAUUUCGCUGAGGAGGAGGCUGUGAG		1-3p			miR2107					
sly-MIR2107-2	GUGGUGGGUUCAAACCCCCAUAGCCCGUCUAUCUUCUUUC UUUUUUUUAAAAAAAAAAGGAGUGGUAGUGAGGUUCUGGG AUCGAAUCCCCACAGCCUCACUUUAUUUCC GUUGUGGGUUCGAACACUCACAACCUCCUUAUUUUUCUUU UAAUUUCGCUGAGGAGGAGGCUGUGAGGUGGUGGGUUCA AACCCCCAUAGCCCGUCUAUCUUCUUUCUUUUUUUUAAAA AAAAAAGGAGUGGUAGUGAGGUUCUGGGAUCGAAUCCCCA CAGCCUCACUUUAUUUCCUUAUUUUUUUGCUUCCCCCUUC AUCGCUGAGGUCGUGGGUUCGAUCCCCACGCU	231	sly-miR2107-2-5p	CAAACCCCCAUAGCCCGUCUA	78-98	gma-miR2107	5	0	21	21	1
sly-MIR6145b	AAGGUCCUAUUACCCCUCUAAACUUAUUUUAUAAAUAAUUU UCUACCCCUUUAGCCUACGUGGCACUAGUUUGAAAAAAAA UAUCAACACAUGUUGGGCCCACAAGAUGGUGUCACGUAGG UCGAAAAGGGAUAGAAAAUUAUUUAUAUAGUAAGUUCAGG AGGGUAAUAGGACCUU	177	sly-miR6145b-5p	UUAGCCUACGUGGCACUAGUU	51-71	nta-miR6145b	5	0	21	21	1
sly-MIR1888b-3	AACUAAUAUAUUUGUAUUCUUAUUCUUUAGCAAAAACCCUA UUUAUUGGGGAACAUACAGAGCCGUCAAUAUGGGCUAGGC CCGUUGGGCGGGCCUGGCUUAACCUGAGAUUUAAUAGGG UUGGACUAAGAUUUUUGAAACCCGUUUAAAAAAGGGCUUU UUAGCCCGACCUGAAUAAGUCUGCUCAUUUGGGGGGCUU GAGAAGUAUCGGUAGGGUCAGCCCGUGGGUCAAUAAAAAU UAAUUAAAAAAUAUAAUAUGAUAUUAAAU	268	sly-miR1888b-3-3p	UUGGACUAAGAUUUUUGAAAC	121-141	ath-miR1888b	5	0	21	21	1
sly-MIR8042	UACCUAUAUAGUAUGUUAAACCACCAGAUAAGCACUUCCAU CUAAUUUCUAAAAGGUGGUCAAGGGAACGAGGUGGUGAAA CACAUGUAACUUGACACAACUUUCAGAAAUUAGACUGAAAU GCUGAUCUGGUUUCUUAUAUACAUUAUACAUAGUUU	158	sly-miR8042-3p	AUUAGACUGAAAUGCUGAUCU	110-130	stu-miR8042	1	0	21	21	1
sly-MIR7992-10	CUUCAACUUUAGUAGCGUACAUCCAGACACCUCAACAACU CAUCCCUACCGAGUCUCGUGGACACCCAAUUCUAACGUGA CACAUAAAUUUUGAAGAUAUGUGAAUGAUCAUUUUGUAAG GUGGAGUGUUCAACUAACACACUAGAACGAGCUGAGGUGU CUAGAUGUGCAUUCUCAAAGUUGGAG	186	sly-miR7992-10-3p	UGUCUAGAUGUGCAUUCUCAAAG	158-180	stu-miR7992-3p	5	0	23	23	1
sly-MIR6281-2	UUAACAAAGUAGAUUUUAUAUAUAUAUAUAUAUAGAGAG AGAGAGAGAGAGAGAGUCAAUUCUCAACUGUACACCAAUA UUUUUAUGGGGGUUCUAUUACCCCCUACACUUUUUAUUUUU GAUAUUAACCCUUAAAAGCUGACAUGUCCAAGAAGGUGAA UACACCUUUUUUAGGGGCGUGAGGAUGUUUUUAAAACACA UUAUCUAAAUUUUAAAAUUCUUGUGUACG	230	sly-miR6281-2-5p	UAUAGAGAGAGAGAGAGAGAG	33-53	ppe-miR6281	4	0	21	21	3
sly-MIR1886h-2	GCCAUGAGAUACCGUAUCGUGGCCUUUGGCCAUGAGAUAU CAUAUCACGAUAUGAAAUCGUGAGAUUGAAUUCGUGUUUG GACAUAUAAUUUUACGUUGAUUUCAUCUCAUGAUUUCAUA UAAUGAGAUGUGAUUUCGUAUUCUCCAAAAAUCAUGAUAU GAGAAUUUCAUAUC	174	sly-miR1886h-2-3p	AUUUUACGUUGAUUUCAUCUCAUG	89-112	stu-miR1886h	0	0	24	24	1
sly-MIR10532-14	AUAGGGAUAAUGCACAAGUAGCCUCAACCUAUUCUCGAAA UCCCCCUGAACUUAUUUUAUAAGUAAUUUUCUACCUUUUU AGCUUACGUGACACUAGUUUGAAAAAAAAGUCAACAAUCG UUGGGCCCACAAGAUAGUGUAAAAAAUUAUUAAUACAAUAA AUUGGGUAAUAGGACCUUAGUAUAAUAUAAGUGUGUCUCU AAGAUUUCGGGCAGAGGUUGAGGGGUACUUGGGCAUUAU CCCCAU	246	sly-miR10532-14-3p	AAGUGUGUCUCUAAGAUUUCGGGC	190-213	sly-miR10532	1	0	24	24	1
sly-MIR536	AAUAAUUUUGUGCAACUUUUUGGCUUAUGUGGCCUCAAAA UAUCUCUCGGUGCCUCAAUCGUGUGGUGUCACGGAGUGU GCCACGUAAGACAAAAGGUGUACAAAAUUAUA	111	sly-miR536-3p	UGGUGUCACGGAGUGUGCCAC	64-84	csi-miR536-3p	5	0	21	21	1
sly-MIR822-1	GUUUGGUAUAGUGUAUUGGUAAAUUGCAUGCAUUAGCUUU AUCUAUUAGUAGUACCUUGUUUGGUACACUUCUUCAACCU ACGUAUAACUACUGCACUCCAUUGUGUAUUGAGGUGUGUA UUGCUAAUACAUGAAAAUCCAUGGUAUUAGUAAUAAGGGU UUUUAAUGCAUGCAUUAGCAAGGUUAAAGUCAAAAUUUCC CCUAAAAAGUUUUUCUGCAUCUUUUCCAUUUUUCUACAUC UUUUCCACUAUACAUGUGGAGGGUAUUUUUGUAUUUUAUU UAGAAAAUGCAAUGCAUGUUAUUUUUAGAACACCAAACCAA AC	323	sly-miR822-1-3p	AUGCAAUGCAUGUUAUUUUUA	287-307	aly-miR822-5p	5	0	21	21	1
sly-MIR2634	UGUCGUAAUUGAUAGUCACGAUUUAAUGCAGAAAUGUGAU CAGCGAUAACGUUUUAUGAUCUGUAAGAUUCCAAUGUAGC AGGAUUUUAUUCUUAAUUUGGUGCUCCGUGAUUAAAUAAA CAUAAAAAGUAAUUGACAGUUACGUUUUACAUAAUAAACGU GAUUGUCAGUUACGUUU	178	sly-miR2634-3p	UUUAUUCUUAAUUUGGUGCUC	86-106	mtr-miR2634	3	0	21	21	1

sly-MIR172d-1	AAAUGAACUUAAUGUGUUGAUUCUGAAUGAUUUAGAUUCA AAGCUAAAAAUCAAACGUACUUAAUGAGCUGAAUCUGAAUG AUUAAGAUUCAGACCUCCAUUAAGUGCAAAC	112	sly-miR172d-1-3p	UCUGAAUGAUUAAGAUUCAGA	74-94	bra-miR172d-5p	5	0	21	21	2
sly-MIR6463-2	UUUUUAUAAUUAUCUUACUUACUUUUUAUUUUAUAGUUUA UUUGGCAAUCUUAUCCGGAAGAUGUUAUUAAUGGAUUGCC UGAAUGGAGUCGGUCAGGACAACUUAUCUGGAUGGCACAU GUGCCACUUAUUUAUGGAAUUUAUCGUGAGUGGCACAUGG UUGAUCAUGUUGUGAGACAGUUUGAUUAUUUACAACAUAU UUUUGGACCGUGUACCCAAUUUUUUGAAUAUUAUUUUAAA CGUGAUAAACGAUCUAAAAUAAAACAAGAAGAUUUAGAUAC AUUUAACUA	290	sly-miR6463-2-3p	UGGUUGAUCAUGUUGUGAGAC	158-178	ptc-miR6463	5	0	21	21	1
sly-MIR164b	UAAUUGGUUAUAGCUGUGAAGCUGUCACGUCAGAGGUUG GUGAGGCGUCAUUGUACUACACACCAAUCAGAAUGAAGGA GGGUGUUUGUCCAACGGAUAAUAACUCUUUAUGUUUGAUA UUUUUAGCAUGACAAAUACCAUAUUAUAUUCAUUCAUCCAA AGAAGGAAGUCAGUUAACAAGCCUUUUCAAGAACUCACAAA GAAGUUUGCAAGGUUAAGACUGCGACGUGAAAAGGUGAAA AGACAGCUGUCAUAAAAGUUGUCACCUCUGAUGUGGUAGG UGCACAUCUUUUCCAACAG	300	sly-miR164b-3p	AGGUGCACAUCUUUUCCAAC	279-298	zma-miR164b-3p	4	0	20	20	1
sly-MIR8030-2	AUAUAUACUAUUGGGUUGGUUUGGUCUCGGAUUGGUUAU UUUUAGUUGAAACCAAACCACCCCAAAUAUAGUC	73	sly-miR8030-2-5p	UUGGGUUGGUUUGGUCUCGGAUU	11-33	stu-miR8030-5p	1	0	23	23	1
			sly-miR8030-2-3p	UUGAAACCAAACCACCCCAAAU	46-67	stu-miR8030-3p	3	0	22	22	1
sly-MIR169l	AACAACAACAGCUGUUUCAUAAAAAAUCUGGCAUGAGAAAA UGAGGCAGAUAUGUAGCCAAAAAUGACUUGCCAGACAUGA AGCAGAAUUGAUCGAGCUUGCCGGCAAGUCAUCCUUGGCU GCAAUUCAAUGACCUUGUUCCCUCAUGCAAGACUUUAACA UGAAUAAAGACAUGUCUAUUCAA	184	sly-miR169l-5p	UAGCCAAAAAUGACUUGCCAGA	55-76	cme-miR169l	2	0	22	22	1
sly-MIR10542-2	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUUAAAAAAA UUUAGAAGUAACAAAUAUAAAUAUAAAACUAAUUUUUUAAC UUCCGUUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACG GCAGGGGUAUAUGUGUACCGUUUGUAUAACGGUAAGAGCA UAUAUGAGCCACUUUUAUAACAAGGGGUAUAUCAGCUCCA AAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUCCCUUA AAAGAAUAGUGGGGAACUAUGAUGUUACUUGCC	275	sly-miR10542-2-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
sly-MIR1917-4	AAAUCCUUCACACUACAACAAAAAUAACUUUUAGCAGCACU AAAUAUUAACAUUAAUAAAGAGUGCUAAAGUCUUUACCGGC AUUAGAUAAAUGUCAUUAGAACCAAUGUCGCUGAAGGCUU AAGGGACAUAUACAAAGAAUGACAAUUGCCGCUAAAAAAUA CAUAUUUAGUGGCAAAUAAGAAUUAAUUGCCGCUAAUAAU UAUUUUGUUGUAGUGUAACGACCC	227	sly-miR1917-4-5p	AUUAAUAAAGAGUGCUAAAGU	52-72	sly-miR1917	0	0	21	21	1
sly-MIR8771f-2	UUAACUUGGCUUUGAAUCAUAUUUAUGCCCUUCAACUUUG GAUGUGCACAAGUAGACACUUAAACUUGUAUUAAGGUGAA CAAACAGACACACAUGUCUUACAUGUCAUCCUACAUGUCA UUUUUUGUCAUUUGUGGUGUCCUACGUGUAUUGUGCCAU GCAGGACUCAUGUGUUUAUUUAUUUAAAAGUUUGAUAGCU AAUGUGUCUGUUUGUGCACUAUGAAAGUUGGAGAUCAAAG UUAAAAUUUGAAGUCAAGUUUA	261	sly-miR8771f-2-3p	UUGGAGAUCAAAGUUAAAAUUUG	227-249	gra-miR8771f	5	0	23	23	1
sly-MIR8771f-3	UUAACUUGGCUUUGAAUCAUAUUUAUGCCCUUCAACUUUG GAUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAA CAAACAGACACACAUGUCUUACACGUUAUCCUACAUAUCAU UUUUUGCCAUAUGUGAUGUCCUACGUGUAUUGUGCCAUG UAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUA ACGUGUCUGUUUGUACAUUAUGAAAGUUGGAGAUCAAAGU UAAAAUUUGAAGUCAAGUUUA	261	sly-miR8771f-3-3p	UUGGAGAUCAAAGUUAAAAUUUG	227-249	gra-miR8771f	5	0	23	23	1
sly-MIR8771f-4	GUUUUGAAUCAUAUUUAUGUCAUUCAACUUUGGAUGUGCA CAAGUAGACACUUAAACUUGUAUAAAGUUGAACGAACAAAC ACACAUGUCUUACAUAUCAUCCUACAUGUUAUUUUUUGUC AUAUGUGGUGUCCUAUGUGGAUUGUGCCAUGUAGGACUC AUGUGUUUAUUAUUUGAAAGUUGGAUAGUUAAAAUUGUCUG UUUGUGCAUUAUGAAAGUUGGAGAUCAAAGUUAAAAUUUG AUGUCAAGUU	250	sly-miR8771f-4-3p	UUGGAGAUCAAAGUUAAAAUUUG	218-240	gra-miR8771f	5	0	23	23	1
sly-MIR2275a-2	AAUGAUUAGAGUGCAAUUUAUUGGAAAGUGACAAGGGUAA GGUAGUAAAAAUACACCUUUUAUUAUGAUUUCUUAAGGGG AGUGCACAAGUGAAGUGUGACAACUAAUAUGGGACAGAGG GAGUACAAAAGACUCUUCAACUCCCUCAAGUGCUCCUUUG	190	sly-miR2275a-2-3p	UUUGUUUUUUUCCAAUAUGGUC	157-178	ata-miR2275a-3p	5	0	22	22	1

sly-MIR7983-6	UUUUUUUCCAAUAUGGUCCACAUAAUCCUA UACAUACUCUACAACAAAAACGACAUUUGGUGGCAUUAAAU AUUGACACUAAUAAAGAGUGCUAAAGUCUUUACCGACAUU AGUUAAGUGUCAUUAGAACCAAUAUCGCUAAAGACUUUAG AGACAUUUACAAAGAGUGGCAAUUGCCGCUAAAAAUACAUA UUUAGCGACAAUUAAGAAUUAAAUGCCUCUAAUGAUCAUU UUUGUUGUAGCGAUAUUCA	221	sly-miR7983-6-5p	UAAAGUCUUUACCGACAUUAGUUA	63-86	stu-miR7983-5p	3	0	24	24	1
sly-MIR11342	UCACAUAGUUAAAUUACAAAAAUUCCUUAAAGUUGAUGGAA UUUGUAAACAUUCUAAAACGACCUAGCACAUCGUGUCCCU GUUUUGAAAACACCGCUCAGUGUCCGCUACAUUGCAUCUC GAUUUUGGAUACAUCACUCAACAUUUUAAUACAUCCCGUA AAGUGACGUAUUAGACUAGCACAUCACACAAAGUGAUGUA UCGAUAGAUACGUCGCGUAAAGUGAUGUAUUAGAUCAAUA CGCGUAAAGUGAAAGUAUCCAAGAAUAGGAGAGACUAUGG AUUUUUAUAUUUUUUUCAAAUUGUAGGAAAUUUUAGAGAA UAUGGUAAAAUAAGUUGUGU	341	sly-miR11342-3p	AUCGAUAGAUACGUCGCGUAAA	201-222	osa-miR11342-3p	5	0	22	22	2
sly-MIR6271-2	AAAUAUAUAGUUCAUGUUCAAGCUAUUGACAACCUUGAAAC UAUCGUUAUAUUUGGCUAAUUAAACUUAAAUACACUCUUAA UCUUGCAACAUGCCUGAAAUACAAUUCAAAAAUUCUCGCC UAGUUUAGGAGUGUUUUCAACACUUUACUCGGCUUAGUAU UAAGAGUCACAUGCUCCUACGAGACUACUUCCGAUGUCAU GUGACAGAUCAUAGAUGUAUCUAAGUUAAUUAUUCAAGUA AAUUAAUAUUUUUAAGACUGUCAAUAGUGAGAGAUAAAACU AAUAAUU	290	sly-miR6271-2-3p	UCAAUAGUGAGAGAUAAAACU	263-283	ppe-miR6271	5	0	21	21	1
sly-MIR821e	AAUAAAUCUUGGCAACAAUUAAUUUGGCAGUCAUACUUGU CGAAAUUACAAGUCACAAAUGUGAAAAUUGAUAGUCAUCAA UGUGAAAGUUGGUAGCCACAUUUGUGGAAGUAGGUAGUCA AAGUUUAGUAGAGUUAGACAGCCAAAUUUUUGUUGAAAUU UGCU	165	sly-miR821e-3p	UAGUCAUCAAUGUGAAAGUUG	72-92	sbi-miR821e	4	0	21	21	2
sly-MIR6248	UGGCAACAAUUAAUUUGGUAGCCAUACUUGUUGAAAUUAC AAGCCACAAAUGUGAAAAUUGGUAGCCACCAAUGUGAAAA UUGGUAGCCACAUUUGUGGAAGUAGGUAGUCAAAGUUUG GUAGAGUUAGGCAGCCAAAUUUUUGUUGAAA	150	sly-miR6248-3p	CAUUUGUGGAAGUAGGUAGUC	91-111	osa-miR6248	5	0	21	21	2
sly-MIR8021-2	UAUUUCAUAUUCAAGGCUCAAACUCGAGACCUCUGGUUAA GGAUGGAUAUUUCAUAUACAUCCCCUCGUAAAUAUUGUUG GUUCUAAACAUAUAAUAAUAACAUAAUUCACCCUCUCUUGC AUAUUCUGCAAUAUGUUGAAUUAAGUUAUUAAGCUCUACC AACAAUAUUGUGUUGGAGAAGAAGUUAAUAUUACUUCAUC CUUAACCAGAAGUUUCAAGUUUGAGUCUUGGCAUGAAUUA AUUCAAGGCUCAAACUCGAGACCUGUGGUUAAGGAUGUAU UUUUCAUAUACAUCCCCUCGUAAAUAUUGUUGGUUCUAAA CUUAUAAUAAUAACAUAAUUCACACUCUCUUGCAUAUUCUG UAGUAUGUUGAAUUAAGUUAUUGAGUUCUACUAACAAUAU UGUGUUGGAGAAGAAGUUAAUAUUACUUCAUCCUUAACCA GAAGUGUCAAGUGUUAGUCUUGCCA	241	sly-miR8021-2-5p	AUUCAAGGCUCAAACUCGAGACCU	9-32	stu-miR8021	0	0	24	24	1
sly-MIR8021-3	UAUUUCAUAUUCAAGGCUCAAACUCGAGACCUCUGGUUAA GGAUAGAUAUUUCAUAUACAUCCCCUCGUAAAUAUUGUUG GUUCUAAACUUAUAAUAAUAACAUAAUUCACUCUCUCUUGC AUAUUCUGCAAUAGGUUAAAUUAAGUUAUUAAGCUCUACC AACAAUAUUGUGUUGGAGAAGAAGUUAAUAUUACUUCAUC CUUAACCAGAAGUGUCAAGUUUGAGUCUUGGCAUGAAUUA ACACUACGUUCACUUUUACUUCUCCACUUUGGACUUCACA UGCCACUUAAAAACAAUGAUUGGUAUGCGUAUUUUAUCAC AAAAUCCAUAUUAAUUGAUGUUUAGUCUUAGGUAUUGACA ACUAAUGUGGGGAAUACGUAAUCAAUGUUGAUUCUUCUCA GGAUAUGCUAAAAGUAGAAAUAUAUUUUUAGUAUAGUGGA CAAGUAAAAGUGAACGGAGGGC	226	sly-miR8021-3-5p	AUUCAAGGCUCAAACUCGAGACCU	1-24	stu-miR8021	0	0	24	24	1
sly-MIR8021-4	UCUUAACCAGAAGUGUCAAGUUUGAGUCUUGGCAUGAAUUA ACACUACGUUCACUUUUACUUCUCCACUUUGGACUUCACA UGCCACUUAAAAACAAUGAUUGGUAUGCGUAUUUUAUCAC AAAAUCCAUAUUAAUUGAUGUUUAGUCUUAGGUAUUGACA ACUAAUGUGGGGAAUACGUAAUCAAUGUUGAUUCUUCUCA GGAUAUGCUAAAAGUAGAAAUAUAUUUUUAGUAUAGUGGA CAAGUAAAAGUGAACGGAGGGC	241	sly-miR8021-4-5p	AUUCAAGGCUCAAACUCGAGACCU	9-32	stu-miR8021	0	0	24	24	1
sly-MIR11564b	UCAUUGGAUAUUGGUGGCACUGUCGUUUAAAAACUAGAGC AUAUAUACUCUUCAUUCUAAUAGGAGACUAAAUAGGGACA CAUGACGCAAUGUUAUCUGUCAGUCUGAUAUUUAAUAAAU AUCGAGUCGAUGGAUAAGAUUAUGACACGUGUAUGUCCGU UAGUAUAAGAUAUAUAUGCUCUAGUUUUUGGACGGCAAAA GCACCAAUAUCCCAAAAA	222	sly-miR11564b-5p	UUUAUCACAAAAUCCAUAUUA	73-93	pab-miR11564b	4	0	21	21	1
sly-MIR8006-6	UUUUAAAAGUUGAUGGCGUCAGAUUGAUAUACGUUACUCA CAGUAACGUUUUAGGAGUAAAACGUUACUGAAAAUAACGU UUUAGGAGUAAAACGUUACUUACAGUGACGUAUAUCAACC	218	sly-miR8006-6-3p	UAGUUUUUGGACGGCAAAAGCACC	182-205	stu-miR8006-5p	4	0	24	24	1
sly-MIR10538-5		141	sly-miR10538-5-5p	AGAUUGAUAUACGUUACUCACAGU	21-44	sly-miR10538	0	0	24	24	1

sly-MIR7980b-5	UAAUGCUGUUAGUUUUUAAAA UCAUGCGAUAUCAUAUCAUGAUAUGGUAUCGUGAGAUGGA AUCAGUGUUUGGACAUGCGAUUUUACGUUGAUUCCAUCUC ACAGUUCCAUAUUAUGAGAUGUGAUCCAAUA	111	sly-miR7980b-5-3p	GAGAUGGAAUCAGUGUUUGGACAU	33-56	stu-miR7980b-3p	0	0	24	24	1
sly-MIR6147	UAGUUAUUCUUUCUUCCAUGUGAAUUUCCCAUAGAAACAU CAACAUCAGCAUCCAUAUUAGUUAUUUCUUCUUAAGGCUU CAUUAUUUUCUUCCCUGUAAUUAAAAAUAGUGCUUACAUA GAUGCGGAUCCCGAAUCUUGAGUUCAUAAAUUUGUAUUCU AGAAAAUGAUACCUUUUCAAAACCCACCAAGUUAUCUUUUA AGAAUUCAUAACCAUAAAAUCAAGAUUCUAGAUUCACCUCU AUGUAAGCGAAGAGAGUUGUGAAGAAUUUAGAGGAAAUAA GUCAUAACUAAGAUGAAUUUUGAUCUCGCUAUGGAAAUUC ACUCAGAAAAAUAAAUA	339	sly-miR6147-3p	AUACCUUUUCAAAACCCACCA	169-189	nta-miR6147	5	0	21	21	3
sly-MIR9470-3	AUUAAAUUUAUGUUAGUUAUUAUACACUAGAAAUAUUUGAA UCAUGAAUUUUAGUUUGCUAGUAAACGGGAAACAGGGAGA AAACUACUAGCCUAUGCCAUCCCAGUGUGGAAAUCGGCAG GCGAGGGAUGCCGUUAGGGGAGUACAAAAGGUUGAGGCG CUGUUAAGCAGUAAUUAUCCGCUAAAGUACGAUGCUUGUA GUGACCGGAAAACAUGAUAAUGAUACUCUAGUUUAUAAUA AACUAAUAUGAAUUUAAC	258	sly-miR9470-3-5p	UUUGAAUCAUGAAUUUUAGU	36-55	sly-miR9470-3p	4	0	20	20	1
sly-MIR4221-2	AAAGGUUCGUAGAACAUCGUGAAUGGUGCUAUGGUAGUAG CUCGUGGCACUAAAUCUUGAACCUUGUACACCAAUGCAGG GUGUAUUAACAUGGACUCUAUUGUUGAAGGUGCUUCCGG UUCAAUUCUGUGGGAAAUACACUUGGACACAAGAGUGCUA AAGGAAUGAAGAUGCUGGUUGCAAAAGGAUCAUUAGAGGG UCUGAAUUCUGUUGAUAUGGGUCUUUGCGAGAGUUGAGU UAUGGGAAAACAGAAAAGAGUAAGCUUUACAAAGACUCCUA GAGAUCCAAAGAAUGUGCGGUUGUAAAUGGUCCAUACGUA UGUUUGCGGACCAUC	334	sly-miR4221-2-3p	AAGAGUGCUAAAGGAAUGAAGA	150-171	aly-miR4221	4	0	22	22	1
sly-MIR10532-15	UAUAAGUGUGUCUCUGAGAUUUCGAGCAUAGAUUGAGGG GGUACUUGUGCAUUAUCCCAAACUAAUUACUAGGAGUACU UGUAAUAAGUUAGUUUGUUUUGGUAACCUAUCUGUAAUCA CUGGUACUUGUGAUAUUGUAACCACUUAAUUAAUUAUAUU AUAUAUAAAAUAUCCUUUUUAUUCAAAAAAAAAAAGGGAAA AUGCGCAAGCAUUCCCUCAACCUAUGUCCGAAAUCCCAAA GACACACUUAUA	252	sly-miR10532-15-5p	AAGUGUGUCUCUGAGAUUUCGAGC	4-27	sly-miR10532	1	0	24	24	1
sly-MIR11498c	CGAAUCAAACCGCAAAUCGAGUCAAAUCGAAAAAAAAACCC CAAUUAGUGAUUUGGUUUGACUUGAUUUGGUGUUGGAUAA A	82	sly-miR11498c-3p	UUAGUGAUUUGGUUUGACUUG	45-65	pab-miR11498c	5	0	21	21	1
sly-MIR11108h	UUUGCGGUGUGAGUUAGGCCUAAGAUCUAAUUUCACAUGG UACCAUAGCAGGGCCCGUCUCACCCGAUGUGGGACCCCC UAUAUCAAAAAUUGUCCACGCACCAGAUUUUAAGAUUGGG CGUGAGGUGGGGUAUUAAAGAAUGACAAAAGUCCCACAUC GGUGGUUAAUGAGAUGGGUGGACUCCUUAUACGGCUUAG ACCAUCAUCCUCCCUUUGAGCAAACUUUUGGGUGUGAGUU AGGCCUAAGAUCUAAUUUCACAUCGCUUU	267	sly-miR11108h-3p	ACAUCGGUGGUUAAUGAGAUGG	155-176	lja-miR11108h-5p	5	0	22	22	1
sly-MIR7997b-3	CUUUUGAAACCAUUGUUUGUACCUAAGUUGCUCGGACUCU UCAAAAAUGUCAGUGGGUGUGUGUCGGAUUCUCCAAAAGU AGUCUGACACGGGUGUGGCAACAAUGUGAAGAGUCCGCAA CUUAGGUUUGUACAAGGUGCAAUUU	145	sly-miR7997b-3-5p	AAGUUGCUCGGACUCUUCAAA	25-45	stu-miR7997b	2	0	21	21	1
sly-MIR3515	UUGUAUAAUAUAUAUGAAUUAUCCAUUAGAUUUAUUCAUUA UUAAAUGGAUUCAUGUAUAGGCAGAGGCAGACCCACAUGG UGUCCGCCGGGUGUUCGAGCACCCAUUAACUUCGUUACG GAAUAUAUAUAUCUAUGUAGAAAUUGAUAGGUAUUUGUAU AAAAUUAACAUAGAGCACCCAAUGAAUAAAUGAUUUAGCUG GCCCAAUGACUCCUGGAUGGGUACUUAAGACUUUUUUAGU GUUGUUGUACUAAGGUUCAAAUCUCAUUGUUAACACAUAU UUUUUAUAUUU	292	sly-miR3515-3p	UAUGUAGAAAUUGAUAGGUAU	134-154	ahy-miR3515	4	0	21	21	2
sly-MIR7822-3	GCCCUUCAACUUUGGUUGUGCACAAGUAGACACUUAAACU UGUAUAAAAUUGAACAAAUAGACACACACGUCCUACAUGUC AUUUUUUGUCGUACGUGUAUUGUGCCAUGUAGGACUCAU GUGUUUAUUUAUUUAAAAGUUGGACAUUUCAAGUGCAUGU UUGUGCAUUAUGAAAGUUGGAGAUC	185	sly-miR7822-3-5p	UAUAAAAUUGAACAAAUAGAC	43-63	ptc-miR7822	5	0	21	21	1
sly-MIR827b	ACUAUGCCCUCCAACUUUGAUUGUGCACAACUAAGCACUU AAACUUGUAUAAAAUUAAACAGACACACGCUAUACAAGUUU AAGUGCUUACUUGUGUACACCAAAAGUUAAAGGUCAUUGU	121	sly-miR827b-5p	UUUGAUUGUGCACAACUAAGC	16-36	gra-miR827b	5	0	21	21	1

sly-MIR821b-2	AAAUUUAUUUAAUAAAACUUCGGUUCUUCGGUGCACCGUAGUUUCGGGACCCUGCAUUGAACUCCGAACCGAAGAAUCGAAGUUCCGAAAAUAAAAAA	98	sly-miR821b-2-3p	AAGUUCCGAAAAUAAAAAA	80-98	sbi-miR821b	5	0	19	21	1
sly-MIR7981-20	UUUCAUAGACACAUUUUGACUAAAUUAAGGUCCUAUUAUCCCUGAAUUUAUUUUUUUGUAACUUUAUACACUUUUGGUCUUACGUGGCAUAGUCUGUGACGACUCCACGCAAUUGAGGCACGUGGGCGAUAUUUAGAUUCCACCUAUGCUUAAAAAGGUGCAUAAAAUUACAAAAAAAAAUGAAUUCAGAGGUAAAUAGAACCUUAGUUUAAUUAAGAUGUGUCUCUGAAA	231	sly-miR7981-20-5p	UUUGACUAAAUUAAGGUCCUAUUA	15-38	stu-miR7981-5p	5	0	24	24	2
			sly-miR7981-20-3p	AUAGAACCUUAGUUUAAUUAAGAU	196-219	stu-miR7981-3p	4	0	24	24	1
sly-MIR3951b-2	AACUCUCUUUUAGACUAACUCUUUCACUCUUUGUUUUCUCUUGUGUUUUGUGUGUAUAACCAAAUGAAGACCACCACUAUUUAUACUACAAGAAGUCUUCCUAGCAAUGAAUAGGAAGAUAAUGGAGGUAGUAAAUAGUGAAGAUAAUGGUCUUAGGAGUUACAUAAGUUACAAUAGGAGUUACAUAGGUUACAAUAGGAGUUACAUAGGUUACAAAGAGUAAUGGAGGAAUUAAGAGUGAUGG	244	sly-miR3951b-2-5p	UUUCUCUUGUGUUUUGUGUGUA	35-56	csi-miR3951b-3p	5	0	22	22	1
sly-MIR171c-3	GGGGUGUGAGUUAGGCCUAAGACCUAACUUCACAUGGUACCAAAGCAGGACCCGUCUCACCCUAUGUUGGAACCCCAAAAUCAAAAUUGUCCACGCACCAGAUGCUAAGCACUGGGCGUGAUGUGGGGUGUUAAAGAAUGACAAAAGUCUCACAUCGGUGGUUAAUGAGAUGGGUGGAAAACUUAUAAGGCUUGGGCAAUCUCCUCCCUUUGAGUUAGCUUUUGGGGUGUGUAUUAGGCCUAAGACCCAAUUUCACACUUU	261	sly-miR171c-3-5p	UGUUGGAACCCCAAAAUCAAA	65-85	csi-miR171c-5p	4	0	21	21	1
sly-MIR3706	GGGACACGUGACACAAUCUUAUUCAUCGAUUCGAUGUCGGGUUGAUGGAUAAGAUUAUGACACAUGUAUG	70	sly-miR3706-3p	UGUCGGGUUGAUGGAUAAGA	35-54	pab-miR3706	5	0	20	20	1
sly-MIR5026-4	CCCCCGAACUAUCAUAAAUGGUAUGGAGAUACCAUCCAUUAUACACGUUUCAUAAUCUUAUUCAUCGACCCGACAUUUUCAAAUAUCAAGUCGACGGAUAAGAUUGUGUCACGUGUUCUCAUUUAGUCUUCUGUUAGAGUGAAAGACAUAUAUGCUCUAGUUAUGGACGGUUAAUGCACCAAUAUCCCAAUAAUAUAAUAAAAGGUGUGUGCAUACCAUUUCUAAUAAUUCGGACA	236	sly-miR5026-4-5p	ACGGAUAAGAUUGUGUCACGU	94-114	ath-miR5026	4	0	21	21	1
sly-MIR7981-22	CACGCCUUAAUUAAACUAAGGUCCUAUUACCCCAUCAAUUCUAUGAAUCCACGCAAUUGAGGCGCGUGUGAAGUAUUUUGGAUGUCACAUAAGCCAAAAAAGUGUAAAAAUUACAAAAAAAAAAAAAUAAGUUGAGGGGGUAAUAGGACCCUAGUUUAGUUAAGGCGUG	168	sly-miR7981-22-5p	CUUAAUUAAACUAAGGUCCUAUUA	6-29	stu-miR7981-5p	2	0	24	24	2
			sly-miR7981-22-3p	AUAGGACCCUAGUUUAGUUAAGGC	142-165	stu-miR7981-3p	3	0	24	24	1
sly-MIR11583b-1	UGUUUUUCUCUCGCUUCAUACAAAAACAGAAACACAAUAUAUACACUUCUGUUGUAUAAAGCGAGAGAAAAUUG	74	sly-miR11583b-1-5p	UUUUCUCUCGCUUCAUACAAA	4-24	pab-miR11583b	4	0	21	21	1
sly-MIR5674b	AAAGAGAUUAUAUGGAUAUAGAUAUAUAAUUUAGAUACGAUAAAAGGUAAUCAAAUGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCACUUUUCAGUGCUACUUCUUUUUCAGAUUUAACCCAAAUUUGUUUCUGUUUACAUUUUAUGUAUCUAAUAUGUCAUUACAUGUUAGAAUUUACCUAAUUUUCUUUUACAUUAUCAAAAUAUAUACAUGUAUAUCUUAAAUUCGAG	273	sly-miR5674b-3p	UAAUUUUCUUUUACAUUAUCA	223-243	gma-miR5674b	3	0	21	21	1
sly-MIR1435b	AGAAGAGAUCGUGAGGGGAAGAGGAGUCGGCAGCAGCAAAUUUUGAAAAUAGAAAAAAAACCCUAAUUUUGACUAAUAUUGUUAAGUCAAAUCUUUUAAAAAAUUUAAAUCAAAAAGGCGGUGCCAUAUUGUCGCCAUUAGCUCGCCAUGGGUCGCCUCGCCUCAGUGUGGAAUGGCGAGAAGGGCUCGCCUUGCCUCGCCUCUCGCCUUUGGCGAUGAGGCGCUCGCCAUUCACAAUACUGCUCCUAGCUCUCUCUAUCUUCAAGAUGUCUAAA	275	sly-miR1435b-5p	AUUGUUAAGUCAAAUCUUUU	78-97	sbi-miR1435b	3	0	20	20	2
sly-MIR2604-2	UGUGUGUGUGUAUAUAUAUAUAUAUUGGGUUUGCUAGAACACACCCACUAAUUUUUAUGUGGAAGUGUUUUAGCAAAGCUACACCUUAAGGUGUAUUUAACUACUUUUUAGUUAUUCACUUGCUAAAAUACUCUUUCUAAAAAAUAAGUGGGUGUAUCCUAGCAAAUGCCUAUAGGAUUUGCUAGAAUUCACCCACUUGUAUUACUUCCUCCGUUUAAAAAAGAACAUCCUUAUUUUCU	199	sly-miR2604-2-5p	UAAUUUUUAUGUGGAAGUGUU	49-69	mtr-miR2604	1	0	21	21	1
sly-MIR5174d-2	UUUUAGUUUGUUUCAGAAAAAAAAUGUCCCCUUUCUUUUUUUGGCAACACUUUAACUUUAACUUUCCACGUAACAUUUUUAAGACCACAAGAUUAAAGGGCAUUUUGGUACAUUUGACAU	262	sly-miR5174d-2-3p	CAAUCUUUUUUAAACGGAGGGAGU	235-258	bdi-miR5174d-3p	4	0	24	24	1

sly-MIR10530	AACUUUAAUUUUGAACCACAAGUUUAAAAAGUCUUCCUUCUUUUUCUUAAACUUCGUUCCAAGUCAAACUAGGCCAAUCUUUUUUAAACGGAGGGAGUACCAACAUGUUGAAUGUUGGGGAACGAACGUCUAAGGUUUGGGUCAACGAUCUCAAUGUUGAUGCGUCCGCUUGUUGUUGAUGCUGCUCCAAAAGGUUCAACAUUGGGAUUUUAGCCCAACAUCAGACGUCCCUUCCCCAUCGUUCAACAUCGU	152	sly-miR10530-3p	ACGUCCCUUCCCCAUCGUUCAACA	125-148	sly-miR10530	0	0	24	24	1
sly-MIR5139b	GCCCAUGUGUCAUAUCUUUACAUGGUCUGAUAAAGAUAUGACACAUGAGCCCAACUCAUCCCCAAGAGUUAGUUUUUGCAUUUUAGGGUUGAGUUAGGCCCAAGUGUCUUAUCUUUACAACGCGCCCAAGCCCAUCUUGUGCGUGGACUGGGAGCCCAACGAGAAUAAACAUGACUCUGAUACCCUGUAAAGAUAUGGCACAUGAGU	208	sly-miR5139b-3p	AUAAACAUGACUCUGAUACCC	166-186	aof-miR5139b	4	0	21	21	1
sly-MIR8006-7	UGCGUUCCUGCCGUCCAAGAACUAGAACAUGUAUAUCCUUUAUACUAACGGACAUACAUGUCAUAUUCUUAUCCGCUGAUUCGACACUUAUUGACGAAUAAGAUUGUGUCAUCUGUCCCUAUUUAGUCUUAUGUUAUAGUGAAGGGCAUAUAUACUCUAGUUUUUGGACGACAGGGACACC	181	sly-miR8006-7-3p	UAGUUUUUGGACGACAGGGACACC	158-181	stu-miR8006-5p	1	0	24	24	1
sly-MIR1130b	AUGUAUAAAAUUGAACAAUUAGACAUAUUUGUCCGACAUGUCGUCCUUGCACCCUACAUAUAUUAUGUCACGUAGGACACAUAUAUCUUCUUGUUCAAUUUUAUAUAA	108	sly-miR1130b-3p	ACAUAUAUUAUGUCACGUAGG	56-76	tae-miR1130b-3p	5	0	21	21	2
sly-MIR10420-2	UCAAAUUCAGACCUGUGAUUGAAAUUUGAGAAUGUCAAAUCUAACUUCAAAUCCAAAUGAUUGAAGUUGAAGUCAAACAUCAGUUUUUUGGGUUUGAAUUAGACUUGGCAGUCCCCAACUUCAAACCUUUUGAAUUAGG	139	sly-miR10420-2-3p	AGUCAAACAUCAGUUUUUU	71-89	gma-miR10420	5	0	19	19	3
sly-MIR5014a-7	UAAUUCACUAUACAUAUAUAACUGUAUAAUUCGCUGGCCUAAAUUGUAUAAUUCGUUGGCCUCGCUGUACAUAUACAAUUGUAUGACUCGCUGGCAUAAAUUGUAUAAUUUGCUGGCCUAUUUCACUGCAAUUGUAUAAUUUGUUGGCCUAUUUCGCUGCAAUAUGAGUAUAAAAUUUGUUUUGCAUACAACUGAAUCGAAGUAAAAUAUUUGUAUAUUGUAUAAUUCUAAGUGUAUAGGAAGAA	245	sly-miR5014a-7-3p	UUGUAUAAUUCUAAGUGUAUA	218-238	ath-miR5014a-3p	5	0	21	21	1
sly-MIR7984d-4	CUAAUACUCUUUAUGUAUGAAAUUGGGAAAAAGGUCUGAAAUAUAUUUGAAUUUUGAUCGAAAUUGUUGUAACGAUGUCAAACUUUGGCAAAGACCUUUUACCCCCUGCACUAUUUAAUAGUGUAUAUU	129	sly-miR7984d-4-3p	AUUUGAAUUUUGAUCGAAAUUGUU	45-68	stu-miR7984d-5p	5	0	24	24	1
sly-MIR5652	AAUUUAAUGGGUUGAAUCUGAAUGAUUCAGUUUCAGACCUAAAAAUCAAACGUACUUAAUAGGCUGAAUCUGAAUGACGAAGAUUUGGACCUCCAUUAAGUG	102	sly-miR5652-5p	UUGAAUCUGAAUGAUUCAGUU	12-32	ath-miR5652	5	0	21	21	1
sly-MIR1917-5	ACUACAACAAAAAUAACUUUUAUCGAUAUUAAAUAUUGACACUAAUAAAGAGUGUUAACGUUUUUAUCGGCAUUAGUUAAGUGUCAUUAGAACCAGUGUAGCUAAAGGCUUUAGAGACAUAUACAAAGAGUGACAAUUGCCGCUAAAAGUACAUAUGUAGCGGCAAUUAAGAAUUAAAUGCCGCUAAUGGUCAUUUUUGUUGUAGU	206	sly-miR1917-5-5p	ACUAAUAAAGAGUGUUAACGU	41-61	sly-miR1917	3	0	21	21	1
sly-MIR11451	UAGGUAUUAGCAAUGCAGUGGUUUUAAUGCUUGCACUAAGCAUGAUUAAAGAUUCAAUUGCCCCCCUCAACACCAUUUUUUACAUCUUUUCCACCAUAAUAGUGGAGGGUAUCUUUGUAUAUAAUUUUUUAUUGCAAUGCAUGCUAUUUAUAAUGUAUCAAACCAAACAAUGCAUAAAAAUAAUCUAUGCAAAAUUAAUCCAAGCAUAACUACUACAUGCAUUGCUAAUACAAA	235	sly-miR11451-3p	UAACUACUACAUGCAUUGCU	208-227	pab-miR11451	5	0	20	20	2
sly-MIR1128-6	UUCUACUCCCUCCGUCCCAUAUUAGUGGUCCACCUUACUAUAAAUAGUUGUUCCAAAUUACGGAAGUGGACAACUAAUAUGGGAUGGAGGGAGUACUU	98	sly-miR1128-6-5p	UUCUACUCCCUCCGUCCCAUA	1-21	ssp-miR1128	2	0	21	21	1
sly-MIR2876	GCCGCAAGGUUCGUAUUUGUACACGGUUGAGUUGGUAAAUGCCACCGAUGAGGGCUUGGCCCCGCAGACUCCCAUGCCAGCCGUGUACAGAAUGACCUGCAGA	103	sly-miR2876-5p	UUCGUAUUUGUACACGGUUGA	10-30	osa-miR2876-3p	5	0	21	21	1
sly-MIR5181b	GACACGUGACACAAUCUUAUUCAUCGAUCUGAUAUUUAAUAAAUGUCGAGUCGGUGAAUAAGAUUAUGACACGUAUA	77	sly-miR5181b-3p	UCUGAUAUUUAAUAAAUGUCG	28-48	bdi-miR5181b	5	0	21	21	1
sly-MIR172d-2	UUAACUUAAUGGGCUAAAUCUAAAUGAUUCAGAUUCAUACCUAAUAACCAAACAUACUUAAUAGGAUGAAUCUAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCG	105	sly-miR172d-2-5p	GCUAAAUCUAAAUGAUUCAGA	13-33	cas-miR172d	5	0	21	21	1
sly-MIR11465	AAUAUUAUUAAAAAAUUAAACUAAAAAAAAUUUCACUUCAGUUAGAGAAAAGGGUAUAUAUGAGUGAUUCCUAUACCGGUAUAGGUAUAUAUGAAUCACUUUCAUAGCGAGGGAUAUAUCA	327	sly-miR11465-3p	CUAUGAAAGAAGAAUGAGACU	167-187	pab-miR11465	5	0	21	21	1

sly-MIR7997c-11	ACUCUAAAUGACAAAGUUAAGAGGUAUAUCAGACCUUCGCCUCAGCUAUGAAAGAAGAAUGAGACUCGAAUCAAUCUUGUAAAAAAUAAUUAGGGGGUUCCUAAAAAUGUGGCUGAUUUGUUCUUUUACCACUUAGCCACACUCUCAAUAUAGUUGAUCUAGAUAGUCUGAAUACAAAUUUAUUUUCUUUUAUGUGUUACAAUUCU	109	sly-miR7997c-11-5p	AUGUUUCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	3	0	24	24	1
sly-MIR10540-3	AGAAGCUAUGUUUCUCGGACUCUCCAAAAAUGCUACGUAAUUCACUAUUUUUGAUGGAUCCGACAUGCAACCCAUAGUGUUUUUGAAGAGUUCGAGAAGCAUAGCUGAGCGGUUGAUUUCUCAUAUAGUCACUUGAUUAAUAGUUAUUAUCUCGAAAGUCCCCUUUCUUCUUGAUUCCAAAACUUUCAACAAAGAAAGUGACUUCCUGAGAUGAUAACAAUUAGUCGAGUGAUCAUCUGAGAAAUCAAACU	142	sly-miR10540-3-3p	AUGAUAACAAUUAGUCGAGUG	102-122	sly-miR10540	4	0	21	21	1
sly-MIR822-2	UUGAACAAAUAGACACACAUGUCCCACAUGUUAUUUUUUAUACUACGUGGUAUCCUACGUGUAUUGUGUCACGUAGGACUCAUGUGUUUAUUUAUUUAA	99	sly-miR822-2-5p	AUGUCCCACAUGUUAUUUUUU	19-39	aly-miR822-5p	5	0	21	21	1
sly-MIR5274b-2	AGAGCUCUAGGGCGUCAGGGUCACAGAUGGGCAGGGGUUUGAGCCAGUCGAGGCCACCUUUGCCUCGGUGUUCUCGUUGUGGUAAGUCUCAUCCUGGGGAAUGUCGUUGGGCUACGGGUGCAUGUUUUUCUUGCGGCCGUCAGGGCCAUACUAUGAGGGAGUGUUAGUGCAGGUGGUAUGGCACAGCCUACAGGGUCCGUUGCUGGUUCAUCUUCUUCUGUGGCUAUGCGCCCUACGGAGCAGG	244	sly-miR5274b-2-3p	CUAUGAGGGAGUGUUAGUGCA	151-171	mtr-miR5274b-5p	5	0	21	21	2
sly-MIR7502c-3	ACUCUUAUUAUAGUUUUUAAAUCUUUUAUCACAAGUUUUUACUUGGUUUCAAGAUGGUGGUACAGUCUGAUAAUACACUGUUAAUGAUAGCGAACAUGUGGUAGUGUAAGUCCCCUUAAGAUGAAUAAAGGGGCAGCCUGAAACCCUUGUUAGAACUGCUAUCCAUUAAUAUGUAUAUUAUUAAGACAGGCUCCAUGCUUGAGUAAAAGUUUACCAUACAGCCGAAACUUAGGAUAAACUUUUAACAAAACUAUAAUAAGUUU	263	sly-miR7502c-3-3p	UUGUUAGAACUGCUAUCCAUU	147-167	gra-miR7502c	5	0	21	21	1
sly-MIR6459a	UUCUUUUUCCAAAAGAAAUAAAACUUGUGGGAUCGUUUGACAUAGGGGUGUCAAAUAGGCGGGUUGAGUUGAAAUUGAAACUGUUAAAAUGAGUUAAACUAUAAAUCGGGUUGGGUCUUGACCCGCCUAAAUUUACUUUGGGAUCAAAUGGGUUGGGUUAAAUGGACUACAAAAUGGGUUGGGUCUUGACCCAUCCAAUUUGAUUCAAUUAAUCUCAAUAAUUUUAACAUAGUGAUAUUUAAAUUUUAUAAUUACAAUUCGAAUUUCGGCUCAAGUUUUUUUUUAUAUAUAAAAUGU	297	sly-miR6459a-3p	UCGAAUUUCGGCUCAAGUUUU	259-279	ptc-miR6459a-3p	5	0	21	21	1
sly-MIR1046-2	UUAUCCCUGUUAGUACACCUCUUGCUGGUCAUAUGAUGUUGAGCAAGAAGAUUUGUCCUACAGCUAGGGAGGAAAAGAGAGAAUGGUCAAAGUUCUAUAUUCCUCCGUUGUCGGAAGUCUAAUGUAUGCAAUGGUAUGCACUAGACCUGAUAUUUCUCACGCCGUUGGUGUUGUCAGUAAAUUUCUUAAAAAUCCGACAAAAGAGCAUUGGGAAGCUGUGAAGUGGAUACUCAGGUAUCUUAGAGGAAACUCAGAUGGAUGCUUUUGUUUUGGAGCAUUAAAUUCAAUCUUGAUAUGCUAUAUAGAUGUUGAUAUAACAGGUGACCU	327	sly-miR1046-2-5p	UAGACCUGAUAUUUCUCACG	142-161	ppt-miR1046-5p	5	0	20	20	1
sly-MIR10532-16	UGGGGAAAAUGCACAAGUACCCCCUCAACCUAUGUCUUAAAUCAUAGAGGCACACUUAUACUAUUACCUAUUAAGUGGGGUAAUAGGACCUUAGUAUAAUAUAAAUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGGGUACUUGUGCAUCGUUCCUAU	160	sly-miR10532-16-3p	AAAUGUGUCUCUGAGAUUUCGGGC	103-126	sly-miR10532	1	0	24	24	1
sly-MIR3623	UCUUUCUCAACAAAACUAAAUGGUAGCUCGUCAACAAUUAUCAUUUUGGCUAAAGCUUUCCUACGUUGUGCUUGGUCAAAUUUCCAAGUGCUAAUGACCCCUUCCUUUGAUCCCGUUGGAGAUGGUAGAAAAUUAAUUAGAUUUUGACCUUUAUCUACGGUGUCACGAGGAAAUUUAGGAUAUAUUCUCAAAUGAGUAUUCAUUGAUGACGUACCAUUAGAUGAUGUAGAAGUU	234	sly-miR3623-5p	UUGUGCUUGGUCAAAUUUCCAA	66-87	vvi-miR3623-3p	5	0	22	22	1
sly-MIR8013-3	AAAAUUAAAAAAUAAUGUUAAAUCGCUGCCCUGGCAGCGAUUUGUAAGAAGAAACAUUUUGAAAUCGCUACUUGAGCAGCGAUUUCAUUUUUUAUUAAAAAAAUUUUUUUUUGGCAAAAUCGCUGCCUCAGCAGCGAUUUUACUUUUUCAGUUGAAGUAAAUCGCUGCGUCGGCAGCGAUUUUACCGUUUUGGUUUAUAUAAA	203	sly-miR8013-3-3p	UGAAGUAAAUCGCUGCGUCGGCAG	153-176	stu-miR8013	5	0	24	24	2
sly-MIR9752	UUGUUGUUGUUCUUCAAUUCGUUGAAGUUAAAGAAGUUUCAGGUACCGCUAUUUUUGUAACAGGUUUAAUCCGUUUUAUC	257	sly-miR9752-3p	UGCUUCAUCUUGUUUCUGUUU	190-210	gma-miR9752	4	0	21	21	1

sly-MIR7992-11	UUGGGAGAAAUUAAUCCAUAACCUUGGGUACAGUGAGGGGAUUAAAUUUCUUAAGGACACACAGUAGUUUCUGUGGACUCGGAUUAAUUCUUGUAUUUUAAAUUUUUUCUGCUUCAUCUUGUUUCUGUUUUUGUUCAUUAACUUCAUAAAUACAAGUUAUUGUAAGAAUAACAAUCUCCAAUCAUUACUCCAACUUUGGAGUACACAUCCAGACACUUCAAAUCAUGUCCACUAUAUCAAUUGAACACUCAACAGUCCAACUUACAAAAUGAACGUGUAGACACCACCAAAAUUUACGUGUCACGUCAACGUUGAGUUCCCACAAGAUCAGUGGGACUGAGUUGAGAUGUCUAGAUGUGCACUCCAAAGUUGGAGAGUAUUAUC	208	sly-miR7992-11-3p	UGUCUAGAUGUGCACUCCAAAGU	172-194	stu-miR7992-3p	2	0	23	23	1
sly-MIR10538-6	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACAUUUUACUCCUAAAACGUUACUCAUAGUAACGUUUUAGGAGUAAAACGUUACUGAAUAUAAUGUUUUAGGAGUAAAACGCUACUUACAAUAACGUAUAUCAACCUAAUGCUGUUCUUCAACGGAUAACUAUAUCCUUCAAUUUUGAGUGUGCACAAGUAAAUACUUAAGUUUAUAUAUGACCAAGUAGACAUAUGUAUUCUACAUGGUAUAAUACGCAUAAGACGUCAUGUAGGAUACAAAAUUUUCAUGUAGGGUGUCAUGUAGGACAAAUGUGUCAAUGUAUUCAAUUUUAUACAAGUUUAAAUGUCUACUCGUGCACAUUCAAAAUUAAUAAAGAUCAUAAUUAUCGAUUGACGC	148	sly-miR10538-6-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
sly-MIR160e	AACUCAGUUACUAACAUUCACUACAAUAAAAAUGAUCAUUAGCGGCAUUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUAUCACUCUUUACGUAUGUCCCUAAAGCCUUUAGCGACAUUCUAAUGCCAGUAAAGAUGUUAGCACUAUUUAUUAAUGUCAAUAUUUAAUGCCGCUAAAAAUUAUCUUUGCUAUAGUGAUUUGAGAUCAUUGACCA	245	sly-miR160e-3p	UCAUGUAGGGUGUCAUGUAGG	133-153	bdi-miR160e-3p	5	0	21	21	2
sly-MIR7983-7	ACCAUGACAAUUAAAAGUGGACGGAUGGAGUAAUUUACGCACUUCUUAAGAAAUUAUAGAUAGAAGACUAAUUUUACUAUAUUGCCCUUUGAAUAUACUCCCUUAGUUCAUUUUAAUAUGUCAUCCU	226	sly-miR7983-7-3p	UCUAAUGCCAGUAAAGAUGUUAGC	131-154	stu-miR7983-3p	5	0	24	24	2
sly-MIR6441	UAGUUUCCUCACUUUUCAUAUUCUCUCUUUUCUUUUCCCAUUCACACUUGCUAAAACCCAACACUUCGUUUAGAAAUAUUUAACUAGAACAAAAUAUAACGUUCUUAUCGAAUUUCUCUCUUGUGAAGUUCAUUUUUUUUAUCUUCUAUUUGAAGAAAUUGUUGCCAAAAAAUAAUGGGUUAUUGUGAGGGGAAAAAUCUAU	127	sly-miR6441-5p	AAGUGGACGGAUGGAGUAAUU	15-35	ptc-miR6441	5	0	21	21	1
sly-MIR859-2	GUGAAUUGGUAAAGGUGAAAUGGAGAUGAAGAGUUAAUAUUGGGUGAAAAUG	254	sly-miR859-2-3p	UUUCUCUCUUGUGAAGUUCAU	113-133	ath-miR859	5	0	21	21	1
sly-MIR7983-8	GUGCAUCCGUCACUACAAUAAAAAUAUCAUUAGCGGCAAUUAAUUCUUAAUUGCUGCUAAAUAUGUAUUUUUAUUUGGCAAUUGUCACUCUUUGUAUAUGUCCCUAAAGCCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUAGCCUUCUUUAUUAAUGUCAAUAUUUAAUGUCGCUAAAAAUUGUUUUUGUUGUCGUGCAUGGGUGAGU	229	sly-miR7983-8-3p	ACUAAUGCCGGUAAAGACUUUAGC	141-164	stu-miR7983-3p	1	0	24	24	1
sly-MIR1919-7	CUGCAAUAUUUGAAGUAAAAUGUUUGUAAAUUAUAUAAUUAAGUGUGUAACACGAAGAUAUACAUUUUUGCAUGUGUAUAUACAAUUUUCUCUCGCUUUUUACAAAAUAGAAACAGAAGUUAUACACUUCUGUGUAUAAAGUGAGAGAGGCGAGAAUGGGAGAGUGGCGAGCGAGACUUCUGGGAGAGAGACGCCUGGAAAAUUUUUGUCAACGUUUGCUAUGGAGCACAAUUAAAUCAAACCCUAGCUAUUCCAUUUAAUUUAGGUUAUUAGUUUGCUAUUUUAUACGAUUUUCCCUUCUAUUAUUGACU	311	sly-miR1919-7-3p	GAGCGAGACUUCUGGGAGAGA	169-189	nta-miR1919	5	0	21	21	1
sly-MIR8011a-5	AUGGAAAGAGUUUACUUUGUGUCUCACACAACUGACACAAGUUGUGUGGGGAUUCUUUUUGUUUCACAAAUUUGUGGACCAAAAGUGUAAGACUAGGGUCCAGUAAUUUGUAGAUCAAAGCCUCACACAACCUGUGUCUGUUGUGUGAGACACAAAAUGAAGUUUCUCUUG	171	sly-miR8011a-5-5p	UUGUGUGGGGAUUCUUUUUGUUUC	42-65	stu-miR8011a-5p	2	0	24	24	1
sly-MIR6271-3	AAGUAAUGAAGCCAAGUACCUAUUUUUGCUUUGUUCCUUGUUCGAGGAAGAUAGAGAUAUAUAAUUACUUUGGAUAUGGAAGUGGGUUUCACAUCUUUCCGGGCAUUGAAAAUUUAGAACAAGCAAGAGAUAGGGCGUGUCUUCUGUUAGAA	152	sly-miR6271-3-5p	GGAAGAUAGAGAUAUAUAAUU	46-66	ppe-miR6271	5	0	21	21	3
sly-MIR6254	AUUUAUGCACAAAUAGACACUUAAACUUCUAUAAAGUUGAACAAAUAGACACACAUGUCCGACAUGUAAUCCUACAUGUCAUUUUUUGUCCUACGUGGUGUGCUACGUGUAUUAUGUCAUGUAGGACUCAUGUGUUUGUUUAUUUAAAAGUUGGAUAGUU	183	sly-miR6254-3p	UGCUACGUGUAUUAUGUCAUG	101-121	osa-miR6254	4	0	21	21	1

sly-MIR10538-7	AAAGUGUCUGUUUGUGCAUAUGA GUCAGAUUGAUAUACGUUACUCACAGUAACAUUUUACUCC UAAACGUUACUCACAGUAACGUUUUAGGAGUAAAACGUUA CUGAAAAUAACGUUUUACGAGUAAAACGUUACUUACAGUAA CGUAUAUCAACCUAAU	137	sly-miR10538-7-5p	AGAUUGAUAUACGUUACUCACAGU	4-27	sly-miR10538	0	0	24	24	1
sly-MIR8037	UAAAAAUGCAUUUAUUUGGAAUAAUAGUAACCAUGAAUAGU AAGAGUCAAGUUACUGUGUAAAUAGUAAGAGUCAAGUAAC UGUGUAAAUAGUAAAGGCCAAUCGUCCUUUAGCAAGGAUG AAAGGUCAUUAUGUAUGUCUAUAUAAGAGGCAUUUACC	159	sly-miR8037-5p	UUUAUUUGGAAUAAUAGUAACC	11-32	stu-miR8037	5	0	22	22	2
sly-MIR5014a-8	UAUUUAUGUCCUUCAAUUUUGGAUGUGCAUAAACAGACAC UUAAAUUUGUAUAAAGUUGAACAAAUAGACACGUAUGUCC UAUAUGUCGUCCUACAUUGUCCUACAUGGUGUCCUAUGUG UAUUGCGUCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAA GUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUU GGAGGUCAAAGUU	213	sly-miR5014a-8-5p	ACACUUAAAUUUGUAUAAAGU	37-57	ath-miR5014a-5p	5	0	21	21	1
sly-MIR7992-12	UGGCUUCGAAUUAUAUUUAUACUCUUUAACUUUGAGUGUG CACAAGUAGACACUUAAACUUGUAUAAAGUUGAGCAAAUAA ACACACGUGUCUUACAUGUCAUUUUUUAUCCUACGUAGUG UCCUACGUGUAUUGUGCAUGUAGGAUUCAUGUGUUUAUUU ACUUAAAAGUUGGACAGUUAAAAUAUCUGUUUGUACAUUA UGAAAGUUGGAGGUCAAAGUUAAAAUUUAAAGUUA	236	sly-miR7992-12-5p	UUUGAGUGUGCACAAGUAGACACU	31-54	stu-miR7992-5p	5	0	24	24	1
sly-MIR10216	GGGACACAUGACACAAUCUUAUCUGUCGAUCUUAUAUUUA AUAAAUGUCGGGUCGAUGGAUAAGAUUAUGACACGUGUAU G	81	sly-miR10216-5p	UAUCUGUCGAUCUUAUAUUUA	20-40	eun-miR10216-5p	5	0	21	21	1
sly-MIR7997c-12	AAGACCUAUGUUGCUCGGACUCUCCAAAAAUCAACUACUU UUGAAGAGUCCUAUACACGUGUUGACAUUUUCAGAGAGUC CGACCAACAUAGGUAAA	97	sly-miR7997c-12-5p	AUGUUGCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	2	0	24	24	1
sly-MIR7983-9	UCCCUAAAGCCUUUAGCGACAUUGGUUUUAAUGACAGUUA ACUAAUGCCGGUAAAGACUUUAGCAC	66	sly-miR7983-9-5p	UAAAGCCUUUAGCGACAUUGGUUU	5-28	stu-miR7983-5p	2	0	24	24	1
			sly-miR7983-9-3p	ACUAAUGCCGGUAAAGACUUUAGC	41-64	stu-miR7983-3p	1	0	24	24	1
sly-MIR399e	GGUGUGUUAAUUCUUUAGAAUACCUUUAUUAAUUAACCAU UAAUAUUAGAAGGGGGCGUGACCAAUAGAUUAGGAAGUUU GUUUUAGUUAUUGAAUGUGCUAAGUAUGAACGGAAACCAU AAUCGGAUUAUUAGUGGUGUCGUGUUGGUGCUUGGGCUG UUUUGAUUAAAGCAAACUGCGGGAAAAUUCUAUUUUGGCA UUAUGUAUAUGUUAAAUGUGAUUAUGAGUAUAUACUCCAA AGGAUGAAUACGAU	253	sly-miR399e-3p	GGAAAAUUCUAUUUUGGCAUU	181-201	csi-miR399e-5p	5	0	21	21	1
sly-MIR172a-1	CUAAACUUGAUUUUAAAUUUCAACUUUACCCUUCAACUUUC AUAAUGCACGAACAUGCAUUUUAACUAUCCAACUUUUAAAU AAAUAAACACAUGAGUCCUACAUGACACAAUACCCAUAGGA CACCAUGUAGGAUAAAAAAUGACAUGUAGGACACGUGUGU CUAUUUGUUCAACUUCAUAAAAAUUUAACUAUCUACUUGU GGACACUCAAAGUUGAAGAUCCUACAUGUAAUUCGAAACC AAGUUAAA	251	sly-miR172a-1-3p	UCAAAGUUGAAGAUCCUACAU	210-230	vvi-miR172a	5	0	21	21	1
sly-MIR1128-7	GGCUAAUGUUUAUUACUCCCUCCGUCCCAAUGUGAGGUAG UUUGACUUGGCAGUUUAAGAAAACAGUCUAAAAUAAGUUA UAGAUGUUGGUGUAGCUGUAGAUCAUUUUAUUAAGGGUAA AAUAGGUACUUUAAAGUUAGAUUGUUACUGAAUAUUGAAA UGCGUCAUUCUUUUUGGGCUGACUUAAAAGAAAAGUGAGC AUAUAAAUUGGGACAGGGAGUAUAUAGAAAGUAAAU	236	sly-miR1128-7-5p	UAUUACUCCCUCCGUCCCAAU	11-31	ssp-miR1128	2	0	21	21	1
sly-MIR172a-2	AAACACUGUCUCAAAUGUAAAUCCUCAGGUCGCCAAAGUC UAUAUCCUCCAAAAAGUAGUGCAUUUUUGGAGUAGAACAA CAUAGACAUUGACGACAUGAAGAUUUACAUCUGAGACAGU GCAU	124	sly-miR172a-2-3p	UUGACGACAUGAAGAUUUACA	89-109	vca-miR172a-5p	5	0	21	21	2
sly-MIR7983-10	UCAUGUAUACACUACAACAAAAAUGACCAUUAACAACAUUU AAUUCUUAAUUGCCUCUAAAUAUGUAUUUUUAGCGGCAAG UGUCACUCUUUGUAUAUGUCUCUAAAACCUUUAGCGAAAU UGCUUCUAAUGACAGUUAACUAAUGCCGGUAAGGACUUUA ACACUCGUUAUUAGUGUUAAUGUUUAAUGCCGCUAAAAGU UGUUUUUGUUGUAGUGAUAUCCAAAU	227	sly-miR7983-10-3p	ACUAAUGCCGGUAAGGACUUUAAC	140-163	stu-miR7983-3p	1	0	24	24	1
sly-MIR5014a-9	GAUUAUGACCUUUAACUUUAGAUGUGUACAAGUAGACAGU UAAACUUGUAUAAAAUUGAGCAAAUGAACACAUUUGUCAUA CAUGAUACUGCUACAUGAUAACUUUGUCUCCUACAUGACA UUCUACGUGUAUUAUGUCAUUUAGGACACUUGUGUCUACU UUUUCAAUCUUGUACAAAUUUAAGUGUAUACUUGUGUACA	223	sly-miR5014a-9-3p	UUGUACAAAUUUAAGUGUAUA	171-191	ath-miR5014a-3p	2	0	21	21	1

sly-MIR8739-3	UUCAAAGUUGAAGGACAUAGUU AUUAUAAUUUUUGAGACAUUGAUUUUCUUGUCGUUUAAAU AUUCGAGCAUAUAUGACCUUUCCUCUAACGAAAGACUAAA UAGAGACACGUGACACAAUCUUAUGCGUUGAUUCGAUAUU UAAUAAAUGUCGAGUUGGUGGAUAAGAUUAUGAUACGCAU AUGUCCGUCAGUAUAAAUAAUAUAUAUGCUCUAGUUUAUG GACGAAAGAUGUACCAAUAUCCCAAAAGUAUGAC GAUUCUUAACUUACGUUAGUUGGCAAUUAUGAUCCUUAAU UUUGGAUGUGCACAAAUAAACACUUAAACUGUUAUAAAAUU AAACAUGUAGACACACAUGUUCUACAUGACAUCAUACGCU UGGACACAAAUUUCCUAUGUUGGGUGCAAUGUAAGACGAA UGUAACAAUCUGUUACAAGUUUAAGAGAAGCAACACAUCU UAUGUUAAGGGUCAUAGUUGCCAACUAACACCAAAUUAAG ACUC GUAGCUCAGUUGGUUUAAUUAGUUGAAUUGUCAUUUUGUU GGUGAGAGUUCGAUUCUCCAUUACGCAAUCUCCUCUUCAA UUUAAGAGAAAAAGAUAUGCUACAAGGUGGAGAAUCGAAC UACCGCUAACAGAAUGGAAGUUCAAAUACUUAAUCAAUUAA GCUAC CCUUAGAUGCAUCCAAUCAUAUCGUGCUUUUGGAUGUAUG ACCAUCUUCAAGUGGUCAAAUCUUUCUUUUAGGUUUUUCC ACAAAACAAAUGGAUCCUUAACUGUCAGAUAUUCGAUUUU UAGAAUCUCGUCAAGAUGAUAAGAAAGAAUAUCAUUGCUC GUGCACAGUUUUGAUUUGAUGCUUUAUUU UUGAAGAAACAUAAUUUUAUUGAUUAAGAUAGCGGGUACA AUUCUGUUGAUCCCUUGAUUCUACUCUCUUCGGAUUUAUC CAUGAUUCGAGAGACGCUAGUAGCGUAUUUCUCGAACUAG GAUGAUCUAGAUGUGAAUAAUCCAUCAAUUUGUGGAGUAU UCGAGAUCUUGAUGUCUUUAAGAAAUUUUUGAGAUGCCUU UUAAGAGAAUUUAGUACCCUUUAUAUAGGCAUAAAUUAGA UUUUUAUG UCCGUAUUUUAAAGGUAUAUAUGUGCCCACGUGGACAUCA UAAAUAUUGCAUCAUUAUAAAUAGUAACGUGCCCAUGUGA GUACAUAUAUACCUUCAAAAUACAGU AGUCUGUGACUUGUUGCUGUUCUUAAGUUCAUUGAAGUUA AAGAAGUUUGAGGUACCACUAUUUCUUUAACAGGUUUAAU CCGUUUUAUCUUGAAAGAAAUUAAUCCAUAACCUUGGUGA GGGGAUUAAAUUUCUUAAGGACACACAGUAGUUUCUGUGG ACUCGGAUUAAUUAUUGUAUUUUUUAUUUUUUCUGCUUCA UCUUAUUUCUGUUUCUGUUUAUUAACUUAUAAAUACAGGU UAUUGUAAGAAUAACAAUAGGUAACAGUGC	234	sly-miR8739-3-5p	AGACUAAAUAGAGACACGUGACAC	73-96	gra-miR8739	5	0	24	24	3
sly-MIR7832		245	sly-miR7832-3p	UAGUUGCCAACUAACACCAAA	216-236	ptc-miR7832	4	0	21	21	1
sly-MIR1918-2		166	sly-miR1918-2-5p	UGUUGGUGAGAGUUCGAUUCUC	37-58	sly-miR1918	0	0	22	22	1
sly-MIR8138-2		189	sly-miR8138-2-3p	UCAAGAUGAUAAGAAAGAAUAU	131-152	cpa-miR8138	5	0	22	22	1
sly-MIR6267a		248	sly-miR6267a-5p	AAGAUAGCGGGUACAAUUCUG	26-46	ppe-miR6267a	5	0	21	21	2
sly-MIR6231-2		106	sly-miR6231-2-5p	UAUAUGUGCCCACGUGGACAU	18-38	sbi-miR6231-3p	5	0	21	21	1
sly-MIR437a		270	sly-miR437a-5p	GAAGUUAAAGAAGUUUGAGGU	34-54	ssp-miR437a	4	0	21	21	2
sly-MIR5021-4	CAGCAGCAGCGACCCGGGAAACUUCUCAGAAUGGAGAAGA AGAAGAAGAAGAAAUUUCCCGGGUUGGUGGCUGUAG	76	sly-miR5021-4-3p	GGAGAAGAAGAAGAAGAAGA	33-52	ath-miR5021	2	0	20	20	2
sly-MIR6273-2	CUCUUUUUGACCUACGUGGCACUAUCUUGUGGGCCCAAC GCUGAUUGACUUUUUUUUCAAGCUAGUGUCACGUAGGCCA GAAAUGG	86	sly-miR6273-2-3p	AACGCUGAUUGACUUUUUUUU	37-57	ppe-miR6273	5	0	21	21	1
sly-MIR5026-5	CCCCUUUUCGACCUACGUGGCACUAACUUGAAAAAAAAUC AAUCAACGUUGGGCCCACAAGAUAGUGCCACGUAGACCGA AAAGGGG	87	sly-miR5026-5-3p	GCCCACAAGAUAGUGCCACGU	53-73	ath-miR5026	5	0	21	21	2
sly-MIR7986-2	ACAGCAUUAGGUUGAUAUACGUCACUGUAAGUAACGUUUU ACUUUUAAAACGUUAUUUUCAGUAACGUUUUAAAACGUUA CUGUGAGUAACGUUUAAGGAGUAAAACGUUACUGUAAGUA ACGUAUACAAUCUGACGCCAU	142	sly-miR7986-2-3p	GUUUUAAAACGUUACUGUGAGUAA	67-90	stu-miR7986	4	0	24	24	3
sly-MIR5654	CUAUGAAGAGUUGCGACUUUUAAGAAAUGUUGCAACUUUU GCUAUGAAAAGUUACGACUUUAUGAAAAAUUGUGACUUUU AUAAAAGGUUGUGAUAUUUCUGAAUAACUUUUCCAAAGGU UUGUGACAUUUCCGAUAAGUCACAACAUUUUCACAC	156	sly-miR5654-3p	AUAAGUCACAACAUUUUCAC	135-154	ath-miR5654-5p	5	0	20	20	1
sly-MIR5163a	UUAUUAUAGUUCUUAAAUCUUUUAUCACAAAUUUUGACUU GGUUUCGAGAUGGUGGUACAGUCUAAUAAUACAUUGUUAA UGGUAGCGAGCAUGUGGUAUUGUAAGUCCCCGUUAAUUG UUGAAGAAAGGGGCAGCCUGAAACCUAUGUUAGAACUGCU AUACAUUAAUAUGUAUAUUAUUAAGACAAGCUCCAUGCUU GAGUAAUAGUUUACCUUAUAGCCAAAACUUAGGAUAAAACA UUUAACAAAACUAUAAUGC	259	sly-miR5163a-3p	CUUAGGAUAAAACAUUUAACA	227-247	bdi-miR5163a-5p	5	0	21	21	1
sly-MIR5303i-5	ACGUAUGUUGCUCGGACUACGCAAAAUGCUCCCGAACUAG AGCGUUGGAUUUUCCAAAAAAAUAUGCUGCUUUUGGAGGA	128	sly-miR5303i-5-	AUAUUUUUGAAGAGUCUGAGCAAC	99-122	stu-miR5303i	0	0	24	24	1

	UCCACCACGCACCUGACAAUAUUUUUGAAGAGUCUGAGCA ACAUAAUC		3p								
sly-MIR172b	UUUAGUCGUUUAUUGCUAAUGCAGCAUCAUCAAGAUUCAC AUUUAAUUGCUUUUUAAAUGUCAGAAUAUUUGAGAAUCUU AAUAGUGCUGCAUUUACAAACAACGACUGUG	111	sly-miR172b-5p	GCAGCAUCAUCAAGAUUCACA	21-41	csi-miR172b-5p	0	0	21	21	1
			sly-miR172b-3p	AGAAUCUUAAUAGUGCUGCAU	73-93	csi-miR172b-3p	3	0	21	21	1
sly-MIR11330	UCUCCCUACUGUUAAAACGAAGUUAUUUUUACCCCUACCG UUACUAAUUUCAUCAUUUUAACAUUGGGUUUGAAAUGGGA AAUGUAUAAAUGAUGAAAUUAGUAACGGUAGGGAUAAAAAU AACUUCAUUUUGACGGUAGGGGCA	145	sly-miR11330-3p	GUAGGGAUAAAAAUAACUUCA	108-128	ppt-miR11330	5	0	21	21	1
sly-MIR6293	GACGACAACAGCAAUAACAUAUCCAGUGAAAUCCCACAAGU GGGAUCAGGGGCUGCGAGAAUAAGGCAGACAAUAGAAAAG GUUACCUAGUAUUUUUAUGUUACUGUUGGGAUUUGAACCU UGGUUUUCAAGAUUUGCACUCACAUUACUGAUUUUUUUUU UGAGUCGAGUAUCUGUUGGAAACAACCUCUCUAUCCCGUA AGAGGUAGAUGACUAGAGAUAAAGUCUGCGGUACAUCCUA CCUUCCCUAAACCGCACUUGUAGGAUCACACUAGGUAUAU AUUAUUGUUGCAGUCCAC	299	sly-miR6293-3p	UAAGAGGUAGAUGACUAGAGA	200-220	ppe-miR6293	5	0	21	21	1
sly-MIR11068c	UAUUCUAAUUCAUGGAUUAGUUAUACCUCAUACAAAAUCUU AUUUUAUUCCUAGAAAAGGGUGGGAUAACUAAUCCAAGGU UUAACAAUCCUUGGAUUAGACCC	104	sly-miR11068c-3p	AUAACUAAUCCAAGGUUUA	66-84	lja-miR11068c-5p	5	0	19	19	1
sly-MIR477e-2	UCAGGAAUAUUAAGCAGUGCCCAAGGACAUAGUGAGGAUC CUUGGGACAGUAAGUAAAUAUUCCAAA	67	sly-miR477e-2-3p	UGAGGAUCCUUGGGACAGUAA	33-53	csi-miR477e-3p	5	0	21	21	1
sly-MIR7696c	UUUUUUUUGUAAUUGCAUGCACCUUUUGGCCUACAUGACA UUCAAACAUCUCUCAUGCGCCUCAAUUGCGUGGAGUCACA AAGUGUGCCACGUAAGACAAAAGGUGCACAAAAUUAAAAAA GAA	124	sly-miR7696c-3p	AGGUGCACAAAAUUAAAAAAG	102-122	mtr-miR7696c-5p	5	0	21	21	1
sly-MIR7540b	GAGGAAAAGGUGAACAUGGAUAAAGUUUCAUAUUCCUCCG UCAUCGGAAGUCUAAUGUAUGCAAUGGUAUGCACUAGAGC UAAUAUUGCUCAUGCAGUUGGUGUUGUGAGCAGAUUUCUC CACAAUCCAGGAAAAGAGCAACGGGAAGUUGUGAAGUGGA UACUCAGGUAUCUUAGAGGAAACUUAGAUGAAGAAUUGUG UUUUAGAGCAUCAAUUCCAAUCUUGAAAGGUUAUACAUAU GUUGAUAUGACAAGUGACCUUGAUAACAGAAAAUCCACUA CUGGAUACUUGUUUACUUUUUCAAG	305	sly-miR7540b-3p	UGAUAUGACAAGUGACCUUG	243-262	lja-miR7540b	5	0	20	20	1
sly-MIR8644-2	CACCCCUAAAUAUUUUUUUUAAAUUACAAGUCAUAAAUAUA AAUUUAAAACUACUUUUUUAACUUUCGUUAAAUGAAGGGU AUAUGUGAGCCAUUUUAUAACGGCAGGGGUAUAUGUGAGC CGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAU GACGAGGGGUAUAUCACCUCUAAGUGACAAAGUUGAGGGG UAUAUCAGACCCUUUUCCAUUUGAAUAUUGUGAUUAUGAC UAUGGGUAACUAAACUCCAUAACUAGGGUUG	272	sly-miR8644-2-3p	CUAAACUCCAUAACUAGGGUU	251-271	gra-miR8644	4	0	21	21	2
sly-MIR10189	GCGGAAAGGUCUAGAGUUGUGGAGAGGUUUGCGGAGAAC UCUAGAACCUUCUACAUUAAUAAGAAGGCUAGAGAAUUCU UAGAAUUCUCUAGAAUAACUUAGACAUUUCAAG	112	sly-miR10189-5p	GAGAACUCUAGAACCUUCUAC	34-54	gma-miR10189	4	0	21	21	2
sly-MIR1514b	UUUAAUAAAGAGACCUCAUGAGGUCUCUUUUCUGCAUUUA UAAAAUAGAAAAUGGUAAUUAGAGACCUCAUGAGAUCUCUA UUAUGAAAUAUCUGGAAAAAUUAAUGCAAAAAAGAGACCUU AUGAGGUCUCUAUUAUGAAUUAUCUGGAAAAUUAAUGCAA AAAAGAGACCUCAUGAGGUCUCUUUUUCUG	192	sly-miR1514b-5p	UGCAUUUAUAAAAUAGAAAAU	33-53	gma-miR1514b-5p	4	0	21	21	1
sly-MIR1886f-2	CGUUCAGGAUAUGGUAUCGUGAGAUGGAAUCAGCGUCUG GACAUGCGAUUUUAUGUUGAUUCCAUCUAUGAUUUCAUAU CAUGAGAU	87	sly-miR1886f-2-5p	AUGGUAUCGUGAGAUGGAAUCAGC	11-34	stu-miR1886f	1	0	24	24	1
sly-MIR8008b-2	UUUUCCAUCACUUUUUUGCAUAAUUCUUUCAAAUAAACCCA GAAAAGCGACAGACAGGGUCCUUUAGUGCGUCGCGUUUC UGGGUUUUUCAAAAAAAAAAAUUUCAGAAAAGAUGGAUAG	120	sly-miR8008b-2-5p	AAACCCAGAAAAGCGACAGACAGG	35-58	stu-miR8008b	2	0	24	24	1
sly-MIR946a	UAAUAAUUUUCUACUCCUUUUCAGUCUACGUGACUUUAUC UUGUGGGCUCAAUAUUGUUUGACUUUUUUUUGUUCAAGCU AGUGUCACGUAGAUCGAAAAGGGUUAGAAAAUUACUU	117	sly-miR946a-3p	CGUAGAUCGAAAAGGGUUAGA	88-108	pta-miR946a-5p	5	0	21	21	2
sly-MIR8014	UUUUACUCCCUCUGUCCAACAAUUCUUGUUCACUAUUGAA UAUAAUAAAUACAAUGUGUUGAAAAAUGUCACAGAGAAAUG AUUAUAAGUAGGUAAAUUAGAAAAGAAGUGUAAAAUAAUCC ACUGAUUUCAUAAAGUGGACAAGUAUUGUUGGACAUCCCA AAUUAGUAUAGUGGACAACUAUUGUUGGACAAAGGGAGUA GUU	205	sly-miR8014-5p	AUAAAUACAAUGUGUUGAAAAAUG	45-68	stu-miR8014-3p	5	0	24	24	1

sly-MIR5180a	AAACUUACGCGUAUCAGGUGUUUACACCAAGUCAAUACAUGCAUAUUAUGUGUUUCAAUUUAUAACUCAUUAAAACAUGUAAUAAUGAAAAUUGCAUAGACUUGGUGUAAACACUUAUACGGAAGGAA	128	sly-miR5180a-3p	UAUGUGUUUCAAUUUAUAACU	47-67	bdi-miR5180a	5	0	21	21	1
sly-MIR156i-4	ACAAGUGAAAUACUACAAAAGAGAGAACACAAAUGUCUUAGUAGGUGAGAAGGCAAGUGAGAGGAUGAUUUGAAAAUGAAUUAAGAACUAUCUAUUUAUAGGAAUGAAUUCAUCCUAUUGAUGUCAUCCAUGACAUCGAUAUAUGUCAAAAAUGUCAAGGUUAAAAAUAUAAAACCAUUUUAUGGUUUGCCUAAACUUCACCUACCAAGAUACUAUCUUGACUUUUAUUUUGUACUAUCUUACUACC	247	sly-miR156i-4-5p	UACAAAAGAGAGAACACAAA	14-33	cas-miR156i	5	0	20	20	2
sly-MIR482b-3	AACCUAAUCCAUGGAUUAGUUAUACCUCAUACAAGGUCUUAUUUUAUCCCUAGAAAAGGGAGGGAGAGAUAGCUAAUCCAAGAUUUAGCAA	91	sly-miR482b-3-3p	GAAAAGGGAGGGAGAGAUAGC	53-73	eun-miR482b-5p	5	0	21	21	1
sly-MIR2655o-1	UUUAACUUGGUUUUAAAUCACAUUUAUGUCCUUCAACUUUGGGUGUGCACAUGUCGACACUUAAACUUGUAUAAAGUUGAACAAAUAGACACACAUGUCCUACAUUUAUCCUACAUGUCAUUUUUUGUUCUACGUGGUGUCCUACGUGUAUUUUGUCAUGUAGGACUCGUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUGGAGGUCAAAAUUAAAAUUUGAAGUUAAGUUUAG	262	sly-miR2655o-1-5p	CAUUUAUGUCCUUCAACUUUG	21-41	mtr-miR2655o	5	0	21	21	1
sly-MIR10538-8	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUAGGAGUAAAACAUUGCUGAAAAUAACGUUUUAGGAGUAAAACGUUACUUACAGUAACGUAUAUCAACCUAAUGCUGU	117	sly-miR10538-8-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
sly-MIR10542-3	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUAAAAAAAAUUAGAAGUAACAAAUAUAAAUUUAAAACUAAUUUUUUAAUUUCCGUUAAAUAAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAAGGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGGUAUACCAGCUCUAAAUGACAAAGUUGAGGGGUAUAUAAGACCCUUUUCCGAGGAGAAGAAUGACAGGGCAAUUCUCCUUUGGCAAAGA	236	sly-miR10542-3-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
sly-MIR399f	UAAUAUAAUGUGUAUGCAAAACAUAUAUAUAUAUAUAUAUAUAUAGGGUUUGCAUAUUCAUUUGCCAAAGGAGAAUUGCACUGUUAUUUCUUACUCCCCA	140	sly-miR399f-5p	GGGCAAUUCUCCUUUGGCAAA	18-38	csi-miR399f-5p	1	0	21	21	1
			sly-miR399f-3p	UGCCAAAGGAGAAUUGCACUG	103-123	ptc-miR399f	1	0	21	21	1
sly-MIR399a-2	AGCAAGAAUCGCAGGUUAUUCUUCUCUGGCAAGAAAACUAUGGUUAUGCAUAAAUUAUUUCUUGCCAAGGGAGAAUUGCCCUACGUUUAU	94	sly-miR399a-2-3p	UGCCAAGGGAGAAUUGCCCUA	63-83	ata-miR399a-3p	2	0	21	21	1
sly-MIR399a-3	AAAUUUCAAGAAUUGAAGAUUAAUUGGAGAGCAAGAAUCGCAGGUUAUUCUCCUCUGGCAAGAAAGCUAUGGUUAUGCAUAAAUUAUUUCUUGUCAAGGGAGAAUUGCCCUACGUUUCUUUAUUUUCCAUAAUAUAUAAUAUUUCAUAAAGUG	153	sly-miR399a-3-3p	UGUCAAGGGAGAAUUGCCCUA	92-112	ata-miR399a-3p	3	0	21	21	1
sly-MIR399a-4	ACUACUCAAAAGAAUUUGAAGAAUUGGAGAGGACAAGAAACGCAGGGUAUUCUCCCUUAGCAAGAUUGCUUUAUGCAUGAAUUAAAUUCUUUCUUGCCAAGGGAGAAUUGCCCUGCGUUUCUUCAUUUCCAUAAAAGUCUAAUUCAUCUGGUGUC	155	sly-miR399a-4-3p	UGCCAAGGGAGAAUUGCCCUG	95-115	ata-miR399a-3p	1	0	21	21	1
sly-MIR7834	CUAGUGGUUGGUUUGACUUGGUUUGGUAUUAAAAAAAACCCGACUAUAUUUGGAUUGGUUUGGUUUUAACUAAAAAGAACCAACCCGAGACCAAACCACCCC	102	sly-miR7834-5p	UAAAAAAAACCCGACUAUAUU	30-50	ptc-miR7834	5	0	21	21	1
sly-MIR10538-9	ACAGCAUUAGGUUGAUGUACGUUACUGUAAGUAACGUUUUACUCCUAAAACGUCAUUUCCAGUAACGUUUUACUCCUAAAACGUUACUAUGAGUAACGUAUAUCAAUCUGACGCCAU	117	sly-miR10538-9-5p	AGGUUGAUGUACGUUACUGUAAGU	9-32	sly-miR10538	5	0	24	24	1
sly-MIR11155e-3	CUGAGUUUGUAAGCGUGUUUGAUUUUAGUCCCUCUGGAGAUAAAUGACGUUUAGUGACAGUCAAAAACUGCUAGUGAUUGUAAAAAUGACUACCACUAAACGUAAUUUUUCUUCAAAGGGACUAAAAUCAAACUCGCUUACAAACUCAG	149	sly-miR11155e-3-5p	UUUGUAAGCGUGUUUGAUUUUAGU	6-29	lja-miR11155e-5p	1	0	24	24	1
sly-MIR7757	UUACUUUUUGGUCUGCGUGACACUAUCUUGUGGGUUCAACGCUAGUUGAUUAUUUUUUUCAAGCUAGUGCCACGUAGGCCGAAAAGGGU	89	sly-miR7757-3p	GCUAGUUGAUUAUUUUUUUCA	41-61	bdi-miR7757-3p-1	5	0	21	21	1
sly-MIR7992-13	AAUUGGUAUUUACGUACUCAAACUUUGAGUGUGCACAAGUAGACACUUAAAAACUUGUAUAAAAUUGAAUAAUUAGAUGCGCACGUCUUAUGUGACAUAUUACACGUAGGAUACCACAUGUAUGAUGCAAAUUGUCCACAUAAGACGUCAUGUAAGAGGUAUAUGUAUCUGUUUGUUCAAUUUUGAACAAGUUUGAAUGACUACUUAUAUACAUCUGAAUUUAAAGGACAUAGAUAUCAC	244	sly-miR7992-13-5p	UUUGAGUGUGCACAAGUAGACACU	24-47	stu-miR7992-5p	5	0	24	24	1

sly-MIR10538-10	UC ACAGCAUUAGAUUGAUAUACGUUACUGUAAGUAACGUUUU ACUCCUAAAACGUUAUUUUCAGUAACGUUUUACUCCUAAAA CGUUACUAUGAGUAAUGUUAUAGGAGUAAAACAUUACUGU GAGUAACGUAUAUCAAUCUGACGCCAU	148	sly-miR10538-10-5p	AGAUUGAUAUACGUUACUGUAAGU	9-32	sly-miR10538	3	0	24	24	1
sly-MIR1917-6	AACUUUUAGCGGCAUUAAAUAUUGACACUAAUAAAGAGUG CUAAAGUCUUUACCGGCAUUAGUUAAGUGUCAGUAGAACC AAUGUCGCUAAAGGCUUUAGGUACAUAUACAAAGUGUGAC AAUUGCCGCUAAAAAUA	137	sly-miR1917-6-5p	ACUAAUAAAGAGUGCUAAAGU	27-47	sly-miR1917	1	0	21	21	1
sly-MIR5181c	ACAAUAUCCUCCAUCAUACUUUUGGGACAUUGGUGCACAU CCCGUCAAAAAACUAGAGCAUAUAUGUCAUUCACUCUAACA GAUCAAUCUUAUCUAUCGAUAUGAUAUUUACUAAAUAUCG GGUCAGUGGAUAAGAUUAUGACACGUGUAUGUUUGUUAGU AUAAAGGUUAUAUAUGCUCUAAUUUUGGAUUGUAGGGGCA CCAAUGUCACAAAAAUAUGACAGAGGGUAUCUG	234	sly-miR5181c-3p	UCUAAUUUUGGAUUGUAGGGG	179-199	bdi-miR5181c-3p	5	0	21	21	2
sly-MIR10538-11	AACAGCAUUAGGUUGAUAUACGUUACUAUAAGUAACGUUU UACUUUUAAAACGUUAUUUUCAGUAAUGUUUUACUCCUAA AACGUUACUGUGAGUAACGUUUAAGGAGUAAAACGUUAUU GUGAGUAACGUAUAUCAAUCUGACGCUAUC	150	sly-miR10538-11-5p	AGGUUGAUAUACGUUACUAUAAGU	10-33	sly-miR10538	4	0	24	24	1
sly-MIR10536-4	AAAUCUCGUUGAAGAAAAGGAAGCUGACGAUUAGAACAUG UCAAAGGAAUCGGUCCAAUGCAGCUGACUAACGUGCUUAU AUCAAGUGUUGUAAACUCGUUAGUUAACUUUGUUAGACAU GUUCUAAUCGUCAGCUUCCUUCUUCACAAUCUACCUCUUC ACACUUUAAAUAUUGAUGAAAAAUCUUAGUAACUUAGUUG GUUGGCUAUAUCAAUUCUCAUAUUAUAAUUCCUGUUUCAU UUUCCCUUCCUCACAUUUUUUUUUUAAAAGAGACUU	276	sly-miR10536-4-5p	AGACAUGUUCUAAUCGUCAGCUUC	115-138	sly-miR10536	0	0	24	24	1
sly-MIR7983-11	UCUCACUACAACAAAAAUGACCACUAACGACAUUUAAUUCU UAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUGUCAC UCUUUGUAUAUGUCAAUAAAACCUUUAGCGACAUUGGUUC UAAUAUCACUUAACUAAUGCCGGUAAAGACUUUAGCACUC UUUAUUAGUAUCAAUAUUUAAUGUCACUAAAAGAUAUUUUU GUUGUAGUGUCU	214	sly-miR7983-11-3p	ACUAAUGCCGGUAAAGACUUUAGC	134-157	stu-miR7983-3p	1	0	24	24	1
sly-MIR5274b-3	AACUAUCGUAAAUGGUAUGCAUGUACCCUCCGUCAUAUUU UUGAGAUAUUGGUGUCCCUGCCGUAAAAAAAAAACUAGAG CAUAUAUGCUCUACGCGUGUCAUAAUCUUAUUCACCGAUC CAACAUUUAUUAAAUAUCGAAUUGACGGAUAAGAUUGUAU CACGUGUCCAUAUUUAGUUUUCCCUUAAAGUGAAAGACAU AUAUGCUCUAAAUUUUGAACGACAUGAAUACAAAUAUCUCA AAAGUAUAAUGGGAGAUUUUCUGCAUAUUAUUUAUGAUAA UU	283	sly-miR5274b-3-5p	CAUGUACCCUCCGUCAUAUUU	20-40	mtr-miR5274b-3p	3	0	21	21	1
sly-MIR1917-7	UGAUAAAAAUAACUUUUAGCGGCAAUAAAUAGACAUAUUAA UAAAGAGUGCUAAAGUCUUUAGUCUUUACCGGCAUUUGUU AAGUGUCAUUAUAUCUAAUGUUUCUGAAGCCUUUAGGGAC AUAUACAAAGAGUGUUAAUUGCCGCUAAAAAUACAUAUUUA GCG	165	sly-miR1917-7-5p	AUUAAUAAAGAGUGCUAAAGU	37-57	sly-miR1917	0	0	21	21	1
sly-MIR5716	GCCUUUUUCUCUGCAAUAUUUGAAGUAAAAUGUUUGUAAA UUGUAUAAUUAAAUGUAUAACACGAAGAUAUAUAUUUUUGC AUGUGUAGAUACAAUUUUCUCUCGCUUUAUACAAAACAGA AACAGAAUUAUACACUUCUGUGUAUAAAGCGAGAGAGGCG AGCGAGAAUGGAGAGUGGCGAGCGAGAUUUUCGGGAGAG AGACGCUGGCAAAUUUUAGCUAACGUUUGCUAUGGAGUAC AAUUAAAUCAAACCCUAGCUAUUCCAUUUAUUUUAGGUUU UUAUUUGCUAUAUACAAUUUUCCCUUUUUAAAACGUAAA GAAAAAUUA	329	sly-miR5716-5p	UUGUAUAAUUAAAUGUAUAAC	41-61	bra-miR5716	5	0	21	21	1
sly-MIR10538-12	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACAUUUU AGGAGUAAACGUUACUAAAAAUAACGUUUUAAAAGUAAAAC GCUACUUACAGUAACGUAUAUCAACCUAAUGCUGU	116	sly-miR10538-12-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
sly-MIR7822-4	AUGUUUAUGUCUUUCAAUUUUGAGUUUGCAUAAGUAAACA CUUAAAAUUGAACAAAUAGAUACAUUCGUCCUACGUAAUAA UUUUGUAUCCUGAUGGUGUGCUACGUGUAUUAUGUUGUG AAGGACGUGUGUGAUUACUUGUUCAAUUUUAUACAAGUUU AAGUGUCUGAUUGUGCAUACAAAAAGUUGGAUGACGUAGA AAGG	204	sly-miR7822-4-5p	CUUAAAAUUGAACAAAUAGAU	41-61	ptc-miR7822	5	0	21	21	2
sly-MIR5014a-10	GAUUUUAAACUUGGUUUCAAAUUUUAACUAUGACUUCCAA UUUUCAUAAUGAACAAACAGAGACUUUAACUAUUCAACAUU AAAUAAAUAAACACAUGAGUCCUACAUGACUAGGACACCAC	259	sly-miR5014a-10-3p	UUAUACAAGUUUAAGUGUCUA	183-203	ath-miR5014a-3p	5	0	21	21	1

sly-MIR399r-2	GUAGGACAAAAAAUGACAUGUAGAAUGAUAUGUAGGACAUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCUACUUGUGCACAUCUAAAAUUGAAGGGCAUAAAUAUAAUUCGAAGUCAAGUUAAAGGG	126	sly-miR399r-2-3p	UGCCAAAGAAGAUUUACCCCG	88-108	mtr-miR399r	1	0	21	21	1
sly-MIR395b-10	CUAUGUAUGGAUGCAUUACUGGGCUAAUCUUCUUUGGCAAAUAGCCACAUUUUCACUAUAUUAUUUAGUGCAAGUUUGUUCAUUUUUUGCCAAAGAAGAUUUACCCCGUAAAUCACCCAUACAAUC	170	sly-miR395b-10-5p	CUGAAGUGUUUGGGGAAACUCC	10-31	sly-miR395b	1	0	22	22	1
sly-MIR395c	GAUGCCCUGCUGAAGUGUUUGGGGAAACUCCUGGGCUCACUCUGAAAUUUUAUGCAAAUUAAACCAAUAGAAGUGUUGGAGUGCUGGUUGUGGAUGAUAAACAUGAUAGUUCACGUAGAAAUCUAUCAAGGUGUUCCCUAGAGUUUCCUUGACCACUUCAUGAGGGCUUACUUUGAUGUUAGAAGCCUUGUUGAAGUGUUUGAGGGAACUCCUGGGUUGACAUUGAAAAUUACGCAAACAAGUAUAUAUAAAUGCAUGA	172	sly-miR395c-3p	UUGAAGUGUUUGAGGGAACUC	104-124	cme-miR395c	1	0	21	21	1
sly-MIR5773	UGUCCACCCACGUAACCCAACCCAGUAAAAAACAUGAUAUGACCCAUUUUAUUUUGUCUUUAAUCUUAAUUCAAGGUUUAAUGAGAGGGAUUAAUUUAGUAUUAAAGAUAUAAUAAAAUGGUUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGUGUGGAUCA	166	sly-miR5773-3p	UUUUUAAUGGGUCGGGUUAGGU	135-156	gma-miR5773	5	0	22	22	1
sly-MIR5722	UUUAGAAGUUAGUAAUUGAUUUUGUUAAUGAGUUUUAUGUCUUCCGCAUUUUUUUCUAUUUAUUAUGAUUGAAAUGUUGGGGUUUAGAUUGGUUGGUCCGCUCACAUCGGAGGUUAAGAGUGGGUGCCACUCGCGGCUCUUUUUGGGUCGUGAAAAACAUGGUAUCAGAGCAUUAGGUUCGUUGGUCUCAUCACACAAGAACAAGUGUAGUAGAGUCUUGAGGAACGGUAGGGGGAUGCCGUUACUUUUCUUUGAGAGGCUACAAGACUUUAGAAAAAUUCAAUUCAUUAUUUCUUUC	298	sly-miR5722-3p	UGUAGUAGAGUCUUGAGGAACG	206-227	bra-miR5722	4	0	22	22	1
sly-MIR952a	UUGGGUCGUGACAAACUUGGUAUCAGAGCAUUACGUUCGUUGGUGUCAUCACACAAGAACGAGUCUAGUAGAGUCUUGAGGAACGGUAGGGGGACGCCUUUACUUUUCUUUGAGAGGCUAUAUGACUUUGGGAAAAUUCCAUUCUUUCUUUCUUUCGUGCAAUUACUUGGAUCCAAUUGGUAUCUAGGUGAUACAAAUUAGUAUCUGACCAUC	213	sly-miR952a-5p	AUCAGAGCAUUACGUUCGUU	22-41	pta-miR952a	4	0	20	20	1
sly-MIR10541	UGCAUAGUUGAGUGACUUUUGAGUGAAAAUUGAAAGUUGAGUGACUUUCUGAGAGAAGAGUGCACAGUUGAGUGACCAUCUGAGGUAUUAACUCCAACUUUGGUUGAGUCAGAUUUUACUCAAAGUCACUUUGACUAUUCU	141	sly-miR10541-3p	AGUCACUUUGACUAUUCU	124-141	sly-miR10541	3	0	18	24	1
sly-MIR7992-14	AUAAACUUGGCUUCAGAUUUUAACUUUGACCUCCAACUUUCAUAAUGCACAAACAGACACUUUAACUAUCUAACUUUUAAAUAAAUAAACACAUGAAUCCUACAUAGCAAAAUACACGUAGGACAAAAAAUGACAUGUAGACAUGUAAGACAUGUUUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUUCUACUUGUGCACUCCCAAAGUUGAAGGACAUAAAUGUAAUUCGAAACCAAGUUAAA	248	sly-miR7992-14-5p	UUUCAUAAUGCACAAACAGACACU	38-61	stu-miR7992-5p	5	0	24	24	1
sly-MIR171j	UGGUUCAUCUAUGUCAUUUCUGUUUUAGAAAACAUUAUACAUGUCAUUAUUUGUUAACUGAAAACAGUUCUAACUUUGCAAAAUUGUUUAUACGCGGUCAGUUAUGAUUGAGACACGUCAUUAAUUAAAUUAUUUUUUAAAAAGUGAAAAAUGUUCAAAUAUGCCAACGAACUUAUAGAAUAGGCUCAUCUAUGCUAUCCGUUAAGAGUUUUCCUCAUCCGUGUCAUUUCAGUUAGGAAAUGCUGACAUGGAUAAGUCUUUUCUCAAACAAAAAUUGCAAUAGAUAAGUC	290	sly-miR171j-5p	UGAUUGAGACACGUCAUUAAU	105-125	lus-miR171j	5	0	21	21	1
sly-MIR1863a	UAAUGGUGUGUGAAAUUAGGUCUUAGGCCUAACUCAUACCCCAAAAGCUAGCUCAAAGGGAGGAGGAUUGCCCAAGCCUUAUAAAGAGUCUACCCAUCUCUUUAAUCACCGAUGUGGGACUUUGUCAUUCUUAACACCCCACCACAUCACGCCCAGUGCUUAGCAUAUGGUGCGUGGGCAAUUUUAAUUUGGUGCCCCCCAAUAUCGGGUGAGACGGGCCCUGCUUUGAUACCAUGUGAAAUUAGGUCUUAGGUCUAACUCACACCCCAAAA	273	sly-miR1863a-3p	UGCUUUGAUACCAUGUGAAAUUAG	223-246	osa-miR1863a	4	0	24	24	2
sly-MIR171c-4	AAACUAAAGAUAUUAAAAUGAGUUGAAAUAGAAUCGGGUUGGGUCUUGACCUGCCCAAGUUUACUUUGGGCUAAAAUGGGUUGGGUUCAAAUGGGCUAAGAACGGGUUGGGUUUUGAA	215	sly-miR171c-4-3p	UAAUUUGACCCGAUUAAUAUC	124-144	aqc-miR171c	5	0	21	21	1

sly-MIR845b	CCACCUAAUUUGACCCGAUUAAUAUCAACAAUUCUAACAUAGUGAUAUUUAACUUUUAUAAUCACAAUUCGAAUUUCAGCUUUAAUAUUUUUAAAGA	285	sly-miR845b-3p	UCAAUUGGUAUCAGAGCAAGU	206-226	aly-miR845b-5p	2	0	21	21	1
sly-MIR1044-2	GAAGUAGUCGGUUAUAGUUAAUUGAGAGUUUUUGUAGUGGUGAGUUUUUGAUUAUUAAGUUGUAAUCAUAAAAUCAUCUAGUUGAAUUAAUAAAACGAGGUUAUUCCUUCCUUGAUUGAGGAAGGUUUUAAUUUAACAAGUGUUUGUGUUCUGACUUAAAACCAACUUACAAGAACUUGGUUCUUGUUCUAGGGGAUAGGUUUCUUCAAUUGGUAUCAGAGCAAGUCUUUUCGAUAAAAGAUUCACACCUUGAAAAGACUCAAUGGCACUACCACCCACCACACA	238	sly-miR1044-2-5p	GCACAAAUAUGCACUUAAACU	53-73	ppt-miR1044-5p	4	0	21	21	1
sly-MIR172d-3	GUGCCCUUUAACUUGGCUUCAAAUCACAUUUAUGCCCUUCAACUUUGGAUGUGCACAAAUAUGCACUUAAACUUGUAUAAAGUUAAACAAAUAGACACACAUGUCAUUUUUUGUCCUACGUGGUAUUACCAUGUAGGACUCGUGUUUAUUUAUUUAAAAGCUGAAUAGUUAAAGUGCCUAAUUGUGCAUUAUGAAAGUUGGAGGUCAAAGUUAAAAUUUAAAGCCAAGUAUAGGGUCCUGAACUUAAUGGACUAAAUCUGAAUGAUUCAGAUUCAGACCUAAAAAUUAAACAUACUCAACAGGCUGAAUCUGAAUUAUUAAGAUUCAGACCUCCAUUAAGUGUA	106	sly-miR172d-3-3p	UCUGAAUUAUUAAGAUUCAGA	71-91	bra-miR172d-5p	5	0	21	21	2
sly-MIR5303i-8	AUGGAAUGACUAUGUUGCUCAGACUCUAUAAAUCAUGUCAGAUCCUUUAUAAGUCCGCAACUUUUAGAGGGGAUUAGACACUCAUUCAUUGAUAUUUUUGAAGAGUCUGAGCAACGUAACAUAUCAGG	128	sly-miR5303i-8-3p	AUAUUUUUGAAGAGUCUGAGCAAC	92-115	stu-miR5303i	0	0	24	24	1
sly-MIR1521b	UAUACUAACUGACAUACACGUGUCAUAAUUUUAUCCACCAACCUGACAUCAGAUCAAUGGAUAAGAUUGUGUCACGUGUCCCUAUUUAGUCUU	93	sly-miR1521b-5p	GACAUACACGUGUCAUAAUUUUA	11-33	gma-miR1521b	5	0	23	23	1
sly-MIR6273-3	AAGACAUGUGCGAUAACGUUUUAUGAUCUGUAAGAUUCUAAUGUAGCAGGAUUUUAUUCUUAAUCCGGUGCCCCGUGAUUAAAUAAACAUAAAACGUGAUUGACAGUUAC	110	sly-miR6273-3-3p	AAUGUAGCAGGAUUUUAUUCU	40-60	ppe-miR6273	4	0	21	21	1
sly-MIR7822-5	GCCCUUCAACUUUAGUUGUGCACAAGUAGACACUUAAACUUGUAUAAAAUUGAACAAAUAGACACACAUGUCCUAUAUGUCAUCCUACAUGUCAUUUUUUGUCCUACGUGUAUUAUGUCAUGUAGGACUCAUGUAAUUAUUUAUUUAAAAGUUGAAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAAUUGGAGUUU	197	sly-miR7822-5-5p	UAUAAAAUUGAACAAAUAGAC	43-63	ptc-miR7822	5	0	21	21	1
sly-MIR5162	AUUAGGUGUCAAUAGAGGGUAUAUGUAUAAUUAUAUCAAUAAUCUGUGAUAGAUUUAUAGAUUGUGUAAGGUGGGAAAAUGACCAAAAUACCCCUAAAGUGACUAUAAUUUAGCUAAUACCUCUCUUUUACACACUCAG	139	sly-miR5162-3p	AAAUGACCAAAAUACCCCUAAAGU	77-100	osa-miR5162	3	0	24	24	1
sly-MIR7983-12	GUUAUCCACUACAACAAAAAUGAUCAUUAGCGGCAAUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUGUCACUCGUUGUAUAUGUCCCUAAAUUCUUUAGAGACAUUGAUUCUAAUGACACUUACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAAUGUCAAUAUUUAAUGCCGCUAAAAGUUAUUUUUGUUGUAGUGAUUCC	218	sly-miR7983-12-3p	ACUAAUGCCGGUAAAGACUUUAGC	136-159	stu-miR7983-3p	1	0	24	24	1
sly-MIR167a	UCAUUUUUAAUUAUUUCUUACUUGAUUCCGUGUUUUUACUUGUGAGUUCCUUUCAACUGCUACCAUUUAAAUUUGACGAUGGAAUGUGCGGUAACAACUACUUCUUCAGCUCAUGUAGCAGUAUUAAGGAACUCACAAGCAAAAACAAGCAAAAAAGAAAAAAUUAAUUUAAAAUGA	191	sly-miR167a-3p	CAGCUCAUGUAGCAGUAUUAA	121-141	vca-miR167a-3p	5	0	21	21	1
sly-MIR482d-3	UUUCUUACUAGAUUGCGCGUUUUUACUUGUGAGUUCCUUUCUACUGCUACCAUUUAAAUUUGACGAUGAAAUGUGCGGUAUGAUCAGCAAUAGAACAACUACUUCUUCAGCUCAUGUAGCAGUAGAAAGGAACUCACAAGUAAAAACAAGCAAUAAAGCAAGAAA	165	sly-miR482d-3-5p	UCCUUUCUACUGCUACCAUU	35-54	pta-miR482d	4	0	20	20	1
sly-MIR12142-2	AAGUUGUGGCUUUUAUAAAGAGUUACGACUUUUAUGAGAGUUGCGACUUUUUUGAAAAGUUAUGACUUUUAUAAAAAUUGCAAGUUUGAUGAAUAGUUUUAACUUUUAUGAAAGAUUGUGACCUUUCAUAAGGGUUGCAACUUUUUCAAAUAGUUGUUACCUUUCCGAAGGGUUGCAACUUUUCCAAAUAGUUGUAACCUUUCUGAUAAGGCAUAAUAA	219	sly-miR12142-2-3p	ACUUUUCCAAAUAGUUGUAAC	178-198	aof-miR12142	5	0	21	21	3
sly-MIR1043-2	GCCCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAACAAAUAGACACAUGUCCUGCUUGUCAUUUUUUAUCCAACAUUAUGUCCUACGUGUAUUUUGCAAUGUAGGAUUCAUGUGUUUAUUUAUUUAAAAAAUUGAUAGUUAAACUGCCUGUUUGUGCGUACUAAAAGUUGGAGAUC	195	sly-miR1043-2-5p	CCUUCAACUUUGGGUGUGCA	3-22	ppt-miR1043-5p	4	0	20	20	1

sly-MIR3950	GGAGAAAUAAUGAAUUAACCCUACACUUGAAAUUUAGGAAACAUGUAAUUAGACCUAUUGGUUGGAAUCAAUAUUUAGGAACUUUAUUAUACAUUUGAGUGAGUUUUGGGUCUAAGCUAGACAUAUGAGUGUUGUUAGUUACGAAAUUUUUUUGUGAUUAUUAAUAUGAAUAGAUUGCUUUGAGUUGGAAGUACAACGAAAAGGAAAGGCUCAAGUCUUAGAGUGAUUGUUCGACUAUUUGAGGCAAGUUGAUUUCUAAACUUUUGUUAUGGGUAUGAAAUUCGUGUAUUUCCUU	295	sly-miR3950-3p	AUUUGAGGCAAGUUGAUUUCU	237-257	csi-miR3950	5	0	21	21	2
sly-MIR11419	UAUUUUAACAGAAAGGGCCUAAACUGCUCUUAAACUAUGAGAGUGAUACAAUAUUUCCCUCCAUCCACCUAAUGAGUAUAUCCGUUAGACAUAAGGGUAUUUUUGAGCCGAAAGAUGAACGGAAGGGGUAUUUUAGUGGUGAUAGGUGGAUGAAAGGUAAUUUUGUACCAAUUCAAAUACUUGAGGGGCAUUAUAGGUCCUUCUCCAUUUAAAUUA	216	sly-miR11419-5p	GCCUAAACUGCUCUUAAACUA	17-37	pab-miR11419	5	0	21	21	2
sly-MIR5218	UGAUUACUUCCGGUUCUUCCCAUAGCUUGUCAAUACUAUUUUGAUUAGUUCACAUUUAAAAUGAAUAAAGAGCCUCGAAUGCACCAAACAAUGCUGUAAGACAUGGGAAGAAACAUUAACAAAACUUGACUUCGUCCGAAUAUUGACAAGCGAUGGGAAGAAUUGGAAGUAAGUU	175	sly-miR5218-3p	GAAGAAUUGGAAGUAAGUU	157-175	mtr-miR5218	5	0	19	22	3
sly-MIR7983-13	GCUAAAAAUGUACUUUUAGCGGCAAUAUACACUCUUUGUAUAUGUUCCUAAAGCAUUUAGCGACAUUGAUUCUGAUGACACUUAAUUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAAUGUCACAUAUUUAAUGCCGCUAAAAGUUAUUUUUGUU	157	sly-miR7983-13-5p	UAAAGCAUUUAGCGACAUUGAUUC	49-72	stu-miR7983-5p	3	0	24	24	1
			sly-miR7983-13-3p	AUUAAUGCCGGUAAAGACUUUAGC	85-108	stu-miR7983-3p	2	0	24	24	1
sly-MIR865-1	UUUUGACCUCCAACUUUCAUAAUGCACAAACAAACACUUCAACUUUCCAACUUUUAAAUAAAUAAACACAUGAGUCUUACAUGACAAAAUACACGUAGGACAAAAAAUGACAUGUAGGACAUUUGCGUCUAUUUGUUCAAUUUUAUGCAAGUCUAAGUGUCUACUUGUGCACAUCCAAAGUUGAAAGGCAUAA	193	sly-miR865-1-3p	UAUUUGUUCAAUUUUAUGCAA	130-150	ath-miR865-3p	5	0	21	21	1
sly-MIR403b	AUUGGAAAAGCCAUAUUACGAGCUUGUGCGUGAAUCUAGCAAACAAUAACAGUUUUUCAGAUGAAAAGAGUUGUUAGAUUCACGCACAAACGUGAAAUAUGCCUCUUCCUGA	112	sly-miR403b-5p	AGCUUGUGCGUGAAUCUAGCA	21-41	csi-miR403b-5p	3	0	21	21	1
			sly-miR403b-3p	UUAGAUUCACGCACAAACGUG	74-94	gma-miR403b	1	0	21	21	1
sly-MIR477d	UAUAAACAAUUUGUAUUAUAGUGAAUGUCUAAUUAUGUGGAGUCCUUGUAGGAUAUGGUUAGGAUUCCUACUUGGGGACCAAGUAAGGUUUUCCCUAUAAAUAAAGGGUUUUCC	114	sly-miR477d-3p	UGGAGUCCUUGUAGGAUAUGG	38-58	ptc-miR477d-3p	5	0	21	21	1
sly-MIR865-2	AUCAAUAAUUAUAUUGUUUUUCCUGCAACUAAUCAAAUUGAUCAAACAACUGAACACAGUUCUCUAACAACUGUCAUAGUUGUGGAAAUAACUUAUUUAAUCGCCUGACAACUACAUGCAGUUUGUUGGACCAUUUUGUAUCUGAAAGAUAUGCAUAAUUAUUCUCUU	165	sly-miR865-2-5p	UUUUUCCUGCAACUAAUCAAA	17-37	ath-miR865-3p	5	0	21	21	1
sly-MIR856	GGAAAUAACUUAUUUAAUCGCCUGACAACUACAUGCAGUUGUUGGACCAUUUUGUAUCUGAAAGAUAUGCAUAAUUAUUCUUAUAAAUAACUUCAGUAGUUGUCCAGACAACUGUAAAAGUUGUUGGC	128	sly-miR856-3p	UAUUCUUAUAAAUAACUUCAGU	76-97	ath-miR856	5	0	22	22	1
sly-MIR1446-1	AAUGGAAAUCCAGUGUUUUCUGAACUCUCUCCCUCAAUGGCUUCUCCAAUAUAUAAAUUAAUUUAAAAGAGCAGCCAUGAGAGAUUGAGUUCAGAAAACUAUGGCUUUCCUAG	113	sly-miR1446-1-5p	UGAACUCUCUCCCUCAAUGGCU	21-42	nta-miR1446	0	0	22	22	1
sly-MIR1446-2	AUAUUAAUGGAAACCCAGAGUUUUCUGAACUCUCUCCCUCAAUGGCUGUUCAUAUAAUAUAUGCUGCUACUUUGCAGCUUAAUUAAAUAACAGCUUUGGGGGUUUGAGUCCAGAAAACUCUUGCUUUCCUAGUUAAGCA	139	sly-miR1446-2-5p	UGAACUCUCUCCCUCAAUGGCU	26-47	nta-miR1446	0	0	22	22	1
sly-MIR6277	AAACACAUUAUAUACAUUUGUGUUUGUAUAAAGCGAGAGAGGCGAGUGAAUGAGCGAGAUCUGGGAGGGGGGAACGAAAUUAUACGUAUAUAUACAAUUUUCUCUUGCUUUAUACAAACACAAACACAUUUUAUACAUUUGUGUUUUUGUAUAAAGUGAGAGAGGCCAGUGAGGGAGCGAGAUUUGGGAGAGUGACGGGCGAUAUCUGGGAGAGGAAAAAGAAAAUAUAUGUAUAUAUACAAUUUUCUCUUGCUUUAUACAAACACACACACAUUUUAUACAUUUGCAU	289	sly-miR6277-5p	UGUGUUUGUAUAAAGCGAGAG	19-39	ppe-miR6277	5	0	21	21	1
sly-MIR11124	UGAUCUGAAAUUUGGGUAAGAUUCAACAAAACAGGACACAACAUUGUUUGCUUAGAGGCUUCUUUGUCAUCUUGGUGCUUGAUCGGAGCCUGAAGCUCCAAUAGAUGGAGCGGUGGGCAUACCAUUUGUUGAUCCAUUUUCAAGUGGUGGAGGGACUC	331	sly-miR11124-3p	ACUGGUUUGGAUCUUGUGGAUG	225-246	lja-miR11124-5p	5	0	22	22	2

sly-MIR1919-8	CCCAUUUGCCUUCAGAUUCAAGUGGUUCAAAAACAUGAAC ACUACCAUCUGACAGACCUAAUGCAAACUGGUUUGGAUCU UGUGGAUGUGCUGCAACUACGACUGGGUGGAUGUUUGAA UUGCUGCAGAAAAAUGACAAGGUUUUAUGAAAAAUUACAU CAAAUAUCAGAAAU	161	sly-miR1919-8-3p	GAGCGAGACUUCUGGGAUAGA	91-111	nta-miR1919	5	0	21	21	1
sly-MIR168a	ACAAUUUUUCUCUCGCUUUAUACAAAAUAGAAACAGAAUUA UACACUUCUGUGUAUAAAGCGAGAGAGGCGAGCGAGAAUG GAGAGUGGCGAGCGAGACUUCUGGGAUAGAAAAGCUGACA AAUUUUAGCUAACGUUUGCUAUGAAGCACAGUUAAAUCAA CCAAACUAUCAUAAAUGGUAUGCAAAUACCUUUCGUCAUAC UUUUGGGACAUUGAUAUUCCUGCCGUUCAUAAACUGGAGC AUAUAUGUCCUUCACUCUAAGGAAGACUAAAUAGGGACAC AUGACGCAAUCUUAUCCGUCGAUAGAUGUCGGAUCAAUGA AUAAGAUUAUGACACAUAUAUGUCCGUCAGUAUAAAGGAU AUAUAUACUCUUUUUCUAAAAUUACAUAUGCAAUUAAUAUU CUAAAAAUAUGAUAGAAAUUAUUUACAUUCCAUUUACGAUA GUUCAA	289	sly-miR168a-5p	CCUGCCGUUCAUAAACUGGAG	60-80	sly-miR168a-3p	5	0	21	21	1
sly-MIR10532-17	AAUAGGACCUUUGUAUGGUAAAAAUGUGUUUCUGAGAUUU CGAGUAUAGAUUGAGGGAUACUUGUGCAUUAUCUCUAUAU UUUUAUAUGUGUACAUAUAGAGAGGCAGGGGAGGGAGGG GGGUAACUCUGUAAUCCAACAUCAAUAUCUUGUCUGAGAA CUCAAUACUCAAAAUAGUAAUUUUUUACAUUAUUUAUAUAU UUUUAGUAUAAGAAGGUGCUUGG	223	sly-miR10532-17-5p	AAAUGUGUUUCUGAGAUUUCGAGU	22-45	sly-miR10532	4	0	24	24	1
sly-MIR7998-2	GUUAGACCUACGGACCGUAGAUCAAACGACAGUCCUUGCU GGUCAUCUAUAGUUUAUGUUAGAGGGUGGGUAACUUGAG UCUUAAUCCACGGACACAGACCACGGACGGUAGUCUGACU UACGGACCGUAGGUCUGUC	138	sly-miR7998-2-5p	ACGGACCGUAGAUCAAACGACAGU	10-33	stu-miR7998	2	0	24	24	1
sly-MIR10204	AGGGUUAUGACAUUUCUAAAGAGUCAUAACUUUUCAGAUG AGUUGUGACCUUUCGAAGGGUUGUGACUUUUCAAUAGGU UGCGACUUUUUCAAGGAAUUGUGACUUUUUCGAAGGAUUG UGACUUUUCCAAAGAGUUAUGACUUUUUGGAUGAGUCAUG AACUUU	165	sly-miR10204-5p	UUGUGACCUUUCGAAGGGUUG	43-63	vca-miR10204-3p	5	0	21	21	1
sly-MIR4994	CAAAUGAAAAAGUGGUGAUAUUAAAUGAUAAAUUAAUGAUA UUAUUGGAUCGGAGUGUCACGUUCCGACACGGUAUUCUU GGAUCGAAGUGUCACGUUCUGACACGGUAUUCUUGGAUC GGAGUGUCACGUUCCGACACGAUAUUCUUGGAUCGGAGU GUCACGUUCCGACACGAUAAUAUUAAAGGAAAAAUAUGUU GAAUUAAUGGAAGAUACUCAAUCUCAAAGAACUCAACUCCC AAAAUGGUUUGGUUUGGAGGCAUGAGUCCUCAUGUGUGA UCUUGAUACCGUUGACUUAAUACGUGCUUAAUUUAUUGUU AUUGACACUUGUUCAUAUU	337	sly-miR4994-3p	UGAUACCGUUGACUUAAUACG	282-302	gma-miR4994-3p	5	0	21	21	1
sly-MIR8008b-3	UUGAUUUAUAUUUGCAGGUAUUGCAGAAAAAAAUGAGGAG CAGAGUGGUUUUGUCCGUCGCUUUUUUGCUUUAUUUAUU UCAAAUAAACCCAGAAAAGCGACGGACAAGGUUCUUUGGU CCGUCACUUCUCUAGGUAUUUUAAAAAAUUAAUUUCAAGG AAAGCGACAGACAUUGUCCUUUAGUCGUCCCUCGCUUUUC UGGAAUUUUCAAAAUAUAAAUUUA	223	sly-miR8008b-3-5p	AAACCCAGAAAAGCGACGGACAAG	86-109	stu-miR8008b	2	0	24	24	1
sly-MIR6230-2	UCAACAGACAACUAAAUACUCCAACGUUGAGAAUGCACGU CCUCGUCCCUACAAGGUCUCGUGGACACCCGAUUUUGAUG UGGGACAUUAAGUUAUGGAGGUGUCUUAAUGAUCAUUUUG GAAGUUGAAGUGUUCAACUGACACCGUAGUGACAAGUUGA GGUGUCUAGAUGUGCAUCCUCAAAGUUAAAGUUUAGUAAU GUGUCAU	207	sly-miR6230-2-3p	UGACAAGUUGAGGUGUCUAGA	150-170	sbi-miR6230-3p	4	0	21	21	1
sly-MIR10532-18	UAAUAGGACCUUAGUAUAGUGUAUGUGUGUUUCUGAGAUU UCGGGCAUAGGUUGAGGGGGUACUUGUGCAUUUUUCCUU AUUUUUUUUAUUUUGUUGGCAAAUGUCAAUUAUAAUGGAA AGGAAGAAAUGUGGUAUAUACAAAAACAUCAUAGAAUUAUA UACAUGUGUCCUAACA	176	sly-miR10532-18-5p	AUGUGUGUUUCUGAGAUUUCGGGC	23-46	sly-miR10532	2	0	24	24	1
sly-MIR1032	AGAGGCUUGUGCACGUGACAACCUGGUUUUGGGGAUUGA AUUAAUAUGACUUGGUUUUUUUUAUAGAAAUUGUUGUUGG AUUGUCAUUUACUUUCGCACUUUGUUAGAUAUUGAGUUUU AGGCUGACUUGUCUUGGUGGGAUAAGACGAGUGCCAUCA CGCCCAUUUUUGGGUCGUGACAAAAUGGUAUUAGAGCCCC AGUUUCAUAGGUCUCACGUGUAUACAAGCCGAG	231	sly-miR1032-5p	ACGUGACAACCUGGUUUUGGG	13-33	ppt-miR1032	5	0	21	21	1
sly-MIR3436	GGAUUGUCAUUUACUUCCGUACUUUGUUAGAUAUUGUGUU UUAGGCUGACUUGUCUUGGUGGAAUAAGACGAGUUCCAUC	138	sly-miR3436-3p	UCACACCCAUUUUUGGGUCGUG	79-100	aly-miR3436-3p	5	0	22	22	3

sly-MIR5303-21	ACACCCAUUUUUGGGUCGUGACACAAUAACAUAUAAAAAUUAAAUAAUUUGACAAAAGCUUACCAUUCUCGACUCAUUGCUCAUGUGUUGUGUUGCUCGGACUCUCAAAAUAGUUGCUGCACCUGUGUCGUAUCUUCCAAAACGCACUAUUUUGGAGUAUCCAACACACACCAGUCGACAUUUUUGAAGAGUUCGAGCAACAUAGUCAUAUCUUGAGUUAAUACUGGUCUG	173	sly-miR5303-21-3p	UUUUUGAAGAGUUCGAGCAAC	123-143	sly-miR5303	0	0	21	21	1
sly-MIR5031	AAUUAAUGAUAUACAAAUAUUUUUCGUCAUACUUUGGGAUAUUGGUGCUCUUGUCGUUAAAAAAUUAAAAUGUAUAUACCCUUUAUACUAAGAGACGAUUUGAUUUUUAAUCAACGGAUAACGUGUUCCUUUUUAGUCUUCCGUUACAGUUAGAGUAAAGGGCAUAUAUGCUCAAGUUUUGGAACAGAAAGGACACCAAUGUCCCAAAAGUAUGACGAAGGUAUCUGCAUACCAUGUACGA	241	sly-miR5031-5p	UUAAUGAUAUACAAAUAUUUU	3-23	gma-miR5031	5	0	21	21	1
sly-MIR10542-4	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUUUUAAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAACCUUCCGUUGAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGAUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUGUGAGCCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUC	238	sly-miR10542-4-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
sly-MIR11583b-2	UUUUCUCUCGCUUUAUACAAACACAAACACAAUGUAUACAUUUGUGUUUGUAUAAAGUGAGAGAGACGAGUGAACGAGCGAGACUUGGAGAGUGGCGAGCGAAAUCUGGGAGUGGGAAGAGAGGGGAACAAAAAUAUAUGUAUAUAUACAAUUUUCUCUCGCUUUAUACAAACACAAACACAUUUAUACAUCGUUUCUAUAAAAACAAGAGAGGC	215	sly-miR11583b-2-5p	UUUUCUCUCGCUUUAUACAAA	1-21	pab-miR11583b	5	0	21	21	1
sly-MIR1917-8	GAGCACUACAAUAGAAAUGACUUUUAGCAGCAUUAAAUAUUGACACUAAUAAAGAGUACUAAAGUUUUUACCGGCAUUAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUACAAAGAAUAACAAUUGCCACUAAAAAUAUAUAUUUAGCGGCAAUUAAAAAUUAAAUGUCGCUAAUGGUCAUUUUAGUUAUAGUGGAG	214	sly-miR1917-8-5p	ACUAAUAAAGAGUACUAAAGU	45-65	sly-miR1917	2	0	21	21	1
sly-MIR7997c-13	AGGCUAUGUUGCUCGAACUCUUCAAAAUGUUGUGAAACUUGUAGGAGUGGUGUUUUUGAAGAUUUCGAGCAAUAUAGGUU	80	sly-miR7997c-13-5p	AUGUUGCUCGAACUCUUCAAAAUG	6-29	stu-miR7997c	4	0	24	24	1
sly-MIR1127-3	UAAUACUCCCUCCGUCCGAUUUUAUGUGGCACAAUUUGACCUAGCACGGAGUUUUAAAAAAAUGAAAACUUUGAAUUGUUUACUAAAUUGUCCUUCAAAAGUAGACUCACUUUUCUCUUUUCUCAUAAACGUAUUAGAGUACUAUGUAAAAUUAAGUGGGACCAACAAGGGUAAAAGAGGAAUUGCACCUUUAAAUACUUACCAUAUAAGAAAAUGUGACAUUCUUUUUGGGACUGAGACAAAAAGGAAAUGGUGCCACAUAAAAUGAGACGGAGGGAGUAACU	284	sly-miR1127-3-5p	UAAUACUCCCUCCGUCCGAUU	1-21	bdi-miR1127	3	0	21	21	2
sly-MIR1043-3	UUGUGUUUGUGUUUCUACUGGCACCCUUCCUUUUCAACAGGGGCGGAUUUAAGAAUGGGGAAGAGGUGUCAUGUGACGCUGCUUCGUCAAAAAAAUGGCUAAAUUGUAUAUGCGGUUAUGAAACAAAAGCAAAUAUAAAAAGUCUAUAUAAUAAAAGUGACAUUACAACAUGAGUUGAUGAAAGUCAUGCAUCAUAUAUUUAUGGGCAUAAUACAUAAAUUUGCCCUUUAACUUGGAUUCGAAUCACAUUUAUGCCCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACAUGU	296	sly-miR1043-3-3p	CCUUCAACUUUGGGUGUGCA	256-275	ppt-miR1043-5p	4	0	20	20	1
sly-MIR1043-4	UUUAACUUGGAUUCGAAUCACAUUUAUGCCCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACAUGUAUAAAGCUGAGCAAAUAGGCAGACAUGUCCAACAUGUCAUCCUACGUGUCAUUUUUUGUCCUACGUGUAUUUUGCCGUAUAGAACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUAAAAGUUGAAGGUCAAAGUUAAAAUUUGAAUCCAUGUUUAG	251	sly-miR1043-4-5p	CCUUCAACUUUGGGUGUGCA	30-49	ppt-miR1043-5p	4	0	20	20	1
sly-MIR6231-3	AUAAUUUUUUACCCCUGCACUAUUUAAUAAUGUAUUUUAAGGAUCUAUAUGUGCCCACGUGGACAUCAUAAAUAUUGCAUCAUUUUAAAUAGUAAAGUAUCCACGCGGACACAUAUAUUUUUAAAAUACACUCCUAAAAAGUGGAGAGGGUAAAAGAUCCU	161	sly-miR6231-3-5p	UAUAUGUGCCCACGUGGACAU	46-66	sbi-miR6231-3p	5	0	21	21	1
sly-MIR10195	CUUUUUCGGCCUACGUGGUACUAUCUUGUGGAUCCAAUGAUGGUUGACUUUUUUUUUUCAAACUAGUGUCACGUAGGCUGAAAGGG	86	sly-miR10195-5p	UACUAUCUUGUGGAUCCAAUGA	19-40	gma-miR10195	5	0	22	22	1

sly-MIR2655o-2	CAUGGCAUAAUACAUAAAUCUGUUCUUUAACUUGGCUUCGAAUCACAUUUAUGUCCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACUUUUAUAAAGUGGAACAAAUAGAUACACAUGUCAUUUUUUAUCCUACAUGGUGUCCUACGUGUAUUGUGCCAUGUAGGACUCAUAUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGAUUUUUUGUACAUUAUGAAAAUUGGAGGUCAAAGUUAAAAUUUGAAGUCAAGCUUAGGGUCCAAUUUAUGUAUUAUACCUUU	292	sly-miR2655o-2-5p	CAUUUAUGUCCUUCAACUUUG	46-66	mtr-miR2655o	5	0	21	21	1
sly-MIR7997c-14	UACUAUGUUGUUCGGACUCUUCAAAAAUGUUGCUGCGCCCAUGUCAGAUCCUCCAAAAAAUGUACUAAUUUUUGAGGAUCCAAUGUGCACUCGGUGCCUUCUUUGAAGAGUUCGAGCAACAUAAUU	126	sly-miR7997c-14-5p	AUGUUGUUCGGACUCUUCAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
sly-MIR9675	CCCUAUGCAUAAUUUCGGUGGAGCUUACAACAGCAAGACAGUGAGAGAGAUUUUUGCUCUCUCUCAUUUUCUUGCUGUUGUAAGCUCCACCGGAAUCAUGCAUAAUA	107	sly-miR9675-3p	UUUUUGCUCUCUCUCAUUUUC	51-71	tae-miR9675-3p	5	0	21	21	1
sly-MIR1512c	GAGGUAAAGCAGAAACUCUUUCAAAUAGAGCCAAAUAGUUCUAAGAAUUCUAAGUUGAUCCUCACUAGCACCACAAAGAUUUUUUUAGUUUCAAAAAACAUAUUCUGUGUGGUGCUGAUGACGAUUAACUUAGAAUUCUUGGAGCAUUUUGCUCUACUUGAAGGAGUUUUUGGUUUACACA	182	sly-miR1512c-3p	UAACUUAGAAUUCUUGGAGCAU	127-148	gma-miR1512c	4	0	22	22	1
sly-MIR5780d	AUCUAGACACCUCAACUUGGUCCCAACUGACAACGAAACACUCCAACUCGGUGUGCAACUGAUACAGUGGAGAGGCGUUUAGAUGUGCAUACUCAAAGUUGGAGUGGUUUACUUGUCAGUUGAGGCUAAGUUUUGAGUGUCUACUC	146	sly-miR5780d-3p	AGUUUUGAGUGUCUACUC	129-146	gma-miR5780d	5	0	18	22	2

Supplementary Table S8. Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum pennellii* (spe).

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
spe-MIR156b-1	AAAAUGGAAUGGGUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUUUCC	149	spe-miR156b-1-5p	UUGACAGAAGAUAGAGAGCAC	22-42	aof-miR156b	0	0	21	21	1
			spe-miR156b-1-3p	GCUCUCUAUGCUUCCGUCAUC	111-131	vca-miR156b-3p	1	0	21	21	1
spe-MIR319b-1	UUAGAUGUAAGUAGGAGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAAUAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAU	198	spe-miR319b-1-3p	AUUGGACUGAAGGGAGCUCCU	168-188	aof-miR319b	1	0	21	21	2
spe-MIR390a-1	GGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGCUU	103	spe-miR390a-1-5p	AAGCUCAGGAGGGAUAGCACC	18-38	sly-miR390a-5p	0	0	21	21	1
			spe-miR390a-1-3p	CGCUAUCCAUCCUGAGUUUUA	67-87	sly-miR390a-3p	0	0	21	21	1
spe-MIR164c-1	AUUAUUUAAGCUGGAGAAGCAGGGCACAUGCUGAAUUACUUGAAACUUUGAUCUUUCAAGAAUUUUGCAUGUGCUCUAGCUCUCCAGCUUAAUUCCUC	98	spe-miR164c-1-5p	UGGAGAAGCAGGGCACAUGCU	12-32	fve-miR164c	0	0	21	21	1
			spe-miR164c-1-3p	CAUGUGCUCUAGCUCUCCAGC	68-88	bdi-miR164c-3p	4	0	21	21	1
spe-MIR7983-1	UUUUAGUGGCAUUAAAUAUUGACACUAAUAAAGAAUGCUAAAGUCUUUACCGGCAUUAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUACAAAGAGUAACAAUUGCCACUAAA	130	spe-miR7983-1-5p	UAAAGUCUUUACCGGCAUUAGUUA	39-62	stu-miR7983-5p	4	0	24	24	1
spe-MIR169r-1	AGUCUAUGAGGUUUGCAUGAAGAUGUAGAGAGUGAAGUUGCAGCCAAGGAUGACUUGCCGGACCAUAAAUUGCUAGGAUUUUCGAGUUUCGGCAAGUUGUUCUUGGCUAUAGUUUGCUCUCUUCUUCUCAUGUCAUCCUCGUUAGAC	147	spe-miR169r-1-5p	CAGCCAAGGAUGACUUGCCGG	41-61	csi-miR169r-5p	0	0	21	21	1
spe-MIR169a-1	UGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGAGUGGAGUGCAGCCAAGGAUGACUUGCCGAGAUGUUUGUAGCCUAAUGCAAUGACAUAUCGGCAGGUCAUCUUUGGCUACAUUUUAUUCUCUCCUAUUCAUGUAAAACUUUAUAAGA	149	spe-miR169a-1-5p	CAGCCAAGGAUGACUUGCCGA	42-62	cas-miR169a	0	0	21	21	1
spe-MIR395b-1	UUCAUGACUACAUAUAUCAAGGUGUUCUCGAGAGUUCCUCUGACCACUUCAUUUCGGAAGUCCUGCUGAAGUGUUUGGGGAAACUCCCGGGUUCACUUUG	100	spe-miR395b-1-3p	CUGAAGUGUUUGGGGAAACUCC	66-87	sly-miR395b	1	0	22	22	1
spe-MIR160h-1	UGCCUGGCUCCUUGUAUGCCAUUUGCAUUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAUGGCAUUCUAGGAGCUAAGCAU	81	spe-miR160h-1-5p	UGCCUGGCUCCUUGUAUGCCAUU	1-23	mes-miR160h	1	0	23	23	1
spe-MIR319a-1	AAUAAGGAGCUCUCUCCGGUCCAGUCCGAGGCACUCAAAGGCUAAAAACACAGCUGACGACUCGUUGAUUCUCAAACACAUCAAGAAGCAUUUUUUGAAUUUGACGUGUUUAAGAUUCAACGAUGCGUGAGCUAUGUUUAGCUAGCGUUGUCACGUCUUGGACUGAAGGGAGCUCCCUAUUA	182	spe-miR319a-1-3p	UUGGACUGAAGGGAGCUCCCU	158-178	aof-miR319a	0	0	21	21	1
spe-MIR1128-1	AGCAUGUCAUUAGUUGUUUUUCUCACAACAAUGACUGCUAAUUGAUUAACUCCUAGAAAAGAAGAUUUCACAAGGAUUUCUGCAUAAAAUUACUACUCC	301	spe-miR1128-1-5p	UACUACUCCCUCCGUCCCAAA	91-111	ssp-miR1128	0	0	21	21	1

spe-MIR172-1	CUCCGUCCCAAAAUAAGUGUCACUUUAGCAAUAAUCACACUCAUUAAGAAAAAUAAUAAAUAGAAAGGUAUCUACCCCUAUUUAUUAGAUGUUUCUUGACAAUUGAGCAUGAUUGAUAAGUAGUUAGUUCUUUAGUACAAAGGUAUACUUGGAAAAACAUACUAAUUUCCGUCUUAAGUUCCUAUGGUGACACUUAUUUUGG	159	spe-miR172-1-3p	UGAGAAUCUUGAUGAUGCUGCAU	118-140	aau-miR172	0	0	23	23	1
spe-MIR5300	UGCAGAUGUAGCAUCAUCAAGAUUCAUACAUGAAAAUUAAGAGGCAAGGUUAAAUAUGUAGCUUUAAUUUGAAAUGGAAAAUAUAAUACAUCAUGACCAUGUCUAUUUAUUUCAAAGUGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAAUAACUAUCGUUGACCAAAAUUCUUCUUCCCCAGUCCAGGCAUUCCAACAGUUGAUAACAUCUAGAUCUGCCAAUCCUUUGUAUUUUUGUUCUUCUAUUUUUCACAUGACAUCUUCAAAAUCCACUGUGAGCUUCAUCAUAAGCUAAGAAAUGGUGAGUUUUGAUGAUGUGAUGCCUAAAAUAGGAUUAAUGAAAGUACUGGUAAAAAGGUGUUCAAAUCUGGAGGUUAUGUUAAGCUGGUGGUAUGCUUUGAUUGGGAAAGAUGACUUAGGUCA	265	spe-miR5300-5p	UCCCCAGUCCAGGCAUUCCAAC	18-39	sly-miR5300	0	0	22	22	1
spe-MIR482c-1	ACAAAAACUUUUGGGAAUGGGUGGGUUGGUAAGCUUUUUCUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUCCUAUGGGUUUUUG	97	spe-miR482c-1-5p	ACUUUUGGGAAUGGGUGGGUUGG	7-29	gma-miR482c-5p	5	0	23	23	1
			spe-miR482c-1-3p	UUACCAAUUCCACCCAUUCCUA	66-87	nta-miR482c	1	0	22	22	1
spe-MIR319a-2	UGGUAUAAGAGAGCUUCCUUUAGUCCACUCAUAGGUAGACGAAGGAUUUGAAUUAUCUCCCGACUCAUUCAUUCAAACGCAAUAGAAAGUAUGUAAUCUUAUACUAUUGUGAAUGUGUGAAUGAUGCGGGAGAUAAAUUCUCUCCUUUUUAUCUGUGCUUGGACUGAAGGGAGCUCCCUUUUACC	185	spe-miR319a-2-5p	AGAGCUUCCUUUAGUCCACUC	10-30	mtr-miR319a-5p	1	0	21	21	1
			spe-miR319a-2-3p	UUGGACUGAAGGGAGCUCCCU	159-179	aof-miR319a	0	0	21	21	1
spe-MIR171a-1	UGAUCAACUUGGGAUGUUGGUGUGGUUCAAUUAGAUAACAAUCUCCACGUAAGAUUGUAGAGUCUGUUAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAAGAAAAUAAC	110	spe-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	72-92	aof-miR171a	0	0	21	21	1
spe-MIR6022	AUACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAGUUAUUUAAACCGAGUUUUAACCAAUUGCACAGUCCUCUACCCAAGAUUGAGGUUUCGUAAACUGUAACUUAAGAUCAAGUCGCGUUAGGUUCAUAAAGUUUUGAAUUGACUUAGGAAGAGUACCAUGCAACUUAAAACUUUGAGCCGAAAUAAGUUAGUGAUGGAAAGGAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGG	236	spe-miR6022-3p	UGGAAAGGAUAAUAUCCAGGA	197-217	sly-miR6022	2	0	21	21	1
spe-MIR482c-2	AAAAACUUUUGGGAAUGGGUGGGUUGGUAAGCUUUUUCUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUCCUAUGGGUUUUUGGGCUUCCCUC	105	spe-miR482c-2-5p	ACUUUUGGGAAUGGGUGGGUUGG	5-27	gma-miR482c-5p	5	0	23	23	1
			spe-miR482c-2-3p	UUACCAAUUCCACCCAUUCCUA	64-85	nta-miR482c	1	0	22	22	1
spe-MIR482c-3	GUGUUUCGAGGAGGUGUUGGAGUGGGUGGUAUGGUAAGAUUUCAUAUUUAUUUUUCAUAAAAAUUGAAAUCUUGCCAAUACCGCCCAUUCCUAUGGCUUCUGAUCAUUUC	110	spe-miR482c-3-3p	UCUUGCCAAUACCGCCCAUUCC	70-91	sly-miR482c	0	0	22	22	1
spe-MIR482b-1	AUUUUUCAGGAAGCUUUUGGAGUGGGUGGCAUGGUAAGAUAUCAUAUUUUAUUUUUCAUAAAGAAAAUGAAAUUAAAAUCUUACCGAUUCCCCCCAUUCCAAUGGCUUCCAGUUAUUUC	119	spe-miR482b-1-5p	GGAGUGGGUGGCAUGGUAAGA	19-39	stu-miR482b-5p	0	0	21	21	1
			spe-miR482b-1-3p	UUACCGAUUCCCCCCAUUCCAA	81-102	stu-miR482b-3p	0	0	22	22	1
spe-MIR482d-1	UUUGGAGUGGGUGGGAUGGAAAAAUAUUGUAUUUGUUUUUUUUUUCUGAAGGGAAAAAGAUGAAUAUUGAGAUUUUUCCUAUUCCACCCAUGCCAAU	113	spe-miR482d-1-5p	GGAGUGGGUGGGAUGGAAAAA	4-24	sly-miR482d-5p	0	0	21	21	1

	GGCUUCCAAUCAUUUA										
			spe-miR482d-1-3p	UUUCCUAUUCCACCCAUGCCAA	75-96	sly-miR482d-3p	0	0	22	22	1
spe-MIR6025e-1	UGAAUAGUUAUUUCAUGUAUACUUGCACAAAAA UAUUAUUGAACCUUGAUGUUAUCUCAGUGUUG GCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAU GUGUAUUUUGGUGUUGUACCAAAUCCAGGCAU GCCAAUUAUUGAGAUGGCAUCUCGGUUUGUUA	162	spe-miR6025e-1-3p	UGCCAAUUAUUGAGAUGGCAUC	130-151	nta-miR6025e	2	0	22	22	1
spe-MIR6025e-2	AAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUG UUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUU GAAUGUGUAUUUUGGUGUUGUACCAAAUCCAG GCAUGCCAAUUAUUGAGAUGGCAUCUCGGUUU GUUAGUUGCUGUGCCGUAUGAUCACUGUGGCA G	162	spe-miR6025e-2-3p	UGCCAAUUAUUGAGAUGGCAUC	101-122	nta-miR6025e	2	0	22	22	1
spe-MIR6027	UUUCCAUAAUUUUACAUGAUUAUGGGUAGCACA AGGAUUAAUGUGAAACAAAUAAGUGAUAUGCAA AGAAGAUGGAGAUUCAAUUGUUUAUUGUUACG AAGAAAACACUUUUGUGUUUCUCGUGAAUCCUU CGGCUAUCCAUAAUCAUGUUGAAUGUGUGACU U	164	spe-miR6027-5p	AUGGGUAGCACAAGGAUUAAUG	22-43	sly-miR6027-5p	0	0	22	22	1
			spe-miR6027-3p	UGAAUCCUUCGGCUAUCCAUAA	123-144	stu-miR6027	0	0	22	22	1
spe-MIR319a-3	AUGUGGAAGAUGGUAUAAGAGAGCUUCCUUUA GUCCACUCAUAGGUAGACGAAGGAUUUGAAUU AUCUCCCGACUCAUUCAUUCAAACGCAAUAGAA AGUAUGUAAUCUUAUACUAUUGUGAAUGUGUG AAUGAUGCGGGAGAUAAAUUCUCUCCUUUUUA UCUGUGCUUGGACUGAAGGGAGCUCCCUUUUA CC	195	spe-miR319a-3-5p	AGAGCUUCCUUUAGUCCACUC	20-40	mtr-miR319a-5p	1	0	21	21	1
			spe-miR319a-3-3p	UUGGACUGAAGGGAGCUCCCU	169-189	aof-miR319a	0	0	21	21	1
spe-MIR395g	UCAAGGUGUUCCCUAGAGUUCCCUUGACCUCU UCAUUAGGGUUUACUCAUUGUUUGAUGUCCUG CUGAAGUGUUUGGGGGAACUUUUGGACUCACA UUGA	100	spe-miR395g-5p	GUUCCCUUGACCUCUUCAUUA	18-38	mdm-miR395g-5p	2	0	21	21	1
			spe-miR395g-3p	UGAAGUGUUUGGGGGAACUUU	66-86	gma-miR395g	0	0	21	21	1
spe-MIR171a-2	AGUAACUUUGAUAUUGGCCUGGUUCACUCAGA CAACAAAAUGAAAACUAUAUUUGAAUGGUUGAG UUUUCGUUUUUCGUUUGAUUGAGCCGUGCCAA UAUCUCAGUUUCUCUUUCACUUUCACUUUCUC	129	spe-miR171a-2-5p	UAUUGGCCUGGUUCACUCAGA	12-32	cas-miR171a-5p	0	0	21	21	1
			spe-miR171a-2-3p	UGAUUGAGCCGUGCCAAUAUC	81-101	aof-miR171a	0	0	21	21	1
spe-MIR171a-3	ACAGUAACUUUGAUAUUGGCCUGGUUCACUCA GACAACAAAAUGAAAACUAUAUUUGAAUGGUUG AGUUUUCGUUUUUCGUUUGAUUGAGCCGUGCC AAUAUCUCAGUUUCU	112	spe-miR171a-3-5p	UAUUGGCCUGGUUCACUCAGA	14-34	cas-miR171a-5p	0	0	21	21	1
			spe-miR171a-3-3p	UGAUUGAGCCGUGCCAAUAUC	83-103	aof-miR171a	0	0	21	21	1
spe-MIR482c-4	GAAAAUCUAUGGGAAUUGGUGAGUUGGAAAGC UUUUCUUUUUCUUCUCUUGUGAUUAGCUUUCC AAUUCCACCCAUUCCUAUGGUUUUUCG	91	spe-miR482c-4-3p	UUUCCAAUUCCACCCAUUCCUA	60-81	nta-miR482c	0	0	22	22	1
spe-MIR1446-1	CAGUGUUUUCUGAACUCUCUCCCUCAAUGGCU UCUUCAAUAUAAUUAAAUUAAUUAAAAAGAGCA GCCAUGAGAGAUUGAGUUCAGAAAACUCUGG	96	spe-miR1446-1-5p	UGAACUCUCUCCCUCAAUGGCU	11-32	nta-miR1446	0	0	22	22	1
spe-MIR482b-2	UUUUCAGGAAGCUUUUGGAGUGGGUGGCAUGG UAAGAUAUCAUAUUUUAUUUUUCAUAAAGAAAA UGAAAUUAAAAUCUUACCGAUUCCCCCCAUUCC AAUGGCUUCCAGUUAUUUCUC	119	spe-miR482b-2-5p	GGAGUGGGUGGCAUGGUAAGA	17-37	stu-miR482b-5p	0	0	21	21	1
			spe-miR482b-2-3p	UUACCGAUUCCCCCCAUUCCAA	79-100	stu-miR482b-3p	0	0	22	22	1
spe-MIR166-1	GAGAAUGUCGUCUGGUUCGAGAUCUUUCAUAA GAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUG UAUCUUGAAUGAUUUCGGACCAGGCUUCAUUC CCCUCAACUCUGAUCCAACAAG	119	spe-miR166-1-3p	AUUUCGGACCAGGCUUCAUUCCCC	77-100	lja-miR166-3p	0	0	24	24	1

spe-MIR156k	GGUGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUUGCAUGAUGUUUAUAUAUAUAUGCUUGAAACUAUGUGUGCUUACUCUCUAUCUGUCACCC	99	spe-miR156k-5p	UGACAGAAGAGAGUGAGCAC	6-25	cas-miR156k-5p	0	0	20	20	1
			spe-miR156k-3p	UGCUUACUCUCUAUCUGUCACC	77-98	cas-miR156k-3p	0	0	22	22	1
spe-MIR156f-1	UAUUGACAGAAGAGAGAGAGUACAAUCUGUCAUCAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUGCUCUCUCUGCUUCUGCCAAU	86	spe-miR156f-1-5p	UUGACAGAAGAGAGAGAGUACA	3-24	gma-miR156f	1	0	22	22	1
spe-MIR160c	AUGUGCCUGGCUCCCUGUAUGCCACACGCAUUCACCAAUUUUUUGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGCAUA	85	spe-miR160c-5p	UGCCUGGCUCCCUGUAUGCCA	4-24	aof-miR160c	0	0	21	21	1
			spe-miR160c-3p	GCGUAUAAGGAGCCAAGCAUA	65-85	aly-miR160c-3p	2	0	21	21	1
spe-MIR397b-1	UGAGUACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGA	116	spe-miR397b-1-5p	UCAUUGAGUGCAGCGUUGAUG	17-37	mes-miR397b	0	0	21	21	1
			spe-miR397b-1-3p	UCAACGCUACACUCGAUCAUG	81-101	eun-miR397b-3p	3	0	21	21	1
spe-MIR156b-2	AUUUAUUGAUUGUGUAAAAUGUAGGGAGGAGAAAAAAGAGGUGAAAAUGGAAUGGGUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUC	183	spe-miR156b-2-5p	UUGACAGAAGAUAGAGAGCAC	65-85	aof-miR156b	0	0	21	21	1
			spe-miR156b-2-3p	GCUCUCUAUGCUUCCGUCAUC	154-174	vca-miR156b-3p	1	0	21	21	1
spe-MIR156b-3	GGUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUUUCCUUCUAUUUUUCUCUCUUCUCUCCCUAAAUCUAUACAAUAACUUGU	183	spe-miR156b-3-5p	UUGACAGAAGAUAGAGAGCAC	11-31	aof-miR156b	0	0	21	21	1
			spe-miR156b-3-3p	GCUCUCUAUGCUUCCGUCAUC	100-120	vca-miR156b-3p	1	0	21	21	1
spe-MIR156b-4	ACUGACAGAAGAGAGUGAGCACACGCUGUCGAAUUGUAUAAAUAUAUAUACAAUUGUCAUUUGCGUGUGCUCACUUCUCAUUCUGUCAGCU	91	spe-miR156b-4-5p	UGACAGAAGAGAGUGAGCACA	3-23	hvu-miR156b	0	0	21	21	1
			spe-miR156b-4-3p	GCUCACUUCUCAUUCUGUCAGCU	69-91	csi-miR156b-3p	2	0	23	23	1
spe-MIR160g	AAUUGUUCUGCCUGGCUCCCUGGAUGCCAACUAAGAACAGUAUUGUCAAAAAAAUUGACACUCUUCCUAGUUGGUACCAGAGGAGACAGGCAGAUCCAU	99	spe-miR160g-5p	UGCCUGGCUCCCUGGAUGCCA	9-29	lus-miR160g	0	0	21	21	1
spe-MIR394-1	AGUGUAGAGCCAUUUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAACUAGCUCUGCAGCUCUCUCUC	94	spe-miR394-1-5p	UUUGGCAUUCUGUCCACCUCC	14-34	cas-miR394	0	0	21	21	1
spe-MIR168c-1	CCUCUUAUUCGCUUGGUGCAGGUCGGGACCUCAUUCGCCGGCGCCGGGAAUAAUGGCGGACGAACGACGGCGGUUUUAAUUCUACUAAGCUGUCACCGACGAAUAUAUGUUUGAUUAGCGGCGAAAUUUGGGUCCUGCCUUGCAUCAACUGAAUUGGAG	159	spe-miR168c-1-5p	UCGCUUGGUGCAGGUCGGGAC	9-29	bra-miR168c-5p	0	0	21	21	1
			spe-miR168c-1-3p	CCUGCCUUGCAUCAACUGAAU	134-154	bra-miR168c-3p	1	0	21	21	1
spe-MIR172-2	CAGUCGUUGUUUGCAAAUGCAGCACUAUUAAGAUUCUCAAAUAUUCGACAUUUAAAAUGCAAUUAAAUGUGAAUCUUGAUGAUGCUGCAUUAGCAAUAAACGACU	105	spe-miR172-2-3p	UGUGAAUCUUGAUGAUGCUGCAU	68-90	aau-miR172	1	0	23	23	1
spe-MIR7528	AAUCGAGUUUUAUAUUCGUUAAUUAUUGUUAUUUGCUUGCUUAAUUUUUCAUUUUUGGAGAAAUAUGGCCGGUGAUGACAAAAAUAUUUGCACGAGCGGCAACAACAUCCUUUUUUGCGCAGUUGUUGUUGCUAUGAUAAAUGUGCCAAUAUGCUAAUCUGAGGCCAAAUUGUUUUUUAUUCUUAGAUGUGUAUGGAGUGAAUUGCUAUUUAAA	214	spe-miR7528-3p	CCAAUAUGCUAAUCUGAGGCCA	146-167	lja-miR7528	5	0	22	22	1

spe-MIR7981-2	ACUAAUUAAACUAAGGUCUUAUAACCCUCCUAAACUUAUUUCUUUUUUGUAAUUUUGUUUACUUUUUGGUUAAGUGACAUCCAAAUAUCUCUUAUGUGCCUCAAUUGCGUGGAGUAUACACGUAAGACAAAAGUUUAAGAGGGUAAUAGGACGUUAGUUUAGUUAAGGUGUGUCUCUGAAAUUUUGAUCUUAGUCUAGAGGGUACU	207	spe-miR7981-2-5p	ACUAAUUAAACUAAGGUCUUAUAA	1-24	stu-miR7981-5p	5	0	24	24	3
			spe-miR7981-2-3p	AUAGGACGUUAGUUUAGUUAAGGU	147-170	stu-miR7981-3p	1	0	24	24	1
spe-MIR7984c-1	GAUAGCAAACUUUAUAAAGGGCCUCUUAUCCUCCUGAACUAUUUAAUAGUGUAUUUUAAAAGUAUAUAUGUGCCUACGUGGAAAUGUUACUAUUAGUAAUUAUGCAUAUUGUUUUAUGUCUAGGUGAACACUUAUAUACCUUUAAAAUACACUAUUAAGUAAUGCACCGGGUAAAAGGUCCUUUCCGAAGUUUGGUAUCG	200	spe-miR7984c-1-3p	CCUUUCCGAAGUUUGGUAUCG	180-200	stu-miR7984c-3p	4	0	21	24	1
spe-MIR5174d-1	UCCGUUCCAAGUCAAACUAAGCCAAUCUUUUUGAAACGGAGGGAGUAAUGUAUUUUAAAAGUAUAUAUGUGCCUACGUGAACACAUUACUAUUUAUAAUGGUGCAAUAUUUAUGAGUCCAUGUGGACACAUAUACUUUUAAUAAAUACUAUUAAAUAGUGAAGAGAUUGUAAAAGGUCCUUUUCAAAGUUCGGCAU	199	spe-miR5174d-1-5p	CAAUCUUUUUGAAACGGAGGGAGU	23-46	bdi-miR5174d-3p	3	0	24	24	1
spe-MIR5174d-2	GUUCCAAGUCAAACUAAGCCAAUCUUUUUGAAACGGAGGGAGUAAUGUAUUUUAAAAGUAUAUAUGUGCCUACGUGAACACAUUACUAUUUAUAAUGGUGCAAUAUUUAUGAGUCCAUGUGGACACAUAUAUACUUUUAAUAAAUACUAUUAAAUAGUGAAGAGAUUGUAAAAGGUCCUUUUCAAAGUUCGGCAUUG	198	spe-miR5174d-2-5p	CAAUCUUUUUGAAACGGAGGGAGU	20-43	bdi-miR5174d-3p	3	0	24	24	1
spe-MIR7984c-2	UACGAUAUCAAACUUUAUGAGGGAUCUUGUACCUCCUGAACUAUUUAAUAAUGUAUUUUAAAGGUAUAUAUGUGUCAACGUAGACACAUUACUAUUUAUAAUUAUGCAAUAUUUUUUAUGUCCACGUGGGCACAUAUAUAUCUUUACAACACACUAUUAAGUAGUGCAGGAGGUAAAAGGUCAUUUCCAAAGUUUGAUAUUGUGA	205	spe-miR7984c-2-5p	ACGAUAUCAAACUUUAUGAGGGAU	2-25	stu-miR7984c-5p	3	0	24	24	1
spe-MIR7984b-1	UACGAUAUCAAACUUUGGAAAUGACCUUUUAACCUCUACAUCAUUUAAUAGUGUAUUCCACGUGGACAUUAUAUAUAUUGCAUAUUACAAAUAGUAAUGUGUCCACGUCGGCACAUAUAUACCUUUAAAAUACACUAUAAAUAGUGCAGAGGGUAAAAGGUCUUUCAUAAAAUUUGGUAUUGUAAUAACACUUUCGAUCAAAGUU	205	spe-miR7984b-1-5p	AUAUCAAACUUUGGAAAUGACCUU	5-28	stu-miR7984b-5p	2	0	24	24	1
			spe-miR7984b-1-3p	GGUCUUUCAUAAAAUUUGGUAUUG	159-182	stu-miR7984b-3p	1	0	24	24	1
spe-MIR8011a-1	AUUAUGUGGGGCUUCUUUUUGUCCCACAAGUUGGUGAACCCAAAUCAUUACACUUCUGGGUCCACCGACUUGUAAAAUAAAAAGAAGCCUCACAGAACU	99	spe-miR8011a-1-5p	UUAUGUGGGGCUUCUUUUUGUCCC	2-25	stu-miR8011a-5p	5	0	24	24	1
			spe-miR8011a-1-3p	AAUAAAAAGAAGCCUCACAGAACU	76-99	stu-miR8011a-3p	1	0	24	24	1
spe-MIR8011a-2	UUCUGUGAGGCUUCUUUUUAUUUUACAAGUCGGUGGACCCAGAAGUGUAAUGAUUUGGGUUCACCAACUUGUGGGACAAAAAGAAGCCCCACAUAAU	97	spe-miR8011a-2-5p	UUCUGUGAGGCUUCUUUUUAUUUU	1-24	stu-miR8011a-5p	4	0	24	24	1
			spe-miR8011a-2-3p	GACAAAAAGAAGCCCCACAUAAU	75-97	stu-miR8011a-3p	5	0	23	24	2
spe-MIR8020-1	GAAUUUCAUUGAGUAUGUUGUUGUUGUAAAGCAUACUGAAUUAAUGCAAGUACAAAAGUUACAACAACAACAUACUUGCUGAAAUACC	88	spe-miR8020-1-5p	AAUUUCAUUGAGUAUGUUGUUGUU	2-25	stu-miR8020	0	0	24	24	1
spe-MIR8024b-1	CUUGGAGUAUUUGAAGACUUUAGCUUGCACUUGGAGGAUUUAAAGACUUCAGCUUGCAAACUUGGAGGAUUUGAAGACUUCAACU	85	spe-miR8024b-1-3p	UUGGAGGAUUUGAAGACUUCAACU	62-85	stu-miR8024b	1	0	24	24	1

spe-MIR8025	UCAUACAUCAUAAAGAAAUAUUUUACCACACAC UACACAUGCAAUUAAAUUAGUAUAAGUCGCCAU UAUGUUUUUCUUAACCAAGCUGAAUCAUAUAAU GGUGACUUAUACUAAUUUAAUUGCAUGCCGAG UGUCUG	137	spe-miR8025-5p	ACACACUACACAUGCAAUUAAAUU	28-51	stu-miR8025-5p	3	0	24	24	1
			spe-miR8025-3p	UUUAAUUGCAUGCCGAGUGUCUG	115-137	stu-miR8025-3p	2	0	23	24	1
spe-MIR8008b-1	AAACCCAGAAAAGCGACGGACAGGGUCCUUAAG UCUGUCGCUUUUCUGGGUUUU	54	spe-miR8008b-1-5p	AAACCCAGAAAAGCGACGGACAGG	1-24	stu-miR8008b	1	0	24	24	1
spe-MIR8036	GGGAGGGAUCGAAAGGUAAUAAGGAUUUAUAU AUUUUUUCGAUUUGAUUGGGAAAAAAAAGAAUU AUGUCUUUCCGAUGCCUCCCA	86	spe-miR8036-5p	GGAGGGAUCGAAAGGUAAUAA	2-22	stu-miR8036-5p	5	0	21	21	1
			spe-miR8036-3p	UAUGUCUUUCCGAUGCCUCCCA	65-86	stu-miR8036-3p	0	0	22	22	1
spe-MIR8038b-1	UCCUUGUGAGUAAGUUGGAUCUCAUGCUCGUU AAACCACAAGAUAUGUAGAAUGCGUCCUAACAU GAGAUUCAGUUUACUCACAAGGAAAAAUUGUU	97	spe-miR8038b-1-5p	CCUUGUGAGUAAGUUGGAUCUC	2-23	stu-miR8038b-5p	1	0	22	22	1
spe-MIR8038b-2	CCUUGUGAGAAAGUUGAAUCUCACGCUUGUUA AGCCUCAAGAAAAGCACAAUGCGUUCCAGCGUC AUCUUGAAAAUCUUGAGUUUUUCAAUUUUCUCA	98	spe-miR8038b-2-5p	CCUUGUGAGAAAGUUGAAUCUC	1-22	stu-miR8038b-5p	1	0	22	22	1
spe-MIR319d-1	AAGGAAACUGUUUAGUCCAACCCAAGGUGGGU UACUGGAACUGAUCUUUGCUGCUGAAUCAUUG GCUCAUGAGCAUGUCAAAGAAGAUGAUUGAACA UUCUGGACAUGUUCUUGCUCCAAUGAUACAGG AGCUGAGCUCGGUUUUUCACCGCCUUUUCUUG GACUGAAGGGUUCCCUUC	179	spe-miR319d-1-5p	AGGAAACUGUUUAGUCCAACC	2-22	sly-miR319d	0	0	21	21	1
			spe-miR319d-1-3p	UUGGACUGAAGGGUUCCCUU	159-178	zma-miR319d-3p	4	0	20	20	1
spe-MIR319d-2	AAGGAAACUGUUUAGUCCAACCCAAGGUGGGC UAUUGGAACUGAUCUUUGCUGUUGAAUCAUUG GCUCAUGAGCAUGUCAAAGAAGAUGAUUUAACA UUCUGGACAUGUUCUUGCUCCAAUGAUGCAGG AGCUGAGCUUNCGGAGUAUAGGUACUUGAGAA AGCAGAGGAGAGAAGGAA	179	spe-miR319d-2-5p	AGGAAACUGUUUAGUCCAACC	2-22	sly-miR319d	0	0	21	21	1
spe-MIR3627	GUCGCAGGAGAGAUGGCACUUACCAUUCCUUU UAAUUGGUACAAUGCCUAAAUGGAACCAUUAAG UGCCUCUGUCUUUCGACA	83	spe-miR3627-5p	UCGCAGGAGAGAUGGCACUUAC	2-23	stu-miR3627-5p	1	0	22	22	1
			spe-miR3627-3p	AAGUGCCUCUGUCUUUCGACA	63-83	stu-miR3627-3p	0	0	21	21	1
spe-MIR171e	UAGAUAUUGAUGCGGUUCAAUCUGAAAGACAU GGCUAGAUAUGUAAUUAGCCUUGUAAUUUUGG AUUGAGCCGCGUCAAUAUCUCU	86	spe-miR171e-3p	UUGAGCCGCGUCAAUAUCUCU	66-86	sly-miR171e	0	0	21	21	1
spe-MIR395c-1	AGUUCCCUUGACCGCUUCAUUAGGGCUUACUU CAUUGUUUGAUGCCCCGCUGAAGUGUUUAGGG GAACUC	70	spe-miR395c-1-3p	CUGAAGUGUUUAGGGGAACUC	50-70	csi-miR395c-3p	1	0	21	21	1
spe-MIR827-1	GUUUGUUGAUGGUCAUCUAUUCAUCAUAUCAU UUGGCAUAGUUUAUGCAACCAUUAAUAUGUCAU GAUUAGAUGAACAUCAACAAACA	88	spe-miR827-1-5p	UUUGUUGAUGGUCAUCUAUUC	2-22	stu-miR827-5p	0	0	21	21	1
			spe-miR827-1-3p	UUAGAUGAACAUCAACAAACA	68-88	sly-miR827	0	0	21	21	1
spe-MIR172c	UGGAGCAUCAUCAAGAUUCACAUAGCUACAUUA GGGAUUUUAUUAUUUUUAAAAACCCUAUGGGC GAUGUGUGGGAAUCUUGAUGAUGCUGCAG	94	spe-miR172c-5p	GGAGCAUCAUCAAGAUUCACA	2-22	cas-miR172c	0	0	21	21	1
			spe-miR172c-3p	GGGAAUCUUGAUGAUGCUGCAG	73-94	csi-miR172c-3p	1	0	22	22	2
spe-MIR156b-5	UUGACAGAAGAUAGAGAGCACUAAUGAUGAUAU GCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAU CUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUC AUC	101	spe-miR156b-5-5p	UUGACAGAAGAUAGAGAGCAC	1-21	aof-miR156b	0	0	21	21	1
			spe-miR156b-5-3p	GCUCUCUAUGCUUCUGUCAUC	81-101	vca-miR156b-3p	0	0	21	21	1
spe-MIR167c-1	GUGAAGCUGCCAGCAUGAUCUAAACUUGGCCA UUUGUAAAGAAAAUGGGUGACUAAGGUUAGGU CAUGCUCGGACAGCCUCACU	84	spe-miR167c-1-5p	UGAAGCUGCCAGCAUGAUCUA	2-22	ata-miR167c-5p	0	0	21	21	1
			spe-miR167c-1-3p	GGUCAUGCUCGGACAGCCUCACU	62-84	stu-miR167c-3p	0	0	23	23	1

spe-MIR167b-1	UGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUAGUUCAAAUAUAAUAUGAGGAAAGAUCAGAUCAUGUGGCAGCCUCAC	80	spe-miR167b-1-5p	UGAAGCUGCCAGCAUGAUCUAA	1-22	bna-miR167b	0	0	22	22	1
			spe-miR167b-1-3p	GAUCAUGUGGCAGCCUCAC	62-80	stu-miR167b-3p	1	0	19	20	1
spe-MIR393b	UUCCAAAGGGAUCGCAUUGAUCCUGUGUCCCAAAUUAAUUAACCAUGGGACUAUGGGAUCAUGUGAUCUCUUCGGAAU	78	spe-miR393b-5p	UUCCAAAGGGAUCGCAUUGAUC	1-22	csi-miR393b-5p	0	0	22	22	1
			spe-miR393b-3p	UCAUGUGAUCUCUUCGGAAU	59-78	csi-miR393b-3p	2	0	20	21	1
spe-MIR477a	GCCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUAUGUUGGGAAAGAAGCUCUAGCAGGGAGAGCCA	70	spe-miR477a-5p	CCUCUCCCUCAAGGGCUUCUC	2-22	stu-miR477a-5p	0	0	21	21	1
			spe-miR477a-3p	GAAGCUCUAGCAGGGAGAGCCA	49-70	stu-miR477a-3p	0	0	22	22	1
spe-MIR477b	CACUCUCCCUCAAAGGCUUCUGGCUUAAAAUGCCAUUUGUGCUAAUGCUAGAGGUCUUUCGAGUGAGAGUGA	72	spe-miR477b-5p	ACUCUCCCUCAAAGGCUUCUG	2-22	stu-miR477b-5p	0	0	21	21	1
			spe-miR477b-3p	GAGGUCUUUCGAGUGAGAGUGA	51-72	stu-miR477b-3p	0	0	22	22	1
spe-MIR397-1	AUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUC	80	spe-miR397-1-5p	AUUGAGUGCAGCGUUGAUGAC	1-21	stu-miR397-5p	0	0	21	21	1
			spe-miR397-1-3p	CAUCAACGCUACACUCGAUC	61-80	stu-miR397-3p	1	0	20	21	1
spe-MIR156b-6	GUGACAGAAGAGAGUGAGCACACAUGGUUCUUUCAUGGAUUAUUCCCCAUGUUUAAAAGCUCUGCGUGCUCACGCUCUAUCUGUCACA	88	spe-miR156b-6-5p	UGACAGAAGAGAGUGAGCACA	2-22	hvu-miR156b	0	0	21	21	1
			spe-miR156b-6-3p	UGCUCACGCUCUAUCUGUCACA	67-88	mtr-miR156b-3p	2	0	22	22	1
spe-MIR169e-1	UCUAUUUGUUUAGUAGCCAAGGAUGACUUGCCUUUCAUCAAUGGAAAAUGAUUACAACACUUUUCAUGGUAUUGGGAAAAUGAGUGGCAAGCAUCUUUGGCGACU	105	spe-miR169e-1-5p	UAGCCAAGGAUGACUUGCCUUU	14-35	sly-miR169e-5p	0	0	22	22	1
			spe-miR169e-1-3p	UGGCAAGCAUCUUUGGCGACU	85-105	sly-miR169e-3p	0	0	21	21	1
spe-MIR394-2	UUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAAC	61	spe-miR394-2-5p	UUUGGCAUUCUGUCCACCUCC	1-21	cas-miR394	0	0	21	21	1
spe-MIR164-1	AGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUACAGCAAAUAGUGUUUGUACUUACAUGUAUGUAGUAAAGUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAU	165	spe-miR164-1-5p	UGGAGAAGCAGGGCACGUGCA	4-24	aof-miR164	0	0	21	21	1
spe-MIR169r-2	UAGUCUAUGAGGUUUGCAUGAAGAUGUAGAGAGUGAAGUUGCAGCCAAGGAUGACUUGCCGGACCAUAAAUUGCUAGGAUUUUCGAGUUUCGGCAAGUUGUUCUUGGCUAUAGUUUGCUCUCUUCUUCUCAUGUCAUCCUCGUUAGA	147	spe-miR169r-2-5p	CAGCCAAGGAUGACUUGCCGG	42-62	csi-miR169r-5p	0	0	21	21	1
spe-MIR169r-3	UCAUGUUAAAGUCUUGCAUGAGGGAAUAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAAUAGCUGUUGUUGUAGGUGUCAAAUCAG	177	spe-miR169r-3-5p	CAGCCAAGGAUGACUUGCCGG	43-63	csi-miR169r-5p	0	0	21	21	1
spe-MIR169c-1	AGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCUACUUUUAUUUUCCUCCAAUUUUUUAUGGAGUAUAUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCGAUUUAUAUUCAUCUCUACUUGAUCAAAA	205	spe-miR169c-1-5p	UAGCCAAGGAUGACUUGCCUA	42-62	ata-miR169c-5p	0	0	21	21	1
spe-MIR2111d	UGGUAAUCUGCAUCCUGAGGUUUAGAUCAAUUUCUAAUUUACUGGAUCUAGUCCUUAGGAUGCAGAUUAUC	71	spe-miR2111d-5p	UAAUCUGCAUCCUGAGGUUUA	4-24	ppe-miR2111d	0	0	21	21	1

			spe-miR2111d-3p	GUCCUUAGGAUGCAGAUUAUC	51-71	mtr-miR2111d-3p	2	0	21	21	2
spe-MIR319b-2	AGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAAUAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAUAUAUAGUUAAGUUAACUAUAUAAAAUAU	211	spe-miR319b-2-3p	AUUGGACUGAAGGGAGCUCCU	153-173	aof-miR319b	1	0	21	21	2
spe-MIR171a-4	UAUUGGUGCGGUUCAAUGAGAAAGCAGUACUUAAGAACAUUUUGAGUCUACUUUUUGAUUGAGCCGCGCCAAUAU	75	spe-miR171a-4-5p	UAUUGGUGCGGUUCAAUGAGA	1-21	nta-miR171a	0	0	21	21	1
			spe-miR171a-4-3p	UGAUUGAGCCGCGCCAAUAU	56-75	cas-miR171a-3p	0	0	20	22	1
spe-MIR171a-5	GUCCAUGUUUGACUUCACAAUUAUGAGGAGUUGGUGUGAUGUUGGAAUGGCUCAAUCUAAUAAAAGUUUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAUAUCGUCUUUGUACAAGAGUCUUGAUGUAUG	147	spe-miR171a-5-3p	UGAUUGAGCCGUGCCAAUAUC	95-115	aof-miR171a	0	0	21	21	1
spe-MIR319c	CAAGAGAGCUUCCUUCAGCCCACUCACGGAGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCCUUGCUUGGACUGAAGGGAGCUCCUUU	178	spe-miR319c-5p	AGAGCUUCCUUCAGCCCACUC	5-25	sly-miR319c-5p	0	0	21	21	1
			spe-miR319c-3p	UUGGACUGAAGGGAGCUCCUU	157-177	sly-miR319c-3p	0	0	21	21	1
spe-MIR164-2	AUCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUACAGCAAAUAGUGUUUGUACUUACAUGUAUGUAGUAAAGUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUGA	171	spe-miR164-2-5p	UGGAGAAGCAGGGCACGUGCA	8-28	aof-miR164	0	0	21	21	1
spe-MIR164e	UGUUGGAGAAGCAGGGCACGUGCAAAUUUUUGUAUUCGACGAUAUAUGCAUUACUAAUGGUAAUGCAUCAAUUUUGCACGUGUUCUCCUUCUCCAAC	97	spe-miR164e-5p	UGGAGAAGCAGGGCACGUGCAA	4-25	bra-miR164e-5p	0	0	22	22	1
			spe-miR164e-3p	CACGUGUUCUCCUUCUCCAAC	77-97	bra-miR164e-3p	3	0	21	21	1
spe-MIR9469	CCAAAGCUAACUCAUGAGGAGAGGUUUGUCCAAGUCCAUAUAAGGAGACCAAAUUCCUUAAGAUGUCCCACAGCGGUAGAGGUAUGGGAAUUCGGUCUUCUUAUAUGGACUUGACAAACCUAUCCUCAUGAGCUAGCUUUG	141	spe-miR9469-5p	CCAUAUAAGGAGACCAAAUUC	36-56	sly-miR9469-5p	3	0	21	21	1
			spe-miR9469-3p	AUUCGGUCUUCUUAUAUGGAC	90-110	sly-miR9469-3p	1	0	21	21	1
spe-MIR394-3	ACGAUCUUGAUUUUCAUGAAGAUUUCUCAAAGGGUUCCUUACACAGUUCUUUGGCAUUCUGUCCACCUCCUUUGUCUUCAUAUUCCUCUAUUUUUUUAGAAAAAUAAUUUUUAUUAAAUUUUUUGUAAAAAAAAAUGGAGGUGGGCAUACUGUCAACAGAUUUGUGUUGGUUUCUCUUUGUGAAAUCUUCUUGAUGUUAAUUG	203	spe-miR394-3-5p	UUUGGCAUUCUGUCCACCUCC	50-70	cas-miR394	0	0	21	21	1
			spe-miR394-3-3p	AGGUGGGCAUACUGUCAACA	139-158	sly-miR394-3p	0	0	20	20	1
spe-MIR166c	UGUGUGUGGUGCGUUUGAGGGGGAUGUUGUCUGGCUCGACACAAUUACUCUCUUGUAUGUAUUUAGUUAUUCGUUAUCAAGAUUGAUGUUGAUAACGAAUAAAUUAAACACAUAUAUACAAGAUGUAAAAAGGGAGUAAAGGCGUCGGACCAGGCUUCAUUCCUCUCAAAUAAUAUUCUACUUCUAC	187	spe-miR166c-5p	GGGAUGUUGUCUGGCUCGACA	21-41	sly-miR166c-5p	0	0	21	21	1
			spe-miR166c-3p	UCGGACCAGGCUUCAUUCCUC	145-165	sly-miR166c-3p	0	0	21	21	1
spe-MIR482c-5	GAAAGGGGAUGAGUGUUUCGAGGAGGUGUUGGAGUGGGUGGUAUGGUAAGAUUUCAUAUUUAUUUUUCAUAAAAAUUGAAAUCUUGCCAAUACCGCC	145	spe-miR482c-5-3p	UCUUGCCAAUACCGCCCAUUCC	82-103	sly-miR482c	0	0	22	22	1

spe-MIR9476-1	CAUUCCUAUGGCUUCUGAUCAUUUCUCUCUUUCCUUUUUCUUCCGUUGCCUGUCCAAAACUGCUAUUGGUCUAGUCCUGCAUCUCUUUUUAUAUUUUUUUCGUUAUCAAAAAAUAUAAAAAAAAAAUGCAGGACUAGACCAAUAGCAGGAUGGAUUG	108	spe-miR9476-1-5p	UCUAGUCCUGCAUCUCUUUUU	22-42	sly-miR9476-5p	1	0	21	21	1
			spe-miR9476-1-3p	AAAAAAAUGCAGGACUAGACC	71-91	sly-miR9476-3p	1	0	21	21	1
spe-MIR9476-2	AGCCAAUCCAUCCUGCUAUUGGUCUAGUCCUGCAUUUUUUUUUUAUAUUUUUUGAUAACGAAAAAAAUAUAAAAAGAGAUGCAGGACUAGACCAAUAGCAGUUUUGGACAG	110	spe-miR9476-2-5p	UCUAGUCCUGCAUUUUUUUUU	23-43	sly-miR9476-5p	1	0	21	21	1
			spe-miR9476-2-3p	AAAGAGAUGCAGGACUAGACC	72-92	sly-miR9476-3p	1	0	21	21	1
spe-MIR1044-1	AUAUGCCAACGUACUUAUAUAAAAGGCUCAUCUAUGCUAUCCGUUAAGAGUUUUCCUCAUCGGUGUCAUUUCAGUUAGGAAAUGCUGACAUGGAUAAGUCUUUUCUCAAACAAAAAUUGCAACAGAUGAGUCAAACUUUUAACGGAUUGCAUAAGUCUUUUUCUCAAAGUUCUAUUGCAUAUUUGAACUUUUUCCCUUGUUUUA	204	spe-miR1044-1-3p	UUCUAUUGCAUAUUUGAACU	170-189	ppt-miR1044-3p	5	0	20	20	1
spe-MIR169e-2	UAGGAGGAGAGGCCUUACAUGAAUUAGAAGAGUUUCUAUUUGUUUAGUAGCCAAGGAUGACUUGCCUUUCAUCAAUGGAAAAUGAUUACAACACUUUUCAUGGUAUUGGGAAAAUGAGUGGCAAGCAUCUUUGGCGACUUGACAAACUCUUCUUUGUCAUGUUAGUCCAUCUUCUUCCU	179	spe-miR169e-2-5p	UAGCCAAGGAUGACUUGCCUUU	48-69	sly-miR169e-5p	0	0	22	22	1
			spe-miR169e-2-3p	UGGCAAGCAUCUUUGGCGACU	119-139	sly-miR169e-3p	0	0	21	21	1
spe-MIR477	AGCUAGGCAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAUCAAGAAAUUCCUUGC	114	spe-miR477-5p	UGUCUCUCCCUCAAGGGCUCC	18-38	sly-miR477-5p	0	0	21	21	1
			spe-miR477-3p	AGUUCUUGUAGGGUGAGACAUC	79-100	sly-miR477-3p	1	0	22	22	1
spe-MIR172-3	UAUUUGCUAGUGCAGCACCAUUAAGAUUCACAUAGAAAAUAUGAAACUAAAUUUGCCCAAUUUUUCAAUACAUGAGAAUCUUGAUGAUGCUGCAUCGGCAAAUGG	105	spe-miR172-3-3p	UGAGAAUCUUGAUGAUGCUGCAU	73-95	aau-miR172	0	0	23	23	1
spe-MIR396b-1	UUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUAUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAG	107	spe-miR396b-1-5p	UUCCACAGCUUUCUUGAACUG	12-32	aof-miR396b	0	0	21	21	1
			spe-miR396b-1-3p	GUUCAAUAAAGCUGUGGGAAG	81-101	csi-miR396b-3p	0	0	21	21	1
spe-MIR166-2	AGGGGAAUGUUGUUUGGUUCGAAAUCAUUCAAACAAAUUAAAAUCCAUGCAUCUCGAUGAUCGAUGAAUUGAAUAAUUUCGGACCAGGCUUCAUUCCCC	99	spe-miR166-2-3p	AUUUCGGACCAGGCUUCAUUCCCC	76-99	lja-miR166-3p	0	0	24	24	1
spe-MIR396b-2	GUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUAUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUA	99	spe-miR396b-2-5p	UUCCACAGCUUUCUUGAACUG	7-27	aof-miR396b	0	0	21	21	1
			spe-miR396b-2-3p	GUUCAAUAAAGCUGUGGGAAG	76-96	csi-miR396b-3p	0	0	21	21	1
spe-MIR10529	AAACAUAACGAGUGAGGCUUGCUCAGUUGGUAAAACACCUCCACGAUCUAACGAAUUAUCUUGGUCGAGGGUUCAAGUAUUGCGGUAAGCAAUGUGGGCGUCCAGCUUAGCAAGCCUCAUCCGUUUUGCUUC	132	spe-miR10529-5p	AACGAGUGAGGCUUGCUCAGUUGG	7-30	sly-miR10529	1	0	24	24	1
spe-MIR398a	CAAUAGGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUUGUUUGUAGCAAUUUAUCGUUUAUAAAUGUGACACAUAUGUUCUCAGGUCGCCCCUGUAGA	100	spe-miR398a-5p	GGGUUGAUUUGAGAACAUAUG	6-26	stu-miR398a-5p	0	0	21	21	1
			spe-miR398a-3p	UAUGUUCUCAGGUCGCCCCUG	76-96	sly-miR398a	0	0	21	21	1

spe-MIR10532-1	AUUUCUUUAUAAAUGCGAGGGGAAAAUGUGGUGCUACAUAUUACAUUACAUUAAUUGAUGAUGUUAUAAGUAAUUUUCUACCCCUUUUCAUCCUUCGUCACACUAGCUUGAAAAUAAAAAAGUCAACUAGCGUUGGACCCACAAGAUAGUGCUACGUAGGCCGAAAAGGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAUGGAGGUAAUAUACCUUAGUUUAGUAUAAGUGUGUCUCUGAGAUUUCAAGCAUAG	253	spe-miR10532-1-3p	AAGUGUGUCUCUGAGAUUUCAAGC	226-249	sly-miR10532	2	0	24	24	1
spe-MIR10531	GAUAUUUGGGGUCCUAGUAGAGUCGGUUCUACAUUGGGUGUUAAGUGUUUUGAGUAAUCAUCAUUGAAAGUAACAUACUUAAAACCAAAUGUUGAACUGACUCUACUCGGAUCCCAAAUAUCG	123	spe-miR10531-5p	UGGGGUCCUAGUAGAGUCGGUUC	7-29	sly-miR10531	0	0	23	23	1
spe-MIR10533-1	CAAAGAUCUUAUGAAUUCUAGGUCUUCUUUCACCAACCCAAUUUCUUCUUUUAUAAAAACAAUUGAAUAAGCUUGAAAUUUAACAAAUUAUUGUAGUUUUUGAUUAGAAGAUUUAUGAAUAGUAAGUAGUCCCGCUUCUCAAUGAGUGAUAGAUCACUCUCUAUGAAUCCUCGACUCAAAAACUUUAAAAAAUUGCUUAAUUUCGAAGCUCAGUCGAUUGCUUCAAAAAAGGAAGAAAUUAGGCCGGUGAAAGACAACUUAGAGUUCAUAAGAUCUAUA	279	spe-miR10533-1-5p	UCUUAUGAAUUCUAGGUCUUCU	7-28	sly-miR10533	0	0	22	22	1
spe-MIR10532-2	CGAGAAAAUGCAUAAAUACCCCAUUAAUUUAUGCCUGAUAUACUAAGGUCAUAUUACCCCUAAACUUAUUUUAUAAAUAAUUUUCUACUCAUUUUCAGCCUACGUGGCACUAUCUUGAAAAAAAUGUCAACACGAGCUUGGCCCACAAGAUAGUGUCACAUACACCGAAAAAGGGUAAAAAAUUAUUUAUAAAAUAAGUUCAGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUUUCUGAGAUUUCGAGCAUGU	256	spe-miR10532-2-3p	AAGUGUGUUUCUGAGAUUUCGAGC	229-252	sly-miR10532	2	0	24	24	1
spe-MIR10532-3	UAUGUCCGAAAUUCCAGAGACGCACUUAUACUAUACUAAGGUCCUAUUACCCUCCUGAACUUAUUUUAUAAGUAAUGUUCUACUCUUUUUCGGCCUACGUGACACUAGGUUAAAAAAAUCAAUCAGCAUUGACCCCACAAAAUAAUAUUAUGUAGGCCAAAAAGAGAUAGAAAAGGACAUUAGUAUAAUAUAAGUGUGUCUCUGAGAUUUCGGGCAUAGAUUGAGGGGGUACUUGGAUAUUAUCCCUU	248	spe-miR10532-3-3p	AAGUGUGUCUCUGAGAUUUCGGGC	192-215	sly-miR10532	0	0	24	24	1
spe-MIR10532-4	UAAAGGGAAAAUACACAAGUACCCCCUCAACCUAUGUCCGAAAUUCCAGAGACGCACUUAUACUAUACUAAGGUCCUAUUACCCUCCUGAACUUAUUUUAUAAGUAAUGUUCUACUCUUUUUCGGCCUACGUGACACUAGGUUAAAAAAAUCAAUCAGCAUUGACCCCACAAAAUAAUAUUAUGUAGGCCAAAAAGAGAUAGAAAAGGACAUUAGUAUAAUAUAAGUGUGUCUCUGAGAUUUCGGGCAUAG	251	spe-miR10532-4-3p	AAGUGUGUCUCUGAGAUUUCGGGC	224-247	sly-miR10532	0	0	24	24	1
spe-MIR10535a-1	AAGGGUUGGCAUAAGUUUGUGAAAGCCGAAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUCGCUCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAAACCCUU	119	spe-miR10535a-1-5p	UUGGCAUAAGUUUGUGAAAGCCGA	6-29	sly-miR10535a	1	0	24	24	1
spe-MIR10535a-2	AAGGGUUGGCAUAAGUUUGUGAAAGACGGAGGUUUAAGACCAAACGAUACAAUUAUUUUCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUUACGAAUCUAUGUCAAUCCUUU	119	spe-miR10535a-2-5p	UUGGCAUAAGUUUGUGAAAGACGG	6-29	sly-miR10535a	1	0	24	24	1
spe-MIR10537	GUUCUACAACGUACGUAGGGUAAGCGGAUGGCUGAAAUUCGUUAGCCUAACCGUGGCCCUGGAAAUGCUUCUCUGCAGGACAAGCUUCAUUUCCAUUACCGGAUAUCAACAGAAAGGUUGAAAAGGACAACAAUUUAGAGGAUUUGGUGGAGUGUGGAAAGAUUUGAAUGCAAACUUAUCGAAGAUUGAUCAUCAUGGAUUUAAGCCACCCACUUACCCCACGUGCGUUGUCAAACG	237	spe-miR10537-3p	ACUUACCCCACGUGCGUUGUC	212-232	sly-miR10537	3	0	21	21	1
spe-MIR5026-1	UUUUUACUUUUUUUUCAGCCUACGUGCCACUAAUUUGAAAAAAAAUCAAUCAACAUUAGACUCACAAGAUAGUGCUACGUAGGUCGAAAAAGGAUAAAAAAU	102	spe-miR5026-1-3p	ACUCACAAGAUAGUGCUACGU	60-80	ath-miR5026	4	0	21	21	1

spe-MIR10532-5	AGGUUCUAUUAUCCUCUUGAACUUAUUUUAUAAGUAAUUUUCUACCCUUUUUUGGCGUAUGUGAUACUAAUUUGAAAAAAAAAAGUUAACUAGCGUUGAGCCACAAUAUAGUGCCACGUAGGCCGAAAGGAGUAGAAAAUUAUUAAUAAAUAAGUUCAGGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAGGAGGAUAAUAGGACCUUAGUAUAAUAUAAGUGUGUCUCUGAGAUUUCAAGCAUAUG	246	spe-miR10532-5-3p	AAGUGUGUCUCUGAGAUUUCAAGC	218-241	sly-miR10532	2	0	24	24	1
spe-MIR159b-1	AAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAGCUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUGUUCUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGUUGUAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUU	180	spe-miR159b-1-5p	AGCUGCUGAUCUAUGGAUCCC	49-69	cas-miR159b-5p	2	0	21	21	1
			spe-miR159b-1-3p	UUGGAAAGAAGGGAGCUCUAC	156-176	sly-miR159b	0	0	21	21	1
spe-MIR171f-1	CCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAG	79	spe-miR171f-1-5p	UAUUGGCCUGGUUCACUCAGA	6-26	csi-miR171f-5p	0	0	21	21	1
			spe-miR171f-1-3p	UGAUUGAGCCGUGUCAAUAUC	55-75	csi-miR171f-3p	1	0	21	21	1
spe-MIR159b-2	AGUUAAUGUUAACUUAUUCGAGAAAGAUUAGAGUUUUGAAUGUAGAGCUCUUCUGAAUUUCAAAGAGGGUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACAUUUGAUAACCUAAUUU	231	spe-miR159b-2-5p	AGCUGCUAAUCUAUGGAUCCC	87-107	cas-miR159b-5p	1	0	21	21	1
			spe-miR159b-2-3p	UUGGAAUGAAGGGAGCUCUAC	194-214	sly-miR159b	1	0	21	21	1
spe-MIR399i-1	UGGUUAUACUAAAUAUAUUAUUGGUAGUGUGCUUAUUAAGUGAAGCAGUUGUAGGGCAGUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUACGAUUGCGUCUGCUUAAU	135	spe-miR399i-1-3p	UGCCAAAGGAGAGUUGCCCUA	97-117	stu-miR399i-3p	0	0	21	21	1
spe-MIR169r-4	GCUUCUCACAAGUUGUGUUUUGUUAGAUGAAGUAGGAAACUGCUAAUUCUAUUUGCAAUAGGGAAUGUUGGAUUUUCUUCUUCGGGAAACUACACUUCCCUAUAAAUCAAUAGACUGCUGGUUAUAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAAUAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAA	285	spe-miR169r-4-3p	CAGCCAAGGAUGACUUGCCGG	178-198	csi-miR169r-5p	0	0	21	21	1
spe-MIR319b-3	GAGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCC	124	spe-miR319b-3-5p	UAGCUGCCGACUCAUUCAUCCA	21-42	ppe-miR319b	1	0	22	22	1
spe-MIR160h-2	UAUAUGCCUGGCUCCCUGUAUGCCAUUUGCAAAGCUCACCGUAAUAUAUCGAUGGGCCUUGUUGAAUGGCGUAUGAGGAGCCAAGCAUAU	90	spe-miR160h-2-5p	UGCCUGGCUCCCUGUAUGCCAUU	5-27	mes-miR160h	0	0	23	23	1
spe-MIR171b-1	AUUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUACGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAU	115	spe-miR171b-1-3p	UUGAGCCGCGCCAAUAUCACU	89-109	aof-miR171b	0	0	21	21	1
spe-MIR390-1	UAUGCAUGGAGAAUCUGUAAAGCUCAGGAGGGAUAGCGCCAUGGAUGACUCAAUUCGAUUUUUUUACACAUCUCUAGCGCUAUCCAUCCUGAGUUUUACAGCUUUUUCAUGCU	113	spe-miR390-1-5p	AAGCUCAGGAGGGAUAGCGCC	20-40	aof-miR390	0	0	21	21	1
			spe-miR390-1-3p	CGCUAUCCAUCCUGAGUUUUA	78-98	stu-miR390-3p	1	0	21	21	1
spe-MIR396b-3	AAAAAAUAAAAUAAAAUGGUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUAUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAU	138	spe-miR396b-3-5p	UUCCACAGCUUUCUUGAACUG	34-54	aof-miR396b	0	0	21	21	1

	AGGGUCA										
			spe-miR396b-3-3p	GUUCAAUAAAGCUGUGGGAAG	103-123	csi-miR396b-3p	0	0	21	21	1
spe-MIR171b-2	AAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUACGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAUUUUCAUUC	110	spe-miR171b-2-3p	UUGAGCCGCGCCAAUAUCACU	76-96	aof-miR171b	0	0	21	21	1
spe-MIR156f-2	UCUGUUGACAGAAGAGAGAAAGCACAAUCUGUCAUCAACAAAAUGGUAUUUGUUGUUUGUUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUAG	92	spe-miR156f-2-5p	UUGACAGAAGAGAGAAAGCACA	5-26	gma-miR156f	1	0	22	22	1
spe-MIR156b-7	AGGGCGGUGACAGAAGAGAGUGAGCACAUAUGGUCUUUUCAAGCAUGAUGUUUACAUGCUUGAAGCUAUGCGUGCUCACUUCUCUAUCUGUCACCCCCAUC	101	spe-miR156b-7-5p	UGACAGAAGAGAGUGAGCACA	8-28	hvu-miR156b	0	0	21	21	1
			spe-miR156b-7-3p	GCUCACUUCUCUAUCUGUCACC	74-95	bdi-miR156b-3p	1	0	22	22	1
spe-MIR156d	UAUAAUUGAAAUUGAUAGGAAGAAAGAGUGAUUAUUGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCAC	140	spe-miR156d-5p	UUGACAGAAGAUAGAGAGCAC	38-58	stu-miR156d-5p	0	0	21	21	1
			spe-miR156d-3p	GCUCUCUAUGCUUCUGUCAUCA	118-139	stu-miR156d-3p	0	0	22	22	1
spe-MIR162-1	ACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGGAAGCUGAAUAUAUAUAUAUAUGCAAAAAUACAGCAAAAGGAAUCGGUCGAUAAACCUCUGCAUCCAGUG	105	spe-miR162-1-5p	UGGAGGCAGCGGUUCAUCGAUC	5-26	csi-miR162-5p	0	0	22	22	1
			spe-miR162-1-3p	UCGAUAAACCUCUGCAUCCAG	83-103	fve-miR162-3p	0	0	21	21	1
spe-MIR166f-1	AUGAAGAAAAACAAGAAAAGUGAUGCUAGAAGAGAAGGAAGAAUAAACAUUUUUUGUUUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCGAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAA	158	spe-miR166f-1-3p	UCGGACCAGGCUUCAUUCCCCU	134-155	cas-miR166f-3p	0	0	22	22	1
spe-MIR171a-6	UCAUACGAGAUGUUGGUGCGGUUCAAUGAGAAAGCAGUUGUUGAAUAAGUUUUUGACCCUACUUUUUGAUUGAGCCGUGCCAAUAUCACGUGUC	94	spe-miR171a-6-5p	UGUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	1	0	21	21	1
			spe-miR171a-6-3p	UGAUUGAGCCGUGCCAAUAUC	67-87	aof-miR171a	0	0	21	21	1
spe-MIR162b-1	AAGAAAAAAAAAAAUCCUAAGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCAUAUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUC	137	spe-miR162b-1-5p	UGGAUGCAGAGGUUUAUCGACC	32-53	ath-miR162b-5p	4	0	22	22	1
			spe-miR162b-1-3p	AUCGAUGAACCGCUGCCUCC	109-128	cas-miR162b	0	0	20	20	1
spe-MIR167b-2	CUACUAUCAGUUGAAGCUGCCAGCAUGAUCUAAACUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGAUCAUGUGGUUGCUUCACCUGUUAGUU	94	spe-miR167b-2-5p	UGAAGCUGCCAGCAUGAUCUAA	12-33	bna-miR167b	0	0	22	22	1
			spe-miR167b-2-3p	GAUCAUGUGGUUGCUUCACC	67-86	stu-miR167b-3p	3	0	20	20	1
spe-MIR169j-1	UGCCUAAUUUGAUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGUUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUGUUUGAUGGCCAGGCAGUCUCCUUGGCUACUCUAAUAGGUUCCUCUCAUUCAUGCUAGACU	156	spe-miR169j-1-5p	UAGCCAAGGAUGACUUGCCUGC	13-34	ppe-miR169j	0	0	22	22	1
spe-MIR169j-2	CUAAUUUGAUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGUUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUGUUUGAUGGCCAGGCAGUCUCCUUGGCUACUCUAAUAGGUUCCUCUCAUUCAUGCUAGACUC	154	spe-miR169j-2-5p	UAGCCAAGGAUGACUUGCCUGC	10-31	ppe-miR169j	0	0	22	22	1
spe-MIR169r-5	AAAGUCUUGCAUGAGGGAAUAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCC	184	spe-miR169r-5-5p	CAGCCAAGGAUGACUUGCCGG	36-56	csi-miR169r-5p	0	0	21	21	1

spe-MIR169j-3	AGAUUUUUUAUGAAAUAGCUGUUGUUGUAGGUGUCAAAUCAGGAAUCGUGGACAAC GAAGAGAAGUCUUACAUGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAUAGUUUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUCCUCUUUCAUGCAAGAACGUCUUGCAUGAUGAAAAGAGUCUUAUUUGGUA	156	spe-miR169j-3-5p	UAGCCAAGGAUGACUUGCCUGC	42-63	ppe-miR169j	0	0	22	22	1
spe-MIR169d-1	GCCAAGAAUGACUUGCCUGCACCAUUUCCGAAAUGUGUCCUUUCGUUCAUGGGGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUCUUUCAUGCAAGACUUUCUCUUCUUCCAAU	155	spe-miR169d-1-5p	UAGCCAAGAAUGACUUGCCUG	31-51	bdi-miR169d	1	0	21	21	1
			spe-miR169d-1-3p	GCAGGUCAUCUUUAGCUAACU	91-111	stu-miR169d-3p	0	0	21	21	1
spe-MIR169a-2	GCCUUGCAUGUUGGUUCAGGAAGAAAGAGUUGCAGCCAAGGAUGACUUGCCGACUUUUGUAUUACUCUUCAUAUAUAUAUAUAUAUAUGUAUAUAUGGAAAUUACAUUAAACUUGGAAGAGAAAGUUGGCAAGUGGUCCUUGGCUACAUCUUUCUUUCUGCCCCUCAUGCCAGGUC	176	spe-miR169a-2-5p	CAGCCAAGGAUGACUUGCCGA	33-53	cas-miR169a	0	0	21	21	1
			spe-miR169a-2-3p	GGCAAGUGGUCCUUGGCUACA	128-148	aly-miR169a-3p	1	0	21	21	1
spe-MIR171a-7	GUAUAGUAAAAUGAUGUUGGAAUGGCUCAAUCAAAUCAAAUUCCUCAAAGUAUUGGGUCAUUUCAUUUGAUUGAGCCGUGCCAAUAUCAUCUUACUU	97	spe-miR171a-7-3p	UGAUUGAGCCGUGCCAAUAUC	68-88	aof-miR171a	0	0	21	21	1
spe-MIR156c-1	AAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGCGUUUUCUGGCAUGAUGUUUAUAUGGUUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCUCCCACC	109	spe-miR156c-1-5p	UGACAGAAGAGAGUGAGCACA	11-31	rco-miR156c	0	0	21	21	1
			spe-miR156c-1-3p	GCUCACUGCUCUAUCUGUCACC	81-102	ata-miR156c-3p	0	0	22	22	1
spe-MIR156b-8	AAAAGAUGAGGUUAUGAAAUAUGUUGUUGACAGAAGAUAGAGAGCACAGAUGAUUAAGUGCAUGAAAAUUGUAUGCACAUUACUCCUUUGUGCUCUUUAUUCUUCUGUCACCAUCUUCAUAUCCUAGAUUUUUUCUU	137	spe-miR156b-8-5p	UUGACAGAAGAUAGAGAGCAC	27-47	aof-miR156b	0	0	21	21	1
spe-MIR437	GUUAUGUUAUGAACUUCGAGUCAAGAGCCGUAAUGGUAUUAUUCAUGUAUUGAAUGAUGAACUUAGGGUUGAUUGACUGGAAUGACAUCAUAUCAUUCU	99	spe-miR437-3p	GAACUUAGGGUUGAUUGACUG	59-79	bdi-miR437	5	0	21	21	1
spe-MIR8014	ACGAUUUCACCCCUUCUCUCUCAUUUCAUGGCUAAGGUUUCACAGUUUUCUUCGUCGAUGGGUUUCAAAGUGGAUAUUCAUGAUUGUAGGUUAGUAAACUUUUUUCUUAUUUUAUUGUGUUUACAAUCACGAAAAUCCACUUUGAAAUUCAGCUCCGAAGAAAGUUAUGAAAUCUUAGCCGCGAAAUGACGGGAAAGUUGUGAAAUUCU	209	spe-miR8014-3p	CUUUUUUCUUAUUUUAUUGUGUUU	99-122	stu-miR8014-5p	5	0	24	24	2
spe-MIR171c-1	UCUAAUCCAAGAUAGUGGUGCACUUCACUACCAUGACUUAGAAACUACUUAAUGUGGUUGAUAUGAACUCAUUAUUCUUGGAAUUUAA	88	spe-miR171c-1-5p	AGAUAGUGGUGCACUUCACUA	10-30	cas-miR171c-5p	5	0	21	21	1
spe-MIR8011a-3	UGAUGAACUUUGUUUUGUGUCUCACACAACUGAUGUAAGUUGUGUGAGGUCUCUUUUUGUUUUAAAAGUCAGUGCGACCCAAAUCGUUGGACUCACCAACUCGUGAAAUAAAAAGAAGUCUCACGCAACUUGCGUUAAUUCUGUGAGCCGCAAAGUAAAUUUUCAAAU	168	spe-miR8011a-3-5p	UUGUGUGAGGUCUCUUUUUGUUUU	40-63	stu-miR8011a-5p	2	0	24	24	1
			spe-miR8011a-3-3p	AAUAAAAAGAAGUCUCACGCAACU	107-130	stu-miR8011a-3p	2	0	24	24	1
spe-MIR5161	ACCCUAAAAACUACACUAUUUCUGGUUCAAUUUGUUUGCCCUACUUUACUUUUAAAGUAAAGUAAAGUGAGACAAACAAAUUGAAUCAGAGAGAGUAUAGUUUUUAGUCC	110	spe-miR5161-3p	AUUGAAUCAGAGAGAGUAUA	80-99	osa-miR5161	4	0	20	20	3
spe-MIR6164b-1	AUUUCUGGUUCAAUUUGUUUGCCCUACUUUACUUUUAAAGUAAAGUAAAGUGAGACAAACAAAUUGAAUCAGAGAGAGUAUAGUUUUUAGUCCGGUU	274	spe-miR6164b-1-3p	UCAAACAAAUUGAAACAGAGU	253-273	nta-miR6164b	4	0	21	21	1

spe-MIR397b-2	CAAAAAAGGUAUCUCCUUACUUUUUGACAACUA UUAUGUUCCAACUUUCCACGUGACAUGUUUAAA ACCAUACAAUUAAAGGGUAUUUUUGGCAUUUGA UGUAUCUCUAUCUGAUGACCAUAAGUUUCUGAA ACUCUAUCUCAAGUUAAAAUAGGUCAAACAAAU UGAAACAGAGUG UCCUUCAGAGAAUUAAAAACAUGAUCGAGUGUA GCGUUGAUGAAAAAUGAGGAAGGCCCAAAUGC AGGAAUUCUCAAAUAUGUCAUCAACGCUGCACU CAAUGAUGUUUCUAAGUACUCAGCAAUAA	127	spe-miR397b-2-5p	AUCGAGUGUAGCGUUGAUGAA	24-44	bdi-miR397b-5p	2	0	21	21	1
			spe-miR397b-2-3p	UCAACGCUGCACUCAAUGAUG	86-106	eun-miR397b-3p	0	0	21	21	1
spe-MIR479	AUGAUGGAGAAGCAGACAUGGCGUGAUAUUGG UUCGGCUCACUAAUUUCUGAUUCGUGAAACAG AUAAGAGAUGAGCCGAACCAAUAUCACUCUUGU AUUCUUCUUCAUACC	112	spe-miR479-5p	CGUGAUAUUGGUUCGGCUCACU	22-43	ghr-miR479	2	0	22	22	1
			spe-miR479-3p	UGAGCCGAACCAAUAUCACUC	73-93	aof-miR479	0	0	21	21	1
spe-MIR403	UCAGGAAGAGGCAUAUUUCGCGUUUGUGCGUG AAUCUAACGACUCUUUUCAUCAGAAAAACUGUU GUUGUUUGCUAGAUUCACGCACAAACUCGUAA UAUGGCUUUUCCAAU	112	spe-miR403-5p	CGUUUGUGCGUGAAUCUAACG	21-41	sly-miR403-5p	1	0	21	21	1
			spe-miR403-3p	CUAGAUUCACGCACAAACUCGU	74-95	cas-miR403	1	0	22	22	2
spe-MIR11085-1	ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAA UCCCCUACCAUAUUGCCAAAUAUUUGCCUUUUU CUUUGUGUUCAUCUAGCUAAAGGCAAAUGUUU GGCAAUAUGGUAGGGGAUUCUGGUCUUCUGUA CACAGGGAAAAGUUGACUUCU	151	spe-miR11085-1-5p	AGUGAACUUCAUCUUUGUAA	4-23	lja-miR11085-3p	5	0	20	20	1
spe-MIR6020a	AAAUGGAGUUUAAUGGCGAAAAUACUCGUAAAA CAUUUACGGAUUAUAUCAGAGCAAUAUGCAUAU AUUGUAGAUCUGUAAAUGUUUUCCGAGUAUCU UUUGCCCAUAACCUUCAAAA	118	spe-miR6020a-3p	AAAUGUUUUCCGAGUAUCUUU	80-100	nta-miR6020a-5p	2	0	21	21	1
spe-MIR6140b-1	AUACCACUCUCUCUCUCUCUCUCUCUGAUCUC UCACUUUCUACAAACAUAAAUUAUACAUUGUUU UUUGUAUAAUUUGUGUUUGUAUAAAGCGAGAAA GAGAGAAAGGAAAAAGAGAAGUGGGCAAGGAAA UAUUUGUAAUGUAUAAUUAUAAGUUUAUAGAAC UAAGAUAUAUGUAUUUGCAUGUAUAUAUAAAAU GUUCUCUCAUUUUAUAUAAACAGAAACGCAAUU UAUACAUUUCUGAUUGUAUAAAGCGAGAGAAGC GAGCAAGACAGGGAGAGUGGCGA	286	spe-miR6140b-1-5p	AUUGUUUUUUGUAUAAUUUGUGUU	59-82	pgi-miR6140b	5	0	24	24	1
spe-MIR7774	GAAUCACUCCUCCAAUUUUUUAUGGUGAGAAUU AUCAACUAUGGUCUGUGAGAAUGGAAACUUACU UGGAGGGUCUUGAUCAAUGGGAAUAUGUGGAA GAGGAUUAUGAAAUCAAUCCGCUGUCAAAUAUU CCCAUUGUGGCUCAUCAAGAGUCAGUAGGAAA AGAAAAUUAUUUAGUCGAAGUCAAAAGCAAUUA UGUUUGUUGCUGUUUCGACAACCGUUUUCACG AAGAUCAUAAUUCUCACAUUCACCAAAAGAUAU UUAAAAUUUUCUGAAGAAAGAUAUGCUGGAGAU GAAAG	299	spe-miR7774-5p	ACUAUGGUCUGUGAGAAUGGAAAC	38-61	bdi-miR7774-5p	2	0	24	24	1
spe-MIR7980b-1	AGAAUAUGAAAUCAUGAGACGGAAUCAGCGUAA AAUCGCAUGUCCAAACGCUGAUUCCAUCUCACG GUACCAUGAUAUG	79	spe-miR7980b-1-3p	GUCCAAACGCUGAUUCCAUCUCAC	42-65	stu-miR7980b-5p	2	0	24	24	1
spe-MIR160e	UAAAAUUGAACAAGUAGACGCAAGUGACUACAU UACACAUAAGACGUCAUGUAGGACACAAAAUUA CCAUGUAGGGUGUCAUGUAGGACGAAUGUGUA UAUUUGCUCAAUUUUA	114	spe-miR160e-3p	CCAUGUAGGGUGUCAUGUAGG	67-87	bdi-miR160e-3p	5	0	21	21	2
spe-MIR5014a-1	UGACAUAAUACAUAAACAUGAGCCUUAACUUAG CGUCAGUUGACAACUAUGACUUUUAACUUUAGA UGUGCGCACAAGUAAAACUUAAACUUAUAUAAA UUUGAACAAAUUAACGCAUUCAUCCUACAUGGC AGCCUACAUGAAAAUUUUGUGUCUAACGUGGC AUUCUAUGUAUAACAUGUCAUGUAGAACACGUG UGUCUGCUUGUUCACUUUUAUACAAUUUAAAGU	288	spe-miR5014a-1-3p	UUAUACAAUUUAAAGUGUAUA	215-235	ath-miR5014a-3p	5	0	21	21	1

spe-MIR169r-6	GUAUACUUAUGAUUACUGACGAAAGCCAAGUUA AGGGUCAUAUUUAUAUACUAUGCCU CUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAA UAAGGUUAUUGAAUUGCAGCCAAGGAUGACUU GCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUC UGGCAAGUCAUUUUUGGCUACAUAUCUGCCUC AUUUUCUCAUGCCAGAUUUUUUAUGAAAUAGCU UGAAUUAAAAUUAUGUUGCUUGGACUCUUCAAA	161	spe-miR169r-6-5p	CAGCCAAGGAUGACUUGCCGG	49-69	csi-miR169r-5p	0	0	21	21	1
spe-MIR7997c-1	AAUGCUGACGGCUGAGAAUUGGAUCCUUCGAA AAUAGUGCAGUUUUCGAGGAUUUGAUACGGGU GCAGCAGCAUUUUCGAAGAGUCAAAGCAACAUA GAAUUAAUGUA	141	spe-miR7997c-1-5p	AUGUUGCUUGGACUCUUCAAAAAU	13-36	stu-miR7997c	2	0	24	24	1
spe-MIR395a-1	UGGGUGUUAAGUCUAUCAAGGUGUUCCCUGGA GUUCCCUUGACCGCUUCAUUAGGGCUUACUUC AUUGUUUGAUGCCCCGCUGAAGUGUUUAGGGG AACUCUUGGACUCACUUUGAAAUUUUACACAAA	129	spe-miR395a-1-3p	UGAAGUGUUUAGGGGAACUCU	82-102	aof-miR395a	1	0	21	21	1
spe-MIR7992-1	UCAAAUUUUAACUUUGACCUCCAACUUUCAUAA UGCACAAACAGACACUUUAACUAUCCAACUUUU AAAUAAAUAAACACAUGAGUCCUACAUGGCACA AUACACGUAGGACACCACGUAGGACAAAAAAUG ACAUGUAGGACACGUGUGUCUAUUUGUUCAAC UUUAUACAAGUUUAAGUGUCUAUUUGUGCACAU CCAAAGUUGAAAGGAAUAAAUGUGAUUGAGCCA ACUUAAAGGGCACAUUUAUGUUUACGCCUAUAA AAAUUAUGAGAGUUAUGAAUAUUAUUAAAAGUA AAAAUUAAA	305	spe-miR7992-1-5p	UUUCAUAAUGCACAAACAGACACU	26-49	stu-miR7992-5p	5	0	24	24	1
spe-MIR11580	UGCUAAGUUAAAAACGUUCUUGAGUGAGAAGG UUUUCAACGUGUAAGACUAUCUUCUUGUUUUG UUCUUGAGUGUAGGUUUCGAUUUAUUGUACAA GGGGUGGGUUUGGCUCUUUGUAGGGUUGAGU UUCAGUGAGGAUUGUAACAAAAGGUGGGUUUG GCCUUUUGGAGAGAUCGAUUGUUGUCAAUCGA GAGAGGUAGAAGAGAUAAGGCUUUUUGAUUAU UGAGUUGUAAUCACAAAAUCUUAUAGUUGAAUU AAUAAAACGAGGUUUUUCCUUCCUUGAGUGAG GAAGGUUUUUAAUUUAAUA	307	spe-miR11580-3p	UUUUGAUUAUUGAGUUGUAAU	214-234	pab-miR11580	5	0	21	21	1
spe-MIR8726	AAAAUAAUCAAAAAGUAAAAUAGAGAGUUGAAU AGUAGUUCUCCAUAUAAAUGGAGUAUAGAGACU AAAGAGUGAUAUGGAGAGUGGUUGGAGAGGGC GUUCUCUAUUUUACUCUUGAAAUAUAGA	126	spe-miR8726-3p	AAAUGGAGUAUAGAGACUAAA	49-69	gra-miR8726	5	0	21	21	3
spe-MIR1044-2	GUUCAAAUAUGCCAACGUACUUAUAUAAAAGGC UCAUCUAUGCUAUCCGUUAAGAGUUUUCCUCA UCGGUGUCAUUUCAGUUAGGAAAUGCUGACAU GGAUAAGUCUUUUCUCAAACAAAAAUUGCAACA GAUGAGUCAAACUUUUAACGGAUUGCAUAAGUC UUUUUCUCAAAGUUCUAUUGCAUAUUUGAAC	194	spe-miR1044-2-3p	UUCUAUUGCAUAUUUGAAC	176-194	ppt-miR1044-3p	5	0	19	20	1
spe-MIR172a-1	CUGUCACCGAUAGUUAUUUAUUGCUGAUGCAG CAUCAUCAAGAUUCUCACUUUGAAAUAAAUAGA CAUGGUCAUGAUGUAUUAUAUUUUCCAUUUCAA AUUAAAGCUACAUAUUUAACCUUGCCUCUUAAU UUUCAUGUAUGAAUCUUGAUGAUGCUACAUCU GCAAACAACAACUGUGUUGAUUA	186	spe-miR172a-1-5p	GCAGCAUCAUCAAGAUUCUCA	29-49	ppe-miR172a-5p	3	0	21	21	1
			spe-miR172a-1-3p	UGAAUCUUGAUGAUGCUACAU	141-161	vvi-miR172a	0	0	21	21	1
spe-MIR11451	GAGUUAGGGGUCGUUUGGUAGAGUUUCUUAGA AAAAAUAAUGCAUGCAUUAGCCUUGUGUAUUAC UAGUACCUUGUUUGGUACUCUUUUCCAACCUA UGUAUAACACUCUAUAGUGUAUUACGAUGUAUA UUGCUAAUACCAUUGAUUUCUAGAUAUGAUUUU AAUGCAUGCAUUAGCAUGAUUAAAGACCAAUUG CCUCUUAAAACCUUUUUUUACAUCCUUUCCACC AUAAUAGUGGAGGUUAUCUUUGUAAAUUCAAUU UAUUAUGCAAUGCAUGCUAUUUUUUUAUGCAUC AAACCAAAUGAUGCAUAAAAA	316	spe-miR11451-5p	GUAUUACGAUGUAUAUUGCU	116-135	pab-miR11451	5	0	20	20	3
spe-MIR8021	AUUCAAGGCUCAAACUCGAGACCUCUGAUUAAG GAUGGAUAUUUCAUAUACAUCCCCUCGUAAUUA	226	spe-miR8021-5p	AUUCAAGGCUCAAACUCGAGACCU	1-24	stu-miR8021	0	0	24	24	1

spe-MIR8051-1	UUGUUGGUUCUUAACUUAUAAUAAUAACAUUAUUCACACUCACUUGCAUAUUAUGCAAUAUGUUGAAUUAAGUUAUUGAGUUCUACCAAUAAUAUUGUGUUGGAGAAGAAGUUAAUAUUACUUCAUCCUUAACCAGAAGUUUCAAGUUUGAGUCUUGGCAGUUGAUAUUUUUAUUUCUUAUUUUUGAGAUUCCGAUCUCUGGAGGUCGGUAUUUUUAUUUUUUAUUUUUUAGAUUCCGACCUAUGGAGGUCGGUAUAUUUAUUUCUUAUUUUUGAGAUUCUGUCCUCUGGAGGUUGGUAUUUCUGCUACAAAACUAACAGCAUUGAGCGGCAAUUUUAGUAUCCCACCUGCUUAUUUAUAUUAAAACAACCCAAAGAAUUCCAAAUAAGCUAUUUCAAAAUAAUCUUC	248	spe-miR8051-1-3p	UAUUUCUGCUACAAAACUAAC	138-158	stu-miR8051-3p	5	0	21	21	1
spe-MIR865-1	UGGGAAGUUCGACAGAAUUGGUAUUUUUUUGGAAAUUGGAAGCAGUUACUAAUUCAUGAUCUGGCAUGUACAGAAUGAAAACUUCAUUCUCAAUUCUACGAGAUUUUUUAUGAAAUCCUUUUAUUUGCUUCUCUUCGAUGGAAGUUUGAUUUUCCAAGAAUGUAUCCAAAUUUUUGCGUAAUUCUUC	187	spe-miR865-1-3p	AUUUUCCAAGAAUGUAUCCAA	149-169	ath-miR865-3p	5	0	21	21	2
spe-MIR1088-1	UACGAAAGAGGUGAAGGUGAUGACAGAAGCAUAGAGAGCACAAAUGAAUUGAGAUGCUUUUGCUGCCCAAAUUGAAUGAAAUUAGCAUAUCAUCAUUAGUGCUCUCUAUCUUCUGUCAACAAUAAUCACUCUUUCUUC	138	spe-miR1088-1-3p	UAGUGCUCUCUAUCUUCUGUC	97-117	smo-miR1088-3p	4	0	21	21	3
spe-MIR9477-1	UAUCUGAACUAUCACUAAACGUUUAUCGACACACACACCUCAACUAUCAGUUGUUCUCUUUUCCUACCUGAAUGAUGGUGAUAUUCCAGGUUGGGAAGGGAACAACUGAUAGUUGAGGUAUGUUUCGAUAAACAUUUGGUGAUAGUUCAGNAA	154	spe-miR9477-1-5p	UAUCAGUUGUUCUCUUUUCCUACC	45-68	sly-miR9477-5p	2	0	24	24	1
			spe-miR9477-1-3p	UUGGGAAAGGGAACAACUGAUAGU	91-114	sly-miR9477-3p	0	0	24	24	1
spe-MIR1127	CGCAACAUGACAAAUAAAAGUGGACGGUAGGAGUAUUAAUUACUCCCUCCGUCCAUAAUUGUUUGUCAUGUUAAG	75	spe-miR1127-3p	AAUUACUCCCUCCGUCCAUAA	38-58	bdi-miR1127	4	0	21	21	1
spe-MIR391i	GCUCCUCUACAUUUUUCUUUUUCAUUUUCCAUUGUUGUUUACUAAUACCCCUAUGCAAUUGUCGAAUUUGAGAUGACAUUGUUGGCUAUUUUGAAUUGUGAUGCCUGUUAUAGUAACAUUGAAACUCCCAUAGCAGCGUGCUCGAUCUGCUGCUCGGAUGACUGCCGGUAAAAGGAAGCCAACAAAAGAAAAUGAAAAGAAAAAUGUAGAGGAGC	215	spe-miR391i-5p	GUCGAAUUUGAGAUGACAUUG	61-81	pab-miR391i	5	0	21	21	3
spe-MIR3513	GGGACUCUACUAGAUGCGUUCGAUUCGAGUUGAGACGCUACAAAUUGUGUUCAACUCAAAUAAGAAUUCUUGGAGGCUAUUCAACCCUAAACCCUAGUUUAUGCCUAUAUAAAGGGUAUUAAAUUCCCUUAAAAGGCAUCUCGGAAAUUCCAUAAAGAGAUCAAGAUCUCGGAUACUCCAUAAAUUGAUGGAUUAUUCAUGUAGAGAGGUCAAAUCUAAAUCAUCAUAGUUCGAGAAAUACGCCACUAACGGCCCUCGAAUCAUGGAUAAAUCCUAGUAGAGUAGA	286	spe-miR3513-5p	UUGAGACGCUACAAAUUGUGU	30-50	ahy-miR3513-3p	5	0	21	21	1
spe-MIR8019-1	AUUAUUAUACUCCCUCUGUUUCAUAAAGAAUGACCUGGUUUGAGUUGACACGGUGUUAAAGAGUAUAAAGAAGACUUUUUGAAUCAGGUUGUCCUAAAUUAAUGUUAGGUGAAAUGUACAAAAUUGUCCUUUGAUCUUGUGGGCUUAAACAUGCUGCAUGGAGAGUUUAAAUUAAAAUCUUACCAAAAAAAAAAGAAAGAGAUUAUUAUUUUUGAAACACACUAAAAAGAAAAGGAGGUCAUCCUUUUAGAAACGGAGGGAGUUCAUGAA	270	spe-miR8019-1-5p	UAAAGAAUGACCUGGUUUGAGUUG	24-47	stu-miR8019-3p	2	0	24	24	2
spe-MIR1436	GUACUCCCUCCAUCCCAUAUUAGUUGUCCGCUUCCGUAAUUUGGGACAACUAUUUAUAGUAAGGUGAACCACUAAUAUGGGACGGAGGGAGCAG	94	spe-miR1436-3p	CUAAUAUGGGACGGAGGGAGC	72-92	hvu-miR1436	4	0	21	21	3
spe-MIR399n	AGGGAAACAGUGGUAGGGCUACUCUCUGUUGGCAUGCAGUGAUAUAGUUAAGCUGAUAUGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGC	92	spe-miR399n-5p	GGGCUACUCUCUGUUGGCAUG	16-36	stu-miR399n-5p	1	0	21	21	1

			spe-miR399n-3p	UGCCAAAGGAGAGCUGCCCUG	59-79	gma-miR399n	0	0	21	21	1
spe-MIR399b-1	UUAUAAGAGAAACAGUGGUAGGGCUACUCUCUAUUGGCAUGCACUUAUACAUUUAAACUGACAUGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUG	103	spe-miR399b-1-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spe-miR399b-1-3p	UGCCAAAGGAGAGCUGCCCUG	64-84	stu-miR399b-3p	0	0	21	21	1
spe-MIR399a-1	AAAGUUCGUGAAUGAUGGUAAUUAUAAGGGAAACAGUGAUAGGGCUACGCUCUAUUGGCAUGCAGCUUUUUUGGUCGCUCCAAGUAGCAACUUGAUCUAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUGUUACUGUCUCUACUUAAUGUAAUGUAAUUACACGCACAUC	175	spe-miR399a-1-5p	GGGCUACGCUCUAUUGGCAUG	42-62	stu-miR399a-5p	1	0	21	21	1
			spe-miR399a-1-3p	UGCCAAAGGAGAGUUGCCCUG	115-135	aof-miR399a	0	0	21	21	1
spe-MIR11066	CCUUGGAAAUAGGUGGUCUUGAACUUUUGCUACAAGGAUAAACCUUCGACGCCAAAAGUCGAUACUUGAUGUUCUGUUCAUGGGGCAAGCAAGAUUAAAAGUUCAAGAUCAUCCACCUCCAAAG	124	spe-miR11066-5p	GAAAUAGGUGGUCUUGAAC	6-24	lja-miR11066-3p	5	0	19	19	2
spe-MIR171t	AAUCCGGUCUCUGCAACUAUGUUGAACUGCGUGACUAUCUCAUCUAAAAGGUUUAGAUGAGAUAGUCAGACACUUCAACAUUGUAUCAAGCCAGGCCC	98	spe-miR171t-5p	UUGAACUGCGUGACUAUCUCA	22-42	gma-miR171t	4	0	21	21	1
spe-MIR9679-1	AAAUUGAUAAUUUAUUACAAAUGGGCCUGAUAAAACCCUCUAAAUUUUUAUGGUCUUGUACUGCAUUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGGUUAGUAAUAAAUUACAAACC	130	spe-miR9679-1-3p	CAGAACAAGAAAGAGGUGUUC	85-105	tae-miR9679-5p	5	0	21	21	1
spe-MIR2608-1	UAUAUGUAAGUAAGAUUAUAUAUAUGAAAUAAAAGUUUGUUUAUAUAUCAAUAUUCUUCAAACUUGAUAAGUAGUUCAAAGUGGAAGUUGCGAUUUCCAGCCUUUAGGAGGAAUAGCAAGGAAAGUAGCCGUAAAGAGUGAAGAAGGCGAAAAAAGCUAUUCAUGGCCGAAGAGGAGAAAUGCUGAGGCAUUGAUAGGACUAAUUAUCAACUAGAGGAAGAAGGUAUAAAAAACUACCUUUUAUUGCAUAUAUUAUAAUCUUAUAUACAUGUU	273	spe-miR2608-1-5p	UUUGUUUAUAUAUCAAUAUUCU	36-57	mtr-miR2608	5	0	22	22	2
spe-MIR156c-2	AGAUAAUUGAAUCGAAGAGGUAAAAUAAAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUAGCAUGAUGUUUUACAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCCCCCAUCGCUUUCUAUAUCUCUCUCUAGAUUUUAUUAGAG	166	spe-miR156c-2-5p	UGACAGAAGAGAGUGAGCACA	38-58	rco-miR156c	0	0	21	21	1
			spe-miR156c-2-3p	GCUCACUGCUCUAUCUGUCACC	105-126	ata-miR156c-3p	0	0	22	22	1
spe-MIR166f-2	UUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCGAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAAAAUCUC	107	spe-miR166f-2-5p	GGAAUGUUGUUUGGCUCGAGG	13-33	cas-miR166f-5p	0	0	21	21	1
			spe-miR166f-2-3p	UCGGACCAGGCUUCAUUCCCCU	77-98	cas-miR166f-3p	0	0	22	22	1
spe-MIR7508	AUUAUUCAAAACCUCGUGUACCUGACUCAAAUUAUAACAGAAGGAAUGAAGUCGGGAUAGAGGCCUGCAACAACCACAUGAAUUUUCCAGGGAAAUUCAUAUGGUUAUCAUUGGUUUCUAUCCCCAAUUUCAUUCCUUCCGUUAAAAUUUGAGCAGAUACCUAGGGUAUUGGAUGUC	177	spe-miR7508-5p	GAAGGAAUGAAGUCGGGAUAG	40-60	ghr-miR7508	4	0	21	21	2
spe-MIR8045-1	ACAUUUACUGCUUGAACUGUCAGUAUAGAUGAGGUAGGAAAAUGGAAGAAUUGAUAGUUGAGGUGUGUUUUAGUAUUCAGGUAGGAAAAUGGUCCAAGUGAUAGUUAGGGAGUGGAAUUUGCGACAAGAUGAUAGUUAUGUAUGUUUUUAACCAUCAUCUGUAUUAUCACGCCUCAACUAUUAGUUUUUCGCUUUCCUAACUGAACUAUCACCAUAGUUAAGGUAGGAAAAAA	234	spe-miR8045-1-5p	AUUGAUAGUUGAGGUGUGUUU	50-70	stu-miR8045	0	0	21	21	1
spe-MIR1886f	GCCAUGUGAUAUCAUAUCACAAUAUGGUAUCGUGAGAUGAAAUCAGCAUUUGGACAUAUCAUUUUA	116	spe-miR1886f-5p	AUGGUAUCGUGAGAUGAAAUCAGC	24-47	stu-miR1886f	0	0	24	24	1

spe-MIR1217-1	CGCUGAUUCCAUCUCAUGAUUUCAUAUCAUGAGAUGUGAUACCAUAUUUCUGUCAUAGAUUGAUAUGUCUAUAUUGAGUUUACCUAGAUCAUUGAGUAUUAUGAGUUUUGUAUUGAAUUGAUUAUCAUGGCCAUGAGUAAGGGCUUUUGAUAUUGAAUUGGAUGAUUUAGCUAUGGAUUGAAGUAGUGAGAAUGGAUUGGUGGUACGCUUCCCUAAUUCUCAUUAUUUUACAUAAUAUAGCUUUUGAAUUAUGAUGU	208	spe-miR1217-1-3p	CUUUUGAAUUAUGAUGU	192-208	ppt-miR1217-3p	4	0	17	21	3
spe-MIR1522	UUUUUAUUUUUUAAAAUAAAAGUUAGAUUCUUCGGUGCACCGAAGUUUUGAGACCCUUGCACCGAAAACUGAACCGAACACACACACAUUAUUUAUUUUAUUUUUUUAAAAUAAAAGUUUGGUUCUUCGGUGCACUGAAGUUUUGAGACCCUUACACCGAAAAUUGAACUGAAGAAUCAAACUUUCAAAAAAAUAAUAC	199	spe-miR1522-5p	UUUAUUUUUUAAAAUAAAAG	3-22	gma-miR1522	4	0	20	20	1
spe-MIR7992-2	GAUCUCUAACUUUUAUAAUGUACAAAUAGACACUCUACCUAUCCAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGGCAUAAUACACGUAGGAUAAAAAUGACAUGUAGGACACGUGUGUUUAUCUGUUCAACUUUAUACAAGUUUAAGUGUCUACUUGUACACACCCAAAGUUAAAGGGU	185	spe-miR7992-2-5p	UUUUAUAAUGUACAAAUAGACACU	11-34	stu-miR7992-5p	5	0	24	24	1
spe-MIR6231-1	AAGGUCCUAUUACCCCCUGAACUUUUUUUUUUUGGUAAUUUUGAACACCUUUUGUCUUACGUUGCAAACUCCGUGACUCCACAAAAUUGAGGUGAGUGGGAGAUAUUUGGAUGCCACGUAAGCCAAAAAGGUGCACAAAAUUAUAUAAAAAAUAAGUUCAUGGGGUAAUAGAACAUU	177	spe-miR6231-1-5p	CUCCGUGACUCCACAAAAUUG	69-89	sbi-miR6231-5p	5	0	21	21	2
spe-MIR7990a-1	CCAAGGCAAAAAGUUUUUACCAUUUGAAGUUUCACAAAUUUACAACUGCUUUUUCUGAGUUACACUCUUUGUUUUUGUGAAACUUCAAAUGAUCGUAACUUUGGCCUCAA	110	spe-miR7990a-1-3p	UUCAAAUGAUCGUAACUUUGGCCU	84-107	stu-miR7990a	0	0	24	24	1
spe-MIR7990a-2	AACAUUUGGGGAAAAAAGUAUGACCGUAUGAAGUUUCAAAAAUUUACAACUACUUUUAUUGAGUAACACUCUUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCCUCAAAUAUC	119	spe-miR7990a-2-3p	UUCAAAUGAUCGUAACUUUGGCCU	88-111	stu-miR7990a	0	0	24	24	1
spe-MIR10538-1	AAAAAAAGUUGACGGCGUUAGGUUGAUAUACGUUACUAUAAGUAAUAUUUUACUCCUAAAACGUUGUUUUGAGUAGCAUUUUAGGAGUAAAACGUUACUAUGAGUAACAUAUAUCAAUCUAACGCCGUCAACUUUUACA	139	spe-miR10538-1-5p	AGGUUGAUAUACGUUACUAUAAGU	20-43	sly-miR10538	4	0	24	24	1
spe-MIR11036	AUCCAUUAUUCUUCUGAAUUGUUUAUCUUCUGCUUUGAUAUGACAGCUUUAUUGUAUUCAUUCAGGAAUAUGAGGAGUAUGAAGAUUUGGAUGAAUAUGAGGAAGAAAGCGGUGCAGAGGAAUAUGAGG	129	spe-miR11036-3p	UUUGGAUGAAUAUGAGGAAGAA	86-107	seu-miR11036	1	0	22	22	1
spe-MIR168a	CAAAGGAUUAUAACUUUGCAAAAUGUCCUUUGUGCAUGUGAUUUUGACAUGCGGUUUAUGUUUAUUGCAGCUGGUUGGGAAGAUAUGAAUCCUAAUGUUUUUCAAUCACAUUGCACAAAAAUGAAUGCCUAUAAUCCUAAU	141	spe-miR168a-3p	UUUAUUGCAGCUGGUUGGGAA	61-81	mtr-miR168a	5	0	21	21	1
spe-MIR477e-1	GAGACAUUAUGUGGUGCAAAUCAAGAUAGCAAGAUUGAUAUCAAGAAUGGUCUCUUUUAAUGAAUCUUUCAUGAUACUUUGAGCCCUUUGUGGGUGAUUGGAAACUUUCAUAUCCAAGAUGGCCCACAACCCCAUUCUUUAUAUCAAUCUUGCUAUCUUGAUUUGCACCACAUAAUGUGUU	181	spe-miR477e-1-3p	UGAGCCCUUUGUGGGUGAUUGG	80-101	ptc-miR477e-3p	4	0	22	22	1
spe-MIR11285	UUCCCUUUCAUAAAAAGUUGUGACUUUCCUGAAAAGUUGUGACUUUUAUGAAAAGUUGUGACAUUUAUGAAGAGUUGCGACUUCUAUGAAAAGUUAUGACUUUUAUGCAAGGUUG	115	spe-miR11285-3p	UCUAUGAAAAGUUAUGACUUUU	83-104	fve-miR11285	5	0	22	22	1
spe-MIR5747	GGGUUUAAUUGAAGAUUUUUUUUUUAGAAUGAAUUAAAAGUUGAAUGAGUUGAAAUUGAACUCAAUUCGAAAUUAUCUUAAGCGAACCUAUAAAAUUAUGAACGGAUUGGGCAUGUUACACAUAUUUGACUUCAUUUUGUCACCUCUACACACGCAAAUAGAA	284	spe-miR5747-3p	AAGAAAAUUCUCAUAAAUAA	265-284	mtr-miR5747	4	0	20	24	1

spe-MIR7997c-2	CGACUCUUGAUAUUGCGCAGUAGACAGGAGUGUCCAAUCGGUUGAUUAAGUUGAUUUAGCGAUUUUUAGUCAUUAACGGUUCGAUUUUCAAUUUAUCUAAUAAGAAAAUUCUCAUAAAUAACUUCUAUGUUGCUCAGACUCUUCAAAAAUGUCGCCAUGUGCAUGUUGGAUCCUUCAAAAGCAAUACGUUUUUUUAUGGAUACCACAGGUGUGGCGACAUUAUUGGAGAGUCCGAGCAACAUAGCUG	126	spe-miR7997c-2-5p	AUGUUGCUCAGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
spe-MIR8029	GGGUUUGAUUUUGAUAGCCGCAUAAUCCAAAAUGUGAAAAAAAUCAUCAGAAAUUAAGCCAUUUUUGUUGAUUUUUUAGCAGAAUCAUAUUGCUUUAUUAUCCGAAAAUGGUAUUCUCAUAUCCUAUAGCCUUGUAGAGCAGAAUCUCUGCUAUUACUAUUUGGGAAUUGCCAUGAGAAGUACAUUUUUUUUUAAAGAUCAAAUUUUGGCCUAUGAGGAGAUCUAUUAUGAAAAAA	236	spe-miR8029-5p	AGCCAUUUUUGUUGAUUUUUUAGC	57-80	stu-miR8029	5	0	24	24	1
spe-MIR168c-2	UUUUUUGCGGCCGCCUCUUAUUCGCUUGGUGCAGGUCGGGACCUCAUUCGCCGGCGCCGGGAAUAAUGGCGGACGAACGACGGCGGUUUUAAUUCUACUAAGCUGUCACCGACGAAUAUAUGUUUGAUUAGCGGCGAAAUUUGGGUCCUGCCUUGCAUCAACUGAAUUGGAGACAGCUGUAAAUCG	186	spe-miR168c-2-5p	UCGCUUGGUGCAGGUCGGGAC	22-42	bra-miR168c-5p	0	0	21	21	1
			spe-miR168c-2-3p	CCUGCCUUGCAUCAACUGAAU	147-167	bra-miR168c-3p	1	0	21	21	1
spe-MIR10540-1	UGCGGGGUUGAAUUCUUGAAUGGUUACUCAACUUAUAGUUAUUAUCUCAGAAAAUCACUUUUCCUUCUUGAUUCUGAUGCACAGAAAGUCACUUUGUUAGAUAUAAACUAUUAGUUGAGUGACCAUCUGUGAAAUCAACUCCUAU	145	spe-miR10540-1-3p	AUAUAAACUAUUAGUUGAGUG	101-121	sly-miR10540	3	0	21	21	1
spe-MIR1127b-1	UUUUAUACUCCCUCUGUCCAACAAUAGUUGUCCACUAUUGACUUGGCACACUUCUUAUAAAUAGAUGGGUAAUUUUAUUAUAUCACCCUUUGAAUAUAAUAAAUACCAUGUCUUGAAAAAUAUAAUAGGGAAAUAGGGAAAUGAGUGAAAUGACUAUAAUUAAUGAUAAGGGUAAAUUAGGAACUAAGUGUAAAAUUAUUCAUGGAUUUCAUAAAGUGGACAAGUAUUGUUGGACGGAGGGAGUAAUAGCU	251	spe-miR1127b-1-3p	ACAAGUAUUGUUGGACGGAGG	220-240	tae-miR1127b-3p	2	0	21	21	1
spe-MIR5568e	GUGGUCCCUCUAGUGCCCAAUUUAACUAGAACUCAGAAUCUUAUUUUCCAGUAGAAUAUGGAAAAGUAGCUUGUAUUUUUUCUUCCAAGAAGAAACGUGUGUUUUAGGUUUUCUUGAGGAAAAAGGAUUUGUGUUCUCUUCUCCUCUUUGGAUUAGGAAGACAUCUCUAAAAGUAGGGAUUAUUCUAACCUAGAGAAAAAGAAUUCAUUAUUCUAUACAAUACUUGCCCACCCAUGUUUGUAGAGAGUUCAAUUGUUAAUUGGGAUCACUGGAGAAGACUGU	282	spe-miR5568e-5p	UGUGUUUUAGGUUUUCUUGAG	98-118	sbi-miR5568e-5p	5	0	21	21	3
spe-MIR7984d	CAAAGGAAAAAAAAUCUGAAAUAUAUCCUAACGCUGACUUGUAAUAAUCCCAAACUUUGGAAAUGACUCUUUGCCCUUGCACUAUUUAAUAGAUCUUGUCCAUGUGGUCACAUAUAUACCUUUAAAAUACACUAUUAAAUAGUGCUGAGGUAAUAGAUCCUAAUCACAGUUUGAAAUUGUUGCAGCAAUUUCGGUCAAAGUUCAGAUAUAUUUCGAACCUUUUUCCUAAA	230	spe-miR7984d-3p	CAAUUUCGGUCAAAGUUCAGAUAU	186-209	stu-miR7984d-3p	1	0	24	24	1
spe-MIR1128-2	AAUUACUCCCUCCGUCCCAAUUUAAGUGUCUUAGUUUAACUAGAAACAGAAUUUAAGAAAAAUGUUUGCAGUCAAGUUUAAAGUUAAAUUGGGACGGAUGAAGUACUC	108	spe-miR1128-2-5p	AAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	3	0	21	21	2
spe-MIR5049-1	UUAUACUCCCUCCGUCCCAAUUUAAGUGUCCUAGUUUAACUGUGCACUAAGUUUAUGAAAGGGGAGACACUGACUCUUUUGGUCUUAAAUUGAAGAUGCAUGUGUGUAUCCCUUUGAUUUUCGGUCUUAGACCUGCCAUGUAGAUUGUUGGAAUUUGGAAGAUUACUAAAUGUAGAAAGAGACGCUCUUUUGGGACAGAUCAAAAGGAAAAUAAGACAACUUAAACUUGGGACGGAGGGAGUACGU	248	spe-miR5049-1-3p	AACUUGGGACGGAGGGAGUAC	226-246	tae-miR5049-3p	4	0	21	21	1

spe-MIR391	AAAAGGCUUGCUACGCAGGAGAGAUGAUGCUG GACGAUAGAGAAAAUGGGAUUUAAUUUAUUGG CCAGCAUCAUACUCCUGCAUAUUAAGCCUAAA	96	spe-miR391-5p	ACGCAGGAGAGAUGAUGCUGGA	13-34	sly-miR391	0	0	22	22	1
			spe-miR391-3p	GCAUCAUACUCCUGCAUAUU	68-87	stu-miR391-3p	0	0	20	20	1
spe-MIR7984c-3	AAAUCUGAAAAAUACUUCAAUUUGAGCUGACAU UGUUGCCAAACUUUAAGAAUGACAUUUUACCCC CUGCACUUUUUAACAAUAUAUUUUAAAAGUAUA UAUGUGUCCACGUGGACACAACACUAUUUAAAA UGAUGCAAUAUUUAUGAUGUCCUAAAAUACAUU AUUAAAUAGUGCAGGGGUAAAAAAGUCCUUCAU AAAGUUUGGUAUCGUAACAACAAUUUCGAUCAA AAUUCGAAUAUAUUUCUCAUUUUCAACCUAAAU UUUACGAGUUAAUACCUCAGAUGGUCACUCAAC UUUGCACUAUUCUCUCAGAAAG	319	spe-miR7984c-3-3p	CCUUCAUAAAGUUUGGUAUCGUAA	192-215	stu-miR7984c-3p	0	0	24	24	1
spe-MIR7983-2	CAUUCACUACAACAAAAUUGACCAUUAGCGGCA UUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUU UAGCGGCAAUUGUCACUCAUUGUAUAUGUCUC UAAAGCCUUUAGCGACAUUGGUUCUAAUGACA GUUAACUAAUGCCGGUAAAGACUUUAGCAUUCU UUGUUAGUGUCAAUAUUUAAUACCGCUAAAAGU UAUUUUUAUUGCAGUGAUUU	216	spe-miR7983-2-3p	ACUAAUGCCGGUAAAGACUUUAGC	135-158	stu-miR7983-3p	1	0	24	24	1
spe-MIR11075b	CUCCAAUGCACUUGGAGCAUUUAUGAUCUGGG UAUUUGUUGCUGAUAAGCUUGCAGUAUCUUAC UAGUAGCUCUUCUGAUAUAAAUUCCUUUUUCAA GGCUCUGGUAGUUGGCUGUUCUUGUGGCUUUA GUAACGAUAAAAUCCAUCUCUGGACUUCAUCCA UAUGUGAUUUCCUUAGCUCUUUGGAGUUUGCA UAAAUCAUUACUUGAUCUCUUGCAUAAUAGCUC CAAAUGGCAUUGCCA	242	spe-miR11075b-5p	CUCUGGUAGUUGGCUGUUCUU	100-120	lja-miR11075b-5p	5	0	21	21	1
spe-MIR8001b-1	ACCCACUAUAAGAAAAAAGUGAAUUACAUGGAG AUUUUUCUAGGAUUAGUAUUAAAAUUUGCAGGA AAAUAGGUUACCUGCAGAUUUUCAUACUAAUCC CUAGGAAAACCUCCAUGUAAUUCAUACUUUUCU UGUAGUGACC	142	spe-miR8001b-1-3p	AGAUUUUCAUACUAAUCCCUAGGA	82-105	stu-miR8001b-3p	3	0	24	24	2
spe-MIR5014a-2	AAUUUUGGAUAUCCACAAGUAAGCACUUAAACU UACAUGGCAUGAUACACAUAGACGUCAUGUAG GAAACAAAAUUUCAUGUAGGACAAAAGUGUCAA UUUGUUCAAUGUUAUACAAGUUUAAGUGUCUAC UUGUGCACAUCUAAAGUU	149	spe-miR5014a-2-3p	UUAUACAAGUUUAAGUGUCUA	110-130	ath-miR5014a-3p	5	0	21	21	1
spe-MIR390-2	CAAGCAUGAAGAAGCCAUAAAACUCAGGAUGGA UAGCGCUAUAGAUAGCCAUUAAGAUGUAUUCAU GGUGCUAUCCCUCCUGAGCUUUAUAGAUUCCC CAUGCCAU	106	spe-miR390-2-5p	UAAAACUCAGGAUGGAUAGCG	18-38	atr-miR390-1	2	0	21	21	1
			spe-miR390-2-3p	UGCUAUCCCUCCUGAGCUUUA	69-89	stu-miR390-3p	4	0	21	21	2
spe-MIR1886h-1	UUGGACAUGCGAUUUUACGUUGAUUUCAUCUC AUGAUAUGUGACUCCAUAUUCUCCAAAAAUCAU GAUAUGAAAUCAUAUGAGAAUAUCAUAUCAUG	97	spe-miR1886h-1-5p	AUUUUACGUUGAUUUCAUCUCAUG	12-35	stu-miR1886h	0	0	24	24	1
spe-MIR5536	UUGUUCAAUAACACUAGCAAAAAAUCUAGUGUA AUUAGCAUGUAUCUCGCGUACCAGAUACGCGA GCGAGACAAGAGGCUGACAAGCAAGAUGGGAG GAAGUGAGGGCGCGAGAUUUGUCUAUGUAUCC UAGAUACAUGUGAAUCUACUUGGAUAGAGUGU AUCGAGAACAAAUUGACUAAUUUUCAGUCCAUA UAUUUCGAGAUACAUGUAUCUGGACAUACCAAA AUCUCGUAAGAUUCAUAAUGUUACAACAUAGUG UGUACUUAAGUAAUAAGAUUAUAUGCUAGUGAA AUUAUUGUAAGUU	306	spe-miR5536-3p	UAUGCUAGUGAAAUUAUUGUAA	282-303	osa-miR5536	5	0	22	22	2
spe-MIR8639e	UAAAUGUGCCUUUAACUUGAUCUUAUUUUACGU UUAUGUCAUCCAACUUUGGAUAUGCACAAGUAG AGUAAAACAAGUAAACACAUGAGUCCUAUAUGA CACAAUAUAUGUAGGACAAAAAAUGACAUGAGG ACAUGUGUGUCUAUUUGUUUAACUUUAUAGAA GUUUAAGUAUCAACUUGUGCACACCCAAAAUUG AAUGGUAUGAAUUUGAUUUAACGCCAAGUUAUA	239	spe-miR8639e-5p	UAUGCACAAGUAGAGUAAAACAAG	54-77	gra-miR8639e	5	0	24	24	1

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spe-MIR472b	CCAAAAUGGGUUGACCCAACCCAACCCAUCCCUAACGGGCUAGAUAGUUAAAUGGGUUGGGACGGGUUGACCCGUUUAGU	80	spe-miR472b-5p	UUGACCCAACCCAACCCAUCCC	11-32	ptc-miR472b	4	0	22	22	1
spe-MIR172a-2	AUGCACUGUCUCAGAUGUAAAUCUUCAUGUCGUCAAUGUCUAUGUUGUUCUACUCCAAAAAUGCACUACUUUUGGAGGAUAUAGAAUUUGGCGACCUGAAGAUUUACAUUUGAGACAGUGUUU	123	spe-miR172a-2-3p	UUGGCGACCUGAAGAUUUACA	88-108	vca-miR172a-5p	5	0	21	21	2
spe-MIR8006-1	UUUAGGGACACUGGUGCCCUUACCUUCAAAAAAACUAGAACACAUAUAUCCUUUAUACUAACGAACAUACACGUGUCAUAAUUUUAUCCAUCGACCCGACAUUGAAUCGACGGAUAAGAUUGUGCCACGUAUUCGUUUAGAGUGAAGGGCAUAUACACUCUAGUUUUUGAACGGCAGGAGCACCAUUGUGUACCUGCA	199	spe-miR8006-1-3p	UAGUUUUUGAACGGCAGGAGCACC	162-185	stu-miR8006-5p	3	0	24	24	1
spe-MIR1919-1	UCCGAAUCGCUCCGACGCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCUUCUAAGGAACGACACUUUCUGUAAAUCUAAUUAAUUUGAAUUCAAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUU	187	spe-miR1919-1-5p	UGUCGCAGAUGACUUUCGCCC	47-67	stu-miR1919-5p	0	0	21	21	1
			spe-miR1919-1-3p	ACGAGAGUCAUCUGUGACAGG	123-143	stu-miR1919-3p	0	0	21	21	1
spe-MIR1919-2	UCCGAAUCGCUCCGACGCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCUUUUAUGGAACCACACUUUCUCUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUU	177	spe-miR1919-2-5p	UGUCGCAGAUGACUUUCGCCC	47-67	stu-miR1919-5p	0	0	21	21	1
			spe-miR1919-2-3p	ACGAGAGUCAUCUGUGACAGG	113-133	stu-miR1919-3p	0	0	21	21	1
spe-MIR169c-2	AAUAUAGAAAUUUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCUACUUUUAUUUUCCUCCAAUUUUUUAUGGAGUAUAUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCGAUUUAUAUUCA	201	spe-miR169c-2-5p	UAGCCAAGGAUGACUUGCCUA	55-75	ata-miR169c-5p	0	0	21	21	1
spe-MIR10538-2	ACUAGUAUAAACGUAUUUCACAGUAACGUUUUAGGGUACAUUUCAAUUUUUAAAAACUAACAGCGUUAGGUUGACAUACGUUACUGUGAGUAACGUUUUACUCCUAAAACGUUUUUUUGAGUAACGUUUUACUCCU	136	spe-miR10538-2-3p	AGGUUGACAUACGUUACUGUGAGU	68-91	sly-miR10538	5	0	24	24	1
spe-MIR6232b-1	GAGCUCUACAGUGCAACUUCAGCAUAGUAAAGAGUAGAGACUAAUUAAUGCCUACAUAUGUAGGCAUUAAUGAGUCUACUCUUUGCUAUACUGAAGUUGCACUGUAGAGAUA	112	spe-miR6232b-1-3p	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-5p	5	0	21	21	1
spe-MIR6232b-2	GAGCUCUACAGUGCAACUUCAGCAUAGUAAAGAGUAGAGACUAAUUAAUGCCUACAUAUGUAGGGAUUAAUGAGUCUACUCUUUGCUAUACUGAAGUUGCACUGUAGAGAUA	112	spe-miR6232b-2-3p	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-5p	5	0	21	21	1
spe-MIR5035	AUGACUUUAGGCGACAUUUACCAAAUGCCUAGAUAAGCCAAAAAAUUGCUUAUAAGCUAGUUUGACCAGCUUAUAAGCUUAGAGGGUGUUUGACUAAGCUUAUAAGCUGGUCAAAUUGGCUUAUUAACACUUUUUAGCUUAUCUACUCAUUUGGUAAAACACCUAAGUGUU	171	spe-miR5035-3p	CUUAUUAACACUUUUUAGCUUA	120-141	gma-miR5035-5p	5	0	22	22	1
spe-MIR8047	CAUAUUUACACCAGGUAGUCAAUUUUGUGCCCUUGUAUCAACAAUUUGACCAUUUUUUCGAAAUUAGACCCAUGGUCUGAAUACCAGUUUUGAACUUUGAAAUACAGACCAGGUGGCCACUUUCGAACUUCAGAUCACUGGGCUAAUUUUGAAAAAGUGGUCAACUUCUAAAUACAAAGCCACAAAUGAGGUUAUUUGUGUAAAUCAG	208	spe-miR8047-5p	CCAUUUUUUCGAAAUUAGACC	50-70	stu-miR8047	0	0	21	21	1

spe-MIR5628	UAAAACCCUGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGAAUAGGUUGCUAAUUCUAGCAUUAGAGAAAUAUGGAAGAGGUGAUUGGAGAAAUAUUUCUAGGUGUUACG	118	spe-miR5628-3p	GAAAUAUGGAAGAGGUGAUUG	75-95	ath-miR5628	5	0	21	21	1
spe-MIR9674c	UUUGAUCUUUUCUAUAACAUCAACGAAAACAGGCAAUCUUAGUUCUUUGAGAGGUUUUUCAAAGAACUAAGAUUGCCUGUUUUCGUUGAUGUUAUACAAUAGAUCUCU	108	spe-miR9674c-5p	UGAUCUUUUCUAUAACAUCAA	3-23	ata-miR9674c-5p	5	0	21	21	1
spe-MIR7540b-1	UAUUUUAGGGAUCAUGUUGUUGGUAUGUGGUGCUAGAUGAUAUUAUAUGUAAUGUUCUUGAAUUAUGAAUGCCGAUUAACCUAUGAAGUUGUGAUCGUAUUAAGUUAAUUGCUUAAAACGUGAAUCAUGAAUCGACAAUGUAUUAGUUACACACGUAAUUGUUGUAAGUGUUGAUGUGUUUGUCCGAAUGUUGCAUUGCUGUUAUAGUGACGUUAUGAAGGUGUUAAAUUCAUAAAGUAUUAAUAUGAUGUUGUCCAAUAUAUCUUAAAACGUUACCCUAAAGUC	285	spe-miR7540b-1-5p	UGAUAUUAUAUGUAAUGUUC	38-57	lja-miR7540b	5	0	20	20	1
spe-MIR917	AGAAAUGAUUUCGCUCCUUCUCUCUCAUUUCGCGGUUAGGAGUUUCAUAGUUUUGUUCGUUGGUUUCAAAGUGGAUAUUCCUGAUUGUAGGUUAGUAAAUCUUUUUUCUUAUUUUAUUAUGUUUACAAUCACGAAUAUCCACUUUGAAACUCAACCCCGAAGAAAUAUAUGAAGCCCUAAUCGGAAAAUGAGGGGAAAGUUGUGAAAUCUUAAC	214	spe-miR917-5p	UUUCAUAGUUUUGUUCGUUG	43-62	cre-miR917	5	0	20	20	1
spe-MIR172-4	AUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGAAGAACUAUUUAAUUAUAUGUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAAUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUA	169	spe-miR172-4-3p	UGGGAAUCUUGAUGAUGCUGCAU	128-150	aau-miR172	1	0	23	23	1
spe-MIR408-1	AAAAGGAAGGAUUGUGGGGAGAGGAAAGCCAGGGAAGAGGCAGUGCAUGGAAUAGGCAAAGCAAAAAUUGCACAUCUCAUGCUCUGGCUCGUCCCCGUCUAUCCAUACCACACCAAUUUUUACCUCAA	128	spe-miR408-1-5p	CAGGGAAGAGGCAGUGCAUGG	30-50	lja-miR408	1	0	21	21	1
			spe-miR408-1-3p	AUGCUCUGGCUCGUCCCCGUC	79-99	cas-miR408	5	0	21	21	1
spe-MIR6145b-1	UUUUAGCAUACGUGGCACUAGUUUGAAAAAAAGUCAAUCAUCGUUGGGCCCACAAGAUAGUGUCACGUAGGCUAAAA	77	spe-miR6145b-1-5p	UUAGCAUACGUGGCACUAGUU	3-23	nta-miR6145b	4	0	21	21	1
spe-MIR11536	UCUCCUUUCAUGAAAAGUUGUGACAUUUAUGAAGAAUUGUGAUUUUUAUGAAAAGUUGUGACUUUUACGUAAAGUUUUGACUUUUACGAAGAGUUGAGACUUUUAUGAAGAAUUGUGACUUUCGUGAAAAGUCGUGACUUUAAUGAAGAGUUGCAACUUAUGAAAAGUUAUGACUUUUAUGAAAGGUUG	189	spe-miR11536-5p	UGAAGAAUUGUGAUUUUUAUG	30-50	pab-miR11536	5	0	21	21	1
spe-MIR8154	CGGUCCUUGCUACAGGAUCAAAGUAUGGUUUGGGGUACGUCCCCACAGAUGAUGAUAUGAAGAUGAAGAGGAAAAGGGAUCAAGGCUUGACUAAGCCGAUCCCGCAUCUCUAUCAAUCCUUUCCAGUCCGGGAGCAUGCCGAGCCUGAAGACGACGGGGAAGGAAUCUGUGACCUGUUCAAGGAGAU	187	spe-miR8154-5p	CAGAUGAUGAUAUGAAGAUGAA	46-67	cpa-miR8154	5	0	22	22	1
spe-MIR5049c	AAAAUGGACAAAGUAAUUAGGCACAAUUAUAAAAGAAAAAGUGGACAAGUAAUUAGGGACGGAGGGAGUAUUACAUAACUCCGCAUGUACGUGCAUUACUACUUAAAAUAUUCUUUUCACAAUAGUCUCUUCGUCUCAUAUUACUUUACCAUUUUCUAUUGUGUACAGUGUUUAAGAAAAUAUUCUCUCCGUCCCAUUUUAUAUGACAUCCCAUUCUAUAAAUAGUUGGCCCAUAAUACUUGUCAUCAU	249	spe-miR5049c-5p	GGACAAGUAAUUAGGGACGGAGG	43-65	hvu-miR5049c	4	0	23	23	2
spe-MIR7495b	ACUUAAACUUGUAUAAAGUUGCACAAAUAGACACAUAUGUCCUACAUGUCAUUUUUGUCCUACGUGGUGUCCUAUGUGUAUUGUGUCACGUAGGACUCACGUGUCUACUUGUUCAAGUUUAAAUGUCUACUU	132	spe-miR7495b-3p	CAAGUUUAAAUGUCUACUU	114-132	ghr-miR7495b	5	0	19	21	3
spe-MIR8006-2	AAAUUUGUGCCCCUCUUGUUCAAAAACUAUAACUAUAUAUAUACUCUUCACUCUAACAGAAUACUA	208	spe-miR8006-2-3p	UAGUUUUUGGACGGCAAGGACAUC	179-202	stu-miR8006-5p	4	0	24	24	1

spe-MIR1511	AAUACAGACACUUGACACAAUCUCAUCCAUCGAUUCGAUAUUUAAUAAAUGUCGGUCGGUGGAUAAGAUUAUGAUACGUGUAUAUCUGUUAGCAUAAAGGCUAUAUGUGCUCUAGUUUUUGGACGGCAAGGACAUCAAAACACAGUCCUAGAGUUUAAAUUAAAGAUGUUGGUGUCAACUCAUAAAAUUUGGGAUUAAAUCUAUCCUAUAUUUAGUUGAGGGUAUUCCCUAAUACCAUGAUAAAUCCUGGAUAACCUGGCUUUGACAUCUUAACUCCAUACUCCUUCAUAACCCACAAACUUAAUUUAAAAUUUGACACCAACAUCUUUAAUUUAAACGCUAGGAGCA	206	spe-miR1511-3p	ACCUGGCUUUGACAUCUUAAC	112-132	ppe-miR1511-3p	4	0	21	21	1
spe-MIR169c-3	AAAGAAGAGAAGUCUUACACGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUCCAUAGUCUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUUUUCUUUUAUGCAAGAUAUCUUUUCAAA	169	spe-miR169c-3-5p	UAGCCAAGGAUGACUUGCCUA	45-65	ata-miR169c-5p	0	0	21	21	1
			spe-miR169c-3-3p	CAGGCAGUCUCCUUGGCUACC	109-129	csi-miR169c-3p	2	0	21	21	1
spe-MIR169j-4	GGGUACAAAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCAUACUUGAAAAGGUCUUUCAUAUGUCCUUUCGUUAUUGGGGUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUUCAUGCAAGGCUUUCUCUUCUUUCGUUUUUAAUUAUGAGAAGAGGAGUCUUGCAUGAUGAAAAGAGUCUUAUUUGGUAGCCAAGAAUGACUUGCCUGCACCAUUUCCGAAAUGUGUCCUUUCGUUCAUGGGGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUCUUUCAUGCAAGACUUUCUCUUCUUCC	192	spe-miR169j-4-5p	UAGCCAAGGAUGACUUGCCUGC	51-72	ppe-miR169j	0	0	22	22	1
spe-MIR169d-2		164	spe-miR169d-2-5p	UAGCCAAGAAUGACUUGCCUG	43-63	bdi-miR169d	1	0	21	21	1
			spe-miR169d-2-3p	GCAGGUCAUCUUUAGCUAACU	103-123	stu-miR169d-3p	0	0	21	21	1
spe-MIR837	AUAAAAAAACAAAAAACUAAUAAAAGGACUCUAAUUAAUAAGAAUUUGUCAAAAUGCGCCCGAGUAGACGGACUCGUGACGGAUUGUCGUGGUUAGGGGUGGGCAUUCGGUAAUUCGGUUCGGUUUCGUUUUUUUUUUGGUUUUUUCGCUUUUUGGUUUUUCAAAUUGGGUACCGAAUACCGAACCGAAAUAUUUCGAUUCGGUUCGGUUUUUGUUAAUUCGGUUCAAUUUUUAUUAAUUCGGUUCGGUUUUUUAUUUCGGUUUUUUAAU	271	spe-miR837-5p	AAAAAAACAAAAAACUAAUAA	3-23	ath-miR837-3p	5	0	21	21	1
spe-MIR9497	GGGGUGCCAAGGUGAGCUUUAUUUUACAUUUUAAGUAAGUGAAUGUAGAGUAUUAUUGCACUAACAACUUUUUUUUUGGUGGCAAUUUGUUCGAACUUACCAUGUGAUAUAUCUGUAUACAUGGUAUAUUCGAACUAAUUCCCACGAAAAAGAAUAAUUGCACUGAUAACUUCUUCGUGGCAAUUGGUUCGAACUUGUGAAAUAUGUAGAUCAUGUUGCCACGAA	225	spe-miR9497-3p	UAUCUGUAUACAUGGUAUAUU	110-130	bdi-miR9497	4	0	21	21	1
spe-MIR1918-1	AGAGUAAAAUAUUAGUAGCUUAAUUGAUUAAGUAUUUGAACUUCCAUCCUGUUAGCGAUAGUCCGAUUCUCCACCUUGUAGCAUAUUUUUUCUCUUAAAUUGAAGAGGAGAUUACGUAAUGGAGAAUCGAACUCUCACCAACAGAAUGACAAUCCAACUAGUUAAACCAACUGAGCUACCAUAAUUAUCUGACAUGGUCUAUAUAGCUCGGACUCUUUAAAAAUGUCG	197	spe-miR1918-1-5p	UGUUAGCGAUAGUCCGAUUCUC	50-71	sly-miR1918	4	0	22	22	1
spe-MIR7997c-3	GUGCACCCAUGUUGGAUCCAACCCAAAUCCUUUGACAUUUUGAAGAGUUCGAGCAACAUAAGU	95	spe-miR7997c-3-5p	AUAUAGCUCGGACUCUUUAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
spe-MIR160-1	GGAAUAUGCUUGGCUCCUCAUACGCCAUUCAACAAGGCCCAUCGAUAUAUUACGGUGAGCUUUGCAAAUGGCAUACAGGGAGCCAGGCAUAUACG	95	spe-miR160-1-5p	UGCUUGGCUCCUCAUACGCCA	7-27	dpr-miR160	4	0	21	21	1
			spe-miR160-1-3p	UGGCAUACAGGGAGCCAGGCA	69-89	aau-miR160	0	0	21	21	1
spe-MIR398-1	CCAAUUUAUGUUGAUAUAUUCACAUUAUUAAUAUGAAUCAUGAUGAACAAUGGUGAAUCCCCAGAG	218	spe-miR398-1-3p	UUGUGUUCUCAGGUCACCCCU	133-153	lja-miR398-3p	0	0	21	21	1

spe-MIR6145e	GAGUGUGCCUGGAAACACAGGUGCAUUUUGGUCCUUUUUUUUGGCAAUUGUUGGACCAAAAUAUAUUUGUGUUCUCAGGUCACCCCUUUGGGAUCACCUUGUUUUUUUAUCGUAUUUUAAUUUUGUAGAAUAAUAGUUAUUACUUAAAUACAGUGCACAAAUACACACUGAACUUGUAUAAAGUUGAACAAAUAGACACACAUGUCCUACAUAUCAUCCUACAUGUCAUUUUUUAUCCUACGUGGUGUCCUACGUGUAUUGUGUCAUGUAGAACUCGUGUGUUUAUUUGUUUAAAAGUUGGAUAGUUAAAGUGUCUAUUUGUGCAU	174	spe-miR6145e-3p	AUUGUGUCAUGUAGAACUCGU	106-126	nta-miR6145e	5	0	21	21	1
spe-MIR5340	AUGUCCCUAAUUACUUGUCAACUUUGAAUUGACACCCAUAUUUAAGAAACAAUUAUUGACAUAGUGAGUUUAUCAUUUUACCGCUAUUAAUUAUGAAGCGGAUGAAUUCAAAAUCUAAGAUUCUUAACAAGUUUUACUUUAUUCAAGGUUGAGGGUACUAUAGGUGAAAAAAGUUGUCCUUUUUUGAUUUGUAGAAAUGAACAAGUAAUUAGGGACAACUAAAAAAGGAAAGUGGACAAGUAAUUAGGGACAG	253	spe-miR5340-5p	UUAUGAAGCGGAUGAAUUCAAAA	91-113	osa-miR5340	5	0	23	23	1
spe-MIR10540-2	AGUUUGAUUUCUCAGAUGAUCACUCGACUAAUUGUUAUCAUCUCAGGAAGUCACUUUCUUUGUUGAAAGUUUUGGAAUCAAGAAGAAAGGGGACUUUCGAGAUAAUAACUAUUAGUCAAGUAACUAUAUGAGAAAUCAACCA	142	spe-miR10540-2-3p	AUAAUAACUAUUAGUCAAGUA	102-122	sly-miR10540	4	0	21	21	1
spe-MIR7803b	CAUACACGUGUCAUAAUUUUAUCCACUGACCCGAUAUCGGAUCGAUGGAUAACAUUAUGUCACGUGUCAC	70	spe-miR7803b-5p	UACACGUGUCAUAAUUUUAU	3-22	rgl-miR7803b-3p	5	0	20	20	1
spe-MIR394b-1	AGAUUAAUUAGUUUCAUGGAGGUUUGACAAAGGGUUUCUUACAGAGUUCAUUGGCAUUCUGUCCACCUCCCUCGUUCUUUUUUCGAAAAAGAAGAAGAAGGGGGGAAGCAAGAUUUAUUGUGGAGGUGGGCAUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUUGUAAAACCCUCGUGAUACACGUCAAGUAAGAU	196	spe-miR394b-1-5p	UUGGCAUUCUGUCCACCUCC	51-70	csi-miR394b-5p	0	0	20	20	1
			spe-miR394b-1-3p	AGGUGGGCAUACUGCCAAUAG	124-144	ath-miR394b-3p	0	0	21	21	1
spe-MIR319	GAUGGGAUAAGGAAGGAAAUUCAUCAGUCCAAACAAGGUGGUAUAUUUGGGCUGAUCUUUGCUGCUGAAUCAUUGGUUCAUCAACAUAUUAUACACAUACAAGGAUAUAUACAUAUGUUGUUGCAUCAAUGAUGCAGGAGCUGAGUUCAGUUUUGGCUACCUUUUCUUGGACUGAAGGGUUUCCUUCUCAACCCCAA	197	spe-miR319-5p	UGCUGCUGAAUCAUUGGUUCA	60-80	ata-miR319-5p	5	0	21	21	2
			spe-miR319-3p	UUGGACUGAAGGGUUUCCUUC	167-187	stu-miR319-3p	1	0	21	21	1
spe-MIR11144-1	AUACUCCCUCUGUCCCUUUUUACUUGUCCACUUUUGAAUUGGCACACCUAAUAAGAAAAUAAUUAAUAACGUAGUGAGUUUACCAUUUUACCCCUAUUAAUUAUGAAGUGGAUAAAAAGUUCUACAUUUUUCAAAGUAAUCAGUCAUUUAAUUGUGGGUUUAGUAGGUAAAAGAAAUUAUCCUUUGUUGAUUUGUCCAAAUGGACAAGUAAUUAGGAACAACUAUAAAAGGAAAAGUGGACAAGUAAUUAGAGACGGAGGUAGUAU	266	spe-miR11144-1-5p	UUUACCAUUUUACCCCUAUUAAU	79-101	lja-miR11144-5p	4	0	23	23	1
spe-MIR7984c-4	AAAACGGUCUCAAACUUUAUGGAGGACCUUUUACUGCCUGCACUAUUUAAUAGUGUACUUUAAAGUUAUAUAUGUGCUUACGUUGACAUCAUAAAUAUUACAUCAUUAUAAAUAGUAACAUGUCCACGUGGACACAUAUAUACUUUUAAAAUACACUAUUUAAUAGUGCAUGGGGGUAAAAGAUCCUCCAUAAAAUUUGGUACCGUAAC	209	spe-miR7984c-4-5p	ACGGUCUCAAACUUUAUGGAGGAC	4-27	stu-miR7984c-5p	4	0	24	24	1
			spe-miR7984c-4-3p	CCUCCAUAAAAUUUGGUACCGUAA	185-208	stu-miR7984c-3p	3	0	24	24	1
spe-MIR10536-1	UACUGUUGAAAAAGAAAGAAGCUGAGGAUUGGAACAUGUAAAAGGAACAGGUUCAACGAAGCUGAC	201	spe-miR10536-1-3p	GGACAUGUUUCAAUCGUCAGCUUC	161-184	sly-miR10536	3	0	24	24	2

spe-MIR156b-9	UGACUUGUCUAUAACAAGUGUUGAUGAAGAAG GAACCUGAGGAUCAGCUGACUGCGGGUUUACA CUUGCUGCAGACACAUCAGUCAGCUUUGUUGG ACAUGUUUCAAUCGUCAGCUUCCUUCUUCUUC AGCAAUG UAUGUUAAAAAGAGGAGGUGGUAGGAGAUGUU GUUGACAGAAGAUAGAGAGCACAGAUGAUAAAG UGCAUAGAAAUUGUCUGCACCUUACUCCUUUG UGCUCUUUAUUCUUCUGUCAUCAUCGUUAAUA CCACCUCUUUUUUUUUAACGUU	151	spe-miR156b-9-5p	UUGACAGAAGAUAGAGAGCAC	34-54	aof-miR156b	0	0	21	21	1
			spe-miR156b-9-3p	GCUCUUUAUUCUUCUGUCAUC	99-119	vca-miR156b-3p	2	0	21	21	1
spe-MIR1128-3	UUUAAUUACUACUCCCUCCGUCCCAUUUUAUUU GACACAUUUUGACUUGGCAUAGUUUUUAAGAAA AAAAAAAGACCUUUGAAACUUGUGUUCUAAACA AUCCUUAGAUAUAUGUGUGGUUGCAAGUCAUU UAAAAGGGGAAUUUUAAAGUUAAUUUGUUUCUA GUUAUAGAAAGGUGACAUUCUUUUUGGGAUGG ACUCAAAAGGAAAGGAUGCCACAUAAAAUGGAA UGGAUGGAGUAUCAUUUUA	248	spe-miR1128-3-5p	UACUACUCCCUCCGUCCCAUU	7-27	ssp-miR1128	2	0	21	21	1
spe-MIR10519-1	UAUUUAUGCUCUUCAACUUUGGAUGUGCACAAA UAGACACUUAAACUUGUAUAAAGUUGAACAAAU AGACACACAUGUCCUACAUGUCACCCUACAUGU CAUUUUUUGUCCUACGUGGUGUCUUACGUGUA UUGUGUCAUGUAGGACUCAUGUGUUUAUUUAU UUAAAAGUUGGAUAGUUAAAGUGUCUGUUUGU ACAUUAUGAAAGUUGGAGGUCAAAGUU	222	spe-miR10519-1-3p	AUUUAAAAGUUGGAUAGU	162-179	tae-miR10519	4	0	18	18	3
spe-MIR168b	AUGCUUGGCCCGCAAGGCUUGGGCCAGGUGG GGCUGGACCAACCCUUUUUGACAACUCUAGAU AAUCAAAAGUAGAGUUGUCAAAACGUGUCGAUC CAGUCUCACCCGGCCCAAGCCUGGCGGGCCAA GGAA	132	spe-miR168b-5p	AGGCUUGGGCCAGGUGGGG	15-33	gma-miR168b	5	0	19	19	3
spe-MIR7980b-2	UUUAAUUUGCUUUGUAACUCCAUGUGAUACCAU AUCACAAUAUGGUAUCGUGAGAUGGAAUCAGU GUUUGGACAUGCGAUUUUACGCUGGUUUCAUC UAAUGAGAUGUGAUUCCAUAUUCUCGAAGAAAU CAUUAUGAGAAUUCCCUAUCAUAAUUUGA	159	spe-miR7980b-2-5p	GAGAUGGAAUCAGUGUUUGGACAU	52-75	stu-miR7980b-3p	0	0	24	24	1
spe-MIR10216	GGGACACAUGACACAAUCUUAUCCGUCGAUCU GAUAUUUAAUAAAUGUCGAGUCGGUGGAUAAG AUUAUGACACGUGUAUG	81	spe-miR10216-5p	UAUCCGUCGAUCUGAUAUUUA	20-40	eun-miR10216-5p	5	0	21	21	1
spe-MIR6434	UGAUUUUGCAAAACUGUUGAUACGUGACCAAUC AUAAUUCGGUCACGUCAUCAAUGUUUUUUAAAA AAA	69	spe-miR6434-5p	CUGUUGAUACGUGACCAAUCA	14-34	ptc-miR6434	5	0	21	21	1
spe-MIR172-5	UACAGUCGUUGUUUGCGUAUGUAGCAUAAUCA AGAUUCACAUGAAAAGUUGCAAAUUGGUUAUAU AAUUAAUGAAAUUAAUGGCUGGCUACUUGAAAC UCAUGAGAAUCUUGAUGAUGCUGCAUCUGCAA UAAACGACUAUU	142	spe-miR172-5-3p	UGAGAAUCUUGAUGAUGCUGCAU	102-124	aau-miR172	0	0	23	23	1
spe-MIR397b-3	CUUGACAUAAAAUGCAUCUGCUUCAACAACUGU CAUUGUAUGAUUAGCUAUUCUAAAGAAAAGGUC AUCAUUGAGUGCAGCGUUGAUUAUACGAAGCA UGUAUGUCUUU	109	spe-miR397b-3-3p	UCAUUGAGUGCAGCGUUGAUU	68-88	mes-miR397b	1	0	21	21	1
spe-MIR7980b-3	GAAAUGGUAUCACAUCUCAUGAUAUGAAAUCAU GAGAUGUAAUCAGCGUAAAAUCGUAUGUCCAAA CACUGAUUCCAUCUCACAAUACAAUAUCAUGAU AUGAUAUCACAUGGU	114	spe-miR7980b-3-3p	GUCCAAACACUGAUUCCAUCUCAC	60-83	stu-miR7980b-5p	1	0	24	24	1
spe-MIR10538-3	UAUUUUUUAAAAGUUGAUGGCGUCAGAUUGAU AUACGUUACUCACGGUAACGUUUUAGGAGUAAA ACGUUACUCAUAGUAACGUUUUAGGAGUAAAAC GUUACUCAUAGUGACGUUUUAGGAGUAAAACG UUACUGAAAACAACGUUUUAGGAGUAAAACGUU ACUUACAGUAACGUAUAUCAACCUAAUGCUGUU AGUUUUUUAAAAUUA	211	spe-miR10538-3-5p	AGAUUGAUAUACGUUACUCACGGU	25-48	sly-miR10538	1	0	24	24	1
spe-MIR171c-2	AAUACGUGAUAUUGGCACGGCUCAAUUAAAUAA CGAAGUUCUAUUUAUAAAGAAGUGCGCUUUCUA AUUGAACCGCACCAAUAUCUCGUUAG	92	spe-miR171c-2-5p	UAUUGGCACGGCUCAAUUAAA	10-30	csi-miR171c-5p	3	0	21	21	1

			spe-miR171c-2-3p	UAAUUGAACCGCACCAAUAUC	65-85	aqc-miR171c	1	0	21	21	1
spe-MIR852-1	UAGAAUAAUAAGGGAGCUAAUUCCUCAAAAAUUUCCCUCUUCUUGAAAAAAAGGAAAACAAAGUCAAAUAUCUUAUUACCUUUAUUUUCCUUUUCCAGAAGAGGGAAAUUUUUGAGGAUUUGACCCCCUUAUAUUGGU	138	spe-miR852-1-3p	AAAACAAAGUCAAAUAUCUUAU	55-76	aly-miR852-5p	5	0	22	22	1
spe-MIR3700	GGAGACAACUAUGACCGUUAACUUUGGAUGACACACAAGUAGACAGUUAAACUUGCAUAAAAUUAAACAAAUAGACACAUUCGUCCUACAUGUCACCUUACAUGGCAAUUUUUUGUCCUACGUGUAUUAUACCAUGUAGGACACAUGUGCUUACUUGUUCAAUUUUAUACAAGUUUAAAUGUCUACUUGUUCACACCCAAAGUUGAAGGGCAUAGUUGUCCGC	223	spe-miR3700-3p	CACACCCAAAGUUGAAGGGCA	192-212	pab-miR3700	5	0	21	21	2
spe-MIR1533-1	AGGGAGCACCUCUGGACAUUCUUAAACAAGUCAAUGAGAAGCUUUUCUAUUUCCACAUGACAUCUCAACUAAAAGAUCAACUUUCUUCAGCAUGGUCUCAAUGCAUCUACGAUCUUGUUAGAGACUCAAACAACUUUUGCUACCGUCAGGCAUGCUGCCAAAGUGUGUUCAUGACCAAUGUUAUCUUCUAUUUUUUCAUUUUUUCAAAGGAAUACUAAAAUUAAUUAUGUGAAAAUAGAAAAGCUUCUCAUUGACUUGAAUUAAAUAAUGUUAAAGAGGUGCUCCUU	287	spe-miR1533-1-3p	AUACUAAAAUUAAUUAUGU	212-230	gma-miR1533	4	0	19	19	1
spe-MIR160-2	GACAUGAAACUCUAUACAUGCUUAGCUCCUAGAAUGCCAUCUGAAAAGGCCAUCAAUUCUUGGUGGAACAAUGCAAAUGGCAUACAAGGAGCCAGGCAUGUUGUGUUAUCGAUCAC	116	spe-miR160-2-5p	UGCUUAGCUCCUAGAAUGCCA	19-39	vca-miR160-5p	4	0	21	21	1
			spe-miR160-2-3p	UGGCAUACAAGGAGCCAGGCA	78-98	aau-miR160	1	0	21	21	1
spe-MIR7997c-4	GACUAUAUUGCUCGUACUUUUCAAAAAUGUUGUCAGACCUGUAUGUAUGUACUUUUGGACGAUCUGACACACACCUGACAGUACUUUUGAAGAGCUCGAGCAACAUAAAA	110	spe-miR7997c-4-5p	AUAUUGCUCGUACUUUUCAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
spe-MIR530	AUUUUUAUCUGCAUUUGCACCUGCACCUUAGUGAACGAAUUUGUUCGCGUAUGAUUCGUGCAGAAAGGUGUAGGUGUUCAUGCAGACAAAAAU	93	spe-miR530-5p	UCUGCAUUUGCACCUGCACCU	8-28	eun-miR530-5p	0	0	21	21	1
			spe-miR530-3p	AGGUGUAGGUGUUCAUGCAGA	66-86	sly-miR530	0	0	21	21	1
spe-MIR7984b-2	UUUUCCAGAAGUUCAGGAUGAAGCACGUUCCACAUGUAGAACAAAUUUAUCUACACGUUGAAUGUGCUUCAUCCUGAACUUUGGACCU	88	spe-miR7984b-2-3p	AUCCUGAACUUUGGACCU	71-88	stu-miR7984b-5p	4	0	18	24	1
spe-MIR395e	UGUUUGAUCCCCUACUGAAGUGUUUGGAGGAACUCUCGGGUUUACUUAGAAAUUUACACAAAAAGUAGAAAUGCAAGAUAAAUGGAAGAUGAUGAAUUUUCAUUGAUAAUACUUAUAUCUGUAUAUCAAGGUGUUCUCGAGAGUUCCCUUGAACACUUCAUUAAGGAUUAAUUU	174	spe-miR395e-5p	CUGAAGUGUUUGGAGGAACUC	15-35	lus-miR395e	0	0	21	21	1
spe-MIR11082l-1	UUCUAUGACUGCAACCAUCACUUUGUGAGAUAACUAUUAUUUUGAAAUUGAAAAAAGAAAUAGUUAUCUCACAAAGUGAUGGUUGCAGUCAUAUGC	96	spe-miR11082l-1-3p	UCACAAAGUGAUGGUUGCAGU	69-89	lja-miR11082l-3p	5	0	21	21	1
spe-MIR5761b-1	GAUAAAUGUUAGAAUGUUUAUUUAUUGAUUUUAUUAAUAAGAUUUUGAGUCUUCUGCAUUAUGUUGGGGUUUAGAUUUGUUGGUUCGCUCACAUAGUAGGAUAAGUGUGGGUGGCACUCGCGGCUCGUUUUGGGUCGUGACAAUUUUGAUGAUUUGAAGAAAAUAAUUUUCAGAACACAUGGCAAUCAGGUAUUUUUCAGAGAAUGUUAUUAGAUUCAUUAUACAUCAAUAUACAUUCUAAUUUUUUUA	249	spe-miR5761b-1-3p	UUUUGGGUCGUGACAAUUUUG	128-148	gma-miR5761b	4	0	21	21	1
spe-MIR1521b-1	UAAUCCAUAAACUAGAACAUGUAUAUCCUUCAUAUUAAUGGACAUACAUGUGUCAUAAUCUUAUCAACCGACUAGAAAUUUAUUAAUGUCAAAUCGAUGAAUAAGAUUGUGUCAGUUGUCCAUGUUUAGUCUUCUUUAAGAGUGAAGGGCAUAUACUCUAGUUUUUGGACGG	174	spe-miR1521b-1-5p	GACAUACAUGUGUCAUAAUCUUA	41-63	gma-miR1521b	5	0	23	23	1
spe-MIR8007a	ACCUACUCCCUCCGUCCCAUUUUAUGUGACACUUUUCGGAUUUCGAGAUUCAAACAAGUGUAUC	268	spe-miR8007a-5p	AUGUGACACUUUUCGGAUUUCGAG	24-47	stu-miR8007a-	2	0	24	24	1

	UUUGACCAUAAAUUUUUCAUAGAUAUUUUAAAC AUUUUGAAUUAUCACCUAUUGUGACUUAUAGUA CUUUUUACGUAGUUUGUAAAUAUAUAAAUUUCG UUUAAAAAAAUUGAAGAUUUCAUGCGCAAAUUC UCGGUCAAAUUUAAACGGUUUGACUCUCGAAAA AUGAAAAGUGCCACAUAAAUUGGGAUAGAGCAA GUAUUA					5p					
			spe-miR8007a-3p	CGAAAAAUGAAAAGUGCCACAUAA	224-247	stu-miR8007a-3p	0	0	24	24	1
spe-MIR9736-1	UGAUCCACCCACCUAACCCGACCUAUUUAAAAA AUAUGAUAUGACCGAUUUUAUUUUUUCUUUAAU CCUAAAUUAUUCCCUCUUAAACCUUGAAUUAGG AUUAAAGACAAAAUAAAAUGGGUAAUAACAUAU UUUUUAAAUGGGUCGGGUUAGGUGGGUGGAUC A	165	spe-miR9736-1-3p	UUAAAGACAAAAUAAAAUGGG	101-121	gma-miR9736	5	0	21	21	1
spe-MIR399r-1	AGUUAUGUGUGGAUGCAUUACUGGGCUAAUCU UCUUUGGCAAAUAAUUUCACUAUUAUUUGGUG CAAAUUUGGUCAUUUAUUGCCAAAGAAGAUUUG CCCCGUAAAUCAUUCAUACAAUAUUA	123	spe-miR399r-1-3p	UGCCAAAGAAGAUUUGCCCCG	82-102	mtr-miR399r	0	0	21	21	1
spe-MIR399r-2	UUCAAGUUAUGUGUGGAUGCAUUACUGGGCUA AUCUUCUUUGGCAAAUAAUUUCACUAUUAUUUG GUGCAAAUUUGGUCAUUUAUUGCCAAAGAAGAU UUGCCCCGUAAAUCACUCAUACCUUUUA	126	spe-miR399r-2-3p	UGCCAAAGAAGAUUUGCCCCG	86-106	mtr-miR399r	0	0	21	21	1
spe-MIR11027	UAUAAGUAAUUUUUUACUUCUUUUCGGCCUCG UGGAACUGACUUGAAAAAAAAAGUCAACUAGCG UUGGGCCCACAAGAUAGUGUCACAUAGGCCAA AAAGGGGUAGAAAAUUCUUAAU	119	spe-miR11027-3p	GGGUAGAAAAUUCUUAAU	102-119	seu-miR11027	5	0	18	23	2
spe-MIR9475	GGCGGAAGAGUCUAGAGUUGUGGAGAGGUUUA UAAAAAACUCUGGAAGCCUCUAGAUAUUUCAAA AAGACUCUAGAAUAACUUAGAAGCUUUCUUGAA AAGCUUUGGUGAGUCCUAUAAUGUAUAGAGAG UUUUAGAAGAGGACUAGAUAUUUUCUAGGAAAG CCUUAGAAUUCUCUAGGCUAGUCGAGAAUUCU AGAACAUGAACCAAAAUGUAAAUAUUUAGGGAC UUGUGUAGUAAUUUUUAUUUACACUUUAUCCCC UAGGAAGUAGUAUCAAUAGAGGGGCUCUCAUU UAUAAAUCAUCCAACAAGUUGUAAACAAUCUUC CAAG	330	spe-miR9475-5p	CUAUAAUGUAUAGAGAGUUUU	114-134	sly-miR9475-3p	4	0	21	21	1
spe-MIR8008b-2	UUGAAAAUUGCAGAAAAGUGACGUACUAAAGGA CCCUAUCCAUCACUUUUCUGAAAAUUAUUUUUU UGAAAAACCCAGAAAAGCGACAGACUUAAGGAC CCUGUCCGUCGCUUUUCUGGGUUUAUUUGAAU GAAUUAUGCAAAAAAGUGAUGGACAAAACGACC CUGUCCGUCGAUUUUUUCUGCAUUUUUUAC	194	spe-miR8008b-2-5p	AAACCCAGAAAAGCGACAGACUUA	71-94	stu-miR8008b	4	0	24	24	1
spe-MIR11131	UACUUACGUCCAACAAAUGACCUAUUUGUUGCA AUAAAUAGGUCAUUUGUUGAACGAAAACUCAAU CAUUUGCUACUGAUUUACUUACGUUCAACAAAU GACCUAUUUGUUGCAACAAAUAGAUCAUUUGUU GGACGAAAUCU	143	spe-miR11131-3p	CUUACGUUCAACAAAUGACC	84-103	lja-miR11131-3p	4	0	20	20	1
spe-MIR10528	UAAUUCACACGUUGAAUAUAUCUCAUAAUGAAU GCAAUGUCAUAUACCAUCAACACUCGGAAACUC AAAUUGAGGUUAAAUCUCGGAGUGAUGAUGGU AUAUGACCUUGCAAUUCACUAUGAGAUAAGUUC AACGUGUGAAUUG	144	spe-miR10528-5p	AAUGCAAUGUCAUAUACCAUC	31-51	sly-miR10528	0	0	21	21	1
spe-MIR6144	UAAUUCAACAACAAUAAUGGCAACUUCUUCAUC AUGUUCUUUAUCUUCCUCUAAAUCUUCUACCAC UUGUGGUUCUCCACGUGGACAUCGUCGGAUCA AUUCCGAUGUUGUGGGGCCCUUCUCUUUCAUC GGGACCGGUGCCGGAGGAGGUUUGAAGAAGAG UAGAUCCAUAGCUUUUGUUGCAAGAU	188	spe-miR6144-5p	UGGCAACUUCUUCAUCAUGUU	18-38	nta-miR6144	2	0	21	21	1
spe-MIR319j	AGGACCUGCAACCUCGACAACCCCGACCUUUU CAUCUCCCUACAAGGCAAGUAGACGUUGUAUCA AACUGUUUCAAAUUCCAAUAAAAUUUAAUACAA UGCCCACUUGCCCUGCAGGGAGAUGAAAAGCU CGGGGUUCUCCAGGUUUCAAGUCCU	155	spe-miR319j-3p	CUUGCCCUGCAGGGAGAUGA	105-124	pab-miR319j	5	0	20	20	1

spe-MIR8175-1	AAUCAAGAAAAUAUUAACUAAACUAUAGUGAUA AGUUCAAGUUAAUCUAAAAGCUAUGAUCCCCGG CAACGGCGCCAAAAUUUAUUACGCUCAAACUUA CUUCUCAAAUAAGAAGUAAAGCGGUCGUGUCAA GUAAAUAACCCAACUAGUAAGGUUGGGAUCGU UCCCACGAGGAAAAUAGUCUAGACUUAACUUCA ACUUGUUAUUACUAUUGUUUGGUUAAUGACUU CCUUGGAA	237	spe-miR8175-1-5p	GAUCCCCGGCAACGGCGCCA	58-77	ath-miR8175	0	0	20	20	1
spe-MIR10224-1	AAAUAAUGCAUGCAUAAGCUUUGUGUAUUAGUA GUACCUUAUUUGGUACACUUCUCAUGCCAUGU AUAACUGAUGCUUGCUGAUGCAAGCAUCAAUUA UACAUUCUAUUGUGUAUUGUGGAGUGUAUAGC UAAUAUAUGAAAAUCCCUGGUAUUAGUUAUACA AGGCGGUUGAUGAAUGCAUUAGCA	187	spe-miR10224-1-3p	UGAUGAAUGCAUUAGCA	171-187	eun-miR10224-3p	4	0	17	21	3
spe-MIR10224-2	AAAUAAUGCAUGCAUAAGCUUUGUGUAUUAGUA GUACCUUAUUUGGUACACUUCUCAUGCCAUGU AUAACUGAUGCUUGCUGAUGCAAGCAUCAAUUA UACAUUCUAUUGUGUAUUGAGGAGUGUAUAGC UAAUAUAUGAAAAUCCCUGGUAUUAGUUAUACA AGGCGGUUGAUGAAUGCAUUAGCA	187	spe-miR10224-2-3p	UGAUGAAUGCAUUAGCA	171-187	eun-miR10224-3p	4	0	17	21	3
spe-MIR10189-1	CCGGAUAGAGGCAGAAGGGUCUAGAGUUGUGG AGAGGUUUACGAAAAACUCUAGAACCUUCUAGA UCAAUCAAG	74	spe-miR10189-1-3p	AAAAACUCUAGAACCUUCUAG	44-64	gma-miR10189	5	0	21	21	1
spe-MIR1106-1	AGGACCUUUUAACCCCUGCACUCUUUAGUAGU GUAUUUUAAAGGUAUAUAUGUGUUCAUAUGGA CACUUACUAUUUAUAAUGAUGCGAUGUUUAUGA UGUCGACGUGGGUACAUAUAUACCCUUAAAAUA CAUUAUUAAAUAGUGCAACGGGCGGGUAAAAAG UUUU	167	spe-miR1106-1-5p	UUUAAAGGUAUAUAUGUGUUC	37-57	smo-miR1106	5	0	21	21	1
spe-MIR395a-2	AGAAUGAUUCAUUUCUAUAUAUAUCAAGGUAUU CUCGAGAGUACCCUUUGACCACUUCAUGAGGG AUUAAUGUUUUUAUUUUUGAUGCUCUGUUGAA GUGUUUGGGGGAACUCUCGGGUUCAGUUUGAA GUAUACACAAACUAGUAAACAUGCA	154	spe-miR395a-2-3p	UGAAGUGUUUGGGGGAACUCU	94-114	aof-miR395a	0	0	21	21	1
spe-MIR159a	AAAUGAACUUAAUGGGCUGAAUCUGAAUGAUUC AGAUUCAGACUUAAAAAUCAAACGUACUUAAUA GGCUGAAUCUAAAUGAUUAAGAUUUAUACCUCC CUUAAGUGCAAAC	112	spe-miR159a-3p	UACCUCCCUUAAGUGCAAAC	93-112	aly-miR159a-5p	5	0	20	21	2
spe-MIR169r-7	UUUGGUCUAUAAGGUUUGCAUGAAGAUGAAGA GAGUGAAGUUGCAGCCAAGGAUGACUUGCCGG ACCAAAAGUUGUGACCAUUUUCUAGUUCCGGC AAGUUGUUUUUGGCUAUAAGUUUGCUCUCUUC UUCUCAUGUUAUCCUCGUUAGACCUUU	155	spe-miR169r-7-5p	CAGCCAAGGAUGACUUGCCGG	44-64	csi-miR169r-5p	0	0	21	21	1
spe-MIR6440a	CUACAAGAUACCAUAGGAAAUAUUAUUGAAUUA UCUUUCAACGUCGCCGAGUUUGAUCAAUUUCG AGUUUGUACGAGGGAGAUAUGCUUUUUUGAAG UUGGGAUGUCUAGAUAAAGAAAGUCAAAACCGG AUUUUAGAAGGGAAUUGUGGUCUUUUCACAAC CCAAUUAAUUAAAUUUCUUUGUGGUAAUUUUGA UG	197	spe-miR6440a-5p	GAGUUUGAUCAAUUUCGAGUU	49-69	ptc-miR6440a	1	0	21	21	1
spe-MIR444b	UUCCUCUUUCAUGAAAAGAUGCGACUUUUAUGA AAAGUUGCAAGUUUAAUGAAGAAUCGCGACUUC UUUCAAAAGUUGUGACUUUUAUGAAAAAUUGUG AUUUCAAUGAAGAGUUGUGACUUUAUGAAAAGU UGUGACUUUAAUGAAUAGUUGUGACUACUUUC AAAAUUUGUGACUUUAAUGAAAAGUUACGACUU UAAUGAAAAGUUGCGACUUUGAUGAAAAGGUU GUGAACUUUACGAAGGGUUGCAACUUUUUUCA AAUAGUUG	269	spe-miR444b-5p	UUGUGACUUUAUGAAAAGUUG	114-134	ssp-miR444b-1	5	0	21	21	1
spe-MIR6287	GAAUGUAUGUUUUAGGAUUUGUGGUAUAUGAG GUGUCUUUUGAGUAAGAAACUUAAGACUUGGA AAUUUUGGUCGGACAUUUUGUAAUAGUGACUU UUCUAUAUAAUUUAGAAAAUUUCUUGAUAGGAG UGGGUUUACGAUAUCCUCAUUCAUAGAAACAUA ACAUAUAAGCAGUUAAACACAUAUAUAUCACGU CCUAACACAUACAGAG	211	spe-miR6287-5p	UAAGACUUGGAAAUUUUGGUC	54-74	ppe-miR6287	5	0	21	21	2

spe-MIR482	GUCAAAAUGGGUCAGCCCAACUCAACCCAAUCC UAACGGGCUAGAGAGUUAAAUGGGUUGGGACG GGCUGAUCCUUUUAAU UAAAAUCUCAAAUCAUGAUAUAGAAUUCUCAUA	81	spe-miR482-5p	UCAGCCCAACUCAACCCAAUCC	12-33	mes-miR482	5	0	22	22	1
spe-MIR7980b-4	UCAUGAUUUUUGGAGAAAAUGGUAUUCCAUCU CAUGACAUGAAACAUGAGAUGGAAUCAACGUGA AAUUGUAUGUCCAAACACUGAUUCCAUCUCAGG AUUCUGUAUCUUGAUAUGAUAUUGCA	157	spe-miR7980b-4-3p	GUCCAAACACUGAUUCCAUCUCAG	107-130	stu-miR7980b-5p	1	0	24	24	1
spe-MIR1509b	AGGUAAUUAUUAUAUGAAUGGACAAAACUUACU CGCAUCGAGUGUUUACACCAAGUCAAUACAUGC AUGUCCUGUGUUUAAAUGUAUUAUUCAUUUUAC UCAAGUAAAUCACAUAUUACUGGAGAUUGCAUU UGCUUGGUGUAAAAACUCGGUGCUUAUAAAUU UUUUUCCUAUAUGAAUUGUUAACA	188	spe-miR1509b-3p	UUACUCAAGUAAAUCACAUAU	96-116	gma-miR1509b	5	0	21	21	1
spe-MIR5014a-3	ACUUUGAACUUGGCUUCAAAUUUUAAUUUUGAC CUCCAACUUUCAUAAUACACAAACAGACACUUA ACUAUCCAACUUUUAAAUAACUAAACACAUGAA UCCUACAUGGAACAAUACACGUAGGACACCAUG UAGGACAAUAAAUGACAUGUAGGAUAAUAUGUG GGACAUGUGUGUCGAUUUGUUCAACUUUAUAC AAGUUUAAGUGUCUAUUUGUGUAUAUCCAAAGU UAAAGGCAUAUAUGUAAUUUGAAGCUAAAUUAA AGG	266	spe-miR5014a-3-3p	UUAUACAAGUUUAAGUGUCUA	192-212	ath-miR5014a-3p	5	0	21	21	1
spe-MIR168	UUUCUCAUUCGCUUGGUGCAGGUCGGGACCUA CCUCGCCGGCAACAAUGGCGGUGGCUGACGGC GACGGCAGCGUACCGGUAAAAAAAAAUCUUAUU UUUACAUGUUGUUGCGUAGUUUGGGUCCCGCC UUGCAUCAACUGAAUAGGAG	149	spe-miR168-5p	UCGCUUGGUGCAGGUCGGGACC	9-30	lja-miR168-5p	1	0	22	22	1
			spe-miR168-3p	UCCCGCCUUGCAUCAACUGAAU	123-144	lja-miR168-3p	0	0	22	22	1
spe-MIR398-2	GUAGGGCAACUUGAGAUCACAUGUUGUCAUUU UUUUCUUUUUGGUUUGAUUUGAUGAAUCAGUA UCUCAACAUGUGUUCUCAGGUCGCCCCUG	93	spe-miR398-2-5p	AGGGCAACUUGAGAUCACAUG	3-23	hbr-miR398	4	0	21	21	2
			spe-miR398-2-3p	UGUGUUCUCAGGUCGCCCCUG	73-93	aof-miR398	0	0	21	21	1
spe-MIR414	UUCAUUACAAAGUUCUAUCGUCCUGAUCCUCCU UCUCCUUUCAUGCCUCCUCUUCUCUAGUUAAA UCUUCUUAUCCUACUUACUAACAAUCUAGAGCU UCUAAAAUCGUUAGCAGGAUGGAAAAAUUUAAC UAAAGAAAGGAAUCCAUGAAGGAAGAACGGGGA UUUGGAUUAGAGAACUUUGUAAUUUU	190	spe-miR414-5p	UCGUCCUGAUCCUCCUUCUCC	18-38	ppt-miR414	5	0	21	21	1
spe-MIR10538-4	UUUUAAAAGUUGAUGGCGUCAGAUUGAUAUAC GUUACUCACAGUAACAUUUUACUCCUAAGACGU UACUCAUAGUAACGUUUUAGGAGUAAAACGUUA CUGAAAAUAGCGUUUUAGGAGUAAAACGUUACU UACAGUAACGUAUAUCAACCUAAUGCUGUUAGU UUUUACAA	172	spe-miR10538-4-5p	AGAUUGAUAUACGUUACUCACAGU	21-44	sly-miR10538	0	0	24	24	1
spe-MIR167c-2	GAUCGUGAACCACUAGCAGCUGAAGCUGCCAG CAUGAUCUAAACUUUUCUAUUGCUCCGUACGA GGAAAGAUCAGAUCAUGUGGCAGCAUCACCUG UUGAUGGUUUCGCGGAA	113	spe-miR167c-2-5p	UGAAGCUGCCAGCAUGAUCUA	21-41	ata-miR167c-5p	0	0	21	21	1
			spe-miR167c-2-3p	AUCAGAUCAUGUGGCAGCAUCACC	71-94	eun-miR167c-3p	1	0	24	24	1
spe-MIR5183	UUUUAAAAAUUAACUUAGGGGAUAAAUUAAGAA AAAAAUGAAAAAUAUUAUUUUUAAUAAAUUAACG CGCUCAGGAAAGUGAAUUACACGUUUUUUGCC AUGUCAGCAUUUUGUGUCUAAUAGGAAUGACU UUUGAACAAAUAAAGUGUUCAAUUGGCACAAGG AUUAGUUGAGGUGUCUAAAUGAAUUAUGCGGA CAACUUUGAGUGGCUGCAGAUAACUUAAGCCU UAAGUUAAUGAUUAGAC	245	spe-miR5183-3p	UAUGCGGACAACUUUGAGUGG	189-209	bdi-miR5183	5	0	21	21	1
spe-MIR7757	UUUGGUCUUGCCUCAAUGCUCAUGAAUUCUAG UGUAGUUUUAUAUGGGCUAUUGGAUGAUGUAA UAAUUGUAUUGAAUUGAUGUGUAGGCCAUCUU AUAUUGAUAAUUUUAUAUUUAAUUGACCUAGAU UCAUUGAGUAUUAUGAUUUUUGUAUUGAAUUG	189	spe-miR7757-3p	UGAUAAUUUUAUAUUUAAUUG	101-121	bdi-miR7757-3p-2	5	0	21	21	2

	AUGAUCAUGACCAUGGGUAAGAGCCUUU										
spe-MIR5139a	ACCAAGAGCUCAAAUAGGAAUGAAUUUUGGCUCUGAUACCAUGUAAAUAUAUGACUUGAGCUUAACUCAACCCCAAAAAGCUAGUUUUUGGAAUUGAGUUAGGCCCAUGUGUCAUAUCUUUACAAGGUGAUCAGAAAUCCAAUCUCCAACCAAUGUGAGACUUUUACC	168	spe-miR5139a-5p	GAAUUUUGGCUCUGAUACCA	22-41	aof-miR5139a	3	0	20	20	1
spe-MIR10542-1	AAAAUAUACCUUGAACUUUGAUAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUGUAAAAUAAUAAGAAGUGAUAAAUAUAAAUUUAAAACUAAUCUUUUAACUUCCGUUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGGUAUAUGUGAGCCAUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGUAUAUCAGCUCCAAAUAACAAAGUUAAGGAGUAUAUCAG	248	spe-miR10542-1-5p	UAGAAGAAUCAUAUAUACCCCUA	22-44	sly-miR10542	0	0	23	23	1
spe-MIR8006-3	CCCUCCGUCAUACUUUUAGGACAGUGGUAAACAUAUAUGUCCUUCACUCUACAAAAGACUAAAUGGGGACACGUGACACAAUCUUAUCCAUCGAUAAUAUUUAAUAAAUGUCUGAUUAGUCGAUAAGAUUAUGUCAUGUAUACGUCCGUUAUCAUAAAAGGUAUAUAUGCUCUAGUUUUUGGACGGCAUGAGCACCAAUGUCUCAAAAGUAUGACAGAAGA	221	spe-miR8006-3-3p	UAGUUUUUGGACGGCAUGAGCACC	173-196	stu-miR8006-5p	3	0	24	24	1
spe-MIR6299-1	GUAUAAUCAUAAGUGUAUAAGACGGAGAUAUAUGUAUUUGCAUGUGUAUAUACAAUUUUCUCUCGCUUUAUACCAUUAGAAACACAAUUUAUACAAUUCUAUGGUAUAAAACGAGAGAGGCGAGCGAAGAAAGCAAGCGAGAGAGGGAGAGUGGCGAGCAAGAAUAUGAGGGAGAGAGGGACUGUUAAAUAGUUUGCUAUUGAAACACAAAUAAAUCAAACGAUAGCUACUAUAUUUAUUUUAUAUUAUUAAUUUGUCAUCCUAUACAAUUAUCCCUUUUUAAAAAUCUAUAUAAUUAGGU	301	spe-miR6299-1-3p	AUUUUAUAUUAUUAAUUUGUCA	238-259	gma-miR6299	3	0	22	22	1
spe-MIR5385	CCUCCACUUCUCUUUGAAGGAAAGAGAUGGCCUCGUUGAGCUUGAGUUCGAGGGUGGACAAACCCUCUUUUUGAACGUCCUCAAGCUCAACAAGGUUGUUCUUCACCUCGUCCAGCCCUUCAAUGGCUACGGAUUCGAGGGAACUAAAGUUGUUUUCAACAACAACAUCCUCCUGUUUAAGGCCAACAACCCCACCUCAACUCCGAUGAUUCUCUCAUCGAGUUGGCUGUUGUCCGCACCUUCCUCCUCUUCAACAGCAGCUCUACCACCAAGAGAAGGGUUA	284	spe-miR5385-3p	GCCAACAACCCCACCUCAACUC	183-204	sbi-miR5385	5	0	22	22	2
spe-MIR477k	GGCUCUCUCACUUUAUAUACAAACACAAAUGUAUAAUGUGUUUGUAUAAAGUGAGAGAAACUGUAUAUAUACAUCUCUUUUCGUCUGCCUCUCCCCCCAGAGAAUCUCGCUCGCCUCUCUCACUCACCUCUCUCACUUUAUACAAACACAAAUGUAUUAUCUCUGUGUUUGUAUAAAACGAGAGAAAA	188	spe-miR477k-3p	CCUCUCCCCCCAGAGAAUCUC	88-108	mes-miR477k	5	0	21	21	2
spe-MIR5303-6	ACCUAAGUUGCUCGGACUCUCCAAAAUUGUUGCCCCACCCCCGUUGGAUCCUCCAAAAAUGCACUACUUUUGGAGGAUCUGACACACACAUGUCGAUAUCUUUGAAGAGUUCGAGCAACAUAACU	125	spe-miR5303-6-3p	UCUUUGAAGAGUUCGAGCAAC	99-119	sly-miR5303	1	0	21	21	1
spe-MIR7997c-5	AUCAAGGCUAUGUUGCUCGGACUCUUCAGAAACGUCGACGGGUGCGUGUCGGAUCCUCCAAAAGUAAAGCAUUUUUGGAAGAUCCGACACGGGUGUGGUAGCAAUUUUGGAGAGUCCGAGCAACUUAGCCUUAAG	135	spe-miR7997c-5-5p	AUGUUGCUCGGACUCUUCAGAAAC	10-33	stu-miR7997c	3	0	24	24	1
spe-MIR8001b-2	GCAUUCAACAGUAAAAUUCAUAGUCAGUGUUACUAAUAUAGAGGAUUACAAAAGUGGCUUAUUAUGAAUGAAAUAUAAUUGAAAGGAACAGGCUAAUUACUAGACGCGUGAACACUAUAAGAAGAGGGUGAUCUAUAUGGAGAUUUUCCUGGGGGUUAAGUAAGAAAAUUUGCAGGAAAAUUUCGUGUGGAUUUUCAUACUAAUUCCUAGGAAAAUCCCAUGUAAUUCACAGUUUGAAUGCAUUAAAAAGGGACAAAUUUUAGCGGAUGGUGCUGCUACGUGGAAAGACAGAA	341	spe-miR8001b-2-3p	GGAUUUUCAUACUAAUUCCUAGGA	189-212	stu-miR8001b-3p	1	0	24	24	1

spe-MIR5167b	AACAGAAAACAGAAAACAAGCACUACUCAGAAUUUUUACUUAGAAUCUGUCCAGAGUUGUUGAGUUAUAUUUUAUGAUUAGGUUGUUGUAUCCUAGAUGGGACAAGUCAAGAGGACUACUGUUGGAUCGGUGAAAAAUAUUUGUUGCAGUGAGUCUGAAUCUCCUUAAAUAGAGCGAGAUAUUCAUGCCUCAGCCUGAAGAGAUUUUAUAUCUUCAUUUUAUUUUCAAUUGUAAUAUUCUAUUUUAUUAUCUCGUAAUUUUUCACUAAAAGAUCUUAACAAGUCUGUUA	241	spe-miR5167b-3p	UCUGAAUCUCCUUAAAUAGAGC	106-127	bdi-miR5167b-3p	5	0	22	22	1
spe-MIR396a-1	AAGCUUGCCAUCUUUUCCCACAGCUUUCUUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAAAUUAUCAAUUUAGAGAUCAAAAUUUAGCAAGAAGAAGUUCAAGAAAGCUGUGGAAAAGCAUGACUAGGAC	131	spe-miR396a-1-5p	CACAGCUUUCUUGGACUUUCA	19-39	hbr-miR396a	2	0	21	21	1
			spe-miR396a-1-3p	GUUCAAGAAAGCUGUGGAAAA	98-118	csi-miR396a-3p	1	0	21	21	2
spe-MIR171f-2	UAGAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAGUUUACGUUUUAUUUUAGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCAUUUCUUUU	100	spe-miR171f-2-5p	CGAUGUUGGUGAGGUUCAAUC	9-29	fve-miR171f-5p	0	0	21	21	1
			spe-miR171f-2-3p	AGAUUGAGCCGCGCCAAUAUC	71-91	mes-miR171f	0	0	21	21	1
spe-MIR5303-7	UAGCUAAGUUACGUGGACUCUUCAAUUUUGAUGUCGUACUCAUGUCUGAUUCACUACUUUUUGGAGAGUCUGACAUGCAUCCAUUGACAUUUUUUGAAGAGAUCGAGCAACAUAGGUU	118	spe-miR5303-7-3p	UUUUUGAAGAGAUCGAGCAAC	91-111	sly-miR5303	1	0	21	21	1
spe-MIR156i-1	UUGUAAAAAGAUAUAUAGGACUACUAGACAACUCAAGUUUUAACACUCUAACUUGUCUACCAGUUGAUUCAGUCCCCUUUGGUUAGGGACUGUCUUCAUUGGUUAUGGUGAUCAACUGGUAGGCAAGUUAGAGUUUUUAAGCUUGAGCUGUCUAGUAGUCUUAUAUACCGUUUUAACG	178	spe-miR156i-1-5p	UUGUAAAAAGAUAUAUAGGAC	1-21	csi-miR156i-5p	5	0	21	21	1
spe-MIR9473-1	CGGAAAAUGUGAGUGAACUAGCAGAUAUUGGCUGUAAACCUAAACUCGUUUCACACCAACCUAAACUCGUUUCACACCACUAGUCAUCAUGUAAUGUCAUUUACUAGAAGAAGAGACUAGUGGAGUAAAACGAGUUCAGAUUUACAGCCAAUAUUGUUUUGCUUGCACGCAUUUUGGU	178	spe-miR9473-1-5p	UGGCUGUAAACCUAAACUCGU	29-49	sly-miR9473-5p	1	0	21	21	1
			spe-miR9473-1-3p	AAACGAGUUCAGAUUUACAGC	128-148	sly-miR9473-3p	0	0	21	21	1
spe-MIR476b	CUACACAGAAGAACAACAAUGUUUUUAAAACUAAACGUUUGUAAGUUUUAUACAUUGAAGUGCUACCAUGAACCUGUCCUCUAAUUCAUGGUGGCACUUCAAUGUAUAAACUUCCAAACGUUUAGUUUUAAAAACAUUGUUGUUCUUCUUUGCGU	154	spe-miR476b-3p	UUGUUGUUCUUCUUUGCGU	136-154	ptc-miR476b	5	0	19	21	1
spe-MIR8019-2	UUGUACUCCCUCCGUUUCAAAAAGAUUGACCUAGUUUGACUUGAACGGAGUUUAAGAAAAGAAAGAAGAGAUUUUUUAAUCUUGUGGUUCUAAUUUAAAGUUAUGUCAAAUGUACCAAAAUACCCUUUAAUCUUGUGGUCUUAAACAUGUCACGUGGAAAGUUAAAGUUAAAGUGUUGCCAAAAAAGGAAAGAAGUCAUUCUUUUUGAAACAGACUAAAAAGAAAAUAGGGUCAUUCUUUUUUAAACGGAGGGAGUAAUU	258	spe-miR8019-2-5p	AAAAGAUUGACCUAGUUUGACUUG	20-43	stu-miR8019-3p	2	0	24	24	1
			spe-miR8019-2-3p	AAGGAAAGAAGUCAUUCUUUUUG	183-205	stu-miR8019-5p	5	0	23	23	1
spe-MIR7983-3	AGCUUUAGCGGCAAUUAAUUAGCAAUUGCUGCUAUGUAUAUUUUUAGCGGCAAUUAACAUUUUUUAUAUGUCCCUAUAAAAGCUUUAGCGACAUUGAAUCUAAUGACACUUUAACUAAUGCCGGUAAAAAAGGGUGAGAUAUUGUUGACAGAAGAUAGAGAGC	131	spe-miR7983-3-3p	UAAAAGCUUUAGCGACAUUGAAUC	77-100	stu-miR7983-5p	4	0	24	24	1
spe-MIR156b-10	ACAAAUAAUGAGGUGCUAAUUGGAAGCUGCACCUUAAUUCUUUGUGCUCUCUAUUCUUCUGUCAUCAUCUUCAGUC	108	spe-miR156b-10-5p	UUGACAGAAGAUAGAGAGCAC	14-34	aof-miR156b	0	0	21	21	1
			spe-miR156b-10-3p	GCUCUCUAUUCUUCUGUCAUC	78-98	vca-miR156b-3p	1	0	21	21	1

spe-MIR2873c	AUACAAAUACAAAUGUAUAAAAUGUAUUUGAGU UUGCAUAAAGCUAGAGAAAAUUGUAUAUAUACA UAUAUUUUCGUUUCAUUCUCUCCCAUCUCCCA GAUAUCGCUCGCCACUCUCCCAUUUCUCGCUC GCUCACUCGCCUCUAUCACUUUAUACAAAAACA CAAAUGUAUAAUAUGUGUUUGUGUUUGUGUUU GUAUAAAGCGAGAGAAAAUUGUAUAUAUACAUA UAUUUUCGUCCCUCUCUCCCAGAUCUCGCUCG CUCGUCUUUCUCACUUUAUACAAACACAAAUAU AUACAUUAUGUUUGUAUUUGUAU	316	spe-miR2873c-5p	AAAAUGUAUUUGAGUUUGCAU	19-39	osa-miR2873c	5	0	21	21	2
spe-MIR10538-5	UUAAAAGCUGACGGCGUUAGAUUGAUAUACGU UACUCACAGUAUAAUGUUACUUACAGUAACAUA UAUCAACCUAACGUUGUUAGUUUAAA	91	spe-miR10538-5-5p	AGAUUGAUAUACGUUACUCACAGU	19-42	sly-miR10538	0	0	24	24	1
spe-MIR1518	GACGGUGUAUAUUUCUACUUAUAUAAUAUCCUA UUUGAAGGACAUGAAUAUCAGUUGAUGACAAAU CAUCACUACAUACGUUUAAUACAUAAACAUGCU ACUUAACUUAACUUCAACUUAUAUUUUGCGUCU UACAAAUAUAUAGACAUUCACAUCCUAUCUGGC AUUCUACGUGACCAUUCUAUGUGUCAUAGACAU AUUAUGUCACGUAGAACGAUAUAUAUUCUACUU AUUUAAUAUCCUAUUUGAAGGACAUGAAUAUCA GUUGACGACAAAUCGUGUAUUUGUAGGAGGAA CAAGAGGAUAUUGUAAAGAGAAGAUCAUCACCA AA	331	spe-miR1518-3p	GAUAUUGUAAAGAGAAGAUCA	303-323	gma-miR1518	5	0	21	21	3
spe-MIR482e	GUUGAAAGGGAUGAGAGUAUUGGGAAGUUGUU GGUUGUGGGUGGGGUGGAAAGAUUUGAUAAAU CUAAUUUUUUUUUCUAAUUGAAAAAAAAAAUGG AAAAGAGAUUAAAUCUUUCCUACUCCUCCCAUA CCCAUGACUUCCACUAGCUUCUCCCUUUCUUC	162	spe-miR482e-5p	UGUGGGUGGGGUGGAAAGAUU	36-56	sly-miR482e-5p	0	0	21	21	1
			spe-miR482e-3p	UCUUUCCUACUCCUCCCAUACC	111-132	sly-miR482e-3p	0	0	22	22	1
spe-MIR7981-6	GUCUAUAAUAUUAUAGGGAUAAGGUGUAAAUAU CCUCUAGACUAUGACUCAAACUUAGAGACACAC CUUAACUAUACUAAGGUUCUAUUACCCCCGAAC CAAUUUGUUUUGUUAUUUUGUAGACCUUUUUG GUUUUCACGUGGCAUCAAAAUAUCUCUCACGC GCCUCAACUGCGUAAGGAGAUAAUAUGACUUUA AUUUAAUUAAGAUAUCUCAGAUUUCGAUCAUAG UCUAAGAGGUACUUAUAUCUUAUCCCUAAUAUU AUAUAU	268	spe-miR7981-6-5p	CUUAACUAUACUAAGGUUCUAUUA	67-90	stu-miR7981-5p	5	0	24	24	2
			spe-miR7981-6-3p	AUAUGACUUUAAUUUAAUUAAGAU	186-209	stu-miR7981-3p	4	0	24	24	1
spe-MIR8006-4	UGUAUAUCCUCCAUCAUACUUUAGGGAUAUUAG UGCUUCUACCGUCCAAAAAUUAUACACUUUAUA CUAACGAACAUAUACGUGUCAUAAUUUUAUCCA UUGAUCCGACAUCGGAUCGGUAGAUAAAAUUG UGUCACGUGUUCCUAUUCAGUCUUCUGUUAGA CUGAAGGGCAUAUAUGCUCUAGUUUUUGGACG ACAUGAACACCAAUGUCCAUAAAGUAUGACGAA GGGUAUCUG	237	spe-miR8006-4-3p	UAGUUUUUGGACGACAUGAACACC	183-206	stu-miR8006-5p	3	0	24	24	1
spe-MIR2611	AAACCACGGUAUAUCAUGAUCUGACCUUGAUAG UUGCAUUUAGGAAUAUUCAGUUAUGAACCAAAU AUAGUAUCCUUGAAUAAUUGGAUACCCUCAUCC CCUCUUGACAACACUAAAGGCCCGCUUGGCCA UGAUUUCCCAAAUAAUAUUCGGGAAAAAAAUUG GCAAAUAAUGUUUGUCCAUAUAAUUUGUCAUUA UUUGAUAAAUUUUUUGGCAAAUAUCCCAAAUUC UCCAAUACUAGUUUUUUCUAGUAUUGAGGUCAA AUCUCAUUACUUGGGAU	280	spe-miR2611-3p	AAUUUGUCAUUAUUUGAUAAA	186-206	mtr-miR2611	4	0	21	21	2
spe-MIR162-2	GUUGGGUGAGAACACUGGAGGCAGCGGUUCAU CGAUCUGUUCCCUGAAAAGCGAUAAAUACAGCA ACAGGAAGCGAUCGAUAAACCUCUGCAUCCAGU GCUUAACCCGCC	110	spe-miR162-2-5p	UGGAGGCAGCGGUUCAUCGAUC	16-37	csi-miR162-5p	0	0	22	22	1
			spe-miR162-2-3p	UCGAUAAACCUCUGCAUCCAG	77-97	fve-miR162-3p	0	0	21	21	1

spe-MIR8126	UUUCCAUUAAGAUCAAGACGUCUGAAUCUGAAUAAACAUCUGAAUAUUAAGAUGUGCAUUGAGAUCAAGAUGUGUAAAUCUGAAUAAACAUCUAAAUAUUAAGAUGUUGUCUCUGAAUCUGAACACUGAAUUAUUGGGAC	140	spe-miR8126-3p	UCUGAAUCUGAACACUGAAUU	112-132	ppe-miR8126-5p	5	0	21	21	1
spe-MIR171b-3	UUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUACGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAUUUUCAUUCCAUUU	127	spe-miR171b-3-3p	UUGAGCCGCGCCAAUAUCACU	88-108	aof-miR171b	0	0	21	21	1
spe-MIR7992-3	UACUUUGAGAGCGCACAUCGAGACACCUCAACUUGGUAUCAAAUGAACACUAAACACUUCAACUAGACCCCACUGUGUUUCAUGGACACCCUGCGUUGACAUGGCACAUAAAUUUUGGAGGUGUCUAGAUGAUCAUAUUUGUAAGUUGGAGUAUUCAUCCGAUACAGUGGAGACAAGUUGAGGUGUCUAGAUGUGCAUUCUGAAAAUU	208	spe-miR7992-3-5p	UUUGAGAGCGCACAUCGAGACACC	4-27	stu-miR7992-5p	5	0	24	24	1
			spe-miR7992-3-3p	UGUCUAGAUGUGCAUUCUGAAAA	184-206	stu-miR7992-3p	5	0	23	23	1
spe-MIR10538-6	CGUAUUUCACGGUAACGUUUUAGGGUAUAUUUUUUUAAAAAGAAACUAACAGCAUUAGGUUGAUAUACGUUACUGUAAGUAACGUUUUACUCCUAAAACGUUAUUUUCAGGAACGUUUUACUCCUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAUUAACUUUUAAAAAAUAAAAUAUAUCCUAAAACGUUACUGUGGAAUACG	213	spe-miR10538-6-5p	AGGUUGAUAUACGUUACUGUAAGU	57-80	sly-miR10538	4	0	24	24	1
spe-MIR398-3	CAGAGGAGUGUGCCUAAGAACACAGGUGUAUUUUGGUCUUCUCCUGUUUUGGACACAAAGUAUGCUUGUGUUCUCAGGUCACCCCUUUG	89	spe-miR398-3-5p	GAGUGUGCCUAAGAACACAGGU	6-27	lja-miR398-5p	4	0	22	22	1
			spe-miR398-3-3p	UUGUGUUCUCAGGUCACCCCU	66-86	lja-miR398-3p	0	0	21	21	1
spe-MIR2608-2	UAUAUGUAAGUAAGAUUAUAUAUAUGAAAUAAAAGUUUGUUUAUAUAUCAAUAUUCUUCAAACUUGAUAAGUAGUUCAAAGUGGAAGUUGCGAUUUCCAGCCUUUAGGAGGAAUAGCAAGGAAAGUAGCCGUAAAGAGUGAAGAAGGCGAAAAAAGCUAUUCAUGGCCGAAGAGGAGAAAUGCUGAGGCAUUGAUAGGACUAAUUAUCAACUAGAGGAAGAAGGUAUAAAAAACUACAUUUUAUUGCAUAUAUUAUAAUCUUAUAUACAUGUU	273	spe-miR2608-2-5p	UUUGUUUAUAUAUCAAUAUUCU	36-57	mtr-miR2608	5	0	22	22	2
spe-MIR5303f-5	AAUCUAUGUUGCUCGGACUCUUCAAAAAUGUCAACGGGUGCGUGUUGGAUUCUCCAAAAGUAGGGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCGAAGCAAGGAGUCCGCGCAACUUAGCUC	126	spe-miR5303f-5-3p	AUUUUUGGAGAAUCUGACACGGGU	67-90	stu-miR5303f	0	0	24	24	1
spe-MIR11891-1	GUUAUACAUGCAAAAUUGAGCAGAUUUGUCCUAUAUUAGUACUUUAGUUCACUUAUGCCCUUACCGUCAAAUACUUGGUCCAAAUACUAUGCGCAAUUGAGCAGAAUAAGGGUGUAUUUGGGCCAAGUAUUUGAUGCUAAGGGCUUAAGUAAAUUGAAGUAUAAACGGAGGAAAAAUACGCUCAAUUUCACAUAGUAUGAG	201	spe-miR11891-1-3p	AGUAAAUUGAAGUAUAAACG	148-167	mes-miR11891	5	0	20	20	3
spe-MIR159	UUCCAAUUGAUCAAUCAUCUCGAGGCAGGAAAGAUUGAGACUAUACCAUAGACUGAAUUAUUGUUUUGAGAAUGAUAAUAAUUCAGUUUAUAGGAUAGUCUCAAUCUUUCUUGCCUCCAAAGACUGAAUUAUUAUUGUUU	140	spe-miR159-3p	AAUCUUUCUUGCCUCCAAAGA	103-123	vca-miR159-5p	5	0	21	21	2
spe-MIR10211a	UAUCUUCACAAUAUGGAGCUUCGAGUGAAGAACAGGAAGCCACUCGCUUGUUCUUCUCAUAAUGCUCCAGACAUUUGAAGCCU	83	spe-miR10211a-3p	CUCCAGACAUUUGAAGCCU	65-83	eun-miR10211a-3p	5	0	19	21	2
spe-MIR8051-2	AACCAGGUCAUAUAAUAAAUCACACAAACAGAUAUAUAAUAGUUGUUCUAUUCUUAGUUCUCUCCAAUUGCAAUGGCCUCUUCAAAAUAGUUUAUAUUUCACAUUAUAAAAAAAAAUUGGGGUGGAGGGAGAAUUAGAGGGGGGGUUAGAUUACAGUUUUGGGAAUUGAAUCCUCACCAACAAGGUGGGAGUUCAAUUGGCCUACCGACUAAGCAAUUAAAAUUCCCCUUCUAUUUCACAUGAAAACUUGGUGAACUAGAAUC	334	spe-miR8051-2-3p	UAGUAUGGUAGAAAGAUUCA	285-304	stu-miR8051-5p	0	0	20	20	1

spe-MIR8762c	GGCGAAAUUCUAAUAGAUAGAUAGUAUGGUAGAAAGAUUCAUCUCAUGUGAGUUUUUUUAUGACCAUGAUAUUUGUGAAAUGACUUGAGAGGUGUAGUAUAAGUGGGAGCCGAAAGGCGAAAGUUAAAUACCACUACUUUUAACGUUAUUUUACUUA	86	spe-miR8762c-3p	UUAACGUUAUUUUACUUA	69-86	gra-miR8762c	4	0	18	24	1
spe-MIR164b	CGGACACAUGUCACAAUCUUAUCCAUCGAUCCGAUAUUUAAUAAAUAUUGGGAUAAGAUUAUGACACGUGUAUG	74	spe-miR164b-5p	CAUGUCACAAUCUUAUCCAUC	7-27	aly-miR164b-3p	5	0	21	21	1
spe-MIR171b-4	GGUAUGAAGAAGAAUACAAGAGUGAUAUUGGUUCGGCUCAUCUCUUAUCUGUUUCACGAAUCAGAAAUUAGUGAGCCGAACCAAUAUCACGCCAUGUCUGCUUCUCCAUCAU	112	spe-miR171b-4-5p	AGUGAUAUUGGUUCGGCUCAUC	21-42	csi-miR171b-5p	1	0	22	22	2
			spe-miR171b-4-3p	UGAGCCGAACCAAUAUCACGC	72-92	fve-miR171b	2	0	21	21	2
spe-MIR166-3	AGCUUCCAGAUUUGAGGGGAAUGUUGUCUGGCUCGAAGUCAUUAUCUCUUCUCGAUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUGAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUCAUUCCCCCCAAUUUGGAAACA	174	spe-miR166-3-3p	UCUUCGGACCAGGCUUCAUUCCCC	137-160	lja-miR166-3p	2	0	24	24	3
spe-MIR6475	UUUAUGUUAAGGAGUCAAGAACGAACCAUACAUGUUCUAUUCAGGCAAGAAACUUGUAUGGUUCGGGUAUUGACUUCUACACAUGAU	87	spe-miR6475-5p	UGUUAAGGAGUCAAGAACGAA	5-25	ptc-miR6475	5	0	21	21	1
spe-MIR162b-2	GUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCAUAUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUCAA	117	spe-miR162b-2-5p	UGGAUGCAGAGGUUUAUCGACC	10-31	ath-miR162b-5p	4	0	22	22	1
			spe-miR162b-2-3p	AUCGAUGAACCGCUGCCUCC	87-106	cas-miR162b	0	0	20	20	1
spe-MIR6137b	UCUCUCUCACUUUAUAUACAGACACAAAUGUAUAAAAUGUGUUUGUGUUUGUAUAAAGUGAGAGAAAAUUGUAUCUAUACAUCUCUUUUCGUUCGCCUAUCUGUCCAGAGAAUCUCGCUCGCCACUCUCACUCGUCUCUCACACUUUAUACAAACACAAAUGUGUAAAAUUACGUUUAUGUUUGUAUAACGCGAGAGUAA	200	spe-miR6137b-5p	GAGAAAAUUGUAUCUAUACAUC	62-83	pgi-miR6137b	5	0	22	22	3
spe-MIR5014a-4	CUUUGGAUGUGCAUAAGUAGACACUUAAACUUCUACAAAAUUAAACAAAUAGACACAUUCGUCCUACAUGGCACACUACAUAACAACUUUGUGUCCUAUGUGGCAUCCUACAUGUAUUAUGUCAUGUAGGACACGUGUGUCUACUUGUUCAAGUUUAUACAAGCUUAAGUGUCUACUUGUGCACAUUCAAAG	192	spe-miR5014a-4-5p	ACACUUAAACUUCUACAAAAU	21-41	ath-miR5014a-5p	5	0	21	21	1
spe-MIR1533-2	CGUGCAGCGAUUUAAUAAAAAAUUUUUUUUUUUAAACAAAUCGCUGCCCCUAGCAGCGAUUUAUGUCAAAAAAAAUUUAUCAAUUUUUUUUUAUUAAAAUCGCUGCACUGGCAGCGAUAUACCUUAAUUUAAAAAAAAAAUUAAAAAUAAUAUGAAAUCGCUGCCAGGGCAGCGAUUUCUAAGAAGAAAAUUUUUGAAAUCGCUGCCCA	209	spe-miR1533-2-3p	AAAUUAAAAAUAAUAUGAA	138-156	gma-miR1533	5	0	19	19	1
spe-MIR4348c	GGAAUAAUGAUCUUACUAAUUUGGUUAAUUCCAUUAAGCAAAGAGUUAAAAUUUUACCUUGCCUUACUCUUGCUAAUCCUAAUUGGAUUAAAAUCAUUGAGACAGAUGCGUCUAACAUUGGUUAUGGUGGGAUUUUAAAGCAGGUUAAUCCCUAUGACAAAAUAGAAUAUCUUGUUAGAUUUCAUUCAGGCAAAUGGUCUGAUUCACAGCGAAAAUAUGCGACUGUGGCACAUGAAAUGCUUUGUGUGGUUAAAUGUGUAUUAAAAUUCCAAGAUGACUUAUAUA	285	spe-miR4348c-3p	UAUUAAAAUUCCAAGAUGACU	259-279	gma-miR4348c	4	0	21	21	1
spe-MIR5168	GUUUUCAUGGUCAGUUUAUGCUUAUCCAGAAGUUGCAGGGGUUGGUUUCUGGUAGAACGAGCUUAUCUUAUACAUGUUUUGUUGAAGAAGCUAUGGUUUCCGAUCUGAUUUGCGUGCACCUUAUGUUUGAGCAUGUGCUACCAUGAACUA	150	spe-miR5168-5p	GGGUUGGUUUCUGGUAGAACG	39-59	ata-miR5168-5p	5	0	21	21	1
spe-MIR10536-2	GUUAAUGUUGAAGAAGAAGGAAGCCGACGAUUGAAAUGUGUCAAAGAAAUAUGUUUCAAUCGUCA	90	spe-miR10536-2-3p	AAAUAUGUUUCAAUCGUCAGCUUC	47-70	sly-miR10536	4	0	24	24	1

	GCUUCCUUCUUCAUCAACACUUGCU										
spe-MIR2089-1	UCUGAUCUCUAUAGCAUGCAUUAAGGUGUGAUCGUACUUGUGCAAUAAGUAAAGAAAUGCUCAAAACCAAUAUCUUUUCUUUUUUGAGAUAAAAAAAAAGUUAUAUUGGUUUUGAGCAUUUCUUUACCUAUUGCACAAGUACGAUCACAACUUAGUAUGACGCUAUAAAGGUCUUU	176	spe-miR2089-1-3p	UUACCUAUUGCACAAGUACGAU	124-145	mtr-miR2089-5p	5	0	22	22	1
spe-MIR3441	GGCAAGUGCUGUACAGCUCCAUUUGAAGAUAGUAGAUUGGUUGCUUGUGUCAAAGCUACAGUUAGAGGAAUGCCACAUGAUUACCGAGGUUGGAUUUUUUGGCAUAGUUUUGUACUGUGGUAAGAAACUGAAGACGCUUUCCUUGGUGAACUGCUUUGGUGGGGAACACUUAAACUAUGCAUUUUCUUUAGAAUCUGUGGCUAUUCGUAACUGUCUUGGAGUAGACAAUGUUAGCAUUGUUGUAGUAGAUACACUGUGUCACAACUAACUCAUCUGGAGCUGUGUAGCUAAUUUUG	296	spe-miR3441-5p	GUAAGAAACUGAAGACGCUUU	120-140	aly-miR3441-5p-2	5	0	21	21	3
spe-MIR8030-1	UAUGGUUUGGUUUGAUUGGUUUGGCAUUGAAAAAGAAAAACCGAUCAUUCUUGAUUUGGUUUGGUACUAAUAAAAAAAAAGUCAAACCAAAUCCAACCCAAACCGAC	106	spe-miR8030-1-3p	AUAAAAAAAAAGUCAAACCAAAU	70-91	stu-miR8030-3p	5	0	22	22	2
spe-MIR8005c	GUUUUAGGGUCUACGACCUAAGAUUUAUGGUUUAGAGUUUAGGAUUUAGUGUUUUGAUUUUAGGGUCUAGGCCUUGAGGUUUAGAGUUUAGGGUUUAGGGUUUAUGCCGUAAGGUUUAGGGUUUAAGGAUUAGGCUUAAGAUUUAGAUUUUGGGGUUUAGACCCUAAGGU	170	spe-miR8005c-3p	UUUAGAGUUUAGGGUUUAGGGUUU	80-103	stu-miR8005c	2	0	24	24	1
spe-MIR6288c-1	AGUAAGGAAAUAGGGGAAGUGUUGCCGGAUUUUCGUUAGAUUAUUAGCUAGCUUAAAAGAUAGUUAAGCGCGACAUUUAUCUAAUUGCGGCACGAUUGUUGCUUGUUAUAGAUUAAUAGCUUGAGCAGUAAAUAUUGGAUGUGCGGCUCGACUAUACGGUAUGUAACGCUGUCCCUUCUUUCUUUGUU	188	spe-miR6288c-1-3p	CUUGUUAUAGAUUAAUAGCUU	102-122	ppe-miR6288c-5p	5	0	21	21	1
spe-MIR5567	UUUACGUUCACAUUCACAUUGACAUUGAUAUUAACAUUCAUAUAGUCGUUUAUGUUUACGUUGACAAUGAGGUUGACAGUGACAUUCACGUUCACGUUGAUGUUUCAAUUUAUGUUGAAGUUCACAUUUAUGUUGACGUUCCAUUGGUGUUGACAUUAAUGAUUCAUUUAUGUGUACAUUAAUAUUGAUGUUGAUGUAGACGUUCA	206	spe-miR5567-3p	UUAAUGAUUCAUUUAUGUGUACAU	156-179	sbi-miR5567	3	0	24	24	1
spe-MIR11508	UAUAUCAAAGGUUGUGACUUUAAUGAAGAGUUGCGAAUUAUUUUAAAAGUUGUGACUCUAAUGAAAAUUUGCGACUUUAAUGAAGAGUUAUGUGACUCGAAAGAAAAAUUGCGACUUUAAUGAAGAGUCGCGACUUUAUGAAAAAUUGUGACUUUUAUGAAAGAUUGUGAAAUUUUCGAAGGGUUCCAACUUUCCAAAUAGUUUUAAGCUUUCUCAUAAGGCACGAUAAACUUUAUUUC	239	spe-miR11508-5p	UUAAUGAAGAGUUAUGUGACU	77-97	pab-miR11508	5	0	21	21	1
spe-MIR11301	UAAUAUGUAAAUAUUAUUUGUCAUAUUUUUAGGAUAUUGAUAUCUCUGUCGUCCAUGAACUAGAGCAUAUAUUCUCUUCAUUCUAAUUUCUAACGGAAGACUAAAUAUAGGAAUACACGGCGCAAUCUUAUCCAUCGAUAAAUGUCGGGUCAGUGGAUAAGAUUAUGACACGUGUAUGUCUGAUAGUAUAAAGGGUACAUAUGCUCUAGUUUUUGAAUGUCGGGACGCAAUGUCCCUAAAAUAUGACAGAAGAUAUUUGAAUACCA	267	spe-miR11301-5p	UCAUAUUUUUAGGAUAUUGAU	21-41	fve-miR11301	5	0	21	21	1
spe-MIR6288c-2	GCUAUCAAAUUAAAAACAGAUGCCUAAUCUGAACUCAUCUACCCCAAAUAAAGCAAGCAGCUUUACUAGGUCCUAGUAAAGCUGCUUGCUUUAUUUGGGGUAGAUGAGCUCAGGUUGGUGUUUUUUAUUUGAUUCU	136	spe-miR6288c-2-3p	GUUGGUGUUUUUUAUUUGAUU	114-134	ppe-miR6288c-5p	4	0	21	21	2
spe-MIR10532-6	AUGCCAGAGGUCCCAAAAACACACUUAUACUAUACUAAGUUUCUAUUAUUAUCCUAAACUUAUUUUAUAAAUAAUUUUCUAUCCUUUUUCGGCCUAUGU	190	spe-miR10532-6-3p	AAGUGUGUCUCUGAGAUUUCGGGA	165-188	sly-miR10532	1	0	24	24	1

spe-MIR10532-7	GACACUAGUUUGAAAAAAAAUAUCAAAAAAUAA GUUCGGGAGGUAUUAGGACCUUAGUAUAGUAU AAGUGUGUCUCUGAGAUUUCGGGAGG UUUAGGGAUAAUGCCCAAGUACCCCCUCAACCU AUGCCCGAAAUUUCGGAGACACACUUAUAUUAU ACUAAGGUCCUCCCUCAACCUAUGCCCGAAAUU CCAGAGACACACUUAUACUAUACUAAGGUCCUA UUACCCCCUCUAAACUUAUUUUAUAAGUGUGUC ACUGAGAUUUCGGGCAUAGAUUGAGGGGGUAC UUGUGUAUUUUCCCUUUC	215	spe-miR10532-7-3p	AAGUGUGUCACUGAGAUUUCGGGC	157-180	sly-miR10532	1	0	24	24	1
spe-MIR2643b	ACUUGUGGUUUGGUUUGAUUGGUUUGGCAAUU GAAAAAAAAAACCCGAUCACUCUUGAUUUGGUU UGGUAUUAGAAAAAAAAGAAUCAAACUGAACUC AAACUAAACCGACACAC	115	spe-miR2643b-3p	UUUGGUAUUAGAAAAAAAAGA	64-84	mtr-miR2643b-3p	5	0	21	21	1
spe-MIR5658	GUUGCGGUGCGGUAAAGAUGUUGAUGAUGAAG AGAUUUUUUUUUGAGAAUGUAUUUUUUGGAUG ACUGAGUCAGUCUCCAAGUGGGAGAACUGUUA GGUAGUGGAGCCUGAUUAAUUUUAGGUUUUCC UAUUUAUUCUCUAUUUUAGGUUUUCCUAUUUAU UCUCUGUAACCAAAAAUACUCUGAUUUAUUAAU AUAAAUAUACCUCACCGCCGU	215	spe-miR5658-5p	AAGAUGUUGAUGAUGAAGAGA	15-35	ath-miR5658	4	0	21	21	1
spe-MIR166f-3	CUCUAGGGCGUCAGGGUCACAGAUGGGCAGGG GUUUGAGCCAGUCGAGGCGACCUUUGCCUCAG UGUUCUCGCUGUGGUAGGUCCCAUCCUGGAGA AUGUCGUUGGGCUACAGGUGCGUGUUUUUCUU GCGGCCGUCAGGGUCAUACUAUGAGGGAGUGU CACCUUAGAGGUAGUGCAGGUGGUAUGGAACA GCCUACUGGGUCCGUUGCUGGUUCAUCUCCUU CUGUGGCUAUGCGCCCUACGG	245	spe-miR166f-3-5p	AGAAUGUCGUUGGGCUACAGG	94-114	cas-miR166f-5p	5	0	21	21	2
spe-MIR396a-2	UACAUCGGGGAGGAUUGAAAUUUGGUGUCAAC UACAGUCCCUCCUUUUACUUGGGAUUGAUGCA AGAAAUCUAAGGAAAAUGAAAUUGACAACCAAU UUUGAUCGACCCCAUCUU	115	spe-miR396a-2-3p	AUGCAAGAAAUCUAAGGAAAA	60-80	csi-miR396a-3p	4	0	21	21	1
spe-MIR7984c-5	AUAUAUCCGAACUUUGAAAAGGACCUUUUACCG CUUGCACUAUUUAAUUGUGUAUUUUAAAGGUAU AUAUGUGUCCACGUGAACAUUAUAAAUAUUGCA UCAUUAUAAAUAAUAAUGUGUCCACGUUGGCAC AUAUAUAUAUUUAGAAUACACUAUAAAUAGUGC AAGGUAAAAGGUCCUCCAUAAAGUUUGGUACC G	198	spe-miR7984c-5-3p	CCUCCAUAAAGUUUGGUACCG	178-198	stu-miR7984c-3p	2	0	21	24	1
spe-MIR166-4	UUUGUUGAGGAGAAUGUCGUCUGGUUCGAGAU CUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUU UCAUAUAUGUAUCUUGAAUGAUUUCGGACCAG GCUUCAUUCCCCUCAACUCU	117	spe-miR166-4-3p	AUUUCGGACCAGGCUUCAUUCCCC	86-109	lja-miR166-3p	0	0	24	24	1
spe-MIR11041	GUCUUGGAGAGCUUCAAAGCAUUUUGAAUUAA UUUACACUGAUUUAUGUGAAUCUAUGCAUAGUA UAUAUUUUUGUGGGAGUCGUUAUUUUCUACUA CUUAGUGAUGAUUGCAGUCGCAUGAGUUGAGA CUUUUUUGAAAAAAAAUUAAAUUUGCCUCAGAA AUUUAAUAAUUUCAAAGCCCAGUUGAGAAGCAA AGUGUUCUGUGCAUAAAAAGUGGUAUGUGCAG CUAGUUCCACUCUCUAAGCAUUUACAACAUUCA UAAGCUCAAAAAACUUCUGAAGCUUUUCAACAA UUAAAGAAUUUGAAGACUUCAGCUUGCAGAAAA	293	spe-miR11041-3p	UAAGCAUUUACAACAUUCAUA	242-262	seu-miR11041	1	0	21	21	1
spe-MIR8024b-2	GAAUUUGAAGACUUCAAGUUGCAGAGUUAAAGA AUCUGAAGACUUCCACCUGGAGACUUAAAGUAU UUGAAGACUUCAACUUGCAUUGUUGAAUGAUU UGAAGACUUCAUCUCGCAUACUCGGGGAAUUU GAAGACUUUAGCUUGCAUACUUGGAGGAUUUG AAGAUUUCAACUUGCAUACUCCGGGAAUUUGAA AACUUCAAUCUUAAA	243	spe-miR8024b-2-3p	UUGGAGGAUUUGAAGAUUUCAACU	184-207	stu-miR8024b	0	0	24	24	1
spe-MIR399a-2	UUUGAAUUUAUAAGCGAAACACUGAUAGGACUA CUCUCUAUUGGCAUGCAGUUGUGUAGUUUAGC UGACACGCCAAAGGAAUGCUGCACUGUUACCA UCUCUUAUUAAUAUUCUAACAAAAAGAAAGAAG UGUAGGUGGAUGAUAAUAAGGGGAACAGUGGU	258	spe-miR399a-2-5p	GGACUACUCUCUAUUGGCAUG	28-48	stu-miR399a-5p	1	0	21	21	1

	AGGACUACUGAUCUCUAUUGGUAUGCAACUAUA UAUUUAAGCUGACAUGCCAAAGGAGAGUUGCC CUGGUACUGUCUCUGCUUACUGUAAUUCUGA										
			spe-miR399a-2-3p	UGCCAAAGGAGAGUUGCCCUG	210-230	aof-miR399a	0	0	21	21	1
spe-MIR7997c-6	GUUCAUCAACAUCUAUGUUGCUCCGACUCUUC AAAAAUGCUAUCAGCUUGCAUGUCGUACUUUU GGAGAGUUCGAGCAACAAUACAGUGUUUAUGC AU	98	spe-miR7997c-6-5p	AUGUUGCUCCGACUCUUCAAAAAU	15-38	stu-miR7997c	2	0	24	24	1
spe-MIR5181b-1	GAUACGUGACACAAUCUUAUCCGUCAAUUCGAU AUUUAAUAAAUGUCGGAUCGGUGGAUAAGAUUA UGAUACGUGUA	77	spe-miR5181b-1-3p	UUCGAUAUUUAAUAAAUGUCG	28-48	bdi-miR5181b	5	0	21	21	1
spe-MIR7992-4	AGUAUGUAAAUAAUUAUUUAGAUACUUCAUAUA CAUCUAGACACCUCAAUUCGUUCUUAUUAUGUU UGUGAUGGCAUUACUCUUAUUUCACGAUUUCG AUGAAGUAAUGGAGGGUGAACUAACAGAAUUUU AGUGGUGUUCCAACUAAUUAUUUUGUAAGUUG GAAUGCUCAACUAACAUAAGAAAAACGAGUUGA UGUGUCUAGAUGUGCAUUCUCAAAAUCAGUGU AUUUAAUUGU	238	spe-miR7992-4-3p	UGUCUAGAUGUGCAUUCUCAAAA	199-221	stu-miR7992-3p	5	0	23	23	1
spe-MIR7484k	AGAGAUCUAUUGUAUAACAUCAACGAAAACAGG CAAUCUUAGUUCUUUGAAAAACCUCUCAAAGAA CUAAGAUUGCCUGUUUUCGUUGAUGUUAUAGA AAAGAUCAAA	108	spe-miR7484k-3p	GUUAUAGAAAAGAUCAAA	91-108	gra-miR7484k	4	0	18	24	2
spe-MIR1521b-2	AUUAGAGCAUAUAUAUCCUUCAUAAUAACGGAC AUACACGUGUCAUAAUCUUAUCUAGAGAUCCGU UAUCUAUUAAAUAUCGGAUCGAUGGAUAAGAUU GUGUCACGUGUCCAUAUUUAGCCUUCUGUUAG AGUGAAGGGCAUAAAUGCUCUAGU	155	spe-miR1521b-2-5p	GACAUACACGUGUCAUAAUCUUA	31-53	gma-miR1521b	4	0	23	23	1
spe-MIR7981-7	AUAUAUAAUAUUAGGGAUAAGAUAUAAGUACCU CUUAGACUAUGAUCGAAAUCUGAGAUAUCUUAA UUAAAUUAAAGUCAUAUUAUCUCCUUACGCAGU UGAGGCGCGUGAGAGAUAUUUUGAUGCCACGU GAAAACCAAAAAGGUCUACAAAAUAACAAAACAA AUUGGUUCGGGGGUAAUAGAACCUUAGUAUAG UUAAGGUGUGUCUCUAAGUUUGAGUCAUAGUC UAGAGGAUAUUUACACCUUAUCCCUAUAAUAUU AUAGAC	268	spe-miR7981-7-5p	CUUAAUUAAAUUAAAGUCAUAUUA	62-85	stu-miR7981-5p	5	0	24	24	2
			spe-miR7981-7-3p	AUAGAACCUUAGUAUAGUUAAGGU	181-204	stu-miR7981-3p	3	0	24	24	1
spe-MIR8005b	UCUAAAUUCGAAUCUAUAAAUUUUAAAUUCUGA AUCUUGUGAUUGAGGAGAAGAACGACAGGGCA AUUCUCCUUUGGCAAAGAUAAUAUAAUGUGUAU GCAAAACAUAUAUAUAGGGUUUGCAUAUAUUCA UUUGCCAAAGGAGAAUUGCACUGUUAUUUCUU ACUCCCCAUUUUUCUUCUUCUAUGAACUUUCAC AUUUUAUGUUUGAUUUUCCA	216	spe-miR8005b-5p	UCUAUAAAUUUUAAAUUCUGAAUC	13-36	stu-miR8005b-5p	3	0	24	24	2
spe-MIR399r-3	AAAACAAUUGGUGAAGAUACAAUUCAAACUAUG UAUGGAUGCAUUACUGGGCUAAUCUUCUUUGG CAAAUAGCCACAUUUUCACUAUAUUAUUUAGUG CAAGUUUGUUCAUUUUUUGCCAAAGAAGAUUU GCCCCGUAAAUCACCAAUACAAUAUAUUAUAAC AUGAGUCACUUCAAUACUUGUAAU	187	spe-miR399r-3-3p	UGCCAAAGAAGAUUUGCCCCG	116-136	mtr-miR399r	0	0	21	21	1
spe-MIR399a-3	AAUUGGAGAGGACAAGAAACGCAGGGUAUUCU CCUUUAGCAAGAUUGCUAUAGAUUGCUUUAUG CAUGAAUUAAAUUCUUUCUUGCCAAGGGAGAAU UGCCCUGCGUUUCUUCAUUUCCACAA	123	spe-miR399a-3-3p	UGCCAAGGGAGAAUUGCCCUG	84-104	ata-miR399a-3p	1	0	21	21	1
spe-MIR166-5	GAAACUAAACAAGAUCAUGUUAAGGAGAAUGUU GUCUGGUUCGUGACCAUAUAUCUUUCUUCAUA UAAAUGAUCUCGGACCAGGCUUCAUUCCCCUC AACUCAUCAAGGUUAUGUCAU	118	spe-miR166-5-3p	AUCUCGGACCAGGCUUCAUUCCCC	72-95	lja-miR166-3p	1	0	24	24	1
spe-MIR5174d-3	AUUUAUUACUCCCUCCGUUUCAAAAAGAUUGGC CUACUUUGACUUGAAACGGAGUUUAAGAAAAGA AAGAAGACUUUUUAAUCUUGUGGUUCUAAUUUA AAGUUAUGUCAAAUUUACCAGAAUACCCUUUAA UCUUGUGGUCUUAAACAUGCCACGUGGAAAGU	266	spe-miR5174d-3-5p	UCCCUCCGUUUCAAAAAGAUUGGC	10-33	bdi-miR5174d-5p	1	0	24	24	1

	UAAAGUUAAAGUGUUGCCAAAAAAGGAAAGGGG UCAUUCUUUUUUAAACAGACUAAAAAGGAAAUG GGGUCAUUCUUUUUGAAACGGAAGGAGUAUAU AUUU		spe-miR5174d-3-3p	CAUUCUUUUUGAAACGGAAGGAGU	235-258	bdi-miR5174d-3p	5	0	24	24	1
spe-MIR5773-1	UGAUCCACCCACCUAACCCGACCCAUUUAAAAA AUAUGUUAUUACCCAUUUUAUUUUGUCUUUAAU CCUAAUUCAAGGUUUAAGAGGGAAUAAUUUAGG AUUAAAGAAAAAAUAAAAUCGGUCAUAUCAUAU UUUUUAAAUAGGUCGGGUUAGGUGGGUGGAUC A	165	spe-miR5773-1-3p	UUUUAAAUAGGUCGGGUUAGGU	134-155	gma-miR5773	5	0	22	22	1
spe-MIR11144-2	UAGAUACUCCCUCUUUCCCUUUUUAAUUGUCCA CUUUUGAAUUGGCACACCUAUUAAGAAAAUAAU UAAUGACGUAGUGAGUUUACCAUUUUACCCCUA UUAAUUAUGAAGUGAAUGAAAAGUUCUACAUUU UUCAAAGUAAUUAGUCAUUGAAUUGUGGGUAUA AUAGGUAAAAAAAUUGCCCUUUCUUGAUUUAUC AAAAUGGACAAGUAAUUAGGGACAACUAUAAAA GGAAAAGUGGACAAGUAAUUAGGGACGGAGGU AGUAUGAG	271	spe-miR11144-2-5p	UUUACCAUUUUACCCCUAUUAAU	82-104	lja-miR11144-5p	4	0	23	23	1
spe-MIR1886-1	AAAUUGAGCAUUUCAAUUUACUUAAGCCCUUAG CAUCAAAUACUUGAUACAAAUACGCCCUUGUUC UGCUCAAUUGCGCAUAGUAUUUGGACCAAGUA UUUGACGGUAAGGGCAUAAAUGAACUUAAGUAC UAACAU	137	spe-miR1886-1-5p	AAUUGAGCAUUUCAAUUUACU	2-22	ath-miR1886-3	5	0	21	21	1
spe-MIR167h-1	UUAUCAAGAAAGGAAGGAGUGAGGCUGUCCGA GCAUGACCUAACCUUAGUCACCCAUUUUCUUUA CAAAUGGCCAAGUUUAGAUCAUGCUGGCAGCU UCACUUGUUCCACUCUAGACCU	119	spe-miR167h-1-3p	AUCAUGCUGGCAGCUUCACUUGUU	83-106	gma-miR167h	3	0	24	24	1
spe-MIR3511	AACUAUUGACAACUUUUAACACAAUACUCUUUU ACUUGACUAACUAAAAUGAAAUACACCCUUAAA UUCUCGCCAAAUUUAGGGGUGUUUUCAAUACU UCUUUCGGUUUUUUAUUAAGAGUCUCAUACUC UUACAAGAGUUUAAUACCGUGUUGCUAUGUCA UGUGGAAAUUAGGAGUGUAUUAAGUUUAGUUA GUCAAGUAGAGACGUGUUUUAAGAUUGUCAAU AUUU	230	spe-miR3511-3p	UGUUGCUAUGUCAUGUGGAAA	150-170	ahy-miR3511-3p	4	0	21	21	1
spe-MIR8713	CAAACCUCUUUAUAACAAUGUCGUUUGUCUGGA UAUGUUUUGGUUGCUAUAACGAGAUGGUGUUA UAGAUAACAUAUAUUAAAGUGGAUGCCAAAAGA UCUAACUAGGCCGUUAAAGUGAAAUUUUGUUAU AAAGGAUGACUGUUAUAGAGAGGUUUG	158	spe-miR8713-3p	AUGACUGUUAUAGAGAGGUUUG	137-158	gra-miR8713	5	0	22	24	1
spe-MIR7992-5	AAACUUGGUCUCUGCUGGCAAGUAAGCGCUCC AACUUUGUGUAUGCACAUCUAGACGCCAAGUU GAGGUGUCUAGAUGUGCACUCUCAAAGUUGGA GUGCGUACUUGCUAGUUGAGGCCAAGUUU	125	spe-miR7992-5-5p	UUUGUGUAUGCACAUCUAGACGCC	36-59	stu-miR7992-5p	5	0	24	24	1
spe-MIR5014a-5	CUCCAACUUUCAUAAUGUACAAACAGACACUUU AACUAUCCAACUUUUAAAUAAAUAAACACAUGA GUCCUACAUGGAAGAAUACACGUAGGAUACCAC GUAGGACAAAAAAUGACAUGUAGUACGACAUGU AGGACGUGUGUGUCUAUUUGUUCAACUUUAUA CAAGUUUAAGUGUCUAUUUGUGCAAAUCCAAAG UUGAAG	203	spe-miR5014a-5-3p	UUAUACAAGUUUAAGUGUCUA	160-180	ath-miR5014a-3p	5	0	21	21	1
spe-MIR8045-2	AUUUUUCCUAACUGAACUAUAUCAACUUAUCAA AUAUUGUUCUCUUUUUUCUACCUGAUCUACUC UGCUGGGCCGACACUGACACUGAGAGACUAAA GCUAGGGGAGCUAAUGGGAUUCAUUAACUAUU UAUCAAUUAUACAUCAGCUGUCAGUUGUUUCCU UUUACUAGAUGAAAUAUCAUCACUGUUCAUUUA GGAUAAGGAAAUUGAUAGUUGAGGUGUGUUUC GAUAAACAUUUGAUAAUAGUUUACCUGGGAAAC UA	262	spe-miR8045-2-3p	AUUGAUAGUUGAGGUGUGUUU	206-226	stu-miR8045	0	0	21	21	1
spe-MIR164c-2	UUAUUUAAGCUGGAGAAGCAGGGCACAUGCUA GAUUACUCGGAUUUCUAUCCUUGAGAAUUUUG	93	spe-miR164c-2-5p	UGGAGAAGCAGGGCACAUGCU	11-31	fve-miR164c	0	0	21	21	1

	CAUGUGCCCUCGCCCUCCAGCUUAAACCC										
			spe-miR164c-2-3p	CAUGUGCCCUCGCCCUCCAGC	65-85	bdi-miR164c-3p	4	0	21	21	1
spe-MIR6116	CGCCUCUGUGUGCAUUCAACAUUAGAGGAUUCAUCAUUAUUGUUAGAAAAUGAUGGAUCCUCUAAUGCUAAAUUCACAUCAGAGAUU	87	spe-miR6116-3p	CAUUAUUGUUAGAAAAUGAUG	35-55	cca-miR6116-5p	5	0	21	21	1
spe-MIR156c-3	AAGGGAGGUGACAGAAGAGAGUGAGCACACAUGAUGUUUUCUCGCAUGAUGUUUACAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCCCACC	101	spe-miR156c-3-5p	UGACAGAAGAGAGUGAGCACA	9-29	rco-miR156c	0	0	21	21	1
			spe-miR156c-3-3p	GCUCACUGCUCUAUCUGUCACC	75-96	ata-miR156c-3p	0	0	22	22	1
spe-MIR156i-2	UCUAAUUAAGUGUGAAGUAUGACAAAAAAGAAGGUGACAGAAGGGCGUGAGCACAUGUGUGUUUUCUAGCAUGAUGUUCAUAUGCUUGAAUCUAUGUGUGCUCACUGCUCUAUCUUUCAUCCUCAUCGCUUUUCCUCUCUCUCUAGAUUUAAUUUUG	157	spe-miR156i-2-5p	UGACAGAAGGGCGUGAGCAC	35-54	stu-miR156i-5p	2	0	20	20	1
			spe-miR156i-2-3p	GCUCACUGCUCUAUCUUUCAUC	100-121	zma-miR156i-3p	1	0	22	22	1
spe-MIR167h-2	AAUUUCUUUCUUUCUCGACGAAGUAGGGUUAAGAUUAUUUUUCGUAGUACGAACUAACAGGUGAAGCAACCACAUGAUCUGAUCUUGCCUUAAUAUAAAUUUAUAGGUAAGUUUAGAUCAUGCUGGCAGCUUCAACUGAUAGUAGUCUACGCUAUCAAUAUGACAAAACCCUAAUAUUGUUGAAGAAGAAGAAGAAUAUUUUUUAAAAGUUGAUGGCGUCAGAUUGAU	196	spe-miR167h-2-3p	AUCAUGCUGGCAGCUUCAACUGAU	117-140	gma-miR167h	1	0	24	24	1
spe-MIR10538-7	AUACGUUACUCACAGUAACGUUUUACUCCUAAAACGUUUCAUCAUAGUAACGUUUUAGGAGUAAAACGUCACUGAAAAUAACGUUUUAGGAGUAAAACGCUACUUACAGUAACGUAUAUCAACCUAAUGCUGUUAGUUUUUUAAAAAUA	181	spe-miR10538-7-5p	AGAUUGAUAUACGUUACUCACAGU	25-48	sly-miR10538	0	0	24	24	1
spe-MIR167d	AUUCAAGUAGUUGCAUCACCUACUUAUGCUCCUUUAUAAUUUAGUACACUAAUUCUAAGGAGGUGCAUCACCUACUUGCUCCUUUUAACUUAAAAUUCAGUCCACUAGCUCUAAGUAGGUGCAUCACCUACUUGUCC	137	spe-miR167d-5p	AUUCAAGUAGUUGCAUCACC	1-20	stu-miR167d-3p	5	0	20	20	3
spe-MIR7980b-5	AAGAUACAGAAUCCUGAGAUGGAAUCAGUGUUUGGACAUACAAUUUCACGUUGAUUCCAUCUCAUGUUUCAUGUCAUGAG	80	spe-miR7980b-5-5p	GAGAUGGAAUCAGUGUUUGGACAU	16-39	stu-miR7980b-3p	0	0	24	24	1
spe-MIR8006-5	CCUGCCGUUAAAAAACUAGAAUAUAUAUACCCUUUAUACUAACGAACAUACAUGUUUCAUAAUCUUAUCUAGUCAUCUGAUAUUUAUUGACGGAUAAGAUUGCAUCACGUAUUCCUAUUUAGUCUUACGUUAGAGUGAAAGACAUAUAUGCUCUAGUUUUUGAACGGCAAG	171	spe-miR8006-5-3p	UAGUUUUUGAACGGCAAG	154-171	stu-miR8006-5p	3	0	18	24	1
spe-MIR5014a-6	AUAAUUUAUAUCCUCCAACUUUGAGUGUGCAUAAAUAGACACUUAAACGUGUAUAAAAAUGAACAAAUAGACACAUAUUUACGUCCGAUAUGGCAUUCUACAUGACAAUUUGUGUCCUACGUGGUGUCAUAUGUUUAUUGUGCCACAUAAGGCAAAUGUGUCUACUUGUUUAACUUUAUACAAGUUUAAGUGUUUGCACACCUAAUGUUGGAGGAUAUAAAUGUG	225	spe-miR5014a-6-3p	UUAUACAAGUUUAAGUGUUUG	176-196	ath-miR5014a-3p	4	0	21	21	1
spe-MIR7981-9	UGCACAAGUUAUUCCUAAAUUAUGACAAAAAUUUUGGACACACAUAUUAAUUAAACUAAGGUCCUAUUAUCCUGAAUAUUAUACACAUUUUGACUUACAUGGCACACUCUAUGACUCCACACGAUUGAAGUGCGUGAGAUAUGUUUGAAGGCCACGAAAGACAAAAAAGUAAACAAAAUUUCUAAAAAAUGGUUCAGUGUAAUGAGAUUUUAAUUUAGUUAAAGUAUGUCUCUAAAUUUCGCUGAUAUUUUAGGGAUACUUGUAUC	267	spe-miR7981-9-5p	AUUAAUUAAACUAAGGUCCUAUUA	46-69	stu-miR7981-5p	2	0	24	24	2
			spe-miR7981-9-3p	AUGAGAUUUUAAUUUAGUUAAAGU	203-226	stu-miR7981-3p	5	0	24	24	1
spe-MIR8142	CAUUUAUGUCCUUCAAUUUUGAGAUAAGUAGACAUUUAAACUUGAACAAGUAGACACGUGAGUCCU	195	spe-miR8142-5p	UGAGAUAAGUAGACAUUUAAACUU	20-43	cpa-miR8142	5	0	24	24	1

spe-MIR156g	ACGUGACACAAUACACAUAGGACACCACGUAGGACAAAAAUGACAUGUAGGACAUAUGUGUCUAUUUGUGCAACUUUAUACAAGUUUAAGUGUUUAUUUGUGUAUACCCAAAGUUGAAGGAUAUAAAUAACAGCUGUGAAGGAAUAUCUGGGCCCAAAGAUGUAUUGACAUAGCUUUCUCUUUUUUUGUGUCAAUACAUCUUUGGGCCCAGACAUAUUCCUUCAUAGCUGU	102	spe-miR156g-3p	GCUUUCUCUUUUUUUGUGUCA	44-64	aly-miR156g-3p	5	0	21	21	1
spe-MIR7992-6	AUCUUCAACUUUCAUAAUGCACAAACAGACACUUUAACUAUCCAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGGCAAAAUACAUGUAGGACACCACGUAGGACAAAAAAUGACAUGUAGGACAUAUGUGUCUAUUUGUUUAAUUUUAUAUAAGUUUAAGUGUUUACUUGUGCAUACCCAAAGUUGAAGGGCAUCUGUCGUUCAUAAACUAGAGCAUAUAUGUC	195	spe-miR7992-6-5p	UUUCAUAAUGCACAAACAGACACU	10-33	stu-miR7992-5p	5	0	24	24	1
spe-MIR8739-1	CUUCAUUCUAACAGAAGACUAAAUAGGAACACGUGGCGUAAUCUUAUCCAACGAUAAACGUCAGAUCGGUGGAUAAGAUUAUGAUACGUGUAUUGUUCGUUAGUAUAAAGGUUAUAUAUGCUCUAGUUUUUGGACGGCAGGAG	176	spe-miR8739-1-5p	AGACUAAAUAGGAACACGUGGCGU	49-72	gra-miR8739	5	0	24	24	3
spe-MIR172b	UUUAGUCGUUUAUUGCUAAUGCAGCAUCAUCAAGAUUCACAUUUAAUUGCAUUUUAAAUGUCGAAUAUUUGAGAAUCUUAAUAGUGCUGCAUUUGCAAACAACGACUGUG	110	spe-miR172b-5p	GCAGCAUCAUCAAGAUUCACA	21-41	csi-miR172b-5p	0	0	21	21	1
			spe-miR172b-3p	AGAAUCUUAAUAGUGCUGCAU	72-92	csi-miR172b-3p	3	0	21	21	1
spe-MIR5174e	UACUACUCCCUCUGUUCAUUAUUACUUGUCCACUAAACCAAUAGAUUUUCAAAUUUACUUGUGGCUUUUAACAUAUCAAGAGAAAACAAUUAUUUUUUCUACGUUUUUCCCAAAACGUUUACUACUUAUUCUCCAAAUCAUUUUCCAAGACCUAAUACUAAACAUCAAUCAAUUGGGUAUUAUAGUAAAAUAUUCAUAUUAAUUAUUGUUUCUUAAGGGGCAUGCAAAGUCCAAAGUGGACAAGUAAAAGUGAACGGCGAGAGUAUUU	268	spe-miR5174e-5p	UACUCCCUCUGUUCAUUAUUA	4-24	bdi-miR5174e-5p-2	5	0	21	21	1
spe-MIR482b-3	UUCAGAAAUUGGGAAAGGGAUGAAGAUUUUUGGGAAGCUUUUGGCGUGAGUGGUGGGGAAAGAUAGAUCUAUUCAUAUUUGUAUGAUAUGAUAAAUCUUGCCUACACCGCCCAUGCCCAUGGCUUCCAAUUAUUUCUCCCUUUCCAUACAAUUUCUUCA	159	spe-miR482b-3-5p	CGUGAGUGGUGGGGAAAGAUA	45-65	nta-miR482b-5p	5	0	21	21	2
			spe-miR482b-3-3p	UCUUGCCUACACCGCCCAUGCC	96-117	sly-miR482b	0	0	22	22	1
spe-MIR482d-2	AGGGAUUUGGGAAUCUUUUGGAGUGGGUGGGAUGGAAAAAUAUUGUAUUUGUUUUUUUUUUCUGAAGGGAAAAAGAUGAAUAUUGAGAUUUUUCCUAUUCCACCCAUGCCAAUGGCUUCCAAUCAUU	127	spe-miR482d-2-5p	GGAGUGGGUGGGAUGGAAAAA	20-40	sly-miR482d-5p	0	0	21	21	1
			spe-miR482d-2-3p	UUUCCUAUUCCACCCAUGCCAA	91-112	sly-miR482d-3p	0	0	22	22	1
spe-MIR171c-3	CUAACGAGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAAAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCACGUAUU	92	spe-miR171c-3-5p	AGAUAUUGGUGCGGUUCAAUU	7-27	cas-miR171c-5p	1	0	21	21	1
			spe-miR171c-3-3p	UUGAGCCGUGCCAAUAUCACG	68-88	cas-miR171c-3p	0	0	21	21	1
spe-MIR5026-2	UUUUACCCUUUUUACGGCCUAUGUGGUACUAGCUUUAAAAAAAAUGUAAACAUGUGAUGGACUCACAAGAUAGUGUCACGUAGACCGAAAAGGGGUAGAA	100	spe-miR5026-2-3p	ACUCACAAGAUAGUGUCACGU	61-81	ath-miR5026	3	0	21	21	1
spe-MIR8042	UACCUAUAUAGUAUGUUAAACCACCAGAUAAGCACUUCCAUCUAAUUUCUAAAAGGUGGUCAAGGGAACGAGGUGGUGAAACACAUGUGACUUGACACAACUUUCAGAAAUUAGACUGAAAUGCUGAUCUGGUUUCUUAUAUACAUUAUACAUAGUUU	158	spe-miR8042-3p	AUUAGACUGAAAUGCUGAUCU	110-130	stu-miR8042	1	0	21	21	1
spe-MIR2111a	CUUCCAAAUUGGUCGGACAAGCCGUGAUGGCCAACGGUAUGCAUAGACAAGGUCAUGACGGAUGUCCACGUAAAAAUUUGGCAUUUUUGACGUCGGAAUCCGGAUCACCCAAAAAUGGUGUGCUAUAGC	264	spe-miR2111a-5p	GACGUCGGAAUCCGGAUCACC	89-109	cas-miR2111a	5	0	21	21	1

spe-MIR7711	ACACGAAAAUCGUCGAAAUGAGGGGUAUGCUCGCUUCGGGGCUCGUUUAACCUUCCAAAUUGGUCGGACAAGCCGUGAUGGCCAACGGUAUGCAUAGACAAGGUCAUGACGGAUGUCCACGUAAAAAUUUGGCAUUGAGAAUCGAUUUCUCAGAUGAUCACUCGAUUGAACUAAUAGUUACUUUGUGAAAUAAUAACUAGUACUCAUAAUUAAUCAGUUGACCGAGUGACCAUUUGAGAAAUCAAUUCAUU	116	spe-miR7711-3p	CCAUUUGAGAAAUCAAUUCAUU	95-116	bdi-miR7711-5p-3	4	0	22	24	1
spe-MIR1043	UGCCCUUCAACUUUAGGUGUGCACAAGUAGACACUUAAACUUGUAUAAAAUUGAACAAAUAGAUACACAUGUCCUACAUGUCACCCUACAUGUCAUUUUUUGUCCUACGUGGUGUCCUACGUUUAUUUUGUCAUAUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGUUUGUACAUUAUGAAAGUUAGAGGUUA	212	spe-miR1043-5p	CCUUCAACUUUAGGUGUGCA	4-23	ppt-miR1043-5p	3	0	20	20	1
spe-MIR7981-10	AUUAAAUGUCAGAGAGGUACACCUUAAUUAAACUAAGGUCCUAUUACCCCCCUAAACUUUUUUUGUAAUUCUGUGCACCUUUUAUCUUAUGUGGCACACUCCGUGACUCUAAGCAAUUGAGGCACGUGAGAUACUUUGAUGUCACGUAAGUAAAAAAGGUACACAAAAUGACAAAAAAAAAUAAGUUCAGGGGAUAAUAGGACCUUAGUUUAGUUAAGGCGUGUCUAUGGAAUUUCGG	239	spe-miR7981-10-5p	CUUAAUUAAACUAAGGUCCUAUUA	23-46	stu-miR7981-5p	2	0	24	24	2
			spe-miR7981-10-3p	AUAGGACCUUAGUUUAGUUAAGGC	198-221	stu-miR7981-3p	2	0	24	24	1
spe-MIR10532-8	UAGGUCGAAAAGGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAGGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUCGGGAAUAGGUUGAGGGGGUACUUGGGCAUUAUCCCUUUAUGCAAAUAUGCUUUUUUCCUUCAAUUUCUUGAUCCUUUUAUAGAUUUGAUUUGCCUUGAACUUCUACAAGGAAAGGAAUUACAAAUUUUUUUCCUUCUUGAACUUGUCUAUAUUUACUUCUUUCCUUAUUUGACUUG	266	spe-miR10532-8-5p	AAGUGUGUCUCUGAGAUUUCGGGA	71-94	sly-miR10532	1	0	24	24	1
spe-MIR7540b-2	UUUUAAGUUCCAAGUGAUUAAAGAAAUAUUCAGCAAGGAUGUUAAUUUCAAAUGUGAUAUUAAGUAUGAUUUGCCUAAUGUAUGUGCCAUUAACUUUAAGUGAGAGAUUAAUUAGUGGCUGAUUAGGAUUAAAUUAAUCUAGUGGGCCCCACCACUCAAGGCAAAUUAAAAGGAAUCAGAUUGGGAGCUGGCCUUAGUGGGACACGUGUAGAGGGGGCCUGCCUCCACUUCAUAUUAUAAAUGAGGUGGUGAAAUGCAUUGCAACAUAUCAUCUUCUUCACCACUUGGCUUAGGC	295	spe-miR7540b-2-3p	UCAUAUUAUAAAUGAGGUGG	230-249	lja-miR7540b	5	0	20	20	1
spe-MIR403b	AUUGGAAAAGCCAUAUUACGAGUUUGUGCGUGAAUCUAGCAAACAACAACAGUUUUUCUGAUGAAAAGAGUCGUUAGAUUCACGCACAAACGCGAAAUAUGCCUCUUCCUGA	112	spe-miR403b-5p	AGUUUGUGCGUGAAUCUAGCA	21-41	csi-miR403b-5p	2	0	21	21	1
			spe-miR403b-3p	UUAGAUUCACGCACAAACGCG	74-94	csi-miR403b-3p	1	0	21	21	1
spe-MIR9758	ACACUUAAAAGCAUUCCGUUACUUUACUAACUGAAUCUCGCAACUUGAGUAUGAAAUACAUCCCUAAUUUCUCGCCAGAUUUAGGUGUAUUUUCAAACUCCAUGUUCCUCCAAGAGUUUGAGAUCACUUGUUAUGUCAUGUGUCAGAUCUGACGUGUAUUGGGGUGUAUAUGAGUUUAGUUAGUCAAGUAUAGAGGUGCUUUUAAGGCU	209	spe-miR9758-3p	AGUUUAGUUAGUCAAGUAUAG	173-193	gma-miR9758	5	0	21	21	2
spe-MIR10538-8	CUAAUAGCAUUAGGUUGAUAUACGUUACUGUAAGUAACGUUUUACUUUUAAAACGUUAUUUUCAGUAAUGUUUUGCCCCUAAAACGUUACUGUGAGUAACGUUUUAGGAGUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGAUGCCAUCAA	154	spe-miR10538-8-5p	AGGUUGAUAUACGUUACUGUAAGU	12-35	sly-miR10538	4	0	24	24	1
spe-MIR5174d-4	UUACUCCCUCCGUUUCAAAAAGAUUGGCUUAGUUUGACUUGGAACGGAGUUUAAGAAAAGAAAGAAAACUUUUUAAUCUUGUGGUUCUAAUUUAAAAU	255	spe-miR5174d-4-5p	UCCCUCCGUUUCAAAAAGAUUGGC	5-28	bdi-miR5174d-5p	1	0	24	24	1

spe-MIR8742b	UAUGUCAAAUGUACCAAAAUACCCUUUAAUCUU GUGAUCUUAAACAUGUCAUGUGGAAAGUUAAAG UUAAAGUGUUGCCAAAAAAGGAAAUUGGUCAUU CUUUUUGAAACAGACUAAAAAGGAAAUAGGACC AUUCUUUUUUAAACAAAGGGAGUAU CCAUAAAAGAUAUAUUUCUAUAUGACAUUAUAC AUAAAUAUAUUAUUUAACUUGGUCUCCAUUCAC AUUUACACCCUCGAGCUCUGGGUGUGGACAAG UAGAGAAUAGAACUUAGACACAUGAGUUCUACU UGACAUGGUAUACAUAGGCCUCAAAUUGUUAU GUAGGACGUGUGUGUCUAUUUGUUCAACUUUA UAAAAAUUGAAGUGCCUACUUGUAUAAAUCCAA AAUUCGCGAGCGCAAGUGUAAAUUGAGUCCAA GUUAAAGGACAUAAUACAUAAAUAUGCCCUUUA AUUUGAUCUCAUUUUACAU UACAUAUAAAUAUACAUAUAUAUAUAUAUAUAUU UGUGGAAGGGAGUUUACAUGAUAGAAAUGGAG AGUGGAUUGCAGCCAGGGAUGACUUGCCGAUG AUUUUUUUUUGUAGUUUUCCUAUUAAAGAUUAU GUUUCGGCAAGUUGUCCCUGGCUACCUUUCGC UCUCUUCUUCUCAUGCGAAUUUUUUUACUCACA CUUAUUUAUUUUUAUUUUGUUAUUUGUCAUAAU	312	spe-miR8742b-5p	UAUAUUAUUUAACUUGGUCUC	39-59	gra-miR8742b	5	0	21	21	1
spe-MIR169a-3		229	spe-miR169a-3-5p	CAGCCAGGGAUGACUUGCCGA	76-96	cas-miR169a	1	0	21	21	1
			spe-miR169a-3-3p	GGCAAGUUGUCCCUGGCUACC	137-157	aly-miR169a-3p	2	0	21	21	1
spe-MIR5021-1	CUUCUUCUUCUUCUCUAUCUUCUUUGUCGUCG UCUUCAGACGUGUCUUCGUGUUCAUCUCCAAA CACUAAUGUGCUCAUGAAGAGUAGAUCAUUGG CUUUGAUUAUGAGAAGAAAAGAAGGUGGAAUUA UAUUGGAAGAUAAUAGUAUUGGGAAGAAGAAGA AGAAAAAAGAAGGAUUUUUGUCAAAAUUAUUAA AUCCUAAGAGAAAUAGAAAGGAUGAAGUAU	225	spe-miR5021-1-3p	UGGGAAGAAGAAGAAGAAAA	149-168	ath-miR5021	1	0	20	20	1
spe-MIR5014a-7	CAUAAUAUAUAAAUAUGCUCAUUGACCUGACUU CAGUCGACAUUUAUACUUUCCAACUUUGAGUG UACACAAGUAGACACACGUGUCUUAUGUGACAU AAUACACUUAGAAUGUCAUGUAGACACAGAAUC GCCAUGUAGAACGUGCGUCUUGUAGGACGAAU GCGUCUAUUUGUUUAAUUUAUAUAAAUUUAAGU GUCUAUUUGUGCACAUCAAAAAUUAAAAAUCAU AGUUAACCAUUAAAGUUAAAUUAAGCAUCAUGU UUACUUUAUUGAA	275	spe-miR5014a-7-3p	UUAUAUAAAUUUAAGUGUCUA	181-201	ath-miR5014a-3p	5	0	21	21	1
spe-MIR6472	CACAAAAUUAGAAUUUAAUGUUAAAAAUUUUUA GUAACGAUUUUUUGGGCUUUUGUGGCGAUUAC UGUCGCCGCUAAAGGUCUAGUUCUUUUGUAGU GAAUCCUAGUUGGCAAUGCUUAGGUGGAAGGA UUAGUCCCACGUGGGUUGCCAAGUCAAUAAAAA UAUGGGGUGUUAAAUCUUGAGGGUAUAUGUGG UCUCUUAAGAUAAUACCAAGGACAUUUUUUAUC CAAAAAUAUAACGAAGGGUAUAAGUGGUCUAUU UCACAUAGUUCAGAGGCAAUUUUGACCCUUUU CAAUUUAAAAUAUAAUAAUUUUAUA	317	spe-miR6472-5p	UAGUGAAUCCUAGUUGGCAAUG	94-115	ptc-miR6472	5	0	22	22	1
spe-MIR5021-2	AAUGGCAAUAGAGAAUAAUGAUCAAUCUUUUUU UUUAGAUGUGCUUUACUGUGAAGAAGAAGAAG AAAAAUGGGGUGAUUUGUUAGAGGAUGAAGAA GGGGUUAUUAUUAACCCAUUGUUGUUAUCUUC CGAAGGAACAACAAAGACUAAUUCUUUAUUAUU AUUACCUCU	171	spe-miR5021-2-5p	UGUGAAGAAGAAGAAGAAAA	50-69	ath-miR5021	1	0	20	20	1
spe-MIR7983-4	UCCCAUCACAACAACAAAAAAGACCAUUAGCGG CAUUUAAUUCUUAAUUGCCGCUAAAUAUAUAUU UUUAGCGGCAAUUGUCACUCUUUGUAUAUGUC CCUAAAGCCUUUAGCGAAAUUGGUUGUAAUGA CAGUUAACUAAUGCCGGUAAAGACUUUAACACU CUUUAUUAGUGUCAAUAUUUAAUGCCGCUAAAU GUUAUUUUUAUUGUAGUGCAUGUUU	221	spe-miR7983-4-3p	ACUAAUGCCGGUAAAGACUUUAAC	137-160	stu-miR7983-3p	0	0	24	24	1
spe-MIR7980b-6	UGACCAUGUGAUAUCAUAUCAUGAUAUUGUAUU GUGAGAUGGAAUCAGUGUUUGGACAUACGAUU UUACGCUGAUUACAUCUCAUGAUUUCAUAUCAU	149	spe-miR7980b-6-5p	GAGAUGGAAUCAGUGUUUGGACAU	36-59	stu-miR7980b-3p	0	0	24	24	1

spe-MIR856	GAGAUGUGAUACCAUUUCCUCCAAAAAUCAUGA UAUGGAAUCAUAUGGGAU GGGAAUAACUUAUUUAAUCGCCUGACAACUACA UGCAGUUGUUGGACCAUUUUGUAUCUGAAAGA UAUGCAUAAUUAUUCUUAUAAAUAACUUCAGUA GUUGUCCAGACAACUGUAAAAGUUGUUGGC	128	spe-miR856-3p	UAUUCUUAUAAAUAACUUCAGU	76-97	ath-miR856	5	0	22	22	1
spe-MIR821c	GCAAUAAAACUCAAAUUCAGAUAUAAGUUGAUU UGUGCAUGCAUUUGCAUAUUUGAACUUUGAUA UAUAAACAUGGACUAUGUUUAGAGCACACAGGU UCAUAGUUGACUGUGUGUUCGUGUACUUUAAA AUGGUAUGAAAUACACGUGCAUUGCACGUGUU CGAGAACUAGUAUUACUAAAAGCAUGAACAAAA AAGUUGAAAGUUGAAUUACGAUUUUAUCCU	225	spe-miR821c-3p	AAAGCAUGAACAAAAAAGUUGAAA	181-204	osa-miR821c	4	0	24	24	1
spe-MIR5303d-4	GGCCUUAGUUGCGCGAACUCUUCACUUUUGAU GCCGCACCCGUCUCGGAUUCUUCAAAAAUACAC UACUUUUGGAGAAUCCGACACGCACCCGUUGG CAUAUUUGAAGAGUCCGAGCAACAUAAGCAA	128	spe-miR5303d-4-3p	UUUUGGAGAAUCCGACACGCACCC	69-92	stu-miR5303d	0	0	24	24	1
spe-MIR9563b	UGAAUUUUUUCACCCUCGCUUUUUGUUGGUGA ACCUUUUUGUUGGCUGACGUAACUUAGGCUAG GUUCAUAAGAAAGAAGAGAUGAAUUCUAAACUG UUAAAAGCAAUGUUUGGCCACUUCUUGGGCAA AAUAACUGCAAGAAAGCUACGUUAGCCUACAAA AAGGUUCACCAACAAAAAACGAUGGUUGAGAAA AAUCCA	201	spe-miR9563b-5p	GAAAGAAGAGAUGAAUUCUAAA	73-94	bra-miR9563b-3p	5	0	22	22	2
spe-MIR10215	GAGAACCCAUUCUCUAUUUUACUUUCUAAAUAU AAAGAAUGGAGAGUAAAAUAGAGAUGGGUUGG A	66	spe-miR10215-3p	AAGAAUGGAGAGUAAAAUAGA	35-55	eun-miR10215-3p	5	0	21	21	2
spe-MIR11089a	UCAGAUAUGAUUUAAGAGAGAAGAGAUGAAGGC AGAUUUGGUCCCACUGGGCGUGCCAAUUUUGU UUGCAACAAAUUUUAAAGUGACAGACAAUAAAU UGCAAUCACAAAUAAAAUAUUAAGAAACAUGAU UUUAUUGAUUAAGAUAGUGGGUACAAUUCUGU UGAUCCUUUGAUUCUACUCUCCUAAGAUUUAUC CAU	199	spe-miR11089a-3p	AAGAAACAUGAUUUUAUUGAU	120-140	lja-miR11089a-5p	5	0	21	21	1
spe-MIR8011a-4	UACUUUGUGUCUCACACAACUGACACAAGUUGU GUGGGGAUUCUUUUUGUUUCACAAAUUUGUGG ACCAAAAGUGUAAGACUAGGGUCCAGAAAUUUG UAGAUCAAAGCCUCACACAACUUGUGUCUGUU GUGUGAGACACAAAAUG	147	spe-miR8011a-4-5p	UUGUGUGGGGAUUCUUUUUGUUUC	30-53	stu-miR8011a-5p	2	0	24	24	1
spe-MIR9779	CAAUCAAAUACAUCACUUUACGCGAUGUAUCAG UCAUAUAUAUAUAUAUAUAUAUAUAUCACUU UACGAUAUAGUAGAACAUACACGAUGUAUCGCG ACGUUACUCUACGAUGUAUUAGCCAGAUAUAUC ACUUUAUACAACGUAUCAGGACGUUGAGUGAU GUAUUCGAAAC	175	spe-miR9779-3p	UUUAUACAACGUAUCAGGAC	135-154	tae-miR9779	5	0	20	20	2
spe-MIR5770b	GGCCUAACACGUGGAGAUCGCCCGUGUUGAGA UCAAGUUAUGAUUAUUUGGGCACGUGGAGAUC GUCCGUGCGAUAGAAAAGUUAUGAUUAUGAUU UGGGCACGUGGAGAUCGUCCGUGCGCAUUUUG UUUGAUUUAUGAUAGUGCAUUGAGAUCGUCCG CACAGACACGUGGAGAUCGUCCGUGUCAGUAU	192	spe-miR5770b-3p	UUAUGAUUAUGAUUUGGGCAC	83-103	gma-miR5770b	5	0	21	21	1
spe-MIR11082l-2	GCAUAUGACUGCAACCAUCACUUUGUGAGAUAA CUAUUUCUUUUUUCAAUUUCAAAAUAAUAGUUA UCUCACAAAGUGAUGGUUGCAGUCAUAGAA	96	spe-miR11082l-2-3p	UCACAAAGUGAUGGUUGCAGU	69-89	lja-miR11082l-3p	5	0	21	21	1
spe-MIR2873b	UUUACAACACCAAACCAAGUCAAACUAAACCAC UAGUCGGGGUUGUUUUUUUUUAGUUUGACUUG AUUUAUGGUUUGGUUCGAUUUUCGGUUUGGUU UUGUGCA	104	spe-miR2873b-3p	UUUGACUUGAUUUAUGGUUUG	57-77	osa-miR2873b	5	0	21	21	1
spe-MIR7993b	CACCUCAACCCCUAAUACAGUGUUCCAAUUAGA CACUUUUGGUUCAAAUGUUGGGGAAAUUUUGA GUGGUCUUGUACGUCUAUUUGGUAGUUAAGUU AACCACAUACAGUAUGUCAUUUCAUUUUAUUUU ACACAUUCACCUCGAUAAGCCGUAAACCACAUG CAUUUUCCACUUGAGGUUGAUGUGUAUAAUUA AUGGACAGCUUAAUUUACGUGGUUAAAUUAACU ACCUGGGUCAAAAGUGUUUACCUCAAACACUUU	276	spe-miR7993b-5p	UUAAGUUAACCACAUACAGUAUGU	91-114	stu-miR7993b-5p	2	0	24	24	1

	AUAGGAGUUGAGGUG										
			spe-miR7993b-3p	UUAAUUUACGUGGUUAAAUUAACU	205-228	stu-miR7993b-3p	4	0	24	24	2
spe-MIR7533b	UAUAAUUAUAAGUGUAUAUGACGAAAAUGUAUG UAUUUGUAUUUGUAUAUACAAUUUUCUCUCGCU UUAUACAAACACAAAAUCAUUUUAUACAUUUGU AUUUGUAUAAAGUGAGAGGGGAGAGGGAGAGG CUGGCAGCAAGAAAUGGACAAUGGCGAGCGAG AAACUCAGGGAGAGAGGCGAAUGACAAUUGUU UGCUACGGGUUACAAUUAAAUCAAACUGUGGU UAUAAUAUUUAAUUUGA	244	spe-miR7533b-3p	GAGGGGAGAGGGAGAGGCUGG	115-135	lja-miR7533b	4	0	21	21	1
spe-MIR7992-7	ACACUAUUGGCCUCAAUUUCCAAUCAAUACUCC AACUUUGGAGUGCACAUCCAGAUACUUCAAAUC AUGUCCACUAUAUCAAUUGAACACUCCAACAGU CCAACUUACAAAAAGAACUUGUAGACACCACCA AAAUUUACGUGUCACGUCAACGUCGAGUGUCC ACAAGAUCAGUGGGACAGAGUUGAGAUGUCUA GAUGUGCACUCCAAAGUUGGAGAGUAUUAUCU AAGUGUUAUGCCAAAAGAAA	248	spe-miR7992-7-3p	UGUCUAGAUGUGCACUCCAAAGU	191-213	stu-miR7992-3p	2	0	23	23	1
spe-MIR7992-8	UUGCUCAAACUUGGUCUCAACUGGCAAGUGAA CACUCCAACUUUAAGUAUGCACAUCUAGACACU UCAACUCGUCUCCAAUGUGUCAUUGUCUCCUU UGUGUCAGACUGUUAGUCGUAUGCUCCAACUU ACAAAUUAUAAUCUAGACACCCCCAAUUAAUCA CAGCGUUGAGUGUUCACAAGACAUAAUGAGGA CGAGUUGGAUUGUUUAGUUGCCAGUUUAGACC GAGUUUAGGUG	237	spe-miR7992-8-5p	UUUAAGUAUGCACAUCUAGACACU	42-65	stu-miR7992-5p	3	0	24	24	1
spe-MIR1088-2	GGAUGACGGAAGCAUAGAGAGCACAAAUGAAG UGAAAUGCUUUUUUUAUUGUUAAGACUCUCCA GAUUUAGCAGCAGCAUUCCAUCAUAUGUGCUC UCUAUCUUCUGUCAACA	113	spe-miR1088-2-3p	AUGUGCUCUCUAUCUUCUGUC	89-109	smo-miR1088-3p	4	0	21	21	3
spe-MIR1446-2	AUAUUAAUGGAAAUCCAGAGUUUUCUGAACUCU CUCCCUCAAUGGCUGUUCAUAUAAUAUAUGCU GCUACUUUGCAGCUUAAUUAAAUAACAGCUUUG GGGUUUUGAGUCCAGAAAACUCUUGCUUUCCU AGUUAAGCA	139	spe-miR1446-2-5p	UGAACUCUCUCCCUCAAUGGCU	26-47	nta-miR1446	0	0	22	22	1
spe-MIR8668	UGGUCGCCUUGGCUUACAGAAACAUUUUGGAA UGAUGACUAUAAUGAGUGGGAUAACCUGAGAAA UGUUUUUGUACAAGGAGAUAU	86	spe-miR8668-5p	UUUUGGAAUGAUGACUAUAA	25-44	gra-miR8668	4	0	20	20	1
spe-MIR395b-2	UGCAGUGAUUCCCGAGAGUUUCCUUGACCACU UCAUGAGGGCUUAAUUACUUUGUUGUUUAUCC CUUGCUGAAGUGUUUGGGGGAACUUCUGGGUU CACUUUA	103	spe-miR395b-2-3p	CUGAAGUGUUUGGGGGAACUUC	69-90	sly-miR395b	1	0	22	22	1
spe-MIR1023e	UCCAUCUCUAAAGACAAGUAUAACGUUUUAGAA AAUGAUUUUGAGAGGUCUCUUUAAGAGUGUCC CGUAUGUAAAAAGAACACAAAAUAUAUACCCCA CUUAACCUAUUUUGUGUUCUUUAUUACACAUG GGAACACUCUUAAAAAGACCUCUCAAAGUGGUU UUCUAAAACACUCUCCUCUUUUACCUUGUCUUU AGAGAUAGG	205	spe-miR1023e-3p	ACACUCUCCUCUUUUACCUUG	171-191	ppt-miR1023e-5p	5	0	21	21	1
spe-MIR8009-1	UCCAUCUCUUUUUUCAACUAAACUCAGAAAAGC GACGGACAGAAACCUUUAGUCCGUCGCUUUUC CGGCUACUUUAAAAAAUUCAUUUCCAGAAAAGU GACGGACAGUGUCCUUUAGUCCGUCGAUUUUC UGAGAUUUUCAAAAUAUAAAUUUA	154	spe-miR8009-1-3p	AUUUCCAGAAAAGUGACGGACAGU	85-108	stu-miR8009	1	0	24	24	1
spe-MIR408-2	UAUGGAUAGACGGGGACGAGCCAGAGCAUGAG AUGUGCAAUUUUUGCUUUGCCUAUUCCAUGCA CUGCCUCUUCCCUGGCUUUCCUCU	88	spe-miR408-2-5p	ACGGGGACGAGCCAGAGCAUG	10-30	sly-miR408	0	0	21	21	1
			spe-miR408-2-3p	UGCACUGCCUCUUCCCUGGCU	61-81	aof-miR408	0	0	21	21	1
spe-MIR529	ACAUGUAUCUGUAUUCGUAUAUACAAUUUUCUC UCGCUUUAUACAAACACAACACAAUGUAUACAU UUCUGUUAGUAUAAAGUGAGAGAGGCGAGCGA AAUCUCGGAGAGGAGAGAGAGCGGAACGAAAA	248	spe-miR529-3p	AGAGGAGAGAGAGCGGAACGA	107-127	aqc-miR529	5	0	21	21	1

spe-MIR7997c-7	UAUAUGUAUAUAUACAAUUUUCUCUCGCUUUUUACAAAUACAAACACAUUUUAUAUAUUUGUGUUUGUAUAAAAGCGAGAGAGACAAGUGAGAUUGUCACCAAACGAGAGUGACAAGCAGAAGCUAUGUUUCUCGGACUCUCCAGAAAUGCUACGUAAUUCACUAUUUUUGAUGGAUCCGACAUGCACCCCAUACUGUUUUUGAAGAGUCCGAGAAGCAUAGCUGAG	109	spe-miR7997c-7-5p	AUGUUUCUCGGACUCUCCAGAAAU	8-31	stu-miR7997c	4	0	24	24	1
spe-MIR5014a-8	UAAUGCACAAACAGACACUUUAACUAUCCAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGGAAGAAUACACGUAGGAUACCACGUAAGACAAAAAAUAACAUGUAGGACGACAUGUAGGACGUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCUAUUUGUGCACAU	179	spe-miR5014a-8-3p	UUAUACAAGUUUAAGUGUCUA	148-168	ath-miR5014a-3p	5	0	21	21	1
spe-MIR7699	UCCAAAGUGUAUUCAAUCCAUUAACUCCUUUGAAGGAAUUCCAAAAUUUGAACAAGUAAACACACAUGUCCUACUUAAUUUCUUAUGUGUACCAUGUCAUGUAGCACAUGUGUGUCUACUUGUUCAACUUUAUGAAGAAGCUUGAGUCUAUGAAUAUGAAUAUAUUUUUAU	171	spe-miR7699-5p	UGUAUUCAAUCCAUUAACUCC	8-28	mtr-miR7699-3p	4	0	21	21	1
spe-MIR6028	CCCCUUUCAUGAAAAGUUGUGACAUUUAUGAAGAGUUGCGACUUUAAUGAAGAGUUGUGACUUUUAUGGAGAGUUGUGACAUUUACAAAAAGUUUCGACUUUUAUGAAGAGUUGCGACUUUUAUGAAAAGUUACGACUUUAAUGAGAGUUG	151	spe-miR6028-3p	UGGAGAGUUGUGACAUUUACA	67-87	bna-miR6028	5	0	21	21	1
spe-MIR396g-1	AUCUUUUUUCUAAUCACAAAAAUUUCUUAAAAUUUAUGAAUUUUGGAUACUUUCGAAUACAUAACUGAGGGAUGUAUCAAGGAGAUAGGAUAUCUGGAUACAUCACUGGACUUCCAGAUAUAUAAGUGAUACAUAAGUGAAGGAUGUAUUAGAGAGGAUAGGAUAUCCGAAUACAUCACUGGACUUCCGGAUACAUAAGCAGACAUCCGGUUACAUACGUAAGAGGAUGUAUUUCGAGAGGGAGAUAGAGAUGUAUCAUCCAGAGGAGAGUGAUAUAUCCGAGAAGAAAUUCUUAAAAUUCUUAUAAAUGAUGGAAAAUUUUAGAGAUUAUGAUAAAAUAA	341	spe-miR396g-1-3p	UUCUUAAAAUUCUUAUAAAUG	290-310	gma-miR396g	5	0	21	21	1
spe-MIR4413b	GCCAUUUAUCUGGUGUCUCAGAUACAUGUAAAUCACUCCAGAUACAUGUACCUAGUGUAUAUCUGGUGUGAUUCACAUGUAUUCGAGAUACAAACAAAUCUU	102	spe-miR4413b-5p	UCAGAUACAUGUAAAUCACU	18-37	gma-miR4413b	5	0	20	20	1
spe-MIR5014a-9	ACUUUUAACUUUAGGUAUGUACAAGUAGGCACUUAAACUUGUAUAAAGUUGAACAAAUAAGACACAUUGUCCUACAUGACACCCUACAUGAAACUUUUGUGUCCUAUGUUAUUAUGUCAUGUAGAACAUGAGUGUGUACUUAUUCAAUUUUAUACAAAUUUAAGGGUCUAAUUGUGCAUACUCAAAGUUAAAGGAAAUUUAAAAAUAAACUUCAAUCAUCAUGCUAUGAUGGCAUUCCCAAUGGUAUCCUACAUGUUGAUCCGCCCUUAGCCCCCUCCCCCAGAUGAGUAGGCAAUUGAUCGCAAAUACCAACCGGUAGAUGUAGGUAUUAGUUCAAUUUCUUGACUCAAGUCAACAACUCGGCAUAAUGACUAGAAUUUGCAUGUUCAUAUUUGCGAUUAAUUUCCUAACCAGUUGCGGGAAUCAACAAGUAGGAUACCCUUGAGAGCAUCAUCAUAACAUGUUUUGCGCUUGUUUUUUAAUUU	195	spe-miR5014a-9-3p	UUAUACAAAUUUAAGGGUCUA	150-170	ath-miR5014a-3p	5	0	21	21	1
spe-MIR10540-3	UAUAAAAUAAAACAUAUAUCGUAAAAUAAAAUUAAAAUAAAUGUAUAAAAUAUUAAAAUAUUAAAUGUUGAGCCCGUGCUUAGCACGGGCAACACUCAUCUAGUACUACAAGAAUUACCUUAUUGCUGCCCCAAAUCUGCAGAUGAGUAAUUCCGGCGAGAUACGACGGCUUUAGCCGUAAUAUUUGGUCUUCACCAUUGUAGACCUUUGACUGUAGUAACUUUUCAUUUCUUUUUGAUGUCCUUGAUUUUAAUUUAUAUUGUUUGUUUAGUUUAUUUUUUC	290	spe-miR10540-3-3p	AUAAUGACUAGAAUUUGCAUG	170-190	sly-miR10540	5	0	21	21	1
spe-MIR2864	ACAAAAUUAUUGAAAAUUGGUCGGAUAAUUUAUUUAAAAGGGGGUUGAUUUAUGGGUCGGAUUAG	282	spe-miR2864-3p	UUUUGAUGUCCUUGAUUUUAA	233-253	osa-miR2864-1	5	0	21	21	1
spe-MIR773b		296	spe-miR773b-3p	CAUAUUUGAACCAAAAGUUGG	208-228	aly-miR773b-5p	5	0	21	21	2

spe-MIR5568b	GUGUUUAUAAGUCCGAAUAUCUUUCCAUUUUCAUAUAAAUGUUAUGUGGUAAGGCCAAAAUGACAUGGCAAUUCCAUGUGGCAUUUAAAGAAAUGAAAAUGAGUUGGAUAUGUCCAACAUGGCAAAUAACGCCCAUAAGGGCAUAUUUGAACCAAAAGUUGGAUGGCGAAGGCAUCAGUGAACCAAAUUUUAAACGGAGGGUAUAUCUAGACAUUUUCUAAUAGUUUAGGCUCAGUAAUUAAUUCUAUGGUCCCUAUAGUGCCCAUAUUUAACUAGAAUUCAGAGUUCUAUUUCUAUGGAAAAAGGAAGAAUAAUAUGGGUUUUUCUAGUUUUCUAGAAAAACUAGGUUUUCUAGUCCUUUUGGAUUAGGAAGACAUCUCUAUAAAUAGAGAUUCUCCUAACCUAGCAAAUAGAGGAAUUAGUUUCUAUUUGAUACUUGCACACUCAAGUAUUGAGAGAGUUCGGAUGUGACUUGGGAUCACUGUAGAAGACCAUAGCUAUUGUUUAUCUUGUUUUAUACUCCCUCUGUCCCUUUUUACUUGUCCACUUUUGAAUUGACACACCUAUUAAGAAAAUAAUUAAUGACGUAGUGAGUUUACCCCUAUUAAUUAUGAAGUGGAUGAAAAGUUCUACAUUUUUCAAAGUAAUUAGUCAUUUAAUUGUGGGUAUAAUAGGUAAAAAAAUUGUCCUUUCUUGAUUUAUCAAAAUGGACAAGUAAUUAGGGACAACUAUAAAAGGAAAAGUGGACAAGUAAUUAGGGACAGAGGUAGUAUCUU	285	spe-miR5568b-5p	UCUAGUUUUCUAGAAAAACUA	95-115	sbi-miR5568b-3p	5	0	21	21	2
spe-MIR5049b-1		264	spe-miR5049b-1-3p	AGUAAUUAGGGACAGAGGUAG	238-258	hvu-miR5049b	3	0	21	21	1
spe-MIR395a-3	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCGCUUCAUUAGGGUUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAU	107	spe-miR395a-3-3p	UGAAGUGUUUGGGGGAACUCU	70-90	aof-miR395a	0	0	21	21	1
spe-MIR395a-4	UGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAAGAGUCCUAGCUGUGGAUGAUGAACAUGAUAAUUCAUGUAUAAAUAUAUUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGA	151	spe-miR395a-4-5p	UGAAGUGUUUGGGGGAACUCU	4-24	aof-miR395a	0	0	21	21	1
spe-MIR395a-5	GAUGCCCUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUAACACAAACAAAUAGAAGUGUAGGAGUCCUGGCUGUGGAUGACGAACAUGAUAGUUCACGUAUAAAAUCUAUUAAGGUGAUCCCUGGAGUUCCCUUGACCACUUCAUGAGGGCUUA	166	spe-miR395a-5-5p	UGAAGUGUUUGGGGGAACUCU	11-31	aof-miR395a	0	0	21	21	1
spe-MIR1432	CCACCAAGAGAAGGGUUACAAGAAGGUUCUCUUACCUUGCUCUUGUCACGUCUCUUGGAAGGUUCCUUCCAAACUUCUGGUUCCUUGUCUUGGACA	96	spe-miR1432-3p	CUUGUCACGUCUCUUGGAA	42-60	vca-miR1432-3p	5	0	19	19	3
spe-MIR11314-1	UAUGAAGAGUUGUGAGUUUUAUGAAAGGUUGUGACUUUUAUGAAAAGUUGUGACUUAUAUGAAAAGCUGCGGCUUUUAUGAAAAGCUGUGAAUUUUAUGAAAGGUGACGACCUCUCCGAAAGAUUCUGACUUUUCCAA	138	spe-miR11314-1-5p	AGAGUUGUGAGUUUUAUGAAA	6-26	fve-miR11314	5	0	21	21	1
spe-MIR7984c-6	AGAGGAAAAUGUUUGAAAUAUAUCCAAAAUUUAACCGAAAUUGUUGUAACAAUUCUGAACUUCGGCUUUUACCUCCGUGCACUAUUUAAUAGUGACUUGAUAAAUAUUGCAUCAUUAUAAAUAGUAACGUAUUCAUGUGGGCACAUAUACCUUUAAAAUACAUAAUUAAAUAGUGUAGGGAGAGGAGGAGGAUAAAAUGUCCUUCAUAAAGUUUGAUAUCGUAACAUAAAUUUCGGACAAAAUUGAAAAAAAUUUCAGACCUUUUGCCGAU	271	spe-miR7984c-6-3p	CCUUCAUAAAGUUUGAUAUCGUAA	201-224	stu-miR7984c-3p	1	0	24	24	1
spe-MIR1530-1	UAAUGCACAAAUAGAAAGUUUAACUAUUCAACUUUUAAAUAAAUAAACAUAUGAGUUCUACAUGGAAAAAUACACAUAGGACACCACGUAGGACUAGGAUGACAUGUAAGACAUGUGUGUCUAUUUGUUCAACUUCAUACAAGUUCAAGUGUGUAUUUGUGCACAU	166	spe-miR1530-1-5p	CUUUUAAAUAAAUAAACAUAU	32-52	gma-miR1530	5	0	21	21	2
spe-MIR5298d	UCUAAUUUUCAACGAUUUAUCUCCAUUCGUUGGAUCAUAUUUCUUCUUUGCUCGUGAAAAUGUU	225	spe-miR5298d-3p	UGAAGGUGAAAUGGAGAUGAAAAG	191-214	mtr-miR5298d	5	0	24	24	1

spe-MIR11068c	AAACUAGAACAAAAUCUGAUCGUUCUUAUCGAA UUUCUCUCUUGAGGAGUUCAUUUUUAUCUUCU AUCUGAAGAAAUUGUUGCUGAAAAAUGAUGUUA UUGUGGGCAAAAAAUCUACAUGAAUUGAUGAAG GUGAAAUGGAGAUGAAAAGUUAAUAUUUGG ACUAUCUAGAAUUAGAGACUGCAUGAUGCGUA GAAAAAUUCCCUUCUUCUGAUCUUAUCGUGCC UUCUCUAAUGCUUGAUUCC	83	spe-miR11068c-3p	UUCUCUAAUGCUUGAUUCC	65-83	lja-miR11068c-5p	5	0	19	19	2
spe-MIR10542-2	AAAAUAUACCUUGAACUUUGAUAGAAGAAUCAU AUAUACCCCUAAAUAAUUUUUUUAAAAAAAUUA GAAGUAACAAAUAUAAAUUUAAAACUAAUUUUU UAACUUCCGUUGAAUGAAGGGUAUAUGUGAGC CAUUUUGUAACGGCAGGGGUAUAUGUGAGCCG UUUGUAUAACGGUAAGGGCAUAUAUGAGCCAC UUUUAAAACGAGGGGUAUAUCAGCUCCAAAUAA CAAAGUUGAGGGGUAUAUCAG	249	spe-miR10542-2-5p	UAGAAGAAUCAUAUAUACCCCUA	22-44	sly-miR10542	0	0	23	23	1
spe-MIR5014a-10	CAAGUACAUACUUAGACUUGUAUAAAAUUGAAC AAGUAGACACAUGUGUCCUACAUGACAUGAUAC ACUUAGGAAUCCACGUAGGACACAAAAUUUUUA UGUAGGGUGUCAUGUAGGACAAGUGAGUCAAU UUGUUAAGUUUUAUAUACAAGUUUAAGUGUCUA CUUG	168	spe-miR5014a-10-5p	AUACUUAGACUUGUAUAAAAU	8-28	ath-miR5014a-5p	5	0	21	21	1
spe-MIR5368	CUAACCUUGUGUCAGGACCUACGGGCCAAGGG ACAGUCUCAGGUAGACAGUUUCUAUGGGGCGU AGGCCUCCCAAAAGGUAAC	83	spe-miR5368-3p	GGACAGUCUCAGGUAGACA	31-49	gma-miR5368	0	0	19	19	1
spe-MIR10420-1	GUCAAAGUGUGUCAAUCAGACACAUCAGUUUUU UUUUCUCACUUCACGCGCUCAAAAUGCGUGCC UCAAACGAUUAGUGACAAGUCAGCCAGGUGUG UUUGAUAGGUACACUUUUUG	117	spe-miR10420-1-5p	UCAGACACAUCAGUUUUUU	16-34	gma-miR10420	5	0	19	19	2
spe-MIR7772	CAAUUAAGAAAUAAUUGCCGCUAAUGAUCAUUU UUUUUUGUAGUGGUUAUUGUGGGGAAAAAAAA UCUACAUGAACUGAUAAAGGUGAAAUGGAGAUG AAGAACUAACAUUUGGUGAAAGUGGUGGCUCA GAUGUAUGAAGACUUUGAUCUUUGUUGGAUAA AAGAAAUAUGCAUUUGUGCUAAUUUAUUUUUAA AGU	198	spe-miR7772-5p	AAAUCUACAUGAACUGAUAAAGGU	63-86	bdi-miR7772-3p	5	0	24	24	1
spe-MIR5205a	UACUCUCUCUAUCCCAAUUUAUGUUGACAUUUU UCGUUUUCCGAGGAUCACUUCAAGUUUUGACC GGAAAUUUGCGCAUUGAAUCUUCAAAAAACUAC GUAAAAAGUACUAUAAGUCAUGAUAAUUGAUAA UUCAAAAUGUUUAAAAGAUCUAUGAAAAUUUAC GGUCAAAGAUAGACUUGUUUGAAUCUCGAAAUU GGAAAGUGCCACAUAAAAUGGGACGGAGGGAG UA	231	spe-miR5205a-3p	CACAUAAAAUGGGACGGAGGGAG	207-229	mtr-miR5205a	4	0	23	23	1
spe-MIR10538-9	ACAGCAUUAGGUUGAUAUACGUUACUGAAAGUA ACGUUUUACUCCUAAAACGUUAUUUUCAGUAAC GUUUUACUCCUAAAACGUUACUAUGAGUAACAU UUUAGGAGUAAACGUUACUGUGAGUAACGUAU AUCAAUCUGACGCAAU	147	spe-miR10538-9-5p	AGGUUGAUAUACGUUACUGAAAGU	9-32	sly-miR10538	3	0	24	24	1
spe-MIR399k	AGAUCUUUAGGUCAAUCUGUUUUUUAAACAGAG ACCAAGAUAGUAUCUCCAAAAGGAGAUAAUGCC AAAGGAGAUUUGCCCUAAAGACAA	90	spe-miR399k-3p	UGCCAAAGGAGAUUUGCCCUA	63-83	gma-miR399k	1	0	21	21	1
spe-MIR11124	UGAUCUGAAAUUUGGGUAAGAUUCAACAAAACA GGACACAACAUUGUUUGCUUAGAGGCUUCUUU GUCAUCUUGGUGCUUGAUCGGAGCCUGAAGCU CCAAUAGAUGGAGCGGUGGGCAUACCAUUUGU UGAUCCAUUUUCAAGUGGUGGAGGGACUCCCC AUUUGCCUUCAGAUUCAAGUGGUUCAAAAACAU GAACACUACCAUCUGACAGACCUAAUGCAAACU GGUUUGGAUCUUGUGGAUGUGCUGCAACUACG ACUGGGUGGAUGUUUGAAUUGCUGCAGAAAAA UGACAAGGUUUUAUGAAAAAUUACAUCAAAUAU CAGAAAU	331	spe-miR11124-3p	ACUGGUUUGGAUCUUGUGGAUG	225-246	lja-miR11124-5p	5	0	22	22	2
spe-MIR8006-6	CUGCCUUUCAAAAACUAGAGUGUGUAUGCACU UUACUCUAAUGGAAGAUUAAAUAGGGACACGUG GCGCAAUCUUAUCCAUCGAUCCAAUGUCGGAU	169	spe-miR8006-6-3p	UAAUUUUUGGACGGUAU	153-169	stu-miR8006-5p	4	0	17	24	1

spe-MIR863-1	CGUGGAUAAGAUUAUGACACAUGUAUGUCCGUUAGUAUAAAGGGUAUAUAUGCUCUAAUUUUUGGACGGUAUCAACUUUGGAAUCACACAAAUAGAAGAUACUUAAGCUUGUAUAAAAGUUGAACAUAUAAACAAACAUGUCCUACAUGGUGUCGUACAUGUAUUAUGUCAUGUAGAACUCAUGUGUUUACUUGUUAAACUUUAUACAAGUUAAAGUGCUUACUUGUGCACAUCCAAAGUUG	170	spe-miR863-1-3p	UUAUGUCAUGUAGAACUCAUG	92-112	ath-miR863-5p	5	0	21	21	1
spe-MIR7993d-1	CUUAUGUAUCAAGUAGAUAAGUUAAACACUUAAAAUGUCAACCUUCUUGAUAAUAUGCAUUUGUCUCAAUAAGCCGUAAAACUUCACCCCUAUGGCAAUUGAGGCUGAUGUGUGUCCUUAAAGGAGAGGAGAUGACAUAUUUUAUGUGGUUAACUUAAAUCUAUCUUCUAUCAUGCU	177	spe-miR7993d-1-3p	AUAUUUUAUGUGGUUAACUUAAAU	137-160	stu-miR7993d	1	0	24	24	1
spe-MIR1027c	UUUUGCUAUUUUCUAUUUCAUUCAGAUAAUGCAUGAUGGGCUAUUAUGUUGAUGCACCAGUGGAUUGGUGUUGUAAGAAUGUGAUAUUGGUAAAUGGAUGAGUGGACUAGAAAAUGUGCAUUA	124	spe-miR1027c-5p	UUGCUAUUUUCUAUUUCAUUC	3-23	ppt-miR1027c	5	0	21	21	1
spe-MIR482b-4	UUCUGCUUAAGUUGGUGUCUUACCUUGUAAUUCACUUCUAUCGUGGAUCGCUUCUGCUUUUGAAGUACCAUAGAAGUGAAUUGCAAGGUAAGACACCAACUUAAGCAGAA	110	spe-miR482b-4-3p	GAAGUGAAUUGCAAGGUAAGA	73-93	stu-miR482b-5p	5	0	21	21	1
spe-MIR8008b-3	UUGUCACUUUUCUGGGUUUUAUUUUUUUAAAAAACCCAGAAAAGCGACGGACAUUGUUCUUUAGUCCAUCGCUUUUCAAGAGUUCCAAAAAAUGAAACUUCCAGAAAAGCGAUGG	115	spe-miR8008b-3-5p	AAACCCAGAAAAGCGACGGACAUU	32-55	stu-miR8008b	1	0	24	24	1
spe-MIR1046	GACUCUACCAGACAUGUUAAAUUUGAGUUGGAAUCUACCUGAUAAUUUUUAUUUGAGUUGAGACUCUACAAGGUGUGUUUAAUUCCAACGAUUUUGGAGGUUACUCAACCCUAAAACCUAUGCAUUUCAAAUAUUUCACAAAUUCAUGAAAUAUUUAUGUAAGAGGUCAAAUCUAAAUCAUUAUGCCACUAAUAGUCUGCCAAUCAUAGAUAAAUUGUAUGAGAGAGAAAUGAAGGGAGGAACAUAAUUGUACCCACAUUAUUAUCAAUAAAAUAUUUCUGUUCUUCAAAUUUUAUAUGUGUGGUUGAUUA	312	spe-miR1046-5p	UGCAUUUCAAAUAUUUCACA	121-140	ppt-miR1046-5p	4	0	20	20	1
spe-MIR1128-4	UAAUUUGUUGACUUCCAAGAAAGCUAUUACUCCCUCCGUCCAACAAUACUUGUCCACUUUAUGAAAUCCAUGAAUAAUUUUACACUUAGUUCCUAAUUUACCCUUAUCAUUAAUUAUAGUCAUUUCACUCAUUUCCCUAUUUCCCUAUUAUAUUUUCAAGACAUGGUAUUUAUUAUAUUCAAAGGGUGAUAUAAUAAAAUUACCCAUCUAUUUAUAAGAAGUGUGCCAAGUCAAUAGUGGACAACUAUUGUUGGACAGAGGGAGUAUAAAAGUUUUGAAAGACACCAAAAUG	293	spe-miR1128-4-5p	UAUUACUCCCUCCGUCCAACA	25-45	ssp-miR1128	3	0	21	21	1
spe-MIR865-2	UAAUGCACAAACACGCACUUUAACUAUCAAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGGCACAAUACACGUAGGACACCAUGUAGGAUAAAAAAUGAUAUGUAGGACAUGUGUGUCUAUUUAUUCAACUUUAUACAAGUUAAGUGUCUAUUUGUGCAAAU	166	spe-miR865-2-3p	UAUUUAUUCAACUUUAUACAA	123-143	ath-miR865-3p	5	0	21	21	1
spe-MIR11109	AAUCAUGUUCAUACUUGUCAUAAUGUUUGGUAGGAAAUAGAAUUUGUACCACCAUUAAAAUGUGCGGUGGUAAUGGAUUGGUUGAAAUUUGUUUAGCCCUACCUAGAAUUUUAGGUGGAUAUGACUUUAGAAAUGAAGCUAGCAUAAAAAGUAUAAAUUUAAUAGUUUUACUUUUGGUCCAACCUUUUAUAAUAAAUUUUAAAAUUUGAAUUCGUCUUUGUGUCAGCAGACAGAUAAAGCAUCAAUGCUAGACGAAGUGAUAGAAUAUUUGAAGCAACUUCAAGCUCAAGUGCACAUGAUGAGUAGGAUGAACAUGUCA	319	spe-miR11109-5p	UAAUGGAUUGGUUGAAAUUUG	71-91	lja-miR11109-5p	4	0	21	21	1
spe-MIR10538-10	UUUUUAAAAGUUGAUGGCGUCAGAUUGAUAUACGUUACUCAUAGUAACAUUUUACUCCUAAAACGUUACUCAUAGUAACAUUUUAGGAGUAAGACGUUACUGAAAAUGACGUUUUAGGAGUAAAACGUUAC	174	spe-miR10538-10-5p	AGAUUGAUAUACGUUACUCAUAGU	22-45	sly-miR10538	1	0	24	24	1

spe-MIR6024	UUACAGUAACGUACAUCAACCUAAUGCUGUUAG UUUUUAAAAA AGAUGAGGAAGUGGAGAAACAACACUUGCUAAA GGAACUUCACCAGUCAUCUCUUUUCUUUUGGA GUUUUUUUAGCAAGAGUUGUUUUCCCUCUUCU CAAUU	102	spe-miR6024-5p	AGAAACAACACUUGCUAAAGGA	15-36	stu-miR6024-5p	1	0	22	22	1
			spe-miR6024-3p	UUUUAGCAAGAGUUGUUUUCCC	70-91	stu-miR6024-3p	0	0	22	22	1
spe-MIR6207	CUUCUCAACCCAAAAGCUAGCUCAAAGGUUGAG ACUUUCCCUCACACUUAUAAAAUUGACCACCAG CCCCUUCCACUUCCGAUGUGGGAUAACCCAAC AAUCUCCCCCUUCACACAUCGGGCCUUGGGCU GGAGAGAACGACAACCCAGUUCCUCCCGGUGG GCUGAGACUUGUUGACAACCUGGGCUCCGAUA CCAAUGUUGGGUGGUCUUGGGCCUUCUCAACC CAAAAGCUAGCUCAAAGGUUGAGGCU	252	spe-miR6207-3p	UUGACAACCUGGGCUCCGAUA	174-194	hvu-miR6207	5	0	21	21	1
spe-MIR2083	CACGAUCGGAGUUGAGAAGGAAGAUAAGAUAAU GAGAAAGAAUAUUUGUUUUGAUAGUCGUGACU UUCAGAUUUUCUAAGGAGGAAGAAUAAGAGAAG AGAGAACAUUGAGAGAAGAAGAAGAGAAAUACC UAUCUUCCUUUUUUUUUUUUUAACAAUGGUUU GAAUAGAAUUAUAAAUGUUGAAAUAAAACUUCA ACUUUUUUCUCUUUCUCUUUCGCUUUCUUUUU CAACUUCUCCAUCUCU	244	spe-miR2083-3p	UUUUUCAACUUCUCCAUCUCU	224-244	ppt-miR2083-5p	4	0	21	21	1
spe-MIR12162-1	UAUAACUGUUUACGCGGUUUAACCUCCGUGGU CAGGUUUCCAGGGGUUAUGGGGUGCGGGAGC CCCCCAUCUGAAGGAGGGGUUUGGUGCAGCGC CCCGACCUAAAUUUUAGGUUGUACUAUUUAUUC UCCAUUUAUUCUCUGUAACCAAAAAUACUCUGA UUUAUUAAUAUAUGUACCCCACCGCCGUGGAAA UUUACUCACGGGGUUUUACCACGAAAUAUUGG G	227	spe-miR12162-1-3p	AAUACUCUGAUUUAUUAAUAU	152-172	aof-miR12162	5	0	21	21	3
spe-MIR2921	AUAAUUUUUUUUUUAAAAAUUAGAAGUAAUAAA UAUAAAUUUAAAACUAAUUUUUUAACUUCCGUU GAAUGAAGGGUAUAUGUGAGCCAUUUUGUAAC GACAGGGGUAUAUGUGAGCCGUUUGUAUAACG GUAAGGGCAUAUGUGAGCCACUUUUAUAACGA GGGGUAUAUCAGCUCCAAAUGACAAAGUUGAG GGGUAUAUCAGACCCUUUUCACUUUAAUUUAUC CAAAGAAAAAAUAUC	242	spe-miR2921-5p	AAGUAAUAAAUAUAAAUUUAAAAC	24-47	osa-miR2921	5	0	24	24	1
spe-MIR8020-2	AGCAAGAUAUAGCUAAUUAGUUGAGUGACCAUU UGAGAAAUCAAUUCCGGUUGAAGUCUGUAUACA CUCUAUCCACCCCAGACUCCACUAAUGCAAUUA UGCUGAAUAUGUUGUUGUUAUACACAAAGUAG GGGCAAAGUUGAGUUGAUUUCUCAUAUCGUCA CUUGACUAAUAGAUAUUAUAUUAGA	188	spe-miR8020-2-3p	AAUUAUGCUGAAUAUGUUGUUGUU	95-118	stu-miR8020	5	0	24	24	1
spe-MIR3951a-1	UGAAUAUGUUGUUGUUAUACACAAAGUAGGGG CAAAGUUGAGUUGAUUUCUCAUAUCGUCACUU GACUAAUAGAUAUUAUAUUAGAAAGUUAGAUUC UUUGUUAAAGAAAAUUGAAAAUAAAAGGUAGCU UUUGAGAAAAUAGCUAAUUAGUUAAGUGACCAU GAAAUCAAAAUGAUGAAGUCUGCAUAUACUCUA CACAGCUCGAGCCCACUUAUGUGAUUACACCAU AUAUCUU	236	spe-miR3951a-1-5p	UUUCUCAUAUCGUCACUUGA	47-66	csi-miR3951a-3p	5	0	20	20	1
spe-MIR7997b-1	AAUUUGUUAGUAUAUAUAUGGUAAUUGAACCCU AUAUGCUGCUCGGACUCUUCAAAAAUGUCGUU ACGUCCGUGUCGGAUCCUCCAAAAGUAGUGCA UUUUUUUAAGGAUCUGACACAUCAACAUUUUUG GGAAAUCCGGAUCUAUUGCUUUUGGUAUAAAC CAUGUAUAAACACAUACAAAGG	184	spe-miR7997b-1-5p	AUGCUGCUCGGACUCUUCAAA	36-56	stu-miR7997b	0	0	21	21	1
spe-MIR8039-1	CGUGUUUCAUAUCUUUACUAUCCAUUGUUCUA UUUACCUAUCUAAACUAUCACUCCCUUUGUAUU AAAGACAAAUCAGCACUGAGCUAUCCAACAUGU AUUUGACCAACUCCGCAUUGAGGUGCCUUUUA AUACAAACUGAGUGAUAGUUUAGCUAAGUACAG AGAACAAUAGAUAGUUGAGGUAAGAAACUAU	194	spe-miR8039-1-5p	UUACCUAUCUAAACUAUCACU	34-54	stu-miR8039	3	0	21	21	1

spe-MIR1167	ACCUGCAAAGUAGAAAUAUUUCGAUAGAUAUUG AAAUAUUUUAUGUUGGGUUCUAAAGGUGUGAA CAGGAAAUGAAGGGUUGUGACUCUCCCGAAUG GUUCUCACUUCCCCAAAGGGUUGUUACCAUUU GAAAGGUUGUGUCUUUUCCAAAGGAUUGUGAC CUUUCUGAAAGACUGUCUUUUUUCAAAGAGUU GUGACCUUUACCCUUUGUUUGCUAUAAAUAGA GAAUUUUCUUUCAUUUUCUUUAUCGAAUUCAUU CUCUUCUCUCACAA	272	spe-miR1167-5p	GGGUUGUUACCAUUUGAAAG	115-134	cre-miR1167	5	0	20	20	1
spe-MIR852-2	CGCCCAUGGCAGAGACAAUACCUGAAUAUGUG AAUCCCGAGGGGGUUGUCACAAAAAAGGCGCU UUUUUUGUGACAACCCCCUCGGGAUCCACAUA CUCAGGUAUUGUCUCUGCCAUGGCAU	122	spe-miR852-2-3p	ACAAAAAAGGCGCUUUUUUUGU	51-72	aly-miR852-5p	5	0	22	22	1
spe-MIR7981-12	UCGAAAUCUCAGACACAUUUUAACUAUACUAAG GUCCUAUUACCCUCAUUAGAUUUAUUUUUUAUA AUUUUGUGCACCUUUUUGGCUUACGUGGCAUC CAAAUAUCUCCUACGCGCCUCAAUUGCAUGGAU UCACGAAGUGUGCCACGUAAGAUAAAAGGUGU AUAAAAUUACAAAAAAAAAUAAUAAAUUCAGGGC GGUAAUAUGACCUUAGUUUGGUUAAGGUGUGU CUCUGAAAUUUUGG	243	spe-miR7981-12-5p	UUUAACUAUACUAAGGUCCUAUUA	19-42	stu-miR7981-5p	4	0	24	24	2
			spe-miR7981-12-3p	AUAUGACCUUAGUUUGGUUAAGGU	202-225	stu-miR7981-3p	3	0	24	24	1
spe-MIR830	UAAAAGAAGGAGUCAAGAACGCACCAUACAAGA AAACAUCUUGAUAAGAAGUGUUGCUAUGUUUAG ACAAUUGUAUGGUUCGGGUAUUGACUUCUGUA CUUGGA	104	spe-miR830-3p	AAAACAUCUUGAUAAGAAGUG	33-53	ath-miR830-3p	5	0	21	21	2
spe-MIR11011a	AACACUUAGGUGUUUUACCAAAUGAGUAGAUAA GCUAAAAAGUGUUAAUAAGCCAAUUUGACCAGC UUAUAAGCUUAGUCAAACACCCUCUAAGCUUAU AAGCUGGUCAAACUAGCUUAUAAGCAAUUUUUU GGCUUAUCUAGGCAUUUGGUAAAUGUCGCCUA AAGUCAU	171	spe-miR11011a-3p	AAGCUUAGUCAAACACCCUCU	71-91	mdm-miR11011a	5	0	21	21	1
spe-MIR8009-2	CAAAAAAAUUGCAGAAAAAGCAAUGGACAGCGU GGUCUAGUCCGUUGCUUUUCUUGGUUUUUUUA AAAAUAAUUUCCAGAAAAGCGACGAACAGUGUC CUUUUGUCCGUCGCUUUUUUGGGAUUUUUCAA UAAUUUCCAGAAAAGCGACGAACAGUGUCCUUU UGUCCGUCGCUUUUUUGGGAUUUUUCAAAAAU	130	spe-miR8009-2-3p	AUUUCCAGAAAAGCGACGAACAGU	72-95	stu-miR8009	1	0	24	24	1
spe-MIR8009-3	GAAAUUUCUACAAAAGUGAUAAACGGCGUCGCA UUUCGGGAAUUAAAAAAAAACAUAUCGGCGGAG UAUGUCGCUUAUGUUUAAAAAAUUAAAAAAUAA UAAUAAUAAGUUCACGACAGUGUCUGUCGCUU UGGGAAAAGC	206	spe-miR8009-3-5p	AUUUCCAGAAAAGCGACGAACAGU	3-26	stu-miR8009	1	0	24	24	1
spe-MIR6473	AAUUUUGUGGGAUUUCAUAAGAUGUGUUCAAU UCGAGUUGGAACUCUACAAAUUGUGUUCAACU CAGAUAAAGAUUCUUGGAGGCUACUCAACCGUA AACUCUAGUUUAUGCCUAUAUAAAGGGUACUAA AUUCUCUUAAAAGGACAUCUCAAAAAUCCCAUA AAGAG	168	spe-miR6473-3p	UCAAAAAUCCCAUAAAGAG	150-168	ptc-miR6473	4	0	19	21	1
spe-MIR8006-7	UUUUUGGGACAUUGGUGCCUCCACCGUCCAAA AACUAGAGUGUAUAUACUAUUUAUAUUAACGGA CAUACACGUGGCAUAAUCUUAUCCACUGAUCCU ACAUUUAUUUAAUAUCGGAUCAAUGAAUAAAAU UGUGUCAUGUGUCCCUAUUUAGUCUUCCAGUA GAGUGAAGGGCAUAUAUACUCUAGUUUUUUGA CAAUAGGGACACCAAUGUCCCAAAAG	221	spe-miR8006-7-3p	UAGUUUUUUGACAAUAGGGACACC	185-208	stu-miR8006-5p	4	0	24	24	1
spe-MIR10519-2	UUAACUUAGCUUUAAAUUACAUUUAUGCCCUUC AACUUUGGAUGUGCACAAGUAGACACUUAAACU UGUAUAAAAUUGAACAAACAGACACACAUGUCC UACUUGUCAUUUUUUGUCCGACGUGGUGUCCU ACGUGUAUUGUGUCAUGUAGGACUCAUGUGUU UAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCU GUUUGUGCAUUAUGAAAGCUGGAGGUCAAAGU UAAAAUUUGAAUCCAAGUUUA	249	spe-miR10519-2-3p	AUUUAAAAGUUGGAUAGU	169-186	tae-miR10519	4	0	18	18	3

spe-MIR1439	CUAUUAUCUAUUGUGGGUAGAAUUGUCAAAAUGGACUAACCCAACCCAACCCUAAUGGGCUAGAGAGUUAAAUGGGUUGGGACGGGCUCACCCUUUUAAUAAAAGAGCCUAUAAAAUAGCAGUUCAACCCAGCCUAAGCGGGCCACAGGUUGGGACGGAUUGACUAUUUAACCAAAAAAUAAACA	185	spe-miR1439-3p	GGUUGGGACGGAUUGACUAUU	148-168	osa-miR1439	5	0	21	21	3
spe-MIR160-3	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAACUAGGAAGAGUGUCAAUUUUUUUGACAAUACUGUUCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACAAUUUC	104	spe-miR160-3-3p	UGGCAUCCAGGGAGCCAGGCA	74-94	aau-miR160	1	0	21	21	1
spe-MIR7992-9	AAUUUUCAGAAUGCACAUCUAGACACCUCAACUUGUCUCCACUGUAUCGGAUGAAUACUCCAACUUACAAAUAUGAUCAUCUAGACACCUCCAAAAUUUAUGUGCCAUGUCAACGCAGGGUGUCCAUGAAACACAGUGGGGUCUAGUUGAAGUGUUUAGUGUUCAUUUGAUACCAAGUUGAGGUGUCUCGAUGUGCGCUCUCAAAGUA	208	spe-miR7992-9-5p	UUUCAGAAUGCACAUCUAGACACC	4-27	stu-miR7992-5p	3	0	24	24	1
spe-MIR10519-3	UGCCCUUUAACUUGGCUUCGAAUCACAUUUAUGCCCUUCAACUUUGGUUGUGCACAAGUAGAACAAAUAGACACACAUGUCCUACAUGUCAUUUUUUGUCCUACGUGGUGUCCUACGUGUAUUGUGUCAUGUAGAACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAUGUCUGUUUGUGCAUUAUGAAAGUUGGAGGUCAAAGUUAAAAUUUGAAGCCAAGUUUAGGAUU	236	spe-miR10519-3-3p	AUUUAAAAGUUGGAUAGU	152-169	tae-miR10519	4	0	18	18	3
spe-MIR7983-5	AUCUUUAUACACUACAUCAAAAAUGAUCAUUAGCGACAAUUAAUUCUUAAUUACCGCUAAAUAUAUAUUUUUAGCGGCAAUUAACUCUCUUUGCAUAUGUCCAGCCUUUAGCGGCAUUCUAAUGUCACUUAACUAAUGCCGGUAAAAAUUUGAACCCUCUUUAUUAAUGUCAAUAUUUAUUACCGCUAAAAGUUAUUUUUGUUGUAGUGAUAGAAACCC	219	spe-miR7983-5-3p	ACUAAUGCCGGUAAAAAUUUGAAC	132-155	stu-miR7983-3p	3	0	24	24	1
spe-MIR419	CAUAACACAUGCCUAAAUAAUUAAUUGUUCAGCUCUUCCUCCACAUCCAUUCAAAUGGUUUGAAUGGACAUGGAGGAAGAGCCGAGUAAUUAAUUAUUAAUGUUGUUGUU	113	spe-miR419-3p	UUAUUAAUGUUGUUGUUGUU	94-113	ath-miR419	5	0	20	21	1
spe-MIR390a-2	AGAGCAUGAAAAAGCUGUAAAACUCAGGAUGGAUAGCGCUAGAGAUGUGUAAAAAAAUCGAAUUGAGUCAUCCAUGGCGCUAUCCCUCCUGAGCUUUACAGAUUCUCCAUGCAUA	115	spe-miR390a-2-5p	AAACUCAGGAUGGAUAGCGCU	20-40	cas-miR390a-5p	3	0	21	21	1
			spe-miR390a-2-3p	CGCUAUCCCUCCUGAGCUUUA	78-98	sly-miR390a-3p	2	0	21	21	1
spe-MIR171b-5	AAAAGAAAUGAUAUUGGCGCGGCUCAAUCUGAGAUCGUUCUUUACUAAAAUAAAACGUAAACUCGUCUUCGGAUUGAACCUCACCAACAUCGCUUCUCUA	100	spe-miR171b-5-5p	GAUAUUGGCGCGGCUCAAUC	10-29	zma-miR171b-5p	1	0	20	20	1
			spe-miR171b-5-3p	GGAUUGAACCUCACCAACAUC	71-91	tcc-miR171b	5	0	21	21	2
spe-MIR396f	GUCCUAGUCAUGCUUUUCCACAGCUUUCUUGAACUUCUUCUUGCUAAAUUUUGAUCUCUAAAUUGAUAAUUUUGAGAUGAGAUUUGAAGCUAUGAAAGUCCAAGAAAGCUGUGGGAAAAGAUGGCAAGCUU	131	spe-miR396f-5p	UUCCACAGCUUUCUUGAACUU	16-36	csi-miR396f-5p	0	0	21	21	1
spe-MIR169e-3	GGUGAAGAGAAGUUCUUGCAUGAAAGAGGAGAGCAUGUCAAGGUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAUUAAACACAUUUUAAACUAUGGAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUAUGACUCUCCUCUUCAUGUAAGACUUCUCUUCUUU	170	spe-miR169e-3-5p	UAGCCAAGGAGACUGCCUGAA	44-64	zma-miR169e	3	0	21	21	1
spe-MIR169e-4	UUUGAAAAGAUAUCUUGCAUAAAAGAAAAGAGCAUGUCAAGGUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAUUAAACACAUUUUAGACUAUGGAGUAGGCAAGUCAUCCUUGGCUACUAAACAAUAUGACUCUCCUCUUCGUGUAAGACUUCUCUUCUUU	169	spe-miR169e-4-5p	UAGCCAAGGAGACUGCCUGAA	43-63	zma-miR169e	3	0	21	21	1

spe-MIR169c-4	AUUAAUUGAAGAGGGGUUUUACAUGAAGUUGAGAGUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAAACCUUAUCUUCUAUUGCU	190	spe-miR169c-4-5p	UAGCCAAGGAUGACUUGCCUA	46-66	ata-miR169c-5p	0	0	21	21	1
spe-MIR6148a	UUCCUGAAUUUAUUUUAUUAAUAAUUUUUUACCCCUUUUGGCCUACGUGACAUUAUCUUGUGGGCUCGACGUUGAUUGAUUUUUUUUAAGCUAGUGCCACGUAGGUCAAAAAGGGAUAGAUUAUUACUUAUAAAAUAAAUUCAGAAA	147	spe-miR6148a-3p	GACGUUGAUUGAUUUUUUUUA	68-88	nta-miR6148a	5	0	21	21	2
spe-MIR8001b-3	AAACACUACAAGAAAAGGGUAAAUUACAUGGGGAUUAGUAUGAAAAUUUGCAGGGAUUACCCUGUAAUUCACACUUUUCUUGUAGUGAAA	90	spe-miR8001b-3-3p	AUGGGGAUUAGUAUGAAAAUUUGC	28-51	stu-miR8001b-5p	0	0	24	24	1
spe-MIR4243	UGGAAGUACUCCCUCCAUAUACUAGUAUAGAUUGGACUUUGCACUAGGAUAAACAGUGAUUGAUAUGGAUAUUUUACUAUAAUACCCAUAUUAGUUGAUAUUUAGUCUUAGGUAUGGGGAAAUGAUUAACAAAUUGUAAAUGCCAAGGGUAAAACAUGAAAAGAAGAUGUUUCGCUCUUGAUAUGCUAACUAGAAGUGACAAGUAAAAGUGAAAUUAUAUUUUUAGUAUAGUGGACAAGUAAAAGUAAAAGUGAAUGGAGUGAGUACUUUAU	272	spe-miR4243-3p	UGAAAUUAUAUUUUUAGUAUA	210-230	aly-miR4243	4	0	21	21	1
spe-MIR11509	GGGUUGCAAGGUGCAAGAAGAAUGUUGCUAAUGAUUGUUAGCAUUGAAUGAUGCUUUUGUGUUUGUUCGUGAGCUUGCUAUUGCUGAUUAAUCAAGUAAGUUCGAAUUGAGUUUGUGAUCAAUUGAGUUUACGGGGUUAUCUAUGAUGAGCAUUGUGCGUGAUUUUACCUAGUACACAUGCUUGGUGAGGGCAUAGAUGCAACAACCAUUCCAUUGUCCAAGCGAUGAAGUAGUGUAAUGACAGAGAGUACAUUGAGAGCUUGCAUCGUAUUUUAUCCGACUUGCAUGUCAUAACUAGCAAAUCAUUUAUCUUGACAUGCAAGUC	325	spe-miR11509-3p	UGAUGAGCAUUGUGCGUGAUU	144-164	pab-miR11509	4	0	21	21	1
spe-MIR9679-2	AAAAGAAAUUUAUAAUUUAUUACAAAAGGGCCUUAUAAAACCCUCUAAAUCUCCAUGGUCUUGUACUGCCUUUUCUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCACAUUAGUAAUAAAUUAUAAACCUCUGAA	141	spe-miR9679-2-3p	CAGAACAAGAAAGAGGUGUUC	90-110	tae-miR9679-5p	5	0	21	21	1
spe-MIR8181	GUCAUCUGUCACCACAAACCAAACAAGACUUGUUUGACACCUUUUAUUUAAUUUUCUCGAGUGUUUUAACUAUUUUUUUUGUGGGGGGGGGGGGUGACACUCCAUGAAGCUAGGGAUUUUUUAGAAAAAUGACAUUAAGGUUUCAAAAUAAAUGGGUGGUUACAUAAGUCUUAAGUAUUGGUUGUAGGUGACAAUUAU	198	spe-miR8181-5p	GUGGGGGGGGGGGGUGACAC	81-100	ath-miR8181	4	0	20	20	3
spe-MIR11068e	UUGCAUUUGAAAGAUAUAUUUUUUAUGAUAUUGGAUACUUGAAUCAUCUUCGUACCUUUGGUUCUGAUUCUUCUGAACACAAAGAUGGAACUAGUGUUGAAGAUGGAACUAGUGUUGAAGAUGAAACUAGUAUUGAUGAUGGAACUACUGCAAAUAUUCUUUCAAGUGUUG	171	spe-miR11068e-3p	AUGAAACUAGUAUUGAUGAUG	121-141	lja-miR11068e-3p	5	0	21	21	1
spe-MIR5556	CUGAUUCGACUACCUAUUUUUUCAAAUUGGUUGUAGCAGCCUCAAGCUACCUGGACUAUAAAUUAUUUUUUUGAUGACAAAAGAAAUUUAAAAAUAUAUAUUCCACGUAGCCUGGGGCUGCUACAAUCAAUUUUGUAAUUCUUGAAAUAGUUAGUCAAAUUGGAAUAGCCAUUAUUUGCCGCUGCAGCAUCAUCAA	163	spe-miR5556-3p	UGAUGACAAAAGAAAUUUAAA	72-92	mtr-miR5556-3p	4	0	21	21	1
spe-MIR172j-1	GAUUCCCACACAUCGCCCAUAGGGUUUUUAAAAUAAUAAAAUCCCUAAUGUAGCUAUGUGAAUCUUGAUGAUGCUCCACCCGCAAAAAAUUGACUUGA	132	spe-miR172j-1-5p	GCAGCAUCAUCAAGAUUCCCA	21-41	lus-miR172j	0	0	21	21	1
			spe-miR172j-1-3p	UGAAUCUUGAUGAUGCUCCAC	93-113	mdm-miR172j	3	0	21	21	2
spe-MIR11314-2	UAUGAAAUGAUGCGACUUUUAUGAAAAGUUGCGAUUUUUAUGAAAAGUUGUGACUUCUAUGAAAAGUUGUGACUUUUAUGAAAGGUGACGACCUUUC	138	spe-miR11314-2-5p	AAAGUUGUGACUUCUAUGAAA	44-64	fve-miR11314	5	0	21	21	1

spe-MIR7993d-2	UGAAAGAUUGUGACUUUUCCAAAGGUUUGUGACAUUUCCGGUCCUUUAAUUAUAUGCAUCAACCUCAAGUAGGAAAUGCCUGAGGUUUAUGACUUUCUGAGGCAAGUGUUAUAAUUAAAGUAAAUGACAUAUUUUAUGUGGUUAACGUAAUUACCUAAUAAACGACAGAGAAUGCCAAAUUAAGUUCAAAAUUUAAAUUGAAAGUGUCUAAUGGGAACUCUUUAUUAGGAGUUGAGGUGUUCAAUUGGAAGAGACUUAGUUUGAGUAUCUAAAUAAAAAU	239	spe-miR7993d-2-5p	AUAUUUUAUGUGGUUAACGUAAUU	88-111	stu-miR7993d	2	0	24	24	1
spe-MIR7990b	GAUUUUUUCACGUAGAUCUUGAAAAAACAACCAGAUUGAAAUAAGAAAUCGCCUCAAUCGAACAUCCAAGACAAGAUUUAUGACCGUUUUAAUUUCACAAAUAUACAACUACUUCAUGGUGAAACUUCAAAUGAUCGUAACUUUUUCCUUGAAUAUCCAUUGGAGGUGAUUCUUUUUUUAAACUUGCUUAUUUUUUCAAGUUCCACGUGGUAAAUGC	217	spe-miR7990b-3p	GAAACUUCAAAUGAUCGUAACUUU	121-144	stu-miR7990b	2	0	24	24	1
spe-MIR7990a-3	UGUUUUUCCGCGUAGAUUAUGAAAAAAUAACUAGGUUGAAAUAAAAUAUUGCCUCAAUCGGACAUUCGAGGCAAGAUUUAUGACUGUUUGAAUUUCACAAAUUUACAACUACUUCAUUUGGUGAAACUUCAAAUGAUCGUAACUUUUGCCUCGAAUAUACGUUGGAGGCGAUUCUUUUUUUAAACUUUCUUAUUUUUUUAAGAUCUAUGUGGUAAACUU	219	spe-miR7990a-3-3p	UUCAAAUGAUCGUAACUUUUGCCU	128-151	stu-miR7990a	1	0	24	24	1
spe-MIR10427b	GGAGAGAAAAAAAAAUUUAGCGAUAAAAUAGAGAAUUGGGUUGGAGUUGGUUGUCUGAAAAAAUAGAGAACUAUAUAUGUGUAGAGUAAAAUAGAGGAUUGGGUUGGAGAUGACCUAACCAUCCUCCAUUUCACUAGUUAUUCUCCAGUUAUUUGGAGAACUAAUAUUCAAACUCUCUGUUUCACUUUUUCGUUAUUAUUUUUAUUAUAUCAAA	214	spe-miR10427b-5p	AUAGAGAAUUGGGUUGGAGUUG	28-49	gma-miR10427b	5	0	22	22	3
spe-MIR10519-4	CACAUUUAUGCCUUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACUUGUAUGAAGUUGAAAAAAUAGACACGCAUGUCAUAUAUGUCAUUUUUUGUCCUACGUGCCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGCCUAUUUGUGCAUUAUGAAAGUUGGAGGUCCAAAUUAAAAGCAAGUUUCAUUCUUUCUCAAUUCUGCAUAUUAAAGUAGGUUAUCAGUGGGCAUUAGAUUGUUGUUUAUUAAGGGUGUUUUUUUUGUUUUCAUGGGUAAGAUGCA	195	spe-miR10519-4-3p	AUUUAAAAGUUGGAUAGU	133-150	tae-miR10519	4	0	18	18	3
spe-MIR7814	GUGUAUAGUGAGUUGAGAAUUUAUUUAUUAUCACGGAUUGGGAUUUCUAGGGACGUUAGUGUGGUUAUUAGGUGAUAGCCUAAUGAAUUCCUAAUUGCUAAUGGUUAUCCCAUGUAGUAUUAUAUAAAGAUGAAAUUUGAAU	271	spe-miR7814-5p	UAGAUUGUUGUUAUUAUUAUA	57-77	ptc-miR7814	5	0	21	21	1
spe-MIR396g-2	UUGUUUAUUAAACUUUGUAUGUAUCGAGACAUUCAAUAGAUCAGUGACAUACAAAAAAUAAAGGAAUGUAGUGGGAUGGUAAGUAUUUUACUCAACCUUAAUCAAACAUUUGGGAUUCAAAUGUUGGGUCGUAGUCAAUGAAUUUGUAAUGACCCGGAUAGUCAUUUUAGUAAAAUU	177	spe-miR396g-2-5p	UUAUUAAACUUUGUAUGUAUC	5-25	gma-miR396g	5	0	21	21	1
spe-MIR8032e	UCGAUCAAAAGUUCAAGAAGAUGACAUCAAAAUCCAAUUCUGAUGAUUCCAUCAGUUCCGGAAGGGUCAUUUUAGGCUAGUAGCAUUGUCGACAUGACUCCCGAAGUUUUCAGUGUGAGUUGGUGUGAUUAGGCGUUUUAACUUUAAGUUAAAGCUAACUUUGACUUUAGUCAACAUUCUGAGUAAACGCGCUCGGAUGAGAAUUCCGUCAGCGCUGCUAGCUCCGGAAUGUCGAGUUUGGUCUAGUUUGACCCUUCUUUCAUGUUCUGAGGUUUUUGAUAUU	283	spe-miR8032e-5p	AGUGUGAGUUGGUGUGAUUAGG	112-133	stu-miR8032e-3p	1	0	22	22	1
spe-MIR475b	AACUGAAGACAGUCAAUGCCACUCCAACUACUGUCCAUGGCAUUUCUCCUAAAGUCCCCAUUGAUUUAGGAGAGUGGACAGGGCAGACUGACUUCACCA	99	spe-miR475b-3p	CUAAAGUCCCCAUUGAUUUAG	49-69	ptc-miR475b-3p	4	0	21	21	2

spe-MIR5303f-7	CCUGACUUAUGUUGCUCGGACUCUUCAAAAAUGUCAAAGGGUGCGUGUCGGAUUCACCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCAAAAGUAAAGAGUCCGCGCAACUAAGCUCCUG	133	spe-miR5303f-7-3p	AUUUUUGGAGAAUCUGACACGGGU	70-93	stu-miR5303f	0	0	24	24	1
spe-MIR1101	UUUCUUUUCGAUUUACGUGGCACUAUCUUGUGGGUUCAAUAUGUGCUGACAUUUUCUUCAAACUAGUGCCACAUAAGAUAAAAAGGGU	88	spe-miR1101-3p	GACAUUUUCUUCAAACUAGUG	48-68	smo-miR1101-5p	5	0	21	21	1
spe-MIR1127b-2	CAGGACAAGUAUGGUUGGACAACUAAUUUUAGUGUAGUGGACAAGUAAAGGUGGAUGGAGGAAGUACUUCCUCCGUCUACUUUUAUUUGUUCACUAUACUGAAAUUAGAUAUCCACUUUUACUUGGUCAUC	131	spe-miR1127b-2-5p	ACAAGUAAAGGUGGAUGGAGG	41-61	tae-miR1127b-3p	5	0	21	21	1
spe-MIR8039-2	UAGAACUAUCAGAAGUUACGUUUUCCUAUCUGAACUAUCACCAUCGUUCAGGUAGGAAGAGGAAACAAUUGACAGUUGAGUUGUGUUUUAAUACAUGGAUGGUGAUAGUUCAGGUAAGAAAAGGGAACAACUGAUAGUUGGA	142	spe-miR8039-2-5p	UUUCCUAUCUGAACUAUCACC	22-42	stu-miR8039	0	0	21	21	1
spe-MIR172j-2	UAGAGUCAUAUGUUAGAUGAUGCAGCAUCAUCAAGAUUCCCAAAGAGAGAAAAUAAGAGAUUUUGAACUAUAUUAUAUAUCCAAUAUUCACCCUAAACAUAAAUUAAAUAGUUCUUCCUUCAAGUUUUGUGAAUCUUGAUGAUGUUGCAUCCUCAAACAUUGACUGAU	169	spe-miR172j-2-5p	GCAGCAUCAUCAAGAUUCCCA	22-42	lus-miR172j	0	0	21	21	1
			spe-miR172j-2-3p	UGAAUCUUGAUGAUGUUGCAU	131-151	mdm-miR172j	2	0	21	21	2
spe-MIR902i	AAGUCUGAAUCUGAAUACACAUCUGAAUAUUAAGAUUUGCAUUAAGAUUCAGGUGUUUCGAUCUGAAUACACAUCUGAAUAUUAAGAUGUGGUUUCUAAAUCUGAACA	108	spe-miR902i-3p	UUAAGAUGUGGUUUCUAAAU	82-101	ppt-miR902i-5p	5	0	20	20	1
spe-MIR9679-3	AAAAGAAAUUGAUAAUUUAUUACAAAAUGGCCUUAUAAAACCCUCUAAAUCUUCAUGGUCUUGUACUGCCUUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGGUUAGUAAUAAAUUAUAAACCUCUGAA	141	spe-miR9679-3-3p	CAGAACAAGAAAGAGGUGUUC	90-110	tae-miR9679-5p	5	0	21	21	1
spe-MIR833a	CAUUAUCAAUGUAAAUGGUACAGAGUUAUAUUUUGACUUAAAAGAGUUGGUUGUUGUAACCGGUCUAAAAUCUGGACCAAUUUCUGAUUUUGUUUCUGAUCCAUCUGUUCCAAAUAGAUUAAUUGCAAAAAUUUCAGAGACUUUGACAAAGUCCCCAAGUCAAAUUUUUACCACAAGUUUAAAUUGGAAAACUUUUGGGAAGAAGAUGACCGUUUAUAAUCAGUUCAUAUAAUUGAUACAC	242	spe-miR833a-5p	UGGUUGUUGUAACCGGUCUAAA	48-69	ath-miR833a-5p	5	0	22	22	1
spe-MIR8011b	GACACUAGUCGAGUGAGACUCAUUUUUGUCUCACAAAAAUUAAGCCCAUUUGAGUCUACACUUUAUGUGAGACAAAAAGAAGUCUCACACAACUAGUAUU	101	spe-miR8011b-5p	ACUCAUUUUUGUCUCACAAAAA	18-39	stu-miR8011b-5p	0	0	22	22	1
spe-MIR863-2	UUGAAACUUGUAUAAAGUAGAACACGUAUACACAUUCAUCCUACGCGACAUUUUACAUGCACUUAUGUGUGAUACGUGGUGUCCUACACGUAUUAUGUCAUGUAGAACUCAUGUGUCUACUUUUUAAAUUUUAGG	135	spe-miR863-2-3p	UUAUGUCAUGUAGAACUCAUG	93-113	ath-miR863-5p	5	0	21	21	1
spe-MIR1106-2	CCCCCCACCCUGCACUAUUCAAUAAUGUAUUUUAAAGGUAUAUAUGUGUCCACGUGGACAUCAUAAAAAUUUCAUCAUUUUAAAAAUUAAUGUGUCAAUGUGAACACAUAUAUACAUUAAAAUGCACUAUUAAAUAGUGUAGAGGGGUAA	151	spe-miR1106-2-5p	UUUAAAGGUAUAUAUGUGUCC	31-51	smo-miR1106	5	0	21	21	1
spe-MIR395a-6	UCUCGAGAGUUCCCUUGACCACUUCAUGAGGGAUUAAUAUCUUUAUUUUUGAUGCCCUACUGAAGUGUUUGGGGGAACUCUCGGGU	86	spe-miR395a-6-3p	UGAAGUGUUUGGGGGAACUCU	61-81	aof-miR395a	0	0	21	21	1
spe-MIR395a-7	UACUGAAGUGUUUGGGGGAACUCUCGGGUUCACUUUGAAGUAUACACAAACUAGUAAACAUGCAAGAGAACUAGAGAUAGAUGAUGAAUGCAAUGCUUCAUGACUACAUAUAUCAAGGUGUUCUCGAGAGUUCCUCUGACCACUUCAUUU	150	spe-miR395a-7-5p	UGAAGUGUUUGGGGGAACUCU	4-24	aof-miR395a	0	0	21	21	1

spe-MIR395c-2	GAUGCCCCACUGAAGUGUUUGGGGGAACUCAUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAAUGUAGGAGUCCUGGCUGUGGAUGAUGAACAUGAUAGUUCACGUAUAAAUCUAUUAAGGUGAUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUUA	165	spe-miR395c-2-5p	CUGAAGUGUUUGGGGGAACUC	10-30	csi-miR395c-3p	0	0	21	21	1
spe-MIR7997c-8	AGAGGCUAUGUUGCUCGGACUCUUUCAAAAUGUGGAAGGUUGUGUGUCAGAUCCUCCAAAAAUAGUGUACUUUUGAAGGAUCCGACACGGGCGAGGCAUCAUUUUGGAGAGUCCGAGCAACUUAGCCCAG	130	spe-miR7997c-8-5p	AUGUUGCUCGGACUCUUUCAAAAU	8-31	stu-miR7997c	3	0	24	24	1
spe-MIR158b	AUUGGGAGGUUGUGGGUUCGAACCCCCACAACCUCCUUAUUUUUGUUUAUAAUUUUGCUAGAGGCUGUGAGGUGGUGGGUUCAACCCCCCACAACUUUCUAUUUUUUUUUUUAUUAAUACUCACUAGGCUAGGCGCUUGGCAGUGAGGUUGUUUGAUCGAGCCCCCACAACCUCACCUCA	180	spe-miR158b-5p	UUUGUUUAUAAUUUUGCUAG	42-61	aly-miR158b-5p	5	0	20	20	1
spe-MIR9473-2	ACCAAAAUGCGUGCAAGCAAAACAAUAUUGGCUGUAAAUCUGAACUCGUUUUACUCCACUAGUCUCUUCUUCAGUAAAUGACAUUACAUGAUGACUAGUGGUGUGAAACGAGUUUAGGUUGGUGUGAAACGAGUUUAGGUUUACAGCCAAUAUCUGCUAGUUCACUCACAUUUUCCG	178	spe-miR9473-2-5p	UGGCUGUAAAUCUGAACUCGU	29-49	sly-miR9473-5p	1	0	21	21	1
			spe-miR9473-2-3p	AAACGAGUUUAGGUUUACAGC	128-148	sly-miR9473-3p	2	0	21	21	1
spe-MIR5253	UAAUAAUAAUAAUAAUAAUAAGGGAGAAGUGCUGAAAACACCCCUAAACUGGGUUUUCUAUUAAGAGCUCCAUACUCCUACAAGAGUUUGACUUGCAAUUUCACGUGGUAAGUCAAAGGUGUAUCUAAGUUUAGUUAGUCAAGUAGAGGGGUGUUUUUAAGGUUGUCAAUAGUUUGGGGAUGAAAAUGAUUAUUAUGCCAAGUUCAGGGGUGUUUUCAAUACUAUUCUCUAUGAUAAAAUAUUUUAGUC	249	spe-miR5253-3p	GAUGAAAAUGAUUAUUAUGCC	179-199	mtr-miR5253	4	0	21	21	1
spe-MIR5174b	UUGUUGCUCUGUUUCAAAAAGAAUGUUUUUUCCCUUUUUUGACGAUACAUAGAGCAUAAGACCAUAAGAUUCAAAUGUUUUAUGUACUUUCUCAAACUCUGUGUCAAGUCAAAACCAGACAAACAAAUUGAAAUAUUGAGAUACUUCUAAUUAUUCAUUUGAGGUUUGCGAAACUUCAAACUUUUUAGAAUUGGUGUGAGGUGAUAACACAUGAUUUUUGCAGCAGUGGAAGAU	234	spe-miR5174b-5p	GCUCUGUUUCAAAAAGAAUGU	6-26	bdi-miR5174b-5p	5	0	21	21	2
spe-MIR9679-4	UUCAAAAUCUCCUUGGUCUUGUACUGCUUUUUAUGUAAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCUUUUUAAAUUACAAAACUCUCUUAAAAUUUAUGGAUUUUGGAUACAUUACUAGACUUCCUGAUACAUUACUAGACUUUCGGAUACAUAGGUGAGGGAUUUAUCUGUGAGGUAAGGGAUGUAUCAGAGAAGGGAUAUGACAUCCGGAUGCAUCACUUGACUUACAAAUACAUCAGCAGACAUCCGGAUACAUAGGUGAGGAUGUAUCAGGGGAUUUAUGUAUUUGAGAGGAGAUAUAAUGUAUCAUCAAGAGGAGAGUGAUGUAUUCGAGAAGAGAUUUUUGAAAUAUUUUUAAAUGAUAGAGAAUUUUAGAGAUUAUGGUAAAAUAAGAU	192	spe-miR9679-4-5p	CAGAACAAGAAAGAGGUGUUC	48-68	tae-miR9679-5p	5	0	21	21	1
spe-MIR1886-2		330	spe-miR1886-2-5p	UCAGAGAAGGGAUAUGACAUC	122-142	ath-miR1886-1	4	0	21	21	1
spe-MIR169n	AACUUUGACCUCCAAUUUUGAUAAUGUUCAAACAGACUCUUUAACUAUCCAACUUUUAAUUAAAUAAACAUGUGAGUCCUACAUGACACAAUAUUAGUAGGACGCCACGUUGGACAAAAAAUUAUAUGUAGGAUGACAUGUAGGACAUGUGUGUCUAUUUGUUCAACUUCAUACAAGUUUAAGUGUCUACUUUUGCACACUCAAAGUUGAAGGGCAUAAAUG	222	spe-miR169n-5p	AACAGACUCUUUAACUAUC	31-49	aly-miR169n-3p	5	0	19	19	3

spe-MIR5181b-2	UGGUAAGUAGAUAUCCUUUGUCAUACUUUUGGGAUAUUGGUCUUCUUGCCAUCAAAAAACUAGAGCAUGUAUACCCUUCAUUCUAACAGAAGACUAAAUAGGGACACAUGACACAAAUUCAUCGAUCUGAUAUUUAAUAAAUGUCGAGUCGGUGAAUAAGAUUAUGACACGUAUAUAUCCGUUAUUAUACAAAGUAUAUAUACUCUAAUU	210	spe-miR5181b-2-3p	UCUGAUAUUUAAUAAAUGUCG	126-146	bdi-miR5181b	5	0	21	21	1
spe-MIR11444	GAGGAUAUGUGAAGGUUUUGUGUGAUUGAUUCAAAAGUAAUUUGGAUGAUCACCUACCUCUCAUUGAGUUUGCUUAUAACAAUGGUUACCACUGUAGCAUCCAAAUGGAUCCUUAUGACGCUCUUUAUUGGAGAAGAUAUUGAUCUCCUAUUAGAUUGGUUGAAUUUGGUUAAGCAGGAUUGCUAGGACCAGAUUUAGUUCAUCAAGCUAUGGAGAAGGUGAAAGUGAUUCAAGAGAAAACUUGAAAACAACACCUAGACUUCAUAAAUCUAC	273	spe-miR11444-3p	AUUUGGUUAAGCAGGAUUGCU	164-184	pab-miR11444	1	0	21	21	1
spe-MIR7813	AAAAUCAAUAAUGCAAGGAUUAGUAAUGCAGGGAUUGGUAAUACCAUGUAGGGUGUAUAACUAAUCCAUGGAUUGAUUAUACA	83	spe-miR7813-5p	UAGUAAUGCAGGGAUUGGUAA	21-41	ptc-miR7813	5	0	21	21	1
spe-MIR7816	UGUAUAACUAAUACCCACAUAACUUAUUCCACCUUCUACCCUGCAUAACUUUAUACAUAGAUUCCCUCAUAAGUUAUGUUGGUAUUAAUUAUGUA	95	spe-miR7816-3p	UAUGUUGGUAUUAAUUAUGUA	75-95	ptc-miR7816	5	0	21	21	2
spe-MIR1039	UUGGGUCGUGACAAACUUGGUAUCAGAGCAUUAGGUUCGUUGGUCUCAUCACACAAGAACGAGUCUAGUAGAGUCUUAAGGAACGGUAGGGGGACGCCUUUACUUUUCUUUGAGAGGCUAUAAGACUUUAGGAAAAUUCCAUUCUUUCUUUCUUUCUUUCGUGCUAUUACUUGGAUCCAAUUGGUAUCUAGGUGAUAUAAAUUUGUAUCUGACCAUC	217	spe-miR1039-3p	UCUUUCUUUCUUUCUUUCGUG	143-163	ppt-miR1039-5p	5	0	21	21	1
spe-MIR11072a	UGAUCCACCCACGUAAUCCGACCAUUAAAAAACAUGAUAUGACCCAUUUUAUUUUGUCUUUAAUCCUAAUUCAAGAUUUAAAGAGAGGGAUUAAUUUAAGAUUAAAGAUAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGGGUGGAUCA	165	spe-miR11072a-3p	GAGAGGGAUUAAUUUAAGA	83-101	lja-miR11072a-3p	3	0	19	19	1
spe-MIR478f	UCGAAAAGCGCAACAUGACAAAUAAAAAUGGACGGAGAGAAUAAAAAUUAAGGUUAUCAUCUUGAUUGGUAAACUUGUUCACAUUCCAAAACAAAAUUUAGGUUCCAUGAUUUGAAAAUAUGGAGUUGGUUUCUACACAUAUCGUGUGGGAUUUAGGUAUUGGUGCAUUGAAUUCUAUGUACCUCUCACUUCCACACGUUGAAUGAACAUAUAUAUAUAUAUGCUCUCUUCGUCCGGUAUUAUUUGUCAUGAUUUCUAUUUUUAG	267	spe-miR478f-3p	UGUCAUGAUUUCUAUUUUUAG	247-267	ptc-miR478f	3	0	21	24	1
spe-MIR160-4	GGUGGUAUGCUUGGCUCCUUAUACGCCACCCACUGAUCAGUCAAUCAAAAAAUUGGUGAAUGCGUGUGGCAUACAGGGAGCCAGGCACAUCCUUC	95	spe-miR160-4-5p	UGCUUGGCUCCUUAUACGCCA	8-28	dpr-miR160	3	0	21	21	1
			spe-miR160-4-3p	UGGCAUACAGGGAGCCAGGCA	67-87	aau-miR160	0	0	21	21	1
spe-MIR7696d	UUUUGAUGGUUUAAGGCUUUCAAGUUUCGUUGUGUGCAUCGUCUCCUAAGGUCCAUUUUAUGUUUUAAUUGGGUUGAUUUAUAGCAAGUGAAUUAUGAAUUGUGACUUCCAAGGAAGGAACUUUUUUUGUUGUAAUACCAUACAAGUCAAUGGUAGAGGUUCUCUCUUUUUUGAAUUAUGAGUACUUGAAACUCAAAUAGCUUCCAACGGAAUUUGGAAAACUAUUUAUAACAUCAUUC	239	spe-miR7696d-3p	UUUUGAAUUAUGAGUACUUGA	169-189	mtr-miR7696d-3p	1	0	21	21	1
spe-MIR1128-5	GGCUAAUGUUUAUUACUCCCUCCGUCCCAAUGUGAGGUAGUUUGACUUGGCAGUUUAAGAAAACAGUCUAAAAUAGGUUAUAGAUGUUGGUGUAGCUGUAAAUCAUUUUAGUAAGGGUAAAAUAGGUACUUUAAAGUUAGAUUGUUACUGAAUAUUGAAAUGCGUCAUUCUUUUUGGGCUGACUUAAAAGAAAAGUGAGCAUAUAAAUUGGGACAGGGAGUAUAUAGAAAGUAAAU	236	spe-miR1128-5-5p	UAUUACUCCCUCCGUCCCAAU	11-31	ssp-miR1128	2	0	21	21	1

spe-MIR172a-3	AAACACUGUCUCAAAUGUAAAUCUUCAGGUCGCCAAAUUCUAUAUCCUCCAAAAGUAGUGCAUUUUUGGAGUAGAACAACAUAGACAUUGACGACAUGAAGAUUUACAUCUGAGACAGUGCAUGCGAAAGAACAUACCUAAAUUAUCACGUUUUCGCGAGUUACAUACCUCAACUACCACUCAAUUAUA	123	spe-miR172a-3-3p	UUGACGACAUGAAGAUUUACA	88-108	vca-miR172a-5p	5	0	21	21	2
spe-MIR9477-2	UUAAAACAUACCUCGAUGUUUUGCCUACAUGUGCUUGUUGUUGAUUGAGAAGGAAUAUUUGGCCAACACAACAUCGAAGUGAGGGAAUGACAAUUUAGAUAGGUAAAGAGAACAAUGGAUAGUUGAGGUAUGAAACUCGCGAAAAAGUCAUAGUUUGGAUGUGUUUUUGAC	237	spe-miR9477-2-3p	UAGGUAAAGAGAACAAUGGAUAGU	166-189	sly-miR9477-3p	5	0	24	24	1
spe-MIR7990a-4	UCGGACAUUAGAGGCAAAAGUUAUGACCGUUUGAUGUUUCACCAAUUUACAACUACUUUUUUUGAGUUACACUUAUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCUUCGAAUAUCAGU	125	spe-miR7990a-4-3p	UUCAAAUGAUCGUAACUUUGGCUU	91-114	stu-miR7990a	1	0	24	24	1
spe-MIR11097a	UCAAAAAUCAACGGAUGAUUGUUUAAAUGUUGAUGCAUCUACAGCGUCAAAAUCAAAACCACCAACAUUGGACGAUUAUCCUGAUUUUACC	91	spe-miR11097a-3p	AUGUUGAUGCAUCUACAGCGU	27-47	lja-miR11097a-5p	5	0	21	21	1
spe-MIR5303d-7	UCUAAGUUGCGGACUCUUCAGUUUCAAUGCGGCACCCGUGUCUGAUUCUCCAAAAAUACACUACUUUUGGAGAAUCCGACACGCACCCAUUGACAAUUUUGAAGAGUCCAGCAAUUGCA	119	spe-miR5303d-7-3p	UUUUGGAGAAUCCGACACGCACCC	65-88	stu-miR5303d	0	0	24	24	1
spe-MIR7504m	CUCAAAAGUCAACGGAUGAUUGUUUAAAUGUUGAUGCAUCUACAACGUCAAAAUCAAAACCACCAACAUUGGACGAUUAUCCUGAUUUUACC	92	spe-miR7504m-3p	AUUAUCCUGAUUUUACC	76-92	gra-miR7504m	5	0	17	24	2
spe-MIR10540-4	CUAGAGUUGAUUUCUCAGAUGGUCACUCGACUAAUAGUUGUAUUAUCUUAGAAAGUCACUUUUUUGGUUGAAGAAAAGCGGAAUCAAGAAGAGAAGUGACUUUUUUUGAUAUAAUGACUAUUAAUCGAGUGAACAUCUGAGCAAUCAAUCCGG	153	spe-miR10540-4-3p	AUAAUGACUAUUAAUCGAGUG	111-131	sly-miR10540	4	0	21	21	1
spe-MIR1918-2	GUCAGAUAAUUAUGGUAGCUCAGUUGGUUUAACUAGUUGGAUUGUCAUUCUGUUGGUGAGAGUUCGAUUCUCCAUUACGUAAUCUCCUCUUCAAUUUAAGAGAAAAAAAUAUGCUACAAGGUGGAGAAUCGGACUAUCGCUAACAGGAUGGAAGUUCAAAUACUUAAUCAAUUAAGCUACUAAUAUUUUACUCUAUG	197	spe-miR1918-2-5p	UGUUGGUGAGAGUUCGAUUCUC	51-72	sly-miR1918	0	0	22	22	1
spe-MIR7984c-7	ACGAUAUCAAAUUUUAUGGAGGACUUUUUACUCCUGCACUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGUCCACGUGGACACGCUACAAGUUAUAAUAAUACAAUAUUUAUUAUGUCCACGUGUGCACAUAUUACACCCUUAAAAUACACUAGCAAAUAGUGCAGGGGUAAAAGGUCAUUUCCAAUAUUUGAUAUUGU	201	spe-miR7984c-7-5p	ACGAUAUCAAAUUUUAUGGAGGAC	1-24	stu-miR7984c-5p	3	0	24	24	1
spe-MIR7828	GAAUGGUGCCCCUAUCGUCUAAAAACUAGAGCAUAUAUACCAGUUAUACUAAUGGACAUACUUGUGUCAUAAUCUUCAACAGGACCGACAUUUAUCAAAUAUUGGAUCGACAAAUAAAAUUGUGUCACAUGUCCUUAUUUAGUCUUCCGUUAGAGUGAAGGGCAUAUAUACUCUAGUUUUUAAAUGGCAGGAACACCAAAA	201	spe-miR7828-3p	AAUGGCAGGAACACCAAAA	183-201	ptc-miR7828	4	0	19	21	2
spe-MIR159c	AGAGCUUUCUUCAGUCCACACAUGGGGAGCGAUAGGGUUCAAUUUGCUGCCGACUCAUUCAUCCAAAUGUUGAGGUCUUGAUAAUCGAAUGUCACCUCAGCAACUGAGUGAAUGAAGCGGGAGUACAAGUUGAGUCUUGAGCUUCCUGUACUUGGACUGAAGGGAGCUCC	170	spe-miR159c-5p	GAGCUUUCUUCAGUCCACAC	2-21	csi-miR159c-5p	3	0	20	20	1
			spe-miR159c-3p	CUUGGACUGAAGGGAGCUCC	151-170	csi-miR159c-3p	0	0	20	21	1
spe-MIR9478-1	GAAAAAGGUUCAAAUAUGCCAUCAAACUUUGAGAAAAGGCUCAUCUAUGCCAUUCGUUAAAAGUUUGGCUCAUCUAUGCUAUUUCAGUGAGCAAAUAAUGGCAUUAAUGAGCCUUUUGUCAAACAAAGACAUAGAUGAGCCAAAUUUCUAAUGGAUGACCUAAAUGAGCUUUUUAUGAAAGUUCGAUGACAUAUUUG	207	spe-miR9478-1-3p	UUCGAUGACAUAUUUGAGCCU	182-202	sly-miR9478-3p	0	0	21	21	1

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spe-MIR9477-3	UUUCAUAGCUGAACUAUCAAGUGUGUGUGAGUUUUCUGUCUGUACUAGUAUCAAAUGCUUGGCGAAGCAAACCUGAUUGUUCAGGUAGGAAAAGUGAACAACUUAUAGUUCAUUUAUGUUU	121	spe-miR9477-3-3p	UAGGAAAAGUGAACAACUUAUAGU	86-109	sly-miR9477-3p	4	0	24	24	1
spe-MIR6283	AGGGAUUAAUUGUCUUCCUAGUUUUCGAAACAAGAAAGGGGUGUAGAAAAAUCCUUUUUUCUUGUGUCGAAACGAAAGAGUAAUGAUUCUUG	92	spe-miR6283-3p	AGAAAGGGGUGUAGAAAAAUC	33-53	ppe-miR6283	5	0	21	21	3
spe-MIR5274b	AAAAUAUCUUCUGUCAUACUUUUGAGACAUUGGUGCUCAUGCCGUCCAAAAACUAGAGCAUAUAUACCUUUUAUGAUAACGGACGUAUACAUGACAUAAUCUUAUCGACUAAUCAGACAUUUAUUAAAUAUUAUCGAUGGAUAAGAUUGUGUCACGUGUCCCCAUUUAGUCUUUUGUAGAGUGAAGGACAUAUAUGUUUACCACUGUCCUAAAAGUAUGACGGAGGGUAUAUG	233	spe-miR5274b-3p	GUAUGACGGAGGGUAUAUG	215-233	mtr-miR5274b-5p	3	0	19	21	2
spe-MIR8001a-1	AAAUAUAUAAAUGCAUAACACUACAAGAAGAUUGUGAAUUACAUAGGAUUUUCCUGGGGAUUAGUACAAAAAUUCACAGGAAACUUAUUUUCCUACAAAUUUUCAUACUAAUUCCCAGGAAAAUCCCCAUGUAAUCCACAGUUUUCUUGUAGUGUAAUUCGCUAUACAUAUACAG	175	spe-miR8001a-1-5p	UCCUGGGGAUUAGUACAAAAAUUC	52-75	stu-miR8001a	2	0	24	24	1
spe-MIR2089-2	UGUUUGGUGUGAAAAAACAAGAGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAUUUAUUUUUUCCACGAAUUG	115	spe-miR2089-2-3p	UUAUUUUUUCCACGAAUUG	97-115	mtr-miR2089-5p	5	0	19	22	1
spe-MIR3447-1	UUGCAUUUGAAAGAUAUAGUUUUUAUGAUAUUGGAUACUUGAAUCAUCUUCGUACCUUUGGUUGUGAUUCUUCUGAAAACAAAGAUGGAACUAGUGUUGAAGAUGGAACUAGUGUUUAAGAUGGAACUCAUGCAAAUAUCCUUUCAAGUGUUG	171	spe-miR3447-1-5p	UUUGGUUGUGAUUCUUCUGAA	57-77	aly-miR3447-3p	5	0	21	21	1
spe-MIR5773-2	CACCCACACAACCCGACCCAUUGAAAAUAUGAUAUGACCCAUUUUAUUUUGUCUUUAAUCCUAAUUCAAGGUUUAAACAGAGGGAUUAAUUUAGGAUUAAAGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGGUGG	155	spe-miR5773-2-3p	UUUUUAAUGGGUCGGGUUAGGU	129-150	gma-miR5773	5	0	22	22	1
spe-MIR1530-2	UAAUGCACAAACAAACACUUUAACUAUCCAACUUUCAAAUAAAUAAACACAUGAGUCCUACAUGGCAAAAUACACGUAGGACACCACGUAAGACAAAAAUGACAUGUAGGACAUGUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUUAAGUGUCUACUUGUGUGCACCC	172	spe-miR1530-2-5p	CUUUCAAAUAAAUAAACACAU	32-52	gma-miR1530	5	0	21	21	2
spe-MIR9773-1	ACUAUGACCAAAAUUACAGAAACACACCUUAACUAAACUAAGAUAUUACUAUUAUCCCUGAACUUUUUUUUUUUUAAUUUUGUGCACCUUUAUGGCUUAUGUGACAUCCAAAUAUCUCCCACGCGCCUCAAUUGCAUGAAGUCACGGAGUGUGUCACCUAAGACAGAAAGUACACAAAAUUAAAAAAAAAUAAAAUUUAAGGGGUAAUAAGAACUUCAUAUAAUUAAGGUGUGUCAUGGUCUAAGUAUUUGUACAUUUU	260	spe-miR9773-1-5p	UUUUUUUUUUUUUAAUUUUGUGCA	64-87	tae-miR9773	5	0	24	24	1
spe-MIR7997c-9	CUUCUAUGUUGCUUGGACUCUUCAAAAAUGUUGACGGGUGCGCGUCGGAUCCUUCUAAAGUAGUGCAUUUUUGGAGGAUCCAAUGGAUGCGGCAACAAUUUUGGAGAGUCCGAGCGACUUAGUCU	125	spe-miR7997c-9-5p	AUGUUGCUUGGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
spe-MIR6248	AGGGAGAGAUUUGUGAUAAUAAAUCUUGGCAACAAUUAAUUUGGCAGCCAUACUUGUUGAAAUUACAAGCCACAAAUGUGAAAAUUGGUAGCCACAUUGUGGAAGUAUGUGAAAGUUGGUAGCCACAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAGAGUUAGGCAGCCAAAUUUUUGUUGAAAUUGGCUACCACAUUAUGUCAUCAAU	201	spe-miR6248-3p	CAUUUGUGGAAGUAGGUAGUC	117-137	osa-miR6248	5	0	21	21	2
spe-MIR1919-3	GACGCCUUUGAUGUUCACAUCUUCUGGUAGUCCUGUCGCAGAUGACUUUCGCCCUUCUAAGGAACCACACUUUCUGUAAAUCUAAUUAAUUUGAAUU	160	spe-miR1919-3-5p	UGUCGCAGAUGACUUUCGCCC	34-54	stu-miR1919-5p	0	0	21	21	1

	CAAUGUGGCAGGACGAGAGUCAUCUGUGACAG GAUAAUGGAAGAUCUAGUUAUCAAAGGCUUA		spe-miR1919-3-3p	ACGAGAGUCAUCUGUGACAGG	110-130	stu-miR1919-3p	0	0	21	21	1
spe-MIR1533-3	UAUAUCGCUGCCUGGUCAGCGAUUUAUAAAAAA AAAAUAAUUAUAAAUCGCUGCCUUGGCAGCGAC UUUAUGAAAUUUUUUUUUUUUUAUUAAAUCGCU GCCUAGGAAGCUAUUUU	116	spe-miR1533-3-5p	AAAAAAAAAAUAAUUAUAA	28-46	gma-miR1533	4	0	19	19	1
spe-MIR7492f	CUACGAUAAAAAUGAUCAUUAGCGGCAUUUAAU UUUUAAUUGCCGCUAAAUAUGUAUUUUUAGCG GCA	68	spe-miR7492f-5p	AAAUGAUCAUUAGCGGCAUUU	10-30	gra-miR7492f	4	0	21	21	3
spe-MIR11090d	GCGACAUUCAUGAAAAGUUAUGACUUUUAUGAA AAGUUGUGACAUUUGAGAAAAGAUGUGACUUU UAUGAAAACUUAUGACCCUUUCAAAGAUUGUGA C	99	spe-miR11090d-3p	AUUUGAGAAAAGAUGUGACUU	44-64	lja-miR11090d-5p	5	0	21	21	1
spe-MIR8030-2	GUAUAAAACCGAACCGAACACCAAACCAAACCG UAAACCGAGUCAAACCGAAAAAAACCCUACUAG CGGUUUGGUUUGACUUGAUUUGGUAUUGGAAA AAAAAACCCGACUAUAUUUGGGUUGGUUUGGU UUUAAAU	137	spe-miR8030-2-3p	UUGGGUUGGUUUGGUUUUAAAU	116-137	stu-miR8030-5p	5	0	22	23	1
spe-MIR8001a-2	CUGACACUAUAACAAUUUGUGAAUUAAAUGGGG AUUUUCCUGGGGAUUAGUAUGAAAAUUCGCGG GGAACUUAUUUUUCUGCAUAUUUUCAUACUAAU CCCCACGGAAAUCUCCAUAUAAUUUACACUUUU CUUGUAGUGUGAA	144	spe-miR8001a-2-5p	UCCUGGGGAUUAGUAUGAAAAUUC	38-61	stu-miR8001a	0	0	24	24	1
spe-MIR1514b-1	GUUAUCUACUUGAUAUCCACACUCAAAAUCUUU GUUAAACACCAAGAGGUCAUUCAUAACAUGAAU CAUAACCUUUGAAUUCCUAAUUCAAAUUCAAGG UAGAGUUAAGAGUCAAGUCUUGAGAGUUCUUC UGAGUCACUUUGAGAAGCUUUUACAAUCUUUUA AACUUGUUUUUAGACUUGAGUUAUUGAGUUCG AGGACGAGUAGAGUUAAGCUUCAUUUUUUAAAA AAAAAAUGAAUGUAUGAGAACUAAGUAUUCCCA AGAGUAAAUGUUUUUAAGAGAGACCUUUUCAGC UUUAAUAUCAAAGUUGAUGAG	316	spe-miR1514b-1-3p	UUCAUUUUUUAAAAAAAAAAU	216-236	gma-miR1514b-5p	5	0	21	21	1
spe-MIR482d-3	CAUGAUAUAUUUUCAUCUUACUGAUGACAUGAC CAUAGAUACGAAGAUAUAGAGGUCGGAAAUUAG GAUAGAAGGGUAGUAAAGUAGCUGAGUGUUGU CAUACUUUUAUGUGGGAUAGGUGAGGCGUAAG UCCCUUCUUGUUGCUUCAUUUGCUUUGUGAU CUUGUCAUUUUAUUGUCAUUAUUUCCAUUUUUA UCUUGUCUUGUCUACAUUUCUUUUAAGAUGAA GAUAUAUCGAA	238	spe-miR482d-3-5p	GAUAGAAGGGUAGUAAAGUAG	67-87	mdm-miR482d	4	0	21	21	2
spe-MIR171b-6	AAAUGGAAUGAAAAUAAGAAGUGAUAUUGGCGC GGCUCAAUCUGAGAUCGUUCUUUACGAAAAUAA GCGUAAAUUCGUCUUCGGAUUGAACCUCACCA ACAUCGCUUCUUCCAUUUUAAUCCCAAAA	127	spe-miR171b-6-5p	GAUAUUGGCGCGGCUCAAUC	23-42	zma-miR171b-5p	1	0	20	20	1
			spe-miR171b-6-3p	GGAUUGAACCUCACCAACAUC	83-103	tcc-miR171b	5	0	21	21	2
spe-MIR8001b-4	ACUUGUAUAAUGUUAAAUAAGUAGACUACAAGA AAACUAUGAAUUACAUGGGCAAUUUCCAGGGGA UUAGUAUGAAAAUUUGCACGAAAAUAAGUAUCC UACGGAUUUACAUACUGAUCCCGAGGAAAAUUC UCAUGUAAUUCACACUUUUCUUGUCCUAUGUG ACAUAAUACACGU	177	spe-miR8001b-4-5p	CAGGGGAUUAGUAUGAAAAUUUGC	60-83	stu-miR8001b-5p	2	0	24	24	3
			spe-miR8001b-4-3p	GGAUUUACAUACUGAUCCCGAGGA	103-126	stu-miR8001b-3p	5	0	24	24	1
spe-MIR9471b	UUGAGAUUCAGUUGAUUUCUGAGGUGCUCACU CAGCUAAUAGUUAUUGUUUAAGAAACUCGAUAA UAUUGGCAGCAAGGAGAAUGGUGACUUUCAGG AUGAUAACUAUUGGCUGAGUGAGCAUCACUGA AAUCGACAUGAUUCUGAG	147	spe-miR9471b-5p	GAGGUGCUCACUCAGCUAAUA	21-41	sly-miR9471b-5p	0	0	21	21	1
			spe-miR9471b-3p	UUGGCUGAGUGAGCAUCACUG	108-128	sly-miR9471b-3p	0	0	21	21	1

spe-MIR9471a	GGUUCUGAGAUUUAGUUGAUUUCUCUGGUGCUUACUCAACUAAUAUUUAUUAUUUAAGAAAAUCAAUAAUAUUGGAAGCAAGUGGAAUGGCGACUAUCAGGAUGAUAACUAUUGGUUGAGCAGCAUUAGAGAAAUCGACGUGAUACUGAGAGGA	154	spe-miR9471a-5p	CUGGUGCUUACUCAACUAAUA	25-45	sly-miR9471a-5p	3	0	21	21	1
spe-MIR1440a-1	CCUUUAUAAUAGUUAAUUCAAUAAGUCUUAAUGUUAAUGUUGAGAUGGCCGAGUUGGUCUAAGGCGCCAGAUUAAGGUUCUGGUCCGAAAGGGCGUGGGUUCAAAUCCCACUCUCAACAACUAUUUUUCUUAUUGCAAAUAUAAUAACAU	150	spe-miR1440a-1-3p	GGUUCAAAUCCCACUCUCAA	98-117	osa-miR1440a	5	0	20	20	2
spe-MIR5180a	CCAAAAACUAAAGCAUAUAUAUCCUUCACUCUAACGAAAUAGGGACAUGUGUGACAGAAUUUUAUUAGUCGAUUCGAUAUUAAAUAAAUGUCGGAUCGGUAGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUUACAAAGGUAUAUAUGUUCCAGUUUUGAA	162	spe-miR5180a-3p	UAUAUGUUCCAGUUUUGAA	144-162	bdi-miR5180a	4	0	19	21	1
spe-MIR11456	UCAGGAACCCUGUUUUCUAGUGAAUGUCGUUUGAGUAAAGCCAAAGAGACUUUACUAGACAAAGUUCCCAU	71	spe-miR11456-3p	AAUGUCGUUUGAGUAAAGCCA	23-43	pab-miR11456	5	0	21	21	2
spe-MIR5303f-9	GGUUGAUUAAAGCUAUGUUGCUUGGAAUCUUCAAAAUUGUCAAGGGGUGUGCGUGUCGGAUUCGCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCAAAAGUAAAGAGUCCGCGCAACUUAGGAUUUAAGCACAA	147	spe-miR5303f-9-3p	AUUUUUGGAGAAUCUGACACGGGU	77-100	stu-miR5303f	0	0	24	24	1
spe-MIR8026	UAGUCGUAAAUUGGUUUCUACCUCCUUGCCCUAACUUUAUAUUACCACAACCGUUAGCGAUGGAAUUAAUGUAGAGAAUAUGUGGUAACCCUAAUGGGUGGAGGGAGGACCAAUUUACAGAGGU	124	spe-miR8026-3p	AUGUAGAGAAUAUGUGGUAACCCU	69-92	stu-miR8026	0	0	24	24	1
spe-MIR7980b-7	GCGUUUGGCUAUGCGAUAUCAUAUCACGAUAUGGUAUCGUGAGAUGGAAUCAGCGUUUGGACAUGCGAUUUCACGCUGAUUCCGUCUCGUGAUUUCAUAUCAUGAGAUGUGAUAUCAUAUUCCCCAAAAAC	131	spe-miR7980b-7-5p	GAGAUGGAAUCAGCGUUUGGACAU	41-64	stu-miR7980b-3p	1	0	24	24	1
spe-MIR1862g	CUAUGGUUUGGUUUGACUUGGUUUGGUAUUGGAAAAAAAAACCCCGACUAUAUUUAGGUUGGUUUAGUUUCAACUUACAAAAACCAACCCAAGACCAAACCAACC	105	spe-miR1862g-3p	UUUAGGUUGGUUUAGUUUCA	53-72	osa-miR1862g	5	0	20	20	2
spe-MIR171h	GAUUAUAAUUAUUUUUUUUUCAUUUCCGUUAGAGGAAAAGGGUAUAUAUGAGCCAUUUGUUUAUAAGUAGGCGUAUAUAUGAGCCACUUUCAUAACACGGGGUAUAUCAGCUCUAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUCCCUUACUAUAAUGAGCAGAAAAAAAAUCAAUAGGC	185	spe-miR171h-3p	AUGAGCAGAAAAAAAAUCAAU	161-181	lus-miR171h	5	0	21	21	1
spe-MIR3706-1	CAUACACGUGUCAUAAUCUUAUCCACCGACCUGACAUCGGAUCGAUGGAUAAGAUUGUAUCACGUGUCCC	70	spe-miR3706-1-3p	CAUCGGAUCGAUGGAUAAGA	35-54	pab-miR3706	5	0	20	20	3
spe-MIR11479	UUUUUCUUGUAGUGAUGAAGAUGUUUGAAAUUCGUUGUGGACAUGAUGAUGAUGAUGAUAAUGAUACAAUUCUGGCUUUACAUCAGCAACAGGAACCCUAAAAUUAGCUGUUGAUGAUGUUGGAUGGACGGAAUUUAAACUUUGGUCUUCCGAAUUCCCGGCAGCAUGAAAAGGACUAAUACCAAACUUUUCUUCAUCACCACAAAAUCC	210	spe-miR11479-5p	GGACAUGAUGAUGAUGAUGAU	39-59	pab-miR11479	1	0	21	21	1
spe-MIR7987-1	UUUAGCGUAAGUACCAACACUAGUUGAUCUUAUUGAUGACAAAGUUAAUUUUCUUGCAAAAUCGAUUUGUGUCCAUCUAGUGUUGAUAUUAAGCUUUAGAGGUAAAGCAGAAACUCUUUCAAAUAGAGCCA	98	spe-miR7987-1-5p	ACACUAGUUGAUCUUAUUGAUGAC	17-40	stu-miR7987	0	0	24	24	1
spe-MIR6023-1	AAUAGUUCUAAGAAUUCUAAGUUGAUCCUCACUAGCACCACAAAGAUUUUUUUUAGUUUCAAAAAACAUAUUCUGCGUGGUGCUGAUGACGAUCAACUUAGAAUUCUUGGAGCAUUUUGCUCUACUUGAAGGAGUUUUUGGUUUACACA	182	spe-miR6023-1-3p	CUACUUGAAGGAGUUUUUGGUU	155-176	sly-miR6023	5	0	22	22	2
spe-MIR5780d	AUCUAGACACCUCAACUUGAUCCCAACUGACAACUAAACACUCCAACUCGGUGUGCAACCGAUACAGUGGAGAGGCGUUUAGAUGUGCAUACUCAAAGUUGGAGUGUUUACUUGUCAGUUGAGGCUAAGUUUUGAGUGUCUACUC	145	spe-miR5780d-3p	AGUUUUGAGUGUCUACUC	128-145	gma-miR5780d	5	0	18	22	2

spe-MIR7997c-10	GGUUAUGUUGCUCGGACUCUUCAAAAAUGUUG CAACAUGCAUGUUGGAUCCUCUGAAAAUGCACA ACUUUUGAAGGAUCUGACAUGUAUUGACGAUA UUUUUGAAGAGCUCGAGCAACAUAGCA	124	spe-miR7997c-10-5p	AUGUUGCUCGGACUCUUCAAAAAU	5-28	stu-miR7997c	1	0	24	24	1
spe-MIR7822	AUGUUUAUGUCUUUUAAUUUUGAGUAUGCAUAA GUAAACACUUAAAAUUGAACAAAUGGAUACAUU CGUCCUACGUAAUAAUUUUGUAUCCUGGUGGU GUGCUACGUGUAUUAUGUUGUGAAGGACGUGU GUGAUUACUUGUUCAAUUUUAUACAAGUUUAAG UGUGUGAUUGUGCAUACAAAAAGUUGGAUGAC GUAGAAAGG	204	spe-miR7822-5p	CUUAAAAUUGAACAAAUGGAU	41-61	ptc-miR7822	4	0	21	21	2
spe-MIR7997b-2	CUUUUGAAACCAUUGUUUGUACCUAAGUUGCU CGGACUCUUCAAAAAAGUCAGUGGGUGUGUGU CGGAUUCUCCAAAAGUAGUCUGACACGGGUGC GGCAACAAAGUGAAGAGUCUGCGCAACUUAGG UUUGUACAAGGUGCAAUUU	147	spe-miR7997b-2-5p	AAGUUGCUCGGACUCUUCAAA	25-45	stu-miR7997b	2	0	21	21	1
spe-MIR7983-6	AACUAUCACUAUAAUAAAAAUGAUCAUUAGCGG CAUUUAAUUCUUAAUUGCCGCUAAAUAUGUAUU UUUAGCGGCAAUUGUCAAUCUUUGUAUAUGUC CCUAAAGCCUUUAGCGAUGUUGGUUCUAAUGC CACUUAACGAAUGCCGGUAAAGACUUUAACACU CUUUAUUAGUGUCAAUAUUUAAUGUCGCUAAAA AUUAUUUUCUUAUAGUAUAUGA	218	spe-miR7983-6-3p	ACGAAUGCCGGUAAAGACUUUAAC	137-160	stu-miR7983-3p	1	0	24	24	1
spe-MIR5162	AUUAGGUGUCAAUAGAGGGUAUAUGUAUUAUU AUAUCAAUAAUCUGUGAUAGAUUUAUAGAUUGU GUAAGGUGGGAAAAAUGACCAAAAUACCCCUAA AGUGACUAUAAUUUAGCUAAUACCUCUCUUUUA CACACUCAG	140	spe-miR5162-3p	AAAUGACCAAAAUACCCCUAAAGU	78-101	osa-miR5162	3	0	24	24	1
spe-MIR7808	CCACUGCGCUUCUUUCUCCUGAGGCGAUGCGA UCUGAAAAAGGCGCUCGCUUCAGAUGAAGAAG CGAGAAG	71	spe-miR7808-3p	AAAGGCGCUCGCUUCAGAUGAA	39-60	rgl-miR7808	5	0	22	22	1
spe-MIR7983-7	ACCACACUACAACAAAAAUGAUCAUUAGCGGCA UUUAAUUCUUAAUUGCCACUAAAUAUGUAUUUU UAGUGGCAAUUGUCACUCUUUGUAUAUGUCCC UAAAGCCUUUAGCGACAUUGGUUCUAAUGGAA CUUAAUUAAUGCCGGUAAAGACUUUAGCAUUCU UUAUUAAUGUCAAUAUUUAAUGCCGCUAAAAGU UGUUUUUGUUGUAGUGUCAU	216	spe-miR7983-7-3p	UAAAGCCUUUAGCGACAUUGGUUC	99-122	stu-miR7983-5p	1	0	24	24	1
spe-MIR1886h-2	GCCAUGAGAUACCAUAUCGUGGCCUUUGGCCA UGAGAUAUCAUAUCACGAUAUGAAAUCGUGAGA UUGAAUUCGUGUUUGGACAUAUAAUUUUACGU UGAUUUCAUCUCAUGAUUUCAUAUAAUGAGAUG UGAUUUCGUAUUCUCCAAAAAUCAUGAUAUGGA AUUUCAUAUC	173	spe-miR1886h-2-3p	AUUUUACGUUGAUUUCAUCUCAUG	89-112	stu-miR1886h	0	0	24	24	1
spe-MIR7992-10	GGUGUCUAGAUGUGCAUUCUCAAAAUUAGAGU GCUUAUUUGCCAGUUGAGGCCCAACUUUAAGU GUCUGCGUAUGUAUUAGUCUAUGGACUAUUGU UGUUGUCUUUCAAAGUGGCAAUGUGAAGCAUU CAGAGAAACAACAUCAAGACUUG	151	spe-miR7992-10-5p	UGUCUAGAUGUGCAUUCUCAAAA	3-25	stu-miR7992-3p	5	0	23	23	1
spe-MIR840	GACUUUUGAGUGAAAAUUGAAAGUUGAGUGAC UUUCUGAGAGAAAGUGCAUAGCUGAGUGAUCA UCUGAGGUAUUAACUCUCCAAAAUCACGUGUUA GCGAUUUUUAAGGUCACUCAAUUUCAAAAAUUU AUGCAUCAAAAUUA	144	spe-miR840-3p	UUUUUAAGGUCACUCAAUUUC	102-122	ath-miR840-3p	5	0	21	21	1
spe-MIR5210	UUCACUAAGGUUAAACUCUAGGAUAUGCUUCCA UAAGCAUAAUCUUAGUUGAUUACGUUUGAUCUC UAAGAGAUUAUUCCUCAAGCAUAACCCUAGACU AUUAAUUGUGUUGGACUCUAGGAUAUGGAUUC UCAAGCUUAAUCUUAGUCCUUCACUAGAGAUG GGAUCUGGGAGAUUCUUUCUCAAGCAUAAUUU UAGAACAUUAACCAUGUUGGAAUCUAGGAGAUU CUACCUUAAGCAUAAUCUUAUCCCAUGAGGUGU GAGCUCUAGGAGAUGCUACCUAGAGCAUAAUC UUAGUUCA	301	spe-miR5210-5p	UAAUUGUGUUGGACUCUAGGAU	102-123	mtr-miR5210	5	0	22	22	1
spe-MIR7981-13	AGACACGCCUUAACUAAACUAAGGUCCUAUUAC CCCGAAUCCAUUUUUCUGUAAUUUUUUGUACAA	214	spe-miR7981-13-5p	CUUAACUAAACUAAGGUCCUAUUA	9-32	stu-miR7981-5p	3	0	24	24	2

	UUUUUCGGCUUAUAUGGCAUCCAAACGUCUCG CACGCGCUUCAUCUAUGUAGAGUCACGGAGUG UGCCACAUAAGCUAAAAUGUGUAUAAACUAACA AAAAAAAUGAUUUUGGAGGUAAUAGGACUUUAG UUUAGUUAAGGCAUGUCU		spe-miR7981-13-3p	AUAGGACUUUAGUUUAGUUAAGGC	185-208	stu-miR7981-3p	1	0	24	24	1
spe-MIR10540-5	UGGUUGAUUUCUCAUAUAGUUACUUGACUAAUA GUUAUUAUCUCGAAAGUCCCCUUUCUUCUUGA UUCCAAAACUUUCAACAAAGAAAGUGACUUCCU GAGAUGAUAACAAUUAGUCGAGUGAUCAUCUGA GAAAUCAAACU	142	spe-miR10540-5-3p	AUGAUAACAAUUAGUCGAGUG	102-122	sly-miR10540	4	0	21	21	1
spe-MIR7992-11	ACUUUUUAGGCAUAAUACAUAAACAGACACUCA AACUCGGUCUGAGUAACCACUCCAACUUUGACA AUGCACAUCUAAACACCGCAACUGACAACUAAA CACUCCAACCCAACCUCACUAUAUCUCGUGGAC ACCUUGCGUUGACAUAUCACAUAAAUUUUCGUA GAUGUACUGUCUAGAUGAUCAUUUAGUAAGUU GGAGUGUUUACUUGUCUGCUGAGGACAAGUUU GAGUGUCGGUUUAUGUAUUAUGUAAAAUUU GCCCUUUAAUCUUGUGUCCUUGAACAUGCCAC	259	spe-miR7992-11-5p	UUUGACAAUGCACAUCUAAACACC	60-83	stu-miR7992-5p	2	0	24	24	1
spe-MIR7983-8	CACUACAACAAAAAUGAUCAUUAGCGGCAAUUA AUUCAGAAUUAAUUGCCGCUAAGUAUGUAUUUU UAGCGGCAAUUGACACUCUUUGUAUAUGUCCC UAAAGCUUUUAGCGACAUCGUUUCUAAUAGCAC UUAACUAAUGCCGGUAAAGACUUUAACACUCUU UAUUAAUGUCUAUAUCUAAUGUCACUAAAAGUU AUUUUUGUUGUAGUGCACGUUGAAAGUUAAAG UUAAAGUUU	270	spe-miR7983-8-3p	ACUAAUGCCGGUAAAGACUUUAAC	167-190	stu-miR7983-3p	0	0	24	24	1
spe-MIR384	ACAAGGGCACCAAUGUCCCAAAAGUAUGACGAA GGGUAGCUGCAUACCAUUUACGAAACUUCAAUU CUUAAACCACUACAGAUAUACUAGAUGGACGAG CAAUCAUGAUAAAUAUGUGUUCUUUUUAGGGAA AAGGGACAAAUAUACUUCUGAAUUAUCAUAAAU AGUAUGCAAAUAUCCUCCGUCAUACUUUAAGGA CAUUGGUGCUCCUAUC	214	spe-miR384-5p	AGGGCACCAAUGUCCCAAAA	4-23	stu-miR384-3p	5	0	20	20	1
spe-MIR166-6	AUUGUUGGGGAGAAUGUUGUCUGGUUCGAAAU CUUUCUAUAGAAAAAUCAGUGGCGGAUUCAGU CAUGAGUUUCAAGAUCGUUAAAUCUUAUAUAUG UACAAAAACAAGUACAAUAUAUAUUUUUAGACC CUAAAAUGUCGAAAUAUAUUCUGAAUCCGUCAU AGAUUAGAUCGUUUGAUCAAUCAAUUUAUUGAG UGAUUUCGGACCAGGCUUCAUUCCCCUCAACU CU	230	spe-miR166-6-3p	AUUUCGGACCAGGCUUCAUUCCCC	199-222	lja-miR166-3p	0	0	24	24	1
spe-MIR162b-3	GGCGGGUUAAGCACUGGAUGCAGAGGUUUAUC GAUCGCUUCCUGUUGCUGUAUUUAUCGCUUUU CAGGGAACAGAUCGAUGAACCGCUGCCUCCAG UGUUCUCACCCAAC	110	spe-miR162b-3-5p	UGGAUGCAGAGGUUUAUCGAUC	15-36	ath-miR162b-5p	3	0	22	22	1
			spe-miR162b-3-3p	AUCGAUGAACCGCUGCCUCC	75-94	cas-miR162b	0	0	20	20	1
spe-MIR8006-8	CCCUGCCGUCCAAAAACUAGAGCAUAUAUACCC UUUAGACUAACAGACAUACAUGUGUCAUAAUCU UAUCCACCGACCUGACAUCGAAUCGAUGGAUAA GAUUGCGCCACGUGUCCCUAUCUAAUCUUCCG UUAGAGUGAAGGGCAUAUAUGCUCUAGUUUUU GGACGGCAGGG	174	spe-miR8006-8-3p	UAGUUUUUGGACGGCAGGG	156-174	stu-miR8006-5p	1	0	19	24	1
spe-MIR1122	GAGCACGAUAUUUGUCUAUGUACCCUAGAUACA UGUGAAUCUACUUGGAUAGAGUGUAACAAAUUA ACCUAAUUUGAGUCUAUAUAUUCCGAGAUACAU GUAUCUGGACGUAGCAAAAUCUGGUA	125	spe-miR1122-5p	UAGAUACAUGUGAAUCUACU	26-45	far-miR1122	5	0	20	20	1
spe-MIR8006-9	AAGAAAGUACUUUUGUGAGAAGCUGUGUGUGU UAGGGUCAAUCAAUUUGAGAAACACUUACAAGU UAGUGUUGACCAAACUUUUAAAAAGGUUUCUAA AUAUAUUUUCUCAAGAAGUGUUUUUUUAAGGG UAUAUAUGCUCUAGUUUUUUGACGGCAGGGGC ACCAAUGUCCCAAAAGUAUGACGAAGGGUAUCU	269	spe-miR8006-9-3p	UAGUUUUUUGACGGCAGGGGCACC	142-165	stu-miR8006-5p	2	0	24	24	1

spe-MIR838	GCAUACUAUUUAUUAUAGUUCCAGGGUAUAUUCGUCCAUUUUACCUUUUUCAGCUUCUGAAAAGCAGCUUUGCCCCAGAGAGUUUGUGAAGAAAGAUCUCUAUGAAGGAAAAAAAAUGGCCAAAAGAAAGCAAAUGCUUUGCUGCAAUCUGUUUUCAGUUAUUUUUCUUCUUCUUCUUGCAGAAGUAAUACAUUUUCCAGAGUGUGUUAAGGCUGCAGGUUCACCUGUUAAGUUUCUUCCAGGCUUUCAAGGACCACUUCCUUUUGAACUUGAAACUGGGUAAGUGUAAAAGUUUCUUCUUUGAUGUUUAGUCGUGUUUUUGUUUCUCAAAGUAUAGUAUAUGAUUGAAAACUUUCAAUAGGCAUAAUACAUAAAGACUCAAAGUUCGCGUCAAUCGGCAAGUAAGCACUCCAAGGUGAGAGUGCACAUAUGGACACCUCAACUGGGUCUCAACUGUCAUAUAAACACUCUCGUCCCCACUCUGUCUCGUGGAUGCUUUAUGUGUCUAGAUGUGCAGACUCAUAGUUGGAGUGCUUACUUGUUAGUUGAGGCCAAGUUUGAGUGUUUGUUUAUGUGUAAGUAUGUUUAUAUAUUCAAAACUUAAAUUUCAUAUAUAUUUAGUUUAAAACUAUAAGAUUCAGGGGCGGACCCAUAUGGUGUCCGCCGGGUGCUCGAGCACCCAUUAACUUCGUUACGAAAUAUAUAUAUCUAUGUAGAAAUUGAUAGGUAUUUGUAUAAAAUUAACAUAGAGUCCUCAGUCAUACAUUUGGGACAUUGGUUGCCGUUUAAAAAUUAGAGCAUAUAUGUCCUUCACUCUAACGGAAGACUAAAUAGGGACACGUGGUGUAAUCUUAUCCGUUGAUAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACGUGUAUGUUCCUUAGUAUAAAAGGUAUAUAUGCUCUAGUUUUUGGCAGAGACACCAAUGCCGCUAAAGUAUGACGAUACUGUUAUCUAAGUCAACACCAAGGGUUGUAGACGAGAUGGAUAAUGAUGCCUUUAUGUUUAACCAGAAGUCUCGGGUUCGAAUCUCAAGAAUGAAAAUAAUUCUUGUAGGUAGUUGUGUACCUUAUUCAGACUCAAAUCCGAGACCUCUGGUUAUGGAUAAAAGUAUUUCAUUCAUCCCGUCACAUCCUUAAUUUUUAUUAGCUACGA	285	spe-miR838-5p	UUUUCUUCUUCUUCUUGCAGA	89-109	aly-miR838-3p	1	0	21	21	1
spe-MIR1044-3	AAAAACCUAUGUUGCUCGGACUCUUGAAAAAGUGUCAUCAGGUACGUGUCAGAUCCUUCAAAAAUAAGCGCAUUUUAGGAGGAUCCGACAUGGCUGCAACAACAUUUUUUGGAGAGUUCGAGCAACUUAGCUUAAAUUAAUUAAGUGUUGAGAUGGCCGAGUUGGUCUAAGGCGCCAGAUUAAGGUUCUGGUCCGAAAGGGCGUGGGUUCAAAUCCCACUCUCAACAUGAAUUUUAUCCAAAAGAAUUGGAUCAAUUGUAUUGUUAGCAUUGUAAAGACGUCUCAAAGUUCUUGUGUAUUUUAUGAACACUAGGUCAUGUUGAGGUGCUUCAGGGUUCUCUUCCUCAAUGACCUAGUGUUCAAAAAUAUAAUAGAAUAUCAAGGCGUCCUUACAAUGCUCACAAUGGAUUGAUCCACUUCUUUUGCAUUGAGUUGCUCGGACUCUCUAGAAAUGUUGUUGCACCCAUCUCGGAUCCUUCAAACAUGCACUACUUUUGAAGGAUCCGGCACACACCCAAAAACAUUUUUGAAGAGUUCGAGCAACAUAAAGUUAUUACUCCCUCCGUUUCAAAAAGAUUGACCUAGUUUGACUUGAACGAAAUUUAAGAAAAGAAAGAAACUUUUUAAUCUUGUGGUUUUAAGUUAAAGUCAUGUCAAAUGUACUAAAAUGCCCUUUAAUCUUGUAGUCCUAAACAUGCCACGUGUAAAGUUAAAGUUAAAGUGUUGCCAAAAAAGGAAAGUGGCCAUUCUUUUUGAAACAAACUAAAAAGGAAAUAGGGACAUUCUUUUUGGAACGGAGGGAGUACGUAA	218	spe-miR1044-3-3p	UUGGAGUGCUUACUUGUUAG	167-186	ppt-miR1044-3p	5	0	20	20	1
spe-MIR3515		174	spe-miR3515-3p	UAUGUAGAAAUUGAUAGGUAU	133-153	ahy-miR3515	4	0	21	21	2
spe-MIR8739-2		223	spe-miR8739-2-5p	AGACUAAAUAGGGACACGUGGUGU	73-96	gra-miR8739	5	0	24	24	3
spe-MIR5157b		207	spe-miR5157b-3p	UAAUUUUUAUUAGCUACGA	189-207	osa-miR5157b-5p	4	0	19	24	2
spe-MIR7997c-11		136	spe-miR7997c-11-5p	AUGUUGCUCGGACUCUUGAAAAAG	9-32	stu-miR7997c	3	0	24	24	1
spe-MIR1440a-2		99	spe-miR1440a-2-3p	GGUUCAAAUCCCACUCUCAA	70-89	osa-miR1440a	5	0	20	20	2
spe-MIR10533-2		193	spe-miR10533-2-5p	UUUUAUGAACACUAGGUCAUGU	64-85	sly-miR10533	5	0	22	22	1
spe-MIR5303-15		119	spe-miR5303-15-3p	UUUUUGAAGAGUUCGAGCAAC	96-116	sly-miR5303	0	0	21	21	1
spe-MIR8019-3		266	spe-miR8019-3-5p	AAAAGAUUGACCUAGUUUGACUUG	24-47	stu-miR8019-3p	2	0	24	24	1

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spe-MIR5773-3	ACCCACCUAACCCGACCAAUUAAAAAAAUAUGAUAUGACCCAUUUUAUAUUGUCUUUAAUCCUAAUUCAAGGUUUAAAGAGAGGGAUUAAUUUAGGAUUGAAGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGUAU	155	spe-miR5773-3-3p	UUUUUAAUGGGUCGGGUUAGGU	130-151	gma-miR5773	5	0	22	22	1
spe-MIR1917-1	CUCAUAGUAACUAAUACUACAAUGAAAAUAACUUUUAGCGGCAAUAGAUAAACACUUAAUAAAGAGUGUUAAAGUCUUUAUGUAGUGUAGUCACAUCCC	232	spe-miR1917-1-5p	AUUAAUAAAGAGUGUUAAAGU	56-76	sly-miR1917	1	0	21	21	1
spe-MIR7983-9	AGUACUACAAUGAAAAUAACUUUUAGCGGCAAUAGAUAAACACAUUAAUAAAGAGUGUUAAAGUCUUUACCGACAUUAGUUAAGCGCCAGUAGAUCCAAUGUCACUAAAUCCUUUAGGAACAUAUACAAAGAGUGAUAGUUACAGCUAAAUAUAUAUUUAGCAGCAAUUGUUAAUUAAUUGCCGCUAAAGGUCAUUUUUGAUGUAGUGUA	212	spe-miR7983-9-5p	UAAAGUCUUUACCGACAUUAGUUA	59-82	stu-miR7983-5p	3	0	24	24	1
spe-MIR8695	AGGAAAACAGUUUGCACUACUAUUUUUCAGUAUGUAAUGGAUUAGGUGAGUCGUACAUAUGAAAAUUGUAGGUCAAGGAGUUUUUUU	87	spe-miR8695-3p	AGUAUGUAAUGGAUUAGGUGA	29-49	gra-miR8695	4	0	21	21	1
spe-MIR11110b	UGAGAAGUGAUUCUGAACAUGGCAGAAUUAUACUCAUGUAUAGACUUAAAGUCUUGUAGCCUUAGAUGCAUCCAAUCAUAUCGUGCCUUUGGAUGUAUGACCAUCUUCAAGUGGUCAAAUCUUUCUUUUAGGUUUUUCCACAAAACAAGUGGAUCCUUAACUGUCAGAUAUUCGAUUUUCAGAAUCUCGUCAAG	194	spe-miR11110b-5p	CUCAUGUAUAGACUUAAAGUC	33-53	lja-miR11110b-3p	5	0	21	21	1
spe-MIR1106-3	GGAACCUUUUACCUCUGUACUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGUCCACGUGGAUAUCAUAAAUAUUGCAUCAUUAUAAAUUGUAACUUGCCCACAUGGACACAUAUAUACCUUUCAAAUACACUAUAAAAUAGUAUAGGGGUAAAAGGUCAU	162	spe-miR1106-3-5p	UUUAAAGGUAUAUAUGUGUCC	36-56	smo-miR1106	5	0	21	21	1
spe-MIR7997c-12	GACAUUAAUUCUAUGUUGCUCGGACUCUUCAAAAAUGUCGACCAGUGUCUCGGAUCCUCCAAAAAUAGUGUAUUUUGAAAGAUCUGACACCGGUGCGGCAACAUUUUUGGAGAGUCCGAGCAACUUAGCAUUAAUUAG	138	spe-miR7997c-12-5p	AUGUUGCUCGGACUCUUCAAAAAU	13-36	stu-miR7997c	1	0	24	24	1
spe-MIR7998	UAUAGACGGUAGGUCCAGUCACGGUCCAUUAGUGGGUAGACCUAGAUUUCUCAUCUAGGAUGUUUGAGUAUGUGUCUAACUACCGAGGCUAGUGACGGACCGUAGAUCAAUCCACGGUCCAUACUGCACGUUUAUCAAUGAUCACUUAGAGUUAAAUUUAAAAGUCUGGAUGAAAAAUUCUAAGUGUGGACCCACGGAGGACCCAUGGACCAUGGAUCGACCCGUACUUCA	231	spe-miR7998-3p	ACGGACCGUAGAUCAAUCCACGGU	95-118	stu-miR7998	1	0	24	24	1
spe-MIR5303-16	UAAGUUGCUCGAACUCUCCAAAAUUGUUGUCGCACCCCUGUCAGAUCCUCCAAAAAUGCAUACUUUUGGAGGAUCCAACACGUACCCGUCUACAUUUUUGAAGAGUUCGAGCAACACA	118	spe-miR5303-16-3p	UUUUUGAAGAGUUCGAGCAAC	95-115	sly-miR5303	0	0	21	21	1
spe-MIR9773-2	AGACACUUUAACUAAAUUGAGGUCCUACUACCCCCUCGAACUUGUCUUCUUCUUUUUUUUUUGUAAUUUUGUGCAACUUUUUGACUUAUCUAGCAUCCAAAUGUCUCUCAGGCCUCAAUUGCGUGGAGUCACGAAGUGUGCCACGUAAGACAAAAGGUGCACAAAAUUUUUAAAAAAUAAGUUGGGGGUGGUGGUGUAAUAGAUCCUUAAUUUAGUUAUGGUGUGU	226	spe-miR9773-2-5p	CUUUUUUUUUUGUAAUUUUGUGCA	52-75	tae-miR9773	5	0	24	24	2
spe-MIR10189-2	AGGUCACGAAACUAAGAGCACUAGACUGAUCUCUUAAGGAGUGGGUCGACAUGAGGUUCAGCCCGAGAGGGUUGGGCCCUAGUCCCAUAUCCAAGCAUUCCCAUCGAAAGAGCGAGUGUGGAUAAGGCGUAGUCUGGAUAGUUUAGACGAGAGGGUGUCCG	250	spe-miR10189-2-5p	AAGAGCACUAGACUGAUCUCU	14-34	gma-miR10189	5	0	21	21	1

spe-MIR6145b-2	AGAGGAACACAUUUGAUAUAGGGUAAGUUGCCGGAGAGGGAACUUACUUUCACUUAAAACUUAGCCUAGUCACGAUUGUUUUGUGAAAUUCCAAGGUCCUAUUACUUCCUGAAUUUAUUUUAUUAAUAAUUUUAUAUUCCUUUUUGGCAUACGUGGCACUAUCGUGUGGGCUCAACACUGGUUGACUUUUUUUUCAACUUAGUACCACGUAGAUCGAAAAGAGGUAGAAAAUUACUUAUAAAAUAAGUUCAGGAGGUAAUAGGACCUUAAU	183	spe-miR6145b-2-5p	UUGGCAUACGUGGCACUAUCG	55-75	nta-miR6145b	5	0	21	21	1
spe-MIR11564b	ACACUACGUUCACUUUUACUUCUCCACUUUGGACUUCACAUGCCACUUAAAAACAAUGAUUGGUAUGCGUAUUUUAUCACAAAAUCCAUAUUAAUUGAUGUUUAGUCUUAGGUAUUGAAAACUAAUUUUGGGAAUACGUAAUCAAUGUUGAUUCUUCUCAGGAUAUGCUAAAAGUAGAAAUAUAUUUUUAGUAUAGUGGACAAGUAAAAGUGAACGGAGGGC	222	spe-miR11564b-5p	UUUAUCACAAAAUCCAUAUUA	73-93	pab-miR11564b	4	0	21	21	1
spe-MIR6140b-2	AAAGUUCUUGUCCAUAUAAUUUUCCUGUUGCUGGAUCCUUUCGAUUUAAUUUGUCCCAAAAGUUUGUGAAAUACUUUCUGUAUAAGCAAGGGAUAUUUUCUCCUGGGGUAUAACCCAUUUCUGGAGUCCAUUUAUGGAUCCAAGGAAUAGAAAAUUCUAUAAAAAGUACAUC	173	spe-miR6140b-2-5p	AAAGUUUGUGAAAUACUUUCUGUA	59-82	pgi-miR6140b	5	0	24	24	1
spe-MIR8006-10	GAGAAAAGGAUAAAUAUAUUCUAAAUUAUCAUAAAUGGUAUACAAAUACUUUUCGUUAUACUUUUAAAACAUUGAUGCAUCUGUCGUUCAAAAACUUAAACAUACACAUAUCGUAAUCUUAUUCACCAACUUGACACUUAUUAGAUACCAGAUCGACGAAUAAGAUUGUAUCACGUGUCCCUAUUUAGUUUUCCGUUAGAGUGAAGGACUAUGCUGGACUAUGCUCUAUCUUUUGAAUGACAGGGACACCAACGUCCCAAAAAAAUGAUGAAGGGUAUCCGUAUACCAUUUAUAGUAGUUCGGUGAUAUAUAUUAUUUUUUUAAC	325	spe-miR8006-10-3p	UAUCUUUUGAAUGACAGGGACACC	227-250	stu-miR8006-5p	5	0	24	24	1
spe-MIR5725	UAAAUAGGGACAUGUGGCACAAUCUUAUCCGUCGAUCGAUAAAUAUCGGAUCGGUAGAUAAUAUUAUGACACAUAUCCGUUAUAAA	86	spe-miR5725-5p	AUGUGGCACAAUCUUAUCCGU	12-32	bra-miR5725	4	0	21	21	1
spe-MIR7997c-13	UAUUGCUCUAAGGCUAUGUUGCUCGGACUCUUCAAAAAUGUCGACGAAUGCGUGUCAGAUUCUCCAAAAGUAGUGUAUUUUAGAAGAACCCAACACGGGUAUGGCAUCAUUUUUGUAAGACCCCGAACAACAUAGCUAUAAGGCAUGU	148	spe-miR7997c-13-5p	AUGUUGCUCGGACUCUUCAAAAAU	16-39	stu-miR7997c	1	0	24	24	1
spe-MIR7983-10	UUGACACUACAACAAAAAUGACCAUUAGCGGCACUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUUAGCGGUCAUUGUCACUCUUUGUGUAUGUCCCUAAAGUCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUAGUACUCUUUAUUAGUGUUAAUAUUUAAUGCCGCUAAAAGUUAUUUUUGUUAUAGUGUGAC	216	spe-miR7983-10-3p	UAAAGUCUUUAGCGACAUUGGUUC	99-122	stu-miR7983-5p	0	0	24	24	1
spe-MIR7997b-3	AUGGCAUGCUGCUCGGACUCUUCAAAUAUGUUGCUAGGUCUUUGUUGGAUCCUCCAAAAGUAGUGCAUAUUUGAAGGAUCCGACAUGAGUGCGGUAACAUUGUUGGAGAGUCCGAGCAACAUAGCAGACGGGGUUAUAUCUAGACCUUUUUGAAUAGUUUAGGGGCAUAUUUGAUCAUUUUCUCUUGAAUAUAAAUGUCAAGUGAAAAUACAUAAAAAUGACGUGGAAAAUCCAUUUGGCAUUUAAAUAAAAGUAAAAUGAGUUGGAUAUUUCAAGUUGGCCAACUAACGUCCAAAAAGGCAUAUGUAGACCAAA	128	spe-miR7997b-3-5p	AUGCUGCUCGGACUCUUCAAA	6-26	stu-miR7997b	0	0	21	21	1
spe-MIR11553		187	spe-miR11553-3p	GUAAAAUGAGUUGGAUAUUUC	125-145	pab-miR11553	4	0	21	21	2
spe-MIR5559	CAAUAAGUCAAAGUAGGUGAUGCACCUACUUGGUUAUUUGGUUGGUCAAUAAGUCAAAGUAGGUGAUGCACCUACUUGUCACCUACUA	88	spe-miR5559-3p	UACUUGGUUAUUUGGUUGGUC	27-47	gma-miR5559	5	0	21	21	1
spe-MIR7696b	UUCCCUUUUAAGUAUUCCAACAUCUCAUAAACCAAAAUCAAUAUUGUCACGCACCAGAUGGUAAGCACUUGGCGUGAGGUGGGGUGUUAAAGAAUGACAAAAGUCCCACAUCAGUGGUUAAUGAGAUGGGUGGACUCCUUAUAAGGCUU	149	spe-miR7696b-5p	CCAACAUCUCAUAAACCAAAA	17-37	mtr-miR7696b-5p	5	0	21	21	2

spe-MIR397-2	GAAGAAUGAGUACUUCAAGACUCGUCUUUGAGUUUCAUCAAGUCUACACUCCGUCAAGCCUUGAAGCAGGCACAUUUGUAGACAUUGAAAUUUUGUGGGACUCUACUAGAUGCGUUCAAUUCGAGUUGAGACACUACAAAUUGUGUUCAACUCAAAUAAGGAUUCUUGGAGGCUACUCAAUCCUA	185	spe-miR397-2-5p	CAUCAAGUCUACACUCCGUCA	36-56	stu-miR397-3p	4	0	21	21	1
spe-MIR8016	AGCAAACGCUUGCUUGCCUAUGCUAGAAAAAGUAUAAUUUUCAUGAUAGCAGUAUGCAUGGUCUUUUCUUUCAAAAAUAUAUAAUUACACCUAGUAAUUAUAUAUUUUUGAAUGGAAGGCCCAUGUGUAUUUCAUUCUUGAAACUUUUUCUCAUAGGUAAUGAACAUUUCCA	172	spe-miR8016-3p	AUUUUUGAAUGGAAGGCCCAUGUG	104-127	stu-miR8016	0	0	24	24	1
spe-MIR11592-1	GAAUCAAAUCGCAAAUCGAGUCAAACCGAAAAAAAACCAACUAGUGCUUUGGUUUGACUUGGUUUGGUAUUGAAAA	77	spe-miR11592-1-5p	AAAUCGAGUCAAACCGAAA	13-31	cas-miR11592	5	0	19	19	2
spe-MIR7983-11	UCAUUAGCGGCAUUUAAUUUUUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUGUUACUCUUUGUAUAUGUCCCUAAAACCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUAACACUCUUUAUUAGUGUCAAUAUUAAUGCCGCUAACAG	173	spe-miR7983-11-3p	ACUAAUGCCGGUAAAGACUUUAAC	114-137	stu-miR7983-3p	0	0	24	24	1
spe-MIR5049-2	CUGCUCCCUCCGUCCCAUAUUAGUGGUUCACCUUACUAUAAAUAGUUGUCCCAAAUUACGGAAGCGGACAACUAAUAUGGGAUGGAGGGAGUAC	94	spe-miR5049-2-5p	UCCCUCCGUCCCAUAUUAGUGGU	5-27	bdi-miR5049-5p	4	0	23	23	1
			spe-miR5049-2-3p	AAUAUGGGAUGGAGGGAGUAC	74-94	tae-miR5049-3p	3	0	21	21	1
spe-MIR8013	AAAAUUAAAAAAUAAUGUCAAAUCGCUGCCCUGGCAGCGAUUUGUAAGAAGAAAAAUUUUGAAAUCGCUGCUUGAGCAGCGAUUUCAUUUUUAUAUUAAAAAAAAAAUUUUUGGCAAAAUCGCUGCCUCAGCAGCGAUUUUACUUUUUCAGUUGAAGUAAAUCGCUGCGUCGGCAGCGAUUUUACCGUUUUGGUUUAUAUAAA	204	spe-miR8013-3p	UGAAGUAAAUCGCUGCGUCGGCAG	154-177	stu-miR8013	5	0	24	24	2
spe-MIR10538-11	GUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUCCCAAAACGUUACUCAUAGUAACGUUUUAGGAGUAAAACGUUACUGAAAAUAACGUUUUAGGAGUAAAACGUUACUUACAGUAACGUAUAUCAACCUAAU	138	spe-miR10538-11-5p	AGAUUGAUAUACGUUACUCACAGU	4-27	sly-miR10538	0	0	24	24	1
spe-MIR8175-2	NNNACGACCGCUUUACUUCUUAUUUGAGAAGUAAGUUUGAGCGUAUCAAAUUUUGUAUAGUGGUACGUAUUCCCGCCUGUCACGCGGGUGACCCGGGUUGGAUCCCCGGCAACGGCGCCAAAAUUUGAUAUACUCAAACUUACUUCUCAAAUAAGAAGUAAUGCGGUCGUUUC	173	spe-miR8175-2-3p	GAUCCCCGGCAACGGCGCCA	101-120	ath-miR8175	0	0	20	20	1
spe-MIR7701-1	AAAGUCUAAAACCGAAACUACUAAGGAAAUUUCCAGAUUUCGGUUAAGACAAGUAAGAGACAACCUAGUACUUAACCUAAGAUGGUCCAAAGAGUUGGUUAUGGUCCUAAAAACUUAGGGGUACUUUAUUAAUUACCCUAGGUCACCUAAUUAAUUAAUUUAGAAACUUAAUUAAUUAAUUUAAAUGACUAAAACCAAAACCAAUGAGGAAAAAUCCAGAUUUUGGUUAAGACAAA	236	spe-miR7701-1-3p	UUUAAAUGACUAAAACCAAAA	180-200	mtr-miR7701-5p	5	0	21	21	2
spe-MIR2673b	CCCAUAUCCAAAUCGACCUCUUCCUCUUCCUCUUCCUCUUCCACUUCCACUUCCACUUCCACUAGUAUGGUAAAAUGAAUUAUGAACAUUGAAAUUUGUUCGAGGUAUAUUGAGAGGAGAAAAGCUGUAGUGGGAGAGAAGAAAUGCUUUGCCACUCAUAGCACCACCAGACACCUGUAGAGGAAGGGGAUUGAUUGGUUGAUAUUUC	208	spe-miR2673b-5p	CCUCUUCCUCUUCCUCUUCCAC	23-44	mtr-miR2673b	0	0	22	22	1
spe-MIR1514b-2	UACAAAAGGGAGACCUCAUGAGGUCUCUUUUCUGCAUUUAUAAAAUAGAAAAUGGUAAAUAGAGACCUCAUGAGGUCUCUACUAUGAAAUAUCUGGAAAAAUUAAUGCAAAAAGAGACCUCGUGAGGUCUCUUUUUCUCUAUUAUGAAAUAUCUGGAAAAUUAAUGCAAAAAAGAGACCUCGUGAGGUCUCUUUUUCUG	192	spe-miR1514b-2-5p	UGCAUUUAUAAAAUAGAAAAU	33-53	gma-miR1514b-5p	4	0	21	21	1

spe-MIR10538-12	AAGCUGACGGCGUUAGAUUGAUAUACGUGUUUCACAGUAACGUUUUACUCUUAAAACGUUACUGUGAAUAACGUCUUACUCUUAAAAAGUUACUCACGGUAAGGUUUUAGGAGUAAAACGUUACUCAAGAAAACGUUUUAGGAGUAAAACCUUACUCACAGUAACGUAUAUCAAUCUAACGCUGUUAGUUU	191	spe-miR10538-12-5p	AGAUUGAUAUACGUGUUUCACAGU	15-38	sly-miR10538	3	0	24	24	1
spe-MIR10540-6	CGAGUUGAUUUCUGAAAUGAUCACUCACCUAAUAGUUAUUAUCUUAGAAAGUCACCCUUCUUUAGAAAUGGUUGCCUAUAAAGAAAGUGACUUUCUGAGAUAAUAACUAUUAGUUGAGUGACCAUCUGAGAAAUCAACCUA	141	spe-miR10540-6-3p	AUAAUAACUAUUAGUUGAGUG	100-120	sly-miR10540	1	0	21	21	1
spe-MIR5303h-11	GGCCUAUGUUGCUCGGACUCUCCAAACAUGUUGUCACACCAGUGUUAGAUCCUCCAAAAAUGUGUAAUUGGAAGAUUCGUCACACACCUUCAAACAUUUUUGAAGAGUCUGAGCAACAUAGAUU	124	spe-miR5303h-11-3p	AACAUUUUUGAAGAGUCUGAGCAA	93-116	stu-miR5303h	0	0	24	24	1
spe-MIR10538-13	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUUCUAAAACGUUACUCGUAGUAACGUUUUAGGAGUAAAACGUUACUUACAGUAACGUAUUUUAGGAGUAAAACGUUACUUACAGUAACGUAUCAACCUAAUGCUGU	148	spe-miR10538-13-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
spe-MIR10538-14	CACAGUAACGUUUUAGGGUAAUAUUUUAUUAUAUUUUAAAAGCUGACGGCAUUAGAUUGAUAUACGUUACUCACACUAAUAUUUUACUCCUGAAGCGUUACUCAC	105	spe-miR10538-14-3p	AGAUUGAUAUACGUUACUCACACU	54-77	sly-miR10538	1	0	24	24	1
spe-MIR1917-2	UCUCACUACAAUAAAAAUAACUUUUAGCGGCAAUAAAUAGAUACAUUAAUAAAGAGUGCUAAAGUCUUUACCGGCAUUAGUUAAGUGUCAUUAGAUCCAAUGUCGCUAAAGCCUUUAGUGACACAUACAAAGAGUGCUAAUUGCCACUAAAAAUAUAUAUUUAGCGGCAAUUGCUAAUUAAUUGCCGCUAAAGCUCAUUUUUAAUGUAGUGUCU	214	spe-miR1917-2-5p	AUUAAUAAAGAGUGCUAAAGU	45-65	sly-miR1917	0	0	21	21	1
spe-MIR5014a-11	CAGAGGAAGAUUUAUAUUGUAUAACUAUAAGUGUAUAGGACGGAGAUAUAUGUAUUUGGAUGUAUAUAUACAAUUUUCUCUCGCUUUUUACAAAUAGGAACACAAUUUGUAUAUAUUUGUUUGUAUAAAGUGAGAGGCGAGAGAGACUGACGAGCGAGAGAGGGAGACUGGCGAGCAAGAAUUUCAUGGGAGAUAGGCAAAUAACAAAGUUUGCUACGUGUUACAGUUAAAUCAUUUGAAUUAAUAGUUUGCUAUUAUAUACAUUUUCCUUAA	274	spe-miR5014a-11-5p	UUGUAUAACUAUAAGUGUAUA	17-37	ath-miR5014a-3p	5	0	21	21	1
spe-MIR394b-2	AAAGGUAUAUAUGUGCUCACGUGGACAUAUUGCAAGUUAUAAUGAUACAAUAUUUAUGAUGUCCAUGUGGGUACAUAUAUACCUUU	86	spe-miR394b-2-5p	ACGUGGACAUAUUGCAAGUU	19-38	aly-miR394b-3p	5	0	20	20	1
spe-MIR7992-12	AAACAUAUCAUGUUCUUCAAUUUUGAGUGUGCACAAGUAGACACUUGAACUUGUAUAAAAUUGAACAAGUAGACACAUGUGUUCUACAUGGUAUAAUGCACAAGAUGCCACGUAGUACACAAAAUUGUCACGUAGGACUAAUAUGUCUAUUUAUUCAACUUUAUAUAAAUUUAAGUGUCUACUUGUAGACACCUAAAGUUAAAGUUCAUAAUUGCCA	217	spe-miR7992-12-5p	UUUGAGUGUGCACAAGUAGACACU	22-45	stu-miR7992-5p	5	0	24	24	1
spe-MIR9752	AAUCCAUAACCUUGGGUACAGUGAGGGGAUUAAAUUUCUUAAGGACACACAGUAGUUUCUGUGGACUCGGAUUAAUUCUUGUAUUAUAUAUUUUUUCUGCUUCAUCUUAUUUCUGUUUCUGUUUAUUAACCUUGUAAAUACAGGUUAUAGUAACAAUAACAAUCUUAAGAAAUUUAACAGUUUCUGUAUCCGAGGUUUCUGGAGA	205	spe-miR9752-3p	UGCUUCAUCUUAUUUCUGUUU	98-118	gma-miR9752	4	0	21	21	1
spe-MIR5142	AAAGGGAAAUUGUUGUCCUUAUAGAAGGAAACACUUCCAUAAGAUCUAAGAAGAAGAUGCCCCCUCGGCUUCUGCUUCUGCUUCGUCUUUGGCUUCGGCUUCGGCUUCGGCUUCGGAUUUGGCAAAUGAUGUGAUUGAUUGAUAAAUUUUUUGGACAAAAUUUAUUUAAUCAGUUAUUGUUAAAUCAAAUAAAUCCUGUUAAAAUUAUCUUUUAUAAAUUUGCAGGUAACGGUAACAUUCUGAAAAGUUGUUACUUUCCGAAAAGUCGUUACUU	336	spe-miR5142-5p	UGAUUGAUUGAUAAAUUUU	132-150	rgl-miR5142	5	0	19	19	3

spe-MIR11102	UCCAAAAAGUCGUUAUUUUCCUAAAAGACACAA UUUUCCAAA ACUUCAUUAAUGUUUAAAAGUUUUAAAUUUUCC GCAAAUUUAACUAUAUGAAUGUGAUGAAGGCUA AGAAGAGGCUUGUCGCGACCUCUAAGAGGUCA ACGACACCGGUUGCAUUCGGAUUUCAGAAUCC GGGUGUGACAGAGGAGCUUCGGACCCAAGGUC CUUGACCCUCACGAUAUGGUAGAGAAAUCCCU CAAAUAUCAUCUUACAAGCUUUUACACACAAAA UGAUUC	233	spe-miR11102-5p	CUAUAUGAAUGUGAUGAAGGC	44-64	lja-miR11102-3p	1	0	21	21	1
spe-MIR3512-1	AAAUUCGAACCAAACCGCAAAUCAAGUCAAAUC GGAAAAAAAUCUGAGUAAUGGUUUGGUUUGAC UUGAUUUGGUGUUGGUGUUGGAAAAA	91	spe-miR3512-1-5p	CGCAAAUCAAGUCAAAUCGG	16-35	ahy-miR3512	5	0	20	20	1
spe-MIR10542-3	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUU UAAAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAA AACUAAUUUUUUAACUUCCGUUAAAUGAAGGGU AUAUGUGAGUCAUUUUGUAACGGCAGGGGUAU AUGUGAGCCGUUUGUAUAACGGUAAGGGCGUA UAUGAGCCACUUUUAUAAUGAGGCGUAUAUCA GCUCCAAAUGACAAAAUUGAGGGGUAUAUCAGA CCCUUUUC	237	spe-miR10542-3-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
spe-MIR7992-13	GAUCCUUAAUUUUGAAUAUGCACAAGUAAACAC UUAAACUUGCAUAAAAUUAAACAAAUAGACAUA UUUGUCCUACAUAGCACCCUACAUGAAAAUUUU GUGUCCUACGCGGCGUCUGACAUGUAUUAUGU CAUGUAGAACACGUGUGUUUACUUGUUCAAUU AUAUACAAUUUUAAGUGCCUACUUGUGUACAUU CAAAGUUGGAGGGGG	211	spe-miR7992-13-5p	UUUGAAUAUGCACAAGUAAACACU	11-34	stu-miR7992-5p	5	0	24	24	1
spe-MIR159b-3	GAGAAAGAUUAGAGUUUUGAAUGUAGAGCUCU UCUGAAUUUCAAAGAGGGUCUGAGAGGGAAAA UCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCU AUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGU GGUUUGCAUAUAUCAGGAGCUGCAUUUACUCU UCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCU ACAUUUGAUAACCUAAUUUUUUUA	217	spe-miR159b-3-5p	AGCUGCUAAUCUAUGGAUCCC	68-88	cas-miR159b-5p	1	0	21	21	1
			spe-miR159b-3-3p	UUGGAAUGAAGGGAGCUCUAC	175-195	sly-miR159b	1	0	21	21	1
spe-MIR159b-4	AGGAAGACCAGAGUUUUGAAGGUAGAGCUCUU CUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUC GAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAU CUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGG UUUGCAUAUAUCAGGAGCUGUAUUUACUCUUC UAGGAUCCUUAUUGGAAAGAAGGGAGCUCUAC ACUUGAUAACCUGGUUUUUUU	215	spe-miR159b-4-5p	AGCUGCUAAUCUAUGGAUCCC	67-87	cas-miR159b-5p	1	0	21	21	1
			spe-miR159b-4-3p	UUGGAAAGAAGGGAGCUCUAC	174-194	sly-miR159b	0	0	21	21	1
spe-MIR11085-2	GAAAGAAGGGAGCUCUACACUUGAUAACCUGG UUUUUUUUAUGAUGGACAUAUAUAAUUUUCUCA UGUUUAAGUAAAGGUUUUUGAAUUUGAUCUUU GAAAAGAAAGUUUUUUGACAGAAAACAUCUUUA UGUUCUUUAAUUAGUCUUACAUGUUGUAACUU CGGACCAGUCGUUGAGAAAUUUCUUCUUUCUU UUUAAGGAUGAUGUAACGUCUAUGUAUAUACUA UAUUUUGCAUACUCUGCUUGUGGAUUACACUA AUAAUCCUAGAGUUGGUUUUAACUUGUUCGAG GAAGACCAGAGUUUUGAAGGUAGAGCUCUUCU GAA	326	spe-miR11085-2-5p	UUUGAAUUUGAUCUUUGAAA	82-101	lja-miR11085-3p	4	0	20	20	2
spe-MIR399i-2	CUUAUUAAGUGAAGCAGUUGUAGGGCAGUUCU CCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAU CUGCCAAAGGAGAGUUGCCCUACGAUUGCGUC UGCUUAAUUAU	107	spe-miR399i-2-3p	UGCCAAAGGAGAGUUGCCCUA	66-86	stu-miR399i-3p	0	0	21	21	1
spe-MIR1440a-3	UUUGGUAAAAUAUAUAAAUAUAUGUUGAGAUGG CCGAGUUGGUCUAAGGCGCCAGAUUAAGGUUC UGGUCCGAAAGGGCGUGGGUUCAAAUCCCACU CUCAACAUAUUAUGAUUUUUUUUCCGCU	125	spe-miR1440a-3-3p	GGUUCAAAUCCCACUCUCAA	83-102	osa-miR1440a	5	0	20	20	2

spe-MIR821e	ACAAAUGUGAAAAUUGGUAGCCAUCAAUAUAAAGUUGGUAGCCAAAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAUAAGUUUGAUAGAGUUAGGCAGCCAAUUUUUUUGUUGAAAUUGGCUACCAUAUUAUUUCAUUAAU	142	spe-miR821e-5p	UAGCCAUCAAUAUAAAAGUUG	18-38	sbi-miR821e	3	0	21	21	2
spe-MIR7987-2	AUUGAUGACAAAAUUGUUUUUCUUGCAAGAUCGAUUUAUGUCCAUCUAGUGUUGACACUUAGCUUCAAUUUAGGAAUAAUGUAUUUGUUGAGUAUAAUACCAACACUAGUUGAUCCUAUUGAUGACAAAACUAAUUUUCUUGCAAGAUCGAUUUGUGUUCAUCUAGUAUUGACACUUGUCUUCAAUUUAUGAAUAAUGUGUUUGUCAAGUAUAAGUACCAACACUAGUUAAUCAUAUUGAUGACAAAAUUGAUAUUCUUGCAAGAUCGAUUUGUGUCCAUCUAG	284	spe-miR7987-2-5p	ACACUAGUUGAUCCUAUUGAUGAC	103-126	stu-miR7987	1	0	24	24	1
spe-MIR10538-15	GUUGACGGCGUUAGAUUGAUAUAUGUUACUCAUAGUAACGUUUUACUCCUAAAAUGCUACUCAAACAACGUUUUAGGAGUAAAAUAUUACUUAUAGUAACGUAUAUCAACCUAACGCCGUCAAC	125	spe-miR10538-15-5p	AGAUUGAUAUAUGUUACUCAUAGU	13-36	sly-miR10538	2	0	24	24	1
spe-MIR6231-2	CCCGUACUUAAAAGGUAUAUAUGUGUCCACGUGGACAUCACAAAUAUUGCAUCAUUAUAAAUAGUAACGUGUCCAUGUUAACACAUAUAUACCUUUAAAAUACACU	106	spe-miR6231-2-5p	UAUAUGUGUCCACGUGGACAU	18-38	sbi-miR6231-3p	5	0	21	21	1
spe-MIR1217-2	UAUCAUAUAUAUGAUUGAUUAAAUUUAUGUUAGUUAUUAUACACUAGAAAUAUUUGAAUCAUGAGUUCUAGUUUGCUAGUAAACGGGAAACAGGGAGAAAACUACUAGACUAUGCCAUCCCACAGUGGAAACCGGUAGGCGAGGGAUGCCGUUAGGGGAGUACACAAGGUUGAGGCGCUGAUAAGCAGUAAUUAUCCGCUAAAGUACGAUGCUAGUAGUGACCGGAAAACAUGAUAAUGAUACUCUAGUUUAUAAUAAACUAAUAUGAAUUUAACUAAAUUAUAAUAUGAUA	292	spe-miR1217-2-5p	UAUUUGAAUCAUGAGUUCUAG	51-71	ppt-miR1217-3p	5	0	21	21	2
spe-MIR8030-3	AUAUAUAACUUCGGGUUGGUUUGGUCUCGGGUUUAUUUCUUUAAGUUAAAACCAAACCAACCCAAAUAUAGUC	73	spe-miR8030-3-5p	UCGGGUUGGUUUGGUCUCGGGUU	11-33	stu-miR8030-5p	1	0	23	23	1
			spe-miR8030-3-3p	UUAAAACCAAACCAACCCAAAU	46-67	stu-miR8030-3p	1	0	22	22	1
spe-MIR1888b	CACAAUGAUUAAUCAUUAAUCAAUAAAUUUUAUUUGGUAUAUUUAGAGCCGUCAAUAUGGGCUAGGCCCGUUGGGCCGGCCUGGCCUAACACGGGAUUUAAUAGGGUUGGGCUAAAAUUUUUGGAGCCCAUUUAAGAAAAGGACUUUUUAGCCCGCCCUGAAUAAGUCUGUUGAUUUGAUGGGCUUGAGAAAAAUAUAGGUAGGGCCGGCCCGUCGGUCAAUAAUAAUUAAUUAAAAAAUAUAAUAUAAUAUUAAAAUUUUA	262	spe-miR1888b-5p	UUGGGCUAAAAUUUUUGGAGC	107-127	ath-miR1888b	5	0	21	21	1
spe-MIR7983-12	UGUAUUUUUAGCGGCAAUUGUCACUCUUUGUAGAUGUCCUUAAAGUCUUUAGCGACAUUGGUUCUAAUGGCACUUAACUAAUGCCGAUAAAGACUUUAACACCUUUAUUAGUGUCAAUAUUUAAUGCCGAUAAAAUUGU	140	spe-miR7983-12-5p	UAAAGUCUUUAGCGACAUUGGUUC	41-64	stu-miR7983-5p	0	0	24	24	1
			spe-miR7983-12-3p	ACUAAUGCCGAUAAAGACUUUAAC	77-100	stu-miR7983-3p	1	0	24	24	1
spe-MIR2648	AGUAACAAACAGAAGUACAGUAAAAAAUAAGUUUGAUAGAAAGCUAGCCUGUAGGAAUAACACAAGUGGACGUGCCGGAGUGGUUAUCGGGCAUGACUAGAAAUCAUGUGGGCUCUGCCCGCGCAGGUUCGAAUCCUGCCGUCCACGAUUUUGAUGUUUUUCUUUUUUAUAGAUCUGUUUGAUUGAU	187	spe-miR2648-5p	UAGCCUGUAGGAAUAACACAA	45-65	mtr-miR2648	5	0	21	21	1
spe-MIR5014a-12	UUUUAGGCAUAAUACAUAAAUAUGUCUCUUAACUUAGCAAAUCACAUUUAUAUCCUCCAACUUUGAGUAUAUACAAGUAGACACAUGAAUCAUAUGUGACGUAAUACAUGUAGGACUCAAAUUGCCAUGUAGGAUGCGUCUGUCUAUUUAUUCAACUUUAUACAAGUUUAAGUGUCUACUUGUGCAUACCUAAAGUUAGAUGACAUAAAUAUGUGCUAAGACUAAGUUAAAGACAUUGUUAUGUUUAUGCCUACUU	256	spe-miR5014a-12-3p	UUAUACAAGUUUAAGUGUCUA	158-178	ath-miR5014a-3p	5	0	21	21	1

spe-MIR399b-2	UUGUAAGGGGAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCGGCUUAGUC	103	spe-miR399b-2-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spe-miR399b-2-3p	CGCCAAAGGAGAGCUGCCCUG	64-84	nta-miR399b	0	0	21	21	1
spe-MIR399b-3	UUAUAAGGGAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCAGCUUAAUC	103	spe-miR399b-3-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spe-miR399b-3-3p	CGCCAAAGGAGAGCUGCCCUG	64-84	nta-miR399b	0	0	21	21	1
spe-MIR7983-13	GAGUACGCACUACAACAAAAAUUACCAUUAGCGGCAUUUAAUUCUUGAUUGCCGCUAAAUAUGUAUUUUAGCGGCAAUUGUAACUCUUUGUAUAUGUCCCUAAAGCCUUUAGCGACAUUGGUUCUAAUGGCACUUAACUAAUGCCGGUAAAGACUUUAGCACCAUUUAUUAGUGUCAAUAUUUAAUGCUGCUAAAUGUUGUUUUUGUUGUAGUGAAGUAAAC	223	spe-miR7983-13-3p	ACUAAUGCCGGUAAAGACUUUAGC	138-161	stu-miR7983-3p	1	0	24	24	1
spe-MIR399b-4	UUGUAAGGGAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUC	103	spe-miR399b-4-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spe-miR399b-4-3p	CGCCAAAGGAGAGCUGCCCUG	64-84	nta-miR399b	0	0	21	21	1
spe-MIR399b-5	UUAUAAGCGAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCGGCUUAAUC	103	spe-miR399b-5-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spe-miR399b-5-3p	CGCCAAAGGAGAGCUGCCCUG	64-84	nta-miR399b	0	0	21	21	1
spe-MIR10538-16	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUCUUAAAACGUUACUCACAGUAACGUUUUAGGAGUAAAACGUUACUGAAAAUAACGUUUUAGGAGUAAAACGUUACUUACAGUAACGUAUAUCAACCUAAUGCUGU	148	spe-miR10538-16-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
spe-MIR5998b	CUGUUCAAAACCGAAUCGAAACCGAUAAGUCGAAUCGAUAAAAAAAUAAUUAGUUUAUAGUAUUGGGUUAUUGAUUUAGUGGUUUUGAUAACGGUUUUGAUUUUUUUUUGUUAUCGGGUUAUCGGUUCUUAACGGUUUGAAGUU	144	spe-miR5998b-3p	ACGGUUUUGAUUUUUUUUUGU	91-111	ath-miR5998b	5	0	21	21	1
spe-MIR9478-2	UAGUCAAAUAUGCCAUUGAACUUUCAGAAAAGACUCAUUUAUGCCAUCCGUUAAAAGUUUGACUCAUCUAUGCCAUUACUAUUCAAGAAAAGGCUCAUUCAUGCCAUUAUUUUUUUUAAUAGUGGUUUGGCAAAAUCAUUUUUGACACGUGAUCAAUUAUAAUUCGGCCACGUCAUCAAUUUUUAAAAUAAAAAAAUUUAACAAAUGGCAUAAAUGAGCCUUUUCUGAAAGUUCAAUGGCAUAUUUGAGUC	251	spe-miR9478-2-3p	UUCAAUGGCAUAUUUGAGUC	232-251	sly-miR9478-3p	3	0	20	21	1
spe-MIR902g	GUUUGCACUUAACGAAGGUCUGAGUCUUAAUAAUUCAGAUUCAGCCUAUUAACUACGUUUGGUUUUAGGUCUGAAUCUGAAUCAUUCAGAUUCAGCUUAUUAAGUUCAUUU	112	spe-miR902g-5p	ACGAAGGUCUGAGUCUUAAU	12-31	ppt-miR902g-3p	4	0	20	20	1
spe-MIR5185k	CCCUUAUGGGCGUUAGUUGCCAUGUUGGACAUAUCUAACUCAUUUUUCAUUUCUUUAAAUGUCACAUGGAAUUGUCAUGUCAUUUUGACCUUACCACAUGACAUUUAUAUAAAAAUGAAAAGAUAUUUGGACUUAUAAACACCUAAUCCGACCCCAUAAAUC	162	spe-miR5185k-5p	AUCUAACUCAUUUUUCAUUUC	33-53	bdi-miR5185k-5p	5	0	21	21	2
spe-MIR4225	UGGUUCAAUUUUUAUGUAAACUUAUUUCCAUUUGAUGGUUAAACAAAAGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAUUUCUUAAUUUUGUUUUUCUGUUAUCGUUCAGAUUUUUAUUUUUUUCAUAUUUAGUUGGUCAAAAUUUUAAAAAUAUUUUUUCUUUAGAAAAGUAAAGUUACCUAAAAAUGAAUUA	239	spe-miR4225-5p	CAUUUGAUGGUUAAACAAAAG	29-49	aly-miR4225	5	0	21	21	2

spe-MIR7980b-8	GGAGAAUAUGAUGUCACAUCUCAUGAUAUGAAA UCAUGAGACAGAAUCAAAAUCGCAUGUCCAAAC GUUGAUUCUAUCUCCAAUACCAUAUUGUGGUA UCACCAUGUGAUUCCAUAUCAUGGUUUUUGGA GAAUAUGAUGUUACAUCUCAUGAUAUGAAAUCA UGAGACAGAAUCAAAAUCACA	184	spe-miR7980b-8-5p	GUCCAAACGUUGAUUCUAUCUCCA	59-82	stu-miR7980b-5p	5	0	24	24	1
spe-MIR9555b	UGUAAAUUAUAUAAUUAAGUGUAUAACACGAAG AUAUAUAUUUUUGCAUGUGUAUAUACAAUUUUC UCUCGCUUUAUACAAAACAGAAACAGAAUUAUA CACUUCUGUGUAUAAAGCGAGAGAGGCGAGCG AGAAUGGAGAGUGGCGAGCGAGAUUUCUGGGA GAGAGACGCUGACAAAUUUUAGCUAACGUUUG CUAUGGAGCACAAUUAAAUCAAACCCUAGCUAU UCCAUUUAUUUUAGGUUAUUAAUUUGCUAUUAU AUACAAUUUUCC	273	spe-miR9555b-3p	UUAUUAAUUUGCUAUUAUAUA	244-264	bra-miR9555b-3p	4	0	21	21	1
spe-MIR7983-14	CAACAAAAAUAACUUUUAGCGGCAUUAAAUAUU GACACUGAUAAAGAGUGCUAAAGUCUUUACCG GCAUUAGUUAAGUGCCAUUAGAACCAAUGUCG CUAAAGGCUUUAGGGACAUACACAAAGAGUGAC AAUUGCCGCUAAAAACACAUAUUUAGCGGCAAU UAAGAAUUAAAUGCCGCUAAUUGUCAUUUUUGU UG	198	spe-miR7983-14-5p	UAAAGUCUUUACCGGCAUUAGUUA	52-75	stu-miR7983-5p	4	0	24	24	1
spe-MIR7992-14	AACUUUGACCUUCAACUUUCAUAAUGCACAAAC AGACACUUUAACUAUCCAACUUUUAAAUAAAUA AACAUAUGAGUCCUACAUGGCACAAUAUACGUA GGACACCAAGUAGGAUAAAAAAUGACAUGUAGG ACAUGUGUGUCUAUUUGUUCAACUUUAUACAAG UUUAAGUGUCUCUUUGUGCAUAUUCAAAGUUG AAGGGCAUAAAUG	210	spe-miR7992-14-5p	UUUCAUAAUGCACAAACAGACACU	17-40	stu-miR7992-5p	5	0	24	24	1
spe-MIR5014a-13	AACUUUGACCUUCAACUUUCAUAAUGCACCAAC AAACACUUUAAAUAUCCAUCUUUUAAAUAAAUAA ACACAUGAGUCCUACAUGACACAAUAUACGUAG GACACCAAGUAGGAUAAAAAUGACAUGUAGGAC AUGUGUGUCUAUUUGUUCAACUUUAUACAAGU UUAAGUGUCUCUUUGUGCACAUUCAAAGUUGA AGGGCAUAAAUG	209	spe-miR5014a-13-3p	UUAUACAAGUUUAAGUGUCUC	156-176	ath-miR5014a-3p	5	0	21	21	1
spe-MIR10541-1	UUCUAGUUACCAACCAAACAUGAGAAAAUAAGU CCAAAAUCUACUUGUUUUCCAGAAAAACAUUUU CUAGGAAACCAUUUUCCAUGGAAAACAUUUUCC UCCAUACCAAACACACCCAUAGAGAUGAAGAAG AGAACUUUUCUUCUUAUUCAAGUAUGUCAUACA UUGAGAAUGACAACUCUAUUUUUAAGUAGAGAA AUCAUCUCAAAAGUCACUUUGAUGAAUGUCAAA UUAAUAGAUACAUCAUUAUCCCCAUAAAGAUUC AUGUUAGCUUGGAAACAUACAU	286	spe-miR10541-1-3p	AGUCACUUUGAUGAAUGUCAAAUU	210-233	sly-miR10541	3	0	24	24	1
spe-MIR3951a-2	AAAAGGCGCUCGCUUCAGAUAAAGAAGCGAGAA GAGACACUAAGGCAAAAGCGCAAUACAGCGCGC UUUUUAUAAAAAAAGCGUCAAUUAGGGUAUUUU UAAAAAAAUUAGGUUUUUUUAAAAAAAUCUGAA AUAUACAAUAUAACUUAAUUUUUCUUUCACGAC UCUUCUUUCGCUUCUUCUCUCUUUACGACAGC GCCUGAG	204	spe-miR3951a-2-5p	CAGAUAAAGAAGCGAGAAGAG	16-36	csi-miR3951a-5p	5	0	21	21	2
spe-MIR8752	CACUCGCGGCUCGUUGUGGGUCGUGACAAACU UGGUAUCAGAGCUUUAGGUUCGUUGGUGUCAU CACACAAGAACGAGUCUAGUAGAGUCUUGAGG AACGGUAGGGGGACGCCCUUACUUUUCUUUGA GAGGCUAUAAGACUUUAGGAAAACUCCAUUCUU UCUUUCUUUCGUGCUAUUACUUGGGUCCAAUU GGUAUCUAGGUGAUAGAAAUUGGUAUCUGACA UCCUCACUCUAUCUCGCAGAUGGUUAGAAUUA GAGCACCAACUGUGUCAACACCAACACCGGCAG GACAG	295	spe-miR8752-3p	UGAUAGAAAUUGGUAUCUGAC	204-224	gra-miR8752	5	0	21	21	1
spe-MIR10538-17	ACAGCAUUAGGUUGAUAUACGUUACUGUAAGUA ACGUUUUACUCCUAAAACGUUAUUUUCAGUAAC GUUUUACUCCUAAAACGUUACUGUGAGUAACG UUUUAAGAGUAAAACGUUACUGUGAGUAACGUA	148	spe-miR10538-17-5p	AGGUUGAUAUACGUUACUGUAAGU	9-32	sly-miR10538	4	0	24	24	1

	UAUCAAUCUGACGCCAU										
spe-MIR7525	UUUUAUACUCCCUCCGUUUCAAAAAGUAUGUCCCUAUUUCCUUUUUAGUUUGUUUCAAAAAGAAUGUCCCAUUUUCUUUUUUGGCAACACUUUAACUUUAACUUUCCACGUGUCAUGUUUAAGACCACAAGAUUAAGGGCGUUUUGGUACAUUUGACAUAACUUUAAUUUAGAACCAAAAGAUUAAAAAGUCUUCUUUCUUUUCUUAAACUCCGUUUCAAGUCAAAUUAAGCCAUCCUUUUUGAAACGGAGGGAGGAAUACAU	263	spe-miR7525-3p	AGGGCGUUUUGGUACAUUUGA	136-156	lja-miR7525	4	0	21	21	1
spe-MIR1112	GGCAACUUUCACAUAUAGCAAACAAAAAAUUUAUAUUUGUAUGCUAUAACAAAGUUUGCAUGAUUGCGCUCCAUAGCAAACUUAUAACUGUAUAAUUCGCUAUACAUAUACAACUGUAUAAUUUGCUGGCCUCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGCCUAAAUUGUAUAAUUCGCUGGCCUAUUUCACUGCAATUGUAUAAUUCGCUGGCCUAUUUCACUGUAAUAUGUGUAUAAAUUUUGCUUUGCAUACAAUUGAAUCGAAGUAAAAUGUUUGUAUAUCGUAUAAUUAUG	300	spe-miR1112-5p	UUGUAUGCUAUAACAAAGUUU	37-57	smo-miR1112-3p	5	0	21	21	3
spe-MIR8006-11	GUAAAUGGUAUGCAAAUUAUCCCAUUAUAUUUUUGAGACGCUGGUGUCUCUACCGUUCAAAAACUAGAGCAUAUACAAUAUGUCCUUCACUCUAACGGAAGACUAAAUAGGGACACGUGACACAAUCUUAUCUGUCGAUAAAUGUUUAAGAUUAUACCAUGUCCGUUAGUAUAAAUGAUAUAUAUGUUCUAGUUUUUGGACGGCAGGGGCACCAAUGUCCCAUAAAUAUGACGAAAUAUAUUUACAUAUCAUUUAU	256	spe-miR8006-11-3p	UAGUUUUUGGACGGCAGGGGCACC	190-213	stu-miR8006-5p	1	0	24	24	1
spe-MIR827-2	AGAAGUCAACUUUUCCCUGUGUACAGAAGACCAGAAUCCCCUACCAUAUUGCCAAACAUUUGCCUUUAGCUAGAUGAACACAAAGAAAAAGGCAAAUAUUUGGCAAUAUGGUAGGGGAUUGGAACUCAUUACAAAGAUGAAGUUCACUAGU	151	spe-miR827-2-3p	CUAGAUGAACACAAAGAAAAA	70-90	sly-miR827	5	0	21	21	2
spe-MIR6164b-2	UUCACAUUUAUAUCCUCCAACUUUGGUCAUGCACAAGUAGACAUAUGAGUCCUACGUGGCAUAAUACAGACACCGUGUAAAACAUAAAUUGUAAUGUAGGAUGUCACACAAGAUAGACAGUUGUAUUUUAUUUGUUCAACUUUAUAUAAGUUUAAAUGUCUACUUGUACAUAUACAAAGUUGAUGAGCAUAAAUGUUAG	199	spe-miR6164b-2-3p	AAACAUAAAUUGUAAUGUAGG	80-100	nta-miR6164b	5	0	21	21	3
spe-MIR10987	AACAGAAGGCUCUAAAAUGCCCUUAAACUAUGAGAUUUGAUACAAUAUUUCCCUCCAUCCACCUAAUGAGUAUGAUCCGUUAGACAUAAGGGUAUUUUUGAGCCGAAAGAUGAACGGAAGGGGUAUUUUAGUGGUGAUAGGUGGAUGAAGGAUAAUUUUGUACCAAUUCAAAUACUUGAGGGGCAUUAUAGGCCCUUCUCCA	202	spe-miR10987-5p	CAAUAUUUCCCUCCAUCCACC	43-63	mdm-miR10987	5	0	21	21	1
spe-MIR477e-2	GAAGAAUGAGUACUUCAAGCCUCGUCUUUGAGUUUCACAAGUCUACACUCCAUCAAGCCUUGAAGCAGGGGCAUUUGUAGACAUUGAAAUUUUGUGGGACUCUACAAGAUGCGUUCAAUUUGAGUUAGACUCUACAAAUUGUGUUCAACUUAAAUAAGGAUUCUUGGAGGCUACUCAAUCCUA	183	spe-miR477e-2-5p	ACACUCCAUCAAGCCUUGAA	45-64	ptc-miR477e-5p	5	0	20	20	1
spe-MIR10532-9	CUUAUAAAAUAAGUUCAGGGGUGAUAGGACCUUAAUAUAGUAUAAGUGUGUCUCUGAGAUUUCGAGUAUAUGUUGAGGGGGUACUUGUGCAUUUUCCCUAGGGGAAAGGGUCUGAUAUACCCCUCAACUUUGUCAUUUG	139	spe-miR10532-9-5p	AAGUGUGUCUCUGAGAUUUCGAGU	44-67	sly-miR10532	2	0	24	24	1
spe-MIR5752b	GGGUGUACAAUAUCGAAUAAAAAAUCAAACCAAAUCGUAAAUCGAGUCAAAUUGAAAAAAACUCGACUGGUGGUUUGGUUUGACUUGGUUUGGUAUUGGACAAAA	105	spe-miR5752b-3p	CUUGGUUUGGUAUUGGACAAA	84-104	mtr-miR5752b	5	0	21	21	1
spe-MIR10993b	UUGACCUCCCUAUGAAUAAUCUACCAAUUUGCGGAUUAUUCGAGAUCUUGAUCUCUUUAUGGAAUUUCCAAGAUGCCUUUUAAGGGAAUUUACUACCA	267	spe-miR10993b-5p	UUACUACCAUUUAUAUAGGCA	90-110	mdm-miR10993b	5	0	21	21	2

spe-MIR5026-3	UUUAUAUAGGCAUAAACUAGGAUUUAUGAUUGAGUAGCCUCCAAGAAUCCUAAUCUGAGUUGGACACAAUUUGUAGAGUCCAACUCGAAUUGAACGCAUCUUGUAGAGUCCCACAAAAUUUCAAUGUCUACAAACACAAAUUAGGGUAGAGUGUUAGUUAGGCGGUUGA	80	spe-miR5026-3-3p	ACCCACAAGAUAGUGCCACGU	49-69	ath-miR5026	4	0	21	21	1
spe-MIR828b	CUUUUCGGCCUACGUGGCACUAGCUUAAAAAGAGUCAACUAGUGUUGGACCCACAAGAUAGUGCCACGUAGACCGAAAAGAUUUACAUUCACUUCUUUGGGAAAGCCUCUUGCUCAAAUGAGUAUUCCAACAAAUGUCUAAUUGACAUACUUUUGAGAUACUCAUUUGGGUAAGAAGUUUUACCAGGAAGGUUGUACUU	119	spe-miR828b-5p	UCUUGCUCAAAUGAGUAUUCCA	28-49	mes-miR828b	0	0	22	22	1
			spe-miR828b-3p	UCAUUUGGGUAAGAAGUUUUA	82-102	ptc-miR828b-3p	5	0	21	21	1
spe-MIR11583b-1	UUUUCUCUCGCUUUAUACAAAUAGAAACGCAAUUUAUACAUUUCGUUUCUGUUUGUAUAAGCAAGAGAGGC	71	spe-miR11583b-1-5p	UUUUCUCUCGCUUUAUACAAA	1-21	pab-miR11583b	5	0	21	21	1
spe-MIR10542-4	UAGAAGAAUCAUAUAUACCCCUAAUAAUUUUUUAAAAAGAAUUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAACUUCCGUUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUC	236	spe-miR10542-4-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
spe-MIR7984b-3	CUGAACUUUAUGGAGGACCUUUUUACCCCCUUGCACUAUUUAAUAGUGUAUUGUGCUCACGUGGACAUCAUAAAUAUUGCAUCUUUUUAAAUAGUAAUGUGUCACGUGGGCACAUAUAUACCUUUAAAAUACACUUUUAAAAAGUGCAGCGGUAAAAAGUCUUUCAUAAAAUUUGG	176	spe-miR7984b-3-3p	AGUCUUUCAUAAAAUUUGG	158-176	stu-miR7984b-3p	1	0	19	24	2
spe-MIR5174d-5	ACCAUUACUCCCUCCGUUUCAGAAAGAUUGACCUAGUUUGACUUGAAACGGAGUUGAAGAAAAGAAAAAUGACUUUUUAAUCCUGUGGUUCUAAUUUAAAGUUAUGUCAAAUGUAUCAAAAUACCCUUUAAUGUUGUGGUCUUAAACAUGCCACGUGGAAAGUUACAAUUAAAGUGUUGUCAAAAAAGGAAAGGAGUUAACUCUUUUUGAACAGACUAAAAAGAAAAUAGAGUCAUUCUUUUUUAAAUGGAGGGAGUAUAUUUA	264	spe-miR5174d-5-5p	UCCCUCCGUUUCAGAAAGAUUGAC	9-32	bdi-miR5174d-5p	2	0	24	24	1
spe-MIR1917-3	GAUUCACUACGACAAAAACGACUUUUAAAGGCAUUAGGUAUUGACAUUAAUGAAGAGUGCUAAAGUCUUUAACGGCAUUAGUUAAAUGCCAUUAGAAACAAUGUCUAAAGUCUUUAGAGACAUAUACAAAGAGUGACAAUUGCCACUAAUGAUCAUUUUUGUUGAAGUGAGUA	173	spe-miR1917-3-5p	AUUAAUGAAGAGUGCUAAAGU	46-66	sly-miR1917	1	0	21	21	1
spe-MIR6271	AACACAUUAUGUGGUGCAAAUCAAGAUAGCAAGAUUGAUAUAAAGAAUGGGGUUGUGGGCCAUCUUGGAUAUGAAAGUUUCCAAUCACCCACAAAGGGCUCAAAGUAUCAUGAAAGAUUCAUUAAAAGAGACCAUUCUUGAUAUCAAUCUUGCUAUCUUGAUUUGCACCACAUAAUGUCUC	181	spe-miR6271-5p	GCAAGAUUGAUAUAAAGAAUG	29-49	ppe-miR6271	5	0	21	21	2
spe-MIR11583b-2	AAUUUUCUCUCGCUUUAUACAAAUAGAAACGCAAUUUAUACACUUCUAUUAUGUUUAUAUAAGCGAGAGGCGAGGGUGGCGAGCGAGAUCUGGGAGAGGAGAGAAACAAAAAUAUAUGUAUUUAUACAAUUUCCUCUGUUUUAUAUAAAUAAAAACAGAUUUUAUACACUUGUGUUUGUAUAAAAGUGAGAGAAAGCG	202	spe-miR11583b-2-5p	UUUUCUCUCGCUUUAUACAAA	3-23	pab-miR11583b	5	0	21	21	1
spe-MIR2275c	UAGUGUAGUUAGUCAUUGGGAAGAAAAGAUAAGACAAGAUGUCCCUCAUUGGUAGAAUAUAAUAUAUCUAACCAGAUAUAUUAAAUUUGAUUUCUCCAAAUUUCUCUUCAGUAUUUUAUUUCAAGUAGUAUUAGAAGUGCGUAAAAACGCUUCUUUCCUUCGGUAUUCUACUAAUGAGGAACAACUUGUCUUGUCU	222	spe-miR2275c-5p	UUUGAUUUCUCCAAAUUUCUCU	86-107	aof-miR2275c	5	0	22	22	1

	UCUCUUUUAAAUCACUAAAUACAUUG										
spe-MIR7992-15	CAUUUAUGCCCUUUAACUUUGAGUGUGCACAAGUAGACACUUAAACUUAUAUGAAGUUGAACAAAUAGACACACAUGUUACAUGUCAUCCUACAUGUCAUUUUUUGUCCUACGUGGUGUCCUACGUGUAUUGUGUGCCAUGUAGGACUCACAUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAUUGUCUAUUUGUGCAUUAUGAAAGUUGAAGGUCAAAGUU	222	spe-miR7992-15-5p	UUUGAGUGUGCACAAGUAGACACU	18-41	stu-miR7992-5p	5	0	24	24	1
spe-MIR2630v	AGGUAACCUAGGGGAAUUACUAAAGUACCCCGUAGUUUAUAGGACCAUAACUAACCUUUUGGACCAUCCUAGGUUAGGUACUAGGUUGUCUCUUUAAAUAGUACUAGGUUAGUGUCAACCCGGUUUUGGUCCUAGGUUGUCGGGUGCACUAGCGGGUCCAUUUCGGUUAGUCCUAGGUUAGUU	183	spe-miR2630v-3p	CGGUUUUGGUCCUAGGUUGUC	121-141	mtr-miR2630v	5	0	21	21	2
spe-MIR11592-2	AAUCAAAUCGCAAAUCGAGUCAAACCGAAAAAAAACUCGACUAAUGGUUUGGUUUGACUUGAUUUGGUGUUGGAA	76	spe-miR11592-2-5p	AAAUCGAGUCAAACCGAAA	12-30	cas-miR11592	5	0	19	19	2
spe-MIR8652	AGCAAACAUAUAACUGUAUAAUUCGCUAUACAUAUACAAUUGUAUAAUACGCUGGCCUCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGCCUAAAUUGUAUAAUUCGCUGGCCUAUUUCGCUGCAAUUGUAUAAUUCGCUGGGCCUAUUUCACUGCAAUUGUAUAAUUCGCUGGCCUAUUUCGCUGCAAUAUGUGUAUAAAAUUUUCUUUGCAUACAAUUGAAUCGAAGUAAAAUGUUUGUAUAUUGUAUAAUUAUAAGUGUAUAGGAAGAAGAUACAUGUUUUUC	308	spe-miR8652-3p	AAUAUGUGUAUAAAAUUUUCUUU	210-232	gra-miR8652	5	0	23	23	1
spe-MIR10542-5	AUUAAAAUAUACCUUGAACUUUGAUAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUUAAAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAACUUCCGUUAGAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGGUAUAUGUGAACCGUUUGUAUAACGGUAAGGGCAUAUACGAGCCACUUUUAUAACGAGGAUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUAACGAGGGGUAUAUAGCCUAUGACUCAUGAAUUUGAAGUGGAUUUUGUG	297	spe-miR10542-5-5p	UAGAAGAAUCAUAUAUACCCCUA	25-47	sly-miR10542	0	0	23	23	1
spe-MIR7992-16	CUAAACUUGGCUUCAAAUUUUAACUUUGACCUCAACUUUCAUAAUGCACAAAUAGACACUUUAACUAUCUAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGACACAAUACACGUAGGACAAAAAAUGACAUGUAGGACAUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGCCUACUUGUGCACACCCAAAGUUGAAGGGCGUAAAUGUGAUUCGAAGCCAAAUUAAA	238	spe-miR7992-16-5p	UUUCAUAAUGCACAAAUAGACACU	37-60	stu-miR7992-5p	4	0	24	24	1
spe-MIR3447-2	AAACACUCCAACUUACAAGAUGAUCAUCUAGACAUCUCCUAAGUCAGCCGAGGCGUCUUGAUGUGCACUCUCAAAGUUGGAGUGCUUACUUGCUUGGUGAUUUAUCAAGUUUGAGUGUAUUGUUUAUGAAUUAUGCCUUAUUUCUUUUGGGUAAAUGAAGUAGAAAUAAGUCAAUAAGAUAUUAGGUGUUGUUAAGGGAUUAUAGUGCUUAUUAUGCAGUGGGAAGUGGGG	231	spe-miR3447-2-3p	UUUGAGUGUAUUGUUUAUGAA	110-130	aly-miR3447-3p	3	0	21	21	1
spe-MIR7983-15	AAGCACUAUAACAAAAAUGAUCAUUAGCGGCAUUUAAUUCUUAAUUGCCGCUAAAUAUGUACUUUUAGCGGCAAUUGUCACUCUUUGUAUAUGUCCCUAAAGGCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGCCAGUAAAGAUUUUAGCACUCUUUAAUAUUAGAAAUAUUUAAUGCCGCUAAAAGUUAUUUUUAUUAUAUUGAAG	214	spe-miR7983-15-3p	UAAAGGCUUUAGCGACAUUGGUUC	98-121	stu-miR7983-5p	1	0	24	24	1
spe-MIR9736-2	CGCUUGCCAAGUUUGCACACUGCAAGGACUUGGCGGGAGUAUGAUGCAACUCUAAGAGAACAACUGCUAGGUGGAGCUGGUAUGUUCAACAAAGGUUUGAUUCUUCUUGUUUCUUACAAUGGGAUUGCCCAGUAAGCUUAGAAGUUUUGGCCGGAGUUGU	331	spe-miR9736-2-3p	UGGAACACAAACCAAGGUGGA	174-194	gma-miR9736	4	0	21	21	1

spe-MIR10532-10	UUAUACGCAUGCUUGGAACACAAACCAAGGUGGAGAUUGAAAGAGUUGGUUUUGGUUCUUGUGGAAUCAAACUAAAUGGAAGAUGAAUUAAUAUGAAUAUUUGGUAGGAAGAUAAUUAGUACAAAAUACAAGUCAAAGAUUGUAUCUUGGUAGGUGAAAGUUAGGCAAACC	198	spe-miR10532-10-5p	AAGUGUGUCUUUGAGAUUUCGGGC	7-30	sly-miR10532	1	0	24	24	1
spe-MIR10420-2	UAGUAUAAGUGUGUCUUUGAGAUUUCGGGCACAGGUUGAGGGGGUACUUGGGCAUUAUCCCAAUAAAUUUUAUCAAUUCUUGGUAAACAAAUUGUAAGAACAAAACUUAAAAGUUUAAGAGAAAUAAUUUAGAUAACGGGAAAAUGCACAAGUACCCCCUGAACCUAUGCCUGAAAUUCCAGAGACGCACUUAUACUA	218	spe-miR10420-2-3p	CCUGAUCGCUCAUUUUUUU	106-124	gma-miR10420	3	0	19	19	1
spe-MIR11076	CCAAAAGUCCAACAUUUUUCAGAUGUGUUGUGAGAAGCUUUCUUGCUUCUCUUAAUUGUAGAAUGUCCUUUCUUUCUAGAGGACUUCUUCUUAGGAGACGAUUUUCCUGAUCGCUCAUUUUUUUGGGGCUUCUUUGCAGAAGGGGGUUUUAGACUAGGGAACCAAAGUCUUAGCAAAAACUUCCAAGCUCGUUACUUGAAAAUUUUUUAUCUUUCUU	72	spe-miR11076-3p	CAUGGUAGUGAAGUGCACC	23-41	lja-miR11076-5p	5	0	19	19	2
spe-MIR156b-11	CCUCAUCGAGUAGUUUCUAAGUCAUGGUAGUGAAGUGCACCACUAUCCUGGAUUAGAGACUACAUGAUGCGUCGUACAAAUAGGCACUUUAAGUAUUCAGCUUUUAAAUAAAUAAGCACAUGAGUCCUACAUGACACAAUACACUUAGCACACCACGUAGGACGAAAAAUGACAUGUAGGAUGACAUGUAGGACAUGUGUGUCUAUCUGUUCAACUUUAUAUAAGUUUAAGUGUCUAUUUGUGCA	173	spe-miR156b-11-5p	UGACACAAUACACUUAGCACA	60-80	hvu-miR156b	5	0	21	21	1
spe-MIR8008b-4	UUUUGUCCGUCGCUUUUUUGCUUUAUUUUUUUCAAAUAAACCCAGAAAAGCGACGGACAAGGUUCUUUGGUCCGUCACUUCUCUAGGUAUUUUAAAAAAUUAAUUUCAAGGAAAGCGACAGACAUUGACUAAUUUACUACUCCCUCCGUUUCAAAAAGAUUGGCCUAGUUUGACUUAGAAUGGAGUUUAAGA	127	spe-miR8008b-4-5p	AAACCCAGAAAAGCGACGGACAAG	38-61	stu-miR8008b	2	0	24	24	1
spe-MIR5174d-6	AAAGAAAGAAGACUUUCUUUUGUGGUUCUAAAUUAAAGUUAUGUCAAAUGUACCAAAAUUCCCUUUAAUCUUGUGGUCUUAAACAUGCCACGUGGAAAGUUAAAGUUAAAGUGUUGCCAAAAAAGGAAAGGAUCAUUCUUUUUUGAGCAAACUAAAAAGGAAAUAGGGACAUUCUUUUUUAAACGGAGGGAGUAUAUAUUUUU	268	spe-miR5174d-6-5p	UCCCUCCGUUUCAAAAAGAUUGGC	14-37	bdi-miR5174d-5p	1	0	24	24	1
			spe-miR5174d-6-3p	CAUUCUUUUUUAAACGGAGGGAGU	235-258	bdi-miR5174d-3p	5	0	24	24	1
spe-MIR5027	UUAUUAUAACUUUUAUGAAAGAUUGUGACCUUUCCUAAGGGUUGCAACUUUUCCAAAUAGUUGUGACCUUUUCGACGGGUUGCAACUUUCCCAAAUAGUUGUAACCU	107	spe-miR5027-3p	ACGGGUUGCAACUUUCCCAAA	75-95	ath-miR5027	5	0	21	21	1
spe-MIR9670	UAUAAACAAUUUGUAUUAUAGUGAAUGUCUAAUUAUGUGGAAUCCUUGUAGGAUAUGGUUAGGAAUCCUACUUGGGGACCAAGUAAGGUUUUCCCUAUAAACAAAGGGUUUUCC	114	spe-miR9670-5p	AUGUGGAAUCCUUGUAGGAUA	35-55	tae-miR9670-3p	5	0	21	21	1
spe-MIR9562-1	UAUAAUUGCGCUCCAUAGCAAACAUAAAACUGUAUAUUUCACUGCAAUUGUAUAAUUCGCAAUUGUAUAAUUCGUUGACCUUUUUCUCUGCAAUAUUUGAAGUAAAAUGUUUGUAAAUUGUAUAAUUAAGUGUAUACCACGAAGAUAUAUAUUUUUGCAUGUGUAUAUACAAUUUUCUCUCGCUUUAUACAAAACAGAAACAGAAUUAUACACUUCUGUGUAUAAAGCGAGAGAGGCGAGCGAGAAUGGAGAGUGGCGAGCGAGAUUUCUGGGAGAGAGACGCUGGCAAAUUUUAGCUAACGUUUUCUAUGGAGCACAAUUAAA	324	spe-miR9562-1-5p	UAAUUCGCAAUUGUAUAAUUC	53-73	bra-miR9562-3p	4	0	21	21	1
spe-MIR1886h-3	GCGAUUUUACGCUGAUUUCAUCUCAUGAUUCCGUAUCAUGAAAUGUGAAUCCAUAUUCUCCAAAAACUAUGAUAUGGAAUCAUAUGAGAAUACCAUC	108	spe-miR1886h-3-5p	AUUUUACGCUGAUUUCAUCUCAUG	4-27	stu-miR1886h	1	0	24	24	1

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spe-MIR9760	CAUGAUUCGGAACUAGGAUGAUUUAGAUUUGA UCUCUAUAUGAAUAUUCCAUGACUUUUGUGGAA UAUUCGAGAUCUUAAUCUCUUUAUGAAAUUUUA GAGAUGUCUUUUAAGAGAACUUAGUAUCUUUUA UAUAUGCGUGAACUAGGAUUUAGAGUUGAGUA GCCUCCAAGAAUCUUAGAGUUGAGUAACUUCAA GUGGAUUAUGCUAGAGGAUUGAGAUUGAAUCC AAUUCAAAUAAUCUUGAGUCCGAUCCUU	256	spe-miR9760-5p	AGGAUGAUUUAGAUUUGAUCU	15-35	gma-miR9760	5	0	21	21	2
spe-MIR9562-2	CGCUAUACAUAUACAACUGUAUAAUUCGCUGGC CUAAAUUGUAUAAUUCGCUGGCUUCGCUAUACA UAUACAAUUGUAUGAUUUGCUGGCCUAGAUUG UAUAAUUCGCUGGCCUAGAUUGUAUAAUUCGC UGGCCUAUUUCACUGCAAUUGUAUAAUUCGCU GGCCUAUUUCGCUGCAAUAUGAGUAAAAAAUUG CUUUGCAUACAAUUGAAUCGAAGUAAAAUGUUU GUAUAUUGUAUAAUU	243	spe-miR9562-2-5p	ACAUAUACAACUGUAUAAUUC	7-27	bra-miR9562-3p	5	0	21	21	3
spe-MIR1128-6	UAUACUACUCCGUCCGUCCCAUUUUAUGUGAC AAUAUUUGACCGGGCACAAAGUUUAAGAAAUAG UGAAUACAUUGAAAUAUUUAUCAAAUAGCCCUU UUGAAAAGUAGACUCACUUUUAUCUCUCCUCGU AAAUGUAUUGAGUACUAUAUUUAAGAUUAAGUG GGACCAACAAGGGUAAAAGAGUAAUUGUACCUU UAAAUAUUUACCAUAUAAGGAAAUGUGACAUUC UUUUUGGAACUGACCAAAUAGAAAAUGGUGCCA CAUAAAAUGGGACAGAGGGAGUAGUUUU	291	spe-miR1128-6-5p	UACUACUCCGUCCGUCCCAUU	3-23	ssp-miR1128	3	0	21	21	1
spe-MIR7701-2	AAAUGAACUUAAUGGGCUGAAUCUGAAUGAUUC AGAUUCAGAUAUAAAAACCAAAUGUACUUAAUA GACUGAAUCUAAAUGAUUAAGAUUCAGACCUCC AUUAAGUGCAAAC	112	spe-miR7701-2-3p	CUUAAUAGACUGAAUCUAAAU	60-80	mtr-miR7701-5p	5	0	21	21	2
spe-MIR10542-6	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUU UAAAAAAAUUAAAAGUAAUAAAUAUAAAUUUAAA ACUAAUUUUUUUAACUUCCGUUAAAUGAAGGGU AUAUGUGAGCCAUUUUGUAACGGCAGGGGUAU AUGUGAGCCGUUUGUAUAACGGUAGGGGCAUA UAUGAGCCACUUUCAUAACGAGGGGUAUAUCA GCUGCAAAUGACAAAGUUGAGGGGUAUAUUAG ACCCUUUUC	237	spe-miR10542-6-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
spe-MIR3512-2	AAUCAAAUCGCAAAUCAAGUCAAAUCGAAAAAAA AACCAACUAGUGAUUUGGUUUGACUUGAUUUG GUGUUGGAA	75	spe-miR3512-2-5p	CGCAAAUCAAGUCAAAUCGA	9-28	ahy-miR3512	4	0	20	20	1
spe-MIR5278	CAUACUUGUUGAAAUUAUUAGCCACAAAUGUGA AAAUUGGUAGCCACCAAUGUGAAAGUUAGUAGC CACAUUUGUGGAAGUAGGUAGUCAAAGUUUGG UAGAGUUAGGCAACCAAUUUUUUGUUGAAAUC GGUUACCACAUUAUGUCAUUAAUGAUGUAAACA AGUGUU	169	spe-miR5278-5p	GAAAUUAUUAGCCACAAAUGUGAA	11-34	mtr-miR5278	5	0	24	24	1
spe-MIR5014a-14	UUACUAUCUAAAUUCUAUCUAUGCACAAGUAGA CACAUAAACUUGUAUAAACUUGAAUAAGUAGAC ACAUGAGUCCUUCGUGACACAACACACGUAAGA CAAAAAAUGACAUGUAGGACAUGUGUGUCUAUU UGUUCAACUUUAUACAAGUUUAAGUGUUUACUU GUGCACACCUAAAGUUGAAGGGU	188	spe-miR5014a-14-3p	UUAUACAAGUUUAAGUGUUUA	142-162	ath-miR5014a-3p	5	0	21	21	1
spe-MIR482b-5	UAGAUAACUGAAUGGUUGGGGGUUCGAGCCCC CACAACUGCUUUGAUUUUUAGAAUUAAAUUCGC UAUAAUAGGGAGGUUGUGGGUUCGAACCCCCA CAACCCCCACUUAUUAUUUUUUUUCAAAUUUUG CUGAGGAGGCUGUGAGGUGGUGGGUUCAAACC CCCACAGCCCCUCUAUCUAUAUUUUAUUUAAAU GGGCGAGUGGCAAUGAGGUUUGUGGGAUCGAA UCCCCACAUCCUCACAUUAUUUC	250	spe-miR482b-5-3p	UAAAUGGGCGAGUGGCAAUGA	191-211	eun-miR482b-5p	5	0	21	21	2
spe-MIR8050	GUCUUGAUGGACGUCCACAAAAACUUUUGUCA UUUUUGACGUCGGAAUCAAGAUCACCCAAAAAA UGGUUUGCUAUAGCACACGAAAGUCGCCGAAA UGAGGGGUAUGCUCGCUCCGGGGCUCGUUUG	204	spe-miR8050-5p	ACGUCGGAAUCAAGAUCACC	39-58	stu-miR8050-5p	5	0	20	20	1

spe-MIR1033e	ACCUUCAAAAUGGGUCGGACGGGCCGUGAGGGCCAACCGGAUGCAUAGACAAGGUCUUGACGGACGUCCACAAAAUGCAAAGACAAGGUCAUGGACGUCCACAAAAACUUUUGUCAUUUUUGACGUCGGAAUCAAGAUCACCCAAAAAAUGGUUUGCUAUAGCACACGAAAGUCGCCGAAAUGAGGGGUAUGCUCGCUCCGGGGCUCGUUUGACCUUCAAAAUGGGUCGGACGGGUCGUGAGGGCCAACAGGAUGCAAAGACAAGGUCUUGAUGGACGUCCACAAAAACUUUUGUCAUUUUUG	231	spe-miR1033e-3p	GGACGGGUCGUGAGGGCCAAC	157-177	ppt-miR1033e	5	0	21	21	2
spe-MIR11317	CGGACUAUUUGCCAUGUCUGAAAUCAUCUUAAGCUAUUCUUUUUAUUUCUCAAAAAACGAAUAGGUGAUGAUGAUUCCAGAUAUGGAAAAUAGUAUCCACUCACUACAACAAAAAUAAUCAUUAGCGGCAAUUAAUCCUUAAUUGCCGCUAGAUAUGUAUUUUAGCGGCAAUUGACAUUCUUUGUAUAUGUCCCUAAAGCCUUUAACGACAUUGGUUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAAUGUCAAUAUUUAAUGCCGCUAAAAGUUAUUUUUGUUGUAGUGAUUUUUACUCCCUCCGUUUCAAAAAGAAUGUCCCUAUUUUUUUUUAGUUUGUUUAAAAAAGAAUGACCUCUUUCCUUUUUUGCAACACUUUAACUUUAACUUUCCACGUGGCGUGUUUAAGACUACAAGAUUAAAUGACAUUUUGGUACAUUUGACAUAACUUUAAUUUAGAACCACAAGAUUAGAAAGUCUUCUUUAUUUUCUUAAACUCCGUUCGAAGUCAAACUAGGUCAUCCUUUUUGAAACGGAGGGAGUAU	216	spe-miR7983-16-3p	ACUAAUGCCGGUAAAGACUUUAGC	135-158	stu-miR7983-3p	1	0	24	24	1
spe-MIR5174d-7		254	spe-miR5174d-7-5p	UCCCUCCGUUUCAAAAAGAAUGUC	5-28	bdi-miR5174d-5p	3	0	24	24	1
			spe-miR5174d-7-3p	CAUCCUUUUUGAAACGGAGGGAGU	229-252	bdi-miR5174d-3p	5	0	24	24	1
spe-MIR6273-1	UGUCGUAAUUGAUAGUCACGAUUUAAUGCAGAAAUGUGAUCAGCGAUAACGUUUUAUGAUCUGUAAGAUUCCAAUGUAGCAGGAUUUUAUUCUUAAUCUGGUGCCCCGUGAUUAAAUAAACAUAAAACGUGAUUGACAGUUACGUUUUAUAUAAUAAACGUGAUUGUCAGUUACGUUU	178	spe-miR6273-1-3p	AAUGUAGCAGGAUUUUAUUCU	73-93	ppe-miR6273	4	0	21	21	1
spe-MIR400	AUUCUAGAAGCUCUUGUACUUAUGACACCAAUUCUUGGGUAGUAUUUUUUUUUAGUUUUCCGCAUUCGUACUUAUAAGGAACUCAUUAUUGGAGAUUUGACUUGUUGUUGUCUUUUACUCAUUAGUUAGUUAAGUUUGUUAAAAUAUGUUGGUUGACUUACCUAUUGGUUGGGAAUAUAGGUGCCAUCACGACUCGUGAUUUUUGGGUCGUGACAAUUUGGUAUCAGAGCAUUAGGUUCAUCGGUCUCACGACUACAAGAGCAUUAUCUAGUAG	274	spe-miR400-5p	UACUUAUAAGGAACUCAUUAU	69-89	bra-miR400-3p	5	0	21	21	2
spe-MIR7992-18	GGUUUCAUAUUUUAACUUUGACCUCCAACCUUCAUAAUGCACAAAUAGACACUUUAACUAUUAAACUUUUAAAUAAAUAAACACAUGAGUCCUACAUGGCAAAAUACAUGUAGGACAUCAUGUAAGACAAAAAUGACAUGUAGCACAUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCUACAUGUGCACAGCCAAAGUUAAAGGGCAUAAUUCUGAUUUGAAGCC	234	spe-miR7992-18-5p	CUUCAUAAUGCACAAAUAGACACU	30-53	stu-miR7992-5p	5	0	24	24	2
spe-MIR7980b-9	AAAUAUGGCAUCACAUCUCAUGAUAUGGAAUCAUGAGAUGGAAUUAGCGUAAAAUCGCUUGUCCAAACACUGAUUCCAUCUCACUAUACCAUAUCGUGAUAUAAUAUCGCAUAGCU	116	spe-miR7980b-9-3p	GUCCAAACACUGAUUCCAUCUCAC	61-84	stu-miR7980b-5p	1	0	24	24	1
spe-MIR3706-2	CAUACACGUGUCAUAAUUAUCCACCGAUCCGACCUCAGAUCAAUGGAUAAGAUUGUGUCACGUGUCCC	68	spe-miR3706-2-3p	CCUCAGAUCAAUGGAUAAGA	33-52	pab-miR3706	5	0	20	20	3
spe-MIR5049b-2	AUUAUAUAAUACUCCCUCUGUCCCUUAUUACUUGUCCAUUUUGACAAAUCAAGAAAGGACAAUUUUUUUUUACCUAUUAUACCCUAAAUUAAUUACUUUGAGAAAGGUAGAACUUCUUGAAAAUAUUAAGUU	266	spe-miR5049b-2-3p	AGUAAUUAGGGACAGAGGGAG	236-256	hvu-miR5049b	2	0	21	21	1

spe-MIR5303h-15	UUCGAUUCAUCCACUUCAUAAUUGAUAAGUGUAAAAUGAUAAACUCACUAUGUCAAUGAUUGUUAUUCAUUUCUUAAUAGGGUGUGCCAAUCCAAAGUGGACAAGUAAUUAGGGACAGAGGGAGUACAUAUCUC	131	spe-miR5303h-15-3p	AACAUUUUUGAAGAGUCUGAGCAA	98-121	stu-miR5303h	0	0	24	24	1
spe-MIR2863a-1	AAGCAGUAUGCUGCUCAGACUCUCCAAAAAUGUUGCCGCACCUGUAUCGUAUCCUUCGGACAAGCACUACUUUUGGAGGAUCGAACAAGCACCUGACAACAUUUUUGAAGAGUCUGAGCAACAUAGUGAAGUGAUCCACCCACCUAACCCGACCCAUUAAAAAA	142	spe-miR2863a-1-5p	AUGACCCAUUUUAUUUUAUCU	41-61	osa-miR2863a	5	0	21	21	2
spe-MIR5303h-16	AUAUGAUAUGACCCAUUUUAUUUUAUCUUUAAUCCUAAAUUAAGAUUAAAAAUAAAAUAAAAUGGGUCAUAUCAUAUUUUUUUAAUGGGUCGGGUUAGUGGGUGGAUCA	128	spe-miR5303h-16-3p	AACAUUUUUGAAGAGUCUGAGCAA	97-120	stu-miR5303h	0	0	24	24	1
spe-MIR7983-17	UGGCUAUGCAGCUUGAACUCUCAUAAAAUGUUAUUUUACCGGUGUCGUGUCCUUCAAAAAUGCUUUACUUUUGGAGGAUCCGGGACGUGCUCGACUAACAUUUUUGAAGAGUCUGAGCAACAUAGAUU	124	spe-miR7983-17-5p	UAAAGCCUUUAGCGAUAUUAAAUC	35-58	stu-miR7983-5p	5	0	24	24	1
	UUUAGCAGCAAUUAACACUCUUUGUAUAUGUCGCUAAAGCCUUUAGCGAUAUUAAAUCCAAUGACACUUGACUAAUGCCGGUAAAGACUUUAGCACAUUAAUGUGUCCAUUUAUUGCCGCUAAA		spe-miR7983-17-3p	ACUAAUGCCGGUAAAGACUUUAGC	71-94	stu-miR7983-3p	1	0	24	24	1
spe-MIR477c-1	CAUAAUAAACUAGUUCUUGAGGUUGAGUUAGGCGCAUGUGUCAUAUCUUUACAUGGUUUGAACCAUGUAAAGAUAUGACACAUGAGCCCAACUCAUCCCCAAGAGUUAGUUUUUGCC	117	spe-miR477c-1-5p	CUAGUUCUUGAGGUUGAGUUA	10-30	csi-miR477c-3p	5	0	21	21	3
spe-MIR477c-2	CAUAACAAACUAGUUCUUGAGGUUGAGUUAGGCUCAUGUGUCAUAUCUUUACAUGGUCUGACAUCUGAGACCAUGUAAAGAUAUGACACCUGAGCCCAACUCAUCCCCAAGAGUUAGUUUUUGCC	125	spe-miR477c-2-5p	CUAGUUCUUGAGGUUGAGUUA	10-30	csi-miR477c-3p	5	0	21	21	3
spe-MIR5014a-15	CAUUUGUCAUACAUGAUACAUCUACAUGACAACUUUGUCUCCUACAUGAUAUUCUACGUGUAUUAUGUCAUGUAGGACACUUGUGUGUACUUGUUCAAUUUUGUACAAAUUUAAGUGUAUACUUGUGCAUAUUCAAAGUUGAAGGACAUAGUUGUUUGUUGAAGCCAAAUUAAGCGUCAUGUAUUAUGCCAGCUAUCUAUAUGUUACGUCUUAGAUAUUGAAAAUUGUUGGUUUUCAUCUCAAUAUAUGUAAUGCAAUUU	260	spe-miR5014a-15-5p	UUGUACAAAUUUAAGUGUAUA	101-121	ath-miR5014a-3p	2	0	21	21	1
spe-MIR7983-18	UCCUUAAAGUCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGUCGGUAAAGACUUUAACAC	66	spe-miR7983-18-5p	UAAAGUCUUUAGCGACAUUGGUUC	5-28	stu-miR7983-5p	0	0	24	24	1
			spe-miR7983-18-3p	ACUAAUGUCGGUAAAGACUUUAAC	41-64	stu-miR7983-3p	1	0	24	24	1
spe-MIR2863a-2	AUAAAGUGACAUAGGGUAAUUACUAAAAUACCACUAUGUCACUAAGACCAUAACCAACCUCUUUGGACCAUCCUAGGUUAGGUACAAGGAUGUUUCUUUAGUUAGUUACCCGGCUAGUAUCACCCGGUUAGGUUUUAGGAUUUUGGGUACACUAUUUGUUUAUUUCGGUUAGUCCUAGGUUAGUUAGAUAGUUAGUUAAGAUACAUAGAGCCUAGUACUGGGU	223	spe-miR2863a-2-5p	UUGGACCAUCCUAGGUUAGGU	63-83	osa-miR2863a	5	0	21	21	1
spe-MIR11891-2	CAUUUGUAGAUAUUGAAAAUUUGUGGGACUAUUCAAGACAUGUUCAAUUCUAGUUGGAAUUGUACAAGAUGUACUUGAUUCCAGGUAGGAUUCUUGGAGGCUACUCAACUUAAAAUUCUAGUUGAUGCCUAUAUAAAUUGUACUAUAUUCCCUUAAAAGGGUAUCUUGAAUAUUCCACAAAUUCAUGAAAUAUUUAUAAGGA	202	spe-miR11891-2-3p	UAUAAAUUGUACUAUAUUCC	132-151	mes-miR11891	4	0	20	20	2
spe-MIR6299-2	UUAUAUAAAGUAUAUUAUAGUCUGUAUGUAAAAUUAAUGAUAUGAAAUAAACAGUUGGUUUUUAUAUCCUUCUUCUUAAAACUCCAUUAAUAGUCGUAAGUGAAGGUUGCGAUCUUCAGCCUCACGGAGGAACAGUAACAGAGUAGCCAAAGACUGAGGUCGUUAGGGUGAAACACUGUUCAUGGCCUAAAGGGAGAACUACUGCGGUAGUGAUAAAGACUAUUCAUC	310	spe-miR6299-2-5p	AUGUAAAAUUAAUGAUAUGAAA	26-47	gma-miR6299	5	0	22	22	1

spe-MIR7986	GACAAAAGAGAAGAAAGGUAUACACGCAAACUU UUUAUUAAAUGUUAUUAAUUUCACAUAUAUACU AUAUAUACUUAUACUU ACAGCAUUAGGUUGAUAUACGUCACUGUAAGUA ACGUUUUACUUUUAAAACGUUAUUUUCAGUAAC GUUUUACUCCUAAAACGUUACUGUGAGUAACG UUUUAGAAGUAAAACGUUACUGUGAGUAACGUA UAUCAAUCUGACGCCAU	148	spe-miR7986-5p	CUUUUAAAACGUUAUUUUCAGUAA	42-65	stu-miR7986	5	0	24	24	3
spe-MIR847	CGAUAGUAGCCAGAGGUCGUGGACGUGGAGAA GCACCAUUAAGAGGUUGUGCUAGAGAGGUCUC UAUAGAACCUCAAAUUGAUGGUAGAGAGGACCA GGUUCCUCCAGAUCCUGUAGUCACACCUUUGC UUCAGGAUACACUAUUGAGGGUGUAAAGUGUU CCAGAGGGAUUUUCUCAGGGUGGUGGUGCGAC UACCACACCACAUGACUCUCGUACUAAAG	222	spe-miR847-3p	UCACACCUUUGCUUCAGGAUA	118-138	aly-miR847-3p	5	0	21	21	1
spe-MIR10542-7	UUUGAUAGAAGAAUCAUAUAUACCCUUAAAUAA UUUUAUAAAAAAAAUUAGAAGUAAUAAAUAUAAAU UUAAAGCUAAUUUUUUAACUUCCGUUAAAUGAA GGGUAUAUGUGAGCCAUUUUGUAACGGCAGGG GUAUAUGCGAGCCGUUUGUAUAACGAUAAGGG CAUAUAUAAGCCACUUUUAUAACGAGGGGUAUA UCAGCUCCAAAUGAGAAAGUUAAGGGGUAUAUC AGACCCUUUUCCCA	244	spe-miR10542-7-5p	UAGAAGAAUCAUAUAUACCCUUA	6-28	sly-miR10542	1	0	23	23	1
spe-MIR10541-2	CAGCUUUUAAGCUGAGCCAAACAGGCUCUAAG UCACUUUGAUAUUUGUCAAACACUCUAAUAAGU CAAAAACUGACUUUUAAGUCAGUUUGACCAGCU UUUAAGUCC	107	spe-miR10541-2-3p	AGUCACUUUGAUAUUUGUCAAACA	31-54	sly-miR10541	2	0	24	24	1
spe-MIR10542-8	AAAAUAUACCUUGAACUUUGAUAGAAGAAUCAU AUAUACCCCAAAAUAAUUUUUAAAAAAAAAUUAG AAGUAAUAAAUAUAAAUUUAAAAAUAAUUUUUUA ACUUCCGUUAAAUGAAGGGUAUAUGUGAGCCA UGUUGUAACAGCAUGGGUAUAUGUGAGCCGUU UGUAUAACGGUAAGGGCAUAUAUGAGCCACUU UUAUAACGAGGGGUAUAUCAGCUCCAAAUGACA AAGUUGAGGGGUAUAUCAG	249	spe-miR10542-8-5p	UAGAAGAAUCAUAUAUACCCCAA	22-44	sly-miR10542	1	0	23	23	1
spe-MIR8766	GAACCAAACAGCAAAUCCAGUCAACCAGAAAAA AACUCGACUAGUGGUUUGGUUUGACUUGAUUU GGUAUUGGAAA	76	spe-miR8766-3p	UUGAUUUGGUAUUGGAAA	59-76	gra-miR8766	4	0	18	24	1
spe-MIR6135k	AUGAUAUUAUAGGAUUGGAGUGUCACGUUCCG ACACAAUAUUCUUGGAUCAGGGUGUCACGUUC CGAUACGGUAUUCUUGGAUCGGAGUGUCACGU UCAGACACGAUAUUCUUGGAUCGGAGUGUCAC GUUCCGACACGAUAAUAUUAA	149	spe-miR6135k-3p	CGUUCCGAUACGGUAUUCUU	60-79	pgi-miR6135k	5	0	20	20	1
spe-MIR5049d	AUGAUAUUAUAGGAUCGGAGUGUGACGUUCCG ACACAAUAUUCUUGGAUCGGAGUGUCACGUUC CGACACAAUAUUCUUGGAUCGGAGUGUCACGU UCCGACACAAUAUUUUUGGAUCGGAGUGUCAC GUUCCGACAAGGUAUUCUUGGAUCGGAGUGUC ACGUUUUGACACGGUAUUCCUGGAUCGGAGUG UCACGUUCCGACACGAUAAUAUUAA	217	spe-miR5049d-3p	CACAAUAUUUUUGGAUCGGAG	102-122	hvu-miR5049d	5	0	21	21	2
spe-MIR6273-2	UGUCGUAAUUGAUAGUCACGAUUUAAUGUAGAA AUGUGAUCAGCGAUAACGUUUUAUGAUCUGUA AGAUUCCAAAGUAGCAGGAUUUUAUUCUUAAUG CGAUGCCCCGUGAUAAAAUAUACAUAAAACGUG AUUGACAGUUACGUUUUAUAUAAUAAACGUGAU UAUCAGUUACGUUU	178	spe-miR6273-2-3p	AAAGUAGCAGGAUUUUAUUCU	73-93	ppe-miR6273	5	0	21	21	1
spe-MIR1428e	UAUUCAUUCAUGCCAUUAUUUUUUAACAAUGGU UUUGCAAACCCAAUUUUGACACGUGACCAAUUA UAAUUGGUCACGUGUCAAAAUUGGGUUUGCAA AACCACUGUUAAAAAAUAAUGGCAUGAAUGAGU C	132	spe-miR1428e-3p	AAAAAUAAUGGCAUGAAUGAG	110-130	osa-miR1428e-3p	5	0	21	21	2
spe-MIR5671a	GUAUCAUAGCACUAGGUUAAAUUCCGAGAAUAA UGAGUUCACAUCAACCACAUUGAGUAGUUUCUA AGUCAUGGUAGUGAAUCGCACCACUAUCCUGG AUUAGAGACUGCAUGAUGCGUAGGAAAAAUUUA CCUUCUUCUGAUCUUAUCGGCAUUUUCCUAAU	172	spe-miR5671a-5p	CAUGGUAGUGAAUCGCACCAC	70-90	gma-miR5671a	5	0	21	21	1

	GUAUGAAUU									
spe-MIR6023-2	UGGUAUUAUUGGAUCGGAGUGUCACGUUCCGACACGUAUUCUUGGAUCGGAGUGUCACGUUCCGACACAGAAUUUUUGGAUCGGAGUGUCACGUUCGACACGGUAUUCUUGGAUCGGAGUGUCACGUUCCGACACGAUAAUAUUA	146	spe-miR6023-2-3p	UUCCGACACAGAAUUUUUGGAU	60-81	sly-miR6023	5	0	22	22	1
spe-MIR5761b-2	AAAGCUCUUGUACUUAUGACACCAAUUCUUGGGUACUACUUUGUUUUAGUUUUGCUAAUUGUUGUGUUUUCACUCAUUAGUUAGUCAAGUUUGUUAAAAUAUGCUGGUUGGUUUACCUAUUGGUUGGGAACAUAGGUGCCAUCACGACUUGUGAAUUUGUGUCGUGACAAAUUUGGUAUCAGAGCCCUAGGUUCAUCGGUCUCACGAGUACAAGAGCACU	220	spe-miR5761b-2-3p	AUUUGUGUCGUGACAAAUUUG	155-175	gma-miR5761b	5	0	21	21	2
spe-MIR6023-3	AAAUUAAUGGUAUUCUUGGAUAGGAGUGUCACGUUCCGACACGAUAUUCUUGGAUCGGAGUGUCACGUUCCGACACAGUAUUUUUGGAUCGGAGUGGUACAUUCUGACACUGUAUACUUGGAUCGGAGUGUCGCGUUCCGACACGGUAUUCUUGGAUCGGAGUGUCACUUUCCGAGAUGAUAAUAUUAAAGGCGCACUUUGUUAGAUAUUGGGGUUUAGGCUGACUUGUCUUGGUGGGAUAAGACGAGUGCCAUCACACCCAUUUUUGGGUCGUGACAUAGAUGGACACAAACACACUAUUUUAAACAAUUGUAAUUGAAUUUUAAAAAUUUAGAAGCACCAACCUUAUCUCCUACUUUGAUGAAAGAAUCAAUAUAGUCUUGUAUUAACUCUUUAGUUGUUGAAGGAAUUACUUUAGGAGAAGGAAAAGUUAAACUACAACCUCAUAUAGCUAAAAAAGUUCU	192	spe-miR6023-3-5p	UUCCGACACAGUAUUUUUGGAU	68-89	stu-miR6023	5	0	22	22	1
spe-MIR3436-1	GGCUUGUGCACGUGACAACCUUGUUUUGGGGAUUAAAUUAAUAUGACUUGGUUUCAUAAUAGAAAUUGUUGUUGGAUUGUCAUUUACUUCCAUACUUUGUUAGAUAUUGUGUUUUAGGCUGACUUGUCUGGUGGGAUAAGACGAGUGCCAUCACACCCAUUUUUGGGUCGUGACAGUAGACCUUAGCUAUACUUAGAUAGUUUAGAUAGGUGCCCUAAAGCGCCUUAAUACGUUAGGUGGCGACUCAUUAAAUUUCAAAUCCCAAAAAAGCUUUUAGGUCGUGCACAAAAC	273	spe-miR3436-1-5p	UCACACCCAUUUUUGGGUCGUG	62-83	aly-miR3436-3p	5	0	22	22	3
spe-MIR3436-2	AGAGGCUUGUGCACGUGACAACCUGAUUUUGGGGAUUGGAUUAAUAUGACUUGGUUUCAUAAUAGGAAUUGUUGUUGGAUUGUCAUUUACUUCCGCACUUUGUUAGAUAUUUGGUUUUAGGCUGACUUGUCUUGGUGGGAUAAGACGAGUGCCAUCACACCCAUUUUUGGGUCGUGACAAAAUGGUAUCAGAGCCCCAGGUUCAUAGGUCUCACGUGUAUACAAUCCGAG	292	spe-miR3436-2-3p	UCACACCCAUUUUUGGGUCGUG	152-173	aly-miR3436-3p	5	0	22	22	3
spe-MIR3436-3	UAAUACUUUAGAGGCUUGUACACGUGAUAACCUGAUUUUGGGGGUGUUUUGAAUUGAUUAUGAAAUUUCCGCAUUUUAUUGUAAUGGUUGAAUUUUAGGCUGACUUGUCUUGGUGGGAUAAGACGAGUGCCAUCACGCCCAUUUUUGGGUCGUGACAAAAUGGUAUCAGAGCCCCAGGUUCAUAGGUCUCACGUGUACAAGUCGAGUCUAAAUAGAG	230	spe-miR3436-3-3p	UCACACCCAUUUUUGGGUCGUG	155-176	aly-miR3436-3p	5	0	22	22	3
spe-MIR1055	AAACAUGGCCAAGUGUUAUAUGGACUAGGUUCAUUAAUCACUAUUAGGUUGUGGAGCCUGAUUUAUAUAUAUAACUGUUUACGCAUUUUAACCUUCGCGGUGAGGUUGUCAGGGGGUUAUGGGGGGCGGGAGCCCCCCAUCCGAAAUGGGGGUUCGGGGCAGCCCCCCGACUUAAAUUUUAGGAUGUACCAUUUAUUCUCUGUAACAAAAAAUACUCUGAUUUAUUAAUAUAUACCCCAUCGCCAUGGAA	219	spe-miR1055-5p	UUGGGGGUGUUUUGAAUUGAUU	38-59	ppt-miR1055	5	0	22	22	1
spe-MIR12162-2	UUUAUACAAAUUUAAGUGUCUACCAACUUUGGAAAUGCACAAGUAGACACUUAAACAUGUAUAAAGUUGAAUAAGUAGACGCAUGAGUCCUAUGUGACAAAGUACACGUAGGACAAAAAAAUGAUAUGUAG	252	spe-miR12162-2-3p	AAUACUCUGAUUUAUUAAUAU	211-231	aof-miR12162	5	0	21	21	3
spe-MIR7992-19		209	spe-miR7992-19-5p	UUUGGAAAUGCACAAGUAGACACU	28-51	stu-miR7992-5p	4	0	24	24	1

spe-MIR7983-19	GACAUGUGUGUUUAUUUGUUCAACUUUAUACAA CUAUAAGUGUGCAAAUCCAAAGUUGAAAAACAU AAAUGUGAUUUG AAAAUACACUACACAAAAAAUGAUCAUUAGCGG CAAUUAAUUCUUAAUUGUCUCUAAACAUGCAUU UUUAGAGGCAAUUAACACUUUUUGUAUGUGUU CCUUAAGCCUGUAGCGACACUGGUUCUAAUGG AACUUAAUUAAUGCCGGUAAAAUGUUAGCACUC UUUAUUAACAUCAAUAUUUAUUGAUGCUAAAGU UGUUUUUGUUAUAGUGAUAUGAG UUUAAUCGAUUUUCAUUAAUGAGUUUUAAGUCU UCCGCAUUAUAUUCUGUUUAUUAUGGUUGAAA	219	spe-miR7983-19-3p	UUAAGCCUGUAGCGACACUGGUUC	101-124	stu-miR7983-5p	4	0	24	24	1
spe-MIR5165	UGUUGGGGUUUAGAUUGGUUGGUUUGCUCACA UAGUAGGAUAAGUGUGGGUGCCACUCGCGGCU CGUUUUGGGUCGUGACAAACUUGGUAUCAGAG CAUUAGGUUCGUUGGUCUCAUCACACAAGAAC GAGUCUAGUAGAGUCUUGAGGAACGGUAGGGG GACGCCUUUACUUUUCUUUGAGAAGCUAUAGG ACUUUAGGAAAAUUCCAUUCUU	279	spe-miR5165-5p	AUGUUGGGGUUUAGAUUGGUU	65-85	bdi-miR5165-5p	5	0	21	21	1
spe-MIR7834	AGAGUUGUAACAUUUACGAAGAGUGCGACUUU UAUGAAGAGGUGUAACUUUAAUGAAGAGUUGC AACUUUCAUUAAGAGUUGCAACUCUUAUAAAAA AAUUGCGACUUUUAUGAAAGAUUGUGACUUUU CCUAAGAGUCGUGACCUUCACGAUAAUGCACAA CAAG	166	spe-miR7834-3p	UAAAAAAAUUGCGACUUUUAU	92-112	ptc-miR7834	4	0	21	21	1
spe-MIR10542-9	AACUUUAAUAGAAGAAUCAUAUAUACCCCUAAA UAAUUUUUUAAAAAAAAUUAGAAGUAAUAAAUAU AAAUUUAAAACUAAUUUUUUAACUUCCAUUAAA UGAAGGGUAUAUGUGAGCCAUUUUGUAACGGC AUGGGUAUAUGUGAGCCGUUUGUAUAACGGUA AGGGCAUAUAUGAGCCACUUUUAUAACGAGGG GUAUAUCAGCUCCAAAUGACAAAGUUGAGGGG UAUAUCAGACCCUUUUCCCUUAAAUCA	255	spe-miR10542-9-5p	UAGAAGAAUCAUAUAUACCCCUA	9-31	sly-miR10542	0	0	23	23	1
spe-MIR1917-4	AACAAAAAAUGACUUUUAGCGGCAUUAAAUAUUG ACAUUAAUAAAGAGUGCUAAAGCCUUUACCGGC AUUGGUUAAGUGCCAUUAGAACCAAUGUCGCU AAAGGCUUUAGGGACAUAUACAAAGAGUGUCAA UUGCCGCUAAAUAUACAUAUUUAGC	156	spe-miR1917-4-5p	AUUAAUAAAGAGUGCUAAAGC	36-56	sly-miR1917	1	0	21	21	1

Supplementary Table S9. Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum galapagense* (Sga).

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
sga-MIR172-1	UAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUAAUUUUCUCCUAUAUAUUGGCUUUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGCAAUGAAUGGCUA	125	sga-miR172-1-3p	UGAGAAUCUUGAUGAUGCUGCAG	87-109	aau-miR172	1	0	23	23	1
sga-MIR164c	UUAUUUAAGCUGGAGAAGCAGGGCACAUGCUGAAUUACUUGAAACUUUGACCUUUCAAGAAUUUUGCAUGUGCUCUAGCUCUCCAGCUUAAU	92	sga-miR164c-5p	UGGAGAAGCAGGGCACAUGCU	11-31	fve-miR164c	0	0	21	21	1
			sga-miR164c-3p	CAUGUGCUCUAGCUCUCCAGC	67-87	bdi-miR164c-3p	4	0	21	21	1
sga-MIR319b-1	UUAGAUGUAAGUAGGAGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAU	198	sga-miR319b-1-3p	AUUGGACUGAAGGGAGCUCCU	168-188	aof-miR319b	1	0	21	21	2
sga-MIR160c	UAAGAAGGAUGUGCCUGGCUCCCUGUAUGCCACACACAUUCACCAAUUCUUUGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGCAUACCACCCGCUU	103	sga-miR160c-5p	UGCCUGGCUCCCUGUAUGCCA	12-32	aof-miR160c	0	0	21	21	1
			sga-miR160c-3p	GCGUAUAAGGAGCCAAGCAUA	73-93	aly-miR160c-3p	2	0	21	21	1
sga-MIR479-1	GAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUU	92	sga-miR479-1-5p	CGUGAUAUUGGUUUGGCUCACU	11-32	ghr-miR479	3	0	22	22	1
			sga-miR479-1-3p	UGAGCCGAACCAAUAUCACUC	62-82	aof-miR479	0	0	21	21	1
sga-MIR1918	AUUGGUUUAAUUAGUUGAAUUGUCAUUUUGUUGGUGAGAGUUCGAUUCUCCGUUACGCAAUCUCCUCUUCAAUUUAAGAGGAAAAGAUAUGCUACAAGAUGGAGAAUCGAACUACCGUUAACAGAAUGCAAGUUCAAAUACUUAAUCAA	149	sga-miR1918-5p	UGUUGGUGAGAGUUCGAUUCUC	29-50	sly-miR1918	0	0	22	22	1
sga-MIR167c-1	AUCGUGCAGCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAUCAGAUCAUGUGGCAGCCUCACCUGUCAAUGCCAUCACGA	117	sga-miR167c-1-5p	UGAAGCUGCCAGCAUGAUCUA	20-40	ata-miR167c-5p	0	0	21	21	1
			sga-miR167c-1-3p	AUCAGAUCAUGUGGCAGCCUCACC	77-100	eun-miR167c-3p	1	0	24	24	1
sga-MIR169c-1	GAAGAGGGGUUUUACAUGAAGUUGAGAGUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAGACCUUAUCUU	175	sga-miR169c-1-5p	UAGCCAAGGAUGACUUGCCUA	39-59	ata-miR169c-5p	0	0	21	21	1

sga-MIR397-1	GCAGAGUACUUAGAAACAUGAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAGUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUAUACUCGAUCAUGUUUUUAAUUCUCUG	117	sga-miR397-1-5p	AUUGAGUGCAGCGUUGAUGAC	21-41	stu-miR397-5p	0	0	21	21	1
			sga-miR397-1-3p	UCAACGCUAUACUCGAUCAUG	83-103	sly-miR397-3p	1	0	21	21	1
sga-MIR171a-1	UAUUGGUGCGGUUCAAUGAGAAAGCAGUACUUAAGAACAUUUUUGAGUCUACUUUUUGAUUGAGCCGCGCCAAUAU	76	sga-miR171a-1-5p	UAUUGGUGCGGUUCAAUGAGA	1-21	nta-miR171a	0	0	21	21	1
			sga-miR171a-1-3p	UGAUUGAGCCGCGCCAAUAU	57-76	cas-miR171a-3p	0	0	20	22	1
sga-MIR160h-1	UGCCUGGCUCCUUGUAUGCCAUUUGCAUUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAUGGCAUUCUAGGAGCUAAGCAU	81	sga-miR160h-1-5p	UGCCUGGCUCCUUGUAUGCCAUU	1-23	mes-miR160h	1	0	23	23	1
sga-MIR319a-1	AAAUAAGGAGCUCUCUCCGGUCCAGUCCGAGGCACUCAAAGGCUAAAAACACAGCUGACGACUCGUUGAUUCUCAAACAUAUCAAGAAGCAUUUUUUGAAAUUGGUGUGUUUAAAAUUCAACGAUGCGUGAGCUAUGUUUGGCUAGCGUUGUCACGUCUUGGACUGAAGGGAGCUCCCUAUUAA	184	sga-miR319a-1-3p	UUGGACUGAAGGGAGCUCCCU	159-179	aof-miR319a	0	0	21	21	1
sga-MIR169d-1	GAUGAAAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGUCUGCACCAUUUCCGAAAUGUGUCCUUUCGUUCAUGGGGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUCUUUCAUGCAAGACUUUCUCUUCU	140	sga-miR169d-1-5p	UAGCCAAGGAUGACUUGUCU	22-41	csi-miR169d-5p	1	0	20	20	1
			sga-miR169d-1-3p	GCAGGUCAUCUUUAGCUAACU	82-102	stu-miR169d-3p	0	0	21	21	1
sga-MIR172-2	AUCAUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUA	164	sga-miR172-2-3p	UGGGAAUCUUGAUGAUGCUGCAU	131-153	aau-miR172	1	0	23	23	1
sga-MIR172-3	CAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAU	164	sga-miR172-3-3p	UGGGAAUCUUGAUGAUGCUGCAU	122-144	aau-miR172	1	0	23	23	1
sga-MIR172-4	CAACACAGUUGUUGUUUGCAGAUGUAGCAUCAUCAAGAUUCAUACAUGAAAAUUAAGAGGCAAGGUUAAAUAUGUAGCUUUAAUUUGAAAUGAAAAAUAUAAUAUAUCAUGACCAUGUCUAUUUAUUUCAAAGUGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAAUAACUAUCGGUGACAGAGUCAGAA	190	sga-miR172-4-3p	UGAGAAUCUUGAUGAUGCUGCAU	134-156	aau-miR172	0	0	23	23	1
sga-MIR5300	UGACCAAAAUUCUUCUUCCCCAGUCCAGGCAUUCCAACAGUUGAUAACAUCUAGAUCUGCCAAUACUUUGUAUUU	264	sga-miR5300-5p	UCCCCAGUCCAGGCAUUCCAAC	17-38	sly-miR5300	0	0	22	22	1

sga-MIR482e	UUGUUCUUCUAUUUUUCACAUGACA UCUUCAAAAUCUACUAUGAGCUUCA UCAUAAGCUAAGAAAUGGUGAGUUU UGAUGAUGUGAUGCCUAAAAUAGGA UUAAAUGAAAGUACUAGUAAAAAGG UGUUCAGAUCUGGAGGUUAUGUUAA GCUGGUGGUAUGCUUUGAUUGGGA AAGAUGACUUAGGUC AGAUCUGUGCUAUGGAAAUAUUGAU GGCGUUGAAAGGGAUGAGAGUAUU GGGAAGUUGUUGGUUGUGGGUGGG GUGGAAAGAUUUGAUAAAUCUAAUU UUAAAGAGAUUAAAUCUUUCCUACU CCUCCCAUACCCAUGACUUCCACUA GCUUCUCCCUUUCUUCAUUUGUCAU CUCCUUUGCUAAGUUC	189	sga-miR482e-5p	UGUGGGUGGGGUGGAAAGAUU	64-84	sly-miR482e-5p	0	0	21	21	1
			sga-miR482e-3p	UCUUUCCUACUCCUCCCAUACC	113-134	sly-miR482e-3p	0	0	22	22	1
sga-MIR5304	UCUAAUUUAGAUCCAUGGUGCAGUU UGCUCAUUCAAUGCUACAUACUCAU CCCCACAACUUUCAUCUCACGUUCA AAGAUGAAAGUUAUAGAGAUGAGUA UGGUGCAUUGGAUGUGUGGCCAUA CCAUGGGUGAUGUUAG	140	sga-miR5304-5p	UCAAUGCUACAUACUCAUCCC	33-53	sly-miR5304	0	0	21	21	1
			sga-miR5304-3p	AGAUGAGUAUGGUGCAUUGGA	92-112	stu-miR5304-3p	0	0	21	21	1
sga-MIR319a-2	UGGUAUAAGAGAGCUUCCUUUAGUC CACUCAUAGGUAGACGAAGGAUUUG AAUUAUCUCCCGACUCAUUCAUUCA AACGCAAUAGGAAGUAUGUAAUCUU AUACUAUUGUGAAUGUGUGAAUGAU GCGGGAGAUAAAUUCUCUCCUUUUU AUCUGUGCUUGGACUGAAGGGAGC UCCCUUUUACC	185	sga-miR319a-2-5p	AGAGCUUCCUUUAGUCCACUC	10-30	mtr-miR319a-5p	1	0	21	21	1
			sga-miR319a-2-3p	UUGGACUGAAGGGAGCUCCCU	159-179	aof-miR319a	0	0	21	21	1
sga-MIR396b-1	AUGGUCCUUUUUGUGUUUUUCCACA GCUUUCUUGAACUGCAUCUACAAUU UCAAUUCAUUAUUGAAAAAGAAAAAA UUGAUUCAUAUUGUUGUUGCGGUUC AAUAAAGCUGUGGGAAGAUACAGAU AGGGUCA	133	sga-miR396b-1-5p	UUCCACAGCUUUCUUGAACUG	19-39	aof-miR396b	0	0	21	21	1
			sga-miR396b-1-3p	GUUCAAUAAAGCUGUGGGAAG	98-118	csi-miR396b-3p	0	0	21	21	1
sga-MIR156i	CAAAAAGAGGUGACAGAAGAGCGUG AGCACAUGUGUGUUUUCUAGCAUGA UGUUUAUAUGCUUGAAUCUAUGCGU GCUCACUGCUCUAUCUUUCAUCCUC AUCG	104	sga-miR156i-5p	UGACAGAAGAGCGUGAGCAC	11-30	stu-miR156i-5p	1	0	20	20	1
			sga-miR156i-3p	GCUCACUGCUCUAUCUUUCAUC	76-97	zma-miR156i-3p	1	0	22	22	1
sga-MIR171a-2	GAUCAACUUGCGAUGUUGGUGUGG UUCAAUUAGAUAACAAUCUCCACGU AAAAUUAUAGAGUUUGUUAUUUGAU UGAGCCGUGCCAAUAUCACAUGUAA AGAAAAUAA	108	sga-miR171a-2-3p	UGAUUGAGCCGUGCCAAUAUC	71-91	aof-miR171a	0	0	21	21	1
sga-MIR6022	AUACCAUCCUGGAUAUUCUCCCUUC CAUCACUAAGUUAUUUAGACCGAGU	236	sga-miR6022-3p	UGGAAAGGAUAAUAUCCAGGA	197-217	sly-miR6022	2	0	21	21	1

sga-MIR5303f-1	UUUAACCAAUUGCACGGUCCUCUAC CCAAGAUUGAGGUUUCGUAAAAUGU AACUUAAGAUCAAGUCGCGUUAGGU UCAUGAAGUUUUGAAUUGACUUAGG AAGAGUACCUUGCAACUUAAAACUU UGAGCCGAAAUAAGUUAGUGAUGGA AAGGAUAAUAUCCAGGAUCGUAUUG UUCCGUUCAGG AAGCAACAAUCUCUGUUCAUAUUCC AUGAGACUGUUUUUGGGUAAGAUUG UUUAUCAUAAUAAUCAUAAAUACUAG AUGACCGUGCUUGUUGUCUAUGUU GCUCGGACUCUUUAAUAAUUUCAAU GGAUGCGUGUUGGAUUCACCAAAAG UAGUGUAUUUUUGGAGAAUUCGACA CGGGCGCGACAUCGGUAAGUGAAUA GUCCGCGCAACAAGUAGGUCCCUCG UCAAGUGUUUGU	237	sga-miR5303f-1-3p	AUUUUUGGAGAAUUCGACACGGGC	157-180	stu-miR5303f	3	0	24	24	1
sga-MIR6024	UAACUGGAAAUGGGGAAGUGGAGAA ACAACACUUGCUAAAGGAAGUUCAC CUGUCAUCUCUUUUCUUUUGGAGUU UUUUUAGCAAGAGUUGUUUUACCUC UUCUCAAUUCCGUCUCUC	118	sga-miR6024-5p	AGAAACAACACUUGCUAAAGGA	22-43	stu-miR6024-5p	1	0	22	22	1
			sga-miR6024-3p	UUUUAGCAAGAGUUGUUUUACC	77-98	sly-miR6024	0	0	22	22	1
sga-MIR482c-1	GAGUUUUUCGAAAAUCUAUGGGGAU UGGUGAGUUGGAAAGCUUUUCUUUU UCUUCUCUUGUGAUUAGCUUUCCAA UUCCACCCAUUCCUAUGGUUUUUCG GUAUUCUCU	109	sga-miR482c-1-3p	UUUCCAAUUCCACCCAUUCCUA	69-90	nta-miR482c	0	0	22	22	1
sga-MIR482b-1	GGAAAGGGAUGAAGAUUUUUGGGAA GCUUUUGGCGUGAGCGGUGGGGAA AGAUAGAUCUAUCAUAUUAGUAUGA UAUGAUAAAUCUUGCCUACACCGCC CAUGCCCAUGGCUUCCAAUGAUUUC AUUUUUCAGGAAGCUUUUGGAGUGG	124	sga-miR482b-1-3p	UCUUGCCUACACCGCCCAUGCC	84-105	sly-miR482b	0	0	22	22	1
sga-MIR482b-2	GUGGCAUGGUAAGAUAUCAUAUCUU GUUUUUCAUAAAAAAAAAAUGAAAUU GAAAUCUUACCGAUUCCCCCCAUUC CAAUGGCUUC	111	sga-miR482b-2-5p	GGAGUGGGUGGCAUGGUAAGA	19-39	stu-miR482b-5p	0	0	21	21	1
			sga-miR482b-2-3p	UUACCGAUUCCCCCCAUUCCAA	83-104	stu-miR482b-3p	0	0	22	22	1
sga-MIR6025b-1	UUGUAUAGUUAUUUCAUCUACACUU GCACAAAAAUAUUAUUGAACCUUGA UGUUAUCUCAGUGUUGGCAUGCAUA AAUUGGGUAAAUUUAUGAUUGAAUG UGUAUUUUGGUGUUGUACCAAAUCC AGGCAUGCCAACUAUUGGGAUGGCA UCUCGGUUUGUUAG	164	sga-miR6025b-1-3p	UGCCAACUAUUGGGAUGGCAUC	131-152	nta-miR6025b	2	0	22	22	1
sga-MIR6025b-2	AAAAAUAUUAUUGAACCUUGAUGUU AUCUCAGUGUUGGCAUGCAUAAAUU GGGUAAAUUUAUGAUUGAAUGUGUA UUUUGGUGUUGUACCAAAUCCAGGC AUGCCAACUAUUGGGAUGGCAUCUC GGUUUGUUAGUUGCUGUGCAGUAU GAUCACUGUGGCAGG	164	sga-miR6025b-2-3p	UGCCAACUAUUGGGAUGGCAUC	102-123	nta-miR6025b	2	0	22	22	1
sga-MIR403-1	CAGGAAGAGGCAUAUUUCACGUUUG UGCGUGAAUCUAACAACUCUUUUCA	105	sga-miR403-1-5p	CGUUUGUGCGUGAAUCUAACA	20-40	sly-miR403-5p	0	0	21	21	1

	UCAGAAAAACUGUUAUUGUUUGCUAGAUUCACGCACAAGCUCGUAAUAUGGCUUU		sga-miR403-1-3p	CUAGAUUCACGCACAAGCUCG	73-93	sly-miR403-3p	0	0	21	21	1
sga-MIR319a-3	AAGAGAGCUUUCUUUAGUCCACACAUGGGGAACGAUAGGGUUCAAUUUGCUGCCGACUCAUUCAUCCAAAUGUUGAGGUCUUGAUAAUCGAGUGCCACCUCAGCAACUGAGUGAAUGAAGCGGGAGUACAAGUUGAGUCUUGAGCUUCCUAUACUUGGACUGAAGGGAGCUCCCU	175	sga-miR319a-3-5p	AGAGCUUUCUUUAGUCCACAC	4-24	stu-miR319a-5p	2	0	21	21	1
			sga-miR319a-3-3p	UUGGACUGAAGGGAGCUCCCU	155-175	aof-miR319a	0	0	21	21	1
sga-MIR172b	UUGUUUAGUCGUUUAUUGCUAAUGCAGCAUCAUCAAGAUUCACAUUUAAUUGCAUUUUAAAUGUCAGAAUAUUUGAGAAUCUUAAUAGUGCUGCAUUUGCAAACAACGACUGUGUAC	117	sga-miR172b-5p	GCAGCAUCAUCAAGAUUCACA	24-44	csi-miR172b-5p	0	0	21	21	1
			sga-miR172b-3p	AGAAUCUUAAUAGUGCUGCAU	76-96	csi-miR172b-3p	3	0	21	21	1
sga-MIR172-5	UGAAACGAUACAGAGAAAAUAGAAUUUUUGAAUUUGAAUCAGGCUUAUCGAUCAAUCGAAUAAUCAACACAGUUGUUGUUUGCAGAUGUAGCAUCAUCAAGAUUCAUACAUGAAAAUUAAGAGGCAAGGUUAAAUAUGUAGCUUUAAUUUGAAAUGAAAAAUAUAAUAUAUCAUGACCAUGUCUAUUUAUUUCAAAGUGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAAUAACUAUCGGUGACAGAG	248	sga-miR172-5-3p	UGAGAAUCUUGAUGAUGCUGCAU	198-220	aau-miR172	0	0	23	23	1
sga-MIR397-2	UUAGAAACAUGAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAGUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUAUACUCGAUCAUGUUUUUAAUUCUCUGAAGGGACAUUUUAU	122	sga-miR397-2-5p	AUUGAGUGCAGCGUUGAUGAC	12-32	stu-miR397-5p	0	0	21	21	1
			sga-miR397-2-3p	UCAACGCUAUACUCGAUCAUG	74-94	sly-miR397-3p	1	0	21	21	1
sga-MIR477b	GUCUUUUUUCACUCUCCCUCAAAGGCUUCUGGCUUAAAAUGCCUUUUGUGCUAAUGCUAGAGGUCUUUCGAGUGAGAGUGAAUAAAUUCU	90	sga-miR477b-5p	ACUCUCCCUCAAAGGCUUCUG	11-31	stu-miR477b-5p	0	0	21	21	1
			sga-miR477b-3p	GAGGUCUUUCGAGUGAGAGUGA	60-81	stu-miR477b-3p	0	0	22	22	1
sga-MIR477-1	GCAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAACAAGAAAUUCCUUGCUCACUUCACAUGGCAACAUACUUAUA	134	sga-miR477-1-5p	UGUCUCUCCCUCAAGGGCUCC	12-32	sly-miR477-5p	0	0	21	21	1
			sga-miR477-1-3p	AGUUCUUGUAGGGUGAGACAAC	73-94	sly-miR477-3p	0	0	22	22	1
sga-MIR1919-1	UCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCUUUUAUGGAACCACACUUUCUCUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUUUUUCAUC	149	sga-miR1919-1-5p	UGUCGCAGAUGACUUUCGCCC	12-32	stu-miR1919-5p	0	0	21	21	1
			sga-miR1919-1-3p	ACGAGAGUCAUCUGUGACAGG	78-98	stu-miR1919-3p	0	0	21	21	1
sga-MIR1446	CAGAGUUUUCUGAACUCUCUCCCUCAAUGGCUGUUCAUAUAAUAUAUGCUGCUACUUUGCAGCUUAAUUAAAUAA	108	sga-miR1446-5p	UGAACUCUCUCCCUCAAUGGCU	11-32	nta-miR1446	0	0	22	22	1

sga-MIR169a	CAGCUUUGGGGGUUUGAGUCCAGAAAACUCUUGUUGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGAGUGGAGUGCAGCCAAGGAUGACUUGCCGAGAUGUUGUAGCCUAAUGCAAUGACAUAUCGGCAGGUCAUCUUUGGCUACAUUUUAUUCUCUCCUAUUCAUGUAAAACUUUAUAGACGUAUAUGUAU	159	sga-miR169a-5p	CAGCCAAGGAUGACUUGCCGA	43-63	cas-miR169a	0	0	21	21	1
sga-MIR394b	GAUGAAGAAAAAAAAUAUGAAGAUUAAUUAGUUUCACGGAGGUUUGACAAAGGGUUUCUUACAGAGUUCAUUGGCAUUCUGUCCACCUCCCUCGUUCUUUUUUCGAGAAAAAAAGAAGAAGGGGGGAAGCAAGAUUUAGUGUGGAGGUGGGCAUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUUGUAAAACCCUCGUGAUACACGUCAAGUAAGAUAGAGAGUGAUUUGAUC	233	sga-miR394b-5p	UUGGCAUUCUGUCCACCUCC	71-90	csi-miR394b-5p	0	0	20	20	1
			sga-miR394b-3p	AGGUGGGCAUACUGCCAAUAG	145-165	ath-miR394b-3p	0	0	21	21	1
sga-MIR166-1	AUAUUGUUGAGGAGAAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUGUAUCGUGAAUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUG	120	sga-miR166-1-3p	AUUUCGGACCAGGCUUCAUUCCCC	88-111	lja-miR166-3p	0	0	24	24	1
sga-MIR171a-3	UCAUACGAGAUGUUGGUGCGGUUCAAUGAGAAAGAAGUUGUUGAAUAAAUUUUUGACCCUACUUUUUGAUUGAGCCGUGCCAAUAUCACGUGUCACUAU	99	sga-miR171a-3-5p	UGUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	1	0	21	21	1
			sga-miR171a-3-3p	UGAUUGAGCCGUGCCAAUAUC	67-87	aof-miR171a	0	0	21	21	1
sga-MIR160g	AUUGUUCUGCCUGGCUCCCUGGAUGCCAACUAAGAACAGUAUUGUCAAAAAAUUGACACUCUUCCUAGUUGGUACCAGAGGAGACAGGCAGAUCCA	97	sga-miR160g-5p	UGCCUGGCUCCCUGGAUGCCA	8-28	lus-miR160g	0	0	21	21	1
sga-MIR164e-1	ACUCAUGUUGGAGAAGCAGGGCACGUGCAAAUUCUUGUAUUCGACGAUAUAUGCAUUACUAAUGGUAAUGCAUGAAUUUUGCACGUGUUCU	91	sga-miR164e-1-5p	UGGAGAAGCAGGGCACGUGCAA	9-30	bra-miR164e-5p	0	0	22	22	1
sga-MIR171c-1	CUAACGAGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCACGUAU	91	sga-miR171c-1-5p	AGAUAUUGGUGCGGUUCAAUU	7-27	cas-miR171c-5p	1	0	21	21	1
			sga-miR171c-1-3p	UUGAGCCGUGCCAAUAUCACG	68-88	cas-miR171c-3p	0	0	21	21	1
sga-MIR172-6	UUGCAGAUGCAGCAUCUUCAAGAUUCACAUAGAUUUAUAUAAAAUAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUAAUUUUCUCCUAUAUAUUGGCUUUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGCAAUGAAUGGCU	168	sga-miR172-6-3p	UGAGAAUCUUGAUGAUGCUGCAG	131-153	aau-miR172	1	0	23	23	1
sga-MIR394-1	AGUGUAGAGCCAUUUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAACUAGCUCUGCAGCUCUCUCUC	94	sga-miR394-1-5p	UUUGGCAUUCUGUCCACCUCC	14-34	cas-miR394	0	0	21	21	1
sga-MIR396f	UAGUCAUGCUUUUCCACAGCUUUCUUGAACUUCUUCUUGCUAAAUUUUGA	122	sga-miR396f-5p	UUCCACAGCUUUCUUGAACUU	12-32	csi-miR396f-5p	0	0	21	21	1

	UCUCUAAAUUGAUAAUUUUGAGAUG AGAUUUGAAGCUAUGAAAGUCCAAG AAAGCUGUGGGAAAAGAUGGCA		sga-miR396f-3p	AAAGUCCAAGAAAGCUGUGGGAAA	91-114	osa-miR396f-3p	6	0	24	24	1
sga-MIR403-2	AAAUUGAAAAUCAGGAAGAGGCAUA UUUCACGUUUGUGCGUGAAUCUAAC AACUCUUUUCAUCAGAAAAACUGUU AUUGUUUGCUAGAUUCACGCACAAG CUCGUAAUAUGGCUUUUCCAAUCUC UGCGCUUUGAUUUCUCCAAUUGGUG UGAC	154	sga-miR403-2-5p	CGUUUGUGCGUGAAUCUAACA	31-51	sly-miR403-5p	0	0	21	21	1
			sga-miR403-2-3p	CUAGAUUCACGCACAAGCUCG	84-104	sly-miR403-3p	0	0	21	21	1
sga-MIR168c-1	CCUCUUAUUCGCUUGGUGCAGGUC GGGACCUCAUUCGCCAGCGCCGGG AAUAAUGCCGGACGAACGACGGCGG UGUUAAUUCUACUAAAGCUGUCACC GACGAAUGUAUGUUUGAUUAGCGGC GAAAUUUGGGUCCUGCCUUGCAUCA ACUGAAUUGGAG	160	sga-miR168c-1-5p	UCGCUUGGUGCAGGUCGGGAC	9-29	bra-miR168c-5p	0	0	21	21	1
			sga-miR168c-1-3p	CCUGCCUUGCAUCAACUGAAU	135-155	bra-miR168c-3p	1	0	21	21	1
sga-MIR479-2	UGGAGAAGAAGACAUGGCGUGAUAU UGGUUUGGCUCACUAAUUUCUGAUU CGCGAAACAGAUAAGAGAUGAGCCG AACCAAUAUCACUCUUGUAUUCUUC UUCAU	105	sga-miR479-2-5p	CGUGAUAUUGGUUUGGCUCACU	18-39	ghr-miR479	3	0	22	22	1
			sga-miR479-2-3p	UGAGCCGAACCAAUAUCACUC	69-89	aof-miR479	0	0	21	21	1
sga-MIR7984b-1	AUAUCAAACUUUAUGGAGGACCUGU UACCCCCUGCACUAUUUAAUAAUGU AUUUUAAAAGUAUAUAUGUGUCCAC AUGGACACAUUACUAUUUAUAAUGA UGCAAUGUGUAUGAUGUCCACGUGG ACACAUAUAUACCUUUAAAAUACACU AUUAAAUAUUGCAUGGGGAUAAAAG GUCCUUUUCAAAAUUUGAUAUU	198	sga-miR7984b-1-3p	GGUCCUUUUCAAAAUUUGAUAUU	176-198	stu-miR7984b-3p	6	0	23	24	1
sga-MIR7990a-1	UGCAAAAGUUAUGACCAUUUGAAGU GUCACAAAUUUACAACUACUUUUUU UGAGUUAUACUCUUUAAUUUGGUGA AACUUCAAAUGAUCGUAACUUUGGC CU	102	sga-miR7990a-1-3p	UUCAAAUGAUCGUAACUUUGGCCU	79-102	stu-miR7990a	0	0	24	24	1
sga-MIR8009-1	UGUCCGUCACUUUUCAGGGAUUUUG AAAAUAAAAUUUCCAGAAAAGCGAUG GACAG	56	sga-miR8009-1-3p	AUUUCCAGAAAAGCGAUGGACAG	34-56	stu-miR8009	1	0	23	24	1
sga-MIR319d	AGGAAACUGUUUAGUCCAACCCAAG GUGGGGUAUUGGAACUGAUCUUUG CUGCUGAAUCAUUGGCUCAUGAGCA UGUCAAAGAAGAUGAUUGAACAUUC UGGACAUGUUCUUGCUCCAAUGAUG CAGGAGCUGAGCUCGGUUUUUCACC GCCUUUUCUUGGACUGAAGGGUUU CCUU	177	sga-miR319d-5p	AGGAAACUGUUUAGUCCAACC	1-21	sly-miR319d	0	0	21	21	1
			sga-miR319d-3p	CUUGGACUGAAGGGUUUCCUU	157-177	ppt-miR319d-3p	6	0	21	21	1
sga-MIR8042	GAUAAGCACUUCCAUCUAAUUUCUA AAAGGUGGUCAAGGGAACGAGGUG	104	sga-miR8042-3p	AUUAGACUGAAAUGCUGAUCU	84-104	stu-miR8042	1	0	21	21	1

sga-MIR7122	GUGAAACACAUGUAACUUGACACAACUUUCAGAAAUUAGACUGAAAUGCUGAUCUUAUAUACAGAGAAACCGCUGUCGAUUAUAAUGAGAAAUUCGGUGUUUCUCAUACUCCACAGCGUUUUUCUGUAUAACC	78	sga-miR7122-5p	AUAUACAGAGAAACCGCUGUCG	2-23	stu-miR7122-5p	1	0	22	22	2
			sga-miR7122-3p	ACAGCGUUUUUCUGUAUAACC	58-78	stu-miR7122-3p	1	0	21	21	1
sga-MIR171m	AGAUAUUGAUGCGGUUCAAUCUGAAAGACAUGGUUAGAUAUGUAAUUAGCCUUGUAAUUUUGGAUUGAGCCGCGUCAAUAUCUC	84	sga-miR171m-3p	GGAUUGAGCCGCGUCAAUAUC	62-82	zma-miR171m-3p	0	0	21	21	1
sga-MIR171a-4	AUAUUGGCCUGGUUCACUCAGACAACAAAAUGUAAACUAUAUUUGAAUGGUUGAGUUUUUGUUUUUCGUUUGAUUGAGCCGUGCCAAUAUC	91	sga-miR171a-4-5p	UAUUGGCCUGGUUCACUCAGA	2-22	cas-miR171a-5p	0	0	21	21	1
			sga-miR171a-4-3p	UGAUUGAGCCGUGCCAAUAUC	71-91	aof-miR171a	0	0	21	21	1
sga-MIR827-1	GUUUGUUGAUGGUCAUCUAUUCAUCAUAUCAUUUGGCAUAGUUUUUGGAACCAUUAAUAUGCCAUGAUUAGAUGAACAUCAACAAACA	88	sga-miR827-1-5p	UUUGUUGAUGGUCAUCUAUUC	2-22	stu-miR827-5p	0	0	21	21	1
			sga-miR827-1-3p	UUAGAUGAACAUCAACAAACA	68-88	sly-miR827	0	0	21	21	1
sga-MIR172c	UGGAGCAUCAUCAAGAUUCACAUAGCUAUAUUAGGGAUUUUAUAAUUUUUAAAAACCCUAUGGGCGAUGUGUGGGAAUCUUGAUGAUGCUGCAG	94	sga-miR172c-5p	GGAGCAUCAUCAAGAUUCACA	2-22	cas-miR172c	0	0	21	21	1
			sga-miR172c-3p	GGGAAUCUUGAUGAUGCUGCAG	73-94	csi-miR172c-3p	1	0	22	22	2
sga-MIR156b-1	UUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUC	101	sga-miR156b-1-5p	UUGACAGAAGAUAGAGAGCAC	1-21	aof-miR156b	0	0	21	21	1
			sga-miR156b-1-3p	GCUCUCUAUGCUUCUGUCAUC	81-101	vca-miR156b-3p	0	0	21	21	1
sga-MIR171d	AGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCAC	81	sga-miR171d-5p	AGAUAUUGGUGCGGUUCAAUU	1-21	stu-miR171d-5p	0	0	21	21	1
			sga-miR171d-3p	UUGAGCCGUGCCAAUAUCAC	62-81	stu-miR171d-3p	0	0	20	21	1
sga-MIR167b-1	UGAAGCUGCCAGCAUGAUCUAAACUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGAUCAUGUGGUUGCUUCAC	74	sga-miR167b-1-5p	UGAAGCUGCCAGCAUGAUCUAA	1-22	bna-miR167b	0	0	22	22	1
			sga-miR167b-1-3p	UCAGAUCAUGUGGUUGCUUCA	53-73	gra-miR167b	4	0	21	21	1
sga-MIR171h-1	GUGAUAUUGGUUCGGCUCAUCUCUUAUCUGUUUCGCGAAUCAGAAAUUAGUGAGCCAAACCAAUAUCACG	70	sga-miR171h-1-5p	UGAUAUUGGUUCGGCUCAUCU	2-22	zma-miR171h-5p	3	0	21	21	1
			sga-miR171h-1-3p	GUGAGCCAAACCAAUAUCACG	50-70	zma-miR171h-3p	2	0	21	21	1
sga-MIR393b-1	UUCCAAAGGGAUCGCAUUGAUCCUGUGUUCCAAAUUAAUUAACCAUGGGACUAUGGGAUCAUGCGAUCUCUUCGGAAU	78	sga-miR393b-1-5p	UUCCAAAGGGAUCGCAUUGAUC	1-22	csi-miR393b-5p	0	0	22	22	1
			sga-miR393b-1-3p	UCAUGCGAUCUCUUCGGAAU	59-78	csi-miR393b-3p	1	0	20	21	1
sga-MIR477a-1	CCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUAUGUUGGGAAAGAAGCUCUAGCAGGGAGAGCC	68	sga-miR477a-1-5p	CCUCUCCCUCAAGGGCUUCUC	1-21	stu-miR477a-5p	0	0	21	21	1
			sga-miR477a-1-3p	GAAGCUCUAGCAGGGAGAGCC	48-68	stu-miR477a-3p	0	0	21	22	1
sga-	ACAAGGACGAGGCAGCGCAUGAGAU	72	sga-miR408-1-5p	CAAGGACGAGGCAGCGCAUGA	2-22	lja-miR408	4	0	21	21	1

MIR408-1	GUACAAUUUUAUUAGUUGUCCAUUC CAUGCACAGCCUCUUCCCUGGC										
			sga-miR408-1-3p	AUGCACAGCCUCUUCCCUGGC	52-72	cas-miR408	1	0	21	21	1
sga-MIR156b-2	GUGACAGAAGAGAGUGAGCACACAU GGUUCUUUCAUGGAUUAUUCCCCAU GUUUAAAAGCUCUGCGUGCUCACGC UCUAUCUGUCACA	88	sga-miR156b-2-5p	UGACAGAAGAGAGUGAGCACA	2-22	hvu-miR156b	0	0	21	21	1
			sga-miR156b-2-3p	UGCUCACGCUCUAUCUGUCACA	67-88	mtr-miR156b-3p	2	0	22	22	1
sga-MIR394-2	UUUGGCAUUCUGUCCACCUCCCAGC UUGCUGAGGACUGAGGAGGGGGCC AAAGUGCCAAAC	61	sga-miR394-2-5p	UUUGGCAUUCUGUCCACCUCC	1-21	cas-miR394	0	0	21	21	1
sga-MIR167c-2	UUACAUCGUGCAGCACUAGCAGUUG AAGCUGCCAGCAUGAUCUAAACUUU CCUUUUAGUUCAAAUAUAAUUCGAG GAAAGAUCAGAUCAUGUGGCAGCCU CACCUGUCAAUG	112	sga-miR167c-2-5p	UGAAGCUGCCAGCAUGAUCUA	24-44	ata-miR167c-5p	0	0	21	21	1
			sga-miR167c-2-3p	AUCAGAUCAUGUGGCAGCCUCACC	81-104	eun-miR167c-3p	1	0	24	24	1
sga-MIR169r-1	UUAGUCUAUGAGGUUUGCAUGAAGA UGUAGAGAGUGAAGUUGCAGCCAAG GAUGACUUGCCGGACCAUAAAUUGC UAGGGUUUUAUAGUUUCGGCAAGUU GUUCUUGGCUAUAGUUUGCUCUCUU CUUCUCAUGUCAUCCUCGUUAGAC	149	sga-miR169r-1-5p	CAGCCAAGGAUGACUUGCCGG	43-63	csi-miR169r-5p	0	0	21	21	1
sga-MIR169c-2	GGAAGAGAGGUCUUACAUGAAAAGA AAAACCUUUGUUAAUUAGCCAAGGA UGACUUGCCUAAUGUACCCACUAUU UAUUUUCCUCCUAUUUUUUAUGGAG UAUUUAAUAGUAUACUAGGCAGUCG UCUUUAGCUAUAUUGACACAUUUUU CUUUAUCAUGCUAGUUCUCUUCUUC CCAUUUAUAUUAAUCUCAUCUCGGA UUU	203	sga-miR169c-2-5p	UAGCCAAGGAUGACUUGCCUA	41-61	ata-miR169c-5p	0	0	21	21	1
sga-MIR172-7	UCUUACAGUCGUUGUUUGCAUAUGU GGCAUAAUCAAGAUUCAAGUGAAAA GUUGCAAAUUGGUUAUAUAAUUGAU GAAAUUAAUGGCUGGCUAUUUGAAA CUCACGAGAAUCUUGAUGAUGCUGC AUCAGCAAUAAAUGACU	142	sga-miR172-7-3p	CGAGAAUCUUGAUGAUGCUGCAU	105-127	aau-miR172	1	0	23	23	2
sga-MIR395a-1	UAUAUCAAGGUAUUCUCGAGAGUUC CCUUGACCACUUCAUGAGGGAUUAA UAUCUUUAUUUUUGAUGCCCUACUA AAGUGUUUGGGGGAACUCUUGGGU UCACUUUGAAGUAU	113	sga-miR395a-1-3p	UAAAGUGUUUGGGGGAACUCU	74-94	aof-miR395a	1	0	21	21	1
sga-MIR2111d	AUGGUAAUCUGCAUCCUGAGGUUUA GAUCAAUUUAUAACUUACUGGAUCU AGUCCUUGGGAUGCAGAUUAUCU	73	sga-miR2111d-5p	UAAUCUGCAUCCUGAGGUUUA	5-25	ppe-miR2111d	0	0	21	21	1
			sga-miR2111d-3p	GUCCUUGGGAUGCAGAUUAUC	52-72	gma-miR2111d	2	0	21	21	1
sga-MIR319b-2	AGCUCCUUUCAGGCCAAGACCGAGG GACGAGGAGCGGCAAGAGCUGCCUA GUCAUGCAUAUUGGUUAACCUUAAC AAACAAAUUAUGUAUAGUGUUAAGA UUAACCAGUUGCAUGGCAAGGGAGC AACUACUUCCGCUAACUUGUCUCAC UUAUUGGACUGAAGGGAGCUCCUAU CCAUUUAUAUAUAGUUAAGUUAACU AUAUAAAAUAU	211	sga-miR319b-2-3p	AUUGGACUGAAGGGAGCUCCU	153-173	aof-miR319b	1	0	21	21	2

sga-MIR319c	AAGAGAGCUUCCUUCAGCCCACUCACGGAGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCCUUGCUUGGACUGAAGGGAGCUCCCUU	176	sga-miR319c-5p	AGAGCUUCCUUCAGCCCACUC	4-24	sly-miR319c-5p	0	0	21	21	1
			sga-miR319c-3p	UUGGACUGAAGGGAGCUCCUU	156-176	sly-miR319c-3p	0	0	21	21	1
sga-MIR164-1	AUCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUGA	173	sga-miR164-1-5p	UGGAGAAGCAGGGCACGUGCA	8-28	aof-miR164	0	0	21	21	1
sga-MIR164e-2	GUUGGAGAAGCAGGGCACGUGCAAAUUCUUGUAUUCGACGAUAUAUGCAUUACUAAUGGUAAUGCAUGAAUUUUGCACGUGUUCUCCUUCUCCAA	95	sga-miR164e-2-5p	UGGAGAAGCAGGGCACGUGCAA	3-24	bra-miR164e-5p	0	0	22	22	1
			sga-miR164e-2-3p	CACGUGUUCUCCUUCUCCAA	76-95	bra-miR164e-3p	3	0	20	21	1
sga-MIR172-8	UGGUGGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUUCAAAAAUGAGAAUCUUGAUGAUGCUGCAUCGACAAAUU	163	sga-miR172-8-3p	UGAGAAUCUUGAUGAUGCUGCAU	132-154	aau-miR172	0	0	23	23	1
sga-MIR403-3	AGAAAUUGAAAAUCAGGAAGAGGCAUAUUUCACGUUUGUGCGUGAAUCUAACACAACUCUUUUCAUCAGAAAAACUGUUAUUGUUUGCUAGAUUCACGCACAAGCUCGUAAUAUGGCUUUUCCAAUCUCUGCGCUUUGAUUUC	141	sga-miR403-3-5p	CGUUUGUGCGUGAAUCUAACA	33-53	sly-miR403-5p	0	0	21	21	1
			sga-miR403-3-3p	CUAGAUUCACGCACAAGCUCG	86-106	sly-miR403-3p	0	0	21	21	1
sga-MIR9471a-1	GGAUCAUUGACGGAUUUGGGGUUCUGAGAUUCAGUUGAUUUCUCAGGUGCUCACUCAGCUAAUAGUUAUUAUUUAAGAAACUCAAUAAUAUUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUGAGUGAGCAUCACUGAAAUCGACAUGAUUCUGAGAGGAAAAUGACU	182	sga-miR9471a-1-5p	CAGGUGCUCACUCAGCUAAUA	44-64	sly-miR9471a-5p	0	0	21	21	1
			sga-miR9471a-1-3p	UUGGCUGAGUGAGCAUCACUG	131-151	sly-miR9471a-3p	1	0	21	21	1
sga-MIR9472	AUGGGUUUCAAUUAUAGCUACAGAUCUUCCCAUAGAUCUACUCGAUUUAUUUUUCAGUAGACGUUGUGAAUAAUUGAUAAAUACAAGUAUACAGAGGUCUUAAUAUAGUCAGAACCUAGAAAUAUGUGUAACUAGAUUCAGACCUUUGUACACUUGUAUUCUGUUGCUAUUCACAAUCUCUGCUGAAAAAUGAUUGACUAGAUCUACGAAUAAUCUAGAUUAUUAAUGCCCG	232	sga-miR9472-5p	UUUCAGUAGACGUUGUGAAUA	52-72	sly-miR9472-5p	0	0	21	21	1

			sga-miR9472-3p	UUCACAAUCUCUGCUGAAAAA	170-190	sly-miR9472-3p	0	0	21	21	1
sga-MIR482d-1	GGAAAGGGAGGAGGGAUUUGGGAA UCUUUUGGAGUGGGUGGGAUGGAA AAAUAUUGUAUUUUUUUUUCUAACG GAAAAAAAGAUGAGAAUUGAGAUUU UUCCUAUUCCACCCAUGCCAAUGGC UUCCAGUCAUUUACUCCUUUUC	145	sga-miR482d-1-5p	GGAGUGGGUGGGAUGGAAAAA	31-51	sly-miR482d-5p	0	0	21	21	1
			sga-miR482d-1-3p	UUUCCUAUUCCACCCAUGCCAA	98-119	sly-miR482d-3p	0	0	22	22	1
sga-MIR9473-1	UAGCAGAUAUUGGCUGUAAAUCUAA ACUCGUUUCACUCCACUAGUCAUCA UGUAAUGUCAUUUACUAGAAGAAGA GACUAUUGGGGUAAAACGAGUUCAG AUUUACAGCCAAUAUUGU	118	sga-miR9473-1-5p	UGGCUGUAAAUCUAAACUCGU	11-31	sly-miR9473-5p	0	0	21	21	1
			sga-miR9473-1-3p	AAACGAGUUCAGAUUUACAGC	89-109	sly-miR9473-3p	0	0	21	21	1
sga-MIR9473-2	CAAAACAAUAUUGGCUGUAAAUCUG AACUCGUUUUACCCCAAUAGUCUCU UCUUCUAGUAAAUGACAUUACAUGA UGACUAGUGGAGUGAAACGAGUUUA GAUUUACAGCCAAUAUCUGC	120	sga-miR9473-2-5p	UGGCUGUAAAUCUGAACUCGU	12-32	sly-miR9473-5p	1	0	21	21	1
			sga-miR9473-2-3p	AAACGAGUUUAGAUUUACAGC	90-110	sly-miR9473-3p	1	0	21	21	1
sga-MIR9476-1	UCCUGUCCAAAACUGCUAUUGGUCU AGUCCUGCAUCUUUUUUUACAUUUU UUCCGUUAUCAAAAAAUAUAAAAAAA GAUGCAGGACUAGACCAAUAGCAGG AUGGAUUGG	110	sga-miR9476-1-5p	UCUAGUCCUGCAUCUUUUUUU	23-43	sly-miR9476-5p	0	0	21	21	1
			sga-miR9476-1-3p	AAAAAGAUGCAGGACUAGACC	72-92	sly-miR9476-3p	0	0	21	21	1
sga-MIR9478	CUUAUAAAAGGGAUAAGGCUUAAAU AUGUAGAUCGAACUUUGAGAAAAGA CUCAUCUAUGUCAUCUGGUAAAGUU UGGUGUGUAAUGGUUUGAAUGAGC CUUUUCUCGAACGAAAAUGGUGUAG AUGAGUUAAAUUUUUAACGGAUUAC AUAAUUGAGCCUUUUCUCAUAGUUC GAUGACAUAUUUGAGCCUUUUUCCA AUUAUAA	206	sga-miR9478-5p	GCUUAAAUAUGUAGAUCGAACU	18-39	sly-miR9478-5p	0	0	22	22	1
			sga-miR9478-3p	UUCGAUGACAUAUUUGAGCCU	172-192	sly-miR9478-3p	0	0	21	21	1
sga-MIR169e-1	UAGGAGGAGAGGCCUUACAUGAAUU AGAAGAGUUUCUAUUUGUUUAGUAG CCAAGGAUGACUUGCCUUUCAUCAA UGCCUUUUGUAAAAUGGAAAUUGAU UACAACACUUUCUAUGGUAUUGGGA AAAUGAGUGGCAAGCAUCUUUGGCG ACUUGACAAACUCUUCUUUGUCAUG UUAGUCCAUCUUCUUCCU	193	sga-miR169e-1-5p	UAGCCAAGGAUGACUUGCCUUU	48-69	sly-miR169e-5p	0	0	22	22	1
			sga-miR169e-1-3p	UGGCAAGCAUCUUUGGCGACU	133-153	sly-miR169e-3p	0	0	21	21	1
sga-MIR477-2	AAGCUAGGCAUUGCUUGUUGUCUCU CCCUCAAGGGCUCCUCUUCAAGAUC CUUAUAAACAAGAAAGCAUGAGGGG GAGGAGUUCUUGUAGGGUGAGACAA CAAGAAAUUCCUUGCU	116	sga-miR477-2-5p	UGUCUCUCCCUCAAGGGCUCC	19-39	sly-miR477-5p	0	0	21	21	1
			sga-miR477-2-3p	AGUUCUUGUAGGGUGAGACAAC	80-	sly-miR477-3p	0	0	22	22	1

					101						
sga-MIR156c-1	CAAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGCGUUUUCUGGCAUGAUGUUUAUAUAUAUAUAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCUCCCACCAAU	117	sga-miR156c-1-5p	UGACAGAAGAGAGUGAGCACA	12-32	rco-miR156c	0	0	21	21	1
			sga-miR156c-1-3p	GCUCACUGCUCUAUCUGUCACC	86-107	ata-miR156c-3p	0	0	22	22	1
sga-MIR172-9	ACUUGCUAGUGCAGCACCAUUAAGAUUCACAUAGAAAAUAUGGAACGAAAUUUGCUCAAUGUUUCAAUACAUGAGAAUCUUGAUGAUGCUGCAUUGGCAAAUC	103	sga-miR172-9-3p	UGAGAAUCUUGAUGAUGCUGCAU	72-94	aau-miR172	0	0	23	23	1
sga-MIR167h-1	UAACAGGUGAAGCAACCACAUGAUCUGAUCUUGCCUUAAUAUAAAUUUAUAGGUAAGUUUAGAUCAUGCUGGCAGCUUCAACUGAU	86	sga-miR167h-1-3p	AUCAUGCUGGCAGCUUCAACUGAU	63-86	gma-miR167h	1	0	24	24	1
sga-MIR395b	GUGUUCCCUAGAGUUCCCUUGACCACUUCAUUAGGGAUUACUUCGUUGUUUGAUGCCCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCA	90	sga-miR395b-3p	CUGAAGUGUUUGGGGGAACUCC	61-82	sly-miR395b	0	0	22	22	1
sga-MIR396b-2	GUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAUAGGGUCAAAUAGAAUUGCUACAAUUGAAUUGAAGUUUA	161	sga-miR396b-2-5p	UUCCACAGCUUUCUUGAACUG	16-36	aof-miR396b	0	0	21	21	1
			sga-miR396b-2-3p	GUUCAAUAAAGCUGUGGGAAG	95-115	csi-miR396b-3p	0	0	21	21	1
sga-MIR408-2	GGAUAGACGGGGACGAGCCAGAGCAUGAGAUGUGCAAUUUUUGCUUUGCCUAUUCCAUGCACUGCCUCUUCCCUGGCUCUCCU	83	sga-miR408-2-5p	ACGGGGACGAGCCAGAGCAUG	7-27	sly-miR408	0	0	21	21	1
			sga-miR408-2-3p	UGCACUGCCUCUUCCCUGGCU	58-78	aof-miR408	0	0	21	21	1
sga-MIR10528	UAAUGAAUGCAAUGUCAUAUACCAUCAACACUUGGAAACUCAAAUUGAGGUUAAAUCUCGGAGUGAUGAUGGUAUAUGACCUUGCAAUUCACUAU	95	sga-miR10528-5p	AAUGCAAUGUCAUAUACCAUC	6-26	sly-miR10528	0	0	21	21	1
sga-MIR172j-1	CCGCUGCAGCAUCAUCAAGAUUCCCACACAUCGCCCAUAGGGUUUUUAAAAAUUAUAAAAUCCCUAAUAUAGCUAUGUGAAUCUUGAUGAUGCUCCACCCAC	102	sga-miR172j-1-5p	GCAGCAUCAUCAAGAUUCCCA	6-26	lus-miR172j	0	0	21	21	1
			sga-miR172j-1-3p	UGAAUCUUGAUGAUGCUCCAC	78-98	mdm-miR172j	3	0	21	21	2
sga-MIR10529-1	AAACAUAACGAGUGAGACUUGCUCAGUUGGUAAAACACCUCCACUGUCUAACCAAUUAUCUUGGUCGAGGGUUCAAGUCAUGUUGGAAGCAAUGUGAGGGCGUCCAGCUUAGCAAGCCUCAUCCGUUUUGCUUC	134	sga-miR10529-1-5p	AACGAGUGAGACUUGCUCAGUUGG	7-30	sly-miR10529	0	0	24	24	1
sga-MIR530-1	UUAUCUGCAUUUGCACCUGCACCUUAGUGAACGAAUUAGUUCGCGUAUAAUUCGUGCAGAAAGGUGUAGGUGUUCAUGCAGACAAA	86	sga-miR530-1-5p	UCUGCAUUUGCACCUGCACCU	4-24	eun-miR530-5p	0	0	21	21	1
			sga-miR530-1-3p	AGGUGUAGGUGUUCAUGCAGA	62-82	sly-miR530	0	0	21	21	1
sga-	AACAUGUUGAAUGUUGGGGAACGAA	153	sga-miR10530-3p	ACGUCCCUUCCCCAUCGUUCAACA	125-	sly-miR10530	0	0	24	24	1

MIR10530	CGUCUAAGGUUUGGGUCAACGAUCUCAAUGUUGAUGCGUCCGCUUGUUGUUGAUGCUGCUCCAAAAGGUUCAACAUUGGGAUUUUAGCCCAAACAUCAGACGUCCCUUCCCCAUCGUUCAACAUCGUU				148						
sga-MIR398a	UCAAUAGGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUUGUUUGUAACAAUUUACCGUUUAUAAAUAUGACACAUAUGUUCUCAGGUCGCCCCUGUAGAC	102	sga-miR398a-5p	GGGUUGAUUUGAGAACAUAUG	7-27	stu-miR398a-5p	0	0	21	21	1
			sga-miR398a-3p	UAUGUUCUCAGGUCGCCCCUG	77-97	sly-miR398a	0	0	21	21	1
sga-MIR10531	GAUAUCUGGGGUCCUAGUAGAGUCGGUUCUACAUUGGGUGUUAAGUGUUUUGAGUAAUCAUCAUUGAAAGUAACAUACUUAAAACCCAAUGUUGAACUGACUCUACUCGGAUCCCAAAUAUCGGGCUCCAAAAUACCCUUGUCAUCCA	123	sga-miR10531-5p	UGGGGUCCUAGUAGAGUCGGUUC	7-29	sly-miR10531	0	0	23	23	1
sga-MIR10534	CCUUUUUGUUCAAAAUGGACCGUUAAAUAAGUGGUCAAUUUUGAAUCCAAUGUUGGAUGACAAGGGUAUUUUGGAGCCA	104	sga-miR10534-5p	CAAAAUACCCUUGUCAUCCAC	6-26	sly-miR10534	1	0	21	21	1
sga-MIR10535b-1	AAGGGUUGGCAUGAGUUUGUGAAAGCCGGAGGUUUAGGAGCAAAGUACAAUUAUUUUUGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUU	119	sga-miR10535b-1-5p	UUGGCAUGAGUUUGUGAAAGCCGG	6-29	sly-miR10535b	0	0	24	24	1
sga-MIR10537	GUUCUACAACGUACGUAGGGUAAGUGGAUGGCUGAAAUUCGUUAGCCUAGCCGUGGCCCUGGAAAUACUUCUCUGCAGGACAAGCUUCAUUUCCAUUACCGGAUAUCAACAGAAAGGUUGAAAAAGACAACAAUGUAGAGGAUUUGGUGGAGUGUGGAAAGAUUUGAAUGCAAACUUAUCGAAGAUUGAUCAUCAUGGAUUUAAGCCAUCCAUUUACCCCAAGUUCGUUGUCAAACG	237	sga-miR10537-3p	AUUUACCCCAAGUUCGUUGUC	212-232	sly-miR10537	0	0	21	21	1
sga-MIR159b-1	AAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACGUUU	180	sga-miR159b-1-5p	AGCUGCUAAUCUAUGGAUCCC	49-69	cas-miR159b-5p	1	0	21	21	1
			sga-miR159b-1-3p	UUGGAAUGAAGGGAGCUCUAC	156-176	sly-miR159b	1	0	21	21	1
sga-MIR171f-1	CUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAGU	81	sga-miR171f-1-5p	UAUUGGCCUGGUUCACUCAGA	7-27	csi-miR171f-5p	0	0	21	21	1
			sga-miR171f-1-3p	UGAUUGAGCCGUGUCAAUAUC	56-76	csi-miR171f-3p	1	0	21	21	1
sga-MIR399i-1	AGAUUAUACUAAAUAUGUUAUUGUUGGUGUGCUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCC	135	sga-miR399i-1-3p	UGCCAAAGGAGAGUUGCCCUA	97-117	stu-miR399i-3p	0	0	21	21	1

sga-MIR169r-2	UCUGCUUAAU CAUCCAAUGAGCUUCUCACAAGUUG UGUUUUGUUAGAUGAAGUAGGAAAC UGCUAAUUCUAUUUGCCAUAGGGAA UGUUGGAUUUUCUUCUUCAGGAAAC UACACUUCCCUAUAAUUGAAUAGAC AUGUCUUUAUUCAUGUUAAAGUCUU GCAUGAGGGAAUAAGGUUAUUGAAU UGCAGCCAAGGAUGACUUGCCGGCA AGCUCGAUCAAUUCUGCUUCAUGUC UGGCAAGUCAUUUUUGGCUACAUAU CUGCCUCAUUUUCUCAUGCCAGAUU UUUUAUGAAA	285	sga-miR169r-2-3p	CAGCCAAGGAUGACUUGCCGG	178-198	csi-miR169r-5p	0	0	21	21	1
sga-MIR169j-1	GAAAUGAUAAAAGAAGAGUGUGUCU UACAUGAAGGGGAAGUGCCUAAUUU GAUAGCCAAGGAUGACUUGCCUGCA UCAUUAGUUCUUGAGGUUUGUGAUA UAUAUCAUGUAUAUGACAUGUAUAC AAGCAUUCUUCUUUGAUGGCCAGGC AGUCUCCUUGGCUACUCUAAUAGGU UCCUCUCAUUCAUGCUAGACUCUUC UCUUCUUAUUUAGAAGUUAAAAAAAA AUAGUGGCAGAUUUGAAAUUUAAAG UUUAUAGGUUUACCU	266	sga-miR169j-1-5p	UAGCCAAGGAUGACUUGCCUGC	53-74	ppe-miR169j	0	0	22	22	1
sga-MIR156c-2	GGCGGUGACAGAAGAGAGUGAGCAC ACAUGGUGUUUUCUAGCAUGAUGUU UUACAUGCUUGAAACUAUGUGUGCU CACUGCUCUAUCUGUCACCC	95	sga-miR156c-2-5p	UGACAGAAGAGAGUGAGCACA	6-26	rco-miR156c	0	0	21	21	1
			sga-miR156c-2-3p	GCUCACUGCUCUAUCUGUCACC	73-94	ata-miR156c-3p	0	0	22	22	1
sga-MIR160h-2	UAUAUGCCUGGCUCCCUGUAUGCCA UUUGCAAAGCUCACCGUAAUAUAUC GAUGGGCCUUGUUGAAUGGCGUAU GAGGAGCCAAGCAUAU	90	sga-miR160h-2-5p	UGCCUGGCUCCCUGUAUGCCAUU	5-27	mes-miR160h	0	0	23	23	1
sga-MIR164-2	CUAGGUGAGUGACGAUCGAGAUGGA GAAGCAGGGCACGUGCAUUACUAAC UCAUACGCAAGAUUUAUCGAUGUUU CGAAAAUUCUGCUAUCAUAGUACUG UAUUUUACAGCAAAUAGUGUUUGUA CUUUACAUGUAUGUGAUAAAAUGAU GAGUUAGUUAUUCAUGUGCCUGUUU UCCCCAUCAUGA	187	sga-miR164-2-5p	UGGAGAAGCAGGGCACGUGCA	22-42	aof-miR164	0	0	21	21	1
sga-MIR164-3	CGAUCGAGAUGGAGAAGCAGGGCAC GUGCAUUACUAACUCAUACGCAAGA UUUAUCGAUGUUUCGAAAAUUCUGC UAUCAUAGUACUGUAUUUUACAGCA AAUAGUGUUUGUACUUUACAUGUAU GUGAUAAAAUGAUGAGUUAGUUAUU CAUGUGCCUGUUUUCCCCAUCAUGA CCGCUCAACCUU	187	sga-miR164-3-5p	UGGAGAAGCAGGGCACGUGCA	10-30	aof-miR164	0	0	21	21	1
sga-MIR167c-3	AUCGUGAACCACUAGCAGUUGAAGC UGCCAGCAUGAUCUAAACUUUUCUA UUGCUCCGUACGAGGAAAGAUCAGA UCAUGUGGCAGCAUCACCUGUUGAU GGUUUCGCGG	110	sga-miR167c-3-5p	UGAAGCUGCCAGCAUGAUCUA	20-40	ata-miR167c-5p	0	0	21	21	1
			sga-miR167c-3-3p	AUCAGAUCAUGUGGCAGCAUCACC	70-93	eun-miR167c-3p	1	0	24	24	1
sga-MIR169d-2	GCAUGAUGAAAAGAGUCUUAUUUGG UAGCCAAGGAUGACUUGUCUGCACC	141	sga-miR169d-2-5p	UAGCCAAGGAUGACUUGUCU	26-45	csi-miR169d-5p	1	0	20	20	1

	AUUUCCGAAAUGUGUCCUUUCGUUCAUGGGGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUCUUUCAUGCAAGACUUUCUCU		sga-miR169d-2-3p	GCAGGUCAUCUUUAGCUAACU	86-106	stu-miR169d-3p	0	0	21	21	1
sga-MIR171a-5	AGUUGGUGUGAUGUUGGAAUGGCUCAAUCUAAUGAAAGUUUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAUAUUGUCUUUUG	100	sga-miR171a-5-3p	UGAUUGAGCCGUGCCAAUAUC	67-87	aof-miR171a	0	0	21	21	1
sga-MIR171b-1	AUUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAU	115	sga-miR171b-1-3p	UUGAGCCGCGCCAAUAUCACU	89-109	aof-miR171b	0	0	21	21	1
sga-MIR390-1	UAUGCAUGGAGAAUCUGUAAAGCUCAGGAGGGAUAGCGCCAUGGAUGACUCAAUUCGAUUUUUGUACACAUCUUUAGCGCUAUCCAUCCUGAGUUUCACGGCUUUUUCAUGUUUUUU	117	sga-miR390-1-5p	AAGCUCAGGAGGGAUAGCGCC	20-40	aof-miR390	0	0	21	21	1
			sga-miR390-1-3p	CGCUAUCCAUCCUGAGUUUC	78-97	mes-miR390	0	0	20	20	1
sga-MIR156b-3	AAAGAGGAGGUGGUAGGAGAUGUUGUUGACAGAAGAUAGAGAGCACAGAUGUGCAUGGAAAUUGUCUGCACCUUACUCCUUUGUGCUCUUUAUUCUUCUGUCAUCAUCGUUAAUCCCACCAUUUUUUUUUUU	132	sga-miR156b-3-5p	UUGACAGAAGAUAGAGAGCAC	26-46	aof-miR156b	0	0	21	21	1
			sga-miR156b-3-3p	GCUCUUUAUUCUUCUGUCAUC	85-105	vca-miR156b-3p	2	0	21	21	1
sga-MIR156b-4	CAAGACUGACAGAAGAGAGUGAGCACACGAUGUCAAAUUGUAUAAAUAUAUAUACAAUUGUCAUUUGCGUGUGCUCACUUCUCAUUCUGUCAGAAUCU	98	sga-miR156b-4-5p	UGACAGAAGAGAGUGAGCACA	7-27	hvu-miR156b	0	0	21	21	1
sga-MIR156k-1	UGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUUGCAUGAUGUUUAUAUAUAUAUGCUUGAAACUAUGUGUGCUUACUCUCUAUCUGUCACC	96	sga-miR156k-1-5p	UGACAGAAGAGAGUGAGCAC	4-23	cas-miR156k-5p	0	0	20	20	1
			sga-miR156k-1-3p	UGCUUACUCUCUAUCUGUCACC	75-96	cas-miR156k-3p	0	0	22	22	1
sga-MIR156f-1	UCUGUUGACAGAAGAGAGAAAGCACAGUCUGUCAUCAACAAAAUGGUAUUUGUUGUUUGUUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUAG	92	sga-miR156f-1-5p	UUGACAGAAGAGAGAAAGCACA	5-26	gma-miR156f	1	0	22	22	1
sga-MIR156d	UAUAAUUGAAAUUGAUAGGAAGAAAGAGUGAUUACCGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCAC	140	sga-miR156d-5p	UUGACAGAAGAUAGAGAGCAC	38-58	stu-miR156d-5p	0	0	21	21	1
			sga-miR156d-3p	GCUCUCUAUGCUUCUGUCAUCA	118-139	stu-miR156d-3p	0	0	22	22	1
sga-MIR162	CACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGGAAGCUGAAUAUAUAUAUACGCAAAAAUACAGCAAAAGGAAUCGGUCGAUAAACCUCUGCAUCCAGU	101	sga-miR162-5p	UGGAGGCAGCGGUUCAUCGAUC	4-25	csi-miR162-5p	0	0	22	22	1
			sga-miR162-3p	UCGAUAAACCUCUGCAUCCAG	80-100	fve-miR162-3p	0	0	21	21	1

sga-MIR166f-1	UGAAGAAAAACAAGAAAAGUGAUGCUAGAAGGGAAGGAAGAAUAAACAUUUUUGUUUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCA	156	sga-miR166f-1-3p	UCGGACCAGGCUUCAUUCCCCU	133-154	cas-miR166f-3p	0	0	22	22	1
sga-MIR171f-2	ACUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAG	81	sga-miR171f-2-5p	UAUUGGCCUGGUUCACUCAGA	8-28	csi-miR171f-5p	0	0	21	21	1
			sga-miR171f-2-3p	UGAUUGAGCCGUGUCAAUAUC	57-77	csi-miR171f-3p	1	0	21	21	1
sga-MIR162b-1	UGAAAAGAAAAAAAAAUCCUUAGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCGUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUCA	139	sga-miR162b-1-5p	UGGAUGCAGAGGUUUAUCGACC	35-56	ath-miR162b-5p	4	0	22	22	1
			sga-miR162b-1-3p	AUCGAUGAACCGCUGCCUCC	110-129	cas-miR162b	0	0	20	20	1
sga-MIR156f-2	UUUGGUUGAGGAUUCAAAGUGAGAAAUUCUAUUGACAGAAGAGAGAGUACAAUCUGUCAUCAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUGGAAACUAUAAAAAUGGAUCCUCAACAAAGA	146	sga-miR156f-2-5p	UUGACAGAAGAGAGAGAGUACA	32-53	gma-miR156f	1	0	22	22	1
sga-MIR169r-3	AAAGUCUUGCAUGAGGGAAUAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAACAGCUGUUGUUGUUAAUUGUCAAAUCAGGAAUUGUGGACAA	184	sga-miR169r-3-5p	CAGCCAAGGAUGACUUGCCGG	36-56	csi-miR169r-5p	0	0	21	21	1
sga-MIR172-10	GCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAUCCUUGUAAAC	160	sga-miR172-10-3p	UGGGAAUCUUGAUGAUGCUGCAU	108-130	aau-miR172	1	0	23	23	1
sga-MIR399i-2	AUACUAAAUAUGUUAUUGUUGGUGUGCUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCCUCUGCUUAAUUAUGUU	136	sga-miR399i-2-3p	UGCCAAAGGAGAGUUGCCCUA	92-112	stu-miR399i-3p	0	0	21	21	1
sga-MIR156c-3	CAAAGGGAGGUGACAGAAGAGAGUGAGCACACAUGAUGUUUUCUCGCAUGAUGUUUACAUGCUUGAAACUAUGCGUGCUCACUGCUCUAUCUGUCACCCCACCAC	105	sga-miR156c-3-5p	UGACAGAAGAGAGUGAGCACA	11-31	rco-miR156c	0	0	21	21	1
			sga-miR156c-3-3p	GCUCACUGCUCUAUCUGUCACC	77-98	ata-miR156c-3p	0	0	22	22	1
sga-MIR159b-2	AUACUCUGUUUGUGGAUUACACUGAUAUUCAUAUAGUUGAUUUUAACUUGUUCGAGGAAGAUUAGAGUUCUGAAUGUAGAGCUUUUCUGAAUUUCAAAGA	272	sga-miR159b-2-3p	AGCUGCUAAUCUAUGGAUCCC	121-141	cas-miR159b-5p	1	0	21	21	1

sga-MIR166-2	GGAUCUGAGAGGGAAAAUCGAGCUG CUAAUCUAUGGAUCCCUCAAACCUA UCUAUUCUCAAAAUAAUUUUAGAUA GGUUUGUGGUUUGCAUAUAUCAGGA GCUUCAUUUACUCUUCUAGGAUCCU UAUUGGAAUGAAGGGAGCUCUACGU UUGAUAACCUAAUUUUUUUCCA GAAACUAAACAAGAUCAUGUUAAGG AGAAUGUUGUCUGGUUCGUGACCAU AUAUCUUUCUUCACAUAAAUGAUCU CGGACCAGGCUUCAUUCCCCUCAAC UCAUCAAGGUUAUGUCAUG	119	sga-miR166-2-3p	AUCUCGGACCAGGCUUCAUUCCCC	72-95	lja-miR166-3p	1	0	24	24	1
sga-MIR171b-2	UUUUGGGAUUAAAAUGGAAGAAGCG AUGUUGGUGAGGUUCAAUCCGAAGA CGAAUUUAUGCUUAUUUUCGUAAAG AACGAUCUCAGAUUGAGCCGCGCCA AUAUCACUUCUUAUUUUC	118	sga-miR171b-2-3p	UUGAGCCGCGCCAAUAUCACU	88-108	aof-miR171b	0	0	21	21	1
sga-MIR396b-3	AAAAAGAAAUGGUCCUUUUUGUGUU UUUCCACAGCUUUCUUGAACUGCAU CUACAAUUUCAAUUCAUUAUUGAAAA AGAAAAAAUUGAUUCAUAUUGUUGU UGCGGUUCAAUAAAGCUGUGGGAAG AUACAGAUA	135	sga-miR396b-3-5p	UUCCACAGCUUUCUUGAACUG	27-47	aof-miR396b	0	0	21	21	1
			sga-miR396b-3-3p	GUUCAAUAAAGCUGUGGGAAG	106-126	csi-miR396b-3p	0	0	21	21	1
sga-MIR8006-1	AUUAUACUUUUGGGUCAUUGGUGCC CCUGUCGUUCAAAAACUAAAGCAUA UAUGCCCUUCACUCAUCGGAUCGGU GGAUAAGAUUGACUUUUUUUAUUAA UGGAUAAAAUUAUGACAUGUGUAUG UCCGUUAGUAUAAAUGAUACAUAUG CUCUAGUUUUUGGACGGCAGGGGC ACCAAUGUCCCCAAAGUAUGAC	196	sga-miR8006-1-5p	GCCCCUGUCGUUCAAAAACUAAA	23-45	stu-miR8006-3p	6	0	23	23	3
			sga-miR8006-1-3p	UAGUUUUUGGACGGCAGGGGCAC C	154-177	stu-miR8006-5p	1	0	24	24	1
sga-MIR5303-1	UUACUCAAACUCUUCAAAAAUGUUG CAGCACACAUGUCGGAUACUCAAAA GUCCACUACUUUUGGAGGAUUUGAC AUGUACGUGUCGACAUUUUUGACGA GUUCGAGCAA	110	sga-miR5303-1-3p	UUUUUGACGAGUUCGAGCAA	91-110	sly-miR5303	1	0	20	21	1
sga-MIR11039	UUCUCUACUUGUUAUGAGGAUAUGC AUGGUAUGUGUCUAUAUGAUGUAGU CUUAUUCUUAUGUGAACUAUGUGAG UCUUAGUGACUAUAGGAUGGAAAUU GUUGAUAGUAAUUGAGUUGUACUUA UGCAUUAUGUUGAUAUAUGAAGUGU UAAGAUUUGUGUUGUCGUGAAGGG UUUACAGAAUGUAUGGAGUUAUGGG GCUUCAUAUGUUCAUUGAACUAGUA GACUA	229	sga-miR11039-3p	UGGAAAUUGUUGAUAGUAAUUGA	93-115	seu-miR11039	2	0	23	23	1
sga-MIR1862g-1	ACAUUAUUCCAGUCUUUAAUAGUAU CUCAUCUCGCCUACAAGAUCUGGGG UUGGUUUACUUUUUGUUGAAACACU UGGGAUCCGUUUGGUAGGCGGUAU UAGGUAAAAUAAUAUAUGGAUUAAAA U	126	sga-miR1862g-1-5p	CUGGGGUUGGUUUACUUUUU	45-64	osa-miR1862g	5	0	20	20	2
sga-	CUUAUAUUUUCUUUUUGUCAUUUAA	240	sga-miR3437-5p	CGUUGGAUCAUGUUUUUUCU	40-59	aly-miR3437-3p	3	0	20	20	1

MIR3437	AUAUUUAUNCUAUUCGUUGGAUCAU GUUUUUUCUUCGCUUGUGAAAAUGU UGAACUAGAACAAAAUCUUAUCGUU CUUAUCGAAUUUCUCUCUCUUGGGG AGUUCAUUUUUAUCUUCUAUUUGAA GAAACUGUUGCGGAAAAAUGAUGGG AUAUUGGCGGGAAAAAAUCUACUUG AAUAGGUGAAGGUGAAAUGGACAUA AAGAGUUAAUAUUUG										
sga-MIR6144	AUAUUGAAGGAUAUUUAUAUGAUUA GUAAUCUAUUUGUUAUAUCUUUGCA GAAUGGCAGGCGGAGAUGAGCCUC CGCCAUGGUCGCAUAUUCGUGGCC GUGGAGGAAAAACUAGAGGAAGAGG AAGAUCAUCCUCUUCAUAGAACAGA AGAUCGUCAUACGAUUCUUCCUUUC CUGUUAUACAGUUAGGAAGAAAAAC UUUAAUCAAUUCAAAGAUUGGGGAA ACUUCUUCAUCAGCUUCAUCUUCUG UGAAUCUAAAAGAUAUCCCAAAGGA UAGUUCAUUAUAUGAACAGAUUCAA GCA	301	sga-miR6144-3p	GGGAAACUUCUUCAUCAGCUU	219-239	nta-miR6144	6	0	21	21	2
sga-MIR1127b	AACAUUUCAGUUGAUCUUGAUCCCA UUUACUCCCUCUCCCUUUGCCGGAC AAUAGUUGUCCACUAUUGACUUGGU ACAGGGAUUAAGAAGCAGUAAAUGA UAGGGGUAAUUUUACCAAAUCACCC UUAUUAAAAGUAAGUCACAUAAACAU CGAAAAAUAAAUAGUAUUUAAUAGCA AGGUAAAAACGACACAACAUGCUAAA UGACUCAUUGAUUUAAUAAACUGGA CAAGUAUUGUUGGACGUCUCAAAAU AGUAUAGUGGACAAGUAAAGAUGGA CAGAGGGAGAGGGAGUAGCUUAGAC UCAUAGCAGCAAAGAAAUUAU	324	sga-miR1127b-3p	ACAAGUAUUGUUGGACGUCUC	228-248	tae-miR1127b-3p	6	0	21	21	1
sga-MIR11167-1	AUAUAAUUAAAGAGUUAAUACCUCAU AUGGUCACUCAACUAUGCACUCUUC UCCCAGAAUGUCACACAAAGUGACU UUCUGAGAGAAGAGUGCAUAGUUGA GUGAUCAUCUGAGGUAUUAACUCUA UAAUUAAAC	135	sga-miR11167-1-5p	UCAUAUGGUCACUCAACUAUGCAC	23-46	lja-miR11167-5p	7	0	24	24	3
sga-MIR5014a-1	GUUUGUUGCCAUAUUUACUUUUAAA UAAAUAAACACAUGAGUCCUAUAUG ACAUAAAACACCACGUAGGAUAAAAA AAUAACAUGUAGGACAUGUGUGUCU AUAUGUUCAACUUUGUACAAAUUUA AGUGUCUAUUUGUGCACACCUAAAG UUAAAGGACAUAAAUAGGAUUCGAG GUCAAGUUAAAGGCAUAUUUAUGUA UUAUGCCUUGUUAAAAGCAAGCAUG CACCACCU	234	sga-miR5014a-1-3p	UUGUACAAAUUUAAGUGUCUA	114-134	ath-miR5014a-3p	3	0	21	21	1
sga-MIR10538-1	AACGUUUUAGGGUAUAUUUCGUUUU UUAAAACUAACAGCGUUAGGUUGAU AUACGUUACUGUAAGUAACAUUUUA CUCCUAAAACAUUAUUUUGAGUAAC GUUUUACUACAGUAAUGUUUUAGGA GCAAAACGUUACUGUGAGUAACGUA	202	sga-miR10538-1-5p	AGGUUGAUAUACGUUACUGUAAGU	43-66	sly-miR10538	4	0	24	24	1

sga-MIR7776	UGUCAAUCUAACGCCGUCAGCUUUUAAAGAGGAGAAAAAGCCCAAGAACCCUUGCACUUAAUGGAGGUCUGAAUCUUAAUCAUUCAAAUUCAGCUCAUUAAGUACGUUUUAUUUUUAGGUCUGAAUCUGAAUCGUGCAGAUUCAGCCCAUUAAGUUUACCCUAUGCAUAAUUUCGGUGGAGCU	106	sga-miR7776-5p	AAAUUCAGCUCAUUAAGUACG	34-54	bdi-miR7776-5p-2	6	0	21	21	1
sga-MIR535	UACAACAGCAAGACAGUGAGAGAGAUUUUUGCUCUCUCUCAUUUUCUUGCUGUUGUAAGCUCCACCGGAAUCAUGCGUAAUAAGAAGCUAUGUUUCUCGGACUCUCC	107	sga-miR535-3p	UUGCUCUCUCUCAUUUUCUUG	54-74	vca-miR535-3p	6	0	21	21	2
sga-MIR7997c-1	AAAAAUGCUAAGUAAUUCACUAUUUUUGAUGGAUCCGACAUGCAACCCAUAGUGUUUUUGAAGAGUUCGAGAAGCAUAGCUGAG	109	sga-miR7997c-1-5p	AUGUUUCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	3	0	24	24	1
sga-MIR3627	GAGAGAGAUUGAGGGAAUCUUGUCGCAGGAGAGAUGGCACUUGCCAUUCCUUUUAAUUGGUACAAUGCCUAAAUGGAACCAAUUAAGUGCCUCUGUCUUUCGACACGAUGCUCACAAUUUCUAUU	125	sga-miR3627-5p	UUGUCGCAGGAGAGAUGGCACU	20-41	vvi-miR3627-5p	1	0	22	22	1
			sga-miR3627-3p	AAGUGCCUCUGUCUUUCGACA	85-105	stu-miR3627-3p	0	0	21	21	1
sga-MIR160-1	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAACUAGGAAGAGUGUCAAUUUUUUUGACAAUACUGUUCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACAAUUUC	104	sga-miR160-1-3p	UGGCAUCCAGGGAGCCAGGCA	74-94	aau-miR160	1	0	21	21	1
sga-MIR8001b-1	UUCUUUUUGGUGGCAAUUGGUUCGAAUUUGCCACGCGAUAUAUCUAGUAUACAUGGUAUAUUCAAACUAAUUCCCACGAAAAAAUC	86	sga-miR8001b-1-3p	GUAUAUUCAAACUAAUUCCCACGA	56-79	stu-miR8001b-3p	6	0	24	24	1
sga-MIR168	GUUUCUCAUUCGCUUGGUGCAGGUCGGGACCUACCUCGCCGGCAACAAUGGCGGUAGCUGACGGCGACGGCAGCGUACCGGUAAAAAAGAAUCUUAUUUUUACAUGUUGUUGCGUAGUAUGGGUCCCGCCUUGCAUCAACUGAAUAGGAGACUG	154	sga-miR168-5p	UCGCUUGGUGCAGGUCGGGACC	10-31	lja-miR168-5p	1	0	22	22	1
			sga-miR168-3p	UCCCGCCUUGCAUCAACUGAAU	124-145	lja-miR168-3p	0	0	22	22	1
sga-MIR5532	UAUUCCAUGAAUAUGAUAUCUAUCUAGUGUGAUGUAUGGAAUAUAUGACAAAGGUGGAUCUAUUGAUCGGUCAUGUCAUAUAGGCCCGAGUUGGACAUCCAAUUGCUUCGAUUUGAAUUAUCCGGAGAAUGCAAUGCCUGAUAUAUAUCAAAAAGAUGGACAA	163	sga-miR5532-5p	AUGGAAUAUAUGACAAAGGUGG	36-57	osa-miR5532	0	0	22	22	1
sga-MIR9751	UAAGAUAUGAAUUCAUUAAAACUUAAGAGUCUAAAUAUAUGCAUUAAAAAAUGUACUCCUUCGUUCGGUAUUUAUUUUGUCAUAGUUUUUAUUUUUAGAGUUAAACUAUAAAAACUUUGACUAAUAUUUUAAGAUGUAUUUUUCGUCAUAUUAAUAUGCAGGGUUGACCCGGUAAAUC	331	sga-miR9751-5p	UUAUUUUUAGAGUUAAACUAUAAA	89-112	gma-miR9751	7	0	24	24	2

sga-MIR9479	CGGUAGCCCACACAUGGUGGGCCG AUCAUUUUUUGUCUACACAAAAAAU GAGUCAGCCGGCUUGACUCAUCAAA CUGCAAAGCCUAUAUUAUUUAACCU GGAUGGGGUGGCUAGCCCAUAUUG ACAACUCUACGUUUUACUAAAUAUA UCAAC UAAGUCCAGUCCUCUACCCUUCUCC ACUUAAAAGACCAAGCUUGUCUACA ACAAGGUUCCAACUCAUGACAAACA UAUGAUGUGUGAGUUAGGCACGUG UCACGGGUUCAAAUGCUACCACCGA CAAAAGUAUGGUAUUUAAGUGGAGA AUGGUAGAGGGUCGGACCCA	169	sga-miR9479-5p	UCCAGUCCUCUACCCUUCUCCA	5-26	sly-miR9479-5p	0	0	22	22	1
			sga-miR9479-3p	GAGAAUGGUAGAGGGUCGGACC	146-167	sly-miR9479-3p	0	0	22	22	1
sga-MIR1127	UAAUACUCCCUCCGUCCGAUUUUAU GUGGCACAAUUUGACCUAGCACGGA GUUUUAAAAAAAUGAAAACUUUGAAU UGUUUACUAAAUUGUCCUUCAAAAG UAGACUCACUUUUCUCUUUUCUCAU AAACGUAUUAGAGUACUAUGUAAAA UUAAGUGGGACCAACAAGGGUAAAA GAGGAAUUGCACCUUUAAAUACUUA CCAUAUAAGAAAAUGUGACAUUCUU UUUGGGACUGAGACAAAAAGGAAAU GGUGCCACAUAAAAUGAGACGGAGG GAGUAACU	284	sga-miR1127-5p	UAAUACUCCCUCCGUCCGAUU	1-21	bdi-miR1127	3	0	21	21	2
sga-MIR534b	AUAUGACCAUUAUAGACUCAUAUUG UCAAGUAGGAAUAACAAUGCAUCAA CUGUAAGACUGUAUACCUAAAGACA UAUACAUAGUCUAACAUGGUCACCU GCUAAUAUUCCCCUUCAUCCUGCUU AAAUAAGCUAUGGAAUUUUUCAUCA AAAAGAAGCUAUUGAAUUAAAACUGA UUUUACAGGUGAGGAUGAUUCCGGA CUAUUUGCCAUGUCUGAAAUCAUCU UAAGCUAUUCUUUUUAUUUCUCAAA AAAUGAAUAGGUGAUGAUGAUUCCA GAUAUGGAAAAUAGUAUCUUUUCUC CAGGAUAUAAGAGGAAAAUGUAGAU AUGUCAAAAAUACGGUCUCUUUUGG CAAGUUAAUUUUUUUAUUUUGGGCA GAGCUUGUCAAGGAAAUAAGAAGGG GAAGGAUUCUU	100	sga-miR534b-5p	UAUGACCAUUAUAGACUCAUAU	2-23	ppt-miR534b	6	0	22	22	1
sga-MIR8577		312	sga-miR8577-3p	AAAAUGAAUAGGUGAUGAUGAUUC	151-174	atr-miR8577	7	0	24	24	1
sga-MIR11036	AUCCAUUAUUCUUCUGAAUUGUUUA UCUUCUGCUUUGAUAUGACAGCUUU AUUGUAUUCAUUCAGGAAUGUGAGG AGUAUGAAGAUUUGGAUGAAUAUGA GGAAGAAAGCGGUGCAGAGGAAUAU GAGG	129	sga-miR11036-3p	UUUGGAUGAAUAUGAGGAAGAA	86-107	seu-miR11036	1	0	22	22	1
sga-MIR6160-1	AUGUUUCACUAGAUAUAUAUAUCCU CUGUUUGAGUUUGGCUCAUCUGUG CCCUCUCCGCCUAACUUUUAGCCUA UAUAUGUCCUAAUAGAAGUUAGUUG UUUUUCUGGAAAUAACCAAUUUAUU UUUCUUUUAUUUAAAUAACAAAUGAA	271	sga-miR6160-1-3p	GUAUAUGUGAGCCAUUUGUAUAAC	187-210	nta-miR6160	6	0	24	24	1

sga-MIR864	AUUGCCACAUCCCCUUUUCAUUUUG UAACGGCAGGGGUAUAUGUGAGCCA UUUGUAUAACGGUAAGGACAUAUAU GAGUCACUUUCAUAACGAGGGGUAU AUCAGCUCCAAGUGACAAAGU CGCCCUUAUUUUCAUUCUUGUGAUC GUUCGGGGACGAACGAUGGGUAAAU UGGUAUCUAAUGUAACGACCCGUUU AGUCGUUUUGAGCAACAGACUUCAA UUCUGGAAAAAAAAGAAUAAUUGGA AUAGCAACAAUUGUACAAGAGUAAG UCAAUAAUUAUUUGAAUGGCAAUGA UAUUUGAAGUUAUUAUGCACGAGAU CAAGUAAUGAUUUAUUCUAAUUCCA AAGAGCUAAGGAAAUCAGAUAUGGA UGAAGUCCAGCGAUGGAUUUUGUCA UUGCUAAAGCCAGAAGAUCAACCAA CUACAAGAGCCUUGAAAAAAGGAUU AGCUACACGUGAUAUUGGCGCGGCU	325	sga-miR864-3p	GUAAGUCAAUAAUUAUUUGAAU	146-167	ath-miR864-3p	6	0	22	22	3
sga-MIR171b-3	CAAUCAAAAAGUAGACUCAAAAAUGU UCUUAAGUACUGCUUUCUCAUUGAA CCGCACCAAUAUCUCGUGUAUUC	99	sga-miR171b-3-5p	GAUAUUGGCGCGGCUCAAUC	11-30	zma-miR171b-5p	1	0	20	20	1
			sga-miR171b-3-3p	UCAUUGAACCGCACCAAUAUC	69-89	tcc-miR171b	4	0	21	21	3
sga-MIR7987-1	CACAAGUACCAACACUAGCUGAUGC UAUUGAUGACAAAAAUUGGUUUUCU UGCAAGAUCAAUUUGUGUCAAUCUA GUGUUGAUACUUAGUUUUAGUUUAG GAAUAAAUGUUUGUUGAUUGUAAGG ACCAACACUAGUUGAUCUUAUUGAU GACAAAAAUUAAUGUUCUUGCAAGA UCGAGUUGUGUCCAUCUAGUGUUGA UACUUAGC	208	sga-miR7987-1-3p	ACACUAGUUGAUCUUAUUGAUGAC	130-153	stu-miR7987	0	0	24	24	1
sga-MIR7987-2	GGUUUUCUUGCAAGAUCAAUUUGUG UCAAUCUAGUGUUGAUACUUAGUUU UAGUUUAGGAAUAAAUGUUUGUUGA UUGUAAGGACCAACACUAGUUGAUC UUAUUGAUGACAAAAAUUAAUGUUC UUGCAAGAUCGAGUUGUGUCCAUCU AGUGUUGAUACUUAGCUUUAAUUUA GUAAUAAUGGUGUUUGUUAGGCAUA AGUACCAACACUAGUUGAUCCUAUU GAUGAAAAAAUUGAUUUUCUUGCAA GAAAAAA	257	sga-miR7987-2-5p	ACACUAGUUGAUCUUAUUGAUGAC	88-111	stu-miR7987	0	0	24	24	1
sga-MIR8025	UACUUAAUUAACUAAUUAAACUUAAA AACACCCCGAUCUUGCCAGUUCAAC UUGAGUGCAAUACACUUUUAAAUUC UUGCCAAGUUUAGGGUUGUUUUCAA CAUUUCUUUCGACGUUUUAUUAAGA GCCUCAUGUUCGUACCUGAGUAUAA GACCACUUCUUAUGUUAUGUGGCAG AUCGGGAGUGUAUCUAAGUUUAGUU AGUUAAAUAAUGA	214	sga-miR8025-5p	UUUAAAUUCUUGCCAAGUUUAGGG	68-91	stu-miR8025-3p	6	0	24	24	1
sga-MIR2875	CGUUAAUUUUAGGUAUGGACAAGUA AACAUUUAAACUUGUAUAAAAUUAAA CAAAUAGACACAUUUGUCCUACAUG ACACCCUACAUGAAAAUUGUGUCCU ACGCGGCGUCCGAUACAUAUUAUGU	202	sga-miR2875-3p	AUGUUCAGUUAUAUACAGUUUUAA	149-172	osa-miR2875	5	0	24	24	1

sga-MIR11124	CAUGUAGAACACGUGUGUUUACAUGUUCAGUUAUAUACAGUUUUAAGUGCCUACUUGUGUACACUCAAAGUUAGAAUGAUCUGAAAUUUGGGUAAGAUUCAACAAAACAGGACACAACAUUGUUUGCUUAGAGGCUUCUUUGUCAUCUUGGUGCUUGAUCGGAGCCUGAAGCUCCAAUAGAUGGAGCGGUGGGCAUACCAUUUGUUGAUCCAUUUUCAAGUGGUGGAGGGACUCCCCAUUUGCCUUCAGAUUCAAGUGGUUCAAAAACAUGAACACUACCAUCUGACAGACCUAAUGCAAACUGGUUUGGAUCUUGUGGAUGUGCUGCAACUACGACUGGGUGGAUGUUUGAAUUGCUGCAGAAAAAUGACAAGGUUUUAUGAAAAAUUACAUCAAAUAUCAGAAAUUUUAUUUUGUCUUUCAUCCUUGAUAAUUCCCUCUCUUUCUCCUCUUAUGUUGUUGGCUUAACCGGCUCUAAACCCUUCCACCGGAUAAAGAAAUGGAAUUUCAAGUACAAGUAGUCGUCUACACUUAAAAGCUUUCUUGUCUUCACUAAUCAACAUUUAGUUUGGCCUAAGAUUUUCUAAGUCCGAUGCAUCACUUACAUUUUUUCUCAUUCUCCGUUGUUGGUGCCUCUCCAAAAAGAAAGUUGAAUGGAGAAUGAAAAAGAAAAAUGUAAAGAAUAAAUAGAGCGAAUAAUUUAGGAUGAAAGGCGAAAUAAAUUUUGACCUCCAACUUUCAUAAUGCACAAACAAACACUUUAACUAUCCAACUUUUAAAUAAAUAAACACACGAGUCCUACAUGGCAAAAUACACGUAGGACACCACGUAGAACAAAAAAUAACAUGUAGGAUAAAUGUAGGACAUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCGACAUGUGCACACCCAAAGUUGAAGGACAUAAUGCCCCUACCGUCAAAAUGAAGUUAUUUUUAUCCCUACCGUUACUAAUUUCAUCAUUUAUACAUUUCCCAUUUCAAACCCAAUGUUAAAAUGAUGAAAUUAGUAACGGUAGGGGUAAAAAUAACUUCGUUUUAACAGUAGGGAGACCAAACUAUCAUAAAUGGUAUGCAAAUACCUUUCGUCAUACUUUUGGGACAUUGAUAUUCCUGCCGUUCAUAAACUGGAGCAUAUAUGUCCUUCACUCUAAGGAAGACUAAAUAGGGACACAUGACGCAAUCUUAUCCGUCGAUAAAUGUCGGAUCAAUGAAUAAGAUUAUGACACAUAUAUGUCCGUCAGUAUAAAGGAUAUAUAUACUCUUUUUCUAAAAUUACAUAUGCAAUUAAUAUUCUAAAAAUAUGAUAGAAAUUAUUUACAUUCCAUU	331	sga-miR11124-3p	ACUGGUUUGGAUCUUGUGGAUG	225-246	lja-miR11124-5p	5	0	22	22	2
sga-MIR8685		316	sga-miR8685-5p	CGUCUACACUUAAAAGCUUUCUUG	116-139	gra-miR8685	7	0	24	24	2
sga-MIR5014a-2		216	sga-miR5014a-2-3p	UUAUACAAGUUUAAGUGUCGA	166-186	ath-miR5014a-3p	5	0	21	21	1
sga-MIR11514-1		145	sga-miR11514-1-5p	GCCCCUACCGUCAAAAUGAAG	2-22	pab-miR11514	6	0	21	21	2
sga-MIR8739-1		289	sga-miR8739-1-5p	AGACUAAAUAGGGACACAUGACGC	105-128	gra-miR8739	7	0	24	24	3

sga-MIR6470	UACGAUAGUUCAA CGACUCAUAAACACCUAAUCCGACC CAUAAAUCAACUCCUUUUAAAUUCAC UAACCGGCCCUUCAUAUUUUUCUAC UUUUAUUAAUGAAUUACUCAUUUUC GGAAUUAAUCAAAAAAAUAAAAAUUA AACAAAAUUAUUGAAAAUUGAUCGG AUAUCUUAUUUAAAAGGGGGUUGAU UUAUGGGUCGGAUUAGGUGUUCAU GAGUCC	207	sga-miR6470-3p	AUCGGAUAUCUUAUUUAAAAG	148-168	ptc-miR6470	5	0	21	21	2
sga-MIR1521b-1	UAUACUAACUGACAUACACGUGUCA UAAUUUUAUCCACCAACCUGACAUC AGAUCAAUGGAUAAGAUUGUGUCAC GUGUCCCUAUUUAGUCUU	93	sga-miR1521b-1-5p	GACAUACACGUGUCAUAAUUUUA	11-33	gma-miR1521b	5	0	23	23	1
sga-MIR11131	UACUUACGUCCAACAAAUGACCUAU UUGUUGCAAUAAAUAGGUCAUUUGU UGAACGAAAACUCAAUCAUUUGCUA UUGAUUUACUUACGUUCAACAAAUG AUCUAUUUGUUGCAACAAAUAGAUC AUUUGUUGGACGAAAUCU	143	sga-miR11131-3p	CUUACGUUCAACAAAUGAUC	84-103	lja-miR11131-3p	3	0	20	20	1
sga-MIR7502c	CUUAUCACACUUUCAAGAAGACUUA UUUAAGUCAUCCGUCAAAAGUUUAG CCAUCUAUGUUAUUUCUGUUUGAGA AAAGUCUCAUCCAUGUCAUUAUUUG UAAAUUGAAAUGACAUAGAUGAUCC AAACUAUUAACGGAUGACAUAGAUG AACCUUUUCUCAAUGUUCGAUGAC	174	sga-miR7502c-3p	UUGAGAAAAGUCUCAUCCAUG	70-90	gra-miR7502c	4	0	21	21	1
sga-MIR5014a-3	AAGUAGACACUUAAAUUUUAAUAAAC UUGAACAAGUAGACACAUGAGUCAU ACAUGACAUGAUACACGUAGGACAA AAAAUGACAUGGAGGAUGUCAUGUA GGACAUGUGUCUAUUUAUUCAACUU UAUACAAAUUAAAGUGUCUAUUA	149	sga-miR5014a-3-3p	UUAUACAAAUUAAAGUGUCUA	126-146	ath-miR5014a-3p	5	0	21	21	1
sga-MIR7697	UAUAUUCAGCCCAUACAAAUCCGAU CAAAUCCAAUGUACAAGCAUAGCAC AGGAAAUAGGCGUAUGACCCAAUCU CCUGUGCUAUGCUUGUACAUUGGAU UUGAUCGGAUUUGCAUGGGCGUAU GAC	127	sga-miR7697-5p	UCCGAUCAAAUCCAAUGUACA	20-40	mtr-miR7697-3p	6	0	21	21	1
sga-MIR10979	CGGAUUUUCCGAUAGAUUUGGAAGG UCAAACUUAAAACGUUAUUUUCAGU AACGUUUUACUCCUAAAACGUUACU GUGAGUAACGUUUAAGGAGUAAAAC GUUACUGUGAGUAACGUAUAUCAAU CUGACGCCAUCAUCUUUUAAAAAAU AAA	153	sga-miR10979-5p	UUUUCCGAUAGAUUUGGAAGG	5-25	mdm-miR10979	5	0	21	21	2
sga-MIR10532-1	GUUCGAAAUUUUCGAGAUACAAUUA UAUUAUACUAAGAUCUAUUACCUUU CUGAACUUAUUUUGUUAGCAAUUUU CUAUUCCUUUUCGGCCUACAUGGCA CUACGUAGGCCGAAAAGAGAUAGAA AAUUAUUAAUAAAAUAAGUUCUAACA GUAAUAAAACCUUAGUUAUAGAAUAA GUGUGUCUGUGAGAUUUCGGGC	199	sga-miR10532-1-3p	AAGUGUGUCUGUGAGAUUUCGGGC	176-199	sly-miR10532	1	0	24	24	1
sga-MIR160-2	GACAUGAAACUCUAUACAUGCUUAG CUCCUAGAAUGCCAUCUGAAAAGGC CAUCAAUUCUUGGUGGAACAAUGCA	116	sga-miR160-2-5p	UGCUUAGCUCCUAGAAUGCCA	19-39	vca-miR160-5p	4	0	21	21	1

	AAUGGCAUACAAGGAGCCAGGCAUG UUGUGUUAUCGAUCAC		sga-miR160-2-3p	UGGCAUACAAGGAGCCAGGCA	78-98	aau-miR160	1	0	21	21	1
sga-MIR9760	UCUUUCUCUCAUGAAAUUGAUGAGA AAUUGGAGGAUUUAGUAUUGACUGU UGAGGAUGAUUUGGGGAUGAAGAU GGUUGGAUGGGUCAUCCUCUCAUG AAAUUCAUGAGAAAUUG	115	sga-miR9760-5p	UGGAGGAUUUAGUAUUGACUG	29-49	gma-miR9760	4	0	21	21	1
sga-MIR156a	GGAGAGACUGGCGAGGGGGAGAGG GAGAGAGGAGAGCGAGAACUUCAGG GAGAGAGGCGAAUGACAAUAAUUUG CUAUGAGAUACAAUUAAAUCAAAUUA UAAUUAUAACAUUUAAUUUGAAUAUA UAUAUAUUUCACCUUUCUCCCACUA UUUUCCCUCUCUCUUGCCUCUCUCC UCUCUCUUCCAGUCUCGCU	195	sga-miR156a-3p	CCUCUCUCCUCUCUCUUCCAGU	168-189	zma-miR156a-3p	5	0	22	22	2
sga-MIR2655o	UACGUUUAUGUCCUUCAACUUUGAG UAUGUACAAAUAGACGCUUAAACUU GUAUAAAGUUGAACAAGUAAACACA UGAGUCCUACAUGACAUUAUACACG UAAGACAUCACUAGGAUAAAAAAAAU GACAUAUAAGAUGUCAUGAAGGACA UGUGUGUCUAUAUGUUCAACUUUAU ACAAAUUUAAAUGUCUACUUGUGUA CAUCGAAAGUUGAAGGCACUACACC AU	228	sga-miR2655o-5p	CGUUUAUGUCCUUCAACUUUG	3-23	mtr-miR2655o	4	0	21	21	1
sga-MIR8709b-1	AUUAGUUGAGGUGUCUAAAUGAAUU AUGCGGACAACUUUGAGUGGCUGGA GAUGACUUAGGCCUUUUAUAAAAUU GAAGAUUUCAUGCAUAAUUUUUCGA UCAAACUUCAACUGUU	116	sga-miR8709b-1-3p	UCAUGCAUAAUUUUUCGAUCAAAC	83-106	gra-miR8709b	7	0	24	24	1
sga-MIR1531	CAUAACACAUGCCUAAAUAAUUAAUU GUUCAGCUCUUCCUCCACAUCCAUU CAAAUGGUUUGAAUGGCCAUGGAGG AAGAGCUGAGUAAUUAAUUAUUAAU GUUGUUGUUGUU	113	sga-miR1531-3p	CCAUGGAGGAAGAGCUGAGUAAUU	68-91	gma-miR1531-5p	7	0	24	24	3
sga-MIR2921	AUGAGAUGGCUCUGAGGUUGAGUU UGAUCCACAUUCAUUUCAUUACACG AUAGUAUAGCAAAAUCUAUGUAUGU ACUACCUUGUAGUGAAAUGGAUGUU GAAUCUAAUUUAACCUUAGAGCUUU CUUUU	129	sga-miR2921-3p	UUGAAUCUAAUUUAACCUUAGAGC	98-121	osa-miR2921	7	0	24	24	3
sga-MIR5568f	UUUGCUCAAACUCUAUUCCAGAUUG UUUGAUAGAGCGCAUUAAAUAGAGU GUACUAACCAACAUUGAUUGUGGUG CACUGAUGGGAGUGUUUCAUUCUUA AUCAGAGAUCUCGAGUUUGAGCCCU UGGUGAAGAGAGACGCAGUCGCGG	125	sga-miR5568f-5p	UCUAUUCCAGAUUGUUUGAUA	12-32	sbi-miR5568f-5p	5	0	21	21	1
sga-MIR7787	UCGUGAAGAAGAGAAGCAACGAAAU AAGAGUAUAAGUCGUGAAAGAAAGC UAAGUUGUAUCUCUUUCAGAUUUUU UUUUAAAAAGCUAUUUUUUUUUUAA AAAAAACCCUAAUUGUCGCUUUUUU AUAAAAAAAAUGCGGUUUAUUGCGC UUUGCCCUUUGUGUUGUUUCUCGC UUCUUCAUCUGAAGCGAGCGCCUUU UUCAUAU	230	sga-miR7787-5p	GCGGUCGUGAAGAAGAGAAGCAAC	21-44	bdi-miR7787-5p	7	0	24	24	1

sga-MIR10532-2	AAGAUAGUGCCACGUAGUCUAAAAA GGGGUAAAAAAUUAUUGAUAUAAUA AGUUCAGGGGGGUAAUAGGACCUUA GUAUAGUAUAAGUGUGUCUGUGAGA UUUCGGGCAUACCUUGAGGGGUAC UUGGGCAUUAUCCCUAACUUAUUUU AUAAGUUACGAUAAUUAUCCUUUCU UACUAUCUGUUGUCUAUAAA	194	sga-miR10532-2-3p	AAGUGUGUCUGUGAGAUUUCGGGC	85-108	sly-miR10532	1	0	24	24	1
sga-MIR9471a-2	GGUUCUGAGAUUUAGUUGAUUUCUC UGGUGCUUACUCAACUAAUAGUUAU UAUGUAAGAAAAUCAAUAAUAUUGG AAGCAAGGAGAAUGGAGACUAUCAG GAUGAUAACUAUUGGUUGAGCAGCA UUAGAGAAAUUGACAUGAUUCUGAG AGGA	154	sga-miR9471a-2-5p	CUGGUGCUUACUCAACUAAUA	25-45	sly-miR9471a-5p	3	0	21	21	1
sga-MIR1919-2	GCAGAAUCGCUCCGACGCCUUUGAU GUUCACAUCUUCCGGUAGUCCUGUC GCAGAUGACUUUCGCCCUUUUAUGG AACCACACUUUCUCUAAUUUGAAUU CUAUGUGGUAGGACGAGAGUCAUCU GUGACAGGAUAAUGGAAGAUCGAGU UAUCAAAGGCUUAUUGGGCGUUUCC UU	177	sga-miR1919-2-5p	UGUCGCAGAUGACUUUCGCCC	47-67	stu-miR1919-5p	0	0	21	21	1
			sga-miR1919-2-3p	ACGAGAGUCAUCUGUGACAGG	113-133	stu-miR1919-3p	0	0	21	21	1
sga-MIR1027c	UGUGCCACAUCCAUCAUUGCUCUUG CAUACAUCUCUUAGAGAAGAUAGGU GGAUGCACCAGGUAUCCCUUCAAUU ACAUAUCAUUUCUAUCUUCUCUAGG AGAUGUAUGCAAGAGCAAUGAUGGA UGUGGCGCC	134	sga-miR1027c-3p	UUUCUAUCUUCUCUAGGAGAU	84-104	ppt-miR1027c	6	0	21	21	1
sga-MIR171b-4	UUUGGGAUUAAAAUGGAAGAAGCGA UGUUGGUGAGGUUCAAUCCGAAGAC GAAUUUAUGCUUAUUUUCGUAAAGA ACGAUCUCAGAUUGAGCCGCGCCAA UAUCACUUCUUAUUUUCAUUCCGUU ACCUAAGUUGCUCGAACUCUCCAAA	125	sga-miR171b-4-3p	UUGAGCCGCGCCAAUAUCACU	87-107	aof-miR171b	0	0	21	21	1
sga-MIR5303-2	AUUGUUGCCCCACCCCCGUCGGAUC CUCCAAAAAUGCACUACUUUUGGAG GAUCUGACACACACAUGUCGAUAUC UUUGAAGAGUUCGAGCAACAUAACU UCUCACUUUUGAAAUAUUACCUGAA	125	sga-miR5303-2-3p	UCUUUGAAGAGUUCGAGCAAC	99-119	sly-miR5303	1	0	21	21	1
sga-MIR12148	GUUCUGCAUGAUCCUUUAGUGGUUC GUACGACUUUAGGAGAAAAUGUAAG AAUGGAUAAAGUAUACAAGGAUGGA CUAAUAGUUGUAUGUGGUAGGACUA UGUGUGCAGACUUGGUUGAAUUACC CAUGCAUGAUUUUGAAAUCAUCUUU GGCAUGUACUAGCUUCAUAAGUGUU U	201	sga-miR12148-5p	CGACUUUAGGAGAAAAUGUAA	54-74	aof-miR12148	6	0	21	21	2
sga-MIR6139	AUUAACAGUAAGUACCCCAAUGACA CAUCCGAUUUCAACAAGAGAAGUUU GAAGGACAUGCAUUUAGUGUAAUCC AACUAUCCCUUGCACCUAACCUUCU UUGUGAAGUGAGUAAAAGUACUGAA GAGGUGACCAAAUAACUUUGGGAAG GGAUGGAAGGACUUUACUGGGACUA	247	sga-miR6139-3p	AAAUAACUUUGGGAAGGGAUGGAA	135-158	pgi-miR6139	6	0	24	24	1

sga-MIR398-1	AUUGGUGACAAGAAGGAUGUUGUUUCAACAACGUCUUUACACAUUUAAGAUGUAGUCGGGUACUUUGUUGCAGUACAACAGGGGCAACUUGAGAUCACAUGUUGUCAUUUUUUUCUUUUUGGUUUGAUUCGAUGAAUCAGUAUCUCAACAUGUGUUCUCAGGUUACCCCUGUUGAAU	105	sga-miR398-1-5p	GGGGCAACUUGAGAUCACAUG	9-29	hbr-miR398	3	0	21	21	1
			sga-miR398-1-3p	UGUGUUCUCAGGUUACCCCUG	79-99	bra-miR398-3p	1	0	21	21	1
sga-MIR5812	AAGACUUGUUGAAUCGUUUGGCAUAGGGGUGUCAAAUAGACGGGUUAGGUUGAAAUUGGAAAUAUUAAAAUAGGUUAAAGUAGAAACCUGAUUGACUUUUGACCCACCCAAGUUUACCUUGGGCUCAAAUGGUUGGGUUCAAAUGGGCUAAAAAUGAGUUGGGACUUAACCCGUCCAAUUUGAUCCGACUAAUCUCAAUGAUUUUAACAUAGUGAU	216	sga-miR5812-3p	CUCAAUGAUUUUAACAUAGUGAU	194-216	osa-miR5812	7	0	23	24	3
sga-MIR156b-5	AUUGAUUUGUGUAAAAUGUAGGGAGGAAAAAAAAAGAGGGGAAAAUGGAAUGGGUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUCUCCUUCUAUUUUUCUCUUUUCUCUCCCUAAAUCUAUACAAUAACUCGUU	246	sga-miR156b-5-5p	UUGACAGAAGAUAGAGAGCAC	63-83	aof-miR156b	0	0	21	21	1
			sga-miR156b-5-3p	GCUCUCUAUGCUUCCGUCAUC	162-182	vca-miR156b-3p	1	0	21	21	1
sga-MIR833a	GAUGACAUGUUCAUUGUCAAUGUAAAUGGUAUAGAGUUACAUUUUGACUUAAAAGAGUUGGUCGUUGUAAUCGGUCUAAAACCUGGACUAAUUUCUGAUUUUAUUUCUGAUCCAUUUGUUCCAAAUAGAUUAAUUGUAGAAAAUCUCGGAGACUUUGACAAAGUACCCAAGUCAAAUUUUUACCACAAGUUUAAAUUGAAAAACUUUUGGGAAGAAGAUGACCGUUUAUAAUCAGUUCAUGUAAUUCAUACACAUUUAAUAUAUCAUUCACUGUCCUA	278	sga-miR833a-5p	UGGUCGUUGUAAUCGGUCUAAA	59-80	ath-miR833a-5p	5	0	22	22	1
sga-MIR6027	GUAAUUUUACAUGAUUAUGGGUAGCACAAGGAUUAAUGUGAAACAGAAAGUGAUAUGCAAAGAAGAUGGAGAUUCAAUUGUUUAUUGUUACGAAGAAAGCACUUUUGUGUUUCUCGUGAAUCCUUCGGCUAUCCAUAAUCAUGUUGAAUGUG	153	sga-miR6027-5p	AUGGGUAGCACAAGGAUUAAUG	17-38	sly-miR6027-5p	0	0	22	22	1
			sga-miR6027-3p	UGAAUCCUUCGGCUAUCCAUAA	118-139	stu-miR6027	0	0	22	22	1
sga-MIR167c-4	UGGUGGCAUACAUACUUCUGUGGCUGGCCGAGCUGGUCAUAUAGUAACACAUUUCAUUUCGUCCAGCCUCAAAUAUAUGUAUGCUACCAAGGCCAAACUGACAUGUGUAACUAUAUGACAUGCUCGACCAGCCACAGAAGUAUGUAUGCC	154	sga-miR167c-4-3p	UGACAUGCUCGACCAGCCACAGA	116-138	stu-miR167c-3p	7	0	23	23	2

sga-MIR10540-1	AUUU CGUAUGGCUCUUGAAUUGUCGGAG UUGAUUUCUCAUAUAGUCACUUAAU UAACUGUUAUUAUCUUGUAAAAUUA CUUUUCUUUAUUGACUUUCUAAGCU AAUAACUGUUAGUUGAGUGAUCAUC UGAGAAAUCAACCUGAAUUGAUGGC AAUCUU	155	sga-miR10540-1-3p	CUAAUAACUGUUAGUUGAGUG	98-118	sly-miR10540	3	0	21	21	2
sga-MIR7984d-1	GGGAAAAUGGUCUAAAAGAUACUUC AAUUUUGGCCGAAAUUAAUGCUACA AUACCAAACUUUAUGGAGGACUUUU UGCCCCCAUGCAAGAUUUAAUAGUA CAUAUGUGCCCGUCUGGACAUAUUA CGAUUUAUAAUUUUUAUGCAAGAUU UUCUAUGUCCACAUGAGCACAUAUA UACCUUUAAAAUACACUGUUAAAUA	288	sga-miR7984d-1-3p	CAAUUUCGGUCAAAGUUCUGAUAU	246-269	stu-miR7984d-3p	1	0	24	24	1
sga-MIR5232	GUGAAGGGAGUAAAAGGUCUUUUCU AAAGUUUGGUACCAUUAUAACAAUU UCGGUCAAAGUUCUGAUAUAUUUCA GACCAUAUUUACU UUUGUAUCUCGAAUACAUGUGAAUC ACACCAGAUAUACACUAGGUACAUG UAUCUGGAUUGAUUUACAUGUAUUU GUGACACCGG	85	sga-miR5232-5p	UACAUGUGAAUCACACCAGAU	14-34	mtr-miR5232	6	0	21	21	1
sga-MIR11068c	AACCUAAUCCAUGGAUUAGUUAUAC CUCAUACAAGAUCUUAUUUUAUCCU UAGGAAAGGGAGGGAUAACUAAUCC AAGGUUUAGCAA	87	sga-miR11068c-3p	AUAACUAAUCCAAGGUUUA	65-83	lja-miR11068c-5p	5	0	19	19	1
sga-MIR10542-1	UCUCUCGUUAUAAAAGAGGCUCAUA UAUUGCCCUUACCGUUAUAUAAACG GCUCACAUAUACCCCUGCCAUUACA AAAUGGCUCACAUAUACCUCUGCCG UUACAAAAUGGCUCACAUAUACCUU UCAUUUAACGGAAGUUAAAAAAUUA GUUUUAAAUUUAUAUUUAUGACUUC GAAUUUGUUUAAAAAAAUUAUUUAG GGGUAAAAAUAAAAAUUUAGAUUAAU AAGUCCACUUGAGGAAAAGGGUAUA UAUGAGCCAUUUGUUUACAAGUAAG GGUAUAUAUGAGUCACUUUCAUAAC AAGGGU	307	sga-miR10542-1-5p	UAAACGGCUCACAUAUACCCCUG	45-67	sly-miR10542	6	0	23	23	1
sga-MIR7997c-2	GUUAUAUUGCUCCGACUCUUCAAAA GUGGUCACACCCAUGUUGAAUCCUC CAAAAAGGCAAUACUUUUGGUGGAU CCAACAUGCACCUGUUGACAUUUCU GAAGAGUUCGAGCAACAUAGU	121	sga-miR7997c-2-5p	AUAUUGCUCCGACUCUUCAAAAGU	4-27	stu-miR7997c	2	0	24	24	1
sga-MIR12151-1	CUCCUUUGCUGAAAUGCUGUGUGAA UUUGCAUCAGUUACUUGCCAAUGCU UUUUAUGUUUCAAGAAUGUCUGAAC UUAGAAAUUGGGGAGUGUAGGAGUA GUUAUUUAAUACCCUUCUUGAGAUU GAGCAGAAACAUUCUUGAAACAUAG AAAGCAAUGUCAAGUAACUGAUGCA AAUUCGCAAUCGCAAGGGUUCGCAA AGAAU	205	sga-miR12151-1-5p	GAACUUAGAAAUUGGGGAGUG	72-92	aof-miR12151	6	0	21	21	2
sga-MIR8763	UUAAAGAAAUAUUAAGCAAGGAUGU UAAUUCCAAAUGUGAUAUUAAGUAU	322	sga-miR8763-3p	UUCAUACUAUUAAAUGAGGUGGA	243-265	gra-miR8763	6	0	23	23	1

sga-MIR5021-1	GAUUUGGCUAAUGUAAGUGUCAUUA ACUUUAAGUGAGAGAUUAAUUAGUG GCUGAUUUGGAUUAAUUUAAUCCAA UGGGCCCCACCACUCAUAAUAAGUG GCUGAUUAGGAUUAAUUUAUGCUAG UGAAUUAAAAAAAGAUCAGAUUGUG AGCUGGCCUUAGUAGAUACGUGUAG AGGGGGGCUGCCUCAACUUCAUACU AUUAAAUGAGGUGGAGAAAUCCACU CUAUGCUAAAUAAAAUGGUGAAAUC CAUUGCUACAUAUCAUCUUCUU GUGGAAAAUUACUUUAUAGAAAAUU ACUUUCCUUCUCUCUUUCACUUUCA UGUCUUCUAAGCUUUUUUACUUUUU GAAGAUUAACAUUGAUGGUUCAGUU GUCGGAUUGGGACAAUCAAUGUUAA UCUUCAAAGUGAAAAAAAGCUUAGA AGCCAUGAAAUCGAAAGAGAGAAGG AGAAGGUGAAAAGGUUAAGUAAUUU UCUAU	205	sga-miR5021-1-3p	AGAGAAGGAGAAGGUGAAAA	168-187	ath-miR5021	4	0	20	20	2
sga-MIR7997c-3	CUUCUAUGUUGCUCGGACUCUUUAA AGAUGUUUACGGGUGCAUGUCUAUU UCUUCCAAACUAGUGCAUGUUUGAA GGAACCGACACAGGUGCAACAGCAU CUUAGGAGAGUCUGAACAACAUAGG UU	127	sga-miR7997c-3-5p	AUGUUGCUCGGACUCUUUAAAGAU	6-29	stu-miR7997c	3	0	24	24	1
sga-MIR8008b-1	UUGAUUUAUAUUUGCAGGUAUUGCA GAAAAAAAUGAGGAGCAGAGUGGUU UUGUCCGUCGCUUUUUUGCUUUAUU UAUUUCAAAUAAACCCAGAAAAGCGA CGGACAAGGUUCUUUGGUCCGUCAC UUCUCUAGGUAUUUUAAAAAAUUAA UUUCAAGGAAAGCGACAGACAUUGU CCUUUAGUCGUCCCUCGCUUUUCUG GAAUUUUCAAAAUAUAAAUUUA	223	sga-miR8008b-1-5p	AAACCCAGAAAAGCGACGGACAAG	86-109	stu-miR8008b	2	0	24	24	1
sga-MIR8730	AUAUAUACUCAUAUAAUAGAUUGAAA UUUUGUGGGACUCUACAAGAUGCGU UUAGUUCGAGUUGAGACUUUACAAA UUGUGUUCAACUCAAAUUAGGAUUC UUGGAGGCUACUCAACUCUAAACCC UAGUUUAUGCGUAUACAA	144	sga-miR8730-5p	AUAAUAGAUUGAAAUUUUGUGGGA	13-36	gra-miR8730	6	0	24	24	2
sga-MIR162b-2	UCCUUAGGGGUUAAGCACUGGAUGC AGAGGUUUAUCGACCGAUUCCUUUU GCUGUAUUUUUGCGUAUAUAUAUU UCAGCUUCCAGGGAACAGAUCGAUG AACCGCUGCCUCCAGUGUCUUCAAC CAACUAAACA	135	sga-miR162b-2-5p	UGGAUGCAGAGGUUUAUCGACC	19-40	ath-miR162b-5p	4	0	22	22	1
			sga-miR162b-2-3p	AUCGAUGAACCGCUGCCUCC	94-113	cas-miR162b	0	0	20	20	1
sga-MIR5035	UUUACCAAAUGCCUAGAUAAGCCAA AAAAUUGCUUAUAAGCUAGUUUGAC CCUCUUAUAAGCUUAGAGGGUGUUU GACUAAGCUUAUAAGCUGGUCAAAU UGGCUUAUUAACACUUUUUAGCUUA UCUACUCAUUUGGUAAA	142	sga-miR5035-3p	CUUAUUAACACUUUUUAGCUUA	104-125	gma-miR5035-5p	5	0	22	22	1
sga-MIR8743a	AAUUGAAUUUGGUGUAAUUACACUG UCUUGUCCUGUUUGGAAGGACACCC	167	sga-miR8743a-3p	AAGGACAAGUAAUUAAUUGGUCAA	95-118	gra-miR8743a	7	0	24	24	2

sga-MIR12162	UGAUAAUUGGAUUUGGUGUAAUUAC AUUGUCUUGUCCUGUUUGGAAGGAC AAGUAAUUAAUUGGUCAAUAGGUAU UGGUGUAAUUAGCAGGGUGUAAUCA CACUCUACAAUUCACCA CGGUGCGGUAAAGAUAUUGAUGAUG AAGAGAUUUUUUUUGAGAAUGUAUU UUUUGAAUGAUUGGAUGACUGAGUA AGUCUCCAAGUGGGAGAAUUGUUAG GUAGUGGAUCCUGAUUAAUAUAUAU AACUGUUUAACAAAAAAUACUCUGAU UUAUUAAUAUAUGUACCCAACC	173	sga-miR12162-3p	AAUACUCUGAUUUAUUAAUAU	141-161	aof-miR12162	5	0	21	21	3
sga-MIR1088	UACGAAAGAGGUGAAGGUGAUGACA GAAGCAUAGAGAGCACAAAUGAAUU GAGAUGCUUUUGCUGCCCAAAUUGA AUGAAAUUAGCAUAUCAUCAUUAGU GCUCUCUAUCUUCUGUCAACGGUAA UCACUCUUUCUUC	138	sga-miR1088-3p	UAGUGCUCUCUAUCUUCUGUC	97-117	smo-miR1088-3p	4	0	21	21	3
sga-MIR8045-1	UAAACUAUCAUCUUCUCGCAAGUGU AAUACCAUAACUAUCUAUUGUUCUA UUUACAUAACAAAUCUAUCAUCAUUU CACGAGUUUCGUACCUCAAGUAUCA GUGUCUUUGUAAUAAAACACACAUU GAAGUUGAAUUGCCUUACACGCGCU UGUUGUCAAUUGGGAACAAAUAAUU GGCCAACUCAGCAUCGAGAUAUGUU UUGAUACAAAGAGAGUGAUAGGUUU AAGUAGUUAAAGAGAACAAUAGAUA GUUGAGGUAUGAAACUUUCAAAGGU GAUAGUUUA	285	sga-miR8045-1-3p	AUAGAUAGUUGAGGUAUGAAA	245-265	stu-miR8045	5	0	21	21	1
sga-MIR1128-1	UAUUACUCCCUCCGUCCCAAUUUAU AUGAGUUAGUUUGACUUGUCAUGGA GUGUAUGAAAGAAGAAAAGACUUUU GAAACUUGUGGUCUAAAAUAAGUCC UAUAUAUUUGUAAGGCUAGAGCCUA GAAAUAAUUUCAUUAAGGGUAACAU GAACAUUUUAAAGUUAAAUCGUUAU UAAUUAUAGAAAUAUGUCAUUCUUU UUGGGACUGAGUAAAAAGGAAAGUA AGUCAUAUAAAGUGGGACAGAGGGA GUAGUU	256	sga-miR1128-1-5p	UAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1
sga-MIR1520l-1	GGGACAUGUGUCAUAAUUUUAUCCA UCGAUCCGAUGUUUAAUAGAUGUCA AGUCGGUAGAUAAGAUUAUGACACG UGUAUG	81	sga-miR1520l-1-3p	GAUAAGAUUAUGACACGUGUAUG	59-81	gma-miR1520l	7	0	23	24	2
sga-MIR5568e	CCCUCUAGUGCCCAAUUUAACUAGA ACUCAGAAUCUUAUUUUCUAGUAGA AGAUGGAAAAGUAGCGUGUAUUUUU UCUUUCAAGAAGAAACGUGUGUUUU AGGUUUUCUUGAGGAAAAAGAAUUU GUGUUCUCUUCUCCUCUUUGGAUUA GGAAGACAUCUCUAAAAGUAGGGAU UAUUUUAACCUAGAGAAAAAGAAUU CAUUUAUUCUAUACAAUACUUGCCC ACCCAAGUCUAUAGAGAGUUCAAUU GUUAAUUGGGAUCACUGGAAAA	272	sga-miR5568e-5p	UGUGUUUUAGGUUUUCUUGAG	93-113	sbi-miR5568e-5p	5	0	21	21	3
sga-	AGUAAUUUGUCUAAGUUUAAACAGG	116	sga-miR4408-5p	AAACAGGCUUGACUGAGGCUUGGA	19-42	gma-miR4408	7	0	24	24	2

MIR4408	CUUGACUGAGGCUUGGACAAUCCUC CUCCCUAUAAGCUAGUUAGUUUUUG GGGCCAUAAGUUAGGCCUAUGACUU AAUUUAACAAAUUUAU										
sga-MIR11514-2	AUAUUAGUACUUAAGUUCACUUAUG CCCUUACCGUCAAAUACUUGGUCCA AAUACUAUGCGCAAUUGAGCAGAAU AAGGGUGUAUGUGGGCCAAGUAUUU GAUGCUAAGGGCUUAAGUACAUUGA AGUAUAAACG	135	sga-miR11514-2-5p	GCCCUUACCGUCAAAUACUUG	25-45	pab-miR11514	6	0	21	21	2
sga-MIR2669b	UCUUCUCUUCAUCCGAAUGAUGAUG CAAGUGAUGCAGGGCCUGAUGGGU GAAUAAUGGAUUUCUACCAAAGUUC UAGGAAUUUCAUCAGUUCAGUCAUC AUGGAAGCCCUACAUCACUACCAUC AACAAUGUUAGAUGGUGAGACAA	147	sga-miR2669b-3p	UCAGUUCAGUCAUCAUGGAAGC	86-107	mtr-miR2669b	6	0	22	22	3
sga-MIR1069	GUGUGUUAAUGGCCUUCAUAAUCCC AAAUAAGCUGAGUUAAUUCAAAGUG CUUAUUUGAUUCAUGGGAGGCCUAA AUCAAUU	82	sga-miR1069-3p	AGUUAAUUCAAAGUGCUUAUU	36-56	ppt-miR1069-3p	5	0	21	21	2
sga-MIR8739-2	UAAUGAUAUGCAUAUACCCUCCGUC AUACUUUUAGGACAGUGGUGAACAU AUAUGUCCUUCACUCUAACGAAAGA CUAAAUAGGGACACGUGACACAAUC UUAUUCAUCGAUAAUAUUUAAUAAAU GUCGGGUCAGUCGAUGAGAUUAUG UCAUGUAUAUGUCCGUAUUCAUAAA GGGUAUAUAUGCUCUAAUUUUUGGA CGGCAUGAGCACCAAUGUCUCAAAA GUAUGACGGCAGAUAUUUUACAUAU CAUUU	255	sga-miR8739-2-5p	AGACUAAAUAGGGACACGUGACAC	73-96	gra-miR8739	5	0	24	24	3
sga-MIR1919-3	UCCGAAUCGCUCCGACGCCUUUGAU GUUCACAUCUUCCGGUAGUCCUGUC GCAGAUGUCUUUCGCCCAUUUAUGG AACCACACUUUCUUUAAUUUGAAUU CUAUGUGGUAGGACGAGAGUCAUCU GUGACAGGAUAAUGGAAGAUCGAGU UAUCAAAGGCUUAUUGGGCGUUUCC UU	177	sga-miR1919-3-5p	UGUCGCAGAUGUCUUUCGCCC	47-67	stu-miR1919-5p	1	0	21	21	1
			sga-miR1919-3-3p	ACGAGAGUCAUCUGUGACAGG	113-133	stu-miR1919-3p	0	0	21	21	1
sga-MIR396a-1	UGGCACUACAAGAAAACUGUGAAUU ACAUGGGAUUUUCCUAGGAUUAGUA UGAAAAUACGUAGGAGACUUAUUUU CCUGCAAAAAUUCAUCCUGAUUUUC AGGAAAAUCUCAAUGUAAUUCAUAC UUUUCUUGUAGUGUGG	141	sga-miR396a-1-5p	CUACAAGAAAACUGUGAAUUA	6-26	csi-miR396a-3p	6	0	21	21	2
sga-MIR12168	AGGCAUUCAAUCAAUUAGUGACAUC CAAAAAAUAAAGGAAUGUAGUGGGA UGGUAAGUAUUGUACUCAACCUUAA UUAAAAGUUUGGGGUUCAAAUAUUG GAUUGAUGUCA	111	sga-miR12168-3p	UUCAAAUAUUGGAUUGAUGUCA	90-111	aof-miR12168	6	0	22	22	1
sga-MIR159a-1	GAGCUCCUUGAAGUCCAACAGAAGA UCUAACAGGUUAGAUUGAGCUGCUG ACCUAUGGAUUCCUCAGCCCUAUCU AUUUAUGAUUUCAAACAUAUAGAUA GGUUUGUGGGUUUGCAUAUGUCAG	174	sga-miR159a-1-5p	GAGCUCCUUGAAGUCCAACAG	1-21	fve-miR159a-5p	1	0	21	21	1

	GAGCUUUAUUUUACCCUUUGUUUGA UCAUUUUUUGGAUUGAAGGGAGCUC		sga-miR159a-1-3p	UUUGGAUUGAAGGGAGCUC	156-174	cas-miR159a	0	0	19	21	1
sga-MIR3932b	UUAAAAAUGGGUUGAAUAGAAAUUA GGUUGGGUCAUGAUCCACCCAAGUU UACUUCAGGCUCAAAUAGGUUGGAC UCGAAUGGGCUAAAUUUGGUUGGG UCAUGACCCACCCAAUUUGACGUGC UUAAUCUGAAUAAUUUUAACAUAUU GUUAUCUAAUUUCUAUAACCACAAU UUGCA	179	sga-miR3932b-3p	UUUGACGUGCUUAAUCUGAAU	115-135	ath-miR3932b-5p	5	0	21	21	1
sga-MIR7828	AAAGAAAAAAAAAAUAAAUACUCCCGA ACUGCUAUAAAUGGUAUAUAAAUAU UCUUUAUUAUUCUUUUGAGAUAUUA AUAUCCCUGUCAUUCAUAAAUUAGA GCACAUAUGUCAUUCACUCUAACGA AGAGGCAGGGGCACCAUGUCCUCAA AGUAUGAUGGCGAGGGCACCAAUGU CCCAAAGUAUGAUGACAAGGACACC AAUAUCCCAAAGUAUGAUGGCGGGG GCAUCAAUGUCCCAAAAGUAUGACG AAGGGUAUUUGCAUACCAUUUACAA UAGUUUGGAGAUAUAUCUGUCCUUU UUCCCA	307	sga-miR7828-3p	GAUGACAAGGACACCAAUAUC	187-207	ptc-miR7828	2	0	21	21	1
sga-MIR11091	CGACUGACUUGUCUACUUCAAGUGU UGAUGAAGAAGGAAGCUGAGUAUUG GAGCAUGUCGAAGGAACAUGUUCAA CGAAGCUGACUGACGAGUUACAACA CUGUUGAAGAUUUAGAGUCAGAUU	124	sga-miR11091-5p	UGAAGAAGGAAGCUGAGUAUU	29-49	lja-miR11091-3p	6	0	21	21	2
sga-MIR1072	CGUAAGUCUUGAUUUCAACCAUGUG CUUGUCAACCUUAUGAAUAUAAAAAA AUAUAUUCAAAAUCAAUGUCAUGGU UUUCCGAGGUUCAUUUCUCUUCAGA AUCAUGGUGACGGGGAGAUUGAUUU AAAAUGGUUUCAUCCAUGACAUUGA GCUCUUCUUGAGUAAAAAUCAUAUU UCUGAGUUUAUGCUAUAGAAAAAAA NAAUAUUGUUUUCUUCAAAUCAUAA AAAAAAUAUGUCAUUUUUGUCUUCC ACUUCAGGAUACGCAGUGUGUGAUC UGAAGCAUGGAUAGCAAUUGUGUUG UCAAAUGGAUGACAACACUCAUGAA ACCAUACUUGCA	338	sga-miR1072-3p	CGCAGUGUGUGAUCUGAAGCAUGG	263-286	ppt-miR1072	6	0	24	24	2
sga-MIR8668	AGUUUGAUUUCUCAGAUGAUCACUC GACUAAUUGUUAUCAUCUCAGGAAG UCACUUUCUUUGUUGAAAGUUUUGG AAUCAAGAAGAAAGGGGACUUUCGA GAUAAUAACUAUUAAUCAAGUGACU AUAUGAGAAAUCAACCG	142	sga-miR8668-3p	UUUUGGAAUCAAGAAGAAAG	70-89	gra-miR8668	4	0	20	20	1
sga-MIR5303-4	GUUUCAUGAGAUUUAUGUUGCUCGG ACUCUCCAAAGUUGCUGGCACACUC CUGUCGGAUCCUCUAGAAAUGCAUU ACUUUUGGAGGAUCCAACAUGCACU UGGUGACAUUUCUGAAGAGUUCGAG CAACAUAGAUUAAUGAGAU	144	sga-miR5303-4-3p	UUUCUGAAGAGUUCGAGCAAC	109-129	sly-miR5303	1	0	21	21	1
sga-	UCUCAGUUGAGGGGAAUGUUGUCU	158	sga-miR166k-3p	UCGGACCAGGCUUCAUUCCCCC	128-	lus-miR166k	0	0	22	22	1

MIR166k	GGCUCGAGGUCACCAAUUAGAUCCA UAAUCCCUAUAUAUACCAUGCUUUU CAAAAAAAAGAUUUAUAAUAUGAAAA GGGGUUAUGAAUCAUGUGUUAGUG UUGUCGGACCAGGCUUCAUUCCCCC CAAUUGUUA			149						
sga-MIR8021-1	UCUUCAUAUUCAAGGCUCAAACUCG AGACCUCUGGUUAAGGAUAGAUGGA UCAUAUACAACCCACCACAACUUUUA UGGUACUAAUAAUGACUUGAUUUAC UUUCUCUUAAAUAUUUGACAAUAUG UUGGAUUUAUUUGUUGUAUUCUACC AACAAAUAUUUUGAUUGAGUGAAAG UUAGUAUUUAUUUAUCCUUAGCCAG AAGUGUCAGUUUCGAAUCUUAGACA UGAGUU	232	sga-miR8021-1-5p	AUUCAAGGCUCAAACUCGAGACCU	8-31	stu-miR8021	0	0	24	24	1
sga-MIR171c-2	UUUGAUUAACAUAGGCAUCAAAAUC AGACAUCAUACUCCAUAACAAACUUU GUGUGCAUAGUAGAUUUUGGUGCC UUGAAAUCUUU	86	sga-miR171c-2-3p	AGAUUUUGGUGCCUUGAAAUC	63-83	cas-miR171c-5p	5	0	21	21	1
sga-MIR5303-5	GUUUGUGUUGUUCGGAUUCUACAAA AAUGUUGCAGUGUUCGUGUCAGAUC CUCCAUAAAUGCGUUCUUUCUGAAA GUUCUGACACAUUUUUUAAGAGUUC GAGCAACACAGAU	113	sga-miR5303-5-3p	UUUUUUAAGAGUUCGAGCAAC	87-107	sly-miR5303	1	0	21	21	1
sga-MIR5085	GGCAACUAAAACCGCCAGUAAAAGC UAAGAAUGUCGUCAUGCAUCUUUUA GUGGCGAUUUUUACCGUCGCUAAAA GUUAUGAAUGUCGUCGCUAAAUGUU AUUUUUUGUGGCGUCUAAAACCACC GCUAAAAGUAAUAAAUAUCGUCACC AAAAGUAAUGAAUAUGUUUUAAUAU UUGUUUUUUAGUUUUA	191	sga-miR5085-3p	AAUGUUAUUUUUUGUGGCGUC	95-115	tae-miR5085	5	0	21	21	1
sga-MIR7997c-4	GUCUAUAUAGCUCGGACUCUUUAAA AAUGUCGGUGCACCCAUGUUGGAUC CAACCCAAAUCCUUUGACAUUUUGA AGAGUUCGAGCAACAUAAGU	95	sga-miR7997c-4-5p	AUAUAGCUCGGACUCUUUAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
sga-MIR8182	CAAAUAUGUCGUUCACUCUAAUGGA AGACUAAAAUGUCACAAUCUUAUCC GUCAAUCCGAUAGUGGAUAAGAUUG UGAUACGUGUAUGUUUGUUAGCAUA AAAGAUAUAUACG	113	sga-miR8182-3p	UUGUGAUACGUGUAUGUUUGUU	73-94	ath-miR8182	6	0	22	22	1
sga-MIR7992-1	UCCAACUUUGAGAAUGCACAUGUAG ACACCUCAACUGAACCCAUUGUGUC UCGUGGACACCCCAUGCUGACGUG GCAUAUGCACCUUGGAGGUGCCGA GAUGACCAUUUUCUAAUUCGGGAGU GUUCAAUUAACACAGUGGAGACUAG UUGAGGUGUCUAGAUGUGCAUUCUC AAGGUUUUU	182	sga-miR7992-1-5p	UUUGAGAAUGCACAUGUAGACACC	7-30	stu-miR7992-5p	3	0	24	24	1
			sga-miR7992-1-3p	UGUCUAGAUGUGCAUUCUCAAGG	155-177	stu-miR7992-3p	4	0	23	23	1
sga-MIR10541	UAUAUUUUGUUGAGUUUCAGUUUGA UGAUCAACAAACGAUGUGAUGACAU UGUGGUGAGCUGGCUAUUGGUGAA UAACACAGUCAUGCUCUAUAAGCUC UUCGAUAGAUUUGUCACAUAAGCUC	289	sga-miR10541-5p	UUUCAGUUUGAUGAUCAACAAACG	15-38	sly-miR10541	7	0	24	24	3

sga-MIR5014a-4	AUUUGAAUUAAGAGUAACUUUUAAU AAUAAUGAAUAUAAUCAAUAAAAUUU CACAAUUGAGAUAUAUAGAGAGGGU GAUGUGUAUGGAGUCUUAUUUCUAU CUUGUGAGGAUAGAAGCGUUGUUUU CGAUAGAUGUUCAGCUCAAUUAAAG UAUAACAAAAUCAG GAUUAUGACCUUUAACUUUAGAUGU GUACAAGUAGACAGUUAAACUUGUA UAAAAUUGAGCAAAUGAACGCAUUU GUCAUACAUGAUACCGCUACAUGAC AACUUUGUCUCCUACAUGACAUUCU ACGUGUAUUAUGUCAUUUAGGACAC UUGUGUCUACUUUUUCAAUCUUGUA CAAAUUUAAGUGUAUACUUGUGUAC AUUCAAAGUUUAAGGACAUAGUU	223	sga-miR5014a-4-3p	UUGUACAAAUUUAAGUGUAUA	171-191	ath-miR5014a-3p	2	0	21	21	1
sga-MIR1133	CAUAUACUCCCUCCGUCCCAAUUUA UGCAAAACAUGCUUGACUGGGCAUG GGCAUGAAGUUCAAGAAAAAUGACU UUUGAAAUUUGUGGUUUAAAACAAU UUUUGAGAACUUUCUUUGGCCGUAA AUUAUUUCAUUAAGGAUAAAAGGUG AAGUUUAAAAUCAAAUUGUUACUAAA AAUAGAAAGAUGUCAUUCUUUUUGG GACUUAAGAAAAGGAAAGAGUAUCA CAUAAAUUGGGACGGAGGAAGUAUG UA	253	sga-miR1133-5p	CAUAUACUCCCUCCGUCCCAAU	1-22	tae-miR1133	2	0	22	22	1
sga-MIR7992-2	UAAUCAAGCUUGAUCUCAGUUGAGC AGUAAACACUCCAACUUAGAAGAUG CACAUCUAGACAGCUCAACUCAAAU CCACUGUGUCAAUUGAGGUGUCUAG AUGUGCAUUCUCAAAGUUGGAGUGC UUACUUGCCAAUUGAGGUCAAGUUU GAGUG	155	sga-miR7992-2-5p	UUAGAAGAUGCACAUCUAGACAGC	41-64	stu-miR7992-5p	5	0	24	24	1
			sga-miR7992-2-3p	UGUCUAGAUGUGCAUUCUCAAAG	94-116	stu-miR7992-3p	5	0	23	23	1
sga-MIR6232b	GAGCUCUACAGUGCAACUUCAGCAU AGUAAAGAGUAGAGACUAAUUAAUG CCUACAUAUGUAGGGAUUAAUGAGU CUACUCUUUGCUAUACUGAAGUUGC ACUGUAGAGAUA	112	sga-miR6232b-3p	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-5p	5	0	21	21	1
sga-MIR5014a-5	ACCCUUUAAUUUUUAAAUGUGCACA AAUAGACACUUAAACUAUUAUAAAAU UGAACAAGUAAACACAAUUAUCCUAC AUGACAUAAUACAUGUAAGAUGCCA UAUAGGAUACAAAAUUGCCAUGCAG GGUGCCACGUAGGACAAUGUGUUUA UUUGUUUAAUUUUGUACAAAUUUAA GUGUCUACUUGUGCACACUCAAAAU AAAGCAU	209	sga-miR5014a-5-3p	UUGUACAAAUUUAAGUGUCUA	164-184	ath-miR5014a-3p	3	0	21	21	1
sga-MIR156b-6	UAUUGUUGACAGAAGAUAGAGAGCA CGAAUAAUGAGGUGCUAAUUGGAAG CUGCACCUUAAUUCUUUGUGCUCUC UAUUCUUCUGUCAUCAUCU	94	sga-miR156b-6-5p	UUGACAGAAGAUAGAGAGCAC	6-26	aof-miR156b	0	0	21	21	1
			sga-miR156b-6-3p	GCUCUCUAUUCUUCUGUCAUC	70-90	vca-miR156b-3p	1	0	21	21	1
sga-MIR156g	GUGUCAAUAACAGCUGUGAAGGAAU AUCUGGGCCCAAAGAUGUAUUGACA	119	sga-miR156g-3p	GCUUUCUCUUUUUUUGUGUCA	53-73	aly-miR156g-3p	5	0	21	21	1

sga-MIR8011a	UAGCUUUCUCUUUUUUUGUGUCAGUACAUCUUUGGGCCCAGACAUAUUCCUUCAUAGCUGUCAUGAUUAAUGGAAAGAGUUUACUUUGUGUCUCACACAACUGACACAAGUUGUGUGGGGAUUCUUUUUGUUUCACAAAUUUGUGGACCAAAAGUGUAAGACUAGGGUCCAGUAAUUUGUAGAUCAAAGCCUCACACAACCUGUGUCUGUUGUGUGAGACACAAAAUGAAGUUUCUCUUG	171	sga-miR8011a-5p	UUGUGUGGGGAUUCUUUUUGUUUC	42-65	stu-miR8011a-5p	2	0	24	24	1
sga-MIR8005c	AGAUUUUAUGUAUUUUUAGCUUCUUAUAAACUCUUAGUUAGUAAUUUGAUUAUAGAUGUUCUUGUGAUGAUGACUUCCAGAUUUUGGGAAUAAUAAUAAUACUUAUUGAUUUUAUUAAUGAGUUUAAGUCUUCCGCCCGAAUUACUUUUGUUGAUAUUAUAUUGAAAUGUUAAGGUUUAGAUUUGGUUGGUUCGCUCAGUGUGGGUGCCAGUCGCGGCUCCGAUUUGGGUCGUGACAUACUAUUACAAAUCUAAAUACAAUUUACACGAAGCAAAAGAAAUAAGAAAACAA	291	sga-miR8005c-3p	UUGAAAUGUUAAGGUUUAGAUUUG	162-185	stu-miR8005c	6	0	24	24	1
sga-MIR7819	AGAGUUUAGUAGCCUUGUAUGUCGAUUACGUAAGUCAUUCUAUAGUCUGAAACAAUCUUUUCAAGCUUGGUUUGGAAUUGCUUAAUGUCGCUAUUUCUGACAGAUCUCUUGAGAAUAUGAUAAUCUCGGUUCCAAUGCUUGAGGACAUACAGCUAGAUAUCACAUACCCUUUGAACUUCCAAACAGACCAUAGAGUGAUUUACGUAAUUAACAUACAAGGCUACUAAACAAC	232	sga-miR7819-3p	UCUUGAGAAUAUGAUAAUCUC	107-127	ptc-miR7819	6	0	21	21	1
sga-MIR5303f-3	UAUGUUGCUCGGACUUUUCAAAAAUAUCAAUGGGUGUUUGUCGGAUACUCUAUAAAUAGUGCAUUUUUGGAGGAUCUGACACGGGUGUGGUAAACAUUAUUGGAGAGUCCGAGCAACGUG	120	sga-miR5303f-3-3p	AUUUUUGGAGGAUCUGACACGGGU	63-86	stu-miR5303f	1	0	24	24	1
sga-MIR1885a	CUUGCUUAGAGAUUCUAUGGAGAAAGUCCGUAUGAUUCAGUAUAGAUUACUGACAGCUCAGAGUCGACAGAAGAGUUAUGCAGACCGGAGAUUUAGAGCCUUAGUGUUUAUGGAGGGUGAUCAUGUUUGGCUUCGAGUAUCAUCAAUGAAAGGUAUGAUGAGGUUCGAAAAGAAGCGCAAGCUUCGCCGUAGAUUCAUUGGACCUUUUGAUAUUUUGAGCCAAGUGGGAGAGGUGGCCCAUAAGUUGGCCUUGUCACCUAGUUUGUCUGCAGUUCAUCCUGUUUUCCAUGUCUCUAUGCUUC	302	sga-miR1885a-3p	CAUCAAUGAAAGGUAUGAUGAG	141-162	bra-miR1885a	3	0	22	22	1
sga-MIR5211	CCUUUUAAGCCAAUGAACUCGAUGAAAUAAUGGUUGUCCCCUCUCACUAUGACAUUAGCUGUGGACAACCAAUGAAGCUUCCAUUGAGUUCGGUGGCUCUCAAGCU	106	sga-miR5211-3p	GUCCCCUCUCACUAUGACAUU	36-56	cpa-miR5211	6	0	21	21	1
sga-MIR9736	CGCUUGCCAAGUUUGCACACUGCAAGGACUUGGCGGGAAUAUGAUGCAAC	331	sga-miR9736-3p	UGGAACACAAACCAAGGUGGA	174-194	gma-miR9736	4	0	21	21	1

sga-MIR5014a-6	UCUAAGAGAACAACUGCUAGGUGGA GCUGGUAUGUUCAACAAAGGUUUGA UUCUUCUUGUUUCUUACAAUGGGAU UGCCCAGUAAGCUUAGAAGUUUUGG CCGGAGUUGUUUAUACGCAUGCUUG GAACACAAACCAAGGUGGAGAUUGA AAGAGUUGGUUUUGGUUCUUGUGG AAUCAAACUAAAUGGAAGAUGAAUUA AUAUGAAUAUUUGGUAGGAAGAUAA UUAGUACAAAAUACAAGUCAAAGAUU GUAUCUUGGUAGGUGAAAGUUAGGC AAACC UACUUAAAAUAUUUAAAGUCAAUUUA GUUUACUAUCGAAAUUCUAUCUAUG CACAAGUAGACACAUAAACUUGAACA AGUAGACACAUGAGUCCUUUGUGGC ACAACACACUUAAGACAAAAAAUGAC AUGUAGGACAUGUGUGUCUAUUAGU UCAACUUUAUACAAGUUUAAGUGUU UACUUGUGCACACCUAAAGUUGAAG GGUAUUAAUGUGAUUUGAAGCCAAU UUAACGG GGUAAGUUUUUCACUCCCCGAAUCA AUUUUUCAAUUCGUGUAACAUAAUA GAAUGGGUGAAUAUUGAUAUUGGGC UUUAUCUAGGGUUUAUCGAAUUGUU AUAAUUUUGAUUAAUUAGCGAUUGU UUAUUGAUUUCUGUGUUAUUGUGAU UGUUUGUAGACCAAGAACAAGCGGA ACAAAUUCUUAAGGGGAAUGAAAAG UCUUUGG UAGUUCAAAGUGGAAGUUGCGAUUU CCAGCCUUUAGAAGGAAUAGCGAAA AAAGUAGCCGUAAGAGAGAAGAAGG CCAAAAAAUCUAUUCAUGGCCGAAG AGGAGAAAUGCUGAAGCAUUGCAAG GACUAAUUAUCAACAAGAGGAAGAA GGUAUAAAAACUUUCUUUUAUUACG UAUAUUAUAAUCUUAUAUACAUGUU AUAAGUUGUUAUCUUGAUUAGACAU UAAUAAAAAUUCUUCAAAAUUGAUAA GUAGUUCAAAGUGGAAGUUGCGAUU UCCAGCCUUUAGAAGGA UGAGUUUGAGGGGGAUGUUGUCUG GCUCGACACAAUUACUCUAUUGUAU GUAUUUAGUUAUUUGUUAUCAAGAU UGAUGUCGAUAACGAAUAAAUUAAA CACAUAUAUACAAGAUGUAAAAAGG GAGUAAAGGCGUCGGACCAGGCUUC AUUCCUCUCAAACAAU	235	sga-miR5014a-6-3p	UUAUACAAGUUUAAGUGUUUA	160-180	ath-miR5014a-3p	5	0	21	21	1
sga-MIR1882e		207	sga-miR1882e-5p	AUAUUGAUAUUGGGCUUUAUCUAG	61-84	osa-miR1882e-3p	7	0	24	24	3
sga-MIR7840		293	sga-miR7840-5p	CAAGGACUAAUUAUCAACAAG	122-142	ptc-miR7840	6	0	21	21	1
sga-MIR166c		165	sga-miR166c-5p	GGGAUGUUGUCUGGCUCGACA	12-32	sly-miR166c-5p	0	0	21	21	1
			sga-miR166c-3p	UCGGACCAGGCUUCAUUCCUC	136-156	sly-miR166c-3p	0	0	21	21	1
sga-MIR172-11	AUCAGUCAAUGUUUGAGGAUGCAAC AUCAUCAAGAUUCACAAAACUUGAA GGGAGAAGUAUUUAAUUAUAUAUUU AGGGUGAAUAUUGGAUAUAUAAUAU AGUUCAAAGUCUCUUAUUUUCUCUC	169	sga-miR172-11-3p	UGGGAAUCUUGAUGAUGCUGCAU	128-150	aau-miR172	1	0	23	23	1

sga-MIR7533b	UUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAUCAACUUGUCUUACUCUAUUUUCCUAAAAAAAGAGUAGAAGAGAAAAGCUUAUUGUCUGUUUCUCCAUUGAUCUCUUGGGCUUAUCGAAGCUUCUUGAGGAGGUUAUGGAAAGAAGGUUGAGUGCUUGUAGUAAAAAAGUAUAGCAAGUCAU	152	sga-miR7533b-3p	GAGGUUAUGGAAAGAAGGUUG	100-120	lja-miR7533b	5	0	21	21	1
sga-MIR5240-1	AUGAGGGAGGAAAAGGUUGAGGAUUUCAUCAACCUUAAGCAAGGCUCUAUGAAGGUCAUAGAGUAUUCCCUUAAGUUUGUUAAGCUAUCAAGGUAUGUUACUUCCCUUAA	110	sga-miR5240-1-5p	AGGAAAAGGUUGAGGAUUUCA	8-28	mtr-miR5240	6	0	21	21	3
sga-MIR395a-2	AGAAUUUCAUUACUACGUUGUUUGAUGCUUUGUUGAAGUGUUCGGGAGAAUUUCCAGGCUCACUUUGAAAUUUACACAAACAAAUAGAAGUGUUAGAGUAUUAAUGGGAGACUGAUUCCCGAGAGUUUUUCGAGAGUUUCCUUGACCACUUCGUGAGGGCUUAAUUACUUUGUUGUCUUAUGCCUUGUUGAAGUGUUUGAGGGAAUUCUGGGUUCACUUUAAAUUUACACAAAUAAGUAGAAGUAAAUGAG	252	sga-miR395a-2-3p	UGAAGUGUUUGAGGGAAUUCU	189-209	aof-miR395a	2	0	21	21	1
sga-MIR395g-1	UUGAAGUGUUGAGGAGAAUUUUCAAGCUCACUUUGAAAUUUACACAAACAAUAGAAGUGUUAGAGUAUUAAUGGGAGACUGAUUCCCGAGAGUUUUCUUGACCACUUCGUGAGGAUUUAAUUACUUUGUUGUUUUAUGCCUUGCUGAAGUGUUUGGGGGAACUUUCGGGUUCACUUUAAAAUUUACACAAAUAAGUAGAAGUAAAUGAGUACUAAUGGAAGAUGAUAGAUGAAUGCAACAAUUUAUUUUAUAUCUAUCAAGGUGUUUUCGAGAUUUCCCUUGACCACUUAAU	293	sga-miR395g-1-3p	UGAAGUGUUUGGGGGAACUUU	146-166	gma-miR395g	0	0	21	21	1
sga-MIR2275a	UAGCAUCUGCCAGGUCUAGUCAUGCCUUGGGCCACGGCUGUUUCUAUGACAAACUUGGGUUUGGCGAGAGUCUUCGAGGUUUGGCGAGAGUCUUCGAGGGCACCAAGGCAACAGCCUUCGCAGGUGUCA	129	sga-miR2275a-3p	AGAGUCUUCGAGGGCACCAA	87-106	ata-miR2275a-5p	5	0	20	20	2
sga-MIR2879	UAAUGUACAAACAGACACUUUAACGAUUCAACUUUUAAAUAAAUAAACACGUGAGUCCUACGUGAUACAAUACACGUAGGACACCACAUGGGACAAAAAAAUGACAUGUAGGAUAUGUGUGUCUAUUUGUUCAACUUCAUACAAGUUUAAGUGUCUACUUGUGCACAC	168	sga-miR2879-3p	ACCACAUGGGACAAAAAAAUGACA	83-106	osa-miR2879	7	0	24	24	2
sga-MIR11107c	CGGUGGGUCGUUUGGUAGAGUGUAUAAAAAUAAUAAUGUAUGCAUUAGUUUUGUGUAUUAUUAGUAUUUUAUUUGGUACUCUUUUUCAACACAAGUAUAACUAAUGAUUGCGUUAGUUAUAAAUUCUAUUGUGUAUUUGGGUGUGUAUUGCUAAUGUCGUGAAUUUCUAGGUA	341	sga-miR11107c-5p	UAGUUUUGUGUAUUAUUAGUA	46-66	lja-miR11107c-3p	5	0	21	21	1

sga-MIR11329	UUAGCAAGACAACGAGUUUAAUGCA UGCAUUAGCAUAAUUAAAGACCCAA UUGUCCCUCACAAUAUUUUCUUACU UCUUUUCUACCAUAAUAGUGGAGGG UAUCUUUGUAAAUUAAUUUUUAUGC AAUGCAUGCUAUUAUUUUAUGCAUC AUACCAAACAACACAUGA UCAAAUUCAGACCUGUGAUUGAAAU UUGAGAAUGUCAAAUCUAACUUCAA AUCCAAAUGAUUGAAGUUGAAGUCA AACAUCAGUUUUUUGGGUUUGAAUU AGACUUGGCAGUCCCCAACUUCAAA CCUUUUGAAUUAGG	139	sga-miR11329-3p	AAAUGAUUGAAGUUGAAGUCA	55-75	ppt-miR11329	6	0	21	21	3
sga-MIR8599	CUAGAUAUUAACAGGAGUAUCAAAU GGGCGGGUCGGGUUGAAACUAAAG AUAUUAAAAUGAGUUGAAAUAGAAU CGGGUUGGGUCUUGACCUGCCCAA GUUUACUUUGGGCUAAAAUGGGUUG GGUUCAAAUGGGCUAAGAACGGGUU GGGUUUUGAACCACCUAAUUUGACC CGAUUAAUAUCAAC	187	sga-miR8599-3p	CUAAAAUGGGUUGGGUUCAAAUGG	111-134	atr-miR8599	7	0	24	24	1
sga-MIR530-2	UGUCAUGUUCAGUAUUUUCUCACUU AAAUUAUUCAAGAGUAAACGAACAUU UACACCCUCGAACUCUGGGUGUGGA UAAGUAGACAAUAGAACUUAGACAC AUGAGUUCUACUUGACAUGAUACAC AUAGGUCUCAAAUUGUUAUGUAGGA CGUGUGUGUCUAUUUGUUCAACUUU AAAAAAAAUUGAAGUGCCUACUUGU AUAAAUCCAAAAUUGGCAGGUGUAA GUGUUAAUUGAGUCCAAGUUAAAGG ACAUAAUACAUAAAUAUGUCC	272	sga-miR530-2-3p	AGGUGUAAGUGUUAAUUGAGU	219-239	sly-miR530	5	0	21	21	1
sga-MIR7997c-5	AUGUUAUGUUGCUCGGGCUCUUCAA AAAUGAUUUAUAAGAUCACCCUCAA CAAUGAGAUACUCACUUUUGAAGAA CCUUUUCAUACGUUAGGUUGUUUGG ACUCUCCAAAAAUAUACUCUCACCAA GUCUAAUCCUCAACAACCGCACUAA CUGUUGUAGGAUCAGCAUAAGCACG UCAACACUUUUGAAGAGUUCGAGCA ACAUAAAAC	210	sga-miR7997c-5-5p	AUGUUGCUCGGGCUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
sga-MIR5781	UGCACCACUAUCCUGAAUUAGAGAC UGCAUGAUGCGUAGAAAAAUUUUCC UUCUUCUAAUCUUAUCGUGCCUUCU CUAAUGUCGGAUUUAUUGGUAUU	98	sga-miR5781-5p	CUGAAUUAGAGACUGCAUGAUG	13-34	gma-miR5781	6	0	22	22	1
sga-MIR9477-1	ACACACACCUCAACUAUUAGUUGUU CUCUUUUCCUACCUGAAUGAUGGUG AUAUUCUAGGUUGGGAAAGGGAACA ACUGAUAGUUGAGGUAUGUUU	96	sga-miR9477-1-5p	UAUUAGUUGUUCUCUUUUCCUACC	15-38	sly-miR9477-5p	3	0	24	24	1
			sga-miR9477-1-3p	UUGGGAAAGGGAACAACUGAUAGU	61-84	sly-miR9477-3p	0	0	24	24	1
sga-MIR7992-3	AACCUUAACUUGGACUCAAUUGACA GCUAGCCAACCUAACUCUGAAAAUG CACAUCUAGACCCCUUAACUUGAUC UAACUUUCCCCCUUUAAGACCUCAA CUUUGAGAAUGCACAUCUAGAAUUC ACAAUUUGAGAAUGCACAUCCGGAA AAGUGUAUUUAGGGGGCCAACUUAC	249	sga-miR7992-3-5p	UUUGAGAAUGCACAUCUAGAAUUC	102-125	stu-miR7992-5p	5	0	24	24	1

	ACCAGGUUAAGAUGUCUAGAUGUGUCUUUUCAAAGUUGGGGUGUCCAAUUGUCAGUUGAGACCAAGUUAAGAUG		sga-miR7992-3-3p	UGUCUAGAUGUGUCUUUUCAAAGU	188-211	stu-miR7992-3p	2	1	24	23	1
sga-MIR9476-2	GCUAUUUAGCGUUAAAACGGUAUAUAAGACUACUAGACAGCUCAAGCUUAAAAACUCUAACUUGCCUACCAGUUGACCACCAUAACCAAUGAAGACAGUCCCUAACCAAAGGGGACUGAGUCAACUGGUAGACAAGUUAGAGUGUUAAAGCUUGAGUUGUCUAGUAGUCCUACAUAUCUUUUUAUGCUUGAAUCCA	196	sga-miR9476-2-3p	AGUAGUCCUACAUAUCUUUUU	163-183	sly-miR9476-5p	5	0	21	21	3
sga-MIR11085	ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAAUUCCCUACCAUAUUGCCAAAUAUUUGCCUUUAUCUUUGUGUUCAUCUAGCUAAAGACAAAUGUUUGGCAAUAUGGUAGGGGAUUCUGGUCUUCUGUACACAGGGAAAAGUUGACUUCU	151	sga-miR11085-5p	AGUGAACUUCAUCUUUGUAA	4-23	lja-miR11085-3p	5	0	20	20	1
sga-MIR167h-2	UUCCGCGAAACCAUCAACAGGUGAUGCUGCCACAUGAUCUGAUCUUUCCUCGUACGGAGCAAUAGAAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGGUUCACGAUC	113	sga-miR167h-2-3p	AUCAUGCUGGCAGCUUCAACUGCU	76-99	gma-miR167h	1	0	24	24	1
sga-MIR2622	UUUUCCAGAAGUUCAGGAUGAAGCACGUUCCACAUGUAGAACAAAUUUAUCUACACGUUGAAUGUGCUUCAUCCUGAACUUUGGACCU	88	sga-miR2622-3p	AAUGUGCUUCAUCCUGAACUUU	61-82	mtr-miR2622	7	0	22	22	3
sga-MIR10186e	GACGACAUGUCACUUUGUUGAGCGAUUGAAGUUCAACAAAGCCAAUGGGAUUUAAAAUGUUAAGUUUCAUUGAGUCUAAGGGCUUAGUUGAGAAAUAGUUAAGUAGAAGGGUUUAGAAUACAAACUGAUACAAGUAUAAGGGUCUACCAGACCAUUCUGUCAAUAAUAAUUAACUAAAUAGUCCUAAAAAUGACGCAUGUCUUG	205	sga-miR10186e-5p	AUGGGAUUUAAAAUGUUAAGUU	46-67	gma-miR10186e	4	0	22	22	2
sga-MIR8739-3	AAGACUAAAUAGGGACAUGUGGCGCAAUCUUAUCCGUUGAUCCGAUAUUUCAGAAAUGUCGGGUCAGUGGAUAAGAUUAUGGCACGUGUAUGUCAGUUAGUAUA	104	sga-miR8739-3-5p	AGACUAAAUAGGGACAUGUGGCGC	2-25	gra-miR8739	6	0	24	24	3
sga-MIR2864	CAUUGCACCUAUGGACGUGUUCGAUAUCAUUUUGGGGCUGGAGUUUUGGUACGAGGUUAACGCGUUUAUUUCACCGCGUCACAACCAGAUGCACAUCAGCGACACCGGAGGUUCAUGCGUGGUACCCCUUAUUCAGGUACCACAAAACGGGAUGCACUUAUCGGUGAUGCAAAUUGUUAAGGUUUUUAAGAGAGGUGAACCAACCUUUCUUGCUGCCCUUGUUGCUUUUCUGAGGCAGUUCCAUUUUCUCAUUGCAUUGAGCACGUCCUUAGUGACAAUA	280	sga-miR2864-3p	UCUUGCUGCCCUUGUUGCUUU	208-228	osa-miR2864-1	6	0	21	21	1
sga-MIR477d	UACAUAAUACCUAUCAGCAGGCUGGGUGUUUGUGGAAGCAGUUAACUAGA	218	sga-miR477d-3p	UGUGGCCUGUGGGUAGAGUGG	156-176	csi-miR477d-3p	4	0	21	21	1

sga-MIR10186l	CUGCAACCACAAUCGCCCUCUUUGUCACCCUUCCUUGCGGAAUUUUACCAAAAGGGUUUAUGUGCUCAGAUGCACCUAAAAUCAGGCUACUAGUUACCACAAAGGUGUGGCCUGUGGGUAGAGUGGGCAAGACAAGUGGCCCAUCCGAGUCUGCUAUGUUAUCAUACCUCAGGUUAUGCUCACAUCAUUAAUAUGACGACGAGAUAAAUCUCUGACAAAUCUUAUAUGAUAAAUCACGAUCAAAAUAUUGAAUAUAUAAAAAAUGUAAGUCUUAGAGACCUUCGGAUACGUUCUACGAAAUAAUGAAUGAAAAAAAAAAAGUGGAGAUGCGGGGGAUCGAACCCCGUGCCUCUCGCAUGCAAAGCGAGCGCUCUAUUUUAAUACCAUUAAUCAAAUUGAGAGUAACUUAUAAGGUCUGCGUAUAUUUUACAUUUUCAGAAUUCACUUGUAAAAUUAUGUAGAAUAUGUUAUAGUUAUUCAAUUUAUAUAUGAUCGAGCAUCACCAUCAUGGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGCUCG	339	sga-miR10186l-3p	UUUUCAGAAUUCACUUGUAAAAUU	264-287	gma-miR10186l	6	0	24	24	1
sga-MIR390a		106	sga-miR390a-5p	AAGCUCAGGAGGGAUAGCACC	20-40	sly-miR390a-5p	0	0	21	21	1
			sga-miR390a-3p	CGCUAUCCAUCCUGAGUUUUA	69-89	sly-miR390a-3p	0	0	21	21	1
sga-MIR8138	GACAUAAGAUAGGUGGACUCCUUGUAAGGUUUGGGCAAUCCUCAUCCCACCUUUUGGGGUGUGAGUUAAGUCUAAGACCUAAUUACACAUGGUAUCAAAGGAUUGUACAAGCUUUAUAAGGAGUCCACUAUCUCAUUAA	139	sga-miR8138-3p	UACACAUGGUAUCAAAGGAUUG	84-105	cpa-miR8138	5	0	22	22	1
sga-MIR9477-2	AAGCCAACUAUCCGUUGUUCACUUUUCCUACCUAAACACUCUGUGUUUUCUAUAUAGAUGGUGAUAGUUCAGGUACAAGAGGGAACAACAAAUAGUUGGGAU	102	sga-miR9477-2-5p	UAUCCGUUGUUCACUUUUCCUACC	9-32	sly-miR9477-5p	1	0	24	24	1
sga-MIR7493b-1	UAAAUGAGUCUCUUUUCUGCAUUUAUAAAAUGUUAAUUAGAGACCUGAUGAGGUCUCCAUUUUGAAAUAGCUGAAAAAAUUAAUACAAAAGGGAGACCUCAUGAGGUCUCUCUUCUGCAUUUAUAAAAUAGAAAAUGGUAAAUAGAGACCUCAUGAGGUCUCUAAUGUGAAAUAUCUGGAAAAAUUAAUGCAAAAAAGAGACCUCAUGAG	210	sga-miR7493b-1-5p	CUGCAUUUAUAAAAUGUUAAUUAG	17-40	gra-miR7493b	7	0	24	24	2
sga-MIR169e-2	AAGACCUUUUCAAGUACGGUGCAGGCAAGUCAUCCUUGGCUACCAAAUAAGACUCUUCUCAUCAUGCUAGACUUCUCUUCUUUUAAAUAAGACUUGUAACCCCGUUUCGAUAUUUUAACGAUGACUAAAACUUCUAUUUUAAAAAGAUAUCUUGCAUAAAAGAAAAGAGCAUGUCAAGGUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAU	218	sga-miR169e-2-5p	GGCAAGUCAUCCUUGGCUACCA	24-45	mtr-miR169e-3p	7	0	22	22	1
			sga-miR169e-2-3p	UAGCCAAGGAGACUGCCUGAA	180-	zma-miR169e	3	0	21	21	1

					200						
sga-MIR5157b	UGAAUUUAUAAUGUUAUCUAAGUCA ACACCAAGGGUUGUAGGCGAGAUGG AUAAUGAUGCCUUUAUGUUUAAUCA GAAGUCUCGGGUUCGAAUCUCAAGA AUGAAAAUAAUUCUUGUAGGUAGUU CUCUACCUUAUUUAGACUCAAAUCC GAGAUCUCUGGUUAUGGAUAAAAGU AUUCCAUUCAUCCCGUCACAUCCUU AAUUUUUAUUAGCUAUGAAUUCAGU AUAUAUCGA	234	sga-miR5157b-3p	UAAUUUUUAUUAGCUAUGAAUUCA	200-223	osa-miR5157b-5p	7	0	24	24	2
sga-MIR8008b-2	UGCAAAUCCCAGAAAAGCGACUGAC AAAAGAACACUAUCCAUCGCUUUUC UGGAAAUUAUUUUUUCAAAAAGUCA AAAAAAAAGUGAAGGACUAAAACACA CUAACUGUCGCUUUUCUUGGUUUUA AAAAAUAAAAACCCAGAAAAGCGACG GACAAAACCAUGUUGUCUGUCGCUU UGUCUGCAAUUUUUU	192	sga-miR8008b-2-3p	AAACCCAGAAAAGCGACGGACAAA	135-158	stu-miR8008b	2	0	24	24	1
sga-MIR10995	CUGAGUGACAAUGCGUCAAGAGCUU UGGAAAUUAUGUCUGUGUAAGUUCU UAAUUAUGGGUGUGAAGCGCGCCAU AUUCAUGGUUAUGAGGUUACAAGCU UCCUUUUCAUACUCGUUAACUUGUC ACUUGU	131	sga-miR10995-3p	CAAGCUUCCUUUUCAUACUCGU	95-116	mdm-miR10995	1	0	22	22	1
sga-MIR8739-4	ACCCUCCGUCAUACUUUUGGGAUAC UAUUAUCCUUGCCGUUCAAAAACUA GAGCAUAUGACCUUCACUCUAACGG AAGACUAAAUAGGGAUACGUGACAC AAUCUUAUCCAUCGAUAUAAUAUGC GGAUCAGUGGAUAAGAUUAUGAGAC GUGUAUGACCAUUAAUAUCAAAGGU AUAUAUGCUUUAAUUUUUUGAACAA CAAAGACACCAAUGUCCGAGAAACG UGACGAAGAUA	236	sga-miR8739-4-5p	AGACUAAAUAGGGAUACGUGACAC	77-100	gra-miR8739	6	0	24	24	3
sga-MIR5303i-2	GUAUUUGUGUCAGAUUCUUCAAAAA UAUAUUGCUUUUGAAGAAACGGACA UGUAAAUAUUUUUGAAGAGUCUGAG CAACAUAGGAAUCCGCUUUCAAUGU UGCAUUUGUAUCAGAUUCUUCAAAA AUACACUACUUUUGAAGAAUCGGAC AUGCAAACAUUUUUGAAGAGUGUGA GCCACAAAGUU	186	sga-miR5303i-2-5p	AUAUUUUUGAAGAGUCUGAGCAAC	56-79	stu-miR5303i	0	0	24	24	1
sga-MIR6459a	UAUAUUUCGGAAACAAAAAAAUCGAA AAAUAAGUUACCUUGUUGAAAUGAC UGGGAUCAACAUUGUCAUCGAGGGA AUGAACAGCCUCAAGCAAAAAUCUG AUCCCAGUCAUUUCGACAAGGUAAC UUAUUUUUCGAUUAUUUUUUGUUUC CGAAAUGUA	160	sga-miR6459a-3p	GCCUCAAGCAAAAAUCUGAUC	84-104	ptc-miR6459a-5p	5	0	21	21	3
sga-MIR9679-1	UGUCAAAUGAAUUCUGAAUUAGUCG AUUUCUGCAAAAAAGAAAUUGAUAAU UUAUUAUCAAAGGGACUUAUAAAAC CCUCUAAAUCUCAUGGUCUUGUACU GCAUUUUAUGUUAAUAAAGCUGCAG AACAAGAAAGAGGUGUUCCCAGGUU GGUAAUAAAUUACAUUAACUUCUUU	209	sga-miR9679-1-3p	CAGAACAAGAAAGAGGUGUUC	124-144	tae-miR9679-5p	5	0	21	21	1

sga-MIR8045-2	AAAAAAUGUCUACUUAUCAGUAUCUUCUUGGUGAAUAACAUACCUCAACUAACAAUUUUUCCCUUUUCCUACCUAAACGAUAGUGAUAUUUCAGGUACGAAAAGGGAAAUUGAUAGUUGAGGUGUGUUUCGCCAUAGGCCUAAAAAAGUUUUGAGA	99	sga-miR8045-2-3p	AUUGAUAGUUGAGGUGUGUUU	77-97	stu-miR8045	0	0	21	21	1
sga-MIR167c-5	AUGUGAAGAACUAACUGAAUUCUAGUAAACUAAUGGGUGAAAGGAAACCCACUAGUGAACUCCCACAUACAUGGUGACAAAAUAUACGAAGAAAUCCUUUUAAAUUUAGGACUAAAAUUUGAAGAACACUUCUUCUUAUUCUUGAGAGGACAUGUUGAUAGUUUCCUCUUGUAUUUGGUCAAAGUAGGAUUAUUUUUCGAGAAUGAGGGAGUUGGGUAGAUUCUUACUAUAUUGUUAGGCUUAGAC	271	sga-miR167c-5-3p	AGGACAUGUUGAUAGUUUCCU	172-192	aly-miR167c-3p	5	0	21	21	1
sga-MIR7983-1	UGCCUCUUAUUCUACAAUAAAAAUAACUUUUAGCGGCAUUAAAUAUUGACGCAUUACCGGCAUUAGUAAGUGCUAUUAGAACCAAUAUCGCUAAAGACUUUAGGAACAUAUACAAAAAGAGUGACAAUUGCCGCUAAAAGUACAUAUUUAGCGGUAAUUAAAAAUUAAAUGCCACUAAUGAUCAUUUUUAUUGUAGUGUUAGAGUUU	207	sga-miR7983-1-5p	ACCAAUAUCGCUAAAGACUUUAGG	81-104	stu-miR7983-3p	6	0	24	24	1
sga-MIR7493b-2	UCCUUUAACUUUGGAUGUGCAUAAAUAAACACUUAAACUAGUAUAAAGUUGAACAAAUAGACACACGUGUCCUACAUGUCAUCCUAUAUGUCAUUUUUUGUCCUACGUGGUGUCCAAGGUGUAUUAUGUCAUGUAGAACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUUUAUUUGUGCAUUAUGAAAGUUGAAAUAU	208	sga-miR7493b-2-3p	UUGGAUAGUUAAAGUGUUUAUUUG	163-186	gra-miR7493b	6	0	24	24	1
sga-MIR9726	UUCUAGAAAAACUAGGUUUUCUAGUCCUUUUUGGAUUAGGAAGACAUCUCUAUAAAUAGGGAUUCUCCUAACCUAGAAAAUAGAGAAAUUAGUUUUCUAUUC	102	sga-miR9726-3p	UAGAGAAAUUAGUUUUCUAUUC	81-102	gma-miR9726	6	0	22	22	1
sga-MIR1044	AAUUUGGCUUCAAAUUUUAACUUUGACCUCCAACUUUCAUAAUGCACAAACAUGCACUUUAACUAUCCAACUCUUAAAUAAAUAAACACAUGAGUCCUACAUGACACAAUACACGUACGACACCACGUAGGACAAAAAAUGACAUGUAGGACACGUGUGUUUAUUUGUUCAACUAUAUACAAGUUUAUGUAUCUACUUGUGCACACCCAAAAUUGAAAGACAUAAAUAUAAUUCGAAGACAAGUU	245	sga-miR1044-5p	GCACAAACAUGCACUUUAACU	44-64	ppt-miR1044-5p	5	0	21	21	1
sga-MIR10994	UAUACUCAAGCCAUAUUUAAUUUAUCCAAAUCUAAUCUAAUUCACGUGUUACUACCCUUAAUUAUAAUUUUGUUGUUGCACAAUACAUGGCUUUCAUUUGUAUUGUGCAACAAAUUUGUUAUAAUCAAGUGGGUUGAAUCCAUUCAAUUCAGACACGUGUUUUAUUUUAGUUUUU	336	sga-miR10994-3p	AGUUUUUUUCUUGAGCAUGAA	178-198	mdm-miR10994-3p	6	0	21	21	2

sga-MIR5303-8	UUAGUUUUUUUCUUGAGCAUGAAUUCAAAUUAAUUUUAAUAAAAUUCCGCACAGACACGUGGAGAUCGUCCGUGUCAGUAUAUGGACCUCGCGAGUCCCCCACUGGGUCAUGAACUCUCGAUGUAUUUCCUAGGAGUACCAUGUAUAUACGGUUGAGUCAGAAUGGAGGGUCACUUCAAGCUAUGUUGUUUAGACUCUUCAAAAAUAUCGAGGGUGUGUGUUGGGUCCUCCAAAAAUAGUGCAUUAGGAGGAUCCAACAUGGGUGCGGCAACACUUUUGAAGAGUUCGAGCAACAUAGACUACAAGUUCCCUCCUAG	156	sga-miR5303-8-3p	CUUUUGAAGAGUUCGAGCAAC	113-133	sly-miR5303	1	0	21	21	2
sga-MIR7746	CUUAAGGAAUAUGUUAGGGUAAUCUAGUCAAAUACUCAUUAUUGUUAAUGUUAUCUACUGGAUUUCUUAAUUGGUGUCUGCCAAAUCUUUAAGCUAGCGUUUGGCCAUAGAUUUCCAAAUAUUCUUGGC	129	sga-miR7746-3p	AUCUACUGGAUUUCUUAAUUGGUG	53-76	bdi-miR7746-3p	7	0	24	24	2
sga-MIR6235	AACAUAUUCAGUAUUUGGGCUGUUGGUUUGUAGUGUGACGCUACAUGUCAGACGUCUCCGGUUCGAACCGAAGGUCCAAAAUGGACAGUGAAAUAAAAAUAAUGUUGCCACUCAUGCUCGAACUGGAGACCCGUGAUAUGUAGUGUCAAGCUCCAACCAACAGCCCAAGUAGCUAAAUAUACA	183	sga-miR6235-3p	CAGUGAAAUAAAAAUAAUGUUGCC	86-109	sbi-miR6235-5p	6	0	24	24	3
sga-MIR8027	UGUCUGAGCCAGCUUAUGAGCUGCUUGAAUCGUUUCAAGUAUCAAGUAACUCAGCCAAAUUAUAAGAUAUAAUAAUCCAGGAUAAAAUGCAGGAUUAUUUUAUAGUAUGUUUAGUUGGAGGUAUUAGGUAAUGCUUGGAUUGUUUAUUCCACUGUUUAUACCUUAGUGAUAAUAUAAGUUUAUCUCAUAUACAUGGUGGAAUAACUUAUAACGGCAUAAUUAAUCUCGAGAUAACUUGUUUCCAACCAAACGACUCAUAAGUGUCUUAGUUUGGAUCCUAUGUUGCUCGGACUCUUCAAAAAAGUCGAGGGGUGUUUGUCAGGUCCUCCGAAAGCAGUGUGCUUUUGAAGGAUCUGACACGGGUGGGGCAACAUACUUGGAGAGUCCGAGCAACAUAGGAGGG	272	sga-miR8027-3p	AUCUCGAGAUAACUUGUUUCCAAC	223-246	stu-miR8027	6	0	24	24	1
sga-MIR7997c-6	ACUACAACAAAAAUAACUUUUAUCGAUAUUAAAUAUUGACACUAAUAAAGAGUGUUAACGUUUUUAUCGGCAUUAGUUAAGUGUCAUUAGAACCAGUGUAGCUAAAGGCUUUAGAGACAUAUACAAAGAGUGACAAUUGCCGCUAAAAGUACAUAUGUAGCGGCAAUUAAGAAUUAAAUGCCGCUAAUGGUCAUUUUUGUUGUAGU	131	sga-miR7997c-6-5p	AUGUUGCUCGGACUCUUCAAAAAA	8-31	stu-miR7997c	2	0	24	24	1
sga-MIR1917-1	UUUUUAUAUGACAUUAUACAUAAAUA	206	sga-miR1917-1-5p	ACUAAUAAAGAGUGUUAACGU	41-61	sly-miR1917	3	0	21	21	1
sga-MIR530-3	UAUUAUUUAACUUGAUCUCUAUUCACAUUUACACCCUCGAACUCUGGGUG	284	sga-miR530-3-3p	AGGUGUAAGUGUUAAUUGAGU	223-243	sly-miR530	5	0	21	21	1

sga-MIR11498a	UGGAUAAGUAGACAAUAGAACUUAG ACACAUGAGUUCUACUUGACAUGAU ACACAUAGGUCUCAAAUUGUUAUGU AGGACGUGUGUGUCUAUUUGUUCAA CUUUAAAAAAAAAUUGAAGUGCCUAC UUGUAUAAAUCCAAAAUUGGCAGGU GUAAGUGUUAAUUGAGUCCAAGUUA AAGGACAUAAUACAUAAAUAUGUCC UUUAAUUU AAAUUACAAAAAUCUCUUAAAAUUUC UGGAUUUUGGAUACAUUACUAGUUC UUGAUACAUGACUCGACUUCUGGAU ACAUAGGUGAGGGAUGUAUCCGCAA GGGGAGGGAUGUAUCAGAGAUGGG AUAUGACAUCCGGAUGCAUCACUUG ACUUACAGAUACAUCAGCAAACAUC CGGAUACAUAGGUGAGGAUGUAUCA GGGGAGUUAUUUAUUUGUGAGGGG AUAUAAUGUAUCAUCGAGAGGAGAG UGAUGUAUUCGAGAAGAGAUUUUUG AAACAUUUUUAAAUGAUAGAGAAUU UUAGAGAUUAUGGUAAAAU UUUUUGGGUGUCCCUGCUGUUAAAA AAUUAGAGCAUAUAUGUUCUUCACU CUACGGGAGACUAAAUAGGAACAUG UGGCACAAUCUUAUUCGUUGAUCCG AUAUUUAAUAAAUGUCAGGUCGGUG GAUAAGAUUAUGAUACGUGUAUGUC CGUUAGUAUAAAUGGUAUAUUUGCU CUAGUUUUUUUUUACGGUAGGAUCA CCAAUGU CGCAAAUUGUAUGUAAAUAUCCCCA UCAUAUUUUUGAGAUAUUGUUGUCC CUGCCGUCAGAAAGCUAGAGCACGU ACUUCCUUCACUCUAACGGAAGAGU AAAUAGGGACAUGUGGCGCAAUCUU AUCGGUCGAUAUGAUAUUUAAUAAA UUGUUGUUAGUGGAUAAGAUUAUGA CACGUGUAUGUCCGUUAGUAUAAAC GGUAUGUAUAUUCUAGUUUUUGAAC GGCAUGGCACCAAUGUUUUAAAAGU AUAACGGAGGAUAUCCGCAUAUACC AUUUACA	318	sga-miR11498a-5p	UAUCAGAGAUGGGAUAUGACA	113-133	pab-miR11498a	4	0	21	21	1
sga-MIR8739-5		207	sga-miR8739-5-5p	AGACUAAAUAGGAACAUGUGGCAC	58-81	gra-miR8739	6	0	24	24	3
sga-MIR8739-6		282	sga-miR8739-6-5p	AGAGUAAAUAGGGACAUGUGGCGC	96-119	gra-miR8739	7	0	24	24	3
sga-MIR7997c-7	CUUCUAUGUUGCUCAGACUCUUCAA AAAUGUCGCCAUGUGCAUGUUGGAU CCUUCAAAAGCAGUACGUCUUUUUA UGGAUACCACAGGUGUGGCGACAUU AUUGGAGAGUCCGAGCAACAUAGCU G	126	sga-miR7997c-7-5p	AUGUUGCUCAGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
sga-MIR3693c	CUUCAUUUAAUAUAGACAAACUUUU CUUUAGUUUCUUCAUCUACUUCAAG AAGAUUGAUUUUCUUCCUUUUUCUU UUGUUUUUAGGACAAUCAAGAGACU UGUGUCUGGACUUUCCACAAGUCCA ACAUUUGUCUUCGUUAGAUGUGUUG UGAGAAGUUUUCUUACUUCUCUUUC CUUUAAAAUAUCUUUUUUCUAUUGA	327	sga-miR3693c-3p	UGAGGAUCUUCUCUUAGGUGU	198-218	pab-miR3693c	5	0	21	21	1

sga-MIR10448	GGAUCUUCUCUUAGGUGUUGAUUG UCUAGAUCGUUCUUUCUUUGAAACC UUUUUUGCAGAAGGGGGUUUUAGAC UUGGGAAACGAAAGUCUUGACAGAA ACUACAAAGUUCGUUACUUGAAAUG UUU UCUUAUCUUCGUAUCUUUGUAAUAC GGAGGAGAAUGAAUAUUUUCAGCGA UAGGGGUCGGGCUGGGAAAGGCUG CCUACGUAGUUCGGGUCUGAGACGA UAGGGAGGGGUAUUUAGGAUUUGU GGUAUGGGAUAUGGGUUUUUUGAG UGAGAAACUUGAGACAGCUUUUUCU CCCUCAACAUUUCCAAUACAAUUUU CAAGUGCUCCUCAUGUUCUUUCAUG CUCUUUGAGUAUAUCAGUAUAUCAU UAAUGAAUACGAUGACAAAGAUAUC CAGAUAUGG	281	sga-miR10448-5p	UUAGGAUUUGUGGUAUGGGAUA	113-134	gma-miR10448	5	0	22	22	1
sga-MIR168c-2	GCGGCCGCCUCUUAUUCGCUUGGU GCAGGUCGGGACCUCAUUCGCCAG CGCCGGGAAUAAUGCCGGACGAACG ACGGCGGUGUUAAUUCUACUAAAGC UGUCACCGACGAAUGUAUGUUUGAU UAGCGGCGAAAUUUGGGUCCUGCC UUGCAUCAACUGAAUUGGAGACAGC UGU	175	sga-miR168c-2-5p	UCGCUUGGUGCAGGUCGGGAC	16-36	bra-miR168c-5p	0	0	21	21	1
			sga-miR168c-2-3p	CCUGCCUUGCAUCAACUGAAU	142-162	bra-miR168c-3p	1	0	21	21	1
sga-MIR7992-4	UGGUAAGUAAGUAAUACCACGUAAC UUUGAGAGUGCACAUCUAGAUACCU CAACUAGACCCUCCAACUCGUGCCC GCUGUGUCUUGUAGACACUUGACAU UAAAGUAGCAGAUAAACUUUAGAGG UGUCUCAAUGAUGAUUUUGUAGAUG UUGGAGUAUUUAACUAACACAUUGG AGACGAGUUGAGGUGUCUAGAUGU GCAUACUCAAAGUUUAAGUGUUUGU UUCUGUAUUAUGC	237	sga-miR7992-4-5p	UUUGAGAGUGCACAUCUAGAUACC	26-49	stu-miR7992-5p	4	0	24	24	1
			sga-miR7992-4-3p	UGUCUAGAUGUGCAUACUCAAAG	189-211	stu-miR7992-3p	6	0	23	23	1
sga-MIR7981-5	CUAUGACCGAAAUCUCAGAGACACA CCUUAACUUAACUAAGGUUCUAUUA AUCUCAACUCAUUUGUUUUGUAAUU UUGUACUGGUACACUCCGUGACUUG AGGCGCGUGAGAGAUGUUUGGAUG UCAGUGUACAGAAUUACAAAAAAAAU GGAUUCGGGGGUAAUAGGACUUUA GUUUAGUUAAGGUCUGUCGCUCGAA UUUCGGUCAUAC	211	sga-miR7981-5-5p	CUUAACUUAACUAAGGUUCUAUUA	27-50	stu-miR7981-5p	5	0	24	24	2
			sga-miR7981-5-3p	AUAGGACUUUAGUUUAGUUAAGGU	164-187	stu-miR7981-3p	0	0	24	24	1
sga-MIR164h	AUGAAUAAACACAUGUGUCCUACAU GGCACAAUACACGUAGGACACCAUA UAGGACAAAAAAUGACAUGUAGGAC ACGUGUGUUCAUUUGU	91	sga-miR164h-3p	AUGACAUGUAGGACACGUGUG	62-82	zma-miR164h-5p	6	0	21	21	3
sga-MIR399b-1	UGAUGAAGCGGAAGCAUGAGAAAGG AAGUCGUUGGUGAAUGAAAAUAAGG	217	sga-miR399b-1-5p	GGGCUACUCUCUAUUGGCAUG	63-83	sly-miR399b	0	0	21	21	1

	GAAAUAGUGAUAGGGCUACUCUCUAUUGGCAUGCGUUAAUAUAUGUACAGUGACUCCAAUUCACUGUAUCGCAUAUUUUAACUGAUACGCCAAAGGAGAGCUGCCCUGCUACUGUCUCUGCUUAAUAUAAUAACUCAAAGGUCCGUUCUUAAUACUCCGAUGCAGAA		sga-miR399b-1-3p	CGCCAAAGGAGAGCUGCCCUG	138-158	nta-miR399b	0	0	21	21	1
sga-MIR167b-2	GGGUCUAGAGUGGAACAAGUGAAGCUGCCAGCAUGAUCUAAACUUGGCCAUUUAUAAAGAAAAUGGGUGACUAAGGUUAGGUCAUGGUCGGACAGCCUCACUCCUUCCUUUCUUGAUAA	119	sga-miR167b-2-5p	UGAAGCUGCCAGCAUGAUCUAA	20-41	bna-miR167b	0	0	22	22	1
			sga-miR167b-2-3p	GGUCAUGGUCGGACAGCCUCACU	80-102	aly-miR167b-3p	2	0	23	23	1
sga-MIR1215	UGUAUAACUAAUACCCACAUAACUUAUUCCACCUUCUACCUUGCAUAACUUUAUACAUAGAUUCCCUCAUAAGUUAUGAGGGUAUUAAUUAUGUA	95	sga-miR1215-3p	ACCUUGCAUAACUUUAUACAU	38-58	ppt-miR1215	6	0	21	21	2
sga-MIR167h-3	UUAUCAAGAAAGGAAGGAGUGAGGCUGUCCGACCAUGACCUAACCUUAGUCACCCAUUUUCUUUAUAAAUGGCCAAGUUUAGAUCAUGCUGGCAGCUUCACUUGUUCCACUCUAGACCC	119	sga-miR167h-3-3p	AUCAUGCUGGCAGCUUCACUUGUU	83-106	gma-miR167h	3	0	24	24	1
sga-MIR7723a	UGUCUUCACAAUAUGGAGCUUCGAGUGAAGAACAGGAAGCCACUUGCUUGUUCUUCUCAUAAUGCUCCAGAUAUUUGAAGCCU	83	sga-miR7723a-3p	GGAAGCCACUUGCUUGUUCUUCUC	35-58	bdi-miR7723a-5p	7	0	24	24	2
sga-MIR6164b	CUGUUACUAAACUAUUCAUUUGUUCAUUUGAUGUCGAAUCAUCUGUGUGAUAGCCAUACCUAUUCAUUCGUUAAAUUGACGUUCAAUCAGGUAUGAAUAGGUGUGGCUAUCAAAUACAUGAUUCGACGUCAACUUAAUGAAUAGGUGCCUCGAUUGUUCCAUUUUGAAUGGUGUCACAUAAAAAGAAACGGAAGGAGUACGUUUGUUACCU	211	sga-miR6164b-3p	UCACAUAAAAAGAAACGGAAG	174-194	nta-miR6164b	3	0	21	21	1
sga-MIR11167-2	UAAAUUGAGCUAAUCAUUGAUAGUCUGGUAAUGAGAUUUUGCAAGCACAUGUAAGACUUAUGAGAUGAGACUACCACCAAAGGGGAUAAUGGUCUCAAAAUUACAGGAAAAUUAUUCCCCGGACUACCUAGUGAGAUAGUAAAUACA	147	sga-miR11167-2-3p	GAUAAUGGUCUCAAAAUUACAGGA	85-108	lja-miR11167-5p	7	0	24	24	1
sga-MIR856	GGAAAUAACUUAUUUAAUCGCCUGACAACUACAUGCAGUUGUUGGACCAUUUUGUAUCUGAAAGAUAUGCAUAAUUAUUCUUAUAAAUAACUUCAGUAGUUGUCCAGACAACUGUAAAAGUUGUUGGC	128	sga-miR856-3p	UAUUCUUAUAAAUAACUUCAGU	76-97	ath-miR856	5	0	22	22	1
sga-MIR166-3	ACAAAAGAAAGAAAACAUUUGUUGAGGGGAAUGUUGUUUGGUUCGAAAUUAUUCAAACAAAUUAAAAUUCAUGCAUCUCGAUGAUCGAUGAAUUGAAUAAUUUCGGACCAGGCUUCAUUCCCCCC	146	sga-miR166-3-3p	AUUUCGGACCAGGCUUCAUUCCCC	100-123	lja-miR166-3p	0	0	24	24	1
sga-	AACUCAAGUUUUUGUUUUAAUGACUUGUGUCCAGACUUUCCACAAG	206	sga-miR5760-3p	UCCUUUGAGGAUCUUCUUUUAGG	97-	mtr-miR5760	7	0	24	24	1

MIR5760	UCCAACAUUUGUCUUCGUUAGAUGU GUUGCGAGAAGUUUUCCUACUUCUC UUUCCUUCAGAAUAUCCUUUUUCCU UUGAGGAUCUUCUUUUAGGUGUCAA UUUUCCAGAUCGUUCUUUCUUUGAA ACCCUUUUUGCAGAAGGGGGUUUUA GACUUGGGAAGCCAAAGUCUUGACA GAAACU			U	120					
sga-MIR7980b-1	AUAUGGUAUCACAUCUCAUUAUAUG AAAUCAUGAGACGGAAUUAACGUAA AAUCGCAUGUCCAAACGCUGAUUUC AUUUCAUGAUAUCAUAUCGUGAUAU GGUAUCACAA	110	sga-miR7980b-1-3p	GUCCAAACGCUGAUUUCAUUUCAU	59-82	stu-miR7980b-5p	3	0	24	24	1
sga-MIR8014-1	UUUUACUCCCUCUGUCCAACAAUUC UUGUUCACUAUUGAAUAUAAUAAAU ACAAUGUGUUGAAAAAUGUCACAGA GAAAUGAUUAUAAGUAGGUAAAUUA GAAAAGAAGUGUAAAAUAAUCCACU GAUUUCAUAAAGUGGACAAGUAUUG UUGGACAUCCCAAAUUAGUAUAGUG GACAACUAUUGUUGGACAAAGGGAG UAGUU	205	sga-miR8014-1-5p	AUAAAUACAAUGUGUUGAAAAAUG	45-68	stu-miR8014-3p	5	0	24	24	1
sga-MIR5303-9	UGAAACCUAAGUUGCUUGGACUCUU CAAAAAUGUUGUCUCACCCGUGUCG GAUCCUUCAAAAUACACUAUUUUUU GGAGGAUCUACACACCCGUCAACAU UUUUGAAGACUUCGAGCAACAAAGC UUGAA	130	sga-miR5303-9-3p	UUUUUGAAGACUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
sga-MIR8132	ACUUAUUUUAUUAGUAAUUUUUUUA CCCGUUUUAGCCUAUGUGACACUAU CUGGUGGGCCCAACGAUGGUUGAC UUCUUUUUUUUCAAACUAGUGCCAC GUAGGCCAAAAAGGGGUAGAAAAUU ACUUAUAAAAUAGAA	139	sga-miR8132-3p	CCCAACGAUGGUUGACUUCUU	59-79	ppe-miR8132	6	0	21	21	2
sga-MIR9679-2	GAAAUUGAUAAUUUAUUAUCAAAGG GACUUAUAAAACCCUCUAAAUCUCC AUGGUCUUGUACUGCAUUUUAUGUU AAUAAAGCUGCAGAACAAGAAAGAG GUGUUCCCAGUUUGUUAAUAAAUUA CAAUACC	132	sga-miR9679-2-3p	CAGAACAAGAAAGAGGUGUUC	86-106	tae-miR9679-5p	5	0	21	21	1
sga-MIR2931	UUCUAUCAGCACCGCUAUCAAGCAA AGCAACUUUGUUAAUAACAAAAUGU UUGUUAAUCACUAUUUUGAUAGGGA UAUGAUGGCUCUGAGGUCUGAUAGA GGAAAUUACUGUUAAACCUGGGAUU GCAGAAGUGGAAGCAUUGUUAUUGG UUUGUGUAAAAACUUCUGGUUCAAC CAGAUGGUUAUUGUUGAUGUCAGGU UCAUUGAUAUCA	212	sga-miR2931-3p	GGUUAUUGUUGAUGUCAGGU	181-200	osa-miR2931	5	0	20	20	3
sga-MIR1850	UGAUUACUUCCGGUUCUUCCCAUAG CUUGUCAAUACUAUUUUGAUUAGUU CACAUUUAAAAUGAAUAAAGAGCCU CGAAUGCACCAAACAAUGCUGUAAG ACAUGGGAAGAAACAUUAACAAAACU UGACUUCGUCCGAAUAUUGACAAGC GAUGGGAAGAAUUGGAAGUAAGUU	175	sga-miR1850-5p	UUGAUUAGUUCACAUUUAAAAU	41-62	osa-miR1850-3	7	0	22	22	2
sga-	UAAAAAAAUGUAGAAUUUAAAGUUG	231	sga-miR5021-2-5p	UGGGAAGAAGAAGAAGAAAA	52-71	ath-miR5021	1	0	20	20	1

MIR5021-2	GGGUUGGGUGGGAGUGGUUGUGGU UGUGGGAAGAAGAAGAAGAAAAGGG AAGGUUGCUCUUUUUUAAUUUUUUU UCUCAAAAAAUAGUUUUAUUUAUUU AAUUGUGUUUUUCUGGGCCCAAUGU CAAAUGUCUCAUUUUUAUUAGCUAC CAUGCCAUGUCAGCCGCGAGUGUAU GACACACCAUCUUUAUUUCUUACAU UUUUAAU										
sga-MIR12151-2	CUGUGUGAAUUUGCAUCAGUUACUU GCCAAUGCUUUUUAUGUUUCAAAGA AUGUCUGAACUUAGAAAUUGGGGAG UAGGAGUAGUUAUUUAAUACCCAUC UUGAGAUUGAGCAGAAACAUUCUUG AAACAUAGAAAGCAAUGUCAAGUAAC UGAUGCAAAUUCGCAAUC	169	sga-miR12151-2-5p	GAACUUAGAAAUUGGGGAGUA	57-77	aof-miR12151	6	0	21	21	2
sga-MIR10538-2	AUUAGGUUGAUAUACGUUACUGUAA GUAACGUUUUACUCCUAAAACGUUA UUUUCAGUAACGUUUUAGGAGUAAA AUGUUACUGUGAGUAACGUAUAUCA AUCUGAC	107	sga-miR10538-2-5p	AGGUUGAUAUACGUUACUGUAAGU	4-27	sly-miR10538	4	0	24	24	1
sga-MIR859-1	AGAUUUCAUUGAUUUUACAAAAAAUA GGAUUGAAUUUCUCAAAUGUUCUCC AGUUUAUACUUUCCAUUAUGUUGGU GGUAGAUACGGCAGAGUGGCAUGG AUCAUGUGAGAAUCAAGUUACUCUU AAACUUGUAUUGGAAUGUGGUUUGC AUGUGUGCAUUGUUGCAAUUAUGAA AUGUUUAGUGCAUGGGAGCUGGGG ACCAUAUGGAAAUUGAUAUGUAGUG AUGUCCAAUUGCAGUAACUAAGGUU UUCUGAGAAAACAAAUAGUUUUUUU UUCUUCUUUUUAAAGUCAAUAAAAAA A	301	sga-miR859-1-5p	UGAUUUUACAAAAAAUAGGAU	10-30	aly-miR859-3p	5	0	21	21	1
sga-MIR408-3	AAAAGGAAGGAUUGUGGGGAGAGGA GAGCCAGGGAAGAGGCAGUGCAUG GAAUAGGCAAAGCAAAAAUUGCACA UCUCAUGCUCUGGCUCGUCCCCGU CUAUCCAUACCACACCAAUUUUUAC CUCAA	128	sga-miR408-3-5p	GAGAGCCAGGGAAGAGGCAGU	24-44	bra-miR408-5p	1	0	21	21	1
			sga-miR408-3-3p	AUGCUCUGGCUCGUCCCCGUC	79-99	cas-miR408	5	0	21	21	1
sga-MIR10532-3	UGAAAAUUACUAAUAAAAUAAGUUCG GGAGUAAUAGGACUUUAGUAUAGUA UAAGUGUGUCUCUGAGAUUUCGAUC AUAGAUUGAGGGCGUACUUGUGCAU UAUUCCUAAAAAUUAAUCAAAAAGAG AGUUCUCAUUUGUUAAAAGAAGGUG UUUAAUUUCUUUUUGUGGAGUUUUG GACUCAACUAUUAUUCCGAGUUUGU UGAGUUAUAAUUUGUG	218	sga-miR10532-3-5p	AAGUGUGUCUCUGAGAUUUCGAUC	53-76	sly-miR10532	2	0	24	24	1
sga-MIR9773-1	AAUGUUCUAGUACCUCUCGAACUUA UCUUUUUGUAAUUUUGUGCAUUUUU UUUAUUUACGUGGUAUUCAAAUAUC UCUCAUGUGCCUCAAUUGCGUGGAG UCACAAAGUGUGUCACGUAAGACAA AAGAUGUAUAAAAUUACCAACAAAAA AAAAAGUUCAGAAAGAUAAUAAAACC	179	sga-miR9773-1-5p	CUUAUCUUUUUGUAAUUUUGUGCA	22-45	tae-miR9773	6	0	24	24	2

sga-MIR9552a	UU UUUGAGUGUGCACAAGUAAAUACUU AAGUUUAUAUAUGACCAAGUAGACA UAUGUAUUCUACAUGGUAUAAUACG CAUAAGACGUCAUGUAGGAUAUAAA AUUUUCAUGUAGGGUGUCAUGUAGG ACAAAUGUGUCAAUGUAUUCAAUUU UAUACAAGUUUAAAUGUCUACUCGU GCACAUCCAA	185	sga-miR9552a-5p	UGACCAAGUAGACAUAUGUAU	37-57	bra-miR9552a-3p	6	0	21	21	1
sga-MIR3946	AAGUUUGCAUAAUUGCGCUCCAUAG CAAACAUACAUACAUAUACAUAUAUA CAUACAUACAUAUAUAUAUAUAUGU GUGUGUGUGUGUGUGUGUAUUAUU CACUAUACAUGUACAAUUGAAGCGA AUUGUAUAAAACGAGAAAGAGAAAG AGACUUGGGCACAGAAUUGUAUAGC AAGAGAGGAGAGUGGCGAGCGAGA GUUUGAGGGAGAGAGGUGACUGGC AAACAGUUUGCUACGGGGCACAAUU AAGUCAAAUGA	259	sga-miR3946-3p	UUGUAUAGCAAGAGAGGAGAGUGG	167-190	csi-miR3946	6	0	24	24	1
sga-MIR7984d-2	AAGGAAAAGAGUCUGAAAAAUACUU UAAUUUUGGUCGGUAUUGCAGUUAC GAUACCAAACUUUAUAAAAGACCUU UUACCGCUGCACUUUUAAAAAGUGU AUUUUAAAGGUAUAUAUGUGUCCAC GUGACGCAUUACUAUUUAAAAAGAU GCAAUAUUUUUUAUGUCCACGUGAG CACAAUACGCUAUUAAAUAGUGCAA GGGGGGUAAAAAGGUCUUCCAUAAA AUUUAGUAUCGUAACACAAUUUCGA UCAAAGUUCAGAUAUAUUUCAAACU UUUUUCCUC	284	sga-miR7984d-2-3p	CAAUUUCGAUCAAAGUUCAGAUAU	242-265	stu-miR7984d-3p	2	0	24	24	1
sga-MIR10542-2	AUACCUUGAACUUUGAUAGAAGAAU CAUAUAUACCCCUAAAUAAUUUCUAA AAAAAAGAAGAAGUAAUAAAUAUAAA UUUAAAACUAAUUUUUUAACUUCCG UUAAAUGAAGGGUAUAUAUGAGCCA UUUUGUAACGGGAGGGGUAUGUGA GCCGUUUGUAUAACGGUAAGAGCAU AUAUGAGCCACUUUUAUAACGAGGG GUAUAUUAGCUCCAAAUAACAAAGU UGAGGGGUA	235	sga-miR10542-2-5p	UAGAAGAAUCAUAUAUACCCCUA	17-39	sly-miR10542	0	0	23	23	1
sga-MIR7981-6	UCGAGCGACAGACCUUAACUAAACU AAAGUCCUAUUACCCCCGAAUCCAU UUUUUUUGUAAUUCUGUACACUGAC AUCCAAACAUCUCUCACGCGCCUCA AGUCACGGAGUGUACCAGUACAAAA UUACAAAACAAAUGAGUUGAGAUUA AUAGAACCUUAGUUAAGUUAAGGUG UGUCUCUGAG	185	sga-miR7981-6-5p	CUUAACUAAACUAAAGUCCUAUUA	14-37	stu-miR7981-5p	4	0	24	24	2
			sga-miR7981-6-3p	AUAGAACCUUAGUUAAGUUAAGGU	151-174	stu-miR7981-3p	3	0	24	24	1
sga-MIR10532-4	CUCUCUGCUGAAAUCAUGUAUAGUA GUGAGUGUGUCUCUGAGAUUUCGG GCAUAGGUUGAGGGGGUACUUGGA CAUUAUCCCUAUCCAAUUCUAUUAA AUAACCAAUUUAUUGCCCAAAUUAU	169	sga-miR10532-4-5p	GAGUGUGUCUCUGAGAUUUCGGGC	28-51	sly-miR10532	1	0	24	24	2

sga-MIR10532-5	UGGCAUAAGAUAGACAAUUCAUUCA AAUGUGAUUUCAUGGAGAUCU UUUUAUUUAGGAAAAAUGCACAAGU ACCCCCAACUUAUGCACAAAUAUCU UGCGGGCCCAACACACGUUGAUAUU UUUUUUCAAGCUAGUGCCACGUAUG ACGAAAAUGGGUAGAAAAUUAUUUA UAAAAUAAGUUCAAGGGGGUAAUAG GACCUUAGUAUAGUAUAAGUGUGUC UCUGUGAUUUCGGGCAUAAGUUGAG GGGGUACUUGUGCAUUUUCCCUUUA UACUU	230	sga-miR10532-5-3p	AAGUGUGUCUCUGUGAUUUCGGGC	167-190	sly-miR10532	1	0	24	24	1
sga-MIR6218	UUGUUUCUAGGAAAAUCAGGAGACU UGUGUCCAGACUUUCCACAAGUCCA ACAUUUAACUUCGUUAGAUGUGUUG UGAGAAAUUUUCUUACUUCUCUUUC CUUUUGAAAAUCCUUUUUCUUUUGA GGAUCUUCUCUUAGUUGUGGAUUUU CCAGAUUGUUCUUUCUUUGAAACCC UUUUUGCAGAAGGGGGUUUUAGACU UGGGAAACCAAAGUCUUGAAAGAAU CUACCAAGUUCGUUACUUGAAAAUU GGCAAGCCCCUUUGUGAAUCAAGUG UCAUUCUCGAAUACAUCGACGAGAC	250	sga-miR6218-5p	GGAAAAUCAGGAGACUUGUGU	10-30	sbi-miR6218-5p	5	0	21	21	2
sga-MIR5670a	AUUUGAAGGCCCUUCCAUCUUGCCU AAAGAACCUUACGAUCGAUCUUUAG CUCGUUUCUGGGCUAAAUUCUUCGA UGAUAAGGUAUAUUGCUUUCAUAAU AUAUUUACUUUAUUAGGUCUUAUAU AUGAUUUUUCAUAAACUUAUGCCAC UUGACUGUAAGGAGAGGGGCUUCAU AAACAAUGUAUACACCUCAACUUGG	225	sga-miR5670a-3p	UUUCAUAAUAUAUUUACUUUAU	142-163	gma-miR5670a	6	0	22	22	3
sga-MIR6230	UUUAAGUUGGCUCCAUAACAAGGCA UUUCACGCGUGUUUACGGGGGCCA ACUUAAAGCAAGUUGAGGUGUCUAG AUGUGCAU	107	sga-miR6230-3p	AAGCAAGUUGAGGUGUCUAGA	80-100	sbi-miR6230-3p	5	0	21	21	2
sga-MIR10536-1	UUGAAUAAGAAGGAAAUUGAAGAUU AAAACAUGUCAAAGGAACUGGUCCG ACGUAGUAGAUUGACUUGUCUACAA CAAGUGUUGAUGAAGAAGGAAGCUG AGGAUCAUAACAUGUUGUUGGACCU UUCUUCAUCAUCACUCGUUGUAGAU AAGUCAAUUAACUGCGUUGUCCUUU GACAUGUUCCAAUCGUUAGUUUUCU UUUUUUUUUU	210	sga-miR10536-1-3p	UGACAUGUUCCAAUCGUUAGUUUU	175-198	sly-miR10536	5	0	24	24	2
sga-MIR7984d-3	GUGAUUUAACAUGUGAUCGAAAUUG CAGUUACGAUACCAAACUGUAUGGA UGACCUUUUAUCCCGCGCUAUUUAA UAGUGUAUUUUAAAGGUAUAUAUGU GUCCAAUGCACGAGAGUAAAAGGUC AUUUCCAAAGUUUAGUAUCGUUACA AUAAUUUCGGUCAAAGUUCGAAUAU A	176	sga-miR7984d-3-3p	UAAUUUCGGUCAAAGUUCGAAUAU	152-175	stu-miR7984d-3p	2	0	24	24	2
sga-MIR7992-5	CUCUGACCUCCAAUUUUCAUAAUGC AUAAAUAGACACUUUAACUAUCCAAC UUUUAAAUAAAUAAAUGCAUGAGUC CCACAUGGCACAAACCACGUAGGAC	193	sga-miR7992-5-5p	UUUCAUAAUGCAUAAAUAGACACU	15-38	stu-miR7992-5p	5	0	24	24	1

sga-MIR10535b-2	AAAAAAUGACAUGUAGGACAUAUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCUACUUGUGCACACCCAAAGUUGAAGGGCAUAAGGUUGGCAUGAGUUUGUGAAAGCCGGAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUAUAUCACUCUUCCAUGUUAACUGAUCAACAACUGAACACAG	111	sga-miR10535b-2-5p	UUGGCAUGAGUUUGUGAAAGCCGG	3-26	sly-miR10535b	0	0	24	24	1
sga-MIR10442	UUGUCCAACAACUAUCGUAGUUGUGGAAACAACUUAUCGAGUUUCCUCCGACAACUACAUGCAGCUGUUGGACCAUUUUUCAUCUGAAUGAUUCUAGUCGUCCAACAACUACAUGCAGUUGUUGGACCAUUUUUCAUCUGAAUGAUUCUAGUCGU	180	sga-miR10442-3p	CUACAUGCAGCUGUUGGACCA	80-100	gma-miR10442	5	0	21	21	1
sga-MIR8707-1	UGUUCUUUUUAAAUUACAAAAAUCUCUUAAAAUUUAUGGAUUUUGGAUACAUUACUAGACUUCCUGGUACAUGAUUCGAAUUUCGGAUACAUAGUGAGGGAUGUAUCUAUGAGGGGAGGGAUGUAUCAGAGAGGGGAUAUUACAUCCAGAUGCAUCACUUGACUUACAGAUACAUCAGCAGACAUCCGGAUACAUACAUGGGAUGUAUCAGGGGAUUUAUGUAUUUGGGAGGAGAUAUAAUGUAUCAUCGAGAGGAGAGCGAUGUAUUCAAGAAGAGAUUUUUGAAAUACUUUUGAAUGAUAGAGAAUUUUAGAGAUUAUGAUAAAAUAAGACGAAGU	338	sga-miR8707-1-3p	UGAAAUACUUUUGAAUGAUAGAGA	283-306	gra-miR8707	7	0	24	24	3
sga-MIR5303-10	CAUCUAUGUUGUUCGGUCUCUCCACAAUGUUAUCGCAUUCAUGUUGGAUCCUCCAAAAAUGCACUAUUUUUGAAGGAUCCGAACAUGCACCGUUCAACAUUUUUCAAGAGUUCGAGCAACUUAGUUU	127	sga-miR5303-10-3p	UUUUUCAAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
sga-MIR5162-1	GCCUCUCUCCUUCAUAUAACAUGUAGUUACAAAUUGUAAUUAUCAAACUAUAGUCAUGAAGAGUAAUUAAUUAUUUUUAAAUGGCUAUAUGUGAAAGUUUUCUAAAAUAGCCGAAUGAAUCGGGUUAUGGAUUUCUGGACCAUGGAUUGUGGAUGUGUAGGUCUGUUCAAGAAUUCAAUUGACCUAAAUGGCCCUAAACAUAAAAUGUUAUUAUAGGAAAGAAUU	225	sga-miR5162-1-3p	AAUUGACCUAAAUGGCCCUAAACA	177-200	osa-miR5162	7	0	24	24	1
sga-MIR8006-2	CUGCGUCAUACUUUUUGGACAUUGGUGUCCUUGCCGUCCAAAAACUCAACAUAUAUGCCCUUCACUCUAAUGGAUGACGAAAUAGGGACAUGUGGCGCAAUGUUAUCCGUCGAUAAAUUUCGGGUCGGUAGAUAAGAUUAUGACACGUGUAUGUCCAUUAGUAUAAGCGGUAUAUAUGCUCUAAAUUUGGGAUGACAGGGGCACCAAUGUUCCUAAAGUAUGACGGAG	229	sga-miR8006-2-5p	GUCCUUGCCGUCCAAAAACUCAA	27-49	stu-miR8006-3p	6	0	23	23	3
			sga-miR8006-2-3p	UAAAUUUGGGAUGACAGGGGCACC	183-	stu-miR8006-5p	4	0	24	24	1

					206						
sga-MIR10532-6	AUUGGGAUAAUGCACAACUACCCCCUCAAACUAGUGUCACGUAGGUCAAAAAGGGAUAGAAAAUUAUUUAUUAAAUAAGUUCGGGGAGUAAUAGGUACUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUUAUGCAUAGAUUGAGGGGGUACUUAUGCAUUUUCCCGGUUUUUCCAUCACUUUUUUGCAUAAUU	168	sga-miR10532-6-3p	AAGUGUGUCUCUGAGAUUUUAUGC	111-134	sly-miR10532	3	0	24	24	1
sga-MIR8008b-3	CUUUCAAAUAAACCCAGAAAAGCGACAGACAGGGUCCUUUAGUGCGUCGCGUUUCUGGGUUUUUCAAAAAAAUAAUUUUCAGAAAAGAUGGAUAGGAAUAGUCACUACAUCAAAAAUGAU	120	sga-miR8008b-3-5p	AAACCCAGAAAAGCGACAGACAGG	35-58	stu-miR8008b	2	0	24	24	1
sga-MIR7983-2	CAUUAGCGGCAGUUAAUUUUUAAUUGCUGCAAAAUAUAUAUUUUUAGCGCCAAUUAACACUCUUUGUAUAUGUUCCUAAAGCUUUUAGCGAAAUUGAUUCUAAUGGCACUUAACUAAUGCCGGUAAAGACUUUAACACUCUUUAUUAAUGUCAAUUUUUAAUGCCGCUAAAAGUUGUUUUGUUGUAGUGAGUACACAAGGAGAAGACCCUAAAAUGCCCCU	222	sga-miR7983-2-3p	ACUAAUGCCGGUAAAGACUUUAAC	138-161	stu-miR7983-3p	0	0	24	24	1
sga-MIR11108u	CAACUAUUUGAAUAGGUGCAAAACUACCCUCAAAGGUGGAUCAAGGGUAUUUUAGGGCCGAAAGGUGGAUGAAGGGUAAUUUUGUACCAAUUCAAAUACUUGAGGGGCACUUUAGGUUCUUGUCUGU	152	sga-miR11108u-3p	GUGGAUGAAGGGUAAUUUUGUA	90-111	lja-miR11108u-3p	7	0	22	22	2
sga-MIR10542-3	AAAAUAUACCUUGAACUUUGAUAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUUAAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAACUUCUGUUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACAGCAGGGGUAUAUGUGAGCCGUUUGUAUGACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAG	249	sga-miR10542-3-5p	UAGAAGAAUCAUAUAUACCCCUA	22-44	sly-miR10542	0	0	23	23	1
sga-MIR5628	CUGGAGAAAUAUGGAAGAGAUGAUCGGAGAAAUAUUAUGUUCUAAUGAGCUAAUGCCACAAGAAAAGUAAUGAUGUCUAUAACUUUAAAGCUCUGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGAA	135	sga-miR5628-5p	GAAAUAUGGAAGAGAUGAUCG	6-26	ath-miR5628	5	0	21	21	1
sga-MIR5723	UAAUCAAUGAUUUGCGAAGAUUGCAAUAUUAUUUUUGGAGUCCCACAUCGUUAGUGGGAUGGGAAUAUGGAUUCCUUAUAUGGUCUUCGAUAAUAUGAAGAAUUAGGUGAAUAUGCUGAGGAGAUGGAGUUGAUAAAUGUUCCUUUGACUCUGGUAUAAGCGACAAAGAAACACUGCCAUCCUCAAUCUUCUCAUCAUAAGCAUCUUUUUUUAAAAAAAUAAUGUUGAAUGAUAUCUUGAAGUAACGUGUUGCAAUCUCUCACUAAAUAUAGAAAU	276	sga-miR5723-3p	AACGUGUUGCAAUCUCUCACU	244-264	bra-miR5723	6	0	21	21	1

sga-MIR8009-2	UUCUUUUGUCAAAAAAUUGCAGAAAAAGUGUCGAAUAAGGUGAGUUUUCCAUCACUUUUUUACAUUACUUUUUUCAACUAAACUCAGAAAAGCGACGAACAUAAACCUUUUGUCCGUCGCUUUUCCGGCUACUUUAAAAAAUUCAUUUCCAGAAAAGUGACGGACAGUGUCCUUUAGUCCGUCGAUUUUCUGAGCUUUUCAAAAUAU	207	sga-miR8009-2-3p	AUUUCCAGAAAAGUGACGGACAGU	145-168	stu-miR8009	1	0	24	24	1
sga-MIR7992-6	GUGCCCUUUCACUUGACUUUAAAUCACAUUUAUGCUCUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACUUAUAUAAAGUUGAAAAAAUAGACACAUCUGUCCUAAAUUUUUUUUUUGUCCUACGUGGUGUCCUACAUUUAUUGUUCCAUGUAGUGCUCAUGUGUAUAUUUAUUUAAAAGUUAGAUAGUUGAAGUGUUUCUCUGUGCAUUAAUAAGGUUGGAGGUUAAGGUUAAAAUUUGAAGCCAAGUGUAGGGUAA	261	sga-miR7992-6-5p	UUUGGAUGUGCACAAAUAGACACU	44-67	stu-miR7992-5p	6	0	24	24	1
sga-MIR6293	GACGACAACAGCAAUAACAUAUCCAGUGAAAUCCCACAAGUGGGAUCAGGGGCUGCGAGAAUAAGGCAGACAAUAGAAAAGGUUACCUAGUAUUUUUAUGUUACUGUUGGGAUUUGAACCUUGGUUUUCAAGAUUUGCACUCACAUUACUGAUUUUUUUUUUGAGUCGAGUAUCUGUUGGAAACAACCUCUCUAUCCCGUAAGAGGUAGAUGACUAGAGAUAAAGUCUGCGGUACAUCCUACCUUCCCUAAACCGCACUUGUAGGAUCACACUAGGUAUAUAUUAUUGUUGCAGUCCACUAGAAUGUAUUAGUAAUGUUUGCAUUAAUUAAACAUAUAUGAUUUCUUAUGCAUUGUUUGGUUUGGUGUAUUUUAUAUUUUUUUUAGUUUCCCACCCUG	299	sga-miR6293-3p	UAAGAGGUAGAUGACUAGAGA	200-220	ppe-miR6293	5	0	21	21	1
sga-MIR5752b	UGUCUGGAGCCCAUGUUGGAGCUCCGUCUAAAUCCGAAUCGCGCUCUGCAGGGGCACAUUCGGGGGUGACACUCCCAAAAGGUUUUCUCCAUAUCGAGGGACCUCUGAUUAAGGAUGAAACACUCCACCAAUGCACCACAACCCAUGUUGGUGGUUUGGUGAAUUAUUAAUAGCAUACAUUGCAUAAAAUAUUUAC	295	sga-miR5752b-5p	CAUUGUUUGGUUUGGUGUAUU	52-72	mtr-miR5752b	5	0	21	21	1
sga-MIR5014a-7	UUCAAAUUUUAACUUUGACCUCCAAUUUUCUUAAUGCACAAACAAACACUUUAGCUAUCCAACUUUUAAAUAAAUAGACACAUGAGUCCUACAUGACGCAACACGUGUAAGACACCACCUAGGACAAAAAUGAUAUGUAGGACAUGUGUGUCUAUUUAUUCAACUUUAUACAAGUUUAAGUGUCUAUUUGUUCACAUCCAAAAUUAAAGGGCAUAAAUAUAAUUUAAA	229	sga-miR5014a-7-3p	UUAUACAAGUUUAAGUGUCUA	167-187	ath-miR5014a-3p	5	0	21	21	1
sga-MIR7984b-2	CCGAAAUUGUUGUAACAAUACCGAACUUUGGAAAGGACCUUUUACCUCCCUAAUCUAUUUAAUAGCAUAUUUUAAA	236	sga-miR7984b-2-5p	AUACCGAACUUUGGAAAGGACCUU	18-41	stu-miR7984b-5p	1	0	24	24	1

	GACAUAUAUGAUAUAUAUGUUCACC UGGACAUCAUAAAUAUUGCAUCACU AUAACUAGUAAUGUGUCCACACGGA CAUAUAUAUACCUUUAAAAUAUGUUA UUAAAUAGUGCAGGGGAAAAUGUCC UCCAUAAAGUUUGGUAUCGCAACAG UAAUUUUGA		sga-miR7984b-2-3p	UGUCCUCCAUAAAGUUUGGUAUCG	198-221	stu-miR7984b-3p	4	0	24	24	2
sga-MIR156t	UAGGGGUACUUUAGUUAUUUCCCUA GGUUACCUAAUUAAUUUAUUUAGCA AAUUAAUUAAUUAAUUUAAAAGACCU AAAACCAAAACUACAAAGGAAAUUUU CAGGUUUUGGUUAAGACAAGAAAGG GACAACCUAGUACCUAACCUAAGAU AGUCCAAAGAGUUAGUUAAGGUUCU AACAACUUAGGGAUACUUUAGUAAG UACCCUGG	210	sga-miR156t-3p	UUAAGACAAGAAAGGGACAAC	113-133	gma-miR156t	5	0	21	21	1
sga-MIR11409d	CUGAACUUUAUUCACUAUAACAGUA UGGUCACAAAACUAUCUUUUGUUGC GUUAAAGAACGUGUUAAUUGCUCAA ACAAUGACUAGAAGGUUAAAUAUUC UUUUAAUAUUAUUUUGAGCCAGAAA UUUAACCUUUGGGCCAUUUGUCUCA UUUGAGCAAUCCACACCCCUAGUUC AGUUACUUUAAUGUGACAAAAAUUA GUUCUGUGAUUCUACCGUUACCGCG GAUAAAAUUAAA	237	sga-miR11409d-3p	CAUUUGUCUCAUUUGAGCAAU	140-160	pab-miR11409d	4	0	21	21	1
sga-MIR396	UAAACUACUCCAAGAAAACUGUGAA UUACAUAGGGAUAGGAAAACUAAUU CCUAGGAAAAUCCCCAUGUAAUUCA UAGUUUUCUUGUAGUGUGCA	95	sga-miR396-5p	CUCCAAGAAAACUGUGAAUUA	8-28	stu-miR396-3p	6	0	21	21	2
sga-MIR8005b	GUGAACUGAAAAUUGAAAAUAUUAAA UCGAGUUGAGAUAGAAGUCGGGUU GGGUAUUGACCCACCCAAGUUUAAU UUGGGCUCGAAUGGACUUAAAAACG GGUUGGAUCUUGACCCGUCAAUUUG AUCCGAUUAAUCUCACUAACCUAAC AUACCACACAUAAGAUAUGACAUAUA UAUUUCUCGAAAUUAUAUAUAUAUU AGCUUAUGAUUUAAGUUUUUCUUUU UCAUUUUGA	235	sga-miR8005b-5p	ACUGAAAAUUGAAAAUAUUAAAUC	5-28	stu-miR8005b-5p	6	0	24	24	1
sga-MIR825	GGUUUCCAUGGUCAGUUUAUGCUUA UCCAGAAGGUGCAGGGGUUGGUUU CUGGUAGAACGAGCUUAUCUUAUAC AUGUUUUGUUGAAGAAGCUAUGGUU UCCGAUCUGAUUUGCCUGCACCUUA UGUUUGAGCAUGCGCUACCAUGAAC UA	151	sga-miR825-5p	UUAUCCAGAAGGUGCAGGGGU	23-43	aly-miR825-3p	6	0	21	21	1
sga-MIR8596	AAGAAACAAUAUGCUUUUUUCUAUU CCAAAAGGCAUUAGGAAAAUCGGAA CAAAUUUCCUUUUCAAAUUUCUCUC GAAGAUUUGCUAUUUUGUUAACAAU CUCCGGGGUUUUUAGAAUUUGCUCA AUUUUCUUAAUACGGAUUUCAUCCU UUAAAAAGGUGAGAUGUUGAGAAAG UUUGUUUAUUUUGAAAACAGUUUUU	318	sga-miR8596-5p	AUACGGAUUUCAUCCUUUAAAAAG	135-158	atr-miR8596	6	0	24	24	1

sga-MIR11419	UCUCUGACAAAAUCACUUUCUUCUU GAGAAAGAGUUUUUACAAAAGGGAA AAGGAGAUCUUUUCCUAGUAUAUUA GUGGAGAUGCCAUUCGGUGAAGUAA AAUAAGGUUUUAUUUGGG UAUUUUAACAGAAAGGGCCUAAACU GCUCUUAAACUAUGAGAGUGAUACA AUAUUUCCCUCCAUCCACCUAAUGA GUAUAUCCGUUAGACAUAAGGGUAU UUUUGAGCCGAAAGAUGAACGGAAG GGGUAUUUUAGUGGUGAUAGGUGG AUGAAGGGUAAUUUUGUACCAAUUC AAAUACUUGAGGGGCAUUAUAGGUC CUUCUCCAUUUAAAUUA	216	sga-miR11419-5p	GCCUAAACUGCUCUUAAACUA	17-37	pab-miR11419	5	0	21	21	2
sga-MIR5664	AUCUCAUUCCGCUUAAAUUGACUAU GUAUGAUUAUUACAAGAACAGAGGU UUAGAUAGAUAUGUUAGUCAAGAAG AGAAUGAGUUACAGAUCUAUCUAAA CCUCUGUUCUUGUAAUAAUCAUACA UAGUCAAUUUAAGCGGAAUGAUUU UUUGAUAGAAGAAUCAUAUAUACCC	149	sga-miR5664-3p	AUAGUCAAUUUAAGCGGAAUG	125-145	ath-miR5664	4	0	21	21	1
sga-MIR10542-4	CUAAAUAAUUUUUUUAAAAAAAAUUA GAAGUAAUAAAUAUAAAUUUAAAACU AAUUUUUUAACUUUUGUUAAAUGAA GGGUAUAUGUGAGCCAUUUCGUAAC AGCAGGGGUAUAUGUGAGCCGUUU GUAUAACGGUAAGGGCAUAUAUGAG CCACUUUUAUAACGAGGGUAUAUCA GCUCCAAAUGACAAAGUUGGGGGUA UAUCAGACCCUUUUCCCU	244	sga-miR10542-4-5p	UAGAAGAAUCAUAUAUACCCCUA	6-28	sly-miR10542	0	0	23	23	1
sga-MIR5773	UGAUCCACCCACGUAACCCGACCCA UUAAAAAACAUGAUAUGACCCAUUU UAUUUUGUCUUUAAUCCUAAUUCAA GGUUUAAAGAAGGAUUAAUUUAUGA UUAAAGAUAAAAUAAAAUGGGUCAUA UCAUAUUUUUUAAUGGGUCGGGUUA GGUGGAUGGAUCA	164	sga-miR5773-3p	UUUUUAAUGGGUCGGGUUAGGU	133-154	gma-miR5773	5	0	22	22	1
sga-MIR821b	AACCACUCAAAUUUUUAAGUUUCAAA UAGGAGCUUAAUGUUUGUAGUUUGA UUGAUUCGGUGUUUACUUAUGAACA UCAAAGUUGCGUAUUAAGCUAGCGU UUGGCCAUAGAUUUCCAAAUAUUCU UGGCAAAUAUUAUUUGAGUGAAAAU UUGGGUGAAA	161	sga-miR821b-3p	UACUUAUGAACAUCAAAGUUG	65-85	sbi-miR821b	3	0	21	21	2
sga-MIR1917-2	UCUCUACAAUAAAAAUAACUUUUAGC GGCAAUAAAUAGAUACAUUAAUAAAG AGUGCUAAAGUCUUUACCGGCAUUA GUUAAGUGUCAUUAGAUCCAAUGUC GCUAAAGCCUUUAGUGACACAUACA AAGAGUGCUAAUUGCCACUAAAACC AUAUAUUUAGCGGCAAUUGCUAAUU AAUUGCCGCUAAAGCUCAUUUUUAA UGUAGUGU	210	sga-miR1917-2-5p	AUUAAUAAAGAGUGCUAAAGU	43-63	sly-miR1917	0	0	21	21	1
sga-MIR11028-1	UCCCUCCGUUUCAAUUUGUUUGUUU UACUUUUCUUGUUGGUCUGUUUCAA AAAGAAUGUUUUUUCCCCUUUUUGA CGAUACAUAGAGCAUAAUAUCAUAA	174	sga-miR11028-1-3p	CAAAUGUUUUAUAUACUUUCUCA	105-127	seu-miR11028	6	0	23	23	3

sga-MIR7997c-8	GAUUCAAAUGUUUUAUAUACUUUCUCAAACUCUGUGUCAAGUCAAAACCAGACAAACAAAUUGAAAUGGAGUGUUACUAUGUUGUUCGGACUCUUCAAAAAUGUUGCUGCGCCCAUGUCAGAUCCUCCAAAAAAUGUACUAAUUUUUGAGGAUCCAAUGUGCACUCGGUGCCUUCUUUGAAGAGUUCGAGCAACAUAAUU	126	sga-miR7997c-8-5p	AUGUUGUUCGGACUCUUCAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
sga-MIR1916	CCUACGAGAGUUUGAGAUUAUUUGUUAUGUAAUGUGAGAGUUUGAGAUUAUUUGUUAUGUAAUGUGACAGAACAGAACAUGGUGUUUCCAAGUUUAAUUUAGGUCCAACCCAUCGGUGGCCCUCUAAACUUGGCAUCAAUUUUCACUUAGACACUUCAAUUAGGCGAUGUUCAUUUUAGACACCUCAUGUAGGGUUCUGUUGUGUCAUUUUGACACUUUUCUGACAAAAAACAAAAAACUAAAGAAGAGUGUAAUACACUUGUCGAUGACAAAUACUUUAAAAGAGAAGAGUAUAUAUUGAAAACAAUUUCAAACUCAACGUGAA	325	sga-miR1916-5p	UUUUCACUUAGACACUUCAA	140-159	sly-miR1916	2	0	20	20	2
sga-MIR8001b-2	CCACACUACAAGAAAAGUAUGAAUUACAUUGAGAUUUUCCUGAAAAUCAGGAUGAAUUUUUGCAGGAAAAUAAGUCUCCUACGUAUUUUCAUACUAAUCCUAGGAAAAUCCCAUGUAAUUCACAGUUUUCUUGUAGUGCCA	141	sga-miR8001b-2-3p	GUAUUUUCAUACUAAUCCUAGGAA	83-106	stu-miR8001b-3p	5	0	24	24	1
sga-MIR11178	UGAUUCAUUGGUGAUAGAUAGGUGUUUAGUCCUAUUGAGACAACAGAACAAUUUAACUAGAAGUUUUGGAGUUCUCUAAAAACUUCUAGUUAAAUUGUUCUAUUGUCUCAAUAGGACUAAACACCUAUGUGUCACCAAUGAACUA	145	sga-miR11178-5p	UAGGUGUUUAGUCCUAUUGAGACA	19-42	lja-miR11178-3p	7	0	24	24	1
sga-MIR395a-3	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCGCUUUAUUAGGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUAGGGGAACUCUUGAACUCACUUUGAAAU	107	sga-miR395a-3-3p	UGAAGUGUUUAGGGGAACUCU	70-90	aof-miR395a	1	0	21	21	1
sga-MIR395a-4	UGCUGAAGUGUUUAGGGGAACUCUUGAACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAAUAGUCCUGGCUGUGGAUGAUGAACAUGAUAGUUCAUGUAUAAAUCUAUUAAGGUGUUCCAUAGAGUUCCCUUGACCACUUCAUGA	151	sga-miR395a-4-5p	UGAAGUGUUUAGGGGAACUCU	4-24	aof-miR395a	1	0	21	21	1
sga-MIR2055	AUAGAACUCUACAAAUUUUCUUCCAACGAAGUUCAAUCUGUGACCUUACAAGUAAAAUGAAAUUUCUGUAAUGCUAUACUCUACCAUAAUCAAUCAGAUCUAUUUCUGCAAAGAGAAGGUAAUCUCUGGUUAAUGACAACGUUUUGCAUUCUACAUAGUACUUUAGCAUUUUAUCUGAUUGAUUAUGGUAGAAUAUUAGUAUUACAGAAAUUUCUUAAGCAAAAUCUCCCAGACAUGCUUUCCUUGGGAGAGAGUUUUUGGCAGAGUUCAGA	272	sga-miR2055-3p	UUUCCUUGGGAGAGAGUUUUU	239-259	osa-miR2055	5	0	21	21	1

sga-MIR396a-2	AUCUUUUCCCACAGCUUUCUUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAAAUUAUCAAUUUAGAGAUCAAAAUUUAGCAAGAAGAAGUUCAAGAAAGCUGUGGAAAAGCA	112	sga-miR396a-2-5p	CACAGCUUUCUUGGACUUUCA	10-30	hbr-miR396a	2	0	21	21	1
			sga-miR396a-2-3p	GUUCAAGAAAGCUGUGGAAAA	89-109	csi-miR396a-3p	1	0	21	21	2
sga-MIR10540-2	UGCGGGGUUGAAUUCUCAAAUGGUUACUCAACUUAUAGUUAUUAUCUCAGAAAAUCUCUUUUCGUUCUUGAUUCUGAUGCAAAGAAAGUCACUUUGUUAGAUAUAAACUAUUAGUUGAGUGACCAUCUGUGAAAUCAACUCCUGU	145	sga-miR10540-2-3p	AUAUAAACUAUUAGUUGAGUG	101-121	sly-miR10540	3	0	21	21	1
sga-MIR7992-7	AAAGCAUAAUACAUAGACAAGACUCUUUAACUUGGCCUUCACCGGCACCUGAUCAUCAAUCCCAGCUCUAAUUGUGAUCAUCUUGACACAGGUGUGUCUCGCAAACAUCUUAACUUUGAUAAUGCACACUUUUGAGAACGUGUCUAGAUGUGCAUUUUCAAAGUUAGGCUGUUUACGGGGUUUUCAAAGUUGGAGUGUUUAGUUACCUGUUGAGGUAAAGUUAAGAUGUCUAUCUAUGUAUUGUGCCAA	249	sga-miR7992-7-3p	UGUCUAGAUGUGCAUUUUCAAAG	141-163	stu-miR7992-3p	4	0	23	23	1
sga-MIR7990a-2	CGCAUAGAUCUCAAAAAAGUAACCGAAUUGAAAAAAAAAAUCGCCUCAAUCGGACAACAGAGACAAAAGUCAUUACCACUUGAAUUUUCAAAACUUUACAACUACUUUUAUUGAGUUACACUCUUCAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCAUCUAAUAUCCGUUUGAGACGGUUUUUUUCAAUUUGGUUAUUUUUUGAGAUCUAUAUG	219	sga-miR7990a-2-3p	UUCAAAUGAUCGUAACUUUGGCAU	140-163	stu-miR7990a	1	0	24	24	1
sga-MIR7990a-3	UAUCUCGAAAAAAUAACCAAUUGAAAAUAAAAAAUCGCCUCGAUCUGACAUCAAAGACAAAAGUUAUGACCGUUUUAAGUUUCACAAAUUUACAACUACCUUUUUUUGAGUUACACUCCUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGACCUUGAAUAUCCGUUUGAGGCGAUUAUUUUUCAAUGAGGUUAUCUUCUGAGUUU	209	sga-miR7990a-3-3p	UUCAAAUGAUCGUAACUUUGACCU	135-158	stu-miR7990a	1	0	24	24	1
sga-MIR9773-2	UAUGUUUAGAUGUUUCUACUAGGUGGAACUCUACAUUUUCGAUGCUUGAUAUAGCACAACAUUUUGAGAUUGCAUUUGAAAUAUAUAGUUUUUAUGAUAUUACUUGAAUCGUCUUCGUACCUUUGGUUCUAAUUCUUUUGAAAACAAAGAUGGAACUAGUGUUGAAGAUGGAACUAGUGUUGAAGAUGAAUUUAGUGUUGAAGAUGGAACUACUGCAAAUAUUCUUUCAAGUGUUGACUAAAAAAAUGUGAGGUCAAUGGUGAAAUUUCUUGAAACUUU	279	sga-miR9773-2-5p	AUAGUUUUUAUGAUAUUACUUGAA	85-108	tae-miR9773	6	0	24	24	2
sga-MIR8001b-3	CAUGGGGAUUAGUAUGAAAAUUCGCAGGGAACUUAUUUUUCUGCAAAUUUUCAUACUAAUCCCCGAA	67	sga-miR8001b-3-5p	AUGGGGAUUAGUAUGAAAAUUCGC	2-25	stu-miR8001b-5p	1	0	24	24	1
			sga-miR8001b-3-3p	AAAUUUUCAUACUAAUCCCCGAA	45-67	stu-miR8001b-3p	6	0	23	24	3

sga-MIR2606c	AGUAGAUCAUCAGGAAUUUGUUUUGGCGUUAAGACAAUUUCUGAGCGUAGUGAAUUAAGAGGGUGUUGUAAAAAGGAAAAAAUGAAAUUCUCUUAAGGAGAUCACUGUCUCACUUCAUAUCGCUGCUGUGACGCCACUACAGCGGGAGGGGUGUCGUUGUCGCAUGUGAGGCGGAGAUGGAAUUAAAGGAUUUUGGGAUUUUUUCGAGGGAAUCUCACUGGUUCGCUUUGUGACACUAUAGCAAUGCUGCUACAAUGAGAUGGAUGUCGUUGUAGCGGGAUGACGAGUUUAAUAACCAUAAAUAAAAUCCUUAGACGAUCUUUU	324	sga-miR2606c-3p	GUUUAAUAACCAUAAAUAAAAUCC	287-310	mtr-miR2606c	7	0	24	24	3
sga-MIR12107	AAUGGUUUUGCAAGAUCAUUUUUGACACGUGGCCAAUUAUAAUUCGGUCACGUCAUCAAUUUUUUUAAUUAAUUUUUUCAUCAGUUUAUGAGUGGCCGAAUUAUAAUUGGCCACGUGUCAAAAAUGGUUUUGCAAAACCACA	142	sga-miR12107-3p	UUUAUGAGUGGCCGAAUUAUA	85-105	csi-miR12107-5p	6	0	21	21	2
sga-MIR827b	AUGUUCCAAACAGACUCAUUGCUGAAAAUUUUGGAGAUUUUAAUAAAGUAUCCAAGUCAGAUUUUUAUUACAAGUUUAAAUUGCAAAUUUUUGGGAAGAAGAUGACCGUCUAAAAAUCGGGAUCUUUUGUACUUUAUUUCUUCAUUUCUAACUGCAUCAGACCCUUCAAAAACAACAAUUCCAAAAUUGUAUUUUGAUUUGGUCGAGAUUCCAAGAACAGCAGAAAUCUCUGGAGCUUUUAGUGUAGCUGUUUAGGAAUAU	261	sga-miR827b-5p	GAAGAUGACCGUCUAAAAAU	98-117	cas-miR827b	5	0	20	20	2
sga-MIR394-3	UUUUCAUGAAGAUUUCUCAAAGGGUUCCUUACAUAGUUCUUUGGCAUUCUGUCCACCUCCUUUACCUUCAUAAUCUUCUAUUUUUUUAGAAAAAUAAUUUUUGUUAUUCUUUUUUUAAAAAAAUGGAGGUGGGCAUACUGUCAACAGAUUUGUGUUAGUUUCUCUUUGUGAAAUCUUCUUGAUGU	185	sga-miR394-3-5p	UUUGGCAUUCUGUCCACCUCC	40-60	cas-miR394	0	0	21	21	1
			sga-miR394-3-3p	AGGUGGGCAUACUGUCAACA	127-146	sly-miR394-3p	0	0	20	20	1
sga-MIR8639e-1	GCAGAUAAAUAUGUUCUCCAAUUUUGAGUGUGCACAAGUAAACACUGAAACUUGUAUAAAAUUAAACAAGUAAAUACACGUAUCCCACAUGACAUAAUACACGUAGGACGCCACGUAAGAAACAAAUUGCAAUGUCGGGUGCCAUGUAGGAUAAAUAUGUUUAUUUGUUCAACUUUAUAUAAGUUUAAGUGUCUACUUGUUUACACUCGAAAUUAAAGAUCAUAGUUGUCAAC	234	sga-miR8639e-1-5p	GAAACUUGUAUAAAAUUAAACAAG	47-70	gra-miR8639e	6	0	24	24	2
sga-MIR10532-7	AACUUUUGUUGCAAAUAAAUGGGAUAAUGCACAAAUACCCUCUCAGCCUAUGCCCAAAAUCUCAGAGCACACUUUCAAACUAGUGUUACGUAGGCCUAAAGGGGUAGAAAAUUAUUUAUAAAAUAAGUUUAGGAAUAAUAGAAUCUUAG	237	sga-miR10532-7-3p	AAGUGUGUCUCUGAUAUUUCGGGC	159-182	sly-miR10532	1	0	24	24	1

sga-MIR8766	UAUAGUAUAAGUGUGUCUCUGAUAU UUCGGGCAUAGAUUAAUGGGGGUAC UUAUGCAUUUUUCCCAAUAAUAUAU CAUAUAAAAAAA UUUACUUGGAUUCAAAUCACAUUUA UGCUCUUCAACUUUGGAUGUGCACA AAUAUAUACUUAAACUUGUAUAAAGU UGAACAAGUAGACACACAUGUCCUA CAUGUCAUUUUUCGUCCUACGUGGU GUCCUACAUGUAUUGUUCCAUAUAG GACUCAUGUGUUUAUAUAUUUAAAA GUUGGAUAGUUAAGUGUCUAUUUGU GCAUUAUAAAAGUUGUGAAGUCAAA GUUAAAAUUUGAAGUCAAGUUUA ACUUUGGAUGUAGACAUUUUAAAUU AUAUAACAUUUAACAAGUAGAAAGAU GAGUCUUACGUGACAUAAUACACGU AGGACACAAUUAAAAUGUCAUGUAG GAUAACGCCAUAUAGGAUAUGUGUG UUUAUAUGUUCAACUUUGUAUAAGU UUAAGUGUCUAGUUGUACAAAUUUA AAGUUGGAGGGUGUAUAUGUGAUUU GAGGCCACGUUAAAGGGCAUAUUUA UGUAUUAUGUCUUUUGGAUUCUAUU ACUUCCUCGGUCUCAAUUUAUGUGA CACUUUUCGAAUUUCAAGAUUCAAA CA	249	sga-miR8766-3p	CUAUUUGUGCAUUAUAAAAGUUGU	194-217	gra-miR8766	6	0	24	24	2
sga-MIR8007b-1	ACACCAUUUAGACUCUUGCAAUGUA CUCAAAUCGUUAUCUAAGCAUAUCU UUUGUGAGUAAUACCUUCUCUUUGG GGUCUCAAUAUCUACUGUUUAGAUA ACAAUUUCAGUUCAUUGCAAGAGUC UAAAUGGCUC	303	sga-miR8007b-1-3p	AUGUGACACUUUUCGAAUUUCAAG	271-294	stu-miR8007b-5p	2	0	24	24	1
sga-MIR2676f	CCGUAUUUUAAAGGUAUAUAUGUGC CCACGUGGACAUCAUAAAUAUUGCA UCAUUAUAAAUAGUAACGUGCCCAU GUGAGUACAUAUAUACCUUCAAAAU AUAG	135	sga-miR2676f-3p	UACUGUUUAGAUAACAAUUUC	88-108	mtr-miR2676f	5	0	21	21	2
sga-MIR1106	UGAAUACCUUCGGUCAUACUUUAGG AUAUUGGUGCUACUGCAAUUCAAAG UUAGAACAUAUAUACCCUUUACUAA CGGAUAUACACGUGUCAUAAUUUUA UCCACCAAUCCGACAUUUAUCGACG GAUAAGAUUGCGCCACUUGUCCCUA UUUAGUUUUCCUUAGAGUGAACGAC AUAUAUGCUCUAAUUUUUGAACGAC GGGGCAUCAAUAUCCCAAAAGUAUG AUGGAGGAUAUCUA	104	sga-miR1106-5p	UUUAAAGGUAUAUAUGUGCCC	7-27	smo-miR1106	6	0	21	21	1
sga-MIR8696	UUUAACAGUCUUUUCAUCUUCUCUA ACGCACUUCUUUUGGGUUUUUGUUU AUCUACCUUUUCUUCAAUGAUCGGA CUCGGUUUUUUUUUUAUUGAUUAAGC UGAAAAAUACAUUAUUUUACCUUUU UAAUUUAUUUCGUUCAUUUUUUUUC CAACUUGGCCAAUAAAAAAAUCAAAA CUGAUCGUUGAAGAGGAGCUAGAGA ACAAAGAGAAACCGAAAGCGUUGCA	239	sga-miR8696-3p	AUGCUCUAAUUUUUGAACGACGGG	180-203	gra-miR8696	6	0	24	24	1
sga-MIR6288c		252	sga-miR6288c-5p	CUCGGUUUUUUUUUAUUGAUU	76-96	ppe-miR6288c-5p	4	0	21	21	1

sga-MIR390b	CUAGAAAUAUGGAAAAGAUUGUUGA A GAGCGAGAUUCAUAUGUAUUCCAAA UACAUUCACAUAAGAUACACAUUAGA UACAUGCAUGUAUUAGGAAUGGUUC ACAUGUAUCUCACAUAUCAGAUACA UGGGAGAGUGGCGAGCGAGAUGGA AGAGAGGCUAUGAAGGCGAUCUAGA UUUGCUAUGUAUCCAAAUACAUGUG AAUCUACUUGGAUAUAUAUAUCUCG AAC	203	sga-miR390b-3p	UACUUGGAUAUAUAUAUCUCGA	180-201	gma-miR390b-3p	5	0	22	22	1
sga-MIR3637	GAGUUGUGACUUUUAUGAAAUGUUG CGACUUUUAUGAAAAGUUGCGACUU UUAUGAAAAGUUGUGACUUUUAUGG AAAGUUGAGACUUUUAUGAAAGGUG ACGACCUUUCUGAAAGAUUAUGACU UUUCCAAAGGUUUGUGACAUUUCCG AUAAGACACAAUAA	164	sga-miR3637-3p	UUCCGAUAAGACACAAUAA	146-164	vvi-miR3637-3p	4	0	19	24	1
sga-MIR172j-2	UAGAGUCAUAUGUUAGAUGAUGCAG CAUCAUCAAGAUUCCCAAAGAGAGA AAAUAAGAGACUUUGAACUAUAUUA UAUAUCCAAUAUUCACCCUAAAUAUA UAAUUAAAUACUUCUCCCUUCAAGU UUUGUGAAUCUUGAUGAUGUUGCAU CCUCAAACAUUGACUGAU	169	sga-miR172j-2-5p	GCAGCAUCAUCAAGAUUCCCA	22-42	lus-miR172j	0	0	21	21	1
			sga-miR172j-2-3p	UGAAUCUUGAUGAUGUUGCAU	131-151	mdm-miR172j	2	0	21	21	2
sga-MIR5014a-8	CAAACACUUUAACUAUCCAACUUUUA AAUAAAUAAAUACAUGAGUCCUACAU GACACAAUACACGUAGGACACCACG UAGGACAAAAAAUGACAUGUAGGAC ACGUGUGUCUGUUUGUUCAACUUUA UACAAGUUUAAGUGUCUA	145	sga-miR5014a-8-3p	UUAUACAAGUUUAAGUGUCUA	125-145	ath-miR5014a-3p	5	0	21	21	1
sga-MIR8007b-2	UCAUUAAUGAGUGAAAUUUAUGAUC GUUUGAAGUUGACCCAAAACUUAAA AAAACUAAGAAAUGACUUGAAAUGAA UUCUAUGUAAUUCUUUUUGAAACUC AAAAUGCUAUAUCUAGUGAUAUUAA UAUUUGAGAAAUUUCAAAUUCCUUG GUAAAAUCCUAUUCACAACGAAGGA UUGCUCGAGUCUUUGGUCAAAAACU UUUUGGGGUGCUACAACUUCAACUU UCACCCCUUUUAACUUUUUAAGGCU UGGGCUCCACUUUUUAACUCAUGCA UAUUACUUUUAACGC	291	sga-miR8007b-2-5p	AUGUAAUUCUUUUUGAAACUCAAA	81-104	stu-miR8007b-5p	7	0	24	24	1
sga-MIR7821	CCAGUUUCUCAAAGGCAUAACACAU ACAUAGACACUCAAGUUUGGCCUCG AUUGGCAAGUAGACAAUCCAAUUUU GGGAGUGGACACACGAUGAUGCUGA CUUGACACAUAAAUUUUGGAUGCGU CCAGAUGAUUAUUUCUUUAAGCUGA GUGUUCAACUGACACAAUGGAGACG AGUUGAAAUUAGUAGAUGUGCAUCG UCCUUGGAGCGUUUUGUCAGUUGA GACCAAGUUUGAGUGUCUAUCUUUA UAUUAUAUACCUUUCUCAAACACC	273	sga-miR7821-3p	AGAUGUGCAUCGUCCUUGGAG	189-209	ptc-miR7821	6	0	21	21	1
sga-MIR860	UUUUGCUAUUUUCUAUUUCAUUCAG	136	sga-miR860-3p	UCAAUUGAGUGGACUAGAAAA	107-	cas-miR860	5	0	21	21	1

sga-MIR10532-8	AUAUUGCAUGAUGGGCCAUUAUGUUGAUGCACCAGUGGAUUGGUGUUGUGAAGAAUGUGAUAUUGAUAAAUGGAUAAUGUUUCAAUUGAGUGGACUAGAAAAUGUGCAUUAAGGGAAAAUGCACAAGUAGCCCCUCAAUCUAUGUCCGAAAUCCCAAAAACACACAAGAUAGUGCCACGUAGGCUAAAAAGGGGUAAAAAAUUAUUAAUAAAAUAAAUUCAGGGGUAACAGGACCUUAAUAUAGUAUAACUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGAUACUUGGGCAUUAUCUCAUAUGCUCUUUAAUUUUAGGUAUGCA	191	sga-miR10532-8-3p	AACUGUGUCUCUGAGAUUUCGGGC	137-160	sly-miR10532	1	0	24	24	1
sga-MIR823	UAAGCAGAUACUUAAAUUUAUAUAAACUUGAACAAGUAGACACAUGAGUCUUACGUAGCACAACACAUGUAGGAGAUCAUAUAGGACAAAAAAUAACAUGUAAGAUGUCAUGCGGGACAUGUGUGUCUACUUGUUCAACUUUAUACAAGUUUAAGUGUCUAUUUAUGCACACCCAAAGUUGAAGAGCAUA	215	sga-miR823-3p	CAUGUAGGAGAUCAUAUAGGAC	91-112	aly-miR823-3p	5	0	22	22	2
sga-MIR7993b-1	UGAAAAUAUGACCAAAUUUACAAAAAUUUGGAAAAUUUGUCUCGGCUAAGCCGUUAGAAGGUUUUUGGGUUUUUGUAAUUCGACUCGGUAGAGGUGUUUAAUAGGUACAUAUUAUAGUUAAGGUGUUCACAUGAAAUAUGCGGACAACUUUAAGGGGCUGUAUAUGACUUAAGCCUAAUUUUAUUAUCUAAUUUUGAGAUUUGGAAUAUUUAUU	214	sga-miR7993b-1-3p	UUAAGGUGUUCACAUGAAAUAUGC	118-141	stu-miR7993b-5p	6	0	24	24	1
sga-MIR7981-9	AUUUUAACUAAACUAAUGCCCUAUUACCACACCCCACAAACUUAUUUUUUUGUAAUUUUAUACACAUUUUUUUACGUGGCACACUGUGUGAUUUCACGCAAUUGAGGCGCGUGAGAGAUAUUUGGAUGCCAUGUAAGUCAAAAAGGUGCAAAUUUUUUUCAAAUAAAGUAUUCAAGGGUAAUAGGACCUUAGUUUAAUUAAGGU	204	sga-miR7981-9-5p	UUUAACUAAACUAAUGCCCUAUUA	3-26	stu-miR7981-5p	5	0	24	24	2
			sga-miR7981-9-3p	AUAGGACCUUAGUUUAAUUAAGGU	181-204	stu-miR7981-3p	2	0	24	24	1
sga-MIR9679-3	GAAAUUGAUAACUUAUUAGCAAAGGGACUUAUAAAACCCUCUAAAUCUCCAUGGUCUUGUACUGCAUUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGUUUGUUAAUAAAUUACAAUACC	132	sga-miR9679-3-3p	CAGAACAAGAAAGAGGUGUUC	86-106	tae-miR9679-5p	5	0	21	21	1
sga-MIR7983-3	UCAUGUAUACACUACAACAAAAAUGACCAUUAACAACAUUUAAUUCUUAAUUGCCUCUAAAUAUGUAUUUUUAGCGGCAAGUGUCACUCUUUGUAUAUGUCUCUAAAACCUUUAGCGAAAUUGCUUCUAAUGACAGUUAACUAAUGCCGGUAAGGACUUUAACACUCGUUAUUAGUGUUAAUGUUUAAUGCCGCUAAAAGUUGUUUUUGUUGUAGUGAUAUCCAAAU	227	sga-miR7983-3-3p	ACUAAUGCCGGUAAGGACUUUAAC	140-163	stu-miR7983-3p	1	0	24	24	1

sga-MIR5014a-9	UUUAUUUCACAUUUACGUCCUUCAACUUUGGGUGUGCAUAAGUAGACACUUAACAUUGUAUAAAAUUGAACAAGUAGACACUGAGUCAUAUGUAUACACGUAGACACAAAUUGUCAUGUAGGAUGUCACGUGGUACGUGUGUAUCUAUUUAUUCAAUUUUAUACAAAUUUAAGUAUUGAUUUGUGCAUGCUCAAGUUGAGGGCAUAAAUGUGAAAUGAU	220	sga-miR5014a-9-5p	ACACUUAACAUUGUAUAAAAU	46-66	ath-miR5014a-5p	5	0	21	21	1
sga-MIR1520k-1	CAAAAAUUAGAGCAUAAAUGCUCUUCACUCUAAGCGAAGACUAAAUAGGGACACACGGGCGUUAUCUUAUCCGUCAAUAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACAUGUAUGUCCGUUAGAAUGAAGGGUAUAUAUGUUCUAGUUUUUG	154	sga-miR1520k-1-3p	GAUAAGAUUAUGACACAUGUAUGU	95-118	gma-miR1520k	7	0	24	24	2
sga-MIR4225	AAUCAAUAAUAAUAUUAUUUAUCCUACAAAUAAUCGAUUGAUCAACAACUAAACACAGUUGUCCAAUAACUGCCUUAGUUGUUCGACCAACUUGUCUAGUCGUCCGGCAACUACAUGCAGUUGUUGGACCAUUUUGUAUUUAAUGGUAUGCCUAAUUAUUCCUAUAAACAACUUUAAUAGUUGUCA	186	sga-miR4225-5p	UAAUCGAUUGAUCAACAACUA	31-51	aly-miR4225	6	0	21	21	2
sga-MIR399i-3	GUUCGUGAACGAUAGUAAUUGUAAGGGAAACAGUGAUACGGCUACACUCUAUUGGCAUGCAACUUGAUCAAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUAUUACUGUCUCUACUUAAUGUAAUGUAAUUACACGCAU	144	sga-miR399i-3-5p	CGGCUACACUCUAUUGGCAUG	39-59	stu-miR399i-5p	1	0	21	21	2
			sga-miR399i-3-3p	UGCCAAAGGAGAGUUGCCCUA	87-107	stu-miR399i-3p	0	0	21	21	1
sga-MIR156f-3	UGGUAUCUUGGAUAUCUCGUCUCCUGUUACUGUAUAUACGGUACUUAGUAGUCCGUAGAUGUAGCAAGUUGCUACUAGAUUUGGAUUUGUUCUGGGUUGUGAAAUUAGCUUAUUAUAUCCUUGUAAAUACUGGGUUAUAUAGUCUUCAGUGGGGUUUUUUGUUUCUUUAGCUCUGGGGUUUUGGUUUAGAAAGUUUUGUACUUUGUAUAUAUUUUCUAUGUAUGUUCUUGCCAAUAGCUAGAGGUAGAGGUGGUCAUGGUAGAGGCCGCCAUUCUGGAGGACGUGGUAGCCAAGGUAAUG	300	sga-miR156f-3-5p	GAUAUCUCGUCUCCUGUUACUG	11-32	csi-miR156f-3p	5	0	22	22	1
sga-MIR12154	CUGCACUAGGUGUUCCUUAAAACCUUGUAUCUAAGUUUGGCAUGGAAAAGAGGCCAAAAGACUUGAUCUCCAAGUCUGUGGAUUCUUUAACUUCUUUUUUUUUUUUUAAAAAGAAAAUAAAGACUUCACAGACUUGGAUAUAAUGUUUUAAAGGAACACCUAGUGGAU	168	sga-miR12154-3p	CUGUGGAUUCUUUAACUUCUU	76-96	aof-miR12154	6	0	21	21	2
sga-MIR1128-2	AAUAUAUAUUACUCCCUCCGUCCCAUUUUAUGUGGCACCAUUUCCUUUUCCGUUAAUCCCAAAAAGAAUGUCACAUUUUCUUAUAAUAUAAGUAUUUAAACAUACAAUUCUUCUUUUACCCUUGU	301	sga-miR1128-2-5p	UAUUACUCCCUCCGUCCCAUU	7-27	ssp-miR1128	3	0	21	21	1

sga-MIR2592bq-1	UAGUCCCACUUCAUUUUAAACAUAG UACUCUAAUACAUUUAUGAGGAGAG AGAAAAGUGAAUUUACUUUUUUGAA GGGAAAUUUGGUAAACAUUUCAAAG UCUUCAUUAUUUUUUAAACUCCGUG CCCGGUCAAAUGUUACCACAUAAAA UGAAACAGAGGGGGUAUUAUCAUCC A UCUUGUCUUCUUCUCUUUAUGAUUA UAGUCUUAUGAACAUAAUUUUAUAA CACGUUAUCAACACGAGACUCUAGC CAAUUGAGAGUGAGUUUAGUUUUUC UUUAGCUCAUGUUUUGGUUGAUCUC GUUUUGAGAAUCAAGAUAUUAUUUG CAUAAAAUCAGGUAUGUACUUUCUA AAAUCAGUUUGAAUAUUAUUUUGAU UGUUUUGAAAGACUCAAAGGGUGAG UCAUGUUGUACUCGAUCUAUUAUAU UGUUGGUUAAGGGAAAGAUGAUGG GUUCAAGCCUCAUCACCAUAAAAAA GGAUAAGACAUCA	312	sga-miR2592bq-1-3p	CAAAGGGUGAGUCAUGUUGUA	215-235	mtr-miR2592bq-3p	5	0	21	21	2
sga-MIR5057	AUUGGUACCAUUGGAAUUUCAUAUG UUUUUGCCAAUGCAUCAGACUUGUA AUGACCUGAUACAUUGGCUAAACCA UAUGUAUCAUGUACAAUAUGUUACC UUA	103	sga-miR5057-5p	GAAUUUCAUAUGUUUUUGCCA	14-34	bdi-miR5057	5	0	21	21	2
sga-MIR1438	AGUCGGAUCCAAGUUGGACGAGGGA AAGUACAUCGACGGUCUUGCGUCAA CAAAAUUGGGGCCGAAUCCGGGUG GAGGCGUGUCCUGCCUUCGCUGCA UCCCAACUCUCAUAUCAGCUAUCUG CUGCAUCAGUUGCGCAAUUAGCUCA UUUUGUUCUGCCACGGUGGGCUGA GCCACCACAACAUCUGUGAGGCUAA CUUUAUCAUUGUUGUCUCCCAUGGC UGUAUUUCCUCUGUCUGAGUUUGG UCCGGCG	253	sga-miR1438-3p	AGGCUAACUUUAUCAUUGUUGU	191-212	osa-miR1438	5	0	22	22	1
sga-MIR10538-3	ACAGCAUUAGGUUGAUAUACGUUAC UGUAAGUAACGUUUUACUCCUAAAA CGUUAUUUUCAGUAACGUUCUACUC CUGAAACGUUACUAUGAGUAACGUA UAUCAAUCUGACGCCAU	117	sga-miR10538-3-5p	AGGUUGAUAUACGUUACUGUAAGU	9-32	sly-miR10538	4	0	24	24	1
sga-MIR827-2	ACAUGAAGUGAUGAAGAUGUUUGUU GAUGUUCAUCUAAUCAUGGCAUAUU AAUGGUUCCAAAAACUAUGCCAAAU GAUAUGAUGAAUAGAUGACCAUCAA CAAACAAAUUCAUAACUACACAA	123	sga-miR827-2-5p	GUUUGUUGAUGUUCAUCUAAUC	19-40	eun-miR827-5p	3	0	22	22	2
			sga-miR827-2-3p	AUAGAUGACCAUCAACAAACA	86-106	aof-miR827	1	0	21	21	2
sga-MIR1919-4	UAGUCCUGUCGCAGAUGACUUUCGC CCUUCUAAGGAACCACACUUUCUGU AAAUCUAAUUAAUUUGAAUUCAAUG UGGCAGGACGAGAGUCAUCUGUGAC AGGAUAA	107	sga-miR1919-4-5p	UGUCGCAGAUGACUUUCGCCC	7-27	stu-miR1919-5p	0	0	21	21	1
			sga-miR1919-4-3p	ACGAGAGUCAUCUGUGACAGG	83-103	stu-miR1919-3p	0	0	21	21	1
sga-MIR391	AAAAGGCUUGCUACGCAGGAGAGAU	96	sga-miR391-5p	ACGCAGGAGAGAUGAUGCUGGA	13-34	sly-miR391	0	0	22	22	1

	GAUGCUGGACGAUAGAGAAAAUGGG AUUUAAUUUAUUGGCCAGCAUCAUA CUCCUGCAUAUUAAGCCUAAA		sga-miR391-3p	GCAUCAUACUCCUGCAUAUU	68-87	stu-miR391-3p	0	0	20	20	1
sga-MIR5049c	AAGAAAAGUGGACAAGUAAUUAGAG ACGGAGGUAGUAUCAUUUAACACAU GUUUUCAAUAAAGUCGAAGGAUAAA AUAGUACUCCCUUUGUCACUAUUUA CUUGCCAUGUUUAAA	115	sga-miR5049c-5p	GGACAAGUAAUUAGAGACGGAGG	10-32	hvu-miR5049c	5	0	23	23	2
sga-MIR8672	UGGAAAUGGAAAUAAUGUUAAAAUA ACUAUAACUAUAAUUAAAAAGAAUGU UGAAAUAAAUAAAGAAUGAAAAAGGA AUCUUAAAGCAACUCAAGAAUGAGA AAUAAUUAGAUGAAAAAGGGGUCUG ACAGCACCUGUAAGGCGCAGAAUAU CAGGCACCUUUUUUUUUAAUGCAAG GCAAAAGCCAUCAUGUGCCUUCCUC UUUUCAUCGGUUGACGCCGUUAACG GCGUAUAGGGGAAGGCACGUGGGC CCCUGUGCCUUUAGCGUUUUGGUU UCCUGAAUAAAUUGUUUGCCCUUUU UGGAACUUUUAGACAAUUAUGUUGC CCUUUUGG	333	sga-miR8672-5p	AUGAGAAAUAAUUAGAUGAAAAAG	97-120	gra-miR8672	5	0	24	24	1
sga-MIR396g	CCUUGGAAAUAGGUGGUCUUGAACU UUUGCUACAUGGUUAAACCUUUGAC GCCAAAAGUCGAUACUUGAUGUUCU GUUCAUGGGGCGCAAGAUUAAAAGU UCAAGAUCAUCCACCUCCAAAG	122	sga-miR396g-5p	GUCUUGAACUUUUGCUACAUG	16-36	gma-miR396g	6	0	21	21	2
sga-MIR7696d	AGCACAUGAUACAUGUGUGUUACGU UACCCAAAAUAUACAUUUGUGUUUU GAAUUAAAAGCACAUGAUACAUUGG CUAAAGCAUAUGUAUCAUGUACG	98	sga-miR7696d-3p	UUUUGAAUUAAAAGCACAUGA	47-67	mtr-miR7696d-3p	4	0	21	21	1
sga-MIR7992-8	ACUAUGCCCUCCAACUUUGAUUGUG CACAACUAAGCACUUAAACUUGUAU AAAAUUAAACAGACACACGCUAUACA AGUUUAAGUGCUUACUUGUGUACAC CAAAAGUUAAAGGUCAUUGU	121	sga-miR7992-8-5p	UUUGAUUGUGCACAACUAAGCACU	16-39	stu-miR7992-5p	6	0	24	24	1
sga-MIR7981-10	UAAUCGAAAUUUCAUAGACACAUUU UGACUAAAUUAAGGUCCUAUUAUCC CUGAAUUUAUUUUUUUGUAACUUUA UACACUUUUGGUCUUACGUGGCAUA GUCUGUGACGACUCCACACAAUUGA GGCACGUAGGCGAUAUUUAGAUUCC ACCUAUGCUUAAAAAGGUGCAUAAA AUUACAAAAAAAAAAAUGAAUUCAGAG GUAAAUAGAACCUUAGUUUAAUUAA GAUGUGUCUCUGAAAUUUUGAACU	250	sga-miR7981-10-5p	UUUGACUAAAUUAAGGUCCUAUUA	24-47	stu-miR7981-5p	5	0	24	24	2
			sga-miR7981-10-3p	AUAGAACCUUAGUUUAAUUAAGAU	206-229	stu-miR7981-3p	4	0	24	24	1
sga-MIR7993b-2	ACAUGUGUGUUGUCAAGCGUAUAUU AGGUCGUUAAGUUAACUACAUAAAA UAUGUCAUCUCUUUUGGAUAUAUAC AUCAGUAUCAAUUGAAUCAGGCCUG AGGUUUAUGGCUUAUUGAGUCGAAU ACUUUAUGAUUAAAGAGAGUGACUU AUUGUAAUUGGUUAACUUAUCUACG UAAGUGUACUUGAGAACACACAAUA	200	sga-miR7993b-2-5p	UUAAGUUAACUACAUAAAAUAUGU	32-55	stu-miR7993b-5p	1	0	24	24	1

sga-MIR7992-9	UCAACAGACAACUAAAUACUCCAACG UUGAGAAUGCACGUCCUCGUCCCUA CAAGGUCUCGUGGACACCCGAUUUU GAUGUGGGACAUUAAGUUAUGGAGG UGUCUUAAUGAUCAUUUUGGAAGUU GAAGUGUUCAACUGACACCGUAGUG ACAAGUUGAGGUGUCUAGAUGUGCA UCCUCAAAGUUAAAGUUUAGUAAUG UGUCAU	207	sga-miR7992-9-3p	UGUCUAGAUGUGCAUCCUCAAAG	163-185	stu-miR7992-3p	6	0	23	23	1
sga-MIR7725b	GAUUAAGUCAUUAAGGUUGACCCUA AAAUCUUAUCCACCAUCCCUUAGCU UAAUGAACAAGCUAUUCUUUAAUUA GGGAAUCGAAAACCAAUUUCCUAUU UAAAGAAUAGUUGGCUCAUUAGGUU AAAGGGUGGUGGAUAAGAUUUUAGG AGUAAUUUUCAGAUAUUUAGUG	172	sga-miR7725b-3p	CGAAAACCAAUUUCCUAUUUA	82-102	bdi-miR7725b-3p-1	6	0	21	21	2
			sga-miR8006-3-3p	UAGUCUUUGAACGACAAUGACACC	188-211	stu-miR8006-5p	5	0	24	24	1
sga-MIR5303i-3	GGAAUGACUAUGUUGCUCAGACUCU AUAAAUCAUGUCAGAUCCUUUAUAA GUCCGCAACUUUUAGAGGGGAUUAG AUACUCAUUCAUUGAUAUUUUUGAA GAGUCUGAGCAACGUAACAUAUU	123	sga-miR5303i-3-3p	AUAUUUUUGAAGAGUCUGAGCAAC	90-113	stu-miR5303i	0	0	24	24	1
sga-MIR5763c	GACGACGUGAAGAACAACCUUGUUG AGCUUGAGGAAGUUCACAAAGAGGG UUCGUCCUACCUCAAACUCAAGCUC AACGAGGCCAUCUCUUCCCUUCAAA UUUGGGACAUUGGUGCCCCAGCAG	100	sga-miR5763c-3p	GGAAGUUCACAAAGAGGGUUC	33-53	gma-miR5763c	6	0	21	21	2
sga-MIR8006-4	UCCAAAAAUUAGAGCGUAUAUUCCC UUCACUCAUACGGAAGACUAAAUAG GAAUACGUGACGCAAUCUUAUCCAU CGAGUCAAUCUUAUCCAUGAGUCUG AUGUCGACUCGAUGGAUAAGAUUAU GACACGUGUAUGUCUGUUAGUAUGA AGGGUAUAUAUACUUUAGUUUUUGA ACGACAGUGAUACCAAUAUCCCUAA	224	sga-miR8006-4-5p	GCCCCAGCAGUCCAAAAAUUAGA	15-37	stu-miR8006-3p	5	0	23	23	3
			sga-miR8006-4-3p	UAGUUUUUGAACGACAGUGAUACC	190-213	stu-miR8006-5p	4	0	24	24	1
sga-MIR10532-9	GGGAAAAUGCACAAGUACCUCCUCA ACCUAUGCGCUAAGGUCCUAUUACC CCCUGAACGUAUUAUAUAAGUAAUU UUCUACCCCUUUUAGGCCUACGUGA CACUAGUUUGAAAGAAAAAGUCAAC CAAUGUUGUGCCACAAGAUAGUGCC ACGUAAAGCGAAAAGGGGUAGAAUA UUAUUAAUAAAAUAAGUUCAGGGAG GUAAUAAGACCUUUGUAUAGUAUAA GUGUGUCUCUGAGAUUUUGGG	246	sga-miR10532-9-3p	AAGUGUGUCUCUGAGAUUUUGGG	224-246	sly-miR10532	1	0	23	24	1
sga-MIR5162-2	UUCUUCAAAGGUAUAUGGGGACUAA GUAUUCCCAAAGAGACUUAAAAUGU UUUUCACAUUUAAAAAAGGAAACUU UCAUUUCCAAUGAGACUUAGGACAU UUUUUUAGAAAAUUGGUGAAAGGCG AUCUCCUUGGGAGGGAUGUAAAGGA GCCAUAGGUCACGGGUUCGAUUCUC CCUUGAGGCUGCAUGCCAAUAAGAG GGGAUUAAAAGAGCGAAUGGCCGCC	315	sga-miR5162-2-3p	AAAUUUCCAAGAUAUCCUUUGAAC	290-313	osa-miR5162	6	0	24	24	1

sga-MIR5303h-4	CAUGGCAGAGACAAUACCUGAGUAUGUGGAUCCCAAGGGGGUUGUCACACAAGCAGGGAAACUAAAAUUUCCAAGAUAUCCUUUGAACUAGGCCUUUGUUGCUCGGACUAUCCAAACAUGUUGUCCCACCAGUGUUAGAUCCUCCAAAAAAUGUGUAAUUGGAAGAUUCGUCACACACCUUCAAACAUUUUUGAAGAGUCUGAGCAACAUAGACU	124	sga-miR5303h-4-3p	AACAUUUUUGAAGAGUCUGAGCAA	93-116	stu-miR5303h	0	0	24	24	1
sga-MIR11028-2	GUCGUUUUGUAGAGUGUAUUAGAAAAAAUAACGUAUGCAUUAGCCUUGUGUAUUACUAGUACCUUGUUUGGUACUCUUUUCUAACCUAUGUAUAACUAAUGCUUGCAUUAGUUAUACACUCUAUAGUGUAUUAAGGUGUGUAUUGCUAAUACCACGGAUUUCUUGGUAGAAUCAAUGCAAUGAUUAUAAUGCAUGCAUUAGCAUGAUUAAAGACCCAAUUGCCCCUCAAAACCUUUUUUACAUCUUUUCCGCCAUAAUAGUGGAGGAUGUCUGUGUAAAUUAAAUUUUUUAUGCAAUGUUUACUAUUUUUUUAAUACAUCAAACCAAACAAU	332	sga-miR11028-2-5p	UGCAUUAGUUAUACACUCUAUAG	104-126	seu-miR11028	7	0	23	23	2
sga-MIR3448	UAAAAGAAGGAGUCAAGAACGCACCAUACAGGAAAACAUCUUGAUAAGAAGUGUUACUAUGUUUAGACAAUUGUAUGGUUCGGGUAUUGACUUCUGUACUUGGA	104	sga-miR3448-5p	ACAGGAAAACAUCUUGAUAAG	28-48	aly-miR3448-5p	5	0	21	21	2
sga-MIR3951a	ACUAUCCUAGAUUAGAGACUGCAUGAUGCGUAGAAAAAUUUCCCUUAUUCUAAUCUUAUCGUGCCUUCUCUAAUGUAGGAUUUC	84	sga-miR3951a-3p	UUUCCCUUAUUCUAAUCUUA	39-58	csi-miR3951a-3p	6	0	20	20	1
sga-MIR8179	AAAGUAUAACUAAUGCUUGCAUUAGUUAUACAUGACAUGAAAAAGUGUACCAAACAAGGUACUACUAAUACACACCUAAUGCAUGCAUUAUAAUGUUUGGUAGAGUGUAUUAGAGAAACUAAUGUUUGCAUUAGCUUGAUGUAUUAGUAGUACCUUAUUUGGUACACUUUUCUAACUCAUGCAUAACUAAUGCUUGUAUUAGUAACACACG	211	sga-miR8179-3p	UGUUUGCAUUAGCUUGAUGUA	123-143	ath-miR8179	6	0	21	21	1
sga-MIR6478-1	UUCAAGAAUCCAACGAACAGGCAAGAUAGGUAUUUCAUGUUUUCAAAACUACAGUAUUGGGAAGAAUCAAUAGAAACCGACCUUAGCUCAGUUGGUAGAGCGGAGGACUGUAGUGGGUCUAAAACCUAUCAGAUAUCCUUAGGUCGCUGGUUCGAAUCCGGCAGGUCGGAUUGAUUCUUUUUGCCAUGUUCUUUCUCUUCUUUUU	205	sga-miR6478-1-5p	CCGACCUUAGCUCAGUUGGUA	77-97	ptc-miR6478	1	0	21	21	1
sga-MIR8038b	UAUUUUUCAAGUCAAAACAGUUUCUCCUUGUGAGUAAGUUGAAUCUCGUGCUCGUUAAACCGCAAGAGACGUAGAAUGCGUCCCAACAUGAGAUUCAACUUACUCACUUGGAAAAAUUGUUUUUGCUUGAGAAGCA	136	sga-miR8038b-5p	CCUUGUGAGUAAGUUGAAUCUC	26-47	stu-miR8038b-5p	0	0	22	22	1
			sga-miR8038b-3p	AUUCAACUUACUCACUUGGAA	93-	stu-miR8038b-3p	3	0	21	21	2

					113						
sga-MIR12142	AUUUGUGGCUUUUAUAAAGAGUUGCAACUUUUGUGAAGAGUUGCAACUUUUUUGAAAAGUUGUGACUUUUAUUUAAAUAAUUUGCAACUUUAAUGAAUAGUUGUAACUUUUAUGAAAGAUUGUGACCUUUCAUAUGGGUUGCAACUUUUCCAAAUAGUUGUGACCUUUCCGAAGGGUUGUAACUUUUCAAAAUAGUUGUAACCUUCAGAUAAGGCACAGUAGGAAAUCAAUAUUGAAGUUGAAUUCACUUCACAGCACUCAACCACAUUAGUUCCUAUGACAUCAUAGGAACUAAUGUGAUUGAGUGCUGUGAAGUGAAUA	222	sga-miR12142-3p	ACUUUUCAAAAUAGUUGUAAC	182-202	aof-miR12142	5	0	21	21	3
sga-MIR1518-1	CACAAAACUGUUACCUUUGUAAAAAAACAAAACAUUAGUUCCUAUCGCGGUGCAAUUUAAAACUGAUGGUAGGUCUAGGAACAGAUGGAGCAUGCACAAAACUUACAAAUUGUAAUGUA	220	sga-miR1518-1-5p	AGUGCUGUGAAGUGAAUACAC	83-103	gma-miR1518	6	0	21	21	2
sga-MIR7980b-2	UCAUGCGAUAUCAUAUCAUGAUAUGGUAUCGUGAGAUGGAAUCAGUGUUUGGACAUGCGAUUUUACGUUGAUUCCAUCUCACAGUUCCAUAUUAUGAGAUGUGAUCCAAUA	111	sga-miR7980b-2-3p	GAGAUGGAAUCAGUGUUUGGACAU	33-56	stu-miR7980b-3p	0	0	24	24	1
sga-MIR169c-3	UUCAUCAAUAUAGAAAUUUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAUUUAUAUUAAUCUC	212	sga-miR169c-3-5p	UAGCCAAGGAUGACUUGCCUA	61-81	ata-miR169c-5p	0	0	21	21	1
sga-MIR1514a	UACGUUCUUCAUUUUCAUAUUAGGCAUAAUACAUAAAUGUAUCUUUUAACUUGGCUUCGAAUCAUAUUUGUGCCCUUCAACUUUGAGUGUGUACAAGUAGACACUUAAAUUUGUAUAAAGUUGAACAAAUAGACACAAAUGUCAUACAUGUCAUUUGUUGGCUUACGUUGUAUCCUAUGUGUAUUAUGACAUGUAGAACUCA	202	sga-miR1514a-5p	UUCAUUUUCAUAUUAGGCAUAA	8-29	pvu-miR1514a	5	0	22	22	1
sga-MIR8006-5	GGAUAAAUAUAUUUCGAACUAUCGUAAAUGUUAUGCAAAUAUUUUCGUCUUAUUUUAUGAACAUUGAUACUAAUGAAAAUACACGUGUCAUAAUUUUAUCCACCGACUAAACAUCGGAUGGAUGGAUAAGACUGCGUCACGUGUCCAUAUUUGGUCUCCCGUUAGAACAAAAGGGCAUAUAUGCUCUAGUUUUUUGAGGACAGAGGCAUCAAUUUUCCAAAAAUAUGACGAAGGAUAUCUGCAUAUCAUUACGAUAGUUCGAAGAUAUAUUUAUUC	276	sga-miR8006-5-3p	UAGUUUUUUGAGGACAGAGGCAUC	187-210	stu-miR8006-5p	4	0	24	24	1
sga-MIR6166-1	UAUUAUUUAGUUUAGAUAAGUUCUUAUAUCAUUAUAAGUGUGAUUGUUGUCUUCUGCUGAGUUAUGUAAGCUAGG	340	sga-miR6166-1-3p	AUUCAAUAACCGUAUUACAUAUG	278-300	hbr-miR6166	7	0	23	23	1

sga-MIR7991c	UCAAGGGCCCGCUCGAGGCCAGCAA UGGUCAUCGAGUUCCAGUCUGGUG CAAGGUGUAGGCUCGGAGCGUGAG AUGGAGAUUGAGGAUUAGAGUAGAA GGUUAGUAGGUAGUUAAAAUUUAUC UAGUUUUUCUUGUUAAUGUUCUUUU UAUCAUUACGGACUAUCUUGUUUCA UAAUUCUGUUAUUACAUUUUUUUUC UUUUAUUCAAUAACCGUAUUACAUA UGGUUGUUACUAAGACAAGGGUCUA UCUAAAACAACAUAUCU UUGAAAUUCUGAUCUCUGGAGGUCG AUAUUUUUAUUUCUUAUUUUUGAGA UUUCAACCUCCGGAGGUUGGUUUUU UAUUUCUUGUUUUUGAAAUUCCGAC CUCUGGAGAUCGGUAUUUUUA	121	sga-miR7991c-5p	UGGAGGUCGAUAUUUUUAUUUCUU	17-40	stu-miR7991c	7	0	24	24	2
sga-MIR5537	UUUAUGUUAAGGAGUCAAGAUCGAA CCAUACAUGUUUUAUUCAGGCAAGA AGUUUGUAUGGUUCGGGUAUUGAC UUCUACACAUGAU	87	sga-miR5537-3p	GAAGUUUGUAUGGUUCGGGUAU	49-70	osa-miR5537	6	0	22	22	2
sga-MIR5499	ACACAACCUGUGUACAAUUAAGCCG AUGCUCCGGACAUUUAAAAAUGAAG GCAGCAUGGUUAUGUGCACAGAGAU UGAAU	80	sga-miR5499-3p	GAAGGCAGCAUGGUUAUGUGC	47-67	osa-miR5499	6	0	21	21	1
sga-MIR6166-2	UCUUUUAUCAUUGUAAGUGUGAUUG UUGUCUUUCGCUGAGUUAAGUCAGU CAGGCCAAGGGUCCGCUCGAGACCA GUAAUGGUCAUCGAGUGUCAAUCCC GCCAAGGGUGUAGGCUCAGGGCGG GAUAUGGGGAUCUAGGAUUAGAGUA GAAGGUUAGUAGGUAGCUAAAUGUU AUUUAGUUUUCUUGUUAGUUUUCUU UUUAUCAUUCAUAGACUAUUUUGUU UCUUAAUUCUAUUAUUAUAUUCUAU UUUCUUUAUUCAAUAAUUGUAUUAC AUGGUUCUUAUUGAGACAAGGGUCU AUCGAAAAACAACAUAUCUACCUUUA CAAGGUUAAACUA	338	sga-miR6166-2-3p	AUUCAAUAAUUGUAUUACAUGGU	257-279	hbr-miR6166	5	0	23	23	1
sga-MIR1520l-2	CACCUGUCGUUCAUAAAUUAGAUUA UAUAUGUCCUUUACUCUUACGGAAG ACUAAAUAGGAACACGUACUGCAAU AUUAUCCGUUGAUAAAUGUCGAGAU CGAUGGAUAAGAUUAUGACACGUGU AUGUCCGUUAGUAUAAAGGGUGUAU AUGCUCUAUUUUUUAGACGAUAGAG A	176	sga-miR1520l-2-3p	GAUAAGAUUAUGACACGUGUAUGU	106-129	gma-miR1520l	7	0	24	24	2
sga-MIR8659b	GCUCAUAUAUGCCAUUACCGUUAAA GAAAAGGUUCAUUCAUGUCAUUAUU UUUUAACGGUGGUUUUGCAAAACCA UUUUGACACGUGACCAAUUAUAAUU UGGCCACACCAUUAAAUUAUUUUUG AAUGAAGAGGUAGUAUGGGCUUCCA CUUUAUGUAAUACAUACGGGUGUCU UAGGGUAACAUAAGUUAGAGACCCU AAAAUGAGGAAUGAACUUCUUAAUG UAUGUGCUUAUGCAU	240	sga-miR8659b-5p	UAUUUUUUAACGGUGGUUUUGCAA	47-70	gra-miR8659b	6	0	24	24	2
sga-	UGGGAUUAAUUAGUGGCUGAUUAGG	161	sga-miR4240-3p	UGAUUAGACCAUUAACUUUAA	98-	ath-miR4240	5	0	21	21	1

MIR4240	CCAUUAACUUUAAGUGGGAUUAAUUAGUGGCUGAUUAGGCCAUUAACUUUAAGUGUGAGAUUAAUUAGUGGCUGAUUAGACCAUUAACUUUAAGUGUGGGAUUAAUUAGUGGCUGAUUAGGAUUAAAUUAAUCUAG				118						
sga-MIR9556	UGUACUUAAGCCCUUAGCAUCAAAUACUUGGCCCACAUACACCCUUAUUCUGCUCAAUUGCGCAUAGUAUUUGGACCAAGUAUUUGACGGUAAGGGCAUAAGUGAA	106	sga-miR9556-3p	CUCAAUUGCGCAUAGUAUUUG	53-73	bra-miR9556-5p	6	0	21	21	2
sga-MIR10538-4	ACAGCAUUAGGUUGAUAUACGUCACUGUAAGUAACGUUUUACUUUUAAAAUGUUAUUUUCAGUAACGUUUUACUCCUAAAACGUUAGGAGUAAAAUGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAU	131	sga-miR10538-4-5p	AGGUUGAUAUACGUCACUGUAAGU	9-32	sly-miR10538	5	0	24	24	1
sga-MIR6111	UUUAAUAGAAAAACUUAAAUGGAGCUAUGUGCUUCGUACAUGGGGAUUUAUAUAGCUGAACCUGAUGGAAUGUAUGCUUCCACUGACUAUGUUGGACAAACAACCUCGUCCAUUCUGAUUGGUAUAGUAUGUUGACGACCUCACCAACCUCUGACAAAACUGUUAGGUAGUGGAGCCUGAUUAAUAUAUAACUGUUAGGUAGUGGAGCCUGAUUAAUAUAUAAGUGUUAGGUAGUGGGGCCUGAUUAAUAUUUAUUCUCUAUAACCAAAACUUUAUUCUCUAUUUUAGGUUUUCCUAUUUAU	306	sga-miR6111-5p	CGUACAUGGGGAUUUAUAUAGC	35-56	cca-miR6111-3p	5	0	22	22	1
sga-MIR5379	ACUGGUUGACUUCAAAUGGGCAUAUCUCCCUCAUCUAAACUCAAAAUUUACAAAACUAGGUGGCUUCGGAAAGAGGAUUGAAAAAAAUUUCAUAUGAUAUCUUAUGGGCCACCUAACUUAUCAUCUUUUGAAAGUUAUGAUCGUUUGAAGUUGACCCAA	159	sga-miR5379-3p	UUGAAAAAAAUUUCAUAUGAUAUC	78-101	gma-miR5379	6	0	24	24	2
sga-MIR2592bq-2	UAGUAGUUCUUGUCCAUAUAACUGACCUGUUGUUGGAUCUUUUCUGUUUAAUUUAUCCCAAAAAUUUGUAAAAUAUUUUCGGUAUAAACAAGGAAUAUUUUCAAUUGGUGUAUAACCCACUUCUGAAGUCCACUUAUGGAUCCAAGGAAUAGAAAAUUCUAUAAAAAAAUACAUUUGAUCAAUUUUCUCAAUGCUUGAGACAUGAUCCUGUAAAGAUAGAUUUGUUAUAAACGGGGAGACUUUUGCCGAAAAAAUUAAAUAGACAAGAUCCCGCAAGUGGACAGAUGUAUGGCCAGGAAUUAAUU	305	sga-miR2592bq-2-3p	CAAUGCUUGAGACAUGAUCCU	189-209	mtr-miR2592bq-3p	5	0	21	21	2
sga-MIR159	GUUUGCACUUAAUGGAGGUCUGAAUCUUAAUCGUUCAGAUUCAGUCCAUCAAGUAUGUUAUGUUUUUAUGACUGAAUCUCAAUGAUUUAGUUCAGCCCAUUAAGUCCAUUU	111	sga-miR159-5p	UUUGCACUUAAUGGAGGUCUG	2-22	aqc-miR159	5	0	21	21	1
sga-MIR8610	UUAUGCACAAAAACUGCAUAUCUUCUCCGGUUUGAUCAACACUCUAAAUA	164	sga-miR8610-5p	AUCUUCUCCGGUUUGAUCAACACU	20-43	atr-miR8610-1	7	0	24	24	1

sga-MIR395g-2	GCUAGAAGCAAAAGAAGGUUGUCGA AUUUCCACCCAAAGAAAUAACCUUC UUUUGCUUCUAGCAUUUCAGAGUGU UGAUCAAACCUGAGAGGAAUCUGCA AUUUUUGUGCAUAA UUGAAGUGUUGAGGAGAAUUUUCAA GCUCACUUUGAAAUUUACACAAACA AAUAGAAGUGUUAGAGUAUUAAUGG GAGACUGAUUCCCGAGAGUUUUCUU GACCACUUCGUGAGGAUUUAAUUAC UUUGUUGUUUUAUGCCUUGCUGAAG UGUUUGGGGGAACUUUCGGGUUCA CUUUAAAAUUUACACAAAUAAGUAGA AGUAAAUGAGUACUAAUGGGAGAUG AUGAAUGCAACGAUUUAUUUUUAUA UCUAUCAAGGUGUUUUCGAGAUUUC CCUUGACCACUUAAU	290	sga-miR395g-2-3p	UGAAGUGUUUGGGGGAACUUU	146-166	gma-miR395g	0	0	21	21	1
sga-MIR8010	AAAUAAAGAAAUAAUGCACAAGUAUC CCUCUAGAUUAUGACCGAAAUCUCA GAGAUACAUAUAAACUUAACUAGAAC CCUAGUUAUGUUUAGGUGUGUCUCU GAAAUUUUGGUUAUAGUCUAGAGGG UAUAUAUACAUAUGUUUUUAGGA	150	sga-miR8010-3p	CUAGAACCCUAGUUAUGUUUAGGU	71-94	stu-miR8010	4	0	24	24	2
sga-MIR8639e-2	GCAUCAGCUGACAACUAUGACCUUU AACUUUGGAUGUGCACAAGUAGACA CUUAAACUUGUAUAAAAUUAAACAAA UAGACACAUUCGUCCUACAUGGCAC CCUAGAUGACAAAUUUAUGUCAUAU GUGUGUCUACUUGUUCAAUUUUAUA UAAGUUCAAAUGACUACUUGUGCAG AAUCAAAGUUGAAGGGCAUAAUUAU CCGCUGAAAG	211	sga-miR8639e-2-5p	UAAACUUGUAUAAAAUUAAACAAA	53-76	gra-miR8639e	6	0	24	24	1
sga-MIR7980b-3	UCUUCAAAGUUAAAUUAGAUUACAU UAAUAUGAUAUUUUAGGAGGUGUUU GGUCAUGCGAUCCAUAUCAUGAUAU GGUAUCGUGAGAUGGAAUCAAUGUU UGGACAUGCGAUUUCAUGCUGAUUC CACAUCAUGAUUCCAUAUCAUGAGA UGUGAUACCACAUUCUCCAAAAACC AUGAUAUGGUAUCACAUGGUGAUAC CAUAUCAUGGUUUGAAUUAUUUUAA UGCAAAAAUUAAUUCACGAGUUUAU AUUUUGUUAAAACAACCCCACAUUU AUAUCUAAUAAUCAUUUUAUUUCACA U	302	sga-miR7980b-3-5p	GAGAUGGAAUCAAUGUUUGGACAU	84-107	stu-miR7980b-3p	1	0	24	24	1
sga-MIR169j-2	GAAAAAGAAGAGAAGUCUUACAUGA AGAGGAGAGUCAUAUUGUUUAGUAG CCAAGGAUGACUUGCCUGCUCCAUA GUCUAAAAUGUGUUUAAUCACAUUU UAAUUUGGUUUCAGGCAGUCUCCUU GGCUACCUUGACAUGCUCUUUUCUU UUAUGCAAGAUAUCUUUUUAAA	172	sga-miR169j-2-5p	UAGCCAAGGAUGACUUGCCUGC	48-69	ppe-miR169j	0	0	22	22	1
sga-MIR169j-3	UUAAAAGAAGAGAAGUCUAGCAUGA UGAGAAGAGUCUUAUUUGGUAGCCA AGGAUGACUUGCCUGCACCGUACUU GAAAAGGUCUUUCAUAUGUCCUUUC GUUUUUGGGGUCAAGCAGGUCAUC	178	sga-miR169j-3-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1

sga-MIR10536-2	UUUAGCUAGCUUGACAAGCUCUUCU UUUUCAUGCAAGGCUUUCUCUUCUU UCGU UGUUGUUAAAGAAGAAGGAAGUUGA CGAUUGAAACAUGUCAAAUGAACAC GUCGAACGCAACUGACUGACGUGUG UGCAGCAACUGUUGAUGAAGAAAGG AAGCUGACGAUAGUGUUGUAAACUA GCCAGUCAGCUUUGUUGGACCUGU UCCUUUAAUAUGUUUCAAUCGUCAG CUUCCUUUCUUCAUCAACACUU	196	sga-miR10536-2-3p	UAAUAUGUUUCAAUCGUCAGCUUC	155-178	sly-miR10536	5	0	24	24	3
sga-MIR11578-1	UUGUAACUAUGACCUUUAACUUUGA GUGUACACAAGUAGACAUUUAAACU UGCAUAAAAUUAGCAAAUGUACGCA UUCGUCCUACAUGAAACCCUACAUG GUAAUUUUAUAUCCUACAUGACAUC CUAGAUGUAUUAUGCCAUGUAGGUU ACUUGUGUCUACUUGUUCGAUUUUA UAUUAAUAGUUUAUGUACAUACUUG UACACAUUUAAAGUUGGAUAACAUA UUUAUUC	232	sga-miR11578-1-3p	UGUAGGUUACUUGUGUCUACU	143-163	pab-miR11578	4	0	21	21	1
sga-MIR7992-10	AACUUUGACCUCCAACUUUCAUAAU GCACAAAUAGACACUUUAACUAUCC AACUUUUAAAUAAAUAAACACAUGAG UCCUACGUGGCAAAAUACACGUAGG ACACCACUUAGGAUAAAAAAUGACAU GUAGGACAUGUGUGUCUACUUGUUC AACUUUAUACAAGUUUAAGUGUCUA UUUGUGCACAUUCAAAGUUGAAGGA CCAAAAGA	210	sga-miR7992-10-5p	UUUCAUAAUGCACAAAUAGACACU	17-40	stu-miR7992-5p	4	0	24	24	1
sga-MIR7981-12	AGACACCUUAAUUAAACUAAGGUCC UAUUACCCCUAAACUUUUUUUAAAAA AAUUUUAUACACUUUUUGUCUUGUG GCAUACUAUGUGACUCCACGCAAUU GAAGCGCGUGAGAGAUAUUUCAAUU GAAGCGCGUGGGAGAUAUUUGAAUG UCACGUAAGCCAAAAGGUGCACAAA AUUACAAAAAAUAAGUUUAGGGGAG GCAAUAAGACCUUAGUUUGGUUAAG GUGUGU	232	sga-miR7981-12-5p	CUUAAUUAAACUAAGGUCCUAUUA	7-30	stu-miR7981-5p	2	0	24	24	2
			sga-miR7981-12-3p	AUAAGACCUUAGUUUGGUUAAGGU	205-228	stu-miR7981-3p	3	0	24	24	1
sga-MIR4351	AAAAUUGAUUUUCUUGAUUAAAAAA GUUCAUGGGUUAUCACACACGUAAA UCGAUAAAAGUAGCAUUCGCCUGAU UUGGGAUUCGUUUGAACUUGAAGAU GCACCAUUUUUCUUCACGGAACGAA CUGGUUUCAUUUUUAAUCUCUUAAC GGACAUCCAUAAAAAAUUUCAGUCA UUUUAUUUUGGAUUUCCGAAUGAAA AAACUCAUGAACUAUAGUACACGAAA AUCGAUAAA	235	sga-miR4351-5p	UUUGGGAUUCGUUUGAACUUGA	75-96	gma-miR4351	6	0	22	22	2
sga-MIR8565h	ACGUAACUUAAGGUUUAAAUGAAUU AGGAAAAUACCAAAAGACCCUUGAA UAAGUUGCUGUCGAACCAAACGACG GUCAGGACUGACGGUCCGUCGUCU GACCGACGCCCCGUUGUUGGGUCC	282	sga-miR8565h-3p	ACUAAAAUUGGCAUAACUUUUUAC	152-175	atr-miR8565h	6	0	24	24	1

sga-MIR8781a-1	GUUGAUUGGGUCUAUUUGACAGGAC UUUACUAAAAUUGGCAUAACUUUUU ACUCGGAGGUUUGAUUUUAUCAAGG UCGGUGGCUAUGGAAAGCUAAUUUA AUUAUUUAUCUGUGGGUAGGUCAUG GGACACCUAACUCAUUUUAUGCUAA GAGUUAUGA CGCCCUUCAACUUUAGAUGUGCACA AGUAGACACUUAAACUUGUAUAAAA UUGAACAAAUAAACAUGUGUCCUAC AUGUCAUUUUUUGUCCUACAUGAUG UAUUACGUGUAUUGUGUCAUGUAGG ACUCAUGUAUUUAUUUAUUUAAAAG UUGGAUAGUUAAAGUGUGUUUGUGC AUUAUGAAAGUUGGAGGUCA	195	sga-miR8781a-1-3p	UAUUUAUUUAUUUAAAAGUUGGAU	133-156	gra-miR8781a	5	0	24	24	1
sga-MIR8137	UCGCCUCGCCUCAGUGUGGAAUGG CGAGAAGGGCUCGCCUCGCCUCGC CUCUCGCCUUUGGCGAUGAGGCGC UCGCCAUUCACAACACUGCGAGAGG GUC	100	sga-miR8137-3p	GGCGCUCGCCAUUCACAACAC	68-88	cpa-miR8137	6	0	21	21	3
sga-MIR164a	UGGUUGAAUUUGAAUAUUAUAUUGA CCGCUAGAUUUGUAGAUUCAAGACG UUCAUUGAUAGGGAGUACACGUGUA CUCCUUAUCAAUGAAUUUCCUGAUU UCUACAACUCUCACGACCACUAUAA GAUCGAAAGUAAUUU	140	sga-miR164a-3p	CACGUGUACUCCUUAUCAAUG	68-88	zma-miR164a-3p	4	0	21	21	1
sga-MIR8006-6	CAUAUAUAUACUCUAGUUUUUGGAU UACAGAGACUCCAAUGUCCCAAAAA UAUGACAGAGAGUAUUUACCUAUCA UUUACCAUAAUGACAAUUUUUUUGG UAAAACAAUAAACUCUACAAAAUGUA UAUUUUUAAGGAAAAAGGACAAAUA UAUCUCAAGCUAUCGUAAAUGGUAU GCAGAUACCCUCCGCCAUAUUUUUG GAACAUUAGUGCCCUGCCGUCCAAA AACUAGAGCAAUAUGCC	243	sga-miR8006-6-5p	UAGUUUUUGGAUUACAGAGACUCC	14-37	stu-miR8006-5p	5	0	24	24	1
			sga-miR8006-6-3p	UGCCCUGCCGUCCAAAAACUAGA	211-233	stu-miR8006-3p	1	0	23	23	1
sga-MIR5014a-10	AAUAGACACUUUAACUAUCCAAUUU UUAAAUAAAUAAACAUGAGUCCUACA UGGCAAAAUACACGUAGGACACCAC GUAGGACAAAAAAUGACAUGUAGGA CAUAUGUGUUUAUUUGUUCAAGUUU AUACAAGUUUAAGUGUCUACU	147	sga-miR5014a-10-3p	UUAUACAAGUUUAAGUGUCUA	125-145	ath-miR5014a-3p	5	0	21	21	1
sga-MIR908	GGAUUGAAAUUGGAGGUAUUAAAAU GGGUUGAAUAGAAGUUAGGUUGGG UCUUCACCCACUUAAGUUUACUCUG GGCUCAAAUGGGCUAAAGUUAGAUU GGGUCUUGACCCGCCUAAUUUGACC CGUUUAAUAUCAGUAAUUUAACAU CUAAACCUAACUUCAAAAUUUACUUU	148	sga-miR908-3p	UGACCCGUUUAAUAUCAGUAAU	120-141	cre-miR908-2	6	0	22	22	1
sga-MIR8587	GACCUCCAACUUUUAUAAUGCACAA ACACACACUUUAACUAUCUAACUUU UAAAUAAAUAAACACAUGAGUCCUAU AUGGCACAAUACAUGUAGGACAACA CAUAGGACAAAAAAUGACAUGUAGG ACAUAUGUGUCUAUUUGUUCAACUU	249	sga-miR8587-5p	UCCAACUUUUAUAAUGCACAAACA	31-54	atr-miR8587	6	0	24	24	1

sga-MIR859-2	UAUACAAGUUUAAGUGUCUAUUGUGCACAUCAAAAGUUGAAGGGCCUAAAUGUGAUUUGAAGCCAAGUUAAAUAGUUUCCUCACUUUUCAUAUUCUCUCUUUUCUUUUCCCAUUCACACUUGCUAAAACCCAACACUUCGUUUAGAAAUAUUUAACUAGAACAAAAUAUAACGUUCUUAUCGAAUUUCUCUCUUGUGAAGUUCAUUUUUUUUUAUCUUCUAUUUGAAGAAAUUGUUGCCAAAAAAUAAUGGGUUAUUGUGAGGGGAAAAAUCUAUGUGAAUUGGUAAAGGUGAAAUGGAGAUGAAGAGUUAAUAUUGGGUGAAAAUG	254	sga-miR859-2-3p	UUUCUCUCUUGUGAAGUUCAU	113-133	ath-miR859	5	0	21	21	1
sga-MIR478d	CCUACUAUAAAUCAUUACCUUGAAUUCAUAAUUCAAAUUAAAGUUAGACUUAAGAGUCAAGUCUUGAGAGUUCUUUUGAGUCUUUUGAGGAAGUCCCUUUGAGUCUUUUGAGAAGUCUUCUACUAUUUCUAAAAACUUGUUUUAAGAUUCAAGUAAGUGAGUAUGAGAUUCAGGAGAAUGUAUUCAUUAGUCUA	194	sga-miR478d-3p	UGAGAAGUCUUCUACUAUUUCUAA	109-132	ptc-miR478d	6	0	24	24	1
sga-MIR7996c	GAGGAGUCCGGAGUCUAAAGGGUAUAAAAUAUUAAUAAAAAUUUUAAAUUUGCAAAAUCGUUGCUACUGCAGCGAUUUUGCUUAUUCCGACAGAGAAAAUCGCUAUUGUUCCAGCAAUUUGCCAUUUUGGUUAAUAUAAAAUUUUAUAUGCCGUUUUAAAAUUUUUGUUAAUAUUUUAUACCCUUUAGGCUCCGGACUCACA	202	sga-miR7996c-3p	UUUUGGUUAAUAUAAAAUUUUAUA	125-148	stu-miR7996c	7	0	24	24	2
sga-MIR9564	UUAUGCAAGAAAUUACCAAAACUAUAUUUCCCUGAUGAAAGUAAAACAUUUACAUAUAUAAUUGAAACAGAUUCAAGUGACCACAGUUAUGGAGGAGUACUAAAAUAUUUUGAAACGAGGCCCCCUCGACGGUCCGUCGUGCCUAUGACGGUCCGUCGUGGGUUUCGUCAUUUCAGCCUAUUUUUCCAGAAAUAAAAUCUGCUGCUCAAAACGACUAAACAGAUCGUUACAAUAGAUACCAAUUUACCCAUCGUUCGUCCCCGAACGAUCACAAGAAGAAAAACAAGGGCGAGAAGAAGUGCCUGAAUCUGUAAACAUGUGUGGGUAUCUUUCUUGCAUAU	341	sga-miR9564-3p	UCAAAACGACUAAACAGAUCGUUA	206-229	bra-miR9564-5p	6	0	24	24	2
sga-MIR3636	GUGUGUGUGUGUGUGUGUAUAUGUAUGUGUAUAUAUAUGUAUUUCGGGUUGGUUUGAGUUCGGUUUGAUUCUUUGUUUAAAUACCAAACCAAAUCAAGAGUGGUCCGAUUUUUUUAUCAAUUGCCAAACCAAUCAAACCAAAUCACAAUUGAGGUUUUGUUCGGUUUGAUUUGGUUCGUCGGUUUGGUUUACUUAAUGGUUCGGUGUAUACACCCCUAAUCAUAAACAAAGACAUAUUAUUGUAGAGUCAAGUUAACAUUUCAUAUCAAUAGAUUAUAUAAACAUAAUAUACAAAACAC	307	sga-miR3636-5p	UCGGUUUGAUUCUUUGUUUAAAUA	60-83	vvi-miR3636-5p	6	0	24	24	1

sga-MIR2929	UUACAAAU UUCACGCGCUCAAAAGGCGUGCUUC AAAUGACAGGUGACAAGUCAGUCAC GUGUGUUUGAUAAAUACACUUUUUA AGUGGUUUA	84	sga-miR2929-3p	GUCACGUGUGUUUGAUAAAUA	46-66	osa-miR2929	5	0	21	21	2
sga-MIR8002	UCCUAACACACGUGUCAUAAUCUUA UUUACUGAUUCGAUAUUUAUCAAUA GAUAAGAUUGUGUCACGUGUCUCUA UUU	78	sga-miR8002-3p	AUUCGAUAUUUAUCAAUAGAUAAG	33-56	stu-miR8002-3p	6	0	24	24	1
sga-MIR6147	UAGUUAUUCUUUCUUCCAUGUGAAU UUCCCAUAGAAACAUCAACAUCAGC AUCCAUAUUAGUUAUUUCUUCUUAA GGCUUCAUUAUUUUCUUCCCUGUAA UUAAAAAUAGUGCUUACAUAGAUGC GGAUCCCGAAUCUUGAGUUCAUAAA UUUGUAUUCUAGAAAAUGAUACCUU UUCAAAACCCACCAAGUUAUCUUUU AAGAAUUCAUAACCAUAAAAUCAAGA UUCUAGAUUCACCUCUAUGUAAGCG AAGAGAGUUGUGAAGAAUUUAGAGG AAAUAAGUCAUAACUAAGAUGAAUUU UGAUCUCGCUAUGGAAAUUCACUCA GAAAAAUAAAUA	339	sga-miR6147-3p	AUACCUUUUCAAAACCCACCA	169-189	nta-miR6147	5	0	21	21	3
sga-MIR5021-3	CAGCAGCAGCGACCCGGGAAACUUC UCAGAAUGGAGAAGAAGAAGAAGAA GAAAUUUCCCGGGUUGGUGGCUGU AG	76	sga-miR5021-3-3p	GGAGAAGAAGAAGAAGAAGA	33-52	ath-miR5021	2	0	20	20	2
sga-MIR7997c-10	UCGCUAUGUUGCUCGGAUUCUCCAA AAUGUUGUCGCACGGAUCCUUAAGA AAUGCACUACAUUUGGAGGAUUGGA CACUCGCCUAUCUGCAUUCUGAAAG AGUCCGAACAGCAUAGGUU	119	sga-miR7997c-10-5p	AUGUUGCUCGGAUUCUCCAAAAUG	6-29	stu-miR7997c	5	0	24	24	1
sga-MIR6283	GGGAUUAUUUGUCUUCCUAGUCUUC GACACAAGAAAGGGGUGUAGAAAAA UCCUUUUUUCUUGUGUCGAAACGAA AGAGUAAUGAUUCU	89	sga-miR6283-3p	AGAAAGGGGUGUAGAAAAAUC	32-52	ppe-miR6283	5	0	21	21	3
sga-MIR7493b-3	GACAAAAUCAACUUCUCUGGCUAAA GAGGCGUAAGUAUCACCUUGCUCUU UUUUCUGCAAAUAUGCCUGAAUUUG UUCAUAUAAUGAACUGUCUUUAGGA AUAUCCCUUAAAUUUAUGGAGGAUG AAGCUGAUGAAGAGGCUUCACCAAU CUUUGAAUUAAUCAAAGUAUUACUU CCUAACUGUAUAACAGGAAAGGAAG AGUCAUAUGACGACCUUGUAGAUUG UGAAAAGGAUGAUUUUCCC	244	sga-miR7493b-3-3p	GUAGAUUGUGAAAAGGAUGAUUUU	218-241	gra-miR7493b	6	0	24	24	2
sga-MIR7493b-4	UAUAAAAAAUCGGGAAGGGAAUUAU CAAUUCCCUUUUUAUACUGAAUUUC AAAGUUGAAUACUUCCUAACUGUAU AACAGGAAAGGAAGAGUCAUAUGAC GACCUUGUAGAUUGUGAAAAGGAUG AUUUUCCCCUUCCUCGUUGAUUUUU UCCC	154	sga-miR7493b-4-3p	GUAGAUUGUGAAAAGGAUGAUUUU	107-130	gra-miR7493b	6	0	24	24	2
sga-MIR1862g-2	UAGAAGAUGAACAAUAACUAGUACU ACUUAAGAGAUGUUACUUAGUAUAG GUAUGGGUAUGAGACUUUACCCAUA UAUUGCACAAGUGGACCUUAAAGGG	174	sga-miR1862g-2-3p	AUGAUGUUGGUUUAUCUUGA	154-173	osa-miR1862g	3	0	20	20	1

sga-MIR8739-7	AAUUCUAGGGUGGAUUCUUUAUUUA UGAAUGAUAUACAUGAUAUUGGUAU UAUAUGAUGUUGGUUUAUCUUGAU GUGCAGAUACCUCCGUCAUACUUUU UAAACAUUGGUGCUCCUGUCGUCCA AAAUUAAGAGCAUAUAUGCCCUUCA CUCUAACAAAAUACUAAAUAGGGACA CGUGGCGCAUGUAAUCUUAGCCGUC GAUCCGAUAUUUAAUAAAUAUCAUG UCGGUAGAUAAGAUUAUGACACGUG UAUAUUCGUUAGUAUAAAAGAUAUA CAUACUUUUAAUUUUUGAAUGACAA AGAUUCCAAUAUCUCAAAAAGUAUG AUGUAGGGUAUCUGUUC	268	sga-miR8739-7-5p	AUACUAAAUAGGGACACGUGGCGC	86-109	gra-miR8739	5	0	24	24	3
sga-MIR10405d	UCUAAUGAAGAAUUGCGACUUUUAU CAAAAGUUGUGACUUUAAUGAAGAG UUGCGACUUUUAUCAACAAUUGUGU UUUUUGUCAAAAGUUGGGACUUUAA UGAAGAGUUGCGACUUUAUGAAAAG UUGCGACUUUUAUGAAAGGUUAUGA ACAUUCCGAAGGGUUGUAACUUUUU CAAAUAGUUGUAGCCUUUCUGAUAA GGCACAGUAAAGAUUAGUUCACACU ACCCUUUGUUUUUUAUAAAUAGUGG GAUUUCCUCUCAUUUUA	267	sga-miR10405d-3p	UUGUUUUUUAUAAAUAGUGGG	231-251	gma-miR10405d	6	0	21	21	1
sga-MIR8006-7	GUGUGCAGAUACUCUUCGUCGUACU UUUGGAAUAUUUGUAACCAUAUCAU CCAAAAGCUAGAGAAUAUGUUCUUC UCUCUAACGGAAGACUAAAUAGGAA CAUGUGACACAAUAUGAUCCAUCGA UCCGAUUUCAAUAAAUGUCAGUCCG GUGGAUAAGAUUAUGACACGUGUGU CUAUUAGUAUAAAUCGUAUAUAUGC UCAAGUUUUUGGAUGAUAGGGGCAA UAUCCCAAAACUAUGGUGGAGGGUA UCUACAUAU	259	sga-miR8006-7-3p	AAGUUUUUGGAUGAUAGGGGCAAU	203-226	stu-miR8006-5p	5	0	24	24	2
sga-MIR394-4	UAUCAAACUCUAGAAAGGACCUUUU ACUUCCUAUACUAUUUAAAGGUAUA UAUGUACCCACGUGGAUGCAACAUU AUAAAUGGCAAUAUGUCCACGUGGG CACAUAUAUAUCUUUAGAAUACAUUA UUAUAUAGUGCACGGGUAAAAGGUC CUUCAAUAAAGUUUGGUA	169	sga-miR394-4-3p	AUGGCAAUAUGUCCACGUGG	80-99	aof-miR394	6	0	20	20	2
sga-MIR7998-1	GUUAGACCUACGGACCGUAGAUCAA ACGACAGUCCUUGCUGGUCAUCUAU AGUUUAUGUUAGAGGGUGGGUAACU UGAGUCUUAAUCCACGGACACAGAC CACGGACGGUAGUCUGACUUACGGA CCGUAGGUCUGUC	138	sga-miR7998-1-5p	ACGGACCGUAGAUCAAACGACAGU	10-33	stu-miR7998	2	0	24	24	1
sga-MIR7992-11	AGGCUCAAACUUGGUCUUAGCUAGC AAGUAAGUUCUCCAACCUUGCAUAU GCACAUCUACACACUUCAACUUGUC UCCACUAUGUCCGAUAAACACUCCA ACUUACAAGAUGGCCAUCUAGACAC CUCCUAAGUCAGCCGAGGCGUCUUG AUGUGCACUCUCAAAGUUGGAGUGC UUACUUGCUAGGUGAGAUCAAGUUU	206	sga-miR7992-11-5p	CUUGCAUAUGCACAUCUACACACU	42-65	stu-miR7992-5p	5	0	24	24	2

sga-MIR1886h-1	UAGUGU ACCAUAUCACGAUAUGGAAUUAUGA GAUGGAAUCAUCGUUUGGACAGCUA AUUUUACGUUGAUUCCAUCUCAUGA UUCCAUAUCAUGAUAUAUG	94	sga-miR1886h-1-3p	AUUUUACGUUGAUUCCAUCUCAUG	51-74	stu-miR1886h	1	0	24	24	1
sga-MIR1520k-2	GGGACACGUGUCACAAUCUUAUCCA UCGAUCUGAUGUCUGGUCGGUGAA UAAGAUUAUGACACAUGUAUG	70	sga-miR1520k-2-3p	AAUAAGAUUAUGACACAUGUAUG	48-70	gma-miR1520k	6	0	23	24	1
sga-MIR5239	UAUACCUGUUAGUACACCUCUUGCU GGUCAUAUGAUGUUGAGCAAGAAGA UUUGUCCUACAGCUAGGGAGGAAAA GAGAGAAUGGUCAAAGUUCUAUAUU CCUCCGUUGUCGGAAGUCUAAUGUA UGCAAUGGUAUGCACUAGACCUGAU AUUUCUCACGCCGUUGGUGUUGUCA GUAAAUUUCUUAAAAAUCCGACAAAA GAGCAUUGGGAAGCUGUGAAGUGG AUACUCAGGUAUCUUAGAGGAAACU CAGAUGGAUGCUUUUGUUUUGGAG CAUUAAAUUCAAUCUUGAUAUGCUA UAUAGAUGUUGAUAUAACAGGUGAC UUGGGUGGUCGUCUUAUGUAGCAC	324	sga-miR5239-5p	GGGAGGAAAAGAGAGAAUGGU	66-86	mtr-miR5239	6	0	21	21	2
sga-MIR7752	CUUUAUAUCCUGCAGGUUUCUGAUC UUCACAUUGUCAUAUUUGAAUCAUA CUCCCCAGCAGUCCCGAAAUCUGUG UUAGGGAGUAUGAUUCAAAUCUGAC AACGUGAACAGCUGAAACCCUACAG GGUACAACAGGUGCUUCAUAAGACG AUGACCUGU	183	sga-miR7752-5p	CUGAUCUUCACAUUGUCAUAUUUG	44-67	bdi-miR7752-5p	7	0	24	24	2
sga-MIR7842	CCGGUGUCACAAAUACAUGUAAAUC AAUCCAGAUACAUGUACCUAGUGUA UAUCUGGUGUGAUUCACAUGUAUUC GAGAUACAAA	85	sga-miR7842-5p	UAAAUCAAUCCAGAUACAUGU	20-40	ptc-miR7842	5	0	21	21	1
sga-MIR5720	UCAUUAAAUCAAACCGAACCGAUGA ACCAAAUCAAAUUGAAAAAAAAAAAC AGACUUGUGGUUUGGUUUGAUUGG UUUGGUGAUUGAAAAA	91	sga-miR5720-3p	UUGUGGUUUGGUUUGAUUGGU	56-76	bra-miR5720	6	0	21	21	1
sga-MIR2873c	UCCUCCGUCAUCGGAAGUCUAAUGU AUGCAAUGGUGUGCAUUAGACCUGA UUUCAGGGGGAGCUAUUUCAUGGAA GUCGAAGCUGUAGAAGUGUGUUGCA CUAUCUACAACUGAAGUUGAGUAUA UUUCGGCUAUUGAAGCCGGCAAGGA UAUAAUAUGGCUCAAGCGAUUUCUU CAAGAGCUUGGUUUGAAUCAGAUGG AGUGUAUUGUUGAUUGUGACAGUCA AAGUGCAAUAGAUGUGAGUAAGAAC UCCAUGUACUAUGUAAGAACAAGAC ACAUCAACGUCAGAUAUCAUUGGAU UCGUGAGGAAGU	312	sga-miR2873c-5p	CAACUGAAGUUGAGUAUAUUU	108-128	osa-miR2873c	6	0	21	21	1
sga-MIR398-2	AUGAACAAUGGUGCAUCCCAGAGGA GUGUGCCUAAGAACACAGGUGUAUU UUGGUCUUCUCCUGUUUUGGACCCA AAGUAUGCUUGUGUUCUCAGGUCAC CCCUUUGGGAUCACCUUGCUUUUU	124	sga-miR398-2-5p	GAGUGUGCCUAAGAACACAGGU	24-45	lja-miR398-5p	4	0	22	22	1
			sga-miR398-2-3p	UUGUGUUCUCAGGUCACCCCU	84-104	lja-miR398-3p	0	0	21	21	1

sga-MIR393b-2	CUUUAAGAGCUCGUUUGGUUGGGAACAAGUUAUCCCAGGACAAGUUAUCCUGAGGUUAGUUAUCUUGGAAUAGCUUAUCACAUACACUAUGAUAUAAAUGGUGGGAUAAGCUAUCCCAAACAUGGCAACCAAACAAGAUAUAAAAACCGUAUCCCAUCAUUAUUUUUCUAUCCCAUUACUAUUUAUUUUUAUCCCUCACACCAAACGACCUCUUAUUA	218	sga-miR393b-2-5p	GUUGGGAACAAGUUAUCCCAG	18-38	gma-miR393b	6	0	21	21	2
sga-MIR5167b	UUGUGGAGCUUUGGACUCUUCAACUAAUCCGGAGUUGCUUGAGUUAUACACUGUUGUUGGGCUGUUGUAUCCUGGAAGAGACAAGUCUAGAGUAUUACUGCUGGAUCGGUGUAGAUUAUGCCGCAGUUGGCUUGAAUCUCCUUAAAGAGAGCGAGAUAUCCGUGCUUCAGCCUAAAGAUUUAUUUCUUCAUUAUAUUUUCAAUUAUAAUCUUACAAUUUUAUUAUAUUGUAAGUUUUUCUUUAACACAAAUUUUAGGGUUAAAGAAUCCAAAUCAUCGCAAGA	283	sga-miR5167b-3p	CUUGAAUCUCCUUAAAGAGAGC	131-152	bdi-miR5167b-3p	5	0	22	22	3
sga-MIR5205a	AUUAUAUACUCCGUCCGUCCCAUUUUCUGUGUCAUACAUUUCGAUAAAUAGUUGGUCCAUAAUACUUGUCAAUUCAUAAAAUCAAUGCAUAAAUUGUCAUAUUGUUCCUUUUUUAUCCUUGUUAGUGAUUAGCCUUGAAAAUAUACAUUUGACCAAUUUAGCAAAGCUAAUAUUGUUUGAAAACUUGAGUUCCAAAAAAAUGAAAUAAGGGUAGAAGGGUAAAGGUACAUUAUUUCUUAAUGCAAGUGCAAACUAAAAAGGUGGCAUAUAAAAUGGGAAGGAGGGAGGAGUAUGUGCUCUAUAAUAAGAUGUAUUUCGAAA	296	sga-miR5205a-3p	CAUAUAAAAUGGGAAGGAGGGAG	265-287	mtr-miR5205a	4	0	23	23	1
sga-MIR10529-2	GACGAGUGAGACUUGCUCAUUUGAUGAAACACCUCCACCUCUAACCAAUUAUAUUGGUCGAGGGUUCAAGUCAUGUUGUAAGCAAUGUGAGCGUACAACAUAGCAAGCCUCAUUCGUUUUGCUUCUCUUGAUUAUACAA	164	sga-miR10529-2-5p	GACGAGUGAGACUUGCUCAUUUGA	26-49	sly-miR10529	3	0	24	24	2
sga-MIR11564b	ACACUACGUUCACUUUUACUUCUCCACUUUGGACUUCACAUGCCACUUAAAAACAAUGAUUGGUAUGCGUAUUUUAUCACAAAAUCCAUAUUAAUUGAUGUUUAGUCUUAGGUAUUGACAACUAAUGUGGGGAAUACGUAAUCAAUGUUGAUUCUUCUCAGGAUAUGCUAAAAGUAGAAAUAUAUUUUUAGUAUAGUGGACAAGUAAAAGUGAACGGAGGGC	222	sga-miR11564b-5p	UUUAUCACAAAAUCCAUAUUA	73-93	pab-miR11564b	4	0	21	21	1
sga-MIR11007	GACAAAUAAACACCCAUGUCCUACAUGUCAUCCAACAUGUCAUUUUUUGUGGUACGUCGUGCCCUACGUGUAUUGUGUCAUGUAGAACCCGUGUGUUUAUUUAUU	105	sga-miR11007-3p	AUGUCAUUUUUUGUGGUACGU	37-57	mdm-miR11007	5	0	21	21	3
sga-MIR8781a-2	UUUACAUGGCUUCAAAUUACAUUUAUACCCUUCAACUUUGGAUGUGCACAAAUAAAUACUUAAACUUGUAUAAAAU	260	sga-miR8781a-2-3p	UAUUUAUUUAUUUAAAAGUUGGAU	172-195	gra-miR8781a	5	0	24	24	1

sga-MIR7807b	UGAACAAAUAGACGCACAUGUCCUACAUGUCAUCAAACAUAUCAUUUUUUGUCCUAUGUGGUGUCCUACAUUUAUUGCGCCAUAUAGGACUCAUGUAUUUAUUUAUUUAAAAGUUGGAUUGUUAAAGUGCCUAUUUGACGUCAUUAAAGUUGGAGGUCAAAGUUAAAAUUUGAAGUCAAGUUUA	66	sga-miR7807b-3p	GUUAGAUUUUCACUUAGUCACU	28-49	rgl-miR7807b-3p	5	0	22	22	2
sga-MIR161	AUGCACUGAUGACUUGCAGUGACUAUAGUUAGAUUUUCACUUAGUCACUGCAAUUCAUUAGUGUAUUAGAUAGAAUUUCACAACUUUCCCGUCAUUUCGCGGUCAAGGUUUCAUCACUUUCUUCAGUGAUGAGUUUCAAAGUGGAUUUUCGUGGUUGUAAACACAAUAAAAUCAGAAGAGUUUACUAACCUAUAACCAUGAAUAUCCACUUUGAAACCCAGUGACGAAGAAAACUAUGAAACCUUAGCCGCGAAAUGAGGGAGAAGGGGUGAAAUCGUUUAUAAA	219	sga-miR161-5p	AAGGUUUCAUCACUUUCUU	39-57	aly-miR161-3p-1	6	0	19	19	3
sga-MIR6148b	ACGUGUAUACAAGCCGAGUCUACAUAAAGUCUCAAGGAUUAGUACGGAAACGUCUGUACUUAUCUUUGAGAGGCUAUAAGGAUUACUAGGAAACUACUUUUAUUCGUUCUUUCUCAUCGUGCGUCGUCACCUUCUUUUGACAGAUGACGAGGACUAGAACUAAUGUUACUGGUGGUAGAGGGAAGGCACUUCUCGAGGCAGUUGUUGAGGCCCCAGCUAGGGGUAGGGGUAGAUCUCGAGCUAGUAGUACAACA	254	sga-miR6148b-5p	ACUUUUAUUCGUUCUUUCUCA	96-116	nta-miR6148b	6	0	21	21	3
sga-MIR5083	UCACAAGGAUAUCAACAAUUACUGCAAUUCUCUAAUCAAGCAACGUGGAGAAAAAACUUAUCAAGCAACGUGGAUACAACAUCCAUCCAACAGAUUAGUUUUUCUCCACGUUGCUUGAUCAGAGAAUUGCAAUAAUUUUUGAUAUCCUUGUGA	153	sga-miR5083-5p	UUACUGCAAUUCUCUAAUCA	19-38	osa-miR5083	5	0	20	20	3
sga-MIR482c-2	ACAAAAAAUGUUACAACUUAAUAAAGGCUUCCACAGCUAAACUGAAAUGGGAGUUGAGCCCAACAAAAACUUUUGGGAAUGGGUGGGUCGGUAAGCUUUUCCUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUCCUAUGGGUUUUUGGGCUUUUAUCCUUUUUCUCUCGCUGUUAUCUAUUAUUCAUUGAGAUUUUUAUA	212	sga-miR482c-2-5p	ACUUUUGGGAAUGGGUGGGUCGG	69-91	gma-miR482c-5p	6	0	23	23	1
			sga-miR482c-2-3p	UUACCAAUUCCACCCAUUCCUA	128-149	nta-miR482c	1	0	22	22	1
sga-MIR7695-1	AGAUCGGAUACGUCACUUGACGAUGUAUCAAGACAUUACUUUGCACAAUGUAACGGUCAGGUACAUUACUUUAAUUAUGCGAUAUAUCGGGAUGCAUGUGAUGUAUCAGGACGUUGAGUGAUGUAUUCGAAAUCGAGACGUGAUGUAUCACGACGU	156	sga-miR7695-1-3p	ACGUGAUGUAUCACGACGU	138-156	osa-miR7695-3p	5	0	19	21	1
sga-	UUAUUUAUAUUUUUGAAGAAGUAGG	192	sga-miR7493-3p	AACUUUAUAAAAAUUUAAACGUCU	146-	ghr-miR7493	7	0	24	24	1

MIR7493	CACUUACUUAGACUUGUAUAAAGUU GAACAAGUAAACACACACGUCCUAC AUGGCAAUUCAGAAUCCUAUGUGCA UUCUAUUUGUAUUAUGUCACGUAUG ACAUGUGUGUCUACUUGUUCAACUU UAUAAAAAUUUAAACGUCUACUUGU AUCUCACAAUUAAAGUU CACAGAGACACCUUAAUUAUUCUAA GGUCCUAUUACUCCUCAACUUUUUU UUAGGUCAUUUUGUGCACCUUUUUG CCUUAAGUGACAUUAAAAUAUCUCU				169						
sga-MIR7981-13	CAUGCGCUUCAAUUGCGUGGAGUCA UGGAGUUUACCACCUAAGACAAAAA CUGUAUAAGAUUAAAAGAAAGUUCG UGGGGGUAAUAGGACCUUACUUUAG UUAAGGUGUGUCUCUG	216	sga-miR7981-13-5p	CUUAAUUAUUCUAAGGUCCUAUUA	12-35	stu-miR7981-5p	4	0	24	24	2
			sga-miR7981-13-3p	AUAGGACCUUACUUUAGUUAAGGU	184-207	stu-miR7981-3p	2	0	24	24	1
sga-MIR6478-2	GAAAAAACAAUUUUAAAAAACUAUAU AAAGUUAUAGAUGAAGUUUACAACA AACCGACCUUAGCUCAGUUGGUAGA GCGGAGGACUGUAGUCUGUUGCUG AAAUCCUUAGGUCGCUGGUUCGAAU CCGGCAGGUCGGAUUUCUUUCUCAU AUUUUUUCGACCUGUGUCACUGAAC UUAUGUUCCGAGAAAUAACUUCGUG UGAUUUUUUUCUUAUGGUUUGAACC CGAGACCUAAGUAUAAACUUGAUUA AUGUCCAUUUGUAUAUUGCUUUUUC AUAUUUUUUCGA	287	sga-miR6478-2-5p	CCGACCUUAGCUCAGUUGGUA	54-74	ptc-miR6478	1	0	21	21	1
sga-MIR7997c-11	UGAAUUAAUAUUAUGUUGCUUGGAC UCUUCAAAAAUGCUGAUGGCUGAGA AUUGGAUCCUUCGAAAAUAGUGCAG UUUUCGAGGAUCUGAUACGGGUGCA GCAGCAUUUUCGAAGAGUCAAAGCA ACAUAGAAUUAAUGUA	141	sga-miR7997c-11-5p	AUGUUGCUUGGACUCUUCAAAAAU	13-36	stu-miR7997c	2	0	24	24	1
sga-MIR8737	UUGCAUUUGAAAGAUAUAGUUUUUA UGAUAUUGGAUACUUGAAUCAUCUU CGUACCUUUGGUUGUGAUUCUUCU GAAAACAAAGAUGGAACUAGUGUUG AAGAUGGAACUAGUGUUGAAGAUGA AUUUAGUGUUGAAGAUGGAACUAUU GCAAAUAUUCUUUCAAGUGGUG	171	sga-miR8737-5p	GUGAUUCUUCUGAAAACAAAGAUG	64-87	gra-miR8737	7	0	24	24	1
sga-MIR5368	CUAACCUUGUGUCAGGACCUACGGG CCAAGGGACAGUCUCAGGUAGACAG UUUCUAUGGGGCGUAGGCCUCCCAA AAGGUAAC	83	sga-miR5368-3p	GGACAGUCUCAGGUAGACA	31-49	gma-miR5368	0	0	19	19	1
sga-MIR5303-13	UGUUUGUUUCAAGCUAUGUUGCUCA GACUCUCCAAAAAGUUUUUGACGGU UGCGUGUAGGGUACUCCAAAAGUAG UGCAUUUUUGGAGAAUAAAUGACAU UUUUGGAGAGUUCGAGCAACAUAGU UUCAGCACAAGUU	138	sga-miR5303-13-3p	UUUUUGGAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
sga-MIR8006-8	UUGUGUUCCUGCCGUUCAAGAACUA GAACAUGUAUAUCCUUUAUACUAAC GGACAUACAUGUCAUAUUCUUAUCC GCUGAUUCGACACUUAUUGACGAAU	183	sga-miR8006-8-3p	UAGUUUUUGGACGACAGGGACACC	159-182	stu-miR8006-5p	1	0	24	24	1

sga-MIR8039	AAGAUUGUGUCAUCUGUCCCUAUUUAGUCUUAUGUUAUAGUGAAGGGCAUAUAUACUCUAGUUUUUGGACGACAGGGACACCACUUGUUUCAUAUCUCUACUAUCCAUGGUUCUAUUUACCUAUCUAAACUAUCACUCCCUUUGUAUUAAAGACAAAUGAGCGCUGAGCUAGCCAAUAUGUAUUUGACCAACUCAGCUUCGAGGUGCCUUUUAAUAAAAACUGAGUGAUAGUUUAGCUAAGUACAGAGAACAAUAGAUAGUUGAGGUAAGAAACUAUGUGUUCUCCUUACUAUUAGUAUUCCAUAUUGUUUUUGUUGUGUCAAGGGACCUGCUCCAUUGACUGAUAGUGGAUGCUUACAUUUCAUCAAUUGGUAUCAGAGCAAGUGUUCUCUAUUUGAUUAACACCAAGUGAGAGAUUUCUGCUAGAAAUAGCAGCUCCACUAAGUCUUGAGGGUCCUUACGUUCCUACCAAGGAAGUGAAGGAUGGAGAUCUAACUCAAGAGGUUCCCAAUUCUAGAAGAGAGUAUGAUGAAGACCAAAAUAAGGAGAAUUC	194	sga-miR8039-5p	UUACCUAUCUAAACUAUCACU	34-54	stu-miR8039	3	0	21	21	1
sga-MIR845b-1		276	sga-miR845b-1-5p	UCAAUUGGUAUCAGAGCAAGU	88-108	aly-miR845b-5p	2	0	21	21	1
sga-MIR7539	UAAUCUCGCUUUAUACAAACACAAACGCAAUGUAUACAUUUGUAUUUGUAUAAAGUGAGAGACGCGAGUGAGAGUGACGAGCGAGAUCUGGGAGAGGAGAGAGAGGGGAACGAAAAUAUAUGAAUAUAUACAAUUUUCUCUCGCUUUUUACAAAGACAAAUGCAUUUUAUACAUUUGUAUUUGUAUAAAAGCGAGAGAG	199	sga-miR7539-5p	ACGCGAGUGAGAGUGACGAGC	62-82	lja-miR7539	5	0	21	21	2
sga-MIR7981-14	ACCUUAACUAAACUAAGGUUUUAUUACCCCUGAAUUUAUUUUUUAGAUAAUUUUGUACACCUUUUUGGCUACGUGGCAUCCAAAAAUCUCCCACGCGUCUCAAUUGCGUGUAGUCACGGAGUGUGUCAAGUAACACGAAAGGUGUAUAAAAUUGGGGGAAAAAAAUAAGUUCAGGGGAUAAUAGGACCUUAGUUUAGUGAAAAU	204	sga-miR7981-14-5p	CUUAACUAAACUAAGGUUUUAUUA	3-26	stu-miR7981-5p	5	0	24	24	2
			sga-miR7981-14-3p	AUAGGACCUUAGUUUAGUGAAAAU	181-204	stu-miR7981-3p	4	0	24	24	1
sga-MIR166-4	AGCUUCCAGAUUUGAGGGGAAUGUUGUUUGGCUCGAAGUCAUUAUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUGAAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUCAUUCCCCCCAAUUUGGAAACA	166	sga-miR166-4-3p	UCUUCGGACCAGGCUUCAUUCCCC	129-152	lja-miR166-3p	2	0	24	24	3
sga-MIR159c	AUUUGUGAAAGAUCAAUGAAUCCUGAAUAUACUUCAAGAUGAAUAGGAAAUCUUUCUCUUCUCCCUACUUUAUUCGUCUUCUAAUUUUAUGUAGUUUCAUAACACGUUAUGAACACGAGACUCUAAUCAAGGUAGGGUCCAUUAUGAUUGACCUAAUCAUAAAAAUAUGAAUCUGU	209	sga-miR159c-5p	GAAAUCUUUCUCUUCUCCCUA	47-67	mdm-miR159c	5	0	21	21	1

sga-MIR395a-5	AAUGUGUUGUGUAUUCAUUGAUGUUACACACGAAUGCCCUGUUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAUGAAUCCUGGCUGUGGAUGAUGAACAUAAUAGUUCACGUAUAAAUCUAUUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUU	163	sga-miR395a-5-5p	UGAAGUGUUUGGGGGAACUCU	10-30	aof-miR395a	0	0	21	21	1
sga-MIR7980b-4	AAUCAUAUCUCAUGAUAUAGAAUCAUAAGAUCGAAUCAAUGUAAAAUUGCACGUCCAAACGCUGAUUCCAUCUCAUGAUACUAUAUCGUAAUAUGCAG	98	sga-miR7980b-4-3p	GUCCAAACGCUGAUUCCAUCUCAU	53-76	stu-miR7980b-5p	1	0	24	24	1
sga-MIR393	AUCAUACUCUCUCUUUGUUCACUUUAGUUGUCCACUAUUCCAAAAAUAGAUUUUCACUUUUACUCGUCACUUCUAACCUAUCAAGAAAAGACAGUAUUUUUCAUGUUUUACCAUUUGCAUCAAAUGGUUAUUUCCAAAUUAUUUUUCAAGACCUAAUAUUAAACAUCGAUGUACUAUGGGUAUUAUAGUAAAAUACUCAUAUCAAUAAUUGUUUCUUAAAAGGAUGUGGCAAAGUCCAAAGUGGACAAGUAAAAGUGAAAGGAGGGAGAGUAUUUG	277	sga-miR393-5p	AUCAUACUCUCUCUUUGUUCA	1-21	cas-miR393-3p	6	0	21	21	1
sga-MIR5160	AUCUAAAACAUGGUUGUGGUCAGAGAAUGUACCAUUUCGAGGGUAGUAUCGCACGUCGUGAUGGAUAUUAUAUUUCGAGGGACAUAUCGCGUGCCUUGAUUGUUUCUAUUAUCGAGGAUCGUGUCGUGCACCGCGACAGAUGCAUUGACAGAUAUGUCCCCCAUGGGUGUGUAUCGGUAGGGAAGACAUGCAUUACUAUUCUUGACAUUGCAUCUCAUGGCAUUACACAUUUUUUAUUA	239	sga-miR5160-5p	CGUGAUGGAUAUUAUAUUUCGA	57-78	osa-miR5160	6	0	22	22	1
sga-MIR5303-14	AGUACCUAACUGCUAAGUUGCUCGGAGUUUCUAAAAUUGUUGGUGCACGCAUGUUGGAUCCUCCAAAAUUGCCUACUUUUGAAGGAUCGACCAGGCACCUGAUCACAUUUUUUAAGAGUUCGAGCAACAUAGCCUUGUAGUGUGUC	146	sga-miR5303-14-3p	UUUUUUAAGAGUUCGAGCAAC	108-128	sly-miR5303	1	0	21	21	1
sga-MIR10532-10	UUUAGGGAAAAUACCCAAGUACCCCCUCAGCCUAUGCCCGAAAUCCCAGUUACACACUUAUACUAUACUAAGGUCCUAUUACCCCAGAAGUGUGUCUCUGAGAUUUCGAGCAUAGGUUGAGGGGGUACUUGGGCAUUAUCCCUUUU	146	sga-miR10532-10-3p	AAGUGUGUCUCUGAGAUUUCGAGC	88-111	sly-miR10532	1	0	24	24	1
sga-MIR156b-7	AAAGGGCGGUGACAGAAGAGAGUGAGCACAUAUGGUCUUUUCAAGCAUGAUGUUUACAUGCUUGAAGCUAUGCGUGCUCACUUCUCUAUCUGUCACCCCCCCAA	104	sga-miR156b-7-5p	UGACAGAAGAGAGUGAGCACA	10-30	hvu-miR156b	0	0	21	21	1
			sga-miR156b-7-3p	GCUCACUUCUCUAUCUGUCACC	76-97	bdi-miR156b-3p	1	0	22	22	1
sga-MIR8643b	CCUUUUAAACACCGUUGGUUGAUGUAGAACCAGAUUUUGUGAGAGGUAUUUAUAGAGGAUACAUAUGUUAUUGUAGAACUUAUUAAUUAGUCUAAUUGAC	280	sga-miR8643b-5p	ACUUAUUAAUUAGUCUAAUUG	78-98	gra-miR8643b	4	0	21	21	1

sga-MIR11108n	AGUGAAAAUAUUCAAGUAUAAUUGUGUUUUACUUCAAGUCAUUUGAACACAUUAGAAAACAAAUGAGACAAACACACAAUUUGUCUUCGUUCCUUCAAUCAAAAUCAUUACAAAACGAACGCAAUUGAAGACAUUUACAAUAUAGAAGCCGAUCAAAAUCAGCCAACAAUGUUUAAAAGGUUAAAGGUACAUAUGUGCUCAUGCGGACAUUAUAAAUAUUGCAUCACUAAAUAGUAAUGUGUCCACGUGGGCACAUAUAUACCUUUAA	88	sga-miR11108n-3p	AUAAAUAUUGCAUCACUAAAUA	32-53	lja-miR11108n-5p	7	0	22	22	2
sga-MIR7997c-12	AAGCUAUGUUGCUCGGACUCUUCAAAAAUGUCGGUGGUAGUGCAUUUUUUUGGAGGAUCCGAUAAGGGUGCUGCAACAUUUUUAAAGAGUUCGAGCAACAUAGAUA	106	sga-miR7997c-12-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
sga-MIR169l	AACAACAACAGCUGUUUCAUAAAAAAUCUGGCAUGAGAAAAUGAGGCAGAUAUGUAGCCAAAAAUGACUUGCCAGACAUGAAGCAGAAUUGAUCGAGCUUGCCGGCAAGUCAUCCUUGGCUGCAAUUCAAUAACCUUAUUCCCUCAUGCAAGACUUUAACAUGAAUAAAGACAUGUCUAUUCAA	184	sga-miR169l-5p	UAGCCAAAAAUGACUUGCCAGA	55-76	cme-miR169l	2	0	22	22	1
sga-MIR5021-4	UUUAUUAAUUAGGUCUAUUAAUUGAAAAGAAAAAGAAAAAAAGAUCAUUUCAAAUGGUUUCACACGCUUGGGGACUGUGAAAUACACAUUUUUUGCCACAUAAGCCAUUUGUGUCCAAUAGGAACUGUUUUUGAACACAUAAGGUGUUCAAUAGGUAUGAGGCUAAAUUGAGGUGUCUAAGUGAAAUAUGUGGACAACUUUAAGGGGCCGCAUAUGACUUAAGCCUUUUAUUUAUGUAUAGAUUAUGGUUAAUUGGUUUAUAGGCUAUUUCAAUUUGAUCAACUGAAUAUUUUACAUUCUUAGAUCUAUUGAAUUUUAAGCUUAUUGAAUUGA	333	sga-miR5021-4-5p	UGAAAAGAAAAAGAAAAAAA	23-42	ath-miR5021	3	0	20	20	1
sga-MIR9761	GAAAAGGGCCUAAAACGCCCUUAAAUUAUGAGAUUAUGUACACUAUUACGCACCAACUACUUAAUGAGUGUGAUCCGUUGGGCAUAAGGUAUUUUUGAGUCGAAAGGUGAAUGUCAAGGAUAUUUUAAGACCGAUAGGUGGAUGGAGGAUAAUUUUAUACCAAUUCAAAUACUUGAGGGGCAUGUUAGGCCCUUCUC	197	sga-miR9761-3p	UGAAUGUCAAGGAUAUUUUAA	108-128	gma-miR9761	4	0	21	21	1
sga-MIR8030	UGAUGAUCCUAAGUACUUGAACUUGUACCAGUAAAUGAUGUAGAUUAAAUGACAUCAGUACAUUGAAUGUACGCGCAUGUAAUAAGGUUGAAUAACACAAUUAACUAAACUGAAAGUAGCGGUGUACAAAACCAAACCAAACCGCACACCGAGUCAAACCGAAAAGAAACCCGACUAGUAGCUUGGUUUGACUUGGUUUGGUAUUGGGAAAAACCCCCCACUAUAUUUGGGUUGGUUUGUUUUUAACUAA	306	sga-miR8030-5p	ACAAAACCAAACCAAACCGCAC	126-147	stu-miR8030-3p	7	0	22	22	3

	AAAAAAUCAACCCGAUUUAAUACAUU AUUUUCAAGUUUAAUACCUAGAAUU CAGAA		sga-miR8030-3p	UUGACUUGGUUUGGUAUUGGGAA	188-210	stu-miR8030-5p	6	0	23	23	1
sga-MIR172a	AAACACUGUCUCAAAUGUAAAUCCU CAGGUCGCCAAAGUCUAUAUCCUCC AAAAAGUAGUGCAUUUUUGGAGUAG AACAACAUAGACAUUGACGACAUGA AGAUUUACAUCUGAGACAGUGCAU	124	sga-miR172a-3p	UUGACGACAUGAAGAUUUACA	89-109	vca-miR172a-5p	5	0	21	21	2
sga-MIR399b-2	GAAACAGUGAUAGGGCUACUCUCUA UUGGCAUGCAAUUGUAUAUUUCAGC UGACACGCCAAAGGAGAGCUGCCCU GUUACUGUCUC	86	sga-miR399b-2-5p	GGGCUACUCUCUAUUGGCAUG	13-33	sly-miR399b	0	0	21	21	1
			sga-miR399b-2-3p	CGCCAAAGGAGAGCUGCCCUG	56-76	nta-miR399b	0	0	21	21	1
sga-MIR7983-4	GAGUACGCACUACAACAAAAAUGAC CAUUAGCGGCAUUUAAUUCUUAAUU UGCCGCUAAAUAUGUAUUUUUAGCG GCAAUUGUCACUCUUUGUAAAUGUC CCUAAACCCUUUAGCAACAUUGGUU CUAAUAGCACUUAACUAAUGCCGGU AAAGACUUUAGCACUAUUUAUUAGU GUCAAUAUUUAAUGCUGCUAAAAGU UGUUUUUGUUGAAGUGACGUAAAC AGUGAUUAAGCAUCUUUUCUAUCAA GUAUCAAUCAACAAAAGUUGGUGAU UCGAGUCACGUUGAACGAUAGGCGA UGGUGCAUAAUACUAGUGAAAAGUU AUAUGUUUUACUAGGGCCGUGUAUC GGUCGGUAUGGUUUGAUUUUUAAAG UUUAUCGGGUUGUCUUAUUGGUUAU CGAUUUGUAGAGAUGCUAAAUCGUU UAAGUACAAUGUCUCGCUAUUUCUU UUAUUUUUUAUCUAACAAUAAUUAG UUUCACCCCAGGGGAUCUUGUUGUC CCUAUAAAGGGGUAGUAGUUAUUGU UGUUGUGGUGUAUGAGCAUGAAAUC UUUAUAUCAACCUUAAAUAGGAAAG CUUAAAGAACUCAAGUGAGCAUUGU GACAUG	224	sga-miR7983-4-3p	ACUAAUGCCGGUAAAGACUUUAGC	139-162	stu-miR7983-3p	1	0	24	24	1
sga-MIR6466		200	sga-miR6466-5p	UAUCAAUCAACAAAAGUUGGU	27-47	ptc-miR6466-3p	3	0	21	21	1
sga-MIR3951b		181	sga-miR3951b-5p	UUUCUUUUAUUUUUUAUCUAAC	20-41	csi-miR3951b-3p	5	0	22	22	1
sga-MIR5174d	AGAUAUACUCCCUCCGUUUAAAAAA GAAUGACCCUGUUUUCUUGUUAGUA UAAAAAAAUGGCCCCUUUCCUUUUU UGACAACACUUUAACUUUAACUUUC CACGUGGCAUGUUUAAGACCACAAG AUUAAAGGGCAUUUUGGUACAUUUG ACAUAACUUUAAUUUUGAACCACAA GAUUAAAAAGUUUUCUUUCUUUUCU UAACUCUGUUCCAAGUCAAACUAGG UCAUCCUUUUUGAAACGGAUGGAGU AUAAUA	256	sga-miR5174d-5p	UCCCUCCGUUUAAAAAAGAAUGAC	9-32	bdi-miR5174d-5p	4	0	24	24	1
			sga-miR5174d-3p	CAUCCUUUUUGAAACGGAUGGAGU	227-250	bdi-miR5174d-3p	6	0	24	24	1
sga-MIR397b	CCCUUCAGAGAAUUAAAAACAUGAU CGAGUAUAGCGUUGAUGAAAAAUGA GGAAGGCCCAAAUGCAGGACUUCUC AAAUAUGUCAUCAACGCUGCACUCA	127	sga-miR397b-5p	AUCGAGUAUAGCGUUGAUGAA	24-44	bdi-miR397b-5p	3	0	21	21	1

	AUCAUGUUUCUAAGUACUCUGCAAUAA		sga-miR397b-3p	UCAACGCUGCACUCAAUCAUG	86-106	eun-miR397b-3p	1	0	21	21	1
sga-MIR5303i-6	AUCAUGUUGUUCGGACUCACCAAAAAUGUCGAUGCAUCCAUGUCGGAUCCUCCAAAAAUGCACUAUUGUUGGAGUAUCCGACACACGCCUGUCGAUAUUUUUGAAGAGUCUGAGCAACAUAAAUCCAUUGGCCUAAGUCAUCCGUAGCCACUUAAAGGAAAAAUAUUAUUUUUAAUAAAUCAACGCGCUCAAAGAAAGUGAAUUAUACGUUUUUUGCCAUUUCAGCAUUUCGUGUCUAAAUAAAUGAUUUUUGAACAAAUAAAGUGUUCAAUUGACACAAGGAUUAGUUGAGGUGUCUAAAUAAAUUAUGCGGACAACUUUGAGUGGCUGCAGAUGACUUAAGCCUAUAUC	123	sga-miR5303i-6-3p	AUAUUUUUGAAGAGUCUGAGCAAC	95-118	stu-miR5303i	0	0	24	24	1
sga-MIR5183	CAUCCAAUUUUCUCCAUUUUCCGUAGAAUUUAGAAACGAUUUCACUGAAUUAAAAUUUCGUAUCGAAUUAAAAAUGAAUAAAUUGAGAUUGGAUGGAGACCAAAUUGUAAAUUAUCAUGUAGCUAUAGAUCCCUAUCCUAUGCGUAUAAUACUAAAUUAAUACUAUUGUAUUUAUUUCCAUUUNUUCUCCAUUUCCUUAGAACGAUUUCACAAAAUACAUAAGUUCUAAGGGAAAGGGGUUUUAUGUUCUUCAGUGAAGUCGUUUCUAAAUUCUAAGGGAAAGAGGAAAUUGGGGG	228	sga-miR5183-3p	UAUGCGGACAACUUUGAGUGG	184-204	bdi-miR5183	5	0	21	21	1
sga-MIR477-3	AUGAACUAUUUGUUGCCUCUUUUAUUCCCUCCUAUUUUUUUUUAGUAACUAGCAAAAAUGAAAAAGUUGGUGAGUAGUUGGGAAAGAAGAAAUGGACGGGAAGGAGCAAAGGGCACCAGAGGGUUUGG	296	sga-miR477-3-3p	AUAAGUUCUAAGGGAAAGGGG	219-239	lja-miR477-3p	5	0	21	21	3
sga-MIR5019	CGACUAUAUUGCUCGUACUUUUCAAAAUGUUGUUAGACCUGUAUGUAUGUACUUUUGAACGAUCUGACACACACCUGACAGUACUUUUGAAGAGCUCGAGCAACAUAGAAA	128	sga-miR5019-3p	AGUUGGGAAAGAAGAAAUGGA	76-96	ath-miR5019	6	0	21	21	2
sga-MIR7997c-13	AAAUAUCUAACCAUGAUUUACUUAAUAAUUACAUUAUAUAUUAAGUCACGUGGAGAUCGUCCGUGUCAGUAUAUGGACCUCGCGAGUCCCCCAUGGGUCAUGAGCUCUCGAUGUAUUUCUAAGGAGUAUGAUGUAUAUACGGUUGAGUGAGUACUGGAUAUUCUGAUAUAUAUCAUUAAAUGGUAUCAUAUUGCAUUGCAUUCCAUCACAUUAUUCAUUCUUGAUGAGUAUAUGUUUCGUUUGGUUUUUUGAAAGUACUUGAUGUUGAUUUCAUUUAUUGACGAAACUUAAAUAGCAAGUGUAAUAUAUAUUUAUUUUGGUAGAUAAAU	111	sga-miR7997c-13-5p	AUAUUGCUCGUACUUUUCAAAAUG	6-29	stu-miR7997c	4	0	24	24	1
sga-MIR8014-2	UGACGGUACCACUUUGAAAUACACU	329	sga-miR8014-2-3p	AUGGUAUCAUAUUGCAUUGCAUUC	180-203	stu-miR8014-5p	5	0	24	24	1
sga-		160	sga-miR12170-5p	CUAGAGCUCACCAAUAACUGCU	57-78	aof-miR12170	7	0	22	22	3

MIR12170	UAGUAAAGACUCGGCAAAGCCUUGA AUUAACCUAGAGCUCACCAAUAACU GCUGAGUAUAAUGUGUUUCUAUUGA GGAGGUCUACUAGUUUAGUACUUAU ACUUUUUACUAAGUGUCUUUACAGG UAUACCGAGU UGUACUCCAGCUUCGAGAGUGCACA UCUACACACCUCAAUUGGACACUCU AACUCGUCCCUAGUGUGUCUCGUG GAUGGAUACCUGAUGCUGACAUGGC AUAUAAAUUUUGGAGACGAGUUGAG GUGUCUAGAUGUGCAUACUCAAAGU UGGAGUGCU	158	sga-miR7992-12-5p	UUCGAGAGUGCACAUCUACACACC	12-35	stu-miR7992-5p	5	0	24	24	1
sga-MIR7992-12			sga-miR7992-12-3p	UGUCUAGAUGUGCAUACUCAAAG	126-148	stu-miR7992-3p	6	0	23	23	1
sga-MIR11108w	AUACAUUUCGGAAACAAAAAAUAAUC GAAAAAUAAGUUACCUUGUCGAAAU GACUGGGAUCAGAUUUUUGCUUGAG GCUGUUCAUUCCCUCGAUGACAAUG UUGAUCUCAGUCAUUUCGACAAGGU AACUUAUUUUUCGAAUUUUUUUUGU UUCCGAAAUGUAU	164	sga-miR11108w-5p	AAUAAGUUACCUUGUCGAAAUGAC	31-54	lja-miR11108w-5p	6	0	24	24	1
sga-MIR9562	ACAUAUAACUGUAUAAUUCGCUAUA CAUAUACAACUGUAUAAUUCGCUGG CCUCGAUAUACAUAUACAAUUGUAU GAUUCACUGGCCUAAAUUGUAUGAU UCAAUGGCCUAAAUUGUAUAAUUUG CUGGCUUAUUUCGCUGCAAUUGUAU AAUUGCUGGCAUAUUUCGCUGCAAU UGUAUAAUGCGUAAUUGUAUAAUUU GCUGGCCUAUUUCGCUGCAAUAUGU GUAUAAAAUUUGCUUUGCAUACAAU UGAAUCGAAGUAAAAUGUUUGUAUA UUGUAUAAUUAUAAGUGUAUAGGA UAUAUUGUAUAAUUAUAAGUGUAUG GGAAGAAGAUAUAUGUUUUUCUCUC ACUUUAUAUAAAGACAGAAACACAAU CUAUACACUUCUGUUGUAUAAAGCU AGAGAAAAUUGUAUUUCACUUUUUU UUAAUGAUACGGCGACCACCGAGAU CUACACUCUUUCCCUACACGACGCU CUUCCGAUCUAAAGCGAGAGAAAAU UAUAUUUCACUACAAUUGUAUAAUU CACAAUUGU	299	sga-miR9562-5p	ACAUAUACAACUGUAUAAUUC	25-45	bra-miR9562-3p	5	0	21	21	3
sga-MIR5014a-11		235	sga-miR5014a-11-5p	UUGUAUAAUUAUAAGUGUAUG	5-25	ath-miR5014a-3p	4	0	21	21	1
sga-MIR1512c	GAGGUAAAGCAGAAACUCUUUCAAA UAGAGCCAAAUAGUUCUAAGAAUUC UAAGUUGAUCCUCACUAGCACCACA AAGAUUUUUUUUAGUUUCAAAAAAC AUAUUCUGUGUGGUGCUGAUGACGA UUAACUUAGAAUUCUUGGAGCAUUU UGCUCUACUUGAAGGAGUUUUUGGU UUACACA	182	sga-miR1512c-3p	UAACUUAGAAUUCUUGGAGCAU	127-148	gma-miR1512c	4	0	22	22	1
sga-MIR10993f	AUUAUAUUUCCUUCAAUGUGAGGGU UAUGACCUAUGAGAAUAAGAUGGGU CAAAUAUGACUUGUGAUGUAACAUU CUGGAAAAUUACAUUUCUAGUGAAG AGCUCAAUAGGUCUUUAAGAAUGUG	173	sga-miR10993f-5p	ACUUGUGAUGUAACAUUCUGG	59-79	mdm-miR10993f	5	0	21	21	1

sga-MIR167h-4	UAUUGGAAGUACAUAGGCAUCCUAACUCCCAAUAUUGAGAAAUAUUUGAAUUCGUGAUGGCAUUGACAGGUGAGGCUGCCACAUGAUCUGAUCUUUCCUCGAAUUAUAUUUGAACUAAAAGGAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGCUGCACGAUGU	122	sga-miR167h-4-3p	AUCAUGCUGGCAGCUUCAACUGCU	84-107	gma-miR167h	1	0	24	24	1
sga-MIR1521b-2	AUACCCUUUAUACUAAUGGACAUACACAUGUCAUAAUCUUAUCCACAUGCUCGACAUCGAAUCGAUGGAUAAGAUUGUAUCACGUGUCCUUCCGUGAGAGUGAAGGGUAU	110	sga-miR1521b-2-5p	GACAUACACAUGUCAUAAUCUUA	19-41	gma-miR1521b	5	0	23	23	1
sga-MIR7984d-4	AUGGUCUGAAAUAUAUCAGAACUUUGACCGAAAUUGUUAUACCAAACUUUAGAAAAGACCUUUUACUCCCUUCACUAUUUAACAGUGUAUUUUAAAGGUAUAUAUGUGCUCAUGUGGACAUAGAAAAUCUUGCAUAAAAAUUAUAAAUCGUAAUAUGUCCAGACGGGCACAUAUGUACUAUUAAAUCUUGCAUGGGGGCAAAAAGUCCUCCAUAAAGUUUGGUAUUGUAGCAUUAAUUUCGGCCAAAAUUGAAGUAUCUUUUAGACCAU	275	sga-miR7984d-4-5p	AUCAGAACUUUGACCGAAAUUGUU	15-38	stu-miR7984d-5p	2	0	24	24	1
			sga-miR7984d-4-3p	UAAUUUCGGCCAAAAUUGAAGUAU	240-263	stu-miR7984d-3p	7	0	24	24	2
sga-MIR7992-13	UCCAAUCAUUACUCCAACUUUGGAGUACACAUCCAGACACUUCAAAUCAUGUCCACUAUAUCAAUUGAACACUCAACAGUCCAACUUACAAAAUGAACGUGUAGACACCACCAAAAUUUACGUGUCACGUCAACGUUGAGUUCCCACAAGAUCAGUGGGACUGAGUUGAGAUGUCUAGAUGUGCACUCCAAAGUUGGAGAGUAUUAUC	208	sga-miR7992-13-3p	UGUCUAGAUGUGCACUCCAAAGU	172-194	stu-miR7992-3p	2	0	23	23	1
sga-MIR7998-2	AUUGUAGGUCCAGUCACGGUCCAUCAGUGGGUAGACCUAGAUUUCUCAUCUAGGAUGUUUGAGUAUGUGUCGAAGUACCGAGGCUAGUGACGGACCGUAGAUCAAUCCACGGUCCAUACUGCAAGUUUAUCAAUGAUCACUUAGAGUUAAAUUUCAAAGUCUGGAUGAAAAAUUCUAAGUGUGGACCCAUAGAGGACCCAUGGAACAUGGAUCGACCCA	219	sga-miR7998-2-3p	ACGGACCGUAGAUCAAUCCACGGU	90-113	stu-miR7998	1	0	24	24	1
sga-MIR10202b-1	CUUUUUUUGCUUACGCGGCACUAUCUUGUGGGCCCAACGAUGGUUGACUUUUUUCUGAACUAGUGCCACGUAGGCUAAAAAGG	83	sga-miR10202b-1-5p	CUUGUGGGCCCAACGAUGG	25-43	vca-miR10202b-3p	6	0	19	19	3
sga-MIR7983-5	GUUCACUACAUCAAAAACGACUAUCAGCGGCAAUUAAUACUUUUUGUAUAUGUCACUAAAGUUUUUAGUGAUAUUGGUUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUACCACUCUUUAUUAAUGUCAAUAUUUAUUGCCGCUAAAAGUUGUUUUAUUGUAUUGGUU	172	sga-miR7983-5-5p	UAAAGUUUUUAGUGAUAUUGGUUC	57-80	stu-miR7983-5p	3	0	24	24	1
			sga-miR7983-5-3p	ACUAAUGCCGGUAAAGACUUUACC	93-116	stu-miR7983-3p	1	0	24	24	1
sga-	CCCUCUGUCCCUAUUUAGUUGUCCG	266	sga-miR11114-5p	UGUCCCUAUUUAGUUGUCCGCUU	6-28	lja-miR11114-5p	5	0	23	23	1

MIR11114	CUUUAGAAGUGACACACAUAUUAAG GCACCAAUUAUCAUCAUAGGUUAGC UACAAUUUUAUCCUUAACUUAAAAGA UUAUGCAUAUCCACAAGUAUAAUAAA UGUAUUUCUGGUUCCAAAAAGCAUG CAUUACAACUUAGUAGUACUAGAAA UUUUCUAGAAUUAAAUAAGGGCAUA UUAGGAAAAAAAAUGUUGUCCUUCC UUGAUUUGUUAAAAUGAACAAGUAA AUAGGGACAGAUAU		sga-miR11114-3p	UGAACAAGUAAAUAGGGACAG	242-262	lja-miR11114-3p	5	0	21	21	1
sga-MIR482c-3	GUUGGAGUGGGUGGUGUGGUAAGA UUUCAUAUUUAUUUUCCAUAAAAAU UGAGAUCUUGCCAAUACCGCCCAUU CCUAU	79	sga-miR482c-3-3p	UCUUGCCAAUACCGCCCAUUCC	55-76	sly-miR482c	0	0	22	22	1
sga-MIR482b-3	UCAGGAAGCUUUUGGAGUGGGUGG CAUGGUAAGAUAUCAUAUCUUGUUU UUCAUAAAAAAAAAAUGAAAUUGAAA UCUUACCGAUUCCCCCCAUUCCAAU GGCUUCCAGU	110	sga-miR482b-3-5p	GGAGUGGGUGGCAUGGUAAGA	14-34	stu-miR482b-5p	0	0	21	21	1
			sga-miR482b-3-3p	UUACCGAUUCCCCCCAUUCCAA	78-99	stu-miR482b-3p	0	0	22	22	1
sga-MIR159a-2	GAAUGAAUUUAAUGGGCUGAAUCUG AAUCUGAUUCAGAUUCAGACCUAAA AAUCAAACGUACUUAAUAGGCUGAA UCUGAAUAAUUUCAGACCUCCAUUA AGUGCAAAC	109	sga-miR159a-2-3p	GACCUCCAUUAAGUGCAAAC	90-109	aly-miR159a-5p	4	0	20	21	1
sga-MIR6273-1	UCGUUUUCGACCUACGUGGCACUAU CUUGUGGGUUCAACGAAGGUUGAUU UUUUUUUUCAAACUGGUGCCACGUA GGCUAAAAAGG	86	sga-miR6273-1-3p	AACGAAGGUUGAUUUUUUUUU	37-57	ppe-miR6273	4	0	21	21	1
sga-MIR5303i-7	UACAAUAUGCUUACGAACAUUAAUC UUGUGUUACUCGGACUCUCCAAAUA UGUUGUUGCAUCCGUGUUAGAUUCU CCAAAACGCAUUACUUUUGGAGGAA CUGACACACACAUACUGAUAUUUUU GAAGAGUCUGAGCAACAUAGUGUUA AACAUUGAACACAUUAAG	168	sga-miR5303i-7-3p	AUAUUUUUGAAGAGUCUGAGCAAC	118-141	stu-miR5303i	0	0	24	24	1
sga-MIR11097c	UUUAUAAUAACAAUUGUGAAAAAAUU ACACAACGUCGCUUUGGCCGAGUGG UUAAGGCGCUUGCCUGCUAAGUAAG UGGGGUUUCCCCGCGUGAGUUCGA AUCUCACAGGCGACGUUGCAUAUGU UUUUGUCGAUACCUAUUAUCGA	147	sga-miR11097c-5p	AAAAAAUUACACAACGUCGCU	19-39	lja-miR11097c-3p	5	0	21	21	1
sga-MIR6271	AUGUCUAGUGAAUAUCCCAAUAGGU CUUUAAGAAUGUGUAUUGGGGUACA UAGGCAUCCCAAUAUCCAAUAUUGA GAAAUAUUGGGCAUAGUAUAGAAAA UAUCAAACAUACCCACCAUAUAAUUU	100	sga-miR6271-3p	CCAAUAUUGAGAAAUAUUGGG	66-86	ppe-miR6271	6	0	21	21	2
sga-MIR8014-3	GUUAAGAGAAUGCAUUUGUUGAUCA AUGGAGUAAUUCAUUUGGGAGGGAU UCUGCAGUCAUUAUAGAUAAGGUAA AUGGGAAAGAAUUAAAGCUUCUUUU ACGGAUUAUCGUUAUCCAUUAUUUC AUAAUGUAUUGUAUUGUAUUGUAUG GUAGAUACAAUGUUUGGUU	195	sga-miR8014-3-3p	AUUAUUUCAUAAUGUAUUGUAUUG	144-167	stu-miR8014-5p	3	0	24	24	1
sga-	GAUGGUGUAUAUUUCUACUUAUUUA	293	sga-miR7695-2-5p	AUCCUAUCUGGCAUCCUACGUGAC	114-	osa-miR7695-5p	7	0	24	24	3

MIR7695-2	AUAUCCUAUUUGAAGGACAUGAGUA UCAGUUGAUGACAAAUCAUCACUAC GUUUAAUACAUAAACGUGCUUCUUA ACUUAAUAUUCAUAUCCUAUCUGGC AUCCUACGUGACCAUUCUAUGUCAU GGAGACAUAUUAUGUCACGUAGGAC GAUGUAUAUUUCUACUUACUUAAUA UCCUAUUUUGAAGGACAUGAAUAUC AGUUGACGACAAAUCAUGUAUUUGU AGGAGGAACAAGAGGAUAUUGUAAA GAGAAGAUCAUCACCAAA				137						
sga-MIR171b-5	AACGGAAUGAAAAUAAGAAGUGAUA UUGGCGCGGCUCAAUCUGAGAUCG UUCUUUACGAAAAUAAGCAUAAAUU CGUCUUCGGAUUGAACCUCACCAAC AUCGCUUCUUCCAUUUUAAUCCCAA A	125	sga-miR171b-5-5p	GAUAUUGGCGCGGCUCAAUC	22-41	zma-miR171b-5p	1	0	20	20	1
			sga-miR171b-5-3p	GGAUUGAACCUCACCAACAUC	82-102	tcc-miR171b	5	0	21	21	2
sga-MIR8036	AGUAUUGGAGUGGGAGGAAUCGAAA GGUAAUAAGGAUUUAUUUAUUUUUC GAUUUGAUUGGGAAAAAAAGAAUUA UGUCUUUCCGAUGCCUCCCAUUCCC AUGGC	105	sga-miR8036-5p	GGAGGAAUCGAAAGGUAAUAA	13-33	stu-miR8036-5p	4	0	21	21	1
			sga-miR8036-3p	UAUGUCUUUCCGAUGCCUCCCA	74-95	stu-miR8036-3p	0	0	22	22	1
sga-MIR5240-2	ACCUAACUUCAAAAGGUCAUAUCUC ACUCAUCCAAACUUGAAACUUAGAAA AAUUGGUUGAUUUGGAAAGAUGAUU CAAACGUCUUUCCUAUGGUAUCUUG UAUCACACCUAGAUCAUCAUGUUCU AGGAGUUAUGAUCGUUUGAAGUUAA CC	153	sga-miR5240-2-5p	UAGAAAAAUUGGUUGAUUUGG	46-66	mtr-miR5240	5	0	21	21	1
sga-MIR2662	UUUGUGAAAUGACUUGAGAGGUGUA GUAUAAGUGGGAGCCGAAAGGCGAA AGUGAAAUACCACUACUUUUAACGU UAUUUUACUUA	86	sga-miR2662-5p	UAGUAUAAGUGGGAGCCGAAA	24-44	mtr-miR2662	6	0	21	21	2
sga-MIR7997c-14	AAAUUAAGGCUAUGUUGCUCGGACU CUUCAAAAAUGUCAACGCGUGCAUG UUGGAUUCUCCAAAAGUAGUGUAUU UUUGGAGAAUCCGACGCGGGUGUG GCAUCGAAGUGAAGAGUCCGUAAAA CUUAGCAUUAAGGU	138	sga-miR7997c-14-5p	AUGUUGCUCGGACUCUUCAAAAAU	12-35	stu-miR7997c	1	0	24	24	1
sga-MIR5298c-1	GGCGCCACAUCCAUCAUUGCUCUUG CAUACAUCUCCUAGAGAAGAUAGAA AUGAUAUGUAAUUGAAGGGAUACCU GGUGCAUCCACCUAUCUUCUCUAAG AGAUGUAUGCAAGAGCAAUGAUGGA UGUGGCACA	134	sga-miR5298c-1-5p	AGAUAGAAAUGAUAUGUAAUUGAA	43-66	mtr-miR5298c	6	0	24	24	2
sga-MIR475b	AACUGAAGACAGUCAAUGCCACUCC CACUUCCGUCUAUGGCUUUGCUCUU AAAGUCCCCAUUGAUUUAGGAGAGU GGACGGGGCAGACUGACUUCACUA	99	sga-miR475b-3p	UUAAAGUCCCCAUUGAUUUAG	49-69	ptc-miR475b-3p	3	0	21	21	1
sga-MIR5021-5	AUGGGUUCGAGCUAGGUUUCGGAU UGGGAAGAGAUUCCCAAGGAAUUAU UGAGCCUGUUCCGGUCCUUGUUAAA GGAUCCAAAUAUGGUUUAGGGUACA UCCCCACAGAUGACGACGUGAAGAU	208	sga-miR5021-5-3p	CGUGAAGAUGAAUAAGAAAA	116-135	ath-miR5021	4	0	20	20	2

sga-MIR8707-2	GAAUAAGAAAAAGGAUCAAGAGUUG GCUAAGCCGAUCCCGCAUCUGUAUC AAUCCUUUCCAAUCCGAGAGUAUGC CGAGCCUGA AAUAGUUUAUUCAAAAGGUAUAUAU GUGCCCACGUGGACAUAAAAAAUAU UGCAUAAUUAUAAACAGUAACGAGC CCAGUGGGAUGAUAUGUACCUUUAA AAUACACUAUU	111	sga-miR8707-2-3p	AUAAAAAAUAUUGCAUAAUUAUAA	40-63	gra-miR8707	7	0	24	24	1
sga-MIR11578-2	GCAUGAACAAGAUAUGAGUUGAAGC CUUUAACUAUAUCAUUGUUUAGGCU GCUUCUGUUGAAGUUGAUAAGUUGU UUCUGGAUUUGGAACCACAAGUAAU CAUUGUUGUAAUUCAACUUUAAUUC AUAUUUUAUUCAACU	140	sga-miR11578-2-5p	UUUAGGCUGCUUCUGUUGAAG	43-63	pab-miR11578	5	0	21	21	1
sga-MIR11563	UUGUUCUUAUUUUAUUAUGUUUACG AUUUCAAAUCAUGAUAGUUAAGAUU AUACAACUUUUCCCUCAUUUCGCGG CUAGGAUUUCUUAAGUUCCUUCAGA GCUGGAUUUUAAAGUGGAUAUUCGU GAUUGUAGGUUAGUAAAUCUUUUUU CUUAUUUAUUAUGCUUACGAUUUCA AAGCAUGCUAGUUAGAAUUUCACAA CUUUUCUCGUAUUUCGUGGCUAGC	295	sga-miR11563-3p	UUCUCGUAUUUCGUGGCUAGC	204-224	pab-miR11563	3	0	21	21	1
sga-MIR5658	GUUUCAUAGCUUUUUACGGGCUGG GUUUCAAGUGGAUAUUCGUGGUUG UAAUCAUAAUGAAAUAAGAAAAA UGCGGUGCGGUAAAGAUGUUGAUG AUGAAGAGAUUUUUUUUUGAGAAUG UAUUUUUUGGAUGACGGAAUCAGUC UCCAAAUCGGAGAAUUGUUAGGUAG UGGAUCCUGAUUAAUAGUUGAUGUA CUUUAACAAAAAAUACUCUGAUUUAU UAAUAUAUGUACCCAACCUCC	171	sga-miR5658-5p	AAGAUGUUGAUGAUGAAGAGA	13-33	ath-miR5658	4	0	21	21	1
sga-MIR172d	AAAUGAACUUAAUGGGCUGAAUCUA AAUGAUUCAAAUUCAGACCUAAAAAC CAAACGUACUUAAUAGGCUGAAUCU GAAUGAUUAAGAUUCAGACCUCCAU UAAGUGCAAAC	112	sga-miR172d-3p	UCUGAAUGAUUAAGAUUCAGA	74-94	bra-miR172d-5p	5	0	21	21	2
sga-MIR7822-1	AUGUUUAUGUCUUUCAGUUUUGAGU UUGCAUAAGUAAACACUUAAAAUUG AACAAAUAGAUACAUUCGUCCUACG UAAUAAUUUUGUAUCCUGAUGGUGU GCUACGUGUAUUAUGUUGUGAAGGA CGUGUAUGAUUACUUGUUCAAUUUU AUACAAGUUUAAGUGUCUGAUUGUG CAUACAAAAAGUUGGAUGACGUAGA AAGG	204	sga-miR7822-1-5p	CUUAAAAUUGAACAAAUAGAU	41-61	ptc-miR7822	5	0	21	21	2
sga-MIR10436	UGGAUUCAAGCAUAAAAAGAUAUGU AGGACUACUAGACAACUCAAGCUUU AACACUCUAACUUGUCUACCAGUUG ACUCAGUCCCCUUUGGUUAGGGACU GUCUUCAUUGGUUAUGGUGGUCAAC UGGUAGGCAAGUUAGAGUUUUUAAG CUUGAGCUGUCUAGUAGUCUUAUAU ACCGUUUUAACGCUAAAUAGC	196	sga-miR10436-5p	ACUAGACAACUCAAGCUUUAACAC	32-55	gma-miR10436	7	0	24	24	2
sga-	GUCUGGGGAGGGUGGUGUGUACAG	86	sga-miR4406-3p	AUUGUUUCUGAUAGACCCUCUCUU	56-79	gma-miR4406	7	0	24	24	1

MIR4406	AACCUAACCCCUACCUUAUGAAGGU AGAGAGAUUGUUUCUGAUAGACCCU CUCUUACCAUUA										
sga-MIR3447	GCGAUGAUGAUGUAAAUAACUGAAU AACUUUCACACAUAUAUGAGUUGGA UAAGGGGCAUAAUUGAACCGUUUAA AAUACGGUCGUAUAUGUGUUUUAAA AUUGGGUCGGAUAGUUAGGGCAUAA GUGACCCCUUUUUGAGUGAGUUUUU AGGUCUAAAAUAGACAUAUAGUAAG AUGAGUGUGUUAGUUUUUAAAUCUU AUUGU	205	sga-miR3447-3p	GAUGAGUGUGUUAGUUUUUAA	175-195	aly-miR3447-3p	5	0	21	21	3
sga-MIR5303-18	ACCCUAUGUUACUCGGACUCUCCUA AAAUGCUUUUGCACCCGGCUCGGAU CUUCAAUAAAUGCACUUAUUUGGAG GUUCUGACACGCACCUAUAAACAUU UUUGAAGAGUUCGAGCAACAUAGUC G	126	sga-miR5303-18-3p	UUUUUGAAGAGUUCGAGCAAC	99-119	sly-miR5303	0	0	21	21	1
sga-MIR8006-9	CUUGUAAGGGGAAAACGACAAAUAU ACCUCUUAUUUAUCGUAAAUAGUAU GGAGAUAUCCUUCAUCAAUGUCCCA AAAGAAUGACAGAUAAGAUUGUUCU ACGUGUUCCUAUUUAGUCUUUCGUU AGAGUGAAGGACAUAUAUGCUUUAG UUUUUGGAUGACAGGGGCACCUAUG UCCCAAAAGUAUGAAGGAGGAUAUU UGCAUGCUGAUUACGAUAGUUCAUG GGUAUAUUUGUCAUUUUUCCGUACU UA	252	sga-miR8006-9-3p	UAGUUUUUGGAUGACAGGGGCAC C	148-171	stu-miR8006-5p	1	0	24	24	1
sga-MIR2949a	CCAAAAAUCAAAUCAAACUGCAAAUC GAGUCAACCCGGAAAAAAACCCGAC UAGUGAUUUGGUUUGACUUGAUUUG GUAUUGAAGAAAAAAACUCGACUAU AUUUGAGUUAGUUUGAUUUUGAC	124	sga-miR2949a-5p	UGCAAAUCGAGUCAACCCGGA	19-39	ghr-miR2949a-3p	6	0	21	21	1
sga-MIR169e-3	UUUAAAAAGAUAUCUUGCAUAAAAGA AAAGAGCAUGUCAAGGUAGCCAAGG AGACUGCCUGAAACCAAAUUAAAAU GUGAUUAACCUUAUAAGUAAUAUUG GAGCAGGCAAGUCAUCCUUGGCUAC UAAACAAUAAUAUAACUCUCCUCUUC AUGUAAGACAUCUCUUCUUUUU	174	sga-miR169e-3-5p	UAGCCAAGGAGACUGCCUGAA	43-63	zma-miR169e	3	0	21	21	1
			sga-miR169e-3-3p	GGCAAGUCAUCCUUGGCUACUA	107-128	mtr-miR169e-3p	6	0	22	22	1
sga-MIR7980b-5	CAUAUUAUGCUCUAUCACAUCUCAU AAUAUAAAAUCAGAAGAUCGAAUCAG CGUAAAAUCGCAUGUCCAAACACUG AUUCCAUUUCAUGAUAUCAUAUUGU GAUAUGAUAUCGCAUGAUCAA	122	sga-miR7980b-5-3p	GUCCAAACACUGAUUCCAUUUCAU	65-88	stu-miR7980b-5p	1	0	24	24	1
sga-MIR1128-3	CUUUUAAGGUGGGAAGGUGUGGGG UACACAUAUUAGGGUAGAAGGUUAG UACUCCCUCUGUCCCUAAUUACUUG UCCACUUUUUCUUUUAUAGUUGUCC CUAAUUACUUGUCCAUUUUGACAAA UCAAGAAAGGACAAACUUUUUUACC UAUACCCUCAAUUAAUUACUUUGAA AAAGGUAGAACUUUUUGAAAAUCUU AAAAAAAAAAUUGUGAAGGUUAAUU	293	sga-miR1128-3-5p	UAGUACUCCCUCUGUCCCUAA	47-67	ssp-miR1128	3	0	21	21	1

sga-MIR477a-2	GUAUUAUAAACAAAAGGAGCACCAA CAGUGUGCUCCUAAAUGUUCUCCAA AUAUGUCCCAAUUUAAGUG UUGAUUAAAUUUAUGUUAGUUAUUA UACACUAGAAAUAUUUGAAUAAUGAA UUCUAGUUUGCUAGUAAACGGGAAA CAGGGAGAAAACUGCUAGACUAUGC CAUCCCAUAGUGGAAACAGGUAGGC GAGGGAUGCCGUUAGGGGAGUACA CAAGGUUGAGGCGCUGAUAAGCAAU AAUUAUACGCUAAAGUAUGAUGCUA GUGGUGACCAGAAAACAUGAUAACA AUACUCUAGUUUAUAAUAAACUAAUA UGAAUUUAAUUGA	264	sga-miR477a-2-3p	GGAUGCCGUUAGGGGAGUACA	130-150	ptc-miR477a-3p	6	0	21	21	1
sga-MIR1514b	CGUGAGGUCUCUAUAAUGAAAUUUA CGGAAAAUAUAAUGCAAACAAGAGG CCUCAUGAGGUCUCUAUAAUGAAAU AUCUGGAAAAAUUAAUGCAAAAAAGA GACCUCAUGAGGUCUCUUUUCUGCA UUUAUAAAAUAGAAAAAAUGUUAAAU AGAGACCUCCUC	164	sga-miR1514b-3p	UGCAUUUAUAAAAUAGAAAAA	123-143	gma-miR1514b-5p	5	0	21	21	1
sga-MIR159b-3	CAGAGUUUUGAAGGUAGAGCUCUUC UGAAUUCCAAAGAGGAUCUAAGAGG GAAAAUCGAGCUGCUAAUCUAUGGA UCCCUCAAUUCUAUCUAUUCUCAAA AUAAUUUUAGAUAGGUUUGUGGUUU GCAUAUAUCAGGAGCUGUAUUUACU CUUCUAGGAUCCUUAUUGGAAAGAA GGGAGCUCUACACUUGAUAACUUUU	200	sga-miR159b-3-5p	AGCUGCUAAUCUAUGGAUCCC	59-79	cas-miR159b-5p	1	0	21	21	1
			sga-miR159b-3-3p	UUGGAAAGAAGGGAGCUCUAC	166-186	sly-miR159b	0	0	21	21	1
sga-MIR159b-4	GAUCUAAGAGGGAAAAUCGAGCUGC UAAUCUAUGGAUCCCUCAAUCCUAU CUAUUCUCAAAAUAAUUUUAGAUAG GUUUGUGGUUUGCAUAUAUCAGGAG CUGCAUUUACUCUUCUAGGAA	121	sga-miR159b-4-5p	AGCUGCUAAUCUAUGGAUCCC	20-40	cas-miR159b-5p	1	0	21	21	1
sga-MIR166f-2	UUAAUUUUGAGGGGAAUGUUGUUUG GCUCGAGGCCACCAACUUCAUCUAA UGUGAGCAAACUCUUUGUUAGUGUC GUCGGACCAGGCUUCAUUCCCCUCA AAAUCUC	107	sga-miR166f-2-5p	GGAAUGUUGUUUGGCUCGAGG	13-33	cas-miR166f-5p	0	0	21	21	1
			sga-miR166f-2-3p	UCGGACCAGGCUUCAUUCCCCU	77-98	cas-miR166f-3p	0	0	22	22	1
sga-MIR9476-3	AUCCUGCUAUUGGUCUAGUCCUGCA UCUUUUUUUAUAUUUUUUGAUAACG GAAAAAAUGUAAAAAAAGAUGCAGGA CUAGACCAAUAGCAGUUU	94	sga-miR9476-3-5p	UCUAGUCCUGCAUCUUUUUUU	14-34	sly-miR9476-5p	0	0	21	21	1
			sga-miR9476-3-3p	AAAAAGAUGCAGGACUAGACC	63-83	sly-miR9476-3p	0	0	21	21	1
sga-MIR1888b	CGUCAAUAUGGGCUAGGCUCGUUG GGCCGGCCUGGCCUAACUCGUGAU UUAAUAGGGUUGGGCUAAGAUUUUU GGAGCACAUUUAAGAAAAGGGCUUU UUAGCCCGGCCUGAAUAAGCUUGUU GAUUUGAUGGGCUUGAGAAAUAUAG GUAGGGUAGGCCCAUUACAAAAAAU AUAAUUUUAAAAAAGUGGGUUGGCC CGUCAAGCCUGUAGCCCACGUACUU GUGG	227	sga-miR1888b-5p	UUGGGCUAAGAUUUUUGGAGC	58-78	ath-miR1888b	4	0	21	21	1

sga-MIR870	GAAAAAAACAUAAAAUUAGAAUUUAA UAUUAAAAACUUCUGGUGAUGAUUU UUUGGGCUUUUGUGGCGACUAUUG UCGCUGCUAUAGGUCUAGUUCUUUU GUAGUGAAUCCUAGUUGGCAACACU UAGAUGGAGGGAUUAGUCCCAUGUG ACAUGUCACAUUACUAAAAAGUUGG GGUGUAUAUUUGUGGUCUCCUACGA UAACAGCGGGAGUAUUUUUUAUCCC AACAUAUAAUGGAGAGUAUAAAUAAU CUAUUUCACAUAAUUUAGAGGCAAU UUUGACCCUUUUCCAUAGUAAUUAU GAUUUAUGAAUUUAGU	317	sga-miR870-5p	AAAAACAUAAAAUUAGAAUUU	4-24	ath-miR870-5p	3	0	21	21	1
sga-MIR7997c-15	UGGACUAUAUUGCUUAUACUCUUCA AAAAUAACGACGGAUGCAUAUCGGA UACUCCAAAAAUAGUGUACUUUUGG AGAAUUCGAUAUGGAUGUGACAACA CUUUUGGAGAGUUCGAGCAACAUAG UUUU	129	sga-miR7997c-15-5p	AUAUUGCUUAUACUCUUCAAAAAU	7-30	stu-miR7997c	3	0	24	24	1
sga-MIR2612	CCUUUUUAACCUACGUGGCACUUUU UUGUGGGCCCAAUAUUGGUUGACUU UUUUUUCAAGAUAGUGUCACAUAGG CCAAAAAAG	84	sga-miR2612-3p	AGAUAGUGUCACAUAGGCCAA	59-79	mtr-miR2612	6	0	21	21	2
sga-MIR4234	CAUAAACACAAUACUUAACUUGACAU CAGCUGACAACCAUGACCUUUAACU UCUGAUAUUCCAUGUAUUAUGUCAU GUAGGACACGUGUUUCUACUUGUUC AAUUUUUAUAUAAGUUUAAGUUUUU AUUUGUACAGACUCAAAGUUGGAGG GCACAGCCGUUGGCUGAAAGCAAGU UAAGAUCAUGUUUGCG	192	sga-miR4234-5p	UAACUUGACAUCAGCUGACAAC	16-37	aly-miR4234	6	0	22	22	2
sga-MIR159b-5	AAGGUAGAGCUCUUCUGAAUUCCAA AAAGGAUCUGAGAGGGAAAAUUGAG CUGCUAAUCUAUGGAUCCCUCAAUC CUAUCUAUUCUCAAAUUAAUUUUAG AUAGGUUUGUGGUUUGCAUAUAUCA GGAGCUGCAUUUACUCUUCUAGGAU CCUUAUUGGAAAGAAGGGAGCUCUA CACU	179	sga-miR159b-5-5p	AGCUGCUAAUCUAUGGAUCCC	49-69	cas-miR159b-5p	1	0	21	21	1
			sga-miR159b-5-3p	UUGGAAAGAAGGGAGCUCUAC	156-176	sly-miR159b	0	0	21	21	1
sga-MIR8739-8	UCCAAAAACUAGAGUGUAUACGCUC UUCAGUCUAACGGAAGACUAAAUAG GGACACAUGGCACAAUCUUAUUCAU CAAUUCAAUAUCGUGUCGAUGGAUA AGAUUAUGACACGUGUAUGUCCGUU AGUAUAAAGGGUAAUAUAUGUUCUA GUUUUUGAA	159	sga-miR8739-8-5p	AGACUAAAUAGGGACACAUGGCAC	40-63	gra-miR8739	5	0	24	24	3
sga-MIR1917-3	UAACUUUAACUUUCCACGUGAACUA CAACAAAAAUAACUUUUAGCGGCAU UAGAUAUAGACAUUAAUAAAGAGUG UUAAAGUAUUUACCGGCAUUAGUUA ACUGCCAUUAGAAACGACGUCGCUA AAAGCUUUAGGAACAUAUACAAAAAG UGUCAAUUGCCGCUAAAAAUCCAUA UUUUAGCGACAAUUAAUUCAGAAUC AGUUGCCGCUAAUGAUCAUUUUUGU	250	sga-miR1917-3-5p	AUUAAUAAAGAGUGUUAAAGU	62-82	sly-miR1917	1	0	21	21	1

sga-MIR1048	UGUAGUGGUGGCAUGUUCAAGGCA UUUACAUUAAUAGGUAAAAACGUGU UUUUUGAUUCAGUCUUAAUUGAUAU CUGUACCCUCCAACUUUAGGUAUAC ACAAGUAGACAUACACGUCCUACAU GAUAAAUCUCACGCGAUUUGACAUG UAGAACAUGCGUGUCUACUUGUUCA AUUUUAUGAUUAUUUAAGUGUUUUU AAUGUACACCCAAAAUUGGAGAGUA UAGAUACUAGCUGAUGCCAAAUUAA AGGACAUGUUUAUGUAUUCUGUCUC UUUUCUCUCAAAUAAAAAUCAAAGU GUCGAUCGACUGAGUCUGUGUGAC	250	sga-miR1048-3p	UAGAACAUGCGUGUCUACUUG	126-146	ppt-miR1048-5p	6	0	21	21	1
sga-MIR437a	UUGUUGUUGUUCUUAAGUUCGUUGA AGUUAAAGAAGUUGGAGGUACCGCU AUUUCUUUAACGGGUUUGAUCCGUU UUAUCUUGGGAGAAAU	140	sga-miR437a-3p	GAAGUUAAAGAAGUUGGAGGU	73-93	ssp-miR437a	5	0	21	21	2
sga-MIR8707-3	GGAUUAAAAGAAAUAUAAAAUUUUGA GGCGUGUGGGAAUCGAACCCACGAC CUCUAGGCAAAAUAAAAGGACUUGU UAGUUAUAGUCCUAAAAACAUAGGA AUACUUUAGUAAUUCCUCUAGUAUA CCUAAGAAAAAGGAAAUUUUUAGAU UUUGAUUUAAACA	164	sga-miR8707-3-3p	CUAAAAACAUAGGAAUACUUUAGU	88-111	gra-miR8707	6	0	24	24	2
sga-MIR8032e	AGCUUUAGUAUUUUUGGAGCUUAUG AACCUUGAACGAUCAUUUUCGAUCA AAAGUUCAAGAAGAUGACAUCAGAA UCCAAUUCUGACGAUUCCAUCAAUU CCAGUAGGGUCAUUUUAGGCUAGUA GCAUUGUUGACAUGACUCCCGAAGU UUUCAGUGUGAGUUGGUGUGAUUA GGUGUUUUAACUUUAAGUUAAAGGC UAAGUUUGACUUCAAAAAUACUAAAA CU	227	sga-miR8032e-3p	AGUGUGAGUUGGUGUGAUUAGG	155-176	stu-miR8032e-3p	1	0	22	22	1
sga-MIR6273-2	UAAUUUUCUAUCCUCUUUCAACCUA CGUGACACUAUCUUGUGGGUCCAAU GCUGAUUGACUUUUUUUUUCAAGCU AGUGUCACGUAGGUCGAAAAAAGCU AGAAAAUUA	109	sga-miR6273-2-3p	AAUGCUGAUUGACUUUUUUUU	48-68	ppe-miR6273	4	0	21	21	1
sga-MIR1128-4	GGCUAAUGUUUAUUACUCCCUCCGU CCCAAUGUGAGGUAGUUUGACUUGG CAGUUUAAGAAAACAGUCUAAAAUAA GUUAUAGAUGUUGGUGUAGCUGUA GAUCAUUUUAUUAAGGGUAAAAUAG GUACUUUAAAGUUAGAUUGUUACUG AAUAUUGAAAUGCGUCAUUCUUUUU GGGCUGACUUAAAAGAAAAGUGAGC AUAUAAAUUGGGACAGGGAGUAUAU AGAAAGUAAAU	236	sga-miR1128-4-5p	UAUUACUCCCUCCGUCCCAAU	11-31	ssp-miR1128	2	0	21	21	1
sga-MIR9750	AGGUAGGGAUAAGGUCUUUCAAUAC UCUACUCUUCUAGGUUCACUUUACG AGAUUACUCUGAAUACGUGUAUUGU UAUUGUAACUCCAUAUGUAUGUACA UUUUACAUAUACGGCAGGGGUAUAU GUGAGCCGUUUGUAUAACGGUAAGG GCAUAUAACCACUUUUAUAACGAAG GGUAUAUCAACUCUAAAUGACGAAG	226	sga-miR9750-5p	UGUAACUCCAUAUGUAUGUACA	79-100	gma-miR9750-3p	7	0	22	22	1

sga-MIR1439	GGUAUAUCAGACCCUUUUCCCUAUAU UUUUAAGUACUCCCUCCGUUUUAAA AUGAAUGACCCUAUUUCCUUUUUAG UUUGUUUCAAAAAGAAUGACCCUUU UCUUUUUUGGCAACACUUUAACUUU AACUUUCCACGUGCUUGUUUAAGAC CAUAUGAUUAAAGGGCAUUUUAGUA CAUUUGACAGAACUUUAAUUUAGAA CACAAGAUUAAAAAGUCUUCUUUCU UUUCUUAAACUCCGUUCCAAGUCAA ACUAGGUCAUCCUGUUUGAAACGGA GGGAGUAUUAUUU	263	sga-miR1439-3p	GUUUGAAACGGAGGGAGUAUU	239-259	osa-miR1439	3	0	21	21	2
sga-MIR6145e	UGCUCUUCAACUUCGGAUGUGCACA AAUAGACACUUAAACUUUUAUAAAGU UGAAAAAAUAAACACACAUGUCCUAU AUGUAAUCCUACGUGACAUUUUUUG UCCUACAUGGUGUCCUACGUGUAUU GUUCCAUGUAGGACUCAUUUGUUUA UUUAUUUAAAAGUUGGAUAGUUAAA GUGUCUGUUUGUGCAUUAUGAAAGU UGGAGGUCAAAGUUUAAAGUUGAAG UCAAGUUUAGGAUCUAAUAUAUGCA UUAUGCCUUUAAAUAACGUUGUUUA AUAACUUUAAGUAUUCACUUGGUAA AGUUAUCAGUAGAAUGAUCU	322	sga-miR6145e-5p	AUUGUUCCAUGUAGGACUCAU	125-145	nta-miR6145e	5	0	21	21	1
sga-MIR5340	GGUGGUUUUGCAAAAAUAAUUUUGA CACAUGACCAAUUAUAAUUGGGCCA CUUCAUCAAUUCUUUUGAUAAAAAAA UCAUAAUUCUGAAANUUAUUUAAAAA AUUGAUGACGUGGCCGAAUUAUAAU UGGCCACGUGUCAAAAAUGGUUUUG UAAAACCACC	162	sga-miR5340-3p	UGAUGACGUGGCCGAAUUAUAAU	105-127	osa-miR5340	5	0	23	23	1
sga-MIR11425d	UGGAGAGUGGAGGGGAUGGCUCCA GCCAUAUGGAUGAAUGGCCUUCCCA AAAGAAGGUUAUAGCUGGUGUCGAU AUCCAACACCUGGAACAUUGCCUCA AACUCUGCG	108	sga-miR11425d-3p	AAAGAAGGUUAUAGCUGGUGUC	50-71	pab-miR11425d	6	0	22	22	1
sga-MIR535f	UAUUACGCAUGAUUCCGGUGGAGCU UACAACAGCAAGAAAAUGAGAGAGA GCAAAAAUCUCUCUCACUGUCUUGC UGUUGUAAGCUCCACCGAAAUUAUG CAUAGGG	107	sga-miR535f-3p	AGAAAAUGAGAGAGAGCAAAA	36-56	csi-miR535f-5p	4	0	21	21	2
sga-MIR8006-10	ACCCUCCGUCAUAUUUUUGAGAUAU UGGUGUCCCUGCCGUAAAAAAAAAC UAGAGCAUAUAUGCUCUACGCGUGU CAUAAUCUUAUUCACCGAUCCAACA UUUAUUAAAUAUCGAAUUGACGGAU AAGAUUGUAUCACGUGUCCAUAUUU AGUUUUCCCUUAAAGUGAAAGACAU AUAUGCUCUAAAUUUUGAACGACAU GAAUACAAAUAUCUCAAAAGUAUAAU GGGAGAUU	234	sga-miR8006-10-5p	GUCCCUGCCGUAAAAAAAAACUA	30-52	stu-miR8006-3p	7	0	23	23	3
sga-MIR11156	UUCCAUUAAGAUUAAGAGGUCUGAA UCUGAAUACACAUCUGAUAUUAAGA GUUGCAGUAAGAUUGGAUGUUUCAA UCUGAAUACACAUCUGAAUAUUAAG	137	sga-miR11156-3p	AAGAUUGGAUGUUUCAAUCUGAAU	59-82	lja-miR11156-5p	7	0	24	24	1

sga-MIR10533	AUGUAGUCUCCAAAUCAGAGCACUA AAUAUAAUGUUG AAAAACUCUAAGAACCAAUGCAAACC AUGCAAUCUUAGUUUUGACUAUUUU AUGGAUUAAGCGAUUGUGUCUCAAU GCUUAUGAAUUCUAGUGUAGUUUUC UUUGGGCUAUUGAAUGAUAUAAGAA UUGUAUUGGAUUGAUGCAUAGGCUG UCUUAGAUUGAU	163	sga-miR10533-3p	GCUUAUGAAUUCUAGUGUAGUU	77-98	sly-miR10533	7	0	22	22	2
sga-MIR1917-4	AGGUACACUACAAUAAAAAUAACUUU UAGCGGCAUUAAUUAUUGACAUUAA UAAAGAGUGCUAAAGUUUUUAUCGG CAUUAGUUAAGUGUCAUUAGAACUA AUGUCGCUAAAGGGUUUAUGGACAU AUACAAAGAGUGACAAUUGCCGCUA AAAAUACAUAUUUAACGACAAUUAAG AAUUAAAUGUCGCUAAUAGUUAUUU UUGCUGUAGUGGUAGAG	219	sga-miR1917-4-5p	AUUAAUAAAGAGUGCUAAAGU	47-67	sly-miR1917	0	0	21	21	1
sga-MIR7992-14	AGUAAGCACUCAAACUUUGAGAGUG CACAUCUAGAUACCUCAACUUGGUC AUAACCGACUACUAAACAAUCCACGA CCACUCGUCUCCACUUUGUCUCAUG CACACUAGACUCUGACAUGACACAU AAAUUUUGGAGGUGUCUAGAUGAUC AUUUUGUAAGUUGAAGUGUUCUUUC UAGAUAUACAUUCUCAAAGUUGGAG UGCUUGAG	209	sga-miR7992-14-5p	UUUGAGAGUGCACAUCUAGAUACC	16-39	stu-miR7992-5p	4	0	24	24	1
			sga-miR7992-14-3p	UGUCUAGAUGAUCAUUUUGUAAG	139-161	stu-miR7992-3p	7	0	23	23	1
sga-MIR167d	ACGAGAAAGAAUUGCUUACGUGGCU AAUAUCUCUAAAUCCUACCAUUAUC GGUUCGAGUCACCGAGCAAUGGAAG CUCCCAGGAAGGUGUUAGCCACUUG AGCAACUCUUUCUUUU	116	sga-miR167d-3p	GGAAGCUCCCAGGAAGGUGUUA	71-92	ppe-miR167d	6	0	22	22	2
sga-MIR4223	UCAAAUCACAUUUAUGCCCUUCAAC UUUGGAUGUGCACAAAUAGACACUU AAACUUGUAUAACGUUGAACAAAUA GACACGCAUGUCCUACAUGUCAUUU UUUGUCCUGCGUGGUGUCCUACGU GUAUUGUGCAAUAUAGGACUCAUGC GUUUAUUUAUUUAAAAGUUGGAUAG UUAAAGUGCCUAUUUGUGCAUUAUG AAAGUUGAUAAACAAAAUAUGUUCC U	225	sga-miR4223-3p	AUGAAAGUUGAUAAACAAAAUA	197-218	aly-miR4223	6	0	22	22	1
sga-MIR8006-11	CCCUCCGUUAUACUUUUGGGAUAUU GGUGCACCCGCCUUCCAAAAACUAG AAAGGGUAUAUACGCUCUAGUUUUU GAACGACAGGGGCACCAAUGUCCCU AAAGUGUGACGGAAUU	116	sga-miR8006-11-3p	UAGUUUUUGAACGACAGGGGCACC	68-91	stu-miR8006-5p	1	0	24	24	1
sga-MIR5303-20	CUUACCAUUCUCGACUCAUUGCUCA UGUGUUGUGUUGCUCGGACUCUCA AAAUAGUUGCUGCACCUGUGUCGUA UCUUCCAAAACUCACUAUUUUGGAG UAUCCAACACACACCAGUCGACAUU UUUGAAGAGUUCGAGCAACAUAGUC	173	sga-miR5303-20-3p	UUUUUGAAGAGUUCGAGCAAC	123-143	sly-miR5303	0	0	21	21	1
sga-	AUAUCUUGAGUUAAUACUGGUCUG AACUGUAUGGUACUCCCUCUGUUUC	188	sga-miR5174e-5p	UACUCCCUCUGUUUCAAUUUG	11-31	bdi-miR5174e-	5	0	21	21	1

MIR5174e	AAUUUGUUUGUCUGGCUUUGACAUG ACACAAAGUUUAGGAAAGUAAAAAAU ACUUUUGAAUCUUGUGAUCUUAAAC AUGUCACGUGAAAAGUUGAAAUUAA AGAGUUGCAAAAAAGGAAAGUAAGA CAAGCAAAUUGAAACGGACUGGAUG UAUCAUGCAAAG					5p-2					
sga-MIR11507	AAGGAAGAAUUCAAACUUAUAGAUA UUUCUGACGAUCGUGAUAUUAAUCA CCAACUUGUUUACAUAAAGCUUAUG GUUUUGAGAGGAUCACUUUCUGUGA ACACAUUGGUGAUCUAAAUCACGAU CAUCAGGAAUAUCUAUAAGUUUGAA UUUUUCUUU	159	sga-miR11507-3p	UCACGAUCAUCAGGAAUAUCUA	119-140	pab-miR11507	5	0	22	22	1
sga-MIR1917-5	UCUCACUACAACAAAAACAACUUUUA GCGGCAUUAAAUAUUGACACUAAUA AAGAGUGCUAAAGUCUUUACCAGCA UUAGUAAAGUGUCAUUAGAACCAAU GUCGCUAAAGGCUUUAAGGACAUAU ACAAAGAGUGACAAUUGCCACUAAA AAUACAUAUUUAGCGAAAAUUAAGAA UUAUAUGUCACUAAUGGUCAUUCUU GUUGUAGUGUCU	214	sga-miR1917-5-5p	ACUAAUAAAGAGUGCUAAAGU	45-65	sly-miR1917	1	0	21	21	1
sga-MIR6427	UUAAAAGGUGUGAGUGAAAAUUAUG AAGAGUUGCGACUUUUAUAAAGAGU UGCGACUAUUAUAAAAAGUUGCGAU UUUUCUGAAGAGUUGUGAUUUUCAU GAAAGGUUGUGACUUUUAUGAAAUA GUGACCUUUUCAGUAAGGCACAAUA UGAAUCUUUUCACACGACCCUUUGU C	176	sga-miR6427-5p	GUGUGAGUGAAAAUUAUGAAG	8-28	ptc-miR6427-3p	5	0	21	21	1
sga-MIR7981-16	AUUUCAGAGACAUAUCUUAACUAAA UUAAAGUCCCAUUACCCUCGAACCC UUUUUUUUUGUAUUUUUGUGCACCU UCUAGCUUACGUGCAUCCUAAUAUC UCUCACGCGCCUCAAUUGUGUGCAG UCACAGAGUGUACCACGUAAGACAA AAUGUGUACGAAGUUACAAAUAAAA UGUUUGGGGGGGGAGAGUAAUAGG ACCUUAUUUUAGUUAAGGUGUGUCU CUUGAAUU	232	sga-miR7981-16-5p	CUUAACUAAAUUAAAGUCCCAUUA	16-39	stu-miR7981-5p	6	0	24	24	2
			sga-miR7981-16-3p	AUAGGACCUUAUUUUAGUUAAGGU	195-218	stu-miR7981-3p	2	0	24	24	1
sga-MIR2920	UAAUGAACUCUUAUUAUAGUUCUUA AAUCUUUUAUCAAAAGUUUUGACUU GGUUUCGAGAUGGUGGUAAGUUUU GAAUAUCAAUGAUAGCGAGCAUGUG GAAUUGUAAGUCCCCGUUAAGAUGA AGAAAGGGGCAGCCUGAAACCCUUG UUAGAACUGCUAUCUAUUGAUGUUU AAAAACGAACUCCAUGCUUGAGUAA AAGUUUACCAUACAGCCAAAACUUA GGAUAAAACUUUUAACACAACUAUAA UACGUUUCAAAG	262	sga-miR2920-3p	ACACAACUAUAAUACGUUUCAAA	239-261	osa-miR2920	5	0	23	23	1
sga-MIR1917-6	GAGCACUACAAUAGAAAUAACUUUU AGCGGCAUUAAAUAUUGACACUAAU AAAGAGUACUAAAGUUUUUACCGGC	214	sga-miR1917-6-5p	ACUAAUAAAGAGUACUAAAGU	45-65	sly-miR1917	2	0	21	21	1

sga-MIR8011b	AUUAGUUAAGUAUCAUUAGAACCAA UGUCGCUAAAGGCUUUAGAGACAUA UACAAAGAAUAACAAUUGCCACUAAA AAUAUAUAUUUAGCGGCAAUUAAAAA UUAAAUGCCGCUAAUGGUCAUUUUA GUUAUAGUGGAG CCUUCACACAACUAACACCAGUUCU UUGAGGCUUCUUUUUAUUUUACAAG UCGGUGGACCCAGAAGUGUAAUAAU UUGGGUUCAUUAACUUGUGGGACAA AAAGAAGCCCUACAUAAUUAGUGUC AGCUGUGUGAGAC	138	sga-miR8011b-3p	CUUGUGGGACAAAAAGAAGCCC	89-110	stu-miR8011b-3p	4	0	22	22	2
sga-MIR8709b-2	UCAUAGGGUAUAAAAGAACUGCCCA AUAGUUGUGAGUGGCAAGUCUAUGU GUGCAAACUUGAUCGAGUUACCCAU GCAUGAUUUUGAUAUUAUUCUUGGC AUGGACUGGCUUCACAGCUAUUAUG CUUGCUUUUAAUGCCGUAGUA ACAUCACAAAUGCAGAUUAUGCCAU CACUGGAGCUGGUAGAAAAGGCAUU AUUGUUUCGCUGAUCAACAUCAUGU AAUGGACCUGAUGGGGUUGUAUAUA	146	sga-miR8709b-2-3p	CCAUGCAUGAUUUUGAUAUUAUUC	72-95	gra-miR8709b	6	0	24	24	2
sga-MIR8130	CAAAAGAGAACCCUAGGCCCGUUUA UGUGGAGCCACCACAAACAAGGAUU UCCUUUUAAUUUAUUUAUUUCAGAA UUUAGUCUUUACCUUUAAUGGAAAG UUGUGACUUUUAUGAAUUGCUGUAA CAUUUAUGAAAGGUUGUGACAUUUU UAAAGUGUUGUGACUUUUCCAAAAA GUUAUGGCCUUUCCAGUAAAGCACA AUAAGCAUUUGUGACAU	317	sga-miR8130-3p	CCUUUCCAGUAAAGCACAAUA	283-303	ppe-miR8130-3p	6	0	21	21	1
sga-MIR6462c	GAUGCGGGCAGGCCACGGCCGACC GUUGUGUGCAGGCACGUCCGACGA CGGCCGACCGUUUGUGCUGUCCAA GGGCUAUGAUGGCAUGCCACGCCC GACGACGGCCGACCGUCUAUGCUG UCAAAGGGCAAAGAUGGCAUGCCAC GCCCGACGUCGUCCGACCGUGUGU GCUGCAAAAAGGCGAAGAUGGCAUG CCACGCCAG	203	sga-miR6462c-3p	AAAGGGCAAAGAUGGCAUGCCA	123-144	ptc-miR6462c-5p	6	0	22	22	1
sga-MIR6135e	AAAGGUAAUUUCACAAUACCUAAUU UAACCAACUUUUGGUGGGGACUAAA UGAGGGGUAAAAUGGUAAAUUGACU AUACCAAACCUAAUAUAACCAAUUUU GGUGGGAAAAUAUCUACAAAUGGGU GGUAAAAUAAGUCUUAAGUAUUGGG UGUAGGUGACAAUUAUGUGAUUAAU GAUUAAGGAUUGUGGAGUUGCCCUC UUUAUAAUUAUCUUAAUUAUUUUUU UAUAGUUUAUUUGGCAACCUUAUUC GUAAGAUGUUAUUAAUGGAUUGCCU GAGUGGUGUCGGUUAGGAAAACGU	201	sga-miR6135e-5p	GGGUAAAAUGGUAAAUUGAC	55-74	pgi-miR6135e-5p	3	0	20	20	1
sga-MIR1112	GUCUGGAUGGCACCAGUGCCACUUA UUUAUGGAAUUUAUCGUGAGUGGCA CAUGGUUGAUCGUGUUGUGAGACA GUUCGGUUAUUUACAACAUAUUCCU GGACCGUGUACCCAAUUUUCCGAAU	276	sga-miR1112-3p	ACUUAUUUAUGGAAUUUAUCG	120-140	smo-miR1112-5p	5	0	21	21	1

sga-MIR8706b	AUCAUUUUAAGUGUGAUAAACAAUCCAAAAUAAAACAAGAAGAUAUAUAUGCAAGGAGUCAAUUCCAAUGAUUUUUCAAAGAUGAUCAAAACAUGAAUUCUCCAAUUUCAUAGUCUAGCCAUGUGUUCUUGCAUACAAGGUUUUGAAUCAGUGUUUUAGGAUUGAAUUGAUGUUAACGCAAUGUUUUAAGGAUAUAAAUUCCUAUGAACCCAUGCAAACUAUACAAUCCUAGUUUUAACUAUUUUAUGGGUUAAGUGAUCAUGCCUUAAUACUUAUGAAUUCUAGUGUAGUUUUGUUUGGGUUACUGAAUGAUGUAAGAAUUGUAUUAAAUUGAUGCAUAGGCUGUCUUACAUUGAUAAACCUAUAUUGAAUUGACUUAG	327	sga-miR8706b-5p	UGUUUUAGGAUUGAAUUGAUGUUA	99-122	gra-miR8706b	4	0	24	24	2
sga-MIR1128-5	UAAUUUGUUGACUUCCAAGAAAGCUAUUACUCCCUCCGUCCAACAAUACUUGUCCACUUCAUGAAAUCCAUGAAUAAUUUUACACUUAGUUCCUAAUUUACCCUUAUCAUAAAUUAUAGUCAUUUCACUCAUUUCCCUAUUUCCCUAUUAUAUUUUUCAAGACAUUGUAUUUAUUAUAUUCAAAGGGUGAUAUAAUAAAAUUACCCAUCUAUAAGAAGUGUGCCAAGUCAAUAGUGGACAACUAUUGUUGGACAGAGGGAGUAUAAAAGUUUUGAAAGACACCAAAAUG	289	sga-miR1128-5-5p	UAUUACUCCCUCCGUCCAACA	25-45	ssp-miR1128	3	0	21	21	1
sga-MIR8021-2	AUUCAAGGCUCAAACUCGAGACCUCUGAUUAAAGAUGGAUAUUUCAUAUACAUCCACUCGUAAAUAUUGUUGGUUCUAAACUUAUAAUAAUAACAUAAUUCACACUCUCUUGCAUAUUCUGCAAUAUGUUGAAUUAAGUUAUUGAGUUCUACCAACAAUAUUGUGUUGGAGAAGAAGUUAAGAUUACUUCAUCCUUAACCAGAAGUGUCAAGUUUGAGUCUUGGCAAAACUCACUAUAUCAAUAAUUUCUUUAUUUAUAGGUGUGUCCGUUCAAAAAUGAACAACUAAUUAGGGACACAGGGAACUCUUUUCUACGUGCCAUGUUGACAAUUUUGUUGAGCAUGGGCCUAAUUGCAUUUCUUUCAUACCUCUUCUGUUUCACAUUAUCAUUGUCCCUGAUUAGUUGUCCACUAUUAAGUUGAUAUACCAAAUAAAAUAAUAAUUCAUAUAGUGAGUUU	226	sga-miR8021-2-5p	AUUCAAGGCUCAAACUCGAGACCU	1-24	stu-miR8021	0	0	24	24	1
sga-MIR5070	UCCUUACUCAAUCUAAGUGAGUAUUUGGGCAUGCGAUACCAUAACACAAUAUGGAAUCGUGAGAUGGAAUCAAUGGUUGGAUAUAUGAUUUUACGUUGAU	232	sga-miR5070-5p	AACUAAUUAGGGACACAGGGA	57-77	bdi-miR5070	4	0	21	21	1
sga-MIR1886h-2	UCCAUCUCAUGAUUUUAUAUCAUGAGAUAUGAUUUCAUAUUCUUCAAAAACUAUGAUAUGAGAAUUU	167	sga-miR1886h-2-3p	AUUUUACGUUGAUUCCAUCUCAUG	88-111	stu-miR1886h	1	0	24	24	1
sga-MIR8009-3	UCGCUUUUCUGGGUUUUAUUUUUUUAAAACCCAAAAAAGAGACGGGCAAU	172	sga-miR8009-3-3p	AUUUCCAGAAAAGCGACGGACAGG	92-115	stu-miR8009	1	0	24	24	1

sga-MIR10532-11	GUCCUUUAGUCCGUCGCUCUUCUG GAUUUCUCACAAAAAUAAUUUCCAG AAAAGCGACGGACAGGGUCCUUUAA UCUGUCGCUAUUCUGGGAUUUUCAA AUAUUAAAUAACCAGAAAAGUGA AUAAUAAUAACAAGGGAAAAUGCACA AGUAUUCUCUAGUGCCACGUAGGCU GAAAAGGGGUAGAAAAUUACUUAUU AAAUAAGUUCAGGGGGUAAUAGAAC CUUAGUAUAGUAUAAGUGUAUCUCU GAGAUUUCGGGCAUAGGUUAAGGAG GUACUUGUACAUUUUUCCUAAUUAA UAUCAA	182	sga-miR10532-11-3p	AAGUGUAUCUCUGAGAUUUCGGGC	115-138	sly-miR10532	1	0	24	24	1
sga-MIR1847	ACUUAUUUUAGAUGUAAUUUUCUAU CUUUUUUUAGCCUACGUGGCAUUAG UUCGAAAAAAGAAGUCAACUAUCGU UGGGCCCACAAGAUAGUGCCACGUA AGCUAAAAAGGGGUAAAAAAUUAUU AAUUUAAUAUAUUA	139	sga-miR1847-3p	GGGCCCACAAGAUAGUGCCACGUA	77-100	osa-miR1847-2	6	0	24	24	2
sga-MIR8019-1	AAGUUAUUACUCCCUCCGUUUCAAA AAGAUUGACCUAGUUUGACUUGGAA CGAAGUUUAAGAAAAGAAACAAACUU UUUAAUCUUGUGGUUUUAAGUUAAA AGUCAUGUCAAAUGUACCAAAAUGC CCUUUAAUCUUGUAGUCCUAAACAU GCCACGUGUAAAGUUAAAGUUAAAG UGUUGCCAAAAACGGAAAAAAACCA UUCUUUUCUAAACAAACUAAAAGGAA AUAGGGACAUUCUUUUUGAAACGGA GGGAGUACGUAAUAU	267	sga-miR8019-1-5p	AAAAGAUUGACCUAGUUUGACUUG	24-47	stu-miR8019-3p	2	0	24	24	1
			sga-miR8019-1-3p	AGGAAAUAGGGACAUUCUUUUUG	223-245	stu-miR8019-5p	6	0	23	23	1
sga-MIR779	UCGUUGAUAAGUUAUCUUGAAGUUU CCUUAUCAAUUAAGUUUCAAUGUAU GUUUCUACUUGGGUCAAAUUGAUAU GACCAUAUCUAGGGGUGUCAAAUGG GCAUGUUGGUUAAAAUUGAAAAUAU UUAAAUGGGUUGAAUAGAAAUUUGG UUGGGUCUUGACCCGUCUAAGUUUA CUUUUAACUCAAAUGGGGGCUAAAA AUGUGUUGGGUCUUGACCAAUCAAU UUGACUUAAUUAAUCUCAAUAAUUU AACAUAUUGAUAUUUAACUUUGAUA AUCACAAUUU	285	sga-miR779-3p	UGAAUAGAAAUUUGGUUGGGU	136-156	ath-miR779-2	5	0	21	21	1
sga-MIR5303-22	UAGUUGUUUGCAUAGCUAUGUUGCU CGGCCCUCCAAAAAUAUUGCUGCGC UCAUAGCUUUAGUAGGAUCAAAACA CACCCAACAAUACUUUUGAAGAGUU CGAGCAAUAUAGUUACAAACAAUGU CAUGGCAUAAUACAUAAAUCUGUUC UUUAACUUGGCUUCGAAUCACAUUU	125	sga-miR5303-22-3p	CUUUUGAAGAGUUCGAGCAAU	88-108	sly-miR5303	2	0	21	21	2
sga-MIR8781a-3	AUGUCCUUCAACUUUGGGUGUGCAC AAGUAGACACUUAAACUUUUAUAAA GUGGAACAAAUAGAUACACAUGUCA UUUUUUAUCCUACAUGGUGUCCUAC GUGUAUUGUGCCAUGUAGGACUCAU AUGUUUAUUUAUUUAAAAGUUGGAU	292	sga-miR8781a-3-3p	UGUUUAUUUAUUUAAAAGUUGGAU	177-200	gra-miR8781a	6	0	24	24	1

sga-MIR390-2	AGUUAAAGUGAUUUUUUGUACAUUA UGAAAAUUGGAGGUCAAAGUUAAAA UUUGAAGUCAAGCUUAGGGUCCAAU UUAUGUAUUAUACCUUU CGAGCAUGAAGAAGCCAUAAAACUC AGGAUGGAUAGCGCUAUAGAUAGCC AUUAAGAUGUAUUCAUGGUGCUAUC CCUCCUGAGCUUUAUAGAUUCCCCA UGCCAU	106	sga-miR390-2-5p	UAAAACUCAGGAUGGAUAGCG	18-38	atr-miR390-1	2	0	21	21	1
			sga-miR390-2-3p	UGCUAUCCCUCCUGAGCUUUA	69-89	stu-miR390-3p	4	0	21	21	2
sga-MIR2630v	CCAUAACUAACCUAUUGGACCAUCC UAGGUUAGGUACUAGGUUAACUCUU UAACUAGUACUAGGUUAGUGUCAAC CCGGUUUUGGUCCUAGGUUAUCGG GUGCACUAUUGGGUCCAUUUCGGU UAGUCCUAGGUUAGUUAGCU	143	sga-miR2630v-3p	CGGUUUUGGUCCUAGGUUAUC	77-97	mtr-miR2630v	5	0	21	21	2
sga-MIR11136	UUGAUAAAUGUUGGGGUUUAGAUUU GUUGGUUCGCUCACUUAGUAGGUUA AGUGUGGGUGUCACUCACGACUCAU UUUGGGUCGUGACAAACUUGGUAUC AGAGCGUUAGGUUCUUUUGUCUCAU CACACAAGCAUAAGUCUAGUAGAGU CUUGAGGAACGGUAUGGGGACGCC UUUACUUUUCUUUGAGAGGUAUUCA AAAAUGCACGGGGCGCGGAACCUAG GGUUUGAUGCUUAGGGGGCACAAU UAACAAGUCUGUUUUUUUCUGCUCA AGGGUUGUUUACUUCUUUAUUUUUG GGUUUAAGUAGUGAAGAAUCAAAUC AGACACAUAAUUUAUAAG	341	sga-miR11136-5p	GAUAAAUGUUGGGGUUUAGAUU	3-24	lja-miR11136-3p	4	0	22	22	1
sga-MIR5298c-2	GAUAUUAUAAUAAUCAAAAACUAAAA UAGAGCGGUGUUAUACCUCUCAUUA AUUGAAUAAUAAAGAGUGGUUGGAA AAUUCAUUCUCUUUUUUACGCUCCA AAUAUAGAGAAGAGAGAGUAAAAUA GAGAUGGAAUGGAGAUGACCUUACA CACCUUAACUACUCAAAGUGAAUUU AUUGUCAUCCUGAGACGUGUAAUGC CACGCUCUCAUUAUGUAUAGUAUUA CAUUGGCGGCCACAUCAACGCUAUG UCAGUGUUAUCUCAUAAAUUAUAAU UUU	279	sga-miR5298c-2-3p	AAAUAGAGAUGGAAUGGAGAUGAC	122-145	mtr-miR5298c	7	0	24	24	3
sga-MIR11174	AAAUUGUAUAAAAUGUGUUUGUGUU UGUAUAAAGCUAGAGAAAAUUGUAU AUAUACAUAUAUUUUCGUUGCUCUC UCUCCCCUCUCCUAAAUCUCACUCG CUCACUCUCCUCUCUCACUUUAUAC AAACACAAAUGCAUACUAAUGCAAAU U	152	sga-miR11174-5p	UGUUUGUGUUUGUAUAAAGCUAGA	16-39	lja-miR11174-3p	7	0	24	24	1
sga-MIR3706-1	AAGACACGUGGCACAAUCUUAUCCA UCUAUCCGAUGUCGGGUCAGUGGA UAAGAUUAUGACACAUGUAUU	70	sga-miR3706-1-3p	UGUCGGGUCAGUGGAUAAGA	35-54	pab-miR3706	5	0	20	20	1
sga-MIR6160-2	GACUUUUUUGUUUCAAUGACUAAUU UAUAAUUAUAGAUCGGAAGAGCGUC GUGUAGGGAAAGAGUGUAGAUCUCG GUGGUCGCCGUAUCAUUAAAAAAAA AGCCGUUUGUAUAACGGUAAGGGCA	235	sga-miR6160-2-3p	GCAUAUAUGAGCCACUUUUAUAAC	123-146	nta-miR6160	5	0	24	24	1

sga-MIR1518-2	UAUAUGAGCCACUUUUAUAACGAGGGUAUAUCAGCUCUAAAUGACAAAGUUGAGAGGUAUAUCAGACCCUUUUCCCUACAUUUAUUAGUAGCGAAUGAAACAAAAAAAAUUUUUCCUUCACUAGAUUUUUUUUCCACUAGAAUUUAUCUGGUAAGGUUUUAACGAGGCACAUAAUCUAACGACAUUCAAGAGGGAGUGUUCGAAAUUGUUAUAAACAAUUUGUAUUAUAGUGAAUAUCUAAUUAUGUGGAGUCCUUGUAGGAUAUGGUUAGGAAUUUUACUUGGGCACCAAGUAAGGUUUUCCCUAUAAAUAAAGAGUUUUCCUUCAUUGUAAAGAAAAUUUGUGAAAGAUCU	243	sga-miR1518-2-3p	UUUGUAUUAUAGUGAAUAUCU	109-129	gma-miR1518	5	0	21	21	1
sga-MIR158	AAUGUAUGUUUUAGGAUUUGUGGUAUAGGAGGUGUCUUUUGAGUGAGAAACUUAAGACUUGGAAAUUUUGGUCGCACAUUUUGUAAUAGUGACUUUUGUAUAUUAUUUAGAAAAUUUCUUGAUAGGAGUGGGUUUACGAUAUCCUCAUUCAUAGAAACAUAACACAUAAGCAGUUAAACACAUAUAUAUCGCAUCCUAACACAUACGGA	209	sga-miR158-3p	UUUUGUAUAUUAUUUAGAAAAU	94-115	bra-miR158-5p	6	0	22	22	2
sga-MIR482d-2	CCAUAAGUUAUCAAGUAGGUGAUCAACCUACUUGGACUUUUCACUUGGGCCUUUUUGGACUUUCGCAUAUUGGGCCUUGACUGUCCAUUUUCCACUUAUUCUUCUAUUCAACUUGGGCAAGAUUAACGCAAGUAGGUGGUAAUGUACUUGGCCUAAUAACGUGGUCCAAAAAAUUCUUAGUAGGUGAUGCAACUACUCAGUGCAUUGGUCUGGUCAACAAGUAAAAGUAGGUGAUGCACCUACUUGUCACUUACUU	256	sga-miR482d-2-5p	GUCCAUUUUCCACUUAUUCUUC	83-104	fve-miR482d	6	0	22	22	2
sga-MIR8014-4	ACAAUAUGAUACAUUAUGAAUCAAUACGUAACAACCAUCUAAACAGAGUGUAAUUAAGCACAACUGAGCUUCUCUCGUAAGUGUUGCAUUAGCUUUAUUUUGUAGCAAUUCAGUAGAAUUUAGAGCUUAAAAAUAAUAUAAUUGAGAAAGAAAAAUGUAGCAAUCCUUUAAGCAAAGCUAAGCUUUUCACCAAACUAUGGUAUAUCAACCAUCACAGUCCUAACAAGGUAGUGUCCUUUUGGUUCCAAAAUGAGACAGAGUACGGGGUGACUUCUUUCUGAUCCCCUAACACUUUGUUUGGAUCAUUGUUACCCAUUGUUUCAUAAUGUAUUGUAUUGU	340	sga-miR8014-4-3p	AUUGUUUCAUAAUGUAUUGUAUUG	316-339	stu-miR8014-5p	2	0	24	24	1
sga-MIR7981-18	AGACACACUUUUAUUAUAUUAAUGUCAUAUUACCCACAUAAACUUAUUUUAUAAGUAAUUCUCUACCCCCAUUCGGACAACGUGACACUAGUUUGAAAAAAAGGUGAACUAACUUUGCGCCCAAGAUAGUGCCACAUAGGCCGAAAGGAGUAGAAAAUUAAUAAAAUAAGUUUAGGGAGUAAUAGGACCUUAGUAUAGUAA	211	sga-miR7981-18-5p	UUUUAUUAUAUUAAUGUCAUAUUA	9-32	stu-miR7981-5p	7	0	24	24	2

	AAGUGUGUCU		sga-miR7981-18-3p	AUAGGACCUUAGUAUAGUAAAAGU	182-205	stu-miR7981-3p	4	0	24	24	1
sga-MIR7992-15	UGUCCUUUAACUUUGAAUGUGCACA AAUAGACACUUAAACUUGUAUAAAG UUGAACAAAUAGACACUAAUGUCCU ACAUGUCAUUUUUUAUCCUACGUGG UGUCCUACGUGUAUUGUGUCAUGU GGGACUCAUGUGUUUAUUUACUUAA AAGUUGGAUAGUUAAAGUGUCUGUU UGUGCAUUAUGAAAGUUAGAGGUCA GGGUGUGAGUUAGGCCUAAGACCUA AUUUCAUGGUAUCAGAGCAGGACCC GUCUCACCUGAUGUUGGGCCCCCAA AAUCAAAAUUGCCCACGCACCAGAU GUCAAGCACUGGACGUGAGGUGGG GUGUUAAAGAAUGACAAAAGUCCCA CAUCGGUGGUUAAUGAGAUGGGUG GACACCUUAUAAGGAUUAGACAAUA CUCAUCCUUUUGAGCUAGCUUUUGG GGUGUGAGUUAGGCCUAAGACCUAA UUUCACAAAA	199	sga-miR7992-15-5p	UUUGAAUGUGCACAAAUAGACACU	12-35	stu-miR7992-5p	5	0	24	24	1
sga-MIR11108h	UAUUGAUUUAGGAUUUGUCAAACUA UACCGUUAUCAAGAACAGAGGAGAU GUGACCAUUACUCAUCUCCUCUGUU CUUGAUAACUGUAUAGUUUGACAAA UCCUAAAUCAAUA	258	sga-miR11108h-3p	ACAUCGGUGGUUAAUGAGAUGG	149-170	lja-miR11108h-5p	5	0	22	22	1
sga-MIR11288c	AUUUAAUUUUUCUAAGCAGUCAAUU AGUGGAGUCCGGAGUCUAAAGAGUA AAUUUUAAAAAAAACAAAAAUCAGUA GCAAUUUUGCUUUUUCCGACAGAGG AAUCCGUUGUUGUUCCAGCGAUUUU GCCGUUUUGGUUAAUAUAAAAUUUC AUAUACUGUUUUGAAAAUUUUAUUA AUAUUUUAUACCCUUUAGGCUCCGG ACUCUCAAUUAGUGCAUGCUUGAUU ACUUACAU	113	sga-miR11288c-5p	UGAUUUAGGAUUUGUCAAACU	4-24	fve-miR11288c-3p	4	0	21	21	1
sga-MIR8727	CAUAACAAACUAGUUCUUGAGGUUG AGUUAGGCGCAUGUGUCAUAUCUUU ACAUGGUCUGACAUCCUUACCAUGU AAGGAUAUGACACAUGAGCCCAACU CAUCCCCAAGAGUUAGUUUUUGCC	234	sga-miR8727-3p	CGGACUCUCAAUUAGUGCAUGCU	199-221	gra-miR8727	6	0	23	23	1
sga-MIR477c	CAUACAUGUGUCACAAUCUUAUCCA CCGAUCUGAUAUUUAUUAAGUAUCG GAUCAACGGAUAAGAUUGUGCAACA UGUCUC	124	sga-miR477c-5p	CUAGUUCUUGAGGUUGAGUUA	10-30	csi-miR477c-3p	5	0	21	21	3
sga-MIR3706-2	UAUUUACAGCCUCUUUCCAAAAAAU AGAAUCAUGUGAAUUGGGGUUUAGA UUGGUUGGUUCGCUCACAUAGGAG GGUAAGUGUGGGUGCCAGUCGCGG CCCGAUUUGGGUCGUGACAAACUUG GUAUCAGAGCAUUAGGUUCGUUGGU CUCAUCACACAAGAACGAGUCUAGU AGAGUCUUAAGGAACGGUAGGGGGA CGCCUUUACUUUUCUUUGAGAGGCU AUAAGAC	81	sga-miR3706-2-3p	UAUCGGAUCAACGGAUAAGA	46-65	pab-miR3706	4	0	20	20	1
sga-MIR845b-2	UCAAAUUUAUGCCCAUCAACUUUGG	230	sga-miR845b-2-3p	AAACUUGGUAUCAGAGCAUUA	117-137	aly-miR845b-5p	6	0	21	21	3
sga-		228	sga-miR7822-2-5p	UAUAAAGUUGAACAAAUGGAC	53-73	ptc-miR7822	5	0	21	21	1

MIR7822-2	AUGUGCACAAAUAGACACUUAAACU UGUAUAAAGUUGAACAAAUGGACAC AUAUGUCCUAAAUGUCAUCCUGCAU AUCGUUUUUCGUUCUACGUGGUAUU CUACGUGUAUUGUGCCAUUUAGGAC UCAUGUGUUCGUUUAUUUAAAAAUU GGAUAGUUAAAGUGUCUGUUUGUGC AUUAUGAAAGUUGGAGGUCAAAGUU AAA GUUAUAUUCAAUGUAUACCUGCAUU AUUGUAGGUUUUGAUUACCUUCAUG AACUUGGCAGCUUGAUGUGACAAAG AGCCUGAAUACACUCGAUCUCUUUC AUAUUAAUGAAACCGAAUCGAAAAUU GAACCAAAUUACAAAUUGAGUCGAA UCGAAAAAAAUUCAACUAAUGGUUU GGUUUGACUUGAUUUGGUAUUUAAA AAAAACGGACUAUAUAUGGGUUUAA UUUAAUAUUUG AGAAACCUAAUUCAAGUUGUAUUCU ACAAAGUCUUGAUGCGGCAGUAAGU UGAAGAAGAACUUAUAAGCGACUGC AGCGUAGACAAAAAGAAGUCCUAAU GCUACAAGGUUGUAUUCCAGUGACA AUUUUCCAGCGACAAAGGGUGGAAA CAAAGUCUAAGUUGAGUUCAACAAU GUUUAUGUAGAGGCAAGACAAAGUU GAAUCAAACAAGGAGUUGAAGAUGC GGCGAAGACAAGUUCAAGUUGAACU AAGAGUUCCACAAGAAGUAGGAUUU CGAGUUGAAAUAGGUUAUG UAUAAACAAUUUGUAUUAUAGUGAA UGCCCAAUUAUGUGGAGUCCUUGUA GGAUAUGGUUAGGAAUCCUACUUGG AGACCAAGUAAGGUUUUUCCUAUAA AUAAAGAGUUUUCC CCGACGCCUUUGAUGUUCACAUCUU CCGGUAGUCCUGUCGCAGAUGACUC UCGCCAAGCCCCUUUCUCUAAGUCU AAUUAAUUUGAAUUCAAUGUGGUAG GACGAGAGUCAUCUGUGACAGGAUU AUGGAUGAUCGAGUUAUCAAAGGCG UUUU										
sga-MIR8019-2		237	sga-miR8019-2-3p	CAACUAAUGGUUUGGUUUGACUUG	164-187	stu-miR8019-3p	6	0	24	24	2
sga-MIR1055		294	sga-miR1055-5p	ACAAGGUUGUAUUCCAGUGACA	104-125	ppt-miR1055	6	0	22	22	3
sga-MIR5030		114	sga-miR5030-5p	UAAACAAUUUGUAUUAUAGUGA	3-24	gma-miR5030	7	0	22	22	3
sga-MIR1919-5		154	sga-miR1919-5-5p	UGUCGCAGAUGACUCUCGCCA	36-56	stu-miR1919-5p	2	0	21	21	1
			sga-miR1919-5-3p	ACGAGAGUCAUCUGUGACAGG	102-122	stu-miR1919-3p	0	0	21	21	1
sga-MIR5225b	AUGAUCGCAAUCAAACAUGAUCGGA UCUGGCCAUCCACGGCUUUCGGCG GCAUGGCCGGAUUGGUUUUUUCUG AUUUGUCCGUGGCGGUGAUGACUG CCGGCGGCGGUUCAGUCUGUGAUA GUUGAGAAGGUGUAUAGGUCUUGU CUUGUGACUUUUGUGGGGAGCAUAA CUCAUGUAGACUUGAUUAUCCUAGA CAUGGUUGAUUUCGAUGUA	214	sga-miR5225b-3p	UCUGUGAUAGUUGAGAAGGUGU	113-134	mdm-miR5225b	6	0	22	22	1
sga-MIR10532-12	AAAUUUUGGGAAAAUACCCAAGUAC CCCCUCGACCUAUGCCCGAAAUUUA CGUAAGCUAAAAAGGGGUAAAAAAU	184	sga-miR10532-12-3p	UAAUGUGUCUCUGAGAUUUCGGGC	122-145	sly-miR10532	2	0	24	24	2

sga-MIR2118a	UAUUAAUAAAAUAAGUUCAGGGGGG UAAUAGGACCUUAGUAUAGUAUAAU GUGUCUCUGAGAUUUCGGGCAUAG GUUGAGGGGGUACUUGAGCAUUAU CCCUAAAAAAA AUUUCUGCAAAAAAGAAAUUGAUAAU UUAUUAUCAAAGGGACUUAUAAAAC CCUCUAAAUCUCAUGGUCUUGUACU GCAUUUUAUGUUAAUAAAGCUGCAG AACAAGAAAGAGGUGUUCCCAGGUU GGUAAUAAAUUACAAGCCUUUGAAC AAAGUUUUAAAAUGCAUAAGGUAUC CCAUUCCUAAUAAAAAAGAUCUUCU UUCCAGAUUA	211	sga-miR2118a-3p	UGCAUAAGGUAUCCCAUUCCUA	164-185	ata-miR2118a-5p	4	0	22	22	1
sga-MIR1313d	GUACUAUUACCACUGAACAUAUUUU AUAAAUUAUUUUUUACACUUUUUCG CGUGGAACUAUCUUGUGGGCAUAAC GCGUGUUGACAUUUUGUUUCAAGCU AGUGUCACGUAGAUCGAAAAGGGGU AAAAAAUUAUUUAUAAAAUAAAUUCA CGAAUAAUAGGAU	164	sga-miR1313d-5p	UACCACUGAACAUAUUUUAUAA	8-29	pab-miR1313d	6	0	22	22	1
sga-MIR8781a-4	CUUUAAAUUGAUUUUCAAAUCACAA UUAUGACUUUCAACUUUGGGUGUGC ACAAGUAGACACUUAAACUUGUAAAA UAGACACACAUAUCCUAUAUGUCAU CCUACAUAUCAUUUUUUGUCCUACG UGGUGUCCUACAUGUAUUUUGUCAU GUAGGACUCGUAUGUUUAUUUAUUU AAAAGUUGGAUAAUUAAAGUGUCUG UUUGUUCAUUAUGAAAGUUGGAGGU CAAAGUUAAAAUUUGAAGCCAAGUU UAGGG	256	sga-miR8781a-4-3p	UGUUUAUUUAUUUAAAAGUUGGAU	164-187	gra-miR8781a	6	0	24	24	1
sga-MIR8006-12	UUAUCAUAUUUUUAGGAUAUUGAUG UCUCUGCCGCCUAAAAACUAGAGUA UAUGUACCCUUCACUCUAACGGAAG ACUAAAUAUGGACAUAUGGUGCAAU UUUAUCCGUCAAUAAAUGUCGAAUG GGUGGAUAAGAUUAUGACACGUGUA UGUCCAUUAGUAUAACAAAUAUAUA UGCUCUAGUUUUUGGACGUCAAGG GCAUCAAUGUCCCAAAAAUAGGACG G	225	sga-miR8006-12-5p	GUCUCUGCCGCCUAAAAACUAGA	25-47	stu-miR8006-3p	6	0	23	23	3
			sga-miR8006-12-3p	UAGUUUUUGGACGUCAAGGGCAUC	181-204	stu-miR8006-5p	3	0	24	24	1
sga-MIR167h-5	CUGAAAAUAGCUAUAAAAUGGGAGA AAUUAAUCCAUAACCUUGGGUACAG UGAGGGGAUUGAAUUUCUUAAGGAC AUACAGUAGUUUCUGUGGACUCGGA UUAAUUCUUGUAUUUUAUGUAUUUU AUG	128	sga-miR167h-5-3p	AGGACAUACAGUAGUUUCUGU	71-91	osa-miR167h-3p	6	0	21	21	1
sga-MIR8033	GCAUUAGCUGGAGUACAAGCUUCCA AAGCUGCAGAAAUGAGUUUUUUUUU UUUAACUGAAAAAGAAAAACUAUUUC UGCAGCUUUGGAAUUUUUUACUCCA GCUAAGUU	109	sga-miR8033-5p	UUCCAAAGCUGCAGAAAUGAGU	21-42	stu-miR8033-5p	0	0	22	22	1
			sga-miR8033-3p	CUAUUUCUGCAGCUUUGGAAUU	70-91	stu-miR8033-3p	6	0	22	22	3
sga-	UUGCAAGUAAGCACUCCAACUUUAA	229	sga-miR7992-16-3p	UGUCUAGAUGUGCAUACUCAAAA	188-	stu-miR7992-3p	6	0	23	23	1

MIR7992-16	AGGGUGCACAUCCAGACAUCUCAAC UGCCAACUAAAAACUCCAACUUGUC UCACUUUGUCUCGUAGACACCUGAU GCUGAUGUGACACAAAUUUUGGAGG UGUCGAGAUGAUCAUUUUUGUCAGC UGGAGUGUUCAACUACCACAAUGGA GAUGAGUUGAGGUGUCUAGAUGUG CAUACUCAAAAGUUGGAGUGUUUUU UGUUU				210						
sga-MIR845b-3	AAGGGUCGUGACAAACUUGGUAUCA GAGCAUUAGGUUCGUUGGUCUCAUC ACACAAGAACGAGUCUAGUAGAGUC UUAAGGAACGGUAGGGGGACGCCU UUACUUUUCUUUGAGAGGCUAUAAG ACUUUAGGAAAAUUCCAUUCUUUCA AUCUUUCUUUCGUGCUAUUACUUGG GUCCAAUUAAUAUCUAGGUGAUACA AAUUGGUAUCUGACCAUC	217	sga-miR845b-3-5p	AAACUUGGUAUCAGAGCAUUA	13-33	aly-miR845b-5p	6	0	21	21	3
sga-MIR1886f	AUUAUAUCACGAUAUGGUAUCGUGA GAUGGAAUCAGCGUUUAGACAUGUG AUUUCACGCUAAUUUCAUCUCAUGA UAUGGAAUCAUGAGAUGUG	94	sga-miR1886f-5p	AUGGUAUCGUGAGAUGGAAUCAGC	14-37	stu-miR1886f	1	0	24	24	1
sga-MIR1888a	ACACACUUAUACUAUACUAAGGUCC UAUUAUCUCUUGAACUUAUUUUAUU AAUAAUUUUCUAUCAUUUUUCGACC UACGUGACACUAUCUUGUGGGCCCA ACGCUGGUUGACUUUUUUCUUCAAG CUAGUGUCACGUAGGUCGAAAAUGG GUAAAAAAUUACUUAUUAAAUAAGUU CAGAUUUUUAAUGAUUAGGAUUAUA AUGCAA	207	sga-miR1888a-3p	UAAGUUCAGAUUUUUAAUGAU	171-191	ath-miR1888a	5	0	21	21	1
sga-MIR8037	UAAAAAUGCAUUUAUUUGGAAUAAU AGUAACCAUGAAUAGUAAGAGUCAA GUUACUGUGUAAAUAGUAAGAGUCA AGUAACUGUGUAAAUAGUAAAGGCC AAUCGUCCUUUAGCAAGGAUGAAAG GUCAUUAUGUAUGUCUAUAUAAGAG GCAUUUACC	159	sga-miR8037-5p	UUUAUUUGGAAUAAUAGUAACC	11-32	stu-miR8037	5	0	22	22	2
sga-MIR399r	AACUAUGUAUGGAUGCAUUACUGGG CUAAUCUUCUUUGGCAAAUAGCCAC AUUUUCACUAUAUUAUUUAGUGCAA GUUUGUUCAUUUUUUGCCAAAGAAG AUUUACCCCGUAAAUCACCCAUACA AUAUAU	131	sga-miR399r-3p	UGCCAAAGAAGAUUUACCCCG	90-110	mtr-miR399r	1	0	21	21	1
sga-MIR399a	GACAAGAAACGCAGGGUAUUCUCCC UUAGCAAGAUUGCUUUAUGCAUGAA UUAAAUUCUUUCUUGCCAAGGGAGA AUUGCCCUGCGUUUCUUCAU	95	sga-miR399a-3p	UGCCAAGGGAGAAUUGCCCUG	64-84	ata-miR399a-3p	1	0	21	21	1
sga-MIR478f	UAACUAUAAAGGAAAAGUGGACAAG UAAUUAGGGACGGAGGUAGUAUUUU GCACUUAUUUUAUCCUUGCUACUCC CUCCGUCCGGAAUUGUUUGUCAUGU UUUCUAUUUUUAGAGU	116	sga-miR478f-3p	UGUCAUGUUUUCUAUUUUUAGAGU	93-116	ptc-miR478f	4	0	24	24	1
sga-MIR7724b	CCAUGAACUUAUUUUAUUAAUAAUU UUUCAUCCCUUUUUGGCCUACAUUA UCUUGUGGGCCAAUACUAGUUGAUU UUUUUUCAAGCUAGUGUCACGUAGG	142	sga-miR7724b-5p	UUGGCCUACAUUAUCUUGUGGGCC	38-61	bdi-miR7724b-3p	7	0	24	24	1

sga-MIR171h-2	CCCAAAAAAAGGUAGAAAAUUACUUA UAAAAUAAGUUCAGUU CGGAAUCGAUAAGCCGAACCGAUAA AAAAGUUAUUGGUUUAUAGUAUUGG GUUAUUGAUUUAGUGGUUUUGAUAA UGGUUUUGACUUUUUUUUUGUUAUC GGCUUAUCGAUUUUU	115	sga-miR171h-2-5p	AUAAGCCGAACCGAUAAAAAA	9-29	lus-miR171h	6	0	21	21	1
sga-MIR482b-4	GUCAUGGCAUGAGGUGUUUAAAAUG AACAAAUCUAAGUUAAUGUGUCAAA GUGAAAAUUAGUGACAAGUUUAGGG GGCCACCGAUGGGUUAGGCCUUUAA AAUAUAUAUGCAUGUGGGACCACUU CUUAGCUACUUGGAAUAAAAAAAUAA GUCUUUUAUGUCAUUAAUUUUUGCU CACUUUAACUAAGUUGAACACUAAAA UCUACAUCAAUGUCAUAAU	221	sga-miR482b-4-5p	GGCAUGAGGUGUUUAAAAUGA	6-26	ptc-miR482b-5p	4	0	21	21	1
sga-MIR7519	AAAUGAACUUAAUGGACUGAAUCUG AUUGAUUCAAAUUCAGACUUAAAAC CAAAUUUACUUAAUGGGCUGAAUCU GAAUGAUUAAGAUUCAGACCUCCAU UAAAUGCAAAC	111	sga-miR7519-3p	CAAAUUUACUUAAUGGGCUGAA	51-72	lja-miR7519	6	0	22	22	1
sga-MIR5014a-12	AUACACAAACAGACACUUUAAUUAUU CAACUUUUAUAUAAAUAAACACAUGA GUCCUACAUGACAUAAUACACGUAA GACACCCCAUAUGACAAAAAAUGAUA CGUUAUGACAUGUAGGACAUGUGUG UCUAUUUGUUCAACUUUAUACAAGU UUAAGUGUCUACUUGUGCAC	173	sga-miR5014a-12-3p	UUAUACAAGUUUAAGUGUCUA	144-164	ath-miR5014a-3p	5	0	21	21	1
sga-MIR5014a-13	UUGGUUUCAAAUUUUAACUUUGACC UCCAACUUUAAUAAUGCACAGACAG ACACUUUAACUAUCCAACUUUUAAAU AAAUAAACACAUGAGUCUUACAUGU CAAAAUACACGUAAGACACCACGCA GGACGAAAAAUGACAUGUAGGACAU GCAUGUCUAUUUGUUCAAUUUUAUA CAAAUUUAAGUGUCUACUUAUGCAC ACCAAAAGUUGAAGGGCAUAAAUGU GAUUUGAAACUAA	239	sga-miR5014a-13-3p	UUAUACAAAUUUAAGUGUCUA	172-192	ath-miR5014a-3p	4	0	21	21	1
sga-MIR7492f	UUUGACAUUAUGACAAUUUGCAUCC UACGUAGUGUCCUACGUCACUAUAA CAAAAAUGAUCAUUAGCGGCAAUUA AUCUUAAUUACCGCUAAAUAUAUAU UUUUAGUGGCAAUUGACACUCAUUG UAUAUGUCCAUAAAGUCUUU	145	sga-miR7492f-3p	AAAUGAUCAUUAGCGGCAAUU	54-74	gra-miR7492f	5	0	21	21	3
sga-MIR7983-6	CCUACGUCACUAUAACAAAAAUGAU CAUUAGCGGCAAUUAAUCUUAAUUA CCGCUAAAUAUAUAUUUUUAGUGGC AAUUGACACUCAUUGUAUAUGUCCA UAAAGUCUUUAGCGACAAUUGACAC UCAUUGUAUAUGUCCAUAAAGCCUU UAGCGACAUUGGUUCUAAUAACACU UAAAUAAUGCCGGUAAAGACUUCAA CACUCUUUAUUAAUGUCAAUAUUUA AUGCCGCUAAAAGUUAUUUUUGUUG UAGUGCAUGUUUU	263	sga-miR7983-6-3p	UAAAGCCUUUAGCGACAUUGGUUC	142-165	stu-miR7983-5p	1	0	24	24	1
sga-MIR5653	GUUCAUAGACGUCAACAUUUGAUAU UCUUUGUAAGAGAGUAAUAUUGUUC	302	sga-miR5653-3p	AGGGUUGGGUUGGGUUGGGUUGGA	179-202	ath-miR5653	5	0	24	24	2

sga-MIR859-3	AUUUUUAGGUUGAAGGGUAAACCCG UCCCAACCCGUGGCCCGCUUGGGA CUGGAUUGAGCCGCUAUAUUAUUGG CCCUUUAAUUAAAAGGGUCAGCCCG CCCCAACCCAUUUAACUCUCUAGCU CGUUAGGGUUGGGUUGGGUUGGGU UGGACCAACCCAUUUUGACACCUCU AAUCCAAAUUUUACAUUAUAAUUUUU UUUUUAUUUGAUAGUGAUCUAGUUA UUAUAGAAUAUAUUCGACAUCUAUG GGA	124	sga-miR859-3-3p	CCUCAAUUGUGUGAAGUCACA	60-80	ath-miR859	6	0	21	21	2
sga-MIR10202b-2	UUUUUUUGUAAUUUUGUGCAACUUU UUAGCUUACGUGACAUCUAAAUAUA UCCCACACGCCUCAAUUGUGUGAAG UCACAGAGUGUGCCACGUAAGACAA AAGGUGUACAAAAUUACUAAAGUC AAAAAAUCUUAUGGCUUACGUGGCA CUAUCUUGUGGGCCCAACGAUGGUU GACUUUUUUUUUGAACUAGUUCCAC GUAGGCUAAUAUUUCAG	92	sga-miR10202b-2-5p	CUUGUGGGCCCAACGAUGG	30-48	vca-miR10202b-3p	6	0	19	19	3
sga-MIR2671i	UUGCAUGUGUAUAUACAAUUUUCUC ACGCUUUAUACAAAUAGAAACGCAA UUUAUACAUUUCGUUUCGGUUUGUA UAAGUGAGAAAGGCGAGGGUGGCG AGCGAGAUCUGGAAGAGGGGAGAGA GAGGAACAAAAAUAUGUGUAUUUAU ACAAUUUUCUAUGUUUUAUACAAUU GGAAACAAUUUUUAUACACUUGUGU UUUUGGAUCUUCCGCAUUAUUUUUG	199	sga-miR2671i-5p	UUAUACAUUUCGUUUCGGUUU	52-72	mtr-miR2671i	5	0	21	21	1
sga-MIR7492d	UUAUUCAUAGUUAAACUAUUUGUAA AUGUUGGGGUUUAGAUUUGUUGGU UCGCUCACCUAGUAGGUUAAGUGUG GGUGGAUAAAAUAAUAAAUCACCAU AAAUGUUCGGGAAGAUUCCACUU	147	sga-miR7492d-5p	GGGGUUUAGAUUUGUUGGUUCGCU	56-79	gra-miR7492d	7	0	24	24	2
sga-MIR10224	AAGUGUAUAGGAUGAAGAUAUAUGU AUUUGCAAGUGUAUAUACAAUUUUC UCUCACUUUAUACAAACAUAAAACAC AAUUUAUACAUUUCCUUUCUGUUUG UAUAAGCGUAGAGACGAGGGUGGC GAGCGAGGUUCGGGAGAGUGACGA GAGAGAUCUGGGAGAGAGCCGAACG GAAAUGUGUAUUAUAUAAUUUAUAA GUAUAUAAGACGAAAAUAUAUGUAU UUGCAGGUGUAUAUAUAAUUUUCUC UCACUUUAUACAAAC	264	sga-miR10224-3p	AAAUAUAUGUAUUUGCAGGUG	213-233	eun-miR10224-3p	5	0	21	21	2
sga-MIR7748a	AAUGAUAUACAUAUCUACUUUUGAG ACAUUAGUGCCCCUGUCGUCAAAGA AUUAGAGCAUAUAUAUCCUAUAUAC UAACGGAUAUACAUGUGUCAUAAUU UUAUCUAUCUAUCCGACAUUUAUAC CAUUUAUACUAACAAACAUACACAUG UCAUAUUCUUAUCUACCGAUCCGAC AUUUAUCGACGGAUAAGAUUAUGCC ACGUGUCCCUAUUUAGUACUUCGUU AGAGUGAAGGGAAUAUAUGCUCUAU UUUUGGACGGCAAGAGCGUCAGGAU CACAAAAGUACGACGAAGGAUAUCU	303	sga-miR7748a-3p	AAUAUAUGCUCUAUUUUUGGACGG	238-261	bdi-miR7748a-3p	4	0	24	24	1

sga-MIR7122a	GC UUAUCUCGCUUUUAUUACAAACACA AACGCAAUGUAUACAUUUGUAUUUG UAUAAAGUAAGAGAGUUGAGCGGCA GUGGCGAGCGAGAUUUAGGAGAGG UGAGAGAUGAGAACAAAAAUAUAUG UAUAUAUACAAUUUUCUCUCGCUUU AUACAAACACAAACACAUUUUAUACG GUUUUUGUUUGUAUAAAAACGAGAG AG	202	sga-miR7122a-3p	ACGGUUUUUGUUUGUAUAAAA	173-193	ppe-miR7122a-3p	5	0	21	21	2
sga-MIR7997c-16	AUCAAGGCUAUGUUGCUCGGACUCU UCAGAAACGUCGCCGGGUGCGUGU CGGAUCCUCCAAAAGUAAAGCAUUU UUGGAAGAUCCGACACAGGUGUGGU AGCAAUUUUGGAGAGUCCGAGCAAC UUAGCCUUAAG	135	sga-miR7997c-16-5p	AUGUUGCUCGGACUCUUCAGAAAC	10-33	stu-miR7997c	3	0	24	24	1

Supplementary Table S10. Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum chilense*.

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
sch-MIR319b-1	AAGAGAGCUUCCUUUAGUCCACUCAUAGGUAGACGAAGGAUUUGAAUUAUCUCCCGACUCAUUCAUUCAAACGCAAUAGGAAGUAUGUAAUCUUAUACUAUUGUGAAUGUGUGAAUGAUGCGGGAGAUAAAUUCUCUCCUUUUUAUCUGUGCUUGGACUGAAGGGAGCUCCCU	173	sch-miR319b-1-5p	GAGCUUCCUUUAGUCCACUCA	5-25	mtr-miR319b-5p	1	0	21	21	1
			sch-miR319a-1-3p	UUGGACUGAAGGGAGCUCCCU	153-173	aof-miR319a	0	0	21	21	1
sch-MIR167d-1	AACUAACAGGUGAAGCAACCACAUGAUCUGAUCUUGCCUUAAUAUAAAUUUAUAGGUAAGUUUAGAUCAUGCUGGCAGCUUCAACUGAUA	90	sch-miR167d-1-5p	UGAAGCAACCACAUGAUCUGA	11-31	eun-miR167d-5p	2	0	21	21	1
			sch-miR167h-1-3p	AUCAUGCUGGCAGCUUCAACUGAU	66-89	gma-miR167h	1	0	24	24	1
sch-MIR169c-1	UGAAGAGGGGUUUUACAUGAAGUUGAGAGUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAGACCUUAGCUUC	177	sch-miR169c-1-5p	UAGCCAAGGAUGACUUGCCUA	40-60	ata-miR169c-5p	0	0	21	21	1
			sch-miR169e-1-3p	GCAAGUUAUCCUGGCUAUC	120-138	stu-miR169e-3p	0	0	19	19	1
sch-MIR395c-1	GAGGGCUUACUUUGAUGUUAGAAGCCUUGUUGAAGUGUUUGGGGGAACUCCUUGGUUGACUUUGAAAAUCAUGCAAACAAGUAUAUACAAAUGCAUGAGUAGGUAUUAGCUAGAGAUGAUGAAUACAAUAUUGAUUCACGUAUAAAUCUACCUCUGGAGUUCCCUAGACCACUUCAUGAGAGCUUAAUAUUUCAUUGUUUUAAGUCAU	208	sch-miR395c-1-5p	UUGAAGUGUUUGGGGGAACUC	30-50	cme-miR395c	0	0	21	21	1
sch-MIR156b-1	GUUGUUGACAGAAGAUAGAGAGCACAGAUGAUAAAGUGCAUGGAAAUUGUCCGCACCUUACUCCUUUGUGCUCUUUAUUCUUCUGUCAUCAU	92	sch-miR156b-1-5p	UUGACAGAAGAUAGAGAGCAC	5-25	aof-miR156b	0	0	21	21	1
			sch-miR156h-1-3p	GCUCUUUAUUCUUCUGUCAUC	70-90	mtr-miR156h-3p	0	0	21	21	1
sch-MIR393	CAGCAACUUAAGGAGGCAUCCAAAGGGAUCGCAUUGAUCCGAUUUCUAUCUAUGUUGUUCAGAUUCUUCAGAAAUAUUAACAGGUACGUGUAGAAUUCUUCAAACAUGUUAUAUUUUUGGAAGGAUUCAAUAUGGUACAACAAUGUUUUUUUUAGGGUUCGAGCAACAUA	170	sch-miR393-5p	UCCAAAGGGAUCGCAUUGAUCC	19-40	cas-miR393-5p	0	0	22	22	1
			sch-miR393-3p	UUUUUUUAGGGUUCGAGCAAC	147-167	sly-miR5303	3	0	21	21	1
sch-MIR172c-1	AACACAGUUGUUGUUUGCAGAUGUAGCAUCAUCAAGAUUCAUACAUGAAAAUUAAGAGGCAAGGUUAAAUAUGUAGCUUUAAUUUGAAAUGAAAUAUAUUAUAUAUCAUGACCAUGUCUAUUUAUUUCAAAGUGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAAUAACUAUCGGUGACAGAGUCAGA	188	sch-miR172c-1-5p	GUAGCAUCAUCAAGAUUCAUACA	23-45	ata-miR172c-5p	2	0	23	23	1
			sch-miR172-1-3p	UGAGAAUCUUGAUGAUGCUGCAU	133-155	aau-miR172	0	0	23	23	1
sch-MIR171f-1	UGAUGUUGGAAUGGCUCAAUCUAAUAAAAGUUUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAUAUCGUC	87	sch-miR171f-1-5p	UGAUGUUGGAAUGGCUCAAUC	1-21	zma-miR171f-5p	2	0	21	21	2
			sch-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	59-79	aof-miR171a	0	0	21	21	1

sch-MIR5300	UGACCAAAAUUCUUCUUCCCCAGUCCAGGCAUU CCAACAGUUGAUAACAUCUAGAUCUGUCAAUCCU UUGUAUUUUUUGUUCUUCUAUUUUUCACAUGAC AUCUUCAAAAUCCACUCUGAGCUUCAUCAUAAGC UAAGAAAUGGUGAGUUUUGAUGAUGUGAUGCCU AAAAUAGGAUUAAAUGAAAGUACUAGUAAAAAGG UGUUCAAAUCUGGAGGUUAUGUUGAGCUGGUGG UAUGCUUUGAUUGGGAAAGAUGACUUAGGUC	265	sch-miR5300-5p	UCCCCAGUCCAGGCAUUCCAAC	17-38	sly-miR5300	0	0	22	22	1
			sch-miR5303p	UGAGUUUUGAUGAUGUGAUGC	145-165	mes-miR172c	5	0	21	21	1
sch-MIR482e	GAUCUGAGCUAUGGAAAUAUUGAUGGCGUUGAA AGGGAUGAGAGUAUUGGGAAGUUGUUGGUUGUG GGUGGGGUGGAAAGAUUUGAUAAAUCUAAAUUU UUUUUCUAAUUGAAAAAAAAAAAUGGAAAAGAGAU UAAAUCUUUCCUACUCCUCCCAUACCCAUGACUU CCACUAGCUUCUCCCUUUCUUCAUUUGUCAUCU CCUUUGCUAAGUU	213	sch-miR482e-5p	UGUGGGUGGGGUGGAAAGAUU	63-83	sly-miR482e-5p	0	0	21	21	1
			sch-miR482e-3p	UCUUUCCUACUCCUCCCAUACC	138-159	sly-miR482e-3p	0	0	22	22	1
sch-MIR396b-1	AUGGUCCUUUUUGUGUUUUUCCACAGCUUUCUU GAACUGCAUCUACAAUUUCAAUUCAUUAUGAAAA AAAGAAAAAAAUUGAUUCAUAUUGUUGUUGCGGUU CAAUAAAGCUGUGGGAAGAUACAGAUAGGGUCA	134	sch-miR396b-1-5p	UUCCACAGCUUUCUUGAACUG	19-39	aof-miR396b	0	0	21	21	1
			sch-miR396c-1-3p	GUUCAAUAAAGCUGUGGGAAG	99-119	fve-miR396c-3p	0	0	21	21	1
sch-MIR6022	UACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAG UUAUUUAGACCCGAGUUUUAACCAAUUGCACAGU CCUCUACCCAAGAUUGAGGUUUCGUAAAAUGUAA CUUAAGAUCAAGUCGCGUUAGGUUCAUGAAGUU UUGAAUUGACUUAGGAAGAGUACCUUGCAACUAA AAACUUUGAGCCGAAAUAAGUUAGUGAUGGAAAG GAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGG	236	sch-miR6022-3p	UGGAAAGGAUAAUAUCCAGGA	197-217	sly-miR6022	2	0	21	21	1
sch-MIR7997b-1	AGCAACAAUCUCUGUUCAUAUUCCAUGAGACUGU UUUUGGGUAAGAUUGUUUAUCAUAAUAAUCAUAA AUACUAGAUGACCGUGCUUGUUGUCUAUGUUGC UCGGACUCUUCAAUAAUUUCAAUGGAUGCGUGU UGGAUUCACCAAAAGUAGUGUAUUUUUGGAGAA CCUGACACGGGCGCGGCAUCGAAAGUGAAUAGU CCGCGCAACAAGUAGGUCCCUCGUCAAGUGUUU GU	235	sch-miR7997b-1-5p	AUGUUGCUCGGACUCUUCAAU	95-115	stu-miR7997b	2	0	21	21	1
			sch-miR7997-1-3p	AUUUUUGGAGAACCUGACACGGGC	156-179	stu-miR5303f	2	0	24	24	1
sch-MIR6024-1	UAACUGGAGAUGGGGAAGUGGAGAAACAACACU UGCUAAAGGAACUUCACCAGUCAUCUCUUUUCU UUUGGAGUUUUUUUAGCAAGAGUUGUUUUCCCU CUUCUCAAUUCCGUCUCUC	118	sch-miR6024-1-5p	AGAAACAACACUUGCUAAAGGA	22-43	stu-miR6024-5p	1	0	22	22	1
			sch-miR6024-1-3p	UUUUAGCAAGAGUUGUUUUCCC	77-98	stu-miR6024-3p	0	0	22	22	1
sch-MIR6024-2	AACUGGAGAUGGGGAAGUGGAGAAACAACACUU GCUAAAGGAACUUCACCAGUCAUCUCUUUUCUU UUGGAGUUUUUUUAGCAAGAGUUGUUUUCCCUC UUCUCAAUUCCGUGUCU	116	sch-miR6024-2-5p	AGAAACAACACUUGCUAAAGGA	21-42	stu-miR6024-5p	1	0	22	22	1
			sch-miR6024-2-3p	UUUUAGCAAGAGUUGUUUUCCC	76-97	stu-miR6024-3p	0	0	22	22	1
sch-MIR6025e-1	AUUUGUAGUUAUUUCAUGUAUACUUGCAUAAAAA UAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGG CAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGU GUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCC AAUUAUUGAGAUGGCAUCUCGGUUUGUUAG	164	sch-miR6025e-1-3p	UGCCAAUUAUUGAGAUGGCAUC	131-152	nta-miR6025e	2	0	22	22	1
sch-MIR6025e-2	AAAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUG UUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUG AAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGC AUGCCAAUUAUUGAGAUGGCAUCUCGGUUUGUU AGUUGCUGUGCAGUAUGAUCACUGUGGCAGG	164	sch-miR6025e-2-3p	UGCCAAUUAUUGAGAUGGCAUC	102-123	nta-miR6025e	2	0	22	22	1
sch-MIR6026	CCACUUUGAUUUGGUAAUACAACUAUAGCCAAGA CAAUGCUUCAUUGUAAGUGCAUAACUUUUCACUU	244	sch-miR6026-5p	AAUACAACUAUAGCCAAGACAA	16-37	stu-miR6026-5p	1	0	22	22	1

	UAUUGUUUGAGCAUUGUGUUGAUUUCUCUUAAC UUGUUUUUCGUUGAACAAAACUGUUUUUUCAUA UACUCGUGAAAUGCAACACUGUGCGCAGAAGUU AAGAGUGAAAUGUUAUGCAUUUGUGAUUAUAUAU UUUCUUGGCUAGAGUUGUAUUGCCAAGUGAAGU GUUUUAAUUG										
			sch-miR6026-3p	UUCUUGGCUAGAGUUGUAUUGC	203-224	sly-miR6026	0	0	22	22	1
sch-MIR395c-2	AUUGUUUGAUUCCCUGCUGAAGUUUUUGGGGGA ACUCUUGGACUCACUUUGAAAUUUUACACAAGCA AAUAGAAGUGUAGGAGUCCUGGAUGUGGAUAAU GAACGAGAUAGUUCACGUAUAAAUCUAUCAAGGU GUUUCCUGGAGUUCCCUUGACCACUUCAUGAGG GCUUACUUUGAUGUUAGAAGCCUUGUUGAAGUG UUUGGGGGAACUCCUUGGUUGACUUUGAAAAUC AUGCAAACAA	243	sch-miR395c-2-3p	UUGAAGUGUUUGGGGGAACUC	193-213	cme-miR395c	0	0	21	21	1
sch-MIR169a-1	UUUUUGUGGAAGGGAGUUUACAUGAUAGAAAUG GAGAGUGGAUUGCAGCCAGGGAUGACUUGCCGA UGAUUUCUUUUGUAGUUUUCCUAUUAAAGAUUA UGUAUCGGCAAGUUGUCCCUGGCUACCUUUCGC UCUCUUCUUCUCAUGCAAAUUUUUUACUAACACU UAUGUAUUUUUAUUUU	182	sch-miR169a-1-5p	CAGCCAGGGAUGACUUGCCGA	46-66	cas-miR169a	1	0	21	21	1
			sch-miR169d-1-3p	GGCAAGUUGUCCCUGGCUACC	106-126	ata-miR169d-3p	2	0	21	21	1
sch-MIR172d-1	AGUCAAUUUUUUGCGGGUGGAGCAUCAUCAAGA UUCACAUAGCUAUAUUAGGGAUUUUAUAAUUUUU AAAAACCCUAUGGGCGAUGUGUGGGAAUCUUGA UGAUGCUGCAGCGGCAAGUAAUGGCUAUUU	130	sch-miR172d-1-5p	GGUGGAGCAUCAUCAAGAUUCACA	16-39	mtr-miR172d-5p	1	0	24	24	2
			sch-miR172e-1-3p	GGAAUCUUGAUGAUGCUGCAGCGG	91-114	gma-miR172e	1	0	24	24	1
sch-MIR167b-1	CUACUAUCAGUUGAAGCUGCCAGCAUGAUCUAAA CUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGA UCAUGUGGUUGCUUCACCUGUUAGUUC	95	sch-miR167b-1-5p	UGAAGCUGCCAGCAUGAUCUAA	12-33	bna-miR167b	0	0	22	22	1
			sch-miR167d-1-3p	AUCAGAUCAUGUGGUUGCUUCACC	63-86	csi-miR167d-3p	2	0	24	24	1
sch-MIR398-1	AUUCAAUAGGGGCAACUUGAGAUCACAUGUUGU CACUUUUUUUUUUCUGGUUUGAUUUGAUGAAUC AGUAUCUCAACAUGUGUUCUCAGGUCGCCCCUG UUGAAUU	106	sch-miR398-1-5p	GGGGCAACUUGAGAUCACAUG	9-29	hbr-miR398	3	0	21	21	1
			sch-miR398-1-3p	UGUGUUCUCAGGUCGCCCCUG	79-99	aof-miR398	0	0	21	21	1
sch-MIR477b-1	GUCUUUUUUCACUCUCCCUCAAAGGCUUCUGGC UUAAGAUGCCUUUUGUGCUAAUGCUAGAGGUCU UUCGAGUGAGAGUGAAUAAAUUCU	90	sch-miR477b-1-5p	ACUCUCCCUCAAAGGCUUCUG	11-31	stu-miR477b-5p	0	0	21	21	1
			sch-miR477b-1-3p	GAGGUCUUUCGAGUGAGAGUGA	60-81	stu-miR477b-3p	0	0	22	22	1
sch-MIR477-1	GCAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCU CUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGG GGAGGAGUUCUUGUAGGGUGAGACAACAAGAAA UUCCUUGCUCACUUCACAUGGUAACAUACUUAUA	134	sch-miR477-1-5p	UGUCUCUCCCUCAAGGGCUCC	12-32	sly-miR477-5p	0	0	21	21	1
			sch-miR477-1-3p	AGUUCUUGUAGGGUGAGACAAC	73-94	sly-miR477-3p	0	0	22	22	1
sch-MIR482a-1	AAAAUCUAUGGGAAUUGGUGAGUUGGAAAGCUU UUCUUUUUCUUCUCCUUCUCUUGUGAUUAGCUU UCCAAUUCCACCCAUUCCUAUGUUUUUUC	95	sch-miR482a-1-5p	GGAAUUGGUGAGUUGGAAAGC	11-31	stu-miR482a-5p	2	0	21	21	1
			sch-miR482c-1-3p	UUUCCAAUUCCACCCAUUCCUA	65-86	nta-miR482c	0	0	22	22	1
sch-MIR1446	CAGAGUUUUCUGAACUCUCUCCCUCAAUGGCUG UUCAUAUAAUAUAUGCUGCUUCUUUGCAGCUUAA UUAAAUAACAGCUUUGGGGGUUUGAGUCCAGAA AAAUCUUG	108	sch-miR1446-5p	UGAACUCUCUCCCUCAAUGGCU	11-32	nta-miR1446	0	0	22	22	1
sch-MIR482b-1	UUCAGGAAGCUUUUGGAGUGGGUGGCAUGGUAA GAUAUCAUAUUUUGUUUUUCAUAAAAAAAAAAAU GAAAUUGAAAUCUUACCGAUUCCCCCCAUUCCAA UGGCUUCCAGUUAUUUCUCC	121	sch-miR482b-1-5p	GGAGUGGGUGGCAUGGUAAGA	15-35	stu-miR482b-5p	0	0	21	21	1

			sch-miR482b-1-3p	UUACCGAUUCCCCCCAUUCCAA	80-101	stu-miR482b-3p	0	0	22	22	1
sch-MIR156b-2	GGUGGUGACAGAAGAGAGUGAGCACACAUGGUG UUUUCUUGCAUGAUGUUUAUAUAUAUAUGCUUG AAACUAUGUGUGCUUACUCUCUAUCUGUCACCC	99	sch-miR156b-2-5p	UGACAGAAGAGAGUGAGCACA	6-26	hvu-miR156b	0	0	21	21	1
			sch-miR156k-2-3p	UGCUUACUCUCUAUCUGUCACC	77-98	cas-miR156k-3p	0	0	22	22	1
sch-MIR156f-1	CUGUUGACAGAAGAGAGAAAGCACAAUCUGUCAU CAACAAAAUGGUAUUUGUUGUUUGUUGAAAUGU GCUCUCUCUGCUUCUGCCAAUA	89	sch-miR156f-1-5p	UUGACAGAAGAGAGAAAGCACA	4-25	gma-miR156f	1	0	22	22	1
sch-MIR160h-1	UAUAUGCCUGGCUCCCUGUAUGCCAUUUGCAAA GUUCACCGUAAUAUAUCGAUGGGCCUUGUUGAA UGGCGUAUGAGGAGCCAAGCAUAU	90	sch-miR160h-1-5p	UGCCUGGCUCCCUGUAUGCCAUU	5-27	mes-miR160h	0	0	23	23	1
			sch-miR160-1-3p	GCGUAUGAGGAGCCAAGCAUA	69-89	eun-miR160-3p	0	0	21	21	1
sch-MIR164c-1	GUGACAGGUUAUUUAAGCUGGAGAAGCAGGGCA CAUGCUAGAAUACUCGGAUUUCUAUCCUUGAGA AUUUUGCAUGUGCCCUCGCCCUCCAGCUUAAAC CCCCGCCA	107	sch-miR164c-1-5p	UGGAGAAGCAGGGCACAUGCU	19-39	fve-miR164c	0	0	21	21	1
			sch-miR164-1-3p	CAUGUGCCCUCGCCCUCCAGC	73-93	stu-miR164-3p	3	0	21	21	1
sch-MIR164	GAUGGAGAAGCAGGGCACGUGCAUUACUAACUC AUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUG CUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGU UUGUACUUUACAUGUAUGUGGUAAAAUGAUGAG UUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUG AC	169	sch-miR164-5p	UGGAGAAGCAGGGCACGUGCA	3-23	aof-miR164	0	0	21	21	1
			sch-miR164a-3p	CAUGUGCCUGUUUUCCCCAUC	144-164	sly-miR164a-3p	0	0	21	21	1
sch-MIR397b-1	CAGAGUACUUAUAAACAUCAUUGAGUGCAGCGU UGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGC CUUCCUCAUUUUUCAUCAACGCUACACUCGAUCA UGUUUUUAAUUCUCUGAA	118	sch-miR397b-1-5p	UCAUUGAGUGCAGCGUUGAUG	18-38	mes-miR397b	0	0	21	21	1
			sch-miR397-1-3p	CAUCAACGCUACACUCGAUCA	80-100	stu-miR397-3p	1	0	21	21	1
sch-MIR166d	UUGAGGAGAAUGUCGUCUGGUUCGAGAUCUUUC AUAAGAAAGGUAAAUGAAUGAUAAGUUUUCAUAU AUGUAUCUUGAAUGAUUUCGGACCAGGCUUCAU UCCCCUCAACUCUG	114	sch-miR166d-5p	AGAAUGUCGUCUGGUUCGAGA	7-27	stu-miR166d-5p	0	0	21	21	1
			sch-miR166-3p	AUUUCGGACCAGGCUUCAUUCCCC	82-105	lja-miR166-3p	0	0	24	24	1
sch-MIR156b-3	GGGUAUUGAUUGUGUAAAAUGUAGGGAGGAGAA AAAAGAGGGGAAAAUGGAAUGGGUGAUAUUGUU GACAGAAGAUAGAGAGCACAUAUGAUGGAAUGC UGCUGCUAAAUCUGGAGAGUCUAAACAAUUAAAA AAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUU CCGUCAUCCCUUUCAUC	183	sch-miR156b-3-5p	UUGACAGAAGAUAGAGAGCAC	65-85	aof-miR156b	0	0	21	21	1
			sch-miR156g-3-3p	GCUCUCUAUGCUUCCGUCAUC	154-174	fve-miR156g-3p	1	0	21	21	1
sch-MIR156b-4	GGUGAUAUUGUUGACAGAAGAUAGAGAGCACAU AUGAUGGAAUGCUGCUGCUAAAUCUGGAGAGUC UAAACAAUUAAAAAAGCAUUUCACUUCAUUUGUG CUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCU UUUCCUUCUAUUUUUCUCUUUUCUCUCCCUAAA UCUAUACAAUAACUUGU	183	sch-miR156b-4-5p	UUGACAGAAGAUAGAGAGCAC	11-31	aof-miR156b	0	0	21	21	1
			sch-miR156g-4-3p	GCUCUCUAUGCUUCCGUCAUC	100-120	fve-miR156g-3p	1	0	21	21	1
sch-MIR160g	AUUGUUCUGCCUGGCUCCCUGGAUGCCAACUAA GAACAGUAUUGUCAAAAAAAUUGACACUCUUCCU AGUUGGUACCAGAGGAGACAGGCAGAUCCA	97	sch-miR160g-5p	UGCCUGGCUCCCUGGAUGCCA	8-28	lus-miR160g	0	0	21	21	1
sch-MIR319b-2	AGUAGGAGCUCCUUUCAGGCCAAGACCGAGGGA CGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUA UUGGUUAACCUUAACAAACAAAUUAUGUAUAGUU UUAAGAUUAACCAGUUGCAUGGCGAGGGAGCAA CUACUUCCGCUAACUUGUCUCACUUAUUGGACU	180	sch-miR319b-2-3p	AUUGGACUGAAGGGAGCUCCU	159-179	aof-miR319b	1	0	21	21	2

	GAAGGGAGCUCCUA										
sch-MIR159c	AAGGAGCUCUCUCCGGUCCAGUCCGAGGCACUC AAAGGCUAAAAACACAGCUGACGACUCGUUGAUU CUCAAACACAUCAAGAAGUAUUUUUUGAAAUUGA CGUGUUUAAGAUUCAACGAUGCGUGAGCUAUGU UUAGCUAGCGUUGUCACGUCUUGGACUGAAGGG AGCUCCC	174	sch-miR159c-3p	CUUGGACUGAAGGGAGCUCCC	154-174	csi-miR159c-3p	0	0	21	21	1
sch-MIR7528	GCUAAUCGAGUUUUAUAUUCGUUAAAUAUUGUUA UUUGCUUAAUUUUUUCAUUUUUGGAAAAAUAUG GCCGGUGAUGACAAAAGUAUUUGCACGAGCGGC AACAACAUCCUUUUUUGCGCAGUUGUUGUUGCU AUGAUAAAUGUGCCAAUAUGCUAAUCUGAGGCC CAAAUUGUUUCUUGUUCUUAGAUGUGUAUCGAG UGAAUUGCUAUUCGA	214	sch-miR7528-3p	CCAAUAUGCUAAUCUGAGGCCC	146-167	lja-miR7528	5	0	22	22	1
sch-MIR8011a-1	AUUAUGUGGGGCUUCUUUUUGUCCCACAAGUUG GUGAACCCAAAUCAUUACACUUCUGGGUCCACC GACUUGUAAAAUAAAAAGAAGCCUCACAGAACU	99	sch-miR8011a-1-5p	UUAUGUGGGGCUUCUUUUUGUCCC	2-25	stu-miR8011a-5p	5	0	24	24	1
			sch-miR8011a-1-3p	AAUAAAAAGAAGCCUCACAGAACU	76-99	stu-miR8011a-3p	1	0	24	24	1
sch-MIR8011a-2	UUCUGUGAGGCUUCUUUUUAUUUUACAAGUCGG UGGACCCAGAAGUGUAAUGAUUUGGGUUCACCA ACUUGUGGGACAAAAAGAAGCCCCACAUAAU	97	sch-miR8011a-2-5p	UUCUGUGAGGCUUCUUUUUAUUUU	1-24	stu-miR8011a-5p	4	0	24	24	1
			sch-miR8011b-2-3p	CUUGUGGGACAAAAAGAAGCCC	68-89	stu-miR8011b-3p	4	0	22	22	2
sch-MIR8021-1	UAUUCAAGGCUCAAACUCGAGACCUCUGGUUAA GGAUAGAUGGAUCAUAUACAACCCACCACAACUU UUAUGGUACUAAUAAUGACUUGAUUUACUUUCUC UUAAAUAUUUGACAAUAUGUUGAAUUUAUUUGUU GUAUUCUACCAACAAAGAUUUUGAUUGAGUGAAA GUUAGUAUUUAUUUAUCCUUAGCUAGAAGUGUC AGGUUCUAGUCUUAGACAU	221	sch-miR8021-1-5p	AUUCAAGGCUCAAACUCGAGACCU	2-25	stu-miR8021	0	0	24	24	1
sch-MIR8033	CUUCCAAAGCUGCAGAAAUGAGUUUUUUUUUCU UAACAGAAAAAGACAAACUAUUUCUGCAGCUUUG GGAUU	72	sch-miR8033-5p	UUCCAAAGCUGCAGAAAUGAGU	2-23	stu-miR8033-5p	0	0	22	22	1
			sch-miR8033-3p	CUAUUUCUGCAGCUUUGGGAUU	51-72	stu-miR8033-3p	5	0	22	22	3
sch-MIR8038b-1	CCUUGUGAGAAAGUUGAAUCUCACGCUUGUUAA GCCUCAAGAAAAGCACAAUGCGUUCCAGCGUCA UCUUGAAAAUCUUGAGUUUUUCAAUUUUCUCA	98	sch-miR8038b-1-5p	CCUUGUGAGAAAGUUGAAUCUC	1-22	stu-miR8038b-5p	1	0	22	22	1
			sch-miR6169-1-3p	GAGUUUUUCAAUUUUCUCA	80-98	hbr-miR6169	5	0	19	21	2
sch-MIR8042	AAUAAGCACUUCCAUCUAAUUUCUAAAAGGUGGU CAAGGAGGUGGUGAAACACAUGUGACUUGACAC AACUUUCAGAAAUUAGACUGAAAUGCUGAUCU	99	sch-miR8042-3p	AUUAGACUGAAAUGCUGAUCU	79-99	stu-miR8042	1	0	21	21	1
sch-MIR7122	UAUAUACAGAGAAACCGCUGUCGAUUAUAAUGAG AAAUUCGGUGUUUCUCAUACUCCACAGCGUUUU UCUGUAUAACC	78	sch-miR7122-5p	AUAUACAGAGAAACCGCUGUCG	2-23	stu-miR7122-5p	1	0	22	22	2
			sch-miR7122-3p	ACAGCGUUUUUCUGUAUAACC	58-78	stu-miR7122-3p	1	0	21	21	1
sch-MIR399j	AGGGCUACUCUCUAUUGGCAUACGCCGUGUAUC ACACAUUACAGCGAACACGCCAAAGGAGAGCUGC CCUA	71	sch-miR399j-5p	GGGCUACUCUCUAUUGGCAUA	2-22	stu-miR399j-5p	0	0	21	21	1
			sch-miR399o-3p	CGCCAAAGGAGAGCUGCCCUA	51-71	stu-miR399o-3p	1	0	21	21	1
sch-MIR399i-1	AGGGCUACACUCUAUUGGCAUGCAGCUUUUUUU GGUCGCUCCGAGUAGCAACUUGAUCAAAUAUUU GAGCUGAAAUGCCAAAGGAGAGUUGCCCUA	96	sch-miR399i-1-5p	GGGCUACACUCUAUUGGCAUG	2-22	stu-miR399i-5p	0	0	21	21	1
			sch-miR399i-1-3p	UGCCAAAGGAGAGUUGCCCUA	76-96	stu-miR399i-3p	0	0	21	21	1
sch-MIR319b-3	AGAGCUUUCUUUAGUCCACACAUGGGGAACGAU AGGGUUCAAUUUGCUGCCGACUCAUUCAUCCAA AUGUUGAGGUCUUGAUAAUCGAAUGCCACCUCA GCAACUGAGUGAAUGAAGCGGGAGUACAAGUUG AGUCUUGAGCUUCCUGUACUUGGACUGAAGGGA GCUCCC	171	sch-miR319b-3-5p	GAGCUUUCUUUAGUCCACACA	2-22	mtr-miR319b-5p	1	0	21	21	1

			sch-miR159c-3-3p	CUUGGACUGAAGGGAGCUCCC	151-171	csi-miR159c-3p	0	0	21	21	1
sch-MIR160c	UGCCUGGCUCCCUGUAUGCCACACACAUUCACCAAUACUUUGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGCAU	81	sch-miR160c-5p	UGCCUGGCUCCCUGUAUGCCA	1-21	aof-miR160c	0	0	21	21	1
			sch-miR160-3p	GCGUAUAAGGAGCCAAGCAU	62-81	eun-miR160-3p	1	0	20	21	1
sch-MIR172c-2	UGGAGCAUCAUCAAGAUUCACAUAGCUAUAUUAGGGAUUUUAUAAUUUUUAAAAACCCUAUGGGCGAUGUGUGGGAAUCUUGAUGAUGCUGCAG	94	sch-miR172c-2-5p	GGAGCAUCAUCAAGAUUCACA	2-22	cas-miR172c	0	0	21	21	1
			sch-miR172d-2-3p	GGAAUCUUGAUGAUGCUGCAG	74-94	sly-miR172d	0	0	21	21	1
sch-MIR172j	GCAGCAUCAUCAAGAUUCCCACACAUCGCCCAUAGGGUUUUUAAAAAUUAUAAAAUCCCUAAUAUAGCUAUGUGAAUCUUGAUGAUGCUCCA	92	sch-miR172j-5p	GCAGCAUCAUCAAGAUUCCCA	1-21	lus-miR172j	0	0	21	21	1
			sch-miR172-3p	UGUGAAUCUUGAUGAUGCUCCA	71-92	aau-miR172	2	0	22	23	1
sch-MIR156b-5	UUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUC	101	sch-miR156b-5-5p	UUGACAGAAGAUAGAGAGCAC	1-21	aof-miR156b	0	0	21	21	1
			sch-miR156g-5-3p	GCUCUCUAUGCUUCUGUCAUC	81-101	fve-miR156g-3p	0	0	21	21	1
sch-MIR167b-2	GUGAAGCUGCCAGCAUGAUCUAAACUUGGCCAUUUAUAAAGAAAAUGGGUGACUAAGGUUAGGUCAUGCUCGGACAGCCUCACU	84	sch-miR167b-2-5p	UGAAGCUGCCAGCAUGAUCUAA	2-23	bna-miR167b	0	0	22	22	1
			sch-miR167c-2-3p	GGUCAUGCUCGGACAGCCUCACU	62-84	stu-miR167c-3p	0	0	23	23	1
sch-MIR167b-3	UGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUAUGAAGAAAGAUCAGAUCAUGUGGCAGCCUCAC	80	sch-miR167b-3-5p	UGAAGCUGCCAGCAUGAUCUAA	1-22	bna-miR167b	0	0	22	22	1
			sch-miR167c-3-3p	AUCAGAUCAUGUGGCAGCCUCAC	58-80	eun-miR167c-3p	1	0	23	24	1
sch-MIR477a	CCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUAUGUUGGGAAAGAAGCUCUAGCAGGGAGAGCC	68	sch-miR477a-5p	CCUCUCCCUCAAGGGCUUCUC	1-21	stu-miR477a-5p	0	0	21	21	1
			sch-miR477a-3p	GAAGCUCUAGCAGGGAGAGCC	48-68	stu-miR477a-3p	0	0	21	22	1
sch-MIR477b-2	ACUCUCCCUCAAAGGCUUCUGGCUUAAGAUGCCUUUUGUGCUAAUGCUAGAGGUCUUUCGAGUGAGAGUG	70	sch-miR477b-2-5p	ACUCUCCCUCAAAGGCUUCUG	1-21	stu-miR477b-5p	0	0	21	21	1
			sch-miR477b-2-3p	GAGGUCUUUCGAGUGAGAGUG	50-70	stu-miR477b-3p	0	0	21	22	1
sch-MIR398a-1	GGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUUGUUUGUAACAAUUUAUCGUUUAUAAAUGUGACACAUAUGUUCUCAGGUCGCCCCU	90	sch-miR398a-1-5p	GGGUUGAUUUGAGAACAUAUG	1-21	stu-miR398a-5p	0	0	21	21	1
			sch-miR398a-1-3p	UAUGUUCUCAGGUCGCCCCU	71-90	sly-miR398a	0	0	20	21	1
sch-MIR408a	ACAGGGACGAGGCAGCGCAUGAGAUGUACAAUUUUACUAAUUGCCCAUUCCAUGCACAGCCUCUUCCCUGGC	72	sch-miR408a-5p	ACAGGGACGAGGCAGCGCAUG	1-21	stu-miR408a-5p	0	0	21	21	1
			sch-miR408-3p	AUGCACAGCCUCUUCCCUGGC	52-72	cas-miR408	1	0	21	21	1
sch-MIR408-1	ACGGGGACGAGCCAGAGCAUGAGAUGUGCAAUUUUUGCUUUGCCUAUUCCAUGCACUGCCUCUUCCCUGGC	71	sch-miR408-1-5p	ACGGGGACGAGCCAGAGCAUG	1-21	sly-miR408	0	0	21	21	1
			sch-miR408-1-3p	AUGCACUGCCUCUUCCCUGGC	51-71	cas-miR408	0	0	21	21	1
sch-MIR156b-6	GUGACAGAAGAGAGUGAGCACACAUGGUUCUUUCAUGGAUUAUUCCCCAUGUUUAAAAGCUCUGCGUGCUCACGCUCUAUCUGUCACA	88	sch-miR156b-6-5p	UGACAGAAGAGAGUGAGCACA	2-22	hvu-miR156b	0	0	21	21	1
			sch-miR156b-6-3p	UGCUCACGCUCUAUCUGUCACA	67-88	mtr-miR156b-3p	2	0	22	22	1
sch-MIR394	UUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAAC	61	sch-miR394-5p	UUUGGCAUUCUGUCCACCUCC	1-21	cas-miR394	0	0	21	21	1

			sch-miR384-3p	AGGGGGCCAAAGUGCCAAAC	42-61	stu-miR384-3p	0	0	20	20	1
sch-MIR156f-2	CUAUUGACAGAAGAGAGAGAGUACAAUCUGUCAU CAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUG CUCUCUCUGCUUCUGCCAAUU	88	sch-miR156f-2-5p	UUGACAGAAGAGAGAGAGUACA	4-25	gma-miR156f	1	0	22	22	1
sch-MIR164e-1	GGGUGGGUAACUCAUGUUGGAGAAGCAGGGCAC GUGCAAAUUUUUUGUAUUCGACGAUAUAUGCAU UACUAAUGGUAAUGCAUGAAUUUUGCACGUGUU CUCCUUCUCCAACCCGAAUUUCCUACCUCCUC	131	sch-miR164e-1-5p	UGGAGAAGCAGGGCACGUGCAA	18-39	bra-miR164e-5p	0	0	22	22	1
			sch-miR164b-1-3p	CACGUGUUCUCCUUCUCCAAC	92-112	sly-miR164b-3p	0	0	21	21	1
sch-MIR169a-2	UGUGGAAGGGAGUUUACAUGAUAGAAAUGGAGA GUGGAUUGCAGCCAGGGAUGACUUGCCGAUGAU UUCUUUUGUAGUUUUCCUAUUAAAGAUUAUGUA UCGGCAAGUUGUCCCUGGCUACCUUUCGCUCUC UUCUUCUCAUGCAAAUUUUUUACUA	157	sch-miR169a-2-5p	CAGCCAGGGAUGACUUGCCGA	42-62	cas-miR169a	1	0	21	21	1
			sch-miR169d-2-3p	GGCAAGUUGUCCCUGGCUACC	102-122	ata-miR169d-3p	2	0	21	21	1
sch-MIR169a-3	UGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGA GUGGAGUGCAGCCAAGGAUGACUUGCCGAGAUG UUGUAGCCUAAUGCAAUGACAUAUCGGCAGGUC AUCUUUGGCUACAUUUUAUUCUCUCCUAUUCAU GUAAAAACUUUAUAAGACGUAUAUGU	158	sch-miR169a-3-5p	CAGCCAAGGAUGACUUGCCGA	42-62	cas-miR169a	0	0	21	21	1
sch-MIR169c-2	AGGAAGAGAGAUCUUACAUGAAAAGAAAAACCUU UGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUA CCUACUAUUUAUUUUCCUCCUAUUUUUUAUGGA GUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAG CUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUU CUCUUCUUCCGAUUUAUAUUAAUCUUUACUUGAC CAAA	205	sch-miR169c-2-5p	UAGCCAAGGAUGACUUGCCUA	42-62	ata-miR169c-5p	0	0	21	21	1
sch-MIR319	UUCUCAACUAAUAAAUUAAAGAAUAUGUAGACGU AAGUAGGAGCUCCUUUCAGGCCAAGACCGAGGG ACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAU AUUGGUUAACCUUAACAAACAAAUUAUGUAUAGU UUUAAGAUUAACCAGUUGCAUGGCGAGGGAGCA ACUACUUCCGCUAACUUGUCUCACUUAUUGGAC UGAAGGGAGCUCC	213	sch-miR319-3p	AUUGGACUGAAGGGAGCUCC	194-213	cpa-miR319	0	0	20	20	1
sch-MIR319b-4	GAGCUCCUUUCAGGCCAAGACCGAGGGACGAGG AGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGU UAACCUUAACAAACAAAUUAUGUAUAGUUUUAAG AUUAACCAGUUGCAUGGCGAGGGAGCAACUACU UCCGCUAACUUGUCUCACUUAUUGGACUGAAGG GAGCUCCUAUCCAUUUAUAUAUAGUUAAGUUAAC UAUAUAAAAUAUA	213	sch-miR319b-4-3p	AUUGGACUGAAGGGAGCUCCU	154-174	aof-miR319b	1	0	21	21	2
sch-MIR319c	AAGAGAGCUUCCUUCAGCCCACUCACGGAGGAG AAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAU CCAACCACUCAGUAGAAAGGAUAGGUUUUGUGC UACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGU UUUCUAUCCCUCUCUUUCCUUGCUUGGACUGAA GGGAGCUCCUU	176	sch-miR319c-5p	AGAGCUUCCUUCAGCCCACUC	4-24	sly-miR319c-5p	0	0	21	21	1
			sch-miR319c-3p	UUGGACUGAAGGGAGCUCCUU	156-176	sly-miR319c-3p	0	0	21	21	1
sch-MIR164e-2	GUUGGAGAAGCAGGGCACGUGCAAAUUUUUUGU AUUCGACGAUAUAUGCAUUACUAAUGGUAAUGCA UGAAUUUUGCACGUGUUCUCCUUCUCCAA	96	sch-miR164e-2-5p	UGGAGAAGCAGGGCACGUGCAA	3-24	bra-miR164e-5p	0	0	22	22	1
			sch-miR164b-2-3p	CACGUGUUCUCCUUCUCCAA	77-96	sly-miR164b-3p	0	0	20	21	1
sch-MIR9469-1	CAAAAGCUAGUUCAUGAGGAGAGGUUUGUCAAG UCCACAUAAGAAGACCGAAUUCCCAUCCCUCUAC CGCUGUGGGACAUCAUAAGGAAUUUGGUCUCCU UAUAUGGACUUGGACAAACCUCUCCUCAUGAGC UAGCUUUU	141	sch-miR9469-1-5p	CCACAUAAGAAGACCGAAUUC	35-55	sly-miR9469-5p	0	0	21	21	1
			sch-miR9469-1-3p	AUUUGGUCUCCUUAUAUGGAC	89-109	sly-miR9469-3p	3	0	21	21	1
sch-MIR9469-2	CCAAAAGCUAGCUCAUGAGGAGAGGUUUGUCCA AGUCCAUAUAAGGAGACCAAAUUCCUUAUGAUGU	143	sch-miR9469-2-5p	CCAUAUAAGGAGACCAAAUUC	37-57	sly-miR9469-5p	3	0	21	21	1

	CCCACAGCGGUAGAGGGAUGGGAAUUCGGUCUU CUUAUGUGGACUUGACAAACCUCUCCUCAUGAA CUAGCUUUUG										
			sch-miR9469-2-3p	AUUCGGUCUUCUUAUGUGGAC	91-111	sly-miR9469-3p	0	0	21	21	1
sch-MIR166c	AUGUGUGUGGUGAGUUUGAGGGGGAUGUUGUC UGGCUCGACACAAUUACUCUCUUGUAUGUAUUU AGUUAUUCGUUAUCAAGAUUGAUGUUGAUAACG AAUAAAUUAAACACAUAUGUACAAGAUGUAAAAA GAGAGUAAAGGCGUCGGACCAGGCUUCAUUCCU CUCAAACAAUAUUCUACUUCUACA	189	sch-miR166c-5p	GGGAUGUUGUCUGGCUCGACA	22-42	sly-miR166c-5p	0	0	21	21	1
			sch-miR166c-3p	UCGGACCAGGCUUCAUUCCUC	146-166	sly-miR166c-3p	0	0	21	21	1
sch-MIR9471a-1	GGAUCUUUGACUGAUUUGGGGUUCUGAGAUUUA GUUGAUUUCUCUGGUGCUUACUCAACUAAUAGU UAUUAUUUAAGAAAAUCAAUAAUAUUGGAAGCAA GGAGAAUGGCGACUAUCAGGAUGAUAACUAUUG GUUGAGCAGCAUUAGAGAAAUUGACAUGAUUCU GAGAGGAAGAUGAUU	181	sch-miR9471a-1-5p	CUGGUGCUUACUCAACUAAUA	44-64	sly-miR9471a-5p	3	0	21	21	1
			sch-miR10540-1-3p	AUGAUAACUAUUGGUUGAGCA	121-141	sly-miR10540	5	0	21	21	1
sch-MIR482b-2	GAAAGGGGAUGAAUUUUUCAGGAAGCUUUUGGA GUGGGUGGCAUGGUAAGAUAUCAUAUUUUGUUU UUCAUAAAAGAAAAAGAAAUUGAAAUCUUACCGA UUCCCCCCAUUCCAAUGGCUUCCAGUUAUUUCU CCCUUUCC	141	sch-miR482b-2-5p	GGAGUGGGUGGCAUGGUAAGA	31-51	stu-miR482b-5p	0	0	21	21	1
			sch-miR482b-2-3p	UUACCGAUUCCCCCCAUUCCAA	94-115	stu-miR482b-3p	0	0	22	22	1
sch-MIR9473	CUAGCAGAUAUUGUCUGUAAAUCUAAACUCGUUU UACUCCACUAGUCAUCAUGUAAUGACAUUUACUA GAAGAAGAGACCAGUGGGGUAAAACGAGUUCGG AUUUACAGCCAAUAUUAUU	120	sch-miR9473-5p	UGUCUGUAAAUCUAAACUCGU	12-32	sly-miR9473-5p	1	0	21	21	1
			sch-miR9473-3p	AAACGAGUUCGGAUUUACAGC	90-110	sly-miR9473-3p	1	0	21	21	1
sch-MIR9476-1	CCUGUCCAAAACUGCUAUUGGUCUAGUCCUGCA UCUUUUUUUAUAUUUUUUUCGUUAUCAAAAAAUA UAAAAAAAAGAUGCAGGACUAGACCAAUAGCAGG AUGGAUUG	109	sch-miR9476-1-5p	UCUAGUCCUGCAUCUUUUUUU	22-42	sly-miR9476-5p	0	0	21	21	1
			sch-miR9476-1-3p	AAAAAGAUGCAGGACUAGACC	72-92	sly-miR9476-3p	0	0	21	21	1
sch-MIR9476-2	AGCCAAUCCAUCCUGCUAUUGGUCUAGUCCUGC AUCUUUUUUUUAUAUUUUUUGAUAACGAAAAAAA UAUAAAAAAAAGAUGCAGGACUAGACCAAUAGCAG UUUUGGACAG	111	sch-miR9476-2-5p	UCUAGUCCUGCAUCUUUUUUU	23-43	sly-miR9476-5p	0	0	21	21	1
			sch-miR9476-2-3p	AAAAAGAUGCAGGACUAGACC	73-93	sly-miR9476-3p	0	0	21	21	1
sch-MIR169e-1	UAGGAGGAGAGGCCUUACAUGAAUUAGAAGAGU UUCUAUUUGUUUAGUAGCCAAGGAUGACUUGCC UUUCAUCAAUGCCUUUUGUAAAAUGGAAAUUGAU UACAACACUUUUUAUGGUAUUGGGAAAAUGAGU GGCAAGCAUCUUUGGCGACUUGACAAACUCUUC UUUGUCAUGUUAGUCCAUCUUCUUCCU	193	sch-miR169e-1-5p	UAGCCAAGGAUGACUUGCCUUU	48-69	sly-miR169e-5p	0	0	22	22	1
			sch-miR169e-1-3p	UGGCAAGCAUCUUUGGCGACU	133-153	sly-miR169e-3p	0	0	21	21	1
sch-MIR477-2	AAGCUAGGCAUUGCUUGUUGUCUCUCCCUCAAG GGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGC AUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAA CAAGAAAUUCCUUGCU	116	sch-miR477-2-5p	UGUCUCUCCCUCAAGGGCUCC	19-39	sly-miR477-5p	0	0	21	21	1
			sch-miR477-2-3p	AGUUCUUGUAGGGUGAGACAAC	80-101	sly-miR477-3p	0	0	22	22	1
sch-MIR395j-1	GGUGUUCCCUAGAGUUCCCUUGACCACUUCAUU AGGGCUUACUUCGUUGUUUGAUGUCCUGCUGAA GUGUUUGGGGGAACUCCUGGGCUCAC	92	sch-miR395j-1-5p	GUUCCCUUGACCACUUCAUUA	14-34	mdm-miR395j	1	0	21	21	1
			sch-miR395b-1-3p	CUGAAGUGUUUGGGGGAACUCC	62-83	sly-miR395b	0	0	22	22	1

sch-MIR172d-2	CUUGCUAGUGCAGCAUCAUUAAGAUUCACAUAGA AAAUAUAGAACGAAAUUUGCUCAAUUUUUCAAUA UAUGAGAAUCUUGAUGAUGCUGCAUUGGCAA	99	sch-miR172d-2-5p	GCAGCAUCAUUAAGAUUCACA	10-30	bra-miR172d-5p	0	0	21	21	1
			sch-miR172-2-3p	UGAGAAUCUUGAUGAUGCUGCAU	71-93	aau-miR172	0	0	23	23	1
sch-MIR396b-2	GGGUUAAAUAUGUUUCCUUUGAGAAAAAAAAAUG GUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAA CUGCAUCUACAAUUUCAAUUCAUUAUGAAAAAAA GAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCA AUAAAGCUGUGGGAAGAUACAGAUAGG	161	sch-miR396b-2-5p	UUCCACAGCUUUCUUGAACUG	50-70	aof-miR396b	0	0	21	21	1
			sch-miR396c-2-3p	GUUCAAUAAAGCUGUGGGAAG	130-150	fve-miR396c-3p	0	0	21	21	1
sch-MIR10528	AUAAUGAAUGCAAUGUCAUAUACCAUCAACACUC GGAAACUCAAAUUGAGGUUAAAUCUCGGAGUGA UGAUGGUAUAUGACCUUGCAAUUCACUAUG	97	sch-miR10528-5p	AAUGCAAUGUCAUAUACCAUC	7-27	sly-miR10528	0	0	21	21	1
			sch-miR11424-3p	AUUGAGGUUAAAUCUCGGAGU	45-65	pab-miR11424	5	0	21	21	1
sch-MIR530	UUUAUCUGCAUUUGCACCUGCACCUUAGUGAAC GAAUUUGUUCGCGUAUAAUUCGUGCAGAAAGGU GUAGGUGUUCAUGCAGACAAAA	88	sch-miR530-5p	UCUGCAUUUGCACCUGCACCU	5-25	eun-miR530-5p	0	0	21	21	1
			sch-miR530-3p	AGGUGUAGGUGUUCAUGCAGA	63-83	sly-miR530	0	0	21	21	1
sch-MIR393b-1	AUUAUUCCAAAGGGAUCGCAUUGAUCCUGUGUC CCAAAUUAAUUAACCAUGGGACUAUGGGAUCAUG CGAUCUCUUCGGAAUUCUC	86	sch-miR393b-1-5p	UUCCAAAGGGAUCGCAUUGAUC	5-26	csi-miR393b-5p	0	0	22	22	1
			sch-miR393-1-3p	AUCAUGCGAUCUCUUCGGAAU	62-82	sly-miR393	0	0	21	21	1
sch-MIR4994	AACAUGUUGAAUGUUGGGGAACGAACAUCUAAG GUUUGGGUCAACGAUCUCAAUGUUGAUGCGUCC GUUGUUGUUGAUGCUGCUCCAAAAGGUUCAACA UUGGGAUUUUAGCCCAAACCUCAGAUGUCCCUU CCCCAUCGUUCAACAUUGAC	152	sch-miR4994-5p	GUUUGGGUCAACGAUCUCAA	34-53	gma-miR4994-5p	5	0	20	20	1
			sch-miR10530-3p	AUGUCCCUUCCCCAUCGUUCAACA	124-147	sly-miR10530	1	0	24	24	1
sch-MIR398a-2	CAAUAGGGUUGAUUUGAGAACAUAUGUAUGUGC AUAUUUUGUUUGUACCAAUUUACCGUUUAUAAAU GUGACACAUAUGUUCUCAGGUCGCCCCUGUAGA	100	sch-miR398a-2-5p	GGGUUGAUUUGAGAACAUAUG	6-26	stu-miR398a-5p	0	0	21	21	1
			sch-miR398a-2-3p	UAUGUUCUCAGGUCGCCCCUG	76-96	sly-miR398a	0	0	21	21	1
sch-MIR10535a	AAGGGUUGGCAUAAGUUUGUGAAAGCCGGAGAU UUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAU UGUAUAUUUUGCUCUAAAACCUUUAGCUUUAACA AAUUUGUGCCAACCCUUU	119	sch-miR10535a-5p	UUGGCAUAAGUUUGUGAAAGCCGG	6-29	sly-miR10535a	0	0	24	24	1
			sch-miR4227-3p	AAAUUUGUGCCAACCCUUU	101-119	aly-miR4227	5	0	19	21	3
sch-MIR159b-1	AAUGUAGAGCUCUUCUGAAUUUCAAAGAGGAUC UGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAU UCCUCAAUCCUAUCUAUUCUCAAAAUAAUUUUAG AUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGC AUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAG GGAGCUCUACGUUU	180	sch-miR159b-1-5p	AGCUGCUAAUCUAUGGAUUCC	49-69	cas-miR159b-5p	2	0	21	21	1
			sch-miR159b-1-3p	UUGGAAUGAAGGGAGCUCUAC	156-176	sly-miR159b	1	0	21	21	1
sch-MIR169r-1	CAUCCAAUGAGCUUCUCACAAGUUGUGUUUUGU UAGAUGAAGUAGGAAACUGCUAAUUCUAUUUGCA AUAGGGAAUGUUGGAUUUUCUUCUUCGGGAAAC UACACUUCCCUAUAAUUGAAUAGACAUGUCUUUA UUCAUGUUAAAGUCUUGCAUGAGGGAAUAAGGU UAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCA AGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGU CAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCA UGCCAGAUUUUUUAUGAAA	285	sch-miR169r-1-3p	CAGCCAAGGAUGACUUGCCGG	178-198	csi-miR169r-5p	0	0	21	21	1
sch-MIR166a-1	GAGGAAGUUCUCUCAGUUGAGGGGAAUGUUGUC UGGCUCGAGGUCACCAAUUAGAUCCAUAAUCCC UAUAUAUACCAUGCUUCUCAAAAAAAGAUUUAUA	165	sch-miR166a-1-5p	GGAAUGUUGUCUGGCUCGAGG	23-43	cas-miR166a	0	0	21	21	1

	AUAUGAAAAGGGGUUAUGAAUCAUGUGUUAGUG UUGUCGGACCAGGCUUCAUUCCCCCCAAUUGU										
			sch-miR166k-1-3p	UCGGACCAGGCUUCAUUCCCCC	137-158	lus-miR166k	0	0	22	22	1
sch-MIR167b-4	GAUCGUGAACCACUAGCAGUUGAAGCUGCCAGC AUGAUCUAAACUUUUCUAUUGCUCCGUACGAGG AAAGAUCAGAUCAUGUGGCAGCAUCACCUGUUAA UGGUUUCGCGGA	112	sch-miR167b-4-5p	UGAAGCUGCCAGCAUGAUCUAA	21-42	bna-miR167b	0	0	22	22	1
			sch-miR167c-4-3p	AUCAGAUCAUGUGGCAGCAUCACC	71-94	eun-miR167c-3p	1	0	24	24	1
sch-MIR171c-1	UAGUAAAAUGAUGUUGGAAUGGCUCAAUCAAAUC AAAUUUCUCAAAGUAUUUGGGUUAUUUCAUUUGA UUGAGCCGUGCCAAUAUCAUCUUACUUAUAU	99	sch-miR171c-1-5p	UGUUGGAAUGGCUCAAUCAAA	12-32	csi-miR171c-5p	1	0	21	21	1
			sch-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	66-86	aof-miR171a	0	0	21	21	1
sch-MIR171f-2	AUUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGG UGAGGUUCAAUCCGAAGACGAAUUUACGCUUGU UUUCGUAAAGAGCGAUCUCAGAUUGAGCCGCGC CAAUAUCACUUCUUAU	115	sch-miR171f-2-5p	CGAUGUUGGUGAGGUUCAAUC	25-45	fve-miR171f-5p	0	0	21	21	1
			sch-miR171b-2-3p	UUGAGCCGCGCCAAUAUCACU	89-109	aof-miR171b	0	0	21	21	1
sch-MIR390-1	AUAUGCAUGGAGAAUCUGUAAAGCUCAGGAGGG AUAGCGCCAUGGAUGACUCAAUUCGAUUUUUUU ACACAUCUUUAGCGCUAUCCAUCCUGAGUUUCA CGGCUUUUUCAUGCUUUUUU	119	sch-miR390-1-5p	AAGCUCAGGAGGGAUAGCGCC	21-41	aof-miR390	0	0	21	21	1
			sch-miR390a-1-3p	CGCUAUCCAUCCUGAGUUUCA	79-99	cas-miR390a-3p	0	0	21	21	1
sch-MIR396f	AAGUCCUAGUCAUGCUUUUCCACAGCUUUCUUG AACUUCUUUUUGCUAAAUUUUGAUCUCUAAAUUG AUAAUUUUGAGAUGAGAUUUGAAGCUAUGAAAGU CCAAGAAAGCUGUGGGAAAAGAUGGCAAGCUUU	134	sch-miR396f-5p	UUCCACAGCUUUCUUGAACUU	18-38	csi-miR396f-5p	0	0	21	21	1
			sch-miR396-3p	GUCCAAGAAAGCUGUGGGAAA	100-120	stu-miR396-3p	0	0	21	21	1
sch-MIR166b	UUUUGUGGGGAAUGUUGUUUGGCUCGAGGCCAC CAACUUCAUCUAAUGUAAGCAAACUCUUUGUUAG UGUCGUCGGACCAGGCUUCAUUCCCCUCAAA	98	sch-miR166b-5p	GGAAUGUUGUUUGGCUCGAGGC	9-30	csi-miR166b-5p	1	0	22	22	1
			sch-miR166f-3p	UCGGACCAGGCUUCAUUCCCCU	73-94	cas-miR166f-3p	0	0	22	22	1
sch-MIR171f-3	AAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCC GAAGACGAAUUUACGCUUGUUUUCGUAAAGAGC GAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCU UAUUUUCAUUC	110	sch-miR171f-3-5p	CGAUGUUGGUGAGGUUCAAUC	12-32	fve-miR171f-5p	0	0	21	21	1
			sch-miR171b-3-3p	UUGAGCCGCGCCAAUAUCACU	76-96	aof-miR171b	0	0	21	21	1
sch-MIR156b-7	CAAGACUGACAGAAGAGAGUGAGCACACGAUGU CGAAUUGUAUAAAUAUAUAUACGAUUGUCAUUUG CGUGUGCUCACUUCUCAUUCUGUCAGAAUCU	98	sch-miR156b-7-5p	UGACAGAAGAGAGUGAGCACA	7-27	hvu-miR156b	0	0	21	21	1
			sch-miR156a-7-3p	UGCUCACUUCUCAUUCUGUCAG	72-93	vca-miR156a-3p	1	0	22	22	1
sch-MIR156b-8	AAGGAGGUGACAGAAGAGCGUGAGCACAUGUGU GUUUUCUAGCAUGAUGUUUAUAUGCUUGAAUCU AUGGGUGCUCACUGCUCUAUAUUUCAUCCUCAU C	100	sch-miR156b-8-5p	UGACAGAAGAGCGUGAGCACA	8-28	hvu-miR156b	1	0	21	21	1
			sch-miR156i-8-3p	GCUCACUGCUCUAUAUUUCAUC	73-94	zma-miR156i-3p	2	0	22	22	1
sch-MIR171a-1	UCAUACGAGAUGUUGGUGCGGUUCAAUGAGAAA GCAGUUGUUGAAUAAGUUUUUGACCCUACUUUU UGAUUGAGCCGUGCCAAUAUCACGUGUC	94	sch-miR171a-1-5p	UGUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	1	0	21	21	1
			sch-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	67-87	aof-miR171a	0	0	21	21	1
sch-MIR156b-9	UGAGAUAUUGUUGACAGAAGAUAGAGAGCACGA AUAAUGAGGUGCUAAUUGGAAGUUGCACCUUAA UUCUUUGUGCUCUCUAUUCUUCUGUCAUCAUCU UCAG	103	sch-miR156b-9-5p	UUGACAGAAGAUAGAGAGCAC	11-31	aof-miR156b	0	0	21	21	1

			sch-miR156g-9-3p	GCUCUCUAUUCUUCUGUCAUC	75-95	csi-miR156g-3p	0	0	21	21	1
sch-MIR169j-1	CUAUUUGAUAGCCAAGGAUGACUUGCCUGCAUC AUUAAUUAAAUCUUGAGGCUAGCUUGUGAUAUAU AUCAUGUAUAUGACAUGUAUACAAGCAAUCUUCU UUGAUGGCCAGGCAGUCUCCUUGGCUACUCUAA UAGGUUCCUCUCAUUCAUGCUAGACUCUU	163	sch-miR169j-1-5p	UAGCCAAGGAUGACUUGCCUGC	9-30	ppe-miR169j	0	0	22	22	1
			sch-miR169e-1-3p	CAGGCAGUCUCCUUGGCUACU	110-130	csi-miR169e-3p	2	0	21	21	1
sch-MIR169r-2	AAAGUCUUGCAUGAGGGAAUAAGGUUAUUGAAU UGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAU CAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUG GCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAU UUUUUAUGAAACAGCUGCUGUUGUUAAUUGUCA AAUCAGGAAUUGUGGACAA	184	sch-miR169r-2-5p	CAGCCAAGGAUGACUUGCCGG	36-56	csi-miR169r-5p	0	0	21	21	1
sch-MIR169j-2	GUCUAGCAUGAUGAAAAGAGUCUUAUUUGGUAG CCAAGGAUGACUUGCCUGCACCAUAUUCGAAAU GUGUCCUUUCGUUCAUGGGGUCAAGCAGGUCAU CUUUAGCUAACUUGACAAGCUCUUCUCUUUCAU GCAAGACUUUCUCUUCUUCCGAU	155	sch-miR169j-2-5p	UAGCCAAGGAUGACUUGCCUGC	31-52	ppe-miR169j	0	0	22	22	1
			sch-miR169d-2-3p	GCAGGUCAUCUUUAGCUAACU	91-111	stu-miR169d-3p	0	0	21	21	1
sch-MIR393b-2	AUGCAAUUAAUUCAUAGUGCUGGUGGAUUAUUC CAAAGGGAUCGCAUUGAUCCUGUGUCCCAAAUU AAUUAACCAUGGGACUAUGGGAUCAUGCGAUCU CUUCGGAAUUCUCCACAAUACUGGCUCUAAUUAA AUUAACGAUUGGUCGAGAAUUUAAUAUCAGUAAA UUCAAA	173	sch-miR393b-2-5p	UUCCAAAGGGAUCGCAUUGAUC	31-52	csi-miR393b-5p	0	0	22	22	1
			sch-miR393-2-3p	AUCAUGCGAUCUCUUCGGAAU	88-108	sly-miR393	0	0	21	21	1
sch-MIR2111d-1	UGUGUUAGGUUAAUGGUAAUCUGCAUCCUGAGG UUUAGAUCAAUUUCUAAUUUACUGGAUCUAGUCC UUGGGAUGCAGAUUAUCUUUACCUUACAAACAG UGUACA	106	sch-miR2111d-1-5p	UAAUCUGCAUCCUGAGGUUUA	17-37	ppe-miR2111d	0	0	21	21	1
			sch-miR2111d-1-3p	GUCCUUGGGAUGCAGAUUAUC	64-84	gma-miR2111d	2	0	21	21	1
sch-MIR7981-1	GACACAAUUUAACUAAACUAAGGUCUUGUUAUUC CAUGCUAUUUUUUUUUUGUAAUUUUAUAUAUCCU UUUGCCUUACGUGACAUCAAAAUAUCUCUCACGU GCCUCAAUCAUGUGGAAUCACGGAGUGUGCCGC GUAAGACAAAAGAUGUACAAUAUUACAAAAAAAAA GGAGUUCAGGGGAAAUAAUAAAACGUUAGUUUA GUUAAGGUGUAUA	216	sch-miR7981-1-5p	UUUAACUAAACUAAGGUCUUGUUA	8-31	stu-miR7981-5p	5	0	24	24	2
			sch-miR7981-1-3p	AUAAAACGUUAGUUUAGUUAAGGU	188-211	stu-miR7981-3p	3	0	24	24	1
sch-MIR408-2	AAAAGGAAGGAUUGUGGGGAGAGGAGAGCCAGG GAAGAGGCAGUGCAUGGAAUAGGCAAAGCAAAAA UUGCACAUCUCAUGCUCUGGCUCGUCCCCGUCU AUCCAUACCACACCAAUUUUUACCUCAA	128	sch-miR408-2-5p	GAGAGCCAGGGAAGAGGCAGU	24-44	bra-miR408-5p	1	0	21	21	1
			sch-miR408-2-3p	AUGCUCUGGCUCGUCCCCGUC	79-99	cas-miR408	5	0	21	21	1
sch-MIR9474-1	AUACUAAGAUCUUAUUACCCCUGAGCUUAUUUUA UAAGUAAUUUUUUAUCUUUUUUUUUGCCUAUAU GACACUAGCUUGAAAAAAAAUGUCAACCAGCGUU GAACCCACAAGAUAGUGUCACAUAGGCCAAAAAG GGGUAGAAAUAAUUAAUAAAAUAAGUUCAGGGGA AAAAUAGGACCUUAGUAU	187	sch-miR9474-1-3p	GGUAGAAAUAAUUAAUAAAAUA	137-158	sly-miR9474-5p	5	0	22	22	2
sch-MIR9474-2	AUUUUAUAAGUAAUUUUUUAUCUUUUUUUUUGCC UAUAUGACACUAGCUUGAAAAAAAAUGUCAACCA GCGUUGAACCCACAAGAUAGUGUCACAUAGGCC AAAAAGGGGUAGAAAUAAUUAAUAAAAUAAGUUC AGGGGAAAAAAUAGGACCUUAGUAUAGUUAAGUG UGUCUCUGAGAUUUUGGGCAUAGGUUGAGGGG GUACUUAUGCAUUAUCCCGAAAUUGGACAAGAAG AAAAUAAAUAAAAAAACUAGAAGAU	259	sch-miR9474-2-5p	GGUAGAAAUAAUUAAUAAAAUA	109-130	sly-miR9474-5p	5	0	22	22	2

			sch-miR10532-2-3p	AAGUGUGUCUCUGAGAUUUUGGGC	164-187	sly-miR10532	1	0	24	24	1
sch-MIR8151	CUGUUUCAUAUUUAUACUCUUCAACUUUGAGUG UAUACAAGUAGACACUUAAACUUGUAUAAAAUUG CACAAGUACACAUGAGUCCAAUGUGACAUAAUAC AAGUAAGACACAAAUUGUCAUGUAGAAUGCGGAC AUGUAUCUAUUUGUUCAACUUUAUACAAGUUUAU AUGUUUAUUGUGCACACCCAAAAUUAAAGAGCAU AAAUGUGAAAUGG	216	sch-miR8151-5p	UGUAUACAAGUAGACACUUA	32-51	cpa-miR8151	4	0	20	20	1
			sch-miR865-3p	UAUUUGUUCAACUUUAUACAA	143-163	ath-miR865-3p	5	0	21	21	1
sch-MIR166a-2	AGAGAGAGAGCUUUUGUAUUGCGGGGAAUGUUG UCUGGCUCGAGGAAUCAAAAAUUGUUUCUUAUA GAUAGAUCUGUAUAUUUUGUUUAUAGAUCUAUAA UGUUUUUGAUGUCGUCGGACCAGGCUUCAUUCC CCACAAUGAAUAUUGCUCUCUCACA	158	sch-miR166a-2-5p	GGAAUGUUGUCUGGCUCGAGG	25-45	cas-miR166a	0	0	21	21	1
			sch-miR166d-2-3p	UCGGACCAGGCUUCAUUCCCC	115-135	aof-miR166d	0	0	21	21	1
sch-MIR1918-1	AUUUGAACUUCCAUCCUGUUAGCGGUAGUCCGA UUCUCCACCUUGUAGCAUAUUUUUUUCUCUUAAA UUGAAGAGGAGAUUGCGUAAUGGAGAAUCGAAC UCUCACCAACAGAAUGACAAUUCAACU	127	sch-miR1918-1-5p	UGUUAGCGGUAGUCCGAUUCUC	17-38	sly-miR1918	5	0	22	22	1
			sch-miR6164b-1-3p	UCUCUUAAAUUGAAGAGGAGA	59-79	nta-miR6164b	5	0	21	21	1
sch-MIR160h-2	GGAAUAUGCUUGGCUCCUCAUACGCCAUUCAAC AAGGCCCAUCGAUAUAUUACGGUGAACUUUGCA AAUGGCAUACAGGGAGCCAGGCAUAUACG	95	sch-miR160h-2-5p	UGCUUGGCUCCUCAUACGCCAUU	7-29	mes-miR160h	5	0	23	23	1
			sch-miR160-2-3p	UGGCAUACAGGGAGCCAGGCA	69-89	aau-miR160	0	0	21	21	1
sch-MIR319a	GAAAAUAAGGAGCUCUCUCCGGUCCAGUCCGAG GCACUCAAAGGCUAAAAACACAGCUGACGACUCG UUGAUUCUCAAACACAUCAAGAAGCAUUUUUUGA AAUUGACGUGUUUAAGAUUCAACGAUGCGUGAG CUAUGUUUAGCUAGCGUUGUCACGUCUUGGACU GAAGGGAGCUCCCUAUUAAA	187	sch-miR319a-3p	UUGGACUGAAGGGAGCUCCCU	161-181	aof-miR319a	0	0	21	21	1
sch-MIR167d-2	UGACAGGUGAGGCUGCCACAUGAUCUGAUCUUU CUUCAUAUUAUAUUUGAACUAAAAGGAAAGUUUA GAUCAUGCUGGCAGCUUCAACUGCUA	93	sch-miR167d-2-5p	UGAGGCUGCCACAUGAUCUGA	8-28	eun-miR167d-5p	1	0	21	21	1
			sch-miR167h-2-3p	AUCAUGCUGGCAGCUUCAACUGCU	69-92	gma-miR167h	1	0	24	24	1
sch-MIR7997c-1	AGAAGCUAUGUUUCUCGGACUCUCCAAAAAUGC UACGUAAUUCACUAUUUUUGAUGGAUCCGACAU GCAACCCAUACUGUUUUUGAAGAGUUCGAGAAG CAUAGCUGAG	109	sch-miR7997c-1-5p	AUGUUUCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	3	0	24	24	1
			sch-miR5303-1-3p	UUUUUGAAGAGUUCGAGAAGC	80-100	sly-miR5303	2	0	21	21	1
sch-MIR1919-1	GACGCCUUUGAUGUUCACAUCUUCUGGUAGUCC UGUCGCAGAUGACUUUCGCCCUUCUAAGGAACC ACACUUUCUGUAGAUCUAAUUAAUUUGAAUUCAA UGUGGCAGGACGAGAGUCAUCUGUGACAGGAUA AUGGAAGAUCUAGUUAUCAAAGGCUUA	160	sch-miR1919-1-5p	UGUCGCAGAUGACUUUCGCCC	34-54	stu-miR1919-5p	0	0	21	21	1
			sch-miR1919-1-3p	ACGAGAGUCAUCUGUGACAGG	110-130	stu-miR1919-3p	0	0	21	21	1
sch-MIR7992-1	UAUUAAACACUCUAACUUACAUAAUGAUCAUCUA GACACCUCCAAAGUUUAUGUCACAUCAGUGUUA GGUGUCCACGAGAUAAAGUGUAAACGAGUUGAA GUGUCUAGAUGUACAUUUCGAAGUUAGAAUGUU UAGUU	138	sch-miR7992-1-3p	UGUCUAGAUGUACAUUUCGAAGU	102-124	stu-miR7992-3p	2	0	23	23	1
sch-MIR7997b-2	UACUGUAAGUUAGCUGCUAGUCUAGACCUACGU UGCUCGGACUCCAAAAAUUGUUGCAGCACCACU GUCAGAUCCUCCAAAAUGCACUAUUUCUGAAGGA UCCGGCACCCAGCAAUCGACAAUUUUAAAGAGUC UGAGCAAUGUAGGUCUAGACUAAGGUCUCACUU ACAACA	173	sch-miR7997b-2-5p	ACGUUGCUCGGACUCCAAAAA	30-50	stu-miR7997b	5	0	21	21	1

			sch-miR5303h-2-3p	GACAAUUUUAAAGAGUCUGAGCAA	118-141	stu-miR5303h	3	0	24	24	2
sch-MIR8045	ACAUUUACUGCUUGAACUGUCAGUAUAGAUGAG GUAGGAAAAUGGAAGAAUUGAUAGUUGAGGUGU GUUUUUAGUAUUCAGGUAGGAAAAUGGUCCAAG UGAUAGUUGGGGAGUGGAAUUUGCGACAAGACG AUAGUUAUGUAUGUUUUUAACCAUCAUAUGUAUU AUCACGCCUCAAACUAUUAGUUUUUCGCUUUCC UAACUGAACUAUCACCAUAGUUGAGGUAGGCAAA AAC	236	sch-miR8045-5p	AUUGAUAGUUGAGGUGUGUUU	50-70	stu-miR8045	0	0	21	21	1
			sch-miR8039-3p	UUUCCUAACUGAACUAUCACC	195-215	stu-miR8039	1	0	21	21	1
sch-MIR8762c	UUUGUGAAAUGACUUGAGAGGUGUAGUAUAAGU GGGAGCCGAAAGGCGAAAGUGAAAUACCACUAC UUUUAACGUUAUUUUACUUA	86	sch-miR8762c-3p	UUAACGUUAUUUUACUUA	69-86	gra-miR8762c	4	0	18	24	1
sch-MIR8021-2	AGGAAAAUCUAACAAUAUAUUUCAUAUUCAAGGC UCAAACUCGAGACCUCUGGUUAAGUUAAAAAUAA UUUUGUACCCCUUUUAGGCCUACGUGGCACUAG UUUGAAAGAAAAAAUCAACCUGUGUUGGUUCCAC ACGAUAGUGCCACGUAAGUCGAAAAGGGGUAGA AUAUUAUUAAUAAAAUAAGUUCAUGGGGGUAGUA GGACCUUUGUAUAGUAUAAGUGUGUCUCUGAGA UUUUGGG	242	sch-miR8021-2-5p	AUUCAAGGCUCAAACUCGAGACCU	26-49	stu-miR8021	0	0	24	24	1
			sch-miR10532-3-3p	AAGUGUGUCUCUGAGAUUUUGGG	220-242	sly-miR10532	1	0	23	24	1
sch-MIR169e-2	UUUGAAAAGAUAUCUUGCAUAAAAGAAAAGAGCA UGUCAAGGUAGCCAAGGAGACUGCCUGAAACCA AAUUAAAAUGUGAUUAAACACAUUUUAGACUAUG GAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUA UGACUCUCCUCUUCAUGUAAGACUUCUCUUCUU U	169	sch-miR169e-2-5p	UAGCCAAGGAGACUGCCUGAA	43-63	zma-miR169e	3	0	21	21	1
			sch-miR169f-2-3p	GGCAAGUCAUCCUUGGCUACU	107-127	zma-miR169f-3p	2	0	21	21	1
sch-MIR7698	UUUUUCCAUCAAGGUUUUCUAUAUCAAUUUCACA CCGGACUAAUCGGGAAACUGAUUUUGAGGACUC UAUUAAAUGUCUACGGUAGUUAAUAGUGUGUAA CCAUAGUGGUUCACUUUUUAUUCUCCGUAGACG UCCAAUUGAGUCAUCUAGAUCAGUUUCUUGAUC AAUCGGGUGUGAAACUGAUAUAUAAAACAUCGGU UGAUGAAUCA	210	sch-miR7698-5p	UUUCCAUCAAGGUUUUCUAUA	3-23	mtr-miR7698-5p	4	0	21	21	1
sch-MIR168c-1	GUUUCUCAUUCGCUUGGUGCAGGUCGGGACCUA CCUCGACGGCAACAAUGGCGGUAGCUGACGGCG ACGGCAGCGUACCGGUAAAAAAAAAUCUUAUUUU UACAUGUUGUUGCGUAGUUUGGGUCCCGCCUUG CAUCAACUGAAUAGGAGACUG	154	sch-miR168c-1-5p	UCGCUUGGUGCAGGUCGGGAC	10-30	bra-miR168c-5p	0	0	21	21	1
			sch-miR168-1-3p	UCCCGCCUUGCAUCAACUGAAU	124-145	lja-miR168-3p	0	0	22	22	1
sch-MIR11330	UCUCCCUACCGUUAAAACGAAGUUAUUUUUACCC CUACCGUUACUAAUUUCAUCAUUUUAACAUUGGG UUUGAAAUGGGAAAUGUAUAAAUGAUGAAAUUAG UAACGGUAGGGAUAAAAAUAACUUCAUUUUAACG GUAGGGGCA	145	sch-miR11330-3p	GUAGGGAUAAAAAUAACUUCA	108-128	ppt-miR11330	5	0	21	21	1
sch-MIR1127-1	CGCAACAUGACAAAUAAAAGUGGACGGUAUGAGU AUUAAUUGCUCCCUCCGUCCAUAAUUGUUUGUC AUGUUAAG	75	sch-miR1127-1-3p	AAUUGCUCCCUCCGUCCAUAA	38-58	bdi-miR1127	5	0	21	21	1
sch-MIR3448	UAAAAGAAGGAGUCAAGAACGCACCAUACAGGAA AACAUCUUGAUAAGAAGUGUUACUAUGUUUAGAC AAUUGUAUGGUUCGGGUAUUGACUUCUGUACUU GGA	104	sch-miR3448-5p	ACAGGAAAACAUCUUGAUAAG	28-48	aly-miR3448-5p	5	0	21	21	2
			sch-miR830-3p	AAAACAUCUUGAUAAGAAGUG	33-53	ath-miR830-3p	5	0	21	21	2
sch-MIR7984b-1	UUGAAAUUGCUGUAAUGAUACCGAACUUUGGAAA UGACCUGUUACCCCCUUGGAUUAUUUAAUAAUG ACGCAAUUUUUAUGAUGUCCACGUGAACAUAAAU AUAACUUUAAAAUACACUACUAAAUAAUGCGGGG GUGGGGGCGUAAAAGGUCCUUUCCAUAGUUCGA	188	sch-miR7984b-1-5p	AUACCGAACUUUGGAAAUGACCUG	18-41	stu-miR7984b-5p	1	0	24	24	1

	UAUCGUUAUAAUAAUUUCGA										
			sch-miR8181-1-3p	CGGGGGUGGGGGCGUAAAAG	131-150	ath-miR8181	4	0	20	20	2
sch-MIR8578	CAUUGAUAUGAUCUGUUUAAUAGUGAUCUUUGA GAAGUUAUAAACAUUCUCAUUAUAUUCUAAGGUG AAGUGCUGAAAUUUCGCACUUCCUGUAUGACUU AGAAUGGCCUCAUAGUAUGAUCGAGUCUUAUAU GAUUGUCCAGGGAAAUAUAAUCCCUUUGUUAAAU ACCUUUGGAGUAUCUUCCAAGGCUCAUUAUUUC UCUGAAUAUCAGAG	214	sch-miR8578-5p	UUUAAUAGUGAUCUUUGAGAA	16-36	atr-miR8578-1	5	0	21	21	1
			sch-miR6020a-3p	AAAUACCUUUGGAGUAUCUUC	164-184	nta-miR6020a-5p	4	0	21	21	1
sch-MIR5035	ACAUUUACCAAAUGCCUAGAUAAGCCAAAAAAUU GCUUAUAAGCUAGUUUGACCAGCUUAUAAGCUU AGAGGGUGUUUGACUAAGCUUAUAAGCUGGUCA AAUUGGCUUAUUAACACUUUUUAGCUUAUCUACU CAUUUGGUAAAACA	148	sch-miR5035-3p	CUUAUUAACACUUUUUAGCUUA	107-128	gma-miR5035-5p	5	0	22	22	1
sch-MIR8038b-2	AAGAAAUUGAUGACUUCAACUUGCAUAUAUGUAA GAUUUGAAGACUUCAACUUCCAUACUUGGAUGA UUUGAAGACUUUAGCUUGCAUACUUGGAGGAUU UGAAGACUUCAUCUUGCAGUUUUGGAUGAUUUA AAGACUUCAGCUUGUAUACUUGGAGGAUUUGAA GACUUCAACUUGCA	180	sch-miR8038b-2-5p	CUUCAACUUCCAUACUUGGAU	45-65	stu-miR8038b-3p	5	0	21	21	2
			sch-miR8024b-2-3p	UUGGAGGAUUUGAAGACUUCAACU	153-176	stu-miR8024b	1	0	24	24	1
sch-MIR2111d-2	AAUACUGUGUUAGGUUAAUGGUAAUCUGCAUCC UGAGGUUUAGAUCAAUUUCUAAUUUACUGGAUC UAGUCCUUGGGAUGCAGAUUAUCUUUACCUUAC AAACAGUGCA	109	sch-miR2111d-2-5p	UAAUCUGCAUCCUGAGGUUUA	22-42	ppe-miR2111d	0	0	21	21	1
			sch-miR2111d-2-3p	GUCCUUGGGAUGCAGAUUAUC	69-89	gma-miR2111d	2	0	21	21	1
sch-MIR5498	AUACUUGUGCAUUCAAAGAAUAUUAUUACAAAGC UAAAUACAAUUUAGACGAAGCAAAAGAAAUGGAA CAAUUGAAGACGAAGCUUGGGAAAUCUACUCUC UCAACAUUUGGUAUGUCCUCAUAUAUUUGAGGA CAUAGUUUAUGUUUUUCAUAGUUUCAAUAUUAAC ACUUAUUGUGUACUUUGCUUUGAAUGUAAAGGG A	202	sch-miR5498-5p	AGAAAUGGAACAAUUGAAGAC	59-79	osa-miR5498	5	0	21	21	2
sch-MIR1919-2	GACGCCUUUGAUGUUCACAUCUUCCGGUAGUCC UGUCGCAGAUGACUUUCGCCCUUUUAUGGAACA AUCCUUCAGGUCUUUUCUCUAAAUCUAAUUAAUU CAAUGUGGUAGGACGAGAGUCAUCUGUGACAGG ACAAUGGAAGAUCGAGUUAUCAAAGGCUUA	163	sch-miR1919-2-5p	UGUCGCAGAUGACUUUCGCCC	34-54	stu-miR1919-5p	0	0	21	21	1
			sch-miR1919-2-3p	ACGAGAGUCAUCUGUGACAGG	113-133	stu-miR1919-3p	0	0	21	21	1
sch-MIR479-1	UUCAGAAGCAGACAUGGCGUGAUAUUGGUUCGG CUCACUAAUUUCUGAUUAGUGUAACAGAUAAGAG AUGAGCCGAACCAAUAUCACUCUUGUAUUCUUCU UCA	104	sch-miR479-1-5p	CGUGAUAUUGGUUCGGCUCACU	18-39	ghr-miR479	2	0	22	22	1
			sch-miR479-1-3p	UGAGCCGAACCAAUAUCACUC	69-89	aof-miR479	0	0	21	21	1
sch-MIR395a-1	GAUGCCCUGCUGAAGUGUUUAGGGGAACUCUUG AACUCACUUUGAAAUUUUACACAAACAAAUAGAA GUGUAAGAGUCCUGGCUGUGGACAAUGAACAUG AUAGUUCAUGUAUAAAUCUAUUAAGGUGUUCCAU AGAGUUCCCUUGACCACUUCAUGAGGGCUUA	165	sch-miR395a-1-5p	UGAAGUGUUUAGGGGAACUCU	11-31	aof-miR395a	1	0	21	21	1
			sch-miR395j-1-3p	GUUCCCUUGACCACUUCAUGA	138-158	mdm-miR395j	2	0	21	21	1
sch-MIR2122	GUAAGAUUAUAUAUAUGAAAUAAAAGUUUGUUUA UAUAUAAAUAUUCUUCAAACUUGAUAAGUAGUUG AAAGUGGAAGUUGCGAUUUCCAGCCUUUAGGAG GAAUAGCAAGGAAAGUAGCCGUAAAGAGUGAAGA AGGCGAAAAAAGCUAUUCAUGGCCGAAGAGGAG AAAUGCUGAGUCAUUGAUAGGACUAAUUAUCAAC UAGAGGAAGAAGGUAUAAAAAAUUACCUUUUAUU	255	sch-miR2122-3p	UAUAAAAAAUUACCUUUUAUUG	216-237	osa-miR2122	5	0	22	22	1

	GCAUAUAUUAUAAUCUUAU										
sch-MIR7981a-2	UAUUAAGGUUCUAUUACCCCUGAACUUAUUUUAU AAGUAAUUUUAUACCCCUUUUCGGCCUACGUGA CACUAGCUUAAAAAAAAAGUGAACAACGUUGGAU CAACAAGAUAGUGUUACGUAGGUCGAAAAUGAUA GAAAAUUAUCAAUAAAAUAAGUUCAGGGAUAAUA AGACCUUAGUA	180	sch-miR7981a-2-5p	ACCCCUUUUCGGCCUACGUGACAC	47-70	sly-miR7981a	1	0	24	24	1
sch-MIR9471a-2	AGUUUGAUUUCUCAGAUGAUCACUCGACUAAUU GUUAUCAUCUCAGGAAGUCACUUUCUUUGUUGA AAGUUUUGGAAUCAAGAAGAAAGGGGACUUUCG AGAUAAUAACUAUUAGUCAAGUGACUAUAUGAGA AAUCAACCG	142	sch-miR9471a-2-5p	CAGAUGAUCACUCGACUAAUU	13-33	sly-miR9471a-5p	5	0	21	21	1
			sch-miR10540-2-3p	AUAAUAACUAUUAGUCAAGUG	102-122	sly-miR10540	3	0	21	21	1
sch-MIR8001b-1	ACCCACUAUAAGAAAAAAGUGAAUUACAUGGGGA UUUUUCUAGAGAUUAGUAUUAAAAUUUGUAGGAA AAUAAGUUACUUGCAGAUUUUCAUACUAACCCCU AGGAAAACCUCCAUGUAAUUCAUACUUUUCUUGU AGUGACG	143	sch-miR8001b-1-5p	CUAGAGAUUAGUAUUAAAAUUUGU	40-63	stu-miR8001b-5p	5	0	24	24	2
			sch-miR8001b-1-3p	AGAUUUUCAUACUAACCCCUAGGA	83-106	stu-miR8001b-3p	4	0	24	24	2
sch-MIR5770b	GGGUAAAGGUCUAACACGUGAAGAUCGUCCGUG UUGAGAUCAAGUUAUGAUUAUUUGGUCACGUGG AGAUCGUUCGUGCGAUAAAAAAGUUAUGAUUAU GAUUUGGGCACGUGGAGAUCGUCCGUGUCAAUU UUAUUU	138	sch-miR5770b-3p	UUAUGAUUAUGAUUUGGGCAC	90-110	gma-miR5770b	5	0	21	21	1
sch-MIR830	GUGACUUUUAUGAAAAGUUGCGACUAUUAUAAAA GGUUGUAACCUUUACGAAGGAUUGUAACUUUUC CAAAGAGUUGU	78	sch-miR830-3p	ACUUUUCCAAAGAGUUGU	61-78	ath-miR830-5p	5	0	18	22	2
sch-MIR5543	AUAACCUAAUUACUUUUCAUAACUAUUAUUUGAU AAUUACAAUUUGUAGUUACAUGUUAUAGAGAGGA GAGAGACGGGCGAGAUUGAGAGAGAGGCGAGAG AGAGGGCAAAGAGUGGGAGAGAUGUGAAUUGUA UAUUAUAUUGGUUAGAUAAUUGUAUAUCAUUCAU AUGUAUUUGCAUAUUCUGCCAAAUUAUACAUAUA CAAACGUGACUAAUCAUACAAACUCGAAGUCAGC CCACAUAAUUAAUGUAUGAUGUUAGUCGUGUGU GGUAAUUAUAACAAAUUAUAGUUAUGAUAAGUAA UUAAGUAGU	312	sch-miR5543-5p	UGUGAAUUGUAUAUUAUAUUG	124-144	osa-miR5543	4	0	21	21	1
			sch-miR2108a-3p	UUAAUGUAUGAUGUUAGUCGU	245-265	gma-miR2108a	5	0	21	21	1
sch-MIR6232b-1	UCAGGUGUUAGGAAAUUAUCCCACCAUCCUCUG AGUUGACCUGUAAAUCCUGCUAUAAUCAUUUUAC AUAUAGCAUGAUCACUAUUCUGAUUUGUAUGAC GACAAAUUGAUGAGUACAUCAACAUUCGAUGUAC CAUAAUGGAAACUUGCCUUUCUGUCAAGGCAUC CAAAUUCCAUUCAUACACCUCAUUACCACUGUAA GAUGUGUUAGUUUGAUUCCAAUCUCUUUCUUCA ACUAGCACAUCUUGGGGAGUAGGACGAGGAUAA UAAUAAGUCAUCAUGGAAGGGAUAAUUGCAUAAC CCCCUU	307	sch-miR6232b-1-5p	CAUUCGAUGUACCAUAAUGGA	123-143	sbi-miR6232b-3p	5	0	21	21	2
			sch-miR396e-1-3p	UUCCAAUCUCUUUCUUCAACU	217-237	fve-miR396e	5	0	21	21	1
sch-MIR7992-2	UAAUCAAGCUUGAUCUCAGUUGAGCAGUAAACAC UCCAACUUAGAAGAUGCACAUCUAGACAGCUCAA CACAAAUCCACUGUGUCAAUUGAGGUGUCUAGA UGUGCAUUCUCAAAGUUGGAGUGCUUACUUGCC AAUUGAGGCCAAGUUUGAGUG	155	sch-miR7992-2-5p	UUAGAAGAUGCACAUCUAGACAGC	41-64	stu-miR7992-5p	5	0	24	24	1
			sch-miR7992-2-3p	UGUCUAGAUGUGCAUUCUCAAAG	94-116	stu-miR7992-3p	5	0	23	23	1
sch-MIR2670g	GGUCUAUAGGAAACAAUCUCUCUACCUCCCAAG GUAUACACUACGUUCCCCAUACUCCACUUGUGG GAUUACACUGGGUUGUUGUGUUGGGGAGGAGG GGGUUGACCUAUAGGGG	115	sch-miR2670g-3p	ACUGGGUUGUUGUGUUGGGGA	73-93	mtr-miR2670g	5	0	21	21	1

sch-MIR7997b-3	CUUAAGGCUAAGUUGCUCGGACUCUCCAAAAUU GCUACCACACCCGUGUCGGAUCUUCCAAAAAUG CUUUACUUUUGGAGGAUCCGACACGCACCCGUC GACGUUUCUGAAGAGUCCGAGCAACAUAGCCUU GAU	135	sch-miR7997b-3-5p	AAGUUGCUCGGACUCUCCAAA	10-30	stu-miR7997b	3	0	21	21	1
			sch-miR5303d-3-3p	UUUUGGAGGAUCCGACACGCACCC	73-96	stu-miR5303d	1	0	24	24	1
sch-MIR6300	CCUAUAUCUUUAUACUCCCUCCAUCCAUGUUUAC UUGUUUAUGUUUGAUUUGCGACACCCUUAAGAA GCAAUAAACAAAAGGGUAAUUUUAAUAUAUCACC UCUAAUUAUUAUAAGUUGGAAGAUGAAUAGUACU UGAUAAAUUAUCUCUUGGUUUUUCAAACUGAACA AGUAAAAGUGGACAUUUAGUUUUAGUAUAGUGG ACAAGUAAAAGUGGAUGGAGGGAGAAUUAGAGA CAUUUU	241	sch-miR6300-3p	UUAGUUUUAGUAUAGUGG	185-202	gma-miR6300	3	0	18	18	2
sch-MIR1128-1	UCGAGACAAAAGUUACUACUCCCUCCGUCCCAUU UUAUGUGAGGUAGUUUGACUCGGCACGGAGUUU AAGAAAGAAAGGAAGACUUUUAAAACUUGUGGUC CAAAUGAAUGAUAGAAAUUUGUGUGGCCGUGAA UCAUUUCAUUAAGGGUAAAAUAGACAAUUCAUAG UUAAAUUGUUACUUAAUAUAGAAAUGUGUCAUUC UUUUUAGGACUGACUAAAGACAAAAGUAAGUCGC ACAAAUUGGGACAAGAGGGAGUAGGUUAUUUCU UCUUAU	275	sch-miR1128-1-5p	UACUACUCCCUCCGUCCCAUU	14-34	ssp-miR1128	2	0	21	21	1
sch-MIR8011a-3	CCCCUUUCUUUAUGACAACACGAAUACUAGUUGU GUGAGGCUUCUUUUUGUCUCACAUAAAAGUAGA CUCAAAUGGGCGAGACAAAAAUGAGUCUCACUC GACUAGUGUCAGUUGUGUGAGUCACAAAAUAGA AC	135	sch-miR8011a-3-5p	UUGUGUGAGGCUUCUUUUUGUCUC	31-54	stu-miR8011a-5p	2	0	24	24	1
sch-MIR169h	AUUGCAAUUUUGGGAGUGUGAAUCUUGAGCAAA CGCUUGCUUGCCUAUGCUAGAAAAAGUAUAAUU UUCAUGAUAGCAGUAUGCAUGGUCUUUUCUUUC AAAAAUAUAUAAUUACUCCUAGUAAUUAUAUAUU UUUGAAUGGAAGGCCCAUGUGUAUUUCAUUCUU GAAACUUUUUCUCAUAGGUAAUGAACAUUUCCUU UUACUGCCUUUUAUGUAAUCAUCAUCAAGAUUCU CCUUCCAAAUUGCACU	250	sch-miR169h-5p	UGAGCAAACGCUUGCUUGCCU	26-46	vvi-miR169h	5	0	21	21	1
			sch-miR8016-3p	AUUUUUGAAUGGAAGGCCCAUGUG	131-154	stu-miR8016	0	0	24	24	1
sch-MIR5773-1	ACCCACCUAACCCGAUCCAUUAAAAAAUAUGAUA UGACCCAUUUUAUUUUGUCUUUAAUCCUAAUUCA AGGUUUAAAGUGAGGGAUUAAUUUAGGAUUAAA GACAAAAUAAUAUGGGUCAUCAUAUUUUUUAAUG GGUCGGGUUAGGUGUUA	152	sch-miR5773-1-3p	UUUUUAAUGGGUCGGGUUAGGU	127-148	gma-miR5773	5	0	22	22	1
sch-MIR11085-1	GUAAUCCACCCACCUAACCCGACCCAUUAAAAAA UAUGACAUGACCCAUUUUAUUUGAUCUUUAAUCG UAAGUUAAUACCUCUCUUUAAACCUUGAAUUAGG AUUAAAGAUAAAAUAAAAUGGGUCAUAUCAUAUU UUUUAAUGGAUCGGGUUAGGUGGGUGGAUCAC	168	sch-miR11085-1-5p	AUUUUAUUUGAUCUUUAAUC	48-67	lja-miR11085-3p	5	0	20	20	1
sch-MIR171o-1	GUAUAGUGAAAAGGAACUGAGAUAUUGACACGG UUCAAUCAAAUCAAAAUAAUAUGUGUCUGAGUGA ACCAGGCCAAUAUCAGAGUUACUAUUUCAUAGAG	101	sch-miR171o-1-5p	AGAUAUUGACACGGUUCAAUC	20-40	gma-miR171o-5p	2	0	21	21	1
			sch-miR171a-1-3p	UGAGUGAACCAGGCCAAUAUC	61-81	aof-miR171a	4	0	21	21	1
sch-MIR7981-2	AUCCCCUAGACUAUGAUCGAAAUUCGAGCGACA GACCUUAACUAAACUAAAGUCCUAUUACCCCCGA AUCCAUUUUUUUUGUAAUUCUGUACAUUGACAUC CAAACAUCUCUCACGCGCCUCGAGUCACGGAGU GUACCACGUAAGCCAAAAGGUGUACAAAAUUACA AAACAAAUGAGUUGGGAGUAAUAGGACCUUAGU UAAGUUAAGGUGUCUCUGAGAUUUCGGUCACAG UCUAAGGAGU	244	sch-miR7981-2-5p	CUUAACUAAACUAAAGUCCUAUUA	37-60	stu-miR7981-5p	4	0	24	24	2
			sch-miR7981-2-3p	AUAGGACCUUAGUUAAGUUAAGGU	189-212	stu-miR7981-3p	2	0	24	24	1
sch-MIR7983-1	UACACUACAAUAAAAAUAACUCUUAGCGGCAUUA AAUAUUGACAUUAAUAAAGAGUAGUGCUAAAGUC	216	sch-miR7983-1-5p	UAAAGUCUUUACCGACAUUAGUUA	62-85	stu-miR7983-5p	3	0	24	24	1

	UUUACCGACAUUAGUUAAUUGCCAUUAGAACCAA UAUCGCUAAAGACUUUAGGAACAUAUACAAAGAG UGUCUACUGCCGCUAAAAAUACACAUUAAGCGGC AAUCGAGAAUUAAUCGCCGCUAGAUGAUCAUUUU UGUUGUAGUACU										
sch-MIR6160	UUUUUUAACUUUCGUUAAAUGAAGGGUAUAUGU GAGCCAUUUUUUAACGGCGGGGGUAUAUGUGAG CCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCC ACUUUUAUAACGAGGGUAUAUCAGCUCCAAAUGA CAAAGUUGAGAGAUAUAUCCCUUUUCCCUUUUAA AUUUAACGAUAUAAAAGGUUCACACAUAUUUCAA UAUUAUAAAGUUAAACUU	219	sch-miR6160-3p	GCAUAUAUGAGCCACUUUUAUAAC	87-110	nta-miR6160	5	0	24	24	1
sch-MIR863-1	GUUCUUCAACUUUGAGUAUGCAAAAAUAAACAUU UAAAUUUGUAUAAAGUUGAAUAAGUAAAUACAUG AGUCCUACAUGACAUAAUACACGUAGAAUACCAC AUAUGACAAAAAUAACAUCGAGGAUGUAGGACAU GUGUGUCGAUUUGUUCAACUUUAUAGAAGCUUA AGUGUCUAUUUAUGCACACCCAGAGUUGAAGGG G	203	sch-miR863-1-5p	AUGAGUCCUACAUGACAUAAU	66-86	ath-miR863-3p	5	0	21	21	2
sch-MIR156h-1	GUUUUGACUUUUUAAUUCUUUUUGUUCCUUUUU UCUCCCUCCUCUCCAUUACCUCUAUCAACAAUCA CUCUUUUUUCUUCCAUCCUCCUUAACUCCCUGC CAACAUUGUUACAAUUACCUCCACCACCAUCUUC UCUUGCACUUCCUACGCUACCCCACCAUCACCU CCACCACUAGAAGGGAAUACGCUAAACGACUUGA ACAUGCAACAUAUAAUAUCAAUUUAAUGCAGGUG UAUAGCUGCAUAUGGGACAAAGGAGGAAGAAAG AUUGAUUGACGAUAGAUGUAGUGGAGGGAAGAG AGAAAGGAGGAAUAAUAAAAGAAAAGGCAAUCU	334	sch-miR156h-1-5p	ACUCUUUUUUCUUCCAUCCUC	67-87	mtr-miR156h-3p	5	0	21	21	2
			sch-miR11440b-1-3p	AUGUAGUGGAGGGAAGAGAGA	284-304	pab-miR11440b	5	0	21	21	1
sch-MIR12142	UAAUAAAUGGUAUGCAGAUAUUUCUCGUCAUAUU UUUGGGACAUUGGUAUCCUUGUCGUCCAAAAGU UAGAGCUAUAUACCUUUUAUACUAACAAACAUAC AUGUAUCAUAAUUUUAUCCACCGACCCGACAUUU AUUAAAUAUUUGAUCAACGGACAAAAUUGCUCCA UGUGUCCCUAUUUAGUCUUCCGUUAGAGUGAAG GGCAUAUAUACUCUAGUUUUUGGAUGGCAGGGG CACCAAUAUUCCGAAAGUAUAAUGAAGGAUAUAU GCAUUACCAUUUACGG	285	sch-miR12142-5p	UAUUUUUGGGACAUUGGUAUC	31-51	aof-miR12142	5	0	21	21	1
			sch-miR8006-3p	UAGUUUUUGGAUGGCAGGGGCACC	216-239	stu-miR8006-5p	2	0	24	24	1
sch-MIR10427b	UUUUAGAGAAUGAUAUAGAGAAUUGGGUUGGAG UUGGUUGUUUGGAUAUAUAGAGAACUCUAUAUU UGGAGAGUAAAAUUCAGUAUAGGGUUGGAGAUG UCUUAACCAACCUCCAAAUCACCCAUUAUUCUUC AUUUAUAGAG	143	sch-miR10427b-5p	AUAGAGAAUUGGGUUGGAGUUG	15-36	gma-miR10427b	5	0	22	22	3
sch-MIR390a	AUGGCAUGGGGAAUCUAUAAAGCUCAGGAGGGA UAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUA GCGCUAUCCAUCCUGAGUUUUAUGGCUUUUUCA UGCUCG	106	sch-miR390a-5p	AAGCUCAGGAGGGAUAGCACC	20-40	sly-miR390a-5p	0	0	21	21	1
			sch-miR390a-3p	CGCUAUCCAUCCUGAGUUUUA	69-89	sly-miR390a-3p	0	0	21	21	1
sch-MIR8739	GCAUCAUACUUUUUGAACAUUGGUGUCCUUGCC GUCCAAAAACUAAAACAUAUAUGCCCUUCACUCU AAUAGAUGACGAAAUAGGGACAUGUGGCAAUCU UAUCCGUCGAUAAAUUUCGAGUCGGUAGAUAAG AUUAUGACACGUGUAUGUCCGUUAGUAUAAGUG GUAUAUAUGCUCUAAUUUUUGGAUGACAGGGGC ACCAAUGUUCCUAAAGUAUGACGG	223	sch-miR8739-5p	UGACGAAAUAGGGACAUGUGGCAA	74-97	gra-miR8739	5	0	24	24	1
			sch-miR8006-3p	UAAUUUUUGGAUGACAGGGGCACC	179-202	stu-miR8006-5p	2	0	24	24	1
sch-MIR1106-1	CCCCCCACCCUGCACUAUUAAAUAAUGUAUUUUA AAGGUAUAUAUGUGUCCACGUGGACAUCAUAAAA AUUGCAUCAUUAUAAAAAUUAAUGUGUCAAUGUG AACACAUAUAUAUCAUUAAAAUGCACUAUUAAAU	151	sch-miR1106-1-5p	UUUAAAGGUAUAUAUGUGUCC	31-51	smo-miR1106	5	0	21	21	1

	AGUGUAGAGGGGUAA										
sch-MIR160-1	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAAC UAGGAAGAGUGUCAAUUUUUUUGACAAUACUGU UCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACA AUUUC	104	sch-miR160-1-3p	UGGCAUCCAGGGAGCCAGGCA	74-94	aau-miR160	1	0	21	21	1
sch-MIR5339	UUCUUCAGCUUCGUCCUCUAUAAACUUAAAGGAU AUUCCUAAAGACAGUUCAUUAUAUGAACAAAUUC AGGCAUAUUUGCAGAAAAAAGAGCAAGGUGAUAC CUACGCCUCUUUAGCCAGAGAAGCUUCUCAGAA GAAACAUCCACAAAAGAGAUUAUAUUUCUUUUGA AAAACUCUGAUAUUCGGAGAAGUAAUGAACCUUG GAAGAUACUCCAAAGGUAUCUAACAAAGGGAUUA UAUUUCCCUGGAGAAGCAUAUAAGACUCGGACA UAUUAUGAGUCUAUUCUAAGUCAUACAGGAAGU GCUGAAUUU	312	sch-miR5339-5p	UAGCCAGAGAAGCUUCUCAGA	114-134	osa-miR5339	4	0	21	21	2
			sch-miR400-3p	UAUGAGUCUAUUCUAAGUCAU	274-294	cas-miR400	4	0	21	21	1
sch-MIR7696b-1	AGGAUUAGGUGAAUUGAUGGGUAUAGACUAGAC AUAGAAUAAUCUGAGUGUUUAUGGCCUUGUGAA CUUACACCUUGUGUGAUAUAUACUUGAUAGUUG AGAAAUUGAAGAGGAUAGGUGUUAGUGCAUGGU GAGUCUGUGUCAUGGUCUGAUUCCACAUAAUUC AAGCCUAAUAGU	177	sch-miR7696b-1-3p	UUGAUAGUUGAGAAAUUGAAG	90-110	mtr-miR7696b-3p	5	0	21	21	1
sch-MIR7992-3	UUGACAUCUAUGUCCUCCAACUUUGAGUAUGUA CAACUAGACACUUAAAGUUGUAUAAAAUUGAACA AAAUAAACACAUGCGUCUUACAUGACAUCCUACA UAGCAAUUUUAUAUCCUACAUGGUGCACUACGUA UUAUUAUGCAACGUAUUACGUGUGUUUCUACUU AUUCAAUUUUAUACAAAAUAAGUGUCUACUUGUG CACACUCAAAGUUGGAGAACAUAGAUGUCAG	233	sch-miR7992-3-5p	UUUGAGUAUGUACAACUAGACACU	22-45	stu-miR7992-5p	4	0	24	24	1
sch-MIR10533-1	AUCCAAAAGAAUUGGAUCAAUUGUUUUGUUAGCA UUGUAAAGACGUCUCAAAGUUCUUGUGUAUUUU AUGAACACUAGGUCAUGUUGAGGUGCUUCAGGG UUCUCUUCCUCAAUGACCUAGUGUUCAAAAAUAU AAUAGAAUAUCAAGGCGUCCUUACAAUGCUCACA AUGGAUUGAUCCACUUCUUUUGCAU	193	sch-miR10533-1-5p	UUUUAUGAACACUAGGUCAUGU	64-85	sly-miR10533	5	0	22	22	1
			sch-miR1446-1-3p	UUCAGGGUUCUCUUCCUCAAU	94-114	gma-miR1446	5	0	21	21	1
sch-MIR5568d	ACGAAAAUAUAUGUAUAUACACAAUUUUUUCUCG CUUUAUACAAACAGAAAUACAUUUUAUACACUUG UGUUUGUAUAAAAGUGAGAGCGAGCGAGAGUUU GAGGGAGAGAGGUGACUGGCAAACAGUUUGCUA CAGGGAACAAUUAAACUAAAUUGUGAUUAUAGCA UUUAAUUUAAU	179	sch-miR5568d-5p	ACACUUGUGUUUGUAUAAAAG	62-82	sbi-miR5568d-3p	5	0	21	21	1
sch-MIR5568b	CGGUAAUUAAUUCUAUGGUCCCUAUAGUGCCCA UAUUUAACUAGAAUUCAGAAUUCUAUUUCUAUGC AAAAAGGAAGAAUAAUAUGGGUUUUUCUAGUUUU CUAGAAAAACUAGGUUUUCUAGUCCUUUUUGGA UUAGGAAGACAUCUCUAUAAAUAGAGAUUCUCCU AACCUAGCAAAUGGAGGAAUUAGUUUUAUAUUUG AUACUUGCACACUCAAGUAUUGAGAGAGUUCGG AUGUGACUUGGGAUCACUGUAGAAGACCAUAGC UAUUGUUUAUCU	280	sch-miR5568b-5p	UCUAGUUUUCUAGAAAAACUA	93-113	sbi-miR5568b-3p	5	0	21	21	2
sch-MIR169r-3	UUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCU UGCAUGAGGGAAUAAGGUUAUUGAAUUGCAGCC AAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCU GCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAU AUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAU GAAACAGCUGCUGUUGUU	184	sch-miR169r-3-5p	CAGCCAAGGAUGACUUGCCGG	63-83	csi-miR169r-5p	0	0	21	21	1
sch-MIR398b-1	AUGAACAAUGGUGCAUCCCAGAGGAGUGUGCCU AAGAACACAGGUGUAUUUUGGUCUUCUCCUGUU UUGGACCCAAAGUAUGCUUGUGUUCUCAGGUCA CCCCUUUGGGAUCACCUUGCUUUUU	124	sch-miR398b-1-5p	GAGUGUGCCUAAGAACACAGGU	24-45	stu-miR398b-5p	1	0	22	22	1
			sch-miR398-1-3p	UUGUGUUCUCAGGUCACCCCU	84-104	lja-miR398-3p	0	0	21	21	1

sch-MIR426	UCACCUCUUUACAACAAAGGGCCAAAAUUUAAAG AAGUCAAGUAGAUGCAUCACCUACUUAACUCCUU GGUUUAUUUGCUUAAGUAGGUGAUGCAACUACU UGUCUUAUUUACAUUUUGGAACUUCGUUCUUAA GUAGGCAC	142	sch-miR426-3p	UUUUGGAACUUCGUUCUUAAG	115-135	osa-miR426	4	0	21	21	1
sch-MIR156b-10	AGGAGAAAAAAGAGGGGAAAAUGGAAUGGGUGA UAUUGUUGACAGAAGAUAGAGAGCACAUAUGAU GGAAUGCUGCUGCUAAAUCUGGAGAGUCUAAAC AAUUAAAAAAGCAUUUCACUUCAUUUGUGCUCUC UAUGCUUCCGUCAUCCCUUUCAUCCUCUUUUCC UUCUAUUUUUCUCUU	181	sch-miR156b-10-5p	UUGACAGAAGAUAGAGAGCAC	39-59	aof-miR156b	0	0	21	21	1
			sch-miR156g-10-3p	GCUCUCUAUGCUUCCGUCAUC	128-148	fve-miR156g-3p	1	0	21	21	1
sch-MIR159	UUUUAAUUGAUCAAUCAUCUCGAGGCAGGAAAGA UUGAGACUAUCCCAUAGACUGAAUUAUUGUUUU GAGAAUGAUAAUAACUCAGUUUAUAGGAUAGUCU CAAUCUUUCUUGCCUCCAAAGACUGAAUUAUUAU UA	137	sch-miR159-3p	AAUCUUUCUUGCCUCCAAAGA	103-123	vca-miR159-5p	5	0	21	21	2
sch-MIR171c-2	UAUAGAUAUUGAUGCGGUUCAAUCUGAAAGACAU GGUUAGAUAUGUAAUUAGCCCUGUAAUUUUGGA UUGAGCCGCGUCAAUAUCUCUC	89	sch-miR171c-2-5p	AGAUAUUGAUGCGGUUCAAUC	4-24	cas-miR171c-5p	1	0	21	21	1
			sch-miR171e-2-3p	UUGAGCCGCGUCAAUAUCUCU	68-88	sly-miR171e	0	0	21	21	1
sch-MIR8666	ACUAUGUUUGGAGCGCACAAGUUCAUAAUUGAC UAUGUGUUCGUGUAGUUAAAAAAUGGUAAGAAAU ACACGUGCGUCGCACGUGUUCGAGAACUAGUAU AAAUAUAAAUAUGGAGUGCGAUUAAAUAUUUACU UAGCUGUUAUCUAUGAUUUAGGCUUCAUUUGUU UCCAUUAAGAUUAAGAGGUCUGAAACUGAAUACA UAUUUGAAUAUUAAAAUUUGCAUAAAGAUUCAGG UGUUUUGAUCUGAAUACACAUCUGAAUAUUAAGA UGUGCUCUCAAAAUUUG	286	sch-miR8666-5p	UUGGAGCGCACAAGUUCAUAA	8-28	gra-miR8666	5	0	21	21	1
			sch-miR1514b-3p	AUACAUAUUUGAAUAUUAAAA	197-217	gma-miR1514b-3p	5	0	21	21	1
sch-MIR7992-4	AGUAAGCACUCAAACUUUGAGAGUGCACAUCUAG AUACCUCAACUUGGUCAUAACCGACUACUAAACA AUCCACGACCACUUGUCUCCACUUUGUCUCAUG CACACCAGACUCUGACAUGACACACGAAUUUUGG AGGUGUCUAGAUCAUUUUGUAAGUUGAAAUGUU CAAUUGACACAGUGGAGAUGAGUUGAGCUGUCU AGAUAUACAUUCUCAAAGUUGGAGUGCUUGAG	233	sch-miR7992-4-5p	UUUGAGAGUGCACAUCUAGAUACC	16-39	stu-miR7992-5p	4	0	24	24	1
			sch-miR11416-4-3p	ACACGAAUUUUGGAGGUGUCU	123-143	pab-miR11416	4	0	21	21	1
sch-MIR3627	GAGAGAGAUUGAGGGAAUCUUGUCGCAGGAGAG AUGGCACUUACCAUUCCUUUUAAUUGGUACAAU GCCUAAAUGGAACCAAUUAAGUGCCUCUGUCUU UCGACAUGAUGCCCACGAUUUCUAUA	125	sch-miR3627-5p	UCGCAGGAGAGAUGGCACUUAC	23-44	stu-miR3627-5p	1	0	22	22	1
			sch-miR3627-3p	AAGUGCCUCUGUCUUUCGACA	85-105	stu-miR3627-3p	0	0	21	21	1
sch-MIR7997c-2	AAGACCUGUGUUGCUCGGACUCUCCAAAAAUUU AAUACUUUUGAAGAGUCCGAUACACACGUGUUU GACAUUUUUAAAGAGUUCGAGCAACAUAAGUAAA	100	sch-miR7997c-2-5p	GUGUUGCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	3	0	24	24	2
			sch-miR5303-2-3p	UUUUUAAAGAGUUCGAGCAAC	71-91	sly-miR5303	1	0	21	21	1
sch-MIR1043-1	ACCCUUAACUUGGAUUCAUCGGACAAUUAUACCC UUCAACUUUGAGUGUGCACAAAGAGACACUUAAA CUUCUAUAAAAUUGAACAAGUAGAUAUACAUAUC CUACGUGGCAUAAUACACGUAAGACGUCAUGUA GGACACAAAAUUGUCAAGUAAGACGAAUGUGUCU AUUUAUUGAUCGAUUUUAUACAAAUUUAAGUGCU ACUUGUGCACACCCAAAAUUAAAGAUUAUAUUUA UUAACUGACGUUAAGUUAAGAAU	260	sch-miR1043-1-5p	CCUUCAACUUUGAGUGUGCA	33-52	ppt-miR1043-5p	4	0	20	20	1
			sch-miR5014a-1-3p	UUAUACAAAUUUAAGUGCUAC	185-205	ath-miR5014a-3p	5	0	21	21	1
sch-MIR6272	UGCGCCAAUUACUACAUUAAAAAUGAUCAUUAGC GACAAUUAAUUCUUAAUUACCAGUAAAUUUGUAU	209	sch-miR6272-5p	UACCAGUAAAUUUGUAUUUUU	52-72	ppe-miR6272	5	0	21	21	1

	UUUUAUCGGCAAUGAACACUCUUUGUAUGUGCC CCGAAAGCCUUUAGCGACAUUGGUUAUAAUGAC ACUUAACUAAUGCGGUAAAGACUUUAGCACUAUU UAAUUUCACUAAAAGUUAUUUUUGUUGUAGAGAU UAGCAUA										
			sch-miR7983-3p	GAAAGCCUUUAGCGACAUUGGUUA	104-127	stu-miR7983-5p	3	0	24	24	2
sch-MIR160-2	GGUGGUAUGCUUGGCUCCUUAUACGCCACCCAC UGAUCAGUCAAUCAAAGUAUUGGUGAAUGUGUG UGGCAUACAGGGAGCCAGGCACAUCCUUC	95	sch-miR160-2-5p	UGCUUGGCUCCUUAUACGCCA	8-28	dpr-miR160	3	0	21	21	1
			sch-miR160-2-3p	UGGCAUACAGGGAGCCAGGCA	67-87	aau-miR160	0	0	21	21	1
sch-MIR399a	AACAAAUAAAAAACUACUCAAAAUAAUUUGAAGAA UUGGAGAGGACAAGAAACGCAGGGUAUUCUCCU UUAGCAAGAUUGCUAUAUAAUGCUUUAUGCAUGA AUUAAAUUCUUUCUUGCCAAGGGAGAAUUGCCC CGCGUUUCUUCAUUUCCACAAAAGUCUAAUUCAU CUGGUGUCUGAUAUUUAGA	188	sch-miR399a-3p	UGCCAAGGGAGAAUUGCCCCG	117-137	ata-miR399a-3p	2	0	21	21	1
sch-MIR7997b-4	AAAGUUGCUCGGACUCUCCAAAAUUGUUGCCCC ACCCCCGUCGGAUCCUCCAAAAAUGCACUACUUU UGGAGGAUCUGACACACACAUGUCGAUAUCUUU GAAGAGUUCGAGCAACAUA	119	sch-miR7997b-4-5p	AAGUUGCUCGGACUCUCCAAA	2-22	stu-miR7997b	3	0	21	21	1
			sch-miR5303-4-3p	UCUUUGAAGAGUUCGAGCAAC	96-116	sly-miR5303	1	0	21	21	1
sch-MIR1170	UUAGUUUAUAUAUGAUCAAUGAAUCUUUUUAGAC UAAAUAUAUUAGAUUCAGCCAAACUCGUAAUAUG UAAUCUCAUUCGGCUCCUAAUUAGAGCUGUCAA UUUGGGCUAGUCCAUUCUAUUUGGGCUAACCCA UAAAGGCUUUGACAUUUUACGGGCCAGGCCGGG CUAACCCAUUUUUGGUAUGGAUCAGAAAACGGU CGGCCCAACCCAUAAGUACGUGGGCUACAGGCU UACCGGGUCAGUUCACUUUUUAAAAAAUUUAUAUU AAUUUUAGAAUUAUUAAAUCAAAAUUAUAAAUUA UAAUUUAAAAUAUUAUCAUAAAUAUCAACAAA	333	sch-miR1170-5p	AUUCAGCCAAACUCGUAAUA	47-66	cre-miR1170-2	5	0	20	20	1
			sch-miR8040-3p	AUUAUAAUUUAAAAUAUUAUC	298-318	stu-miR8040-3p	5	0	21	21	2
sch-MIR11444	UCAAACCUCUUUAUAACAGUAUCGUUUGUCUGG AUAUGUUUUGGUUGCUAUAACGAGAUGGUGUUA UAGAUAACAUAUAUUAAAGUCAAUUCCAAAAGAU CUAACUAGGCCGUUAAUGUGAAAUUUUGUUAUAA AGGAUGACUGUUAUAGAGAGAUUUGA	160	sch-miR11444-3p	AUUUUGUUAUAAAGGAUGACU	123-143	pab-miR11444	5	0	21	21	1
sch-MIR9471b	UUGAGAUUCAGUUGAUUUCUGGGGUGCUCACUC AGCUAAUAGUUAUUGUUUAAGAAACUCAAUAAUA UUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUG AUAACUAUUGGCUGAGUGAGCAUCACGGAAAUC GACGUGAUUCUGAG	147	sch-miR9471b-5p	GGGGUGCUCACUCAGCUAAUA	21-41	sly-miR9471b-5p	1	0	21	21	1
			sch-miR9471a-3p	UUGGCUGAGUGAGCAUCACGG	108-128	sly-miR9471a-3p	0	0	21	21	1
sch-MIR169j-3	AAACAUGAAGAGGAGAGUUAUAUUAUUGUUUAGU AGCCAAGGAUGACUUGCCUGCUCCAUAGUUUAA AAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAG GCAGUCUCCUUGGCUACCUUGACAUGCUCUCCU CUUUCAUGCAA	144	sch-miR169j-3-5p	UAGCCAAGGAUGACUUGCCUGC	34-55	ppe-miR169j	0	0	22	22	1
			sch-miR169e-3-3p	CAGGCAGUCUCCUUGGCUACC	98-118	csi-miR169e-3p	2	0	21	21	1
sch-MIR169j-4	AUGAGAAGAGGAGUCUAGCAUGAUGAAAAGAGU CUUAUUUGGUAGCCAAGGAUGACUUGCCUGCAC CAUAUUCGAAAUGUGUCCUUUCGUUCAUGGGGU CAAGCAGGUCAUCUUUAGCUAACUUGACAAGCU CUUCUCUUUCAUGCAAGACUUUCUCUUCUUCC	164	sch-miR169j-4-5p	UAGCCAAGGAUGACUUGCCUGC	43-64	ppe-miR169j	0	0	22	22	1
			sch-miR169d-4-3p	GCAGGUCAUCUUUAGCUAACU	103-123	stu-miR169d-3p	0	0	21	21	1
sch-MIR11131	UACUUACGUCCAACAAAUGACCUAUUUGUUGCAA UAAAUAGGUCAUUUGUUGAACGAAAACUCAAUCA UUUGCUACUGAUUUACUUACGUUCAACAAAUGAC CUAUUUGUUGCAACAAAUAGAUCAUUUGUUGGA	143	sch-miR11131-3p	CUUACGUUCAACAAAUGACC	84-103	lja-miR11131-3p	4	0	20	20	1

	CGAAAUCU										
sch-MIR6024-3	CAAGUGCAGCUAACUGGAGAUGGGGAAGUGGAG AAACAACACUUGCUAAAGGAUCUUCACAAGUCAU CUCUUUUCUUUUGGAGUUUUCUCUUUUCUUUUG GAGUUUUUUUAGCAAGUGUUGUUUUACCUCUUC ACAAUUCCGUCUAUCUUUCACAGU	157	sch-miR6024-3-5p	AGAAACAACACUUGCUAAAGGA	32-53	stu-miR6024-5p	1	0	22	22	1
			sch-miR6024-3-3p	UUUUAGCAAGUGUUGUUUUACC	107-128	sly-miR6024	1	0	22	22	1
sch-MIR6024-4	CUAACUGGAGAUGGGGAAGUGGAGAAACAACAC UUGCUAAAGGAACUUCACCAGUCAUCUCUUUUC UUUUGGAGUUUUUUUAGCAAGAGUUGUUUUCCC UCUUCUCAAUUCCGUCUC	117	sch-miR6024-4-5p	AGAAACAACACUUGCUAAAGGA	23-44	stu-miR6024-5p	1	0	22	22	1
			sch-miR6024-4-3p	UUUUAGCAAGAGUUGUUUUCCC	78-99	stu-miR6024-3p	0	0	22	22	1
sch-MIR7992-5	CCUCAACUUGGUUACAACUGACAACUAACCCACU CCAACUUGUCCUCACUUUGUCUCAUGGACACCC UGACGUGACACAUAAAUUUUGGAAAUGUCUAGAU GAUCAUUUUGUAAGUUGGGGUGUUCAAGUGACA CAGUGGAGACGAGUUGAGGUGUCUAGAUGUGUA UAUUCAAAGUUGGAG	182	sch-miR7992-5-3p	UGUCUAGAUGUGUAUAUUCAAAGU	154-177	stu-miR7992-3p	2	1	24	23	1
sch-MIR482d-1	CAUGAUACAUUUUUAUCUUACUGAUGACAUGACC AUAGAUACGAAGAUAUAGAGGUCGGGAAUUAGG GUAGAAGGGUAGUAAAGUAGCUGAGUGUUGUCG UACUUUUAUGUGGGAUAUGUGAGGCGUAAGACC CUUCUUGUUGCUUCAUUUGCUUUGUGUAUCUUG UCAUUUUAUUGUCAUUAUUUUCAUUUUUAUCUU GUCUUAUCUUCAUUUCUUUUGAGAUGAAGAUAU AUCGAA	238	sch-miR482d-1-5p	GGUAGAAGGGUAGUAAAGUAG	67-87	mdm-miR482d	5	0	21	21	3
			sch-miR774b-1-3p	UGAGAUGAAGAUAUAUCGAA	219-238	ath-miR774b-5p	5	0	20	21	1
sch-MIR169r-4	CAUUUGAUAGACAAAUCUAAAAUUUUUGGUCUAU AAGGUUUGCAUGAAGAUGAAGAGAGUGAAGUUG CAGCCAAGGAUGACUUGCCGGACCAAAAGUUGU GACCAUUUUCUAGUUCCGGCAAGUUGUUUUUGG CUAUAAGUUUGCUCUCUUCUUCUCAUGUUAUCC UCGUUAGACCUAUUUUUUCCCUAUUCUCUACAA GAG	202	sch-miR169r-4-5p	CAGCCAAGGAUGACUUGCCGG	68-88	csi-miR169r-5p	0	0	21	21	1
			sch-miR169l-4-3p	CCGGCAAGUUGUUUUUGGCUAU	116-137	gma-miR169l-3p	2	0	22	22	1
sch-MIR7992-6	AGGCUCAAACUUGGUCUUAGCUAGCAAGUAAGU UCUCAAACCUUGCAUAUGCACAUCUACACACUUC AACUUGUCUCCACUAUGUCCGUUAAACACUCCAA CUUACAAGAUGGCCAUCUAGACACCUCCUAAGUC AGCCGAGGCGUCUUGAUGUGCACUCUCAAAGUU GGAGUGCUUACUUGCUAGGUGAGAUCAAGUUUU AGUGU	206	sch-miR7992-6-5p	CUUGCAUAUGCACAUCUACACACU	42-65	stu-miR7992-5p	5	0	24	24	2
			sch-miR1033e-6-3p	CGAGGCGUCUUGAUGUGCACU	139-159	ppt-miR1033e	5	0	21	21	2
sch-MIR1033e	CUCCACUAUGUCCGUUAAACACUCCAACUUACAA GAUGGCCAUCUAGACACCUCCUAAGUCAGCCGA GGCGUCUUGAUGUGCACUCUCAAAGUUGGAGUG CUUACUUGCUAGGUGAGAUCAAGUUUUAGUGUA UAGUUUAUGAAUUAUGCCUUAUUUCUUUUGGGU GAAUGAAGUAGAAAUAAUUCAAUAAGAUGUUAGG UGUUUUUAAGGGAUUAUAGUGCUU	224	sch-miR1033e-5p	CGAGGCGUCUUGAUGUGCACU	65-85	ppt-miR1033e	5	0	21	21	2
			sch-miR7823-3p	UUGGGUGAAUGAAGUAGAAAU	161-181	ptc-miR7823	5	0	21	21	1
sch-MIR2119	CUAAGAGUCCGUUUGGGUUGGCUUAAAAAAUGU AGCUUUUUAGUCAAAAUAAGAAGUAGGGGAAGC CUACUUUUGGUUUAACUUAUUUUAAGUUAUUUU UAACCUUGCCAAACACUUCCUAAGUUAUUUUAAG UUAUUUUUAUAUUGACAAAUACUUCCAGGAGUCA AAAACCGACUUAAAAGUAGGUUUGACCAACUUUU AAGUCAAUCCAAACACACUCUAAU	225	sch-miR2119-5p	UCAAAAUAAGAAGUAGGGGAA	44-64	pvu-miR2119	5	0	21	21	1

			sch-miR11011b-3p	UAAGUCAAUCCAAACACACUC	201-221	mdm-miR11011b	5	0	21	21	1
sch-MIR394b-1	UGGGCAAGUAAAAUAUUGGUGCUCUCAAUUUGU AAGAAAGUUUACUAGGGAAUGCAUCAUGACCAAC CAAGGUAAAGACUUCUAAAUAGAACUAUUUACCU UGGUUGGUCCUGAGGCAUUUCCUUUGUAAACUU CUUUACUAAUGGAAUGCACCAAUAUUUUCCUAGC UGU	171	sch-miR394b-1-5p	UUGGUGCUCUCAAUUUGUAA	16-35	ptc-miR394b-3p	5	0	20	20	2
			sch-miR11891-1-3p	UCUAAAUAGAACUAUUUACC	81-100	mes-miR11891	5	0	20	20	3
sch-MIR9478-1	AAAGUUUUGCUGAUCUAUGCCGUUUCCGCUUGA GAAAAGGCUCACCCAUGUCAUUAUUUGUAAACUG AAAUGGCGUAGUGAGCCAAGCUUUUAACGGAUG ACAUAGAUGAGCCUUUUCUCAAAGUUUGAUUGC AUAUUUGAGCCUUUUCUAUUCAAAAAUGAUUUAA UUACUAACGUGGCAGAGUCAUAAUUGACCACGU GUAAAAAAUGAUUUUGCAAAACCGGAACUGUUUU CUGUUAACAAAUAAUGACAUGGAUGAACCUUUUA UCUAACAGAAAUGACAUAGAUUAGCCAAACUUU	301	sch-miR9478-1-5p	UUUGAUUGCAUAUUUGAGCCU	125-145	sly-miR9478-3p	3	0	21	21	1
			sch-miR8586-1-3p	UUUUCUGUUAACAAAUAAUGA	231-251	atr-miR8586	5	0	21	21	1
sch-MIR11085-2	AUUUAGGAUAAUUAUUACAAUAAUGAAUAUCAUU UCAUGUUUGAGCUAGAUCGUGUUGAAGUGGUUA AUCUGAUCUCCGAGUUCUCAUCUUCUCUAUUGA CUCAAAGAAAAUAUCUUGGAGAUCAAAUUAGUAG CUCGAAUAUGAUGUCGUUCAAACAUGAAAUGAUG UUGAACAUUGCAAUAGCUAUCCUAGAU	195	sch-miR11085-2-5p	AUAUCAUUUCAUGUUUGAGC	27-46	lja-miR11085-3p	5	0	20	20	1
			sch-miR5185l-2-3p	CUUGGAGAUCAAAUUAGUAGC	115-135	bdi-miR5185l-3p	5	0	21	21	2
sch-MIR6157	AAAUUGACAUCAACGAAUAAUUAUGUCCUCCAAC UUUGAAUGUGUAGACACUUAAAUUAUUAUAAAAU UGAACAAGUAGACACAAGUGUCCUACAUGGCAU GAUACACGUAGGAUGUGAUGCCAUGUAAGAUAC AAAAUUGUCAUGUAGGGUGCCACGUAAGACGAU AGUGUUCAUUUGCUUCAUUUUAUACAAGUUUAAU GUCUACAUGUGCACACCCAAAGUCAAAGGUCAUA AUUGUCAAUUGAUGUUAAAUU	256	sch-miR6157-5p	UGAUACACGUAGGAUGUGAUGC	101-122	nta-miR6157	5	0	22	22	1
			sch-miR9652-3p	AAGUUUAAUGUCUACAUGUG	193-212	tae-miR9652-3p	4	0	20	20	1
sch-MIR2673b-1	ACAAUACUAAGUUUAUAAUUUAGGCUCAUAAUUU UUUGGUGUGGAUAAUAUUUGUGGGUAGAGGAUA AAAAGAAAAGAAAACUCUCUCCCCUUCCUCUUUC CCAGCCCUUCCUCUUCCUCAUUCCCUCUCCGUU UUUCCCUCCUGCCAGUAGCCCCUUUCGCGCCCC UUCUCCCCCUUACCUUAGUAUUGUGGCUCAAAA UUUUCCUUUUUUUCUUUUUCAUUCUCUACUACAA AUAUUAUUCACAUCAAAAAAUUAUGGGCCUAAGU UAUGAACUUAGUAUUGU	285	sch-miR2673b-1-5p	GCCCUUCCUCUUCCUCAUUCCC	105-126	mtr-miR2673b	5	0	22	22	2
			sch-miR5184-1-3p	UACAAAUAUUAUUCACAUCAA	230-250	bdi-miR5184	5	0	21	21	1
sch-MIR857-1	GAUCAACAACUGAACACAGUUGUCUAACAACUGU CGUAGUUGCGGGAACAACUUACCUAAUCGUCCG AUAACUACAUGCAGUUGUUGGACCAUUUUGUAU CUGAAAGAUGUACAUAAUUAUUUUUAUAAAUAAC UUCAGUAGUUGUCAAGACAACUGUAAAAGUUGU UGGCU	172	sch-miR857-1-3p	UUUUGUAUCUGAAAGAUGUAC	93-113	aly-miR857-3p	5	0	21	21	1
sch-MIR1513b	GUUACUGUGAGUAACGUUUAACUCCUUAGACAU UUUUUGAGUAACGUUUUACUUCUAAAAUGUUACU UUGACUAACGUUUUAAGAGUAAGACGUUACUUAC AGUAAC	107	sch-miR1513b-3p	UAAGAGUAAGACGUUACUUAC	81-101	gma-miR1513b	5	0	21	21	1
sch-MIR11122	GUCGAAAGACAUACUGUUUUAUCAAACCUAAAAU UGAACCAAAUUUCAAAACGAUAGCAUUUUGAACU CGUAAGCUUCGCCUAAUUUAAAUUUUAGGAAGU UUGACUUCAAACAAAAUUUGCAAAUUUUAAACAA GUAUUAGCCAAAUAGUUAGUGGCGGAAAGCCGC AUUAAGCAGAAUGUCUUAGGUGCCUUCAAAACCU	294	sch-miR11122-5p	UUAAAUUUUAGGAAGUUUGAC	86-106	lja-miR11122-3p	4	0	21	21	1

	UCCUAAGACGUUAAUAAGAAUCCUCGAACCCCUU UGAAUGUUUUCAAAUGAUUUUUCUGUUUAAGUU AUUUGAAAACAAGUCUUUUUUCUAA										
			sch-miR10204-3p	UUGAAUGUUUUCAAAUGAUUU	236-256	vca-miR10204-3p	5	0	21	21	1
sch-MIR10405d-1	GCCAUAUGAAGAUUCUUUUAAUGAGGAAAAUAUU CCUACAAAAUCUCGCCCAUGCCAAAUGAAUUCUG AACUUGUCGAUUUCUGUAAAAAAGAAAUUGAUAG UUUAUUAUCAAAGGGACUUAUAAAACCCUCUAAA UCACCAUGGUCUUGUACUGCUUUUUAUGUUAAU AAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGG UUGGUAAUAAAUUACAAACCUUUAAACAAAGUUU UAAAAUGGAUUAGGUAUCCUAUUCCUAAUAAAAA AGAUCUUUUAUCAA	284	sch-miR10405d-1-5p	UAGUUUAUUAUCAAAGGGACU	100-120	gma-miR10405d	5	0	21	21	1
			sch-miR9679-1-3p	CAGAACAAGAAAGAGGUGUUC	177-197	tae-miR9679-5p	5	0	21	21	1
sch-MIR1533-1	CAACAUAUUCAGUACUUGGGCAGUUGGUUCAUA GUGUGACGCUACAUGUCAAACUUCUCCGAUUCG AAUCUGAGGUCCAAAAUGGACAGUGAAAUAAAAA UAAUGUUGUCACUCAUGCUCGAACCGGAGACCC GUGACAUGUAGUGUCAAGCUCCUACCAACAGCC CAAGUAGCUAAAUAUGCAC	185	sch-miR1533-1-3p	GAAAUAAAAAUAAUGUUGU	91-109	gma-miR1533	5	0	19	19	3
sch-MIR1533-2	AACAUAUUCAGUAUUUGGGCUGGUGGUUUGUAG UGUGACACUACAUGUCAAACGUCUCCGGUUCGA ACCUGGGUCCAAAAUGGACAGUGAAAUAAAAAUA AUGUUGUCACUCACGCUCGAACUGAAGACCCGU GAUAUGUAGUGUCAAGCUCCAACCAACAGCCCAA GUAGCUAAAUAUACA	182	sch-miR1533-2-3p	GAAAUAAAAAUAAUGUUGU	89-107	gma-miR1533	5	0	19	19	3
sch-MIR172b-1	CACAGUCGUUGUUUGCAAAUGCAGCACUAUUAA GAUUCUCAAAUAUUCGACAUUUAAAAUGCAAUUA AAUGUGAAUCUUGAUGAUGCUGCAUUAGCAAUAA ACCACUAAA	110	sch-miR172b-1-5p	GCAGCACUAUUAAGAUUCUCA	21-41	bra-miR172b-5p	2	0	21	21	1
			sch-miR172-1-3p	UGUGAAUCUUGAUGAUGCUGCAU	70-92	aau-miR172	1	0	23	23	1
sch-MIR7997c-3	UGACUAUACUGCUCGUACUUUUCAAAAAUGUUG UCAGGCCUGUAUGUAUGUACUUUUGGACGAUCU GACACACACCUGACAGUAUUUUUGAAGAGCUCG AGCAACAUAGAAA	112	sch-miR7997c-3-5p	AUACUGCUCGUACUUUUCAAAAAU	6-29	stu-miR7997c	3	0	24	24	1
			sch-miR5303-3-3p	UUUUUGAAGAGCUCGAGCAAC	85-105	sly-miR5303	1	0	21	21	1
sch-MIR5163b	GGGGAAUUGAACCCUACCAAUAAGAGGAGAGUU CAGGUAGUCAACCAACUGAACUACUAAGAUUCUC CUAUUUGUUGCAACAGUUACAUUUCAAU	95	sch-miR5163b-3p	CAACCAACUGAACUACUAAGA	42-62	bdi-miR5163b-5p	5	0	21	21	1
sch-MIR1028b	AAAGUUGGAGGACAUAGAUAUCAGUUGAAGCCAA GUUAAACGGCAUAUUUAUAUAAUGCCUUUUUUUU AUGAUAGUCUACACACCUUGACUUAUUACACGUG UUUUGUCUCCAAGGAGUUUUGGACCUGAGACCU CAAGAUUCUGAAUAAUUUCAUUGACCACUAGGCC ACACCCUUAGGUGAAUAAUGAAAGAGGUUUUUU UAUUCAAACUAUUAACAAUAGACACAUUUUAGGU CAAAUUCUUAACAAUUAGUUAUUUAAUACAUAAA CAUGUAAUUUGGACUCAACUGACAUUUAUAUCUU GCAACUUU	312	sch-miR1028b-5p	AGGAGUUUUGGACCUGAGACC	114-134	ppt-miR1028b-3p	5	0	21	21	2
			sch-miR5014a-3p	ACAAUUAGUUAUUUAAUACAU	247-267	ath-miR5014a-5p	5	0	21	21	1
sch-MIR162-1	UGUUUAGUUGGUUGAAGACACUGGAGGCAGCGG UUCAUCGAUCUGUUCCCUGGAAGCUGAAUAUAU AUAUAUGCAAAAAUACAGCAAAAGGAAUCGGUCG AUAAACCUCUGCAUCCAGUGCUUAACCCCUAAGG A	135	sch-miR162-1-5p	UGGAGGCAGCGGUUCAUCGAUC	22-43	csi-miR162-5p	0	0	22	22	1
			sch-miR162-1-3p	UCGAUAAACCUCUGCAUCCAG	98-118	fve-miR162-3p	0	0	21	21	1
sch-MIR395	AACACUCUGUAAUUAGAAUGUAGAACUGCUCUCA CACCUAUUUCAAAUUUGAAAAGAGGUGGUUACAA ACUAAGAAUUCAAGAAUAAUGUCAAGAUGUGAUG GGAUUCUGAAGUGUUUGGAGGAACGUCUCAUUA	200	sch-miR395-3p	CUGAAGUGUUUGGAGGAACGU	108-128	pab-miR395	1	0	21	21	1

	UGUUUAGGAGUGUAAGGGAAACUCCGAACCCUA CCUUCUAUUUUACUCUCUAAAUAUAGAGUUCU										
sch-MIR10215-1	GAGAACCCAUUCUCUGUUUUACUCUCCAAAUAUA GAGAAUGGAGAGUAAAAUAGAGAUGGAUUGGA	66	sch-miR10215-1-3p	GAGAAUGGAGAGUAAAAUAGA	35-55	eun-miR10215-3p	4	0	21	21	1
sch-MIR8020	UUAGACCCCACUUAGUGGAAUUUCAUUGAGUAU GUUGUUGUUGUAAAGCAUACUGAAUUAAUGCAA GUACACAAGUUACGACAACAACAUACUUACUGAA AUGCCACAAAAAGGGGUCUAG	121	sch-miR8020-5p	AAUUUCAUUGAGUAUGUUGUUGUU	19-42	stu-miR8020	0	0	24	24	1
sch-MIR156b-11	AAAGGGGCGGUGACAGAAGAGAGUGAGCACACA UGGUGUUUUCUAGCAUGAUGUUUUACAUGCUUG AAACUAUGUGUGCUCACUGCUCUAUCUGUCACC CCCCAUC	106	sch-miR156b-11-5p	UGACAGAAGAGAGUGAGCACA	11-31	hvu-miR156b	0	0	21	21	1
			sch-miR156c-11-3p	GCUCACUGCUCUAUCUGUCACC	78-99	ata-miR156c-3p	0	0	22	22	1
sch-MIR3434	AGUUCGAACCAAGAACAAGAAAUGGAAGAAUGAA AGUCGUAUGGGUUCACAAAGACUCUGUGGCUAA AAAGUAAAAAAGAUAUAUCGAAGUUGUUUUGAUG AUUCAAGAAUCUUAUUACUUCAAUCCGAAGUUCU UAGUUACUUCGACUGGAUGAGUCCUAGUGAGGG AAUAAUUAAGUCAUAAUUCAUUGGUUGAUUGUAU CAUUAACCAUUUCUUUUUUUGGUACGAGGA	232	sch-miR3434-3p	CAUUGGUUGAUUGUAUCAUU	187-206	ath-miR3434-5p	5	0	20	20	3
sch-MIR8006-1	GUCUUGAACUAUCGUAAAUGGUAUGCAGAUAUC UUCCGUCAUACCUUUGGGUCAUCUGUGCCCUGC CGUCCAAAAACUAGAGCAUUCACCCUUUAUACUG ACGGACCUACAUGUGUCAUAAUCUUAUCAAAUUG AUUGAGAAAUUCAUACCAACCUUAACAUUUUAUU AAAUAUUGCAUCUAUGAAUAAGAUUGUGUCACGU GUCCGUUUCUAGUCUUCCAUUAGAGUGAAGAGC AUAUAUGCUCUAGUUUUUUAACAAUAGAAGCGUC UAUAUCUCAAAAAUAUGGUAGAGAAUAUCCGAUU UCAUUUAUGAUAGUUCGAAUAU	325	sch-miR8006-1-5p	UGCCCUGCCGUCCAAAAACUAGA	59-81	stu-miR8006-3p	1	0	23	23	1
			sch-miR2645-1-3p	AUUAGAGUGAAGAGCAUAUAU	221-241	mtr-miR2645	5	0	21	21	2
sch-MIR479-2	AUGAUGGAGAAGCAGACAUGGCGUGAUAUUGGU UCGGCUCACUAAUUUCUGAUUCGUGUAACAGAU AAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUU CUUCUUCAUACC	112	sch-miR479-2-5p	CGUGAUAUUGGUUCGGCUCACU	22-43	ghr-miR479	2	0	22	22	1
			sch-miR479-2-3p	UGAGCCGAACCAAUAUCACUC	73-93	aof-miR479	0	0	21	21	1
sch-MIR1128-2	UACUACUCCCUCCGUCCCAAAAUAAGUGUCACUU UAGCAAUAAUCAUACUCAUUAAGAAAAAUAAUAAA UAGAAAGGUAUAGUUCACCAAGUUACCCCUAUUU AUUAGAUGUUUCUUGACAAUUGAGCAUGAUUGA UAAGUAGUUCUUUAGUACAAAGGUAUACUUGGAA AAACAUACUAAUUUCUGUCUUAAGUUCCUAUGGU GACACUUAUUUUGGAAAAAAUUUUAUUGCUAAAG UGACACUUAUUUUGGGACGGAUGGAGUAUUU	269	sch-miR1128-2-5p	UACUACUCCCUCCGUCCCAAA	1-21	ssp-miR1128	0	0	21	21	1
			sch-miR5049c-2-3p	UGACACUUAUUUUGGGACGGAUG	239-261	hvu-miR5049c	3	0	23	23	2
sch-MIR399f-1	GUUAUGUGUGGAUGCAUUACUGGGCUAAUCUUC UUUGGCAAAUAAUUUCACUAUUAUUUGGUGCAAA UUUGGUCAUUUAUUGCCAAAGAAGAUUUGCCCC GUAAAUCACUCAUACAUGUU	120	sch-miR399f-1-5p	GGGCUAAUCUUCUUUGGCAAA	22-42	csi-miR399f-5p	4	0	21	21	1
			sch-miR399r-1-3p	UGCCAAAGAAGAUUUGCCCCG	81-101	mtr-miR399r	0	0	21	21	1
sch-MIR399f-2	AAAUGGGGAGUAAGAAAUAACAGUGCAAUUCUCC UUUGGCAAAUGAAUAUAUGCAAACCAUAUAUAUA UAUAUAUGUUUUGCAUACACAUUAUAUUAUCUUU GCCAAAGGAGAAUUGCCCUGUCAUUCUUCUCCU CAAUC	140	sch-miR399f-2-5p	GUGCAAUUCUCCUUUGGCAAA	23-43	csi-miR399f-5p	2	0	21	21	1
			sch-miR399a-2-3p	UGCCAAAGGAGAAUUGCCCUG	102-122	ata-miR399a-3p	0	0	21	21	1
sch-MIR5773-2	AUCCACCCACCUAACCCGAUCCAUUAAAAAAAUA UGAUAUGACCCAUUUUAUUUUGUCUUUAAUCCUA AUUCAAGGUUUAAAGAGAGGGAUUAAUUUAGGA UUAAAGACAAAAUAAAAUGAGUCAUCAUAUUUUU	161	sch-miR5773-2-3p	UUUUUAAUGGGUCGGGUUAGGU	132-153	gma-miR5773	5	0	22	22	1

	UAAUGGGUCGGGUUAGGUGGGUGAAU										
sch-MIR8032e	CUCAAAAGCUAAUUGGGUUGAAAUGCAUUGAGU UAAAAUGAGUGGUUUAUUGACCAGCCCAAACGC UAAUUGUUAAUCCAUUGAAUUUAAAUGGGCUAAA AUGUCAACUACUUCUAAGUUUUAGUUGGUGUGA UUAUUUUAUUUAAAUAAAUUUUUNCUUUUGAGUG AAAAUUGAAAGUUGAGUGACUUUCUGAGAGAAGA GUGCAUAGUUGAGUGAUCAUCUGAGGUAUUAAC UCGUUACUCAUUUUUUCAGAUAAAGAACUCCAAC CCAAUUCUCUAUUUUAC	285	sch-miR8032e-5p	AGUUUUAGUUGGUGUGAUUAUU	117-138	stu-miR8032e-3p	5	0	22	22	1
			sch-miR1137a-3p	GAGUGCAUAGUUGAGUGAUC	200-219	tae-miR1137a	4	0	20	20	2
sch-MIR482h	GAUGUGAUACAUAAAUACUUUACGGAAAAAGAGA UAAAUAUAUAUUCGAACUAUCGUUAAUGAUAUAU AUGAAGAUACCUUCGUCAUACUUUGGAUACAUU GGUGCCUCUUCGGAUAUAUGAAAAAGGGUAUAU AUGAAAAAGGGUAUAUAUGAAUGUCCCACAAGUA UAACGGAGGAUACUUGCAUACCAUUUAUGAUAG UUUGAUAUAUAUUUAUCCUUUUCCCCAUAUUUUA UCUCAUAACCAG	247	sch-miR482h-3p	AAAGGGUAUAUAUGAAUGUCC	140-160	pab-miR482h	5	0	21	21	1
sch-MIR8022-1	UGCGUAACCUCACUACUGAAUUUAACUCUCUUAA CUUUGUGACGGAUCUGUAGGACGGACCGUCAUA GAUACGACGGACCGUCACAAGCUACAUAACUCCA CCCUGGGUCGGAUUUCCACUAAAAUUUAAAUGG GUGUUUUGGACUAUUCAUGAUUAUAAUUAUGAAA UUAGUGGGGUAAGUUUAAUAAUUUAUUUACUUG GGGGUUGAAGAAGAUAAUAGGGGUGGGUUACUU U	235	sch-miR8022-1-3p	UUUAAAUGGGUGUUUUGGACUAUU	126-149	stu-miR8022	3	0	24	24	1
sch-MIR5021-1	UUAGAGAAGGUUAGAAUAGAGAAGAAGAAGAAGA AAGAGAGCUUUUCCACAUUUUGCAUUCCCUGAC UGUUUGCUAGUGUGUGCCCCUCUCUCUCUUUCU CUCCUCAUCUCUCUACCAAUUUUCUCUCC	129	sch-miR5021-1-5p	AGAGAAGAAGAAGAAGAAAG	18-37	ath-miR5021	2	0	20	20	2
			sch-miR156d-1-3p	CCUCUCUCUCUUUCUCUCCUC	86-106	cas-miR156d-3p	5	0	21	21	2
sch-MIR7983-2	CUCAUGACACUACAACAAAAAUGAUCAUUAGCGA CAAUUGUCACUCGUUGUAUAUGUUCCUAAAGCC UUUAGCGACAUUGGUUCUAAUGACACUUAACUAA UGCCGAUAAAUACUUUAACAUUUUUUUAUAAUGU CAAUAUUUAAUGCCGCUAAAAGUUAUUUUUAUUG UAGUGUGAUAUG	181	sch-miR7983-2-5p	UAAAGCCUUUAGCGACAUUGGUUC	61-84	stu-miR7983-5p	1	0	24	24	1
			sch-miR7983-2-3p	ACUAAUGCCGAUAAAUACUUUAAC	97-120	stu-miR7983-3p	2	0	24	24	1
sch-MIR8006-2	CUCCGUCAUACUUUUGAGAUAUUGGUGCCUCUG CCGUCUAAAAACUAGAACAUAUAUAUCCUUUAUA CUAAUCUUAUCCACCGACUCGAUAUUUAUCGACG GAUAAGAUUGUAUCACGUGUCCCUAUUUAGUCU UCCGUUAGAGUGAAGGGCAUACAUGUUUUACUU UAUGGACAGCAGAAGCACCAAUAUCUUAAAAGUA UAACGAUG	209	sch-miR8006-2-5p	GCCUCUGCCGUCUAAAAACUAGA	27-49	stu-miR8006-3p	5	0	23	23	3
			sch-miR5026-2-3p	ACGGAUAAGAUUGUAUCACGU	99-119	ath-miR5026	5	0	21	21	1
sch-MIR5379	AAGUGUUAUCAUUCCAAUUAGAGCUAAAUUAGUU AUUUGCGAUCAACUGAGCACUAUUAGCUGACUA GAUAUCAAGAACAUAAUCGAUAUGAAAAUUAGUC AUUAUGAUAUUUUUUUGUUUGAAUAAUGAAGCGA GAUGAACAAUGAAGAUUAGUGAUAUAGCUGAUCC GACUUGCUUGAUAUUGAAGUAUGUUGUUGUAUG AAACCUAUAUAUUUUAAUAUAGUAUUCCAAUCGA AGCAGAAUGGAGAUUGAGAUAACAUAUAGCUCU GAUGGGUAGAAACAUAG	286	sch-miR5379-5p	AUGAAAAUUAGUCAUUAUGAUAUU	89-112	gma-miR5379	3	0	24	24	1
			sch-miR9729-3p	CUGAUGGGUAGAAACAUAG	268-286	gma-miR9729	5	0	19	24	2
sch-MIR403	AUUGAAAAUCAGGAAGAGGCAUAUUUCACGUUU GUGCGUGAAUCUAACAACUCUUUUCAUCAGAAAA ACUGUUAGUGUUUGCUAGAUUCACGCACAAGCU	127	sch-miR403-5p	CGUUUGUGCGUGAAUCUAACA	29-49	sly-miR403-5p	0	0	21	21	1

	CGUAAUAUGGCUUUUUCGAAUCUCUGC										
			sch-miR403-3p	CUAGAUUCACGCACAAGCUCG	82-102	sly-miR403-3p	0	0	21	21	1
sch-MIR10538-1	CAGCGUUAGGUUGAUAUACGUCACUGUGAGUAA CGUUUUACUUCUAAAACAUUUUUUUGAGUAACGU UUUACUCCUAAAACCUUAACCUUGCUGUGAGUAA CGUUUUAAGAGUAAGACGUUACUCACAGUAACG UUUUAGGAGUAAAACGUUAUUGUGAGUAACGUA UAUCAAUCUGACGUCA	183	sch-miR10538-1-5p	AGGUUGAUAUACGUCACUGUGAGU	8-31	sly-miR10538	5	0	24	24	1
sch-MIR6427	GACUCACUUGAUUACUUCCAGUUCUUCCCAUAG CUUGUCAAUACUAUUUUGAUUAGUUCAUGUUUAA GAUGAAUAAAGAGCCUCGAAUGCACCAAACAAUG CUGUAAGACAUGGGAAGAAACAUUAACAGAACUU GACUUCGUCCGAAUAUUGACAAGCGAUGGGAAG AACUGGAAGUAAGUUUCAAUGAUAU	193	sch-miR6427-3p	AUGGGAAGAAACAUUAACAGA	111-131	ptc-miR6427-3p	5	0	21	21	2
sch-MIR5174d-1	AAAAAAUAAUUACUCCCUCCGUUUCAAAAAGAUU GGCCUAGUUUUUCUUGGAACGGAGUUCAAGAAA AAAAAAGACUUUUUAAUCUUGUGGUUCUAAAUUA AAGUUGUGUCAAAUAUACAAAAAUUCCCUUUAAU CUUGUGUUCCUAAACAUAACACACGGAAAGUUAA AGGUAAGGUGUUGCCAAAAAAGGAAAGGGGUCA UUCUUUCUGAAACAAACUAAAAAGGUAAUAGGAU UGUUUUUGAAAUGGAGGGAGUAUUACUUACC	267	sch-miR5174d-1-5p	UCCCUCCGUUUCAAAAAGAUUGGC	14-37	bdi-miR5174d-5p	1	0	24	24	1
			sch-miR1439-1-3p	UUUUGAAAUGGAGGGAGUAUU	240-260	osa-miR1439	3	0	21	21	1
sch-MIR1128-3	GGCUAAUGUUUAUUACUCCCUCCGUCCCAAUGU GAGGUAGUUUGACUUGGCAGUUUAAGAAAACAG UCUAAAAUAAGUUAUAGAUGUUGGUGUAGCUGU AAAUCAUUUUAUUAAGGGUAAAAUAGGUACUUUA AAGUUAGAUUGUUACUGAAUAUUGAAAUGCGUCA UUCUUUUUGGGCUGACUUAAAAGAAAAGUGAGC AUAUAAAUUGGGAUAGGGAGUAUAUAGAAAGUAA AU	236	sch-miR1128-3-5p	UAUUACUCCCUCCGUCCCAAU	11-31	ssp-miR1128	2	0	21	21	1
			sch-miR810b-3-3p	UGAAUAUUGAAAUGCGUCAUU	149-169	osa-miR810b-1	5	0	21	21	1
sch-MIR7808	CCACUGCGCUUCUUUCUCCUGAGGCGAUGCGAU CUGAAAAAGGCGCUCGCUUCAGAUGAAGAAGCG AGAAG	71	sch-miR7808-3p	AAAGGCGCUCGCUUCAGAUGAA	39-60	rgl-miR7808	5	0	22	22	1
sch-MIR171f-4	CUAUGAAACAGUAACUUUGAUAUUGGCCUGGUU CACUCAGACAACAAAAUGAAAACUAUAUUUGAAU GGUUGAGUUUUCGUUUUUCGUUUGAUUGAGCCG UGCCAAUAUCUCAGUUUCUCUUUCACUU	128	sch-miR171f-4-5p	UAUUGGCCUGGUUCACUCAGA	21-41	csi-miR171f-5p	0	0	21	21	1
			sch-miR171a-4-3p	UGAUUGAGCCGUGCCAAUAUC	90-110	aof-miR171a	0	0	21	21	1
sch-MIR7757-1	CAUUUUUGGCCUACGUGGCAGUAUCUUGUGGAC CCAAUGUUGGUUGACUUUUUUUUUUAAACUAGU GCCACGUAGGCCGAAAAGG	85	sch-miR7757-1-3p	GUUGGUUGACUUUUUUUUUA	39-59	bdi-miR7757-3p-1	5	0	21	21	1
sch-MIR171o-2	UCAACUUGGGAUGUUGGUGUGGUUCAAUUAGAU AACAAUCUCCACGUAAAAAUUGUAGAGUCUGUUA UUUGAUUGAGCCGUGCCAAUAUCACAUGUAAA	99	sch-miR171o-2-5p	UGGGAUGUUGGUGUGGUUCAA	7-27	mdm-miR171o	1	0	21	21	1
			sch-miR171a-2-3p	UGAUUGAGCCGUGCCAAUAUC	70-90	aof-miR171a	0	0	21	21	1
sch-MIR166-1	GAAACUAAACAAGAUUAUGUUAAGGAGAAUGUUG UCUGGUUCGUGACCAUAUAUCUUUCUUCAUAUA AAUGAUCUCGGACCAGGCUUCAUUCCCCUCAAC UCAUCAAGGUUAUGUCAU	118	sch-miR166-1-3p	AUCUCGGACCAGGCUUCAUUCCCC	72-95	lja-miR166-3p	1	0	24	24	1
sch-MIR7993b	CACCUCGACCCCUAAUACAGUGUUCCAAUUAGAC ACUUUUGGUUCAAAUGUUGGGGAAAUUUUGAGU GGUCUUGUACGUCUAUUUGGUAGUUAAGUUAAC CACAUACAGUAUGUCAUUUCAUUUUAUUUUACAC AUUCACCUCGAUAAGCCGUAAACCACAUGCAUUU UCUACUUGAGGUUGAUGUGUAUAAUUAAUGGAC AGCUUAAUUUACGUGGUUAAAUUAACUACCUGG GUCAAAAGUGUUUACCUGAAACACUUUAUAGGAG UUGAGGUG	276	sch-miR7993b-5p	UUAAGUUAACCACAUACAGUAUGU	91-114	stu-miR7993b-5p	2	0	24	24	1

			sch-miR7993d-3p	UUAAUUUACGUGGUUAAAUUAACU	205-228	stu-miR7993d	4	0	24	24	2
sch-MIR1078-1	CAGAGUAUGACGACUCUUUUUUGAAUCAUGUGU GAUUACAUAAUAUUUUGUGCAUCUGAUCAGAGUA UGAUAACACUUGAAUCAUGAAUGCAAAAUGUUUU GUGCAUCUGAUUGUUCAGAAUUAAUACAUGGUC CUACUAUU	142	sch-miR1078-1-5p	CUUUUUUGAAUCAUGUGUGAU	16-36	ssl-miR1078	5	0	21	21	1
sch-MIR171a-2	AUACACGAGAUAUUGGUGCGGUUCAAUGAGAAA GCAGUACUUAAGAACAUUUUGAGUCUACUUUUU GAUUGAGCCGCGCCAAUAUCACGUGUAG	94	sch-miR171a-2-5p	UAUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	0	0	21	21	1
			sch-miR171a-2-3p	UGAUUGAGCCGCGCCAAUAUCA	66-87	cas-miR171a-3p	1	0	22	22	1
sch-MIR7997c-4	AAGCUAUGUUGCUCGGACUCUUCAAAAAUGUCG GUGGUAGUGCAUUUUUUUGGAGGAUCCGAUAAG GGUGCUGCAACAUUUUUAAAGAGUUCGAGCAAC AUAGAUA	106	sch-miR7997c-4-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
			sch-miR5303-4-3p	UUUUUAAAGAGUUCGAGCAAC	79-99	sly-miR5303	1	0	21	21	1
sch-MIR10532-1	AGAUAUAUAUAUAUUGUAACGAAGUUAAUGGGUG UUCGAGCACCCGACGGACAACAUGUGGGUCCAC CAUUGAGUUCAGGGUAAUAGGACCUUAUUAUAG UAUAAGUGUGUCUCUGAGAUUUUAGGCAUAGAU UGAGUGGGUAUUUGUGCAUUUUUCUUUUUUGUA AUCAUGUGUACGAUAUAUAUAUACAA	192	sch-miR10532-1-3p	AAGUGUGUCUCUGAGAUUUUAGGC	104-127	sly-miR10532	2	0	24	24	1
sch-MIR393b-3	UGACCCUAAAAUCUUAUCCACCAUCCCUUAGCUU AGUGAACAUGCUAUUCUUUAAUUAGGGAAUCGAA AACCAAUUUCCUAUUUAAAGAACAGUUUGUUCAU AGGGGAUUGAAAAUCAAUUCCCUAUUUAAAGAAU AGUUGGCUCAUUAGGUUAAAGGGUGGUGGAUAA GAUUUUAGGGGUA	182	sch-miR393b-3-5p	UUAGUGAACAUGCUAUUCUUU	33-53	gma-miR393b	5	0	21	21	1
sch-MIR11509	GGCACUUCUUAAUCUACAUGAUCAUUUUAAAUGA UCAUGUUCUAUGGUAUCUAGACUUGACACUUGG AUGCCUUGUACCUAAUGUGUGUAAGAUAAGAAG UCAA	104	sch-miR11509-5p	ACAUGAUCAUUUUAAAUGAUC	16-36	pab-miR11509	5	0	21	21	2
			sch-miR5824-3p	UGUAAGAUAAGAAGUCAA	87-104	osa-miR5824	3	0	18	24	2
sch-MIR2931	UAAGCUCUUACUCUUCACUUUUGAUGUCAAAUCC GUGUCGGGUUUUCCAAAAAUAUACUACUUUUGC CAAAUUCGACACAUACUAUUGACAUUUCUGAAGA GUUCGAGCAAC	112	sch-miR2931-5p	CUUCACUUUUGAUGUCAAAU	13-32	osa-miR2931	4	0	20	20	1
			sch-miR5303-3p	UUUCUGAAGAGUUCGAGCAAC	92-112	sly-miR5303	1	0	21	21	1
sch-MIR5303-1	CUUACUCUUCACUUUUGAUGUCAAAUCCGUGUC GGGUUUUCCAAAAAUAUACUACUUUUGCCAAAUU CGACACAUACUAUUGACAUUUCUGAAGAGUUCGA GCAACAUAGCAUUCAAUAUCUAUUCUAAAAGAAA AAACAAGCCUAAUUAAGCUCUUUGUUGAACGGAC UCCUCACUUUUUAUGCCGCAACCGUGUCGAAUU CUCCAAAAAUACACUACUUUUGGCAAAUCCGACA CGCAACCAUUGACAUAUCUGAAGAGUCCG	265	sch-miR5303-1-5p	UUUCUGAAGAGUUCGAGCAAC	86-106	sly-miR5303	1	0	21	21	1
			sch-miR5303d-1-3p	UUUUGGCAAAUCCGACACGCAACC	220-243	stu-miR5303d	3	0	24	24	1
sch-MIR156b-12	GGGUGAGAUAUUGUUGACAGAAGAUAGAGAGCA CGAAUAAUGAGGUGCUAAUUCGAAGUUGCACCU UAAUUCUUUGUGCUCUCUAUUCUUCUGUCAUCA UCUUCAGUC	108	sch-miR156b-12-5p	UUGACAGAAGAUAGAGAGCAC	14-34	aof-miR156b	0	0	21	21	1
			sch-miR156g-12-3p	GCUCUCUAUUCUUCUGUCAUC	78-98	csi-miR156g-3p	0	0	21	21	1
sch-MIR7519	UGAUUGGAUGUGCAUAAGUAGUCAUUUUAGUAU AAAAUUGAACAAUUAGACAGACGUAUCUUACAUG GGAUUAUACACGUAAGACACCACGUAGACAUAAA UUUUCUAUGUAGGGUGGCAUGCAGGAUGAAUGC GUCAAUUUGUAUAAUUUUAUACAAAAUUUAAGUA UCUACAUGUGCACAUCUAAAGU	190	sch-miR7519-3p	UAAAUUUUCUAUGUAGGGUGGC	98-119	lja-miR7519	5	0	22	22	2
sch-MIR400	CUCUGAUAUUCAAAGAAGUAAUGAACCUUGGAAG AUACUCCAAAGGUAUUUAACAAAGGGAUUAUAUU	194	sch-miR400-3p	UAUGAGUCUAUUCUAAGUCAU	101-121	cas-miR400	4	0	21	21	1

sch-MIR6137b	UUUCUGGCGAAGCAUAUAAGACUCGGACAUAUU AUGAGUCUAUUCUAAGUCAUACAGGAAGUGCUG AAUUUCAGCAUUUCACUUCAGAAUAUGACAAGAA UGUUUAUAACUUCUCUAAAAUCACUA CCUCUCUCACUUUAUAUACAGACACAAAUGUAUA AAAUGUGUUUGUGUUUGUAUAAAGUGAGAGAAA AUUGUAUCUAUACAUCUCUUUUCGUUCGCUUAU CUGCCUAGAGAAUCUUGCUCGUCACUCUCACUC GUCUCUCUCACUUUAUACUAACACAAAUGUAUAA AAUUACGUUUAUGUUUGUAUAAAGCGAGAGUAA	200	sch-miR6137b-5p	GAGAAAAUUGUAUCUAUACAUC	62-83	pgi-miR6137b	5	0	22	22	3
			sch-miR7122a-3p	UACGUUUAUGUUUGUAUAAAG	171-191	ppe-miR7122a-3p	5	0	21	21	3
sch-MIR395j-2	UUAUAUAUAUCAAGGUAUUCUCGAGAGUUCCCU UGACCACUUCACGAGGGAUUAAUAUCUUUAUUU UUGAUGCCCUACUAAAGUGUUUGGGGGAACUCU CGGGUUCACUUUGAAGUAUACAC	122	sch-miR395j-2-5p	GUUCCCUUGACCACUUCACGA	27-47	mdm-miR395j	3	0	21	21	1
			sch-miR395a-2-3p	UAAAGUGUUUGGGGGAACUCU	79-99	aof-miR395a	1	0	21	21	1
sch-MIR156aa	UGGUAUGUGAAUAUCCUCAGUCAUAUUUUUGGG AUAUUGUUGUCUUUGCCGUUCAAAAAUAGAGCG UAUAUACUCUUUAUACUAACGGACGUAUACGUGU CACAAUCUUAUCCAUCGAUCCGACAUUUAUCAAC GAAUAAUAUUGCGCCACAUGUCUCUAUUUUAGC CUUUAAUUAGAGAUAGAGCGUAUAUACUUUGUAU AUUAACGGACGUAUACGUGUCAUAAUCUUAUCCA UCGAUCCGACAUUUAUCAACGAAUAAUAUUGUGC CACAUGUCCCUAUUUUAGCAUUUCAUUAGUGUG AAGGGCGACAAAAGUACGACGGAGGAUAUCUGC AUACCA	341	sch-miR156aa-3p	AUUAGUGUGAAGGGCGAC	294-311	gma-miR156aa	5	0	18	18	1
sch-MIR1106-2	CUUUUAUCCCCAUGCAAUAUUUAAUAGUGUAUUU UAAAGGUAUAUAUGUGUCCACGUGGACAUCAUAA CAUUGCAUCAUUAUAAAUAGUAAUGUGUCCACGU GGACACAUAUAUACUUUUAAAAUUCAUUAUUAAA UAGUGCAGGGGGUAACAU	154	sch-miR1106-2-5p	UUUAAAGGUAUAUAUGUGUCC	33-53	smo-miR1106	5	0	21	21	1
sch-MIR9762	CAAAUCUAUUGAUAUGUCAUUUAUUGAAUCAUUA UUAGUUUCUGAAUAUAUUUGUUGUUUUUACCCU ACUACACUUAAAAGAUAUUUGGGAACAAGCAACA AAUAUAUUGAUUCAUCGAUAUUUGGGAACAAGCA ACAAAUAUAAUGAUAUAGUAAAUAAUAUUUCAAA GGAUAAGAGCUACUUCUCUUCUGGAGAAGUCUG CAGGAAGUCCCUCUAUGUAGAGGGUGUUAGAUA CACCAGGAGGGAGAUGUAGUAUUUCACGAUACA UGGACAUAAAUAGCAUAGU	287	sch-miR9762-5p	AAAAGAUAUUUGGGAACAAGC	77-97	gma-miR9762	5	0	21	21	2
			sch-miR5562-3p	UUCUGGAGAAGUCUGCAGG	188-206	mtr-miR5562-3p	5	0	19	19	2
sch-MIR1078-2	AACAUUUUUUCAUGUAUAUGCAGCUCAAAAAUCA ACGGAUGAUUGUUUAAAUUUUGAUGCAUCAACA GCGUCAAAAUCAAAACCACCAACAUUGGACGAUU AUCCUGAUUUUACCAUGACACAAAUAAU	129	sch-miR1078-2-5p	GAUGAUUGUUUAAAUUUUGAU	38-58	ssl-miR1078	5	0	21	21	3
			sch-miR11097a-2-3p	AUUUUGAUGCAUCAACAGCGU	51-71	lja-miR11097a-5p	4	0	21	21	1
sch-MIR160e	UAUACAUGCUUAGCUCCUAGAAUGCCAUCUGAAA AGGCCAUCAAUUCUUGGUGGAACAAUGCAAAUG GCAUACAAGGAGCCAGGCAUGUUGU	92	sch-miR160e-5p	UGCUUAGCUCCUAGAAUGCCAUC	7-29	mes-miR160e	4	0	23	23	1
			sch-miR160-3p	UGGCAUACAAGGAGCCAGGCA	66-86	aau-miR160	1	0	21	21	1
sch-MIR7981-6	GUUGACAGAUUUCAGAAAUUUCAGAGACACGCU UUAACUAAACUAAGGUCCUAUUACCCAACAAAUC CAUUUUUUUUGUAAUUUUGUGCACCUUUAUGGC UUACGUGAUAUCCAAAUAUCUCUAAUGCGCUUUA UUUGUCUGGAGUCACAGAGUGUGUCGCAUAACA CAAAAGGUGUACAAAAUUACCAAAAAUUAAGUUC AAUAGUAUGACCUUAGUUUAGUUAAGGUAUGUC UCUGAGAUUUCAGUCAUUGUCCGC	258	sch-miR7981-6-5p	UUUAACUAAACUAAGGUCCUAUUA	33-56	stu-miR7981-5p	3	0	24	24	2
			sch-miR7981-6-3p	GUAUGACCUUAGUUUAGUUAAGGU	206-229	stu-miR7981-3p	3	0	24	24	2

sch-MIR7988	AGCUUAUUUUUAAAUAAUUUCAAAUUAUUUUAAC GGAAAAUGGUCUAAAAUGCCCUUAAACUAUGAGA UUUGGCAUAAUAUGACCCUGCAUCCAUUUAAUGA GUAUGAUCUGUUUGACAUAAGGUUAUGUUUCAG CCGAAAGGUGGACGUCAGGGGUAUUUUAGGGCC GAUAGGUGGAUGGAGGGUAAUGUUAUACCAAUU CAAAUACUUGAGGGGCAUUUUAGGCCCUUUUCU CUAUUAAGAAAAUAUUAUCAUCUAUUGAAAUAUA AUAU	272	sch-miR7988-5p	AACGGAAAAUGGUCUAAAAUGCCC	32-55	stu-miR7988	4	0	24	24	1
sch-MIR1511	GAAAAUUUUGGAUCUAUCCCUCAUGCAAUUUUUC UAAAUAUGCCUAUUAUUUAUACGAAGAUUAUCGG UUCAAAUAAUCUAGGCUCUGAUGCCACAUGUAAA AUUAAAUACUUGAAUACAUAAUAUCAGGAACUUG AACACGAUAAUCUUACAUAGAGAUUGUUUGGAGC AUAUACCUGAUGAGGAAGACAUCAACACAGAGAA AAGCGCAAGGGUUAGUCAUAAAUUGAU	231	sch-miR1511-5p	AUCUAGGCUCUGAUGCCACA	77-96	gma-miR1511	5	0	20	20	1
sch-MIR863-2	UUGAAACUUGUAUAAAGUAGAACACGUAUACACA UUCAUCCUAUGUGACAUUUUACAUGCACUUAUG UGUGAUACAUGAUGUCCUACACGUAUUAUGUCA UGUAGAACUCAUGUGUCUACUUUUAAAAUUUUAU A	135	sch-miR863-2-3p	UUAUGUCAUGUAGAACUCAUG	93-113	ath-miR863-5p	5	0	21	21	1
sch-MIR169k	UUGAGAGUCUGAGACAUGAUGGUUUAUCGGUUA CAGAGUAUGAGGCGCGUUUUUGCCAGUUGUCUA GGCAUGCGUUGGCCAUUAUUCCAAAUGAGACAC AGAGGAUCCUCAGAUUUGUGAGGGGAUUGACUU UCUCUAUCAGGUCAGCUGUGUUUCGGGCAUCUA GGUAGGGGGCUUCUUUCGAGUCCAUUGAGAGCG CCGCCAAAGAGGCGGAAUUGAUGGAGAGAGAAU GGCCCAAACCUAUCAAUUCAGACGCUGUC	260	sch-miR169k-5p	UGAGACAUGAUGGUUUAUCGG	10-30	mtr-miR169k	5	0	21	21	1
sch-MIR6288c-1	UUUUUUUGGUGGCAAUUUGUUCGAACUUACCAU GUGAUAUAUCUAGUAUACAUGGUAAAUUUUAACU GAUUCCCACGAAAACGA	84	sch-miR6288c-1-3p	CAUGGUAAAUUUUAACUGAUU	51-71	ppe-miR6288c-5p	5	0	21	21	1
sch-MIR11144-1	UAGAUACUCCCUCUGUCCCUUUUUACUUGUCCA CUUUUGAAUUGGCACACCUAUUAAGAAAAUAAUU AAUGACGUAGUGAGUUUACCAUUUUACCCCUAU UAAUUAUGAAGUGACUGAAAAGUUGUACAUUUUU CAAAGUAAUUAGUCAUUGAAUUGUGGGUAUAAUA GGUAAAAAAAAUUGCCCUUUCUUGAUUUAUCAAA AUGGACAAGUAAUUAGGGACAACUAUAAAAGGAA AAGUGGACAAGUAAUUAGGGAUGGAGGUAGUAU GAG	272	sch-miR11144-1-5p	UUUACCAUUUUACCCCUAUUAAU	82-104	lja-miR11144-5p	4	0	23	23	1
			sch-miR6248-1-3p	UAAUUAGGGAUGGAGGUAGUA	248-268	osa-miR6248	3	0	21	21	1
sch-MIR7757-2	UUUCAAUAUCAAAUCAAGUCACACAAAAUCAUUA GUCGGGUUUUUUUCAGUUUAACUCGAUUUAUGG UUUGGUUCGAUUGUCGAUUUGAUUUUGUAC	97	sch-miR7757-2-5p	UUUCAAUAUCAAAUCAAGUCA	1-21	bdi-miR7757-5p-2	5	0	21	21	2
sch-MIR8001b-2	AAGAUAACUACAUCUCUAAUACUACAAGAAAACU GUGAAUUACAUGGAGAUUUUGUAGGCAUUAGUA UGAAAAUUUGGUUUCCUGCAAAUUUUCAUACGAA UUUCCUCAUGUAAUUCACCAGUUUUCUUGUAGU GUAACGAGGAGAAGUAUGUA	154	sch-miR8001b-2-5p	GUAGGCAUUAGUAUGAAAAUUUGG	55-78	stu-miR8001b-5p	4	0	24	24	2
			sch-miR2275c-2-3p	UUUGGUUUCCUGCAAAUUUUCA	74-95	ata-miR2275c-3p	4	0	22	22	1
sch-MIR8003	UGGAUCCUGCAUUUGUAUAUUUCAGUAUAUAAAC GGGUUCUGCAUUUGUAUAUUUCGGUCUAAUUGU AUAUUUUGGUAUACAAACGGGUUCUACAUUUAUA UAUUUCGGUAUACAAAUGGGAUGAC	126	sch-miR8003-3p	AUUUCGGUAUACAAAUGGGAUGAC	103-126	stu-miR8003	0	0	24	24	1
sch-MIR162-2	GGGGGGUUAAGCACUGGAUGCAGAGGUUUAUCG AUCGCUUCCUGUUGCUGUAUUUAUCGCUUUUCA GGGAACAGAUCGAUGAACCGCUGCCUCCAGUGU UCUCACCCAAC	110	sch-miR162-2-5p	UGGAUGCAGAGGUUUAUCGAUC	15-36	csi-miR162-5p	3	0	22	22	1
			sch-miR162b-2-3p	AUCGAUGAACCGCUGCCUCC	75-94	cas-miR162b	0	0	20	20	1
sch-MIR1428a	UAUAAAAGUCGCUGCCAAGGCAGCGACUUCCAC GUUUCAAAAAAAAAUUAAAAAAAAAAUCGCUGCC UAGGCAGCGACUUUAAAAAAAACACUAAAAUCGC	177	sch-miR1428a-3p	CAUUUUGCAAAAUCGCUGCCU	141-161	osa-miR1428a-5p	5	0	21	21	1

sch-MIR156b-13	UGCCUAGGUAGCGAUUUCAUUUUUUUUAAAAAAA AUUCACAUUUUGCAAAAUCGCUGCCUCUGCAGC GAUUUUGCU GUUAAAAGAUGAGGUUGUGAAAUAUGUUGUUGA CAGAAGAUAGAGAGCACAGAUGAUUAAGUGCAU GAAAAUUGUAUGCACAUUACUCCUUUGUGCUCU UUAUUCUUCUGUCACCAUCUUCAUAUCCUAGAUU UUUUCUU	140	sch-miR156b-13-5p	UUGACAGAAGAUAGAGAGCAC	30-50	aof-miR156b	0	0	21	21	1
			sch-miR156h-13-3p	GCUCUUUAUUCUUCUGUCACC	95-115	mtr-miR156h-3p	1	0	21	21	1
sch-MIR5051-1	UUUAAAUUUGGGGAAGAUGACAUAAAUUGAUUAA AUAAUUAAUAAUAAAGAAAAAUAAUGACACAUGAC ACCUUUAAACUGGUACAUGGCAGUAAAACUACUG CAUGACGCGCCUCAUGUGCGUGGUAACAACCCA GACUUGAGAAUGAGUCAAAAUGGUCCAUUUACAA AGAAAUUAAAUAGUUCUGUGGGGGUGAUAGGAC ACUUUAAAAGUUAAGGUGUCAUUAUACAAAUACG GGACAACUUUGAUGGUUUUUUUUAUGUCUUCUC UCUUUAUUUGUAUGUUAUUUAAGUCGAUAUUUG UUUUUUCCAGCUAAAUUUUCA	324	sch-miR5051-1-5p	CAUGACACCUUUAAACUGGUA	64-84	hvu-miR5051	5	0	21	21	3
			sch-miR5741e-1-3p	ACGGGACAACUUUGAUGGUUU	235-255	mtr-miR5741e	5	0	21	21	3
sch-MIR7822-1	UAUAUUUAUGUCCUCGAAUUUUGAAUGUGAACAA AUAGACACUGAAACUUGUCUAAAAUAGAACAAAU AGACACAAAUCAUAUGUAUCAUAAUACACGCUGG ACACAAAUUUUCAUGUAGGAUGCAAUGUAGGAC GUUUGUGUCUAUUUGUUCAAUUUUAUACAAAUU UAAAUAUCUACAUGUGCACACCCAAAGUAGGAUG ACAUAAAUGUG	213	sch-miR7822-1-5p	UUUGAAUGUGAACAAAUAGAC	20-40	ptc-miR7822	5	0	21	21	1
			sch-miR1530-1-3p	AUUUUAUACAAAUUUAAAUAU	155-175	gma-miR1530	5	0	21	21	2
sch-MIR5020b	UCUGAUCUGUAUAGCAUGCAUAAAGGUGUGAUC GUACUUGUGCAAUAGGUAAAGAAAUGCUCAAAAC CAAUAUCUUUUCUUUUUUGAGAUUAAAAAAAAAG UUAUAUUGGUUUUGAGCAUUUCUUUACCUAUUG CACAAGUACGAUCACAACAUAGUAUGACGCUAUA AAGGUCUUU	177	sch-miR5020b-5p	AUAGCAUGCAUAAAGGUGUGA	11-31	ath-miR5020b	5	0	21	21	1
			sch-miR2089-3p	UUACCUAUUGCACAAGUACGAU	125-146	mtr-miR2089-5p	5	0	22	22	1
sch-MIR169n	GGAAGCAUCAUUGGUUGUCCACGCCUAAUGUCA UAGUAAGAGGGGAUGACCGAUAUUUCAUCGAGC UUAUUGGCUUAAAGGGUGUCCAACCAUAUGAAG CUCUU	104	sch-miR169n-5p	GGAAGCAUCAUUGGUUGUCC	1-20	ptc-miR169n-3p	3	0	20	20	1
			sch-miR2657-3p	CGAUAUUUCAUCGAGCUUAUUG	51-72	mtr-miR2657	5	0	22	22	2
sch-MIR2655o	CAUUUAUGUCCUUUAACUUUGAGUGUGCGCAAG UAGACACUUAAACUUGUAUGAAGUUGAAAAAAUA GACACACAUGUUACAUGUCCUCCUACAUGUCAU GUCCUACGUGUAUUGUGUCACGUAGGACUCACG UGUUUAUUUAUUUAAAAGUUGAAUAGUUAAAAUG UCUAUUUGUGCAUUAUGAAAGUUGAAGGUCAAAA UU	203	sch-miR2655o-5p	CAUUUAUGUCCUUUAACUUUG	1-21	mtr-miR2655o	4	0	21	21	1
			sch-miR2101-3p	AAAAGUUGAAUAGUUAAAAUGU	147-168	osa-miR2101-5p	5	0	22	22	1
sch-MIR396h	AAUCCGGGCUCUGCAACUAUGUUGAACUGUGUG ACUCUCAUCUAAAAGGUUUAGAUGAGAUAGUCAG ACACUUCAACAUUGUAUCAAGCCAGGCCC	96	sch-miR396h-5p	UCUGCAACUAUGUUGAACUG	10-29	gma-miR396h	5	0	20	20	1
sch-MIR829	CUUGAUUUAGUGGAGCAGUCAUUCCUCUAGGAU AUUUCUUUUCUUGGUGUUAACCAAAUUUAAAAAU AAAGCUCUGAUACCAAUUGUUGGAAUGUAUGCA UCCACUUAUCUUA	113	sch-miR829-3p	AGCUCUGAUACCAAUUGUUGGAAU	70-93	ath-miR829-3p-1	2	0	24	24	1
sch-MIR8001b-3	AAUAGAUACUAUACACUACAAGAAAAUGAUAAAU UAAAUGGGGAUAUUCUGCGGAUUAGUAUGAAAA UUUGCAGGAUAAUAAGUUUCCUGCGGAUUUUCA UACUAAUUCCUAGGAAAAUCUCCAUGUAAUUCAU AGUUUUCCUAGUGAUACUUGUUUCUUCG	162	sch-miR8001b-3-5p	CUGCGGAUUAGUAUGAAAAUUUGC	49-72	stu-miR8001b-5p	2	0	24	24	2

			sch-miR8001b-3-3p	GGAUUUUCAUACUAAUUCCUAGGA	92-115	stu-miR8001b-3p	1	0	24	24	1
sch-MIR8025-1	UUCAUGACUUGAUGAAAAUGAUAGCAUAGUCAAA CAUCAUAAAGAAAUAUUUUACCACACACUACUCA UGCAAUUAAAUUAGUAUAAGUCGCCAUUAUGUUU UUCUUAACCAAGCUGAAUCAUAUAAUGGUGACUU AUACUAAUUUAAUUGCAUGUCGAGUGUGUGUAU UUCCGCAUGUGUGUAACUACUCUAUCUUUUUGA UGAAGUUCAUAAA	215	sch-miR8025-1-5p	ACACACUACUCAUGCAAUUAAAUU	57-80	stu-miR8025-5p	4	0	24	24	1
			sch-miR8025-1-3p	UUUAAUUGCAUGUCGAGUGUGUGU	144-167	stu-miR8025-3p	3	0	24	24	1
sch-MIR6231	AUCAGGUUUUUUAAAACCCCCCCUUCCCGCACUA UUUAAUAGUGUAUUUUUAAAGUAUGUAUGUGGU CACGUGGACAUAAAAAAAAUUGCAUAACUAUAAUA UUAAUGUGUCCACGUGGGCACAUAUAUACCUUU AAAAUACAUUAUUAGAUAAUUUGGGAGGUAAAAA AUACACUAUUAAAUAGUUAGGAGGGGGGGGGGG GGUAAAAAGUCCUCCA	217	sch-miR6231-5p	UGUAUGUGGUCACGUGGACAU	58-78	sbi-miR6231-3p	5	0	21	21	1
			sch-miR2919-3p	AGGGGGGGGGGGGGUAAAA	190-208	osa-miR2919	3	0	19	19	1
sch-MIR7488	UGAAAUAAAAUAAGUUAAUAUUCAAUUAAAUAUU GAGCUUCUCUAACUUUAUUGAGAUAAAAUAAUUA UUUCAAUAUAAAUCUUAAAUAAAGGCUUAUUAUA AAUAUGUAACCUAACUACUUUUGAGUAGAGCCGU CAAUAUAGGCUAGACUGUUGGGCCGGUCUGGCC UAAUCCGAGAUUUAAUAGGGUGGGCUAAGAUUU UUGGAGCACAUUUAAAAAAAGGGUUUUUUAGCC CGACUUGAAUAAGUCUGUUGAUUUGAUGGGUUU GAGAAAUAUAUGUAGGGCCGGCCCGUGGGCCAA UAAUAAUUAAUUGGAAAAUAUAAUAUAAUAUUAAA	336	sch-miR7488-5p	UUUUGAGUAGAGCCGUCAAUA	121-141	ghr-miR7488	5	0	21	21	1
			sch-miR1888b-3p	GUGGGCUAAGAUUUUUGGAGC	189-209	ath-miR1888b	5	0	21	21	2
sch-MIR1043-2	UGUCCUUCAACUUUAGGUGUACACAAGUAGACA CUUAAACUUGUAUAAAGUUGAACAAAUAGACAUA CAUGUCCUACAUGUCAUUUUUUGUCCUACGUGG UGUCUUACGUAUAUUGUGUCAAGUAGGACUCGU GUUUUAUUUAUUUAAAAGUUGAACAGUUAAAAUG UCUGCUUGUGCAUUAUGAAAGUUGGAGGGAG	198	sch-miR1043-2-5p	CCUUCAACUUUAGGUGUACA	4-23	ppt-miR1043-5p	4	0	20	20	1
			sch-miR2101-2-3p	AAAAGUUGAACAGUUAAAAUGU	147-168	osa-miR2101-5p	5	0	22	22	1
sch-MIR7984d-1	UGGAAUAUAUCCAAAUUUUGACCAAAAUUGUUAU AACAAUCCCAAAAUUUGGGUCGCACCUAUUACCC UCCUGCACUAUUUAUUAGUGCAUUUUAGAGAUA UAUAUAUAUAUGCGCCACGUGGACAUCAUAAAAA UUGUAUCAUCAUAAAUAGUAAAUUGUCGAGAUGA GAACGUAUAUAUCCUUAAAAUACACUAUUAAAUA GUGUAAUGGGUAAUAGGUCCUGCCCAAAGUUUG AGAUUAUUACAUCGAUUUCGAUCAAAGUUCGGAU AUAUUUUU	278	sch-miR7984d-1-5p	AUCCAAAUUUUGACCAAAAUUGUU	9-32	stu-miR7984d-5p	4	0	24	24	1
			sch-miR7984d-1-3p	CGAUUUCGAUCAAAGUUCGGAUAU	249-272	stu-miR7984d-3p	2	0	24	24	1
sch-MIR1085	UUUUGAAUUAUUGACAACCUAGAAAUAUCUUUUU ACUUGAUUAACUAAAUUAAAAUACACCUCCGAUC AUGCAACAUGAGCGAAAUAGACCCCUAAAUUCUU UCUAAGUUUACAGGGGUUUUCAACACCUUUCUC AGUUGUUCAUUAAGAGUCUCAUGCUCCUAUAAG AGCUUGUGACCACUUGCUAUGUCUUGUUGCAAA UUAGGGGUGUAAUUAAUUUUAGUUAGUCUUUGG AUAAAAAAUUAGUUAGUCAAGUAGAGAUGUGUUC AUAAAAUUGUCAAUAUUUCAGGA	291	sch-miR1085-3p	UUGCUAUGUCUUGUUGCAAA	182-201	smo-miR1085-3p	5	0	20	20	1
sch-MIR172a-1	AAACACUGUCUCAAAUGUAAAUCUUCAGGUCGCC AAAGUCUAUAUCGUCCAGAAGUAGUGCAUUUUU GGAGUAGAACAACAUAGACAUUGACGACAUGAAG AUUUACAUCUGAGACAGUGCAU	123	sch-miR172a-1-3p	UUGACGACAUGAAGAUUUACA	88-108	vca-miR172a-5p	5	0	21	21	2
sch-MIR6232b-2	GAGCUCUACAGUGCAACUUCAGCAUAGUAAAGA GUAGAGACUAAUUAAUGCCUACAUAUGUAGGCAU	112	sch-miR6232b-2-3p	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-5p	5	0	21	21	1

	UAAUGAGUCUACUCUUUGCUAUACUGAAGUUGC ACUGUAGAGAUA										
sch-MIR828b	AUUUACAUUCACUUCUUUGGGAAAGCCUCUUGC UCAAAUGAGUAUUCCAACAAAUGUCUAAUUGACA UACUUUUGAGAUACUCAUUUGGGCAAGAAGUUU UACCAGGAAGGUUGUACUU	119	sch-miR828b-5p	UCUUGCUCAAAUGAGUAUUCCA	28-49	mes-miR828b	0	0	22	22	1
			sch-miR828-3p	AGAUACUCAUUUGGGCAAGAAG	76-97	aly-miR828-3p	4	0	22	22	1
sch-MIR319j	AGGACAUGCAACCUCGACAACCCCGACCUUUUCA UCUCCCUACAAGGCAAGUAGAAGUUGUAUCAAAC UGUUUCAAAUUCCAAUAAAAUUUAAUACAACGCC CACUUGCCCUGCAGGGAGAUGAAAAGGUCGGGG UUCUCAAGGUUGCAAGUUUU	155	sch-miR319j-3p	CUUGCCCUGCAGGGAGAUGA	105-124	pab-miR319j	5	0	20	20	1
sch-MIR2077	CAAUCAUCUUCGCAACUGGUUUCACAUCGCCAA GAGAUAUUGCUAUCGAUAGCCCUAAUAAAGAUAU GGCAAUUCUAUUUAAUAAAAUCGCCAUAUAUCUC CUUUAUUAAUUAGGAUCGAUGUUAAAAUCUCCUG GUAAUGUGAAACCAGCUGCGAAGGUGAUUA	165	sch-miR2077-3p	UAAUAAAAUCGCCAUAUAUCU	80-100	ppt-miR2077	5	0	21	21	1
sch-MIR5014a-1	AAAUUAAACAAAUAAACACAUUAUUUCUGCAGUG UCACCCUACAUGACAAUUUUGUGUCCUAACUGG AGUCUUAUGUAUAUUAUGUCAUGUAGGACACGU GUGUCUAUUUGUUCAUUUUUAUACAAAUAUAAGU GUCUACUUAUGUACACUUAAAGUUGGAGGGCAU AGUUAUCCGUUGAAAUCAAGUUAAAGAUCAUAUG UAGACUUCACACUUGACCCCAUAUAGAUAAUGUC UCCAUUGCUUUAAUGC	251	sch-miR5014a-1-3p	UUAUACAAAUAUAAGUGUCUA	119-139	ath-miR5014a-3p	5	0	21	21	1
sch-MIR160-3	ACUUGGAUCCAACUGAAAACUAUAACUUUUAACU UUGGGUGUUUAGAACUAGACACUUAAGCUUGUA UAAGAUAAAAAAAAAUAAACAUAUUCAUCCUACCU GGCGCCUUAUAUGACAAUUUUGUGUGCUACAUG AUAUCCUACGUGUAUUAUGUCAUGUAGGACACG UGUGUUUACUUGUUCAAUUCUAUACAAGUUUAA GUGUCUACUUGUGCACUUCAAAAGUUGGAGGGC AUGGUUGUCAGGUGAAGCCAAGU	257	sch-miR160-3-5p	UACCUGGCGCCUUAUAUGACA	98-118	dpr-miR160	4	0	21	21	1
			sch-miR7992-3-3p	UGUCUACUUGUGCACUUCAAAAG	203-225	stu-miR7992-3p	5	0	23	23	1
sch-MIR5213	UUGCAAGUAAGCACUCCAACUUUAAAGAGUGCAC AUCCAGACAUCUCAACUGCCAACUUAACACUCCA ACUUGUCUCACUUUGUCUCGUAGACACCUGAUG CUGAUGUGACACAUAAAUUUUGGAGGUGUCGAG AUGAUCAUUUUUGUUAGCUGGAGUGUUCAACUA CCACAAUGGAGAUGAGUUGAGGUGUCUAGAUGU GCAUACUCAAAAGUUGGAGUGUUUUUUGUUU	231	sch-miR5213-5p	AAGAGUGCACAUCCAGACAUC	25-45	mtr-miR5213-3p	5	0	21	21	2
			sch-miR10519-2-3p	ACUCAAAAGUUGGAGUGU	205-222	tae-miR10519	5	0	18	18	3
sch-MIR7981d-4	GCCCGAAAUUUUAGAGAUACACUUAUACUAUAUU AAGGUCCUAUUACCCCCCUGAACUUAUUUUAUAA GUAAUUUUCUAUCGUUUUUCGGCCUACAUGACA CUAGUUUGAAAAAAAAGUCAGCCAGCAUUGGGC CCAAAAGAUAGUGCCCCAUAGACCGAAAAGCGGU AGAAAAUUAUUAAUAAAAUAAGUUCAGGGGAUAA UAAGACCUUAAAAUAAUAAUAAAUAUGUCUCUGA GAUUUCGAAC	246	sch-miR7981d-4-5p	CCGAAAUUUUAGAGAUACACUUAU	3-26	sly-miR7981d	4	0	24	24	2
			sch-miR7981e-4-3p	AAAUAUGUCUCUGAGAUUUCGAAC	223-246	sly-miR7981e	4	0	24	24	1
sch-MIR11891-1	AUGUUAGUACUUUAGUUCAUUUAUGCCCUUACU GUCAAAUACUUGGUCCAAAUACUAUGCGCAAUUG AGCAGAAUAAGGGCGUAUUUGGAUCAAGUAUUU GAUGCUAAGGGCUUAAGUAAAUUGAAGUAUAAAC G	135	sch-miR11891-1-3p	AGUAAAUUGAAGUAUAAACG	116-135	mes-miR11891	5	0	20	20	3
sch-MIR8038b-3	UAUUUUUCAAGUCAAAGCAGUUUCUCCUUGUGA GUAAGUUGAAUCUCAUGCUCGUUAAACUGCAAG AGACGUAGAAUGCGUCCCAACAUGAGAUUCAUU UUACUCACAAGGAAAACUUGUUUUUGCUUGAGAA GCA	136	sch-miR8038b-3-5p	CCUUGUGAGUAAGUUGAAUCUC	26-47	stu-miR8038b-5p	0	0	22	22	1

sch-MIR171f-5	GUGAGUACAUAUUGAAUUAGAGAAGCGAUGUUG GUGAGGUUCAAUCUGAAGACGAGUUUACGUUUU AUUUCAGUAAAGAACGAUCUCAGAUUGAGCCGC GCCAAUAUCAUUUCUUUUUACCAAUUCAUUUACU AGU	136	sch-miR171f-5-5p	CGAUGUUGGUGAGGUUCAAUC	26-46	fve-miR171f-5p	0	0	21	21	1
			sch-miR171f-5-3p	AGAUUGAGCCGCGCCAAUAUC	88-108	mes-miR171f	0	0	21	21	1
sch-MIR9652	AAUUAUCUUACUUAAUUAUUUUUUAUAGUUUAUU UGGCAACCUUAUUCAGAAGAUGUUAUAAUUGGA UUGCCUGAGUGGUGUCGGUUAGGACAACAUGUC UGUAUGACACAGGUGCCACUUAUUUAUGGAAUU UAUCGUGAGUGGCACAUGGUUUAUCGUGUUGUG AGACAGUUUGGUAUUUACAACAUAUUCCUAGACA GUGUACCCAAUUUUUCGAAUAUCAUUUUAAGCG UGAUAAACGAUCCAAAAUAAAACAAGAAGAUAUA G	268	sch-miR9652-5p	AACCUUAUUCAGAAGAUGUU	39-58	tae-miR9652-3p	5	0	20	20	1
			sch-miR5014a-3p	ACAGUUUGGUAUUUACAACAU	169-189	ath-miR5014a-5p	5	0	21	21	1
sch-MIR7983-3	UCCCUAAUGCCUUUAGCGAUAUUGGUUCUAAUG ACAGUUAACUAAUGCCGGUAAAGGCUUUAGCAC	66	sch-miR7983-3-5p	UAAUGCCUUUAGCGAUAUUGGUUC	5-28	stu-miR7983-5p	3	0	24	24	1
			sch-miR7983-3-3p	ACUAAUGCCGGUAAAGGCUUUAGC	41-64	stu-miR7983-3p	2	0	24	24	1
sch-MIR479-3	AAUACGUGAUAUUGGCACGGCUCAAUUAAAUAAC GAAGUUCUAUAUAUAAAGAAGUGCGCUUUCUAAU UGAACCGCACCAAUAUCUCGUUAG	92	sch-miR479-3-5p	CGUGAUAUUGGCACGGCUCAAU	5-26	ghr-miR479	4	0	22	22	1
			sch-miR171c-3-3p	UAAUUGAACCGCACCAAUAUC	65-85	aqc-miR171c	1	0	21	21	1
sch-MIR5303d	ACCCUAAGUUACUCAGACUUUCCAAAAUUGCUGC CUCACCCGUGUCGGAUCCUCCAAAAAUGCCAUA CUUUUGGAGGAUCCGACACGCACCUGUCAACGU UUCUGAAGAGUCCGAGCAACAUAGCUC	127	sch-miR5303d-3p	UUUUGGAGGAUCCGACACGCACCU	69-92	stu-miR5303d	2	0	24	24	1
sch-MIR396a-1	AGUCCAAAGCUUGCCAUCUUUUCCCACAGCUUU CUUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAA AUUAUCAAUUUAGAGAUCAAAAUUUAGCAAAAAG AAGUUCAAGAAAGCUGUGGAAAAGCAUGACUAG GACUUGGUCA	144	sch-miR396a-1-5p	CACAGCUUUCUUGGACUUUCA	25-45	hbr-miR396a	2	0	21	21	1
			sch-miR396a-1-3p	GUUCAAGAAAGCUGUGGAAAA	104-124	csi-miR396a-3p	1	0	21	21	2
sch-MIR1886f-1	GCGUUUGGCCAUGUGAUAUCAUAUCACCAUAUG GUAUCGUGAGAUGAAAUCAGCGUUUGAAUAUAC AAUUUUAUGAUGAUUCCAUCUCAUGAUACAGUAU CGUGAGAUGUGAUACCAUAUUCUCCAAAUAA	131	sch-miR1886f-1-5p	AUGGUAUCGUGAGAUGAAAUCAGC	31-54	stu-miR1886f	0	0	24	24	1
			sch-miR1886h-1-3p	AUUUUAUGAUGAUUCCAUCUCAUG	68-91	stu-miR1886h	3	0	24	24	1
sch-MIR5174d-2	AAAUACUCCCUCCGUUUCAAAAAGAUUGGCCUAG UUUGACUUGAAACGGAGUUAAAGAAAAGAAAGAA GACUUUUUAAUCUUGUGGUUCCAAUUUAAAGUU AUGUCAAAUGUACCAAAAUACCCUUUAAUCUUGU GGUCUUAAACAUGCCACGUGGAAAGUUAAAGUU UAAGUGUUGCCAAAAAAGGAAAGGGGUCAUUCU UUUUGAAACAAACUAAAAAGGAAAUAGGGUCAUU CUUUUUGAAACGGAGGGAGUAGCA	259	sch-miR5174d-2-5p	UCCCUCCGUUUCAAAAAGAUUGGC	7-30	bdi-miR5174d-5p	1	0	24	24	1
			sch-miR5174e-2-3p	UUUUUGAAACGGAGGGAGUAG	237-257	bdi-miR5174e-3p-2	2	0	21	21	1
sch-MIR7983-4	CAAUCACUACAAUUACAAUGACCAUUAACGGUAU UUAAUUCUUAAUUGCCUCUAAAUAUGUAUUUUUA GUGGUUAUUGUCACUCUUUACGUAUGUCCCUAA AGUCUUUAGCGACAUUGGUUCUAAUGUCACUUA ACUAAUACCGGUAAAGACGUUAUCACUCUUUAUU AAUGUCAAUAUUUAAUGCCGCUAAAAGUUAUUUU UGUUGUAGUGAAUC	216	sch-miR7983-4-3p	UAAAGUCUUUAGCGACAUUGGUUC	99-122	stu-miR7983-5p	0	0	24	24	1
sch-MIR166-2	CCAAAAGAAAGAAAACAUUUGUUGAGGGGAACGU UGUUUGGUUCGAAAUCAUUCAAACAAAUUAAAAU UCAUGCAUCUCGAUGAUCGAUGAAUUGAAUAAUU UCGGACCAGGCUUCAUUCCCCCCAACUCAAGUU UUUGUUUUAAU	146	sch-miR166-2-3p	AUUUCGGACCAGGCUUCAUUCCCC	100-123	lja-miR166-3p	0	0	24	24	1

sch-MIR7990a	UUGCGUAUAUAUCAGAGGCAAUCUUAUGACCGU UUGAAGUUUCACAAAUUUACAAAUACUUUUUUUU UUGAGUUACACUCUUUAAUGUGGUGAAACUUCA AAUGAUCGUAACUUUGGCCUUGAAUAUCCGUUU	133	sch-miR7990a-3p	UUCAAAUGAUCGUAACUUUGGCCU	97-120	stu-miR7990a	0	0	24	24	1
sch-MIR10197	UAAAAAAUCGCCUCAAUCGGACAUCUAAGACAAA AUUUAUGACCGUUUUAAGUUUCACAAAUUUACAA CUACUUUUUCUGGGUUACACUCUUUAUUUUGGU GAAACUUCAAAUGAUCGUUACUUUAACAUUGAAU GUCCGUUUGAGGCGAUUUUACU	157	sch-miR10197-5p	AAUUUACAACUACUUUUUCUG	60-80	gma-miR10197	5	0	21	21	1
			sch-miR7990b-3p	GAAACUUCAAAUGAUCGUUACUUU	102-125	stu-miR7990b	3	0	24	24	1
sch-MIR164c-2	UAUUUAAGCUGGAGAAGCAGGGCACAUGCUGAA UUACUUGAAACUUUGAUCUUUCAAGAAUUUUGCA UGUGCUCUUGCUCUCCAGCUUAAUUC	93	sch-miR164c-2-5p	UGGAGAAGCAGGGCACAUGCU	10-30	fve-miR164c	0	0	21	21	1
			sch-miR164-2-3p	CAUGUGCUCUUGCUCUCCAGC	66-86	stu-miR164-3p	1	0	21	21	1
sch-MIR7997b-5	UGAAGUCUGACCGUUUAGUUGCUCGGACUCUUC AUUUUUGAUGUCGCACUCGUGUCGGAUUCUCCA AAAAUACACUACUUUUGGCUAAUCCGACACGCUA CCGUUGAAACUUUUGAAGAGUUCGAGCAACAUA GGGCCAGUCUAGG	146	sch-miR7997b-5-5p	UAGUUGCUCGGACUCUUCAUU	16-36	stu-miR7997b	5	0	21	21	3
			sch-miR5303-5-3p	CUUUUGAAGAGUUCGAGCAAC	110-130	sly-miR5303	1	0	21	21	2
sch-MIR827	GGUAAUUGGAUUUGGUGUAAUUACACUGUCCUG UUUUGUUGGCCAUGUAAUUGCCUGGUCAGCAGU UAAUUGGGUGUAGUUGGCAGGGUGCAAUUACAC UCUCCAAUUCAU	111	sch-miR827-5p	CUGUUUUGUUGGCCAUGUAAUU	31-52	eun-miR827-5p	5	0	22	22	1
			sch-miR171i-3p	AGUUGGCAGGGUGCAAUUACA	78-98	zma-miR171i-5p	5	0	21	21	2
sch-MIR7997c-5	AACUAUGUUGCUCAUACUCUCCAAAAAUGAUGCC ACAUCCGUGUCGGGUCCUUCGAAAAUGUACUAC UUUUGAAGGAUCCAAAACGCACUCGCCGACAUU UUUGAAGAGAUCGAGCAACAUAACA	125	sch-miR7997c-5-5p	AUGUUGCUCAUACUCUCCAAAAAU	5-28	stu-miR7997c	4	0	24	24	1
			sch-miR5303-5-3p	UUUUUGAAGAGAUCGAGCAAC	99-119	sly-miR5303	1	0	21	21	1
sch-MIR1919-3	UCCGAAUCGCUCCGACGCCUUUGAUGUUCACAU CUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCC CUUCUAAGGAACCACUUUUUCUGUAAAUCUAAUU AAUUUGAAUUCAAUGUGGUAGGGCGAGAGUCAU CUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAA AGGCUUAUUGGGCGUUUCCUU	187	sch-miR1919-3-5p	UGUCGCAGAUGACUUUCGCCC	47-67	stu-miR1919-5p	0	0	21	21	1
			sch-miR1919-3-3p	GCGAGAGUCAUCUGUGACAGG	123-143	stu-miR1919-3p	1	0	21	21	2
sch-MIR812o	UUUCUAGUUUGCCUUUCGCGGAAGAAAUUUGAU UUCCAUCUUGAAGGUUUACCAUGAAAUAGUCAUU CUUGUCUUGAAUGUUUGACUGACCUCUGCUUAU UUCAUGGGCAAACUUUCAAGACGGAAAAUCAAGU UUCUUUUCGAGGAGGCAAACGAGGUC	160	sch-miR812o-3p	UGUCUUGAAUGUUUGACUGAC	70-90	osa-miR812o-5p	5	0	21	21	2
sch-MIR5205d	AUCUUAUAAUCAGAGGCGGAGCUAGGUAGAGAU UUAUGGGUUCGGACGAACCUAUUAACUUUUGUG UAAAUUCUAUAUUUGUAUUUUAAUUUUUUUUUAA AAUAUAUGUAUAUUAACUUGUGAAUCCCCAACAA AUUGAUUUAGAACCCCUCAAACUUCUAAUUUUAA CCCCGCCUCUACUUAUAACCG	189	sch-miR5205d-5p	CUUAUAAUCAGAGGCGGAGCUAGG	3-26	mtr-miR5205d	5	0	24	24	1
sch-MIR1514b-1	CAAUAUUUUUUCUUGCCAUAAGUUGAAUAAAAGU UAUCGACUUCUUUUUUACGAUAGAUAUCUAGAAA AGAAUGACUUAUUUUUGAAUAUCGAGGAAAUUUC AGGUAUUGGAGAUUAAUUGGAGUACAAGAAUCG CAGGUUAUUCUCCUUUGGCAAGAACAACUAUGU	168	sch-miR1514b-1-5p	UUCUUUUUUACGAUAGAUAUC	42-62	gma-miR1514b-5p	5	0	21	21	1
			sch-miR399f-1-3p	AGGUUAUUCUCCUUUGGCAAG	137-157	csi-miR399f-5p	5	0	21	21	2
sch-MIR9477	AUGUUUAUCGACACACACACCUCAACUAUCAGUU GUUCCCUUUUCCUACCUGAAUGAUGGUGAUAUU UCUAGGUUGGGAAAGGGAACAACUGAUAGUUGA GGUAUGUUUCGAUAAACAU	119	sch-miR9477-5p	UAUCAGUUGUUCCCUUUUCCUACC	27-50	sly-miR9477-5p	1	0	24	24	1

			sch-miR9477-3p	UUGGGAAAGGGAACAACUGAUAGU	74-97	sly-miR9477-3p	0	0	24	24	1
sch-MIR8046-1	UGGAUAAGGGCGCAAGUACCCCUGGACUAUAAC CAAAAUUUCAGAGGCACACCUAAACAUAAUUAGG GUUCUAGUUAAGUUUAGAUGUAUCUCUGAGAUU UUGGACAUAAUCUAGGGGAUACUUGUGCAUUAU UCG	136	sch-miR8046-1-3p	CUCUGAGAUUUUGGACAUAAU	91-111	stu-miR8046-3p	5	0	21	21	1
sch-MIR5376	UGCACAUCAAGAGGGCCAUAAAGGUCCGAAUUU UUUCAUAUUUUCAUUUCAAGUCAACCAGCCCAUA AAGCCGACGAACGGUUCUUAGGACUAAAGUUCA AAGCGAUUGGAGAAGUUGAAGAUUUGAAGAAGU UGGGCCAGAGGAGCCCUACUUUAUGUAUU	162	sch-miR5376-3p	UGAAGAUUUGAAGAAGUUGGGC	117-138	gma-miR5376	2	0	22	22	1
sch-MIR1128-4	UACUACUCCCUCCAUCCCAAUUUAAGUGUCUUCC CAAUUUAGUCUGUCCCAGCAAGACUGCCUCUUU CUAUAUUUAGUAAGUUCUCCAAUUCCAACAUUAU ACAUGGAAAGUUUGAGACCACAAGAUUUAAAGGA CUACACACAUCUUUAAUUGAAGACCACAAGAUUC AAAAACUUUGUGUCCAAUCGAACUAAAACACUUA AAUUUGGGACGGAGGGAGUAAUU	226	sch-miR1128-4-5p	UACUACUCCCUCCAUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1
			sch-miR1436-4-3p	UAAAUUUGGGACGGAGGGAGU	202-222	hvu-miR1436	4	0	21	21	3
sch-MIR7517	UUUCCUACAAUUUUAAAAAUUACAAAAAUUCCUA CUCUCUCCUAUUGUCGGAUACAUCACUUAACAU GAUAUAUCGGUCGGAUAUAUCAUUUUACGCGAU GUAUCAGGACGUUGAGUGAUGUAUCCGAAAGUG AGACGCAAUUUAUCGGGACGUCGAGGGAUGAUC CGACAUCGGGAUACGAUGUUUGGGACGUUUUUG GAUAUAUCCGGAUUCCACCAAAUUUAAGGAUUUU UUGUUAUUUGGAAAAGAGUAGGGAU	258	sch-miR7517-3p	AUUUGGAAAAGAGUAGGGAU	239-258	lja-miR7517	5	0	20	21	1
sch-MIR3628	UGUAAGUAUGAUAUGUAAUAGUAAUAUUUAAGGA UUGUACGGAUAGAUAGAGGCAUCUAACCUUAAG CAGAGGUCUCGAAUUCGAGAGGAAAAAAAGAUAU AUUUUCAGAAGUUUGAGGCUUCAACAUGCUCAAA AUUACUAUAACAACAUACAUUGUU	159	sch-miR3628-3p	UUAAGCAGAGGUCUCGAAUUC	63-83	vvi-miR3628-3p	5	0	21	21	2
sch-MIR5014a-2	AUAUCAAAUAUAGCUCUUUCUCUCGCUUUAUACA AACAUAAAUUGUACAUGGUAUUUUUGUAUAAUUU GUGUUUGUAUAAAGCCAGAAAGAGUGAAAGGCA AAACAGAACUGGACAGGGGAAUAUUUGUAUUGU AUAAUUAUAAGUGUAUAAGACGAAGAUAUAUGUA UUUGCAUGUGUAUAUACAAUUUUCUCUCGCCUU AUAUAAACAGAAACACAAUUUAUACAUUUUUGAU UGUAUAAAGCGAGAGAGGGAACGAGCGAGAGUU UGAGGG	274	sch-miR5014a-2-3p	UUGUAUAAUUAUAAGUGUAUA	131-151	ath-miR5014a-3p	5	0	21	21	1
sch-MIR396a-2	UCCAUUCAUACACCUCAUUACCACUGUAAGAUGU GUUAGUUUGAUUUCAAUCUCUUUCUUCAACUAG CACAUUUUGAGGAGUAGGACGGGGAUAAUAAU	99	sch-miR396a-2-3p	UUCAAUCUCUUUCUUCAACUA	46-66	pab-miR396a-5p	5	0	21	21	1
sch-MIR415	GCAUUUGUAUACAAUUGAAUCGAAGUAAAAUAUU UGUAAAUUGUAUAAUUAAGUGUAUAGCACGAAGA UAUAUGUUUUUGCAUGUGUAUAUAUAAUUCUCU CUCGCUUUAUACAAAACAGAAACACAAUAUAUAC ACUUCUGUUAUAUAAAGCGAGAGAGGCGAGCAG AGGGAGAGUGGCGAGAGAGAGAGUUGCGAGAGA GAGUUUCAGGAGAGAGGCGACCGGCAAACUUUG GCAAAUAUUUGCUUUGGUGCACAAUUAAAUCAAA CAG	271	sch-miR415-5p	UACAAAACAGAAACACAAUAU	111-131	ath-miR415	5	0	21	21	2
			sch-miR1432-3p	UUCAGGAGAGAGGCGACCGGCA	206-227	bdi-miR1432	4	0	22	22	1
sch-MIR8030-1	GACUAGUAAUUUGGUUUGACUUGAUUUGGUGUU GGAAAAAAAAUCCGAAUACAUUUGGGUUGGGUU GGUUUCAUGUAAAAAAAAUCAACCCGAGAUCAAA CCAAUCCAACAUUAUAUAU	119	sch-miR8030-1-3p	UUGGGUUGGGUUGGUUUCAUGUA	55-77	stu-miR8030-5p	5	0	23	23	1
sch-MIR169c-3	UUAGGAAGAGAGAUCUUACAUGAAAAGAAAAGCC UUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUG CACCUACUAUUUUCCUUCAUUUUUUUUAUGGAG UACUUAAUAGUAUACUAGGCAGUCUUCUUUAGC UAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUC	179	sch-miR169c-3-5p	UAGCCAAGGAUGACUUGCCUA	44-64	ata-miR169c-5p	0	0	21	21	1

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sch-MIR7816	UGUAUAACUAAUACCCACAUAACUUAUUCCACCU UCUACCCUGCAUAACUUUAUACAUAGAUUCCCUC AUAAGUUAUGUUGGUAUUAAUUAUGUA	95	sch-miR7816-3p	UAUGUUGGUAUUAAUUAUGUA	75-95	ptc-miR7816	5	0	21	21	2
sch-MIR1312a	GUUCAAAUAUGUCAACGAACUUAUAGAAUAGGCU CAUCUAUGCUAUCGGUUAAAAGUUUUCUUCGUC GAUGUCAUUUCAGUUAGAAAAUGCUGACAUGAAU AAGUCUUUUCUCAAACAAAAAUUGCAACAGAUAA GUCAAACUUUUAACGGAGUGCAUAAAUGAGUCU UUUUCUCAAAGUUCUGUUGCAUAUUUGAAC	198	sch-miR1312a-5p	UUCAGUUAGAAAAUGCUGACAU	76-97	pab-miR1312a	5	0	22	22	1
sch-MIR7997c-6	UGAAACCUAUAUUGCUUUGACUCUUCUAAAAUGA AAUCGGGUGUGUGUCGGAUCAUUCAAAAGUAGU GCAUUUUUGGAGGAUCCGACACGGGUGCGGCAA CAUUUUUGGAGUGUCCGAGCAACUUAGGUUGAA	133	sch-miR7997c-6-5p	AUAUUGCUUUGACUCUUCUAAAAU	9-32	stu-miR7997c	3	0	24	24	1
			sch-miR5303f-6-3p	AUUUUUGGAGGAUCCGACACGGGU	70-93	stu-miR5303f	2	0	24	24	1
sch-MIR8040	UAACUUGGCUUCAAAUCACAUUUAUGCUCUUCAA CUUUGGAUGUACACAAAUAGACACUUAAACUUGU AUAAAGUUGAACAAAUAGACACUCGUGUCCUACA UGUCAUUUUUUGUCCUACGUGGUGUCAUACGUG UAUUGUGCCAUGUAAGACCCAUGUGUUUAUUUA UCUAAGUUGGAUAGUUAAAGUGUCUGUUUGUAC AUUAUGAAAGUUGGAGGUCAAAAUUAAAAUUUGA AGCCAAGUUU	245	sch-miR8040-3p	UCAAAAUUAAAAUUUGAAGCC	219-239	stu-miR8040-5p	4	0	21	21	1
sch-MIR6299	UAUAAUAUUUCAGUUGAUCUUGAAUCCCAUUUAC UCCCUCUCCCUUUGCCGGACAAUAGUUGUCCAC UAUUGACUUGGUACAGGGAUUAAGAAGCAGUAA AUGAUAGGGGUAAAUUUAACAAAUCACCCUUAUU AAAAGUAAGUCACGUAACAUUGAAAAAUAUUGAU UUAAUAAACUGGACAAGUAUUGUUGGACGUCUC AAAGUAGUUUAGUGAACAAGUAAAGAUGGACAGA GAGAGAGGGAGUAGCUUAGACUCAUAGCAGCAA AGAAAUUAUUGGU	281	sch-miR6299-3p	AUUGAAAAAUAUUGAUUUAAUA	153-174	gma-miR6299	5	0	22	22	1
sch-MIR5014a-3	UCUCCAACUUUCAUUAUGCACAAACAAACACUUU AACUAUCAAACUUUUAAAUAAAUAAACACAUGAG UCCUACAUGACAAAAUACACGUAGGACACCACGU UAGACAAAAAAUGACAUGUAUGAUGACAUGUAAG ACAUGUGUGUCUAUAUGUUCAACUUUAUACAAGU UUAAGUGUCUACUUGUGCACACCCAAAGUUGGC UU	205	sch-miR5014a-3-3p	UUAUACAAGUUUAAGUGUCUA	161-181	ath-miR5014a-3p	5	0	21	21	1
sch-MIR156b-14	UACGAAAGAGGUGAAGGUGAUGACAGAAGCAUA GAGAGCACAAAUGAAUUGAGAUGCUUUUGCUGC CCAAAUUGAAUGAAAUUAGCAUAUCAUCAUUAGU GCUCUCUAUCUUCUGUCAACAAUAAUCACUCUUU CUUC	138	sch-miR156b-14-5p	AUGACAGAAGCAUAGAGAGCAC	20-41	aof-miR156b	2	1	22	21	2
			sch-miR1088-14-3p	UAGUGCUCUCUAUCUUCUGUC	97-117	smo-miR1088-3p	4	0	21	21	3
sch-MIR5070-1	UCCAUUUAUAAUUAGGGCUUAUAAGCCUGGUAU AAAUAAGUCAUUGGGUCUUAAGGCUUGAUCUAA GUUGGGUCGAGGUUGGUGGUUGGCCCACAGGC CAUUGAAAUUACUUCCCUGUUACAUUUUAUGUG GCACUUUUUGAAUUUUGAGAUUCAAAAAGAUCUG UCUUUAACCGUGAAUUUUUCAUGAAUCUUUUAUA CAUUUUGAAUUAUCAAUUACUAUUAAUUAUAGUA CUUUUAACGUCGUUUAUAAAUAUA	257	sch-miR5070-1-5p	UUGAUCUAAGUUGGGUCGAGG	58-78	ata-miR5070-3p	4	0	21	21	1
			sch-miR8007b-1-3p	AUGUGGCACUUUUUGAAUUUUGAG	127-150	stu-miR8007b-5p	2	0	24	24	1
sch-MIR9760-1	AUGAUUCCGUUAGUAGCGUAUCUCGAACUAGGA UGAUUUAGAUUUGAUCUCUCUAUAUGAAUAAUCC AUUAAUUUGUGGAGUAUUCGAGAUUUUGAUAUC UUUGUGGAUUUUUCGAGAUGCCUUUUAAGGGAA UUUA	137	sch-miR9760-1-5p	AGGAUGAUUUAGAUUUGAUCU	30-50	gma-miR9760	5	0	21	21	2
			sch-miR393-1-3p	AUUUUGAUAUCUUUGUGGAUU	90-110	cas-miR393-3p	5	0	21	21	1

sch-MIR5070-2	GACUUAUGGUUUGGUUUGAUUGGUUUGGCAUUA AAAAAAUCUGACCAUUCUUGGUUUAGUUUGGUA UUUACAAAAAACGCCAAACUAAAUUCAAUCCAAA UCGACAUAAUAC	112	sch-miR5070-2-3p	UCUGACCAUUCUUGGUUUAGU	40-60	ata-miR5070-5p	5	0	21	21	1
sch-MIR396c	UGCUAAGCAUGAGCAGAAACCAUGAUCGGAUUG CUAGCGGUGUUAUGUUAGUGUUUGGGCUGUUUU GAUUAAAGUAAGCUGCUGGAAAUUCUGUUUUGG UGUUAUGCAUAUGUUAAUA	118	sch-miR396c-3p	UUAAAGUAAGCUGCUGGAAAU	69-89	cca-miR396c	5	0	21	21	1
sch-MIR11066	ACCUUGGAAAUAGGUGGUCUUGAACUUUUGCUA CAUGGAUAAACCUUCGACGCCAAAAGUCGAUACU UGAUGUUCUGUUCAUGGGGCAAGCAAGAUUGAA AGUUCAAGAUCAUCCACCUCCAAAGU	126	sch-miR11066-5p	GAAAUAGGUGGUCUUGAAC	7-25	lja-miR11066-3p	5	0	19	19	2
sch-MIR7984d-2	UUUUUAGGAAAAGAGUUCAAAAUGUAUCCGAACU UUAAUCGAAAUUUGCGUAGCAAUCCCAACUUUUG AGCUGGACAAGUUACUAUUUAUAAUGAUGCAAUA UUUAUGAUGUCCACACGAGCACAUGUAUACCUG UAAAUUGCACUAUUAAUACUGCAGCGGUAAAUGU CAUUCCCAAAGUUUGGUACUGUUGCAACAAUUU CGAUCAAAGUUCAGAUAUAUUUCAAACAUUUUCC CAAUUU	242	sch-miR7984d-2-5p	AUCCGAACUUUAAUCGAAAUUUGC	26-49	stu-miR7984d-5p	5	0	24	24	1
			sch-miR7984d-2-3p	CAAUUUCGAUCAAAGUUCAGAUAU	197-220	stu-miR7984d-3p	2	0	24	24	1
sch-MIR2605	ACUGCCCCCUUACGUAUAUUAUAUGAACUAUUUG UUGCCUCUUUUAUUCCCUCCUAUUUUUUUUUAG UAACUAGCAAAAAUGAAAAAGUUGGUGAGUAGUU GGGAAAGAAGAAAUGGACGGGAAGGAGCAAAGG GCACCAGAGGGUUUGGCAAGAAAAUGUAAGGAA GGGCUAC	174	sch-miR2605-5p	ACGUAUAUUAUAUGAACUAU	12-31	mtr-miR2605	5	0	20	20	1
			sch-miR482d-3p	AAUGGACGGGAAGGAGCAAAG	113-133	mdm-miR482d	5	0	21	21	1
sch-MIR5026-1	AUUCCUUUUCGAUUUAUGUGGCACUAGCUUAAA AAAAAGUCAAUCAUCGUUGGGCUCACAAGAUAGU GUCACGUAGGCGGAAAAGGAGU	89	sch-miR5026-1-3p	GCUCACAAGAUAGUGUCACGU	54-74	ath-miR5026	4	0	21	21	2
sch-MIR1886f-2	UAUGAUAUCACAUCUCAUGAUAUGGAAUCAUGAG AUGGAAUCAGCGUAAAAUCGCUUGUCCAAACACU GAUUCCAUCUCACGAUACUAUAUCGUGAUAUGAU AUCGCA	108	sch-miR1886f-2-5p	AUGGAAUCAUGAGAUGGAAUCAGC	22-45	stu-miR1886f	3	0	24	24	1
			sch-miR7980b-2-3p	GUCCAAACACUGAUUCCAUCUCAC	58-81	stu-miR7980b-5p	1	0	24	24	1
sch-MIR2868-1	AAAGUGUAUUACAAAAUGCUGAAUAAAGUGUAUU AGUAAUGCUUGUAUUCGUUAUGCUUGCAUCAUU UUUUAUGCAUUGUUUGGUUUGGUGUAUUAAAAA UAACAUCCAUUGCAUAAUUUCCAGAAAAAAGUAU UUUUUUACCAAAAUAGCCUCAACAAAUAUGGUGG AAAGGAUGUGGACAAGGUUUUGACGGGCAAUUG UAUCUUUCGUCAUGCCAAUGCAUGCAUCAAAACC CUUUGCAUUACUAAUACCAUGGAUUUCCAUGUAU UAGUAAUACACAAU	283	sch-miR2868-1-5p	UUGGUUUGGUGUAUUAAAAA	81-100	osa-miR2868	3	0	20	20	1
			sch-miR396b-1-3p	CUCAACAAAUAUGGUGGAAA	152-171	vca-miR396b-3p	5	0	20	20	2
sch-MIR2678	CCUACGGACCGUAGGUCCACCUACGGACCAUGC UGGUCAUCCGUAGCUCUUUCCAGAGAGAGGGUG AAGGGAGUAUUGAUCGACGUUCACAGACUAUGG ACCGUCAUCUGACCUACGGAUUGUAAGUUUGUA CGUCGUCCAAGACUUAACCAAUUAAUUUGGGCU GAAAUUUUUGGGAGUUUCUGAUCCCAUUGACGG UUGUGCAGGACGGACUGUGGGUCAGGCUACAGU CCGUCAA	238	sch-miR2678-3p	UGAAAUUUUUGGGAGUUUCUG	165-185	mtr-miR2678	4	0	21	21	1
sch-MIR5370	AACUGUAUGGUACUCUCUCUGUUUUAAUUUGUU UGUCUGGCUUUGACAUGACACAAAGUUUAAGAAA GUAAAAAAUACUUUUGAAUCUUGUGAUCUUAAAC AUGUCACGUGAAAAGUUGAAACUAAAGAGUUGCA AAAAGGAAAGUAAGACAAGCAAAUUGAAACGGAC CGGAUGUAUCAUGCAAAG	187	sch-miR5370-3p	CUAAAGAGUUGCAAAAAGGAA	123-143	gma-miR5370	4	0	21	21	1
sch-MIR6283	GGGAUUAUUUGUCUUCCUAGUCUUCGACACAAG AAAGGGGUGUAGAAAAAUCCUUUUUUCUUGUGU	89	sch-miR6283-3p	AGAAAGGGGUGUAGAAAAAUC	32-52	ppe-miR6283	5	0	21	21	3

	CGAAACGAAAGAGUAAUGAUUCU										
sch-MIR2675	AGGGCCACUUCCUGCCUCAAGAUGUGAAGAGAG CUAGAGUCAAUAGAUUCUUGCGUUUGAGGCAGA AUGGCAGG	74	sch-miR2675-3p	UGAGGCAGAAUGGCAGG	58-74	mtr-miR2675	4	0	17	21	2
sch-MIR2595	AUAAAAUUGUUGAAAAUCGUCGGAUAAUUUUUUU UAAAGGGGGUUGAUUUAUGGGUCGGAUUAGGUG UUUAUGAGUCCGAAUAUCUUUUCAUUUUCAUAUA UAUGUCAUGUGGUAAGGUCAAAAUGACAUGACA UAUCCAUGUGACAUUUAAAGAAAUUAAAAAUGAG UUGGAUACGUCCAACAUGACAACUAACGCCCACA AGGGCAUAUUUGGACCAAAAGUUGGAUGGUGAG GGCAUGAAUGAACCAAAUUUUAAACGGAAUAUAU AUCUAGACUUUUUCGAAUAAUUUAGG	295	sch-miR2595-5p	UUCAUUUUCAUAUAUAUGUCA	88-108	mtr-miR2595	5	0	21	21	1
			sch-miR11553-3p	UAAAAAUGAGUUGGAUACGUC	159-179	pab-miR11553	4	0	21	21	1
sch-MIR7533c	UUGUUGAAAAUCGUCGGAUAAUUUAUUUAAAAGG GGGUUGAUUUAUGGGUCGGAUUAGGUGUUUAUG AGUCCGAAUAUCUUUUCAUUUUCAUAUAAAUGUC AUGUGGUAAGGUCAAAAUGACAUGACAUAUCCAU GUGGCAUUUAAAGAAAUCAAAUGGAUACGUCCAA CAUGUCAACUAACGCCCAUAAGGGCAUAUUUGCA CCAAAAGUUGGAUGGCGAGGGCAUGAAUGAACC AAACUUUAAACGGAGGAUAUAUCUAGACUUUUUC AAAUA	275	sch-miR7533c-3p	AAGUUGGAUGGCGAGGGCA	208-226	lja-miR7533c-5p	4	0	19	19	1
sch-MIR7984c-1	UUACGAUACCAAACUUUAUGAAGGGUCUUUUACC CCUGCUCUUUUUGAAAGUGUAUUUUAAAGGUAU AUAUGUGUCUACGUAAACACAUUACUAUUCAAAA UGAUGCAACAUUUAUGAUGUCCACGUGAGUACG CAUAUGCCUUUAAAAUGCACUAUCAAAUAUUGCA GUGAUAAAUGGUCCUCCGUAAAGUUCGGUAUCG CAG	204	sch-miR7984c-1-5p	ACGAUACCAAACUUUAUGAAGGGU	3-26	stu-miR7984c-5p	2	0	24	24	1
			sch-miR7984c-1-3p	CCUCCGUAAAGUUCGGUAUCGCAG	181-204	stu-miR7984c-3p	5	0	24	24	1
sch-MIR7699-1	AAUACUAGAGAUUCAAGCGAUAGAAUUUCUCAAU UCUAAUACAAGGUACUUAUUAGAUCGAAUGUACU UAUUCGAUCUAAUAGAAUGAUUUUGCCGUAUCCA GACUAAUACCAAUCCAAGCCAUUUCAUGAAUAAA AUGUGACCAAUUAACCAACCAACAAAACCACUUG UUACAAAUAAGAUCUUGUUGUUGCAUCGAAAGAG AUAAAUGUUGAGUAAUUUGACUAACAUUGAACUU CGUAAAAUGAAAUGGUUGAAUAAUUGAAAAAUGA GAUUAUUCAGGAAUACACAUUGAAUGCUGAGAUU ACGCAUUGAAUUUCUGGUAGU	327	sch-miR7699-1-3p	AUUGAAUGCUGAGAUUACGCA	291-311	mtr-miR7699-5p	5	0	21	21	1
sch-MIR7719	UGUAUACAAAUCAAUUGUAUAAUUUGUGUAUGUA UAAAACGAGAAAGAGAGAAAGACAAAAGAAAAUU GGGCAGGGAAAUAUUUGUAUUGCAUAAUUAUAA GCGUAUAGGACGAAGAUAUAUGUAUCUGCAAGU GUAUAUACAAUUUUCUCUAGCUUUAUACAAACAG AAGCGAUAGAGGCUAGGGUAACAAGCGAGAUCU GAGAGAGUAGGGAGCGAGAUCUAGGAGAGGGGA ACGAAAAUAUAUGUAUAUAUACAUUUUUUUCUCG CUUCAUACUAACAUAAACACAUUUUAUACACUUG UAUUUGUAUAAA	314	sch-miR7719-5p	UAUAAGCGUAUAGGACGAAGA	97-117	bdi-miR7719-3p	4	0	21	21	1
			sch-miR9555b-3p	UUAUACACUUGUAUUUGUAUA	292-312	bra-miR9555b-3p	5	0	21	21	1
sch-MIR9760-2	UUCUUCUUAUGAAAUUGAUGAGAAAUUGGAGGA UUUAGUGUUGAUUGUUGAGGAUGAUUUGGGGAU GAAGAUGGUUGGAUGGGUCUUCCUCUCAUGAAA UUGAUGAGAAAUU	112	sch-miR9760-2-5p	UGGAGGAUUUAGUGUUGAUUG	27-47	gma-miR9760	3	0	21	21	1
sch-MIR7997c-7	AAGUAUGUUGACCGGACUCUUCAAAAAUGCUGG CUGGUGCAUGUCGAUCCUUCAAAAGUAGUAUAU UUUUGAAGGAUCUGACACGGGUGCGGCAACAUU AAUUGAGAGUCUGAGCAACAUAGGA	124	sch-miR7997c-7-5p	AUGUUGACCGGACUCUUCAAAAAU	5-28	stu-miR7997c	3	0	24	24	1
			sch-miR5303f-7-3p	AUUUUUGAAGGAUCUGACACGGGU	65-88	stu-miR5303f	2	0	24	24	1

sch-MIR169r-5	UGCAGCCAAGGAUGACUUGCCGGACCAUAAAAU UGCUAGGAUUUUCUAGUUUCGGCAAGUUGUUCU UGGCUAUA	74	sch-miR169r-5-5p	CAGCCAAGGAUGACUUGCCGG	3-23	csi-miR169r-5p	0	0	21	21	1
			sch-miR169b-5-3p	GGCAAGUUGUUCUUGGCUAUA	54-74	zma-miR169b-3p	1	0	21	21	1
sch-MIR1044	UGUAUGACAUUAUACAUAAAUAUAUUAUUUAACU UGAUCUCCAUUCACAUUUACACCCUCGAACUCUA GGUGUGGACAAGUAGAUAAUAGAACUUAGACACA UGAGUUCUACUUGACAUGGUAUACAUAGGCCUC AAAUUGUUAUGUAGGACGUGUGUGUCUAUUUGU UCAACUUUAUAAAAAUUGAAGUGCCUACUUGUAU AAAUCCAAAAUUGGCGGGCGUAAGUGUAAAUUG AGUCCAAGUUAAAGGACAUAAUACAUAAAUAUGC CAUUUA	275	sch-miR1044-3p	UUGAAGUGCCUACUUGUAUA	184-203	ppt-miR1044-3p	5	0	20	20	1
sch-MIR7997c-8	UGACAUAUAGGUUAUGUUGCUCGAACUCUUCAA AAAUGUUGCUACAUUCAUGUUGGAUCCUCUAAAA AUGCACAACUUUUGAAGGAUCUGACAUGUAUUG ACGAUAUUUUUGAAGAGCUCGAGCAACAUAGCAU AGAGUGAAA	143	sch-miR7997c-8-5p	AUGUUGCUCGAACUCUUCAAAAAU	14-37	stu-miR7997c	2	0	24	24	1
			sch-miR5303-8-3p	UUUUUGAAGAGCUCGAGCAAC	107-127	sly-miR5303	1	0	21	21	1
sch-MIR11576	UCUUCUUCACGUUUUUUGGUAUAGUUUUGAACU GUGGUAAGAAACUGAAGCCGAGGCUGGAUUUUU UGGUAUAGUUUUGAACUGUGGUAAGAAACUGAA GCCAAGGCUGGAUUUUUUGGUAUAGUUUUGAAC UGUGGUAAGAAACUGAAGCCAAGGUUGGAUUUU UUGGCAUAGUUUUGAACUGUGGUAAGAAACUGA AGACGC	204	sch-miR11576-5p	UUUUGGUAUAGUUUUGAACUG	14-34	pab-miR11576	5	0	21	21	1
			sch-miR5656-3p	ACUGAAGCCAAGGUUGGAUUU	144-164	ath-miR5656	5	0	21	21	1
sch-MIR391i	GGUCUAUAGGAAACAAUCUCUCUACCUCCCAAG GUACACACUAUGCUUCCCAGACUCCACUUGUGA GAUUACACUGGGUUGUUGUGUUGGGGAGGAGG GGGUUGACCUAUAGGGG	115	sch-miR391i-3p	UCCACUUGUGAGAUUACACUG	56-76	pab-miR391i	5	0	21	21	1
sch-MIR2928	AGAAGAAGAUGGUAGUUUGUUGGUGAUUGUGGU UCCAAAAUUGAUGUUGAUUAUCCCUUUAUAUUAG UCUGGUAUUCUCUCGGUUUCAGUUUAUUUAUUC UACUUAUUUUUAUUAUCUGUUUUAAAUUUUUAUA UAUUUAAAUUCUGAACUCGCAUACACGUGACGUA CAAAAUGUAUAGACCCAACAUUACAAUCUUGGAA CCACAGUUACCACCAUACUAUCAAAUUUCUCAG	235	sch-miR2928-5p	AAGAAGAUGGUAGUUUGUUG	3-22	osa-miR2928	4	0	20	20	1
			sch-miR10539-3p	CUUGGAACCACAGUUACCACC	196-216	sly-miR10539	0	0	21	21	1
sch-MIR8030-2	UUCGUGUUGGUUUGGUCUCGGGUUGAUUUUUC UAGUUAAAACCAAAUCAACCCAAAUAUAGCCAGA CUUUGUUUUCCAAUAUCAAACCAAGUCAAACCAA ACCAC	105	sch-miR8030-2-5p	UCGUGUUGGUUUGGUCUCGGGUU	2-24	stu-miR8030-5p	2	0	23	23	1
			sch-miR8030-2-3p	UUAAAACCAAAUCAACCCAAAU	36-57	stu-miR8030-3p	0	0	22	22	1
sch-MIR7981a-14	AGAACUAUACUACGAUCUUAUUACCCCUGAACUU AUUCUAUAAGUAAUUUCAUGUCCCUUUUCGGCC UACGUGACACUAGCUUGAAAAAAAAAGUCAAUCAG CAUUCGACCAACAAGAUAGUGUUACGUAGGCCAA AAAGGAGUAGAAAAUUAUUAAUAAAAUAAGUUCA GUGGUAAUAGGACCUUAAUAUAGUAUA	196	sch-miR7981a-14-5p	GUCCCUUUUCGGCCUACGUGACAC	54-77	sly-miR7981a	3	0	24	24	3
			sch-miR7981-14-3p	AUAGGACCUUAAUAUAGUAUA	176-196	stu-miR7981-3p	5	0	21	24	1
sch-MIR8006-3	GAUAUUGGUGCACACGCCAUCCAAAAACUAGAAA GGGUAUAUACGCUCUAGUUUUUGGACGACAGGG GCACCAAUGUG	78	sch-miR8006-3-3p	UAGUUUUUGGACGACAGGGGCACC	49-72	stu-miR8006-5p	0	0	24	24	1
sch-MIR6191	GCACACUCAACGUUGACGUGGCACAUAAAUUUU GGAGGUGUCUAGAUGUGCAUACUCAAUGUUGGA GUGCUU	72	sch-miR6191-3p	UGGAGGUGUCUAGAUGUGCA	33-52	hvu-miR6191	5	0	20	20	1
sch-MIR168c-2	GUGGUCUCUCAUUCGCUUGGUGCAGGUCGGGA CCUACCUCGCCGGCAACGAUGGCGGUAGCUGAC GGCGACGGCAGCGUACCGGUAAAGAAAAUCUUA	157	sch-miR168c-2-5p	UCGCUUGGUGCAGGUCGGGAC	13-33	bra-miR168c-5p	0	0	21	21	1

	UUUUUACAUGUUGUUGCGUAGUUUGGGUCCCGC CUUGCAUCAACUGAAUAGGAGACUGC										
			sch-miR168-2-3p	UCCCGCCUUGCAUCAACUGAAU	126-147	lja-miR168-3p	0	0	22	22	1
sch-MIR8022-2	UGCGUAACCUCACUACUGAAUUUAACUCUCUGAA CUUCGUGACGGACCGUCAUAGAUACGACGGACC GUCACAAGCUGCAUAACUCCACCCUGGGUCGGA CUUCCGCUAAAAUUUAAAUGGGUGUUUUGGACU AUUCAUGAUUAUAAUUAUGAAAUUAGUGGGGUAA GUUUAAUAAUUUAUUUAGUUGGGGGUUAAAGAA GAUAAUAGGGAAAUAAAUAGUGGGUUACUUU	231	sch-miR8022-2-3p	UUUAAAUGGGUGUUUUGGACUAUU	113-136	stu-miR8022	3	0	24	24	1
sch-MIR11018-1	AAAUAAGAAAUAAAAAUACCAACUUCUGGAGGUC GCAAUCUCAAAAGUAAGAAGAAAAAAAAUACCGA UCUCUGGAGGUCGGUGUUCUAAAAUUUGAUAAU UAAAAUAUUCUGACCUCCGGAAGAUGAAAAUAAU AAAAAUAAUAAAUAAAUAAAUAUAUCAAAGUGACC UCCGGAAGCCGGAAAAUAAAAUAAUGAAUUUUAC CGACUUAAAUUAAAACGGACCUCUGGAGGUCAG UAAAUACCGACCUCUAGAGGUUAGAUUUUUUAU GUCUUAAGC	279	sch-miR11018-1-5p	GCAAUCUCAAAAGUAAGAAGAA	35-56	mdm-miR11018	5	0	22	22	2
			sch-miR1533-1-3p	AUAAUAAAAAUAAUAAAUA	131-149	gma-miR1533	2	0	19	19	1
sch-MIR163	CAACAGAGUUUUGUGAAUUCUAAUCCCCAUAGG GGUGCUACACCUAAAGUAGGAACACCUGAGUCC AAGAAGGGAAAUGGAGGUGAGAUGCAGCGUCCU AAGAAUAACUUUGCUAAGUGUGGCCGAGCUCAC AGUGGAGAGUGAAAAUAGGGCAGAAAUUCCUGC UUUGGUUGUGAUAAGAGUGGACAAAUGGUAAGA GAAUGUCCAUUAAACAGAGGUUAGGCUUCACAUA AUGCUCUGCCU	243	sch-miR163-5p	UGAGAUGCAGCGUCCUAAGA	84-103	aly-miR163-5p-1	5	0	20	20	2
			sch-miR156e-3p	UCACAGUGGAGAGUGAAAAU	129-148	vvi-miR156e	5	0	20	20	1
sch-MIR7981-7	CACAAGUACUUCCUACACUAUGAACGAUAUCCUA GAGACAUACCUUAACUAAACUAAGGUCCUAUUCC ACCCCCCCCCCCCCCCCCCCCAAAAAAAAAGGUUU GUUUGUAAUUUAAUACACCUUUUGGCUUACAUUA CACACUACACGACUACACACAAUUGAGAUGUGUU GGACAUGUUUGUAUGCCAUGUAAGUGGAAAAGG UGUACAAAACUAUAAAAAAAAAAUGGGAUCACGGG GUAUUAGGAUCUAAGUUAGUUAACACAUGUAUAU GGGGUUUCGAUCAUAAUCUAGGUAAUACUUAUA	304	sch-miR7981-7-5p	CUUAACUAAACUAAGGUCCUAUUC	44-67	stu-miR7981-5p	4	0	24	24	2
sch-MIR7492f-1	AGUAUCACUACAAUAAAAAUGAUCAUUAGCGGCA UUUAAUUCUUAAUUGCCGCUAAAUAUGUUUUUAG CGGCAAUUGUCACUCUUUGUAUGUGUCGCUAAA GCCUUUAGCGACAUUGUGUCUAAUGACACUUAA CUAAUGCCCGUAAAGACUUUAACACUCUUUAUUA GUGUCAAUGUUUAAUGCCGCUAAAAGUUAUUUU UGUUUCAGUGUAUCAA	217	sch-miR7492f-1-5p	AAAUGAUCAUUAGCGGCAUUU	17-37	gra-miR7492f	4	0	21	21	3
			sch-miR7983-1-3p	ACUAAUGCCCGUAAAGACUUUAAC	134-157	stu-miR7983-3p	1	0	24	24	1
sch-MIR156b-15	AAGGGGCGGUGACAGAAGAGAGUGAGCACACAU GGCGUUUUCUGGCAUGAUGUUUAUAUGGUUGCU UGAAACUAUGUGUGCUCACUGCUCUAUCUGUCA CCUCCCACA	108	sch-miR156b-15-5p	UGACAGAAGAGAGUGAGCACA	10-30	hvu-miR156b	0	0	21	21	1
			sch-miR156c-15-3p	GCUCACUGCUCUAUCUGUCACC	80-101	ata-miR156c-3p	0	0	22	22	1
sch-MIR7992-7	UAACUUUGACCUUCAACUUUCAUAAUGCACAAAC AGACACUUUAACUAUCCAACUUCUAAAUAAAUAA ACACAUGAGUCAUACAUGGCACAAUACAUGUAGG ACGCCACGUAGGACAAAAAAUGACAUGUAGGAUG ACAUUUAGGACGUGUGUGUCUAUUUGUUCAACU UUAUACAAGUUUAAUUGUCUAUUUGUGCACAUCC AAAGUUGAAGGACAUAGACG	223	sch-miR7992-7-5p	UUUCAUAAUGCACAAACAGACACU	18-41	stu-miR7992-5p	5	0	24	24	1
			sch-miR865-7-3p	UAUUUGUUCAACUUUAUACAA	157-177	ath-miR865-3p	5	0	21	21	1

sch-MIR12168	UCAUUAAGAUUAAGAGGUAUGAAUCUGAAUAUUA AGAUUUGCACUAAGAUUUGAGUGUUUUGAUCUG AAUAUUGAAAUGUGGCCUCUAAAUCUGAACAC	99	sch-miR12168-3p	UCUGAAUAUUGAAAUGUGGCCU	64-85	aof-miR12168	5	0	22	22	1
sch-MIR167b-5	GCAGCACUAGCAGUUGAAGCUGCCAGCAUGAUC UAAACUUUCCUUUUAGUUCAAAUAUAAUACGAGG AAAGAUCAGAUCAUGUGGCAGCCUCGCCUGUCA AUGCCAU	107	sch-miR167b-5-5p	UGAAGCUGCCAGCAUGAUCUAA	15-36	bna-miR167b	0	0	22	22	1
			sch-miR167c-5-3p	AUCAGAUCAUGUGGCAGCCUCGCC	72-95	eun-miR167c-3p	2	0	24	24	1
sch-MIR444b-1	AGAAUUUUGACUUUAAUGAAAUGUUGCAACAUUU AUGAAAAGUUGUGACAUUUAUGAAAAGUUGCAAU UUUAUGAAAAAUUGUGACUUUUAUGGAAGGUGG UGACCUUUCCGAAAGAUUGUGACCUUUCCGCUA AGGCACAAUAAG	146	sch-miR444b-1-3p	UUGUGACUUUUAUGGAAGGUG	80-100	ssp-miR444b-1	5	0	21	21	1
sch-MIR1127-2	AACUACUCCCUCCGUCCCAUUUUAUGUGGCUCC GUUACCUUUUUGGUCAGUCCCAAAAGAGUCACA UUUCCUUAUAUGGUAAAUAUUUAAAGGUACAAUU CCUCUUUUAUCCUUGUUGGUCCCACUUAAUUUU AAAAAUAGUAUACAUUUAUGAGGAGAGAAAAGUA AGUCUACUUUUGAAGGGUAAUUUGGUAAACAUU UCAAAGUCGGUCAUAUGUUGCCACGUAAAAUGG GACGGAGGGAGUAUAA	249	sch-miR1127-2-5p	AACUACUCCCUCCGUCCCAUU	1-21	bdi-miR1127	2	0	21	21	1
			sch-miR5049-2-3p	CACGUAAAAUGGGACGGAGGGAGU	222-245	bdi-miR5049-3p	5	0	24	24	1
sch-MIR5181c	UUAUACUCCCUCCGUCCCAAUUUAAGUGUCCUA GUUUAACUGUGCACUAAGUUUAUGAAAUGGGAG ACACUGACUCUUUUGGUCUUAAAUUAAAGAUGCA UGUGUGUAUCCCUUUGAUUUUCGGUCUUAGACC UGCCCAUGUAGAAUGUUGGAAUUGGAAAGAUUA CUAAAUAUAGAAAGAGACGCUCUUUUUGGGACA GAUCAAAAGGAAAAUAAGGCAACUUAAACUUGGG ACGGAGGGAGUACCA	248	sch-miR5181c-5p	CCUCCGUCCCAAUUUAAGUGU	9-29	bdi-miR5181c-5p	5	0	21	21	1
			sch-miR5049-3p	AACUUGGGACGGAGGGAGUAC	226-246	tae-miR5049-3p	4	0	21	21	1
sch-MIR837	UAAUACUUUAGAGUCUUGUACACGUGACAACCAG AUUUUUGGGAUGUUUUGAAUUGUUUCUGAAAUU UUUCACAUUUUAUUGUAAUGGUUGAGUUGUAGG UUGACUUGUCUUGGUGGGAUAAGACGAGCGUCA UCACAUCCAUUUUUGGGUCGUGACUACAUGGUA UCAGAGCCCAGGUUCAUAGGUCUCACGUGUGUA CAAACCGAGUCUAAAUAGAG	219	sch-miR837-5p	AAUUGUUUCUGAAAUUUUUCA	52-72	aly-miR837-5p	5	0	21	21	2
			sch-miR3436-3p	UCACAUCCAUUUUUGGGUCGUG	134-155	aly-miR3436-3p	5	0	22	22	3
sch-MIR7981d-6	GACUAUGAGCAAAAUCUCAGAGACACACCUAACU AAACUAAGGUCUUAUUACCCCCUCCCCCGAACU UUUUUUUUUUUGUAAUUUUAUACACCUUUUGUC UUACAUGGCACACUUCGUGACUCCAUGCAAUUG AGGCGCGUGGAGAUAUUUGAAUGCCACAUAAGC CAGAAAGAUUCACAAAAUUACAAAAUAAAAUAAAA UUCAUAGGGGUAAUAGAACCUUAGAAUAGUUAAA GUGUGUCUCUGGAAUUUCGAUCAUAUUA	264	sch-miR7981d-6-5p	GCAAAAUCUCAGAGACACACCUAA	9-32	sly-miR7981d	4	0	24	24	2
			sch-miR7981f-6-3p	AAGUGUGUCUCUGGAAUUUCGAUC	235-258	sly-miR7981f	2	0	24	24	1
sch-MIR7983-5	CAUCACUAUAACAAAAAUAACUUUUAGCAGCAUU AAAUAUAGACACUAAUAAAGAAUGUUAAAGUUUU UACCGGCAUUAGUUAAGUAUCAUUGGAACCAAUA UCGCUAAAGACUUUAGGAACAUAUACAAAGAGUG ACAACUGCCGCUAAAAAUACAUAUUUAGCGGCAA UUAAGAAUUAAAUGCCGCUAGUGAUCAUGUUUG UUGUAGUGCGU	214	sch-miR7983-5-5p	UAAAGUUUUUACCGGCAUUAGUUA	60-83	stu-miR7983-5p	5	0	24	24	1
			sch-miR833a-5-3p	UGUUUGUUGUAGUGCGU	198-214	ath-miR833a-5p	3	0	17	22	1
sch-MIR8026-1	GAGAAAAAUGGAAGUGUCAGUUGUAAAUUGGUU CUACUUCCUUGCACUAACUUUAUGUUACCACAAC CAUCAGAGAUGGAAUUAAUGUAGAGAAUAUGUG GUAACCCUAAUGGGUGGAGGAGGGACCAAUUUA	203	sch-miR8026-1-3p	AUGUAGAGAAUAUGUGGUAACCCU	85-108	stu-miR8026	0	0	24	24	1

	UAGAGGUUAUGACUUAAUCUGGUCGUCCAAGAA GUAACCAAUGUACGACUGAGAUCUAUUCGUUAU UAAA										
sch-MIR1127b-1	CAGGACAAGUAUGGUUGGACAACUAAUUUUAGU GUAGUGGACAAGUAAAGGUGGAUGGAGGAAGUA CUUCCUCCGUCCACUUUUAUUUGUUCACUAUAC UAAAAUUAGAUAUCCACUUUUACUUGGUCAUC	131	sch-miR1127b-1-5p	ACAAGUAAAGGUGGAUGGAGG	41-61	tae-miR1127b-3p	5	0	21	21	1
			sch-miR1127-1-3p	AAGUACUUCCUCCGUCCACUU	62-82	bdi-miR1127	5	0	21	21	1
sch-MIR5205b	GACUUAUAAUAUGGGACGGAGGGAGUAAUUAAU AGUUUCUCUGCCUAAUACUCCCUCCAUUACAUAA UAACUU	73	sch-miR5205b-5p	CUUAUAAUAUGGGACGGAGGGAGU	3-26	mtr-miR5205b	2	0	24	24	1
			sch-miR5174e-3p	UACUCCCUCCAUUACAUAAUA	49-69	bdi-miR5174e-5p-2	5	0	21	21	1
sch-MIR168c-3	GCGGCCGCCUCUUAUUCGCUUGGUGCAGGUCG GGACCUCAUUCGCCGGCGCCGGAGAUAAUGGCG GACGAACGACGGCGGUGUUAAUUCUACUAAAGC UGUCACCGACGAAUAUAUGUUUGAUUAGCGGCG AAAUUUGGGUCCUGCCUUGCAUCAACUGAAUUG GAGACGGCUGU	175	sch-miR168c-3-5p	UCGCUUGGUGCAGGUCGGGAC	16-36	bra-miR168c-5p	0	0	21	21	1
			sch-miR168a-3-3p	CCUGCCUUGCAUCAACUGAAU	142-162	sly-miR168a-3p	0	0	21	21	1
sch-MIR390-2	CGAGCAUGAAAAAGCCAUAAAACUCAGGAUGGAU AGCGCUAUAGAUAGCCAUUAAGAUGUAUUCAUG GUGCUAUCCCUCCUGAGCUUUAUAGAUUCCCCA UGCCAU	106	sch-miR390-2-5p	UAAAACUCAGGAUGGAUAGCG	18-38	atr-miR390-1	2	0	21	21	1
			sch-miR390a-2-3p	UGCUAUCCCUCCUGAGCUUUA	69-89	sly-miR390a-3p	3	0	21	21	2
sch-MIR838	AGUAUUUAUAUGUAUAACUAUUUUACUGUAUGAA CAUGGAUUGUGGUGCACUGUUGAGAGUGUUUCA CCCUUAACCAGAUAUCUCAGAUUCGAGCUCUGG GCAUAGAGAAAUUCUGUAGGGAGCGUCACUCCG AAUAGACCCUACAGAGAGCUAUUCAAAUUAAGUC GAAGCUCCAAUAUGAGCUUCGAACACCAGGUGG GAGACCAAAAGAAAAAACUAUUCUACUGGAUACA AAUUUGACAAUCACACAAACCUUAGUCUCUUUUU AUUCAUGUUCUUCUUGUACCAUAUAUAUAUAUAU AUAUAUA	309	sch-miR838-3p	UAUUCAUGUUCUUCUUGUACC	268-288	aly-miR838-3p	5	0	21	21	1
sch-MIR1122	UGAAAAUCGAUCGGAUAAUUUAUUUAAAAGGGG GUUGAUUUAUGGGUCGGAUUAGGUGUUUAUGAG UUCGAAUAUCUUUCCAUUUUCAUAUAAAUGUCAU GUGGUAAGGUCAAAAUGACAUGACAAUUUCCAU GUGACAUUUAAAGAAAUAAACAAUGAGUUGGAUA UGUCCAACAUGACAACUAACGCAUAUAAAUGCAU AUUUGGACCAGAAAUUGGAAGGAGAUGACAUGA GUGAACCAAACUUUAAAAAAAUGAUAUAUCUAAA CCUUUUCAAAUAAUUUAGAGACGUAUUUGAG	299	sch-miR1122-3p	CAUAUAAAUGCAUAUUUGGA	189-208	bdi-miR1122	5	0	20	20	2
sch-MIR8026-2	AGGAAAUUGGUUUCUACCUCCUUGCCCUAACUU UAUGUUACCACAACCGUCACCGAUGGAAUUAAUG UAGAGAAUAUGUGGUAACCCUAAUGGGUGGAGG GAGGACCAAUUUAUA	115	sch-miR8026-2-3p	AUGUAGAGAAUAUGUGGUAACCCU	65-88	stu-miR8026	0	0	24	24	1
sch-MIR394c	AGAUUAAUUAGUUUCAUGGAGGUUUGACAAAGG GUUUCUUACAGAGUUCAUUGGCAUUCUGUCCAC CUCCCUCGUUCUUUUUUCGAGAAAAAAGAAGAAG GGGGGAAGCAAGAUUAGUGUGUGGAGGUGGGC AUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUU GUAAAACCCUCGUGAUACACGUCAAGUAAGAU	197	sch-miR394c-5p	UUGGCAUUCUGUCCACCUCCCU	51-72	mes-miR394c	1	0	22	22	1
			sch-miR394b-3p	AGGUGGGCAUACUGCCAAUAG	125-145	ath-miR394b-3p	0	0	21	21	1
sch-MIR8039-1	AUUGGUCAAAAACACACCUAGGAUAUACCCAUUU UUUGAGUUUCAUAUAGGAAAUAUCAUCAUCGUUC AGGUAGGAAAGGUAAACAAUUGAUAGUUGAGGU GUGUUUUGAUGAAUAACGGUGAUAGUUUAGGUA GGAAAUUCGCACACAUGAUAGUUUAGGUUUGAA ACUCGAAAAACCGGAGUACUUUAGGUGUGUUUU UGACCCUU	208	sch-miR8039-1-5p	UUUCAUAUAGGAAAUAUCAUC	41-61	stu-miR8039	5	0	21	21	1

			sch-miR8045-1-3p	AUUGAUAGUUGAGGUGUGUUU	87-107	stu-miR8045	0	0	21	21	1
sch-MIR399f-3	AACUAUGUAUGGAUGCAUUACUGGGCUAAUCUU CUUUGGCAAAUAGCCACAUUUUCACUAUAUUAUU UAGUGCAAGUUUGUUCAUUUUUUGCCAAAGAAG AUUUGCCCCGUAAAUCACCCAUACAAUAUAU	131	sch-miR399f-3-5p	GGGCUAAUCUUCUUUGGCAAA	23-43	csi-miR399f-5p	4	0	21	21	1
			sch-miR399r-3-3p	UGCCAAAGAAGAUUUGCCCCG	90-110	mtr-miR399r	0	0	21	21	1
sch-MIR11011a	GAGUAGAUAAGCUAAAAAGUGUUAAUAAGCCAAU UUGACCAGCUUAUAAGCUUAGUCAAACACCCUCU AAGCUUAUAAGCUGGUCAAACUAGCUUAUAAGCA AUUUUUUGGCUUAUCUAGGC	122	sch-miR11011a-3p	AAGCUUAGUCAAACACCCUCU	48-68	mdm-miR11011a	5	0	21	21	1
sch-MIR395b-1	GUAUAAUUCUAUUAAGGUGUUCCCUAGUGUUCC CUUGACCACUUCAUGAGGGCUUACUUUGAUGUU AGAAGCCUUGCUGAAGUGUUUGGGGGAACUCCU GGGUUGACUUUCAAAAUUACGC	121	sch-miR395b-1-3p	CUGAAGUGUUUGGGGGAACUCC	77-98	sly-miR395b	0	0	22	22	1
sch-MIR399b-1	UUUGAAUUUAUAAGCGAAACACUGAUAGGGCUAC UCUCUAUUGGCAUGCAGUUGUGUAGUUUAACUG ACACGCCGAAGGAGUGCUGCCCUGUUACAGUCU CUUAUUAAUAUUCUAACAAAAAGAAAGAAGAGUA GGUGGAUGAUAAUAAGGGGAACAGUGGUAGGAC UACUGAUCUCUAUUUGUAUGCAACUAUAUAUUUA AGCAGACAUGCCAAAGGAGAGUUGCCCUGGUAC UGUCUCUGCUUACUGUAAUUCUGA	258	sch-miR399b-1-5p	GGGCUACUCUCUAUUGGCAUG	28-48	sly-miR399b	0	0	21	21	1
			sch-miR399a-1-3p	UGCCAAAGGAGAGUUGCCCUG	210-230	aof-miR399a	0	0	21	21	1
sch-MIR399b-2	AACAAUGAUAGGGCUACUCUCUAUUGGCAUGUA GUUGUGUAGUUUAGCUGACACACCAAAGGAGUG CUGCCCUGUUACCGUUUCUUAUUAAUAUCCUAA CAAAAAGAAAGAAGAGUAGGUGGAUUAUAAUAAG GGGAACAGUGGUAGGACUACUGAUCUCUAUUGG UAUGCAAUUAUAUAUUUAAGCUGAUAUGCCAAAG GAGAGUUGCCCUGAUACUUUCUC	223	sch-miR399b-2-5p	GGGCUACUCUCUAUUGGCAUG	11-31	sly-miR399b	0	0	21	21	1
			sch-miR399a-2-3p	UGCCAAAGGAGAGUUGCCCUG	193-213	aof-miR399a	0	0	21	21	1
sch-MIR7501	AAUACAGAUGAUGACGUUACUGCGGAGGGAAGG UUCAAUCUAUGCUAUUGACGGAAAAUUUCCCGAU AAGAUAUCGGAUUCCGACAAGAAGAAGAUUGAAG GAGUUGCAUUGAGUGUAAUUCAACUGUCCCUUG CACCUAACGUACUCUGUGAA	154	sch-miR7501-3p	AUAUCGGAUUCCGACAAGAAGAAG	71-94	ghr-miR7501	5	0	24	24	1
sch-MIR782	ACUUUCAAACAUCUUGGACGUUCUUGGACGUUU GACCUCUAAAUGUUAGGAAACUUAGCAUACAGAC UAAGAACAUCAUUAUAACUUAUAUAAGGACCUCA UAAGCUCAUGAAAAACACAUAAGCACAUAAAAUC ACAUAAGGCCCCUUAGGUGACUAGUCGUCAAAC GUCUUGGUUGUCCUUGACGUUUGAAUUC	196	sch-miR782-5p	UCAAACAUCUUGGACGUUCUU	5-25	ath-miR782	3	0	21	21	2
sch-MIR5368	CUAACCUUGUGUCAGGACCUACGGGCCAAGGGA CAGUCUCAGGUAGACAGUUUCUAUGGGGCGUAG GCCUCCCAAAAGGUAAC	83	sch-miR5368-3p	GGACAGUCUCAGGUAGACA	31-49	gma-miR5368	0	0	19	19	1
sch-MIR158a-1	UGAAAUCACAAAUCGAGUCAAACCAAAAAAAAUU GACUAGUGGUUUGGUUUGACUUGAUUUGGUGUU GAA	70	sch-miR158a-1-5p	UCACAAAUCGAGUCAAACCA	6-25	aly-miR158a-3p	5	0	20	20	1
sch-MIR2111d-3	AAUACUGUGUUAGGUUAAUGGUAAUCUGCAUCC UGAGGUUUAGAUCAAUUUCUAAUUUACUGGAUC UAGUCCUUGGGAUGCAGAUUAUCUUUACCUUAC AAACAGUGUA	109	sch-miR2111d-3-5p	UAAUCUGCAUCCUGAGGUUUA	22-42	ppe-miR2111d	0	0	21	21	1
			sch-miR2111d-3-3p	GUCCUUGGGAUGCAGAUUAUC	69-89	gma-miR2111d	2	0	21	21	1
sch-MIR10538-2	UUUAAAAGCUGACGGCGUUAGAUUGAUAUACGU UACUCACAGUAACGUUUUAGGAGUAAAACCUUAC UUACAUUAACGUUUUAGGAGUAAAACCUUACUUA CAUUAACGUUUUAGGAGUAAAAACGUUACUCAAA AUAACGUUUUAGGAGUAAAACAUUACUUACAGUA ACGUAUAUCAACCUAAUGCUGUUAGUUUUUAAA	202	sch-miR10538-2-5p	AGAUUGAUAUACGUUACUCACAGU	20-43	sly-miR10538	0	0	24	24	1
sch-MIR10538-3	UUAAAAAACUAACAGCAUUAGGUUGAUAUACGUU ACUAUAAGUAACGUUUUACUCCUAAAACGUUAUU	169	sch-miR10538-3-5p	AGGUUGAUAUACGUUACUAUAAGU	20-43	sly-miR10538	4	0	24	24	1

	UUCAGUAACGUUUACUCCUAAAACGUUACUCACA GUAACGUUUUAGGAGUAAAACGUUACUGUGAGU AACGUAUAUCAAUCUGACGCUAUCAAUUUUUAAA										
			sch-miR12108-3-3p	UGACGCUAUCAAUUUUUAAA	150-169	csi-miR12108-5p	5	0	20	24	2
sch-MIR6024-5	CACUAAAUCUAUGUUGAUAAUUCUUUUCCUAUUA UCUACCUCCUUGGUCCGGCAAGUAGCAUUAAGG CGAUUUCUAACGUUGGCCAUCCAUUAAAAAGACU UCUAUGCGAAAUAAGCUUAGAAGUUUUGGCCGG AGUUGUUUAUACGCAUGCUUGGAACACAAACCAA GGUGGAGAUUGAAAGAGUUGGUUUUGGUUCUUG UGGAAUCAAACUAAAUGGAAGAUGAAUUAAUAUG AAUAUUUGGUAGGAAGAUAAUUAGUACAAAAUAC AAGUCAAAGAUUGUAUCU	287	sch-miR6024-5-5p	UUUUGGCCGGAGUUGUUUAUAC	125-146	nta-miR6024	5	0	22	22	1
			sch-miR9736-5-3p	UGGAACACAAACCAAGGUGGA	154-174	gma-miR9736	4	0	21	21	1
sch-MIR10542-1	UAGAAGAAUCAUAUAUACCCCUAAUUAAUUUUAA AAAAAAAUUAAAAGUAAAAAAUAUAAAUUUAAAAC AAAUUUUUUAACUUCCGUUAAAUGAAGGGUAUAU GUGAGCUCAUUUUGUAACGGCAGGGGUAUAUGU GAGCCGUUUGUAUAAUGGUAAGGGCAUAUAUGA GCCACUUUCAUAACGAGGGGUAUAUCAGCUCCA AAUGACAAAGUUGAGGGGUAUAUCAGACUCUUU UC	237	sch-miR10542-1-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
sch-MIR169l	AACAACAGCAGCUGUUUCAUAAAAAAUCUGGCAU GAGAAAAUGAGGCAGAUAUGUAGCCAAAAAUGAC UUGCCAGACAUGAAGCAGAAUUGAUCGAGCUUG CCGGCAAGUCAUCCUUGGCUGCAAUUCAAUAAC CUUAUUCCCUCAUGCAAGACUUUAACAUGAAUAA AGACAUGUCUAUUCAA	184	sch-miR169l-5p	UAGCCAAAAAUGACUUGCCAGA	55-76	cme-miR169l	2	0	22	22	1
			sch-miR169s-3p	CGGCAAGUCAUCCUUGGCUGC	103-123	gma-miR169s-3p	2	0	21	21	1
sch-MIR8138-1	ACAGCUAGGAAAAUAUUGGUGCAUUCCAUUAGUA AAGAAGUUUACAAAGGAAAUGCCUCAGGACCAAC CAAGGUAAAUAGUUCUAUUUAGAAGUCUUUACCU UGGUUGGUCAUGAUGCAUUCCCUAGUAAACUUU CUUACAAAUUGAGAGCACCAAUAUUUUACUUGCC CA	171	sch-miR8138-1-5p	UAAAGAAGUUUACAAAGGAAAU	33-54	cpa-miR8138	5	0	22	22	1
sch-MIR8138-2	UGAGCUAGGAAAAUAUUGGUGCAUUCCAUUAGU AAAGAAGUUUACAAAGGAAAUGCCUCAGGACCAA CCAAGGUAAAUAGUUCUAUUUAGAAGUCUUUACC UUGGUUGGUCAUGAUGCAUUCCCUAGUAAACUU UCUUACAAAUUGAGAGCACCAAUAUUUUACUUGC CCA	171	sch-miR8138-2-5p	UAAAGAAGUUUACAAAGGAAAU	33-54	cpa-miR8138	5	0	22	22	1
sch-MIR5012	UUUUUGCUUGUUUUUACUUGUGAGUUCCUUUUU ACUGCUACAUGAGCUGAUGAAGUAGUUGUUCUG UUGCUGAUCAUACCGCACAUUCCAUCGUCAAAUU UAAAUGGUAGCAGUAGAAAGGAACUCACAAGUAA AAACACGGAAUCA	147	sch-miR5012-5p	UUUUACUGCUACAUGAGCUGA	30-50	ath-miR5012	5	0	21	21	1
sch-MIR8610	UUGAUUGACGGUCAUAGACUACGGACUGUAGGU CCGUCCAUCGAUCAGGACUUAACCAAAUUUUCCU GGGCUGAUAUUUGGGGUUUCUGACCCCAUUGAC GGAUGUCCAGGACGGACUGUGGGUCAGGCUACA AUCCGUCAAUAGC	146	sch-miR8610-3p	UUCUGACCCCAUUGACGGAUG	85-105	atr-miR8610-2	4	0	21	21	1
sch-MIR773b	UAUAUCAUUCAAUCAAGGAUAUGUAGCCGAUCCG GGCGGAAGACAUUGUCAGGUGGGGAGUUUGGC UGGGGCGGCACAUUCCUUGAUCGAGAUCAUUUC	99	sch-miR773b-5p	UAUCAUUCAAUCAAGGAUAUG	3-23	aly-miR773b-3p	5	0	21	21	2
sch-MIR169e-3	UUGCAUGAAAGAGGAGAGCAUGUCAAGGUAGCC AAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAU UAAACACAUUUUAAACUAUGGAGCAGGCAAGUCA UCCUUGGCUACUAAACAAUAAUAUAACUCUCCUC UUCAUGUUU	144	sch-miR169e-3-5p	UAGCCAAGGAGACUGCCUGAA	29-49	zma-miR169e	3	0	21	21	1
			sch-miR169f-3-3p	GGCAAGUCAUCCUUGGCUACU	93-113	zma-miR169f-3p	2	0	21	21	1
sch-MIR8001b-4	AUUUGUGAAUUAUAUGGGGAUUAGUAUGAAAAU UCGCAGGAAACUUAUUUUCCUGCAAAUUUUCAUA	92	sch-miR8001b-4-5p	AUGGGGAUUAGUAUGAAAAUUCGC	14-37	stu-miR8001b-5p	1	0	24	24	1

	CUGAUUCCCAGGAAAAUCCUCAUGU										
			sch-miR8001b-4-3p	AAAUUUUCAUACUGAUUCCCAGGA	57-80	stu-miR8001b-3p	5	0	24	24	3
sch-MIR1886i-1	CCCAUGUGAUACCAUAUCACGAUAUGAUAUCAUG AGAUGAAAUCAGCGUUUGGACAUGUCAUUUUAC GCUGAUUCCGUCUCAUAAUUUCAUAUCAUGAGA UGUGAUACCAUAUUCU	116	sch-miR1886i-1-5p	AUGAGAUGAAAUCAGCGUUUGGAC	32-55	stu-miR1886i-5p	2	0	24	24	1
			sch-miR1886h-1-3p	AUUUUACGCUGAUUCCGUCUCAUA	61-84	stu-miR1886h	4	0	24	24	1
sch-MIR7984b-2	CGAUAACGAAUCUUGGAAAUGAUCUUUUAUCCUC UACACUAUUUGAUAUUGUAUUUUAAGAGUAUAUA CAUGUUCACGUGGACAUCAUAAAUAUUGCAUCAU UAGAAAUAGUAACGUAUCCACGUGGGCACAUAUA UACCUUUAAAAUACACUAUUAAAUAGUGCGGUUA AAAGGUCUUCCGUAAAAUUUGCUAGCA	197	sch-miR7984b-2-5p	AUAACGAAUCUUGGAAAUGAUCUU	3-26	stu-miR7984b-5p	4	0	24	24	1
			sch-miR7984b-2-3p	GGUCUUCCGUAAAAUUUGCUAGCA	174-197	stu-miR7984b-3p	5	0	24	24	1
sch-MIR6288c-2	ACUGAAAAGAAGUGAUUAGACAAGACAUGACACA ACUCUAGCUGACUAAGGAAACAACCUUAGAUAGA AUAUUAUGGAGAACACAUAUGGGUAGAUAGAUAA UUAGUUAGGUAGUUGUGAGUUAUUUUGCUUUAA UCUGUAAUAAUACUUAUAGUUUAUCUUUGAGGG UCUUGUUAUUAUUUAUUUAGUUAGGUAGUGUGU UUGUCAUACUUGUUUAGCAUUUUUGUCUUG	231	sch-miR6288c-2-3p	CUUGUUAUUAUUUAUUUAGUU	170-190	ppe-miR6288c-5p	4	0	21	21	1
sch-MIR171b-1	ACUAGUAAAUGAAUUGGUAAAAAGAAAUGAUAUU GGCGCGGCUCAAUCUGAGAUCGUUCUUUACUGA AAUAAAACGUAAACUCGUCUUCAGAUUGAACCUC ACCAACAUCGCUUCUCUAAUUCAAUAUGUACUCA C	136	sch-miR171b-1-5p	GAUAUUGGCGCGGCUCAAUC	29-48	zma-miR171b-5p	1	0	20	20	1
			sch-miR171-1-3p	AGAUUGAACCUCACCAACAUC	90-110	cca-miR171	4	0	21	21	2
sch-MIR10531	CGUAGUACCGAGGGUUGUUAAGAGUCUAUUUUU UCAUUAGUUCAUUCUGAUAUUUGGGGUCCUAGU AGAGUCAGUUCUACUUUAGGAUUUCGUUAUUUU GUUAGUUUCAUUGAUGAUUAUUCGAGAUGCACU UGGGUUUUCUUAAUGAAAGAUUGUUUAGAGUUA CUUUCUAUUUUCAAAAGUUCCUUUGCUGAAAUUC AAAAUCAGUUUGGUGUUUCCAUUCAUACUUUCA GUAGUGAUCAACAAAAAGGUGUAGCUGAAAGAAA GAAUAAGCAUCUCAUAAAGACUGCUGGCACUCUC	300	sch-miR10531-5p	UGGGGUCCUAGUAGAGUCAGUUC	55-77	sly-miR10531	1	0	23	23	1
			sch-miR5244-3p	CAUCUCAUAAAGACUGCUGGC	274-294	mtr-miR5244	5	0	21	21	2
sch-MIR482a-2	GUUUAGCAGAUCUGAAAUUGGAGAUGAGUUUUU CGAAAAUCUAUGGGAAUUGGUGAGUUGGAAAGC UUUUCUUUUUCUUCUCUUGUGAUUAGCUUUCCA AUUCCACCCAUUCCUAUGGUUUUUUGGUAUUCU CUCCCUUUUCGAAUGCUAUAG	153	sch-miR482a-2-5p	GGAAUUGGUGAGUUGGAAAGC	46-66	stu-miR482a-5p	2	0	21	21	1
			sch-miR482c-2-3p	UUUCCAAUUCCACCCAUUCCUA	94-115	nta-miR482c	0	0	22	22	1
sch-MIR7997c-9	CUUUUCAUACGUUAUGUUGCUCGGACUCACUAA AAUUGUUGUCUCACCCAACUCUAAUCCUCCAACC UGCACAAACUGUUGGAGGAUCGGACAUGAGCAC AUGAACACUUUUGAAGAGUCCGAGCAACAGAAAA CGUGUAGAAUAU	146	sch-miR7997c-9-5p	AUGUUGCUCGGACUCACUAAAAUU	14-37	stu-miR7997c	5	0	24	24	1
			sch-miR5303h-9-3p	AACACUUUUGAAGAGUCCGAGCAA	104-127	stu-miR5303h	2	0	24	24	1
sch-MIR9736	UAACACCUAACCCGACCCAUUAAAAAAUAUGAUG ACCCAUAUUAUUUUGUCUUUAAUCCUAAAUUAAU CCCUCACUUUAAACCUUGAAUUAGGAUUAAAGAC AAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGG AUCGGGUUAGGUGGGU	152	sch-miR9736-3p	UUAAAGACAAAAUAAAAUGGG	95-115	gma-miR9736	5	0	21	21	1
sch-MIR7502c-1	UCAGAAUUAUUGAAAUGUUUUAUCUACAAACAUU AUAGUUGUUGUUAAAAGUUUCUUCCAUUCAGGA UAUCUCUUACCCUCUUGGAAUGAAACUUUUAUUA CUUUAACCCUUAAGUCUUUAAAUACCGGCCACGU	206	sch-miR7502c-1-5p	UUGUUAAAAGUUUCUUCCAUU	42-62	gra-miR7502c	1	0	21	21	1

	CCACGAUGUAGCUCGGGGCAUGACAAUAUUAAA CUUGUAUGUAGGUGGCAAGAUACAUUGCAUAAU UCAAC										
sch-MIR6439a	UAUCUUCACAAUAUGGAGCUUCGAGUGAAGAACA AGAAGCCACUCGCUUGUUCUUCUCAUAAUGCUC CAGAUAUUUGAAGCCU	83	sch-miR6439a-5p	UCGAGUGAAGAACAAGAAGCC	21-41	ptc-miR6439a	5	0	21	21	2
			sch-miR10211a-3p	CUCCAGAUAUUUGAAGCCU	65-83	eun-miR10211a-3p	5	0	19	21	2
sch-MIR7997c-10	GGACUUAAGAGUCUAUUUUGCUCGGAUUCUUAA AAAAAAUGAUGUUGCUCCCAGUCGAGUCCUCCAA UGGAGGAUCCGACAUGUACCCUAUUUACAUUUU UUAAGAGUUCGAGCAACAUAGCUUAAGGUU	130	sch-miR7997c-10-5p	AUUUUGCUCGGAUUCUUAAAAAAA	15-38	stu-miR7997c	4	0	24	24	1
			sch-miR5303-10-3p	UUUUUUAAGAGUUCGAGCAAC	97-117	sly-miR5303	1	0	21	21	1
sch-MIR6108e	UUUAAGAAUAGAUCUUCUUCCUUGGAUCUUCAAA GCUCUUAAAUGGAGGUUUUGAAGAGAGUGAAUU UUGAGAGAAGAGAGCUUUUCGUUUUC	93	sch-miR6108e-5p	UUAAGAAUAGAUCUUCUUCCUUGG	2-25	cca-miR6108e-5p	5	0	24	24	2
			sch-miR10200-3p	AGGUUUUGAAGAGAGUGAAUU	47-67	gma-miR10200	5	0	21	21	1
sch-MIR7831	AUACAUAUACAGACGCUCAAACAUGGCCUCAACU CUCACCUGGCAACUAAAGACUCCAACUUGUCCCC ACUAUGUCUCGUUUGAUACCCUGCACUGGUGUA GCUCUUAAAUUAUGUAGGUGCCUAGAUGAUCAU UUUGUAAGUUGGAGUGUUCAACGGACACGGUGG AGACGAGUUGCAGUGUCAAGAUGGAGUGCUUAC UUGCUAGCUAAGGGAAUGUUUGAGUGUCUGUUU AUGUAU	239	sch-miR7831-5p	UACAUAUACAGACGCUCAAAC	2-22	ptc-miR7831	5	0	21	21	1
			sch-miR2604-3p	CAUUUUGUAAGUUGGAGUGUU	132-152	mtr-miR2604	5	0	21	21	2
sch-MIR7535-1	UCUUUUGUUGAUAUUGUAUUAAAAUGUUAAAGG UUAGAUUGGUUGGUUCGCUCACAUAGGAGGGUA AAUGUGGGUGCCAGUCGCGGCCCCGAUUUGGG UCGUGACAGAUUUGCAUUAAGAUUCAGGUGUUU UGAUCUGAAUACAAUUCUGAAUAUUAAGAUGUGG UCUCUAAAUUUGAAUACUAAAUAACUAAUAU	196	sch-miR7535-1-5p	GGGUAAAUGUGGGUGCCAG	62-80	lja-miR7535	5	0	19	19	1
sch-MIR7997c-11	UAUGUUGCUGGAGCUCUUCAAAAAUGUCAUCGG GUGCGUGUUGAAUCCUUCAAAAGUAGAGCAAUU UUGGAGGAUCCAACACGGGUGCGGCAACAUUUU GGAGUGUCCGAGCAACUCA	118	sch-miR7997c-11-5p	AUGUUGCUGGAGCUCUUCAAAAAU	2-25	stu-miR7997c	4	0	24	24	1
			sch-miR5303c-11-3p	ACGGGUGCGGCAACAUUUUGG	81-101	nta-miR5303c	1	0	21	21	1
sch-MIR11108e	UGCAAAAAUCGAACCGACCGAUAAAUCGAACAAU AAAAAUGUGAUUGGCUUAUUGUUAUUGGAUUUU UAAUGGGUUUAUAAAAAAAAUUGGGGUUAUUGG UUCGGUAUCGAUUUUUACU	119	sch-miR11108e-5p	AAAUGUGAUUGGCUUAUUGUU	37-57	lja-miR11108e-3p	5	0	21	21	2
sch-MIR397b-2	UCCUUCAGAGAAUUAAAAACAUGAUCGAGUGUAG CGUUGAUGAAAAAUGAGGAAGGCCCAAAUGCAG GAAUUCUCAAAUAUGUCAUCAACGCUGCACUCAA UGAUGUUUAUAAGUACUCUGCAAUAA	127	sch-miR397b-2-5p	AUCGAGUGUAGCGUUGAUGAA	24-44	bdi-miR397b-5p	2	0	21	21	1
			sch-miR397b-2-3p	UCAACGCUGCACUCAAUGAUG	86-106	eun-miR397b-3p	0	0	21	21	1
sch-MIR156g-1	GUGUCAAUAACAGCUGUGAAGGAAUAUCUGGGC CCAAAGAUGUAUUGACAUAGCUUUCUCUUUUUU UGUGUCAAUACAUCUUUGGGCCCAGACAUAUUC CUUCAUAGCUGUCAUGAUUA	119	sch-miR156g-1-3p	GCUUUCUCUUUUUUUGUGUCA	53-73	aly-miR156g-3p	5	0	21	21	1
sch-MIR1128-5	AAUUACUCCCUCCGUCCCAAAUUUAAGUGUUUUA GUUCGAUUGGACACAAAGUUUUUGAAUCUUGUG GUCUUCAAUUAAAGAUGUGUGUAGUCCUUUAAA UCUUGUGGUCUCAAACUUUCCAUGUAUAAUGUU GGAAUUGGAGAACUUACUAAAUAUAGAAAGAGGC AGUCUUGCUGGGACAGACUAAAUUGGGAAGACA CUUAAAUUGGGAUGGAGGGAGUAGUA	226	sch-miR1128-5-5p	AAUUACUCCCUCCGUCCCAAA	1-21	ssp-miR1128	2	0	21	21	2
			sch-miR5049c-5-3p	AGACACUUAAAUUGGGAUGGAGG	196-218	hvu-miR5049c	4	0	23	23	1
sch-MIR10538-4	ACAGCAUUAGGUUGAUAUACGUUACUGUAAGUAA CGUUUUACUCUUAAAACGUUAUUUUCAGUAACAU	148	sch-miR10538-4-5p	AGGUUGAUAUACGUUACUGUAAGU	9-32	sly-miR10538	4	0	24	24	1

	UUUACUCCUAAAACGUUACUCAUGGUAACGUUUU AGGAGUAAAACGUUACUGUGAGUAACGUAUAUCA AUCUGACGCAAU										
sch-MIR10419-1	UUGAUUUAGCACAACAUUUUGAGCUUGCAUUUG AAAGAUAUAGUUUUUAUGGUAUUGGAUACUUGAA UCAUCUUCGUACCUUUAGUUUUUAUUCUUCUAAA AACAAAGAUGGAACUAGUGUUGAAUAUGGAACUA GUGUUGAAGAUGAAUUUAGUGUUGAAGAUGGAA CUGCUGCAAAUAUUCUUUCAAGUGUUGACUGGA AAAAUGUGUGUUCAAUGGU	220	sch-miR10419-1-3p	CUAAAAACAAAGAUGGAACUA	97-117	gma-miR10419	5	0	21	21	1
sch-MIR11108a	AUGACUUUGUUCUUUAUCAGUGGCUAAAAGAUC CAUGAGAUGUCCAAGAAGGGACUUUGAGUGUUA AAAUACUAUGGUAGUUCCACACUACCUUGGAGU UUUACUUAUUCAACUUUCCAUCUUAUCGAGGCAU UCAAUCGAUUAGUGACUUCUAAAAAAAUAAAGGA AUGUAGUGGGAUGGUAAGUAUUGUACUCAACCU UAAUCAAAUAUUUGGGGUUCGAAUGAUGGAUUG GAGUUAAUGAAUUACCCCUCAAAGUUGAUAAAUC UAUAUUAAUCUAAUGUUAAAGAAAUAGUUAA	298	sch-miR11108a-5p	GUGGCUAAAAGAUCCAUGAGA	20-40	lja-miR11108a-5p	5	0	21	21	2
sch-MIR5026-2	UUGGGCCUACGUGACACUAACUUGGAAAAAAAAA GUCAAUCAACGUUGGGCUCACAAGAUAGUGUCA CGUAGGCCGAA	78	sch-miR5026-2-3p	GCUCACAAGAUAGUGUCACGU	50-70	ath-miR5026	4	0	21	21	2
sch-MIR1043-3	UUUAUGUCCUUCAACUUAAGGUAUGCACAAGUA GACACUUAAAUUUUAAUAAACUUGAACAAGUAGA CACAUGAGUCAUACAUGACAUGAUACACGUAGGA CAAAAAUGACAUGUAGGAUGUCAUGUAGGACAU GUGUGUCUAUUUAUUCAACUUUAUACAAGUUAAA GUGUCUACUAGUGCACACCCAAAAUUAAAAGAUA UAAA	206	sch-miR1043-3-5p	CCUUCAACUUAAGGUAUGCA	8-27	ppt-miR1043-5p	4	0	20	20	1
			sch-miR2612-3-3p	UUAAAGUGUCUACUAGUGCAC	164-184	mtr-miR2612	5	0	21	21	1
sch-MIR8006-4	UAUUUUUGGGAUAUUGGUAAUCAUGCCAUCUAA AAACUUAGAGUGUAUAUCUACCCCUUUAUACUAG CAGAUCUACCCGACCCAAUAUUUAUUAAAUAUCG GAUCGAUGAAUGAGAAUGUGAUACGUUUCCCUA UUUAGUCUUUCGUUAGAGUGAAGGGCAUAUAUA CUCUAGUUUUUGGAUGGCAGGUGCACCAGUGUC CCAAAAGUA	209	sch-miR8006-4-3p	UAGUUUUUGGAUGGCAGGUGCACC	171-194	stu-miR8006-5p	3	0	24	24	1
sch-MIR5265	UUUUUCUAAAUAUGUGCUAAUACAUAAUGUCUUU GAAAUGUUUCCGUGGAGAAUGUAAUCUUGGAAU GUUUUGCUUUGGUGUCAAACAACACCAAAGCUAA AUGUUCCAAGUCCACAUUUCCACCGAAACAUUUC AAAGACAUCAUGUAUUAGCACAUAAUUAGAAGAG	169	sch-miR5265-5p	AUGUAAUCUUGGAAUGUUUU	53-72	mtr-miR5265	5	0	20	20	1
			sch-miR5826-3p	UAGCACAUAAUUAGAAGAG	151-169	osa-miR5826	4	0	19	24	1
sch-MIR10211b	CAAAACCGAAAUCACAAAGCAAUUUCCAGAUUUC GGUUAAGACAAGAAAAAGACAACCUAGUAACUAA CCUAAGAUUGUCCAAAGGGUUCGUUAUGGUCCG AAUAACUUAGGGAUACUUUAGUAAUUAACCUAGG AUAGUUUAUUAAUUAAUUAAUCAGAUUAAUUAAU UAAUUUAAAAGGGCAAAACCAAAAUCACAAAGCA GUUUUCAGAUUUCGGUUAAG	223	sch-miR10211b-5p	CAAUUUCCAGAUUUCGGUUAA	20-40	eun-miR10211b-5p	5	0	21	21	1
sch-MIR7997c-12	GGAGGAGGUCAACAGCCCGUUGAAACCUAUGUU GCUCAGACGUUUCAAAAAUGUUGACAUACUUGUA UCGGAACCUCAAGAAGUAGUGCAUUUUCAACAC GAAUGUGACAACAGUUUUGAAGAGUCCGAGCAA CAUAGAUCACCAGUGUUGAAUCCAAU	159	sch-miR7997c-12-5p	AUGUUGCUCAGACGUUUCAAAAAU	29-52	stu-miR7997c	4	0	24	24	1
			sch-miR5303h-12-3p	AACAGUUUUGAAGAGUCCGAGCAA	110-133	stu-miR5303h	2	0	24	24	1
sch-MIR2275c	UAGUGUAGUUAGUCAUUGGGAAGAAAAGAUAAG ACAAGAUGUCCCUCAUUGGUAGAAUAUAAUAUAU CUAACCAGAUAUAUUAAAUUUGAUUUCUCCAAAU UUCUCUUCAGUAUUUUAUUUCAAGUAGUAUUAGA AGUGCGUAAAAACGCUUCUUUCCUUCGGUAUUC UACUAAUGAGGAACAACUUGUCUUGUAUUCUCU UUUGAAUCACUAAAUACAUUC	222	sch-miR2275c-5p	UUUGAUUUCUCCAAAUUUCUCU	86-107	aof-miR2275c	5	0	22	22	1

			sch-miR11118-3p	UUCGGUAUUCUACUAAUGAGG	159-179	lja-miR11118-3p	4	0	21	21	1
sch-MIR10419-2	UUUGUAUGCACAAGUAGGCACUUAAACUUGUAUA AGUUGAACAACUAGGCACAUGAGUCAUAUAUGAC ACAAUACACAUAUGACACCAUGUAGGAUAAAAAA UGACAUGUAGGAUGUUAUGUAGGACAUGUGUGU CUACUUGUUCAACUUUAUAUAAAUUUAAGCGUCC ACUUCUGCACACCCA	184	sch-miR10419-2-5p	CACAAUACACAUAUGACACCA	68-88	gma-miR10419	5	0	21	21	1
			sch-miR5014a-2-3p	UUAUAUAAAUUUAAGCGUCCA	150-170	ath-miR5014a-3p	5	0	21	21	1
sch-MIR7822-2	UAUUAUGACUUUUAAUUUUAGGUGUGCACAAGU AGACACUUAAACUUGUAUAAAAUUGAACAAAUAG ACACAUUUGUCCUACAUGACACCCUACAUGGAAC UUUUGUGUCCUAUGUUAUUAUGUCAUGUAGAAC AUGAGUGUGUACUUAUUCAAUUUUAUACAAAUUU AAGGGUCUAAUUGUGCAUACUCAAAGUUGAAAGA CAUAGUU	209	sch-miR7822-2-5p	UAUAAAAUUGAACAAAUAGAC	49-69	ptc-miR7822	5	0	21	21	1
			sch-miR5014a-2-3p	UUAUACAAAUUUAAGGGUCUA	157-177	ath-miR5014a-3p	5	0	21	21	1
sch-MIR7980b-1	GGUAUCUUGAGAUGGAAUCAGUGUUUGGACAUG CGAUUUUACGCUGAUUCCAUUUCAUUAGAUGUA	66	sch-miR7980b-1-5p	GAGAUGGAAUCAGUGUUUGGACAU	9-32	stu-miR7980b-3p	0	0	24	24	1
			sch-miR1886h-1-3p	AUUUUACGCUGAUUCCAUUUCAUU	36-59	stu-miR1886h	4	0	24	24	1
sch-MIR8005c	ACCAAAACUAGUCUUCCCCUUUCAUGAAAAGUUG UGACAUUUAUGAAAAGUUGUUACUUUGUAAAAAC UUGAGGCUUUUAUGAAAAGUUCUGACUUUUAUA AAAAGUUGCGACCUUUAGGAAGAGUUACAACUUU UAUGAAGAGUUGCGACUUUUAUGAAAAGUUGAG AGUUUAAGGUUUUCGC	184	sch-miR8005c-3p	UUGAGAGUUUAAGGUUUUCGC	164-184	stu-miR8005c	5	0	21	24	1
sch-MIR159a-1	GGAGUGGAGCUCCUUGAAGUCCAACAGAAGAUC UAACAGGUUAGAUUGAGCUGCUGACCUAUGGAU UCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUA UAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAG CUUUAUUUUACCCUUUGUUUGAUCAUUUUUUGG AUUGAAGGGAGCUCUACAUU	186	sch-miR159a-1-5p	GAGCUCCUUGAAGUCCAACAG	7-27	fve-miR159a-5p	1	0	21	21	1
			sch-miR159-1-3p	UUUGGAUUGAAGGGAGCUCUA	162-182	aof-miR159	0	0	21	21	1
sch-MIR319d	AGCAGAGGAGAGAAGGAAACUGUUUAGUCCAAC CCAAGGUGGGUUAUUGGAACUGACCUUUGCUGC UGAAUCAUUGGCUCAUGAGCAUGUCAAAGAAGA UGAUUUAACAUUCUGGACAUGUUCUUGCUCCAA UGAUGCAGGAGCUGAGCUCGGUUUUCCACCGCC UUUUCUUGGACUGAAGGGUUCCCUUCCCUUCUC UUUA	202	sch-miR319d-5p	AGGAAACUGUUUAGUCCAACC	14-34	sly-miR319d	0	0	21	21	1
			sch-miR319-3p	UUGGACUGAAGGGUUCCCUUC	171-191	stu-miR319-3p	0	0	21	21	1
sch-MIR5142-1	GACCAUAUGAUGAUGGUCUAUACUUGUCUUAUU GAUGUAUGAAGUGCAUAUUAAGGCUUGUAGUCU CUUUUUAGAUUUACAUAGUAUGUGUGAGAUUAU GGGACUUCAGAUGUACAUUGUACUAGCAAGCUU AUGCUAGGAUUUUAAGUAGGGUUCUAUGAUGUU UUAUUAUGUGAAUUCCAAGUAUGUGUUGUUUAC UAUUGCCUAGAAUGAUGUUGUUGAUAGUGUUGA CUUACAUGAUGGCUUGAAUUAAAUCAUAUAUGAU AUUUAUGCAUUAUAUUGAUUUGUAUGUGAAGUU UGUACUAUCAUGAUAUGCUA	318	sch-miR5142-1-3p	AUAUUGAUUUGUAUGUGAA	277-295	rgl-miR5142	4	0	19	19	1
sch-MIR7992-8	AUCGAUAGACACCUUAAAUUGGCCUUCACGAGCA AGUAAAGACCCAAACUAAAACGGGGCCAACUUAA ACCAAGUUCAUGUGUCUAGAUGUGCAUUCUCAA AGUGUAGGUCUUUACAUGUCAGUUAAGUCCAAG UUAAGGUGUCUAUCUAC	151	sch-miR7992-8-3p	UGUCUAGAUGUGCAUUCUCAAAG	81-103	stu-miR7992-3p	5	0	23	23	1
sch-MIR169c-4	GGUAGAAGAGAGGUGUUUCAUGAAGGGAAAGUG CCUGCUCUGAUAGCCAAGGAUGACUUGCCUAAA ACCAUUUUUAUAAAGGGUCUUAACUAAUUAAACU UUAGUUACUAAAAUUAAAGUUUAAAUUAUAUGAU CCUAAAAUUGGGAUUUUAGGCGUUGUCUGAAGC	212	sch-miR169c-4-5p	UAGCCAAGGAUGACUUGCCUA	44-64	ata-miR169c-5p	0	0	21	21	1

	UAAUCUGAGAGGCACUUAUCUUUCAUGUAACACC UUCAUUCUCUU										
			sch-miR169f-4-3p	UAGGCGUUGUCUGAAGCUAAU	151-171	sly-miR169f	2	0	21	21	1
sch-MIR5051-2	AUGACAUAAAUUGAUUAAAUAAUUAAUAAUAAAG AAAAAUAAUGACACAUGGCACCUUUAAAAUGGUA CAUGGCAGUAAAAAUACUGCAUGGCGCGCCUCA UAUUCGUGUUAACAACCCAGACUUGAGAAUGGA UCAAAAUGGUCCAUUUACAAAUAAAUUAACUAGU UCUGUGGGGUGAUAGGACACUUUAAAAGUUAAG GUGUCUUUAUACAAAUACGGGACAACUUUGAUG GUGUUUUUUUAUGUCUUUUCUCUUAUUAUAAUG AAUAUAAAUUGGAUGUUUA	286	sch-miR5051-2-5p	CAUGGCACCUUUAAAAUGGUA	48-68	hvu-miR5051	5	0	21	21	3
			sch-miR8045-2-3p	UUUAAAAGUUAAGGUGUCUUU	189-209	stu-miR8045	5	0	21	21	2
sch-MIR9471a-3	CGAGUUGGUUUCUCAGAUGGUCACUCGACUAAU AGUUGUAUUAUCUUAGAAAGUCACUUUUUUGGU UGAAGAAAAGCGGAAUCAAGAAGAGAAGUGACUU UUUUUUUUAUAUAAUGACUAAAUCGAGUGAACAU CUGAGCAAUCAACACU	150	sch-miR9471a-3-5p	CAGAUGGUCACUCGACUAAUA	14-34	sly-miR9471a-5p	4	0	21	21	1
			sch-miR171e-3-3p	UGACUAAAUCGAGUGAACAUC	115-135	aqc-miR171e	5	0	21	21	1
sch-MIR5556	UGUCUUGAAUACCUACGAUUAGACCGGGUUCAC ACGGAUUGAUGUGCAUAGAACCAGACCUCGGAA CCCUUGCGACAUCCAAGCCAACUAACUUGGGGA GUUAGUUGAGCUAGGAAUGGUUGGGUCCUUUCA UGAAGUGUUCCUGAAUACUAGGAUUCACCCGGA UGAGUCUUAACCUGACUUAGAGGGUUAGUCCUA GGUUUUAAGUGU	210	sch-miR5556-5p	CGGAACCCUUGCGACAUCCAA	62-82	mtr-miR5556-5p	5	0	21	21	2
			sch-miR6256-3p	UUAGUCCUAGGUUUUAAGUGU	190-210	osa-miR6256	5	0	21	22	2
sch-MIR397	GAAUGAGUACCUCAAGCCACGUCUUUGAGUUUC AUCAAGUCUACACUCCGUUAAACCUUGAAGCAGG GGGCGUUUGUAGACAUUGAAAUUUUGUGGGACU UUACAAGAUGUGUUCAAUGCGAGUUGGGACCUA CAAAUUGUAUUCAACUCACAUAAAGAUUCUUGGA GGCUACUCAACC	179	sch-miR397-5p	CAUCAAGUCUACACUCCGUUA	33-53	stu-miR397-3p	5	0	21	21	1
sch-MIR5214	CAUCAACUCUAUGAACAAUUAUAAGGACCUUUUA CCCCCUUACACUAUUUAAUAGUGUAUUUUAAAGG UAUAUAUAUGUCCACGUGGAUAUAAUUUUUUUUU GUAUAAUUAUAAACAGUAAUGUGUCCACGUGGG CACACAUAUACCUUUAAAAUACUCUAUUAAAUAG CUCUAGAUAAAAGGCCCUCCAGAAAGUUAAGUGU UGUAA	208	sch-miR5214-5p	CAACUCUAUGAACAAUUAUAA	4-24	mtr-miR5214-5p	5	0	21	21	2
sch-MIR10538-5	UUUUUAAAAGUUGAUGGCGUCAGAUUGAUAUAC GUUACUCACAGUAACGUUUUAGGAGUAAAACGU UACUCAUAGUAACGUUUUAGGAGUAAAACGUUAC UGAAAAUAACGUUUUAGGAGUAAAACGUUAUUUA CAGUAACGUAUAUCAACCUACUGCUGUUAGUUU UUAAAAA	174	sch-miR10538-5-5p	AGAUUGAUAUACGUUACUCACAGU	22-45	sly-miR10538	0	0	24	24	1
sch-MIR7699-2	UGUACAUGUAUCAUAAUUUUAUCCAUCGAUUCGA CAUUUAUUAAUUAUUGGGUCGAUGAAUAAGAUU GUAUCACGUGUCCC	81	sch-miR7699-2-5p	AUUUUAUCCAUCGAUUCGACA	16-36	mtr-miR7699-5p	5	0	21	21	1
sch-MIR7981d-8	CCCUAGACUAUAAUCGAAAUCUCAGAGACGUACA UUACCUAAACUAAGCUCCUAUUAUCCCUGAACUU AUUUUUUUUGGUAAUUCACGCGGCUCAAUUGCG UGGAGUCACGGAGUGUGCCACGUAGGACAAAGG GUGCACAAUUUUUUUAAAAAAAAAUAAGUUCAGG GUAAUAUGACCUUAGUUUAGUUAAGGUCUGUCU CUGAAAUUUCGGUCACAGCCUAAAC	226	sch-miR7981d-8-5p	UCGAAAUCUCAGAGACGUACAUUA	14-37	sly-miR7981d	5	0	24	24	1
			sch-miR7981-8-3p	AUAUGACCUUAGUUUAGUUAAGGU	172-195	stu-miR7981-3p	2	0	24	24	1
sch-MIR9562-1	AAAAAUUCAUAUUUGUAUGUUAUAGCAAACUUUG CAUACUUGCGCUCCAUAGUAAAUAUAUAACUGUA UAAUUCGCUAUAUAUAUAUAACUGUAUAAUUCGC UGGCCUAAAUUGUAUAAUUCGUUGGCCUCGCUA	314	sch-miR9562-1-5p	AUAUAUAUAACUGUAUAAUUC	80-100	bra-miR9562-3p	5	0	21	21	2

	UGCAUAUACAAUUGUAUGAUUCGCUGCCUAAAUU GUAUAAUUUGUUGGCCUAUUUCGCUGCAAUUGU AUAAUUCGCUGGCUUAUUUCACUGCAAUUGUAU AAUACGCAAUCGUAUAAUUCGUUGGCCUAUUUU GCUGCAAUAUGUGUAUAAAAUUUGUUUUGCAUA CAAUUGAAUUGAA										
			sch-miR11309-1-3p	UUUGUUUUGCAUACAAUUGAA	289-309	fve-miR11309	5	0	21	21	1
sch-MIR10521	UGCCAAAAAAAAAAUGUAUACUACUAAUGCCAAC CCUAAUAAGCCUCUUCCUUUUAGGGGUGGGCAU UCGGUAAUUCGGUUCGGUUUCGUUUUUUUUCCG AUUUUUUCGGUUUUCGAUUCUUGUACAAUGUGU ACCGAACACCGAAUUGAAAUAAUUCGGUUCGGU UCGUUUUGUUAUUUCGGUUUUUUUUAAUGGGCC UGCUUAGUUGGGCUUUUAAAAAUUUACAAUUUU UGUUUUUGUUU	243	sch-miR10521-5p	UUCGUUUUUUUUCCGAUUU	86-104	tae-miR10521	5	0	19	19	1
			sch-miR2614-3p	CGGUUCGGUUCGUUUUGUUA	158-177	mtr-miR2614	5	0	20	20	1
sch-MIR7983-6	AUGUUCCUAAAGUCUUUAGCGACAUUGGUUCUA AUGGCACUUAACUAAUGUCGGUAAAGACUUUAG CAAUCU	72	sch-miR7983-6-5p	UAAAGUCUUUAGCGACAUUGGUUC	8-31	stu-miR7983-5p	0	0	24	24	1
			sch-miR7983-6-3p	ACUAAUGUCGGUAAAGACUUUAGC	44-67	stu-miR7983-3p	2	0	24	24	1
sch-MIR5658-1	UCCACAAUCAUCAUUCUUCACACAUAUUACACUG UCAAGUUGAGCACUGCAUUCCUUGGCCAUGACU UGGUGAUUUUGGGCCAUUUUGGGGUUGAGGAC UACAAUAAUAAUAAUUUAAAAAAAUUAUUAGUACU AAAAUUAGUCUAAUUUAAGUAAGUAAAUAAAUUU AUGUUCGUUAAUUAUAGUGGAGAUAGUUUGUUG UAGUGGAGGCGGCGAUGGUUGAUGAUGGUAUG UAACUAGUAACGAUGAAUGUGAUUGGUGUUGUA GUGACUGGUGUGAUGAUGAUGGUGAUUGUAAU	298	sch-miR5658-1-3p	GUGAUGAUGAUGGUGAUUGUA	276-296	ath-miR5658	5	0	21	21	2
sch-MIR396e	AGAUAUACCUCAUUACCACUGUAAGAUGUGUUAG UUUGAUUCCAAUCUCUUUCUUCAACUAGCACAUC UUGAGGAGUAGGACGAGGAUAAUA	92	sch-miR396e-3p	UUCCAAUCUCUUUCUUCAACU	40-60	fve-miR396e	5	0	21	21	1
sch-MIR399b-3	UUAUAAGAGAAACAGUGGUAGGGCUACUCUCUA UUGGCAUGCACUUAUAUAUUUAAACUGACAUGCC AAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUA AUG	103	sch-miR399b-3-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			sch-miR399n-3-3p	UGCCAAAGGAGAGCUGCCCUG	64-84	gma-miR399n	0	0	21	21	1
sch-MIR7981b-8	AUUUUAACUAAAUUAAGGUUUUAUUACCUUCUAA CUUUUUUUUUAUAAUUUUGUGCACCUUUUUGGC UUACGUGACAUCCAAAUAUCUCCCACGCAUCUCA AUUGCGUGGAGUCACAGAAUGUGCCACGUAAAA CAAAAGGUGCACAAAAUUACAAAAAAAAAAAAUAA GUUCAGGGGAUAAUAGGACCUUAGUUUAGUUAA UAU	205	sch-miR7981b-8-5p	GCACCUUUUUGGCUUACGUGACAU	55-78	sly-miR7981b	5	0	24	24	2
			sch-miR7981-8-3p	AUAGGACCUUAGUUUAGUUAAUAU	182-205	stu-miR7981-3p	3	0	24	24	1
sch-MIR8001a	CAACUUCUAUAUCUCACCUUUAUUGCACCAACAC UACAAGAAAACUGUGAAUUAUAUGGGGAUUUUCC UAUGGAUUGAUAUGAAAAUUCGUAGAAACUUAUU UUCCUGCAAUUUGGAAAAUACCCAUGUAAUUCAC AGUUUUCUUGUAGUGCGUCAAAACAUCAGUGUA GAAGCAU	176	sch-miR8001a-3p	UCCUAUGGAUUGAUAUGAAAAUUC	66-89	stu-miR8001a	4	0	24	24	1
sch-MIR444b-2	UUAUCAUGAAAAGUUUGGACUUUUAUGAAGAGUA ACAACAUUUAUUUAAGGUUCUGACUUUUACGCAA AGUUGUGACUUUCAUGCAAAGUUGUGACUUUUA UGAAAAGUUGUGACUUUUAUGAAGAGUUGCGAC UUUAAUGAAGAGUUGCGACUUUUGUGAAAAGUU GCGACUUUAGAGUAGAGUUGCAACUUUUAUGAA AGGUUGUGACUUUUAUGAAUG	221	sch-miR444b-2-5p	UUGUGACUUUCAUGCAAAGUU	71-91	ssp-miR444b-1	5	0	21	21	1
sch-MIR7984b-3	UACUGUUACGAUAUCAAAUUUUGAAAAUGACCUU UUACCCCCUGCAUUAUUCAUUAUGUAUUUAAAAG GUAUACAUGUGUUCAUGUGGACAGAAAAAAUAUU	215	sch-miR7984b-3-5p	AUAUCAAAUUUUGAAAAUGACCUU	11-34	stu-miR7984b-5p	4	0	24	24	1

	CCAUAAUUAUAAUAGUAAUGUGUCCACGUGGGC ACAUACAUACCUUUAAAAUAUACUAUUAAAUAGU UCGGGGGUGAAGGAGGUCCUUCAUAAAGUUUGA UAUCGUAACAACA		sch-miR7984c-3-3p	CCUUCAUAAAGUUUGAUAUCGUAA	187-210	stu-miR7984c-3p	1	0	24	24	1
sch-MIR10538-6	UUUUAAAAACUAACAGCAUUAGGUUGAUAUACGU UACUGUAAGUAACGUUUUACUCCUAAAACGUUAU UUUCAGUAACGUUUUACUCCUAAAACGUUACUAU GAGUAACGUUUUAGUAGUAAAACGUUACUGUGA GUAACGUAUAUCAAUCUGACGCCAUCAACUUUUA CUC	172	sch-miR10538-6-5p	AGGUUGAUAUACGUUACUGUAAGU	21-44	sly-miR10538	4	0	24	24	1
sch-MIR6145c	UGCAUAAUUGUACUCUAUAGUAAACAUAUAACUG UAUAAUUCGCUAUACAUAUACAAUUGUAUAAUUC GCUGGCCUCGCUAUACAUAUACAAUUGUAUGAU UCGCUGGCCUAAAUUGUAUAAUUCGCUGGCUUA UUUCGCUGCAAUUGUAUAAUUCGCUGGCCUAUA UCACUGCAAUUGUAUUAAUGCGCAAUCGUAUUAU UCGCUACCUAUUUCGCUGCAAUAUUUGUAUAAAA UUUGUUUUGUAUACAAUUGAAUUGAAGUAAAAUG UUUGUAUAUUGUAUAAUUAUAAG	292	sch-miR6145c-5p	UAGUAAACAUAUAACUGUAU	18-37	nta-miR6145c	5	0	20	20	2
sch-MIR3951a	UCAAACUUUUUCUGUUACGUUUAUCUUUUUUUG GAUCCAUGCAAAAGUUCACACUGUCAACUCAAGU UCUGAAACUGUUGGUGUCAGAAGUUUGUGUUGA AAUUGUGAACUUUUGCAUGGAUCCAAAAAAAGAU AAGCGUAACAGAAAAAGUUAAA	156	sch-miR3951a-5p	UUUCUGUUACGUUUAUCUUU	9-28	csi-miR3951a-3p	5	0	20	20	1
sch-MIR399b-4	UUAUAAGGGAAACAGUAGUAGGGCUACUCUCUA UUGGCAUGCAGUGAUAUAUUUAAACUGACAUGC CAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUU AGUG	103	sch-miR399b-4-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			sch-miR399n-4-3p	UGCCAAAGGAGAGCUGCCCUG	64-84	gma-miR399n	0	0	21	21	1
sch-MIR7997c-13	UAAAAGCUAUAUUGCUCGGACUCUUCAAAAAUAU UGAUGGUUGCAUGUUGGAUCCUCCAAAAAUACA UAGAUCCGACACAAGUGCGACAACAUUUUUGGAA AGUUCAAGCAACAUGCUUAAA	122	sch-miR7997c-13-5p	AUAUUGCUCGGACUCUUCAAAAAU	9-32	stu-miR7997c	0	0	24	24	1
			sch-miR5303-13-3p	UUUUUGGAAAGUUCAAGCAAC	93-113	sly-miR5303	3	0	21	21	1
sch-MIR1521b	CUGAACUAUCGUGAAUGGUAUAUAUACAAAUACC CUCCGUCGUACUUUUGGGAUAUUGAUGCUCCUA UCGUCAAAAAAGUAGAACACAUACGCCCUUUAUA CUAACUGACAUACACGUGUCAUAAUUUUAUCCAU CGAUCAAACAUUUAUUGACAGAAAAGAUUGCGCA ACGUAUCCCUUUUUAUUUUUUUUCAGGGUGAAG AGCAUAUAUACUCUAGUUUUUGAACGGUAGAUG CUUCAAUAUCGCAAAAAUAUGACGGAGAAUAUUU ACAUGCCAUUUACAAUAGUUAAA	292	sch-miR1521b-5p	GACAUACACGUGUCAUAAUUUUA	108-130	gma-miR1521b	5	0	23	23	1
			sch-miR156e-3p	UUGACAGAAAAGAUUGCGCAA	150-170	fve-miR156e	4	0	21	21	1
sch-MIR4248c	CCCCCCUCUGAACAUAUUUUUUUUGGCCAUUUU GUGCACCUUUUUGGCUGAUGUGGCAUCCAAAUA UCUCCCACGCGUCUCAAUUGCGUGGAUUCAUGG AAUAUGCCAUGUAAGACAAAAGAUGUAUAAAAUU ACAAAAAAAAAAAGAAGUUCAGGGGUGU	161	sch-miR4248c-5p	ACAUAUUUUUUUUGGCCAUUU	12-32	aly-miR4248c	5	0	21	21	1
sch-MIR8001b-5	AAUCACUACAAGAAAAGGGUAAAUUACAUGGGGA UUAGUAUGAAAAUUUUGCAGGGAUUACCCUGUA GUUCACACUUUCUUGUAAUGAAA	91	sch-miR8001b-5-3p	AUGGGGAUUAGUAUGAAAAUUUUG	28-51	stu-miR8001b-5p	2	0	24	24	1
sch-MIR1432	UCGUGAAGUCAGUCUGCCCCGUCCACUCUCCUA AAUCGAUGGGGACUUUAGGAGCGAAGACAUGGA CGGUAGUGGGAGUGGCGUUGACUGUCUUCAAUU	99	sch-miR1432-3p	UUAGGAGCGAAGACAUGGACG	48-68	ata-miR1432-5p	5	0	21	21	1
sch-MIR1309	GAUGGUGUAUAUUUCUACUUAUUUAAUAUCCUAU UUGAAGGACAUGAGUAUCAGUUAAUGACAAAUCA UCACUACGUUUAAUACAUAAACGUGCUUCUUAAC UUAAUAUUCAUAUCCUAUCUGGCAUCCUACGUGA CCAUUCUAUGUCAUGGAGACAUAUUAUGUCACG UAGGACGAUGUAUAUUUCUACUUAUUUAAUAUCC	292	sch-miR1309-5p	UAAUAUCCUAUUUGAAGGACA	24-44	pta-miR1309	5	0	21	21	1

	UAUUUGAAGGACAUGAAUAUCAGUUGAUGACAAA UCGUGUAUUCGUAGGAGGAACAAGAGGAUAUUG UAAAGAGAAGAUCAUCACCAAA										
			sch-miR1518-3p	GAUAUUGUAAAGAGAAGAUCA	264-284	gma-miR1518	5	0	21	21	3
sch-MIR171f-6	UCUGAUAUUGGCCUGGUUCACUCAGACACAUAU UAUUUUGAUUUGAUUGAACCGUGUCAAUAUCUC A	67	sch-miR171f-6-5p	UAUUGGCCUGGUUCACUCAGA	6-26	csi-miR171f-5p	0	0	21	21	1
			sch-miR171c-6-3p	UGAUUGAACCGUGUCAAUAUC	44-64	stu-miR171c-3p	1	0	21	21	1
sch-MIR9555b-1	GCUACUCCUUUUAUUUUAGAUUAUUAGUUUGCU AUUAUAUACAAUUAUCCCUUUAAAAUUAGAGCCG UCAAUAUGGGCUAGGCCUGUUGUGCUGGUCUGG CCUAACCGAGAUUUAAUAGGGUUGGACUAUGAU UUUUGGAGCCCAUUUGAGAAAAGAGUUGUUUAG CUCGACCUGAAUAAGCCUGCUGAUUUGUGGGGC UUGAUAAAUAUCGGUAGAGCUGACCCGUGGGCC AGUAAAAAUUAAUUAAAAAAUAUAAUAUAAAAUUA AAAUUUAAAAUUAAUGAGAGUCCA	291	sch-miR9555b-1-5p	UUAUUAGUUUGCUAUUAUAUA	21-41	bra-miR9555b-3p	5	0	21	21	1
sch-MIR7997c-14	AGUCUAUGUUGCAUGGACUCUUCAAAAGUGUUA CUUAGUGCAUGUCAUAUCCUCCAAAAGUAUCUGA UAUAGGUGCAACAACAUUUUUGAAGAGUCUGAG CAACAUAGUUU	111	sch-miR7997c-14-5p	AUGUUGCAUGGACUCUUCAAAAGU	6-29	stu-miR7997c	4	0	24	24	1
			sch-miR5303h-14-3p	AACAUUUUUGAAGAGUCUGAGCAA	80-103	stu-miR5303h	0	0	24	24	1
sch-MIR5640	GCAUUCAUAGUUAAAAGAAAAAAUUAAAUUCAAC UGCGAGUUCUAUGACUGCAACCAUCACUGAGAU AACUAUUAUUUUGAAAUUGAAACAAAAAAUAGUU AUCUCACAAAGUGAUGGUUGCAGUCAUAUGCAU GCAUUAUAAGGUGCUAUCACAAAGUGAUGGUUG CAGUCAUUUGACAGAAGCAACUUUACAACAAACU UCUGGUUUGUAAAUUCAAAAG	222	sch-miR5640-5p	UAAAAGAAAAAAUUAAAUUCA	12-32	ath-miR5640	5	0	21	21	1
			sch-miR11082l-3p	UCACAAAGUGAUGGUUGCAGU	105-125	lja-miR11082l-3p	5	0	21	21	1
sch-MIR1525	UGUUUUAAUUAUGUUUCUAGGCUUAAACUGACU AAAAUAUGAUGAUUUAGGGUCAAAAUGACGUAAC UUUGGGUUUAAACGGAGUGGGAAAGGUCAAAAA GACACCUGGAAAGGUUGCUGUCGGGUCUUACGA CGGUCAGGACUGACGGUCCGUCGUGCGCCCGAC GCCCCAUCUUUGGGUCCGUCGUGAGGGCUUGU UCGACAGAGCUUUACUAAAAUUAGAGUAACUUUU UGCUCGUAGGUCUGAUUUAUCAAGGUUGGUGCC AUGGAAAGAUAAUUCAAUUA	285	sch-miR1525-5p	UGUUUUAAUUAUGUUUCUAGG	1-21	gma-miR1525	5	0	21	21	1
			sch-miR444c-3p	UGAUUUAUCAAGGUUGGUGCC	245-265	osa-miR444c-1	5	0	21	21	1
sch-MIR159b-2	AGGAAGACCAGAGUUUUGAAGGUAGAGCUCUUC UGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGA GCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUA UUCUCAAAUAAUUUUAGAUAGGUUUGUGGUUUG CAUAUAUCAGGAGCUGUAUUUACUCUUCUAGGA UCCUUAUUGGAAAGAAGGGAGCUCUACACUUGA UAACCUGGUUUUUUU	214	sch-miR159b-2-5p	AGCUGCUAAUCUAUGGAUCCC	67-87	cas-miR159b-5p	1	0	21	21	1
			sch-miR159b-2-3p	UUGGAAAGAAGGGAGCUCUAC	173-193	sly-miR159b	0	0	21	21	1
sch-MIR156b-16	UGGAAGAGUGGGACUGACAGAAGAGAGUGAGCA UACACAUAUAAUUAUAUAAACAUGUUUACAUAAU UCUUUUGAUAUAUAUAUAUAUAAUUUUGCGUGU GCUCACUUUUCUUUCUGUCAAUCUCUCUUGAA	132	sch-miR156b-16-5p	UGACAGAAGAGAGUGAGCAUA	15-35	cca-miR156b	0	0	21	21	1
			sch-miR156f-16-3p	CUCACUUUUCUUUCUGUCAAUC	102-123	stu-miR156f-3p	1	0	22	22	1
sch-MIR10532-2	UAAGUUCAGGGGGUUAAUAGGACCUUAAUAUAG UAUAAGUGUGUCUCUGAGAUUUUGGGCAUAGGU UGAGGGGGUACUUAUGCAUUAUCCCAUAAAAAA GGUAUUUACAUUAGAACUCGACAAGAUGUGUAAA AGUAAAGUGUAUGUCAUUUAAAGAGAAAAUAAUC AAAUGCACCCUUAAUCUAUUACCAUAUUAUCGAU	245	sch-miR10532-2-5p	AAGUGUGUCUCUGAGAUUUUGGGC	37-60	sly-miR10532	1	0	24	24	1

	UACACACUUAUACUUUAGAAAAACCUAUUACCUC UCUGGACUAU										
			sch-miR8039-2-3p	UUACCUCUCUGGACUAU	229-245	stu-miR8039	3	0	17	21	1
sch-MIR7981-8	UAUGUUCAAAAUUUCAGAGACACACAUUAACUAA ACUAAGGUUCUAUUAUUCUUGAACUUAUUCUUUU UGUAAUUUUGUUUACCUUUUUUGCUUACGUGAC AUUCAAAUAUCUCCUACUCGCCUCUAUUGCGUG GAGUCCCGGAGUGUGCCACGUAAGACAAAAGAU GCACAAAUUACAAAAAAAAAUUAAAAAAAUUCAAA GAAUAAUAGGACUUUAAUUUAGUUAAAGUGUGUC UCUGAAAUUUUAACGAC	253	sch-miR7981-8-5p	AUUAACUAAACUAAGGUUCUAUUA	26-49	stu-miR7981-5p	4	0	24	24	2
			sch-miR7981-8-3p	AUAGGACUUUAAUUUAGUUAAAGU	208-231	stu-miR7981-3p	2	0	24	24	1
sch-MIR7981d-9	AUUAUGACCGAAAUCUCAGAGACAUACCUUAACU AAACUAAUGUUCUAUUACCCCUCAAUUCUAUGAA UCCACGCAAUUGAGGCGCGUGUGAAGUAUUUGG AUGUCACGUAAGCCAAAAAAGUGUAAAAAUUACA AAAAAUAAAUAAAUUAAGUUCAGGGAUAAUAGGA CCCUAGUUUAGUUAAGACGUGUCUCUGAAAUUU CAGUCAUAGU	212	sch-miR7981d-9-5p	CCGAAAUCUCAGAGACAUACCUUA	8-31	sly-miR7981d	5	0	24	24	2
			sch-miR7981-9-3p	AUAGGACCCUAGUUUAGUUAAGAC	164-187	stu-miR7981-3p	4	0	24	24	1
sch-MIR7997c-15	AAUAUUGCUAUGUUGCUUGGACUCUUCAAAAAU GUCUUGGAUACUCCAAAAGUAGUGCAUUUUUGG AGAAUCCGACACUGGUAUGGCAACAUUUUUGGA GAGUUCGAGCAAACAUGCAAUUAG	123	sch-miR7997c-15-5p	AUGUUGCUUGGACUCUUCAAAAAU	10-33	stu-miR7997c	2	0	24	24	1
			sch-miR5303f-15-3p	AUUUUUGGAGAAUCCGACACUGGU	59-82	stu-miR5303f	2	0	24	24	1
sch-MIR171b-2	AGCUACACGUGAUAUUGGCGCGGCUCAAUCAAA AAGUAGACUCAAAAUGUUCUUAAGUACUGCUUUC UCAUUGAACCGCACCAAUAUCUCGUGUAUUC	98	sch-miR171b-2-5p	GAUAUUGGCGCGGCUCAAUC	11-30	zma-miR171b-5p	1	0	20	20	1
			sch-miR171e-2-3p	UCAUUGAACCGCACCAAUAUC	68-88	ppe-miR171e	2	0	21	21	1
sch-MIR7997b-6	GGUCUAUGCUGCUCGGACUCUUCAAAAAUGUCG AGGGGUGUGUGUGGGAUCCUCCAUAUAUAGUAC AUUUUUGAAGGAUCCGACACGGAUGCGCCAACA UUUUUGGAGAACCUGAGCAACUUAGUGU	127	sch-miR7997b-6-5p	AUGCUGCUCGGACUCUUCAAA	6-26	stu-miR7997b	0	0	21	21	1
			sch-miR5303h-6-3p	AACAUUUUUGGAGAACCUGAGCAA	96-119	stu-miR5303h	3	0	24	24	1
sch-MIR444a	CUGAUUCGACUACCUAUUUUUUCAAAUUGGUUG UAGCAGCCUCAAGCUACCUGGACUAUAAAUUAUU UUUUUGAUGACAAAAGAAAUUUAAAAAGAUAUAU UCCACGUAGCCUGGGGCUGCUACAAUCAAUUUG UAAUUCUUGAAAUAGUUAGUCAAAUUGG	162	sch-miR444a-5p	UAGCAGCCUCAAGCUACCUGG	34-54	hvu-miR444a	5	0	21	21	1
			sch-miR5556-3p	UGAUGACAAAAGAAAUUUAAA	72-92	mtr-miR5556-3p	4	0	21	21	1
sch-MIR7492c	AGGAACAUUCACUACAUCAAAAAUGAUCUUUAGC GGCAAUUAAUUAACAACAAUAACUUAAUUGUCAC UAAAUAUGUACUAUUAGAGGCAAUUAGCACUCUU UGAAUAUGUCCCAAAAGUCUUUAGCGACAUUGG AUACAAUGACAAUUAACUAGUGUCGUUAAAGUUU UUAACAAUCUUUGUUAAUAUGUAUAUUUACUGCC GCUAAAUGAUGUGUUUGUUGUAGUGAUUGUUGG G	237	sch-miR7492c-5p	ACAUCAAAAAUGAUCUUUAGCGG	14-36	ghr-miR7492c	5	0	23	23	3
			sch-miR7983-3p	AAAAGUCUUUAGCGACAUUGGAUA	115-138	stu-miR7983-5p	3	0	24	24	2
sch-MIR7984b-4	UUUUCCAGAAGUUCAGGAUGAAGCACGUUCCAC AUGUAGAACAAAUUUAUCUACACGUUGAAUGUGC UUCAUCCUGAACUUUGGACCU	88	sch-miR7984b-4-3p	AUCCUGAACUUUGGACCU	71-88	stu-miR7984b-5p	4	0	18	24	1
sch-MIR169c-5	UUAAGAAGAGAGGCCUUACCUGAAGUGAAGAGU CUUUGUUUGUUAGCCAAGGAUGACUUGCCUACA UACCCCUCCUCCCACAAGGUUAUUAUUUCUUAAU UUCCCUUGUGGGGUUGCUAUGCUAGGCAGUUAU CCUGGCUAUCUUGACAGGCUGUUCUUCAUCACG	185	sch-miR169c-5-5p	UAGCCAAGGAUGACUUGCCUA	44-64	ata-miR169c-5p	0	0	21	21	1

	UUAGGCCUCUUCUUCUCGU										
sch-MIR11891-2	AUAUUAGUACUUUAGCUCACUUAUGCCCUUACCA UCAAAUACUUGGUUUAAAUACUAUGCGCAAUUGA GCAGAAUAAGGGUGUAUGUGGGCCAAGUAUUUG AUGCUAAGGGCUUAAGUAAAUUGAAGUAUAAACG	135	sch-miR11891-2-3p	AGUAAAUUGAAGUAUAAACG	116-135	mes-miR11891	5	0	20	20	3
sch-MIR169j-5	GAUAAAAGAAGAGUGUGUCUUACAUGAAGGGUA AGUGCCUAAUUUGAUAGCCAAGGAUGACUUGCC UGCAUCAUUAGUUCUUGAGGCUAGUUUGUGAUA UAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCU UCUUUGAUGGCCAGGCAGUCUCCUUGGCUACUC UGAUAGGUUCCUCUCAUUCAUGCUAGACUCUUC UCUUCUUAUUUAG	212	sch-miR169j-5-5p	UAGCCAAGGAUGACUUGCCUGC	48-69	ppe-miR169j	0	0	22	22	1
			sch-miR169e-5-3p	CAGGCAGUCUCCUUGGCUACU	145-165	csi-miR169e-3p	2	0	21	21	1
sch-MIR5303f-1	GUUGCUUGGACUCUUCAAAAAUGUUGAUGGGUG UGUGUCGGAUACUUCAAAAGUUGUGUAUGUCUG GAGGAUCUGACACGGGUGCGACAACAAUUUCAG AGAGUCCGAGCUUA	113	sch-miR5303f-1-3p	AUGUCUGGAGGAUCUGACACGGGU	60-83	stu-miR5303f	3	0	24	24	1
sch-MIR7997b-7	CAAUCUAUGCUGCUCGGACUCUUCAAAAAUGUC GACAGGUGCAUGUAAGAUACUUCAAAAAUUAUGC AUUUUCAACGAAUUCGACACGGGUGCUGCAACA UUUUUGGAGAGUCUGAGCAACAUAGACGA	129	sch-miR7997b-7-5p	AUGCUGCUCGGACUCUUCAAA	7-27	stu-miR7997b	0	0	21	21	1
			sch-miR5303h-7-3p	AACAUUUUUGGAGAGUCUGAGCAA	97-120	stu-miR5303h	1	0	24	24	1
sch-MIR11424	CCCUUCUCCCUCAUUUUGCUGCUAGGGUUUUAC AACUGUCUUUAUAUCUGGGUUUGUAAGUGGAUA UUCGUGAUUGUAGGUUAGUAAAACUUUUUCUU UUUUUUAUUGUGUUUGCAACCAUGAAAAUUCACU UUGAAACUCAGCUCCGAAGAAAGUUAUGAAAGAU UAGCCGCGUAAUGAGGGGAAAGU	190	sch-miR11424-5p	ACUGUCUUUAUAUCUGGGUUU	35-55	pab-miR11424	5	0	21	21	1
			sch-miR1052-3p	UUUCUUUUUUUUAUUGUGUUU	94-114	ppt-miR1052	5	0	21	21	1
sch-MIR5654	UUGACCAAAUUCCAUAGACACACCUUAACUAAAC UAAUGUCUUAUUUCCCCCUAAACCCAAUUUUUA AUGUAAUUCUGUGCACCUUUUGGGUUACGUGAC AUCCAAAUAUCUUCCACACGCUUCAACUGCAUGU AGUUAUGAAGUAUGCAACGUAAGCCAAAAGGUG UACAUAUUUUUAAAAAAAUGAAUUCAGGGGUAAU AAGACUUAAGUCUCUGAGAUUUCGGUCAUAGUC UAGGGCUACUUGUGUUUU	253	sch-miR5654-5p	UGACAUCCAAAUAUCUUCCA	98-117	ath-miR5654-5p	5	0	20	20	3
			sch-miR8046-3p	CUCUGAGAUUUCGGUCAUAGU	214-234	stu-miR8046-3p	4	0	21	21	1
sch-MIR8008b-1	GUUGUUUAGUUCGUCGCUUUUGGGUUUUAAUUU UUUUAAAACCCAGAAAAGCGACGGACUAAACUUU	67	sch-miR8008b-1-3p	AAACCCAGAAAAGCGACGGACUAA	39-62	stu-miR8008b	3	0	24	24	1
sch-MIR319g	UCUUCUCUUCAUCCGACAAUGUUGAUGCAAGUG AUGCAGGGCCUGAUGGGUGAAUAAUGGAUUUCU ACCGAAGUUCUAGGGAUUUCAUCAGUUCAGUCA UCAUGGAAGCCCUACAUCACUACCAUUAACAAUG UUAGAUGGUGAGACAA	149	sch-miR319g-3p	GGGAUUUCAUCAGUUCAGUC	79-98	mdm-miR319g	5	0	20	20	1
sch-MIR5014a-4	AAUAUUUGUAUUGUACAAUUAUAAGUGUAUAUGA CGAAGAUAUAUGAAUUUGCAUGUGUAUAUACAAU UUUCUCUCGCUUUUUACAAAUAGAAACACAAUUU AUACAUUUAUGUUUGUAUAAAGCGAGAGAGACGA GGAAGAAACUGGUGAGCAAGAGAUGGAGAGUGG CAAUCGAGAAUUUCAGGAAGAGAGGCGACUGAC AAAAGUUUGCUACGAGGCACAAUUAUUAUAACAU UCAAUUUGAAUUAAUAGUUUGCCAUUAUAUACGA UUUUCUUUUCUUAAUUUUAUCCAAUACAAAUUAC	304	sch-miR5014a-4-5p	UUGUACAAUUAUAAGUGUAUA	11-31	ath-miR5014a-3p	4	0	21	21	1
			sch-miR865-4-3p	UCUUUUCUUAAUUUUAUCCAA	274-294	ath-miR865-3p	4	0	21	21	1
sch-MIR857-2	AUCUACUACAUAUACCUAAAAAAAUACUUUAACC AUAUAAAAAUAACAAAAAUUUUCCGCCGAAGGUG GUUCGGAUGAACCCCUAAUGACAAUGUGGCUCU GCCACUGUAAGGUAGAUACAAUUUUUGGGUAGA CGAUAUUGUUUGUUGUUGUUUAAUAACAUUUUA	199	sch-miR857-2-5p	AUACUUUAACCAUAUAAAAAUA	24-45	cas-miR857	5	0	22	22	1

	AUUGUUUGGUUUGAUUGUAUCGUGUAGUAUUG										
			sch-miR8014-2-3p	AUUGUAUCGUGUAGUAUUG	181-199	stu-miR8014-5p	4	0	19	24	1
sch-MIR5014a-5	GUCAAGUAGACACUUAAACUUGUAUAAAAUUGAA CAAGUAGACACAUGUGUCCUAAAUGACAUGAUAC ACGUAGGACACCAUGUAGGACACAAAAUUUCUAU GUAGGGUGCCAUGUAGGACGAAUUUGUCAAUUU GUUCAAUUUUAUACAAGUUUAAGUGUCUACUUAC G	170	sch-miR5014a-5-5p	ACACUUAAACUUGUAUAAAAU	10-30	ath-miR5014a-5p	5	0	21	21	1
			sch-miR5014a-5-3p	UUAUACAAGUUUAAGUGUCUA	144-164	ath-miR5014a-3p	5	0	21	21	1
sch-MIR2118a	UUUUCUCCAUUUUUCAUCGAAUUUAGAAACGAUU UCAUUGAAAAACAUAGAACCCCUUUUCCUCAUUU CUCCAUUUCCUGAGAACGAUUUCACAAUAUACAU AAGUUCUAAGCGAAAGGGGUUUUAUGUUCUUCA GUGAAAUCGUUUCUAAAUUCUAAGAGAAAUAGAG AAAA	173	sch-miR2118a-5p	UUCCUCAUUUCUCCAUUUCCUG	59-80	ata-miR2118a-5p	5	0	22	22	1
sch-MIR7997b-8	CUGCUAAGUUGUUCGGACUCUUCAAAAUUGCUA CUGCACCCGUGUCAGAUUCUCCAAAAAUGCACUA CUUUUGGAGGAUCCCACACACUCCCGUCGACGU UUUUGAAGAGUCCGAGCAACAUAGAUG	127	sch-miR7997b-8-5p	AAGUUGUUCGGACUCUUCAAA	6-26	stu-miR7997b	3	0	21	21	1
			sch-miR5303h-8-3p	GACGUUUUUGAAGAGUCCGAGCAA	96-119	stu-miR5303h	3	0	24	24	2
sch-MIR171b-3	GGUAUGAAGAAGAAUACAAGAGUGAUAUUGGUU CGGCUCAUCUCUUAUCUGUUACACGAAUCAGAAA UUAGUGAGCCGAACCAAUAUCACGCCAUGUCUG CUUCUCCAUCAU	112	sch-miR171b-3-5p	AGUGAUAUUGGUUCGGCUCAUC	21-42	csi-miR171b-5p	1	0	22	22	2
			sch-miR171h-3-3p	GUGAGCCGAACCAAUAUCACG	71-91	zma-miR171h-3p	1	0	21	21	1
sch-MIR7997c-16	GACCUAUGUUGCUCGGACUUCUCAAAAUUAUCAA CAGUGUGUCAGAUACUCCAAAAAUAGUACAUUUU GGAGAAUCUGACACGGGUGCGACAACAAUUUUG GAGAGUCCGAGCAAUAUAGCAU	123	sch-miR7997c-16-5p	AUGUUGCUCGGACUUCUCAAAAUU	6-29	stu-miR7997c	4	0	24	24	1
			sch-miR5303e-16-3p	UUUUGGAGAAUCUGACACGGGUGC	65-88	stu-miR5303e	1	0	24	24	1
sch-MIR7981d-11	CCUGAAAUUUUAGAGACACACUUAUAUUAUACUA AGGUCCGAUUACCCUUCGAACUUAUUUUAUAAAU GAUUUUAUGUUACGUGACACUAUCUUUUGGAUC CUGCGCGUGUUGACAAUUUUUUCAAGCUAUCUA GUUGAUAGUGUCAUGUAAGCCGAAAAGGGAUAG AAAUUAUUUGAAAAUAAGUUUGGGGGUAAUAAAA CCUUAGUAUAAGUGUGUCUCUGAGAUUUCGAA	233	sch-miR7981d-11-5p	CUGAAAUUUUAGAGACACACUUAU	2-25	sly-miR7981d	4	0	24	24	3
			sch-miR7981e-11-3p	AAGUGUGUCUCUGAGAUUUCGAA	211-233	sly-miR7981e	1	0	23	24	1
sch-MIR5997	AAUAAGACAAGUAGUUGCAUCACCUACUUAAGCA AAUAAACCAAGGAGUUAAGUAGGUGAUGCAUCUA CUUGACUUCUU	79	sch-miR5997-3p	AUAAACCAAGGAGUUAAGUAG	36-56	ath-miR5997	5	0	21	21	3
sch-MIR7997c-17	GCUACUAUGUUGUUCGGACUCUUCAAAAAUGUU GCUGCGCCCACGUCAGAUCCUCCAAAAAUUGUA CUAAUUUUUGAGGAUCCAACGUGCACUUGGUGC CUUCUUUGAAGAGUUCGAGCAACAUAGUUUU	130	sch-miR7997c-17-5p	AUGUUGUUCGGACUCUUCAAAAAU	7-30	stu-miR7997c	2	0	24	24	1
			sch-miR5303-17-3p	UCUUUGAAGAGUUCGAGCAAC	102-122	sly-miR5303	1	0	21	21	1
sch-MIR11497-1	UACAUAAUCAAUAUCAACAUAACUUCUUAGGAAA UCUCGGUAUAAAAUUAUGCAGGGUAGAAGGUGG AAUAAGUUAUGUGGGUAUUAGUUAUACA	95	sch-miR11497-1-3p	GGAAUAAGUUAUGUGGGUAUU	66-86	pab-miR11497	5	0	21	21	2
sch-MIR7997b-9	CAUCUAUGUUGUUCGGUCUCUCCAAAAUGUUAU CGCAUUCACGUUGAAUCCUCCAAAAAUGCACUAU UUUUGAAGGAUCCGAACAUGCACCGAUCAACAUU UUUUAAGAGUUCGAGCAACUUAGUUU	127	sch-miR7997b-9-5p	AUGUUGUUCGGUCUCUCCAAA	6-26	stu-miR7997b	4	0	21	21	1
			sch-miR5303-9-3p	UUUUUUAAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
sch-MIR1888a	CAAAUCACAAGAGAAAACAAAGAAUGAAAGAAUU AGUCUAAAAGAGAGUUCUUAUUAGUUGAAGGGA	289	sch-miR1888a-5p	UGAGUUAUAAUUUGUGAAGGU	116-136	ath-miR1888a	5	0	21	21	1

	GGUGUUCUUCUUUGUGGAGCUUUGGACUCAACU CUUGUCCAGAGUUGUUGAGUUAUAAUUUGUGAA GGUUGUUGUAUCUUGGAGGGGACAAGUCAAAAG GACUACUGCUGGACCGGUGAAAAUAUUUGGUGC AGUGGGCUUGAAUCUCAUUAAAGAGAGCGACAU AUUCACACCUUAGCCUGAAGAGAUUAAUUUCUUC AUUUUAUUUUCAAUUGUAAUCUU										
sch-MIR390-3	AGCAGAUUAAAAAUAAAAAUAAUAUAUUAUAAAAA AAAGCAUGAAAAAGCCGUGAAACUCAGGAUGGAU AGCGCUAAAGAUGUGUAAAAAAAUCGAAUUGAGU CAUCCAUGGCGCUAUCCCUCCUGAGCUUUACAG AUUCUCCAUGCAUAUCCACUAGAAAUUAAUUUGU UUUUUCACUAUA	182	sch-miR390-3-5p	AAACUCAGGAUGGAUAGCGCU	55-75	aof-miR390	3	0	21	21	1
			sch-miR390a-3-3p	CGCUAUCCCUCCUGAGCUUUA	113-133	sly-miR390a-3p	2	0	21	21	1
sch-MIR171b-4	AAAUGGAAUGAAAAUAAGAAGUGAUAUUGGCGCG GCUCAAUCUGAGAUCGCUCUUUACGAAAACAAGC GUAAAUUCGUCUUCGGAUUGAACCUCACCAACAU CGCUUCUUCCAUUUUAAUCCCAAAA	127	sch-miR171b-4-5p	GAUAUUGGCGCGGCUCAAUC	23-42	zma-miR171b-5p	1	0	20	20	1
			sch-miR171-4-3p	GGAUUGAACCUCACCAACAUC	83-103	cca-miR171	4	0	21	21	2
sch-MIR9478-2	GAGCCUUUUUUUAAACGGUAAUGGCAUGGAUGA GCCAAACUUUUAACGAAUGGCAUAAAUGAGCCUU UUUUGAAAGUUCGAUGACAUAUUUGAGCCUUUU CCCUUAAAAAAAAGGUAA	118	sch-miR9478-2-3p	UUCGAUGACAUAUUUGAGCCU	77-97	sly-miR9478-3p	0	0	21	21	1
sch-MIR172c-3	UCGAAGGGCAACAUGACAAAUAAAAGUGGAUGGA UGGAGUAUAUGAUUAUAAGAACGUAUUAAGUAAU AUGUUCACAUGAGGCUCUUCGAGAUUCAUUCUA UCUGAUACUCCCUUCAUUUCAAUUUAUUUCGUC UUACUUUCCUUUUUA	149	sch-miR172c-3-3p	AGGCUCUUCGAGAUUCAUU	80-98	stu-miR172c-5p	5	0	19	19	1
sch-MIR6222	AACAGCUAAUUAAGUCAAAAACCAGCUUUUAGGU CAGUUUGAUCAACUUUUAAGCUGAGCCAAACAG GCUCUAAGUCACUUUGAUAUUUGUCAAACACUCU AAUAAGUCAAAAACUGACUUUUAAGUCAGUUUGA UCAGCUUUUAAGUCCAUCCAAACUGGCUCUUAAU CUAUAUUAGGAAUUAUAGCUAUA	192	sch-miR6222-5p	UAAGCUGAGCCAAACAGGCUC	51-71	sbi-miR6222-3p	4	0	21	21	3
			sch-miR10541-3p	AGUCACUUUGAUAUUUGUCAAACA	74-97	sly-miR10541	2	0	24	24	1
sch-MIR1222d	GAGAUUUCACGAGGAUGAAUCCUCUUAUUCACAA UUGUUAAGACAUCAGAGGAUCCUCAAGAGUUUG UAGAUGAGGUGGAUAAGAUCCUGGUGUCUAUGG GGGUCACUGAUAUUGAGAAGGCUGAGCUGGCUU CCUACCAGCUCAAGGAUGUUGCACAGAUUUGGU GUAAGAUGUGGCAAGAUAGUCGUGUCUUAAGUG GAAUGCGAGUCACAUGGGAGAUGUUCAAAAAAG CAUUUCUGAAGAGAUUCUUCCACAGAGACAUGA G	266	sch-miR1222d-5p	UCUAUGGGGGUCACUGAUAUU	94-114	ppt-miR1222d	5	0	21	21	1
sch-MIR169f	AGAACUAUUGUUCAACUAUAAAUUUGAAGAAUAG AGAGUAAUUUGGAGGUGGGUUGGAGUGCCCGUU CUCUAUUUUACUCUCCAAAUAUAGAGAAUAGAGA GUAAAAUAGAGAUGGAUUGGAGAUGGUCUUAAC CGUUACGUUGACAUUCAACUUUGUUAUGAUAGU UUCAAAGUUCUGCAUAAAGUAUUUUAUUCGUUAA AUAGUUGAAAAUGUGUA	218	sch-miR169f-5p	UGAAGAAUAGAGAGUAAUUUGG	25-46	mdm-miR169f	5	0	22	22	1
			sch-miR10215-2-3p	GAGAAUAGAGAGUAAAAUAGA	91-111	eun-miR10215-3p	5	0	21	21	1
sch-MIR7992-9	AACACUCAAACUUGGGCUCGACUGGCAAGUAAG CACUCCAACUUUGACAGUGCACAUGUAGACACCU CAACUUGGUCUUACUUUUCAUUGAAGGUGUCUA AAUGAUCAUUUGGUAAGUUGGAGCAUACAACUG ACACAUUGGAGACGAGUUGAGUAGA	158	sch-miR7992-9-5p	UUUGACAGUGCACAUGUAGACACC	43-66	stu-miR7992-5p	3	0	24	24	1
			sch-miR7806-9-3p	UUGAAGGUGUCUAAAUGAUCA	88-108	rgl-miR7806	5	0	21	21	1
sch-MIR4235	CUUUAGAAUUUUAAAACUAUUCUACUGAAGAACA UAGAACCCCUAUCCCUUAGAACUUGUGUAUUUU GUGAAAUCGUUCUAAGGAAAUGGAGAAAUGAGG	147	sch-miR4235-5p	ACUGAAGAACAUAGAACCCCU	24-44	aly-miR4235	5	0	21	21	1

	AAAAGGGGUUUUAUGUUCUUCAGUGAAAUCGUU UCUAAAUUAUACGG										
sch-MIR11093	UCCUCCUAAUACCCUCUGAACUUAUUUAAUAAAU AAUUUUCUAUCUCUUUUUGACUUACGUGAUACUA GCUUGAAAAAAAUGUCAACCGUUAGAUCCACGAG AUAGUGCCACGUAGGCUGAAAAGGGAUAGAAAA UUGUUAAUAAAAUAAGUUCAGGGGAUAAUAGGAC CU	171	sch-miR11093-3p	AAAAAUGUCAACCGUUAGAUC	76-96	lja-miR11093-3p	4	0	21	21	1
sch-MIR7997c-18	UAUGUUGCUCAGACUUUUCAAAAAUAUCAAUGGG UGUUUGUCGGAUACUCUAUAAAUAGUGCAUUUU UGGAGGAUCUGACACGGGUGCGGUAAACAUUAU UGGAGAGUCCGAGCAACGUG	120	sch-miR7997c-18-5p	AUGUUGCUCAGACUUUUCAAAAAU	2-25	stu-miR7997c	3	0	24	24	1
			sch-miR5303f-18-3p	AUUUUUGGAGGAUCUGACACGGGU	63-86	stu-miR5303f	1	0	24	24	1
sch-MIR2863a	UGAUCCACCCACCUAAUCCGACCCAUUUAAAAAA UAUGAUAUGACCCAUUUUAUUUUAUCUUUAAUCC UAAAUCAAGGUUUAAAGAGGGAAUAAUUUAGGAU UAAAGAGAAAAUAAAAUGGGUCAUAUCAUAUUUU UUAAAUGGAUCGGGUUAAGUGGGUGGAUCA	166	sch-miR2863a-5p	AUGACCCAUUUUAUUUUAUCU	41-61	osa-miR2863a	5	0	21	21	2
			sch-miR11072a-3p	AAGAGGGAAUAAUUUAGGA	83-101	lja-miR11072a-3p	5	0	19	19	3
sch-MIR11425f	UUUAAAUUUAAUAAAGUAGUUGGGAAAUGAUGAG AAUAUAUCGAUACAUCAGAGGGACAGUUUAAUCU GUGCUUUGCUGAAUAAAUUUUGCACGUCAGUCU GAUCCCAAUUACUUCUAAAUCUUUUG	127	sch-miR11425f-3p	AUUACUUCUAAAUCUUUUG	109-127	pab-miR11425f	4	0	19	21	2
sch-MIR7696d	GUAAAAAAUAUACGCACAAGCAAGCUAUGCUAUU UGAACUCCACAUGUUGAAUUAUGCAAAAAUGACU AUUUUUAAGGAUUCAACACACACUCAAUGGCAUU UUGAAGAGUUCGAGCAACAUAGCCUAAUUGUAUA AAUAUUUUUACA	148	sch-miR7696d-5p	UGUUGAAUUAUGCAAAAAUGA	46-66	mtr-miR7696d-3p	5	0	21	21	1
			sch-miR5303-3p	AUUUUGAAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	2
sch-MIR10538-7	UUUUAAAAGUUGAUGGCGUCAGAUUGAUAUACG UUACUCACAGUAACAUUUUACUCCUAAUAGUAAC GUUUUAGGAGUAAAACGUUACUGAAAAUAACGUU UUAGGAGUAAAGCGUUACUUAUAGUAACGUACAU CAACCUAAUGCUGUUAGUUUUUAAAA	161	sch-miR10538-7-5p	AGAUUGAUAUACGUUACUCACAGU	21-44	sly-miR10538	0	0	24	24	1
			sch-miR6288c-7-3p	GCUGUUAGUUUUUAAAA	145-161	ppe-miR6288c-5p	5	0	17	21	3
sch-MIR10405d-2	UGUCAAAUGAAUUCUGAACUUGUCGAUUUCUGC AAAAAAGAAAUUGAUAGUUUAUUAUCAAAGGGAC UUAUAAAACCCUCUAAAUCACCAUGGUCUUGUAC UGCAUUUUAUGUUAAUAAAGCUGCAGAACAAGAA AGAGGUGUUCCUAGGUUGGUAAUAAAUUACAAA CCUUUGGUUGGGGGGGGGCGGGGGAUGAUAA UGUUAUGUUAGACUUUGAAAAACCUAUUAAUAUA GAUAUGUGAAUAUUCAUUUUCUAAAUGGAAAAUU AUCAUAUUUACUUUUGUAU	287	sch-miR10405d-2-5p	UAGUUUAUUAUCAAAGGGACU	48-68	gma-miR10405d	5	0	21	21	1
			sch-miR9679-2-3p	CAGAACAAGAAAGAGGUGUUC	125-145	tae-miR9679-5p	5	0	21	21	1
sch-MIR11018-2	CAAUUCAUUUCUGGCUGUAGUUUAUGGUGUCUU UAAUGCAACAUAACAAGUAAAAGUGAACGAAGCU UAUAAAUACAAAGCUAGGCACCAUAUAUAGCCAU AUUAUGAAAAG	112	sch-miR11018-2-5p	GCAACAUAACAAGUAAAAGUGA	38-59	mdm-miR11018	5	0	22	22	2
sch-MIR5083	AACGUAUAGAGAUGUCCACGUGGAUAUUAUAAUU AUUUCAUCAUUUUAAAUAGUAAUGUGUCCACGUG GACACAUAUAUACCUU	84	sch-miR5083-3p	AUAUUAUAAUUAUUUCAUCA	24-43	osa-miR5083	5	0	20	20	1
sch-MIR3706-1	AUAGGAAUACGUGGAACAAAAUUAUUCAUCGAUC UGAAGUUCGGAUCAGUGGAUAAGAUUAUGACAC AUGUAUGUCCGUU	80	sch-miR3706-1-3p	GUUCGGAUCAGUGGAUAAGA	39-58	pab-miR3706	4	0	20	20	2
sch-MIR7997c-19	UUUCUUGAUUUUUUUUUGUCAGUAACUAAUGUU CGUUAUGUUGCUCAGACUCUCCAAAAUCAAUGU CACAUCAGUUUUGAAUAUAGUCCUCCAAAAUAAU GUACUUUAUUGUACUGUUUUUGAAGGAUCUGAC AUGCAUCUGUCACUAUUUUUGAAGAGUUUAGAG CAAUAUAACUUAAAAUGUUCGAUUUUUUUUUUAU	329	sch-miR7997c-19-5p	AUGUUGCUCAGACUCUCCAAAAUC	38-61	stu-miR7997c	5	0	24	24	1

	AAGUAAUGUGGAUUUGGGAUAUUUGAUAGGGGA UAGAAGAAUUGAAGCAUUCAUUGGUGUACACAAC AUUGGAAUUGGAGAAUACUGUGAUUUCAGCUCA UGAGGAACUUGCAAGAAAAGAUGAAGAGA										
			sch-miR1886i-19-3p	AAUACUGUGAUUUCAGCUCAUGA	281-303	stu-miR1886i-3p	5	0	23	23	3
sch-MIR5026-3	UUCGGCCUACGUGGCACUAGCUUGAAAAAAAGU CAAUCAGCGCCCACAAGAUAGUGUCACGUAGGC CUUA	70	sch-miR5026-3-3p	GCCCACAAGAUAGUGUCACGU	42-62	ath-miR5026	5	0	21	21	2
sch-MIR156i	UUGUAAAAAGAUAUAUAGGACUACUAGACAACUC AAGCUUUAACACUCUAACUUGUCUACCAGUUUAU UCAGUCCCCUUUGGUUAGGGACUGUCUUCAUUG GUUAUGGUGAUCAACUGGUAGGCAAGUUAGAGU UUUUAAGCUUGAGCUGUCUAGUAGUCUUAUAUA CCAUUUUAACG	178	sch-miR156i-5p	UUGUAAAAAGAUAUAUAGGAC	1-21	csi-miR156i-5p	5	0	21	21	1
			sch-miR11115-3p	UGGUAGGCAAGUUAGAGUUUU	117-137	lja-miR11115-5p	5	0	21	21	1
sch-MIR7997b-10	GAAGUUAUAAUACCUAUGCUGCUCGGACUCUUC AAAAAUGUCGACCGGUGCGUGUUGGAUCCUCCA AAAAUACUGUAUCCGGAAGGAUCCGACACGUGC GGCAACAUUUUUGGAGAGUCCGAGCAACUUAGA AAAUAACAAC	142	sch-miR7997b-10-5p	AUGCUGCUCGGACUCUUCAAA	16-36	stu-miR7997b	0	0	21	21	1
			sch-miR5303h-10-3p	AACAUUUUUGGAGAGUCCGAGCAA	103-126	stu-miR5303h	2	0	24	24	1
sch-MIR8011a-4	UAACUUAUAUUGUUAUAAGUGAAGUACCAAUUGA UUGGUGUUUACAUGGUGAAUUUUUUUACCAUGU GACGUUAGUUGUGUGAGGUUCCUUUUUGUGAGA CGAAAAAAUGGACCCACGGAAAAGACAUCUUUCU AUAGGGCAUAUUUAUGCAGGUAUCCAGUGAAAU AAUCGAGAUACAUGCAAACUGACUAGUCGUUACC AUCAUUAGAAAAUAAAUGGGUCAUAGCUGUGUAG GGCAAAAACCAGAUAGAUUGAUGUUAAUCCACAC AUGAAUCUAAGAUAAGACC	288	sch-miR8011a-4-5p	UUGUGUGAGGUUCCUUUUUGUGAG	76-99	stu-miR8011a-5p	4	0	24	24	1
sch-MIR399f-4	GUGUGGAUGCAUUACUGGGCUAAUCUUCUUUGG CAAAUAAACCACACAAUUUCACUAUUAUUUGGUG CAAAUUUGGUCAUUUAUUGCCAAAGUAGAUUUG CCCCGUAAAUCAUUCAUGC	119	sch-miR399f-4-5p	GGGCUAAUCUUCUUUGGCAAA	17-37	csi-miR399f-5p	4	0	21	21	1
			sch-miR399a-4-3p	UGCCAAAGUAGAUUUGCCCCG	85-105	cme-miR399a	1	0	21	21	1
sch-MIR11314	AUGAAAGGUUGUGACUUUUAUGAAAAGUUGCGA CUUUUAUGAAGGGUUGCGACUUUAAUGAAGAGU CAUGACUUUUAUGAGAAGUUGUGACUUUUAUGA AGAGUUGCGCAUUUUAUGAAAAGUUGUGAAUUU UAUGAUAAGUUGUGACCUUUUCG	155	sch-miR11314-3p	AGAGUUGCGCAUUUUAUGAAA	100-120	fve-miR11314	5	0	21	21	1
sch-MIR9563a	UAGUACUGCUUAGUUGCGCGGACUCUUCACUUU UGAUGCCGCACCCGUCUCGGAUUCUUUAAAACU ACACUACUUUUGGUGAAUCCGACACGCAACAGU CGGCAUUUUUGAAGAGUACGAGCAACAUAGGGU AGUAGUG	139	sch-miR9563a-5p	ACCCGUCUCGGAUUCUUUAAA	43-63	bra-miR9563a-5p	5	0	21	21	1
			sch-miR5303d-3p	UUUUGGUGAAUCCGACACGCAACA	74-97	stu-miR5303d	3	0	24	24	1
sch-MIR6027-1	UUUUCUCAUAUUUUUACAUGAUUAUGGGUAGCA CAAGGAUUAAUGUGAAACAAAUAAGUGAUAUGCA AAGAAGAUGGAGAUUCCAUUGUUUAUUGUUACG AAGAAAACACUUUUGUGUUUCUCGUGAAUCCUU CGGCUAUCCAUAAUCACGUUGAAUGUGUGACUU	166	sch-miR6027-1-5p	AUGGGUAGCACAAGGAUUAAUG	24-45	sly-miR6027-5p	0	0	22	22	1
			sch-miR6027-1-3p	UGAAUCCUUCGGCUAUCCAUAA	125-146	stu-miR6027	0	0	22	22	1
sch-MIR8008b-2	UGUGGUUUUGUAAGUCGCUUUUUGUAUUUUUUU UAUAAAAAAUAAACCCAGAAAAGUGACGGACAGG AACCUUU	74	sch-miR8008b-2-3p	AAACCCAGAAAAGUGACGGACAGG	44-67	stu-miR8008b	2	0	24	24	1
sch-MIR399b-5	AUGAGAAAGGAAGUCAUUGGUGAAUGAAAAUAAG GGAAAUAGUGAUAGGGCUACUCUCUAUUGGCAU GCGUUAAUGUAUGUAUAGUGACUCCACUUCACU AUAUCGCAUAUUUUAACCAACACGCCAAAGGAGA GCUGCCCUGCUACUGUCUCUGCUUAAUAUAAUA	187	sch-miR399b-5-5p	GGGCUACUCUCUAUUGGCAUG	48-68	sly-miR399b	0	0	21	21	1

	ACUCAAAGGUCCGUUCUUAA										
			sch-miR399o-5-3p	CGCCAAAGGAGAGCUGCCCUG	123-143	stu-miR399o-3p	0	0	21	21	1
sch-MIR6287	UGAAUGUAUUAGGAUUUGUGAUAUAGGAGGUGU CUUUUGAGUGAGAAACUUAAGACUUGGAAAUUU UGGUCGGACAUUUUGUAAUGGUGACUUCUGUAU AUUCUUUGGAAAUUUCUGGAUAAGAGUGGGUUU ACGAUAUCCUCAUUCAUAUCAACAUAACACAUAA GAAGUUAAACGCACAUAUAUCGCAUCCUAACACA UAAA	204	sch-miR6287-5p	UAAGACUUGGAAAUUUUGGUC	51-71	ppe-miR6287	5	0	21	21	2
			sch-miR5161-3p	UCUGGAUAAGAGUGGGUUUA	114-133	osa-miR5161	4	0	20	20	1
sch-MIR171d	CUAACGAGAUAUUGGUGCGGUUCAAUUAGAAAG CGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAA UUGAGCCGUGCCAAUAUCACGUAUU	92	sch-miR171d-5p	AGAUAUUGGUGCGGUUCAAUU	7-27	stu-miR171d-5p	0	0	21	21	1
			sch-miR171c-3p	UUGAGCCGUGCCAAUAUCACG	68-88	cas-miR171c-3p	0	0	21	21	1
sch-MIR7492f-2	AGACACUACAAUAAAAAUGAUCAUUAGCGGCAUU UAAUUCUUAAUUGCCGCUAGCGGCAAUUGUCAC UCUUUGUAUAUGUCCCUAAUGCCUUUAACGACA UUGGUUCUAAGUGCACUUAACUAAUGCCGGUAA AGAUUUUAGCACUCUUUAUUAGUGUCAAUAUUUA AUGCCGCUGAAAGUUAUUUUUGUUAUAAUGAGA	200	sch-miR7492f-2-5p	AAAUGAUCAUUAGCGGCAUUU	15-35	gra-miR7492f	4	0	21	21	3
			sch-miR7983-2-3p	ACUAAUGCCGGUAAAGAUUUUAGC	120-143	stu-miR7983-3p	2	0	24	24	1
sch-MIR7997b-11	CCCUCUAAGUUGCGCGGACUCUUCACUUUCGAU GCCGUACCCGUGUCGGAUUCUCCAAAAAUACAC UAAUUUUGGAGAAUCCGACACGCACCCAUUGAC CUUUUUGAACAAUCCGAGCAACAUAGAUUG	129	sch-miR7997b-11-5p	AAGUUGCGCGGACUCUUCACU	7-27	stu-miR7997b	5	0	21	21	1
			sch-miR5303d-11-3p	UUUUGGAGAAUCCGACACGCACCC	70-93	stu-miR5303d	0	0	24	24	1
sch-MIR391	AAAAGGCUUGCUACGCAGGAGAGAUGAUGCUGG ACGAUAGAGAAAAUGGGAUUUAAUUUAUUGGCCA GCAUCAUACUCCUGCAUAUUAAGCCUAAA	96	sch-miR391-5p	ACGCAGGAGAGAUGAUGCUGGA	13-34	sly-miR391	0	0	22	22	1
			sch-miR391-3p	GCAUCAUACUCCUGCAUAUU	68-87	stu-miR391-3p	0	0	20	20	1
sch-MIR8018	AAAGACUUUCACGGGGCCAUCUAUGGUUCGUGA UUUAUUCUACGAACCGUAGAUCCCAUCCGUGAAA UUCAUA	73	sch-miR8018-3p	ACGAACCGUAGAUCCCAUCCGUGA	42-65	stu-miR8018	1	0	24	24	1
sch-MIR5759	GUUAAAUAAGUUCUAGUUAUUUUAACGGAGAAAA AAGCCAAAGCCCCCUAACCUAUAUCCGGAUUUCC AACAACUUCACUUGAGUAUUAUCACCCCGUGAAC UAUUUAAAACUGAAACUCCAUCUCCCUGGGGGU GAGAGGAUUCAAGUGAAGUUGAAGAGUGUGGUU GAAAAUCCGGAUAUAAGUUAGGGGGCUUUUGGC UAUUUUCUCUAUUUAAACUACAAACAUUUGUG	233	sch-miR5759-3p	CUGGGGGUGAGAGGAUUCAAG	128-148	mtr-miR5759	5	0	21	21	3
sch-MIR2645	AAAUGUACCUUUAUCCAUAUGUCAAUUAAUCAAU GGAGGGUCACCCAACUAUUGUUGGUUGGACCUC UCCCAUUGUAAAAUUUUUCAAGAGAUGCAUAUAU GUCAAGAAAAAGUGUCUAUCUGGUCACUAGAUAA GUUUUAAGUGUCUAAUUUGCAAAUUGUGCCAAG UUUGAGGGACUAUCUAGGUAUUUAAACUAAAUUA UUUAGGGAUAAAGGGACAGAU	223	sch-miR2645-5p	UUUCAAGAGAUGCAUAUAUGU	83-103	mtr-miR2645	5	0	21	21	1
			sch-miR5049e-3p	AAUUAUUUAGGGAUAAAGGGA	198-218	hvu-miR5049e	3	0	21	21	1
sch-MIR4243-1	UGGAAGUACUCCCUCCAUAUACUAGUAUAGAUU GGACUUUGCACUAGGAUAAACAGUUAUUGAUAU GGAUAUUUUACUAUAAUACCCAUAUUAGUUGAUA UUUAGUCUUAGGUAUGGGGAAAUGAUUAACAAA UAGUAAAUGCCAAGGGUAAAACAUGAAAAGAAGA UGUUUCGCCCUUGAUAUGCUAACUAGAAGUGAC AAGUAAAAGUGAAAUUAUAUUUUUAGUAUAGUGG ACAAGUAAAAGUAAAAGUGAAUGGAGUGAGUACU UUAU	272	sch-miR4243-1-3p	UGAAAUUAUAUUUUUAGUAUA	210-230	aly-miR4243	4	0	21	21	1

sch-MIR8743e	UACAGUCGUUGUUUGCGUAUGUGGCAUAAUCAA GAUUCAUAUGAAAAGUUGCAAAUUGGUUAUAUAA UUGAUGAAAUUAAUGACUGGCUAUUUGAAACUCA UGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAAC GACUAUU	142	sch-miR8743e-5p	UAUGAAAAGUUGCAAAUUGGUUAU	40-63	gra-miR8743e	3	0	24	24	1
			sch-miR172-3p	UGAGAAUCUUGAUGAUGCUGCAU	102-124	aau-miR172	0	0	23	23	1
sch-MIR10538-8	UGUUCAGCUGUUAGUAAGUAUCUCUUAUCUUUG AGAGUGAGGAGUUCUAUCUAUAAAUACAGGUAUA UCCGUCACACUAGACAGUUGAGACUUCUUAGAG UGUUACAACUGGAAUAUGUUUUCUAAAAUUUUAC AAAACUAGUAUAAACGUAUUCCACAGUAACGUUU UAGGAUAUAUUUUAUUUUUUAAAAGUUGAUGGC GUCAGAUUGAUAUACGUUACUCACAGUGACGU	233	sch-miR10538-8-3p	AGAUUGAUAUACGUUACUCACAGU	205-228	sly-miR10538	0	0	24	24	1
sch-MIR10538-9	CAGUAAAAGUUGAUGGCGUCAGAUUGAUAUACG UUACUCACAGUAACGUUUUACUCCUAAAACGUUA CUCACAGUAACGUUUUAGGGGUAGAACGUUACU GAAAAUAACAUUUUAAAAGUAAAAUAUUACUUAC AGUAACGUAUAUCAACCUAAUGCUGUUAGUUUUU AAAA	172	sch-miR10538-9-5p	AGAUUGAUAUACGUUACUCACAGU	21-44	sly-miR10538	0	0	24	24	1
			sch-miR5555-9-3p	UAAAAGUAAAAUAUUACUUAC	114-134	mtr-miR5555-5p	5	0	21	21	1
sch-MIR6472	CUAAAUCGCCACUAAAAAUCACUAAAAACCCUUU AGUGACAAUAUUUUGGGAUUUUAUGGCGACUUU UGUCGCCGCUAAAGUAUAAUUCUUUGUAGUGAA UCCUAGUUGGCAAUUCUU	118	sch-miR6472-3p	UAGUGAAUCCUAGUUGGCAAUU	94-115	ptc-miR6472	5	0	22	22	1
sch-MIR860	UUACACAAUGUAUCAAUCAAUUAGAUUAUGUAAG UGAUGUAUAGAUCGGAUACAUCACUUGACGAUG UAUCAGGACAUUACUUUGCACAAUGUAACGGUCA GAUACAUUACUUUAAUUAUGCGAUAUAUCGGGAU GUAUGUGAUGUAUCAGGACGUUGAGUGAUGUAU UCGAAAUCGAGACGUAAUGUAUCACGAUGUUGA GUAUGUAUUCAAAAUCGGAAUGUGAUGUGUCAA UACGUUUUGAGU	246	sch-miR860-5p	UCAAUCAAUUAGAUUAUGUAA	13-33	ath-miR860	5	0	21	21	1
sch-MIR7776	UGAAUCUUAAUCAUUCAGAUUCAGCUCAUUAAGU AUGUUUAAUUUUUAGGUCUGAAUCUGAAUCGUG CAGAUUCAACCUAUUAAUGGGUCUGAAAAAGGUC UGAACGAAUCAGAUCUG	118	sch-miR7776-5p	AGAUUCAGCUCAUUAAGUAUG	17-37	bdi-miR7776-5p-2	5	0	21	21	1
sch-MIR1167	CUCUUAGUCUAUUAUUAAAAAAGACUUUAAUGAC AUGUUAUACCAACUAGGAGAGAGUGAUGAUUUU AAAGUGCCGAGUAUAUUCAGAGGAAAAUAGUGAU ACUUGAGUGAUAUUUUGGUCCUAAAUGAAACAUA AAUGAUAUUUCAAGACAAUUCUCUUAACUUGGGU GACCAUUUAGGGAAUUGAUUCCAAAAUCAUCACU CUCCUAGUUGACAUGACAUGUCAUCAAUUUUUU UCAAUAAUAGACUAAUUU	254	sch-miR1167-5p	AGAGAGUGAUGAUUUUAAAG	52-71	cre-miR1167	5	0	20	20	2
			sch-miR478d-3p	UGACAUGUCAUCAAUUUUUUUCAA	217-240	ptc-miR478d	5	0	24	24	1
sch-MIR5662	UAGAACUUUGACCAAAAUUGUUGUAACGAUAUGA ACAUUGGAGAUAACCUUUUACCCCUGCACUAUUU AAUAGUGUAUUCUAAAGGUAUAUAUAUGUCCACG UGGACAUAAAAAAUAUUCAUCAUUAAAAAAUAGC AAUCUAUACACAUGGAUAUGCACACAUACGUACU UUUAAAAUAUACUACGAAUUAGUGCAGCGGUAAA AGGUCCUCUAUAAAGUUUGAUAUCGUAACGACAU UUUCGAUUAAAGUUUAA	255	sch-miR5662-5p	CGAUAUGAACAUUGGAGAUA	27-46	ath-miR5662	5	0	20	20	2
			sch-miR7984c-3p	CCUCUAUAAAGUUUGAUAUCGUAA	209-232	stu-miR7984c-3p	3	0	24	24	1
sch-MIR8047	CAUAUUUACACCAGGUAGUCAAUUUUGUGCCCU UGUAUUAACAAUUUGACCAUUUUUUCGAAAUUAG ACCCAUGGUCUGAAUACCAGUUUUGAACUUUGA AAUACAGACCAGGUGGCCACUUUCGAACUUCAG AUCACUAGGCUAAUUUUGAAAAACUGGUCAACUU CUAAAUACAAAGCCACAAAUGAGGUUAUUUGUGU AAAUCAG	208	sch-miR8047-5p	CCAUUUUUUCGAAAUUAGACC	50-70	stu-miR8047	0	0	21	21	1

sch-MIR8030-3	UACAAAAUCGAACCAAAUCGUAAAUCGAGUCAAU UUGAAAAGAAACCCGACUAGUGGUUUAGUUUGA CUUGAUUUGGUAUUGCAAAAAAAAAUUCGACUAU AUUUGGGUUGGUUUGGUUUUAAC	124	sch-miR8030-3-3p	UUGGGUUGGUUUGGUUUUAAC	104-124	stu-miR8030-5p	5	0	21	23	1
sch-MIR444b-3	GGAACCUUAAUGAAGAGUUGUGACUUUAUGAAAA GUUGUGACUUUUAUGAAAGGUUGUGAACUUUUU AAAAGGUUGCAACAUUUCUAAUAAGGUGCA	97	sch-miR444b-3-5p	UUGUGACUUUAUGAAAAGUUG	18-38	ssp-miR444b-1	5	0	21	21	1
sch-MIR6457b-1	GUUCCUUUAGGCUUAGUUGCGCGGACUCUUCAC UUUUGAUGCCGCACCCGUCUCGGAUUCUUCAAA AACACACUACUUUUAGCGAAUCCGACACGCACCC GUUGGCAUUUUUGAAGAGUACGAGCAACAUAGC CUUUAGGGUG	143	sch-miR6457b-1-5p	UUAGUUGCGCGGACUCUUCAC	13-33	ptc-miR6457b	5	0	21	21	1
			sch-miR5303d-1-3p	UUUUAGCGAAUCCGACACGCACCC	77-100	stu-miR5303d	2	0	24	24	1
sch-MIR6475	UUUAUGUUAAGGAGUCAAGAACGAACCAUACAUG UUUUAUUCAGGCAAGAAAUUUGUAUGGUUCGGG UAUUGACUUCUGCACAUGAU	87	sch-miR6475-5p	UGUUAAGGAGUCAAGAACGAA	5-25	ptc-miR6475	5	0	21	21	1
sch-MIR8008b-3	GCAGAAAAAGCGACGAAUAAGGUGAGUUUUCCA UCACUUUUUUACAUUACUUUUUUCAACUAAACUC AGAAGAGCGACGGACAUAAACCUUUUGUCCGUC GCUUUUCCGGCUACUUUAAAAAAUUCAUUUCCAG AAAAGUGACGGACAGUGUCCUUUAGUCCGUCGA UAUUUUCAAA	177	sch-miR8008b-3-5p	AAACUCAGAAGAGCGACGGACAUA	62-85	stu-miR8008b	4	0	24	24	1
			sch-miR8009-3-3p	AUUUCCAGAAAAGUGACGGACAGU	127-150	stu-miR8009	1	0	24	24	1
sch-MIR1133-1	GUCGUUAGAUUUAUACUCCCUCCGUCCCAUUUU AUGUGACACCAUUUCCUUUUUGGUCAGUCCCAA AAAGAAUGUCACAUUUUCUUAUAUGGUAAAGUAU UUAAAGAUAGAAUUCCUCUUUUAUCCUUGUUGG UCCCACUUAAUUUUUUAUAUUUAAUAGUACUUUA AUACAUUUAUGAGGAGAGAGAAAAGUGAGUCCAC UUUUGAAGUACAAUUUGAUAAACAUUUCAAAGUC UUCAUUAUUUCUUAAACUGCGUGCUGGGUUAAA UGGUGCCACAUAAAAUGAAAUGGAGGGAGUAUA GUUUAACAAG	311	sch-miR1133-1-5p	UUUAUACUCCCUCCGUCCCAUU	10-31	tae-miR1133	5	0	22	22	3
			sch-miR6164b-1-3p	CCACAUAAAAUGAAAUGGAGG	274-294	nta-miR6164b	3	0	21	21	2
sch-MIR5176	CAAUAUCCUUAUAACUCUCAAAUGGUAGAAAUAU ACCAUAUCGUCACUCAACUAAUAGUAGUUAUUUC AGAAAGUGACUUCUGAAAUAAUAAUGAUUAGUUG AGUGACCAUCUGAGAAAUCAACUCGAGAAUAUAA GAGAUACGU	145	sch-miR5176-5p	UAUACCAUAUCGUCACUCAAC	32-52	bdi-miR5176-5p	5	0	21	21	1
			sch-miR10540-3p	AUAAUAAUGAUUAGUUGAGUG	86-106	sly-miR10540	3	0	21	21	1
sch-MIR6027-2	UUUUCAUAAUUUUACAUGAUUAUGGGUAGCACAA GGAUUAAUGUGAAACAAAUAAGUGAUAUGCAAAG AAGAUGGAGAUUCCAUUGUUUAUUGUUACGAAG AAAACACUUCUGUGUUUCUCGUGAAUCCUUCGG CUAUCCAUAAUCACGUUGAAAUGUGUGACUU	165	sch-miR6027-2-5p	AUGGGUAGCACAAGGAUUAAUG	22-43	sly-miR6027-5p	0	0	22	22	1
			sch-miR6027-2-3p	UGAAUCCUUCGGCUAUCCAUAA	123-144	stu-miR6027	0	0	22	22	1
sch-MIR5303-3	GCCAUGUUGCUAGGUUCCUCUAAAAGUGUUGCU GCACCCGUGUCAGAUCCAAAAACAUGAUUUUGG AGAAUUUGGCACAUACCUGACAAUACUUUUGAAG AACUCGAGCAACAUAUA	117	sch-miR5303-3-3p	CUUUUGAAGAACUCGAGCAAC	92-112	sly-miR5303	3	0	21	21	2
sch-MIR8724	ACCUCUGUCGUGUCAGUUGAACGCUCCAACUUA CUAGAUGAUCAUCUAGACACCUCUAGAGUUUUU GUGUUACAUGCACACACGAGACACGAUGGGGAU GAGUGGGAGUGUUUAGUUGCCAUUUGAGAUCAA GUUGAGGUGUCUAGAUGUGCACUCUCAAAGUUG GAGUGCUUACUUGCCAGUCAAGACCA	191	sch-miR8724-5p	UCUGUCGUGUCAGUUGAACGCUC	4-26	gra-miR8724	5	0	23	23	2
			sch-miR6230-3p	GAUCAAGUUGAGGUGUCUAGA	127-147	sbi-miR6230-3p	5	0	21	21	2
sch-MIR171h-1	AAAGACCUUUAUAGCGUCAUACUAUGUUGUGAU CGUACUUGUGCAAUAGGUAAAGAAAUGCUCAAAA CCAAUAUAACUUUUUUUUUAAUCUCAAAAAAGAA	177	sch-miR171h-1-5p	AUGCUCAAAACCAAUAUAACU	58-78	lus-miR171h	5	0	21	21	1

	AAGAUAUUGGUUUUGAGCAUUUCUUUACCUAUU GCACAAGUACGAUCACACCUUUAUGCAUGCUAUA CAGAUCAGA										
			sch-miR2089-1-3p	UUACCUAUUGCACAAGUACGAU	126-147	mtr-miR2089-5p	5	0	22	22	1
sch-MIR6457b-2	AUGGUAACCUUAGUUGCGCGGACUCUUCACUUU UGAUGCCACACCCGUCUCGGAUUCUUCACAAAU ACACUACUUUUGGCGAAUCCGACACGCACCCAU UGACAUUUUUGAAGAGUCCGAGCAACAUAGAUG GUAACUUG	140	sch-miR6457b-2-5p	UUAGUUGCGCGGACUCUUCAC	10-30	ptc-miR6457b	5	0	21	21	1
			sch-miR5303d-2-3p	UUUUGGCGAAUCCGACACGCACCC	74-97	stu-miR5303d	1	0	24	24	1
sch-MIR5163a	UUACCCUCCCCUACAUUAUUUAAUAAUGUAUUUU AAAGAUAUAUAUGUCCCCACAUGGACACGUUACU AUUUAUAAUGAUGCAAUAUAUAUGAUGUUCAUAU GGACACAUAUAUACCUUUAAAAUGCACUAUUAAA UAGUGUGGGGAGGGGGG	153	sch-miR5163a-5p	CCUCCCCUACAUUAUUUAAUA	5-25	bdi-miR5163a-5p	5	0	21	21	1
sch-MIR7997c-20	UCUGCUAUGUUGCUCGGACUCUCCAACAAUGUU GCCGCACUCAUGUCGGAUCCUUCAAAUAUGCAC UACUUUUGGAGGAUCCAACAUAGACCUAGAAACA UUUUUGAAGAGUUCGAGCAGCAUGCCAU	128	sch-miR7997c-20-5p	AUGUUGCUCGGACUCUCCAACAAU	7-30	stu-miR7997c	3	0	24	24	1
			sch-miR5303h-20-3p	AACAUUUUUGAAGAGUUCGAGCAG	97-120	stu-miR5303h	3	0	24	24	1
sch-MIR8025-2	UGAACUUCAUCAAAAAGAUAGAGUAGUUACACAC AUGCGGAAAUACACACACUCGACAUGCAAUUAAA UUAGUAUAAGUCACCAUUAUAUGAUUCAGCUUG GUUAAGAAAAACAUAAUGGCGACUUAUACUAAUU UAAUUGCAUGAGUAGUGUGUGGUAAAAUAUUUC UUUAUGAUGUUUGACUAUGCUAUCAUUUUCAUC AAGUCAU	208	sch-miR8025-2-5p	ACACACUCGACAUGCAAUUAAAUU	47-70	stu-miR8025-5p	1	0	24	24	1
			sch-miR8025-2-3p	UUUAAUUGCAUGAGUAGUGUGUGG	134-157	stu-miR8025-3p	3	0	24	24	1
sch-MIR11409d	AACUUUAUUCACUAUAACAGUAUGGUCACAAAAC UAUCUUUUGUUGCGUUAAAGUACGUGUUAAUUG AUCAAACAAUGACUAGAACUAGAAGGUUAAGUAU UCUUUUAAUAUUAUUUCUACCAUUUAAUAUUAUU UGUGCCAGAAAUUAACCUUUGGGCCAUUUGUCU CAUUUGAGCAAUCCACACCUAGUUCAGUUACUUU AAUGUGACAAAAAUUAGUUCUGUGAUUCUACCGU UACCGCGGAUAAAAUG	252	sch-miR11409d-3p	CAUUUGUCUCAUUUGAGCAAU	160-180	pab-miR11409d	4	0	21	21	1
sch-MIR7997c-21	AGAACCUAUGUUGGUCGGACUCUUCAAAAAUGU CAACUGGUGCGUGUAAAGUUCUCCAAAAAAUAGU GUACUUUUGGAGAAUCUGACACGGGUGCGGCAU GGAAAGUGAAGAGUCCGCACAACUUAGAGUAGA	133	sch-miR7997c-21-5p	AUGUUGGUCGGACUCUUCAAAAAU	8-31	stu-miR7997c	2	0	24	24	1
			sch-miR5303e-21-3p	UUUUGGAGAAUCUGACACGGGUGC	72-95	stu-miR5303e	1	0	24	24	1
sch-MIR7997c-22	CUCCUAUGUUGCUCGGACUCUUCAAAAAUACUG CUAGGAUCCAACAUGUAGUCGGCACAUUUUUGA AGAGUCCAAGCAAUAUAGAUAAUUAAUGUCUUUG AGACAUUCUCUUGGAGUGUUCAAAGUUAACAAAU AACAUGUGUUGCUCGGACUUGUGGCGUAUCCUC AGAAAAUGAACUACUUUUGGAGGAUCCGACAUUA UGCACUCAGCACAUUUUUGAAGAGUCCGAGCAA UGUAGAAA	242	sch-miR7997c-22-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
			sch-miR5303h-22-3p	CACAUUUUUGAAGAGUCCGAGCAA	211-234	stu-miR5303h	2	0	24	24	2
sch-MIR7502c-2	AAUCAAGUUAUAAUAAAUUCUUAUUAUAGUUCUU AAAUCUUUUAUCACAAGUUUUGACUUGGUUUCAA GAUGGUGGUAAGUCUGAUAUUAAUGAUAGCGAG CAUGUGGUAUUGUAAGUCCCGUUAAAGAUGAAG AAAGGGGCAGCCUGAAACCCUUGUUAGAACUGC UAUCCAUUAAUAUUAAGGCAAGCUCCAUGCUUGA GUAAAAGUUUACCAUACAGCCGAAACUUAGGAUA AAACUUUUAACAUAACUAUAAUACGUUUCAAAGU AUAACUUGGUC	280	sch-miR7502c-2-3p	UUGUUAGAACUGCUAUCCAUU	155-175	gra-miR7502c	5	0	21	21	1

sch-MIR7997c-23	GACGCUAUGUUUCUCGGACUCUCCAAAAAUGCUAAUGCACUAUUUUUGAAGGAUCCAACAUACACCCCCACACUGUUUUUGAAGAGUCCGAGAAGCAUAGCUAA	104	sch-miR7997c-23-5p	AUGUUUCUCGGACUCUCCAAAAAU	7-30	stu-miR7997c	3	0	24	24	1
			sch-miR5303i-23-3p	CUGUUUUUGAAGAGUCCGAGAAGC	73-96	stu-miR5303i	5	0	24	24	2
sch-MIR6020a	AGGAUAAUAUUGAUAAAUUAUUCCUUAGAUAUUGAUGUCUUUUAAGUAUCUUCUUCAGGUACUGUGUCAUUGUAGAGAUUAAAUUUUGUGAGACUCUACAAGAUGCGUUCAAUUUGAGUUGGGACUCUACAAAUUGUGUUCAACUCAAACGAGGAUUCUUCGAGACUAUUCAACCCUAAACCCUAAUUUAUGCCUAUAUAAAGAGUACUAAAUUCUCUUAAAAGGCAUCUCGAAAAUUUCAUAAAGAGAUCAAGAUCUCGAAUACUCCACAAAUUGAUGGA	281	sch-miR6020a-5p	UGAUGUCUUUUAAGUAUCUUC	33-53	nta-miR6020a-5p	5	0	21	21	3
sch-MIR1916-1	CCUUAAAGUUGUCUGUAUAUUUCACUUAGACACCUCAAUUUAGCCUCAUACCUAUUGAACACUUUAUGUGUUCAAAAACAGUUCCUAGUGAAAUAUAUGAACAACUUUAUUU	112	sch-miR1916-1-5p	AUUUCACUUAGACACCUCAA	19-38	sly-miR1916	0	0	20	20	1
			sch-miR1046-1-3p	UAGUGAAAUAUAUGAACAACU	86-106	ppt-miR1046-3p	5	0	21	21	1
sch-MIR7828	UAUAAAUGGAAUGUAGAUAUUCUUCGUUAUUCUUUUAAGGUAUUAGCGUCUCUGUCUUUCAUAAAUUAGAGCAUAUAUGUUCUUCACUUUAACGAAGGGGCAGGAGCACUAAUGUCCUCAACGUAUGAUGACCGGGGCACCAAUACCCUAAAAGUAUGACGACAAGGGCAUUAAUGUCUCAAAAGUAUGACGGCAGGGGAAUCAAUGUCCCAAAAGUAUGACGAAGGGUAUUUGCAUACCAUUUACA	247	sch-miR7828-3p	GAUGACCGGGGCACCAAUACC	127-147	ptc-miR7828	5	0	21	21	1
sch-MIR4243-2	UGGUACGCUAAUCUUUACAAUUGUUGAAUUCGUAUAUAUAAAUAUUUCUAUCUUCUGUGAAGAUGUAACAAAAGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAAAUAUAUUUUUAUUUGUGUAGUAUCAUACCAUUGAAAUAGGGUGGCGUAUCG	198	sch-miR4243-2-5p	UUACAAUUGUUGAAUUCGUAU	15-35	ath-miR4243	5	0	21	21	1
sch-MIR5185m	UAAAUGCGUCAUUUAACUUUGAGUGGGCAGAUUUAGGUAUUCAAACACGUAUAAAAAUUGAACAAGCAGACAUAUGAGUUCUACAUGAUAAUACGCGUAGAAAAUCAUGUAGGAUGCAAAUUGUCAUGUAGGUUGUCAUGUAGGACGUAUGUAUCGAUUUCGUGUAAUUUUAUACGAGUUUAGCUGUCUAUUUAUACACACUAAAAGUUAAAGGGCAUAAA	221	sch-miR5185m-5p	UAUAAAAAUUGAACAAGCAGA	50-70	bdi-miR5185m-3p	5	0	21	21	1
sch-MIR812f	UAUACUUUAGGGACAUUGGUCCCCAUGCAUUUCAAAAAUUAAAUCGUAUAUGCCAUUCAUUCUAACGGAAGAUUAAACAAGGACACGUGACACAAUUUUAUCCAUCGAUCUGAUGUCGAGUCGAUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAUAUUAAGGGUAUAUAUGCUCUAGUUUUUGGACGGCAAGGACACCAAUGUCCCUAAAGUAUG	217	sch-miR812f-5p	ACGGAAGAUUAAACAAGGACACGU	65-88	osa-miR812f	5	0	24	24	1
			sch-miR8006-3p	UAGUUUUUGGACGGCAAGGACACC	177-200	stu-miR8006-5p	3	0	24	24	1
sch-MIR1847	CCCUUUUCGACCUACGUGGUACUGCUUGAAAAAAGUCAAUCAGCGUUGGCCCACAAGAUAGUGCCACGUAGGUCAAAAAAAG	83	sch-miR1847-3p	UGGCCCACAAGAUAGUGCCACGUA	48-71	osa-miR1847-2	5	0	24	24	1
sch-MIR159b-3	GAGAAAGACCAGAGUAUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUAGUAUUUUAU	216	sch-miR159b-3-5p	AGCUGCUAAUCUAUGGAUCCC	68-88	cas-miR159b-5p	1	0	21	21	1
			sch-miR159b-3-3p	UUGGAAAGAAGGGAGCUCUAC	174-194	sly-miR159b	0	0	21	21	1
sch-MIR7696b-2	GAGGACCUUUUACUCCUGCACUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUAUGUCCACGUGGACACGUUACAAGUUAUAAUAAUGCAAUAUGUAUUAUGU	165	sch-miR7696b-2-3p	ACAAGUUAUAAUAAUGCAAUA	71-91	mtr-miR7696b-5p	5	0	21	21	2

	CCACGUGUGCAUAUAUUACACCCUUAAAAUACAC UAUCAAAUAGUGUAGGGGUAAAAGGUCAUU										
sch-MIR5142-2	CUUUACUUUAACGAAAUAGAGAUAUGUGGCGCU AUCUUAUUUAUUGAUAAAUGUCGGAUCAAUAGAU AAGAUUGUGACACGUGUAUGUCUGUUAGUAUAA CGGUAUGU	108	sch-miR5142-2-5p	UUAUUUAUUGAUAAAUGUC	37-55	rgl-miR5142	5	0	19	19	2
			sch-miR3706-2-3p	UGUCGGAUCAAUAGAUAAGA	52-71	pab-miR3706	4	0	20	20	1
sch-MIR398b-2	GAGCAAUGGUGAAUUCCCAGAGGAGUGUGCCUG GAAACACAGGUGCAUUUUGGUCUUUUUUUUUUU UAAUUGCCGGACCAAAGUACACUUGUGUUCUCA GGUCACCCCUUUGGGAUCACCUUGUUU	126	sch-miR398b-2-5p	GAGUGUGCCUGGAAACACAGGU	23-44	stu-miR398b-5p	3	0	22	22	1
			sch-miR398-2-3p	UUGUGUUCUCAGGUCACCCCU	89-109	lja-miR398-3p	0	0	21	21	1
sch-MIR399i-2	CUUAUUAAGUGAAGCAUUUGUAGGGCAGUUCUC CGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCU GCCAAAGGAGAGUUGCCCUACGAUUGUUUCUGC UUAAUUAU	107	sch-miR399i-2-3p	UGCCAAAGGAGAGUUGCCCUA	66-86	stu-miR399i-3p	0	0	21	21	1
sch-MIR1440a	GGUAAAACAUAUAAAUAUAUGUUGAGAUGGCCGA GUUGGUCUAAGGCGCCAGAUUAAGGUUCUGGUC CGAAAGGGCGUGGGUUCAAAUCCCACUCUCAAC AUAUUAUAAUAUUUUUUUUC	120	sch-miR1440a-3p	GGUUCAAAUCCCACUCUCAA	80-99	osa-miR1440a	5	0	20	20	2
sch-MIR7997b-12	CUUUUUAAAACCUACGUUGCUCGGACUGUUCAA AAAUGUCGAAGGGUGCGUGUGUCAGAUUCUCCA GAAUUAGUGUAUUUUUGAAGAAUCCGACACUGG UGCAGCAUCAUUUUGAAGAGCCCGAGCAACAUA GUUUAAAACU	142	sch-miR7997b-12-5p	ACGUUGCUCGGACUGUUCAAA	14-34	stu-miR7997b	3	0	21	21	1
			sch-miR5303f-12-3p	AUUUUUGAAGAAUCCGACACUGGU	77-100	stu-miR5303f	3	0	24	24	1
sch-MIR482d-2	UUCAGAAAUUGGGAAAGGGAUGAAAAUUUUUGG GAAGCUUUUGGCGUGAGCGGUGGGGAAAGAUAG AUCUAUCAUAUUCGUAUGAUAUGAUAAAUCUUGC CUACACCGCCCAUGCCCAUGGCUUCCAAUUAUU UCUCCCUUUCCAUACAAUUUCUAUU	158	sch-miR482d-2-5p	CGUGAGCGGUGGGGAAAGAUA	45-65	stu-miR482d-5p	2	0	21	21	1
			sch-miR482b-2-3p	UCUUGCCUACACCGCCCAUGCC	95-116	sly-miR482b	0	0	22	22	1
sch-MIR5029	GCCUCUCUCACUUUAUAUACAAACACAAAUGUAU AAAUGUGUUUGUACAAAGUGAGAGAAAACUGCAU AUAUACAUCUCUUUUCGUCUAGCUCUCCCCUAG AGAAUCUCGUUCGCCUCUCUCACUCACCUUUCU CACUUUAUACAAACACAGAGACAAUUUGUGUUUG UAUAAAGUGAGAGAAAA	185	sch-miR5029-5p	AAAGUGAGAGAAAACUGCAUA	49-69	ath-miR5029	4	0	21	21	1
sch-MIR172d-3	GAUUCAGACCUAAAAAUCAAAAGUACUGAAUAGG CUGAAUCUGAAUGAUUAAGAUUCAGACCUCCAUU GAGUGCAAACAAAUGAGGCCUUAGUUGUCAUUU GUUUUCAUUAAGAUUAAGAGGUCUGAAUCUGAA UAAACAUCUGAAUAUUAAGAUUUGCAUUAAGAUU UGAGUGCUUUAAUCUGAGUA	188	sch-miR172d-3-5p	UCUGAAUGAUUAAGAUUCAGA	40-60	bra-miR172d-5p	5	0	21	21	2
sch-MIR8046-2	AGUUAAGGUGUUUCUCUGAAAUUUCGAUCAUAG UCUAAGAGGUACUUAGACAUUUUCCCAUUUCUG CUUCCUAGUUUCAUACUAGAAGAGCUUGUUGAA UUCUGAGGGAUACACCUAUAUCG	122	sch-miR8046-2-5p	CUCUGAAAUUUCGAUCAUAGU	14-34	stu-miR8046-3p	2	0	21	21	1
			sch-miR2093-2-3p	ACAUUUUCCCAUUUCUGCUU	50-69	osa-miR2093-3p	5	0	20	20	1
sch-MIR3706-2	UACACACGUCAUAAUCUUAUCCAUCGACCUGACA UCGGAUUGAUGGAUAAGAUUGUGUCACGUGUCC C	68	sch-miR3706-2-3p	CAUCGGAUUGAUGGAUAAGA	33-52	pab-miR3706	5	0	20	20	3
sch-MIR10532-3	GUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCU CUGCGAUUUCAGGCAUAGGUUGAGGGGGUACUU GGGUAUUUUCCCUUUAAUCUUACUCAUACUUUG AAUAAAAAGCCAGAUAUAUAGGGCAACCUAGGGA UCAAUGAGUGCUCUUUAUAAAAUACACAUUAGUU UAAAUGGGAUGGGCUAACUUACUCGUACUAAAAC GUACGACUUUCUAAAUGACAAGUUUAAGUUAUUA GAGCGAGUUUACAUUUAUAUACAUAAUUUGUCCU AUCAC	274	sch-miR10532-3-5p	AAGUGUGUCUCUGCGAUUUCAGGC	24-47	sly-miR10532	2	0	24	24	1

sch-MIR172b-2	UUUAGUGGUUUAUUGCUAAUGCAGCAUCAUCAA GAUUCACAUUUAAUUGCAUUUUAAAUGUCGAAUA UUUGAGAAUCUUAAUAGUGCUGCAUUUGCAAACA ACGACUGUG	110	sch-miR172b-2-5p	GCAGCAUCAUCAAGAUUCACA	21-41	csi-miR172b-5p	0	0	21	21	1
			sch-miR172-2-3p	UGAGAAUCUUAAUAGUGCUGCAU	70-92	aau-miR172	3	0	23	23	1
sch-MIR8039-2	UAGAACUAUUAGAUGUUACGUUUUCCUAUCUGAA CUAUCACCAUCGUUCAGGUAGGAAGAGGAAACAA UUGACAGUUGAGUUGUGUUUUAAUACAUAGAUG GUGAUAGUUCAGGUAAGCAAGGGGAACAACUGA UAGUUGGA	142	sch-miR8039-2-5p	UUUCCUAUCUGAACUAUCACC	22-42	stu-miR8039	0	0	21	21	1
			sch-miR8045-2-3p	AUUGACAGUUGAGUUGUGUUU	68-88	stu-miR8045	2	0	21	21	1
sch-MIR7997c-24	UAGUUCUUCAAUGUUUAAAGCUAUGUUGCUCAAA CCCUCCAAAAAUAUUGUUGCACCUAGGUCGGUU CCUUCAAAAAUGCAAUACUUUUGGAGGAUCCGAC ACGCAUCCAUCAACAUUUUUGAAGAGUACGAGCA ACAUAGGUUUAAAGAGAAAGAAGGG	160	sch-miR7997c-24-5p	AUGUUGCUCAAACCCUCCAAAAAU	23-46	stu-miR7997c	5	0	24	24	1
			sch-miR5303h-24-3p	AACAUUUUUGAAGAGUACGAGCAA	113-136	stu-miR5303h	2	0	24	24	1
sch-MIR8006-5	CUUAAACUAUCGUAAAUCAUAUACAAGUAUUCUU AGACAUACUUUAGAGAUAUUGUGUCCCUGCCGU UUAAAAACUAGAGUAUAUAUACCCUUCAGUCUAA CAUAAGACUAAAUAGGGACACAUGAUGCUAUCUU AUCCAUUCAUUCGAUGUCACCGGUGGAUAAGAU UAUGACACGUGUAUAUCCACUAGUAUAAAGGGCA UAUAUGUUCUAAUUAUUUAACGAUAGAGGCACCA AUGUCCCCAAAGUAUGACGGGAGAUAAUCGCAU ACUAUUUAUAAUAGUUUGGG	289	sch-miR8006-5-5p	GUCCCUGCCGUUUAAAAACUAGA	57-79	stu-miR8006-3p	5	0	23	23	3
			sch-miR5049e-5-3p	AAUUAUUUAACGAUAGAGGCA	213-233	hvu-miR5049e	5	0	21	21	1
sch-MIR1918-2	GAUAAUCAUAGUAGCUCAGUUGGUUUAACUAGU UGAAUUGUCAUUCUGUUGGUGAGAGUUCGAUUC UCCAUUACGCAAUCUCCUCUUCAAUUUAAGAGAA AAAAAUAUGCUACAAGGUGGAGAAUCGGACUACC GCUAACAGGAUGGAAGUUCAAAUACUUAAUCAAU UAAGCUACUAAUAUUUUA	186	sch-miR1918-2-5p	UGUUGGUGAGAGUUCGAUUCUC	47-68	sly-miR1918	0	0	22	22	1
sch-MIR11426b	CAAGGAGAAAUGAGGAUUAAAUUUCUUCCACCAG UAAAUACUACAACACUUGUUGUUGGUGAUCAAGU UCCGAAUCAACACACUCUUCCUCUACCUCUUCCU CUUCCUCUUCCUCUUCCAGUACUACUCGAUAUG AUGUAUCCAUUCGAAACUUGAUCAUAAUCAACCA GUAGUGUUGCAUUUACGAUGGAAGAAAUUGAUU UCUCCAUUCUCCUUA	217	sch-miR11426b-5p	CGAAUCAACACACUCUUCCUCU	71-92	pab-miR11426b	4	0	22	22	2
			sch-miR2673b-3p	CCUCUUCCUCUUCCUCUUCCAG	100-121	mtr-miR2673b	1	0	22	22	1
sch-MIR8727	CUCUCUACGUUGCUCGGACUCUCAAAAAAUGUC GCUACACCCAUGUCAGAUCCUCCAAAAAUCCACA AGUUUUGGAGAAUACACGCCCCUUGAUAUUUUU GAAGAGUCCGAGCAACAUAGAUGU	124	sch-miR8727-5p	CGGACUCUCAAAAAAUGUCGCUA	15-37	gra-miR8727	5	0	23	23	1
			sch-miR5303i-3p	AUAUUUUUGAAGAGUCCGAGCAAC	93-116	stu-miR5303i	1	0	24	24	1
	GGUUGGGGGUUCGAGCCCCCACAACCUCUUUGA UUUUUAGAGUUAAAUUCCCUACAAUAGGGAGGU UGUGGGUUCGAACCCCUCAGCCCCACCUUAUUA UUUUAGUUCAAGUUUCGCUAAGGAGGCUGUGAG GUGGUGGGUUCAAACCCCACAGCCCCUCUAUCU UUAUUUUAUUUAAAUGGGCGAGUGGCAAUGAGG UUUGUGGGAUCGAAUCCCCACUG	221	sch-miR482b-3-3p	UAAAUGGGCGAGUGGCAAUGA	176-196	eun-miR482b-5p	5	0	21	21	2
sch-MIR6111	UGGCAGCAAUUAAUUUUGCAGCCAUACAUGUUG AAAUUACUAGCCACAAAUGUGAAAAUUUGUAGCC ACAAAUGUGAAAGUUGGUAGCCACAUUUGUGGA AGUAGGUAGUCAAAGUUUGAUAUAAGUUUGGUA UAAGUUUGAUACACUUAGGCAGCCAAAUUUUUG UUGAAA	172	sch-miR6111-5p	CAUACAUGUUGAAAUUACUAGC	23-44	cca-miR6111-3p	5	0	22	22	1

			sch-miR6248-3p	CAUUUGUGGAAGUAGGUAGUC	91-111	osa-miR6248	5	0	21	21	2
sch-MIR8039-3	UAGAACUAUCAGAAGUUACGUUUUCCUAUCUGAA CUAUCACCAUCUUUCAGGUAGGAAGUGAAAACAA UUGACAGUUGAGUUGUGUUUAAAUACAUAGAUG GUGAUAGUUCACGUAAGAAAGGGGAACAACUGA UAAUUGGA	142	sch-miR8039-3-5p	UUUCCUAUCUGAACUAUCACC	22-42	stu-miR8039	0	0	21	21	1
			sch-miR8045-3-3p	AUUGACAGUUGAGUUGUGUUU	68-88	stu-miR8045	2	0	21	21	1
sch-MIR156j	UCAAAGGCUAAAAACACAGCUGACGACUCGUUGA UUCUCAAACACAUCAAGAAGUAUUUUUUGAAAUU GACGUGUUUAAGAUUCAACGAUGCGUGAGCUAU GUUUAGCUAGCGUUGUC	118	sch-miR156j-5p	AGCUGACGACUCGUUGAUUCU	18-38	csi-miR156j-5p	4	0	21	21	1
			sch-miR4414a-3p	AUUCAACGAUGCGUGAGCUAU	81-101	mtr-miR4414a-3p	4	0	21	21	1
sch-MIR395a-2	UUGAAGUCCUGCUGAAGUGUUUGGGGGAACUCU UGGACUCACUUUGAAAUUUUACACAAACAAAUAA AAGUGUAGGAGUCCUGGCUGUGGAUGAUGAACA UGAUAGUUCACGUAUAAAUCUAUUAAGGUGAUCC CUAGAGUUCCCUUGAGCACUUCAUGAGGGCUUA CU	169	sch-miR395a-2-5p	UGAAGUGUUUGGGGGAACUCU	13-33	aof-miR395a	0	0	21	21	1
sch-MIR395c-3	AGUGUAGGAGUCCUGGCUGUGGAUGAUGAACAU GAUAGUUCACGUAUAAAUCUAUUAAGGUGAUCCC UAGAGUUCCCUUGAGCACUUCAUGAGGGCUUAC UUUGAUGUUAGAAGCAUUGUUGAAGUGUUUGGG GGAACUCCUGGGUUGACUUUAAAAAUUACGCAAA CAAGUUUAUAUAAAUGCAUGACUACGUACUAG	199	sch-miR395c-3-3p	UUGAAGUGUUUGGGGGAACUC	120-140	cme-miR395c	0	0	21	21	1
sch-MIR1533-3	UUUUUUAUAAAUAAAUCGCUGCCCGGGGCAGCG AUUUAUGUAAUUUUUUUUUUUUUUUUAAUAAAUC GCUGCUUGGGCAGCGAUUUAAUAAAAAAAAAAAG CAGCGAUUUCAUUUUUUUAUUAAAAAAAAAAAAU UUGCUAAAUCGCUGCCGGAGCAGCGAUUUACCU UUGUAAAUCG	178	sch-miR1533-3-3p	UUAAUAAAAAAAAAAAGCA	85-103	gma-miR1533	5	0	19	19	2
sch-MIR5628-1	UAAAACCCUGAAGUAAUAUCUCUCCAGUCAUCUC AUCCGUAUUUCUCGAAUAGGUUGCUAAUUCUAG CAUUAGAGAAAUAUGGAAGAGGUGAUUGGAGAA AUAUUUCUAGGUGUUACG	118	sch-miR5628-1-3p	GAAAUAUGGAAGAGGUGAUUG	75-95	ath-miR5628	5	0	21	21	1
sch-MIR6196-1	UAAUCAAUGAUUUGCGAAGAUUGCAAUAUUAUUU UUGGAGUCCCACAUCGUCAGUGGGAUGGGAAUA UGGAUUCCUUAUAUGGUCUUCGGUAAUAUGAAG AAUUAGGUGAAUAUGAUAAGGAGAUGGAGUUGA UAAAUGUUCCUUUGACUCUGGUAUAAGCGGCAA AGAAACACUGCCAUCCUCAAUCUUCUCAUCAUAA GCAUCUUUUUUUUUUUAAAGAAUAAUGUAGGAU GAUAUCUUGAAGUAAAGUGUUGCAAUCUCUCAC UAAAUAUAGAAAU	279	sch-miR6196-1-5p	AUGAUAAGGAGAUGGAGUUGA	113-133	hvu-miR6196	5	0	21	21	1
			sch-miR3631b-1-3p	UGUAGGAUGAUAUCUUGAAGU	226-246	vvi-miR3631b-3p	5	0	21	21	1
sch-MIR6273-2	AAAUCGCUGCUCCGGCAGCGAUUUAGCAAAAUU UUUUUUUUUUAAUAAAAAAAUGAAAUCGCUGCCC AAGCAGCGAUUUCAAAAAAAAAAAAAAAAAUUUUU UUUAAUAAAUCGCUGCCGGGGCAGCGAUUUAUA AAAAAAAAAAUUUUUUUAUUAAAUCGCUGCCCA AGCAGGGAUUU	179	sch-miR6273-2-5p	GAUUUAGCAAAAUUUUUUUUU	20-40	ppe-miR6273	5	0	21	21	2
sch-MIR5720	AAUCAAAAAAAAUAAAUAAAUAAUGAAAUCGCUGCA GGGGCAGCGAUUUCAUUUUUUUAUUAUUAUUAA AAUCGCAUUUUGCAAAAUUGUUGCAGAGGCAGC GAUUUUGCUUUUUCCGGUGGGGUAAGUCGCUGU UGGUGCAGCGAUUUUUACCUUUUUGGUUAAUAU AAAAUUUUAUAUACCGUUUUGAAAUUUUUGUUAA UAUUUUAUACCCUUUAGGCUCCGGACUCUCAGU UGUAGUUAGUUGUUGAUUCAUUCAAGUUGUAUU AGUACAAUUUGUAGACAAGUUUGAUUCAAAAUUU GUGAUUUUUUUGGAA	316	sch-miR5720-3p	UUGUGAUUUUUUUGGAA	300-316	bra-miR5720	2	0	17	21	1
sch-MIR1054	AUUCACCCACCUAACCCGACCCAUUAAAAAAUAU GAUGACUCAUUUUAUUUUGUCUUUAAUCCUAAAU	161	sch-miR1054-3p	UAAUCCCUCUCUUUAAACCUU	69-89	ppt-miR1054	5	0	21	21	1

sch-MIR9563b	UAAUCCCUCUCUUUAAACCUUGAAUUAGGAUUAA AGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUU AAUGGAUCGGGUUAGGUGGGUGGAU UGAAUUUUUUCACCCUCGCUUUUGUUGGUGAA CCUUUUUGUUGGCUGACGUAACUUAGGCUAGGU UCAUAAGAAAGAAGAGAUGAAUUCUAAACUGUUA AAAGCAAUGUUUGGCCACUUCUUGGGCAAAAUAA CUGCAAGAAAGCUACGUUAGCCUACAAAAAGGUU CACCAACAAAAAACGAUGGUUUAGAAAAAUCCA	201	sch-miR9563b-5p	GAAAGAAGAGAUGAAUUCUAAA	73-94	bra-miR9563b-3p	5	0	22	22	2
			sch-miR2592bl-3p	GAUGAAUUCUAAACUGUUAAA	82-102	mtr-miR2592bl-3p	5	0	21	21	1
sch-MIR11466b	GACCUCGUUUGCCUCCUCGAAAAGAAACUUGAU UUUCCGUCUUGAAAGUUUGCCCAUGAAAUAAGC AGAGGUCAGUCAAACAUUCAAGACAAGAAUGACU AUUUCAUGGUAAACCUUCAAGAUGGAAAUCAAAU UUCUUCCGCGAAAGGCAAACUAGAAA	160	sch-miR11466b-5p	GCCUCCUCGAAAAGAAACUUG	11-31	pab-miR11466b	5	0	21	21	2
			sch-miR4348c-3p	UGGUAAACCUUCAAGAUGGAA	107-127	gma-miR4348c	5	0	21	21	1
sch-MIR1886f-3	GCCAUGCAAUGCCAUAUCACGAUAUGAUAUCGU GAGAUGGAAUCAGCGUUUGAAUAUGCAAUUUCA CGCUGAUUCCAUCUCAUGAUACCAUAUCAUGAGA UGUGAUUUCAUAUU	114	sch-miR1886f-3-5p	AUGAUAUCGUGAGAUGGAAUCAGC	24-47	stu-miR1886f	2	0	24	24	1
			sch-miR1886h-3-3p	AUUUCACGCUGAUUCCAUCUCAUG	61-84	stu-miR1886h	3	0	24	24	1
sch-MIR1886f-4	UACCAUAUCACGAUAUGAAAUCAUGAGAUGGAAU CAGCUUUUAUGACAUGCGAUUUUAUGUUCAUUC CAUCUCAUGAUUUCAUAUGAUGAGAUGUGA	97	sch-miR1886f-4-5p	AUGAAAUCAUGAGAUGGAAUCAGC	15-38	stu-miR1886f	4	0	24	24	1
			sch-miR1886h-4-3p	AUUUUAUGUUCAUUCCAUCUCAUG	53-76	stu-miR1886h	3	0	24	24	1
sch-MIR5256-1	UCCAACCUCUUAAUAGAUUAUACUUAUUUAUUAU GUAAUAAUAAUGGUUUAAUAAUCAUGUCGUCUG GUCACUACUACAGUUUUCUUCUUUGAUCAGUUA CCCUAACAGCGCCUCAAUUUUGUUUACUCCCCU AAACGGCCUUCUUGCCUAUCGGUUUCAACCUUA GGAUGACAUAGUCUGGGCAUACUUAUUCGCAGA AUAUUUCUGUAGUAAACUUUCUAAUGAUGGUUAU UAUAACAUUAUUAAAACAUAAUAGACAAUUAUAAU CAAUAAGAGAUUAUC	283	sch-miR5256-1-5p	UUAUUUAUUAUGUAAUAAUAA	24-44	mtr-miR5256	5	0	21	21	1
			sch-miR1438-1-3p	AUGGUUAUUAUAACAUUAUUAA	226-247	osa-miR1438	5	0	22	22	1
sch-MIR7981-12	GAUACACAUUUUAAUUAAACUAAGGUCCUAUUAC CGCCAAACUCAUUCUUUUUGUGAUUUGAUAAUU UUUUUUUGCUUAUAUGGUACACUCUAUGACUUC AUGCAAUUGAGGUGCAUUGGAAAUGUUUGGCUU AUGUGGCACAAUCCAAGUAAAAGAUGUAUUUUUA AAAUUACACAAAAAUGGGCUCGGGGGAAUAAUAA GACCUUAGUCUAGUUAAAAUGUGUCUU	228	sch-miR7981-12-5p	UUUAAUUAAACUAAGGUCCUAUUA	10-33	stu-miR7981-5p	2	0	24	24	2
			sch-miR7981-12-3p	AUAAGACCUUAGUCUAGUUAAAAU	198-221	stu-miR7981-3p	5	0	24	24	1
sch-MIR319h	CUUCUCGCUUCUUCAUCUGAAGCGAGCGCCUUU UUCAGAUCGCAUCGCCUCAGGAGAAAGAAGCGC AGUGG	71	sch-miR319h-5p	CUUCAUCUGAAGCGAGCGCCU	11-31	mes-miR319h	5	0	21	21	1
sch-MIR7986	ACAGCAUUAGGUUGAUAUAUGUUACUGUAAGUAA CGUUUUACUUUUAAAACGUUAUUUUCAGUAACGU UUUACUCCUAAAACGUUACUGUGAGUAACGUUU UAGGAGUAAAACGUUACUGUGAGUAACGUAUAU CAAUCUGACGCCAA	148	sch-miR7986-5p	CUUUUAAAACGUUAUUUUCAGUAA	42-65	stu-miR7986	5	0	24	24	3
sch-MIR1886f-5	GUCAUGCAAUACCAUAUCAUGAUAUGGUAUCGU GAGAUGAAAUCAGCGUUUGGACAUGCGAUUUUA CGCUGAUUCCAUCUCAUGAUUCUAUAUCAUGAG AUGUGAUUCCAUAUU	114	sch-miR1886f-5-5p	AUGGUAUCGUGAGAUGAAAUCAGC	24-47	stu-miR1886f	0	0	24	24	1
			sch-miR1886h-5-3p	AUUUUACGCUGAUUCCAUCUCAUG	61-84	stu-miR1886h	2	0	24	24	1
sch-MIR167d-3	UUCCGCGAAACCAUUAACAGGUGAUGCUGCCAC AUGAUCUGAUCUUUCCUCGUACGGAGCAAUAGA AAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCU	113	sch-miR167d-3-5p	UGAUGCUGCCACAUGAUCUGA	22-42	eun-miR167d-5p	1	0	21	21	1

	AGUGGUUCACGAUC										
			sch-miR167h-3-3p	AUCAUGCUGGCAGCUUCAACUGCU	76-99	gma-miR167h	1	0	24	24	1
sch-MIR167h	UUAUCAAGAAAGGAAGGAGUGAGGCUGUCCGAG CAUGACCUAACCUUAGUCACCCAUUUUCUUUAUA AAUGGCCAAGUUUAGAUCAUGCUGGCAGCUUCA CUUGUUCCACUCUAGACCC	119	sch-miR167h-3p	AUCAUGCUGGCAGCUUCACUUGUU	83-106	gma-miR167h	3	0	24	24	1
sch-MIR11592-1	AACACCGGAAAACCGAAAUACCGAACCGAACCGA ACCGAAAUUUUUCAGAAUUUCGGUUUCGGUAUU UCGGUUUUUGGUUCG	82	sch-miR11592-1-5p	GAACCGAACCGAACCGAAA	23-41	cas-miR11592	0	0	19	19	1
sch-MIR11079	UGUAUAUGUAUAUUGGUUGCUGUCUAGUUUUUC GAGCAAAUGUUGGUCGGCUAAUUUUAUUAGUAU UCUUUCUUGUUGAAAGUUUUUGGAUGUUGGUGU GGUGUCGAAUGUCUUCAUGACGACCACAUUGAU CGCAUUUAUGUGGAAGAGGGCUUUUUUGGUAGA UGCUUUGAAAGUAUUUGAUGCAAUGGUUAGCGA CGAGUUUGUCGGGAAAACGCGGACGAGCACAAA AAUAUAUAUGGU	243	sch-miR11079-5p	GUGGUGUCGAAUGUCUUCAUGA	98-119	lja-miR11079-3p	5	0	22	22	1
sch-MIR6164b-1	UACUUUAAUAUUGCGAGUCUUAAAAGUAUUUAUU UCCUUUUUCUAUUUUCGUACGAUUUAUGAACGU CACGUAAAUUGAAAUAGAAGAAGGUCUAUAAACU UAAUUAUAGAUGCCAAUGCACACUUGGGGAUGU AGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCG AGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAU AUUUUUUCAUAAUUUUCCUAUUUUUAAUCGGAAU AUAAUUAACAACGUAUGAUUAAAUUAAAAGAAAU ACAUUUAUAUAACUAUCAAUAUGAAACAU	297	sch-miR6164b-1-5p	UCACGUAAAUUGAAAUAGAAG	67-87	nta-miR6164b	4	0	21	21	1
sch-MIR7984c-2	UCCGAACUUUGAUAGAAAUUUGUGUUACGAUAU UGAACUUUAUGGAGGACCUUUUUACCCCUUUGC ACUAUUUAAUAUUGUAUUGUGCUCACGUAGACAU CAUAAAUGUUGCAUCUUUUUAAAUAGUAAUGUGU CACGUGGGCACAUAUAUACCUUUAAAAUACACUU UUAAAAAGGGUAGCGGUAAAAGGUCUUUCAUAAA AUUUGGUAUCGUAACUGCUAUUCCGCCAAAGUU CAAA	239	sch-miR7984c-2-5p	ACGAUAUUGAACUUUAUGGAGGAC	27-50	stu-miR7984c-5p	4	0	24	24	1
			sch-miR7984b-2-3p	GGUCUUUCAUAAAAUUUGGUAUCG	190-213	stu-miR7984b-3p	0	0	24	24	1
sch-MIR11088a	UGUUUGGUUUGACUUGAUUUGGUGUUGGAAAAA AACCCGACUAUAUUUGGGUUGGGUUGGUUUCAA CUGGAAAAAAACCAACUCGAGCCCAAACCAACCC	100	sch-miR11088a-3p	AUAUUUGGGUUGGGUUGGUUU	43-63	lja-miR11088a-5p	5	0	21	21	1
sch-MIR8586	CAAAAAUUCUAAAACGGUAUAUGAAUUUUUAUUU UAACAAAAAAGGGAAAAUCGCUGAAAGAGCAGCG AUUUCGCUCGCCGGAAAAAAUAAAAUCGCUGCAA UAGCAGCGAUUUGCAAAAUUUGAUUUAAAAAAAA AUUAAAGAAAUCGUUGUCUUGACGAUUUCCA	167	sch-miR8586-5p	UUUUAUUUUAACAAAAAAGGG	27-47	atr-miR8586	5	0	21	21	1
			sch-miR6232b-3p	AAUUUGAUUUAAAAAAAAAUU	119-139	sbi-miR6232b-3p	5	0	21	21	1
sch-MIR8008b-4	UUAUCCGUCGCUUUUUUGCUUUAUUUUUUUCAA AUAAACCCAGAAAAGCGACGGACAAGGUUCUUUG GUCCGUCACUUCUCUAGGUAUUUUAAAAAAUUAA UUUCAAUGAAAGCGACAAACAUUGUCCUUUAGUC GUCCCUCGCUUUUCUGGGAUUUUCAAAAUAUAA AUUUAAAGAAAGGCGACGGACUG	191	sch-miR8008b-4-5p	AAACCCAGAAAAGCGACGGACAAG	36-59	stu-miR8008b	2	0	24	24	1
sch-MIR902j	CGUUCAGACAUUAGGUCAUUAAAUGCAUUUUUU UAUCACUUAAAAAUCUCUUAAUGAGUCUAAAAGG AUCUGAAUUGAACCAAAUUUGAGGCAAAGUCUUA GGCCUCAUUUUUGCACUUAAUGAGGAUCUGAAU AUAAUUAUUCAUAUUUAGUCCAUUAAGUGCGUUG GACUUUUAGGUCUGAAUCUUAAUCAUAUGGGUC UUAAUGAGUCUAAAUGAGUAAGAUCUAUAACAUA GCCUUAGGCCUCAUUUGUUUCCAUUAAGAUUAA GACGUCUGAAUCUGAAUAUUAAGAUAUGCAUGAA GAUCUAGAUGUGUAGAUCU	321	sch-miR902j-3p	AGUAAGAUCUAUAACAUAGCC	218-238	ppt-miR902j-3p	5	0	21	21	1
sch-MIR7981a-33	ACUAUACUAAGGUUCUAUUACCCCCCUGAACUUA UUUUAGAAGUAAUUUUCUACCCACUUUCGACCUA	193	sch-miR7981a-33-5p	ACCCACUUUCGACCUACGUGACAC	53-76	sly-miR7981a	4	0	24	24	1

	CGUGACACUAGCUUUUAGAAAAAAGUCAACCAAC GUUGGGCCACAAGAUAGUGCCACGUAGGUCAAA AAGGAGCAGAAAAUUAUUAAUAAAAUAAAUUCAG GGGGUAACAGGACCUUAGUAUAGU		sch-miR7981-33-3p	ACAGGACCUUAGUAUAGU	176-193	stu-miR7981-3p	3	0	18	24	1
sch-MIR5721	ACUAUUAAAUUAGUGAAAACAAAAGUAGUGUGUA CUUCCUAGUGAUAUCUAAGAGAAUAUUGAAAAAU GAAGUGUGAACUGUGAAGACAAGUGUUAAUACC AAUAGGGGGUGUCAAAUGGGAGGGUAGUGUUGA AAUUGGAGAUACUAAAAUGGGUUAAGACAAAAAU UAGGUUGGCUCUUGACCCGCCCAAGUUUACUUU GGGCUCAAAUGGAUUGGGUUCAAAAGGGCUAGA AACAGGUUGAGUCUUGACCAGCCCAAUUUGACC UGAUUAAUCUAAAUAAUUAACAUAGUGAUAUUUA ACUUUUAUAAUCACAAUUUGAAUUUU	327	sch-miR5721-5p	AAAAAUGAAGUGUGAACUGUG	63-83	bra-miR5721	5	0	21	21	1
			sch-miR7734-3p	UUAACAUAGUGAUAUUUAACU	284-304	bdi-miR7734-3p	5	0	21	21	1
sch-MIR7984c-3	UUGUUGUUACGAUAUCAAACUUUAUGGAGGACA UGUUACCCCCUGCACUAUUUAAUAAUGAAUUUUA AAAGUAUAUAUGUGUCCACGUGGACACAUUACUA UUUAUAAUGAUGCAAUGUUAUGAUGUCCACGUG GACACAUAUAUACCUUUAAAAUACACUAUUAAAU AUUGCAUGGGGAUAAAAGGUCCUUUUCAAAAUU CGAUAUUCUCACAACAA	218	sch-miR7984c-3-5p	ACGAUAUCAAACUUUAUGGAGGAC	9-32	stu-miR7984c-5p	2	0	24	24	1
sch-MIR8006-6	GCCGUCAUAUUUUUGGAACAUUGGUGUCCUGCC GUCAAUAAACUAGAACAUAUGUACCUUUAUAUUA AUGGACAAACACGUGUCAUAAUCUUAUUCAUCGA UCCAACAAUUAUCGACGAAUAAAAUUAGUCAUGU CUCCCCUAUUUAAUUUUCAGUUAGAGUGAAAGAC AUAUAUGCUCUAGUUUAUGGACGGCAGGGGCAC CAAUGUCCCAAAAAUAUAACAUA	225	sch-miR8006-6-5p	UGUCCUGCCGUCAAUAAACUAGA	25-47	stu-miR8006-3p	4	0	23	23	1
			sch-miR8006-6-3p	UAGUUUAUGGACGGCAGGGGCACC	180-203	stu-miR8006-5p	2	0	24	24	1
sch-MIR8601	UUUAAUGUCUUUCAGAUCUCUUUUAGAAAAUUUU UUGGCAAAUUUGGUCGCCUUGCGAUGAGCUGUU UUAGCUUCCUUCUUUUCCUUAUAUCGUUUUGAA CGAUGACGUCUUUUGUAGGAUCUCUUUUUAUCA ACCUCUUCAUGAGAUUUCUUCUUUCUAUUAGGG UGAGAAGGUCCUUCAAUAACGAAUUGUGCACAAA AGUCUCCUAAUUGAGAUCUUUUUGACAUUUGG	232	sch-miR8601-5p	UGCGAUGAGCUGUUUUAGCUU	54-74	atr-miR8601	5	0	21	21	1
			sch-miR11466a-3p	CUCUUCAUGAGAUUUCUUCUU	136-156	pab-miR11466a	5	0	21	21	1
sch-MIR7985-1	AAACCUUCGGGGUUGCCCAGUGGUUUGGGCUUU GGACUUCCAUGUUAGAGGUCUCAAGAAGCAAGG GGUUUGCCUUCCGGGUCGAGCUCGUCGCACCG GGCUUGCCUAGUGCGGGUUACCUCUCCUAUGUG GUUUGCGAGCUAUUGCAUAGGAGCGAGAGUCUU ACCAUGUGCACACCCAAAGGGUA	187	sch-miR7985-1-3p	CGGGCUUGCCUAGUGCGGGUUACC	97-120	stu-miR7985	2	0	24	24	1
sch-MIR7992-10	UUUAUUCCAUUCAACUUUGGGUAUGCACAAGUA GACACUUAAACUUGAACAAGUAGACACAUGAGUC UUACGUGGUACGAUAAAUGUAGGACAUCACGUA GGGUAAAAAAUGACAUUUAGGAGGUCAUGUUAG ACAUGUGUGUCUAUAUGUUCAGCUUUUAUACAA GUUUAAAUGUCUACUUGUUCACACCCAAAGUUGA AGGGCAUAAA	210	sch-miR7992-10-5p	UUUGGGUAUGCACAAGUAGACACU	16-39	stu-miR7992-5p	5	0	24	24	1
			sch-miR2101-10-3p	GCUUUUAUACAAGUUUAAAUGU	155-176	osa-miR2101-5p	5	0	22	22	2
sch-MIR394b-2	AAAGGUAUAUAUGUGCUCACGUGGACAUAUUGC AAGUUAUAAUGAUACAAUAUUUAUGAUGUCCAUG UGGGUACAUAUAUACCUUU	86	sch-miR394b-2-5p	ACGUGGACAUAUUGCAAGUU	19-38	aly-miR394b-3p	5	0	20	20	1
sch-MIR535f	UAUUAUGCAUGAUUCCGGUGGAGCUUACAAUAG CAAGAAAAUGAGAGAGAGUAAAAAUCUCUCUCAC UGUCUUGCUGUUGUAAGCUCCACCGAAAUUAUG CUUAGGG	107	sch-miR535f-3p	AGAAAAUGAGAGAGAGUAAAA	36-56	csi-miR535f-5p	5	0	21	21	2

sch-MIR7997c-25	UAACCUAUGUUGUUCGUACGCUUCAGAAAUGUU UGCAAGCCAGUGUUGGAUCCUCAAAAAAUGUGU AGCUUUCCGAAGUAUCUAACACACGCUAGGCUA UAUUUUUGAAGAGUUCGAGUAACAUGGACU	129	sch-miR7997c-25-5p	AUGUUGUUCGUACGCUUCAGAAAU	7-30	stu-miR7997c	5	0	24	24	1
			sch-miR5303-25-3p	UUUUUGAAGAGUUCGAGUAAC	102-122	sly-miR5303	1	0	21	21	1
sch-MIR2868-2	ACUUUGUUUUGUGUAGUAGAAAUCGUAUUGUAG GUAAAGUCGAGAGGUUCAUCGCGAUAAUUUCAC GUGCAAUAGUACAAUUUUUUCUUUUCCUCCAAAG UCAUAUGAUAAAGUAUUCUUAAGUUUAGCUGUAG UAAUAUUUCUAGUGAACAGAACAAGGU	161	sch-miR2868-2-5p	UUUGUUUUGUGUAGUAGAAA	3-22	osa-miR2868	1	0	20	20	1
			sch-miR2275a-2-3p	UUUCUUUUCCUCCAAAGUCAUA	84-105	bdi-miR2275a	5	0	22	22	1
sch-MIR6108f	GUCGCCAUUAGCUCGCCAUACCUCGCCAUAGGU CGCCUUUUUUGGGUCGCCUCGCCUCGGUGUGG AAUGGCGAGAAGGGCUCG	83	sch-miR6108f-3p	AAUGGCGAGAAGGGCUCG	66-83	cca-miR6108f	5	0	18	21	2
sch-MIR5669	AUAUGGACGACCCUUUACCCCCCUGCACUAUUU AAUAAUAUAUAUUAAAGGUAUAUAUGUGCCCACG UGGACACAUUACUAUUUAGUGAUGUAAUAUUUAC GAUGUCCGCAUGAGCACAUAAGUACCUUUAAAAU ACACUAUUAAAUAAUGUAGAGGGGUAAAAGGUCC GUUCCAAAG	178	sch-miR5669-3p	UAAUGUAGAGGGGUAAAAGGUC	147-168	gma-miR5669	5	0	22	22	2
sch-MIR7980b-2	GCCAUGCGAUACCAUAUCAGGAUAUGAUAUCGU GAGAUGGAAUCAGCGUUUGGAUAUGCGAUUUCA CGCUGAUUCAAUCUCAUGAUUCCGUAUCAUGAG AUGUGAUUCCAUAUU	114	sch-miR7980b-2-5p	GAGAUGGAAUCAGCGUUUGGAUAU	34-57	stu-miR7980b-3p	2	0	24	24	1
			sch-miR1886h-2-3p	AUUUCACGCUGAUUCAAUCUCAUG	61-84	stu-miR1886h	4	0	24	24	1
sch-MIR7992-11	GACAUAUACGAACAAACAUUCAAACUUGGUCUCA GAUCGUUAGUAAGCACUCCAACUUUGAGAGUGC ACAUCUAGAGAUUUCAGUUCGUCUCCACUGUGU CAGUUGAACACUUCGAAGUGCUUACUUGCCGGU UGAGGCCAAGUUUGAGCGUAUGUUUAUAUAUUA C	167	sch-miR7992-11-5p	UUUGAGAGUGCACAUCUAGAGAUU	57-80	stu-miR7992-5p	4	0	24	24	1
sch-MIR6430	UUUUUGUACUGUGUCAAUGUACAUAGUUAUGGU AUACCUGGCUAAGAUGAUAAGUAAAUGACUGAAC AUCAUUUUCAUGCCUAUUAAUUUAUAUAGGCAUA GUGCAUAAACAAACGAACUUGGAGUCAGCUGGC GAGUAAGCACUCCAACUUUGAGAGUGCACAUCU AGAUACCUUAACUUGGUCUCAUUGGCAACUAAAC CC	203	sch-miR6430-5p	UGAUAAGUAAAUGACUGAACA	48-68	ptc-miR6430	5	0	21	21	1
			sch-miR7992-3p	UUUGAGAGUGCACAUCUAGAUACC	151-174	stu-miR7992-5p	4	0	24	24	1
sch-MIR8634	GGGAGAGGGGAGCUGCAUUUCAUGCCCGCAGGU GUAGACGCACAGNUUAUAUGUGUGAUUGGUAUU UCUGUGGAUAAUUUGGGUUGUUGUCGGAUUGG GAUGAAGUAAGGAAAAUAGGGGAAGUGAUGCCG AAUUUUCGUUAGAUUAUUAGCUAGCUUACGAUAA GUAGUAAAGCGCGACGUUUCUCUAAUUGCGGCA UGAUUGUUCUUGUUAUUGAUUAAUAGCUUGAGC AAUAAAUAUUGGACGUGCAGCUCGACAAUACGG UAUGUAAUGCUACCCCUUCUUUC	287	sch-miR8634-5p	UUGGGAUGAAGUAAGGAAAAU	95-115	gra-miR8634	5	0	21	21	1
			sch-miR6288c-3p	CUUGUUAUUGAUUAAUAGCUU	207-227	ppe-miR6288c-5p	4	0	21	21	1
sch-MIR7985-2	CUCACCCUUUGGGGUGGCCCGAUGGUUUGGGC UUGGGACUUUCAUGUUGUUGGUCUCAAGUUCGA AACAACUUACCAGUGAAAGUAAGGGGUUUGCUU UCUGGGUCGAGCUCGUCACACCGGGCUUGCCUA GUGCGGGUUACCUCUCCUAUGUGGUUUCCGAGC UAUUGCAUAGGAGCGGGGUUUUUACCAUGUGCG CACCCAAAGGGUAAC	212	sch-miR7985-2-3p	CGGGCUUGCCUAGUGCGGGUUACC	120-143	stu-miR7985	2	0	24	24	1
sch-MIR403b	GCAGAGAUUCGAAAAAGCCAUAUUACGAGCUUG UGCGUGAAUCUAGCAAACACUAACAGUUUUUCU GAUGAAAAGAGUUGUUAGAUUCACGCACAAACGU GAAAUAUGCCUCUUCCUGAUUUUCAAU	127	sch-miR403b-5p	AGCUUGUGCGUGAAUCUAGCA	28-48	csi-miR403b-5p	3	0	21	21	1

			sch-miR403b-3p	UUAGAUUCACGCACAAACGUG	81-101	gma-miR403b	1	0	21	21	1
sch-MIR7984b-5	UUGAGAAAAAAGUCUGAAAUAUAUUUGAACUUUA AUCGAAAUUAUUAUAACGAUAUCGAACUAUGGAA AGGACCUUUUACGCCCCCACCCCCGCAUUAUUU AGUAGUGUAUUUUAAAGUUAUAUUUAUGUUCAC GUGGACAUCAUAAAAAUUGCGUCAUUAUUAAAUA AUCCAAGGGGGUAACAGGUCAUUUCCAAAGUUC GGUAUCAUUACAGCAAUUUCAAUCAAAAUUUGGA UAUAUUUCAAACCAUUUCCUUUG	258	sch-miR7984b-5-5p	AUAUCGAACUAUGGAAAGGACCUU	53-76	stu-miR7984b-5p	3	0	24	24	1
			sch-miR7984d-5-3p	CAAUUUCAAUCAAAAUUUGGAUAU	215-238	stu-miR7984d-3p	4	0	24	24	1
sch-MIR7983-7	AUGCCUAUAUCACUACAACAAAAAUGACCAUUAG CAGCAUUUAAUUCUUAGUUGCCGCUAAAUAUGUA UUUUUAGCGGCAAUUUUCACUCUUUGUAUAUGU CCGUAAAGCCUUUAGUGAAUUGGUUCUAAUGAC ACUUAACUAAUGCCGGUAAAGACUUUAACACUCU UUAUUAGUGUCAAUAUUUAAUGCCGCUAAAAGUU AUUUUUGUUGUGGUGUAUAAAGGGUA	228	sch-miR7983-7-3p	ACUAAUGCCGGUAAAGACUUUAAC	140-163	stu-miR7983-3p	0	0	24	24	1
sch-MIR5026-4	CUACCUUUUUCAGCCUACGAGACACUAGCUUGA AAAAAUGUCAACACGCACUGGACCUAGAAGAUAG UGUCACGUAGGCCGAAAAGGGGAU	91	sch-miR5026-4-3p	ACCUAGAAGAUAGUGUCACGU	55-75	ath-miR5026	5	0	21	21	1
sch-MIR1533-4	AGGGUGAAGUGGGAGGACGACCAAGGACAAAUA UGUAAUUUAACUCUAACAAAAAUCUAAGAAGAAA GAAAUAAAUAGUUCUAGAAUUAUCUUUUUAUAUA CGAAGUGAAUAAUGAUCAAGGGAAAAAUGUGAUU CACGCUAACAAAAAAUUAGUAAGAAAAAUAAUAAA CAAUUCUAGAAACAUCUUUUUGUCUUUGGUCGC CCUCCCACUUCACUUU	219	sch-miR1533-4-3p	GUAAGAAAAAUAAUAAACA	154-172	gma-miR1533	4	0	19	19	2
sch-MIR8030-4	AUAUAUAAUGUUGGGUUGGUUUGGUCUCGGGUU GGUUAUUUUAAAUUGAAACCAACCCAACCCAAAU AUAGUC	73	sch-miR8030-4-5p	UUGGGUUGGUUUGGUCUCGGGUU	11-33	stu-miR8030-5p	0	0	23	23	1
			sch-miR8030-4-3p	UUGAAACCAACCCAACCCAAAU	46-67	stu-miR8030-3p	3	0	22	22	1
sch-MIR8030-5	UGUUGGGUUGGUUUGGUCUCGGGUUGGUUAUU UUAAAUUGAAACCAACCCAACCCAAAUAUAGUCG GAUUUUUUUUCCAACACCAAACCAAGUCAAACCA AACCACUA	108	sch-miR8030-5-5p	UUGGGUUGGUUUGGUCUCGGGUU	3-25	stu-miR8030-5p	0	0	23	23	1
			sch-miR8030-5-3p	UUGAAACCAACCCAACCCAAAU	38-59	stu-miR8030-3p	3	0	22	22	1
sch-MIR5248	ACAUUAAUUUGUUUGUCUGGUUUUCACUUGGCA CGCGUUUAAGAAAACAAAGAAAACUUUUGAAUCU UGUGUCUUAAACUAAAGAUACAUAGUAGAAUGUA CCAAAAUGUCCUUUAAUCUUGUGUUCUUAAGCAU GCCAUGUGGAACUUUUAACUCAAAGAGUUGCCA AUAAAAAGGAAAGAGACAUUCUUUUUUAAACGGA CUGAAAAGGAAAGUGAGACAAACAAAUUGAAACG	236	sch-miR5248-5p	UUUUCACUUGGCACGCGUUUA	21-41	mtr-miR5248	5	0	21	21	1
			sch-miR6452-3p	UGAAAAGGAAAGUGAGACAAA	204-224	ptc-miR6452	4	0	21	21	1
sch-MIR2867	CAACUUCCAACUUUCAUAAUGCACAAACAGACAC CUUAAGUAUCCAACUUUUAAAUAAAUAAACACAU GAGUCGUACAUGACACAAUACACGUAGGACACCA CGUAGGACAAAAAAUGACGUGUAGGAUGACAUG UAGGAAAUGUGUGUCUAUUUGUUUAACUUUAUA CAAGUUUAAGUUUCUAUUUGUGCACACCCAAAGU UGAAGGGC	210	sch-miR2867-3p	AAAUGACGUGUAGGAUGACA	114-133	osa-miR2867-3p	5	0	20	20	3
sch-MIR7980b-3	AGUAUGUGUUUGGUCAUAAGGUAUCAUAUCACA AUACGGUAUCGUGAGAUGGAAUCAGCGUUUGGA CAUGCGAUUUCACGCUGAUUCCAUCUCAUGAUU CCAUAUCAUAAGAUAUGAUUUCAUAUUUUCCAAA AAACAUGAU	142	sch-miR7980b-3-5p	GAGAUGGAAUCAGCGUUUGGACAU	46-69	stu-miR7980b-3p	1	0	24	24	1
			sch-miR1886h-3-3p	AUUUCACGCUGAUUCCAUCUCAUG	73-96	stu-miR1886h	3	0	24	24	1
sch-MIR6023	AUAUUCCAUGAAAGAGUUUUUGGGUAAGAUCUU UUACCGUAGUAAUCACAAAUACUAGGCAACCGUG CUGUUGGACAGAAAUUUCUGAUCAAAGCAUUUC	198	sch-miR6023-5p	UUCCAUGAAAGAGUUUUUGGGU	4-25	sly-miR6023	1	0	22	22	1

sch-MIR5026-5	CCUUCUUAAAUUCAAGAGAAUGCUUACAGUAGGU CCCUCAUCGAGUGUUUGUGAUUACUACGGUCAG GAAUCUUAUCCAGAGACAAUUCAUGGAAUAU AAUAAGAGGGCUUCAAUUAGUCCUACACUCCAAC UGUAAAAGUAUUUAAAAACAAAUGAUAAGAAGGU GACAUGUCAAUUAAACCUUACUUGACAUAUACUU AUCUGCAAUUUAAAUGCAGAAAAGUAUAUGUCAG GUAUUGUUUAGCUGACUUCUUAGUUCUUAUCGU CUGUGAACUUAGACAGUUAGACUAAUUGAAGCC CUUUUGGG	210	sch-miR5026-5-5p	AAUGAUAAGAAGGUGACAUGU	55-75	ath-miR5026	5	0	21	21	1
			sch-miR169d-5-3p	UCAGGUAUUGUUUAGCUGACU	133-153	stu-miR169d-3p	5	0	21	21	2
sch-MIR6116	CGCCUCUGUGUGCAUUCAACAUUAGAGGAUUCA UCAUUAUUGUUAGAAAAUGAUGGAUCCUCUAAUA CUAAAUUCACAUCAGAGAUU	87	sch-miR6116-3p	CAUUAUUGUUAGAAAAUGAUG	35-55	cca-miR6116-5p	5	0	21	21	1
sch-MIR159b-4	UACUAAGGUCCUAUUAUUCCCCUGAGCUUAUUU UGUAAAUAAUUUUGUACACAUUUUGCCUUACGU GGCAUUAGCUUGAAAAAAGAGUCAAUCACCAUUG GGCCCACAAGAUAGUGUCACGUAGGCCUAAAAU GGGUAGAAAAUUAUUAAUAAAAUAAGUUUAGGAG GGGUAAUAGGACCUUAAAG	186	sch-miR159b-4-5p	AAGGUCCUAUUAUUCCCCUGA	5-25	bdi-miR159b-5p-1	5	0	21	21	2
			sch-miR5026-4-3p	GCCCACAAGAUAGUGUCACGU	102-122	ath-miR5026	5	0	21	21	2
sch-MIR1916-2	AAAAAAUAGAAAAUUGGUUUAAAUAAUUGAAGCU CGGGUACAUUAAUAUGUAGCUAGGAUAUAUUAA GGCCUAACCCAUAACUAUUUUUCAUUUAGACACU CUAACUAGACUUUGUUCAUUUUGGACAGCUCAU GUCAUGUUUCGUUGUGUCACUUUUUGCUGACAU GACAUAGUGAGUGUGAUACACUCCUUGAAGAGC UUAUAUUUAACUAUUUUUAUUUAAU	225	sch-miR1916-2-5p	UUUUCAUUUAGACACUCUAA	86-105	sly-miR1916	5	0	20	20	2
			sch-miR477k-2-3p	ACACUCCUUGAAGAGCUUAUA	185-205	mes-miR477k	5	0	21	21	1
sch-MIR5303h	CUCUUAGUUGCACGGACUCUUCACUUUUGAUGC CGCACCCGUCUCGGAUUCUCCAAAAAUACACUAC CUUUGGCGAAUCCGACACGUACCCGUUGGCAUU UUUGAAGAGUCCGAGCAAAAUAAUAC	126	sch-miR5303h-3p	GGCAUUUUUGAAGAGUCCGAGCAA	95-118	stu-miR5303h	3	0	24	24	3
sch-MIR7997b-13	CUACUAAGUUGCUCGAGCUCUCCAAAAAUGUUG CCGCAAUAUUAUUGGAGGAUCAGCCACGCAACC GUCGACAUUUUUGAAGAGAUCGAGCAACAUAGC CC	101	sch-miR7997b-13-5p	AAGUUGCUCGAGCUCUCCAAA	6-26	stu-miR7997b	5	0	21	21	1
			sch-miR5303-13-3p	UUUUUGAAGAGAUCGAGCAAC	74-94	sly-miR5303	1	0	21	21	1
sch-MIR172a-2	AUGCACUGUCUCAGAUGUAAAUCUUCAUGUCGU CAAUGUCUAUGUUGUUCUACUCCAAAAAUGCACU ACUUCUGGACGAUAUAGACUUUGGCGACCUGAA GAUUUACAUUUGAGACAGUGUUU	123	sch-miR172a-2-3p	UUGGCGACCUGAAGAUUUACA	88-108	vca-miR172a-5p	5	0	21	21	2
sch-MIR7981-13	ACCUUAACUAAACUAAGGUCCUAUUACCCUUGAA CUUAUUUUUUUUUUUAUAAUUUUGUAAACCUUUUA UCUUACGUGGCACCCUUCGUGACUUAACGCAAU UGAGACGCGUGAGAGAUAUUUGGAUGCCACGUA AGCCAAAAAGUGCACAAAAUUACAAAACAUAGGU UUAUGGUAAUAGGAUCUUAGUUUAGUUAAAAU	200	sch-miR7981-13-5p	CUUAACUAAACUAAGGUCCUAUUA	3-26	stu-miR7981-5p	3	0	24	24	2
			sch-miR7981-13-3p	AUAGGAUCUUAGUUUAGUUAAAAU	177-200	stu-miR7981-3p	4	0	24	24	1
sch-MIR11107c	UAGUUUCAUUGAUGAUUAUUCGAGAUGCACUUG GGUUUUCUUAAUGAAAGAUCGUUUUGAGUUAUU UUUUCAUUAGUUCAUUCUGAUAUUUGGGGUCCU AGUAGAGUCAGUUCCCCCGUAAGAUUUCGUUAU UUUGUUAGUUUCAUUGAUGAUUAUUCGAGAUGC ACUUGGGUUUUCUUAAUGAAAGAU	189	sch-miR11107c-5p	UAGUUCAUUCUGAUAUUUGGG	74-94	lja-miR11107c-3p	5	0	21	21	1
			sch-miR10531-3p	UGGGGUCCUAGUAGAGUCAGUUC	91-113	sly-miR10531	1	0	23	23	1
sch-MIR11498c	AAAAAUGACUAGUGAUUUAGUUUGACUUGGUUU GGUAUUGGGGGGAAAACCCGACUAUAUUUGUGU UGGUUUGGUUUUAACUAGAAAAAUCAACUCGAGA CCAAAUCAGUCCGACAUUAUA	121	sch-miR11498c-5p	CUAGUGAUUUAGUUUGACUUG	9-29	pab-miR11498c	5	0	21	21	3

			sch-miR11086-3p	UAGAAAAAUCAACUCGAGACC	82-102	lja-miR11086-3p	5	0	21	21	1
sch-MIR1134	UUUUUUUUGUAAUUUGUACACCUUAUGUCUUAC GUGACACGCUCCAUGACUCCACGUAAUUGAGAC GCGUGAGAGAUAUUUGGAUGCCUCGUAAGCAAA AAAGGUGCACAAAAAUUACAAAAAGAA	126	sch-miR1134-3p	CAAAAAUUACAAAAAGAA	109-126	tae-miR1134	4	0	18	24	1
sch-MIR11077a	AUUUCAAUUGAGAAGUGAUUUUGAACAUGACAGA AUUAUACUCAUGUAUAGACUUAAAGUCUUGUAGC CUUAGAUGCAUCCAAUCAUAUCGUGCCUUUGGA UGUAUGACCAUCUUCAAGUGGUCAAAUCUUUCU UUUAGGUUUUUCCACAAAACAAGUGGAUCCUUAA CUAUCAGAUAUUCAAUUUUCAGAAUCUUGUCAAG AUGAUGA	209	sch-miR11077a-5p	CAAUUGAGAAGUGAUUUUGA	5-24	lja-miR11077a-5p	5	0	20	20	2
			sch-miR1217-3p	AAUUUUCAGAAUCUUGUCAAG	182-202	ppt-miR1217-3p	5	0	21	21	1
sch-MIR1886i-2	AAAAUUGAUGAGAAUACAAGAUUCCCAGAGUAUA UUUCUGAUCAAUAUGAUAUUUAUUACGAUUAUUU GACGACAAUUACAACAAAGGGACAAGAUUAUGAU UCUGUUAGAAUUUUGGAUUCUAACAUGAUUAUCA AUCUCUCAAAGAACAGAUUUGAAGGUCAUAUUCC AAGCAUUAUUGGAGAUCUUGUUGGACUUCGUAC GUUGAAUUUAUCUCAUAAUGUCUUGGAAGGUCA UAUACCGGCAUCAUUGCAAAAUUUAUCAGUACUG AAUCAUUGGAUCUCUCAUCUAAUAAA	296	sch-miR1886i-2-3p	CGUACGUUGAAUUUAUCUCAUAA	199-221	stu-miR1886i-3p	5	0	23	23	3
sch-MIR7987	ACCCAUCUAAUAUUGAUACUUAGCUUUAAAUAUG UGUUGACACUUAGCUUUUUCUUAAGCUUAAGUA CCAACACUAGUUGAUCCUAUUGAUGACGAAACUG AUUUCUUUCAAAAUCAAUUUGCGUCCAUCUAGUG UUGACACUUAGCUUUAAAGUUUAGAAAUAAUUAU UUGUUAAGCAUAAGUACCAACACUAGUUGAUC	201	sch-miR7987-5p	ACACUAGUUGAUCCUAUUGAUGAC	71-94	stu-miR7987	1	0	24	24	1
			sch-miR774a-3p	UUAUUUGUUAAGCAUAAGUAC	166-186	aly-miR774a-3p-2	5	0	21	21	1
sch-MIR5303i-1	CUAUGUUGCUCCGGGCUUUCCAAAAAAUUUGUU GUGCCCAUGUGGGAUCCAAACAUACACUAAUUU UGGAGUAUCCAACAUGGUGCUAUAUUUUUGAAG AGUCCGAGCAAACAUAG	116	sch-miR5303i-1-3p	AUAUUUUUGAAGAGUCCGAGCAAA	88-111	stu-miR5303i	2	0	24	24	1
sch-MIR397b-3	GAGUCUAUGCUGCCGGACUUCCCAAGAAUGUCG UUGCACCCCUGUCGAAUACUAUAAAAAUAACUAC UUUUGUAGGAUUCAACAUGUAUCUAUGUCAUUU UUGAAGAGUCCGAGCAACAUAGAUGA	126	sch-miR397b-3-5p	UGCACCCCUGUCGAAUACUAU	35-55	eun-miR397b-5p	5	0	21	21	1
			sch-miR5303i-3-3p	UCAUUUUUGAAGAGUCCGAGCAAC	95-118	stu-miR5303i	3	0	24	24	3
sch-MIR477b-3	GGUUGACAGUCUUUUUUCACUCUCCCUCAAAGG CUUCUGGCUUAAAAUGCCUUUUGUGCUAAUGCU AGAGGUCUUUCGAGUGAGAGUGAAUAAAUUCUG CCAUGA	105	sch-miR477b-3-5p	ACUCUCCCUCAAAGGCUUCUG	19-39	stu-miR477b-5p	0	0	21	21	1
			sch-miR477b-3-3p	GAGGUCUUUCGAGUGAGAGUGA	68-89	stu-miR477b-3p	0	0	22	22	1
sch-MIR7983-8	UUUCAGUACAACAAAAAUGACUAUUAGCGGCAUU UAAUUCUUAAUUGCCGCUAAAUAUGUACUUUUAG CGGCAAUUGCCACUCUUUGUAUAUGUCCCUUAA AGCCUUUAGCGACAUUGGUUCUAAUGGCACUUA ACUAAUGCCGGUAAAGACUUUAGCACUCUUUGU UAGUGUCAAUAAUUAAUGCCGCUAAAAGUUGUUU UUGUUGUAGUGUUU	215	sch-miR7983-8-3p	ACUAAUGCCGGUAAAGACUUUAGC	135-158	stu-miR7983-3p	1	0	24	24	1
sch-MIR2604	AUCAAUUUUAUGUAUGUGUGUUAGUUGGCGAAU AUAUUGGUGAUAUGAGUUUCGUAAGUUAGCUCA UGGGUUAACACACAUGAAAAAAUUGAGAAAAUUA UCUAAUUUAUAAAAUUGGCCCCUAAAUUUCCAAA AUGUGCUCUAAAAAUUGUGAGACUACGUAUUACU AUCAAAACUCCCUACGGAGGGUUUCAUAAAGGU UUCACAAGAAAAUCAUCAUAAAGUUAAAUCACCA AGAUAUUCAUGGGCUAACACACACGAAAAAUUGA G	270	sch-miR2604-5p	UCAAUUUUAUGUAUGUGUGUU	2-22	mtr-miR2604	5	0	21	21	1
			sch-miR1153-3p	UGAGACUACGUAUUACUAUCAA	152-173	cre-miR1153-5p-1	5	0	22	22	1

sch-MIR1530-1	GUAAUGCACAAACAGACACCUUUACUAUCUAACU UUUAAAUAAAUAAACAUAUGAGUCCUACAUGACA CAUUACACGUAGGACACCACGUAGGACAAAAAAU GACAUAUAGGAUGACAUGUAGGACGUGUGUGUC UAUUUGUUCAACUUUAUACAAUUUUAAGUGUCUA UUUGUGCAUAUC	181	sch-miR1530-1-5p	CUUUUAAAUAAAUAAACAUAU	33-53	gma-miR1530	5	0	21	21	2
			sch-miR5014a-1-3p	UUAUACAAUUUUAAGUGUCUA	149-169	ath-miR5014a-3p	5	0	21	21	1
sch-MIR156g-2	GGAUGACGGAAGCAUAGAGAGCACAAAUGAAGU GAAAUGCUUUUUUAAUUGUUUAGACUCUCCAGA UUUAGCAGCAGCAUUCCAUCAUAUGUGCUCUCU AUCUUCUGUCAACA	113	sch-miR156g-2-5p	AUGACGGAAGCAUAGAGAGCAC	3-24	csi-miR156g-5p	2	1	22	21	2
			sch-miR1088-2-3p	AUGUGCUCUCUAUCUUCUGUC	89-109	smo-miR1088-3p	4	0	21	21	3
sch-MIR867	AAGGUCCUAUGAUUCCUGAACUUGUUUUAUAAG UAAUAUUUUACCCAUUUUCUAUCUACGUGACAUU AGCUUGAAAAAAUAAGUCAACCAGCAUUGAGUCC ACAAGAUAGUGUCACGUAGACAGAAAAAGGGUAG AGAAUUAUUAAUAAAAUAAGUUCAAGGGUUAUAG AACCUU	175	sch-miR867-5p	CUGAACUUGUUUUAUAAGUAA	16-36	ath-miR867	5	0	21	21	2
sch-MIR5251	UUUAAGUGUUGAAUAUUCACAUUUCCAAUCACCC UUUAUAGUUUAACGACAUAAUCCACUGUGCGUCA UGGACACCUGAUGUUGAUGUGGCAAAUAUAUUU CGUUGGUGUCUAGAUGAUCAUUUUGUAAGUUGG AGUGUUCAACUGACACAGUGGAGAUGAGUUGAG GUGUAGAUGUGCAUACUCAAAGUUGGA	194	sch-miR5251-3p	AAUAUAUUUCGUUGGUGUCUA	93-113	mtr-miR5251	5	0	21	21	1
sch-MIR9562-2	CAUAGCAAACAUAUAACUGUAUAAUUCGCUAUAC AUAUACAACUGUAUAAUUCACUGGCCUAAAUUGU AUAAUUCGCUGGCCUCGCUAUACAUAUACAAUUG UAUGAUUCGCUGGCCUAUAUUGUAUCAUUCGCU GGCCUAUUCGCUGCAAUUGUAUAAUUCACUGGC CUAAAUUGUAUAAUUCGUUGGCCUCGCUAUACA UAUACAAUUGUAUGAUUCGCUGGC	225	sch-miR9562-2-5p	ACAUAUACAACUGUAUAAUUC	33-53	bra-miR9562-3p	5	0	21	21	3
sch-MIR6149	AAAUGAACUCAAUGGGCUGAAUAUGAAUGAUUCA GAUUCAGAUUCAAACCUAAAUACCAAACGUACUU AAUAGGCUGAAUCUGAAUGAUUAAGAUUCAGACC UCCAUUAAGUGCAAAC	118	sch-miR6149-5p	UGAUUCAGAUUCAGAUUCAAAC	28-49	stu-miR6149-3p	5	0	22	22	1
			sch-miR172d-3p	UCUGAAUGAUUAAGAUUCAGA	80-100	bra-miR172d-5p	5	0	21	21	2
sch-MIR1530-2	ACUUGACUUCAAAUUUUAACUGACCUUUAACUUU CAUAAUGCACAAACAAACACUUUAACUAUCCAAC UUUUAAAUAAAUUAACACAUGAGUCCUACAUGAC ACAAUACACGUAAGACACCACGUAGGACAAAAAA UGACAUGUAGGAUUACAUGUAGGACAUGUGUGU CUAUUUGUUUAACUUUAUACAAGUUUAAGUGUCU ACUUGUGCACACCCAAAGUUGAAGGGCAUAAAUA UAAUUCGAAGUCAAGU	253	sch-miR1530-2-5p	CUUUUAAAUAAAUUAACACAU	68-88	gma-miR1530	5	0	21	21	2
			sch-miR5014a-2-3p	UUAUACAAGUUUAAGUGUCUA	184-204	ath-miR5014a-3p	5	0	21	21	1
sch-MIR398a-3	AACUUUGAGUGUACACAAGUAGACACACGUGUC UUAUAUGACAUAAUACACUUAGAAUGUCAUGUAG ACACAGAAUCGUCAUGUAGAACGUGCGUCUUGU AGGACGAAUGCGUCUAUUUGUUUAAUUUAUACAA AUUUAAGUGUCUAUUUGUGCACACCCAAAUAU	166	sch-miR398a-3-5p	AGAAUGUCAUGUAGACACAGA	54-74	aly-miR398a-5p	5	0	21	21	2
			sch-miR5014a-3-3p	UUAUACAAAUUUAAGUGUCUA	127-147	ath-miR5014a-3p	4	0	21	21	1
sch-MIR5205a	CGCAACAUGACAAACAAUUCCGGACGGAGGGAG UAUAAUUAUGAUCUAUUUUAUAUUUGAAACAUUU UAAAGAAGUAUUUUUCCAUCAUAUUAAUAUGCAA AAAAUUACUCCAUCCGUCCGGUAUUGUUUGUCA UAGUUUCU	142	sch-miR5205a-5p	CAAACAAUUCCGGACGGAGGGAG	11-33	mtr-miR5205a	3	0	23	23	1
			sch-miR1127-3p	AAUUACUCCAUCCGUCCGGUA	104-124	bdi-miR1127	3	0	21	21	1
sch-MIR2099	CCCACUACAUUAAAAAGAGCUUUAGCGACAAUUA AUUAGCAAUUGCCGCUAAGUAUAUAUAUUUUAGC GGCAAUUAGCACUCUUUGUAUAUGUUCCUAAAA	213	sch-miR2099-5p	UGUAUAUGUUCCUAAAAGCUUU	85-106	osa-miR2099-5p	4	0	22	22	1

	GCUUUAGCAACAUUGGAUCUAAUGACACUUUAAC UAAUGCCGAUAAAGACUUUAACACUCUUUAUUAA CGUAUCUAUUUAUUGCCGCUAAAAGUUAUUUUU GUUAUAGUACC										
			sch-miR7983-3p	ACUAAUGCCGAUAAAGACUUUAAC	134-157	stu-miR7983-3p	1	0	24	24	1
sch-MIR10538-10	GUCAGAUUGAUAUACGUUACUCACAGUAACGUU UUACUCCUAAAACGUUACUCAUAGUAACGUUUUA GGAGUAAAACGUUACUGAAAAUAACGUUUUAGGA GUAAAACGUUACUUACAGUAAUGUAUAUCAACCU AAU	138	sch-miR10538-10-5p	AGAUUGAUAUACGUUACUCACAGU	4-27	sly-miR10538	0	0	24	24	1
sch-MIR7822-3	GCUCUUCAACUUUGAACGUGCACAAAUAGACAUU UAAACUUGUAUAAAAUUGAACAAAUAGACACACA UGUCCUACAUGUCAUUUUUUUCCUACGUGGUGU CCUACGUGUAUUAUGUCAUGUAGGACUCAUGUG UUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUC UAUUUGUGCAUUAUGAAAGUUGUAGGUC	196	sch-miR7822-3-5p	UAUAAAAUUGAACAAAUAGAC	43-63	ptc-miR7822	5	0	21	21	1
			sch-miR10519-3-3p	AUUUAAAAGUUGGAUAGU	142-159	tae-miR10519	4	0	18	18	3
sch-MIR865-1	UAAUGCACAAACAGACACUUUAACUAUCCAACUU UUAAAUAAAUAAACACUUGAGUCCUACAUGACAC GAUACACGUAGGACAUAACGUAGGACAAAAAAUG ACAUGUAGGACAUAUGUGUCUAUUUGUUCAACU UUAUACAAGUAAAUGUUUAUUUGUGCACAU	165	sch-miR865-1-3p	UAUUUGUUCAACUUUAUACAA	123-143	ath-miR865-3p	5	0	21	21	1
sch-MIR5015	UUUUUCACAGACUAUUUUCUUGUAUAGUCUAUG GAAUACCUCACUUUGCUCUCAAAAUGGUUUUUC UCCGUCGUCGGAAGUCUAAUGUAUGCAAUGGUG UGCACUAGACCUGAUAUUGCUCAUGCAGUUGGU GUUGUCAGUAGAUUUCUCAAAAAUCCAGGAAAAG AGCACUGGGAAGCU	180	sch-miR5015-3p	UUGGUGUUGUCAGUAGAUUUC	128-148	ath-miR5015	5	0	21	21	1
sch-MIR3706-3	UGACAUAUUUUUGGGACAUUGGUGCUCCUGCCG UUUAAAAACUAGAGCACAUAUGUCCUCACUCUAA CGGAAGACUAAAUACAGAUACGUGACACAAUCUU AUCCGUAGAUAAAUUUUGGAUUGAUGGAUAAGA UUAUGACACGUGUAUGUAUGUUAGUAUAAAGGG UAUAUAUGAUCUAAUUUUUCGACGGCUGGGGUA UUAAUGUCAUAAAAGUGUGACG	222	sch-miR3706-3-3p	UUUUGGAUUGAUGGAUAAGA	115-134	pab-miR3706	4	0	20	20	1
sch-MIR8014	UUUUACUCCCUCUGUCCAACAAUUCUUGUUCAC UAUUGAAUAUAAUAAAUACAAUGUGUUGAAAAAU GUCACAGAGAAAUGAUUAUAAGUAGGUAAAUUAG AAAAGAAGUGUAAAAUAAUCCACUGAUUUCAUCA AGUGGACAAGUAUUGUUGGACAUCCCAAAUUAG UAUAGUGGACAACUAUUGUUGGACAAAGGGAGU AGUU	205	sch-miR8014-5p	AUAAAUACAAUGUGUUGAAAAAUG	45-68	stu-miR8014-3p	5	0	24	24	1
			sch-miR6444-3p	UAGGUAAAUUAGAAAAGAAGU	90-110	ptc-miR6444	5	0	21	21	1
sch-MIR7997c-26	UAUGUUGCUUGGACUCUUCAAAAAUGUUGAUGG GUGCGUGUCGGAUCAUCCAAAAGGUAGUGCAUU UUUGGAGGAUCUGUUUCGGGUGCGGCAACAAUU UUGGAGAGUCUGAGCAACUUA	120	sch-miR7997c-26-5p	AUGUUGCUUGGACUCUUCAAAAAU	2-25	stu-miR7997c	2	0	24	24	1
			sch-miR5303h-26-3p	AACAAUUUUGGAGAGUCUGAGCAA	93-116	stu-miR5303h	2	0	24	24	1
sch-MIR1866	UGCAAUAAAGAGACCUCAUGAGGUCUCUAUUAU GAAAUAUCUGGAAAAUUAAUGCAAAAAAGAGACC UCAUGAGGUCUCUUUUUCUG	87	sch-miR1866-3p	UGAAAUAUCUGGAAAAUUAAUG	33-54	osa-miR1866-3p	5	0	22	22	1
sch-MIR11008	AAACUAGGGUCAUAUUAUCUCUGAACUUAUUUUU UUGGUAAUUUUAUACAUCUUUUGUCUUACGUGG UACACUCUGUGACUCCACAAAAUUGAGGCGCGU AGGAGAUAUUUGGAUGCCACGUAAGUGUCUCCA CGAAAUUGAGGCGCGUGAGAGAUAUUUGGAUGU CACGUAACCCAAAAAGGUGCACAAAAUUAUAAAA AAAAAAAUAAGUUUAGGGGUAAUAGGACCUUAGU UU	236	sch-miR11008-5p	GUGACUCCACAAAAUUGAGGC	76-96	mdm-miR11008	5	0	21	21	1
			sch-miR2923-3p	GCACAAAAUUAUAAAAAAAAAA	185-206	osa-miR2923	5	0	22	22	3

sch-MIR7983-9	UUCCACUACAACAAAAAUGAUCAUUAGCGGCAAU AAAAAAAUUUUAGCCGCUAAAUAUGAAUUUUUAG CGGCAAUUGUCACUCUUUGUAUAUGUCCCUAAA GUCUUUAGCGACAUUGGUUCUAGUGACACUUAA CUAAUGCCGAUAAAAUUUUUAGCACUCUUUAUUA AUGUCAACAUUUAAUGCUGCUAUAAGUUAUUUUU AUUGUAGUGUUU	214	sch-miR7983-9-3p	UAAAGUCUUUAGCGACAUUGGUUC	98-121	stu-miR7983-5p	0	0	24	24	1
sch-MIR8011a-5	AUGGAAAGAGUUUACUUUGUGUCUCACACAACU GACACAAGUUGUGUGGGGAUUCUUUUUGUUUCA CAAAUUUGUGGACCAAAAGUGUAAGACUAGGGU CCAGUAAUUUGUAGAUCAAAGCCUCACACAACUU GUGUCUGUUGUGUGAGACACAAAAUUAAGUUUC UCUUG	171	sch-miR8011a-5-5p	UUGUGUGGGGAUUCUUUUUGUUUC	42-65	stu-miR8011a-5p	2	0	24	24	1
sch-MIR6230	CACUCCAACUUUAGGUAUGCAUAGUUAGACACCU CAACUGGUCUCCAUUGUGUUUAUUGAAUGACUC CAACUCACAAAAGGAUCAUCUAGACACCUCCAAA AUUUAUGUGUCACAUAAGCGUCAGGUGUCCAUG AGUUGGAGUAUCUAGUUUUCGGUUGACACCAAG UUGAGGUGUCUAGAUGUGCAAGCUCAAAGUUGG AAUA	204	sch-miR6230-3p	CACCAAGUUGAGGUGUCUAGA	161-181	sbi-miR6230-3p	5	0	21	21	2
sch-MIR9773-1	CCAAGGUUCUAUUACCCCUCUGAACUUUUUUUU UUUUGUAAUUUUGUGCACCUUUCUAGCUUAUGU AGCAUUCAAAUAUCUCCGCUGCGCUUCAAUUGC AUGGAGUCAUGGAGUGUGCUAUGUAAGACAAAA GGUGUAUAAAAUUACAAAAAAAAAAGUUCAGGAG GGUAAUAGGACCUUAG	182	sch-miR9773-1-5p	UUUUUUUUUUUGUAAUUUUGUGCA	27-50	tae-miR9773	4	0	24	24	1
sch-MIR857-3	AGGCAUAAUACAGAUAUUAAACCUUAAAUUUGGC UUCAAAUUUUAACUUUGACCUCCAACUUUCACCA UGCACAAACAAACACUUUAUAAACACAUAAGUCC UAAGUGACACAAUACACGUGGAGACCACGUCGG ACAAAAAAUGACAUGUAGGACAUAUGUUUUUAUU UGUUCAACUUUAUACAAGUUUAAGUGUCUAUUU GUGUACAUACGAAAUUGAAGGGCAUAAAUGUGA UUUGAAGCCAAGUUAAAGGGUACAUUUAUGUAU UAUGUCU	275	sch-miR857-3-5p	CAACUUUCACCAUGCACAAACA	57-78	cas-miR857	5	0	22	22	2
			sch-miR5014a-3-3p	UUAUACAAGUUUAAGUGUCUA	179-199	ath-miR5014a-3p	5	0	21	21	1
sch-MIR3707	ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAAU CCCCUACCAUAUUGCCAAAUUAUUUGCCUUUAUC UUUGUGUUCAUCUAGCUAAAGGCAAAUGUUUGG CAAUAUGGUAGGGGAUUCUGGUCUUCUGUACAC AGGGAAAAGUUGACUUCG	152	sch-miR3707-5p	AUUAUUUGCCUUUAUCUUUGU	53-73	pab-miR3707	5	0	21	21	1
sch-MIR1530-3	UAAUGCACAAACAGACACUUUAACUAUCCAAUUU UUAAAUAAAUAAAUACAUGAGUCCUACAUGACAA AAUACACGUAGGAGAUCACAUAAGACAAAAAAUG ACAGGUAGACAUUUAGGACGUGUGUGUCGAUUU GUUCAACUUUAUACAAGUUUCAGUGUCUACUUG UGCAAAC	175	sch-miR1530-3-5p	UUUUUAAAUAAAUAAAUACAU	32-52	gma-miR1530	5	0	21	21	1
sch-MIR11114	CCCUCUGUCCCUAUUUAGUUGUCCACUUUAGAA GUGGCACGCAUAUUAAGGCACCAAUUAUCAUCAU AGUUUAGUUACAAUUUUAUCCUUAACUUAAAAGA UUAUGCAUAUCCACAAGUAUAAUAAAUGUAUUUU CUGAUUUCCAAAAGGCAUGCAUUACAACUUAGUA GAACUAGAAAUUUUCUAGAAUUAAAUAAGGGCAU AUUAGGAAAAAAAUUGUUGUCCUUCCUUGAUUU GUUAAAAUGAACAAGUAAAUAGGGACAGAUAU	268	sch-miR11114-5p	UGUCCCUAUUUAGUUGUCCACUU	6-28	lja-miR11114-5p	4	0	23	23	1
			sch-miR11109-3p	UCCUUGAUUUGUUAAAAUGAA	227-247	lja-miR11109-5p	5	0	21	21	1
sch-MIR10540-1	CGGUUGAUUUCUCAUAUAGUCACUUGACUAAUA GUUAUUAUCUCGAAAGUCCCCUUUCUUCUUGAU UCCAAAACUUUCAACAAAGAAAGUGACUUCCUGA GAUGAUAACAAUUAGUCGAGUGAUCAUCUGAGAA AUCAAACU	142	sch-miR10540-1-3p	AUGAUAACAAUUAGUCGAGUG	102-122	sly-miR10540	4	0	21	21	1
sch-MIR11497-2	UACAUAAUUAAUACCAACAUAACUUAUGAGGGAA UCUAUGUAUAAAGUUAUGCAGGGUAGAAGGUGG AAUAAGUUAUGUGGGUAUUAGUUAUACA	95	sch-miR11497-2-3p	GGAAUAAGUUAUGUGGGUAUU	66-86	pab-miR11497	5	0	21	21	2

sch-MIR10540-2	GGCAGAUUGAUUUCUCAUAUGGUCACUUUAACA AAGAAAGUGACUUAUAUUACUCAAAUAAUUACUA UUAGUUGAACGACCAACUGAGAAAUUAACUUCG	100	sch-miR10540-2-3p	AUAAUUACUAUUAGUUGAACG	58-78	sly-miR10540	2	0	21	21	1
sch-MIR8006-7	CAUUGGUGUCCCUGUCGUCCAAAAACUAGAAUG UAUAUGCCCUUGACAAAAUAGGGUCACGUGGUC AAUCUUAUCCAUCGAUCCGAUGUCGGGUCAGUG GAUAAGAUUAUGACACAUGUAUGUCAGUUAGUAU AAAAAUUAGUUUUGGAUGACAGGGACACCAGGG	166	sch-miR8006-7-5p	GUCCCUGUCGUCCAAAAACUAGA	8-30	stu-miR8006-3p	4	0	23	23	3
			sch-miR7828-7-3p	GAUGACAGGGACACCAGGG	148-166	ptc-miR7828	4	0	19	21	1
sch-MIR7822-4	GAUAUGCAUAAGUAUGUAUACACUUCAGUUUGUA UGAAAUUGAACAAGUAGACACAUGAGUCAUACGU GACACAAUACAUGUAGGAUGUCAUAUAGUAUAUG UGUGUCUAUUUGUUCAAAUUUUAUACAAGUUUAA GCGUUUACUUUUGUGCAUCCA	157	sch-miR7822-4-5p	UAUGAAAUUGAACAAGUAGAC	33-53	ptc-miR7822	5	0	21	21	1
			sch-miR5183-4-3p	UAUUUGUUCAAAUUUUAUACA	109-129	bdi-miR5183	5	0	21	21	1
sch-MIR865-2	AUUUUUGAUGUUCAUAUGUAGGCAAUUAAACUUU UAUAAAGUUGAAUAAAUAGACACAUGAGUCCUAC GUGAUAUAAUACACCACAUAGGAUACAAAUUGUC AUGUAGGAUGUCGCGUAGGACGUGUGUGUCUAU UUGUUCAACUUUAUACAAGUUUACGUGUCUACU UGUGCACAGUCAAAGUU	185	sch-miR865-2-3p	UAUUUGUUCAACUUUAUACAA	133-153	ath-miR865-3p	5	0	21	21	1
sch-MIR5796	AAUCUUUUUCGGUCUACGUGGUAUUAGCUUGAA UAAAAAUCAAUCAGCAUUGAGGCCACAAGAUAGU GUCACGUAGGCCAAAAAGGGU	88	sch-miR5796-3p	UCAAUCAGCAUUGAGGCCACA	40-60	osa-miR5796	5	0	21	21	1
sch-MIR7981-14	UUUUAACUUUGAACUAAUAUAGAGACACGCCUUA ACUAAACUAAGGUCCUAUUAACCCACCCACCCAC CCACCCCCCGAACUUAUUUUUAUACACCUUUUGU CUUACUGGCACACUCUGUGACUCCACGCAAUUG AGGAGUGUAGGAGAUAUUUGGAUGCCACGUAAG CCAAAAAGGUGCAAAAAAUUACAAAAAAUAAGUU CAGGGAGUAAUAGGACCUUAGAAUAGUUAAGGU GAGUUUCUGGAAUUUCGAUCAUAGUCUAGGG	266	sch-miR7981-14-5p	CUUAACUAAACUAAGGUCCUAUUA	31-54	stu-miR7981-5p	3	0	24	24	2
			sch-miR7981-14-3p	AUAGGACCUUAGAAUAGUUAAGGU	212-235	stu-miR7981-3p	3	0	24	24	1
sch-MIR917	ACGAUUUCAUCCAUUCACCCUCAUUUCGCGGCU AGGUUUCACAGUUUUCUUCGUCGCUGGUUUUCA AAGUGGAUAUUCUUGAUUGUAGGUUAGUAAAAC UUUUUUCUUAUUUUAUUGUGUUUACAACCAUGAA AAUCCACUUUGAAACUUAGCUCCGAAAAUUUUUA UGAAACCUUGGCCGUGAAAUGACGGUAAAGUUG UGAAAUUCU	209	sch-miR917-5p	UUUCACAGUUUUCUUCGUCG	37-56	cre-miR917	5	0	20	20	1
			sch-miR8014-3p	CUUUUUUCUUAUUUUAUUGUGUUU	99-122	stu-miR8014-5p	5	0	24	24	2
sch-MIR162-3	GAACACUGGAGGCAGCGGUUCAUCGAUCUGUUC CCUGAAAAGCGAUAAAUACAGCAACAGGAAGCGA UCGAUAAACCUCUGCAUCCAGUGCUU	93	sch-miR162-3-5p	UGGAGGCAGCGGUUCAUCGAUC	7-28	csi-miR162-5p	0	0	22	22	1
			sch-miR162-3-3p	UCGAUAAACCUCUGCAUCCAG	68-88	fve-miR162-3p	0	0	21	21	1
sch-MIR1888b-1	UUGUAUUUAUUUUCACAUCUUUUAAAUUAAUAGU GUAUAAUACUUUCUAAAUUUGUGCAUCAAUGACU AUUAGAGCCGUCAAUAUGGGCUAAGCUUGUUGG GACGGUCUGGCCUAGCCCGGGAUUUAAUAGGGU UGGGCUAAGAUUUUUGAAGCCCAUUUAAGAAAAA GACUUUUUAGCCCGGCCUGAAUAAGCUUGUUGA UUUGAUGGGCUUGAGAAAUAUAGGUAGGGCCGG CCCGUGGGCCAAUAGUAAUUAAUUAAAAAAUAUA AAAUAAAAUUAAAUUUUAAAAUUAAAGAGAGUCC AAAUUCAAAAUAAUU	317	sch-miR1888b-1-5p	UUGGGCUAAGAUUUUUGAAGC	134-154	ath-miR1888b	3	0	21	21	1
sch-MIR844-1	CUUGGCUUCAAAUCACAUUUAUGCCCUUUAACUU UGGAUGUGCACAAGUAGACACUUAAACUUGUAUA AAGUUGAACAAACAGACACACAUGUCCUACAUGU CAUCCUACUUGUCAUUUUUUGUCCGACGUGGUG UCUUACGUGUAUUGUGUCAUGUAGGACUCAUGU GUUUAUUUAUUAAAAAGUUGGAUAGUUAAAGUGU	253	sch-miR844-1-5p	UCAUCCUACUUGUCAUUUUUU	102-122	aly-miR844-3p	5	0	21	21	2

	CUGUUUGUGCAUUAUGAAAGUUGGAGGUCAAAG UUAAAAUUUGAANCCUAC										
			sch-miR10519-1-3p	AUUAAAAAGUUGGAUAGU	177-194	tae-miR10519	4	0	18	18	3
sch-MIR7997c-27	GAUGCUUUGUAGCUCAGACUCUUCUAAAAUGUU GCAGCUUCCGUGGUGGAUCCUUAAAAAAUUUAC UACUUUUGGAGGAUAGUCGACAUUUUGAAGAGU UUGAGCAACAUAGCCAA	116	sch-miR7997c-27-5p	UUGUAGCUCAGACUCUUCUAAAAU	7-30	stu-miR7997c	5	0	24	24	2
			sch-miR5303-27-3p	AUUUUGAAGAGUUUGAGCAAC	88-108	sly-miR5303	2	0	21	21	2
sch-MIR3635	CUUUUGACUAUUAAUAAUUGGUGUAAAUAACCCG AUUUGGCGGCAAUUAUGUCUUACACGAGCCUCA GAGUUUAAAACACUGCCUCAAAAAUGAUAAUUAG CGGUAAUUGAUCGCUAAAGAUGUAUUUUUAGCG GUAAUUAACACUUGCCUUUUGUAUAUGUCUCUAA AGUCUUUAGCUACAUUGGUUCUAAUGACACUUAA UUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUA AUAUCAAUAU	246	sch-miR3635-5p	AUUAUGUCUUACACGAGCCUC	46-66	vvi-miR3635-3p	4	0	21	21	1
			sch-miR7983-3p	UAAAGUCUUUAGCUACAUUGGUUC	166-189	stu-miR7983-5p	1	0	24	24	1
sch-MIR10538-11	ACAGCAUUAGGUUGAUAUACAUUACUGUAAGUAA CGUUUUAGGAGUAAAACGUUACUGUGAGUAACG UAUAUCAAUCUGACGCCAU	86	sch-miR10538-11-5p	AGGUUGAUAUACAUUACUGUAAGU	9-32	sly-miR10538	5	0	24	24	1
sch-MIR6164b-2	ACUAAGAGAAAGUGUUUUUUAGGACUUCAUAGAA AUUGAAAGAGAGUAAUUAAUAUUUGUUGUGCUAU UAAAUAUAUUGGUUCCACUUUAUGCUUAUAUGCC AAAGGCAGAAGUCAUCGGUGGCCCCCUAAACUU GGCACAAUCUUUCACUUAGACACCUCAACUUGAG GAUUUUCAUUUUAAAUACCUAACGAGGGUCCCUA UGUGUCACUUAAAACACUUUUUUUUCAU	231	sch-miR6164b-2-5p	UCAUAGAAAUUGAAAGAGAGU	27-47	nta-miR6164b	5	0	21	21	1
			sch-miR1916-2-3p	CUUUCACUUAGACACCUCAA	144-163	sly-miR1916	1	0	20	20	2
sch-MIR164a	UUUAAGUAGGUGAUGCACCUAGUUUUCUAUUAA AAUUAUUUCUUGUGGGCUUUGGAAGAUUGGGCC UUGGCUGUCCAUUUUCCCAUUAUUCUUCUAUUC AACUUGGGCUAAAUUAAUGUAAAUGGGUGAAGU GUACUUGGCCCAAUUACAUAGUCAAAAGAGUUUU AGUAGUUGAUGUACCUACUAGGUCUGGUCAAUA AGUCAAAGUAGGUGAUGCACCUACUUGUC	228	sch-miR164a-5p	AUUGGGCCUUGGCUGUCCAUU	59-79	gra-miR164a	5	0	21	21	3
sch-MIR8740	UUGUUAGGUACUCUCUCUGUCCAAUAAUAGUUG UACACUAUUGACUUGGCACAAGAUUAAGAAGCAG UAACUAUUAAAUAUAAGUCAUCAAACAUUGAAAA AUGAAUGGUAUUUCAAAGCAAGGGUAAAAUAUGC ACAAAGUGGUAAAUUAUUUAUUUAUUUUGUAAGC CAUACAAGGAUUGUUGGACAUCCCAAAAUAGUUG AGUGGACAAGUAAAGAUGGACGGAGGGAGUAUU AAACG	241	sch-miR8740-5p	UAUUGACUUGGCACAAGAUUA	39-59	gra-miR8740	4	0	21	21	1
			sch-miR11021-3p	AAGCAAGGGUAAAAUAUGCACA	117-138	seu-miR11021	5	0	22	22	2
sch-MIR7822-5	AUUUGGCUUCGAAUUACAUUUAUGCGCUUCAAC UUUAGGUGUGCACAAGUAGACACUUAAACUUGU AUAAAAUUGAACAAAUAGACACACAUGUCCUACA UAUCAUCCAACAUGUCAUUUUUUGUCCUACGUG GUAUCUUACGUGUAUUGUGCCAUUUAAACAUGU GUUUAUUUAUUUGAAAGUUGGAUAGUUAAAGUG AUUGUUUGUGCAUUAUGAAAGUUGGAGGUCAAA GUUAAAAUUUGAAGCCAAGU	252	sch-miR7822-5-5p	UAUAAAAUUGAACAAAUAGAC	66-86	ptc-miR7822	5	0	21	21	1
			sch-miR8040-5-3p	UCAAAGUUAAAAUUUGAAGCC	228-248	stu-miR8040-5p	5	0	21	21	1
sch-MIR7997c-28	AAGUCACUUUUGUAACAAGGGGUUAUAUCAGCC UAUGUUGCUCGGAAUCCUAAGAAAUGAUGCCAC ACCCGUGUCGGAUUCUUAGAAAUAUACUACUUU UGGAGAAUCUGACACGUACCCGCCGACAUUUUU GAAGAGUUUGAGCAACAUAGAUAUCAUCAGACUC UAAAUAACAAAAUUGAGGG	185	sch-miR7997c-28-5p	AUGUUGCUCGGAAUCCUAAGAAAU	35-58	stu-miR7997c	5	0	24	24	1

			sch-miR5303h-28-3p	GACAUUUUUGAAGAGUUUGAGCAA	124-147	stu-miR5303h	2	0	24	24	2
sch-MIR780	AUAGGUAUAAUGCACAGCCCCUCAACCUAUGUCUUGAAAUAGUAAAGACGCAAUUGUGUUAUACUAAGUUCCUAUUAUUCGUGAAUUUAUUGUAUUAAUAAUUUUCUAUUUAUAUGGGGCUCAGUACUGAUUGAAUUUUUUUCAAUCUAAUACCAGCGUAAUAGGACCUUAGUAUAAUAUAAGGGUGUCUCUAAGAUUUUGGGCAUAGAUUGAGGGGAUACUUGUGCAUUUUUCCAAA	238	sch-miR780-5p	UUAUUCGUGAAUUUAUUGUAU	75-95	ath-miR780-2	5	0	21	21	1
			sch-miR10532-3p	AAGGGUGUCUCUAAGAUUUUGGGC	181-204	sly-miR10532	3	0	24	24	1
sch-MIR7997c-29	GUUUCUGCUCUAAAAAGUUAUGUUGCUCAGACUCUUCAAAAUGUUGCCACACUGUCAGAUCCUCCAAAAGCACUGCUUUCGGAGCAUUCAUCAUGCACCCAGUGGCAUUUUUGAAGAGUUUGAGCAACAUAGCUAAAGAGUGCAGAGAG	149	sch-miR7997c-29-5p	AUGUUGCUCAGACUCUUCAAAAUG	20-43	stu-miR7997c	4	0	24	24	1
			sch-miR5303i-29-3p	GCAUUUUUGAAGAGUUUGAGCAAC	105-128	stu-miR5303i	3	0	24	24	3
sch-MIR3438	GGGCUUAUACGGCGCGUGGCAUCUUUGAGGAAUGCUACCUGGUUGUUCCUGCCAGUAGUCAUAUGCUUGUCUCAAAGAUUAAGCCAUGCAUGUGUAAGUAU	101	sch-miR3438-3p	UCAAAGAUUAAGCCAUGCAUG	72-92	aly-miR3438-5p	5	0	21	21	1
sch-MIR7980b-4	UCCAUGUGAUACCUUAUCAUGAUAUGAUAUCCAUGAGAAGGAAUCAACGUUUGGUCAUGCGAUUUUACGUUGAUUUCAUCUCAUGAUACCAUAUCAUGAGAUGUGAUACCAUAUUCU	117	sch-miR7980b-4-5p	GAGAAGGAAUCAACGUUUGGUCAU	35-58	stu-miR7980b-3p	4	0	24	24	1
			sch-miR1886h-4-3p	AUUUUACGUUGAUUUCAUCUCAUG	62-85	stu-miR1886h	0	0	24	24	1
sch-MIR8009-1	UUUGUCUGUCACUUUUCUGGGUUUGAUUUUUUUUUAAAAGACCCCAAAAAGAGACAGACAAAGUCCCUUAGACUGUCUCUUUUCUGAAUUUUUCAAAAAAUAAUUUCCAGAAAAGCGACGGACGGA	126	sch-miR8009-1-3p	AUUUCCAGAAAAGCGACGGACGGA	103-126	stu-miR8009	2	0	24	24	1
sch-MIR1133-2	UCAUAUACUUCCUCCGUCCCAUUUUAUGUGGCGACGUCGACCGGACACGGAGUUUAAGAAAUAAUAAACACUUUAAAAUGUUUACCAAAUUGUCCUUCGAAAAAGUAAACUCACUUUUCUCUCUUCUCAUAAAUGUAUUAGGUACCAUCUUUAAAAUUAAGUGGGACCAAUAAGGGUAAAAAAUGAAUUGUACCUUUAAAUACUUACCAUAUAGAAAAUGUGAUAUUCUUUUUGGACUGACAAAAAAAAAAAAUGGUAACACGUAAAAUGGGACGGAGAAAGUAUAAAG	288	sch-miR1133-2-5p	CAUAUACUUCCUCCGUCCCAUU	2-23	tae-miR1133	4	0	22	22	1
			sch-miR812v-2-3p	AUGGUAACACGUAAAAUGGGACGG	252-275	osa-miR812v	4	0	24	24	1
sch-MIR6149b	UUAUAGCCUUUGUAUGUCAAAGCUUCGAUACGCACCUGAAUCGACAGAUAUAUAUAUUAUUCAGACUUUAUAAGAAUAUCACGCGUUCAUUAUUUCUAUAAGUCUGAAUAACAUAAAUCAUAUAUAUGUCGAUUCAGGUUCGUAUGAAAACUAUGGCAUACCUCAAAGGGUAACG	175	sch-miR6149b-5p	UCGAUACGCACCUGAAUCGAC	25-45	nta-miR6149b	2	0	21	21	1
			sch-miR6149-3p	CGAUUCAGGUUCGUAUGAAAAC	130-151	stu-miR6149-3p	3	0	22	22	2
sch-MIR159a-2	AAAUGAACUUAAUGAGCUGAAUCUGAAUGAUUCAGAUUCAGACCUAAAAAUCAAACGUACUUAAUAGGCUGAAUUUGAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCAAGC	112	sch-miR159a-2-3p	GACCUCCAUUAAGUGCAAGC	93-112	aly-miR159a-5p	5	0	20	21	1
sch-MIR8009-2	AAAAAAAGCGACGGACAACGUGGUUUUGUCCGUCGCUUUUCAGGGAUUUUGAAAAUAAAAUUUCCAGAAAAGCGAUGGACAGGGUCCUUUUGUCCGUUGCCUUUCUG	107	sch-miR8009-2-3p	AUUUCCAGAAAAGCGAUGGACAGG	60-83	stu-miR8009	2	0	24	24	1
sch-MIR7997c-30	CCUCUAUGUUGCUUGGACUCUUCAAAAAUGUCGAUGAGUUUGUGUCGGAUCCUCCAAAAAGGAUCCUCCAAAAAUGUAUAUUUUUGAAGGAUCUGACACGGGUGCGGCAACAUUUUUGGAGAAUCCGAGCAACGUAGUUC	140	sch-miR7997c-30-5p	AUGUUGCUUGGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1

			sch-miR5303f-30-3p	AUUUUUGAAGGAUCUGACACGGGU	80-103	stu-miR5303f	2	0	24	24	1
sch-MIR399i-3	CUUAUUAAGUGAAACAGUUGUAGGGCAGUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUAUAAUCUGCCAAAGGAGAGUUGCCCUACGAUUGCCUCUGCUUAAUUAU	107	sch-miR399i-3-3p	UGCCAAAGGAGAGUUGCCCUA	66-86	stu-miR399i-3p	0	0	21	21	1
sch-MIR7122a	CGGUAAAAUCGCUGCUGAGGCAGCGAUUUAGCAAAAAAAAAUUUUUUUAAUUAAAAAAAUGAAAUCGCUGCCCAAGCAGCGAUUUCAAAAAAAAAAUUUUUUUUUAUUAAAUCGCUGCCCUAGCAGCGAUUUAUAAAA	137	sch-miR7122a-3p	UUAAAAAAUGAAAUCGCUGCCC	52-73	ppe-miR7122a-5p	5	0	22	22	1
sch-MIR7983-10	GUGCUAAAGUCUUUACCGGCAUUAGUUAAGUGCCAUUAGAACCAAUGUCGCUAAAGGCUUUAGGGA	66	sch-miR7983-10-5p	UAAAGUCUUUACCGGCAUUAGUUA	5-28	stu-miR7983-5p	4	0	24	24	1
sch-MIR5628-2	UGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGAAUAGGUUGCUAAUUCUAGCAUUAGAGAAAUAUGGAAGAGAUGAUUGGAGAAAUAUUUCUAGG	103	sch-miR5628-2-3p	GAAAUAUGGAAGAGAUGAUUG	67-87	ath-miR5628	4	0	21	21	1
sch-MIR7484m	AUUUGUAUGUUAUAGCAAAGUUUGCAUAAUUGCGCACCAUAGCAAACAUAAAACAAUAUAAUUCGCUAUACAUAUACAAUUGUAUAAUUCGCUGGCCUAAAUUGUAUAAUUUGCUGGCCUAUUUCGCUGCAAUUGUAUAAUUUGCUUUGCAUACAGUU	158	sch-miR7484m-5p	UUUGUAUGUUAUAGCAAAGUU	2-22	gra-miR7484m	5	0	21	21	1
			sch-miR11309-3p	UUUGCUUUGCAUACAGUU	141-158	fve-miR11309	3	0	18	21	1
sch-MIR7997c-31	UUCAAUCUAUGUUGCUCGGACCCUUCAAAAAUGUCAAUGGGUGUGUAUCGGAUUCUCCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCGAAAGUGAAGAGUCCGUGCAACUUAGCUUUCA	133	sch-miR7997c-31-5p	AUGUUGCUCGGACCCUUCAAAAAU	9-32	stu-miR7997c	2	0	24	24	1
			sch-miR5303f-31-3p	AUUUUUGGAGAAUCUGACACGGGU	70-93	stu-miR5303f	0	0	24	24	1
sch-MIR7992-12	AACUUUGAGUGUGCACAAGUAGACACUUAAACUUGUGUAAAAUUGAACAAAUAGAUAGACACAUCCUAUAUGGUAUCCUACAUGGCAAUUUGCGUCCUACGUGGAGUCCUAUGUGUAUUGUGCCACAUAGGAAUAAUGUGUCAACUUGUUCAACUUUAUACAAGUUUAAGUGUCUAUUUGUGCACAGCCAAAUAG	195	sch-miR7992-12-5p	UUUGAGUGUGCACAAGUAGACACU	4-27	stu-miR7992-5p	5	0	24	24	1
			sch-miR5014a-12-3p	UUAUACAAGUUUAAGUGUCUA	156-176	ath-miR5014a-3p	5	0	21	21	1
sch-MIR6464	GGAGACAAUUGUGACCGUUAACUUUGGAUGACACACAAGUAGACACUUAAACUUGCAUAAAAUUAAACAAAUAGACACAUUCGUCCUACAUGUCACCUUACAUGGCAAUUUUGUGUCCUACGUGUAUUAUACCAUGUAGGACACGUGUGCUUACUUGUUCAAUUUUAUACAAGUUUAAAUGUCUACUUGUGCACACCCAAAGUUGGAGGGCAUAGUUGUCCGC	223	sch-miR6464-3p	UGCUUACUUGUUCAAUUUUAU	148-168	ptc-miR6464	5	0	21	21	1
sch-MIR5238	CAUGAUACGUGAUUAUAGUCAUUGUAAUGUACACAGUAACCUCAAUAAGUGUUUUUUUAAUUAAAUGUAGAUGAUACAUUGGGCAAAGCACAUGAUACAUGUGUGUUACGUUACCCAAAAUACACAUUUGUGUUUUGAAUUAAAAGUACAUGAUACAUUGGCUAAAGCAUAUGUAUCAUC	180	sch-miR5238-5p	UGUAGAUGAUACAUUGGGCAA	66-86	mtr-miR5238	5	0	21	21	1
			sch-miR7696d-3p	UUUUGAAUUAAAAGUACAUGA	133-153	mtr-miR7696d-3p	4	0	21	21	1
sch-MIR10542-2	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUUUUAAAAGAUUAGAAGUAAUAAACAUAAAUUUAAAACUAAUUUUUUAACUUCUAUUAAAUGAAGGGUAUAUGUGAGUCAUUUUGUAACCGCAGUGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAACCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUC	268	sch-miR10542-2-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
sch-MIR3706-4	GAGACACGUGACACAAUCUUAUCCAUCGAUCCGAUGUCGGAUAGGUGGAUAAGAUUAUGAGACGUGUAUG	70	sch-miR3706-4-3p	UGUCGGAUAGGUGGAUAAGA	35-54	pab-miR3706	5	0	20	20	1

		278	sch-miR11108h-5p	ACAUCGGUGGUUAAUGAGAUGG	43-64	lja-miR11108h-5p	5	0	22	22	1
sch-MIR5499	UUUGUUUCAAAAAAAUUGAUUUUUUUCCUUUUUU GACAACACUUUAACUUUAACUUUCCACGUGACAU GUUUAUAACCAUGCUGCUGAGUUGGAAUGGUCG AUAGUAAUUGAGUGUGAAUGGGGUGGGAGGUAG GGUUUGCUCGAUUUGAAGGUAUUCUAAAAAAAG GAAGAAUAAUUAUUGAAACUUU	189	sch-miR5499-3p	AAAGGAAGAAUAAUUAUUGAA	164-184	osa-miR5499	4	0	21	21	2
sch-MIR160h-3	ACAACAUGCCUGGCUCCUUGUAUGCCAUUUGCA UUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAU GGCAUUCUAGGAGCUAAGCAUGUAUA	92	sch-miR160h-3-5p	UGCCUGGCUCCUUGUAUGCCAUU	7-29	mes-miR160h	1	0	23	23	1
			sch-miR160c-3-3p	GCAUUCUAGGAGCUAAGCAUG	68-88	ata-miR160c-3p	4	0	21	21	1
sch-MIR844-2	UGUCCUUCAACUUUGGAUGUGCACAAGUAGACA CUUAAACUUGUAUAAAGUUAAACAAACAGACACA CAUGUCCUACAUGUCAUCCUACUUGUCAUUUUU UGUCCUACGUGGUGUCCUACGUGUAUUGUGUCA UGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUU GGACAGUUAAAGUGUCUGUUUGUGCAUUAUGAA AGUUGGAGGUCA	211	sch-miR844-2-5p	UCAUCCUACUUGUCAUUUUUU	81-101	aly-miR844-3p	5	0	21	21	2
sch-MIR529	AUACAUGCAUUUGUAUUCGUAUAUACAAUUUUCU AUCGCUUUAUACAAACACAACACAAUGUAUACAU UUGUGUUUUUAUAAAGUGAGAGAGGCGAGCGAA AUCUCGGAGAAGAGAGAGAGUGGAACGAAAAUA UAUGUAUAUACAAUUUUCUCUCGCUUUUUACAAA UAUAAACACGUUUUAUAUAUUUGUGUUCGUAUAA AAGCGAGAGAGACAAGUGAGAUUGUCACCAAAU GACAGUGACA	245	sch-miR529-5p	AGAAGAGAGAGAGUGGAACGA	109-129	bdi-miR529-5p	5	0	21	21	1
			sch-miR529-3p	AGAAGAGAGAGAGUGGAACGA	109-129	aqc-miR529	5	0	21	21	1
sch-MIR10542-3	AAAAAUUAAAAUAUACCUUGAACUUUGAUAGAAG AAUCAUAUAUACCCCUAAAUAAUUUUUUUUUAAA AAAAAUUACACGUAAUAAAUAUAAAUUUAAAACUA AUUUUUUAACUUUCGUUAAAUGAAGGGUAUAUG UGAGCCAUUUUUUAACGGCAGGGGUAUAUGUGA GCCGUUUGUAUAACGGUAAGGGCAUGUAAGAAC CACUUUUAUAGCGAAGGGUAUACAAGCUCCAAAU GACAAAGUUGAGGGGUAGAUCAGACCUUUUUCC CUUUCUAUAUUCACAGCUACAAUCUUCAUUCGU	302	sch-miR10542-3-5p	UAGAAGAAUCAUAUAUACCCCUA	29-51	sly-miR10542	0	0	23	23	1
sch-MIR10538-12	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUA AUGUUUUACUCCUAAAACGUUACUAUGAGUAACG UUCCUAAAACGUUACUGAAAAUAACGUUUUAGGA GUAAAACGUUACUUACAGUAACGUAUAUCAACCU AAUGCUGU	143	sch-miR10538-12-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
sch-MIR7512	GAGAAGUCUGCUGAUGUGGUCACACGUAUGCUG CAAGUAUUAUCAAUUUCUUUUUAUGCUCUACUUG AUCUAGGGUCUACGCUUUCUUUUCUGACUCCUC UUCUUGCUCUUACUUUUGAAAUACUACCUGAAG UUCUGCAUGAUCCUAUAGUGGUUAGUACGCCUU UAGGAGAAAGUGUAAGAACUAAUAGAGUAUAUAA GGAUUGCACAAUAGUUGUUCGUGGUAGGACUAU AUGUGCAGACUUGGU	248	sch-miR7512-3p	UACUACCUGAAGUUCUGCAUG	122-142	ghr-miR7512	4	0	21	21	1
sch-MIR902a	AAAUGAACUUAAUGGGAUUAAUCUAAAUGAUUCA GAUUCAUACCUAAAAUCAAACGUACUUAAUAGGC UGAAUCUGAAUGAUUAAGAUUCAGACCUCCAUUA AGUGCAAAC	111	sch-miR902a-5p	AAUGAUUCAGAUUCAUAC	26-43	ppt-miR902a-5p	5	0	18	18	2
			sch-miR172d-3p	UCUGAAUGAUUAAGAUUCAGA	73-93	bra-miR172d-5p	5	0	21	21	2
sch-MIR1917-1	UGUAUCACUACAACAAACUAACUUUUAGAGGCAU UAAAUAUUGACACUAAUAAAGAGUGCUAAAGUCU UUACCGGCACUAAUUAAGUGUCAUUAGAACCAAU GUCGCUAUAGGCUUUAGAGACAUAUACAAAGAG UAACAAUCAUCGCUAAAAUACAUAUUUAGCGGCA AUUAAGAAUUAAAUGCCGCUAAUGUUCAUUUUGU UGUAGUGUAUGUC	216	sch-miR1917-1-5p	ACUAAUAAAGAGUGCUAAAGU	46-66	sly-miR1917	1	0	21	21	1

sch-MIR10540-3	UAAGUUGAUUUGUCAGUUGGUUAUUCGACUAGU AGUUAUUAUUUCAGAAAGUCACUUUCUUUUGCU GAGGAAAAAGUUGGAAUCAAGAAAAAAGAUGACU UCCUAAUAUAAUAACUAUUAGUUGAAUGACCAUG UGAGAAAUCGACCCU	149	sch-miR10540-3-3p	AUAAUAACUAUUAGUUGAAUG	108-128	sly-miR10540	0	0	21	21	1
sch-MIR7980b-5	CAAAAAAAAUACGUGACACAAAAACUCAUAUUGC AUGUCCAAACAAAACUUCAACUCUUCUAUCUCAU GAUUUUAUAUAUCACAUUGCCAAACAAAGACGUA UGGAGCAAUAUGAAAUCAUGAGUCUCCAUUUGA CGAUAUAUGAAAUCAUGAGAUGAAAUCAGUGUUU GGACAUGCGAUUUCAUUUGAUUUCAUCGCAUGA UUUCAU	208	sch-miR7980b-5-3p	GAGAUGAAAUCAGUGUUUGGACAU	152-175	stu-miR7980b-3p	1	0	24	24	1
sch-MIR7490	AAUAAAAUAUGAAGAAACGUGAUUUUAUUCAUCA AGAUUGUGAGUACAAAUCUGUUCCUCCCUUGAU UCUACUCUCCAAGAUGAUUUAUCCAUGAUUCGA GAAUCGUUAGUGGCGUAUUUCUCGAAUUAGGAU GAUUUAGAUUUGACCUCUCUAUAUGAAUAAUCCA UCAAUGUCUACAAAAUUUCAA	188	sch-miR7490-3p	UGUCUACAAAAUUUCAA	172-188	ghr-miR7490	4	0	17	24	2
sch-MIR7484e	AUCCUUCAACUCAAAGAUUGAAUUUUAUGUAUUU UGACUUAUUAUUUGAUAAGUUAAGGGUAAGACG AUAUAUUCAUGUCCAAUCACCAAAAAAGGAUAAG ACAAUGAGUCAUGUCUAAUUGCACUAAAAGGGUA AGAUAUCAGGUUUAAGCCUUGGUGUACCGUGAU AAAUUAAAGAUCUUGAGUUCAAGUCU	194	sch-miR7484e-5p	AUUUUAUGUAUUUUGACUUAU	22-42	gra-miR7484e	5	0	21	21	1
			sch-miR2660-3p	UAAGAUAUCAGGUUUAAGCCU	134-154	mtr-miR2660	5	0	21	21	1
sch-MIR395a-3	GUUCCCUGGAGUUCCCUUGACCGCUUCAUUAUG GUUUACUUCAUCGUUUGAUGCUCUGCUGAAGUG UUUGGGGGAACUCUUGGACUCACUUUGAAAUUU UACACAAACAAAUAGAAGUGUAAGAGUCCUGGCU GUGGAUGAUGAACAUGAUAGUUCACGUAUAAAU CUAUUAAGGUGAUCCCUAGAGUUCCCUUGACCA CUUCAUGAGGGCUUACUUUGAUGUUAGAAGCAU UGCUGAAGUAUUUGUGGAAACUCCUGGGUUG	263	sch-miR395a-3-5p	UGAAGUGUUUGGGGGAACUCU	60-80	aof-miR395a	0	0	21	21	1
sch-MIR395b-2	AAAUAGUUUUCAAGUCUAUCAAGGUGUUCCCUA GAGUUUCCUUGACCGCUUCAUCAUGGCAUACUU CGCUGUUUGAUGCCCUGCUGAAGUGUUUGGGG GAACUCCCGGAUUCACUUUGAAAAUUACGC	128	sch-miR395b-2-3p	CUGAAGUGUUUGGGGGAACUCC	84-105	sly-miR395b	0	0	22	22	1
sch-MIR395b-3	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCG CUUCAUUAGGGUUUACUUCGCUGUUUGAUGCCC UGCUGAAGUGUUUGGGGGAACUCCUGGGCUCAC UUUGAAAU	107	sch-miR395b-3-3p	CUGAAGUGUUUGGGGGAACUCC	69-90	sly-miR395b	0	0	22	22	1
sch-MIR5026-6	GUUAAACAAUAGGUUGAGUCAUAAGAUUGUGUC ACGUGUCACUAAUUAUUCUUCCAUUAGAGGGAG GGACAAAUGUGAUUUUGGACGGUAACACUUUAU UUGUAUCAUUGUUUCAUAAUGUAUUGUAUUGUA GUGUAUUCUAUUGUACUGUAUUGUAUGAUAGAU AUAAUGUUUGACUAGAUUGUAUUGUUUGUU	195	sch-miR5026-6-5p	AGUCAUAAGAUUGUGUCACGU	17-37	ath-miR5026	3	0	21	21	1
			sch-miR8014-6-3p	AUUGUUUCAUAAUGUAUUGUAUUG	107-130	stu-miR8014-5p	2	0	24	24	1
sch-MIR11592-2	GUGUACAAAACCGAACCAAACCGCAAACCGAAAA AAAAAAUCCAACUAGUGGUUUGGUUUGACUUGG UUUGGUAUUG	77	sch-miR11592-2-5p	AAACCGAACCAAACCGCAA	8-26	cas-miR11592	3	0	19	19	2
			sch-miR8030-2-3p	UUGACUUGGUUUGGUAUUG	59-77	stu-miR8030-5p	4	0	19	23	1
sch-MIR11583b-1	UGUAAAUUGUAUAAUUAAGUGUAUAACACUAAGA UAUAUAUUUUUGCAUGUGUAUAUACAAUUUUCUC UCGCUUUAUACAAAACAGAAUUAUACACUUCUAU GUAUAAAGCGAGAGAGGCGAGCGAGAAUGGAGA GUGGCGAGCGAGAUUUUUGGGAGAGACGCUGG CAAAUUUUAUCUAAUGUUUGCUAUGGAGCACAAU UAAAUCAAACCCUAGCUAUUCCAUUUAUUUUAGG UUAUUAGUUUGCUAUUAUAUACAAUUUUCC	265	sch-miR11583b-1-5p	UUUUCUCUCGCUUUAUACAAA	62-82	pab-miR11583b	5	0	21	21	1
			sch-miR9555b-1-3p	UUAUUAGUUUGCUAUUAUAUA	236-256	bra-miR9555b-3p	5	0	21	21	1

sch-MIR6254	AAACACAAGAAAGCACCUAAACUUGUAUAAACUU GAACAAAUCGACACAUUCAUCCUACAUGGCAUCC CAUGUGAAAAUUUUGUAUCUUACAUGGUUUCCU ACGUGUAUUAUGUCAUGUAGGAUAUGUGUGUCU ACUUGUUCAACUUUCUAGAGUAUUAAGUGUCUA CUUGUGCAU	176	sch-miR6254-3p	UCCUACGUGUAUUAUGUCAUG	98-118	osa-miR6254	5	0	21	21	1
sch-MIR2118b	AUAGGGAGGUUGUGGGUUCGAACCCCCACACCC CCCCCUUAUUUUUCAGUUAUCUUCGCUGGGAUG GAGGCUGUGAGGUGGUGGGUUCAAACCCCCACA GCCUCCCCUU	109	sch-miR2118b-3p	CCCCCACAGCCUCCCCUU	92-109	aof-miR2118b	5	0	18	22	3
sch-MIR1888b-2	AGGUUAUUUUCUUACUUUAUAAUUCUCACUUUAU UCAUUUUGCUUGGCCCAUAUUGAUCUGUCAUAA CUAGAGUUGUCAAUAAGGGUUAGGCCCGUUGGG CCGGCUUGGUCUAACCCGAGAUUUAAUAGGGUU GGACUAAGAUUUUUGAAGCCCAUUUUAGAAAAAG GUUUUUUAGCUCGACCUUAAUAAGUCUGUUGAU UUGAUUGGCUUGAGAAAUAUAGGUAGGGCCGAC CCCUAGGCCAAUAAUAAUUAAUUAAAAAAUAUAA UAUAAUAUUAAAAUUUAAAAU	288	sch-miR1888b-2-3p	UUGGACUAAGAUUUUUGAAGC	132-152	ath-miR1888b	4	0	21	21	1
sch-MIR7983-11	NNNACAACAGAAAUGAUCAUUAAUAGCAUUUAAU UCUUAAUUGCCGCUAAAUAUGUAUUUUUAGUGG CAACUGUCACUCUUUGUAUAUGUCCCUAAAGCC UUUAACUACAUUGGUUCUAAUGGCACUUAACUAA UGCCGGUAAAGACUUUAGCACUCUUUAUUAGGG UCAAUAUUUAAUGCCGCUAAAAAUUAUUUUUGUU GUAGU	206	sch-miR7983-11-3p	ACUAAUGCCGGUAAAGACUUUAGC	130-153	stu-miR7983-3p	1	0	24	24	1
sch-MIR7997c-32	CAGGCUAUGUUGCUCGGACUCUUCAAUAAUGUC AAGGGGUGCGUAUCGGAUUUACCAAAAGUAGUG UAAGUUUAGAAAAUCCGACACGGGUGCGGCAUC GAAAGUGAAGAGUCCGCGCAACUUAGCUUC	129	sch-miR7997c-32-5p	AUGUUGCUCGGACUCUUCAAUAAU	7-30	stu-miR7997c	2	0	24	24	1
			sch-miR5303e-32-3p	GUUUAGAAAAUCCGACACGGGUGC	70-93	stu-miR5303e	5	0	24	24	2
sch-MIR2667b	AUAUGUCCUUGAUGUGAUGACUAUCAGAUUUUG GGAUGAUAAGUAUUAAACUUUAGAAACUUAUUUA AAUUGGUUGCUUAGUAUCUUUUGGAGCUUCCUC AUUAUUUAUAUUAUUUAUAGUUGAAUUAUUGGUA CAUGUUGGGAUUUGAAUUUUUUUUGGUUCGGCC ACCUAGGUAGUUAAGUGUGGAUGCCACUCACGA CUCGUUUUGGAUCGUGACAAACUUGGUAUCAGA GCGUUAGGUUCCUUGAUCUCAUCACACAAGGAC AAGU	270	sch-miR2667b-5p	UCCUUGAUGUGAUGACUAUC	6-25	mtr-miR2667b	4	0	20	20	1
			sch-miR7543-3p	UUAUUGGUACAUGUUGGGAU	126-145	lja-miR7543	5	0	20	20	1
sch-MIR10538-13	AAACUAACGGCGUUAGGUUGAUAUACGUUACUG UGAGUAACGUUUUACUCCUAAAAACAUUUUUUUU GAGUAACGUAUAUCAACCUAACGCCGUCAGCUU	100	sch-miR10538-13-5p	AGGUUGAUAUACGUUACUGUGAGU	15-38	sly-miR10538	4	0	24	24	1
sch-MIR11068f	AACUUAACGUCAAUAAACUAUGAUCUUUAACUUU GGAUGUGCACAAGUAGACACUUAAACUUGUAUAA AAUUGAGCAAAUAGACACAUUUUUCCUACAUGAC AAUUUUGUAUACUACAUGGCAUCCUACGUGUAU UAUGCCAUGUAAGACACUUGUGUCUACUUGUUC AAUUUUAUAAUGGUUUAAAUGUCUCCUUAUGUAC AUUCAAAGUUGAAGACAUAGUUAUUCGUUAACGC	236	sch-miR11068f-5p	CUAUGAUCUUUAACUUUGGAUG	18-39	lja-miR11068f-3p	5	0	22	22	1
			sch-miR6254-3p	UCCUACGUGUAUUAUGCCAUG	124-144	osa-miR6254	5	0	21	21	1
sch-MIR3700	AACUUUGACCUCCACUUUCAUAAUGCACAAACAG GCACUGUAACUAUCCAACUUUUAAAUAAAUAAAC ACAUGAGUCCUACAUGGCACAAUACACGUAGGU CACCACGUAGGACAAAAAAUGACAUGUAGGACAU AUGUGUCUAUUUGUUCAACGUUAUACAAGUUUAA GUGCUUACUUGUGCACACCCAAAGUUGAAGGAC AUAAAUG	209	sch-miR3700-3p	CACACCCAAAGUUGAAGGACA	183-203	pab-miR3700	5	0	21	21	2
sch-MIR7997b-14	UUUCUAAGUUUCUCGGACUCUCCAAAAAUGUUG CCGAACCCGUGUCUGAUCCUUCAAAAAUACAUUA UUUUUGUAGGACACCUAUUGACCUUUUUGAAGA GUUCGAGCAACAUAGGUU	118	sch-miR7997b-14-5p	AAGUUUCUCGGACUCUCCAAA	6-26	stu-miR7997b	4	0	21	21	1

			sch-miR5303-14-3p	UUUUUGAAGAGUUCGAGCAAC	91-111	sly-miR5303	0	0	21	21	1
sch-MIR7997c-33	AUCAAGGCUAUGUUGCUCGGACUCUUCAGAAAC GUCGACGGGUGCGUGUCGGAUCCUCCAAAAGUA AAGCAUUUUUGGAAGAUCCGACACGGGUGUGGU AGCAAUUUUGGAGAGUCCGAGCAACUUAGCCUU AAG	135	sch-miR7997c-33-5p	AUGUUGCUCGGACUCUUCAGAAAC	10-33	stu-miR7997c	3	0	24	24	1
			sch-miR5303f-33-3p	AUUUUUGGAAGAUCCGACACGGGU	71-94	stu-miR5303f	3	0	24	24	1
sch-MIR11144-2	AGUUACUCUCUCUGUCCCUUUUUACUUGUCCAC UUUUGAAUUGACACACCUAUUAAGAAAAUAAAUA AUGACGUAGUGAGUUUACCAUUUUAACCCUAUUA AUUAUGAAGUGGAUGAAAAGUUCUACAUUUUUCA AAGUAAUUAGUCAUUUAGUUGUGGGUAUAAUAG GUAAGAAAAAAUUAUCCUGUCUUGAUUUGUCAAA AUGGACAAAUAAUUAGAGACAACUAUAAAAGGAA AAGUGGACAAGUAAUUAGGGACGGAGGUAGUAU UU	271	sch-miR11144-2-5p	UUUACCAUUUUAACCCUAUUAAU	81-103	lja-miR11144-5p	5	0	23	23	1
			sch-miR5049c-2-3p	GGACAAGUAAUUAGGGACGGAGG	241-263	hvu-miR5049c	4	0	23	23	2
sch-MIR6145b-1	AUUCCUUUUUGACCUACGUGGCACUAGCUUGGA AAAAAAAGUCAACCAGCGCUGGGCCUACAAGAUA GUGUCACGUAGGCCAAAAAGGGGU	91	sch-miR6145b-1-5p	UUGACCUACGUGGCACUAGCU	9-29	nta-miR6145b	5	0	21	21	1
sch-MIR10189-1	ACAUAACCACCUAUGUGUUUUCGCCUUGCUCAA GAGAGAGGUCACAAAAUUAAGACCACUAGAAUAA UCUCCUAAGGAGAGGGUCGAUAUGAGGUUCAGC CUGAGAGGGUGAGCCCUAGUCCCAUAUCCAAGC ACUCUCGUGGAAAGAGCGAGUGUGGAUAAGGCG UAGGUUGGUUAGUU	180	sch-miR10189-1-5p	AAGACCACUAGAAUAAUCUCC	52-72	gma-miR10189	3	0	21	21	1
sch-MIR845e	UUGUGUGUCUCUAAAACCAAAUGAAGACUAUCAC UAUUUAUACUACAAGAAGUCUUCCUAGAAAUGAA UAGGAAGAUAAUGGAGGUAGUAAAUAGUGAAGA UAAUGGUCUUAGGAGUUACAUAG	124	sch-miR845e-5p	UGUCUCUAAAACCAAAUGAAG	6-26	vvi-miR845e	5	0	21	21	1
			sch-miR6103-3p	CAAGAAGUCUUCCUAGAAAUG	46-66	cca-miR6103-3p	5	0	21	21	1
sch-MIR7983-12	CUAAUCCACUGCAUCAAAAAUGAUCAUUAGCGGC AAUUAACACUCUUUAUAUAUAUGUCGUUAAAGUC UUUAGCGACAUUGAUCUAAAUGUCACUUAACUAA UGCCGGUAAAGACUUUAACACUCUUUAUUAAUGU CAAUAUAUCUAACGCCGCUAAAAGUUAUUUUUGU UGUAGUGAUCAA	182	sch-miR7983-12-5p	UAAAGUCUUUAGCGACAUUGAUCU	62-85	stu-miR7983-5p	3	0	24	24	1
			sch-miR7983-12-3p	ACUAAUGCCGGUAAAGACUUUAAC	98-121	stu-miR7983-3p	0	0	24	24	1
sch-MIR8001b-6	AUGUAAGGGAAUUACAUGGGGAUUAGUAUGAAA UUUGCAGGAAAGUAAGUUCCUUGCGGAUUUUCA UACUAAUUCCUAGGAAAAUUCCAUAUAACU	96	sch-miR8001b-6-5p	AUGGGGAUUAGUAUGAAAUUUGCA	16-39	stu-miR8001b-5p	4	0	24	24	1
			sch-miR8001b-6-3p	GGAUUUUCAUACUAAUUCCUAGGA	58-81	stu-miR8001b-3p	1	0	24	24	1
sch-MIR5262	UGGAGUGUCACGUACCGACUCAAGAGGAAUAAA GAGAAUGAAUCUUGGAUUAUGUUAAUAUACUCAA UUUGAAGAACCUAAUUCCUAAAUGAGUAUGGUG UGGAGGCUUGAGUCCUCAUAGGUGUGUUUUCGU GUUGUUGCAGAUGAUUCUUAUACUUGUUGCUAU CACCUGUUAAGUAUUUGGUUCGUUUAAUGCUAU UAUUCGAUAUAUAUUGUUUUCUAUUUUGAGUUG GCCGAUGAUACUUAC	247	sch-miR5262-5p	UAUGUUAAUAUACUCAAUUUG	51-71	mtr-miR5262	5	0	21	21	1
sch-MIR158b	CCAUCGGAAAAUUUUUGAGUCCGGAGUCUAAAG GGUAUAAAUUUUUAUUUUAGAAAAUCGCUACUUA AAAAAAAUCACAUUUUGCAAAAUCGUUGCAGUAG CAGCGAUUUUGCUUUUUCCAGUGGAGGAAAUCG CUAUUGUUCCAGCGAUUUUGCCGUUUUGGUUAA UAUAAAAUUUUAUAUACCGUUUUGGAAUUUUUGU UAAUAUUUUAUACCCUUUAGGCUCCGGACUCCAA UUAUUUUAAACUU	248	sch-miR158b-3p	UUUAUAUACCGUUUUGGAAU	176-195	aly-miR158b-5p	5	0	20	20	1
sch-MIR9555b-2	CAUUUAUGAACUUUAACUUUGAGUGUGCAUAAUU AGACACUUAAACUUGUAUAAAGUUGAAAAAAUAG	222	sch-miR9555b-2-5p	UUAGACACUUAAACUUGUAUA	33-53	bra-miR9555b-3p	5	0	21	21	1

	ACACACAUCUCCGACAUGUCAUUUUACAUUUCAU UUUUUGUCCUACGUGGUGUCCUACGUGUUUUUC GUCAUGUAGGACUCAUGUGUUUAUUUAUUUAAA AGUUGGAUACUUAAAUUUCUUGUUUGUGCAUUA UGAAAGUUGGAGGUCAAAUUU										
			sch-miR11552-2-3p	UGUUUUUCGUCAUGUAGGACU	128-148	pab-miR11552	5	0	21	21	1
sch-MIR6462c	UCCUUGAAUUCUAUGGUAUGUAUUCUGUUUAUU UUGCAUAUUGUCAAUUGGUCUUUAUGGUUAAUC AGCUAUCGUUGGUUGGGUGAUAGCAAGGCACAA AAAUUGCAAAGGUAACUUGUUUGCCAAAUAUUUA GCUGAAAUUACUUUUGUAAUUUUUUCUUGUCCU UUUUUUUUUUUUUGGCAUAAUACAUAAAUAUGUC UUUUAAUUUGACUUCGAAUUAUAUUUAUGGCUU UCAAUUUUGGAUGUGCACAAGUAGACACUUAGG ACCCGUUUGGUAGGCGGUAUUAGGUAGAAUAAU CCAUGGAUUAAAAUU	314	sch-miR6462c-5p	AAGGCACAAAAAUUGCAAAGGU	91-112	ptc-miR6462c-5p	5	0	22	22	1
			sch-miR9476-3p	UCUUGUCCUUUUUUUUUUUUU	158-178	sly-miR9476-5p	5	0	21	21	1
sch-MIR7997b-15	UUUUCACUAAGUUGCUCGAACUCUCCAAAAAUGU AAUGAAGUACUACUACUUUUGAACGAUCCAACAC GUACCUAACGAUCACAUUUUUGAAGAGUCCGAG CAACAUAGGAUUU	114	sch-miR7997b-15-5p	AAGUUGCUCGAACUCUCCAAA	9-29	stu-miR7997b	4	0	21	21	1
			sch-miR5303h-15-3p	CACAUUUUUGAAGAGUCCGAGCAA	81-104	stu-miR5303h	2	0	24	24	2
sch-MIR6196-2	UCUCACGCUUUAUACAAAUAGAAACGCAAUUUAU ACAUUUCGCUUCUGUUUGUAUAAGAGAGAAAGG CGAAGGUUGCGAGCGAGAUCUGGAAGAGGAGAU AAAGGGGAACAAAAAUAUAUGUAUUUGUACAAUU UUCUCUGCUUUAUACAAAUAGAAACAGUUUUUAU ACACUUAUAUUUGUAUAAAAAGUGAGG	195	sch-miR6196-2-3p	UGGAAGAGGAGAUAAAGGGGA	88-108	hvu-miR6196	5	0	21	21	2
sch-MIR10519-4	CUUAAACUUGUAUAAAGUUGAACAAAUAGACACA CAUGUCCUACAUGUCAUCCUACAUAUCAUUUUUU UGUCCUACGUGGUGUCCUACGUGUAUUAUGCCA UGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUU GGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAA AAUUGGAGGUCAAAGUUAAAAUUUGAAGCCAAGU UUAGGGUGUAAUAUAUGUAUUAUACCUUUUUGA UAUUGUGAUGGACUAUUUUCUUUCAAAUGAGUA UUUACAAAAAAGUGUUUGUUGUUUGUCUCAAGC UUCAAAAACUUUAGA	315	sch-miR10519-4-5p	AUUUAAAAGUUGGAUAGU	124-141	tae-miR10519	4	0	18	18	3
			sch-miR166k-3p	UGUUUGUUGUUUGUCUCAAGC	280-300	osa-miR166k-5p	5	0	21	21	2
sch-MIR5181b	CCCUAAUGCCACUGUUGUUCAAAAACUAGAGCAU AUAUGCUCUUCACUUUAAUAGAAGACUAUAUAGG CAUACGAGACACAAUCUUAUUUGUCGAUUCGAUA UUUAAUAAAUGUCGAGUCAGUGGAUAAGAUUAC GAUACAUGUAUGUUCGUGGCAAAAAGGGUAUAU AACUAUAUAUGCUCUAGAUUUUGGACAGCAUUG CAGCAAUAUCC	212	sch-miR5181b-3p	UUCGAUAUUUAAUAAAUGUCG	96-116	bdi-miR5181b	5	0	21	21	1
sch-MIR2673b-2	AACAUACUCUUCUUCCUCUUCCUCUUCCUCUACC UAUACCUCUUUCCCUUCCCGUACUUCUAUUCGA GAUGUUUUGUUGAUUCAGAAGUUGAUCAUCACG AAAAAGUGGUGUAGCAUUUUUAGUGGAAGAGAU UGAUUUUUCUUUUCUCCUUAAACUUGUACCAACA ACAAGAGGAGCAGGAGGAGGAGGCGAUGGUAGA GUAUCCA	207	sch-miR2673b-2-5p	CUUCUUCCUCUUCCUCUUCCUC	9-30	mtr-miR2673b	2	0	22	22	1
			sch-miR5829-2-3p	AGCAGGAGGAGGAGGCGAUGGUAG	176-199	osa-miR5829	5	0	24	24	1
sch-MIR5021-2	UAACAAUGGAGAAACGAGUAAAAACUGCAAAAGA AAGGGAGAAGAAGAAGAAGAAGAAGAAUAAACCC AUGAAGAAAAAGGGUGGAUUUGAUGUCAUCGCU AGAGAAAUGUAAAAGUAAUUUACAGAUUCAAACA CCCAAAUUCAGAUUAGUUUCUUCAUUUCUUCGC UUUCUUAGCCGGAGACUUGAUAGUUUUCGGCUU CUUCACAACUUUCUUCGCUGGAGUUUUCUUCAC	248	sch-miR5021-2-5p	GGAGAAGAAGAAGAAGAAGA	38-57	ath-miR5021	2	0	20	20	2

	UUUCGCAACUGCGG										
sch-MIR1917-2	UUGCUAUACACUACAACAAAAACAACUUUUAGCG GCAUUAAAUAUUGACAUUAAUAAAGAGUGUUAAA GUCUUUACAGGUAUUAGUUAAGUGUCAUUAGAA CCAAUAUAGCUAAAGGCUUUAGGGACAUAUACAA AGAGUGUCAAUUGCCGCUAAAAAUACAUAUAUAG CGGCAAUUUAAAAUUAAUUGCCGCUAAUGAUCUU UUUUGUUGUAGUGAUAGUAC	223	sch-miR1917-2-5p	AUUAAUAAAGAGUGUUAAAGU	50-70	sly-miR1917	1	0	21	21	1
sch-MIR156b-17	AAGGGGGGUGACAGAAGAGAGUGAGCACAUAUG GUCUUUUCAAGCAUGAUGUUUACAUGCUUGAAG CUAUGCGUGCUCACAUCUCUAUCUGUCACCCCC ACC	102	sch-miR156b-17-5p	UGACAGAAGAGAGUGAGCACA	9-29	hvu-miR156b	0	0	21	21	1
sch-MIR156b-18	GGAGGUGACAGAAGAGCGUGAGCACAUGUGUGU UUUCUAGCAUGAUGUUUAUAUGCUUGAAUCUAU GGGUGCUCACUGCUCUAUAUUUCAUCCUCAUCG CUUUUCCUAUCUCUCUAGAUUUAAUUUUCUGUC UCUAUUUUGUAUAUAUUAUGCAUGUAUUUAUGUA UAUAUAUCAGUUAUUCCAAGUAUAUAUUAAUCUA GUUAGUACAUAUUAUGUGCUCAAUUUUCAUCACC AAG	237	sch-miR156b-18-5p	UGACAGAAGAGCGUGAGCACA	6-26	hvu-miR156b	1	0	21	21	1
sch-MIR158a-2	AUGUGUACACAGAGGCGGAGCUAAGUGGAGAUU CAUAAGUUCGGACGAAUUCAUUAACCUUUUCACA AAUUUAAUAUUUAUAUUUAUAUUUAUAAACUAAA UAAAUAUAUGUACGUUGACAGGCAAACCCCCAAA CGCCUACAUUGGCUCCGCUUCUAUGUGUACAAG U	169	sch-miR158a-2-3p	CUCCGCUUCUAUGUGUACAAG	148-168	cas-miR158a	5	0	21	21	1
sch-MIR2642	UUAUGUUACUCAGAUUCUUUAAUAAUGUUGCUG CACCCAUAUUAGAUUCUUCAAAAGAUGUACUGCU UUUGAAGGAUCCGACAUGCAUUUGGCGAUAUCU UUAAAGAGUCUGAGCAACAGAG	122	sch-miR2642-5p	AUUAGAUUCUUCAAAAGAUGU	41-61	mtr-miR2642	5	0	21	21	1
			sch-miR5303i-3p	AUAUCUUUAAAGAGUCUGAGCAAC	95-118	stu-miR5303i	2	0	24	24	1
sch-MIR10533-2	AUCCAUUAUUCUUCUGAAUUGUUUAUCUUCUGC UUUGAUAUGACAGCUUUAUUGUAUUCAUUCAGG AAUAUGAGGAGUAUGAAGAUUUGGAUGAAUAUG AGGAAGAAAGCGGUGCAGAGGAAUAUGAGG	129	sch-miR10533-2-5p	UCUUCUGAAUUGUUUAUCUUCU	10-31	sly-miR10533	5	0	22	22	1
			sch-miR11036-2-3p	UUUGGAUGAAUAUGAGGAAGAA	86-107	seu-miR11036	1	0	22	22	1
sch-MIR4223	CAAGUGUAUUUGUGUCAAAGUUAUAUGGGGGAU ACAAUAUAUUUUCUUAUUGGCAUAAUACAUAAUU GUGUCCUUUAACUUAGCUUCGAAUCACAUAUAC GCCUUCAACUUUGGGUGUGCACAAGUAGACACU UAAACUUGUAUAAAAUUGAACAAAUAAACACA	165	sch-miR4223-3p	AUAAAAUUGAACAAAUAAACAC	143-164	aly-miR4223	5	0	22	22	1
sch-MIR10538-14	GUUGACGGCGUCAGAUUGAUAUACGUUACUCAC AGUAACGUUUUACUCCUAAAACGUUACUGUGAG UAACGUCUUACUCUUUAAAUGUUACUUACAGUAA GGUUUUAGGAGUAAAACGUUACUCAAAAAAACGU UUUAAGAGUAAAAUGUUACUUAAAGUAACGUAUA UUGUCCCUUAUCUUCAAAUUGUCAAACACACGUC AAUGAAUAUACUAUCACUUACUAAUGACUGAAUU ACUCGAUACCAACCAUAACGUUUAUAACUAAAUC AACCCGACCCGAUCCGA	287	sch-miR10538-14-5p	AGAUUGAUAUACGUUACUCACAGU	13-36	sly-miR10538	0	0	24	24	1
			sch-miR8030-14-3p	UUAUAACUAAAUCAACCCGACC	258-279	stu-miR8030-3p	5	0	22	22	1
sch-MIR156h-2	GCCUCUCUCACUUUAUAUACAGACAUAAAUGUAU AAAUGUGUUUGUAUAAAGUGAGAGAAAACUGUAU AUAUAUACAUCUCUUUUCUUCUGCCUCUCCCCCA GAGAAUCUCGCUCGCCUCUCUUACUCACCUCUC UCACUUUAUACAAACACAAAUCUAUUGUCUCUGU GUUUGUAUAAAGCGAAAGAAAA	191	sch-miR156h-2-5p	CAUCUCUUUUCUUCUGCCUCU	76-96	aly-miR156h-3p	5	0	21	21	3
			sch-miR838-2-3p	UUUUCUUCUGCCUCUCCCCCA	82-102	aly-miR838-3p	5	0	21	21	1
sch-MIR7701	UGACAAAUAUGUGAUUAAUGAUUAAGGAUUGUG GAGUUGCCCUCAAGCUUAUAAGUUGACAGUUUG GUCCAUUCAAUUAAAUGAAGGGUAAAAGGGUAAU	131	sch-miR7701-3p	UUUGGUCCAUUCAAUUAAAUG	63-83	mtr-miR7701-3p	5	0	21	21	1

	UUCACAUACCUAAUUUAAUCAACUUUUGGUG										
sch-MIR10189-2	AGCGGAAGGGUCUAGAGUUGUGGAGAGGUUUGCGGAGAACUCUAGAACCUUCUAGACUAAUAUAGAAUUCUCUAGAAUAACUUAGAUAUUUUCUUGGAAAGAUUUAGAAAUUCCAAGAAUGUGUAGAAUUUUCUAGAGAGGGACUAAAGUGUAAAUAAAGAGGGACUUGUAAAGUAAAUAAUAUUUACACUUAGAUCCUUAUGAGGUAGUAUAAAUAGGGAGUGACAUUCAUUUGCAAGGCAUCCAAGCUUGAAAUAAGCAAACCAUGAAAGUUGUAAAGAAAUCUUCCAAGUUGUAAAAAACCUUCUUCCAAAAUUCUCUAAGUCUUCCUUU	333	sch-miR10189-2-5p	GAGAACUCUAGAACCUUCUAG	35-55	gma-miR10189	5	0	21	21	2
			sch-miR5014b-2-3p	AUAUUUACACUUAGAUCCUUA	181-201	ath-miR5014b	5	0	21	21	1
sch-MIR5026-7	UUAAGGUCCUAUUACCCCCCUAAACUUAUUUUAUAAACAAUUUUCUAUUCCUUUUCGGCCUACGUGACACUAGCUUGAAAAAAUAAAUAUCAAAACACACUAGACCCACAAGAUAGUACCACGUAGGCCGAAAAGGGGUAGAAAAUUAUUUAUAAAUUAAGUUCAGGGGGAUAAUAGGACCUUAG	185	sch-miR5026-7-3p	ACCCACAAGAUAGUACCACGU	104-124	ath-miR5026	5	0	21	21	1
sch-MIR7997c-34	AACCUAUGUUGGUCGGACUCUUCAAAAAUGUCGUUAGACGUGUGUGAAAUCCUCCAAAAGCUAUCCAUUUUGGAGGAUCAGAUACGAGUUUGACAAUACUUUAAAAAAACGAGAAACAUAGACA	124	sch-miR7997c-34-5p	AUGUUGGUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
			sch-miR5303e-34-3p	UUUUGGAGGAUCAGAUACGAGUUU	68-91	stu-miR5303e	5	0	24	24	1
sch-MIR159a-3	AAAUGAACUUAAUGGACUGAAUCUGAAUCCAAACCUAAGAACCAAACGUACUUAAUAGGCUGAAUUUGAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCAAAC	103	sch-miR159a-3-3p	GACCUCCAUUAAGUGCAAAC	84-103	aly-miR159a-5p	4	0	20	21	1
sch-MIR1919-4	UCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCGCUUCUAAGGAACCACUUUUUCUGUAAAUCUAAUUAAUUUGAAUUCAAUGUGGUAGGGCGAGAGUCAUCUGUGACAGGAUAAUGGAAGA	122	sch-miR1919-4-5p	UGUCGCAGAUGACUUUCGCGC	15-35	stu-miR1919-5p	1	0	21	21	1
			sch-miR1919-4-3p	GCGAGAGUCAUCUGUGACAGG	91-111	stu-miR1919-3p	1	0	21	21	2
sch-MIR10542-4	AACUUUGAUAGAAGAAUCAUAUAUACCACUAAAUAAUUUUUUUAAAAAAAAUUAGAAGUAAUAAAUAUAAAUUAAAAAUUAAUUUUUUAACUUCCGUUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGGUAUAUGUGAGCUGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUCCCUAUCAAAUAA	257	sch-miR10542-4-5p	UAGAAGAAUCAUAUAUACCACUA	9-31	sly-miR10542	1	0	23	23	1
			sch-miR6160-4-3p	GCAUAUAUGAGCCACUUUUAUAAC	168-191	nta-miR6160	5	0	24	24	1
sch-MIR9749-1	GCAUUAGUUGCUUUCACUUUUCCUUUGCAAUUCUCAGUCGGAAAAGGAGGAAGUGAACUCUUUGAUCGCGUGUGAUAAGCCAUGGUCUACAGAUCAGCCAUUGAGAAUUGGUAAAGGAAAUAAAAAAAAUAAAAG	135	sch-miR9749-1-5p	UUAGUUGCUUUCACUUUUCCU	4-24	gma-miR9749	4	0	21	21	1
			sch-miR821e-1-3p	AAAUAAAAAAAAAUAAAAG	118-135	sbi-miR821e	4	0	18	21	1
sch-MIR171b-5	UAUAGAUAUUGAUGCGGCUCAAUCUGAAAGACAUGGUUAGAUAUGUAAUUAGCCUUGUAAUUUUGGAUUGAGCCGCGUCAAUAUCUCUC	89	sch-miR171b-5-5p	AGAUAUUGAUGCGGCUCAAUC	4-24	stu-miR171b-5p	1	0	21	21	1
			sch-miR171e-5-3p	UUGAGCCGCGUCAAUAUCUCU	68-88	sly-miR171e	0	0	21	21	1
sch-MIR8132	CUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAACAAAUAGACACACAUGUCCUACAUGUCAUCCUACAUGUCAUUUUUCGUCCUACGUGGCGUAUUACGUGUAUUUUGCCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGGUUGUGCAUUAUGAAAGUUGGAC	203	sch-miR8132-5p	UUCAACUUUGGGUGUGCACAA	2-22	ppe-miR8132	5	0	21	21	1

			sch-miR812f-3p	GUGCAUUAUGAAAGUUGGAC	184-203	osa-miR812f	5	0	20	24	3
sch-MIR482d-3	UUGGGAAUCUUUUGGAGUGGGUGGGAUGGAAAA AUAUUGUAUUUAUUUUUUUUCUGAAGGGAAAAAG AUAAGAAUUGAAUUUUUUCCUAUUCCACCCAUGC CAAUGGCUUCCAGU	115	sch-miR482d-3-5p	GGAGUGGGUGGGAUGGAAAAA	14-34	sly-miR482d-5p	0	0	21	21	1
			sch-miR482d-3-3p	UUUCCUAUUCCACCCAUGCCAA	83-104	sly-miR482d-3p	0	0	22	22	1
sch-MIR7997c-35	AUUUAUGUUGCUCGAAAUCUUCAAAAAUGUCAUU AGAUACGUGUCGGAUCCUUUAAAAGUAGUGCAU UGUGGAGGAUUGUGGCAACAUUUUUGGAGAGUU CGAGCAACUUAGAG	114	sch-miR7997c-35-5p	AUGUUGCUCGAAAUCUUCAAAAAU	5-28	stu-miR7997c	3	0	24	24	1
			sch-miR5303-35-3p	UUUUUGGAGAGUUCGAGCAAC	88-108	sly-miR5303	1	0	21	21	1
sch-MIR7992-13	UGACCUCCAACUUUCAUAAUGCACAAAUAGACAC UUUAACUAUCCAAUUUUAAAUAAAUAAACAUGAG UCCUACAUGGCAAAAUACACGUAAGACAACACGU AGGACAAAAAAUGACAUGUAGGACAUGUGUUUAU UUGUUCAAGUUUAUACAAGUUUAAGUGUCUACU UGUGCACACCCAAAGUUGAAGGGCA	194	sch-miR7992-13-5p	UUUCAUAAUGCACAAAUAGACACU	12-35	stu-miR7992-5p	4	0	24	24	1
			sch-miR5014a-13-3p	UUAUACAAGUUUAAGUGUCUA	147-167	ath-miR5014a-3p	5	0	21	21	1
sch-MIR8013-1	AAUGUUAAAUCGCUGCCCUGGCAGCGAUUUGUA AGAAGAAAAAUUUUGAAAUCGCUGCUGGAGCAG CGAUUUCAUUUUUUUAUUAAAAAAAAAAAAUUUU GCAAAAUCGCUGCCUCAGCAGCGAUUUUACUUU UUCAGUUGAAGUAAAUCGCUGCGUCGGCAGCGA UUUUACCGU	175	sch-miR8013-1-3p	UGAAGUAAAUCGCUGCGUCGGCAG	140-163	stu-miR8013	5	0	24	24	2
sch-MIR7535-2	AUAUAUGUUGCUCACGCUCUUUGAAAAUUGUGG GUGUUGGAUCGAGGAUCCUCCAAAUGUAGUCUA UUUUGAGAGUAUCUGGUAUGGGUGAGGCAUCAG UUUUGGAGAGUCCGAGCAACAUAGGU	125	sch-miR7535-2-5p	UGAAAAUUGUGGGUGUUGG	22-40	lja-miR7535	5	0	19	19	2
			sch-miR5303h-2-3p	AUCAGUUUUGGAGAGUCCGAGCAA	95-118	stu-miR5303h	4	0	24	24	1
sch-MIR7997b-16	AAGUUGCUCGGACUCUCCUAAAAUGUUGCGGCA CCCGUGUUGGAUCCUUUAAAAAUGCACUACUUU UGAGGGUCUGACACACCCGAUGACAUUUUUGAA GAGUCCGAGCAAUGU	114	sch-miR7997b-16-5p	AAGUUGCUCGGACUCUCCUAA	1-21	stu-miR7997b	4	0	21	21	1
			sch-miR5303h-16-3p	GACAUUUUUGAAGAGUCCGAGCAA	88-111	stu-miR5303h	2	0	24	24	2
sch-MIR5021-3	CAAGGGAUUAUUGAACCAAUUCUGGUCCUUGCU AAAGGAUCAAAAUAUGGUUUGGGGUACAUCCCC ACAGAUGACGAUGUGAAGAUGAAGAAGAAAAAGG AUCAAGAGUUGGCUAAACCGAUCCCGCA	128	sch-miR5021-3-3p	UGUGAAGAUGAAGAAGAAAA	78-97	ath-miR5021	2	0	20	20	1
sch-MIR7997c-36	CUUAUUUAUAGAAGGGUUCUACCUCUAUGAAUU GACCGUGUAAAAAAUUACAGUGUCAAGCUAUGCU GUUCAAAUUCUUAAAACGUCAACGGGUGUGUGC GGAUACUUCAAAAAGUAGUGCAUAUUUGAAGGAU CCAGCAAACCAUUUUUGGAAAGUAAGAGCAGUAU AAAUAUCAAGUCAAUUUUGAUGUAAUUAAAGGCU AUGUUGCUCGGACUCUUCAAUAUGGAGCCUUAC CAGUGUAGGAUCCUCUAUAAAUUCU	260	sch-miR7997c-36-3p	AUGUUGCUCGGACUCUUCAAUAUG	203-226	stu-miR7997c	4	0	24	24	1
sch-MIR7803b	CAUACACGUGUCAUAAUUUUAUCUACCGACCCAA GUGUUAAAUAUCGAAACGAUGGAUAAGAUUGUG UCACGUGUCCC	78	sch-miR7803b-5p	UACACGUGUCAUAAUUUUAU	3-22	rgl-miR7803b-3p	5	0	20	20	1
			sch-miR3706-3p	UAUCGAAACGAUGGAUAAGA	43-62	pab-miR3706	5	0	20	20	1
sch-MIR7484j	AUCAAAUCGCUGCCAUGGCAGCGAUUUGUAAGA AGAAAAAUUUUGAAAUUGCUGCCAGUGCAGCGA UUUUAUUUUUUUAUUAAAAAUUUUUUUUUUUUGC AAAAUCGCUGCCUCAGCAGCGAUUUUACUUUUU CAGCUAAAGUAAAUCGCUGCACCGGCAGCGAUU UUAC	170	sch-miR7484j-3p	UUUACUUUUUCAGCUAAAGUAAA	124-146	gra-miR7484j	5	0	23	23	1
sch-MIR7997b-17	UUAUCACUUUUGAUUCUCGGAUUCUUCAAAAAUA CACUACUUUUGGCUAAUCCGACAUGCAACCCCU UGACAUUUUUGAAGAGUCCGAGCAACAUAAGUG	104	sch-miR7997b-17-5p	UUGAUUCUCGGAUUCUUCAAA	10-30	stu-miR7997b	4	0	21	21	2

	AGUG										
			sch-miR5303h-17-3p	GACAUUUUUGAAGAGUCCGAGCAA	69-92	stu-miR5303h	2	0	24	24	2
sch-MIR8013-2	AAAAUUAAAAAAUAAUGUUAAAUCGCUGCCCUGG CAGCGAUUUGUAAGAAGAAAAAUUUUGAAAUCGC UGCUGGAGCAGCGAUUUCAUUUAUUUUUUUUGC AAAAUCGCUGCCUCAGCAGCGAUUUUACUUUUU CAGUUGAAGUAAAUCGCUGCGUCGGCAGCGAUU UUACCGUUUUGGUUUAUAUAAA	189	sch-miR8013-2-3p	UGAAGUAAAUCGCUGCGUCGGCAG	139-162	stu-miR8013	5	0	24	24	2
sch-MIR7997b-18	AAGAAGCUAUGCUGCUCGGACUCUUCAAAGAUA UUGGUGGGUUUGUGUCGCAUCAGCUAUACAUUU UUGGAGAUCUAACACAGGUGCAGCAACAUCUUU AGAGAGUUCGAGCAACAUAGUUUAGC	125	sch-miR7997b-18-5p	AUGCUGCUCGGACUCUUCAAA	9-29	stu-miR7997b	0	0	21	21	1
			sch-miR5303-18-3p	UCUUUAGAGAGUUCGAGCAAC	95-115	sly-miR5303	3	0	21	21	1
sch-MIR7981a-57	GCAUUGUUAUAUUUCUACUUUUUUUCUCCCUUA UUUAUUUUUUCAUUAGUUGAAAAUAAUUAUAAUG GUAUUUUUUACUCCUUUUCGACCUACGUGGCAC UAUCUUGUGGGCCCAACGAAGGUUGACUUUUUU UUAAACUAGUGCCACGUAGGCUAAAAAGGGGUA GAAAAUUACUUAUAAAAUAAGUUCAGGGGGGUAA UAGGACCUUAGUAUAGUACAAGUGUGUCUCUGG GAUUUCGGGCAUAGGUUGAGGGGGUACUUGUG CAUUAUCCAAAAAAAAAAAAAGAUAAAAGAAGAAA AAGAAACAAAGA	312	sch-miR7981a-57-5p	ACUCCUUUUCGACCUACGUGGCAC	77-100	sly-miR7981a	2	0	24	24	1
			sch-miR7981f-57-3p	AAGUGUGUCUCUGGGAUUUCGGGC	220-243	sly-miR7981f	1	0	24	24	1
sch-MIR7525	UCCGUUUCAAAAAGAAUGACUUCAUUUCCUUUUU AGUCUGUUUAAAAAAGAAUGACCUUUUCUUUUUU UGGUAACACUUUAACUUUAACUUUCCACGUGACA UGUUUAAGACCACAAGAUUUAAGGGCAUUUUGG UACAUUUGACAUAACUUUAAUUUAUAACCACAAG AUUAAAAAGUCUUCUUUCUUUUCUUAAACUCCGU UCCAAGACAAACUAGGUCAUUCUUUUUGAAACGG A	238	sch-miR7525-3p	AGGGCAUUUUGGUACAUUUGA	124-144	lja-miR7525	5	0	21	21	1
sch-MIR11583b-2	UUGAAGUAAAAUGUUUGUAAAUUGUAUAAUUAAG UGUAUAACACAAAGAUAUACAUUUUUACAUGUGU AUAUACAAUUUUCUCUCGCUUUAUACAAAACAGA AACAGAAUUAUACACUUCUGUGUAUAAAGCGAGA GAGGCGAGCGAGAAUGGAGAGUGGCGAGCGAGA UUCCUGGGAGAGAGACUCUAGCAAAUUUUAGAU AAUGUUUGCUAUGGAGCACAAUUAAAUCAAACCC UAGCUAUUCCAUUUAAUUUAGGUUAUUAGUUUG CUAUUUUAUACAAUUUUCCCAUUUAACAACUCAU CUUUUAAUUGGA	315	sch-miR11583b-2-5p	UUUUCUCUCGCUUUAUACAAA	77-97	pab-miR11583b	5	0	21	21	1
			sch-miR6451-2-3p	AUUUUAGAUAAUGUUUGCUAU	194-214	ptc-miR6451	5	0	21	21	1
sch-MIR865-3	GGCGAAGUAAGUUCUACGUGACAUAAUACACGU AGGAUAUUACGUAGGACAAAAAAUGACAUGUAGG ACAUGUGUGUUUAUUGUUCAACUUUAUACAAGU UUAAAUGUCUACUUGUGCACACCAAAAGUUGAAG GGCGUAAAUAUGAUUCGAAGCCAAGUUAAAGAG CACAAUUAUGUAUUAUGCCUAUAUAAAAACGCAA AUAAAAUUUUUAUCGUUGUGUUAUUUUAAUAUCA UCUUUAUUAAGUUGCAUGUUAUAACUUCUAUCAU G	270	sch-miR865-3-5p	UUAUUGUUCAACUUUAUACAA	78-98	ath-miR865-3p	5	0	21	21	1
			sch-miR1514b-3-3p	AUGCCUAUAUAAAAACGCAAA	182-202	gma-miR1514b-3p	4	0	21	21	1
sch-MIR7992-14	CUAAACUUGGAUUCAAAUUUUAACUUUGACCUCC AACUUUCAUAAUGCACAAACAGACACUUUAAUUA UCCAACUUUUAAAUAAAUAAACAAAUGAGCCCUA CGUGACACAAUACACGUAAGACACCACGUAGGAC AAAAAAUGACGCAUUGGAUGACAUAUGUGUCUAU UUCUGUAACUUUAUACAAGUUUAAGUGUCUAUAU GUGCACAUCCAAAGUUGAAGUGCAUAAAUAUAAU	254	sch-miR7992-14-5p	UUUCAUAAUGCACAAACAGACACU	38-61	stu-miR7992-5p	5	0	24	24	1

	UUGAAACCAAAUUAAA										
			sch-miR1130-14-3p	UCUGUAACUUUAUACAAGUUU	172-192	hvu-miR1130	5	0	21	21	1
sch-MIR7983-13	AUCACUACAACAAAAAUGAUCAUUAGUAGCAUUU AAUUCUUUAUUGUCGCUAAAUAUGUAUUUUUAGC GGCAAUUGUCACUCUUUGUAUAUGUCCCUAAAG CCUUGAACAUUGGUUCUAAUGUAUCUUAACUAAU GCCGGUAAAGACUUUACCACUCUUUAUUAGUGU CAAUAUUUAAUGCCGCUAAAAGUUGUUUUUGUU GUAGUCAA	209	sch-miR7983-13-3p	ACUAAUGCCGGUAAAGACUUUACC	130-153	stu-miR7983-3p	1	0	24	24	1
sch-MIR10538-15	UUAACAGCGUUAGGUUGAUAUACGUUACUGUAA GUAACAUUUUACUCCUAAAAUGUUAUUUUGAAUU AACGUUUUAGGAGUAAAACGUUACUGUGAGUAA UGUUCUAGGAGUAAAACGUUACUGUGAGUAACG UAUAUCAAUUUAACGCUGUCAG	155	sch-miR10538-15-5p	AGGUUGAUAUACGUUACUGUAAGU	12-35	sly-miR10538	4	0	24	24	1
sch-MIR7997c-37	GUUUUUUGCAAGCUAUGUUGGUUGGACUCUUCA GAAAUGUUGACGGAUCCUGUCGGAUCCUUGGAA AGUAAUCCAUUCUUGGAGGAUCCAACAUGAGCG CCACACCCUUUUUGAAGAGUCCGAGCAAACAUAG UGUUACUAAAUUU	146	sch-miR7997c-37-5p	AUGUUGGUUGGACUCUUCAGAAAU	15-38	stu-miR7997c	4	0	24	24	1
			sch-miR5303h-37-3p	ACCCUUUUUGAAGAGUCCGAGCAA	104-127	stu-miR5303h	3	0	24	24	1
sch-MIR5014a-6	CACAAACAGACACUUUAACUAUCCAACUUUUAAA UAAAUAGACACAUGAGUCUUACAUGGCACAAUAC ACGUAGGACAUAAAAUGACAUGUAGGACAUGUG UGUCUAUUUGUUCAACUUUAUACAAGUUUAAGU GUCUAUUUGUG	145	sch-miR5014a-6-3p	UUAUACAAGUUUAAGUGUCUA	119-139	ath-miR5014a-3p	5	0	21	21	1
sch-MIR6273-4	UCAUUUCAAUACGUGACACUAUUUUGUGAGUCU UAAUGCUGGUUGACUUUUUUUUUCAAGCUAGUG UCAUGUAGAUCGAAAAAG	84	sch-miR6273-4-3p	AAUGCUGGUUGACUUUUUUUU	35-55	ppe-miR6273	4	0	21	21	1
sch-MIR482b-4	GCUAUUAGGGGUGUCAAAUGGGCGGGUUGGGU UAAAUAUGGGCUGGUUAGAAUGGAUUGGUACAA CAAAUGGUCGUGACCCAACCCACCCAAAGGAUAC CAAGUUCAAGAUGGGUUGAGCAAUGGGUUAUAA CCCAACCCACCCAAUUCUCCCCAAUGUU	160	sch-miR482b-4-5p	AAAUGGGCGGGUUGGGUUAAA	16-36	hbr-miR482b	5	0	21	21	2
			sch-miR8030-4-3p	UUAUAACCCAACCCACCCAAUU	127-148	stu-miR8030-3p	5	0	22	22	1
sch-MIR7997b-19	UCAUAAGUUUAAGUUGCGCGGACUCUUCAAUGU AGAUGCCGCACUCGUGCCUGAUCUCCAAAAAUA UGCUACUUUUGGAGAAUCCGACACGCACCCAUU GACAUUUUUGAAGAGUCCGAGCAACAUAACUGUA GGU	136	sch-miR7997b-19-5p	AAGUUGCGCGGACUCUUCAAU	11-31	stu-miR7997b	4	0	21	21	1
			sch-miR5303d-19-3p	UUUUGGAGAAUCCGACACGCACCC	73-96	stu-miR5303d	0	0	24	24	1
sch-MIR3447	GUGGUUUGGUUUGACUUGGUUUGGUAUUAAAAA AAACUCAACUAUUUUUGGGUUGGUUUGAUUUUA ACUAAAAAAAAUCAACCCGAGACCAA	92	sch-miR3447-5p	UUUGACUUGGUUUGGUAUUAA	10-30	aly-miR3447-3p	5	0	21	21	1
			sch-miR7834-3p	UAAAAAAAACUCAACUAUUUU	28-48	ptc-miR7834	4	0	21	21	1
sch-MIR10992	AAAAACGUGCAUAAUAGAAUAAUAUAAUAUUUUA GUAUAUGGUCACUUAGAUAUAUUGGAAAUAAGUA ACUCAAUUAUUGAAAUGUUCAACAGUUCUGUACA AGUUAAAAAUUGAGGAGUAUCAAUAUCAUCAAAA AUUAUUACUCUUUCGUUUUGAUACAAGAAAAAAG GAUUUUCUGUUAAAAAAUGACAAAAGUCCCACAU CGGUGAUUAAUGAGAUGGGUAGACUCUUUAUAA GGCUUGGGGAAUCCUCCUCCCUUAGAGCUAGCU UUUGGAGUGUGAGUUUGACCUAACACCUAAUUU UACAUUUUACUAUUGAUCACCUUGUG	329	sch-miR10992-5p	CAUCAAAAAUUAUUACUCUUU	129-149	mdm-miR10992	4	0	21	21	1
			sch-miR11108h-3p	ACAUCGGUGAUUAAUGAGAUGG	201-222	lja-miR11108h-5p	4	0	22	22	1
sch-MIR7981-18	GCGGACAAUGACUGAAAUCUCAGAGACAUACCUU AACUAAACUAAGGUCAUACUAUUGAACUUAAUUU UUGGUAAUUUUGUACACCUUUUGUGUUAUGCGA CACACUCUGUGACUCCAGACAAAUAAAGCGCAUU	258	sch-miR7981-18-5p	CUUAACUAAACUAAGGUCAUACUA	32-55	stu-miR7981-5p	5	0	24	24	2

	AGAGAUAUUUGGAUAUCACGUAAGCCAUAAAGGUGCACAAAAUUACAAAAAAAAUGGAUUUGUUGGGUAAUAGGACCUUAGUUUAGUUAAAGCGUGUCUCUGAAAUUUCUGAAAUCUGUCAAC										
			sch-miR7981-18-3p	AUAGGACCUUAGUUUAGUUAAAGC	205-228	stu-miR7981-3p	3	0	24	24	1
sch-MIR398-2	GGAAUGAUGGAUUUAAGGUUGAUUGACUGGAACGACAUCAUAUCAAACCUUAGGAAAUUCAUCAUGAG	68	sch-miR398-2-3p	GGAACGACAUCAUAUCAAACC	29-49	cpa-miR398	5	0	21	21	1
sch-MIR8006-8	UUUUGGGACAUUGAUGCUCCUGCUAUCUAAAAAAAAAAAAGCUAAAGCUUAUAUGCCGUUAACUCUAAAGGAAGACUAAAUAGGAACACAUGGCGCAAUCUUCUUCCUCGAUAAAUGUAGUUUUGGUGGAUAAGAUUAUGACACGUGUGUGUGCAUUAGUAUAAAGGGUACAUAUUAUUUCUAGUUUUAGGACGACAGGAGCAUUAAUGUCCCAAAA	217	sch-miR8006-8-3p	UAGUUUUAGGACGACAGGAGCAUU	182-205	stu-miR8006-5p	4	0	24	24	1
sch-MIR9749-2	GGUAUAUAGAUACCUUUUGUCAUGCUUUUGGGACAUUGAUGUCCCGAUAUUCAAAAACAAGAGCAUAUAUACCCUUUAUGCUAACGGACAUAUACAUUUCAUAAUCUUAUCCACAGAUCCAAUAUUUAUUAAAUAUCGGAUCGACGAAUAAGAUUGUUUCACGUGUCCCUAUUUAAUAUUCUGUUAGAGUGAAAGACAAAUACUCUAAUUUUUGAACGGUAAAGCCACCUAUAUCCCAAAAAAAUGACAGAAGUUAUCAAUAUACU	266	sch-miR9749-2-3p	UAAGAUUGUUUCACGUGUCCC	149-169	gma-miR9749	5	0	21	21	1
sch-MIR169j-6	AAAGAAGAGAAGUCUUACAUGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAUAGUCUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUUUUCUUUUAUGCAAGAUAUCUUUUCAAA	169	sch-miR169j-6-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1
			sch-miR169e-6-3p	CAGGCAGUCUCCUUGGCUACC	109-129	csi-miR169e-3p	2	0	21	21	1
sch-MIR169j-7	UUAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCAUACUUGAAAAGGUCUUUCAUAUGUCCUUUCGUUUUUGGGAUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUUCAUGCAAGGCUUUCUCUUCUUUCGU	178	sch-miR169j-7-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1
			sch-miR169d-7-3p	GCAGGUCAUCUUUAGCUAACU	115-135	stu-miR169d-3p	0	0	21	21	1
sch-MIR863-3	UCACUUUUUUUAUUUAUUUUUUAUCUCUAUAUAUUUGGGCAAACCAUUACAGCAACAACACACAUUUCUCUACUUAUUUCUUACCCUCUUUUCAGAAAUUUCUCAGAUCUUCUUAGAUCUGAGCUAUGGAAAUAUUGAUGGCGUUGAAAGGGAUGAGAGUAUUGGGAAGUUGUUGGUUGUGGGUGGGGUGGAAAGAUUUGAUAAAUCUAAAUUUUUUUCUAAUUGAAAAAAAAAAUGGAAAAGAGAUU	249	sch-miR863-3-5p	UUAUUUAUUUUUUAUCUCUAU	10-30	ath-miR863-5p	5	0	21	21	1
			sch-miR482e-3-3p	UGUGGGUGGGGUGGAAAGAUU	178-198	sly-miR482e-5p	0	0	21	21	1
sch-MIR7981a-64	UCCGAAAUUCAAAAGACACAUUUAUAUUAUAUUAAGGUUCUUUUACCUUCGAAUUUAUUUUAUAAGUAAUUUUCUACCCCUUUUCGAUCUAUGUAGUACUAGCUUGAAAAAAAAUCAACCAGCGUUGGGCCCAUAAGAUAGUGCCAUGUAAGCCGAAAAGUGGUACAAAAUUAUUAAUAAAAUAAGUUCAGGGGAAUAAUAGAACCUUUGUAUAGUAUAAGUGUGUCUCUGAAAUUUCUAA	241	sch-miR7981a-64-5p	ACCCCUUUUCGAUCUAUGUAGUAC	76-99	sly-miR7981a	5	0	24	24	1
			sch-miR7981f-64-3p	AAGUGUGUCUCUGAAAUUUCUAA	219-241	sly-miR7981f	4	0	23	24	1
sch-MIR10405d-3	UCGUUUAUUAUCAAAGGGACUUAUAAAACCCUCUAAAUCACCAUGGUCUUGUACUGCAUUUUAUGUUAAUAAGGCUGCAGAACAAGAAAGAGGUGUUCCCAGGUUGGUAAUAAAUUACAAACCUUUAAAUAAAGUU	136	sch-miR10405d-3-5p	UCGUUUAUUAUCAAAGGGACU	1-21	gma-miR10405d	5	0	21	21	1

			sch-miR9679-3-3p	CAGAACAAGAAAGAGGUGUUC	78-98	tae-miR9679-5p	5	0	21	21	1
sch-MIR11076-1	CCACAUUAAGUAGUUUCUAAGUCAUGGUAGUGA AGUGCACCACUAUCCUGGAUUAGAGACUGCAUG AUGCGU	72	sch-miR11076-1-3p	CAUGGUAGUGAAGUGCACC	23-41	lja-miR11076-5p	5	0	19	19	2
sch-MIR6288c-3	UUUUGAUGGUUUAAGGCUUUCAAGUUUCGUUGU GUGCAUCGUCUUCUAAGGUCCAUUUUAUGUUUU AAUUGGGUUGAUUUAUAGCAAGUGAAUUAUGAA UUGUGACUUCCAAGGAAGAAACUUUUUUUGUUC UAAUACCAUACAAGUCAAUGGUAGAGGUUUUCUC UUUUUUGAAUUAUGAGUACUUGAAACUCAAAUAG CUUCCAACGGAAUUUGGAAAACUAUUUAUAACAU CAUUC	239	sch-miR6288c-3-5p	CAUUUUAUGUUUUAAUUGGGU	54-74	ppe-miR6288c-5p	5	0	21	21	1
			sch-miR7696d-3-3p	UUUUGAAUUAUGAGUACUUGA	169-189	mtr-miR7696d-3p	1	0	21	21	1
sch-MIR7981b-27	CUGAAAUUCCAGAGACACACUUAUACUAUACUAA ACUCUUAUUACCCCUGAACUUACUUUAUAAGUAA UUUUCUACCCCUUUUUAGCCUACGUGGCACCAG UUUGAAAAAAAAAAAAAGUCAAUCAUCGUUGGGCU CACAAGAUAGUGCCACGUAGGUCGAAAAGGGUA AAAUAUUAUUAAUAAAAUAAAUUCAGAGGUAAUA GGACCUUAGUAUAGUAUAAGUGUGUCUGAAUUU AAA	238	sch-miR7981b-27-5p	ACCCCUUUUUAGCCUACGUGGCAC	75-98	sly-miR7981b	1	0	24	24	1
			sch-miR7981-27-3p	AUAGGACCUUAGUAUAGUAUAAGU	200-223	stu-miR7981-3p	5	0	24	24	1
sch-MIR6145b-2	UCAGCCUACGUGGCACUAGCUUGAAAAAAAGUCA ACCAGUAUUGGCCCACAAGAUAAUGUCAUGUAG GCCAA	72	sch-miR6145b-2-5p	UCAGCCUACGUGGCACUAGCU	1-21	nta-miR6145b	5	0	21	21	1
sch-MIR5256-2	UCACUAAAAUUUUAUUCCUUCCAACCUCUUAAUG GAUUAUACUUAUUUAUUAUGUAAUAAUAAUGGUU UAAUAAUCAUCUCGUCUGGUCACUACUACAGUUU UCUUCUUUGAUCAGUACCAUAACAGCGCCUCAAC UUUGUUUACUCCCCUAACGGACUUCUUGCCUAU CGGUUUCAACCUUAGGAUGACAUAGUCUGGGCA UACUUAUUCGCAGAAUAUUUCUAUAGCAAACUUU CUAAAGAUGGUUAUUGUAACAUUAUUAAGACAUG AUAAAAAAUUAUAAUCAACAAGAGAUUAUCAGGA AUAAAUAGAUUUAGCUA	321	sch-miR5256-2-5p	UUAUUUAUUAUGUAAUAAUAA	43-63	mtr-miR5256	5	0	21	21	1
			sch-miR2590f-2-3p	UUCUAAAGAUGGUUAUUGUAAC	235-256	mtr-miR2590f	5	0	22	22	2
sch-MIR6145e	AAUGUCCUACAUGUCAUCCAACAUGUCAUUUUUU GUCCUACGUGGUGUCCUACGUGUAUUGUGUCAU GUAGGACUCA	77	sch-miR6145e-3p	AUUGUGUCAUGUAGGACUCA	58-77	nta-miR6145e	5	0	20	21	1
sch-MIR8668	UGGUCGCCUUGGCUUACAGAAACAUUUUGGAAU GAUGACUAUAAUGAGUGGGAUAACCUGAGAAAU GUUUUUGUACAAGGAGAUAU	86	sch-miR8668-5p	UUUUGGAAUGAUGACUAUAA	25-44	gra-miR8668	4	0	20	20	1
			sch-miR11323-3p	UUUGGAAUGAUGACUAUAAUG	26-46	ppt-miR11323	5	0	21	21	1
sch-MIR162-4	UCCUUAGGGGUUAAGCACUGGAUGCAGAGGUUU AUCGACCGAUUCCUUUUGCUGUAUUUUUGCAUA UAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAU GAACCGCUGCCUCCAGUGUCUUCAACCAACUAAA CA	135	sch-miR162-4-5p	UGGAUGCAGAGGUUUAUCGACC	19-40	csi-miR162-5p	4	0	22	22	1
			sch-miR162b-4-3p	AUCGAUGAACCGCUGCCUCC	94-113	cas-miR162b	0	0	20	20	1
sch-MIR7997b-20	GAGCUAUGUUGCAUGGACUCUUCACUUUCGAUG CCACAACCGUGUCGGAUUCUCCAAAAAUACACUA CUUUUGGCGAAUCCGACACGCGCCCCUUAACAU UUUUGAAGAGUCCGAGCAACAUAGGUA	127	sch-miR7997b-20-5p	AUGUUGCAUGGACUCUUCACU	6-26	stu-miR7997b	5	0	21	21	1
			sch-miR5303h-20-3p	AACAUUUUUGAAGAGUCCGAGCAA	96-119	stu-miR5303h	1	0	24	24	1
sch-MIR1514b-2	AUACAAAAGGGAGACCUCAUGAGGUCUCUUUUC UGCAUUUAUAAAAUAGAAAAUGGUAAAUAGAGAC CUCAUGAAGUCUCUAUUAUGAAAUAUCUGGAAAA AUUAAUGCAAAAAAGAGACCUCAUGAGGUCUCUA UUAUGAAA	143	sch-miR1514b-2-5p	UGCAUUUAUAAAAUAGAAAAU	34-54	gma-miR1514b-5p	4	0	21	21	1

			sch-miR11163-2-3p	AGGUCUCUAUUAUGAAA	127-143	lja-miR11163-5p	5	0	17	24	1
sch-MIR11076-2	UCCAAGGAUAAUUAGUUCACAUCAACCACAUCGA GUAGUUUCUAAGUCAUGGUAGUGAAGUGCACCA CUAUCCUGGAUUAGAGACUGCAUGAUGUGUAGG AAAAUUUCCCUUCUU	115	sch-miR11076-2-3p	CAUGGUAGUGAAGUGCACC	48-66	lja-miR11076-5p	5	0	19	19	2
sch-MIR11583b-3	UUUUCUCUCGUUUUAUACAAACACAAACGGAAUG UAUACAAUUUGUGUUUGUAUAAGGUGAGAGAGG CAAACGAGACCUGAGAGAGUCGCGAGCGAGAUU UGGGAGAGGGGAUAGAUGUAACAAAAAUAUAUG AAUAUAUACAAUUUUCUCUCGCUUUUUACAAACA CAGACACAUCUUAUACAUUUGUGUUUGUAUAAAA GCUAGAGAGGC	212	sch-miR11583b-3-5p	UUUUCUCUCGUUUUAUACAAA	1-21	pab-miR11583b	4	0	21	21	1
			sch-miR5568d-3-3p	ACAUUUGUGUUUGUAUAAAAG	182-202	sbi-miR5568d-3p	5	0	21	21	1
sch-MIR477g	CUUCAUCAAAUUGUUGAGAAAUAAUAAGGUAUGG GUUAUAUUCACCUUUGAGAUCCUUUCCUCAAAG GGUUCCUUCAAAAAUGUAUUUCAAAAAUUUAAGU UUUCUGAUCUUGAAGUUCUUGGAGUUGUGGUGA GCUGCGUGGUUGUUCCGUGGCCCACACCUCCCU CUAUAUUUUAUUUAUUCUGUUAUUAGUAUUCAG GCAGUAUAUCCCUUAUGUAAGAUUUGACAUUUAC UUUCAGUCUUGCAUCGGAUUUUAGAAGCUCUUG UACUUAAGACACCAAUUCUUGGGGUGAUAUACU UUUUUUUACCCAUUUGAUGGUU	322	sch-miR477g-5p	UUCCUCAAAGGGUUCCUUCAA	58-78	ppt-miR477g-5p	4	0	21	21	1
sch-MIR7992-15	ACUUUCAUAAUGCACAAACAGACACUUUAGCUAU UCAGCUUUUAAAUAAAUAAACACGUGAGUUUUAC AUACAUGUAUGAUUUCACGUAGGACCAAAAAUGA CACAUAAAAUGACAUGUAUAUCUAUUUGUUCAAC UCUAUACGAGUUUAAGUGUCUAUUUGUGCACAU GAAGGG	175	sch-miR7992-15-5p	UUUCAUAAUGCACAAACAGACACU	3-26	stu-miR7992-5p	5	0	24	24	1
sch-MIR11466c	UGUUGCACGUGUAGACACUUAAACUUAUAUACAG UAAAAUAAAUAUACGCACAUGUUCUACAUGUCAU UUUUUGUCCUACGUGGUAUUCUACGUGUAUUGU GUCAUGUAGAACUCAUAUGUUUAUUUAUUAAAAA GUUGGAUAGUUAAAGUGCAUGU	157	sch-miR11466c-5p	UCUACAUGUCAUUUUUUGUCC	57-77	pab-miR11466c	5	0	21	21	1
			sch-miR10519-5-3p	AUUAAAAAGUUGGAUAGU	128-145	tae-miR10519	4	0	18	18	3
sch-MIR1046	GUUCAACUAACACUACAAGAAAACUGGGGUUUUU UCUGGAGAUAAUUUUCAUACUAAUUGCCACGAAA AUCCUCAUGUAAUUCAUAGUUUUCUUGUAGUGU AAGUUGUUU	110	sch-miR1046-3p	UGUAAUUCAUAGUUUUCUUG	76-95	ppt-miR1046-5p	5	0	20	20	1
sch-MIR5658-2	GUUACGGUGCAGUAAAGAUGUUGAUGAUGAAGA GAUUUUUUUUUGAGAAUGUAUUUUUUUUGGAUG ACGGAAUCAGUCUCCAAGUGGGAGAAUUGUUAG GUCGUGGAGCCUGAUUUAUAUAUAUAACUGUUU ACGAGGUUUGACCUAUUUAUUCUCCAUUUAUUC UCUGUAAAAAAAAAAUACUCUGAUUUAUUAAUAU AUAUACCCCUUCACCGUGGA	219	sch-miR5658-2-5p	AAGAUGUUGAUGAUGAAGAGA	15-35	ath-miR5658	4	0	21	21	1
			sch-miR12162-2-3p	AAUACUCUGAUUUAUUAAUAU	179-199	aof-miR12162	5	0	21	21	3
sch-MIR171h-2	GUUGCGGUGCGGUAAAGAUGUUGAUGAUAAAAA GAUUUUUUUUGAGAAUGUAUUGUUUGGAUGACU GAAUCAGUCUCCAAGUAGGAGAAUUGUUAGGUU GUGGAGCCUGAUUAAUAUAUAUUCUCCAUUUAU UUUCCGUAACCAAAAAUACUCUGAUUUAUUAAUA UAUAUAUAUCCCACCGCUGU	186	sch-miR171h-2-5p	UGUUUGGAUGACUGAAUCAGU	54-74	ptc-miR171h-5p	5	0	21	21	1
			sch-miR12162-2-3p	AAUACUCUGAUUUAUUAAUAU	147-167	aof-miR12162	5	0	21	21	3

Supplementary Table S11 - Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum peruvianum* (spr).

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
spr-MIR10528-1	AUAAUGAAUGCAAUGUCAUAUACCAUCAACACUCGGAAACUCAAAUUGAGGUUAAAUCUCGGAGUGAUGAUGGUAUAUGACCUUGCAAUUCACUAUG	97	spr-miR10528-1-5p	AAUGCAAUGUCAUAUACCAUC	7-27	sly-miR10528	0	0	21	21	1
spr-MIR10528-2	AGUGAAUUGCAAGGUCAUAUACCAUCAUCACUCCGAGAUUUAACCUCAAUUUGAGUUUCCGAGUGUUGAUGGUAUAUGACAUUGCAUUCAUUAUG	95	spr-miR10528-2-5p	AUUGCAAGGUCAUAUACCAUC	6-26	sly-miR10528	2	0	21	21	1
spr-MIR11091	AAAGGGAUAUGAAGAAGAAGAAGAGAUUUUCUUUGAAGAACUCUCUCUUUCUCUACAGAGAAGAAAAAGAAGAGAGAAAUUGAGAAGAGAAAACCCUUAUUGGCUUCUUAUCCCCCA	117	spr-miR11091-3p	AGAAGAGAGAAAUUGAGAAGA	68-88	lja-miR11091-3p	2	0	21	21	1
spr-MIR1511	AGUAAUGUUCUUCUUGCUUCCAUUGAGAACAUGCAGUAUGCAGUAACCCUGGAUGUCCUAUACACGGUUUUCUCAGCUUUUGGUCCUGUCCUAAAGAUUGCUAUGUUUGAUAAGAAUGGAGGGCUUCAGGCUCUGAUACAAUAUCCAGAUGUGCGCACAGCUGCUGUUGCGAAGGAAGCUUUGGAAGGACAUUCCA	196	spr-miR1511-3p	UUCAGGCUCUGAUACAAUAUC	125-145	ppe-miR1511-3p	5	0	21	21	3
spr-MIR1520a	GUGACACCAUGACAAUGUUGGUCAGCAUCACCAUGAUGAUGGUGUCCAUGAUUAUGGUCAUGGGAGUGAUCAUGAGGAUGAGGAGUAUUAUUUUCAUUCCAUUCUUUUUCUUUCUUGCUUUGGUUUUUAUAGUCAGCAUUAUGUCCAUGACCAGCAUGACUAGAACAUGAUUCAUGGCAUUCAUGGACAAUACUGAUUUGUUCCUGUUGUAUA	213	spr-miR1520a-3p	UAGAACAUGAUUCAUGGCAUUCA	161-183	gma-miR1520a	3	0	23	23	1
spr-MIR1521a	UUUCUUUUAAGGGAAAAGGCUCAAAUAUGCCAUCGAACUUUCAAAAAAGGCUCAUUUAUGCCAUCCGUUAAAAGUUU	77	spr-miR1521a-5p	CUUUUAAGGGAAAAGGCUCA	4-23	gma-miR1521a	5	0	20	20	1
spr-MIR166k	UCUCAGUUGAGGGGAAUGUUGUCUGGCUCGAGGUCACCAAUUAGAUCCAUAAUCCCUAUAUAUACCAUGCUUUUCAAAAAAAGAUUUAUAAUAUGAAAAGGGGUUAUGAAUCAUGUGUUAGUGUUGUCGGACCAGGCUUCAUUCCCCCCAAUUGUUA	157	spr-miR166k-3p	UCGGACCAGGCUUCAUUCCCCC	127-148	lus-miR166k	0	0	22	22	1
spr-MIR1886f	ACCAUAUCAUCUAAAUUUCCAUUAAGUAUAUGGAUUGCUGAUGUUCUAAGUAGGCAUUUGGACAUGCAAUUUCAUAUCGCGAUAUGAAAUCAUUAGAUGAAAUCAA	106	spr-miR1886f-3p	AUGAAAUCAUUAGAUGAAAUCAA	84-106	stu-miR1886f	5	0	23	24	1
spr-MIR1918	UGGAAGACACAAAUAGGAGGACCAAAGUGUCCAUGAUAUUUAUAUAUUAAUCGUGGAAAAAUAGCGUGUCGGAGAAUCUUAGUAGUUCAGUUGGUUGUAUUGGUUGUGACUGGUUUUACUUGGAUUUUCACUUUGUUGGUGAUUGUUCGAUUCUCCACCUUGUAAUUUUCUGUCUUUCACUGUAUACGUUUUAUGUGUAUUUUUCUUUUAUUUGUUCUUCUC	222	spr-miR1918-3p	UGUUGGUGAUUGUUCGAUUCUC	134-155	sly-miR1918	2	0	22	22	1
spr-MIR3448	UAAAAGAAGGAGUCAAGAACGCACCAUACAGGAAAACAUCUUGAUAAGAAGUGUUACUAUGUUUAGACAAUUGUAUGGUUCGGGUAUUGACUUCUGUACUUGGA	104	spr-miR3448-5p	ACAGGAAAACAUCUUGAUAAG	28-48	aly-miR3448-5p	5	0	21	21	2
spr-MIR3710h	UUUCGAGUUUGAAACAGCUGAAUUUGUCGUACAACCCGUUUUCACCGGGUCGGGUCCCGCCGGAGAUUGGGAACCUCACGAAUCUCGAGGUGCUUUGGUUAACUGACUGUGGGUUAAUUGGUGAGGUUCCGGGUACAUUAAGGAGAUUAAAUAAGCUUGUUAACUUGGACCUUGCGUUAAACAACUUGUAUGGUCCGAUUCCGAGCUGGCUCACUGAGUUAACUAGUGUUGAGCAAAUUGAGCUGUAUAAUAACUCGUUC	260	spr-miR3710h-5p	UUGGGAACCUCACGAAUCUCG	67-87	pab-miR3710h	3	0	21	21	1
spr-MIR393	CCGUACCUCCUAGUCCUCUCACACUCGUGGAAGCUACUGGCAUGAAAUUGUGGUCAUCAACAUCAGGAGCCAUUCCGUACCUAUACUCCUUAUUAGUUAUCCCAUAGGAGGCGGGCUCCAUCUGCAGUUUCGUGGUGGUGCUUCCGUAACUUAUUCCAUCUGAAUUAGCGACAGAAUAUAAUGGCAUAUUUUGGAAGCUUCCACUGCUAUUGCUUUGGAAACUUCCACUUCUAUUGCUGCUCCCAGUAGCAGUGUGUGAUUUACUUGUCGACAAGGACUGGGAAGUAGUU	290	spr-miR393-3p	CCACUGCUAUUGCUUUGGAAA	201-221	vca-miR393-3p	5	0	21	21	2
spr-MIR482b	GGGAAGAAGCAGAUUUAAUCCAAUCUCUAGUCAAGAAAGUUCUGGGGAAACUUGAUAAUACACCUAUAGGUGUGGCUAAAUACCCCGUAGGACUUCAUUCUCGUCUUGAUCAAUUGCUCACGCUACUCGACGUUAAAGCAAAUGGUGUGAAAGUUGUAGGAUUGUACGGAAUGGGAGGAGUGGGCAAGACCACUCUUGCCAAGGCUUUGUACAAUCAGCUUGUUGUUAGGAAAUUACUCCUGGUGUCCUUGGAAAUGGUUGGUCUUGAACUUUUAACCCUCGCUUGUUGCAUGGAUAAACCUAAAAAGGACAAAAUUAAA	227	spr-miR482b-3p	GGAAUGGGAGGAGUGGGCAAG	168-188	ppe-miR482b-5p	3	0	21	21	1
spr-MIR5016	AUUUGUUAACUUCAAUAUUUCGCCCAUGGAGCAAGUGAGGAUAAAAGUUAAACAUCAUCUUGUAAAUCAUCGAGGGUGAAUUUAAU	179	spr-miR5016-5p	UACUCCUGGUGUCCUUGGAAA	8-28	ath-miR5016	5	0	21	21	1

spr-MIR5021-1	AAUGGCAAUAGAGAAUAAUGAUCAAUCUUUUUUGCUUUACUGUGAAGAAGAAGAAAAAUGGGGUGAUUUGUUAGAGGAUGAAGAAGGGGUUAUUAUUAACCCAUUGUUGUUAUCUUCUGAAGGAACAACAAAAACUAAUUCUUUAUUAUUAUUACCUCU	162	spr-miR5021-1-5p	UGUGAAGAAGAAGAAGAAAA	41-60	ath-miR5021	1	0	20	20	1
spr-MIR5021-2	AUCUCUUUUUUCUACUAUUUGCUUGUUACAAAGUCAUUUUUGUGCAUCUAUAGUUUGGUGUAUCUACCAUUACCAAACCCAAAAUCCCAUUACAACAAGUGUUGUAGGGGGAAGAAGAAGAAGAAGAAGAAAGAUGU	137	spr-miR5021-2-3p	GAAGAAGAAGAAGAAGAAAG	114-133	ath-miR5021	3	0	20	20	3
spr-MIR5303	GUAGUUUUCUUUAUGGCUGUGUUGUUUGGCUCUCAAAAAAUGUUACUCGUGUCGGAUCUUCCAAAGGUACAUUACUUUUGGAGGACUGACAUGCACCGGCUGACAUUUUUGAAGAGUUCGAGCAGCAUAGACAUUUACAAAACGAA	146	spr-miR5303-3p	UUUUUGAAGAGUUCGAGCAGC	106-126	sly-miR5303	1	0	21	21	1
spr-MIR5303d-1	UCUCUAUGUUGCCGGGACUCUCCAAAAUUGCUGUCACAGUUGUGUCGGAUUCUCUAAAAUGCACUACUUUUGGAGAAUCCGACACGCAUCCGUUGGCAUAUUUGAAGAGUCCGAGCAACAUAGGGC	126	spr-miR5303d-1-3p	UUUUGGAGAAUCCGACACGCAUCC	68-91	stu-miR5303d	1	0	24	24	1
spr-MIR5303f-1	UAUGUUGCUCGGUCUCUUCAAGAAUUGCAACAGGUGCGUGUCAGGUUCUUCAAAAGUAGUGCAUUUUUGGAGAGUCUGACACGGGUGUGGCAUCAAAAGUGAAGAGUCCGCGCAACUAAA	120	spr-miR5303f-1-3p	AUUUUUGGAGAGUCUGACACGGGU	63-86	stu-miR5303f	1	0	24	24	1
spr-MIR5303f-2	AAACUAUGUUGCUCGGACUCUUCAAAGAUGUCACGAAGUGCGUGUUGGAUCCUCCAAAAGUAGUGCAUUUUUGGAGGAUCUGACACGGGUGCAGUAGCAAUUUUGAAGAGUCCGAACAACUUAGCAG	127	spr-miR5303f-2-3p	AUUUUUGGAGGAUCUGACACGGGU	67-90	stu-miR5303f	1	0	24	24	1
spr-MIR5303h-1	UGUUCGGACUCUUCAAAAUUGCUACUGCACCCGUGUCAGAUCCUCCAAAAAUGCACUACUUUUGGAGGAUCCAACACGCACUUCGUGACAUCUUUGAAGAGUCCGAGCAA	110	spr-miR5303h-1-3p	GACAUCUUUGAAGAGUCCGAGCAA	87-110	stu-miR5303h	3	0	24	24	2
spr-MIR5303h-3	AGUACUCUAUGUCGCUCGGACUCUUCAAAAUGCUUCCCUGGGUGCACAUCCGAUCCUCCAAAAGUAGUGCAUUUUGGGACAUCAUUUUUGGAGAGUCCGAGCAACAUAGCAGUUAG	116	spr-miR5303h-3-3p	AUCAUUUUUGGAGAGUCCGAGCAA	81-104	stu-miR5303h	3	0	24	24	1
spr-MIR5303h-4	ACAAUCUAAGUUGCGCAGACUCUUCACUUACGUUGCUGAAGCAGUGUCAGAUUCCUCAAAGUACACUACUUUUGGAGAAUCCAACACACAUCCAUCAACAUUUUCGAAGAGUCCGAGCAACAUAGAUAAA	130	spr-miR5303h-4-3p	AACAUUUUCGAAGAGUCCGAGCAA	97-120	stu-miR5303h	2	0	24	24	1
spr-MIR5303h-5	UUUUAUAACACACUGACUAUUCUUUAAAACUUAUGUUGCUCGGAUACUACAAAAAUGUUGUCGUACCAAGUGUCAGAUCCUUAACGACACACACCAUCUGUCAACAUUAUUGAAGAAUCCGAGCAACAUAGAGGGGAAGAAGAAGAAGUGUGUUUACUA	159	spr-miR5303h-5-3p	AACAUUAUUGAAGAAUCCGAGCAA	103-126	stu-miR5303h	3	0	24	24	1
spr-MIR5303h-6	GCAAUAACCUAUGUUGCUCGAACUGUUCAUAAAUGGUGAUGGGCUAUGUCGGAUCCUCCAAAAGUAGUACAGUUUUAGAGGAUCUUGCACAUAUGUGACAACAUUUUUGGAAAGUCCGAGCAACAUAGAUAAUAAC	136	spr-miR5303h-6-3p	AACAUUUUUGGAAAGUCCGAGCAA	100-123	stu-miR5303h	3	0	24	24	1
spr-MIR5303i-1	UCCUGUUGCUCGGACUUUACAAAAAUACAAUUGCACCCGUGUCAGAUCCUCUAAAAAAACACUAUUUUUGGUGGAUCAAACUAACAUCCGAUAAUAUUUUUGAAGAGACUGAGCAACAUAG	121	spr-miR5303i-1-3p	AUAUUUUUGAAGAGACUGAGCAAC	94-117	stu-miR5303i	1	0	24	24	1
spr-MIR5303i-2	GCUGAAUCUCUUCAUAUAGGUUAUGUUGCUUUGACUCCCCGAAAAUGGGGCCACACUCAUGUUGGAUCCUCCAAAAAGCUCUACUUUUGGACGAUCCAGUACACACAUGUCGAUAUUUUUGAAGAGUCCGAGUAACAUAUAUUACAAUUCAAGUGAUUCUUU	162	spr-miR5303i-2-3p	AUAUUUUUGAAGAGUCCGAGUAAC	113-136	stu-miR5303i	2	0	24	24	1
spr-MIR5368-1	CACUGUUCCCUGGGAUUGGCUUUGGGCCUUUCCUGCGCAGCUUAGGUGGAAGGCGAAGAAGGCCUCCUUCCGGGGGGGCCCGAGCCAUCAGUGAGAUACCACUCUGGAAGGGCUAGAAUUCUAACCUUGUGUCAGGACCUACGGGCAAGGGACAGUCUCAGGUAGACAGU	171	spr-miR5368-1-3p	GGACAGUCUCAGGUAGACA	151-169	gma-miR5368	0	0	19	19	1
spr-MIR5368-2	CUAACCUUGUGUCAGGACCUACGGGCCAAGGGACAGUCUCAGGUAGACAGUUUCUAUGGGGCGUAGGCCUCCCAAAAGGUAAC	83	spr-miR5368-2-3p	GGACAGUCUCAGGUAGACA	31-49	gma-miR5368	0	0	19	19	1
spr-MIR5566	AUAUUUUCGUAUCAGCAUCACCUGCCUCUUGAGAGCUCAUUGGUACUUCUGAAGCACUGAGAGCAGCAGAGGCAGCUUUAGCUGACCAGAAAAGAA	96	spr-miR5566-5p	UCAGCAUCACCUGCCUCUUGA	12-32	sbi-miR5566	3	0	21	21	1
spr-MIR5633	UCAGAUCAACUAGAGGAUCCACUGCCUCUGAUGAAGGAGAAGUCUCUGGAAUCAACAAGUCCUCAGAGGCAGAUUCAGUGAGUAGACUAUGAUCAUCUGAAAACAGAGAAGAAGUGCCGAUCGAUGAUUGAGAAAAUGAGGAGGCAGCUUGCGAUUCAAACACAGAAUUCAAGUUCUUCCUAGUGCUUUUGAUCUGCUUCUUAGUUUGAUCGGC	214	spr-miR5633-3p	UAUGAUCAUCUGAAAACAGAG	88-108	ath-miR5633	2	0	21	21	1
spr-MIR5658	CAAAACAACAACCCAAAUGAUCUUCUUGAAGAAGAUGAUGAAGAUCAAGAUGAUGAUGUUGAGAUCAACGCCACUAUAGCAUCCACCAUUUUUGCUGAUUUUAACAAAGAUGGUUCCUCAGAUAGUGACAAUUCAAGUGCAAUCUUGAAUGAAGAUAACAGUCCAAAUGCUGCUGCAAUUUCAUCAUCUGGUGCAUUCUUGAUCUCUAAUGAUGGUGGGGUUGGUUGUUCAU	232	spr-miR5658-5p	AUCAAGAUGAUGAUGUUGAGA	44-64	ath-miR5658	4	0	21	21	1
spr-MIR6022-1	CCUGAACGGAACAAUACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAGUUAUUUAGACCCGAGUUUUAACCAAUUGCACAGUCCUCUACCCAAGAUUGAGGUUUCGUAAAAUGUAACUUAAGAUCAAGUCGCGUUAGGUU	238	spr-miR6022-1-3p	UGGAAAGGAUAAUAUCCAGGA	211-231	sly-miR6022	2	0	21	21	1

spr-MIR6022-2	CAUGAAGUUUUGAAUUGACUUAGGAAGAGUACCUUGCAACUUAAAACUUAGAGCCGAAAUAAGUUAGUGAUGGAAAGGAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGGG	238	spr-miR6022-2-3p	UGGAAAGGAUAAUAUCCAGGA	198-218	sly-miR6022	2	0	21	21	1
spr-MIR6034	AAAUGAAAAAUGUGAUGUAUAUAGCUUCGGUGUCAUACUAUGGGAGCUCUGUACUUUACAGCAACCAUGGGGAGGAAUGAAUCCAAUGCAAGUCGUUGGUGCUGUGGGGUUUCAGCACCGUCGUCUUGACAUACCAGAUGACACGGAUCCAGCUAUUGCAGACAUUAUCAGGA	173	spr-miR6034-5p	UGUGAUGUAUAUAGCUUCGGU	11-31	bna-miR6034	3	0	21	21	1
spr-MIR6284	ACCUUGGAAAUAGGUGGUCUUGAACUUUUGGUACAUGGAUAAACCUUCGACGCCAAAAGUCGAUACUUGAUGUUCUGUUCAUGGGGCAAGCAAGAUUGAACGUUCAAGAUCAUCCACCUCCAAAGU	126	spr-miR6284-5p	UUUGGUACAUGGAUAAACCUU	27-47	ppe-miR6284	5	0	21	21	1
spr-MIR7822	GGUAGACACUUAACUUGUAUAAAAUUGAACAAAUAGACACACAUGUCCUACAUGUCAUCCUACAUAUCGUUUUUCGUCCUACGUGGUGUCCUAAGUGUAUUUUGCCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGUU	160	spr-miR7822-5p	UAUAAAAUUGAACAAAUAGAC	18-38	ptc-miR7822	5	0	21	21	1
spr-MIR7981a	GUCCUACCCUUUUCGGCCUACGUGGCACUAUCUUGUGGGCCCAACGAUGGUUGACUUUUUUUUUCGAACUAGUGCCACGUAGGCUAAAAAGGGGUAGAAA	100	spr-miR7981a-5p	UACCCUUUUCGGCCUACGUGGCAC	5-28	sly-miR7981a	2	0	24	24	3
spr-MIR7981b	UUUCUACCCCUUUUUAGCCUACGUGGCACUAGUUCGAAAAAAAAAGUCAACCAUCGUUGGGCCCACAAGAUAGUGCCACGUAGGCCGAAAAGGGUAGGAC	100	spr-miR7981b-5p	ACCCCUUUUUAGCCUACGUGGCAC	6-29	sly-miR7981b	1	0	24	24	1
spr-MIR7983-1	CUUUUAGCGGCAUUAAUUACUGACAUUAAUAAAGAGGGAUAAAGUCUUUAUCGAUAUUAGUUAAGUGUCAUUAGAACCAAUGUCGUUAAAGGCUUUAGGGACAUAUACAAAGAGUGCUAAUUGCUGCUAAAA	132	spr-miR7983-1-5p	UAAAGUCUUUAUCGAUAUUAGUUA	40-63	stu-miR7983-5p	4	0	24	24	1
spr-MIR7983-2	AACAACUUUUAGCGGCAUUAAUUACUGACAUUAAUAAAGAGGGAUAAAGUCUUUAUCGAUAUUAGUUAAGUGUCAUUAGAACCAAUGUCGUUAAAGGCUUUAG	103	spr-miR7983-2-3p	UAAAGUCUUUAUCGAUAUUAGUUA	45-68	stu-miR7983-5p	4	0	24	24	1
spr-MIR7992	AAGUAUGUCCUUCAACUUUGAAUAUGCACAGACAGACACUUAAACUAUUAUAAAAUUGAACAAAUAGACAGAAGUGUCCUACAUGGCAUAUUACACGUAGGAUUCCAUGUAGAAUACAAAAUUGUCAUGUAGGGUGCCACGUAGGACGAAUGUGUUCAUUUGCUCAAUUUUAUACAAGGAUCAUGUUUAUGAGUUAUGCCUAUUGAAAACAUAGAG	216	spr-miR7992-5p	UUUGAAUAUGCACAGACAGACACU	17-40	stu-miR7992-5p	5	0	24	24	1
spr-MIR7997c-1	GUUAUUAUCUAUGUUGCUCGGACUUUCCAAAAAUGUUGUCACAUAUGUGCAAGAUCCUCUAAAACUGUACUACUUUUGGAGGAUCCGACAUAGCCCAUCACCAUUUAUGAACAGUUCGAGCAACAUAGGUUAUUGC	136	spr-miR7997c-1-5p	AUGUUGCUCGGACUUUCCAAAAAU	11-34	stu-miR7997c	3	0	24	24	1
spr-MIR7997c-2	GACCCUAUCUUGCUCGAAAUCUUCAAAAGUAGUGUGUUUUUAGAAGUAUUCAACACAGGUGCGACAACAUUUUGGAGAGUCCGAGCAACAUAGGCUU	97	spr-miR7997c-2-5p	AUCUUGCUCGAAAUCUUCAAAAGU	7-30	stu-miR7997c	4	0	24	24	1
spr-MIR7997c-3	CGGUUCGUUGUUGCUCGGAUUAUUCAAAAAUGUUGAUAAACUCAGUAAUACAGAGGUUCUGAAUCAUCAUCAUCAUCUUCGUUCGGAUUAUUCAAAAAUGUUGGUUACCAUCUGUUGAUAAUUUCGAAGAGUUCGAGUAAUAUAAGUUUUGAAUAAUCAUAGCUAAGUUCUAUUUUGUGUUGUUCGGAUUAUUUGAAAAUGUAGUUUGAAUUCUGAUAUGUACUUGUUGAUAAUUUUUGAAGAGUCCGAGGAAAAAAAGAAGAG	264	spr-miR7997c-3-5p	UUGUUGCUCGGAUUAUUCAAAAAU	8-31	stu-miR7997c	4	0	24	24	2
spr-MIR7997c-4	GAGCUAUAUUGCUCGGACUCUUCAAUAAAAUCGAUGAGUGUGUGUCGGAUCCAGCACGAGUACAGCAACAUUUUUGGAGAGUUCGAGUAACAUAGGUA	98	spr-miR7997c-4-5p	AUAUUGCUCGGACUCUUCAAUAAA	6-29	stu-miR7997c	2	0	24	24	1
spr-MIR7997c-5	AAGCCUAUGUUGCUCGGACUCUCCAAAAUGUUGUCGCACCUGUGUUGAAUACUUCUAAAAACACACUACUUUUGAAGAUUUCGAGCAAGAUAGGGUC	97	spr-miR7997c-5-5p	AUGUUGCUCGGACUCUCCAAAAUG	7-30	stu-miR7997c	4	0	24	24	1
spr-MIR8011a	ACCCUUUCUUUAUGACAACACGAAUACUAGUUGUGUGAGGCUUCUUUUUGUCUCACAUAACAGUAGACUCAAAUGGGCGAGACAAAAAUGAGUCUCACUCGACUAGUGUCAGUUGUGUGAGUCACAAAAUAGAAC	135	spr-miR8011a-5p	UUGUGUGAGGCUUCUUUUUGUCUC	31-54	stu-miR8011a-5p	2	0	24	24	1
spr-MIR8047	GACUCUGCUACACAAUAUAACGGUUGAUUUACACAAAUAGCCACUUUUUACGGCUUUGUACAUAGAAGAUGGCCAUUUUUUCAAAACUAGACCAGUAGUCUGAAGUUUAUAAUCCAAAAAACUACUAUUCAAACCAUGGGUCUAAUGUAGAAAAAAGUGGCCAACUUCUAAAUACAACGCGACGAAAGUGGCUACCUGAUGUAAACAUCGCCAUUUUAUCUUGCAACAUGAAUGGUCUCAUAAUCAAGAUGAAACUGAUGUUAAGUUUUUGGUAAGCUUGGUCUGGCAGAAGACUGAAGGUCUUCGUUAUUGCUCUUUUAUCGAGA	234	spr-miR8047-5p	CCAUUUUUUCAAAACUAGACC	73-93	stu-miR8047	2	0	21	21	1
spr-MIR8718	GAGUAUAUGUAUGGAUCUUCUAUAAGAUGGAUGGAGCUGUUUGAUU	332	spr-miR8718-3p	AUUUUGGGUGCAUUUCUGCUA	195-215	gra-miR8718	5	0	21	21	1

spr-MIR8767c	GUAGCUUUAUGUGAUCUUCUGUGCAGAUUGAUGGUUUUGCAGCCAA CUGACAUCCAAUUUUGGGUGCAUUUCUGCUACAGCUCAUCUAGGUG UUCUCUCUUUUGGUGGCAGUGCAACUAAAACAGGGUGAUAUUCAUU GGAAAAUUAAUACAUCAGAUGCCAAAAGAUUGACUCUCUUCUCUUGU GACUGACGC UUAAACGUCUUCGUGCUCUUAGCUCACUUUGGGCUGGACGUCUUUC UGAACCGGCUUAAAGAAGUAAGAAAGAACCGGUGGGUUUUUCAACU UUGCCAAUCAAAGCUGUGUGAGCUAAGUAACAAGUAUGAGUUGGC	137	spr-miR8767c-3p	UUUUCAACUUUGCCAAUCAAA	84-104	gra-miR8767c	3	0	21	21	1
spr-MIR9478	AAACUUUUAACGGAUGGCAUAAAUGAGCCUUUUUUGAAAGUUCGAU GGCAUAUUUGAGCCUUUUCCCUUAAAAGAAA	77	spr-miR9478-3p	UUCGAUGGCAUAUUUGAGCCU	41-61	sly-miR9478-3p	1	0	21	21	1

Supplementary Table S12. Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum pimpinellifolium* LA0480 (spiLA0480).

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
spiLA0480-MIR169a-1	AUAGAAAUGGAGAGUGGAUUGCAGCCAGGGAUGACUUGCCGAUGAUUUCUUUCCUAGUUUUCCUAUUAAAGAUUAUGUAUCGGCAAGUUGUCCCUGGCUACCUUUCGCUCUCUUCUUCU	119	spiLA0480-miR169a-1-5p	CAGCCAGGGAUGACUUGCCGA	22-42	cas-miR169a	1	0	21	21	1
			spiLA0480-miR169a-1-3p	GGCAAGUUGUCCCUGGCUACC	82-102	aly-miR169a-3p	2	0	21	21	1
spiLA0480-MIR319b-1	UUAGAUGUAAGUAGAAGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAU	198	spiLA0480-miR319b-1-3p	AUUGGACUGAAGGGAGCUCCU	168-188	aof-miR319b	1	0	21	21	2
spiLA0480-MIR159b-1	UGGAUACUCUGUUUGUGGAUUACACUAAUAUUCAUAUAGUUGAUUUUAACUUGUUCGAGGAAGAUUAGAGUUCUGAAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACGUU	254	spiLA0480-miR159b-1-3p	AGCUGCUAAUCUAUGGAUCCC	124-144	cas-miR159b-5p	1	0	21	21	1
spiLA0480-MIR479-1	GAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUU	92	spiLA0480-miR479-1-5p	CGUGAUAUUGGUUUGGCUCACU	11-32	ghr-miR479	3	0	22	22	1
			spiLA0480-miR479-1-3p	UGAGCCGAACCAAUAUCACUC	62-82	aof-miR479	0	0	21	21	1
spiLA0480-MIR1919-1	GCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUAUGGAACCACACUUUCUUUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGG	143	spiLA0480-miR1919-1-5p	UGUCGCAGAUGACUUUCGCCC	31-51	stu-miR1919-5p	0	0	21	21	1
			spiLA0480-miR1919-1-3p	ACGAGAGUCAUCUGUGACAGG	97-117	stu-miR1919-3p	0	0	21	21	1
spiLA0480-MIR395b-1	UUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUUACUUUGAUGUUAGAAGCGUUGCUGAAGUGUUUGGGGGAACUCCUGGGUUGACUUUA	100	spiLA0480-miR395b-1-3p	CUGAAGUGUUUGGGGGAACUCC	66-87	sly-miR395b	0	0	22	22	1
spiLA0480-MIR160h-1	AUGCCUGGCUCCUUGUAUGCCAUUUGCAUUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAUGGCAUUCUAGGAGCUAAGCAUG	83	spiLA0480-miR160h-1-5p	UGCCUGGCUCCUUGUAUGCCAUU	2-24	mes-miR160h	1	0	23	23	1
spiLA0480-MIR319a-1	AAAUAAGGAGCUCUCUCCGGUCCAGUCCGAGGCACUCAAAGGCUAAAAACACAGCUGACGACUCGUUGAUUCUCAAACAUAUCAAGAAGCAUUUUUUGAAAUUGGUGUGUUUAAGAUUCAACGAUGCGUGAGCUAUGUUUGGCUAGCGUUGUCACGUCUUGGACUGAAGGGAGCUCCCUAUUAA	184	spiLA0480-miR319a-1-3p	UUGGACUGAAGGGAGCUCCCU	159-179	aof-miR319a	0	0	21	21	1
spiLA0480-MIR156f-1	AAUUCUAUUGACAGAAGAGAGAGAGUACAAUCUGUCAUCAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUGGAAAC	97	spiLA0480-miR156f-1-5p	UUGACAGAAGAGAGAGAGUACA	8-29	gma-miR156f	1	0	22	22	1
spiLA0480-MIR171a-1	UGAUGUUGGAAUGGCUCAAUCUAAUGAAAGUUUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAUAUCGUC	87	spiLA0480-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	59-79	aof-miR171a	0	0	21	21	1
spiLA0480-MIR5300	UUGACCAAAAUUCUUCUUCCAGUCCAGGCAUUCCAACAGUUGAUAACAUCUAGAUCUGCCAAUACUUUGUAUUUUUGUUCUUCUAUUUUUCACAUGACAUCUUCAAAAUCUACUAUGAGCUUCAUCAUAAGCUAAGAAAUGGUGAGUUUUGAUGAUGUGAUGCCUAAAAUAGGAUUAAAUGAAAGUACUAGUAAAAAGGUGUUCAGAUCUGGAGGUUAUGUUAAGCUGGUGGUAUGCUUUGAUUGGGAAAGAUGACUUAGGUCA	266	spiLA0480-miR5300-5p	UCUCCAGUCCAGGCAUUCCAAC	18-39	sly-miR5300	1	0	22	22	1
spiLA0480-MIR482b-1	UAUUCAUAAAAAAAAAAAAAUUCAGAAAUUGGGAAAGGGAUGAAGAUUUUUGGGAAGCUUUUGGCGUGAGCGGUGGGGAAAGAUAGAUCUAUCAUAUUAGUAUGAUAUGAUAAAUCUUGCCUACACCG	190	spiLA0480-miR482b-1-3p	UCUUGCCUACACCGCCCAUGCC	114-135	sly-miR482b	0	0	22	22	1

spiLA0480-MIR319a-2	CCCAUGCCCAUGGCUUCCAAUGAUUUCUUCCUUUCCAUACAAUUUCUUCAUGUUAUUUUUUUU UGGUAUAAGAGAGCUUCCUUUAGUCCACUCAUAGGUAGACGAAGGAUUUGAAUUAUCUCCCGACUCAUUCAUUCAAACGCAAUAGGAAGUAUGUAAUCUUAUACUAUUGUGAAUGUGUGAAUGAUGCGGGAGAUAAAUUCUCUCCUUUUAUCUGUGCUUGGACUGAAGGGAGCUCCCUUUUACC	185	spiLA0480-miR319a-2-5p	AGAGCUUCCUUUAGUCCACUC	10-30	mtr-miR319a-5p	1	0	21	21	1
			spiLA0480-miR319a-2-3p	UUGGACUGAAGGGAGCUCCCU	159-179	aof-miR319a	0	0	21	21	1
spiLA0480-MIR171a-2	GAUCAACUUGCGAUGUUGGUGUGGUUCAAUUAGAUAACAAUCUCCACGUAAAAUUAUAGAGUUUGUUAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAAGAAAAUAA	108	spiLA0480-miR171a-2-3p	UGAUUGAGCCGUGCCAAUAUC	71-91	aof-miR171a	0	0	21	21	1
spiLA0480-MIR6022-1	AAUACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAGUUAUUUAGACCGAGUUUUAACCAAUUGCACGGUCCUCUACCCAAGAUUGAGGUUUCGUAAAAUGUAACUUAAGAUCAAGUCGCGUUAGGUUCAUGAAGUUUUGAAUUGACUUAGGAAGAGUACCUUGCAACUUAAAACUUUGAGGCGAAAUAAGUUAGUGAUGGAAAGGAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGGG	238	spiLA0480-miR6022-1-3p	UGGAAAGGAUAAUAUCCAGGA	198-218	sly-miR6022	2	0	21	21	1
spiLA0480-MIR6024-1	AACUGGAAAUGGGGAAGUGGAGAAACAACACUUGCUAAAGGAAGUUCACCAGUCAUCUCUUUUCUUUUGGAGUUUUUUUAGCAAGAGUUGUUUUACCUCUUCUCAAUUCCGUCUCU	116	spiLA0480-miR6024-1-5p	AGAAACAACACUUGCUAAAGGA	21-42	stu-miR6024-5p	1	0	22	22	1
			spiLA0480-miR6024-1-3p	UUUUAGCAAGAGUUGUUUUACC	76-97	sly-miR6024	0	0	22	22	1
spiLA0480-MIR482c-1	GAGUUUUUCGAAAAUCUAUGGGGAUUGGUGAGUUGGAAAGCUUUUCUUUUUCUUCUCUUGUGAUUAGCUUUCCAAUUCCACCCAUUCCUAUGGUUUUUCGGUAUUCUCU	109	spiLA0480-miR482c-1-3p	UUUCCAAUUCCACCCAUUCCUA	69-90	nta-miR482c	0	0	22	22	1
spiLA0480-MIR482c-2	GUGUUUCGAGGAGGUGUUGGAGUGGGUGGUGUGGUAAGAUUUCAUAUUUAUUUUCCAUAAAAAUUGAGAUCUUGCCAAUACCGCCCAUUCCUAUGGCUUCUGAUCAUUUC	110	spiLA0480-miR482c-2-3p	UCUUGCCAAUACCGCCCAUUCC	70-91	sly-miR482c	0	0	22	22	1
spiLA0480-MIR482b-2	AUUUUUCAGGAAGCUUUUGGAGUGGGUGGCAUGGUAAGAUAUCAUAUCUUGUUUUUCAUAAAAAAAAAAAUGAAAUUGAAAUCUUACCGAUUCCCCCCAUUCCAAUGGCUUCCAGUUAUAAC	121	spiLA0480-miR482b-2-5p	GGAGUGGGUGGCAUGGUAAGA	19-39	stu-miR482b-5p	0	0	21	21	1
			spiLA0480-miR482b-2-3p	UUACCGAUUCCCCCCAUUCCAA	83-104	stu-miR482b-3p	0	0	22	22	1
spiLA0480-MIR6025b-1	UGUAUAGUUAUUUCAUGUACACUUGCACAAAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACUAUUGGGAUGGCAUCUCGGUUUGUUA	162	spiLA0480-miR6025b-1-3p	UGCCAACUAUUGGGAUGGCAUC	130-151	nta-miR6025b	2	0	22	22	1
spiLA0480-MIR6025b-2	AAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACUAUUGGGAUGGCAUCUCGGUUUGUUAGUUGCUGUGCAGUAUGAUCACUGUGGCAG	162	spiLA0480-miR6025b-2-3p	UGCCAACUAUUGGGAUGGCAUC	101-122	nta-miR6025b	2	0	22	22	1
spiLA0480-MIR172-1	UUCAUCAUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAU	176	spiLA0480-miR172-1-3p	UGGGAAUCUUGAUGAUGCUGCAU	134-156	aau-miR172	1	0	23	23	1
spiLA0480-MIR172-2	UGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUCAAAAAUGAGAACUUGAUGAUGCUGCAUCGACAAAUUAUGACUUUUUCCCCUCGAAUUAAAAGAAUUCAGGAUGAUCUCGACUUUACUAUUUAUUUUUGGUAAGUAUGCAAUUUGGACUUUGACU	246	spiLA0480-miR172-2-3p	UGAGAAUCUUGAUGAUGCUGCAU	127-149	aau-miR172	0	0	23	23	1
spiLA0480-MIR166-1	GGAAUGUUGUUUGGCUCGAAGUCAUUAUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUAAAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUCAUUCCCCCCAAUUUGGAAACAAAAAUUACAUUCCGUAAUUCUCUCUCCGUCUCUGGU	185	spiLA0480-miR166-1-3p	UCUUCGGACCAGGCUUCAUUCCCC	112-135	lja-miR166-3p	2	0	24	24	3
spiLA0480-MIR166b	CAGAUUUGAGGGGAAUGUUGUUUGGCUCGAAGUCAUUAUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUAAAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUCA	140	spiLA0480-miR166b-5p	GGAAUGUUGUUUGGCUCGAAGU	12-33	csi-miR166b-5p	2	0	22	22	1
			spiLA0480-miR166b-3p	CUUCGGACCAGGCUUCA	124-140	aof-miR166b	2	0	17	21	3
spiLA0480-MIR167b-1	UACUAUCAGUUGAAGCUGCCAGCAUGAUCUAAACUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGAUCAUGUGGUUGCUUCACC	93	spiLA0480-miR167b-1-5p	UGAAGCUGCCAGCAUGAUCUAA	11-32	bna-miR167b	0	0	22	22	1

	UGUUAGUU										
spiLA0480-MIR172-3	GUGUACACAGUUGUUGUUUGCAAAUGCAGCACUAUUAAGAUUCUCAAAUAUUCUGACAUUUAAAAUGCAAUUAAAUGUGAAUCUUGAUGAUGCUGCAUUAGCAAUAAA	108	spiLA0480-miR167b-1-3p	GAUCAUGUGGUUGCUUCACC	66-85	stu-miR167b-3p	3	0	20	20	1
			spiLA0480-miR172-3-3p	UGUGAAUCUUGAUGAUGCUGCAU	76-98	aau-miR172	1	0	23	23	1
spiLA0480-MIR398-1	UAUUCAACAGGGGCAACUUGAGAUCACAUGUUGUCAUUUUUUUCUUUUUGGUUUGAUUCGAUGAAUCAGUAUCUCAACAUGUGUUCUCAGGUUACCCCUGUUGAAUUA	108	spiLA0480-miR398-1-5p	GGGGCAACUUGAGAUCACAUG	10-30	hbr-miR398	3	0	21	21	1
			spiLA0480-miR398-1-3p	UGUGUUCUCAGGUUACCCCUG	80-100	bra-miR398-3p	1	0	21	21	1
spiLA0480-MIR399i-1	UUCGUGAACGAUAGUAAUUGUAAGGGAAACAGUGAUAGGGCUACACUCUAUUGGCAUGCAACUUGAUCAAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUAUUACUGUCUC	116	spiLA0480-miR399i-1-5p	GGGCUACACUCUAUUGGCAUG	38-58	stu-miR399i-5p	0	0	21	21	1
			spiLA0480-miR399i-1-3p	UGCCAAAGGAGAGUUGCCCUA	86-106	stu-miR399i-3p	0	0	21	21	1
spiLA0480-MIR399o	AACAGUGAUAGGGCUACUCUCUAUAGGCAUAUGCCGUUUAUCACACAUUACAGCUGACACGCCAAAGGAGAGCUGCCCUAUUACUGUCU	89	spiLA0480-miR399o-5p	GGGCUACUCUCUAUAGGCAUA	11-31	stu-miR399o-5p	2	0	21	21	1
			spiLA0480-miR399o-3p	CGCCAAAGGAGAGCUGCCCUA	60-80	stu-miR399o-3p	1	0	21	21	1
spiLA0480-MIR477b	GUCUUUUUUCACUCUCCCUCAAAGGCUUCUGGCUUAAAAUGCCUUUUGUGCUAAUGCUAGAGGUCUUUCGAGUGAGAGUGAAUAAAUUCU	90	spiLA0480-miR477b-5p	ACUCUCCCUCAAAGGCUUCUG	11-31	stu-miR477b-5p	0	0	21	21	1
			spiLA0480-miR477b-3p	GAGGUCUUUCGAGUGAGAGUGA	60-81	stu-miR477b-3p	0	0	22	22	1
spiLA0480-MIR1919-2	CCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUAUGGAACCACACUUUCUUUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUUUUUCAU	147	spiLA0480-miR1919-2-5p	UGUCGCAGAUGACUUUCGCCC	11-31	stu-miR1919-5p	0	0	21	21	1
			spiLA0480-miR1919-2-3p	ACGAGAGUCAUCUGUGACAGG	77-97	stu-miR1919-3p	0	0	21	21	1
spiLA0480-MIR156k	UGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUUGCAUGAUGUUUAUAUAUAUAUGCUUGAAACUAUGUGUGCUUACUCUCUAUCUGUCACC	96	spiLA0480-miR156k-5p	UGACAGAAGAGAGUGAGCAC	4-23	cas-miR156k-5p	0	0	20	20	1
			spiLA0480-miR156k-3p	UGCUUACUCUCUAUCUGUCACC	75-96	cas-miR156k-3p	0	0	22	22	1
spiLA0480-MIR160c	AUGUGCCUGGCUCCCUGUAUGCCACACACAUUCACCAAUUCUUUGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGCAUA	85	spiLA0480-miR160c-5p	UGCCUGGCUCCCUGUAUGCCA	4-24	aof-miR160c	0	0	21	21	1
			spiLA0480-miR160c-3p	GCGUAUAAGGAGCCAAGCAUA	65-85	aly-miR160c-3p	2	0	21	21	1
spiLA0480-MIR164-1	GAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUGAC	169	spiLA0480-miR164-1-5p	UGGAGAAGCAGGGCACGUGCA	3-23	aof-miR164	0	0	21	21	1
spiLA0480-MIR169a-2	UGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGAGUGGAGUGCAGCCAAGGAUGACUUGCCGAGAUGUUGUAGCCUAAUGCAAUGACAUAUCGGCAGGUCAUCUUUGGCUACAUUUUAUUCUCUCCUAUUCAUGUAAAACUUUAUAGACGUAUAUGUA	157	spiLA0480-miR169a-2-5p	CAGCCAAGGAUGACUUGCCGA	42-62	cas-miR169a	0	0	21	21	1
spiLA0480-MIR394b	GAUGAAGAAAAAAAAUAUGAAGAUUAAUUAGUUUCACGGAGGUUUGACAAAGGGUUUCUUACAGAGUUCAUUGGCAUUCUGUCCACCUCCUUCGUUCUUUUUUCGAGAAAAAAAGAAGAAGGGGGGAAGCAAGAUUUAGUGUGGAGGUGGGCAUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUUGUAAAACCCUCGUGAUACACGUCAAGUAAGAUAGAGAGUGAUUUGAUC	233	spiLA0480-miR394b-5p	UUGGCAUUCUGUCCACCUCC	71-90	csi-miR394b-5p	0	0	20	20	1
			spiLA0480-miR394b-3p	AGGUGGGCAUACUGCCAAUAG	145-165	ath-miR394b-3p	0	0	21	21	1
spiLA0480-MIR397b-1	CAGAGUACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGAA	118	spiLA0480-miR397b-1-5p	UCAUUGAGUGCAGCGUUGAUG	18-38	mes-miR397b	0	0	21	21	1
			spiLA0480-miR397b-1-3p	UCAACGCUACACUCGAUCAUG	82-102	eun-miR397b-3p	3	0	21	21	1
spiLA0480-MIR166-2	AUAUUGUUGAGGAGAAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUGUAUCGUGAA	120	spiLA0480-miR166-2-3p	AUUUCGGACCAGGCUUCAUUCCCC	88-111	lja-miR166-3p	0	0	24	24	1

	UGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUG										
spiLA0480-MIR156b-1	GUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUCUCCUUCUAUUUUUCUCUUUUCUCUCCCUAAAUCUAUA	181	spiLA0480-miR156b-1-5p	UUGACAGAAGAUAGAGAGCAC	10-30	aof-miR156b	0	0	21	21	1
			spiLA0480-miR156b-1-3p	GCUCUCUAUGCUUCCGUCAUC	109-129	vca-miR156b-3p	1	0	21	21	1
spiLA0480-MIR160g	AAUUGUUCUGCCUGGCUCCCUGGAUGCCAACUAAGAACAGUAUUGUCAAAAAAAAUUGACACUCUUCCUAGUUGGUACCAGAGGAGACAGGCAGAUCCAU	99	spiLA0480-miR160g-5p	UGCCUGGCUCCCUGGAUGCCA	9-29	lus-miR160g	0	0	21	21	1
spiLA0480-MIR167c-1	UCGUGCAGCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAUCAGAUCAUGUGGCAGCCUCACCUGUCAAUGCCAUCACGAAUUAUUAAA	125	spiLA0480-miR167c-1-5p	UGAAGCUGCCAGCAUGAUCUA	19-39	ata-miR167c-5p	0	0	21	21	1
			spiLA0480-miR167c-1-3p	AUCAGAUCAUGUGGCAGCCUCACC	76-99	eun-miR167c-3p	1	0	24	24	1
spiLA0480-MIR168c	CUCUUAUUCGCUUGGUGCAGGUCGGGACCUCAUUCGCCGGCGCCGGGAAUAAUGCCGGACGAACGACGGCGGUGUUAAUUCUACUAAAGCUGUCACCGACGGAUAGAUGUUUGAUUAGCGGCGAAAUUUGGGUCCUGCCUUGCAUCAACUGAAUUGGA	158	spiLA0480-miR168c-5p	UCGCUUGGUGCAGGUCGGGAC	8-28	bra-miR168c-5p	0	0	21	21	1
			spiLA0480-miR168c-3p	CCUGCCUUGCAUCAACUGAAU	134-154	bra-miR168c-3p	1	0	21	21	1
spiLA0480-MIR397b-2	UACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGAAGGGACAUU	121	spiLA0480-miR397b-2-5p	UCAUUGAGUGCAGCGUUGAUG	13-33	mes-miR397b	0	0	21	21	1
			spiLA0480-miR397b-2-3p	UCAACGCUACACUCGAUCAUG	77-97	eun-miR397b-3p	3	0	21	21	1
spiLA0480-MIR7990a-1	GCAAAAGUUAUGACCAUUUGAAGUGUCACAAAUUUACAACUACUUUUUUUGAGUUAUACUCUUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCC	100	spiLA0480-miR7990a-1-3p	UUCAAAUGAUCGUAACUUUGGCC	78-100	stu-miR7990a	0	0	23	24	1
spiLA0480-MIR8009	AAUUUCCAGAAAAGCGACGGACAGGGUCCUUUAAUCUGUCGCUAUUCUGGGAUUUU	56	spiLA0480-miR8009-5p	AUUUCCAGAAAAGCGACGGACAGG	2-25	stu-miR8009	1	0	24	24	1
spiLA0480-MIR1886h-1	CGUGAGAUGAAAUCAGCAUUUGGAUAUGCAAUUUUACGUUGAUUUCAUCUCAUGA	55	spiLA0480-miR1886h-1-3p	AUUUUACGUUGAUUUCAUCUCAUG	31-54	stu-miR1886h	0	0	24	24	1
spiLA0480-MIR8025-1	CACACACUACACAUGCAAUUAAAUUAGUAUAAGUCGCCAUUAUGUUUUUCUUAACCAAGCUGAAUCAUAUAAUGGUGACUUAUACUAAUUUAAUUGCAUGCCGACUGUGUGUAUUUUCCGCAUGUGUGUAACUACUCUAU	140	spiLA0480-miR8025-1-5p	ACACACUACACAUGCAAUUAAAUU	2-25	stu-miR8025-5p	3	0	24	24	1
			spiLA0480-miR8025-1-3p	UUUAAUUGCAUGCCGACUGUGUGU	89-112	stu-miR8025-3p	3	0	24	24	1
spiLA0480-MIR8025-2	GUCAAACAUCAUAAAGAAAUAUUUUACCACACACUACACAUGCAAUUAAAUUAGUAUAAGUCGCCAUUAUGUUUUUCUUAACCAAGCUGAAUCAUAUAAUGGUGACUUAUACUAAUUUAAUUGCAUGCCGACUGUGUGU	139	spiLA0480-miR8025-2-5p	ACACACUACACAUGCAAUUAAAUU	29-52	stu-miR8025-5p	3	0	24	24	1
			spiLA0480-miR8025-2-3p	UUUAAUUGCAUGCCGACUGUGUGU	116-139	stu-miR8025-3p	3	0	24	24	1
spiLA0480-MIR7122	UAUAUACAGAGAAACCGCUGUCGAUUAUAAUGAGAAAUUCGGUGUUUCUCAUACUCCACAGCGUUUUUCUGUAUAACC	78	spiLA0480-miR7122-5p	AUAUACAGAGAAACCGCUGUCG	2-23	stu-miR7122-5p	1	0	22	22	2
			spiLA0480-miR7122-3p	ACAGCGUUUUUCUGUAUAACC	58-78	stu-miR7122-3p	1	0	21	21	1
spiLA0480-MIR5304	UCAAUGCUACAUACUCAUCCCCACAACUUUCAUCUCACGUUCAAAAGAUGAAAGUUAUAGAGAUGAGUAUGGUGCAUUGGA	81	spiLA0480-miR5304-5p	UCAAUGCUACAUACUCAUCCC	1-21	sly-miR5304	0	0	21	21	1
			spiLA0480-miR5304-3p	AGAUGAGUAUGGUGCAUUGGA	61-81	stu-miR5304-3p	0	0	21	21	1
spiLA0480-MIR171c-1	AGAUAUUGAUGCGGUUCAAUCUGAAAGACAUGGUUAGAUAUGUAAUUAGCCUUGUAAUUUUGGAUUGAGCCGCGUUAAUAUCUC	84	spiLA0480-miR171c-1-5p	AGAUAUUGAUGCGGUUCAAUC	1-21	cas-miR171c-5p	1	0	21	21	1
			spiLA0480-miR171c-1-3p	UUGAGCCGCGUUAAUAUCUC	65-84	aof-miR171c	1	0	20	21	1
spiLA0480-MIR166-3	GGAAUGUUGUUUGGUUCGAAAUCAUUCAAACAAAUUAAAAUUCAUGCAUCUAGAUGAUCGAUGAAUUGAAUAAUUUCGGACCAGGCUUCAUUCCC	95	spiLA0480-miR166-3-3p	AUUUCGGACCAGGCUUCAUUCCC	73-95	lja-miR166-3p	0	0	23	24	1
spiLA0480-MIR399i-2	UAGUAAUUGUAAGGGAAACAGUGAUAGGGCUACACUCUAUUGGCAUGCAACUUGAUCAAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUA	95	spiLA0480-miR399i-2-5p	GGGCUACACUCUAUUGGCAUG	27-47	stu-miR399i-5p	0	0	21	21	1

			spiLA0480-miR399i-2-3p	UGCCAAAGGAGAGUUGCCCUA	75-95	stu-miR399i-3p	0	0	21	21	1
spiLA0480-MIR172c	GGAGCAUCAUCAAGAUUCACAUAGCUAUAUUAGGGCUUUUAUAAUUUUUAAAAACCCUAUGGGCGAUGUGUGGGAAUCUUGAUGAUGCUGCA	92	spiLA0480-miR172c-5p	GGAGCAUCAUCAAGAUUCACA	1-21	cas-miR172c	0	0	21	21	1
			spiLA0480-miR172c-3p	GGAAUCUUGAUGAUGCUGCA	73-92	ata-miR172c-3p	0	0	20	21	1
spiLA0480-MIR172j	UGCAGCAUCAUCAAGAUUCCCACACAUCGCCCAUAGGGUUUUUAAAAAUUAUAAAAGCCCUAAUAUAGCUAUGUGAAUCUUGAUGAUGCUCCAC	94	spiLA0480-miR172j-5p	GCAGCAUCAUCAAGAUUCCCA	2-22	lus-miR172j	0	0	21	21	1
			spiLA0480-miR172j-3p	UGAAUCUUGAUGAUGCUCCAC	74-94	mdm-miR172j	3	0	21	21	2
spiLA0480-MIR156b-2	UUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUC	101	spiLA0480-miR156b-2-5p	UUGACAGAAGAUAGAGAGCAC	1-21	aof-miR156b	0	0	21	21	1
			spiLA0480-miR156b-2-3p	GCUCUCUAUGCUUCUGUCAUC	81-101	vca-miR156b-3p	0	0	21	21	1
spiLA0480-MIR167b-2	UGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAUCAGAUCAUGUGGCAGCCUCAC	80	spiLA0480-miR167b-2-5p	UGAAGCUGCCAGCAUGAUCUAA	1-22	bna-miR167b	0	0	22	22	1
			spiLA0480-miR167b-2-3p	GAUCAUGUGGCAGCCUCAC	62-80	stu-miR167b-3p	1	0	19	20	1
spiLA0480-MIR477a-1	CCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUGUGUUGGGAAAGAAGCUCUAGCAGGGAGAGCC	68	spiLA0480-miR477a-1-5p	CCUCUCCCUCAAGGGCUUCUC	1-21	stu-miR477a-5p	0	0	21	21	1
			spiLA0480-miR477a-1-3p	GAAGCUCUAGCAGGGAGAGCC	48-68	stu-miR477a-3p	0	0	21	22	1
spiLA0480-MIR408-1	ACGGGGACGAGCCAGAGCAUGAGAUGUGCAAUUUUUGCUUUGCCUAUUCCAUGCACUGCCUCUUCCCUGGC	71	spiLA0480-miR408-1-5p	ACGGGGACGAGCCAGAGCAUG	1-21	sly-miR408	0	0	21	21	1
			spiLA0480-miR408-1-3p	AUGCACUGCCUCUUCCCUGGC	51-71	cas-miR408	0	0	21	21	1
spiLA0480-MIR156b-3	GUGACAGAAGAGAGUGAGCACACAUGGUUCUUUCAUGGAUUAUUCCCCAUGUUUAAAAGCUCUGCGUGCUCACGCUCUAUCUGUCACA	88	spiLA0480-miR156b-3-5p	UGACAGAAGAGAGUGAGCACA	2-22	hvu-miR156b	0	0	21	21	1
			spiLA0480-miR156b-3-3p	UGCUCACGCUCUAUCUGUCACA	67-88	mtr-miR156b-3p	2	0	22	22	1
spiLA0480-MIR169j-1	AUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGUUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUCUUUGAUGGCCAGGCAGUCUCCUUGGCUACU	115	spiLA0480-miR169j-1-5p	UAGCCAAGGAUGACUUGCCUGC	2-23	ppe-miR169j	0	0	22	22	1
spiLA0480-MIR394-1	UUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAA	59	spiLA0480-miR394-1-5p	UUGGCAUUCUGUCCACCUCC	1-20	aof-miR394	0	0	20	20	1
spiLA0480-MIR169c-1	AGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAUUUAUAUUAAUCUCAUCUCGGAUUUA	205	spiLA0480-miR169c-1-5p	UAGCCAAGGAUGACUUGCCUA	42-62	ata-miR169c-5p	0	0	21	21	1
spiLA0480-MIR172-4	CUUACAGUCGUUGUUUGCAUAUGUGGCAUAAUCAAGAUUCACGUGAAAAGUUGCAAAUUGGUUAUAUAAUUGAUGAAAUUAAUGGCUGGCUAUUUGAAACUCACGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAACGAC	140	spiLA0480-miR172-4-3p	CGAGAAUCUUGAUGAUGCUGCAU	104-126	aau-miR172	1	0	23	23	2
spiLA0480-MIR2111d	UGGUAAUCUGCAUCCUGAGGUUUAGAUCAAUUUAUAACUUACUGGAUCUAGUCCUUGGGAUGCAGAUUAUC	71	spiLA0480-miR2111d-5p	UAAUCUGCAUCCUGAGGUUUA	4-24	ppe-miR2111d	0	0	21	21	1
			spiLA0480-miR2111d-3p	GUCCUUGGGAUGCAGAUUAUC	51-71	gma-miR2111d	2	0	21	21	1
spiLA0480-MIR319b-2	AGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAUAUAUAGUUAAGUUAACUAUAUAAAAUAUAAGAGAGCUUCCUUCAGCCCACUCACGGAGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCCUUGCUUGGACUGAAGGGAGCUCCUU	211	spiLA0480-miR319b-2-3p	AUUGGACUGAAGGGAGCUCCU	153-173	aof-miR319b	1	0	21	21	2
spiLA0480-MIR319c		176	spiLA0480-miR319c-5p	AGAGCUUCCUUCAGCCCACUC	4-24	sly-miR319c-5p	0	0	21	21	1
			spiLA0480-miR319c-3p	UUGGACUGAAGGGAGCUCCUU	156-176	sly-miR319c-3p	0	0	21	21	1
spiLA0480-MIR164-2	UCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUG	171	spiLA0480-miR164-2-5p	UGGAGAAGCAGGGCACGUGCA	7-27	aof-miR164	0	0	21	21	1

spiLA0480-MIR164e	UAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUG UGUUGGAGAAGCAGGGCACGUGCAAAUUCUUGUAUUCGACGAUAUAUGCAUUACUAAUGGUAAUGCAUGAAUUUUGCACGUGUUCUCCUUCUCCAAC	97	spiLA0480-miR164e-5p	UGGAGAAGCAGGGCACGUGCAA	4-25	bra-miR164e-5p	0	0	22	22	1
			spiLA0480-miR164e-3p	CACGUGUUCUCCUUCUCCAAC	77-97	bra-miR164e-3p	3	0	21	21	1
spiLA0480-MIR172-5	UGGUUGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUCAAAAAUGAGAAUCUUGAUGAUGCUGCAUCGACAAAU	161	spiLA0480-miR172-5-3p	UGAGAAUCUUGAUGAUGCUGCAU	131-153	aau-miR172	0	0	23	23	1
spiLA0480-MIR9471a-1	GAUCUUUGACGGAUUUGGGGUUCUGAGAUUCAGUUGAUUUCUCAGGUGCUCACUCAGCUAAUAGUUAUUAUUUAAGAAACUCAAUAAUAUUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUGAGUGAGCAUCACGGAAAUCAACGUGAUUCUGAGAGGAAAAUGAU	180	spiLA0480-miR9471a-1-5p	CAGGUGCUCACUCAGCUAAUA	43-63	sly-miR9471a-5p	0	0	21	21	1
			spiLA0480-miR9471a-1-3p	UUGGCUGAGUGAGCAUCACGG	130-150	sly-miR9471a-3p	0	0	21	21	1
spiLA0480-MIR9472	AUGGGUUUCAAUUAUAGCUACAGAUCUUCCCAUAGAUCUACUCGAUUUAUUUUUCAGUAGACGUUGUGAAUAAUUGAUAAAUACAGGUAUACAGAGGUCUUAAUAUAGUCAGAACCUAGAAAUAUGUGUAACUAGAUUCAGACCUUUGUACACUUGUAUUCUGUUGCUAUUCACAAUCUCUGCUGAAAAAUGAUUGACUAGAUCUACGAAUAAUCUAGAUUAUUAAUGCCCG	232	spiLA0480-miR9472-5p	UUUCAGUAGACGUUGUGAAUA	52-72	sly-miR9472-5p	0	0	21	21	1
			spiLA0480-miR9472-3p	UUCACAAUCUCUGCUGAAAAA	170-190	sly-miR9472-3p	0	0	21	21	1
spiLA0480-MIR482d	UGGAAAGGGAGGAGGGAUUUGGGAAUCUUUUGGAGUGGGUGGGAUGGAAAAAUAUUGUAUUUUUUUUUCUAACGGAAAAAAAGAUGAGAAUUGAGAUUUUUCCUAUUCCACCCAUGCCAAUGGCUUCCAGUCAUUUACUCCUUUUCC	147	spiLA0480-miR482d-5p	GGAGUGGGUGGGAUGGAAAAA	32-52	sly-miR482d-5p	0	0	21	21	1
			spiLA0480-miR482d-3p	UUUCCUAUUCCACCCAUGCCAA	99-120	sly-miR482d-3p	0	0	22	22	1
spiLA0480-MIR9473-1	CUAGCAGAUAUUGGCUGUAAAUCUAAACUCGUUCUACUCCACUAGUCAUCAUGUAAUGACAUUUACUAGAAGAAGAGACUAUUGGGGUAAAACGAGUUCAGAUUUACAGCCAAUAUUGUU	120	spiLA0480-miR9473-1-5p	UGGCUGUAAAUCUAAACUCGU	12-32	sly-miR9473-5p	0	0	21	21	1
			spiLA0480-miR9473-1-3p	AAACGAGUUCAGAUUUACAGC	90-110	sly-miR9473-3p	0	0	21	21	1
spiLA0480-MIR9473-2	AAAACAAUAUUGGCUGUAAAUCUGAACUCGUUUUACCCCAAUAGUCUCUUCUUCUAGUAAAUGUCAUUACAUGAUGACUAGUGGAGUAGAACGAGUUUAGAUUUACAGCCAAUAUCUG	118	spiLA0480-miR9473-2-5p	UGGCUGUAAAUCUGAACUCGU	11-31	sly-miR9473-5p	1	0	21	21	1
			spiLA0480-miR9473-2-3p	GAACGAGUUUAGAUUUACAGC	89-109	sly-miR9473-3p	2	0	21	21	2
spiLA0480-MIR9478	UUAUAAAAGGGAUAAGGCUUAAAUAUGUCGAUCGAACUUUGAGAAAAGACUCAUCUAUGUCAUCUGGUAAAGUUUGGUGUGUAAUGGUUUGAAUGAGCCUUUUCUCGAACGAAAAUGGUGUAGAUGAGUUAAAUUUUUAACGGAUUACAUAAUUGAGUCUUUUCUCAUAGUUCGAUGACAUAUUUGAGCGUUUUCCCAAUUAUA	204	spiLA0480-miR9478-5p	GCUUAAAUAUGUCGAUCGAACU	17-38	sly-miR9478-5p	1	0	22	22	1
			spiLA0480-miR9478-3p	UUCGAUGACAUAUUUGAGCGU	171-191	sly-miR9478-3p	1	0	21	21	1
spiLA0480-MIR169e-1	UAGGAGGAGAGGCCUUACAUGAAUUAGAAGAGUUUCUAUUUGUUUAGUAGCCAAGGAUGACUUGCCUUUCAUCAAUGCCUUUUGUAAAAUGGAAAUUGAUUACAACACUUUCUAUGGUAUUGGGAAAAUGAGUGGCAAGCAUCUUUGGCGACUUGACAAACUCUUCUUUGUCAUGUUAGUCCAUCUUCUUCCU	193	spiLA0480-miR169e-1-5p	UAGCCAAGGAUGACUUGCCUUU	48-69	sly-miR169e-5p	0	0	22	22	1
			spiLA0480-miR169e-1-3p	UGGCAAGCAUCUUUGGCGACU	133-153	sly-miR169e-3p	0	0	21	21	1
spiLA0480-MIR395b-2	GGUGUUCCCUAGAGUUCCCUUGACCACUUCAUUAGGGAUUACUUCGUUGUUUGAUGCCCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCAC	92	spiLA0480-miR395b-2-3p	CUGAAGUGUUUGGGGGAACUCC	62-83	sly-miR395b	0	0	22	22	1
spiLA0480-MIR156c-1	AAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGCGUUUUCUGGCAUGAUGUUUAUAUAUAUAUAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCUCCCACCAA	115	spiLA0480-miR156c-1-5p	UGACAGAAGAGAGUGAGCACA	11-31	rco-miR156c	0	0	21	21	1
			spiLA0480-miR156c-1-3p	GCUCACUGCUCUAUCUGUCACC	85-106	ata-miR156c-3p	0	0	22	22	1

spiLA0480-MIR159b-2	UUUAACUUGUUCGAGGAAGAUCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAGCUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUAUUUUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCUUUAUUGGAAAGAAGGGAGCUCUA	206	spiLA0480-miR159b-2-5p	AGCUGCUGAUCUAUGGAUCCC	80-100	cas-miR159b-5p	2	0	21	21	1
			spiLA0480-miR159b-2-3p	UUGGAAAGAAGGGAGCUCUA	187-206	sly-miR159b	0	0	20	21	1
spiLA0480-MIR159b-3	UUUAACUUGUUCGAGGAAGAUUAGAGUUCUGAAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUA	206	spiLA0480-miR159b-3-5p	AGCUGCUAAUCUAUGGAUCCC	80-100	cas-miR159b-5p	1	0	21	21	1
			spiLA0480-miR159b-3-3p	AUUGGAAUGAAGGGAGCUCUA	186-206	fve-miR159b	2	0	21	21	1
spiLA0480-MIR167h-1	UAACAGGUGAAGCAACCACAUGAUCUGAUCUUGCCUUAAUAUAAAAUUUAUAGGUAAGUUUAGAUCAUGCUGGCAGCUUCAACUGAU	86	spiLA0480-miR167h-1-3p	AUCAUGCUGGCAGCUUCAACUGAU	63-86	gma-miR167h	1	0	24	24	1
spiLA0480-MIR172-6	GCAGAUGCAGCAUCUUCAAGAUUCACAUAGAUUUAUAUAAAAUAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUAAUUUUCUCCUAUAUAUUGGCUCUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGCA	156	spiLA0480-miR172-6-3p	UGAGAAUCUUGAUGAUGCUGCAG	129-151	aau-miR172	1	0	23	23	1
spiLA0480-MIR10528-1	UAAUGAAUGCAAUGUCAUAUACCAUCAACACUCGGAAACUCAAAUUGAGGUUAAAUCUCGGAGUGAUGAUGGUAUAUGACCUUGCAAUUCACUAU	95	spiLA0480-miR10528-1-5p	AAUGCAAUGUCAUAUACCAUC	6-26	sly-miR10528	0	0	21	21	1
spiLA0480-MIR10529	AACAUAACGAGUGAGACUUGCUCAGUUGGUAAAACACCUCCACGGUCUAACCAAUUAUCUUGGUCGAGGGUUCAAGUCAUGUUGGAAGCAAUGUGGGGGCGUCCAGCUUAGCAAGCCUCAUCCGUUUUGCUU	132	spiLA0480-miR10529-5p	AACGAGUGAGACUUGCUCAGUUGG	6-29	sly-miR10529	0	0	24	24	1
spiLA0480-MIR530	UUUAUCUGCAUUUGCACCUGCACCUUAGUGAACGAAUUAGUUCGCGUAUAAUUCGUGCAGAAAGGUGUAGGUGUUCAUGCAGACAAAA	88	spiLA0480-miR530-5p	UCUGCAUUUGCACCUGCACCU	5-25	eun-miR530-5p	0	0	21	21	1
			spiLA0480-miR530-3p	AGGUGUAGGUGUUCAUGCAGA	63-83	sly-miR530	0	0	21	21	1
spiLA0480-MIR10530	AACAUGUUGAAUGUUGGGGAACGAACGUCUAAGGUUUGGGUCAACGAUCUCAAUGUUGAUGCGUCCGCUUGUUGUUGAUGCUGCUCCAAAAGGUUCAACAUUGGGAUUUUAGCCCAAACAUCAGACGUCCCUUCCCCAUCGUUCAACAUCGUU	153	spiLA0480-miR10530-3p	ACGUCCCUUCCCCAUCGUUCAACA	125-148	sly-miR10530	0	0	24	24	1
spiLA0480-MIR398a	UCAAUAGGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUUGUUUGUAACAAUUUACCGUUUAUAAAUAUGACACAUAUGUUCUCAGGUCGCCCCUGUAGAC	102	spiLA0480-miR398a-5p	GGGUUGAUUUGAGAACAUAUG	7-27	stu-miR398a-5p	0	0	21	21	1
			spiLA0480-miR398a-3p	UAUGUUCUCAGGUCGCCCCUG	77-97	sly-miR398a	0	0	21	21	1
spiLA0480-MIR10531-1	AUAUCUGGGGUCCUAGUAGAGUCGGUUCUACAUUGGGUGUUAAGUGUUUUGAGUAAUCAUCAUUGAAAGUAACAUACUUAAAACCCAAUGUUGAAUUGACUCUACUCGGAUCCCAAAUAUC	121	spiLA0480-miR10531-1-5p	UGGGGUCCUAGUAGAGUCGGUUC	6-28	sly-miR10531	0	0	23	23	1
spiLA0480-MIR10534-1	UGGCUCCAAAAUACCCUUGUCAUCCAACAUUGGAUUCAAAAUUGACCACUUAUUUAACGGUCCAUUUUGAACAAAAAGGUGGAUGACAAGGGUAUUUUGGAGCCAA	106	spiLA0480-miR10534-1-5p	CAAAAUACCCUUGUCAUCCAA	7-27	sly-miR10534	0	0	21	21	1
spiLA0480-MIR10534-2	GGCUCCAAAAUACCCUUGUCAUCCACCUUUUUGUUCAAAAUGGACCGUUAAAUAAGUGGUCAAUUUUGAAUCCAAUGUUGGAUGACAAGGGUAUUUUGGAGCCA	104	spiLA0480-miR10534-2-5p	CAAAAUACCCUUGUCAUCCAC	6-26	sly-miR10534	1	0	21	21	1
spiLA0480-MIR10535a	AAAGGGUUGGCAUAAGUUUGUGAAAGCCGGAGAUUUAGGAGUAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUUG	121	spiLA0480-miR10535a-5p	UUGGCAUAAGUUUGUGAAAGCCGG	7-30	sly-miR10535a	0	0	24	24	1
spiLA0480-MIR10535b	AAAGGGUUGGCAUGAGUUUGUGAAAGCCGGAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUUG	121	spiLA0480-miR10535b-5p	UUGGCAUGAGUUUGUGAAAGCCGG	7-30	sly-miR10535b	0	0	24	24	1
spiLA0480-MIR159b-4	AAGGUAGAGCUCUUCUGAAUUCCAAAAAGGAUCUGAGAGGGAAAAUUGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUU	180	spiLA0480-miR159b-4-5p	AGCUGCUAAUCUAUGGAUCCC	49-69	cas-miR159b-5p	1	0	21	21	1
			spiLA0480-miR159b-4-3p	UUGGAAAGAAGGGAGCUCUAC	156-176	sly-miR159b	0	0	21	21	1
spiLA0480-MIR159b-5	AAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUC	180	spiLA0480-miR159b-5-5p	AGCUGCUAAUCUAUGGAUCCC	49-69	cas-miR159b-5p	1	0	21	21	1

	UCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACGUUU		spiLA0480-miR159b-5-3p	UUGGAAUGAAGGGAGCUCUAC	156-176	sly-miR159b	1	0	21	21	1
spiLA0480-MIR171f-1	CUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAGU	81	spiLA0480-miR171f-1-5p	UAUUGGCCUGGUUCACUCAGA	7-27	csi-miR171f-5p	0	0	21	21	1
			spiLA0480-miR171f-1-3p	UGAUUGAGCCGUGUCAAUAUC	56-76	csi-miR171f-3p	1	0	21	21	1
spiLA0480-MIR399i-3	AAGAUUAUACUAAAUAUGUUAUUGUUGGUGUGCUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCCUCUGCUUAAUU	137	spiLA0480-miR399i-3-3p	UGCCAAAGGAGAGUUGCCCUA	98-118	stu-miR399i-3p	0	0	21	21	1
spiLA0480-MIR169r-1	CAUCCAAUGAGCUUCUCACAAGUUGUGUUUUGUUAGAUGAAGUAGGAAACUGCUAAUUCUAUUUGCCAUAGGGAAUGUUGGAUUUUCUUCUUCAGGAAACUACACUUCCCUAUAAUUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAA	285	spiLA0480-miR169r-1-3p	CAGCCAAGGAUGACUUGCCGG	178-198	csi-miR169r-5p	0	0	21	21	1
spiLA0480-MIR169j-2	GUCUUAUUUAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCGUACUUGAAAAGGUCUUUCAUAUGUCCAUCAACAAGAAGAACCUGAGUCAAGUGAUCAGCCGUCUUUUAUAAUCCCUAUGUCAUCUGCCCAUAGAGAAAACAAUGCUACUACUCCUCCAGUUUUUGGGGUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUUCAUGCAAGGCUUUCUCU	265	spiLA0480-miR169j-2-5p	UAGCCAAGGAUGACUUGCCUGC	52-73	ppe-miR169j	0	0	22	22	1
spiLA0480-MIR319b-3	AGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCUUUAUGUGUUAUGGGAGUGGAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAUUGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAGCUUUAUUUUACCCUUUGUUUGAUCACUUUUUGGAUUGAAGGGAGCUCUACAUUCAUUUC	122	spiLA0480-miR319b-3-5p	UAGCUGCCGACUCAUUCAUCCA	20-41	ppe-miR319b	1	0	22	22	1
spiLA0480-MIR159		205	spiLA0480-miR159-3p	UUUGGAUUGAAGGGAGCUCUA	175-195	aof-miR159	0	0	21	21	1
spiLA0480-MIR160h-2	UAUAUGCCUGGCUCCCUGUAUGCCAUUUGCAAAGCUCACCGUAAUAUAUCGAUGGGCCUUGUUGAAUGGCGUAUGAGGAGCCAAGCAUAU	90	spiLA0480-miR160h-2-5p	UGCCUGGCUCCCUGUAUGCCAUU	5-27	mes-miR160h	0	0	23	23	1
spiLA0480-MIR164-3	UAGGUGAGUGACGAUCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUG	185	spiLA0480-miR164-3-5p	UGGAGAAGCAGGGCACGUGCA	21-41	aof-miR164	0	0	21	21	1
spiLA0480-MIR166k	AGGAAGUUCUCUCAGUUGAGGGGAAUGUUGUCUGGCUCGAGGUCACCAAUUAGAUCCAUAAUCCCUAUAUAUACCAUGCUUUUCAAAAAAAGAUUUAUAAUAUGAAAAGGGGUUAUGAAUCAUGUGUUAGUGUUGUCGGACCAGGCUUCAUUCCCCCCAAUUG	163	spiLA0480-miR166k-3p	UCGGACCAGGCUUCAUUCCCCC	136-157	lus-miR166k	0	0	22	22	1
spiLA0480-MIR166-4	AAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUGUAUCGUGAAUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUGAUC	109	spiLA0480-miR166-4-3p	AUUUCGGACCAGGCUUCAUUCCCC	74-97	lja-miR166-3p	0	0	24	24	1
spiLA0480-MIR167c-2	AUCGUGAACCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUUCUAUUGCUCCGUACGAGGAAAGAUCAGAUCAUGUGGCAGCAUCACCUGUUGAUGGUUUCGCGG	110	spiLA0480-miR167c-2-5p	UGAAGCUGCCAGCAUGAUCUA	20-40	ata-miR167c-5p	0	0	21	21	1
			spiLA0480-miR167c-2-3p	AUCAGAUCAUGUGGCAGCAUCACC	70-93	eun-miR167c-3p	1	0	24	24	1
spiLA0480-MIR171a-3	UAGUAAAAUGAUGUUGGAAUGGCUCAAUCAAAUCAAAUUUCUCAAAGUAUUGGGUCAUUUCAUUUGAUUGAGCCGUGCCAAUAUCAUCUUACUUAUAU	98	spiLA0480-miR171a-3-3p	UGAUUGAGCCGUGCCAAUAUC	65-85	aof-miR171a	0	0	21	21	1
spiLA0480-MIR171b-1	AUUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAU	115	spiLA0480-miR171b-1-3p	UUGAGCCGCGCCAAUAUCACU	89-109	aof-miR171b	0	0	21	21	1
spiLA0480-MIR827-1	AGUGAUGAAGAUGUUUGUUGAUGUUCAUCUAAUCAUGGCAUAUUAAUGGUUCCAAAAACUAUGCCAAAUGAUAUGAUGAAUAGAUGACCAUCAACAAACAAAUUCAUAACUACACAAU	118	spiLA0480-miR827-1-5p	GUUUGUUGAUGUUCAUCUAAUC	13-34	eun-miR827-5p	3	0	22	22	2
			spiLA0480-miR827-1-3p	AUAGAUGACCAUCAACAAACA	80-100	aof-miR827	1	0	21	21	2

spiLA0480-MIR171a-4	UUGAUCAACUUGCGAUGUUGGUGUGGUUCAAUUAGAUAACAAUCUCCACGUAAAAUUAUAGAGUUUGUUAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAAGAAAAU	108	spiLA0480-miR171a-4-3p	UGAUUGAGCCGUGCCAAUAUC	73-93	aof-miR171a	0	0	21	21	1
spiLA0480-MIR156f-2	UUCUGUUGACAGAAGAGAGAAAGCACAGUCUGUCAUCAACAAAAUGGUAUUUGUUGUUUGUUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUAGA	94	spiLA0480-miR156f-2-5p	UUGACAGAAGAGAGAAAGCACA	6-27	gma-miR156f	1	0	22	22	1
spiLA0480-MIR156i-1	AAAAGAGGUGACAGAAGAGCGUGAGCACAUGUGUGUUUUCUAGCAUGAUGUUUAUAUGCUUGAAUCUAUGCGUGCUCACUGCUCUAUCUUUCAUCCUCAUCG	102	spiLA0480-miR156i-1-5p	UGACAGAAGAGCGUGAGCAC	9-28	stu-miR156i-5p	1	0	20	20	1
			spiLA0480-miR156i-1-3p	GCUCACUGCUCUAUCUUUCAUC	74-95	zma-miR156i-3p	1	0	22	22	1
spiLA0480-MIR156d	UAUAAUUGAAAUUGAUAGGAAGAAAGAGUGAUUAUUGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCAC	140	spiLA0480-miR156d-5p	UUGACAGAAGAUAGAGAGCAC	38-58	stu-miR156d-5p	0	0	21	21	1
			spiLA0480-miR156d-3p	GCUCUCUAUGCUUCUGUCAUCA	118-139	stu-miR156d-3p	0	0	22	22	1
spiLA0480-MIR162-1	ACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGGAAGCUGAAUAUAUAUAUACGCAAAAAUACAGCAAAAGGAAUCGGUCGAUAAACCUCUGCAUCCAGUG	103	spiLA0480-miR162-1-5p	UGGAGGCAGCGGUUCAUCGAUC	5-26	csi-miR162-5p	0	0	22	22	1
			spiLA0480-miR162-1-3p	UCGAUAAACCUCUGCAUCCAG	81-101	fve-miR162-3p	0	0	21	21	1
spiLA0480-MIR166a	UGCGGGGAAUGUUGUCUGGCUCGAGGAAUCAAAAAUUGUUUCUUAUAGAUAGAUCUGUAUAUUUUGUUUAUAGAUCUAUAAUGUUUUUGAUGUCGUCGGACCAGGCUUCAUUCCC	115	spiLA0480-miR166a-5p	GGAAUGUUGUCUGGCUCGAGG	6-26	cas-miR166a	0	0	21	21	1
			spiLA0480-miR166a-3p	UCGGACCAGGCUUCAUUCCC	96-115	fve-miR166a	0	0	20	21	1
spiLA0480-MIR166f-1	AUGAAGAAAAACAAGAAAAGUGAUGCUAGAAGGGAAGGAAGAAUAAACAUUUUUUGUUUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAA	158	spiLA0480-miR166f-1-3p	UCGGACCAGGCUUCAUUCCCCU	134-155	cas-miR166f-3p	0	0	22	22	1
spiLA0480-MIR171f-2	ACUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAG	81	spiLA0480-miR171f-2-5p	UAUUGGCCUGGUUCACUCAGA	8-28	csi-miR171f-5p	0	0	21	21	1
			spiLA0480-miR171f-2-3p	UGAUUGAGCCGUGUCAAUAUC	57-77	csi-miR171f-3p	1	0	21	21	1
spiLA0480-MIR171a-5	AUACACGAGAUAUUGGUGCGGUUCAAUGAGAAAGCAGUACUUAAGAACAUUUUUGAGUCUACUUUUUGAUUGAGCCGCGCCAAUAUCACGUGUA	94	spiLA0480-miR171a-5-5p	UAUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	0	0	21	21	1
			spiLA0480-miR171a-5-3p	UGAUUGAGCCGCGCCAAUAUCA	67-88	cas-miR171a-3p	1	0	22	22	1
spiLA0480-MIR162b-1	GAAAAGAAAAAAAAAUCCUUCGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCGUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUC	137	spiLA0480-miR162b-1-5p	UGGAUGCAGAGGUUUAUCGACC	34-55	ath-miR162b-5p	4	0	22	22	1
			spiLA0480-miR162b-1-3p	AUCGAUGAACCGCUGCCUCC	109-128	cas-miR162b	0	0	20	20	1
spiLA0480-MIR169c-2	GUUUUACAUGAAGUUGAGAGUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAGA	158	spiLA0480-miR169c-2-5p	UAGCCAAGGAUGACUUGCCUA	31-51	ata-miR169c-5p	0	0	21	21	1
spiLA0480-MIR169r-2	AAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAACAGCUGUUGUUGUUAAUUGUCAAAUCAGGAAUUGUGGACAA	184	spiLA0480-miR169r-2-5p	CAGCCAAGGAUGACUUGCCGG	36-56	csi-miR169r-5p	0	0	21	21	1
spiLA0480-MIR156c-2	CCAAAGGGAGGUGACAGAAGAGAGUGAGCACACAUGAUGUUUUCUCGCAUAAUGUUUAUAUGCUUGAAAUUAUGCUUGCUCACUGCUCUAUCUGUCACCCCACCACU	107	spiLA0480-miR156c-2-5p	UGACAGAAGAGAGUGAGCACA	12-32	rco-miR156c	0	0	21	21	1
			spiLA0480-miR156c-2-3p	GCUCACUGCUCUAUCUGUCACC	78-99	ata-miR156c-3p	0	0	22	22	1
spiLA0480-MIR156i-2	CAAAAGGGAGGUGACAGAAGAGAGUGAGCACGUAUGGUAUUUUCUCGCAUGCUUGAAACUAUGUCUGCUCACUUCUCUAUCUGUCAUCCCUACCAU	96	spiLA0480-miR156i-2-5p	UGACAGAAGAGAGUGAGCAC	12-31	stu-miR156i-5p	0	0	20	20	1
			spiLA0480-miR156i-2-3p	UGCUCACUUCUCUAUCUGUCAUC	66-88	mtr-miR156i-3p	1	0	23	23	1

spiLA0480-MIR159b-6	UACUCUGCUUGUGGAUUAUACUGAUAUUCAUAUAGUUGAUUUUAACUUGUUCGGGGAAGACCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGUAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACUUUUUUUUUCUA	270	spiLA0480-miR159b-6-3p	UUGGAAAGAAGGGAGCUCUAC	227-247	sly-miR159b	0	0	21	21	1
spiLA0480-MIR6271-1	AAAUAUAUAGUUCAUGUUCAAGCUAUUGACAACCUUGAAACUAUCGUUAUAUUUGGCUAAUUAAACUUAAAUACACUCUUAAUCUUGCAACAUGCCUGAAAUACAAUUCAAAAAUUCUCGCCUAGUUUAGGAGUGUUUUCAACACUUUACUCGGCUUAGUAUUAAGAGUCACAUGCUCCUACGAGACUACUUCCGAUGUCAUGUGACAGAACUAGAUGUAUCUAAGUUAAUUAUUCAAGUAAAUUAAUAUUUUUAAGACUGUCAAUAGUGAGAGAUAAAACUAAUAAUU	290	spiLA0480-miR6271-1-3p	UCAAUAGUGAGAGAUAAAACU	263-283	ppe-miR6271	5	0	21	21	1
spiLA0480-MIR8011a-1	ACAUGAACUUUGUUUUGUGUCUCACACAACUGAUGUAAGUUGUGUGAGGUCUCUUUUUGUUUUACAAGUCAGUGCGACCCAAAUCGUUGGACUCACCAACUCGUGAAAUAAAAAGAAGUCUCACGCAACUUGUGUUAAUUCUGUGAGUCGCAAAGUAAAUUUUCAAAU	168	spiLA0480-miR8011a-1-5p	UUGUGUGAGGUCUCUUUUUGUUUU	40-63	stu-miR8011a-5p	2	0	24	24	1
			spiLA0480-miR8011a-1-3p	AAUAAAAAGAAGUCUCACGCAACU	107-130	stu-miR8011a-3p	2	0	24	24	1
spiLA0480-MIR6299	GAGAUUUUGGCAGGGAAGUAAUUUUAUUGUAUAAUCAUAAGUGUAUAAGACGGAGAUAUAUGUAUUUGCAUAUGUAUAUACAAUUUUCUCUCACUUUAUACAAUUAGAAACACACUUUAUACAAUUCUAUUGUAUGAAGCGAGAGAGGCGAGCGAAGAAAGCGAGCGAGAGUGGCAAGUGAAAAUAUGCGGGAGAGAGGGACUGACAAACAGUUUGCUAUGAAACACAAAAUAAAUUAAACGGUAGCUACUAUAUUUAUUUUAUAUUAUUAGUUUGUCAUUAUUUAUAUAUAAUUAUCCCUUAAUCAAAAUGAU	314	spiLA0480-miR6299-3p	AUUUUAUAUUAUUAGUUUGUCA	258-279	gma-miR6299	4	0	22	22	1
spiLA0480-MIR172a-1	AAACACUGUCUCAAAUGUAAAUCUUCAGGUCGCCAAAGUCUAUAUCCUCCAAAAAGUAGUGCAUUUUUGGAGUAGAACAACAUAGACAUUGACGACAUGAAGAUUUACAUCUGAGACAGUGCAU	124	spiLA0480-miR172a-1-3p	UUGACGACAUGAAGAUUUACA	89-109	vca-miR172a-5p	5	0	21	21	2
spiLA0480-MIR1919-3	GACGCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUCUCGCCAAGCCCCUUUCUCUAAGUCUAAUUAAUUUGAAUUCAAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUUAUGGAAGAUCGAGUUAUCAAAGGCUUA	150	spiLA0480-miR1919-3-5p	UGUCGCAGAUGACUCUCGCCA	34-54	stu-miR1919-5p	2	0	21	21	1
			spiLA0480-miR1919-3-3p	ACGAGAGUCAUCUGUGACAGG	100-120	stu-miR1919-3p	0	0	21	21	1
spiLA0480-MIR1886i	GGCGAUACGGUAUCAUGAGAUGGAAUUAGCGUUUGGACAUGCGAUUUUGUGCUGAUUCAGUCUGAUGAUUCCAUAUCAUG	80	spiLA0480-miR1886i-5p	AUGAGAUGGAAUUAGCGUUUGGAC	15-38	stu-miR1886i-5p	2	0	24	24	1
spiLA0480-MIR169r-3	UGCAGCCAAGGAUGACUUGCCGGACCAUAAAUUGCUAGGGUUUUAUAGUUUCGGCAAGUUGUUCUUGGCUAUA	73	spiLA0480-miR169r-3-5p	CAGCCAAGGAUGACUUGCCGG	3-23	csi-miR169r-5p	0	0	21	21	1
spiLA0480-MIR1088	UAUGAAAGAGGUGAAGGUGAUGACAGAAGCAUAGAGAGCACAAAUGAAUUGAGAUGCUUUUGCUGCCCAAAUUGAAUGAAAUUAGCAUAUCAUCAUUAGUGCUCUCUAUCUUCUGUCAACAAUAAUCACUCUUUCUUC	138	spiLA0480-miR1088-3p	UAGUGCUCUCUAUCUUCUGUC	97-117	smo-miR1088-3p	4	0	21	21	3
spiLA0480-MIR7991c-1	AUCAAAUUUUAGAAUAUCGACCUCCGGAAGUUGGUAUUUUUAUUUUCUAUUUUUUAGAUUUUGACCUCUGGAGGUCGGUAUUUUCAUUUCUAUUUUUUUGAUUCUGAUCUCUGGAGGUCGGUAUUUCUAUUUCUUAUUUUUUAGAUUCCGACCUCCAGAGGUCGGUAUUUCUAUUUCUUAAUUCUUUAGAUUCCGACUUUCGGAGGUCGGUAUUUUAUAUUUCCU	225	spiLA0480-miR7991c-1-5p	UGGAGGUCGGUAUUUUCAUUUCUU	69-92	stu-miR7991c	7	0	24	24	2
spiLA0480-MIR156c-3	AGAUAAUUGAAUCGAAGAGGUAAAAUAAAAGGGGCGGUGACAGAAGAGUGAGCACACAUGGUGUUUUCUAGCAUGAUGUUUUACAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCCCCCAUCGCUUUCUAUAUCUCUCUCUAGAUUUUAUUAGAG	166	spiLA0480-miR156c-3-5p	UGACAGAAGAGAGUGAGCACA	38-58	rco-miR156c	0	0	21	21	1
			spiLA0480-miR156c-3-3p	GCUCACUGCUCUAUCUGUCACC	105-126	ata-miR156c-3p	0	0	22	22	1
spiLA0480-MIR8011b	CCUUCACACAACUAACACCAGUUCUUUGAGGCUUCUUUUUAUUUUACAAGUCGGUGGACCCAGAAGUGUAAUAAUUUGGGUUCAUUAACUUGUGGGACAAAAAGAAGCCCUACAUAAUUAGUGUCAGCUGUGUGAGAC	138	spiLA0480-miR8011b-3p	CUUGUGGGACAAAAAGAAGCCC	89-110	stu-miR8011b-3p	4	0	22	22	2
spiLA0480-MIR7997c-1	UCGCUAUGUUGCUCGGAUUCUCCAAAAUGUUGUCGCACGGAUCCUUAAGAAAUGCACUACAUUUGGAGGAUUGGACACUCGCCUAUCUGCAUUCUGAAAGAGUCCGAACAGCAUAGGUU	119	spiLA0480-miR7997c-1-5p	AUGUUGCUCGGAUUCUCCAAAAUG	6-29	stu-miR7997c	5	0	24	24	1
spiLA0480-MIR10532-1	GCUCUAUACCCGAAAUUUCAGAGACACACUUAUAUUAUACUAAGGUCACUUUUUUCGGUCUACGUGACACUAGCUUGAAAAAAUG	222	spiLA0480-miR10532-1-3p	AAGUGUGUCUCUGAGAUUUCGAGC	192-215	sly-miR10532	1	0	24	24	1

spiLA0480-MIR11551b-1	UCAAAACGCGCUGAGCCCAGAAAAUAGUGUCACGUAGGCCAAAACGGGUAGAAAAUUCUUUUUAUAAAAUAAGUUAUGGAGAGUAAUAAGACCUUAGUAUAAUAUAAGUGUGUCUCUGAGAUUUCGAGCAUAGCUU	308	spiLA0480-miR11551b-1-3p	UUUUCCACCAUAAUUGUGACUG	266-287	pab-miR11551b	5	0	22	22	1
spiLA0480-MIR479-2	ACCAUUUAUUUGACAAAUUUCCAUGUCAGCGCGAGUGUGCUACACUCAUUUUAUAUUUUUAGCUGAUUGUCAAAAAAAUGCUCAAAUGGUUAUAAUUCAACUCGGUAGAGGUGUUUAAUAGGUACAUGUUAUAGUUAAGGUGUUUAAAUGAAAUAUGCGAACAACUUUAAUGGGCUGUAAAUGACUUAAGUCGUAAUGCAAAUGAUUUAAUGCAUGCAUUGAUAUGAUUAAAGACUCAAUUACCCCUCAAAAGUACUUUUACAUCUUUUCCACCAUAAUUGUGACUGAUAUUUUAGUAAAUAAAUAUU	112	spiLA0480-miR479-2-5p	CGUGAUAUUGGUUUGGCUCACU	22-43	ghr-miR479	3	0	22	22	1
			spiLA0480-miR479-2-3p	UGAGCCGAACCAAUAUCACUC	73-93	aof-miR479	0	0	21	21	1
spiLA0480-MIR5298c	AUGAUGGAGAAGAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUUCUUCAUACC	134	spiLA0480-miR5298c-5p	AGAUAGAAAUGAUAUGUAAUUGAA	43-66	mtr-miR5298c	6	0	24	24	2
spiLA0480-MIR5157b-1	GGCGCCACAUCCAUCAUUGCUCUUGCAUACAUCUCCUAGAGAAGAUAGAAAUGAUAUGUAAUUGAAGGGAUACCUGGUGCAUCCACCUAUCUUCUCUAAGAGAUGUAUGCAAGAGCAAUGAUGGAUGUGGCACA	234	spiLA0480-miR5157b-1-3p	UAAUUUUUAUUAGCUAUGAAUUCA	200-223	osa-miR5157b-5p	7	0	24	24	2
spiLA0480-MIR167h-2	UAAAUUUAUAAUGUUAUCUAAGUCAACACCAAGGGUUGUAGGCGAGAUGGAUAAUGAUGCCUUUAUGUUUAACCAGAAGUCUCGGGUUCGAAUCUCAAGAAUGAAAAUAAUUCUUGUAGGUAGUUCUGUACCUUAUUUAGACUCAAAUCCGAGAUCUCUGGUUAUGGAUAAAAGUAUUCCAUUCAUCCCGUCACAUCCUUAAUUUUUAUUAGCUAUGAAUUCAGUAUAUAUCGA	122	spiLA0480-miR167h-2-3p	AUCAUGCUGGCAGCUUCAACUGCU	84-107	gma-miR167h	1	0	24	24	1
spiLA0480-MIR2111	AAUUCGUGAUGGCAUUGACAGGUGAGGCUGCCACAUGAUCUGAUCUUUCCUCGAAUUAUAUUUGAACUAAAAGGAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGCUGCACGAUGU	76	spiLA0480-miR2111-5p	UCAUCUGAAUAUUCAGAUUUGC	3-24	atr-miR2111	6	0	22	22	1
spiLA0480-MIR1046-1	ACUCAUCUGAAUAUUCAGAUUUGCUUUAAGAUUUGAGUGCUUUGAUCUGAAUACACAUCUGAAUAUUAAGAUGUGG	179	spiLA0480-miR1046-1-3p	AGGUUAAGAAUAUGAAAUAAU	125-145	ppt-miR1046-3p	6	0	21	21	2
spiLA0480-MIR167d	UGCCUUGGAAGGUGAGAAGGCAAGUGAGAGGAUGAUUUGAAAUGAACUAAGAGCCACCUAUUUAUAGGAAUAAAUUCAUCCUAUUAAUGUCAUCCAUGACAUCACUAUGUGUCAAAAAUGCCAAGGUUAAGAAUAUGAAAUAAUUUUAUGGUUUGCCUAAAUUUCACCUACCAAGAUA	116	spiLA0480-miR167d-3p	GGAAGCUCCCAGGAAGGUGUUA	71-92	ppe-miR167d	6	0	22	22	2
spiLA0480-MIR403	ACGAGAAAGAAUUGCUUACGUGGCUAAUAUCUCUAAAUCCUACCAUUAUCGGUUCGAGUCACCGAGCAAUGGAAGCUCCCAGGAAGGUGUUAGCCACUUGAGCAACUCUUUCUUUU	112	spiLA0480-miR403-5p	CGUUUGUGCGUGAAUCUAACA	21-41	sly-miR403-5p	0	0	21	21	1
	UCAGGAAGAGGCAUAUUUCACGUUUGUGCGUGAAUCUAACAACUCUUUUCAUCAGAAAAACUGUUAUUGUUUGCUAGAUUCACGCACAAGCUCGUAAUAUGGCUUUUCCAAU		spiLA0480-miR403-3p	CUAGAUUCACGCACAAGCUCG	74-94	sly-miR403-3p	0	0	21	21	1
spiLA0480-MIR10538-1	UUAUUGUUUAAAAGUUGACGACGUUAGAUUGAUAUACAUUACUCACAGUAACGUUGUACUCACAUUUUAGUAGUAAAACGGUACUCAAAAUAACGUUUUAGGAGUAAAACGCUACUUACAGUAAUGUAUAUCAACCUAACGCUGUUCGUUUUUAAAAAAUGA	162	spiLA0480-miR10538-1-5p	AGAUUGAUAUACAUUACUCACAGU	26-49	sly-miR10538	1	0	24	24	1
spiLA0480-MIR156b-4	AAAGGGCGGUGACAGAAGAGAGUGAGCACAUAUGGUCUUUUCAAGCAUGAUGUUUACAUGCUUGAAGCUAUGCGUGCUCACUUCUCUAUCUGUCACCCCCCCCC	104	spiLA0480-miR156b-4-5p	UGACAGAAGAGAGUGAGCACA	10-30	hvu-miR156b	0	0	21	21	1
			spiLA0480-miR156b-4-3p	GCUCACUUCUCUAUCUGUCACC	76-97	bdi-miR156b-3p	1	0	22	22	1
spiLA0480-MIR6024-2	CAUGAAAAGUUGUGACAUUUAUGAAAAGUUGCAACUUUUAUGAAGAGUUGUUACUUUUAUGAAGAAUUGUGACUUUUACGAAAUGUUGUGUCCUUUCCGAAGGGUUGUAACUCUUUCAAAGAGUUGUAUCCUUAUGGAUAAGUGACAAUAAUCAUUUUCUAC	162	spiLA0480-miR6024-2-5p	UUUUAUGAAGAGUUGUUACUUU	36-57	sly-miR6024	7	0	22	22	1
spiLA0480-MIR396f-1	GGGUCUAGAGUUGUGGAGAGGUUUACGGAGAACUCUAGAACCUUCUAGAUUAAUCAAGAAGGCUAGAGAAUUCCUUAGAAUUCUCUAGAAUAACUUAGGCAUUUCAAGAAAGUCUUUGGAAGAUCUUCGAAAGUAUACACUUUUCUAGAAUA	152	spiLA0480-miR396f-1-3p	GCAUUUCAAGAAAGUCUUUGGAAG	99-122	osa-miR396f-3p	5	0	24	24	3
spiLA0480-MIR11519	UGGUAAGGUUAUAUGUAUGUUGAAGUCAAAAGCCGUAAUGGUAUACUUCAAGUAAAGGAAUGAUGGAAUUAAGGUUGAUUGACUGGAAUGACAUCAUAUCAAACCUUAGUA	111	spiLA0480-miR11519-3p	ACUUCAAGUAAAGGAAUGAUGG	45-66	pab-miR11519	6	0	22	22	2

spiLA0480-MIR1881	AUGUUUAUGUCUUUCAGUUUUGAGUUUGCAUAAGUAAACACUUAAAAUUGAACAAAUAGAUACAUUCGUCCUACGUAAUAAUUUUGUAUCCUGGUGGUGUGCUACGUGUAUUAUGUUGUGAAGGAUGCGUGUGAUUACUUGUUCAAUUUUAUACAAGUUUAAAUGUUUGAUUGUGCAUACAAAAAGUUGGAUGACGUAGAAAGG	204	spiLA0480-miR1881-5p	AAUAAUUUUGUAUCCUGGUGGUGU	77-100	osa-miR1881	5	0	24	24	1
spiLA0480-MIR399a-1	UACAAGAAUCGCAGGUUAUUCUCCUUUGGCAAGAACAACUAUGUCAUGCAUAAAUCUUUCCUUGCCAAGGGAGAAUUGCCCUACGUUUCUUCAU	94	spiLA0480-miR399a-1-3p	UGCCAAGGGAGAAUUGCCCUA	63-83	ata-miR399a-3p	2	0	21	21	1
spiLA0480-MIR159a-1	GAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAUUGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAGCUUUAUUUUACCCUUUGUUUGAUCACUUUUUGGAUUGAAGGGAGCUC	174	spiLA0480-miR159a-1-5p	GAGCUCCUUGAAGUCCAACAG	1-21	fve-miR159a-5p	1	0	21	21	1
			spiLA0480-miR159a-1-3p	UUUGGAUUGAAGGGAGCUC	156-174	cas-miR159a	0	0	19	21	1
spiLA0480-MIR319d	AGCAGAGGAGAGAAGGAAACUGUUUAGUCCAACCCAAGGUGGGGUAUUGGAACUGAUCUUUGCUGCUGAAUCAUUGGCUCAUGAGCAUGUCAAAGAAGAUGAUUGAACAUUCUGGACAUGUUCUUGCUCCAAUGAUGCAGGAGCUGAGCUCGGUUUUUCACCGCCUUUUCUUGGACUGAAGGGUUCCCUUCCCUUCUCUUUA	202	spiLA0480-miR319d-5p	AGGAAACUGUUUAGUCCAACC	14-34	sly-miR319d	0	0	21	21	1
			spiLA0480-miR319d-3p	UUGGACUGAAGGGUUCCCUU	171-190	zma-miR319d-3p	4	0	20	20	1
spiLA0480-MIR171c-2	AAUACGUGAUAUUGGCACGGCUCAAUUAAAUAACGAAGUUCUAUAUAUAAAGAAGUGCGCUUUCUAAUUGAACCGCACCAAUAUCUCGUUAG	92	spiLA0480-miR171c-2-5p	UAUUGGCACGGCUCAAUUAAA	10-30	csi-miR171c-5p	3	0	21	21	1
			spiLA0480-miR171c-2-3p	UAAUUGAACCGCACCAAUAUC	65-85	aqc-miR171c	1	0	21	21	1
spiLA0480-MIR8011a-2	AAAUUAAUUAUCAAUCCGUAACUGUCAAUUGAAUGAGGUCUCUUUUUAUUUCACAAGUAGUUAGAAACUUAAAUCUUACAAAAAGUCCACAUUACUUUGUGUCCUGUCCACUUGUGAGAUAAAAAAGAGGUUCUGACAAAUAUUGUUAGCUUGUGGCACAUGUCAUCAAGGGCGGAGUCACUUUGUAGGUAGGGGUUCAUCUGAACCUCAUUCAACGGAAAAUUAUAUUAUUUAAACA	238	spiLA0480-miR8011a-2-5p	UUGAAUGAGGUCUCUUUUUAUUUC	29-52	stu-miR8011a-5p	4	0	24	24	1
spiLA0480-MIR167c-3	CCAUAGGCCUAAAAAAGUUUUGAGAAUGUGAAGAACUAACUGAAUUCUAGUAAACUAAUGGGUGAAAGGAAACCCACUAGUGAACUCCCACAUACAUGGUGACAAAAUAUACGAAGAAAUCCUUUUAAAUUUAGGACUAAAAUUUGAAGAACACUUCUUCUUAUUCUUGAGAGGACAUGUUGAUAGUUUCCUCUUGUAUUUGGUCAAAGUAGGAUUAUUUUUCGAGAAUGAGGGAGUUGGUAGAUUCUUACUAUAUUGUUAGGCUUAGAC	271	spiLA0480-miR167c-3-3p	AGGACAUGUUGAUAGUUUCCU	172-192	aly-miR167c-3p	5	0	21	21	1
spiLA0480-MIR7997c-2	UGGAAAAUUUCUAUGUUGCUCGGACUCUUUAAAAAUGUUGAUGAGUGUGUGUUGGAUACUCCAAAAGUAGUGCAUUUUGGAGGAUACGACACGGGUGUGGUGAUAAUUUUGAGAGUUUGAGUAACGUAGGCAAAAUUUAUU	141	spiLA0480-miR7997c-2-5p	AUGUUGCUCGGACUCUUUAAAAAU	13-36	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR9477-1	CUACCUGAUCUAUCACCAUCUAUGUAUUAAAAAACACCUCGAAGAUGACAAGUCCAACUAUCAAUUGUUUCCUUUUUCAACCUGAACUAUCAUACCAUCUACUCAACUAGGUGUGUCUUAAUAUAUAGAUGGUGAUACUCCAGGUAG	147	spiLA0480-miR9477-1-3p	UAUCAAUUGUUUCCUUUUUCAACC	59-82	sly-miR9477-5p	5	0	24	24	1
spiLA0480-MIR11414	GUUGGAUCCAAGUUGGACGAGGGGAAAUAUAUUGGAGGCCUCGCAUCAACAAAAUUAGGGCCGAAUUCGGGUGGAGGCGUGUCCUGCCUUCGCUGGAUCUCGACCCUCAUAUCUUCUAUCAGCUGCAUCAGGUGUGCAAUUAAUUCAUUUUGUUCUGCCACGGUGGGCUGAGCCCCCACAACAUUUGUGAGGCUAACUUCAUCAUUGUUGUCUCCCAUGGCUGUAUUUCCUCUGUCUAAGUUUGGUCCGGG	251	spiLA0480-miR11414-3p	AACUUCAUCAUUGUUGUCUCC	195-215	pab-miR11414	6	0	21	21	1
spiLA0480-MIR5499	ACACAACCUGUGUACAAUUAAGCCGAUGCUCCGGACAUUUAAAAAUGAAGGCAGCAUGGUUAUGUGCACAGAGAUUGAAUUACUUAAUUAACUAAUUAAACUUAAAAACACCCCGAUCUUGCC	80	spiLA0480-miR5499-3p	GAAGGCAGCAUGGUUAUGUGC	47-67	osa-miR5499	6	0	21	21	1
spiLA0480-MIR8025-3	AGUUCAACUUGAGUGCAAUACACUUUUAAAUUCUUGCCAAGUUUAGGGUUGUUUUCAACAUUUCUUUCGGCGUUUUAUUAAAAGCCUCAUGUUCCUACCUGAGUAUAAGACCACUUCUUAUGUUAUGUGGCAGAUCGGGAGUGUAUCUAAGUUUAGUUAGUUAAAUAACGA	214	spiLA0480-miR8025-3-5p	UUUAAAUUCUUGCCAAGUUUAGGG	68-91	stu-miR8025-3p	6	0	24	24	1
spiLA0480-MIR6235-1	AAAUAUAAGUAUGUAGUUGAAAAUCAUAUAAUUAAAGCUGUUAAAAUGGGUCGGUCCAACUCAACCCAAUCCUAACGGGCUAGAGAGUUAAAUGGGUUGGGACGGGCUGAUCCUUUUAAUUAAAGGACCUGUAAAAUAGCAAUCCAACCAAGCCCUAAGCGGGCCACGG	288	spiLA0480-miR6235-1-3p	AACGGACAACAUUUUUCUCUUUGA	198-221	sbi-miR6235-3p	5	0	24	24	1

spiLA0480-MIR1850	GUUGGGAUGGGUUGACCCUUCAACGAAAAACGGACAACAUUUUUCUCUUUGAAAGAACACGAACGUUGAUGAAUUACACAUACUUUAGUGAAUAUUUACAAAAUAAAUACAUAAUAGCCUGAUUACUUCCGGUUCUUCCCAUAGCUUGUCAAUACUAUUUUGAUUAGUUCACAUUUAAAAUGAAUAAAGAGCCUCGAAUGCACCAAACAAUGCUGUAAGACAUGGGAAGAAACAUUAACAAAACUUGACUUCGUCCGAAUAUUGACAAGCGAUGGGAAGAAUUGGAAGUAAGUU	175	spiLA0480-miR1850-5p	UUGAUUAGUUCACAUUUAAAAU	41-62	osa-miR1850-3	7	0	22	22	2
spiLA0480-MIR8179	CUUGCAUUAGUUAUACAUGACAUGAAAAAGUGUACCAAACAAGGUACUACUAAUACACACCUAAUGCAUGCAUUAUAAUGUUUGGUAGAGUGUAUUAGAGAAACUAAUGUUUGCAUUAGCUUGAUGUAUUAGUAGUACCUUAUUUGGUACACUUUUCUAACUCAUGCAUAACUAAUGCUUG	181	spiLA0480-miR8179-3p	UGUUUGCAUUAGCUUGAUGUA	108-128	ath-miR8179	6	0	21	21	1
spiLA0480-MIR11068f	UUUGAGGUGUAGUAGUAGUUGGUUAUAUUUAUAGUGGUGGAGCAUGUGGUUUAAUUCGAUGCAAAGCUAAGAACCUUACCAGGGCUUGACAUUAUAUGUUUUCUUUGCAUUAAGUAACAAUUGAGCAAAAGUCUAGUAGAGACCGAACCAACUUUUACUGUACAUCGAUAACAAAAUUAUUAAAAAUGGGUCGGAUAACGUAUUUAAAAGGAGUUGAUUUAUGGGUUGGAUUAGGUGUUUAUGAGUCCGGAUAUCUUUUCAUUUUCAUAUAAAUGUCACGUGGUAAGGUCAAAAUGACAUAGCAAUUCCAUGUGGCAUUUUAAAAAAUGAAAAAUGAGUUGGAUAUGUCCAACAUGAAAACUAACGUCCAUAAGGGCAUAUUGGACCAAAAGUUGGACGGCGAGGGCAUGAGUGAACCAAACUUUAAAUGGAAGGUAUAUCUAGACCUUUUCGAAUAGUUUAGGAGCAUAUUUGAUCCUUUUCCC	170	spiLA0480-miR11068f-5p	CUAAGAACCUUACCAGGGCUUG	67-88	lja-miR11068f-3p	6	0	22	22	1
spiLA0480-MIR11553-1	ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAAUUCCCUACCAUAUUGCCAAAUAUUUGCCUUUAUCUUUGUGUUCAUCUAGCUAAAGACAAAUGUUUGGCAAUAUGGUAGGGGAUUCUGGUCUUCUGUACACAGGGAAAAGUUGACUUCU	316	spiLA0480-miR11553-1-3p	GAAAAAUGAGUUGGAUAUGUC	160-180	pab-miR11553	6	0	21	21	3
spiLA0480-MIR11085	CGUUGUGGCUUGUGCUUGAGUAGUAAUGGCUUGGUCCAUUUUAGAAGGAAUUACCCUCAUCUCCGCCUCCAUCAUAGGUGGAGGGUUAUCCGGGUCUUGAUCAACACUAGCAUUCUCCUCAUGUGGAGGAACUUGAUCAACAUGGGGAGGAGCUCAUGCUUUAGCAACUUUCUCCUCAAGUAUUCGAGCCACAUUC	151	spiLA0480-miR11085-5p	AGUGAACUUCAUCUUUGUAA	4-23	lja-miR11085-3p	5	0	20	20	1
spiLA0480-MIR11504-1	GCAUUAGCUGGAGUACAAGCUUCCAAAGCUGCAGAAAUGAGUUUUUUUUUUUAACUGAAAAAGAAAAACUAUUUCUGCAGCUUUGGAAUUUUUUACUCCAGCUAAGUU	196	spiLA0480-miR11504-1-3p	UCAACAUGGGGAGGAGCUCAUG	137-158	pab-miR11504	2	0	22	22	1
spiLA0480-MIR8033		108	spiLA0480-miR8033-5p	UUCCAAAGCUGCAGAAAUGAGU	21-42	stu-miR8033-5p	0	0	22	22	1
			spiLA0480-miR8033-3p	CUAUUUCUGCAGCUUUGGAAUU	69-90	stu-miR8033-3p	6	0	22	22	3
spiLA0480-MIR8051	UAUGCAAAUUCCUUCUGCCAUACUAUUGGGGCAAUGAUACCCCUGCUAUCUAAAAGCUAGAGCAUAUACACCCUCUACUUUAACAGAAGACUAAUAGGGAUACAUAACACAAUCUUAUCUGUCAUCAGAUAUUUAAUCAGUGGAUAAAAUUACGACAAUAUAUAUCCGUUAGUAUAAAGGACGUAUAUGCUUUAAUUUUUGGACGGCAUGAACAUCAAUGUUCAAAAAAUAUGACGAAAAAUAUUUGCUCA	251	spiLA0480-miR8051-5p	AAUUCCUUCUGCCAUACUAUU	7-27	stu-miR8051-3p	3	0	21	21	2
spiLA0480-MIR1518-1	AGUUGAAUUCACUUCACAGCACUCAACCACAUUAGUUCCUAUGACAUCAUAGGAACUAAUGUGAUUGAGUGCUGUGAAGUGAAUACACAA	90	spiLA0480-miR1518-1-3p	AGUGCUGUGAAGUGAAUACAC	68-88	gma-miR1518	6	0	21	21	2
spiLA0480-MIR5157b-2	UUGUGAUUUUUAUGAAAAGUUGCGACUUUUAUGAAGGGUUGCGACUUUAACGAAGAGUCAUGACUUUUAUGAGAAGUUGUGACUUUUAUGAAGAGUUGCGUCUUUUAUGAAAAGUUGUGAAUUUUAUGAUAGGGUGUGACUUUUCCGAAGGAUUGUAACUUUUCCAAAGAGUCGUGACCUUUUCAAUAAAGAACAGUG	198	spiLA0480-miR5157b-2-5p	AGAAGUUGUGACUUUUAUGAAGAG	72-95	osa-miR5157b-3p	7	0	24	24	1
spiLA0480-MIR395b-3	GAUGCCCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCACUCUGAAAUUUUAUGCAAAUUAAACCAAUAGAAGUGUUGGAGUGCUGGUUGUGGAUGAUAAACAUGAUAGUUCACGUAGAAAUCUAUCAAGGUGUUCCCUAGAGUUUCCUUGACCACUUCAUGAGGGCUUA	170	spiLA0480-miR395b-3-5p	CUGAAGUGUUUGGGGGAACUCC	10-31	sly-miR395b	0	0	22	22	1
spiLA0480-MIR395c	UUGAAGUGUUUGAGGGAACUCCUGGGUUGACAUUGAAAAUUACGCAAACAAGUAUAUAUAAAUGCAUGAUGAGUACGUAUUAGCUAGAGAUGAUGAAUACAAUAUUGAUUCACGUAUAAAACUACCUCUGGAGUUUCCUUGACCACUUUAU	151	spiLA0480-miR395c-5p	UUGAAGUGUUUGAGGGAACUC	1-21	cme-miR395c	1	0	21	21	1
spiLA0480-MIR10540-1	UGCGGGGUUGAAUUCUCAAAUGGUUACUCAACUUAUAGUUAUUAUCUCAGAAAAUCUCUUUUCGUUCUUGAUUCUGAUGCAAAGAAAGUCACUUUGUUAGAUAUAAACUAUUAGUUGAGUGACCAUCUGUGAAAUCAACUCCUGU	145	spiLA0480-miR10540-1-3p	AUAUAAACUAUUAGUUGAGUG	101-121	sly-miR10540	3	0	21	21	1

spiLA0480-MIR7997c-3	CGACUAUAUUGCUCGUACUUUUCAAAAAUGUUGUCAGACCUGUAUGUAUGUACUUUUGGACGAUCUGACACACACCUGACAGUACUUUUGAAGAGCUCGAGCAACAUAGAAA	112	spiLA0480-miR7997c-3-5p	AUAUUGCUCGUACUUUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR5017	UAUAAAUUUGCAGGUAACGGUAACAUUCUGAAAAGUUGUUACUCUUUUCGAAAAGUCGUUACUUUCCGAAAAGUCGUUACUUUCCUAACAGACACAAUUUUCUGAAAAGUUGUUAUUUUUUCCAAAAGACACAACUCUCUGGAUAAAAUGGGUCUGAACAGAUUUCACUGAACAGACACGUUCCUUGCUGAAAAUGGCUAUAAAAGGAAGUCAAUUUUCAAUUUUUCAAACCCUGAAAUUUUUU	244	spiLA0480-miR5017-5p	AGUUGUUACUCUUUUCGAAAA	34-54	ath-miR5017-5p	6	0	21	21	1
spiLA0480-MIR9477-2	AUGUUUAUCGACACACACACCUCAACUAUUAGUUGUUCUCUUUUCCUACCUGAAUGAUGGUGAUAUUCUAGGUUGGGAAAGGGAACAACUGAUAGUUGAGGUAUGUUUCGAUAAACAU	118	spiLA0480-miR9477-2-5p	UAUUAGUUGUUCUCUUUUCCUACC	27-50	sly-miR9477-5p	3	0	24	24	1
			spiLA0480-miR9477-2-3p	UUGGGAAAGGGAACAACUGAUAGU	73-96	sly-miR9477-3p	0	0	24	24	1
spiLA0480-MIR169e-2	UUUAAAAAGAUAUCUUGCAUAAAAGAAAAGAGCAUGUCAAGAUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAUUAAACACAUUUUAGACUAUGGAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUAUGACUCUCCUCUUCAUGUAAGACUUCUCUUCUUUUUC	172	spiLA0480-miR169e-2-5p	UAGCCAAGGAGACUGCCUGAA	43-63	zma-miR169e	3	0	21	21	1
			spiLA0480-miR169e-2-3p	GGCAAGUCAUCCUUGGCUACUA	107-128	mtr-miR169e-3p	6	0	22	22	1
spiLA0480-MIR2089	UCUGAUCUGUAUAGCAUGCAUUAAGGUUUGAUCGUACUUCUGCAAUAAGUAAAGAAAUGCUCAAAACCAAUAUCUUUUCUUUUUUGAGAUAAAAAAAAAAGUUAUAUUGGUUUUGAGCAUUUCUUUACCUAUUGCACAAGUACGAUCACAAUUUAGUAUGACGCUAUAAAGGUCUUC	177	spiLA0480-miR2089-3p	UUACCUAUUGCACAAGUACGAU	125-146	mtr-miR2089-5p	5	0	22	22	1
spiLA0480-MIR11078d	AAGUGCUAUUCUUAUUUUUGCUUAUCUGGAGUUACAAGUUGAGGAUCUUAUUGGUUAACGAUAGUUAUUAUCCCACUGUAAUAAAUACUUCUAACCAUGAAGAUCCUCAACUUGUCGCUUCAGAUAAGAAAAUUAGUCAUUGCAUGG	147	spiLA0480-miR11078d-5p	GGAUCUUAUUGGUUAACGAU	43-62	lja-miR11078d-3p	5	0	20	20	3
spiLA0480-MIR7984c	CUUACUUAGUGAAAAGAGUGAAAAAAAUUUCAACGUUGAUCAAAAUUGUUAUGAUACCAAAGUUUAUGGAGGAGCUUUUACCCUCCUCAACUAUUAAUAGUAUAUUUUAAAGGUAUAUAUGUGUCCACCUGGACAUAUUACUAUUUAUAGUUAUGCAAUAUUUUUUAUGUCCACGUGGGACUUUUAAAUAGUGCAUGGGUAAAAAGUCAUUUCCAACGUUUGGUAUCGUAGCAACAAAUUUUGAUUGAAGUUCGGAUAUAUUUCGGAUCUUCUUCUCAUUUAGUUAU	287	spiLA0480-miR7984c-5p	AUGAUACCAAAGUUUAUGGAGGAG	51-74	stu-miR7984c-5p	4	0	24	24	1
spiLA0480-MIR10538-2	UCGUAAAACUAACAGCAUUAGGUUGAUGUACGUUACUGUAAGUAACGUUUUACUCCUAAAACAUUAUUUUCAGUAACGUUUUAGGAGUAAAAUGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAUCAACUUUUAAAA	140	spiLA0480-miR10538-2-5p	AGGUUGAUGUACGUUACUGUAAGU	20-43	sly-miR10538	5	0	24	24	1
spiLA0480-MIR7993b	UGUGUGUUCCCAUUUGUAUGUGAGGUAGUUAAGUUAACCACAUAAAAUAUAUUGUCAUCUCCUUUAAUUCUAUGCAUUCGCCUUACCAAGUCGUAAACACCCAAGAUGUUUUCUACAAAGGUUGAUGUAUAAUUAAAGGAGACAGCAUAUUUUUAUAUAGUUAACUUAACUACAUAAUAGACAAAUGAAAACACGCU	199	spiLA0480-miR7993b-5p	UUAAGUUAACCACAUAAAAUAUAU	29-52	stu-miR7993b-5p	1	0	24	24	1
spiLA0480-MIR10540-2	CGUAUGGCUCUUGAAUUGUCGGAGUUGAUUUCUCAUAUAGUCACUUAAUUAACUGUUAUUAUCUUGUAAAAUUAUUUUUCUUUAUUGACUUUCUAAGCUAAUAACUGUUAGUUGAGUGAUCAUCUGAGAAACAACCUGAAUUGAUGGCAAUCUU	155	spiLA0480-miR10540-2-3p	CUAAUAACUGUUAGUUGAGUG	98-118	sly-miR10540	3	0	21	21	2
spiLA0480-MIR6139	AUUAACAGUAAGUACCCCAAUGACACAUCCGAUUUCAACAAGAGAAGUUUGAAGGACAUGCAUUUAGUGUAAUCCAACUAUCCCUUGCACCUAACCUUCUUUGUGAAGUGAGUAAAAGUACUGAAGAGGUGACCAAAUAACUUUGGGAAGGGAUGGAAGGACUUUACUGGGACUAAUUGGUGACAAGAAGGAUGUUGUUUCAACAACGUCUUUACACAUUUAAGAUGUAGUCGGGUACUUUGUUGCA	247	spiLA0480-miR6139-3p	AAAUAACUUUGGGAAGGGAUGGAA	135-158	pgi-miR6139	6	0	24	24	1
spiLA0480-MIR9726-1	UCCUUCUAUAAAUAGAGCAUUGUUGCUCAUUUGGUAAGAUUUACAACCAUUUUUGACUUUGCUAUAUUUACCUAUGUCAUUAGUGACAUAAGCAUGAUUUUAUCCUUCUAUAAAUAGAGCAUUCUUGCUCAUUUGUAGAACAC	143	spiLA0480-miR9726-1-3p	CAUAAGCAUGAUUUUAUCCUUC	87-108	gma-miR9726	5	0	22	22	2
spiLA0480-MIR5781	UGCACCACUAUCCUGAAUUAGAGACUGCAUGAUGCGUAGAAAAAUUUUCCUUCUUCUAAUCUUAUCGUGCCUUCUCUAAUGUCGGAUUUAUUGGUAUU	98	spiLA0480-miR5781-5p	CUGAAUUAGAGACUGCAUGAUG	13-34	gma-miR5781	6	0	22	22	1
spiLA0480-MIR5558	GAAGAUAUUUCAUGUGAUAAAUUUUAAUUCCGCACUACUUUUCAUACAUACAUGUAUGCAAUGAAUGAUGUCAAAGGGCUUGUACAAGACCUCCGUGAGGUCAAGUACGCCAUGUCGCACUCCGAGAG	326	spiLA0480-miR5558-3p	CAGAUUUAGAAUUAGUUAAGC	216-236	mtr-miR5558-3p	3	0	21	21	2

spiLA0480-MIR7992-1	UGUCAUAUCUUCUAGUGUGUGCUCUCGGGGUGUGACAUAUACACAAUGGAAUUAUCAACCUUGAUGAUACAAAUACAAUAUAUGAUACAGAUUUAGAAUUAGUUAAGCAAAUAUGAUCAGUCUUAAUGAUACAAAUACAAUAUAUGAUAUUAAUUUAAUAUUAGUUAAACAAAAAUUAUCAGUCAUAAUAAUAUCAAGGUGCCCUUUCACUUGACUUUAAAUCACAAUUAUGCUCUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACUUAUAUAAAGUUGAAAAAAUAGACACAUCUGUCCUAAUUUUUUUUUUUGUCCUACGUGGUGUCCUACAUUUAUUGUGCCAUGUAGUGCUCAUGUGUAUAUUUAUUUAAAAGUUAGAUAGUUGAAGUGUUUCUCUGUGCAUUAAUAAGGUUGGAGGUUAAGGUUAAAAUUUGAAGCCAAGUGUAGGGUAA	260	spiLA0480-miR7992-1-5p	UUUGGAUGUGCACAAAUAGACACU	44-67	stu-miR7992-5p	6	0	24	24	1
spiLA0480-MIR5773-1	GAUCCAUCCAUCUAACCCGAUCCAUUAAAAAAUAUAAUAUGAUCCAUUUUAUUUUGUCUUUAAUCCUAAAUUAAUCCCUCUCUUUAAACCUUGAAUUAGGAUUAAAGACGAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGUGUGGAUC	164	spiLA0480-miR5773-1-3p	UUUUUAAUGGGUCGGGUUAGGU	134-155	gma-miR5773	5	0	22	22	1
spiLA0480-MIR950	UCAUGCCUUGGGCCACGGUCGUUUCUAUGACAAACUUGGGUUUGGCAAGAGUCUUCGAGGGCACCAAGGCAACA	74	spiLA0480-miR950-5p	CUUGGGCCACGGUCGUUUCU	7-26	pde-miR950	5	0	20	20	3
spiLA0480-MIR8006-1	UGCGUUCCUGCCGUCCAAGAACUAGAACAUGUAUAUCCUUUAUACUAACGGACAUACAUGUCAUAUUCUUAUCCGCUGAUUCGACACUUAUUGACGAAUAAGAUUGUGUCAUCUGUCCCUAUUUAGUCUUAUGUUAUAGUGAAGGGCAUAUAUACUCUAGUUUUUGGACGACAGGGACACC	181	spiLA0480-miR8006-1-3p	UAGUUUUUGGACGACAGGGACACC	158-181	stu-miR8006-5p	1	0	24	24	1
spiLA0480-MIR1886f-1	GUCAUGCAAUACCAUAUCAUGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGGACAUGCGAUUUUACGCUGAUUCCAUCUCAUGAUUCUAUAUCAUGAGAUGUGAUUCCAUAUU	114	spiLA0480-miR1886f-1-5p	AUGGUAUCGUGAGAUGAAAUCAGC	24-47	stu-miR1886f	0	0	24	24	1
spiLA0480-MIR10532-2	UGGGGAAAAUGCACAAGUACCCCCUCAACCUAUGUCUUAAAUCAUAGAGGCACACUUAUACUAUUACCUAUUAAGUGGGGUAAUAGGACCUUAGUAUAAUAUAAAUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGGGUACUUGUGCAUCGUUCCUAU	160	spiLA0480-miR10532-2-3p	AAAUGUGUCUCUGAGAUUUCGGGC	103-126	sly-miR10532	1	0	24	24	1
spiLA0480-MIR10538-3	AACAGCAUUAGGUUGAUAUACGUUACUGUAAGUAACAUUUUACUCCUAAAACGUUACUAUGAGUAAUGUUUUAGGAGUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGACGCUAUC	119	spiLA0480-miR10538-3-5p	AGGUUGAUAUACGUUACUGUAAGU	10-33	sly-miR10538	4	0	24	24	1
spiLA0480-MIR1919-4	UAGUCCUGUCGCAGAUGACUUUCGCCCUUCUAAGGAACCACACUUUCUGUAAAUCUAAUUAAUUUGAAUUCAAUGUGGCAGGACGAGAGUCAUCUGUGACAGGAUAA	107	spiLA0480-miR1919-4-5p	UGUCGCAGAUGACUUUCGCCC	7-27	stu-miR1919-5p	0	0	21	21	1
			spiLA0480-miR1919-4-3p	ACGAGAGUCAUCUGUGACAGG	83-103	stu-miR1919-3p	0	0	21	21	1
spiLA0480-MIR10215-1	AUAAUAACCUUGAAUCAAUAAUUCAAAUUCAAGUUAGAUUGAAGAGUUAAAUUUUGAGAAUUCUUUCCAAAAUUCUAAGAAAGUCCCUUUUGACACAUUCGAGAGUUCGAGUUAGCUAUGGUGAGUCUCCUUGCUUCCAUAGGAUUUCAUUUACUUUUCAGUUUAGUCAGGAUCUCAUGGGUCGUAUCCCGACUUCCAUAUUUCUCUGUUAGAGGCUUCAUCGAUUGUUAGUAUAGUUGAGGAGUCUGUAUUAAUCUUUUAUUUUAUUAAAUGUUAUAAA	280	spiLA0480-miR10215-1-5p	UAGAUUGAAGAGUUAAAUUUU	35-55	eun-miR10215-3p	6	0	21	21	2
spiLA0480-MIR7992-2	UCCAAUCAUUACUCCAACUUUGGAGUGCACAUCCAGACACUUCAAAUCAUGUCCACUAUAUCAAUUGAACACUCAACAGUCCAACUUACAAUAUGAACGUGUAGACACCACCAAAAUUUACGUGUCACGUCAAUGUUGAGUUCCCACAAGAUCAGUGGGACUGAGUUGAGAUGUCUAGAUGUGCACUCCAAAGUUGGAGAGUAUUAUC	208	spiLA0480-miR7992-2-3p	UGUCUAGAUGUGCACUCCAAAGU	172-194	stu-miR7992-3p	2	0	23	23	1
spiLA0480-MIR2118a	AUAUUCCGUAGAAUUUAGAAACGAUUUCACUGAAUUACAUAGAACCCCUUUUCCUCAUUUCUCCAUUUCCUUAGAACGAUUUCACAAAUACAUAAGUUCUAAGGGAAAGGGGUUUUAUGUUCUUCAGUGAAGUCGUUUCUAAAUUCUAAGGGAAAGA	158	spiLA0480-miR2118a-5p	UUCCUCAUUUCUCCAUUUCCUU	51-72	ata-miR2118a-5p	5	0	22	22	1
spiLA0480-MIR7695	CCAUUUCCUUAGAACGAUUUCACAAAAUACAUAAGUUCUAAGGGAAAGGGGUUUUAUGUUCUUCAGUGAAGUCGUUUCUAAAUUCUAAGGGAAAGAGGAAAUUGGGGGAAAUUAGGGGUAAGUUUAUUAGUCUACGUGGCAUGAGUGGAACUCUAUUGGCUUAUGUGGCAUGUCAUGUGACAUUCACAUGGCAUUUAAGUGAUAUUUAACCGAUUCUGUUAAUAAAAAGAGUAUUUUUGACCCUAUAGUUUAAGGAAAAAG	261	spiLA0480-miR7695-3p	GGCUUAUGUGGCAUGUCAUGUGAC	158-181	osa-miR7695-5p	6	0	24	24	2
spiLA0480-MIR6198	GUUUACAAAGGAAAUGCCUCUGGACCAACCAGAGUAAAGAGUUCUAUUUAGAAGUCUUUACCUUGGUUGGUCAUGAUGCAUUUCCCUAGUAAAC	94	spiLA0480-miR6198-3p	UCUUUACCUUGGUUGGUCAUGA	55-76	hvu-miR6198	7	0	22	22	2
spiLA0480-MIR1134-1	UUGAAACUUUAUGCACAAAAAUUGCAGCUUCCUCUCCGGUUUGAUCAACAACUAGAAGCAAAAGAAGGUUGUCGAAUUUCCACCA	173	spiLA0480-miR1134-1-5p	GAUCAACAACUAGAAGCAAAAGAA	43-66	tae-miR1134	6	0	24	24	2

spiLA0480-MIR6027	AAAAAAAAUAGCCUUCCUUUGCUUCUAGAAAUUCAGAGUGUUGAUCAAACCCGAGAGGAAUCUGCAGUUUUUGUGCAUAAAGUUUCAAGUAAUUUUACAUGAUUAUGGGUAGCACAAGGAUUAAUGUGAAACAGAAAAGUGAUAUGCAAAGAAGAUGGAGAUUCAAUUGUUUAUUGUUACGAAGAAAACACUUUUGUGUUUCUCGUGAAUCCUUCGGCUAUCCAUAAUCAUGUUGAAUGUG	153	spiLA0480-miR6027-5p	AUGGGUAGCACAAGGAUUAAUG	17-38	sly-miR6027-5p	0	0	22	22	1
			spiLA0480-miR6027-3p	UGAAUCCUUCGGCUAUCCAUAA	118-139	stu-miR6027	0	0	22	22	1
spiLA0480-MIR11605	UGAAUAGUUUAGGGGGCAUAUUUGACAUUUUUUCCUUUAAAGAAUUAUCAAUGUAUUAAAAAGGGUCAAGACAAGUACCCCCAGACUAUGAU	92	spiLA0480-miR11605-5p	UUUAGGGGGCAUAUUUGACAU	8-28	pla-miR11605	6	0	21	21	1
spiLA0480-MIR7986	ACAGCAUUAGGUUGAUAUACGUCACUGUAAGUAACGUUUUACUUUUAAAACGUUAUUUUCAGUAACGUUUUAAAACGUUACUGUGAGUAACGUUUAAGGAGUAAAACGUUACUGUAAGUAACGUAUAUCAAUCUGACGCCAA	142	spiLA0480-miR7986-3p	GUUUUAAAACGUUACUGUGAGUAA	67-90	stu-miR7986	4	0	24	24	3
spiLA0480-MIR6149b	UUAUAGCCUUUGUAUGUCAAAGCUUCGAUACGCACCUGAAUCGACAAAUACAUAUAUUAUCAGACUUUUUAAGAAUAUCACGCGUUUAUUAUUUUUAUAAGUCUGAAUAACAUAAAUCAUAUAUAACAUAUAUGUCGAUUCGGGUUCGUAUGAAAACUAUGGCAUACCUCAAAGGGUAACG	182	spiLA0480-miR6149b-5p	UCGAUACGCACCUGAAUCGAC	25-45	nta-miR6149b	2	0	21	21	1
spiLA0480-MIR8678	ACACCGUUUCAUAUUUAUACUCUUCAACUUUGAGUGUAUACAAGUAGACACUUAAACUUGUAUAAAAUUGCACAAGUACACAUGAGUCCAAUGUGACAUAAUACAAGUAGGACACAAAUUGUCAUGUAGAAUGUCACGUAGGACAUGUAUGUAUUUGUUCAACUUUAUACAAGUUUAUAUGUUUAUUGUGCACGCCCAAAAUUAAAGAGCAUAUAUGUGAAAUGGGAC	228	spiLA0480-miR8678-3p	CAUGUAGAAUGUCACGUAGGA	123-143	gra-miR8678	4	0	21	21	2
spiLA0480-MIR396a-1	UGGCACUACAAGAAAACUGUGAAUUACAUGGGAUUUUCCUAAGAUUAGUAUGAAAAUACGUAGGAAACUUAUUUUCCUGCAAAAAUUCAUCCUGAUUUUCAGGAAAAUCUCAAUGUAAUUCAUACUUUUCUUGUAGUGUGG	141	spiLA0480-miR396a-1-5p	CUACAAGAAAACUGUGAAUUA	6-26	csi-miR396a-3p	6	0	21	21	2
spiLA0480-MIR1128-1	UAUUACUCCCUCCGUCCCAAUUUAUAUGAGUUAGUUUGACUUGUCAUGGAGUGUAUGAAAGAAGAAAAGACUUUUGAAACUUGUGGUCUAAAAUAAGUCCUAUAUAUUUGUAAGGCUAGAGCCUAGAAAUAAUUUCAUUAAGGGUAACAUGAACAUUUUAAAGUUAAAUCGUUAUUAAUUAUAGAAAUAUGUCAUUCUUUUUGGGACUGAGUAAAAAGGAAAGUAAGUCAUAUAAAGUGGGACAGAGGGAGUAGUU	256	spiLA0480-miR1128-1-5p	UAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1
spiLA0480-MIR172e	UAAAAAAAUAAGGUAUAUCGCUGCCAGGGAAGCGAUUUAAAAUAAAAAAUAAAAAAUUUAUAAAACGCUGCCCAGGCAGCGACUUUAUGAAAAUUUUUUUUUUUUAUAAAAUAAAUCGCUGCCAAGGCAGCGAUUUAUAGAAUUUUUUUUUUCUAAACGCUGCCCAGGCAGCGACAUUAUGAUUUUUCUU	189	spiLA0480-miR172e-3p	GCAGCGACAUUAUGAUUUUU	167-186	aly-miR172e-5p	6	0	20	20	1
spiLA0480-MIR166-5	ACGGUUGGGGAGAAUGUUGUCUGGUUCGAAAUCUUUCUAUAGAAAAAUCAGUGGCGGAUUCAGUCAUGGAUUUCAAAAUCGUUAAAUCUUAUAUAUGUACAAAAACAAGUACAAUAUAUAUUUUUAGACCCUAAAAAUGUUGAAUAUAUAUUCUGAAUCCGUCAUAGAUUAGAUCGUUUGAUCAAUCAAAUUAUUGAGUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCU	232	spiLA0480-miR166-5-3p	AUUUCGGACCAGGCUUCAUUCCCC	201-224	lja-miR166-3p	0	0	24	24	1
spiLA0480-MIR396f-2	UGACCAAGUCCUAGUCAUGCUUUUCCACAGCUUUCUUGAACUUCUUCUUGCUAAAUUUUGAUCUCUAAAUUGAUAAUUUUGAGAUGAGAUUUGAAGCUAUGAAAGUCCAAGAAAGCUGUGGGAAAAGAUGGCAAGCUUUGGACU	144	spiLA0480-miR396f-2-5p	UUCCACAGCUUUCUUGAACUU	23-43	csi-miR396f-5p	0	0	21	21	1
			spiLA0480-miR396f-2-3p	AAAGUCCAAGAAAGCUGUGGGAAA	102-125	osa-miR396f-3p	6	0	24	24	1
spiLA0480-MIR5049b	UGUCAAAUCAUAAAUAGACAAGUAAUUAGGGACAGAAGGAGUACUAUCUAUCAUGAACACACAUAUAUUUAUUUUUUUAAAAAAAAUUGUGUAUGUGUGUGGUGGUGGUGGUGAUAGGGUGGGGGUGGUGGUUAAAAAUGUGGGAAGUCGUAAUUCGUAUCCUCACCUACAAAAAAUUUAGAUAGUCAACCAACUGAGCUAGCUAAUGAGAUCCGAAAAUAAUUUUCUAUAUAUUUUUUGCUU	243	spiLA0480-miR5049b-5p	AGUAAUUAGGGACAGAAGGAG	21-41	hvu-miR5049b	3	0	21	21	1
spiLA0480-MIR827-2	CUAGCCUGACCAGUGAGGACUUGCUAUUUUACUUUCUAGAUGGCCUUCAAAACUGGGCCAAGCAAGAUCUUCAAAGACGUCAAGUUCACGACGUGGAUGAGGCGAU	106	spiLA0480-miR827-2-5p	CUUUCUAGAUGGCCUUCAAAAC	32-53	eun-miR827-5p	5	0	22	22	1
spiLA0480-MIR166-6	UAAACUAAACAAGAUCAUGUUAAGGAGAAUGUUGUCUGGUUCGUGACCAUAUAUCUUUCUUCACAUAAAUGAUCUCGGACCAGG	118	spiLA0480-miR166-6-3p	AUCUCGGACCAGGCUUCAUUCCCC	72-95	lja-miR166-3p	1	0	24	24	1

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spiLA0480-MIR8121	UUUCACUUUACCCGCUCAAAAGGCGUGCCUAAACGACAGGUGACAAGUCAGUCAGGUGUGUUUGAUAGGUACACUUGUUGAGUGGUUUAAGUGUUC	96	spiLA0480-miR8121-3p	UAGGUACACUUGUUGAGUGGUUUA	66-89	ath-miR8121	7	0	24	24	2
spiLA0480-MIR10215-2	AAUUAGUAACGUAAUAGAAAUAACAUUGUAAUAAUCAAAAAGUAAAAUAGAGAUGUGAAUCAUAGUUCUCCAAAUUGGAGAACUACUAUCCACCUCUUUAUAAUUGCAGAAUAGAGAGUUAAAUAGAGAGUGGUCUAUUUUACUUUCCAAAUAUAGAGAAUGGAGAGUAAAAUAGAGAUGGAUUGGAGAUGGUCUAAGGGGUACGAGAGCCACUCAUACUAUGUCACUUACUCAUAACUCAUGCCCAAGAGCUCGUCACAUAGCUACAGUUUCUAUAAUGAUAGAUGAAGCUUUGGGUACUUACAUUAUUUUUCUUGUUACUAGGC	326	spiLA0480-miR10215-2-3p	GAGAAUGGAGAGUAAAAUAGA	156-176	eun-miR10215-3p	4	0	21	21	1
spiLA0480-MIR1072	UUGGGUGGUCGUCUUAUGUAGCACCUUUAUAUCCUGCAGGUUUCUGAUCUUCACAUUGUCAUAUUUGAAUCUUACUCCCCAGCAGUCCCGAAAUCUGUGUUAGGGAGUAUGAUUCAAAUCUGACAACGUGAACAGCUGAAACCCUACAGGGUACAACAGGUGCUUCAUAAGACGAUGACCUGU	183	spiLA0480-miR1072-5p	CACAUUGUCAUAUUUGAAUCUUAC	52-75	ppt-miR1072	7	0	24	24	3
spiLA0480-MIR1863	CGUCAAAGUCAAUACCCUUUCUUUGACCGAAUUUCUUAUUAAGGUCAGUAGUCGAUUGCAACAAAGGUGUGCCCAAUUUGCUGCAAAUCUUGCCAAAAAGAUUUUCUUCCUUUAAAGAUGGGAUUUGGACCCCAUAACUUGAAGCUCAGGUACAAAGUUAGAUUGGUUGUUAAGCUAUUUGGCCGAAGGAAGGGUAUUGACUUUGAAG	208	spiLA0480-miR1863-3p	AGCUCAGGUACAAAGUUAGAUU	143-164	pab-miR1863	3	0	22	22	1
spiLA0480-MIR7696d-1	UUUUGAUGGUUUAAGGCUUUCAAGUUUCGUUGUGUGCAUCGUCUCCUAAAGGUCCAUUUUAUGUUUUAAUUGGGUUGAUUUAUAGCCAGUGAAUUAUGAAUUGUGACUUCCAAGGAAGGAGCUUUUUUUAUUCUAAUACCAUACAAGUCAAUGGUAGAGGUUCUCUCUUUUUGAAUUAUGAGUACUUGAAACUCAAAUAGCUUCCAACGGAAUUUGGAAAACUAUUUAUAACAUCAUUC	240	spiLA0480-miR7696d-1-3p	UUUUGAAUUAUGAGUACUUGA	170-190	mtr-miR7696d-3p	1	0	21	21	1
spiLA0480-MIR11499b	CUUAGUAUGUGAUGCACCUACUUUGUCCUUUUGGUUGGCCAAUAAGUCAAAGUUUGUUAUGCACCUACAUGGUCUUUUGAGUUGGUCAAUAAGUCAAAGUAGGUGAUGCAACUACUUGU	119	spiLA0480-miR11499b-3p	CAAUAAGUCAAAGUAGGUGAUG	87-108	pab-miR11499b	6	0	22	22	3
spiLA0480-MIR160-1	GGUAACUUUAUAUGACGAGAUGGUUACAUAUUUCAACAUCAUAUACACGAUAUCGGAAUAUGCUUGGCUCCUCAUACGCCAUUCAACAAGGCCCAUCGAUAUAUUACGGUGAGCUUUGCAAAUGGCAUACAGGGAGCCAGGCAUAUACGUGUACACGACUUGUAUCAGUACAUAUAUACACACUCAUAUGUAUAUAUAAAAUUUUU	206	spiLA0480-miR160-1-5p	UGCUUGGCUCCUCAUACGCCA	61-81	dpr-miR160	4	0	21	21	1
			spiLA0480-miR160-1-3p	UGGCAUACAGGGAGCCAGGCA	123-143	aau-miR160	0	0	21	21	1
spiLA0480-MIR5083-1	UCACAAGGAUAUCAAAAAUUAUUGCAAUUCUCUGAUCAAGCAACGUGGAGAAAAACUAAUCUGUUGGAUGGAUGUUGUAUCCACGUUGCUUGAUAAGUUUUUUCUCCACGUUGCUUGAUCAGAGAAUUGCAGUAAUUGUUGAUAUCCUUGUGA	153	spiLA0480-miR5083-1-5p	UUAUUGCAAUUCUCUGAUCA	19-38	osa-miR5083	5	0	20	20	3
spiLA0480-MIR7987-1	CACAAGUACCAACACUAGCUGAUGCUAUUGAUGACAAAAAUUGGUUUUCUUGCAAGAUCAAUUUGUGUCAAUCUAGUGUUGAUACUUAGUUUUGAUUUAAGGAUAAAUGUUUGUUGAUUGUAAGGACCAACACUAGUUGAUCUUAUUGAUGACAAAAAUUAAUGUUCUUGCAAGAUCGAGCAAGAUCGAGUUGUGUCCAUCUAGUGUUGAUACUUAGC	208	spiLA0480-miR7987-1-3p	ACACUAGUUGAUCUUAUUGAUGAC	130-153	stu-miR7987	0	0	24	24	1
spiLA0480-MIR7987-2	AAGAUCAAUUUGUGUCAAUCUAGUGUUGAUACUUAGUUUUAGUUUAGGAAUAAAUGUUUGUUGAUUGUAAGGACCAACACUAGUUGAUCUUAUUGAUGACAAAAAUUAAUGUUCUUGCAAGAUCGAGUUGUGUCCAUCUAGUGUUGAUACUUAGCUUUAAUUUAGUAAUAAUGGUGUUUGUUAGGCAUAAGUACCAACACUAGUUGAUCCUAUUGAUGAA	220	spiLA0480-miR7987-2-5p	ACACUAGUUGAUCUUAUUGAUGAC	77-100	stu-miR7987	0	0	24	24	1
spiLA0480-MIR11514-1	UGCCCCUACCGUCAAAAUGAAGUUAUUUUUAUCCCUACCGUUACUAAUUUCAUCAUUUAUACAUUUCCCAUUUCAAACCCAAUGUUAAAAUGAUGAAAUUAGUAACGGUAGGGGUAAAAAUAACUUCGUUUUAACAGUAGGGAGA	145	spiLA0480-miR11514-1-5p	GCCCCUACCGUCAAAAUGAAG	2-22	pab-miR11514	6	0	21	21	2
spiLA0480-MIR7710	CAGUCCUAGAGUUUAAAUUAAAGAUGUUGGUGUCAACUCAUAAAAUUUGGGAUUAAAUCUAUCCUAUAUUUGGUUGAGGGUAUUCCCUAAUACCAUGAUAAAUCCUGGAUAACCUGACUUUGACACCUUAACUCCAUACUCCUUCAUAACCCACAAACUUAAUUUAAAAUUUGACAUCAACAUCUUUAAUUUAAACGCUAGGAGCG	206	spiLA0480-miR7710-5p	AAUUAAAGAUGUUGGUGUCAACUC	16-39	bdi-miR7710-5p	7	0	24	24	2
spiLA0480-MIR5379	AAAGAAAAGAGAGAAUAUGAAAAGUGAGGGAACUACUUUGGAAGGAAAAUUAAAAGUCAUUUGCAAAGUGCAAAUGAAAGUCAUUUCUUAUAAAUUCUUAUAAAUUUGCAGGUAACGGUAACAUUCUGAAAAGUUGUUA	158	spiLA0480-miR5379-3p	AUGAAAGUCAUUUCUUAUAAAUUU	74-97	gma-miR5379	7	0	24	24	1

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spiLA0480-MIR9746i-1	UACCCUUUAACUUGGCUUCGAAUCACAUUUAUGCCCUUCAACUUUGAGUGUGCAUAAAUAGACACUUAAACUUGUAGAAAGUUGAACAAAUAGACACACAUGUCCUAUAUGUCAUUUUUUGUCCUACGUGUAUUUUGUCAUGUAGGACUCACGUGUUUAAUUAUUUAAAAGGUGGAUAGUUAAAGUGUUUGUUUGUCCAUUAUGAAAGUUGGAGGUCAUAGUUAAAGUAUUUGUUUGUGCAUAAUGAAAGUUGGAGGUCAAAGUUAAAAUUUGAGUCAAGUUUAGGAUC	284	spiLA0480-miR9746i-1-3p	AAAGUGUUUGUUUGUCCAUUAUGA	182-205	gma-miR9746i	7	0	24	24	1
spiLA0480-MIR818e	CAAGAGCAUAUAUACCUUUAUAUUAACGGAAUCUUAUUCAUCGACUCAACAUCGAAUCAAUAGAUAAGAUUGUGUCACGUGUCCCUAUUUAAUCUUCCGUUAGUGUGAAGGGGCAUAUACGCUCUAGGGCAGACUGACGAGGGCAAGUAAAACAUGACUGACAGACUUCUAAACAGACAAAUUUUUGAAACAGAAGUGCAUAUGAUAUAUCAGACGAAUCUCAUAUCUCCAUGAGGGAGGAAAGUGAAUUUAUUAUGCACACUUCUGUUUCAGAAGCUUGUCAAUUUAGAAGUCUG	128	spiLA0480-miR818e-5p	UAUCCUUUAUAUUAACGGAAUC	13-34	osa-miR818e	7	0	22	22	2
spiLA0480-MIR2083	UCAAUCCUGCUUGACCUGCCCUCAUCAGUCUAGA	203	spiLA0480-miR2083-5p	AGACUGACGAGGGCAAGUAAA	4-24	ppt-miR2083-3p	4	0	21	21	1
spiLA0480-MIR10532-3	ACUUAAACUAUGACUGAAAUUUCAAAGAUACACUUUAACGAAUUAAAUUCCUAUUACCCCCCUAAGCUUACUUUUUUUUUUUUUGCAUUUUCAUACACCUUUUUCGCUUAUGUGGCAUCAAAAAAUAUCUUCAACGUGCCACAAUUGUAUGGAGUCAUGAAGUCUGCUACGUUAAAAAAAAAAGAGGUAAUAGGACCUUAGUUUAUGAAGGUGUGUCUCUGAGAUUUCGGUCAUAGUCUAGGG	273	spiLA0480-miR10532-3-3p	AGGUGUGUCUCUGAGAUUUCGGUC	239-262	sly-miR10532	2	0	24	24	1
spiLA0480-MIR10532-4	GACUGAAAUUUCAAAGAUACACUUUAACGAAUUAAAUUCCUAUUACCCCCCUAAGCUUACUUUUUUUUUUUUUGCAUUUUCAUACACCUUUUUCGCUUAUGUGGCAUCAAAAAAUAUCUUCAACGUGCCACAAUUGUAUGGAGUCAUGAAGUCUGCUACGUUAAAAAAAAAAGAUGUACGAAAUUACAAAAAAAUAAAAGUUCAAGGGUAAUAGGACCUUAGUUUAUGAAGGUGUGUCUCUGAGAUUUCGGUCAUAGUCUAGGGAUACUUGUAUCUUAUCCCAAAUAUAUCCUCUAAACUAUUAAAUGUACUUAUAUUCUCAAUC	323	spiLA0480-miR10532-4-3p	AGGUGUGUCUCUGAGAUUUCGGUC	228-251	sly-miR10532	2	0	24	24	1
spiLA0480-MIR7486c	CCACCCUCCUACAAUUUUUAGUAGAGUAUGUUAAACGUAUAUAUGUGUCCACGUGGAUAUGAAAAGUCCACGUGGGCACAUAUAUAUCUUUAAAAUACAGUUUUAAAUAGUUCCGAGGGCAU	122	spiLA0480-miR7486c-3p	UGUGUCCACGUGGAUAUGAAAAGU	44-67	gra-miR7486c	7	0	24	24	1
spiLA0480-MIR8001a-1	GUGCACUACAAGAAAACUAUGAAUUAUAUGGGCAUUUUUCUGGGGAUUAGUAUGAAAAUUCGCAGAAAACUUAUAUUCCUGCAAAUUUUCAUACUAAUUCCUCGAAAAAUCCCCAUGUAAUUCACAGUUUUCUUGUAGUGGGA	143	spiLA0480-miR8001a-1-5p	UUCUGGGGAUUAGUAUGAAAAUUC	38-61	stu-miR8001a	1	0	24	24	1
spiLA0480-MIR8013	ACACAGCAGCAAUUUUUGUGUUUUUUAAAAAAAUUAACAAGUCAAUUUUGUCAGAAGAAAAUCGCUCCGUCAGAAGCGAUUUAGCCCUUUUGAUUAAAAAAAUAAUUAUAGCAGCUAUUUCCUUUUUCCUUAAAUAGAGGCAGGCAUUUUGGUCCUAACAUUUGGUCUGCCCAGCAACAUUUGUUAAUUUUUUUUUUUUGACAAAAUCGCUGCUGGAA	218	spiLA0480-miR8013-5p	AGAAGAAAAUCGCUCCGUCAGAAG	53-76	stu-miR8013	0	0	24	24	1
spiLA0480-MIR1127b	AACAUUUCAGUUGAUCUUGAUCCCAUUUACUCCCUCUCCCUUUGCCGGACAAUAGUUGUCCACUAUUGACUUGGUACAGGGAUUAAGAAGCAGUAAAUGAUAGGGGUAAUUUUACCAAAUCACCCUUAUUAAAAGUAAGUCACAUAAACAUCGAAAAAUAAAUAGUAUUUAAUAGCAAGGUAAAAACGACACAACAUGCUAAAUGACUCAUUGAUUUAAUAAGCUGGACAAGUAUUGUUGGACGUCUCAAAAUAGUAUAGUGGACAAGUAAAGAUGGACAGAGGGAGAGGGAGUAGCUUAGACUCAUAGCAGCAAAGAAAUUAU	324	spiLA0480-miR1127b-3p	ACAAGUAUUGUUGGACGUCUC	228-248	tae-miR1127b-3p	6	0	21	21	1
spiLA0480-MIR8714	CAACAAGUGAUAUCACAUUCGACGAGAUGAACAUAGAGGUAACUGAGUUACAAUAUAUGACUUGCUUUACUAUGUUUAUCAUGUCAAGGUAACUUGAAA	99	spiLA0480-miR8714-5p	UUCGACGAGAUGAACAUAGAG	18-38	gra-miR8714	5	0	21	21	2
spiLA0480-MIR5628-1	CUGGAGAAAUAUGGAAGAGAUGAUCGGAGAAAUAUUAUGUUCUAAUGAGCUAAUGCCACAAGAAAAGUAAUGAUGUCUAUAACUUUAAAGCUCUGAAGUAAUAUCUCUCCAGUCACCUCAUCCCUAUUUCUCGAA	135	spiLA0480-miR5628-1-5p	GAAAUAUGGAAGAGAUGAUCG	6-26	ath-miR5628	5	0	21	21	1
spiLA0480-MIR5628-2	UGAAGUAAUAUCUCUCCAGUCACCUCAUCCCUAUUUCUCGAAUAGGUUGCUAAUUCAAGCAUUAGAGAAAUAUGGAAGAGGUGAUUGGAGAAAUAUUUCUAGG	103	spiLA0480-miR5628-2-3p	GAAAUAUGGAAGAGGUGAUUG	67-87	ath-miR5628	5	0	21	21	1
spiLA0480-MIR172a-2	AUGAAGAAUUAGGUGAAUAUGCUGAGGAGAUGGAGUUGAUAAAUGUUCCUUUGACUCUGGUAUAAGCGACAAAGAAACACUGCCAUCCUCAAUCUUCUCAUCAUAAGCAUCUUUUUUUUAAA	122	spiLA0480-miR172a-2-3p	CUGCCAUCCUCAAUCUUCUCA	80-100	cas-miR172a-5p	6	0	21	21	2

spiLA0480-MIR397b-3	AAUUAUCUUACUUAAUUAUUUUUUAUAGUUUAUUUGGCAACCUUAUUCGGAAGAUGUUAUUAUUGGAUUGUCUGAGUGGUGUCGGUUAGGACAACAUGUCUGGAUGACACAGGUGCCACUUAUUUAUGAAAUUUAUCGUGAGUGGCACAUGGUUAAUCGUGUUGUGAGACAGUUUGGUUAUUUACAACAUAUUCUUAGACCGUGUACCCAAUUUUUCGAAUAUCAUUUUAAACGUGAUAAACGAGCCAAAAUAAAACAAGAAGAUAUAG	269	spiLA0480-miR397b-3-3p	CUUAGACCGUGUACCCAAUUU	194-214	bdi-miR397b-3p	5	0	21	21	1
spiLA0480-MIR156g	GUGUCAAUAACAGCUGUGAAGGAAUAUCUGGGCCCAAAGAUGUAUUGACAUAGCUUUCUCUUUUUUUGUGUCAGUACAUCUUUGGGCCCAGACAUAUUCCUUCAUAGCUGUCAUGAUUA	119	spiLA0480-miR156g-3p	GCUUUCUCUUUUUUUGUGUCA	53-73	aly-miR156g-3p	5	0	21	21	1
spiLA0480-MIR1128-2	AAUUACUCCCUCCGUCCCAAUUUAAGUGUUUUAGUUCGAUUGGACACAAAGUUUAAGAAAUAAAGGGAGACUUUGAAUCUUGUGGUCUUCAAUUAAAGAUGUGUGUAGUCCUUUAAAUCUUGUGGUCUCAAAACUUUCCAUGUAUAAUGUUGGAAUUGGAGAACUUAUUAAAUAUUGAAAGAGGCAGUCUUGCUGGGACAGACUAAAUGGGAAGACACUUAAAUUGGGAUGGAGGGAGUAGUA	243	spiLA0480-miR1128-2-5p	AAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	3	0	21	21	2
spiLA0480-MIR2622-1	UUUUCCAGAAGUUCAGGAUGAAGCACGUUCCACAUGUAGAACAAAUUUAUCUACACGUUGAAUGUGCUUCAUCCUGAACUUUGGACCU	88	spiLA0480-miR2622-1-3p	AAUGUGCUUCAUCCUGAACUUU	61-82	mtr-miR2622	7	0	22	22	3
spiLA0480-MIR7998-1	AUUGUAGGUCCAGUCACGGUCCAUCAGUGGGUAGACCUAGAUUUCUCAUCUAGGAUGUUUGAGUAUGUGUCGAACUACCGAGGCUAGUGACGGACCGUAGAUCAAUCCACGGUCCAUACUGCAAGUUUAACAAUGAUCACUUAGAGUUAAAUUUCAAAGUCUGGAUGAAAAUUCUAAGUGUGGACCCACAGAGGACCCAUGGAACAUGGAUCGACCCA	219	spiLA0480-miR7998-1-3p	ACGGACCGUAGAUCAAUCCACGGU	90-113	stu-miR7998	1	0	24	24	1
spiLA0480-MIR10448	UUAUAUCUUUUUUAGACUUAGUUAAUGAAUACACAAACAAGUUAGGCUUUGUGGGUGUGCAAGAACUAAUUGUUCUUGCUCCAAGCGAAUUUUUUUUUUUUGAAAUAAUAGGUGAUGAGGGGGUUAGGACCUUAGCAUCUUUUGUAUCUAGUGAGUAUAAUCAAUUCACUUGUUUGCUACGGAUUAAUGUGACUUGUCUGUUAAAGUAACU	211	spiLA0480-miR10448-5p	UUAGGCUUUGUGGGUGUGCAAG	42-63	gma-miR10448	7	0	22	22	1
spiLA0480-MIR9679-1	GACUUAUAAAACCCUCUAAAUCUCAUGGUCUUGUACUGCAUUUUAUGUUAAUAAAGCUGCAGAACAAGAAAGAGGUGUUCCCAGGUUUGUAAUAAAUU	98	spiLA0480-miR9679-1-3p	CAGAACAAGAAAGAGGUGUUC	60-80	tae-miR9679-5p	5	0	21	21	1
spiLA0480-MIR7531	CAUCCUAAAUUAUUCGCUCUAUUUAUUCUUUACAUUUUUCUUUUUCAUUCUCCAUUCAACUUUCUUUUUGGAGAGGCACCAACAACGGAGAAUGAGAAAAAAAUGUAAGUGAUGCAUCAGACUUAGAAAAUCUUAGGCCA	140	spiLA0480-miR7531-5p	AUUUUUCUUUUUCAUUCUCCA	34-54	lja-miR7531	6	0	21	21	3
spiLA0480-MIR5035	UUUACCAAAUGCCUAGAUAAGCCAAAAAAUUGCUUAUAAGCUAGUUUGACCAGCUUAUAAGCUUAGAGGGUGUUUGACUAAGCUUAUAAGCUGGUCAAAUUGGCUUAUUAACACUUUUUAGCUUAUCUACUCAUUUGGUAAA	142	spiLA0480-miR5035-3p	CUUAUUAACACUUUUUAGCUUA	104-125	gma-miR5035-5p	5	0	22	22	1
spiLA0480-MIR7983-1	UCCCUAAAGCCUUUAGCGACAUUGGUUUAAUGACAGUUAACUAAUGCCGGUAAAGACUUUAGCAC	66	spiLA0480-miR7983-1-5p	UAAAGCCUUUAGCGACAUUGGUUU	5-28	stu-miR7983-5p	2	0	24	24	1
			spiLA0480-miR7983-1-3p	ACUAAUGCCGGUAAAGACUUUAGC	41-64	stu-miR7983-3p	1	0	24	24	1
spiLA0480-MIR1106-1	AAUCCCCAUGCACUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGCCCACGUGGACACACUACUAUUUAUAAUUAUGAAAUAUUUAUGAUGUCCACGUGGACACAUAUAUACCUUCAAAAGACACACUAUUAAGUAGUGUGUGUGGGGUG	151	spiLA0480-miR1106-1-5p	UUUAAAGGUAUAUAUGUGCCC	29-49	smo-miR1106	6	0	21	21	1
spiLA0480-MIR8564-1	CGACUGAGAAUUGCAAAGGUAAAGUGAAAGCGACUAAUGCUAAGGAGGAAGUUUUGCACAUAACCUUAGCAUUACUGUUGGUUUCAUAUUUUCCUUUCUUUCUUAGGUA	109	spiLA0480-miR8564-1-3p	UACUGUUGGUUUCAUAUUUUCCUU	73-96	atr-miR8564	7	0	24	24	3
spiLA0480-MIR395a-1	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUUUGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAU	107	spiLA0480-miR395a-1-3p	UGAAGUGUUUGGGGGAACUCU	70-90	aof-miR395a	0	0	21	21	1
spiLA0480-MIR1106-2	UUACCCCAGCAUUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGCGCAUGUGGACAUCAAAGAUAUUGCAUAAUUAUGAAUAGUAAUGUGUCCACGUGGACACAUAUAUACCUUUAAAAUACAGUUUUAAAUAGUUCAGGGGGUG	146	spiLA0480-miR1106-2-5p	UUUAAAGGUAUAUAUGUGCGC	28-48	smo-miR1106	5	0	21	21	1
spiLA0480-MIR2864	CAUUGCACCUAUGGACGUGUUCGAUAUCAUUUUAGGGCUGGAGUUUUGGUACGAGGUUAACGCGUUUAUUUCACCGCGUCACAACCAGAUGCACAUCAGCGACACCGGAGGUUCAUGCGUGGUACCCCUUAUUCAGGUACCACAAAACGGGAUGCACUUAUCGGUGAUGCAAAUUGUUAAGGUUUUUAAGAGAGGUGAACCAACCUUUCUUGCUGCCCUUGUUGCUUUUCUGAGGCAGUUCCAUUUUCUCAUUGCAUUGAGCACGUCCUUAGUGACAAUA	280	spiLA0480-miR2864-3p	UCUUGCUGCCCUUGUUGCUUU	208-228	osa-miR2864-1	6	0	21	21	1

spiLA0480-MIR11546e	UAAAAUGGAUGAUUUAGCUAUGGAUUGAAGUAGUGAGAAUGGAUUGGUGGUACACUGCCCUAUUCUCCUUAUUUUAUCUAAUGUAAAUCUUGAAUUACG	99	spiLA0480-miR11546e-5p	AGCUAUGGAUUGAAGUAGUGAG	16-37	pab-miR11546e	7	0	22	22	2
spiLA0480-MIR8038b	UAUUUUUCAAGUCAAAACAGUUUCUCCUUGUGAGUAAGUUGAAUCUCGUGCUCGUUAAACCGCAAGAGACGUAGAAUGCGUCCCAACAUGAGAUUCAACUUACUCACUUGGAAAAAUUGUUUUUGCUUGAGAAGCA	136	spiLA0480-miR8038b-5p	CCUUGUGAGUAAGUUGAAUCUC	26-47	stu-miR8038b-5p	0	0	22	22	1
			spiLA0480-miR8038b-3p	AUUCAACUUACUCACUUGGAA	93-113	stu-miR8038b-3p	3	0	21	21	2
spiLA0480-MIR9726-2	AUAAGGAGUGUCCAUAAAUAACUCUUUUCAAAAAGUAGAACUAGUGAAAUUCGAACACACAAGCACUACCUCAUCCUAAGGAGGUAAAACCACUGGAGUACAGUAGCUUGUUGUGUUAAGGGUGUUAAAAAUAUGUUAUUUAAUUAUUUUGUGUAUUAUAUUACUUGUAUACACAAUAUUUUUUUCUGACGAAGGGUAUUCAAUUGGACACCCUAAC	217	spiLA0480-miR9726-2-3p	UAUACACAAUAUUUUUUUCUGA	168-189	gma-miR9726	5	0	22	22	1
spiLA0480-MIR6140b	UAUCUCUCUCUCUCUCUCUCCCUCGCUUUAUACAAACAUAAAAUAUGCAAUGUAUUUUGUAUAAUUUGUAUUUGUAUAAAGCGAGAAAGAAAGAACGGAAAAGAGAACUGGGCAAGGGUAUAUUUGUAUUGUAUAAUUACGAGUAUAUAAGACGAAGAUAUAUGUAUUUGCAUGUGUCUAUACAAUUUUUUCUCGUUUUAUACAAAUAAAGCCGCAAUUUAUACUGAUUGUAUAAAGUGAGAGAGGCGAGCGACAGAGGGA	261	spiLA0480-miR6140b-5p	AAUGUAUUUUGUAUAAUUUGUAUU	49-72	pgi-miR6140b	6	0	24	24	1
spiLA0480-MIR6108c	AGGUCUGAAUCUGAAUCAUUCAGAUUCAGCCCAAUAAGUACGUUUGAUUUUUAGGUCUGAAUGUGAAUCAUUCAGAUUCAGCCCAUUAAGUUAAUUUGUUUUAAUUUUUAGAAAACCUCUUAAUGGGUCUGAAGAGAUCUGAACGAAUAAGAUCUGUAGGA	161	spiLA0480-miR6108c-3p	AUGGGUCUGAAGAGAUCUGAACG	123-145	cca-miR6108c	5	0	23	23	1
spiLA0480-MIR11032	UGGUGGCUGCCGAAAAGCAGCAAGAGAAGGCUGCAACGCAAAUCGAAAGUUCUGCCGGGGAGCAACGAGGGCAGAAUAGCGGGACAGACAAGGGCAAGAACGUUGUUGUUGGCAUGUUCAAUCACAUGGCGUUGAUCAACCAUAUUUCUAUUGCUGCUUUGGCUGCCAAAC	171	spiLA0480-miR11032-3p	GAACGUUGUUGUUGGCAUGUUC	98-119	seu-miR11032	7	0	22	22	3
spiLA0480-MIR167b-3	GCUAUCAAAUUAAAAACAGAUGCCUAAUCUGAACUCAUCUACCCCAAAUAAAGCAAGCAGUUUUACUAGGUCCUAGUAAAGCUGCUUGCUUUAUUUGGGGUAGAUGAGCUCAGGUUGGUGUUUUUAUUUGAUUCU	135	spiLA0480-miR167b-3-3p	UAAAGCUGCUUGCUUUAUUUGG	77-98	sly-miR167b-5p	5	0	22	22	1
spiLA0480-MIR395a-2	AUGCCCUAUUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAUGAAUCCUGGCUGUGGAUGAUGAACAUAAUAGUUCACGUAUAAAUCUAUUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUU	163	spiLA0480-miR395a-2-5p	UGAAGUGUUUGGGGGAACUCU	10-30	aof-miR395a	0	0	21	21	1
spiLA0480-MIR395b-4	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCGCUUCAUUAGGGCUUACUUCAUUGUUUGAUGCCCUGUUGAAGUGUAUGGGGGAACUCUUGGACUCACUUUGAAAU	107	spiLA0480-miR395b-4-3p	UUGAAGUGUAUGGGGGAACUC	69-89	aof-miR395b	1	0	21	21	2
spiLA0480-MIR1128-3	GGCUAAUAAUGUACUACUCCCUCCGUCCCAUUUUAUGUGGCACCAUUUCCUUUUUGGUCAGUCCCAAAAAGAAUGUCACAUUUUCUUAUAUGGUAAGUAUUUAAAGGUACAAUUCCUCUUUUACCCUUGUUGGUCCCACUUAAGUACUCUAAUACAUUUAUGAGGAGAGAGAAAGGCGAGUUUACUUUUUUGAAGGGCAAUUUGGUAAACAUUUCAAAGUCUUCAUUAUUUCUUAAACUCCGUGCCGGGUCAAAUGUUGCCACAUAAAAUGGGACAGAGGGAGUAUUAUUUUAUCUAUUA	300	spiLA0480-miR1128-3-5p	UACUACUCCCUCCGUCCCAUU	12-32	ssp-miR1128	2	0	21	21	1
spiLA0480-MIR482b-3	UUCUGCUUAAGUUGGUGUCUUAACUUGUAAUUCACUUCUAUCGUGGAUCGCUUCUGCUUUUGAAGUACCAUAGAAGUGAAUUGCAAGGUAAGACACCAACUUAAGCAGAA	110	spiLA0480-miR482b-3-3p	GAAGUGAAUUGCAAGGUAAGA	73-93	stu-miR482b-5p	5	0	21	21	1
spiLA0480-MIR7992-3	AACCUUAACUUGGACUCAAUUGACAGCUAGCCAACCUAACUCUGAAAAUGCACAUCUAGACCCCUUAACUUGAUCUAACUUUCCCCCUUUAAGACCUCAACUUUGAGAAUGCACAUCUAGAAUUCACAAUUUGAGAAUGCACAUCCGGAAAAGUGUAUUUAGGGGGCCAACUUACACCAGGUUAAGAUGUCUAGAUGUGUCUUUUCAAAGUUGGGGUGUCCAAUUGUCAGUUGAGACCAAGUUAAGAUG	249	spiLA0480-miR7992-3-5p	UUUGAGAAUGCACAUCUAGAAUUC	102-125	stu-miR7992-5p	5	0	24	24	1
			spiLA0480-miR7992-3-3p	UGUCUAGAUGUGUCUUUUCAAAGU	188-211	stu-miR7992-3p	2	1	24	23	1
spiLA0480-MIR6273	UAAUUUUCUACCCCUUUUGGUCUAUGUGGCAUUAUCUUGUGGGCCCAACGCUGUUUGACUUUUUUUUUCAAACUAGUGUCACGUAGGCAGAAAAGGGGUAGAAAAUUA	108	spiLA0480-miR6273-3p	AACGCUGUUUGACUUUUUUUU	47-67	ppe-miR6273	5	0	21	21	1
spiLA0480-MIR5565d	AAAUUCCCGAGGUUGUCAUUUCUCUUGUAUUCAUGUGUGUGUGUGUGUAUAUAUAUAUACACACACACACGUGAAUACAAGAGAAAU	102	spiLA0480-miR5565d-5p	UCUUGUAUUCAUGUGUGUGUGU	23-46	sbi-miR5565d	7	0	24	24	2

	GACAACCUCGUGAAUUU										
spiLA0480-MIR814c	AUUUUUUGUAGCUCAUCGAGCAUCUAGGGUGGCAAGUUGUACUAUGAACUGCUCAUAUCUUGAUAUACCUUUUAAGCACCUCCAUACCUUUUCAGAAUAAGCAGUUCAUAGUACAACUUGCCACCCUAGAUGCUAGAUGAGCUACAAAAUCA	152	spiLA0480-miR814c-3p	CAGUUCAUAGUACAACUUGCCA	102-123	osa-miR814c	6	0	22	22	1
spiLA0480-MIR7992-4	CUGGCAAGUAAGCGCUCCAACUUUGUGUAUGCACAUCUAGACGCCAAGUUGAGGUGUCUAGAUGUGCACUCUCAAAGUUGGAGUGCGUACUUGCUAG	97	spiLA0480-miR7992-4-5p	UUUGUGUAUGCACAUCUAGACGCC	22-45	stu-miR7992-5p	5	0	24	24	1
			spiLA0480-miR7992-4-3p	UGUCUAGAUGUGCACUCUCAAAG	55-77	stu-miR7992-3p	6	0	23	23	1
spiLA0480-MIR7711-1	AAUAUAGAAAUCGCUGCCUCAGCAACGAUUUAUAAAUUAUUAUUUUUUUAAUAAAUCGCUGCCCUGGUAAGGUUAUCCUUGCUGCUGACGAGUCUACUGGUACAAUUGGCAAGCAUCUAUCCAGCAUUAAUGUUGAGAAUGUCGAGUCAAACAGGAGGACUCUUCGAGAGUUGCUCUUCUGCGCACCUGGUGCUCUUCAGUACCUUAGUGAAAUCAUCUUGUUCGAGGAAACCCUUUAUCAGAAGACAACAACUGGUACGUUUAUAUGAAUUCUAAUGUCUAAUUUUUUUUUAAAAAAAAUUGCUGUCUCAGCAGCGAUUUCUAUAUU	329	spiLA0480-miR7711-1-3p	ACCUUAGUGAAAUCAUCUUGUUCG	203-226	bdi-miR7711-5p-3	7	0	24	24	2
spiLA0480-MIR7997c-4	UACUAUGUUGUUCGGACUCUUCAAAAAUGUUGCUGCGCCCAUGUCAGAUCCUCCAAAAAAUGUACUAAUUUUUGAGGAUCCAAUGUGCACUCGGUGCCUUCUUUGAAGAGUUCGAGCAACAUAAUU	126	spiLA0480-miR7997c-4-5p	AUGUUGUUCGGACUCUUCAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR1888b-1	CUAGGCCCAUUGGGCCGGCCUGGCCUAACCCGGGAUUUAAUAGGGUUGGGCUAAGAUUUUUGGAGCCCAUUUAAGGAAAAGGCUUUUUAGCCCGACCUAAUUAAGUCUGUUGAUUUAAGGGGCUUGAGAAAUAUAGGUAUGGCCGGCCCGUGGGCCAAU	159	spiLA0480-miR1888b-1-5p	UUGGGCUAAGAUUUUUGGAGC	46-66	ath-miR1888b	4	0	21	21	1
spiLA0480-MIR6112	AAAUUUAUUUAAUAAAACUUUGGUUCUUCGGUGCACCGUAGUUUCGGGACUCUUGCACCAAACUUCGAACCGAAGUUUCAAAAAUAAAAAA	91	spiLA0480-miR6112-3p	GAAGUUUCAAAAAUAAAAAA	72-91	cca-miR6112	3	0	20	24	1
spiLA0480-MIR8781a-1	UUUAACUUGGGUUCGAAUUACAUUUACGCCCUUCAACUUUAGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAAUUGAACAAAUAAACAUGUGUCCUACAUGUCAUUUUUUGUCCUACAUGAUGUCUUACGUGUAUUGUGCCAUGUAGGACUCAUGUAUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUGUUUGUGCAUUAUGAAAGUUGGAGGUCAAAGUUAAAAUUUGAAAUCAAGUUUAG	247	spiLA0480-miR8781a-1-3p	UAUUUAUUUAUUUAAAAGUUGGAU	159-182	gra-miR8781a	5	0	24	24	1
spiLA0480-MIR166f-2	UUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAAAAUCUC	107	spiLA0480-miR166f-2-5p	GGAAUGUUGUUUGGCUCGAGG	13-33	cas-miR166f-5p	0	0	21	21	1
			spiLA0480-miR166f-2-3p	UCGGACCAGGCUUCAUUCCCCU	77-98	cas-miR166f-3p	0	0	22	22	1
spiLA0480-MIR7992-5	UUUAUACAAAUUUAAGUGUCUACCAACUUUGGAAAUGCACAAGUAGACACUUAAACAUGUAUAAAGUUGAAUAAGUAGACGCAUGAGUCCUAUGUGACAAAAUACACGUAGGACAAAAAAAUGAUAUGUAGGACAUGUGUGUUUAUUUGUUCAACUUUAUACAACUAUAAGUGAGCAAAUCCAAAGUUGAAAAACAUAAAUGUGAUUUGACAAAAAAAGAAAAAAAGGAUACGUGUGAGGAGGAUCAAAUAUACCCACUAUAUGGAUUUUUAUUUUUUCACGUCCGUUAGAGGAAAAAGGUAUAUAUGAGCCAUUUGUAUAAUAGUUGGGGUAUAUAUGAACCACUUUCAUAACGAGAGAUAUAUCAACUCUAAAUGACAAAGUGGAGGGGAAUGUUAGGCCCUUUUCCCUAUUAAUUAUACUUAAUAAAAUAUUUCAGUUCGAUUGAUUCGGUUGUAUUGCCUCCUCCCCGUACUUUUCUUGGUUUUCAC	209	spiLA0480-miR7992-5-5p	UUUGGAAAUGCACAAGUAGACACU	28-51	stu-miR7992-5p	4	0	24	24	1
spiLA0480-MIR7722	UGAAUUAAUAUUAUGUUGCUUGGACUCUUCAAAAAUGCUGAUGGCUGAGAAUUGGAUCCUUCGAAAAUAGUGCAGUUUUCGAGG	281	spiLA0480-miR7722-3p	CCUCCUCCCCGUACUUUUCUU	252-272	bdi-miR7722-5p	4	0	21	21	2
spiLA0480-MIR7997c-5	AUCUGAUACGGGUGCAGCAGCAUUUUCGAAGAGUCAAAGCAACAUAGAAUUAAUGUA	141	spiLA0480-miR7997c-5-5p	AUGUUGCUUGGACUCUUCAAAAAU	13-36	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR393b	CUUUAAGAGCUCGUUUGGUUGGGAACAAGUUAUCCCAGGACAAGUUAUCCUGAGGUUAGUUAUCUUGGAAUAGCUUAUCACAUACACUAUGAUAUAAAUGGUGGGAUAAGCUAUCCCAAACAUGGCAACCAAACAAGAUAUAAAAACCGUAUCCCAUCAUUAUUUUUCUAUCCCAUUACUAUUUAUUUUUAUCCCUCACACCAAACGACCUCUUAUUA	218	spiLA0480-miR393b-5p	GUUGGGAACAAGUUAUCCCAG	18-38	gma-miR393b	6	0	21	21	2
spiLA0480-MIR11078e	UGAUCCACCCACCUAACCCGACCCAUUUAAAAAAUAUGAUAUGACCCAUUUUAUUUUCUCUUUAAUCCUAAGUUAUUCCCUCCUUAAACCUUGAAUUAUGAUUAAAGACAAAAUAAAAUGGUUCAUAUCAUAUUUUUUAAAUGGGUCGGGUUAGGUAGGUGGAUCA	166	spiLA0480-miR11078e-3p	AAACCUUGAAUUAUGAUUAA	86-105	lja-miR11078e-3p	6	0	20	20	2

spiLA0480-MIR7990b	GAGUUGUGACUUUUAUGAAGAGUUACGACUUUUAUAAAGAGUUGCGACUUCUAUGAAAAGUUGUGACUUUUAUGAAAAGUUGCGAUUUUAAUGAAGAGUUGUAACUUUUAUGAAAAAAUUGUUACUUUUAUGAAAGAUUGUGACUUUUUCGAAGUGUUGCAACUUUUCCAAGUAGUUUUGACCUUUAAUAAGGGUUGCAACUUUUCAAAUAGUUGUAACCUUUCCGAUAAGGCACAAUAU	240	spiLA0480-miR7990b-3p	AACUUUUCAAAUAGUUGUAACCUU	199-222	stu-miR7990b	6	0	24	24	2
spiLA0480-MIR395g-1	CUAUCAAGGUGUUCCCUAAAGUUCCCUUGACCUCUUCAUUAGGGUUUAGUUCAUUGUUUGAUGUCUUGCUGAAGUGUUUGGGGGAACUUUUGGACUCACAUUGAAAU	107	spiLA0480-miR395g-1-5p	GUUCCCUUGACCUCUUCAUUA	21-41	mdm-miR395g-5p	2	0	21	21	1
			spiLA0480-miR395g-1-3p	UGAAGUGUUUGGGGGAACUUU	70-90	gma-miR395g	0	0	21	21	1
spiLA0480-MIR1886h-2	GCCAUGAGAUACCGUAUCGUGGCCUUUGGCCAUGAGAUAUCAUAUCACGAUAUGAAAUCGUGAGAUUGAAUUCGUGUUUGGACAUAUAAUUUUACGUUGAUUUCAUCUCAUGAUUUUAUAUAAUGAGAUGUGAUUUCGUAUUCUCCAAAAAUCAUGAUAUGGGAAUUUCAUAUC	174	spiLA0480-miR1886h-2-3p	AUUUUACGUUGAUUUCAUCUCAUG	89-112	stu-miR1886h	0	0	24	24	1
spiLA0480-MIR1128-4	UACUACUCCCUCCGUCCCAAAAUAAGUGUCACUUUAGCAAUAAUCAUACUCACUAAGAAAAAUAAUAAAUAGAAAGGUAUAGUUCACCAAGUUACCCCUAUUUAUUAGUUGUUUCUUGACAAUUGAGCAUGAUUGAUAAGUAGUUCUUUAGUACAAAGGUAUACUUGGAAAAACAUACUAAUUUCUGUCUUAAGUUCCUAUGGUGACACUUAUUUUGGAAAAAAAUUUAUUGCUAAAGUGACACUUAUUUUGGGACGGAUGGAGUAUUU	269	spiLA0480-miR1128-4-5p	UACUACUCCCUCCGUCCCAAA	1-21	ssp-miR1128	0	0	21	21	1
spiLA0480-MIR8011a-3	GACACUAGUCAAGUGAGACUCAUUUUUGCCUCACAAAAAAUUAAGCCCAUUUGAGUCUACUUUUAUGUGAGACAAAAAGAAGCCUCACACAACUAGUAUU	100	spiLA0480-miR8011a-3-3p	GACAAAAAGAAGCCUCACACAAC U	71-94	stu-miR8011a-3p	2	0	24	24	2
spiLA0480-MIR11068c	UAUUCUAAUUCAUGGAUUAGUUAUACCUCAUACAAAAUCUUAUUUUAUUCCUAGAAAAGGGUGGGAUAACUAAUCCAAGGUUUAACAAUCCUUGGAUUAGACCC	104	spiLA0480-miR11068c-3p	AUAACUAAUCCAAGGUUUA	66-84	lja-miR11068c-5p	5	0	19	19	1
spiLA0480-MIR7539	AUUCUCUCUCUCUCUCUCUCGCUUUACACAAACCUAAAUUAUACAUUGUAUUUUGUAUAAUUUGUGUUUGUAUAAAACGAGAAAGAGAGAAAGACAAAAGAGAACUGGGAAGGGGUAAUGUUUGUAUUGUAUAAUUAUAAGGAUAUCGGACGAAAAUAUAUGUAUUUGCAUGUUUGUAAUAAUUUUCUCUCGCUUUAUACAAACAGAAACACAAUUUAUAAAUUUCUGAUUGUAUAAAGCGAGAGAGACAGCGACAAAGGGA	264	spiLA0480-miR7539-3p	GCGAGAGAGACAGCGACAAAG	241-261	lja-miR7539	4	0	21	21	2
spiLA0480-MIR167e	UGGACCUUCAAUCGUACGCUUAAUCUUCAUCCUCUUACAGCCUUACCUGGGAAUGACUAAUGAGCAAUUUAGAUUUGUUAUUAUCAGGAGCUACUUGGAUUGCAUGGUUCGUCAAGAAAAAAGCUUUCAUAAUAUGGUCGGGAGUUGAAACUUUUAUAGUACAAAUCCAAUGAUGUUACAACAUUCCUUGCAAGGGUUAUUUGUUAAUGAGAGUGAUGAUACAUUCAAAGAACUUAACCAUCUUUUGAUAAUAACAAAUUCAAAUCUCUUAGUGAACCAUCCUCAGACCAUGCUGCUUAGGGGAAGAAGUUAAGAAUACUGAUGAAGGUUGA	333	spiLA0480-miR167e-5p	CUUCAUCCUCUUACAGCCUUACC	25-47	csi-miR167e-3p	6	0	23	23	3
spiLA0480-MIR8014-1	UUUUACUCCCUCUGUCCAACAAUUCUUGUUCACUAUUGAAUAUAAUAAAUAUAAUGUGUUGAAAAAUGUCACAGAGAAAUGAUUAUAAGUAGGUAAAUUAGAAAAGAAGUGUAAAAUAAUCCACUGAUUUCAUAAAGUGGACAAGUAUUGUUGGACAUCCCAAAUUAGUAUAGUGGACAACUAUUGUUGGACAAAGGGAGUAGUU	205	spiLA0480-miR8014-1-5p	AUAAAUAUAAUGUGUUGAAAAAU G	45-68	stu-miR8014-3p	6	0	24	24	1
spiLA0480-MIR390a	AUGGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGCUCG	106	spiLA0480-miR390a-5p	AAGCUCAGGAGGGAUAGCACC	20-40	sly-miR390a-5p	0	0	21	21	1
			spiLA0480-miR390a-3p	CGCUAUCCAUCCUGAGUUUUA	69-89	sly-miR390a-3p	0	0	21	21	1
spiLA0480-MIR7992-6	AGUAAGCACUCAAACUUUGAGAGUGCACAUCUAGAUACCUCAACUUGGUCAUAACCGACUACUAAACAAUCCACGACCACUCGUCUCCACUUUGUCUCAUGCACACUAGACUCUGACAUGACACAUAAAUUUUGGAGGUGUCUAGAUGAUCAUUUUGUAAGUUGAAGUGUUCUGUCUAGAUAUACAUUCUCAAAGUUGGAGUGCUUGAG	209	spiLA0480-miR7992-6-5p	UUUGAGAGUGCACAUCUAGAUAC C	16-39	stu-miR7992-5p	4	0	24	24	1
			spiLA0480-miR7992-6-3p	UGUCUAGAUGAUCAUUUUGUAAG	139-161	stu-miR7992-3p	7	0	23	23	1
spiLA0480-MIR2607-1	UCUGUUUUAGAAAACAUUAUACAUGUCAUUAUUUGUUAACUGAAAACAGUUCUAACUUUGCAAAAUUGUUUAUACGCGGUCAGUUAUGAUUGGGGCACGUCAUUAAUUAAAUUAUUUUUUAAAAAGUGAAAAAUGUUCAAAUAUGCCAACGAACUUAUAGAAUAGGCUCAUCUAUGCUAUCCGUUAAGAGUUUUCCUCAUCCGUGUCAUUUUAG	254	spiLA0480-miR2607-1-5p	AUGUCAUUAUUUGUUAACUGA	23-43	mtr-miR2607	5	0	21	21	1

	UUAGGAAAUGCUGACAUGGAUAAGUCUUUUCUCAAACAAA										
spiLA0480-MIR11578	GCAUGAACACGAUAUGAGUUGAAGCCUUUAACUAUAUCAUUGUUUAGGCUGCUUCUGUUGAAGUUGAUAAGUUGUUUCUGGAUUUGGAACCACAAGUGAUCAUUGUUGUAAUUCAACUUUAAUUCAUAUUUUAUUCAACU	140	spiLA0480-miR11578-5p	UUUAGGCUGCUUCUGUUGAAG	43-63	pab-miR11578	5	0	21	21	1
spiLA0480-MIR8042	UACCUAUAUAGUAUGUUAAACCACCAGAUAAGCACUUCCAUCUAAUUUCUAAAAGGUGGUCAAGGGAACGAGGUGGUGAAACACAUGUAACUUGACACAACUUUCAGAAAUUAGACUGAAAUGCUGAUCUGGUUUCUUAUAUACAUUAUACAUAGUUU	158	spiLA0480-miR8042-3p	AUUAGACUGAAAUGCUGAUCU	110-130	stu-miR8042	1	0	21	21	1
spiLA0480-MIR408-2	AAAAGGAAGGAUUGUGGGGAGAGGAGAGCCAGGGAAGAGGCAGUGCAUGGAAUAGGCAAAGCAAAAAUUGCACAUCUCAUGCUCUGGCUCGUCCCCGUCUAUCCAUACCACACCAAUUUUUACCUCAA	128	spiLA0480-miR408-2-5p	GAGAGCCAGGGAAGAGGCAGU	24-44	bra-miR408-5p	1	0	21	21	1
			spiLA0480-miR408-2-3p	AUGCUCUGGCUCGUCCCCGUC	79-99	cas-miR408	5	0	21	21	1
spiLA0480-MIR7983-2	UAAUAAAUAGCAAAUCACAUUACAACAAAAAUAACUUUUAGCGUCAUUAAAUAUUGACACUAAUAAAGAGUGCUAAAGUCUUUACCGACAUUAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUACAAAGAGUAACAACUGCCGCUAAAAAUACAUAUUUAGCGGCAAUUAAGAAUUAAAUGUCGCUAAUGGUCAUUUUUGUUGUAGUGUCAUGGUAUGUAAUC	240	spiLA0480-miR7983-2-5p	UAAAGUCUUUACCGACAUUAGUUA	74-97	stu-miR7983-5p	3	0	24	24	1
			spiLA0480-miR7983-2-3p	ACCAAUGUCGCUAAAGGCUUUAGA	110-133	stu-miR7983-3p	6	0	24	24	1
spiLA0480-MIR12162	UGAUGAAGAGAUUUCUUUUGAAAAUGUAUUUUUGGAUGACUGAGUCAGUCUCCAAGUGGGAGAACUGUUAGGUAGUGGAGCCUGAUUAAUUUUAGGUUUUCCUAUUUAUUCUCUAUUUUAGGCUUUCCUAUUUAUUCUCUAUUUUAGGUUUUCCUAUUUAUUAUCUGUAACCAAAAAUACUCUGAUUUAUUAAUAUAAAUAUACCUCACCG	211	spiLA0480-miR12162-3p	AAUACUCUGAUUUAUUAAUAU	176-196	aof-miR12162	5	0	21	21	3
spiLA0480-MIR399a-2	AGCAAGAAUCGCAGGUUAUUCUUCUCUGGCAAGAAAACUAUGGUUAUGCAUAAAUUAUUUCUUGCCAAGGGAGAAUUGCCCUACGUUUCUUUAU	94	spiLA0480-miR399a-2-3p	UGCCAAGGGAGAAUUGCCCUA	63-83	ata-miR399a-3p	2	0	21	21	1
spiLA0480-MIR399a-3	ACUACUCAAAAGAAUUUGAAGAAUUGGAGAGGACAAGAAACGCAGGGUAUUCUCCCUUAGCAAGAUUGCUUUAUGCAUGAAUUAAAUUCUUUCUUGCCAAGGGAGAAUUGCCCUGCGUUUCUUCAUUUCCACAAAAGUCUAAUUCAUCUGGUGUC	155	spiLA0480-miR399a-3-3p	UGCCAAGGGAGAAUUGCCCUG	95-115	ata-miR399a-3p	1	0	21	21	1
spiLA0480-MIR399i-4	CUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCCUCUGCUUAAUUAU	107	spiLA0480-miR399i-4-3p	UGCCAAAGGAGAGUUGCCCUA	66-86	stu-miR399i-3p	0	0	21	21	1
spiLA0480-MIR156t	GGGAUUAUUUGUCUUCCUAGUCUUUGACACAAGAAAGGGGUGUAGAAAAAUCCUUUUUUCUUGUGUCGAAACAAAAGAGUAAUGAUUCU	89	spiLA0480-miR156t-5p	UUGACACAAGAAAGGGGUGUA	24-44	gma-miR156t	6	0	21	21	1
spiLA0480-MIR2669b	UCUUCUCUUCAUCCGACAAUGAUGAUGCAAGUGAUGCAGGGCCUGAUGGGUGAAUAAUGGAUUUCUACCAAAGUUCUAGGAAUUUCAUCAGUUCAGUCAUCAUGGAAGCCCUACAUCACUACCAUCAACAAUGUUAGAUGGUGAGACAA	149	spiLA0480-miR2669b-3p	UCAGUUCAGUCAUCAUGGAAGC	88-109	mtr-miR2669b	6	0	22	22	3
spiLA0480-MIR10528-2	UUUUAAGUUCCAAGUGAUUAAAGAAAUAUUAGGCAAGGAUGUUAAUUCCAAAUGUGGUAUUAAGUAUGAUUUGGCUAACGUAACUGCCAUUAACUUUAAGUUAGAGAUUAAUUAGUGGCUGAUUAGGAUUAAAUUAAUCUAGUGGGCCCCACCACUCAAGGCAAAUUAAAAGGAAUCAGAUUAGGAGCUGGCCUUAGUGGGACACGUGUAGAGGGGGGUUGCCUCCACUUCAUAUUAUAAAUGGGUGGUGAAAUGCAUUGCAACAUACCAUCUUCUUUACCACUUGGCUUAGGC	294	spiLA0480-miR10528-2-3p	AAUGCAUUGCAACAUACCAUC	252-272	sly-miR10528	4	0	21	21	1
spiLA0480-MIR8001b-1	GGGAAUUACAUGGGGAUUAGUAUGAAAUUUGCAGGAAAAUAAUUUUUUGCGGAUUUUCAUACUAAUUCCUAGGAAAAUUUCU	82	spiLA0480-miR8001b-1-5p	AUGGGGAUUAGUAUGAAAUUUGCA	10-33	stu-miR8001b-5p	4	0	24	24	1
			spiLA0480-miR8001b-1-3p	GGAUUUUCAUACUAAUUCCUAGGA	51-74	stu-miR8001b-3p	1	0	24	24	1
spiLA0480-MIR11891	AUGUUAGUACUUUAGUUCAUAUAUGCCCUUACCGUCAAAUACUUGGUCUAAAUACUAUGCGCAAUUGAGCAGAAUAAGGGCGUAUUUGGAUCAAGUAUUUGAUGCUAAGGGCUUAAGUAAAUUGAAGUAUAAACG	135	spiLA0480-miR11891-3p	AGUAAAUUGAAGUAUAAACG	116-135	mes-miR11891	5	0	20	20	3
spiLA0480-MIR7997c-6	AUUCUAUGUUGCUCGGACUCUUAAAAGAUGUCGAUGAGUGUGAGUCCAAUCCUCCAAAAAUAUUAAAUUAUAAGAUCUGACAUGUGUGACAAUAUUUUCGGGAAGUUUGAGCAACAUAGUCU	124	spiLA0480-miR7997c-6-5p	AUGUUGCUCGGACUCUUAAAAGAU	6-29	stu-miR7997c	3	0	24	24	1
spiLA0480-MIR6155	UUAAGCGACUCAUGAUGUAUCAACAAGGUUGCUUUGCUGGUGGGACCGUUAUCCGACUGGCAAAGGACUUAGCUGAGAACAACAAGGGUGCUCGA	95	spiLA0480-miR6155-5p	CAAGGUUGCUUUGCUGGUGGG	24-44	nta-miR6155	6	0	21	21	2

spiLA0480-MIR12168	AGGCAUUCAAUCAAUUAGUGACAUCCAAAAAAUAAAGGAAUGUAGUGGGAUGGUAAGUAUUGUACUCAACCUUAAUUAAAAGUUUGGGGUUCAAAUAUUGGAUUGAUGUCA	111	spiLA0480-miR12168-3p	UUCAAAUAUUGGAUUGAUGUCA	90-111	aof-miR12168	6	0	22	22	1
spiLA0480-MIR7992-7	UCUUUUAUUCCAUUCCAAUUUGGGUAUGCACAAGUAGACUCUUAAACUUGAACAAGUAGACACAUGAGUCUUACGUGGUACGAUACAUAUAGUUAUCACAUAGGAUAAAAAAUGACAUGUGGGAGGUCAUGUUAUACAUGUAUGUCUAUUUUUUAAGCUUUUAUACAAGUUUAAUAGUCUACUUGUGCACACGCAAAGUUUAAGGGCAUAAACGU	215	spiLA0480-miR7992-7-5p	UUUGGGUAUGCACAAGUAGACUCU	19-42	stu-miR7992-5p	6	0	24	24	1
spiLA0480-MIR8706b-1	UUUGGUCUUGCCUCAAUGCUCAUGAAUUCUAGUGUAGUUUUAUAUGGGCUAUUGAAUGAUGUAAUAAUUGUAUUGAAUUGAUGUGUAGGCCAUCUUAUAUUGAUAAGUUUAUAUUGAAUUGACCUAGAUUCAUUGAGUAUUAUGAUUUUUGUAUUGAAUUGAUGAUCAUGACCAUGGGUAAGAGCCUUU	189	spiLA0480-miR8706b-1-3p	GAUUUUUGUAUUGAAUUGAUGAUC	144-167	gra-miR8706b	7	0	24	24	3
spiLA0480-MIR6483	UUUAUCCAUGUGUCAAUUAAUCAAUGGAGGGUCACCCAACUAUUGUUGGUUGGACCUCUCCCAUUGUAAAUUUUUUCAUGAGAUGCA	87	spiLA0480-miR6483-3p	CAUUGUAAAUUUUUUCAUGAGA	62-83	hbr-miR6483	7	0	22	22	2
spiLA0480-MIR2868-1	GAAAUAAUGCAUGCAUUAGCUUUGUGUAUUAGUAGUACCUUGUUUGGUACACUUUUUGAACCUAUGUAUAGCUAAUGAUUGCAUUAGUUAUACAUUCUAUUGUGUAUUGAGUGUAUUUUCCUACGAAUACAUGGAAAUUCAUGGUAUUAGUAAUGCAAGAGGGUUCAAUGUAUGCAUUAUCAUGGUAUUAGUAAUGCAAGAGGGUUCAAUGUAUGCAUUAUCAUGGUAAAGACCCAAUCGCCCCUCAACUUUUUUUACAUGUUAUCACCAUACUUGUGGAGGGUAUCUUUGUAAA	183	spiLA0480-miR2868-1-5p	UUAGCUUUGUGUAUUAGUAG	16-35	osa-miR2868	5	0	20	20	1
spiLA0480-MIR4412	UAAUUUUUUUUUAAAAACUAUACAAUACAUACUAUAUUUAAUACACCAAACAAAACAACGCAUAAG	319	spiLA0480-miR4412-3p	UGUGGAGGGUAUCUUUGUAAA	233-253	gma-miR4412-5p	6	0	21	21	1
spiLA0480-MIR852-1	AUAAUAAGGGUGCUAAUUCCUCAAAAAUUUCCCUCCUCUUGAAAAAAAGGAAACAAAGUCAAAUAUCUUAUUACCUUUAUUUUCCUUUUCCAGAAGAGGGAAAUUUUUGAGGAUUUGACCCCCUUAUGUU	131	spiLA0480-miR852-1-3p	GAAACAAAGUCAAAUAUCUUAU	51-72	aly-miR852-5p	6	0	22	22	3
spiLA0480-MIR7508	AAUAAAAGUUUGUUUAUAUACCAAUAUUCUUCAAAAUUGAUAAGUAGUUCAAAGUGGAAGUUGCGCUUUCCAACCUUUAGGAGGAAUAGCAAAAAAAGUAGCCGUAAGAGUGAAGAAGGCGAAAAAAGCUAUUCAUGGCCAAAGAGGAGAAAUGGUGAAGCAUUGAUAGGAAUAAUUAUCAACAAGAGGAAGAAGGUAUAAAAAUAUCUUUUAUU	215	spiLA0480-miR7508-3p	CAAAAAAAGUAGCCGUAAGAG	90-110	ghr-miR7508	5	0	21	21	1
spiLA0480-MIR5014a-1	AUUUUUCAUUUUAGGUGUGCACAAGUAGGCACUUAAACUUGUAUAAACUUGAACAAAUAGACACAUUUGUUCUACAUGACACCCUACAUGAAACUUUUGUGUCCUAUUUUAUUAUGUCAUGUAGAACAUGAGCGUGUACUUAUUCAAUUUUAUACAAAUUUAAGGGUCUAAUUAUGCAUACUCAAAGUUGAAAGAC	196	spiLA0480-miR5014a-1-3p	UUAUACAAAUUUAAGGGUCUA	150-170	ath-miR5014a-3p	5	0	21	21	1
spiLA0480-MIR8006-2	CAUAUACCCUCCGUCAUACUUUUAGGGCAGUGGUGAACAUAUAUGUCAUUCACUCUAACGAAAGACUAAAUAGGGUCACGUGACACAACUUAUUCAUCGAUAAUAUUUAAUAAAUAUCGGGUCAGUCGAUGAGAUUAUGUCAUGUAUAUGUCCGUAUUCAUAAAGGGUAUAUAGCUCUAAUUUUUGGACGGCAUGAGCACCAAUGUCUCAAAAGUAUGACGGCAGAUAUUUU	234	spiLA0480-miR8006-2-3p	UAAUUUUUGGACGGCAUGAGCACC	180-203	stu-miR8006-5p	4	0	24	24	1
spiLA0480-MIR482c-3	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGUCCAUGGCUUUGCUCCUUAAGUCCCCAUUGAUUUAGGAGAGUGGACGGGGCAGACUGACUUCACGA	99	spiLA0480-miR482c-3-5p	CUCCCACUUCCGUCCAUGGCU	22-42	gma-miR482c-3p	5	0	21	21	2
spiLA0480-MIR9562-1	CAUAAUUGCGUUCCAUAGCAAACAUAUAACUGUAUAAUUCGCUAUACAUAUACAAUUGUAUAAUUCGCUGGCUCGCUAUGCAUAUACAAUUGUAUUAUUCGCUGGCCUAAAUUGUAUAAUUUGUUGGCCUAUUCGGCUGCAAUUGUAACUAUUAGUGUACAGUCAGACCUCUUUAUAACAGUGUCGUUUGUCUGGAUAUGUUUUGGUUGCUAUAACGAGAUGGUGUUAUAGAUAACAUAUAUUAAAGUCGAUUCCAAAAGAUCUAACUAGGCCGUUAAAGUGAAAUUUUGUUAUAAAGGAUGACUGUUAUAGAGAGGUUUGACUGUAAAUUGAUCUC	170	spiLA0480-miR9562-1-5p	ACAUAUACAAUUGUAUAAUUC	46-66	bra-miR9562-3p	6	0	21	21	3
spiLA0480-MIR8713	ACCCUUUAAUUUUAAAUGUGCACAAAUAGACACUUAAACUAUUAUAAAAUUGAACAAGUAAACACAAUUAUCCUACAUGACAUAAUACAUGUAAGAUGCCAUAUAGGAUACAAAAUUGCCAUGCAGGGU	190	spiLA0480-miR8713-3p	AUGACUGUUAUAGAGAGGUUUGAC	153-176	gra-miR8713	7	0	24	24	1
spiLA0480-MIR5014a-2		208	spiLA0480-miR5014a-2-3p	UUGUACAAAUUUAAGUGUCUA	163-183	ath-miR5014a-3p	3	0	21	21	1

spiLA0480-MIR10436	GCCACGUAGGACAAUGUGUUUAUUUGUUUAAUUUUGUACAAUUUAAGUGUCUACUCGUGCACACUCAAAAUAAAGCAUUUGUAAAAAGAUAUGUAGGACUACUAGACAACUCAAGCUUUAACACUCUAACUUGUCUACCAGUUGAUUCAGUUCCCUUUGGUUAGGGACUGUCUUCAUUGGUUAUGGUGGUCAACUGGUAGGCAAGUUAGAGUUUUUAAGCUUGAGCUGUCUAGUAGUCUUAUAUACCGUUUUAACG	178	spiLA0480-miR10436-5p	ACUAGACAACUCAAGCUUUAACAC	23-46	gma-miR10436	7	0	24	24	2
spiLA0480-MIR393d	AUCCAAAAGAAUUGGAUUAAUUGUUUUGUUAGCAUUGUAAAGACGUCUCAAAGUUCUUGUGUAUUUUAUGAACACUAGGUCAUGUUGAGGUGCUUCAGGGUUCUCUUCCUCAAUGACCAAGUGUUCAAAAUAUAAUAGAAUAUCAAGGCGUCCUUGCAAUGCUCACAAUGGAUUGAUCCACUUCUUUUGCAU	193	spiLA0480-miR393d-5p	UCCAAAAGAAUUGGAUUAAUUG	2-23	pab-miR393d	5	0	22	22	1
spiLA0480-MIR7980b-1	AUAUGGUAUCACAUCUCAUUAUAUGAAAUCAUGAGACGGAAUUAACGUAAAAUCGAAUGUCCAAACGCUGAUUUCAUUUCAUGAUAUCAUAUCGUGAUAUGGUAUCACAA	110	spiLA0480-miR7980b-1-3p	GUCCAAACGCUGAUUUCAUUUCAU	59-82	stu-miR7980b-5p	3	0	24	24	1
spiLA0480-MIR395g-2	UUGAAGUGUUGAGGAGAAUUUCCAAGCUCACUUUGAAAUUUACACAAACAAAUAGAAGUGUUAGAGUAUUAAUGGGAGACUGAUUCCCGAGAGUUUCCUUGACCACUUCGUGAGGAUUUAAUUACUUUGUUGUUUUAUGCCUUUCUGAAGUGUUUGGGGGAACUUUAGGGUUCACUUUAAAAUUUACACAAAUAAGUAGAAGUAAAUGAGUACUAAUGGAAGAUGAUAGAUGAAUGCAACGAUUUAUUUUAUAUCUAUCAAGGUGUUUUCGAGAUUUCCCUUGACCACUUAAU	293	spiLA0480-miR395g-2-3p	UGAAGUGUUUGGGGGAACUUU	146-166	gma-miR395g	0	0	21	21	1
spiLA0480-MIR5167b-1	UGCCCUUACUUUAAAUGGUCAAACUAGCCGUUAACUAGUCGUUGUAGAGUUUUAGGAGCUUUAAUAAAGAACUAGUUUAGGUAUAAUAACCAUAAAUCGUAAGGUUU	107	spiLA0480-miR5167b-1-3p	ACUAGUUUAGGUAUAAUAACC	71-91	bdi-miR5167b-5p	6	0	21	21	2
spiLA0480-MIR5160	AUCUAAAACAUGGUUGUGGUCAGAGAAUGUAUCAUUUCGAGGGUAGUAUCGCACGUCGUGAUGGAUAUUAUAUUUCGAGGGACAUAUCGCGUGCCUUGAUUGUUUCUAUUAUCGAGUAUCGUGUCGUGCGCCGCGACAGAUGCAUUGACAGAUAUGUCCCCCAUGGGUGUGUAUCGUUAGGGAAGACAUGCAUUACUAUUCUUGACAUUGCAUCUCAUGGCAUUACACAUUUUUUAUUA	239	spiLA0480-miR5160-5p	CGUGAUGGAUAUUAUAUUUCGA	57-78	osa-miR5160	6	0	22	22	1
spiLA0480-MIR7504g	GUUCUAGUUUGCCUUUCGGGGAAGAAAUUUGAUUUUCCAUCUUGAAGGUUUACCAUGAAAUAGUCAUUCUUGUCUUGAAUGUUUGACUGACCUCUGCUUAUUUCAUGGGCAAACUUUCAAGACGAAAAACAAGUUUCUUUUCCAAGAGGCAAACAAGGUC	161	spiLA0480-miR7504g-5p	GGGAAGAAAUUUGAUUUUCCAUCU	19-42	gra-miR7504g	7	0	24	24	2
spiLA0480-MIR8763-1	UUUUAUGUAAGACUAUUAAUAGUGUUGGACUUGUUCGUCCUCAUGCCUUUCGUCUAAAUUCAGUCAACAAUAGUUAUGCUUAGUCAACAAUAUGGUUCAUGUGACUUUUUUAGGAUAAAACCCUAAACAUAAUUUUUGUCGGCUAAAUUUAGAUGUAGGGCGUAAGUACGAACUAGUCCAACACUAUGAAUAGCCUUACAUACCU	205	spiLA0480-miR8763-1-5p	UUAAUAGUGUUGGACUUGUUCGU	16-38	gra-miR8763	5	0	23	23	1
spiLA0480-MIR7727	GUACAAAACCAAACCAAAAUGCAAACCGAGUCAGAUCGAAAAAACCCGACUAGUGGUUUAGUUUGACUUGGUUUGGUGUUGGAA	85	spiLA0480-miR7727-3p	GGUUUAGUUUGACUUGGUUUGGUG	56-79	bdi-miR7727-5p	7	0	24	24	2
spiLA0480-MIR2949a	CCAAAUGGCAAAUCGAGUCAAACGAAAAAAAAACGACUAGUGAUUUGGUUUGACUUGAUUUGGUAUUGAA	70	spiLA0480-miR2949a-5p	GGCAAAUCGAGUCAAACGAAA	7-27	ghr-miR2949a-3p	5	0	21	21	2
spiLA0480-MIR7981-4	CUUAACUAAAGUAAGGUCCUAUUAUCUUGAACUUAUUUUUUUUUUUAAUUUUGUAAACCUUUUAUCUUACGUGGCACACUUCGUGACUUCACACAAUUGAGACGCGUGAGAGAUAUUUGGAUGCCACGUAAGCCAAAAGUGCACAAAAUUACAAAAAAUAGGUUUAGGUAAUAUGAUCUUAGUUUAGUUAAA	193	spiLA0480-miR7981-4-5p	CUUAACUAAAGUAAGGUCCUAUUA	1-24	stu-miR7981-5p	4	0	24	24	2
			spiLA0480-miR7981-4-3p	AUAUGAUCUUAGUUUAGUUAAA	172-193	stu-miR7981-3p	4	0	22	24	1
spiLA0480-MIR7993d-1	GUGUAUUCUCAAGUGCUCAUACGUAGAUAAGCUAACCACAUAGAUUAUGUACUUUAAUUAUUCACAUCAGACUAAACUGGAACAUGCUUGAGCCUUUACUUGAUGUGUAUAACUAAAGGAGGUGACAUAUUUUUAGUGGUUAACUUAUCUAGGUAACGGAUACUUGAGAAUAUGU	175	spiLA0480-miR7993d-1-3p	AUAUUUUUAGUGGUUAACUUAUCU	127-150	stu-miR7993d	3	0	24	24	1
spiLA0480-MIR9476-1	AUCCUGCUAUUGGUCUAGUCCUGCAUCUUUUUUUAUAUUUUUUGAUAACGGAAAAAAUGUAAAAAAAGAUGCAGGACUAGACCAAUAGCAGUUU	94	spiLA0480-miR9476-1-5p	UCUAGUCCUGCAUCUUUUUUU	14-34	sly-miR9476-5p	0	0	21	21	1
			spiLA0480-miR9476-1-3p	AAAAAGAUGCAGGACUAGACC	63-83	sly-miR9476-3p	0	0	21	21	1
spiLA0480-MIR7823	AAAUAAUGCAUGCAUUAGCUUGAUGUAUUAGUAGUACCUUGUUUGGUACACUUUUCUAACCUAUGCAUCACCAAUGCUUGUAUUAGUA	88	spiLA0480-miR7823-5p	AUGCAUGCAUUAGCUUGAUGU	6-26	ptc-miR7823	5	0	21	21	2
spiLA0480-MIR6110-1	UGUAUAGGGAAAAAUACUCAAAUAUGCUAUCGAACUUUCAGAAAAGACUCAUUUAUGCCAUUCGUUAAAAGUUUGACUCAUCUAUG	276	spiLA0480-miR6110-1-3p	GGCCACGUCAUCAAUUUUUAAAAU	178-201	cca-miR6110-3p	6	0	24	24	3

spiLA0480-MIR477a-2	CCAUUACCGUUCAAGAAAAGACUCAUUUAUGCCAUUAUUUUUUAAUAGUGAUUUUGCAAAACCAUUUUUGACACGUGAUCAAUUAUAAUUCGGCCACGUCAUCAAUUUUUAAAAUAAAAAAAAUGUAACUGAUGGCAUAAAUGAGCCUUUUCUGGAAGUUCAAUGGUAUAUUUAUGUCUUUUCCCAUUUGAUUAAAUUUAUGUAAGUUAUUAUACACUAGAAAUAUUUGAAUCAUGAAUUCUAGUUUGCUAGUAAACGGGAAACAGGGAGAAAACUGCUAGACUAUGCCAUCCCAUAGUGGAAACAGGUAGGCGAGGGAUGCCGUUAGGGGAGUACACAAGGUUGAGGCGCUGAUAAGCAAUAAUUAUACGCUAAAGUAUGAUGCUAGUGGUAACCAGAAAACAUGAUAACAAUACUCUAGUUUAUAAUAAACUAAUAUGAAUUUAAU	258	spiLA0480-miR477a-2-3p	GGAUGCCGUUAGGGGAGUACA	127-147	ptc-miR477a-3p	6	0	21	21	1
spiLA0480-MIR8007b-1	AAAUUUUCUUACAUAGAGGUGGAUCCCGAAUCUUGAGUUUAUGGAUUUAGAUUCUAGAAAAGGUUACAUUUUCAAAACCCAACAAGUUACAUUUUUAGAAUUUCGUAUCCACAAACUCAAAAUUCUGGAUUCACCUCUACGUAAGCGAAAAGAG	154	spiLA0480-miR8007b-1-3p	AAGUUACAUUUUUAGAAUUUCGUA	84-107	stu-miR8007b-5p	6	0	24	24	1
spiLA0480-MIR3448	UAAAAGAAGGAGUCAAGAACGCACCAUACAGGAAAACAUCUUGAUAAGAAGUGUUACUAUGUUUAGACAAUUGUAUGGUUCGGGUAUUGACUUCUGUACUUGGA	104	spiLA0480-miR3448-5p	ACAGGAAAACAUCUUGAUAAG	28-48	aly-miR3448-5p	5	0	21	21	2
spiLA0480-MIR1918	GUAGCUCAGUUGGUUUAAUUAGUUGAAUUGUCAUUUUGUUGGUGAGAGUUCGAUUCUCCAUUACGCAAUCUCCUCUUUAAUUUAAGAGAAAAAGAUAUGCUACAAGGUGGAGAAUCGAACUACCGCUAACAGAAUGGAAGUUCAAAUACUUAAUCAAUUAAGCUAC	166	spiLA0480-miR1918-5p	UGUUGGUGAGAGUUCGAUUCUC	37-58	sly-miR1918	0	0	22	22	1
spiLA0480-MIR171b-2	GAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUA	97	spiLA0480-miR171b-2-3p	UUGAGCCGCGCCAAUAUCACU	72-92	aof-miR171b	0	0	21	21	1
spiLA0480-MIR5340	AUGGUUUUGCAAAGCCAUUUUUGACACGUGGUCAAUUAUAAUUUGGUCAUGUCAUCAAUUUUUUAAUUAAAAAAUUCAAAAAAAUUGAUGACGUGGCCGAAUUACAAUUGGUCACGUCUCAAAAAUGGUUUUACAAAACUAC	142	spiLA0480-miR5340-3p	UGAUGACGUGGCCGAAUUACAAU	86-108	osa-miR5340	4	0	23	23	1
spiLA0480-MIR5173	UUGCAUGUGUAUAUACAAUUUUCUCACACUUUAUACAAAUAGAAACGCAAUUUAUACAUUUCGCUUCUGUUUGUAUAAAUGAGAAAAGCGAGGGUGGCGAGCGAGAUUUGAGAGAGUGGCGAGCGAGAUCUGAAAGAGGGGAGAGAGGGGAACAAAAAUAUAUGUAUUUAUAUAAUUUUCUCUGCUUUAUACAAUUAGAAACAUUUUUUAUACACUUGUGU	221	spiLA0480-miR5173-5p	UGCAUGUGUAUAUACAAUUUU	2-22	bdi-miR5173-3p	6	0	21	21	1
spiLA0480-MIR6293	GACGACAACAGCAAUAACAUAUCCAGUGAAAUCCCACAAGUGGGAUCAGGGGCUGCGAGAAUAAGGCAGACAAUAGAAAAGGUUACCUAGUAUUUUUAUGUUACUGUUGGGAUUUGAACCUUGGUUUUCAAGAUUUGCACUCACAUUACUGAUUUUUUUUUUUGAGUCGAGUAUCUGUUGGAAACAACCUCUCUAUCCCGUAAGAGGUAGAUGACUAGAGAUAAAGUCUGCGGUACAUCCUACCUUCCCUAAACCGCACUUGUAGGAUCACACUAGGUAUAUAUUAUUGUUGCAGUCCAC	300	spiLA0480-miR6293-3p	UAAGAGGUAGAUGACUAGAGA	201-221	ppe-miR6293	5	0	21	21	1
spiLA0480-MIR11136-1	UGUAAAAAUCGAACCGACCAAUAAAUCGAACCGAUAAAAUGUUAUUGGGUUAUUGUAAUUGGGUUAUUGGGUUUUUAAUGGGUUUAGAAAAAAUAAUUAUUGGGUUAUUGGGUCGGUUUCGGUUUUUCCU	130	spiLA0480-miR11136-1-3p	AAUAAUUAUUGGGUUAUUGGGU	92-113	lja-miR11136-3p	5	0	22	22	2
spiLA0480-MIR8739-1	CGCAAAUUGUAUGUAAAUAUCCCCAUCAUACUUUUGAGAUAUUGUUGUCCCUGCCGUCAGAAAGCUAGAGCACGUACUUCCUUCACUCUAACGGAAGACUAAAUAGGGACAUGUGGCGCAAUCUUAUCGGUCGAUAUGAUAUUUAAUAAGUUGUUGUUAGUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAACGGUAUGUAUAUUCUAGUUUUUGAACGGCAUGGCACCAAUGUUUUAAAAGUAUAACGGAGGAUAUCCGCAUAUACCAUUUACA	282	spiLA0480-miR8739-1-5p	AGACUAAAUAGGGACAUGUGGCGC	96-119	gra-miR8739	6	0	24	24	3
spiLA0480-MIR835	CGCUUUGCCCUCAUGUUUGCUUCACCUACCACCCUAUUUUAUAUACUUUUAUGCAUUGGGGACAAUUGUAUGUCUUUUUGUUGGGGUGGGGUAAAUGGAAAGUAAGUGUUAGGGUGAAGUUUGAGUAUCCCAACUCACGAUCCUCUCUUGGGGUUUUCUUGCAUGUGUUCUUUAUCCCCAAGAGACUGGUUAUUUUAUUGUUGAAACGGCAUGUUGGUAUCUUUUGUACAUAGUAUAGAAAUGGAAUCUAAAGCAUGAUGGCUAAACAA	269	spiLA0480-miR835-3p	UUCUUGCAUGUGUUCUUUAUC	156-176	aly-miR835-5p	1	0	21	21	1
spiLA0480-MIR7997c-7	GGUUAUAUUGCUCCGACUCUUCAAAAGUGGUCACACCCAUGUUGAAUCCUCCAAAAAGGCAAUACUUUUGGUGGAUCCAACAUGCACCUGUUGACAUUUCUGAAGAGUUCGAGCAACAUAGUU	123	spiLA0480-miR7997c-7-5p	AUAUUGCUCCGACUCUUCAAAAGU	5-28	stu-miR7997c	2	0	24	24	1

spiLA0480-MIR8577	CGGACUAUUUGCCAUGUCUGAGAUCAUCUUAAGCUAUUCUUUUUAUUUCUCAAAAAAUGAAUAGGUGAUGAUGAUUCCAGAUAUGGAAAAUAGUAUC	97	spiLA0480-miR8577-3p	AAAAUGAAUAGGUGAUGAUGAUUC	54-77	atr-miR8577	7	0	24	24	1
spiLA0480-MIR1525	UGAAAAAAUCGAACCGACUGAUAAAUCGAAUCGAAAAAAAUGUUAUUGGGUUAUUGGGUUUUCAAUGGGUUUAUAAAUUUUUUUAUUGGGUUAUGGGUUCGGUAUCGGUUUUUACU	116	spiLA0480-miR1525-3p	UGGGUUUAUAAAUUUUUUUAU	66-86	gma-miR1525	5	0	21	21	1
spiLA0480-MIR7983-3	UUGCAACAAAAAUGAUCAUUAGCGGCAUUUAAUUUUUAAUUGUCGCUAAAUAUGUAUUUUUAGCGACAAUUAUCACUUUGUAUAUGUCCUCAAAGCCUUUAGCGACAUUGGUUCUAAUGGCACUUAACUACUGUCGGUAAAGACUUUAGCGCUCUUUAUUAAUGUCAAUAUUUAAUGCCGCUAAAAGUUGUUUUUGUUGUAG	202	spiLA0480-miR7983-3-3p	CAAAGCCUUUAGCGACAUUGGUUC	91-114	stu-miR7983-5p	2	0	24	24	2
spiLA0480-MIR169r-4	UUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAACAGCUGUUGUUGUU	184	spiLA0480-miR169r-4-5p	CAGCCAAGGAUGACUUGCCGG	63-83	csi-miR169r-5p	0	0	21	21	1
spiLA0480-MIR6234b	CUUUUAAAUAAAUAAACACAUGAGUCCUACACGGCACAAUAAACGUAGGUUACCACGUAGGACAAAAAAUGACAUGUAGGACACGUGUGUUUAUUUAUUUAACUU	105	spiLA0480-miR6234b-3p	ACGUGUGUUUAUUUAUUUAACUU	83-105	sbi-miR6234b-5p	7	0	23	24	1
spiLA0480-MIR5174e-1	AACUGUAUGGUACUCCCUCUGUUUCAAUUUGUUUGUCUGGCUUUGACAUGACACAAAGUUUAGGAAAGUAAAAAAUACUUUUGAAUCUUGUGAUCUUAAACAUGUCACGUGAAAAGUUGAAAUUAAAGAGUUGCAAAAAAGGAAAGUAAGACAAGCAAAUUGAAACGGACUGGAUGUAUCAUGCAAAG	188	spiLA0480-miR5174e-1-5p	UACUCCCUCUGUUUCAAUUUG	11-31	bdi-miR5174e-5p-2	5	0	21	21	1
spiLA0480-MIR827-3	ACAUGAAGUGAUGAAGAUGUUUGUUGAUGUUCAUCUAAUCAUGGCAUAUUAAUGGUUCCAAAAACUAUGCCAAAUGAUAUGAUGAAUAGAUGACCAUCAACAAACAAAUUCAUAACUACACAA	123	spiLA0480-miR827-3-5p	GUUUGUUGAUGUUCAUCUAAUC	19-40	eun-miR827-5p	3	0	22	22	2
			spiLA0480-miR827-3-3p	AUAGAUGACCAUCAACAAACA	86-106	aof-miR827	1	0	21	21	2
spiLA0480-MIR5303f-6	GAAUUAUGUUGCUCGGACUCUUCAAAAAUGUCAAAGGGUGCGUGUCGGAUUCGCCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCAAAAGUGAAGAGUCCGCGCAACUAAGCUUUCCGCGAAACCAUCAACAGGUGAUGCUGCCACAUGAUCUGA	126	spiLA0480-miR5303f-6-3p	AUUUUUGGAGAAUCUGACACGGGU	67-90	stu-miR5303f	0	0	24	24	1
spiLA0480-MIR167h-3	UCUUUCCUCGUACGGAGCAAUAGAAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGGUUCACGAUC	113	spiLA0480-miR167h-3-3p	AUCAUGCUGGCAGCUUCAACUGCU	76-99	gma-miR167h	1	0	24	24	1
spiLA0480-MIR10540-3	AGUCACUCAACUACUUGCUAGUAUCUCAGAAAAUCACUUUUUUGUUGAAGAAAAUAGGAAUCACGAAGAAAGCCGUCUUUCUGAGAUAAUAACUAUUAGUUGAAUGUUC	110	spiLA0480-miR10540-3-3p	AUAAUAACUAUUAGUUGAAUG	87-107	sly-miR10540	0	0	21	21	1
spiLA0480-MIR3706-1	AUAUUUUUAAGAGAAAGUGGAUAAAUAAAUUUCGAACUAUCGUAAAUGUUAUGAAGAUAUUUUCGUCUUAUUUUAUGAACAUUGAUAUUAAUGAAAAUACACGUGUCAUAAUUUUAUCCACCGACCAAACAUCGGAUGGAUGGAUAAGACUACGUCACGUGUCCAUAUUUGGUCUCUCGUUAGAACAAAAGGGCAUAUAUGCUCUAGUUUUUUUAGGAUAGAGGCAUCAAUUUUCCAAAAAUAUGACGAAGGAUAUCUGCAUAUCAUUACGAUAGUUCGAAGAUAUACUUAUUCUUUUCACUAUUUUUUUAAAAAGGC	318	spiLA0480-miR3706-1-5p	CAUCGGAUGGAUGGAUAAGA	130-149	pab-miR3706	4	0	20	20	3
spiLA0480-MIR1046-2	AAAAAUAAUAUCAAAUCGCUGCCCUGGCAGCGAUUUGUAAGAAGAAAAAUUUUGAAAUCGCUGCUUGAGCAGCGAUUUCAUUUUUUAU	88	spiLA0480-miR1046-2-3p	GCGAUUUCAUUUUUUAU	72-88	ppt-miR1046-5p	5	0	17	20	3
spiLA0480-MIR8613	AUGACUCAGUUGGUUUGGAGGGUGGUUAUCCACACGGAUGACCUGGGAUCAAUCCCCUCAAUGCCUUCUGAGUUGA	76	spiLA0480-miR8613-3p	UAUCCACACGGAUGACCUGGGAUC	27-50	atr-miR8613	7	0	24	24	2
spiLA0480-MIR169c-3	UUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAU	182	spiLA0480-miR169c-3-5p	UAGCCAAGGAUGACUUGCCUA	44-64	ata-miR169c-5p	0	0	21	21	1
spiLA0480-MIR172b	UUUAGUCGUUUAUUGCUAAUGCAGCAUCAUCAAGAUUCACAUUUAAUUGCAUUUUAAAUGUCAGAAUAUUUGAGAAUCUUAAUAGUGCUGCAUUUGCAAACAACAACUGUG	111	spiLA0480-miR172b-5p	GCAGCAUCAUCAAGAUUCACA	21-41	csi-miR172b-5p	0	0	21	21	1
			spiLA0480-miR172b-3p	AGAAUCUUAAUAGUGCUGCAU	73-93	csi-miR172b-3p	3	0	21	21	1
spiLA0480-MIR7748a	CGGUGGAUAUGUUGCUGAGAAAAGAGAAAAGCACAUGAAUAUUUUUUCACCUUUUGGAUGAAGCAGUAAUCAUGGUGAUUGUUUUAGUUCUGCUUAACAUUUCACAUACUUUGUGAUACUGUGGAUAUGUUACUGAGAAAAGAGAAAAGGACAUGAAUAUUUUUUCACCUUUUGGAUGAAGCAGUAAUCAUGGUGAUUGUUUUUGUUCUGC	227	spiLA0480-miR7748a-5p	AAUAUUUUUUCACCUUUUGGAUGA	38-61	bdi-miR7748a-3p	7	0	24	24	1

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spiLA0480-MIR10519	AUGUGCAUAAAUAGACACUUAAACUUGUAUAAAGUUGACAAAUAGACACACAUGUCCUACAUGUCAUCCUACAUAUCAUUUUUUUUCUUACGUGAUGUCGUACGUGUAUUGUGUCAUGUAGAACUCAUGUAUUUAUUUAUUCAAAAGUUGGAUAAUUAAAGUGUCUGUUUGUGCAUUA	178	spiLA0480-miR10519-3p	AUUCAAAAGUUGGAUAAU	139-156	tae-miR10519	3	0	18	18	3
spiLA0480-MIR7988-1	UUUUAAGGGAAAAGGGACAAACAUACUUCGAUACUAACAUAAAUGGUACGCAGAUAAUCUUUCGUCAUACUUUUGAGAUAUUAGUACCACCGUCGUCCAAAAACUAGAGUAUAUAUAUCCUUUGUACUAACGGACAUACACGUGUCAUAAUUUUAUCCACCGAUUGUAUAUCGAAUACGGAUAAAAUUGUGUCAUGAUGGAGAGUAUUUGCAUAUCAUUUACUAAUAUUAUAGAGAUAUAUUUAUCGUUUUCCCUAUAUUU	261	spiLA0480-miR7988-1-5p	AAGGGAAAAGGGACAAACAUACUU	5-28	stu-miR7988	5	0	24	24	1
spiLA0480-MIR5016	UACAACCCAUUGCGAUACUAGAAGUUUUAUGUUUUAUUGAGUGACUCAAGAUUGGAGUCGUGCAGGCGGAGAUCCUUUUGUCGAUUCCUUGGGUUAAAUGUUGUUCCACUGUAGUUUGGGUUAUAGAUGAUACAUGAUACUUCUAUGUUCUUAUUGGUUCCC	162	spiLA0480-miR5016-3p	CUUUUGUCGAUUCCUUGGGUU	75-95	ath-miR5016	6	0	21	21	2
spiLA0480-MIR162-2	GAACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGAAAAGCGAUAAAUACAGCAACAGGAAGCGAUCGAUAAACCUCUGCAUCCAGUGCUU	93	spiLA0480-miR162-2-5p	UGGAGGCAGCGGUUCAUCGAUC	7-28	csi-miR162-5p	0	0	22	22	1
			spiLA0480-miR162-2-3p	UCGAUAAACCUCUGCAUCCAG	68-88	fve-miR162-3p	0	0	21	21	1
spiLA0480-MIR5256	UAAGGGGUAAUAGGAAAGGGGGUAGGGAAGGGGGGGGGAAAAUUUCAUAUAUGGCAAACUUAAUUGAUUAAAUAACAUUAUAUGGGUAUAGUUUACCUAAUUACAUUCUAUGCGUAUAGUUUGGUUAUUAAAAUAGACGCUACCCGACAAAGGGAGAAUAUUCUAACGGGCAUUUAAGUAAUAUAUUCAAAGUUAGCAAUAAAAAUAAAAUAAAUAAAAUUAGCGAUUGUUUCUUCCCGGCAUACUGUACGACACAUUUUGUCGUCCUCCCCUUCCCUUCCCUUCCCUUCCCUUCCCCAAC	301	spiLA0480-miR5256-5p	UAAUUGAUUAAAUAACAUUAU	61-81	mtr-miR5256	5	0	21	21	1
spiLA0480-MIR5303-7	AGUACCUACCUGCUAAGUUGCUCGGAGUUUCUAAAAUUGUUGGUGCACGCAUGUUGGAUCCUCCAAAAUUGCCUACUUUUGAAGGAUCGACCAGGCACCUGAUCACAUUUUUUAAGAGUUCGAGCAACAUAGCCUUGUAGUGUGUC	146	spiLA0480-miR5303-7-3p	UUUUUUAAGAGUUCGAGCAAC	108-128	sly-miR5303	1	0	21	21	1
spiLA0480-MIR10538-4	UUUAAAAGUUGAUGGCGUCAGAUUGAUAUGCGUUACUGUAAAUAACGUUUUACUCCUAAAACGUUACUCAAAGUAACGUUUUAGGAGUAAAACGUUACUUACAGUGACGAAUAUCAACCUAAUGCUGUUAAUUUUUUAA	139	spiLA0480-miR10538-4-5p	AGAUUGAUAUGCGUUACUGUAAAU	20-43	sly-miR10538	5	0	24	24	1
spiLA0480-MIR11077b	GAUCAAGGCUUACUUCGAGCGAAUAUCAACCAGAUCUUGAUGAUGAGGCUAUAGUAGCAAAUAUCGAAAACAUUUUAACAUUAGAUUGUCUUGGUAAUUAACAAGAACAUGAACAACAAUAAUAUGUAAUUUUAUUUCUCAAGUUUAAUUGAUGAAUUAAGAAUAUGUAAAGGCCUACAAGACACUAUUACAAACUUCACUUUGUUAUAUUAAUCAAGCAAUACAUUGAUGAAAUGUAAGAUCUUUGCUUCAUUUUGCCUCUUUCAUCAUGAGGACUAUAGUUUCAUCUAGUCGAGUUAGCUUGCAC	307	spiLA0480-miR11077b-3p	UAAUUGAUGAAUUAAGAAUAU	146-166	lja-miR11077b-5p	5	0	21	21	3
spiLA0480-MIR169j-3	GAAAAAGAAGAGAAGUCUUACAUGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAUAGUCUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUAUCUUGACAUGCUCUUUUCUUUUAUGCAAGAUAUCUUUUUAAA	172	spiLA0480-miR169j-3-5p	UAGCCAAGGAUGACUUGCCUGC	48-69	ppe-miR169j	0	0	22	22	1
			spiLA0480-miR169j-3-3p	GGCAGUCUCCUUGGCUAUC	114-132	aly-miR169j-3p	0	0	19	19	1
spiLA0480-MIR169j-4	UUAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCGUACUUGAAAAGGUCUUUCAUAUGUCCAUCAACAAGAAGAACCUGAGUCAAGUGAUCAGCCGUCUUUUAUAAUCCCUAUGUCAUCUGCCCAUAGAGAAAACAAUGCUACUACUCCUCCAGUUUUUGGGGUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUUCAUGCAAGGCUUUCUCUUCUUUCGU	266	spiLA0480-miR169j-4-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1
spiLA0480-MIR1128-5	UUCUACUCCCUCCGUCCCAUAUUAGUGGUCCACCUUACUAUAAAUAGUUGUUCCACAUUACGGAAGUGGACAACUAAUAUGGGAUGGAGGGAGUACUU	98	spiLA0480-miR1128-5-5p	UUCUACUCCCUCCGUCCCAUA	1-21	ssp-miR1128	2	0	21	21	1
spiLA0480-MIR8007a-1	AUGUAUUUAUACUAAGUUUAUGGUCACUGUCACAAGUAUCAACCAGUGUAAUGGUACUUCCUCUGUGCCAUUUUAUGUGGCACUU	149	spiLA0480-miR8007a-1-3p	AUGUGGCACUUUUCGGAUUUCGAG	75-98	stu-miR8007a-5p	1	0	24	24	1

spiLA0480-MIR8006-3	UUCGGAUUUCGAGUAAACAUUUUGAAUUAUUAAUUAUUGUGACCAAUACUUUUUAUAAAUAGUU	155	spiLA0480-miR8006-3-3p	UAAUUUUUAGACGACAGGAGCAAC	120-143	stu-miR8006-5p	4	0	24	24	1
spiLA0480-MIR11592	UUUUGGGACAUUGGUGCUCCUACCGUCCAAAAACUGGAGCAUAUUCGUAGAUAAAUGUCGGAUCAGUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAAGGGUAUAUAUGCUUUAAUUUUUAGACGACAGGAGCAACGAUGUCCCAAAA	141	spiLA0480-miR11592-3p	GAACGGAACGAAACCGAAG	98-116	cas-miR11592	4	0	19	19	1
spiLA0480-MIR1128-6	GAUGUACCGGUACCGGUCCAGUACCUUCCGAUUUGUUUCGGUUCGUCCCGAUUCGGUUGCCUACGAGACGAAAUGGGACAUCCUGAAUCGGGACACGGAACGGAACGAAACCGAAGUUUGGUACCGGUGUACUGGUACCGA	236	spiLA0480-miR1128-6-5p	UAUUACUCCCUCCGUCCCAAU	11-31	ssp-miR1128	2	0	21	21	1
spiLA0480-MIR2608	GGCUAAUGUUUAUUACUCCCUCCGUCCCAAUGUGAGGUAGUUUGACUUGGCAGUUUAAGAAAACAGUCUAAAAUAAGUUAUAGAUGUUGGUGUAGCUGUAGAUCAUUUUAUUAAGGGUAAAAUAGGCACUUUAAAGUUAGAUUGUUACUGAAUAUUGAAAUGCGUCAUUCUUUUUGGGCUGACUUAAAAGAAAAGUGAGCAUAUAAAUUGGGACAGGGAGUAUAUAGAAAGUAAAU	216	spiLA0480-miR2608-5p	UUUGUUUAUAUACCAAUAUUCU	9-30	mtr-miR2608	6	0	22	22	2
spiLA0480-MIR319n	AAUAAAAGUUUGUUUAUAUACCAAUAUUCUUCAAAAUUGAUAAGUAGUUCAAAGUGGAAGUUGCGAUUUCCAGCCUUUAGGAGGAAUAGCGAAAAAAGUAGCCGUAAGAGUGGAGAAGGCGAAAAAAGCUAUUCAUGGCCGAAGAGGAGAAAUGUUGAGGCAUUGAUAGGACUAAUUAUCAACUAGAGGAAGAAGGUAUAAAAACUAUCUUUUAUU	159	spiLA0480-miR319n-3p	UUUCCUCCGAAGGGAACCCCU	113-133	gma-miR319n	4	0	21	21	1
spiLA0480-MIR7981-5	AGAGGCGGAGUCAGAAUUUUCAAUAAGGGGUUCAAAAUCUGUAGAUAUAGAUAGUCAAAGAGGGUUCGACAUCUACUAUAAACUUAUUUUAACCAUGUACAAUUAAUAUAAUUUUCCUCCGAAGGGAACCCCUUGUAUGAAGGUAGCUCCUCCGCCCCU	185	spiLA0480-miR7981-5-5p	CUUAACUAAACUAAAGUCCUAUUA	14-37	stu-miR7981-5p	4	0	24	24	2
	UCGAGCGACAGACCUUAACUAAACUAAAGUCCUAUUACCCCCGAAUCCAUUUUUUUUGUAAUUCUGUACACUGACAUCCAAACAUCUCUCACGCGCCUCGAGUCACGGAGUGUACCAGUACAAAAUUACAAAACAAAUGAGUUGAGAUUAAUAGAACCUUAGUUAAGUUAAGGUGUGUCUCUGAG		spiLA0480-miR7981-5-3p	AUAGAACCUUAGUUAAGUUAAGGU	151-174	stu-miR7981-3p	3	0	24	24	1
spiLA0480-MIR8739-2	UUGGGUGUCCCUGCUGUUAAAAAAUUAGAGCAUAUAUGUUCUUCACUCUACGGGAGACUAAAUAGGAACAUGUGGCACAAUCUUAUUCGUUGAUCCGAUAUUUAAUAAAUGUCGGGUCGGUGGAUAAGAUUAUGAUACGUGUAUGUUCGUUAGUAUAAAUGGUAUAUUUGCUCUAGUUUUUUUUACGGUAGGAUCACCAAU	201	spiLA0480-miR8739-2-5p	AGACUAAAUAGGAACAUGUGGCAC	55-78	gra-miR8739	6	0	24	24	3
spiLA0480-MIR319h	UUGUGUCGCUUCUUCAUCUGAAGCGAGCGCCUUUUUCAGAUCGCAUCGCCUCAGGAGAAAGAAGCGCAGUG	71	spiLA0480-miR319h-5p	CUUCAUCUGAAGCGAGCGCCU	12-32	mes-miR319h	5	0	21	21	1
spiLA0480-MIR7504j	AAAGCCCCCUAACCUAUAUCCGGAUUUCCAACAACUUCACUUGAGUCUUAUCACCCUGUGAACUAUUUAAAACUGAAAUUCCAUCUCCCUGGAGGUGAUAGGACUCAAGUGAAGUUGAAGAGUGUGGUUGAAAAUCCGGAUAUAAGUUAGGGGGCUUU	158	spiLA0480-miR7504j-3p	AUUUAAAACUGAAAUUCCAUC	65-85	gra-miR7504j	5	0	21	21	1
spiLA0480-MIR6232b	GAGCUCUACAGUGCAACUUCAGCAUAAUAAAGAGUAGAGACUAAUUAAUGCCUACAUAUGUAGGGAUUAAUGAGUCUACUCUUUGCUAUACUGAAGUUGCACUGUAGAGAUA	112	spiLA0480-miR6232b-3p	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-5p	5	0	21	21	1
spiLA0480-MIR5014a-3	GAUGUGCGCAAGUAGGCACUUAAAUUGUAUAAAAUUGAACAAGUAGACACAUGUGUCCUACAUGACAUGAUACACGUAACACACCACGUUAGACACAACUUUUUCAUGUAGGGUGUCAUAUAGGAUGAAUGUAUAGACUUGUUUAAUUUUAUACAAGUUUAAGUGUCUAUUUGUGCACAUC	181	spiLA0480-miR5014a-3-3p	UUAUACAAGUUUAAGUGUCUA	149-169	ath-miR5014a-3p	5	0	21	21	1
spiLA0480-MIR1130b-1	AUGUAUAAAAUUGAACAAUUAGACAUAUUUGUCCGACAUGUCGUCCUUGCACCCUACAUAUAUUAUGUCACGUAGGACACAUAUAUCUUCUUGUUCAAUUUUAUAUAA	108	spiLA0480-miR1130b-1-3p	ACAUAUAUUAUGUCACGUAGG	56-76	tae-miR1130b-3p	5	0	21	21	2
spiLA0480-MIR3951b-1	UAAGUACAAUCUCUCGCUAUUUCUUUUAUUUUUUAUCUAACAAUAAUUAGUUUCACCCCAGGGGAUCUUGUUGUCCCUAUAAAGGGGUAGUAGUUAUUGUUGUUGUGGUGUAUGAGCAUGAAAUCUUUAUAUCAACCUUAAAUAGGAAAGCUUAAAGAACUCAAGUGAGCAUUGUGACAUG	181	spiLA0480-miR3951b-1-5p	UUUCUUUUAUUUUUUAUCUAAC	20-41	csi-miR3951b-3p	5	0	22	22	1
spiLA0480-MIR9556	UGUACUUAAGCCCUUAGCAUCAAAUACUUGGCCCACAUACACCCUUAUUCUGCUCAAUUGCGCAUAGUAUUUGGACCAAGUAUUUGACGGUAAGGGCAUAAGUGAA	106	spiLA0480-miR9556-3p	CUCAAUUGCGCAUAGUAUUUG	53-73	bra-miR9556-5p	6	0	21	21	2
spiLA0480-MIR168b	AUGCUUGGCCCGCAAGGCUUGGGCCAGGUAGGGCUGGACCAACCCUUUUUGACAACUCUAGAUACAUCAAAAGUAGAGUUGUCAAAACGUGUCGAUCCAGUCUCACCCGGCCCAAGCCUGGCGGGC	133	spiLA0480-miR168b-5p	AGGCUUGGGCCAGGUAGGGCU	15-35	osa-miR168b	6	0	21	21	1

	CAAGGAA										
spiLA0480-MIR9679-2	AAAUUGAUAAUUUAUUAUCAAAGGGACUUAUAAAACCCUCUAAAUCUCCAUGGUCUUGUACUGCAUUUUAUGUUAAUAAAGUUGCAGAACAAGAAAGAGGUGUUCCCAGUUUGGUAAUAAAUUACAAGCC	130	spiLA0480-miR9679-2-3p	CAGAACAAGAAAGAGGUGUUC	85-105	tae-miR9679-5p	5	0	21	21	1
spiLA0480-MIR7804-1	GAUAUUUGUAUGAUUACUAAUCUAUUUGUUAUAUCUUUUGUAGUAUGGAAGGCGACGAGCCUCCGCCAUGGUCACAUAUUUGUGGUCGUGGGGGAAGAGGUAGAGGAAGGGGAAGAUCAUCCUCUUCACAGUCUAGAAGAUUAUUAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCGAAUCAACGAUUGGCGAAGCCUCCUAAUCAGCUUCAUCCUCUGUAAAUUUAAAAGAUAUUCCUAAGGACAGUUCAUUAUAUGAACAAAUUUA	286	spiLA0480-miR7804-1-3p	UUUAAUCGAAUCAACGAUUGGCG	188-210	rgl-miR7804-3p	7	0	23	23	1
spiLA0480-MIR10538-5	ACAGCAUUAGGUUGAUAUACGUAACUGUAAGUAACGUUUUACUUUUAAAACGUUAUUUUGAAUAACGUUUUACUCCUAAAAUGUUACUGUGAGUAACGUUUUAGGAGUAAAACAUUAUUGUGAGUAACGUAUAUCAAUCUGACGCCAU	148	spiLA0480-miR10538-5-5p	AGGUUGAUAUACGUAACUGUAAGU	9-32	sly-miR10538	5	0	24	24	1
spiLA0480-MIR7987-3	UAGGAAUAAUGUAUCUGUUAAGCAUAAGUACCAACAGUAGUUGAUCCUAUUGAUGACAAAAUUGAUUUUCUUGCAAGAUCGACUCGUGUCCAUCUAGUGUUGAUACUAAGUUUUAUUUAGGAAUAAUAUGUUUGUUAAGCAUAAGUAUCAACACUAGUUGAUCUUAUUGAUGACAAAUUGAUUUUCUUG	189	spiLA0480-miR7987-3-3p	ACACUAGUUGAUCUUAUUGAUGAC	151-174	stu-miR7987	0	0	24	24	1
spiLA0480-MIR1847-1	UUUGGCCUACGUGACACUAACUUGAAAAAAAGUCAACCAGCGUUGUGCCCACAAGAUAGUGCCACGUAGACCGAA	75	spiLA0480-miR1847-1-3p	GUGCCCACAAGAUAGUGCCACGUA	45-68	osa-miR1847-2	7	0	24	24	3
spiLA0480-MIR5567	UUAUACUCCCUCCGUCCCAAUUUAAGUGUCCUAGUUUAACUGUGCACUAAGUUUAUGAAAGGGGAGACACUGACUCUUUUAGUCUUAAAUUAAAGAUGCAUGUGUGUAUCCCUUUGAUUUUUGGUCUUAGACCUGCCAUGUAGAAUGUUGGAACUGGAAAGGUUACUAAAUAUAGAAAGACGCUCUUUUUGGGACAGAUCAAAAGGAAAAUAAGACAACUUAAACUUGGGACGGAGGGAGUACCA	245	spiLA0480-miR5567-5p	UUAAAGAUGCAUGUGUGUAUCCCU	90-113	sbi-miR5567	6	0	24	24	1
spiLA0480-MIR5014a-4	UUCAAAUUUUAACUUUGACCUCCAAUUUUCUUAAUGCACAAACAAACACUUUAGCUAUCCAACUUUUAAAUAAAUAGACACAUGAGUCCUACAUGACGCAACACGUGUAAGACACCACCUAGGACAAAAAAUGAUAUGUAGGACAUGUGUGUCUAUUUAUUCAACUUUAUACAAGUUUAAGUGUCUAUUUGUUCACAUCCAAAAUUAAAGGGCAUAAAUAUAAUUUAAA	229	spiLA0480-miR5014a-4-3p	UUAUACAAGUUUAAGUGUCUA	167-187	ath-miR5014a-3p	5	0	21	21	1
spiLA0480-MIR8007b-2	CGGGGACUUUCUUAAAGAGGAACCUCAUGUAAAUACCAUGGAAUAAGGUUUGAUCCUAUUCAUGGAGAUUCCGUAACUAUUCCAAAAAUGGAAAGUUCGACACAAUUGGUAUUUUUUUUUUGAAAUUGGAAGCAGUUACUAAUUCAUGAUCUGGCAUGUACAGAAUGAAAACUUCAUUCUCGAUUCUACGAGAAUUUUUAUGAAAGCCUUU	211	spiLA0480-miR8007b-2-5p	CCAAAAAUGGAAAGUUCGACACAA	82-105	stu-miR8007b-3p	5	0	24	24	1
spiLA0480-MIR5026-1	CGCCUUUUCGGCCUACGUGACACUAGCUUAAAAAAAUCAACUAGUCUUGAGCUCACAAGAUAGUGCCACGUAAGCCAAAAAGAAACUUGUUUCAUAUCUCUACUAUCCAUGGUUCUAUUUACCUAUCUAAACUAUCACUCCCUUUGUAUUAAAGACAAAUGAGCGCUGAGCUAGCCAAUAUGUAUUUGACCAACUCAGCUUCGAGGUGCCUUUUAAUAAAAACUGAGUGAUAGUUUAGCUAAGUACAGAGAACAAUAGAUAGUUGAGGUAAGAAACUAU	85	spiLA0480-miR5026-1-3p	GCUCACAAGAUAGUGCCACGU	51-71	ath-miR5026	4	0	21	21	2
spiLA0480-MIR8039-1	UUAUAAGAGAAACAGUGGUAGGGCUACUCUCUAUUGGCAUGCACUUAUAUAUUUAAACUGACAUGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUG	194	spiLA0480-miR8039-1-5p	UUACCUAUCUAAACUAUCACU	34-54	stu-miR8039	3	0	21	21	1
spiLA0480-MIR399b-1		103	spiLA0480-miR399b-1-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spiLA0480-miR399b-1-3p	UGCCAAAGGAGAGCUGCCCUG	64-84	stu-miR399b-3p	0	0	21	21	1
spiLA0480-MIR9742	UUGCUGGAUUGGGUGUUUUUACUUGUGAGUUCCUUUCUACUACUACUGUUUAAAUUUGACGAUAGAAUGUGUGGUUUGAUCUGUAACACAAUAGCUACUUCUUCAGCUUAUGUAGCAGUAGAAAGGAACUCACAAGUAAAAACACGCAAUCAAGAUU	157	spiLA0480-miR9742-3p	UGUGUGGUUUGAUCUGUAACA	68-88	gma-miR9742	4	0	21	21	1
spiLA0480-MIR8021-1	AUAUUCAAGGCUCAAACUCGAGACCUCUAGUUAAGGAUCGAUGUUUCAUAUACAUCCCUUCAUAACUAUUGUUGGUUCUAAUAAUAACUUAAUUCACUCUCUCUUUUAUAUAAAUAGAAAUACGUUAAUAUUAUUGAGUUCUACCAACAAUAUUGUGUUGGUGAAGAAGUUAAUAUUACUUCAUCCUUAACUAGAAGUGUCAAGUUUGAGUCUUGGAAAUG	221	spiLA0480-miR8021-1-5p	AUUCAAGGCUCAAACUCGAGACCU	3-26	stu-miR8021	0	0	24	24	1
spiLA0480-MIR169c-4	GUUGAAGAGAGGUAUUGCAUGAAGAUAAAGUGCCUGCUCUGAUAGCCAAGGAUGACUUGCCUAAAAUCAUUUUUAUGAAGGGUCUUAACUAAUUAAACUUUAGUUACUAAAAUUAAAGUUUAUAUUA	209	spiLA0480-miR169c-4-5p	UAGCCAAGGAUGACUUGCCUA	43-63	ata-miR169c-5p	0	0	21	21	1

spiLA0480-MIR10536-1	UAUGAUCUUAAAAUUGGGAUUUUAGGCGUUGUCUGAGGCUAAUUGAGAGACACUUAUCUUUCAUGAAACACCUUCAUUCUCUUUGAAUAAGAAGGAAAUUGAAGAUUAAAACAUGUCAAAGGAACUGGUCCGAUGUAGUAGAUUGACUUGUCUACAACAAGUGUUGAUGAAGAAGGAAGCUGAGGAUCAUAACAUGUUGUUGGACCUUUCUUCAUCACACUCGUUAUAGAUAAGUCAAUUAACUGCGUUGUCCUUUGACAUGUUCUAAUCGUUAGUUUUCUUUUUUUUUUU	210	spiLA0480-miR10536-1-3p	UGACAUGUUCUAAUCGUUAGUUUU	175-198	sly-miR10536	4	0	24	24	2
spiLA0480-MIR1432	UAAAUUCACGAGGUUGUCAUUUCUCUUGUAUUCACGUGUGUGUGUGUAUAUAUAUACACACACACACAUGAAUACAAGAGAAAUGACAACCUCGGGAAUUUA	104	spiLA0480-miR1432-3p	ACAAGAGAAAUGACAACCU	76-94	vca-miR1432-5p	5	0	19	19	2
spiLA0480-MIR8045	ACACACCUAGGAUAUACCCAUUUUUUGAGUUUCAUAUAGGAAAUAUCAUCAUCGUUCAGGUAGGAAAAGUAAACAAUUGAUAGUUGAGGUGUGUUUUGAUGAAUAACGGUGAUAGUUUAGGUAGGAAAUUCGCACACAUGAUAGUUUAGGUUUGAAACUCGAAAAAUCGGAGUACUUUAGGUGUGU	186	spiLA0480-miR8045-3p	AUUGAUAGUUGAGGUGUGUUU	76-96	stu-miR8045	0	0	21	21	1
spiLA0480-MIR11285	UGACUUUCCUGAAAAGUUGUGACUUUUAUGGAAAGUUGUGACUUUCAUGAAAAGUUGUGACAUUUAUGAAGAGUUGCGACUUCUAUGAAAAGUUAUGACUUUUAUGAAAGGUU	113	spiLA0480-miR11285-3p	UCUAUGAAAAGUUAUGACUUUU	82-103	fve-miR11285	5	0	22	22	1
spiLA0480-MIR7984d-1	UUUGGGAAAAAGUGUGAAAUAUAUUUGAAUUUUGAUUGAAAUUGCCGUUACGAUACCAAACUUUGAGAAUGACACGUGGACAUAAAUUUUUUUGCCGAAUUAUCAAUAAUAAUGUCCUCCAUAAAGUUUGAUACGUAACAACAAUUUCGGUCAAAGUUUGAGUAUUUUUUUAGACCCUUUUCCCUAU	187	spiLA0480-miR7984d-1-5p	AUUUGAAUUUUGAUUGAAAUUGCC	23-46	stu-miR7984d-5p	6	0	24	24	1
			spiLA0480-miR7984d-1-3p	CAAUUUCGGUCAAAGUUUGAGUAU	142-165	stu-miR7984d-3p	3	0	24	24	1
spiLA0480-MIR7997c-8	AAGCUAUGUUGCUCGGACUCUUCAAAAAUGUCGCUGGUAGUGCAUUUUUUUGGAGGAUCCGAUAAGGGUGCUGCAACAUUUUUAAAGAGUUCGAGCAACAUAGAUA	106	spiLA0480-miR7997c-8-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
spiLA0480-MIR10410c	UUGCUUAGGAUGGAUGAAAGAGAUGUGAGGCAAACGAAAUUGACAAAUCCAAUUUGGUCCGACCAUUAAUUCAUUUUCUCCUAAAUGAAAUUGCCUCUCCCACAUCGUUUCUCAAACAAUUUUCAAUUUUACAAUAGUCUCACAUCGGUAUUUCAUCCUUUUUGAGGAU	169	spiLA0480-miR10410c-3p	CUCCCACAUCGUUUCUCAAACAAU	97-120	gma-miR10410c	7	0	24	24	2
spiLA0480-MIR10532-5	CAAGUAUAGAGAUUAUUGUCGGGAUAAGGAACAAGUACCCUAUAGACUAUAAACAAAAUUUGAAAGGCACACAUAAGCUUAACUAGGGUCUUAUCCCCGGCCCAACGAUGGUUGACUUUUUUUUUCAAACUAGUGUCACGUAGGCUAAAAAGGGGUAGAAAAUUACUUAUAAAACAAGUUCAGGGGAGUAAUAGGACCUUAGUAUAGUAUGAGUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAAGGGUACUUGUGCAUUUUCCCUAAAAUCUAUAUACAAA	281	spiLA0480-miR10532-5-3p	GAGUGUGUCUCUGAGAUUUCGGGC	211-234	sly-miR10532	1	0	24	24	2
spiLA0480-MIR7484k	UUCAAACCAAAGCCUAUAAUUCCUCCUCUUGCCAUUUACAAUUAAGACCUUUUCCAUCAAUCUCAAGAGAGGUAUGUUUCUAUGUAUUUGGCGUUAAUUUUUCUUGAAUCAUUUAUGUGAGAUAUCACAUUUAGAAAUAAACAAAAUUUCUAAAUGAAAUCAAAGACCAGUGUUGCAUAUUGGUCGGUUUGGUUCGGUUUUGAAAUUUAUUGGGUUGACUUAUUGGUUAUCGAUUUGUAGAGAUGCUAAAAAGUUGUAGAACGACUAAGAUCUUGACUUAUCGGUUAUUGGUUUAUC	297	spiLA0480-miR7484k-3p	UUUCUAAAUGAAAUCAAAGACCAG	147-170	gra-miR7484k	6	0	24	24	1
spiLA0480-MIR7997c-9	UGGACUAUAUUGCUUAUACUCUUCAAAAAUAACGACGGAUGCAUAUCGGAUACUCCAAAAAUAGUGUACUUUUGGAGAAUUCGAUAUGGAUGUGACAACACUUUUGGAGAGUUCGAGCAACAUAGUUU	129	spiLA0480-miR7997c-9-5p	AUAUUGCUUAUACUCUUCAAAAAU	7-30	stu-miR7997c	3	0	24	24	1
spiLA0480-MIR3636	GUGUGUGUGUGUGUGUGUAUAUGUAUGUGUAUAUAUAUGUAUUUCGGGUUGGUUUGAGUUCGGUUUGAUUCUUUGUUUAAAUACCAAACCAAAUCAAGAGUGGUCCGAUUUUUUUAUCAAUUGCCAAACCAAUCAAACCAAAUCACAAUUGAGGUUUUGUUCGGUUUGAUUUGGUUCGUCGGUUUGGUUUACUUAAUGGUUCGGUGUAUACACCCCUAAUCAUAAACAAAGACAUAUUAUUGUAGAGUCAAGUUAACAUUUCAUAUCAAUAGAUUAUAUAAACAUAAUAUACAAAACACUUACAAAU	307	spiLA0480-miR3636-5p	UCGGUUUGAUUCUUUGUUUAAAUA	60-83	vvi-miR3636-5p	6	0	24	24	1
spiLA0480-MIR5303i-2	ACCUAUGUUGCUCGGACUAUGCAAAAUGCUCCCGAACUAGAGCGUUGGAUUUUCCAAAAAAAUAUGCUGCUUUUGGAGGAUCCACCACGCACCUGACAAUAUUUUUGAAGAGUCUGAGCAACAUAAUC	128	spiLA0480-miR5303i-2-3p	AUAUUUUUGAAGAGUCUGAGCAAC	99-122	stu-miR5303i	0	0	24	24	1
spiLA0480-MIR11288c	ACUACAGGAAUCUAUUGAUUUAGGAUUUGUCAAACUAUACCGUUAUCAAGAACAGAGGAGAUGUGACCAUUACUCAUCUCCUCUGUUCUUGAAUAGUUUGACAAAUCAUAAAUCAAUAGAUUCCUGUGAA	130	spiLA0480-miR11288c-5p	UGAUUUAGGAUUUGUCAAACU	16-36	fve-miR11288c-3p	4	0	21	21	1

spiLA0480-MIR838	AAUUAUUUGGUCCCUAUAGUGCCCAUAUUUAACUAGAACUCAGAAUCCUAUUUCUAUGCAAAAAGGAAGAAUAAUAUGGAUUUUUUUCUAGUCUUCUAGAAAAAUUAGGUUUUCUAGUUCUUUUUGGAUUAGGAAGACAUCUCAUAAACAGGGAUUCUCCUAACCUAGCAAAUAGAGGAAUUAGUAUUAUAUUCAUGCUUACCCACCCAAGUAUUGAGAGAGUUCAGAUAUGACUUGGGAUCACUGUAGAAGACCAUAACUAUCU	266	spiLA0480-miR838-5p	UUUUCUAGUUCUUUUUGGAUU	110-130	aly-miR838-3p	6	0	21	21	1
spiLA0480-MIR5303d-3	UCAUAAGUUUAAGUUGCGCGGACUCUUCAAUGUAGAUGCUGCACUCGUGCCUGAUCUCCAAAAAUAUGCUACUUUUGGAGAAUCCGACACGCACCCACUGACAUUUUUGAAGAGUCCGAGCAACAUAACUAUAGGU	136	spiLA0480-miR5303d-3-3p	UUUUGGAGAAUCCGACACGCACCC	73-96	stu-miR5303d	0	0	24	24	1
spiLA0480-MIR5030-1	AUGUAUAUCGCUGCCCAGGCAGCGACUUUAUGAAAAACAAUUUGUUUUUUAUAAAACGCUGCACAGGCAGCGACUUUAUGAAAAACAAUUUUUUUUUAUUUUAUGAAACGCUGCCCAGGCAGCGACUUUAUGA	133	spiLA0480-miR5030-1-5p	AAAACAAUUUGUUUUUUAUAAA	34-55	gma-miR5030	6	0	22	22	1
spiLA0480-MIR825	GGUUUCCAUGGUCAGUUUAUGCUUAUCCAGAAGGUGCAGGGGUUGGUUUCUGGUAGAACGAGCUUAUCUUAAACAUGUUUUGUUGAAGAAGCUAUGGUUUCGAUCUGAUUUGCCUGCACCUUAUGUUUGAGCAUGCGCUACCAUGAACUA	150	spiLA0480-miR825-5p	UUAUCCAGAAGGUGCAGGGGU	23-43	aly-miR825-3p	6	0	21	21	1
spiLA0480-MIR11039-1	UUCUCUACUUGUUAUGAGGAUAUGCAUGGUAUGUGUCUAUAUGAUGUAGUCUUAUUCUUAUGUGAACUAUGUGAGUCUUAGUGACUAUAGGAUGGAAAUUGUUGAUAGUAAUUGAGUUGUACUUAUGCAUUAUGUUGAUGUAUGAAGUGUUAAGAUUUGUGGUGUCGUGAAGGGUUUACAGAAUGUAUGGAGUUAUGGGGCUUCAUAUGUUCAUUGAACUAGUAGACUA	229	spiLA0480-miR11039-1-3p	UGGAAAUUGUUGAUAGUAAUUGA	93-115	seu-miR11039	2	0	23	23	1
spiLA0480-MIR8739-3	CCAAACUAUCAUAAAUGGUAUGCAAAUACCUUUCGUCAUACUUUUGGGACAUUGAUAUUCCUGCCGUUCAUAAACUGGAGCAUAUAUGUCCUUCACUCUAAGGAAGACUAAAUAGGGACACAUGACGCAAUCUUAUCCGUCGAUAGAUGUCGGAUCAAUGAAUAAGAUUAUGACACAUAUAUGUCCGUCAGUAUAAAGGAUAUAUAUACUCUUUUUCUAAAAUUACAUAUGCAAUUAAUAUUCUAAAAAUAUGAUAGAAAUUAUUUACAUUCCAUUUACGAUAGUUCAA	289	spiLA0480-miR8739-3-5p	AGACUAAAUAGGGACACAUGACGC	105-128	gra-miR8739	7	0	24	24	3
spiLA0480-MIR7840	GGCAAUGGAAUAGGUGGUCACUAGAAUGCAUUAAUUGCACUCCAAUUAUAGGAGUAAUUAAUGUCAUUGGAAUUGUCUAAACAAUUAAUUGACUUUUUAAAAAAAUGAAAACAAACGGUCGUAUAUGUGUUUUAAAAUUGGGUCGGAUAAUUAGGGCAUAAGUGACCCCUUUCUCUUUUAA	181	spiLA0480-miR7840-5p	AUAGGAGUAAUUAAUGUCAUU	48-68	ptc-miR7840	5	0	21	21	3
spiLA0480-MIR2868-2	AGUACUCUAUUUGGGGUCGUUUGGUAGGGCGUAUACGAAUAGUGUUGAAUAUGGUGUAUUGGUAUUGUUGCCUUUAGUAAUGGUGGUAUUAAUUAUUUUUUAUGCAUUGUUUGGUUUGGUGUAUUAAAAAUAGCAUGUAUAUCACAACUUUCAAUAAAAAAAAAAUUGUUAACAAAAGUACCCUCUACAAAUAUGGUGGAAAUGAUGCGGAAAAGGUUUUGAGGGACAAUUGUGGCUUUAACCAUGCUAAUGCAUGCAUUAAAAACCCUUGUAUUGCUAAUAACAUAGUUUGCUAUGUACUAGUUAUGCAUACCAUAAUACCAAAUAGAGUGCA	334	spiLA0480-miR2868-2-5p	UUGGUUUGGUGUAUUAAAAA	111-130	osa-miR2868	3	0	20	20	1
spiLA0480-MIR10999b	ACAGGUGCGUGUUUUUCUUGCGACCGUCAGGGUCAUACUAUGAGGAAAUGUAACCUUAGAGGUAGUGCAGGUGGUAUGGCUCAGCCUACUGGGUCCGUGGAUGGUUCAUCUUCUUCUGUGGUUAUGCACCCUACGGGGCAGGGUAUUCAGGCACCAAC	158	spiLA0480-miR10999b-3p	GGGCAGGGUAUUCAGGCACCA	136-156	mdm-miR10999b	6	0	21	21	1
spiLA0480-MIR6447	UAUGAAGAGUUCUGACUUUUAUGAAAAGUUGCGACUUUUAUGAAAAAAAGGUUGCGACUUUUAUGAAAAGUUGUGACUUUUAUGGAAAGUUGUAACUUUUAUGAAAGAUGACGACUAUUCCGAAAGAAUUUAUGGACUUCUUCUUC	161	spiLA0480-miR6447-3p	UUUAUGAAAGAUGACGACUAU	113-133	ptc-miR6447	5	0	21	21	1
spiLA0480-MIR10532-6	AGGGAAAAUGCACAAGUACCCCCUCAAUCUAUGUCCGAAAUCCCAAAAACACACAAGAUAGUGCCACGUAGGCUAAAAGGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAGGGGUAAUAGGACCUUAAUAUAGUAUAACUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGAUACUUGAGCAUUAUCUCA	190	spiLA0480-miR10532-6-3p	AACUGUGUCUCUGAGAUUUCGGGC	136-159	sly-miR10532	1	0	24	24	1
spiLA0480-MIR859-1	AGAUUUCAUUGAUUUUACAAAAAAUAGGAUUGAAUUUCUCAAAUGUUCUCCAGUUUAUACUUUCCAUUAUGUUGGUGGUAGAUACGGUAGAGUGGCAUGGAUCAUGUGAGAAUCAAGUUACUCUUAAACUUGUAUUGGAAUGUGGUUUGCAUGUGUGCAUUGUUGCAAUUAUGAAAUGUUUAGUGCAUGGGAGCUGGGGACCAUAUGGAAAUUGAUAUGUAGUGAUGUCCAAUUGCAGUAACUAAGGUUUUCUGAGAAAACAAAUAGUUUUUUUUUUCUUCUUUUUAAAGUCAAUAAAAAAA	302	spiLA0480-miR859-1-5p	UGAUUUUACAAAAAAUAGGAU	10-30	aly-miR859-3p	5	0	21	21	1

spiLA0480-MIR841a	CCAAACCGACGAACCAAAUCAAACUGAAAAAAAAAAUCGGCUUGUGGUUUGGUUUGAUUGGUUUGGCGAUUGAA	74	spiLA0480-miR841a-5p	GACGAACCAAAUCAAACUGAA	8-28	ath-miR841a-5p	5	0	21	21	2
spiLA0480-MIR5720	GCUUGUGGUUUGGUUUGAUUGGUUUGGCGAUUGAAAAAAAAAAUCGACCACUCUUGGUUUGGUAUGGUAUUAGAAAAAAAGAAUCAAACUGAACUCAAACCAAACCGACACAC	113	spiLA0480-miR5720-5p	UUGUGGUUUGGUUUGAUUGGU	3-23	bra-miR5720	6	0	21	21	1
spiLA0480-MIR10542-1	AAAUAUACCUUGAACUUUGAUUGAAGAAUCGUAUAUACCCCUAAAUAAUAUUUUUAAAAAAAAAUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUCAACUUCCGCUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAAGGGUAUAUCA	278	spiLA0480-miR10542-1-5p	UUGAAGAAUCGUAUAUACCCCUA	21-43	sly-miR10542	2	0	23	23	1
spiLA0480-MIR8007b-3	AUGCUAACAUGAUACUCCCUCUGUCCCAUUUUAUGUGACACUUUUUGUUUUUCGAGAGUCAAACGAUUUAACUUUGAUCAGACAUUUGCGCAUGGAAUCUUCAAUUUUUUUUUGAAAUGAAAUUUAUAUAUUUGUAACUACGUAAAGAGUUACUAAUGAGUCACAGUAAUUGAUAAUUCAAAAUGUUAAAAGGAUCUAUGAAAAACUUACGGUCAAAAAUAGACUUAUUUAAAUCUCGAAAUGCGAAAAGUGCAACGUAAAAUGGGACGGAGGGAGUAUUUAUUUAGUCG	290	spiLA0480-miR8007b-3-5p	AUGUGACACUUUUUGUUUUUCGAG	33-56	stu-miR8007b-5p	2	0	24	24	1
			spiLA0480-miR8007b-3-3p	CGAAAUGCGAAAAGUGCAACGUAA	237-260	stu-miR8007b-3p	6	0	24	24	1
spiLA0480-MIR9760-1	UUGAAGAAACAUAAUUUUAUUGAUUAAGAUAGCGGGUACAAUUCUGUUGAUCCCUUGAUUCUACUCUCUUCGGAUUUAUCCAUGAUUCGAGAGACGCUAGUAGCGUAUUUCUCGAACUAGGAUGAUUUAGAUUUGAUCUUUCUAUGUGAAUAAUCCAUCAAUUUGUGGAGUAUUCGAGAUCUUGAUGUCUUUAAGAAAUUUUUGAGAUGCCUUUUAAGAGAAUUUAGUACCCUUUAUAUAGGCAUAAAUUAGAUUUUAUG	261	spiLA0480-miR9760-1-3p	AGGAUGAUUUAGAUUUGAUCU	119-139	gma-miR9760	5	0	21	21	2
spiLA0480-MIR9560	CGACUUUUAUGAAGAGUUGUGACAUAUAUGAAAUGUUGCGACUUUUAUGAAAAAUUGCGACUUUUAUGAAAAGUUGUGACAUUUAUGGAAAGUGUGACCACCUUUCUGAAAGAUU	115	spiLA0480-miR9560-5p	UGAAGAGUUGUGACAUAUAUGAAA	10-33	csi-miR9560-5p	7	0	24	24	3
spiLA0480-MIR11464a-1	UAGACACAUUCGUCCUACAUAACAUCCUACAUGGCGAUUUUUUGUCCUACUUGGCGUCCUACAUGUAUUAUGUCAUGUAGGACACGUGUGUGCA	94	spiLA0480-miR11464a-1-3p	GUAGGACACGUGUGUGCA	77-94	pab-miR11464a	4	0	18	21	2
spiLA0480-MIR5303h-6	AAGCAGUAUGCUGCUCAGACUCUCCAAAAAUAUUGCCACACCUGUAUCGUAUCCUUCGGACAGGCACUACUUUUGGAGGAUCGAACAAGCACCUGACAACAUUUUUGAAGAGUCUGAGCAACAUAGUGAAG	131	spiLA0480-miR5303h-6-3p	AACAUUUUUGAAGAGUCUGAGCAA	98-121	stu-miR5303h	0	0	24	24	1
spiLA0480-MIR7998-2	ACCACCGACAGACCGUAGGGUGACCUACGGUCCAUAGGUAGGGUCUAUAGAUGGUCACCUGCAACUCUCCCCGGAAAAGUCCAAAAAAUUGUUCACGGUCGAACCCACGGACCGUAGGUCAAUCCACGGUUGUGGUCCU	139	spiLA0480-miR7998-2-3p	ACGGACCGUAGGUCAAUCCACGGU	107-130	stu-miR7998	2	0	24	24	1
spiLA0480-MIR2923	UGGCCUAAGAUUUUCUAAGUCUGAUGCAUCACUUACAUUUUUUUCUCAUUCUCCGUUGUUGGUGCCUCUCCAAAAAGAAAGUUGAAUGGAGAAUGAAAAAGAAAAAUGUAAAGAAUAAAUAGAGCGAAUAAUUUAGGAUG	140	spiLA0480-miR2923-3p	AAAGAAAAAUGUAAAGAAUAAA	98-119	osa-miR2923	5	0	22	22	1
spiLA0480-MIR8675b	GUUAUUGGUGCUUCUGCUGUUCAAAAACUAGAGCAUAUAUUGUCACUCACUCUAACGGAAAACUAAGUGGGAACAUGUGGCACAAUCUCAUCCGUCGAUUUGAUAUUUAAUAAAUGUCAGGUUAGUGGAUAAGAUUGUGACACGUGUAUGUAUGUUAGCAUAAAAGGUAUAUAUGCUCUAUUUUUUUGACUGCAGAAACACCAAUGUU	208	spiLA0480-miR8675b-5p	GUGGGAACAUGUGGCACAAUCUCA	67-90	gra-miR8675b	6	0	24	24	3
spiLA0480-MIR397b-4	CCCUUCAGAGAAUUAAAAACAUGAUCGAGUGUAGCGUUGAUGAAAAAUGAGGAAGGCCCAAAUGCAGGAAUUCUCAAAUAUGUCAUCAACGCUGCACUCAAUGAUGUUUCUAAGUACUCUGCAAUAA	127	spiLA0480-miR397b-4-5p	AUCGAGUGUAGCGUUGAUGAA	24-44	bdi-miR397b-5p	2	0	21	21	1
			spiLA0480-miR397b-4-3p	UCAACGCUGCACUCAAUGAUG	86-106	eun-miR397b-3p	0	0	21	21	1
spiLA0480-MIR399r	AGUUAUGUGUGGAUGCAUUACUGGGCUAAUCUUCUUUGGCAAAUAAUUUCACUAUUAUUUGGUGCAAAUUUGGUCAUUUAUUGCCAAAGAAGAUUUGCCCCGUAAAUCAUUCAUACAAUAUUA	123	spiLA0480-miR399r-3p	UGCCAAAGAAGAUUUGCCCCG	82-102	mtr-miR399r	0	0	21	21	1
spiLA0480-MIR7805	GCCCUGGUAAUUGGAUUUGGUGUAAUUACAUUGUCUGUCCUAUUUAGUUUGACAGGGUAAUUACAUGGUCAGCAGGUAUUUGGUGUAAUUGACAGUGAGUAAUUACACUCUCCAAUUCACAGUCA	125	spiLA0480-miR7805-3p	GUAUUUGGUGUAAUUGACAGU	76-96	rgl-miR7805-5p	6	0	21	21	3
spiLA0480-MIR7504c	CCUCUCUCACUUUAUGUACAGACACAAAUGUAUAAAAUGUGUUUGUAUUUGUAUAAAAUGAGAGAAAAUUGUAUUUAUACAUCUCUUUUCGUUUGCCUAUCUGUCCUAAAAAUCUCGCUCGUUACUCUCACUCGUCUCUCUCACUUUAUACAAACACAAAUGUAUAAAAUU	200	spiLA0480-miR7504c-5p	AUGAGAGAAAAUUGUAUUUAUACA	58-81	gra-miR7504c	7	0	24	24	1

	ACGUUUAUGUUUGUAUAAAGCGAGAGUAA										
spiLA0480-MIR8039-2	UAGAACUAUCAGAAGUUACGUUUUCCUAUCUGAACUAUCACCA UCGUUCAGGAAAGAAGAGGAAACAAUUGACAGUUGACUUGUG UUUUAAUACAUGGAUGGUGAUAGUUCAAGUAAGAAAGGGGAA CAACUGAUAGUUGGA	142	spiLA0480-miR8039-2-5p	UUUCCUAUCUGAACUAUCACC	22-42	stu-miR8039	0	0	21	21	1
spiLA0480-MIR1530	AAUGGAGUUUGAGUGGUUAGGAGGAAGGUUGAUGGUGGAUG CUUUGAGAAGAUGGUGGUUUCACUAUUUUGAAAUAAAUUAAUA UUUUAUUUUAAAAUAGAUAAUACAUAAUUAUGACGUGGUAUUA AUGUGAGUGACAUGGAUUUGACUUGUCAUCUAUGCAAGAGAG AGUGAGGUACUCACAUGGUUAGAGUGGUUUAGCAAUCAUUUU UUUAUUGAGUUCAGGGGUCUAGAUGACAAAAGGGUAAGUAGA AGGAUUCACACUUUAAACGCAUACAAGUACAAGGGUCCACCAG ACCAUUCCACCUAAAUUCUAAUCCUGA	323	spiLA0480-miR1530-5p	UUUUGAAAUAAAUUAAUAUUU	67-87	gma-miR1530	4	0	21	21	1
spiLA0480-MIR7504f	AUAAAGUUGAACAAGUAAACACAUGAGUCCUACAUGACAUUAU ACACGUAAGACACCACUAGGAUAAAAAAAAAUGACAUAUAAGA UGUCAUGAAGGACAUGUGUGUCUAUAUGUUCAACUUUAU	125	spiLA0480-miR7504f-3p	AGGAUAAAAAAAAAAUGACAUAUAA	61-84	gra-miR7504f	7	0	24	24	1
spiLA0480-MIR1520k-1	CAAAAAUUAGAGCAUAAAUGCUCUUCACUCUAAGCGAAGACUA AAUAGGGACACACGGGCGUUAUCUUAUCCGUCAAUAAAUGUC GGAUCGGUGGAUAAGAUUAUGACACAUGUAUGUCCGUUAGAA UGAAGGGUAUAUAUGUUCUAGUUUUUG	154	spiLA0480-miR1520k-1-3p	GAUAAGAUUAUGACACAUGUAUG U	95-118	gma-miR1520k	7	0	24	24	2
spiLA0480-MIR8575	AAGUUGUGACUUAUGAAAAGUUGUGACAUUUGUGAAAGGUAG UAACCUCUUCGAAGCGUUGAAACCUUUCAAAUAGUUGUAACCU UUCCGAUGAGACAUAAUAA	104	spiLA0480-miR8575-5p	AGUUGUGACAUUUGUGAAAGGUA G	19-42	atr-miR8575	7	0	24	24	1
spiLA0480-MIR5014a-5	UAGUUUGCAACUAUGAUCCUUAACUUUGGAUGUGCACAAGUA GGGACUUAAAGCUUGUAUAAAAUUGAACAAGUAGACACAUGUG UCUUAGAUGGAAUGAUACUUGUAGGACGCCACAUAGGACACA AAAUUUUCAUGUAGGAUGCCAUGUAGCAUGAAUGUGUCAAUU UGCUCAAUUUUACACAAAUUUAGGUGCCAAUUGUGCAAAUUUA AAGUUACGGAUCAUAAUUGCCAAAUGA	239	spiLA0480-miR5014a-5-3p	UUGUGCAAAUUUAAAGUUACG	200-220	ath-miR5014a-3p	4	0	21	21	1
spiLA0480-MIR7985-1	GGACUUCCAUGUUGGAGGUCUCAAGUUUGAAACCCCUUGUCA GUGAAAGCAAAGUGUUUGCCUUCUGGGUCGAGCUUGUCGCAC CGGGCUUGCCUAGUGCGGGUUACCACUCCUAUGUGGUUGUG AGUUAUUGCAUAGGAGCGGGGGUUUUACCCUGUGCGCAUCCA AAGGGUAGCGG	178	spiLA0480-miR7985-1-3p	CGGGCUUGCCUAGUGCGGGUUA CC	85-108	stu-miR7985	2	0	24	24	1
spiLA0480-MIR172d-1	AUUCAGACCUAAAAAUCAAACGUACUGAAUAGGCUGAAUCUGA AUGAUUAAGAUUCACACCUCCAUUGAGUGCAAACAAAUGAGGC CUUAGUUGUCAUUUGUUUUCAUUAAGAUUAAGAGGUCUGAAU CUGAAUAAACAUCUGAAUAUUAAGAUUUGCAUUAAGAUUUGAG UGCUUUAAUCUGAGU	186	spiLA0480-miR172d-1-5p	UCUGAAUGAUUAAGAUUCACA	39-59	bra-miR172d-5p	4	0	21	21	2
spiLA0480-MIR10532-7	ACGUGGCACUAGUUUGAAAAAAAAAAGCCAACCAUCGUUGGGC CACAGGAUAGUGCCACGUAGGCUAAAAUGGGAUAAAAAAUUAU UAAUUAAAUAAGUUCAGGGAGGUAAUAGGACGUUAGUAUAGUA UAAGUGUGUCUCUAAGAUUUCAGGCAUAGGUUGAGGGGGUAC UUGGGCAUUAUCCCCCGAGGGCCCUAAAUCUUAUAUAGCGUG UUCAAUAAAAAUUAGUCACGUAAAACUAAACUUGACUUCAUAG GCACCUCCCUCAAUAAUAAUUAUUAUUGUAUCUUUUUCUUGUU UUUUUUUUUUUUCAUAUUUGUGUCCAUCU	328	spiLA0480-miR10532-7-5p	AAGUGUGUCUCUAAGAUUUCAGG C	131-154	sly-miR10532	2	0	24	24	1
spiLA0480-MIR860	UCCUAACACACGUGUCAUAAUCUUAUUUACUGAUCCGAUAUUU AUCAAUAGAUAAGAUUGUGUCACGUGUCUCUAUUU	78	spiLA0480-miR860-3p	UCAAUAGAUAAGAUUGUGUCA	45-65	ath-miR860	6	0	21	21	1
spiLA0480-MIR3637	UUAAUGAACUCUGUAACUCUAUAUUUUUAUCUUGUGUUUUGU CUCUUCCAAACCAAAUGAAGACCAUCACUAUUUAUACUAGAAG AAGUCUUCCUAGCAAGGAAUAGGAAGAUAAUGGAGUAGUAAAA UGAAGAUAAUGGUCUUAGGAGUUACAUAUGUUUCAUAGG	167	spiLA0480-miR3637-5p	AUUUUUAUCUUGUGUUUUGUCUC U	23-46	vvi-miR3637-5p	6	0	24	24	1
spiLA0480-MIR2607-2	UGGACAUACCCAUUUAAGGGAAAAUUACAUGGGAUGUCAAACA UCCCCAUGUAAUUAGUUAAUAAGGGUAUAGUUUA	77	spiLA0480-miR2607-2-3p	AUGUAAUUAGUUAAUAAGGGU	49-69	mtr-miR2607	5	0	21	21	1
spiLA0480-MIR1514b	AUCAAAUCGCUGCCCUGGCAGCGAUUUGUAAGAAGAAAAAUUU UGAAAUCACUGCUUGAGCAGCGAUUUCAUUUUUUUAUUAAACA AAAUUUUUUUUGGCAAAAUCGCUGCCUCAGUAGCGAUUUUAC GUGAAUGUAUCCGGUUUUUCAAAUUUUAUAUCUAAACUAACAC UAAAUGUUUAUCGACAUACACACCUCAACUAUCAGUUGUUCUC UUUUCCUACCUGAAUGAUGGUGAUAUUCUAGGUUGGGAAAGG	128	spiLA0480-miR1514b-3p	UUCAUUUUUUUAUUAAACAAA	68-88	gma-miR1514b-5p	6	0	21	21	1
spiLA0480-MIR9477-3	GAACAACUGAUAGUUGAGGUAUGUUUCUAUAAACAUUUGGUG AUAGUUCAGGUUGGGAACUCGGAAAAAGGAAUACUUGAU	209	spiLA0480-miR9477-3-5p	UAUCAGUUGUUCUCUUUUCCUAC C	73-96	sly-miR9477-5p	2	0	24	24	1
			spiLA0480-miR9477-3-3p	UUGGGAAAGGGAACAACUGAUAG U	119-142	sly-miR9477-3p	0	0	24	24	1

spiLA0480-MIR7711-2	AAGUGUUAAUAAGCCAAUUUGACCAGCUUAUAAGCUUAGUCAACACCCUCUAAGCUUAUAAGCUGGUCAAACUAGCUUAUAAGCAAUU	89	spiLA0480-miR7711-2-5p	UAAUAAGCCAAUUUGACCAGCUUA	7-30	bdi-miR7711-5p-1	7	0	24	24	1
spiLA0480-MIR10538-6	UAAAAGCUGACGGCAUUAUAUUGAUAUACGUUACUCAUUGUAACGUUUUACUCCUAAAACGUUACCCAAAAAAAUGUUUUACGCCUAAAACGUUACUCACAGUAAUGCAUAUCAACCUAACACCGUCAACUUAUG	135	spiLA0480-miR10538-6-5p	AUAUUGAUAUACGUUACUCAUUGU	18-41	sly-miR10538	3	0	24	24	1
spiLA0480-MIR7997c-10	CUUCUAUGUUGCUCGGACUCUUUAAAGAUGUUUACGGGUGCAUGUCUAUUUCUUCCAAACUAGUGCAUGUUUGAAGGAACCGACACAGGUGCAACAGCAUCUUAGGAGAGUCUGAACAACAUAGGUU	127	spiLA0480-miR7997c-10-5p	AUGUUGCUCGGACUCUUUAAAGAU	6-29	stu-miR7997c	3	0	24	24	1
spiLA0480-MIR8030-1	GUACAAAACUGAACCGAAAAUCAAACCAAAUCGCAAAUCGAGUCAACCCAAAAAAAAUCCGACUAGUGAUUUGGUUUGACUUGGUUUGGUAUUGGAA	97	spiLA0480-miR8030-1-3p	UUGACUUGGUUUGGUAUUGGAA	76-97	stu-miR8030-5p	6	0	22	23	1
spiLA0480-MIR7981-6	AUUUUAACUAAACUAAUGCCCUAUUACCACACCCCACAAACUUAUUUUUUUGUAAUUUUAUACACAUUUUUUUACGUGGCACACUGUGUGACUUCACGCAAUUGAGGCGCGUGAGAGAUAUUUGGAUGCCAUGUAAGUCAAAAAGGUGCAAAUUUUUUUCAAAUAAAGUAUUCAAGGGUAAUAGGACCUUAGUUUAAUUAAGGU	204	spiLA0480-miR7981-6-5p	UUUAACUAAACUAAUGCCCUAUUA	3-26	stu-miR7981-5p	5	0	24	24	2
			spiLA0480-miR7981-6-3p	AUAGGACCUUAGUUUAAUUAAGGU	181-204	stu-miR7981-3p	2	0	24	24	1
spiLA0480-MIR8034	UUUAAAUACUGAAUUAAGAAAAAGUAAAAUCAGAUUGUUGUUCUUAACUAAUUAAUUAAUGGGGCGGUUUGGGUCGGGUUGACCUUGAGGGACCCGUUUUUGCGAUGGGGACAUCACGGGUUAGAACCGAUGGAAGAAACAUUUAAGUGGAUGAAAUUGAGGUUUAUAAUCUAAUUUAUAAAUUAAUUAACUUUUAUUAUGUUAACAGCUUUUAAGGGUAUUUCAGACAUUUUGAUUUAAAAAGCUGUUUAUAAGCACUUAUUUGCCAAACACAUCAACAACUUUUUUUUUUACUUCAGCACUUUUAU	309	spiLA0480-miR8034-3p	UUUGCCAAACACAUCAACAACU	263-284	stu-miR8034	5	0	22	22	1
spiLA0480-MIR7992-8	UAAUCAAGCUUGAUCUCAGUUGAGCAGUAAACACUCCAACUUAGAAGAUGCACAUCUAGACAGCUCAACUCAAAUCCACUGUGUCAAUUGAGGUGUCUAGAUGUGCAUUCUCAAAGUUGGAGUGCUUACUUGCCAAUUGAGGUCAAGUUUGAGUG	155	spiLA0480-miR7992-8-5p	UUAGAAGAUGCACAUCUAGACAGC	41-64	stu-miR7992-5p	5	0	24	24	1
			spiLA0480-miR7992-8-3p	UGUCUAGAUGUGCAUUCUCAAAG	94-116	stu-miR7992-3p	5	0	23	23	1
spiLA0480-MIR2921	AUGAGAUGGCUCUGAGGUUGAGUUUGAUCCACAUUCAUUUCAUUACACGAUAGUAUAGCAAAAUCUAUGUAUGUACUACCUUGUAGUGAAAUGGAUGUUGAAUCUAAUUUAACCUUAGAGCUUUCUUUU	129	spiLA0480-miR2921-3p	UUGAAUCUAAUUUAACCUUAGAGC	98-121	osa-miR2921	7	0	24	24	3
spiLA0480-MIR9386	GUCCUCCAACUUUGGGUAUGCACAAAUACACUUAGUUUAAAAUUGAACAAGUAGACACAUGAGUCCUAUGUGGCAUGAUACAUGUAGGAAAUCACAUAGGACACAAAUUGAUAUGUAGGAUGCCGCGUGGUACGUGUGUUUUUUAAGUGCCCAUUUUUGCACUUCCAAAGUUGGAGGGU	179	spiLA0480-miR9386-3p	UUUGCACUUCCAAAGUUGGAGG	156-177	mes-miR9386	5	0	22	22	1
spiLA0480-MIR8006-4	AGAUUCGUCAUAUUUUUUGGAUAUAUUUAUCUUAGUCGUCCAAAAACUAGAGCAUAUAUACCCUUUAUACUAACGGACAUGCACGUAUUAUAAUCUUAUUAACCGACCCGACAUUUAUUAAAUAUCAGAUCGACGGAUAAGGUUGUGUUACGUGUCCUUAUUUAGUCUUUCGUUAGAAUAAAUGACAUAUAUGACCUAGGUUUUGGACGACAGGGCACCAAUGUCCCAAAAGUAUGACGAAGAG	244	spiLA0480-miR8006-4-3p	UAGGUUUUGGACGACAGGGCACCA	197-220	stu-miR8006-5p	5	0	24	24	1
spiLA0480-MIR396a-2	AGUCCAAAGCUUGCCAUCUUUUCCCACAGCUUUCUUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAAAUUAUCAAUUUAGAGAUCAAAAUUUAGCAAGAAGAAGUUCAAGAAAGCUGUGGAAAAGCAUGACUAGGACUUGGUCA	144	spiLA0480-miR396a-2-5p	CACAGCUUUCUUGGACUUUCA	25-45	hbr-miR396a	2	0	21	21	1
			spiLA0480-miR396a-2-3p	GUUCAAGAAAGCUGUGGAAAA	104-124	csi-miR396a-3p	1	0	21	21	2
spiLA0480-MIR8001b-2	CCACACUACAAGAAAAGUAUGAAUUACAUUGAGAUUUUCCUGAAAAUCAGGAUGAAUUUUUGCAGGAAAAUAAGUUUCCUACGUAUUUUCAUACUAAUCUUAGGAAAAUCCCAUGUAAUUCACAGUUUUCUUGUAGUGCCA	141	spiLA0480-miR8001b-2-3p	GUAUUUUCAUACUAAUCUUAGGAA	83-106	stu-miR8001b-3p	6	0	24	24	1
spiLA0480-MIR5303d-4	AACCUAUGUUGCUCAUACUCUCCAAAAAUGUUGCUGCACCCCUGUCGGAUUCUCCAAAAGUGCAGUACUUUUGGAGAAUCCGACACGCACCCGCCGACAUUUCUGAAGAGUCCAAGCAACAAGACU	126	spiLA0480-miR5303d-4-3p	UUUUGGAGAAUCCGACACGCACCC	69-92	stu-miR5303d	0	0	24	24	1
spiLA0480-MIR7981-7	ACAAACAUCCCAAAGACACAUUAACUAAACUAAAGUCCUAUUACUCCCCUGAACUUUUUUUUUGUAAUUUUAUACACCUUUUGUCUUACGUGGCACACUCCAUGACUCCACACAAUUGAGGAAUGUGA	241	spiLA0480-miR7981-7-5p	AUUAACUAAACUAAAGUCCUAUUA	20-43	stu-miR7981-5p	4	0	24	24	2

	CAGAUAUUUGAAGGUCACGUAAGCCAAGAAGUUGCACAAAAUUACAAAAAAAAAAAAGAAGUUCAGGAGGUAAUAGGACCUUAGAAUAGUUAAGGUGUGUCUUUGGGAUUUCGG		spiLA0480-miR7981-7-3p	AUAGGACCUUAGAAUAGUUAAGGU	200-223	stu-miR7981-3p	3	0	24	24	1
spiLA0480-MIR6459a	UAUAUUUCGGAAACAAAAAAAUCGAAAAAUAAGUUACCUUGUUGAAAUGACUGGGAUCAACAUUGUCAUCGAGGGAAUGAACAGCCUCAAGCAAAAAUCUGAUCCCAGUCAUUUCGACAAGGUAACUUAUUUUUUGAUUUUUUUUUGUUUCCGAAAUGUA	160	spiLA0480-miR6459a-3p	GCCUCAAGCAAAAAUCUGAUC	84-104	ptc-miR6459a-5p	5	0	21	21	3
spiLA0480-MIR391	AAAAGGCUUGCUACGCAGGAGAGAUGAUGCUGGACGAUAGAGAAAAUGGGAUUUAAUUUAUUGGCCAGCAUCAUACUCCUGCAUAUUAAGCCUAAA	96	spiLA0480-miR391-5p	ACGCAGGAGAGAUGAUGCUGGA	13-34	sly-miR391	0	0	22	22	1
			spiLA0480-miR391-3p	GCAUCAUACUCCUGCAUAUU	68-87	stu-miR391-3p	0	0	20	20	1
spiLA0480-MIR10445	AUGAAACCGUUGCCUUGGCAGCGAUUUGUAAGAAGCAAAAUUUUGAAAUAAAAUUUUUUUUGGCAAAAUCGCUGCUGAGGCAGCGAUUUUAC	92	spiLA0480-miR10445-3p	AAGAAGCAAAAUUUUGAAAUAAAA	30-53	gma-miR10445	6	0	24	24	1
spiLA0480-MIR2099	GCCUCUCUCACUUUAUAUACAAACACAUAUAUAUUGUCUCUGUGUUUGUACAAAAGUGAUAUAAAAUGCAUACAUACAUCUCUUUUCGUCUGCCUCUCCCCUAGAGAAUCUCGUUUGCCUCUCUCACUCACCUCUCUCACUUUAUACAAACACAUAUAUAUUGUCUCUGUGUUUGUAUAAAGCGAGAGAAAA	189	spiLA0480-miR2099-5p	CAAAUGUGUUUGUACAAAAGUG	34-55	osa-miR2099-5p	7	0	22	22	3
spiLA0480-MIR1513a	UGUAUAAUUAUAUGUGUAUAAGACGGAGAUAUAUGUAUUUACAUGUGUAUAUACAAUUUUCUCUCGCUUUAUACAAUUAGAAACACAAUUUAUACAAUUCUAUUGUAUAAAGCGAGAGAGGCAAGCGAAGGAAGCGAGCGAGAGAGGGAGAGUGGCGAGCGAGAAUAUGAGGAAUAGAGAGACUGACAAAUAGUUUGCUAUGAAACAGAAAUAAAUCAAAUGAUAGCUACUAUAAUUAUUUU	242	spiLA0480-miR1513a-5p	AUUAUAUGUGUAUAAGACGGAGA	7-29	gma-miR1513a-3p	7	0	23	23	2
spiLA0480-MIR9477-4	AAGCCAACUAUCCGUUGUUCACUUUUCCUACCUAAACACUCUGUGUUUUCUAUAUAGACGGUGAUAGUUCAGGUACAAGAGGGAACAACAAAUAGUUGGGAU	102	spiLA0480-miR9477-4-5p	UAUCCGUUGUUCACUUUUCCUACC	9-32	sly-miR9477-5p	1	0	24	24	1
spiLA0480-MIR7992-9	AAAGCAUAAUACAUAGACAAGACCCUUUAACUUGGCCUUCACCGGCACCUGAACAUCAAUCCCAGCUCUAAUUGUGAUCAUCUUGACACAGGUGUGUCUCGCAAACAUCUUAACUUUGAUAAUGCACACUUUUGAGAACGUGUCUAGAUGUGCAUUUUCAAAGUUAGGCUGUUUACGGGGUUUUCAAAGUUGGAGUGUUUAGUUACCUGUUGAGGUAAAGUUAAGAUGUCUAUCUAUGUAUUGUGCCAA	249	spiLA0480-miR7992-9-3p	UGUCUAGAUGUGCAUUUUCAAAG	141-163	stu-miR7992-3p	4	0	23	23	1
spiLA0480-MIR11136-2	UCUUAGAUAACAGAAUGGUUGGGAGUUUGAGCCCCCACGACCCCUUAGAUUUUUAGAGUUAAAUUCGAUACAAUAUGGAGGUUGUGGGCUCAAACACCCACAACCCCCCUUAUAUUUUUUUUAAAUUUCGCUUAGGAGGCUGUGAGGUGGUGGGUUCAAAUCCCACAGCCCCUCAUCAUUUAUUU	186	spiLA0480-miR11136-2-5p	CAGAAUGGUUGGGAGUUUGAGC	11-32	lja-miR11136-3p	7	0	22	22	2
spiLA0480-MIR8599-1	AAACUAAAGAUAUUAAAAUGAGUUGAAAUAGAAUCGGGUUGGGUCUUGACCUGCCCAAGUUUACUUUGGGCUAAAAUGGGUUGGGUUCAAAUGGGCUAAGAACGGGUUGGGUUUUGAACCACCUAAUUUGACCCGAUUAAUAUCAACAAUUCUAACAUAGUGAUAUUUAACUUUUAUAAUCACAAUUCGAAUUUCAGCUUUAAUAUUUUUAAAGA	215	spiLA0480-miR8599-1-5p	CUAAAAUGGGUUGGGUUCAAAUGG	71-94	atr-miR8599	7	0	24	24	1
spiLA0480-MIR6145b-1	AUUUUCUAUCCUUUUUACGUACGUGGCACUAUCUUGUGGGUUCAACGAUGUUUGACUUUUUUUUAAGCUAGUGUAACGUAGGCCGAAAAGGGGUAGAAAAU	101	spiLA0480-miR6145b-1-5p	UUUACGUACGUGGCACUAUCU	14-34	nta-miR6145b	6	0	21	21	1
spiLA0480-MIR3520	CUGUCUUAUCACUCUUCUCUUUGAAGGGAGAGGCUUUAAUCAGUGUACCUGCAAUAGGAAUAUUGAUUCCUUCAAGAGGAGGAGUGGUAGAUUC	94	spiLA0480-miR3520-5p	AAGGGAGAGGCUUUAAUCAGU	24-44	ahy-miR3520-3p	6	0	21	21	1
spiLA0480-MIR8672	UGGAAAUGGAAAUAAUGUUAAAAUAACUAUAACUAUAAUUAAAAAGAAUGUUGAAAUAAAUAAAGAAUGAAAAAGGAAUCUUAAAGCAACUCAAGAAUGAGAAAUAAUUAGAUGAAAAAGGGGUCUGACAGCACCUGUAAGGCGCAGAAUAUCAGGCACCUUUUUUUUUAAUGCAAGGCAAAAGCCAUCAUGUGCCUUCCUCUUUUCAUCGGUUGACGCCGUUAACGGCGUAUAGGGGAAGGCACGUGGGCCCCUGUGCCUUUAGCGUUUUGGUUUCCUGAAUAAAUUGUUUGCCCUUUUUGGAACUUUUAGACAAUUAUGUUGCCCUUUUGG	333	spiLA0480-miR8672-5p	AUGAGAAAUAAUUAGAUGAAAAAG	97-120	gra-miR8672	5	0	24	24	1
spiLA0480-MIR7774	UGAGCAGAAAAAUGGAUUUCGAAAAUAAUUUUUCACGAAUUAGUCCUCUUUUUUUAUGGUGAGAAUUAUCAACUAUGGUCUGUGAGAAUGGAAACUUACUUGGAGGUUCUUGAUCUUUGAGAAGUCGUGGAAGAGGAUUAUGAAAUCAAUUUACUGCGAA	160	spiLA0480-miR7774-3p	ACUAUGGUCUGUGAGAAUGGAAAC	72-95	bdi-miR7774-5p	2	0	24	24	1

spiLA0480-MIR171b-3	AGCUACACGUGAUAUUGGCGCGGCUCAAUCAAAAAGUAGACUCAAAAAUGUUCUUAAGUACUGCUUUCUCAUUGAACCGCACCAAUAUCUCGUGUAUUC	99	spiLA0480-miR171b-3-5p	GAUAUUGGCGCGGCUCAAUC	11-30	zma-miR171b-5p	1	0	20	20	1
			spiLA0480-miR171b-3-3p	UCAUUGAACCGCACCAAUAUC	69-89	tcc-miR171b	4	0	21	21	3
spiLA0480-MIR5014a-6	AUUUACGUCCUUCAACUUUGGGUGUGCAUAAGUAGACACUUAACAUUGUAUAAAAUUGAACAAGUAGACACAUGAGUCAUAUGUAUACACGUGGACACAAAUUGUCAUGUAGGAUGUCACGUAGUACGUGUGUAUCUAUUUAUUCAAUUUUAUACAAAUUUAAGUAUUGAUUUGUGCAUGCUCAAGUUGAGGGCAUAAAU	200	spiLA0480-miR5014a-6-5p	ACACUUAACAUUGUAUAAAAU	36-56	ath-miR5014a-5p	5	0	21	21	1
			spiLA0480-miR5014a-6-3p	UUAUACAAAUUUAAGUAUUGA	150-170	ath-miR5014a-3p	5	0	21	21	1
spiLA0480-MIR11114	CCCUCUGUCCCUAUUUAGUUGUCCGCUUUAGAAGUGACACACAUAUUAAGGCACCAAUUAUCAUCAUAGGUUAGCUACAAUUUUAUCCUUAACUUAAAAGAUUAUGCAUAUCCACAAGUAUAAUAAAUGUAUUUCUGGUUCCAAAAAGCAUGCAUUACAACUUAGUAGUACUAGAAAUUUUCUAGAAUUAAAUAAGGGCAUAUUAGGGAAAAAAAUGUUGUCCUUCCUUGAUUUGUUAAAAUGAACAAGUAAAUAGGGACAGAUAU	266	spiLA0480-miR11114-5p	UGUCCCUAUUUAGUUGUCCGCUU	6-28	lja-miR11114-5p	5	0	23	23	1
			spiLA0480-miR11114-3p	UGAACAAGUAAAUAGGGACAG	242-262	lja-miR11114-3p	5	0	21	21	1
spiLA0480-MIR9781	AAAUUGAACAAGUAGACACAUGUGUCCUACAUGUCAUCCCACAUGUCAUUUUUUGUCAUACAUGGUGUCCUACGUGUAUUUUGUCAUAUAGAACUCAUGUGUUUAUUUAUUUAAAAG	117	spiLA0480-miR9781-3p	UUUUGUCAUAUAGAACUCAUG	79-99	tae-miR9781	5	0	21	21	1
spiLA0480-MIR8007b-4	ACUGUUAAAUAAAUAAACACAUGAGUCCUAUAUGGCACAAUACAUGUAGGACAACACAUAGGACAAAAAAUGACAUGUAGGACAUAUGUGUCUAUUUGUUCAACUUU	107	spiLA0480-miR8007b-4-3p	CAAAAAAUGACAUGUAGGACAUAU	64-87	stu-miR8007b-3p	6	0	24	24	1
spiLA0480-MIR8020-1	CUCUCCUCAGACCUCACUUAGUAGAAUUUCAUUGAGUAUGUUGUUGUUGUAAAGCAUACUGAAUUAAUGCAAGUACACAAGUUACAACAACAACAUACUUACUGAAAUGCCACAAAAAGGGGUCUAGGAAGG	132	spiLA0480-miR8020-1-5p	AAUUUCAUUGAGUAUGUUGUUGUU	25-48	stu-miR8020	0	0	24	24	1
spiLA0480-MIR5559	GUUGGAAGCACAACGAAAAGGAAAGGCUCAAGUCUCAUAGUGAUUGUUAAACUAUUUGAGGCAAGUGGAUUUCUAAACUCUUGUUAAGCGUAUGAAAUUCGUGUAUUCCUUGUGUGGUGUUGAGAAUGACUUGGAGACUUGUUGCUUAUUUGUUGGUGUUGUAUUCCUUG	170	spiLA0480-miR5559-3p	GACUUGGAGACUUGUUGCUUA	128-148	gma-miR5559	6	0	21	21	2
spiLA0480-MIR8643b	AUACACAUCUGAAUAUUAAGAUCUGCAUUAAUAUCCAUGUGUUUCGAUCUGAAUGCACAUCUACAUAUUAAGAUGUGGUC	80	spiLA0480-miR8643b-3p	ACAUAUUAAGAUGUGGUC	63-80	gra-miR8643b	4	0	18	21	1
spiLA0480-MIR9739	GUUUUCAUGGGUAAGAUAUAGUGUAUAGUGAGUUGAGAAUUUAUUUAUUAUCACGGAUUGGGAUUUCUAGGGACGUUAGUGUGGUUAUUAGGUGAUAGUCUAUUAAAAUCCUUACUCGCUUAGGGAUUUCUAGGGACGUUAGUGAGUGAGUUUAGGGUCUAUGAUAUACCUAUAAUAAUUUGAAUGUCCACAAACUUGCUUACUUAUGAAUAU	213	spiLA0480-miR9739-3p	UUUGAAUGUCCACAAACUUGC	179-199	gma-miR9739	4	0	21	21	1
spiLA0480-MIR8007b-5	CUCCCUCUCUCCCAUUUUAUGUGACACUUUUCGGAUUUCGAGAUUCAAACAAGUCUAUCUUUGACCGUAAAUUUUUCAUAGAUCUUUUAAACAUUUUAAAUUAUCAAUUGUGGGUGACUUAUAGUACUUUUUAUGUAGUUUACAAAUAUAUAAAUUCAUUCAAAAGAAUUAAAGAUUCCAUGCGCAAAUUUUCGGUCAAACUUAAACUACUUGACUCUUGGAAAACGAAAAGUGCCACAUAAAUUGGGACAAAGGGAG	257	spiLA0480-miR8007b-5-5p	AUGUGACACUUUUCGGAUUUCGAG	19-42	stu-miR8007b-5p	2	0	24	24	1
			spiLA0480-miR8007b-5-3p	UGGAAAACGAAAAGUGCCACAUAA	218-241	stu-miR8007b-3p	4	0	24	24	2
spiLA0480-MIR8610	UUGACGGUCACAAACUACGGAUUGUAGGUUCGUCCAUCAAUCAGGACUUAACCAAAUUUUCCUGGGCUGAGAUUUGGGGUUUUUGACCCCAUUGAUGGAUGUGCAGGACGGACUGUGGGUCAGGCUACGAUCCGUCGAUAGCCACCGUUUG	151	spiLA0480-miR8610-3p	UUUUGACCCCAUUGAUGGAUG	81-101	atr-miR8610-2	5	0	21	21	1
spiLA0480-MIR7992-10	CUUCAAUUUUGGGUAUACACAAGUAGACACUUAAACCUGUAUAAACUUGAACAAGUAGACACAUGAGUUCUACGUAGCACAAUACACGUAAAAUACCACAUAUGACGAAAAAUGAUAUACAUGAUGUCAUGUAGAACAUGUGUGUCUAUUUGUUCAACCUUCUAUAAGUUUAAGUGUCUAUUUGUACACACUCAAAGUUGAAG	203	spiLA0480-miR7992-10-5p	UUUGGGUAUACACAAGUAGACACU	8-31	stu-miR7992-5p	6	0	24	24	1
spiLA0480-MIR8027	UGUCUGAGCCAGCUUAUGAGCUGCUUGAAUCGUUUCAAGUAUCAAGUAACUCAGCCAAAUUAUAAGAUAUAAUAAUCCAGGAUAAAAUGCAGGAUUAUUUUAUAGUAUGUUUAGUUGGAGGUAUUAGGUAAUGCUUGGAUUGUUUAUUCCACUAUUUAUACCUUAGUGAUAAUAUAAGUUUAUCUCAUAUACAUGGUGGAAUAACUUAUAAC	272	spiLA0480-miR8027-3p	AUCUCGAGAUAACUUGUUUCCAAC	223-246	stu-miR8027	6	0	24	24	1

spiLA0480-MIR477a-3	GGCAUAAUUAAUCUCGAGAUAACUUGUUUCCAACCAAACGACUCAUAAGUGUCUUAGUUUAUAUAUUCCUGAAUAUCAUAUAUAUGAUUGAUUAAAUUUAUGUUAGUUAUUAUACACUAGAAAUAUUUGAAUCAUGAAUUCUAGUUUGCUAGUAAACGGGAAACAGGGAGAAAACUGCUAGACUAUGCCAUCCCACAGUGGAAAUCGGUAGGUGAGGGAUGCCGUUAGGGGAGUACACAAGGUUGAGGCGCUGAUAAGCAGUAAUUAUCCGCUAAAGUACGAUGCUAGUAGUGACCGGAAAACAUGAUAACGAUACUCUAGUUUAUAAUAAACUAAUAUGAAUUUAAUUAGAUUAUGAUAUGAGGAAGGAAUAACU	318	spiLA0480-miR477a-3-3p	GGAUGCCGUUAGGGGAGUACA	157-177	ptc-miR477a-3p	6	0	21	21	1
spiLA0480-MIR2622-2	AUGCCCUCGGAACUAUUUAAAACUGUAUUUUAAAGAUAUAUAUGUGCCCACGUGGACUUUCAUAUCCACGUGGACACAUAUAUACGUUUAACAUACUCUACUAAAAAUUGUAGGAGGGUGG	122	spiLA0480-miR2622-2-5p	UAUAUGUGCCCACGUGGACUUU	39-60	mtr-miR2622	6	0	22	22	1
spiLA0480-MIR7755	UUCAUAUAAUGAACUGUCUUUAGGAUUAUCCUUUAUAUUUAUAGAGGAUGAAGCUAAUGAAGAGGCUUCGCCAAUCUUUGAAUUAAUCAAAGUUUUACUUCCUAACUGUAUAACAGGAAAGGAAGAGUCAUAUGACGACCUUGUAGAUUGUAAAGAGGACGAUCUUCCCCUUCCUCGUUGAUUUUUUUCCAACGACUACGAACAUGUUGACAUGGCGGAGGGUCAGUACCUCCAUACUGCAAAAUGAAUAACUCUAAUCAUAAAAACAUCCUGAUAUAUC	280	spiLA0480-miR7755-3p	CCUCCAUACUGCAAAAUGAAU	229-249	bdi-miR7755-5p	5	0	21	21	3
spiLA0480-MIR10542-2	AAAACAUACCUUGAACUUUGAUAGAAGAAUCAUAUAUACCCAUAAAUAAUUUAAAAAAAUUAAAAGUACAAAUAUAAACUUAAAACUGUUUUUUUAACUUCCGUUAAAUGAAGGAUAUGUGUGAGCUCAUUUUGUAACGGCAGGGGUAUAUGUGAGCCAUUUGUAUAACGGUAAGGACAUAUAUGAGUCACUUUCAUAACGAGGGGUAUAUCAGCUCCAAGUGACAAAGUUGAGGGGUAUGUCAA	245	spiLA0480-miR10542-2-5p	UAGAAGAAUCAUAUAUACCCAUA	22-44	sly-miR10542	1	0	23	23	1
spiLA0480-MIR477c	CAUAACAAACUAGUUCUUGAGGUUGAGUUAGGCGCAUGUGUCAUAUCUUUACAUGGUCUGAUAUCUGAGACCAUGUAAGGAUAUGACACAUGAGCCCAACUCAUCCCCAAGAGUUAGUUUUUGCC	125	spiLA0480-miR477c-5p	CUAGUUCUUGAGGUUGAGUUA	10-30	csi-miR477c-3p	5	0	21	21	3
spiLA0480-MIR1888b-2	CUGAGAUUUAAUAGGGUUGGGCUAAGGUUUUUGAAGCCUAUUUAAGAAAAGGGCUUUUUAGCCCGACCUGAAUAAGUCUGUU	82	spiLA0480-miR1888b-2-5p	UUGGGCUAAGGUUUUUGAAGC	17-37	ath-miR1888b	4	0	21	21	1
spiLA0480-MIR11036	AUCCAUUAUUCUUCUGAAUUGUUUAUCUUCUGCUUUGAUAUGACAGCUUUAUUGUAUUCAUUCAGGAAUUGUGAGGAGUAUGAAGAUUUGGAUGAAUAUGAGGAAGAAAGCGGUGCAGAGGAAUAUGAGG	129	spiLA0480-miR11036-3p	UUUGGAUGAAUAUGAGGAAGAA	86-107	seu-miR11036	1	0	22	22	1
spiLA0480-MIR3706-2	AAGACACGUGGCACAAUCUUAUCCAUCUAUCCGAUGUCGGGUCAGUGGAUAAGAUUAUGACACAUGUAUU	70	spiLA0480-miR3706-2-3p	UGUCGGGUCAGUGGAUAAGA	35-54	pab-miR3706	5	0	20	20	1
spiLA0480-MIR9471b	UUGAGAUUCAGUUGAUUUCUGAGGUGCUCACUCAGCUAAUAGUUAUUGUUUAAGAAACUCAAUAAUAUUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUGAGUGAGCAUCACUGAAAUCGACAUGAUUCUGAG	147	spiLA0480-miR9471b-5p	GAGGUGCUCACUCAGCUAAUA	21-41	sly-miR9471b-5p	0	0	21	21	1
			spiLA0480-miR9471b-3p	UUGGCUGAGUGAGCAUCACUG	108-128	sly-miR9471b-3p	0	0	21	21	1
spiLA0480-MIR9471a-2	GGUUCUGAGAUUUAGUUGAUUUCUCUGGUGCUUACUCAACUAAUAGUUAUUAUUUAAGAAAAUCAAUAAUAUUGGAAGCAAGGAGAAUGGAGACUAUCAGGAUGAUAACUAUUGGUUGAGCAGCAUUAGAGAAAUUGACAUGAUUCUGAGAGGA	154	spiLA0480-miR9471a-2-5p	CUGGUGCUUACUCAACUAAUA	25-45	sly-miR9471a-5p	3	0	21	21	1
spiLA0480-MIR10199	UUUAUUUUCUCAUAUACCAAGCAUGGUAUGAUUUUAUACAGUUGGCUCGACUACUACAACUGGUAUGAUACUAGAGUUGGGUUAAGUUUUAUUAGAGGAAAUUAAUUUUAAGAAUAUUCAUUUAAAAUAGUGGUCAAAAUUGAUUGUCAACAAUAUAGCUGAGAGACAACGGGUGUGUAUCAUUAGGUCAGACAUGCAUCAUUAUACUUGACAUUGCAUUCCAUUGCAUUGCACGUACUUAUUAUUAGUGAACUUGAUAUCGUGUUUUGCUGAUCUUCUGAUUUCCUCCUGUGGAACUUGUAAUAGAUCAAUAUUGAGCUUGUUAUUGUGAAUAUGUA	338	spiLA0480-miR10199-3p	AUCAAUAUUGAGCUUGUUAUU	307-327	gma-miR10199	6	0	21	21	1
spiLA0480-MIR8006-5	UGCUUUUGGGACAUUGGUACCCCUACCGUCCAAAGACUAGAGCAUAUACCAUUUAUAUUAAUUGACAUACACGUUUCAUAAUUUUAUCCACCAACCUGACAUCAGAUCAAUGGAUAAGAUUGUGUCACGUGUCCCUAUUUAGUCUUUCUUUAGAGUGAAAGAUAUAUACGCUCAAAUUUUUGAAUGACAGGAGCACUAAUGUCCCAAAAAAG	212	spiLA0480-miR8006-5-5p	ACCCCUACCGUCCAAAGACUAGA	19-41	stu-miR8006-3p	5	0	23	23	3
			spiLA0480-miR8006-5-3p	AAAUUUUUGAAUGACAGGAGCACU	174-197	stu-miR8006-5p	6	0	24	24	2
spiLA0480-MIR7997b-1	ACAAUUAAAACAGCAGACUUCAUAUAAUUUAUGCUGCUCGGACUCUUCAAAAAUAUCAAGGGGUGUGUGUCGGAACUCGGAUCCUCCAAAAGUUGUGCAUUUUUGGGGGAUCUGGCAUCGGCGGAACAACAUUUUGAAGAGCCUGAGCAACAUAAAACAUAAUUAUAAAG	190	spiLA0480-miR7997b-1-5p	AUGCUGCUCGGACUCUUCAAA	31-51	stu-miR7997b	0	0	21	21	1

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spiLA0480-MIR11330	UCUCCCUACUGUUAAAACGAAGUUAUUUUUACCCCUACCGUUACUAAUUUCAUCAUUUUAACAUUGGGUUUGAAAUGGGAAAUGUAUAAAUGAUGAAAUUAGUAACGGUAGGGAUAAAAAUAACUUCAUUUUGACGGUAGGGGCA	145	spiLA0480-miR11330-3p	GUAGGGAUAAAAAUAACUUCA	108-128	ppt-miR11330	5	0	21	21	1
spiLA0480-MIR11124	UGAUCUGAAAUUUGGGUAAGAUUCAACAAAACAGGACACAACAUUGUUUGCUUAGAGGCUUCUUUGUCAUCUUGGUGCUUGAUCGGAGCCUGAAGCUCCAAUAGAUGGAGCGGUGGGCAUACCAUUUGUUGAUCCAUUUUCAAGUGGUGGAGGGACUCCCCAUUUGCCUUCAGAUUCAAGUGGUUCAAAAACAUGAACACUACCAUCUGACAGACCUAAUGCAAACUGGUUUGGAUCUUGUGGAUGUGCUGCAACUACGACUGGGUGGAUGUUUGAAUUGCUGCAGAAAAAUGACAAGGUUUUAUGAAAAAUUACAUCAAAUAUCAGAAAU	331	spiLA0480-miR11124-3p	ACUGGUUUGGAUCUUGUGGAUG	225-246	lja-miR11124-5p	5	0	22	22	2
spiLA0480-MIR7997c-11	AUUAUUUUAGUCUAUAUUGCUCGGACUCUUCAAAAAUGUCAAUGGUAGUGUAUUUUUGAAGAAUCUCAGACGGGUGCGGCAUCAAAAGUGAAGAGUCCGUGCAACUAAGAUUUUAAUUGC	120	spiLA0480-miR7997c-11-5p	AUAUUGCUCGGACUCUUCAAAAAU	14-37	stu-miR7997c	0	0	24	24	1
spiLA0480-MIR8182	CAAAUAUGUCGUUCACUCUAAUGGAAGACUAAAAUGUCACAAUCUUAUCCGUCAAUCCGAUAGUGGAUAAGAUUGUGAUACGUGUAUGUUUGUUAGCAUAAAAGAUAUAUACG	113	spiLA0480-miR8182-3p	UUGUGAUACGUGUAUGUUUGUU	73-94	ath-miR8182	6	0	22	22	1
spiLA0480-MIR10538-7	AUUAGGUUGAUAUACGUUACUGUAAGUAACGUUUUACUCUUAAAACGUUAUUUUCAGUAACGUUUUACUCCUAAAACGUUACUGUGAGUAACGUUUUAGGAGUAAAACGUUACUGUGAGUAACAUCUAUCAAUCUGAC	138	spiLA0480-miR10538-7-5p	AGGUUGAUAUACGUUACUGUAAGU	4-27	sly-miR10538	4	0	24	24	1
spiLA0480-MIR11108h	UGUAGGGAGGAUAGUGUUAAAGUAUGACAAAAGUCUCACAUCGGUGAUUAAUGAGAUGGGUGGACUCUUUAUAAGGCUUGGACAAUUCUCCUCCCUUUG	99	spiLA0480-miR11108h-3p	ACAUCGGUGAUUAAUGAGAUGG	38-59	lja-miR11108h-5p	4	0	22	22	1
spiLA0480-MIR1520k-2	UAAAUAGGGACAUGUGGCGCAAUCUUAUCCGUCGACAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACAUGUCCGUUAUAAA	82	spiLA0480-miR1520k-2-3p	GAUAAGAUUAUGACACAUGUCCGU	53-76	gma-miR1520k	6	0	24	24	2
spiLA0480-MIR8006-6	CAUAUAUAUACUCUAGUUUUUGGAUUACAGAGACACCAAUGUCCCAAAAAUAUGACAGAGAGUAUUUACCUAUCAUUUACCAUAAUGACAAUUUUUUUGGUAAAACAAUAAACUCUACAAAAUGUAUAUUUUUAAGGAAAAAGGACAAAUAUAUCUCAAGCUAUCGUAAAUGGUAUGCAGAUACCCUCCGUCAUAUUUUUGGAACAUUAGUGCCCUGCCGUCCAAAAACUAGAGCAAUAUGCC	243	spiLA0480-miR8006-6-5p	UAGUUUUUGGAUUACAGAGACACC	14-37	stu-miR8006-5p	4	0	24	24	1
			spiLA0480-miR8006-6-3p	UGCCCUGCCGUCCAAAAACUAGA	211-233	stu-miR8006-3p	1	0	23	23	1
spiLA0480-MIR164c	UAUUUAAGCUGGAGAAGCAGGGCACAUGCUGAAUUACUUGAAACUUUGACUUUUCAAGAAUUUUGCAUGUGCUCUAGCUCUCCAGCUUAAUUC	93	spiLA0480-miR164c-5p	UGGAGAAGCAGGGCACAUGCU	10-30	fve-miR164c	0	0	21	21	1
			spiLA0480-miR164c-3p	CAUGUGCUCUAGCUCUCCAGC	66-86	bdi-miR164c-3p	4	0	21	21	1
spiLA0480-MIR3513	AUAGGGCUUGAGUUGACACUUGUAAAGCAAGAGAUGGAGCGAGAGAGGGAGAGUGGCGAGCGAGAGUUUGAGGGAGAGAGGUGACUGGCAAACAGUUUGCUAAAAGGUACAAUUAAAUCAAAGUGUAGUUAUAAAAUUUAAUUUAAUUUAUUAGUUUGUUAUUAUAUAUAAUUUUCCGAUAUUAAAAAGCACAAACUCAUUUGAAGGUCAUACCUCAAAAGGCCGGCCCAAAUGCUUUACAGGUGUCAACUCAAGCCCAAA	261	spiLA0480-miR3513-3p	UUAAUUUAUUAGUUUGUUAUU	143-163	ahy-miR3513-5p	4	0	21	21	1
spiLA0480-MIR5272e	UUUCUCUCGCUUUAUACAAAUAGAAACGCAAUUUAUACAAUUCGUUUCUGUUUGUAUAAGCGAUAUAGGUGAGGGUGGCGAGCAAGAUCUGAGAGGGGAUAAAGGAGAGAGGGGAACAAAAAUAUAUGUAUAUAUACAAUUUUUCUCGUUUUAUACAAACACAAACACAUUUUAUACACUUGUGUUUGUAUAAAAGUGAGAGGGA	205	spiLA0480-miR5272e-5p	CAAUUCGUUUCUGUUUGUAUAAGC	38-61	mtr-miR5272e	7	0	24	24	2
spiLA0480-MIR6469	GGCUAAUGUAAGUGCCAUUAACUUUAAGCGAGAGAUUAAUUAGUGGCUGAUUAGGAUUAAUUUAACCAGUGGGCCCCACCACUUAUAAUUAGUGGCUGAUUAGGAUUAAUU	112	spiLA0480-miR6469-3p	UGGCUGAUUAGGAUUAAUUUA	44-64	ptc-miR6469	5	0	21	21	1
spiLA0480-MIR7804-2	CUCGAGUUGAUUUCUCAGAUGGUCACUCGACUAAUAGCUGUAUUAUCUUAGAAAGUCACUUUUUUGGUUGAAGAAAAGCGGAAUCAAGAAGAGAAGUGACUUUUUUUUAUAUAAUGACUAUUAAUCGAGUGAACAUCUGAGCAAUCAAUUCCGU	154	spiLA0480-miR7804-2-3p	AUUAAUCGAGUGAACAUCUGAGC	120-142	rgl-miR7804-3p	6	0	23	23	2
spiLA0480-MIR7997c-12	AGGCUAUGUUGCUCGAACUCUUCAAAAUGUUGUGAAACUUGUAGAAGUGGUGUUUUUGAAGAUUUCGAGCAAUAUAGGUU	80	spiLA0480-miR7997c-12-5p	AUGUUGCUCGAACUCUUCAAAAUG	6-29	stu-miR7997c	4	0	24	24	1
spiLA0480-MIR162b-2	CGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGAUUUUUUGCGUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUCAACCAAC	124	spiLA0480-miR162b-2-5p	UGGAUGCAGAGGUUUAUCGACC	14-35	ath-miR162b-5p	4	0	22	22	1

			spiLA0480-miR162b-2-3p	AUCGAUGAACCGCUGCCUCC	89-108	cas-miR162b	0	0	20	20	1
spiLA0480-MIR6281	UACAUUUAUGUUUGUACUCCCUCUAUCCCUACUUACUUGUCCAUAUUUCUCUUUUAAAUGUCCCCAUUUGCUUGUCCAUUUUGACAAAUUAAGAAAGGAAAAAAUUGUUUUUCCUAUUAUACCCUCAUUUAAACUUAUUGAAAAUUUCUAAGUUUUAAUUCAUCCUUUCUGAAACCAUAUUUAAUAAAGGUAAAACUGUAAUUACUAUGUUAAUUAUUGUUAUCUUAAGAUGUGUCCCUUUUCUAAAGUGGACAACUAAAUAGGGACAGAUGGAGUAUUAAGUGAGAGAGAGAGAGAGUGACGAACAAGAUCAG	315	spiLA0480-miR6281-3p	GUGAGAGAGAGAGAGAGUGAC	283-303	ppe-miR6281	3	0	21	21	1
spiLA0480-MIR5026-2	CCUUUUCGGCCUACGUAGCACUAGCUUGAAACAAAAAGUCAACCGGCGUUGGACCCACAAGAUAGUGUUACGUAGGCCAAAGAAUUUUCCAUCACUUUUUUGCAUAAUUCUUUCAAAUAAACCCAGA	84	spiLA0480-miR5026-2-3p	ACCCACAAGAUAGUGUUACGU	53-73	ath-miR5026	5	0	21	21	1
spiLA0480-MIR8008b-1	AAAGCGACAGACAGGGUCCUUUAGUGCGUCGCGUUUCUGGGUUUUUCAAAAAAAUAAUUUUCAGAAAAGAUGGAUAG	120	spiLA0480-miR8008b-1-5p	AAACCCAGAAAAGCGACAGACAGG	35-58	stu-miR8008b	2	0	24	24	1
spiLA0480-MIR10538-8	AUUAGGUUGAUAUACGUUACUGUAAGUGACGUUUUACUUUUAAAACGUUAUUUUCAGUAACGUUUUAUUACUCCUGUGAGUAACGUAUUACUCCUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGAC	130	spiLA0480-miR10538-8-5p	AGGUUGAUAUACGUUACUGUAAGU	4-27	sly-miR10538	4	0	24	24	1
spiLA0480-MIR8001a-2	UCCUGGGGAUUAGUAUGAAAAUUCAAAAGAAACUUAUUUUCCUGCAAAUUUUCACACUAAUUCCCAUGA	69	spiLA0480-miR8001a-2-5p	UCCUGGGGAUUAGUAUGAAAAUUC	1-24	stu-miR8001a	0	0	24	24	1
spiLA0480-MIR7997b-2	AAGAAACUAUGCUGCUCGGACUCUUCAAAGAUAUUGGUGGGUUUGUGUAGCAUCAGCUAUACAUUUUUGGAGAUCUAACACAGGUGCAGCAACAUCUUUAGAGAGUUCGAGCAACAUAGGUUAGC	125	spiLA0480-miR7997b-2-5p	AUGCUGCUCGGACUCUUCAAA	9-29	stu-miR7997b	0	0	21	21	1
spiLA0480-MIR11563	GAAGAGAUAGUACUAUCUAUACAUUUCAUUAAAAUGAUUUUCUGGGAUUUUGUGGCGAUUGUUGUCCCCGCUAAUGGUCUAAUUCUUUUUGAUGUGAACUCUAGUUGGCAACGCUUAGGUGGAAGAAUUAGUCCCACAUUGUCUUGCCAUGUCACGAAAACUUGGGGAUUAACCUUAGAAUAACGGCAGGGCAUUUUUUAUCCCAAAAUGUAAUGAAGGGUAUAAGUGGUCUAUUUCGCA	239	spiLA0480-miR11563-5p	UUCUGGGAUUUUGUGGCGAUU	40-60	pab-miR11563	5	0	21	21	1
spiLA0480-MIR6228	CAUGACACCUUUAAACUGGUCCAUGGCAGUAAAAAUAAUGCAUGACACGCCUCAUGUGCGUAGUAACAACUCAGACUAGGAAAUGGGUCAAAAUUGUCCAUUUACAAAGAAAUUAAAUAGUUCUGUGGGGUGAUAGAACACUUUAAAAAUUAAGGUGUCUUAAUACAAAUACAGGACAACUUUGAUGGUGUCUUU	195	spiLA0480-miR6228-5p	AUGGCAGUAAAAAUAAUGCAUGAC	23-46	sbi-miR6228-3p	7	0	24	24	2
spiLA0480-MIR475b	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGUCUAUGGCUUUGCUCUUAAAGUCCCCAUUGAUUUAGGAGAGUGGACGGGGCAGACUGACUUCACUA	99	spiLA0480-miR475b-3p	UUAAAGUCCCCAUUGAUUUAG	49-69	ptc-miR475b-3p	3	0	21	21	1
spiLA0480-MIR8005c	UGUACCUUACAAAUCAAAAUCUUCUUUUUAAACUCAUUCAAAUUCUCAUCCUCAAAUUGGUUGGCCUUGAUCUCUUUAAUGAAUUUGGCCCUCAAUUCAAUACUAGAUAGUUUUAGGUUUAGGGUUUAGGAUUUAGGGUUUGGAUAUAGGGUUUAGAGUUUAGGGUUUUGAGUUUAGGGUUUU	183	spiLA0480-miR8005c-3p	UUUAGAGUUUAGGGUUUUGAGUUU	152-175	stu-miR8005c	2	0	24	24	1
spiLA0480-MIR1062	UGACCACACGUGGGGUUUGGGGAGGGUGGUGUGUACGCAAACCUUGCCCCUAACUUAUGCAGGUAGAGUUAAGGUAUGCGUACAUCCUACCCUCCCCAGACCCUAUUUGUGGGAU	115	spiLA0480-miR1062-5p	GACCACACGUGGGGUUUGGGGA	2-23	ppt-miR1062	7	0	22	22	3
spiLA0480-MIR7992-11	UUAUGCCCUUUAACUUUGAGUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAACAAAUAGACACACAUGUCCUACAUGUCAUCCUACAUGUCAUUUUUUGUCCUACGUGGUGUUUUACGUGUAUUGUGUCAUGUAUGACUCAUGUGUUUAUUUAUUUAAAAGCUGGAUAGUAAAGUGUUUAUUUGUGCAUUAUGACAGUUGGAGGUCAAAG	216	spiLA0480-miR7992-11-5p	UUUGAGUGUGCACAAGUAGACACU	15-38	stu-miR7992-5p	5	0	24	24	1
spiLA0480-MIR8005b-1	GUGAACUGAAAAUUGAAAAUAUUAAAUCGAGUUGAGAUAGAAGUCGGGUUGGGUAUUGACCCACCCAAGUUUAAUUUGGGCUCGAAUGGACAUAAAAACGGGUUGGAUCUUGACCCGUCAAUUUGAUCCGAUUAAUCUAACAUACCACACAUAUUGAUAUUUAACUUUUAUAAUCACAAUUUGAAUUUUAGCUCGAAAUUAUAUAUAUAUUAGCUUAUGAUUUAAGUUUUUCUUUUUCAUUUUGA	245	spiLA0480-miR8005b-1-5p	ACUGAAAAUUGAAAAUAUUAAAUC	5-28	stu-miR8005b-5p	6	0	24	24	1
spiLA0480-MIR2622-3	UAUCAAUCUAGCAAGGAACCAGAUCCUUGUUAUUGAAACUGCUGACAGUGAGAUGAAUGACAAACUCAGUGUGAGGUAUAUUUGUGUGCUAUCAUCAAAAAGGGAAAAAAUGUUAUAUUCUAGGUGUUUUGAUGAUCCUCACAAAUGCAAGGACCUGGUCCCUGUCAGAGUGCUC	175	spiLA0480-miR2622-3-3p	UUUGUGUGCUAUCAUCAAAAAG	81-102	mtr-miR2622	7	0	22	22	1
spiLA0480-MIR8562c	GGCACAAGGAUUAGUUGAGGUGUCUAAAUGAAUUAUGCGGACAACUUUGAGUGGCUGCAGAUGACUUAAGCCUAAGAAUAAAAUGAAAUUUGUAGUAAAAGUGGAUGCCACGUAAGCUUCACAUUAUG	269	spiLA0480-miR8562c-5p	UAAGAAUAAAAUGAAAUUUGUAGU	73-96	atr-miR8562c	6	0	24	24	1

spiLA0480-MIR2875	GCAAAUUAAUGACCAAAGUAAAAUUAUGGGAGAAAGGAUAAAA AUUACCUCUCAACUUGGUUUAUAGUUGCCAUAAGUCAUAUGU GAUCCCUUUAAAUUAUCCGUAUAAUUUAUUUAGACAUUUUAAU UAGUACUAGUACC	202	spiLA0480-miR2875-3p	UUGUUCAGUUAUAUACAGUUUUA A	149-172	osa-miR2875	6	0	24	24	2
spiLA0480-MIR7992-12	CGUUAAUUUUAGGUAUGGACAAGUAAACAUUUAAACUUGUAUA AAAUUGAACAAAUAGACACAUUUGUCCUACAUGACACCCUACA UGAAAAUUGUGUCCUACGCGGCGUCCGAUACAUAUUAUGUCA UGUAGAACACGUGUGUUUACUUGUUCAGUUAUAUACAGUUUU AAGUGCCUACUUGUGUACACUCAAAGUUAGAG	244	spiLA0480-miR7992-12-5p	UUUGAGUGUGCACAAGUAGACAC U	24-47	stu-miR7992-5p	5	0	24	24	1
spiLA0480-MIR319a-3	AAUUGGUAUUUACGUACUCAAACUUUGAGUGUGCACAAGUAG ACACUUAAAAACUUGUAUAAAAUUGAAUAAUUAAAUGCACACG UCUUAUGUGACAUAUUACACGUAGGAUACCACAUGUAUGAUG CAAAUUGUCCACAUAAGACGUCAUGUAAGAGGUAUAUAUGUAU CUGUUUGUUCAAUUUUGAACAAGUUUGAAUGACUACUUAUAUA CAUCUGAAUUUAAAGGACAUAGAUAUCACUC	174	spiLA0480-miR319a-3-5p	AGAGCUUUCUUUAGUCCACAC	3-23	stu-miR319a-5p	2	0	21	21	1
	AGAGAGCUUUCUUUAGUCCACACAUAGGGAACUAUAGGGUUC AAUUUGCUGCCGACUCAUUCAUCCAAAUGUUGAGGUCUUGAU AAUCGAAUGCCACCUCAGCAACUGAGUGAAUGAAGCGGGAGU ACAAGUUGAGUCUUGAGCUUCCUGUACUUGGACUGAAGGGAG CUCCCU		spiLA0480-miR319a-3-3p	UUGGACUGAAGGGAGCUCCCU	154-174	aof-miR319a	0	0	21	21	1
spiLA0480-MIR7997c-13	CUUCUAUGUUGCUCAGACUCUUCAAAAAUGUCGCCAUGUGCA UGUUGGAUCCUUCAAAAGCAGUACGUCUUUUUAUGGAUACCA CAGGUGUGGCGACAUUAUUGGAGAGUCCGAGCAACAUAGCUG UUCUUUUUGGUGGCAAUUGGUUCGAAUUUGCCACGCGAUAUA	126	spiLA0480-miR7997c-13-5p	AUGUUGCUCAGACUCUUCAAAAA U	6-29	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR8001b-3	UCUAGUAUACAUGGUAUAUUCAAACUAAUUCCCACGAAAAAAU C	86	spiLA0480-miR8001b-3-3p	GUAUAUUCAAACUAAUUCCCACG A	56-79	stu-miR8001b-3p	6	0	24	24	1
spiLA0480-MIR8738b	UGUUCACUCUCCUUUUUUGUUUAAACUCACAUAUUAUUUAUUU UAGGAUAAAUUUGAGAGUGUUAACUUUAAUGAUCACCAUGAUC AUACAUUUGGAUGGAUGAAUGAGUUAUGGAACAAAUUGAGAG GAUACUUGUAUGCUACUUAUGUGAAGAAUAAGCCUAUUAUUCC AGCUCUUAAGAAUAAUCCAAAGGGAGUAGAAACAAGGAAUGGG AGUGAUUA	222	spiLA0480-miR8738b-5p	GUUAACUUUAAUGAUCACCAUGA	62-84	gra-miR8738b	7	0	23	23	1
spiLA0480-MIR812f	AAUAUCGUAAUGGUAAGUAAAUACCCUCUGUCACACUUUUGGA AUAUUAAGUCUAUGAUGUUUAAAAAUUAGAGUUAUAUGUCCGU CAUUUUAACGGAAGAUUAAAUAUUGACACGUGCCGCAAUUUUA UUUAUCGCUCUGAUGUCGGAUCAGUGGAUAAGAUUAUGAUAC GUGAAUGUCCGUUAGUAUAUAAAGGGUAUAUAGGCUCUAGUU UUUGAACAAUAGGGAACCUAUGUCCCAAAAGUAUGACGGAGG UUAUCUGCAUAACAUUUAUGAUGGU	280	spiLA0480-miR812f-5p	ACGGAAGAUUAAAUAUUGACACG U	94-117	osa-miR812f	5	0	24	24	1
spiLA0480-MIR1046-3	GGGGUCGUUUGGUAGAGUGUAUAAAAGUAAUGCUAAAUAUAG UGUAUUAGCAAUACUGGCAUUAGUAAUUUUUGCAUUAGUUAUA CUUGCAUUAGUUGUACAUACAUUAUUUCUUAUGCAUUGUUUG GUUUGGUGUAUUAAAAUUAACAUGUAUUGUACAAAAGUAUCCU UCACAUUAUGGUGAAAAAGAUGAAAAAGUGUUUUUGAGGGGU GUUUGUAUCUUUUAAGUGCUAAUGCAUGCAUUAAAUCCCUUU GCAUUACUAAUACCUAGAAAUCCAUGGUAUUAGUAAUGUACUC UCCAAUACACAAU	310	spiLA0480-miR1046-3-3p	UGGUGAAAAAGAUGAAAAAGU	179-199	ppt-miR1046-3p	3	0	21	21	1
spiLA0480-MIR7997c-14	AGAAGCUAUGUUUCUCGGACUCUCCAAAAAUGCUACAUAAUUC ACUAUUUUUGAUGGAUCCGACAUGCAACCCAUAGUGUUUUUG AAGAGUUCGAGAAGCAUAGCUGAG	109	spiLA0480-miR7997c-14-5p	AUGUUUCUCGGACUCUCCAAAAA U	8-31	stu-miR7997c	3	0	24	24	1
spiLA0480-MIR11553-2	GAUUUAUGGGCCGGAUUAGUUGUUUAUGAGUUCGAAUAUCUU UCCAUUUUCAUAUAAAUGUCAUGUUUUAAGGUCAAAAUUACAU GUCAAUUCCAUGUGGCAUUUAAAGAAAUGAAAAAUGAGUUGGA UAUAUCCAACAUGACAACUAACGCUCAUAAGGG	161	spiLA0480-miR11553-2-3p	GAAAAAUGAGUUGGAUAUAUC	114-134	pab-miR11553	6	0	21	21	3
spiLA0480-MIR7997b-3	AUGGCAUGCUGCUCGGACUCUUCAAAAAUGUUGCUAGGUCUG UGUUGGAUCCUCCAAAAGUAGUGCAUAUUUGAAGGAUCCGAC AUGAGUGCGGCAACAUUGUUGGAGAGUCUGAGCAACAUAGCA GA	128	spiLA0480-miR7997b-3-5p	AUGCUGCUCGGACUCUUCAAA	6-26	stu-miR7997b	0	0	21	21	1
spiLA0480-MIR399b-2	UGAUGAAGCGGAAGCAUGAGAAAGGAAGUCGUUGGUGAAUGA AAAUAAGGGAAAUAGUGAUAGGGCUACUCUCUAUUGGCAUGC GUUAAUAUAUGUACAGUGACUCCAAUUCACUGUAUCGCAUAUU UUAACCGAUACGCCAAAGGAGAGCUGCCCUGCUACUGUCUCU GCUUAAUAUAAUAACUCAAAGGUCCAUUCUUAAUACUCCGAUG CAGAA	217	spiLA0480-miR399b-2-5p	GGGCUACUCUCUAUUGGCAUG	63-83	sly-miR399b	0	0	21	21	1

			spiLA0480-miR399b-2-3p	CGCCAAAGGAGAGCUGCCCUG	138-158	nta-miR399b	0	0	21	21	1
spiLA0480-MIR11156	UUCCAUUAAGAUUAAGAGGUCUGAAUCUGAAUACACAUCUGAUAUUAAGAGUUGCAGUAAGAUUGGAUGUUUCAAUCUGAAUACACAUCUGAAUAUUAAGAUGUAGUCUCCAAAUCAGAGCACUAAAUAUAAUGUUG	137	spiLA0480-miR11156-3p	AAGAUUGGAUGUUUCAAUCUGAAU	59-82	lja-miR11156-5p	7	0	24	24	1
spiLA0480-MIR6116	CGCCUCUGUGUGCAUUCAACAUUAGAGGAUUCAUCAUUAUUGUUAGAAAAUGAUGGAUCCUCUAAUACUAAAUUCACAUCAGAGAUU	87	spiLA0480-miR6116-3p	CAUUAUUGUUAGAAAAUGAUG	35-55	cca-miR6116-5p	5	0	21	21	1
spiLA0480-MIR7984b	UACGAUACCAAACGUUGGAAAUGACUUUUUACCCAUGCACUAUUUAAAAGUCCCACGUGGACAUAAAAAAUAUUGCAUAACUAUAAAUAGUAAUAUGUCCAGGUGGACACAUAUAUACCUUUAAAAUAUACUAUUAAUAGUUGAGGAGGGUAAAAGCUCCUCCAUAAACUUUGGUAUCAUA	181	spiLA0480-miR7984b-5p	AUACCAAACGUUGGAAAUGACUUU	5-28	stu-miR7984b-5p	3	0	24	24	1
			spiLA0480-miR7984b-3p	GCUCCUCCAUAAACUUUGGUAUCA	156-179	stu-miR7984b-3p	5	0	24	24	1
spiLA0480-MIR7981-8	CUUAAUUAAACUAAGGUCCUAUUAUCACACCGAACUCAAUAAUUUUGUAAUUUUGUACACCUUUUAUUGGCUUACGUGACAUCCAAACAUCUUCCACACGUCUUAACUAUAUGGAGUCACAGAGUGUGCAACGUAAGCCAAAAUGUGUAUAAAAUUACAAAAGAAAAUGAGUUCAACGGGUUAAUAGGAUCUUAGUUUAGUUAAG	205	spiLA0480-miR7981-8-5p	CUUAAUUAAACUAAGGUCCUAUUA	1-24	stu-miR7981-5p	2	0	24	24	2
			spiLA0480-miR7981-8-3p	AUAGGAUCUUAGUUUAGUUAAG	184-205	stu-miR7981-3p	2	0	22	24	1
spiLA0480-MIR156b-5	UAUUGUUGACAGAAGAUAGAGAGCACGAAUAAUGAGGUGCUAAUUGGAAGCUGCACCUUAAUUCUUUGUGCUCUCUAUUCUUCUGUCAUCAUCU	94	spiLA0480-miR156b-5-5p	UUGACAGAAGAUAGAGAGCAC	6-26	aof-miR156b	0	0	21	21	1
			spiLA0480-miR156b-5-3p	GCUCUCUAUUCUUCUGUCAUC	70-90	vca-miR156b-3p	1	0	21	21	1
spiLA0480-MIR823	CAUCUCCUCAUUAGGUAUUAUGUUCAUCCUCUUGUAACCAGAUGAUUCAAUACAAAGUGUAUAUGUAUAAUUCUGAAUGUACGUACAAUACUUUUAGCUUAAAGACACUUCCUUGAGGAAAUGCAGAUAUUGAAGUAGAUGUGUGAUCAUAUAGCAACAAUAUGAUUAGAAAUGAAGAUAUCUGAAAUAAGGUGGGACUGAUCUCCACGUUGGAGUGAGACUGAGAUGAUUUGGACAUGUGAAUAGGAGAUGCAUAGACGCACCAAUGAGGAGGUG	276	spiLA0480-miR823-3p	UAGAUGUGUGAUCAUAUAGCAA	136-157	aly-miR823-3p	5	0	22	22	1
spiLA0480-MIR8006-7	CUAAACAAAUGUGAACACAUCAUUGGUCCGAUGUCGGGUCGGUGGAUAAGAUUAUGACACGUGUAUAUCCGUUAGUAUAAAGGGUAUAUAUGCUCUAGUUUUUGGAUGACAGGGGCACCUAUGUCACAAAAGCAUGAUGGAGGGUAUUAUAAUACCAUUAAUGAUAGUUCGGGGGUAUAUUUGUCCUUUUUCCCUAUUUAUAACGAGUGAGUGCUCUUUACAUUUGUUACG	231	spiLA0480-miR8006-7-3p	UAGUUUUUGGAUGACAGGGGCACC	96-119	stu-miR8006-5p	1	0	24	24	1
spiLA0480-MIR8748	CUACAUUUGAAGAACAGAGAGUAACAUAGAGAUGGAUUGAAGUGUUUAUUCUCUAUUUUACUCUCCAAAUAUAGAGAAUAGAGAGUAAAUAGAGGUGGGGUGGAGAUGGUCAAAAUGAUAAUGAUUAGUAAUUAAAUCGAAGACUAUGAAGGGAAAUUGGACUCCCUUGGACUAUCUAAUUGUCCUAUUCUUCAAUUGGUC	201	spiLA0480-miR8748-3p	GGGGUGGAGAUGGUCAAAAUGAUA	97-120	gra-miR8748	6	0	24	24	3
spiLA0480-MIR171c-3	CUAACGAGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCACGUAUU	92	spiLA0480-miR171c-3-5p	AGAUAUUGGUGCGGUUCAAUU	7-27	cas-miR171c-5p	1	0	21	21	1
			spiLA0480-miR171c-3-3p	UUGAGCCGUGCCAAUAUCACG	68-88	cas-miR171c-3p	0	0	21	21	1
spiLA0480-MIR5368	CUAACCUUGUGUCAGGACCUACGGGCCAAGGGACAGUCUCAGGUAGACAGUUUCUAUGGGGCGUAGGCCUCCCAAAAGGUAAC	83	spiLA0480-miR5368-3p	GGACAGUCUCAGGUAGACA	31-49	gma-miR5368	0	0	19	19	1
spiLA0480-MIR8639e-1	CAACUACGCCCUUCAACUUUGAAUGUGCACAAAUAAACACGUAAACUUGUAUAAAAUUGAACAAGUAGACGCAAGUGCCCUACAUGGCAUAAUACACGUUGGCAUGUAGGACACAAAAUUGUCAUGUAGGAUGAAUGUGUAUAUUUGCUCAAUUUUAUAGAAGUUUAAGUACCUACUUGUGCACACCCAAAGUUAAAGGUCAUAGUUA	208	spiLA0480-miR8639e-1-5p	UAAACUUGUAUAAAAUUGAACAAG	42-65	gra-miR8639e	6	0	24	24	1
spiLA0480-MIR8668-1	UGGUCGCCUUGGCUUACAGAAACAUUUUGGAAUGAUGACUAUAACGAGUGGGAUAAUCUGAGAAAUGUUUUUGUACAAGGAGAUAU	86	spiLA0480-miR8668-1-5p	UUUUGGAAUGAUGACUAUAA	25-44	gra-miR8668	4	0	20	20	1
spiLA0480-MIR9555b	UAAAAUUUGCAUUUCUAUACAAUUGAAUCGAAGUAAAAUAUUUGUAAAUUGUAUAAUUAAGUGUAUAGCACGAAGAUGUAUGUUUUUGCAUGUGUAUAUAUAAUUUUCUCUCGCUUUAUACAAAACAGAAACACAAUAUAUACAAUUCUGUUAUAUAAAGCGAGAGAGGCGAACAGAGGGAGAAUGGCGAGCGAGAAUGCGAGAGUUGCGAGCG	336	spiLA0480-miR9555b-3p	UUAUUAAUUUGCUAUUAUAUA	308-328	bra-miR9555b-3p	4	0	21	21	1

spiLA0480-MIR8130	AGAGUUUCGGGAGAGAGGCGACUGACAAACUUUGGCAAAUGUUUGCUUUGGUGCACAAUUAAAUCAAACAGUAACUACUCCAUUUAUUUUAGGUUAUUAAUUUGCUAUUAUAUACAAUUAUCACAUCACAAAUGCAGAUUAUGCCAUCACUGGAGCUGGUAGAAAAGGCAUUAUUGUUUCGCUGAUCAACAUCAUGUAAUGGACCUGAUGGGGUUGUAUAUACAUAAGAGAACCCUAGGCCCGUUUAUGUGGAGCCACCACAAACAAGGAUUUCCUUUUAAUUUAUUUAUUUCAAAAUUUAGUCUUUACCUUUAAUGGAAAGUUGUGACUUUUAUGAAUUGCUGUAACAUUUAUGAAAGGUUGUGACAUUUUUAAAGUGUUGUGACUUUUCCAAAAAGUUAUGGCCUUUCCAGUAAAGCACAAUAAGCAUUUGUGACAU	317	spiLA0480-miR8130-3p	CCUUUCCAGUAAAGCACAAUA	283-303	ppe-miR8130-3p	6	0	21	21	1
spiLA0480-MIR1520f	CUACUACCAAGAGAAGGGUUACAAGAAGGUUCUCUUACCUUGCUCUUGUCACGUUUCUUGGAAGGAU	67	spiLA0480-miR1520f-3p	CUUGUCACGUUUCUUGGAAGGAU	45-67	gma-miR1520f-5p	7	0	23	24	2
spiLA0480-MIR1128-7	UACUACUCCCUCCAUCCCAAUUUAAGUGUCUUCCCAUUUAGUCUGUCCCAGCAAGACUGCCUCUUUCAAUAUUUAAUAAGUUCUCCAAUUCCAACAUUAUACAUGGAAAGUUUUGAGACCACAAGAUUUAAAGGACUACACACAUCUUUAAUUGAAGACCACAAGAUUCAAAGUCUCCCUUUAUUUCUUAAACUUUGUGUCCAAUCGAACUAAAACACUUAAAUUGGGACGGAGGGAGUAAUU	243	spiLA0480-miR1128-7-5p	UACUACUCCCUCCAUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1
spiLA0480-MIR417	AACAAAAACACUUAAAUUGUUCCAAUUUGUUGAGUUUCAUAGCUAAACUAUCAAGUGUGUGAGUUUUCUGUCUGUACUAGUAUCAAAUGCUUCGCGAAGCAAACCUGAUUGUUCAGGUAGGAAAAGUGAACAACUUGUAGUUCAUUUGUGUUUCCGUAAACAUUUGGUGAUAGUACAGGUAGGAAACUCACACACCUGAUAGUUCAUGUAUGAAACUCAAAAAUGAAAAAAUGUAAUGAAUUUGUU	248	spiLA0480-miR417-3p	AAAUGUAAUGAAUUUGUU	231-248	osa-miR417	2	0	18	21	2
spiLA0480-MIR8567	AUGCACUGUCUCAGAUGUAAAUCUUCAUGUCGUCAAUGUCUAUGUUGUUCUACUCCAAAAAUGCACUACUUUUUGGAGGAUAUAGACUUUGGCGACCUGAAGAUUUACAUUUGAGACAGUGUUU	124	spiLA0480-miR8567-3p	CAAAAAUGCACUACUUUUUGGAGG	56-79	atr-miR8567	7	0	24	24	3
spiLA0480-MIR7983-4	UGGCACUAUGACAAAAAUGAUCAUUAGCGACAAUUAAUUCUUAAUUGCUAUUAAAUAUGUAUUUUUAGCGGCAAUUGUCACUCUUUGUAUAUGUCCCUAAAGCCUUUAGCGACAUUGGUUCUUAUGAAUCUUAACUAAUGCCGGUAAAAACUUUAACACUCUUUAUUAGUGUCAAUAUUUAAUGUCGCUAAAAGUUAUUUUUGUUGUAGUGUGA	214	spiLA0480-miR7983-4-3p	ACUAAUGCCGGUAAAAACUUUAAC	134-157	stu-miR7983-3p	1	0	24	24	1
spiLA0480-MIR2873b	CCUACGGGACGGGACAUCCUGAAUCUGGACACGAAACUAAAUGGAAUCGAGGUUUGGUACCGGUGUACCGAUACCUAUUUCAUCCCGGUUUAUUCCGAUUCUGGUUCGGUCUGGUCCGGUUUG	123	spiLA0480-miR2873b-5p	AUGGAAUCGAGGUUUGGUACC	41-61	osa-miR2873b	6	0	21	21	2
spiLA0480-MIR7985-2	CUACUAUCCUUCGGGGUGGCCCAGUGGUUUGGGCUUGGGACUUCCAUGUUGGAGGUCUCAAGUUUGAAACGGGUUUUGACUUCUGGGUCGAGCUUGUUGCUCCGGGCUUGCCUAGUGCGGGUUACCUCUCCUAUGAGGUUAGCGAGCUUAUCGCAUAGGAGGGGGUUUUUACCCUGUGCGCACCCAAAGGGUAGCGG	197	spiLA0480-miR7985-2-3p	CGGGCUUGCCUAGUGCGGGUUACC	103-126	stu-miR7985	2	0	24	24	1
spiLA0480-MIR171a-6	CUAUGAAACAGUAACUUUGAUAUUGGCCUGGUUCACUCAGACAACAAAAUGUAAACUAUAUUUGAAUGGUUGAGUUUUCGUUUUUCGUUUGAUUGAGCCGUGCCAAUAUCUCAGUUUCUCUUUCACUU	128	spiLA0480-miR171a-6-5p	UAUUGGCCUGGUUCACUCAGA	21-41	cas-miR171a-5p	0	0	21	21	1
			spiLA0480-miR171a-6-3p	UGAUUGAGCCGUGCCAAUAUC	90-110	aof-miR171a	0	0	21	21	1
spiLA0480-MIR1027c	UGUGCCACAUCCAUCAUUGCUCUUGCAUACAUCUCUUAGAGAAGAUAGGUGGAUGCACCAGGUAUCCCUUCAAUUACAUAUCAUUUCUAUCUUCUCUAGGAGAUGUAUGCAAGAGCAAUGAUGGAUGUGGCGCC	134	spiLA0480-miR1027c-3p	UUUCUAUCUUCUCUAGGAGAU	84-104	ppt-miR1027c	6	0	21	21	1
spiLA0480-MIR1521b	AAUUAAUGAUAUACAAAUAUUUUUCGUCAUACUUUGGGAUAUUGGUGCUCUUGUCGUUAAAAAAUUAAAAUGUAUAUACCCUUUAUACUAAGAGACAUACACAUGUCAUAAUCUUAUCUACUGAUUUGAUUUUUAAUCAACGGAUAACGUGUUCCUUUUUAGUCUUCCGUUACAGUUAGAGUAAAGGGCAUAUAUGCUCAAGUUUUGGAACGGAAAGGACACCAAUGUCCCAAAAGUAUGACGAAGGUAUCUGCAUACCAUGUACGA	267	spiLA0480-miR1521b-5p	GACAUACACAUGUCAUAAUCUUA	94-116	gma-miR1521b	5	0	23	23	1
spiLA0480-MIR8001b-4	UCCCACUACAAGAAAACUGUGAAUUACAUGGGGAUUUUUCGAGGAAUUAGUAUGAAAAUUUGCAGGAAUAUAAGUUUUCUGCGAAUUUUCAUACUAAUCCCCAGAAAAAUGCCCAUAUAAUUCAUAGUUUUCUUGUAGUGCAC	143	spiLA0480-miR8001b-4-3p	GAAUUUUCAUACUAAUCCCCAGAA	83-106	stu-miR8001b-3p	3	0	24	24	1
spiLA0480-MIR10203	CUCCGUGAAAAGUUGCGACUUUUAUGAAGAGUUGCGACUUUCAUAAAGAAUUGCGACUUGUAUGAAAAGUUGUGACUUUAUGAAAUAUUGUGUUCUUUUAGAAGGAUUGUAACUUUUCCAAAGAGU	143	spiLA0480-miR10203-3p	GUGUUCUUUUAGAAGGAUUGUAAC	91-114	vca-miR10203-5p	7	0	24	24	2

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spiLA0480-MIR7130	UUUGUUGGGACUCUACAAGAUGCGUUCAAUUUGAGUUGGGAA UCUACAAAUUGUGUUCAACUCAAAUUAGGAUUCUUAGAGUCUA CUCAACCCC	94	spiLA0480-miR7130-3p	GUUGGGAAUCUACAAAUUGUGUU C	35-58	cme-miR7130	7	0	24	24	1
spiLA0480-MIR5293-1	CCAUGAUAAUGUUGCAGAAUGGGUUCGAGCCAAUUUUCAGAU UGGGAAGAGAUUCACAAGGAAUUAUUGGGCCUGUUCCGGUCC UUCCUAAAGAGUCCAAAUAUGGUUUGGGGUAUACCCCCACAG AUGACGAUAUGAAGAUGAAGAAGAAAAAGGAUCAAGAGUUGGC UAAACCGAUCCUGCAUCUGUAUCAAUC	196	spiLA0480-miR5293-1-3p	GAUGAAGAAGAAAAAGGAUCAAG A	140-163	mtr-miR5293	5	0	24	24	1
spiLA0480-MIR828b	AUUUACAUUCACUUCUUUGGGAAAGCCUCUUGCUCAAAUGAG UAUUCCAACAAAUGUCUAAUUGACAUACUUUUGAGAUACUCAU UUGGGUAAGAAGUUUUACCAGGAAGGUUGUACUU	119	spiLA0480-miR828b-5p	UCUUGCUCAAAUGAGUAUUCCA	28-49	mes-miR828b	0	0	22	22	1
			spiLA0480-miR828b-3p	UCAUUUGGGUAAGAAGUUUUA	82-102	ptc-miR828b-3p	5	0	21	21	1
spiLA0480-MIR8008b-2	UUUGUCCGUCGCUUUUUUGCUUUAUUUAUUUCAAAUAAACCC AGAAAAGCGACGGACAAGGUUCUUUGGUCCGUCACUUCUCUA GGUAUUUUAAAAAAUUAAUUUCAAGGAAACCGACAGACAUUGU CCUUUAGUCGUCCCUCGCUUUUCUGGAAUUUUCAAAAUAUAAA UUUAAAGAAAGGCGACGGACUGC	193	spiLA0480-miR8008b-2-5p	AAACCCAGAAAAGCGACGGACAA G	37-60	stu-miR8008b	2	0	24	24	1
spiLA0480-MIR1520l-1	AAGACUAAACAUGGACACGUGACGCGAUCUUAUCCGUCAAUAA AUGUCGGAUUGGUGGAUAAGAUUAUGACACGUGUAUGUCCGU UAGUAUA	92	spiLA0480-miR1520l-1-3p	GAUAAGAUUAUGACACGUGUAUG U	58-81	gma-miR1520l	7	0	24	24	2
spiLA0480-MIR10197	UGGUUCAAUUUUUAUGUGAACUUACUUUCGUUUAAUGGUUAA ACAAAAGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGC AUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAUUUCU UAAUUUUGUUUUUCUGUUUUCGGUCAGAUUUUUAUUUUUUCA UGUUGGUUAAAAUUUUAAAAAUAUUUUUUCUUUAGAAAAAGUA AGUUACCUAAAAAAUGAAUUA	232	spiLA0480-miR10197-3p	AUUUUAAAAAUAUUUUUUCUU	180-200	gma-miR10197	5	0	21	21	1
spiLA0480-MIR395a-3	UGUUUGAUGCCUUGCUGAAGUGUUUGGGGGAACUCUUGGAC UCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAGGAGUCC UGGCUAUGGAUGAUGAACAUGAUAGUUCAUGUUUAAAUCUAU UAAGGUGAUCCCUAGAGUUCACUUGACCACUUCAUGAGGGCU UAAUUU	174	spiLA0480-miR395a-3-5p	UGAAGUGUUUGGGGGAACUCU	16-36	aof-miR395a	0	0	21	21	1
spiLA0480-MIR11028	UCCCUCCGUUUCAAUUUGUUUGUUUUACUUUUCUUGUUGGUC UGUUUCAAAAAGAAUGUUUUUUCCCCUUUUUGACGAUACAUAG AGCAUAAUAUCAUAAGAUUCAAAUGUUUUAUAUACUUUCUCAA ACUCUGUGUCAAGUCAAAACCAGACAAACAAAUUGAAAUGGAG UGU	174	spiLA0480-miR11028-3p	CAAAUGUUUUAUAUACUUUCUCA	105-127	seu-miR11028	6	0	23	23	3
spiLA0480-MIR171t	AAUCCGGGCUCUGCAACUAUGUUGAACUGCGUGACUAUCUCA UUUAAAAGGUUUAGAUGAGAUAGUCAGACACUUCAACAUUGUA UCAAGCCAGGCCC	98	spiLA0480-miR171t-5p	UUGAACUGCGUGACUAUCUCA	22-42	gma-miR171t	4	0	21	21	1
spiLA0480-MIR5014a-7	UAAUGCAUAAAUAGACACUUUAACUAUCCAACUUUUAAAUAAA UAAACGCAUGAGUCCCACAUGGCACAAACCACGUAGGACAAAA AAUGACAUGUAGGACAUAUGUGUCUAUUUGUUCAACUUUAUAC AAGUUUAAGUGUCUACUUGUGCACAC	155	spiLA0480-miR5014a-7-3p	UUAUACAAGUUUAAGUGUCUA	124-144	ath-miR5014a-3p	5	0	21	21	1
spiLA0480-MIR1514a	AAGGGUAUAAUUAUAUAUUAUGCCUAUUACAUAAUGCACACGG GACACCACAUAGAACACAGAUUGUCAUGUAGGAUGUCAUGUA GAACAUGUGUGUCUAUUUGUUCAAUUUUAUACAAAUUUGAGA GUCUACUUAUGCAUUUUCAAAAUAGGAGAGCAUAAAUAUUAAA UGAGACCAAGUUAGAAGGCAUAUUUAUAUAUUAUGCCUAA	210	spiLA0480-miR1514a-5p	AUGCCUAUUACAUAAUGCACA	20-40	gma-miR1514a-3p	5	0	21	21	1
			spiLA0480-miR1514a-3p	UGCAUUUUCAAAAUAGGAGAGC	137-158	pvu-miR1514a	7	0	22	22	1
spiLA0480-MIR8739-4	AAGACUAAAUAGGGACACGUGAUGUGAUCUUAUCCGUUAAGU CGGUGGAUAAGAUUAUGACACGUGUACGUUCAUUAGUAUA	82	spiLA0480-miR8739-4-5p	AGACUAAAUAGGGACACGUGAUG U	2-25	gra-miR8739	6	0	24	24	3
spiLA0480-MIR11103c-1	UGUGGAGUAUUCGUGGUCUUGAUCUCUUUGUGGAUUUUUCGA GAUGCCUUUUAAGGGAAUUUAAUAGCCUUUAUAUAGGCAUAAA GUAGGGUUUAGGGUUGAGUAGCAUUCAAGAAUCCUAAUCUGA AUUGAACACAAUUUGUAGAGUCCCAACUCGAAUUGAACGCAUC UUCUAGAAUUCCACAAAAUUUCAAUGUCUACAAAUGCCCCCUG GGUAUUUCAUCCUUUUUGAGGAUUUUUUGGUUUCUAUAUAAA	213	spiLA0480-miR11103c-1-3p	ACAAAAUUUCAAUGUCUACAA	183-203	lja-miR11103c-3p	5	0	21	21	1
spiLA0480-MIR8016	UCCACUUCAUUCACUAUUUUUAGAGGAGAUUUUUGAGGGGA AGACCAAAGAGUACCCAUAAAAUUUUGAGAAUUCU	119	spiLA0480-miR8016-3p	AUUUUUGAGGGGAAGACCAAAGA G	72-95	stu-miR8016	6	0	24	24	1
spiLA0480-MIR10531-2	UACUCAUGCUACAUUUUCUCGUAGUACUGAGGGUUGUUAAGA GUCUAUUUUUUCAUUAGUUCAUUCUGAUAUUUGGGGUCCUAG UAGAGUCAGUUCUACUUUAGGAUUUCGUUAUUUUGUUAGUUU	282	spiLA0480-miR10531-2-5p	UGGGGUCCUAGUAGAGUCAGUU C	74-96	sly-miR10531	1	0	23	23	1

spiLA0480-MIR5569	CAUUGAUGAUUAUUCGAGAUGCACUUGGGUUUUCUUAAUGAAAGAUUGUUCUGAGUUACUUUCUAUUUUCAAAAGUUCCUUUGCUGAAAUGCAAAAUCAGUUUGGUGUUUCCAUUCAUACUUUCAGUAGUGAUCAACAAAAAGGUGUAGCUGAAAGCCUAUGGACCGUAGGUGGCCUCCGUAGUUUGUGAUUGAGGCUGAGUUUUGCCUUCCUAUUGCAUGCUUGAAUUAUGGAGGAAGACCUAAGGUGCAUCAU	99	spiLA0480-miR5569-3p	UAUUGCAUGCUUGAAUUAUGGAGG	57-80	sbi-miR5569	4	0	24	24	1
spiLA0480-MIR5658-1	UGCGGUGCGGUAAAGAUGUUGAUGAUGAAGAGAUUUUUUUUUGAGAAUGUAUUUUUUGGAUGACGGAAUCAGUCUCCAAAUCGGAGAAUUGUUAGGUAGUGGAUCCUGAUUAAUAGUUGAUGUACUUUAACAAAAAAUACUCUGAUUUAUUAAUAUAUGUACCCAACCUCC	171	spiLA0480-miR5658-1-5p	AAGAUGUUGAUGAUGAAGAGA	13-33	ath-miR5658	4	0	21	21	1
spiLA0480-MIR160-2	GGUGGUAUGCUUGGCUCCUUAUACGCCACCCACUGAUCAGUCAAUCAAAGAAUUGGUGAAUGUGUGUGGCAUACAGGGAGCCAGGCACAUCCUUC	95	spiLA0480-miR160-2-5p	UGCUUGGCUCCUUAUACGCCA	8-28	dpr-miR160	3	0	21	21	1
			spiLA0480-miR160-2-3p	UGGCAUACAGGGAGCCAGGCA	67-87	aau-miR160	0	0	21	21	1
spiLA0480-MIR7992-13	CCUCUUUACUUGACCUCAUUUUACAUUUAUUUUGGGUAUGCACAAGUAGAUACUUAAACUUGUAUAAACUUGAACAAGUAGACACAUGAGUCCUACGUGACACAACACACACAUAGGGCAAAAAUGACAUGUAGGACAUGUGCGUCUAUUUGUUCAACUUUAUAUAAGUUUAAGUGUCUACUUGGACACAUCCAAAGCUGAAAGGCAUAAACAUAAUUUGAAGCCAAGUUA	231	spiLA0480-miR7992-13-5p	UUUGGGUAUGCACAAGUAGAUACU	31-54	stu-miR7992-5p	6	0	24	24	1
spiLA0480-MIR1886f-2	CGGUGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGAAUAUAUGAUUUUACCCUAAUUUCAUCUCAUGAUUUCAUAACAUGA	82	spiLA0480-miR1886f-2-5p	AUGGUAUCGUGAGAUGAAAUCAGC	8-31	stu-miR1886f	0	0	24	24	1
spiLA0480-MIR8668-2	AGUUUGAUUUCUCAGAUGAUCACUCGACUAAUUGUUAUCAUCUCAGGAAGUCACUUUCUUUGUUGAAAGUUUUGGAAUCAAGAAGAAAGGGGACUUUCGAGAUAAUAACUAUUAAUCAAGUGACUAUAUGAGAAAUCAACCG	142	spiLA0480-miR8668-2-3p	UUUUGGAAUCAAGAAGAAAG	70-89	gra-miR8668	4	0	20	20	1
spiLA0480-MIR8030-2	UAGUGGUUUGGUUUGACUUGGUUUGGUAUUGGACAAAAAUACCCGACUAUAUUUGGGUUGGUUUAGUUUUAGCUAAAAAAACAAACUCGAGACCAAACCAACC	103	spiLA0480-miR8030-2-3p	UUGGGUUGGUUUAGUUUUAGCUA	53-75	stu-miR8030-5p	6	0	23	23	1
spiLA0480-MIR8660-1	UAAUGCACAAACAGAAACUUUAACUAUCCAACUUUUAAAUAAAUAAAACACUGAAUCCUACAUGGCACAAUACAUGUAGGACACCAUGUAGGACAAAAAAUGAUAUGGAGGACAUGUGUGUCUAUUUGUUUAACUUUAUACAAGUUUAAGUUGAUAUUUGUGCACAU	167	spiLA0480-miR8660-1-3p	ACAAAAAAUGAUAUGGAGGACAU	93-115	gra-miR8660	6	0	23	23	1
spiLA0480-MIR11088b-1	GUUAAAAUUGAAAAUAUUUAAAUGGGUUGAAUAGAAAUUGGGUUGGGUCUUGACCUGCCCAAGUUUACUUUGGACUCAAAUGGGGGCUAAAAUAUGUGUUGGGUCUUGACCCACCCAAUUUGACUUGAUUAAUUUCAAUAAUUUAACAUAUUGAU	155	spiLA0480-miR11088b-1-3p	AAUAUGUGUUGGGUCUUGACCC	91-112	lja-miR11088b-5p	6	0	22	22	1
spiLA0480-MIR169l	AACAACAACAGCUGUUUCAUAAAAAAUCUGGCAUGAGAAAAUGAGGCAGAUAUGUAGCCAAAAAUGACUUGCCAGACAUGAAGCAGAAUUGAUCGAGCUUGCCGGCAAGUCAUCCUUGGCUGCAAUUCAAUAACCUUGUUCCCUCAUGCAAGACUUUAACAUGAAUAAAGACAUGUCUAUUCAA	184	spiLA0480-miR169l-5p	UAGCCAAAAAUGACUUGCCAGA	55-76	cme-miR169l	2	0	22	22	1
spiLA0480-MIR1863a-1	AAUUGUGAAAUUAGGUCCUAGAGCUAACUCACACUUCAAAAGCUAGCUCAAAGAGAGGAUGAUUUUUCAAGUCUUAUAAGGAGUCCACCCAUCUUAUUUAUCACCGAUGUGGACUUUUUGUCAUUCUUUAACACUCCACCUCACGCCCAGUGCUUACCAUCUGGUGCGUGGGCAAUUUUGAUUUUGGGGGUCCCAACAUCGGGUGAGAUGGGCCCUGCUCUGAUACCAUGUAAAAUUAGGUAUUAGGCCUAAUUCACACCC	261	spiLA0480-miR1863a-1-3p	UGCUCUGAUACCAUGUAAAAUUAG	216-239	osa-miR1863a	3	0	24	24	2
spiLA0480-MIR9728	AUGGAAAGAGUUUACUUUGUGUCUCACACAACUGACACAAGUUGUGGGGAUUCUUUUUGUUUCACAAAUUUGUGGACCAAAAGUGUAAGACUAGGGUCCAGUAAUUUGUAGAUCAAAGCCUCACACAACCUGUGUCUGUUGUGUGAGACACAAAAUGAAGUUUCUCUUGAUGAUAUUUAGCGUGCACAAGUAGAAACUCAAACUUGUAUAAAAUUGAACAAAUAGAAACAUUUAUUCUACAUGACAAAAUUUGUAUCCUACGUGGCGUCUCAUGUGUAUUAUGUCAUGUAGAACACAUGUGUCUACUUAUUCAAUUUUAUGCAAAUUUAAGUGUCUACUUGUGCACACUCAAAAUUGA	169	spiLA0480-miR9728-5p	CACACAACUGACACAAGUUGU	25-45	gma-miR9728	4	0	21	21	1
spiLA0480-MIR5014a-8	AACUUAUUUUAUAAAUGAUUUUUUACCCCUUUUUAAGCAUAAUGGAACUAUCUUGAAAAACAUAUGUCAACACGCACUUGGCCGACAAGAUAGUGUCACGUAGGCCAAAAAGGGGUAGAGUAUUAUUUAUAAUAUAACUG	140	spiLA0480-miR1847-2-3p	UGGCCGACAAGAUAGUGUCACGUA	79-102	osa-miR1847-2	7	0	24	24	1

spiLA0480-MIR7696d-2	AGCACAUGAUACAUGUGUGUUACGUUACCCAAAAUAUACAUUUGUGUUUUGAAUUAAAAGCACAUGAUACAUUGGCUAAAGCAUAUGUAUCAUGUACG	98	spiLA0480-miR7696d-2-3p	UUUUGAAUUAAAAGCACAUGA	47-67	mtr-miR7696d-3p	4	0	21	21	1
spiLA0480-MIR8709a	GGAGAAAUAAUGAAUUAACCCUACACUUGAAAUUUAGGAAACAUGUAAUUAGACCUAUUGGUUGGAAUCAAUAUUUAGGAACUUUAUUAUACAUUUGAGUGAGUUUUGGGUCUAAGCUAGACAUAUGAGUGUUGUUAGUUACGAAAUUUUUUUGUGAUUAUUAAUAUGAAUAGAUUUCUUUGAGUUGGAAGUACAACGAAAAGGAAAGGCUCAAGUCUUAGAGUGAUUGUUCGACUAUUUGAGGCAAGUUGAUUUCUAAACUUUUGUUAUGGGUAUGAAAUUCGUGUAUUUCCUU	295	spiLA0480-miR8709a-5p	GAAUUAACCCUACACUUGAAAUUU	12-35	gra-miR8709a	7	0	24	24	3
spiLA0480-MIR8040	AGCAUGGAUGAAUAAAUUGUCAACAUUAUAAUUCAGUUUAUAAUGUUAAUUGUGAAAAGUUUGCACAGCGUCGCUUUGGCCGAGUGGUUAAGGCGCUUGCCUGCUAAGUAAGUGGGGUUUCCCCGCGUGAGUUCGAAUCUCACAGGCGACGUUGCAUAUGUUUUUGUCGAUACUGUUAUCGACAAUUUUUUACACCUAUUUA	202	spiLA0480-miR8040-5p	UUUAUAAUGUUAAUUGUGAAA	37-57	stu-miR8040-3p	6	0	21	21	2
spiLA0480-MIR11103c-2	UCAAUUUGUAGAUUAUUCGAGAUCUUGAUCUCUUUAAUCUUUAUAGAAUUUCUGAGAUGCCUUUUAAGGGAAUUUAGUACCCUUUAUAUAGGCAUAAACUAGGGUUUAGGGUUGAGUAGCAUCCAAGAAUCCUAGAAUUGAACACAAUUUGUAGUGUCCCAACUCGAAUUGAACGCAUCUUCUAGAGUUCCACAAAAUUUCAAUGUCUACAAAUGCC	217	spiLA0480-miR11103c-2-3p	ACAAAAUUUCAAUGUCUACAA	192-212	lja-miR11103c-3p	5	0	21	21	1
spiLA0480-MIR8639e-2	GCAUCAGCUGACAACUAUGACCUUUAACUUUGGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAAUUAAACAAAUAGACACAUUCGUCCUACAUGGCACCCUAGAUGAAAAAUUUAUGUCAUAUGUGUGUCUACUUGUUCAAUUUUAUAUAAGUUCAAAUGACUACUUGUGCAGAAUCAAAGUUGAAGGGCAUAAUUAUCCGCUGAAAG	211	spiLA0480-miR8639e-2-5p	UAAACUUGUAUAAAAUUAAACAAA	53-76	gra-miR8639e	6	0	24	24	1
spiLA0480-MIR7992-14	UGUACUCCAGCUUCGAGAGUGAACAUCUACACACCUCAAUUGGACACUCCAACUCGUCCCUAGUGUGAUGCUGACAUGGCAUAUAAAUUUUGGAGACGAGUUGAGGUGUCUAGAUGUGCAUACUCAAAGUUGGAGUGCU	139	spiLA0480-miR7992-14-5p	UUCGAGAGUGAACAUCUACACACC	12-35	stu-miR7992-5p	6	0	24	24	1
			spiLA0480-miR7992-14-3p	UGUCUAGAUGUGCAUACUCAAAG	107-129	stu-miR7992-3p	6	0	23	23	1
spiLA0480-MIR5650-1	ACACUAGAUGCAUGUAUCUGAUGUAAUUCACAUAUAUAUGAGAUAUAAGAUACAUAGGAGAGUGACGAGAGCUGGGAGAGAGGCGAGCCAGAUAGGUAAGGAGGCAAAUAAGAUUUGUUAUGUAGCUCAGAUACAUGUGAAUCUACUUGGAUACAAUGUAUCUAGAACUAAUACUUCCUCUGUUCCAAUUUAUGUGGCAUAUUUCGGAUU	168	spiLA0480-miR5650-1-3p	UUGUUAUGUAGCUCAGAUACA	115-135	ath-miR5650	4	0	21	21	1
spiLA0480-MIR8007a-2	UUGAGAUUCUAACAAGUUUAAGUGGUUAAUACUUCCUCCAUUCCAAUUUAUGUGCACAUUUUGAAUCUCGAAAUCUGAACUGUACCAUACAAAUUGGGACAAAGGUAGUAACA	155	spiLA0480-miR8007a-2-5p	AUGUGGCAUAUUUCGGAUUUUGAG	24-47	stu-miR8007a-5p	2	0	24	24	1
			spiLA0480-miR8007a-2-3p	CGAAAUCUGAACUGUACCAUACAA	111-134	stu-miR8007a-3p	7	0	24	24	1
spiLA0480-MIR7981-9	ACAUUUAGGAAAAAGCACAAGUACUUCCUACACUAUGAAUGAUAUCCUAGAGACAUACCUUAACUAAACUAAAGUCCUAUUCCCCCCCCCCCCAAAAAAAAGGUUUGUUUGUAAUUCGAUACACCUUUUGGCUUACAUGACACACUCCAUGACUACACACAACUAAGAUUUAUUGGAUAUGUUUGGAUGCCACAAGUGGAAAAGGUGAACAAAAUUAUAAAAAAUGGGAUCACGGGGUAUUAGGAUCUAAGUUUAGUUAACACAUGUAUAUGGGGUUUCGGUCAUAAUCUAGGUAGUACUUGUACUUUAUCUCGCUAAAAUU	322	spiLA0480-miR7981-9-5p	CUUAACUAAACUAAAGUCCUAUUC	59-82	stu-miR7981-5p	5	0	24	24	2
			spiLA0480-miR7981-9-3p	UUAGGAUCUAAGUUUAGUUAACAC	240-263	stu-miR7981-3p	7	0	24	24	2
spiLA0480-MIR7993d-2	AACUUUUUGCGUGUGUUUUCAUUCGUCUAUUAGUUAGUGAAGUUAAUUACAUGAAAUGUAUCAUCUUUUUUAACCGUACACAUUAACUUCAAGUAAAAAAUGCUUGAGGUUUUAAGGCGUAUUGAGGCGCAAGCGUAUAAUUAAAGGAGAUAGAGAUAUUUUAUGUUGUUAACUUAACUACAUCGUAGAUAAAUGAGUGAGCACAAACCAGAAAAAA	218	spiLA0480-miR7993d-2-3p	AUAUUUUAUGUUGUUAACUUAAC U	156-179	stu-miR7993d	1	0	24	24	1
spiLA0480-MIR5303i-4	AUCAUGUUGUUCGGACUCACCAAAAAUGUCGAUGCAUCCAUGUCGGAUCCUCCAAAAAUGCACUAUUGUUGGAGUAUCCGACACACGCCUGUUGAUAUUUUUGAAGAGUCUGAGCAACAUAAA	123	spiLA0480-miR5303i-4-3p	AUAUUUUUGAAGAGUCUGAGCAA C	95-118	stu-miR5303i	0	0	24	24	1
spiLA0480-MIR9761	AAAAGGGCCUAAAACGCCCUUAAAUUAUGAGAUUAUGUACACUAUUACGCACCAACUACUUAAUGAGUGUGAUCCGUUGGGCAUAAGGUAUUUUUGAGUCGAAAGGUAAAUGUCAAGGAUAUUUUAAGACCGAUAGGUGGAUGGAGGAUAAUUUUAUACCAAUUCAAAUACUUGAGGGGCAUGUUAGGCCCUUCU	195	spiLA0480-miR9761-3p	UAAAUGUCAAGGAUAUUUUAA	107-127	gma-miR9761	5	0	21	21	1

spiLA0480-MIR7988-2	CACUCCCGUUAGAACAAAAUGGUAUAUUUUAGAAUAUUUAUGUAAUAAUAUGAGUGUAUGUAAGCCACUUUUUUAAUAAGGGAAAAGGCUCAAAUAUGCCGUUGAACUUUUAGAAAAGACUCAUUUAUGUCAUCCGUUAAAAGUUUGACUCGUUCAUGUUAUUACCAUUUAGGAAAAGACUCAUUCAUGCCAUUAGUUUUUAACGGCGAUUUGUUGCACGUACAAGGAUGUUCUACAACGUACGUAGGGUAAGUGGAUGGCUGAAAUUCGUUAGCCUAACCGUGGCCCUGGAAAUACUUCUUUGCAGGACAAGCUUCAUUUCCAUUACCGGAUAUCAACAGAAAGGUUGAAAAAGACAACAAUGUAGAGGAUUUGGUGGAGUGUGGAAAGAUUUGAAUGCAAACUUAUCGAAGAUUGAUCAU	212	spiLA0480-miR7988-2-5p	AAGGGAAAAGGCUCAAAUAUGCCG	78-101	stu-miR7988	6	0	24	24	1
spiLA0480-MIR10537	CAUGGAUUUAAGCCAUCCAUUUACCCCAAGUUCGUUGUCAAACGCCUUUGUAAGUGCGCG	270	spiLA0480-miR10537-3p	AUUUACCCCAAGUUCGUUGUC	229-249	sly-miR10537	0	0	21	21	1
spiLA0480-MIR9476-2	CGUUAAAACGGUAUAUAAGACUACUAGACAGCUCAAGCUUAAAAACUCUAACUUGCCUACCAGUUGACCACCAUAACCAAUGAAGACAGUCCCUAACCAAAGGGAACUGAAUCAACUGGUAGACAAGUUAGAGUGUUAAAGCUUGAGUUGUCUAGUAGUCCUACAUAUCUUUUUACAA	178	spiLA0480-miR9476-2-3p	AGUAGUCCUACAUAUCUUUUU	154-174	sly-miR9476-5p	5	0	21	21	3
spiLA0480-MIR172d-2	CAAACUUAAUGGGCUAAAUCUAAAUUAUUCAAAUUCAGACCUAAAAACCAAACGUACUUAAUAGGCUGAAUCUGAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCA	106	spiLA0480-miR172d-2-3p	UCUGAAUGAUUAAGAUUCAGA	71-91	bra-miR172d-5p	5	0	21	21	2
spiLA0480-MIR8037	UAAAAAUGCAUUUAUUUGGAAUAAUAGUAACCAUGAAUAGUAAGAGUCAAGUUACUGUGUAAAUAGUAAGAGUCAAGUAACUGUGUAAAUAGUAAAGGCCAAUCGUCCUUUAGCAAGGAUGAAAGGUCAUUAUGUAUGUCUAUAUAAGAGGCAUUUACC	159	spiLA0480-miR8037-5p	UUUAUUUGGAAUAAUAGUAACC	11-32	stu-miR8037	5	0	22	22	2
spiLA0480-MIR7803b	CAUACACGUGUCAUAAUCUUAUCCACCGACCUGACAUUGGAUCGAUGGAUAAGAUUGUAUCACGUGUCCC	70	spiLA0480-miR7803b-5p	UACACGUGUCAUAAUCUUAU	3-22	rgl-miR7803b-3p	6	0	20	20	1
spiLA0480-MIR408a	AAGUGGAGAGGAUAGACAGGGACGAGGCAGCGCAUGAGAUGUACAAUUUUAUUAGUUGUCCAUUCCAUGCACAGCCUCUUCCCUGGCUUUCCUCCCCAAAA	101	spiLA0480-miR408a-5p	ACAGGGACGAGGCAGCGCAUG	16-36	stu-miR408a-5p	0	0	21	21	1
			spiLA0480-miR408a-3p	UGCACAGCCUCUUCCCUGGCU	68-88	stu-miR408a-3p	1	0	21	21	1
spiLA0480-MIR10538-9	AAAAGCUGACGGUGUUAGGUUGAUAUACGUUACUACAGGUAACGUUUUCAUCCUAAAACGUUACUAUGAGUAACGUUUUAGCAGUAAAACGUUACUGUGAGUAACAUAUAUCAAUGUAACACCGUCAGCUUUU	133	spiLA0480-miR10538-9-5p	AGGUUGAUAUACGUUACUACAGGU	17-40	sly-miR10538	5	0	24	24	1
spiLA0480-MIR5014a-9	GAUUAUGACCUUUAACUUUAGAUGUGUACAAGUAGACAGUUAAACUUGUAUAAAAUUGAGCAAAUGAACGCAUUUGUCAUACAUGAUACCGCUACAUGACAACUUUGUCUCCUACAUGACAUUCUACGCGUAUUAUGUCAUUUAGGACACUUGUGUCUACUUUUUCAAUCUUGUACAAAUUUAAGUGUAUACUUGUGUACAUUCAAAGUUGAAGGACAUAGUU	223	spiLA0480-miR5014a-9-3p	UUGUACAAAUUUAAGUGUAUA	171-191	ath-miR5014a-3p	2	0	21	21	1
spiLA0480-MIR5157b-3	GAGUUGUGACUUUUUUGAAGAGUUGCGACUUUUUUGAAAAGUUGUGGCUUUUAUAAAAAAAUUGCAACUUUAAUGAUUAGUUGUAAAUUUUAUGAAAGAUUGUGACCUUUCAUAAGGGUUGUCAGUUUUCCAAAUAGUUGUGACUUUUCCGAAGGGUUGCAACUUUUCCAAAUAGUUGUAUCCUUUUCGAUAAGGCACAAUAA	203	spiLA0480-miR5157b-3-5p	AAAAGUUGUGGCUUUUAUAAAAAA	37-60	osa-miR5157b-3p	7	0	24	24	1
spiLA0480-MIR1917-1	GGAAUCAAUACAACAAAAAUAACUUUUAGCGGCAUUAAAUAUUGACAUUAAUAAAGAGUGUUAAAGUCUUUACCGGCAUUAGUAAGUGCCAUUAGAAUCAAUGUCUCUAAAGACUUUAGGGACAUAUACAACCAGUGACAAUUGCCACUAAAAAUCCAUAUUUUGCGACAAUUAAGAAUUAAUUGUCGCUAAUGAUCAUUUUUGUUGUAGUGGAUAAU	218	spiLA0480-miR1917-1-5p	AUUAAUAAAGAGUGUUAAAGU	47-67	sly-miR1917	1	0	21	21	1
spiLA0480-MIR5167b-2	UUGUGGAGCUUUGGACUCUUCAACUAAUCCGGAGUUGCUUGAGUUAUACACUGUUGUUGGGCUGUUGUAUCCUGGAAGAGACAAGUCUAGAGUAUUACUGCUGGAUCGGUGUAGAUUAUGCCGCAGUUGGCUUGAAUCUCCUUAAAGAGAGCGAGAUAUCCGUGCUUCAGCCUAAAGAUUUAUUUCUUCAUUAUAUUUUCAAUUAUAAUCUUACAAUUUUAUUAUAUUGUAAGUUUUCUUUAACACAAAUUUUAGGGUUAAAGAAUCCAAAUCAUCGCAAGA	282	spiLA0480-miR5167b-2-3p	CUUGAAUCUCCUUAAAGAGAGC	131-152	bdi-miR5167b-3p	5	0	22	22	3
spiLA0480-MIR779	GUUAAGCUUAUCUGCAUCGAGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUGAAACUUGUUGUUCAUUUUACUUCAUUAAAUCACAUAAUAAUGGAAAUUGCAUUGGCUUGGUGUAAACAUUCGAUGCGGGUAAGUUGUU	146	spiLA0480-miR779-3p	AUAAUGGAAAUUGCAUUGGCU	95-115	ath-miR779-2	6	0	21	21	3
spiLA0480-MIR419	AAAUAGUAAAGGCCAAUCGUCCUUUAACAAGGAUGAAAGGUCAUUAUGUAUGUCUAUAUAAGGGGCAUUUGCCUUCAUAAAU	82	spiLA0480-miR419-3p	GGAUGAAAGGUCAUUAUGUAU	31-51	ppt-miR419	6	0	21	21	2

spiLA0480-MIR5014a-10	CAUUUAUGCCCUUCAACUUUGGAUGUGCACAAAUAAACACUUAAAUUUGUAUAAAAUUGAACAAAUAGACACAUAUGUCCUACAUGUCAUCUUACAUAUCAUAUUUUGUCCUAUGUGGUGUCCUACGUGUAUUGUGUCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGAAUAGUUAAAGUGUCUAUUUGUGCAUUGUGAAAGUUGGAGGUCAAAGUU	222	spiLA0480-miR5014a-10-5p	ACACUUAAAUUUGUAUAAAAU	37-57	ath-miR5014a-5p	4	0	21	21	1
spiLA0480-MIR160-3	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAACUAGGAAGAGUGUCAAUUUUUUUGACAAUACUGUUCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACAAUUUC	104	spiLA0480-miR160-3-3p	UGGCAUCCAGGGAGCCAGGCA	74-94	aau-miR160	1	0	21	21	1
spiLA0480-MIR11083c	AUAAUAAUAAGGGAGAAGUGUUGAAAACACCCCUAAACUCGGUUUUCUAUUAAGAGACCCAUACUCCUACAAGAGUUUGAGACCACUUGCAAUUUCACGUAGUAGAUCAAAGGUGUAUCUAAGUUUAGUUAGUCAAGUAGAGGGGUGUUUUUAAGGUUGUCAAUAGUUUGGGAUGAAAAUGAUAAUUAUGCCAAGUUCAGGGGUGUUUUCAAUACUAUUCUCUAUGAUAAA	232	spiLA0480-miR11083c-3p	GGGGUGUUUUCAAUACUAUUCU	201-222	lja-miR11083c-5p	5	0	22	22	2
spiLA0480-MIR8706b-2	ACGGGUAAAACUUAUCUGCACAUGGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUCAAAUUUAUAGUUCAUUUUACUUCUUUAAAUAUCGUAAUAAUAUUUUUUGCAUUUACUUGAUGUAAACACCCGGUACGAAUAAGUUUUUCCUUU	155	spiLA0480-miR8706b-2-3p	AUUUUUUGCAUUUACUUGAUGUAA	104-127	gra-miR8706b	6	0	24	24	1
spiLA0480-MIR11409d	CUGAACUUUAUUCACUAUAACAGUAUGGUCACAAAACUAUCUUUUGUUGCGUUAAAGUACGUGUUAAUUGCUCAAACAAUGACUAGAAGGUUAAAUAUUCUUUUAAUAUUAUUUUGAGCCAGAAAUUUAACCUUUGGGCCAUUUGUCUCAUUUGAGCAAUCCACACCCCUAGUUCAGUUACUUUAAUGUGACAAAAAUUAGUUCUGUGAUUCUACCGUUACCGAGGAUAAAAUUAAA	237	spiLA0480-miR11409d-3p	CAUUUGUCUCAUUUGAGCAAU	140-160	pab-miR11409d	4	0	21	21	1
spiLA0480-MIR8001b-5	UAAACUACUCCUAGAAAACUGUGAAUUACAUAGGGAUAGGAAAACUAAUUCCUAGGAAAAUCCCCAUGUAAUUCAUAGUUUUCUUGUAGUGUGCA	95	spiLA0480-miR8001b-5-3p	GGAUAGGAAAACUAAUUCCUAGGA	34-57	stu-miR8001b-3p	6	0	24	24	1
spiLA0480-MIR7992-15	CUUCAACUUUAGUAGCGUACAUCCAGACACCUCAACAACUCAUCCCUACCGAGUCUCGUGGACACCCAAUUCUAACGUGACACAUAAAUUUUGAAGAUAUGUGAAUGAUCAUUUUGUAAGGUGGAGUGUUCAACUAACACACUAGAACGAGCUGAGGUGUCUAGAUGUGCAUUCUCAAAGUUGGAG	186	spiLA0480-miR7992-15-3p	UGUCUAGAUGUGCAUUCUCAAAG	158-180	stu-miR7992-3p	5	0	23	23	1
spiLA0480-MIR868	UAUAAAUGAUAUGCAGAUAUCUUCAUCAUACUUUUGGGACAUUUAGUGCCCCUGCUGUAAAAAACUAGAGCAUAUAUAUACCCUUUAUAUUAACGGAUAUAUGCGUGUCGUAAUCUUAUUCACUAACCGAAUAUUUAUUAAAUAUCAGAUCAACGGAUAAGAUUUCACCAUGUAUCCCAAUUUAGGUUUCUCUUAGAGUGAAAGACAUAUAUGCUCUAACACGAUAACACAUAUAUCCCAAAAAUAUGACGGAGGAUAUAUCUAUAUCAUUUUUU	275	spiLA0480-miR868-5p	GCGUGUCGUAAUCUUAUUCAC	103-123	ath-miR868-5p	5	0	21	21	2
spiLA0480-MIR7983-5	UUCCUAAAGUCUUUAGCGACAUUGGUUCUAACAACACUUAACUAAUGUCAGUAAAGACGUUAGCAC	66	spiLA0480-miR7983-5-5p	UAAAGUCUUUAGCGACAUUGGUUC	5-28	stu-miR7983-5p	0	0	24	24	1
			spiLA0480-miR7983-5-3p	ACUAAUGUCAGUAAAGACGUUAGC	41-64	stu-miR7983-3p	4	0	24	24	1
spiLA0480-MIR9736	CGCUUGCCAAGUUUGCACACUGCAAGGACUUGGCGGGAAUAUGAUGCAACUCUAAGAGAACAACUGCUAGGUGGAGCUGGUAUGUUCAACAAAGGUUUGAUUCUUCUUGUUUCUUACAAUGGGAUUGCCCAGUAAGCUUAGAAGUUUUGGCCGGAGUUGUUUAUACGCAUGCUUGGAACACAAACCAAGGUGGAGAUUGAAAGAGUUGGUUUUGGUUCUUGUGGAAUCAAACUAAAUGGAAGAUGAAUUAAUAUGAAUAUUUGGUAGGAAGAUAAUUAGUACAAAAUACAAGUCAAAGAUUGUAUCUUGGUAGGUGAAAGUUAGGCAAACC	331	spiLA0480-miR9736-3p	UGGAACACAAACCAAGGUGGA	174-194	gma-miR9736	4	0	21	21	1
spiLA0480-MIR7745	CUGUGAGUAACAUUUUACUCCUAAAACGUUACUGUGAGUAACGUCUUACUCUUAAAACGUUACUCACAGUAAGGUUUUAGGAGUAAAACGUUAGUCUCAAAAAAACGUUUUAGGAGUAAAACGUUACUCAUAU	131	spiLA0480-miR7745-3p	AGUAAGGUUUUAGGAGUAAAACGU	68-91	bdi-miR7745-5p	7	0	24	24	1
spiLA0480-MIR2101-1	UUCAUUUCAUUAUGUGCAUCACUUGAGGCUGACCUCAUUCUUUCAUUGGGAAAUUUAACUCAAGUGAGCAUCAUGAAAUCCA	82	spiLA0480-miR2101-1-3p	AUUUAACUCAAGUGAGCAUCAU	53-74	osa-miR2101-3p	2	0	22	22	1
spiLA0480-MIR2619b	CGUGGUGGAGCUUCCAGUUCUAGCGGUCCCUCAAACCGUAUAUAUGCUUUGAGUAAUAGGCAAGAUCAGGAGGCGUCACCUAA	83	spiLA0480-miR2619b-3p	AUAUGCUUUGAGUAAUAGGCA	42-62	mtr-miR2619b-5p	5	0	21	21	1
spiLA0480-MIR7983-6	UAUGUUUCUAGAGUCUUUAGCGACAUUGGUUCUAAUAACACUUAACUAAUGCCGGUAAAGACUUUAACACUCU	73	spiLA0480-miR7983-6-5p	UAGAGUCUUUAGCGACAUUGGUUC	9-32	stu-miR7983-5p	1	0	24	24	1
			spiLA0480-miR7983-6-3p	ACUAAUGCCGGUAAAGACUUUAAC	45-68	stu-miR7983-3p	0	0	24	24	1
spiLA0480-MIR1435	UGAUUUUCGUGUGCUAUAGUCCAUGGAUUUUUUGUGAUUCAGGAUUACAGAUUUUCUUUUGUCAAAAUUUUUCAUGAUAGAUUG	234	spiLA0480-miR1435-5p	UUUCUUUUGUCAAAAUUUUU	53-72	osa-miR1435	3	0	20	20	1

spiLA0480-MIR5773-2	GCUCCUAAAUAUAAAAAAUGGACUCUCGAAUUGGUGACUGUACAUAUUACUCCUCCAACUCCCUACAGAGAGUUCUCUAAUGGUUUCAAAUUGAAAUCGUUUGAAAGCAAUAUGACCAAAAUAUUCAUGGGCUAACACACACAAAAAAUUUGAUCCACCCACUUAAUCCGACCCAUUUAAAAAAUAUGAUAUGACCCAUUUUAUAUUUCUCUUUAAUCCUAAAUUAUUCCCUCUUUAAACCUUGAAUUAGGAUUAAAGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAAUGGGUCAGGUUAGGUCGGUGGAUCA	166	spiLA0480-miR5773-2-3p	UUUUUAAAUGGGUCAGGUUAGG	134-155	gma-miR5773	6	0	22	22	1
spiLA0480-MIR7997c-15	CUACUAUGAUAUUGCUCAGACUCUUUAAAAAUAUCACUAGCUGCGUGUUGGAGGUGUUGGAUCCUCCAAAAGUAAGUGCAUUUCUAGAUGAUUUGAUAUAGGUGCAACAAUGUUUUUGAAGAGUUCGAGAAUUUCCUAGCAC	143	spiLA0480-miR7997c-15-5p	AUAUUGCUCAGACUCUUUAAAAAU	9-32	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR7983-7	UCUCACUACAACAAAAAUGAUCAUUAGCGGCAUUUAAUAUGUAUUUUUAGCGCCAAUUGUCAUUCUUUAUAUAUGUCCCUAAAGCCUUUAGACAUUGGUUCUAAUGACACUUAACUAAUGCCGAUAAAGACUUUAGCACUCUUUAUUAGUGUCAAUAUUUAAUGCCGCUAAAAAUUGCUUUUGUUGCGGUGUCU	194	spiLA0480-miR7983-7-3p	ACUAAUGCCGAUAAAGACUUUAGC	114-137	stu-miR7983-3p	2	0	24	24	1
spiLA0480-MIR7732	AUUUCUUUGUACAAGGAUCACAAUUUUCUGAUCUUUCCCUAGCUGAUGAUAACUGGGAACUAGAUAUUGAAGGAUAUUGAUUACUAAUCUAUUUGUAAUACUUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUUCGUGGUCGUGGAGGAAGAAGUAGAGGAAGGGGAAGAUCAUCCUCUUCCAAGUCUAGAAGAUCAUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAACUCAAAGAUUA	274	spiLA0480-miR7732-3p	AUUCGUGGUCGUGGAGGAAGA	145-165	bdi-miR7732-3p	6	0	21	21	3
spiLA0480-MIR414-1	AUUACUAAUCUAUUUGUAAUACUUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUUCGUGGUCGUGGAGGAAGAAGUAGAGGAAGGGGAAGAUCAUCCUCUUCCAAGUCUAGAAGAUCAUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAACUCAAAGAUUAAUGAAGCAUCUUCAUCAGCUUCGUCCUUUGUAAAUUUAAAGGAUAUUCCCAAUGAUAGUUCA	257	spiLA0480-miR414-1-3p	GCAUCUUCAUCAGCUUCGUCC	201-221	ath-miR414	4	0	21	21	2
spiLA0480-MIR7697	UAUAUUCAGCCCAUACAAAUCCGAUCAAAUCCAAUGUACAAGCAUAGCACAGGAAAUAGGCGUAUGACCCAAUCUCCUGUGCUAUGCUUGUACAUUCGAUUUGAUCGGAUUUGCAUGGGCGUAUGAC	127	spiLA0480-miR7697-5p	UCCGAUCAAAUCCAAUGUACA	20-40	mtr-miR7697-3p	6	0	21	21	1
spiLA0480-MIR9563a-1	CAUACACGUCUCAUAAUCUUAUCCACUGAUCCGCACAUUAUAUCGAUGGAUAAGAUUGUGUCACGUGUCCC	71	spiLA0480-miR9563a-1-5p	ACACGUCUCAUAAUCUUAUCC	4-24	bra-miR9563a-5p	6	0	21	21	1
spiLA0480-MIR8014-2	ACAAUAUGAUACAUUAUGAAUCAAUACGUAACAACCAUCUAAACAGAGUGUAAUUAAGCACAACUGAGCUUCUCUCGUAAGUGUUGCAUUAGCUUUAUUUUGUAGCAAUUCAGUAGAAUUUAGAGCUUAAAAAUAAUAUAAUUGAGAAAGAAAAAAUGUAGCAAUCCUUUAAGCAAAGCUAAGCUUUUCACCAAACUAUGGUAUAUCAACCAUCACAGUCCUAACAAGGUAGUGUCCUUUUGGUUCCAAAAUGAGACAGAGUAUGGGGUGACUUCUUUCUGAUCCCCUAACACUUUGUUUGGAUCAUUGUUACCCAUUGUUUCAUAAUGUAUUGUAUUGUGGAUCCUAUGUUGCUCGGACUCUUCAAAAAAGUCGAGGGGUG	340	spiLA0480-miR8014-2-3p	AUUGUUUCAUAAUGUAUUGUAUUG	316-339	stu-miR8014-5p	2	0	24	24	1
spiLA0480-MIR7997c-16	UUUGUCAGGUCCUCCGAAAGCAGUGUGCUUUUGAAGGAUCUGACACGGGUGGGGCAACAUACUUGGAGAGUCCGAGCAACAUAGGAGGG	131	spiLA0480-miR7997c-16-5p	AUGUUGCUCGGACUCUUCAAAAAA	8-31	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR1313d	UACUAUAAAACUCUCUCAGACCGUCUUCUAAGCAUAUAAUGUCAUACUGGCUUCAAAAAAACCACUGAAAAUCUUUUGCAACCACAAAGAGAAAUAUAUAUAUAUAUAUAUAUAUGCUUAGAGGACGGUCUGAGAGAGUUUUAUACAA	148	spiLA0480-miR1313d-3p	AACCACUGAAAAUCUUUUGCAA	60-81	pab-miR1313d	6	0	22	22	2
spiLA0480-MIR5083-2	UCACAAGGAUAUCAACAAUUACUGCAAUUCUCUGAUCAAGCAACGUGGAGAAAAAACUUAUCAAGCAACGUGGAUACAACAUCCAUCCAACAGAUUAGUUUUUCUCCACGUUGCUUGAUCAGAGAAUUGCAAUAAUUUUUGAUAUCCUUGUGA	153	spiLA0480-miR5083-2-5p	UUACUGCAAUUCUCUGAUCA	19-38	osa-miR5083	4	0	20	20	3
spiLA0480-MIR7486b	CACCCCACACACACUACUUAAUAGUGUGUCUUUUGAAGGUAUAUAUGUGUCCACGUGGACAUCAUAAAUAUUUCAUAAUUAUAAAUAGUAGUGUGUCCACGUGGGCACAUAUAUACCUUUAAAAUACACUAUUAAAUAGUGCAUGGGGAUU	151	spiLA0480-miR7486b-5p	AAGGUAUAUAUGUGUCCACGUGGA	36-59	ghr-miR7486b	6	0	24	24	1
spiLA0480-MIR5185m	AAUAUUAUUAAAAAUUAAACUAAAAAAAAUUUCACUUCAGUUAGAGAAAAGGGUAUAUAUGAGUGAUUCCUAUACCGGUAUAGGUAUAUAUGAGUCACUUUCAUAGCGAGGGAUAUAUCAACUCUAAAUGACAAAGUUAGGAGAUAUAUCAGACCUUCGCCUCAGCUAUGAAAGAAGAAUGAGACUCGAAUCGAUCUUGUAAAAAAUAAUUAGGGGGUUCCUAAAAAUGUGGCUAAUUUGUUCUUUUACCACUUAGC	326	spiLA0480-miR5185m-5p	AUUAAAAAUUAAACUAAAAAA	7-27	bdi-miR5185m-3p	6	0	21	21	2

spiLA0480-MIR8006-8	CACACUCUCAAUAUAGUUGAUCUAGAUAGUCUGAAUACAAAUUUAUUUUCUUUUAUGUGUUACAAUUCUUUUGUCAUAUUUUUAGUAUGUGUCUUUAUCAUUAAAAAAUAAAGCAUAUAUUAUGUCCUUUAAUCUAACAGAAGACUAAAUAUUGACAUACAUGUGCGUAAUCUUCUCCAUCGAUUCGAUGUCGGAUCGGUGGAUAAGAUUAUGACCACGUGUAUGUCUGUUAGUAUAAAGCGUAUAUAUGCUCUAGUUUUUGGACGGCAGAAACACCAAUAUCUCUAAUAUAUGACGGA	230	spiLA0480-miR8006-8-3p	UAGUUUUUGGACGGCAGAAACACC	185-208	stu-miR8006-5p	4	0	24	24	1
spiLA0480-MIR11039-2	AUGCAAGUUUAGAUCUAAUUUUCAACGAUUUAUCUCUAUUCGUUGGAUCAUAUUUCUUCUUCGCUCGUGAAAAUGUUUAACUAGAAUAAAAUUUGAUCGCUCUUAUUGAAUUUCUCUAUUGAGAAGUUCGUUUUUAUCUUCUAUUUGAAGAAAUUGUUGCUCGAAAAUGAUGGGUUGUUGUGGUGAACAAAUCUACGUGAAUUGAUAAAGGUGAAAUGGAGAUGAAGAGUUAAUAUUUGGUGAAAAUGGUGGGUCAACUUGAGU	264	spiLA0480-miR11039-2-3p	AAGAAAUUGUUGCUCGAAAAUGA	148-170	seu-miR11039	6	0	23	23	3
spiLA0480-MIR11078f	GAUUUCAAUAAGUAUUUGCAAUAAAGACAGAGAUUUGGGUCUUCAAGUUAUCUGAGGCUGUUUUGCGUAAAAAAAAAUGCUUCAUUCCAGGCAAUGGAUUGGUUGCUGGUGUCAAAAGCUUCACUUAGAGGAAUGCCACAUGAUUACCGAGGCUGGACUUUUUGGCAUAGUUUUGAACUGUGGUAAGAACCUGAAGCCGAGGCUGGAUAUUUUGGCAUAGUUUUGAACUGUGGUAAGAAACUGAAGCCCGAGGCUGGAUUUUUUGGCAUAGUUUUGAACUG	281	spiLA0480-miR11078f-5p	GGAUUGGUUGCUGGUGUCAAA	96-116	lja-miR11078f-3p	4	0	21	21	2
spiLA0480-MIR7756	UUUUUGGCAUAGUUUUGAACUGUGAUAAGAAACUGAAGCCAAGGCUGGAUAUUUUGGCAUAGUUUUGAACUGUGGUAAGAAACUGAAGCCAAGGC	95	spiLA0480-miR7756-3p	UGGAUAUUUUGGCAUAGUUUUGAA	46-69	bdi-miR7756-3p	7	0	24	24	1
spiLA0480-MIR1128-8	UAAUUUGUUGACUUCCAAGAAAGCUAUUACUCCCUCCGUCCAACAAUACUUGUCCACUUCAUGAAAUCCAUGAAUAAUUUUACACUUAGUUCCUAAUUUACCCUUAUCAUAAAUUAUAGUCAUUUCACUCAUUUCCCUAUUUCCCUAUUAUAUUUUUCAAGACAUUGUAUUUAUUAUAUCAAAGGGUGAUAUAAUAAAAUUACCCAUCUAUAAGAAGUGUACCAAGUCAAUAGUGGACAACUAUUGUUGGACAGAGGGAGUAUAAAAGUUUUGAAAGACACCAAAAUG	289	spiLA0480-miR1128-8-5p	UAUUACUCCCUCCGUCCAACA	25-45	ssp-miR1128	3	0	21	21	1
spiLA0480-MIR1127	GUGUAGUGGACAAGUAAAGGUGGAUGGAAGAAUUACUUCCUCCGUCCACUUUUAUUUGUUCACUAUAC	68	spiLA0480-miR1127-3p	AAUUACUUCCUCCGUCCACUU	31-51	bdi-miR1127	5	0	21	21	1
spiLA0480-MIR167a	UUCAGACUACGUGGCAGUAUCUUGUGGGCCCAACACUGGUUUAUUUUUUUCAAGCUAGUGCCACGUAGGCUAAA	75	spiLA0480-miR167a-5p	CAGACUACGUGGCAGUAUCUU	3-23	vca-miR167a-3p	5	0	21	21	1
spiLA0480-MIR9562-2	UGUAUGCUAUAGCAAAGUUUGCAUAAUUGCGCUCCAUAGCGAACAUAAAACUGUAUAAUUCGCUAUACAUAUACAAUUGUAUAAUUUGCUGGCCUAAAUUGUAUAAUUCGCUGGCCUAUUUCGCUGUAAUUGUAUAAUUUGCUAUCCUAUUUAACUGCAAUUGUAUAAUGCACAAUUGAAUAAUUCGCUGCCUAUUUCGCUGCAAUUUUUAUAUAAAAUUUGCUUUGCAUACA	233	spiLA0480-miR9562-2-3p	UAAUGCACAAUUGAAUAAUUC	166-186	bra-miR9562-3p	4	0	21	21	1
spiLA0480-MIR7981-10	AUAUAUAAUAUUAGGGGUAAGAUAUAAGUACCUCUUAGAUUAUGAUCGAAAUUUGAGAUAUCUUAAUUAAACUAAAUUCAUAUUAUCUCCUCACGCAGUUGAGGCGCGUGAGAGAUAUUUUGAUGCCAUGUAAAAGCCAAAAAGGUCUACGAAAUAACAAAACAAAUUGGUUCGGGGGUAAUAGAACCUUAAUAUAGUUAAGGUGUGUCUCUAAGUUUCAGUCAUAGUCUAGAGGAUAUUUACACCUUAUCCCUAUAAUAUUGUAGAC	268	spiLA0480-miR7981-10-5p	CUUAAUUAAACUAAAUUCAUAUUA	62-85	stu-miR7981-5p	5	0	24	24	2
			spiLA0480-miR7981-10-3p	AUAGAACCUUAAUAUAGUUAAGGU	181-204	stu-miR7981-3p	4	0	24	24	1
spiLA0480-MIR8003	AGGUAGGUUCUUCAUUAUUUCGAUAUACAAAUGGGUCCUGUAUUUUUUUCGGUAUACAAUGGAUCCUGCAUUUGUAUAUUUCAGUAUAUAAACGGGUUCUGCAUUUGAAUAUUUCGGUCUAAUUGUAUAUUUUGAUAUACAAAUGGGUCCUACAUUUGUAUAUUUCGGUAUACAAAUGGGAUGACAAAAAAUAUGGAAUGUUUGCUACGAAUUACAAAUAGAAGAAACUAUGG	233	spiLA0480-miR8003-3p	AUUUCGGUAUACAAAUGGGAUGAC	162-185	stu-miR8003	0	0	24	24	1
spiLA0480-MIR7997b-4	CUUUUGAAACCAUUGUUUGUACCUAAGUUGCUCGGACUCUUCAAAAAUGUCAGUGGGUGUGUGUCGGAUUCUCCAAAAGUAGUCUGACACGGGUGUGGCAACAAUGUGAAGAGUCCGCAACUUAGGUUUGUACAAGGUGCAAUUU	145	spiLA0480-miR7997b-4-5p	AAGUUGCUCGGACUCUUCAAA	25-45	stu-miR7997b	2	0	21	21	1
spiLA0480-MIR10538-10	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUAGGAGUAAAACGUUACUGAAAAUAACGUUUUAAAAGUAAAACGUUACUUACAGUGACGUAUAUCAACCUAAUGCUGU	117	spiLA0480-miR10538-10-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
spiLA0480-MIR8132-1	UACCCCCCUGAACUUAUUUUAUUAGUAAUUUUUUUACCCGUUUUAGCCUAUGUGACACUAUCUGGUGGGCCCAACGAUGGUUGAC	161	spiLA0480-miR8132-1-3p	CCCAACGAUGGUUGACUUCUU	70-90	ppe-miR8132	6	0	21	21	2

spiLA0480-MIR7997c-17	UUCUUUUUUUUCAAACUAGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUACUUAUAAAAUAGGUUCAGGGGGUAACCUAUGUUGCUCGGACUCUCCAAAAAUAAGGAUCAGAUACACAACCAUCGAUAUUUUUGACGAGUUCGAGCAACAUUAA	79	spiLA0480-miR7997c-17-5p	AUGUUGCUCGGACUCUCCAAAAAU	4-27	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR8011a-4	UUCUUUAUGACAACACGAAUACUAGUUGUGUGAGGCUUCUUUUUGUCUCACAUAAAAGUAGACUCAAAUGGGCUUAAUUUUUUGUGAGGCAAAAAUGAGUCUCACUUGACUAGUGUCAGAUGUGUGAGUCACAAAAUA	138	spiLA0480-miR8011a-4-5p	UUGUGUGAGGCUUCUUUUUGUCUC	26-49	stu-miR8011a-5p	2	0	24	24	1
spiLA0480-MIR8648	CGGUAUAAUUUACUAUACAUAUACAAUUAUAUAAGUUGCUGGCCUAAAUUGUAUAAUUCGCUGGCUUCGCUAUACAUAUACAAUUGUAUGAUUCGCUAGUCUAUUUUGCUGCAAUUGUAUAAUUCGGUGGCCUAUUUCAGCGCAAUUGUAUAAUUCGCUGGCCUAUUUCGCUGCAAUAUCUGUAUAAAAUUUGCUUUGUAUACAAUUGAAUCGAAGUAAAAUGUUUGUAUAUUGUAUAAUUAUAAAU	247	spiLA0480-miR8648-3p	UUUCAGCGCAAUUGUAUAAUU	135-155	gra-miR8648	5	0	21	21	1
spiLA0480-MIR11514-2	AUAUUAGUACUUAAGUUCACUUAUGCCCUUACCGUCAAAUACUUGGUCCAAAUACUAUGCGCAAUUGAGCAGAAUAAGGGUGUAUGUGGGCCAAGUAUUUGAUGCUAAGGGCUUAAGUACAUUGAAGUAUAAACG	135	spiLA0480-miR11514-2-5p	GCCCUUACCGUCAAAUACUUG	25-45	pab-miR11514	6	0	21	21	2
spiLA0480-MIR168	GUUUCUCAUUCGCUUGGUGCAGGUCGGGACCUACCUCGCCGGCAACAAUGGCGGUAGCUGACGGCGACGGCAGCGUACCGGUAAAAAGAAUCUUAUUUUUACAUGUUGUUGCGUAGUUUGGGUCCCGCCUUGCAUCAACUGAAUAGGAGACUG	154	spiLA0480-miR168-5p	UCGCUUGGUGCAGGUCGGGACC	10-31	lja-miR168-5p	1	0	22	22	1
			spiLA0480-miR168-3p	UCCCGCCUUGCAUCAACUGAAU	124-145	lja-miR168-3p	0	0	22	22	1
spiLA0480-MIR405d	UCGGAUUAGGUGUUUAUGAGUCCGAAAAUCUUUCCAUUUUCAUAUAAAUGUUAUGUGGUAAGGUCAAAAUGACAUGACAAUUCCAUGUGGCAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUAAUGCACAAAUCAUC	136	spiLA0480-miR405d-3p	AUGAGUUGGAUAUAAUGCACAAAU	109-132	ath-miR405d	6	0	24	24	1
spiLA0480-MIR158	CUUAUUAGCAUCUAGCCAAGCUUUUUAAAGAGUCCGGAGCCUAAAGGGUACAAAAUAUUAACAAAAAUUUCAAAACGUCUGCAGCGAUUUUGCUUUUUCCGGUGGAGUAAAUCGCUGUUGAUGCAACGAUUUUAUCGUUUUUGUUAAUAUAAAAUUUUAUAUAUCGUUUUGAAUUUUUCAUUAAUAUUUUAUACCCUUUAGGCUCCGGACUCGCUUUUUAAAAGUGUUUGGGGAGGAAACUAAUUUU	247	spiLA0480-miR158-3p	UUUUAUAUAUCGUUUUGAAUUU	155-176	bra-miR158-5p	7	0	22	22	2
spiLA0480-MIR535	CCCUAUGCAUAAUUUCGGUGGAGCUUACAACAGCAAGACAGUGAGAGAGAUUUUUGCUCUCUCUCAUUUUCUUGCUGUUGUAAGCUCCACCGGAAUCAUGCGUAAUA	107	spiLA0480-miR535-3p	UUGCUCUCUCUCAUUUUCUUG	54-74	vca-miR535-3p	6	0	21	21	2
spiLA0480-MIR1128-9	AAAUAAUACUCCCUCCGUCCCAUUUUAUGAGGCAAAAUUUGACCGGGCACGGAGUUUAAGAAAUAAUGAAGACUUUGAAAUGUUUAUCAAAUUGUCCUUCAAAAAAGUAAAUUCACUUUUCUCUCUCCUCAUAAAUGUAUUAGAGUACUAUGUUUAAAAUUAAGUGGGACCAACAAGAGUAAAAGAGGAAUUGUACCUUUAAAGACUUACCAUAUAAGGAAACAUGACAUUCUUAUUGAGACUGACCAAAAAGGAAAUGGUGCCACAUAAAAUGGAACGGGGGGAGUAGUACAU	294	spiLA0480-miR1128-9-5p	UAAUACUCCCUCCGUCCCAUU	4-24	ssp-miR1128	3	0	21	21	1
spiLA0480-MIR11504-2	AUAUUGUUCAGCUGAAUCAACAGGAGGAAGAGGUUGCAGUUCUGGAUAAGUGGCCGGCGGUGGAACAGCCGCUGGCAAAGGAAAAGGUCCAGCUGCUAAUGCUGGAACUUGCACACCAGCUGGCUGUGGAUGGUUAAAUUUACAGGUGAUACCAAAUUUACAGUGCCCUGUUUUCAUAUAGUGUGCACAUUCCUUUUCAUUCUGUGAAACAAACU	215	spiLA0480-miR11504-2-5p	UCAACAGGAGGAAGAGGUUGCA	17-38	pab-miR11504	7	0	22	22	1
spiLA0480-MIR10532-8	UAAAAUAAGUUCAGGGGGGUAAUAGUACCUUAGUAUAGUAUAAGUGUGUUUCUGAGAUUUCGAGCAUAGGUUGAGGGGGUACUUGGGCUUUAUCCCUAAGAACAACUAUAAAUGAGUAAAGACAAAAUUCCCUCUUGAACUUGUACCGAAAAGUUAGUUACACGCUUAAACUAUCACAGUAACAUAUUACACACCUAUAUUAUUCAG	207	spiLA0480-miR10532-8-5p	AAGUGUGUUUCUGAGAUUUCGAGC	42-65	sly-miR10532	2	0	24	24	1
spiLA0480-MIR840-1	GUAUACCCUAAGAUUAUCCUAUUAGGGGUACAUAGGCACCCCAAUGCCCAAUAUUGAGAAAUAUUGGGCAUCAAAUAGAAAAAUUGGCUAAGAUAUAUUAGCUAAUUUUCUAUAUACGAAUAAUUAAAUAUACUUUUUGGACGUUCAUACCGCAAUCCAAGAUUGUUGUUCAAUAAAUGUACCUUCAAUGAAGACCCUAAACUAAAAUUGUUUUUACUUUAACUCACAAAAAGGUAUGAGGCAUCCAAGUGUCAAGCCUAGAUACCAUGUCAUAUGAUCAAUUAAAAUGAUAAUGUAGAGUAAGC	305	spiLA0480-miR840-1-3p	UCAAUGAAGACCCUAAACUAAA	185-206	ath-miR840-5p	5	0	22	22	2
spiLA0480-MIR8006-9	UGGGACAUUGGUGUCCCUACCAUCUAAAAACUAGUAUAUACCCUUUAUACUAACGCACAUACACAUGUCAUAAUCUAAUCCACCGACCCGACAUUUAUUAAAUAUUGGAUCGAUGGUUAAUAUUGUGU	208	spiLA0480-miR8006-9-5p	GUCCCUACCAUCUAAAAACUAGU	13-35	stu-miR8006-3p	7	0	23	23	3

	CACGUGUGUCUAUUUAGUCCUCCGUUAGAGUGAAGGGUAUAUAUACUCUAGUUUUUGGACAUCAAGGGCACCAUGUCUCA		spiLA0480-miR8006-9-3p	UAGUUUUUGGACAUCAAGGGCACC	177-200	stu-miR8006-5p	3	0	24	24	1
spiLA0480-MIR7997c-18	UGACAUAUAUGUUAUGUUGCUCGGACUCUUCAAAAAUGUUGUAACAUUCAUGUUAGAUCCUCUGAAAAUGUACAACUUUUGAAGAAUCUGACAUGUAUUGACGAUAUUUUUGAAGAGCUCGAGCAACAUAGCAUAGAGUGAAA	143	spiLA0480-miR7997c-18-5p	AUGUUGCUCGGACUCUUCAAAAAU	14-37	stu-miR7997c	1	0	24	24	1
spiLA0480-MIR5637-1	ACAAAACUGUAUAAUUCGCUAUACAUAUACAAUUGUACAAUUCGCUGGCCUAAAUUGUAUAAUUUGCUGGCCUAUUUCGCUGCAAUUGUAUAAUUCGCUAUCCUAUUUCACUGCAAUUGUAUAAUGCACAAUUGUAUAGUUUGCU	145	spiLA0480-miR5637-1-3p	AAUGCACAAUUGUAUAGUUUG	123-143	ath-miR5637	6	0	21	21	1
spiLA0480-MIR12156	UCCCCUGCACGUCGCAAGGCUGAGCGCGGGGGAGAAAGCUGGCCUCCCGUGCGCCCGGCCUAAAUGUGAGUCCACGUCGACGGACGUCGCGGCAAGGGGUUGUUGAAACUCAAUUCUCUCUAGUUGUCGCGACUACAGCCCGUUGCGCGUCUGGACU	157	spiLA0480-miR12156-3p	CUCUCUAGUUGUCGCGACUAC	116-136	aof-miR12156	6	0	21	21	1
spiLA0480-MIR1134-2	GAUAAAAUCAUUGAUGAUCUUCUCAUGAAUUACUUUCUGCAAGGAUCACAAUUUGCUGAUCUUUCCCUAGCUGAUGAUAGUUGGGAAUUGGAUAUUGAAGGAUAUUUAUAUGAUUACUAAUCUAUUUGUUAUAUCUUUGCAGAAUGGCAGGCGGAGAUGAGCCUCCGCCAUGGUCGCAUAUUCGUGGCCGUGGAGGAAAAACUAGAGGAAGAGGAAGAUCAUCCUCUUCACAGACCAGAAGAUCGUCAUACGAUUCUUCCU	261	spiLA0480-miR1134-2-3p	GAAAAACUAGAGGAAGAGGAAGAU	196-219	tae-miR1134	6	0	24	24	2
spiLA0480-MIR2650	CGUGUUAAAAUUAAAAAUAUUUAAUGGGUUGAAUAGAAAUUGGGUUGGGUCUUGACGUGCCCAAGUUUACUUUGGACUCAAAUGGGGGCUAAAAUAUGUGUUCGGUCUUGACCCACCCAAUUUGACUUGAUUAAUCUCAAUAAUUUAACAUAUUGAUAUUUAACUUUAAACCAAGAACAAGAAAUGGAAGAAUGAAAGUCGUAUGGGUUCACAAAGACUCUGUGGCUAAAAAGUAAAAAAGAUAUAUUGAAGUUGUUUUGAUGAUUCAAGAAUCUUAUUACUUCAAUCUGAAGUUCUUAGUUACUUCGACUGGAUGAGUCCUAGUGAGGGAAUAAUUAAGUCAUAAUUCAUUGGUUGAUUGUAUCAUUAACCAUUUCUUUUUUUGGUAC	167	spiLA0480-miR2650-3p	GGCUAAAAUAUGUGUUCGGUCU	87-108	mtr-miR2650	6	0	22	22	3
spiLA0480-MIR8024a	CGCUACUCCCUUCGUCCCUAAUUACUUGUCCACUUUUCCUUUUAUAGUUGUCCGUAAUUACUUGUCCAUUUUGACAAAUUAAGAAAGGACGAAUUUUUUUUACCUAUUCUAUUAAAUGACUAAUUACUUUGAAAAAUGUAGAACUUUUCAUCCAUUUUAAAAUUAAUAGGGGUAAAAUGAUAAAACUCACUACGUCAUUAAUUAUUUUCUUAAUAGGUGUGCCAAUUCAAAAGUGGAAAAGUAAAACGGGAUGGAGGGAAUAUUA	222	spiLA0480-miR8024a-3p	UUCAAGAAUCUUAUUACUUCAAUC	98-121	stu-miR8024a-5p	7	0	24	24	1
spiLA0480-MIR1128-10	GGAUUAUUCAUAUAGAGAUGUCAAAUCUGAAUCAUCCUAGUUCGAGAAAUACGCCACUAACGGCCCUCGAAUCAUGGAUAAAUCAUCUUAGAGAGUAGAAUCAAGGGAUGAACGGAUUUGUACUCACAAUCUUUAUGAAUAAAAU	265	spiLA0480-miR1128-10-5p	CGCUACUCCCUUCGUCCCUAA	1-21	ssp-miR1128	4	0	21	21	3
spiLA0480-MIR10407b	GCCAGUGGGCCACCCCAAAGGAUAUAUAUUGCUACUUUUGAGGAUAUGUAAGUCGGCUAAUCCUCAAAAGUAGAAAUAUAUAUCCUUUGGGGUGGGCCCACUUGA	145	spiLA0480-miR10407b-3p	AAUCAAGGGAUGAACGGAUUUGUA	99-122	gma-miR10407b	6	0	24	24	1
spiLA0480-MIR11108s	AACGAAGCUGAUGACGUGUCUGCAGCAAGUGUUGAUGAAGAAGGAAGCUGACGAUAGGAACAGGUCCAACAAAGCUGACUGGCGAGUUUACAGCACUUGCUUCAGACACGUCAGCCAGCUUCGUUAUCGUCAAUUUCCUUCUUCAUCAACAGUUGUCC	104	spiLA0480-miR11108s-3p	UUUUGAGGAUAUGUAAGUCGGC	36-57	lja-miR11108s-5p	7	0	22	22	3
spiLA0480-MIR1098	UUUAGUUAUCUUUAACACUUGUAAGGAUAUGAUCUAUGGAAAUAAAUCUUGGCAACAAUUAAUUUGGCAGUCAUACUUGUCGAAAUUACAAGUCACAAAUGUGAAAAUUGAUAGUCAUCAAUGUGAAAGUUGGUAGCCACAUUUGUGGAAGUAGGUAGUCAAAGUUUAGUAGAGUUAGACAGCCAAAUUUUUGUUGAAAUUUGCUACCACAUUAUGUCAUUGAUGAUGUAAACAAGUGUUCAAAAAAACUCUA	253	spiLA0480-miR821e-1-3p	UAGUCAUCAAUGUGAAAGUUG	112-132	sbi-miR821e	4	0	21	21	2
spiLA0480-MIR172-7	UACAGUCGUUGUUUGCAUAUGUGGCAUAAUCAAGAUUCACGUGAAAAGUUGCAAAUUGGUUAUAUAAUUGAUGAAAUUAAUGGCUGGCUAUUUGAAACUCACGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAACGACUAUU	142	spiLA0480-miR172-7-3p	CGAGAAUCUUGAUGAUGCUGCAU	102-124	aau-miR172	1	0	23	23	2
spiLA0480-MIR7813	CAUUAAUUCAGGGAUUAGUAAUGCAUGGAUUGGUAAUGCAGGGAUUAAUAAUGCAUGGAUUGGUAAUGCAAGGAUUAGUAAUGC	95	spiLA0480-miR7813-3p	UGGUAAUGCAAGGAUUAGUAA	61-81	ptc-miR7813	4	0	21	21	1

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spiLA0480-MIR7984d-2	CACGGUAAAUUUAUGGAAAAAGGGUCUGAAAUAUAUCUGAACUUUAACCCAAAUUAUUGUAACAAUCUCCAGCUUUUGGGAGGACCUUUUACUCCGUACCUUAUAAAUACAUUAUUAAAUAGUGCAGAGGGUAAUAGGUCCUCCCCAAAGUUAGGAUUGUUACCACAAUUUCGAUCAAAGUUCGAAUAUAUUUAAAACCCUUUUCCCCUAAAUUUAUCCUUU	222	spiLA0480-miR7984d-2-5p	AUCUGAACUUUAACCCAAAUUAUU	35-58	stu-miR7984d-5p	5	0	24	24	1
			spiLA0480-miR7984d-2-3p	CAAUUUCGAUCAAAGUUCGAAUAU	166-189	stu-miR7984d-3p	2	0	24	24	1
spiLA0480-MIR8751a	UGGUUGAAUUUGAAUAUUAUAUUGACCGCUAGAUUUGUAGAUUCAAGACGUUCAUUGAUAGGGAGUACACUUGUACUCCUUAUCAAUGAAUUUCCUGAUUUCUACAACUCUCACGACCACUAUAAGAUCGAAAGUAAUUU	140	spiLA0480-miR8751a-5p	CUAGAUUUGUAGAUUCAAGACGUU	29-52	gra-miR8751a	7	0	24	24	3
spiLA0480-MIR11068e	UUCUUCAUCUUCUUAAAGCUCAUUGAUAGAGCUUUUCUUCACAUGGUAUCAGAGCACAGGAGAAUUUGAAACUCUCUGUUGAGCUCUUCAUAAUCUGAAGACAAGAGUCUAAAGAAUCUUGAAUUGAAGAUCAAUUG	137	spiLA0480-miR11068e-3p	AAGAAUCUUGAAUUGAAGAUC	112-132	lja-miR11068e-3p	3	0	21	21	1
spiLA0480-MIR5303-20	ACCCUAUGUUACUCGGACUCUCCUAAAAUGCUUUUGCACCCGGCUCGGAUCUUCAAUAAAUGCACUUAUUUGGAGGUUCUGACACGCACCUAUAAACAUUUUUGAAGAGUUCGAGCAACAUAGUCG	126	spiLA0480-miR5303-20-3p	UUUUUGAAGAGUUCGAGCAAC	99-119	sly-miR5303	0	0	21	21	1
spiLA0480-MIR5278	CAUACUUGUUGAAAUUAUUAGCCACAAAUGUGAAAAUUGGUAGACACCAAUGUGAAAGUUAGUAGCCACAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAGAGUUAGGAAACCAAUUUUUGUUGAAAUCGGUUACCACAUUAUGUCAUUAAUGAUGUAAACAAGUGUU	169	spiLA0480-miR5278-5p	GAAAUUAUUAGCCACAAAUGUGAA	11-34	mtr-miR5278	5	0	24	24	1
spiLA0480-MIR3693	AACGUAGAUAUGAAAGGUUCUGAUAGAUGGAUCCACCUAAGUUUCAGGGUGGGAAGAGUGAGGAUGCUCAUGACUUUCUGACAACAUGUCGAGACUUGCUAGAUGUUGUUGGAUUAGCUGAGUCACAUAAGUUUCGAUAUGCUACAAU	148	spiLA0480-miR3693-3p	UGAGGAUGCUCAUGACUUUCUG	59-80	pab-miR3693	6	0	22	22	2
spiLA0480-MIR5049c	ACCAUGACAAUUAAAAGUGGACGGAGGGAGUAAUUUACGCACUUCUUAAGAAAUUAUAGGUAGAAAACUAAUUUUACUAUAUUACCCUUUGAAUAUACUCCCUUAGUUCAUUUUAAUAUGUCAUCCU	127	spiLA0480-miR5049c-5p	UGACAAUUAAAAGUGGACGGAGG	5-27	hvu-miR5049c	6	0	23	23	2
spiLA0480-MIR6429	AAUCUUGAUUGCGUGUUUUUACUUGUGAGUUCCUUUCUACUGCUACAUAAGCUGAAGAAGUAGCUAUUGUGUUACAGAUCAAACCACACAUUCUAUCGUCAAAUUUAAACAGUAGUAGUAGAAAGGAACUCACAAGUAAAAACACCCAAUCCAGCAA	157	spiLA0480-miR6429-3p	UAGUAGAAAGGAACUCACAAG	116-136	ptc-miR6429	5	0	21	21	1
spiLA0480-MIR399b-3	GAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUC	86	spiLA0480-miR399b-3-5p	GGGCUACUCUCUAUUGGCAUG	13-33	sly-miR399b	0	0	21	21	1
			spiLA0480-miR399b-3-3p	CGCCAAAGGAGAGCUGCCCUG	56-76	nta-miR399b	0	0	21	21	1
spiLA0480-MIR399b-4	UUAUAAGCGAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUC	103	spiLA0480-miR399b-4-5p	GGGCUACUCUCUAUUGGCAUG	21-41	sly-miR399b	0	0	21	21	1
			spiLA0480-miR399b-4-3p	CGCCAAAGGAGAGCUGCCCUG	64-84	nta-miR399b	0	0	21	21	1
spiLA0480-MIR396g	CCUUGGAAAUAGGUGGUCUUGAACUUUUGCUACAUGGUUAAACCUUUGACGCCAAAAGUCGAUACUUGAUGUUCUGUUCAUGGGGCGCAAGAUUAAAAGUUCAAGAUCAUCCACCUCCAAAG	122	spiLA0480-miR396g-5p	GUCUUGAACUUUUGCUACAUG	16-36	gma-miR396g	6	0	21	21	2
spiLA0480-MIR5303-21	GAGCUAUGUUGCUCGGACUAUUCUAAAAUAUUGACAGGUACAUGUUGGGUACUCUAGAAAUAGUGCAUGUUUGGAGGAUCCGACAUGGGUAUGACAACAUUUUUGAAGAGUUCGAGCAACUAGGCG	126	spiLA0480-miR5303-21-3p	UUUUUGAAGAGUUCGAGCAAC	100-120	sly-miR5303	0	0	21	21	1
spiLA0480-MIR8657b-1	ACAAAGAUCCUAUUACCCCCCUAUACUUAUUAUAUAAGUAAUUUUCUAUCCCUUUUGGCCUACGUGACACUAGCUUGAAAAAAUAAUCAACCAGCGUUGAGCCCACAAGAUAGUGUCACGUAGAUCGAAAAGGAUAGAAAAUUAUUAAUAAAAGAAAUUCAGGGAGGUAAUAAAACCUUAGC	182	spiLA0480-miR8657b-1-3p	AUUAUUAAUAAAAGAAAUUCAGGG	141-164	gra-miR8657b	7	0	24	24	3
spiLA0480-MIR9563a-2	AUACUACAAGACUAUUUGUUGUUGAAGCUUCUGCUUAAGUUGGUGUCUUACCUUGCAAUUCACUUCUAUGGUACUUCAAAAGCAGAAGCGAUCCACGAUAGAAGUGAAUUACAAGUUAAGACACCAACUUAAGCAGAAGCUUCAACAACAAAUAGUCUGGAGAGG	165	spiLA0480-miR9563a-2-3p	UACAAGUUAAGACACCAACUU	110-130	bra-miR9563a-3p	6	0	21	21	1
spiLA0480-MIR8001a-3	AUGGGGAUUUUCCUGGGGAUUAGUAUGAAAAUUCGUACCAAACUUAUUUUUCUGCAAAUUUUCAUACUAAUUCCAGGAAAAUCCCCUU	88	spiLA0480-miR8001a-3-5p	UCCUGGGGAUUAGUAUGAAAAUUC	11-34	stu-miR8001a	0	0	24	24	1
spiLA0480-MIR7992-16	UGGUAAGUAAGUAAUACCACGUAACUUUGAGAGUGCACAUCUAGAUACCUCAACUAGACCCUCCAACUCGUGCCCGCUGUGUCUU	237	spiLA0480-miR7992-16-5p	UUUGAGAGUGCACAUCUAGAUAC	26-49	stu-miR7992-5p	4	0	24	24	1

	GUAGACACUUGACAUUAAAGUAGCAGAUAAACUUUAGAGGUGUCUCAAUGAUGAUUUUGUAGAUGUUGGAGUAUUUAACUAACACAUUGGAGACGAGUUGAGGUGUCUAGAUGUGCAUACUCAAAGUUUAAGUGUUUGUUUCUGUAUUAUGC	spiLA0480-miR7992-16-3p	UGUCUAGAUGUGCAUACUCAAAG	189-211	stu-miR7992-3p	6	0	23	23	1
spiLA0480-MIR7981-11	CUAUGACCGAAAUCUCAGAGACACACCUUAACUUAACUAAGGUUCUAUUAAUCUCAACUCAUUUGUUUUGUAAUUUUGUACUGGUACACUCCGUGACUCGAGGCGCGUGAGAGAUGUUUGGAUGUCAGUGUACAGAAUUACAAAAAAAAUGGAUUCGGGGGUAAUAGGACUUUAGUUUAGUUAAGGUCUGUCGCUCGAAUUUCGAUCAUAC	211	spiLA0480-miR7981-11-5p	CUUAACUUAACUAAGGUUCUAUUA	27-50	stu-miR7981-5p	5	0	24	24	2
			spiLA0480-miR7981-11-3p	AUAGGACUUUAGUUUAGUUAAGGU	164-187	stu-miR7981-3p	0	0	24	24	1
spiLA0480-MIR3515	UCGAAUCCUUAUUAAUUUGGAUGUCAAUCAAAAUAUAUUGUUUCAUGUUUAAUAUCUACAUUCAUAUGUUUUUGAGGUUAUCACGGGCCGAUGACCCCUACCCUUGGGUAGGUCCAGAGGCGGACCGACAUGGUGUUCGCCGGGUGCUUGAGUACCUAUUAACUUCGUUACGGAAUAUAUAUAUCUAUGUAGAAAUUGAUAUGGUAUUUGUAUAAAAUUAACAUAGAGCACCCAAUGAAUAAAUGAUUUAG	250	spiLA0480-miR3515-3p	UAUGUAGAAAUUGAUAGGUAU	186-206	ahy-miR3515	4	0	21	21	2
spiLA0480-MIR5174d-1	AUGCUACUCUCCAGCUUCGUGGAACAGCGAGAGACUGGUGGAGGACUUAUUUUGGAUGUUUGCCAGUUGGAUCUCCUCCAGUGAAUUGGGAGCAGUUUGCUAGUGCAUUCCAAGAUCGUUUUAUCCCAUGGAGCGUGAGAGAGGAGAGU	149	spiLA0480-miR5174d-1-5p	CCAGCUUCGUGGAACAGCGAGAGA	11-34	bdi-miR5174d-3p	7	0	24	24	1
spiLA0480-MIR6204	AUCAACCGUAAAGAAGGAUCUAUGACGGUCAGGGAGUAUUUCUGAAGUUUGUGAAGCUAUCAAGGUAUGUUACUUCCCUUGAUAUUUAAUAGAAAGAAUGAGGAGAGUACUUAGAUUUGUUGAAAUUAUCCAGGUAUGCUACUUCCCUGGUUUCGAACAACAGGGAUGAGAUGCGAAGGUUCCUCACAGGAAUCAAUGGAGACCUGGAGGAUGAGUGUCGGUCUGCGAUGCUCCAUGAUAAUAUUGACCUUUCUAGGUUAAU	263	spiLA0480-miR6204-5p	AGGAGAGUACUUAGAUUUGUUG	102-123	hvu-miR6204	6	0	22	22	1
spiLA0480-MIR10532-9	AAUGCACAAGUACCCCUCAACAUAUCCUGAAAUUUCAGAGACAAACUUAUAUUAUACUAAGAUCCUUUGUAUAGUAUAAGUGUGUCUCUGAGAUUUCAGGCAUAUGUUGAGGAGGUACUGGUGCAUUGCUAUAUCGGCUUCUCUGGCUAAAGAGGCAUAGGUAUUACCUUGCUCUUUUUUAUGCAGAUAUGCUUGAAUCUGUUCAUAUACU	127	spiLA0480-miR10532-9-3p	AAGUGUGUCUCUGAGAUUUCAGGC	78-101	sly-miR10532	1	0	24	24	1
spiLA0480-MIR8170	GAACUAUCUUUUGGGAUAUCUUUUAUAUUCAGAGAGGAUGAAACUGAUGAAGAAGCUUCGCCAAUCUUUGAAUUGAUUAAAGUUUUUCUUCCUAACUGUAUAACAGGAAAGGAAGAAUCGUAUGACGAUCUUCUGGUCUGUGAAGAGGAUGAUCUU	240	spiLA0480-miR8170-3p	UUGAUUAAAGUUUUUCUUCCU	157-177	ath-miR8170-3p	5	0	21	21	1
spiLA0480-MIR846	UGGCUAAGAUUUUUGGAGCCCAUCUAAGAAAAGGACUUUUUAGUCCGGCCUGAAUAAGCCUGUUGAUUUGAUGGGCUUGAGAAAUAUAGGUA	92	spiLA0480-miR846-3p	UUGAUUUGAUGGGCUUGAGAA	63-83	aly-miR846-3p	6	0	21	21	1
spiLA0480-MIR10532-10	GUACCCCCUCAACCUAUGCCUGAAAUUCCAGAGACUCACUUGUACUUUACUAAGGUCCUAUAAUUUAAAAUUUGUCAAUACACGCUGGGUCCACAAGAUAGUGCUACGUAAGUCGAAAAGGGAUAAAAAUUAUUUAUAAAAUAAGUUCGGGGGGAGNAAGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAUGAGGGGGGGGGGGUAAUAGGACCUUAGUAUAGUAGAAGUGUGUCUCUAAGAUUUCGGGCAUAGUUCAGGGGGGUA	265	spiLA0480-miR10532-10-3p	AAGUGUGUCUCUAAGAUUUCGGGC	226-249	sly-miR10532	1	0	24	24	1
spiLA0480-MIR3434	GUUCAAGACAACAUUUCUAGAGAGAUUCUUCCCCAGAGAGAUGAGGGAGGACAAGGUUGAGGAGUUCAUCAACCUUAAGGCCCUAUGACGGUCAGGGAGUAUUCCCAGAAGUUUGUUAAGCUAUCAAGGUAUGUUACUUCCCUUAAUAUUUAAUAACAAGAAUGAGAAGAUUACUUAGUUGGUUGUAAUUAUCCAGGUAUGCUAAUUCCCUGGUUUUGAAUAGUAGGGGUGAGAUGAGCAGGUUCCUCACAGAAUCAAUGGAGACCUAGAGGAGGAGUGUCGAUAUGCGAUGCUCCAUGAUAAUAUGGAUCUUUCUAGGUUAAUGGUGCUUGUCCAUUCGGUUUUUGUAUUUUGGACUUAGGGAUUUGAGUUUGUGGUGUAUAAGAGUCAAGUUACUGUGUAAAUAGUAAGAGUCAAGUAACUGUGUAAAUAGUAAAGGCCAAUCAUCCUUUAACAAGGAUGAAAGGUCAUUAUGUAUGUCUAUAUAAGGGGCAUUUGCCUUCAUAAAUAAAAUAUCCUUCUUCCAACAAUCUUCUCUCUACUCUAAAAUAACAAAACCGCUU	335	spiLA0480-miR3434-3p	GCUAAUUCCCUGGUUUUGAAU	201-221	aly-miR3434-5p	4	0	21	21	1
spiLA0480-MIR1520b		228	spiLA0480-miR1520b-3p	AGGCCAAUCAUCCUUUAACAAGG	102-124	gma-miR1520b	7	0	23	23	3
spiLA0480-MIR11091	CGACUGACUUGUCUACUUCAAGUGUUGAUGAAGAAGGAAGCUGAGUAUUGGAGCAUGUCGAAGGAACAUGUUCAACGAAGCUGACUGACGAGUUACAACACUGUUGAAGAUUUAGAGUCAGAUU	124	spiLA0480-miR11091-5p	UGAAGAAGGAAGCUGAGUAUU	29-49	lja-miR11091-3p	6	0	21	21	2

spiLA0480-MIR1886f-3	GAUAUGGUAUCGUGAGAUGAAAUCAGCAUUUGGACAUUUGAUUUCACGUUGAUUCCAUCUCAUGAUUCCAUGAG	74	spiLA0480-miR1886f-3-5p	AUGGUAUCGUGAGAUGAAAUCAGC	4-27	stu-miR1886f	0	0	24	24	1
spiLA0480-MIR5773-3	ACCCACCUAACCCGACCAAUUAAAAAAAUAUGAUAUGACCCAUUUUAUUUUGUCUUUAAUCCUAAUUUCAGGUUUAAAGAGAGGGAUUAAUUUAGGAUCGAAGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGUAU	155	spiLA0480-miR5773-3-3p	UUUUUAAUGGGUCGGGUUAGGU	130-151	gma-miR5773	5	0	22	22	1
spiLA0480-MIR7983-8	UUGCACUACAACAAAAAUAACCAUUAGCGGCAUUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUGUCACACUUUGUAUAUGUACCUAAAGCUUUUAGCGACAUUGGUUCUACUGACACUUAACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAGUGUCAAUAUUUAAUGCCGCUAAAAGUUGUUUUUGUUGUAGUGUUG	214	spiLA0480-miR7983-8-3p	ACUAAUGCCGGUAAAGACUUUAGC	134-157	stu-miR7983-3p	1	0	24	24	1
spiLA0480-MIR5253	AAAAUUCUUUUUCCUUUAACUAACUAAAAGGUAUGAGGCAUCCAAGUGUCAAGCCUAGAUAUGAUGUCACAUGAUCAAUUAAAAUGAUUAUGUAGAGUAAGCAGUGCCCAAGGACAUAGCGAGGAUCCUUGGGACAAUUAGUAAACAUUCCCAAAGGAACCAUAAAUAAUAGUUACUUAGGAAAUUACAACCAACCCAUGUGCAAGCACAUGUACAACACAUGUGAAUAAGCACCAAAGGAGGGGACCACCCUAACCGAAUUCGGUUAGGUUAGUUAAGGGGAAAAAAAUGUG	293	spiLA0480-miR5253-5p	AAUUAAAAUGAUUAUGUAGAG	77-97	mtr-miR5253	5	0	21	21	2
spiLA0480-MIR7981-12	ACCUUAACUAAACUAAGUUUUUAUUACCCCUGAAUUUAUUUUUUAGAUAAUUUUGUACACCUUUUUAGCUACGUGGCAUCCAAAAAUCUCCCACGCGUCUCAAUUGCGUGUAGUCACGGAGUGUGUCAAGUAACACGAAAGGUGUAUAAAAUUGGGGAAAAAAAAUAAGUUCAGGGGAUAAUAGGACCUUAGUUUAGUAAAAAU	204	spiLA0480-miR7981-12-5p	CUUAACUAAACUAAGUUUUUAUUA	3-26	stu-miR7981-5p	6	0	24	24	2
			spiLA0480-miR7981-12-3p	AUAGGACCUUAGUUUAGUAAAAAU	181-204	stu-miR7981-3p	4	0	24	24	1
spiLA0480-MIR8006-10	UAUCCUCUGUCAUAUUUUGGAGACAUUGCAUAUAUGCCUUUUACUCUGACGAAAGACUAAACAGGAACACAUGGUGCAAUCUUAUCUGUCGAUUCAAUAUUUAAUAAAUGUUGGAUCGGUGAAUAAGAUUAUGACACGUGAAUGUCAGUUAGUAUAAAAGGUAUGUAUGCUCUAAUUUUUUGACGACAUGGGUACCAAUGUCCCAAAAGUAUGACGGAGGAUA	223	spiLA0480-miR8006-10-3p	UAAUUUUUUGACGACAUGGGUACC	173-196	stu-miR8006-5p	4	0	24	24	1
spiLA0480-MIR1531	CAUAACACAUGCCUAAAUAAUUAAUUGUUCAGCUCUUCCUCCACAUCCAUUCAAAUGGUUUGAAUGGCCAUGGAGGAAGAGCUGAGUAAUUAAUUAUUAAUGUUGUUGUUGUU	113	spiLA0480-miR1531-3p	CCAUGGAGGAAGAGCUGAGUAAUU	68-91	gma-miR1531-5p	7	0	24	24	3
spiLA0480-MIR8639e-3	CUACAUUUUUAGGCAUAAUACAUAAACAUGACAUUUAACUUACAUUUAGCGGACAACUGUAACCUCCUACUUUGAGUGUACACAAGUAGACACUUAAAUUUUUAUAAAAUUAAACAAGUAGACAUAUGUGUUCUACAUGACAUAACGCAUGUAGGAUGUCGUGUAGGACCAAAAUUGUCAUGUAUGGUGCCAUGUAAAAUGGAU	205	spiLA0480-miR8639e-3-3p	UAAAUUUUUAUAAAAUUAAACAAG	95-118	gra-miR8639e	6	0	24	24	1
spiLA0480-MIR5174d-2	AGAUAUACUCCCUCCGUUUAAAAAAGAAUGACCCUGUUUUCUUGUUAGUAUAAAAAAAUGGCCCCUUUCCUUUUUUGACAACACUUUAACUUUAACUUUCCACGUGGCAUGUUUAAGACCACAAGAUUAAAGGGCAUUUUGGUACAUUUGACAUAACUUUAAUUUUGAACCACAAGAUUAAAAAGUUUUCUUUCUUUUCUUAACUCUGUUCCAAGUCAAACUAGGUCAUCCUUUUUGAAACGGAUGGAGUAUAAUA	256	spiLA0480-miR5174d-2-5p	UCCCUCCGUUUAAAAAAGAAUGAC	9-32	bdi-miR5174d-5p	4	0	24	24	1
			spiLA0480-miR5174d-2-3p	CAUCCUUUUUGAAACGGAUGGAGU	227-250	bdi-miR5174d-3p	6	0	24	24	1
spiLA0480-MIR5637-2	AAUAUAUAACUAUAUAAUUCGCCAUACAUAUACAAUGGUAUAAUUCGCUGGCCAAAAUUGUAUAAUUCGGUAGUCUCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGCCUAUUUCGUUGCAAUUGUAUAAUGCGCAAUUGUAUAUUUCGCUGGCCUAUUUCGCCGCAAUAUGUGUAUAAAAUUUGCUUUGCGAUCAAAGUAAAAUGUUUGUAUAUUGUAUAAUUAAGAGUAUAUGAA	269	spiLA0480-miR5637-2-3p	AAUGCGCAAUUGUAUAUUUCG	161-181	ath-miR5637	3	0	21	21	1
spiLA0480-MIR7983-9	UAUGUCCUUAAAGUCUUUAGCGACAUUGGUUCUAAUGACAGUUAACUAAUGCUGGUAAAGACUUUAGCACUCU	73	spiLA0480-miR7983-9-5p	UAAAGUCUUUAGCGACAUUGGUUC	9-32	stu-miR7983-5p	0	0	24	24	1
			spiLA0480-miR7983-9-3p	ACUAAUGCUGGUAAAGACUUUAGC	45-68	stu-miR7983-3p	2	0	24	24	1
spiLA0480-MIR8564-2	GCCCUUCAACUUUGGAUGUGCACAAGUAGACACUUAAACUUAUAUAAAGUUGAACAAACAGACACACAUGUCUUACAUGUCAUCCUACAUGUCAUUUUGUUGCCAUAUGUGAUGCCCUACGUGUAUUGUGCCCUGUUGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAACGUGUCUGUUUGUACAUUAUGAAAGUUGGAGAUC	210	spiLA0480-miR8564-2-3p	CCCUGUUGGACUCAUGUGUUUAUU	131-154	atr-miR8564	6	0	24	24	3
spiLA0480-MIR8766	GUAUAACUAAUACCCACAUAACUUAUUUCACUUUCUACCCUGCAUAACUUUAUACAUAGAUUCCCUCAUAAGUUAUGUUGGUAUUA	93	spiLA0480-miR8766-3p	UUAUGUUGGUAUUAGUUAGGU	73-93	gra-miR8766	5	0	21	24	1

	GUUAGGU										
spiLA0480-MIR159b-7	AGAGUUUUGAAUGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUG	198	spiLA0480-miR159b-7-5p	AGCUGCUAAUCUAUGGAUCCC	58-78	cas-miR159b-5p	1	0	21	21	1
			spiLA0480-miR159b-7-3p	UUGGAAAGAAGGGAGCUCUAC	165-185	sly-miR159b	0	0	21	21	1
spiLA0480-MIR159b-8	AGGAAGAUCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAGCUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUAUUUUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCUUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUGGUUUUUUU	215	spiLA0480-miR159b-8-5p	AGCUGCUGAUCUAUGGAUCCC	67-87	cas-miR159b-5p	2	0	21	21	1
			spiLA0480-miR159b-8-3p	UUGGAAAGAAGGGAGCUCUAC	174-194	sly-miR159b	0	0	21	21	1
spiLA0480-MIR11044	UAGAUAAGUAUUUUUUAGUUUGUAUGUAAAAUUAUUAAUAUGAAAUAAAAAGUGAGUUUUUAUAUCAUUCUUCUUAAAACUCCAUAUAUAGUCGAAAGUGAAGGUUGCGAUCUUCAGCCUUAAGGAGGAACAGUAACAAAGUAGCCAAAGACUGCGGUCGCCAGGGUGAAACACUGUUCAUGGCCUGAAAGGAGAAAUACUGCGGCAUUGAUAGAGACUAUUCAUCGACAAAAGAGAAGAAAGGUAUACACACAAACUUUUUAUUACAUACUAUAUAAUUUUACAGAUAUACUAUAUACACUUAUUUU	308	spiLA0480-miR11044-5p	AAGUAUUUUUUAGUUUGUAUGUA	6-28	seu-miR11044	6	0	23	23	2
spiLA0480-MIR9751	UUGGAUUAUUCCGUUAAAUGGGGGCUGAUUUUGGUGAAAUUAGUAACGGGAGGGGUAAAAUUAACUCCAUUUUAACGGAGAGGAUAAAUUUAAACAAUAAAUUAAAGUCGAGGGUAUUUUUAACCCUUAUCCCUUUAAAUAACUAAAUAUAGCCAUGGUUUAAUAAUCAAUCAUU	175	spiLA0480-miR9751-3p	GUAUUUUUAACCCUUAUCCCUUUA	114-137	gma-miR9751	6	0	24	24	1
spiLA0480-MIR8763-2	UCCAUUCAUACACCUCAUUACCACUGUAAGAUGUGUUAGUUUGAUUUCAAUCUCUUUCUUCAACUAGCACAUCUUGAGGAGUAGGACGAGGAUAAUAAU	99	spiLA0480-miR8763-2-5p	UUACCACUGUAAGAUGUGUUAGU	18-40	gra-miR8763	6	0	23	23	1
spiLA0480-MIR398-2	AUGAACAAUGGUGCAUCCCAGAGGAGUGUGCCUAAGAACACAGGUGUAUUUUGGUCUUCUCCUGUUUUGGACCCAAAGUAUGCUUGUGUUCUCAGGUCACCCCUUUGGGAUCACCUUGCUUUUU	124	spiLA0480-miR398-2-5p	GAGUGUGCCUAAGAACACAGGU	24-45	lja-miR398-5p	4	0	22	22	1
			spiLA0480-miR398-2-3p	UUGUGUUCUCAGGUCACCCCU	84-104	lja-miR398-3p	0	0	21	21	1
spiLA0480-MIR319a-4	GUAUAAUAUAUGUAGAGAGCUUUCUUUAGUCCACAUAAAGGGGGCAGUAUGGUUCAAUUAGCUGCUGACUCAUUCACACAAAUGCUAAGGCUUUGAGAAUUAUUAGGAGGAAAAACCUUAGUAACUGAGUGAAUGAUGCGGUAGGCUGACUGAAUCUUAAGCUUUUUUUGCUUGGACUGAAGGGAGCUCCCUCUUCGUAAUUACUU	206	spiLA0480-miR319a-4-5p	AGAGCUUUCUUUAGUCCACAU	16-36	stu-miR319a-5p	3	0	21	21	1
			spiLA0480-miR319a-4-3p	UUGGACUGAAGGGAGCUCCCU	172-192	aof-miR319a	0	0	21	21	1
spiLA0480-MIR11464a-2	GCCCUUCAACUUAGGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAAUAAACGGACACACAUAUCUUAAAUGUCAUCCUACAUGUCAUUUAUUGUCAUAUGUGGUGUCCUACGUAUAUUGCGCCAUGUAGGACUCAUGUUUUAAUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUGGAGAUA	209	spiLA0480-miR11464a-2-3p	GUAGGACUCAUGUUUUAAUUU	134-154	pab-miR11464a	6	0	21	21	2
spiLA0480-MIR8739-5	AGUAUAAAUAUAUCCACUUAAACUAUCGUAAAUAAUAUACAGAUACCUUUCGUCAUACUUUAAGAAUAUUGAUGUCUCCGUCGUCCAAAAAACUAGAGUAUGCCUUUUAGUCCAACGGAAGACUUAAUAGGGACACAUGUCACAAUCUCAUCCAUCGAUCUGAUCGAUGUCGAGUCAAUGGAUAAGAUUAUGAUACGUGUAUGUCUGUUUGUAUAAAGUGUAUAUAUAUCUAAUUUUUGGACGGCAAAGAAACCAACAUUCCUAAAAUAUGACAAAAAAUAUCUACCUACCGUUUAUGAUAGUUCAAGGGUAUAUUUAUUUU	323	spiLA0480-miR8739-5-5p	AGACUUAAUAGGGACACAUGUCAC	120-143	gra-miR8739	7	0	24	24	3
spiLA0480-MIR7992-17	AAGUGUCUAUUUGUGCACAUCCAAAGUUGAAGGACAUAAAUGUAAUUUGAAGCCAAGUUAAAAGACACAUUUAAGUAUCGUAUAAUACAUAAAUAUAUCCUUUAACUUGGCUUCGAAUCACAUUUAUGCCCUUCAACUUUGGGUGUGCACAAGUAGACACUU	162	spiLA0480-miR7992-17-5p	UGUCUAUUUGUGCACAUCCAAAG	4-26	stu-miR7992-3p	7	0	23	23	1
			spiLA0480-miR7992-17-3p	UUUGGGUGUGCACAAGUAGACACU	138-161	stu-miR7992-5p	6	0	24	24	1
spiLA0480-MIR9476-3	AAACUGCUAUUGGUCUAGUCCUGCAUCUUUUUUUACAUUUUUUCCGUUAUCAAAAAAUAUAAAAAAAGAUGCAGGACUAGACCAA	94	spiLA0480-miR9476-3-5p	UCUAGUCCUGCAUCUUUUUUU	14-34	sly-miR9476-5p	0	0	21	21	1

	UAGCAGGAU		spiLA0480-miR9476-3-3p	AAAAAGAUGCAGGACUAGACC	63-83	sly-miR9476-3p	0	0	21	21	1
spiLA0480-MIR5205a	GUAGUCUAAAUUAUUACUCCCACCGUCCUAUUUUAUGUGUCA UCAUUUCCUUUUUGGUCCGUCCCAAAAAGAAUGUCACAUUUU CUUAUAUGUUAAAUAUUUAAAGGUACAAUUUCUCUUUUACCAU UGUUGGUCCCACUUAAUUUUAAAUAAUACUCUAAUACAUUUAU GAGGAGAGAGAAAAGUGAGUCUACUUUUAAAGGACAAUUUGA UAAACAAUUCAAAGUCUUCAUUUAUUUCCUUAACUCCGUGUCG GGUCAAAUGAUGCCACAUAAAAUAGGACGGAGGGAGUAUUAU UUUAACAAU	306	spiLA0480-miR5205a-3p	CACAUAAAAUAGGACGGAGGGAG	269-291	mtr-miR5205a	5	0	23	23	1
spiLA0480-MIR10532-11	UUUAUUGAAUCAUUGAACCACACAUAAGUGUGUCUCUGAGAUU UCGAGCACAGGUUGAGGAGGUACUUGUGCAUUAUCCCAAGUU AAAUUGGUGAAUAUCAUGUUGGAAUUAAGUUAAAACUAAACUA AUUAGACUUAGAAAGUUCUUAAGUUCUUCAAAUUAGCUAAUGU GAUUAAGUUGGUUAAUAUAGUGUUGGAAUUGAGUUAAAACUAA ACUAAUUAGACAUGGGAAGUUGUUAAGUUGUUCAAUGAGUUA AAUUGG	262	spiLA0480-miR10532-11-5p	AAGUGUGUCUCUGAGAUUUCGA GC	26-49	sly-miR10532	1	0	24	24	1
spiLA0480-MIR160-4	GACAUGAAACUCUAUACAUGCUUAGCUCCUAGAAUGCCAUCUG AAAAGGCCAUCAAUUCUUGGUGGAACAAUGCAAAUGGCAUACA AGGAGCCAGGCAUGUUGUGUUAUCGAUCAC	116	spiLA0480-miR160-4-5p	UGCUUAGCUCCUAGAAUGCCA	19-39	vca-miR160-5p	4	0	21	21	1
			spiLA0480-miR160-4-3p	UGGCAUACAAGGAGCCAGGCA	78-98	aau-miR160	1	0	21	21	1
spiLA0480-MIR7983-10	AUCAUAUACACUACAUCAAAAAUGAGCUUUAGCGGCUAUUAAC ACUUUCUGUAUGUGUCUCUAACGGCUUUAGCAACAUUGGAUC UAGUGACAGUUAACUAAUGCCGGUAAAGACUUUAACAAUUUUU AUUAAUGUAUCUAUUUAUUGUCGCUAAAAAUUAUUUUUGUUGU AGUGACAUCAA	182	spiLA0480-miR7983-10-5p	UAACGGCUUUAGCAACAUUGGAU C	62-85	stu-miR7983-5p	4	0	24	24	1
			spiLA0480-miR7983-10-3p	ACUAAUGCCGGUAAAGACUUUAA C	98-121	stu-miR7983-3p	0	0	24	24	1
spiLA0480-MIR171a-7	GUGUGAUGUUGGAAUGGCUCAAUCUAAUGAAAGUUUCCAAAC AUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAU AU	86	spiLA0480-miR171a-7-3p	UGAUUGAGCCGUGCCAAUAUC	62-82	aof-miR171a	0	0	21	21	1
spiLA0480-MIR8707	AAAGACGUUUUACCCCUGCACUGUUUAAUAAUGUAUUUUAAAG GUAUAUAUGUGCUUACAUGGGCAUAAAAAAUAUUGCAUAAUUA UAAAUAGUAAUGUGUCCACGUGGACACAUAUAUACCUUUAAAA UACACUAUUAAGUAGUUCAGGGGCUAAAUGGUCCUC	165	spiLA0480-miR8707-3p	AUAAAAAAUAUUGCAUAAUUAUAA	66-89	gra-miR8707	7	0	24	24	1
spiLA0480-MIR11466a	NNNAACCUCUUAAUGGAUUAUACUUAUUUAUUAUGAAAUAAUA AUGAUUUAAUAAUCAUCUUGUCUAGUCACUACUACAGCUUUCU UCUUUGGUUAGUUACCCUAACAGCGCCUCAACUUUGUUUACU CCCCUAAACGGCUUUCUUGCCUACCGGUUUCAACCUUAGGAU GACAUAGUCUGGGCAUACUUAUCCAGAGAAUAUUUCUGUAGC AAACCUUCUAGAGAUGUUUAUUAAAGCAUUAUUAAGUCAUGAU AAACAAUUAUAAUCAACAAGAGAUUUUC	283	spiLA0480-miR11466a-3p	AUCAACAAGAGAUUUUC	267-283	pab-miR11466a	4	0	17	21	2
spiLA0480-MIR6110-2	UUUUUGACACGUGGCCAAUUAUAAUUCGGCCACGUCAUCAAU UUUUUUAAGAAAAUAAAAUUAUUUUAAAAUUGAUGACGUGGCC AAUUGUAAUUCGUCCACGUCAUCAAUUU	113	spiLA0480-miR6110-2-5p	GGCCACGUCAUCAAUUUUUUUAA G	28-51	cca-miR6110-3p	6	0	24	24	3
			spiLA0480-miR6110-2-3p	AUUAUUUUAAAAUUGAUGACGUG G	60-83	cca-miR6110-5p	7	0	24	24	1
spiLA0480-MIR1512c	GAGGUAAAGCAGAAACUCUUUCAAAUAGAGCCAAAUAGUUCUA AGAAUUCUAAGUUGAUCCUCACUAGCACCACAAAGAUUUUUUU UAGUUUCAAAAAACAUAUUCUGUGUGGUGCUGAUGACGAUUA ACUUAGAAUUCUUGGAGCAUUUUGCUCUACUUGAAGGAGUUU UUGGUUUACACA	182	spiLA0480-miR1512c-3p	UAACUUAGAAUUCUUGGAGCAU	127-148	gma-miR1512c	4	0	22	22	1
spiLA0480-MIR167b-4	GGAAGUUUGUUUUAGUUAUUGAAUGUGCUAAGUACGAACGGA AACCAUAAUCGGAUUAUUAGUGGUGUCAUGUUGGUGCUUGGG CUGUUUUGAUUAAAUCAAACUGUG	108	spiLA0480-miR167b-4-3p	UGUCAUGUUGGUGCUUGGGC	66-85	mtr-miR167b-3p	6	0	20	20	3
spiLA0480-MIR11451	GAGUUAGGGGUCGUUUGGUAGAGUUUCUUAGAAAAAAUAAUG CAUGCAUUAGCCUUGUGUAUUACUAGUACCUUGUUUGGUACU CUUUUCCAACCUAUGUAUAACACUCUAUAGUGUAUUACGAUGU AUAUUGCUAAUACCAUUGAUUUCUAGAUAUGAUUUUAAUGCAU GCAUUAGCAUGAUUAAAGACCAAUUGCAUCUUAAAACCUUUUU UUACAUCCUUUCCACCAUAAUAGUGGAGGUUAUCUUUGUAAAU UAAAUUUAUUAUGCAAUGCAUGCUAUUUUUUUAUGCAUCAAAC CAAAUGAUGCAUAAAAA	316	spiLA0480-miR11451-5p	GUAUUACGAUGUAUAUUGCU	116-135	pab-miR11451	5	0	20	20	3

spiLA0480-MIR6230-2	AGCGCACAUCGAGACACCUCAACUUGGUAUCAAAUGAACACUAAACACUUCAACUAGACCCCACUGUGUUUCAUGGACACCCUGCGUUGACAUGGCACAUAAAUUUUGGAGAUGUCUAGAUGAUCAUAUUUGUAAGUUGGAGUGUUCAUCCGAUACAGUGGAGACAAGUUGAGGUGUCUAGAUGUGCAUU	190	spiLA0480-miR6230-2-3p	AGACAAGUUGAGGUGUCUAGA	162-182	sbi-miR6230-3p	5	0	21	21	3
spiLA0480-MIR10429	UAAUUUUAUGCACCUUUUGGCUUACGUAACAUCUAAAUAUCUCGCACGGGUCUCAAUUUCGUGGAGUUACGGAGUGUGUUACGUAAGACAAAAGAUGUACAAAAUUA	107	spiLA0480-miR10429-3p	GUAAGACAAAAGAUGUACAAAAUU	83-106	gma-miR10429	7	0	24	24	3
spiLA0480-MIR11574	AAACUUUAUGGAAGAUCUUUUACCCCUAAGCUAUUUAAUAGUGUUAAAGGUAUAUAUGUGCCCACGUGUACACGUCACUAUUUAUCAUUAUGCAGUAUUUUUUAUGCUCAUGUGAACACAUAUUUACCUUUAAAAUACACUAUUAAAUAGUACACGGGAUGAAAGGUCCUUCCCAAAGUUU	181	spiLA0480-miR11574-5p	AUGGAAGAUCUUUUACCCCUA	8-28	pab-miR11574	4	0	21	21	2
spiLA0480-MIR7825	UAUUAUAGUCUGUAUGUAAAACUAAAAAUAUGAAAUAAACAGUUGAUUUUUUAUAUCCUUUUUCUUAAAACUUCAUUAAUAGUCGUAAGUGAAGGUUGCAAUCUUCAGCCUCAGGGAGGAACAGUAACAGAGUAGCCAAAGACUGAGGUCGUUAGGGUGAAACAUUGUUCAUGGCCUAUAGGGAGAACUACUGCGGUAGUGAUAAAGACUAUUGAUCGACAAAAGAGAAGAAAGGUAUACACGCAAACUUUUUUUAAAUAUUAUUAAAUUUACAAAUAUACUAUAUGU	288	spiLA0480-miR7825-3p	GAGAAGAAAGGUAUACACGCAA	224-245	ptc-miR7825	7	0	22	22	3
spiLA0480-MIR827-4	UUGUGUAGUUAUGAAUUUGUUUGUUGAUGGUCAUCUAUUCAUCAUAUCAUUUGGCAUAGUUUUUGGAACCAUUAAUAUGCCAUGAUUAGAUGAACAUCAACAAACAUCUUCAUCACUUCAUGU	123	spiLA0480-miR827-4-5p	UUUGUUGAUGGUCAUCUAUUC	20-40	stu-miR827-5p	0	0	21	21	1
			spiLA0480-miR827-4-3p	UUAGAUGAACAUCAACAAACA	86-106	sly-miR827	0	0	21	21	1
spiLA0480-MIR5532-1	ACCCUUAUUGGAUGAUAUAUAUGCCAAAUAUGAUUAAUGUAACAUUCUGAAAAAUUACAUGUCUAAUGAAGAUCCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGAUACAUAGGCAUAUCAAUUCCGAAUAUUGAGAAAUACUGGGCAUAGUAUAGUUGCUUAAGGGGUAUUAGCCAAUUUCUAUAUAAUACCCAAAUAAGCAG	203	spiLA0480-miR5532-1-5p	AUGAUAUAUAUGCCAAAUAUGA	12-33	osa-miR5532	6	0	22	22	1
spiLA0480-MIR3444b	CCAAAUAUGAUUAAUGUAACAUUCUGAAAAAUUACAUGUCUAAUGAAGAUCCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGAUACAUAGGCAUAUCAAUUCCGAAUAUUGAGAAAUACUGGGCAUAGUAUAGUUGCUUAAGGGGUAUUAGCCAAUUUCUAUAUAAUACCCAAAUAAGCAGAAUAUUGGCUUAAAGGGUGUUAGACAAUUUUUCUAAGUAUUAAUGAGAUUGUU	233	spiLA0480-miR3444b-5p	GUCUAAUGAAGAUCCCAAUAG	38-58	aly-miR3444b	6	0	21	21	2
spiLA0480-MIR1534-1	GAACCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGGUACAUAGGCAUCCCAAUGCUCAAAAUUGAGAAUUAUUGGGUAG	78	spiLA0480-miR1534-1-3p	UAUUGGGGGUACAUAGGCAU	27-46	gma-miR1534	4	0	20	20	1
spiLA0480-MIR156b-6	AUUGAUUUGUGUAAAAUGUAGGGAGGAAAAAAAAAGAGGGGAAAAUGGAAUGGGUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUCUCCUUCUAUUUUUCUCUUUUCUCUCCCUAAAUCUAUACAAUAACUCGUU	246	spiLA0480-miR156b-6-5p	UUGACAGAAGAUAGAGAGCAC	63-83	aof-miR156b	0	0	21	21	1
			spiLA0480-miR156b-6-3p	GCUCUCUAUGCUUCCGUCAUC	162-182	vca-miR156b-3p	1	0	21	21	1
spiLA0480-MIR7991c-2	CAUCUUCCGUAGGUCAGAAUUUUUAAUUAUCAAAUUUUAGAAACCAACCUCCGGAAGUUGGUAUUUUUAUUUCUUAUUUUUUUAGAUUCUUACCUCUGGAGGUCGGUAUUUUCAUUUCUUAUUUUUUUAAUUCCGAUCUCUGGAGGUCGGUAUUUCUAUUUCUUAUUGUUUAGAUUCCGACCUCCGAAGGUU	192	spiLA0480-miR7991c-2-5p	CGUAGGUCAGAAUUUUUAAUUAUC	8-31	stu-miR7991c	6	0	24	24	2
spiLA0480-MIR11042	UUUAAAAACUACAGCAUAUAUACCAUUUAUAUUAACAAAUAUACACGUGUCAUAAUCUUAUCGACCGACCUCACAUUUAUCAAAUAUCCGAAUCGACGGAUAAGAUUGUGCCAUAUGUUCCUAUUAAGUCUUCUGUUAGAGUGAAGGGCAUGUAUACUCUAGUUUUUGGA	169	spiLA0480-miR11042-3p	UGUUCCUAUUAAGUCUUCUGUUA	115-137	seu-miR11042	7	0	23	23	3
spiLA0480-MIR394-2	UUUUCAUGAAGAUUUCUCAAAGGGUUCCUUACAUAGUUCUUUGGCAUUCUGUCCACCUCCUUUACCUUCAUAAUCUUCUAUUUUUUUAGAAAAAUAAUUUUUGUUAUUCUUUUUAAAAAAAAAUGGAGGUGGGCAUACUGUCAACAGAUUUGUGUUAGUUUCUCUUUGUGAAAUCUUCUUGAUGU	185	spiLA0480-miR394-2-5p	UUUGGCAUUCUGUCCACCUCC	40-60	cas-miR394	0	0	21	21	1
			spiLA0480-miR394-2-3p	AGGUGGGCAUACUGUCAACA	127-146	sly-miR394-3p	0	0	20	20	1
spiLA0480-MIR7533c	UUGAAAAUCGUCGGAUAAUUUAUUUAAAAGGGGGUUGAUUUAUGGGUCGGAUUAGGUGUUUAUGAGUCCGAAUAUCUUUUCAUUUUCAUAUAAAUGUCAUGUGGUUAGGUCAAAAUGACAUGGCAAAUCCAUGUGGCAUUUACAAAAAUUAAAAAUGAGUUGAAUAUGUC	330	spiLA0480-miR7533c-3p	AAGUUGGAUGGCGAGGGCA	212-230	lja-miR7533c-5p	4	0	19	19	1

spiLA0480-MIR159a-2	CAACAUGACAUCUAACGCCCAUAAGGGCAUAUUUGGACCAAAAGUUGGAUGGCGAGGGCAUGAGUGAACCAAACUUUAAACGGAGGGUACAUUUAGACCUUUUUGAAUAGUUUAGGGGCAUAUUUGACCCUUUUCCCAUUAAAUAAUUGGACUUUUUACCUCCAAAGCAGAGAAGUUAUGAUUUAUUAUUUGAUAACUUAUCGAAUGAGUCUGAAUGUUGUUAAGGGUCUCCCACAUAUAUGAUUCGUUCAUACCUCUUCAGACUCAUUAAGAGAUUUUUUAAAAAAAUAAAACAAAUGAACUUAAUGGGCUCAUUUAGAUUCAGACCUAAAAAUCAAACGUACUUAAUGGGGUGAAUCUGAAAAAUUAAGAUUCAGACCUCCAUUAAGUGCAAACAAAUGAGGCCUAAGCUUCGUUUGCUUUCAA	266	spiLA0480-miR159a-2-3p	GACCUCCAUUAAGUGCAAACA	217-237	aly-miR159a-5p	5	0	21	21	1
spiLA0480-MIR5290	UGGCAUAAUAGAUAUAUGCCCUUUAACUUGACUUCAAAUCAUACUUAUGCUCUUCAACUUUGUGUGCGUAGAAACUUAAACUUGUAUAAAGUUGGAGAAAUAGACACACAUAUCCUACAUGUCAUUUUUUGUCCUACGUGAUGUCCUACAUGUAUUUUGCCGUGUAGUACUCAUGUAUUUAUUUAUUUAAAAGUUGAAAUGUUAAAGUGUCUGUUUGUGCAUUAUGAAAAUUGGAGGUCAAAAUUAAAAUUUGAAGCCAAGUUUAGAAUCCAAUAUAUGUAUUAUGAUUUGCACAAGUAGACACUUAAACUUAUAUAAAAGUUGAAUAAAUAGAUACACAUGUCCUGCAUGUCAUUUUUUUGUCUUACAUGGUGUCCUACGUGUAUUGUGUCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGAUUGUUUGUACA	289	spiLA0480-miR5290-5p	AAGUUGGAGAAAUAGACACACAUA	89-112	mtr-miR5290	5	0	24	24	1
spiLA0480-MIR8614	GUCUCACACAGCUGACACUAAUUAUGUAGGGCUUCUUUUUGUCCCACAAGUUAAUGAACCCAAAUUAUUACACUUCUGGGUCCACCGACUUGUAAAAUAAAAAGAAGCCUCAAAGAACUGGUGUUAGUUGUGUGAAGG	163	spiLA0480-miR8614-3p	GGAUAGUUAAAGUGAUUGUUUGU	138-160	atr-miR8614	7	0	23	23	3
spiLA0480-MIR8011a-5		138	spiLA0480-miR8011a-5-5p	UUAUGUAGGGCUUCUUUUUGUCCC	22-45	stu-miR8011a-5p	6	0	24	24	1
			spiLA0480-miR8011a-5-3p	AAUAAAAAGAAGCCUCAAAGAACU	96-119	stu-miR8011a-3p	2	0	24	24	1
spiLA0480-MIR11551b-2	AAAAAAACUAACAGCAUUAGGUUGAUAUACUAGAAUGUAAGUAACGUUGUACUCCUAAAACGUUAUUUUCAGUAACGUUUUACUCCUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAUCAAUUUUUUU	137	spiLA0480-miR11551b-2-3p	UUUUACUCCUAAAACGUUACUG	78-99	pab-miR11551b	6	0	22	22	1
spiLA0480-MIR781b	CGUGAAAAGGGAAAAAUAGAAGAAAGAGAUGUUAGAGUUAUGUGGAUAAUUUGGAGAUUGUAUAAAAAUAUUAAGGGCAAAAAGGUAAAAAUGUGGUCAACUUAAAACAGCUUAUAAGCUGGAAAAAAAAAAGCACCCCUACCCCAGCUUUUAACUUUUAGCUUAAAAUAAGUUUUUUUUUAACUUAAAAUAAGUUGUUUUGAGUAUUGCCAAACAGGUAAAUAAGUCAAAAAUCAGCUUUUAAGUCAGUUUGACCAGCUUUUAAGCUGAGCCAAAUAUGCUCUUAAUCCCUUCUUCUCUUUUUUUUCUAU	312	spiLA0480-miR781b-5p	UUAGAGUUAUGUGGAUAAUUU	32-52	ath-miR781b	4	0	21	21	1
spiLA0480-MIR2931	AAGGGGGUAAAACUUACCCGCAUCGGGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUUAAGUUUAUUGUUCAUGUCAUGUUACUUCAUUAAAUCACAUAAUAAUGAAAAUUGUAUUGACUUGGUGUAAACACAAAGUGCAGGUAGUUUUUUCCCAAG	163	spiLA0480-miR2931-3p	GUUUAUUGUUCAUGUCAUGU	67-86	osa-miR2931	5	0	20	20	2
spiLA0480-MIR8573	UAUUAUUUAGUUUAGAUAAGUUCUUAUAUCAUUAUAAGUGUGACUGUUGUCUUCUGUUGAGUUAUGUAAGCUAGGUCAAGGGCCCGCUCGAGGCCAGCAAUGGUCAUCGAGUUCCAGUCUGGCGCAAGGUGUAGGCUCGGAGCGUGAGAUGGAGAUUGAGGAUUAGAGUAGAAGGUUAGUAGGUAGUUAAAAUUUAUCUAGUUUUUCUUGUUAAUGUUCUUUUUAUCAUUACGGACUAUCUUGUUUCAUAAUUCUUUUAUUACAUUUUUUUUCUUUUAUUCAAUAACCGUAUUACAUAUGGUUGUUACUGAGACAAGGGUCUAUCUAAAACAACAUAUCU	340	spiLA0480-miR8573-5p	CCAGUCUGGCGCAAGGUGUAG	114-134	atr-miR8573	5	0	21	21	1
spiLA0480-MIR6145b-2	CCCUUUUGGCCUACGUGGCACUAGCUUGAAGAAAAAUUUAACCAACGUUGGGCCCACAAAAUAGUGUCACGUAGGCCAAAAAAGUUUAUCAUUAUAAGUGUAAUUUUUUUUCUUCAAUUGAUUUAAGUAAGUUAGGCCAAGGGUCCGCUCGAGGCCAGUAAUGGUCAUCGAGUAUCAGUCUCAUCCAGGAUGUAGGAUCGCGAUGUGAAAUUUUUAGCGUCAAACUAUAAAAACUUUGACCAAUAUUUUACGAUGUAUAUUUUCAUCAUAUUGAUAUGAAAAAAGAUUACAAUUUAUAGUAUUUU	84	spiLA0480-miR6145b-2-5p	UUGGCCUACGUGGCACUAGCU	6-26	nta-miR6145b	5	0	21	21	1
spiLA0480-MIR9726-3	UGGUAAAUAGCGUCUUGAUGUGAAGCGAAGACACUUUACGCGAUGUAUCGGUCAAAUAUAUCACUUUAUGCUAUGUAUUAAUAGGUUGAAUGAUGUAUCUUAAAUUGAGACGCGAUAUAUCAGGACGUUGAGUGAUGUAUUCGACAUCAGGACGCAAUAUAUUG	220	spiLA0480-miR9726-3-5p	UAUAAGUGUAAUUUUUUCUUC	9-30	gma-miR9726	4	0	22	22	1
spiLA0480-MIR8580		164	spiLA0480-miR8580-3p	UGUAUUAAUAGGUUGAAUGAUGUA	74-97	atr-miR8580	6	0	24	24	1

spiLA0480-MIR8175-1	CUAUAGUAAAAAGUUCAAGUUAAUCUAAAAUCUAUGAUCCCCGGCAACGGCGCCAAAAUUUGAUACACUCAAACUUACUUCUCAAAUAAGAAGUAAAGCGGUCGUGUCAAGUAAAUAACCCAACUAGUGAGGUUGGGAUCGUUCCCACGAGGAAAAUAGUCUAGACUUAACUUCAACGUGUUAUUACUAUUA	192	spiLA0480-miR8175-1-5p	GAUCCCCGGCAACGGCGCCA	36-55	ath-miR8175	0	0	20	20	1
spiLA0480-MIR1134-3	GUUUCAAUAUUUCUCUUUGUAUUGGCUAUCAACAACAACAAGAAGAAGAAUGCCGCAUAUACGUAUUUGUAGAAAUCAGUUCUGAUGUGGCUGAAUGCCACGUUAGAGUUGAGAUGAAUAAAAAUAAAGUAUUGACUA	138	spiLA0480-miR1134-3-5p	CAACAACAACAAGAAGAAGAAUGC	30-53	tae-miR1134	3	0	24	24	1
spiLA0480-MIR5240	ACCUAACUUCAAAAGGUCAUAUCUCACUCAUCCAAACUUGAAACUUAGAAAAAUUGGUUGAUUUGGAAAGAUGAUUCAAACGUCUUUCCUAUGGUAUCUUGUAUCACACCUAGAUCAUCAUGUUCUAGGAGUUAUGAUCGUUUGAAGUUAACC	153	spiLA0480-miR5240-5p	UAGAAAAAUUGGUUGAUUUGG	46-66	mtr-miR5240	5	0	21	21	1
spiLA0480-MIR10542-3	UUUGAUAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUUUUAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAACUUCCGUCAAAUGAAGGGUAUAUCUGAGCCAUUUUGUAACGGCAGGGGUAUAUAUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGUGAGUAUAUCAGCUCUAAAUGACAAAGUUAAGGGGUAUAUCAGACCCUUUACCCUU	248	spiLA0480-miR10542-3-5p	UAGAAGAAUCAUAUAUACCCCUA	6-28	sly-miR10542	0	0	23	23	1
spiLA0480-MIR7997c-19	AAGACCUAUGUUGCUCGGACUCUCCAAAAAUCAACUACUUUUGAAGAGUCCUAUACACGUGUUGACAUUUUCAGAGAGUCCGACCAACAUAGGUAAA	97	spiLA0480-miR7997c-19-5p	AUGUUGCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	2	0	24	24	1
spiLA0480-MIR7981-13	CAGAUAUUGCUGUUCUAUCAUGCAAAGUUUAGUUUCAUUUUUAUAUGUCUUAUGUGGCACACUCCGUGACUCCACACAAUUGAUGCGUGUGGGAGAUACUUGAAAUCCAUGUAAGCUAUAAAGGUGUAUAAAUUAUAAAAAAAUAAGUUCAGGGGUAAUAGGACCUUAGUUUAGUUAAGAUGUGUCUUUGAGAUUUCGGUCAUAGUCUAGCGAGGUACUUGUGCAUUUUCCCUUUACUUAUUAAAGAAGAUCUAUAGUUCUUUCUUAUGCAUUUUGCCUGAGAAUGAUAAGCAAUAUGCA	300	spiLA0480-miR7981-13-3p	AUAGGACCUUAGUUUAGUUAAGAU	158-181	stu-miR7981-3p	2	0	24	24	1
spiLA0480-MIR7981a-37	AUAUCCCUUCUCGGCCUACGUGGCACUACCUUGAAGAAAAAAGUCAACCAGCGUUGGGCCCACAAGAUAGUGUCACGUAGGCUGAAAAGGGAGAG	95	spiLA0480-miR7981a-37-5p	AUCCCUUCUCGGCCUACGUGGCAC	3-26	sly-miR7981a	2	0	24	24	1
spiLA0480-MIR8006-11	AUAUAUUCUCGAAUUAUUAUGACUAAUAUCCUCGUCAUAUUUUUGAGACAUUAAUGUUUUUUUGUCCAAAAACUAGAACAUAUAUACCAUUUAUAUUAAUGGAUAUACAUGUGACGUAAUCUUGUUCCUAUUUAGUCUUCCGUUAGAGUAAAGGAAAUAUAUACUCUAGUUUUUGGACGGCAAGGGAACCAAUGUCCCAAAAGUAUGACGGAGGAGGGUAUGCGCAUAUCAUUAUAAUAGUC	242	spiLA0480-miR8006-11-3p	UAGUUUUUGGACGGCAAGGGAACC	167-190	stu-miR8006-5p	3	0	24	24	1
spiLA0480-MIR169ad	UGGAAAAGGGAGGUUGUGGGUUCGAACCCCCACAACCUCCUUAUUUUAAUUUAAAUUCGCUAGAGGCUGUGAGGUGGUGGGUUCAAACCCCCACAGCCUCCUAUUUUUUU	110	spiLA0480-miR169ad-3p	CCACAGCCUCCUAUUUUUUU	91-110	mes-miR169ad	5	0	20	22	2
spiLA0480-MIR7981b-22	GUCCUAUUACCUCCCUGAACUUAUUUUAUUAAUAAUUUUUUACCCCUUUUUAGCUUACGUGACACUAUAUUGUGGGCCCAACGAUGAUUAACUUUUUUUUCGAACUAGUGCCACAUAGGCUAAAAAGGGAUAGAAAAUUACAUAUAAAAUAAGUUCAGGGGGUAAUAGAACUUGAACUUUGAUAGAAGAAUCAUAUAUACCCCUAAAUAGUUUUUUUAAAAAAACUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAAUUUCCGUUAAAUGAAGGGUAUAUGUGAGUCAUUUGGUAACUACAGGGGUAUAUGUGUGCCGUUUGUAUAAUGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGAUAUAUCAGCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUCCCAAGUUUUA	171	spiLA0480-miR7981b-22-5p	ACCCCUUUUUAGCUUACGUGACAC	42-65	sly-miR7981b	1	0	24	24	1
spiLA0480-MIR10542-4	AUCAACUUAUUUUAUUAAUAAUUUUUUACCCCUUUUUAGCCUACGUGACACUAUCUUGUGGGUCCAACGAUGGAUGGUUGACUUUUUUUUCAAACUAGUGCCACGUAAGCUAAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUCAA	258	spiLA0480-miR10542-4-5p	UAGAAGAAUCAUAUAUACCCCUA	12-34	sly-miR10542	0	0	23	23	1
spiLA0480-MIR7981b-23	GAACACUACAUCAAAAAUGAGUUUUAGUCGUAAUUAAUUAGUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUAACACUCUUUGUAUAUGUCCCUAAAGGUUUCAGCGACAUUGAAUCUAAGGACACUUAACUAAUGCCGGUAAAGACUUUAACACUCUAUAUGAAUGUGUCUUUUAUUGUCGCUAAAAGUUAUUUUUGUUGUAGUGAAAGAACUUAUUUUAUCAAUAACUUUCUACUCCUUUUCUGCUUACGUGACACUAUCUAGUGGGUAUGACGCUGGUUGACUUUUUUUUCAAGCUAGUGUCACGUAGGUCGAAAAGGGGUAACAAAUUACUUAUAAAAUAAGAAA	213	spiLA0480-miR7983-11-3p	ACUAAUGCCGGUAAAGACUUUAAC	134-157	stu-miR7983-3p	0	0	24	24	1
spiLA0480-MIR7981b-24		140	spiLA0480-miR7981b-24-5p	ACUCCUUUUCUGCUUACGUGACAC	26-49	sly-miR7981b	4	0	24	24	1

spiLA0480-MIR10538-11	GACAUACAGCUAGAUAUCACAUACCCUUUGAACUUCCCAAACAGACCAUAGAGUGAUUUACGUAAUUAACAUACAAGGCUACUAAACAACCCCAAGAAACAAAAUUAGGUGGUUGCUCAGGGGUAGUCUUGUAUGUCGUUUAUGUAUGUAUGGUCUGGAACAGUCUUUGCACGCUUGGGUUGGGAAGUUCAACUGUAAUUUUAUUAGUGUAUUUU	215	spiLA0480-miR10538-11-5p	AGAGUGAUUUACGUAAUUAACAUA	50-73	sly-miR10538	7	0	24	24	1
spiLA0480-MIR9774	ACUAAGGAAUGAGUCAAAAUGACCCAUUUACAAAGAUAUUAAAUAGUUCUGUGGGGUGAUAGGACACUUUGAAAGUUAAAGUGUCUUUAUACAAAUACUGGACAACUUUGAUGGUGUCUUUAUGUCUUUUCUCUUUUU	138	spiLA0480-miR9774-5p	AAAGAUAUUAAAUAGUUCUGUG	32-53	tae-miR9774	6	0	22	22	2
spiLA0480-MIR8032e	GAAUGAUCAUUUUUUAUCAAAAAGUUCAAGAAGAUGACAUCAGAAUCAAAUUCUGACGAUUCCAUCAGUUUCGGAAGGGUCAUUUUAGGCUAGUAGCAUUGUCACCCUGACUCCCAAAGUUUUCAGUGUGAGUUGGUGUGAUUAGGCGUUUUUACUUUAAGAUAAAGGCAAAGUUUGAAUUUAGUCAACAUUCUGAGUAAACGCGCUCGGAUGAGAAUUUCGUCAGCGCGACUUGCUCCGGAAUGUCGAGUUUUGUCUAGUUUGAUCCUUCUUUUGGGUUUUGAGGUUUUUGAUAUUUUUCCAAGCCCUUUUGUGGUUUUUGACUUAAAAUGACCAAAG	339	spiLA0480-miR8032e-5p	AGUGUGAGUUGGUGUGAUUAGG	125-146	stu-miR8032e-3p	1	0	22	22	1
spiLA0480-MIR7992-18	UUUAACUUGGCUUCAAAUCACAUUUAUGCCUUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACCUGUAUGAAGUUAAAUAAAUACACACGUGUCCUACAUGUCAUUUCUUGUCCUAUUUAGUGUCCUACGUGUACUGUUUCAUGUAGGACCCAUGUGUUUAUUUAUUUAAAAGGUGGAUAUUUAAAGUAUCUGUUUAUGCAUUAUGAAAGUUGGGUCAAAGUUAAAAUUUGAAGUCAAGUUUAG	247	spiLA0480-miR7992-18-5p	UUUGGAUGUGCACAAAUAGACACU	38-61	stu-miR7992-5p	6	0	24	24	1
spiLA0480-MIR7696b	AAUUGGCUUCAAACCACAUUUAUGUCCUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACCUGUAUAGAGUUGAACAAAUAGACACACAUGUCCUACAUAUCAUUUUUCGUCCUACGUGGUGUCCUACGUGUAUUGUGUCAUGUAGGACUUAUGUGUUUAUUUAUUUAAAAAUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAAAUUGAAGGUCUAAGUUUUGAAGCCAGGU	239	spiLA0480-miR7696b-3p	GUGCAUUAUGAAAAAUUGAAG	198-218	mtr-miR7696b-3p	4	0	21	21	2
spiLA0480-MIR9746i-2	UCUUUCUCAACAAAACUAAAUGGUAGCUCGUCAACAAUUAUCGUUUUGGCUAAAGCUUUCCUACUUUGUACUUGGUCAAAUUUCCAAGUGCUAAUGACCCCUUCCUGUGAUCCCGUUGAAGAUGGUAGAAAAUUAAUUAGAUUUUGAUAUCUACGGUGUCACGAGGAAAUUUAGGACAUAUUCUCAAAUGAGUAUUCAUUGAUGACGUACCAUUAGAUGAUGUAGAAGUU	230	spiLA0480-miR9746i-2-3p	AAGAUGGUAGAAAAUUAAUUAGAU	119-142	gma-miR9746i	7	0	24	24	1
spiLA0480-MIR7997c-20	AUAUUGCUCGGACUCUUCAAAAAUGUGGACGGGUGUGUGUCGGAUGAUCCUCCAAAAGUAGUGCAUUUUUGGAGGAUCUGGCUUAGGUGCGGCAACAAUUUUGGAGAGUCCGGGUAAGUU	120	spiLA0480-miR7997c-20-5p	AUAUUGCUCGGACUCUUCAAAAAU	1-24	stu-miR7997c	0	0	24	24	1
spiLA0480-MIR11602	UUAUUUUAUAAGUAAUUUUCUGCCCCUUUUUAGCCUACGUGGCACUAAUUUUUUUAAAAAAGCUAACCAUCGUUGGCCCACAAGAUAGUGCUAUGUAGGUCGAUCUUUCCAUUCUAAUACUCUAUCCGAGAGUUAUCAGUAUUUAUCAAAUCUGUUCUUAUCUAACGGAACGCUAUUGGAUCAAAUGCCAAAGACAUUGUUGAAAAAAAGAUGGCUUUUCCCGGAUGAAAUGAAAAUUGGAUUCAUGUAACAGGAGAAAGAUUUCCCAUUCCUUAGCCGGAAAGAUAUGUGGCCAUGAAAGAGGGAAAAGGGGUAAAAAAUUAUUAAUAAAAUAA	335	spiLA0480-miR11602-3p	UCUAACGGAACGCUAUUGGAUC	161-182	pla-miR11602	0	0	22	22	1
spiLA0480-MIR8175-2	UAAGUUCAAGUUAAUCUUAAAGCUAUGAUCCCCGGCAACGGCGCCAAAAUUUGAUACGCUCAAACUUACUUCUCAAAUAAGAAGUAAAGCAGUCGUGUCAAGUAAAUAACCCAACUAGUGAGGUUGGGAUCGUUCCAACGAGGAAAAUAGUCUAGACUUAACUUCAACCUG	171	spiLA0480-miR8175-2-5p	GAUCCCCGGCAACGGCGCCA	27-46	ath-miR8175	0	0	20	20	1
spiLA0480-MIR7981a-38	UAAUUUUCUACUCCUUUUUCGGCCUACGUGACACUAGCUUAAAAAAGUCAACCAACGUUGGUACCACAAGAUAGUGCCACGUAGGUCAAAAAGGGACAUAAAAUUA	107	spiLA0480-miR7981a-38-5p	CUCCUUUUUCGGCCUACGUGACAC	11-34	sly-miR7981a	4	0	24	24	3
spiLA0480-MIR1130b-2	GAAAACUAGUACUUACUUCCAAUGUCCAACAAUAGUUGUCCAUUAUUGACUUGACACAUGAAUUAGAAACAGUUAAUGAUAAGAGUAAUUUUACCAAAUCACCCUUAUUAAGUACAAGUCAUCUAACAUUAUAAAAUGGGACAGAGGAAGAAGUAUUUAAUAGCAAGGGUAAAAUAGACAUAACAUGGUAAACUAUUCAUUGCUUUUAUGAACUUCACAAGUAUUGUUAACAUUCCAAAGUAAUAUGAUGGACAAGUAAAGAUGGACGAAAGGAGUAAUUAACUGUUAUG	290	spiLA0480-miR1130b-2-3p	CAUUAUAAAAUGGGACAGAGG	127-147	tae-miR1130b-3p	5	0	21	21	3
spiLA0480-MIR7992-19	CCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACUUGUAGAAGUUGAACAAAUAGACACUCAUGUCCUACAUGUCCAUUUUUCAUCCUACGUGGUGUCUUACAUGUAUUUUGCCAUGUAGGACU	194	spiLA0480-miR7992-19-5p	UUUGGGUGUGCACAAGUAGACACU	9-32	stu-miR7992-5p	6	0	24	24	1

spiLA0480-MIR8006-12	CAUGUGUUUAUUUAUUUAAAAGUUAGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUAGAGGUAUCUUAGUGCCCCUGUCGUCCAAAACUAGAGCAUAUAUACUUUUUAUACUAACGGACAUACAUGUGUCAUAAUCUUAUCCACUGACCCGACAUCAGAUCGAUGGAUAAGAUUGACCACGUGACUCUAUUUUGUCAAGGGCAUAUACAUUCUAGUUUUUGGACGACAGGGGCACCAAUGU	179	spiLA0480-miR8006-12-3p	UAGUUUUUGGACGACAGGGGCACC	151-174	stu-miR8006-5p	0	0	24	24	1
spiLA0480-MIR7981d-7	UGCACAAGUAUCCCCUCAACAUAUACUCGAAAAUCCAGCGACACACCUAUACGAUAAUAAAGUACUAUUACCCCCUGAACUUAUAUUAUAAGUUAUUGUAGGCCGAAAAUGGGUAGAAAAUUAUUAGUAAAUAAAUUCAGGGGGGUAAUAGGACCUUGGUAUAUUAUAAGUGUUUCCUAAGAUUUCGUUCAUAGGUUGAGGGGGUACUUGUACA	215	spiLA0480-miR7981d-7-5p	UCGAAAAUCCAGCGACACACCUAU	27-50	sly-miR7981d	5	0	24	24	1
spiLA0480-MIR6464	UAACAUAAUACAAAAGUGCCCGAAGUCAUUACCUUAACCGCAAGGAGGGGGAUGCCGAAGGCAGGGCUAGUGACUGGAGUGAAGUCGUAACAAGGUAGCCGUACUGGAAGGUGCGGCUGGAUCACCUCCUUUUCAGGGAGAGCUAAUGCUUGUUGGGUAUUUUGAUUUGACA	172	spiLA0480-miR6464-3p	CUAAUGCUUGUUGGGUAUUUU	143-163	ptc-miR6464	5	0	21	21	3
spiLA0480-MIR7981a-39	UUAUAAGUAAUUUUCUACCCCUUUUCGGCUUAUGUGGCACUAGCUUGAAGAAAAAAGUAAACCAGCGUUGGGCCCACAAGAUACUGUCAUGUAGGCCGAAAAGGGGUAGAAAAUUAUUAACA	122	spiLA0480-miR7981a-39-5p	ACCCCUUUUCGGCUUAUGUGGCAC	17-40	sly-miR7981a	2	0	24	24	1
spiLA0480-MIR7981d-8	AAAUAAUUCUGAGGGAAAAUGCACAGGUACCCCCUCAACCUAUGUCCGAAAUUUCAGAGACACACUUAUACAACACUAAGGUCCUAUUACCCCCUCAACUUAUUUUAUAAGUAAUUUUCUAUCUCUUUUCGACCUAUCGGACAUAGGUUGAGGGGUACUUGUGCAUUUUUUCCCUGAACUUAUUU	185	spiLA0480-miR7981d-8-5p	CCGAAAUUUCAGAGACACACUUAU	46-69	sly-miR7981d	2	0	24	24	2
spiLA0480-MIR7725b	GAUUAAGUCAUUAAGGUUGACCCUAAAAUCUUAUCCACCAUCCCUUAGCUUAAUGAACAAGCUAUUCUUUAAUUAGGGAAUCGAAAACCAAUUUCCUAUUUAAAGAAUAGUUGGCUCAUUAGGUUAAAGGGUGGUGGAUAAGAUUUUAGGAGUAAUUUUCAGAUAUUUAGUG	172	spiLA0480-miR7725b-3p	CGAAAACCAAUUUCCUAUUUA	82-102	bdi-miR7725b-3p-1	6	0	21	21	2
spiLA0480-MIR11110b	AGUGAUUCUGAACAUGGCAGAAUUAUACUCAUGUAUAGACUUAAAUUCUUGUAGCCUUAGAUGCAUCCAAUCAUAUCGUGCAUUUAGAUGUAUGACCAUCUUCAAGUGGUCAAAUCUUUCUUUUAGGUUUUUCCACAAAACAAGUGGAUCCUUAACUGUCAGAUAUUUGAUUUUCAGAAUCUUG	184	spiLA0480-miR11110b-5p	CUCAUGUAUAGACUUAAAUUC	28-48	lja-miR11110b-3p	5	0	21	21	1
spiLA0480-MIR2118b	CUAGGGAAACGCAUCAUGACCAACCAAGGUAAAGAAUUCUAAAUAGAACUCUUUACCUUGCCUUGGUUGGUCCCGAUGCGUUCCCUUU	88	spiLA0480-miR2118b-3p	GUCCCGAUGCGUUCCCUUU	70-88	ata-miR2118b-5p	5	0	19	22	2
spiLA0480-MIR9776	GCAUUCCACUUUCAUGAAAAGAUGUGACUUUUAUGAAAUUUUGCUACUUUAACGAGGAGGUGCGACUUUAAUCAAAAGUUGUAACUUUUAUGAAAAGUUGUGACUCUAAUGAAGAGUUACGAUUUUUAUGAAAAAUUGUGACUUUUGUGAAGAGUUGCGACUUUAAUGAAGAGUUGCGACUUUAUGAAAAGUUGUAACUUUUACGAAAGGUUGUGAACUU	220	spiLA0480-miR9776-5p	UUUAACGAGGAGGUGCGACUU	48-68	tae-miR9776	5	0	21	21	1
spiLA0480-MIR8030-3	GGCAUGUAAUAAGGUUGAAUAACACAAUUAACUAAACUGAAAGUAGCGGUGUACAAAACCAAACCAAACCGCACACCGAGUCAAACCGAAAAGAAACCCGACUAGUAGCUUGGUUUGACUUGGUUUGGUAUUGGGAAAACCCCCCCACUAUAUUUGGGUUGGUUUGUUUUUAACUAAAAAAAAAUCAACCCGAGACCAGACCAACCCGACUUCAUUUUUGUAAUUUUGAAAUAUAAUUUUAUACAUAAA	248	spiLA0480-miR8030-3-5p	ACAAAACCAAACCAAACCGCAC	53-74	stu-miR8030-3p	7	0	22	22	3
			spiLA0480-miR8030-3-3p	UUGACUUGGUUUGGUAUUGGGAA	115-137	stu-miR8030-5p	6	0	23	23	1
spiLA0480-MIR5293-2	AUGGGUUCGAGCCAGGUUUUGGAUUUGGAAGAGAUUCCCAAGGAAUUAUCGAACCUGUUCCGAUCCUUGAUAAGGGAUCCAAAUAUGGUUUGGGGUAUACCCCCACAGAUGACGAUAUGAAGAUGAAGAAAAAAGGAUCAAGAGUUGGCUAAACCGAUACCGCAUCUGUAUCAAUCCUUUCCAAUCCAAGAGUGCGUCGAGCCUGA	208	spiLA0480-miR5293-2-3p	GAUGAAGAAGAAAAAGGAUCAAGA	122-145	mtr-miR5293	5	0	24	24	1
spiLA0480-MIR812q	AACUUUUUUUUUGUAAUUAUUUGUACCUCUUUGGCUUACGUGGCAUCCAAAUAUCUCCGGCGCGCCUCAAUUGCGUGGAGUCAAAUAGAGUGCCACAUAAGACAAAAGGUGUAUAAAAUUACAAAAAAAAAAAA	134	spiLA0480-miR812q-5p	ACGUGGCAUCCAAAUAUCUCCGGC	38-61	osa-miR812q	6	0	24	24	1
spiLA0480-MIR7981b-25	GUAAUUUUCUACCCCUUUUUUGGCUACGUGGCACUAGUUUGAAAAAAAGUCAACCAUCGUUGGGCCCACAAGAUAGUGCCACGUAGGACGAAAAGGGGUAACAAAUGAU	110	spiLA0480-miR7981b-25-5p	ACCCCUUUUUUGGCUACGUGGCAC	11-34	sly-miR7981b	3	0	24	24	1

spiLA0480-MIR7981a-40	AAUUUCAGAGACACACUUAUAGUAUACUAAGGUCCUAUUACCCUCCUGAACUUAUUUUAUAAGUAAUUUUCCACCUCUUUUCGGUCUACGUGGCACUAACUUGAAGAAAAAAGUCAAUCAACGUUGGGUCCACAAGAUAAUGCCACGUAAGUCGAAAAGGGAUAGAAAAUUAUUAAUAAAAUAACUUUAGUAGAUAAUAGGACCUUAGUAUAGUAUAAAUAUGUCUCUGAAAAU	234	spiLA0480-miR7981a-40-5p	ACCUCUUUUCGGUCUACGUGGCAC	73-96	sly-miR7981a	2	0	24	24	1
spiLA0480-MIR8005b-2	UCUAUAAUUAUAGACAUAAACAUUUUGUGGAGCUCUACAAGACUUGUUUAAUUUGUGUUGGGAUUCCACAAAUUGUGAUCAACUCAAAUUAGGAUUCUUGGAGACUAGUCAACUCUAAAUUCUAAUUUAUGCC	133	spiLA0480-miR8005b-2-3p	ACUCUAAAUUCUAAUUUAUGCC	112-133	stu-miR8005b-5p	6	0	22	24	1
spiLA0480-MIR7980b-2	UCUCAUGAUAUGAAAUCAUGAGAUGGAAUUAACGUGAAAUUAUAUGUCCAAACGCUGAUUUCAUCUCAUGAUUUCAUAUUGCAUGUCC	88	spiLA0480-miR7980b-2-3p	GUCCAAACGCUGAUUUCAUCUCAU	46-69	stu-miR7980b-5p	2	0	24	24	1
spiLA0480-MIR7990a-2	CGCAUAGAUCUCAAAAAAGUAACCGAAUUGAAAAAAAAAUCGCCUCAAUCGGACAACAGAGACAAAAGUCAUUACCACUUGAAUUUUCAAAACUUUACAACUACUUUUAUUGAGUUACACUCUUCAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCAUCUAAUAUCCGUUUGAGACGAUUUUUUUUCAAUUUGGUUAUUUUUUUGAGAUCUAUAUG	220	spiLA0480-miR7990a-2-3p	UUCAAAUGAUCGUAACUUUGGCAU	139-162	stu-miR7990a	1	0	24	24	1
spiLA0480-MIR7990a-3	UGUGUAUAUCUCGAAAAAAUAACCAAUUGGAAAUAAAAAAUCGCCUCGAUCGGACAUCAAAGACAAAAGUUAUGACCGUUUUAAGUUUCACAAAUUUACAACUACCUUUUUUUGAGUUACACUCCUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGACCUUGAAUAUCUGUUUGAGGCGAUUAUUUUUCAAUGAGGUUAUCUUCUGAGAUCUACGUG	221	spiLA0480-miR7990a-3-3p	UUCAAAUGAUCGUAACUUUGACCU	141-164	stu-miR7990a	1	0	24	24	1
spiLA0480-MIR7990a-4	AAGAUCUCGAAAAAUUAUCAGAUUGAAAAAGAUUGCCUCAAUCACACAUCCAAGGCAAAAAAAUUUACCAUUUGAAGUUUCACAAAUUUACAACUACUUUUUCUGAGUUGCACUCUUUAUUUUUUGUGAAUCUUCAAAUGAUCGUAACUUUGGCCUCGAAUAUCCGUUUGAGGCGAUUUCUUUUUCAAUUGCACUAUUUUCUCGAGAUAUACGUGUAGAUCUCUAAAAAAUAAUCAAAUUGAAGGAAAAAUUGCCUCAAUAAAACAUCUGGGGGGGAAAGUAAGAUCGUAUGAAAUUUCAAAAAUUUACAACUACUUUUAUUGAGUAACACUCUUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGACCUCGAAUAUCCUUUUUAGGCUAUUUCAUUUUUCAAUGAUGUUAUAUUUUCGAGAUCUACGUG	211	spiLA0480-miR7990a-4-3p	UUCAAAUGAUCGUAACUUUGGCCU	133-156	stu-miR7990a	0	0	24	24	1
spiLA0480-MIR7990a-5	AACAAUACGAUCCUGGAUAUUAUCCUUUCCAUCACUAACUUAUUUCGCCUCAAAGUUUUAAGUUGCAAGGUACUCUUCCUAAGUCAAUUCAAAACUUCAUGAACCUAACGCGACUUGAUCUUAAGUUACAUUUUACGAAACCUCAAUCUUGGGUAGAGGACCGUGCAAUUGGUUAAAACUCGGUCUAAAUAACUUAGUGAUGGAAGGGAGAAUAUCCAGGAUGGUAUUGUU	222	spiLA0480-miR7990a-5-3p	UUCAAAUGAUCGUAACUUUGACCU	139-162	stu-miR7990a	1	0	24	24	1
spiLA0480-MIR6022-2	UUCUUUUUCCAAAAGAAAUAAAACUUGUGGGAUCGUUUGACAUAGGGGUGUCAAAUAGGCGGGUUGAGUUGAAAUUGAAACUGUUAAAAUGAGUUAAACUAUAAAUCGGGUUGGGUCUUGACCCGCCUAAAUUUACUUUGGGAUCAAAUGGGUUGGGUUAAAUGGACUACAAAAUGGGUUGGGUCUUGACCCAUCCAAUUUGAUUCAAUUAAUCUCAAUAAUUUUAACAUAGUGAUAUUUAAAUUUUAUAAUUACAAUUCGAAUUUCGGCUCAAGUUUUUUUUUUAUAUAUAAAAUGUCUUUCAUGAAAAGAUGUGACUCUUAUGAAAAAUUGCAACUUUAAUGAAGAGUUGCGACUUUAUGAAAGGUUGUGACUUUUAUGAAAGAUUGUGAACUUUAUGAAAGGUUGCACCUUUUCCAAUUAGUUGUAUCAUUUCUGAUAC	297	spiLA0480-miR8599-2-3p	ACAAAAUGGGUUGGGUCUUGACCC	169-192	atr-miR8599	7	0	24	24	2
spiLA0480-MIR444b	UCAUGAGUCGAUUUAAUCAAUUUUAUACGAUUUAAGUAAUUAUUUGUGUGCAUUUUAAAUUGGAAGGCAUAGGCGUAAGAUAAGGCUAAGUUUAAAAAAAUGUUGUAUUAAGCGUAAUGCAUAAUAUGUCAUCUAACUUGGUUUGAGCUCAUAUUGUUGUCCUCCAAUUUUUGGUGUGCACAAGUAGACACUUAAAUUUCUAUAGAGUUGAACAAAUAGACACACGC	144	spiLA0480-miR444b-3p	UUGUGACUUUUAUGAAAGAUU	70-90	ssp-miR444b-1	6	0	21	21	1
spiLA0480-MIR2275b	UAGAAUGUAUUAGUAAUGUUUGCAUUAAUUAAACAUAGAUGAUUUCUUAUGCAUUGUUUGGUUUGGUGUAUUUUAUAUUUUUUUUAGUUUCCCACCCUGUGUCUGGAGCCCAUGUUGGAGCUCCGUCUAAAUCCGAAUCGCGCUCUGCAGGGGCCCAUUCGGGGGUGACACUCCCAAAAGGUUUUCUCCAUAUCGAGGGACCUCUGAUUAAGGAUGAAACACUCCACCAAUGCACCACAACCCAUGUUGGUGGUUUGGUGAAUUAUUAAUAGCAUACAUUGCAUAAAAUAUUUAC	227	spiLA0480-miR2275b-3p	AUUGUUGUCCUCCAAUUUUUGG	153-174	ata-miR2275b-3p	6	0	22	22	2
spiLA0480-MIR5752b		295	spiLA0480-miR5752b-5p	CAUUGUUUGGUUUGGUGUAUU	52-72	mtr-miR5752b	5	0	21	21	1

spiLA0480-MIR8006-13	GUUUCCCUAUUUAGUCUUUUGUUAGAGUGAAGGACAUAUAUACUCUAGUUUUUGGAUGGCAGGUGCACCAGUGUUCCAAAAGUAUGACAGAGGUAUCUGCAUACCAUUUACGAUAGUUCAGGGCUAUAUUUGUCCUUUUUCUAUAUAUUAUUAUAUAUUUACUGCUUAAGAGUUUACUACGUAUCUUACACUUAGAUACAUAUAUUUUUGCUACAGAUACACAUAAAUAGGGAGCU	236	spiLA0480-miR8006-13-5p	UAGUUUUUGGAUGGCAGGUGCACC	46-69	stu-miR8006-5p	3	0	24	24	1
spiLA0480-MIR9782	UGCGUUGAGACAGUUGUAGUGUCUAAAUCUUGUUAAUUGAGGCCAAGUUUGAGAGUGUUUAUAGCGGCAAUUUAUUGUGUAUACAAUUUGACAUAAUACAUAAAUAGUUUCUUUAACUUGGGUAUGAAUUACGUUUAUACCCUUCAAUUUUGGGUGUGCACAAGUAGACACUUAAACUAGUAUAAAGUUGGACAAAUAGACACACAUGUCCUACAUG	217	spiLA0480-miR9782-3p	GUAUAAAGUUGGACAAAUAGACAC	180-203	tae-miR9782	6	0	24	24	1
spiLA0480-MIR9760-2	UCUUUCUCUCAUGAAAUUGAUGAGAAAUUGGAGGAUUUAGUAUUGACUGUUGAGGAUGAUUUGGGGAUGAAGAUGGUUGGAUGGGUCAUCCUCUCAUGAAAUUCAUGAGAAAUUG	115	spiLA0480-miR9760-2-5p	UGGAGGAUUUAGUAUUGACUG	29-49	gma-miR9760	4	0	21	21	1
spiLA0480-MIR8001a-4	UUUUCCUGGGGAUUAGUAUGAAAGUUCGCAGGAAACUUAUUUUCCUGCAAAUUUUCAUAUAAAUUUCCAGGAAAA	75	spiLA0480-miR8001a-4-5p	UCCUGGGGAUUAGUAUGAAAGUUC	4-27	stu-miR8001a	1	0	24	24	1
spiLA0480-MIR6197-1	AAUUUUCUCACGCUUUAUACAAAUAGAAACGCAAUUUAUACAUUUCGCUUCUGUUUGUAUAUGUGAGAAAGGC	73	spiLA0480-miR6197-1-3p	UCUGUUUGUAUAUGUGAGAAA	50-70	hvu-miR6197	6	0	21	21	1
spiLA0480-MIR7981a-41	UUUCCCUUUUUGGCCUACGUGGCACUACUUUGAAAAAAAAAAGUCAACAAGCAUUGGGCUCACAAGAUAGUGUCACGUAGGCCGAAAAGGGGUA	94	spiLA0480-miR7981a-41-5p	UUCCCUUUUUGGCCUACGUGGCAC	2-25	sly-miR7981a	3	0	24	24	3
spiLA0480-MIR840-2	CCAAUAGGUCUUUAAGAAUGUGUAUUGGGGUACAUAGGCAUCCCAAUGCCCAAUAUUUUGAAAUAUUGGGCAUAGUAUAGAAAAUUGGCUAAGAUGUAUUAGCCAAUUUCUAUAUAAUACCCAAAUAAGCAAAUAUUGGCAUAUUAGAAAAUAUUGGCUUAAAGGGUGUUAGCCAAUUUUCUAGCAUUAAUGAGCUUGUUUAAGAAAUGCACUUGCAAUGAAGACCCUAAUCUAAAAACAUUUAUUCACAACUUAGCACUUUAGAUACGAGGCACCCAAGUGUCAAGCCUAGGUACCAUUCCACAUGACCAUUUAAAAUGAUCAUGUA	328	spiLA0480-miR840-2-3p	GCAAUGAAGACCCUAAUCUAAA	215-236	ath-miR840-5p	6	0	22	22	2
spiLA0480-MIR8781a-2	UUUCAAAUUUGGAUGUGCACAAAUAGACGCUCAAACUUGUACAAAAUUGAAUAAAUAGACACACAUGUCAUUUUUUGUCCUACGUGGUGUCCUACGUGUAUUGUGUCAUGUAGGACUCAUGUAUUUAUUUUAUUUAAAAGUUGGAUAGUUAAAGUGUCUUUUUGUGAAUUAUAAAAGUUGGAG	182	spiLA0480-miR8781a-2-3p	UAUUUAUUUAUUUAAAAGUUGGAU	122-145	gra-miR8781a	5	0	24	24	1
spiLA0480-MIR8651	GCAUUAUUUAUUAAUUAGGUCUAUUAAUUGAAAAGAAAAAAGAUCAUUUCAAAUGGUUUCACGCGCUUGGGGACCGUGAAAUACACAUUUUUUGCCACAUAAGUCAUUUGUGUCCAAUAGGAACUGUUUUUGAACACAUAAGGUGUUCAAUAGGUAUGAGGCUAAAUUGAGGUGUCUAAGUGAAAUAUACGGACAACUUUAAGGGGCCGCAUAUGACUUAAGCCUUUUGGGAAGUUUAAUUUGUCUCAUCUCAUGUUGAUGUUUAAUCCUUAAUUAAUGGAUAAUAACAAUAUAAAAA	298	spiLA0480-miR8651-3p	UUAAUGGAUAAUAACAAUAUAAAA	274-297	gra-miR8651	7	0	24	24	1
spiLA0480-MIR10538-12	GUCAGAUUGAUAUACGUUACUCACAGUAACAUUUUACUCCUAAAACGUUACUCACAGUAACGUUUUAGGAGUAAAACGUUAUUGAAAAUAACGUUUUAAAAGUAAAACGUUACUUGCAGUAACGUAUAUCAACCUAAU	138	spiLA0480-miR10538-12-5p	AGAUUGAUAUACGUUACUCACAGU	4-27	sly-miR10538	0	0	24	24	1
spiLA0480-MIR7822-1	GGGACACGUGACACAAUCUUAUUCGUCGAUUUGAUAUUUAAUAAAUGUCGAGUCGAUGGAUAAGAUUAUGACACAUGUAUG	81	spiLA0480-miR7822-1-3p	UUUGAUAUUUAAUAAAUGUCG	30-50	ptc-miR7822	6	0	21	21	1
spiLA0480-MIR1520l-2	GGGACACAUGGCACAAUCUUAUCCAUCAAUUCAAUAUCGUGUCGAUGGAUAAGAUUAUGACACGUGUAUG	70	spiLA0480-miR1520l-2-3p	GAUAAGAUUAUGACACGUGUAUG	48-70	gma-miR1520l	7	0	23	24	2
spiLA0480-MIR9773	UCAUCAGAAAUUUCUUUUAUCCUCAAGACUUAAACGCGAUAUAUCUACUUAAGAAUGAAGGGAUUUUAUUCAUUUCAUCAGUACCCCUUGAUAAAGCGUAUGGUUUAUUAAAAUCGAACUACCAUAAAUGUGUAGUUUAACUUUCUUUGGCUUAGAUAUUUGUUUUUAUAUUUUAGGACCAUUAGAGAUUUCGGACAG	199	spiLA0480-miR9773-3p	UUUGUUUUUAUAUUUUUAGGACCA	159-182	tae-miR9773	7	0	24	24	1
spiLA0480-MIR8019	CCCCCCCCCGUUUUAAAAAGAAUAAUCUAGUUUGACUUGACAAGGAGUUUAAAAAAAGAAAGAAGACUUUUUAAUCUUGUGGUUCUAUAUUAAAUUUAUGUCAAAUGUAUCAAAAUGCCCUUCAAUCUUGUGGUCUUAAACAUGCCACGUGGAAAGUUAAGGUUAAAGUGUUGCCAAAAAAAGAAAAGGUCAUUCUUUUUUAAACAGACUAACAAGGAAACAAGGUCAUUCUUUUUUAGACGGAGGGAGU	250	spiLA0480-miR8019-5p	AAAAGAAUAAUCUAGUUUGACUUG	16-39	stu-miR8019-3p	3	0	24	24	1
			spiLA0480-miR8019-3p	AGGAAACAAGGUCAUUCUUUUUU	215-237	stu-miR8019-5p	5	0	23	23	1
spiLA0480-MIR10538-13	ACAGCAUUAGGUUGAUAUACGUUAUUGUAAGUAGCGUUUUACUCCUAAAACAUUAUAUUCAGUAACGUUUUACUCCUAAAACGUU	148	spiLA0480-miR10538-13-5p	AGGUUGAUAUACGUUAUUGUAAGU	9-32	sly-miR10538	5	0	24	24	1

spiLA0480-MIR1847-3	ACUAUGAGUAACGUUUUAGGAGUAAAAUGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAUAUUCCUUUUCAGCCUACCUAGCACUAACUUGAAAAAAAAAAAGGCAAUCAGUGUUGGGCCCACAAGAUAGUGUCACGUAGGCCGAAAAGGAGU	93	spiLA0480-miR1847-3-3p	GGGCCCACAAGAUAGUGUCACGUA	56-79	osa-miR1847-2	7	0	24	24	2
spiLA0480-MIR172d-3	AAAUGAACUUAAUGGAUUUAAUCUGAAUGAUUCAGAUCCAAACCUAAAAAUCAUACGUACUUAAUAGGUUGAAUCUGAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCAAAC	112	spiLA0480-miR172d-3-3p	UCUGAAUGAUUAAGAUUCAGA	74-94	bra-miR172d-5p	5	0	21	21	2
spiLA0480-MIR3951b-2	CAUGAGAACAUAAGAGAGGUUUUCAACAAGAGAAAAGAGAGAAAGAAAAAGGUUCUUUUGCUGCAGUCUUUUUCUCCGACCAGCAACAUUCAGAUCGUCUUUCUUGCUUAACUAACCGUUGGAUCGGGUUGAAAUUCGGACUGAGUGUUCCUGACAUUUUGUUGGUUGAUUUUAACGGUGGAGAUUGAAUUGAAGGUCAUAAAGAUCCUGUUGUUAGUCCCGAACAGAAAUUGGGUUUGAGUAGUGUUUCUUUCUAUUAUCUUUUGUUGGUGUAGCUAUUGUUUGUUCUCUUU	293	spiLA0480-miR3951b-2-3p	UUUCUAUUAUCUUUUGUUGGUG	251-272	csi-miR3951b-3p	4	0	22	22	1
spiLA0480-MIR7981a-42	UUACCCCCUGAACUUAUUUUAUAAAUAAUUUUCUACCCCUUUUCGGCCUACGUGGCACUAGCUUGAAAAAAAAAGUCAAUCAGCGUUGGGCCCACAAGAUAGUGUCACAUAGGUCCAAAAGAGAUAGAAAAUUAUUAUAAAACAAGUUUAGGGGGGUA	158	spiLA0480-miR7981a-42-5p	ACCCCUUUUCGGCCUACGUGGCAC	35-58	sly-miR7981a	0	0	24	24	1
spiLA0480-MIR7981a-43	UCCAAGGUCCUAUUACCUCCUGAACUUAUUUUAUUAAUAAUUUUAUAUCCCUUUUCGACAUACGUGGCACUAUCGUGUGGGUCCAAUACUGGUUGACUUUUUUUCAAGUUAGUACCACGUAGAUCGAAAAGGGUAGAAAAUUACUUAUAAAAUAAGUUCAGGAGGUAAUAGGACCUUAAU	181	spiLA0480-miR7981a-43-5p	AUCCCUUUUCGACAUACGUGGCAC	47-70	sly-miR7981a	3	0	24	24	1
spiLA0480-MIR5716	AACAAGGUUAAUAUAUAUUUAUAUAUACUGAUGAGGAAUGAAUACAACAAAAUGGUAUGUAAUAAUAUUCUAUUUUAUAGUUGUAAUUUAAAUAAUAACAAUUAGCAAAUUGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAUUUUUUUCCCUCUGAAAUAUGGAUCUUUGUAUAUAUAAAUGCAUAUAUUUUCGUCGGAUCUUUGUAUAUAUAAAUGCAUAUAUUUUCGUCUUAUA	279	spiLA0480-miR5716-3p	AUGGAUCUUUGUAUAUAUAAA	203-223	bra-miR5716	5	0	21	21	2
spiLA0480-MIR827-5	UAACAACUUUUUUUUUGGUGGCAAUUUGUUCGAACUUACCAUGUGAUAUAUCUACUAUACAUGGUAUAUUCGAACUAGUUCCCACGAAAAAGAAUAAUUGCAC	103	spiLA0480-miR827-5-5p	UUUUUUGGUGGCAAUUUGUUC	11-31	zma-miR827-5p	6	0	21	21	1
spiLA0480-MIR7981d-9	UGUGUCUCUGGGAUUUCGGGCGUAGGUUGAGGGGCUACUUGUGCAUUUUCCCUUUUUAUAUACUCUUAAAGUUAAGGUUAAUAUUAACACUCCACACAUAAUGUUUUUUUAUUUUUAGGGAUAAUGCAUAAGUACCCUCUCAACCUAUGCCCGAAAUUUCAGAGACAUAAUAACACUACAAUAAAAAUGACUUUUAGCGGCAUUAAAUAUUGACAUUAAUAAAGAGUGCUAAAGCCUUUACCGACAUUGGUUAAGUGCCAUUAGAACCAAUGUCGCUAAAGGCUUUAGGGACAUAUACAAAGAGUGUCAAUUGCCGCUAAAUAUACAUAUUUAGCUACAAUUGAGAAUUAAUUGCCUCUAUUAAUCAUUUUUGUUGUAGUGUAAC	169	spiLA0480-miR7981d-9-3p	CCGAAAUUUCAGAGACAUA	151-169	sly-miR7981d	3	0	19	24	2
spiLA0480-MIR1917-2	UUUGUGAAAUGACUUGAGAGGUGUAGUAUAAGUGGGAGCCGAAAGGCGAAAGUGAAAUACCACUACUUUUAACGUUAUUUUACUUA	216	spiLA0480-miR1917-2-5p	AUUAAUAAAGAGUGCUAAAGC	46-66	sly-miR1917	1	0	21	21	1
spiLA0480-MIR2662		86	spiLA0480-miR2662-5p	UAGUAUAAGUGGGAGCCGAAA	24-44	mtr-miR2662	6	0	21	21	2
spiLA0480-MIR3951a-1	GUGCGCUUCUUUCUCCUGAGGCGAUGCGAUCUGAAAAAGGCGCUCGCUUCAGAUAAAGAAGCGAGA	66	spiLA0480-miR3951a-1-3p	CAGAUAAAGAAGCGAGA	50-66	csi-miR3951a-5p	3	0	17	21	2
spiLA0480-MIR8132-2	UCUCACUUCACGCGCUCAAAAGGCGUGCUUCAAACGAUAGGUGACAAGUCAGUCACGUGUGUUUGAUAGGUACACUUUUUAAGUGGUUUAAGUGUUC	97	spiLA0480-miR8132-2-5p	UCAAACGAUAGGUGACAAGUC	30-50	ppe-miR8132	6	0	21	21	1
spiLA0480-MIR171b-4	AACGGAAUGAAAAUAAGAAGUGAUAUUGGCGCGGCUCAAUCUGAGAUCGUUCUUUACGAAAAUAAGCAUAAAUUCGUCUUCGGAUUGAACCUCACCAACAUCGCUUCUUCCAUUUUAAUCCCAAA	125	spiLA0480-miR171b-4-5p	GAUAUUGGCGCGGCUCAAUC	22-41	zma-miR171b-5p	1	0	20	20	1
			spiLA0480-miR171b-4-3p	GGAUUGAACCUCACCAACAUC	82-102	tcc-miR171b	5	0	21	21	2
spiLA0480-MIR1106-3	CACCCCCUGAACUAUUUAAAACUGUAUUUUAAAGGUAUAUAUGUGUCCACGUGGACACAUUACUAUUCAUAAUUAUGCAAUAUCUUUGAUGUCCACAUGCGCACAUAUAUACCUUUAAAAUACACUAUUAAAUAAUGCUGGGGUAA	146	spiLA0480-miR1106-3-5p	UUUAAAGGUAUAUAUGUGUCC	28-48	smo-miR1106	5	0	21	21	1
spiLA0480-MIR5303-23	CCCCUAUGUUUUCGGACUUUCCAAAAAUGUUAUCAUACCUAUGUCGGAUCCUUCAAAAUAGUGUAAUUUUGGAGGACACGACACGCAGGCAUCAGCAAUUUUGAAGAGUUCGAGCAACAUAGCUU	125	spiLA0480-miR5303-23-3p	AUUUUGAAGAGUUCGAGCAAC	98-118	sly-miR5303	1	0	21	21	2
spiLA0480-MIR7816	UGUAUAACUAAUACCCACAUAACUUUUUCCACCUUCUACCCUGCAUAUCUGUAUACAUAGAUUCCCUCAUAAGUUAUGUUGGUAUU	95	spiLA0480-miR7816-3p	UAUGUUGGUAUUAAUUAUGUA	75-95	ptc-miR7816	5	0	21	21	2

	AAUUAUGUA										
spiLA0480-MIR8006-14	GAACUAUCGUAAAUGGUAUGCAGAUAUCCUUCCUCAUACUUUAGGGACGUUGGUGCCUCUGCUAUCCAAAAAACUAAAGCAUAUAUACCUUUUACACCAACAAACAUACACGUGUCAUAAUUUUAUACCGACCUGACAUCGGAUCGAUGAAUAAGAUUGUAUCACGUGUCCCUAUUUAGUCUUCCGCUACACUCUAGUUUUUGAACGACAAUGGCACCAAUAUGUUCCAAAAGUAUGACCGAGAGUAUCUGCAUAUCAUUUACUAUAGCUC	271	spiLA0480-miR8006-14-3p	UAGUUUUUGAACGACAAUGGCACC	195-218	stu-miR8006-5p	3	0	24	24	1
spiLA0480-MIR821e-2	ACAAAUGUGAAAAUUGGUAGCCAUCAAUAUGAAAGUUGGUAGCCAAAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAUAAGUUUGAUAGAGUUAGGCAGCCAAUUUUUUUGUUGAAAUUGGCUACCAUAUUUUUUCAUUACU	142	spiLA0480-miR821e-2-5p	UAGCCAUCAAUAUGAAAGUUG	18-38	sbi-miR821e	4	0	21	21	2
spiLA0480-MIR7981a-44	AGUAAUUUUCUACCCCUUUUCGGCCUACAUGGUACUAGCUUGAAAAAAAGUCAACCAGUGUCGGGCCUACAAGAUAGUGUCAUGUAGGCCGAAAAGGGGUAGAAAAUUAUU	112	spiLA0480-miR7981a-44-5p	ACCCCUUUUCGGCCUACAUGGUAC	12-35	sly-miR7981a	2	0	24	24	1
spiLA0480-MIR11553-3	UGACAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUACCCAACAUGGCAACUAACGCUCAUUAGGGCAUAUUUGGACCAAAAGUUGGACGGCGAGGGCAUGAGUGAACCAAUCUUUAAACGGAGAAUAUAUCUAAACUUUUUCGAAUAGUUUAGAGGCAUAUUUGACUCUUUUCCUUUCUUUAAAUGAAA	188	spiLA0480-miR11553-3-5p	GAAAAAUGAGUUGGAUAUACC	17-37	pab-miR11553	5	0	21	21	3
spiLA0480-MIR396a-3	GUCAUCUAGAAAAACUAGGUUUUCUAGUCCUUUUUGGAUUAGGAAGAAAUCUCUAUAUAUAGGGAUUCUUCUAACAUAGAAAAUAGAUGAUUAGUUUUCUAUUCAUACUUGCCCACCCAAGUAUUGAGAGUUCGGAUGUGACUUGAGAUCACUAUAGAAGACCAUAGCUAUCUUGUAGAUUCU	185	spiLA0480-miR396a-3-3p	CAUAGCUAUCUUGUAGAUUCU	165-185	hbr-miR396a	5	0	21	21	1
spiLA0480-MIR6235-2	AACAUAUUCAGUAUUUGGGUUGUUGGUUUGUAGUGUGACACUACAUGUCAGACGUCUCCGGUUCGAACCGAAGGUCCAAAAUGGACAGUGAAAUAAAAAUAAUGUUGUCACUCAUGCUCGAACUGGAGACCCGUGAUAUGUAGUGUCAAACUCCAACCAACAGCCCAAGUAGCUAAAUAUACA	183	spiLA0480-miR6235-2-3p	CAGUGAAAUAAAAAUAAUGUUGUC	86-109	sbi-miR6235-5p	6	0	24	24	3
spiLA0480-MIR477j	GUCACAAAAAAGGCGCAGCUUAAUUGGUGAAAGGCGAUCCCCUUGGGAGGGAUGUAAAAGAGUCAUAAGUCACGGGUUCGAUUCUCCCUUGAGGCUGCAUGCUAAUAAGAGGGGAUUAAAAGAGCGAAUGGCCGCCCAUGGCAGAGACAAUACCUGAGUAUGUGGAUCCCGAGGGGGUUGUCACAAAAAAGGCGCCUUUUUUGUGAC	207	spiLA0480-miR477j-5p	AUUCUCCCUUGAGGCUGCAUG	81-101	mes-miR477j	6	0	21	21	1
spiLA0480-MIR8665	AAAGGAAAUUUUUAGAUUUCGGUUAAGACAUAAAAGGGACAACCUAGUACCUAACCUAGGAUGGUCCGAAGAGUUAGUUAAGAUACUAAAUACUUAAGGGUACUCUAGUAAUUACCCUAGGAUACUUAAUUAAUAAAUAUAUCAACAUAAUUAAUUAAUUUAAAGGUGCAAAACCGAAAUCAGAAAGCAAUAUCCAGA	198	spiLA0480-miR8665-3p	UUAAUUAAUAAAUAUAUCAACAUA	126-149	gra-miR8665	7	0	24	24	1
spiLA0480-MIR9668	CACCAUUUUUGGGGUGAUCCGGAUUACGACGUCAAAAAUGUCAAAUAUUUUCGUGGACAUCUCUCAAGACCUUGUCUAUGCAUGCGGUUGGCCAUCACGGCUUUUCCGGCCCAUUUAGAGGGUCAAACAAGCGUAGAAGCGAGCAUACGCCUCAUUUCGACGAUUUUCGUGUGCUAUAGCACACCAUUUUUUGGGUGAUCCGGAUUCCGACGUUAAAAAUGUCA	224	spiLA0480-miR9668-5p	AAAAUGUCAAAUAUUUUCGUG	35-55	tae-miR9668-5p	6	0	21	21	3
spiLA0480-MIR7981b-26	NNCGAACUUAUUUUAUAAAUAAUUUUCUACCCCUUUUUAGCCUACGUGGCACUAGUUUGAAAAAAAAGUCAACCUUCGUUGGGCCCACAAGAUAGUGCCACGUAGGUCGAAAAGGGGUAAAAAAUAUUAACAAAAUAAGUUCAGG	145	spiLA0480-miR7981b-26-5p	ACCCCUUUUUAGCCUACGUGGCAC	29-52	sly-miR7981b	1	0	24	24	1
spiLA0480-MIR11089a	AUUUAGGAGAGAAGAGAUGAAGGGCAAAUCUGGUCCCACUGGGCGUGCCAAUUUUGCAACAAAUUUUAAAGUGAUUAAAAAUAAACUGCAAUCACAAAUAAAAUCUGGAGAAACAUGAUUUUAUUGAUAAAUAUUGCGGGUACAAUUCUGUUGAUCCCUUGAUUCUACUCUCCUAGGC	178	spiLA0480-miR11089a-3p	GAGAAACAUGAUUUUAUUGAU	108-128	lja-miR11089a-5p	6	0	21	21	2
spiLA0480-MIR7708a	AGCCCACGACUCUUAAGAUAAUGGUAUUGUACUAAGGCGAAUUUCAAUUUUCUAUUGAAACAAUUUCUUAGUCAUUAAGUUAGUGGUGGUGG	92	spiLA0480-miR7708a-5p	GAUAAUGGUAUUGUACUAAGGCGA	17-40	bdi-miR7708a-3p	7	0	24	24	3
spiLA0480-MIR3627	GAGAGAGAUUGAGGGAAUCUUGUCGCAGGAGAGAUGGCACUUGCCAUUCCUUUUAAUUGGUACAAUGCCUAAAUGGAACCAAUUAAGUGCCUCUGUCUUUCGACACGAUGCUCACAAUUUCUAUU	125	spiLA0480-miR3627-5p	UUGUCGCAGGAGAGAUGGCACU	20-41	vvi-miR3627-5p	1	0	22	22	1
			spiLA0480-miR3627-3p	AAGUGCCUCUGUCUUUCGACA	85-105	stu-miR3627-3p	0	0	21	21	1
spiLA0480-MIR1534-2	AGAGCCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGGUACAUAGGCAUCCAAUUCCAAAUAUUGAGAAAUAUUGGGCAUA	79	spiLA0480-miR1534-2-3p	UAUUGGGGGUACAUAGGCAU	28-47	gma-miR1534	4	0	20	20	1

spiLA0480-MIR7981a-45	UAGAUUUUUACCCCUUUUCGACCUACGUGGCACUAUCUUGUGGGCCCAACGAAGGUUGACUUUUUUUUUCAAACUAGUGUCACGUAGGCUAAAAAGGGGUAUAAAAUUAC	110	spiLA0480-miR7981a-45-5p	ACCCCUUUUCGACCUACGUGGCAC	10-33	sly-miR7981a	1	0	24	24	1
spiLA0480-MIR8021-2	UCUUCAUAUUCAAGGCUCAAACUCGAGACCUCUGGUUAAGGAUAGAUGGAUCAUAUACAACCCACCACAACUUUUAUGGUACUAAUAAUGACUUGAUUUACUUUCUCUUAAAUAUUUGACAAUAUGUUGGAUUUAUUUGUUGUAUUCUACCAACAAAUAUUUUGAUUGAGUGAAAGUUAGUAUUUAUUUAUCCUUAGCCAGAAGUGUCAGGUUCGAAUCUUAGACAUGAGUU	232	spiLA0480-miR8021-2-5p	AUUCAAGGCUCAAACUCGAGACCU	8-31	stu-miR8021	0	0	24	24	1
spiLA0480-MIR7533b	UCAACUUGUCUUACUCUAUUUUCCUAAAAAAAGAGUAGAAGAGAAAAGCUUAUUGUCUGUUUCUCCAUUGAUCUCUUGGGCUUAUCGAAGCUUCUUGAGGAGGUUAUGGAAAGAAGGUUGAGUGCUUGUAGUAAAAAAGUAUAGCAAGUCAU	152	spiLA0480-miR7533b-3p	GAGGUUAUGGAAAGAAGGUUG	100-120	lja-miR7533b	5	0	21	21	1
spiLA0480-MIR1518-2	GUAUUCACUUCACAGCACUCAAUCACAUUAGUUCCUAUGAUGUCAUAGGAACUAAUGUGGUUGAGUGCUGUGAAGUGAAUUC	82	spiLA0480-miR1518-2-3p	AGUGCUGUGAAGUGAAUUC	64-82	gma-miR1518	5	0	19	21	2
spiLA0480-MIR6197-2	AAGAUUAAACGGGGACACACGUCGUAAUCUUAUCUGUCAAUAAAUGUCGGAUCGAUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAAUAUA	92	spiLA0480-miR6197-2-3p	UCUGUCAAUAAAUGUCGGAUC	33-53	tae-miR6197-5p	5	0	21	21	1
spiLA0480-MIR7981d-10	CUCCUAGACUAUUGACUGAAAUUUCAGAGACACACUUUAACUAAACUAAGAUCCUAUUUAUAAUUUUAUACACCUUUUAUCUUAUGUGGCUCUCUCCGUGACUCUGCGCAAUUAAUGUGCGUGUGAGAUAUUGGAUUUCACGUAAGCUAAAAAUGUGCACAAAAUAACAAAACAAAAUGAAUUCUGCAGGUAAUAAGAUCUUAGUUUAGUUAAAGCGUGCCUCUGAAAUUUCGAUCAUAGUAUAGAAGAGAUAGCUUUCAACAAGAGAAAAGGAGAGAAAGAACAGGGUUCUUUUGCUGCAGUCUUUUCUACGACCAGUCACGUUCAGAUCAUGUUUCCUGAUUAACUAACCGUUGGAUCGGACUGAAAUUUGGAGAGAGUGUCCCUGACAUCUUGGUGGUUGAUUUGAACGAUGGAGAUCGGAUUCAGAGGUUAGAAAGAUCCUGUUUUAGGUCCCGUACAAAAGUUGGGUUUGGGUGGUGUUUCUUUCUAUUUAUCUUUUGUUGGUGUAGCUAUUGU	249	spiLA0480-miR7981d-10-5p	CUGAAAUUUCAGAGACACACUUUA	16-39	sly-miR7981d	5	0	24	24	3
spiLA0480-MIR11175	UGUAGGUCCUAUUAUUCCCUGAACUUAUUUUGUAAGUAAUUUUUUACUCCUUCUCGGCCUACAUGACACUAACUUGAAAAAAAAAGUCAACCAACGUUGAACCCACAAAAUAGUGUCACGUAGGCCGAAAAGGGAUAGAAAAUUAUUAAUAAAAUAAGUUCAGGGGUAAUAGGACCUUAG	272	spiLA0480-miR11175-3p	UUGAUUUGAACGAUGGAGAUCGGA	154-177	lja-miR11175-5p	6	0	24	24	1
spiLA0480-MIR7981a-46	UAUUAUUUAUCUGAACUUAUUUUAUAAGUAAUUUUUACUUCUUUUCGGCUUACGUGACACUAGUUUAAAAGAAAAAGUCAACCAGCGUUGAACCCACAAGAUAGUGCCACGUAGGCCAAAAAGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAGAGAUAAUAGGA	180	spiLA0480-miR7981a-46-5p	ACUCCUUCUCGGCCUACAUGACAC	46-69	sly-miR7981a	4	0	24	24	1
spiLA0480-MIR7981a-47	CGAGCAUGAAGAAGCCAUAAAACUCAGGAUGGAUAGCGCUAUAGAUAGCCAUUAAGAUGUAUUCAUGGUGCUAUCCCUCCUGAGCUUUAUAGAUUCCCCAUGCCAU	164	spiLA0480-miR7981a-47-5p	ACUUCUUUUCGGCUUACGUGACAC	37-60	sly-miR7981a	4	0	24	24	1
spiLA0480-MIR390		106	spiLA0480-miR390-5p	UAAAACUCAGGAUGGAUAGCG	18-38	atr-miR390-1	2	0	21	21	1
			spiLA0480-miR390-3p	UGCUAUCCCUCCUGAGCUUUA	69-89	stu-miR390-3p	4	0	21	21	2
spiLA0480-MIR8771f	UAACUUGGCUUUGAAUCAUAUUUAUGCCCUUCAACUUUGGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAACAACCAGACACACAUGUCUUACAUGUCAUUUUUUGUCAUAUGUGGUGUCCUACGUGUAUUGUGCCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAACGUGUCUAUUCGUGCAUUAUGGAAGUUGGAGAUCAAAGUUAAAAUUUGAAGUCAAGUUU	247	spiLA0480-miR8771f-3p	UUGGAGAUCAAAGUUAAAAUUUG	214-236	gra-miR8771f	5	0	23	23	1
spiLA0480-MIR855	UAAGACUAUAAAUAUGAGAUUAGGUCCCUCUCCUAGCUUAAGAAAAAGAUGUAUUCCCAUAAGGUGGAUACGUCAUAAGCUAAAGGAGAGGAAGACUCAGCCUAGCUUAUAUUCAGU	117	spiLA0480-miR855-3p	GUCAUAAGCUAAAGGAGAGGAA	72-93	ath-miR855	6	0	22	22	3
spiLA0480-MIR5014a-11	GAUAACUAUGCCCUUCAACUUUGAGUGUGCACAAAUAGACACCUAAACUAAUAUAAAUUAAAUAAGUAGACACAAUAUCCUACAUGGCAUAAUACACGUAGGACGCCACAUAAGACAUAAAAUUUGUUAUAUAGGGUGUCAUGAAGGACGAAUAUGUCUAAUUAUUUGAUUUUGUACAAGUUUAAGUGUCUACUUAUGCACAUUCAAAGUUAAAGGUCAUAUUUGUU	227	spiLA0480-miR5014a-11-3p	UUGUACAAGUUUAAGUGUCUA	172-192	ath-miR5014a-3p	4	0	21	21	1
spiLA0480-MIR8594	ACAAUACCCUCCAUCAUACUUUUGGGACAUUGGUACACAUCCCGUCAAAAAACUAGAGCAUAUAUGUCAUUCACUCUAACAGAUCAAUCUUAUCUAUCGAUAUGAUAUUUACUAAAUAUCGGGUCAGUGGAUAAGAUUAUGACACGUGUAUGUUUGUUAGUAUAAAGGUUAUAUAUGCUCUAAUUUUGGAUGGUAGGGGCACCAAUGUCACAAAAAUGACAGAGGGUAUCUG	234	spiLA0480-miR8594-5p	AGAUCAAUCUUAUCUAUCGAUAUG	81-104	atr-miR8594-1	7	0	24	24	3

spiLA0480-MIR1917-3	AGAUAUAUAUGCUCACGUGGACAUGAAUUAUUUAUAAUUAUUACUACAAAAAAAUAACUUUUAGCGGCAUUAAAUAUGACACUAAUAAAGAGUGCUAAAGUCUUUACCGGCAUUAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGGGACAUAUACAAAGAGUGACAAUUGCCUCUAAAAUUACAUAUUUAGCGGGCUAAUAGUUAUUUUUGUUGUAAUGUAUACAAUAUUUAUGAUGCUUACGUGAGCACAUAUAUACCU	271	spiLA0480-miR1917-3-5p	ACUAAUAAAGAGUGCUAAAGU	83-103	sly-miR1917	1	0	21	21	1
spiLA0480-MIR8046	GGAGGUAAUAGGACCUUAGUAUAAUAUAAGUGUCUCUGAAAUUUCGAGCAUAGUUUGAGGGGUAAUUGUGCAUUAUCCCUUAUUUUUAUUAAAAACAUAGAGAAAAUGGUCUAAACUCACCCUAAACUAUACCUGAAAUUCACCUACACACUCUUAUUUCACAGGUCCUAUUACCCUC	178	spiLA0480-miR8046-5p	CUCUGAAAUUUCGAGCAUAGU	34-54	stu-miR8046-3p	3	0	21	21	1
spiLA0480-MIR5030-2	GACAUUCAAGGGGAGUGUUAUAAACAAUUUGUAUUAUAGUGAAUGUCUAAUUAUGUGGAGUCCUUGUAGGAUAUGGUUAGGAAUCCUACUUGGGGACCAAGUAAGGUUUUCCUUAUAAAUAAAGGGUUUUCCUUCAUUGUAAACAAGAUUUGUAAAAGAUCUCUGAAUCCU	171	spiLA0480-miR5030-2-5p	UAAACAAUUUGUAUUAUAGUGA	21-42	gma-miR5030	7	0	22	22	3
spiLA0480-MIR482b-4	UCUUCUAAAAUAACUAGGUUUUCUAGUCCUUUUUGGAUUAGGAAGAAAUCUCUAUAUAUAGGGAUUCUUCUAACCUAGAAAUAGAUUAUUAGUUUUCUAUUCAUACUUUUCCACCCAAGUAUUGAGAGAGUUCGGAUGUGACUUGGGAUCACUGUAGAAGACCAUAGAUAUCUUGUAGAUUU	182	spiLA0480-miR482b-4-3p	UUUUCUAUUCAUACUUUUCCAC	93-114	eun-miR482b-3p	6	0	22	22	1
spiLA0480-MIR4405	AUGAUAUUAUUGGAUCGGAGUGUCACGUUCUGACACGGUAUUAUGGGAUCGGAGUGUCACAUUCCGACACGGAAUACGGGAUCGGAGUGUCACGUCCCGACACAAUAACAUUAA	114	spiLA0480-miR4405-5p	GUUCUGACACGGUAUUAUGGGAUC	27-50	gma-miR4405	7	0	24	24	2
spiLA0480-MIR6271-2	AAGUAAUGAAGCCAAGUACCUAUUUUUGCUUUGUUCCUUGUUCGAGGAAGAUAGAGAUAUAUAAUUACUUUGGAUAUGGAAGUGGGUUUCACAUCUUUCCGGGCAUUGAAAAUUUAGAACAAGCAAGAGAUAGGGCGUGUCUUCUGUUAGAA	152	spiLA0480-miR6271-2-5p	GGAAGAUAGAGAUAUAUAAUU	46-66	ppe-miR6271	5	0	21	21	3
spiLA0480-MIR10434	GAUAAAUAUAUAUUAGAAAAUGUGUAGUGAGUACUAAUUAUAGAGUUAAUACCUCAGAUGGUCACUCAAUUAUGCACUCUUAUUCAAAGUUAAGUGACUUUCUGAGAAAGAAAGCAAUAGUUGAGUGACUUUUGAGUGAAAAUUGAAAGUUGAGUGACUUUCUGAGAAAGAAGCAAUAGUUGAGUGGUAUUAACUCACUAAUUAUAUACAAAAGAUACAAAAACACACAUGUUUGGCAGCUAUUAUUUUGA	312	spiLA0480-miR10434-5p	GUACUAAUUAUAGAGUUAAUACCUC	31-55	gma-miR10434	8	0	25	25	2
spiLA0480-MIR7997b-5	GAAUCCUCCAAAAGUAGUGUAUUUUUUGAGGAUCCAAAACACGAGUGCGGCAACAUUUUAGGAGAGUACAAGCAACCAUUUUUCUCUUUUUGGAUUGAUUGAUUUGGUAAUGUAUGUGAUUCUAAAUCUCUCUCAUUCUCAAUAAUGGCUGUGAAUAUUUCUUAAUAAAGAUUGUUAAUUUGGAGUAAGAAUCUUAUUAUUUCCUCCUACGUUGCUUGGACUCUUCAAAAAUGUUGAAGGGUGUGUGUCGGAUCCUCCAAAAGUAGUGUAUUUUUGGAGGAUCC	284	spiLA0480-miR7997b-5-3p	ACGUUGCUUGGACUCUUCAAA	209-229	stu-miR7997b	3	0	21	21	1
spiLA0480-MIR414-2	UUCAUUACAAAGUUCUAUCAUCCUGAUCCUCCUUCUCCUUUCAUGCCUCCUCUUCUCUAGUUAAAUCUUCUGAUCGUACUUAUUAACAAUCUAGAGCUUCUAAAAUUGUUAGCAGGAUCGAAAAAUUUAACUAAAGAGAGGAAUCCAUGAAGGAAGAACGGGGAUUUGGAUUAGAGAACUUUAUAAUUUU	190	spiLA0480-miR414-2-5p	UCAUCCUGAUCCUCCUUCUCC	18-38	ppt-miR414	4	0	21	21	1
spiLA0480-MIR10542-5	AACUUUUAUAGAAGAAUCAUAUAUACCCCUAAAUAAUUUCUUUAAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUUAACUUCCGUUAAAUGAAGGGUAUAUGUGAGUCUUGUUGUAACGGCAGAGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAGAGCCACUUUUAUAACGAGGGGUAUAUUAGCUUCAAAUGACAGAGUUGAGGGGUAUAUCAGACCUUUUUCCCAUAAAACAAAAAACUCUAAGAACCAAUGCAAACCAUGCAAUCUUAGUUUUGACUAUUUUAUGGAUUAAGCGAUUGUGUCUCAAUGCUUAUGAAUUCUAGUGUAGUUUUCUUUGGGCUAUUGAAUGAUAUAAGAAUUGUAUUGGAUUGAUGCAUAGGCUGUCUUAGAUUGAU	256	spiLA0480-miR10542-5-5p	UAGAAGAAUCAUAUAUACCCCUA	9-31	sly-miR10542	0	0	23	23	1
spiLA0480-MIR10533	CACCUGUCGUUCAUAAAUUAGAUUAUAUAUGUCCUUUACUCUUACGGAAGACUAAAUAGGAACACGUAGUGCAAUAUUAUCCGUUGAUAAAUGUCGAGAUCGAUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAAGGGUGUAUAUGCUCUGUUUUUUAGACGAUAGAGA	163	spiLA0480-miR10533-3p	GCUUAUGAAUUCUAGUGUAGUU	77-98	sly-miR10533	7	0	22	22	2
spiLA0480-MIR1520l-3	CACAUCUCAUGAGAUGGAAUCAGCGUGAAAUCGCAUGUCCAAA	176	spiLA0480-miR1520l-3-3p	GAUAAGAUUAUGACACGUGUAUGU	106-129	gma-miR1520l	7	0	24	24	2
spiLA0480-MIR7980b-3	CGCUGAUUCCAUCUCAUGAUAUCAU	68	spiLA0480-miR7980b-3-3p	GUCCAAACGCUGAUUCCAUCUCAU	37-60	stu-miR7980b-5p	1	0	24	24	1

spiLA0480-MIR5532-2	UAUUCCAUGAAUAUGAUAUCUAUCUAGUGUGAUGUAUGGAAUAUAUGACAAAGGUGGAUCUAUUGAUCGGUCAUGUCAUAUAGGCCCGAGUUGGACAUCCAAUUGCUUCGAUUUGAAUUAUCCGGAGAAUGCAAUGCCUGAUAUAUAUCAAAAAGAUGGACAA	163	spiLA0480-miR5532-2-5p	AUGGAAUAUAUGACAAAGGUGG	36-57	osa-miR5532	0	0	22	22	1
spiLA0480-MIR8004	AUAAGUGGGGUCUUGAGAGGGUAGAGUGUAUGCAAAUCUUACCCCUGCCUCUUUAUCUUUACGAGGUAGGGGUAAAGUAUGCGUAUAACCUACCCUCCCCAGACCCCACUUGU	113	spiLA0480-miR8004-3p	AGGGGUAAAGUAUGCGUAUAACCU	68-91	stu-miR8004	7	0	24	24	1
spiLA0480-MIR5652	AAAUGAACUUAAUGAGUUGAAUCUGAAUGAUUCAGAUUCAGACUUAAAAAUCAAACGUAGUUAAUAGGCUGAAUCUGAAUUAUUAAGAUUCAGACCUCCAUUAAGUGCAAAC	112	spiLA0480-miR5652-5p	UUGAAUCUGAAUGAUUCAGAU	17-37	ath-miR5652	5	0	21	21	1
spiLA0480-MIR7981a-48	AAAAUCUCAGAGACACGCUUAUAUUAUACUAAGAUCCUAUUAUCCAUGAAUCCCUUUUCGGCUUACGCGGCACUAGUUUGAAAGAAAAGUCAACCAGCAUUGGGCCUACAAGAUAGUUUCACGUAGGCCGAAAAGGGAUAGAAUACUAUCAAUAAAAUAAGUUCAGGGGUAAUCGAACCUUAGUAUAGUAUAAAUGUGUCUCUGAGAUUUCUUAAUAGUCAAAAACACAUUUGAACUGUUACUUUUUCGGUAGUUUCACACUUUAACUACCGGUUAUUCCUUUUUCCUAUCUGAACUAUGACCAUCGUUCAGGUAGGAAAAGGAAACAACUGAUAGUUGAAAUGUGAAACUGACGAGAGAACAAUAGUUCAUUUGAGUUUUUGAGCUAUGCU	212	spiLA0480-miR7981a-48-5p	AUCCCUUUUCGGCUUACGCGGCAC	50-73	sly-miR7981a	3	0	24	24	1
spiLA0480-MIR8039-3	UCCUAGGUUAGUAGUUAAGAUAGUUAGUUAGGGCCUAGAGUUAUUUAGGAAGUUAGGCCCCACAUCGAGGGACCCGUACACCAUGCUGCCCCUUAACUACCCUAACCGAAUUUGGUUAGGGUGGUCCCCUCCUUUGGUCGAUUCUCACUUGCUUUGCCCAUGUUCAUGCACAUGGGCGGGUUGUACUUUUCUAACUAACUAUUUGGAAUAGUUACUUAUCG	181	spiLA0480-miR8039-3-3p	UUUCCUAUCUGAACUAUGACC	72-92	stu-miR8039	1	0	21	21	1
spiLA0480-MIR9767	CUAAGGUCCUAUUACCCCCCUGAAGUUAUUUUAUAAGUAAUUUUCUACCCCUUUUAGGCCUACGUGGCACUAGUUUGAAAGAAAAAGUCAACCAGUGUUGGGCCCACAAGAUAGUGCCACGUAAGUCAAAAAGGGGUAGAAUAUUACUAAUAAAAUAAGUUCAGGGGGUAAUAAGACCUUUG	221	spiLA0480-miR9767-3p	UUGGAAUAGUUACUUAUCG	203-221	gma-miR9767	4	0	19	24	2
spiLA0480-MIR7981a-49	UAAUAAUUUUCUAUUUUUUUUCGGUCUACGUGGUACUAUCAUAUGGGUCCAACGCUGAUUAUUUUUUUUUUCAAGCUAGUGCCACGUAGGUCGAAAAGGAAUAGAAAAUUACCU	182	spiLA0480-miR7981a-49-5p	ACCCCUUUUAGGCCUACGUGGCAC	47-70	sly-miR7981a	1	0	24	24	1
spiLA0480-MIR1312c	CUCUACUAAAGUUCAAUUACCCUCCUAAAUUUAUUUUAUAAAUAUUUUUCUACCCCUUUUCGGCCUACGUGGCACUAGUUUUGAAAAUAAUGUGAACACACGUUGGACCCACAAUAUAGUCUCUCAUAAGAGGAAAAGUGGUAAAAAUUUAUUUAUAAAAUAAGUUUUAGGGGUUAUAAAACCUUAGUAUAC	114	spiLA0480-miR1312c-3p	GAAAAGGAAUAGAAAAUUACC	93-113	pab-miR1312c	6	0	21	21	2
spiLA0480-MIR7981a-50	UAUAGGUUUUAUUACCCUCUGAAUUUAUAUUAUAAAUAAUUUUCUACUCUUUUUCGGUCGAUGUGACACUAGCUUGAAAAAAAAGUCAACAAGCAUUGAACCCACAAGAUAGUGUUACGUAGGUCAAAAUGGGGUAGAAAAUUAUUAAUAGAAUAAGUUCAGGGGGUAAUAGGACCUUAG	194	spiLA0480-miR7981a-50-5p	ACCCCUUUUCGGCCUACGUGGCAC	52-75	sly-miR7981a	0	0	24	24	1
spiLA0480-MIR8657b-2	AUUAAAUGUCAGAGAGGCACACCUUAAUUAAACUAAGGUCAUAUUACCACCUAAAUCUUUUUUUGGUAAUUUUGUGCACCUUUAUCUUAUGUGGCACGCUCCGUGACUUUAUGUAAUUGAGGCGCGUGAGAUAUUUUGAUAUCACGUAAGUAAAAAAGGUACACAAAAUGGCAAAAAAAAAAGUUCAGGGGAUAAUAGGACCUUAGUAUGGUUAAGGUGUCUCUGGAAUUUCGG	180	spiLA0480-miR8657b-2-3p	AUUAUUAAUAGAAUAAGUUCAGGG	141-164	gra-miR8657b	6	0	24	24	3
spiLA0480-MIR7981-14		234	spiLA0480-miR7981-14-5p	CUUAAUUAAACUAAGGUCAUAUUA	23-46	stu-miR7981-5p	3	0	24	24	2
			spiLA0480-miR7981-14-3p	AUAGGACCUUAGUAUGGUUAAGGU	195-218	stu-miR7981-3p	3	0	24	24	1
spiLA0480-MIR10538-14	GUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUCCUAAAACGUUACUCACAGUAAAACGUUACUGAAAAUAACGUUUUAAAAGUGAAACGUUACUUACAGUAACGUAUAUCAACCUAAU	124	spiLA0480-miR10538-14-5p	AGAUUGAUAUACGUUACUCACAGU	4-27	sly-miR10538	0	0	24	24	1
spiLA0480-MIR482c-4	CCAACAAAAACUUUUGGGAAUGGGUGGGUUGGUAAGCUUUUCCUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUCCUAUGGGUUUUUGUGCU	104	spiLA0480-miR482c-4-5p	ACUUUUGGGAAUGGGUGGGUUGG	10-32	gma-miR482c-5p	5	0	23	23	1
			spiLA0480-miR482c-4-3p	UUACCAAUUCCACCCAUUCCUA	69-90	nta-miR482c	1	0	22	22	1
spiLA0480-MIR859-2	UUUUUUAUAAUUUUGUGCAACUUUUUAGCUUACGUGACAUCCAAAUAUAUCCCACACGCCUCAAUUGUGUGAAGUCACAGAGUGUGCCACGUAAGACAAAAGGUGUACAAAAUUACUAAAGUC	123	spiLA0480-miR859-2-3p	CCUCAAUUGUGUGAAGUCACA	59-79	ath-miR859	6	0	21	21	2
spiLA0480-MIR5670a	UGCAAUAUUUGAAGUAAAAUGUUUGUAAAUUGUAUAAUUAAGUGUAUAACACGAAGAUAUAUAUAUUUUUACAUGUGUAUAUACAAUUUUCUCUCGCUUUUUACAAAACAGAAACAGAAUUUAUACACU	255	spiLA0480-miR5670a-3p	AAUCAAACCCUAUCUACUUCAU	226-247	gma-miR5670a	5	0	22	22	2

spiLA0480-MIR7822-2	UCUGUGUAUAAAGCGAGAAUGGAGAGUGGCGAGCGCGAUUUUGGGAGAGAGACGCCUGGCAAACUUUAGUUAACAUUUGCUAUGGAGCACAAUUAAAUCAAACCCUAUCUACUUCAUUUAUUUUAUCAAAUGGGCGGAGUAGGUUUGAAAUUGAAAAUAUUAAAAUGGGUUUAAUAUAAAUCGGAUUGGGUCUUGACCUAUCCAAAUUUAUUUUGGGCUCGAAUGGGCUAAAAAACGGGUUGGGUCUUGACCUGUUCAGUUUAACCCGAUUAAUCUCAAUAAUUUAACAUAUUGAUAUUUAACUUUUUAUAAUCACAAUUUGAAUUUCCGCUCAUUAAU	214	spiLA0480-miR7822-2-5p	UUUGAAAUUGAAAAUAUUAAA	19-39	ptc-miR7822	5	0	21	21	1
spiLA0480-MIR2108a	AUGUAUUUGUAUACUCUGGCGAAUUAUACAUAUACAAACGUGACUAAUUAUACAAACUUGAAGUCAACCAACGUAAUUAAUGUAUAAUGUUAGUCGCGAGUGACAAUUAUAG	112	spiLA0480-miR2108a-3p	UUAAUGUAUAAUGUUAGUCGC	77-97	gma-miR2108a	5	0	21	21	1
spiLA0480-MIR5214	UAAGAAUUCAAGUAUUCAAGUUUAAGAAUUCAAGUAUUCAAGAUAAAGUUCAAGAACGAUCAAGAUAAAGUUAAGUUCAAGAACGAUCAAAAGAUCAAGACCAUCGGAUUCAUGAUCAAGCUUGAAGCCCUUGAAUUCAAC	141	spiLA0480-miR5214-3p	CAAAAGAUCAAGACCAUCGGAU	88-109	mtr-miR5214-3p	6	0	22	22	3
spiLA0480-MIR8020-2	CAAGAUAUAGCUAAUUAGUUGAGUGACCAUCUGAGAAAUCAAUUCGAUUGAAGUCUGUAUACACUCUAUCCAUCCCAGACUUCACUAAUGUAAUUAUGCUGAAUAUGUUGUUGUUAUACACAAAGUAGGGGCAAAGUUGAGUUGAUUUCUCAUAUCGUCACUUGACUAAUAGAUAUUAUCCUA	183	spiLA0480-miR8020-2-3p	AAUUAUGCUGAAUAUGUUGUUGUU	92-115	stu-miR8020	5	0	24	24	1
spiLA0480-MIR6160	AUUAUAUUUUUUUUCAUUUCCGUUAGAGGAAAAGGGUAUAUGUGAGCCAUUUGUUUACAAGUAAGGGUAUAUAUGUGCCACUUUCAUAACAAUGGGUAUAUCAGCUCUAAAUGACAAAGUUGAGGGGUAGAUCAGACCCUUUUCCCUUUAACUUAAUUCGAAUAAUAUAUUCA	173	spiLA0480-miR6160-3p	GUAUAUAUGUGCCACUUUCAUAAC	67-90	nta-miR6160	7	0	24	24	1
spiLA0480-MIR7504b	AUGUAAAUAACAAAAGAAUUUACACAUAUAUGAGUCGGAUUAGGGGCAUAAUUGAACCAUUUAAAAGACGGUCGUAUAUGUGUUUUAAAAUUGGGUCGGAUAGUUAGGGCAUAAGUGACCCCUUUCCCUUUUAAUGUAAAUGUCAAAUGAUAAUAUAUAUAAAUGAUGUGAAAUCUCAUUUGGCAUUUAAAG	192	spiLA0480-miR7504b-3p	AUGAUGUGAAAUCUCAUUUGGCAU	163-186	ghr-miR7504b	6	0	24	24	1
spiLA0480-MIR2101-2	AUGUGAUUAAUGAUUAAGGAUUGUGGAGUUGCCCUCAUGUUUAUAAGUUGACAGUUGGUCCACUUAAUUAAAUGAAGGGUAAAAGGGUAAUUUCACAAUACCUAAUUUAACCAACU	116	spiLA0480-miR2101-2-5p	UCAUGUUUAUAAGUUGACAGUU	35-56	osa-miR2101-5p	6	0	22	22	2
spiLA0480-MIR159c	CCAAGUUUACUUUGGGCUAAAAUGGAUUGGGUUAAAGUGAGCUAACCCAAUUCAAUUUGACCCGAUUAAUCUCAA	75	spiLA0480-miR159c-3p	AUUGGGUUAAAGUGAGCUAAC	26-46	fve-miR159c	5	0	21	21	1
spiLA0480-MIR7981a-51	AUUAUUUUCUACUCCUUUUCGGUCUACGUGACACUAUAUUGUGGGCUCAACGCUGGUUGAUUUUUUUUCAAGCUAGUGCCACGUAGGUCGAAAAGGGACAGAAAAUUAC	109	spiLA0480-miR7981a-51-5p	ACUCCUUUUCGGUCUACGUGACAC	11-34	sly-miR7981a	3	0	24	24	1
spiLA0480-MIR12169	CACAUACCGACACAAGAGAAAUAAUAGUUAUUGAAUUGGUUUUUAUUAAUGAGUUAAGUCUUCCGCAUUACUUUAUGUUUAUAUUACAUUGAAAUGUUAAGGCUUAGAUUGAUUGGUUCGCUCACAUAGGAGGGUAAGUGUGGGUGUCAGUCGCGGCUCGGUUUUGGGUCGUGACAAACUUGGUAUCUCAUCACACAAGAACGAGUCUAGUAGAGUCUUAAGGAACGGUAGGGGGACGCCUUUACUUUUCUUUGAGAGGCUAUAAGACUUUAGGAAAAUUCCAUUCUUUCUUUCUUUCUUUCGUGCUAUUAC	312	spiLA0480-miR12169-5p	UAAUAGUUAUUGAAUUGGUUU	22-42	aof-miR12169	4	0	21	21	1
spiLA0480-MIR7981b-27	UAUCCCUUUUUAGCUUACGUGGCACUAUCUUGUGGGCCCACGCCCAACGAUGAUUGACUUUUUUUUCCGAACUAGUGCCACGUAGGCUAAAAAGAGGUAG	100	spiLA0480-miR7981b-27-5p	AUCCCUUUUUAGCUUACGUGGCAC	2-25	sly-miR7981b	1	0	24	24	1
spiLA0480-MIR395n-1	GACAAGUCUAGUAGAGUCUUGAGGAACGGUAUGGGGACGCCUUUACUUUUCUUCGAGAGGCUAUAGGACUUUAG	74	spiLA0480-miR395n-1-5p	UAGUAGAGUCUUGAGGAACGG	9-29	vvi-miR395n	6	0	21	21	3
spiLA0480-MIR5174e-2	GUACUCCCUCCAUCCCAUAUUAGUUGUCCACUUCCGUAAUGUGGAACAACUAUUUAUAGUAAGGUGGACCACUAAUAUGGGACGGAGGGAGUAG	94	spiLA0480-miR5174e-2-5p	UACUCCCUCCAUCCCAUAUUA	2-22	bdi-miR5174e-5p-2	6	0	21	21	1
			spiLA0480-miR5174e-2-3p	AAUAUGGGACGGAGGGAGUAG	74-94	bdi-miR5174e-3p-2	3	0	21	21	3
spiLA0480-MIR6458	UGACAAUUAUGUGAUUAAUGAUUAAGGAUUGUGGAGUUGCCCUCAAGUUUAUAAGUUGACAGUUUGGUCCACUGAAUUAAAUAAAGGAUAAAAGGGUAACUUCACAAUGCCUAAUUUAACCAACUAUUGGUG	132	spiLA0480-miR6458-5p	GCCCUCAAGUUUAUAAGUUGAC	39-60	ptc-miR6458	7	0	22	22	2
spiLA0480-MIR1886h-3	ACCAUAUCACGAUAUGGAAUUAUGAGAUGGAAUCAUCGUUUGGACAUCUAAUUUUACGUUGAUUCCAUCUCAUGAUUCCAUAUCAUGAUAUAUG	94	spiLA0480-miR1886h-3-3p	AUUUUACGUUGAUUCCAUCUCAUG	51-74	stu-miR1886h	1	0	24	24	1
spiLA0480-MIR10532-12	AUGAAUUCAAAGAAAUUAAAUAUAGAUUUAUAAAUCCCCCUGAACUUAUUUUAUAUGUAUUUUUCUACCCCUUUUUAGCCUACAUG	232	spiLA0480-miR10532-12-3p	AAGUGUGUCUCUGAGAUUUCG	212-232	sly-miR10532	0	0	21	24	1

spiLA0480-MIR5380b	GCACUAGUUCGAAAAAAAAAGUCAACCAUCGUUGGGCCCACAAGAUAGUGCCACGUAAGCUAAAAAUGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAGGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUCG	112	spiLA0480-miR5380b-3p	GAAUCUGAAUGAUGAAGAUUUGGA	71-94	gma-miR5380b	5	0	24	24	1
spiLA0480-MIR5026-3	AAAUGAAUUUAAUGGGUUGAAUCUGAAUGAUUCAGUUUCAGACCUAAAAAUCAAACGUACUUAAUAGGCUGAAUCUGAAUGAUGAAGAUUUGGACCUCCAUUAAGUGCAAAC	96	spiLA0480-miR5026-3-3p	ACCCACAAGAUAGUGUCACGU	58-78	ath-miR5026	4	0	21	21	1
spiLA0480-MIR8660-2	UGUAUUCCUUUUCGGCCUACGUGAUACUAGCUUGAAAAAGAAGUCAAUCAGAGUUGGACCCACAAGAUAGUGUCACGUAGGCCGAAAAGGGAUAGA	87	spiLA0480-miR8660-2-3p	ACGAAAAAUGACAUGUAGGACAC	53-75	gra-miR8660	6	0	23	23	1
spiLA0480-MIR7981a-52	AAAUAAACACAUGAGUCCUACAUGGCAAAAUACACGUAGAACACCACGUAGGACGAAAAAUGACAUGUAGGACACGUGUGUCUAUUU	113	spiLA0480-miR7981a-52-5p	ACCCCUUUUCGACCUACGUGACAC	13-36	sly-miR7981a	2	0	24	24	1
spiLA0480-MIR7981b-28	AAGUAAUUUUCUACCCCUUUUCGACCUACGUGACACUAGGUUGAAAGAAAAAGUCAAUCAGAAUUGGGCACAAGAUAGUGCUAUGUAGGCCGAAAAGGGGUAGAAAAUUAUUA	95	spiLA0480-miR7981b-28-5p	ACCCCUUUUUAGCCUACGUGGCAC	3-26	sly-miR7981b	1	0	24	24	1
spiLA0480-MIR395n-2	CUACCCCUUUUUAGCCUACGUGGCACUAGUUCGAAAGAAAAAGUCAACUAUCGUUGGGCCCACAAGAUAGUGCCACGUAAGCUAAAAAGGGGUAA	74	spiLA0480-miR395n-2-5p	UAGUAGAGUCUUGAGGAACGG	9-29	vvi-miR395n	6	0	21	21	3
spiLA0480-MIR3951a-2	AACAAGUCUAGUAGAGUCUUGAGGAACGGUAUGGGGACGCCUUUACUUUUCUUCGAGAGGCUAUAAGACUUUAG	66	spiLA0480-miR3951a-2-3p	CAGAUAAAGAAGCGAGA	50-66	csi-miR3951a-5p	3	0	17	21	2
spiLA0480-MIR5014a-12	GUGCGCUUCUUUCUCCUGAUGCGAUGCGAUCUGAAAAAGGCGCUCGCUUCAGAUAAAGAAGCGAGA	221	spiLA0480-miR5014a-12-3p	UUAUACAAAUUUAAGCAUCUA	145-165	ath-miR5014a-3p	6	0	21	21	1
spiLA0480-MIR7997c-21	AAUUUUAACUUUGACCUCGAACUUUCAUAAUGCAUAAACAAGCACUUUAACUAUCCAACUUUUAUAAACACAUGAGUCCUACAUGACACAAUACACGUAGGACAAAAAAUGACAUGUAGGACAUGUGUGUCUAUUUGUUCAACUUUAUACAAAUUUAAGCAUCUACUUAUGCACACCCAAAGUUGAAGAGCAUAAAUGUAAUUCGAAGUCAAGUUAAAGAG	128	spiLA0480-miR7997c-21-5p	AUGUUGCUCGGACUCUUUCAAAAU	8-31	stu-miR7997c	3	0	24	24	1
spiLA0480-MIR7992-20	AGAGGCUAUGUUGCUCGGACUCUUUCAAAAUGUGGAAGGUUGUGUCAGACCCUCCAAAAAUAGUGUAUUUUUGAAGGAUCCGACACGGGCGAGGCAUCAUUUUGGAGAGUCCGAGCAACUUAGCCCAG	169	spiLA0480-miR7992-20-3p	UGUCUAGAUGUGCAUUCUCAAAG	90-112	stu-miR7992-3p	5	0	23	23	1
spiLA0480-MIR7699	GCAUAAUAUAUAGAUAGACACCUUAAAUUGGCCUUAACGAGCAAGUAAAGACCCAAACUAACACGGGGCCAACUUAAACCAAGUUCAUGUGUCUAGAUGUGCAUUCUCAAAGUGUAGGUCUUUACAUGUCAGUUAAGUCCAAGUUAAGGUGUCUAUCUACGUGUUACAA	88	spiLA0480-miR7699-5p	ACUUAAUCCAUGGAUUAGUUA	3-23	mtr-miR7699-5p	6	0	21	21	1
spiLA0480-MIR7981a-53	UAACUUAAUCCAUGGAUUAGUUAUACCUCAUACAAAGUCUUAUUUUAUCCCUAGGAAAGGGAAGGAUAGCUAAUCCAAGAUUUAGCAA	115	spiLA0480-miR7981a-53-5p	ACCCCUUUUCGGCCUACGUGGCAC	13-36	sly-miR7981a	0	0	24	24	1
spiLA0480-MIR7981b-29	UUAUAAUUUUUUACCCCUUUUCGGCCUACGUGGCACUAUCUUGUAGGCCCAACGAUGGUUGACUUUUUUUUCAAACCAGUGUCACGUAGGCUAAAAAGGGAUAGAAAACCCCCCUGAACUUAUUUUAUUAAUAAUUUUUUACCCCUUUUUAGCCUACGUGGCACUAUCUUGUGGGCCCGACGAUGGUUGACUUUUUUUCAAACUAGUGCCACGUAAGCUAAAAAGGGGUAGAAAACUACUUAUAAAAUAAGUUCAGGGGGGU	156	spiLA0480-miR7981b-29-5p	ACCCCUUUUUAGCCUACGUGGCAC	34-57	sly-miR7981b	1	0	24	24	1
spiLA0480-MIR7981b-30	UUUUACCCCUUUUUAGCUUACGUGGCACUAUCUUGUGGGACCAACGAUGGUUGACUUUUCUUUUCGAGUCACGUAGGCUAAAAAGAGGUAGAA	93	spiLA0480-miR7981b-30-5p	ACCCCUUUUUAGCUUACGUGGCAC	5-28	sly-miR7981b	0	0	24	24	1
spiLA0480-MIR5826	ACAUAACUCACAUCUCAAAACUAGCCCAAAGGGAGGAGCAUUGUCCAUGCACCCAAAUCUCAUUAACCACAAUUCUUAAAGAAUGACAAAGUCCUGCAUCGGUGGUUAAUGAGAUGGGUGGACUCCUUAUAAGGCUUGAGCAAUCCUUCUCCGUUUGAGCUAGCUUUUGGGGUGUGAAUUAGGC	184	spiLA0480-miR5826-5p	UAGCCCAAAGGGAGGAGCAUUGUC	22-45	osa-miR5826	7	0	24	24	1
spiLA0480-MIR2673b	GUCCAGUCCUCUUCCUCUUCCUCUACCACCGCUGUCAUUGAUUCAAAAUCAAAAUUUUCAAUUAAAGAUUGAAAUCAACAAUAAAGAAGAUUUUUCGUUUUACCUCCUAUUGGAAUGAGAAAAGGCAGAGUAGGAUGAGGAUGAGGAUGAGGAUGAAG	158	spiLA0480-miR2673b-5p	CCUCUUCCUCUUCCUCUACCAC	8-29	mtr-miR2673b	1	0	22	22	1
spiLA0480-MIR7981f-15	UGUUUUGUUAAAAAGGGAUAAUGCACAAGUAGAAAAUUACUUAUCUAAUAAGUUCAGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGGGAUUUCGGCCAUAGGUUGAGGGGGUACUUGUGCAUUUUCCCUUUUUAAAAAUUU	151	spiLA0480-miR7981f-15-3p	AAGUGUGUCUCUGGGAUUUCGGCC	84-107	sly-miR7981f	2	0	24	24	1
spiLA0480-MIR6162	UUGUUGAUAUUACUAGUCACAAAUGUGAAAAUUGGUAGCCAUCAAUGUGAAAGUUGGUAGCUACAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAUAAGUUUGAUAGAGUUAGGCAACCAAUUUUUU	173	spiLA0480-miR6162-5p	UGAAAAUUGGUAGCCAUCAAU	26-46	nta-miR6162	6	0	21	21	2

spiLA0480-MIR7981f-16	UGUUGAAAUUGGCUACCAUAUAUGUCAUUAAUGAUGUAAACAAGUG GCUUUUAUUAAAGGGAUAAUGCACAAAUACCCCUCAAUCUACG CCCGAAAUUACUUAUAAAAUAAGUUCAAAAGGGUAAUAAGACC UUAGUAUAUUAUAAGUGUGUCUCUGAAAUUUUGGGCAUAAAU UGAAGGGGUACUUGUGCAUUUUCCCUUUAUUAAAUUU	165	spiLA0480-miR7981f-16-3p	AAGUGUGUCUCUGAAAUUUUGGGC	99-122	sly-miR7981f	2	0	24	24	1
spiLA0480-MIR10532-13	UAAAACAAGUUCAGGGGGUAAUAGGACCUUAGUAUAGUAUAAG UGUGUCUCUGAGAUUUCGAGCAUAGGUUGGGGGGUACUUGU ACAUUUUUCCAUUAAAAAGAUAAUCUAACAUAACUUGUUACAU CAUUAAUAAAAUGCAUAAAUUUCCCCUUUAACUUGUAUUGAAA AGUCAGUUACACACUUCAAUUAUUAUGAUGACCUAUUACACAC UUAUUCUUGUUCAA	227	spiLA0480-miR10532-13-5p	AAGUGUGUCUCUGAGAUUUCGAGC	41-64	sly-miR10532	1	0	24	24	1
spiLA0480-MIR403b	AUUGGAAAAGCCAUAUUACGAGCUUGUGCGUGAAUCUAGCAA ACAAUAACAGUUUUUCUGAUGAAAAGAGUUGUUAGAUUCACGC ACAAACGUGAAAUAUGCCUCUUCCUGA	112	spiLA0480-miR403b-5p	AGCUUGUGCGUGAAUCUAGCA	21-41	csi-miR403b-5p	3	0	21	21	1
			spiLA0480-miR403b-3p	UUAGAUUCACGCACAAACGUG	74-94	gma-miR403b	1	0	21	21	1
spiLA0480-MIR7764	UGUUAAUUCUUUAGAAUACCUUUGUUAAUUAUCCAUUAAUAUU AAGAAGGGGGUGUGACCAGUAGCUUAGGAAGUUUGUUUUAGU UAUUGAAUGUGCUAAGUAUGAACGAAAACCAUAAUCGGAUUAU UAGUGGUGUCGUGUUGGUGCUUGGGCUGUUUUGAUUAAAGC AAACUGCGGGAAAAUUCUAUUUUGGCGUUAUGUAUAUGUUAA AUAUGUAUGAGUAUAUACUCCAAAGGAUGAAUACGAUAAGGUA GAUGUGUUGAGAAUUAUAA UUUGUUAUUGCAUACUUUUCUUCAGAUGAUAAGAAAUUAUCCC ACCAUCCUCUGAGUUGACCUGUAAAUCCUGCUAUAAUCAUUUU ACAUAUAGCAUGAUCACUAUUCUGAUUCGUAUGACGACAAAUU GAUGAGUACAUCAACAUCCGAUGUACCAUAAUGGAAACCUGCC UUUCAGUCAAGGCAUCCAAAUUCCAUUCAUACACCUCAUUACC	273	spiLA0480-miR7764-3p	AAUUCUAUUUUGGCGUUAUGUA	182-203	bdi-miR7764-3p	6	0	22	22	1
spiLA0480-MIR395m	ACUGUAAGAUGUGUUAGUUUGAUUCCAAUCUCUUUCUUCGAC UAACACAUCUUGGGGAGUAGGACGAGGAUAAUAAUAAGUCAU CAUUGAAGGGAGAGUUGCAUAACCCC	325	spiLA0480-miR395m-3p	AUUCCAUUCAUACACCUCAUUA	192-213	zma-miR395m-5p	7	0	22	22	2
spiLA0480-MIR7981a-54	AUUUAUCCCUUUUCGACCUACGUGACACUAUCUUGUGGGUCC AAUGAUGAUUGAUUUUUUUUUCAAACUAGUGUCACGUAGAUUA AAAAGGGGUAGAA	98	spiLA0480-miR7981a-54-5p	AUCCCUUUUCGACCUACGUGACAC	5-28	sly-miR7981a	3	0	24	24	1
spiLA0480-MIR9748	ACGAGUCUAGUAGAGUCUUAAGGAACGGUAGGGGGACGCCAU UACUUUUCUUUGAGAGGCUAUAAGACUUUA	72	spiLA0480-miR9748-3p	UAAGGAACGGUAGGGGGACGCC	19-40	gma-miR9748	6	0	22	22	2
spiLA0480-MIR1917-4	UCUCUACAAUAAAAAUAACUUUUAGCGGCAAUAAAUAGAUACA UUAAUAAAGAGUGCUAAAGUCUUUACCGGCAUUAGUUAAGUG UCAUUAGAUCCAAUGUCGCUAAAGCCUUUAGUGACACAUACAA AGAGUGCUAAUUGCCACUAAAACCAUAUAUUUAGCGGCAAUUG CUAAUUAAUUGCCGCUAAAGCUCAUUUUUAAUGUAGUGU	210	spiLA0480-miR1917-4-5p	AUUAAUAAAGAGUGCUAAAGU	43-63	sly-miR1917	0	0	21	21	1
spiLA0480-MIR482	CUUGGGUAGUGUCAUCCUUGAGAUGUGCCACAGACUUGGUGC AAAAUGUGGCGAGAUAGUCGUGUCCUAGGAGGGGUGCCAGUC ACCUGGGAGCUGUUCAAGACAACAUUUUUGGAAAGGUUCUUC CCUAGGGAGAUGAAGGAGGCCAAGGUUGAGGAGUUCAUCAAC CUUAACCAAGGGUCUAUGACGGUCAGGGAGCAUUCUCUGAAG UUUGUGAAGCUAUCAAGGUAUGUUACUUCCCUUG	244	spiLA0480-miR482-3p	AGGGAGAUGAAGGAGGCCA	130-148	zma-miR482-5p	4	0	19	19	2
spiLA0480-MIR7981a-55	UUACCCUCCUGAACUUAUUUUAUUAAUAAUUUUCUACCCUUUU UUGGCCUACGUGGCACUAUCUUGUGGGCCCAAUGCUGAUUGA CUUUUUUUUUUCAAGCUAGUGCCACGUAGGCUUAAAAGGGGU AGAAAAUUACUUAUAAAAUAAGUUCAUGGGGGUAA	162	spiLA0480-miR7981a-55-5p	ACCCUUUUUUGGCCUACGUGGCAC	36-59	sly-miR7981a	2	0	24	24	1
spiLA0480-MIR11525b	CGCUAUAGGAAAAGGGUAUAUGUGAGCCAUUUGUUUACAAAU AAGGGUAUAUAUGAGCCACUUUCAUAACUAGGGGUAUAUAAG CUCUAAAUGACAAAGUAGAGGGCUUUAUCAGACCCUUUUCCC UUUAUGU	133	spiLA0480-miR11525b-3p	AGUAGAGGGCUUUAUCAGACC	98-118	pab-miR11525b	6	0	21	21	3
spiLA0480-MIR8028	AUCUAUUUCUAUUUGUAUAAAGCGAGAUGAAAUUGUAUAAAUA CAUAUAUUUUUGUUCACCUCUCUCCCUAAUCUCGCUCGUCAC CCUCACCUCUCUCGCUUAUACAAACAGAAACGAAGUGUAUAAA UUGUGUUUGUGUUUGUAUAAAGCGAGAGAAAAUUGUAUAUAC ACAUGCAAAUACAUAUAUUUUCAUCCUAUACACUUAUAAUUAU ACAAUAAAGAUACUC	228	spiLA0480-miR8028-3p	ACUUAUAAUUAUACAAUAAAGAUA	202-225	stu-miR8028-3p	7	0	24	24	3
spiLA0480-MIR852-2	UUCCUCAAAAAUUUCCCUCUUCUUGAAAAAAAAGGAAAACGAA GUCAAAUAUCUUAUUACCUUUGUUUUCCUUUUCCAGAAGAGG GAACUUUUUGAGGAU	100	spiLA0480-miR852-2-3p	AAAACGAAGUCAAAUAUCUUAU	36-57	aly-miR852-5p	6	0	22	22	1

spiLA0480-MIR8007b-6	UAUAAAUAAACACAUGAGUCUUACAUGGCACAAUACACGUAGGACACCACGUAGGACAAAAAAUGACAUGUAGGACAUGUGUGUCUAUUUGUU	93	spiLA0480-miR8007b-6-3p	CAAAAAAUGACAUGUAGGACAUGU	57-80	stu-miR8007b-3p	7	0	24	24	1
spiLA0480-MIR10205	CACACACAAUACACAAGAGAAAAAAACAUAAAGUGAAAGUGUUAGUCUAAAAGAGAGUUCUUAUUACUUGAAUGGAGGUGUUUUUUUUUUUUUGUGGAGCUUUGGACUCAACUCUUGUCCAGAGUUGUUGAGUUAUACUUUGUGAAGGUUGUUGUAUCAUGGAGGGGACAAGUCAAAGAGGACUACUGUUGGACCGGUGAAAACAUUUGCUACAGUAGACUUGAAUCUCUUUAAAGAGAGCGAGAUAUCCGCGCCUCAGCCUUGAAGAGAUUUAUUUUCUUCAUUUUUUAUUUUCAAUUGUAAUUAUGUAUU	311	spiLA0480-miR10205-3p	GGUUGUUGUAUCAUGGAGGGGACA	146-169	vca-miR10205-3p	7	0	24	24	3
spiLA0480-MIR7981b-31	ACACCUAUUAUCCCCCUGAACUUAUUUUAUAAGUAAUUUUCUACCCCUUUUUAGCCUACGUGGCACUAGUUUAAAAAAAUAAGUCAACCAUCGUUCGAGCCAUAAGAUAGUGCCACAUAGGCUAAAAAGGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAAGGGGGUAAUAGGACC	175	spiLA0480-miR7981b-31-5p	ACCCCUUUUUAGCCUACGUGGCAC	43-66	sly-miR7981b	1	0	24	24	1
spiLA0480-MIR5658-2	GUUGCGGUGCGGUAAAGAUGUUGAUGAUGAAGAGAUUUUUUUUAGAAUGUAUUUUUUGAAUGAUUGAAUCAGUCUCCAAGUGGGAAAAUUGUUAGGUUGUGGAGUCUGAUUAAUAUUUGAUGUAUUGUCAUAUAUUACUGUUUACGCGGUUUAGGCUGUACUAUUUAUUCUCCAUUUAUUCUCUGUAACCAAAAAUACUCUGAUUUAUUAAUAUAUACCCCACUGCCGU	231	spiLA0480-miR5658-2-5p	AAGAUGUUGAUGAUGAAGAGA	15-35	ath-miR5658	4	0	21	21	1
spiLA0480-MIR5039	UUGUUAUUGGAUUGUCAUUUACUUCCGCACUUUGUUAGAUAUUGGGUUUUAGGCUGACUUGUCUUGGUGGGGAUAAGACGAGUGCCAUUCACGUCCAUUUUUGAAUCGUGACAUUAGACCUAAGACCUAAUUUCACAAAUGAAAAAGUCAAAAUUUCAUUAAUAAGGU	167	spiLA0480-miR5039-3p	CCAUUUUUGAAUCGUGACAUU	94-114	gma-miR5039	5	0	21	21	1
spiLA0480-MIR1078	CUCAAAAGUCAACGGAUGAUUGUUUAAAUGUUGAUGCAUCUACAACGUCAAAAUCAAAACCACCAACAUUGGACGAUUAUCCUGAUUUUACC	92	spiLA0480-miR1078-5p	GAUGAUUGUUUAAAUGUUGAU	15-35	ssl-miR1078	6	0	21	21	3
spiLA0480-MIR11088b-2	UAGUGGUUUGGUUUGACUUGAUUUGGUGUUGGGAAAAAAACCCGACUAUAUUUGGGUUGGGUUGAUUUCAACUAAAAUAAACCAACCCCGAGACCAAACCAACC	103	spiLA0480-miR11088b-2-3p	UAUUUGGGUUGGGUUGAUUUCA	49-70	lja-miR11088b-5p	7	0	22	22	2
spiLA0480-MIR7981a-56	UAUUAUAAUUUUUUUGAGAAAUUACCUAACCGACAACUUUUCGGCCUACGUGACACUAUCUUGUGGGCCCAACGCUGGUUGACUUUUUCUUCAAGCUAGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUUAG	152	spiLA0480-miR7981a-56-5p	ACAACUUUUCGGCCUACGUGACAC	33-56	sly-miR7981a	3	0	24	24	1
spiLA0480-MIR10532-14	UUAUAAUUUUUUUGAGAAAUUACCUAACCGACAACUUUUCGGCCUACGUGACACUAUCUUGUGGGCCCAACGCUGGUUGACUUUUUCUUCAAGCUAGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUUAGGGGGUAAUAGGACCUUAGUAUAGUAUAAAUGUGUCUCUGAGAUUUCGGGCAUAGAUUGACGGGGUACUUGUGCAUUUUCCCCCGUUCAUUAUAACAGUAAUAUUAUUAAAAACAAUUAUUU	269	spiLA0480-miR10532-14-3p	AAAUGUGUCUCUGAGAUUUCGGGC	175-198	sly-miR10532	1	0	24	24	1
spiLA0480-MIR7981a-57	CUACCCCCUUUCCGUCUACGUUGCACUAUUUUGAGAAAAAAGUCAAUCAGCAUUGUGCCCACAAAAUAGUGCCACGUAGGCUGAAAAUGGGUAG	94	spiLA0480-miR7981a-57-5p	ACCCCCUUUCCGUCUACGUUGCAC	3-26	sly-miR7981a	4	0	24	24	1
spiLA0480-MIR7981d-11	GCCCGAAAUCUCAUAGAUAUACUUAUACUAUACUAAGAUCCUAGUGCCACGUAGACCGAAAAGGGGUAGAAAAUUUACUUAUAAAAUAAGUUCAGAGAGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGACUCUCUGAUUUCGAAU	147	spiLA0480-miR7981d-11-5p	CCGAAAUCUCAUAGAUAUACUUAU	3-26	sly-miR7981d	4	0	24	24	2
spiLA0480-MIR7981b-32	UAUACUAUCCUAAGGUCCUAUUACCCCCUGAACAUAUUUUAUAUGUAAUUUUCUACCCCUUUUUAGCCUAUGUGGCACUAGUUCAGAAAAAAAGUCAACCACUGUUGGGCCCACAAGAUAGUGCCACGUAAGCAAAAAAGGGGUACAAAAUUAUUAAUAAAAUAAGUUCAGGGGAAUUAAAAGAACAAUUCUAGAAUAGUGUC	204	spiLA0480-miR7981b-32-5p	ACCCCUUUUUAGCCUAUGUGGCAC	55-78	sly-miR7981b	2	0	24	24	1
spiLA0480-MIR7981b-33	UGCUUGCCCCCAGAUCAUUAUUAAUAAUUUUUUACCCCUUUUUAGCUUACGUGGCACUAUCUUGUGGGCCCAACGAUGAAUGACUUUUUUUUUUAACUAGUGCCACAUAGGUUAAAAAGGGGUAGCAAAUUACAUAUAAAAUAAGUUCAGGGGGUAAUAG	160	spiLA0480-miR7981b-33-5p	ACCCCUUUUUAGCUUACGUGGCAC	34-57	sly-miR7981b	0	0	24	24	1
spiLA0480-MIR169j-5	UAAAUUAAUGGUAUUAUUGGAUCGGAGUGUCACGUUCCAAUACAGUAUUCUUGGAUCAGAGUGUCACGUUCCGACACGGUAAUUUUGGAUCGGAGUAUCACGUUUCGACACGAUAUUCUUGGAUCAGAGUGUCACAUUUCGACACGGUAUUCUUGGAUCGGAGUGUCACGUUCCGACACGAUAAUAUUAAUGGA	194	spiLA0480-miR169j-5-3p	UUUCGACACGAUAUUCUUGGA	103-123	gma-miR169j-3p	5	0	21	21	1
spiLA0480-MIR7981b-34	AACCCCCUGAACUUCUUUUAUUAAUAAUUUUUUACCCCUUUUUAGCUUACGUGGCACUAUCUUGUGGGUCCAACGAUGGUUGACU	156	spiLA0480-miR7981b-34-5p	ACCCCUUUUUAGCUUACGUGGCAC	34-57	sly-miR7981b	0	0	24	24	1

spiLA0480-MIR7992-21	UUUUUUCUGAACUAGUGCCACAUAGGCUAAAAAGGGGUAGAAAAUUACAUAUAAAAUAAGUUCAGGGGAUAAUAAUGCACAUAUAGACACUUUAACUAUCCAACUUUUAAGUAAAUAAAUGUGUCCUACGUGACAUAAUACAUGUAGGACACCACGUAGGACAAAAAAUGACAUGUAGGAUGAUAUGUAGGUCAUGUGUGUCUAUUUGUUCAACUUUAAACAAGUUUAAAUGUCUAUUUGUGCAUAUC	181	spiLA0480-miR7992-21-3p	UGUCUAUUUGUGCAUAUC	164-181	stu-miR7992-3p	3	0	18	23	1
spiLA0480-MIR1863a-2	UUAAUAUAGAAAUUAGGUUUUAGGCCUAACUCACACCUCAAAAGUUAACUUAAAGGGAGGAAGAAUACACAAUUCUUAUAAAAAGUCCACUCAUCUCAUUAACCACCGAUUUAGACUUUUGUCAUUCUUUAACAUCCCACCUCAAGUACAGUGCUUAGCAUCGGGUGAGACGAACCUGCUCUGAUACCAUCUGAAAUUAGGUUUUAGGCCUAAUUCAAACCCCAAAAGCUAGCUUUUCGGGUGUGAGUUAAGCCUAAAAUAUUUCACAUAAA	272	spiLA0480-miR1863a-2-3p	UGCUCUGAUACCAUCUGAAAUUAG	177-200	osa-miR1863a	4	0	24	24	2
spiLA0480-MIR5650-2	CAACCGCAACUCUAGCCAGUCUUCAUCACACCAGAUUUCAGGGUGAGCUAAAGCUUNCUAGCUUGGACUGGAUCUUCUUCUUCAUGUCUUGAUGCCUUGAAGUUCUGGCAUAGACUAGCUAUUAUUUAUGUUUAGUUUCUUAGAUACUCUUAGCUUUAAUAAUUUGAGGAUAGAUGUUCUUGUGAUGAUGACUUCCAGAUUUUGGGGAUAACUUCAGCUGACAAGUAAGCCACUCCAACUUUGAGAGUGAAUAUCUAAACGCCUCAACUUGGUCUCAACAUUCAAUUUGUCCUCG	210	spiLA0480-miR5650-2-3p	AUGUUUAGUUUCUUAGAUACU	128-148	ath-miR5650	5	0	21	21	2
spiLA0480-MIR11092	UGCCACAUAAAUUUUGCAUGUGUGUAUAGAUGAUCAUUUUGUAACUGACACAGAGGAGACGAGUUGAAGUGUUUAGAUGUACAUACUCAAAGCUGGAGUGUUUAAUUGUUAGCUGAGAC	204	spiLA0480-miR11092-3p	AUUUUGUAACUGACACAGAGG	121-141	lja-miR11092-3p	5	0	21	21	1
spiLA0480-MIR7981f-17	UUGUUUAAAAGGGAUAAUGCACAAGUACCCAGGCACUAUCUUGUGGGUCCAAUGUUGGUUGACUUUUUUUCAUGAUAGUGCCAUGUAGGCCGAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUUAGGGGGGCAAUAAGACCUUAGUAUAAUAUAAGUGUGUCUCUGGGAUUUCGGGCAUAGGUUGAGGGGAUACUUGUGCAUUUUCCCUAUAUAAAAUG	222	spiLA0480-miR7981f-17-3p	AAGUGUGUCUCUGGGAUUUCGGGC	157-180	sly-miR7981f	1	0	24	24	1
spiLA0480-MIR396b	UUUUCUUUCUAGAUUAGCUUUCCUCACCCUUUCAUAAUUUAGUGUCAGAUCCGCCACAUUCUAGUUAAAUUUGGCAUCCGUAUAGAGGCGGAAGUGUCUAGAGUUGUGGAGAGGUUUGCGAAAAAAUCUAGAACCUUCUAGAUCAAUCAAGAAUGCUUGGAAUUCUCUAGAAUAACUUAGACUUUUUAAGAAAGGCUUUGGAAGAUCCUAGAAAGAGUA	219	spiLA0480-miR396b-3p	UUUUAAGAAAGGCUUUGGAA	184-203	ata-miR396b-3p	4	0	20	20	2
spiLA0480-MIR7981a-58	UUUUCUACCCCUUUUCGGCCUACAUGGCACUAUCUUAUGGGCUCAGCGCGUGUUGACAAUUUUUUCAAUGAUAGUGUCACGUAGGUUGAAAAGUGGUAGAAAA	103	spiLA0480-miR7981a-58-5p	ACCCCUUUUCGGCCUACAUGGCAC	7-30	sly-miR7981a	1	0	24	24	1
spiLA0480-MIR11045	UCCGCAAUGUAUUUAGUUCAUUAUGUUUGAAAUGAUGGGGUUUAGAUUGGUUGGUUCGCUCACAUAGGAGGAUAAAUGUAGAUGCCACUCACGGCCCGAUUUGGGUCGUGACAUUAACCCAAUCCGACUCGAAUCUGCGCGCGAUCUGUUUUAUUUAAAAAGAUAUUUCAUCAUUUUGGAAAUGACUGUUCUGAAAGAUUGCAAC	205	spiLA0480-miR11045-5p	UUUGAAAUGAUGGGGUUUAGAUU	26-48	seu-miR11045	7	0	23	23	1
spiLA0480-MIR7981a-59	UGGACUUAUUUAUAAGUAAUUUUCAACCCCUUUUCGGCCUACGUGGCACUAGCUUGAAAAAAAAGUCAACCAACAUUGGGCCCAAAAUAUACUGCCACGUGGGCCGAAAAGAGGUAGAAAAUUAUUUAUAAAAUAAGUGUA	142	spiLA0480-miR7981a-59-5p	ACCCCUUUUCGGCCUACGUGGCAC	27-50	sly-miR7981a	0	0	24	24	1

Supplementary Table S13. Characterization of families, mature sequences and pre-miRNAs of miRNAs in *Solanum pimpinellifolium* LA1589 (spiLA1589).

Precursor name	Sequence	Len	Mature Name	Mature Sequence	Start and End	Orthology mature name	Number of mismatches With Orthology MiRNA	Number of gaps with Orthology MiRNA	Size of the miRNA	Size of the Orthology miRNA	Subject start
spiLA1589-MIR319b-1	AGAGAGCUUCCUUUAGUCCACUCAUAGGUAGACGAAGGAUUUGAAUUAUCUCCCGACUCAUUCAUUCAAACGCAAUAGGAAGUAUGUAAUCUUAUACUAUUGUGAAUGUGUGAAUGAUGCGGGAGAUAAAUUCUCUCCUUUUUAUCUGUGCUUGGACUGAAGGGAGCUCCC	171	spiLA1589-miR319b-1-5p	GAGCUUCCUUUAGUCCACUCA	4-24	mtr-miR319b-5p	1	0	21	21	1
			spiLA1589-miR159c-1-3p	CUUGGACUGAAGGGAGCUCCC	151-171	csi-miR159c-3p	0	0	21	21	1
spiLA1589-MIR172	UAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUAAUUUUCUCCUGUAUAUUGGCUCUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGCAAUGAAUGGCUA	125	spiLA1589-miR172-3p	UGAGAAUCUUGAUGAUGCUGCAG	87-109	aau-miR172	1	0	23	23	1
spiLA1589-MIR159b-1	CUUGUUCGAGGAAGAUUAGAGUUCUGAAUGUAGAGCUUUCUGAAUUUCAAAGAGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACGUUUGAUAACCUAAUUU	219	spiLA1589-miR159b-1-5p	AGCUGCUAAUCUAUGGAUCCC	75-95	cas-miR159b-5p	1	0	21	21	1
			spiLA1589-miR159b-1-3p	UUGGAAUGAAGGGAGCUCUAC	182-202	sly-miR159b	1	0	21	21	1
spiLA1589-MIR319b-2	UUAGAUGUAAGUAGGAGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAU	198	spiLA1589-miR319b-2-3p	AUUGGACUGAAGGGAGCUCCU	168-188	aof-miR319b	1	0	21	21	2
spiLA1589-MIR159b-2	UGGAUAUUCUGUUUGUGGAUUACACUGAUAUUCAUAUAGUUGAUUUUAACUUGUUCGAGGAAGAUUAGAGUUCUGAAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCUACGUU	254	spiLA1589-miR159b-2-3p	AGCUGCUAAUCUAUGGAUCCC	124-144	cas-miR159b-5p	1	0	21	21	1
spiLA1589-MIR479a-1	GAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUU	92	spiLA1589-miR479a-1-5p	CGUGAUAUUGGUUUGGCUCACU	11-32	nta-miR479a	2	0	22	22	1
			spiLA1589-miR479-1-3p	UGAGCCGAACCAAUAUCACUC	62-82	aof-miR479	0	0	21	21	1
spiLA1589-MIR171d-1	ACGAGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGUCAAUAUCACG	85	spiLA1589-miR171d-1-5p	AGAUAUUGGUGCGGUUCAAUU	4-24	stu-miR171d-5p	0	0	21	21	1
			spiLA1589-miR171c-1-3p	UUGAGCCGUGUCAAUAUCACG	65-85	cas-miR171c-3p	1	0	21	21	1
spiLA1589-MIR160g	CUGCCUGGCUCCCUGGAUGCCAACUAAGAACAGUAUUGUCAAAAAAAUUGACACUCUUCCUAGUUGGUACCAGAGGAGACAGGCAGA	87	spiLA1589-miR160g-5p	UGCCUGGCUCCCUGGAUGCCA	2-22	lus-miR160g	0	0	21	21	1
spiLA1589-MIR160h-1	UGCCUGGCUCCUUGUAUGCCAUUUGCAUUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAUGGCAUUCUAGGAGCUAAGCAU	81	spiLA1589-miR160h-1-5p	UGCCUGGCUCCUUGUAUGCCAUU	1-23	mes-miR160h	1	0	23	23	1
			spiLA1589-miR160b-1-3p	GCAUUCUAGGAGCUAAGCAU	62-81	csi-miR160b-3p	4	0	20	21	1
spiLA1589-MIR319a	AAUAAGGAGCUCUCUCCGGUCCAGUCCGAGGCACUCAAAGGCUAAAAACACAGCUGACGACUCGUUGAUUCUCAAACAUAUCAAGAAGCAUUUUUUGAAAUUGGUGUGUUUAAGAUUCAACGAUGCGUGAGCUAUGUUUGGCUAGCGUUGUCACGU	182	spiLA1589-miR319a-3p	UUGGACUGAAGGGAGCUCCCU	158-178	aof-miR319a	0	0	21	21	1

	CUUGGACUGAAGGGAGCUCCCUAUUA										
spiLA1589-MIR156b-1	GUUGUUGACAGAAGAUAGAGAGCACAGAUGAUAAAGUGCAUGGAAAUUGUCUGCACCUUACUCCUUUGUGCUCUUUAUUCUUCUGUCAUCAU	92	spiLA1589-miR156b-1-5p	UUGACAGAAGAUAGAGAGCAC	5-25	aof-miR156b	0	0	21	21	1
			spiLA1589-miR156h-1-3p	GCUCUUUAUUCUUCUGUCAUC	70-90	mtr-miR156h-3p	0	0	21	21	1
spiLA1589-MIR156b-2	AUGGCCAUGGAAGAGAGGGACUGACAGAAGAGAGUGAGCAUACACAUAUAAUUAUAUAAACAUGUUUACAUAAUUCUUUUGAUAUAUAUAUAUAUAAUUUUGCGUGUGCUCACUUCUCUUUC	122	spiLA1589-miR156b-2-5p	UGACAGAAGAGAGUGAGCAUA	22-42	cca-miR156b	0	0	21	21	1
spiLA1589-MIR172e-1	UCAUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAU	162	spiLA1589-miR172e-1-5p	GCAACAUCAUCAAGAUUCACA	23-43	stu-miR172e-5p	0	0	21	21	1
			spiLA1589-miR172-1-3p	UGGGAAUCUUGAUGAUGCUGCAU	130-152	aau-miR172	1	0	23	23	1
spiLA1589-MIR172c	CAACACAGUUGUUGUUUGCAGAUGUAGCAUCAUCAAGAUUCAUACAUGAAAAUUAAGAGGCAAGGUUAAAUAUGUAGCUUUAAUUUGAAAUGAAAAAUAUAAUAUAUCAUGACUAUGUCUAUUUAUUUCAAAGUGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAAUAACUAUCGGUGACAGAGUCAGAA	190	spiLA1589-miR172c-5p	GUAGCAUCAUCAAGAUUCAUACA	24-46	ata-miR172c-5p	2	0	23	23	1
			spiLA1589-miR172-3p	UGAGAAUCUUGAUGAUGCUGCAU	134-156	aau-miR172	0	0	23	23	1
spiLA1589-MIR5300	UUGACCAAAAUUCUUCUUCUCCAGUCCAGGCAUUCCAACAGUUGAUAACAUCUAGAUCUGCCAAUACUUUGUAUUUUUGUUCUUCUAUUUUUCACAUGACUUCUUCAAAAUCUACUAUGAGCUUCAUCAUAAGCUAAGAAAUGGUGAGUUUUGAUGAUGUGAUGCCUAAAAUAGGAUUAAAUGAAAGUACUAGUAAAAAGGUGUUCAGAUCUGGAGGUUAUGUUAAGCUGGUGGUAUGCUUUGAUUGGGAAAGAUGACUUAGGUCA	266	spiLA1589-miR5300-5p	UCUCCAGUCCAGGCAUUCCAAC	18-39	sly-miR5300	1	0	22	22	1
			spiLA1589-miR5300c-3p	UGAGUUUUGAUGAUGUGAUGC	145-165	mes-miR172c	5	0	21	21	1
spiLA1589-MIR482e-1	AGAUCUGUGCUAUGGAAAUAUUGAUGGCGUUGAAAGGGAUGAGAGUAUUGGGAAGUUGUUGGUUGUGGGUGGGGUGGGAAAGAUUUGAUAAAUCUAAUUUUAAAGAGAUUAAAUCUUUCCUACUCCUCCCAUACCCAUGACUUCCACUAGCUUCUCCCUUUCUUCAUUUGUCAUCUCCUUUGCUAAGUUC	189	spiLA1589-miR482e-1-5p	UGUGGGUGGGGUGGAAAGAUU	64-84	sly-miR482e-5p	0	0	21	21	1
			spiLA1589-miR482e-1-3p	UCUUUCCUACUCCUCCCAUACC	113-134	sly-miR482e-3p	0	0	22	22	1
spiLA1589-MIR5304	UCUAAUUUAGAUCCAUGGUGCAGUUUGCUCAUUCAAUGCUACAUACUCAUCCCCACAACUUUCAUCUCACGUUCAAAAGAUGAAAGUUAUAGAGAUGAGUAUGGUGCAUUGGAUGUGUGGCCAUACCAUGGGUGAUGUUAG	141	spiLA1589-miR5304-5p	UCAAUGCUACAUACUCAUCCC	33-53	sly-miR5304	0	0	21	21	1
			spiLA1589-miR5304-3p	AGAUGAGUAUGGUGCAUUGGA	93-113	stu-miR5304-3p	0	0	21	21	1
spiLA1589-MIR396b-1	UGGUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAUAGGGUC	131	spiLA1589-miR396b-1-5p	UUCCACAGCUUUCUUGAACUG	18-38	aof-miR396b	0	0	21	21	1
			spiLA1589-miR396c-1-3p	GUUCAAUAAAGCUGUGGGAAG	97-117	fve-miR396c-3p	0	0	21	21	1
spiLA1589-MIR156b-3	CAAAAAGAGGUGACAGAAGAGCGUGAGCACAUGUGUGUUUUCUAGCAUGAUGUUUAUAUGCUUGAAUCUAUGCGUGCUCACUGCUCUAUCUUUCAUCCUCAUCG	104	spiLA1589-miR156b-3-5p	UGACAGAAGAGCGUGAGCACA	11-31	hvu-miR156b	1	0	21	21	1
			spiLA1589-miR156i-3-3p	GCUCACUGCUCUAUCUUUCAUC	76-97	zma-miR156i-3p	1	0	22	22	1
spiLA1589-MIR171f-1	UGAUCAACUUGCGAUGUUGGUGUGGUUCAAUUAGAUAACAAUCUCCACGUAAAAUUAUAGAGUUUGUUAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAAGAAAAUAAC	110	spiLA1589-miR171f-1-5p	CGAUGUUGGUGUGGUUCAAUU	12-32	fve-miR171f-5p	2	0	21	21	1
			spiLA1589-miR171a-1-3p	UGAUUGAGCCGUGCCAAUAUC	72-92	aof-miR171a	0	0	21	21	1
spiLA1589-MIR6022-1	AAUACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAGUUAUUUAGACCGAGUUUUAACCAAUUGCACGGUCCUCUACCCAAGAUUGAGGUUUCGUAAAAUGUAACUUAAGAUCAAGUCG	238	spiLA1589-miR6022-1-3p	UGGAAAGGAUAAUAUCCAGGA	198-218	sly-miR6022	2	0	21	21	1

spiLA1589-MIR6023-1	CGUUAGGUUCAUGAAGUUCUGAAUUGACUUAGGAAGAGUACCUUGCAACUUAAAACUUUGAGGCGAAAUAAGUUAGUGAUGGAAAGGAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGGG	235	spiLA1589-miR6023-1-5p	UUCCAUGAAAGAGUUUUUGAAU	22-43	sly-miR6023	1	0	22	22	1
spiLA1589-MIR6023-2	AAGCAGUAAUCUCUGUUCAUAUUCCAUGAAAGAGUUUUUGAAUAAGAUCUUUUACCGUAGUAAUCACAAAUCCUAGACGACUGUGCUCUUGGACAGAAAUUUCUGAUCAAAGCAUUUCCCUUCUUAAAUUCAAGAGAAUGCUUACAGUAGGUCCCUCAUCGAGUGUUUGUGAUUACUACGGUCAGGAAUCUUAUCCAGAGACAAUUCAUGGAAUAUGAGCUGAGAUUGGUGUCUA	237	spiLA1589-miR6023-2-5p	UUCCAUGAGACUGUUUUUGGGU	22-43	stu-miR6023	3	0	22	22	1
			spiLA1589-miR5303f-2-3p	AUUUUUGGAGAAUUCGACACGGGC	157-180	stu-miR5303f	3	0	24	24	1
spiLA1589-MIR6024	AAGCAACAAUCUCUGUUCAUAUUCCAUGAGACUGUUUUUGGGUAAGAUUGUUUAUCAUAAUAAUCAUAAAUACUAGAUGACCGUGCUUGUUGUCUAUGUUGCUCGGACUCUUUAAUAAUUUCAAUGGAUGCGUGUUGGAUUCACCAAAAGUAGUGUAUUUUUGGAGAAUUCGACACGGGCGCGACAUCGAAAGUGAGGUCCCUCGUCAAGUGUUUGUGAUUACUACAAUCAACAAUC	118	spiLA1589-miR6024-5p	AGAAACAACACUUGCUAAAGGA	22-43	stu-miR6024-5p	1	0	22	22	1
			spiLA1589-miR6024-3p	UUUUAGCAAGAGUUGUUUUACC	77-98	sly-miR6024	0	0	22	22	1
spiLA1589-MIR482a-1	GAGUUUUUCGAAAAUCUAUGGGGAUUGGUGAGUUGGAAAGCUUUUCUUUUUCUUCUCUUGUGAUUAGCUUUCCAAUUCCACCCAUUCCUAUGGUUUUUCGGUAUUCUCU	109	spiLA1589-miR482a-1-5p	GGGAUUGGUGAGUUGGAAAGC	21-41	stu-miR482a-5p	3	0	21	21	1
			spiLA1589-miR482c-1-3p	UUUCCAAUUCCACCCAUUCCUA	69-90	nta-miR482c	0	0	22	22	1
spiLA1589-MIR482d-1	GAUUUUUGGGAAGCUUUUGGCGUGAGCGGUGGGGAAAGAUAGAUCUAUCAUAUUAGUAUGAUAUGAUAAAUCUUGCCUACACCGCCCAUGCCCAUGGCUUCCAAUGAUUUC	111	spiLA1589-miR482d-1-5p	CGUGAGCGGUGGGGAAAGAUA	21-41	stu-miR482d-5p	2	0	21	21	1
			spiLA1589-miR482b-1-3p	UCUUGCCUACACCGCCCAUGCC	71-92	sly-miR482b	0	0	22	22	1
spiLA1589-MIR6025b-1	UGUAUAGUUAUUUCAUGUACACUUGCACAAAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACUAUUGGGAUGGCAUCUCGGUUUGUUA	162	spiLA1589-miR6025b-1-3p	UGCCAACUAUUGGGAUGGCAUC	130-151	nta-miR6025b	2	0	22	22	1
spiLA1589-MIR6025b-2	AAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACUAUUGGGAUGGCAUCUCGGUUUGUUAGUUGCUGUGCAGUAUGAUCACUGUGGCAG	162	spiLA1589-miR6025b-2-3p	UGCCAACUAUUGGGAUGGCAUC	101-122	nta-miR6025b	2	0	22	22	1
spiLA1589-MIR166b-1	AGAUUUGAGGGGAAUGUUGUUUGGCUCGAAGUCAUUAUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUAAAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUC	138	spiLA1589-miR166b-1-5p	GGAAUGUUGUUUGGCUCGAAGU	11-32	csi-miR166b-5p	2	0	22	22	1
			spiLA1589-miR166-1-3p	UCUUCGGACCAGGCUUC	122-138	lja-miR166-3p	2	0	17	24	3
spiLA1589-MIR394-1	GUAGAGCCAUUUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAACUAGCUCUGCA	81	spiLA1589-miR394-1-5p	UUUGGCAUUCUGUCCACCUCC	11-31	cas-miR394	0	0	21	21	1
			spiLA1589-miR384-1-3p	AGGGGGCCAAAGUGCCAAAC	52-71	stu-miR384-3p	0	0	20	20	1
spiLA1589-MIR398	AUUCAACAGGGGCAACUUGAGAUCACAUGUUGUCAUUUUUUUCUUUUUGGUUUGAUUCGAUGAAUCAGUAUCUCAACAUGUGUUCUCAGGUUACCCCUGUUGAAUU	106	spiLA1589-miR398-5p	GGGGCAACUUGAGAUCACAUG	9-29	hbr-miR398	3	0	21	21	1
			spiLA1589-miR398-3p	UGUGUUCUCAGGUUACCCCUG	79-99	bra-miR398-3p	1	0	21	21	1
spiLA1589-MIR399j-1	GUUCGUGAACGAUAGUAAUUGUAAGGGAAACAGUGAUAGGGCUACACUCUAUUGGCAUGCAACUUGAUCAAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUAUUACUGUCU	116	spiLA1589-miR399j-1-5p	GGGCUACACUCUAUUGGCAUG	39-59	stu-miR399j-5p	2	0	21	21	1
			spiLA1589-miR399i-1-3p	UGCCAAAGGAGAGUUGCCCUA	87-107	stu-miR399i-3p	0	0	21	21	1

spiLA1589-MIR477-1	CAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAACAAGAAAUUCCUUGCUCACUUCACAUGGCAAACAUACUUA	132	spiLA1589-miR477-1-5p	UGUCUCUCCCUCAAGGGCUCC	11-31	sly-miR477-5p	0	0	21	21	1
			spiLA1589-miR477-1-3p	AGUUCUUGUAGGGUGAGACAAC	72-93	sly-miR477-3p	0	0	22	22	1
spiLA1589-MIR1446	CAGAGUUUUCUGAACUCUCUCCCUCAAUGGCUGUUCAUAUAAUAUAUGCUGCUACUUUGCAGCUUAAUUAAAUAACAGCUUUGGGGGUUUGAGUCCAGAAAACUCUUG	108	spiLA1589-miR1446-5p	UGAACUCUCUCCCUCAAUGGCU	11-32	nta-miR1446	0	0	22	22	1
			spiLA1589-miR7490-3p	AGUCCAGAAAACUCUUG	92-108	ghr-miR7490	5	0	17	24	1
spiLA1589-MIR164-1	AGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUC	165	spiLA1589-miR164-1-5p	UGGAGAAGCAGGGCACGUGCA	4-24	aof-miR164	0	0	21	21	1
			spiLA1589-miR164a-1-3p	CAUGUGCCUGUUUUCCCCAUC	145-165	sly-miR164a-3p	0	0	21	21	1
spiLA1589-MIR169a	UUGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGAGUGGAGUGCAGCCAAGGAUGACUUGCCGAGAUGUUGUAGCCUAAUGCAAUGACAUAUCGGCAGGUCAUCUUUGGCUACAUUUUAUUCUCUCCUAUUCAUGUAAAACUUUAUAGACGUAUAUGUAU	159	spiLA1589-miR169a-5p	CAGCCAAGGAUGACUUGCCGA	43-63	cas-miR169a	0	0	21	21	1
spiLA1589-MIR394c	GAUGAAGAAAAAAAAUAUGAAGAUUAAUUAGUUUCACGGAGGUUUGACAAAGGGUUUCUUACAGAGUUCAUUGGCAUUCUGUCCACCUCCCUCGUUCUUUUUUCGAGAAAAAAAGAAGAAGGGGGGAAGCAAGAUUUAGUGUGGAGGUGGGCAUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUUGUAAAACCCUCGUGAUACACGUCAAGUAAGAUAGAGAGUGAUUUGAUC	233	spiLA1589-miR394c-5p	UUGGCAUUCUGUCCACCUCCCU	71-92	mes-miR394c	1	0	22	22	1
			spiLA1589-miR394b-3p	AGGUGGGCAUACUGCCAAUAG	145-165	ath-miR394b-3p	0	0	21	21	1
spiLA1589-MIR397b-1	CAGAGUACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGAA	118	spiLA1589-miR397b-1-5p	UCAUUGAGUGCAGCGUUGAUG	18-38	mes-miR397b	0	0	21	21	1
			spiLA1589-miR397-1-3p	CAUCAACGCUACACUCGAUCA	80-100	stu-miR397-3p	1	0	21	21	1
spiLA1589-MIR2111d-1	UGUUAGGUUAAUGGUAAUCUGCAUCCUGAGGUUUAGAUCAAUUUAUAACUUACUGGAUCUAGUCCUUGGGAUGCAGAUUAUCUUUACCUUACA	93	spiLA1589-miR2111d-1-5p	UAAUCUGCAUCCUGAGGUUUA	15-35	ppe-miR2111d	0	0	21	21	1
			spiLA1589-miR2111d-1-3p	GUCCUUGGGAUGCAGAUUAUC	62-82	gma-miR2111d	2	0	21	21	1
spiLA1589-MIR166d-1	AAUAUUGUUGAGGAGAAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUGUAUCGUGAAUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUGA	122	spiLA1589-miR166d-1-5p	AGAAUGUCGUCUGGUUCGAGA	14-34	stu-miR166d-5p	0	0	21	21	1
			spiLA1589-miR166-1-3p	AUUUCGGACCAGGCUUCAUUCCCC	89-112	lja-miR166-3p	0	0	24	24	1
spiLA1589-MIR171f-2	AUGAAAUAGUAACUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAGUUCCUUUUCACUAUACUUCAUCAUAUUAAGCUCCCAUAU	131	spiLA1589-miR171f-2-5p	UAUUGGCCUGGUUCACUCAGA	19-39	csi-miR171f-5p	0	0	21	21	1
			spiLA1589-miR171c-2-3p	UGAUUGAGCCGUGUCAAUAUC	68-88	stu-miR171c-3p	0	0	21	21	1
spiLA1589-MIR397b-2	UACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGAAGGGACAUU	121	spiLA1589-miR397b-2-5p	UCAUUGAGUGCAGCGUUGAUG	13-33	mes-miR397b	0	0	21	21	1
			spiLA1589-miR397-2-3p	CAUCAACGCUACACUCGAUCA	75-95	stu-miR397-3p	1	0	21	21	1
spiLA1589-MIR6231-1	AUAUCAAACUUUAUGGAGGACCUGUUACCCCCUGCACUAUUUAAUAAUGUAUUUUAAAAGUAUAUAUGUGUCCACAUGGACACAUUACUAUUUAUAAUGAUGCAAUGUGUAUGAUGUCCACGUGGACACAUAUAUACCUUUAAAAUACACUAUUAAAUAUUGCAUGGGGAUAAAAGGUCCUUUUCAAAAUUUGAUAUU	198	spiLA1589-miR6231-1-5p	UAUAUGUGUCCACAUGGACAC	63-83	sbi-miR6231-3p	5	0	21	21	1

spiLA1589-MIR7990a	UGCAAAAGUUAUGACCAUUUGAAGUGUCACAAAUUUACAACUACUUUUUUUGAGUUAUACUCUUUAAUUUGGUGAAACUUCAAAUGAUCGUAACUUUGGCCU	102	spiLA1589-miR5507-1-3p	AAUGUGUAUGAUGUCCACGUG	104-124	osa-miR5507	5	0	21	21	1
			spiLA1589-miR7990a-3p	UUCAAAUGAUCGUAACUUUGGCCU	79-102	stu-miR7990a	0	0	24	24	1
spiLA1589-MIR8009-1	AUUUCCAGAAAAGCGACGGACAGGGUCCUUUAAUCUGUCGCUAUUCUGGGAUUU	54	spiLA1589-miR8009-1-5p	AUUUCCAGAAAAGCGACGGACAGG	1-24	stu-miR8009	1	0	24	24	1
spiLA1589-MIR8020-1	GAAUUUCAUUGAGUAUGUUGUUGUUGUAAAGCAUACUGAAUUAAUGCAAGUACACAAGUUACAACAACAACAUACUUACUGAAAUGCC	88	spiLA1589-miR8020-1-5p	AAUUUCAUUGAGUAUGUUGUUGUU	2-25	stu-miR8020	0	0	24	24	1
spiLA1589-MIR1886i-1	CGUGAGAUGAAAUCAGCAUUUGGAUAUGCAAUUUUACGUUGAUUUCAUCUCAUGA	55	spiLA1589-miR1886i-1-5p	GUGAGAUGAAAUCAGCAUUUGGAU	2-25	stu-miR1886i-5p	3	0	24	24	2
			spiLA1589-miR1886h-1-3p	AUUUUACGUUGAUUUCAUCUCAUG	31-54	stu-miR1886h	0	0	24	24	1
spiLA1589-MIR8038b-1	UCCUUGUGAGGAAGUUGAAUCUCAUGCUUGUUAAGCCUCAAGAAAAGCACAAUGCGUUCCAGCGUCAUCUUGAAAAUCUUGAGUUUUUCAAUUUUCUCAU	100	spiLA1589-miR8038b-1-5p	CCUUGUGAGGAAGUUGAAUCUC	2-23	stu-miR8038b-5p	1	0	22	22	1
spiLA1589-MIR171c-1	UAGAUAUUGAUGCGGUUCAAUCUGAAAGACAUGGUUAGAUAUGUAAUUAGCCUUGUAAUUUUGGAUUGAGCCGCGUUAAUAUCUCU	86	spiLA1589-miR171c-1-5p	AGAUAUUGAUGCGGUUCAAUC	2-22	cas-miR171c-5p	1	0	21	21	1
			spiLA1589-miR171e-1-3p	UUGAGCCGCGUUAAUAUCUCU	66-86	sly-miR171e	1	0	21	21	1
spiLA1589-MIR827-1	GUUUGUUGAUGGUCAUCUAUUCAUCAUAUCAUUUGGCAUAGUUUUUGGAACCAUUAAUAUGCCAUGAUUAGAUGAACAUCAACAAACA	88	spiLA1589-miR827-1-5p	UUUGUUGAUGGUCAUCUAUUC	2-22	stu-miR827-5p	0	0	21	21	1
			spiLA1589-miR827-1-3p	UUAGAUGAACAUCAACAAACA	68-88	sly-miR827	0	0	21	21	1
spiLA1589-MIR319b-3	AGAGCUUUCUUUAGUCCACACAUAGGGAACUAUAGGGUUCAAUUUGCUGCCGACUCAUUCAUCCAAAUGUUGAGGUCUUGAUAAUCGAAUGCCACCUCAGCAACUGAGUGAAUGAAGCGGGAGUACAAGUUGAGUCUUGAGCUUCCUGUACUUGGACUGAAGGGAGCUCCC	171	spiLA1589-miR319b-3-5p	GAGCUUUCUUUAGUCCACACA	2-22	mtr-miR319b-5p	1	0	21	21	1
			spiLA1589-miR159c-3-3p	CUUGGACUGAAGGGAGCUCCC	151-171	csi-miR159c-3p	0	0	21	21	1
spiLA1589-MIR171d-2	AGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGUCAAUAUCAC	81	spiLA1589-miR171d-2-5p	AGAUAUUGGUGCGGUUCAAUU	1-21	stu-miR171d-5p	0	0	21	21	1
			spiLA1589-miR171c-2-3p	UAAUUGAGCCGUGUCAAUAUC	59-79	stu-miR171c-3p	1	0	21	21	1
spiLA1589-MIR167b-1	GUGAAGCUGCCAGCAUGAUCUAAACUUGGCCAUUUAUAAAGAAAAUGGGUGACUAAGGUUAGGUCAUGCUCGGACAGCCUCACU	84	spiLA1589-miR167b-1-5p	UGAAGCUGCCAGCAUGAUCUAA	2-23	bna-miR167b	0	0	22	22	1
			spiLA1589-miR167c-1-3p	GGUCAUGCUCGGACAGCCUCACU	62-84	stu-miR167c-3p	0	0	23	23	1
spiLA1589-MIR477a	GCCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUGUGUUGGGAAAGAAGCUCUAGCAGGGAGAGCCA	70	spiLA1589-miR477a-5p	CCUCUCCCUCAAGGGCUUCUC	2-22	stu-miR477a-5p	0	0	21	21	1
			spiLA1589-miR477a-3p	GAAGCUCUAGCAGGGAGAGCCA	49-70	stu-miR477a-3p	0	0	22	22	1
spiLA1589-MIR477b	CACUCUCCCUCAAAGGCUUCUGGCUUAAAAUGCCUUUUGUGCUAAUGCUAGAGGUCUUUCGAGUGAGAGUGA	72	spiLA1589-miR477b-5p	ACUCUCCCUCAAAGGCUUCUG	2-22	stu-miR477b-5p	0	0	21	21	1
			spiLA1589-miR477b-3p	GAGGUCUUUCGAGUGAGAGUGA	51-72	stu-miR477b-3p	0	0	22	22	1
spiLA1589-MIR398a	AGGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUUGUUUGUAACAAUUUACCGUUUAUAAAUAUGACACAUAUGUUCUCAGGUCGCCCCUA	92	spiLA1589-miR398a-5p	GGGUUGAUUUGAGAACAUAUG	2-22	stu-miR398a-5p	0	0	21	21	1
			spiLA1589-miR398a-3p	UAUGUUCUCAGGUCGCCCCUA	72-92	sly-miR398a	1	0	21	21	1
spiLA1589-MIR408a	ACAGGGACGAGGCAGCGCAUGAGAUGUACAAUUUUAUUAGUUGUCCAUUCCAUGCACAGCCGCUUUCCUCCC	72	spiLA1589-miR408a-5p	ACAGGGACGAGGCAGCGCAUG	1-21	stu-miR408a-5p	0	0	21	21	1
			spiLA1589-miR408a-3p	UGCACAGCCGCUUUCCUCCC	53-72	stu-miR408a-3p	5	0	20	21	1
spiLA1589-MIR408-1	ACGGGGACGAGCCAGAGCAUGAGAUGUGCAAUUUUUGCUUUGCCUAUUCCAUGCACUGCCUCUUCCCUGGC	71	spiLA1589-miR408-1-5p	ACGGGGACGAGCCAGAGCAUG	1-21	sly-miR408	0	0	21	21	1
			spiLA1589-miR408-1-3p	AUGCACUGCCUCUUCCCUGGC	51-71	cas-miR408	0	0	21	21	1

spiLA1589-MIR156a	UGACAGAAGAGAGUGAGUACAUAUGGUAUUUUCUCGCAUGCUUGAAACUAUGUCUGCUCACUUCUCUAUCUGUCAU	76	spiLA1589-miR156a-5p	UGACAGAAGAGAGUGAGUAC	1-20	hci-miR156a	0	0	20	20	1
			spiLA1589-miR156i-3p	UGCUCACUUCUCUAUCUGUCAU	55-76	mtr-miR156i-3p	1	0	22	23	1
spiLA1589-MIR394-2	UUUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAAC	61	spiLA1589-miR394-2-5p	UUUGGCAUUCUGUCCACCUCC	1-21	cas-miR394	0	0	21	21	1
			spiLA1589-miR384-2-3p	AGGGGGCCAAAGUGCCAAAC	42-61	stu-miR384-3p	0	0	20	20	1
spiLA1589-MIR167b-2	UACAUCGUGCGGCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUACGAGGAAAGAUCAGAUCAUGUGGCAGCCUCACCUGUCAAU	110	spiLA1589-miR167b-2-5p	UGAAGCUGCCAGCAUGAUCUAA	23-44	bna-miR167b	0	0	22	22	1
			spiLA1589-miR167c-2-3p	AUCAGAUCAUGUGGCAGCCUCACC	80-103	eun-miR167c-3p	1	0	24	24	1
spiLA1589-MIR169c-1	GGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAUUUAUAUUAAUCUCAUCUCGGAUUU	203	spiLA1589-miR169c-1-5p	UAGCCAAGGAUGACUUGCCUA	41-61	ata-miR169c-5p	0	0	21	21	1
spiLA1589-MIR172d-1	AGUCAAUUUUUUGCGGGUGGAGCAUCAUCAAGAUUCACAUAGCUAUAUUAGGGCUUUUAUAAUUUUUAAAAACCCUAUGGGCGAUGUGUGGGAAUCUUGAUGAUGCUGCAGCGGCAAAUAAUGGCU	126	spiLA1589-miR172d-1-5p	GGUGGAGCAUCAUCAAGAUUCACA	16-39	mtr-miR172d-5p	1	0	24	24	2
			spiLA1589-miR172e-1-3p	GGAAUCUUGAUGAUGCUGCAGCGG	91-114	gma-miR172e	1	0	24	24	1
spiLA1589-MIR319b-4	AGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAUAUAUAGUUAAGUUAACUAUAUAAAAUAU	211	spiLA1589-miR319b-4-3p	AUUGGACUGAAGGGAGCUCCU	153-173	aof-miR319b	1	0	21	21	2
spiLA1589-MIR319c	AAGAGAGCUUCCUUCAGCCCACUCACGGAGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCCUUGCUUGGACUGAAGGGAGCUCCUU	176	spiLA1589-miR319c-5p	AGAGCUUCCUUCAGCCCACUC	4-24	sly-miR319c-5p	0	0	21	21	1
			spiLA1589-miR319c-3p	UUGGACUGAAGGGAGCUCCUU	156-176	sly-miR319c-3p	0	0	21	21	1
spiLA1589-MIR164-2	AUCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUGA	173	spiLA1589-miR164-2-5p	UGGAGAAGCAGGGCACGUGCA	8-28	aof-miR164	0	0	21	21	1
			spiLA1589-miR164a-2-3p	CAUGUGCCUGUUUUCCCCAUC	149-169	sly-miR164a-3p	0	0	21	21	1
spiLA1589-MIR164e	UGUUGGAGAAGCAGGGCACGUGCAAAUUCUUGUAUUCGACAAUAUAUGCAUUUCUAAUGGUAAUGCAUGAAUUUUGCACGUGUUCUCCUUCUCCAAC	97	spiLA1589-miR164e-5p	UGGAGAAGCAGGGCACGUGCAA	4-25	bra-miR164e-5p	0	0	22	22	1
			spiLA1589-miR164b-3p	CACGUGUUCUCCUUCUCCAAC	77-97	sly-miR164b-3p	0	0	21	21	1
spiLA1589-MIR172b-1	UGGUUGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUUCAAAAAUGAGAAUCUUGAUGAUGCUGCAUCGACAAAU	161	spiLA1589-miR172b-1-5p	GCAGCAUCAUCAAGAUUCACA	34-54	csi-miR172b-5p	0	0	21	21	1
			spiLA1589-miR172-1-3p	UGAGAAUCUUGAUGAUGCUGCAU	131-153	aau-miR172	0	0	23	23	1
spiLA1589-MIR9471a-1	UGAGAUUCAGUUGAUUUCUCAGGUGCUCACUCAGCUAAUAGUUAUUAUUUAAGAAACUCAAUAAUAUUGGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUGAGUGAGCAUCAC	125	spiLA1589-miR9471a-1-5p	CAGGUGCUCACUCAGCUAAUA	20-40	sly-miR9471a-5p	0	0	21	21	1
			spiLA1589-miR9471a-1-3p	UUGGCUGAGUGAGCAUCAC	107-125	sly-miR9471a-3p	0	0	19	21	1
spiLA1589-MIR166c-1	UAUGUGUGGUGAGUUUGAGGGGGAUGUUGUCUGGCUCGACACAAUUACUCUAUUGUAUGUAUUUAGUUAUUCGUUAU	187	spiLA1589-miR166c-1-5p	GGGAUGUUGUCUGGCUCGACA	21-41	sly-miR166c-5p	0	0	21	21	1

	CAAGAUUGAUGUUGAUAACGAAUAAAUUAAACACAUAUAUACAAGAUGUAAAAAGGGAGUAAAGGCGUCGGACCAGGCUUCAUUCCUCUCAAACAAUAUUCUACUUUUAC										
			spiLA1589-miR166c-1-3p	UCGGACCAGGCUUCAUUCCUC	145-165	sly-miR166c-3p	0	0	21	21	1
spiLA1589-MIR482d-2	GGAAAGGGAGGAGGGAUUUGGGAAUCUUUUGGAGUGGGUGGGAUGGAAAAAUAUUGUAUUUUUUUUUCUAACGGAAAAAAAGAUGAGAAUUGAGAUUUUUCCUAUUCCACCCAUGCCAAUGGCUUCCCAUCAUUUACUCCCUUUC	145	spiLA1589-miR482d-2-5p	GGAGUGGGUGGGAUGGAAAAA	31-51	sly-miR482d-5p	0	0	21	21	1
			spiLA1589-miR482d-2-3p	UUUCCUAUUCCACCCAUGCCAA	98-119	sly-miR482d-3p	0	0	22	22	1
spiLA1589-MIR9473-1	UAGCAGAUAUUGGCUGUAAAUCUAAACUCGUUCUACUCCACUAGUCAUCAUGUAAUGACAUUUACUAGAAGAAGAGACUAUUGGGGUAAAACGAGUUCAGAUUUACAGCCAAUAUUGU	118	spiLA1589-miR9473-1-5p	UGGCUGUAAAUCUAAACUCGU	11-31	sly-miR9473-5p	0	0	21	21	1
			spiLA1589-miR9473-1-3p	AAACGAGUUCAGAUUUACAGC	89-109	sly-miR9473-3p	0	0	21	21	1
spiLA1589-MIR9473-2	CAAAACAAUAUUGGCUGUAAAUCUGAACUCGUUUUACCCCAAUAGUCUCUUCUUCUAGUAAAUGUCAUUACAUGAUGACUAGUGGAGUAGAACGAGUUUAGAUUUACAGCCAAUAUCUGC	120	spiLA1589-miR9473-2-5p	UGGCUGUAAAUCUGAACUCGU	12-32	sly-miR9473-5p	1	0	21	21	1
			spiLA1589-miR9473-2-3p	GAACGAGUUUAGAUUUACAGC	90-110	sly-miR9473-3p	2	0	21	21	2
spiLA1589-MIR8039-1	AGUUAAUCUAUUGAGGGAGUGUAUCCGGUUUUUCGAAUUUUAUAUCUGAACUAUCACUAAGUGUUUAUCGACACACACCUCAACUAUCCGUUGUUCCCUUUUCCUACCUGAAUGAUGGUGAUAUUCUAGGUUGGGAAAGGGAACAA	146	spiLA1589-miR8039-1-5p	UUUUAUAUCUGAACUAUCACU	38-58	stu-miR8039	3	0	21	21	1
			spiLA1589-miR9477-1-3p	UAUCCGUUGUUCCCUUUUCCUACC	85-108	sly-miR9477-5p	0	0	24	24	1
spiLA1589-MIR9478	CUUAUAAAAGGGAUAAGGCUUAAAUAUGUCGAUCGAACUUUGAGAAAAGACUCAUCUAUGUCAUCUGGUAAAAGUUUGGUGUAUAAUGGUAUGAAUGAGCCUUUUCUCGAACGAAAAUGGUGUAGAUGAGUUAAAUUUUUAACGGAUUACAUAAUUGAGUCUUUUCUCAUAGUUCGAUGACAUAUUUGAGCGUUUUCCCAAUUAUAA	207	spiLA1589-miR9478-5p	GCUUAAAUAUGUCGAUCGAACU	18-39	sly-miR9478-5p	1	0	22	22	1
			spiLA1589-miR9478-3p	UUCGAUGACAUAUUUGAGCGU	173-193	sly-miR9478-3p	1	0	21	21	1
spiLA1589-MIR169e-1	AGGAGGAGAGGCCUUACAUGAAUUAGAAGAGUUUCUAUUUGUUUAGUAGCCAAGGAUGACUUGCCUUUCAUCAAUGCCUUUUGUAAAAUGGAAAUUGAUUACAACACUUUCUAUGGUAUUGGGAAAAUGAGUGGCAAGCAUCUUUGGCGACUUGACAAACUCUUCUUUGUCAUGUUAGUCCAUCUUCUUCC	191	spiLA1589-miR169e-1-5p	UAGCCAAGGAUGACUUGCCUUU	47-68	sly-miR169e-5p	0	0	22	22	1
			spiLA1589-miR169e-1-3p	UGGCAAGCAUCUUUGGCGACU	132-152	sly-miR169e-3p	0	0	21	21	1
spiLA1589-MIR477-2	AGCUAGGCAUUGCUUGUUGUCUCUCCCUCAAGGGCUCCUCUUCAAGAUCCUUAUAAACAAGAAAGCAUGAGGGGGAGGAGUUCUUGUAGGGUGAGACAACAAGAAAUUCCUUGC	114	spiLA1589-miR477-2-5p	UGUCUCUCCCUCAAGGGCUCC	18-38	sly-miR477-5p	0	0	21	21	1
			spiLA1589-miR477-2-3p	AGUUCUUGUAGGGUGAGACAAC	79-100	sly-miR477-3p	0	0	22	22	1
spiLA1589-MIR156b-4	UGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUUGCAUGAUGUUUAUAUAUAUAUGCUUGAAACUAUGUGUGCUUACUCUCUAUCUGUCACCC	97	spiLA1589-miR156b-4-5p	UGACAGAAGAGAGUGAGCACA	4-24	hvu-miR156b	0	0	21	21	1
			spiLA1589-miR156k-4-3p	UGCUUACUCUCUAUCUGUCACC	75-96	cas-miR156k-3p	0	0	22	22	1
spiLA1589-MIR156b-5	AAAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUAGCAUGAUGUUUUACAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCCCCCAUCGCU	110	spiLA1589-miR156b-5-5p	UGACAGAAGAGAGUGAGCACA	12-32	hvu-miR156b	0	0	21	21	1
			spiLA1589-miR156c-5-3p	GCUCACUGCUCUAUCUGUCACC	79-100	ata-miR156c-3p	0	0	22	22	1
spiLA1589-MIR159-1	UUUAACUUGUUCGAGGAAGAUCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAGCUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUAUUUUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCUUUAUUGGAAAGAAGGGAGCUCUA	206	spiLA1589-miR159-1-5p	AGCUGCUGAUCUAUGGAUCCC	80-100	eun-miR159-5p	1	0	21	21	1

spiLA1589-MIR172d-2	CUUGCUAGUGCAGCAUCAUUAAGAUUCACAUAGAAAAUAUGGAACGAAAUUUGCUCAAUUUUUCAAUAUAUGAGAAUCUUGAUGAUGCUGCAUUGGCAA	99	spiLA1589-miR159b-1-3p	UUGGAAAGAAGGGAGCUCUA	187-206	sly-miR159b	0	0	20	21	1
			spiLA1589-miR172d-2-5p	GCAGCAUCAUUAAGAUUCACA	10-30	bra-miR172d-5p	0	0	21	21	1
			spiLA1589-miR172-2-3p	UGAGAAUCUUGAUGAUGCUGCAU	71-93	aau-miR172	0	0	23	23	1
spiLA1589-MIR167b-3	UAUCAGUUGAAGCUGCCAGCAUGAUCUAAACUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGAUCAUGUGGUUGCUUCACCUGUU	86	spiLA1589-miR167b-3-5p	UGAAGCUGCCAGCAUGAUCUAA	8-29	bna-miR167b	0	0	22	22	1
			spiLA1589-miR167d-3-3p	AUCAGAUCAUGUGGUUGCUUCACC	59-82	csi-miR167d-3p	2	0	24	24	1
spiLA1589-MIR395j-1	GUGUUCCCUAGAGUUCCCUUGACCACUUCAUUUGGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUGGGGGAACUCUUGGACUCA	90	spiLA1589-miR395j-1-5p	GUUCCCUUGACCACUUCAUUU	13-33	mdm-miR395j	1	0	21	21	1
			spiLA1589-miR395a-1-3p	UGAAGUGUUUGGGGGAACUCU	62-82	aof-miR395a	0	0	21	21	1
spiLA1589-MIR396b-2	UCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAUAGGGUCAAAUAGAAUUGCUACAAUUGAAUUGAAGUUU	159	spiLA1589-miR396b-2-5p	UUCCACAGCUUUCUUGAACUG	15-35	aof-miR396b	0	0	21	21	1
			spiLA1589-miR396c-2-3p	GUUCAAUAAAGCUGUGGGAAG	94-114	fve-miR396c-3p	0	0	21	21	1
spiLA1589-MIR172b-2	GCAGAUGCAGCAUCUUCAAGAUUCACAUAGAUUUAUAUAAAAUAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUAAUUUUCUCCUGUAUAUUGGCUCUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGCA	156	spiLA1589-miR172b-2-5p	GCAGCAUCUUCAAGAUUCACA	7-27	csi-miR172b-5p	1	0	21	21	1
			spiLA1589-miR172-2-3p	UGAGAAUCUUGAUGAUGCUGCAG	129-151	aau-miR172	1	0	23	23	1
spiLA1589-MIR10528	AUAAUGAAUGCAAUGUCAUAUACCAUCAACACUCGGAAACUCAAAUUGAGGUUAAAUCUCGGAGUGAUGAUGGUAUAUGACCUUGCAAUUCACUAUG	97	spiLA1589-miR10528-5p	AAUGCAAUGUCAUAUACCAUC	7-27	sly-miR10528	0	0	21	21	1
			spiLA1589-miR11424-3p	AUUGAGGUUAAAUCUCGGAGU	45-65	pab-miR11424	5	0	21	21	1
spiLA1589-MIR172j-1	CCGCUGCAGCAUCAUCAAGAUUCCCACACAUCGCCCAUAGGGUUUUUAAAAAUUAUAAAAGCCCUAAUAUAGCUAUGUGAAUCUUGAUGAUGCUCCACCCGC	102	spiLA1589-miR172j-1-5p	GCAGCAUCAUCAAGAUUCCCA	6-26	lus-miR172j	0	0	21	21	1
			spiLA1589-miR172f-1-3p	UGAAUCUUGAUGAUGCUCCAC	78-98	egu-miR172f	1	0	21	21	1
spiLA1589-MIR10529	AAACAUAACGAGUGAGACUUGCUCAGUUGGUAAAACACCUCCACGGUCUAACCAAUUAUCUUGGUCGAGGGUUCAAGUCAUGUUGGAAGCAAUGUGGGGGCGUCCAGCUUAGCAAGCCUCAUCCGUUUUGCUUC	134	spiLA1589-miR10529-5p	AACGAGUGAGACUUGCUCAGUUGG	7-30	sly-miR10529	0	0	24	24	1
			spiLA1589-miR3441-3p	UUCAAGUCAUGUUGGAAGCAA	72-92	aly-miR3441-5p-1	5	0	21	21	1
spiLA1589-MIR530	UUAUCUGCAUUUGCACCUGCACCUUAGUGAACGAAUUAGUUCGCGUAUAAUUCGUGCAGAAAGGUGUAGGUGUUCAUGCAGACAAA	86	spiLA1589-miR530-5p	UCUGCAUUUGCACCUGCACCU	4-24	eun-miR530-5p	0	0	21	21	1
			spiLA1589-miR530-3p	AGGUGUAGGUGUUCAUGCAGA	62-82	sly-miR530	0	0	21	21	1
spiLA1589-MIR399b-1	GUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACU	75	spiLA1589-miR399b-1-5p	GGGCUACUCUCUAUUGGCAUG	7-27	sly-miR399b	0	0	21	21	1
			spiLA1589-miR399o-1-3p	CGCCAAAGGAGAGCUGCCCUG	50-70	stu-miR399o-3p	0	0	21	21	1
spiLA1589-MIR399b-2	UAGUAGGGCUACUCUCUAUUGGCAUGCAGUGAUAUAUUCAAACUGAUAUGCCAAAGGAGAGCUGCCCUGUUAC	73	spiLA1589-miR399b-2-5p	GGGCUACUCUCUAUUGGCAUG	6-26	sly-miR399b	0	0	21	21	1
			spiLA1589-miR399n-2-3p	UGCCAAAGGAGAGCUGCCCUG	49-69	gma-miR399n	0	0	21	21	1
spiLA1589-MIR10531	GAUAUCUGGGGUCCUAGUAGAGUCGGUUCUACAUUGGGUGUUAAGUGUUUUGAGUAAUCAUCAUUGAAAGUAACAUACUUAAAACCCAAUGUUGAAUUGACUCUACUCGGAUCCAAAUAUCG	122	spiLA1589-miR10531-5p	UGGGGUCCUAGUAGAGUCGGUUC	7-29	sly-miR10531	0	0	23	23	1
			spiLA1589-miR397u-3p	UCAUCAUUGAAAGUAACAUAC	58-78	pab-miR397u	5	0	21	21	1

spiLA1589-MIR10534-1	GGCUCCAAAAUACCCUUGUCAUCCAACAUUGGAUUCAAAAUUGACCACUUAUUUAACGGUCCAUUUUGAACAAAAAGGUGGAUGACAAGGGUAUUUUGGAGCCA	104	spiLA1589-miR10534-1-5p	CAAAAUACCCUUGUCAUCCAA	6-26	sly-miR10534	0	0	21	21	1
spiLA1589-MIR10534-2	UGGCUCCAAAAUACCCUUGUCAUCCACCUUUUUGUUCAAAAUGGACCGUUAAAUAAGUGGUCAAUUUUGAAUCCAAUGUUGGAUGACAAGGGUAUUUUGGAGCCAU	106	spiLA1589-miR10534-2-5p	CAAAAUACCCUUGUCAUCCAC	7-27	sly-miR10534	1	0	21	21	1
spiLA1589-MIR7981d-1	UUUUGCUCGAAAUCUCAGAGACACACUUAUAAUAUAUUAGGCUCCUAUUACCACACUCCCUUAAACUUAUUGUAUAAGUAAUUUUCUAUCCCUUUUCGACAUACGUGACACUAACUUGAAAAAAAAAGUCAAUCAUGGGUCCACAAGAGUGUCACGUAGGUCGAAAAGGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAAGAAUAAUAGAACCUUAUUAUAGUAUAACUGUGUCUCUGAGAUUUCGGACAUAGG	253	spiLA1589-miR7981d-1-5p	UCGAAAUCUCAGAGACACACUUAU	7-30	sly-miR7981d	0	0	24	24	1
			spiLA1589-miR7981e-1-3p	AACUGUGUCUCUGAGAUUUCGGAC	225-248	sly-miR7981e	2	0	24	24	1
spiLA1589-MIR9470-1	GUUCUACAACGUACGUAGGGUAAGUGGAUGGCUGAAAUUCGUUAGCCUAACCGUGGCCCUGGAAAUACUUCUCUGCAGGACAAGCUUCAUUUCCAUUACCGGAUAUCAACAGAAAGGUUGAAAAAGACAACAAUGUAGAGGAUUUGGUGGAGUGUGGAAAGAUUUGAAUGCAAACUUAUCGAAGAUUGAUCAUCAUGGAUUUAAGCCAUCCAUUUACCCCAAGUUCGUUGUCAAACG	237	spiLA1589-miR9470-1-5p	UGAAAUUCGUUAGCCUAACCG	33-53	sly-miR9470-5p	5	0	21	21	1
			spiLA1589-miR10537-1-3p	AUUUACCCCAAGUUCGUUGUC	212-232	sly-miR10537	0	0	21	21	1
spiLA1589-MIR171f-3	UCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAG	79	spiLA1589-miR171f-3-5p	UAUUGGCCUGGUUCACUCAGA	6-26	csi-miR171f-5p	0	0	21	21	1
			spiLA1589-miR171c-3-3p	UGAUUGAGCCGUGUCAAUAUC	55-75	stu-miR171c-3p	0	0	21	21	1
spiLA1589-MIR159a-1	UAUUUUAUGUGUUAUGGGAGUGGAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAUUGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAGCUUUAUUUUACCCUUUGUUUGAUCAUUUUUUGGAUUGAAGGGAGCUCUACAUUCAUUUCUUCUUACUAGUUUAAUCUAUGUUGG	233	spiLA1589-miR159a-1-5p	GAGCUCCUUGAAGUCCAACAG	23-43	fve-miR159a-5p	1	0	21	21	1
			spiLA1589-miR159-1-3p	UUUGGAUUGAAGGGAGCUCUA	178-198	aof-miR159	0	0	21	21	1
spiLA1589-MIR169r-1	CAUCCAAUGAGCUUCUCACAAGUUGUGUUUUGUUAGAUGAAGUAGGAAACUGCUAAUUCUAUUUGCCAUAGGGAAUGUUGGAUUUUCUUCUUCAGGAAACUACACUUCCCUAUAAUUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAA	285	spiLA1589-miR169r-1-3p	CAGCCAAGGAUGACUUGCCGG	178-198	csi-miR169r-5p	0	0	21	21	1
spiLA1589-MIR169j-1	GAAAUGAUAAAAGAAGAGUGUGUCUUACAUGAAGGGGAAGUGCCUAAUUUGAUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGUUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUCUUUGAUGGCCAGGCAGUCUCCUUGGCUACUCUAAUAGGUUCCUCUCAUUCAUGCUAGACUCUUCUCUUCUUAUUUAGAAGUUAAAAAAAAAUAGUGGCAGACUGAACUUUAAAGUUUAUAGGUUUACCUU	266	spiLA1589-miR169j-1-5p	UAGCCAAGGAUGACUUGCCUGC	53-74	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169e-1-3p	CAGGCAGUCUCCUUGGCUACU	146-166	csi-miR169e-3p	2	0	21	21	1
spiLA1589-MIR160h-2	GUAUAUGCCUGGCUCCCUGUAUGCCAUUUGCAAAGCUCACCGUAAUAUAUCGAUGGGCCUUGUUGAAUGGCGUAUGAGGAGCCAAGCAUAUU	92	spiLA1589-miR160h-2-5p	UGCCUGGCUCCCUGUAUGCCAUU	6-28	mes-miR160h	0	0	23	23	1
			spiLA1589-miR160-2-3p	GCGUAUGAGGAGCCAAGCAUA	70-90	eun-miR160-3p	0	0	21	21	1
spiLA1589-MIR167b-4	AUCGUGAACCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUUCUAUUGCUCCGUACGAGGAAAGAUCAGAUCAUGUGGCAGCAUCACCUGUUGAUGGUUUCGCGG	110	spiLA1589-miR167b-4-5p	UGAAGCUGCCAGCAUGAUCUAA	20-41	bna-miR167b	0	0	22	22	1
			spiLA1589-miR167c-4-3p	AUCAGAUCAUGUGGCAGCAUCACC	70-93	eun-miR167c-3p	1	0	24	24	1
spiLA1589-MIR171f-4	UUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAAC	113	spiLA1589-miR171f-4-5p	CGAUGUUGGUGAGGUUCAAUC	24-44	fve-miR171f-5p	0	0	21	21	1

	GAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUA									
spiLA1589-MIR827-2	GUGAUGAAGAUGUUUGUUGAUGUUCAUCUAAUCAUGGCAUAUUAAUGGUUCCAAAAACUAUGCCAAAUGAUAUGAUGAAUAGAUGACCAUCAACAAACAAAUUCAUAACUACACAA	116	spiLA1589-miR171b-4-3p	UUGAGCCGCGCCAAUAUCACU	88-108	aof-miR171b	0	0	21	21	1
			spiLA1589-miR827-2-5p	GUUUGUUGAUGUUCAUCUAAUC	12-33	eun-miR827-5p	3	0	22	22	2
			spiLA1589-miR827-2-3p	AUAGAUGACCAUCAACAAACA	79-99	aof-miR827	1	0	21	21	2
spiLA1589-MIR171f-5	AUUGAUCAACUUGCGAUGUUGGUGUGGUUCAAUUAGAUAACAAUCUCCACGUAAAAUUAUAGAGUUUGUUAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAAGAAAAUA	110	spiLA1589-miR171f-5-5p	CGAUGUUGGUGUGGUUCAAUU	14-34	fve-miR171f-5p	2	0	21	21	1
			spiLA1589-miR171a-5-3p	UGAUUGAGCCGUGCCAAUAUC	74-94	aof-miR171a	0	0	21	21	1
spiLA1589-MIR171f-6	AUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAUUUUCAUU	108	spiLA1589-miR171f-6-5p	CGAUGUUGGUGAGGUUCAAUC	11-31	fve-miR171f-5p	0	0	21	21	1
			spiLA1589-miR171b-6-3p	UUGAGCCGCGCCAAUAUCACU	75-95	aof-miR171b	0	0	21	21	1
spiLA1589-MIR156b-6	GGGUGACAGAAGAGAGUGAGCACACAUGGUUCUUUCAUGGAUUAUUCCCCAUGUUUAAAAGCUCUGCGUGCUCACGCUCUAUCUGUCACA	90	spiLA1589-miR156b-6-5p	UGACAGAAGAGAGUGAGCACA	4-24	hvu-miR156b	0	0	21	21	1
			spiLA1589-miR156b-6-3p	UGCUCACGCUCUAUCUGUCACA	69-90	mtr-miR156b-3p	2	0	22	22	1
spiLA1589-MIR156f-1	UCUGUUGACAGAAGAGAGAAAGCACAGUCUGUCAUCAACAAAAUGGUAUUUGUUGUUUGUUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUAG	92	spiLA1589-miR156f-1-5p	UUGACAGAAGAGAGAAAGCACA	5-26	gma-miR156f	1	0	22	22	1
spiLA1589-MIR156b-7	AUAUAAUUGAAAUUGAUAGGAAGAAAGAGUGAUUAUUGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCACC	142	spiLA1589-miR156b-7-5p	UUGACAGAAGAUAGAGAGCAC	39-59	aof-miR156b	0	0	21	21	1
			spiLA1589-miR156d-7-3p	GCUCUCUAUGCUUCUGUCAUCA	119-140	stu-miR156d-3p	0	0	22	22	1
spiLA1589-MIR156b-8	UUAUUGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCACCUUCACCUCUUUCAUAAAAAUAUUUAAAUCUGU	142	spiLA1589-miR156b-8-5p	UUGACAGAAGAUAGAGAGCAC	7-27	aof-miR156b	0	0	21	21	1
			spiLA1589-miR156d-8-3p	GCUCUCUAUGCUUCUGUCAUCA	87-108	stu-miR156d-3p	0	0	22	22	1
spiLA1589-MIR162-1	ACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGGAAGCUGAAUAUAUAUAUACGCAAAAAUACAGCAAAAGGAAUCGGUCGAUAAACCUCUGCAUCCAGUG	103	spiLA1589-miR162-1-5p	UGGAGGCAGCGGUUCAUCGAUC	5-26	csi-miR162-5p	0	0	22	22	1
			spiLA1589-miR162-1-3p	UCGAUAAACCUCUGCAUCCAG	81-101	fve-miR162-3p	0	0	21	21	1
spiLA1589-MIR166f	UAAAGAAAAACAAGAAAAGUGAUGCUAGAAGGGAAGGAAGAAUAAACAUUUUUUGUUUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCA	156	spiLA1589-miR166f-3p	UCGGACCAGGCUUCAUUCCCCU	133-154	cas-miR166f-3p	0	0	22	22	1
spiLA1589-MIR171f-7	CUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCA	79	spiLA1589-miR171f-7-5p	UAUUGGCCUGGUUCACUCAGA	7-27	csi-miR171f-5p	0	0	21	21	1
			spiLA1589-miR171c-7-3p	UGAUUGAGCCGUGUCAAUAUC	56-76	stu-miR171c-3p	0	0	21	21	1
spiLA1589-MIR171a	AUACACGAGAUAUUGGUGCGGUUCAAUGAGAAAGCAGUACUUAAGAACAUAUUUGAGUCUACUUUUUGAUUGAGCCGCGCCAAUAUCACGUGUA	94	spiLA1589-miR171a-5p	UAUUGGUGCGGUUCAAUGAGA	11-31	nta-miR171a	0	0	21	21	1
			spiLA1589-miR171a-3p	UGAUUGAGCCGCGCCAAUAUCA	67-88	cas-miR171a-3p	1	0	22	22	1
spiLA1589-MIR162-2	GAAAAGAAAAAAAAAUCCUUAGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCGUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUC	137	spiLA1589-miR162-2-5p	UGGAUGCAGAGGUUUAUCGACC	34-55	csi-miR162-5p	4	0	22	22	1
			spiLA1589-miR162b-2-3p	AUCGAUGAACCGCUGCCUCC	109-128	cas-miR162b	0	0	20	20	1

spiLA1589-MIR169j-2	UAGUAGCCAAGGAUGACUUGCCUGCUCCAAUAUUACUUAUAAGGUUUUUAAUUAUAUCAUUAUUAAUAUAAUGGUGACCUUUUAUUGGUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUCCUCUUUCAUGCAAGAACUU	148	spiLA1589-miR169j-2-5p	UAGCCAAGGAUGACUUGCCUGC	4-25	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169e-2-3p	CAGGCAGUCUCCUUGGCUACC	96-116	csi-miR169e-3p	2	0	21	21	1
spiLA1589-MIR156f-2	UUUGGUUGAGGAUUCAAAGUGAGAAAUUCUAUUGACAGAAGAGAGAGAGUACAAUCUGUCAUCAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUGCUCUCUCGUCUUCGCCAAUGGAAACUAUAAAAAUGGAUCCUCAACAAAGA	146	spiLA1589-miR156f-2-5p	UUGACAGAAGAGAGAGAGUACA	32-53	gma-miR156f	1	0	22	22	1
spiLA1589-MIR169c-2	GUUUUACAUGAAGUUGAGAGUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAGA	158	spiLA1589-miR169c-2-5p	UAGCCAAGGAUGACUUGCCUA	31-51	ata-miR169c-5p	0	0	21	21	1
			spiLA1589-miR169e-2-3p	GCAAGUUAUCCUGGCUAUC	111-129	stu-miR169e-3p	0	0	19	19	1
spiLA1589-MIR169r-2	AAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAACAGCUGUUGUUGUUAAUUGUCAAAUCAGGAAUUGUGGACAA	184	spiLA1589-miR169r-2-5p	CAGCCAAGGAUGACUUGCCGG	36-56	csi-miR169r-5p	0	0	21	21	1
spiLA1589-MIR169j-3	AUUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAAUAUUACUUAUAAGGUUUUUAAUUAUAUCAUUAUUAAUAUAAUGGUGACCUUUUAUUGGUUGGUUUCAGGCAGUCUCCUUGGCUACCUUGACAUGCUCUCCUCUUUCAUGCAAGAA	154	spiLA1589-miR169j-3-5p	UAGCCAAGGAUGACUUGCCUGC	13-34	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169e-3-3p	CAGGCAGUCUCCUUGGCUACC	105-125	csi-miR169e-3p	2	0	21	21	1
spiLA1589-MIR169j-4	UCUAGCAUGAUGAAAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCAUUUCCGAAAUGUGUCCUUUCGUUCAUGGGGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUCUUUCAUGCAAGACUUUCUCUUCUUCCGA	153	spiLA1589-miR169j-4-5p	UAGCCAAGGAUGACUUGCCUGC	30-51	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169d-4-3p	GCAGGUCAUCUUUAGCUAACU	90-110	stu-miR169d-3p	0	0	21	21	1
spiLA1589-MIR171f-8	GAGGAGUUGGUGUGAUGUUGGAAUGGCUCAAUCUAAUGAAAGUUUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCCGUGCCAAUAUCAUAUCGUCUU	101	spiLA1589-miR171f-8-5p	UGAUGUUGGAAUGGCUCAAUC	13-33	zma-miR171f-5p	2	0	21	21	2
			spiLA1589-miR171a-8-3p	UGAUUGAGCCGUGCCAAUAUC	71-91	aof-miR171a	0	0	21	21	1
spiLA1589-MIR396b-3	AAAAGAAAUGGUCCUUUUUGUGUUUUUCCACAGCUUUCUUGAACUGCAUCUACAAUUUCAAUUCAUUAUUGAAAAAGAAAAAAUUGAUUCAUAUUGUUGUUGCGGUUCAAUAAAGCUGUGGGAAGAUACAGAU	133	spiLA1589-miR396b-3-5p	UUCCACAGCUUUCUUGAACUG	26-46	aof-miR396b	0	0	21	21	1
			spiLA1589-miR396c-3-3p	GUUCAAUAAAGCUGUGGGAAG	105-125	fve-miR396c-3p	0	0	21	21	1
spiLA1589-MIR9760-1	CUCUUUCUCUCUUUUUGGCUGCUGAAAAAACUCUCUGUGUAUAUGAGGGUGCAUUAUGAAUUGCUGAAGGUUCAUCGUCCGAGGAUGAUGAAGUUUUGAGGUGUUAAGUAGAUCAGUGUUCUGUUUUUCAACCUUGGUAGACAUUAUCGUAAUCCUCGAUGUUGACAGUGAAUUGUGAUUGAAGAUGCAUUAGCUGGAGUACAAGCUUCCAAAGCUGCAGAAAUGAGUUUUUUUUUUUAACUGAAAAAGAAAAACUA	257	spiLA1589-miR9760-1-5p	AGGAUGAUGAAGUUUUGAGGU	82-102	gma-miR9760	5	0	21	21	2
			spiLA1589-miR8033-1-3p	UUCCAAAGCUGCAGAAAUGAGU	207-228	stu-miR8033-5p	0	0	22	22	1
spiLA1589-MIR3512-1	CGUCAAAGUCAAUACCCUUUCUUUGACCGAAUUUCUUAUUAAGGUCAGUAGUCGAUUGCAACAAAGGUGUGCCCAAUUUGCUGCAAAUCUUGCCAAAAAGAUUUUCUUCCUUUAAAGAUGGGAUUUGGACCCCAUAACUUGAAGCUCAGGUACAAAGUUAGAUUGGUUGUUAAGCUAUUUGGCCGAAGGAAGGGUAUUGACUUUGAAG	208	spiLA1589-miR3512-1-5p	UGCAAAUCUUGCCAAAAAGA	82-101	ahy-miR3512	5	0	20	20	2
			spiLA1589-miR1863-1-3p	AGCUCAGGUACAAAGUUAGAUU	143-164	pab-miR1863	3	0	22	22	1
spiLA1589-MIR7997c-1	GGAUCCUAUGUUGCUCGGACUCUUCAAAAAAGUCGAGGGGUGUUUGUCAGGUCCUCCGAAAGCAGUGUGCUUUUGAAGGAUCUGACACGGGUGGGGCAACAUACUUGGAGAGUCCGAGCAACAUAGGAGGG	131	spiLA1589-miR7997c-1-5p	AUGUUGCUCGGACUCUUCAAAAAA	8-31	stu-miR7997c	2	0	24	24	1

			spiLA1589-miR5303e-1-3p	UUUUGAAGGAUCUGACACGGGUGG	71-94	stu-miR5303e	3	0	24	24	1
spiLA1589-MIR8011a-1	AAAUUAAUUAUCAAUCCGUAACUGUCAAUUGAAUGAGGUCUCUUUUUAUUUCACAAGUAGUUAGAAACUUAAAUCUUACAAAAAGUCCACAUUACUUUGUGUCCUGUCCACUUGUGAGAUAAAAAAGAGGUUCUGACAAAUAUUGUUAGCUUGUGGCACAUGUCAUCAAGGGCGGAGUCACUUUGUAGGUAGGGGUUCAUCUGAACCUCAUUCAACGGAAAAUUAUAUUAUUUAAACA	238	spiLA1589-miR8011a-1-5p	UUGAAUGAGGUCUCUUUUUAUUUC	29-52	stu-miR8011a-5p	4	0	24	24	1
			spiLA1589-miR6209-1-3p	UGAGAUAAAAAAGAGGUUCU	115-134	hvu-miR6209	5	0	20	20	1
spiLA1589-MIR6273-1	UGUCGUAAUUGAUAGUCACGAUUUAAUGCAGAAAUGUGAUCACCGAUAACGUUUUAUGAUCUGUAAGAUUCCAAUGUAGCAGGAUUUUAUUCUUAAUUUGGUGUCCCGUGAUUAAAUAAACAUAAAAAGUGAUUGACAGUUACGUUUUACAUAAUAAACGUGAUUGUCAGUUACGUUU	178	spiLA1589-miR6273-1-3p	AAUGUAGCAGGAUUUUAUUCU	73-93	ppe-miR6273	4	0	21	21	1
spiLA1589-MIR156e	AAUUUGCUUUAGUAUGCAUUUGUGUUUGUAUAAAGUGAGAGAGGAGAGUGAGCGAGCGAGAUUUAGGAGAGGGGGGAGAGAGCAACGAAAAUAUAUGUAUAUAUACAAUUUUCUCUAGCUUUAUACAAACACAAACGCAUUUUAUACAAUAG	152	spiLA1589-miR156e-5p	UGAGAGAGGAGAGUGAGCGA	36-55	vvi-miR156e	3	0	20	20	1
spiLA1589-MIR167d-1	UUCCGCGAAACCAUCAACAGGUGAUGCUGCCACAUGAUCUGAUCUUUCCUCGUACGGAGCAAUAGAAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGGUUCACGAUC	113	spiLA1589-miR167d-1-5p	UGAUGCUGCCACAUGAUCUGA	22-42	eun-miR167d-5p	1	0	21	21	1
			spiLA1589-miR167h-1-3p	AUCAUGCUGGCAGCUUCAACUGCU	76-99	gma-miR167h	1	0	24	24	1
spiLA1589-MIR9675	CCCUAUGCAUAAUUUCGGUGGAGCUUACAACAGCAAGACAGUGAGAGAGAUUUUUGCUCUCUCUCAUUUUCUUGCUGUUGUAAGCUCCACCGGAAUCAUGCAUAAUA	107	spiLA1589-miR9675-3p	UUUUUGCUCUCUCUCAUUUUC	51-71	tae-miR9675-3p	5	0	21	21	1
spiLA1589-MIR5568f	UUUGCUCAAACUCUAUUCCAGAUUGUUUGAUAGAGCGCAUUAAAUAGAGUGUACUAACCAACAUUGAUUGUGGUGCACUGAUGGGAGUGUUUUAUUCUUAAUCAGAGAUCUCGAGUUUGAGCCCU	125	spiLA1589-miR5568f-5p	UCUAUUCCAGAUUGUUUGAUA	12-32	sbi-miR5568f-5p	5	0	21	21	1
spiLA1589-MIR8030-1	AUGUGUAUAAUGUCGGGUUGAUUUGGUCUCGGGUUAAUUUUUUUAAGUUAAAACCAAAUCAACCCAAAAUUUCCAAAA	78	spiLA1589-miR8030-1-5p	UCGGGUUGAUUUGGUCUCGGGUU	13-35	stu-miR8030-5p	2	0	23	23	1
			spiLA1589-miR8030-1-3p	UUAAAACCAAAUCAACCCAAAA	48-69	stu-miR8030-3p	1	0	22	22	1
spiLA1589-MIR6463	UUGGGUCAGUGUUGUCCUUGUUGUCCAAAAAUUAGAACAUAUAUACCCUUUAUGCUAACAGACAUACAUGUAUCAUCAUCUUACCAACCGAUCGGAUAUUUAUUUAAUACCGAAUCGACGAAUAAGAUUAUUUCAUAUGUCCCUAUUUAGUCUUUUGUUAGAGUGAAGGGCAUAUAUAUGCUCUAAUUUUUGGAUGGCAGGGGCACCAAUGUCCGAA	217	spiLA1589-miR6463-5p	UGUAUCAUCAUCUUACCAACC	69-89	ptc-miR6463	5	0	21	21	1
			spiLA1589-miR8006-3p	UAAUUUUUGGAUGGCAGGGGCACC	184-207	stu-miR8006-5p	3	0	24	24	1
spiLA1589-MIR5057-1	UGAUUCAAAAUAUAUAUUUGAAUAAUUACUAAUGAUGAUCAGUGGUGGAGCCACGUGUAGUGAAGGGUGUUGAUCGACAUUUCUUCAUUGGAAAAUUACAUUGUAAAAAUAUUUUUUUAAUAUGUAAUCAUAUUGACACCCCUUAGACAAAAUUCUAGCUCCGUCACUGAUGAUGAUAGUGAUAGUUAGUGAUGAUAGUUGAAGGC	206	spiLA1589-miR5057-1-3p	UAAUAUGUAAUCAUAUUGACA	118-138	bdi-miR5057	5	0	21	21	2
spiLA1589-MIR319h	UUGUGUCGCUUCUUCAUCUGAAGCGAGCGCCUUUUUCAGAUCGCAUCGCCUCAGGAGAAAGAAGCGCAGUG	71	spiLA1589-miR319h-5p	CUUCAUCUGAAGCGAGCGCCU	12-32	mes-miR319h	5	0	21	21	1
spiLA1589-MIR8001b-1	GGGAAUUACAUGGGGAUUAGUAUGAAAUUUGCAGGAAAAUAAUUUUUUGCGGAUUUUCAUACUAAUUCCUAGGAAAAUUUCU	82	spiLA1589-miR8001b-1-5p	AUGGGGAUUAGUAUGAAAUUUGCA	10-33	stu-miR8001b-5p	4	0	24	24	1
			spiLA1589-miR8001b-1-3p	GGAUUUUCAUACUAAUUCCUAGGA	51-74	stu-miR8001b-3p	1	0	24	24	1
spiLA1589-MIR8011a-2	UUCUUUAUGACAACACGAAUACUAGUUGUGUGAGGCUUCUUUUUGUCUCACAUAAAAGUAGACUCAAAUGGGCUUAAUUUUUUGUGAGGCAAAAAUGAGUCUCACUUGACUAGUGUCAGAUGUGUGAGUCACAAAAUA	138	spiLA1589-miR8011a-2-5p	UUGUGUGAGGCUUCUUUUUGUCUC	26-49	stu-miR8011a-5p	2	0	24	24	1
			spiLA1589-miR8011b-2-3p	UUUGUGAGGCAAAAAUGAGUCU	81-102	stu-miR8011b-3p	5	0	22	22	1
spiLA1589-MIR5725-1	UAAAUAGGGACAUGUGGCGCAAUCUUAUCCGUCGACAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACAUGUCCGUUAUAAA	82	spiLA1589-miR5725-1-5p	AUGUGGCGCAAUCUUAUCCGU	12-32	bra-miR5725	5	0	21	21	1

			spiLA1589-miR3706-1-3p	UGUCGGAUCGGUGGAUAAGA	40-59	pab-miR3706	5	0	20	20	1
spiLA1589-MIR8710b	AAAGUACAUGAACAUUGGCUAAAGCAUAUGUAUCAUGAGAUAUAAAUUCAAGGAUUAUUGGGUAACAUAUCGUACAUGAUACAUAUGCUUUAGCCAAUGUUCUCAUGGACAAG	113	spiLA1589-miR8710b-5p	GUACAUGAACAUUGGCUAAA	4-23	gra-miR8710b	5	0	20	20	2
spiLA1589-MIR479	AAUACGUGAUAUUGACACGGCUCAAUUAAAUAACGAAGUUCUAUAUAUAAAGAAGUGCGCUUUCUAAUUGAACCGCACCAAUAUCUCGUUAG	92	spiLA1589-miR479-5p	CGUGAUAUUGACACGGCUCAAU	5-26	ghr-miR479	5	0	22	22	1
			spiLA1589-miR171c-3p	UAAUUGAACCGCACCAAUAUC	65-85	aqc-miR171c	1	0	21	21	1
spiLA1589-MIR5337a	UGCGGGGUUGAAUUCUCAAAUGGUUACUCAACUUAUAGUUAUUAUCUCAGAAAAUCUCUUUUCGUUCUUGAUUCUGAUGCAAAGAAAGUCACUUUGUUAGAUAUAAACUAUUAGUUGAGUGACCAUCUGUGAAAUCAACUCCUGU	145	spiLA1589-miR5337a-5p	AAAUCUCUUUUCGUUCUUGAU	52-72	osa-miR5337a	5	0	21	21	1
			spiLA1589-miR10540-3p	AUAUAAACUAUUAGUUGAGUG	101-121	sly-miR10540	3	0	21	21	1
spiLA1589-MIR5051	UUUCAAAUAUGUAACAAAUUAGAUGGGGAAGAUGACAUAAAUUGAUAAAAUAAUUAAUAAUAAAGAAAAAUACUGACACAUGGCACCUUUAAACUGGUCCAUGGCAGUAAAAAUAAUGCAUUACGCGCCUCAAGUGCGUGGUAACAACUCAGACUAGGAAAUGGGUCAAAAUGGUCCAUUUACAAAGAAAUUAAAUAGUUCUGUGGGGUGAUAGGACAUUUUAAAAGUUAAGGUGUCUUAAUGCAAAUACAGGACAACUUUGAUGGUAUCUUUAUGUCUUUUCUCUUAUAUAAGCUUUGUAAAUUUGUGA	310	spiLA1589-miR5051-5p	CAUGGCACCUUUAAACUGGUC	79-99	hvu-miR5051	5	0	21	21	3
spiLA1589-MIR6271	AAGUAAUGAAGCCAAGUACCUAUUUUUGCUUUGUUCCUUGUUCGAGGAAGAUAGAGAUAUAUAAUUACUUUGGAUAUGGAAGUGGGUUUCACACUCUUUCCGGGCAUUGAAAAUUUAGAACAAGCAAGAGAUAGGGCGUGUCUUCUGUUAGAA	152	spiLA1589-miR6271-5p	GGAAGAUAGAGAUAUAUAAUU	46-66	ppe-miR6271	5	0	21	21	3
			spiLA1589-miR408-3p	ACAAGCAAGAGAUAGGGCGUG	119-139	pab-miR408	4	0	21	21	1
spiLA1589-MIR11484	CUGAACUUUAUUCACUAUAACAGUAUGGUCACAAAACUAUCUUUUGUUGCGUUAAAGUACGUGUUAAUUGCUCAAACAAUGACUAGAAGGUUAAAUAUUCUUUUAAUAUUAUUUUGAGCCAGAAAUUUAACCUUUGGGCCAUUUGUCUCAUUUGAGCAAUCCACACCCCUAGUUCAGUUACUUUAAUGUGACAAAAAUUAGUUCUGUGAUUCUACCGUUACCGAGGAUAAAAUUAAA	237	spiLA1589-miR11484-5p	UAAUUGCUCAAACAAUGACUA	65-85	pab-miR11484	5	0	21	21	1
			spiLA1589-miR11409d-3p	CAUUUGUCUCAUUUGAGCAAU	140-160	pab-miR11409d	4	0	21	21	1
spiLA1589-MIR5083-1	UCACAAGGAUAUCAAAAAUUAUUGCAAUUCUCUGAUCAAGCAACGUGGAGAAAAACUAAUCUGUUGGAUGGAUGUUGUAUCCACGUUGCUUGAUAAGUUUUUUCUCCACGUUGCUUGAUCAGAGAAUUGCAGUAAUUGUUGAUAUCCUUGUGA	153	spiLA1589-miR5083-1-5p	UUAUUGCAAUUCUCUGAUCA	19-38	osa-miR5083	5	0	20	20	3
spiLA1589-MIR7992-1	AACCUUAACUUGGACUCAAUUGACAGCUAGCCAACCUAACUCUGAAAAUGCACAUCUAGACCCCUUAACUUGAUCUAACUUUCCCCCUUUAAGACCUCAACUUUGAGAAUGCACAUCUAGAAUUCACAAUUUGAGAAUGCACAUCCGGAAAAGUGUAUUUAGGGGGCCAACUUACACCAGGUUAAGAUGUCUAGAUGUGUCUUUUCAAAGUUGGGGUGUCCAAUUGUCAGUUGAGACCAAGUUAAGAUG	249	spiLA1589-miR7992-1-5p	UUUGAGAAUGCACAUCUAGAAUUC	102-125	stu-miR7992-5p	5	0	24	24	1
			spiLA1589-miR7992-1-3p	UGUCUAGAUGUGUCUUUUCAAAGU	188-211	stu-miR7992-3p	2	1	24	23	1
spiLA1589-MIR11330	UCUCCCUACUGUUAAAACGAAGUUAUUUUUACCCCUACCGUUACUAAUUUCAUCAUUUUAACAUUGGGUUUGAAAUGGGAAAUGUAUAAAUGAUGAAAUUAGUAACGGUAGGGAUAAAAAUAACUUCAUUUUGACGGUAGGGGCA	145	spiLA1589-miR11330-3p	GUAGGGAUAAAAAUAACUUCA	108-128	ppt-miR11330	5	0	21	21	1
spiLA1589-MIR395a-1	UGUUUGAUGCCUUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAGGAGUCCUGGCUAUGGAUGAUGAACAUGAUAGUUCAUGUUUAAAUCUAUUAAGGUGAUCCCUAGAGUUCACUUGACCACUUCAUGAGGGCUUAAUUU	174	spiLA1589-miR395a-1-5p	UGAAGUGUUUGGGGGAACUCU	16-36	aof-miR395a	0	0	21	21	1
spiLA1589-MIR7980b-1	UCUCAUGAUAUGAAAUCAUGAGAUGGAAUUAACGUGAAAUUAUAUGUCCAAACGCUGAUUUCAUCUCAUGAUUUCAUAUUGCAUGUCC	88	spiLA1589-miR7980b-1-3p	GUCCAAACGCUGAUUUCAUCUCAU	46-69	stu-miR7980b-5p	2	0	24	24	1
spiLA1589-MIR172d-3	AUUCAGACCUAAAAAUCAAACGUACUGAAUAGGCUGAAUCUGAAUGAUUAAGAUUCACACCUCCAUUGAGUGCAAACAAA	186	spiLA1589-miR172d-3-5p	UCUGAAUGAUUAAGAUUCACA	39-59	bra-miR172d-5p	4	0	21	21	2

spiLA1589-MIR447a	UGAGGCCUUAGUUGUCAUUUGUUUUCAUUAAGAUUAAGA GGUCUGAAUCUGAAUAAACAUCUGAAUAUUAAGAUUUGCA UUAAGAUUUGAGUGCUUUAAUCUGAGU UGGCUAUAUUCCCUUGUAAAGUGUCCUUCUUGUCCGCAU UUGUAGCAUCCCUCUCCUCCUCCACCGCCUCCUUGGCUA CAUUCCCUUGUGAAAGAAGGAAGGGGCUGCUACAAAUGU GGGGAAGAAGGGCAUUUUGGAAGGGAUUGUAGAAU	152	spiLA1589-miR447a-3p	UUUGGAAGGGAUUGUAGAAU	133-152	ath-miR447a-2-3p	4	0	20	21	1
spiLA1589-MIR171b-1	AACGGAAUGAAAAUAAGAAGUGAUAUUGGCGCGGCUCAA UCUGAGAUCGUUCUUUACGAAAAUAAGCAUAAAUUCGUC UUCGGAUUGAACCUCACCAACAUCGCUUCUUCCAUUUUA AUCCCAAA	125	spiLA1589-miR171b-1-5p	GAUAUUGGCGCGGCUCAAUC	22-41	zma-miR171b-5p	1	0	20	20	1
			spiLA1589-miR171-1-3p	GGAUUGAACCUCACCAACAUC	82-102	cca-miR171	4	0	21	21	2
spiLA1589-MIR167a-1	UCAUUUUUAAUUAUUUCUUACUUGAUUCCGUGUUUUUAC UUGUGAGUUCCUUUCAACUGCUACCAUUUAAAUUUGACG AUGGAAUGUGCGGUAUGAUCAGCAAAAGAACAACUACUU CUUCAGCUCAUGUAGCAGUAUUAAGGAACUCACAAGCAAA AACAAGCAAAAAAGAAAAAAUUAAUUUAAAAUGA	191	spiLA1589-miR167a-1-3p	CAGCUCAUGUAGCAGUAUUAA	121-141	vca-miR167a-3p	5	0	21	21	1
spiLA1589-MIR11304	GUACAAAACCAAACCAAAAUGCAAACCGAGUCAGAUCGAA AAAAACCCGACUAGUGGUUUAGUUUGACUUGGUUUGGUG UUGGAA	85	spiLA1589-miR11304-3p	UAGUGGUUUAGUUUGACUUG	52-71	fve-miR11304	5	0	20	20	1
spiLA1589-MIR827b-1	UCAUGUAUACACUACAACAAAAAUGACCAUUAACAACAUU UAAUUCUUAAUUGCCUCUAAAUAUGUAUUUUUAGCGGCA AGUGUCACUCUUUGUAUAUGUCUCUAAAACCUUUAGCGA AAUUGCUUCUAAUGACAGUUAACUAAUGCCGGUAAGGAC UUUAACACUCGUUAUUAGUGUUAAUGUUUAAUGCCGCUA AAAAUUGUUUUUGUUGUAGUGAUAUCCAAAU	227	spiLA1589-miR827b-1-5p	AAAAAUGACCAUUAACAACA	19-38	cas-miR827b	5	0	20	20	2
			spiLA1589-miR7983-1-3p	ACUAAUGCCGGUAAGGACUUUAAC	140-163	stu-miR7983-3p	1	0	24	24	1
spiLA1589-MIR7997c-2	CCUCUAUGUUGCUUGGACUCUUCAAAAAUGUCGAUGAGU UUGUGUCGGAUCCUCCAAAAAGGAUCCUCCAAAAAUGUA UAUUUUUGAAGGAUCUGACACGGGUGCGGCAACAUUUUU GGAGAAUCCGAGCAACGUAGUUC	140	spiLA1589-miR7997c-2-5p	AUGUUGCUUGGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303f-2-3p	AUUUUUGAAGGAUCUGACACGGGU	80-103	stu-miR5303f	2	0	24	24	1
spiLA1589-MIR1074	GAAAAAACAUAUUUUUAAUGAUUAAGAUAGCGGUACAAUU GUGUUGAUCCCUUGAUUGUACUCUCUUAGGAUUUAUCCA UGAUUCGAGGGUUGUUAGUGGUGUAUCUCUCGGAUUAG GAUGAUUUAGAUUUGACCUCUCUAUAUGAAUAUUCCAUU AAUUUGCGGAGUAUUCGAGAUCUUGAUAUCUUUAAGAAA UUUUUGAG	203	spiLA1589-miR1074-3p	AGGGUUGUUAGUGGUGUAUCU	87-107	ppt-miR1074	4	0	21	21	1
spiLA1589-MIR835-1	CGCUUUGCCCUCAUGUUUGCUUCACCUACCACCCUAUUU UAUAUACUUUUAUGCAUUGGGGACAAUUGUAUGUCUUUU UGUUGGGGUGGGGUAAAUGGAAAGUAAGUGCUAGGGUG AAGUUUGAGUAUCCCAACUCACGAUCCUCUCUUGGGGUU UUCUUGCAUGUGUUCUUUAUCCCCAAGAGACUGGUUAUU UUAUUGUUGAAACGGCAUGUUGGUAUCUUUUGUACAUAG UAUAGAAAUGGAAUCUAAAGCAUGAUGGCUAAACAA	269	spiLA1589-miR835-1-3p	UUCUUGCAUGUGUUCUUUAUC	156-176	aly-miR835-5p	1	0	21	21	1
spiLA1589-MIR8127	UGAUCUGAAAUUUGGGUAAGAUUCAACAAAACAGGACACA ACAUUGUUUGCUUAGAGGCUUCUUUGUCAUCUUGGUGCU UGAUCGGAGCCUGAAGCUCCAAUAGAUGGAGCGGUGGG CAUACCAUUUGUUGAUCCAUUUUCAAGUGGUGGAGGGAC UCCCCAUUUGCCUUCAGAUUCAAGUGGUUCAAAAACAUG AACACUACCAUCUGACAGACCUAAUGCAAACUGGUUUGG AUCUUGUGGAUGUGCUGCAACUACGACUGGGUGGAUGU UUGAAUUGCUGCAGAAAAAUGACAAGGUUUUAUGAAAAAU UACAUCAAAUAUCAGAAAU	331	spiLA1589-miR8127-5p	GAGCGGUGGGCAUACCAUUUG	108-128	ppe-miR8127-5p	5	0	21	21	2
			spiLA1589-miR11124-3p	ACUGGUUUGGAUCUUGUGGAUG	225-246	lja-miR11124-5p	5	0	22	22	2
spiLA1589-MIR1521a-1	UUGUUCUAACUCUCCAAAGAUGCAUCACUACUUUUGAAG GAUCUGACAUGCAUCUGUCGUCAUUAUUGAAGACACAGA UGUGUUGUGUCAAUGCUAAUAGAAAUUGUUGUGUCUUUA GAGUGAAGUUAAAUUU	133	spiLA1589-miR1521a-1-3p	AUGCUAAUAGAAAUUGUUGU	91-110	gma-miR1521a	5	0	20	20	2
spiLA1589-MIR7997c-3	CGACUAUAUUGCUCGUACUUUUCAAAAAUGUUGUCAGAC CUGUAUGUAUGUACUUUUGGACGAUCUGACACACACCUG ACAGUACUUUUGAAGAGCUCGAGCAACAUAGAAA	112	spiLA1589-miR7997c-3-5p	AUAUUGCUCGUACUUUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1

			spiLA1589-miR5303-3-3p	CUUUUGAAGAGCUCGAGCAAC	85-105	sly-miR5303	2	0	21	21	2
spiLA1589-MIR6145b-1	UUAUUUUUAGCUUACGUGGCACUAUCAUGUGGGCCCAACGAUGGUUGACUUUCUUUUCGAACUAGUGUCACGUAGGCUUAAAAGGG	86	spiLA1589-miR6145b-1-5p	UUAGCUUACGUGGCACUAUCA	7-27	nta-miR6145b	5	0	21	21	1
spiLA1589-MIR7980b-2	GCCAUGAGAUACCGUAUCGUGGCCUUUGGCUAUGAGAUAUCAUAUCACGAUAUGAAAUCGUGAGAUUGAAUUCGUGUUUGGACAUAUAAUUUUACGUUGAUUUCAUCUCAUGAUUUUAUAUAAUGAGAUGUGAUUUCGUAUUCUUCAAAAAUCAUGAUAUGGGAAUUUCAUAUC	174	spiLA1589-miR7980b-2-5p	GAGAUUGAAUUCGUGUUUGGACAU	62-85	stu-miR7980b-3p	3	0	24	24	1
			spiLA1589-miR1886h-2-3p	AUUUUACGUUGAUUUCAUCUCAUG	89-112	stu-miR1886h	0	0	24	24	1
spiLA1589-MIR7822-1	CGUUAAUUUUAGGUAUGGACAAGUAAACAUUUAAACUUGUAUAAAAUUGAACAAAUAGACACAUUUGUCCUACAUGACACCCUACAUGAAAAUUGUGUCCUACGCGGCGUCCGAUACAUAUUAUGUCAUGUAGAACACGUGUGUUUACUUGUUCAGUUAUAUACAGUUUUAAGUGCCUACUUGUGUACACUCAAAGUUAGAG	202	spiLA1589-miR7822-1-5p	UAUAAAAUUGAACAAAUAGAC	40-60	ptc-miR7822	5	0	21	21	1
spiLA1589-MIR5274b	AAAAAGGAAAAAUAAUAUUCAGCACUAUCAUUAAUGAUAUGCAUAUACCCUCCGUCAUACUUUUAGGGCAGUGGUGAACAUAUAUGUCAUUCACUCUAACGAAAGACUAAAUAGGGUCACGUGACACAAUCUUAUUCAUCGAUAAUAUUUAAUAAAUAUCGGGUCAGUCGAUGAGAUUAUGUCAUGUAUAUGUCCGUAUUCAUAAAGGGUAUAUAUGCUCUAAUUUUUGGACGGCAUGAGCACCAAUGUCUCAAAAGUAUGACGGCAGAUAUUUUACAUAUCAUUUACGAUAGUUCGAAAAUAUAUUCGUCCUUCCC	317	spiLA1589-miR5274b-5p	CAUAUACCCUCCGUCAUACUU	42-62	mtr-miR5274b-3p	4	0	21	21	1
			spiLA1589-miR8006-3p	UAAUUUUUGGACGGCAUGAGCACC	221-244	stu-miR8006-5p	4	0	24	24	1
spiLA1589-MIR7992-2	CUGGCAAGUAAGCGCUCCAACUUUGUGUAUGCACAUCUAGACGCCAAGUUGAGGUGUCUAGAUGUGCACUCUCAAAGUUGGAGUGCGUACUUGCUAG	97	spiLA1589-miR7992-2-5p	UUUGUGUAUGCACAUCUAGACGCC	22-45	stu-miR7992-5p	5	0	24	24	1
			spiLA1589-miR1033e-2-3p	UGAGGUGUCUAGAUGUGCACU	50-70	ppt-miR1033e	5	0	21	21	1
spiLA1589-MIR1069-1	GUGUGUUAAUGGCCUUCAUAAUCCCAAAUAAGCUGAGUUAAUUCAAAGUGCUUAUUUGAUUCAUGGGAGGCCUAAAUCAAUU	82	spiLA1589-miR1069-1-3p	AGUUAAUUCAAAGUGCUUAUU	36-56	ppt-miR1069-3p	5	0	21	21	2
spiLA1589-MIR7983-1	UGUAUCUUGAACAUGCCACCACUACAACAAAAAUGAUCAUUAGCGACAAUUAAUUCAGAAUUAGUUGCUGCUAAAUAUGUAUUUUUAGCGGCAAUUGACGCUCUUUGUAUAUGUCCCUAAAGAUUUUAGCGACAUCGUUUCUAAUGGCACUUAAAUAAUGCCGGUAAAUACUUUAACACUCUUUAUUAAUGUCUAUAUCUAAUGCCGCUAAAAGUUGUUUUUGUUGUAGUUCACGUGGAAAGUUGAAAUUAA	252	spiLA1589-miR7983-1-3p	AAUAAUGCCGGUAAAUACUUUAAC	154-177	stu-miR7983-3p	2	0	24	24	1
spiLA1589-MIR1046-1	ACAAAAAAGAAAAAAAGGAUACGUGUGAGGAGGAUCAAAUAUACCCACUAUAUGGAUUUUUAUUUUUUCACGUCCGUUAGAGGAAAAAGGUAUAUAUGAGCCAUUUGUAUAAUAGUUGGGGUAUAUAUGAACCACUUUCAUAACGAGAGAUAUAUCAACUCUAAAUGACAAAGUGGAGGGGAAUGUUAGGCCCUUUUCCCUAUUAAUUAUACUUAAUAAAAUAUUUCAGUUCGAUUGAUUCGGUUGUAUUGCCUCCUCCCCGUACUUUUCUUGGUUUUCAC	281	spiLA1589-miR1046-1-5p	UGGAUUUUUAUUUUUUCACG	53-72	ppt-miR1046-5p	4	0	20	20	1
			spiLA1589-miR7722-1-3p	CCUCCUCCCCGUACUUUUCUU	252-272	bdi-miR7722-5p	4	0	21	21	2
spiLA1589-MIR8048	GAUCAAGGCUUACUUCGAGCGAAUAUCAACCAGAUCUUGAUGAUGAGGCUAUAGUAGCAAAUAUCGAAAACAUUUUAACAUUAGAUUGUCUUGGUAAUUAACAAGAACAUGAACAACAAUAAUAUGUAAUUUUAUUUCUCAAGUUUAAUUGAUGAAUUAAGAAUAUGUAAAGGCCUACAAGACACUAUUACAAACUUCACUUUGUUAUAUUAAUCAAGCAAUACAUUGAUGAAAUGUAAGAUCUUUGCUUCAUUUUGCCUCUUUCAUCAUGAGGACUAUAGUUUCAUCUAGUCGAGUUAGCUUGCAC	307	spiLA1589-miR8048-5p	AGAUUGUCUUGGUAAUUAACA	83-103	stu-miR8048-3p	5	0	21	21	1
			spiLA1589-miR11077b-3p	UAAUUGAUGAAUUAAGAAUAU	146-166	lja-miR11077b-5p	5	0	21	21	3
spiLA1589-MIR7823-1	AAAUAAUGCAUGCAUUAGCUUGAUGUAUUAGUAGUACCUUGUUUGGUACACUUUUCUAACCUAUGCAUCACUAAUGCU	88	spiLA1589-miR7823-1-5p	AUGCAUGCAUUAGCUUGAUGU	6-26	ptc-miR7823	5	0	21	21	2

	UGUAUUAGUA										
spiLA1589-MIR5658-1	UGCGGUGCGGUAAAGAUGUUGAUGAUGAAGAGAUUUUUUUUUGAGAAUGUAUUUUUUGGAUGACGGAAUCAGUCUCCAAAUCGGAGAAUUGUUAGGUAGUGGAUCCUGAUUAAUAGUUGAUGUACUUUAACAAAAAAUACUCUGAUUUAUUAAUAUAUGUACCCAACCUCC	171	spiLA1589-miR5658-1-5p	AAGAUGUUGAUGAUGAAGAGA	13-33	ath-miR5658	4	0	21	21	1
			spiLA1589-miR12162-1-3p	AAUACUCUGAUUUAUUAAUAU	136-156	aof-miR12162	5	0	21	21	3
spiLA1589-MIR159c	CCAAGUUUACUUUGGGCUAAAAUGGAUUGGGUUAAAGUGAGCUAACCCAAUUCAAUUUGACCCGAUUAAUCUCAA	75	spiLA1589-miR159c-3p	AUUGGGUUAAAGUGAGCUAAC	26-46	fve-miR159c	5	0	21	21	1
spiLA1589-MIR5014a-1	AUUUGAGUGUGCAGAAGUAGACACUUAAACUUGUAUAAAAUUGAACAAUUAGACACAAGUCCUACAUGACAUUAAUAUACGUCGGAUGCCACGUAGGACACAAAAUUUCGAUGUAAGGUGUCAUGCAGGACGAGUGUGUCUAUUUAUUCAAUUAUAUACAAAUUUAAGUUUUACUUGUGCAUACCCAAAAU	192	spiLA1589-miR5014a-1-5p	ACACUUAAACUUGUAUAAAAU	22-42	ath-miR5014a-5p	5	0	21	21	1
spiLA1589-MIR169j-5	GAAAAAGAAGAGAAGUCUUACAUGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAUAGUCUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUAUCUUGACAUGCUCUUUUCUUUUAUGCAAGAUAUCUUUUUAAA	172	spiLA1589-miR169j-5-5p	UAGCCAAGGAUGACUUGCCUGC	48-69	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169e-5-3p	CAGGCAGUCUCCUUGGCUAUC	112-132	csi-miR169e-3p	2	0	21	21	1
spiLA1589-MIR169j-6	UUAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCGUACUUGAAAAGGUCUUUCAUAUGUCCUUUCGUUUUUGGGGUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUUCAUGCAAGGCUUUCUCUUCUUUCGU	178	spiLA1589-miR169j-6-5p	UAGCCAAGGAUGACUUGCCUGC	45-66	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169d-6-3p	GCAGGUCAUCUUUAGCUAACU	115-135	stu-miR169d-3p	0	0	21	21	1
spiLA1589-MIR395g-1	UUGAAGUGUUGAGGAGAAUUUCCAAGCUCACUUUGAAAUUUACACAAACAAAUAGAAGUGUUAGAGUAUUAAUGGGAGACUGAUUCCCGAGAGUUUCCUUGACCACUUCGUGAGGAUUUAAUUACUUUGUUGUUUUAUGCCUUGCUGAAGUGUUUGGGGGAACUUUCGGGUUCACUUUAAAAUUUACACAAAUAAGUAGAAGUAAAUGAGUACUAAUGGAAGAUGAUAGAUGAAUGCAACGAUUUAUUUUAUAUCUAUCAAGGUGUUUUCGAGAUUUCCCUUGACCACUUAAU	293	spiLA1589-miR395g-1-3p	UGAAGUGUUUGGGGGAACUUU	146-166	gma-miR395g	0	0	21	21	1
spiLA1589-MIR5181c	UUAUACUCCCUCCGUCCCAAUUUAAGUGUCCUAGUUUAACUGUGCACUAAGUUUAUGAAAGGGGAGACACUGACUCUUUUAGUCUUAAAUUAAAGAUGCAUGUGUGUAUCCCUUUGAUUUUUGGUCUUAGACCUGCCAUGUAGAAUGUUGGAACUGGAAAGGUUACUAAAUAUAGAAAGACGCUCUUUUUGGGACAGAUCAAAAGGAAAAUAAGACAACUUAAACUUGGGACGGAGGGAGUACCA	245	spiLA1589-miR5181c-5p	CCUCCGUCCCAAUUUAAGUGU	9-29	bdi-miR5181c-5p	5	0	21	21	1
			spiLA1589-miR5049-3p	AACUUGGGACGGAGGGAGUAC	223-243	tae-miR5049-3p	4	0	21	21	1
spiLA1589-MIR167c-1	UAGGCCUAAAAAAGUUUUGAGAAUGUGAAGAACUAACUGAAUUCUAGUAAACUAAUGGGUGAAAGGAAACCCACUAGUGAACUCCCACAUACAUGGUGAAAAAAUAUACGAAGAAAUCCUUUUAAAUUUAGGACUAAAAUUUGAAGAACACUUCUUCUUAUUCUUGAGAGGACAUGUUGAUAGUUUCCUCUUGUAUUUGGUCAAAGUAGGAUUAUUUUUCGAGAAUGAGGGAGUUGGGUAGAUUCUUACUAUAUUGUUAGGCUUA	265	spiLA1589-miR167c-1-3p	AGGACAUGUUGAUAGUUUCCU	169-189	aly-miR167c-3p	5	0	21	21	1
spiLA1589-MIR5773	GAUCCAUCCACCUCACCCGACCCAUUAAAAAAUAUGAUAUGACCCAUUUUAUUGUCUUUAAUCCUAAAUUAAUUCCUCUCUUUAAACCUUGAAGGGAUUCAAGACAAAAUAAAAUGGGUCAUAUGAUAUUUUUUAAUGGGUCGGGUUAGGUGGGUGGAUA	160	spiLA1589-miR5773-3p	UUUUUAAUGGGUCGGGUUAGGU	130-151	gma-miR5773	5	0	22	22	1
spiLA1589-MIR5568g	GCGAUAACGUUUUAUGAUUUGUAAGAUUCCAAUGUAGCAGGAUUUUAUUCUUAAUCUGAUGCCCCGUGAUUAAAUAAACAUAAAACGUAAUUGA	94	spiLA1589-miR5568g-5p	AUAACGUUUUAUGAUUUGUAA	4-24	sbi-miR5568g-3p	5	0	21	21	1
			spiLA1589-miR6273-3p	AAUGUAGCAGGAUUUUAUUCU	31-51	ppe-miR6273	4	0	21	21	1
spiLA1589-MIR390-1	UAUGCAUGGAGAAUCUGUAAAGCUCAGGAGGGAUAGCGCCAUGGAUGACUCAAUUCGAUUUUUGUACACAUCUUUAGC	115	spiLA1589-miR390-1-5p	AAGCUCAGGAGGGAUAGCGCC	20-40	aof-miR390	0	0	21	21	1

	GCUAUCCAUCCUGAGUUUCACGGCUUUUUCAUGCUUU										
			spiLA1589-miR390a-1-3p	CGCUAUCCAUCCUGAGUUUCA	78-98	cas-miR390a-3p	0	0	21	21	1
spiLA1589-MIR477-3	CAUUAUCAAUGUAAAUGGUACAGAGUUAUAUUUUGACUUAAAAGAGUUAGUUGUUGUAACCGGUCUAAAAUCUGGACCAAAUUCUGAUUUUGUUUCUGAUCCAUCUGUUCCCAAUAGAUUAAUUGCAGAAAAUUUCAGAGAUUUUGACAAAGUCCCCAAGUCAAAUUUUUACCACAAGUUUAAAUUGGAAAACUUUUGGGAAGAAGAUGACCGUUUAUAAUCAGUUCAUAUAAUUGAUACAC	242	spiLA1589-miR477-3-3p	AUUGGAAAACUUUUGGGAAGA	184-204	cpa-miR477	5	0	21	21	1
spiLA1589-MIR169r-3	UUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCA	184	spiLA1589-miR169r-3-5p	CAGCCAAGGAUGACUUGCCGG	63-83	csi-miR169r-5p	0	0	21	21	1
spiLA1589-MIR8001b-2	GAUUUUUUAUGAAACAGCUGUUGUUGUAAACACUACAAGAAAAGGGUAAAUUAAAUGGGGAUUAGUAUGAAAAUUUGCAGGGAUUACCCUGUAGUUCACACUUUUCUUGUAGUGAAA	90	spiLA1589-miR8001b-2-3p	AUGGGGAUUAGUAUGAAAAUUUGC	28-51	stu-miR8001b-5p	0	0	24	24	1
spiLA1589-MIR9472-1	CCAUAGAUCUACUCGAUUUAUUUUUCAGUAGACGUUGUGAAUAAUUGAUAAAUACAGGUAUACAGAGGUCUUAAUAUAGUCAGAACCUAGAAAUAUGUGUAACUAGAUUCAGACCUUUGUACACUUGUAUUCUGUUGCUAUUCACAAUCUCUGCUGAAAAUGAUUGACUAGAUCUACGA	180	spiLA1589-miR9472-1-5p	UUUCAGUAGACGUUGUGAAUA	23-43	sly-miR9472-5p	0	0	21	21	1
			spiLA1589-miR9472-1-3p	UUCACAAUCUCUGCUGAAAAA	141-161	sly-miR9472-3p	0	0	21	21	1
spiLA1589-MIR11039	UUCUCUACUUGUUAUGAGGAUAUGCAUGGUAUGUGUCUAUAUGAUGUAGUCUUAUUCUUAUGUGAACUAUGUGAGUCUUAGUGACUAUAGGAUGGAAAUUGUUGAUAGUAAUUGAGUUGUACUUAUGCAUUAUGUUGAUGUAUGAAGUGUUAAGAUUUGUGGUGUCGUGAAGGGUUUACAGAAUGUAUGGAGUUAUGGGGCUUCAUAUGUUCAUUGAACUAGUAGACUA	229	spiLA1589-miR11039-3p	UGGAAAUUGUUGAUAGUAAUUGA	93-115	seu-miR11039	2	0	23	23	1
spiLA1589-MIR8006-1	CAUAUAUAUACUCUAGUUUUUGGAUUACAGAGACACCAAUGUCCCAAAAAUAUGACAGAGAGUAUUUACCUAUCAUUUACCAUAAUGACAAUUUUUUUGGUAAAACAAUAAACUCUACAAAAUGUAUAUUUUUAAGGAAAAAGGACAAAUAUAUCUCAAGCUAUCGUAAAUGGUAUGCAGAUACCCUCCGUCAUAUUUUUGGAACAUUAGUGCCCUGCCGUCCAAAAACUAGAGCAAUAUGCC	243	spiLA1589-miR8006-1-5p	UAGUUUUUGGAUUACAGAGACACC	14-37	stu-miR8006-5p	4	0	24	24	1
			spiLA1589-miR8006-1-3p	UGCCCUGCCGUCCAAAAACUAGA	211-233	stu-miR8006-3p	1	0	23	23	1
spiLA1589-MIR5165	UAAGACUAUAAAUAUGAGAUUAGGUCCCUCUCCUAGCUUAAGAAAAAGAUGUAUUCCCAUAAGGUGGAUACGUCAUAAGCUAAAGGAGAGGAAGACUCAGCCUAGCUUAUAUUCAGUAAAACAUACCUUGAACUUUGAUAGAAGAAUCAUAUAUACC	117	spiLA1589-miR5165-5p	CCUAGCUUAAGAAAAAGAUGU	32-52	bdi-miR5165-3p	5	0	21	21	1
spiLA1589-MIR10542-1	CAUAAAUAAUUUAAAAAAAUUAAAAGUACAAAUAUAAACUUAAAACUGUUUUUUUAACUUCCGUUAAAUGAAGGAUAUGUGUGAGCUCAUUUUGUAACGGCAGGGGUAUAUGUGAGCCAUUUGUAUAACGGUAAGGACAUAUAUGAGUCACUUUCAUAACGAGGGGUAUAUCAGCUCCAAGUGACAAAGUUGAGGGGUAUGUCAA	245	spiLA1589-miR10542-1-5p	UAGAAGAAUCAUAUAUACCCAUA	22-44	sly-miR10542	1	0	23	23	1
			spiLA1589-miR395b-1-3p	AUGAAGGAUAUGUGUGAGCUC	108-128	aof-miR395b	5	0	21	21	1
spiLA1589-MIR10542-2	UAGAAGAAUCAUAUAUACCCCUAAAUAACUUUUUUAAAAAAAUUAGAAGUAAUAAAUAUAAAUUUAAAGCUAAUUUUUUAACUUCCGUUAUAUGAAGGGUAUAUGUGAGCAGCCGUUUGUAUAGCGGUAAGGGCAUAUAUGAGCUACUUUUAUAACGAGGGAUAUAUCAGCUCUAAAUGACAAAGUUGAGGGGUAUAUCAGACCCUUUUC	211	spiLA1589-miR10542-2-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
spiLA1589-MIR867-1	AUAAAAACAAGCUUUUAACGGUAAUUGUUGUCAAUUUGUGUUAUGAAAAUCAGAAAUUACUGGUUAUAAUAAAUCAUUCAGAAACACGAAGUAUCUGAGAUUUUUAGAACCAGUAAGUAAGAUGAACAUAAUUUAUUUGUAAAAAAUAAUUGAAUCUGUAAAAACUUACCAGAAUCUGGGCUGCCUCAAGGUCCUCUAGAACCUGGUCCUUGGGGGUAGUACGUCGAUAUUUACACCCAAAAGCAUCUAUAUCCAGUCCCAGAGGUUAUUUUAGGA	313	spiLA1589-miR867-1-5p	AUGAACAUAAUUUAUUUGUAA	122-142	ath-miR867	5	0	21	21	2

	CUAUGAUCAUUAAAUUAAACCUUAAACUAGUUUUAUG										
			spiLA1589-miR3433-1-3p	GGUUAUUUUAGGACUAUGAUC	264-284	aly-miR3433-5p	5	0	21	21	1
spiLA1589-MIR10519-1	CCAAAAAGUAGAUGAAGUAACAAGUUAGAAAUUUGAUUUCCAACUGAAAUUUAUGUGUGGAUCGAUUUCAAAAGUUAGAAAUUUGAUUUCCAACUGAAAUUUGUUUUUCGAUAUUGGAUUUUGAUAGUUAAUUUUUGGUUGCAGUGAUGCAUGUGUGGAUCGAUUUCAAUCGUGAAAGUGUGGGUCGAUUUCAUUCAGCAAAAAUCGUGACUGACUUGAGUUCAAAGGUUAGUUUUUUCUUCAUUUAUUUUAUU	254	spiLA1589-miR10519-1-5p	UUUCAAAAGUUAGAAAUU	66-83	tae-miR10519	3	0	18	18	1
			spiLA1589-miR1515b-1-3p	UAAUUUUUGGUUGCAGUGAUGC	129-150	csi-miR1515b-5p	5	0	22	22	1
spiLA1589-MIR5021-1	AAUAGAGAAUAAUGAUCAAUCUUUUUUUUUAGAUGUGCUUUACUGUGAAGAAGAAGAAGAAAAAUGGGGUGAUUUGUUAGAGGAUGAAGAAGGGGUUAUUAUUAACCCAUUGUUGUUAUCUUCCGAAGGAACAACAAAAACUAAUUCUUUAUUAUUAUUACCUCUGCU	168	spiLA1589-miR5021-1-5p	UGUGAAGAAGAAGAAGAAAA	44-63	ath-miR5021	1	0	20	20	1
spiLA1589-MIR5303-1	CAACUAUGUUCUCGGACUUUCCAAAAGUGCUGCUGCACUGUGUCGGAUCAUCCAAAAAUGCACUUUUUUUGGAAGACACGACACACAUCUGAAGGUAUUUUGAAGAGUUCGUGCAACACAGGUA	124	spiLA1589-miR5303-1-3p	AUUUUGAAGAGUUCGUGCAAC	97-117	sly-miR5303	2	0	21	21	2
spiLA1589-MIR11106	GAAAACUAGUACUUACUUCCAAUGUCCAACAAUAGUUGUCCAUUAUUGACUUGACACAUGAAUUAGAAACAGUAAAUGAUAAGAGUAAUUUUACCAAAUCACCCUUAUUAAGUACAAGUCAUCUAACAUUAUAAAAUGGGACAGAGGAAGAAGUAUUUAAUAGCAAGGGUAAAAUAGACAUAACAUGGUAAACUAUUCAUUGCUUUUAUGAACUUCACAAGUAUUGUUAACAUUCCAAAGUAAUAUGAUGGACAAGUAAAGAUGGACGAAAGGAGUAAUUAACUGUUAUG	290	spiLA1589-miR11106-5p	UAGAAACAGUAAAUGAUAAGA	64-84	lja-miR11106-3p	5	0	21	21	1
			spiLA1589-miR1130b-3p	CAUUAUAAAAUGGGACAGAGG	127-147	tae-miR1130b-3p	5	0	21	21	3
spiLA1589-MIR11115	AAACUCAAGCUUUAACACUCUAACUUGUCUACCAGUUGAUUCAGUUCCCUUUGGUUAGGGACUGUCUUCAUUGGUUAUGGUGGUCAACUGGUAGGCAAGUUAGAGUUUUUAAGCUUGAGCUG	122	spiLA1589-miR11115-3p	UGGUAGGCAAGUUAGAGUUUU	89-109	lja-miR11115-5p	5	0	21	21	1
spiLA1589-MIR399b-3	UGAUGAAGCGGAAGCAUGAGAAAGGAAGUCGUUGGUGAAUGAAAAUAAGGGAAAUAGUGAUAGGGCUACUCUCUAUUGGCAUGCGUUAAUAUAUGUACAGUGACUCCAAUUCACUGUAUCGCAUAUUUUAACCGAUACGCCAAAGGAGAGCUGCCCUGCUACUGUCUCUGCUUAAUAUAAUAACUCAAAGGUCCGUUCUUAAUACUCCGAUGCAGAA	217	spiLA1589-miR399b-3-5p	GGGCUACUCUCUAUUGGCAUG	63-83	sly-miR399b	0	0	21	21	1
			spiLA1589-miR399o-3-3p	CGCCAAAGGAGAGCUGCCCUG	138-158	stu-miR399o-3p	0	0	21	21	1
spiLA1589-MIR160e-1	UCUUCAACGGAUAACUAUAUCCUUCAAUUUUGAGUGUGCACAAGUAAAUACUUAAGUUUAUAUAUGACCAAGUAGACAUAUGUAUUCUACAUGGUAUAAUACGCAUAAGACGUCAUGUAGGAUACAAAAUUUUCAUGUAGGGUGUCAUGUAGGACAAAUGUGUCAAUGUAUUCAAUUUUAUACAAGUUUAAAUGUCUACUCGUGCACAUUCAAAAUUAAUAAAGAUCAUAAUUAUCGAUUGACGC	245	spiLA1589-miR160e-1-3p	UCAUGUAGGGUGUCAUGUAGG	133-153	bdi-miR160e-3p	5	0	21	21	2
spiLA1589-MIR11295	AUGCAAGUUUAGAUCUAAUUUUCAACGAUUUAUCUCUAUUCGUUGGAUCAUAUUUCUUCUUCGCUCGUGAAAAUGUUUAACUAGAAUAAAAUUUGAUCGCUCUUAUUGAAUUUCUCUAUUGAGAAGUUCGUUUUUAUCUUCUAUUUGAAGAAAUUGUUGCUCGAAAAUGAUGGGUUGUUGUGGUGAACAAAUCUACGUGAAUUGAUAAAGGUGAAAUGGAGAUGAAGAGUUAAUAUUUGGUGAAAAUGGUGGGUCAACUUGAGU	264	spiLA1589-miR11295-5p	CUUAUUGAAUUUCUCUAUUGAG	102-123	fve-miR11295	5	0	22	22	1
			spiLA1589-miR8183-3p	UCUAUUUGAAGAAAUUGUUGC	140-160	ath-miR8183	5	0	21	21	1
spiLA1589-MIR11563-1	UUGUUCUUAUUUUAUUAUGUUUACGAUUUCAAAUCAUGAUAGUUAAGAUUAUACAACUUUUCCCUCAUUUCGCGGCUAGGAUUUCUUAAGUUCCUUCAGAGCUGGAUUUUAAAGUGGAUAUUCGUGAUUGUAGGUUAGUAAAUCUUUUUUCUUAUUUAUUAUGCUUACGAUUUCAAAGCAUGCUAGUUAGAAUUUCACAACUUUUCUCGUAUUUCGUGGCUAGCGUUUCAUAGC	295	spiLA1589-miR11563-1-3p	UUCUCGUAUUUCGUGGCUAGC	204-224	pab-miR11563	3	0	21	21	1

spiLA1589-MIR5574	UUUUUACGGGCUGGGUUUCAAGUGGAUAUUCAUGGUUGUAAUCAUAAUGAAAUAAGAAAAAUUGAAACUUUAUGCACAAAAAUUGCAGCUUCCUCUCCGGUUUGAUCAACAACUAGAAGCAAAAGAAGGUUGUCGAAUUUCCACCAAAAAAAAAUAGCCUUCCUUUGCUUCUAGAAAUUCAGAGUGUUGAUCAAACCCGAGAGGAAUCUGCAGUUUUUGUGCAUAAAGUUUCAA	173	spiLA1589-miR5574-5p	UUUGAUCAACAACUAGAAGCA	40-60	rgl-miR5574	5	0	21	21	1
spiLA1589-MIR7987-1	ACAAGUACCAACACUAGCUGAUGCUAUUGAUGACAAAAAUUGGUUUUCUUGCAAGAUCAAUUUGUGUCAAUCUAGUGUUGAUACUUAGUUUUAGUUUAGGAAUAAAUGUUUGUUGAUUGUAAGGACCAACACUAGUUGAUCUUAUUGAUGACAAAAAUUAAUGUUCUUGCAAGAUCGAGUUGUGUCCAUCUAGUGUUGAUACUUAGCUUUAAUUUAGUAAUAAUGGUGUUUGUUAGGCAUAAGUACCAACACUAGUUGAUCCUAUUGAUGAAAAAUUGAUUUUCUUGCAAGAUCAAUUUGUGUCCAUCUAGUUUUGAUACUAGC	324	spiLA1589-miR7987-1-5p	ACACUAGUUGAUCUUAUUGAUGAC	129-152	stu-miR7987	0	0	24	24	1
			spiLA1589-miR5142-1-3p	CUAUUGAUGAAAAAUUGAU	262-280	rgl-miR5142	5	0	19	19	2
spiLA1589-MIR2083	GGCAGACUGACGAGGGCAAGUAAAACAUGACUGACAGACUUCUAAACAGACAAAUUUUUGAAACAGAAGUGCAUAUGAUAUAUCAGACGAAUCUCAUAUCUCCAUGAGGGAGGAAAGUGAAUUUAUUAUGCACACUUCUGUUUCAGAAGCUUGUCAAUUUAGAAGUCUGUCAAUCCUGCUUGACCUGCCCUCAUCAGUCUAGA	203	spiLA1589-miR2083-5p	AGACUGACGAGGGCAAGUAAA	4-24	ppt-miR2083-3p	4	0	21	21	1
spiLA1589-MIR7997c-4	UGGAAAAUUUCUAUGUUGCUCGGACUCUUUAAAAAUGUUGAUGAGUGUGUGUUGGAUACUCCAAAAGUAGUGCAUUUUGGAGGAUACGACACGGGUGUGGUGAUAAUUUUGAGAGUUUGAGUAACGUAGGCAAAAUUUAUU	141	spiLA1589-miR7997c-4-5p	AUGUUGCUCGGACUCUUUAAAAAU	13-36	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303e-4-3p	UUUUGGAGGAUACGACACGGGUGU	75-98	stu-miR5303e	3	0	24	24	1
spiLA1589-MIR1106	AUAUCAAACUUCAUGGAGGACCUUAUACCCCCUUACACUUUUUAAAAGUGCAUUUUAAAGGUAUAUAUGUGUCCACGUGGACACAUUACUAUUUAAAAUGUUUAUGAUGUCCACGUGGACACAUAUAUAUCUUUAAAAUACAUUAUUUAAUAGUACAGGGACAUGAAAGGUCCUACAUAAACUUCGAGAU	190	spiLA1589-miR1106-5p	UUUAAAGGUAUAUAUGUGUCC	54-74	smo-miR1106	5	0	21	21	1
			spiLA1589-miR5780c-3p	UUUAAUAGUACAGGGACAUGAA	146-167	gma-miR5780c	5	0	22	22	1
spiLA1589-MIR11068c-1	UAUUCUAAUUCAUGGAUUAGUUAUACCUCAUACAAAAUCUUAUUUUAUUCCUAGAAAAGGGUGGGAUAACUAAUCCAAGGUUUAACAAUCCUUGGAUUAGACCC	104	spiLA1589-miR11068c-1-3p	AUAACUAAUCCAAGGUUUA	66-84	lja-miR11068c-5p	5	0	19	19	1
spiLA1589-MIR8668	UGGUCGCCUUGGCUUACAGAAACAUUUUGGAAUGAUGACUAUAAUGAGUGGGAUAAUCUGAGAAAUGUUUUUGUACAAGGAGAUAU	86	spiLA1589-miR8668-5p	UUUUGGAAUGAUGACUAUAA	25-44	gra-miR8668	4	0	20	20	1
			spiLA1589-miR11323-3p	UUUGGAAUGAUGACUAUAAUG	26-46	ppt-miR11323	5	0	21	21	1
spiLA1589-MIR399f-1	UGGGGAGUAAGAAAUAACAGUGCAAUUCUCCUUUGGCAAAUGAAUAUGCAAACCCUAUAUAUAUAUAUAUAUAUAUGUUUUGCAUACACAUUAUAUUAUCUUUGCCAAAGGAGAAUUGCCCUGUCAUUCUUCUCCUCG	138	spiLA1589-miR399f-1-5p	GUGCAAUUCUCCUUUGGCAAA	20-40	csi-miR399f-5p	2	0	21	21	1
			spiLA1589-miR399a-1-3p	UGCCAAAGGAGAAUUGCCCUG	103-123	ata-miR399a-3p	0	0	21	21	1
spiLA1589-MIR7997c-5	GUCUAUAUAGCUCGGACUCUUUAAAAAUGUCGGUGCACCCAUGUUGGAUCCAACCCAAAUCCUUUGACAUUUUGAAGAGUUCGAGCAACAUAAGU	95	spiLA1589-miR7997c-5-5p	AUAUAGCUCGGACUCUUUAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-5-3p	AUUUUGAAGAGUUCGAGCAAC	69-89	sly-miR5303	1	0	21	21	2
spiLA1589-MIR1521b-1	AAUUAAUGAUAUACAAAUAUUUUUCGUCAUACUUUGGGAUAUUGGUGCUCUUGUCGUUAAAAAAUUAAAAUGUAUAUACCCUUUAUACUAAGAGACAUACACAUGUCAUAAUCUUAUCCACUGAUUUGAUUUUUAAUCAACGGAUAACGUGUUCCUUUUUAGUCUUCCGUUACAGUUAGAGUAAAGGGCAUAUAUGCUCAAGUUUUGGAACGGAAAGGACACCAAUGUCCCAAAAGUAUGACGAAGGUAUCUGCAUACCAUGUACGA	267	spiLA1589-miR1521b-1-5p	GACAUACACAUGUCAUAAUCUUA	94-116	gma-miR1521b	5	0	23	23	1
spiLA1589-MIR1888b-1	AUAGGGUUGGGCUAAGAUUUUUGGAGCCCAUUAAAAAAAAGGUCUUUUUAGCCCAGCCUGAAUAAGCCUGUUGAUUUGAUGGGUUUGAGAAAUAUAGGUAGGGCCAACCCGUG	113	spiLA1589-miR1888b-1-5p	UUGGGCUAAGAUUUUUGGAGC	7-27	ath-miR1888b	4	0	21	21	1

			spiLA1589-miR4249-1-3p	UGGGUUUGAGAAAUAUAGGUA	80-100	aly-miR4249	5	0	21	21	1
spiLA1589-MIR399a-1	AGCAAGAAUCGCAGGUUAUUCUUCUCUGGCAAGAAAACUAUGGUUAUGCAUAAAUUAUUUCUUGCCAAGGGAGAAUUGCCCUACGUUUCUUUAU	94	spiLA1589-miR399a-1-3p	UGCCAAGGGAGAAUUGCCCUA	63-83	ata-miR399a-3p	2	0	21	21	1
spiLA1589-MIR11078d	AAGUGCUAUUCUUAUUUUUGCUUAUCUGGAGUUACAAGUUGAGGAUCUUAUUGGUUAACGAUAGUUAUUAUCCCACUGUAAUAAAUACUUCUAACCAUGAAGAUCCUCAACUUGUCGCUUCAGAUAAGAAAAUUAGUCAUUGCAUGG	147	spiLA1589-miR11078d-5p	GGAUCUUAUUGGUUAACGAU	43-62	lja-miR11078d-3p	5	0	20	20	3
spiLA1589-MIR9744	GCCUCUCUCACUUUAUAUACAAACACAAAUGUACAAAUGUGUUUGUACAAAAGUGAUAUAAAAUGCAUACAUACAUCUCUUUUCGUCUGCCUCUCCCCUAGAGAAUCUCGUUUGCCUCUCUCACUCACCUCUCUCACUUUAUACAAACACAAAUAUAUUGUCUCUGUGUUUGUAUAAAGCGAGAGAAAA	189	spiLA1589-miR9744-5p	AAGUGAUAUAAAAUGCAUACA	51-71	gma-miR9744	5	0	21	21	1
			spiLA1589-miR6277-3p	UGUGUUUGUAUAAAGCGAGAG	165-185	ppe-miR6277	5	0	21	21	1
spiLA1589-MIR7993b	UGUGUGUUCCCAUUUGUAUGUGAGGUAGUUAAGUUAACCACAUAAAAUAUAUUGUCAUCUCCUUUAAUUCUAUGCAUUCGCCUUACCAAGUCGUAAACACCCAAGAUGUUUUCUACAAAGGUUGAUGUAUAUAAUUAAAGGAGACAGCAUAUUUUUAUAUAGUUAACUUAACUACAUAAUAGACAAAUGAAAACACGCU	199	spiLA1589-miR7993b-5p	UUAAGUUAACCACAUAAAAUAUAU	29-52	stu-miR7993b-5p	1	0	24	24	1
			spiLA1589-miR821d-3p	AAGUCGUAAACACCCAAGAUG	88-108	sbi-miR821d	5	0	21	21	1
spiLA1589-MIR390-2	GAAAAAGAGUGUCGAGGGAUCUGUAAAGCUCAGGAGGGAUAGCGCCAUGAAAAAUAAUAUGAUGUUUUCUUUUUAAUUAUUUUAUUGGUACAUAAAUUCAUCUUUUUAAUUGUUAUUAUUUUCGGUAUAAUAAAUUCAUCAAUUAUAUUUGGCGCUAUCCAUCCUGAGUUCUACGGCUCCUUCAUACUUUUUGC	194	spiLA1589-miR390-2-5p	AAGCUCAGGAGGGAUAGCGCC	26-46	aof-miR390	0	0	21	21	1
			spiLA1589-miR390a-2-3p	CGCUAUCCAUCCUGAGUUCUA	153-173	sly-miR390a-3p	1	0	21	21	1
spiLA1589-MIR172a-1	AAACACUGUCUCAAAUGUAAAUCUUCAGGUCGCCAAAGUCUAUAUCCUCCAAAAAGUAGUGCAUUUUUGGAGUAGAACAACAUAGACAUUGACGACAUGAAGAUUUACAUCUGAGACAGUGCAU	124	spiLA1589-miR172a-1-3p	UUGACGACAUGAAGAUUUACA	89-109	vca-miR172a-5p	5	0	21	21	2
spiLA1589-MIR7997c-6	CUUCUAUGUUGCUCAGACUCUUCAAAAAUGUCGCCAUGUGCAUGUUGGAUCCUUCAAAAGCAGUACGUCUUUUUAUGGAUACCACAGGUGUGGCGACAUUAUUGGAGAGUCCGAGCAACAUAGCUG	126	spiLA1589-miR7997c-6-5p	AUGUUGCUCAGACUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303h-6-3p	GACAUUAUUGGAGAGUCCGAGCAA	95-118	stu-miR5303h	4	0	24	24	2
spiLA1589-MIR8643b	AUACACAUCUGAAUAUUAAGAUCUGCAUUAAUAUCCAUGUGUUUCGAUCUGAAUGCACAUCUACAUAUUAAGAUGUGGUC	80	spiLA1589-miR8643b-3p	ACAUAUUAAGAUGUGGUC	63-80	gra-miR8643b	4	0	18	21	1
spiLA1589-MIR9760-2	ACAACAAUAUUAAAUAUUUGUUCUUUAGUUUUACAUUGGUUUAGACAAUUGAAAUGGAUAAUCUAAUUUUAAUUUUCCUUAAAUAUUUAAUAAUGUAACUAAUACUAGGGUAAGUGUGGGUGCCAGUCGCGGCCCGGAUUUGGGUCGUGACACCCGGCCCACCCCUAUUACAUAUGUCACUGUGUGCUGUUGAUGGAGAAGAAAUUUGAAUUUUGUAUU	219	spiLA1589-miR9760-2-5p	UGGAUAAUCUAAUUUUAAUUU	55-75	gma-miR9760	5	0	21	21	1
spiLA1589-MIR1128-1	GGCUAAUGUUUAUUACUCCCUCCGUCCCAAUGUGAGGUAGUUUGACUUGGCAGUUUAAGAAAACAGUCUAAAAUAAGUUAUAGAUGUUGGUGUAGCUGUAGAUCAUUUUAUUAAGGGUAAAAUAGGUACUUUAAAGUUAGAUUGUUACUGAAUAUUGAAAUGCGUCAUUCUUUUUGGGCUGACUUAAAAGAAAAGUGAGCAUAUAAAUUGGGACAGGGAGUAUAUAGAAAGUAAAU	236	spiLA1589-miR1128-1-5p	UAUUACUCCCUCCGUCCCAAU	11-31	ssp-miR1128	2	0	21	21	1
			spiLA1589-miR810b-1-3p	UGAAUAUUGAAAUGCGUCAUU	149-169	osa-miR810b-1	5	0	21	21	1
spiLA1589-MIR5182	AAAGCAUAAUACAUAGACAAGACCCUUUAACUUGGCCUUCACCGGCACCUGAACAUCAAUCCCAGCUCUAAUUGUGAUCAUCUUGACACAGGUGUGUCUCGCAAACAUCUUAACUUUGAUAAUGCACACUUUUGAGAACGUGUCUAGAUGUGCAUUUUCAAAGUUAGGCUGUUUACGGGGUUUUCAAAGUUGGAGUGUUUAGUUACCUGUUGAGGUAAAGUUAAGAUGUCUAUCUAUGUAUUGUGCCAA	249	spiLA1589-miR5182-5p	UGAUCAUCUUGACACAGGUGU	75-95	bdi-miR5182	5	0	21	21	1

			spiLA1589-miR7992-3p	UGUCUAGAUGUGCAUUUUCAAAG	141-163	stu-miR7992-3p	4	0	23	23	1
spiLA1589-MIR1217	UGAAUAUCAUACAUAUGAUUGAUUAAAUUUAUGUUAGUUA UUAUACACUAGAAAUAUUUGAAUCAUGAAUUCUAGUUUGC UAGUAACGGGAAACAGGGAAAAAACUGCUAGACUAUUCCA UCCCACAGUGGAAACCGGUAGGCGAGGGAUGCCGUUAG GGGAGUACACAAGGUGAAGGCGCUGAUAAGCAGUAAUUA UCCGCUAAAGUACUAUGCUAGUAGUGACCGGAAAACAUG AUAACGAUACUCUAGUUUAUAAUAAACUAAUAUGAAUUUA AUUAGAUUAUGAUAUGGU	294	spiLA1589-miR1217-5p	UAUUUGAAUCAUGAAUUCUAG	55-75	ppt-miR1217-3p	5	0	21	21	2
spiLA1589-MIR848	AAAUAAAUCUAACUAGUGGUUUGGUUUGACUUGAUUUGG UGUUGAAAAAAGACCCGACUAUAUUUAAGUUGAUUUGGU UUCAGCUUAAAAAACCAAUCCGAUGUCAAAUCAUCCCAAC CCGACAUUAUAUAUUUAAUC	138	spiLA1589-miR848-3p	ACCAAUCCGAUGUCAAA	92-108	aly-miR848-5p	3	0	17	17	3
spiLA1589-MIR7997b-1	CAUCUAUGUUGUUCGGUCUCUCCACAAUGUUAUCGCAUU CAUGUUGGAUCCUCCAAAAAUGCACUAUUUUUGAAGGAU CCGAACAUGCACCGUUCAACAUUUUUCAAGAGUUCGAGC AACUUAGUUU	127	spiLA1589-miR7997b-1-5p	AUGUUGUUCGGUCUCUCCACA	6-26	stu-miR7997b	5	0	21	21	1
			spiLA1589-miR5303-1-3p	UUUUUCAAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
spiLA1589-MIR11066	CCUUGGAAAUAGGUGGUCUUGAACUUUUGCUACAUGGUU AAACCUUUGACGCCAAAAGUCGAUACUUGAUGUUCUGUU CAUGGGGCGCAAGAUUAAAAGUUCAAGAUCAUCCACCUC CAAAG	122	spiLA1589-miR11066-5p	GAAAUAGGUGGUCUUGAAC	6-24	lja-miR11066-3p	5	0	19	19	2
spiLA1589-MIR857-1	CCAAAUUUAUGGAGGAUUUUUUACCCCCACUAUUUAAUAU UGGAUUUUGAAGGUAUAUAUGUGUCCACGUGGACACGUU ACUAUUUAUAAUGAUGCAAUAUUUAUGAUGUACACGUAGA CACAUAUAUAACUUUAAGAUACACUAAUAAAUAGUGCAUG UGUAAAAGGUCCUUUUCAAAAUUCGA	185	spiLA1589-miR857-1-5p	UAUUGGAUUUUGAAGGUAUAU	38-58	aly-miR857-3p	4	0	21	21	1
spiLA1589-MIR8011a-3	ACAUGAACUUUGUUUUGUGUCUCACACAACUGAUGUAAG UUGUGUGAGGUCUCUUUUUGUUUUACAAGUCAGUGCGAC CCAAAUCGUUGGACUCACCAACUCGUGAAAUAAAAAGAAG UCUCACGCAACUUGCGUUAAUUCUGUGAGUCGCAAAGUA AAUUUUCAAAU	168	spiLA1589-miR8011a-3-5p	UUGUGUGAGGUCUCUUUUUGUUUU	40-63	stu-miR8011a-5p	2	0	24	24	1
			spiLA1589-miR8011a-3-3p	AAUAAAAAGAAGUCUCACGCAACU	107-130	stu-miR8011a-3p	2	0	24	24	1
spiLA1589-MIR5014a-2	GUGUGCAUAAGUAGACACUUAAACUUGUAUAAAGUUGAA CAAAUACACACAUGUCCUACAUGUCAUUGUUUGUUCUAC GUGUAUUGUGUCACGUAGGACUCAUUAUUUGUUCAAGUU UAUACAAAUUUAAGUGUCUACUUAUGCAUAU	148	spiLA1589-miR5014a-2-3p	UUAUACAAAUUUAAGUGUCUA	117-137	ath-miR5014a-3p	4	0	21	21	1
spiLA1589-MIR8006-2	UGAUAUGCAGAUACCUCCGUCAUGCUUUUGGGACAUUGG UACCCCUACCGUCCAAAGACUAGAGCAUAUACCAUUUAUA UUAACUGACAUACACGUUUCAUAAUUUUAUCCACCAACCU GACAUCAGAUCAAUGGAUAAGAUUGUGUCACGUGUCCCU AUUUAGUCUUUCUUUAGAGUGAAAGAUAUAUACGCUCAAA UUUUUGAAUGACAGGAGCACUAAUGUCCCAAAAAAGUAU GACGGAUGAUAUCUACAUACUA	259	spiLA1589-miR8006-2-5p	ACCCCUACCGUCCAAAGACUAGA	41-63	stu-miR8006-3p	5	0	23	23	3
			spiLA1589-miR3706-2-3p	CAUCAGAUCAAUGGAUAAGA	122-141	pab-miR3706	5	0	20	20	3
spiLA1589-MIR11314-1	UUGGUCAUUUUAAAUAUAUAAUUUAGAUUAUAAUUUUUUU CAUUAUGAAGUAUGCACAAAAUUUACAUGCUUUCGCUGG CAAGGGAUUUCGAACUUGAGACCUCCAACAUGGAAGUUA CAAGCUCAAAACACUGGGCCACUGUAUCUUGUUUCUUCA GUUCUUCCACUGUGAAAGAGGUCACAAACUGUUUUUGUG CCACUAUAGACAAAUGUUGUAUGGUAGUGAAUGUUGGAC UGCUAGAGUCCAACAUAUCCACAAGAUGAGUGUUGUGGA GAUGCGGAUGCUAUGAUGGAUGUGCGGGCAUAUCAUAUU AGAUAAGAUUAAAAAUGACUUU	335	spiLA1589-miR11314-1-3p	GGAGAUGCGGAUGCUAUGAUG	272-292	fve-miR11314	5	0	21	21	2
spiLA1589-MIR7715	AGUGGCUAACAAAAUUCACUAUUGAUGUCUUCUUUGUUA GCUUCAAAAACGUACUCAAUAAAAUCUAACACCAUUUCUC CUACGUUCUCUAACAAAACUUUACUAUUUUCUCUUUUCUA AAAUAUUAUUCUACUUGCCUAGUAUUCAUUUCUGUUUUC UCUAAAAGUUACAAAAGGGAUCCAAACAAAAAAAGAUUCA AGUCUGAUCUUUUCUAUGUGUACAUGCGCAUUUUAGAGC UAACAAAGAAGACAACAAUGGUGGACAUUGUUAACCAUA	276	spiLA1589-miR7715-5p	UAACAAAAUUCACUAUUGAUG	7-27	bdi-miR7715-3p	5	0	21	21	1

spiLA1589-MIR5532	CUGCUACCGAAUUUCUUCAAAUUCCAGGAGAAUUGUCCCUUGAAGAGGACUCGAACCUCCACGCUCUUUAGCACGAGAUUUUAAGUCUCGCAUGUCUACAAUUUCACAACCAAGGCAUCUUGAAAGUGAAUCGUAUUCCAUGAAUAUUAUAUCUAUUUAGUAUGAUGUAUGGAAUAUAUGACAAAGGUGGAUCUAUUGAUCCGUCAUGUCAUAAAGGCCCUAGUUGGACAUCCAAUUGCUUCGAUUUGAAUUAUUCGGAGAAU	263	spiLA1589-miR5532-3p	AUGGAAUAUAUGACAAAGGUGG	169-190	osa-miR5532	0	0	22	22	1
spiLA1589-MIR773b-1	ACCCCAUUUCGACUAUGUGGCACUAGCUUGAAAAAAAAGUCAACCAACGUUGAAUCCACAAGAUAGUAUCACGUAGAUCGAAAAGGAAU	89	spiLA1589-miR773b-1-5p	GGCACUAGCUUGAAAAAAAA	19-38	ath-miR773b-5p	5	0	20	20	1
spiLA1589-MIR1127-1	CGGGACAAGUAUCGUUGGACAACUACUUUUAGUGUAGUGGACAAGUAAAGGUGGAUGGAAGAAUUACUUCCUCCGUCCACUUUUAUUUGUUCACUAUACUAAAAUUAGAUAUCCACUUUUACUUUGUCAUC	131	spiLA1589-miR1127-1-3p	AAUUACUUCCUCCGUCCACUU	62-82	bdi-miR1127	5	0	21	21	1
spiLA1589-MIR5752b	GGGGUCGUUUGGUAGAGUGUAUAAAAGUAAUGCUAAAUAUAGUGUAUUAGCAAUACUGGCAUUAGUAAUUUUUGCAUUAGUUAUACUUGCAUUAGUUGUACAUACAUUAUUUCUUAUGCAUUGUUUGGUUUGGUGUAUUAAAAUUAACAUGUAUUGUACAAAAGUAUCCUUCACAUUAUGGUGAAAAAGAUGAAAAAGUGUUUUUGAGGGGUGUUUGUAUCUUUUAAGUGCUAAUGCAUGCAUUAAAUCCCUUUGCAUUACUAAUACCUAGAAAUCCAUGGUAUUAGUAAUGUACUCUCCAAUACACAAU	310	spiLA1589-miR5752b-5p	CAUUGUUUGGUUUGGUGUAUU	119-139	mtr-miR5752b	5	0	21	21	1
			spiLA1589-miR1046-3p	UGGUGAAAAAGAUGAAAAAGU	179-199	ppt-miR1046-3p	3	0	21	21	1
spiLA1589-MIR1512c	GAGGUAAAGCAGAAACUCUUUCAAAUAGAGCCAAAUAGUUCUAAGAAUUCUAAGUUGAUCCUCACUAGCACCACAAAGAUUUUUUUAGUUUCAAAAAACAUAUUCUGUGUGGUGCUGAUGACGAUUAACUUAGAAUUCUUGGAGCAUUUUGCUCUACUUGAAGGAGUUUUUGGUUUACACA	182	spiLA1589-miR1512c-3p	UAACUUAGAAUUCUUGGAGCAU	127-148	gma-miR1512c	4	0	22	22	1
spiLA1589-MIR5066	ACAUAUACAAUUGUAUAAUUCGAUGGCCUAAAUUGUAUAAUUUGCUGGCCUAUUUCGCUAGAAUUGUAUAAUUCGCUAUCCUAUUUCACUGCGAUUGUAUAAUGCACAAUUGUAUAAUU	119	spiLA1589-miR5066-5p	AAUUGUAUAAUUCGAUGGCCU	9-29	bdi-miR5066	5	0	21	21	1
			spiLA1589-miR9562-3p	UAAUGCACAAUUGUAUAAUU	100-119	bra-miR9562-3p	4	0	20	21	1
spiLA1589-MIR5185l	GAAUUCAGAGGCGGAGCUAGGUAGGGAUUUUGUGGGUUCGGAAGAACUCAGUAAAAUUUUCGUAGAUCGUACUUGAAAAUUAAUUAAAUAUAUAUGUGCAUUUAUUUAAGAAUCCUUAACAAAAUUGAUUGACAAUUCUAAAAGAAAUUUGAAAUCUCCAAACUCUUUAUUCUAGUUCCACCUCUAAUUC	190	spiLA1589-miR5185l-3p	UUCUAGUUCCACCUCUAAUUC	170-190	bdi-miR5185l-5p	5	0	21	21	1
spiLA1589-MIR774a	CGUUGUGGCUUGUGCUUGAGUAGUAAUGGCUUGGUCAAUUUUAGAAGGAAUUACCCUCAUCUCCGCCUCCAUCAUAGGUGGAGGGUUAUCCGGGUCUUGAUCAACACUAGCAUUCUCCUCAUGUGGAGGAACUUGAUCAACAUGGGGAGGAGCUCAUGCUUUAGCAACUUUCUCCUCAAGUAUUCGAGCCACAUUC	196	spiLA1589-miR774a-5p	UACCCUCAUCUCCGCCUCCAU	52-72	aly-miR774a-3p-1	5	0	21	21	1
			spiLA1589-miR11504-3p	UCAACAUGGGGAGGAGCUCAUG	137-158	pab-miR11504	2	0	22	22	1
spiLA1589-MIR8008b-1	UGCAAAUCCCAGAAAAGCGACUGACAAAAGAACACUAUCCAUCGCUUUUCUGGAAAUUAUUUUUUCAAAAAGUCAAAAAAAAAAAGUGAAGGACUAAAACACACUAACUGUCGCUUUUCUUGGUUUUAAAAAAUAAAAACCCAGAAAAGCGACGGACAAAACCAUGUUGUCUGUCGCUUUGUCUGCAAUUUUUU	194	spiLA1589-miR8008b-1-3p	AAACCCAGAAAAGCGACGGACAAA	137-160	stu-miR8008b	2	0	24	24	1
spiLA1589-MIR156b-9	GAAGAAAGAGUGAUUAUUGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCACCUUCACCUCUUUCAUA	138	spiLA1589-miR156b-9-5p	UUGACAGAAGAUAGAGAGCAC	20-40	aof-miR156b	0	0	21	21	1
			spiLA1589-miR156d-9-3p	GCUCUCUAUGCUUCUGUCAUCA	100-121	stu-miR156d-3p	0	0	22	22	1
spiLA1589-MIR7997c-7	AAGACCUAUGUUGCUCGGACUCUCCAAAAAUCAACUACUUUUGAAGAGUCCUAUACACGUGUUGACAUUUUCAGAGAGUCCGACCAACAUAGGUAAA	97	spiLA1589-miR7997c-7-5p	AUGUUGCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-7-3p	UUUUCAGAGAGUCCGACCAAC	68-88	sly-miR5303	5	0	21	21	1
spiLA1589-MIR399i	CUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAG	107	spiLA1589-miR399i-3p	UGCCAAAGGAGAGUUGCCCUA	66-86	stu-miR399i-3p	0	0	21	21	1

	UUGCCCUAUGAUUGCCUCUGCUUAAUUAU										
spiLA1589-MIR156b-10	UGGAAGAGAGGGACUGACAGAAGAGAGUGAGCAUACACAUAUAAUUAUAUAAACAUGUUUACAUAAUUCUUUUGAUAUAUAUAUAUAUAAUUUUGCGUGUGCUCACUUCUCUUUCUGUCAAUCUCUCUUAGA	132	spiLA1589-miR156b-10-5p	UGACAGAAGAGAGUGAGCAUA	15-35	cca-miR156b	0	0	21	21	1
			spiLA1589-miR156f-10-3p	CUCACUUCUCUUUCUGUCAAUC	102-123	stu-miR156f-3p	0	0	22	22	1
spiLA1589-MIR3700	CAACUACGCCCUUCAACUUUGAAUGUGCACAAAUAAACACGUAAACUUGUAUAAAAUUGAACAAGUAGACGCAAGUGCCCUACAUGGCAUAAUACACGUUGGCAUGUAGGACACAAAAUUGUCAUGUAGGAUGAAUGUGUAUAUUUGCUCAAUUUUAUAGAAGUUUAAGUACCUACUUGUGCACACCCAAAGUUAAAGGUCAUAGUUA	208	spiLA1589-miR3700-3p	CACACCCAAAGUUAAAGGUCA	182-202	pab-miR3700	5	0	21	21	2
spiLA1589-MIR6149b	UUAUAGCCUUUGUAUGUCAAAGCUUCGAUACGCACCUGAAUCGACAAAUACAUAUAUUAUUCAGACUUUUUAAGAAUAUCACGCGUUUAUUAUUUUUAUAAGUCUGAAUAACAUAAAUCAUAUAUAACAUAUAUGUCGAUUCGGGUUCGUAUGAAAACUAUGGCAUACCUCAAAGGGUAACG	182	spiLA1589-miR6149b-5p	UCGAUACGCACCUGAAUCGAC	25-45	nta-miR6149b	2	0	21	21	1
			spiLA1589-miR6149-3p	CGAUUCGGGUUCGUAUGAAAAC	137-158	stu-miR6149-3p	4	0	22	22	2
spiLA1589-MIR7997c-8	CGAAAAAGCUAUGUUGCUCGGACUUUUCAAACAUGUCGACGGGUGCGUGUCCAAUCCCCCCAAAAUAGUGUAUUUUUGAAGGAUCCGACACGGGUGGGGCAUCAUUUUUGGAGUGUCCGAGCAACAUGUUUUAGA	135	spiLA1589-miR7997c-8-5p	AUGUUGCUCGGACUUUUCAAACAU	11-34	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303f-8-3p	AUUUUUGAAGGAUCCGACACGGGU	72-95	stu-miR5303f	3	0	24	24	1
spiLA1589-MIR5303-2	AGUACCUAACUGCUAAGUUGCUCGGAGUUUCUAAAAUUGUUGGUGCACGCAUGUUGGAUCCUCCAAAAUUGCCUACUUUUGAAGGAUCGACCAGGCACCUGAUCACAUUUUUUAAGAGUUCGAGCAACAUAGCCUUGUAGUGUGUC	146	spiLA1589-miR5303-2-3p	UUUUUUAAGAGUUCGAGCAAC	108-128	sly-miR5303	1	0	21	21	1
spiLA1589-MIR172j-2	UAGAGUCAUAUGUUAGAUGAUGCAGCAUCAUCAAGAUUCCCAAAGAGAGAAAAUAAGAGACUUUGAACUAUAUUAUAUAUCCAAUAUUCACCCUAAAUAUAUAAUUAAAUACUUCUCCCUUCAAGUUUUGUGAAUCUUGAUGAUGUUGCAUCCUCAAACAUUGACUGAU	169	spiLA1589-miR172j-2-5p	GCAGCAUCAUCAAGAUUCCCA	22-42	lus-miR172j	0	0	21	21	1
			spiLA1589-miR172-2-3p	UGUGAAUCUUGAUGAUGUUGCAU	129-151	aau-miR172	2	0	23	23	1
spiLA1589-MIR6027	GUAAUUUUACAUGAUUAUGGGUAGCACAAGGAUUAAUGUGAAACAGAAAAGUGAUAUGCAAAGAAGAUGGAGAUUCAAUUGUUUAUUGUUACGAAGAAAACACUUUUGUGUUUCUCGUGAAUCCUUCGGCUAUCCAUAAUCAUGUUGAAUGUG	153	spiLA1589-miR6027-5p	AUGGGUAGCACAAGGAUUAAUG	17-38	sly-miR6027-5p	0	0	22	22	1
			spiLA1589-miR6027-3p	UGAAUCCUUCGGCUAUCCAUAA	118-139	stu-miR6027	0	0	22	22	1
spiLA1589-MIR11068c-2	UUAUGCUCUUUAACUUUGGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAACAAAUAGACACGCAUGUCGUACAUGUCAUUUUUUGUCCUACGUGUAUUGUGGCAUGUAGGACUCAUGUGUUUUUUUAUAUAAAAGUUGGAUAGUUAAAGUGUUUGUUUGUACAUUAUUAAGUUGAAGAUCAACG	192	spiLA1589-miR11068c-2-5p	UCUUUAACUUUGGAUGUGC	7-25	lja-miR11068c-3p	4	0	19	19	2
			spiLA1589-miR6254-2-3p	UCCUACGUGUAUUGUGGCAUG	94-114	osa-miR6254	5	0	21	21	1
spiLA1589-MIR9781-1	AAAUUGAACAAGUAGACACAUGUGUCCUACAUGUCAUCCCACAUGUCAUUUUUUGUCAUACAUGGUGUCCUACGUGUAUUUUGUCAUAUAGAACUCAUGUGUUUAUUUAUUUAAAAG	117	spiLA1589-miR9781-1-3p	UUUUGUCAUAUAGAACUCAUG	79-99	tae-miR9781	5	0	21	21	1
spiLA1589-MIR1435	UGAUUUUCGUGUGCUAUAGUCCAUGGAUUUUUUGUGAUUCAGGAUUACAGAUUUUCUUUUGUCAAAAUUUUUCAUGAUAGAUUGGCUCCUAAAUAUAAAAAAUGGACUCUCGAAUUGGUGACUGUACAUAUUACUCCUCCAACUCCCUACAGAGAG	234	spiLA1589-miR1435-5p	UUUCUUUUGUCAAAAUUUUU	53-72	osa-miR1435	3	0	20	20	1
spiLA1589-MIR390a	UUCUCUAAUGGUUUCAAAUUGAAAUCGUUUGAAAGCAAUAUGACCAAAAUAUUCAUGGGCUAACACACACAAAAAAUUAUGGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGCUCG	106	spiLA1589-miR390a-5p	AAGCUCAGGAGGGAUAGCACC	20-40	sly-miR390a-5p	0	0	21	21	1
			spiLA1589-miR390a-3p	CGCUAUCCAUCCUGAGUUUUA	69-89	sly-miR390a-3p	0	0	21	21	1

			spiLA1589-miR5026-5-3p	GCUCACAAGAUAGUGUCACGU	58-78	ath-miR5026	4	0	21	21	2
spiLA1589-MIR11085-1	ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAAUUCCCUACCAUAUUGCCAAAUAUUUGCCUUUAUCUUUGUGUUCAUCUAGCUAAAGACAAAUGUUUGGCAAUAUGGUAGGGGAUUCUGGUCUUCUGUACACAGGGAAAAGUUGACUUCU	151	spiLA1589-miR11085-1-5p	AGUGAACUUCAUCUUUGUAA	4-23	lja-miR11085-3p	5	0	20	20	1
spiLA1589-MIR8739-1	GUGCAGAUACCUCCGUCAUACUUUUUAAACAUUGGUGCUCCUGUCGUCCAAAAUUAAGAGCAUAUAUGCCCUUCACUCUAACAAAAUACUAAAUAGGGACACGUGGCUCAUGUAAUCUUAGCCGUCGAUCCGAUAUUUAAUAAAUAUCAUGUCGGUAGAUAAGAUUAUGACACGUGUAUAUUCGUUAGUAUAAAAGAUAUACAUACUCUUAAUUUUUGAAUGACAAAGAUUCCAAUAUCUCAAAAAGUAUGAUGUAGGGUAUCUGUUC	268	spiLA1589-miR8739-1-5p	AUACUAAAUAGGGACACGUGGCUC	86-109	gra-miR8739	5	0	24	24	3
			spiLA1589-miR417-1-3p	UGAUGUAGGGUAUCUGUUC	250-268	osa-miR417	5	0	19	21	3
spiLA1589-MIR10540-1	AGGCGGAUUGAUUUCUCAUAUGGUCACUUUGCUAAAUAGUUAUUAUCUCAAGAAGUCAUUUUUCAACUUGAUUCCAAUUUUCUUCAACAAAGAAAGUGACUUAUAUUACUCAAAUAAUUACUAUUAGUUGAACGACCAACUGAGAAAUUAACUUCGGUA	159	spiLA1589-miR10540-1-3p	AUAAUUACUAUUAGUUGAACG	114-134	sly-miR10540	2	0	21	21	1
spiLA1589-MIR11078f	GAUUUCAAUAAGUAUUUGCAAUAAAGACAGAGAUUUGGGUCUUCAAGUUAUCUGAGGCUGUUUUGCGUAAAAAAAAAUGCUUCAUUCCAGGCAAUGGAUUGGUUGCUGGUGUCAAAAGCUUCACUUAGAGGAAUGCCACGUGAUUACCGAGGCUGGACUUUUUGGCAUAGUUUUGAACUGUGGUAAGAAACUGAAGCCCGAGGCUGGAUUUUUUGGCAUAGUUUUGAACUG	281	spiLA1589-miR11078f-5p	GGAUUGGUUGCUGGUGUCAAA	96-116	lja-miR11078f-3p	4	0	21	21	2
			spiLA1589-miR7803b-3p	AGAGGAAUGCCACGUGAUUA	127-146	rgl-miR7803b-5p	5	0	20	20	2
spiLA1589-MIR5168	GGUUUCCAUGGUCAGUUUAUGCUUAUCCAGAAGGUGCAGGGGUUGGUUUCUGGUAGAACGAGCUUAUCUUAAACAUGUUUUGUUGAAGAAGCUAUGGUUUCGAUCUGAUUUGCCUGCACCUUAUGUUUGAGCAUGCGCUACCAUGAACUA	150	spiLA1589-miR5168-5p	GGGUUGGUUUCUGGUAGAACG	40-60	ata-miR5168-5p	5	0	21	21	1
spiLA1589-MIR8020-2	UGACCUUGUGAAUUUCAUGUAGUAUGUUGUGGUUCUGUCACAAUGUUAUUGUGCUUAUGGACGGUCAAGUGCUGUUUAGAUGAAUUAACAACAGUACUUAACAAAAAUACAUAAGCUACAUUGAAAAUCCACUAGGGUU	139	spiLA1589-miR8020-2-5p	AAUUUCAUGUAGUAUGUUGUGGUU	11-34	stu-miR8020	3	0	24	24	1
spiLA1589-MIR7997c-9	UGACAUAUAUGUUAUGUUGCUCGGACUCUUCAAAAAUGUUGUAACAUUCAUGUUAGAUCCUCUGAAAAUGCACAACUUUUGAAGAAUCUGACAUGUAUUGACGAUAUUUUUGAAGAGCUCGAGCAACAUAGCAUAGAGUGAAA	143	spiLA1589-miR7997c-9-5p	AUGUUGCUCGGACUCUUCAAAAAU	14-37	stu-miR7997c	1	0	24	24	1
			spiLA1589-miR5303-9-3p	UUUUUGAAGAGCUCGAGCAAC	107-127	sly-miR5303	1	0	21	21	1
spiLA1589-MIR823-1	GAUAUUUGUAUGAUUACUAAUCUAUUUGUUAUAUCUUUUGUAGUAUGGAAGGCGACGAGCCUCCGCCAUGGUCACAUAUUUGUGGUCGUGGGGGAAAAGGUAGAGGAAGGGGAAGAUCAUCCUCUUCACAGUCUAGAAGAUUAUUAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCGAAUCAACGAUUGGCGAAGCCUCCUAAUCAGCUUCAUCCUCUGUAAAUUUAAAAGAUAUUCCUAAGGACAGUUCAUUAUAUGAACAAAUUUA	286	spiLA1589-miR823-1-5p	UUUGUAUGAUUACUAAUCUA	5-24	aly-miR823-5p	5	0	20	20	2
spiLA1589-MIR9479	UAAGUCCAGUCCUCUACCCUUCUCCACUUAAAAGACCAAGCUUGUCUACAACAAGGUUCCAACUCAUGACAAACAUAUGAUGUGUGAGUUAGGCACGUGUCACGGGUUCAAAUGCUACCACCGACAAAAGUAUGGUAUUUAAGUGGAGAAUGGUAGAGGGUCGGACCCA	169	spiLA1589-miR9479-5p	UCCAGUCCUCUACCCUUCUCCA	5-26	sly-miR9479-5p	0	0	22	22	1
			spiLA1589-miR9479-3p	GAGAAUGGUAGAGGGUCGGACC	146-167	sly-miR9479-3p	0	0	22	22	1
spiLA1589-MIR10533	AUCCAUUAUUCUUCUGAAUUGUUUAUCUUCUGCUUUGAUAUGACAGCUUUAUUGUAUUCAUUCAGGAAUGUGAGGAGUAUGAAGAUUUGGAUGAAUAUGAGGAAGAAAGCGGUGCAGAGGAAUAUGAGG	129	spiLA1589-miR10533-5p	UCUUCUGAAUUGUUUAUCUUCU	10-31	sly-miR10533	5	0	22	22	1
			spiLA1589-miR11036-3p	UUUGGAUGAAUAUGAGGAAGAA	86-107	seu-miR11036	1	0	22	22	1
spiLA1589-MIR8039-2	CUUGUUUCAUAUCUCUACUAUCCAUGGUUCUAUUUACCUAUCUAAACUAUCACUCCCUUUGUAUUAAAGACAAAUGAGC	194	spiLA1589-miR8039-2-5p	UUACCUAUCUAAACUAUCACU	34-54	stu-miR8039	3	0	21	21	1

	GCUGAGCUAGCCAAUAUGUAUUUGACCAACUCAGCUUCGAGGUGCCUUUUAAUAAAAACUGAGUGAUAGUUUAGCUAAGUACAGAGAACAAUAGAUAGUUGAGGUAAGAAACUAU		spiLA1589-miR7710-2-3p	GUUGAGGUAAGAAACUAU	177-194	bdi-miR7710-3p	4	0	18	24	2
spiLA1589-MIR8039-3	GUAUAGAGUUAAUGGCGAAAGAACAUACCUAAAUUAUCAAGUUUUCGCGAGUUUCAUACCUCAACUACCACUCAAUUAUAUUAAAAACAUACCUCGAUGUUUUGCCUACAUGUGCUUGUUGUUGACUGAGAAGGAAUAUUUGGCCAACACAACAUCGAAGUGUGUCUUAACACUAAGGGAAUGACAAUUUAGAUAGGUAAGAGAACAAUGGAUAGUUGAGGUAUAAAACUCGCGAAAAAGUCAUAGUUUGGAUGUGUUUUUGAUCAUUAACUCUAAAA	277	spiLA1589-miR8039-3-5p	UUUCAUACCUCAACUACCACU	52-72	stu-miR8039	5	0	21	21	1
			spiLA1589-miR5675-3-3p	UAGGUAAGAGAACAAUGGAUA	193-213	gma-miR5675	5	0	21	21	1
spiLA1589-MIR8001a-1	UCCUGGGGAUUAGUAUGAAAAUUCAAAAGAAACUUAUUUUCCUGCAAAUUUUCACACUAAUUCCCAUGA	69	spiLA1589-miR8001a-1-5p	UCCUGGGGAUUAGUAUGAAAAUUC	1-24	stu-miR8001a	0	0	24	24	1
spiLA1589-MIR167d-2	GAUGGCAUUGACAGGUGAGGCUGCCACAUGAUCUGAUCUUUCCUCGUAUUAUAUUUGAACUAAAAGGAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGCCGCA	109	spiLA1589-miR167d-2-5p	UGAGGCUGCCACAUGAUCUGA	16-36	eun-miR167d-5p	1	0	21	21	1
			spiLA1589-miR167h-2-3p	AUCAUGCUGGCAGCUUCAACUGCU	77-100	gma-miR167h	1	0	24	24	1
spiLA1589-MIR7997c-10	AGAACCUAUGUUGGUCGGACUCUUCAAAAAUGUCUACUGAUGCGCGUCAGAUACUCCAAAAAAUAGUGUAUUUUUGGAGAAUCCAACACGGGUGUGUGGCAUGGAAAGUGAAGAGUCAGCACAACUUAGAGUAGA	135	spiLA1589-miR7997c-10-5p	AUGUUGGUCGGACUCUUCAAAAAU	8-31	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303f-10-3p	AUUUUUGGAGAAUCCAACACGGGU	70-93	stu-miR5303f	2	0	24	24	1
spiLA1589-MIR169c-3	GUUGAAGAGAGGUAUUGCAUGAAGAUAAAGUGCCUGCUCUGAUAGCCAAGGAUGACUUGCCUAAAAUCAUUUUUAUGAAGGGUCUUAACUAAUUAAACUUUAGUUACUAAAAUUAAAGUUUAUAUUAUAUGAUCUUAAAAUUGGGAUUUUAGGCGUUGUCUGAGGCUAAUUGAGAGACACUUAUCUUUCAUGUAACACCUUCAUUCUCU	209	spiLA1589-miR169c-3-5p	UAGCCAAGGAUGACUUGCCUA	43-63	ata-miR169c-5p	0	0	21	21	1
			spiLA1589-miR169f-3-3p	UAGGCGUUGUCUGAGGCUAAU	150-170	sly-miR169f	1	0	21	21	1
spiLA1589-MIR7504j	AAAGCCCCCUAACCUAUAUCCGGAUUUCCAACAACUUCACUUGAGUCUUAUCACCCUGUGAACUAUUUAAAACUGAAAUUCCAUCUCCCUGGAGGUGAUAGGACUCAAGUGAAGUUGAAGAGUGUGGUUGAAAAUCCGGAUAUAAGUUAGGGGGCUUU	158	spiLA1589-miR7504j-3p	AUUUAAAACUGAAAUUCCAUC	65-85	gra-miR7504j	5	0	21	21	1
spiLA1589-MIR7997b-2	ACUAUGUUGCUUGGACUCUUAAGUAAACCGCUAGGUUCAUGUCAUCCUUCAAAAACAGGACAUUUUUUAAGGAUCUGACAUGAGUGCAGCAUUAUUGGAGAGUCCGAGCAACAUGCA	117	spiLA1589-miR7997b-2-5p	AUGUUGCUUGGACUCUUAAGU	4-24	stu-miR7997b	5	0	21	21	1
			spiLA1589-miR5303h-2-3p	AGCAUUAUUGGAGAGUCCGAGCAA	88-111	stu-miR5303h	4	0	24	24	1
spiLA1589-MIR3513	AUCCAUCAUUGCUCUUGCAUACAUCUCCUAGAGAAGAUAGAAAUGAUAUGUAAUUGAAGGGAUACCUGGUGCAUCCACCUAUCUUCUCUAAGAGAUGUAUGCAAGAGCAAUGAUGCAA	118	spiLA1589-miR3513-5p	UAGAGAAGAUAGAAAUGAUAU	29-49	ahy-miR3513-3p	4	0	21	21	1
spiLA1589-MIR1514a	UGGUUAUUCAACAAUGUAAGGGCCCGUUUGGAUGGGCUUAAUAAAAGCAGCUUUAAAAAAGUACUUUUAAAAGUGCUGAAACUUAUUUUUGAAAUAAGCAGUUAUGCGUUUGGAUAAAAGUGCUGAAAUUGUUAUGUCAAAUCCCCUUUUCCUCUCAUCCUCCCCCGGUUCUGGUUCAGGAAAGGGUCAUGAGCAUUGUUGAAAAAAAA	209	spiLA1589-miR1514a-5p	CUUAUUUUUGAAAUAAGCAGU	82-102	gma-miR1514a-5p	5	0	21	21	2
			spiLA1589-miR11509-3p	UCAUGAGCAUUGUUGAAAAAA	187-207	pab-miR11509	5	0	21	21	1
spiLA1589-MIR7817a	AAUCUUCACCCUCUUACAGCCUGAUCUGGGAAUGACUUAUAAGAAAUUUGGAUUUGUUUAUUAUCUAGAGCUAGUUAAAUUUAUUUGGAUGCAACCAUGCAUUUCUUUGUGCAGUGCACAAUUCAUCAAGCAAAUAGCUUCAGAAUAUGGUCGGGAGUCGAAACUUUUAUAGUACGGAUCCAAUGAUGUUACAACAUUCCUUGGUAGGUUUAUUUGUUGAAGAGAGUGAUGAUACAACAAAGAACUUAACCAUCUUCUAAUAAUAACAAAUUAAAAUCUCUUAGUGAACCAUCCUCAGACCAUGCUGCUUAGGGGAAGAAGGUU	324	spiLA1589-miR7817a-5p	UUUGUUUAUUAUCUAGAGCUA	53-73	ptc-miR7817a	5	0	21	21	1

			spiLA1589-miR9482-3p	GCUUAGGGGAAGAAGGUU	307-324	bdi-miR9482	4	0	18	21	2
spiLA1589-MIR1044-1	GCGUCCUCUAACUUGGCUUCAAAUCACAUUUAUGCUCUUCAACUUUGGAUGUGCACAAAUAUACACUUAAACUUAUAUAAAAGUUGAACAAACAGACACACAUGUCCUACAUGUAAUUUUUUGUCUUACGUGUAUUGUGUCAUGUAGGACUUCAUGUGUUUAUUUAUUUAAAAGUUUAUGUUUGUACAUUAUGAAAUUUGGAUGUCAAAGUUAGAAUUUGAAGCCAAGUUUAGGAUUA	237	spiLA1589-miR1044-1-5p	GCACAAAUAUACACUUAAACU	53-73	ppt-miR1044-5p	5	0	21	21	1
			spiLA1589-miR8771f-1-3p	UUGGAUGUCAAAGUUAGAAUUUG	197-219	gra-miR8771f	5	0	23	23	1
spiLA1589-MIR5303i-1	AAAACCUAUGUUGCUUGGGGCUUUCCAAAAAAUUUGUUGUGCCCAUGUGGGAUCCAAACAUGCACUAAUUUUGGGGUAUCCAACAUGGUGCUAUAUUUUUGAAGAGUCCGAGCAAACAUAGGUCAA	126	spiLA1589-miR5303i-1-3p	AUAUUUUUGAAGAGUCCGAGCAAA	93-116	stu-miR5303i	2	0	24	24	1
spiLA1589-MIR396d	GACCCUAUCUGUAUCUUCCCACAGCUUUAUUGAACCGCACACAACAAUAUGAAUCAAUUUUUUCUUUUUCAAUAAUGAAUUGAAAUUGUAGAUGCAGUUCAAGAAAGCUGUGGAAAAACACAAAAAGGACC	130	spiLA1589-miR396d-5p	UCCCACAGCUUUAUUGAACCG	17-37	lus-miR396d	1	0	21	21	1
			spiLA1589-miR396a-3p	GUUCAAGAAAGCUGUGGAAAA	96-116	csi-miR396a-3p	1	0	21	21	2
spiLA1589-MIR1130b	AUGUAUAAAAUUGAACAAUUAGACAUAUUUGUCCGACAUGUCGUCCUUGCACCCUACAUAUAUUAUGUCACGUAGGACACAUAUAUCUUCUUGUUCAAUUUUAUAUAA	108	spiLA1589-miR1130b-3p	ACAUAUAUUAUGUCACGUAGG	56-76	tae-miR1130b-3p	5	0	21	21	2
spiLA1589-MIR1886i-2	GGCGAUACGGUAUCAUGAGAUGGAAUUAGCGUUUGGACAUGCGAUUUUGUGCUGAUUCAGUCUGAUGAUUCCAUAUCAUG	80	spiLA1589-miR1886i-2-5p	AUGAGAUGGAAUUAGCGUUUGGAC	15-38	stu-miR1886i-5p	2	0	24	24	1
spiLA1589-MIR902a	CAACUAUGUUAUGCAGACUCUUCAGAAAUGUUGCUAAACGUGUAUCAGAUUCUCAAAAGAUAAAUUGUUGUUGGAGAAUUGAGCACGCAGUUAGCGACAUUUUUAAAGAGUUCGAGCAACAUUAGCUC	128	spiLA1589-miR902a-5p	UGUUAUGCAGACUCUUCA	7-24	ppt-miR902a-5p	3	0	18	18	1
			spiLA1589-miR5303-3p	UUUUUAAAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
spiLA1589-MIR5049	GUACUCCCUCCAUCCCAUAUUAGUUGUCCACUUCCGUAAUGUGGAACAACUAUUUAUAGUAAGGUGGACCACUAAUAUGGGACGGAGGGAGUAG	94	spiLA1589-miR5049-5p	UCCCUCCAUCCCAUAUUAGUUGU	5-27	bdi-miR5049-5p	4	0	23	23	1
			spiLA1589-miR5174e-3p	AAUAUGGGACGGAGGGAGUAG	74-94	bdi-miR5174e-3p-2	3	0	21	21	3
spiLA1589-MIR7504f	UCUUUACAUUUUUCUUUUUCAUUCUCCAUUCAACUUUCUUUUUGGAGAGGCACCAACAACGGAGAAUGAGAAAAAAAUGUAAGUG	85	spiLA1589-miR7504f-3p	AUGAGAAAAAAAUGUAAGUG	66-85	gra-miR7504f	5	0	20	24	1
spiLA1589-MIR11419-1	CAUCCAACAAAUGUGUUUACCUAAGUUGCUCAGACUCUCCACAAAUGUUGUCAUAUCCGUGUCAGAUCCUUAAAAAAAAUACUUUUUUCAAAGGAUCUGAUACGUACCUAUAAAUAUUUAUGAAGAGUUCGAGCAACAUUGGUGUUCAGAGUUGCUGGCAA	161	spiLA1589-miR11419-1-5p	ACCUAAGUUGCUCAGACUCUC	19-39	pab-miR11419	5	0	21	21	1
			spiLA1589-miR5303-1-3p	UUUAUGAAGAGUUCGAGCAAC	117-137	sly-miR5303	1	0	21	21	1
spiLA1589-MIR827-3	CUAGCCUGACCAGUGAGGACUUGCUAUUUUACUUUCUAGAUGGCCUUCAAAACUGGGCCAAGCAAGAUCUUCAAAGACGUCAAGUUCACGACGUGGAUGAGGCGAU	106	spiLA1589-miR827-3-5p	CUUUCUAGAUGGCCUUCAAAAC	32-53	eun-miR827-5p	5	0	22	22	1
spiLA1589-MIR6283-1	CCCAAUCAAGUCAUCGAGUGACAUUAAACAACAUAUCCAAAACAAGAAAGGGGUGUAGAAAAAUCCUUUUUUCUUGUGUCGAAACGAAAGAGUAAUGAUUCAUGAUCCAGUUUGUUUUUUAUAUAUACAUAUAUAUAUUGCAUUCUAGUCAAGAACGAACUGACAAUGUGUGAUGACACAUGAUGACACUUGUAUUUUG	199	spiLA1589-miR6283-1-5p	AGAAAGGGGUGUAGAAAAAUC	45-65	ppe-miR6283	5	0	21	21	3
			spiLA1589-miR860-1-3p	AUAUAUUGCAUUCUAGUCAAG	133-153	aly-miR860-5p	5	0	21	21	1
spiLA1589-MIR159-2	UUAUCGUCUAUCAUUUGAUUCCAAUUGAUCAAUCAUCUCGAGGCAGGAAAGAUUGAGACUAUCCCAUAGACUGAAUUAUUAUUUUGAGAAUGAUAAUAAUUCAGUUUAUAGGAUAGUCUCAAUCUUUCUUGCCUCCAAAGACUGAAUUAUUAUUAUUUCAGUAAUAACCAUAGACUGAAUU	181	spiLA1589-miR159-2-3p	AAUCUUUCUUGCCUCCAAAGA	121-141	vca-miR159-5p	5	0	21	21	2
spiLA1589-MIR7997c-11	CUUCUAUGUUGCUCGGACUCUUUAAAGAUGUUUACGGGUGCAUGUCUAUUUCUUCCAAACUAGUGCAUGUUUGAAGGAACCGACACAGGUGCAACAGCAUCUUAGGAGAGUCUGAAC	127	spiLA1589-miR7997c-11-5p	AUGUUGCUCGGACUCUUUAAAGAU	6-29	stu-miR7997c	3	0	24	24	1

	AACAUAGGUU										
spiLA1589-MIR396a	AGUCCAAAGCUUGCCAUCUUUUCCCACAGCUUUCUUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAAAUUAUCAAUUUAGAGAUCAAAAUUUAGCAAGAAGAAGUUCAAGAAAGCUGUGGAAAAGCAUGACUAGGACUUGGUCA	144	spiLA1589-miR5303h-11-3p	AGCAUCUUAGGAGAGUCUGAACAA	96-119	stu-miR5303h	5	0	24	24	1
			spiLA1589-miR396a-5p	CACAGCUUUCUUGGACUUUCA	25-45	hbr-miR396a	2	0	21	21	1
			spiLA1589-miR396a-3p	GUUCAAGAAAGCUGUGGAAAA	104-124	csi-miR396a-3p	1	0	21	21	2
spiLA1589-MIR8011a-4	CCUUCACACAACUAACACCAGUUCUUUGAGGCUUCUUUUUAUUUUACAAGUCGGUGGACCCAGAAGUGUAAUAAUUUGGGUUCAUUAACUUGUGGGACAAAAAGAAGCCCUACAUAAUUAGUGUCAGCUGUGUGAGAC	138	spiLA1589-miR8011a-4-5p	UUCUUUGAGGCUUCUUUUUAUUUU	22-45	stu-miR8011a-5p	5	0	24	24	1
			spiLA1589-miR8011b-4-3p	CUUGUGGGACAAAAAGAAGCCC	89-110	stu-miR8011b-3p	4	0	22	22	2
spiLA1589-MIR8002	AAUCAUUUAUUAUAAAGAAAAAGGCUCAAAUAUGCCAUCGAAUCUAAAGUUUGGCUCAACUAUGCCAUUUCAGUGAACAAAUAAUGUUUUAAUGGCAUGGAUGAGCCUUUACUCAAAACGGAAAUGGCAUAUAUGAGCAAACUUUUAACGGAUGACAUAAAUGAGCCUUUUCUCAAUGUUAAAUGGCA	188	spiLA1589-miR8002-5p	AAUCAUUUAUUAUAAAGAAAAAGG	1-24	stu-miR8002-3p	5	0	24	24	1
			spiLA1589-miR904b-3p	UUUUCUCAAUGUUAAAUGGCA	168-188	ppt-miR904b	5	0	21	21	1
spiLA1589-MIR837	UAUCUCUCUCUCUCUCUCUCCCUCGCUUUAUACAAACAUAAAAUAUGCAAUGUAUUUUGUAUAAUUUGUAUUUGUAUAAAGCGAGAAAGAAAGAACGGAAAAGAGAACUGGGCAAGGGUAUAUUUGUAUUGUAUAAUUACGAGUAUAUAAGACGAAGAUAUAUGUAUUUGCAUGUGUCUAUACAAUUUUUUCUCGUUUUAUACAAAUAAAGCCGCAAUUUAUACUGAUUGUAUAAAGUGAGAGAGGCGAGCGACAGAGGGA	261	spiLA1589-miR837-3p	AAUUUUUUCUCGUUUUAUACA	184-204	aly-miR837-5p	5	0	21	21	2
spiLA1589-MIR7992-3	UGGUAAGUAAGUAAUACCACGUAACUUUGAGAGUGCACAUCUAGAUACCUCAACUAGACCCUCCAACUCGUGCCCGCUGUGUCUUGUAGACACUUGACAUUAAAGUAGCAGAUAAACUUUAGAGGUGUCUCAAUGAUGAUUUUGUAGAUGUUGGAGUAUUUAACUAACACAUUGGAGACGAGUUGAGGUGUCUAGAUGUGCAUACUCAAAGUUUAAGUGUUUGUUUCUGUAUUAUGC	237	spiLA1589-miR7992-3-5p	UUUGAGAGUGCACAUCUAGAUACC	26-49	stu-miR7992-5p	4	0	24	24	1
			spiLA1589-miR5226-3-3p	UUUGUAGAUGUUGGAGUAUUUA	141-162	mtr-miR5226	5	0	22	22	1
spiLA1589-MIR7981d-4	CUAUGACCGAAAUCUCAGAGACACACCUUAACUUAACUAAGGUUCUAUUAAUCUCAACUCAUUUGUUUUGUAAUUUUGUACUGGUACACUCCGUGACUCGAGGCGCGUGAGAGAUGUUUGGAUGUCAGUGUACAGAAUUACAAAAAAAAUGGAUUCGGGGGUAAUAGGACUUUAGUUUAGUUAAGGUCUGUCGCUCGAAUUUCGAUCAUAC	211	spiLA1589-miR7981d-4-5p	CCGAAAUCUCAGAGACACACCUUA	7-30	sly-miR7981d	4	0	24	24	2
			spiLA1589-miR7981-4-3p	AUAGGACUUUAGUUUAGUUAAGGU	164-187	stu-miR7981-3p	0	0	24	24	1
spiLA1589-MIR7997c-12	AUGUUAUGUUGCUCGGGCUCUUCAAAAAUGAUUUAUAAGAUCACCCUCAACAAUGAGAUACUCACUUUUGAAGAACCUUUUCAUACGUUAGGUUGUUUGGACUCUCCAAAAAUAUACUCUCACCAAGUCUAAUCCUCAACAACCGCACUAACUGUUGUAGGAUCAGCAUAAGCACGUCAACACUUUUGAAGAGUUCGAGCAACAUAAAAC	210	spiLA1589-miR7997c-12-5p	AUGUUGCUCGGGCUCUUCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-12-3p	CUUUUGAAGAGUUCGAGCAAC	183-203	sly-miR5303	1	0	21	21	2
spiLA1589-MIR160e-2	GACAUGAAACUCUAUACAUGCUUAGCUCCUAGAAUGCCAUCUGAAAAGGCCAUCAAUUCUUGGUGGAACAAUGCAAAUGGCAUACAAGGAGCCAGGCAUGUUGUGUUAUCGAUCAC	116	spiLA1589-miR160e-2-5p	UGCUUAGCUCCUAGAAUGCCAUC	19-41	mes-miR160e	4	0	23	23	1
			spiLA1589-miR160-2-3p	UGGCAUACAAGGAGCCAGGCA	78-98	aau-miR160	1	0	21	21	1
spiLA1589-MIR8038b-2	UAUUUUUCAAGUCAAAACAGUUUCUCCUUGUGAGUAAGUUGAAUCUCGUGCUCGUUAAACCGCAAGAGACGUGGAAUGCGUCCCAACAUGAGAUUCAGCUUACUCACUUGGAAAAAUUGUUUUUGCUUGAGAAGCA	136	spiLA1589-miR8038b-2-5p	CCUUGUGAGUAAGUUGAAUCUC	26-47	stu-miR8038b-5p	0	0	22	22	1
			spiLA1589-miR8038b-2-3p	AUUCAGCUUACUCACUUGGAA	93-113	stu-miR8038b-3p	4	0	21	21	2

spiLA1589-MIR7984d	CACGGUAAAUUUAUGGAAAAAGGGUCUGAAAUAUAUCUGAACUUUAACCCAAAUUAUUGUAACAAUCUCCAGCUUUUGGGAGGACCUUUUACUCCGUACCUUAUAAAUACAUUAUUAAAUAGUGCAGAGGGUAAUAGGUCCUCCCCAAAGUUAGGAUUGUUACCACAAUUUCGAUCAAAGUUCGAAUAUAUUUAAAACCCUUUUCCCCUAAAUUUAUCCUUU	222	spiLA1589-miR7984d-5p	AUCUGAACUUUAACCCAAAUUAUU	35-58	stu-miR7984d-5p	5	0	24	24	1
			spiLA1589-miR7984d-3p	CAAUUUCGAUCAAAGUUCGAAUAU	166-189	stu-miR7984d-3p	2	0	24	24	1
spiLA1589-MIR5162	AUUAGGUGUCAAUAGAGGGUAUAUGUAUAAUUAUAUCAAUAAUCUGUGAUAGAUUUAUAGAUUGUGUAAGGUGGGAAAUGACCAAAAUACCCCUAAAGUGACUAUAAUUUAGCUAAUACCUCUCUUUUACACACUCAG	139	spiLA1589-miR5162-3p	AAAUGACCAAAAUACCCCUAAAGU	77-100	osa-miR5162	3	0	24	24	1
spiLA1589-MIR2607-1	UUUUUAAUCCUCGAGAGUAGUAUAUAAGAAUCUUGUUCAAUUUCUAAAUACGUGCAAUUUUUUUUUUAACUGAGAUUACCUUUUGAUGCAAUAUAUGUUUUUGUUAACGAGAGAAAGGAGACUGAGAUGUAGUUUGGACAUGUGAAUAGGAGAUAUGUGGAUGUACUACUAAGGAGGUGUAAGAG	185	spiLA1589-miR2607-1-3p	AUGUGAAUAGGAGAUAUGUGG	140-160	mtr-miR2607	5	0	21	21	1
spiLA1589-MIR408-2	AAAAGGAAGGAUUGUGGGGAGAGGAGAGCCAGGGAAGAGGCAGUGCAUGGAAUAGGCAAAGCAAAAAUUGCACAUCUCAUGCUCUGGCUCGUCCCCGUCUAUCCAUACCACACCAAUUUUUACCUCAA	128	spiLA1589-miR408-2-5p	GAGAGCCAGGGAAGAGGCAGU	24-44	bra-miR408-5p	1	0	21	21	1
			spiLA1589-miR408-2-3p	AUGCUCUGGCUCGUCCCCGUC	79-99	cas-miR408	5	0	21	21	1
spiLA1589-MIR9760-3	AUUAUCAAAACAAGAUAAUUAUUGUCAAUCAAGACAAUGCAUUACCCCAGGGUACUUUCUUGACCUUCCAAAAUCGAGCACACAACUACAACUUAUUCACUCUCUUGUAAAUAGAGAGUUAAAACACACAUGGAUGAUGUGUUUGCUAUUGAAAUAAAUAACAAAAUGUUAUUUUUUGGUCUUAGAGAGUUACGGGCUCAAAUUGUGUCAGUGAUGACACUUCUAUCAAUGUUGUUGAUUCU	243	spiLA1589-miR9760-3-3p	UGGAUGAUGUGUUUGCUAUUG	132-152	gma-miR9760	5	0	21	21	1
spiLA1589-MIR159b-3	UUGAAUUAUCAUGAAUGAUAUGCAGAUACUUUCUGUUAUAUUUUUGGAACACUAGGGCUCAUAUCAUUCCAAAACCAGAGCAUAUAUACAGUUUGUACUAAUGGAUAUGCAUGUGUCAUAAUCUUAUUUAACGAUAUGAUAUUUAUUGAAUAUUGAAUCGAUCGAUAAGAUUGUAUCACGUGUCCCUAUUUAGUAUUUCGUUAGAGUGAAGGAUAUUUAUUCUCUAAUUUUUUUUAAAUGACAGGUGCAUCAACGUCUCAAAAGUAUGACGAAGAAUUUCUGUAUACCAUUUACGAUAGUUUGG	304	spiLA1589-miR159b-3-5p	GGGCUCAUAUCAUUCCAAAAC	55-75	bdi-miR159b-5p-1	5	0	21	21	1
			spiLA1589-miR2636-3-3p	UUUCGUUAGAGUGAAGGAUAU	196-216	mtr-miR2636	5	0	21	21	1
spiLA1589-MIR5837	AUUAACAGUAAGUACCCCAAUGACACAUCCGAUUUCAACAAGAGAAGUUUGAAGGACAUGCAUUUAGUGUAAUCCAACUAUCCCUUGCACCUAACCUUCUUUGUGAAGUGAGUAAAAGUACUGAAGAGGUGACCAAAUAACUUUGGGAAGGGAUGGAAGGACUUUACUGGGACUAAUUGGUGACAAGAAGGAUGUUGUUUCAACAACGUCUUUACACAUUUAAGAUGUAGUCGGGUACUUUGUUGCA	247	spiLA1589-miR5837-5p	AAGUUUGAAGGACAUGCAUUU	45-65	osa-miR5837-1	5	0	21	21	1
			spiLA1589-miR4221-3p	AAGUGAGUAAAAGUACUGAAGA	106-127	aly-miR4221	5	0	22	22	1
spiLA1589-MIR950	UCAUGCCUUGGGCCACGGUCGUUUCUAUGACAAACUUGGGUUUGGCAAGAGUCUUCGAGGGCACCAAGGCAACA	74	spiLA1589-miR950-5p	CUUGGGCCACGGUCGUUUCU	7-26	pde-miR950	5	0	20	20	3
			spiLA1589-miR2275a-3p	AGAGUCUUCGAGGGCACCAA	48-67	ata-miR2275a-5p	5	0	20	20	2
spiLA1589-MIR8006-3	GAACUAUCGUAAAUGGUAUGCAGAUAUCCUUCCUCAUACUUUAGGGACGUUGGUGCCUCUGCUGUCCAAAAAACUAAAGCAUAUAUACCUUUUACACCAACAAACAUACACGUGUCAUAAUUUUAUACCGACCUGACAUCGGAUCGAUGAAUAAGAUUGUAUCACGUGUCCCUAUUUAGUCUUCCGCUACACUCUAGUUUUUGAACGACAAUGGCACCAAUAUGUUCCAAAAGUAUGACCGAGAGUAUCUGCAUAUCAUUUACUAUAGCUC	271	spiLA1589-miR8006-3-3p	UAGUUUUUGAACGACAAUGGCACC	195-218	stu-miR8006-5p	3	0	24	24	1
spiLA1589-MIR11575-1	UUGGGUGGUCGUCUUAUGUAGCACCUUUAUAUCCUGCAGGUUUCUGAUCUUCACAUUGUCAUAUUUGAAUCUUACUCCCCAGCAGUCCCGAAAUCUGUGUUAGGGAGUAUGAUUCAAAUCUGACAACGUGAACAGCUGAAACCCUACAGGGUACAACAGGUGCUUCAUAAGACGAUGACCUGU	183	spiLA1589-miR11575-1-5p	UUGUCAUAUUUGAAUCUUACU	56-76	pab-miR11575	5	0	21	21	1

spiLA1589-MIR7997b-3	AAACUAUGUUGCCUGGACUCUUCUAAAUGUCACCAGGUGAAAGUCAAAUCCUCCAAAAGUAGUGUACUUUAUGGAGGAUCCAACACAAGUAUAGGAACAUUUUUGAAGAGUUGGAGCAACAUAGCGU	127	spiLA1589-miR7997b-3-5p	AUGUUGCCUGGACUCUUCUAA	6-26	stu-miR7997b	4	0	21	21	1
			spiLA1589-miR5303h-3-3p	AACAUUUUUGAAGAGUUGGAGCAA	96-119	stu-miR5303h	2	0	24	24	1
spiLA1589-MIR9742	UUGCUUGAUUGGGUGUUUUUACUUGUGAGUUCCUUUCUACUACUACUGUUUAAAUUUGACGAUAGAAUGUGUGGUUUGAUCUGUAACACAAUAGCUACUUCUUCAGCUUAUGUAGCAGUAGAAAGGAACUCACAAGUAAAAACACGCAAUCAAGAUUUAAAUAUGUCAUUUAACUUGAUUUCAAAUCACAUUUAAGU	157	spiLA1589-miR9742-3p	UGUGUGGUUUGAUCUGUAACA	68-88	gma-miR9742	4	0	21	21	1
spiLA1589-MIR7696d	GUGCACAAGUAGACAUUUAAAAUUGUGUAAACUUGAACAAGUAGACUCAUGAGUCCUAAGUGACACAAUACAUCUAGGAUGCCACGUAGGAUAAAAACUGACAUGUAGAACAUGUGUGUCGAUUUGUUCAACUUUAUGCAAGUUUAAGUGUUUACUUGUGCAUACUCAAAGUUGAAGGGCAUAAAUGUGAAAUAAUAUCAA	241	spiLA1589-miR7696d-5p	UUUAAAAUUGUGUAAACUUGA	56-76	mtr-miR7696d-3p	5	0	21	21	1
spiLA1589-MIR479a-2	AUGAUGGAGAAGAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCUUCUUCAUACC	112	spiLA1589-miR479a-2-5p	CGUGAUAUUGGUUUGGCUCACU	22-43	nta-miR479a	2	0	22	22	1
			spiLA1589-miR479-2-3p	UGAGCCGAACCAAUAUCACUC	73-93	aof-miR479	0	0	21	21	1
spiLA1589-MIR9472-2	GGUGUCCAAGUAUGGAUACAUGUACAGGUGAUGAUUGUUAUGGAUCCAGAUAGACAGGUAAGUCUAGCCUUUCCAUAAUUCUAGUUUAUUCAUUUUCAGUAGAGGUUGUGAAUAAUUUAAAAAUACAAACUAAGUUGUUCGUACUCCAGUGCAAGUAUGGAUCUAGAGAUCGGAUCCAGGGACAACUGUCUUCAGAACAGGGGAUCCACUUGAACUAU	218	spiLA1589-miR9472-2-3p	UUUCAGUAGAGGUUGUGAAUA	94-114	sly-miR9472-5p	1	0	21	21	1
spiLA1589-MIR10532-1	GGCCAAAAAGAGGUAGAAAAUUAUUAAUAAAAUAAAUUUAGGGGGUAAAGAACCUUAGUAUAGUAUAAGUGUGUCUCUGAUAUUUCGGGCAUAUGUUGAGGGGAUACUUGUGCAUUAUCCCUGAUUAUUAAUAUACAAUUUCUCUAUUUUUGUAU	155	spiLA1589-miR10532-1-3p	AAGUGUGUCUCUGAUAUUUCGGGC	67-90	sly-miR10532	1	0	24	24	1
spiLA1589-MIR5035	UUUACCAAAUGCCUAGAUAAGCCAAAAAAUUGCUUAUAAGCUAGUUUGACCCUCUUAUAAGCUUAGAGGGUGUUUGACUAAGCUUAUAAGCUGGUCAAAUUGGCUUAUUAACACUUUUUAGCUUAUCUACUCAUUUGGUAAA	142	spiLA1589-miR5035-3p	CUUAUUAACACUUUUUAGCUUA	104-125	gma-miR5035-5p	5	0	22	22	1
spiLA1589-MIR8748	GGGUUAUGUUUAACCAGAAGUCUCGGGUUCGAAUCUCAAGAAUGAAAAUAAUUCUUGUAGGUAGUUCUGUACCUUAUUUAGACUCAAAUCCGAGAUCUCUGGUUAUGGAUAAAAG	115	spiLA1589-miR8748-3p	UCUCUGGUUAUGGAUAAAAG	96-115	gra-miR8748	5	0	20	24	1
spiLA1589-MIR11342	AAAAUUCCUUAAAUUUGAUGGAAUUUGUAAACAUUCUAAAACGACCUAGCACAUCGUGUCCCUGUUUUGAAAACACCGCUCAGUGUCCGCUACAUUGCAUCUCGAUUUUGGAUACAUCACUCAACAUUUUAAUACAUCCCGUAAAGUGACGUAUUAGACUAGCACAUCACACAAAGUGAUGUAUCGAUAGAUACGUCGCGUAAAGUGAUGUAUUAGAUCAAUACGCGUAAAGUGAAAGUAUCCAAGAAUAGGAGAGACUAUGGAUUUUUAUAUUUUUUUCAAAUUGCAGGAAAUUUUAGAGAAUAUG	307	spiLA1589-miR11342-3p	AUCGAUAGAUACGUCGCGUAAA	183-204	osa-miR11342-3p	5	0	22	22	2
spiLA1589-MIR10192	UAUCUUCUUGAUUUACAUAUGUAAUUCUAUAGAAUCACAUUUGGUAGGAAAAUAUCAUGUUCAUAUGUUUGAUGUCUUGUAUGUGUAUUUUGUUUUCUUUAUAGGUGGUCUUAAGGAUCAUUUAGGUGUUCCUAGAGAGGGUGUGGGGAGGUCUCUUUUGUCUUACAUAAGUGAGUAUUAGGAUAGCUUUUAGUGAGUGGAUUACAUUUUAGAAGGUGUCUAGAGUGAAAAUAGGAAACAUCAUUGUAACAGUGAAGAAGUUC	264	spiLA1589-miR10192-5p	CAUAUGUUUGAUGUCUUGUAU	62-82	gma-miR10192	5	0	21	21	2
			spiLA1589-miR828-3p	UCUUACAUAAGUGAGUAUUAG	162-182	cas-miR828	5	0	21	21	1
spiLA1589-MIR1048	GAUUCUUAACUUACGUUAGUUGGCAAUUAUGAUCCUUAAUUUUGGAUGUGCACAAAUAAACACUUAAACUGUUAUAAAAUUAAACAUGUAGACACACAUGUUCUACAUGACAUCAUACGCUUGGACACAAAUUUCCUAUGUUGGGUGCAAUGUAAGACGAAUGUAACAAUCUGUUACAAGUUUAAGAGCAACACAUCUUAUGUUAAGGGUCAUAGUUGCCAACUAACACCAAAUUAAGACUC	242	spiLA1589-miR1048-5p	UGUAGACACACAUGUUCUACA	87-107	ppt-miR1048-3p	4	0	21	21	1
			spiLA1589-miR7832-3p	UAGUUGCCAACUAACACCAAA	213-233	ptc-miR7832	4	0	21	21	1

spiLA1589-MIR828b-1	UCACUUCUUUGGGAAAGCCUCUUGCUCAAAUGAGUAUUCCAACAAAUGUCUAAUUGACAUACUUUUGAGAUACUCAUUUGGGUAAGAAGUUUUACCAGGAAGGUC	105	spiLA1589-miR828b-1-5p	UCUUGCUCAAAUGAGUAUUCCA	20-41	mes-miR828b	0	0	22	22	1
			spiLA1589-miR828-1-3p	AGAUACUCAUUUGGGUAAGAAG	68-89	aly-miR828-3p	5	0	22	22	1
spiLA1589-MIR7992-4	UUUAUACAAAUUUAAGUGUCUACCAACUUUGGAAAUGCACAAGUAGACACUUAAACAUGUAUAAAGUUGAAUAAGUAGACGCAUGAGUCCUAUGUGACAAAAUACACGUAGGACAAAAAAAUGAUAUGUAGGACAUGUGUGUUUAUUUGUUCAACUUUAUACAACUAUAAGUGAGCAAAUCCAAAGUUGAAAAACAUAAAUGUGAUUUG	209	spiLA1589-miR7992-4-5p	UUUGGAAAUGCACAAGUAGACACU	28-51	stu-miR7992-5p	4	0	24	24	1
			spiLA1589-miR821e-4-3p	AAGUGAGCAAAUCCAAAGUUG	169-189	sbi-miR821e	5	0	21	21	1
spiLA1589-MIR6191	CCUUUUACUUUGGCCUUAUCUGGCUUAUAUGCUCUCUAAUUUGAAAUUUGCAAAAGUAAGACACUUAAAUUUGUAUAUAUAUAAUUGAAUAAGUAGACACACAUGUCAUACAUGACAAUUUGCAGUCUUACGUGGUGCCUUAAGUGUAUUUUGCCGCGUAGAACAUGUGUGUCUACUUGUUCAACUUUAUACAAGUUGAAGUGGUUAUUUGUAUACAUCCAAAGUUGGAGAGUACACAUGUCAGCUGAGUCCAAAUUAAAGAA	263	spiLA1589-miR6191-5p	UAAAUUUGUAUAUAUAUAAU	66-85	hvu-miR6191	5	0	20	20	1
			spiLA1589-miR1044-3p	UUGAAGUGGUUAUUUGUAUA	196-215	ppt-miR1044-3p	5	0	20	20	1
spiLA1589-MIR1128-2	UAAUUUGUUGACUUCCAAGAAAGCUAUUACUCCCUCCGUCCAACAAUACUUGUCCACUUCAUGAAAUCCAUGAAUAAUUUUACACUUAGUUCCUAAUUUACCCUUAUCAUAAAUUAUAGUCAUUUCACUCAUUUCCCUAUUUCCCUAUUAUAUUUUUCAAGACAUUGUAUUUAUUAUAUUCAAAGGGUGAUAUAAUAAAAUUACCCAUCUAUAAGAAGUGUACCAAGUCAAUAGUGGACAACUAUUGUUGGACAGAGGGAGUAUAAAAGUUUUGAAAGACACCAAAAUG	289	spiLA1589-miR1128-2-5p	UAUUACUCCCUCCGUCCAACA	25-45	ssp-miR1128	3	0	21	21	1
			spiLA1589-miR5049c-2-3p	GGACAACUAUUGUUGGACAGAGG	236-258	hvu-miR5049c	5	0	23	23	2
spiLA1589-MIR5725-2	UUGGGUGUCCCUGCUGUUAAAAAAUUAGAGCAUAUAUGUUCUUCACUCUACGGGAGACUAAAUAGGAACAUGUGGCACAAUCUUAUUCGUUGAUCCGAUAUUUAAUAAAUGUCGGGUCGGUGGAUAAGAUUAUGAUACGUGUAUGUUCGUUAGUAUAAAUGGUAUAUUUGCUCUAGUUUUUUUUACGGUAGGAUCACCAAU	201	spiLA1589-miR5725-2-5p	AUGUGGCACAAUCUUAUUCGU	70-90	bra-miR5725	5	0	21	21	1
			spiLA1589-miR5543-2-3p	UAUAAAUGGUAUAUUUGCUCU	154-174	osa-miR5543	4	0	21	21	1
spiLA1589-MIR868-1	UAUAAAUGAUAUGCAGAUAUCUUCAUCAUACUUUUGGGACAUUUAGUGCCCCUGCUGUAAAAAACUAGAGCAUAUAUAUACCCUUUAUAUUAACGGAUAUAUGCGUGUCGUAAUCUUAUUCACUAACCGAAUAUUUAUUAAAUAUCAGAUCAACGGAUAAGAUUUCACCAUGUAUCCCAAUUUAGGUUUCUCUUAGAGUGAAAGACAUAUAUGCUCUAACACGAUAACACAUAUAUCCCAAAAAUAUGACGGAGGAUAUAUCUAUAUCAUUUUUU	275	spiLA1589-miR868-1-5p	GCGUGUCGUAAUCUUAUUCAC	103-123	ath-miR868-5p	5	0	21	21	2
			spiLA1589-miR11078c-1-3p	GAUCAACGGAUAAGAUUUCA	148-167	lja-miR11078c-5p	5	0	20	20	3
spiLA1589-MIR391	AAAAGGCUUGCUACGCAGGAGAGAUGAUGCUGGACGAUAGAGAAAAUGGGAUUUAAUUUAUUGGCCAGCAUCAUACUCCUGCAUAUUAAGCCUAAA	96	spiLA1589-miR391-5p	ACGCAGGAGAGAUGAUGCUGGA	13-34	sly-miR391	0	0	22	22	1
			spiLA1589-miR391-3p	GCAUCAUACUCCUGCAUAUU	68-87	stu-miR391-3p	0	0	20	20	1
spiLA1589-MIR6232b-1	GAGCUCUACAGUGCAACUUCAGCAUAGUAAAGAGUAGAGACUAAUUAAUGCCUACAUAUGUAGGGAUUAAUGAGUCUACUCUUUGCUAUACUGAAGUUGCACUGUAGAGAUA	112	spiLA1589-miR6232b-1-3p	UCUUUGCUAUACUGAAGUUGC	80-100	sbi-miR6232b-5p	5	0	21	21	1
spiLA1589-MIR156h	GUUUUGACUUUUUAAUUCUUUUUGUUCCUUUUUUCUCCCUCCUCUCCAUUACCUCUAUCAACAAUCACUCUUUAUUCUUCCAUCCUCCUUAACUCCCUGCCAACAUUGUUACCAUUACCUCCACCACCAUCUUCUCUUGCACUUCCUACGCUACCCCAUCAUCACCUCCACCACUAGGAGGGAAUACGCUAAACGACUUGAACAUGCAACAUAUAAUAUCAAUUUAAUGCAGGUGUAUAGCUGCAUAUGGGACAAAGGAGGAAGAAAGAUUGAUUGACGAUAGAUGUAGUGGAGGGAAGAGAGAAAGGAGGAAUAAUAAAAGAAAAGACAAUCU	334	spiLA1589-miR156h-5p	ACUCUUUAUUCUUCCAUCCUC	67-87	mtr-miR156h-3p	4	0	21	21	2

			spiLA1589-miR11440b-3p	AUGUAGUGGAGGGAAGAGAGA	284-304	pab-miR11440b	5	0	21	21	1
spiLA1589-MIR7983-2	ACACACUACGACAAAAUGACUAUCAGCGGUAUUUAAUUAUUAAAUGCCGCUAAAUAUGUAUUUUUAGUGGCAAUUAUCACUCUUUGUAUAUGUCCCUAAAGUCUUUAGCGACAUUGGUUCUACUGGCACUUAACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAGUAUCAAUAUUUAAUACCGCUAAAAGUUGAUUUUGUUAUAGUGACA	213	spiLA1589-miR7983-2-3p	UAAAGUCUUUAGCGACAUUGGUUC	97-120	stu-miR7983-5p	0	0	24	24	1
spiLA1589-MIR5014a-3	UUCAACUUUAGGUAUGCACAAGUAGAUACUUAAACUUGUAUACAGUUGAACAAAUAGACACACAUUUCCUACAUGUCAUUUUUAGUCCUACGUAGUGUUUACGUGUAUUGUGUCACGUAGGACUCGUGUAUCUAUUUGUUCAAAUUUAUACAAGUUUAAGUGUCUACUUGUACAUAACUAAAAUUUUU	188	spiLA1589-miR5014a-3-3p	UUAUACAAGUUUAAGUGUCUA	146-166	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR2673b-1	CCCAUAUCCAAAUCGACCUCUUCCUCUUCCUCUUCCACUUCCACUUUCACUAGUAUGGUAAAAUGAAUUAUGAACAUUGAAAUUUGUUCGAGGUAUAUUGGGAGGAGAAAAGCUGUAGUGGGAGAGAAGAAAUGCUUUGCCACUCAUAGCACCACCAGACAGCUGUAGUGGAAGGGGAUUGAUUGGUUGAUAUUUC	196	spiLA1589-miR2673b-1-5p	CCUCUUCCUCUUCCUCUUCCAC	17-38	mtr-miR2673b	0	0	22	22	1
			spiLA1589-miR11109-1-3p	GGAUUGAUUGGUUGAUAUUUC	176-196	lja-miR11109-5p	5	0	21	21	3
spiLA1589-MIR867-2	UACCCCCCUGAACUUAUUUUAUUAGUAAUUUUUUUACCCGUUUUAGCCUAUGUGACACUAUCUGGUGGGCCCAACGAUGGUUGACUUCUUUUUUUUCAAACUAGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUACUUAUAAAAUAGGUUCAGGGGGUAA	161	spiLA1589-miR867-2-5p	CUGAACUUAUUUUAUUAGUAA	8-28	ath-miR867	5	0	21	21	2
spiLA1589-MIR7997c-13	UACUAUGUUGUUCGGACUCUUCAAAAAUGUUGCUGCGCCCAUGUCAGAUCCUCCAAAAAAUGUACUAAUUUUUGAGGAUCCAAUGUGCACUCGGUGCCUUCUUUGAAGAGUUCGAGCAACAUAAUU	126	spiLA1589-miR7997c-13-5p	AUGUUGUUCGGACUCUUCAAAAAU	5-28	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-13-3p	UCUUUGAAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
spiLA1589-MIR9497	GCGUUAUGUGGUUGUAGGCUUUUUUAUCUUGGUUUAAACUUUCUGAGUAAGUAUGUAUUUGUGGUGGUAUAAAUAAUGAGUCUUUUUGGUUCUUUGGAAUAAAUGGUUUAUCGAAGAUUUAUUCAUAUUUACAUUUGUAUAUCUUAUUCCAAUGGCUCCUUUUAUUGUAGAUGUGCUUGCUCUAGCUGCAUUUAAACAAACAUUGUCAUGGGUUUUAUGGAGUUUCCCAACCUUGGCAUACUUACAAGAUGCAUAAGUCUUGUAUCACAUAAUCU	276	spiLA1589-miR9497-5p	CUUUGGAAUAAAUGGUUUAUC	92-112	bdi-miR9497	5	0	21	21	2
			spiLA1589-miR5797-3p	UCAUGGGUUUUAUGGAGUUUC	207-227	osa-miR5797	5	0	21	21	1
spiLA1589-MIR399b-4	UAUAAGGGAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAU	101	spiLA1589-miR399b-4-5p	GGGCUACUCUCUAUUGGCAUG	20-40	sly-miR399b	0	0	21	21	1
			spiLA1589-miR399o-4-3p	CGCCAAAGGAGAGCUGCCCUG	63-83	stu-miR399o-3p	0	0	21	21	1
spiLA1589-MIR11146	CAUGUCAUGCCAAUUAGGAGAUAGUGAUGAUUUUGAAAUGUCAAGUAUAUUUGGAGGAAAAUAGUGAUAGUUGAGUGAUAUUUUGGUCUUAAAUGAAAUAUAAAUGAUAUUUCAAGACAAUUCUCUUAACUCGGGUGACCAC	142	spiLA1589-miR11146-5p	GAAAUGUCAAGUAUAUUUGGAGG	35-57	lja-miR11146-3p	5	0	23	23	1
			spiLA1589-miR8045-3p	AGUGAUAGUUGAGUGAUAUUU	63-83	stu-miR8045	5	0	21	21	1
spiLA1589-MIR1533-1	AACAUAUUCAGUAUUUGGGCUGUUGGUUUGUAGUGUGACACUACAUGUCAGACGUCUCCGGUUCGAACCUAAGGUCCAAAAUGGACAGUGAAAUAAAAAUAAUGUUGUCACUCAUGCUCGAACUGGAGACCCGUGAUAUGUAGUGUCAAGCUCCAACCAACAGCCCAAGUAGCUAAAUAUACA	183	spiLA1589-miR1533-1-3p	GAAAUAAAAAUAAUGUUGU	90-108	gma-miR1533	5	0	19	19	3
spiLA1589-MIR9470-2	GCAUGUCCAGUAAAGAACUCAGUAAGUCCGUAAGAAUAUAUAUUGGGGGUACAUAGGACUUCUCAAUGCCCAAUAUUAUAAAAUAUUGGGCAUAGUAUAAAAAAUUGGCUAAGGGGUGUUAGCCAAUUUCUAUGUAUAUAUCGGAAAAAGCAUAGUAUGAUCCAAGCUUUUUUAAAAUUGUACCUGCAUUGAAAACCCUAAAAUGAUUUAUUAUUUAACUCACAAAUUAGGUACGAGGCAUCCAAGUGUCAAGCCUUGGUACCAUCGCACAUGAUCAUUUAAAAUUAUCAUGUAGAUAAGUAGUGCCCAAGGACAUAGUGAGGAUCUUUGGGACAAUA	338	spiLA1589-miR9470-2-5p	AUUGGCUAAGGGGUGUUAGC	104-123	sly-miR9470-3p	5	0	20	20	2

			spiLA1589-miR477e-2-3p	UGAGGAUCUUUGGGACAAUA	319-338	csi-miR477e-3p	4	0	20	21	1
spiLA1589-MIR9471a-2	GAUAACUAUUGGCUGAGUGAGCAUCACAACUUAUAUUUA UAUAAAAGAAUCCUAAACUAAUUUGAAAAUAAAAUAUAGAA AAUUUGAGUUUGGACGCGGUUUUAUUUGAGAAUAGCAAC GUGCAGACUGCGGAUCAGCCAAUGGUUUGC	149	spiLA1589-miR9471a-2-5p	UUGGCUGAGUGAGCAUCACAA	9-29	sly-miR9471a-3p	2	0	21	21	1
			spiLA1589-miR11443-2-3p	AUUUGAGAAUAGCAACGUGCAG	104-125	pab-miR11443	5	0	22	22	1
spiLA1589-MIR1046-2	UGGCACUACAAGAAAACUGUGAAUUACAUGGGAUUUUCC UAAGAUUAGUAUGAAAAUACGUAGGAAACUUAUUUUCCUG CAAAAAUUCAUCCUGAUUUUCAGGAAAAUCUCAAUGUAAU UCAUACUUUUCUUGUAGUGUGG	141	spiLA1589-miR1046-2-3p	UGUAAUUCAUACUUUUCUUG	114-133	ppt-miR1046-5p	5	0	20	20	1
spiLA1589-MIR11498a	UUAAAUUACAAAAAUCUCUUAAAAUUUAUGGAUUUUGGAU ACAUUACUAGUUCUUGAUACAUGACUCGACUUCUGGAUA CAUAGGUGAGGGAUGUAUCCGCAAGGGGAGGGAUGUAU CAGAGAUGGGAUAUGACAUCCGAAUGCAUCACUUGACUU ACAGAUACAUCAGCAAACAUCCGGAUACAUAGGUGAGGA UGUAUCAGGGGAGUUAUUUAUUUGUGAGGGGAUAUAAUG UAUCAUCGAGAGGAGAGUGAUGUAUUCGAGAAGAGAUUU UUGAAACAUUUUUAAAUGAUAGAGAAUUUUAGAGAUUAUG	313	spiLA1589-miR11498a-5p	UAUCAGAGAUGGGAUAUGACA	115-135	pab-miR11498a	4	0	21	21	1
			spiLA1589-miR11554-3p	UUACAGAUACAUCAGCAAACA	155-175	pab-miR11554	5	0	21	21	1
spiLA1589-MIR835-2	AAAUUAAGGGAAAAAUAAAAUGAAGGCUUUUGGGGUUUU CUUGCAUGUGUUCUUUAUCCCCAAAAGACUGAUUACUUU UUCUGUUAAACC	90	spiLA1589-miR835-2-3p	UUCUUGCAUGUGUUCUUUAUC	38-58	aly-miR835-5p	1	0	21	21	1
spiLA1589-MIR169r-4	UGCAGCCAAGGAUGACUUGCCGGACCAUAAAUUGCUAGG UUUUAUAGUUUCGGCAAGUUGUUCUUGGCUAUA	72	spiLA1589-miR169r-4-5p	CAGCCAAGGAUGACUUGCCGG	3-23	csi-miR169r-5p	0	0	21	21	1
			spiLA1589-miR169b-4-3p	GGCAAGUUGUUCUUGGCUAUA	52-72	zma-miR169b-3p	1	0	21	21	1
spiLA1589-MIR169m	UAGCCAUCUUCCUGGCUAUAUUCCCUUGUAAAGUGUCCU UCUUGUCCGCAUUUGUAGCAUCCCUCUCCUCCUCCACCG CCUCCUUGGCUACAUUCCCUUGUGAAAGAAGGAAGGGGC UGCUACAAAUGUGGGGAAGAAGGGCAUUUUGGAAGGGAU UGUAGACAAAAGAAGGAAA	175	spiLA1589-miR169m-5p	AGCCAUCUUCCUGGCUAUA	2-20	aly-miR169m-3p	5	0	19	19	2
			spiLA1589-miR169c-3p	ACCGCCUCCUUGGCUACA	75-92	stu-miR169c-3p	4	0	18	18	2
spiLA1589-MIR7122	AUAUAUACAGAGAAACCGCUGUCGAUUAUAAUGGGAAAUU CGGUGUUUCUCAUACUCCACAGCGUUUUUCUGUAUAACC	79	spiLA1589-miR7122-5p	AUAUACAGAGAAACCGCUGUCG	3-24	stu-miR7122-5p	1	0	22	22	2
			spiLA1589-miR7122-3p	ACAGCGUUUUUCUGUAUAACC	59-79	stu-miR7122-3p	1	0	21	21	1
spiLA1589-MIR821b	AAAUUUAUUUAAUAAAACUUCGGUUCUUCGGUGCACCGU AGUUUCGGGACCCUUGCAUUGAACUCCGAACCGAAGAAU CGAAGUUCCGAAAAUAAAAAA	99	spiLA1589-miR821b-3p	AAGUUCCGAAAAUAAAAAA	81-99	sbi-miR821b	5	0	19	21	1
spiLA1589-MIR3693i	UGAUUCAUUGGUGAUAGAUAGGUGUUUAGUCCUAUUGAG ACAACAGAACAAUUUAACUAGAAGUUUUGGAGUUCUCUAA AAACUUCUAGUUAAAUUGUUCUAUUGUCUCAAUAGGACUA AACACCUAUGUGUCACCAAUGAACUA	145	spiLA1589-miR3693i-5p	UCAUUGGUGAUAGAUAGGUGU	5-25	pab-miR3693i	5	0	21	21	1
spiLA1589-MIR3951b	UAAGUACAAUCUCUCGCUAUUUCUUUUAUUUUUUAUCUAA CAAUAAUUAGUUUCACCCCAGGGGAUCUUGUUGUCCCUA UAAAGGGGUAGUAGUUAUUGUUGUUGUGGUGUAUGAGCA UGAAAUCUUUAUAUCAACCUUAAAUAGGAAAGCUUAAAGA ACUCAAGUGAGCAUUGUGACAUG	181	spiLA1589-miR3951b-5p	UUUCUUUUAUUUUUUAUCUAAC	20-41	csi-miR3951b-3p	5	0	22	22	1
spiLA1589-MIR6273-2	UGUCUGAGCCAGCUUAUGAGCUGCUUGAAUCGUUUCAAG UAUCAAGUAACUCAGCCAAAUUAUAAGAUAUAAUAAUCCA GGAUAAAAUGCAGGAUUAUUUUAUAGUAUGUUUAGUUGG AGGUAUUAGGUAAUGCUUGGAUUGUUUAUUCCACUGUUU AUACCUUAGUGAUAAUAUAAGUUUAUCUCAUAUGCAUGG UGGAAUAACUUAUAACGGCAUAAUUAAUCUCGAGAUAACU UGUUUCCAACCAAACAAUUCAUAAGUGUCUUAGUUU	272	spiLA1589-miR6273-2-5p	AAUGCAGGAUUAUUUUAUAGU	86-106	ppe-miR6273	5	0	21	21	1
			spiLA1589-miR5025-2-3p	ACUGUUUAUACCUUAGUGAUA	151-171	ath-miR5025	5	0	21	21	1
spiLA1589-MIR2868	GAAAUAAUGCAUGCAUUAGCUUUGUGUAUUAGUAGUACC UUGUUUGGUACACUUUUUGAACCUAUGUAUAGCUAAUGA UUGCAUUAGUUAUACAUUCUAUUGUGUAUUGAGUGUAUU UUCCUACGAAUACAUGGAAAUUCAUGGUAUUAGUAAUGC AAGAGGGUUCAAUGUAUGCAUUAUCAU	183	spiLA1589-miR2868-5p	UUAGCUUUGUGUAUUAGUAG	16-35	osa-miR2868	5	0	20	20	1

spiLA1589-MIR477c	CAUAACAAACUAGUUCUUGAGGUUGAGUUAGGCGCAUGUGUCAUAUCUUUACAUGGUCUGAUAUCUGAGACCAUGUAAGGAUAUGACACAUGAGCCCAACUCAUCCCCAAGAGUUAGUUUUUGCC	125	spiLA1589-miR477c-5p	CUAGUUCUUGAGGUUGAGUUA	10-30	csi-miR477c-3p	5	0	21	21	3
spiLA1589-MIR1098	AACGAAGCUGAUGACGUGUCUGCAGCAAGUGUUGAUGAAGAAGGAAGCUGACGAUAGGAACAGGUCCAACAAAGCUGACUGGCGAGUUUACAGCACUUGCUUCAGACACGUCAGCCAGCUUCGUA	125	spiLA1589-miR1098-5p	UGAUGACGUGUCUGCAGCAAG	9-29	smo-miR1098	5	0	21	21	1
spiLA1589-MIR171f-9	CUAUGAAACAGUAACUUUGAUAUUGGCCUGGUUCACUCAGACAACAAAAUGUAAACUAUAUUUGAAUGGUUGAGUUUUCGUUUUUCGUUUGAUUGAGCCGUGCCAAUAUCUCAGUUUCUCUUUCACUU	128	spiLA1589-miR171f-9-5p	UAUUGGCCUGGUUCACUCAGA	21-41	csi-miR171f-5p	0	0	21	21	1
			spiLA1589-miR171a-9-3p	UGAUUGAGCCGUGCCAAUAUC	90-110	aof-miR171a	0	0	21	21	1
spiLA1589-MIR5174d	GUUUCCUAGUGUGAAGUCGGUAGAGUACUAAUAAUGUGAUAUAGUUAUAGUGUAAUUAUAUAUUAAAUUAUUACUCCCUCCGUUUCAACAAGGAUGA	97	spiLA1589-miR5174d-3p	UCCCUCCGUUUCAACAAGGAUGA	75-97	bdi-miR5174d-5p	5	0	23	24	1
spiLA1589-MIR7997b-4	ACAAUUAAAACAGCAGACUUCAUAUAAUUUAUGCUGCUCGGACUCUUCAAAAAUAUCAAGGGGUGUGUGUCGGAACUCGGAUCCUCCAAAAGUUGUGCAUUUUUGGGGGAUCUGGCAUCGGCGGAACAACAUUUUGAAGAGCCUGAGCAACAUAAAACAUAAUUAUAAAGUAACACCUCCUUUUAAUAUU	190	spiLA1589-miR7997b-4-5p	AUGCUGCUCGGACUCUUCAAA	31-51	stu-miR7997b	0	0	21	21	1
			spiLA1589-miR5303-4-3p	AUUUUGAAGAGCCUGAGCAAC	131-151	sly-miR5303	4	0	21	21	2
spiLA1589-MIR7492f-1	UGAUACCUCUACAACAAAAAUGAUCAUUAGCGGCAUUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUGUCACUGUUUGUAUAUUUCGCUAAUGCCUUUAGCGACAUUGGUUCUAAUGGCACUUAAGUAAUGCCGGUAAAGACUUUAACACUCUUUAUUAGUGUCAAUAUUUAAUGCCGCUAAAAGUUAUUUUUAUUGUAGUGUACUA	219	spiLA1589-miR7492f-1-5p	AAAUGAUCAUUAGCGGCAUUU	18-38	gra-miR7492f	4	0	21	21	3
			spiLA1589-miR7983-1-3p	AGUAAUGCCGGUAAAGACUUUAAC	137-160	stu-miR7983-3p	1	0	24	24	1
spiLA1589-MIR403	UCAGGAAGAGGCAUAUUUCACGUUUGUGCGUGAAUCUAACAACUCUUUUCAUCAGAAAAACUGUUAUUGUUUGCUAGAUUCACGCACAAGCUCGUAAUAUGGCUUUUCCAAU	112	spiLA1589-miR403-5p	CGUUUGUGCGUGAAUCUAACA	21-41	sly-miR403-5p	0	0	21	21	1
			spiLA1589-miR403-3p	CUAGAUUCACGCACAAGCUCG	74-94	sly-miR403-3p	0	0	21	21	1
spiLA1589-MIR7997b-5	UCAUAAGUUUAAGUUGCGCGGACUCUUCAAUGUAGAUGCCGCACUCGUGCCUGAUCUCCAAAAAUAUGCUACUUUUGGAGAAUCCGACACGCACCCACUGACAUUUUUGAAGAGUCCGAGCAACAUAACUGUAGGU	136	spiLA1589-miR7997b-5-5p	AAGUUGCGCGGACUCUUCAAU	11-31	stu-miR7997b	4	0	21	21	1
			spiLA1589-miR5303d-5-3p	UUUUGGAGAAUCCGACACGCACCC	73-96	stu-miR5303d	0	0	24	24	1
spiLA1589-MIR4249-1	UGAACUUAGAUUUUUGAAGCCCAUUUAAUAAAAAGGUUUUUUUAGCCCAGUCUGAAUAAGCCUGUUGAUUUGAUGGGUUUGAGAAAUAUAGGUAGG	96	spiLA1589-miR4249-1-3p	UGGGUUUGAGAAAUAUAGGUA	74-94	aly-miR4249	5	0	21	21	1
spiLA1589-MIR7828	UGCUAUAAAUGGUAUAUAAAUAUUCUUCGUUAUUCUUUUGAGAUAUUGAUAUUCCUGUCAUUUAUAAAUUAGAGCACAUAUGCCAUUUACUCUAACGAAGGGGCAGGGGCACCAUGUCCCCAAAGUAUGAUGGCGAGGGCACCAAUGUCCCAAAGUAUGAUGACAAGGACACCAAUAUCCCAAAGUAUGAUGGCGGGGGCAUCAAUGUCCCAAAAGUAUGACGAAGGGUAUUUGCAUACCAUUUAUAAUA	250	spiLA1589-miR7828-3p	GAUGACAAGGACACCAAUAUC	159-179	ptc-miR7828	2	0	21	21	1
spiLA1589-MIR7983-3	CGGUUGAGUUGAAGGUGGUUACACUACAACAAAAAUGAUCAAUAGCGGCAAUUAAUUCUCAAUUGUAGCUAAAUAUGUAUAUUUAGCGGCAAUUGACACUUUGUAUAUGUCCCUAAAGUCUUUAGCGACAUUGGUUCUAAUGGCACUUAACCAAUGCCGGUAAAGGCUUUAGCACAAUUUAUUAAUGUCAAUAUUUAAUGCCGCUAAAAGUCAUUUUUGUUGUAGUGUUAUAGCAUCUCACCCCAAAUA	249	spiLA1589-miR7983-3-3p	UAAAGUCUUUAGCGACAUUGGUUC	114-137	stu-miR7983-5p	0	0	24	24	1
spiLA1589-MIR7981d-7	UACAAGUACCCUCUAGACUAUGAUCGAAAUCUCAGAUACACACAUUAACUAAACUAAGAUCAUAUUAUCCUCCUCAAAUUAUUUUAUUUUGUAAUUUUGUGCACCUUUCACUUAUGUGGCAUUCAAGUAUCUCUCACACGCCUAUAUUUUGUGGAGUACUCAUGGAGUGUGUUAUGUAAGACAAAAGAUGUAUAAAAUUAAAAAAAAAAGUUCAGGAGGUAAUUGUACCUUAAUUUA	285	spiLA1589-miR7981d-7-5p	UCGAAAUCUCAGAUACACACAUUA	24-47	sly-miR7981d	4	0	24	24	1

	GUUAAGGUAUGUCUCUUGAUUUCGUUCAUAGUCUAGUGGAUACUUGUG										
			spiLA1589-miR7981-7-3p	AUUGUACCUUAAUUUAGUUAAGGU	222-245	stu-miR7981-3p	4	0	24	24	1
spiLA1589-MIR7997c-14	AACCUAUGUUGCUCGGACUCUCCAAAAAUAAGGAUCAGAUACACAACCAUCGAUAUUUUUGACGAGUUCGAGCAACAUAGAAG	83	spiLA1589-miR7997c-14-5p	AUGUUGCUCGGACUCUCCAAAAAU	6-29	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-14-3p	UUUUUGACGAGUUCGAGCAAC	56-76	sly-miR5303	1	0	21	21	1
spiLA1589-MIR11583b-1	UUUUCUCUCGCUUUAUACAAAACAGAAACACAAUAUAUACAAUUCUGUUAUAUAAAGCGAGAGAGGC	67	spiLA1589-miR11583b-1-5p	UUUUCUCUCGCUUUAUACAAA	1-21	pab-miR11583b	5	0	21	21	1
			spiLA1589-miR415-1-3p	UACAAAACAGAAACACAAUAU	16-36	ath-miR415	5	0	21	21	2
spiLA1589-MIR9668-1	CGGAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUCA	66	spiLA1589-miR9668-1-3p	CAAAGUACAAUUAUUUUCGCA	15-35	tae-miR9668-5p	5	0	21	21	1
spiLA1589-MIR9668-2	GCCGGAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUCCAUA	71	spiLA1589-miR9668-2-3p	CAAAGUACAAUUAUUUUCGCA	17-37	tae-miR9668-5p	5	0	21	21	1
spiLA1589-MIR5160	AAAAAAAUGAUUUUAUUCAUCAAGAUAGAGGGUAUAAUUCUGUUGAUCCCUUGAUUUUACUCUCGUAAGAUUUAUCCAUGAUUCGAAGGCCGUUAGUGGUGUAUUUCUUGAACUAGGAUGAUUUAGAUUUUAUCCCUCUAUAUGAAUAAUCUAUCAAUUUGUG	163	spiLA1589-miR5160-5p	CAAGAUAGAGGGUAUAAUUCUG	21-42	osa-miR5160	4	0	22	22	1
spiLA1589-MIR5026-1	UAGUAAAUAAUUUUCUAUCUCUUUUCGGCCUAAGUAGGCACUAUAAAUCAGAUUACUUGAAAACACGCGCUGGGGCCCAGAAGAUAGUGUCACGUAGGCCGAAAAGCGAAAGAAAAUUAUUUAUAA	126	spiLA1589-miR5026-1-3p	GCCCAGAAGAUAGUGUCACGU	75-95	ath-miR5026	5	0	21	21	2
spiLA1589-MIR5371	AAAUUAGAAUUUAUUAUUAAAAAAUUUCAGUGACGAUUUUCUAGGCUUUUGUGACGACUAUUGUCGCCGCUAAAGGUCUAAUUCUUUUGUAGUGAAUCCUAGUUGGCAAUGCUUAGGUGGAAGAAUUAGUCUCACGUGGCUUGCCAAGUCAAUAAAAAUGUGGGUGUUAACUCUUGAGGGUAUAUGUGGUCUCUUACGAUAACAUCAAGGGCAAUUUUGACUCUUUUCCGUAGAAUGUAUAUUCAAAGGAGAAUCAAAUGUCUAGAUAAUUCUUUAAAUAGAAUUUAAUAGAUAAAAUCAAGGG	304	spiLA1589-miR5371-5p	UUUCAGUGACGAUUUUCUAGG	25-45	gma-miR5371-3p	4	0	21	21	1
			spiLA1589-miR4223-3p	AUAGAAUUUAAUAGAUAAAAUC	278-299	aly-miR4223	5	0	22	22	1
spiLA1589-MIR11423i	GUGGGAGAGAUGACCGCAAUCAAAGAUGAUCGGAUCUGGCCAUCUACGGCUUUCCAGGCGGUAUGGGCCGGAUUGGUUUUUUCUGAUUUGUCCGUGGCGGUGAUGACUGCCGGCGGCGGUUCUGUGCGUCCAUCGACGUAUUUGAGAAGGUAAUUGGCCUCAAGGGCUGUAAGAACAAAGGAAGAAUUAUUGACGUUAUCAAAAAUCAUGCAUGAUCUUCCAGAGUUGUUGUUCAUCUCUCCAUG	245	spiLA1589-miR11423i-3p	CUGCCGGCGGCGGUUCUGUGC	107-127	pab-miR11423i	5	0	21	21	1
spiLA1589-MIR8003	AGGUAGGUUCUUCAUUAUUUCGAUAUACAAAUGGGUCCUGUAUUUUUUUCGGUAUACAAUGGAUCCUGCAUUUGUAUAUUUCAGUAUAUAAACGGGUUCUGCAUUUGAAUAUUUCGGUCUAAUUGUAUAUUUUGAUAUACAAAUGGGUCCUACAUUUGUAUAUUUCGGUAUACAAAUGGGAUGACAAAAAAUAUG	233	spiLA1589-miR8003-3p	AUUUCGGUAUACAAAUGGGAUGAC	162-185	stu-miR8003	0	0	24	24	1
spiLA1589-MIR5180a	GAAUGUUUGCUACGAAUUACAAAUAGAAGAAACUAUGGGGCGUUAGUUGGCAACUAUGACCCUUAACUUUAGAUGUGCACAAGUAGGCACUUAAACUUGUAUAAAAUUGAACAAAAUUUGACACACUCAUCCUACAAGGCAUCCUACAUGGAAAAUUUCUGUCCUACAUGACGUCCUACUUGUAUCAUUCACAUUUUAAGUUAAGGGUCAUAGUUGUAAACUAACACC	190	spiLA1589-miR5180a-3p	UAAGGGUCAUAGUUGUAAACU	164-184	bdi-miR5180a	5	0	21	21	1
spiLA1589-MIR6230	AAACAAUGUAUACACCUCAACUUGGUUUAAGUUGGCUCCAUAACAAGGCAUUUCACGCGUGUUUACGGGGGCCAACUUAAAGCAAGUUGAGGUGUCUAGAUGUGCAU	107	spiLA1589-miR6230-3p	AAGCAAGUUGAGGUGUCUAGA	80-100	sbi-miR6230-3p	5	0	21	21	2
spiLA1589-MIR10532-2	GGGACUCUAUUUGUAUAAGUGUGUUUCUGAGAUUUCGAGCAUAGGUUGAGGGGGUACUUGGGCUUUAUCCCUAAGAACAACUAUAAAUGAGUAAAGACAAAAUUCCCUCUUGAACUUGUACCGAAAAGUUAGUUACACGCUUAAACUAUCACAGUAAC	158	spiLA1589-miR10532-2-5p	AAGUGUGUUUCUGAGAUUUCGAGC	17-40	sly-miR10532	2	0	24	24	1
spiLA1589-MIR11563-2	GAAGAGAUAGUACUAUCUAUACAUUUCAUUAAAAUGAUUUUCUGGGAUUUUGUGGCGAUUGUUGUCCCCGCUAAUGGUCUAAUUCUUUUGUAGUGAAUCCUAGUUGGCAACGCUUAGGUGGAAGAAUUAGUCCCACAUUGUCUUGCCAUGUCACGA	239	spiLA1589-miR11563-2-5p	UUCUGGGAUUUUGUGGCGAUU	40-60	pab-miR11563	5	0	21	21	1

spiLA1589-MIR6231-2	AAACUUGGGGAUUAACCUUAGAAUAACGGCAGGGCAUUUUUUAUCCCAAAAUGUAAUGAAGGGUAUAAGUGGUCUAUUUCGCAAACUUUUGAAAGGCAUAUAUCGUUUAUACGACAGCGAAAUCGAGAAAACUCGACAUUUUAAGGUAUAUUUGUGUCCACAUGGACACAUUACUAUUUAAAAUGAUGCAAUAUUUAUCAUAUCCACGUGAUCACAUAUAUACCUUAAAAUAC	151	spiLA1589-miR6231-2-3p	UAUUUGUGUCCACAUGGACAC	66-86	sbi-miR6231-3p	4	0	21	21	1
spiLA1589-MIR5181b-1	GGGACACAUGACACAAUUUUAUCCAUUGAUCCGAUAUUUAAUAAAUGUCGGGUCAGUGGAUAAGAUUAUGACACGUGUAUG	81	spiLA1589-miR5181b-1-3p	UCCGAUAUUUAAUAAAUGUCG	30-50	bdi-miR5181b	4	0	21	21	1
spiLA1589-MIR6145b-2	UUAAAUUUAACCUAUUAUUUUUUAGCUUACGUGGCACUAUCUUUGUGGGCCCAACGAGGGUUGAUUUUUUUUCUGAACUAGUGCCACGUAGGCUAAAAAGGAGUAGAAAAUUACA	114	spiLA1589-miR6145b-2-5p	UUAGCUUACGUGGCACUAUCU	22-42	nta-miR6145b	5	0	21	21	1
			spiLA1589-miR6035-2-3p	AGGAGUAGAAAAUUACA	98-114	bna-miR6035	5	0	17	21	2
spiLA1589-MIR7993d-1	AGCGUGUUUUCAUUUGUCUAUUAUGUAGUUAAGUUAACUAUAUAAAAAUAUGCUGUCUCCUUUAAUUAUAUACAUCAACCUUUGUAGAAAACAUCUUGGGUGUUUACGACUUGGUAAGGCGAAUGCAUAGAAUUAAAGGAGAUGACAAUAUAUUUUAUGUGGUUAACUUAACUACCUCACAUACAAAUGGGAACACACA	199	spiLA1589-miR7993d-1-3p	AUAUUUUAUGUGGUUAACUUAACU	150-173	stu-miR7993d	0	0	24	24	1
spiLA1589-MIR10532-3	GGUCCUAUUAUCUCUUGAACUUAUUUUUUUUUUUGUAAUUUUAUACAUCUUUUGUCUUACGUGGCACAUUUCGUGACUCCACGCAAAUGAGGCGCGUGAGAGAUAUUUGGUUGCCACGUAAAUAAAAAAGGUGCACAGAAUUACAAAAAAAAAAAGAGUUCAGGGGGUAAUAGAACCUUAGAAUAGUUAAGGUGUGUCUCUGAGAUUUCGGUCAUAGUCUAAAGGAAUACUUGUGCAUUUUUCCUAUAAUUUACUAUAAUAGAUAAAUAUUACGAGAGAUGAAAGUGAGU	290	spiLA1589-miR10532-3-3p	AGGUGUGUCUCUGAGAUUUCGGUC	190-213	sly-miR10532	2	0	24	24	1
spiLA1589-MIR8047	CAUAUUUACACCAGGUAGUCAAUUUUGUGCCCUUGUAUUAACAAUUUGACCAUUUUUUCGAAAUUAGACCCAUGGUCUAAAUACCAGUUUUGAACUUUGAAAUACAGACCAGGUGGCCACUUUCGAACUUCAGAUCACUGGGCUAAUUUUGAAAAACUGGUCAACUUCUAAAUACAAAGCCACAAAUGAGGUUAUUUGUGUAAAUCAG	208	spiLA1589-miR8047-5p	CCAUUUUUUCGAAAUUAGACC	50-70	stu-miR8047	0	0	21	21	1
spiLA1589-MIR403b	AUUGGAAAAGCCAUAUUACGAGCUUGUGCGUGAAUCUAGCAAACAAUAACAGUUUUUCUGAUGAAAAGAGUUGUUAGAUUCACGCACAAACGUGAAAUAUGCCUCUUCCUGA	112	spiLA1589-miR403b-5p	AGCUUGUGCGUGAAUCUAGCA	21-41	csi-miR403b-5p	3	0	21	21	1
			spiLA1589-miR403b-3p	UUAGAUUCACGCACAAACGUG	74-94	gma-miR403b	1	0	21	21	1
spiLA1589-MIR865-1	UUUUUUUAUCAAUUUCGGUCUACUUGACACUAGUUUGAAAAAAAUGUAAACACGCGCUAGGCUCACAAGAUAGUGUCACAUAGGCCAAAAAGGGAUAGAAAAU	104	spiLA1589-miR865-1-5p	AUCAAUUUCGGUCUACUUGAC	8-28	ath-miR865-5p	5	0	21	21	1
			spiLA1589-miR5026-1-3p	GCUCACAAGAUAGUGUCACAU	62-82	ath-miR5026	5	0	21	21	2
spiLA1589-MIR7981-1	AAAUACUCACUAAACUAUAGCUGAAAUUUUAGAGAUACAUCUUAACUAAACUAAGGUCCUAUUAACCCCACCCUCCCCCCAAACUUUUUUUUGUAAUUUUAUACACCUUUUGUCUUACGUGGUACACUCUAUGACUCCACGCAUUUGAGGCGCGUGAGAGAUAAUUACAAAAAAAAAAAGUUCAGGGAGGUAAUAAGAUCUUAGUUUAGUUAAGGUGUGUCUCUGAAAUUUCGAUCAUAGUCUAGGGGAGUACUU	255	spiLA1589-miR7981-1-5p	CUUAACUAAACUAAGGUCCUAUUA	41-64	stu-miR7981-5p	3	0	24	24	2
			spiLA1589-miR7981-1-3p	AUAAGAUCUUAGUUUAGUUAAGGU	193-216	stu-miR7981-3p	3	0	24	24	1
spiLA1589-MIR5183	UUUGUCUAAAUGAAUUAUGCGGACAACUUUGAGUGGCUGCAGAUGACUUAAUCCUUUUUUUUUUAAUUCCAAAGGCCAACAGGCCACUUUAUUAAAAAGAAAAAAAGAAUAGCCUUAAGUCAUGUCCAGCCACUCAAAGUUGUCCGCGUAAUUCAUUUAGACUCC	165	spiLA1589-miR5183-5p	UAUGCGGACAACUUUGAGUGG	16-36	bdi-miR5183	5	0	21	21	1
spiLA1589-MIR160h-3	GGUAACUUUAUAUGACGAGAUGGUUACAUAUUUCAACAUCAUAUACACGAUAUCGGAAUAUGCUUGGCUCCUCAUACGCCAUUCAACAAGGCCCAUCGAUAUAUUACGGUGAGCUUUGCAAAUGGCAUACAGGGAGCCAGGCAUAUACGUGUACACGACUUGUAUCAGUACAUAUAUACACACUCAUAUGUAUAUAUAAAAUUUUU	206	spiLA1589-miR160h-3-5p	UGCUUGGCUCCUCAUACGCCAUU	61-83	mes-miR160h	5	0	23	23	1

			spiLA1589-miR160-3-3p	UGGCAUACAGGGAGCCAGGCA	123-143	aau-miR160	0	0	21	21	1
spiLA1589-MIR10186e	UUUAAAAUCUGACGUGGAUGACGACAUGUCACUUUUGUUGAGCGAUUGAAGUUCAACAAAGCCAAUGGGAUUUAAAAUGUUAAGUUUCAUUGAGUCUAAGGGCUUAGUUGAGAAAUAGUUAAGUAGAAGGGUUUAGAAUACAAACUGAUACAAGUAUAAGGGUCUACCAGACCAUUCUGUCAAUAAUAAUUAACUAAAUAGUCCUAAAAAUGACGCAUGUCUUGAUCUUAGCCUAGAUUUUCUU	244	spiLA1589-miR10186e-5p	AUGGGAUUUAAAAUGUUAAGUU	65-86	gma-miR10186e	4	0	22	22	2
			spiLA1589-miR902h-3p	AGAAGGGUUUAGAAUACAAAC	125-145	ppt-miR902h-3p	5	0	21	21	1
spiLA1589-MIR8766	GUAUAACUAAUACCCACAUAACUUAUUUCACUUUCUACCCUGCAUAACUUUAUACAUAGAUUCCCUCAUAAGUUAUGUUGGUAUUAGUUAGGU	93	spiLA1589-miR8766-3p	UUAUGUUGGUAUUAGUUAGGU	73-93	gra-miR8766	5	0	21	24	1
spiLA1589-MIR8005c	UGUACCUUACAAAUCAAAAUCUUCUUUUUAAACUCAUUCAAAUUCUCAUCCUCAAAUUGGUUGGCCUUGAUCUCUUUAAUGAAUUUGGCCCUCAAUUCAAUACUAGAUAGUUUUAGGUUUAGGGUUUAGGAUUUAGGGUUUGGAUAUAGGGUUUAGAGUUUAGGGUUUUGAGUUUAGGGUUUU	183	spiLA1589-miR8005c-3p	UUUAGAGUUUAGGGUUUUGAGUUU	152-175	stu-miR8005c	2	0	24	24	1
spiLA1589-MIR8021-1	UUUAGUGAAUAAGUUUACAAGAAAACUAACAAUAUAUUUCAUAUUCAAGGCUCAAACUCGAGACCUCUGCUUAAGGAUGGAUGUUUUAUACAUCCCUUCAUGACUAUUGUUGGUUCUAAUAGUAACUUAAUUUACUCUC	139	spiLA1589-miR8021-1-5p	AUUCAAGGCUCAAACUCGAGACCU	43-66	stu-miR8021	0	0	24	24	1
spiLA1589-MIR7997c-15	GUUAUAUUGCUCCGACUCUUCAAAAGUGGUCACACCCAUGUUGAAUCCUCCAAAAAGGCAAUACUUUUGGUGGAUCCAACAUGCACCUGUUGACAUUUCUGAAGAGUUCGAGCAACAUAGU	121	spiLA1589-miR7997c-15-5p	AUAUUGCUCCGACUCUUCAAAAGU	4-27	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-15-3p	UUUCUGAAGAGUUCGAGCAAC	96-116	sly-miR5303	1	0	21	21	1
spiLA1589-MIR5658-2	UGCUUGGAGAAGAUAGAGGGUGCAAAGAACCCGGUAGACAUGUUGACGAAAUGUGUUGAUGUUGGGAAACUGAGGUUAUGUAAAAUUUCGGUUGGUCUUCUGUAGUUGUUACUACAGGUGUUACGGUGCAGUAAAGAUGUUGAUGAUGAAGAGAUUUUUUUUUGAGAAUCUAUUUUUUGGAUGACUAAGUCAGUUUCCAAGUGGGAGAACUGUUAGGUAGUGGAGCCUGAUUAAUUUUAGGUUUUCCUAUUUAUUCUCUAUUUUAGGCUUUCCUAUUUAUUCUCUAUUUUUUUGUGUACUAAAAUACACCUCCUUUCUUCCUGUUCUUUCUCCAAUUC	339	spiLA1589-miR5658-2-5p	AAGAUGUUGAUGAUGAAGAGA	134-154	ath-miR5658	4	0	21	21	1
			spiLA1589-miR4248c-2-3p	AGAUUUUUUUUUUGAGAAUCU	152-172	aly-miR4248c	5	0	21	21	1
spiLA1589-MIR161	UGGUGGCUGCCGAAAAGCAGCAAGAGAAGGCUGCAACGCAAAUCGGAAGUUCUGCCGGGGAGCAACGAGGGCAGAAUAGCGGGACGGACAAGGGCAAGAACGUUGCUGUUGGCAUGUUCAAUUACAUGGCGUUGAUCAACCAUAUUUCUAUUGCUGCUUUGGCUGCCAAAC	171	spiLA1589-miR161-3p	UUCAAUUACAUGGCGUUGAUC	117-137	bra-miR161-3p	5	0	21	21	2
spiLA1589-MIR475b	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGUCUAUGGCUUUGCUCUUAAAGUCCCCAUUGAUUUAGGAGAGUGGACGGGGCAGACUGACUUCACUA	99	spiLA1589-miR475b-3p	UUAAAGUCCCCAUUGAUUUAG	49-69	ptc-miR475b-3p	3	0	21	21	1
spiLA1589-MIR11083c	UUGGUUUCUUAAAUACUCUUAGACUUGGCAAUUUAAGGAUAGAUGUUCUUGAUGUGAUGAAUUCCAGAUUUUGGGGGUAAUAAGUGUUAAACUUUAGAAGCUUAUUUACUUGGUUACAUUAAUAAGUUUUGGAUCUUCCGCAUUAUUUUUGAUAUUCAUAGUUGAACUAUUGGUAAAUGUUGGGGUUUAUAAUUGUUGGUUCGUUCACCUAGUAAGUUAAGUGUGGGUGCCACUCACGACUCGUUUUGGAUCGUGACAAACUUGGUAUUAGAGCGUUAGGUUCGUUGGUCUCAUCACACAAGGACAAGUCUAGUAGAGUUUUGAGGAACGGU	332	spiLA1589-miR11083c-5p	UUGGUUUCUUAAAUACUCUUAG	1-22	lja-miR11083c-5p	5	0	22	22	1
			spiLA1589-miR1507-3p	AGAGUUUUGAGGAACGGU	315-332	mtr-miR1507-5p	5	0	18	22	1
spiLA1589-MIR395j-2	UGACAACAUUAAACAAACAAUUGAAGUGCAAGAGUAUUACUACUAGCUAGUUGGAGAUGAUGAACAAAAAUGAUUUUCUAAGUCUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUUAGGGCUUACUUCGUUGUUUGAUGUUCUGCUGGAGUGUUUGGGGGAACUCCUGGGCUCACUCUGAAAUUUUACGCAAAUUAAACAAAUAGAAGUGUUGGAGUGUUGAUUGUGGAUGAUGAACGAGAUAGUUCACGUAUAAAUCUAUCAAGG	326	spiLA1589-miR395j-2-5p	GUUCCCUUGACCACUUCAUUA	104-124	mdm-miR395j	1	0	21	21	1

	UGUUCCCUAGAAUUCCCUUGACCACUUCAUGAGGGCUUACUUUGAUGUUGGAA		spiLA1589-miR395b-2-3p	CUGGAGUGUUUGGGGGAACUCC	152-173	sly-miR395b	1	0	22	22	1
spiLA1589-MIR7827	UCCUUUUUAAGUUGAUUCUUCUAUAUGGAUUAGGUUCAUUGAGCCGGCCUGAUCUAACCCGAUGGGUAAUAGGUUGGACAAAUUUUUCGGAGUCCAUUUAAGAAAAUGACUUUUUGCCUGGUUUGAAUAAACCUAUUGAUUUGGGGCUUGAGAAAUAUAGGUAGGGUCGGCUCGUGGGCCAAUAAAAAUUAACUAAAAACUA	203	spiLA1589-miR7827-5p	GGUUGGACAAAUUUUUUCGGA	72-92	ptc-miR7827	5	0	21	21	1
			spiLA1589-miR6425d-3p	UCCAUUUAAGAAAAUGACUUU	94-114	ptc-miR6425d-3p	5	0	21	21	1
spiLA1589-MIR11116	AUUUACGUAAUUAACAUACAAGGCUACUAAACAACCCCAAGAAACAAAAUUAGGUGGUUGCUCAGGGGUAGUCUUGUAUGUCGUUUAUGUAUGU	94	spiLA1589-miR11116-3p	UGUAUGUCGUUUAUGUAUGU	75-94	lja-miR11116-3p	5	0	20	21	1
spiLA1589-MIR6145b-3	GUAAUUUUCUAUUCCUUUUUGGCAUACGUGGCACUAGCUUGAAGAAAAAAGUCAACCAGCGUUCGACCCACAAGAUAGUUUCACGUAGGCCGAAAAGGGGUAGAAAAUAUU	111	spiLA1589-miR6145b-3-5p	UUGGCAUACGUGGCACUAGCU	19-39	nta-miR6145b	4	0	21	21	1
			spiLA1589-miR5166-3-3p	AGUCAACCAGCGUUCGACCCA	50-70	bdi-miR5166	5	0	21	21	2
spiLA1589-MIR156b-11	UAUUGUUGACAGAAGAUAGAGAGCACGAAUAAUGAGGUGCUAAUUGGAAGCUGCACCUUAAUUCUUUGUGCUCUCUAUUCUUCUGUCAUCAUCU	94	spiLA1589-miR156b-11-5p	UUGACAGAAGAUAGAGAGCAC	6-26	aof-miR156b	0	0	21	21	1
			spiLA1589-miR156g-11-3p	GCUCUCUAUUCUUCUGUCAUC	70-90	csi-miR156g-3p	0	0	21	21	1
spiLA1589-MIR1128-3	CGCUACUCCCUUCGUCCCUAAUUACUUGUCCACUUUUCCUUUUAUAGUUGUCCGUAAUUACUUGUCCAUUUUGACAAAUUAAGAAAGGACGAAUUUUUUUUACCUAUUCUAUUAAAUGACUAAUUACUUUGAAAAAUGUAGAACUUUUCAUCCAUUUUAAAAUUAAUAGGGGUAAAAUGAUAAAACUCACUACGUCAUUAAUUAUUUUCUUAAUAGGUGUGCCAAUUCAAAAGUGGAAAAGUAAAACGGGAUGGAGGGAAUAUUA	265	spiLA1589-miR1128-3-5p	CGCUACUCCCUUCGUCCCUAA	1-21	ssp-miR1128	4	0	21	21	3
			spiLA1589-miR7502c-3-3p	AUGUAGAACUUUUCAUCCAUU	136-156	gra-miR7502c	5	0	21	21	2
spiLA1589-MIR7997c-16	AGUUAUGUUGUAUGGACUCUCCAAAAAUGUUGCUGCACUUGUGAUGGAUCCUACAAAAAUGCACUACUUUUGGAGGAUCUGACCCACAUCCGGUGGCAUUUUUGAAGAGUCCGAGCAAACAUAGAU	126	spiLA1589-miR7997c-16-5p	AUGUUGUAUGGACUCUCCAAAAAU	5-28	stu-miR7997c	5	0	24	24	1
			spiLA1589-miR5303h-16-3p	GGCAUUUUUGAAGAGUCCGAGCAA	95-118	stu-miR5303h	3	0	24	24	3
spiLA1589-MIR171b-2	ACUAGUAAAUGAAUUGGUAAAAAGAAAUGAUAUUGGCGCGGCUCAAUCUGAGAUCGUUCUUUACUGAAAUAAAACGUAAACUCGUCUUCAGAUUGAACCUCACCAACAUCGCUUCUCUAAUUCAAUAUAUACUCAC	136	spiLA1589-miR171b-2-5p	GAUAUUGGCGCGGCUCAAUC	29-48	zma-miR171b-5p	1	0	20	20	1
			spiLA1589-miR171-2-3p	AGAUUGAACCUCACCAACAUC	90-110	cca-miR171	4	0	21	21	2
spiLA1589-MIR162-3	UCCUUAGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUUGCGUAUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUCAACCAACUAAACA	135	spiLA1589-miR162-3-5p	UGGAUGCAGAGGUUUAUCGACC	19-40	csi-miR162-5p	4	0	22	22	1
			spiLA1589-miR162b-3-3p	AUCGAUGAACCGCUGCCUCC	94-113	cas-miR162b	0	0	20	20	1
spiLA1589-MIR1127-2	AACUACUCCCUCCGUCCCAUUUUAUAUGGCUCCGUUUCCUUUUUGGUCAGUCCCAAAAAGAAUGUCACAUUUCCUUAUAUGGUAAAUAUUUAAAGGUACAAUUCCUCUUUUAUCCUUGUUGGUCCCACUUAAUUUUAAAAAUAGUACUCUUAAACAUUUAUGAGGAGAGAAAAGUAAGUCUACUUUUGAAGGGUAAUUUGGUAAACAUUUCAAAGUCGGUCAAAUGUUGCCACAUAAAAUGGGACGGAGGGAGUAUAA	258	spiLA1589-miR1127-2-5p	AACUACUCCCUCCGUCCCAUU	1-21	bdi-miR1127	2	0	21	21	1
			spiLA1589-miR5205a-2-3p	CACAUAAAAUGGGACGGAGGGAG	231-253	mtr-miR5205a	4	0	23	23	1
spiLA1589-MIR5725-3	GUUAUUGGUGCUUCUGCUGUUCAAAAACUAGAGCAUAUAUUGUCACUCACUCUAACGGAAAACUAAGUGGGAACAUGUGGCACAAUCUCAUCCGUCGAUUUGAUAUUUAAUAAAUGUCAGGUUAGUGGAUAAGAUUGUGACACGUGUAUGUAUGUUAGCAUAAAAGGUAUAUAUGCUCUAUUUUUUGACUGCAG	208	spiLA1589-miR5725-3-5p	AUGUGGCACAAUCUCAUCCGU	75-95	bra-miR5725	4	0	21	21	1

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spiLA1589-MIR7997b-6	UAUGUUGCUUGGACACUCCACAGAAAUGUAGGUGCACCCAUGUCGUAUCCUCCAAAAAGGAUAGGUUUUGGAGGAUUGACACAAAUACUGUAGACAAUACUUUUGAAGAGUCCGAGCAACCUU	123	spiLA1589-miR5181a-3-3p	UGAUAUUUAAUAAAUGUCAGG	101-121	bdi-miR5181a-5p	4	0	21	21	1
			spiLA1589-miR7997b-6-5p	AUGUUGCUUGGACACUCCACA	2-22	stu-miR7997b	5	0	21	21	1
			spiLA1589-miR5303i-6-3p	AUACUUUUGAAGAGUCCGAGCAAC	97-120	stu-miR5303i	2	0	24	24	1
spiLA1589-MIR167a-2	GAGUUCAUUGAUGAUAUCCUCAUUUACUCUAGGAGUGAGGAAGAACAUGCAAGUCAUUUGAGAGUUGUUCUGCAGACUCUCAAAGAUUGCCAGUUAUUCGCUAAGUUUAGUAAAUGUGAGUUUUUGUUGCAAUCUGUUGCUGGAUAUAUUUUAUUUUUUAAAAGUUGAUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUCCUAAAGCGUUUAUGUUUCAUUGUAAAGCGAGCGAUACAUAUCUGUUUUGGAUGAUUUCCAAGUUACUGCUCUUCUACCAAAAGUAAAUACAUACUCAUUUGUGAAUUU	319	spiLA1589-miR167a-2-5p	UUCAUUGAUGAUAUCCUCAUUU	4-25	osa-miR167a-3p	5	0	22	22	2
			spiLA1589-miR10538-2-3p	AGAUUGAUAUACGUUACUCACAGU	176-199	sly-miR10538	0	0	24	24	1
spiLA1589-MIR1069-2	UAAGUCAUCCGUAGCCACUUAAAGGAAAAAUAUUAUUUUUAAUAAAUCAACGCGCUCAAAGAAAGUGAAUUACACGUUUUUUGCCAUUUCAGCAUUUUGUGUCUAAAUGAAUGAUUUUUGAACAAAUAAAGUGUUCAAUUGACACAAGGAUUAGUUGAGGUGUCUAAAUAAAUUAUGCGGACAACUUUGAGUGGCUGCAGAUGACUUA	208	spiLA1589-miR1069-2-5p	UAAUAAAUCAACGCGCUCAAA	40-60	ppt-miR1069-3p	5	0	21	21	1
			spiLA1589-miR5183-2-3p	UAUGCGGACAACUUUGAGUGG	174-194	bdi-miR5183	5	0	21	21	1
spiLA1589-MIR4994	AACAUGUUGAAUGUUGGGGAACGAACGUCUAAGGUUUGGGUCAACGAUCUCAAUGUUGAUGCGUCCGCUUGUUGUUGAUGCUGCUCCAAAAGGUUCAACAUUGGGAUUUUAGCCCAAACAUCAGACGUCCCUUCCUCAUCGUUCAACAUUGU	152	spiLA1589-miR4994-5p	GUUUGGGUCAACGAUCUCAA	34-53	gma-miR4994-5p	5	0	20	20	1
			spiLA1589-miR10530-3p	ACGUCCCUUCCUCAUCGUUCAACA	125-148	sly-miR10530	1	0	24	24	1
spiLA1589-MIR7997b-7	CUACUAAGUUGCUCGAGCUCUCCAAAAAUGUUGCCGCAAUAUUAUUGGAGGAUCAGCCACGCAACCGUCGACAUUUUUGAAGAGAUCGAGCAACAUAGCCC	101	spiLA1589-miR7997b-7-5p	AAGUUGCUCGAGCUCUCCAAA	6-26	stu-miR7997b	5	0	21	21	1
			spiLA1589-miR5303-7-3p	UUUUUGAAGAGAUCGAGCAAC	74-94	sly-miR5303	1	0	21	21	1
spiLA1589-MIR167b-5	UGCGGCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUACGAGGAAAGAUCAGAUCAUGUGGCAGCCUCACCUGUCAAUGCCAUC	109	spiLA1589-miR167b-5-5p	UGAAGCUGCCAGCAUGAUCUAA	16-37	bna-miR167b	0	0	22	22	1
			spiLA1589-miR167c-5-3p	AUCAGAUCAUGUGGCAGCCUCACC	73-96	eun-miR167c-3p	1	0	24	24	1
spiLA1589-MIR11419-2	AAAAAAUAGUGACCACCUAAGUUGCGCAAACUCUUCACUUCGAUGCCGCACCCGUGUCUGAUUCUCCAAUAAUACACUACUUUGGGAGAAUCCAACACGCACCCGUUGACAUUUCUGAAGAGUCCGAGCAACAUAGGUGACCACACAUUUGCA	153	spiLA1589-miR11419-2-5p	ACCUAAGUUGCGCAAACUCUU	15-35	pab-miR11419	5	0	21	21	1
			spiLA1589-miR5303d-2-3p	UUUGGGAGAAUCCAACACGCACCC	81-104	stu-miR5303d	2	0	24	24	1
spiLA1589-MIR8011b	GACACUAGUCAAGUGAGACUCAUUUUUGCCUCACAAAAAAUUAAGCCCAUUUGAGUCUACUUUUAUGUGAGACAAAAAGAAGCCUCACACAACUAGUAUU	100	spiLA1589-miR8011b-5p	ACUCAUUUUUGCCUCACAAAAA	18-39	stu-miR8011b-5p	1	0	22	22	1
			spiLA1589-miR8011a-3p	GACAAAAAGAAGCCUCACACAACU	71-94	stu-miR8011a-3p	2	0	24	24	2
spiLA1589-MIR7997b-8	GCUAUUAUCUAAGUUGCUCAGACUCUCCUAAAUUGUUGUCAUAUACACCUGUCGAUAUUUUUUUAAGAGUUCGAGCAACAUAGGUUAUCAU	91	spiLA1589-miR7997b-8-5p	AAGUUGCUCAGACUCUCCUAA	11-31	stu-miR7997b	5	0	21	21	1
			spiLA1589-miR5303-8-3p	UUUUUUAAGAGUUCGAGCAAC	59-79	sly-miR5303	1	0	21	21	1
spiLA1589-MIR3448	UAAAAGAAGGAGUCAAGAACGCACCAUACAGGAAAACAUCUUGAUAAGAAGUGUUACUAUGUUUAGACAAUUGUAUGGUUCGGGUAUUGACUUCUGUACUUGGA	104	spiLA1589-miR3448-5p	ACAGGAAAACAUCUUGAUAAG	28-48	aly-miR3448-5p	5	0	21	21	2

			spiLA1589-miR830-3p	AAAACAUCUUGAUAAGAAGUG	33-53	ath-miR830-3p	5	0	21	21	2
spiLA1589-MIR11137	UGGCAUUUUUGACGUCACGUUACUGUGAGUAACGUUUUACUCCUAAAACGUUUUUUUGAGUAACGCUUUACUCCUAAAACCUUACUGUAAGUAACGUUUUAAGAAUAAGACGUUAUUCACAGUAACGUUUUAGGAGUAAAAAGUUACUGUGAGUAACGUAUAUCAAUAUGACG	173	spiLA1589-miR11137-5p	UUUUUGACGUCACGUUACUGUG	6-27	lja-miR11137-5p	4	0	22	22	1
spiLA1589-MIR1886f-1	UGCGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGGACAUGCGAUUUUAUAUUGAUUUCAUCUCAUGAUUUCAUAUCAUG	80	spiLA1589-miR1886f-1-5p	AUGGUAUCGUGAGAUGAAAUCAGC	7-30	stu-miR1886f	0	0	24	24	1
			spiLA1589-miR1886h-1-3p	AUUUUAUAUUGAUUUCAUCUCAUG	44-67	stu-miR1886h	2	0	24	24	1
spiLA1589-MIR5014a-4	AAUUUAUCUUCAGAUUACAUUUAUGAUCUUCAAUUUUGGUGUGUACAAGUAGACACUUAAUUUUGUAUACGAUUGAAGAAAUAAACGCACAUGUUCUAUAUGAUAUUUUUCGUCCUACGUGUAUUGUGUCACGUAGGACUCAUGUGUCUAUUUGUUCAAGGUUAUACAAGUUUAAGUGUCGACUUGUUCAUAUCCAAUGUUGAAGGACAUAAAUGUACAAUGAAGUUAAGUU	232	spiLA1589-miR5014a-4-5p	ACACUUAAUUUUGUAUACGAU	53-73	ath-miR5014a-5p	4	0	21	21	1
			spiLA1589-miR5014a-4-3p	UUAUACAAGUUUAAGUGUCGA	162-182	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR4348b	CUUAGUAUGUGAUGCACCUACUUUGUCCUUUUGGUUGGCCAAUAAGUCAAAGUUUGUUAUGCACCUACAUGGUCUUUUGAGUUGGUCAAUAAGUCAAAGUAGGUGAUGCAACUACUUGU	119	spiLA1589-miR4348b-3p	UCUUUUGAGUUGGUCAAUAAG	73-93	gma-miR4348b	5	0	21	21	1
spiLA1589-MIR8674a	UACUAGUACCUUCUGCUACCGAUUUUCCCUUCUGGGCAGCUGUCGCUUUCUUUGGAGGCAUAGCUGAAAGCACAGGGAUUCGUUAGAGAGGGACUAUCC	99	spiLA1589-miR8674a-3p	UUAGAGAGGGACUAUCC	83-99	gra-miR8674a	4	0	17	24	1
spiLA1589-MIR390-3	AAAGCAUGAAAAAGCCGUGAAACUCAGGAUGGAUAGCGCUAAAGAUGUGUACAAAAAUCGAAUUGAGUCAUCCAUGGCGCUAUCCCUCCUGAGCUUUACAGAUUCUCCAUGCAUA	115	spiLA1589-miR390-3-5p	AAACUCAGGAUGGAUAGCGCU	20-40	aof-miR390	3	0	21	21	1
			spiLA1589-miR390a-3-3p	CGCUAUCCCUCCUGAGCUUUA	78-98	sly-miR390a-3p	2	0	21	21	1
spiLA1589-MIR319b-5	GUAUAAUAUAUGUAGAGAGCUUUCUUUAGUCCACAUAAAGGGGGCAGUAUGGUUCAAUUAGCUGCUGACUCAUUCACACAAAUGCUAAGGCUUUGAGAAUUAUUAGGAGGAAAAACCUUAGUAACUGAGUGAAUGAUGCGGUAGGCUGACUGAAUCUUAAGCUUUUUUUGCUUGGACUGAAGGGAGCUCCCUCUUCGUAAUUACUU	206	spiLA1589-miR319b-5-5p	GAGCUUUCUUUAGUCCACAUA	17-37	mtr-miR319b-5p	2	0	21	21	1
			spiLA1589-miR319a-5-3p	UUGGACUGAAGGGAGCUCCCU	172-192	aof-miR319a	0	0	21	21	1
spiLA1589-MIR10519-2	AUGUGCAUAAAUAGACACUUAAACUUGUAUAAAGUUGACAAAUAGACACACAUGUCCUACAUGUCAUCCUACAUAUCAUUUUUUUCUUACGUGAUGUCGUACGUGUAUUGUGUCAUGUAGAACUCAUGUAUUUAUUUAUUCAAAAGUUGGAUAAUUAAAGUGUCUGUUUGUGCAUUA	178	spiLA1589-miR10519-2-3p	AUUCAAAAGUUGGAUAAU	139-156	tae-miR10519	3	0	18	18	3
spiLA1589-MIR390-4	CGAGCAUGAAGAAGCCAUAAAACUCAGGAUGGAUAGCGCUAUAGAUAGCCAUUAAGAUGUAUUCAUGGUGCUAUCCCUCCUGAGCUUUAUAGAUUCCCCAUGCCAU	106	spiLA1589-miR390-4-5p	UAAAACUCAGGAUGGAUAGCG	18-38	atr-miR390-1	2	0	21	21	1
			spiLA1589-miR390a-4-3p	UGCUAUCCCUCCUGAGCUUUA	69-89	sly-miR390a-3p	3	0	21	21	2
spiLA1589-MIR166-1	AGCAAAAGAAAACAUUUGUUGAGGGGAAUGUUGUUUGGUUCGAAAUCAUUCAAACAAAUUAAAAUUCAUGCAUCUCGAUGAUCGAUGAAUUGAAUAAUUUCGGACCAGGCUUCAUUCCCCCCAACUCAAGUUUUUGUUUUAAU	143	spiLA1589-miR166-1-3p	AUUUCGGACCAGGCUUCAUUCCCC	97-120	lja-miR166-3p	0	0	24	24	1
spiLA1589-MIR6145b-4	CCCUUUUGGCCUACGUGGCACUAGCUUGAAGAAAAAUUUAACCAACGUUGGGCCCACAAAAUAGUGUCACGUAGGCCAAAAAG	84	spiLA1589-miR6145b-4-5p	UUGGCCUACGUGGCACUAGCU	6-26	nta-miR6145b	5	0	21	21	1
spiLA1589-MIR6441	ACCAUGACAAUUAAAAGUGGACGGAGGGAGUAAUUUACGCACUUCUUAAGAAAUUAUAGGUAGAAAACUAAUUUUACUAUAUUACCCUUUGAAUAUACUCCCUUAGUUCAUUUUAAUAUGUCAUCCU	127	spiLA1589-miR6441-5p	AAGUGGACGGAGGGAGUAAUU	15-35	ptc-miR6441	5	0	21	21	1
spiLA1589-MIR7997c-17	AGGCUAUGUUGCUCGAACUCUUCAAAAUGUUUUGAAACUUGUAGGAGUGGUGUUUUUGAAGAUUUCGAGCAAUAUAGGUU	80	spiLA1589-miR7997c-17-5p	AUGUUGCUCGAACUCUUCAAAAUG	6-29	stu-miR7997c	4	0	24	24	1
			spiLA1589-miR5303-17-3p	UUUUUGAAGAUUUCGAGCAAU	53-73	sly-miR5303	2	0	21	21	1

spiLA1589-MIR11003	ACUUUUAAAUAAAUAAACACACGAGUCCUACAUGACACAAUACACGUAGGACAAAAAAUGAUAUGUAGGACAUGUGUGUCUAUUUGUUCAAAUUU	95	spiLA1589-miR11003-3p	ACACAAUACACGUAGGACAAA	35-55	mdm-miR11003	5	0	21	21	1
spiLA1589-MIR7997c-18	CUUCACUAUGUUGCUCAGACUCUUCAAAAAUGUUGUCAGGUGCUUGUUCGAUCCUCCAAAAGUAGUGCCUGUCCGAAGGAUACGAUACAGGUGUGGCAACAUUUUUGGAGAGUCUGAGCAGCAUACUGCUU	131	spiLA1589-miR7997c-18-5p	AUGUUGCUCAGACUCUUCAAAAAU	8-31	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303h-18-3p	AACAUUUUUGGAGAGUCUGAGCAG	98-121	stu-miR5303h	2	0	24	24	1
spiLA1589-MIR172b-3	UUUAGUCGUUUAUUGCUAAUGCAGCAUCAUCAAGAUUCACAUUUAAUUGCAUUUUAAAUGUCAGAAUAUUUGAGAAUCUUAAUAGUGCUGCAUUUGCAAACAACGACUGUG	111	spiLA1589-miR172b-3-5p	GCAGCAUCAUCAAGAUUCACA	21-41	csi-miR172b-5p	0	0	21	21	1
			spiLA1589-miR172-3-3p	UGAGAAUCUUAAUAGUGCUGCAU	71-93	aau-miR172	3	0	23	23	1
spiLA1589-MIR10197	AAGAUCUCGAAAAAUUAUCAGAUUGAAAAAGAUUGCCUCAAUCACACAUCCAAGGCAAAAAAAUUUACCAUUUGAAGUUUCACAAAUUUACAACUACUUUUUCUGAGUUGCACUCUUUAUUUUUUGUGAAUCUUCAAAUGAUCGUAACUUUGGCCUCGAAUAUCCGUUUGAGGCGAUUUCUUUUUCAAUUGCACUAUUUUCUCGAGAUAUA	211	spiLA1589-miR10197-5p	AAUUUACAACUACUUUUUCUG	85-105	gma-miR10197	5	0	21	21	1
			spiLA1589-miR7990a-3p	UUCAAAUGAUCGUAACUUUGGCCU	133-156	stu-miR7990a	0	0	24	24	1
spiLA1589-MIR10541	CUCGCAUAACUUUUAGCUUUUGACUUAAAAUAAGUCACUUUUAUAAUUGUCAAACACUCUAAUAAGGGCCCGUUUGGAUGGGCUUAAUAAAAACAGCUUUAAAAAAGUACUUUUGAAAGUGCUGAAACUUAUUUUUAGAAUAAGCAGUUAUGCCCC	156	spiLA1589-miR10541-5p	AGUCACUUUUAUAAUUGUCAAACA	33-56	sly-miR10541	2	0	24	24	1
			spiLA1589-miR1514a-3p	CUUAUUUUUAGAAUAAGCAGU	128-148	gma-miR1514a-5p	5	0	21	21	2
spiLA1589-MIR10540-2	AGUCACUCAACUACUUGCUAGUAUCUCAGAAAAUCACUUUUUUUGUUGAAGAAAAUAGGAAUCACGAAGAAAGCCGUCUUUCUGAGAUAAUAACUAUUAGUUGAAUGUUC	110	spiLA1589-miR10540-2-3p	AUAAUAACUAUUAGUUGAAUG	87-107	sly-miR10540	0	0	21	21	1
spiLA1589-MIR7980b-3	AUAUGGUAUCACAUCUCAUUAUAUGAAAUCAUGAGACGGAAUUAACGUAAAAUCGAAUGUCCAAACGCUGAUUUCAUUUCAUGAUAUCAUAUCGUUAUAUGGUAUCACAA	110	spiLA1589-miR7980b-3-3p	GUCCAAACGCUGAUUUCAUUUCAU	59-82	stu-miR7980b-5p	3	0	24	24	1
spiLA1589-MIR823-2	CAUCUCCUCAUUAGGUAUUAUGUUCAUCCUCUUGUAACCAGAUGAUUCAAUACAAAGUGUAUAUGUAUAAUUCUGAAUGUACGUACAAUACUUUUAGCUUAAAGACACUUCCUUGAGGAAAUGCAGAUAUUGAAGUAGAUGUGUGAUCAUAUAGCAACAAUAUGAUUAGAAAUGAAGAUAUCUGAAAUAAGGUGGGACUGAUCUCCACGUUGGAGUGAGACUGAGAUGAUUUGGACAUGUGAAUAGGAGAUGCAUAGACGCACCAAUGAGGAGGUG	276	spiLA1589-miR823-2-3p	UAGAUGUGUGAUCAUAUAGCAA	136-157	aly-miR823-3p	5	0	22	22	1
spiLA1589-MIR167d-3	AGUUUCUUUCUCCACGAAGUAGGGUUAAGAUUAUUUUUCGUAGUACGAACUAACAGGUGAAGCAACCACAUGAUCUGAUCUUGCCUUAAUAUAAAUUUAUAGGUAAGUUUAGAUCAUGCUGGCAGCUUCAACUGAUAGUAGUCUACGCUAUCAAUAUGACAAAACCCUAAUAUUGUUGAAGAAGAAGAA	189	spiLA1589-miR167d-3-5p	UGAAGCAACCACAUGAUCUGA	58-78	eun-miR167d-5p	2	0	21	21	1
			spiLA1589-miR167h-3-3p	AUCAUGCUGGCAGCUUCAACUGAU	113-136	gma-miR167h	1	0	24	24	1
spiLA1589-MIR9477-1	CACACACACCUCAACUAUCAGUUGUUCUCAUUUCCUACCUGAAUAUUGGUGAUAUUCUAGGUUGGGAAAGGGAACAACUGAUAGUUGAGGUAUGUCUU	98	spiLA1589-miR9477-1-5p	UAUCAGUUGUUCUCAUUUCCUACC	16-39	sly-miR9477-5p	3	0	24	24	1
			spiLA1589-miR9477-1-3p	UUGGGAAAGGGAACAACUGAUAGU	62-85	sly-miR9477-3p	0	0	24	24	1
spiLA1589-MIR8001a-2	AUGGGGGUUUUCCUGGGGAUUAGUAUGAAAAUUCGUACCAAACUUAUUUUUCUGCAAAUUUUCAUACUAAUUCCAGGAAAAUCCCCUU	88	spiLA1589-miR8001a-2-5p	UCCUGGGGAUUAGUAUGAAAAUUC	11-34	stu-miR8001a	0	0	24	24	1
			spiLA1589-miR8001b-2-3p	AAAUUUUCAUACUAAUUCCAGGAA	56-79	stu-miR8001b-3p	4	0	24	24	3
spiLA1589-MIR5725-4	CGCAAAUUGUAUGUAAAUAUCCCCAUCAUACUUUUGAGAUAUUGUUGUCCCUGCCGUCAGAAAGCUAGAGCACGUACUUCCUUCACUCUAACGGAAGACUAAAUAGGGACAUGUGGCGCAAUCUUAUCGGUCGAUAUGAUAUUUAAUAAGUUGUUGUUAGUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAACGGUAUGUAUAUUCUAGUUUUUGAACGGCAUGGCACCAAUGUUUUAAAAGUAUAACGGAGGAUAUCCGCAUAUACC	282	spiLA1589-miR5725-4-5p	AUGUGGCGCAAUCUUAUCGGU	111-131	bra-miR5725	5	0	21	21	1

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spiLA1589-MIR9760-4	UCUUUCUCUCAUGAAAUUGAUGAGAAAUUGGAGGAUUUAGUAUUGACUGUUGAGGAUGAUUUGGGGAUGAAGAUGGUUGGAUGGGUCAUCCUCUCAUGAAAUUCAUGAGAAAUUG	115	spiLA1589-miR2866-4-3p	UCUAGUUUUUGAACGGCAUG	212-231	osa-miR2866	5	0	20	20	1
			spiLA1589-miR9760-4-5p	UGGAGGAUUUAGUAUUGACUG	29-49	gma-miR9760	4	0	21	21	1
			spiLA1589-miR1866-4-3p	UGAAAUUCAUGAGAAAUUG	97-115	osa-miR1866-3p	4	0	19	22	1
spiLA1589-MIR1530-1	UAUUUCUAAUUUUUCAAACAACAUCAAAUAUGUCAUAACUGAUUUGGAAAACAUUUUCCGAAACUUUUGUCCCAACCAAACAUGAGAAGAUUGGAAAACAUUUUCCAGAAAAUGUUUUCCUUUAUACCAAACACAAACAGACUCUCAAUGUGUCUCUGAGAUUUCGAGCAUAGGUUGAGGGGCUACUUGUGCAUUAUCCCUUUUGAUAAUGUGUUUUAAGAAUUGAAGGU	230	spiLA1589-miR1530-1-5p	UUUUCAAACAACAUCAAAUAU	11-31	gma-miR1530	5	0	21	21	1
			spiLA1589-miR10532-1-3p	CAAUGUGUCUCUGAGAUUUCGAGC	146-169	sly-miR10532	3	0	24	24	2
spiLA1589-MIR8184	AAGAAGGGCCGAUGACGUUCGAAAGAUAGCCUUGAGACAUGCAUGUGUGUCUUAGGCCUCAUCUAUUUUUUUAAAGAAUAAGAGGUUUGAAUUUGAAUACACAUAUGUAAAUUGGGAUUUUUAUUACGAUUCAGGUGUUUUGAUCUGAAUACACAUUUAAAUAAUAUGAUGUGGUCUCUAAAUCUGAACACUAAAU	231	spiLA1589-miR8184-3p	UUUGAUCUGAAUACACAUUUA	139-159	ath-miR8184	5	0	21	21	1
spiLA1589-MIR8030-2	AAUUAAUAGGCUUAAGUCAACGAUCGGCCGUUAAACGCAAAUCGAGUCAACCCAAAAAAAAUCCGACUAGUGAUUUGGUUUGACUUGGUUUGGUAUUGGAAAAAAAUUCGACUAUAUUUUGAUUGGGUUGGGUUGGUUUUAA	107	spiLA1589-miR8030-2-3p	UUGGGUUGGGUUGGUUUUAA	88-107	stu-miR8030-5p	5	0	20	23	1
spiLA1589-MIR1862e	AAAUUGAACAAGUAGACACAUGUGUCCUACAUGACAUGAUACACGUAACACACCACGUUAGACACAACUUUUUCAUGUAGGGUGUCAUAUAGGAUGAAUGUAUAGACUUGUUUAAUUU	118	spiLA1589-miR1862e-3p	AUAGACUUGUUUAAUUU	102-118	osa-miR1862e	3	0	17	24	2
spiLA1589-MIR2609b	GGGAUAGAAAAUUAUUAACAAAAUAAGUUCAGGGAGGUAAUAGGACCUCAUUAUAGUAUAAGUAUGUCUCUGAGAUUUCGGGCAUAGAUUGAGGGGGUACUUGUGCAUUAUCCCUAAAAUAUAUUUUCUUAUUUUUCUUAUUAU	144	spiLA1589-miR2609b-5p	GGGAGGUAAUAGGACCUCAUU	32-52	mtr-miR2609b	5	0	21	21	2
			spiLA1589-miR10532-3p	AAGUAUGUCUCUGAGAUUUCGGGC	60-83	sly-miR10532	1	0	24	24	1
spiLA1589-MIR1128-4	UAUUACUCCCUCCGUCCCAAUUUAUAUGAGUUAGUUUGACUUGUCAUGGAGUGUAUGAAAGAAGAAAAGACUUUUGAAACUUGUGGUCUAAAAUAAGUCCUAUAUAUUUGUAAGGCUAGAGCCUAGAAAUAAUUUCAUUAAGGGUAACAUGAACAUUUUAAAGUUAAAUCGUUAUUAAUUAUAGAAAUAUGUCAUUCUUUUUGGGACUGAGUAAAAAGGAAAGUAAGUCAUAUAAAGUGGGACAGAGGGAGUAGUU	256	spiLA1589-miR1128-4-5p	UAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1
			spiLA1589-miR5205a-4-3p	CAUAUAAAGUGGGACAGAGGGAG	229-251	mtr-miR5205a	4	0	23	23	1
spiLA1589-MIR6145b-5	UAUUUUUUAGCUUACGUGGCACUAUCUUGUGGGCCCAACAAUGGUUGACUUUAUUUUUCGAACUAGUGCCACGUAGGCUAAAAAGGG	87	spiLA1589-miR6145b-5-5p	UUAGCUUACGUGGCACUAUCU	7-27	nta-miR6145b	5	0	21	21	1
spiLA1589-MIR1530-2	CUUUAAGAGCUCGUUUGGUUGGGAACAAGUUAUCCCAGGACAAGUUAUCCUGAGGUUAGUUAUCUUGGAAUAGCUUAUCACAUACACUAUGAUAUAAAUGGUGGGAUAAGCUAUCCCAAACAUGGCAACCAAACAAGAUAUAAAAACCGUAUCCCAUCAUUAUUUUUCUAUCCCAUUACUAUUUAUUUUUAUCCCUCACACCAAACGACCUCUUAUUA	218	spiLA1589-miR1530-2-5p	UUAUCACAUACACUAUGAUAU	75-95	gma-miR1530	5	0	21	21	1
spiLA1589-MIR164c	UAUUUAAGCUGGAGAAGCAGGGCACAUGCUGAAUUACUUGAAACUUUGACCUUUCAAGAAUUUUGCAUGUGCUCUAGCUCUCCAGCUUAAUUC	93	spiLA1589-miR164c-5p	UGGAGAAGCAGGGCACAUGCU	10-30	fve-miR164c	0	0	21	21	1
			spiLA1589-miR164-3p	CAUGUGCUCUAGCUCUCCAGC	66-86	stu-miR164-3p	0	0	21	21	1
spiLA1589-MIR11299	GGCUUGGGACUUUCAAUAUGCCGGAUAAAGUUGUUAAGGAUUACGAUGUGACGGAGAGAUUGUCUGAUCGUCACGAAGAUAACUUACAAAACAUCAACAACUUUCUCAAAAAGGAUUGGAUAAUAAUAAUUAUUCAAUCCUAUCCUUCAAAACCUGAGAUAAUCUUUGGUUUUUUAGAGUGUCAUACUUACAAAAAUUAGUGACACCUUCUAGCGUAGAAAUAACUUCUUUGACACAUCAUAAGCCCUUACAGCUUUCUAUUGUGUUUAGAAUGUACCAAUCU	283	spiLA1589-miR11299-5p	CAAAAAGGAUUGGAUAAUAAU	107-127	fve-miR11299	5	0	21	21	1

spiLA1589-MIR171f-10	UUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAAUAUCACUUCUUAUUUUCAUUCCGUU	125	spiLA1589-miR171f-10-5p	CGAUGUUGGUGAGGUUCAAUC	23-43	fve-miR171f-5p	0	0	21	21	1
			spiLA1589-miR171b-10-3p	UUGAGCCGCGCCAAUAUCACU	87-107	aof-miR171b	0	0	21	21	1
spiLA1589-MIR2672	UGUAAAAUUAUCCAUUGAUUUCACAAAGUGGACAAAUAUUGUUGGACAUCCCAAAUAGUAUAGUGAACAACUAUUAUUGGACAGAGAGGGUACUAUUUAAAUUUUGUACUCAUGUCCAAAUCAAUUGAAAGUUGUUUGU	139	spiLA1589-miR2672-3p	UUAUUGGACAGAGAGGGUACUA	74-95	mtr-miR2672	5	0	22	22	1
spiLA1589-MIR159-3	AGGAAGAUCAGAGUUUUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAGCUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUAUUUUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCUUUAUUGGAAAGAAGGGAGCUCUACACUUGAUAACCUGGUUUUUUU	215	spiLA1589-miR159-3-5p	AGCUGCUGAUCUAUGGAUCCC	67-87	eun-miR159-5p	1	0	21	21	1
			spiLA1589-miR159b-3-3p	UUGGAAAGAAGGGAGCUCUAC	174-194	sly-miR159b	0	0	21	21	1
spiLA1589-MIR159b-4	GGAAAAUUGAGCUGCUAAUCUAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAUUAAUUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUAGG	101	spiLA1589-miR159b-4-5p	AGCUGCUAAUCUAUGGAUCCC	10-30	cas-miR159b-5p	1	0	21	21	1
			spiLA1589-miR159-4-3p	UUUGCAUAUAUCAGGAGCUGC	74-94	eun-miR159-3p	4	0	21	21	2
spiLA1589-MIR1888b-2	GCGCUAGGCCCAUUGGGCCGGCCUGGCCUAACCCGGGAUUUAAUAGGGUUGGGCUAAGAUUUUUGGAGCCCAUUUAAGGAAAAGGCUUUUUAGCCCGACCUAAUUAAGUCUGUUGAUUUAAGGGGCUUGAGAAAUAUAGGUAUGGCCGGCCCGUGGGCCAAGGUA	165	spiLA1589-miR1888b-2-5p	UUGGGCUAAGAUUUUUGGAGC	49-69	ath-miR1888b	4	0	21	21	1
spiLA1589-MIR7539	UAUUCUCUCUCUCUCUCUCUCUCGCUUUACACAAACCUAAAUUAUACAUUGUAUUUUGUAUAAUUUGUGUUUGUAUAAAACGAGAAAGAGAGAAAGACAAAAGAGAACUGGGAAGGGGUAAUGUUUGUAUUGUAUAAUUAUAAGGAUAUCGGACGAAAAUAUAUGUAUUUGCAUGUUUGUAAUAAUUUUCUCUCGCUUUAUACAAACAGAAACACAAUUUAUAAAUUUCUGAUUGUAUAAAGCGAGAGAGACAGCGACAAAGGGAGUG	270	spiLA1589-miR7539-3p	GCGAGAGAGACAGCGACAAAG	244-264	lja-miR7539	4	0	21	21	2
spiLA1589-MIR11451	GAGUUAGGGGUCGUUUGGUAGAGUUUCUUAGAAAAAAUAAUGCAUGCAUUAGCCUUGUGUAUUACUAGUACCUUGUUUGGUACUCUUUUCCAACCUAUGUAUAACACUCUAUAGUGUAUUACGAUGUAUAUUGCUAAUACCAUUGAUUUCUAGAUAUGAUUUUAAUGCAUGCAUUAGCAUGAUUAAAGACCAAUUGCAUCUUAAAACCUUUUUUUACAUCCUUUCCACCAUAAUAGUGGAGGUUAUCUUUGUAAAUUAAAUUUAUUAUGCAAUGCAUGCUAUUUUUUUAUGCAUCAAACCAAAUGAUGCAUAAAAA	316	spiLA1589-miR11451-5p	GUAUUACGAUGUAUAUUGCU	116-135	pab-miR11451	5	0	20	20	3
			spiLA1589-miR822-3p	AUGCAAUGCAUGCUAUUUUUU	267-287	aly-miR822-5p	5	0	21	21	1
spiLA1589-MIR9781-2	UUUUUUUGUAAUUUUGUACACCUUUUGUCUUAUAUGACACAUUCCGUGACUCCACGUAGUUGAGGCGCGUGAGAGAUAUUUGGAUGCCAUGUUAGUCAAAAAGGUGCACAAAAUUAUAAAAGGA	124	spiLA1589-miR9781-2-5p	UUUUGUCUUAUAUGACACAUU	23-43	tae-miR9781	5	0	21	21	1
spiLA1589-MIR9556	ACAAGUAGGUGCAUCAUCUACUUUGACUUAUUGACCAACUCAAAGGACCAAGUAGGUGCAUCACCUACUUUGACUUAUUGACAAACCUAAAGGAUCAAGUAGAUGCAUCACCUACUAAG	119	spiLA1589-miR9556-5p	UCUACUUUGACUUAUUGACCA	17-37	bra-miR9556-3p	5	0	21	21	1
			spiLA1589-miR4343a-3p	ACAAACCUAAAGGAUCAAGUAGAU	81-104	gma-miR4343a	5	0	24	24	1
spiLA1589-MIR856	GGGAAUAACUUAUUUAAUCGCCUGACAACUACAUGCAGUUGUUGGACCAUUUUGUAUCUGAAAGAUAUGCAUAAUUAUUCUUAUAAAUAACUUCAGUAGUUGUCCAGACAACUGUAAAAGUUGUUGGC	128	spiLA1589-miR856-3p	UAUUCUUAUAAAUAACUUCAGU	76-97	ath-miR856	5	0	22	22	1
spiLA1589-MIR8040-1	UCUUUUAUCAUUGUAAGUGUGAUUGUUGUCUUUCGCUGAGUUAAGUCAGUCAGGCCAAGGGUCCGCUCGAGACCAGUAAUGGUCAUCGAGUGUCAAUCCCGCCAAGGGUGUAGGCUCAGGGCGGGAUAUGGGGAUCUAGGAUUAGAGUAGAAGGUUAGUAGGUAGCUAAAUGUUAUUUAGUUUUCUUGUUAGUUUUCUUUUUAUCAUUCAUAGACUAUUUUGUUUCUUAAUUC	338	spiLA1589-miR8040-1-5p	UUUAUCAUUGUAAGUGUGAUU	4-24	stu-miR8040-3p	5	0	21	21	2

	UAUUAUUAUAUUCUAUUUUCUUUAUUCAAUAAUUGUAUUA CAUGGUUCUUAUUGAGACAAGGGUCUAUCGAAAAACAAC AUAUCUACCUUUACAAGGUUAAACUA		spiLA1589-miR6166-1-3p	AUUCAAUAAUUGUAUUACAUGGU	257-279	hbr-miR6166	5	0	23	23	1
spiLA1589-MIR4243-1	AUUAGUUGAGGUGUCUAAAUGAAUUAUGCGGACAACUUU GAGCGGCUGGAGAUGACUUAGGCCUUUUAUAAAAUUGAA GAUUUCAUGCAUAAUUUUUCGAUCAAACUUCAACUGUU	116	spiLA1589-miR4243-1-3p	AUAAAAUUGAAGAUUUCAUGC	68-88	ath-miR4243	5	0	21	21	2
spiLA1589-MIR1525-1	CUAUUGGUUGGUUUGACUUGAUUUGGUAUUAAAAAAAAA UUGACUAUGUUGGGUUAGUUUGGUUUUAACUAAAGAAAA UCAACCUGAGACCAAACCAACCC	101	spiLA1589-miR1525-1-3p	UGGGUUAGUUUGGUUUUAACU	50-70	gma-miR1525	5	0	21	21	1
spiLA1589-MIR172e-2	AUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCA CAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGG GUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUU UUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAA CAUAUGACUCUA	169	spiLA1589-miR172e-2-5p	GCAACAUCAUCAAGAUUCACA	21-41	stu-miR172e-5p	0	0	21	21	1
			spiLA1589-miR172-2-3p	UGGGAAUCUUGAUGAUGCUGCAU	128-150	aau-miR172	1	0	23	23	1
spiLA1589-MIR10204	UAUUAUGCAUGAUUCCGGUGGAGCUUACAACAGCAAGAA AAUGAGAGAGAGCAAAAAUCUCUCUCACUGUCUUGCUGU UGUAAGCUCCACCGAAAUUAUGCAUAGGG	107	spiLA1589-miR10204-5p	UUCCGGUGGAGCUUACAACAG	13-33	vca-miR10204-5p	5	0	21	21	1
			spiLA1589-miR535f-3p	AGAAAAUGAGAGAGAGCAAAA	36-56	csi-miR535f-5p	4	0	21	21	2
spiLA1589-MIR164b	UAAUUGGUUAUAGCUGUGAAGCUAUCACGUCAGAGGUUG GUGAGGCGUCAGUGUACUACACACCAAUCAAAAUGAAGG AGGGUGUUUGUCCAACGGAUAAUAACUCUUUAUGUUUGA UAUUUUUAGCAUGACAAAUACCAUAUUAUAUUCAUUCAUC CAAAGAAGGAAGUCAGUCAACAAGCCUUUUCAAGAACUCA CAAAGAAGUUUGCAAGGUUAUGACUGCGACGUGAAAAGG UGAAAAGACAGCUGUCAUAAAAGUUGUCACCUCUGAUGC GGUAGGUGCACAUCUUUUCCAACAG	300	spiLA1589-miR164b-3p	AGGUGCACAUCUUUUCCAAC	279-298	zma-miR164b-3p	4	0	20	20	1
spiLA1589-MIR7997c-19	AUUAUUUUAGUCUAUAUUGCUCGGACUCUUCAAAAAUGU CAAUGGUAGUGUAUUUUUGAAGAAUCUCAGACGGGUGCG GCAUCAAAAGUGAAGAGUCCGUGCAACUAAGAUUUUAAU UGC	120	spiLA1589-miR7997c-19-5p	AUAUUGCUCGGACUCUUCAAAAAU	14-37	stu-miR7997c	0	0	24	24	1
			spiLA1589-miR5303f-19-3p	AUUUUUGAAGAAUCUCAGACGGGU	52-75	stu-miR5303f	3	0	24	24	1
spiLA1589-MIR7997c-20	CUACUAUGAUAUUGCUCAGACUCUUUAAAAAUAUCACUAG CUGCGUGUUGGAGGUGUUGGAUCCUCCAAAAGUAAGUGC AUUUCUAGAUGAUUUGAUAUAGGUGCAACAAUGUUUUUG AAGAGUUCGAGAAUUUUCCUAGCAC	143	spiLA1589-miR7997c-20-5p	AUAUUGCUCAGACUCUUUAAAAAU	9-32	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303-20-3p	UUUUUGAAGAGUUCGAGAAUU	113-133	sly-miR5303	3	0	21	21	1
spiLA1589-MIR2118-1	AAAGGAAAAGGGUAUAUGUGAGUCAUUUGUUUACAUGUA GGGGUAUAUAUGAGCCACUUUCAUAAUAAGGGAUAUAUC AGCUCUAAAUGACAAAGUUGAGGGGUAUAUCAGACUCUU UUCCCAA	124	spiLA1589-miR2118-1-5p	GAAAAGGGUAUAUGUGAGUCA	5-25	hbr-miR2118	5	0	21	21	1
spiLA1589-MIR171c-2	AAACUAAAGAUAUUAAAAUGAGUUGAAAUAGAAUCGGGUU GGGUCUUGACCUGCCCAAGUUUACUUUGGGCUAAAAUGG GUUGGGUUCAAAUGGGCUAAGAACGGGUUGGGUUUUGA ACCACCUAAUUUGACCCGAUUAAUAUCAACAAUUCUAACA UAGUGAUAUUUAACUUUUAUAAUCACAAUUCGAAUUUCAG CUUUAAUAUUUUUAAAGA	215	spiLA1589-miR171c-2-3p	UAAUUUGACCCGAUUAAUAUC	124-144	aqc-miR171c	5	0	21	21	1
spiLA1589-MIR7981-3	AUGACAUUAGUAACUAAACUAAGGUCCUAUUGCUUCCGAA UUUAUUUUUUGUAAUUUUGUGCAUUUUUUGGCUCAUGUG ACAUUCAAAUAUCUCUCACGUGCCUCAAUUGCGUGAAAG UCACGGAGUGGAUCACGUAAGACAAAAAGUAUACAAAAUU AAAAAAAAUUAGUUCAGGAGGUAAUAGGACCUUAGUUUAG UUAAGAUGUGUC	210	spiLA1589-miR7981-3-5p	AGUAACUAAACUAAGGUCCUAUUG	9-32	stu-miR7981-5p	5	0	24	24	3
			spiLA1589-miR7981-3-3p	AUAGGACCUUAGUUUAGUUAAGAU	182-205	stu-miR7981-3p	2	0	24	24	1
spiLA1589-MIR9761	AAAAGGGCCUAAAACGCCCUUAAAUUAUGAGAUUAUGUAC ACUAUUACGCACCAACUACUUAAUGAGUGUGAUCCGUUG GGCAUAAGGUAUUUUUGAGUCGAAAGGUGAAUGUCAAGG AUAUUUUAAGACCGAUAGGUGGAUGGAGGAUAAUUUUAU ACCAAUUCAAAUACUUGAGGGGCAUGUUAGGCCCUUCU	195	spiLA1589-miR9761-3p	UGAAUGUCAAGGAUAUUUUAA	107-127	gma-miR9761	4	0	21	21	1

spiLA1589-MIR2607-2	UCUGUUUUAGAAAACAUUAUACAUGUCAUUAUUUGUUAACUGAAAACAGUUCUAACUUUGCAAAAUUGUUUAUACGCGGUCAUUUAUGAUUGGGGCACGUCAUUAAUUAAAUUAUUUUUUAAAAAGUGAAAAAUGUUCAAAUAUGCCAACGAACGUAUAGAAUAGGCUCAUCUAUGCUAUCCGUUAAGAGUUUUCCUCAUCCGUGUCAUUUCAGUUAGGAAAUGCUGACAUGGAUAAGUCUUUUCUCAAACAAA	254	spiLA1589-miR2607-2-5p	AUGUCAUUAUUUGUUAACUGA	23-43	mtr-miR2607	5	0	21	21	1
			spiLA1589-miR171g-2-3p	UAUAGAAUAGGCUCAUCUAUG	156-176	zma-miR171g-5p	5	0	21	21	1
spiLA1589-MIR2118b	UGAUUUCUUAUAGUCUAGCAUGGUAUAAAAUGGACCUGCAAACCAAAAUUGUAAAUGGGAUUAGUGGUGCAAAUAGUCUUGGAGAUGGGAGGUACUUUAAUGGGCUAUGUUGCUCCUCCAAAAAUGAUGUCAUACCUGUGUUGGAUUCUUUGAAAAUGCACUACUUUUGAAGGAUCCAACACCACUGUUGACAUUUUUGAAGAGUUGGAGCAACAUAGUUGAUAGGAACCUUGACAUGACAUUGAGUUGAUGUGGGGAUAAUAGUUUCUAGUGACAUGCUAGGUGAAAAGAAAGAA	296	spiLA1589-miR2118b-5p	GGAGAUGGGAGGUACUUUAAUG	81-102	gma-miR2118b-5p	5	0	22	22	1
			spiLA1589-miR5303h-3p	GACAUUUUUGAAGAGUUGGAGCAA	190-213	stu-miR5303h	3	0	24	24	2
spiLA1589-MIR8583	CCACACAAGUGAAAAUCUUGCAGAUAUGUUGACCAAGGAGAUACCGAAAGACAAGGGCGAGUUAUGCCAAGAACUUUCGGGCAUGAGCUCUCUCUAAAAAAGAUGAAGAUACCUUCUUCCAGUAAAUGGUACUGGAGCGGGAGAUUUGUUGAAUCCAUUUCAUUUUUUGGUCAACUUUUGCUAUUCAAUUGCUAAACAAUUGUUAAAAAGGAAUAGUAAUUGGAGUUGAAAAUAAAAGAUUUGGUGGUUGGCAAAUUGGUAAGAUUUACAACCAUUUUUGACUUUGCUA	289	spiLA1589-miR8583-3p	CAACCAUUUUUGACUUUGCUA	269-289	atr-miR8583	5	0	21	24	3
spiLA1589-MIR1530-3	AAUGGAGUUUGAGUGGUUAGGAGGAAGGUUGAUGGUGGAUGCUUUGAGAAGAUGGUGGUUUCACUAUUUUGAAAUAAAUUAAUAUUUUAUUUUAAAAUAGAUAAUACAUAAUUAUGACGUGGUAUUAAUGUGAGUGACAUGGAUUUGACUUGUCAUCUAUGCAAGAGAGAGUGAGGUACUCACAUGGUUAGAGUGGUUUAGCAAUCAUUUUUUUAUUGAGUUCAGGGGUCUAGAUGACAAAAGGGUAAGUAGAAGGAUUCACACUUUAAACGCAUACAAGUACAAGGGUCCACCAGACCAUUCCACCUAAAUUCUAAUCCUGA	323	spiLA1589-miR1530-3-5p	UUUUGAAAUAAAUUAAUAUUU	67-87	gma-miR1530	4	0	21	21	1
			spiLA1589-miR7488-3-3p	UAUUGAGUUCAGGGGUCUAGA	214-234	ghr-miR7488	5	0	21	21	1
spiLA1589-MIR11533a	GAAAAAUGGAUUUCGAAAAUAAUUUUUCACGAAUUAGUCCUCUUUUUUUAUGGUGAGAAUUAUCAACUAUGGUCUGUGAGAAUGGAAACUUACUUGGAGGUUCUUGAUCUUUGAGAAGUCGUGGAAGAGGAUUAUGAAAUCAAUUUACU	149	spiLA1589-miR11533a-5p	UGAGAAUUAUCAACUAUGGU	54-73	pab-miR11533a	5	0	20	20	1
			spiLA1589-miR7774-3p	ACUAUGGUCUGUGAGAAUGGAAAC	66-89	bdi-miR7774-5p	2	0	24	24	1
spiLA1589-MIR11123	CCACUUUACUCUUCUAUAUAAUAGAACUAGAUGGCCUAACAAUUUCCCCCGGAUGGAGAAGUGAGUUACUUACGUUAUUGUCUUCAGCAGGCAGGCUGCACUCUAGGCUGCUAAGAAGUUGUAGACAUUGAAAUUUUAUGUGACUCUACAAGAUGCGUUCAAUUUGAGUUGCGAUUUUACAAAUUGUGUUAGACUCAAAUUAGGAUUCUUGGAGGUUACUCAACCCUAUACCCUAGUUUAUGCCUAUAUAAAGGGUACUAAAUUCUCUUUAAAGGCAUCUAGGAAAUUAUAUAAAGAGAUCAAGAUC	307	spiLA1589-miR11123-5p	AGAACUAGAUGGCCUAACAAU	23-43	lja-miR11123-5p	3	0	21	21	1
			spiLA1589-miR11288a-3p	UGCGAUUUUACAAAUUGUGUU	170-190	fve-miR11288a	5	0	21	21	1
spiLA1589-MIR3627	GAGAGAGAUUGAGGGAAUCUUGUCGCAGGAGAGAUGGCACUUGCCAUUCCUUUUAAUUGGUACAAUGCCUAAAUGGAACCAAUUAAGUGCCUCUGUCUUUCGACACGAUGCUCACAAUUUCUAUU	125	spiLA1589-miR3627-5p	UUGUCGCAGGAGAGAUGGCACU	20-41	vvi-miR3627-5p	1	0	22	22	1
			spiLA1589-miR3627-3p	AAGUGCCUCUGUCUUUCGACA	85-105	stu-miR3627-3p	0	0	21	21	1
spiLA1589-MIR6429	AAUCUUGAUUGCGUGUUUUUACUUGUGAGUUCCUUUCUACUGCUACAUAAGCUGAAGAAGUAGCUAUUGUGUUACAGAUCAAACCACACAUUCUAUCGUCAAAUUUAAACAGUAGUAGUAGAAAGGAACUCACAAGUAAAAACACCCAAUCAAGCAA	157	spiLA1589-miR6429-3p	UAGUAGAAAGGAACUCACAAG	116-136	ptc-miR6429	5	0	21	21	1
spiLA1589-MIR10419	CAACUUUCAUAAUGCACAAACAGACAUUUUAACUAUCUAACUUUUAAAUGAAUAAACAAAUGAGUCCGACAUGUCACAAA	185	spiLA1589-miR10419-3p	CACAAAACACAUAGGACACCA	75-95	gma-miR10419	5	0	21	21	1

spiLA1589-MIR4243-2	ACACAUAGGACACCACGUAGGACAAAAAAUGACAUGUAGGACAUAUGUGUCGAUUUGUUCAACUUUAUACAAGUUUAAGUAUCUAUUUGUGCACAUCCAAAGUUGGUGACAAGUAAAAGUGAAAUUAUAUUUUUAGUAUAGUGGACAAGUAAAAGUUAAAGUGAAUGGAGUGAGUACUUUAUUUGAGUCCCAGCAAAGACGCGACUUCAAGAUUGAAUUUUGGAAGACAUUAAUUUAGAGGGUGGCUCAUAGGUUUUUUAUUAAGAAUUUAGCUAUUAUUCCCUCAUUAUUUUUGGAGUUUUUAUGUUUCAGAUGGGGAAGAAUAUGAUUUCAUGCUUUACUGUUAU	242	spiLA1589-miR4243-2-5p	UGAAAUUAUAUUUUUAGUAUA	15-35	aly-miR4243	4	0	21	21	1
			spiLA1589-miR2641-2-3p	AUUUCAUGCUUUACUGUUAU	223-242	mtr-miR2641	5	0	20	20	2
spiLA1589-MIR10538-1	GUUUUUUAAAACUAACAGCGUUAGGUUGAUAUACGUUACUGUAAGUAACAUUUUACUCCCAAAACAUUAUUUUGAGUAACGUUUUACUACAGUAAUGUUUUAGGAGCAAAACGUUACUGUGAGUAACGUAUGUCAAUCUAACGCCGUCAGCUUUUAAAAUUA	162	spiLA1589-miR10538-1-5p	AGGUUGAUAUACGUUACUGUAAGU	23-46	sly-miR10538	4	0	24	24	1
			spiLA1589-miR11575-1-3p	CCGUCAGCUUUUAAAAUUA	144-162	pab-miR11575	5	0	19	21	3
spiLA1589-MIR2922	GUCACCCACAAUAUUAUACCAACAUUGUAUACAUGGUGUAGAAAUUAAUAACUAUAUAGUAUUAUAUUGACUACUAAAUUUUCUGAAUGGUGAUGAUACAAUAACAAUUAAUAACUGGAUAGCGAAAUUGAUCAAAGUUAUCCCAAUAUAUACGUAAUACAACGACCUAUUAAUUAAACUUAUGUUGUUGUAUACGUACCUAGAUAAACUAUGUUUGGUCAUGUCAGAAGCAGCGGCGAAACUAUGGUGCAUGUCAGGAUGUCCAAUUAGAUAUGCAUCCUCAUUAAAAAAACUUUCUGAGUAAGUAGUUGUUUGUGGUGGUAUAAAUAAUGGGUCUU	338	spiLA1589-miR2922-5p	AAUAACUGGAUAGCGAAAUU	110-129	osa-miR2922	4	0	20	20	1
			spiLA1589-miR856-3p	AGUUGUUUGUGGUGGUAUAAA	307-327	aly-miR856-3p	5	0	21	21	2
spiLA1589-MIR156b-12	AAGGGAGGUGACAGAAGAGAGUGAGCACACAUGAUGUUUUCUCGCAUAAUGUUUAUAUGCUUGAAAUUAUGCUUGCUCACUGCUCUAUCUGUCACCCCACC	101	spiLA1589-miR156b-12-5p	UGACAGAAGAGAGUGAGCACA	9-29	hvu-miR156b	0	0	21	21	1
			spiLA1589-miR156c-12-3p	GCUCACUGCUCUAUCUGUCACC	75-96	ata-miR156c-3p	0	0	22	22	1
spiLA1589-MIR156b-13	AACAAAAGGGAGGUGACAGAAGAGAGUGAGCACACAUGAUGUUUUCUCGCAUGAUGUUUACAUGCUUGAAACUAUGCGUGCUCACUGCUCUAUCUGUCACCCCACCUCUUUCUC	114	spiLA1589-miR156b-13-5p	UGACAGAAGAGAGUGAGCACA	14-34	hvu-miR156b	0	0	21	21	1
			spiLA1589-miR156c-13-3p	GCUCACUGCUCUAUCUGUCACC	80-101	ata-miR156c-3p	0	0	22	22	1
spiLA1589-MIR156i-1	AGAGGUGACAGAAGAGCGUGAGCACAUGUGUGUUUUCUAGCAUGAUGUUUAUAUGCUUGAAUCUAUGCGUGCUCACUGCUCUAUCUUUCAUCCUCAUCGCUUUUCCUCUCUCUCUAGAUUUAAUUUUCUGUCUCUAUUUUGUAUAUAUUAUGUAUGUAUUUAUGUAUAUAUAUAUCAGUUAUUCCAAGUAUAUAUAAAACUAGUUAGUACAUAUUAUGUGCUCAAUUUUCAUCACCAAG	239	spiLA1589-miR156i-1-5p	GCUCACUGCUCUAUCUUUCAUC	71-92	zma-miR156i-3p	1	0	22	22	1
spiLA1589-MIR1886f-2	AAUAUGGAUUCACAUCUCGUGAAAUAGAAUCAUGAGAUGAAAUCAGCAUAAAAUCGCAUGUCCAAACAUUGAUUCCAUCUCAUGAUAUCAUAUCGUGAUAUGAUAUCGCAUGGC	114	spiLA1589-miR1886f-2-5p	AUAGAAUCAUGAGAUGAAAUCAGC	24-47	stu-miR1886f	3	0	24	24	1
			spiLA1589-miR7980b-2-3p	GUCCAAACAUUGAUUCCAUCUCAU	60-83	stu-miR7980b-5p	1	0	24	24	1
spiLA1589-MIR7822-2	AAGCAUAUCAUGUUCUUCAAUUUUGAGUGUCAACAAGUAGACAAUUGAACUUGUAUGAAAUUGAACAAGUAGACACAUGUGUUCUACAUAGUAUAAUGCACAUAAGAUGCCACGUAGUACACAAAAUUAUCAUGCAGGACUAAUAUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCUACUUGUUGACACCUAAAGUUAAAGAUCAUAAUUGUCA	219	spiLA1589-miR7822-2-5p	UAUGAAAUUGAACAAGUAGAC	54-74	ptc-miR7822	5	0	21	21	1
			spiLA1589-miR5014a-2-3p	UUAUACAAGUUUAAGUGUCUA	163-183	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR160e-3	UACAACCCAUUGCGAUACUAGAAGUUUUAUGUUUUAUUGAGUGACUCAAGAUUGGAGUCGUGCAGGCGGAGAUCCUUUUGUCGAUUCCUUGGGUUAAAUGUUGUUCCACUGUAGUUUGGGUUAUAGAUGAUACAUGAUACUUCUAUGUUCUUAUUGGUUCCC	162	spiLA1589-miR160e-3-5p	UCAAGAUUGGAGUCGUGCAGG	46-66	ptc-miR160e-3p	5	0	21	21	2

			spiLA1589-miR12173-3-3p	AAUGUUGUUCCACUGUAGUUU	97-117	aof-miR12173	5	0	21	21	2
spiLA1589-MIR5303i-2	UAAAUUGUGCAGAAUCUUCAUUUUCAAUAUCGUAUUUGUGUCAGUUUCUUCAAAAAUAUAUUGCUUUUGAAGAAACGGACAUGUAAAUAUUUUUGAAGAGUCUGAGCAACAUAGGAAUCCGCUUUCAAUGUUGCAUUUGUAUCAGAUUCUUCAAAAAUACACUACUUUUGAAGAAUCGGACAUGCAAACAUUUUUGAAGAGUGUGAGCCACAAAGUUUGAGACAAGAUUUGAAUAAUACU	240	spiLA1589-miR5303i-2-5p	AUAUUUUUGAAGAGUCUGAGCAAC	87-110	stu-miR5303i	0	0	24	24	1
			spiLA1589-miR5303d-2-3p	UUUUGAAGAAUCGGACAUGCAAAC	166-189	stu-miR5303d	5	0	24	24	1
spiLA1589-MIR166b-2	UUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAAAAUCUC	107	spiLA1589-miR166b-2-5p	GGAAUGUUGUUUGGCUCGAGGC	13-34	csi-miR166b-5p	1	0	22	22	1
			spiLA1589-miR166f-2-3p	UCGGACCAGGCUUCAUUCCCCU	77-98	cas-miR166f-3p	0	0	22	22	1
spiLA1589-MIR397b-3	CCCUUCAGAGAAUUAAAAACAUGAUCGAGUGUAGCGUUGAUGAAAAAUGAGGAAGGCCCAAAUGCAGGAAUUCUCAAAUAUGUCAUCAACGCUGCACUCAAUGAUGUUUCUAAGUACUCUGCAAUAA	127	spiLA1589-miR397b-3-5p	AUCGAGUGUAGCGUUGAUGAA	24-44	bdi-miR397b-5p	2	0	21	21	1
			spiLA1589-miR397b-3-3p	UCAACGCUGCACUCAAUGAUG	86-106	eun-miR397b-3p	0	0	21	21	1
spiLA1589-MIR5014a-5	UAGUUUGCAACUAUGAUCCUUAACUUUGGAUGUGCACAAGUAGGGACUUAAAGCUUGUAUAAAAUUGAACAAGUAGACACAUGUGUCUUAGAUGGAAUGAUACUUGUAGGACGCCACAUAGGACACAAAAUUUUCAUGUAGGAUGCCAUGUAGCAUGAAUGUGUCAAUUUGCUCAAUUUUACACAAAUUUAGGUGCCAAUUGUGCAAAUUUAAAGUUACGGAUCAUAAUUGCCAAAUGA	239	spiLA1589-miR5014a-5-3p	UUGUGCAAAUUUAAAGUUACG	200-220	ath-miR5014a-3p	4	0	21	21	1
spiLA1589-MIR7997c-21	UUGAACUAUAUUGCUCAAACUCUUCAAAACUUUUUAGAGGUACAAGUCAGAUCCUCCAAAACUAGUGCAUUUUUGGAGGAUCCGACAUGGGGGCGGCAAUAUUUUUGAAGAGUCUGAGCAACAUAGGUUGUU	132	spiLA1589-miR7997c-21-5p	AUAUUGCUCAAACUCUUCAAAACU	8-31	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303i-21-3p	AUAUUUUUGAAGAGUCUGAGCAAC	99-122	stu-miR5303i	0	0	24	24	1
spiLA1589-MIR8714	CAACAAGUGAUAUCACAUUCGACGAGAUGAACAUAGAGGUAACUGAGUUACAAUAUAUGACUUGCUUUACUAUGUUUAUCAUGUCAAGGUAACUUGAAA	99	spiLA1589-miR8714-5p	UUCGACGAGAUGAACAUAGAG	18-38	gra-miR8714	5	0	21	21	2
spiLA1589-MIR8764	ACGGGUAAAACUUAUCUGCACAUGGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUCAAAUUUAUAGUUCAUUUUACUUCUUUAAAUAUCGUAAUAAUAUUUUUUGCAUUUACUUGAUGUAAACACCCGGUACGAAUAAGUUUUUCCUUU	155	spiLA1589-miR8764-3p	UUAUAGUUCAUUUUACUUCUU	67-87	gra-miR8764	5	0	21	21	1
spiLA1589-MIR482a-2	CCAACAAAAACUUUUGGGAAUGGGUGGGUUGGUAAGCUUUUCCUUUUUUAUAUGUGUGUUCCCUUAGCUUACCAAUUCCACCCAUUUCUAUGGGUUUUUGUGCU	104	spiLA1589-miR482a-2-5p	GGAAUGGGUGGGUUGGUAAGC	17-37	stu-miR482a-5p	3	0	21	21	1
			spiLA1589-miR482c-2-3p	UUACCAAUUCCACCCAUUUCUA	69-90	nta-miR482c	2	0	22	22	1
spiLA1589-MIR1886f-3	UUUGGCCAUGUGAUACCAUAUCACGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGGGCAUGCGAUUUUACGCUGAUUCCAUCUCAUGAUAUGAUAUCAUCAGAUGUGAUACCAUAUCGUCCUCC	125	spiLA1589-miR1886f-3-5p	AUGGUAUCGUGAGAUGAAAUCAGC	28-51	stu-miR1886f	0	0	24	24	1
			spiLA1589-miR1886h-3-3p	AUUUUACGCUGAUUCCAUCUCAUG	65-88	stu-miR1886h	2	0	24	24	1
spiLA1589-MIR10215	GAGAACCUAUUCUCUAUUUUACUCUCCAAAUAUAGAGAAUGGAGAGUAAAAUAGAGAUGGGUUGGA	66	spiLA1589-miR10215-3p	GAGAAUGGAGAGUAAAAUAGA	35-55	eun-miR10215-3p	4	0	21	21	1
spiLA1589-MIR6147	AAAUUUUCUUACAUAGAGGUGGAUCCCGAAUCUUGAGUUUAUGGAUUUAGAUUCUAGAAAAGGUUACAUUUUCAAAACCCAACAAGUUACAUUUUUAGAAUUUCGUAUUCACAAACUCAAAAUUCUGGAUUCACCUCUACGUAAGCGAAAAGAG	154	spiLA1589-miR6147-3p	UUACAUUUUCAAAACCCAACA	64-84	nta-miR6147	4	0	21	21	1
spiLA1589-MIR7997c-22	AAAUUAAGGCUAUGUUGCUCGGACUCUUCAAAAAUGUCAACGCGUGCAUGUUGGAUUCUCCAAAAGUAGUGUAUUUUUGGAGAAUCCGACGCGGGUGUGGCAUCGAAUGAAGAGUCCGUAAAACUUAGCAUUAAGGU	137	spiLA1589-miR7997c-22-5p	AUGUUGCUCGGACUCUUCAAAAAU	12-35	stu-miR7997c	1	0	24	24	1
			spiLA1589-miR5303f-22-3p	AUUUUUGGAGAAUCCGACGCGGGU	73-96	stu-miR5303f	2	0	24	24	1

spiLA1589-MIR4240	GGAUUAAUUAGUGGCUGAUUAUGCCAUUAACUUUAAGUGUGGGAUUAAUUAGUGGCUGAUUAGGCCAUUAACUUUAAGUGUGGGAUUAAUUAGUGCUGAUUAGGCCAUUAACUUUAAGUGUGGGAUUAAUUAGUGGCUGAUUAGGCCAUUAACUUUAAGUGUGAGAUUAAUUAGUGGCUGAUUAGACCAUUAACUUUAAGUG	241	spiLA1589-miR4240-3p	UGAUUAGACCAUUAACUUUAA	218-238	ath-miR4240	5	0	21	21	1
spiLA1589-MIR5174e	AUGUAUUUAUACUAAGUUUAUGGUCACUGUCACAAGUAUCAACCAGUGUAACGGUACUCCCUCUGUGCCAUUUUAUGUGGCACUUUUCGGAUUUCGAGUAAACAUUUUGAAUUAUUAAUUAUUGUGACCCAUACUUUUUAUAAAUAGUU	149	spiLA1589-miR5174e-5p	UACUCCCUCUGUGCCAUUUUA	55-75	bdi-miR5174e-5p-2	5	0	21	21	1
			spiLA1589-miR8007a-3p	AUGUGGCACUUUUCGGAUUUCGAG	75-98	stu-miR8007a-5p	1	0	24	24	1
spiLA1589-MIR398b	AUGAACAAUGGUGCAUCCCAGAGGAGUGUGCCUAAGAACACAGGUGUAUUUUGGUCUUCUCCUGUUUUGGACCCAAAGUAUGCUUGUGUUCUCAGGUCACCCCUUUGGGAUCACCUUGCUUUUU	124	spiLA1589-miR398b-5p	GAGUGUGCCUAAGAACACAGGU	24-45	stu-miR398b-5p	1	0	22	22	1
			spiLA1589-miR398-3p	UUGUGUUCUCAGGUCACCCCU	84-104	lja-miR398-3p	0	0	21	21	1
spiLA1589-MIR169j-7	AAUCGAUGGAUAUACAUUUUUUGCCUAUCCAAGGGUCAUUUUAGUUACAAUCUUACGAUUACAUAUCUACUGAGCGAUGUGAAUACCAUGAAAAGCCAUAUUGGUGAUCUUCACUUUUGAACUAACCGCGCUCAAUAAAUAUUUAACUGUAAGAUCGUAGCUAACACGAGCUCAUGGAUAGGCAGGAAAUGCUUCUCUAUCGGCU	205	spiLA1589-miR169j-7-3p	UAGGCAGGAAAUGCUUCUCUA	179-199	bdi-miR169j-5p	5	0	21	21	1
spiLA1589-MIR1128-5	UUCUACUCCCUCCGUCCCAUAUUAGUGGUCCACCUUACUAUAAAUAGUUGUUCCACAUUACGGAAGUGGACAACUAAUAUGGGAUGGAGGGAGUACUU	98	spiLA1589-miR1128-5-5p	UUCUACUCCCUCCGUCCCAUA	1-21	ssp-miR1128	2	0	21	21	1
			spiLA1589-miR5049-5-3p	AAUAUGGGAUGGAGGGAGUAC	76-96	tae-miR5049-3p	3	0	21	21	1
spiLA1589-MIR10538-2	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUCCUAAAAUGUUACUCAUAGUAAUGUUUUAAGAGUAAAAUGUUACUGAAAAAAACGUUUUAGGAGUAAAACGUUACUUAAAGUAACGUAUAUCAACCUAAUGCUGU	148	spiLA1589-miR10538-2-5p	AGAUUGAUAUACGUUACUCACAGU	9-32	sly-miR10538	0	0	24	24	1
spiLA1589-MIR5568a	UCCAAUCAUUACUCCAACUUUGGAGUGCACAUCCAGACACUUCAAAUCAUGUCCACUAUAUCAAUUGAACACUCAACAGUCCAACUUACAAUAUGAACGUGUAGACACCACCAAAAUUUACGUGUCACGUCAAUGUUGAGUUCCCACAAGAUCAGUGGGACUGAGUUGAGAUGUCUAGAUGUGCACUCCAAAGUUGGAGAGUAUUAUC	208	spiLA1589-miR5568a-5p	CAGUCCAACUUACAAUAUGAA	77-97	sbi-miR5568a	5	0	21	21	1
			spiLA1589-miR7992-3p	UGUCUAGAUGUGCACUCCAAAGU	172-194	stu-miR7992-3p	2	0	23	23	1
spiLA1589-MIR8001a-3	AUUUACAAGAAAACUUUGAAUUACAUGGGAAUUUCCGUGGGGAUUAGUAUGAAUAUUCCCAGGAAACUUAUUUUCCUACAAAUAUUCAUACUAAUUUCCAGGAAAAUCCUCAUGUAAUUCACAGUUUUCUUGUAGUG	137	spiLA1589-miR8001a-3-5p	CCGUGGGGAUUAGUAUGAAUAUUC	35-58	stu-miR8001a	3	0	24	24	2
			spiLA1589-miR396b-3-3p	AUUCACAGUUUUCUUGUAGUG	117-137	aof-miR396b	5	0	21	21	2
spiLA1589-MIR9470-3	CGGAAUCGAUAAGCCGAACCGAUAAAAAAGUUAUUGGUUUAUAGUAUUGGGUUAUUGAUUUAGUGGUUUUGAUAAUGGUUUUUGACUUUUUUUUUGUUAUCGGCUUAUCGAUUUUU	115	spiLA1589-miR9470-3-3p	AUCGGCUUAUCGAUUUUU	98-115	sly-miR9470-3p	5	0	18	20	2
spiLA1589-MIR7997b-9	UACUGUAAGUUAGCUGCUAGUCUAGACCUACGUUGCUCGGACUCCAAAAAUUGUUGCAGCACCACUAUCAGAUCCUCCAAAAUGCACUAUUUCUGAAGGAUCCGGCACCCAGCCAUCGACAAUUUUAAAGAGUCUGAGCAAUGUAGGUCUAGACUAAGGUCUCACUUACAACA	173	spiLA1589-miR7997b-9-5p	ACGUUGCUCGGACUCCAAAAA	30-50	stu-miR7997b	5	0	21	21	1
			spiLA1589-miR5303h-9-3p	GACAAUUUUAAAGAGUCUGAGCAA	118-141	stu-miR5303h	3	0	24	24	2
spiLA1589-MIR6025c	GUGGAUGUUUGAACCAAGUGAUGUUAAAAAAUCAACGGAUAAGUUGUGGUUAGGGGUGAAAUGUCACUCUAACCCAGAGCUAGCUAGUUCUCCCUGAAAUGCUUUGUGGCACAUCAUUUGACUAGACAUCUAG	133	spiLA1589-miR6025c-3p	UCAUUUGACUAGACAUCUAG	114-133	nta-miR6025c	4	0	20	21	1
spiLA1589-MIR1435b	AAACCCUUUUUGCAGAAGGGGGUUUUAGACUUGGGAAGCAAAAGUCUUGACAGAAACUACCAAGUUCAUUACUUGAGAAUUUUUUAUCUUUCUUAAGCUGAUCCAUUAGCUUUAAAUCAGUACAUAACUCCAUUGCUACGAAAUGAAUCAAAAUGGUA	246	spiLA1589-miR1435b-3p	UAUUUUAGAUCAAACCUUUU	212-231	sbi-miR1435b	4	0	20	20	1

spiLA1589-MIR6151i	AGGUCUCCAUAAGUCAUUUAUGAAUAUGGAAUUUUACCUUCAUAUCGAUCUCUUAUUUUAGAUCAAACCUUUUCUGCAAAAUGGGGAGUUUUUAAGGAUAAGGGGCUAAAAUGCCCUUAACUUAUGAGAUUUUGUACACUAUUACCCUCCAACCACCUAAUGAGUGUGAUACGUUGGACAUAAGGGUAUUUUUUGAGUCGAAAGGUGGACGUCAAGGGUAUUUUAGGACCGAUAGGCGGAUGGAGGGUAAUGUCGUACCAAUUCAAAUACUUGAGGGGCAUGUUAGACCCUUCUCUGUAAUUU	215	spiLA1589-miR6151i-5p	UGAGUGUGAUACGUUGGACAUA	73-94	nta-miR6151i	5	0	22	22	1
spiLA1589-MIR1520d	GAGACUUGCCACAAUUUUAUUCAUCGAUUCAAUAUUUAAUAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACGUGUA	77	spiLA1589-miR1520d-3p	AUAAGAUUAUGACACGUGUA	58-77	gma-miR1520d	5	0	20	22	1
spiLA1589-MIR7543-1	GGGACACGUGUCACAAUCUUAUCCAUCGAUCUAAUGUCUGGUCGGUGAAUAAGAUUAUGACACAUGUAUG	70	spiLA1589-miR7543-1-3p	AUUAUGACACAUGUAUG	54-70	lja-miR7543	4	0	17	20	2
spiLA1589-MIR171t	AAUCCGGGCUCUGCAACUAUGUUGAACUGCGUGACUAUCUCAUUUAAAAGGUUUAGAUGAGAUAGUCAGACACUUCAACAUUGUAUCAAGCCAGGCCC	98	spiLA1589-miR171t-5p	UUGAACUGCGUGACUAUCUCA	22-42	gma-miR171t	4	0	21	21	1
			spiLA1589-miR5237-3p	UUUAAAAGGUUUAGAUGAGAU	43-63	mtr-miR5237	4	0	21	21	1
spiLA1589-MIR7980b-4	UUUGACUAUGUAAUACCAUAUCAAGAUAUGGUAUCGUGAGAUGGAAUCAGCGUUUGGACAUGCGAUUUUACGCUGGUUCCAUCUCAUGAUUUCAUAUCAUGGGAUGUGAUUCUAUAUUCUCC	122	spiLA1589-miR7980b-4-5p	GAGAUGGAAUCAGCGUUUGGACAU	38-61	stu-miR7980b-3p	1	0	24	24	1
			spiLA1589-miR1886h-4-3p	AUUUUACGCUGGUUCCAUCUCAUG	65-88	stu-miR1886h	3	0	24	24	1
spiLA1589-MIR868-2	AAGUAUUAGCACGGAGACGUCUAUGCUCAUCUCUGAGAGGCUAUAAAGAUUACUAGGAAACUCCCUUUUGUUCAUUCUUUCUCAUCGUGCGUAGUUACCUUCCUUAGUACUGAGUUGUUAUAUACUCUUUUGACAGAUGACGAAGACUAGAAGUAAUGUUACUAGUGGUAGAGGGGAGGCAUUUCCCGAGGUAGUUGUUAAGGCCCAUGCCAGGCGUCGGGGUAGAUAUCGAGCUAGAUGUCGUGCUAGUAGUA	254	spiLA1589-miR868-2-3p	AGAUGUCGUGCUAGUAGUA	236-254	ath-miR868-5p	5	0	19	21	3
spiLA1589-MIR773b-2	UUGUACACCUUUUGGCUUACGUGGCAUUAGCUUGAAAAAAAAAGUCAAUCACCGUUGAGCCCACAAGAUAGUGUCACGUAGGCCUAAAAUGGGUAGAA	98	spiLA1589-miR773b-2-5p	GGCAUUAGCUUGAAAAAAAA	23-42	ath-miR773b-5p	5	0	20	20	1
			spiLA1589-miR5026-2-3p	GCCCACAAGAUAGUGUCACGU	59-79	ath-miR5026	5	0	21	21	2
spiLA1589-MIR7823-2	AAAUAAUGCAUGCAUUAGCUUGAUGUAUUAGUAGUACCUUGUUUGGUACACUUUUCUAACCUAUGCAUCACCAAUGCUUGUAUUAGUA	88	spiLA1589-miR7823-2-5p	AUGCAUGCAUUAGCUUGAUGU	6-26	ptc-miR7823	5	0	21	21	2
spiLA1589-MIR4229	AUGACUCAGUUGGUUUGGAGGGUGGUUAUCCACACGGAUGACCUGGGAUCAAUCCCCUCAAUGCCUUCUGAGUUGA	76	spiLA1589-miR4229-5p	UUUGGAGGGUGGUUAUCCACAC	14-35	aly-miR4229	5	0	22	22	1
			spiLA1589-miR11076-3p	AUCCCCUCAAUGCCUUCUG	52-70	lja-miR11076-3p	5	0	19	19	2
spiLA1589-MIR7543-2	GCUCACACAUGUCUUUCAUUCAACGAAAAUGAAAAAAAUAGUUUUAAAUUUAUAUUUUUGACUUUUAAUUUUAUAAAAAAAAAAAAAAGACAAUAUACCCAUAGCUGUCGUAAAUGGUAUGCAGAUACCCUCUGUCAUACUUUUGGGCAUUGGUACAAAUGUCGUCCAAAAACUAGAGCAUAUGUAUCCUUUAGACAACCGAACAUACACGUGUCAUAAUUUUAUCCACCAACCCGACAUGUAAUAAAUAUUGGAUCGAUGGAUUAAUUGUGUCACGUGUCCCUAUUUAGUCUUUCGUUAGAGUGAAUGACAUAUAUGCUC	321	spiLA1589-miR7543-2-5p	UUAAAUUUAUAUUUUUGACU	44-63	lja-miR7543	5	0	20	20	1
			spiLA1589-miR11108b-2-3p	AUAUGUAUCCUUUAGACAACC	180-200	lja-miR11108b-3p	5	0	21	21	3
spiLA1589-MIR171b-3	GGUAUGAAGAAGAAUACAAGAGUGAUAUUGGUUCGGCUCAUCUCUUAUCUGUUUCGCGAAUCAGAAAUUAGUGAGCCAAACCAAUAUCACGCCAUGUCUUCUUCUCCAUCAU	112	spiLA1589-miR171b-3-5p	AGUGAUAUUGGUUCGGCUCAUC	21-42	csi-miR171b-5p	1	0	22	22	2
			spiLA1589-miR171h-3-3p	GUGAGCCAAACCAAUAUCACG	71-91	zma-miR171h-3p	2	0	21	21	1
spiLA1589-MIR9471a-3	CUCGAGUUGAUUUCUCAGAUGGUCACUCGACUAAUAGCUGUAUUAUCUUAGAAAGUCACUUUUUUGGUUGAAGAAAAGCGGAAUCAAGAAGAGAAGUGACUUUUUUUUAUAUAAUGACUAUUAAUCGAGUGAACAUCUGAGCAAUCAAUUCCGU	154	spiLA1589-miR9471a-3-5p	CAGAUGGUCACUCGACUAAUA	16-36	sly-miR9471a-5p	4	0	21	21	1
			spiLA1589-miR10540-3-3p	AUAAUGACUAUUAAUCGAGUG	111-131	sly-miR10540	4	0	21	21	1

spiLA1589-MIR1159	UGUCGUAAUUGAUAGUCACGAUUUAAUGCAGAAACGUGAUCAGUGAUAACGUUUUAUGAUCUGUAAAAUUCCAAUGUAGCAGGAUUUUAUUCUUAAUCCGAUGCCCGGUGAUUAAAUUUUCAUAAAACGAGAUUGACAGUUACGUUUAAUAUAAUAAACGUGAUUAUCAGUUACGUUU	178	spiLA1589-miR1159-5p	AAAAUUCCAAUGUAGCAGGAU	65-85	cre-miR1159-2	5	0	21	21	1
			spiLA1589-miR6273-3p	AAUGUAGCAGGAUUUUAUUCU	73-93	ppe-miR6273	4	0	21	21	1
spiLA1589-MIR156i-2	UAAUGCACAAACAGACACUUUAACUAUCCAACUUUUAAAUAAAUAAACACUUGAGUCCUACAUGACAGAAUAUACGUAGGACAUCACGUAGGACAAAAAAAAUGACAUGUAGGACAUAUGUGUGUAUUUGUUCAACUUUAUACAAGUUUAAGUGUUUAUUUAUGCACAU	169	spiLA1589-miR156i-2-5p	AUGACAGAAUAUACGUAGGAC	62-82	csi-miR156i-5p	5	0	21	21	2
			spiLA1589-miR5014a-2-3p	UUAUACAAGUUUAAGUGUUUA	138-158	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR7997c-23	AAAUUGAUGGAAUUACAAAAUGAUUUUUGGUUGUUAAAAGCUAUGUUGCUUGGACUCUCCAAAAGUGUUGUCACACCAUGUCGGAUCCUCAAGAAAUGCACUACUUUUGGAAGAUCCGACACACAUCCGGCAGGACUUUUGAAGAGUUCGACCAACAUAGGUGUUACAUAAGCAGAUAAAAUCUUGUGUUAAUGUCCCAUAACUC	205	spiLA1589-miR7997c-23-5p	AUGUUGCUUGGACUCUCCAAAAGU	43-66	stu-miR7997c	4	0	24	24	1
			spiLA1589-miR5303-23-3p	CUUUUGAAGAGUUCGACCAAC	136-156	sly-miR5303	2	0	21	21	2
spiLA1589-MIR2673b-2	GACUUCUUCCUCUUCCUCUUCCUCUUCAUCUUCGAGUUCAUUUGCUGAUAAAGAAAAAGGUAAAGGGCAAUCAAUGAAAGAGAAACAUGUGAAGAGGAUUAAGAAAGGAUUAGAGAGGUGUAAAUCAGAAACUUUAAGAGUUAGACCUGUGAUUCAUGUGCCAAUUUGUUCACAGGGGAAAAACUCUGCUCUGCCACCUCUGUUUUCACUUAAGAAAAAAGGAAGAGCAAUAGAGAGAUGAAAAA	245	spiLA1589-miR2673b-2-5p	CCUCUUCCUCUUCCUCUUCAUC	9-30	mtr-miR2673b	2	0	22	22	1
			spiLA1589-miR8586-2-3p	UUUUCACUUAAGAAAAAAGGA	203-223	atr-miR8586	4	0	21	21	1
spiLA1589-MIR393b	CUGGUGGAUUAUUCCAAAGGGAUCGCAUUGAUCCUGUGUUCCAAAUUAAUUAACCAUGGGACUAUGGGAUCAUGCGAUCUCUUCGGAAUUCUCCACAAU	99	spiLA1589-miR393b-5p	UUCCAAAGGGAUCGCAUUGAUC	12-33	csi-miR393b-5p	0	0	22	22	1
			spiLA1589-miR393-3p	AUCAUGCGAUCUCUUCGGAAU	69-89	sly-miR393	0	0	21	21	1
spiLA1589-MIR391a	UUGCAUCAUUGCUCUUGCAUACAUCUCUUAGAGAAGAUAGGUGGAUGCACCAGGUAUCCCUUCAAUUACAUAUCAUUUCUAUCUUCUCUAGGAGAUGUAUGCAAGAGCAAUGAUGGAU	118	spiLA1589-miR391a-5p	UGCAUCAUUGCUCUUGCAUAC	2-22	gma-miR391a-3p	5	0	21	21	2
			spiLA1589-miR7806-3p	UAGGAGAUGUAUGCAAGAGCA	89-109	rgl-miR7806	5	0	21	21	1
spiLA1589-MIR419	CAUAACACAUGCCUAAAUAAUUAAUUGUUCAGCUCUUCCUCCACAUCCAUUCAAAUGGUUUGAAUGGCCAUGGAGGAAGAGCUGAGUAAUUAAUUAUUAAUGUUGUUGUUGUU	113	spiLA1589-miR419-3p	UUAUUAAUGUUGUUGUUGUU	94-113	ath-miR419	5	0	20	21	1
spiLA1589-MIR1879	CACCCUAAUAAAGAAAGAGUAAUUUCCCUAGAUAGUCACUCGUGUUUGGGAAAUUAUCUAGGAAUAUCACUUCUGUUUGUUUUAGGAUU	89	spiLA1589-miR1879-3p	CUGUUUGUUUUAGGAUU	73-89	osa-miR1879	4	0	17	24	2
spiLA1589-MIR169c-4	UUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAU	182	spiLA1589-miR169c-4-5p	UAGCCAAGGAUGACUUGCCUA	44-64	ata-miR169c-5p	0	0	21	21	1
spiLA1589-MIR6231-3	UCCGUAUUUUAAAGGUAUAUAUGUGCCCACGUGGACAUCAUAAAUAUUGCAUCAUUAUAAAUAGUAACGUGCCCAUGUGAGUACAUAUAUACCUUCAAAAUACAGU	106	spiLA1589-miR6231-3-5p	UAUAUGUGCCCACGUGGACAU	18-38	sbi-miR6231-3p	5	0	21	21	1
spiLA1589-MIR10211a	UGUCUUCACAAUAUGGAGCUUCGAGUGAAGAACAGGAAGCCACUUGCUUGUUCUUCUCAUAAUGCUCCAGAUAUUUGAAGCCU	83	spiLA1589-miR10211a-3p	CUCCAGAUAUUUGAAGCCU	65-83	eun-miR10211a-3p	5	0	19	21	2
spiLA1589-MIR7980b-5	ACCAUGUGAUACUAUAUCACGAUAUGAUAUCGUGAGAUGGAAUCAGCGUUUGGAUAUGCGAUUUCACGCUGAUUCAAUCUCAUGAUUCCGUAUCCUGAGAUGUGAUUCCAUAUU	114	spiLA1589-miR7980b-5-5p	GAGAUGGAAUCAGCGUUUGGAUAU	34-57	stu-miR7980b-3p	2	0	24	24	1
			spiLA1589-miR1886h-5-3p	AUUUCACGCUGAUUCAAUCUCAUG	61-84	stu-miR1886h	4	0	24	24	1
spiLA1589-MIR6288c-1	UUUUGAUGGUUUAAGGCUUUCAAGUUUCGUUGUGUGCAUCGUCUCCUAAAGGUCCAUUUUAUGUUUUAAUUGGGUUGA	240	spiLA1589-miR6288c-1-5p	CAUUUUAUGUUUUAAUUGGGU	55-75	ppe-miR6288c-5p	5	0	21	21	1

	UUUAUAGCCAGUGAAUUAUGAAUUGUGACUUCCAAGGAA GGAGCUUUUUUUAUUCUAAUACCAUACAAGUCAAUGGUA GAGGUUCUCUCUUUUUUGAAUUAUGAGUACUUGAAACUC AAAUAGCUUCCAACGGAAUUUGGAAAACUAUUUAUAACAU CAUUC		spiLA1589-miR7696d-1-3p	UUUUGAAUUAUGAGUACUUGA	170-190	mtr-miR7696d-3p	1	0	21	21	1
spiLA1589-MIR1428e	AAGGAAUUCUACAUGGUUGAUCCUGCCAGUAGUCAUAUG CUUGUCUUAAAGAUUAAGCCAUGCAUGUGUAAGUAUGAA AAAAUUCAGACUGUGAAACUUCGAAUGGCUCAUUAAAUAA GUUAUAGUUUGUUUUAUGGUAUCUACUGCUCAAAUAACC GUAGUAAUUCUAG	170	spiLA1589-miR1428e-5p	AAAGAUUAAGCCAUGCAUGUG	48-68	osa-miR1428e-3p	5	0	21	21	2
spiLA1589-MIR10424d	CAGUGGACAUUUCUAGACAUUGAAAUUUUGCAGGACUCU ACAAGAUAUUUUCUAUUUGAGUUGGGACUUUACAAGGUG UGUUCUAUUCAAAUAGGAUUCUUGGAGGCUACUCAAUCC UAACCCUAGUUCACACUUCUACAAAGGGUAUGAAAUUCCC UUAAAACACAUCUCAAAUAUCACAUAAACUCUUGGGUAUU UUUUAAAGAUCAAUGUCUCAAAAAUUCCAUAA	229	spiLA1589-miR10424d-5p	UUUUCUAUUUGAGUUGGGACU	48-68	gma-miR10424d	4	0	21	21	1
			spiLA1589-miR10984a-3p	UCUCAAAUAUCACAUAAACUC	168-188	mdm-miR10984a-3p	5	0	21	21	3
spiLA1589-MIR11444	ACUAUUAGUGUACAGUCAGACCUCUUUAUAACAGUGUCG UUUGUCUGGAUAUGUUUUGGUUGCUAUAACGAGAUGGUG UUAUAGAUAACAUAUAUUAAAGUCGAUUCCAAAAGAUCUA ACUAGGCCGUUAAAGUGAAAUUUUGUUAUAAAGGAUGAC UGUUAUAGAGAGGUUUGACUGUAAAUUGAUCUC	190	spiLA1589-miR11444-3p	AUUUUGUUAUAAAGGAUGACU	138-158	pab-miR11444	5	0	21	21	1
spiLA1589-MIR10542-3	UAGAAGAAUCAUAUAUACCCCUAAAUAAUUUUUAAAAAAA AAUAGAAGUAACAAAUAUAAAUUUAAAACUAAUAUUUUAAC UUCCGUUAAAUGAAGGGUAUAUGUGAGCAAUUUUGUAAC GGUAGGGAUAUAUGUGAGCCGUUUGUAUAACGGUAAGGG CAUACAUGAGCCACUUUUAUAACGAGGAGUAUAUCAGCU	237	spiLA1589-miR10542-3-5p	UAGAAGAAUCAUAUAUACCCCUA	1-23	sly-miR10542	0	0	23	23	1
spiLA1589-MIR11592-1	CCAAAUGACAUAGUUGAGGGGUAUAUCAGACUCAUUUCC GAUGUACCGGUACCGGUCCAGUACCUUCCGAUUUGUUUC GGUUCGUCCCGAUUCGGUUGCCUACGAGACGAAAUGGGA CAUCCUGAAUCGGGACACGGAACGGAACGAAACCGAAGU UUGGUACCGGUGUACUGGUACCGA	141	spiLA1589-miR11592-1-3p	GAACGGAACGAAACCGAAG	98-116	cas-miR11592	4	0	19	19	1
spiLA1589-MIR7502c-1	UGUAUAGGGAAAAAUACUCAAAUAUGCUAUCGAACUUUCA GAAAAGACUCAUUUAUGCCAUUCGUUAAAAGUUUGACUCA UCUAUGCCAUUACCGUUCAAGAAAAGACUCAUUUAUGCCA UUAUUUUUUAAUAGUGAUUUUGCAAAACCAUUUUUGACAC GUGAUCAAUUAUAAUUCGGCCACGUCAUCAAUUUUUAAAA UAAAAAAAAUGUAACUGAUGGCAUAAAUGAGCCUUUUCUG GAAGUUCAAUGGUAUAUUUAUGUCUUUUCCCAUUUG	276	spiLA1589-miR7502c-1-5p	UCGUUAAAAGUUUGACUCAUC	62-82	gra-miR7502c	5	0	21	21	1
			spiLA1589-miR5160-1-3p	GAAGUUCAAUGGUAUAUUUAUG	241-262	osa-miR5160	5	0	22	22	3
spiLA1589-MIR8021-2	AUCAUUCAUAUUCAAGGCUCAAACUCGAGACCUCUGGUU AAGGAUGGAUAUUUCAUAUACAUCCCCUCGUAAAUAUUG UUGGUUCUAAACUUAUAAUAAUAACAUAAUUCACUCUCC UUGCAUAUUCUGCAAUAUGUUGAAUUAAGUUAUUAAGCU CUAUCAACAAUAUUGUGUUGGAGAAGAAGUUAAUAUUACU UCAUCCUUAACCAGAAGUGUCAAGUUUGAGUCUUGGCAU GAAUUAA	243	spiLA1589-miR8021-2-5p	AUUCAAGGCUCAAACUCGAGACCU	10-33	stu-miR8021	0	0	24	24	1
spiLA1589-MIR5303h-1	UUAAAGCUAAGUUGCUGAAACUCUCCAAAAAUGUCAUUGC ACUCCUGUCGGAUCCUUCAAAAAUACACUGUUUUGGAGA ACCCGACAUUGUACCCAUUGACAUUUUUGAAGAGUCCGA GCAAUAGCUUAUG	131	spiLA1589-miR5303h-1-3p	GACAUUUUUGAAGAGUCCGAGCAA	99-122	stu-miR5303h	2	0	24	24	2
spiLA1589-MIR7981-4	AUGAUUGAAAUUCCAGAGACACACCUUAACUAGACUAAGU UCCUAUUACCCCCUCCCCCCCUCGAACCCAUUUUUUUU GUAAUUUUGUGCACUUUUUUGGCUUACGUAACAUCCAAA UAUCUCCCGCGCACCUCAAUUGCGUGGUGUCACAGAGUG UGCCUCGUAAGACAAAAGGUGUAAAAAUUAAAAAAAAAAA GUUCAUGGAGAUACUAGAACCUUAGUUUAGUUAAGGUAU GUCUCUGAAAUUUCGAUCAU	256	spiLA1589-miR7981-4-5p	CUUAACUAGACUAAGUUCCUAUUA	25-48	stu-miR7981-5p	5	0	24	24	2
			spiLA1589-miR7981-4-3p	CUAGAACCUUAGUUUAGUUAAGGU	211-234	stu-miR7981-3p	3	0	24	24	2
spiLA1589-MIR7997c-	GGCCUAUGUUGCUCGGACUCUCUAAUAAUGUUGACAAGC CCGUGUCAAAUCCUUCAAAUAUGCACUGCUUUUGAAGGA	127	spiLA1589-miR7997c-24-5p	AUGUUGCUCGGACUCUCUAAUAAU	6-29	stu-miR7997c	4	0	24	24	1

24	UCCGACAUGCACCUUAUGACAUUUUUGAAGAGUUUGAGCAACAUAGUAU										
			spiLA1589-miR5303h-24-3p	GACAUUUUUGAAGAGUUUGAGCAA	96-119	stu-miR5303h	2	0	24	24	2
spiLA1589-MIR7992-5	GCAUAAUAUAUAGAUAGACACCUUAAAUUGGCCUUAACGAGCAAGUAAAGACCCAAACUAACACGGGGCCAACUUAAACCAAGUUCAUGUGUCUAGAUGUGCAUUCUCAAAGUGUAGGUCUUUACAUGUCAGUUAAGUCCAAGUUAAGGUGUCUAUCUACGUGUUACAA	169	spiLA1589-miR7992-5-3p	UGUCUAGAUGUGCAUUCUCAAAG	90-112	stu-miR7992-3p	5	0	23	23	1
spiLA1589-MIR6457b	UUUUAGUUGCGCGGACUCUUCACUUUUGUUGCUGCAUUUAUUUCAAAUUCUUAAAAAAUACAUUAUUUUUUGUGAAUUUGACCCAUAUUCAUUGACAUUUUUGAAGAGUCCGAGCAAUAUAG	122	spiLA1589-miR6457b-5p	UUAGUUGCGCGGACUCUUCAC	3-23	ptc-miR6457b	5	0	21	21	1
			spiLA1589-miR5303h-3p	GACAUUUUUGAAGAGUCCGAGCAA	94-117	stu-miR5303h	2	0	24	24	2
spiLA1589-MIR9749	UUCUAACUUAGUCUUUGGUUUGCUUUUAUUUUUUUUAUUUUCUUUACCCUCUCCCAAUGGUUGAUUUGUAGACCAUGGUUUACCAUACGCGAUCAAAGGGUUCAUUACCUUCUCUUCCGACUGAGGAUUGCAAAGGAAAAGUGAAAGCGACUAAUGCUAGAGUUAUAU	168	spiLA1589-miR9749-5p	UUAUUUUCUUUACCCUCUCCC	35-55	gma-miR9749	5	0	21	21	1
			spiLA1589-miR1211-3p	UUCAUUACCUUCUCUUCCGAC	101-121	ppt-miR1211-3p	5	0	21	21	1
spiLA1589-MIR8042	UACCUAUAUAGUAUGUUAAACCACCAGAUAAGCACUUCCAUCUAAUUUCUAAAAGGUGGUCAAGGGAACGAGGUGGUGAAACACAUGUAACUUGACACAACUUUCAGAAAUUAGACUGAAAUGCUGAUCUGGUUUCUUAUAUACAUUACACAUAGUUU	158	spiLA1589-miR8042-3p	AUUAGACUGAAAUGCUGAUCU	110-130	stu-miR8042	1	0	21	21	1
spiLA1589-MIR162-4	GAACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGAAAAGCGAUAAAUACAGCAACAGGAAGCGAUCGAUAAACCUCUGCAUCCAGUGCUU	93	spiLA1589-miR162-4-5p	UGGAGGCAGCGGUUCAUCGAUC	7-28	csi-miR162-5p	0	0	22	22	1
			spiLA1589-miR162-4-3p	UCGAUAAACCUCUGCAUCCAG	68-88	fve-miR162-3p	0	0	21	21	1
spiLA1589-MIR1173	UUAAAAAUGGGUUGAAUAGAAAUUAGGUUGGGUCAUGAUCCGCCCAAGUUUACUUCAGGCUCAAAUAGGUUGGACUCGAAUGGGCUAAAUUUGGUUGGGUCAUGACCCACCCAAUUUGACGUGCUUAAUCUGAAUAAUUUUAACAUAUUGUUAUCUAAUUUCUAUAACCACAAUUUGCA	179	spiLA1589-miR1173-5p	AUGGGUUGAAUAGAAAUUAGG	7-27	cre-miR1173	5	0	21	21	1
			spiLA1589-miR3932b-3p	UUUGACGUGCUUAAUCUGAAU	115-135	ath-miR3932b-5p	5	0	21	21	1
spiLA1589-MIR1054	UGGUGGCUGCCGAAAAGCAGCAAGAGAAGGCUGCAACGCAAAUCGAAAGUUCUGCCGGGGAGCAACGAGGGCAGAAUAGCGGGACAGACAAGGGCAAGAACGUUGUUGUUGGCAUGUUCAAUCACAUGGCGUUGAUCAACCAUAUUUCUAUUGCUGCUUUGGCUGCCAAAC	171	spiLA1589-miR1054-3p	UCAACCAUAUUUCUAUUGCUG	136-156	ppt-miR1054	5	0	21	21	1
spiLA1589-MIR11078c	AACUGAGAGCUAUGGUGGCUGCCGAAAAGCAGCAAGAGAAGGCUGCAACGCAAACCGGAAGUUCUGCCGGGGAGCAACGAGGGCAGAAUAGCGGGACAGACAAGGGAAAGAACGUUGUUGUUGGCAUGUUCAAUCACAUGGCGUUGAUCAAUCAUAUUUCUAUUGCUGCUUUGGCUGCCAAACCAGCUAGUAUCAAAU	198	spiLA1589-miR11078c-3p	CGUUGAUCAAUCAUAUUUCU	142-161	lja-miR11078c-5p	5	0	20	20	1
spiLA1589-MIR8727	CUCUCUACUUGCUCGGACUCUCAAAAAAUGUCGCUACACCCAUGUCAGAUCCUCCAAAAAUCCACAAGUUUUGGAGAAUACGCGCCCCUUGAUAUUUUUGAAGAGUCCGAGCAACAUAGAUGU	123	spiLA1589-miR8727-5p	CGGACUCUCAAAAAAUGUCGCUA	14-36	gra-miR8727	5	0	23	23	1
			spiLA1589-miR5303i-3p	AUAUUUUUGAAGAGUCCGAGCAAC	92-115	stu-miR5303i	1	0	24	24	1
spiLA1589-MIR1046-3	GUUCAACUUGCAUGUUCAUAGUUUGAUAAGUCAGCUCAAAAAAAUGAAAAAUUUUGCUGAUCAAAAGCAGCGACAAGUCGACUAUCAAAUUGGGGAUUGAGUUAUGAUAAAACUCAAUCUUAGACAAUUCAAGUUGCUG	139	spiLA1589-miR1046-3-5p	AGCUCAAAAAAAUGAAAAAUU	33-53	ppt-miR1046-3p	5	0	21	21	2
			spiLA1589-miR10211a-3-3p	UCGACUAUCAAAUUGGGGAUU	78-98	eun-miR10211a-5p	5	0	21	21	1
spiLA1589-MIR8040-2	UAGAAACCAACCUCCGGAAGUUGGUAUUUUUAUUUCUUAUUUUUUUAGAUUCUUACCUCUGGAGGUCGGUAUUUUCAUUUCUUAUUUUUUUAAUUCCGAUCUCUGGAGGUCGGUAUUUCU	120	spiLA1589-miR8040-2-3p	CUUAUUUUUUUAAUUCCGAUC	81-101	stu-miR8040-3p	5	0	21	21	1

spiLA1589-MIR7997c-25	AUAUUGCUCGGACUCUUCAAAAAUGUGGAUGGGUUUGUGUCGGAUGAUCCUCCAAAAGUAGUGCAUUUUUGGAGGAUCUGGCUUAGGUGUGACAACAAUUUUGGAGAGUCCGGGUAAGUU	120	spiLA1589-miR7997c-25-5p	AUAUUGCUCGGACUCUUCAAAAAU	1-24	stu-miR7997c	0	0	24	24	1
			spiLA1589-miR5303h-25-3p	AACAAUUUUGGAGAGUCCGGGUAA	94-117	stu-miR5303h	5	0	24	24	1
spiLA1589-MIR11317	CGGACUAUUUGCCAUGUCUGAGAUCAUCUUAAGCUAUUCUUUUUAUUUCUCAAAAAAUGAAUAGGUGAUGAUGAUUCCAGAUAUGGAAAAUAGUAUC	97	spiLA1589-miR11317-5p	UCUGAGAUCAUCUUAAGCUAU	17-37	ppt-miR11317	5	0	21	21	1
spiLA1589-MIR7992-6	AGUAAGCACUCAAACUUUGAGAGUGCACAUCUAGAUACCUCAACUUGGUCAUAACCGACUACUAAACAAUCCACGACCACUCGUCUCCACUUUGUCUCAUGCACACUAGACUCUGACAUGACACAUAAAUUUUGGAGGUGUCUAGAUGAUCAUUUUGUAAGUUGAAGUGUUCUGUCUAGAUAUACAUUCUCAAAGUUGGAGUGCUUGAG	209	spiLA1589-miR7992-6-5p	UUUGAGAGUGCACAUCUAGAUACC	16-39	stu-miR7992-5p	4	0	24	24	1
			spiLA1589-miR857-6-3p	UUUUGUAAGUUGAAGUGUUCU	153-173	aly-miR857-3p	5	0	21	21	1
spiLA1589-MIR9471a-4	AGUUUGAUUUCUCAGAUGAUCACUCGACUAAUUGUUAUCAUCUCAGGAAGUCACUUUCUUUGUUGAAAGUUUUGGAAUCAAGAAGAAAGGGGACUUUCGAGAUAAUAACUAUUAAUCAAGUGACUAUAUGAGAAAUCAACCG	142	spiLA1589-miR9471a-4-5p	CAGAUGAUCACUCGACUAAUU	13-33	sly-miR9471a-5p	5	0	21	21	1
			spiLA1589-miR8668-4-3p	UUUUGGAAUCAAGAAGAAAG	70-89	gra-miR8668	4	0	20	20	1
spiLA1589-MIR5303j	AACUAGCUCGGACUGUUCAAAAAUAUCUGACAUGUGUGUCAAGCUUCCCAAAUAGUGGAUUUUUGAAUGAUCCAACAUGAGUAUAACAAUAUUUUUGAAGAGUUCGAGUAAUG	113	spiLA1589-miR5303j-3p	AAUAUUUUUGAAGAGUUCGAGUAA	88-111	stu-miR5303j	3	0	24	24	1
spiLA1589-MIR7980b-6	GAUAUGAAAUCAUGAGAUGGAAUUAGCGUAAAAUGACAUGUCCAAACGCUGAUUCCAUCUCACGAUACCAUUUG	74	spiLA1589-miR7980b-6-3p	GUCCAAACGCUGAUUCCAUCUCAC	40-63	stu-miR7980b-5p	2	0	24	24	1
spiLA1589-MIR1043-1	AUUUACGUCCUUCAACUUUGGGUGUGCAUAAUUAGACACUUAACAUUGUAUAAAAUUGAACAAGUAGACACAUGAGUCAUAUGUAUACACGUAGACACAAAUUGUCAUGUAGGAUGUCACGUAGUACGUGUGUAUCUAUUUAUUCAAUUUUAUACAAAUUUAAGUAUUGAUUUGUGCAUGCUCAAGUUGAGGGCAUAAAU	200	spiLA1589-miR1043-1-5p	CCUUCAACUUUGGGUGUGCA	9-28	ppt-miR1043-5p	4	0	20	20	1
			spiLA1589-miR5014a-1-3p	UUAUACAAAUUUAAGUAUUGA	150-170	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR7981a-23	AGAAUACUAUACUAAGGUCCUAUUCCCUUCUGAAGUUUUUUAAAGUAAUUUUCUACCCCUUUUCGGCCUACAUUACCCUAAUUUGAAAAAAAAAGUCAACCAGCGUUGGACCCACAAGAUAUUGCCACAUAGGCCGAAAAGGGAUAGAAAAUUAUUAAUAAAAUAAGUUUAGGUGGGUAAUAGGACCUUAGUAUAGUAUAAG	202	spiLA1589-miR7981a-23-5p	ACCCCUUUUCGGCCUACAUUACCC	55-78	sly-miR7981a	4	0	24	24	1
			spiLA1589-miR7981-23-3p	AUAGGACCUUAGUAUAGUAUAAG	180-202	stu-miR7981-3p	5	0	23	24	1
spiLA1589-MIR3637-1	UUUACAUUAAUACGUAAAAACGUGUUUUUUUUUAUUUAGUCUUAAUUGACAUUUGUACUCUCCAACUUUAGGUAUACACAAGUAGACAUACACGUCCUACGUGAUAAAUCUCACGCGAUUUGACAUGUAGAACAUGCGUGUCUACAUAUUCAAUUUUAUAAUUAUUUAAGUGUUUCUUAUGCACAACCAAAAUUGGAGGGUAUAGAUACUAGCUGAUGCCAAAUUAAAGAACACGUUUAUGUAUUCUGUCUC	252	spiLA1589-miR3637-1-3p	GUUUAUGUAUUCUGUCUC	235-252	vvi-miR3637-5p	4	0	18	24	2
spiLA1589-MIR5057-2	AGGACUAGUUUGAAUUCGAAAUUUUAGGACUAGUUUAAGUUAAGGUAUUUUAGGACUUGUUUGAAUUUGGAAUUUUAGGACAAAUUCGAUUUUGAAAUUUCUAGUCAGUUUGAAUUAGAGUAUUUUAGGACUAGCUAGCUUGAGUCAACGUAUGUA	192	spiLA1589-miR5057-2-3p	AAAUUUCUAGUCAGUUUGAAU	95-115	bdi-miR5057	5	0	21	21	1
spiLA1589-MIR11553	GGAUUUGUUUGAAUUUGGGAUCUUAAGACUAGUUUGUGACAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUACCCAACAUGGCAACUAACGCUCAUUAGGGCAUAUUUGGACCAAAAGUUGGACGGCGAGGGCAUGAGUGAACCAAUCUUUAAACGGAGAAUAUAUCUAAACUUUUUCGAAUAGUUUAGAGGCAUAUUUGACUCUUUUCCUUUCUUUAAAUGAAA	188	spiLA1589-miR11553-5p	GAAAAAUGAGUUGGAUAUACC	17-37	pab-miR11553	5	0	21	21	3
			spiLA1589-miR1522-3p	UUCCUUUCUUUAAAUGAAA	170-188	gma-miR1522	4	0	19	20	1
spiLA1589-MIR7699	CUGGUUGUGCUAUUAGCUUAUUAUAUCCUUGUAGUUUUUGGGUUAUGAAAUCAGUAUGAGGGUCUUUGGCAGUUGGAGAUCUAGGUGUUGAUUUUAAAUAUUUUUGAAACUAAUAAA	305	spiLA1589-miR7699-3p	UGAUAUCAAUACAUCAAAUGU	249-269	mtr-miR7699-3p	5	0	21	21	1

spiLA1589-MIR1917-1	ACAAUGAAAAAUAAUGUCCUCCGGAAUGCAAGGAGGAUCACCACUAACUCAGGAACUUGGUCUGGAUAAAUGAAGCAUUGCGUGCUGAUCCUGAGUACUUGCGUCUGCAUCAUAAAACAAUGCAGGCUAACUGAUAUCAAUACAUCAAAUGUACGUGUAUACAAGUUGGAGAGCUAAACGACAACUUACGGAUCAGCGGAUAAGAUUAUGAUACUUGUACCACUACAACAAAAACAACUUUUAGCGGCAUUAAUAUAUUGAUACUAAUAAAGAGUGCUAAAGUCUUUACCGGCAUUAGUUAAUUGCCAUUAGAACCAAUAUCGCUAAAGACUUUAGGGACAUAUACAAAGAGUGACAAUUGUCGCUAAAAAUUAGCGGCAAUUAAGAAUUAAAUGCCGCUAAUGGUCAUUUUUGUUGUAGUUAGCAAACACAAAUUAAUAAGCUAUAAA	261	spiLA1589-miR1917-1-5p	ACUAAUAAAGAGUGCUAAAGU	75-95	sly-miR1917	1	0	21	21	1
			spiLA1589-miR6137b-1-3p	GUGACAAUUGUCGCUAAAAAUU	164-185	pgi-miR6137b	5	0	22	22	2
spiLA1589-MIR7981-5	CUGGAUCAAGUAAAGCAUAAACAUAAUAAAAUAAGUUCAGGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGGGAUUUCGGGUAUAGAUUGAGGGGGUACUUGGGCAUUAUCCCUUAGUGAAUUUGAUAUCAUGUUUAGUUGAUCUUC	156	spiLA1589-miR7981-5-5p	AUAGGACCUUAGUAUAGUAUAAGU	48-71	stu-miR7981-3p	5	0	24	24	1
			spiLA1589-miR7981f-5-3p	AAGUGUGUCUCUGGGAUUUCGGGU	68-91	sly-miR7981f	2	0	24	24	1
spiLA1589-MIR437a	CCUCUCUCACUUUAUAUACAGACACAAAUGUAUAAAAUGUGUUUGUGUUUGUAUAAAGUGAGAGAAAAUUGUAUUUAUACAUCUCUUUUCGUUUGCCUAUCUACCCAGAAAAUCUCGCUCGUUACUCUCACUCGUCUCUCUCACUUUAUACAAACACAAAUGUAUAAAAUUACGUUUAUGUUUGUAUAAAGCGAGAGUAA	200	spiLA1589-miR437a-5p	AAAGUGAGAGAAAAUUGUAUU	55-75	ssp-miR437a	5	0	21	21	1
			spiLA1589-miR7122a-3p	UACGUUUAUGUUUGUAUAAAG	171-191	ppe-miR7122a-3p	5	0	21	21	3
spiLA1589-MIR4223	UUUAACUUGGCUUCAAAUCACAUUUAUGCCUUUCAACUUUGGAUGUGCACAAAUAGACACUUAAACUUGUAUGAAGUUAAAUAAAUACACACGUGUCCUACAUGUCAUUUCUUGUCCUAUUUAGUGUCCUACGUGUACUGUUUCAUGUAGGACCCAUGUGUUUAUUUAUUUAAAAGGUGGAUAUUUAAAGUAUCUGUUUAUGCAUUAUGAAAGUUGGGUCAAAGUUAAAAUUUGAAGUCAAGUUUAG	247	spiLA1589-miR4223-5p	AUGAAGUUAAAUAAAUACACAC	71-92	aly-miR4223	5	0	22	22	1
			spiLA1589-miR10519-3p	AUUUAAAAGGUGGAUAUU	168-185	tae-miR10519	4	0	18	18	3
spiLA1589-MIR1525-2	UGAAAAAAUCGAACCGACUGAUAAAUCGAAUCGAAAAAAAUGUUAUUGGGUUAUUGGGUUUUCAAUGGGUUUAUAAAUUUUUUUAUUGGGUUAUGGGUUCGGUAUCGGUUUUUACU	116	spiLA1589-miR1525-2-3p	UGGGUUUAUAAAUUUUUUUAU	66-86	gma-miR1525	5	0	21	21	1
spiLA1589-MIR7502c-2	AAGCGUUGCGACUUUAUGAAAUGUUGCAAAUUUUAUAAAAAGUUGCGACUUUAUGAAAAGUUGCAUCUUUUAUGAAAAAUUAUGACUUACAUGAAAAGUUGUGACUUUUAUGAAAGGUGACGCCCUUUCUGAAAGAUUGUGACUUUUCCAAAGGUUUGUGACAUUUAUAGUAAGGCACGACA	183	spiLA1589-miR7502c-2-5p	UUAUGAAAAGUUGCAUCUUUU	52-72	gra-miR7502c	5	0	21	21	1
			spiLA1589-miR444b-2-3p	UUGUGACUUUUAUGAAAGGUG	100-120	ssp-miR444b-1	5	0	21	21	1
spiLA1589-MIR8573	UAUUAUUUAGUUUAGAUAAGUUCUUAUAUCAUUAUAAGUGUGACUGUUGUCUUCUGUUGAGUUAUGUAAGCUAGGUCAAGGGCCCGCUCGAGGCCAGCAAUGGUCAUCGAGUUCCAGUCUGGCGCAAGGUGUAGGCUCGGAGCGUGAGAUGGAGAUUGAGGAUUAGAGUAGAAGGUUAGUAGGUAGUUAAAAUUUAUCUAGUUUUUCUUGUUAAUGUUCUUUUUAUCAUUACGGACUAUCUUGUUUCAUAAUUCUUUUAUUACAUUUUUUUUCUUUUAUUCAAUAACCGUAUUACAUAUGGUUGUUACUGAGACAAGGGUCUAUCUAAAACAACAUAUCU	340	spiLA1589-miR8573-5p	CCAGUCUGGCGCAAGGUGUAG	114-134	atr-miR8573	5	0	21	21	1
			spiLA1589-miR835-3p	UUCUUGUUAAUGUUCUUUUUA	205-225	aly-miR835-5p	5	0	21	21	1
spiLA1589-MIR160	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAACUAGGAAGAGUGUCAAUUUUUUUGACAAUACUGUUCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACAAUUUC	104	spiLA1589-miR160-3p	UGGCAUCCAGGGAGCCAGGCA	74-94	aau-miR160	1	0	21	21	1
spiLA1589-MIR158b	AAGUAAUAUAUUUUUCUAAAAUUUUACAAAACUAGUAUAAACGUAUUUCACGGUAACGUAAGGUUUAGAUUGGUUGGUUCGCUCACAUAGGAGGGUAAGUGUGGGUGCCAGUCGCGGCCCGGAUUUGGGUCGUGACAUAGAGACAUACCUUAAUCAUCCAUACCUACACUUUGUGUAAAAUGUAAAGAAGAAUUGA	203	spiLA1589-miR158b-5p	UUUUUCUAAAAUUUUACAAA	11-30	aly-miR158b-5p	4	0	20	20	1

	GUUAGUA										
			spiLA1589-miR8136-3p	UAAAGAAGAAUUGAGUUAGUA	183-203	cpa-miR8136	5	0	21	21	1
spiLA1589-MIR5029	GCCUCUCUCACUUUAUAUACAAACACAAAUGAAUAAAUGUGUUUGUACAAAGUGAGAGAAAACUGCAUACAUAAAUCUCUAUUCCUCUGCCUCUCCCCUAGAGAAUCUCGUUCGCCUCUCUCACUCACCUCUCUCACUUUAUACAAACACAAAUGUAUUGUCUUUGUGUUUGUAUAAAGCGAGAGAAAA	189	spiLA1589-miR5029-5p	AAAGUGAGAGAAAACUGCAUA	49-69	ath-miR5029	4	0	21	21	1
			spiLA1589-miR6277-3p	UGUGUUUGUAUAAAGCGAGAG	165-185	ppe-miR6277	5	0	21	21	1
spiLA1589-MIR169c-5	GUUUGGAAGAUAGGACUUGCAUGAAGGGAAGAGCCUUUGUUUAUUAGCCAAGGAUGACUUGCCUACAUAAUACUACUAAUUUCGAGCUGAAAUACUACUUGUUUGGUUGACAUGUUAGGCAGUCAUCUAUGGCUUUGUUGACAGACUCUUCUCCAUCAUGUUAGUCCUUCUCUUCUCAUUU	181	spiLA1589-miR169c-5-5p	UAGCCAAGGAUGACUUGCCUA	45-65	ata-miR169c-5p	0	0	21	21	1
spiLA1589-MIR5302b	UAGGAAUAUUGAUUCCUUCAAGAGGAGGAGUGGUAGAUUCUACUAUUUUGUUAGAAGAUGUAUACCAUUUAUUAAUGAUAACUUGUAAGGACUCAGUACAAUUUUCAAUUCUACCAUUCAUUUCAAACCACUUGAAGAAUUAGAUUUCACA	151	spiLA1589-miR5302b-3p	UUUUCAAUUCUACCAUUCAUUU	102-123	sly-miR5302b-3p	5	0	22	22	1
spiLA1589-MIR7981-6	UCGAGCGACAGACCUUAACUAAACUAAAGUCCUAUUACCCCCGAAUCCAUUUUUUUGUAAUUCUGUACACUGACAUCCAAACAUCUCUCACGCGCCUCGAGUCACGGAGUGUACCAGUACAAAAUUACAAAACAAAUGAGUUGAGAUUAAUAGAACCUUAGUUAAGUUAAGGUGUGUCUCUGAG	185	spiLA1589-miR7981-6-5p	CUUAACUAAACUAAAGUCCUAUUA	14-37	stu-miR7981-5p	4	0	24	24	2
			spiLA1589-miR7981-6-3p	AUAGAACCUUAGUUAAGUUAAGGU	151-174	stu-miR7981-3p	3	0	24	24	1
spiLA1589-MIR167a-3	UUCGAUCUCGAAAAAAUAACCGACUUGAAAAAAAUUUGCCUCAAGCGGACAUCCGAGACAAAAGUUAUGAUGUUUGUAGUUUCACAAAUUUACAAUAAUCUUUUUGAUUUACUCUUUAAUUUGGUGAAACUUCAAAUGAUCGUGAUGUUGACCUUAAAUAUUCGACUGAGGAUUUUUUUUUCAAUUCGAUUAUUUCUUCGAUAUCUAC	208	spiLA1589-miR167a-3-5p	UAUGAUGUUUGUAGUUUCACA	66-86	cas-miR167a	5	0	21	21	2
			spiLA1589-miR7990a-3-3p	UUCAAAUGAUCGUGAUGUUGACCU	131-154	stu-miR7990a	4	0	24	24	1
spiLA1589-MIR159a-2	GAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAUUGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAGCUUUAUUUUACCCUUUGUUUGAUCAUUUUUUGGAUUGAAGGGAGCUC	174	spiLA1589-miR159a-2-5p	GAGCUCCUUGAAGUCCAACAG	1-21	fve-miR159a-5p	1	0	21	21	1
			spiLA1589-miR159-2-3p	UUUGGAUUGAAGGGAGCUC	156-174	aof-miR159	0	0	19	21	1
spiLA1589-MIR7992-7	UGGCUUUAAAUUACAUUUAUGUCCUUCAACUUUGAGUGUGCACAAGUAGACACUUAAACUUGUAUAAAGUUGAAUAAAUAGAUACACAUGUCCUACAUGUCAUUUUUGUCCUACGUGGUGUUCUACGUGUAUUGUGUCAUCUAGGACUCAUGUGUUUAUUUAUUUAAAAAUUGGAUAGUUAACGUGAUUGUUUGUG	236	spiLA1589-miR7992-7-5p	UUUGAGUGUGCACAAGUAGACACU	31-54	stu-miR7992-5p	5	0	24	24	1
spiLA1589-MIR2093	CAUUAUGAAAUUUGGAGGUCAAAAUUAAAAUUUGAAGUAAGCUCCAUCUUAAAAUAAAUGCCUCAAACGACAGGUGACAAGUCAGUCACGUGUGUUUGAUAGGUACACUUUUUAAGUGGUUC	82	spiLA1589-miR2093-5p	CCAUCUUAAAAUAAAUGCCU	4-23	osa-miR2093-3p	5	0	20	20	2
			spiLA1589-miR8649-3p	ACACUUUUUAAGUGGUUC	65-82	gra-miR8649	4	0	18	24	1
spiLA1589-MIR167c-2	AGAUCUCUAGCUAGAGGUCAUGCUAGUAGUACGAUAGUAGCCAGAGGUCGUGGACGUGGAGCAGCACCAGUGAGAGGUCGUGCUAGAGAGGUCUCCACAAAACCUCUGAUUGAUGGCAAGGAGGACCAGGUUCCUCCAGAUCCUGUAGUCACACCUUUUCUUCAGGAUAUACUAUUGAGGGUUGUAAGUGUGCUUGAUGGAUUUUCUAAGGCUGGUGGUAUGUUUACCACACCACAUGACUCUCGUACUAGAGAGGG	257	spiLA1589-miR167c-2-5p	AGGUCAUGCUAGUAGUACGAU	15-35	aly-miR167c-3p	5	0	21	21	1
			spiLA1589-miR847-2-3p	UCACACCUUUUCUUCAGGAUA	149-169	aly-miR847-3p	4	0	21	21	1
spiLA1589-MIR1521a-2	GGGGUGUAUUGUUGGGUUAUAAAAGUUGUGAAUGGAAAAUGAAGAGUUGCGACUUUUAUGAAGAGUUCUGACUUUUAUGAAAGGUUGUGACUUUUAUGAAAGGUUGCGACUUUUAUGAACACACACACACACACACA	137	spiLA1589-miR1521a-2-5p	UUGUGAAUGGAAAAUGAAGA	26-45	gma-miR1521a	4	0	20	20	2

spiLA1589-MIR7997c-26	UGGACUAUAUUGCUUAUACUCUUCAAAAAUAACGACGGAUGCAUAUCGGAUACUCCAAAAAUAGUGUACUUUUGGAGAAUUCGAUAUGGAUGUGACAACACUUUUGGAGAGUUCGAGCAACAUAGUUUU	129	spiLA1589-miR7997c-26-5p	AUAUUGCUUAUACUCUUCAAAAAU	7-30	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303-26-3p	CUUUUGGAGAGUUCGAGCAAC	101-121	sly-miR5303	2	0	21	21	2
spiLA1589-MIR1064	AAUUCAGUCUAUGGUUAUUACUGAAAUAAUAAUAAUUCAGUCUUUGGAGGCAAGAAAGAUUGAGACUAUCCUAUAAACUGAAUUAUUAUCAUUCUCAAAAUAAUAAUUCAGUCUAUGGGAUAGUCUCAAUCUUUCCUGCCUCGAGAUGAUUGAUCAAUUGGAAUCAAAUGAUAGACGAUAA	181	spiLA1589-miR1064-3p	CAUUCUCAAAAUAAUAAUUCA	90-110	ppt-miR1064-5p	5	0	21	21	1
spiLA1589-MIR172d-4	AAAUGAACUUAAUGGACUGAAUUUGAAUGAUUCAGUUCGAGACCUAAAAACAAAACGUACUUAAUAGGCUGAAUCUGAAUCAUUAAGAUUCACCUCCAUUAAGUGCAAAC	110	spiLA1589-miR172d-4-3p	UCUGAAUCAUUAAGAUUCACC	74-94	bra-miR172d-5p	4	0	21	21	2
spiLA1589-MIR7981-7	AUAUAUAAUAUUAGGGGUAAGAUAUAAGUACCUCUUAGAUUAUGAUCGAAAUUUGAGAUAUCUUAAUUAAACUAAAUUCAUAUUAUCUCCUCACGCAGUUGAGGCGCGUGAGAGAUAUUUUGAUGCCAUGUAAAAGCCAAAAAGGUCUACGAAAUAACAAAACAAAUUGGUUCGGGGGUAAUAGAACCUUAAUAUAGUUAAGGUGUGUCUCUAAGUUUCAGUCAUAGUCUAGAGGAUAUUUACACCUUAUCCCUAUAAUAUUGUAGAC	268	spiLA1589-miR7981-7-5p	CUUAAUUAAACUAAAUUCAUAUUA	62-85	stu-miR7981-5p	5	0	24	24	2
			spiLA1589-miR7981-7-3p	AUAGAACCUUAAUAUAGUUAAGGU	181-204	stu-miR7981-3p	4	0	24	24	1
spiLA1589-MIR11425f	AUGUGGAACCAUAACAAGUCAGAAUCCCUUUAAAUUUAUUCAUUUCCAAGAUUAGCUAUCUCUUUUCAUGAAAAGUUGUGACAUUUAUGAAAAGUUGAUUAGUAUGAUGCUAUUCAUGUUGAUAUGAACUUAUGUUGAUAAUAUGCAUGUGAAAAUGCCUUUAUGAUGAUGGUGGUCUUGUGUUGAAUAUGGACUUGUCUCAAGUAAUGUUAUGUCUAUUGGCUUGUAUGCAUUCCUAAUUUGUGCAUAAAGGCUUUUUAAGUGACUUAGCAUAGUUUUGAACAAAUAGUCCUUUUUUAGCAUGAUUUCAAUGGUUUUACUUGUAUAUGUUUUCAUAC	338	spiLA1589-miR11425f-3p	UUUACUUGUAUAUGUUUUCAU	316-336	pab-miR11425f	4	0	21	21	1
spiLA1589-MIR8030-3	AUAUAUAUAAUGUUGGGUUGGUUUGGUCUCGGAUUGGUUUCUUUUAGUUGAAACCAAAUCAACCCAAAUAUAGUAAGG	78	spiLA1589-miR8030-3-5p	UUGGGUUGGUUUGGUCUCGGAUU	13-35	stu-miR8030-5p	1	0	23	23	1
			spiLA1589-miR8030-3-3p	UUGAAACCAAAUCAACCCAAAU	48-69	stu-miR8030-3p	1	0	22	22	1
spiLA1589-MIR7741	CGAGGAGAUAUUGAAUGAGAAAAUAUGUCUCAAGUGAAAGCAUAAACAAAAUGUCGCUUUGGCCGAGUGGUUAAGGCGUGUGCCUGCUAAGUACAUGGGGUUUCCCCGCGAGAGUUCGAAUCUCUCAGGCGACGAUUACUUUUUUUAAAAAAUUUAUUUUGUUCUGUAAUCGUAUUUUUUUUUUCUCUCGAAUAAACAAGUGAUUUUCUCACUCAUUUUCCAAU	224	spiLA1589-miR7741-5p	AGAUAUUGAAUGAGAAAAUAU	6-26	bdi-miR7741-3p-1	5	0	21	21	1
			spiLA1589-miR6169-3p	UCGUAUUUUUUUUUUCUCUCG	170-190	hbr-miR6169	4	0	21	21	1
spiLA1589-MIR7993d-2	AACUUUUUGCGUGUGUUUUCAUUCGUCUAUUAGUUAGUGAAGUUAAUUACAUGAAAUGUAUCAUCUUUUUUAACCGUACACAUUAACUUCAAGUAAAAAAUGCUUGAGGUUUUAAGGCGUAUUGAGGCGCAAGCGUAUAAUUAAAGGAGAUAGAGAUAUUUUAUGUUGUUAACUUAACUACAUCGUAGAUAAAUGAGUGAGCACAAACCAGAAAAAAA	218	spiLA1589-miR7993d-2-3p	AUAUUUUAUGUUGUUAACUUAACU	156-179	stu-miR7993d	1	0	24	24	1
spiLA1589-MIR7997c-27	UGUUUGUUUCAAGCUAUGUUGCUCAGACUCUCCAAAAUGUUUUUGACGGUUGCGUGUAGGAUACUCCAAAAGUAGUGCAUUUUUGGAGAAUAAAUGACAUUUUUGGAGAGUUCGAGCAACAUAGUUUCAGCACAAGUU	138	spiLA1589-miR7997c-27-5p	AUGUUGCUCAGACUCUCCAAAAUG	16-39	stu-miR7997c	5	0	24	24	1
			spiLA1589-miR5303-27-3p	UUUUUGGAGAGUUCGAGCAAC	100-120	sly-miR5303	1	0	21	21	1
spiLA1589-MIR8006-4	CAUUGGUACCCGUGUCGUCCAAAAACUAGAAUGUAUAUGCCCUUGACAAAAUAGGGUCACGUGGUCAAUCUUAUCCAUCGAUCCGAUGUCGGGUCAGUGGAUAAGAUUAUGACACAUGUAUGUCCGUUAGUAUAAAAAGUAUGUAUGCUCUAGUUUUGGACGACAGGGGCACCAGGG	177	spiLA1589-miR8006-4-5p	ACCCGUGUCGUCCAAAAACUAGA	8-30	stu-miR8006-3p	5	0	23	23	3
spiLA1589-MIR1128-6	UACUACUCCCUCCAUCCCAAUUUAAGUGUCUUCCCAUUUAGUCUGUCCCAGCAAGACUGCCUCUUUCAAUAUUUAAUAAGUUCUCCAAUUCCAACAUUAUACAUGGAAAGUUUUGAGACCACAAGAUUUAAAGGACUACACACAUCUUUAAUUGAAGACCACAAGAUUCAAAGUCUCCCUUUAUUUCUUAAACUUUGU	243	spiLA1589-miR1128-6-5p	UACUACUCCCUCCAUCCCAAU	1-21	ssp-miR1128	2	0	21	21	1

	GUCCAAUCGAACUAAAACACUUAAAUUGGGACGGAGGGAGUAAUU										
			spiLA1589-miR5049c-6-3p	AAACACUUAAAUUGGGACGGAGG	213-235	hvu-miR5049c	4	0	23	23	1
spiLA1589-MIR166-2	UAAACUAAACAAGAUCAUGUUAAGGAGAAUGUUGUCUGGUUCGUGACCAUAUAUCUUUCUUCACAUAAAUGAUCUCGGACCAGGCUUCAUUCCCCUCAACUCAUCAAGGUUAUGUCAU	118	spiLA1589-miR166-2-3p	AUCUCGGACCAGGCUUCAUUCCCC	72-95	lja-miR166-3p	1	0	24	24	1
spiLA1589-MIR7984c	UUUGGGAAAAAGUGUGAAAUAUAUUUGAAUUUUGAUUGAAAUUGCCGUUACGAUACCAAACUUUGAGAAUGACACGUGGACAUAAAUUUUUUUGCCGAAUUAUCAAUAAUAAUGUCCUCCAUAAAGUUUGAUACGUAACAACAAUUUCGGUCAAAGUUUGAGUAUUUUUUUAGACCCUUUUCCCUAU	187	spiLA1589-miR7984c-5p	ACGAUACCAAACUUUGAGAAUGAC	50-73	stu-miR7984c-5p	3	0	24	24	1
			spiLA1589-miR7984d-3p	CAAUUUCGGUCAAAGUUUGAGUAU	142-165	stu-miR7984d-3p	3	0	24	24	1
spiLA1589-MIR169e-2	UUUAAAAAGAUAUCUUGCAUAAAAGAAAAGAGCAUGUCAAGAUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAUUAAACACAUUUUAGACUAUGGAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUAUGACUCUCCUCUUCAUGUAAGACUUCUCUUCUUUUUC	172	spiLA1589-miR169e-2-5p	UAGCCAAGGAGACUGCCUGAA	43-63	zma-miR169e	3	0	21	21	1
			spiLA1589-miR169f-2-3p	GGCAAGUCAUCCUUGGCUACU	107-127	zma-miR169f-3p	2	0	21	21	1
spiLA1589-MIR7840	GGCAAUGGAAUAGGUGGUCACUAGAAUGCAUUAAUUGCACUCCAAUUAUAGGAGUAAUUAAUGUCAUUGGAAUUGUCUAAACAAUUAAUUGACUUUUUAAAAAAAUGAAAACAAACGGUCGUAUAUGUGUUUUAAAAUUGGGUCGGAUAAUUAGGGCAUAAGUGACCCCUUUCUCUUUUAA	181	spiLA1589-miR7840-5p	AUAGGAGUAAUUAAUGUCAUU	48-68	ptc-miR7840	5	0	21	21	3
spiLA1589-MIR8014	UUUUACUCCCUCUGUCCAACAAUUCUUGUUCACUAUUGAAUAUAAUAAAUACAAUGUGUUGAAAAAUGUCACAGAGAAAUGAUUAUAAGUAGGUAAAUUAGAAAAGAAGUGUAAAAUAAUCCACUGAUUUCAUAAAGUGGACAAGUAUUGUUGGACAUCCCAAAUUAGUAUAGUGGACAACUAUUGUUGGACAAAGGGAGUAGUU	205	spiLA1589-miR8014-5p	AUAAAUACAAUGUGUUGAAAAAUG	45-68	stu-miR8014-3p	5	0	24	24	1
			spiLA1589-miR6444-3p	UAGGUAAAUUAGAAAAGAAGU	90-110	ptc-miR6444	5	0	21	21	1
spiLA1589-MIR169j-8	AUGAGAAGAGGAGUCUAGCAUGAUGAAAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCAUUUCCGAAAUGUGUCCUUUCGUUCAUGGGGUCAGGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUCUUUCAUGCAAGACUUUCUCUUCUUCC	164	spiLA1589-miR169j-8-5p	UAGCCAAGGAUGACUUGCCUGC	43-64	ppe-miR169j	0	0	22	22	1
			spiLA1589-miR169d-8-3p	GCAGGUCAUCUUUAGCUAACU	103-123	stu-miR169d-3p	0	0	21	21	1
spiLA1589-MIR7981-8	AGACACCUUAAUUAAACUAAGGUCCUAUUACUCCUAAACUUUUUUUAAAAAAAAUUUAUACACUUUUUGUCUUGUGGCAUACUAUGUGACUCCACGCAAUUGAAGCGCGUGAGAGAUGUUUCUAUUGAAGCGCGUGGGAGAUAUUUGAAUGCCACGUAAGCCAAAAGGUGCACAAAAUUACAAAAAAAUAAGUUUAGGGGAGGCAAUAAGACCUUAGUUUGGUUAAGGUGUGU	233	spiLA1589-miR7981-8-5p	CUUAAUUAAACUAAGGUCCUAUUA	7-30	stu-miR7981-5p	2	0	24	24	2
			spiLA1589-miR7981-8-3p	AUAAGACCUUAGUUUGGUUAAGGU	206-229	stu-miR7981-3p	3	0	24	24	1
spiLA1589-MIR8008b-2	UUUUCCAUCACUUUUUUGCAUAAUUCUUUCAAAUAAACCCAGAAAAGCGACAGACAGGGUCCUUUAGUGCGUCGCGUUUCUGGGUUUUUCAAAAAAAUAAUUUUCAGAAAAGAUGGAUAG	120	spiLA1589-miR8008b-2-5p	AAACCCAGAAAAGCGACAGACAGG	35-58	stu-miR8008b	2	0	24	24	1
			spiLA1589-miR156i-2-3p	UUCAGAAAAGAUGGAUAG	103-120	csi-miR156i-5p	4	0	18	21	1
spiLA1589-MIR7981-9	CAGAGACACACCAUAACUAAACUAAGGUCCUAUUACCCCCAUAAACGUAUUUUUUUAAAAUUUUGUGAACCUUUUGUCUUACUUGAAAUAUUGCGUGACUCCAGGCAAUUGAGGCGCGUGAGAGAUAUUUGGAUGCCACAUAUGCCAAAAAGUUGCACAAAAUUACAAAAAAAAAAAAUAAGUUUAGGGGUAAUAAAAUCUUAGUUUAGUUAAGGUGUAUCUGAU	225	spiLA1589-miR7981-9-5p	CAUAACUAAACUAAGGUCCUAUUA	12-35	stu-miR7981-5p	4	0	24	24	3
			spiLA1589-miR7981-9-3p	AUAAAAUCUUAGUUUAGUUAAGGU	193-216	stu-miR7981-3p	4	0	24	24	1
spiLA1589-MIR10420	UCAAAUUCAGACCUGUGAUUGAAAUUUGAGAAUGUCAAAUCUAACUUCAAAUCCAAAUGAUUGAAGUUGAAGUCAAACAU	139	spiLA1589-miR10420-3p	AGUCAAACAUCAGUUUUUU	71-89	gma-miR10420	5	0	19	19	3

spiLA1589-MIR4995	CAGUUUUUUGGGUUUGAAUUAGACUUGGCAGUCCCCAACUUCAAACCUUUUGAAUUAGGUAAACAAAUGUAUAUAUAUAUAUAUAUAUAUAUAAUAUAUAUAUAUAUACCACGUAAUUUAUGCCUCAAGGUGAACCUUUUGAGUUGUUCUGCCAGAUCGGUCGCUCAAGAUCUUUGGUCUUUAUCCAUACCCGAUGAAAAAAAUGGUUCUUAUGGAUUCGCAGUGGGAGGAGCAAGGGCUCUGACCGCGUGCCUGUUGAAGAAUGAGUCGGCGACUCAUAGGCAGUGACUUGGUACAUUGUUCUUGUCUUAUGCUCUUUAUUAUUUAUGUUUUAUAUAAAUUGUGUCUU	290	spiLA1589-miR4995-3p	AGGCAGUGACUUGGUACAUUG	221-241	gma-miR4995	5	0	21	21	1
spiLA1589-MIR5205a	AAUUACUCCCUUUGCCCCAUUUUAUGUGCCACCAUUUCCUUUUUGGUCAAUCCCAAAAAGAAUGUCACAUUUCUUAUAUGGGUAAGUAUUUAAAGGUAUAACUUCUCUUUUACCUUUGUUGGUCACAGUUAAUUUUAAACAUAGUACUCUAAUAUAUUUAUGAGGAGAGUGAAAAGUGAGUUUAAUUUUUUGAAGGGAAAUUUGGUAAAACAUUUCAAAGUCUUCUUUUUUUCUUACACUCCGUGUCCGGUCAAAUAUUGCUACAUAAAAUGGGACGGAGGGAGUAUAA	290	spiLA1589-miR5205a-3p	UACAUAAAAUGGGACGGAGGGAG	263-285	mtr-miR5205a	5	0	23	23	2
spiLA1589-MIR7983-4	GUAAUUGUCACCUUUUGUAUAUGUCCUAAAGUCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGUCAAUAAAGACGUUAGCACUAUUUAUUAGUGUCAAUAUU	108	spiLA1589-miR7983-4-5p	UAAAGUCUUUAGCGACAUUGGUUC	27-50	stu-miR7983-5p	0	0	24	24	1
			spiLA1589-miR7983-4-3p	ACUAAUGUCAAUAAAGACGUUAGC	63-86	stu-miR7983-3p	5	0	24	24	1
spiLA1589-MIR8006-5	UGAGACAUUGCCGCCCCCGUUGUUAAAAAACUAAAGCAUAUAUUCCCUUUAUACUAAUAAACAUACACGUAUCACAAUUUUAUCCAUCGACCCGAUAUUUAUCAAUAUCAAAUCGAUAGAUAAUAUUGCGCCAUGUGUCCCUAUUUAGUCUUCCGUUAGAGUGAAGGAAAUAUAAACUAUAUUUUUUGGACGGCAGGGGCACCAAUGUCCCA	212	spiLA1589-miR8006-5-3p	UAUUUUUUGGACGGCAGGGGCACC	180-203	stu-miR8006-5p	2	0	24	24	1
spiLA1589-MIR8039-4	UAGAACUAUCAGAAGUUACGUUUUCCUAUCUGAACUAUCACCAUCGUUCAGGAAAGAAGAGGAAACAAUUGACAGUUGACUUGUGUUUUAAUACAUGGAUGGUGAUAGUUCAAGUAAGAAAGGGGAACAACUGAUAGUUGGA	142	spiLA1589-miR8039-4-5p	UUUCCUAUCUGAACUAUCACC	22-42	stu-miR8039	0	0	21	21	1
			spiLA1589-miR8045-4-3p	AUUGACAGUUGACUUGUGUUU	68-88	stu-miR8045	3	0	21	21	1
spiLA1589-MIR10223	UAGCACAACAUUUUGAGCUUGCAUUUGAAAGAUAUAGUUUUUUAUGAUAUUGGAUACUUGAAUCAUCUUCGUACCUUUGGUUCUGAUUCUUCUGAAAACAAAGAUGGAAUUAGUGUUGAACAUGGAACUAGUGUUGAAGAUGAAUUUAGUGUUGAAGAUGGAACUACUGUAAAUAUUCUUUCAAGUGUUGACUGAAAAUAUGUGAGG	207	spiLA1589-miR10223-5p	UUUGGUUCUGAUUCUUCUGAA	76-96	eun-miR10223-3p	5	0	21	21	1
spiLA1589-MIR2118-2	AAUAUUAUUAAAAAUUAAACUAAAAAAAAUUUCACUUCAGUUAGAGAAAAGGGUAUAUAUGAGUGAUUCCUAUACCGGUAUAGGUAUAUAUGAGUCACUUUCAUAGCGAGGGAUAUAUCAACUCUAAAUGACAAAGUUAAGAGAUAUAUCAGACCUUCGCCUCAGCUAUGAAAGAAGAAUGAGACUCGAAUCGAUCUUGUAAAAAAUAAUUAGGGGGUUCCUAAAAAUGUGGCUAAUUUGUUCUUUUACCACUUAGCCACACUCUCAAUAUAGUUGAUCUAGAUAGUCUGAAUACAAAUUUAUUUUCUUUUAUGUGUUACAAUUCU	326	spiLA1589-miR2118-2-5p	GAAAAGGGUAUAUAUGAGUGA	46-66	hbr-miR2118	5	0	21	21	1
			spiLA1589-miR11465-2-3p	CUAUGAAAGAAGAAUGAGACU	166-186	pab-miR11465	5	0	21	21	1
spiLA1589-MIR821e	AAUACCAAUCAUCUAUGGAGAUGUUGCAUGUUCAUUUCCAUUUUUUAUUUCAUCUUCUUAGUAGUAUAAUCUUUUAAUUUUAUUUUCUUCAUCGUUUCCUUCAUCAAUCAUGUAAUUAAGUAAUCAAAAAAGAAGAUAUUAGAAAAGAUGAUGUCACGAUAUGAUCUUCACUUUGAUGAAGAUCAUUAGUAAACUUUCUUGCCCAUACUGCUAUACGCAGAAAGAGACUUGGCAAGUACAUCCCAGUAGAGAUUGGUUCC	260	spiLA1589-miR821e-3p	AAGUAAUCAAAAAAGAAGAUA	118-138	sbi-miR821e	5	0	21	21	1
spiLA1589-MIR7985	GGACUUCCAUGUUGGAGGUCUCAAGUUUGAAACCCCUUGUCAGUGAAAGCAAAGUGUUUGCCUUCUGGGUCGAGCUUGUCGCACCGGGCUUGCCUAGUGCGGGUUACCACUCCUAUGUGGUUGUGAGUUAUUGCAUAGGAGCGGGGGUUUUACC	178	spiLA1589-miR7985-3p	CGGGCUUGCCUAGUGCGGGUUACC	85-108	stu-miR7985	2	0	24	24	1
spiLA1589-MIR7997c-	CUGUGCGCAUCCAAAGGGUAGCGGAAGUAUGUUGUUCGGAUUCUUCAAAAAAUGUCGACGGGUGCGUGCCAGAUACUCCAAAAGUAGUGCAACGUUGGAGAA	126	spiLA1589-miR7997c-28-5p	AUGUUGUUCGGAUUCUUCAAAAAA	5-28	stu-miR7997c	4	0	24	24	1

28	UCCGACACGGGUGCGGCUACAUUUUUGGAGAGUCCGGGCAACAUAUGG										
			spiLA1589-miR5303e-28-3p	CGUUGGAGAAUCCGACACGGGUGC	69-92	stu-miR5303e	4	0	24	24	3
spiLA1589-MIR839	CAUUGCACCUAUGGACGUGUUCGAUAUCAUUUUAGGGCUGGAGUUUUGGUACGAGGUUAACGCGUUUAUUUCACCGCGUCACAACCAGAUGCACAUCAGCGACACCGGAGGUUCAUGCGUGGUACCCCUUAUUCAGGUACCACAAAACGGGAUGCACUUAUCGGUGAUGCAAAUUGUUAAGGUUUUUAAGAGAGGUGAACCAACCUUUCUUGCUGCCCUUGUUGCUUUUCUGAGGCAGUUCCAUUUUCUCAUUGCAUUGAGCACGUCCUUAGUGACAAUA	280	spiLA1589-miR839-3p	AACCAACCUUUCUUGCUGCCC	198-218	ath-miR839-5p	5	0	21	21	2
spiLA1589-MIR1886f-4	CGAUACUAUAUCACGAUAUGGUAUCGUGAGAUGGAAUCAGUGUUUGUACAUGCGAUUUCACGCUGAUUCCACCUCAUGAUUCCAUUUCAUUAGAUGUAAUU	101	spiLA1589-miR1886f-4-5p	AUGGUAUCGUGAGAUGGAAUCAGU	18-41	stu-miR1886f	2	0	24	24	1
			spiLA1589-miR7980b-4-3p	GAGAUGGAAUCAGUGUUUGUACAU	28-51	stu-miR7980b-3p	1	0	24	24	1
spiLA1589-MIR1886i-3	GGACAUGCAAUAUGAAAUCAUGAGAUGAAAUCAGCGUUUGGACAUAUAAUUUCACGUUAAUUCCAUCUCAUGAUUUCAUAUCAUGAGA	88	spiLA1589-miR1886i-3-5p	AUGAGAUGAAAUCAGCGUUUGGAC	20-43	stu-miR1886i-5p	2	0	24	24	1
			spiLA1589-miR7980b-3-3p	GAGAUGAAAUCAGCGUUUGGACAU	22-45	stu-miR7980b-3p	2	0	24	24	1
spiLA1589-MIR172a-2	AUGCACUGUCUCAGAUGUAAAUCUUCAUGUCGUCAAUGUCUAUGUUGUUCUACUCCAAAAAUGCACUACUUUUUGGAGGAUAUAGACUUUGGCGACCUGAAGAUUUACAUUUGAGACAGUGUUU	124	spiLA1589-miR172a-2-3p	UUGGCGACCUGAAGAUUUACA	89-109	vca-miR172a-5p	5	0	21	21	2
spiLA1589-MIR11068f	GCAUCAGCUGACAACUAUGACCUUUAACUUUGGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAAUUAAACAAAUAGACACAUUCGUCCUACAUGGCACCCUAGAUGACAAAUUUAUGUCAUAUGUGUGUCUACUUGUUCAAUUUUAUAUAAGUUCAAAUGACUACUUGUGCAGAAUCAAAGUUGAAGGGCAUAAUUAUCCGCUGAAAG	211	spiLA1589-miR11068f-5p	CUAUGACCUUUAACUUUGGAUG	15-36	lja-miR11068f-3p	5	0	22	22	1
			spiLA1589-miR160g-3p	UACAUGGCACCCUAGAUGACA	92-112	lus-miR160g	5	0	21	21	1
spiLA1589-MIR6112	AAAUUUAUUUAAUAAAACUUUGGUUCUUCGGUGCACCGUAGUUUCGGGACUCUUGCACCAAACUUCGAACCGAAGUUUCAAAAAUAAAAAA	91	spiLA1589-miR6112-3p	GAAGUUUCAAAAAUAAAAAA	72-91	cca-miR6112	3	0	20	24	1
spiLA1589-MIR7997c-29	UCGCUAUGUUGCUCGGAUUCUCCAAAAUGUUGUCGCACGGAUCCUUAAGAAAUGCACUACAUUUGGAGGAUUGGACACUCGCCUAUCUGCAUUCUGAAAGAGUCCGAACAGCAUAGGUU	119	spiLA1589-miR7997c-29-5p	AUGUUGCUCGGAUUCUCCAAAAUG	6-29	stu-miR7997c	5	0	24	24	1
spiLA1589-MIR5185m	UUAUUUUUUUUUUCAUUUUUCGCACCUUUUUGAUUUAUGUGGCAUCUAAAUAUCUCCACGCGUCUCAAUUGCAUGGAGUCACAGAGUGUGUCAUGUAAGACAAAAGAUGUAUAAAAUUACAAAAAAAACUC	131	spiLA1589-miR5185m-5p	UUUUUUUUCAUUUUUCGCACC	6-26	bdi-miR5185m-5p	5	0	21	21	1
spiLA1589-MIR1128-7	UACUACUCCCUCCGUCCCAUUUUAUGUGGCAUCAAAAGAAUGUCACAUAUAUAGUAAGUAUUUAAAGGUACAAUUCUUUUUUUACUCUUGUUGGUCCCACUUAAUUUUAAAGAUAGUACCUAAUACAUUUUUGAGAAGAAAGAAAAAUGAGUUUACUUUUUGAAGGGCAAUUCGGUAAACAUUUCAAAGUAUCCAUUAUUUCUUAGACUCCAUGCCCGACCAAAAGUUGCAACCUAAAAUGGGACGGAGGGAAUAACU	260	spiLA1589-miR1128-7-5p	UACUACUCCCUCCGUCCCAUU	1-21	ssp-miR1128	2	0	21	21	1
			spiLA1589-miR5171b-7-3p	ACCUAAAAUGGGACGGAGGGA	234-254	bdi-miR5171b	4	0	21	21	1
spiLA1589-MIR11891	UUCACAUUUAUAACCUCCAACUUUGGUGAUGCACAAGUAGACAUAUGAGUCCUACGUGGCAUAAUACAGACACCACGUAAAACAUAAAUUGUAAUAUAGGAUGUCACACAAGAUAGAGAAUUGUAAUUUUAUUUGUUCAACUUUAUAUAUGUUUAAAUGUCUACUUGUACACAUACAAAGUUGAUGACCAUAAAUGUUAG	200	spiLA1589-miR11891-5p	CAUAAAUUGUAAUAUAGGAU	83-102	mes-miR11891	5	0	20	20	1
			spiLA1589-miR156-3p	GUCACACAAGAUAGAGAAU	103-121	hbr-miR156	5	0	19	19	2
spiLA1589-MIR399j-2	ACCUAACAAAAUAGUGAUAGGGCAACUCUCUAUUGGCAUAUGCCGUUUAUCACACAUUACAGCUGACACGCCAAAGGAGAGCUGCCCUAUUACUGUCUCUGCUUAAUC	108	spiLA1589-miR399j-2-5p	GGGCAACUCUCUAUUGGCAUA	20-40	stu-miR399j-5p	1	0	21	21	1

spiLA1589-MIR1044-2	GUGAUGUACCUCCAACUUUCAUAAUGCACAAAUAAGCACUUUAACUAUCCAACUUUAAAAUAAAUAAACACAUGAAUCCUACAUGGCACAGUACACGUAGGACACCUCGUAGGACAAAAAAUGACAUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUGUCUACAUGUGCACACCCAAAGUUGAAGGGCAUAAA	199	spiLA1589-miR399o-2-3p	CGCCAAAGGAGAGCUGCCCUA	69-89	stu-miR399o-3p	1	0	21	21	1
			spiLA1589-miR1044-2-5p	GCACAAAUAAGCACUUUAACU	26-46	ppt-miR1044-5p	5	0	21	21	1
			spiLA1589-miR5014a-2-3p	UUAUACAAGUUUAAGUGUCUA	148-168	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR1027c	GGGAAAACGAUAAAUAUAUAUCGAACUAUCAUAAAUAGUAUACAAGUAUCCUCCGUUAUACUUGUGGGACAUUCAUAUAUACCCUUUAUACCGAUAAAUAUACACAUGUUAUAAUUUUAUCUACCUAUUCGAUAUAUAUCGACGGAUAAGAUUAUGCCACUUGUUUCUAUUUACUCUUCCGUUAGAGUGAAGGGCAUAUAUGUUCAAGUUUUCAAUGGAAGAGGCACCAAUGUAUUCAAAAGUAUGACAAAGAUAUCUUCAUAUAUACCAUUAACAAUAGUUCGAAUAUAUAUUUAUCCCUUUUUCC	307	spiLA1589-miR1027c-3p	UUUCUAUUUACUCUUCCGUUA	164-184	ppt-miR1027c	5	0	21	21	1
spiLA1589-MIR6149	ACACUUAAAAACAUUCCGUUACUUUACUAACUGAAGUGUGAAAUACAUCUCUAAUUUCUCGCCAGAUUUAGGUGUGUUUUCAAACUUCAUGUUCCUCCAAUAGUUUGAGAUCACUUGUUAUGUCACGUGUCAGAUCUGACGUGUAUUGGGAUGUAUCUGAGUUUAGUUAGUCAAGUAGAGAGGUACUUUUAAGGCU	196	spiLA1589-miR6149-5p	AGAUUUAGGUGUGUUUUCAAAC	64-85	stu-miR6149-3p	5	0	22	22	2
			spiLA1589-miR11577-3p	UAGUUUGAGAUCACUUGUUAUG	101-122	pab-miR11577	5	0	22	22	1
spiLA1589-MIR166a	ACGGUUGGGGAGAAUGUUGUCUGGUUCGAAAUCUUUCUAUAGAAAAAUCAGUGGCGGAUUCAGUCAUGGAUUUCAAAAUCGUUAAAUCUUAUAUAUGUACAAAAACAAGUACAAUAUAUAUUUUUAGACCCUAAAAAUGUUGAAUAUAUAUUCUGAAUCCGUCAUAGAUUAGAUCGUUUGAUCAAUCAAAUUAUUGAGUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCU	232	spiLA1589-miR166a-5p	AGAAUGUUGUCUGGUUCGAAA	11-31	vca-miR166a-5p	1	0	21	21	2
			spiLA1589-miR166-3p	AUUUCGGACCAGGCUUCAUUCCCC	201-224	lja-miR166-3p	0	0	24	24	1
spiLA1589-MIR7997b-10	CUUUUGAAACCAUUGUUUGUACCUAAGUUGCUCGGACUCUUCAAAAAUGUCAGUGGGUGUGUGUCGGAUUCUCCAAAAGUAGUCUGACACGGGUGUGGCAACAAUGUGAAGAGUCCGCAACUUAGGUUUGUACAAGGUGCAAUUU	145	spiLA1589-miR7997b-10-5p	AAGUUGCUCGGACUCUUCAAA	25-45	stu-miR7997b	2	0	21	21	1
			spiLA1589-miR5014a-10-3p	CAACUUAGGUUUGUACAAGGU	118-138	ath-miR5014a-5p	5	0	21	21	3
spiLA1589-MIR9764	CCAUCUCACUUUUAUACAAGCACAAAUGUAUAAAAUGUGUUUGUGUUUGUGUAAAGCAAGAAAAAAUUGUAUAUGUACAUAUAUUUCGUUACCCUCUCCCUUUCUCAAUCUCGCGCGCCACCUUCACUUAUACAAAAAGAAACGGAAUGUAUAAAUUGUGUUUCUGAUUGUAUAAAGCGAGAGAA	186	spiLA1589-miR9764-3p	UCGUUACCCUCUCCCUUUCUC	87-107	gma-miR9764	5	0	21	21	1
spiLA1589-MIR9387	UCCAUAGCAAACAUAUAACUGUAUAAUUCGCUAUACAUAUACAAUUAUAUGAUUCGUUGGCCUAAAUUGUAUAAUUCGCUGGCUCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGUCGCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGCCUAAAUUGUAUAAUUCGUUGGCCUAUUUCACUGCAAUAUCUGUAUAAGAUUUGCUUUGUAUACAAUUAAAUCGAAGUAAAAUGUUUGUAUAUU	245	spiLA1589-miR9387-5p	AUAUACAAUUAUAUGAUUC	37-55	hbr-miR9387	5	0	19	19	3
			spiLA1589-miR5214-3p	UUGCUUUGUAUACAAUUAAAU	203-223	mtr-miR5214-5p	5	0	21	21	1
spiLA1589-MIR11068c-3	GUCCUUUAACUUUGGAUGUGCACAAAUAGACACUUAAACUUGUAUAAAGUUGAACAAAUAGGCAAACAUGUCCUACAUGUCAUCCUAUAUGUUAUUUUUUUUUGUCUUACGUGUUUUGUGCCAUGGAGGAGUCAUGCGUUUAUUUAUUUAAAAGUUAGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUGAAGAUC	200	spiLA1589-miR11068c-3-5p	CCUUUAACUUUGGAUGUGC	3-21	lja-miR11068c-3p	4	0	19	19	2
			spiLA1589-miR5041-3-3p	AUUAUGAAAGUUGAAGAUC	182-200	gma-miR5041-3p	5	0	19	21	2
spiLA1589-MIR2122	UCCCUCCGUUUCAAUUUGUUUGUUUUACUUUUCUUGUUGGUCUGUUUCAAAAAGAAUGUUUUUUCCCCUUUUUGACGAUACAUAGAGCAUAAUAUCAUAAGAUUCAAAUGUUUUAUAUACUUUCUCAAACUCUGUGUCAAGUCAAAACCAGACAAACAAAUUGAAAUGGAGUGU	174	spiLA1589-miR2122-5p	UUUCAAAAAGAAUGUUUUUUCC	45-66	osa-miR2122	5	0	22	22	1

			spiLA1589-miR6164b-3p	ACAAACAAAUUGAAAUGGAGU	152-172	nta-miR6164b	5	0	21	21	2
spiLA1589-MIR1917-2	CCUCCUUGUCCAAGCUUUAUGCAAUACAACAAAAAUAACUUUUAGCGACAUUAAAUAUUGAUAUUAAUAAAGAGUGUUAAAGUCUUUACUGGCAUUAGCUAAGUGUCAUUGAACCGAUGUCGCUAAAAGGCUUUAGGACAUAUACAAAGAGUAUAACUUAAAGAGAAUAACUUGUUCGGCCAAAAUGUCACUUUAUUUUUGUAGAAAAUUACAUUUAGUUUAGAAAAGGGUG	232	spiLA1589-miR1917-2-5p	AUUAAUAAAGAGUGUUAAAGU	63-83	sly-miR1917	1	0	21	21	1
spiLA1589-MIR7997c-30	GGUUGAUUAAAGCUAUGUUGCUUGGGAUCUUCAAAAUUGUCAAGGGGUGCCCGUUGGAUUCGUCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGUGGCAUCAAAAGUGAAGAGUCCGCGCAACUUAGGAUUUAAGCACAG	146	spiLA1589-miR7997c-30-5p	AUGUUGCUUGGGAUCUUCAAAAUU	15-38	stu-miR7997c	5	0	24	24	1
			spiLA1589-miR5303f-30-3p	AUUUUUGGAGAAUCUGACACGGGU	76-99	stu-miR5303f	0	0	24	24	1
spiLA1589-MIR1886f-5	AAGAAUAUGAGAUUUCAUCUCAAAGUAUGAAAUCAUGAGAUGAAAUCACCAUGAAAUUGCACGUCCAAACGCUUAUUACAUCUCAUGAUUUCAUAUAUCACAUGAUUUGAUUUCAUCUCAUGAUUUCAUAGCACAUGUUCAAAGGUCUUUGUUUAGUCAUGUGAUAUAUGAAAUCAUGCGAUGAAAUCAAAUGAAAUCUCAUGUCCAAACACUGAUUUCAUCUCAUGAUUUCAUAUAUCGUCAAAUGGAGACUCAUGAUUUCA	263	spiLA1589-miR1886f-5-5p	AUGAAAUCAUGAGAUGAAAUCACC	27-50	stu-miR1886f	4	0	24	24	1
			spiLA1589-miR7980b-5-3p	GUCCAAACACUGAUUUCAUCUCAU	203-226	stu-miR7980b-5p	1	0	24	24	1
spiLA1589-MIR167h	UUAUCAAGAAAGGAAGGAGUGAGGCUGUCCGAGCAUGACCUAACCUUAGUCACCCAUUUUCUUUAUAAAUGGCCAAGUUUAGAUCAUGCUGGCAGCUUCACUUGUUCCACUCUAGACCC	119	spiLA1589-miR167h-3p	AUCAUGCUGGCAGCUUCACUUGUU	83-106	gma-miR167h	3	0	24	24	1
spiLA1589-MIR9553	GUCUCACACAGCUGACACUAAUUAUGUAGGGCUUCUUUUUGUCCCACAAGUUAAUGAACCCAAAUUAUUACACUUCUGGGUCCACCGACUUGUAAAAUAAAAAGAAGCCUCAAAGAACUGGUGUUAGUUGUGUGAAGG	138	spiLA1589-miR9553-5p	CACACAGCUGACACUAAUUAUG	5-26	bra-miR9553-5p	4	0	22	22	2
			spiLA1589-miR8011a-3p	AAUAAAAAGAAGCCUCAAAGAACU	96-119	stu-miR8011a-3p	2	0	24	24	1
spiLA1589-MIR396f	UGACCAAGUCCUAGUCAUGCUUUUCCACAGCUUUCUUGAACUUCUUCUUGCUAAAUUUUGAUCUCUAAAUUGAUAAUUUUGAGAUGAGAUUUGAAGCUAUGAAAGUCCAAGAAAGCUGUGGGAAAAGAUGGCAAGCUUUGGACU	144	spiLA1589-miR396f-5p	UUCCACAGCUUUCUUGAACUU	23-43	csi-miR396f-5p	0	0	21	21	1
			spiLA1589-miR396-3p	GUCCAAGAAAGCUGUGGGAAA	105-125	stu-miR396-3p	0	0	21	21	1
spiLA1589-MIR8763	UUUUAUGUAAGACUAUUAAUAGUGUUGGACUUGUUCGUCCUCAUGCCUUUCGUCUAAAUUCAGUCAACAAUAGUUAUGCUUAGUCAACAAUAUGGUUCAUGUGACUUUUUUAGGAUAAAACCCUAAACAUAAUUUUUGUCGGCUAAAUUUAGAUGUAGGGCGUAAGUACGAACUAGUCCAACACUAUGAAUAGCCUUACAUACCU	205	spiLA1589-miR8763-5p	UUAAUAGUGUUGGACUUGUUCGU	16-38	gra-miR8763	5	0	23	23	1
spiLA1589-MIR10538-3	GUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUAGGAGUAAUACGUUACUCACAGGAGUAAUAAAACGUUACUGAAAAUAACGUUUUAAAAGUAAAACGUCACUUACAGUAACGUAUAUCAACCUAAU	130	spiLA1589-miR10538-3-5p	AGAUUGAUAUACGUUACUCACAGU	4-27	sly-miR10538	0	0	24	24	1
spiLA1589-MIR399f-2	CGAGGAGAAGAAUGACAGGGCAAUUCUCCUUUGGCAAAGAUAAUAUAAUGUGUAUGCAAAACAUAUAUAUAUAUAUAUAUAGGGUUUGCAUAUUCAUUUGCCAAAGGAGAAUUGCACUGUUAUUUCUUACUCCCCA	138	spiLA1589-miR399f-2-5p	GGGCAAUUCUCCUUUGGCAAA	18-38	csi-miR399f-5p	1	0	21	21	1
			spiLA1589-miR399a-2-3p	UGCCAAAGGAGAAUUGCACUG	101-121	ata-miR399a-3p	1	0	21	21	1
spiLA1589-MIR399f-3	CUAUGUAUGGAUGCAUUACUGGGCUAAUCUUCUUUGGCAAAUAGCCACAUUUUCACUAUAUUAUUUAGUGCAAGUUUGUUCAUUUUUUGCCAAAGAAGAUUUACCCCGUAAAUCACCCAUACAAUC	126	spiLA1589-miR399f-3-5p	GGGCUAAUCUUCUUUGGCAAA	21-41	csi-miR399f-5p	4	0	21	21	1
			spiLA1589-miR399r-3-3p	UGCCAAAGAAGAUUUACCCCG	88-108	mtr-miR399r	1	0	21	21	1
spiLA1589-MIR171c-3	UCCAAUUCAAAGAGAAUGCUCAUUGAAUGAGCAUUCUCAAUAUUAUGCCUUGAAGAGGACUCGAACCUCCACGCUCUUUAGCACGAGAUUUUGAGUCUCGCGUGUCAACCAUUUCGCCACCAAGGCAUCAUGAAAGUGAAUCGUAUUCCAUGAAUAUGAUAUUUUUCUAGUGUGAUGUAUGGAAUAUAUGAGAAAG	265	spiLA1589-miR171c-3-5p	UGAAUGAGCAUUCUCAAUAUU	24-44	stu-miR171c-3p	5	0	21	21	1

	GUGGAUCUAUUGAUCGGUCAUGUCAUAUAGGCCCAAGUUGGACAUCCAAUUGCUUCGAUUUGAAUUAUC		spiLA1589-miR5532-3-3p	AUGGAAUAUAUGAGAAAGGUGG	179-200	osa-miR5532	1	0	22	22	1
spiLA1589-MIR5026-3	CGCCUUUUCGGCCUACGUGACACUAGCUUAAAAAAAUCAACUAGUCUUGAGCUCACAAGAUAGUGCCACGUAAGCCAAAAAGAAA	85	spiLA1589-miR5026-3-3p	GCUCACAAGAUAGUGCCACGU	51-71	ath-miR5026	4	0	21	21	2
spiLA1589-MIR397b-4	GAGUCUAUGUUGCCGGACUUCCCAAGAAUGUCGUUGCAUCCCUGUCGAAUACUAUAAAAAUAAUUACUUUUGUAGGAUUCAACAUGUAUCUAUGUCAUUUUUGAAGAGUCCGAGCAACAUAGAUGA	126	spiLA1589-miR397b-4-5p	UGCAUCCCUGUCGAAUACUAU	35-55	eun-miR397b-5p	5	0	21	21	1
			spiLA1589-miR5303i-4-3p	UCAUUUUUGAAGAGUCCGAGCAAC	95-118	stu-miR5303i	3	0	24	24	3
spiLA1589-MIR6277	AUUAUAAGUGUAUAGGAUGAAAAUAUAUGUACUUGUAUUUAUAUGUACAGUUUUCUCUCGCCUUAUACAAACACAAACAUAUUUUAUACAUUUGUGUUUGUGUAAAGUGAGAGAGGCGAGGGAGAGACCGGCAAGCGAGAAAUCUAGGGAGAGAGGCGAAUGACAAUUGUUUGGUACGGGUUACUAAAUCAAACUUUGAUUAUAACAUUUAAGUGAUUUGUUAUUUUUAUACAUUUUCACCUUAUUUU	247	spiLA1589-miR6277-5p	UGUUUGUGUAAAGUGAGAGAG	95-115	ppe-miR6277	5	0	21	21	1
			spiLA1589-miR7805-3p	UAUACAUUUUCACCUUAUUUU	227-247	rgl-miR7805-3p	5	0	21	22	1
spiLA1589-MIR399a-2	CAGAAUAAGAAACUACUCAAAAGAAUUUGAAGAAUUGGAGAGGACAAGAAACGCAGGGUAUUCUCCCUUAGCAAGAUUGCUUUAUGCAUGAAUUAAAUUCUUUCUUGCCAAGGGAGAAUUGCCCUGCGUUUCUUCAUUUCCACAAAAGUCUAAUUCAUCUGGUGUCUGAUAUUUAU	176	spiLA1589-miR399a-2-3p	UGCCAAGGGAGAAUUGCCCUG	106-126	ata-miR399a-3p	1	0	21	21	1
spiLA1589-MIR1917-3	GGCAUUAAUAAAGAGUGCUAAAGUCUUUUAUCAACAUUGGUGAAGUGUCAUUAGAAUCAAUGUCGCUAAAGGCUUUAGAAAUUUUAUGUUAUCUA	95	spiLA1589-miR1917-3-5p	AUUAAUAAAGAGUGCUAAAGU	4-24	sly-miR1917	0	0	21	21	1
			spiLA1589-miR5262-3-3p	AGUGUCAUUAGAAUCAAUGUC	44-64	mtr-miR5262	5	0	21	21	3
spiLA1589-MIR7997c-31	AGGGCUAUGUAGCUCGAACUCUUCAAAAAUGUCAACGGGUGAGUGUCGGACUCUUCAAAAUUAGUGUACUUUUGGAGAAUCUGACACGGGUGCAACAUCGAAAGUGAAGAGUCCGGGCAACUUAGCAUG	129	spiLA1589-miR7997c-31-5p	AUGUAGCUCGAACUCUUCAAAAAU	7-30	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303e-31-3p	UUUUGGAGAAUCUGACACGGGUGC	70-93	stu-miR5303e	1	0	24	24	1
spiLA1589-MIR8006-6	UGCGUUCCUGCCGUCCAAGAACUAGAACAUGUAUAUCCUUUAUACUAACGGACAUACAUGUCAUAUUCUUAUCCGCUGAUUCGACACUUAUUGACGAAUAAGAUUGUGUCAUCUGUCCCUAUUUAGUCUUAUGUUAUAGUGAAGGGCAUAUAUACUCUAGUUUUUGGACGACAGGGACACC	181	spiLA1589-miR8006-6-3p	UAGUUUUUGGACGACAGGGACACC	158-181	stu-miR8006-5p	1	0	24	24	1
spiLA1589-MIR8006-7	CAUACUAUGGAGACGUUGGUGCCCCUGCCGUCCAAAAACUAGAGCAUAUGUAUCAUUUAUACUAACGGACAUACACAUGUCAUAAUUUUAUCCAUUAAUAAAAAAAAGUCAAUCUUAUCCACCGAUCCGAUGAGUGAAGGGCAUAUAUGCUUUAGUUUUUGAACGACAGGGGCACCAAUGACCCAAAAGUAUA	193	spiLA1589-miR8006-7-5p	GCCCCUGCCGUCCAAAAACUAGA	21-43	stu-miR8006-3p	3	0	23	23	3
			spiLA1589-miR8006-7-3p	UAGUUUUUGAACGACAGGGGCACC	153-176	stu-miR8006-5p	1	0	24	24	1
spiLA1589-MIR5049b-1	UGUCAAAUCAUAAAUAGACAAGUAAUUAGGGACAGAAGGAGUACUAUCUAUCAUGAACACACAUAUAUUUAUUUUUUUAAAAAAAUUGUGUAUGUGUGUGGUGGUGGUGGUGAUAGGGUGGGGGUGGUGGUUAAAAAUGUGGGAAGUCGUAAUUCGUAUCCUCACCUACAAAAAAUUUAGAUAGUCAACCAACUGAGCUAGCUAAUGAGAUCCGAAAAUAAUUUUCUAUAUAUUUUUUGCUU	243	spiLA1589-miR5049b-1-5p	AGUAAUUAGGGACAGAAGGAG	21-41	hvu-miR5049b	3	0	21	21	1
			spiLA1589-miR1046-1-3p	UGGUUAAAAAUGUGGGAAGUC	129-149	ppt-miR1046-3p	5	0	21	21	1
spiLA1589-MIR3515	AAAAAGAAAUUUCAUAUACUGUUUUGAAAUUUUUGUUAACAUUUUUCACCCUUUAGGCUCCAGAAUCUGUGUUUGAUAGGUAUACUUUUUUGAAUGGUUUAAGCAGAGGCGGACCCACAUGGUGUCCGUCAGGUGCUCGAGCACCCAUUAAAUAUAUCUAUGUAGAAAUUGAUAGGUAUUUGUAUAAAAUUAACAUAGAGACCCGGGUCUCCUGGGUGAAAGCCAGAUAUCCUAACCGCUGGACGACAACGGAUUGUUGUUUUCAUACUUCAAAA	294	spiLA1589-miR3515-3p	UAUGUAGAAAUUGAUAGGUAU	159-179	ahy-miR3515	4	0	21	21	2

	CUUAUUAUGUUUUCUUAAA										
spiLA1589-MIR7992-8	UAAUCAAGCUUGAUCUCAGUUGAGCAGUAAACACUCCAACUUAGAAGAUGCACAUCUAGACAGCUCAACUCAAAUCCACUGUGUCAAUUGAGGUGUCUAGAUGUGCAUUCUCAAAGUUGGAGUGCUUACUUGCCAAUUGAGGUCAAGUUUGAGUG	155	spiLA1589-miR7992-8-5p	UUAGAAGAUGCACAUCUAGACAGC	41-64	stu-miR7992-5p	5	0	24	24	1
			spiLA1589-miR7992-8-3p	UGUCUAGAUGUGCAUUCUCAAAG	94-116	stu-miR7992-3p	5	0	23	23	1
spiLA1589-MIR10532-5	UCUUAUACUAUACUAAGGUCCUAGUAACCCUUAGUAUAUUAUAAGUGUGUCUCUGAGAUUUAUUUAAAAAAUAAGUUCAGGGGGGUAAUAGGACCUUAGUAUAGUAUACUA	111	spiLA1589-miR10532-5-3p	AAGUGUGUCUCUGAGAUUUAUUUA	43-66	sly-miR10532	5	0	24	24	1
spiLA1589-MIR7983-5	AUUUGGAUAUCACUACAACAAAAACAAUUUUUAGCGGCAUUAAACAUUAACACUAAUAACGAGUGUUAAAGUCCUUACCGGCAUUAGUUAACUGUCAUUAGAAGCAAUUUCGCUAAAGGUUUUAGAGACAUAUACAAAGAGUGACACUUGCCGCUAAAAAUACAUAUUUAGAGGCAAUUAAGAAUUAAAUGUUGUUAAU	227	spiLA1589-miR7983-5-5p	UAAAGUCCUUACCGGCAUUAGUUA	67-90	stu-miR7983-5p	5	0	24	24	1
spiLA1589-MIR5569	GGUCAUUUUUGUUGUAGUGUAUACAUGACCUAUGGACCGUAGGUGGCCUCCGUAGUUUGUGAUUGAGGCUGAGUUUUGCCUUCCUAUUGCAUGCUUGAAUUAUGGAGGAAGACCUAAGGUGCAUCAU	99	spiLA1589-miR5569-3p	UAUUGCAUGCUUGAAUUAUGGAGG	57-80	sbi-miR5569	4	0	24	24	1
spiLA1589-MIR6299	UUUUAGUUUGUAUGUAAAAUUAUUAAUAUGAAAUAAAAAGUGAGUUUUUAUAUCAUUCUUCUUAAAACUCCAUAUAUAGUCGAAAGUGAAGGUUGCGAUCUUCAGCCUUAAGGAGGAACAGUAACAAAGUAGCCAAAGACUGCGGUCGCCAGGGUGAAACACUGUUCAUGGCCUGAAAGGAGAAAUACUGCGGCAUUGAUAGAGACUAUUCAUCGACAAAAGAGAAGAAAGGUAUACACACAAACUUUUUAUUACAUACUAUAUAAUUUUACAGAUAUACUAUAU	285	spiLA1589-miR6299-5p	AUGUAAAAUUAUUAAUAUGAAA	12-33	gma-miR6299	5	0	22	22	1
spiLA1589-MIR4249-2	UGCCAACAUGAACACAAAUGUAAUCAUGAAUUGUAUAUGGAAAAAAAUAAACAAUUCUAGAAGUUGAGGUAUAUGAAGAAUAUAUUUUUGGUCCCUUUCAUCUAGUGGUUAGGACAUUGUAUUUUCAUGUUGAGG	135	spiLA1589-miR4249-2-3p	ACAAUUCUAGAAGUUGAGGUA	51-71	aly-miR4249	4	0	21	21	3
spiLA1589-MIR5530	GUUGGAAGCACAACGAAAAGGAAAGGCUCAAGUCUCAUAGUGAUUGUUAAACUAUUUGAGGCAAGUGGAUUUCUAAACUCUUGUUAAGCGUAUGAAAUUCGUGUAUUCCUUGUGUGGUGUUGAGAAUGACUUGGAGACUUGUUGCUUAUUUGUUGGUGUUGUAUUCCUUG	170	spiLA1589-miR5530-3p	GUUGGUGUUGUAUUCCUUG	152-170	osa-miR5530	5	0	19	21	3
spiLA1589-MIR6288c-2	AAACCUAUGACUCAAGUUAUCAUGGAUAUACAAGAAUGUAGCAUAAUUUGCAGCUACACAUCUAGCGUAAGUUAGUUUUGUUGUUUAUUGCUAAAGCAUGUUGUAUUUUAAUUGAUAUAUGUAUAAGGUGGAAUUGUUGCUAUUGUGCAACUACUAUCUUACUUUAGCUUAUCAUAUUGUGUUAGAUAUUAUGAGA	232	spiLA1589-miR6288c-2-5p	CAUGUUGUAUUUUAAUUGAUA	97-117	ppe-miR6288c-5p	4	0	21	21	1
spiLA1589-MIR6293	CAGUGUGAUCAUGAUACUGUUGAAGCUCAAAGGACUGACGACAACAGCAAUAACAUAUCCAGUGAAAUCCCACAAGUGGGAUCAGGGGCUGCGAGAAUAAGGCAGACAAUAGAAAGGUUACCUAGUAUUUUUAUGUUACUGUUGGGAUUUGAACCUUGGUUUUCAAGAUUUGCACUCACAUUACUGAUUUUUUUUUUUGAGUCGAGUAUCUGUUGGAAACAACCUCUCUAUCCCGUAAGAGGUAGAUGACUAGAGAUAAAGUCUGCGGUACAUCCUACCUUCCCUAAACCGCACUUGUAGGAUCACACUAGGUAUAUAUUAUUGUUGCAGUCCAC	300	spiLA1589-miR6293-3p	UAAGAGGUAGAUGACUAGAGA	201-221	ppe-miR6293	5	0	21	21	1
spiLA1589-MIR6135e	ACAUAAGUCUGAAGUAUUGGGUGUAGUUGACAAUUAUGUGAUUAAUGAUUAAGGAUUGUGGAGUUGCCCUCAAGUUUAUAAGUUGACAGUUUGGUCCACUGAAUUAAAUGAAGGGUAAAAGGGUAAUUUCACAAUACCUAAUUUAACCAACUUUUUGUGGGGAUUAAAUGAGAGGUAAAAUGGUAAAUUGACUACACCAUACCUAAUUUAACA	213	spiLA1589-miR6135e-3p	AGGUAAAAUGGUAAAUUGAC	173-192	pgi-miR6135e-5p	4	0	20	20	2
spiLA1589-MIR10532-6	AUUUUUUUGUAUUUUUAACAUAUGAAUGUAAUGAUGAAUUCUAAGAGGCUAGUCUUAGUCCUCUUCUAAGUUCAGAGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUUCGGGCAUAGGUUGAAGGGGUACUUGUGCAUUAUCUCAAAAAUCAUUGCUAAUAAUAUUACUAAAAAUGCGAAAACUC	198	spiLA1589-miR10532-6-3p	AAGUGUGUCUCUGAGAUUUUCGGG	102-125	sly-miR10532	3	0	24	24	1
spiLA1589-MIR7822-3	AUGAUAUUUAGCGUGCACAAGUAGAAACUCAAACUUGUAUAAAAUUGAACAAAUAGAAACAUUUAUUCUACAUGACAAAAUUUGUAUCCUACGUGGCGUCUCAUGUGUAUUAUGUCAUG	189	spiLA1589-miR7822-3-5p	UAUAAAAUUGAACAAAUAGAA	38-58	ptc-miR7822	4	0	21	21	1

	UAGAACACAUGUGUCUACUUAUUCAAUUUUAUGCAAAUUUAAGUGUCUACUUGUGCACACUCAAAAUUGA		spiLA1589-miR5014a-3-3p	UUAUGCAAAUUUAAGUGUCUA	148-168	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR1886i-4	GCGUUUGGUAAUGUGAUAUCAUAUCACGAUAUAGUAUCAUGAGAUGAAAUCAGCGUUUGGACAUGCGAUUUUACCCUGAUAUCAUCUCAUGAUUCCAUAUCAUGAGAUUUGAUACCAUAUUCUCUAAAAAC	131	spiLA1589-miR1886i-4-5p	AUGAGAUGAAAUCAGCGUUUGGAC	39-62	stu-miR1886i-5p	2	0	24	24	1
			spiLA1589-miR1886h-4-3p	AUUUUACCCUGAUAUCAUCUCAUG	68-91	stu-miR1886h	3	0	24	24	1
spiLA1589-MIR9477-2	CUACCUGAUCUAUCACCAUCUAUGUAUUAAAAAACACCUCGAAGAUGACAAGUCCAACUAUCAAUUGUUUCCUUUUUCAACCUGAACUAUCAUACCAUCUACUCAACUAGGUGUGUCUUAAUAUAUAGAUGGUGAUACUCCAGGUAG	147	spiLA1589-miR9477-2-3p	UAUCAAUUGUUUCCUUUUUCAACC	59-82	sly-miR9477-5p	5	0	24	24	1
spiLA1589-MIR5628-1	CUGGAGAAAUAUGGAAGAGAUGAUCGGAGAAAUAUUAUGUUCUAAUGAGCUAAUGCCACAAGAAAAGUAAUGAUGUCUAUAACUUUAAAGCUCUGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGAA	135	spiLA1589-miR5628-1-5p	GAAAUAUGGAAGAGAUGAUCG	6-26	ath-miR5628	5	0	21	21	1
			spiLA1589-miR1025-1-3p	UGCCACAAGAAAAGUAAUGAU	54-74	ppt-miR1025	5	0	21	21	1
spiLA1589-MIR5628-2	UGAAGUAAUAUCUCUCCAGUCACCUCAUCCGUAUUUCUCGAAUAGGUUGCUAAUUCAAGCAUUAGAGAAAUAUGGAAGAGGUGAUUGGAGAAAUAUUUCUAGG	103	spiLA1589-miR5628-2-3p	GAAAUAUGGAAGAGGUGAUUG	67-87	ath-miR5628	5	0	21	21	1
spiLA1589-MIR390-5	ACAUAUAACUGUAUAAUUCGCUAUACAUAUACAGUUGUAUAAUUUGCUAGCCUAAAUUGAAUUAAUUCGCAGCUCUCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGCCUAUUUCGCUGCAAUUGUGUAAUUCGCUGGCCAAUUAAUACGCAAUUGUAUAAUUCGCUGGCCUAUAUUCGCUGCAAUAUCUGUAUAAAAUUUGUUUUGCAUACAAUUGAAUUGAAGCAAAAUGUUUGUAUAUUGUAUAUUGUAUAAUUAUAAGUGUAUAAGA	272	spiLA1589-miR390-5-5p	CGCUAUACAUAUACAGUUGUA	19-39	stu-miR390-3p	5	0	21	21	1
			spiLA1589-miR11309-5-3p	UUUGUUUUGCAUACAAUUGAA	200-220	fve-miR11309	5	0	21	21	1
spiLA1589-MIR1863	CAUGUGAUUUUUUUAAUUAUUUUUUUAAUAAAUACUCAGAGAGCGGAAGAGCUUUAAGCUCUGAUACCAUGUUAGAAAUUCAUGUAGAAAUCUCACGUC	99	spiLA1589-miR1863-3p	AGCUCUGAUACCAUGUUAGAAAUU	57-80	cme-miR1863	3	0	24	24	1
spiLA1589-MIR8006-8	CUAUUUAUAAUAAAAGGAUAAAGAAUAAAUAUACCCUUGAAUUAUCAUAAAUGGUAUAUAAAUACUCUUUGUCAUACUUUAGGAAUAUUGGUGCCCUGCCGUCCAAAAACUAGAGCCUAUGUCCCUUAAGGAUGACGGAGGGUAUCCGCAUACUAUUUACACUAGUUCGGAAGUAUAUUUAUCCUUUUUCCAUGAUAAAAUC	203	spiLA1589-miR8006-8-3p	UGCCCUGCCGUCCAAAAACUAGA	92-114	stu-miR8006-3p	1	0	23	23	1
spiLA1589-MIR482d-3	UAUGAACUAUUUGUUGCCUCUUUUAUUCCCUCCUAUUUUUUUUUAGUACUAGCAAAAAUGAAAAAGUUGGUGAGUAGUUGGGAAAGAAGAAAUGGACGGGAAGGAGCAAAGGGCACCAGAGGGUUCGGC	129	spiLA1589-miR482d-3-3p	AAUGGACGGGAAGGAGCAAAG	91-111	mdm-miR482d	5	0	21	21	1
spiLA1589-MIR5171b	CCAAAAAUCAAAUCAAACUGCAAAUCGAGUCAACCCGGAAAAAAACCCGACUAGUGAUUUGGUUUGACUUGAUUUGGUAUUGAAGAAAAAAACUCGACUAUAUUUGAGUUAGUUUGAUUUUGAC	124	spiLA1589-miR5171b-3p	ACUUGAUUUGGUAUUGAAGAA	67-87	bdi-miR5171b	5	0	21	21	1
spiLA1589-MIR7997c-32	UUUUGUUGCUUGGACUCUUCAAAAAUGUUGAUGGGGCGUGUAUUAGAUUCUCCAAAAGCAGUUAUUUUUGGAGAGUCGACACAGGUGUGACAAUAUUUUUUUGAGAGUUCGAGCAACAGUC	121	spiLA1589-miR7997c-32-5p	UUGUUGCUUGGACUCUUCAAAAAU	3-26	stu-miR7997c	3	0	24	24	2
			spiLA1589-miR5303-32-3p	UUUUUUGAGAGUUCGAGCAAC	97-117	sly-miR5303	2	0	21	21	1
spiLA1589-MIR11131	CUUUUCGAUCUACAUGACAUUAGCUUGAAAAAAAAAUCAACUAGUGUUGGUUCCACAAGAUAGUGUCACGUAGAUCGAAUCA	82	spiLA1589-miR11131-5p	AUUAGCUUGAAAAAAAAAUC	19-38	lja-miR11131-3p	5	0	20	20	2
spiLA1589-MIR5049b-2	AACAUUUCAGUUGAUCUUGAUCCCAUUUACUCCCUCUCCCUUUGCCGGACAAUAGUUGUCCACUAUUGACUUGGUACAGGGAUUAAGAAGCAGUAAAUGAUAGGGGUAAUUUUACCAAAUCACCCUUAUUAAAAGUAAGUCACAUAAACAUCGAAAAAUAAAUAGUAUUUAAUAGCAAGGUAAAAACGACACAACAUGCUAAAUGACUCAUUGAUUUAAUAAGCUGGACAAGUAUUGUUGGACGUCUCAAAAUAGUAUAGUGGACAAGUAAAGAUGGACAGAGGGAGAGGGAGUAGCUUAGACUCAUAGCAGCA	324	spiLA1589-miR5049b-2-3p	AGUAAAGAUGGACAGAGGGAG	267-287	hvu-miR5049b	5	0	21	21	1

	AAGAAAUUAU										
spiLA1589-MIR2863a	UUGAAAUUUGGCCACCUAUGUCAAAUAGGAUAAGUGUGGGUGCCACUCGCGGCUCGAUUUGGGUCGUGACAAUAACCAACCUUUUGGACCAUCCUAGGUUAGGUAUUAUGUUGUCUCCUUAACUAGUACUAGGUUAGUGUCAACCCAGUUUUUGGUCCUAGGUUUUGGGUACACUAGUGGGUCCAUUUCGGUUAGUCCUAGGUUAAUUAGCUAUUUGAAGUAGUAGGUUAGGUCUAAAUUUGUU	244	spiLA1589-miR2863a-5p	UUGGACCAUCCUAGGUUAGGU	84-104	osa-miR2863a	5	0	21	21	1
			spiLA1589-miR2630v-3p	AGUUUUUGGUCCUAGGUUUUG	147-167	mtr-miR2630v	5	0	21	21	2
spiLA1589-MIR11575-2	AGCAUGGAUGAAUAAAUUGUCAACAUUAUAAUUCAGUUUAUAAUGUUAAUUGUGAAAAGUUUGCACAGCGUCGCUUUGGCCGAGUGGUUAAGGCGCUUGCCUGCUAAGUAAGUGGGGUUUCCCCGCGUGAGUUCGAAUCUCACAGGCGACGUUGCAUAUGUUUUUGUCGAUACUGUUAUCGACAAUUUUUUACACCUAUUUA	202	spiLA1589-miR11575-2-5p	UUGUCAACAUUAUAAUUCAGU	17-37	pab-miR11575	5	0	21	21	1
spiLA1589-MIR1533-2	AAUUAGUAACGUAAUAGAAAUAACAUUGUAAUAAUCAAAAAGUAAAAUAGAGAUGUGAAUCAUAGUUCUCCAAAUUGGAGAACUACUAUCCACCUCUUUAUAAUUGCAGAAUAGAGAGUUAAAUAGAGAGUGGUCUAUUUUACUUUCCAAAUAUAGAGAAUGGAGAGUAAAAUAGAGAUGGAUUGGAGAUGGUCUAAGGGGUACGAGAGCCACUCAUACUAUGUCACUUACUCAUAACUCAUGCCCAAGAGCUCGUCACAUAGCUACAGUUUCUAUAAUGAUAGAUGAAGCUUUGGGUACUUACAUUAUUUUUCUUGUUACUAGGC	326	spiLA1589-miR1533-2-5p	GUAAUAGAAAUAACAUUGU	11-29	gma-miR1533	5	0	19	19	2
			spiLA1589-miR10215-2-3p	GAGAAUGGAGAGUAAAAUAGA	156-176	eun-miR10215-3p	4	0	21	21	1
spiLA1589-MIR1534	UGAACAUCCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGAUACAUAGGCAUUCCAAUGCCCAACAUUGAUAAAAUAUUGGGCAUAGUGUA	89	spiLA1589-miR1534-3p	UAUUGGGGAUACAUAGGCAU	31-50	gma-miR1534	5	0	20	20	1
spiLA1589-MIR2111d-2	GAGUAUUCUUUUAUUCUUAAUCAAGAGGUUUAAGGUUCAGUUCCCUUUGGGUUACCCCGAUGGGGCUUUACGACGCAAAUUCAAAUUUAAUCGGGCUCCAAUAUAGAUAUUGGACAUCGAUGGAGAAUCUUUUGUUAAGAAAAAACACUAAUU	153	spiLA1589-miR2111d-2-5p	UAUUCUUAAUCAAGAGGUUUA	12-32	ppe-miR2111d	5	0	21	21	1
spiLA1589-MIR1886f-6	GUCAUGCAAUACCAUAUCAUGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGGACAUGCGAUUACGCUGAUUCCAUCUCAUGAUUCUAUAUCAUGAGAUGUGAUUCCAUAUU	112	spiLA1589-miR1886f-6-5p	AUGGUAUCGUGAGAUGAAAUCAGC	24-47	stu-miR1886f	0	0	24	24	1
			spiLA1589-miR7980b-6-3p	GAGAUGAAAUCAGCGUUUGGACAU	34-57	stu-miR7980b-3p	2	0	24	24	1
spiLA1589-MIR865-2	UAAUGCACAAACAGACACUUUAACUAUCCAACUUUUAAAUGAAUAAACACAUGAGUCCCACAUAACAUAAUACACGUAGGACUCCACGCAAGACAAAAAAAUGAUAUGUAGGACAUGUGUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGUAUCUACUUGUGCAAAC	168	spiLA1589-miR865-2-3p	UAUUUGUUCAACUUUAUACAA	124-144	ath-miR865-3p	5	0	21	21	1
spiLA1589-MIR7984b-1	CGAUAACGAAUCUUGGAAAUGAUCUUUUAUCCUCUACACUAUUUGAUAUUGUAUUUUAAGAGUAUAUACAUGUUCACGUGGACAUCAUAAAUAUUGCAUCAUUAGAAAUAGUAACGUAUCCACGUGGGCACAUAUAUACCUUUAAAAUACACUAUUAAAUAGUGCGGUUAAAAGGUCUUCCGUAAAAUUUGCUAGCA	197	spiLA1589-miR7984b-1-5p	AUAACGAAUCUUGGAAAUGAUCUU	3-26	stu-miR7984b-5p	4	0	24	24	1
			spiLA1589-miR7984b-1-3p	GGUCUUCCGUAAAAUUUGCUAGCA	174-197	stu-miR7984b-3p	5	0	24	24	1
spiLA1589-MIR7502c-3	GAAGACUUAUUUAAGUCAUCCGUCAAAAGUUUAGCCAUCUAUGUUAUUUCUGUUUGAGAAAAGUCUCAUCCAUGUCAUUAUUUGUAAAUUGAAAUGACAUAGAUGAUCCAAACUAUUAACGGAUGACAUAGAUGAUCCAA	140	spiLA1589-miR7502c-3-3p	UUGAGAAAAGUCUCAUCCAUG	54-74	gra-miR7502c	4	0	21	21	1
spiLA1589-MIR7981a-38	UUAUACUAUACUAAGGUCCUAUUACCUCCCUGAAUUUAUUUUAUUAAUAAUUUUCUACUCCUCUUCGGCUUACGUAGCACUAUCUUAUGGGGUAACGCUGAUUGACUUUUUUUUCAACCUAGUGUCACGUAAGCCGAAAAACGGUAAGAAAUUACUUAUAAAAUAAGUUCAGGGGAUAAUAGGACCUUAGUAUAGUAAUU	200	spiLA1589-miR7981a-38-5p	ACUCCUCUUCGGCUUACGUAGCAC	57-80	sly-miR7981a	4	0	24	24	1
			spiLA1589-miR7981-38-3p	AUAGGACCUUAGUAUAGUAAUU	179-200	stu-miR7981-3p	5	0	22	24	1
spiLA1589-MIR1127-3	ACCAAGUACACCCUCCGUCCAUUUUUACUUGUCCAGUAUUAACUUGACACCCCCUUUUAAGGAGCAAUAAAUAGAAUGA	265	spiLA1589-miR1127-3-5p	AAGUACACCCUCCGUCCAUUU	4-24	bdi-miR1127	5	0	21	21	1

	CAAUUUUACUAUAUCACCCUUUGGAUAUAAUAAAUUCAAUGCUUUGGGAAAUGACUAGAGUUAAUAAUAAGGGUAAAUUAGGAACUAAGUGAUAAAUAUCUCUUGAUUUUACAAAAUGGAUAAGUAAAAGUGGACAUCUAUCUUAGUAUAGUGGACAAGUAAAAUUGGAUGGAAGGAGUACUUACA		spiLA1589-miR5373-3-3p	UCUCUUGAUUUUACAAAAUGG	178-198	gma-miR5373	5	0	21	21	1
spiLA1589-MIR1886f-7	CGGUGAUAUGGUAUCGUGAGAUGAAAUCAGCGUUUGAAUAUAUGAUUUUACCCUAAUUUCAUCUCAUGAUUUCAUAACAUGA	82	spiLA1589-miR1886f-7-5p	AUGGUAUCGUGAGAUGAAAUCAGC	8-31	stu-miR1886f	0	0	24	24	1
			spiLA1589-miR1886h-7-3p	AUUUUACCCUAAUUUCAUCUCAUG	45-68	stu-miR1886h	3	0	24	24	1
spiLA1589-MIR7981-10	AUUUUAACUAAACUAAUGCCCUAUUACCACACCCCACAAACUUAUUUUUUUGUAAUUUUAUACACAUUUUUUUACGUGGCACACUGUGUGACUUCACGCAAUUGAGGCGCGUGAGAGAUAUUUGGAUGCCAUGUAAGUCAAAAAGGUGCAAAUUUUUUUCAAAUAAAGUAUUCAAGGGUAAUAGGACCUUAGUUUAAUUAAGGU	204	spiLA1589-miR7981-10-5p	UUUAACUAAACUAAUGCCCUAUUA	3-26	stu-miR7981-5p	5	0	24	24	2
			spiLA1589-miR7981-10-3p	AUAGGACCUUAGUUUAAUUAAGGU	181-204	stu-miR7981-3p	2	0	24	24	1
spiLA1589-MIR156g	AACCUCUUUUCUUUUGUGGAGAAUUUUAAAAGGAAAAAGCUAGGGAGGAAAAAGAGAACAUGGCCAAAGUUCCAUAUUCCUCCGUCAUCGGAAGUCUAAUGUAUGCAAUGGUGUGCACUAGAUCUGAUAUUGCUCACGCAGUUGGUGUUGUCAGUAGAUUUCUCGAAAAUUCAAGAAAAGAGCAU	185	spiLA1589-miR156g-5p	GUUCCAUAUUCCUCCGUCAUC	69-89	csi-miR156g-3p	5	0	21	21	1
			spiLA1589-miR5015-3p	UUGGUGUUGUCAGUAGAUUUC	142-162	ath-miR5015	5	0	21	21	1
spiLA1589-MIR8009-2	UAAUUUCCAGAAAAGCGACGGACAGGGUCCUUUAAUCUGUCGCUAUUCUGGGAUUUUCAAAUAUUAAAUAACCAGAAAAGUGAUGGACUAUAUCGCCUUUAGAAAAUUCAAUUAAAAAAAGCAACGGAGUGUCGCUUUUAUUUAAAAAAAUUAUAAAGCGACGCAGUCCAUCGCAUUUUGAAAAGCG	187	spiLA1589-miR8009-2-5p	AUUUCCAGAAAAGCGACGGACAGG	3-26	stu-miR8009	1	0	24	24	1
spiLA1589-MIR1886f-8	UGUUCAGGAUAUGGUAUCGUGAGAUGGAAUCAGCGUCUGGACAUGCGAUUUUAUGUUGAUUCCAUCUAUGAUUUCAUAUCAUGAGAU	87	spiLA1589-miR1886f-8-5p	AUGGUAUCGUGAGAUGGAAUCAGC	11-34	stu-miR1886f	1	0	24	24	1
			spiLA1589-miR7980b-8-3p	GAGAUGGAAUCAGCGUCUGGACAU	21-44	stu-miR7980b-3p	2	0	24	24	1
spiLA1589-MIR7981a-39	UUGUUUGAUUUAAUUAUUGGGAUAAUGCACAAUUACCAUGUUAAUCUAUACUUGAAAUUUCAGAGACACUUUUCCAUCUCUUUUUGACCUACGUGACACUAUCUUGUGGACUCAACGCUGAUUGAUUUUUUUCCAAGCUAGUGCCGCAUAGGCCGAAAAAGGAUAGAAAAUUACUAAUAAAAUAAGUUCAGGGAUAAUAGGAGCUUAGUAUUGUAUAAGUGUGUCUCUUGAAUUUCGGACAUAGGUAAAGGUACUUGUGCAUUUUCCCUUAAUUAUUUUAAAAUU	286	spiLA1589-miR7981a-39-5p	AUCUCUUUUUGACCUACGUGACAC	76-99	sly-miR7981a	5	0	24	24	1
			spiLA1589-miR7981f-39-3p	AAGUGUGUCUCUUGAAUUUCGGAC	218-241	sly-miR7981f	2	0	24	24	1
spiLA1589-MIR5163a	UCUUAUUAUAGUUCUUCAAUCUUUUAUCACAAGUUUUGACUUGUUUUCGAGAUGGUGGUACAGUAUGAUAAUACACUAUUAAUGGUAGCGAACAUGUGGUAUUGUAAGUCCCCGUUAAUGUUGAAGAAAGGGGCAGCCUGAAACCCUUGAUAGAAUUGCUAUCCAUUAAUAUGUAUAUUAUUAAGACAUGUUCCAUGCUUGAGUAAAAGUAUACCAUACAGCCUAAACUUAGGAUAAAAUUUUUAACAAAACUAUAAUACAU	262	spiLA1589-miR5163a-3p	CUUAGGAUAAAAUUUUUAACA	228-248	bdi-miR5163a-5p	5	0	21	21	1
spiLA1589-MIR5181b-2	AGGUACACGUGACACAAUCUUAUUCAUGGAUCCGAUAUUUAAUAAAUGUCCAGUUAGUGGAUAAGAUUAUGACACAUGUAUGU	83	spiLA1589-miR5181b-2-3p	UCCGAUAUUUAAUAAAUGUCC	31-51	bdi-miR5181b	5	0	21	21	1
spiLA1589-MIR5287a	UGGUUGAAUUUGAAUAUUAUAUUGACCGCUAGAUUUGUAGAUUCAAGACGUUCAUUGAUAGGGAGUACACGUGUACUCCUUAUCAAUGAAUUUCCUGAUUUCUACAACUCUCACGACCACUAUAAGAUCGAAAGUAAUUU	140	spiLA1589-miR5287a-5p	UUUGAAUAUUAUAUUGACCGC	9-29	lja-miR5287a-3p	5	0	21	21	1
			spiLA1589-miR164a-3p	CACGUGUACUCCUUAUCAAUG	68-88	zma-miR164a-3p	4	0	21	21	1
spiLA1589-MIR5382	CAGCUCAAGCUUAAAAACUCUAACUUGCCUACCAGUUGACCACCAUAACCAAUGAAGACAGUCCCUAACCAAAGGGAACUGAAUCAACUGGUAGACAAGUUAGAGUGUUAAAGCUUGAG	122	spiLA1589-miR5382-3p	CCAAUGAAGACAGUCCCU	49-66	sbi-miR5382	4	0	18	18	1

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spiLA1589-MIR477-4	UCCUUAGAACGAUUUCACAAAAUACAUAAGUUCUAAGGGAAAGGGGUUUUAUGUUCUUCAGUGAAGUCGUUUCUAAAUUUUCUUAAACCUCUUAUCACAAGUUUUGACUUGGUUUUGA	79	spiLA1589-miR477-4-3p	AUAAGUUCUAAGGGAAAGGGG	26-46	lja-miR477-3p	5	0	21	21	3
spiLA1589-MIR11463	GGUGGUGGCAAGUUAUGAAUAUCAAUGAUAGCGAGCAUCUGGUAUUGUAAGUCCCCGUGAAGAUGAAGAAAGGGGCAGCCUGAAACCCUUGUUAGAACUGCUAUCUAUUGAUAUUUGAAACGAACUCCAUGCUCGAGUAAUAGUUUACCAUACAUCCAAAACUUAGGAUAAGAUAUUUAAUAU	222	spiLA1589-miR11463-5p	AUGAUAGCGAGCAUCUGGUAU	64-84	pab-miR11463	5	0	21	21	2
			spiLA1589-miR8044-3p	UAUCUAUUGAUAUUUGAAACG	141-161	stu-miR8044-3p	5	0	21	21	1
spiLA1589-MIR6248	GGGAAUAAAAUCUUGGAAGCCAUACUUGUUGAAAUUAUUAGUCAAAAUGUGAAAGUUGGUAGCCACAUUUGUGGAAGUAGGUAGUCAAAGUUUCGUAAAUUUAGGUAAAGUUUGGCAGCCAAAUUUUGUGAAAAUUGGCUACCACAGUUAUGUCAAAGUUGUUUACCUACAAGUUUGAAUUGUUAGUUUCCAUUGAUGUCAUUAGU	206	spiLA1589-miR6248-5p	CAUUUGUGGAAGUAGGUAGUC	66-86	osa-miR6248	5	0	21	21	2
spiLA1589-MIR11285	UGACUUUCCUGAAAAGUUGUGACUUUUAUGGAAAGUUGUGACUUUCAUGAAAAGUUGUGACAUUUAUGAAGAGUUGCGACUUCUAUGAAAAGUUAUGACUUUUAUGAAAGGUU	113	spiLA1589-miR11285-3p	UCUAUGAAAAGUUAUGACUUUU	82-103	fve-miR11285	5	0	22	22	1
			spiLA1589-miR837-18-3p	CACUGGUUGAUAUUUUUUUCA	54-74	aly-miR837-5p	5	0	21	21	1
spiLA1589-MIR477d	CAUAAACAAUUUGUAUUAUAGUGAAUGUCUAAUUAUGUGGAGUCCUUGUAGGAUAUGGUUAGGAAUCCUACUUGGGGACCAUGUAAGGUUUUUCCUAUAAAUAAAGUUGUUUUCC	115	spiLA1589-miR477d-3p	UGGAGUCCUUGUAGGAUAUGG	38-58	ptc-miR477d-3p	5	0	21	21	1
spiLA1589-MIR11409d	AGAAAGGGAGCUAAUUCCUCAAAAAUUUCCCUCUUCUUGAAAAAAAAGGAAACAAAGUCAUAUAUCUUAUUACCUUUAUUUUCCUUUUCCAAAAGAGGGAAUUUUUUGAGGAUUUGACCCCUUAUG	127	spiLA1589-miR11409d-3p	GAUUUGACCCCCUUAUG	111-127	pab-miR11409d	4	0	17	21	2
spiLA1589-MIR7997b-11	GCCUUUCUAUAUGGUAGUCCUCAUAAGCUAAGUUGCUCGGACUCUCCAAAAAUGUUGCCACACCGUGUCAGAUCUUUCAGAAAUACACUAUUUUUGGAGGAUCCGACACGCACCCAUCGACAUUUUUGAAGAGUCUAAGCAACAUAGCUCAUAAAUGACUCUCCAAAGAGUAAUAC	176	spiLA1589-miR7997b-11-5p	AAGUUGCUCGGACUCUCCAAA	30-50	stu-miR7997b	3	0	21	21	1
			spiLA1589-miR5303d-11-3p	UUUUGGAGGAUCCGACACGCACCC	92-115	stu-miR5303d	1	0	24	24	1
spiLA1589-MIR1917-4	AACUUUUAGCAGCAUUAAAUAUUGACACUAAUAAAAAGUGUUAAAGUCUUUACUGACAUAAGUGUCCUGAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUAUAAAGAGUAACAAUUGCCGCUAAGAAUAC	133	spiLA1589-miR1917-4-5p	ACUAAUAAAAAGUGUUAAAGU	27-47	sly-miR1917	3	0	21	21	1
spiLA1589-MIR827b-2	ACUAUGCCCUCCAACUUUGAUUGUGCACAACUAAGCACUUAAACUUGUAUAAAAUUAAACAGACACACGCUAUACAAGUUUAAGUGCUUACUUGUGUACACCAAAAGUUAAAGGUCAUUGU	121	spiLA1589-miR827b-2-5p	UUUGAUUGUGCACAACUAAGC	16-36	gra-miR827b	5	0	21	21	1
spiLA1589-MIR6273-3	CCUCACUAGUACCUAGUGAAAUAUUCAAAGAUGUGUGUACCUACUCCUACCUACGUGGCACUAUCUUGUGGGCCCAAUGCUGGUUGACUUUUUUUCAAGCUAGUGUCACGUAGAUCGAAAAAGAGUAGAAAAUUACUUAUAAUAUAAGUUCAGGGGUACUUGUGCAU	167	spiLA1589-miR6273-3-3p	AAUGCUGGUUGACUUUUUUUC	76-96	ppe-miR6273	5	0	21	21	1
spiLA1589-MIR171b-4	AGCUACACGUGAUAUUGGCGCGGCUCAAUCAAAAAGUAGACUCAAAUAUGUUCUUAAGUACUGCUUUCUCAUUGAACCGCACCAAUAUCUCGUGUAUUC	99	spiLA1589-miR171b-4-5p	GAUAUUGGCGCGGCUCAAUC	11-30	zma-miR171b-5p	1	0	20	20	1
			spiLA1589-miR171e-4-3p	UCAUUGAACCGCACCAAUAUC	69-89	ppe-miR171e	2	0	21	21	1
spiLA1589-MIR1917-5	UUGCUUAUGCAUUUACGUACACUUCUCUAAAAAAAUUUGAUCAGUUAUGUAUUUAACCGAUUAAUACUACAACAAAAAUAAUUUUUAGCGGCCUUAAAUAUUGACACUAAUAAAAAGUGAUAAAAUCUUACUGGCAUUAGUUAAGUGCCGUUAGAACCAAUGUCGCUAAAGGCUUUAGGGACAAAUACAAAGAGUGACAAUUGUCGCUAAAAAUACAUAUUUAGCGGCAAUUAAGAAUUAAAUGUCGUUGAUGGUCAUUUUUAUCGUAGUGUAAAUGGCCAUGCAUGUACUUAUAUUCAGAUUUGUAAUUUAGUAUGGACAAAAUGCAUAAGUAC	335	spiLA1589-miR1917-5-5p	ACUAAUAAAAAGUGAUAAAAU	106-126	sly-miR1917	4	0	21	21	1
			spiLA1589-miR6137b-5-3p	GUGACAAUUGUCGCUAAAAAUA	194-215	pgi-miR6137b	5	0	22	22	2

spiLA1589-MIR1886f-9	UUGAUCAUGCGAUACCAAAUCACGAUAUGGUAUCGUGAGAUGGAAUCAACGUUUAGACAUGCGAUUUUACGUUGAUUCCAUCUCAUGAUUCCAUAUCAUGAGAUAUGAUUCCAUAUUCU	119	spiLA1589-miR1886f-9-5p	AUGGUAUCGUGAGAUGGAAUCAAC	27-50	stu-miR1886f	2	0	24	24	1
			spiLA1589-miR1886h-9-3p	AUUUUACGUUGAUUCCAUCUCAUG	64-87	stu-miR1886h	1	0	24	24	1
spiLA1589-MIR159a-3	AAAUGAACUUAAUGGGCUGAAUCUGAAUGAUUUGAAUUCAGAUCUAAAAAUCAAACGUACUUAAUAGGCUGAAUCUGAAUUAUUAAGAUCCAGACCUCCAUUAGGUGCAAAC	112	spiLA1589-miR159a-3-3p	GACCUCCAUUAGGUGCAAAC	93-112	aly-miR159a-5p	5	0	20	21	1
spiLA1589-MIR7701-1	AGAUCGGAUACGUCACUUGACGAUGUAUCAAGACAUUACUUUGCACAAUGUAACGGUUAGGUACAUUACUUUAAUUAUGCGAUAUAUCGGGAUGCAUGUGAUGUAUCAGGACGUUGAGUGAUGUAUUCGAAAUCGAGACGUGAUGUAUCACGACGU	156	spiLA1589-miR7701-1-5p	UUAGGUACAUUACUUUAAUUA	57-77	mtr-miR7701-3p	5	0	21	21	1
			spiLA1589-miR7695-1-3p	ACGUGAUGUAUCACGACGU	138-156	osa-miR7695-3p	5	0	19	21	1
spiLA1589-MIR5303-3	CUGCUAUGUUUCUCAGACUCUCCAAUUGUUGUUGCACCCAUGUCGAAUCCUCCAAGAAUGCACUACUUUUGGAGGAUCCAACAUGCAGCUGUCCACAUUUUUGAAAAGUUCGAGCAACAUAGUUU	125	spiLA1589-miR5303-3-3p	UUUUUGAAAAGUUCGAGCAAC	98-118	sly-miR5303	1	0	21	21	1
spiLA1589-MIR8046-2	UUAAGUUUAGGGGAGGUAAUAGGACCUUAGUAUAAUAUAAGUGUCUCUGAAAUUUCGAGCAUAGUUUGAGGGGUAAUUGUGCAUUAUCCCUUAUUUUUAUUAAAAACAUAGAGAAAAUGGUCUAAACUCACCCUAAACUAUACCUGAAAUUCACCUACACACUCUUAUUUCACAGGUCCUAUUACCCUCGUGAACUAUU	199	spiLA1589-miR8046-2-5p	CUCUGAAAUUUCGAGCAUAGU	45-65	stu-miR8046-3p	3	0	21	21	1
			spiLA1589-miR437-2-3p	AAACAUAGAGAAAAUGGUCUA	104-124	far-miR437	5	0	21	21	1
spiLA1589-MIR3706	GGGACACGUAACGCAAUCUUAUUCAUCGAUCCGAUGUCGGAUCGGUGGAUAAGAUUAUGACACGUGUAUG	70	spiLA1589-miR3706-3p	UGUCGGAUCGGUGGAUAAGA	35-54	pab-miR3706	5	0	20	20	1
spiLA1589-MIR7997c-33	AAUCUAUGUUGCUCGGACUCUUCAAAAAUGUCAACGGGUGCGUGUUGGAUUCUCCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCAAAGCGAGGAGUCCGCGCAACUUAGCUC	126	spiLA1589-miR7997c-33-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
			spiLA1589-miR5303f-33-3p	AUUUUUGGAGAAUCUGACACGGGU	67-90	stu-miR5303f	0	0	24	24	1
spiLA1589-MIR156b-14	AUUGAUUUGUGUAAAAUGUAGGGAGGAAAAAAAGAGAGGGGAAAAUGGAAUGGGUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUCUCCUUCUAUUUUUCUCUUUUCUCUCCCUAAAUCUAUACAAUAACUCGUU	243	spiLA1589-miR156b-14-5p	UUGACAGAAGAUAGAGAGCAC	63-83	aof-miR156b	0	0	21	21	1
			spiLA1589-miR156g-14-3p	GCUCUCUAUGCUUCCGUCAUC	159-179	fve-miR156g-3p	1	0	21	21	1
spiLA1589-MIR3512-2	CGAAUCAAACCGCAAAUCGAGUCAAAUCGAAAAAAAACCCCAAUUAGUGAUUUGGUUUGACUUGAUUUGGUGUUGGAUAAA	81	spiLA1589-miR3512-2-5p	CGCAAAUCGAGUCAAAUCGA	11-30	ahy-miR3512	5	0	20	20	1
			spiLA1589-miR11498c-2-3p	UUAGUGAUUUGGUUUGACUUG	44-64	pab-miR11498c	5	0	21	21	1
spiLA1589-MIR1043-2	AGGUACAUUUAUGUCCUUCAACUUUGUGUGUGCACAAGUAGACACUUAAACUUUUAUAAAAUUGAACAAAUAGACUUACAUGUCAUCCUACAUGUCAUUUUUUGUCCUACGUAAUUUCUUACGUGUAUUUUGUCAUGUAGGACUCAUGUGUCUAUUUAUUUAAAGUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUGGAGAUCAAAGUUAAAA	221	spiLA1589-miR1043-2-5p	CCUUCAACUUUGUGUGUGCA	15-34	ppt-miR1043-5p	3	0	20	20	1
			spiLA1589-miR8771f-2-3p	UUGGAGAUCAAAGUUAAAA	203-221	gra-miR8771f	4	0	19	23	1
spiLA1589-MIR8672	UGGAAAUGGAAAUAAUGUUAAAAUAACUAUAACUAUAAUUAAAAAGAAUGUUGAAAUAAAUAAAGAAUGAAAAAGGAAUCUUAAAGCAACUCAAGAAUGAGAAAUAAUUAGAUGAAAAAGGGGUCUGACAGCACCUGUAAGGCGCAGAAUAUCAGGCACCUUUUUUUUUAAUGCAAGGCAAAAGCCAUCAUGUGCCUUCCUCUUUUCAUCGGUUGACGCCGUUAACGGCGUAUAGGGGAAGGCACGUGGGCCCCUGUGCCUUUAGCGUUUUGGUUUCCUGAAUAAAUUGUUUGCCCUUUUUGGAACUUUUAGACAAUUAUGUUGCCCUUUUGG	333	spiLA1589-miR8672-5p	AUGAGAAAUAAUUAGAUGAAAAAG	97-120	gra-miR8672	5	0	24	24	1

			spiLA1589-miR8041b-3p	GUGCCUUCCUCUUUUCAUCG	192-211	stu-miR8041b-5p	4	0	20	20	1
spiLA1589-MIR1886f-10	UCAUGCGAUAUCAUAUCAUGAUAUGGUAUCGUGAGAUGGAAUCAGCGUUUGGACAUGCGAUUUUACGUUGAUUCCAUCUCACAGUUCCAUAUUAUGAGAUGUGAUCCAAUA	111	spiLA1589-miR1886f-10-5p	AUGGUAUCGUGAGAUGGAAUCAGC	23-46	stu-miR1886f	1	0	24	24	1
			spiLA1589-miR7980b-10-3p	GAGAUGGAAUCAGCGUUUGGACAU	33-56	stu-miR7980b-3p	1	0	24	24	1
spiLA1589-MIR7981-11	CCCUGUAGACAAUGACUGAAAUCUCAGAGACAUACCUUAACUAAACUAAGGUCAUAUUACUCUUGAACUUAAUUUUUGGUAAUUUUGUACACCUUUCGUGUUGUGCGACACACUCUGUGACUCCAGAAAAAUGAAGCGCAUGAGAGAUAUUUGUAUAUCACGCAAGCCAUAAAGGUGCACAAAAUUACAAAAGAAUGGAUUCGUGGGGUAAUAGGACCUUAUUUAGUUAAAGCGUGUCUCUGAAAUUUCUGAAAUCUGUCAACAUCA	267	spiLA1589-miR7981-11-5p	CUUAACUAAACUAAGGUCAUAUUA	36-59	stu-miR7981-5p	4	0	24	24	2
			spiLA1589-miR7981e-11-3p	AAGCGUGUCUCUGAAAUUUCUGAA	230-253	sly-miR7981e	4	0	24	24	1
spiLA1589-MIR8610	UUGACGGUCACAAACUACGGAUUGUAGGUUCGUCCAUCAAUCAGGACUUAACCAAAUUUUCCUGGGCUGAGAUUUGGGGUUUUUGACCCCAUUGAUGGAUGUGCAGGACGGACUGUGGGUCAGGCUACGAUCCGUCGAUAGCCACCGUUUG	151	spiLA1589-miR8610-3p	UUUUGACCCCAUUGAUGGAUG	81-101	atr-miR8610-2	5	0	21	21	1
spiLA1589-MIR7997c-34	UUGACUAUGUUGCUCGGACUCUACAAAACUGGUGACAGGUGUGUGUUGGAUACUUCAAAAAUUAGUGCGUUUUUUUGAGGAUUUUACACAGGUGCGACAACAAUUCUGGAGUGUCCGAGCAACAAAGUGUC	131	spiLA1589-miR7997c-34-5p	AUGUUGCUCGGACUCUACAAAACU	7-30	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303-34-3p	AUUCUGGAGUGUCCGAGCAAC	103-123	sly-miR5303	5	0	21	21	2
spiLA1589-MIR7492f-2	ACACUACAUUAAAAAUGAGCUUUAGCGGCAAUUAAUUAGCAAUUGCCGCUAAAUAUAUGGUUUUAGUGGCAAUUAGCACUCUUUGUAUGUGUCACUAAAGGCUUUAGCGACAUUGGAUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAAUGUAUCUAUUUAUUGCCGCUAAAAGUUAUUUUUAUUGUAGAGA	210	spiLA1589-miR7492f-2-5p	AAAUGAGCUUUAGCGGCAAUU	13-33	gra-miR7492f	5	0	21	21	3
			spiLA1589-miR7983-2-3p	ACUAAUGCCGGUAAAGACUUUAGC	132-155	stu-miR7983-3p	1	0	24	24	1
spiLA1589-MIR7997c-35	AGAGGCUAUGUUGCUCGGACUCUUUCAAAAUGUGGAAGGUUGUGUCAGACCCUCCAAAAAUAGUGUAUUUUUGAAGGAUCCGACACGGGCGAGGCAUCAUUUUGGAGAGUCCGAGCAACUUAGCCCAG	128	spiLA1589-miR7997c-35-5p	AUGUUGCUCGGACUCUUUCAAAAU	8-31	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303f-35-3p	AUUUUUGAAGGAUCCGACACGGGC	67-90	stu-miR5303f	4	0	24	24	1
spiLA1589-MIR9409	AUUAUUUUGGUACGUUUACACACUUAAAGAGAGUAAACCACACGUUUUUUGUCAUGUCAGCAUUUUGUGUCCAAUAGGUAUGACUUUUGAACCAUUGAGGAGUUCAAUAGGGACAUCAUAUAGUUAAGGUGUCCAAGUGAAAUAUACAGACAACUUUAAGGGGCUGCAUAUGAUUUAAGCCUUUCUUUUUUGCACGAAUGACAUGACAGAGUGUAAAAGACCACAAUUUU	230	spiLA1589-miR9409-5p	UUUUUGUCAUGUCAGCAUUUUG	46-67	bol-miR9409	5	0	22	22	1
			spiLA1589-miR5274b-3p	ACAUGACAGAGUGUAAAAGAC	201-221	mtr-miR5274b-5p	4	0	21	21	1
spiLA1589-MIR7997c-36	AGAAGCUAUGUUUCUCGGACUCUCCAAAAAUGCUACAUAAUUCACUAUUUUUGAUGGAUCCGACAUGCAACCCAUAGUGUUUUUGAAGAGUUCGAGAAGCAUAGCUGAG	109	spiLA1589-miR7997c-36-5p	AUGUUUCUCGGACUCUCCAAAAAU	8-31	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR5303-36-3p	UUUUUGAAGAGUUCGAGAAGC	80-100	sly-miR5303	2	0	21	21	1
spiLA1589-MIR8615	AACUUGGUUUCAAUUGACAUCUAUGUUCUCCGACUUUGAUUGUGGUCAAGUAGACACUUAAACUUGUAUAUAAUUGAACGACUAGACACAUUCGUCUUACGUCGCAUCCUACAUGACAAUUUUGUUUCCUAUGUGGCGUCUGAUAUGUAUUAUGCCACGCAGAACAUGUGUGUCUACUUGUACACAUCCAAAAUUGAAGGGAUUAGAUGCUUGUUGAAGUCAAUAU	226	spiLA1589-miR8615-3p	CUGAUAUGUAUUAUGCCACGCA	140-161	atr-miR8615	5	0	22	22	1
spiLA1589-MIR7984b-2	CCGAAAUAUAUCCGAACUUCAAUCAAAAUUUGUUGCUACGAUACCAAACGUUGGAAAUGACUUUUUACCCAUGCACUAUUUAAAAGUCCCACGUGGACAUAAAAAAUAUUGCAUAACUAUAAAUAGUAAUAUGUCCAGGUGGACACAUAUAUACCUUUAAAAUACUAUUAAAUAGUUGAGGAGGGUAAAAGCUCCUCCAUAAACUUUGGUAUCAUAACAAUUUUGAUCAACGUUGAAAUUUUUUUC	248	spiLA1589-miR7984b-2-5p	AUACCAAACGUUGGAAAUGACUUU	41-64	stu-miR7984b-5p	3	0	24	24	1

			spiLA1589-miR7984c-2-3p	CCUCCAUAAACUUUGGUAUCAUAA	196-219	stu-miR7984c-3p	3	0	24	24	1
spiLA1589-MIR5021-2	GAAUAAGAAGAGGAAGAGGAAGAGGAGAAGGAGAAGAAG AAGAAGAAGAACGGACGCAUACUCUUCUCCACAUCUUCU UGUGAGUCCUCAUUCUUAGAG	99	spiLA1589-miR5021-2-5p	GGAGAAGAAGAAGAAGAAGA	30-49	ath-miR5021	2	0	20	20	2
spiLA1589-MIR6283-2	GGGAUUAUUUGUCUUCCUAGUCUUUGACACAAGAAAGGG GUGUAGAAAAAUCCUUUUUUCUUGUGUCGAAACAAAAGA GUAAUGAUUCU	89	spiLA1589-miR6283-2-3p	AGAAAGGGGUGUAGAAAAAUC	32-52	ppe-miR6283	5	0	21	21	3
spiLA1589-MIR5567	GGGACACGUGCCGCAAUCUUAUCUAUCGGUCCAAUAUUG GGUCUGUGGAUAAGAUUAUGAUACGUGUAUG	70	spiLA1589-miR5567-3p	AUUAUGAUACGUGUAUG	54-70	sbi-miR5567	4	0	17	24	2
spiLA1589-MIR11085-2	GAACACUACAAUAAAAAUGACUAUUGCAUUUAAUUCUUAA UUGCCGCUAAAUAUGUAUUUUUAACGGUAAUUGUCACUC UUUGUAUAUGUCCCUAAAGCCUUUAGCGACAUUGGUUCU AAUGCCACUUAACUAAUGCCGGUAAAGACUUUACCACUCU UUAUUAGUGUCAAUAUUUAAUGCCACUAAAAGUUAUUUUU GUUGUAGUGGAA	210	spiLA1589-miR11085-2-5p	AUUGCAUUUAAUUCUUAAUU	23-42	lja-miR11085-3p	5	0	20	20	1
			spiLA1589-miR7983-2-3p	ACUAAUGCCGGUAAAGACUUUACC	130-153	stu-miR7983-3p	1	0	24	24	1
spiLA1589-MIR1513c	UUUUAAUUCCACGGUACUUUUCAUACCUAUGUGAUGAAU GAAAGCCAAGAGGUUUGAACGAGACCUCUGUGAGGUCAA GUACACCUGGGAUGCCUAGGGGAGGGGGUAAUAGGACC UUAGUAUAGUAUAAUUGUGUCUCUGAGAUUUCGAGCAUA GGUUGAGGAGGUACUUGGACAUUAUCC	182	spiLA1589-miR1513c-5p	GAUGAAUGAAAGCCAAGAG	33-51	gma-miR1513c	5	0	19	19	2
			spiLA1589-miR10532-3p	AAUUGUGUCUCUGAGAUUUCGAGC	129-152	sly-miR10532	2	0	24	24	1
spiLA1589-MIR11314-2	ACAUCACAAAUGCAGAUUAUGCCAUCACUGGAGCUGGUA GAAAAGGCAUUAUUGUUUCGCUGAUCAACAUCAUGUAAU GGACCUGAUGGGGUUGUAUAUACAUAAGAGAACCCUAGG CCCGUUUAUGUGGAGCCACCACAAACAAGGAUUUCCUUU UAAUUUAUUUAUUUCAAAAUUUAGUCUUUACCUUUAAUGG AAAGUUGUGACUUUUAUGAAUUGCUGUAACAUUUAUGAA AGGUUGUGACAUUUUUAAAGUGUUGUGACUUUUCCAAAA AGUUAUGGCCUUUCCAGUAAAGCACAAUAAGCAUUUGUG ACAU	317	spiLA1589-miR11314-2-3p	AAAGUUGUGACUUUUAUGAAU	197-217	fve-miR11314	5	0	21	21	1
spiLA1589-MIR482c-1	AAAUAUAAGUAUGUAGUUGAAAAUCAUAUAAUUAAAGCUG UUAAAAUGGGUCGGUCCAACUCAACCCAAUCCUAACGGG CUAGAGAGUUAAAUGGGUUGGGACGGGCUGAUCCUUUUA AUUAAAGGACCUGUAAAAUAGCAAUCCAACCAAGCCCUAA GCGGGCCACGGGUUGGGAUGGGUUGACCCUUCAACGAA AAACGGACAACAUUUUUCUCUUUGAAAGAACACGAACGUU GAUGAAUUACACAUACUUUAGUGAAUAUUUACAAAAUAAA UACAUAAUAGCC	288	spiLA1589-miR482c-1-5p	GGUCCAACUCAACCCAAUCCUA	53-74	nta-miR482c	5	0	22	22	3
			spiLA1589-miR6235-1-3p	AACGGACAACAUUUUUCUCUUUGA	198-221	sbi-miR6235-3p	5	0	24	24	1
spiLA1589-MIR5026-4	GGUCCUAUUACCCCCCUGAACUUAUUUUUCAAGUAAUUU UCUACCCCUUUUUAGCCUACAUGCACUAGAUUUAAAAAAA AGUCAACCAUCGUUGGACCCAUAAGAUAGUGUCACAUUG GUCGAAAAGGGGCAAAAAAAUAUUAAUAAAAUAAGUUCAG GGGGGUAAUAGGACC	173	spiLA1589-miR5026-4-3p	ACCCAUAAGAUAGUGUCACAU	96-116	ath-miR5026	4	0	21	21	1
spiLA1589-MIR11580	AAAUGCUAUAGCAAAGUUUGCAUAAUUGCGUUCCAUAGC AAACAUAUAACUGUAUAAUUCGCUAUACAUAUACAAUUGU AUAAUUCGCUGGCCUAAAUUGUAUAAUUCGCUGGUCUCG CUAUGCAUAUACAAUUGUAUUAUUCGCUGGCCUAAAUUG UAUAAUUUGUUGGCCUAUUCGGCUGCAAUUGUAUAAUUC GCUGGCCUAUUUCGCUGCAAUUGUAUAUUGCGUAAUUGU AUAAUUCGUUGCCUAUUUCGCUGCAAUAUCUGUAUAAAA UUUGCUUUGCAAAC	288	spiLA1589-miR11580-5p	UUUGCAUAAUUGCGUUCCAUA	17-37	pab-miR11580	5	0	21	21	1
			spiLA1589-miR4243-3p	CUGCAAUUGUAUAUUGCGUAA	211-231	ath-miR4243	5	0	21	21	2
spiLA1589-MIR5057-3	AAUUUUCUACCCCUUUUGACAUAGGUGUUACUAGCUUGA AAAAAAAAUCAACCGUCAUUGGGUCCACAAGAUAGUGUUA CGUAGGCCGAAAAGGGUUAGAAAAUU	105	spiLA1589-miR5057-3-5p	AAUUUUCUACCCCUUUUGACA	1-21	bdi-miR5057	5	0	21	21	1
spiLA1589-MIR7997c-37	UGCCUAUAUUGCUCAGACUCUUCACAAAUGUCAUCGGAU GCGUGUCGGAUCCUUAAAAAUAGUGCAUUUUGAAGUAUC CAACACGAGUGUGAGAACAUUUUUUGAAGAGUUUGAGCA ACUUAGAUG	126	spiLA1589-miR7997c-37-5p	AUAUUGCUCAGACUCUUCACAAAU	6-29	stu-miR7997c	2	0	24	24	1

			spiLA1589-miR5303-37-3p	UUUUUGAAGAGUUUGAGCAAC	99-119	sly-miR5303	1	0	21	21	1
spiLA1589-MIR7543-3	GGGACACGUGACACAAUCUUAUCCGUCGAUUUGAUAUUCAACAGAUGUCGAGUUGGUGGAUAAGAUUAUGAUACAUGUAUG	81	spiLA1589-miR7543-3-3p	AUUAUGAUACAUGUAUG	65-81	lja-miR7543	3	0	17	20	2
spiLA1589-MIR5014a-6	AUUUUUCAUUUUAGGUGUGCACAAGUAGGCACUUAAACUUGUAUAAACUUGAACAAAUAGACACAUUUGUUCUACAUGACACCCUACAUGAAACUUUUGUGUCCUAUUUUAUUAUGUCAUGUAGAACAUGAGCGUGUACUUAUUCAAUUUUAUACAAAUUUAAGGGUCUAAUUAUGCAUACUCAAAGUUGAAAGAC	196	spiLA1589-miR5014a-6-3p	UUAUACAAAUUUAAGGGUCUA	150-170	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR7997c-38	UGUUUAAGUACAUAUCAUGUUGGAUACGUAUGUUACUCGAAUUCUUCAAAAAUGUUGCAGCACACAUGUCGGAUACUCAAAAGUCCACUACUUUUGGAGGAUUUGACAUGUACGUGUCGACAUUUUUGACGAGUUCGAGCAACAUAGCUAUAAGAAUGGUAAUACCUCUAAUAG	174	spiLA1589-miR7997c-38-5p	AUGUUACUCGAAUUCUUCAAAAAU	30-53	stu-miR7997c	4	0	24	24	1
			spiLA1589-miR5303-38-3p	UUUUUGACGAGUUCGAGCAAC	123-143	sly-miR5303	1	0	21	21	1
spiLA1589-MIR1128-8	AAUUACUCCCUCCGUCCCAAUUUAAGUGUCUUAGUUUAACUAGAAACAGAAUUUAAGAAAAAUGUGUGCAUUCAAAUUUAAAGUUAAAUUGGGAUGGAUGAAGUACUC	108	spiLA1589-miR1128-8-5p	AAUUACUCCCUCCGUCCCAAU	1-21	ssp-miR1128	3	0	21	21	2
			spiLA1589-miR5171b-8-3p	AGUUAAAUUGGGAUGGAUGAA	82-102	bdi-miR5171b	5	0	21	21	1
spiLA1589-MIR7981a-46	GAACAACUACAUAUAAAUGAAUAAUUAAUAACAAAAUUUAGGGAUAAUGCCCAAGUACCCCCUCAACCUAUGCCCGAAAUCUCCUUUUCGGCCUACGUGACAUUAUCCUGUGGGCCCAACGUUGGUUGACUUUUUUUUCAAGUUAGUGCCACGUAGACCGAAAAGAGGUAGAAAAUUACUUAUGAAAUAAGUUCAGGGAGUAAUAACCCUUAGUAUAAGUGUGUCUCUGGGAUUUCGGACAUAAGUUAAGGGGAUACUUCUACAUUAUCCCUAAUUUUUUUCUUUACGUAGAUGAUAUUGUAUUAAUUGAAA	312	spiLA1589-miR7981a-46-5p	UCUCCUUUUCGGCCUACGUGACAU	80-103	sly-miR7981a	4	0	24	24	2
			spiLA1589-miR7981e-46-3p	AAGUGUGUCUCUGGGAUUUCGGAC	217-240	sly-miR7981e	2	0	24	24	1
spiLA1589-MIR7983-6	UACAUACUCUACAACAAAAACGACAUUUGGUGGCAUUAAAUAUUGACACUAAUAAAGAGUGCUAAAGUCUUUACCGACAUUAGUUAAGUGUCAUUAGAACCAAUAUCGCUAAAGACUUUAGAGACAUUUACAAAGAGUGGCAAUUGCCGCUAAAAAUACAUAUUUAGCGACAAUUAAGAAUUAAAUGCCUCUAAUGAUCAUUUUUGUUGUAGCGAUAUUCA	221	spiLA1589-miR7983-6-5p	UAAAGUCUUUACCGACAUUAGUUA	63-86	stu-miR7983-5p	3	0	24	24	1
spiLA1589-MIR8739-2	UCGAACUAUCUCCGUCGUACUUUUGGUAUAUUGGUACCCCUGUCGUCCAAAAAUUAGAGUGUAUAUGCCCUUAGCUCUAACGAAAGACUAAAUAGGGACACGUGGCGCAAUAUUAUCUUCGAUCCGAUGAUGGUUCGGUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAAGGAUAUGUAUGCUUUAGUUUUUGAAUGACAGGAAUACCAAUAUCCCUAAAAUAUGACAGAGGAUAUUUUCA	248	spiLA1589-miR8739-2-5p	AGACUAAAUAGGGACACGUGGCGC	85-108	gra-miR8739	5	0	24	24	3
			spiLA1589-miR8006-2-3p	UAGUUUUUGAAUGACAGGAAUACC	192-215	stu-miR8006-5p	5	0	24	24	1
spiLA1589-MIR7701-2	AUAUUAUGUUUAUUAUGGUUGAAAUGUUGGGGUUUAGAUUGCUUGGUUCGAUCACAUAGGAGGGUAAGUGUGGGUUCCACUCGCGGUCCGCUUUGGGUCGUGACAAACAUGGUAUCAGAGCAUUAGGUUCGUUGGUCUCAUUACAGAUUAACGAGUCUAGUAGAGUCUUAAGGAACGGUAGGGGGACACCUUUACUUUUCUUUGAGAGGCUAUUUAUCAUUGAAAUAGUAGCUAAAUAAUCGUGUAUCAUAGUUUUGAAUAACUAUUUUUACAUGAAAGAACAUAAAAG	289	spiLA1589-miR7701-2-3p	UUUACAUGAAAGAACAUAAAA	268-288	mtr-miR7701-5p	5	0	21	21	2
spiLA1589-MIR395a-2	AUGCCCUAUUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAUGAAUCCUGGCUGUGGAUGAUGAACAUAAUAGUUCACGUAUAAAUCUAUUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUU	163	spiLA1589-miR395a-2-5p	UGAAGUGUUUGGGGGAACUCU	10-30	aof-miR395a	0	0	21	21	1
			spiLA1589-miR395j-2-3p	GUUCCCUUGACCACUUCAUGA	137-157	mdm-miR395j	2	0	21	21	1
spiLA1589-MIR482d-4	UAAUUUCUUACUUGAUCGCGUGUUUUUACUUGUGAGUUCCUUUCUACUGCUACCAUUUAAAUUUGACGACGGAAUGUGCGGUAUGAUCAACAACAGAACAACUACUUCUUCAGCUCAUGUAGCAGUAGAAAGGAACUCACAAGUUAAAACAAGCAAUA	171	spiLA1589-miR482d-4-5p	UCCUUUCUACUGCUACCAUU	38-57	pta-miR482d	4	0	20	20	1

	AAGCAAGAAAUAA										
			spiLA1589-miR3623-4-3p	UCACAAGUUAAAACAAGCAAUA	137-158	vvi-miR3623-5p	5	0	22	22	1
spiLA1589-MIR9477-3	ACACACCUAGGAUAUACCCAUUUUUUGAGUUUCAUAUAGGAAAUAUCAUCAUCGUUCAGGUAGGAAAAGUAAACAAUUGAUAGUUGAGGUGUGUUUUGAUGAAUAAUGGUGAUAGUUUAGGUAGGAAAUUCGCACACAUGAUAGUUUAGGUUUGAAACUCGAAAAAUCGGAGUACUUUAGGUGUGU	186	spiLA1589-miR9477-3-5p	UAGGAAAAGUAAACAAUUGAUAGU	61-84	sly-miR9477-3p	5	0	24	24	1
			spiLA1589-miR8045-3-3p	AUUGAUAGUUGAGGUGUGUUU	76-96	stu-miR8045	0	0	21	21	1
spiLA1589-MIR1043-3	UGACAUAAUACAUAAAGAUGUCAUUUAACUUGGAUUCGAAUCACAUUUAUGCCCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACUUGUGUAAAGUUGAACAAAGAGACACACAUGUCCUAUAUGUUAUUUUUCGUCCUACUUGGUGUUUUACGUGUAUUUUUUCAUGCAGAACUCAUGUAUUUACUUAUUUAAAAGUUGGAUAGUUAAAGUGCCUGUUUGUGCAUUAUAAAAGAUGGAGGUCAAAGUUAAAAUGUGAAGCUAAGUUUAGGGUCUAAUAUAUGUAUUAUGCCU	297	spiLA1589-miR1043-3-5p	CCUUCAACUUUGGGUGUGCA	53-72	ppt-miR1043-5p	4	0	20	20	1
			spiLA1589-miR8781a-3-3p	UAUUUACUUAUUUAAAAGUUGGAU	184-207	gra-miR8781a	5	0	24	24	1
spiLA1589-MIR1040	UCUGAACCGUGGGAGAGAUGACCGCAAUCAAACAUGAUCGGAUCUGUCCAUCCACUGCUUUCCAGGCGGCAUGGGCCGGAUUGAUUUUUUCUGAUUUGUCCGUUGCGGUGAUGACUGCCGGUUCUGU	127	spiLA1589-miR1040-5p	UGACCGCAAUCAAACAUGAUC	19-39	ppt-miR1040	5	0	21	21	1
spiLA1589-MIR857-2	GUUCUAGUUUGCCUUUCGGGGAAGAAAUUUGAUUUUCCAUCUUGAAGGUUUACCAUGAAAUAGUCAUUCUUGUCUUGAUGUUUGACUGACCUCUGCUUAUUUCAUGGGCAAACUUUCAAGACGAAAAAACAAGUUUCUUUUCCAAGAGGCAAACAAGGUC	161	spiLA1589-miR857-2-5p	UUUUCCAUCUUGAAGGUUUAC	33-53	aly-miR857-3p	5	0	21	21	1
			spiLA1589-miR812o-2-3p	UGUCUUGAAUGUUUGACUGAC	71-91	osa-miR812o-5p	5	0	21	21	2
spiLA1589-MIR7997c-39	GUUUGUGUUGUUCGGAUUCUACAAAAAUGUUGCAGUGUUCGUGUCAGAUCCUCCAUAAAUGCGUUCUUUCUGAAAGUUCUGACACAUUUUUUAAGAGUUCGAGCAACACAGAU	113	spiLA1589-miR7997c-39-5p	GUGUUGUUCGGAUUCUACAAAAAU	5-28	stu-miR7997c	5	0	24	24	2
			spiLA1589-miR5303-39-3p	UUUUUUAAGAGUUCGAGCAAC	87-107	sly-miR5303	1	0	21	21	1
spiLA1589-MIR8006-9	UCAUUGGAUAUUGGUGGCACUGUCGUUUAAAAACUAGAGCAUAUAUACUCUUCAUUCUAAUAGGAGACUAAAUAGGGACACAUGACGCAAUGUUAUCUGUCAGUCUGAUAUUUAAUAAAUAUCGAGUCGAUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAGAUAUAUAUGCUCUAGUUUUUGGACGGCAAAAGCACCAAUAUCCCAAAAA	218	spiLA1589-miR8006-9-3p	UAGUUUUUGGACGGCAAAAGCACC	182-205	stu-miR8006-5p	4	0	24	24	1
spiLA1589-MIR319d	AGCAGAGGAGAGAAGGAAACUGUUUAGUCCAACCCAAGGUGGGGUAUUGGAACUGAUCUUUGCUGCUGAAUCAUUGGCUCAUGAGCAUGUCAAAGAAGAUGAUUGAACAUUCUGGACUUGUUCUUGCUCCAAUGAUGCAGGAGCUGAGCUCGGUUUUUCACCGCCUUUUCUUGGACUGAAGGGUUCCCUUCCCUUCUCUUUA	202	spiLA1589-miR319d-5p	AGGAAACUGUUUAGUCCAACC	14-34	sly-miR319d	0	0	21	21	1
			spiLA1589-miR319-3p	UUGGACUGAAGGGUUCCCUUC	171-191	stu-miR319-3p	0	0	21	21	1
spiLA1589-MIR7728	GUAAUAACGGUGAUAAUGGUAUUCUAAUAUUGCUAAAGUUAAACAGAUUUACUGCCUUUUGUUAUUUCAGAUGCAGGAACACCAAUACAAGAAGCAAUGAGCUUGCUUGGGCAUGUCAAAAGCCGUAAAUCCAUUCAAUUUUAGCAAUAUUGGAAUACCAUCAUCACCGUUAUUAC	176	spiLA1589-miR7728-3p	AAAUCCAUUCAAUUUUAGCAA	127-147	bdi-miR7728-3p	5	0	21	21	1
spiLA1589-MIR6145e	UGGAUAUGCACAAAUGGAUACUUAAACUUGUAUAAAGUUGAACAAAUAGAUACGCAUAUCCUACGUGUCAUCCUACAUGUCAUUUUUUGUCCUACGUAAUGUCCUACAUGUAUUGUUACAUGUAGAACUCAUGAGUUUAUUUAUCUAAAAGUUGGAU	186	spiLA1589-miR6145e-3p	AUUGUUACAUGUAGAACUCAU	112-132	nta-miR6145e	4	0	21	21	1
spiLA1589-MIR482e-2	AGUUAAAGUGUCUGUUUGUGCAUUAUGAAGUUGGAGUGGGUGGUGUGGUAAGAUUUCAUAUUUAUUUUCCAUAAAAAUUGAGAUCUUGCCAAUACCGCCCAUUCCUAU	79	spiLA1589-miR482e-2-5p	AGUGGGUGGUGUGGUAAGAUU	6-26	stu-miR482e-5p	0	0	21	21	1
			spiLA1589-miR482c-2-3p	UCUUGCCAAUACCGCCCAUUCC	55-76	sly-miR482c	0	0	22	22	1

spiLA1589-MIR7997c-40	AAUGGAGGGUCACUUCAAGCUAUGUUGUUUAGACUCUUCAAAAAUAUCGAGGGUGUGUGUUGGGUCCUCCAAAAAUAGUGCAUUAGGAGGAUCCAACAUGGGUGCGGCAACAUUUUUGAAGAGUUCGAGCAACAUAGACUACAAGUUCCCUCCUAG	156	spiLA1589-miR7997c-40-5p	AUGUUGUUUAGACUCUUCAAAAAU	22-45	stu-miR7997c	4	0	24	24	1
			spiLA1589-miR5303-40-3p	UUUUUGAAGAGUUCGAGCAAC	113-133	sly-miR5303	0	0	21	21	1
spiLA1589-MIR816	CAUAGCAAACAUAUAACUGUAUAAUUCACUAUACAUAUACAACUGUAUAAUUUGCUGACCUAAAUUGUAUAAUUCGCUGGCCUCACUAUACGCAUACAAUUGUAUGAUCGCUGGCCUAAAUUGUAUAAUUUGUUGGCCUAUUUCGCUGCAAUUGUAUAAUUCACUGGCCUAUUUUACUGCAAUUAUAUAAUAUGCAAUUCUAUAAUUUGCUGGU	215	spiLA1589-miR816-3p	CUGGCCUAUUUUACUGCAAU	165-184	osa-miR816	5	0	20	20	2
spiLA1589-MIR6022-2	AACAAUACGAUCCUGGAUAUUAUCCUUUCCAUCACUAACUUAUUUCGCCUCAAAGUUUUAAGUUGCAAGGUACUCUUCCUAAGUCAAUUCAGAACUUCAUGAACCUAACGCGACUUGAUCUUAAGUUACAUUUUACGAAACCUCAAUCUUGGGUAGAGGACCGUGCAAUUGGUUAAAACUCGGUCUAAAUAACUUAGUGAUGGAAGGGAGAAUAUCCAGGAUGGUAUUGUU	231	spiLA1589-miR6022-2-3p	UGGAAGGGAGAAUAUCCAGGA	201-221	sly-miR6022	0	0	21	21	1
spiLA1589-MIR396b-4	AUAAUAACCUUGAAUCAAUAAUUCAAAUUCAAGUUAGAUUGAAGAGUUAAAUUUUGAGAAUUCUUUCCAAAAUUCUAAGAAAGUCCCUUUUGACACAUUCGAGAGUUCGAGUUAGCUAUGGUGAGUCUCCUUGCUUCCAUAGGAUUUCAUUUACUUUUCAGUUUAGUCAGGAUCUCAUGGGUCGUAUCCCGACUUCCAUAUUUCUCUGUUAGAGGCUUCAUCGAUUGUUAGUAUAGUUGAGGAGUCUGUAUUAAUCUUUUAUUUUAUUAAAUGUUAUAAA	280	spiLA1589-miR396b-4-5p	GUUCGAGUUAGCUAUGGUGAG	105-125	eun-miR396b-3p	5	0	21	21	1
			spiLA1589-miR7502c-4-3p	CUGUUAGAGGCUUCAUCGAUU	206-226	gra-miR7502c	5	0	21	21	2
spiLA1589-MIR7997c-41	CAAAUAUUGCGCGGACUCUUCAAAUAUGCAGCCUAUUGUUUGUCUGAUCCUCCAAAAUUAGUGUAUAUCCGGACGGAUCAGACAGAUGCUACAACAUUUUUGGAGAGUCCGAGCAACAUAGC	122	spiLA1589-miR7997c-41-5p	AUAUUGCGCGGACUCUUCAAAUAU	4-27	stu-miR7997c	2	0	24	24	1
			spiLA1589-miR5303h-41-3p	AACAUUUUUGGAGAGUCCGAGCAA	93-116	stu-miR5303h	2	0	24	24	1
spiLA1589-MIR7533c	ACAUUUAAAGAAAUAGAAAAUGAGUUGGAUAUGUCCAGCUGACCAACUAAUCAUAAGGGCAUACCUAUGUGAAAAGUUGGACGGCGAGGACAUGAGUGAGCCAAACUUUAAACGGAGACUAUACUAAACUUUUUCAAAUAUUGCAGAGGCAUAUUUGACCAUUUUCCCUUUUUUAAAAUA	180	spiLA1589-miR7533c-5p	AAGUUGGACGGCGAGGACA	74-92	lja-miR7533c-5p	4	0	19	19	1
			spiLA1589-miR11144-3p	UUGACCAUUUUCCCUUUUUUAAA	155-177	lja-miR11144-5p	5	0	23	23	1
spiLA1589-MIR482b	UUCUGCUUAAGUUGGUGUCUUAACUUGUAAUUCACUUCUAUCGUGGAUCGCUUCUGCUUUUGAAGUACCAUAGAAGUGAAUUGCAAGGUAAGACACCAACUUAAGCAGAA	110	spiLA1589-miR482b-3p	GAAGUGAAUUGCAAGGUAAGA	73-93	stu-miR482b-5p	5	0	21	21	1
spiLA1589-MIR3637-2	AAGUUGUGACUUUUAUGAAACGUGAAGACCUUUCUGAAAGAUUAUGACUUUUUCCAAAGGUUUGUGACAUUUUCGGUAAGGCACAAUAA	89	spiLA1589-miR3637-2-3p	UUUCGGUAAGGCACAAUAA	71-89	vvi-miR3637-3p	5	0	19	24	1
spiLA1589-MIR3434	AUCUAAAACAUGGUUGUGGUCAGAGAAUGUAUCAUUUCGAGGGUAGUAUCGCACGUCGUGAUGGAUAUUAUAUUUCGAGGGACAUAUCGCGUGCCUUGAUUGUUUCUAUUAUCGAGUAUCGUGUCGUGCGCCGCGACAGAUGCAUUGACAGAUAUGUCCCCCAUGGGUGUGUAUCGUUAGGGAAGACAUGCAUUACUAUUCUUGACAUUGCAUCUCAUGGCAUUACACAUUUUUUAUUA	239	spiLA1589-miR3434-5p	CCUUGAUUGUUUCUAUUAUC	94-113	ath-miR3434-5p	5	0	20	20	2
			spiLA1589-miR5260-3p	UUACUAUUCUUGACAUUGCAU	193-213	mtr-miR5260	5	0	21	21	1
spiLA1589-MIR8138	GACAUAAGAUAGGUGGACUCCUUGUAAGGUUUGGGCAAUCCUCCUCCCACCUUUUGGGUGUGAGUUAAGUCUAAGACCUAAUUACACAUGGUAUCAAAGGAUUGUACAAGCUUUAUAAGGAGUCCACUAUCUCAUUAA	138	spiLA1589-miR8138-3p	UACACAUGGUAUCAAAGGAUUG	83-104	cpa-miR8138	5	0	22	22	1
spiLA1589-MIR8557	UUUUGUCUAGUUGCAACAUCACCCAUAUAGUUGGGAACAAGUUAUUACCUUGAGAUUAGUUAUUAGGUCAUAAUACAUAAAUAUGCCCUUUAACUUGACUUCUGAUUACGUUUAUGUCUUUCAACUUUGGGUGUGCACAAGUAGACACUU	150	spiLA1589-miR8557-5p	CCAUAUAGUUGGGAACAAGUU	23-43	atr-miR8557	4	0	21	21	1
			spiLA1589-miR2655o-3p	CGUUUAUGUCUUUCAACUUUG	109-129	mtr-miR2655o	5	0	21	21	1

spiLA1589-MIR7505b	CUUCAACUUUAGUAGCGUACAUCCAGACACCUCAACAACUCAUCCCUACCGAGUCUCGUGGACACCCAAUUCUAACGUGACACAUAAAUUUUGAAGAUAUGUGAAUGAUCAUUUUGUAAGGUGGAGUGUUCAACUAACACACUAGAACGAGCUGAGGUGUCUAGAUGUGCAUUCUCAAAGUUGGAG	186	spiLA1589-miR7505b-5p	ACACCUCAACAACUCAUCCCU	27-47	gra-miR7505b	5	0	21	21	1
			spiLA1589-miR7992-3p	UGUCUAGAUGUGCAUUCUCAAAG	158-180	stu-miR7992-3p	5	0	23	23	1
spiLA1589-MIR11076	AAAUUCCUAGAAUAAUGAGUUCACAUAAACCACAUUGAGUAGUUUCUAAGUCAUGGUAGUGAAGUGCACCACUAUCCUGGAUUAGAGACUGCAUGAUGCAUAGGAAAAA	109	spiLA1589-miR11076-3p	CAUGGUAGUGAAGUGCACC	52-70	lja-miR11076-5p	5	0	19	19	2
spiLA1589-MIR8771f	ACCAGAUUGAAAUAAGAAAUCGCCUCAAUUGAACAUCCAAGACAAGAUUUAUGACCGUUUUAAUUUCACAAAUAUACAACUACUUCAUUUGGUGAAACUUCAAAUGAUCGUAACUUUUUCCUUGAAUAUCCGUUGGAGGUGAUUUUUUUUUUAAACUUGC	160	spiLA1589-miR8771f-5p	UUGAACAUCCAAGACAAGAUUUA	29-51	gra-miR8771f	5	0	23	23	1
			spiLA1589-miR7990b-3p	GAAACUUCAAAUGAUCGUAACUUU	94-117	stu-miR7990b	2	0	24	24	1
spiLA1589-MIR482c-2	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGUCCAUGGCUUUGCUCCUUAAGUCCCCAUUGAUUUAGGAGAGUGGACGGGGCAGACUGACUUCACGA	99	spiLA1589-miR482c-2-5p	CUCCCACUUCCGUCCAUGGCU	22-42	gma-miR482c-3p	5	0	21	21	2
spiLA1589-MIR7997c-42	AAACCUAUGUUGAUCGGACUCUCCAAAAAAUGAUGCCGCUCAGAUGUCUUAUCUUACAAAAAUGCACUACUUCUGAAGGAUCCGACAAACAUUCGAUUUCAUUUUUGAAGAGUCCAAGCAACAUAGGAAA	130	spiLA1589-miR7997c-42-5p	AUGUUGAUCGGACUCUCCAAAAAA	7-30	stu-miR7997c	4	0	24	24	1
			spiLA1589-miR5303i-42-3p	UCAUUUUUGAAGAGUCCAAGCAAC	99-122	stu-miR5303i	4	0	24	24	3
spiLA1589-MIR8594	CAAGUCUUAAAUAUCAUUGAUAGCGAGCAUGUGGUAUUGUAAGUCCCCGUUAAAAUGAGAAAAGGGGAAGCCUGAAACCCUUGUUAGAACUGCUAUUUAUUGAUAUUUUAGACAAA	116	spiLA1589-miR8594-3p	UAUUGAUAUUUUAGACAAA	98-116	atr-miR8594-2	5	0	19	24	2
spiLA1589-MIR3950	GGAGAAAUAAUGAAUUAACCCUACACUUGAAAUUUAGGAAACAUGUAAUUAGACCUAUUGGUUGGAAUCAAUAUUUAGGAACUUUAUUAUACAUUUGAGUGAGUUUUGGGUCUAAGCUAGACAUAUGAGUGUUGUUAGUUACGAAAUUUUUUUGUGAUUAUUAAUAUGAAUAGAUUUCUUUGAGUUGGAAGUACAACGAAAAGGAAAGGCUCAAGUCUUAGAGUGAUUGUUCGACUAUUUGAGGCAAGUUGAUUUCUAAACUUUUGUUAUGGGUAUGAAAUUCGUGUAUUUCCUU	295	spiLA1589-miR3950-3p	AUUUGAGGCAAGUUGAUUUCU	237-257	csi-miR3950	5	0	21	21	2
spiLA1589-MIR7997c-43	UUUACCUAUGUUGGUCGGACUCUCUGAAAAUGUCAACACGUGUAUAGGACUCUUCAAAAGUAGUUGAUUUUUGGAGAGUCCGAGCAACAUAGGUCUU	97	spiLA1589-miR7997c-43-5p	AUGUUGGUCGGACUCUCUGAAAAU	8-31	stu-miR7997c	5	0	24	24	1
			spiLA1589-miR5303i-43-3p	UGAUUUUUGGAGAGUCCGAGCAAC	65-88	stu-miR5303i	4	0	24	24	3
spiLA1589-MIR156b-15	UAUGAAAGAGGUGAAGGUGAUGACAGAAGCAUAGAGAGCACAAAUGAAUUGAGAUGCUUUUGCUGCCCAAAUUGAAUGAAAUUAGCAUAUCAUCAUUAGUGCUCUCUAUCUUCUGUCAACAAUAAUCACUCUUUCUUC	138	spiLA1589-miR156b-15-5p	AUGACAGAAGCAUAGAGAGCAC	20-41	aof-miR156b	2	1	22	21	2
			spiLA1589-miR1088-15-3p	UAGUGCUCUCUAUCUUCUGUC	97-117	smo-miR1088-3p	4	0	21	21	3
spiLA1589-MIR394-3	UUUUCAUGAAGAUUUCUCAAAGGGUUCCUUACAUAGUUCUUUGGCAUUCUGUCCACCUCCUUUACCUUCAUAAUCUUCUAUUUUUUUAGAAAAAUAAUUUUUGUUAUUCUUUUUUAAAAAAAUGGAGGUGGGCAUACUGUCAACAGAUUUGUGUUAGUUUCUCUUUGUGAAAUCUUCUUGAUGU	185	spiLA1589-miR394-3-5p	UUUGGCAUUCUGUCCACCUCC	40-60	cas-miR394	0	0	21	21	1
			spiLA1589-miR394-3-3p	AGGUGGGCAUACUGUCAACA	127-146	sly-miR394-3p	0	0	20	20	1
spiLA1589-MIR11592-2	AAUCAAACCGACGAACCAAACCAAACCGAAAAAAUGACUUGUGGUUUGGUUUGAUUGGUUUGGCG	65	spiLA1589-miR11592-2-5p	GAACCAAACCAAACCGAAA	13-31	cas-miR11592	2	0	19	19	1
spiLA1589-MIR9726	UUUAUCAUUAUAAGUGUAAUUUUUUUCUUCAAUUGAUUUAAGUAAGUUAGGCCAAGGGUCCGCUCGAGGCCAGUAAUGGUCAUCGAGUAUCAGUAUCAUCCAGGAUGUAGGAUCGCGAUGUGAAAUUUUUAGCGUCAAACUAUAAAAACUUUGACCAA	220	spiLA1589-miR9726-5p	UAUAAGUGUAAUUUUUUUCUUC	9-30	gma-miR9726	4	0	22	22	1
spiLA1589-MIR7987-2	UAUUUUACGAUGUAUAUUUUCAUCAUAUUGAUAUGAAAAAAGAUUACAAUUUAUAGUAUUUUAAUAUAUUUGUUAAGCAUAAGUACCAACACUAGUUGAUCCUAUUGAUGACUAAAUUGAUUUUCUUGCAAGAUCGGUUUGUGUCCAUCUAGUGUUGACACUUAGGACAACGAAUAUCUC	118	spiLA1589-miR7987-2-5p	ACACUAGUUGAUCCUAUUGAUGAC	27-50	stu-miR7987	1	0	24	24	1

spiLA1589-MIR6020a	AAAUGGAGUUUAAUGGCGAAAAUACUCGUAAAACAUUUACGGAUCACUUCUAGGUAGGAUUGAAUAUCAGAGCAAUAUCAUAUAUUGUAGAUCUGUAAAUGUUUUCCGAGUAUCUUUUGCCCAUAACCUUCAAAA	135	spiLA1589-miR6020a-3p	AAAUGUUUUCCGAGUAUCUUU	97-117	nta-miR6020a-5p	2	0	21	21	1
spiLA1589-MIR1917-6	AACUUUUAGCGGCAUUAAAUAUUGACAUUAAUAAAGAGUGCUAAAGUCUUUACCGACAUUAGUUAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAUGGACAUAUACAAAGAGUGACAAGUGCCGCUAAAAAUA	136	spiLA1589-miR1917-6-5p	AUUAAUAAAGAGUGCUAAAGU	27-47	sly-miR1917	0	0	21	21	1
spiLA1589-MIR828b-2	AAUUUACUUGCACCAGGCGUUUACACCAAGUCAAUACAUGCAUGUCAUGUGUUUAAUUUAUAUUUUAUUUAACUUCAUUAAAUCACGUAAUAUUAAAAAUUGCAUUGACUUGGCAUAAACACCCGAAGCGGGUAAGUU	138	spiLA1589-miR828b-2-3p	UCAUUAAAUCACGUAAUAUUA	75-95	ptc-miR828b-3p	5	0	21	21	1
spiLA1589-MIR859	AGAUUUCAUUGAUUUUACAAAAAAUAGGAUUGAAUUUCUCAAAUGUUCUCCAGUUUAUACUUUCCAUUAUGUUGGUGGUAGAUACGGCAGAGUGGCAUGGAUCAUGUGAGAAUCAAGUUACUCUUAAACUUGUAUUGGAAUGUGGUUUGCAUGUGUGCAUUGUUGCAAUUAUGAAAUGUUUAGUGCAUGGGAGCUGGGGACCAUAUGGAAAUUGAUAUGUAGUGAUGUCCAAUUGCAGUAACUAAGGUUUUCUGAGAAAACAAAUAGUUUUUUUUUUCUUCUUUUUAAAGUCAAUAAAAAAA	302	spiLA1589-miR859-5p	UGAUUUUACAAAAAAUAGGAU	10-30	aly-miR859-3p	5	0	21	21	1
			spiLA1589-miR6288b-3p	GCAAUUAUGAAAUGUUUAGUG	165-185	ppe-miR6288b-3p	5	0	21	21	2
spiLA1589-MIR9477-4	UUAAUAGUCAAAAACACAUUUGAACUGUUACUUUUUCGGUAGUUUCACACUUUAACUAUCGGUUAUUCCUUUUUCCUAUCUGAACUAUGACCAUCGUUCAGGUAGGAAAAGGAAACAACUGAUAGUUGAAAUGUGAAACUGACGAGAGAACAAUAGUUCAUUUGAGUUUUUGAGCUAUGCU	181	spiLA1589-miR9477-4-5p	UAUCGGUUAUUCCUUUUUCCUAUC	57-80	sly-miR9477-5p	4	0	24	24	1
			spiLA1589-miR8039-4-3p	UUUCCUAUCUGAACUAUGACC	72-92	stu-miR8039	1	0	21	21	1
spiLA1589-MIR8006-10	AUUGGUGCCCGUCGUCCAAAAACUAGAGCGUAGAUGCCCUUCACUCUAACAGAAGACUAAAUAGGGCGCAAUCUUAUUCAUCGAUCCGAUGUUAGGUCGGUGGAUAAGAUUAUGACACAUGUAUUUCUGUUAGUAUAAAGGGUAUAUAUGCUCUAGUUUUUGGACGGCAGGGGCACCCUA	180	spiLA1589-miR8006-10-3p	UAGUUUUUGGACGGCAGGGGCACC	154-177	stu-miR8006-5p	1	0	24	24	1
spiLA1589-MIR7997c-44	AGGCUAUGUUGCUCGGACUCUUCAAAGGUGCUGCAGGAUCCUCCAAAGCUUGUGCAACUUUUGAGGAACUGAGACGGGGUGUGACAGCAUUUUUGGAGAGUGAGCAACAUAGGGU	115	spiLA1589-miR7997c-44-5p	AUGUUGCUCGGACUCUUCAAAGGU	6-29	stu-miR7997c	3	0	24	24	1
			spiLA1589-miR9779-44-3p	CUUGUGCAACUUUUGAGGAA	49-68	tae-miR9779	4	0	20	20	1
spiLA1589-MIR11136	GUGUGCCAAGAUCUCGAUAUUGAUAUUUGUAGGCAAUAGUAUUUUUGAACAUUUAUUCACGUAUGACUUAUGUAUCAAUAUGGAAUUUGGGCAAGG	96	spiLA1589-miR11136-5p	UCUCGAUAUUGAUAUUUGUAGG	12-33	lja-miR11136-5p	5	0	22	22	1
			spiLA1589-miR11517-3p	UCAAUAUGGAAUUUGGGCAAG	75-95	pab-miR11517	5	0	21	21	1
spiLA1589-MIR1916	UUGAGCAACAAACUUCAAUUAUGGAAAAACAUGUCCAAUAGGUACAAGUCCUAGUUGAGGUGUCUAAGUGAAUUAUGCGGCAAUUUUAAGGGGCAAAUGAUGAAUUUAAACUAUUUUAUAGGCUUAAGUCAUCGACAACUCUUAGAGUUGUUCACAUAUUUCACUUAGACACCUCAACUAGGGUCAAUACAUAUUGAACACUUUUGUCUAUAAAAAUGUUGUUCUAUU	228	spiLA1589-miR1916-3p	AUUUCACUUAGACACCUCAA	158-177	sly-miR1916	0	0	20	20	1
spiLA1589-MIR10532-8	UUUAGUCAUUUAGUUUAAGUUUUUGCUAGAUUUAGUUGGGGCUUGUCCCGACCUUAGUAUAGUAUAAGUGUGUCUGUGAGAUUUCGGGCAUAGGUUGAGGGGGUACUUGUGCAUUUUUCCUAUUUUAAAUGAUACUAGUUUCUGGAAAAAUGCGUUGCAUGUUUAUCGCUUACUACUUUAUAAAACUUAUACAUGAUUGACUUUA	205	spiLA1589-miR10532-8-5p	AAGUGUGUCUGUGAGAUUUCGGGC	66-89	sly-miR10532	1	0	24	24	1
			spiLA1589-miR11144-8-3p	UUGUGCAUUUUUCCUAUUUUAAA	107-129	lja-miR11144-5p	5	0	23	23	1
spiLA1589-MIR7998	AUUGUAGGUCCAGUCACGGUCCAUCAGUGGGUAGACCUAGAUUUCUCAUCUAGGAUGUUUGAGUAUGUGUCGAACUACCGAGGCUAGUGACGGACCGUAGAUCAAUCCACGGUCCAUACUGCAAGUUUAUCAAUGAUCACUUAGAGUUAAAUUUCAAAGUCUGGAUGAAAAAUUCUAAGUGUGGACCCACAGAGGA	219	spiLA1589-miR7998-3p	ACGGACCGUAGAUCAAUCCACGGU	90-113	stu-miR7998	1	0	24	24	1
spiLA1589-MIR865-3	CCCAUGGAACAUGGAUCGACCCAGAAUGAACUUAAUGGGCUGAAUCUGAAUCUGAUUCAGAUUCAGUCCUAAAAAUUAAACGUACUUAAUAGGCUGAAUCUG	109	spiLA1589-miR865-3-5p	CUGAAUCUGAAUCUGAUUCAG	17-37	ath-miR865-5p	5	0	21	21	2

	AAUAAUUUCAGACCUCCAUUAAGUGCAAAC										
			spiLA1589-miR159a-3-3p	GACCUCCAUUAAGUGCAAAC	90-109	aly-miR159a-5p	4	0	20	21	1
spiLA1589-MIR536	AAGCAUACUGCGUGGGCACUUGACGGCAUGCAUGGCUCGUCCGUGCUACGCUGUGGGCGUUUACAAAAACACGCCUGCGACAUCUGCAGGGCGUUUGAGGCGGUGGCAGGCAAACGUCAUGGGCGUCCUGUGGGCUUAGUAGGCGUGCUGCGUGGGCGCUUGACGGCAUGCAUGGCUUGUCCAUGCUACGCCGUUGGGC	199	spiLA1589-miR536-5p	CCGUGCUACGCUGUGGGCGUU	41-61	aof-miR536	4	0	21	21	2
spiLA1589-MIR10538-4	GGUGUUAGAUUGAUAUACGUUACUCAUAGUAAAGUUUUACUCCUAAAACGUUACUGUGAGUAACGUCUUACUCUUAAAACGUUACUCACGUAGGAGUAAAAUGUUACUCACGGUAAUAUAUAUUAAUCUAACGCU	135	spiLA1589-miR10538-4-5p	AGAUUGAUAUACGUUACUCAUAGU	7-30	sly-miR10538	1	0	24	24	1
spiLA1589-MIR5369	CGACUGACUUGUCUACUUCAAGUGUUGAUGAAGAAGGAAGCUGAGUAUUGGAGCAUGUCGAAGGAACAUGUUCAACGAAGCUGACUGACGAGUUACAACACUGUUGAAGAUUUAGAGUCAGAUU	124	spiLA1589-miR5369-5p	UGAGUAUUGGAGCAUGUCG	42-60	gma-miR5369	5	0	19	19	1
			spiLA1589-miR5140-3p	ACUGUUGAAGAUUUAGAG	100-117	rgl-miR5140	4	0	18	18	2
spiLA1589-MIR395g-2	UGCUGAAGUGUUUGGGGGAACUUUUGGACUCACAUUGAAAUUUUACACAAAUUAAACAAAUACAAGUGUAGCAGUGUUGGCUGUGGAUGAUAAAAGUUCACGUAUAAAUCUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGA	150	spiLA1589-miR395g-2-5p	UGAAGUGUUUGGGGGAACUUU	4-24	gma-miR395g	0	0	21	21	1
			spiLA1589-miR395j-2-3p	GUUCCCUUGACCACUUCAUGA	130-150	mdm-miR395j	2	0	21	21	1
spiLA1589-MIR6273-4	CGAUCCUAUUACCCCCCUGAACUUAUUUUAUUCAUAAUUUUCUACCCCUUUUGGCCUAUGUGGCAUUAUCUUGUGGGCCCAACGCUGUUUGACUUUUUUUUUUCAAACUAGUGUCACGUAGGCAGAAAAGGGGUAGAAAAUUAAUUAUAAAAUAAGUUCAUGAGGGGUAAUAGGACCU	178	spiLA1589-miR6273-4-3p	AACGCUGUUUGACUUUUUUUU	81-101	ppe-miR6273	5	0	21	21	1
spiLA1589-MIR7120b	GACCGGAGUGUCACGUUCUGACACGGUAUUAUGGGAUCGGAGUGUCACGUUUCGACACGGUAUUAUGGGAACGGAGUGUCACAUUCCGACACGGUAUUAUAGGAUCAGAGUGUCACGUUCCGACA	125	spiLA1589-miR7120b-3p	UAUUAUAGGAUCAGAGUGUCA	95-115	mdm-miR7120b-5p	5	0	21	21	1
spiLA1589-MIR7997c-45	CUGCUAUGUUGCUCGGACUCUUCAAAAAUACACUACUUUUGAAGAACCUGACAUGCAUCCAGCCACAUUUUUGAAGAGUCGGAGCAACAUAGGAU	95	spiLA1589-miR7997c-45-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
			spiLA1589-miR5303h-45-3p	CACAUUUUUGAAGAGUCGGAGCAA	64-87	stu-miR5303h	2	0	24	24	2
spiLA1589-MIR5014a-7	UUGGACCCUAAACUUGGCUUUAAAUUUUAACUUUGACCUCCAACUUUCAUAAUUUAUCCAACUUUUAAGUAAAUAAACACAUGAGUCCUACAUGACACAAUACACGUAGGACAUCAUGUAGGACAAAAAAUGACAUGUAGAAUGACGUGUAGGACAUGUGUGUCUGUUUGUUCAAAUUUAUACAAGUUUAAGUGUCUAC	199	spiLA1589-miR5014a-7-3p	UUAUACAAGUUUAAGUGUCUA	178-198	ath-miR5014a-3p	5	0	21	21	1
spiLA1589-MIR6160	UAUGUAUUAUAUAACUCUCUAGAUUUUGUAUAAAUGCUACUUUUACAAUCUUCAACACUAGGAGUUUCAUCAUUUAACUUCCGUUAAAUGAAGGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUGGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGAUAUAUCAGCUCCAAACGACAAAGUUGAGGGAUAUAUCAAACCCU	229	spiLA1589-miR6160-3p	GCAUAUAUGAGCCACUUUUAUAAC	156-179	nta-miR6160	5	0	24	24	1
spiLA1589-MIR11085-3	UAUUUUGUCUUUCAUCCUUGAUAAUUCCCUCUCUUUCUCCUCUUAUGUUGUUGGCUUAACCGGCUCUAAACCCUUCCACCGGAUAAAGAAAUGGAAUUUCAAGUACAAGUAGUCGUCUACACUUAAAAGCUUUCUUGUCUUCACUAAUCAACAUUUAGUUUGGCCUAAGAUUUUCUAAGUCCGAUGCAUCACUUACAUUUUUUUCUCAUUCUCCGUUGUUGGUGCCUCUCCAAAAAGAAAGUUGAAUGGAGAAUGAAAAAGAAAAAUGUAAAGAAUAAAUAGAGCGAAUAAUUUAGGAUGAAAGGCGAAAUA	312	spiLA1589-miR11085-3-5p	UUUGUCUUUCAUCCUUGAUA	4-23	lja-miR11085-3p	4	0	20	20	2
			spiLA1589-miR2923-3-3p	AAAGAAAAAUGUAAAGAAUAAA	258-279	osa-miR2923	5	0	22	22	1
spiLA1589-MIR11088b	UUCCAAGUAUCUUGUAUUAUUUUGAGUCAUUUGUAUUGGUGCAAAAUCGGCAGGUUGGGUUGAAAUUGAAAAUAUAAAAAUGGGUUGAAUAGAAAUUGGGUUGGGUUUUGACUCGUCCAACUUUACUUUGGGCAGAAAUGAUCUAAAAAUUGGGUU	211	spiLA1589-miR11088b-3p	AAAUUGGGUUGGGUUUUGACUC	93-114	lja-miR11088b-5p	5	0	22	22	1

spiLA1589-MIR3693c	GGAUUUUAUCCACCCAAUUGAACCCAAUUAAUCUAAAUAAUUUAAUAUAUUGAUACUUCAUUUAAUAUAGACAAACUUUUCUUUAGUUUCUUCAUCUACUUCAAGAAGAUUGAUUUUCUUCCUUUUUCUUUUGUUUUUAGGACAAUCAAGAGACUUGUGUCUGGACUUUCCACAAGUCCAACAUUUGUCUUCGUUAGAUGUGUUGUGAGAAGUUUUCUUACUUCUCUUUCCUUUAAAAUAUCCUUUUUCUAUUGAGGAUCUUCUCUUAGGUGUUGAUUUUCUAGAUCGUUCUUUCUUUGAAACCCUUUUUACAGAAGGGGGUUUUAGACUUGGGAAACGAAAGUCUUGACAGAAACUACAAAGUUCGUUACUUGAAAUGUUU	327	spiLA1589-miR3693c-3p	UGAGGAUCUUCUCUUAGGUGU	198-218	pab-miR3693c	5	0	21	21	1
spiLA1589-MIR5083-2	AUUUCUUUGUACAAGGAUCACAAUUUUCUGAUCUUUCCCUAGCUGAUGAUAACUGGGAACUAGAUAUUGAAGGAUAUUGAUUACUAAUCUAUUUGUAAUACUUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUUCGUGGUCGUGGAGGAAGAAGUAGAGGAAGGGGAAGAUCAUCCUCUUCCAAGUCUAGAAGAUCAUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAACUCAAAGAUUA	274	spiLA1589-miR5083-2-5p	GGAUCACAAUUUUCUGAUCU	15-34	osa-miR5083	5	0	20	20	2
			spiLA1589-miR844-2-3p	UCAUCAUACGAUUCUUCCUUU	208-228	aly-miR844-3p	5	0	21	21	2
spiLA1589-MIR1147	AUUACUAAUCUAUUUGUAAUACUUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUUCGUGGUCGUGGAGGAAGAAGUAGAGGAAGGGGAAGAUCAUCCUCUUCCAAGUCUAGAAGAUCAUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAACUCAAAGAUUAAUGAAGCAUCUUCAUCAGCUUCGUCCUUUGUAAAUUUAAAGGAUAUUCCCAAUGAUAGUUCA	257	spiLA1589-miR1147-5p	CCUCUUCCAAGUCUAGAAGA	109-128	cre-miR1147-2	5	0	20	20	2
			spiLA1589-miR414-3p	GCAUCUUCAUCAGCUUCGUCC	201-221	ath-miR414	4	0	21	21	2
spiLA1589-MIR10532-9	UAAGUGUGGAGAAAAUUACAAUGUUUAUUAUGAUGCAUCUAUGCCGAAAAGGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGCGUCUCUGAGAUUUCGCGCAUAGGUUGAGGGGUACUUGUGCAUUAUCCCUAUAUUUUAUAACAAUUAGGAGUUAUUUUCUAAUAAUUCCCACUAAAUUAAGAGUUUCUUUAGAGUUUUUAGCCUCACACCAUCAUCAAAAACAAAAAUGAUUUACUAUCACACAAA	279	spiLA1589-miR10532-9-5p	AAGUGCGUCUCUGAGAUUUCGCGC	109-132	sly-miR10532	2	0	24	24	1
spiLA1589-MIR10519-3	UCUAAUGAAGAAUUGCGACUUUUAUCAAAAGUUGUGACUUUAAUGAAGAGUUGCGACUUUUAUCAACAAUUGUGUUUUUUGUCAAAAGUUGGGACUUUAAUGAAGAGUUGCGACUUUAUGAAAAGUUGCGACUUUUAUGAAAGGUUAUGAACAUUCCGAAGGGUUGUAACUUUUUCAAAUAGUUGUAGCCUUUCUGAUAAGGCACAGUAAAGAUUUGUUCACACUACCCUUUGUUUUCUAUAAAUAGUGGAUUUCCUCUCAUUUUA	266	spiLA1589-miR10519-3-5p	UGUCAAAAGUUGGGACUU	80-97	tae-miR10519	3	0	18	18	1
			spiLA1589-miR10214a-3-3p	UAUAAAUAGUGGAUUUCCUCU	239-259	eun-miR10214a-3p	5	0	21	21	1
spiLA1589-MIR395b-1	GAUGCCCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCACUCUGAAAUUUUAUGCAAAUUAAACCAAUAGAAGUGUUGGAGUGCUGGUUGUGGAUGAUAAACAUGAUAGUUCACGUAUAAAUCUAUCGAGGUGUUCCGUAGAGUUUCCUUGAACACUUCAUGAGGGCUUA	170	spiLA1589-miR395b-1-5p	CUGAAGUGUUUGGGGGAACUCC	10-31	sly-miR395b	0	0	22	22	1
spiLA1589-MIR395b-2	GAUGCCCUGCUGAAGUGUUUGGGGGAACUCCUGGGCUCACUCUGAAAUUUUAUGCAAAUUAAACCAAUAGAAGUGUUGGAGUGCUGGUUGUGGAUGAUAAACAUGAUAGUUCACGUAGAAAUCUAUCAAGGUGUUCCCUAGAGUUUCCUUGACCACUUCAUGAGGGCUUA	170	spiLA1589-miR395b-2-5p	CUGAAGUGUUUGGGGGAACUCC	10-31	sly-miR395b	0	0	22	22	1
spiLA1589-MIR395j-3	AGAAAUCUAUCAAGGUGUUCCCUAGAGUUUCCUUGACCACUUCAUGAGGGCUUACUUUGAUGUUAGAAGCCUUGUUGAAGUGUUUGAGGGAACUCCUGGGUUGACAUUGAAAAUUACG	118	spiLA1589-miR395j-3-5p	GUUUCCUUGACCACUUCAUGA	27-47	mdm-miR395j	3	0	21	21	1
			spiLA1589-miR395c-3-3p	UUGAAGUGUUUGAGGGAACUC	75-95	cme-miR395c	1	0	21	21	1
spiLA1589-MIR395c	UUGAAGUGUUUGAGGGAACUCCUGGGUUGACAUUGAAAAUUACGCAAACAAGUAUAUAUAAAUGCAUGAUGAGUACGUAUUAGCUAGAGAUGAUGAAUACAAUAUUGAUUCACGUAUAA	151	spiLA1589-miR395c-5p	UUGAAGUGUUUGAGGGAACUC	1-21	cme-miR395c	1	0	21	21	1

	AACUACCUCUGGAGUUUCCUUGACCACUUUAU										
spiLA1589-MIR7997c-46	AAAAUCUAUGUUGCUUGGACUCUCCAAUAAUGUUGGCCCACCCGUGUAAGAUCCUUCAAAAAUGUACUGACUUUAAAGGAUCUGAUAUACACCUAGCGACAUUUUUGAAGAGUCCGAGCAACAUAGAUCCA	131	spiLA1589-miR7997c-46-5p	AUGUUGCUUGGACUCUCCAAUAAU	8-31	stu-miR7997c	4	0	24	24	1
			spiLA1589-miR5303h-46-3p	GACAUUUUUGAAGAGUCCGAGCAA	98-121	stu-miR5303h	2	0	24	24	2
spiLA1589-MIR8124	UUCUAUAGUUCUUAAAUCUUUUAUCACAAGUUUUGACUUGGUUUCGAGGUGGAGGUACAAUUUGAUAAUACAUUGUUAAUGGUAGCGAGCAUGUGGUAUUGUAAGUCCCCGUUAAUUGUUGAAGAAAGGGGCAGCCUGAAACCCAUGUUAGAAUUGCUAUACAUUAAUAUGUUUAUUAUUAUGAUAGGCCUCAUGCUUGAGUAAAAGUUUACCAUGUAGCCGAAACUUAGGAUAAAAUUUUUAUAAACUAUAAUA	255	spiLA1589-miR8124-5p	ACUUGGUUUCGAGGUGGAGGU	36-56	ppe-miR8124-5p	5	0	21	21	1
			spiLA1589-miR3981-3p	AUUAUUAUGAUAGGCCUCAUG	175-195	osa-miR3981-3p	5	0	21	21	1
spiLA1589-MIR7997b-12	AGUUAAGUUGCUCAGACUCUUCAAAACUGUUACCAUACCUGUGUCGGAUCCUUCAAAAAUACACUGUUUUGGAGGAUCCAACACGUACCCAUCAAUAUUUUUGAAGAGUUCGAGCAACAUAGCC	124	spiLA1589-miR7997b-12-5p	AAGUUGCUCAGACUCUUCAAA	5-25	stu-miR7997b	3	0	21	21	1
			spiLA1589-miR5303-12-3p	UUUUUGAAGAGUUCGAGCAAC	98-118	sly-miR5303	0	0	21	21	1
spiLA1589-MIR6430	UUUUUGUACUGUGUCAAUGUACAUAGUUAUGGUAUGCCUGGCUAAGAUGAUAAGUAAAUGACUGAACAUCAUUUUCAUGCCUAUUAAUUUUAUAUAGGCAUAGUGCAUAAACAAACGAACUUGGCCUCAGCUGGCGAGUAAGCACUCCAACUUUGAGAGUGCACAUCUAGAUACCUUAACUUGGUCUCAUUGGCAACUAAAUCC	204	spiLA1589-miR6430-5p	UGAUAAGUAAAUGACUGAACA	48-68	ptc-miR6430	5	0	21	21	1
			spiLA1589-miR7992-3p	UUUGAGAGUGCACAUCUAGAUACC	152-175	stu-miR7992-5p	4	0	24	24	1
spiLA1589-MIR2597	UUCCAAGUUAAUAUAUGCUUUCUUUCGGAGCAAAUUUUGGUACUCCCUCCGUUUUAAAAAGAUUGGCUAGUUUGACUUGAAACGGAGUUUAAGAAAAGAAAGAAAUAUUUUAAUCUUGUGG	121	spiLA1589-miR2597-5p	UUUGGUACUCCCUCCGUUUUA	36-56	mtr-miR2597	5	0	21	21	1
			spiLA1589-miR5174d-3p	UCCCUCCGUUUUAAAAAGAUUGGC	44-67	bdi-miR5174d-5p	2	0	24	24	1
spiLA1589-MIR8639e	ACGUUUAUGUCAUCCAAUUUUGGAUAUGCACAAGUAGAAUAAAACAAGUAAACACACGAGUCCUAUAUGACACAAUAUUUAUAAGACAAAAAAUGACAUGAGGACAUGUGUGUCUAUUUGUUUAACUUUAUACAAGUCAACUUGUGCACACCCAAAGUUGAAUGAUAUGAAUUU	174	spiLA1589-miR8639e-5p	UAUGCACAAGUAGAAUAAAACAAG	25-48	gra-miR8639e	4	0	24	24	1
			spiLA1589-miR7982b-3p	AAGUUGAAUGAUAUGAAUUU	155-174	stu-miR7982b	4	0	20	24	1
spiLA1589-MIR7492f-3	ACUGAUACUACACUUGCUAUGUCUUUCACUAUAACAAAAAUGACCAUUAGCGGCAUUUAGUUCUUAAUUGCCGCUAAAAUAUGUAUUUUUAGUGUCAAUUGUUACUCUUUGUAUAUGUCCCUAAAGCCUUUAGCGACAUUGGUUCUAAUGACACUUAACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAGAGUUAAUAUUUAAUGCCGCUAAAAGUUAUUUUUUGUUGUAGUAUUUUGACAUAGUCUGUAUGUAGUUUCUCU	264	spiLA1589-miR7492f-3-5p	AAAUGACCAUUAGCGGCAUUU	38-58	gra-miR7492f	5	0	21	21	3
			spiLA1589-miR7983-3-3p	ACUAAUGCCGGUAAAGACUUUAGC	157-180	stu-miR7983-3p	1	0	24	24	1
spiLA1589-MIR5218	UGAUUACUUCCGGUUCUUCCCAUAGCUUGUCAAUACUAUUUUGAUUAGUUCACAUUUAAAAUGAAUAAAGAGCCUCGAAUGCACCAAACAAUGCUGUAAGACAUGGGAAGAAACAUUAACAAAACUUGACUUCGUCCGAAUAUUGACAAGCGAUGGGAAGAAUUGGAAGUAAGUU	175	spiLA1589-miR5218-3p	GAAGAAUUGGAAGUAAGUU	157-175	mtr-miR5218	5	0	19	22	3
spiLA1589-MIR7983-7	CUAAAGCAUUUAGCGACAUUGAUUCUGAUGACACUUAAUUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAAUGUCACAUAUUUAAUGCCGCUAAAAGUUAUU	104	spiLA1589-miR7983-7-5p	UAAAGCAUUUAGCGACAUUGAUUC	2-25	stu-miR7983-5p	3	0	24	24	1
			spiLA1589-miR7983-7-3p	AUUAAUGCCGGUAAAGACUUUAGC	38-61	stu-miR7983-3p	2	0	24	24	1
spiLA1589-MIR1044-3	GACCUUCAACUUUCGUAAUGCACAAACAUGCACUUUAACUAUCCAACUUUUAAAUAAACAAACACACGAGUCCUACAUGGCACAAUACACAUAGAACACCAGAUAGGAGAAAAAAAUGAC	198	spiLA1589-miR1044-3-5p	GCACAAACAUGCACUUUAACU	20-40	ppt-miR1044-5p	5	0	21	21	1

	AUAUAGGACAUGUGUGUCUAUUUGUUCAACUUUAUACAA AUUUAAGUGUCUACUUGUGCAAACCCAAAGUUGAAGGUC		spiLA1589-miR5014a-3-3p	UUAUACAAAUUUAAGUGUCUA	152-172	ath-miR5014a-3p	4	0	21	21	1
spiLA1589-MIR8006-11	UUUGGGACAUUGGUGCCCCAACAGUCUAAAAAUUAGAGC GUAUAUUCCCUUCACUCAUACGGAAGACUAAAUAGAAAUA CGUGACGCAAUCUUAUCCAUCGAGUCAAUCUUAUCCAUG AGUCUGAUGUCGACUCGAUGGAUAAGAUUAUGACACGUG UAUGUCUGUUAGUAUGAAGGGUAUAUAUACUUUAGUUUU UGAACGACAGAGAUACCAAUAUCCCUAA	224	spiLA1589-miR8006-11-3p	UAGUUUUUGAACGACAGAGAUACC	190-213	stu-miR8006-5p	4	0	24	24	1
spiLA1589-MIR169l	AACAACAACAGCUGUUUCAUAAAAAAUCUGGCAUGAGAAA AUGAGGCAGAUAUGUAGCCAAAAAUGACUUGCCAGACAU GAAGCAGAAUUGAUCGAGCUUGCCGGCAAGUCAUCCUUG GCUGCAAUUCAAUAACCUUGUUCCCUCAUGCAAGACUUU AACAUGAAUAAAGACAUGUCUAUUCAA	184	spiLA1589-miR169l-5p	UAGCCAAAAAUGACUUGCCAGA	55-76	cme-miR169l	2	0	22	22	1
			spiLA1589-miR169s-3p	CGGCAAGUCAUCCUUGGCUGC	103-123	gma-miR169s-3p	2	0	21	21	1
spiLA1589-MIR2873b	UUUAGAUGAGACAUCAACACUAGGGGUGUACAAAAUCGA ACCGAAAAUCGAAUCAAAUCGCAACUCGAGUCAUAAAAAA AAUUCGACUAGUGAUUUGGUUUGACUUGGUUUGGUGUU GGAAAAAAAAUCCGACUAUAUUUGGGUUGGCGUUAACUA UAAAGCCCAGAAGGCAUAAACGUAUCAAGUUUUGUUAUUA ACCAUUAGUGUAAGUUUCAUCUUCU	221	spiLA1589-miR2873b-5p	UUCGACUAGUGAUUUGGUUUG	82-102	osa-miR2873b	4	0	21	21	1
			spiLA1589-miR2868-3p	UUGGUUUGGUGUUGGAAAAA	105-124	osa-miR2868	4	0	20	20	1
spiLA1589-MIR1521b-2	UAUUUUAGGGACAUUGAUAUCCCUGCUGUCCAAAACUAG AAUAUAUAUACCCUUUAUAUUAACAGACAUACACGUGUCA UAAUUUUAUCCACCGACCUGGCUCUGAUAGAUGAAUAAC AUUGUGUCACGUGUUCCUAUUUAGUUUUCUAUUAGACUG AAGAGUAUAUACGUUCUAGUUUUUGGACGACGGGGGCAU CAAUGUUCGUAAAGUA	212	spiLA1589-miR1521b-2-5p	GACAUACACGUGUCAUAAUUUUA	65-87	gma-miR1521b	5	0	23	23	1
			spiLA1589-miR8006-2-3p	UAGUUUUUGGACGACGGGGGCAUC	174-197	stu-miR8006-5p	2	0	24	24	1
spiLA1589-MIR172a-3	UACAGUCGUUGUUUGCAUAUGUGGCAUAAUCAAGAUUCA CGUGAAAAGUUGCAAAUUGGUUAUAUAAUUGAUGAAAUUA AUGGCUGGCUAUUUGAAACUCACGAGAAUCUUGAUGAUG CUGCAUCAGCAAUAAACGACUAUU	142	spiLA1589-miR172a-3-5p	GUGGCAUAAUCAAGAUUCACG	21-41	cas-miR172a-5p	2	0	21	21	1
			spiLA1589-miR172-3-3p	CGAGAAUCUUGAUGAUGCUGCAU	102-124	aau-miR172	1	0	23	23	2
spiLA1589-MIR7997c-47	GCCUAUAUUGCUCCGACUCUUCAAAAAUACCAACAGAUAU AUGUCGGAUCCUCAAAAAGCUAUCUUUUUUUAAGAGGAU UCGAUAUGUGUGCAACAUUUUUGGAGGGUCCGAGCAACA UACUA	123	spiLA1589-miR7997c-47-5p	AUAUUGCUCCGACUCUUCAAAAAU	5-28	stu-miR7997c	1	0	24	24	1
			spiLA1589-miR5303h-47-3p	AACAUUUUUGGAGGGUCCGAGCAA	93-116	stu-miR5303h	3	0	24	24	1
spiLA1589-MIR11583b-2	CGAGAUCUGAGACAGUGAAGAGCGAGAUCUGGGAGAGAG GAGAGCGAAAAUAUAUGUAUAUAUACAAUUUUCUCUCGCU UUAUACAAAAACAAACACAUUUUAUACAUUUGUGUUUGUA UAAAAUUCAAGUUUAUGUGGAUGACAUAAUUUUUGGAGC UACUUCAGAACAUUUGUGUGAAGAAUUCUCAUCACUGAU GGGAAAGGAGUUUGAAAUGAGCAUGAUGGGUGAACUAUC GUUCUUCCUGGGUCUGCAAAUCGAG	261	spiLA1589-miR11583b-2-5p	UUUUCUCUCGCUUUAUACAAA	68-88	pab-miR11583b	5	0	21	21	1
spiLA1589-MIR6144	CCGCAACUCUAGUAAGUCUUCAUCACAUCAGAUUUGAGG GUGAGCUAAAGCUUAUAGCUUGGAUUGGAUCUUCUUCUU CAUGUCUUGAUGCCUUGAAGUUCUGGCAUAGACUAGCUA UUACUUAUGUUUAGUUUCUUAGAUACUCUUGGCUCUAGU AAUUUGAGGAUAGAUGUUCUUGUGAUGAUGACUUCCAGA UUUGUCU	202	spiLA1589-miR6144-5p	UUGGAUCUUCUUCUUCAUGUC	64-84	nta-miR6144	5	0	21	21	1
			spiLA1589-miR5650-3p	AUGUUUAGUUUCUUAGAUACU	124-144	ath-miR5650	5	0	21	21	2
spiLA1589-MIR5026-5	CUGCCCCUUUCAACCUACAUGGCACAAACUUCAAAAAAAA AGUCAACCAGCGUUGGGCCCAUAAUAUAGUGCCACGUAG GCCAAAAAGGGGUAG	94	spiLA1589-miR5026-5-3p	GCCCAUAAUAUAGUGCCACGU	57-77	ath-miR5026	5	0	21	21	2
spiLA1589-MIR2607-3	UGGACAUACCCAUUUAAGGGAAAAUUACAUGGGAUGUCA AACAUCCCCAUGUAAUUAGUUAAUAAGGGUAUAGUUUA	77	spiLA1589-miR2607-3-3p	AUGUAAUUAGUUAAUAAGGGU	49-69	mtr-miR2607	5	0	21	21	1

spiLA1589-MIR7997c-48	AAGCUAUGUUGCUCGGACUCUUCAAAAAUGUCGGUGGUAGUGCAUUUUUUUGGAGGAUCCGAUAAGGGUGCUGCAACAUUUUUAAAGAGUUCGAGCAACAUAGAUA	106	spiLA1589-miR7997c-48-5p	AUGUUGCUCGGACUCUUCAAAAAU	6-29	stu-miR7997c	1	0	24	24	1
			spiLA1589-miR5303-48-3p	UUUUUAAAGAGUUCGAGCAAC	79-99	sly-miR5303	1	0	21	21	1
spiLA1589-MIR10532-10	GAUAAAAUAUAGUGUGUCUCUGAUAUUUCGGGCAUAGGUUGAGGGGGUACUUGUGCAUUAUCCCAAUAUUCAACAAAGAAUACUAUAUUUUUUU	94	spiLA1589-miR10532-10-5p	UAGUGUGUCUCUGAUAUUUCGGGC	10-33	sly-miR10532	2	0	24	24	2
			spiLA1589-miR5543-10-3p	AAAGAAUACUAUAUUUUUUU	75-94	osa-miR5543	5	0	20	21	2
spiLA1589-MIR6232b-2	AACUAUCGCAAAUGGUACGCAUAUACCCUUCGUUAUAUUUUUGGGAUAUUGGUCCAAAAACUAGAGUUUAUAUAUGCCCUUGGUUCUAAAGGAAGACUAAAUAGAGACACAUACGCAAUCUUAUAAUGUCGAGUCGGUAGAUAAGAUUAUGACUACGUGUGUGUAUGUGCGUUAGUAUAAAGGGUAUAUAUGAUCUAGUUUUGAACAACAAGAAGUUCAAUGUCCCAAAAAUAUGACGGAGAAUAUCUGUAUACCAUAUACGAUAUCA	269	spiLA1589-miR6232b-2-3p	AGUUCAAUGUCCCAAAAAUAU	215-235	sbi-miR6232b-3p	5	0	21	21	1
spiLA1589-MIR11036	CCACACUACAAGAAAAGUAUGAAUUACAUUGAGAUUUUCCUGAAAAUCAGGAUGAAUUUUUGCAGGAAAAUAAGUUUCCUACGUAUUUUCAUACUAAUCUUAGGAAAAUCCCAUGUAAUUCACAGUUUUCUUGUAGUGCCA	141	spiLA1589-miR11036-5p	UUUUCCUGAAAAUCAGGAUGAA	35-56	seu-miR11036	5	0	22	22	1
			spiLA1589-miR396b-3p	AUUCACAGUUUUCUUGUAGUG	118-138	aof-miR396b	5	0	21	21	2
spiLA1589-MIR7822-4	GUCCUCCAACUUUGGGUAUGCACAAAUACACUUAGUUUAAAUUGAACAAGUAGACACAUGAGUCCUAUGUGGCAUGAUACAUGUAGGAAAUCACAUAGGACACAAAUUGAUAUGUAGGAUGCCGCGUGGUACGUGUGUUUUUUAAGCGCCCAUUUUUGCACUUCCAAAGUUGGAGGGU	179	spiLA1589-miR7822-4-5p	UUUAAAAUUGAACAAGUAGAC	36-56	ptc-miR7822	5	0	21	21	1
			spiLA1589-miR9386-4-3p	UUUGCACUUCCAAAGUUGGAGG	156-177	mes-miR9386	5	0	22	22	1
spiLA1589-MIR172d-5	UUAACUUAAUGGGCUAAAUCUAAAUGAUUCAGAUUCAUACCUAAUAACCAAACGUACUUAAUAGGAUGAAUCUAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCG	105	spiLA1589-miR172d-5-5p	GCUAAAUCUAAAUGAUUCAGA	13-33	cas-miR172d	5	0	21	21	1
spiLA1589-MIR10540-3	AAUAGAGUUGAUUUCUCGGAUGGUCACUUGUUUUAGAAAGUCACUUUCUUUGUUGAAGAAAAUUUGAAUCAGAAGAAAUGUGAUUUUCUAAGAUAAUAACUAUUAGUUGAGUGACCAUCUGAGAAAUCAACCCUCAC	137	spiLA1589-miR10540-3-3p	AUAAUAACUAUUAGUUGAGUG	93-113	sly-miR10540	1	0	21	21	1
spiLA1589-MIR7987-3	AGUACCAACACUAGUUGAUCCUAUUGAUGACCAAAUUGAUUUUCUUUUGAAAAUCAAUUUGUGUCCAUCUAGUGUUGACACUUAGCUUUAAAUUUUAGAAAUAAUUAUUUGUUAAAUUUGUAACUAUCGUGUUAGUAUUAAGGUAAAACUAAACUACAUAAGCUGAGGUGCACAUGUCAAAGGAGGGACCAGGGCCAACACAUUGGUCCCAGAAAAGAUCAGUUGGGGUGAAAAAGAAAGGUCUAAUAUAAGCUUAGAUCAUUUGGAUCAAACGAGGAUAAAUUUCAUUUGGUUUU	296	spiLA1589-miR7987-3-5p	ACACUAGUUGAUCCUAUUGAUGAC	8-31	stu-miR7987	1	0	24	24	1
spiLA1589-MIR2678	ACCAAACGACGACAAGGAUUGACGAUCCGUAGUCUGACCUAUAGACCGUUAGUCCGUCUGUCAUCAAAGACUUAACCAAUUUUUCUGAGGAGUCUUGAUCAGCGGUCACGAACUACGGACUCGUCUUACCCAUGAACUGUAAAUCUGUCCGUCGUCCAAGAUUUAACCAACUUUUCUGGGCUGAAAUUUAUGUGAGUUUCUGAUCCCAUGGACAGUUGUGCAGGACGGACCGUGGGUCAGGCUACGGUCCGUCGAUGCUCAUCUGUGGAUCUUUCAU	277	spiLA1589-miR2678-3p	UGAAAUUUAUGUGAGUUUCUG	182-202	mtr-miR2678	5	0	21	21	1
spiLA1589-MIR7981a-68	CCCCUAAUACUAAGGUCCUAUUAUCCUCGUGAACUUAUUUUAUUAAUAAUUUUUUCUACCCCUUUUCGGCCUACGUGGCCCUAUCUUGUGGGUUCAACGCUGGUUAACUCUUUUUUCAAGUUAGUCCCACGUAGGUCAAAAAGGGGUAGAAAAUUACUUAUUCUUUCAGGGGGUAAUAGGACCUUAGUAUAGUAU	195	spiLA1589-miR7981a-68-5p	ACCCCUUUUCGGCCUACGUGGCCC	58-81	sly-miR7981a	1	0	24	24	1
			spiLA1589-miR7981-68-3p	AUAGGACCUUAGUAUAGUAU	176-195	stu-miR7981-3p	4	0	20	24	1
spiLA1589-MIR1309	GAUGGUGUAUAUUUCUACUUAUUUAAUAUCCUAUUUGAAGGACAUGAGUAUCAGUUGAUGACAAAUCAUCACUACGUUUAAUACAUAAACAUGCUUCUUAACUUAAUAUUCAUAUCCUAUCUGGCAUCCUACGUGACCAUUCUAUGUCAUGGAGACAUAUUAUGUCACGUAGGACGAUGUGUAUUUCUACUUACUUAAUAUCCUAUUUUGAAGGACAUGAAUAUCAGUUGACGACA	293	spiLA1589-miR1309-5p	UAAUAUCCUAUUUGAAGGACA	24-44	pta-miR1309	5	0	21	21	1

	AAUCAUGUAUUUGUAGGAGGAACAAGAGGAUAUUGUAAA GAGAAGAUCAUCACCAAA									
			spiLA1589-miR1518-3p	GAUAUUGUAAAGAGAAGAUCA	265-285	gma-miR1518	5	0	21	21	3
spiLA1589-MIR159-4	GUUUGCACUUAAUGGAGGUCUGAAUCUUAAUCGUUCAGA UUCAGUCCAUCAAGUAUGUUAUGUUUUUAUGACUGAAUC UCAAUAAUUUAGUUCAGCCCAUUAAGUCCAUUU	111	spiLA1589-miR159-4-5p	UUUGCACUUAAUGGAGGUCUG	2-22	aqc-miR159	5	0	21	21	1
spiLA1589-MIR6267a	UUGAAGAAACAUAAUUUUAUUGAUUAAGAUAGCGGGUACA AUUCUGUUGAUCCCUUGAUUCUACUCUCUUCGGAUUUAU CCAUGAUUCGAGAGACGCUAGUAGCGUAUUUCUCGAACU AGGAUGAUUUAGAUUUGAUCUUUCUAUGUGAAUAAUCCA UCAAUUUGUGGAGUAUUCGAGAUCUUGAUGUCUUUAAGA AAUUUUUGAGAUGCCUUUUAAGAGAAUUUAGUACCCUUU AUAUAGGCAUAAAUUAGAUUUUUAUG	261	spiLA1589-miR6267a-5p	AAGAUAGCGGGUACAAUUCUG	26-46	ppe-miR6267a	5	0	21	21	2
			spiLA1589-miR9760-3p	AGGAUGAUUUAGAUUUGAUCU	119-139	gma-miR9760	5	0	21	21	2

Supplementary Table S14. Thermodynamic and structural characterization of *Solanum lycopersicum* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Size	G content	A content	C content	U content	GC content	AU content	UA-ratio	GC-ratio	MFE	MFEE	Freq	Div	AMFE	MFEI
sly-MIR10186e	244	19,262295	34,42623	14,344262	31,967213	33,606557	66,393443	0,9285714	1,3428571	-64,9	-62,1	0,0010587	21,28	-26,598361	-0,7914634
sly-MIR10189	112	24,107143	33,928571	14,285714	27,678571	38,392857	61,607143	0,8157895	1,6875	-35,6	-24,35	0,0101989	32,96	-31,785714	-0,7172043
sly-MIR10195	86	24,418605	19,767442	17,44186	38,372093	41,860465	58,139535	1,9411765	1,4	-33,1	-31,6	0,0795009	11,49	-38,488372	-0,7708333
sly-MIR10204	165	23,030303	25,454545	12,727273	38,787879	35,757576	64,242424	1,5238095	1,8095238	-62,3	-58,3	0,0091627	17,55	-37,757576	-1,1057692
sly-MIR10211a	83	20,481928	26,506024	21,686747	31,325301	42,168675	57,831325	1,1818182	0,9444444	-28,3	-28,1	0,107074	6,12	-34,096386	-0,8085714
sly-MIR10215-1	326	18,711656	36,196319	14,723926	30,368098	33,435583	66,564417	0,8389831	1,2708333	-89,8	-89,7	8,44E-05	36,82	-27,546012	-0,8263158
sly-MIR10215-2	66	22,727273	36,363636	12,121212	28,787879	34,848485	65,151515	0,7916667	1,875	-33,2	-33,2	0,34445	1,69	-50,30303	-1,0632911
sly-MIR10216	81	22,222222	30,864198	14,814815	32,098765	37,037037	62,962963	1,04	1,5	-32,5	-32,5	0,420238	2,16	-40,123457	-1,1983607
sly-MIR1023e	217	19,354839	30,414747	17,050691	33,179724	36,40553	63,59447	1,0909091	1,1351351	-56,7	-49,5	0,0057313	43,1	-26,129032	-1,2230769
sly-MIR1032	231	25,541126	22,943723	15,584416	35,930736	41,125541	58,874459	1,5660377	1,6388889	-72,7	-62,2	0,0002923	47,11	-31,471861	-0,7173228
sly-MIR10405d	191	17,277487	30,366492	15,183246	37,172775	32,460733	67,539267	1,2241379	1,137931	-84,8	-82,1	0,0113113	21,5	-44,397906	-1,3677419
sly-MIR10419	103	15,533981	38,834951	15,533981	30,097087	31,067961	68,932039	0,775	1	-23,1	-22,8	0,0920933	11,03	-22,427184	-1,0645833
sly-MIR10420-1	113	21,238938	24,778761	21,238938	32,743363	42,477876	57,522124	1,3214286	1	-35,3	-22,51	0,106681	16,59	-31,238938	-0,9783505
sly-MIR10420-2	139	17,266187	33,093525	16,546763	33,093525	33,81295	66,18705	1	1,0434783	-41,5	-37,3	0,0133714	22,4	-29,856115	-0,9878788
sly-MIR10424d	229	14,847162	32,751092	18,777293	33,624454	33,624454	66,375546	1,0266667	0,7906977	-54,4	-50,3	0,0137052	38,14	-23,755459	-0,9795181
sly-MIR10430	83	26,506024	25,301205	26,506024	21,686747	53,012048	46,987952	0,8571429	1	-36,6	-36,6	0,280684	2,52	-44,096386	-0,7053191
sly-MIR1043-1	255	17,647059	30,588235	15,294118	36,470588	32,941176	67,058824	1,1923077	1,1538462	-86,5	-85,2	0,0020511	30,76	-33,921569	-1,15
sly-MIR1043-2	195	17,948718	29,230769	15,897436	36,923077	33,846154	66,153846	1,2631579	1,1290323	-57,7	-55,45	0,0042551	21,82	-29,589744	-1,0414286
sly-MIR1043-3	296	19,932432	32,77027	15,878378	31,418919	35,810811	64,189189	0,9587629	1,2553191	-76,5	-69,2	0,000236	52,44	-25,844595	-1,06
sly-MIR1043-4	251	18,7251	29,880478	15,139442	36,25498	33,864542	66,135458	1,2133333	1,2368421	-80,4	-68,22	0,0003558	39,67	-32,031873	-1,3
sly-MIR1044-1	227	19,823789	31,718062	15,418502	33,039648	35,242291	64,757709	1,0416667	1,2857143	-84	-83,5	0,0550654	8,01	-37,004405	-1,0771429
sly-MIR1044-2	238	17,647059	31,932773	16,386555	34,033613	34,033613	65,966387	1,0657895	1,0769231	-88,8	-88,2	0,0128099	11,97	-37,310924	-0,9382353
sly-MIR1046-1	141	17,730496	32,624113	14,893617	34,751773	32,624113	67,375887	1,0652174	1,1904762	-68,5	-66,1	0,111212	3,27	-48,58156	-1,03
sly-MIR1046-2	327	23,24159	29,051988	15,902141	31,804281	39,143731	60,856269	1,0947368	1,4615385	-92,8	-88	0,0002837	47,05	-28,379205	-1,0357143
sly-MIR10528	97	18,556701	35,051546	16,494845	29,896907	35,051546	64,948454	0,8529412	1,125	-41,2	-41,2	0,0573338	6,74	-42,474227	-1,2117647
sly-MIR10529	134	23,880597	26,119403	23,134328	26,865672	47,014925	52,985075	1,0285714	1,0322581	-46,4	-46,4	0,165106	9,05	-34,626866	-0,7365079
sly-MIR1053	125	18,4	25,6	20,8	35,2	39,2	60,8	1,375	0,8846154	-40,3	-37,3	0,0068566	12,13	-32,24	-0,7545455
sly-MIR10530	152	23,026316	24,342105	23,026316	29,605263	46,052632	53,947368	1,2162162	1	-70,7	-68,8	0,049442	6,74	-46,513158	-0,7632813
sly-MIR10531	123	21,138211	29,268293	17,073171	32,520325	38,211382	61,788618	1,1111111	1,2380952	-64,7	-64,7	0,282752	4,41	-52,601626	-1,3765957
sly-MIR10532-1	246	19,105691	30,081301	15,853659	34,95935	34,95935	65,04065	1,1621622	1,2051282	-99,3	-97,5	0,0060984	15,13	-40,365854	-1,1546512
sly-MIR10532-10	174	18,390805	37,356322	12,068966	32,183908	30,45977	69,54023	0,8615385	1,5238095	-37,6	-28,9	0,0079023	32,08	-21,609195	-0,8761905
sly-MIR10532-11	278	15,467626	30,935252	18,705036	34,892086	34,172662	65,827338	1,127907	0,8269231	-79,5	-70,99	1,81E-05	36,29	-28,597122	-0,7523077
sly-MIR10532-12	161	18,63354	31,055901	13,043478	37,267081	31,677019	68,322981	1,2	1,4285714	-36,1	-34,4	0,0588077	39,07	-22,42236	-0,945098
sly-	148	22,972973	30,405405	10,135135	36,486486	33,108108	66,891892	1,2	2,2666667	-35,9	-35,3	0,0269522	19,9	-24,256757	-1,026087

MIR10532-13															
sly-MIR10532-14	246	18,699187	33,333333	17,073171	30,894309	35,772358	64,227642	0,9268293	1,0952381	-73,1	-53,96	0,0005022	61,55	-29,715447	-0,9462963
sly-MIR10532-15	252	15,873016	34,126984	16,269841	33,730159	32,142857	67,857143	0,9883721	0,9756098	-88,2	-80,5	0,0002308	45,56	-35	-0,9262136
sly-MIR10532-16	160	22,5	28,75	18,125	30,625	40,625	59,375	1,0652174	1,2413793	-95,3	-95,3	0,27076	10,48	-59,5625	-0,8325581
sly-MIR10532-17	223	21,973094	30,941704	10,762332	36,32287	32,735426	67,264574	1,173913	2,0416667	-54,1	-26	0,000768	67,21	-24,26009	-0,7095588
sly-MIR10532-18	176	21,590909	30,113636	10,227273	38,068182	31,818182	68,181818	1,2641509	2,1111111	-42,9	-38,7	0,0035541	26,14	-24,375	-0,7652632
sly-MIR10532-2	253	17,391304	33,596838	16,600791	32,411067	33,992095	66,007905	0,9647059	1,047619	-92,3	-87,9	0,0048474	14,82	-36,482213	-1,0732558
sly-MIR10532-3	189	19,047619	30,687831	15,873016	34,391534	34,920635	65,079365	1,1206897	1,2	-51,1	-51,1	0,0286038	19,72	-27,037037	-0,7742424
sly-MIR10532-4	191	21,465969	37,172775	17,277487	24,08377	38,743455	61,256545	0,6478873	1,2424242	-70,1	-69,8	0,010814	19,23	-36,701571	-1,0857143
sly-MIR10532-5	282	19,148936	35,815603	13,829787	31,205674	32,978723	67,021277	0,8712871	1,3846154	-67,5	-54,5	0,0004404	43,13	-23,93617	-0,7122449
sly-MIR10532-6	207	18,84058	34,782609	15,942029	30,434783	34,782609	65,217391	0,875	1,1818182	-55,9	-44,37	0,0013106	32,26	-27,004831	-0,925
sly-MIR10532-7	111	19,81982	28,828829	12,612613	38,738739	32,432432	67,567568	1,34375	1,5714286	-29,3	-29,3	0,0246203	10,15	-26,396396	-1,7575
sly-MIR10532-8	221	19,004525	34,38914	17,19457	29,411765	36,199095	63,800905	0,8552632	1,1052632	-93,8	-89,3	0,0035424	25,54	-42,443439	-0,8227273
sly-MIR10532-9	195	17,948718	33,846154	19,487179	28,717949	37,435897	62,564103	0,8484848	0,9210526	-82,4	-80,4	0,0121632	11,84	-42,25641	-0,89
sly-MIR10534	104	20,192308	28,846154	18,269231	32,692308	38,461538	61,538462	1,1333333	1,1052632	-59,2	-58,3	0,0919056	4,92	-56,923077	-1,48
sly-MIR10535a	119	18,487395	30,252101	15,12605	36,134454	33,613445	66,386555	1,1944444	1,2222222	-61,9	-60,6	0,0601894	5,46	-52,016807	-1,5475
sly-MIR10535b-1	119	20,168067	28,571429	15,12605	36,134454	35,294118	64,705882	1,2647059	1,3333333	-67	-65,7	0,0667144	5,24	-56,302521	-1,5952381
sly-MIR10535b-2	119	19,327731	29,411765	15,966387	35,294118	35,294118	64,705882	1,2	1,2105263	-63,5	-62,2	0,0468733	6,2	-53,361345	-1,5119048
sly-MIR10536-1	126	20,634921	29,365079	19,047619	30,952381	39,68254	60,31746	1,0540541	1,0833333	-59,9	-57,2	0,0965686	8,03	-47,539683	-1,198
sly-MIR10536-2	221	19,004525	32,126697	15,384615	33,484163	34,38914	65,61086	1,0422535	1,2352941	-95,6	-91,2	0,0552799	14,92	-43,257919	-1,9433333
sly-MIR10536-3	85	17,647059	36,470588	18,823529	27,058824	36,470588	63,529412	0,7419355	0,9375	-51,4	-51	0,310221	2,36	-60,470588	-0,7054348
sly-MIR10536-4	276	14,492754	29,710145	18,84058	36,956522	33,333333	66,666667	1,2439024	0,7692308	-76,1	-61,87	0,0008478	44,5	-27,572464	-0,816
sly-MIR10537	237	23,628692	30,801688	18,565401	27,004219	42,194093	57,805907	0,8767123	1,2727273	-77,5	-76,2	0,0075891	26,6	-32,700422	-0,775
sly-MIR10538-1	150	16	32,666667	15,333333	36	31,333333	68,666667	1,1020408	1,0434783	-80,4	-80,4	0,291106	7,63	-53,6	-1,3769231
sly-MIR10538-10	148	15,540541	33,783784	16,216216	34,459459	31,756757	68,243243	1,02	0,9583333	-76,7	-76,7	0,502924	1,45	-51,824324	-0,8708333
sly-MIR10538-11	150	16,666667	32,666667	14	36,666667	30,666667	69,333333	1,122449	1,1904762	-79,2	-79,2	0,388143	3,12	-52,8	-0,8792208
sly-MIR10538-12	116	15,517241	37,931034	16,37931	30,172414	31,896552	68,103448	0,7954545	0,9473684	-37,1	-36,1	0,141019	10,85	-31,982759	-0,8857143
sly-MIR10538-2	162	15,432099	35,185185	14,814815	34,567901	30,246914	69,753086	0,9824561	1,0416667	-49,3	-48,4	0,0175848	12,05	-30,432099	-1,273913
sly-MIR10538-3	105	17,142857	27,619048	14,285714	40,952381	31,428571	68,571429	1,4827586	1,2	-28,8	-27	0,0506997	14,93	-27,428571	-0,8075269
sly-MIR10538-4	122	17,213115	33,606557	15,57377	33,606557	32,786885	67,213115	1	1,1052632	-64,2	-64,2	0,195366	3,27	-52,622951	-0,7655172
sly-MIR10538-5	141	18,439716	34,751773	12,765957	34,042553	31,205674	68,794326	0,9795918	1,4444444	-59,8	-59,8	0,164495	17,15	-42,411348	-1,2688525
sly-MIR10538-6	148	15,540541	35,135135	16,891892	32,432432	32,432432	67,567568	0,9230769	0,92	-63,8	-58,9	0,098629	38,79	-43,108108	-0,9490566
sly-MIR10538-7	137	13,868613	36,49635	18,248175	31,386861	32,116788	67,883212	0,86	0,76	-59,3	-57,6	0,0320718	25,01	-43,284672	-0,925
sly-MIR10538-8	117	18,803419	35,042735	15,384615	30,769231	34,188034	65,811966	0,8780488	1,2222222	-44,6	-44,4	0,10897	15,59	-38,119658	-1,125641
sly-	117	15,384615	30,769231	20,512821	33,333333	35,897436	64,102564	1,0833333	0,75	-50,2	-50	0,243498	3,6	-42,905983	-0,9380952

MIR10538-9															
sly-MIR10540-1	155	16,129032	27,741935	14,193548	41,935484	30,322581	69,677419	1,5116279	1,1363636	-49,2	-48	0,0237255	10,89	-31,741935	-1,0468085
sly-MIR10540-2	145	17,241379	28,965517	16,551724	37,241379	33,793103	66,206897	1,2857143	1,0416667	-53,5	-51,3	0,0245621	15,52	-36,896552	-0,7986842
sly-MIR10540-3	142	14,788732	32,394366	19,014085	33,802817	33,802817	66,197183	1,0434783	0,7777778	-58,9	-56,4	0,0507256	5,88	-41,478873	-0,7228571
sly-MIR10541	141	23,404255	28,368794	14,184397	34,042553	37,588652	62,411348	1,2	1,65	-42,1	-22,42	0,0028644	37,99	-29,858156	-0,8275
sly-MIR10542-1	317	15,772871	31,861199	14,511041	37,85489	30,283912	69,716088	1,1881188	1,0869565	-72,7	-65,5	4,83E-05	44,78	-22,933754	-0,9837838
sly-MIR10542-2	275	18,545455	36,363636	13,818182	31,272727	32,363636	67,636364	0,86	1,3421053	-64,6	-38,62	4,14E-05	99,23	-23,490909	-0,9807692
sly-MIR10542-3	236	18,220339	37,711864	12,711864	31,355932	30,932203	69,067797	0,8314607	1,4333333	-59,5	-52,5	0,0011715	44,89	-25,211864	-0,8297297
sly-MIR10542-4	238	19,327731	35,294118	13,02521	32,352941	32,352941	67,647059	0,9166667	1,483871	-57,6	-42,1	0,0009537	77,9	-24,201681	-1,038
sly-MIR1069	82	19,512195	30,487805	15,853659	34,146341	35,365854	64,634146	1,12	1,2307692	-22,2	-22,2	0,0657563	8,68	-27,073171	-0,9622222
sly-MIR1070	152	16,447368	29,605263	22,368421	31,578947	38,815789	61,184211	1,0666667	0,7352941	-90,4	-89,7	0,100476	7,29	-59,473684	-0,816129
sly-MIR1078	231	20,34632	34,199134	12,554113	32,900433	32,900433	67,099567	0,9620253	1,6206897	-54,8	-43	0,0003741	42,69	-23,722944	-1,0226415
sly-MIR1088	138	18,84058	33,333333	18,115942	29,710145	36,956522	63,043478	0,8913043	1,04	-55,1	-55	0,0398162	7,48	-39,927536	-0,9268657
sly-MIR10992	242	16,115702	35,123967	14,876033	33,884298	30,991736	69,008264	0,9647059	1,0833333	-54,5	-50	0,0004553	39,88	-22,520661	-2,1133333
sly-MIR10995	194	18,556701	33,505155	17,525773	30,412371	36,082474	63,917526	0,9076923	1,0588235	-49,1	-43,8	0,0058624	36,72	-25,309278	-0,7197802
sly-MIR11003	251	13,944223	37,051793	16,733068	32,270916	30,677291	69,322709	0,8709677	0,8333333	-56,7	-56,6	0,0024778	18,44	-22,589641	-0,8034483
sly-MIR11011a	89	14,606742	35,955056	20,224719	29,213483	34,831461	65,168539	0,8125	0,7222222	-43,6	-43,6	0,49261	1,54	-48,988764	-1,0615385
sly-MIR11039	229	25,327511	26,200873	8,2969432	40,174672	33,624454	66,375546	1,5333333	3,0526316	-58,1	-39,7	0,0011809	54,43	-25,371179	-0,7545455
sly-MIR11048	241	21,161826	31,53527	19,087137	28,215768	40,248963	59,751037	0,8947368	1,1086957	-71,2	-69,2	0,0004208	44,29	-29,543568	-1,18
sly-MIR1106-1	146	19,178082	33,561644	13,013699	34,246575	32,191781	67,808219	1,0204082	1,4736842	-69	-66,1	0,134117	7,33	-47,260274	-0,707874
sly-MIR1106-2	189	14,814815	34,920635	16,931217	33,333333	31,746032	68,253968	0,9545455	0,875	-68,5	-68,4	0,0041178	16,06	-36,243386	-0,7928571
sly-MIR1106-3	146	13,013699	34,246575	19,178082	33,561644	32,191781	67,808219	0,98	0,6785714	-59,4	-58,9	0,228449	6,33	-40,684932	-1,0164384
sly-MIR11066-1	122	21,311475	28,688525	20,491803	29,508197	41,803279	58,196721	1,0285714	1,04	-39,9	-39,9	0,148352	6,86	-32,704918	-0,93
sly-MIR11066-2	194	22,164948	26,28866	14,43299	37,113402	36,597938	63,402062	1,4117647	1,5357143	-50,7	-25,9	0,0211471	64,58	-26,134021	-1,0033333
sly-MIR11068c	104	14,423077	33,653846	17,307692	34,615385	31,730769	68,269231	1,0285714	0,8333333	-29	-20,58	0,143131	23,98	-27,884615	-0,7395833
sly-MIR11068e	171	21,052632	32,163743	11,111111	35,672515	32,163743	67,836257	1,1090909	1,8947368	-41,5	-33	0,0009645	47,69	-24,269006	-0,7746988
sly-MIR11074	121	19,834711	36,363636	13,22314	30,578512	33,057851	66,942149	0,8409091	1,5	-30,8	-22,2	0,0034327	31,95	-25,454545	-0,9666667
sly-MIR11077b	307	15,309446	35,179153	15,635179	33,876221	30,944625	69,055375	0,962963	0,9791667	-66,5	-57,3	0,0001111	44,42	-21,661238	-1,0590909
sly-MIR11077d	312	14,423077	33,012821	16,025641	36,538462	30,448718	69,551282	1,1067961	0,9	-85,1	-84,3	0,0030664	20,94	-27,275641	-1,0076923
sly-MIR11078d	147	17,006803	29,931973	16,326531	36,734694	33,333333	66,666667	1,2272727	1,0416667	-60,1	-57,7	0,0396981	12	-40,884354	-1,2
sly-MIR11085	151	18,543046	26,490066	18,543046	36,423841	37,086093	62,913907	1,375	1	-64,1	-63,9	0,0414341	11,75	-42,450331	-0,7011494
sly-MIR11108h	267	24,344569	25,468165	21,722846	28,464419	46,067416	53,932584	1,1176471	1,1206897	-89,9	-59,24	2,96E-05	51,57	-33,670412	-1,1
sly-MIR11114	266	14,661654	36,466165	16,165414	32,706767	30,827068	69,172932	0,8969072	0,9069767	-61,2	-58,2	0,0001879	44,25	-23,007519	-1,3896552
sly-MIR11115	172	20,930233	26,744186	18,023256	34,302326	38,953488	61,046512	1,2826087	1,1612903	-92,8	-90,1	0,016872	11,02	-53,953488	-1,3850746
sly-MIR11118	75	25,333333	34,666667	6,6666667	33,333333	32	68	0,9615385	3,8	-22,3	-21,5	0,0718215	9,7	-29,733333	-0,7651515
sly-MIR11124	331	23,26284	29,607251	17,824773	29,305136	41,087613	58,912387	0,9897959	1,3050847	-96,5	-74,5	0,0010334	88,54	-29,154079	-1,2470588
sly-MIR11131	143	13,986014	33,566434	16,783217	35,664336	30,769231	69,230769	1,0625	0,8333333	-77,2	-77,2	0,229391	4,05	-53,986014	-0,7962025
sly-MIR11155e-1	188	16,489362	33,510638	16,489362	33,510638	32,978723	67,021277	1	1	-97,9	-97,9	0,125604	5,95	-52,074468	-1,5790323
sly-MIR11155e-2	164	17,682927	32,317073	17,073171	32,926829	34,756098	65,243902	1,0188679	1,0357143	-88,8	-88,8	0,182261	3,25	-54,146341	-1,5578947
sly-MIR11155e-3	149	18,120805	33,557047	17,449664	30,872483	35,57047	64,42953	0,92	1,0384615	-82,2	-82,2	0,269643	4,89	-55,167785	-1,7217391
sly-MIR1127-1	258	17,054264	31,007752	17,829457	34,108527	34,883721	65,116279	1,1	0,9565217	-78,6	-73,25	0,0003959	39,63	-30,465116	-1,2352113
sly-MIR1127-2	131	19,083969	27,480916	18,320611	35,114504	37,40458	62,59542	1,2777778	1,0416667	-63,4	-63,4	0,107865	4,17	-48,396947	-0,8468085

sly-MIR1127-3	284	18,309859	35,915493	16,197183	29,577465	34,507042	65,492958	0,8235294	1,1304348	-84,1	-66,61	0,0004534	62,04	-29,612676	-1,0701754
sly-MIR1128-1	256	20,3125	35,546875	10,9375	33,203125	31,25	68,75	0,9340659	1,8571429	-74,2	-72,2	0,0043251	42,98	-28,984375	-0,8153846
sly-MIR1128-2	300	17,666667	28	18,666667	35,666667	36,333333	63,666667	1,2738095	0,9464286	-97,7	-97,7	0,0069308	17,95	-32,566667	-0,95
sly-MIR1128-3	243	23,045267	31,687243	13,168724	32,098765	36,213992	63,786008	1,012987	1,75	-81,5	-74	0,0004101	56,73	-33,539095	-1,5483871
sly-MIR1128-4	288	18,402778	37,5	15,277778	28,819444	33,680556	66,319444	0,7685185	1,2045455	-70,9	-60,5	0,0005067	61,48	-24,618056	-0,76
sly-MIR1128-5	289	12,456747	33,910035	18,685121	34,948097	31,141869	68,858131	1,0306122	0,6666667	-72,2	-65,72	0,0004728	42,45	-24,989619	-1,05
sly-MIR1128-6	98	20,408163	27,55102	21,428571	30,612245	41,836735	58,163265	1,1111111	0,952381	-54,4	-54,4	0,262027	4,47	-55,510204	-0,7282051
sly-MIR1128-7	236	22,457627	33,474576	10,59322	33,474576	33,050847	66,949153	1	2,12	-57,5	-56	0,0001297	53,9	-24,364407	-0,7107143
sly-MIR11288c-1	137	16,058394	32,846715	18,248175	32,846715	34,306569	65,693431	1	0,88	-98,9	-98,7	0,685271	1,48	-72,189781	-0,8138889
sly-MIR11288c-2	137	18,248175	32,846715	16,058394	32,846715	34,306569	65,693431	1	1,1363636	-97,2	-97	0,702301	1,17	-70,948905	-0,8633803
sly-MIR11288d	213	19,248826	30,046948	17,370892	33,333333	36,619718	63,380282	1,109375	1,1081081	-81,2	-76,6	0,0063457	18,65	-38,122066	-1,040625
sly-MIR11295	264	20,833333	29,545455	10,606061	39,015152	31,439394	68,560606	1,3205128	1,9642857	-60,4	-57	0,000579	44,85	-22,878788	-1,07
sly-MIR1130b	108	12,037037	32,407407	18,518519	37,037037	30,555556	69,444444	1,1428571	0,65	-32,6	-28,49	0,142363	11,53	-30,185185	-0,7887324
sly-MIR11314-1	179	22,905028	31,284916	7,2625698	38,547486	30,167598	69,832402	1,2321429	3,1538462	-76,2	-72	0,016872	29,2	-42,569832	-0,7516129
sly-MIR11314-2	183	21,311475	29,508197	11,47541	37,704918	32,786885	67,213115	1,2777778	1,8571429	-61,2	-52,2	0,0009052	50,56	-33,442623	-0,7592593
sly-MIR11317	97	16,494845	32,989691	14,43299	36,082474	30,927835	69,072165	1,09375	1,1428571	-37,2	-36	0,120865	6,91	-38,350515	-0,7021505
sly-MIR1133	279	13,978495	32,97491	17,921147	35,125448	31,899642	68,100358	1,0652174	0,78	-69,9	-56,02	0,0004926	59,34	-25,053763	-0,7733333
sly-MIR11330	145	18,62069	33,103448	14,482759	33,793103	33,103448	66,896552	1,0208333	1,2857143	-81,1	-81,1	0,193063	3,93	-55,931034	-1,2647059
sly-MIR11342	341	17,595308	34,897361	16,129032	31,378299	33,72434	66,27566	0,8991597	1,0909091	-85,7	-82,9	0,0001411	37,17	-25,131965	-0,7772727
sly-MIR11404	253	20,55336	28,063241	10,671937	40,711462	31,225296	68,774704	1,4507042	1,9259259	-57,7	-52,7	0,0003472	55,11	-22,806324	-0,9735294
sly-MIR11409d	237	15,189873	31,223629	17,299578	36,28692	32,489451	67,510549	1,1621622	0,8780488	-78,3	-76,7	0,0309315	8,36	-33,037975	-0,9354167
sly-MIR11413a	159	18,867925	33,333333	18,238994	29,559748	37,106918	62,893082	0,8867925	1,0344828	-84,4	-81,42	0,0220576	14,85	-53,081761	-0,7063492
sly-MIR11416-1	273	20,879121	28,937729	19,047619	31,135531	39,92674	60,07326	1,0759494	1,0961538	-76,9	-70,7	0,0003167	47,92	-28,168498	-0,7055046
sly-MIR11416-2	229	21,834061	27,074236	20,087336	31,004367	41,921397	58,078603	1,1451613	1,0869565	-91,8	-89,2	0,0051192	33,65	-40,087336	-1,5703704
sly-MIR11419	216	21,296296	31,944444	15,277778	31,481481	36,574074	63,425926	0,9855072	1,3939394	-57,5	-53,1	0,0001366	35,13	-26,62037	-0,7347826
sly-MIR11425f	340	17,941176	28,529412	12,352941	41,176471	30,294118	69,705882	1,443299	1,452381	-80,4	-72,3	2,41E-05	46,76	-23,647059	-0,7064516
sly-MIR11451	235	12,340426	35,319149	18,297872	34,042553	30,638298	69,361702	0,9638554	0,6744186	-59,3	-54,41	0,0135416	31,39	-25,234043	-1,3909091
sly-MIR11465	327	15,902141	36,697248	14,373089	33,027523	30,275229	69,724771	0,9	1,106383	-75	-72,7	0,0013022	30,12	-22,93578	-1,0196721
sly-MIR11472	70	21,428571	22,857143	22,857143	32,857143	44,285714	55,714286	1,4375	0,9375	-23,9	-23,9	0,172512	7,31	-34,142857	-0,9320755
sly-MIR11492	261	17,241379	28,35249	13,793103	40,613027	31,034483	68,965517	1,4324324	1,25	-64,1	-63	0,0041964	41,37	-24,559387	-0,8473684
sly-MIR11498c	82	19,512195	37,804878	15,853659	26,829268	35,365854	64,634146	0,7096774	1,2307692	-26	-26	0,218412	3,62	-31,707317	-1,0347826
sly-MIR11553	188	19,148936	35,638298	14,893617	30,319149	34,042553	65,957447	0,8507463	1,2857143	-48,3	-45,2	0,0036923	22,75	-25,691489	-0,7428571
sly-MIR11564b	222	18,018018	32,882883	15,315315	33,783784	33,333333	66,666667	1,0273973	1,1764706	-66,5	-47,4	0,0014982	57,34	-29,954955	-1,2382979
sly-MIR11575	183	21,311475	25,68306	22,404372	30,601093	43,715847	56,284153	1,1914894	0,9512195	-92,3	-91,7	0,035276	8,51	-50,437158	-1,4534884
sly-MIR11583b-1	74	13,513514	37,837838	17,567568	31,081081	31,081081	68,918919	0,8214286	0,7692308	-27,1	-27,1	0,240266	3,09	-36,621622	-1,1595238
sly-MIR11583b-2	215	21,395349	36,744186	15,348837	26,511628	36,744186	63,255814	0,721519	1,3939394	-60,3	-55	0,0016681	36,7	-28,046512	-0,7216981
sly-MIR11592	141	29,078014	22,695035	24,822695	23,404255	53,900709	46,099291	1,03125	1,1714286	-64,5	-63	0,0105917	13,06	-45,744681	-1,0338235
sly-MIR11891	135	20,740741	32,592593	14,074074	32,592593	34,814815	65,185185	1	1,4736842	-58,1	-54,5	0,0915536	11,02	-43,037037	-0,724
sly-MIR12142-1	242	16,528926	31,818182	14,46281	37,190083	30,991736	69,008264	1,1688312	1,1428571	-78,6	-78,6	0,0023452	31,33	-32,479339	-1,048
sly-MIR12142-2	219	18,26484	30,593607	11,872146	39,269406	30,136986	69,863014	1,2835821	1,5384615	-76,4	-20,5	0,0034466	105,28	-34,885845	-0,7789474
sly-MIR12162	217	16,129032	26,728111	14,285714	42,857143	30,414747	69,585253	1,6034483	1,1290323	-49,8	-48,8	0,0058492	46,27	-22,949309	-0,7740741
sly-MIR1217	245	22,040816	35,510204	15,510204	26,938776	37,55102	62,44898	0,7586207	1,4210526	-64,9	-61	0,0008735	43,2	-26,489796	-1,0493827

sly-MIR1435	234	15,811966	32,051282	17,094017	35,042735	32,905983	67,094017	1,0933333	0,925	-54,8	-46,9	0,0002763	50,38	-23,418803	-0,8963303
sly-MIR1435b	275	22,909091	28,727273	22,545455	25,818182	45,454545	54,545455	0,8987342	1,016129	-93,1	-73,87	0,0001643	59,28	-33,854545	-0,774
sly-MIR1446-1	113	16,814159	32,743363	19,469027	30,973451	36,283186	63,716814	0,9459459	0,8636364	-47,3	-44,9	0,115697	4,34	-41,858407	-0,7406593
sly-MIR1446-2	139	17,266187	28,057554	20,143885	34,532374	37,410072	62,589928	1,2307692	0,8571429	-57,5	-54,7	0,0508995	9,48	-41,366906	-0,720339
sly-MIR1512a	195	15,897436	32,820513	16,923077	34,358974	32,820513	67,179487	1,046875	0,9393939	-45,1	-35,24	0,0028734	39,82	-23,128205	-0,9851852
sly-MIR1512c	182	18,131868	31,868132	15,934066	34,065934	34,065934	65,934066	1,0689655	1,137931	-92,8	-90,5	0,102169	10,72	-50,989011	-0,7632911
sly-MIR1514b	192	16,666667	37,5	13,541667	32,291667	30,208333	69,791667	0,8611111	1,2307692	-85,6	-85,6	0,0124477	9,63	-44,583333	-0,7421053
sly-MIR1518	293	16,723549	33,447099	15,699659	34,129693	32,423208	67,576792	1,0204082	1,0652174	-77,2	-71,5	8,67E-05	43,88	-26,348123	-0,86
sly-MIR1521a	133	19,548872	28,571429	15,037594	36,842105	34,586466	65,413534	1,2894737	1,3	-35,6	-33,1	0,0256473	20,03	-26,766917	-0,7078431
sly-MIR1521b	93	13,978495	30,107527	22,580645	33,333333	36,55914	63,44086	1,1071429	0,6190476	-31,9	-31,9	0,241649	5,42	-34,301075	-0,8877193
sly-MIR1525	116	22,413793	29,310345	8,6206897	39,655172	31,034483	68,965517	1,3529412	2,6	-30,6	-29,8	0,0098947	14,34	-26,37931	-0,85
sly-MIR1529	307	15,960912	37,785016	14,65798	31,596091	30,618893	69,381107	0,8362069	1,0888889	-70,5	-61,4	0,0007363	41,6	-22,964169	-0,709434
sly-MIR1530-1	323	23,839009	32,50774	12,074303	31,578947	35,913313	64,086687	0,9714286	1,974359	-85,5	-79	0,0001089	45,6	-26,470588	-0,8764706
sly-MIR1530-2	247	18,218623	35,62753	12,550607	33,603239	30,769231	69,230769	0,9431818	1,4516129	-58,1	-46,4	8,97E-05	58,36	-23,522267	-0,7384615
sly-MIR1533-1	183	21,857923	31,693989	20,765027	25,68306	42,622951	57,377049	0,8103448	1,0526316	-89,7	-89,4	0,023423	7,57	-49,016393	-1,4891304
sly-MIR1533-2	263	19,011407	33,840304	11,787072	35,361217	30,798479	69,201521	1,0449438	1,6129032	-61,4	-51,8	4,57E-05	37,28	-23,346008	-1,7545455
sly-MIR156a	308	19,480519	38,636364	11,688312	30,194805	31,168831	68,831169	0,7815126	1,6666667	-69,9	-61,6	0,0003803	40,85	-22,694805	-0,728125
sly-MIR156b-1	101	17,821782	29,70297	18,811881	33,663366	36,633663	63,366337	1,1333333	0,9473684	-43,5	-42,2	0,119446	6,96	-43,069307	-1,1756757
sly-MIR156b-2	88	21,590909	25	23,863636	29,545455	45,454545	54,545455	1,1818182	0,9047619	-44,1	-44,1	0,312754	2,54	-50,113636	-1,1025
sly-MIR156b-3	98	18,367347	32,653061	18,367347	30,612245	36,734694	63,265306	0,9375	1	-48,3	-42,9	0,0433508	5,76	-49,285714	-1,3416667
sly-MIR156b-4	101	23,762376	24,752475	23,762376	27,722772	47,524752	52,475248	1,12	1	-62,5	-62,5	0,221714	5,23	-61,881188	-1,3020833
sly-MIR156b-5	147	21,088435	27,210884	15,646259	36,054422	36,734694	63,265306	1,325	1,3478261	-68,2	-67,8	0,0309898	8,08	-46,394558	-1,262963
sly-MIR156b-6	246	18,699187	29,674797	18,699187	32,926829	37,398374	62,601626	1,109589	1	-83	-70,5	0,0038961	28,95	-33,739837	-0,9021739
sly-MIR156b-7	94	20,212766	26,595745	18,085106	35,106383	38,297872	61,702128	1,32	1,1176471	-48,4	-48,4	0,0852724	4,15	-51,489362	-1,3444444
sly-MIR156c-1	102	24,509804	24,509804	18,627451	32,352941	43,137255	56,862745	1,32	1,3157895	-57,3	-57,3	0,419204	4,94	-56,176471	-1,3022727
sly-MIR156c-2	101	24,752475	23,762376	23,762376	27,722772	48,514851	51,485149	1,1666667	1,0416667	-50,7	-50,7	0,0662223	7,13	-50,19802	-1,0346939
sly-MIR156c-3	166	21,686747	28,313253	18,674699	31,325301	40,361446	59,638554	1,106383	1,1612903	-75,5	-75,1	0,0316798	15,36	-45,481928	-1,1333333
sly-MIR156c-4	101	23,762376	25,742574	23,762376	26,732673	47,524752	52,475248	1,0384615	1	-51,1	-51,1	0,104576	4,98	-50,594059	-0,8163043
sly-MIR156d	140	15	30	19,285714	35,714286	34,285714	65,714286	1,1904762	0,7777778	-44,7	-43,4	0,0776389	8,6	-31,928571	-0,93125
sly-MIR156f-1	92	22,826087	26,086957	17,391304	33,695652	40,217391	59,782609	1,2916667	1,3125	-38,3	-38,3	0,259233	2,69	-41,630435	-1,0351351
sly-MIR156f-2	144	22,222222	33,333333	14,583333	29,861111	36,805556	63,194444	0,8958333	1,5238095	-63,6	-63,6	0,177809	4,38	-44,166667	-1,2
sly-MIR156f-3	132	17,424242	31,818182	14,393939	36,363636	31,818182	68,181818	1,1428571	1,2105263	-51,2	-47,2	0,0212865	14,18	-38,787879	-0,7692308
sly-MIR156g	119	20,168067	25,210084	19,327731	35,294118	39,495798	60,504202	1,4	1,0434783	-74,5	-74,5	0,171764	3,48	-62,605042	-0,9876923
sly-MIR156i-1	104	22,115385	25	20,192308	32,692308	42,307692	57,692308	1,3076923	1,0952381	-42,4	-42,4	0,328687	4,15	-40,769231	-0,9636364
sly-MIR156i-2	100	19	20	25	36	44	56	1,8	0,76	-36,4	-36,4	0,191241	5,24	-36,4	-0,8272727
sly-MIR156i-3	94	22,340426	26,595745	22,340426	28,723404	44,680851	55,319149	1,08	1	-41	-41	0,119007	9,2	-43,617021	-0,9761905
sly-MIR156i-4	247	15,789474	38,05668	14,979757	31,174089	30,769231	69,230769	0,8191489	1,0540541	-60,6	-58,8	0,0001041	38,92	-24,534413	-1,004
sly-MIR156k	101	22,772277	24,752475	15,841584	36,633663	38,613861	61,386139	1,48	1,4375	-56,6	-56,6	0,350764	4,9	-56,039604	-1,4512821
sly-MIR156t	222	16,216216	39,189189	13,963964	30,630631	30,18018	69,81982	0,7816092	1,1612903	-48,7	-37,4	0,0005567	51,44	-21,936937	-0,7313953
sly-MIR158b	108	26,851852	22,222222	22,222222	28,703704	49,074074	50,925926	1,2916667	1,2083333	-37,9	-34,8	0,0775822	16,67	-35,092593	-1,0245283
sly-MIR159a	174	21,83908	24,712644	17,241379	36,206897	39,08046	60,91954	1,4651163	1,2666667	-76,6	-74	0,0215353	12,01	-44,022989	-1,1264706
sly-MIR159b-1	254	21,259843	27,952756	14,566929	36,220472	35,826772	64,173228	1,2957746	1,4594595	-88,2	-80,2	5,78E-05	33,41	-34,724409	-0,9692308
sly-MIR159b-2	254	18,897638	29,92126	16,141732	35,03937	35,03937	64,96063	1,1710526	1,1707317	-83,2	-74,84	0,0002179	30	-32,755906	-0,9348315
sly-MIR159b-	180	20	30	17,222222	32,777778	37,222222	62,777778	1,0925926	1,1612903	-72,7	-67,4	0,0038648	15,42	-40,388889	-1,0850746

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sly-MIR159b-4	180	20,555556	28,888889	16,111111	34,444444	36,666667	63,333333	1,1923077	1,2758621	-77,2	-75,3	0,0053671	11,58	-42,888889	-1,169697
sly-MIR159b-5	270	18,148148	29,62963	15,925926	36,296296	34,074074	65,925926	1,225	1,1395349	-89,6	-81	0,000738	31,21	-33,185185	-0,973913
sly-MIR159b-6	270	20	28,518519	15,925926	35,555556	35,925926	64,074074	1,2467532	1,255814	-94,6	-92,7	0,0019266	20,52	-35,037037	-0,9752577
sly-MIR159b-7	198	20,707071	29,79798	17,171717	32,323232	37,878788	62,121212	1,0847458	1,2058824	-76,7	-74,8	0,0059664	14,42	-38,737374	-0,8052632
sly-MIR159b-8	215	22,325581	27,906977	14,883721	34,883721	37,209302	62,790698	1,25	1,5	-92,1	-89,2	0,0058915	13,96	-42,837209	-0,9517241
sly-MIR159e	283	18,021201	37,809187	12,720848	31,448763	30,742049	69,257951	0,8317757	1,4166667	-71,3	-66	0,000526	37,6	-25,194346	-1,1233766
sly-MIR160-1	116	21,551724	31,896552	21,551724	25	43,103448	56,896552	0,7837838	1	-41,7	-40,3	0,0514112	9,2	-35,948276	-0,834
sly-MIR160-2	206	17,475728	32,524272	19,902913	30,097087	37,378641	62,621359	0,9253731	0,8780488	-64,9	-61,2	0,0128627	27,85	-31,504854	-0,8428571
sly-MIR160-3	148	17,567568	37,162162	13,513514	31,756757	31,081081	68,918919	0,8545455	1,3	-39,5	-37,5	0,0097562	13,18	-26,689189	-0,8586957
sly-MIR160-4	95	26,315789	24,210526	24,210526	25,263158	50,526316	49,473684	1,0434783	1,0869565	-42,1	-38,1	0,0541257	13,48	-44,315789	-1,009434
sly-MIR160-5	104	23,076923	24,038462	21,153846	31,730769	44,230769	55,769231	1,32	1,0909091	-52,3	-51,4	0,100504	4,55	-50,288462	-0,9295082
sly-MIR160c	81	23,45679	23,45679	25,925926	27,160494	49,382716	50,617284	1,1578947	0,9047619	-39,4	-39,4	0,383978	2,73	-48,641975	-0,985
sly-MIR160e	245	15,918367	35,510204	14,693878	33,877551	30,612245	69,387755	0,954023	1,0833333	-64,7	-64	0,0061964	29,86	-26,408163	-1,3291667
sly-MIR160g	99	21,212121	30,30303	23,232323	25,252525	44,444444	55,555556	0,8333333	0,9130435	-48,9	-48,9	0,136739	3,41	-49,393939	-1,1113636
sly-MIR160h-1	81	22,222222	20,987654	23,45679	33,333333	45,679012	54,320988	1,5882353	0,9473684	-33,6	-33,4	0,303642	3,48	-41,481481	-0,9081081
sly-MIR160h-2	90	24,444444	24,444444	22,222222	28,888889	46,666667	53,333333	1,1818182	1,1	-46,8	-46,8	0,126945	3,09	-52	-1,1142857
sly-MIR161	171	30,994152	27,48538	21,637427	19,883041	52,631579	47,368421	0,7234043	1,4324324	-68,4	-66,2	0,0504454	10,2	-40	-0,9472973
sly-MIR162-1	135	22,962963	31,111111	21,481481	24,444444	44,444444	55,555556	0,7857143	1,0689655	-50	-49,3	0,00759	12,19	-37,037037	-1,7106383
sly-MIR162-2	98	23,469388	32,653061	24,489796	19,387755	47,959184	52,040816	0,59375	0,9583333	-42	-42	0,173594	5,92	-42,857143	-1,0586207
sly-MIR162b-1	137	22,627737	27,737226	19,708029	29,927007	42,335766	57,664234	1,0789474	1,1481481	-54,9	-52,4	0,0508337	11,14	-40,072993	-0,9465517
sly-MIR162b-2	135	21,481481	24,444444	22,962963	31,111111	44,444444	55,555556	1,2727273	0,9354839	-58,3	-57,4	0,0962136	9,62	-43,185185	-0,8586207
sly-MIR162b-3	110	25,454545	20	25,454545	29,090909	50,909091	49,090909	1,4545455	1	-55	-55	0,172243	4,95	-50	-2,0680851
sly-MIR164-1	165	19,393939	29,090909	16,363636	35,151515	35,757576	64,242424	1,2083333	1,1851852	-59,4	-57,3	0,0027898	17,41	-36	-1,0067797
sly-MIR164-2	173	19,653179	29,479769	16,184971	34,682081	35,83815	64,16185	1,1764706	1,2142857	-62,2	-60,1	0,0019867	17,99	-35,953757	-1,0032258
sly-MIR164a	140	17,142857	30,714286	17,142857	35	34,285714	65,714286	1,1395349	1	-51,1	-51,1	0,170251	4,43	-36,5	-0,75
sly-MIR164b	300	22	32,333333	17	28,666667	39	61	0,8865979	1,2941176	-83,2	-72,94	3,65E-05	54,98	-27,733333	-0,8581818
sly-MIR164c	88	20,454545	27,272727	20,454545	31,818182	40,909091	59,090909	1,1666667	1	-50,5	-47,5	0,178181	2,29	-57,386364	-1,4027778
sly-MIR164e	97	20,618557	26,804124	19,587629	32,989691	40,206186	59,793814	1,2307692	1,0526316	-48,3	-47,6	0,0509358	8,8	-49,793814	-1,2384615
sly-MIR166-1	120	21,666667	28,333333	16,666667	33,333333	38,333333	61,666667	1,1764706	1,3	-52,7	-51,5	0,335949	5,46	-43,916667	-1,1456522
sly-MIR166-2	97	18,556701	30,927835	18,556701	31,958763	37,113402	62,886598	1,0333333	1	-41,1	-41,1	0,33726	2,44	-42,371134	-1,1416667
sly-MIR166-3	151	18,543046	29,139073	17,880795	34,437086	36,423841	63,576159	1,1818182	1,037037	-56,4	-51	0,0684176	16,58	-37,350993	-1,0254545
sly-MIR166-4	119	16,806723	29,411765	21,848739	31,932773	38,655462	61,344538	1,0857143	0,7692308	-33	-30,4	0,0399008	10,56	-27,731092	-0,7173913
sly-MIR166c	187	21,390374	30,481283	14,973262	33,15508	36,363636	63,636364	1,0877193	1,4285714	-72,2	-64,6	0,0118421	15,6	-38,609626	-1,0617647
sly-MIR166d-1	129	21,705426	25,581395	14,728682	37,984496	36,434109	63,565891	1,4848485	1,4736842	-56	-56	0,201716	4,93	-43,410853	-1,0123288
sly-MIR166f-1	98	23,469388	21,428571	23,469388	31,632653	46,938776	53,061224	1,4761905	1	-41,7	-38,4	0,0245813	13,29	-42,55102	-0,9065217
sly-MIR166f-2	158	23,417722	31,64557	16,455696	28,481013	39,873418	60,126582	0,9	1,4230769	-47	-43,7	0,0042127	20,18	-29,746835	-0,7460317
sly-MIR166k	165	21,212121	29,090909	18,181818	31,515152	39,393939	60,606061	1,0833333	1,1666667	-58,5	-58,2	0,0580752	12,14	-35,454545	-0,9
sly-MIR167a	191	14,136126	36,649215	16,230366	32,984293	30,366492	69,633508	0,9	0,8709677	-52,3	-44,7	0,0014371	35,52	-27,382199	-1,0962963
sly-MIR167b-1	110	19,090909	30	21,818182	29,090909	40,909091	59,090909	0,969697	0,875	-38,7	-38,5	0,0810606	6,96	-35,181818	-0,86
sly-MIR167b-2	94	17,021277	29,787234	19,148936	34,042553	36,170213	63,829787	1,1428571	0,8888889	-35,3	-35,3	0,0639905	5,86	-37,553191	-1,0382353
sly-MIR167b-3	122	18,852459	30,327869	22,95082	27,868852	41,803279	58,196721	0,9189189	0,8214286	-47,1	-46,9	0,116637	5,55	-38,606557	-0,7892857
sly-MIR167c-1	84	25	29,761905	20,238095	25	45,238095	54,761905	0,84	1,2352941	-41,7	-41,7	0,476326	3,16	-49,642857	-1,0973684
sly-MIR167c-2	110	21,818182	29,090909	21,818182	27,272727	43,636364	56,363636	0,9375	1	-48,3	-48,3	0,450688	3,3	-43,909091	-1,00625
sly-MIR167c-3	271	20,295203	33,948339	13,653137	32,103321	33,948339	66,051661	0,9456522	1,4864865	-66,7	-61,3	0,0004795	59,78	-24,612546	-0,725
sly-MIR167c-4	113	24,778761	26,548673	22,123894	26,548673	46,902655	53,097345	1	1,12	-53,5	-53,5	0,0786897	4,46	-47,345133	-0,7853933

sly-MIR167h-1	122	22,95082	27,868852	18,852459	30,327869	41,803279	58,196721	1,0882353	1,2173913	-57,7	-57,7	0,175549	4,67	-47,295082	-1,1761905
sly-MIR167h-2	113	22,123894	26,548673	24,778761	26,548673	46,902655	53,097345	1	0,8928571	-46,1	-46,1	0,0248159	9,32	-40,79646	-1,02
sly-MIR167h-3	119	20,168067	26,890756	24,369748	28,571429	44,537815	55,462185	1,0625	0,8275862	-49,4	-49,4	0,0393334	8,91	-41,512605	-0,9352941
sly-MIR168	170	30	20,588235	22,352941	27,058824	52,352941	47,647059	1,3142857	1,3421053	-77,5	-76,2	0,0126023	15,25	-45,588235	-0,8707865
sly-MIR168a	289	14,186851	35,640138	17,301038	32,871972	31,487889	68,512111	0,9223301	0,82	-67,4	-52,47	0,0001923	47,41	-23,321799	-0,7282051
sly-MIR168b	133	27,819549	24,81203	27,067669	20,300752	54,887218	45,112782	0,8181818	1,0277778	-89,4	-87,2	0,32578	2,78	-67,218045	-1,2246575
sly-MIR168c	160	29,375	21,25	23,75	25,625	53,125	46,875	1,2058824	1,2368421	-65,9	-61,6	0,0150613	19,69	-41,1875	-0,7752941
sly-MIR169a-1	158	24,683544	27,21519	15,189873	32,911392	39,873418	60,126582	1,2093023	1,625	-82	-82	0,0616001	4,18	-51,898734	-1,3015873
sly-MIR169a-2	181	15,469613	29,834254	16,574586	38,121547	32,044199	67,955801	1,2777778	0,9333333	-70,9	-68,34	0,0102268	21,59	-39,171271	-1,2224138
sly-MIR169a-3	176	15,909091	31,25	15,909091	36,931818	31,818182	68,181818	1,1818182	1	-70,1	-66,54	0,0076468	25,52	-39,829545	-1,2517857
sly-MIR169a-4	141	21,276596	22,695035	19,858156	36,170213	41,134752	58,865248	1,59375	1,0714286	-68,6	-67,7	0,0902048	6,75	-48,652482	-1,1409836
sly-MIR169c-1	170	15,294118	28,823529	17,647059	38,235294	32,941176	67,058824	1,3265306	0,8666667	-62	-62	0,0872699	5,93	-36,470588	-1,1071429
sly-MIR169c-2	205	14,146341	27,317073	18,04878	40,487805	32,195122	67,804878	1,4821429	0,7837838	-65,7	-64,6	0,0076332	19,06	-32,04878	-0,9954545
sly-MIR169c-3	183	14,754098	27,322404	18,032787	39,89071	32,786885	67,213115	1,46	0,8181818	-64,5	-63,4	0,0142082	17,53	-35,245902	-0,7459459
sly-MIR169c-4	188	19,148936	28,723404	12,765957	39,361702	31,914894	68,085106	1,3703704	1,5	-76,6	-73,8	0,0023734	16,45	-40,744681	-1,0150943
sly-MIR169d	136	22,058824	23,529412	20,588235	33,823529	42,647059	57,352941	1,4375	1,0714286	-53,4	-53,4	0,0311945	6,46	-39,264706	-0,9206897
sly-MIR169e-1	193	20,725389	26,943005	17,098446	35,233161	37,823834	62,176166	1,3076923	1,2121212	-78,5	-74,8	0,006646	15,08	-40,673575	-1,0753425
sly-MIR169e-2	215	16,27907	39,069767	18,139535	26,511628	34,418605	65,581395	0,6785714	0,8974359	-78,9	-73,6	0,0018786	25,24	-36,697674	-0,7458333
sly-MIR169e-3	169	17,159763	35,502959	18,934911	28,402367	36,094675	63,905325	0,8	0,90625	-69,6	-66,9	0,151292	3,99	-41,183432	-0,8065934
sly-MIR169f	209	18,181818	32,057416	14,354067	35,406699	32,535885	67,464115	1,1044776	1,2666667	-72,1	-70,8	0,0020279	16,18	-34,497608	-1,0602941
sly-MIR169j-1	163	19,018405	23,312883	21,472393	36,196319	40,490798	59,509202	1,5526316	0,8857143	-56,6	-53,7	0,0067252	16,76	-34,723926	-0,8575758
sly-MIR169j-2	163	21,472393	24,539877	19,631902	34,355828	41,104294	58,895706	1,4	1,09375	-60,4	-57,5	0,0042864	18,87	-37,055215	-0,9014925
sly-MIR169j-3	156	20,512821	26,923077	17,307692	35,25641	37,820513	62,179487	1,3095238	1,1851852	-66,6	-66,6	0,0093667	9,94	-42,692308	-1,1288136
sly-MIR169j-4	169	18,934911	28,402367	17,159763	35,502959	36,094675	63,905325	1,25	1,1034483	-75,4	-75,4	0,0091711	9,92	-44,615385	-1,2360656
sly-MIR169j-5	208	20,192308	25,480769	19,230769	35,096154	39,423077	60,576923	1,3773585	1,05	-82,7	-82,6	0,0064032	19,9	-39,759615	-0,7443299
sly-MIR169l	184	19,021739	35,869565	20,652174	24,456522	39,673913	60,326087	0,6818182	0,9210526	-59,8	-51,9	0,0060482	20,3	-32,5	-0,7465909
sly-MIR169n	171	22,807018	24,561404	9,9415205	42,690058	32,748538	67,251462	1,7380952	2,2941176	-49,5	-48,5	0,0149419	32,24	-28,947368	-0,8839286
sly-MIR169r-1	285	19,298246	26,666667	18,947368	35,087719	38,245614	61,754386	1,3157895	1,0185185	-98,6	-93,77	0,0004317	33,54	-34,596491	-0,9045872
sly-MIR169r-2	184	21,73913	26,630435	19,021739	32,608696	40,76087	59,23913	1,2244898	1,1428571	-71,3	-71,3	0,0110152	10,34	-38,75	-0,9506667
sly-MIR169r-3	124	23,387097	23,387097	18,548387	34,677419	41,935484	58,064516	1,4827586	1,2608696	-58,1	-57,3	0,0220759	10,21	-46,854839	-1,125
sly-MIR169r-4	184	20,652174	24,456522	19,021739	35,869565	39,673913	60,326087	1,4666667	1,0857143	-73,9	-68,5	0,0262777	16,74	-40,163043	-0,7050847
sly-MIR169r-5	73	26,027397	23,287671	17,808219	32,876712	43,835616	56,164384	1,4117647	1,4615385	-34,7	-34,7	0,0847862	7,34	-47,534247	-1,140678
sly-MIR171a-1	91	20,879121	30,769231	14,285714	34,065934	35,164835	64,835165	1,1071429	1,4615385	-40,5	-40,5	0,0765296	2,83	-44,505495	-1,265625
sly-MIR171a-2	99	23,232323	26,262626	16,161616	34,343434	39,393939	60,606061	1,3076923	1,4375	-44,7	-44,7	0,6406	1,18	-45,151515	-1,1461538
sly-MIR171a-3	106	23,584906	28,301887	15,09434	33,018868	38,679245	61,320755	1,1666667	1,5625	-44,7	-44,7	0,591224	1,62	-42,169811	-1,0902439
sly-MIR171a-4	110	19,090909	33,636364	13,636364	33,636364	32,727273	67,272727	1	1,4	-42,8	-42,8	0,148276	4,48	-38,909091	-1,1888889
sly-MIR171a-5	92	22,826087	28,26087	17,391304	31,521739	40,217391	59,782609	1,1153846	1,3125	-52,8	-52,8	0,546334	1,11	-57,391304	-1,427027
sly-MIR171a-6	97	17,525773	30,927835	15,463918	36,082474	32,989691	67,010309	1,1666667	1,1333333	-45,5	-45,5	0,305523	1,96	-46,907216	-1,421875
sly-MIR171a-7	86	19,767442	27,906977	13,953488	38,372093	33,72093	66,27907	1,375	1,4166667	-40,3	-40,3	0,105416	3,78	-46,860465	-0,9945205
sly-MIR171a-	128	17,1875	25,78125	17,96875	39,0625	35,15625	64,84375	1,5151515	0,9565217	-46	-46	0,136677	6,85	-35,9375	-1,2265306

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sly-MIR171b-1	115	22,608696	30,434783	15,652174	31,304348	38,26087	61,73913	1,0285714	1,4444444	-43	-37,7	0,131277	7,03	-37,391304	-0,9772727
sly-MIR171b-2	118	22,033898	28,813559	16,101695	33,050847	38,135593	61,864407	1,1470588	1,3684211	-43	-40	0,101445	8,33	-36,440678	-0,9555556
sly-MIR171b-3	99	17,171717	30,30303	23,232323	29,292929	40,40404	59,59596	0,9666667	0,7391304	-40,6	-40,6	0,313587	2,49	-41,010101	-0,7147059
sly-MIR171b-4	125	21,6	28,8	16,8	32,8	38,4	61,6	1,1388889	1,2857143	-49,3	-45,4	0,0528652	6,32	-39,44	-0,7576923
sly-MIR171b-5	99	18,181818	29,292929	23,232323	29,292929	41,414141	58,585859	1	0,7826087	-33,9	-28,7	0,0714709	9,28	-34,242424	-0,7140845
sly-MIR171b-6	136	14,705882	35,294118	20,588235	29,411765	35,294118	64,705882	0,8333333	0,7142857	-35,8	-30,6	0,0232514	9,97	-26,323529	-0,7018692
sly-MIR171c-1	101	16,831683	28,712871	17,821782	36,633663	34,653465	65,346535	1,2758621	0,9444444	-42,2	-42,2	0,636931	1,01	-41,782178	-1,2057143
sly-MIR171c-2	92	17,391304	34,782609	18,478261	29,347826	35,869565	64,130435	0,84375	0,9411765	-28,2	-27,8	0,480796	1,93	-30,652174	-0,8545455
sly-MIR171c-3	261	25,287356	27,203065	21,455939	26,05364	46,743295	53,256705	0,9577465	1,1785714	-87	-74,1	0,0009068	49,8	-33,333333	-1,1435484
sly-MIR171c-4	215	19,069767	33,488372	13,953488	33,488372	33,023256	66,976744	1	1,3666667	-56,4	-56	0,0002589	41,68	-26,232558	-1,2121212
sly-MIR171d	81	18,518519	29,62963	17,283951	34,567901	35,802469	64,197531	1,1666667	1,0714286	-39,5	-39,5	0,73619	0,6	-48,765432	-1,362069
sly-MIR171e	86	22,093023	27,906977	13,953488	36,046512	36,046512	63,953488	1,2916667	1,5833333	-45,7	-45,7	0,487215	1,75	-53,139535	-1,4741935
sly-MIR171f-1	131	12,977099	26,717557	19,847328	40,458015	32,824427	67,175573	1,5142857	0,6538462	-31,5	-31,5	0,160306	10,28	-24,045802	-0,7325581
sly-MIR171f-2	79	17,721519	22,78481	17,721519	41,772152	35,443038	64,556962	1,8333333	1	-24,3	-24,3	0,435288	5,09	-30,759494	-0,8678571
sly-MIR171f-3	79	16,455696	22,78481	18,987342	41,772152	35,443038	64,556962	1,8333333	0,8666667	-24,3	-24,3	0,494065	4,21	-30,759494	-0,8678571
sly-MIR171f-4	100	23	28	16	33	39	61	1,1785714	1,4375	-45,4	-45,4	0,2285	3,6	-45,4	-1,1641026
sly-MIR171j	290	15,172414	33,448276	15,172414	36,206897	30,344828	69,655172	1,0824742	1	-67,5	-51,7	0,0002466	39,51	-23,275862	-1,3661765
sly-MIR171l	253	26,086957	19,367589	26,482213	28,063241	52,56917	47,43083	1,4489796	0,9850746	-95,3	-84,5	0,0019151	23,61	-37,667984	-1,4829787
sly-MIR171t	98	20,408163	29,591837	22,44898	27,55102	42,857143	57,142857	0,9310345	0,9090909	-42,6	-40,9	0,111429	11,49	-43,469388	-1,0142857
sly-MIR172-1	164	17,073171	33,536585	13,414634	35,97561	30,487805	69,512195	1,0727273	1,2727273	-52,9	-47,57	0,0178513	21,68	-32,256098	-1,058
sly-MIR172-2	164	17,073171	32,926829	13,414634	36,585366	30,487805	69,512195	1,1111111	1,2727273	-52,9	-47,57	0,0104285	22,6	-32,256098	-1,058
sly-MIR172-3	248	15,322581	33,870968	14,919355	35,887097	30,241935	69,758065	1,0595238	1,027027	-68,6	-60,2	0,0001817	36,46	-27,66129	-0,9146667
sly-MIR172-4	142	20,422535	32,394366	14,788732	32,394366	35,211268	64,788732	1	1,3809524	-54,9	-54	0,0223995	15,36	-38,661972	-1,098
sly-MIR172-5	154	18,181818	30,519481	12,337662	38,961039	30,519481	69,480519	1,2765957	1,4736842	-54,3	-53,5	0,0104065	14,75	-35,25974	-1,1553191
sly-MIR172-6	160	15,625	33,125	15	36,25	30,625	69,375	1,0943396	1,0416667	-42,2	-36,87	0,0120814	24,46	-26,375	-0,8612245
sly-MIR172-7	104	17,307692	34,615385	16,346154	31,730769	33,653846	66,346154	0,9166667	1,0588235	-41,9	-41,9	0,175805	7,29	-40,288462	-1,1971429
sly-MIR172-8	169	17,159763	33,136095	13,609467	36,094675	30,769231	69,230769	1,0892857	1,2608696	-58,4	-53,07	0,0160855	21,81	-34,556213	-1,0806452
sly-MIR172a-1	251	11,553785	37,848606	19,920319	30,677291	31,474104	68,525896	0,8105263	0,58	-55,8	-55,7	0,0028099	16,21	-22,231076	-0,9013889
sly-MIR172a-2	124	17,741935	36,290323	20,16129	25,806452	37,903226	62,096774	0,7111111	0,88	-53,4	-53,4	0,240194	2,99	-43,064516	-0,7742857
sly-MIR172b	111	15,315315	31,531532	15,315315	37,837838	30,630631	69,369369	1,2	1	-37,4	-37,4	0,0807936	5,37	-33,693694	-0,9875
sly-MIR172c	94	23,404255	28,723404	15,957447	31,914894	39,361702	60,638298	1,1111111	1,4666667	-42,2	-38,7	0,0789023	8,39	-44,893617	-1,1405405
sly-MIR172d-1	112	16,071429	39,285714	14,285714	30,357143	30,357143	69,642857	0,7727273	1,125	-29,6	-24,1	0,0282779	19,73	-26,428571	-0,9966102
sly-MIR172d-2	105	13,333333	39,047619	17,142857	30,47619	30,47619	69,52381	0,7804878	0,7777778	-30,7	-30,7	0,195275	4,26	-29,238095	-0,8236111
sly-MIR172d-3	106	14,150943	39,622642	16,981132	29,245283	31,132075	68,867925	0,7380952	0,8333333	-40	-40	0,293467	2,22	-37,735849	-1,402439
sly-MIR172e	188	14,893617	32,446809	15,425532	37,234043	30,319149	69,680851	1,147541	0,9655172	-58,7	-50,1	0,0027847	19,61	-31,223404	-1,0298246
sly-MIR172j	109	16,513761	30,275229	25,688073	27,522936	42,201835	57,798165	0,9090909	0,6428571	-46,2	-45,2	0,157	3,73	-42,385321	-0,924
sly-MIR1863	208	21,634615	28,846154	17,788462	31,730769	39,423077	60,576923	1,1	1,2162162	-72,6	-69,5	0,005693	33,88	-34,903846	-0,8853659
sly-MIR1863a	273	21,245421	26,739927	25,274725	26,739927	46,520147	53,479853	1	0,8405797	-89,2	-89,2	0,0297416	15,64	-32,673993	-0,7943396
sly-MIR1865	76	22,368421	26,315789	25	26,315789	47,368421	52,631579	1	0,8947368	-34,1	-34,1	0,163678	2,92	-44,868421	-0,9472222
sly-MIR1886f-1	187	20,320856	26,203209	20,320856	33,15508	40,641711	59,358289	1,2653061	1	-56,7	-44,8	0,0008493	48,29	-30,320856	-0,773913
sly-MIR1886f-2	87	24,137931	25,287356	14,942529	35,632184	39,08046	60,91954	1,4090909	1,6153846	-34,8	-34,7	0,0458517	6,3	-40	-0,8787879
sly-MIR1886h-1	71	21,126761	25,352113	12,676056	40,84507	33,802817	66,197183	1,6111111	1,6666667	-33,9	-33,9	0,29984	3,19	-47,746479	-1,4125
sly-	174	18,390805	29,885057	15,517241	36,206897	33,908046	66,091954	1,2115385	1,1851852	-58,8	-51,47	0,0064982	41,44	-33,793103	-1,2653333

MIR1886h-2															
sly-MIR1888b-1	271	20,295203	32,472325	14,760148	32,472325	35,055351	64,944649	1	1,375	-90,9	-82,7	0,0005106	44,51	-33,542435	-1,0875
sly-MIR1888b-2	340	21,470588	34,411765	11,176471	32,941176	32,647059	67,352941	0,957265	1,9210526	-88,1	-72,3	2,27E-05	74,43	-25,911765	-0,9568421
sly-MIR1888b-3	268	22,761194	30,970149	15,671642	30,597015	38,432836	61,567164	0,9879518	1,452381	-75,1	-54,3	0,0002988	80,49	-28,022388	-0,7839623
sly-MIR1917-1	130	17,692308	34,615385	16,923077	30,769231	34,615385	65,384615	0,8888889	1,0454545	-32,5	-29,5	0,0074152	11,98	-25	-0,7222222
sly-MIR1917-2	191	16,753927	34,554974	16,230366	32,460733	32,984293	67,015707	0,9393939	1,0322581	-52,9	-51,8	0,0018751	27,67	-27,696335	-0,7507042
sly-MIR1917-3	94	19,148936	37,234043	11,702128	31,914894	30,851064	69,148936	0,8571429	1,6363636	-25,3	-25,3	0,0829368	5,24	-26,914894	-1,1414634
sly-MIR1917-4	227	14,977974	40,088106	16,740088	28,193833	31,718062	68,281938	0,7032967	0,8947368	-62	-61,1	0,0013714	32,7	-27,312775	-0,9921053
sly-MIR1917-5	206	17,961165	36,893204	13,592233	31,553398	31,553398	68,446602	0,8552632	1,3214286	-59,7	-56,6	0,0028632	26,41	-28,980583	-0,71
sly-MIR1917-6	137	18,978102	36,49635	16,058394	28,467153	35,036496	64,963504	0,78	1,1818182	-44,9	-44,9	0,0481727	9,5	-32,773723	-1,040678
sly-MIR1917-7	165	16,969697	35,757576	13,333333	33,939394	30,30303	69,69697	0,9491525	1,2727273	-40,8	-38	0,0078832	17,98	-24,727273	-1,6032787
sly-MIR1917-8	214	16,82243	39,719626	13,551402	29,906542	30,373832	69,626168	0,7529412	1,2413793	-59,8	-59,1	0,0095628	15,07	-27,943925	-0,9458824
sly-MIR1918-1	127	16,535433	29,92126	20,472441	33,070866	37,007874	62,992126	1,1052632	0,8076923	-41,5	-27,8	0,0199569	20,41	-32,677165	-0,8829787
sly-MIR1918-2	166	19,277108	32,53012	16,26506	31,927711	35,542169	64,457831	0,9814815	1,1851852	-69,6	-68,9	0,0343249	9,13	-41,927711	-0,9047619
sly-MIR1919-1	124	21,774194	25	20,16129	33,064516	41,935484	58,064516	1,3225806	1,08	-60,1	-59,62	0,0612351	8,57	-48,467742	-1,1557692
sly-MIR1919-2	149	22,818792	23,489933	19,463087	34,228188	42,281879	57,718121	1,4571429	1,1724138	-56,2	-52,7	0,0136523	17,97	-37,718121	-0,8920635
sly-MIR1919-3	177	22,033898	23,163842	22,033898	32,768362	44,067797	55,932203	1,4146341	1	-83,2	-78,5	0,0318773	16,25	-47,00565	-1,1142857
sly-MIR1919-4	177	22,59887	22,59887	22,033898	32,768362	44,632768	55,367232	1,45	1,025641	-83,2	-79,7	0,0263846	15,25	-47,00565	-0,7306452
sly-MIR1919-5	164	20,731707	32,926829	22,560976	23,780488	43,292683	56,707317	0,7222222	0,9189189	-62,8	-62,8	0,0061429	13,18	-38,292683	-0,8784615
sly-MIR1919-6	107	20,560748	28,971963	20,560748	29,906542	41,121495	58,878505	1,0322581	1	-46,6	-46,6	0,116525	10,67	-43,551402	-0,746
sly-MIR1919-7	311	19,292605	31,832797	13,826367	35,048232	33,118971	66,881029	1,1010101	1,3953488	-73,6	-58,2	3,44E-05	60,37	-23,665595	-0,7111111
sly-MIR1919-8	161	22,981366	36,024845	15,52795	25,465839	38,509317	61,490683	0,7068966	1,48	-45,5	-42,8	0,0093182	11,55	-28,26087	-0,7514286
sly-MIR2089	177	15,254237	33,333333	15,254237	36,158192	30,508475	69,491525	1,0847458	1	-79,7	-74	0,0432896	18,41	-45,028249	-1,6051724
sly-MIR2101	82	15,853659	26,829268	20,731707	36,585366	36,585366	63,414634	1,3636364	0,7647059	-23,5	-23,5	0,477366	3,55	-28,658537	-0,7833333
sly-MIR2107-1	189	22,222222	23,809524	21,164021	32,804233	43,386243	56,613757	1,3777778	1,05	-77,8	-65,7	0,0066917	53,93	-41,164021	-0,7259259
sly-MIR2107-2	231	21,645022	19,047619	24,242424	35,064935	45,887446	54,112554	1,8409091	0,8928571	-83,1	-62,07	0,0005663	58,83	-35,974026	-0,7326531
sly-MIR2111d	71	21,126761	25,352113	16,901408	36,619718	38,028169	61,971831	1,4444444	1,25	-36,4	-36,4	0,232791	2,07	-51,267606	-1,3481481
sly-MIR2118	154	18,181818	33,116883	12,337662	36,363636	30,519481	69,480519	1,0980392	1,4736842	-38,2	-37,6	0,0026705	22,05	-24,805195	-1,2102564
sly-MIR2118a	185	17,297297	30,27027	17,837838	34,594595	35,135135	64,864865	1,1428571	0,969697	-90,8	-90	0,0111843	13,97	-49,081081	-0,9842105
sly-MIR2120	210	15,714286	37,142857	15,238095	31,904762	30,952381	69,047619	0,8589744	1,03125	-48,9	-37,3	0,0056659	52,41	-23,285714	-0,9092593
sly-MIR2275a-1	74	27,027027	24,324324	25,675676	22,972973	52,702703	47,297297	0,9444444	1,0526316	-29,2	-29,2	0,495684	1,69	-39,459459	-0,7039216
sly-MIR2275a-2	190	21,052632	33,157895	15,789474	30	36,842105	63,157895	0,9047619	1,3333333	-51,7	-44,9	0,0198953	28,21	-27,210526	-0,9224719
sly-MIR2604-1	287	14,982578	31,010453	17,421603	36,585366	32,404181	67,595819	1,1797753	0,86	-73,5	-49,9	0,0002789	69,06	-25,609756	-0,7903226
sly-MIR2604-2	199	17,085427	29,648241	15,577889	37,688442	32,663317	67,336683	1,2711864	1,0967742	-69,5	-63,1	0,0081451	31,66	-34,924623	-0,7131148
sly-MIR2607-1	77	19,480519	36,363636	14,285714	29,87013	33,766234	66,233766	0,8214286	1,3636364	-26,2	-25	0,0298097	8,43	-34,025974	-0,7727273
sly-MIR2607-2	185	22,702703	31,351351	9,1891892	36,756757	31,891892	68,108108	1,1724138	2,4705882	-43,9	-38,5	0,0059417	30,72	-23,72973	-0,8559322
sly-MIR2634	178	18,539326	32,58427	12,359551	36,516854	30,898876	69,101124	1,1206897	1,5	-47,2	-37,3	0,0121937	35,31	-26,516854	-1,1514706

sly-MIR2654	87	22,988506	27,586207	13,793103	35,632184	36,781609	63,218391	1,2916667	1,6666667	-34,3	-33,4	0,13061	7,16	-39,425287	-0,9218391
sly-MIR2655o-1	262	18,70229	27,862595	13,358779	40,076336	32,061069	67,938931	1,4383562	1,4	-85,1	-83	0,0015685	22,68	-32,480916	-1,09
sly-MIR2655o-2	292	17,123288	30,821918	14,041096	38,013699	31,164384	68,835616	1,2333333	1,2195122	-83,2	-66,32	0,0001478	71,41	-28,493151	-1,4967742
sly-MIR2673b	196	21,938776	28,571429	19,897959	29,591837	41,836735	58,163265	1,0357143	1,1025641	-57,7	-31,2	0,0131078	53,51	-29,438776	-0,7036585
sly-MIR2676f	135	14,814815	28,148148	20	37,037037	34,814815	65,185185	1,3157895	0,7407407	-57,8	-57,4	0,170187	6,05	-42,814815	-1,0918367
sly-MIR2680e	151	17,880795	29,801325	15,89404	36,423841	33,774834	66,225166	1,2222222	1,125	-87,9	-86,3	0,061938	7,45	-58,211921	-0,7771429
sly-MIR2863b	170	17,058824	28,235294	13,529412	41,176471	30,588235	69,411765	1,4583333	1,2608696	-45	-45	0,0639295	7,49	-26,470588	-1,1310811
sly-MIR2864	196	22,44898	29,081633	16,836735	31,632653	39,285714	60,714286	1,0877193	1,3333333	-80,3	-80,3	0,036843	10,15	-40,969388	-1,0428571
sly-MIR2872	291	14,089347	32,646048	16,838488	36,426117	30,927835	69,072165	1,1157895	0,8367347	-64	-61,2	0,0020639	32,51	-21,993127	-0,7111111
sly-MIR2875	202	16,336634	33,663366	17,326733	32,673267	33,663366	66,336634	0,9705882	0,9428571	-66,2	-66,2	0,0310893	11,02	-32,772277	-1,395
sly-MIR2876	103	29,126214	22,330097	27,184466	21,359223	56,31068	43,68932	0,9565217	1,0714286	-41,8	-41,8	0,0515955	11,14	-40,582524	-0,9288136
sly-MIR2923	255	20,784314	32,156863	10,588235	36,470588	31,372549	68,627451	1,1341463	1,962963	-56,3	-41,8	3,75E-05	58,02	-22,078431	-0,7805825
sly-MIR2928	305	16,393443	33,770492	14,098361	35,737705	30,491803	69,508197	1,0582524	1,1627907	-66,3	-61,4	3,56E-05	51,47	-21,737705	-0,7444444
sly-MIR2929	96	22,916667	27,083333	20,833333	29,166667	43,75	56,25	1,0769231	1,1	-32,7	-32,7	0,198109	3,58	-34,0625	-1,0034091
sly-MIR2931-1	261	21,072797	28,735632	14,559387	35,632184	35,632184	64,367816	1,24	1,4473684	-65,7	-42,7	0,0001361	82,6	-25,172414	-0,8368421
sly-MIR2931-2	163	19,018405	31,288344	15,337423	34,355828	34,355828	65,644172	1,0980392	1,24	-67,9	-64,2	0,0370557	11,27	-41,656442	-1,2233333
sly-MIR319a-1	182	23,626374	27,472527	20,879121	28,021978	44,505495	55,494505	1,02	1,1315789	-82,2	-77	0,0402093	22,69	-45,164835	-1,0148148
sly-MIR319a-2	185	21,081081	27,027027	18,378378	33,513514	39,459459	60,540541	1,24	1,1470588	-92,3	-91,6	0,0174515	9,73	-49,891892	-1,2643836
sly-MIR319a-3	189	24,867725	25,925926	21,164021	28,042328	46,031746	53,968254	1,0816327	1,175	-82,8	-76,3	0,0164531	16,07	-43,809524	-1,0168831
sly-MIR319b	198	23,232323	29,79798	20,20202	26,767677	43,434343	56,565657	0,8983051	1,15	-95,6	-95,6	0,102878	5,75	-48,282828	-1,1116279
sly-MIR319c	178	25,280899	23,595506	21,910112	29,213483	47,191011	52,808989	1,2380952	1,1538462	-77,1	-65,9	0,0238786	17,43	-43,314607	-0,9178571
sly-MIR319d	179	25,139665	23,463687	20,111732	31,284916	45,251397	54,748603	1,3333333	1,25	-86,8	-86	0,0371958	6,34	-48,49162	-1,0716049
sly-MIR319h	71	26,760563	21,126761	25,352113	26,760563	52,112676	47,887324	1,2666667	1,0555556	-27,6	-27,2	0,078875	5,83	-38,873239	-0,7082474
sly-MIR319n	159	19,496855	32,075472	19,496855	28,930818	38,993711	61,006289	0,9019608	1	-45,3	-44,1	0,0111482	22,12	-28,490566	-0,96875
sly-MIR3436	138	18,84058	30,434783	15,217391	35,507246	34,057971	65,942029	1,1666667	1,2380952	-36,5	-35,3	0,0297956	20,79	-26,449275	-0,7647059
sly-MIR3447	212	20,754717	23,113208	16,509434	39,622642	37,264151	62,735849	1,7142857	1,2571429	-55,7	-50,2	0,0006991	44,07	-26,273585	-0,7050633
sly-MIR3448-1	293	20,477816	31,399317	19,112628	29,010239	39,590444	60,409556	0,923913	1,0714286	-84	-78,6	0,0007536	42,18	-28,668942	-1,0096774
sly-MIR3448-2	104	23,076923	34,615385	13,461538	28,846154	36,538462	63,461538	0,8333333	1,7142857	-29	-29	0,201646	6,65	-27,884615	-0,7283951
sly-MIR3509	105	21,904762	24,761905	19,047619	34,285714	40,952381	59,047619	1,3846154	1,15	-56,2	-56,1	0,0744708	4,92	-53,52381	-0,7111111
sly-MIR3511	269	23,048327	24,907063	16,728625	35,315985	39,776952	60,223048	1,4179104	1,3777778	-76,3	-73,1	0,0015858	43,16	-28,364312	-0,7793103
sly-MIR3513	134	22,38806	30,597015	20,895522	26,119403	43,283582	56,716418	0,8536585	1,0714286	-87,3	-87	0,407195	3,32	-65,149254	-0,9166667
sly-MIR3515	292	17,808219	31,164384	14,726027	36,30137	32,534247	67,465753	1,1648352	1,2093023	-66,6	-60,68	0,0010605	41,75	-22,808219	-0,9651515
sly-MIR3623	234	18,376068	29,059829	17,521368	35,042735	35,897436	64,102564	1,2058824	1,0487805	-63,2	-59,1	0,0007627	24,33	-27,008547	-0,7755319
sly-MIR3627	125	22,4	27,2	20	30,4	42,4	57,6	1,1176471	1,12	-47,6	-47,6	0,149706	5,08	-38,08	-0,7066667
sly-MIR3706	70	25,714286	28,571429	15,714286	30	41,428571	58,571429	1,05	1,6363636	-30	-30	0,671559	1,48	-42,857143	-1,1782609
sly-MIR390-1	113	22,123894	23,893805	21,238938	32,743363	43,362832	56,637168	1,3703704	1,0416667	-56,9	-56,9	0,590138	1,36	-50,353982	-1,1612245
sly-MIR390-2	106	20,754717	30,188679	22,641509	26,415094	43,396226	56,603774	0,875	0,9166667	-43,7	-43,7	0,157079	5,71	-41,226415	-0,9030303
sly-MIR390a-1	103	22,330097	26,213592	21,359223	30,097087	43,68932	56,31068	1,1481481	1,0454545	-51,1	-48,4	0,109752	6,21	-49,61165	-1,1355556
sly-MIR390a-2	102	22,54902	26,470588	20,588235	30,392157	43,137255	56,862745	1,1481481	1,0952381	-49,4	-46,7	0,140767	5,83	-48,431373	-1,1227273
sly-MIR390a-3	181	15,469613	39,226519	17,127072	28,176796	32,596685	67,403315	0,7183099	0,9032258	-50,5	-48,17	0,0204094	13,12	-27,900552	-0,8637931
sly-MIR391	96	23,958333	34,375	16,666667	25	40,625	59,375	0,7272727	1,4375	-46,7	-46,7	0,336484	3,38	-48,645833	-1,1974359
sly-MIR3932b	179	18,994413	30,726257	16,759777	33,519553	35,75419	64,24581	1,0909091	1,1333333	-56,4	-54,3	0,0037964	24,3	-31,50838	-0,7294872
sly-MIR393b	78	21,794872	26,923077	20,512821	30,769231	42,307692	57,692308	1,1428571	1,0625	-39,9	-39,9	0,199073	2,73	-51,153846	-1,2090909
sly-MIR394-1	81	28,395062	22,222222	27,160494	22,222222	55,555556	44,444444	1	1,0454545	-43,7	-43,4	0,247506	3,21	-53,950617	-0,9711111
sly-MIR394-2	61	29,508197	21,311475	27,868852	21,311475	57,377049	42,622951	1	1,0588235	-31,2	-30,9	0,175055	3,56	-51,147541	-0,8914286
sly-MIR394b	235	25,531915	31,06383	14,468085	28,93617	40	60	0,9315068	1,7647059	-81,2	-74,37	0,0028271	29,21	-34,553191	-0,8638298
sly-MIR3950	295	21,355932	31,525424	9,8305085	37,288136	31,186441	68,813559	1,1827957	2,1724138	-67,6	-56	1,83E-05	60,85	-22,915254	-1,1575758
sly-MIR3951b-1	181	19,889503	28,729282	14,364641	37,016575	34,254144	65,745856	1,2884615	1,3846154	-49,4	-46,9	0,0116787	26,09	-27,292818	-1,5851064
sly-MIR3951b-2	244	20,901639	34,42623	12,704918	31,967213	33,606557	66,393443	0,9285714	1,6451613	-62,9	-55,7	0,0024047	44,48	-25,778689	-1,1289474
sly-MIR395a-1	88	22,727273	18,181818	22,727273	36,363636	45,454545	54,545455	2	1	-42,1	-42,1	0,321886	3,22	-47,840909	-1,0525
sly-MIR395a-	165	22,424242	29,090909	16,969697	31,515152	39,393939	60,606061	1,0833333	1,3214286	-61,6	-60	0,0354107	16,45	-37,333333	-0,9348485

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sly-MIR395a-2	88	21,590909	18,181818	23,863636	36,363636	45,454545	54,545455	2	0,9047619	-38,7	-38,3	0,138292	4,73	-43,977273	-0,9675
sly-MIR395a-3	115	20,869565	25,217391	16,521739	37,391304	37,391304	62,608696	1,4827586	1,2631579	-48,3	-48,3	0,354595	4,23	-42	-1,1232558
sly-MIR395a-4	146	20,547945	30,821918	18,493151	30,136986	39,041096	60,958904	0,9777778	1,1111111	-55	-52,2	0,122285	9,89	-37,671233	-0,893617
sly-MIR395a-5	107	23,364486	17,757009	23,364486	35,514019	46,728972	53,271028	2	1	-50,9	-50,9	0,270938	4,1	-47,570093	-1,0666667
sly-MIR395a-6	151	22,516556	28,476821	16,556291	32,450331	39,072848	60,927152	1,1395349	1,36	-56,7	-56,7	0,069146	10,43	-37,549669	-1,2081081
sly-MIR395a-7	174	22,988506	28,16092	15,517241	33,333333	38,505747	61,494253	1,1836735	1,4814815	-59,1	-58,5	0,0491573	14,87	-33,965517	-1,0965116
sly-MIR395a-8	165	22,424242	28,484848	17,575758	31,515152	40	60	1,106383	1,2758621	-61,7	-61,7	0,0577673	16,72	-37,393939	-0,9939759
sly-MIR395a-9	107	23,364486	17,757009	22,429907	36,448598	45,794393	54,205607	2,0526316	1,0416667	-49,9	-49,9	0,18711	5,72	-46,635514	-0,8289474
sly-MIR395b-1	88	23,863636	19,318182	22,727273	34,090909	46,590909	53,409091	1,7647059	1,05	-35,2	-34,1	0,0058219	11,54	-40	-0,8585366
sly-MIR395b-10	170	24,705882	27,058824	17,647059	30,588235	42,352941	57,647059	1,1304348	1,4	-61,8	-55,4	0,0395848	23,81	-36,352941	-0,8271739
sly-MIR395b-2	88	29,545455	20,454545	18,181818	31,818182	47,727273	52,272727	1,5555556	1,625	-34,1	-34,1	0,0914568	5,27	-38,75	-0,8119048
sly-MIR395b-3	88	28,409091	20,454545	19,318182	31,818182	47,727273	52,272727	1,5555556	1,4705882	-34,1	-34	0,0987628	5,21	-38,75	-0,8119048
sly-MIR395b-4	88	23,863636	17,045455	22,727273	36,363636	46,590909	53,409091	2,1333333	1,05	-41,1	-40	0,0747377	6,11	-46,704545	-1,002439
sly-MIR395b-5	102	24,509804	20,588235	19,607843	35,294118	44,117647	55,882353	1,7142857	1,25	-42,4	-42,2	0,230176	3,63	-41,568627	-0,9422222
sly-MIR395b-6	100	25	15	23	37	48	52	2,4666667	1,0869565	-39,9	-39,9	0,108636	6,91	-39,9	-0,83125
sly-MIR395b-7	100	26	17	22	35	48	52	2,0588235	1,1818182	-42,8	-42,7	0,0428689	7,51	-42,8	-0,8916667
sly-MIR395b-8	107	23,364486	19,626168	20,560748	36,448598	43,925234	56,074766	1,8571429	1,1363636	-51,4	-51,4	0,0956258	5,93	-48,037383	-0,8020619
sly-MIR395b-9	170	25,882353	26,470588	15,882353	31,764706	41,764706	58,235294	1,2	1,6296296	-61,3	-61,3	0,11163	14,14	-36,058824	-0,98125
sly-MIR395c	172	22,674419	30,232558	15,116279	31,976744	37,790698	62,209302	1,0576923	1,5	-55,3	-54,4	0,0156216	23,63	-32,151163	-0,7191781
sly-MIR396a-1	144	16,666667	34,027778	20,138889	29,166667	36,805556	63,194444	0,8571429	0,8275862	-51,6	-50,2	0,0321931	10,38	-35,833333	-0,9735849
sly-MIR396a-2	130	14,615385	36,923077	19,230769	29,230769	33,846154	66,153846	0,7916667	0,76	-35,8	-30,61	0,0207255	16,47	-27,538462	-0,9466667
sly-MIR396b-1	133	18,796992	30,075188	14,285714	36,842105	33,082707	66,917293	1,225	1,3157895	-56,8	-53,51	0,0300123	14,47	-42,706767	-1,2909091
sly-MIR396b-2	161	18,012422	32,298137	13,043478	36,645963	31,055901	68,944099	1,1346154	1,3809524	-57	-51,81	0,0059019	24,77	-35,403727	-1,14
sly-MIR396b-3	135	17,037037	34,074074	13,333333	35,555556	30,37037	69,62963	1,0434783	1,2777778	-49,6	-46,31	0,0245187	16,84	-36,740741	-1,2097561
sly-MIR396f	134	19,402985	29,850746	15,671642	35,074627	35,074627	64,925373	1,175	1,2380952	-49,5	-46	0,0025905	19,62	-36,940299	-1,0531915
sly-MIR397-1	115	18,26087	26,086957	20	35,652174	38,26087	61,73913	1,3666667	0,9130435	-52,8	-52,4	0,0749916	7,19	-45,913043	-1,2
sly-MIR397-2	120	19,166667	26,666667	18,333333	35,833333	37,5	62,5	1,34375	1,0454545	-50,4	-50	0,0689571	8,64	-42	-1,12
sly-MIR397b	127	18,110236	35,433071	20,472441	25,984252	38,582677	61,417323	0,7333333	0,8846154	-48	-48	0,0469476	9,52	-37,795276	-0,9730769
sly-MIR398-1	108	17,592593	24,074074	17,592593	40,740741	35,185185	64,814815	1,6923077	1	-50,3	-48,2	0,163333	11,44	-46,574074	-1,3236842
sly-MIR398-2	211	18,483412	29,85782	15,165877	36,492891	33,649289	66,350711	1,2222222	1,21875	-71,8	-65,3	0,0001324	38,99	-34,028436	-0,786
sly-MIR398a	100	19	29	15	37	34	66	1,2758621	1,2666667	-38,6	-37	0,045403	12,28	-38,6	-1,1352941
sly-MIR399a-1	140	15	32,142857	17,857143	35	32,857143	67,142857	1,0888889	0,84	-63	-53,7	0,023523	18,93	-45	-1,3695652
sly-MIR399a-2	94	19,148936	28,723404	18,085106	34,042553	37,234043	62,765957	1,1851852	1,0588235	-32,9	-32,6	0,0741787	7,24	-35	-1,115
sly-MIR399a-3	153	17,647059	33,333333	13,72549	35,294118	31,372549	68,627451	1,0588235	1,2857143	-41,8	-41,3	0,002636	17,9	-27,320261	-0,8150685
sly-MIR399a-4	155	19,354839	30,322581	18,709677	31,612903	38,064516	61,935484	1,0425532	1,0344828	-61,4	-59,8	0,0104712	11,68	-39,612903	-0,7619718
sly-MIR399b-1	103	21,359223	28,15534	19,417476	31,067961	40,776699	59,223301	1,1034483	1,1	-47,6	-47,6	0,203168	6,7	-46,213592	-0,8020202
sly-MIR399b-	217	22,119816	32,258065	18,43318	27,18894	40,552995	59,447005	0,8428571	1,2	-70,8	-70,4	0,0013189	15,6	-32,626728	-1,1825397

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sly-MIR399b-3	86	23,255814	25,581395	23,255814	27,906977	46,511628	53,488372	1,0909091	1	-43,5	-43,5	0,369104	2,13	-50,581395	-1,3675
sly-MIR399b-4	103	21,359223	26,213592	22,330097	30,097087	43,68932	56,31068	1,1481481	0,9565217	-50,1	-50,1	0,478969	1,93	-48,640777	-0,743662
sly-MIR399e	253	23,320158	30,434783	9,8814229	36,363636	33,201581	66,798419	1,1948052	2,36	-59,7	-41,6	3,21E-05	52,24	-23,596838	-0,83
sly-MIR399f	140	17,857143	35	15	32,142857	32,857143	67,142857	0,9183673	1,1904762	-66,2	-66	0,050466	8,52	-47,285714	-1,1952381
sly-MIR399i-1	80	22,5	30	18,75	28,75	41,25	58,75	0,9583333	1,2	-37	-37	0,589033	1,75	-46,25	-1,1212121
sly-MIR399i-2	107	21,495327	28,037383	15,88785	34,579439	37,383178	62,616822	1,2333333	1,3529412	-55,8	-53,5	0,237852	2,78	-52,149533	-1,0631579
sly-MIR399o	89	20,224719	28,089888	25,842697	25,842697	46,067416	53,932584	0,92	0,7826087	-36,6	-36,6	0,510615	4,59	-41,123596	-0,8926829
sly-MIR399r-1	123	17,073171	29,268293	15,447154	38,211382	32,520325	67,479675	1,3055556	1,1052632	-50,2	-48,5	0,0626769	15,68	-40,813008	-1,255
sly-MIR399r-2	126	14,285714	28,571429	20,634921	36,507937	34,920635	65,079365	1,2777778	0,6923077	-47,6	-45,7	0,0813954	8,9	-37,777778	-0,8507692
sly-MIR403	112	17,857143	27,678571	19,642857	34,821429	37,5	62,5	1,2580645	0,9090909	-44,9	-42,2	0,048325	8,94	-40,089286	-1,1507937
sly-MIR403b	112	19,642857	34,821429	17,857143	27,678571	37,5	62,5	0,7948718	1,1	-43	-41,7	0,0982045	8,89	-38,392857	-0,8888889
sly-MIR407	258	19,379845	31,395349	12,015504	37,209302	31,395349	68,604651	1,1851852	1,6129032	-58,8	-44,4	0,0001987	47,53	-22,790698	-1,0776471
sly-MIR408-1	71	25,352113	18,309859	28,169014	28,169014	53,521127	46,478873	1,5384615	0,9	-32	-32	0,704395	1,32	-45,070423	-0,8421053
sly-MIR408-2	128	25,78125	32,03125	22,65625	19,53125	48,4375	51,5625	0,6097561	1,137931	-46,6	-41,4	0,0291793	9,07	-36,40625	-0,8145161
sly-MIR408-3	291	19,931271	30,584192	17,525773	31,958763	37,457045	62,542955	1,0449438	1,1372549	-77,9	-75,7	0,0012903	47,98	-26,769759	-0,7923077
sly-MIR408a	72	23,611111	23,611111	26,388889	26,388889	50	50	1,1176471	0,8947368	-37,5	-36	0,713897	0,93	-52,083333	-1,0416667
sly-MIR414	190	15,263158	31,052632	18,421053	35,263158	33,684211	66,315789	1,1355932	0,8285714	-63,5	-61,9	0,0042301	16,36	-33,421053	-1,3114754
sly-MIR415	273	19,413919	33,699634	12,087912	34,798535	31,501832	68,498168	1,0326087	1,6060606	-66,9	-63,2	0,000119	37,3	-24,505495	-0,7684932
sly-MIR417	248	18,951613	33,870968	14,516129	32,66129	33,467742	66,532258	0,9642857	1,3055556	-96,7	-96,7	0,0013888	16,6	-38,991935	-0,7115108
sly-MIR419	113	17,699115	30,088496	16,814159	35,39823	34,513274	65,486726	1,1764706	1,0526316	-53,7	-53,7	0,0532811	8,75	-47,522124	-0,9115385
sly-MIR4221-1	247	22,267206	32,388664	17,004049	28,340081	39,271255	60,728745	0,875	1,3095238	-68,4	-57,8	0,0010276	49,41	-27,692308	-1,7270833
sly-MIR4221-2	334	26,946108	29,94012	15,269461	27,844311	42,215569	57,784431	0,93	1,7647059	-99,9	-93,5	0,0001519	69,38	-29,91018	-0,7489362
sly-MIR4348c	161	18,012422	34,782609	19,254658	27,950311	37,267081	62,732919	0,8035714	0,9354839	-62,6	-62,6	0,0550423	11,12	-38,881988	-0,7460526
sly-MIR437a	270	17,407407	28,148148	12,962963	41,481481	30,37037	69,62963	1,4736842	1,3428571	-62,4	-51,69	0,0002033	41,94	-23,111111	-0,7493827
sly-MIR4415b	180	17,777778	33,888889	18,888889	29,444444	36,666667	63,333333	0,8688525	0,9411765	-79,7	-70,9	0,0114588	25,93	-44,277778	-1,6311111
sly-MIR444b	201	17,412935	30,348259	13,432836	38,80597	30,845771	69,154229	1,2786885	1,2962963	-43,8	-42,8	0,0050138	23,72	-21,791045	-0,8836066
sly-MIR477-1	132	21,212121	28,787879	22,727273	27,272727	43,939394	56,060606	0,9473684	0,9333333	-53,2	-50,1	0,054659	9,94	-40,30303	-0,9172414
sly-MIR477-2	114	25,438596	27,192982	21,052632	26,315789	46,491228	53,508772	0,9677419	1,2083333	-56,7	-56,2	0,136212	7,34	-49,736842	-1,0698113
sly-MIR477-3	242	16,115702	33,884298	14,876033	35,123967	30,991736	69,008264	1,0365854	1,0833333	-58,8	-58	0,0053984	16,56	-24,297521	-1,2767857
sly-MIR477a	70	25,714286	20	27,142857	27,142857	52,857143	47,142857	1,3571429	0,9473684	-35,9	-34,5	0,0498196	3,89	-51,285714	-0,9702703
sly-MIR477b	72	23,611111	22,222222	22,222222	31,944444	45,833333	54,166667	1,4375	1,0625	-34,4	-29,2	0,188148	4,56	-47,777778	-1,0424242
sly-MIR477d	114	21,929825	28,947368	12,280702	36,842105	34,210526	65,789474	1,2727273	1,7857143	-28,4	-28,4	0,0632152	20,3	-24,912281	-1,08
sly-MIR477e-1	180	18,888889	29,444444	17,777778	33,888889	36,666667	63,333333	1,1509434	1,0625	-85,6	-81,7	0,0243647	17,83	-47,555556	-1,2969697
sly-MIR477e-2	67	23,880597	37,313433	16,41791	22,38806	40,298507	59,701493	0,6	1,4545455	-22,2	-21,3	0,198337	4,75	-33,134328	-0,733913
sly-MIR478f	116	19,827586	26,724138	16,37931	37,068966	36,206897	63,793103	1,3870968	1,2105263	-39,2	-37,2	0,0983085	10,45	-33,793103	-1,3661538
sly-MIR479-1	92	21,73913	29,347826	18,478261	30,434783	40,217391	59,782609	1,037037	1,1764706	-40,9	-39,7	0,0909347	7,81	-44,456522	-1,1054054
sly-MIR479-2	112	20,535714	31,25	18,75	29,464286	39,285714	60,714286	0,9428571	1,0952381	-54,3	-53,1	0,0848896	7,74	-48,482143	-0,9610169
sly-MIR482b-1	80	23,75	27,5	20	28,75	43,75	56,25	1,0454545	1,1875	-37,7	-37,7	0,24015	3,21	-47,125	-0,8820896
sly-MIR482b-2	110	20	28,181818	18,181818	33,636364	38,181818	61,818182	1,1935484	1,1	-67,6	-67,5	0,111525	3,91	-61,454545	-0,9942857
sly-MIR482b-3	91	18,681319	36,263736	17,582418	27,472527	36,263736	63,736264	0,7575758	1,0625	-26,1	-23	0,0409701	12,56	-28,681319	-1,3078431
sly-MIR482c-1	97	20,618557	19,587629	18,556701	41,237113	39,175258	60,824742	2,1052632	1,1111111	-43,7	-43,7	0,275596	2,69	-45,051546	-1,15
sly-MIR482c-2	105	20,952381	18,095238	18,095238	42,857143	39,047619	60,952381	2,3684211	1,1578947	-41,3	-41,3	0,214573	3,19	-39,333333	-1,0073171
sly-MIR482c-3	91	19,78022	18,681319	18,681319	42,857143	38,461538	61,538462	2,2941176	1,0588235	-42,4	-42,4	0,366359	1,78	-46,593407	-1,2114286
sly-MIR482c-4	99	23,232323	24,242424	28,282828	24,242424	51,515152	48,484848	1	0,8214286	-35,9	-34,7	0,111243	9,73	-36,262626	-1,1746269
sly-MIR482c-5	149	23,489933	22,818792	16,107383	37,583893	39,597315	60,402685	1,6470588	1,4583333	-67,3	-65,8	0,0116463	24,72	-45,167785	-0,7580247
sly-MIR482d-1	113	23,00885	28,318584	13,274336	35,39823	36,283186	63,716814	1,25	1,7333333	-45,7	-45,3	0,0756935	11,07	-40,442478	-0,7757576
sly-MIR482d-2	128	26,5625	31,25	12,5	29,6875	39,0625	60,9375	0,95	2,125	-37,3	-35,4	0,0299416	19,35	-29,140625	-0,70375

sly-MIR482d-3	165	17,575758	34,545455	18,181818	29,69697	35,757576	64,242424	0,8596491	0,9666667	-68,4	-63,79	0,0162891	21,8	-41,454545	-1,2490196
sly-MIR482e	189	22,222222	24,338624	17,460317	35,978836	39,68254	60,31746	1,4782609	1,2727273	-76	-75,9	0,0196879	12,81	-40,21164	-1,0133333
sly-MIR482j	315	21,587302	27,619048	18,730159	32,063492	40,31746	59,68254	1,1609195	1,1525424	-93,4	-77,6	2,10E-05	68,89	-29,650794	-1,0678571
sly-MIR4994	337	21,661721	29,673591	16,023739	32,64095	37,68546	62,31454	1,1	1,3518519	-91,1	-57,41	5,14E-05	89,51	-27,032641	-1,0741935
sly-MIR5014a-1	172	16,27907	36,627907	18,023256	29,069767	34,302326	65,697674	0,7936508	0,9032258	-58,7	-58,7	0,0516028	4,96	-34,127907	-1,122449
sly-MIR5014a-10	259	15,830116	38,223938	14,671815	31,274131	30,501931	69,498069	0,8181818	1,0789474	-59,9	-56,4	0,0004669	24,71	-23,127413	-0,9897436
sly-MIR5014a-2	209	13,875598	38,277512	16,267943	31,578947	30,143541	69,856459	0,825	0,8529412	-72,5	-72,5	0,0059024	14,08	-34,688995	-0,8690476
sly-MIR5014a-3	270	16,666667	36,296296	14,074074	32,962963	30,740741	69,259259	0,9081633	1,1842105	-99,4	-96,8	0,005738	13,32	-36,814815	-0,7358025
sly-MIR5014a-4	187	14,973262	38,502674	15,508021	31,016043	30,481283	69,518717	0,8055556	0,9655172	-60,6	-60,6	0,0235103	10,84	-32,406417	-0,7809524
sly-MIR5014a-5	252	14,285714	34,920635	16,666667	34,126984	30,952381	69,047619	0,9772727	0,8571429	-84,2	-83,9	0,0024707	20,16	-33,412698	-0,8396825
sly-MIR5014a-6	155	20	38,064516	10,967742	30,967742	30,967742	69,032258	0,8135593	1,8235294	-34,4	-34,4	0,0099905	20,98	-22,193548	-0,8041667
sly-MIR5014a-7	245	16,326531	31,428571	14,285714	37,959184	30,612245	69,387755	1,2077922	1,1428571	-56,7	-54,5	0,0045376	58,98	-23,142857	-0,8740741
sly-MIR5014a-8	213	20,187793	28,169014	13,14554	38,497653	33,333333	66,666667	1,3666667	1,5357143	-83,7	-83,6	0,0224299	14,88	-39,295775	-1,0833333
sly-MIR5014a-9	223	15,695067	31,838565	15,246637	37,219731	30,941704	69,058296	1,1690141	1,0294118	-79,1	-76,9	0,0066941	10,21	-35,470852	-0,7553571
sly-MIR5021-1	289	17,301038	36,678201	13,148789	32,871972	30,449827	69,550173	0,8962264	1,3157895	-64,4	-31,7	2,00E-05	106,65	-22,283737	-0,7318182
sly-MIR5021-2	115	20,869565	33,913043	13,043478	32,173913	33,913043	66,086957	0,9487179	1,6	-29,7	-28,5	0,0775402	19,1	-25,826087	-0,7648649
sly-MIR5021-3	232	23,706897	27,586207	9,0517241	39,655172	32,758621	67,241379	1,4375	2,6190476	-53,4	-32,08	0,0006952	63,02	-23,017241	-0,9255814
sly-MIR5021-4	76	32,894737	32,894737	18,421053	15,789474	51,315789	48,684211	0,48	1,7857143	-35	-35	0,347484	3,32	-46,052632	-1,0785714
sly-MIR5026-1	153	15,686275	38,562092	15,03268	30,718954	30,718954	69,281046	0,7966102	1,0434783	-55,3	-55,2	0,0695	11,77	-36,143791	-0,7268657
sly-MIR5026-2	77	22,077922	32,467532	20,779221	24,675325	42,857143	57,142857	0,76	1,0625	-29,8	-29,8	0,45238	2,29	-38,701299	-0,783
sly-MIR5026-3	169	15,976331	32,544379	18,343195	33,136095	34,319527	65,680473	1,0181818	0,8709677	-52,6	-49,1	0,037784	12,75	-31,12426	-1,6563636
sly-MIR5026-4	236	16,101695	32,20339	19,915254	31,779661	36,016949	63,983051	0,9868421	0,8085106	-70,7	-66,6	0,0114348	27,68	-29,957627	-0,7123596
sly-MIR5026-5	87	21,83908	33,333333	26,436782	18,390805	48,275862	51,724138	0,5517241	0,826087	-45,3	-45,3	0,681709	1,17	-52,068966	-1,2781818
sly-MIR5031	241	17,842324	33,195021	15,352697	33,609959	33,195021	66,804979	1,0125	1,1621622	-77,9	-68,6	0,0005109	36,97	-32,323651	-0,8581633
sly-MIR5035	142	16,901408	31,690141	16,197183	35,211268	33,098592	66,901408	1,1111111	1,0434783	-74,2	-73	0,0279829	9,39	-52,253521	-1,5787234
sly-MIR5049	247	22,267206	30,769231	16,194332	30,769231	38,461538	61,538462	1	1,375	-79,3	-47,3	0,0001255	76,72	-32,105263	-0,954717
sly-MIR5049b	324	19,135802	37,654321	16,358025	26,851852	35,493827	64,506173	0,7131148	1,1698113	-88,4	-73,47	0,0004736	49,91	-27,283951	-1,1114943
sly-MIR5049c-1	295	17,627119	34,237288	12,881356	35,254237	30,508475	69,491525	1,029703	1,3684211	-79,2	-69,34	0,0009768	37,41	-26,847458	-0,88
sly-MIR5049c-2	290	17,241379	36,206897	13,103448	33,448276	30,344828	69,655172	0,9238095	1,3157895	-88,3	-78,2	3,14E-05	47,44	-30,448276	-1,2766667
sly-MIR5083	153	15,686275	34,640523	20,261438	29,411765	35,947712	64,052288	0,8490566	0,7741935	-91,1	-89,4	0,0485835	5,86	-59,542484	-1,1725
sly-MIR5139b	208	21,634615	27,884615	23,076923	27,403846	44,711538	55,288462	0,9827586	0,9375	-83,6	-83,6	0,0341219	18,83	-40,192308	-0,9306818
sly-MIR5140	124	26,612903	31,451613	15,322581	26,612903	41,935484	58,064516	0,8461538	1,7368421	-40	-40	0,055982	8,23	-32,258065	-0,8723404
sly-MIR5161	186	13,44086	35,483871	17,204301	33,870968	30,645161	69,354839	0,9545455	0,78125	-63,5	-61,6	0,0748358	14,57	-34,139785	-1,1140351
sly-MIR5162	139	17,266187	35,971223	13,669065	33,093525	30,935252	69,064748	0,92	1,2631579	-33,5	-27,17	0,0231865	15,62	-24,100719	-1,0278689
sly-MIR5163a	259	17,760618	33,590734	14,285714	34,362934	32,046332	67,953668	1,0229885	1,2432432	-61,7	-56,6	8,77E-05	32,74	-23,822394	-1,1485714
sly-MIR5165	117	20,512821	35,897436	17,094017	26,495726	37,606838	62,393162	0,7380952	1,2	-40,7	-40,7	0,14275	4,9	-34,786325	-1,0234568
sly-MIR5168	150	25,333333	21,333333	17,333333	36	42,666667	57,333333	1,6875	1,4615385	-54,2	-47,1	0,0099286	19,16	-36,133333	-0,7220339
sly-MIR5171b	124	17,741935	37,096774	16,129032	29,032258	33,870968	66,129032	0,7826087	1,1	-33,3	-28,1	0,0081116	16,83	-26,854839	-1,3179104
sly-MIR5174d-1	248	19,758065	34,677419	13,709677	31,854839	33,467742	66,532258	0,9186047	1,4411765	-64,3	-50,65	6,23E-05	48,49	-25,927419	-0,9051724
sly-MIR5174d-2	262	11,450382	30,534351	19,465649	38,549618	30,916031	69,083969	1,2625	0,5882353	-58,2	-54,99	0,0006021	41,35	-22,206107	-0,8317647
sly-MIR5174e	188	20,212766	37,234043	13,297872	29,255319	33,510638	66,489362	0,7857143	1,52	-62,8	-60,2	0,0079949	15,83	-33,404255	-0,9968254
sly-MIR5180a	128	15,625	38,28125	14,84375	31,25	30,46875	69,53125	0,8163265	1,0526316	-43,9	-41,2	0,0569173	13,2	-34,296875	-0,7909091

sly-MIR5181b	77	18,181818	35,064935	15,584416	31,168831	33,766234	66,233766	0,8888889	1,1666667	-34,2	-34,2	0,415099	1,73	-44,415584	-1,3268293
sly-MIR5181c	234	18,376068	32,478632	16,666667	32,478632	35,042735	64,957265	1	1,1025641	-87,2	-86	0,0062345	16,31	-37,264957	-1,2837209
sly-MIR5185k	145	20,689655	37,241379	10,344828	31,724138	31,034483	68,965517	0,8518519	2	-35,3	-27,5	0,0036176	22,9	-24,344828	-1,0926829
sly-MIR5185l	198	16,666667	34,848485	14,646465	33,838384	31,313131	68,686869	0,9710145	1,137931	-50,5	-42,4	0,0011343	45,5	-25,505051	-0,7258065
sly-MIR5205a-1	116	16,37931	37,068966	19,827586	26,724138	36,206897	63,793103	0,7209302	0,826087	-30,6	-30,2	0,0209637	10,15	-26,37931	-0,7285714
sly-MIR5205a-2	290	16,551724	29,655172	16,206897	37,586207	32,758621	67,241379	1,2674419	1,0212766	-74,8	-61,59	0,0004794	53,91	-25,793103	-1,1853659
sly-MIR5218	175	18,857143	35,428571	17,142857	28,571429	36	64	0,8064516	1,1	-56	-52,4	0,0078454	23,47	-32	-0,952
sly-MIR5237	182	18,131868	36,813187	12,637363	32,417582	30,769231	69,230769	0,880597	1,4347826	-40,9	-29,8	0,0089883	41,82	-22,472527	-0,7936937
sly-MIR5274b-1	212	17,924528	32,075472	21,698113	28,301887	39,622642	60,377358	0,8823529	0,826087	-88,1	-88,1	0,0366873	12,64	-41,556604	-0,7234568
sly-MIR5274b-2	244	34,836066	15,163934	22,540984	27,459016	57,377049	42,622951	1,8108108	1,5454545	-99,6	-86,5	0,0024089	49,55	-40,819672	-0,9909091
sly-MIR5274b-3	283	15,194346	33,922261	16,607774	34,275618	31,80212	68,19788	1,0104167	0,9148936	-93,6	-88	0,001414	23	-33,074205	-0,7233333
sly-MIR5282	128	17,1875	35,15625	16,40625	31,25	33,59375	66,40625	0,8888889	1,047619	-50,7	-50,1	0,172215	3,46	-39,609375	-1,1790698
sly-MIR530	88	22,727273	28,409091	18,181818	30,681818	40,909091	59,090909	1,08	1,25	-42,8	-42,1	0,204281	3,04	-48,636364	-1,1888889
sly-MIR5300	266	19,548872	30,075188	15,789474	34,586466	35,338346	64,661654	1,15	1,2380952	-98,2	-95,8	0,0026441	14,82	-36,917293	-1,0446809
sly-MIR5303-21	173	18,49711	24,855491	23,699422	32,947977	42,196532	57,803468	1,3255814	0,7804878	-62,6	-57,9	0,0190687	18,43	-36,184971	-0,97375
sly-MIR5303-7	130	16,923077	30	21,538462	31,538462	38,461538	61,538462	1,0512821	0,7857143	-50,8	-50,8	0,275719	6,07	-39,076923	-1,7574074
sly-MIR5303-8	125	16,8	28,8	28,8	25,6	45,6	54,4	0,8888889	0,5833333	-56,1	-56,1	0,293605	2,85	-44,88	-1,123913
sly-MIR5303-9	113	20,353982	25,663717	17,699115	36,283186	38,053097	61,946903	1,4137931	1,15	-39,8	-39,8	0,181235	11,19	-35,221239	-1,0531646
sly-MIR5303d-1	136	20,588235	27,941176	24,264706	27,205882	44,852941	55,147059	0,9736842	0,8484848	-45,9	-44,2	0,0057457	19,74	-33,75	-0,8981132
sly-MIR5303d-2	126	18,253968	28,571429	29,365079	23,809524	47,619048	52,380952	0,8333333	0,6216216	-55,8	-55,2	0,0801491	6,25	-44,285714	-1,2361702
sly-MIR5303f-6	126	27,777778	28,571429	17,460317	26,190476	45,238095	54,761905	0,9166667	1,5909091	-58,3	-56,5	0,0818526	5,34	-46,269841	-0,8054054
sly-MIR5303i-5	128	20,3125	30,46875	22,65625	26,5625	42,96875	57,03125	0,8717949	0,8965517	-47,1	-47,1	0,0779094	9,94	-36,796875	-0,7433735
sly-MIR5303i-8	128	19,53125	31,25	17,1875	32,03125	36,71875	63,28125	1,025	1,1363636	-43	-40,4	0,0225097	22,42	-33,59375	-0,7023622
sly-MIR5304	81	17,283951	33,333333	20,987654	28,395062	38,271605	61,728395	0,8518519	0,8235294	-35,5	-35,3	0,456836	1,08	-43,82716	-1,1451613
sly-MIR535f	107	22,429907	31,775701	19,626168	26,168224	42,056075	57,943925	0,8235294	1,1428571	-73,5	-73,5	0,411599	1,15	-68,691589	-1,144186
sly-MIR536	111	22,522523	27,927928	18,018018	31,531532	40,540541	59,459459	1,1290323	1,25	-46,6	-42,8	0,239922	13,01	-41,981982	-0,7487179
sly-MIR5368-1	171	31,578947	20,467836	23,976608	23,976608	55,555556	44,444444	1,1714286	1,3170732	-69,1	-44,3	0,0127819	51,36	-40,409357	-0,7273684
sly-MIR5368-2	83	28,915663	25,301205	24,096386	21,686747	53,012048	46,987952	0,8571429	1,2	-31,2	-31,2	0,442785	1,96	-37,590361	-1,1313725
sly-MIR5532	263	19,011407	29,657795	19,011407	32,319392	38,022814	61,977186	1,0897436	1	-75,5	-62,2	0,0004462	33,8	-28,707224	-0,7693182
sly-MIR5542	315	21,587302	30,47619	12,380952	35,555556	33,968254	66,031746	1,1666667	1,7435897	-75,1	-59	0,0001973	63,82	-23,84127	-0,8219512
sly-MIR5543	207	21,256039	27,536232	14,009662	37,198068	35,2657	64,7343	1,3508772	1,5172414	-74,2	-73,4	0,0072824	22,73	-35,845411	-1,5875
sly-MIR5558	191	23,560209	32,984293	14,659686	28,795812	38,219895	61,780105	0,8730159	1,6071429	-56,1	-49,6	0,0031069	19,66	-29,371728	-1,2234375
sly-MIR5568e	272	18,014706	31,985294	15,441176	34,558824	33,455882	66,544118	1,0804598	1,1666667	-73,8	-66,8	0,0004515	39,44	-27,132353	-1,0085366
sly-MIR5569	99	28,282828	20,20202	19,191919	32,323232	47,474747	52,525253	1,6	1,4736842	-37,6	-37,6	0,205842	5,02	-37,979798	-1,0466667
sly-MIR5570	259	16,216216	36,679537	13,899614	33,204633	30,11583	69,88417	0,9052632	1,1666667	-99	-90	0,0003631	40,48	-38,223938	-0,812766
sly-MIR5628-1	135	18,518519	34,814815	17,777778	28,888889	36,296296	63,703704	0,8297872	1,0416667	-45	-44,7	0,10438	15,69	-33,333333	-0,9183673
sly-MIR5628-2	103	21,359223	32,038835	15,533981	31,067961	36,893204	63,106796	0,969697	1,375	-49,7	-49,1	0,128409	7,13	-48,252427	-1,3078947
sly-MIR5652	102	19,607843	35,294118	14,705882	30,392157	34,313725	65,686275	0,8611111	1,3333333	-30,6	-28,6	0,101054	8,92	-30	-0,7406977
sly-MIR5654	156	16,666667	32,692308	14,102564	36,538462	30,769231	69,230769	1,1176471	1,1818182	-47,4	-38,5	0,0171257	33,87	-30,384615	-0,7609756
sly-MIR5658	171	21,637427	30,409357	12,280702	35,672515	33,918129	66,081871	1,1730769	1,7619048	-42,6	-33,5	0,0159618	37,8	-24,912281	-0,7344828
sly-MIR5670b	150	14,666667	38	17,333333	30	32	68	0,7894737	0,8461538	-66,2	-60,7	0,0574325	22,36	-44,133333	-1,0969697
sly-MIR5674b	273	16,483516	30,769231	16,117216	36,630037	32,600733	67,399267	1,1904762	1,0227273	-63,4	-59,6	0,0003147	69,11	-23,223443	-0,7670732
sly-MIR5716	329	18,237082	33,738602	13,677812	34,346505	31,914894	68,085106	1,018018	1,3333333	-80,2	-72,4	0,0003089	61,68	-24,3769	-0,7823529
sly-MIR5722	298	24,496644	24,496644	14,09396	36,912752	38,590604	61,409396	1,5068493	1,7380952	-83,6	-78,4	0,000132	48,1	-28,053691	-1,4519231
sly-MIR5725-1	70	28,571429	25,714286	18,571429	27,142857	47,142857	52,857143	1,0555556	1,5384615	-35,5	-35,5	0,614178	1	-50,714286	-0,8871795
sly-MIR5725-2	168	21,428571	30,357143	16,666667	31,547619	38,095238	61,904762	1,0392157	1,2857143	-78,3	-78,3	0,0830313	6,5	-46,607143	-1,4759259

sly-MIR5725-3	282	19,503546	30,851064	17,021277	32,624113	36,524823	63,475177	1,0574713	1,1458333	-85,9	-69,61	0,0004366	45,29	-30,460993	-1,0433333
sly-MIR5752b	295	20	26,101695	19,322034	34,576271	39,322034	60,677966	1,3246753	1,0350877	-81,9	-62,9	2,03E-05	69,23	-27,762712	-0,9029126
sly-MIR5773	166	17,46988	33,13253	13,855422	35,542169	31,325301	68,674699	1,0727273	1,2608696	-75,5	-75	0,0437941	13,5	-45,481928	-1,16
sly-MIR5780c	280	14,642857	36,071429	16,785714	32,5	31,428571	68,571429	0,9009901	0,8723404	-66,9	-62,4	0,0001223	52,47	-23,892857	-0,9692308
sly-MIR5780d	146	23,972603	26,712329	21,232877	28,082192	45,205479	54,794521	1,0512821	1,1290323	-66,2	-66	0,0175707	10,11	-45,342466	-0,8575342
sly-MIR5812	181	17,679558	28,176796	17,127072	37,016575	34,80663	65,19337	1,3137255	1,0322581	-76,2	-72,8	0,0095764	19,14	-42,099448	-0,7303571
sly-MIR6020a	135	17,037037	34,814815	15,555556	32,592593	32,592593	67,407407	0,9361702	1,0952381	-49,3	-49,3	0,204405	5,78	-36,518519	-1,1204545
sly-MIR6021	321	17,133956	29,595016	13,084112	40,186916	30,218069	69,781931	1,3578947	1,3095238	-73,7	-70,3	3,80E-05	52,32	-22,959502	-0,7597938
sly-MIR6022	236	19,915254	30,084746	18,644068	31,355932	38,559322	61,440678	1,0422535	1,0681818	-81	-60,77	0,0065962	54,63	-34,322034	-0,8901099
sly-MIR6024	116	19,827586	25,862069	18,965517	35,344828	38,793103	61,206897	1,3666667	1,0454545	-43	-42,8	0,0913448	6,74	-37,068966	-0,9555556
sly-MIR6025b-1	162	20,987654	27,160494	13,580247	38,271605	34,567901	65,432099	1,4090909	1,5454545	-52,9	-50,2	0,021433	24,61	-32,654321	-0,9446429
sly-MIR6025b-2	162	24,691358	25,308642	13,580247	36,419753	38,271605	61,728395	1,4390244	1,8181818	-59,7	-59,7	0,0307663	16,86	-36,851852	-0,9629032
sly-MIR6025c	133	24,06015	28,571429	17,293233	30,075188	41,353383	58,646617	1,0526316	1,3913043	-40,2	-40,2	0,024304	18,96	-30,225564	-1,05
sly-MIR6027	153	21,568627	33,333333	11,764706	33,333333	33,333333	66,666667	1	1,8333333	-57,7	-52	0,0615353	15,59	-37,712418	-1,6333333
sly-MIR6116	87	16,091954	32,183908	18,390805	33,333333	34,482759	65,517241	1,0357143	0,875	-36	-36	0,262563	3,47	-41,37931	-0,7676471
sly-MIR6140b	244	16,803279	30,327869	15,983607	36,885246	32,786885	67,213115	1,2162162	1,0512821	-57,1	-50,1	7,15E-05	25,55	-23,401639	-0,7792453
sly-MIR6145b	177	18,644068	33,898305	17,514124	29,943503	36,158192	63,841808	0,8833333	1,0645161	-89,8	-89,7	0,0515833	12,68	-50,734463	-0,7715596
sly-MIR6147	339	13,274336	35,39823	17,109145	34,218289	30,383481	69,616519	0,9666667	0,7758621	-95,4	-90,4	0,0004	30,56	-28,141593	-1,3590909
sly-MIR6149	196	19,387755	27,040816	17,346939	36,22449	36,734694	63,265306	1,3396226	1,1176471	-54,4	-48,4	0,0007139	30,02	-27,755102	-1,12875
sly-MIR6149b	182	14,835165	34,615385	15,934066	34,615385	30,769231	69,230769	1	0,9310345	-65,2	-63,3	0,0255056	17,25	-35,824176	-0,8770833
sly-MIR6151i	179	17,318436	29,050279	15,083799	38,547486	32,402235	67,597765	1,3269231	1,1481481	-45,2	-41,1	0,0009263	28,32	-25,251397	-1,4390625
sly-MIR6164b	174	13,793103	29,310345	17,241379	39,655172	31,034483	68,965517	1,3529412	0,8	-49,1	-49,1	0,0239275	9,29	-28,218391	-0,7025974
sly-MIR6169	239	15,899582	19,246862	15,062762	49,790795	30,962343	69,037657	2,5869565	1,0555556	-84,9	-81,4	0,0063914	25,5	-35,523013	-0,7342857
sly-MIR6218	250	18	24,8	17,2	40	35,2	64,8	1,6129032	1,0465116	-72,4	-68	0,0048884	20,51	-28,96	-0,8013333
sly-MIR6224c	82	19,512195	30,487805	18,292683	31,707317	37,804878	62,195122	1,04	1,0666667	-23,7	-23,7	0,181394	7,01	-28,902439	-1,0820513
sly-MIR6230-1	190	22,105263	29,473684	20,526316	27,894737	42,631579	57,368421	0,9464286	1,0769231	-70,5	-65,95	0,0107426	38,64	-37,105263	-1,4392857
sly-MIR6230-2	207	23,188406	28,502415	18,357488	29,951691	41,545894	58,454106	1,0508475	1,2631579	-65,1	-64,7	0,0051271	17,8	-31,449275	-0,7426471
sly-MIR6231-1	121	17,355372	31,404959	19,834711	31,404959	37,190083	62,809917	1	0,875	-56,7	-56,7	0,13078	6,78	-46,859504	-1,0862069
sly-MIR6231-2	106	15,09434	34,90566	17,924528	32,075472	33,018868	66,981132	0,9189189	0,8421053	-40,2	-40,2	0,306319	5,67	-37,924528	-0,7125
sly-MIR6231-3	161	14,285714	36,024845	16,770186	32,919255	31,055901	68,944099	0,9137931	0,8518519	-54	-54	0,0616859	8,09	-33,540373	-0,9194444
sly-MIR6232b	112	21,428571	33,035714	16,071429	29,464286	37,5	62,5	0,8918919	1,3333333	-70,1	-69,8	0,178559	4,07	-62,589286	-1,6690476
sly-MIR6235	288	20,138889	36,111111	18,055556	25,694444	38,194444	61,805556	0,7115385	1,1153846	-77	-69,3	0,0014187	49,96	-26,736111	-1,0972222
sly-MIR6248	150	23,333333	34	13,333333	29,333333	36,666667	63,333333	0,8627451	1,75	-46,3	-42,7	0,0903456	13,74	-30,866667	-1,0766234
sly-MIR6254	183	18,579235	29,508197	14,754098	37,15847	33,333333	66,666667	1,2592593	1,2592593	-73,1	-73,1	0,0376507	14,49	-39,945355	-0,7
sly-MIR6267a	248	18,951613	29,435484	13,709677	37,903226	32,66129	67,33871	1,2876712	1,3823529	-60,7	-52,7	8,47E-05	53,74	-24,475806	-1,1463768
sly-MIR6271-1	223	15,246637	33,632287	17,93722	33,183857	33,183857	66,816143	0,9866667	0,85	-83,7	-82,6	0,005007	19,39	-37,533632	-1,06
sly-MIR6271-2	290	13,793103	35,172414	16,551724	34,482759	30,344828	69,655172	0,9803922	0,8333333	-68,4	-67,5	0,0001632	28,27	-23,586207	-0,8506329
sly-MIR6271-3	152	23,684211	30,263158	13,157895	32,894737	36,842105	63,157895	1,0869565	1,8	-39,9	-39,8	0,0089113	12,28	-26,25	-0,8549296
sly-MIR6273-1	178	19,662921	31,460674	12,921348	35,955056	32,58427	67,41573	1,1428571	1,5217391	-52,5	-47,2	0,0112703	22,74	-29,494382	-0,8
sly-MIR6273-2	86	23,255814	19,767442	23,255814	33,72093	46,511628	53,488372	1,7058824	1	-32,7	-32,7	0,0873532	4,35	-38,023256	-0,8297297
sly-MIR6273-3	110	19,090909	32,727273	15,454545	32,727273	34,545455	65,454545	1	1,2352941	-29,6	-29,6	0,341156	2,89	-26,909091	-0,7366667
sly-MIR6277	289	22,491349	34,602076	12,802768	30,103806	35,294118	64,705882	0,87	1,7567568	-80,3	-69,9	0,0015008	28,18	-27,785467	-1,1536585
sly-MIR6281-1	304	14,802632	31,907895	15,789474	37,5	30,592105	69,407895	1,1752577	0,9375	-75,1	-64,8	3,06E-05	57	-24,703947	-1,3791667
sly-MIR6281-2	230	16,956522	33,913043	13,913043	35,217391	30,869565	69,130435	1,0384615	1,21875	-54,5	-50,2	0,0029103	25,16	-23,695652	-1,403125
sly-MIR6293	299	20,735786	29,765886	19,732441	29,765886	40,468227	59,531773	1	1,0508475	-87,8	-84,6	0,0003583	39,32	-29,364548	-1,4765625
sly-MIR6299	308	17,532468	37,337662	13,961039	31,168831	31,493506	68,506494	0,8347826	1,255814	-80,7	-78,1	0,0031126	14,77	-26,201299	-0,8319588
sly-MIR6440a	111	26,126126	25,225225	10,810811	37,837838	36,936937	63,063063	1,5	2,4166667	-28,7	-23,1	0,0045322	27,95	-25,855856	-1,1764706
sly-MIR6441	127	14,173228	33,858268	16,535433	35,433071	30,708661	69,291339	1,0465116	0,8571429	-27,3	-26,2	0,00703	14,09	-21,496063	-0,9078947
sly-MIR6447	161	21,118012	29,813665	10,559006	38,509317	31,677019	68,322981	1,2916667	2	-60	-58	0,0163106	15,53	-37,267081	-1,2586207
sly-MIR6451	262	14,503817	37,78626	16,412214	31,29771	30,916031	69,083969	0,8282828	0,8837209	-62,7	-61,5	0,0004207	36,49	-23,931298	-0,7148148

sly-MIR6459a	297	19,52862	31,986532	12,121212	36,363636	31,649832	68,350168	1,1368421	1,6111111	-72,9	-66,4	1,76E-05	60,1	-24,545455	-0,8365079
sly-MIR6463-1	233	23,60515	27,038627	16,309013	33,04721	39,914163	60,085837	1,2222222	1,4473684	-65,3	-59	8,78E-05	33,52	-28,025751	-1,3489362
sly-MIR6463-2	290	17,586207	30,344828	12,758621	39,310345	30,344828	69,655172	1,2954545	1,3783784	-65,7	-61,6	3,70E-05	66,46	-22,655172	-0,8705882
sly-MIR6474	236	17,79661	35,169492	18,644068	28,389831	36,440678	63,559322	0,8072289	0,9545455	-62,9	-58,3	0,0055594	19,37	-26,652542	-1,1313725
sly-MIR7122	78	16,666667	29,487179	20,512821	33,333333	37,179487	62,820513	1,1304348	0,8125	-31,5	-31,5	0,154352	3,65	-40,384615	-1,0862069
sly-MIR7122a	200	13	31,5	19	36,5	32	68	1,1587302	0,6842105	-62,8	-54,3	0,0044487	59,08	-31,4	-0,9316667
sly-MIR7492f	82	15,853659	31,707317	14,634146	37,804878	30,487805	69,512195	1,1923077	1,0833333	-23,8	-23,8	0,0794001	6,56	-29,02439	-0,7241379
sly-MIR7493	119	18,487395	28,571429	13,445378	39,495798	31,932773	68,067227	1,3823529	1,375	-26,8	-23,9	0,0069998	19,21	-22,521008	-0,7046875
sly-MIR7493b	182	19,78022	28,571429	19,230769	32,417582	39,010989	60,989011	1,1346154	1,0285714	-52,8	-52,8	0,0085412	15,22	-29,010989	-0,7171053
sly-MIR7502c-1	174	14,367816	32,758621	17,241379	35,632184	31,609195	68,390805	1,0877193	0,8333333	-54,1	-49,8	0,0092076	21,45	-31,091954	-0,9836364
sly-MIR7502c-2	289	16,608997	28,719723	15,224913	39,446367	31,83391	68,16609	1,373494	1,0909091	-64,9	-60,9	0,000719	50,71	-22,456747	-0,8571429
sly-MIR7502c-3	263	17,110266	33,460076	15,589354	33,840304	32,69962	67,30038	1,0113636	1,097561	-71,6	-64,8	0,0004065	41,89	-27,224335	-0,8
sly-MIR7502f	132	15,909091	31,818182	20,454545	31,818182	36,363636	63,636364	1	0,7777778	-44,2	-44,2	0,050073	9,18	-33,484848	-0,8733333
sly-MIR7504f	85	15,294118	30,588235	17,647059	36,470588	32,941176	67,058824	1,1923077	0,8666667	-26,5	-25,7	0,0962127	4,91	-31,176471	-0,9565789
sly-MIR7504j	158	20,886076	29,746835	20,886076	28,481013	41,772152	58,227848	0,9574468	1	-83,9	-80	0,0423929	9	-53,101266	-1,2712121
sly-MIR7508	254	20,472441	39,76378	9,8425197	29,92126	30,314961	69,685039	0,7524752	2,08	-66	-63,7	0,0096834	17,82	-25,984252	-0,8727273
sly-MIR7525	187	24,59893	18,181818	21,925134	35,294118	46,524064	53,475936	1,9411765	1,1219512	-61	-60,3	0,0021244	23,3	-32,620321	-1,3096774
sly-MIR7539	263	17,870722	35,741445	13,307985	33,079848	31,178707	68,821293	0,9255319	1,3428571	-87,6	-82	0,0108589	24,75	-33,307985	-0,7316327
sly-MIR7540b	305	22,622951	32,459016	15,081967	29,836066	37,704918	62,295082	0,9191919	1,5	-84,4	-78,3	0,0002544	57,19	-27,672131	-0,7256198
sly-MIR7543	70	22,857143	28,571429	18,571429	30	41,428571	58,571429	1,05	1,2307692	-30,7	-30,7	0,668782	0,89	-43,857143	-1,24
sly-MIR7695	156	23,717949	30,128205	16,666667	29,487179	40,384615	59,615385	0,9787234	1,4230769	-44,5	-33,6	0,0187391	36,12	-28,525641	-0,9444444
sly-MIR7696c	124	17,741935	33,064516	20,967742	28,225806	38,709677	61,290323	0,8536585	0,8461538	-35,5	-28,6	0,0096853	32,82	-28,629032	-1,6895833
sly-MIR7696d	98	17,346939	34,693878	15,306122	32,653061	32,653061	67,346939	0,9411765	1,1333333	-30,5	-29,7	0,0335336	9,46	-31,122449	-0,7389381
sly-MIR7711	109	16,513761	39,449541	14,678899	29,357798	31,192661	68,807339	0,744186	1,125	-26,8	-25,6	0,137094	14,99	-24,587156	-1,0774194
sly-MIR7722	281	18,86121	32,02847	15,658363	33,451957	34,519573	65,480427	1,0444444	1,2045455	-68,7	-58,87	0,0013193	55,09	-24,448399	-1,4305085
sly-MIR773b-1	194	18,041237	27,835052	19,072165	35,051546	37,113402	62,886598	1,2592593	0,9459459	-53,6	-48,3	0,0032705	25,8	-27,628866	-0,7
sly-MIR773b-2	118	22,033898	35,59322	16,101695	26,271186	38,135593	61,864407	0,7380952	1,3684211	-43,3	-43,3	0,0401836	7,23	-36,694915	-0,8096154
sly-MIR773b-3	261	22,222222	28,735632	18,007663	31,034483	40,229885	59,770115	1,08	1,2340426	-81,3	-68,96	0,0004874	59,31	-31,149425	-1,093617
sly-MIR7740	282	19,858156	36,879433	13,829787	29,432624	33,687943	66,312057	0,7980769	1,4358974	-67,4	-64,5	0,0005675	52,55	-23,900709	-0,7094737
sly-MIR7748a	282	15,957447	31,914894	19,503546	32,624113	35,460993	64,539007	1,0222222	0,8181818	-78,3	-78,2	0,0014766	43,73	-27,765957	-0,78
sly-MIR7757	89	24,719101	20,224719	17,977528	37,078652	42,696629	57,303371	1,8333333	1,375	-38,7	-38,7	0,199981	4,16	-43,483146	-0,9354167
sly-MIR7805-1	247	20,242915	32,388664	11,740891	35,62753	31,983806	68,016194	1,1	1,7241379	-62,9	-43,9	0,0001584	78,66	-25,465587	-0,8363636
sly-MIR7805-2	306	16,339869	31,372549	16,339869	35,947712	32,679739	67,320261	1,1458333	1	-75,1	-63,4	6,19E-05	58,37	-24,542484	-1,2051724
sly-MIR7806	134	20,895522	26,119403	22,38806	30,597015	43,283582	56,716418	1,1714286	0,9333333	-93,1	-93,1	0,416422	3,78	-69,477612	-0,7
sly-MIR7822-1	125	18,4	36	15,2	30,4	33,6	66,4	0,8444444	1,2105263	-54,7	-45,48	0,0637166	21,26	-43,76	-0,953125
sly-MIR7822-2	219	15,068493	36,52968	15,525114	32,876712	30,593607	69,406393	0,9	0,9705882	-86,6	-82,64	0,0234187	22,56	-39,543379	-1,605
sly-MIR7822-3	185	19,459459	28,648649	16,216216	35,675676	35,675676	64,324324	1,245283	1,2	-63,7	-62,5	0,0126563	12,48	-34,432432	-0,8965517
sly-MIR7822-4	204	20,588235	30,392157	11,27451	37,745098	31,862745	68,137255	1,2419355	1,826087	-68	-67,3	0,0226486	8,2	-33,333333	-1,147619
sly-MIR7822-5	197	16,243655	30,964467	14,720812	38,071066	30,964467	69,035533	1,2295082	1,1034483	-62,7	-62,3	0,0086099	16,7	-31,827411	-0,7340206
sly-MIR7823	122	16,393443	29,508197	14,754098	39,344262	31,147541	68,852459	1,3333333	1,1111111	-44,3	-43,3	0,0697607	7,02	-36,311475	-0,7
sly-MIR7832	245	15,918367	35,918367	17,55102	30,612245	33,469388	66,530612	0,8522727	0,9069767	-79,8	-77,4	0,0072628	28,31	-32,571429	-0,9159091
sly-MIR7834	102	19,607843	31,372549	19,607843	29,411765	39,215686	60,784314	0,9375	1	-29,2	-27,3	0,0158855	31,33	-28,627451	-0,7230769
sly-MIR7840	181	19,337017	34,80663	12,154696	33,701657	31,491713	68,508287	0,968254	1,5909091	-41,5	-36,5	0,0015288	45,28	-22,928177	-1,015
sly-MIR7842	85	17,647059	34,117647	18,823529	29,411765	36,470588	63,529412	0,862069	0,9375	-31,3	-29,5	0,216838	4,64	-36,823529	-0,77
sly-MIR7980b-1	88	15,909091	31,818182	17,045455	35,227273	32,954545	67,045455	1,1071429	0,9333333	-36,4	-36,4	0,375896	3,29	-41,363636	-1,2551724
sly-MIR7980b-2	110	15,454545	36,363636	16,363636	31,818182	31,818182	68,181818	0,875	0,9444444	-32,8	-32,8	0,207741	5,26	-29,818182	-0,9371429
sly-MIR7980b-3	111	16,216216	35,135135	20,720721	27,927928	36,936937	63,063063	0,7948718	0,7826087	-36,9	-35,6	0,0793932	7,75	-33,243243	-0,7266667
sly-	114	20,175439	27,192982	19,298246	33,333333	39,473684	60,526316	1,2258065	1,0454545	-42,3	-39,5	0,0223888	13,61	-37,105263	-0,7649123

MIR7980b-4															
sly-MIR7980b-5	111	20,720721	27,927928	16,216216	35,135135	36,936937	63,063063	1,2580645	1,2777778	-46,6	-46,6	0,131222	6,37	-41,981982	-1,0328947
sly-MIR7981-10	220	20	31,363636	17,272727	31,363636	37,272727	62,727273	1	1,1578947	-93	-91,1	0,0007303	18,4	-42,272727	-0,9594595
sly-MIR7981-11	184	15,76087	33,152174	22,282609	28,804348	38,043478	61,956522	0,8688525	0,7073171	-51,4	-51,4	0,0171165	14,48	-27,934783	-0,7354167
sly-MIR7981-12	295	15,254237	34,915254	18,305085	31,525424	33,559322	66,440678	0,9029126	0,8333333	-88,1	-82,2	0,0034513	25,06	-29,864407	-1,0433333
sly-MIR7981-14	239	16,736402	30,125523	19,665272	33,472803	36,401674	63,598326	1,1111111	0,8510638	-96,7	-86,3	0,0002919	32,63	-40,460251	-0,9310345
sly-MIR7981-15	210	21,428571	29,047619	16,666667	32,857143	38,095238	61,904762	1,1311475	1,2857143	-86,2	-82,6	0,0036702	26,71	-41,047619	-0,7014286
sly-MIR7981-16	266	16,917293	36,466165	14,285714	32,330827	31,203008	68,796992	0,8865979	1,1842105	-82,5	-77,6	0,0012571	29,83	-31,015038	-1,1810127
sly-MIR7981-18	245	20	32,653061	14,285714	33,061224	34,285714	65,714286	1,0125	1,4	-87,6	-82,3	0,003338	26,42	-35,755102	-0,852
sly-MIR7981-19	256	18,75	32,03125	14,453125	34,765625	33,203125	66,796875	1,0853659	1,2972973	-96,3	-91,5	0,0014512	23,51	-37,617188	-1,0428571
sly-MIR7981-20	231	16,883117	32,900433	16,017316	34,199134	32,900433	67,099567	1,0394737	1,0540541	-85,8	-84,7	0,0031829	25,83	-37,142857	-0,8545455
sly-MIR7981-22	168	20,238095	37,5	16,666667	25,595238	36,904762	63,095238	0,6825397	1,2142857	-70,9	-68,6	0,0205673	19,63	-42,202381	-1,0142857
sly-MIR7981-5	224	17,857143	36,160714	16,517857	29,464286	34,375	65,625	0,8148148	1,0810811	-87	-83,2	0,0239828	21,24	-38,839286	-1,0682927
sly-MIR7981-6	214	15,420561	29,906542	22,429907	32,242991	37,850467	62,149533	1,078125	0,6875	-58,6	-55,7	0,0051591	21,48	-27,383178	-0,9208333
sly-MIR7981-7	277	18,772563	33,212996	12,635379	35,379061	31,407942	68,592058	1,0652174	1,4857143	-85,1	-83,9	0,0051431	21,4	-30,722022	-0,925
sly-MIR7983-1	240	15,416667	39,166667	15	30,416667	30,416667	69,583333	0,7765957	1,0277778	-72,6	-69,8	0,0013729	25,91	-30,25	-0,9389474
sly-MIR7983-10	227	14,537445	31,718062	16,740088	37,004405	31,277533	68,722467	1,1666667	0,8684211	-58	-56	0,0010477	19,77	-25,550661	-0,7371795
sly-MIR7983-11	214	12,616822	32,242991	17,757009	37,383178	30,373832	69,626168	1,1594203	0,7105263	-58,3	-57,1	0,0089513	17,96	-27,242991	-1,0027027
sly-MIR7983-12	218	14,678899	30,275229	17,431193	37,614679	32,110092	67,889908	1,2424242	0,8421053	-72,9	-72,5	0,0059922	22,8	-33,440367	-1,159322
sly-MIR7983-13	157	14,649682	30,573248	16,56051	38,216561	31,210191	68,789809	1,25	0,8846154	-44,4	-43,5	0,0268189	12,4	-28,280255	-0,7078431
sly-MIR7983-2	109	14,678899	30,275229	16,513761	38,53211	31,192661	68,807339	1,2727273	0,8888889	-26,3	-24,7	0,0269927	13,49	-24,12844	-0,9428571
sly-MIR7983-3	137	14,59854	29,927007	17,518248	37,956204	32,116788	67,883212	1,2682927	0,8333333	-36,8	-36,8	0,0726236	9,3	-26,861314	-1,4111111
sly-MIR7983-4	222	14,864865	31,981982	15,765766	37,387387	30,630631	69,369369	1,1690141	0,9428571	-58,5	-50,2	0,0019702	44,42	-26,351351	-0,7116279
sly-MIR7983-5	265	16,603774	40,377358	13,962264	29,056604	30,566038	69,433962	0,7196262	1,1891892	-78,3	-72,8	0,0005622	28,86	-29,54717	-0,8698113
sly-MIR7983-6	221	15,384615	38,00905	16,289593	30,316742	31,674208	68,325792	0,797619	0,9444444	-59,8	-58,9	0,0013464	24,97	-27,058824	-1,046
sly-MIR7983-7	226	13,274336	32,743363	18,141593	35,840708	31,415929	68,584071	1,0945946	0,7317073	-60,7	-59,9	0,0026142	19,54	-26,858407	-0,7155844
sly-MIR7983-8	229	16,593886	27,947598	16,593886	38,864629	33,187773	66,812227	1,390625	1	-69	-68,6	0,0118856	14,37	-30,131004	-0,8458824
sly-MIR7983-9	66	18,181818	30,30303	21,212121	30,30303	39,393939	60,606061	1	0,8571429	-20,5	-20,1	0,267845	2,96	-31,060606	-1,2692308
sly-MIR7984b-1	199	15,075377	35,175879	15,075377	34,673367	30,150754	69,849246	0,9857143	1	-61,2	-60,2	0,0195412	24,78	-30,753769	-1,02
sly-MIR7984b-2	88	19,318182	28,409091	20,454545	31,818182	39,772727	60,227273	1,12	0,9444444	-49,8	-49,8	0,204221	2,96	-56,590909	-1,4228571
sly-MIR7984b-3	272	13,970588	36,764706	16,176471	33,088235	30,147059	69,852941	0,9	0,8636364	-80,2	-77,2	0,0009717	41,78	-29,485294	-1,0488095
sly-MIR7984b-4	220	15,454545	35,909091	15	33,636364	30,454545	69,545455	0,9367089	1,030303	-78,7	-78,5	0,0020249	20,44	-35,772727	-0,7309091
sly-MIR7984c-1	204	14,705882	33,823529	16,666667	34,803922	31,372549	68,627451	1,0289855	0,8823529	-93	-87,3	0,0073595	17,85	-45,588235	-1,453125
sly-	225	15,555556	35,111111	15,111111	34,222222	30,666667	69,333333	0,9746835	1,0294118	-87,9	-87,5	0,0518188	13,04	-39,066667	-0,9327273

MIR7984c-2															
sly-MIR7984c-3	243	15,226337	35,390947	17,283951	32,098765	32,510288	67,489712	0,9069767	0,8809524	-84	-72,5	0,0154124	21,69	-34,567901	-2,1042553
sly-MIR7984c-4	278	17,625899	33,093525	14,388489	34,892086	32,014388	67,985612	1,0543478	1,225	-66,2	-46,6	0,0002581	65,31	-23,81295	-1,415942
sly-MIR7984c-5	226	18,141593	31,858407	15,044248	34,955752	33,185841	66,814159	1,0972222	1,2058824	-97,9	-97,8	0,0219098	17,1	-43,318584	-0,7742857
sly-MIR7984d-1	216	16,666667	32,87037	18,055556	32,407407	34,722222	65,277778	0,9859155	0,9230769	-91,6	-87,2	0,0086314	26,27	-42,407407	-1,2213333
sly-MIR7984d-2	277	15,884477	35,018051	15,162455	33,935018	31,046931	68,953069	0,9690722	1,047619	-90,9	-86,9	0,0001687	29,53	-32,815884	-0,8347368
sly-MIR7984d-3	187	16,57754	32,085561	14,973262	36,363636	31,550802	68,449198	1,1333333	1,1071429	-63,1	-63,1	0,0467909	17,21	-33,743316	-1,15375
sly-MIR7984d-4	129	16,27907	32,55814	13,953488	37,209302	30,232558	69,767442	1,1428571	1,1666667	-28,4	-25,5	0,0237125	17,75	-22,015504	-0,756
sly-MIR7985	178	31,460674	17,977528	21,910112	28,651685	53,370787	46,629213	1,59375	1,4358974	-67,8	-58,7	0,0030071	44,94	-38,089888	-0,7296703
sly-MIR7986-1	83	16,86747	30,120482	19,277108	33,73494	36,144578	63,855422	1,12	0,875	-31	-30,8	0,180561	4,25	-37,349398	-1,0333333
sly-MIR7986-2	142	17,605634	33,098592	14,788732	34,507042	32,394366	67,605634	1,0425532	1,1904762	-74,9	-74,9	0,418074	1,76	-52,746479	-0,8175
sly-MIR7987-1	208	19,230769	30,288462	13,942308	36,538462	33,173077	66,826923	1,2063492	1,3793103	-59,2	-50,5	0,003571	46,77	-28,461538	-0,857971
sly-MIR7987-2	220	19,545455	30,454545	11,363636	38,636364	30,909091	69,090909	1,2686567	1,72	-53,4	-22,4	0,0010897	91,18	-24,272727	-0,7852941
sly-MIR7988	261	15,32567	34,099617	15,708812	34,8659	31,034483	68,965517	1,0224719	0,9756098	-59,6	-54,5	5,94E-05	39,22	-22,835249	-1,2340909
sly-MIR7990a-1	102	14,705882	30,392157	15,686275	39,215686	30,392157	69,607843	1,2903226	0,9375	-32,6	-32,6	0,100386	7,6	-31,960784	-1,0516129
sly-MIR7990a-2	211	13,270142	31,753555	18,483412	36,492891	31,753555	68,246445	1,1492537	0,7179487	-62,1	-60,7	0,0093892	22,57	-29,43128	-0,8126316
sly-MIR7990a-3	324	14,506173	31,790123	16,666667	37,037037	31,17284	68,82716	1,1650485	0,8703704	-77,5	-62,9	4,08E-05	74,73	-23,919753	-1,016
sly-MIR7990a-4	219	15,981735	31,050228	15,981735	36,986301	31,96347	68,03653	1,1911765	1	-83,4	-82,1	0,0130431	13,03	-38,082192	-0,7882353
sly-MIR7992-1	209	17,22488	40,191388	12,91866	29,665072	30,143541	69,856459	0,7380952	1,3333333	-71,5	-71,5	0,100086	15,58	-34,210526	-1,1349206
sly-MIR7992-10	186	19,892473	30,645161	22,043011	27,419355	41,935484	58,064516	0,8947368	0,902439	-58,4	-57,7	0,0076555	20,02	-31,397849	-0,8204545
sly-MIR7992-11	208	16,826923	33,173077	24,038462	25,961538	40,865385	59,134615	0,7826087	0,7	-71,9	-65,3	0,0024681	16,3	-34,567308	-1,064557
sly-MIR7992-12	236	17,79661	31,355932	12,711864	38,135593	30,508475	69,491525	1,2162162	1,4	-64,9	-57,4	0,0013761	33,03	-27,5	-0,9871795
sly-MIR7992-13	244	16,803279	35,245902	14,754098	33,196721	31,557377	68,442623	0,9418605	1,1388889	-67,7	-50,5	0,0001507	43,47	-27,745902	-0,94
sly-MIR7992-14	248	12,5	38,709677	18,145161	30,645161	30,645161	69,354839	0,7916667	0,6888889	-58,8	-46,67	0,0010295	32,23	-23,709677	-1,2626667
sly-MIR7992-2	209	18,181818	29,665072	22,488038	29,665072	40,669856	59,330144	1	0,8085106	-62,6	-44,3	0,0036899	47,74	-29,952153	-0,7364706
sly-MIR7992-3	249	18,473896	30,923695	22,088353	28,514056	40,562249	59,437751	0,9220779	0,8363636	-98,9	-96,9	0,0362719	19,69	-39,718876	-1,0569767
sly-MIR7992-4	238	16,386555	34,033613	17,647059	31,932773	34,033613	65,966387	0,9382716	0,9285714	-82,9	-82,9	0,0094865	11,35	-34,831933	-0,7555556
sly-MIR7992-5	169	18,934911	33,727811	19,526627	27,810651	38,461538	61,538462	0,8245614	0,969697	-64,2	-64,2	0,0596601	12,29	-37,988166	-1,1287671
sly-MIR7992-6	97	26,804124	23,71134	21,649485	27,835052	48,453608	51,546392	1,173913	1,2380952	-69,7	-68,1	0,703449	0,66	-71,85567	-0,8263889
sly-MIR7992-7	182	24,175824	24,725275	21,428571	29,67033	45,604396	54,395604	1,2	1,1282051	-98,1	-97,6	0,228977	4,92	-53,901099	-0,7411765
sly-MIR7992-8	237	21,940928	28,691983	16,877637	32,489451	38,818565	61,181435	1,1323529	1,3	-84,1	-80,9	0,0038903	26,45	-35,485232	-0,9333333
sly-MIR7992-9	84	21,428571	26,190476	17,857143	34,52381	39,285714	60,714286	1,3181818	1,2	-34,6	-32	0,0795132	7,21	-41,190476	-1,1648148
sly-MIR7993d-1	218	18,348624	35,321101	12,844037	33,486239	31,192661	68,807339	0,9480519	1,4285714	-70,3	-69,4	0,0137925	15,33	-32,247706	-1,0106383
sly-MIR7993d-2	175	18,857143	32	14,857143	34,285714	33,714286	66,285714	1,0714286	1,2692308	-60,9	-60,9	0,0096291	16,19	-34,8	-1,7235294
sly-	125	24	29,6	17,6	28,8	41,6	58,4	0,972973	1,3636364	-50,6	-50,6	0,121895	5,24	-40,48	-1,0760563

MIR7997b-1															
sly-MIR7997b-2	128	27,34375	27,34375	18,75	26,5625	46,09375	53,90625	0,9714286	1,4583333	-66,4	-63,8	0,025604	10,01	-51,875	-1,2638298
sly-MIR7997b-3	145	25,517241	25,517241	17,931034	31,034483	43,448276	56,551724	1,2162162	1,4230769	-59,2	-59,2	0,0599793	5,96	-40,827586	-1,3910714
sly-MIR7997c-1	131	32,824427	24,427481	19,083969	23,664122	51,908397	48,091603	0,96875	1,72	-70,8	-69,77	0,0350722	10,95	-54,045802	-1,0411765
sly-MIR7997c-10	205	14,146341	33,658537	23,902439	28,292683	38,04878	61,95122	0,8405797	0,5918367	-57,3	-54,4	0,0094772	22,83	-27,95122	-0,7774648
sly-MIR7997c-11	109	21,100917	29,357798	19,266055	30,275229	40,366972	59,633028	1,03125	1,0952381	-43,6	-41,22	0,135655	13	-40	-0,8757576
sly-MIR7997c-12	97	17,525773	32,989691	22,680412	26,804124	40,206186	59,793814	0,8125	0,7727273	-38,5	-38,5	0,0847405	8,39	-39,690722	-1,3477273
sly-MIR7997c-13	80	26,25	26,25	11,25	36,25	37,5	62,5	1,3809524	2,3333333	-31,8	-31,8	0,157095	3,68	-39,75	-0,7765957
sly-MIR7997c-14	126	19,047619	26,984127	21,428571	32,539683	40,47619	59,52381	1,2058824	0,8888889	-52,6	-50,8	0,0718719	15,85	-41,746032	-1,0030303
sly-MIR7997c-2	112	18,75	30,357143	20,535714	30,357143	39,285714	60,714286	1	0,9130435	-36,5	-35,2	0,0688978	9,08	-32,589286	-0,8295455
sly-MIR7997c-3	126	23,015873	25,396825	21,428571	30,15873	44,444444	55,555556	1,1875	1,0740741	-63	-63	0,0493363	4,5	-50	-0,7615385
sly-MIR7997c-4	120	21,666667	30	15,833333	32,5	37,5	62,5	1,0833333	1,3684211	-36,2	-35,2	0,0712003	12,88	-30,166667	-1,1102041
sly-MIR7997c-5	129	20,155039	32,55814	15,503876	31,782946	35,658915	64,341085	0,9761905	1,3	-51,7	-51,7	0,166614	3,47	-40,077519	-0,7615385
sly-MIR7997c-6	109	21,100917	28,440367	14,678899	35,779817	35,779817	64,220183	1,2580645	1,4375	-42,2	-42	0,278275	4,82	-38,715596	-0,8318182
sly-MIR7997c-7	141	27,659574	27,659574	10,638298	34,042553	38,297872	61,702128	1,2307692	2,6	-52,4	-51,9	0,0057766	10,38	-37,163121	-1,1369565
sly-MIR7997c-8	143	18,881119	33,566434	15,384615	32,167832	34,265734	65,734266	0,9583333	1,2272727	-63,4	-57,5	0,0833743	12,43	-44,335664	-0,8136364
sly-MIR7997c-9	121	19,008264	28,92562	23,140496	28,92562	42,14876	57,85124	1	0,8214286	-48,2	-45,4	0,0088954	9,07	-39,834711	-0,7057692
sly-MIR7998-1	139	25,179856	25,899281	28,776978	20,143885	53,956835	46,043165	0,7777778	0,875	-54,3	-51,5	0,0251781	27,04	-39,064748	-0,752459
sly-MIR7998-2	138	26,811594	24,637681	22,463768	26,086957	49,275362	50,724638	1,0588235	1,1935484	-50,5	-49,7	0,0266762	18,6	-36,594203	-1,0406593
sly-MIR8001a-1	69	13,043478	34,782609	18,84058	33,333333	31,884058	68,115942	0,9583333	0,6923077	-22,6	-22,2	0,160219	5,15	-32,753623	-1,0272727
sly-MIR8001a-2	143	16,083916	33,566434	16,783217	33,566434	32,867133	67,132867	1	0,9583333	-83,3	-83,3	0,110346	4,1	-58,251748	-1,0390244
sly-MIR8001b-1	171	16,959064	32,163743	16,374269	34,502924	33,333333	66,666667	1,0727273	1,0357143	-41,1	-31	0,0089224	29,03	-24,035088	-0,7210526
sly-MIR8001b-2	79	13,924051	31,64557	17,721519	36,708861	31,64557	68,35443	1,16	0,7857143	-20,9	-20,3	0,0583485	5,67	-26,455696	-0,836
sly-MIR8001b-3	84	22,619048	33,333333	13,095238	30,952381	35,714286	64,285714	0,9285714	1,7272727	-27,9	-26,8	0,0358574	14,92	-33,214286	-0,9703704
sly-MIR8001b-4	141	14,893617	34,751773	17,730496	32,624113	32,624113	67,375887	0,9387755	0,84	-52,6	-50,8	0,0387926	6,8	-37,304965	-1,1416667
sly-MIR8001b-5	143	16,783217	33,566434	16,783217	32,867133	33,566434	66,433566	0,9791667	1	-82,9	-82,9	0,567608	2,4	-57,972028	-1,1146341
sly-MIR8001b-6	67	17,910448	31,343284	17,910448	32,835821	35,820896	64,179104	1,047619	1	-38,1	-38,1	0,434263	1,23	-56,865672	-0,9716667
sly-MIR8001b-7	132	14,393939	33,333333	15,909091	36,363636	30,30303	69,69697	1,0909091	0,9047619	-54,2	-54,2	0,27874	3,22	-41,060606	-0,8368421
sly-MIR8002	188	17,021277	37,234043	15,957447	29,787234	32,978723	67,021277	0,8	1,0666667	-63,1	-60,8	0,0052864	15,31	-33,56383	-1,0177419
sly-MIR8003	233	18,88412	31,330472	12,017167	37,76824	30,901288	69,098712	1,2054795	1,5714286	-59,5	-58,2	0,0026651	35,79	-25,536481	-1,1927536
sly-MIR8005b	323	18,885449	32,817337	16,099071	32,198142	34,98452	65,01548	0,9811321	1,1730769	-79,1	-73,8	4,90E-05	61,23	-24,489164	-0,9375
sly-MIR8005c	183	19,672131	25,136612	13,114754	42,076503	32,786885	67,213115	1,673913	1,5	-49,4	-33,02	0,0076779	34,27	-26,994536	-0,7438202
sly-MIR8006-1	199	26,130653	26,633166	14,572864	32,663317	40,703518	59,296482	1,2264151	1,7931034	-75,9	-75,9	0,0091256	12,77	-38,140704	-0,937037
sly-MIR8006-2	228	19,298246	29,824561	16,22807	34,649123	35,526316	64,473684	1,1617647	1,1891892	-92,1	-88,9	0,0059267	18,61	-40,394737	-1,0690476
sly-MIR8006-3	231	23,376623	27,705628	15,151515	33,766234	38,528139	61,471861	1,21875	1,5428571	-63,7	-50,6	0,0002553	52,81	-27,575758	-1,0794872
sly-MIR8006-	243	13,99177	37,037037	18,930041	30,041152	32,921811	67,078189	0,8111111	0,7391304	-68,5	-56,81	0,0010347	35,22	-28,1893	-0,822449

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sly-MIR8006-5	232	17,672414	29,741379	20,258621	32,327586	37,931034	62,068966	1,0869565	0,8723404	-93,8	-88,7	0,0448003	13,38	-40,431034	-1,1914286
sly-MIR8006-6	218	19,266055	33,944954	15,59633	31,192661	34,862385	65,137615	0,9189189	1,2352941	-86,1	-80,8	0,0037063	22,44	-39,495413	-1,4211538
sly-MIR8006-7	181	18,232044	27,071823	20,994475	33,701657	39,226519	60,773481	1,244898	0,8684211	-67,3	-66,9	0,0920172	11,21	-37,18232	-0,8989247
sly-MIR8007a	146	15,753425	35,616438	17,123288	31,506849	32,876712	67,123288	0,8846154	0,92	-36,6	-36,6	0,0246477	18,53	-25,068493	-0,7709677
sly-MIR8007b-1	79	18,987342	41,772152	18,987342	20,253165	37,974684	62,025316	0,4848485	1	-23,2	-21,9	0,122687	7,1	-29,367089	-1,3296296
sly-MIR8007b-2	291	17,182131	34,364261	13,745704	34,707904	30,927835	69,072165	1,01	1,25	-94,6	-86,89	8,93E-05	39,39	-32,508591	-0,8233333
sly-MIR8008b-1	193	14,507772	38,860104	19,170984	27,46114	33,678756	66,321244	0,7066667	0,7567568	-57,1	-52,7	0,0154305	32,79	-29,585492	-1,2254237
sly-MIR8008b-2	120	17,5	33,333333	17,5	31,666667	35	65	0,95	1	-33,9	-35	0,006543	12,92	-28,25	-0,8222222
sly-MIR8008b-3	223	18,38565	29,596413	16,143498	35,874439	34,529148	65,470852	1,2121212	1,1388889	-72,5	-71	0,0006238	21,32	-32,511211	-1,1206897
sly-MIR8009-1	206	18,446602	28,15534	18,932039	34,466019	37,378641	62,621359	1,2241379	0,974359	-86,5	-83,7	0,0111222	42,9	-41,990291	-0,9792079
sly-MIR8009-2	179	16,201117	29,050279	20,670391	34,078212	36,871508	63,128492	1,1730769	0,7837838	-55,8	-55,8	0,0202292	14,65	-31,173184	-1,0301887
sly-MIR8011a-1	168	19,047619	29,166667	19,047619	32,738095	38,095238	61,904762	1,122449	1	-70	-69,6	0,0268794	10,2	-41,666667	-1,09375
sly-MIR8011a-2	238	17,647059	32,773109	16,386555	33,193277	34,033613	65,966387	1,0128205	1,0769231	-59,9	-52,3	0,0010532	35,43	-25,168067	-0,9416667
sly-MIR8011a-3	138	20,289855	29,710145	15,217391	34,782609	35,507246	64,492754	1,1707317	1,3333333	-55	-52,8	0,0209002	11,3	-39,855072	-0,9921875
sly-MIR8011a-4	100	15	36	21	28	36	64	0,7777778	0,7142857	-29,3	-29,2	0,345427	3,67	-29,3	-0,7146789
sly-MIR8011a-5	171	22,222222	28,654971	16,959064	32,163743	39,181287	60,818713	1,122449	1,3103448	-83,5	-82,5	0,0835789	11,66	-48,830409	-0,8626667
sly-MIR8011b	137	20,437956	29,19708	18,978102	31,386861	39,416058	60,583942	1,075	1,0769231	-60,7	-60,7	0,10052	5,57	-44,306569	-0,7122222
sly-MIR8013-1	289	16,262976	37,716263	14,186851	31,83391	30,449827	69,550173	0,8440367	1,1463415	-67,7	-54,3	9,67E-05	58,45	-23,425606	-1,1914894
sly-MIR8013-2	169	18,934911	27,218935	18,343195	35,502959	37,278107	62,721893	1,3043478	1,0322581	-74,5	-71,1	0,0077904	29,94	-44,08284	-0,7645161
sly-MIR8013-3	203	17,73399	31,034483	15,763547	35,46798	33,497537	66,502463	1,1428571	1,125	-74,7	-71,1	0,0003263	54,8	-36,79803	-0,725
sly-MIR8014	205	18,04878	38,04878	12,682927	31,219512	30,731707	69,268293	0,8205128	1,4230769	-59,1	-57,9	0,0092321	30,26	-28,829268	-0,7973684
sly-MIR8019-1	283	19,434629	34,275618	13,074205	33,215548	32,508834	67,491166	0,9690722	1,4864865	-89,3	-87,3	0,0018184	48,54	-31,55477	-0,7116883
sly-MIR8019-2	258	18,217054	39,147287	12,790698	29,844961	31,007752	68,992248	0,7623762	1,4242424	-57	-50	0,0001889	39,27	-22,093023	-1,1352941
sly-MIR8019-3	262	16,793893	41,603053	14,122137	27,480916	30,916031	69,083969	0,6605505	1,1891892	-57,6	-47,58	0,00019	50,51	-21,984733	-1,3880597
sly-MIR8020	88	15,909091	36,363636	15,909091	31,818182	31,818182	68,181818	0,875	1	-32,3	-32,3	0,266514	5,32	-36,704545	-1,1535714
sly-MIR8021-1	218	16,055046	31,651376	15,59633	36,697248	31,651376	68,348624	1,1594203	1,0294118	-82,3	-81,3	0,04637	11,23	-37,752294	-1,0659091
sly-MIR8021-2	241	14,522822	32,365145	17,427386	35,684647	31,950207	68,049793	1,1025641	0,8333333	-82,9	-77,8	0,0090512	27,41	-34,39834	-1,28
sly-MIR8021-3	226	15,929204	30,973451	16,371681	36,725664	32,300885	67,699115	1,1857143	0,972973	-65,4	-55,3	0,0026657	27,16	-28,938053	-1,1719298
sly-MIR8021-4	241	14,522822	32,780083	17,012448	35,684647	31,53527	68,46473	1,0886076	0,8536585	-77,7	-69	0,0009944	21,76	-32,240664	-0,8542857
sly-MIR8025	137	12,408759	35,766423	18,248175	33,576642	30,656934	69,343066	0,9387755	0,68	-56,7	-56,7	0,538625	3,44	-41,386861	-1,35
sly-MIR8030-1	110	19,090909	33,636364	13,636364	33,636364	32,727273	67,272727	1	1,4	-30,2	-30,2	0,0309867	10,3	-27,454545	-0,7491803
sly-MIR8030-2	73	19,178082	27,39726	16,438356	36,986301	35,616438	64,383562	1,35	1,1666667	-25,5	-21,5	0,117366	6,19	-34,931507	-0,9196078
sly-MIR8033	108	17,592593	31,481481	15,740741	35,185185	33,333333	66,666667	1,1176471	1,1176471	-60,1	-59,1	0,115534	5,36	-55,648148	-0,8486842
sly-MIR8034	289	15,570934	34,602076	15,570934	34,256055	31,141869	68,858131	0,99	1	-69	-53,65	0,0001165	75,02	-23,875433	-1,9117647
sly-MIR8037	159	20,125786	38,36478	11,320755	30,188679	31,446541	68,553459	0,7868852	1,7777778	-37,2	-35,9	0,0321117	18,86	-23,396226	-0,7125
sly-MIR8038b	136	19,852941	29,411765	19,117647	31,617647	38,970588	61,029412	1,075	1,0384615	-62,8	-62,1	0,086087	6,23	-46,176471	-0,8195402
sly-MIR8039	194	15,979381	32,474227	18,556701	32,989691	34,536082	65,463918	1,015873	0,8611111	-63,6	-61,3	0,0302743	8,87	-32,783505	-0,7166667
sly-MIR8042	158	17,088608	34,810127	17,088608	31,012658	34,177215	65,822785	0,8909091	1	-51,1	-51,1	0,0483277	13,37	-32,341772	-0,8452381

sly-MIR8045	186	23,11828	32,795699	11,827957	32,258065	34,946237	65,053763	0,9836066	1,9545455	-48	-37,63	0,0004667	39,84	-25,806452	-0,783908
sly-MIR8046-1	324	20,987654	32,716049	16,049383	30,246914	37,037037	62,962963	0,9245283	1,3076923	-84,8	-74,8	5,38E-05	49,74	-26,17284	-1,26
sly-MIR8046-2	332	12,951807	35,843373	19,879518	31,325301	32,831325	67,168675	0,8739496	0,6515152	-84,1	-82,09	0,0004011	25,81	-25,331325	-1,1329412
sly-MIR8050-1	131	13,740458	33,587786	18,320611	34,351145	32,061069	67,938931	1,0227273	0,75	-49,4	-46,7	0,0185586	10,83	-37,709924	-1,5322034
sly-MIR8050-2	131	12,977099	33,587786	17,557252	35,877863	30,534351	69,465649	1,0681818	0,7391304	-42,4	-39,9	0,012346	11,2	-32,366412	-1,0658537
sly-MIR8050-3	131	12,977099	33,587786	18,320611	35,114504	31,29771	68,70229	1,0454545	0,7083333	-48,6	-46	0,0138022	11,56	-37,099237	-0,7064935
sly-MIR8051	251	15,139442	37,051793	17,131474	30,677291	32,270916	67,729084	0,827957	0,8837209	-61,5	-56,5	0,0002083	39,69	-24,501992	-1,1642857
sly-MIR812o	161	19,254658	27,950311	18,012422	34,782609	37,267081	62,732919	1,2444444	1,0689655	-64,5	-62,3	0,016799	14,97	-40,062112	-1,075
sly-MIR8138-1	138	21,014493	28,985507	19,565217	30,434783	40,57971	59,42029	1,05	1,0740741	-59,8	-54,3	0,0174319	16,34	-43,333333	-1,1827586
sly-MIR8138-2	189	16,402116	28,042328	17,460317	38,095238	33,862434	66,137566	1,3584906	0,9393939	-45,6	-44,4	0,0343625	28,53	-24,126984	-1,179661
sly-MIR816	104	14,423077	27,884615	18,269231	39,423077	32,692308	67,307692	1,4137931	0,7894737	-26,1	-26,1	0,157567	5,92	-25,096154	-1,7723404
sly-MIR8172	164	20,731707	31,707317	11,585366	35,97561	32,317073	67,682927	1,1346154	1,7894737	-55,3	-50,8	0,0057625	26,89	-33,719512	-1,0433962
sly-MIR8175	235	16,595745	37,021277	18,723404	27,659574	35,319149	64,680851	0,7471264	0,8863636	-58,4	-58,4	0,0086135	18,14	-24,851064	-0,8703704
sly-MIR821b-1	282	19,148936	29,432624	13,120567	38,297872	32,269504	67,730496	1,3012048	1,4594595	-66,4	-54,7	7,25E-05	54,96	-23,546099	-0,7
sly-MIR821b-2	98	18,367347	34,693878	20,408163	26,530612	38,77551	61,22449	0,7647059	0,9	-30,8	-27,4	0,155524	11,85	-31,428571	-0,7308943
sly-MIR821e	165	20,606061	35,151515	12,121212	32,121212	32,727273	67,272727	0,9137931	1,7	-41,1	-34,3	0,0479235	17,43	-24,909091	-0,7452174
sly-MIR822-1	323	16,099071	28,79257	15,789474	39,318885	31,888545	68,111455	1,3655914	1,0196078	-79,8	-63	0,0001017	75,13	-24,705882	-0,8306818
sly-MIR822-2	99	16,161616	27,272727	17,171717	39,393939	33,333333	66,666667	1,4444444	0,9411765	-28,9	-26,2	0,0262673	19,32	-29,191919	-1,0942029
sly-MIR823-1	276	22,463768	33,695652	13,768116	30,072464	36,231884	63,768116	0,8924731	1,6315789	-77,5	-67,6	0,0012595	38,37	-28,07971	-0,775
sly-MIR823-2	263	21,673004	27,376426	16,34981	34,60076	38,022814	61,977186	1,2638889	1,3255814	-76	-73,2	0,0002529	41,92	-28,897338	-0,7131579
sly-MIR827-1	88	15,909091	31,818182	15,909091	36,363636	31,818182	68,181818	1,1428571	1	-34,9	-34,9	0,0956756	6,03	-39,659091	-1,2464286
sly-MIR827-2	123	15,447154	40,650407	15,447154	28,455285	30,894309	69,105691	0,7	1	-44,3	-44,3	0,16497	5,9	-36,01626	-0,8138889
sly-MIR827b	121	14,049587	35,53719	20,661157	29,752066	34,710744	65,289256	0,8372093	0,68	-48,7	-48,7	0,247828	2,97	-40,247934	-0,8105263
sly-MIR828b	119	17,647059	29,411765	16,806723	36,134454	34,453782	65,546218	1,2285714	1,05	-48,2	-48,2	0,0901791	5,37	-40,504202	-0,8724138
sly-MIR829	129	18,604651	28,682171	13,953488	38,75969	32,55814	67,44186	1,3513514	1,3333333	-57,2	-56,2	0,0710057	4,89	-44,341085	-1,8407407
sly-MIR830	335	22,985075	28,358209	9,8507463	38,80597	32,835821	67,164179	1,3684211	2,3333333	-78	-54,99	7,66E-05	73,52	-23,283582	-0,7090909
sly-MIR837	261	19,157088	34,482759	13,409962	32,950192	32,56705	67,43295	0,9555556	1,4285714	-90,3	-87,8	0,0153028	22,53	-34,597701	-1,0623529
sly-MIR839	280	22,857143	23,571429	22,5	31,071429	45,357143	54,642857	1,3181818	1,015873	-89,9	-86,4	0,0003095	38,59	-32,107143	-0,8296296
sly-MIR845b	285	19,298246	30,877193	14,736842	35,087719	34,035088	65,964912	1,1363636	1,3095238	-71,2	-67,3	0,0002034	56,26	-24,982456	-0,9148936
sly-MIR846	311	20,257235	33,440514	11,254019	35,048232	31,511254	68,488746	1,0480769	1,8	-71,7	-68,6	0,0001482	33,28	-23,054662	-0,8653846
sly-MIR856	128	17,1875	32,8125	15,625	34,375	32,8125	67,1875	1,047619	1,1	-32,4	-31,8	0,0055146	15,45	-25,3125	-1,0956522
sly-MIR857	130	16,153846	33,846154	14,615385	35,384615	30,769231	69,230769	1,0454545	1,1052632	-70,3	-70,3	0,132349	5,22	-54,076923	-0,9625
sly-MIR8573-1	216	19,907407	31,018519	17,592593	31,481481	37,5	62,5	1,0149254	1,1315789	-67,2	-63,1	0,0159499	13,54	-31,111111	-1,0405063
sly-MIR8573-2	160	23,125	30	10	36,875	33,125	66,875	1,2291667	2,3125	-54,2	-48,9	0,0083573	47,34	-33,875	-0,925
sly-MIR8578	278	11,151079	34,532374	19,064748	35,251799	30,215827	69,784173	1,0208333	0,5849057	-65,6	-64,1	0,0025188	34,07	-23,597122	-1,0897059
sly-MIR859-1	301	21,262458	30,564784	11,295681	36,877076	32,55814	67,44186	1,2065217	1,8823529	-69,8	-61,8	4,69E-05	74,01	-23,189369	-1,0214286
sly-MIR859-2	254	16,141732	31,496063	14,173228	38,188976	30,314961	69,685039	1,2125	1,1388889	-55,1	-49	0,0012283	36,17	-21,692913	-0,9705882
sly-MIR8644-1	142	12,676056	42,957746	17,605634	26,760563	30,28169	69,71831	0,6229508	0,72	-38,3	-38,3	0,145444	14,1	-26,971831	-1,0506667
sly-MIR8644-2	272	19,485294	31,617647	14,705882	34,191176	34,191176	65,808824	1,0813953	1,325	-66,7	-45	0,0005328	71,97	-24,522059	-0,9818182
sly-MIR865-1	193	12,953368	37,305699	19,689119	30,051813	32,642487	67,357513	0,8055556	0,6578947	-45,2	-44,3	0,0312535	6,99	-23,419689	-0,9061224
sly-MIR865-2	165	12,727273	33,939394	17,575758	35,757576	30,30303	69,69697	1,0535714	0,7241379	-36,6	-36	0,0111493	13,42	-22,181818	-1,0783333
sly-MIR8656	116	19,827586	34,482759	12,068966	33,62069	31,896552	68,103448	0,975	1,6428571	-36,4	-36,4	0,146623	3,95	-31,37931	-0,7395062
sly-MIR8668-1	142	19,014085	33,802817	14,788732	32,394366	33,802817	66,197183	0,9583333	1,2857143	-52	-52	0,0438196	6,62	-36,619718	-1,4680851
sly-MIR8668-2	86	25,581395	31,395349	10,465116	32,55814	36,046512	63,953488	1,037037	2,4444444	-25,3	-25,3	0,458091	5,92	-29,418605	-0,8238532
sly-MIR867	161	19,875776	27,329193	18,63354	34,161491	38,509317	61,490683	1,25	1,0666667	-75,8	-74,6	0,019215	19,23	-47,080745	-0,7277108
sly-MIR8672	333	21,321321	33,033033	15,915916	29,72973	37,237237	62,762763	0,9	1,3396226	-88,4	-74,6	2,37E-05	69,84	-26,546547	-0,8339806
sly-MIR868	247	14,979757	34,412955	19,433198	31,174089	34,412955	65,587045	0,9058824	0,7708333	-69,4	-65,4	0,0015807	27,76	-28,097166	-1,1714286
sly-MIR8714	82	18,292683	34,146341	15,853659	31,707317	34,146341	65,853659	0,9285714	1,1538462	-21,7	-21,7	0,103368	6,48	-26,463415	-1,0952381
sly-MIR8739-1	234	18,803419	31,623932	17,948718	31,623932	36,752137	63,247863	1	1,047619	-77,2	-76	0,0071294	21,84	-32,991453	-0,8976744
sly-MIR8739-	190	16,315789	35,263158	17,368421	31,052632	33,684211	66,315789	0,880597	0,9393939	-47,1	-41,7	0,0023237	32,31	-24,789474	-0,9

2															
sly-MIR8739-3	234	17,094017	34,188034	14,529915	34,188034	31,623932	68,376068	1	1,1764706	-61,4	-61,2	0,0048587	18,35	-26,239316	-1,15
sly-MIR8763	205	16,585366	30,243902	18,04878	35,121951	34,634146	65,365854	1,1612903	0,9189189	-87,7	-86,6	0,0150827	8,59	-42,780488	-1,1298701
sly-MIR8764	155	13,548387	29,677419	17,419355	39,354839	30,967742	69,032258	1,326087	0,7777778	-38,6	-38,6	0,0361932	14,92	-24,903226	-1,6509091
sly-MIR8766	93	10,752688	30,107527	20,430108	38,709677	31,182796	68,817204	1,2857143	0,5263158	-27	-27	0,407838	2,66	-29,032258	-0,7316327
sly-MIR8771f-1	256	18,75	32,03125	12,890625	36,328125	31,640625	68,359375	1,1341463	1,4545455	-67,8	-64	0,0003252	31,7	-26,484375	-1,155102
sly-MIR8771f-2	261	18,773946	28,35249	15,32567	37,547893	34,099617	65,900383	1,3243243	1,225	-82,1	-78,9	0,0022072	33,33	-31,455939	-0,7258427
sly-MIR8771f-3	261	17,624521	30,268199	14,942529	37,164751	32,56705	67,43295	1,2278481	1,1794872	-75,8	-71	0,0005808	43,45	-29,042146	-0,8611111
sly-MIR8771f-4	250	19,2	29,6	12,4	38,8	31,6	68,4	1,3108108	1,5483871	-67,2	-52,2	0,0018834	56,23	-26,88	-1,1491525
sly-MIR908	145	15,172414	39,310345	16,551724	28,965517	31,724138	68,275862	0,7368421	0,9166667	-32,5	-27,97	0,0458492	14,21	-22,413793	-1,2529412
sly-MIR946a	117	17,094017	24,786325	15,384615	42,735043	32,478632	67,521368	1,7241379	1,1111111	-42,1	-41,1	0,0521512	11,2	-35,982906	-0,8222222
sly-MIR9470-1	192	17,708333	29,6875	17,708333	34,895833	35,416667	64,583333	1,1754386	1	-48,6	-45,2	0,0076152	31,28	-25,3125	-0,702
sly-MIR9470-2	115	21,73913	24,347826	8,6956522	45,217391	30,434783	69,565217	1,8571429	2,5	-34,8	-32,4	0,0649658	15,66	-30,26087	-0,7625
sly-MIR9470-3	258	22,48062	34,883721	13,953488	28,682171	36,434109	63,565891	0,8222222	1,6111111	-70,4	-62,1	0,0001407	39,21	-27,286822	-0,8986486
sly-MIR9471a-1	180	25,555556	30,555556	13,888889	30	39,444444	60,555556	0,9818182	1,84	-74,3	-74,3	0,112858	11,67	-41,277778	-1,0464789
sly-MIR9471a-2	154	23,376623	34,415584	10,38961	31,818182	33,766234	66,233766	0,9245283	2,25	-58,5	-58,5	0,120957	6,66	-37,987013	-1,0511111
sly-MIR9471b	147	23,809524	30,612245	14,285714	31,292517	38,095238	61,904762	1,0222222	1,6666667	-65,2	-65,1	0,0700697	7,91	-44,353741	-0,9261364
sly-MIR9472	234	16,239316	32,051282	16,239316	35,470085	32,478632	67,521368	1,1066667	1	-82,1	-80,2	0,0015802	16,22	-35,08547	-1,0802632
sly-MIR9473-1	120	17,5	34,166667	17,5	30,833333	35	65	0,902439	1	-53	-52,9	0,0399228	8,28	-44,166667	-1,2619048
sly-MIR9473-2	118	16,949153	32,20339	16,949153	33,898305	33,898305	66,101695	1,0526316	1	-55,9	-55	0,118759	7,94	-47,372881	-1,3975
sly-MIR9476-1	94	17,021277	32,978723	14,893617	35,106383	31,914894	68,085106	1,0645161	1,1428571	-63,4	-63,4	0,890285	0,53	-67,446809	-1,0694915
sly-MIR9476-2	94	14,893617	35,106383	17,021277	32,978723	31,914894	68,085106	0,9393939	0,875	-58,3	-58,3	0,77138	0,58	-62,021277	-0,7823529
sly-MIR9476-3	172	18,023256	34,302326	20,930233	26,744186	38,953488	61,046512	0,779661	0,8611111	-88,3	-88,3	0,134661	4,94	-51,337209	-0,7116667
sly-MIR9477	102	19,607843	30,392157	18,627451	31,372549	38,235294	61,764706	1,0322581	1,0526316	-34,6	-30,7	0,113704	7,96	-33,921569	-0,71375
sly-MIR9478-1	206	19,902913	31,553398	12,621359	35,92233	32,524272	67,475728	1,1384615	1,5769231	-75,5	-68,13	0,0058672	25,61	-36,650485	-1,1268657
sly-MIR9478-2	204	18,137255	35,294118	12,745098	33,823529	30,882353	69,117647	0,9583333	1,4230769	-49,7	-46,9	0,0033366	27,02	-24,362745	-0,7888889
sly-MIR9479	169	21,893491	30,769231	23,668639	23,668639	45,56213	54,43787	0,7692308	0,925	-64,4	-53,24	0,0198283	29,81	-38,106509	-0,8363636
sly-MIR952a	213	23,474178	24,882629	17,840376	33,802817	41,314554	58,685446	1,3584906	1,3157895	-65,4	-57,5	0,0070913	30,03	-30,704225	-0,7269565
sly-MIR9555b	260	18,461538	29,615385	14,230769	37,692308	32,692308	67,307692	1,2727273	1,2972973	-79,5	-77,2	0,0014116	19,85	-30,576923	-1,1575
sly-MIR9556	335	19,701493	29,253731	12,835821	38,208955	32,537313	67,462687	1,3061224	1,5348837	-78,4	-69,1	0,0006276	62,73	-23,402985	-0,7192661
sly-MIR9563a	253	20,158103	34,782609	11,857708	33,201581	32,01581	67,98419	0,9545455	1,7	-59	-55,8	0,0002397	36,13	-23,320158	-0,7346154
sly-MIR9565	284	24,295775	29,225352	13,380282	33,098592	37,676056	62,323944	1,1325301	1,8157895	-75,7	-48	0,0005317	72,94	-26,65493	-0,7074766
sly-MIR9668	66	16,666667	30,30303	15,151515	37,878788	31,818182	68,181818	1,25	1,1	-32,1	-30,8	0,168323	4,19	-48,636364	-0,952
sly-MIR9674b	235	20	28,93617	13,617021	37,446809	33,617021	66,382979	1,2941176	1,46875	-56,8	-35,7	0,0004795	59,35	-24,170213	-0,7627451
sly-MIR9675	107	19,626168	26,168224	22,429907	31,775701	42,056075	57,943925	1,2142857	0,875	-74,9	-74,9	0,602081	0,94	-70	-1,5290323
sly-MIR9679-1	98	17,346939	33,673469	16,326531	32,653061	33,673469	66,326531	0,969697	1,0625	-26,1	-24,4	0,094145	6,72	-26,632653	-1,0103896
sly-MIR9679-2	132	15,151515	37,121212	15,909091	31,818182	31,060606	68,939394	0,8571429	0,952381	-33,7	-33,7	0,101679	6,65	-25,530303	-1,1403226
sly-MIR9726-1	143	13,286713	28,671329	17,482517	40,559441	30,769231	69,230769	1,4146341	0,76	-34	-27,2	0,0067136	43,92	-23,776224	-0,755
sly-MIR9726-2	220	17,272727	31,818182	13,636364	37,272727	30,909091	69,090909	1,1714286	1,2666667	-51,3	-48,8	0,000726	32,49	-23,318182	-0,8164706
sly-MIR9736-1	165	15,151515	32,727273	17,575758	34,545455	32,727273	67,272727	1,0555556	0,862069	-99,4	-99,4	0,012463	8,23	-60,242424	-1,2628205
sly-MIR9736-2	165	18,181818	34,545455	15,151515	32,121212	33,333333	66,666667	0,9298246	1,2	-90,8	-86,2	0,0362521	10,68	-55,030303	-1,1819277
sly-MIR9752	257	17,509728	26,848249	13,618677	42,023346	31,128405	68,871595	1,5652174	1,2857143	-59,4	-57,4	0,0004932	42,28	-23,11284	-0,72
sly-MIR9760	115	27,826087	27,826087	9,5652174	34,782609	37,391304	62,608696	1,25	2,9090909	-30,6	-25,7	0,0255981	26,25	-26,608696	-0,7309091

sly-MIR9761	327	21,100917	29,663609	13,455657	35,779817	34,556575	65,443425	1,2061856	1,5681818	-83,5	-57,6	3,65E-05	86,88	-25,535168	-1,6095238
sly-MIR9764	186	15,053763	33,333333	18,27957	33,333333	33,333333	66,666667	1	0,8235294	-45,4	-40,5	0,0034872	25,86	-24,408602	-0,9476923
sly-MIR9772b	147	19,727891	37,414966	15,646259	27,210884	35,37415	64,62585	0,7272727	1,2608696	-41,2	-41,2	0,176784	4,53	-28,027211	-0,7363636
sly-MIR9773	215	17,209302	29,302326	18,604651	34,883721	35,813953	64,186047	1,1904762	0,925	-89,7	-89,7	0,0656485	11,58	-41,72093	-0,9310345

Supplementary Table S15. Thermodynamic and structural characterization of *Solanum pennellii* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Len	G	A	C	U	GC	AU	UA-ratio	GC-ratio	MFE	MFE-ensemble	frequency	diversity	AMFE	MFEI
spe-MIR10189-1	**74**	28,378378	33,783784	16,216216	21,621622	44,594595	55,405405	0,64	1,75	-25,2	-25,2	0,163457	3,42	-34,054054	-0,7636364
spe-MIR10189-2	**250**	28,8	28,4	18,4	24,4	47,2	52,8	0,8591549	1,5652174	-84,5	-80,2	0,0006855	41,31	-33,8	-0,7161017
spe-MIR10211a	**83**	19,277108	27,710843	24,096386	28,915663	43,373494	56,626506	1,0434783	0,8	-26,5	-26,5	0,339153	5,02	-31,927711	-0,7361111
spe-MIR10215	**66**	21,212121	37,878788	10,606061	30,30303	31,818182	68,181818	0,8	2	-30,6	-30,6	0,351823	1,72	-46,363636	-1,4571429
spe-MIR10216	**81**	23,45679	30,864198	16,049383	29,62963	39,506173	60,493827	0,96	1,4615385	-32	-32	0,326206	2,84	-39,506173	-1
spe-MIR10224-1	**187**	19,786096	29,946524	14,438503	35,828877	34,224599	65,775401	1,1964286	1,3703704	-65,6	-59,2	0,0104151	43,45	-35,080214	-1,025
spe-MIR10224-2	**187**	19,786096	30,481283	14,438503	35,294118	34,224599	65,775401	1,1578947	1,3703704	-68,5	-66,2	0,0135701	25,65	-36,631016	-1,0703125
spe-MIR1023e	**205**	14,146341	32,682927	19,512195	33,658537	33,658537	66,341463	1,0298507	0,725	-99,9	-96,7	0,041305	6,75	-48,731707	-1,4478261
spe-MIR1027c	**124**	25,806452	27,419355	8,8709677	37,903226	34,677419	65,322581	1,3823529	2,9090909	-32,1	-32,1	0,0210959	15,63	-25,887097	-0,7465116
spe-MIR1033e	**231**	25,974026	28,571429	20,779221	24,675325	46,753247	53,246753	0,8636364	1,25	-77,6	-69,2	0,0005239	43,08	-33,593074	-0,7185185
spe-MIR1039	**217**	22,119816	24,884793	17,511521	35,483871	39,631336	60,368664	1,4259259	1,2631579	-66,1	-60,2	0,0045943	36,37	-30,460829	-0,7686047
spe-MIR10420-1	**117**	20,512821	25,641026	21,367521	32,478632	41,880342	58,119658	1,2666667	0,96	-34,5	-34,5	0,0517384	11,84	-29,487179	-0,7040816
spe-MIR10420-2	**218**	18,807339	23,853211	18,348624	38,990826	37,155963	62,844037	1,6346154	1,025	-57	-44,5	0,0048541	44,89	-26,146789	-0,7037037
spe-MIR10427b	**214**	19,158879	34,579439	11,682243	34,579439	30,841121	69,158879	1	1,64	-51,5	-47,9	0,0002752	44,55	-24,065421	-0,780303
spe-MIR1043	**212**	17,45283	28,773585	15,566038	38,207547	33,018868	66,981132	1,3278689	1,1212121	-58,1	-55,7	0,0024981	30,79	-27,40566	-0,83
spe-MIR1044-1	**204**	15,196078	29,411765	18,137255	37,254902	33,333333	66,666667	1,2666667	0,8378378	-56,6	-53,3	0,0124341	15,53	-27,745098	-0,8323529
spe-MIR1044-2	**194**	15,979381	31,443299	18,041237	34,536082	34,020619	65,979381	1,0983607	0,8857143	-66,4	-66,4	0,0438435	11,85	-34,226804	-1,0060606
spe-MIR1044-3	**218**	23,394495	25,688073	20,642202	30,275229	44,036697	55,963303	1,1785714	1,1333333	-91,1	-87,99	0,0082698	27,01	-41,788991	-0,9489583
spe-MIR1046	**312**	15,705128	34,615385	14,423077	35,25641	30,128205	69,871795	1,0185185	1,0888889	-67,5	-60	0,0001904	50,1	-21,634615	-0,7180851
spe-MIR10519-1	**222**	18,918919	28,378378	14,864865	37,837838	33,783784	66,216216	1,3333333	1,2727273	-81	-75,6	0,0057905	21,18	-36,486486	-1,08
spe-MIR10519-2	**249**	18,473896	29,718876	14,859438	36,947791	33,333333	66,666667	1,2432432	1,2432432	-76,1	-62,98	0,0017919	61,92	-30,562249	-0,9168675
spe-MIR10519-3	**236**	19,915254	27,118644	15,677966	37,288136	35,59322	64,40678	1,375	1,2702703	-85,4	-84	0,0027977	21,39	-36,186441	-1,0166667
spe-MIR10519-4	**195**	18,461538	31,282051	14,358974	35,897436	32,820513	67,179487	1,147541	1,2857143	-64,3	-63,2	0,0201892	12,68	-32,974359	-1,0046875
spe-MIR10528	**144**	18,055556	34,722222	16,666667	30,555556	34,722222	65,277778	0,88	1,0833333	-78,3	-78,3	0,041324	7,03	-54,375	-1,566
spe-MIR10529	**132**	24,242424	25,757576	22,727273	27,272727	46,969697	53,030303	1,0588235	1,0666667	-50,4	-45,9	0,0305468	13,67	-38,181818	-0,8129032
spe-MIR10531	**123**	21,138211	30,081301	16,260163	32,520325	37,398374	62,601626	1,0810811	1,3	-64,6	-64,6	0,18915	4,91	-52,520325	-1,4043478
spe-MIR10532-1	**253**	18,972332	34,387352	14,624506	32,01581	33,596838	66,403162	0,9310345	1,2972973	-68,6	-55,5	0,0005588	43,5	-27,114625	-0,8070588
spe-MIR10532-10	**198**	19,69697	35,858586	16,161616	28,282828	35,858586	64,141414	0,7887324	1,21875	-97	-90,71	0,0186713	21,82	-48,989899	-1,3661972
spe-MIR10532-2	**256**	16,015625	35,9375	17,1875	30,859375	33,203125	66,796875	0,8586957	0,9318182	-97,6	-91,6	0,0247765	21,62	-38,125	-1,1482353
spe-MIR10532-3	**248**	17,741935	33,064516	18,145161	31,048387	35,887097	64,112903	0,9390244	0,9777778	-98,4	-97,5	0,020615	17,06	-39,677419	-1,105618
spe-MIR10532-4	**251**	15,936255	35,856574	20,318725	27,888446	36,25498	63,74502	0,7777778	0,7843137	-97,7	-96,8	0,0260365	17,18	-38,924303	-1,0736264
spe-MIR10532-5	**246**	18,699187	36,585366	11,788618	32,926829	30,487805	69,512195	0,9	1,5862069	-94,4	-89	0,0095938	16,02	-38,373984	-1,2586667
spe-MIR10532-6	**190**	16,315789	33,684211	15,263158	34,736842	31,578947	68,421053	1,03125	1,0689655	-62,5	-61,8	0,0067794	13,17	-32,894737	-1,0416667
spe-MIR10532-7	**215**	16,27907	26,976744	25,581395	31,162791	41,860465	58,139535	1,1551724	0,6363636	-95,4	-93,7	0,0436712	17,04	-44,372093	-1,06
spe-MIR10532-8	**266**	19,548872	27,443609	13,533835	39,473684	33,082707	66,917293	1,4383562	1,4444444	-64,6	-54,2	0,0003355	53,74	-24,285714	-0,7340909
spe-MIR10532-9	**139**	25,179856	25,899281	14,388489	34,532374	39,568345	60,431655	1,3333333	1,75	-41,8	-39,6	0,0101823	18,58	-30,071942	-0,76
spe-MIR10533-1	**279**	14,695341	36,200717	16,129032	32,97491	30,824373	69,175627	0,9108911	0,9111111	-99,8	-83,4	0,0020986	27,51	-35,770609	-1,1604651
spe-MIR10533-2	**193**	18,134715	29,533679	17,61658	34,715026	35,751295	64,248705	1,1754386	1,0294118	-91,2	-90,2	0,0303955	8,98	-47,253886	-1,3217391
spe-MIR10535a-1	**119**	18,487395	31,092437	16,806723	33,613445	35,294118	64,705882	1,0810811	1,1	-66,2	-66,2	0,0539014	4,31	-55,630252	-1,5761905
spe-MIR10535a-2	**119**	16,806723	31,092437	15,12605	36,97479	31,932773	68,067227	1,1891892	1,1111111	-60,4	-60,4	0,309866	1,83	-50,756303	-1,5894737
spe-MIR10536-1	**201**	24,378109	30,348259	18,40796	26,865672	42,78607	57,21393	0,8852459	1,3243243	-95	-94,6	0,0847741	7,18	-47,263682	-1,1046512
spe-MIR10536-2	**90**	20	32,222222	17,777778	30	37,777778	62,222222	0,9310345	1,125	-48,6	-48,6	0,501948	2,14	-54	-1,4294118
spe-MIR10537	**237**	24,050633	29,957806	20,253165	25,738397	44,303797	55,696203	0,8591549	1,1875	-76,9	-62,9	0,0007872	45,01	-32,447257	-0,732381
spe-MIR10538-1	**139**	16,546763	35,251799	14,388489	33,81295	30,935252	69,064748	0,9591837	1,15	-74,2	-74,2	0,173152	6,35	-53,381295	-1,7255814
spe-MIR10538-10	**174**	16,091954	35,057471	14,367816	34,482759	30,45977	69,54023	0,9836066	1,12	-75,3	-75,3	0,131307	3,64	-43,275862	-1,4207547
spe-MIR10538-11	**138**	15,217391	36,231884	17,391304	31,15942	32,608696	67,391304	0,86	0,875	-69,2	-69,2	0,299395	4,76	-50,144928	-1,5377778
spe-MIR10538-12	**191**	17,801047	32,984293	16,753927	32,460733	34,554974	65,445026	0,984127	1,0625	-96,9	-96,7	0,116727	8,34	-50,732984	-1,4681818
spe-MIR10538-13	**148**	17,567568	33,783784	16,216216	32,432432	33,783784	66,216216	0,96	1,0833333	-78,4	-78,4	0,283924	2,9	-52,972973	-1,568
spe-MIR10538-14	**105**	14,285714	31,428571	17,142857	37,142857	31,428571	68,571429	1,1818182	0,8333333	-24,9	-23	0,0593107	17,52	-23,714286	-0,7545455
spe-MIR10538-15	**125**	15,2	34,4	18,4	32	33,6	66,4	0,9302326	0,826087	-68,7	-68,7	0,48531	2,01	-54,96	-1,6357143
spe-MIR10538-16	**148**	16,891892	34,459459	16,891892	31,756757	33,783784	66,216216	0,9215686	1	-79,6	-79,6	0,297297	2,25	-53,783784	-1,592
spe-MIR10538-17	**148**	16,891892	31,756757	16,891892	34,459459	33,783784	66,216216	1,0851064	1	-85	-85	0,604314	0,99	-57,432432	-1,7
spe-MIR10538-2	**136**	15,441176	30,147059	16,176471	38,235294	31,617647	68,382353	1,2682927	0,9545455	-33,9	-33,1	0,0077875	32,37	-24,926471	-0,7883721

spe-MIR10538-3	**211**	18,483412	34,123223	12,796209	34,597156	31,279621	68,720379	1,0138889	1,4444444	-86,9	-83,3	0,0611283	19,77	-41,184834	-1,3166667
spe-MIR10538-4	**172**	16,860465	33,72093	15,116279	34,302326	31,976744	68,023256	1,0172414	1,1153846	-81,7	-81,7	0,233517	5,23	-47,5	-1,4854545
spe-MIR10538-5	**91**	15,384615	35,164835	15,384615	34,065934	30,769231	69,230769	0,96875	1	-38,9	-38,9	0,567889	1,5	-42,747253	-1,3892857
spe-MIR10538-6	**213**	15,023474	34,741784	15,492958	34,741784	30,516432	69,483568	1	0,969697	-97,6	-91,4	0,0296883	15,91	-45,821596	-1,5015385
spe-MIR10538-7	**181**	15,469613	34,80663	14,917127	34,80663	30,38674	69,61326	1	1,037037	-79,7	-79,7	0,084052	10,3	-44,033149	-1,4490909
spe-MIR10538-8	**154**	17,532468	31,168831	14,935065	36,363636	32,467532	67,532468	1,1666667	1,173913	-88,5	-88,5	0,4467	1,61	-57,467532	-1,77
spe-MIR10538-9	**147**	16,326531	33,333333	16,326531	34,013605	32,653061	67,346939	1,0204082	1	-77,6	-75,7	0,140492	5,52	-52,789116	-1,6166667
spe-MIR10540-1	**145**	16,551724	28,965517	17,241379	37,241379	33,793103	66,206897	1,2857143	0,96	-49	-43,7	0,0151529	19,02	-33,793103	-1
spe-MIR10540-2	**142**	18,309859	34,507042	14,788732	32,394366	33,098592	66,901408	0,9387755	1,2380952	-52,3	-51,7	0,0314814	7,06	-36,830986	-1,112766
spe-MIR10540-3	**290**	16,896552	29,655172	21,724138	31,724138	38,62069	61,37931	1,0697674	0,7777778	-90,2	-89,3	0,0004983	22,78	-31,103448	-0,8053571
spe-MIR10540-4	**153**	20,915033	32,679739	13,72549	32,679739	34,640523	65,359477	1	1,5238095	-67,7	-67,7	0,156277	6,32	-44,248366	-1,2773585
spe-MIR10540-5	**142**	14,788732	32,394366	18,309859	34,507042	33,098592	66,901408	1,0652174	0,8076923	-58,8	-56,4	0,0556965	5,9	-41,408451	-1,2510638
spe-MIR10540-6	**141**	16,312057	34,042553	17,021277	32,624113	33,333333	66,666667	0,9583333	0,9583333	-71	-69,8	0,333616	3,6	-50,35461	-1,5106383
spe-MIR10541-1	**286**	11,888112	38,461538	19,230769	30,41958	31,118881	68,881119	0,7909091	0,6181818	-62,5	-48	0,0001677	43,52	-21,853147	-0,7022472
spe-MIR10541-2	**107**	14,953271	31,775701	21,495327	31,775701	36,448598	63,551402	1	0,6956522	-31,6	-27,1	0,0373637	10,82	-29,53271	-0,8102564
spe-MIR10542-1	**248**	17,741935	38,709677	12,5	31,048387	30,241935	69,758065	0,8020833	1,4193548	-58,5	-55,3	0,0016332	53,34	-23,58871	-0,78
spe-MIR10542-2	**249**	18,875502	37,751004	12,449799	30,923695	31,325301	68,674699	0,8191489	1,516129	-66,9	-66,3	0,0007931	31,06	-26,86747	-0,8576923
spe-MIR10542-3	**237**	18,565401	36,28692	12,658228	32,489451	31,223629	68,776371	0,8953488	1,4666667	-58,7	-44,34	0,001269	79,83	-24,767932	-0,7932432
spe-MIR10542-4	**236**	19,491525	35,59322	13,135593	31,779661	32,627119	67,372881	0,8928571	1,483871	-61,5	-55,2	0,0020942	68,47	-26,059322	-0,7987013
spe-MIR10542-5	**297**	19,52862	36,700337	11,784512	31,986532	31,313131	68,686869	0,8715596	1,6571429	-74,4	-71,2	0,0003829	36,46	-25,050505	-0,8
spe-MIR10542-6	**237**	19,409283	35,864979	12,658228	32,067511	32,067511	67,932489	0,8941176	1,5333333	-62,2	-40,6	0,0046634	64,79	-26,244726	-0,8184211
spe-MIR10542-7	**244**	18,442623	36,885246	13,114754	31,557377	31,557377	68,442623	0,8555556	1,40625	-61,7	-56,8	0,0061956	56,33	-25,286885	-0,8012987
spe-MIR10542-8	**249**	18,473896	39,35743	11,646586	30,522088	30,120482	69,879518	0,7755102	1,5862069	-69,2	-58,2	0,0025106	55,8	-27,791165	-0,9226667
spe-MIR10542-9	**255**	16,862745	37,254902	13,72549	32,156863	30,588235	69,411765	0,8631579	1,2285714	-58,1	-38,9	0,0013358	73,42	-22,784314	-0,7448718
spe-MIR1055	**219**	25,570776	25,114155	15,525114	33,789954	41,09589	58,90411	1,3454545	1,6470588	-74,3	-74	0,0010995	26,48	-33,926941	-0,8255556
spe-MIR1088-1	**138**	18,84058	33,333333	18,115942	29,710145	36,956522	63,043478	0,8913043	1,04	-55,1	-55	0,0398162	7,48	-39,927536	-1,0803922
spe-MIR1088-2	**113**	19,469027	30,088496	19,469027	30,973451	38,938053	61,061947	1,0294118	1	-44,8	-44,8	0,0568571	6,67	-39,646018	-1,0181818
spe-MIR10987	**202**	22,277228	31,683168	16,831683	29,207921	39,108911	60,891089	0,921875	1,3235294	-66,6	-66,2	0,012243	12,92	-32,970297	-0,843038
spe-MIR10993b	**267**	18,726592	31,086142	17,977528	32,209738	36,70412	63,29588	1,0361446	1,0416667	-69,2	-67,3	0,000531	34,4	-25,917603	-0,7061224
spe-MIR1101	**88**	19,318182	26,136364	17,045455	37,5	36,363636	63,636364	1,4347826	1,1333333	-23,7	-22,7	0,0491744	14,85	-26,931818	-0,740625
spe-MIR11011a	**171**	16,959064	33,918129	17,54386	31,578947	34,502924	65,497076	0,9310345	0,9666667	-87,3	-85,1	0,0515776	5,23	-51,052632	-1,479661
spe-MIR11027	**119**	20,168067	34,453782	16,806723	28,571429	36,97479	63,02521	0,8292683	1,2	-41,2	-41,2	0,281737	10,47	-34,621849	-0,9363636
spe-MIR11036	**129**	24,806202	30,232558	10,077519	34,883721	34,883721	65,116279	1,1538462	2,4615385	-34,3	-31,1	0,0047931	28,27	-26,589147	-0,7622222
spe-MIR11041	**293**	17,406143	32,423208	15,017065	35,153584	32,423208	67,576792	1,0842105	1,1590909	-67	-61,4	0,0002409	47,24	-22,866894	-0,7052632
spe-MIR1106-1	**167**	19,161677	30,538922	14,371257	35,928144	33,532934	66,467066	1,1764706	1,3333333	-59,9	-50,4	0,0075296	25,31	-35,868263	-1,0696429
spe-MIR1106-2	**151**	13,907285	37,086093	16,556291	32,450331	30,463576	69,536424	0,875	0,84	-59,2	-55,3	0,13824	9,5	-39,205298	-1,2869565
spe-MIR1106-3	**162**	14,814815	35,185185	15,432099	34,567901	30,246914	69,753086	0,9824561	0,96	-81,2	-79,8	0,0395659	11,23	-50,123457	-1,6571429
spe-MIR11066	**124**	20,967742	31,451613	20,967742	26,612903	41,935484	58,064516	0,8461538	1	-41,2	-41,2	0,112761	9,03	-33,225806	-0,7923077
spe-MIR11068c	**83**	15,662651	25,301205	22,891566	36,144578	38,554217	61,445783	1,4285714	0,6842105	-22,9	-22,9	0,12045	4,4	-27,590361	-0,715625
spe-MIR11068e	**171**	20,467836	30,409357	11,695906	37,426901	32,163743	67,836257	1,2307692	1,75	-47,6	-46,6	0,0067071	13,49	-27,836257	-0,8654545
spe-MIR11072a	**165**	18,181818	35,151515	13,333333	33,333333	31,515152	68,484848	0,9482759	1,3636364	-94,1	-90,7	0,0362598	12,72	-57,030303	-1,8096154
spe-MIR11075b	**242**	18,595041	23,140496	19,834711	38,429752	38,429752	61,570248	1,6607143	0,9375	-67,1	-65,2	0,001697	34,64	-27,727273	-0,7215054
spe-MIR11076	**72**	23,611111	26,388889	20,833333	29,166667	44,444444	55,555556	1,1052632	1,1333333	-30,9	-30,4	0,387498	3,53	-42,916667	-0,965625
spe-MIR11082I-1	**96**	16,666667	35,416667	14,583333	33,333333	31,25	68,75	0,9411765	1,1428571	-59	-56,8	0,276702	6,2	-61,458333	-1,9666667
spe-MIR11082I-2	**96**	14,583333	33,333333	16,666667	35,416667	31,25	68,75	1,0625	0,875	-57,2	-57,2	0,189928	4,52	-59,583333	-1,9066667
spe-MIR11085-1	**151**	19,205298	25,165563	19,205298	36,423841	38,410596	61,589404	1,4473684	1	-73	-72,8	0,0430411	11,05	-48,344371	-1,2586207
spe-MIR11085-2	**326**	18,711656	28,527607	12,883436	39,877301	31,595092	68,404908	1,3978495	1,452381	-81,4	-79,6	5,10E-05	41,55	-24,969325	-0,7902913
spe-MIR11089a	**199**	18,090452	35,175879	14,070352	32,663317	32,160804	67,839196	0,9285714	1,2857143	-47,3	-37,7	0,0017055	26,35	-23,768844	-0,7390625
spe-MIR11090d	**99**	19,191919	35,353535	12,121212	33,333333	31,313131	68,686869	0,9428571	1,5833333	-22,2	-22,2	0,125547	11,31	-22,424242	-0,716129
spe-MIR11097a	**91**	14,285714	36,263736	20,879121	28,571429	35,164835	64,835165	0,7878788	0,6842105	-25,7	-25,7	0,0903954	5,42	-28,241758	-0,803125
spe-MIR11102	**233**	20,171674	31,330472	20,600858	27,896996	40,772532	59,227468	0,890411	0,9791667	-67,4	-48,1	0,0015033	54,22	-28,927039	-0,7094737
spe-MIR11109	**319**	19,435737	34,482759	12,539185	33,54232	31,974922	68,025078	0,9727273	1,55	-78,4	-70,9	1,45E-05	68,85	-24,576803	-0,7686275
spe-MIR11110b	**194**	18,041237	28,865979	18,556701	34,536082	36,597938	63,402062	1,1964286	0,9722222	-51,1	-47,8	0,0097071	22,35	-26,340206	-0,7197183
spe-MIR1112	**300**	14,666667	32	16,666667	36,666667	31,333333	68,666667	1,1458333	0,88	-73	-68	0,0013543	29,53	-24,333333	-0,7765957
spe-MIR11124	**331**	23,26284	29,607251	17,824773	29,305136	41,087613	58,912387	0,9897959	1,3050847	-96,5	-74,5	0,0010334	88,54	-29,154079	-0,7095588
spe-MIR11131	**143**	13,986014	33,566434	18,181818	34,265734	32,167832	67,832168	1,0208333	0,7692308	-78,9	-78,9	0,236719	2,98	-55,174825	-1,7152174
spe-MIR11144-1	**266**	17,293233	35,338346	13,909774	33,458647	31,203008	68,796992	0,9468085	1,2432432	-78,1	-68,57	0,0008187	41,23	-29,360902	-0,9409639
spe-MIR11144-2	**271**	18,081181	35,424354	13,284133	33,210332	31,365314	68,634686	0,9375	1,3611111	-72,3	-58,77	0,0006384	55,94	-26,678967	-0,8505882
spe-MIR1122	**125**	19,2	32,8	16	32	35,2	64,8	0,9756098	1,2	-35,3	-33,6	0,0153642	16,5	-28,24	-0,8022727
spe-MIR1127	**75**	20	32	18,666667	29,333333	38,666667	61,333333	0,9166667	1,0714286	-42,2	-42,2	0,652747	0,82	-56,266667	-1,4551724
spe-MIR1127b-1	**251**	18,7251	36,653386	11,952191	32,669323	30,677291	69,322709	0,8913043	1,5666667	-75,9	-68,06	0,000417	44,31	-30,239044	-0,9857143
spe-MIR1127b-2	**131**	21,374046	28,244275	16,030534	34,351145	37,40458	62,59542	1,2162162	1,3333333	-73	-72,9	0,0472174	5,66	-55,725191	-1,4897959

spe-MIR1128-1	**301**	14,285714	34,551495	17,275748	33,887043	31,561462	68,438538	0,9807692	0,8269231	-74	-68,6	0,001492	28,91	-24,584718	-0,7789474
spe-MIR1128-2	**108**	17,592593	35,185185	15,740741	31,481481	33,333333	66,666667	0,8947368	1,1176471	-30,6	-27,6	0,0337962	11,03	-28,333333	-0,85
spe-MIR1128-3	**248**	18,548387	33,064516	12,903226	35,483871	31,451613	68,548387	1,0731707	1,4375	-61,1	-53,97	0,0015645	46,67	-24,637097	-0,7833333
spe-MIR1128-4	**293**	12,627986	33,447099	18,088737	35,836177	30,716724	69,283276	1,0714286	0,6981132	-75,6	-75,5	0,0008737	30,66	-25,8157	-0,8404444
spe-MIR11285	**115**	20	29,565217	12,173913	38,26087	32,173913	67,826087	1,2941176	1,6428571	-35,5	-31,2	0,002829	14,67	-30,869565	-0,9594595
spe-MIR1128-5	**236**	22,881356	33,474576	10,59322	33,050847	33,474576	66,525424	0,9873418	2,16	-56,9	-31,1	0,0003453	77,95	-24,110169	-0,7202532
spe-MIR1128-6	**291**	17,869416	35,395189	15,120275	31,61512	32,989691	67,010309	0,8932039	1,1818182	-79,3	-74,57	0,0004949	66,3	-27,250859	-0,8260417
spe-MIR11301	**267**	18,35206	32,958801	14,981273	33,707865	33,333333	66,666667	1,0227273	1,225	-91,6	-82,4	0,0002555	27,66	-34,307116	-1,0292135
spe-MIR11314-1	**138**	23,188406	30,434783	11,594203	34,782609	34,782609	65,217391	1,1428571	2	-39,7	-36,6	0,0054039	23,06	-28,768116	-0,8270833
spe-MIR11314-2	**138**	22,463768	28,985507	11,594203	36,956522	34,057971	65,942029	1,275	1,9375	-45,6	-41,2	0,02262	10,92	-33,043478	-0,9702128
spe-MIR11317	**97**	16,494845	32,989691	15,463918	35,051546	31,958763	68,041237	1,0625	1,0666667	-37,2	-36	0,149596	5,86	-38,350515	-1,2
spe-MIR11444	**273**	21,245421	31,868132	15,018315	31,868132	36,263736	63,736264	1	1,4146341	-72,3	-68,8	0,0007078	47,92	-26,483516	-0,730303
spe-MIR11451	**316**	15,189873	30,379747	15,822785	38,607595	31,012658	68,987342	1,2708333	0,96	-74,6	-67,47	0,0001541	45,13	-23,607595	-0,7612245
spe-MIR11456	**71**	19,71831	30,985915	19,71831	29,577465	39,43662	60,56338	0,9545455	1	-20,7	-20,7	0,130248	5,83	-29,15493	-0,7392857
spe-MIR11479	**210**	20	30,952381	17,142857	31,904762	37,142857	62,857143	1,0307692	1,1666667	-55,2	-44,4	0,0121462	48,16	-26,285714	-0,7076923
spe-MIR11508	**239**	18,828452	34,309623	11,715481	35,146444	30,543933	69,456067	1,0243902	1,6071429	-67,6	-64,6	0,0021481	18,52	-28,284519	-0,9260274
spe-MIR11509	**325**	24,307692	27,076923	14,769231	33,846154	39,076923	60,923077	1,25	1,6458333	-90,3	-76,1	1,57E-05	75,34	-27,784615	-0,7110236
spe-MIR11536	**189**	21,164021	31,216931	8,994709	38,624339	30,15873	69,84127	1,2372881	2,3529412	-62,6	-60,5	0,0001987	23,23	-33,121693	-1,0982456
spe-MIR11553	**187**	18,716578	37,433155	12,834225	31,016043	31,550802	68,449198	0,8285714	1,4583333	-44,5	-43,8	0,0088199	19,25	-23,796791	-0,7542373
spe-MIR11564b	**222**	17,117117	33,333333	14,864865	34,684685	31,981982	68,018018	1,0405405	1,1515152	-69	-64,6	0,0070794	15,1	-31,081081	-0,971831
spe-MIR11580	**307**	26,384365	26,384365	9,4462541	37,785016	35,830619	64,169381	1,4320988	2,7931034	-83,4	-64,8	6,71E-05	89,98	-27,166124	-0,7581818
spe-MIR11583b-1	**71**	15,492958	29,577465	16,901408	38,028169	32,394366	67,605634	1,2857143	0,9166667	-30,3	-30,1	0,0847751	6,63	-42,676056	-1,3173913
spe-MIR11583b-2	**202**	20,29703	36,633663	11,881188	31,188119	32,178218	67,821782	0,8513514	1,7083333	-49,6	-45,1	0,0002734	32,78	-24,554455	-0,7630769
spe-MIR11592-1	**77**	19,480519	38,961039	15,584416	25,974026	35,064935	64,935065	0,6666667	1,25	-26,1	-25,4	0,173033	4,39	-33,896104	-0,9666667
spe-MIR11592-2	**76**	21,052632	36,842105	14,473684	27,631579	35,526316	64,473684	0,75	1,4545455	-26,3	-24,7	0,0970221	8,25	-34,605263	-0,9740741
spe-MIR1167	**272**	18,382353	26,470588	16,911765	38,235294	35,294118	64,705882	1,4444444	1,0869565	-70,9	-69,2	0,0017965	23,62	-26,066176	-0,7385417
spe-MIR11891-1	**201**	20,39801	33,333333	15,422886	30,845771	35,820896	64,179104	0,9253731	1,3225806	-90,6	-90,6	0,154048	4,65	-45,074627	-1,2583333
spe-MIR11891-2	**202**	17,326733	33,168317	13,366337	36,138614	30,693069	69,306931	1,0895522	1,2962963	-63,5	-62,5	0,0129115	12,94	-31,435644	-1,0241935
spe-MIR12162-1	**227**	23,348018	22,907489	22,026432	31,718062	45,374449	54,625551	1,3846154	1,06	-77,5	-76,4	0,0036902	28,03	-34,140969	-0,7524272
spe-MIR12162-2	**252**	23,412698	26,587302	19,444444	30,555556	42,857143	57,142857	1,1492537	1,2040816	-78,3	-63	0,0003508	66,2	-31,071429	-0,725
spe-MIR1217-1	**208**	21,634615	27,403846	9,6153846	41,346154	31,25	68,75	1,5087719	2,25	-48,1	-45,8	0,0007053	37,61	-23,125	-0,74
spe-MIR1217-2	**292**	20,890411	36,643836	13,356164	29,109589	34,246575	65,753425	0,7943925	1,5641026	-79,3	-69,19	0,0001961	46,24	-27,157534	-0,793
spe-MIR1428e	**132**	15,909091	33,333333	16,666667	34,090909	32,575758	67,424242	1,0227273	0,9545455	-98,1	-98,1	0,581505	1,12	-74,318182	-2,2813953
spe-MIR1432	**96**	20,833333	20,833333	26,041667	32,291667	46,875	53,125	1,55	0,8	-32,4	-32,4	0,20757	4,59	-33,75	-0,72
spe-MIR1436	**94**	23,404255	26,595745	22,340426	27,659574	45,744681	54,255319	1,04	1,047619	-42,7	-38,3	0,132597	10,48	-45,425532	-0,9930233
spe-MIR1439	**185**	21,621622	34,594595	20,540541	23,243243	42,162162	57,837838	0,671875	1,0526316	-57	-51,7	0,0512324	25,51	-30,810811	-0,7307692
spe-MIR1440a-1	**150**	19,333333	30	17,333333	33,333333	36,666667	63,333333	1,1111111	1,1153846	-39,1	-33,4	0,015565	22,15	-26,066667	-0,7109091
spe-MIR1440a-2	**99**	27,272727	25,252525	18,181818	29,292929	45,454545	54,545455	1,16	1,5	-33	-27,3	0,0651244	16,1	-33,333333	-0,7333333
spe-MIR1440a-3	**125**	23,2	26,4	16,8	33,6	40	60	1,2727273	1,3809524	-38	-30,6	0,0101074	23,37	-30,4	-0,76
spe-MIR1446-1	**96**	16,666667	33,333333	18,75	31,25	35,416667	64,583333	0,9375	0,8888889	-40,4	-38	0,177184	5,5	-42,083333	-1,1882353
spe-MIR1446-2	**139**	16,546763	28,057554	19,42446	35,971223	35,971223	64,028777	1,2820513	0,8518519	-53,3	-50,5	0,0352644	12,23	-38,345324	-1,066
spe-MIR1509b	**188**	17,1875	31,25	15,625	35,9375	32,8125	67,1875	1,15	1,1	-52,9	-52,9	0,10481	8,69	-41,328125	-1,2595238
spe-MIR1511	**206**	13,106796	33,980583	19,902913	33,009709	33,009709	66,990291	0,9714286	0,6585366	-66,4	-61,8	0,0096103	22,72	-32,23301	-0,9764706
spe-MIR1514b-1	**316**	16,772152	34,177215	14,240506	34,810127	31,012658	68,987342	1,0185185	1,1777778	-68,9	-43,3	1,51E-05	90,45	-21,803797	-0,7030612
spe-MIR1514b-2	**192**	18,75	37,5	15,104167	28,645833	33,854167	66,145833	0,7638889	1,2413793	-94,1	-91,9	0,015971	10,02	-49,010417	-1,4476923
spe-MIR1518	**331**	14,501511	35,347432	16,616314	33,534743	31,117825	68,882175	0,9487179	0,8727273	-76,8	-59,1	1,57E-05	69,49	-23,202417	-0,7456311
spe-MIR1521b-1	**174**	16,666667	32,758621	14,942529	35,632184	31,609195	68,390805	1,0877193	1,1153846	-51,4	-49,9	0,0067168	17,64	-29,54023	-0,9345455
spe-MIR1521b-2	**155**	18,709677	30,967742	16,774194	33,548387	35,483871	64,516129	1,0833333	1,1153846	-71,2	-71,2	0,275855	3,24	-45,935484	-1,2945455
spe-MIR1522	**199**	13,567839	35,678392	17,085427	33,668342	30,653266	69,346734	0,943662	0,7941176	-52,7	-52,6	0,0311203	15,59	-26,482412	-0,8639344
spe-MIR1530-1	**166**	16,26506	37,951807	15,060241	30,722892	31,325301	68,674699	0,8095238	1,08	-37,9	-33,6	0,0218528	27,06	-22,831325	-0,7288462
spe-MIR1530-2	**172**	14,534884	37,209302	20,348837	27,906977	34,883721	65,116279	0,75	0,7142857	-43,1	-41,6	0,0231651	18,49	-25,05814	-0,7183333
spe-MIR1533-1	**287**	15,33101	32,055749	19,163763	33,449477	34,494774	65,505226	1,0434783	0,8	-99,1	-96,6	0,0045482	45,72	-34,529617	-1,0010101
spe-MIR1533-2	**209**	13,875598	37,799043	16,267943	32,057416	30,143541	69,856459	0,8481013	0,8529412	-87,1	-81,2	0,0079669	28,87	-41,674641	-1,3825397
spe-MIR1533-3	**116**	15,517241	30,172414	15,517241	38,793103	31,034483	68,965517	1,2857143	1	-47,7	-45,3	0,0426051	7,95	-41,12069	-1,325
spe-MIR156b-1	**149**	18,791946	29,530201	19,463087	32,214765	38,255034	61,744966	1,0909091	0,9655172	-52,9	-51,47	0,0373213	12,7	-35,503356	-0,9280702
spe-MIR156b-10	**108**	22,222222	26,851852	17,592593	33,333333	39,814815	60,185185	1,2413793	1,2631579	-51,7	-51,6	0,0192466	8,32	-47,87037	-1,2023256
spe-MIR156b-11	**173**	17,919075	34,682081	17,34104	30,057803	35,260116	64,739884	0,8666667	1,0333333	-51,9	-49,6	0,023118	19,73	-30	-0,8508197
spe-MIR156b-2	**183**	22,95082	33,333333	13,661202	30,054645	36,612022	63,387978	0,9016393	1,68	-49	-39,97	0,0041893	30,97	-26,775956	-0,7313433
spe-MIR156b-3	**183**	14,20765	26,229508	22,404372	37,15847	36,612022	63,387978	1,4166667	0,6341463	-48,3	-47,27	0,0472508	11,12	-26,393443	-0,7208955
spe-MIR156b-4	**91**	19,78022	28,571429	19,78022	31,868132	39,56044	60,43956	1,1153846	1	-50,6	-47,6	0,068923	4,78	-55,604396	-1,4055556
spe-MIR156b-5	**101**	17,821782	29,70297	18,811881	33,663366	36,633663	63,366337	1,1333333	0,9473684	-43,5	-42,2	0,119446	6,96	-43,069307	-1,1756757
spe-MIR156b-6	**88**	21,590909	25	23,863636	29,545455	45,454545	54,545455	1,1818182	0,9047619	-44,1	-44,1	0,312754	2,54	-50,113636	-1,1025

spe-MIR156b-7	**101**	23,762376	23,762376	23,762376	28,712871	47,524752	52,475248	1,2083333	1	-62,5	-62,5	0,320774	2,71	-61,881188	-1,3020833
spe-MIR156b-8	**137**	17,518248	29,927007	15,328467	37,226277	32,846715	67,153285	1,2439024	1,1428571	-54,6	-53,3	0,0331925	9,21	-39,854015	-1,2133333
spe-MIR156b-9	**151**	20,529801	27,81457	15,89404	35,761589	36,423841	63,576159	1,2857143	1,2916667	-72,7	-72,7	0,0051816	12,7	-48,145695	-1,3218182
spe-MIR156c-1	**109**	26,605505	22,93578	22,018349	28,440367	48,623853	51,376147	1,24	1,2083333	-60,2	-60,2	0,0979289	7,82	-55,229358	-1,1358491
spe-MIR156c-2	**166**	21,686747	28,313253	18,674699	31,325301	40,361446	59,638554	1,106383	1,1612903	-75,5	-75,1	0,0316798	15,36	-45,481928	-1,1268657
spe-MIR156c-3	**101**	23,762376	25,742574	22,772277	27,722772	46,534653	53,465347	1,0769231	1,0434783	-55	-55	0,104866	4,96	-54,455446	-1,1702128
spe-MIR156d	**140**	15	30	19,285714	35,714286	34,285714	65,714286	1,1904762	0,7777778	-44,7	-43,4	0,0776389	8,6	-31,928571	-0,93125
spe-MIR156f-1	**86**	22,093023	27,906977	16,27907	33,72093	38,372093	61,627907	1,2083333	1,3571429	-38,8	-38,8	0,335177	2,27	-45,116279	-1,1757576
spe-MIR156f-2	**92**	21,73913	27,173913	17,391304	33,695652	39,130435	60,869565	1,24	1,25	-38,3	-38,3	0,308362	2,29	-41,630435	-1,0638889
spe-MIR156g	**102**	19,607843	24,509804	20,588235	35,294118	40,196078	59,803922	1,44	0,952381	-72,1	-72,1	0,307249	1,93	-70,686275	-1,7585366
spe-MIR156i-1	**178**	20,224719	26,966292	16,853933	35,955056	37,078652	62,921348	1,3333333	1,2	-92,3	-85,9	0,0057728	15,67	-51,853933	-1,3984848
spe-MIR156i-2	**157**	19,745223	24,840764	18,471338	36,942675	38,216561	61,783439	1,4871795	1,0689655	-47,4	-47,3	0,022454	16,37	-30,191083	-0,79
spe-MIR156k	**99**	23,232323	24,242424	17,171717	35,353535	40,40404	59,59596	1,4583333	1,3529412	-58,3	-58,3	0,310263	5,29	-58,888889	-1,4575
spe-MIR158b	**180**	21,666667	20	23,888889	34,444444	45,555556	54,444444	1,7222222	0,9069767	-61,8	-56,6	0,0042678	51,4	-34,333333	-0,7536585
spe-MIR159	**140**	16,428571	32,142857	15	36,428571	31,428571	68,571429	1,1333333	1,0952381	-65,6	-63,6	0,135206	6,79	-46,857143	-1,4909091
spe-MIR159a	**112**	15,178571	39,285714	16,071429	29,464286	31,25	68,75	0,75	0,9444444	-30,1	-26,7	0,0634264	11,05	-26,875	-0,86
spe-MIR159b-1	**180**	22,222222	27,777778	16,111111	33,888889	38,333333	61,666667	1,22	1,3793103	-77,2	-75,1	0,0086919	12,11	-42,888889	-1,1188406
spe-MIR159b-2	**231**	20,34632	29,87013	14,718615	35,064935	35,064935	64,935065	1,173913	1,3823529	-85,7	-83,8	0,003423	13,3	-37,099567	-1,0580247
spe-MIR159b-3	**217**	20,737327	29,493088	14,746544	35,023041	35,483871	64,516129	1,1875	1,40625	-89,2	-87,3	0,0093381	11,04	-41,105991	-1,1584416
spe-MIR159b-4	**215**	21,395349	29,302326	16,27907	33,023256	37,674419	62,325581	1,1269841	1,3142857	-91,3	-88,4	0,006026	12,72	-42,465116	-1,1271605
spe-MIR159c	**170**	26,470588	25,294118	21,176471	27,058824	47,647059	52,352941	1,0697674	1,25	-88,8	-88,2	0,0809317	6,12	-52,235294	-1,0962963
spe-MIR160-1	**95**	24,210526	28,421053	24,210526	23,157895	48,421053	51,578947	0,8148148	1	-47,8	-47,8	0,358832	2,11	-50,315789	-1,0391304
spe-MIR160-2	**116**	21,551724	31,896552	21,551724	25	43,103448	56,896552	0,7837838	1	-41,7	-40,3	0,0514112	9,2	-35,948276	-0,834
spe-MIR160-3	**104**	23,076923	24,038462	21,153846	31,730769	44,230769	55,769231	1,32	1,0909091	-52,3	-51,4	0,100504	4,55	-50,288462	-1,1369565
spe-MIR160-4	**95**	25,263158	25,263158	25,263158	24,210526	50,526316	49,473684	0,9583333	1	-39,5	-32,9	0,0117631	15,55	-41,578947	-0,8229167
spe-MIR160c	**85**	24,705882	23,529412	23,529412	28,235294	48,235294	51,764706	1,2	1,05	-42	-42	0,411232	2,25	-49,411765	-1,0243902
spe-MIR160e	**114**	20,175439	36,842105	14,912281	28,070175	35,087719	64,912281	0,7619048	1,3529412	-30,5	-30	0,0748294	12,7	-26,754386	-0,7625
spe-MIR160g	**99**	21,212121	30,30303	23,232323	25,252525	44,444444	55,555556	0,8333333	0,9130435	-48,9	-48,9	0,136739	3,41	-49,393939	-1,1113636
spe-MIR160h-1	**81**	22,222222	20,987654	23,45679	33,333333	45,679012	54,320988	1,5882353	0,9473684	-33,6	-33,4	0,303642	3,48	-41,481481	-0,9081081
spe-MIR160h-2	**90**	24,444444	24,444444	22,222222	28,888889	46,666667	53,333333	1,1818182	1,1	-46,8	-46,8	0,126945	3,09	-52	-1,1142857
spe-MIR162-1	**105**	21,904762	33,333333	20,952381	23,809524	42,857143	57,142857	0,7142857	1,0454545	-41,2	-41,2	0,0440347	10,93	-39,238095	-0,9155556
spe-MIR162-2	**110**	25,454545	29,090909	25,454545	20	50,909091	49,090909	0,6875	1	-49,1	-49,1	0,0450458	7,98	-44,636364	-0,8767857
spe-MIR162b-1	**137**	20,437956	29,927007	19,708029	29,927007	40,145985	59,854015	1	1,037037	-50,2	-46,9	0,0541981	9,36	-36,642336	-0,9127273
spe-MIR162b-2	**117**	20,512821	24,786325	21,367521	33,333333	41,880342	58,119658	1,3448276	0,96	-46,2	-43,7	0,0584315	9,02	-39,487179	-0,9428571
spe-MIR162b-3	**110**	25,454545	20	25,454545	29,090909	50,909091	49,090909	1,4545455	1	-55	-55	0,172243	4,95	-50	-0,9821429
spe-MIR164-1	**165**	20	29,090909	16,363636	34,545455	36,363636	63,636364	1,1875	1,2222222	-59,3	-54,6	0,0023044	22,51	-35,939394	-0,9883333
spe-MIR164-2	**171**	20,467836	29,239766	16,374269	33,918129	36,842105	63,157895	1,16	1,25	-60,8	-56,1	0,0016071	23,18	-35,555556	-0,9650794
spe-MIR164b	**74**	17,567568	33,783784	17,567568	31,081081	35,135135	64,864865	0,92	1	-25,8	-25,8	0,194689	2,98	-34,864865	-0,9923077
spe-MIR164c-1	**98**	18,367347	26,530612	20,408163	34,693878	38,77551	61,22449	1,3076923	0,9	-51,1	-48,1	0,249912	2,23	-52,142857	-1,3447368
spe-MIR164c-2	**93**	20,430108	23,655914	25,806452	30,107527	46,236559	53,763441	1,2727273	0,7916667	-51,2	-51,2	0,367833	1,75	-55,053763	-1,1906977
spe-MIR164e	**97**	20,618557	25,773196	19,587629	34,020619	40,206186	59,793814	1,32	1,0526316	-46,2	-45,3	0,0465132	8,87	-47,628866	-1,1846154
spe-MIR166-1	**119**	19,327731	30,252101	19,327731	31,092437	38,655462	61,344538	1,0277778	1	-40	-38,8	0,07688	9,19	-33,613445	-0,8695652
spe-MIR166-2	**99**	19,191919	31,313131	19,191919	30,30303	38,383838	61,616162	0,9677419	1	-39,7	-36,81	0,121796	10,52	-40,10101	-1,0447368
spe-MIR166-3	**174**	18,390805	28,735632	18,965517	33,908046	37,356322	62,643678	1,18	0,969697	-69,5	-69,2	0,0172446	12,73	-39,942529	-1,0692308
spe-MIR166-4	**117**	20,512821	27,350427	17,094017	35,042735	37,606838	62,393162	1,28125	1,2	-52,9	-51,7	0,331121	6,15	-45,213675	-1,2022727
spe-MIR166-5	**118**	16,949153	29,661017	21,186441	32,20339	38,135593	61,864407	1,0857143	0,8	-33,4	-31,9	0,0182815	12,66	-28,305085	-0,7422222
spe-MIR166-6	**230**	17,391304	31,73913	16,086957	34,782609	33,478261	66,521739	1,0958904	1,0810811	-84,9	-82,7	0,0102225	20,63	-36,913043	-1,1025974
spe-MIR166c	**187**	21,390374	29,411765	15,508021	33,68984	36,898396	63,101604	1,1454545	1,3793103	-76,5	-72,4	0,0124291	17,61	-40,909091	-1,1086957
spe-MIR166f-1	**158**	23,417722	31,64557	16,455696	28,481013	39,873418	60,126582	0,9	1,4230769	-47,2	-43,7	0,0043755	21,01	-29,873418	-0,7492063
spe-MIR166f-2	**107**	22,429907	21,495327	23,364486	32,71028	45,794393	54,205607	1,5217391	0,96	-44,4	-41	0,0431609	13,05	-41,495327	-0,9061224
spe-MIR166f-3	**245**	33,877551	15,102041	23,265306	27,755102	57,142857	42,857143	1,8378378	1,4561404	-99,5	-98,3	0,0002237	43,49	-40,612245	-0,7107143
spe-MIR167b-1	**80**	18,75	32,5	20	28,75	38,75	61,25	0,8846154	0,9375	-35,9	-35,9	0,169061	3,93	-44,875	-1,1580645
spe-MIR167b-2	**94**	17,021277	29,787234	19,148936	34,042553	36,170213	63,829787	1,1428571	0,8888889	-35,3	-35,3	0,0639905	5,86	-37,553191	-1,0382353
spe-MIR167c-1	**84**	26,190476	28,571429	20,238095	25	46,428571	53,571429	0,875	1,2941176	-41,3	-41,3	0,373498	6,31	-49,166667	-1,0589744
spe-MIR167c-2	**113**	24,778761	26,548673	23,00885	25,663717	47,787611	52,212389	0,9666667	1,0769231	-53,5	-53,5	0,0789463	4,44	-47,345133	-0,9907407
spe-MIR167d	**137**	13,138686	27,007299	24,817518	35,036496	37,956204	62,043796	1,2972973	0,5294118	-36,9	-36,9	0,165251	10,58	-26,934307	-0,7096154
spe-MIR167h-1	**119**	20,168067	26,890756	24,369748	28,571429	44,537815	55,462185	1,0625	0,8275862	-48,9	-48,1	0,0900057	8,77	-41,092437	-0,9226415
spe-MIR167h-2	**196**	18,367347	34,183673	15,816327	31,632653	34,183673	65,816327	0,9253731	1,1612903	-71,1	-67,3	0,00191	18,71	-36,27551	-1,061194
spe-MIR168	**149**	28,187919	21,47651	23,489933	26,845638	51,677852	48,322148	1,25	1,2	-65,2	-59,9	0,0062203	18,75	-43,758389	-0,8467532
spe-MIR168a	**141**	18,439716	30,496454	14,893617	36,170213	33,333333	66,666667	1,1860465	1,2380952	-39,7	-39,7	0,0257591	9,25	-28,156028	-0,8446809
spe-MIR168b	**132**	28,030303	25	27,272727	19,69697	55,30303	44,69697	0,7878788	1,0277778	-91,4	-89,2	0,344772	2,53	-69,242424	-1,2520548
spe-MIR168c-1	**159**	28,301887	21,383648	23,27044	27,044025	51,572327	48,427673	1,2647059	1,2162162	-63,9	-63,2	0,0338833	19,52	-40,188679	-0,7792683

spe-MIR168c-2	**186**	27,956989	20,967742	23,11828	27,956989	51,075269	48,924731	1,3333333	1,2093023	-75,1	-73,4	0,0243662	20,06	-40,376344	-0,7905263
spe-MIR169a-1	**149**	24,832215	27,516779	15,436242	32,214765	40,268456	59,731544	1,1707317	1,6086957	-74,3	-72,5	0,0278336	6,77	-49,865772	-1,2383333
spe-MIR169a-2	**176**	21,022727	27,272727	18,181818	33,522727	39,204545	60,795455	1,2291667	1,15625	-81,9	-79,44	0,0086511	19,02	-46,534091	-1,1869565
spe-MIR169a-3	**229**	17,030568	25,764192	13,973799	43,231441	31,004367	68,995633	1,6779661	1,21875	-81	-78,5	0,003821	20,61	-35,371179	-1,1408451
spe-MIR169c-1	**205**	14,146341	29,268293	17,560976	39,02439	31,707317	68,292683	1,3333333	0,8055556	-67,9	-64,4	0,004868	17,34	-33,121951	-1,0446154
spe-MIR169c-2	**201**	14,427861	30,348259	15,920398	39,303483	30,348259	69,651741	1,295082	0,90625	-68,8	-65,5	0,0039843	19,43	-34,228856	-1,1278689
spe-MIR169c-3	**169**	18,343195	28,994083	17,751479	34,911243	36,094675	63,905325	1,2040816	1,0333333	-70,8	-70,8	0,0271053	8,62	-41,893491	-1,1606557
spe-MIR169c-4	**190**	18,421053	28,947368	13,157895	39,473684	31,578947	68,421053	1,3636364	1,4	-82	-79,3	0,0027117	15,74	-43,157895	-1,3666667
spe-MIR169d-1	**155**	19,354839	22,580645	23,225806	34,83871	42,580645	57,419355	1,5428571	0,8333333	-61,1	-61,1	0,0097468	9,76	-39,419355	-0,9257576
spe-MIR169d-2	**164**	21,341463	23,780488	21,95122	32,926829	43,292683	56,707317	1,3846154	0,9722222	-74,3	-74,3	0,002458	12,25	-45,304878	-1,0464789
spe-MIR169e-1	**105**	21,904762	28,571429	16,190476	33,333333	38,095238	61,904762	1,1666667	1,3529412	-35,4	-35,4	0,131651	10,78	-33,714286	-0,885
spe-MIR169e-2	**179**	21,22905	27,374302	17,318436	34,078212	38,547486	61,452514	1,244898	1,2258065	-71,8	-68,1	0,0079569	17,71	-40,111732	-1,0405797
spe-MIR169e-3	**170**	20,588235	33,529412	18,823529	27,058824	39,411765	60,588235	0,8070175	1,09375	-93,5	-90,8	0,0428789	5,52	-55	-1,3955224
spe-MIR169e-4	**169**	17,751479	34,911243	18,343195	28,994083	36,094675	63,905325	0,8305085	0,9677419	-68,1	-65,4	0,136147	4,14	-40,295858	-1,1163934
spe-MIR169j-1	**156**	19,871795	23,717949	19,871795	36,538462	39,74359	60,25641	1,5405405	1	-55,4	-54,1	0,0103737	10,78	-35,512821	-0,8935484
spe-MIR169j-2	**154**	19,480519	24,025974	20,12987	36,363636	39,61039	60,38961	1,5135135	0,9677419	-50,9	-47,3	0,0055117	13,57	-33,051948	-0,8344262
spe-MIR169j-3	**156**	20,512821	26,923077	19,230769	33,333333	39,74359	60,25641	1,2380952	1,0666667	-73,9	-73,9	0,0119891	10,85	-47,371795	-1,1919355
spe-MIR169j-4	**192**	20,833333	26,041667	18,229167	34,895833	39,0625	60,9375	1,34	1,1428571	-77,4	-75,1	0,0009494	15,36	-40,3125	-1,032
spe-MIR169n	**222**	16,216216	34,234234	17,117117	32,432432	33,333333	66,666667	0,9473684	0,9473684	-54,8	-53,5	0,0094847	25,95	-24,684685	-0,7405405
spe-MIR169r-1	**147**	25,170068	22,44898	18,367347	34,013605	43,537415	56,462585	1,5151515	1,3703704	-68,9	-67,9	0,0156396	9,65	-46,870748	-1,0765625
spe-MIR169r-2	**147**	25,170068	22,44898	17,687075	34,693878	42,857143	57,142857	1,5454545	1,4230769	-66,2	-65,2	0,0113674	10,1	-45,034014	-1,0507937
spe-MIR169r-3	**177**	22,033898	24,858757	18,079096	35,028249	40,112994	59,887006	1,4090909	1,21875	-71,4	-71,2	0,0347675	12,08	-40,338983	-1,0056338
spe-MIR169r-4	**285**	20	25,964912	17,54386	36,491228	37,54386	62,45614	1,4054054	1,14	-98,1	-92,7	0,0004444	39,85	-34,421053	-0,9168224
spe-MIR169r-5	**184**	22,826087	26,086957	18,478261	32,608696	41,304348	58,695652	1,25	1,2352941	-71	-70,6	0,0238827	12,4	-38,586957	-0,9342105
spe-MIR169r-6	**161**	19,875776	24,84472	19,254658	36,024845	39,130435	60,869565	1,45	1,0322581	-69,6	-69,6	0,0358784	9,63	-43,229814	-1,1047619
spe-MIR169r-7	**155**	23,225806	22,580645	18,064516	36,129032	41,290323	58,709677	1,6	1,2857143	-74,7	-73,9	0,0149928	9,78	-48,193548	-1,1671875
spe-MIR171a-1	**110**	21,818182	31,818182	14,545455	31,818182	36,363636	63,636364	1	1,5	-44,2	-44,2	0,226006	2,8	-40,181818	-1,105
spe-MIR171a-2	**129**	16,27907	24,031008	19,379845	40,310078	35,658915	64,341085	1,6774194	0,84	-45,6	-45,6	0,198512	3,15	-35,348837	-0,9913043
spe-MIR171a-3	**112**	18,75	26,785714	16,964286	37,5	35,714286	64,285714	1,4	1,1052632	-45,8	-45,8	0,235347	2,84	-40,892857	-1,145
spe-MIR171a-4	**75**	22,666667	28	16	33,333333	38,666667	61,333333	1,1904762	1,4166667	-40,9	-40,9	0,489064	1,27	-54,533333	-1,4103448
spe-MIR171a-5	**147**	21,088435	26,530612	14,285714	38,095238	35,37415	64,62585	1,4358974	1,4761905	-53,5	-53,5	0,0413943	11,04	-36,394558	-1,0288462
spe-MIR171a-6	**94**	24,468085	24,468085	17,021277	34,042553	41,489362	58,510638	1,3913043	1,4375	-44,7	-44,7	0,654507	1,08	-47,553191	-1,1461538
spe-MIR171a-7	**97**	17,525773	30,927835	16,494845	35,051546	34,020619	65,979381	1,1333333	1,0625	-44,7	-44,7	0,250042	3,27	-46,082474	-1,3545455
spe-MIR171b-1	**115**	22,608696	30,434783	16,521739	30,434783	39,130435	60,869565	1	1,3684211	-44,8	-42,5	0,142031	5,08	-38,956522	-0,9955556
spe-MIR171b-2	**110**	20,909091	29,090909	19,090909	30,909091	40	60	1,0625	1,0952381	-45,2	-44,9	0,0972518	4,98	-41,090909	-1,0272727
spe-MIR171b-3	**127**	20,472441	28,346457	17,322835	33,858268	37,795276	62,204724	1,1944444	1,1818182	-52	-51,1	0,0952714	4,07	-40,944882	-1,0833333
spe-MIR171b-4	**112**	19,642857	29,464286	21,428571	29,464286	41,071429	58,928571	1	0,9166667	-46,2	-44,7	0,0403651	12,41	-41,25	-1,0043478
spe-MIR171b-5	**100**	16	33	23	28	39	61	0,8484848	0,6956522	-29	-26,5	0,132327	5,16	-29	-0,7435897
spe-MIR171b-6	**127**	17,322835	33,858268	20,472441	28,346457	37,795276	62,204724	0,8372093	0,8461538	-44,3	-37,7	0,0468289	13,87	-34,88189	-0,9229167
spe-MIR171c-1	**88**	15,909091	31,818182	17,045455	35,227273	32,954545	67,045455	1,1071429	0,9333333	-21,1	-20,2	0,0271494	14,3	-23,977273	-0,7275862
spe-MIR171c-2	**92**	17,391304	33,695652	18,478261	30,434783	35,869565	64,130435	0,9032258	0,9411765	-28,2	-27,8	0,407749	5,55	-30,652174	-0,8545455
spe-MIR171c-3	**92**	18,478261	30,434783	17,391304	33,695652	35,869565	64,130435	1,1071429	1,0625	-42,2	-42,2	0,646251	0,94	-45,869565	-1,2787879
spe-MIR171e	**86**	22,093023	27,906977	15,116279	34,883721	37,209302	62,790698	1,25	1,4615385	-48,1	-48,1	0,491398	1,7	-55,930233	-1,503125
spe-MIR171f-1	**79**	17,721519	22,78481	18,987342	40,506329	36,708861	63,291139	1,7777778	0,9333333	-24,3	-24,3	0,430885	5,3	-30,759494	-0,837931
spe-MIR171f-2	**100**	23	28	16	33	39	61	1,1785714	1,4375	-40,7	-37,7	0,213889	3,86	-40,7	-1,0435897
spe-MIR171h	**185**	18,918919	33,513514	14,594595	32,972973	33,513514	66,486486	0,983871	1,2962963	-44,3	-40,9	0,0029965	32,54	-23,945946	-0,7145161
spe-MIR171t	**98**	19,387755	29,591837	23,469388	27,55102	42,857143	57,142857	0,9310345	0,826087	-42	-39,3	0,0813088	7,32	-42,857143	-1
spe-MIR172-1	**159**	16,981132	38,993711	13,207547	30,81761	30,188679	69,811321	0,7903226	1,2857143	-57,3	-54,1	0,0271342	11,52	-36,037736	-1,19375
spe-MIR172-2	**105**	16,190476	35,238095	16,190476	32,380952	32,380952	67,619048	0,9189189	1	-44,3	-44,3	0,399103	4,45	-42,190476	-1,3029412
spe-MIR172-3	**105**	17,142857	35,238095	17,142857	30,47619	34,285714	65,714286	0,8648649	1	-37,3	-36,8	0,166108	10,58	-35,52381	-1,0361111
spe-MIR172-4	**169**	15,976331	33,727811	14,201183	36,094675	30,177515	69,822485	1,0701754	1,125	-58,7	-55,7	0,037414	12,68	-34,733728	-1,1509804
spe-MIR172-5	**142**	19,014085	33,802817	14,084507	33,098592	33,098592	66,901408	0,9791667	1,35	-54,4	-54,4	0,0382791	15,79	-38,309859	-1,1574468
spe-MIR172a-1	**186**	13,44086	31,182796	17,741935	37,634409	31,182796	68,817204	1,2068966	0,7575758	-51,8	-49,7	0,0026377	18,81	-27,849462	-0,8931034
spe-MIR172a-2	**123**	19,512195	27,642276	17,073171	35,772358	36,585366	63,414634	1,2941176	1,1428571	-67,7	-67,7	0,467028	1,91	-55,04065	-1,5044444
spe-MIR172a-3	**123**	17,073171	35,772358	19,512195	27,642276	36,585366	63,414634	0,7727273	0,875	-54	-54	0,300546	2,76	-43,902439	-1,2
spe-MIR172b	**110**	16,363636	30,909091	15,454545	37,272727	31,818182	68,181818	1,2058824	1,0588235	-41,9	-41,9	0,112378	8,38	-38,090909	-1,1971429
spe-MIR172c	**94**	23,404255	28,723404	14,893617	32,978723	38,297872	61,702128	1,1481481	1,5714286	-43,1	-39,6	0,0269567	10,06	-45,851064	-1,1972222
spe-MIR172j-1	**132**	15,151515	33,333333	23,484848	28,030303	38,636364	61,363636	0,8409091	0,6451613	-43,6	-38,2	0,0150737	8,78	-33,030303	-0,854902
spe-MIR172j-2	**169**	14,201183	36,094675	15,976331	33,727811	30,177515	69,822485	0,9344262	0,8888889	-55	-53,8	0,0357955	13,26	-32,544379	-1,0784314
spe-MIR1862g	**105**	17,142857	33,333333	20	29,52381	37,142857	62,857143	0,8857143	0,8571429	-31,7	-27,1	0,0193648	19,54	-30,190476	-0,8128205
spe-MIR1886-1	**137**	16,058394	33,576642	18,978102	31,386861	35,036496	64,963504	0,9347826	0,8461538	-41,9	-38,1	0,0632021	9,82	-30,583942	-0,8729167
spe-MIR1886-2	**330**	22,424242	34,848485	10,606061	32,121212	33,030303	66,969697	0,9217391	2,1142857	-91,3	-81,81	0,0001214	50,98	-27,666667	-0,8376147

spe-MIR1886f	**116**	16,37931	30,172414	17,241379	36,206897	33,62069	66,37931	1,2	0,95	-44	-43,8	0,116035	8,37	-37,931034	-1,1282051
spe-MIR1886h-1	**97**	14,43299	32,989691	16,494845	36,082474	30,927835	69,072165	1,09375	0,875	-23,9	-23,9	0,24274	9,68	-24,639175	-0,7966667
spe-MIR1886h-2	**173**	17,919075	30,057803	15,606936	36,416185	33,526012	66,473988	1,2115385	1,1481481	-63	-58,97	0,0116439	22,27	-36,416185	-1,0862069
spe-MIR1886h-3	**108**	13,888889	33,333333	17,592593	35,185185	31,481481	68,518519	1,0555556	0,7894737	-27,8	-26,3	0,0414749	12,05	-25,740741	-0,8176471
spe-MIR1888b	**262**	21,374046	32,442748	14,885496	31,29771	36,259542	63,740458	0,9647059	1,4358974	-79,2	-64,4	0,0001089	80,53	-30,229008	-0,8336842
spe-MIR1917-1	**232**	12,931034	38,793103	17,672414	30,603448	30,603448	69,396552	0,7888889	0,7317073	-52	-47,3	0,0007873	36,04	-22,413793	-0,7323944
spe-MIR1917-2	**214**	15,420561	35,981308	16,82243	31,775701	32,242991	67,757009	0,8831169	0,9166667	-65,2	-62,3	0,0032547	31,94	-30,46729	-0,9449275
spe-MIR1917-3	**173**	18,49711	37,572254	13,872832	30,057803	32,369942	67,630058	0,8	1,3333333	-45,2	-34,4	0,0241334	46,41	-26,127168	-0,8071429
spe-MIR1917-4	**156**	18,589744	36,538462	16,666667	28,205128	35,25641	64,74359	0,7719298	1,1153846	-55,9	-55,6	0,0383104	10,4	-35,833333	-1,0163636
spe-MIR1918-1	**197**	15,736041	34,010152	18,781726	31,472081	34,517766	65,482234	0,9253731	0,8378378	-51,6	-49,7	0,0320851	13,75	-26,192893	-0,7588235
spe-MIR1918-2	**197**	19,28934	31,472081	15,228426	34,010152	34,517766	65,482234	1,0806452	1,2666667	-71,4	-70,4	0,0024058	22,32	-36,243655	-1,05
spe-MIR1919-1	**187**	22,459893	24,59893	21,390374	31,550802	43,850267	56,149733	1,2826087	1,05	-81,2	-77,47	0,0181656	21,47	-43,42246	-0,9902439
spe-MIR1919-2	**177**	22,59887	22,033898	22,59887	32,768362	45,19774	54,80226	1,4871795	1	-85,8	-85,8	0,120754	8,43	-48,474576	-1,0725
spe-MIR1919-3	**160**	21,25	27,5	20	31,25	41,25	58,75	1,1363636	1,0625	-69,2	-69,2	0,0483214	12,84	-43,25	-1,0484848
spe-MIR2083	**244**	17,622951	33,606557	12,704918	36,065574	30,327869	69,672131	1,0731707	1,3870968	-59,7	-47,1	0,0002935	76,9	-24,467213	-0,8067568
spe-MIR2089-1	**176**	15,909091	32,954545	15,340909	35,795455	31,25	68,75	1,0862069	1,037037	-92,8	-89,6	0,119921	15,58	-52,727273	-1,6872727
spe-MIR2089-2	**115**	27,826087	23,478261	20,869565	27,826087	48,695652	51,304348	1,1851852	1,3333333	-42,1	-42,1	0,150011	10,88	-36,608696	-0,7517857
spe-MIR2111a	**264**	26,515152	28,409091	21,590909	23,484848	48,106061	51,893939	0,8266667	1,2280702	-93,4	-89,4	0,007395	29,55	-35,378788	-0,7354331
spe-MIR2111d	**71**	19,71831	25,352113	16,901408	38,028169	36,619718	63,380282	1,5	1,1666667	-37,7	-37,7	0,367076	1,82	-53,098592	-1,45
spe-MIR2275c	**222**	14,864865	32,432432	15,315315	37,387387	30,18018	69,81982	1,1527778	0,9705882	-78,8	-78,8	0,010883	17,55	-35,495495	-1,1761194
spe-MIR2608-1	**273**	20,512821	39,194139	10,622711	29,67033	31,135531	68,864469	0,7570093	1,9310345	-78,1	-75,8	0,0217639	12,49	-28,608059	-0,9188235
spe-MIR2608-2	**273**	20,512821	39,56044	10,25641	29,67033	30,769231	69,230769	0,75	2	-76	-73,7	0,0106955	15,41	-27,838828	-0,9047619
spe-MIR2611	**280**	14,642857	32,142857	18,571429	34,642857	33,214286	66,785714	1,0777778	0,7884615	-69,8	-61,48	0,0014302	48,47	-24,928571	-0,7505376
spe-MIR2630v	**183**	25,136612	22,95082	19,125683	32,786885	44,262295	55,737705	1,4285714	1,3142857	-59,3	-57,6	0,0009713	28,8	-32,404372	-0,7320988
spe-MIR2643b	**115**	18,26087	37,391304	15,652174	28,695652	33,913043	66,086957	0,7674419	1,1666667	-28,9	-29,04	0,0351084	12,53	-25,130435	-0,7410256
spe-MIR2648	**187**	24,59893	28,877005	17,112299	29,411765	41,71123	58,28877	1,0185185	1,4375	-54,9	-51,1	0,0200182	16,45	-29,358289	-0,7038462
spe-MIR2673b	**208**	19,711538	28,365385	22,596154	29,326923	42,307692	57,692308	1,0338983	0,8723404	-63,4	-57,51	0,0106278	37,53	-30,480769	-0,7204545
spe-MIR2863a-1	**142**	14,084507	35,915493	16,197183	33,802817	30,28169	69,71831	0,9411765	0,8695652	-98,1	-98,1	0,10218	3,41	-69,084507	-2,2813953
spe-MIR2863a-2	**223**	21,076233	28,251121	16,591928	34,080717	37,668161	62,331839	1,2063492	1,2702703	-65,2	-56,4	0,0065246	33,05	-29,237668	-0,7761905
spe-MIR2864	**282**	14,539007	31,914894	15,957447	37,588652	30,496454	69,503546	1,1777778	0,9111111	-64,5	-55,1	8,19E-05	53,71	-22,87234	-0,75
spe-MIR2873b	**104**	20,192308	22,115385	15,384615	42,307692	35,576923	64,423077	1,9130435	1,3125	-37,8	-37,8	0,176257	5,79	-36,346154	-1,0216216
spe-MIR2873c	**316**	11,708861	29,746835	21,202532	37,341772	32,911392	67,088608	1,2553191	0,5522388	-74,3	-59,89	0,0001231	47,23	-23,512658	-0,7144231
spe-MIR2921	**242**	18,595041	35,123967	12,396694	33,884298	30,991736	69,008264	0,9647059	1,5	-56	-52,4	0,0082698	28,15	-23,140496	-0,7466667
spe-MIR319	**197**	21,827411	28,426396	17,766497	31,979695	39,593909	60,406091	1,125	1,2285714	-86,8	-85,1	0,0612374	7,18	-44,060914	-1,1128205
spe-MIR319a-1	**182**	22,527473	28,021978	21,978022	27,472527	44,505495	55,494505	0,9803922	1,025	-79,3	-74,6	0,0127949	25,87	-43,571429	-0,9790123
spe-MIR319a-2	**185**	20,540541	27,567568	18,378378	33,513514	38,918919	61,081081	1,2156863	1,1176471	-92,3	-90,5	0,0223102	10,3	-49,891892	-1,2819444
spe-MIR319a-3	**195**	21,538462	28,205128	17,435897	32,820513	38,974359	61,025641	1,1636364	1,2352941	-92,3	-90,5	0,021731	10,41	-47,333333	-1,2144737
spe-MIR319b-1	**198**	23,737374	29,292929	19,69697	27,272727	43,434343	56,565657	0,9310345	1,2051282	-95,9	-95,9	0,100503	5,85	-48,434343	-1,1151163
spe-MIR319b-2	**211**	20,853081	31,753555	18,957346	28,436019	39,810427	60,189573	0,8955224	1,1	-88,3	-88,3	0,0240325	9,04	-41,848341	-1,0511905
spe-MIR319b-3	**124**	25,806452	25	18,548387	30,645161	44,354839	55,645161	1,2258065	1,3913043	-43,7	-32,5	0,0723298	15,56	-35,241935	-0,7945455
spe-MIR319c	**178**	25,280899	23,595506	21,910112	29,213483	47,191011	52,808989	1,2380952	1,1538462	-77,1	-65,9	0,0238786	17,43	-43,314607	-0,9178571
spe-MIR319d-1	**179**	24,022346	24,022346	21,22905	30,726257	45,251397	54,748603	1,2790698	1,1315789	-82,3	-81,5	0,0640995	6,73	-45,977654	-1,0160494
spe-MIR319d-2	**179**	27,374302	30,167598	15,642458	26,256983	43,01676	56,424581	0,8703704	1,75	-54,3	-46,5	0,0036656	29,81	-30,335196	-0,7051948
spe-MIR319j	**155**	18,064516	29,032258	27,741935	25,16129	45,806452	54,193548	0,8666667	0,6511628	-75,2	-73,7	0,0941966	6,36	-48,516129	-1,0591549
spe-MIR3436-1	**273**	18,315018	33,333333	15,750916	32,600733	34,065934	65,934066	0,978022	1,1627907	-65,4	-30,27	0,0001158	75,03	-23,956044	-0,7032258
spe-MIR3436-2	**292**	21,917808	26,712329	16,780822	34,589041	38,69863	61,30137	1,2948718	1,3061224	-81,4	-73,5	0,0002485	67,3	-27,876712	-0,720354
spe-MIR3436-3	**230**	25,652174	23,478261	16,956522	33,913043	42,608696	57,391304	1,4444444	1,5128205	-73,4	-68,8	0,0009088	25,67	-31,913043	-0,7489796
spe-MIR3441	**296**	25	25,337838	15,540541	34,121622	40,540541	59,459459	1,3466667	1,6086957	-88,7	-77,5	0,0002251	62,62	-29,966216	-0,7391667
spe-MIR3447-1	**171**	21,637427	30,994152	11,111111	36,25731	32,748538	67,251462	1,1698113	1,9473684	-41,1	-34,8	0,0023282	34,75	-24,035088	-0,7339286
spe-MIR3447-2	**231**	23,809524	28,138528	13,419913	34,632035	37,229437	62,770563	1,2307692	1,7741935	-61,4	-51,7	0,0009208	27,64	-26,580087	-0,7139535
spe-MIR3511	**230**	15,652174	30,869565	14,782609	38,695652	30,434783	69,565217	1,2535211	1,0588235	-70,8	-65,2	0,0010271	36,83	-30,782609	-1,0114286
spe-MIR3512-1	**91**	23,076923	36,263736	12,087912	28,571429	35,164835	64,835165	0,7878788	1,9090909	-30,1	-26,8	0,0211408	11,9	-33,076923	-0,940625
spe-MIR3512-2	**75**	18,666667	40	13,333333	28	32	68	0,7	1,4	-24,1	-22,5	0,119184	6,49	-32,133333	-1,0041667
spe-MIR3513	**286**	18,881119	34,265734	19,230769	27,622378	38,111888	61,888112	0,8061224	0,9818182	-78,8	-72,8	0,0028285	53,68	-27,552448	-0,7229358
spe-MIR3515	**174**	17,241379	35,057471	13,793103	33,908046	31,034483	68,965517	0,9672131	1,25	-43,8	-39,1	0,0048385	36,67	-25,172414	-0,8111111
spe-MIR3627	**83**	20,481928	26,506024	22,891566	30,120482	43,373494	56,626506	1,1363636	0,8947368	-33,4	-33,4	0,345021	2,22	-40,240964	-0,9277778
spe-MIR3700	**223**	16,591928	31,838565	20,179372	31,390135	36,7713	63,2287	0,9859155	0,8222222	-95,8	-92,5	0,0105582	13,01	-42,959641	-1,1682927
spe-MIR3706-1	**70**	18,571429	27,142857	27,142857	27,142857	45,714286	54,285714	1	0,6842105	-33,9	-33,9	0,625685	1,84	-48,428571	-1,059375
spe-MIR3706-2	**68**	17,647059	27,941176	27,941176	26,470588	45,588235	54,411765	0,9473684	0,6315789	-26	-26	0,226896	2,43	-38,235294	-0,8387097
spe-MIR384	**214**	17,28972	35,514019	19,158879	28,037383	36,448598	63,551402	0,7894737	0,902439	-77,8	-77,4	0,0191701	16,35	-36,35514	-0,9974359
spe-MIR390-1	**113**	20,353982	24,778761	21,238938	33,628319	41,59292	58,40708	1,3571429	0,9583333	-58,3	-58,3	0,400087	2,43	-51,59292	-1,2404255
spe-MIR390-2	**106**	19,811321	31,132075	22,641509	26,415094	42,45283	57,54717	0,8484848	0,875	-43,7	-43,7	0,157098	5,71	-41,226415	-0,9711111

spe-MIR390a-1	**103**	22,330097	26,213592	20,38835	31,067961	42,718447	57,281553	1,1851852	1,0952381	-51,1	-48,4	0,111964	6,15	-49,61165	-1,1613636
spe-MIR390a-2	**115**	21,73913	33,913043	20	24,347826	41,73913	58,26087	0,7179487	1,0869565	-51,5	-51,5	0,22682	3,73	-44,782609	-1,0729167
spe-MIR391	**96**	23,958333	34,375	16,666667	25	40,625	59,375	0,7272727	1,4375	-46,7	-46,7	0,336484	3,38	-48,645833	-1,1974359
spe-MIR391i	**215**	20	29,302326	18,604651	32,093023	38,604651	61,395349	1,0952381	1,075	-71,9	-67,3	0,0010459	37,33	-33,44186	-0,8662651
spe-MIR393b	**78**	21,794872	26,923077	20,512821	30,769231	42,307692	57,692308	1,1428571	1,0625	-40,9	-40,9	0,200824	2,59	-52,435897	-1,2393939
spe-MIR394-1	**94**	26,595745	20,212766	28,723404	24,468085	55,319149	44,680851	1,2105263	0,9259259	-44,4	-43,2	0,0896826	4,96	-47,234043	-0,8538462
spe-MIR394-2	**61**	29,508197	21,311475	27,868852	21,311475	57,377049	42,622951	1	1,0588235	-31,2	-30,9	0,175055	3,56	-51,147541	-0,8914286
spe-MIR394-3	**203**	15,763547	25,615764	15,270936	43,349754	31,034483	68,965517	1,6923077	1,0322581	-67,2	-61,15	0,0057424	28,79	-33,103448	-1,0666667
spe-MIR394b-1	**196**	25	27,040816	16,326531	31,632653	41,326531	58,673469	1,1698113	1,53125	-78,6	-78,5	0,0036383	13,84	-40,102041	-0,9703704
spe-MIR394b-2	**86**	18,604651	32,55814	12,790698	36,046512	31,395349	68,604651	1,1071429	1,4545455	-41,3	-40,6	0,0249794	11,37	-48,023256	-1,5296296
spe-MIR3951a-1	**236**	17,372881	36,440678	13,135593	33,050847	30,508475	69,491525	0,9069767	1,3225806	-52,2	-33,94	1,18E-05	51,13	-22,118644	-0,725
spe-MIR3951a-2	**204**	16,176471	35,294118	18,137255	30,392157	34,313725	65,686275	0,8611111	0,8918919	-55,2	-50,2	0,0008496	33,68	-27,058824	-0,7885714
spe-MIR395a-1	**129**	23,255814	20,930233	20,930233	34,883721	44,186047	55,813953	1,6666667	1,1111111	-55,8	-55,8	0,123573	7,27	-43,255814	-0,9789474
spe-MIR395a-2	**154**	20,779221	27,922078	14,935065	36,363636	35,714286	64,285714	1,3023256	1,3913043	-45,8	-45,6	0,0305642	13,04	-29,74026	-0,8327273
spe-MIR395a-3	**107**	23,364486	18,691589	21,495327	36,448598	44,859813	55,140187	1,95	1,0869565	-51,6	-51,6	0,239298	5,7	-48,224299	-1,075
spe-MIR395a-4	**151**	21,192053	31,125828	15,89404	31,788079	37,086093	62,913907	1,0212766	1,3333333	-54,2	-54,2	0,157497	5,76	-35,89404	-0,9678571
spe-MIR395a-5	**166**	24,698795	28,313253	18,674699	28,313253	43,373494	56,626506	1	1,3225806	-63,9	-51,13	0,0249283	24,29	-38,493976	-0,8875
spe-MIR395a-6	**86**	24,418605	19,767442	19,767442	36,046512	44,186047	55,813953	1,8235294	1,2352941	-46	-46	0,558547	2,87	-53,488372	-1,2105263
spe-MIR395a-7	**150**	21,333333	31,333333	18	29,333333	39,333333	60,666667	0,9361702	1,1851852	-57,7	-55,8	0,142871	9,95	-38,466667	-0,9779661
spe-MIR395b-1	**100**	23	21	23	33	46	54	1,5714286	1	-36,3	-36,1	0,0512895	10,31	-36,3	-0,7891304
spe-MIR395b-2	**103**	24,271845	17,475728	19,417476	38,834951	43,68932	56,31068	2,2222222	1,25	-42	-40,1	0,0632991	10,38	-40,776699	-0,9333333
spe-MIR395c-1	**70**	24,285714	17,142857	24,285714	34,285714	48,571429	51,428571	2	1	-31,8	-31,8	0,256702	3,62	-45,428571	-0,9352941
spe-MIR395c-2	**165**	23,030303	29,69697	18,787879	28,484848	41,818182	58,181818	0,9591837	1,2258065	-57,3	-54,9	0,0217562	22,87	-34,727273	-0,8304348
spe-MIR395e	**174**	18,965517	32,758621	13,793103	34,482759	32,758621	67,241379	1,0526316	1,375	-54,5	-47,5	0,0066501	27,98	-31,321839	-0,9561404
spe-MIR395g	**100**	24	18	20	38	44	56	2,1111111	1,2	-36,3	-34,1	0,0211285	11,82	-36,3	-0,825
spe-MIR396a-1	**131**	16,030534	35,114504	19,847328	29,007634	35,877863	64,122137	0,826087	0,8076923	-45,1	-45,1	0,0260434	10,18	-34,427481	-0,9595745
spe-MIR396a-2	**115**	20	31,304348	19,130435	29,565217	39,130435	60,869565	0,9444444	1,0454545	-33,1	-29,2	0,0294223	11,54	-28,782609	-0,7355556
spe-MIR396b-1	**107**	18,691589	30,841121	13,084112	37,383178	31,775701	68,224299	1,2121212	1,4285714	-48,2	-47,9	0,0277768	8,77	-45,046729	-1,4176471
spe-MIR396b-2	**99**	19,191919	32,323232	13,131313	35,353535	32,323232	67,676768	1,09375	1,4615385	-43,1	-42,8	0,033524	8,68	-43,535354	-1,346875
spe-MIR396b-3	**138**	18,115942	36,231884	12,318841	33,333333	30,434783	69,565217	0,92	1,4705882	-57,1	-56,8	0,0228057	9,76	-41,376812	-1,3595238
spe-MIR396f	**131**	19,847328	29,007634	16,030534	35,114504	35,877863	64,122137	1,2105263	1,2380952	-49,5	-46,1	0,0044882	17,93	-37,78626	-1,0531915
spe-MIR396g-1	**341**	20,527859	37,829912	12,02346	29,618768	32,55132	67,44868	0,7829457	1,7073171	-81	-70,1	2,01E-05	77,59	-23,753666	-0,7297297
spe-MIR396g-2	**177**	19,20904	35,028249	11,299435	34,463277	30,508475	69,491525	0,983871	1,7	-39,9	-38,6	0,0039826	13,58	-22,542373	-0,7388889
spe-MIR397-1	**80**	18,75	22,5	23,75	35	42,5	57,5	1,5555556	0,7894737	-32,5	-32,3	0,138367	4,26	-40,625	-0,9558824
spe-MIR397-2	**185**	20	29,72973	20	30,27027	40	60	1,0181818	1	-55,1	-51,6	0,0062984	18,7	-29,783784	-0,7445946
spe-MIR397b-1	**116**	17,241379	25	20,689655	37,068966	37,931034	62,068966	1,4827586	0,8333333	-45	-44,8	0,124293	4,97	-38,793103	-1,0227273
spe-MIR397b-2	**127**	19,685039	37,007874	18,110236	25,19685	37,795276	62,204724	0,6808511	1,0869565	-46,4	-46,4	0,0923041	7,7	-36,535433	-0,9666667
spe-MIR397b-3	**109**	18,348624	31,192661	16,513761	33,944954	34,862385	65,137615	1,0882353	1,1111111	-28,3	-27,1	0,26599	4,64	-25,963303	-0,7447368
spe-MIR398-1	**218**	17,431193	27,981651	15,137615	39,449541	32,568807	67,431193	1,4098361	1,1515152	-75,1	-63	0,0012002	41,81	-34,449541	-1,0577465
spe-MIR398-2	**93**	21,505376	19,354839	18,27957	40,860215	39,784946	60,215054	2,1111111	1,1764706	-34,6	-31,27	0,0949317	13,39	-37,204301	-0,9351351
spe-MIR398-3	**89**	24,719101	20,224719	21,348315	33,707865	46,067416	53,932584	1,6666667	1,1578947	-45,1	-45,1	0,697069	1,24	-50,674157	-1,1
spe-MIR398a	**100**	21	27	14	38	35	65	1,4074074	1,5	-37,6	-31,4	0,0210989	14,39	-37,6	-1,0742857
spe-MIR399a-1	**175**	22,285714	29,142857	17,714286	30,857143	40	60	1,0588235	1,2580645	-62,4	-59,4	0,0068091	26,21	-35,657143	-0,8914286
spe-MIR399a-2	**258**	22,093023	30,620155	16,666667	30,620155	38,75969	61,24031	1	1,3255814	-78,2	-74,4	0,0016506	44,49	-30,310078	-0,782
spe-MIR399a-3	**123**	20,325203	28,455285	18,699187	32,520325	39,02439	60,97561	1,1428571	1,0869565	-54,4	-47,9	0,0144853	13,53	-44,227642	-1,1333333
spe-MIR399b-1	**103**	21,359223	28,15534	20,38835	30,097087	41,747573	58,252427	1,0689655	1,047619	-47,6	-47,6	0,226369	6,15	-46,213592	-1,1069767
spe-MIR399b-2	**103**	26,213592	23,300971	21,359223	29,126214	47,572816	52,427184	1,25	1,2272727	-47	-45,7	0,111272	6,28	-45,631068	-0,9591837
spe-MIR399b-3	**103**	22,330097	27,184466	21,359223	29,126214	43,68932	56,31068	1,0714286	1,0454545	-47	-47	0,464074	2,91	-45,631068	-1,0444444
spe-MIR399b-4	**103**	23,300971	25,242718	21,359223	30,097087	44,660194	55,339806	1,1923077	1,0909091	-47,9	-47,9	0,296977	6,84	-46,504854	-1,0413043
spe-MIR399b-5	**103**	22,330097	26,213592	22,330097	29,126214	44,660194	55,339806	1,1111111	1	-50,1	-50,1	0,252815	2,67	-48,640777	-1,0891304
spe-MIR399i-1	**135**	24,444444	26,666667	13,333333	35,555556	37,777778	62,222222	1,3333333	1,8333333	-62,9	-57,2	0,0141805	11,92	-46,592593	-1,2333333
spe-MIR399i-2	**107**	24,299065	26,168224	15,88785	33,64486	40,186916	59,813084	1,2857143	1,5294118	-59,2	-56,9	0,146903	3,67	-55,327103	-1,3767442
spe-MIR399k	**90**	18,888889	38,888889	16,666667	25,555556	35,555556	64,444444	0,6571429	1,1333333	-23,8	-21,3	0,0510011	17,83	-26,444444	-0,74375
spe-MIR399n	**92**	29,347826	23,913043	19,565217	27,173913	48,913043	51,086957	1,1363636	1,5	-47,3	-47	0,0634144	6,87	-51,413043	-1,0511111
spe-MIR399r-1	**123**	17,073171	29,268293	15,447154	38,211382	32,520325	67,479675	1,3055556	1,1052632	-50,2	-48,5	0,0626769	15,68	-40,813008	-1,255
spe-MIR399r-2	**126**	16,666667	26,984127	17,460317	38,888889	34,126984	65,873016	1,4411765	0,9545455	-44,3	-41,4	0,0478547	23,82	-35,15873	-1,0302326
spe-MIR399r-3	**187**	13,903743	34,224599	17,112299	34,759358	31,016043	68,983957	1,015625	0,8125	-51,1	-42,18	0,000812	38,12	-27,326203	-0,8810345
spe-MIR400	**274**	20,80292	24,087591	14,963504	40,145985	35,766423	64,233577	1,6666667	1,3902439	-70,1	-60,9	0,0011208	42,52	-25,583942	-0,7153061
spe-MIR403	**112**	19,642857	26,785714	19,642857	33,928571	39,285714	60,714286	1,2666667	1	-52,3	-52,3	0,158716	8,61	-46,696429	-1,1886364
spe-MIR403b	**112**	19,642857	33,928571	19,642857	26,785714	39,285714	60,714286	0,7894737	1	-45,4	-42,8	0,101614	9,61	-40,535714	-1,0318182
spe-MIR408-1	**128**	25	32,8125	22,65625	19,53125	47,65625	52,34375	0,5952381	1,1034483	-46,6	-41,4	0,0479359	8	-36,40625	-0,7639344
spe-MIR408-2	**88**	23,863636	18,181818	26,136364	31,818182	50	50	1,75	0,9130435	-37,4	-37,4	0,505233	1,93	-42,5	-0,85

spe-MIR414	**190**	15,263158	30,526316	20	34,210526	35,263158	64,736842	1,1206897	0,7631579	-69,8	-69,8	0,01292	13,78	-36,736842	-1,041791
spe-MIR419	**113**	17,699115	30,973451	16,814159	34,513274	34,513274	65,486726	1,1142857	1,0526316	-51,8	-51,8	0,0550167	8,69	-45,840708	-1,3282051
spe-MIR4225	**239**	17,154812	28,033473	14,225941	40,585774	31,380753	68,619247	1,4477612	1,2058824	-52,8	-42,3	0,0002676	45,35	-22,09205	-0,704
spe-MIR4243	**272**	20,588235	37,132353	10,294118	31,985294	30,882353	69,117647	0,8613861	2	-67,9	-65,4	0,0001524	28,17	-24,963235	-0,8083333
spe-MIR4348c	**285**	18,596491	32,982456	14,035088	34,385965	32,631579	67,368421	1,0425532	1,325	-67,7	-65,5	0,0003952	32,46	-23,754386	-0,727957
spe-MIR437	**99**	22,222222	29,292929	12,121212	36,363636	34,343434	65,656566	1,2413793	1,8333333	-30,2	-29,6	0,182463	9,79	-30,505051	-0,8882353
spe-MIR4413b	**102**	16,666667	30,392157	19,607843	33,333333	36,27451	63,72549	1,0967742	0,85	-39,9	-38,7	0,144685	7	-39,117647	-1,0783784
spe-MIR444b	**269**	19,702602	32,713755	10,780669	36,802974	30,483271	69,516729	1,125	1,8275862	-75,2	-63,2	4,88E-05	58,9	-27,95539	-0,9170732
spe-MIR472b	**80**	26,25	26,25	25	22,5	51,25	48,75	0,8571429	1,05	-42,8	-42,8	0,451489	4,09	-53,5	-1,0439024
spe-MIR475b	**99**	20,20202	29,292929	27,272727	23,232323	47,474747	52,525253	0,7931034	0,7407407	-37	-37	0,100594	4,56	-37,373737	-0,787234
spe-MIR476b	**154**	14,285714	31,818182	18,181818	35,714286	32,467532	67,532468	1,122449	0,7857143	-95,7	-95,2	0,400819	2,34	-62,142857	-1,914
spe-MIR477	**114**	25,438596	26,315789	21,052632	27,192982	46,491228	53,508772	1,0333333	1,2083333	-52,8	-52,3	0,130267	7,43	-46,315789	-0,9962264
spe-MIR477a	**70**	25,714286	20	27,142857	27,142857	52,857143	47,142857	1,3571429	0,9473684	-35,9	-34,5	0,0498196	3,89	-51,285714	-0,9702703
spe-MIR477b	**72**	23,611111	23,611111	22,222222	30,555556	45,833333	54,166667	1,2941176	1,0625	-33,8	-33	0,183134	4,64	-46,944444	-1,0242424
spe-MIR477c-1	**117**	19,65812	29,059829	19,65812	31,623932	39,316239	60,683761	1,0882353	1	-67,3	-67,3	0,254926	3,22	-57,521368	-1,4630435
spe-MIR477c-2	**125**	18,4	28,8	22,4	30,4	40,8	59,2	1,0555556	0,8214286	-73,7	-73,7	0,305365	2,94	-58,96	-1,445098
spe-MIR477e-1	**181**	17,679558	28,729282	18,78453	34,80663	36,464088	63,535912	1,2115385	0,9411765	-91,9	-90,2	0,0165669	12,6	-50,773481	-1,3924242
spe-MIR477e-2	**183**	20,218579	29,508197	19,125683	31,147541	39,344262	60,655738	1,0555556	1,0571429	-53,7	-33,1	0,0090982	41,46	-29,344262	-0,7458333
spe-MIR477k	**188**	20,212766	26,595745	22,87234	30,319149	43,085106	56,914894	1,14	0,8837209	-93,9	-91,2	0,0167554	7,94	-49,946809	-1,1592593
spe-MIR478f	**267**	17,602996	32,209738	14,981273	35,205993	32,58427	67,41573	1,0930233	1,175	-72,1	-63,8	3,32E-05	48,19	-27,003745	-0,8287356
spe-MIR479	**112**	21,428571	29,464286	19,642857	29,464286	41,071429	58,928571	1	1,0909091	-52,6	-51,4	0,108285	8,75	-46,964286	-1,1434783
spe-MIR482	**81**	25,925926	28,395062	22,222222	23,45679	48,148148	51,851852	0,826087	1,1666667	-36,8	-36,5	0,178887	7,45	-45,432099	-0,9435897
spe-MIR482b-1	**119**	16,806723	29,411765	16,806723	36,97479	33,613445	66,386555	1,2571429	1	-49	-48,6	0,1398	6,03	-41,176471	-1,225
spe-MIR482b-2	**119**	16,806723	28,571429	17,647059	36,97479	34,453782	65,546218	1,2941176	0,952381	-49	-48,6	0,129263	6,28	-41,176471	-1,195122
spe-MIR482b-3	**159**	21,383648	26,415094	18,238994	33,962264	39,622642	60,377358	1,2857143	1,1724138	-69,2	-69	0,0084506	10,26	-43,522013	-1,0984127
spe-MIR482b-4	**110**	20	27,272727	19,090909	33,636364	39,090909	60,909091	1,2333333	1,047619	-74,3	-74,2	0,195069	3,37	-67,545455	-1,727907
spe-MIR482b-5	**250**	22,4	24	21,6	32	44	56	1,3333333	1,037037	-95,7	-94,2	0,0028795	25,26	-38,28	-0,87
spe-MIR482c-1	**97**	20,618557	19,587629	17,525773	42,268041	38,14433	61,85567	2,1578947	1,1764706	-47,3	-47,3	0,24716	2,59	-48,762887	-1,2783784
spe-MIR482c-2	**105**	20,952381	17,142857	20	41,904762	40,952381	59,047619	2,4444444	1,047619	-47,3	-47,3	0,171711	3,93	-45,047619	-1,1
spe-MIR482c-3	**110**	22,727273	23,636364	15,454545	38,181818	38,181818	61,818182	1,6153846	1,4705882	-50,9	-47,8	0,0320347	12,21	-46,272727	-1,2119048
spe-MIR482c-4	**91**	18,681319	19,78022	18,681319	42,857143	37,362637	62,637363	2,1666667	1	-42,9	-42,9	0,365926	1,78	-47,142857	-1,2617647
spe-MIR482c-5	**145**	22,758621	21,37931	16,551724	39,310345	39,310345	60,689655	1,8387097	1,375	-62,5	-56,4	0,0069922	29,53	-43,103448	-1,0964912
spe-MIR482d-1	**113**	21,238938	27,433628	12,389381	38,938053	33,628319	66,371681	1,4193548	1,7142857	-42,9	-41,8	0,0582037	16,47	-37,964602	-1,1289474
spe-MIR482d-2	**127**	23,622047	26,771654	11,811024	37,795276	35,433071	64,566929	1,4117647	2	-50,7	-47	0,0348856	18,48	-39,92126	-1,1266667
spe-MIR482d-3	**238**	20,588235	26,05042	13,02521	40,336134	33,613445	66,386555	1,5483871	1,5806452	-61,2	-58,9	0,0002818	38,72	-25,714286	-0,765
spe-MIR482e	**162**	20,987654	29,012346	15,432099	34,567901	36,419753	63,580247	1,1914894	1,36	-72,2	-72,1	0,0281287	10,02	-44,567901	-1,2237288
spe-MIR5014a-1	**288**	15,277778	33,680556	17,361111	33,680556	32,638889	67,361111	1	0,88	-73,5	-72,1	0,0016197	29,97	-25,520833	-0,7819149
spe-MIR5014a-10	**168**	19,047619	34,52381	14,285714	32,142857	33,333333	66,666667	0,9310345	1,3333333	-70,8	-70,4	0,0333837	10,69	-42,142857	-1,2642857
spe-MIR5014a-11	**274**	21,89781	34,671533	10,583942	32,846715	32,481752	67,518248	0,9473684	2,0689655	-68,8	-53,3	0,0009267	56,05	-25,109489	-0,7730337
spe-MIR5014a-12	**256**	14,84375	33,59375	16,015625	35,546875	30,859375	69,140625	1,0581395	0,9268293	-83,6	-79,8	0,0026879	20,07	-32,65625	-1,0582278
spe-MIR5014a-13	**209**	14,354067	36,842105	18,181818	30,62201	32,535885	67,464115	0,8311688	0,7894737	-55,9	-55,9	0,0033744	15,77	-26,746411	-0,8220588
spe-MIR5014a-14	**188**	16,489362	35,638298	17,021277	30,851064	33,510638	66,489362	0,8656716	0,96875	-78,2	-77,4	0,0624376	10,1	-41,595745	-1,2412698
spe-MIR5014a-15	**260**	16,538462	28,846154	14,615385	40	31,153846	68,846154	1,3866667	1,1315789	-62,4	-47,1	0,0007243	59,25	-24	-0,7703704
spe-MIR5014a-2	**149**	16,778523	36,241611	15,436242	31,543624	32,214765	67,785235	0,8703704	1,0869565	-45,5	-44,7	0,0162446	25,93	-30,536913	-0,9479167
spe-MIR5014a-3	**266**	15,037594	36,842105	16,165414	31,954887	31,203008	68,796992	0,8673469	0,9302326	-75,5	-61,43	0,0032525	50,74	-28,383459	-0,9096386
spe-MIR5014a-4	**192**	16,145833	31,25	20,3125	32,291667	36,458333	63,541667	1,0333333	0,7948718	-88,1	-86,1	0,0140114	18,72	-45,885417	-1,2585714
spe-MIR5014a-5	**203**	16,256158	36,945813	17,73399	29,064039	33,990148	66,009852	0,7866667	0,9166667	-62,5	-62,4	0,0168392	12,6	-30,788177	-0,9057971
spe-MIR5014a-6	**225**	17,333333	32,444444	15,555556	34,666667	32,888889	67,111111	1,0684932	1,1142857	-91,3	-85,5	0,0155755	27,44	-40,577778	-1,2337838
spe-MIR5014a-7	**275**	14,909091	34,545455	16	34,545455	30,909091	69,090909	1	0,9318182	-62,4	-48,7	1,34E-05	63,01	-22,690909	-0,7341176
spe-MIR5014a-8	**179**	16,201117	37,988827	17,318436	28,49162	33,519553	66,480447	0,75	0,9354839	-57,9	-57,8	0,0499607	7,01	-32,346369	-0,965
spe-MIR5014a-9	**195**	15,897436	34,358974	14,871795	34,871795	30,769231	69,230769	1,0149254	1,0689655	-81,6	-81,6	0,0933481	6,67	-41,846154	-1,36
spe-MIR5021-1	**225**	20,888889	34,666667	12,444444	32	33,333333	66,666667	0,9230769	1,6785714	-55,1	-32,15	0,002136	54,82	-24,488889	-0,7346667
spe-MIR5021-2	**171**	20,467836	34,502924	10,526316	34,502924	30,994152	69,005848	1	1,9444444	-39,3	-38	0,0053528	22,7	-22,982456	-0,7415094
spe-MIR5026-1	**102**	13,72549	39,215686	16,666667	30,392157	30,392157	69,607843	0,775	0,8235294	-28,4	-28,4	0,229639	8,83	-27,843137	-0,916129
spe-MIR5026-2	**100**	22	34	16	28	38	62	0,8235294	1,375	-36,8	-36,8	0,103081	5,18	-36,8	-0,9684211
spe-MIR5026-3	**80**	23,75	31,25	23,75	21,25	47,5	52,5	0,68	1	-39,4	-39,4	0,344341	3,16	-49,25	-1,0368421
spe-MIR5027	**107**	16,82243	26,168224	18,691589	38,317757	35,514019	64,485981	1,4642857	0,9	-39	-38,9	0,130924	4,13	-36,448598	-1,0263158
spe-MIR5035	**171**	17,54386	31,578947	16,959064	33,918129	34,502924	65,497076	1,0740741	1,0344828	-81,7	-78,1	0,0186177	13,06	-47,777778	-1,3847458
spe-MIR5049-1	**248**	23,387097	29,435484	16,129032	31,048387	39,516129	60,483871	1,0547945	1,45	-79,3	-74,2	0,0006884	54,88	-31,975806	-0,8091837
spe-MIR5049-2	**94**	22,340426	27,659574	23,404255	26,595745	45,744681	54,255319	0,9615385	0,9545455	-47,1	-41,3	0,053666	18,91	-50,106383	-1,0953488
spe-MIR5049b-1	**264**	17,045455	35,227273	13,257576	34,469697	30,30303	69,69697	0,9784946	1,2857143	-84,1	-81,2	0,0004363	42,5	-31,856061	-1,05125
spe-MIR5049b-2	**266**	14,285714	33,834586	16,165414	35,714286	30,451128	69,548872	1,0555556	0,8837209	-84,9	-71,19	0,0005051	51,13	-31,917293	-1,0481481

spe-MIR5049c	**249**	14,457831	33,73494	18,072289	33,73494	32,53012	67,46988	1	0,8	-61,8	-61,5	0,0014932	20,52	-24,819277	-0,762963
spe-MIR5049d	**217**	25,345622	24,423963	19,815668	30,414747	45,16129	54,83871	1,245283	1,2790698	-85,5	-69,35	0,0042458	67,33	-39,400922	-0,872449
spe-MIR5139a	**168**	17,261905	33,333333	20,238095	29,166667	37,5	62,5	0,875	0,8529412	-59,9	-59,6	0,0307096	6,64	-35,654762	-0,9507937
spe-MIR5142	**336**	16,964286	30,357143	16,964286	35,714286	33,928571	66,071429	1,1764706	1	-86,1	-72,4	1,62E-05	66,31	-25,625	-0,7552632
spe-MIR5157b	**207**	18,84058	29,951691	17,874396	33,333333	36,714976	63,285024	1,1129032	1,0540541	-68,9	-65,9	0,0161552	11,92	-33,285024	-0,9065789
spe-MIR5161	**110**	14,545455	35,454545	16,363636	33,636364	30,909091	69,090909	0,9487179	0,8888889	-51,2	-50,2	0,409386	1,98	-46,545455	-1,5058824
spe-MIR5162	**140**	17,142857	35,714286	13,571429	33,571429	30,714286	69,285714	0,94	1,2631579	-31,9	-31,3	0,0331973	15,97	-22,785714	-0,7418605
spe-MIR5165	**279**	25,448029	23,297491	15,053763	36,200717	40,501792	59,498208	1,5538462	1,6904762	-79,8	-59,4	0,0004282	58,06	-28,602151	-0,7061947
spe-MIR5167b	**241**	18,672199	28,630705	13,278008	39,419087	31,950207	68,049793	1,3768116	1,40625	-55	-46,2	0,0048463	50,22	-22,821577	-0,7142857
spe-MIR5168	**150**	24,666667	21,333333	16	38	40,666667	59,333333	1,78125	1,5416667	-47	-45,3	0,0097825	11,08	-31,333333	-0,7704918
spe-MIR5174b	**234**	17,094017	32,478632	14,529915	35,897436	31,623932	68,376068	1,1052632	1,1764706	-53,6	-46,3	0,0004164	33,98	-22,905983	-0,7243243
spe-MIR5174d-1	**199**	17,085427	34,673367	14,070352	34,170854	31,155779	68,844221	0,9855072	1,2142857	-52,9	-52	0,0062873	21,81	-26,582915	-0,8532258
spe-MIR5174d-2	**198**	17,676768	34,848485	13,131313	34,343434	30,808081	69,191919	0,9855072	1,3461538	-51,7	-46,9	0,0075519	23,84	-26,111111	-0,847541
spe-MIR5174d-3	**266**	18,796992	34,586466	13,533835	33,082707	32,330827	67,669173	0,9565217	1,3888889	-73,7	-56,95	5,85E-05	63,57	-27,706767	-0,8569767
spe-MIR5174d-4	**255**	17,254902	36,862745	12,941176	32,941176	30,196078	69,803922	0,893617	1,3333333	-59,9	-54,7	0,0004117	56,97	-23,490196	-0,7779221
spe-MIR5174d-5	**264**	18,181818	36,363636	13,257576	32,19697	31,439394	68,560606	0,8854167	1,3714286	-66	-46,59	0,001044	67,14	-25	-0,7951807
spe-MIR5174d-6	**268**	18,283582	35,074627	13,432836	33,208955	31,716418	68,283582	0,9468085	1,3611111	-76,9	-58,4	0,0025444	51,01	-28,69403	-0,9047059
spe-MIR5174d-7	**254**	13,779528	29,527559	18,110236	38,582677	31,889764	68,110236	1,3066667	0,7608696	-63,5	-51,57	6,34E-05	54,97	-25	-0,7839506
spe-MIR5174e	**268**	12,313433	33,955224	17,910448	35,820896	30,223881	69,776119	1,0549451	0,6875	-61,8	-57,4	0,0005227	48,09	-23,059701	-0,762963
spe-MIR5180a	**162**	18,518519	35,185185	14,197531	32,098765	32,716049	67,283951	0,9122807	1,3043478	-54,6	-51,2	0,0097982	20,37	-33,703704	-1,0301887
spe-MIR5181b-1	**77**	20,779221	32,467532	14,285714	32,467532	35,064935	64,935065	1	1,4545455	-33,1	-33,1	0,321414	1,98	-42,987013	-1,1259259
spe-MIR5181b-2	**210**	15,714286	34,761905	16,190476	33,333333	31,904762	68,095238	0,9589041	0,9705882	-50,2	-47,2	0,0017174	26,05	-23,904762	-0,7492537
spe-MIR5183	**245**	19,183673	37,142857	11,020408	32,653061	30,204082	69,795918	0,8791209	1,7407407	-52,1	-43,4	0,0001505	48,8	-21,265306	-0,7040541
spe-MIR5185k	**162**	12,962963	31,481481	20,37037	35,185185	33,333333	66,666667	1,1176471	0,6363636	-39,1	-38,6	0,0277504	19,01	-24,135802	-0,7240741
spe-MIR5205a	**231**	17,748918	35,064935	15,151515	32,034632	32,900433	67,099567	0,9135802	1,1714286	-69,9	-62,79	0,0002414	29,22	-30,25974	-0,9197368
spe-MIR5210	**301**	18,272425	29,568106	18,272425	33,887043	36,54485	63,45515	1,1460674	1	-83,9	-66,8	3,80E-05	77,67	-27,873754	-0,7627273
spe-MIR5253	**249**	20,883534	32,53012	12,449799	34,136546	33,333333	66,666667	1,0493827	1,6774194	-63,8	-54,7	0,0005543	48,81	-25,62249	-0,7686747
spe-MIR5274b	**233**	18,025751	31,759657	16,738197	33,476395	34,763948	65,236052	1,0540541	1,0769231	-76	-61,1	0,0075357	42,08	-32,618026	-0,9382716
spe-MIR5278	**169**	21,301775	33,136095	13,017751	32,544379	34,319527	65,680473	0,9821429	1,6363636	-43,5	-43,1	0,0459981	37,43	-25,739645	-0,75
spe-MIR529	**248**	18,951613	36,290323	15,322581	29,435484	34,274194	65,725806	0,8111111	1,2368421	-77,9	-66,9	0,0009746	45,81	-31,41129	-0,9164706
spe-MIR5298d	**225**	17,777778	31,111111	12,888889	38,222222	30,666667	69,333333	1,2285714	1,3793103	-49	-32,08	0,0008511	56,36	-21,777778	-0,7101449
spe-MIR530	**93**	22,580645	26,88172	17,204301	33,333333	39,784946	60,215054	1,24	1,3125	-43,5	-43,5	0,157591	9,04	-46,774194	-1,1756757
spe-MIR5300	**265**	20	29,056604	16,603774	34,339623	36,603774	63,396226	1,1818182	1,2045455	-91,8	-89,4	0,0014535	16	-34,641509	-0,9463918
spe-MIR5303-15	**119**	18,487395	29,411765	25,210084	26,890756	43,697479	56,302521	0,9142857	0,7333333	-54,4	-54,4	0,17029	3,55	-45,714286	-1,0461538
spe-MIR5303-16	**118**	16,949153	28,813559	27,118644	27,118644	44,067797	55,932203	0,9411765	0,625	-53,8	-52,9	0,400313	2,06	-45,59322	-1,0346154
spe-MIR5303-6	**125**	17,6	28	28	26,4	45,6	54,4	0,9428571	0,6285714	-52,8	-52,8	0,287736	2,92	-42,24	-0,9263158
spe-MIR5303-7	**118**	20,338983	25,423729	17,79661	36,440678	38,135593	61,864407	1,4333333	1,1428571	-35,2	-31,6	0,133421	7,09	-29,830508	-0,7822222
spe-MIR5303d-4	**128**	20,3125	26,5625	27,34375	25,78125	47,65625	52,34375	0,9705882	0,7428571	-50,9	-50,5	0,0358179	6,39	-39,765625	-0,8344262
spe-MIR5303d-7	**119**	18,487395	27,731092	26,05042	27,731092	44,537815	55,462185	1	0,7096774	-55,9	-55,9	0,174031	4,28	-46,97479	-1,054717
spe-MIR5303f-5	**126**	27,777778	25,396825	20,634921	26,190476	48,412698	51,587302	1,03125	1,3461538	-58,6	-57,3	0,087852	6,26	-46,507937	-0,9606557
spe-MIR5303f-7	**133**	25,56391	27,819549	21,052632	25,56391	46,616541	53,383459	0,9189189	1,2142857	-56,3	-54,5	0,0753844	5,7	-42,330827	-0,9080645
spe-MIR5303f-9	**147**	27,891156	29,251701	14,965986	27,891156	42,857143	57,142857	0,9534884	1,8636364	-45,7	-42,9	0,0103002	24,09	-31,088435	-0,7253968
spe-MIR5303h-11	**124**	18,548387	29,83871	22,580645	29,032258	41,129032	58,870968	0,972973	0,8214286	-48,5	-48,5	0,289283	5,88	-39,112903	-0,9509804
spe-MIR5303h-15	**131**	21,374046	30,534351	23,664122	24,427481	45,038168	54,961832	0,8	0,9032258	-55,4	-54	0,0237299	7,17	-42,290076	-0,9389831
spe-MIR5303h-16	**128**	21,875	25,78125	18,75	33,59375	40,625	59,375	1,3030303	1,1666667	-41,4	-41,3	0,0141772	8,06	-32,34375	-0,7961538
spe-MIR5340	**253**	18,181818	36,758893	12,252964	32,806324	30,434783	69,565217	0,8924731	1,483871	-72,8	-70,6	0,0013396	32,67	-28,774704	-0,9454545
spe-MIR5368	**83**	28,915663	25,301205	25,301205	20,481928	54,216867	45,783133	0,8095238	1,1428571	-33	-33	0,448662	1,92	-39,759036	-0,7333333
spe-MIR5385	**284**	19,366197	24,295775	29,577465	26,760563	48,943662	51,056338	1,1014493	0,6547619	-97,9	-93,1	0,000821	39,56	-34,471831	-0,7043165
spe-MIR5536	**306**	21,24183	34,640523	14,705882	29,411765	35,947712	64,052288	0,8490566	1,4444444	-78,9	-66,3	0,0002979	66,06	-25,784314	-0,7172727
spe-MIR5556	**163**	15,95092	31,90184	15,95092	36,196319	31,90184	68,09816	1,1346154	1	-62,5	-55,2	0,0162657	20,25	-38,343558	-1,2019231
spe-MIR5559	**88**	21,590909	29,545455	18,181818	30,681818	39,772727	60,227273	1,0384615	1,1875	-28,6	-26,7	0,006266	14,45	-32,5	-0,8171429
spe-MIR5567	**206**	17,961165	26,699029	13,592233	41,747573	31,553398	68,446602	1,5636364	1,3214286	-51,2	-48,1	0,0007617	49,76	-24,854369	-0,7876923
spe-MIR5568b	**285**	18,596491	30,526316	14,736842	36,140351	33,333333	66,666667	1,183908	1,2619048	-90,7	-87,7	0,0011082	25,04	-31,824561	-0,9547368
spe-MIR5568e	**282**	19,503546	29,787234	15,957447	34,751773	35,460993	64,539007	1,1666667	1,2222222	-78,5	-73	4,29E-05	58,08	-27,836879	-0,785
spe-MIR5628	**118**	20,338983	31,355932	16,949153	31,355932	37,288136	62,711864	1	1,2	-54,4	-51,9	0,0294461	12,75	-46,101695	-1,2363636
spe-MIR5658	**215**	20,465116	25,581395	13,488372	40,465116	33,953488	66,046512	1,5818182	1,5172414	-71,1	-71,1	0,0407948	13,1	-33,069767	-0,9739726
spe-MIR5671a	**172**	18,604651	30,232558	18,604651	32,55814	37,209302	62,790698	1,0769231	1	-45	-40,17	0,0024853	24,88	-26,162791	-0,703125
spe-MIR5725	**86**	18,604651	36,046512	16,27907	29,069767	34,883721	65,116279	0,8064516	1,1428571	-23	-23	0,0413856	6,32	-26,744186	-0,7666667
spe-MIR5747	**284**	17,253521	33,802817	13,380282	35,56338	30,633803	69,366197	1,0520833	1,2894737	-64,3	-42,36	4,30E-05	58,12	-22,640845	-0,7390805
spe-MIR5752b	**105**	21,904762	38,095238	12,380952	27,619048	34,285714	65,714286	0,725	1,7692308	-33,6	-33,6	0,0480283	5,14	-32	-0,9333333
spe-MIR5761b-1	**249**	20,481928	28,11245	10,441767	40,963855	30,923695	69,076305	1,4571429	1,9615385	-56,4	-39,7	6,84E-05	68,57	-22,650602	-0,7324675
spe-MIR5761b-2	**220**	21,818182	23,636364	16,818182	37,727273	38,636364	61,363636	1,5961538	1,2972973	-67,4	-55,9	0,0018054	50,65	-30,636364	-0,7929412

spe-MIR5770b	**192**	29,6875	22,916667	17,708333	29,6875	47,395833	52,604167	1,2954545	1,6764706	-66,1	-59,7	0,0072386	24,37	-34,427083	-0,7263736
spe-MIR5773-1	**165**	16,363636	34,545455	15,151515	33,939394	31,515152	68,484848	0,9824561	1,08	-91	-91	0,108527	6,44	-55,151515	-1,75
spe-MIR5773-2	**155**	18,709677	33,548387	15,483871	32,258065	34,193548	65,806452	0,9615385	1,2083333	-91,2	-88,7	0,0095111	13,95	-58,83871	-1,7207547
spe-MIR5773-3	**155**	17,419355	36,129032	13,548387	32,903226	30,967742	69,032258	0,9107143	1,2857143	-85,4	-81,2	0,0220257	11,92	-55,096774	-1,7791667
spe-MIR5780d	**145**	22,068966	27,586207	22,068966	28,275862	44,137931	55,862069	1,025	1	-64,3	-64,1	0,0526732	8,12	-44,344828	-1,0046875
spe-MIR5998b	**144**	20,833333	28,472222	9,7222222	40,972222	30,555556	69,444444	1,4390244	2,1428571	-34,4	-23,67	0,0025569	60,23	-23,888889	-0,7818182
spe-MIR6020a	**118**	16,101695	35,59322	15,254237	33,050847	31,355932	68,644068	0,9285714	1,0555556	-43,4	-42,3	0,12879	11,43	-36,779661	-1,172973
spe-MIR6022	**236**	18,644068	31,355932	19,067797	30,932203	37,711864	62,288136	0,9864865	0,9777778	-75,7	-68,8	0,0028846	34,04	-32,076271	-0,8505618
spe-MIR6023-1	**182**	18,131868	31,868132	17,032967	32,967033	35,164835	64,835165	1,0344828	1,0645161	-93,5	-91,2	0,118315	10,45	-51,373626	-1,4609375
spe-MIR6023-2	**146**	26,712329	21,917808	19,863014	31,506849	46,575342	53,424658	1,4375	1,3448276	-55,5	-55,3	0,0377978	11,12	-38,013699	-0,8161765
spe-MIR6023-3	**192**	26,5625	23,958333	17,708333	31,770833	44,270833	55,729167	1,326087	1,5	-67	-61,1	0,0048709	24,86	-34,895833	-0,7882353
spe-MIR6024	**102**	18,627451	26,470588	18,627451	36,27451	37,254902	62,745098	1,3703704	1	-41	-41	0,0702447	12,97	-40,196078	-1,0789474
spe-MIR6025e-1	**162**	20,37037	28,395062	12,345679	38,888889	32,716049	67,283951	1,3695652	1,65	-53,5	-50,3	0,0191978	19,5	-33,024691	-1,009434
spe-MIR6025e-2	**162**	24,074074	25,308642	13,580247	37,037037	37,654321	62,345679	1,4634146	1,7727273	-55,1	-52,3	0,0087339	21,14	-34,012346	-0,9032787
spe-MIR6027	**164**	19,512195	32,317073	12,804878	35,365854	32,317073	67,682927	1,0943396	1,5238095	-55,7	-45,9	0,0130049	27,23	-33,963415	-1,0509434
spe-MIR6028	**151**	22,516556	30,463576	11,258278	35,761589	33,774834	66,225166	1,173913	2	-54,5	-51,9	0,0041931	17,7	-36,092715	-1,0686275
spe-MIR6116	**87**	17,241379	31,034483	18,390805	33,333333	35,632184	64,367816	1,0740741	0,9375	-39,1	-39,1	0,320862	3,07	-44,942529	-1,2612903
spe-MIR6135k	**149**	24,832215	25,503356	18,791946	30,872483	43,624161	56,375839	1,2105263	1,3214286	-47,5	-44,5	0,0109382	21,09	-31,879195	-0,7307692
spe-MIR6137b	**200**	14,5	30	20,5	35	35	65	1,1666667	0,7073171	-58,3	-52,6	0,0018885	26,75	-29,15	-0,8328571
spe-MIR6140b-1	**286**	17,832168	36,363636	12,937063	32,867133	30,769231	69,230769	0,9038462	1,3783784	-94,5	-88	0,0009861	45,21	-33,041958	-1,0738636
spe-MIR6140b-2	**173**	16,763006	30,057803	16,763006	36,416185	33,526012	66,473988	1,2115385	1	-41,1	-37,1	0,0123103	17,92	-23,757225	-0,7086207
spe-MIR6144	**188**	21,276596	22,87234	22,87234	32,978723	44,148936	55,851064	1,4418605	0,9302326	-58,4	-44,07	0,0312777	29,81	-31,06383	-0,7036145
spe-MIR6145b-1	**77**	22,077922	33,766234	18,181818	25,974026	40,25974	59,74026	0,7692308	1,2142857	-27,6	-27,5	0,11778	4,81	-35,844156	-0,8903226
spe-MIR6145b-2	**183**	16,939891	30,054645	15,846995	37,15847	32,786885	67,213115	1,2363636	1,0689655	-78,7	-78,7	0,0735337	10,59	-43,005464	-1,3116667
spe-MIR6145e	**174**	17,816092	28,735632	16,666667	36,781609	34,482759	65,517241	1,28	1,0689655	-62,1	-60,4	0,0479125	12,1	-35,689655	-1,035
spe-MIR6148a	**147**	16,326531	29,251701	14,285714	40,136054	30,612245	69,387755	1,372093	1,1428571	-53,7	-53,2	0,0169573	17,3	-36,530612	-1,1933333
spe-MIR6164b-1	**274**	15,693431	33,576642	15,693431	35,036496	31,386861	68,613139	1,0434783	1	-66,8	-54,82	0,0003604	49,54	-24,379562	-0,7767442
spe-MIR6164b-2	**199**	16,080402	34,673367	15,577889	33,668342	31,658291	68,341709	0,9710145	1,0322581	-53,7	-50	0,0054048	34,36	-26,984925	-0,852381
spe-MIR6207	**252**	21,428571	24,603175	30,952381	23,015873	52,380952	47,619048	0,9354839	0,6923077	-92,6	-92,6	0,039427	20,28	-36,746032	-0,7015152
spe-MIR6231-1	**177**	19,20904	32,20339	16,949153	31,638418	36,158192	63,841808	0,9824561	1,1333333	-66,6	-64,9	0,0015503	19,79	-37,627119	-1,040625
spe-MIR6231-2	**106**	12,264151	36,792453	19,811321	31,132075	32,075472	67,924528	0,8461538	0,6190476	-38,1	-38,1	0,29583	5,12	-35,943396	-1,1205882
spe-MIR6232b-1	**112**	20,535714	33,035714	16,964286	29,464286	37,5	62,5	0,8918919	1,2105263	-74,2	-73,9	0,180751	4,04	-66,25	-1,7666667
spe-MIR6232b-2	**112**	21,428571	33,035714	16,071429	29,464286	37,5	62,5	0,8918919	1,3333333	-70,1	-69,8	0,178559	4,07	-62,589286	-1,6690476
spe-MIR6248	**201**	22,885572	33,333333	13,930348	29,850746	36,81592	63,18408	0,8955224	1,6428571	-57,1	-53,6	0,0109887	39,29	-28,40796	-0,7716216
spe-MIR6271	**181**	18,78453	34,80663	17,679558	28,729282	36,464088	63,535912	0,8253968	1,0625	-87,6	-86,8	0,0144688	11,21	-48,39779	-1,3272727
spe-MIR6273-1	**178**	19,101124	31,460674	13,483146	35,955056	32,58427	67,41573	1,1428571	1,4166667	-54,1	-48,8	0,0201132	26,22	-30,393258	-0,9327586
spe-MIR6273-2	**178**	18,539326	33,146067	12,921348	35,393258	31,460674	68,539326	1,0677966	1,4347826	-53,4	-46,45	0,012385	25,26	-30	-0,9535714
spe-MIR6283	**92**	22,826087	31,521739	11,956522	33,695652	34,782609	65,217391	1,0689655	1,9090909	-26,4	-25,1	0,0076598	14,86	-28,695652	-0,825
spe-MIR6287	**211**	18,957346	33,649289	11,848341	35,545024	30,805687	69,194313	1,056338	1,6	-50	-39,4	0,0005492	40,25	-23,696682	-0,7692308
spe-MIR6288c-1	**188**	24,468085	26,06383	14,361702	35,106383	38,829787	61,170213	1,3469388	1,7037037	-51,4	-28,37	0,0005648	59,75	-27,340426	-0,7041096
spe-MIR6288c-2	**136**	19,117647	28,676471	18,382353	33,823529	37,5	62,5	1,1794872	1,04	-85,3	-85,3	0,226999	6,48	-62,720588	-1,672549
spe-MIR6299-1	**301**	18,936877	37,541528	12,292359	31,229236	31,229236	68,770764	0,8318584	1,5405405	-67	-58,84	0,0002428	46,02	-22,259136	-0,712766
spe-MIR6299-2	**310**	18,064516	36,129032	14,193548	31,612903	32,258065	67,741935	0,875	1,2727273	-86,5	-75,6	0,0003585	39,04	-27,903226	-0,865
spe-MIR6434	**69**	14,492754	34,782609	15,942029	34,782609	30,434783	69,565217	1	0,9090909	-21,7	-20,7	0,183826	4,57	-31,449275	-1,0333333
spe-MIR6440a	**197**	20,812183	30,964467	12,690355	35,532995	33,502538	66,497462	1,147541	1,64	-47,2	-47,2	0,0037718	22,18	-23,959391	-0,7151515
spe-MIR6472	**317**	20,189274	31,230284	12,933754	35,646688	33,123028	66,876972	1,1414141	1,5609756	-79,6	-67,1	3,79E-05	52,61	-25,11041	-0,7580952
spe-MIR6473	**168**	17,261905	34,52381	16,666667	31,547619	33,928571	66,071429	0,9137931	1,0357143	-43,6	-39,9	0,0038157	20,54	-25,952381	-0,7649123
spe-MIR6475	**87**	20,689655	31,034483	16,091954	32,183908	36,781609	63,218391	1,037037	1,2857143	-35,5	-35,5	0,167667	3,96	-40,804598	-1,109375
spe-MIR7484k	**108**	15,740741	38,888889	15,740741	29,62963	31,481481	68,518519	0,7619048	1	-69,2	-69,2	0,810126	0,44	-64,074074	-2,0352941
spe-MIR7492f	**68**	16,176471	32,352941	14,705882	36,764706	30,882353	69,117647	1,1363636	1,1	-21,1	-21,1	0,130626	4,09	-31,029412	-1,0047619
spe-MIR7495b	**132**	17,424242	25,757576	18,939394	37,878788	36,363636	63,636364	1,4705882	0,92	-38,5	-29,5	0,0259069	32,46	-29,166667	-0,8020833
spe-MIR7504m	**92**	14,130435	35,869565	21,73913	28,26087	35,869565	64,130435	0,7878788	0,65	-23,1	-23,1	0,100261	5,27	-25,108696	-0,7
spe-MIR7508	**177**	18,644068	31,073446	19,774011	30,508475	38,418079	61,581921	0,9818182	0,9428571	-80,4	-80,4	0,216289	4,91	-45,423729	-1,1823529
spe-MIR7525	**263**	13,307985	29,277567	19,011407	38,403042	32,319392	67,680608	1,3116883	0,7	-60,8	-47,4	0,0002465	46,89	-23,117871	-0,7152941
spe-MIR7528	**214**	19,626168	27,102804	12,616822	40,654206	32,242991	67,757009	1,5	1,5555556	-50,3	-48,3	0,0005835	36,15	-23,504673	-0,7289855
spe-MIR7533b	**244**	22,540984	35,245902	10,655738	31,557377	33,196721	66,803279	0,8953488	2,1153846	-61,9	-61,9	0,0184583	22,26	-25,368852	-0,7641975
spe-MIR7540b-1	**285**	20,701754	29,824561	10,526316	38,947368	31,22807	68,77193	1,3058824	1,9666667	-63,9	-58,7	0,0001847	49,26	-22,421053	-0,7179775
spe-MIR7540b-2	**295**	22,372881	30,847458	15,932203	30,847458	38,305085	61,694915	1	1,4042553	-81,4	-76,9	0,0007652	40,42	-27,59322	-0,720354
spe-MIR7696b	**149**	22,147651	30,872483	19,463087	27,516779	41,610738	58,389262	0,8913043	1,137931	-47,2	-45,3	0,0433011	13,39	-31,677852	-0,7612903
spe-MIR7696d	**239**	18,828452	27,615063	13,807531	39,748954	32,635983	67,364017	1,4393939	1,3636364	-54,9	-54,4	0,00225	32,44	-22,970711	-0,7038462
spe-MIR7699	**171**	14,035088	32,163743	16,959064	36,842105	30,994152	69,005848	1,1454545	0,8275862	-50,2	-50,2	0,0424275	13,67	-29,356725	-0,9471698
spe-MIR7701-1	**236**	15,254237	41,525424	15,254237	27,966102	30,508475	69,491525	0,6734694	1	-57,7	-54,7	0,0016626	24,67	-24,449153	-0,8013889

spe-MIR7701-2	**112**	15,178571	41,964286	15,178571	27,678571	30,357143	69,642857	0,6595745	1	-33,9	-33,9	0,0202944	20,17	-30,267857	-0,9970588
spe-MIR7711	**116**	15,517241	35,344828	15,517241	33,62069	31,034483	68,965517	0,9512195	1	-36,2	-31,52	0,0467302	21,9	-31,206897	-1,0055556
spe-MIR773b	**296**	22,297297	34,797297	12,162162	30,743243	34,459459	65,540541	0,8834951	1,8333333	-81,1	-76,9	0,0003374	23,88	-27,398649	-0,795098
spe-MIR7757	**189**	20,10582	26,455026	10,05291	43,386243	30,15873	69,84127	1,64	2	-40,5	-36,6	0,0001329	36,24	-21,428571	-0,7105263
spe-MIR7772	**198**	22,222222	34,848485	8,0808081	34,848485	30,30303	69,69697	1	2,75	-45	-44,1	0,0188738	19,8	-22,727273	-0,75
spe-MIR7774	**299**	20,401338	34,113712	14,715719	30,769231	35,117057	64,882943	0,9019608	1,3863636	-88,9	-86,37	0,0022875	36,25	-29,732441	-0,8466667
spe-MIR7803b	**70**	17,142857	28,571429	24,285714	30	41,428571	58,571429	1,05	0,7058824	-31,8	-31,8	0,616818	0,9	-45,428571	-1,0965517
spe-MIR7808	**71**	28,169014	25,352113	25,352113	21,126761	53,521127	46,478873	0,8333333	1,1111111	-34	-34	0,115047	4,7	-47,887324	-0,8947368
spe-MIR7813	**83**	21,686747	38,554217	10,843373	28,915663	32,53012	67,46988	0,75	2	-22,3	-22,3	0,106245	6,06	-26,86747	-0,8259259
spe-MIR7814	**271**	21,402214	26,937269	8,8560886	42,804428	30,258303	69,741697	1,5890411	2,4166667	-63,4	-59,4	0,0006464	41,52	-23,394834	-0,7731707
spe-MIR7816	**95**	8,4210526	31,578947	22,105263	37,894737	30,526316	69,473684	1,2	0,3809524	-22,7	-22,7	0,236631	3,8	-23,894737	-0,7827586
spe-MIR7822	**204**	22,058824	29,901961	10,294118	37,745098	32,352941	67,647059	1,2622951	2,1428571	-70,4	-70,4	0,0425711	8,37	-34,509804	-1,0666667
spe-MIR7828	**201**	16,915423	34,328358	18,40796	30,348259	35,323383	64,676617	0,884058	0,9189189	-59,5	-58	0,0434276	12,75	-29,60199	-0,8380282
spe-MIR7834	**166**	19,879518	34,337349	14,457831	31,325301	34,337349	65,662651	0,9122807	1,375	-53,3	-48,2	0,0027826	46,94	-32,108434	-0,9350877
spe-MIR7980b-1	**79**	20,253165	35,443038	21,518987	22,78481	41,772152	58,227848	0,6428571	0,9411765	-27,5	-27,5	0,445047	1,89	-34,810127	-0,8333333
spe-MIR7980b-2	**159**	18,238994	28,930818	15,72327	37,106918	33,962264	66,037736	1,2826087	1,16	-42,7	-38,1	0,0035868	27,12	-26,855346	-0,7907407
spe-MIR7980b-3	**114**	14,912281	37,719298	18,421053	28,947368	33,333333	66,666667	0,7674419	0,8095238	-33,4	-33,4	0,117473	5,54	-29,298246	-0,8789474
spe-MIR7980b-4	**157**	15,923567	35,031847	15,923567	33,121019	31,847134	68,152866	0,9454545	1	-52,4	-52,3	0,0699047	9,06	-33,375796	-1,048
spe-MIR7980b-5	**80**	20	30	17,5	32,5	37,5	62,5	1,0833333	1,1428571	-27,4	-26,6	0,115573	11,26	-34,25	-0,9133333
spe-MIR7980b-6	**149**	18,791946	30,872483	14,765101	35,57047	33,557047	66,442953	1,1521739	1,2727273	-61,5	-58,6	0,0458673	9,11	-41,275168	-1,23
spe-MIR7980b-7	**131**	22,137405	25,954198	19,847328	32,061069	41,984733	58,015267	1,2352941	1,1153846	-59	-59	0,0663273	11,15	-45,038168	-1,0727273
spe-MIR7980b-8	**184**	16,847826	35,869565	17,391304	29,891304	34,23913	65,76087	0,8333333	0,96875	-57,2	-52,3	0,0089159	30,8	-31,086957	-0,9079365
spe-MIR7980b-9	**116**	15,517241	34,482759	20,689655	29,310345	36,206897	63,793103	0,85	0,75	-38,5	-38,5	0,100871	8,72	-33,189655	-0,9166667
spe-MIR7981-10	**239**	19,246862	33,054393	17,154812	30,543933	36,401674	63,598326	0,9240506	1,1219512	-98,7	-94,7	0,0035657	17,34	-41,297071	-1,1344828
spe-MIR7981-12	**243**	17,283951	31,27572	17,283951	34,156379	34,567901	65,432099	1,0921053	1	-96,2	-93,5	0,0010023	25,07	-39,588477	-1,1452381
spe-MIR7981-13	**214**	17,757009	30,841121	19,158879	32,242991	36,915888	63,084112	1,0454545	0,9268293	-92,5	-92	0,0243737	18,17	-43,224299	-1,1708861
spe-MIR7981-2	**207**	18,357488	28,985507	14,009662	38,647343	32,36715	67,63285	1,3333333	1,3103448	-57,6	-51	0,0054844	36,8	-27,826087	-0,8597015
spe-MIR7981-6	**268**	17,164179	35,820896	19,776119	27,238806	36,940299	63,059701	0,7604167	0,8679245	-71,2	-70,4	0,0015177	26,08	-26,567164	-0,7191919
spe-MIR7981-7	**268**	18,283582	36,19403	14,179104	31,343284	32,462687	67,537313	0,8659794	1,2894737	-88,3	-76,61	0,0008272	40,36	-32,947761	-1,0149425
spe-MIR7981-9	**267**	15,355805	36,70412	14,981273	32,958801	30,337079	69,662921	0,8979592	1,025	-61,6	-40,6	0,0008072	40,97	-23,071161	-0,7604938
spe-MIR7983-1	**130**	16,923077	38,461538	15,384615	29,230769	32,307692	67,692308	0,76	1,1	-37,1	-36,7	0,050511	13,52	-28,538462	-0,8833333
spe-MIR7983-10	**216**	16,203704	28,703704	17,12963	37,962963	33,333333	66,666667	1,3225806	0,9459459	-76,1	-74	0,0065248	18,79	-35,231481	-1,0569444
spe-MIR7983-11	**173**	15,028902	28,901734	18,49711	37,572254	33,526012	66,473988	1,3	0,8125	-53,2	-49,6	0,0108952	30,59	-30,751445	-0,9172414
spe-MIR7983-12	**140**	16,428571	29,285714	16,428571	37,857143	32,857143	67,142857	1,2926829	1	-38,6	-38,6	0,0587153	10,75	-27,571429	-0,8391304
spe-MIR7983-13	**223**	17,488789	29,596413	17,040359	35,874439	34,529148	65,470852	1,2121212	1,0263158	-77	-71,6	0,0050302	19,97	-34,529148	-1
spe-MIR7983-14	**198**	18,181818	36,363636	17,171717	28,282828	35,353535	64,646465	0,7777778	1,0588235	-74,1	-73,8	0,0343533	10,7	-37,424242	-1,0585714
spe-MIR7983-15	**214**	14,485981	33,17757	15,88785	36,448598	30,373832	69,626168	1,0985915	0,9117647	-58,2	-47,8	0,0021297	35,96	-27,196262	-0,8953846
spe-MIR7983-16	**216**	14,351852	31,018519	18,055556	36,574074	32,407407	67,592593	1,1791045	0,7948718	-79,2	-77,2	0,0016806	35,14	-36,666667	-1,1314286
spe-MIR7983-17	**124**	15,322581	31,451613	20,16129	33,064516	35,483871	64,516129	1,0512821	0,76	-30,9	-30,9	0,0163257	12,49	-24,919355	-0,7022727
spe-MIR7983-18	**66**	15,151515	31,818182	19,69697	33,333333	34,848485	65,151515	1,047619	0,7692308	-28,1	-28,1	0,306531	2,62	-42,575758	-1,2217391
spe-MIR7983-19	**219**	15,525114	32,876712	14,611872	36,986301	30,136986	69,863014	1,125	1,0625	-51,4	-49,2	0,000246	36,15	-23,47032	-0,7787879
spe-MIR7983-2	**216**	15,277778	29,62963	17,12963	37,962963	32,407407	67,592593	1,28125	0,8918919	-65,2	-61,5	0,0033008	15,05	-30,185185	-0,9314286
spe-MIR7983-3	**131**	15,267176	33,587786	16,030534	35,114504	31,29771	68,70229	1,0454545	0,952381	-31,2	-25,8	0,0073784	34,02	-23,816794	-0,7609756
spe-MIR7983-4	**221**	14,932127	30,769231	17,647059	36,651584	32,579186	67,420814	1,1911765	0,8461538	-67,2	-65,4	0,0136402	17,74	-30,40724	-0,9333333
spe-MIR7983-5	**219**	11,872146	32,420091	18,721461	36,986301	30,593607	69,406393	1,1408451	0,6341463	-54,1	-52,2	0,0041826	20,42	-24,703196	-0,8074627
spe-MIR7983-6	**218**	14,220183	31,651376	16,055046	38,073394	30,275229	69,724771	1,2028986	0,8857143	-58,3	-55,4	0,0043739	30,1	-26,743119	-0,8833333
spe-MIR7983-7	**216**	15,277778	30,092593	16,666667	37,962963	31,944444	68,055556	1,2615385	0,9166667	-75,7	-73,9	0,0068934	17,58	-35,046296	-1,0971014
spe-MIR7983-8	**270**	15,185185	30,740741	18,148148	35,925926	33,333333	66,666667	1,1686747	0,8367347	-72,5	-71	0,00045	43,74	-26,851852	-0,8055556
spe-MIR7983-9	**212**	16,509434	38,207547	14,150943	31,132075	30,660377	69,339623	0,8148148	1,1666667	-57,7	-52,9	0,0015428	30,94	-27,216981	-0,8876923
spe-MIR7984b-1	**205**	14,146341	35,609756	16,097561	34,146341	30,243902	69,756098	0,9589041	0,8787879	-67,3	-62,7	0,0072323	17,82	-32,829268	-1,0854839
spe-MIR7984b-2	**88**	18,181818	28,409091	21,590909	31,818182	39,772727	60,227273	1,12	0,8421053	-49,8	-49,8	0,204618	2,96	-56,590909	-1,4228571
spe-MIR7984b-3	**176**	16,477273	31,25	17,045455	35,227273	33,522727	66,477273	1,1272727	0,9666667	-66,7	-66,7	0,0223406	12,97	-37,897727	-1,1305085
spe-MIR7984c-1	**200**	17	31,5	15	36,5	32	68	1,1587302	1,1333333	-77,2	-75,7	0,0577433	14,81	-38,6	-1,20625
spe-MIR7984c-2	**205**	16,097561	33,170732	14,146341	36,585366	30,243902	69,756098	1,1029412	1,137931	-87,1	-86,3	0,0227281	11,2	-42,487805	-1,4048387
spe-MIR7984c-3	**319**	12,539185	36,050157	17,554859	33,855799	30,094044	69,905956	0,9391304	0,7142857	-79,9	-71,3	2,77E-05	52,62	-25,047022	-0,8322917
spe-MIR7984c-4	**209**	14,832536	34,92823	16,746411	33,492823	31,578947	68,421053	0,9589041	0,8857143	-93,5	-93,5	0,0356836	11,2	-44,736842	-1,4166667
spe-MIR7984c-5	**198**	15,656566	34,848485	15,151515	34,343434	30,808081	69,191919	0,9855072	1,0333333	-87,5	-82,8	0,0304106	15,17	-44,191919	-1,4344262
spe-MIR7984c-6	**271**	16,605166	37,638376	13,653137	32,103321	30,258303	69,741697	0,8529412	1,2162162	-66,2	-65,8	0,0010771	25,35	-24,428044	-0,8073171
spe-MIR7984c-7	**201**	15,920398	33,333333	15,920398	34,825871	31,840796	68,159204	1,0447761	1	-98,6	-98,6	0,0449709	8,29	-49,054726	-1,540625
spe-MIR7984d	**230**	13,913043	34,782609	18,26087	33,043478	32,173913	67,826087	0,95	0,7619048	-66,5	-65,7	0,0250228	15,8	-28,913043	-0,8986486
spe-MIR7986	**148**	16,891892	31,756757	16,216216	35,135135	33,108108	66,891892	1,106383	1,0416667	-82,5	-82,5	0,576781	1,08	-55,743243	-1,6836735
spe-MIR7987-1	**98**	16,326531	29,591837	14,285714	39,795918	30,612245	69,387755	1,3448276	1,1428571	-23,3	-22,2	0,0591509	17,14	-23,77551	-0,7766667

spe-MIR7987-2	**284**	15,84507	30,985915	14,43662	38,732394	30,28169	69,71831	1,25	1,097561	-71,2	-70,7	5,33E-05	30,85	-25,070423	-0,827907
spe-MIR7990a-1	**110**	13,636364	29,090909	19,090909	38,181818	32,727273	67,272727	1,3125	0,7142857	-34,9	-34,9	0,197113	7,37	-31,727273	-0,9694444
spe-MIR7990a-2	**119**	15,12605	36,134454	15,12605	33,613445	30,252101	69,747899	0,9302326	1	-32,3	-23,3	0,0536674	16,03	-27,142857	-0,8972222
spe-MIR7990a-3	**219**	15,981735	30,593607	14,611872	38,812785	30,593607	69,406393	1,2686567	1,09375	-82,1	-81,8	0,0083378	13,44	-37,488584	-1,2253731
spe-MIR7990a-4	**125**	16,8	29,6	16	37,6	32,8	67,2	1,2702703	1,05	-43,3	-43,3	0,0679038	8,54	-34,64	-1,0560976
spe-MIR7990b	**217**	13,824885	33,179724	17,97235	35,023041	31,797235	68,202765	1,0555556	0,7692308	-53,5	-52,9	0,0001197	18,21	-24,654378	-0,7753623
spe-MIR7992-1	**305**	14,42623	39,016393	16,721311	29,836066	31,147541	68,852459	0,7647059	0,8627451	-84,3	-83,3	0,001455	23,46	-27,639344	-0,8873684
spe-MIR7992-10	**151**	23,178808	27,152318	15,89404	33,774834	39,072848	60,927152	1,2439024	1,4583333	-43,8	-41,7	0,0169534	14,05	-29,006623	-0,7423729
spe-MIR7992-11	**259**	16,216216	31,274131	21,621622	30,888031	37,837838	62,162162	0,9876543	0,75	-80,6	-66,09	0,0019001	62,27	-31,119691	-0,822449
spe-MIR7992-12	**217**	15,207373	35,9447	16,129032	32,718894	31,336406	68,663594	0,9102564	0,9428571	-76,7	-76,7	0,0382663	8,13	-35,345622	-1,1279412
spe-MIR7992-13	**211**	17,061611	32,227488	17,061611	33,649289	34,123223	65,876777	1,0441176	1	-73,1	-70,6	0,0141029	8,67	-34,64455	-1,0152778
spe-MIR7992-14	**210**	15,238095	36,666667	17,142857	30,952381	32,380952	67,619048	0,8441558	0,8888889	-68,3	-67,5	0,0092965	11,79	-32,52381	-1,0044118
spe-MIR7992-15	**222**	18,468468	28,828829	15,315315	37,387387	33,783784	66,216216	1,296875	1,2058824	-73,4	-72,1	0,0037343	30,87	-33,063063	-0,9786667
spe-MIR7992-16	**238**	14,285714	36,97479	18,907563	29,831933	33,193277	66,806723	0,8068182	0,7555556	-72	-72	0,0040331	11,82	-30,252101	-0,9113924
spe-MIR7992-18	**234**	14,529915	36,324786	17,948718	31,196581	32,478632	67,521368	0,8588235	0,8095238	-68,7	-62,1	0,0021674	31,93	-29,358974	-0,9039474
spe-MIR7992-19	**209**	17,703349	39,23445	12,91866	30,143541	30,62201	69,37799	0,7682927	1,3703704	-74	-74	0,0148795	18,22	-35,406699	-1,15625
spe-MIR7992-2	**185**	14,054054	36,756757	18,378378	30,810811	32,432432	67,567568	0,8382353	0,7647059	-54,9	-55,01	0,0148124	13,13	-29,675676	-0,915
spe-MIR7992-3	**208**	21,634615	29,807692	19,711538	28,846154	41,346154	58,653846	0,9677419	1,097561	-73,5	-69,58	0,0032707	38,7	-35,336538	-0,8546512
spe-MIR7992-4	**238**	17,647059	31,932773	13,02521	37,394958	30,672269	69,327731	1,1710526	1,3548387	-74,5	-66,2	0,0009497	43,62	-31,302521	-1,0205479
spe-MIR7992-5	**125**	26,4	23,2	20,8	29,6	47,2	52,8	1,2758621	1,2692308	-91,5	-89,9	0,371929	1,33	-73,2	-1,5508475
spe-MIR7992-6	**195**	14,871795	37,435897	16,923077	30,769231	31,794872	68,205128	0,8219178	0,8787879	-69,1	-69,1	0,0413782	9,52	-35,435897	-1,1145161
spe-MIR7992-7	**248**	16,935484	34,677419	22,983871	25,403226	39,919355	60,080645	0,7325581	0,7368421	-83,6	-77,7	0,0016145	22,87	-33,709677	-0,8444444
spe-MIR7992-8	**237**	18,987342	27,42616	22,362869	31,223629	41,350211	58,649789	1,1384615	0,8490566	-77,5	-72,24	0,0135081	54,82	-32,700422	-0,7908163
spe-MIR7992-9	**208**	19,711538	28,846154	21,634615	29,807692	41,346154	58,653846	1,0333333	0,9111111	-84,5	-84,5	0,102421	12,1	-40,625	-0,9825581
spe-MIR7993b	**276**	18,115942	28,623188	18,115942	35,144928	36,231884	63,768116	1,2278481	1	-87,2	-81,42	0,000135	33,99	-31,594203	-0,872
spe-MIR7993d-1	**177**	16,949153	31,638418	16,949153	34,463277	33,898305	66,101695	1,0892857	1	-51,8	-45,2	0,0015097	18,51	-29,265537	-0,8633333
spe-MIR7993d-2	**239**	18,828452	36,401674	11,297071	33,472803	30,125523	69,874477	0,9195402	1,6666667	-51,3	-43,2	0,001013	62,74	-21,464435	-0,7125
spe-MIR7997b-1	**184**	17,934783	30,434783	17,934783	33,695652	35,869565	64,130435	1,1071429	1	-48,6	-44,8	0,0050777	31,25	-26,413043	-0,7363636
spe-MIR7997b-2	**147**	25,85034	26,530612	18,367347	29,251701	44,217687	55,782313	1,1025641	1,4074074	-61	-60,7	0,0650761	7,93	-41,496599	-0,9384615
spe-MIR7997b-3	**128**	26,5625	26,5625	18,75	28,125	45,3125	54,6875	1,0588235	1,4166667	-65	-63,7	0,0342332	9,28	-50,78125	-1,1206897
spe-MIR7997c-1	**141**	23,404255	32,624113	14,184397	29,787234	37,588652	62,411348	0,9130435	1,65	-60,1	-60,1	0,075321	6,91	-42,624113	-1,1339623
spe-MIR7997c-10	**124**	21,774194	29,83871	17,741935	30,645161	39,516129	60,483871	1,027027	1,2272727	-66,3	-65,9	0,0779504	7	-53,467742	-1,3530612
spe-MIR7997c-11	**136**	21,323529	32,352941	19,117647	27,205882	40,441176	59,558824	0,8409091	1,1153846	-61,6	-61,6	0,22392	4,72	-45,294118	-1,12
spe-MIR7997c-12	**138**	21,014493	28,985507	20,289855	29,710145	41,304348	58,695652	1,025	1,0357143	-64,4	-63,9	0,083581	10,23	-46,666667	-1,1298246
spe-MIR7997c-13	**148**	20,945946	30,405405	20,27027	28,378378	41,216216	58,783784	0,9333333	1,0333333	-51,1	-47,7	0,0600041	9,99	-34,527027	-0,8377049
spe-MIR7997c-2	**126**	22,222222	26,190476	20,634921	30,952381	42,857143	57,142857	1,1818182	1,0769231	-63,7	-63,7	0,14201	4,21	-50,555556	-1,1796296
spe-MIR7997c-3	**95**	18,947368	29,473684	22,105263	29,473684	41,052632	58,947368	1	0,8571429	-33,1	-33,1	0,0923641	8,16	-34,842105	-0,8487179
spe-MIR7997c-4	**110**	18,181818	30,909091	20	30,909091	38,181818	61,818182	1	0,9090909	-33,8	-32,5	0,0495805	10,22	-30,727273	-0,8047619
spe-MIR7997c-5	**135**	28,148148	25,925926	20,740741	25,185185	48,888889	51,111111	0,9714286	1,3571429	-79,7	-79,7	0,288205	3,27	-59,037037	-1,2075758
spe-MIR7997c-6	**98**	18,367347	26,530612	21,428571	33,673469	39,795918	60,204082	1,2692308	0,8571429	-31,4	-30,5	0,0304848	11,31	-32,040816	-0,8051282
spe-MIR7997c-7	**109**	21,100917	27,522936	22,018349	29,357798	43,119266	56,880734	1,0666667	0,9583333	-42,2	-39,3	0,10088	9,57	-38,715596	-0,8978723
spe-MIR7997c-8	**130**	27,692308	26,153846	20	26,153846	47,692308	52,307692	1	1,3846154	-66,2	-66	0,0461473	5,75	-50,923077	-1,0677419
spe-MIR7997c-9	**125**	27,2	22,4	19,2	31,2	46,4	53,6	1,3928571	1,4166667	-62,9	-60	0,0784014	11,58	-50,32	-1,0844828
spe-MIR7998	**231**	23,809524	28,138528	21,212121	26,839827	45,021645	54,978355	0,9538462	1,122449	-75,1	-67,6	0,0016351	45,87	-32,510823	-0,7221154
spe-MIR8001a-1	**175**	13,142857	37,142857	17,714286	32	30,857143	69,142857	0,8615385	0,7419355	-77,4	-75,5	0,0454348	9,18	-44,228571	-1,4333333
spe-MIR8001a-2	**144**	17,361111	29,166667	16,666667	36,805556	34,027778	65,972222	1,2619048	1,0416667	-72,8	-72	0,136319	6,44	-50,555556	-1,4857143
spe-MIR8001b-1	**142**	15,492958	35,211268	16,901408	32,394366	32,394366	67,605634	0,92	0,9166667	-75,8	-75,8	0,0678798	4,4	-53,380282	-1,6478261
spe-MIR8001b-2	**341**	20,821114	38,416422	13,196481	27,565982	34,017595	65,982405	0,7175573	1,5777778	-87,2	-85,2	0,0001359	28,98	-25,571848	-0,7517241
spe-MIR8001b-3	**90**	20	37,777778	13,333333	28,888889	33,333333	66,666667	0,7647059	1,5	-34,1	-34,1	0,32729	5,28	-37,888889	-1,1366667
spe-MIR8001b-4	**177**	16,384181	36,158192	16,384181	31,073446	32,768362	67,231638	0,859375	1	-63,3	-60,3	0,0169978	9,83	-35,762712	-1,0913793
spe-MIR8005b	**216**	14,814815	30,555556	15,740741	38,888889	30,555556	69,444444	1,2727273	0,9411765	-63,4	-56,79	0,001425	35,3	-29,351852	-0,9606061
spe-MIR8005c	**170**	30	21,764706	7,6470588	40,588235	37,647059	62,352941	1,8648649	3,9230769	-61,2	-61,1	0,0125856	35,46	-36	-0,95625
spe-MIR8006-1	**199**	18,592965	31,155779	22,110553	28,140704	40,703518	59,296482	0,9032258	0,8409091	-76,1	-74,2	0,0028567	13,61	-38,241206	-0,9395062
spe-MIR8006-10	**325**	15,076923	34,461538	16,615385	33,846154	31,692308	68,307692	0,9821429	0,9074074	-86,2	-74,8	0,0001122	50,81	-26,523077	-0,8368932
spe-MIR8006-11	**256**	16,796875	33,203125	17,1875	32,8125	33,984375	66,015625	0,9882353	0,9772727	-90,9	-88,3	0,0012669	24,68	-35,507813	-1,0448276
spe-MIR8006-2	**208**	15,384615	34,134615	18,75	31,730769	34,134615	65,865385	0,9295775	0,8205128	-60,8	-52,8	0,002123	24,34	-29,230769	-0,856338
spe-MIR8006-3	**221**	17,647059	33,484163	18,552036	30,316742	36,199095	63,800905	0,9054054	0,9512195	-62,2	-50,2	0,0015033	45,58	-28,144796	-0,7775
spe-MIR8006-4	**237**	17,721519	29,535865	19,409283	33,333333	37,130802	62,869198	1,1285714	0,9130435	-98,3	-96,6	0,0204166	9,96	-41,476793	-1,1170455
spe-MIR8006-5	**171**	14,619883	32,748538	17,54386	35,087719	32,163743	67,836257	1,0714286	0,8333333	-49,7	-46,19	0,0062013	20,96	-29,064327	-0,9036364
spe-MIR8006-6	**169**	21,893491	29,585799	16,568047	31,952663	38,461538	61,538462	1,08	1,3214286	-73,2	-73,2	0,287631	3,36	-43,313609	-1,1261538
spe-MIR8006-7	**221**	17,19457	30,769231	19,004525	33,031674	36,199095	63,800905	1,0735294	0,9047619	-90,4	-90,4	0,0185178	16,49	-40,904977	-1,13
spe-MIR8006-8	**174**	20,114943	28,16092	24,712644	27,011494	44,827586	55,172414	0,9591837	0,8139535	-95,5	-92,2	0,165066	5,66	-54,885057	-1,224359

spe-MIR8006-9	**269**	20,074349	28,996283	15,241636	35,687732	35,315985	64,684015	1,2307692	1,3170732	-69,4	-67,7	0,0001547	37,84	-25,799257	-0,7305263
spe-MIR8007a	**268**	14,179104	33,208955	16,044776	36,567164	30,223881	69,776119	1,1011236	0,8837209	-80,1	-75,4	0,0009212	29,31	-29,88806	-0,9888889
spe-MIR8008b-1	**54**	25,925926	24,074074	22,222222	27,777778	48,148148	51,851852	1,1538462	1,1666667	-35	-35	0,295605	2,4	-64,814815	-1,3461538
spe-MIR8008b-2	**194**	17,525773	31,443299	19,072165	31,958763	36,597938	63,402062	1,0163934	0,9189189	-73,9	-73,9	0,0203015	12,64	-38,092784	-1,0408451
spe-MIR8008b-3	**115**	17,391304	31,304348	18,26087	33,043478	35,652174	64,347826	1,0555556	0,952381	-45,1	-42,7	0,0489642	10,47	-39,217391	-1,1
spe-MIR8008b-4	**127**	17,322835	28,346457	18,110236	36,220472	35,433071	64,566929	1,2777778	0,9565217	-42,6	-40,8	0,0105015	19,08	-33,543307	-0,9466667
spe-MIR8009-1	**154**	14,935065	30,519481	21,428571	33,116883	36,363636	63,636364	1,0851064	0,6969697	-49,7	-45,7	0,0225628	11,33	-32,272727	-0,8875
spe-MIR8009-2	**130**	20	28,461538	16,923077	34,615385	36,923077	63,076923	1,2162162	1,1818182	-49,6	-49,6	0,0160238	11,71	-38,153846	-1,0333333
spe-MIR8009-3	**206**	19,417476	35,436893	15,048544	30,097087	34,466019	65,533981	0,8493151	1,2903226	-55	-28,8	0,0023639	78,49	-26,699029	-0,7746479
spe-MIR8011a-1	**99**	18,181818	30,30303	23,232323	28,282828	41,414141	58,585859	0,9333333	0,7826087	-50,2	-50,2	0,400147	1,79	-50,707071	-1,2243902
spe-MIR8011a-2	**97**	22,680412	27,835052	18,556701	30,927835	41,237113	58,762887	1,1111111	1,2222222	-50,9	-50,9	0,274503	3,31	-52,474227	-1,2725
spe-MIR8011a-3	**168**	19,642857	29,166667	18,452381	32,738095	38,095238	61,904762	1,122449	1,0645161	-66,1	-65,7	0,0185356	12,98	-39,345238	-1,0328125
spe-MIR8011a-4	**147**	21,768707	29,251701	17,687075	31,292517	39,455782	60,544218	1,0697674	1,2307692	-84,8	-83,8	0,134711	7,84	-57,687075	-1,462069
spe-MIR8011b	**101**	15,841584	34,653465	19,80198	29,70297	35,643564	64,356436	0,8571429	0,8	-37,4	-35,67	0,0884615	8,95	-37,029703	-1,0388889
spe-MIR8013	**204**	18,137255	33,333333	15,686275	32,843137	33,823529	66,176471	0,9852941	1,15625	-81,9	-79,7	0,0011815	24,29	-40,147059	-1,1869565
spe-MIR8014	**209**	18,181818	27,272727	17,703349	36,842105	35,885167	64,114833	1,3508772	1,027027	-91,5	-91,5	0,10181	7,43	-43,779904	-1,22
spe-MIR8016	**172**	14,534884	31,976744	15,697674	37,790698	30,232558	69,767442	1,1818182	0,9259259	-63,9	-62,8	0,0714572	6,87	-37,151163	-1,2288462
spe-MIR8019-1	**270**	19,62963	37,037037	12,222222	31,111111	31,851852	68,148148	0,84	1,6060606	-65,1	-58	0,0001195	48,19	-24,111111	-0,7569767
spe-MIR8019-2	**258**	18,604651	36,046512	12,790698	32,55814	31,395349	68,604651	0,9032258	1,4545455	-70,3	-39,88	0,0010682	83,03	-27,248062	-0,8679012
spe-MIR8019-3	**266**	18,421053	36,842105	13,909774	30,827068	32,330827	67,669173	0,8367347	1,3243243	-75	-60,5	0,0021122	57,55	-28,195489	-0,872093
spe-MIR8020-1	**88**	15,909091	38,636364	14,772727	30,681818	30,681818	69,318182	0,7941176	1,0769231	-32	-32	0,231983	3,42	-36,363636	-1,1851852
spe-MIR8020-2	**188**	18,085106	32,446809	17,021277	32,446809	35,106383	64,893617	1	1,0625	-52,5	-51,5	0,0012937	21,7	-27,925532	-0,7954545
spe-MIR8021	**226**	15,044248	31,858407	16,371681	36,725664	31,415929	68,584071	1,1527778	0,9189189	-71,9	-65,97	0,0023074	33,09	-31,814159	-1,0126761
spe-MIR8024b-1	**85**	23,529412	28,235294	15,294118	32,941176	38,823529	61,176471	1,1666667	1,5384615	-24	-24	0,072726	5,16	-28,235294	-0,7272727
spe-MIR8024b-2	**243**	19,753086	33,333333	15,63786	31,27572	35,390947	64,609053	0,9382716	1,2631579	-62	-55,2	0,0006413	53,56	-25,514403	-0,7209302
spe-MIR8025	**137**	12,408759	35,036496	18,248175	34,306569	30,656934	69,343066	0,9791667	0,68	-56,1	-56,1	0,345907	3,73	-40,948905	-1,3357143
spe-MIR8026	**124**	23,387097	29,032258	17,741935	29,83871	41,129032	58,870968	1,0277778	1,3181818	-39,4	-38,2	0,0105642	19,12	-31,774194	-0,772549
spe-MIR8029	**236**	16,949153	33,050847	13,559322	36,440678	30,508475	69,491525	1,1025641	1,25	-55,1	-49,9	0,0016839	28,5	-23,347458	-0,7652778
spe-MIR8030-1	**106**	17,924528	36,792453	16,037736	29,245283	33,962264	66,037736	0,7948718	1,1176471	-32,5	-21,1	0,0175157	30,38	-30,660377	-0,9027778
spe-MIR8030-2	**137**	18,978102	36,49635	18,978102	25,547445	37,956204	62,043796	0,7	1	-47,1	-44,7	0,0145154	16,83	-34,379562	-0,9057692
spe-MIR8030-3	**73**	16,438356	30,136986	17,808219	35,616438	34,246575	65,753425	1,1818182	0,9230769	-22,7	-22,2	0,184762	7,62	-31,09589	-0,908
spe-MIR8032e	**283**	22,614841	25,088339	18,374558	33,922261	40,989399	59,010601	1,3521127	1,2307692	-89	-80,4	0,0001753	50,88	-31,448763	-0,7672414
spe-MIR8036	**86**	23,255814	32,55814	11,627907	32,55814	34,883721	65,116279	1	2	-28	-25,9	0,0679914	15,77	-32,55814	-0,9333333
spe-MIR8038b-1	**97**	19,587629	31,958763	17,525773	30,927835	37,113402	62,886598	0,9677419	1,1176471	-38,1	-38,1	0,294566	7,4	-39,278351	-1,0583333
spe-MIR8038b-2	**98**	17,346939	28,571429	21,428571	32,653061	38,77551	61,22449	1,1428571	0,8095238	-27,2	-27,2	0,200082	4,53	-27,755102	-0,7157895
spe-MIR8039-1	**194**	14,948454	32,474227	19,587629	32,989691	34,536082	65,463918	1,015873	0,7631579	-65,7	-63,6	0,0149731	14,68	-33,865979	-0,980597
spe-MIR8039-2	**142**	24,647887	33,802817	12,676056	28,873239	37,323944	62,676056	0,8541667	1,9444444	-56,8	-53,1	0,0621646	9,51	-40	-1,0716981
spe-MIR8042	**158**	12,658228	36,708861	18,35443	32,278481	31,012658	68,987342	0,8793103	0,6896552	-38,3	-36,2	0,0482052	19,26	-24,240506	-0,7816327
spe-MIR8045-1	**234**	22,649573	31,623932	12,393162	33,333333	35,042735	64,957265	1,0540541	1,8275862	-73,1	-70,4	0,000824	38,28	-31,239316	-0,8914634
spe-MIR8045-2	**262**	17,175573	29,770992	16,793893	36,259542	33,969466	66,030534	1,2179487	1,0227273	-67,4	-52,8	8,14E-05	47,26	-25,725191	-0,7573034
spe-MIR8047	**208**	17,307692	31,730769	19,230769	31,730769	36,538462	63,461538	1	0,9	-69,3	-62,1	0,0010112	23,38	-33,317308	-0,9118421
spe-MIR8050	**204**	26,960784	27,941176	23,039216	22,058824	50	50	0,7894737	1,1702128	-74,8	-67,97	0,009067	20,89	-36,666667	-0,7333333
spe-MIR8051-1	**248**	15,322581	26,209677	16,129032	42,33871	31,451613	68,548387	1,6153846	0,95	-56,4	-47	0,0027172	55,57	-22,741935	-0,7230769
spe-MIR8051-2	**334**	19,161677	34,431138	15,269461	31,137725	34,431138	65,568862	0,9043478	1,254902	-83,3	-58,45	2,71E-05	85,19	-24,94012	-0,7243478
spe-MIR8126	**140**	17,142857	37,142857	13,571429	32,142857	30,714286	69,285714	0,8653846	1,2631579	-36	-29,9	0,019909	44,72	-25,714286	-0,8372093
spe-MIR8142	**195**	17,948718	35,897436	15,384615	30,769231	33,333333	66,666667	0,8571429	1,1666667	-81,2	-77,34	0,0575934	7,52	-41,641026	-1,2492308
spe-MIR8154	**187**	28,877005	27,807487	21,925134	21,390374	50,802139	49,197861	0,7692308	1,3170732	-67,7	-58,4	0,0081558	27,46	-36,203209	-0,7126316
spe-MIR8175-1	**237**	16,877637	35,864979	18,14346	29,113924	35,021097	64,978903	0,8117647	0,9302326	-69,3	-67	0,0004234	27,82	-29,240506	-0,8349398
spe-MIR8175-2	**173**	21,965318	24,855491	21,965318	29,479769	43,930636	54,33526	1,1860465	1	-93,7	-91,6	0,133943	20,41	-54,16185	-1,2328947
spe-MIR8181	**198**	22,222222	28,787879	13,131313	35,858586	35,353535	64,646465	1,245614	1,6923077	-53,7	-41,9	0,0027357	37,06	-27,121212	-0,7671429
spe-MIR821c	**225**	18,666667	34,666667	13,333333	33,333333	32	68	0,9615385	1,4	-55,4	-52	0,0029171	31,48	-24,622222	-0,7694444
spe-MIR821e	**142**	21,126761	33,802817	9,8591549	35,211268	30,985915	69,014085	1,0416667	2,1428571	-44,7	-42,9	0,0139392	18,47	-31,478873	-1,0159091
spe-MIR827-1	**88**	14,772727	32,954545	15,909091	36,363636	30,681818	69,318182	1,1034483	0,9285714	-33,5	-33,5	0,106373	10,78	-38,068182	-1,2407407
spe-MIR827-2	**151**	19,205298	36,423841	19,205298	25,165563	38,410596	61,589404	0,6909091	1	-63,1	-63,1	0,0370405	12,36	-41,788079	-1,087931
spe-MIR828b	**119**	17,647059	29,411765	16,806723	36,134454	34,453782	65,546218	1,2285714	1,05	-48,2	-48,2	0,0901791	5,37	-40,504202	-1,1756098
spe-MIR830	**104**	23,076923	34,615385	13,461538	28,846154	36,538462	63,461538	0,8333333	1,7142857	-27,5	-20,7	0,0242152	15,97	-26,442308	-0,7236842
spe-MIR833a	**242**	16,115702	34,297521	14,876033	34,710744	30,991736	69,008264	1,0120482	1,0833333	-54,5	-44,9	0,0009757	41,84	-22,520661	-0,7266667
spe-MIR837	**271**	21,402214	24,723247	13,284133	40,590406	34,686347	65,313653	1,641791	1,6111111	-66,7	-61	8,97E-05	50,06	-24,612546	-0,7095745
spe-MIR838	**285**	19,298246	28,421053	15,438596	36,842105	34,736842	65,263158	1,2962963	1,25	-71,1	-66,1	0,0009707	45,25	-24,947368	-0,7181818
spe-MIR840	**144**	19,444444	34,027778	13,888889	32,638889	33,333333	66,666667	0,9591837	1,4	-39,5	-24,7	0,003582	36,12	-27,430556	-0,8229167
spe-MIR847	**222**	27,927928	26,576577	20,720721	24,774775	48,648649	51,351351	0,9322034	1,3478261	-78,3	-75	0,0045762	46,02	-35,27027	-0,725
spe-MIR852-1	**138**	14,492754	34,782609	16,666667	34,057971	31,15942	68,84058	0,9791667	0,8695652	-56,9	-53,9	0,0112295	10,91	-41,231884	-1,3232558

spe-MIR852-2	**122**	23,770492	25,409836	26,229508	24,590164	50	50	0,9677419	0,90625	-99,3	-99,3	0,132076	3,95	-81,393443	-1,6278689
spe-MIR856	**128**	17,96875	32,03125	15,625	34,375	33,59375	66,40625	1,0731707	1,15	-32,4	-31,8	0,0036575	17,32	-25,3125	-0,7534884
spe-MIR863-1	**170**	15,882353	35,294118	15,882353	32,941176	31,764706	68,235294	0,9333333	1	-57	-54,9	0,0030241	17,66	-33,529412	-1,0555556
spe-MIR863-2	**135**	17,037037	28,888889	17,777778	36,296296	34,814815	65,185185	1,2564103	0,9583333	-33,4	-31,1	0,0138475	20,66	-24,740741	-0,7106383
spe-MIR8639e	**239**	16,317992	35,564854	14,225941	33,891213	30,543933	69,456067	0,9529412	1,1470588	-67,1	-66	0,0175272	28,11	-28,075314	-0,9191781
spe-MIR865-1	**187**	17,647059	27,807487	14,438503	40,106952	32,085561	67,914439	1,4423077	1,2222222	-43,5	-37	0,0011832	28,46	-23,262032	-0,725
spe-MIR8652	**308**	16,233766	30,519481	16,233766	37,012987	32,467532	67,532468	1,212766	1	-80	-77,8	0,0029837	41,66	-25,974026	-0,8
spe-MIR865-2	**166**	14,457831	38,554217	16,86747	30,120482	31,325301	68,674699	0,78125	0,8571429	-45,7	-42,74	0,0056753	15,34	-27,53012	-0,8788462
spe-MIR8668	**86**	25,581395	31,395349	11,627907	31,395349	37,209302	62,790698	1	2,2	-24,5	-24,3	0,486608	5,02	-28,488372	-0,765625
spe-MIR8695	**87**	22,988506	31,034483	9,1954023	36,781609	32,183908	67,816092	1,1851852	2,5	-21,2	-21,2	0,0243355	11,39	-24,367816	-0,7571429
spe-MIR8713	**158**	22,151899	32,278481	10,759494	34,810127	32,911392	67,088608	1,0784314	2,0588235	-45,9	-45,9	0,0117075	15,59	-29,050633	-0,8826923
spe-MIR8726	**126**	23,809524	39,68254	7,9365079	28,571429	31,746032	68,253968	0,72	3	-29	-26,2	0,0250295	29,94	-23,015873	-0,725
spe-MIR8739-1	**176**	21,590909	31,25	15,909091	31,25	37,5	62,5	1	1,3571429	-80,3	-77,5	0,0080543	9,77	-45,625	-1,2166667
spe-MIR8739-2	**223**	21,973094	30,044843	17,040359	30,941704	39,013453	60,986547	1,0298507	1,2894737	-88,7	-82,3	0,0234155	11,55	-39,775785	-1,0195402
spe-MIR8742b	**312**	16,025641	33,653846	16,666667	33,653846	32,692308	67,307692	1	0,9615385	-92,5	-92,5	0,0162346	16,83	-29,647436	-0,9068627
spe-MIR8752	**295**	24,40678	24,745763	21,355932	29,491525	45,762712	54,237288	1,1917808	1,1428571	-97,8	-95	0,0003616	33,03	-33,152542	-0,7244444
spe-MIR8762c	**86**	23,255814	32,55814	11,627907	32,55814	34,883721	65,116279	1	2	-23,7	-23,7	0,340226	6,76	-27,55814	-0,79
spe-MIR8766	**76**	21,052632	36,842105	17,105263	25	38,157895	61,842105	0,6785714	1,2307692	-21,8	-21,7	0,168979	4,16	-28,684211	-0,7517241
spe-MIR902g	**112**	16,964286	26,785714	16,071429	40,178571	33,035714	66,964286	1,5	1,0555556	-44,4	-44,4	0,214749	4,2	-39,642857	-1,2
spe-MIR902i	**108**	16,666667	35,185185	13,888889	34,259259	30,555556	69,444444	0,9736842	1,2	-33,2	-33,2	0,0694763	3,85	-30,740741	-1,0060606
spe-MIR917	**214**	18,224299	28,504673	16,35514	36,915888	34,579439	65,420561	1,295082	1,1142857	-97,4	-97,4	0,120323	7,65	-45,514019	-1,3162162
spe-MIR9469	**141**	22,695035	29,078014	21,276596	26,950355	43,971631	56,028369	0,9268293	1,0666667	-85,1	-85,1	0,191857	4,69	-60,35461	-1,3725806
spe-MIR9471a	**154**	23,376623	33,116883	11,688312	31,818182	35,064935	64,935065	0,9607843	2	-53	-49,99	0,019786	15,07	-34,415584	-0,9814815
spe-MIR9471b	**147**	24,489796	29,931973	14,285714	31,292517	38,77551	61,22449	1,0454545	1,7142857	-64,5	-64,4	0,056318	9,57	-43,877551	-1,1315789
spe-MIR9473-1	**178**	19,101124	32,022472	19,662921	29,213483	38,764045	61,235955	0,9122807	0,9714286	-56,8	-47,8	0,0037896	33,8	-31,910112	-0,8231884
spe-MIR9473-2	**178**	19,662921	29,213483	19,101124	32,022472	38,764045	61,235955	1,0961538	1,0294118	-63,9	-55,69	0,0059442	35,25	-35,898876	-0,926087
spe-MIR9475	**330**	20,30303	34,545455	14,242424	30,909091	34,545455	65,454545	0,8947368	1,4255319	-84,6	-58,9	2,57E-05	94,8	-25,636364	-0,7421053
spe-MIR9476-1	**108**	15,740741	33,333333	17,592593	33,333333	33,333333	66,666667	1	0,8947368	-58,4	-58,4	0,429571	1,75	-54,074074	-1,6222222
spe-MIR9476-2	**110**	17,272727	33,636364	16,363636	32,727273	33,636364	66,363636	0,972973	1,0555556	-64,8	-64,8	0,642104	1,56	-58,909091	-1,7513514
spe-MIR9477-1	**154**	19,480519	29,87013	18,181818	31,818182	37,662338	61,688312	1,0652174	1,0714286	-92,3	-86,7	0,0769943	9,4	-59,935065	-1,5913793
spe-MIR9477-2	**237**	20,675105	34,177215	16,033755	29,113924	36,708861	63,291139	0,8518519	1,2894737	-77,1	-58,57	0,0012807	43,26	-32,531646	-0,8862069
spe-MIR9477-3	**121**	21,487603	28,099174	14,049587	36,363636	35,53719	64,46281	1,2941176	1,5294118	-32,5	-31,6	0,087224	13,32	-26,859504	-0,755814
spe-MIR9478-1	**207**	17,874396	33,816425	15,942029	32,36715	33,816425	66,183575	0,9571429	1,1212121	-90,2	-88,4	0,0143954	10,33	-43,574879	-1,2885714
spe-MIR9478-2	**251**	13,944223	34,262948	16,733068	35,059761	30,677291	69,322709	1,0232558	0,8333333	-95,7	-92,8	0,0010142	23,75	-38,12749	-1,2428571
spe-MIR9497	**225**	20	29,777778	14,666667	35,555556	34,666667	65,333333	1,1940299	1,3636364	-71,6	-70,5	0,0017017	29,55	-31,822222	-0,9179487
spe-MIR9555b	**273**	18,681319	34,065934	14,285714	32,967033	32,967033	67,032967	0,9677419	1,3076923	-67,1	-53,31	4,54E-05	73,07	-24,578755	-0,7455556
spe-MIR9562-1	**324**	19,135802	33,641975	14,506173	32,716049	33,641975	66,358025	0,9724771	1,3191489	-96	-72,6	4,83E-05	72,36	-29,62963	-0,8807339
spe-MIR9562-2	**243**	17,283951	28,806584	16,872428	37,037037	34,156379	65,843621	1,2857143	1,0243902	-62	-58,9	0,0036004	41,52	-25,514403	-0,746988
spe-MIR9563b	**201**	19,900498	33,830846	17,412935	28,855721	37,313433	62,686567	0,8529412	1,1428571	-79,7	-70,9	0,00529	23,29	-39,651741	-1,0626667
spe-MIR9670	**114**	21,052632	30,701754	13,157895	35,087719	34,210526	65,789474	1,1428571	1,6	-30,4	-28	0,0981234	13,9	-26,666667	-0,7794872
spe-MIR9674c	**108**	15,740741	29,62963	15,740741	38,888889	31,481481	68,518519	1,3125	1	-68,5	-68,5	0,410942	1,59	-63,425926	-2,0147059
spe-MIR9679-1	**130**	16,153846	36,923077	14,615385	32,307692	30,769231	69,230769	0,875	1,1052632	-36,9	-36,9	0,108323	8,02	-28,384615	-0,9225
spe-MIR9679-2	**141**	13,475177	38,297872	17,730496	30,496454	31,205674	68,794326	0,7962963	0,76	-33,9	-33,5	0,0664609	12,8	-24,042553	-0,7704545
spe-MIR9679-3	**141**	14,893617	38,297872	15,602837	31,205674	30,496454	69,503546	0,8148148	0,9545455	-34,5	-34,5	0,0414769	8,14	-24,468085	-0,8023256
spe-MIR9679-4	**192**	18,229167	34,375	15,104167	31,770833	33,333333	66,145833	0,9242424	1,2068966	-47,7	-41,01	0,0342777	64,76	-24,84375	-0,7453125
spe-MIR9736-1	**165**	15,151515	33,939394	16,363636	34,545455	31,515152	68,484848	1,0178571	0,9259259	-97,6	-97,6	0,19519	3,57	-59,151515	-1,8769231
spe-MIR9736-2	**331**	25,679758	31,117825	13,897281	29,305136	39,577039	60,422961	0,9417476	1,8478261	-94,8	-92,3	0,0002384	25,94	-28,640483	-0,7236641
spe-MIR9752	**205**	17,073171	28,780488	14,634146	39,512195	31,707317	68,292683	1,3728814	1,1666667	-59,3	-58,2	0,0068827	16,36	-28,926829	-0,9123077
spe-MIR9758	**209**	19,617225	26,794258	17,703349	35,885167	37,320574	62,679426	1,3392857	1,1081081	-66,2	-62,7	0,0025975	26,04	-31,674641	-0,8487179
spe-MIR9760	**256**	19,53125	30,46875	12,890625	37,109375	32,421875	67,578125	1,2179487	1,5151515	-64,4	-43,7	8,98E-05	79,95	-25,15625	-0,7759036
spe-MIR9773-1	**260**	13,846154	36,153846	17,307692	32,692308	31,153846	68,846154	0,9042553	0,8	-68,6	-66,4	0,0003739	25,12	-26,384615	-0,8469136
spe-MIR9773-2	**226**	19,911504	26,548673	17,699115	35,840708	37,610619	62,389381	1,35	1,125	-82,7	-73,6	0,0077011	28,1	-36,59292	-0,9729412
spe-MIR9779	**175**	14,285714	35,428571	17,714286	32,571429	32	68	0,9193548	0,8064516	-48	-46,6	0,0275793	25,77	-27,428571	-0,8571429

Supplementary Table S16. Thermodynamic and structural characterization of *Solanum galapagense* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Size	G content	A content	C content	U content	GC content	AU content	UA-ratio	GC-ratio	MFE	MFEE	Freq	Div	AMFE	MFEI
sga-MIR10186e	205	20,4878049	36,097561	13,6585366	29,7560976	34,1463415	65,8536585	0,82432432	1,5	-53	-52	0,00409879	18,24	-25,853659	-0,7571429
sga-MIR10186l	339	16,519174	36,8731563	15,9292035	30,6784661	32,4483776	67,5516224	0,832	1,03703704	-79,8	-78	0,00030973	53,2	-23,539823	-0,7254545
sga-MIR10202b-1	83	24,0963855	20,4819277	21,686747	33,7349398	45,7831325	54,2168675	1,64705882	1,11111111	-30,2	-29,8	0,0812552	14,35	-36,385542	-0,7947368
sga-MIR10202b-2	92	20,6521739	25	18,4782609	35,8695652	39,1304348	60,8695652	1,43478261	1,11764706	-25,6	-25,2	0,133117	10,09	-27,826087	-0,7111111
sga-MIR10224	264	21,2121212	34,469697	12,1212121	32,1969697	33,3333333	66,6666667	0,93406593	1,75	-66,9	-59,8	0,00039716	40,22	-25,340909	-0,7602273
sga-MIR1027c	134	20,8955224	26,119403	22,3880597	30,5970149	43,2835821	56,7164179	1,17142857	0,93333333	-93,1	-93,1	0,416422	3,78	-69,477612	-1,6051724
sga-MIR10405d	267	19,1011236	29,588015	13,1086142	38,2022472	32,2097378	67,7902622	1,29113924	1,45714286	-72,8	-63,7	3,82E-05	90,73	-27,265918	-0,8465116
sga-MIR10436	196	20,9183673	27,5510204	18,3673469	33,1632653	39,2857143	60,7142857	1,2037037	1,13888889	-99,3	-98,2	0,0195999	11,76	-50,663265	-1,2896104
sga-MIR1044	245	12,244898	38,3673469	20,4081633	28,9795918	32,6530612	67,3469388	0,75531915	0,6	-57,4	-51,3	0,00327325	20,35	-23,428571	-0,7175
sga-MIR10442	180	16,6666667	28,3333333	22,7777778	32,2222222	39,4444444	60,5555556	1,1372549	0,73170732	-57,3	-53,4	0,0163692	22,53	-31,833333	-0,8070423
sga-MIR10448	281	24,911032	25,9786477	15,3024911	33,8078292	40,2135231	59,7864769	1,30136986	1,62790698	-79,3	-40,3	4,14E-05	68,81	-28,220641	-0,7017699
sga-MIR1048	250	16	31,2	16,4	36,4	32,4	67,6	1,16666667	0,97560976	-78,5	-74,7	0,00303934	19,02	-31,4	-0,9691358
sga-MIR10528	95	17,8947368	34,7368421	16,8421053	30,5263158	34,7368421	65,2631579	0,87878788	1,0625	-40,6	-40,6	0,0558446	6,29	-42,736842	-1,230303
sga-MIR10529-1	134	23,1343284	26,119403	23,1343284	27,6119403	46,2686567	53,7313433	1,05714286	1	-45,9	-43,5	0,0769176	13,68	-34,253731	-0,7403226
sga-MIR10529-2	164	18,2926829	29,8780488	20,1219512	31,7073171	38,4146341	61,5853659	1,06122449	0,90909091	-47,5	-39,2	0,00762307	25,45	-28,963415	-0,7539683
sga-MIR10530	153	22,875817	24,1830065	22,875817	30,0653595	45,751634	54,248366	1,24324324	1	-71,3	-70,1	0,0484994	6,73	-46,601307	-1,0185714
sga-MIR10531	123	21,1382114	29,2682927	17,8861789	31,7073171	39,0243902	60,9756098	1,08333333	1,18181818	-67,5	-67,5	0,284642	4,4	-54,878049	-1,40625
sga-MIR10532-1	199	16,080402	33,6683417	14,5728643	35,678392	30,6532663	69,3467337	1,05970149	1,10344828	-83,6	-83,6	0,0403359	6,92	-42,01005	-1,3704918
sga-MIR10532-10	146	19,8630137	26,0273973	25,3424658	28,7671233	45,2054795	54,7945205	1,10526316	0,78378378	-85,4	-85,4	0,360131	3,2	-58,493151	-1,2939394
sga-MIR10532-11	182	21,4285714	36,2637363	12,0879121	30,2197802	33,5164835	66,4835165	0,83333333	1,77272727	-47,4	-36,6	0,00406755	34,31	-26,043956	-0,7770492
sga-MIR10532-12	184	22,2826087	35,8695652	15,2173913	26,6304348	37,5	62,5	0,74242424	1,46428571	-72,5	-69,32	0,00084971	26,71	-39,402174	-1,0507246
sga-MIR10532-2	194	21,6494845	30,9278351	12,8865979	34,5360825	34,5360825	65,4639175	1,11666667	1,68	-50,8	-50	0,00404967	21,74	-26,185567	-0,758209
sga-MIR10532-3	218	20,6422018	31,1926606	9,63302752	38,5321101	30,2752294	69,7247706	1,23529412	2,14285714	-53,4	-47,9	0,00328247	29,62	-24,495413	-0,8090909
sga-MIR10532-4	169	20,1183432	28,9940828	16,5680473	34,3195266	36,6863905	63,3136095	1,18367347	1,21428571	-43,8	-41,2	0,00618609	32,04	-25,91716	-0,7064516
sga-MIR10532-5	230	20,8695652	30	16,0869565	33,0434783	36,9565217	63,0434783	1,10144928	1,2972973	-72,1	-45,1	0,00226535	57,75	-31,347826	-0,8482353
sga-MIR10532-6	168	23,2142857	31,547619	13,6904762	31,547619	36,9047619	63,0952381	1	1,69565217	-54,3	-51	0,00279556	25,9	-32,321429	-0,8758065
sga-MIR10532-7	237	16,8776371	37,1308017	14,7679325	31,2236287	31,6455696	68,3544304	0,84090909	1,14285714	-68,8	-53,64	0,00330503	37,1	-29,029536	-0,9173333
sga-MIR10532-8	191	21,4659686	37,1727749	17,2774869	24,0837696	38,7434555	61,2565445	0,64788732	1,24242424	-70,1	-69,8	0,010814	19,23	-36,701571	-0,9472973
sga-MIR10532-9	246	20,7317073	33,3333333	17,8861789	28,0487805	38,6178862	61,3821138	0,84146341	1,15909091	-87,2	-84,1	0,00369862	21,71	-35,447154	-0,9178947
sga-MIR10533	163	19,6319018	30,0613497	12,2699387	38,0368098	31,9018405	68,0981595	1,26530612	1,6	-37	-30,34	0,0067247	27,45	-22,699387	-0,7115385
sga-MIR10534	104	20,1923077	28,8461538	19,2307692	31,7307692	39,4230769	60,5769231	1,1	1,05	-61,9	-61	0,0925874	4,91	-59,519231	-1,5097561
sga-MIR10535b-1	119	20,1680672	28,5714286	15,1260504	36,1344538	35,2941176	64,7058824	1,26470588	1,33333333	-69,7	-68,4	0,0667639	5,23	-58,571429	-1,6595238
sga-MIR10535b-2	111	19,8198198	26,1261261	16,2162162	37,8378378	36,036036	63,963964	1,44827586	1,22222222	-45,1	-41,5	0,0208612	13,6	-40,630631	-1,1275
sga-MIR10536-1	210	20,4761905	29,5238095	14,7619048	35,2380952	35,2380952	64,7619048	1,19354839	1,38709677	-99,6	-97,3	0,0488307	11,74	-47,428571	-1,3459459
sga-MIR10536-2	196	22,4489796	29,5918367	18,3673469	29,5918367	40,8163265	59,1836735	1	1,22222222	-88	-83,5	0,0128077	12,24	-44,897959	-1,1
sga-MIR10537	237	23,628692	30,8016878	18,5654008	27,0042194	42,1940928	57,8059072	0,87671233	1,27272727	-77,5	-76,2	0,00758913	26,6	-32,700422	-0,775
sga-MIR10538-1	202	17,8217822	33,1683168	15,8415842	33,1683168	33,6633663	66,3366337	1	1,125	-88,5	-88,1	0,0241267	13,45	-43,811881	-1,3014706
sga-MIR10538-2	107	17,7570093	31,7757009	13,0841121	37,3831776	30,8411215	69,1588785	1,17647059	1,35714286	-66,2	-66,2	0,411798	1,13	-61,869159	-2,0060606
sga-MIR10538-3	117	15,3846154	30,7692308	19,6581197	34,1880342	35,042735	64,957265	1,11111111	0,7826087	-50,7	-50,7	0,128717	5,7	-43,333333	-1,2365854
sga-MIR10538-4	131	16,7938931	32,0610687	15,2671756	35,8778626	32,0610687	67,9389313	1,11904762	1,1	-60	-60	0,246878	2,81	-45,801527	-1,4285714
sga-MIR10540-1	155	16,1290323	27,7419355	14,8387097	41,2903226	30,9677419	69,0322581	1,48837209	1,08695652	-48,8	-47,6	0,0269435	10,79	-31,483871	-1,0166667
sga-MIR10540-2	145	17,2413793	28,9655172	16,5517241	37,2413793	33,7931034	66,2068966	1,28571429	1,04166667	-53,5	-51,3	0,0245621	15,52	-36,896552	-1,0918367
sga-MIR10541	289	20,0692042	33,2179931	11,4186851	35,2941176	31,4878893	68,5121107	1,0625	1,75757576	-67	-60,1	0,0001157	47,34	-23,183391	-0,7362637
sga-MIR10542-1	307	14,9837134	35,8306189	15,9609121	33,2247557	30,9446254	69,0553746	0,92727273	0,93877551	-94,4	-87,1	0,00011897	41,95	-30,749186	-0,9936842
sga-MIR10542-2	235	19,1489362	38,7234043	11,9148936	30,212766	31,0638298	68,9361702	0,78021978	1,60714286	-59,3	-54,3	0,00071162	48,28	-25,234043	-0,8123288
sga-MIR10542-3	249	18,875502	37,3493976	11,6465863	32,1285141	30,5220884	69,4779116	0,86021505	1,62068966	-67,5	-64,3	0,00122311	33,86	-27,108434	-0,8881579
sga-MIR10542-4	244	18,0327869	35,6557377	13,1147541	33,1967213	31,147541	68,852459	0,93103448	1,375	-62,3	-59,2	0,00231552	36,05	-25,532787	-0,8197368
sga-MIR1055	294	24,1496599	37,414966	14,2857143	24,1496599	38,4353741	61,5646259	0,64545455	1,69047619	-80,2	-74,8	0,00101392	32,31	-27,278912	-0,7097345
sga-MIR1069	82	19,5121951	30,4878049	15,8536585	34,1463415	35,3658537	64,6341463	1,12	1,23076923	-22,2	-22,2	0,0657563	8,68	-27,073171	-0,7655172
sga-MIR1072	338	16,8639053	32,8402367	15,6804734	34,3195266	32,5443787	67,1597633	1,04504505	1,0754717	-89,3	-87,6	0,00166247	71,87	-26,420118	-0,8118182
sga-MIR1088	138	20,2898551	31,884058	18,115942	29,7101449	38,4057971	61,5942029	0,93181818	1,12	-54,7	-54,5	0,0402885	7,38	-39,637681	-1,0320755
sga-MIR10979	153	16,9934641	34,6405229	15,6862745	32,6797386	32,6797386	67,3202614	0,94339623	1,08333333	-62	-62	0,181964	12,24	-40,522876	-1,24
sga-MIR10993f	173	20,2312139	33,5260116	12,716763	33,5260116	32,9479769	67,0520231	1	1,59090909	-44,9	-40,3	0,00895931	21,72	-25,953757	-0,7877193
sga-MIR10994	336	16,3690476	27,6785714	18,1547619	37,797619	34,5238095	65,4761905	1,3655914	0,90163934	-88,5	-84,2	1,68E-05	43,97	-26,339286	-0,762931
sga-MIR10995	131	22,9007634	23,6641221	16,7938931	36,6412214	39,6946565	60,3053435	1,5483871	1,36363636	-38	-37,9	0,041588	7,63	-29,007634	-0,7307692
sga-MIR11007	105	18,0952381	23,8095238	21,9047619	36,1904762	40	60	1,52	0,82608696	-29,6	-29,6	0,240415	3,93	-28,190476	-0,7047619

sga-MIR11028-1	174	13,7931034	29,3103448	17,2413793	39,6551724	31,0344828	68,9655172	1,35294118	0,8	-49,1	-49,1	0,0239275	9,29	-28,218391	-0,9092593
sga-MIR11028-2	332	15,3614458	30,4216867	15,9638554	38,253012	31,3253012	68,6746988	1,25742574	0,96226415	-81,2	-68,5	7,35E-05	60,68	-24,457831	-0,7807692
sga-MIR11036	129	25,5813953	29,4573643	10,0775194	34,8837209	35,6589147	64,3410853	1,18421053	2,53846154	-34,1	-28,74	0,00445188	28,73	-26,434109	-0,7413043
sga-MIR11039	229	24,8908297	26,2008734	8,29694323	40,6113537	33,1877729	66,8122271	1,55	3	-61,2	-52,09	0,00932463	34,74	-26,724891	-0,8052632
sga-MIR1106	104	15,3846154	35,5769231	17,3076923	31,7307692	32,6923077	67,3076923	0,89189189	0,88888889	-38,2	-38,2	0,254924	6,03	-36,730769	-1,1235294
sga-MIR11068c	87	17,2413793	35,6321839	17,2413793	29,8850575	34,4827586	65,5172414	0,83870968	1	-28	-26,4	0,0884418	10,71	-32,183908	-0,9333333
sga-MIR11085	151	18,5430464	26,4900662	18,5430464	36,4238411	37,0860927	62,9139073	1,375	1	-64,1	-63,9	0,0414341	11,75	-42,450331	-1,1446429
sga-MIR11091	124	26,6129032	31,4516129	15,3225806	26,6129032	41,9354839	58,0645161	0,84615385	1,73684211	-40	-40	0,055982	8,23	-32,258065	-0,7692308
sga-MIR11097c	147	23,8095238	25,170068	19,7278912	31,292517	43,537415	56,462585	1,24324324	1,20689655	-49,1	-41,8	0,0184322	23,91	-33,401361	-0,7671875
sga-MIR11107c	341	17,0087977	29,9120235	13,1964809	39,8826979	30,2052786	69,7947214	1,33333333	1,28888889	-89,8	-78,9	1,52E-05	72,44	-26,334311	-0,8718447
sga-MIR11108h	258	25,9689922	28,6821705	20,5426357	24,8062016	46,5116279	53,4883721	0,86486486	1,26415094	-86,8	-81,8	8,53E-05	27,25	-33,643411	-0,7233333
sga-MIR11108n	88	17,0454545	34,0909091	17,0454545	31,8181818	34,0909091	65,9090909	0,93333333	1	-39,6	-39,6	0,147848	8,18	-45	-1,32
sga-MIR11108u	152	25	30,9210526	17,1052632	26,9736842	42,1052632	57,8947368	0,87234043	1,46153846	-68,1	-67,3	0,0507536	11,71	-44,802632	-1,0640625
sga-MIR11108w	164	17,0731707	30,4878049	15,8536585	36,5853659	32,9268293	67,0731707	1,2	1,07692308	-96,4	-95,1	0,147162	6,44	-58,780488	-1,7851852
sga-MIR11114	266	14,6616541	36,4661654	16,1654135	32,7067669	30,8270677	69,1729323	0,89690722	0,90697674	-61,2	-58,2	0,00018792	44,25	-23,007519	-0,7463415
sga-MIR1112	276	19,9275362	29,3478261	14,1304348	36,5942029	34,057971	65,942029	1,24691358	1,41025641	-66,3	-56,9	1,81E-05	52,84	-24,021739	-0,7053191
sga-MIR11124	331	23,2628399	29,6072508	17,8247734	29,305136	41,0876133	58,9123867	0,98979592	1,30508475	-96,5	-74,5	0,0010334	88,54	-29,154079	-0,7095588
sga-MIR11131	143	13,986014	33,5664336	16,7832168	35,6643357	30,7692308	69,2307692	1,0625	0,83333333	-77,2	-77,2	0,229391	4,05	-53,986014	-1,7545455
sga-MIR11136	341	25,5131965	24,6334311	14,9560117	34,8973607	40,4692082	59,5307918	1,41666667	1,70588235	-98,1	-81,8	1,18E-05	71,93	-28,768328	-0,7108696
sga-MIR11156	137	17,5182482	36,4963504	13,8686131	32,1167883	31,3868613	68,6131387	0,88	1,26315789	-30,6	-27,8	0,00906128	12,69	-22,335766	-0,7116279
sga-MIR11167-1	135	16,2962963	34,8148148	18,5185185	30,3703704	34,8148148	65,1851852	0,87234043	0,88	-90,7	-90,7	0,595307	1,01	-67,185185	-1,9297872
sga-MIR11167-2	147	20,4081633	37,414966	15,6462585	26,5306122	36,0544218	63,9455782	0,70909091	1,30434783	-38,9	-38,9	0,104186	7,5	-26,462585	-0,7339623
sga-MIR11174	152	9,86842105	30,9210526	22,3684211	36,8421053	32,2368421	67,7631579	1,19148936	0,44117647	-35,5	-32,28	0,0343765	13,78	-23,355263	-0,7244898
sga-MIR11178	145	17,2413793	33,1034483	15,1724138	34,4827586	32,4137931	67,5862069	1,04166667	1,13636364	-98,1	-98,1	0,0780953	4,99	-67,655172	-2,087234
sga-MIR1127	284	18,3098592	35,915493	16,1971831	29,5774648	34,5070423	65,4929577	0,82352941	1,13043478	-84,1	-66,61	0,00045337	62,04	-29,612676	-0,8581633
sga-MIR1127b	324	19,1358025	37,654321	16,3580247	26,8518519	35,4938272	64,5061728	0,71311475	1,16981132	-88,4	-73,47	0,00047357	49,91	-27,283951	-0,7686957
sga-MIR1128-1	256	20,3125	35,546875	10,9375	33,203125	31,25	68,75	0,93406593	1,85714286	-74,2	-72,2	0,00432507	42,98	-28,984375	-0,9275
sga-MIR1128-2	301	12,6245847	32,2259136	18,9368771	36,2126246	31,5614618	68,4385382	1,12371134	0,66666667	-66,7	-65,2	0,0020437	36,1	-22,159468	-0,7021053
sga-MIR1128-3	293	16,3822526	32,7645051	16,7235495	34,1296928	33,105802	66,894198	1,04166667	0,97959184	-70,8	-66,6	0,00032429	44,1	-24,163823	-0,7298969
sga-MIR1128-4	236	22,4576271	33,4745763	10,5932203	33,4745763	33,0508475	66,9491525	1	2,12	-57,5	-56	0,0001297	53,9	-24,364407	-0,7371795
sga-MIR1128-5	289	12,4567474	33,9100346	18,6851211	34,9480969	31,1418685	68,8581315	1,03061224	0,66666667	-72,2	-65,72	0,00047279	42,45	-24,989619	-0,8024444
sga-MIR11288c	113	15,0442478	32,7433628	17,699115	34,5132743	32,7433628	67,2566372	1,05405405	0,85	-78,3	-78,1	0,522625	1,8	-69,292035	-2,1162162
sga-MIR11329	139	17,2661871	33,0935252	16,5467626	33,0935252	33,8129496	66,1870504	1	1,04347826	-41,5	-37,3	0,0133714	22,4	-29,856115	-0,8829787
sga-MIR1133	253	19,7628458	36,3636364	12,6482213	31,2252964	32,4110672	67,5889328	0,85869565	1,5625	-75,7	-69,3	0,00054014	53,09	-29,920949	-0,9231707
sga-MIR11409d	237	14,7679325	32,0675105	17,721519	35,443038	32,4894515	67,5105485	1,10526316	0,83333333	-72,7	-71,1	0,018301	10,57	-30,675105	-0,9441558
sga-MIR11419	216	21,7592593	31,4814815	15,2777778	31,4814815	37,037037	62,962963	1	1,42424242	-63,6	-59,3	0,00022	32,52	-29,444444	-0,795
sga-MIR11425d	188	17,5531915	36,7021277	19,6808511	26,0638298	37,2340426	62,7659574	0,71014493	0,89189189	-70,3	-67,3	0,0183766	11,56	-37,393617	-1,0042857
sga-MIR11498a	318	24,5283019	33,3333333	11,6352201	30,5031447	36,163522	63,836478	0,91509434	2,10810811	-94	-73,77	8,90E-05	82,74	-29,559748	-0,8173913
sga-MIR11507	159	16,3522013	32,7044025	14,4654088	36,4779874	30,8176101	69,1823899	1,11538462	1,13043478	-79,3	-72,4	0,0446116	14,15	-49,874214	-1,6183673
sga-MIR11514-1	145	14,4827586	33,7931034	18,6206897	33,1034483	33,1034483	66,8965517	0,97959184	0,77777778	-79,4	-79,4	0,448539	1,76	-54,758621	-1,6541667
sga-MIR11514-2	135	21,4814815	31,8518519	16,2962963	30,3703704	37,7777778	62,2222222	0,95348837	1,31818182	-56,4	-55,5	0,0742568	13,11	-41,777778	-1,1058824
sga-MIR11563	295	17,9661017	26,1016949	13,8983051	42,0338983	31,8644068	68,1355932	1,61038961	1,29268293	-68,4	-57	0,00028029	80,37	-23,186441	-0,7276596
sga-MIR11564b	222	18,018018	32,8828829	15,3153153	33,7837838	33,3333333	66,6666667	1,02739726	1,17647059	-66,5	-47,4	0,00149821	57,34	-29,954955	-0,8986486
sga-MIR11578-1	232	13,7931034	31,4655172	16,3793103	38,362069	30,1724138	69,8275862	1,21917808	0,84210526	-60,3	-53,3	0,0026175	45,99	-25,991379	-0,8614286
sga-MIR11578-2	140	17,1428571	29,2857143	13,5714286	40	30,7142857	69,2857143	1,36585366	1,26315789	-35,9	-34,7	0,0489624	12,25	-25,642857	-0,8348837
sga-MIR12107	142	16,9014085	29,5774648	16,1971831	37,3239437	33,0985915	66,9014085	1,26190476	1,04347826	-83,9	-83,9	0,0978429	4,13	-59,084507	-1,7851064
sga-MIR12142	222	18,4684685	29,7297297	12,1621622	39,6396396	30,6306306	69,3693694	1,33333333	1,51851852	-79,5	-74,84	0,00443771	36,62	-35,810811	-1,1691176
sga-MIR12148	201	22,3880597	28,8557214	13,4328358	35,3233831	35,8208955	64,1791045	1,22413793	1,66666667	-52,4	-43,5	0,00563524	49,94	-26,069652	-0,7277778
sga-MIR1215	95	9,47368421	32,6315789	21,0526316	36,8421053	30,5263158	69,4736842	1,12903226	0,45	-24,1	-24,1	0,236358	3,93	-25,368421	-0,8310345
sga-MIR12151-1	205	21,4634146	31,2195122	15,6097561	31,7073171	37,0731707	62,9268293	1,015625	1,375	-91,9	-91,9	0,0143258	14,89	-44,829268	-1,2092105
sga-MIR12151-2	169	20,1183432	33,1360947	14,7928994	31,9526627	34,9112426	65,0887574	0,96428571	1,36	-75,5	-69,2	0,00850046	22,11	-44,674556	-1,279661
sga-MIR12154	168	17,8571429	32,1428571	15,4761905	34,5238095	33,3333333	66,6666667	1,07407407	1,15384615	-72,7	-67,8	0,0266779	21,5	-43,27381	-1,2982143
sga-MIR12162	173	21,3872832	32,9479769	9,8265896	35,8381503	31,2138728	68,7861272	1,0877193	2,17647059	-39,7	-35,4	0,00315985	37,26	-22,947977	-0,7351852
sga-MIR12168	111	21,6216216	36,9369369	10,8108108	30,6306306	32,4324324	67,5675676	0,82926829	2	-25,7	-25,5	0,00972516	13,63	-23,153153	-0,7138889
sga-MIR12170	160	18,75	30	18,125	33,125	36,875	63,125	1,10416667	1,03448276	-42,3	-41,1	0,0255964	14,47	-26,4375	-0,7169492
sga-MIR1313d	164	17,0731707	33,5365854	13,4146341	35,9756098	30,4878049	69,5121951	1,07272727	1,27272727	-46	-45,5	0,022516	10,51	-28,04878	-0,92
sga-MIR1438	253	26,0869565	19,3675889	26,0869565	28,458498	52,173913	47,826087	1,46938776	1	-93,1	-82,3	0,00151147	30,16	-36,798419	-0,705303
sga-MIR1439	263	13,6882129	28,8973384	18,2509506	39,1634981	31,9391635	68,0608365	1,35526316	0,75	-66,9	-50,7	0,00052708	53,51	-25,437262	-0,7964286
sga-MIR1446	108	18,5185185	25,9259259	20,3703704	35,1851852	38,8888889	61,1111111	1,35714286	0,90909091	-51	-51	0,177923	3,7	-47,222222	-1,2142857
sga-MIR1512c	182	18,1318681	31,8681319	15,9340659	34,0659341	34,0659341	65,9340659	1,06896552	1,13793103	-92,8	-90,5	0,102169	10,72	-50,989011	-1,4967742
sga-MIR1514a	202	15,3465347	30,6930693	15,8415842	38,1188119	31,1881188	68,8118812	1,24193548	0,96875	-46,8	-40,8	0,00152458	37,32	-23,168317	-0,7428571
sga-MIR1514b	164	17,0731707	40,2439024	15,2439024	27,4390244	32,3170732	67,6829268	0,68181818	1,12	-59,2	-55,4	0,00784614	14,84	-36,097561	-1,1169811
sga-MIR1518-1	220	18,1818182	37,7272727	16,8181818	27,2727273	35	65	0,72289157	1,08108108	-83,6	-80,1	0,0273635	26,71	-38	-1,0857143
sga-MIR1518-2	243	18,5185185	31,2757202	12,7572016	37,4485597	31,2757202	68,7242798	1,19736842	1,4516129	-55,6	-42,1	0,00010076	34,71	-22,880658	-0,7315789
sga-MIR1520k-1	154	22,0779221	32,4675325	15,5844156	29,8701299	37,6623377	62,3376623	0,92	1,41666667	-54,9	-51,4	0,0238332	10,85	-35,649351	-0,9465517
sga-MIR1520k-2	70	24,2857143	27,1428571	18,5714286	30	42,8571429	57,1428571	1,10526316	1,30769231	-30,7	-30,7	0,673728	0,84	-43,857143	-1,0233333

sga-MIR1520l-1	81	23,4567901	29,6296296	13,5802469	33,3333333	37,037037	62,962963	1,125	1,72727273	-37,1	-37,1	0,454728	1,01	-45,802469	-1,2366667
sga-MIR1520l-2	176	19,8863636	31,8181818	14,7727273	33,5227273	34,6590909	65,3409091	1,05357143	1,34615385	-54,4	-52,5	0,0372119	8,27	-30,909091	-0,8918033
sga-MIR1521b-1	93	13,9784946	30,1075269	22,5806452	33,3333333	36,5591398	63,4408602	1,10714286	0,61904762	-31,9	-31,9	0,241649	5,42	-34,301075	-0,9382353
sga-MIR1521b-2	110	19,0909091	30	20,9090909	30	40	60	1	0,91304348	-44,2	-44,2	0,195729	5,69	-40,181818	-1,0045455
sga-MIR1531	113	17,699115	30,0884956	16,8141593	35,3982301	34,5132743	65,4867257	1,17647059	1,05263158	-53,7	-53,7	0,0532811	8,75	-47,522124	-1,3769231
sga-MIR156a	195	20,5128205	29,2307692	20	30,2564103	40,5128205	59,4871795	1,03508772	1,02564103	-76,6	-66,1	0,00246542	27,29	-39,282051	-0,9696203
sga-MIR156b-1	101	17,8217822	29,7029703	18,8118812	33,6633663	36,6336634	63,3663366	1,13333333	0,94736842	-43,5	-42,2	0,119446	6,96	-43,069307	-1,1756757
sga-MIR156b-2	88	21,5909091	25	23,8636364	29,5454545	45,4545455	54,5454545	1,18181818	0,9047619	-44,1	-44,1	0,312754	2,54	-50,113636	-1,1025
sga-MIR156b-3	132	21,969697	24,2424242	17,4242424	36,3636364	39,3939394	60,6060606	1,5	1,26086957	-57	-56,6	0,0500151	6,87	-43,181818	-1,0961538
sga-MIR156b-4	98	18,3673469	32,6530612	18,3673469	30,6122449	36,7346939	63,2653061	0,9375	1	-48,3	-42,9	0,0433508	5,76	-49,285714	-1,3416667
sga-MIR156b-5	246	18,699187	29,6747967	18,2926829	33,3333333	36,9918699	63,0081301	1,12328767	1,02222222	-85,1	-81,7	0,00861711	27,5	-34,593496	-0,9351648
sga-MIR156b-6	94	20,212766	26,5957447	18,0851064	35,106383	38,2978723	61,7021277	1,32	1,11764706	-48,4	-48,4	0,0852724	4,15	-51,489362	-1,3444444
sga-MIR156b-7	104	23,0769231	25,9615385	24,0384615	26,9230769	47,1153846	52,8846154	1,03703704	0,96	-62	-56	0,149631	6,04	-59,615385	-1,2653061
sga-MIR156c-1	117	23,0769231	26,4957265	21,3675214	29,0598291	44,4444444	55,5555556	1,09677419	1,08	-63,9	-63,9	0,217665	8,54	-54,615385	-1,2288462
sga-MIR156c-2	95	25,2631579	23,1578947	21,0526316	30,5263158	46,3157895	53,6842105	1,31818182	1,2	-57,9	-57,9	0,47385	2,23	-60,947368	-1,3159091
sga-MIR156c-3	105	22,8571429	26,6666667	24,7619048	25,7142857	47,6190476	52,3809524	0,96428571	0,92307692	-51,1	-51,1	0,0798115	6,21	-48,666667	-1,022
sga-MIR156d	140	15	30	20,7142857	34,2857143	35,7142857	64,2857143	1,14285714	0,72413793	-43,9	-42,2	0,073607	8,76	-31,357143	-0,878
sga-MIR156f-1	92	22,826087	26,0869565	17,3913043	33,6956522	40,2173913	59,7826087	1,29166667	1,3125	-38,3	-38,3	0,259233	2,69	-41,630435	-1,0351351
sga-MIR156f-2	146	21,9178082	33,5616438	14,3835616	30,1369863	36,3013699	63,6986301	0,89795918	1,52380952	-63,6	-63,6	0,0980466	6,13	-43,561644	-1,2
sga-MIR156f-3	300	26	21	13	40	39	61	1,9047619	2	-85,4	-75,1	0,0002451	82,86	-28,466667	-0,7299145
sga-MIR156g	119	20,1680672	25,210084	19,3277311	35,2941176	39,4957983	60,5042017	1,4	1,04347826	-74,5	-74,5	0,171764	3,48	-62,605042	-1,5851064
sga-MIR156i	104	22,1153846	25	20,1923077	32,6923077	42,3076923	57,6923077	1,30769231	1,0952381	-42,4	-42,4	0,328687	4,15	-40,769231	-0,9636364
sga-MIR156k-1	96	21,875	25	16,6666667	36,4583333	38,5416667	61,4583333	1,45833333	1,3125	-57,5	-57,5	0,335821	5,09	-59,895833	-1,5540541
sga-MIR156t	210	16,6666667	37,6190476	14,7619048	30,952381	31,4285714	68,5714286	0,82278481	1,12903226	-51,4	-40,2	0,0016243	44,8	-24,47619	-0,7787879
sga-MIR158	209	19,6172249	32,5358852	12,4401914	35,4066986	32,0574163	67,9425837	1,08823529	1,57692308	-48,4	-43	0,00117352	43,05	-23,157895	-0,7223881
sga-MIR159	111	17,1171171	26,1261261	17,1171171	39,6396396	34,2342342	65,7657658	1,51724138	1	-35,6	-34,4	0,00934161	11,05	-32,072072	-0,9368421
sga-MIR159a-1	174	21,8390805	24,7126437	17,2413793	36,2068966	39,0804598	60,9195402	1,46511628	1,26666667	-76,6	-74	0,0215353	12,01	-44,022989	-1,1264706
sga-MIR159a-2	109	16,5137615	37,6146789	17,4311927	28,440367	33,9449541	66,0550459	0,75609756	0,94736842	-37,5	-36,3	0,0549871	14	-34,40367	-1,0135135
sga-MIR159b-1	180	20,5555556	29,4444444	17,2222222	32,7777778	37,7777778	62,2222222	1,11320755	1,19354839	-81,4	-79,2	0,0114567	10	-45,222222	-1,1970588
sga-MIR159b-2	272	19,4852941	28,3088235	15,0735294	37,1323529	34,5588235	65,4411765	1,31168831	1,29268293	-96,7	-94,8	0,00036166	22,72	-35,551471	-1,0287234
sga-MIR159b-3	200	20,5	29,5	16	34	36,5	63,5	1,15254237	1,28125	-79,2	-76,3	0,00935741	12,3	-39,6	-1,0849315
sga-MIR159b-4	121	19,0082645	29,7520661	17,3553719	33,8842975	36,3636364	63,6363636	1,13888889	1,0952381	-37,5	-30,5	0,0794512	11,24	-30,991736	-0,8522727
sga-MIR159b-5	179	20,6703911	29,6089385	17,3184358	32,4022346	37,9888268	62,0111732	1,09433962	1,19354839	-73,2	-70,4	0,00460345	13,75	-40,893855	-1,0764706
sga-MIR159c	209	15,3110048	32,0574163	16,2679426	36,3636364	31,5789474	68,4210526	1,13432836	0,94117647	-48,4	-44,8	0,00070686	33,87	-23,157895	-0,7333333
sga-MIR160-1	104	23,0769231	24,0384615	21,1538462	31,7307692	44,2307692	55,7692308	1,32	1,09090909	-52,3	-51,4	0,100504	4,55	-50,288462	-1,1369565
sga-MIR160-2	116	21,5517241	31,8965517	21,5517241	25	43,1034483	56,8965517	0,78378378	1	-41,7	-40,3	0,0514112	9,2	-35,948276	-0,834
sga-MIR160c	103	23,3009709	25,2427184	26,2135922	25,2427184	49,5145631	50,4854369	1	0,88888889	-44,9	-44,9	0,320949	5,37	-43,592233	-0,8803922
sga-MIR160g	97	21,6494845	29,8969072	23,7113402	24,742268	45,3608247	54,6391753	0,82758621	0,91304348	-48,9	-48,9	0,183973	3,15	-50,412371	-1,1113636
sga-MIR160h-1	81	22,2222222	20,9876543	23,4567901	33,3333333	45,6790123	54,3209877	1,58823529	0,94736842	-33,6	-33,4	0,303642	3,48	-41,481481	-0,9081081
sga-MIR160h-2	90	24,4444444	24,4444444	22,2222222	28,8888889	46,6666667	53,3333333	1,18181818	1,1	-46,8	-46,8	0,126945	3,09	-52	-1,1142857
sga-MIR161	219	19,6347032	34,2465753	17,8082192	28,3105023	37,4429224	62,5570776	0,82666667	1,1025641	-99,8	-93,4	0,0020875	19,54	-45,570776	-1,2170732
sga-MIR162	101	21,7821782	32,6732673	22,7722772	22,7722772	44,5544554	55,4455446	0,6969697	0,95652174	-38,5	-38,1	0,0970113	5,79	-38,118812	-0,8555556
sga-MIR162b-1	139	21,5827338	28,7769784	19,4244604	30,2158273	41,0071942	58,9928058	1,05	1,11111111	-50,4	-48,7	0,0498402	9,3	-36,258993	-0,8842105
sga-MIR162b-2	135	20,7407407	25,1851852	22,962963	31,1111111	43,7037037	56,2962963	1,23529412	0,90322581	-53,8	-52,1	0,118759	6,73	-39,851852	-0,9118644
sga-MIR164-1	173	19,6531792	29,4797688	16,1849711	34,6820809	35,8381503	64,1618497	1,17647059	1,21428571	-62,2	-60,1	0,00198674	17,99	-35,953757	-1,0032258
sga-MIR164-2	187	21,3903743	28,8770053	16,0427807	33,6898396	37,4331551	62,5668449	1,16666667	1,33333333	-62,2	-60,1	0,00111811	19,79	-33,262032	-0,8885714
sga-MIR164-3	187	19,2513369	28,342246	18,7165775	33,6898396	37,9679144	62,0320856	1,18867925	1,02857143	-64	-61,9	0,00215359	18,08	-34,224599	-0,9014085
sga-MIR164a	140	17,1428571	30,7142857	17,1428571	35	34,2857143	65,7142857	1,13953488	1	-51,1	-51,1	0,170251	4,43	-36,5	-1,0645833
sga-MIR164c	92	19,5652174	27,173913	19,5652174	33,6956522	39,1304348	60,8695652	1,24	1	-51,1	-48,1	0,252239	2,19	-55,543478	-1,4194444
sga-MIR164e-1	91	23,0769231	27,4725275	16,4835165	32,967033	39,5604396	60,4395604	1,2	1,4	-32,2	-31,4	0,0208932	12,61	-35,384615	-0,8944444
sga-MIR164e-2	95	22,1052632	26,3157895	18,9473684	32,6315789	41,0526316	58,9473684	1,24	1,16666667	-45,5	-44,7	0,0177693	10,28	-47,894737	-1,1666667
sga-MIR164h	91	19,7802198	37,3626374	18,6813187	24,1758242	38,4615385	61,5384615	0,64705882	1,05882353	-32,2	-31,12	0,0648748	7,4	-35,384615	-0,92
sga-MIR166-1	120	21,6666667	28,3333333	16,6666667	33,3333333	38,3333333	61,6666667	1,17647059	1,3	-52,7	-51,5	0,335949	5,46	-43,916667	-1,1456522
sga-MIR166-2	119	17,6470588	29,4117647	21,8487395	31,092437	39,4957983	60,5042017	1,05714286	0,80769231	-33	-31,7	0,0334998	10,65	-27,731092	-0,7021277
sga-MIR166-3	146	17,1232877	34,2465753	15,7534247	32,8767123	32,8767123	67,1232877	0,96	1,08695652	-58,5	-57,3	0,090135	8,89	-40,068493	-1,21875
sga-MIR166-4	166	18,6746988	30,1204819	17,4698795	33,7349398	36,1445783	63,8554217	1,12	1,06896552	-66,3	-60,9	0,0344526	17,97	-39,939759	-1,105
sga-MIR166c	165	21,2121212	32,7272727	14,5454545	31,5151515	35,7575758	64,2424242	0,96296296	1,45833333	-68,7	-65,9	0,042982	8,57	-41,636364	-1,1644068
sga-MIR166f-1	156	23,7179487	30,7692308	16,6666667	28,8461538	40,3846154	59,6153846	0,9375	1,42307692	-46,1	-42,6	0,00367698	22,13	-29,551282	-0,731746
sga-MIR166f-2	107	21,4953271	22,4299065	23,364486	32,7102804	44,8598131	55,1401869	1,45833333	0,92	-44,2	-41	0,0417107	13,02	-41,308411	-0,9208333
sga-MIR166k	158	20,2531646	29,1139241	18,3544304	32,278481	38,6075949	61,3924051	1,10869565	1,10344828	-58,5	-58,2	0,116365	9,88	-37,025316	-0,9590164
sga-MIR167b-1	74	17,5675676	32,4324324	18,9189189	31,0810811	36,4864865	63,5135135	0,95833333	0,92857143	-27,5	-27,5	0,0608085	5,77	-37,162162	-1,0185185
sga-MIR167b-2	119	25,210084	28,5714286	19,3277311	26,8907563	44,5378151	55,4621849	0,94117647	1,30434783	-50,2	-48,6	0,153238	5,27	-42,184874	-0,9471698
sga-MIR167c-1	117	19,6581197	29,9145299	23,9316239	26,4957265	43,5897436	56,4102564	0,88571429	0,82142857	-48,8	-48,6	0,110335	5,36	-41,709402	-0,9568627
sga-MIR167c-2	112	19,6428571	29,4642857	22,3214286	28,5714286	41,9642857	58,0357143	0,96969697	0,88	-40,9	-40,7	0,0807021	6,93	-36,517857	-0,8702128
sga-MIR167c-3	110	24,5454545	25,4545455	22,7272727	27,2727273	47,2727273	52,7272727	1,07142857	1,08	-53,5	-53,5	0,0801293	4,39	-48,636364	-1,0288462
sga-MIR167c-4	154	20,1298701	27,9220779	23,3766234	28,5714286	43,5064935	56,4935065	1,02325581	0,86111111	-85,9	-83,1	0,082826	11,41	-55,779221	-1,2820896

sga-MIR167c-5	271	20,295203	33,9483395	14,0221402	31,7343173	34,3173432	65,6826568	0,93478261	1,44736842	-69,3	-65,7	0,00053908	49,5	-25,571956	-0,7451613
sga-MIR167d	116	20,6896552	27,5862069	23,2758621	28,4482759	43,9655172	56,0344828	1,03125	0,88888889	-49,5	-49,5	0,172191	5,15	-42,672414	-0,9705882
sga-MIR167h-1	86	18,6046512	32,5581395	17,4418605	31,3953488	36,0465116	63,9534884	0,96428571	1,06666667	-38,9	-38,4	0,194618	4,23	-45,232558	-1,2548387
sga-MIR167h-2	113	22,1238938	26,5486726	24,7787611	26,5486726	46,9026549	53,0973451	1	0,89285714	-46,1	-46,1	0,0248159	9,32	-40,79646	-0,8698113
sga-MIR167h-3	119	19,3277311	26,8907563	25,210084	28,5714286	44,5378151	55,4621849	1,0625	0,76666667	-44	-44	0,0441684	8,75	-36,97479	-0,8301887
sga-MIR167h-4	122	23,7704918	27,0491803	18,852459	30,3278689	42,6229508	57,3770492	1,12121212	1,26086957	-62,7	-62,7	0,159834	4,66	-51,393443	-1,2057692
sga-MIR167h-5	128	21,875	31,25	10,9375	35,9375	32,8125	67,1875	1,15	2	-31,2	-30,3	0,0332807	14,7	-24,375	-0,7428571
sga-MIR168	154	28,5714286	22,0779221	23,3766234	25,974026	51,9480519	48,0519481	1,17647059	1,22222222	-70,3	-68,8	0,0115726	15,46	-45,649351	-0,87875
sga-MIR168c-1	160	28,125	21,875	23,75	26,25	51,875	48,125	1,2	1,18421053	-63,8	-62,7	0,00925608	21,04	-39,875	-0,7686747
sga-MIR168c-2	175	29,1428571	21,1428571	24,5714286	25,1428571	53,7142857	46,2857143	1,18918919	1,18604651	-71,4	-69,3	0,00776791	21,29	-40,8	-0,7595745
sga-MIR169a	159	24,5283019	27,0440252	15,0943396	33,3333333	39,6226415	60,3773585	1,23255814	1,625	-82	-82	0,0608701	4,2	-51,572327	-1,3015873
sga-MIR169c-1	175	20	28,5714286	13,1428571	38,2857143	33,1428571	66,8571429	1,34	1,52173913	-77,6	-74,9	0,00358005	15,07	-44,342857	-1,337931
sga-MIR169c-2	203	14,2857143	27,0935961	18,226601	40,3940887	32,5123153	67,4876847	1,49090909	0,78378378	-65,8	-62,8	0,00488823	16,4	-32,413793	-0,9969697
sga-MIR169c-3	212	13,2075472	29,245283	17,4528302	40,0943396	30,6603774	69,3396226	1,37096774	0,75675676	-66,3	-63,3	0,00286997	23,08	-31,273585	-1,02
sga-MIR169d-1	140	20,7142857	22,1428571	22,1428571	35	42,8571429	57,1428571	1,58064516	0,93548387	-46,9	-46,9	0,00276464	14,21	-33,5	-0,7816667
sga-MIR169d-2	141	21,2765957	22,6950355	21,9858156	34,0425532	43,2624113	56,7375887	1,5	0,96774194	-55,4	-55,4	0,0221595	7,79	-39,29078	-0,9081967
sga-MIR169e-1	193	20,7253886	26,9430052	17,0984456	35,2331606	37,8238342	62,1761658	1,30769231	1,21212121	-78,5	-74,8	0,006646	15,08	-40,673575	-1,0753425
sga-MIR169e-2	218	16,0550459	34,8623853	19,7247706	29,3577982	35,7798165	64,2201835	0,84210526	0,81395349	-58,8	-53,19	0,00532306	25,29	-26,972477	-0,7538462
sga-MIR169e-3	174	15,5172414	37,3563218	17,816092	29,3103448	33,3333333	66,6666667	0,78461538	0,87096774	-55,2	-52,5	0,0232162	11,03	-31,724138	-0,9517241
sga-MIR169j-1	266	19,924812	29,6992481	15,4135338	34,962406	35,3383459	64,6616541	1,17721519	1,29268293	-88	-81,4	0,00038224	31,09	-33,082707	-0,9361702
sga-MIR169j-2	172	19,1860465	29,0697674	16,2790698	35,4651163	35,4651163	64,5348837	1,22	1,17857143	-73,3	-73,3	0,00801673	11,06	-42,616279	-1,2016393
sga-MIR169j-3	178	21,9101124	23,5955056	19,1011236	35,3932584	41,011236	58,988764	1,5	1,14705882	-78,5	-75,6	0,00477325	12,93	-44,101124	-1,0753425
sga-MIR169l	184	17,9347826	36,9565217	20,6521739	24,4565217	38,5869565	61,4130435	0,66176471	0,86842105	-58,5	-50,6	0,00867538	19,45	-31,793478	-0,8239437
sga-MIR169r-1	149	24,8322148	22,147651	17,4496644	35,5704698	42,2818792	57,7181208	1,60606061	1,42307692	-69	-68,8	0,00837833	12,37	-46,308725	-1,0952381
sga-MIR169r-2	285	19,2982456	26,6666667	18,245614	35,7894737	37,5438596	62,4561404	1,34210526	1,05769231	-99,5	-94,67	0,00038669	33,49	-34,912281	-0,9299065
sga-MIR169r-3	184	21,7391304	26,6304348	17,9347826	33,6956522	39,673913	60,326087	1,26530612	1,21212121	-72,2	-72,2	0,00986728	10,29	-39,23913	-0,9890411
sga-MIR171a-1	76	22,3684211	27,6315789	15,7894737	34,2105263	38,1578947	61,8421053	1,23809524	1,41666667	-41,7	-41,7	0,589963	1,08	-54,868421	-1,437931
sga-MIR171a-2	108	19,4444444	34,2592593	13,8888889	32,4074074	33,3333333	66,6666667	0,94594595	1,4	-42,8	-42,8	0,175856	3,72	-39,62963	-1,1888889
sga-MIR171a-3	99	22,2222222	27,2727273	16,1616162	34,3434343	38,3838384	61,6161616	1,25925926	1,375	-44,7	-44,7	0,640461	1,18	-45,151515	-1,1763158
sga-MIR171a-4	91	19,7802198	26,3736264	15,3846154	38,4615385	35,1648352	64,8351648	1,45833333	1,28571429	-34,7	-34,7	0,392431	3,5	-38,131868	-1,084375
sga-MIR171a-5	100	21	25	13	41	34	66	1,64	1,61538462	-41,9	-41,2	0,0463227	4,9	-41,9	-1,2323529
sga-MIR171b-1	115	22,6086957	30,4347826	15,6521739	31,3043478	38,2608696	61,7391304	1,02857143	1,44444444	-43	-37,7	0,131277	7,03	-37,391304	-0,9772727
sga-MIR171b-2	118	22,0338983	28,8135593	16,1016949	33,0508475	38,1355932	61,8644068	1,14705882	1,36842105	-43	-40	0,101445	8,33	-36,440678	-0,9555556
sga-MIR171b-3	99	17,1717172	30,3030303	23,2323232	29,2929293	40,4040404	59,5959596	0,96666667	0,73913043	-40,6	-40,6	0,313587	2,49	-41,010101	-1,015
sga-MIR171b-4	125	21,6	28	16,8	33,6	38,4	61,6	1,2	1,28571429	-49,3	-45,4	0,0539825	6,28	-39,44	-1,0270833
sga-MIR171b-5	125	16,8	33,6	21,6	28	38,4	61,6	0,83333333	0,77777778	-38,9	-33,7	0,0464737	13,27	-31,12	-0,8104167
sga-MIR171c-1	91	18,6813187	29,6703297	17,5824176	34,0659341	36,2637363	63,7362637	1,14814815	1,0625	-42,2	-42,2	0,651468	0,91	-46,373626	-1,2787879
sga-MIR171c-2	86	15,1162791	32,5581395	17,4418605	34,8837209	32,5581395	67,4418605	1,07142857	0,86666667	-24,1	-24,1	0,321764	4,32	-28,023256	-0,8607143
sga-MIR171d	81	18,5185185	29,6296296	17,2839506	34,5679012	35,8024691	64,1975309	1,16666667	1,07142857	-39,5	-39,5	0,73619	0,6	-48,765432	-1,362069
sga-MIR171f-1	81	17,2839506	22,2222222	18,5185185	41,9753086	35,8024691	64,1975309	1,88888889	0,93333333	-24,6	-24,6	0,271433	6	-30,37037	-0,8482759
sga-MIR171f-2	81	17,2839506	23,4567901	18,5185185	40,7407407	35,8024691	64,1975309	1,73684211	0,93333333	-24,5	-24,5	0,269034	5,56	-30,246914	-0,8448276
sga-MIR171h-1	70	20	27,1428571	21,4285714	31,4285714	41,4285714	58,5714286	1,15789474	0,93333333	-32,3	-31,9	0,12089	5,18	-46,142857	-1,1137931
sga-MIR171h-2	115	21,7391304	24,3478261	8,69565217	45,2173913	30,4347826	69,5652174	1,85714286	2,5	-34,8	-32,4	0,0649658	15,66	-30,26087	-0,9942857
sga-MIR171m	84	22,6190476	28,5714286	14,2857143	34,5238095	36,9047619	63,0952381	1,20833333	1,58333333	-45,3	-45,3	0,430562	1,87	-53,928571	-1,4612903
sga-MIR172-1	125	20,8	28	9,6	41,6	30,4	69,6	1,48571429	2,16666667	-27,4	-23,7	0,00326075	15,93	-21,92	-0,7210526
sga-MIR172-10	160	15,625	33,125	15	36,25	30,625	69,375	1,09433962	1,04166667	-42,2	-36,87	0,0120814	24,46	-26,375	-0,8612245
sga-MIR172-11	169	17,1597633	33,1360947	13,6094675	36,0946746	30,7692308	69,2307692	1,08928571	1,26086957	-58,4	-53,07	0,0160855	21,81	-34,556213	-1,1230769
sga-MIR172-2	164	17,0731707	33,5365854	13,4146341	35,9756098	30,4878049	69,5121951	1,07272727	1,27272727	-52,9	-47,57	0,0178513	21,68	-32,256098	-1,058
sga-MIR172-4	190	17,8947368	38,4210526	13,1578947	30,5263158	31,0526316	68,9473684	0,79452055	1,36	-65,8	-59,3	0,00664007	21,08	-34,631579	-1,1152542
sga-MIR172-5	248	17,7419355	39,1129032	12,5	30,6451613	30,2419355	69,7580645	0,78350515	1,41935484	-71,8	-57,7	0,0004926	44,95	-28,951613	-0,9573333
sga-MIR172-6	168	19,047619	30,3571429	11,3095238	39,2857143	30,3571429	69,6428571	1,29411765	1,68421053	-57	-56,2	0,0109254	15,05	-33,928571	-1,1176471
sga-MIR172-7	142	20,4225352	33,0985915	13,3802817	33,0985915	33,8028169	66,1971831	1	1,52631579	-51,4	-50,5	0,0225746	15,35	-36,197183	-1,0708333
sga-MIR172-8	163	16,5644172	37,4233129	14,1104294	31,9018405	30,6748466	69,3251534	0,85245902	1,17391304	-52,5	-43,9	0,00974715	26,91	-32,208589	-1,05
sga-MIR172-9	103	18,4466019	34,9514563	17,4757282	29,1262136	35,9223301	64,0776699	0,83333333	1,05555556	-40,1	-32,6	0,0438801	16,19	-38,932039	-1,0837838
sga-MIR172a	124	17,7419355	36,2903226	20,1612903	25,8064516	37,9032258	62,0967742	0,71111111	0,88	-53,4	-53,4	0,240194	2,99	-43,064516	-1,1361702
sga-MIR172b	117	16,2393162	30,7692308	15,3846154	37,6068376	31,6239316	68,3760684	1,22222222	1,05555556	-40,6	-38,8	0,031595	13,61	-34,700855	-1,0972973
sga-MIR172c	94	23,4042553	29,787234	13,8297872	32,9787234	37,2340426	62,7659574	1,10714286	1,69230769	-42,8	-39,3	0,069746	9,2	-45,531915	-1,2228571
sga-MIR172d	112	15,1785714	41,0714286	17,8571429	25,8928571	33,0357143	66,9642857	0,63043478	0,85	-39,5	-39,5	0,131563	5,01	-35,267857	-1,0675676
sga-MIR172j-1	102	13,7254902	31,372549	27,4509804	27,4509804	41,1764706	58,8235294	0,875	0,5	-36,5	-36,5	0,204011	4,47	-35,784314	-0,8690476
sga-MIR172j-2	169	13,6094675	36,0946746	17,1597633	33,1360947	30,7692308	69,2307692	0,91803279	0,79310345	-54,4	-54,4	0,131028	13,83	-32,189349	-1,0461538
sga-MIR1847	139	16,5467626	35,2517986	13,6690647	34,5323741	30,2158273	69,7841727	0,97959184	1,21052632	-44,9	-36,3	0,0507454	15,87	-32,302158	-1,0690476
sga-MIR1850	175	18,8571429	35,4285714	17,1428571	28,5714286	36	64	0,80645161	1,1	-56	-52,4	0,00784537	23,47	-32	-0,8888889
sga-MIR1862g-1	126	20,6349206	27,7777778	14,2857143	37,3015873	34,9206349	65,0793651	1,34285714	1,44444444	-31,2	-30,7	0,00466879	12,01	-24,761905	-0,7090909
sga-MIR1862g-2	174	21,2643678	32,183908	9,77011494	36,7816092	31,0344828	68,9655172	1,14285714	2,17647059	-39,7	-31,9	0,0015591	40,16	-22,816092	-0,7351852
sga-MIR1882e	207	21,2560386	28,9855072	10,6280193	39,1304348	31,884058	68,115942	1,35	2	-47,5	-44,5	0,0113532	18,36	-22,94686	-0,719697
sga-MIR1885a	302	26,1589404	24,8344371	17,5496689	31,4569536	43,7086093	56,2913907	1,26666667	1,49056604	-93,7	-77,4	0,0003597	41,47	-31,02649	-0,7098485

sga-MIR1886f	94	22,3404255	29,787234	13,8297872	34,0425532	36,1702128	63,8297872	1,14285714	1,61538462	-33,5	-32	0,036676	10,53	-35,638298	-0,9852941
sga-MIR1886h-1	94	17,0212766	30,8510638	17,0212766	35,106383	34,0425532	65,9574468	1,13793103	1	-49,5	-49,5	0,568037	2,61	-52,659574	-1,546875
sga-MIR1886h-2	167	17,3652695	32,3353293	13,7724551	36,5269461	31,1377246	68,8622754	1,12962963	1,26086957	-51,4	-43,9	0,00302913	37,56	-30,778443	-0,9884615
sga-MIR1888a	207	14,4927536	30,4347826	16,4251208	38,647343	30,9178744	69,0821256	1,26984127	0,88235294	-69,1	-66,9	0,00184314	20,95	-33,381643	-1,0796875
sga-MIR1888b	227	28,1938326	25,9911894	17,1806167	28,6343612	45,3744493	54,6255507	1,10169492	1,64102564	-81,3	-80	0,00046113	42,53	-35,814978	-0,7893204
sga-MIR1916	325	18,4615385	33,5384615	15,3846154	32,6153846	33,8461538	66,1538462	0,97247706	1,2	-82,1	-75,5	0,00013611	55,63	-25,261538	-0,7463636
sga-MIR1917-1	206	17,961165	36,8932039	13,592233	31,5533981	31,5533981	68,4466019	0,85526316	1,32142857	-59,7	-56,6	0,00286319	26,41	-28,980583	-0,9184615
sga-MIR1917-2	210	15,7142857	35,7142857	17,1428571	31,4285714	32,8571429	67,1428571	0,88	0,91666667	-61	-58	0,00323743	31,79	-29,047619	-0,884058
sga-MIR1917-3	250	17,2	35,6	16,8	30,4	34	66	0,85393258	1,02380952	-66,7	-66,7	0,00910939	15,84	-26,68	-0,7847059
sga-MIR1917-4	219	18,2648402	37,4429224	11,8721461	32,4200913	30,1369863	69,8630137	0,86585366	1,53846154	-61	-42,33	0,00327204	69,86	-27,853881	-0,9242424
sga-MIR1917-5	214	15,4205607	38,317757	16,3551402	29,9065421	31,7757009	68,2242991	0,7804878	0,94285714	-53,6	-48,43	0,00129702	29,81	-25,046729	-0,7882353
sga-MIR1917-6	214	16,3551402	40,1869159	14,0186916	29,4392523	30,3738318	69,6261682	0,73255814	1,16666667	-61,3	-60,6	0,00790997	14,26	-28,64486	-0,9430769
sga-MIR1918	149	18,7919463	32,885906	15,4362416	32,885906	34,2281879	65,7718121	1	1,2173913	-56,2	-54,9	0,0119187	11,31	-37,718121	-1,1019608
sga-MIR1919-1	149	22,8187919	22,8187919	20,1342282	34,2281879	42,9530201	57,0469799	1,5	1,13333333	-58,8	-58,8	0,0624817	11,14	-39,463087	-0,91875
sga-MIR1919-2	177	23,1638418	22,5988701	22,0338983	32,2033898	45,1977401	54,8022599	1,425	1,05128205	-85,7	-85,7	0,113702	8,67	-48,418079	-1,07125
sga-MIR1919-3	177	22,5988701	22,0338983	22,0338983	33,3333333	44,6327684	55,3672316	1,51282051	1,02564103	-79,2	-75,7	0,0262689	15,26	-44,745763	-1,0025316
sga-MIR1919-4	107	20,5607477	28,9719626	20,5607477	29,9065421	41,1214953	58,8785047	1,03225806	1	-46,6	-46,6	0,116525	10,67	-43,551402	-1,0590909
sga-MIR1919-5	154	22,7272727	23,3766234	22,0779221	31,8181818	44,8051948	55,1948052	1,36111111	1,02941176	-74,3	-73,44	0,012205	14,75	-48,227273	-1,0763768
sga-MIR2055	272	15,8088235	32,7205882	16,9117647	34,5588235	32,7205882	67,2794118	1,05617978	0,93478261	-89,6	-76,2	5,97E-05	35,88	-32,941176	-1,0067416
sga-MIR2111d	73	20,5479452	26,0273973	16,4383562	36,9863014	36,9863014	63,0136986	1,42105263	1,25	-37,6	-37,6	0,2639	1,91	-51,506849	-1,3925926
sga-MIR2118a	211	14,6919431	37,9146919	15,6398104	31,7535545	30,3317536	69,6682464	0,8375	0,93939394	-48,3	-42,5	0,00348862	37,95	-22,890995	-0,7546875
sga-MIR2275a	129	31,0077519	19,379845	24,0310078	25,5813953	55,0387597	44,9612403	1,32	1,29032258	-51,7	-51,7	0,0759803	11,21	-40,077519	-0,728169
sga-MIR2592bq-1	312	17,9487179	30,1282051	13,4615385	38,4615385	31,4102564	68,5897436	1,27659574	1,33333333	-69,9	-48,9	1,39E-05	103,48	-22,403846	-0,7132653
sga-MIR2592bq-2	305	17,0491803	34,7540984	14,7540984	33,442623	31,8032787	68,1967213	0,96226415	1,15555556	-84,7	-81,7	0,00047179	34,79	-27,770492	-0,8731959
sga-MIR2606c	324	26,5432099	28,3950617	14,8148148	30,2469136	41,3580247	58,6419753	1,06521739	1,79166667	-95	-74,8	5,39E-05	101,24	-29,320988	-0,7089552
sga-MIR2612	84	19,047619	25	19,047619	36,9047619	38,0952381	61,9047619	1,47619048	1	-22,9	-21,8	0,095617	10,18	-27,261905	-0,715625
sga-MIR2622	88	18,1818182	28,4090909	21,5909091	31,8181818	39,7727273	60,2272727	1,12	0,84210526	-49,8	-49,8	0,204618	2,96	-56,590909	-1,4228571
sga-MIR2630v	143	23,0769231	21,6783217	20,2797203	34,965035	43,3566434	56,6433566	1,61290323	1,13793103	-45,5	-45,3	0,00586821	21,82	-31,818182	-0,733871
sga-MIR2655o	228	15,7894737	37,7192982	16,2280702	30,2631579	32,0175439	67,9824561	0,80232558	0,97297297	-82,5	-78,47	0,00085155	25,5	-36,201754	-1,1306849
sga-MIR2662	86	24,4186047	32,5581395	11,627907	31,3953488	36,0465116	63,9534884	0,96428571	2,1	-23,7	-23,7	0,457726	5,52	-27,55814	-0,7645161
sga-MIR2669b	147	21,0884354	29,9319728	20,4081633	28,5714286	41,4965986	58,5034014	0,95454545	1,03333333	-51,4	-51,4	0,00979808	12,39	-34,965986	-0,842623
sga-MIR2671i	199	22,1105528	32,6633166	11,5577889	33,6683417	33,6683417	66,3316583	1,03076923	1,91304348	-48	-37,5	0,0049708	31,7	-24,120603	-0,7164179
sga-MIR2676f	135	14,8148148	28,1481481	20	37,037037	34,8148148	65,1851852	1,31578947	0,74074074	-57,8	-57,4	0,170187	6,05	-42,814815	-1,2297872
sga-MIR2864	280	23,5714286	22,8571429	22,5	31,0714286	46,0714286	53,9285714	1,359375	1,04761905	-93,1	-84,2	0,00075419	50,33	-33,25	-0,7217054
sga-MIR2873c	312	25,6410256	29,4871795	15,3846154	29,4871795	41,025641	58,974359	1	1,66666667	-94,6	-64,2	0,00027749	91	-30,320513	-0,7390625
sga-MIR2875	202	16,3366337	33,6633663	17,3267327	32,6732673	33,6633663	66,3366337	0,97058824	0,94285714	-66,2	-66,2	0,0310893	11,02	-32,772277	-0,9735294
sga-MIR2879	168	16,0714286	36,9047619	18,452381	28,5714286	34,5238095	65,4761905	0,77419355	0,87096774	-50,9	-45	0,0425214	12,74	-30,297619	-0,8775862
sga-MIR2920	262	18,3206107	34,351145	15,2671756	32,0610687	33,5877863	66,4122137	0,93333333	1,2	-71,4	-55,67	0,00098009	30,24	-27,251908	-0,8113636
sga-MIR2921	129	18,6046512	28,6821705	14,7286822	37,9844961	33,3333333	66,6666667	1,32432432	1,26315789	-59,9	-58,9	0,0712501	4,89	-46,434109	-1,3930233
sga-MIR2929	84	22,6190476	28,5714286	17,8571429	30,952381	40,4761905	59,5238095	1,08333333	1,26666667	-27,1	-24,7	0,0793072	14,35	-32,261905	-0,7970588
sga-MIR2931	212	22,1698113	29,7169811	13,6792453	34,4339623	35,8490566	64,1509434	1,15873016	1,62068966	-56,2	-42,6	0,00386408	48,82	-26,509434	-0,7394737
sga-MIR2949a	124	17,7419355	37,0967742	16,1290323	29,0322581	33,8709677	66,1290323	0,7826087	1,1	-33,3	-28,1	0,00811161	16,83	-26,854839	-0,7928571
sga-MIR319a-1	184	22,826087	28,8043478	20,6521739	27,7173913	43,4782609	56,5217391	0,96226415	1,10526316	-77,8	-72,6	0,0487764	22,54	-42,282609	-0,9725
sga-MIR319a-2	185	21,0810811	27,027027	18,3783784	33,5135135	39,4594595	60,5405405	1,24	1,14705882	-92,3	-91,6	0,0174515	9,73	-49,891892	-1,2643836
sga-MIR319a-3	175	25,7142857	26,2857143	21,1428571	26,8571429	46,8571429	53,1428571	1,02173913	1,21621622	-82,7	-80,4	0,0605567	8,72	-47,257143	-1,0085366
sga-MIR319b-1	198	23,7373737	29,2929293	20,2020202	26,7676768	43,9393939	56,0606061	0,9137931	1,175	-97,8	-97,8	0,114249	5,34	-49,393939	-1,1241379
sga-MIR319b-2	211	20,8530806	31,7535545	19,4312796	27,9620853	40,2843602	59,7156398	0,88059701	1,07317073	-90,2	-90,2	0,0273192	8,53	-42,748815	-1,0611765
sga-MIR319c	176	25,5681818	23,8636364	21,5909091	28,9772727	47,1590909	52,8409091	1,21428571	1,18421053	-76,5	-65,1	0,0169927	17,33	-43,465909	-0,9216867
sga-MIR319d	177	25,4237288	23,1638418	19,7740113	31,6384181	45,1977401	54,8022599	1,36585366	1,28571429	-85,9	-85,1	0,0475253	6,14	-48,531073	-1,07375
sga-MIR3437	240	18,75	28,75	11,6666667	40,4166667	30,4166667	69,1666667	1,4057971	1,60714286	-52,5	-47,6	8,12E-05	28,03	-21,875	-0,7191781
sga-MIR3447	205	22,9268293	31,7073171	9,75609756	35,6097561	32,6829268	67,3170732	1,12307692	2,35	-48,3	-47,5	0,0016788	21,6	-23,560976	-0,7208955
sga-MIR3448	104	23,0769231	34,6153846	13,4615385	28,8461538	36,5384615	63,4615385	0,83333333	1,71428571	-29	-29	0,201646	6,65	-27,884615	-0,7631579
sga-MIR3627	125	22,4	27,2	20	30,4	42,4	57,6	1,11764706	1,12	-47,6	-47,6	0,149706	5,08	-38,08	-0,8981132
sga-MIR3636	307	17,9153094	30,6188925	13,6807818	37,7850163	31,5960912	68,4039088	1,23404255	1,30952381	-76,7	-51	0,00013591	94,83	-24,983713	-0,7907216
sga-MIR3637	164	21,3414634	31,097561	11,5853659	35,9756098	32,9268293	67,0731707	1,15686275	1,84210526	-57	-56,8	0,00353386	16,34	-34,756098	-1,0555556
sga-MIR3693c	327	16,5137615	23,853211	16,2079511	43,4250765	32,7217125	67,2782875	1,82051282	1,01886792	-81	-76	9,16E-05	56,59	-24,770642	-0,7570093
sga-MIR3706-1	70	21,4285714	30	20	28,5714286	41,4285714	58,5714286	0,95238095	1,07142857	-28,7	-28,7	0,428936	2,82	-41	-0,9896552
sga-MIR3706-2	81	16,0493827	30,8641975	20,9876543	32,0987654	37,037037	62,962963	1,04	0,76470588	-39,3	-39,3	0,293519	2,22	-48,518519	-1,31
sga-MIR390-1	117	21,3675214	23,0769231	19,6581197	35,8974359	41,025641	58,974359	1,55555556	1,08695652	-54,8	-54,8	0,539138	1,52	-46,837607	-1,1416667
sga-MIR390-2	106	20,754717	30,1886792	22,6415094	26,4150943	43,3962264	56,6037736	0,875	0,91666667	-43,7	-43,7	0,157079	5,71	-41,226415	-0,95
sga-MIR390a	106	22,6415094	26,4150943	20,754717	30,1886792	43,3962264	56,6037736	1,14285714	1,09090909	-51,5	-48,8	0,102755	6,65	-48,584906	-1,1195652
sga-MIR390b	203	21,6748768	34,4827586	15,7635468	28,0788177	37,4384236	62,5615764	0,81428571	1,375	-56,5	-48,2	0,00393645	32,29	-27,832512	-0,7434211
sga-MIR391	96	23,9583333	34,375	16,6666667	25	40,625	59,375	0,72727273	1,4375	-46,7	-46,7	0,336484	3,38	-48,645833	-1,1974359
sga-MIR393	277	14,4404332	33,5740072	15,8844765	36,101083	30,3249097	69,6750903	1,07526882	0,90909091	-75,2	-72,8	0,00088741	31,95	-27,148014	-0,8952381
sga-MIR3932b	179	18,9944134	30,726257	16,7597765	33,5195531	35,7541899	64,2458101	1,09090909	1,13333333	-56,4	-54,3	0,0037964	24,3	-31,50838	-0,88125
sga-MIR393b-1	78	21,7948718	26,9230769	20,5128205	30,7692308	42,3076923	57,6923077	1,14285714	1,0625	-39,9	-39,9	0,199073	2,73	-51,153846	-1,2090909

sga-MIR393b-2	218	14,2201835	32,1100917	21,559633	32,1100917	35,7798165	64,2201835	1	0,65957447	-59,1	-56	0,0253873	23,32	-27,110092	-0,7576923
sga-MIR394-1	94	26,5957447	20,212766	28,7234043	24,4680851	55,3191489	44,6808511	1,21052632	0,92592593	-44,4	-43,2	0,0896826	4,96	-47,234043	-0,8538462
sga-MIR394-2	61	29,5081967	21,3114754	27,8688525	21,3114754	57,3770492	42,6229508	1	1,05882353	-31,2	-30,9	0,175055	3,56	-51,147541	-0,8914286
sga-MIR394-3	185	14,5945946	24,3243243	15,6756757	45,4054054	30,2702703	69,7297297	1,86666667	0,93103448	-66,2	-64	0,0684765	8,85	-35,783784	-1,1821429
sga-MIR394-4	169	16,5680473	34,3195266	16,5680473	32,5443787	33,1360947	66,8639053	0,94827586	1	-69,3	-69,1	0,0122318	14,24	-41,005917	-1,2375
sga-MIR3946	259	24,7104247	36,2934363	12,7413127	26,2548263	37,4517375	62,5482625	0,72340426	1,93939394	-80	-68	0,00022361	50,14	-30,888031	-0,8247423
sga-MIR394b	233	25,3218884	30,9012876	14,5922747	29,1845494	39,9141631	60,0858369	0,94444444	1,73529412	-81,2	-79,7	0,0100066	25,35	-34,849785	-0,8731183
sga-MIR3951a	84	15,4761905	27,3809524	20,2380952	36,9047619	35,7142857	64,2857143	1,34782609	0,76470588	-30,9	-30,1	0,255678	2,47	-36,785714	-1,03
sga-MIR3951b	181	19,3370166	29,281768	14,3646409	37,0165746	33,7016575	66,2983425	1,26415094	1,34615385	-49,1	-46,6	0,0124464	25,67	-27,127072	-0,804918
sga-MIR395a-1	113	21,2389381	23,8938053	16,8141593	38,0530973	38,0530973	61,9469027	1,59259259	1,26315789	-47,1	-47,1	0,279231	4,54	-41,681416	-1,0953488
sga-MIR395a-2	252	22,6190476	28,1746032	13,4920635	35,7142857	36,1111111	63,8888889	1,26760563	1,67647059	-68	-55,62	0,00018919	42,95	-26,984127	-0,7472527
sga-MIR395a-3	107	21,4953271	20,5607477	21,4953271	36,4485981	42,9906542	57,0093458	1,77272727	1	-48,9	-48,9	0,160511	5,57	-45,700935	-1,0630435
sga-MIR395a-4	151	20,5298013	31,1258278	15,8940397	32,4503311	36,4238411	63,5761589	1,04255319	1,29166667	-50,8	-45,7	0,0279526	15,98	-33,642384	-0,9236364
sga-MIR395a-5	163	22,0858896	28,2208589	17,791411	31,9018405	39,8773006	60,1226994	1,13043478	1,24137931	-61,7	-61,7	0,0634031	16,4	-37,852761	-0,9492308
sga-MIR395b	90	26,6666667	15,5555556	23,3333333	34,4444444	50	50	2,21428571	1,14285714	-42,5	-42,5	0,145097	4,99	-47,222222	-0,9444444
sga-MIR395g-1	293	20,4778157	31,0580205	12,9692833	35,4948805	33,447099	66,552901	1,14285714	1,57894737	-79,2	-74,1	9,36E-05	42,07	-27,030717	-0,8081633
sga-MIR395g-2	290	21,0344828	30	13,1034483	35,862069	34,137931	65,862069	1,1954023	1,60526316	-76,3	-65,5	8,71E-05	50,8	-26,310345	-0,7707071
sga-MIR396	95	16,8421053	36,8421053	16,8421053	29,4736842	33,6842105	66,3157895	0,8	1	-42,7	-41,7	0,173775	4,09	-44,947368	-1,334375
sga-MIR396a-1	141	18,4397163	31,9148936	14,893617	34,751773	33,3333333	66,6666667	1,08888889	1,23809524	-68,6	-66,2	0,122485	3,16	-48,652482	-1,4595745
sga-MIR396a-2	112	14,2857143	36,6071429	18,75	30,3571429	33,0357143	66,9642857	0,82926829	0,76190476	-41,8	-41,8	0,0525966	7,72	-37,321429	-1,1297297
sga-MIR396b-1	133	18,7969925	30,075188	14,2857143	36,8421053	33,0827068	66,9172932	1,225	1,31578947	-56,8	-53,51	0,0300123	14,47	-42,706767	-1,2909091
sga-MIR396b-2	161	18,0124224	32,2981366	13,0434783	36,6459627	31,0559006	68,9440994	1,13461538	1,38095238	-57	-51,81	0,00590194	24,77	-35,403727	-1,14
sga-MIR396b-3	135	17,037037	34,0740741	13,3333333	35,5555556	30,3703704	69,6296296	1,04347826	1,27777778	-49,6	-46,31	0,0245187	16,84	-36,740741	-1,2097561
sga-MIR396f	122	19,6721311	30,3278689	14,7540984	35,2459016	34,4262295	65,5737705	1,16216216	1,33333333	-49,4	-46	0,00899036	16,78	-40,491803	-1,1761905
sga-MIR396g	122	21,3114754	28,6885246	20,4918033	29,5081967	41,8032787	58,1967213	1,02857143	1,04	-39,9	-39,9	0,148352	6,86	-32,704918	-0,7823529
sga-MIR397-1	177	24,8587571	28,8135593	21,4689266	24,8587571	46,3276836	53,6723164	0,8627451	1,15789474	-91,1	-91,1	0,108967	5,21	-51,468927	-1,1109756
sga-MIR397-2	122	18,852459	25,4098361	18,0327869	37,704918	36,8852459	63,1147541	1,48387097	1,04545455	-51,9	-51,5	0,053591	8,93	-42,540984	-1,1533333
sga-MIR397b	127	18,1102362	36,2204724	20,4724409	25,1968504	38,5826772	61,4173228	0,69565217	0,88461538	-48	-48	0,0469476	9,52	-37,795276	-0,9795918
sga-MIR398-1	105	20	22,8571429	18,0952381	39,047619	38,0952381	61,9047619	1,70833333	1,10526316	-46,4	-46,1	0,172909	8,87	-44,190476	-1,16
sga-MIR398-2	124	23,3870968	20,1612903	22,5806452	33,8709677	45,9677419	54,0322581	1,68	1,03571429	-63,9	-63,8	0,088157	7,49	-51,532258	-1,1210526
sga-MIR398a	102	18,627451	28,4313725	15,6862745	37,254902	34,3137255	65,6862745	1,31034483	1,1875	-39,3	-37,7	0,0412401	12,62	-38,529412	-1,1228571
sga-MIR399a	95	20	26,3157895	21,0526316	32,6315789	41,0526316	58,9473684	1,24	0,95	-49,6	-49,6	0,0879684	5,79	-52,210526	-1,2717949
sga-MIR399b-1	217	22,5806452	31,797235	17,9723502	27,6497696	40,5529954	59,4470046	0,86956522	1,25641026	-70,3	-68,4	0,00215295	15,68	-32,396313	-0,7988636
sga-MIR399b-2	86	23,255814	25,5813953	23,255814	27,9069767	46,5116279	53,4883721	1,09090909	1	-43,5	-43,5	0,369104	2,13	-50,581395	-1,0875
sga-MIR399i-1	135	22,2222222	28,1481481	13,3333333	36,2962963	35,5555556	64,4444444	1,28947368	1,66666667	-59,7	-57,4	0,0229381	7,48	-44,222222	-1,24375
sga-MIR399i-2	136	22,0588235	27,2058824	13,2352941	37,5	35,2941176	64,7058824	1,37837838	1,66666667	-59	-55,1	0,0210961	7,9	-43,382353	-1,2291667
sga-MIR399i-3	144	20,8333333	31,9444444	17,3611111	29,8611111	38,1944444	61,8055556	0,93478261	1,2	-44,7	-43,9	0,0326895	16,8	-31,041667	-0,8127273
sga-MIR399r	131	13,740458	30,5343511	19,0839695	36,6412214	32,8244275	67,1755725	1,2	0,72	-47,6	-45,7	0,0682294	9,63	-36,335878	-1,1069767
sga-MIR403-1	105	19,047619	28,5714286	19,047619	33,3333333	38,0952381	61,9047619	1,16666667	1	-37,4	-34,4	0,0546323	11,2	-35,619048	-0,935
sga-MIR403-2	154	18,1818182	27,9220779	19,4805195	34,4155844	37,6623377	62,3376623	1,23255814	0,93333333	-49,2	-45,4	0,0089026	17,93	-31,948052	-0,8482759
sga-MIR403-3	141	17,7304965	29,0780142	19,1489362	34,0425532	36,8794326	63,1205674	1,17073171	0,92592593	-47,4	-44,4	0,0413199	16,76	-33,617021	-0,9115385
sga-MIR408-1	72	22,2222222	25	26,3888889	26,3888889	48,6111111	51,3888889	1,05555556	0,84210526	-30,9	-29,4	0,63272	1,42	-42,916667	-0,8828571
sga-MIR408-2	83	25,3012048	18,0722892	27,7108434	28,9156627	53,0120482	46,9879518	1,6	0,91304348	-37	-37	0,541603	1,83	-44,578313	-0,8409091
sga-MIR408-3	128	25,78125	32,03125	22,65625	19,53125	48,4375	51,5625	0,6097561	1,13793103	-46,6	-41,4	0,0291793	9,07	-36,40625	-0,7516129
sga-MIR4223	225	17,3333333	30,2222222	16,8888889	35,5555556	34,2222222	65,7777778	1,17647059	1,02631579	-66,7	-66,7	0,00603392	15,63	-29,644444	-0,8662338
sga-MIR4225	186	12,9032258	32,7956989	19,3548387	34,9462366	32,2580645	67,7419355	1,06557377	0,66666667	-46,9	-46,9	0,0451103	25,75	-25,215054	-0,7816667
sga-MIR4234	192	17,7083333	29,6875	17,7083333	34,8958333	35,4166667	64,5833333	1,1754386	1	-48,6	-45,2	0,00761515	31,28	-25,3125	-0,7147059
sga-MIR4240	161	24,8447205	29,8136646	8,69565217	36,6459627	33,5403727	66,4596273	1,22916667	2,85714286	-51,1	-26,8	0,00379025	62,52	-31,73913	-0,9462963
sga-MIR4351	235	15,3191489	34,893617	16,1702128	33,6170213	31,4893617	68,5106383	0,96341463	0,94736842	-52,3	-41,2	0,00039043	54,07	-22,255319	-0,7067568
sga-MIR437a	140	22,8571429	25	13,5714286	38,5714286	36,4285714	63,5714286	1,54285714	1,68421053	-36	-27,5	0,00511527	30,27	-25,714286	-0,7058824
sga-MIR4406	86	25,5813953	24,4186047	20,9302326	29,0697674	46,5116279	53,4883721	1,19047619	1,22222222	-29,4	-26	0,0828878	8,02	-34,186047	-0,735
sga-MIR4408	116	18,9655172	28,4482759	17,2413793	35,3448276	36,2068966	63,7931034	1,24242424	1,1	-31,5	-30,3	0,0203379	18,99	-27,155172	-0,75
sga-MIR475b	99	22,2222222	25,2525253	26,2626263	26,2626263	48,4848485	51,5151515	1,04	0,84615385	-34	-32,3	0,0549769	7,87	-34,343434	-0,7083333
sga-MIR477-1	134	21,641791	28,358209	22,3880597	27,6119403	44,0298507	55,9701493	0,97368421	0,96666667	-52,9	-49,8	0,0354548	11,25	-39,477612	-0,8966102
sga-MIR477-2	116	25	27,5862069	20,6896552	26,7241379	45,6896552	54,3103448	0,96875	1,20833333	-58,4	-57,9	0,114479	7,54	-50,344828	-1,1018868
sga-MIR477-3	296	16,2162162	33,7837838	14,1891892	35,472973	30,4054054	69,2567568	1,05	1,14285714	-96	-91,6	0,00274294	40,65	-32,432432	-1,0666667
sga-MIR477a-1	68	25	19,1176471	27,9411765	27,9411765	52,9411765	47,0588235	1,46153846	0,89473684	-35,4	-34	0,219683	2,56	-52,058824	-0,9833333
sga-MIR477a-2	264	21,969697	37,1212121	12,5	28,4090909	34,469697	65,530303	0,76530612	1,75757576	-64,1	-53,2	3,55E-05	54,15	-24,280303	-0,7043956
sga-MIR477b	90	20	22,2222222	20	37,7777778	40	60	1,7	1	-37,2	-32	0,0386397	6,86	-41,333333	-1,0333333
sga-MIR477c	124	19,3548387	27,4193548	22,5806452	30,6451613	41,9354839	58,0645161	1,11764706	0,85714286	-67,4	-65,9	0,226367	4,11	-54,354839	-1,2961538
sga-MIR477d	218	23,3944954	26,146789	23,853211	26,6055046	47,2477064	52,7522936	1,01754386	0,98076923	-76,7	-72,6	0,00846161	25,34	-35,183486	-0,7446602
sga-MIR478d	194	17,0103093	31,443299	13,4020619	38,1443299	30,4123711	69,5876289	1,21311475	1,26923077	-41,6	-40,8	0,00066128	29,02	-21,443299	-0,7050847
sga-MIR478f	116	20,6896552	25,862069	15,5172414	37,9310345	36,2068966	63,7931034	1,46666667	1,33333333	-38,5	-36,5	0,0942929	10,57	-33,189655	-0,9166667
sga-MIR479-1	92	21,7391304	29,3478261	18,4782609	30,4347826	40,2173913	59,7826087	1,03703704	1,17647059	-40,9	-39,7	0,0909347	7,81	-44,456522	-1,1054054
sga-MIR479-2	105	21,9047619	29,5238095	18,0952381	30,4761905	40	60	1,03225806	1,21052632	-52,2	-51	0,0716574	7,86	-49,714286	-1,2428571
sga-MIR482b-1	124	26,6129032	27,4193548	16,9354839	29,0322581	43,5483871	56,4516129	1,05882353	1,57142857	-51,5	-51,1	0,0308083	10,37	-41,532258	-0,9537037

sga-MIR482b-2	111	18,018018	30,6306306	17,1171171	34,2342342	35,1351351	64,8648649	1,11764706	1,05263158	-42,7	-42,3	0,0724983	8,87	-38,468468	-1,0948718
sga-MIR482b-3	110	19,0909091	30,9090909	18,1818182	31,8181818	37,2727273	62,7272727	1,02941176	1,05	-47,5	-47,1	0,0774172	8,75	-43,181818	-1,1585366
sga-MIR482b-4	221	18,5520362	34,841629	14,0271493	32,5791855	32,5791855	67,4208145	0,93506494	1,32258065	-53,4	-46,71	0,00361779	28,66	-24,162896	-0,7416667
sga-MIR482c-1	109	19,266055	17,4311927	18,3486239	44,9541284	37,6146789	62,3853211	2,57894737	1,05	-48,7	-48,5	0,323046	2,47	-44,678899	-1,1878049
sga-MIR482c-2	212	17,4528302	25,4716981	18,8679245	38,2075472	36,3207547	63,6792453	1,5	0,925	-69,7	-66,8	0,00654784	19,74	-32,877358	-0,9051948
sga-MIR482c-3	79	21,5189873	25,3164557	16,4556962	36,7088608	37,9746835	62,0253165	1,45	1,30769231	-42,3	-42,3	0,125589	6,35	-53,544304	-1,41
sga-MIR482d-1	145	24,8275862	27,5862069	13,7931034	33,7931034	38,6206897	61,3793103	1,225	1,8	-58,9	-54,3	0,00833772	15,12	-40,62069	-1,0517857
sga-MIR482d-2	256	20,3125	25,78125	20,3125	33,59375	40,625	59,375	1,3030303	1	-84,1	-76,4	0,00015207	25,02	-32,851563	-0,8086538
sga-MIR482e	189	22,2222222	24,3386243	17,4603175	35,978836	39,6825397	60,3174603	1,47826087	1,27272727	-76	-75,9	0,0196879	12,81	-40,21164	-1,0133333
sga-MIR5014a-1	234	16,2393162	36,7521368	15,3846154	31,6239316	31,6239316	68,3760684	0,86046512	1,05555556	-52,9	-48,9	0,00246137	31,26	-22,606838	-0,7148649
sga-MIR5014a-10	147	14,9659864	38,7755102	15,6462585	30,6122449	30,6122449	69,3877551	0,78947368	0,95652174	-43,1	-42,3	0,0295548	11,56	-29,319728	-0,9577778
sga-MIR5014a-11	235	13,6170213	34,0425532	17,4468085	34,893617	31,0638298	68,9361702	1,025	0,7804878	-54	-48,9	0,00884755	30,01	-22,978723	-0,739726
sga-MIR5014a-12	173	12,716763	37,5722543	18,4971098	31,2138728	31,2138728	68,7861272	0,83076923	0,6875	-49,3	-49,3	0,0845954	7,14	-28,49711	-0,912963
sga-MIR5014a-13	239	13,8075314	38,0753138	17,9916318	30,125523	31,7991632	68,2008368	0,79120879	0,76744186	-63,1	-63,1	0,0105593	23,66	-26,401674	-0,8302632
sga-MIR5014a-2	216	14,3518519	39,3518519	19,9074074	26,3888889	34,2592593	65,7407407	0,67058824	0,72093023	-58,7	-56,3	0,0264606	8,61	-27,175926	-0,7932432
sga-MIR5014a-3	149	16,7785235	40,2684564	13,4228188	29,5302013	30,2013423	69,7986577	0,73333333	1,25	-54,5	-54,5	0,059754	6,56	-36,577181	-1,2111111
sga-MIR5014a-4	223	15,6950673	31,3901345	16,1434978	36,7713004	31,838565	68,161435	1,17142857	0,97222222	-74	-73,5	0,00912982	15,76	-33,183857	-1,0422535
sga-MIR5014a-5	209	13,8755981	38,277512	16,2679426	31,5789474	30,1435407	69,8564593	0,825	0,85294118	-72,5	-72,5	0,00590235	14,08	-34,688995	-1,1507937
sga-MIR5014a-6	235	16,5957447	36,1702128	15,3191489	31,9148936	31,9148936	68,0851064	0,88235294	1,08333333	-66,5	-64,1	0,00101118	27,58	-28,297872	-0,8866667
sga-MIR5014a-7	229	11,790393	37,9912664	18,3406114	31,8777293	30,1310044	69,8689956	0,83908046	0,64285714	-52,9	-52,9	0,00485741	17,75	-23,100437	-0,7666667
sga-MIR5014a-8	145	14,4827586	37,9310345	19,3103448	28,2758621	33,7931034	66,2068966	0,74545455	0,75	-38,9	-38,1	0,095771	6,15	-26,827586	-0,7938776
sga-MIR5014a-9	220	18,6363636	32,2727273	13,6363636	35,4545455	32,2727273	67,7272727	1,09859155	1,36666667	-92,4	-91,1	0,00115288	27,09	-42	-1,3014085
sga-MIR5019	128	26,5625	31,25	12,5	29,6875	39,0625	60,9375	0,95	2,125	-37,3	-35,4	0,0299416	19,35	-29,140625	-0,746
sga-MIR5021-1	205	18,5365854	33,6585366	12,6829268	35,1219512	31,2195122	68,7804878	1,04347826	1,46153846	-98,4	-95,2	0,00262083	18,33	-48	-1,5375
sga-MIR5021-2	231	21,6450216	27,7056277	11,6883117	38,961039	33,3333333	66,6666667	1,40625	1,85185185	-58,3	-52,7	0,00134457	42,6	-25,238095	-0,7571429
sga-MIR5021-3	76	32,8947368	32,8947368	18,4210526	15,7894737	51,3157895	48,6842105	0,48	1,78571429	-35	-35	0,347484	3,32	-46,052632	-0,8974359
sga-MIR5021-4	333	18,6186186	33,033033	11,7117117	36,6366366	30,3303303	69,6696697	1,10909091	1,58974359	-74,4	-57,1	1,43E-05	73,16	-22,342342	-0,7366337
sga-MIR5021-5	208	25,9615385	28,8461538	20,1923077	25	46,1538462	53,8461538	0,86666667	1,28571429	-78,3	-77,6	0,0749193	13,06	-37,644231	-0,815625
sga-MIR5030	114	20,1754386	31,5789474	13,1578947	35,0877193	33,3333333	66,6666667	1,11111111	1,53333333	-32,4	-32,4	0,193984	6,1	-28,421053	-0,8526316
sga-MIR5035	142	16,1971831	30,9859155	16,9014085	35,915493	33,0985915	66,9014085	1,15909091	0,95833333	-65,4	-64,2	0,0277947	9,42	-46,056338	-1,3914894
sga-MIR5049c	115	18,2608696	37,3913043	13,9130435	30,4347826	32,173913	67,826087	0,81395349	1,3125	-31,7	-28,9	0,0231823	13,49	-27,565217	-0,8567568
sga-MIR5057	103	15,5339806	30,0970874	17,4757282	36,8932039	33,0097087	66,9902913	1,22580645	0,88888889	-26,5	-25,5	0,0379534	9,39	-25,728155	-0,7794118
sga-MIR5070	232	14,2241379	30,1724138	17,6724138	37,9310345	31,8965517	68,1034483	1,25714286	0,80487805	-66,4	-64,6	0,00222073	19,86	-28,62069	-0,8972973
sga-MIR5083	153	15,0326797	35,2941176	20,2614379	29,4117647	35,2941176	64,7058824	0,83333333	0,74193548	-84,7	-83	0,043063	6,08	-55,359477	-1,5685185
sga-MIR5085	191	17,2774869	31,9371728	15,7068063	35,078534	32,9842932	67,0157068	1,09836066	1,1	-46,7	-44,5	0,0198345	25,13	-24,450262	-0,7412698
sga-MIR5157b	234	17,5213675	30,7692308	16,2393162	35,4700855	33,7606838	66,2393162	1,15277778	1,07894737	-72,5	-70,5	0,0156478	15,37	-30,982906	-0,9177215
sga-MIR5160	239	24,2677824	24,6861925	18,4100418	32,6359833	42,6778243	57,3221757	1,3220339	1,31818182	-79,5	-77,2	0,00089942	22,9	-33,263598	-0,7794118
sga-MIR5162-1	225	18,2222222	34,2222222	12,8888889	34,6666667	31,1111111	68,8888889	1,01298701	1,4137931	-50,6	-27,8	0,0007035	46,27	-22,488889	-0,7228571
sga-MIR5162-2	315	24,1269841	32,3809524	17,4603175	26,031746	41,5873016	58,4126984	0,80392157	1,38181818	-92,5	-87,3	0,00091433	59,62	-29,365079	-0,7061069
sga-MIR5167b	283	19,7879859	27,5618375	15,9010601	36,7491166	35,6890459	64,3109541	1,33333333	1,24444444	-71,9	-66,6	0,00056052	46,05	-25,40636	-0,7118812
sga-MIR5174d	256	13,671875	31,25	18,75	36,328125	32,421875	67,578125	1,1625	0,72916667	-59,3	-49,66	0,00014754	45,41	-23,164063	-0,7144578
sga-MIR5174e	188	20,212766	37,2340426	13,2978723	29,2553191	33,5106383	66,4893617	0,78571429	1,52	-62,8	-60,2	0,00799488	15,83	-33,404255	-0,9968254
sga-MIR5183	228	17,5438596	35,0877193	16,6666667	30,7017544	34,2105263	65,7894737	0,875	1,05263158	-98,5	-95,1	0,0143548	14,36	-43,201754	-1,2628205
sga-MIR5205a	296	18,2432432	34,7972973	13,5135135	33,4459459	31,7567568	68,2432432	0,96116505	1,35	-67,1	-39,19	2,60E-05	80,47	-22,668919	-0,7138298
sga-MIR5211	106	19,8113208	26,4150943	24,5283019	29,245283	44,3396226	55,6603774	1,10714286	0,80769231	-34,6	-33,1	0,0332811	8,49	-32,641509	-0,7361702
sga-MIR5225b	214	29,9065421	19,1588785	18,2242991	32,7102804	48,1308411	51,8691589	1,70731707	1,64102564	-78,8	-73,9	0,00252829	25,29	-36,82243	-0,7650485
sga-MIR5232	85	18,8235294	29,4117647	17,6470588	34,1176471	36,4705882	63,5294118	1,16	1,06666667	-34,4	-34,4	0,249685	4,23	-40,470588	-1,1096774
sga-MIR5239	324	23,4567901	29,6296296	15,4320988	31,4814815	38,8888889	61,1111111	1,0625	1,52	-93,8	-89	0,00026449	46,77	-28,950617	-0,7444444
sga-MIR5240-1	110	22,7272727	30,9090909	15,4545455	30,9090909	38,1818182	61,8181818	1	1,47058824	-36,4	-36,4	0,131675	6,41	-33,090909	-0,8666667
sga-MIR5240-2	153	15,6862745	32,0261438	18,9542484	33,3333333	34,6405229	65,3594771	1,04081633	0,82758621	-44,5	-44,4	0,0258992	9,21	-29,084967	-0,8396226
sga-MIR5298c-1	134	22,3880597	30,5970149	20,8955224	26,119403	43,2835821	56,7164179	0,85365854	1,07142857	-87,3	-87	0,407195	3,32	-65,149254	-1,5051724
sga-MIR5298c-2	279	16,8458781	35,483871	15,7706093	31,8996416	32,6164875	67,3835125	0,8989899	1,06818182	-67,3	-58,8	0,00163907	34,15	-24,121864	-0,7395604
sga-MIR5300	264	19,6969697	29,9242424	15,9090909	34,469697	35,6060606	64,3939394	1,15189873	1,23809524	-96,4	-94	0,00403445	14,41	-36,515152	-1,0255319
sga-MIR530-1	86	23,255814	27,9069767	18,6046512	30,2325581	41,8604651	58,1395349	1,08333333	1,25	-42,7	-42,7	0,345573	2,23	-49,651163	-1,1861111
sga-MIR530-2	272	18,0147059	34,1911765	15,4411765	32,3529412	33,4558824	66,5441176	0,94623656	1,16666667	-77,1	-73,3	0,00686593	30,54	-28,345588	-0,8472527
sga-MIR530-3	284	15,8450704	34,1549296	14,4366197	35,5633803	30,2816901	69,7183099	1,04123711	1,09756098	-88,1	-85,5	0,00215941	18,63	-31,021127	-1,0244186
sga-MIR5303-1	110	19,0909091	30	20,9090909	30	40	60	1	0,91304348	-46,7	-46,7	0,101238	5,02	-42,454545	-1,0613636
sga-MIR5303-10	127	16,5354331	25,984252	22,8346457	34,6456693	39,3700787	60,6299213	1,33333333	0,72413793	-44,5	-44,2	0,0437971	5,8	-35,03937	-0,89
sga-MIR5303-13	138	23,1884058	27,5362319	15,2173913	34,057971	38,4057971	61,5942029	1,23684211	1,52380952	-53,4	-52,9	0,0133095	12,48	-38,695652	-1,0075472
sga-MIR5303-14	146	21,9178082	25,3424658	21,2328767	31,5068493	43,1506849	56,8493151	1,24324324	1,03225806	-48,4	-47,7	0,047362	13,33	-33,150685	-0,768254
sga-MIR5303-18	126	18,2539683	26,984127	24,6031746	30,1587302	42,8571429	57,1428571	1,11764706	0,74193548	-40	-37,7	0,00741304	11,56	-31,746032	-0,7407407
sga-MIR5303-2	125	16,8	28,8	28,8	33,5260116	45,6	54,4	0,88888889	0,58333333	-56,1	-56,1	0,293605	2,85	-44,88	-0,9842105
sga-MIR5303-20	173	17,9190751	24,8554913	23,699422	41,6184971	58,3815029	1,34883721	0,75609756	-62,6	-57,9	0,0190699	18,43	-36,184971	-0,8694444
sga-MIR5303-22	125	18,4	28	25,6	28	44	56	1	0,71875	-42	-39,5	0,107229	11,7	-33,6	-0,7636364
sga-MIR5303-4	144	22,2222222	26,3888889	20,1388889	31,25	42,3611111	57,6388889	1,18421053	1,10344828	-62,2	-62	0,0235338	12,38	-43,194444	-1,0196721
sga-MIR5303-5	113	20,3539823	25,6637168	17,699115	36,2831858	38,0530973	61,9469027	1,4137931	1,15	-39,8	-39,8	0,181235	11,19	-35,221239	-0,9255814

sga-MIR5303-8	156	25	28,8461538	19,2307692	26,9230769	44,2307692	55,7692308	0,93333333	1,3	-70,3	-68,7	0,0728902	11	-45,064103	-1,0188406
sga-MIR5303-9	130	16,9230769	30	23,0769231	30	40	60	1	0,73333333	-54,1	-53,7	0,32715	6,19	-41,615385	-1,0403846
sga-MIR5303f-1	237	22,3628692	27,0042194	17,2995781	33,3333333	39,6624473	60,3375527	1,234375	1,29268293	-70,8	-69,9	0,00111995	30,34	-29,873418	-0,7531915
sga-MIR5303f-3	120	26,6666667	26,6666667	14,1666667	32,5	40,8333333	59,1666667	1,21875	1,88235294	-52,9	-52,9	0,050769	5,88	-44,083333	-1,0795918
sga-MIR5303h-4	124	18,5483871	29,0322581	23,3870968	29,0322581	41,9354839	58,0645161	1	0,79310345	-39,4	-39,4	0,1184	10,91	-31,774194	-0,7576923
sga-MIR5303i-2	186	18,2795699	33,8709677	14,516129	33,3333333	32,7956989	67,2043011	0,98412698	1,25925926	-60,1	-52,7	0,00573993	23,07	-32,311828	-0,9852459
sga-MIR5303i-3	123	18,699187	30,8943089	16,2601626	34,1463415	34,9593496	65,0406504	1,10526316	1,15	-41,5	-38,9	0,0256143	14,58	-33,739837	-0,9651163
sga-MIR5303i-6	123	19,5121951	30,0813008	22,7642276	27,6422764	42,2764228	57,7235772	0,91891892	0,85714286	-60,2	-60	0,100624	4	-48,943089	-1,1576923
sga-MIR5303i-7	168	16,6666667	32,1428571	19,047619	32,1428571	35,7142857	64,2857143	1	0,875	-52,1	-44,4	0,0298463	14,71	-31,011905	-0,8683333
sga-MIR5304	140	21,4285714	27,1428571	19,2857143	32,1428571	40,7142857	59,2857143	1,18421053	1,11111111	-60,4	-60,1	0,106203	3,77	-43,142857	-1,0596491
sga-MIR5340	162	15,4320988	36,4197531	14,8148148	32,7160494	30,2469136	69,1358025	0,89830508	1,04166667	-75	-68,7	0,0518644	10,66	-46,296296	-1,5306122
sga-MIR534b	100	14	39	19	28	33	67	0,71794872	0,73684211	-23,3	-20,7	0,0458097	9,65	-23,3	-0,7060606
sga-MIR535	107	20,5607477	25,2336449	22,4299065	31,7757009	42,9906542	57,0093458	1,25925926	0,91666667	-74,5	-74,5	0,602335	0,94	-69,626168	-1,6195652
sga-MIR535f	107	22,4299065	31,7757009	20,5607477	25,2336449	42,9906542	57,0093458	0,79411765	1,09090909	-69,8	-69,8	0,465199	1,86	-65,233645	-1,5173913
sga-MIR5368	83	28,9156627	25,3012048	25,3012048	20,4819277	54,2168675	45,7831325	0,80952381	1,14285714	-33	-33	0,448662	1,92	-39,759036	-0,7333333
sga-MIR5379	159	16,9811321	33,3333333	18,2389937	31,4465409	35,2201258	64,7798742	0,94339623	0,93103448	-42,8	-38,01	0,00839765	17,75	-26,918239	-0,7642857
sga-MIR5499	80	22,5	35	18,75	23,75	41,25	58,75	0,67857143	1,2	-25,6	-25,1	0,104881	5,45	-32	-0,7757576
sga-MIR5532	163	21,4723926	32,5153374	14,7239264	31,2883436	36,196319	63,803681	0,96226415	1,45833333	-46,4	-46,2	0,0434157	10,9	-28,466258	-0,7864407
sga-MIR5537	87	21,8390805	28,7356322	13,7931034	35,6321839	35,6321839	64,3678161	1,24	1,58333333	-34,3	-33,4	0,130632	7,16	-39,425287	-1,1064516
sga-MIR5568e	272	18,0147059	31,9852941	15,4411765	34,5588235	33,4558824	66,5441176	1,08045977	1,16666667	-73,8	-66,8	0,00045146	39,44	-27,132353	-0,810989
sga-MIR5568f	125	21,6	26,4	17,6	34,4	39,2	60,8	1,3030303	1,22727273	-35	-25,7	0,0156916	37,47	-28	-0,7142857
sga-MIR5628	135	18,5185185	35,5555556	17,037037	28,8888889	35,5555556	64,4444444	0,8125	1,08695652	-43,7	-40,6	0,055683	22,11	-32,37037	-0,9104167
sga-MIR5653	302	20,1986755	25,1655629	19,205298	35,4304636	39,4039735	60,5960265	1,40789474	1,05172414	-89,5	-82,7	0,00032956	42,81	-29,635762	-0,7521008
sga-MIR5658	171	21,6374269	30,4093567	12,2807018	35,6725146	33,9181287	66,0818713	1,17307692	1,76190476	-42,6	-33,5	0,0159618	37,8	-24,912281	-0,7344828
sga-MIR5664	149	16,7785235	35,5704698	13,4228188	34,2281879	30,2013423	69,7986577	0,96226415	1,25	-97,8	-97	0,418463	1,55	-65,637584	-2,1733333
sga-MIR5670a	225	18,2222222	26,6666667	19,5555556	35,5555556	37,7777778	62,2222222	1,33333333	0,93181818	-64,2	-59,7	0,00114078	42,44	-28,533333	-0,7552941
sga-MIR5720	91	18,6813187	41,7582418	12,0879121	27,4725275	30,7692308	69,2307692	0,65789474	1,54545455	-27	-25,5	0,0438382	9,96	-29,67033	-0,9642857
sga-MIR5723	276	19,2028986	32,9710145	14,1304348	33,6956522	33,3333333	66,6666667	1,02197802	1,35897436	-74,5	-69,2	0,00080252	25,63	-26,992754	-0,8097826
sga-MIR5752b	295	20	26,1016949	19,3220339	34,5762712	39,3220339	60,6779661	1,32467532	1,03508772	-81,9	-62,9	2,03E-05	69,23	-27,762712	-0,7060345
sga-MIR5760	206	18,9320388	21,3592233	20,8737864	38,8349515	39,8058252	60,1941748	1,81818182	0,90697674	-64,7	-61,1	0,0252352	10,89	-31,407767	-0,7890244
sga-MIR5763c	100	21	30	27	22	48	52	0,73333333	0,77777778	-35,9	-35	0,325736	4,19	-35,9	-0,7479167
sga-MIR5773	164	17,0731707	34,7560976	14,6341463	33,5365854	31,7073171	68,2926829	0,96491228	1,16666667	-96,6	-95	0,0803915	8,86	-58,902439	-1,8576923
sga-MIR5781	98	16,3265306	24,4897959	20,4081633	38,7755102	36,7346939	63,2653061	1,58333333	0,8	-29	-28,2	0,0965677	5,05	-29,591837	-0,8055556
sga-MIR5812	216	23,1481481	31,4814815	14,8148148	30,5555556	37,962963	62,037037	0,97058824	1,5625	-61,5	-44	0,00042041	48,04	-28,472222	-0,75
sga-MIR6022	236	19,9152542	30,0847458	18,6440678	31,3559322	38,559322	61,440678	1,04225352	1,06818182	-81	-60,77	0,00659624	54,63	-34,322034	-0,8901099
sga-MIR6024	118	19,4915254	24,5762712	19,4915254	36,440678	38,9830508	61,0169492	1,48275862	1	-41,5	-41,3	0,0874159	6,64	-35,169492	-0,9021739
sga-MIR6025b-1	164	20,7317073	26,8292683	14,0243902	38,4146341	34,7560976	65,2439024	1,43181818	1,47826087	-50,7	-46,9	0,00516056	21,49	-30,914634	-0,8894737
sga-MIR6025b-2	164	25	25,6097561	13,4146341	35,9756098	38,4146341	61,5853659	1,4047619	1,86363636	-59,7	-57,3	0,0157497	19,08	-36,402439	-0,947619
sga-MIR6027	153	22,2222222	32,6797386	11,7647059	33,3333333	33,9869281	66,0130719	1,02	1,88888889	-58,5	-52,92	0,0463577	16,29	-38,235294	-1,125
sga-MIR6111	306	19,2810458	29,4117647	15,6862745	35,620915	34,9673203	65,0326797	1,21111111	1,22916667	-77,2	-66,1	0,00030297	56,72	-25,228758	-0,7214953
sga-MIR6135e	201	22,3880597	35,3233831	11,4427861	30,8457711	33,8308458	66,1691542	0,87323944	1,95652174	-49	-35,61	0,00091038	42,9	-24,378109	-0,7205882
sga-MIR6139	247	22,2672065	32,388664	17,0040486	28,340081	39,2712551	60,7287449	0,875	1,30952381	-68,4	-57,8	0,0010276	49,41	-27,692308	-0,7051546
sga-MIR6144	301	20,2657807	32,8903654	16,9435216	29,9003322	37,2093023	62,7906977	0,90909091	1,19607843	-93	-83,9	0,00091021	43,11	-30,89701	-0,8303571
sga-MIR6145e	322	17,3913043	31,3664596	13,3540373	37,8881988	30,7453416	69,2546584	1,20792079	1,30232558	-90,1	-80,9	1,52E-05	60,74	-27,981366	-0,910101
sga-MIR6147	339	13,2743363	35,3982301	17,1091445	34,2182891	30,3834808	69,6165192	0,96666667	0,77586207	-95,4	-90,4	0,00040001	30,56	-28,141593	-0,9262136
sga-MIR6148b	254	25,984252	26,7716535	18,8976378	28,3464567	44,8818898	55,1181102	1,05882353	1,375	-83,7	-67,7	0,00049157	59,67	-32,952756	-0,7342105
sga-MIR6160-1	271	16,9741697	28,0442804	18,0811808	36,900369	35,0553506	64,9446494	1,31578947	0,93877551	-67,9	-63,3	0,00019616	76,72	-25,055351	-0,7147368
sga-MIR6160-2	235	21,2765957	34,4680851	14,4680851	29,787234	35,7446809	64,2553191	0,86419753	1,47058824	-58,9	-55,4	0,0019466	35,61	-25,06383	-0,7011905
sga-MIR6164b	211	19,4312796	29,3838863	16,5876777	34,5971564	36,0189573	63,9810427	1,17741935	1,17142857	-75,1	-63,5	0,00146901	44,26	-35,592417	-0,9881579
sga-MIR6166-1	340	21,1764706	26,1764706	13,5294118	39,1176471	34,7058824	65,2941176	1,49438202	1,56521739	-86,1	-78,7	0,0003934	29,81	-25,323529	-0,729661
sga-MIR6166-2	338	20,7100592	26,035503	14,7928994	38,4615385	35,5029586	64,4970414	1,47727273	1,4	-95,1	-91,2	1,19E-05	45,03	-28,136095	-0,7925
sga-MIR6218	250	18	24,8	17,2	40	35,2	64,8	1,61290323	1,04651163	-72,4	-68	0,00488836	20,51	-28,96	-0,8227273
sga-MIR6230	107	23,364486	28,9719626	19,6261682	28,0373832	42,9906542	57,0093458	0,96774194	1,19047619	-53,1	-50,8	0,162778	8,46	-49,626168	-1,1543478
sga-MIR6232b	112	21,4285714	33,0357143	16,0714286	29,4642857	37,5	62,5	0,89189189	1,33333333	-70,1	-69,8	0,178559	4,07	-62,589286	-1,6690476
sga-MIR6235	183	22,4043716	31,147541	21,3114754	25,136612	43,715847	56,284153	0,80701754	1,05128205	-87,9	-87,6	0,0257238	7,95	-48,032787	-1,09875
sga-MIR6271	100	21	36	13	30	34	66	0,83333333	1,61538462	-29	-28,7	0,11976	11,14	-29	-0,8529412
sga-MIR6273-1	86	24,4186047	22,0930233	18,6046512	34,8837209	43,0232558	56,9767442	1,57894737	1,3125	-31,2	-30,3	0,0709258	8,46	-36,27907	-0,8432432
sga-MIR6273-2	109	16,5137615	27,5229358	19,266055	36,6972477	35,7798165	64,2201835	1,33333333	0,85714286	-41,8	-41,7	0,0567579	5,06	-38,348624	-1,0717949
sga-MIR6283	89	22,4719101	29,2134831	14,6067416	33,7078652	37,0786517	62,9213483	1,15384615	1,53846154	-34,5	-33,7	0,114464	6,21	-38,764045	-1,0454545
sga-MIR6288c	252	15,0793651	30,5555556	15,4761905	38,8888889	30,5555556	69,4444444	1,27272727	0,97435897	-74,6	-73,88	0,00081858	27,57	-29,595238	-0,9685714
sga-MIR6293	299	20,735786	29,7658863	19,7324415	29,7658863	40,4682274	59,5317726	1	1,05084746	-87,8	-84,6	0,00035827	39,32	-29,364548	-0,7256198
sga-MIR6427	176	21,0227273	31,25	11,9318182	35,7954545	32,9545455	67,0454545	1,14545455	1,76190476	-56,2	-55	0,0151111	31,25	-31,931818	-0,9689655
sga-MIR6459a	160	16,875	35,625	16,25	31,25	33,125	66,875	0,87719298	1,03846154	-91,6	-90,8	0,115428	5,02	-57,25	-1,7283019
sga-MIR6462c	203	33,4975369	20,1970443	31,0344828	15,270936	64,5320197	35,4679803	0,75609756	1,07936508	-93,8	-92,6	0,0123659	14,23	-46,206897	-0,7160305
sga-MIR6466	200	24	27	12	37	36	64	1,37037037	2	-53	-42,1	0,00098572	49,68	-26,5	-0,7361111
sga-MIR6470	207	13,0434783	35,2657005	17,3913043	34,2995169	30,4347826	69,5652174	0,97260274	0,75	-74,4	-68,64	0,00020931	37,77	-35,942029	-1,1809524

sga-MIR6478-1	205	22,4390244	26,8292683	19,0243902	31,7073171	41,4634146	58,5365854	1,18181818	1,17948718	-59,5	-56,9	0,0101317	22,83	-29,02439	-0,7
sga-MIR6478-2	287	18,815331	27,8745645	16,7247387	36,5853659	35,5400697	64,4599303	1,3125	1,125	-74,3	-71,9	0,00118229	51,43	-25,888502	-0,7284314
sga-MIR7122	78	16,6666667	29,4871795	20,5128205	33,3333333	37,1794872	62,8205128	1,13043478	0,8125	-31,5	-31,5	0,154352	3,65	-40,384615	-1,0862069
sga-MIR7122a	202	19,8019802	36,1386139	12,8712871	31,1881188	32,6732673	67,3267327	0,8630137	1,53846154	-48,4	-44,74	0,00194907	41,45	-23,960396	-0,7333333
sga-MIR7492d	147	21,0884354	26,5306122	12,244898	40,1360544	33,3333333	66,6666667	1,51282051	1,72222222	-35,4	-31,4	0,00710157	30,23	-24,081633	-0,722449
sga-MIR7492f	145	13,1034483	32,4137931	17,9310345	36,5517241	31,0344828	68,9655172	1,12765957	0,73076923	-36,2	-36	0,0154754	10,79	-24,965517	-0,8044444
sga-MIR7493	192	14,0625	32,2916667	16,1458333	37,5	30,2083333	69,7916667	1,16129032	0,87096774	-55,8	-52	0,00821723	16,94	-29,0625	-0,962069
sga-MIR7493b-1	210	18,0952381	38,5714286	13,8095238	29,5238095	31,9047619	68,0952381	0,7654321	1,31034483	-76,3	-66,2	0,00280961	45,51	-36,333333	-1,138806
sga-MIR7493b-2	208	17,3076923	31,25	12,9807692	38,4615385	30,2884615	69,7115385	1,23076923	1,33333333	-66,7	-65,7	0,024688	17,24	-32,067308	-1,0587302
sga-MIR7493b-3	244	18,852459	32,3770492	16,8032787	31,9672131	35,6557377	64,3442623	0,98734177	1,12195122	-62,1	-57,9	0,00130385	29,99	-25,45082	-0,7137931
sga-MIR7493b-4	154	17,5324675	31,8181818	16,8831169	33,7662338	34,4155844	65,5844156	1,06122449	1,03846154	-42,1	-41,7	0,0140043	19,06	-27,337662	-0,7943396
sga-MIR7502c	174	14,3678161	32,7586207	17,816092	35,0574713	32,183908	67,816092	1,07017544	0,80645161	-50,6	-46,3	0,00983886	21,3	-29,08046	-0,9035714
sga-MIR7519	111	14,4144144	39,6396396	16,2162162	29,7297297	30,6306306	69,3693694	0,75	0,88888889	-30,4	-28,7	0,0390247	8,65	-27,387387	-0,8941176
sga-MIR7533b	152	21,7105263	30,9210526	13,8157895	33,5526316	35,5263158	64,4736842	1,08510638	1,57142857	-38,3	-33,3	0,00195673	24,21	-25,197368	-0,7092593
sga-MIR7539	199	22,6130653	36,6834171	12,5628141	28,1407035	35,1758794	64,8241206	0,76712329	1,8	-58,7	-53,59	0,00189787	28,97	-29,497487	-0,8385714
sga-MIR7695-1	156	24,3589744	29,4871795	16,025641	30,1282051	40,3846154	59,6153846	1,02173913	1,52	-48,8	-38,2	0,0197417	36,21	-31,282051	-0,7746032
sga-MIR7695-2	293	16,7235495	33,447099	16,0409556	33,7883959	32,7645051	67,2354949	1,01020408	1,04255319	-79	-73,3	8,68E-05	43,87	-26,962457	-0,8229167
sga-MIR7696d	98	17,3469388	34,6938776	15,3061224	32,6530612	32,6530612	67,3469388	0,94117647	1,13333333	-30,5	-29,7	0,0335336	9,46	-31,122449	-0,953125
sga-MIR7697	127	20,4724409	29,9212598	22,0472441	27,5590551	42,519685	57,480315	0,92105263	0,92857143	-84,8	-84,8	0,123586	5,57	-66,771654	-1,5703704
sga-MIR7723a	83	20,4819277	26,5060241	21,686747	31,3253012	42,1686747	57,8313253	1,18181818	0,94444444	-28,3	-28,1	0,107074	6,12	-34,096386	-0,8085714
sga-MIR7724b	142	14,084507	30,9859155	16,1971831	38,7323944	30,2816901	69,7183099	1,25	0,86956522	-46	-44,7	0,0202033	16,09	-32,394366	-1,0697674
sga-MIR7725b	172	18,6046512	33,1395349	13,9534884	34,3023256	32,5581395	67,4418605	1,03508772	1,33333333	-80,6	-78,5	0,0375707	10,47	-46,860465	-1,4392857
sga-MIR7746	129	17,8294574	27,1317829	15,503876	39,5348837	33,3333333	66,6666667	1,45714286	1,15	-31	-31	0,0589681	9	-24,031008	-0,7209302
sga-MIR7748a	303	16,1716172	32,3432343	19,4719472	32,0132013	35,6435644	64,3564356	0,98979592	0,83050847	-82,4	-80,8	0,00121806	45,14	-27,194719	-0,762963
sga-MIR7752	183	21,3114754	26,2295082	22,4043716	30,0546448	43,715847	56,284153	1,14583333	0,95121951	-96,3	-95,7	0,0378704	8,38	-52,622951	-1,20375
sga-MIR7776	106	16,9811321	28,3018868	16,9811321	37,7358491	33,9622642	66,0377358	1,33333333	1	-31,2	-30,2	0,0554639	6,78	-29,433962	-0,8666667
sga-MIR7787	230	20	29,1304348	15,2173913	35,6521739	35,2173913	64,7826087	1,2238806	1,31428571	-62,2	-57,8	0,0003622	32,62	-27,043478	-0,7679012
sga-MIR779	285	18,245614	30,877193	11,9298246	38,9473684	30,1754386	69,8245614	1,26136364	1,52941176	-63,4	-50	3,33E-05	60,2	-22,245614	-0,7372093
sga-MIR7807b	66	18,1818182	27,2727273	16,6666667	37,8787879	34,8484848	65,1515152	1,38888889	1,09090909	-34,5	-34,5	0,178763	3	-52,272727	-1,5
sga-MIR7819	232	17,2413793	31,4655172	18,9655172	32,3275862	36,2068966	63,7931034	1,02739726	0,90909091	-85,8	-73,7	0,00182728	43,08	-36,982759	-1,0214286
sga-MIR7821	273	20,8791209	28,9377289	19,047619	31,1355311	39,9267399	60,0732601	1,07594937	1,09615385	-76,9	-70,7	0,00031668	47,92	-28,168498	-0,7055046
sga-MIR7822-1	204	20,5882353	30,3921569	11,2745098	37,745098	31,8627451	68,1372549	1,24193548	1,82608696	-60,5	-59,3	0,00534032	12,23	-29,656863	-0,9307692
sga-MIR7822-2	228	18,8596491	29,8245614	14,9122807	36,4035088	33,7719298	66,2280702	1,22058824	1,26470588	-84,3	-84,1	0,0250789	15,25	-36,973684	-1,0948052
sga-MIR7828	307	18,2410423	34,8534202	18,8925081	28,0130293	37,1335505	62,8664495	0,80373832	0,96551724	-92,6	-86,8	0,00054905	24,01	-30,162866	-0,8122807
sga-MIR7840	293	20,4778157	38,5665529	12,2866894	28,668942	32,7645051	67,2354949	0,74336283	1,66666667	-67,5	-62,5	5,04E-05	52,6	-23,037543	-0,703125
sga-MIR7842	85	17,6470588	34,1176471	18,8235294	29,4117647	36,4705882	63,5294118	0,86206897	0,9375	-31,3	-29,5	0,216838	4,64	-36,823529	-1,0096774
sga-MIR7980b-1	110	15,4545455	35,4545455	17,2727273	31,8181818	32,7272727	67,2727273	0,8974359	0,89473684	-32,8	-32,8	0,219581	5,09	-29,818182	-0,9111111
sga-MIR7980b-2	111	20,7207207	27,9279279	16,2162162	35,1351351	36,9369369	63,0630631	1,25806452	1,27777778	-46,6	-46,6	0,131222	6,37	-41,981982	-1,1365854
sga-MIR7980b-3	302	14,9006623	32,781457	15,5629139	36,7549669	30,4635762	69,5364238	1,12121212	0,95744681	-93,8	-78,2	0,00035074	61,97	-31,059603	-1,0195652
sga-MIR7980b-4	98	13,2653061	37,755102	19,3877551	29,5918367	32,6530612	67,3469388	0,78378378	0,68421053	-26,8	-26,6	0,20544	7,22	-27,346939	-0,8375
sga-MIR7980b-5	122	12,295082	36,8852459	19,6721311	31,147541	31,9672131	68,0327869	0,84444444	0,625	-31,7	-31,7	0,17912	7,04	-25,983607	-0,8128205
sga-MIR7981-10	250	15,6	34,4	15,6	34,4	31,2	68,8	1	1	-91,1	-85,9	0,00440591	24,76	-36,44	-1,1679487
sga-MIR7981-12	232	20,2586207	33,6206897	15,5172414	30,6034483	35,7758621	64,2241379	0,91025641	1,30555556	-86,6	-80,17	0,00062243	27,38	-37,327586	-1,0433735
sga-MIR7981-13	216	18,5185185	28,2407407	18,5185185	34,7222222	37,037037	62,962963	1,2295082	1	-86,4	-86,4	0,0141026	20,98	-40	-1,08
sga-MIR7981-14	204	20,0980392	32,3529412	16,1764706	31,372549	36,2745098	63,7254902	0,96969697	1,24242424	-87,9	-87,7	0,0435196	17,29	-43,088235	-1,1878378
sga-MIR7981-16	232	18,9655172	28,0172414	18,9655172	34,0517241	37,9310345	62,0689655	1,21538462	1	-87,7	-87,3	0,00431074	22,17	-37,801724	-0,9965909
sga-MIR7981-18	211	17,0616114	37,4407583	16,5876777	28,9099526	33,6492891	66,3507109	0,7721519	1,02857143	-82,5	-78	0,053173	7,12	-39,099526	-1,1619718
sga-MIR7981-5	211	21,8009479	28,436019	17,0616114	32,7014218	38,8625592	61,1374408	1,15	1,27777778	-89,9	-86,4	0,00766997	22,3	-42,606635	-1,0963415
sga-MIR7981-6	185	16,2162162	32,972973	22,7027027	28,1081081	38,9189189	61,0810811	0,85245902	0,71428571	-54,3	-49,57	0,0120135	18,94	-29,351351	-0,7541667
sga-MIR7981-9	204	16,6666667	31,8627451	16,1764706	35,2941176	32,8431373	67,1568627	1,10769231	1,03030303	-53,4	-43,62	0,0018633	37	-26,176471	-0,7970149
sga-MIR7983-1	207	15,4589372	37,1980676	14,9758454	32,3671498	30,4347826	69,5652174	0,87012987	1,03225806	-53,4	-49	0,0084829	42,02	-25,797101	-0,847619
sga-MIR7983-2	222	14,8648649	31,981982	15,7657658	37,3873874	30,6306306	69,3693694	1,16901408	0,94285714	-58,5	-50,2	0,00197022	44,42	-26,351351	-0,8602941
sga-MIR7983-3	227	14,5374449	31,7180617	16,7400881	37,0044053	31,277533	68,722467	1,16666667	0,86842105	-58	-56	0,00104768	19,77	-25,550661	-0,8169014
sga-MIR7983-4	224	16,0714286	31,25	17,8571429	34,8214286	33,9285714	66,0714286	1,11428571	0,9	-75,6	-72	0,0231503	9,66	-33,75	-0,9947368
sga-MIR7983-5	172	14,5348837	30,2325581	15,6976744	39,5348837	30,2325581	69,7674419	1,30769231	0,92592593	-44,8	-44,6	0,0031981	15,44	-26,046512	-0,8615385
sga-MIR7983-6	263	13,6882129	32,6996198	17,4904943	36,121673	31,1787072	68,8212928	1,10465116	0,7826087	-73,8	-69,6	0,00126919	29,96	-28,060837	-0,9
sga-MIR7984b-1	198	14,6464646	34,3434343	15,6565657	35,3535354	30,3030303	69,6969697	1,02941176	0,93548387	-91,2	-85,5	0,00714248	17,35	-46,060606	-1,52
sga-MIR7984b-2	236	14,4067797	35,5932203	16,9491525	33,0508475	31,3559322	68,6440678	0,92857143	0,85	-84,3	-83,3	0,0141148	29,7	-35,720339	-1,1391892
sga-MIR7984d-1	288	15,9722222	33,3333333	16,3194444	34,375	32,2916667	67,7083333	1,03125	0,9787234	-98,2	-95,1	0,00252128	26,29	-34,097222	-1,055914
sga-MIR7984d-2	284	16,1971831	34,8591549	15,4929577	33,4507042	31,6901408	68,3098592	0,95959596	1,04545455	-98,6	-93,8	0,00021727	27,98	-34,71831	-1,0955556
sga-MIR7984d-3	176	18,75	32,3863636	14,7727273	34,0909091	33,5227273	66,4772727	1,05263158	1,26923077	-53,4	-43,6	0,00269555	24,68	-30,340909	-0,9050847
sga-MIR7984d-4	275	16,7272727	34,5454545	15,6363636	33,0909091	32,3636364	67,6363636	0,95789474	1,06976744	-94,7	-90,07	0,00177287	26,1	-34,425455	-1,0637079
sga-MIR7987-1	208	19,2307692	30,2884615	13,9423077	36,5384615	33,1730769	66,8269231	1,20634921	1,37931034	-59,2	-50,5	0,00357102	46,77	-28,461538	-0,857971
sga-MIR7987-2	257	19,0661479	31,1284047	11,2840467	38,5214008	30,3501946	69,6498054	1,2375	1,68965517	-71,3	-64,04	0,00078617	59,86	-27,743191	-0,9141026
sga-MIR7990a-1	102	14,7058824	30,3921569	15,6862745	39,2156863	30,3921569	69,6078431	1,29032258	0,9375	-32,6	-32,6	0,100386	7,6	-31,960784	-1,0516129
sga-MIR7990a-2	219	14,1552511	34,7031963	17,3515982	33,7899543	31,5068493	68,4931507	0,97368421	0,81578947	-65,6	-54,7	6,05E-05	40,84	-29,954338	-0,9507246

sga-MIR7990a-3	209	13,8755981	33,492823	17,2248804	35,4066986	31,1004785	68,8995215	1,05714286	0,80555556	-61	-54,47	0,00539854	20,79	-29,186603	-0,9384615
sga-MIR7991c	121	19,0082645	19,0082645	14,0495868	47,9338843	33,0578512	66,9421488	2,52173913	1,35294118	-43,4	-37,29	0,0851517	25,32	-35,867769	-1,085
sga-MIR7992-1	182	24,1758242	24,7252747	21,978022	29,1208791	46,1538462	53,8461538	1,17777778	1,1	-97,4	-96,9	0,182853	6,74	-53,516484	-1,1595238
sga-MIR7992-10	210	14,7619048	37,6190476	19,047619	28,5714286	33,8095238	66,1904762	0,75949367	0,775	-67,9	-56,2	0,00235776	25,59	-32,333333	-0,956338
sga-MIR7992-11	206	18,9320388	26,6990291	25,7281553	28,6407767	44,6601942	55,3398058	1,07272727	0,73584906	-80	-73,9	0,0182985	26,83	-38,834951	-0,8695652
sga-MIR7992-12	158	24,6835443	24,6835443	21,5189873	29,1139241	46,2025316	53,7974684	1,17948718	1,14705882	-74,7	-74,7	0,0431158	8,72	-47,278481	-1,0232877
sga-MIR7992-13	208	16,8269231	33,1730769	24,0384615	25,9615385	40,8653846	59,1346154	0,7826087	0,7	-71,9	-65,3	0,00246805	16,3	-34,567308	-0,8458824
sga-MIR7992-14	209	17,7033493	29,6650718	22,0095694	30,6220096	39,7129187	60,2870813	1,03225806	0,80434783	-67,1	-67,1	0,0123275	31,8	-32,105263	-0,8084337
sga-MIR7992-15	199	19,5979899	28,6432161	14,0703518	37,6884422	33,6683417	66,3316583	1,31578947	1,39285714	-82,5	-80,1	0,0593008	8,75	-41,457286	-1,2313433
sga-MIR7992-16	229	21,8340611	27,510917	19,650655	31,0043668	41,4847162	58,5152838	1,12698413	1,11111111	-87	-65,9	0,00163225	51,61	-37,991266	-0,9157895
sga-MIR7992-2	155	21,2903226	29,6774194	20	29,0322581	41,2903226	58,7096774	0,97826087	1,06451613	-89,2	-88,7	0,0713096	6,39	-57,548387	-1,39375
sga-MIR7992-3	249	18,4738956	30,9236948	22,0883534	28,5140562	40,562249	59,437751	0,92207792	0,83636364	-98,9	-96,9	0,0362719	19,69	-39,718876	-0,9792079
sga-MIR7992-4	237	21,9409283	28,6919831	16,8776371	32,4894515	38,8185654	61,1814346	1,13235294	1,3	-84,1	-80,9	0,00389026	26,45	-35,485232	-0,9141304
sga-MIR7992-5	193	14,507772	36,2694301	20,2072539	29,015544	34,7150259	65,2849741	0,8	0,71794872	-53,9	-53,9	0,0219934	7,49	-27,927461	-0,8044776
sga-MIR7992-6	261	18,0076628	29,5019157	14,1762452	38,3141762	32,183908	67,816092	1,2987013	1,27027027	-76,6	-76,5	0,0010704	22,7	-29,348659	-0,9119048
sga-MIR7992-7	249	20,0803213	27,7108434	18,875502	33,3333333	38,9558233	61,0441767	1,20289855	1,06382979	-90,4	-87,7	0,00304854	22,54	-36,305221	-0,9319588
sga-MIR7992-8	121	14,0495868	35,5371901	20,661157	29,7520661	34,7107438	65,2892562	0,8372093	0,68	-48,7	-48,7	0,247828	2,97	-40,247934	-1,1595238
sga-MIR7992-9	207	23,1884058	28,5024155	18,3574879	29,9516908	41,5458937	58,4541063	1,05084746	1,26315789	-65,1	-64,7	0,0051271	17,8	-31,449275	-0,7569767
sga-MIR7993b-1	214	20,5607477	31,3084112	10,2803738	37,8504673	30,8411215	69,1588785	1,20895522	2	-50,2	-37,3	0,00179414	50,95	-23,457944	-0,7606061
sga-MIR7993b-2	200	19	32	13	36	32	68	1,125	1,46153846	-60,4	-57,1	0,00123087	30,16	-30,2	-0,94375
sga-MIR7996c	202	16,3366337	31,6831683	15,3465347	36,6336634	31,6831683	68,3168317	1,15625	1,06451613	-94,8	-94,8	0,0621323	9,8	-46,930693	-1,48125
sga-MIR7997c-1	109	21,1009174	30,2752294	18,3486239	30,2752294	39,4495413	60,5504587	1	1,15	-43,7	-41,9	0,112458	11,79	-40,091743	-1,0162791
sga-MIR7997c-10	119	22,6890756	26,0504202	22,6890756	28,5714286	45,3781513	54,6218487	1,09677419	1	-37,8	-35,4	0,180913	7,43	-31,764706	-0,7
sga-MIR7997c-11	141	23,4042553	31,9148936	14,1843972	30,4964539	37,5886525	62,4113475	0,95555556	1,65	-64,5	-64,5	0,054351	6,51	-45,744681	-1,2169811
sga-MIR7997c-12	106	25,4716981	28,3018868	15,0943396	31,1320755	40,5660377	59,4339623	1,1	1,6875	-49,5	-49,5	0,10552	8,23	-46,698113	-1,1511628
sga-MIR7997c-13	111	18,018018	30,6306306	19,8198198	31,5315315	37,8378378	62,1621622	1,02941176	0,90909091	-33,5	-32,2	0,0944295	8,3	-30,18018	-0,797619
sga-MIR7997c-14	138	26,0869565	28,9855072	16,6666667	28,2608696	42,7536232	57,2463768	0,975	1,56521739	-68,4	-68,4	0,11766	3,78	-49,565217	-1,159322
sga-MIR7997c-15	129	20,1550388	32,5581395	15,503876	31,7829457	35,6589147	64,3410853	0,97619048	1,3	-51,7	-51,7	0,166614	3,47	-40,077519	-1,123913
sga-MIR7997c-16	135	27,4074074	25,9259259	21,4814815	25,1851852	48,8888889	51,1111111	0,97142857	1,27586207	-80,4	-80,1	0,236051	2,43	-59,555556	-1,2181818
sga-MIR7997c-2	121	19,0082645	28,9256198	23,1404959	28,9256198	42,1487603	57,8512397	1	0,82142857	-48,2	-45,4	0,00889544	9,07	-39,834711	-0,945098
sga-MIR7997c-3	127	22,8346457	26,7716535	19,6850394	30,7086614	42,519685	57,480315	1,14705882	1,16	-52,1	-52,1	0,061159	8,41	-41,023622	-0,9648148
sga-MIR7997c-4	95	18,9473684	29,4736842	22,1052632	29,4736842	41,0526316	58,9473684	1	0,85714286	-33,1	-33,1	0,0923641	8,16	-34,842105	-0,8487179
sga-MIR7997c-5	210	15,2380952	32,8571429	22,8571429	29,047619	38,0952381	61,9047619	0,88405797	0,66666667	-60,5	-58,2	0,00153736	31,65	-28,809524	-0,75625
sga-MIR7997c-6	131	32,8244275	24,4274809	19,0839695	23,6641221	51,9083969	48,0916031	0,96875	1,72	-70,8	-69,77	0,0350722	10,95	-54,045802	-1,0411765
sga-MIR7997c-7	126	23,015873	25,3968254	21,4285714	30,1587302	44,4444444	55,5555556	1,1875	1,07407407	-63	-63	0,0493363	4,5	-50	-1,125
sga-MIR7997c-8	126	19,047619	26,984127	21,4285714	32,5396825	40,4761905	59,5238095	1,20588235	0,88888889	-52,6	-50,8	0,0718719	15,85	-41,746032	-1,0313725
sga-MIR7998-1	138	26,8115942	24,6376812	22,4637681	26,0869565	49,2753623	50,7246377	1,05882353	1,19354839	-50,5	-49,7	0,0266762	18,6	-36,594203	-0,7426471
sga-MIR7998-2	219	24,2009132	29,2237443	20,0913242	26,4840183	44,2922374	55,7077626	0,90625	1,20454545	-68,7	-65	0,00018865	49,27	-31,369863	-0,7082474
sga-MIR8001b-1	86	16,2790698	30,2325581	18,6046512	34,8837209	34,8837209	65,1162791	1,15384615	0,875	-27,1	-26,9	0,320398	4,03	-31,511628	-0,9033333
sga-MIR8001b-2	141	14,893617	34,751773	18,4397163	31,9148936	33,3333333	66,6666667	0,91836735	0,80769231	-50,3	-48,5	0,0439097	7,26	-35,673759	-1,0702128
sga-MIR8001b-3	67	17,9104478	31,3432836	17,9104478	32,8358209	35,8208955	64,1791045	1,04761905	1	-38,1	-38,1	0,434263	1,23	-56,865672	-1,5875
sga-MIR8002	78	12,8205128	28,2051282	17,9487179	41,025641	30,7692308	69,2307692	1,45454545	0,71428571	-29,6	-29,6	0,742726	0,63	-37,948718	-1,2333333
sga-MIR8005b	235	17,0212766	32,7659574	15,3191489	34,893617	32,3404255	67,6595745	1,06493506	1,11111111	-58,3	-51,2	0,00048182	51,43	-24,808511	-0,7671053
sga-MIR8005c	291	18,556701	30,5841924	12,371134	38,4879725	30,9278351	69,0721649	1,25842697	1,5	-65,7	-61,3	0,00017431	59,28	-22,57732	-0,73
sga-MIR8006-1	196	20,4081633	28,0612245	17,8571429	33,6734694	38,2653061	61,7346939	1,2	1,14285714	-89,3	-81,59	0,0033999	23,86	-45,561224	-1,1906667
sga-MIR8006-10	234	15,3846154	34,1880342	17,9487179	32,4786325	33,3333333	66,6666667	0,95	0,85714286	-74	-64,5	0,00191605	22,42	-31,623932	-0,9487179
sga-MIR8006-11	116	22,4137931	26,7241379	23,2758621	27,5862069	45,6896552	54,3103448	1,03225806	0,96296296	-62,5	-62,2	0,106655	3,82	-53,87931	-1,1792453
sga-MIR8006-12	225	19,5555556	32,4444444	16,4444444	31,5555556	36	64	0,97260274	1,18918919	-84,5	-84	0,0114267	11,7	-37,555556	-1,0432099
sga-MIR8006-2	229	23,580786	28,3842795	18,7772926	29,2576419	42,3580786	57,6419214	1,03076923	1,25581395	-97,3	-97,3	0,0454224	10,19	-42,489083	-1,0030928
sga-MIR8006-4	224	20,0892857	30,3571429	19,1964286	30,3571429	39,2857143	60,7142857	1	1,04651163	-85,8	-75,41	0,00366534	24,61	-38,303571	-0,975
sga-MIR8006-5	276	17,3913043	33,3333333	15,942029	33,3333333	33,3333333	66,6666667	1	1,09090909	-98,3	-92,5	9,99E-05	37,82	-35,615942	-1,0684783
sga-MIR8006-6	243	13,9917695	36,6255144	18,9300412	30,4526749	32,9218107	67,0781893	0,83146067	0,73913043	-64,9	-54,21	0,00080135	35,69	-26,707819	-0,81125
sga-MIR8006-7	259	20,0772201	31,6602317	16,6023166	31,6602317	36,6795367	63,3204633	1	1,20930233	-95,7	-94,1	0,000948	19,44	-36,949807	-1,0073684
sga-MIR8006-8	183	18,0327869	27,3224044	19,6721311	34,9726776	37,704918	62,295082	1,28	0,91666667	-68	-67,6	0,087457	11,36	-37,15847	-0,9855072
sga-MIR8006-9	252	20,6349206	29,7619048	15,0793651	34,5238095	35,7142857	64,2857143	1,16	1,36842105	-88,6	-78,6	0,00197813	35,21	-35,15873	-0,9844444
sga-MIR8007b-1	303	18,8118812	32,0132013	12,2112211	36,9636964	31,0231023	68,9768977	1,15463918	1,54054054	-79,1	-70,1	4,24E-05	62,34	-26,105611	-0,8414894
sga-MIR8007b-2	291	14,0893471	32,6460481	16,838488	36,4261168	30,9278351	69,0721649	1,11578947	0,83673469	-64	-61,2	0,00206386	32,51	-21,993127	-0,7111111
sga-MIR8008b-1	223	18,3856502	29,5964126	16,1434978	35,8744395	34,529148	65,470852	1,21212121	1,13888889	-72,5	-71	0,00062376	21,32	-32,511211	-0,9415584
sga-MIR8008b-2	192	15,1041667	38,0208333	19,2708333	27,6041667	34,375	65,625	0,7260274	0,78378378	-58,2	-52,6	0,00947255	61,53	-30,3125	-0,8818182
sga-MIR8008b-3	120	17,5	31,6666667	17,5	33,3333333	35	65	1,05263158	1	-34,7	-31,8	0,00927145	14,13	-28,916667	-0,8261905
sga-MIR8009-1	56	21,4285714	33,9285714	16,0714286	28,5714286	37,5	62,5	0,84210526	1,33333333	-24,4	-22,6	0,229227	8,14	-43,571429	-1,1619048
sga-MIR8009-2	207	14,9758454	30,4347826	19,3236715	35,2657005	34,2995169	65,7004831	1,15873016	0,775	-59,6	-58,3	0,00256048	21,79	-28,792271	-0,8394366
sga-MIR8009-3	172	18,0232558	30,2325581	19,1860465	32,5581395	37,2093023	62,7906977	1,07692308	0,93939394	-65,7	-64,6	0,0198433	18,45	-38,197674	-1,0265625
sga-MIR8010	150	17,3333333	36	13,3333333	33,3333333	30,6666667	69,3333333	0,92592593	1,3	-70	-70	0,130154	10,89	-46,666667	-1,5217391
sga-MIR8011a	171	22,2222222	28,6549708	16,9590643	32,1637427	39,1812865	60,8187135	1,12244898	1,31034483	-83,5	-82,5	0,0835789	11,66	-48,830409	-1,2462687
sga-MIR8011b	138	20,2898551	28,9855072	19,5652174	31,1594203	39,8550725	60,1449275	1,075	1,03703704	-58,2	-58,2	0,0502544	7,29	-42,173913	-1,0581818

sga-MIR8014-1	205	18,0487805	38,0487805	12,6829268	31,2195122	30,7317073	69,2682927	0,82051282	1,42307692	-59,1	-57,9	0,00923205	30,26	-28,829268	-0,9380952
sga-MIR8014-2	329	18,2370821	29,4832827	13,3738602	38,9057751	31,6109422	68,3890578	1,31958763	1,36363636	-76,1	-65,3	1,26E-05	68,09	-23,130699	-0,7317308
sga-MIR8014-3	195	19,4871795	31,7948718	10,7692308	37,9487179	30,2564103	69,7435897	1,19354839	1,80952381	-42,5	-35,7	0,00494502	19,23	-21,794872	-0,720339
sga-MIR8014-4	340	16,1764706	33,8235294	17,3529412	32,6470588	33,5294118	66,4705882	0,96521739	0,93220339	-95,3	-86,2	0,00066244	57,85	-28,029412	-0,8359649
sga-MIR8019-1	267	16,8539326	37,8277154	15,3558052	29,9625468	32,2097378	67,7902622	0,79207921	1,09756098	-71,8	-53	0,00066899	61,96	-26,891386	-0,8348837
sga-MIR8019-2	237	16,8776371	34,5991561	13,5021097	35,021097	30,3797468	69,6202532	1,01219512	1,25	-53,8	-48,1	0,00419636	53,66	-22,700422	-0,7472222
sga-MIR8021-1	232	15,5172414	30,6034483	15,9482759	37,9310345	31,4655172	68,5344828	1,23943662	0,97297297	-61,6	-60,3	0,00205525	30,06	-26,551724	-0,8438356
sga-MIR8021-2	226	15,4867257	33,1858407	16,8141593	34,5132743	32,300885	67,699115	1,04	0,92105263	-71,5	-65,4	0,0068288	28,69	-31,637168	-0,9794521
sga-MIR8025	214	16,3551402	29,4392523	17,2897196	36,9158879	33,6448598	66,3551402	1,25396825	0,94594595	-60,7	-56,4	0,00142469	32,52	-28,364486	-0,8430556
sga-MIR8027	272	17,6470588	31,9852941	14,3382353	36,0294118	31,9852941	68,0147059	1,12643678	1,23076923	-64,8	-57	0,00016794	70,69	-23,823529	-0,7448276
sga-MIR8030	306	17,3202614	36,9281046	17,6470588	28,1045752	34,9673203	65,0326797	0,76106195	0,98148148	-78,1	-69,5	3,55E-05	52,16	-25,522876	-0,7299065
sga-MIR8032e	227	19,8237885	30,3964758	15,4185022	34,3612335	35,2422907	64,7577093	1,13043478	1,28571429	-57,4	-53,4	0,00034227	45,75	-25,286344	-0,7175
sga-MIR8033	109	17,4311927	31,1926606	15,5963303	35,7798165	33,0275229	66,9724771	1,14705882	1,11764706	-61,3	-60,3	0,112968	4,5	-56,238532	-1,7027778
sga-MIR8036	105	23,8095238	29,5238095	13,3333333	33,3333333	37,1428571	62,8571429	1,12903226	1,78571429	-35,7	-27,6	0,0142164	21,41	-34	-0,9153846
sga-MIR8037	159	20,1257862	38,3647799	11,3207547	30,1886792	31,4465409	68,5534591	0,78688525	1,77777778	-37,2	-35,9	0,0321117	18,86	-23,396226	-0,744
sga-MIR8038b	136	19,1176471	30,1470588	19,1176471	31,6176471	38,2352941	61,7647059	1,04878049	1	-62,8	-62,1	0,0861435	6,23	-46,176471	-1,2076923
sga-MIR8039	194	16,4948454	32,4742268	18,556701	32,4742268	35,0515464	64,9484536	1	0,88888889	-63	-63	0,00721321	10,05	-32,474227	-0,9264706
sga-MIR8042	104	21,1538462	35,5769231	17,3076923	25,9615385	38,4615385	61,5384615	0,72972973	1,22222222	-37,2	-37,2	0,214876	3,9	-35,769231	-0,93
sga-MIR8045-1	285	17,1929825	34,3859649	15,7894737	32,6315789	32,9824561	67,0175439	0,94897959	1,08888889	-90,1	-80,04	0,00027936	33,58	-31,614035	-0,9585106
sga-MIR8045-2	99	17,1717172	33,3333333	17,1717172	32,3232323	34,3434343	65,6565657	0,96969697	1	-46,6	-46,6	0,0523576	7,81	-47,070707	-1,3705882
sga-MIR8130	317	19,2429022	30,9148265	16,0883281	33,7539432	35,3312303	64,6687697	1,09183673	1,19607843	-83,3	-71,9	2,22E-05	66,73	-26,277603	-0,74375
sga-MIR8132	139	17,9856115	29,4964029	16,5467626	35,971223	34,5323741	65,4676259	1,2195122	1,08695652	-50,3	-50,1	0,0292398	15,38	-36,18705	-1,0479167
sga-MIR8137	100	31	15	34	20	65	35	1,33333333	0,91176471	-54,3	-53,7	0,16438	8,56	-54,3	-0,8353846
sga-MIR8138	139	21,5827338	29,4964029	18,705036	30,2158273	40,2877698	59,7122302	1,02439024	1,15384615	-62,2	-59,9	0,0384037	11,67	-44,748201	-1,1107143
sga-MIR8179	211	16,1137441	35,07109	15,1658768	33,6492891	31,2796209	68,7203791	0,95945946	1,0625	-95,7	-95,1	0,0499396	7,7	-45,35545	-1,45
sga-MIR8182	113	18,5840708	34,5132743	15,0442478	31,8584071	33,6283186	66,3716814	0,92307692	1,23529412	-36	-36	0,0978592	6,06	-31,858407	-0,9473684
sga-MIR821b	161	19,2546584	31,0559006	11,8012422	37,8881988	31,0559006	68,9440994	1,22	1,63157895	-41,3	-37,8	0,00192358	20,51	-25,652174	-0,826
sga-MIR823	215	17,6744186	36,2790698	15,3488372	30,6976744	33,0232558	66,9767442	0,84615385	1,15151515	-94,9	-94,9	0,0672384	10,22	-44,139535	-1,3366197
sga-MIR825	151	25,1655629	21,192053	17,8807947	35,7615894	43,0463576	56,9536424	1,6875	1,40740741	-56	-52	0,00620872	12,07	-37,086093	-0,8615385
sga-MIR827-1	88	15,9090909	31,8181818	15,9090909	36,3636364	31,8181818	68,1818182	1,14285714	1	-34,9	-34,9	0,0956756	6,03	-39,659091	-1,2464286
sga-MIR827-2	123	15,4471545	40,6504065	15,4471545	28,4552846	30,8943089	69,1056911	0,7	1	-44,3	-44,3	0,16497	5,9	-36,01626	-1,1657895
sga-MIR827b	261	16,4750958	32,9501916	15,3256705	35,2490421	31,8007663	68,1992337	1,06976744	1,075	-61,2	-46,34	0,00184212	47,18	-23,448276	-0,7373494
sga-MIR833a	278	15,8273381	33,4532374	14,7482014	35,971223	30,5755396	69,4244604	1,07526882	1,07317073	-62	-61,1	0,00184303	26,76	-22,302158	-0,7294118
sga-MIR845b-1	276	21,7391304	29,3478261	17,7536232	31,1594203	39,4927536	60,5072464	1,0617284	1,2244898	-78,2	-62	8,18E-05	56,68	-28,333333	-0,7174312
sga-MIR845b-2	230	28,2608696	25,2173913	17,3913043	29,1304348	45,6521739	54,3478261	1,15517241	1,625	-80	-72,6	0,0500027	38,83	-34,782609	-0,7619048
sga-MIR845b-3	217	22,1198157	27,1889401	17,9723502	32,718894	40,0921659	59,9078341	1,20338983	1,23076923	-61,4	-42,8	0,00377554	51,21	-28,294931	-0,7057471
sga-MIR856	128	17,1875	32,8125	15,625	34,375	32,8125	67,1875	1,04761905	1,1	-32,4	-31,8	0,00551455	15,45	-25,3125	-0,7714286
sga-MIR8565h	282	23,7588652	27,6595745	17,3758865	31,2056738	41,1347518	58,8652482	1,12820513	1,36734694	-82	-68	0,00053809	58,04	-29,078014	-0,7068966
sga-MIR8577	312	18,9102564	33,0128205	13,4615385	34,6153846	32,3717949	67,6282051	1,04854369	1,4047619	-85,6	-81,2	5,40E-05	46,96	-27,435897	-0,8475248
sga-MIR8587	249	13,253012	38,5542169	18,0722892	30,1204819	31,3253012	68,6746988	0,78125	0,73333333	-64,7	-62,62	0,00204481	34,14	-25,983936	-0,8294872
sga-MIR859-1	301	21,2624585	30,5647841	11,2956811	36,8770764	32,5581395	67,4418605	1,20652174	1,88235294	-69,8	-61,8	4,69E-05	74,01	-23,189369	-0,7122449
sga-MIR859-2	254	16,1417323	31,496063	14,1732283	38,1889764	30,3149606	69,6850394	1,2125	1,13888889	-55,1	-49	0,00122828	36,17	-21,692913	-0,7155844
sga-MIR859-3	124	16,9354839	31,4516129	18,5483871	33,0645161	35,483871	64,516129	1,05128205	0,91304348	-39	-37,5	0,0145196	12,85	-31,451613	-0,8863636
sga-MIR8596	318	17,9245283	31,4465409	12,8930818	37,7358491	30,8176101	69,1823899	1,2	1,3902439	-75,3	-68,6	0,0008273	72,16	-23,679245	-0,7683673
sga-MIR8599	187	26,7379679	30,4812834	14,4385027	28,342246	41,1764706	58,8235294	0,92982456	1,85185185	-55,9	-55,9	0,00286805	19,59	-29,893048	-0,725974
sga-MIR860	136	23,5294118	27,9411765	9,55882353	38,9705882	33,0882353	66,9117647	1,39473684	2,46153846	-35,3	-31,4	0,0166779	22,5	-25,955882	-0,7844444
sga-MIR8610	164	16,4634146	32,9268293	20,1219512	30,4878049	36,5853659	63,4146341	0,92592593	0,81818182	-94,3	-94,3	0,0490033	8,21	-57,5	-1,5716667
sga-MIR8639e-1	234	16,2393162	37,1794872	16,2393162	30,3418803	32,4786325	67,5213675	0,81609195	1	-80,1	-75,99	0,00721196	17,42	-34,230769	-1,0539474
sga-MIR8639e-2	211	16,5876777	34,5971564	18,0094787	30,8056872	34,5971564	65,4028436	0,89041096	0,92105263	-85,6	-84,4	0,0339795	10,61	-40,56872	-1,1726027
sga-MIR864	325	20,6153846	35,6923077	14,7692308	28,9230769	35,3846154	64,6153846	0,81034483	1,39583333	-82,9	-73,8	0,00029991	55,53	-25,507692	-0,7208696
sga-MIR8643b	280	15,3571429	38,5714286	15	31,0714286	30,3571429	69,6428571	0,80555556	1,02380952	-60,3	-50	0,00074973	55,38	-21,535714	-0,7094118
sga-MIR8659b	240	18,75	31,25	15,4166667	34,5833333	34,1666667	65,8333333	1,10666667	1,21621622	-58,5	-35,3	0,00065792	76,1	-24,375	-0,7134146
sga-MIR8668	142	19,0140845	33,8028169	14,7887324	32,3943662	33,8028169	66,1971831	0,95833333	1,28571429	-52	-52	0,0438196	6,62	-36,619718	-1,0833333
sga-MIR8672	333	21,3213213	33,033033	15,9159159	29,7297297	37,2372372	62,7627628	0,9	1,33962264	-88,4	-74,6	2,37E-05	69,84	-26,546547	-0,7129032
sga-MIR8685	316	15,8227848	31,3291139	18,6708861	34,1772152	34,4936709	65,5063291	1,09090909	0,84745763	-80,6	-66,5	1,36E-05	64,62	-25,506329	-0,7394495
sga-MIR8696	239	17,1548117	30,5439331	20,083682	32,2175732	37,2384937	62,7615063	1,05479452	0,85416667	-74,8	-63,7	0,00066813	30,81	-31,297071	-0,8404494
sga-MIR870	317	19,5583596	30,5993691	13,2492114	36,5930599	32,807571	67,192429	1,19587629	1,47619048	-73,4	-62	0,00013127	71,8	-23,154574	-0,7057692
sga-MIR8706b	327	17,4311927	31,4984709	13,1498471	37,9204893	30,5810398	69,4189602	1,2038835	1,3255814	-74,5	-71,1	5,85E-05	41,45	-22,782875	-0,745
sga-MIR8707-1	338	23,3727811	34,0236686	11,2426036	31,3609467	34,6153846	65,3846154	0,92173913	2,07894737	-91,1	-81,7	2,86E-05	52,59	-26,952663	-0,7786325
sga-MIR8707-2	111	16,2162162	39,6396396	14,4144144	29,7297297	30,6306306	69,3693694	0,75	1,125	-30,2	-27,2	0,0765571	8,42	-27,207207	-0,8882353
sga-MIR8707-3	164	17,6829268	40,2439024	12,804878	29,2682927	30,4878049	69,5121951	0,72727273	1,38095238	-36,1	-36,1	0,0262062	28,24	-22,012195	-0,722
sga-MIR8709b-1	116	20,6896552	30,1724138	12,9310345	36,2068966	33,6206897	66,3793103	1,2	1,6	-30	-30	0,045051	11,44	-25,862069	-0,7692308
sga-MIR8709b-2	146	22,6027397	26,0273973	17,1232877	34,2465753	39,7260274	60,2739726	1,31578947	1,32	-45,1	-42,8	0,028682	16,2	-30,890411	-0,7775862
sga-MIR8727	234	15,8119658	30,7692308	14,957265	38,4615385	30,7692308	69,2307692	1,25	1,05714286	-65,4	-53,3	0,00104735	37,86	-27,948718	-0,9083333
sga-MIR8730	144	17,3611111	31,9444444	15,9722222	34,7222222	33,3333333	66,6666667	1,08695652	1,08695652	-34,8	-34,8	0,0335843	14,69	-24,166667	-0,725
sga-MIR8737	171	22,8070175	30,4093567	9,35672515	37,4269006	32,1637427	67,8362573	1,23076923	2,4375	-41,2	-39,7	0,00141225	30,39	-24,093567	-0,7490909

sga-MIR8739-1	289	13,8408304	35,9861592	17,3010381	32,8719723	31,1418685	68,8581315	0,91346154	0,8	-67,4	-52,47	0,00021916	45,5	-23,321799	-0,7488889
sga-MIR8739-2	255	18,0392157	32,1568627	17,254902	32,5490196	35,2941176	64,7058824	1,01219512	1,04545455	-84,8	-83,6	0,00323417	23,4	-33,254902	-0,9422222
sga-MIR8739-3	104	25,9615385	29,8076923	14,4230769	29,8076923	40,3846154	59,6153846	1	1,8	-48,2	-48,2	0,314571	3,02	-46,346154	-1,147619
sga-MIR8739-4	236	17,7966102	35,1694915	19,0677966	27,9661017	36,8644068	63,1355932	0,79518072	0,93333333	-69,8	-69,7	0,023684	13,23	-29,576271	-0,8022989
sga-MIR8739-5	207	21,2560386	27,5362319	14,0096618	37,1980676	35,2657005	64,7342995	1,35087719	1,51724138	-74,2	-73,4	0,00728238	22,73	-35,845411	-1,0164384
sga-MIR8739-6	282	20,212766	30,4964539	16,6666667	32,6241135	36,8794326	63,1205674	1,06976744	1,21276596	-95,8	-91,9	0,0025084	35,81	-33,971631	-0,9211538
sga-MIR8739-7	268	16,7910448	33,2089552	17,5373134	32,4626866	34,3283582	65,6716418	0,97752809	0,95744681	-77,9	-72,5	0,00066662	35,89	-29,067164	-0,8467391
sga-MIR8739-8	159	19,4968553	33,3333333	15,7232704	31,4465409	35,2201258	64,7798742	0,94339623	1,24	-54,7	-53	0,0492969	7,45	-34,402516	-0,9767857
sga-MIR8743a	167	22,1556886	27,5449102	14,3712575	35,9281437	36,5269461	63,4730539	1,30434783	1,54166667	-51,2	-45,3	0,0132847	36,05	-30,658683	-0,8393443
sga-MIR8763	322	20,4968944	33,8509317	13,3540373	32,2981366	33,8509317	66,1490683	0,95412844	1,53488372	-81,2	-69,1	0,00015382	74,18	-25,217391	-0,7449541
sga-MIR8766	249	16,4658635	31,3253012	14,0562249	38,1526104	30,5220884	69,4779116	1,21794872	1,17142857	-66,7	-53,6	0,00017187	47,25	-26,787149	-0,8776316
sga-MIR8781a-1	195	18,974359	30,2564103	13,3333333	37,4358974	32,3076923	67,6923077	1,23728814	1,42307692	-67,6	-67,6	0,0239304	14,88	-34,666667	-1,0730159
sga-MIR8781a-2	260	15	32,6923077	15,3846154	36,9230769	30,3846154	69,6153846	1,12941176	0,975	-69,3	-68,3	0,00208628	33,79	-26,653846	-0,8772152
sga-MIR8781a-3	292	17,1232877	30,8219178	14,0410959	38,0136986	31,1643836	68,8356164	1,23333333	1,2195122	-83,2	-66,32	0,00014784	71,41	-28,493151	-0,9142857
sga-MIR8781a-4	256	17,1875	30,46875	14,0625	38,28125	31,25	68,75	1,25641026	1,22222222	-74,3	-68,2	0,00167213	40,34	-29,023438	-0,92875
sga-MIR908	148	23,6486486	28,3783784	14,8648649	33,1081081	38,5135135	61,4864865	1,16666667	1,59090909	-49,9	-43,2	0,00421547	18,01	-33,716216	-0,8754386
sga-MIR9471a-1	182	24,7252747	30,7692308	14,2857143	30,2197802	39,010989	60,989011	0,98214286	1,73076923	-71,9	-71	0,0352594	14,44	-39,505495	-1,0126761
sga-MIR9471a-2	154	24,025974	34,4155844	10,3896104	31,1688312	34,4155844	65,5844156	0,90566038	2,3125	-57,4	-57,4	0,167319	6,03	-37,272727	-1,0830189
sga-MIR9472	232	15,9482759	32,7586207	16,3793103	34,9137931	32,3275862	67,6724138	1,06578947	0,97368421	-81,4	-79,5	0,00136598	16,06	-35,086207	-1,0853333
sga-MIR9473-1	118	18,6440678	33,0508475	16,9491525	31,3559322	35,5932203	64,4067797	0,94871795	1,1	-53,6	-52,2	0,054637	7,54	-45,423729	-1,2761905
sga-MIR9473-2	120	16,6666667	32,5	19,1666667	31,6666667	35,8333333	64,1666667	0,97435897	0,86956522	-56	-55,1	0,057338	7,71	-46,666667	-1,3023256
sga-MIR9476-1	110	17,2727273	31,8181818	18,1818182	32,7272727	35,4545455	64,5454545	1,02857143	0,95	-66,1	-66,1	0,605077	1,1	-60,090909	-1,6948718
sga-MIR9476-2	196	18,3673469	33,1632653	20,9183673	27,5510204	39,2857143	60,7142857	0,83076923	0,87804878	-98,1	-94,8	0,014696	12,32	-50,05102	-1,274026
sga-MIR9476-3	94	17,0212766	32,9787234	14,893617	35,106383	31,9148936	68,0851064	1,06451613	1,14285714	-63,4	-63,4	0,890285	0,53	-67,446809	-2,1133333
sga-MIR9477-1	96	21,875	27,0833333	16,6666667	34,375	38,5416667	61,4583333	1,26923077	1,3125	-54,8	-54,8	0,214537	4,18	-57,083333	-1,4810811
sga-MIR9477-2	102	19,6078431	30,3921569	18,627451	31,372549	38,2352941	61,7647059	1,03225806	1,05263158	-34,6	-30,7	0,113704	7,96	-33,921569	-0,8871795
sga-MIR9478	206	19,9029126	31,5533981	12,6213592	35,9223301	32,5242718	67,4757282	1,13846154	1,57692308	-75,5	-68,13	0,00586716	25,61	-36,650485	-1,1268657
sga-MIR9479	169	21,8934911	30,7692308	23,0769231	24,260355	44,9704142	55,0295858	0,78846154	0,94871795	-64,4	-53,24	0,0197494	29,82	-38,106509	-0,8473684
sga-MIR9552a	185	17,8378378	34,5945946	13,5135135	34,0540541	31,3513514	68,6486486	0,984375	1,32	-45,9	-41,1	0,00729885	45,06	-24,810811	-0,7913793
sga-MIR9556	106	18,8679245	29,245283	22,6415094	29,245283	41,509434	58,490566	1	0,83333333	-43,7	-41,1	0,189229	6,15	-41,226415	-0,9931818
sga-MIR9562	299	16,722408	30,7692308	14,0468227	38,4615385	30,7692308	69,2307692	1,25	1,19047619	-76,4	-67,7	0,00014271	51,12	-25,551839	-0,8304348
sga-MIR9564	341	18,7683284	33,431085	20,8211144	26,9794721	39,5894428	60,4105572	0,80701754	0,90140845	-96	-82	5,02E-05	58,08	-28,152493	-0,7111111
sga-MIR9679-1	209	15,7894737	34,9282297	14,354067	34,9282297	30,1435407	69,8564593	1	1,1	-48,6	-45,8	0,00237625	30,03	-23,253589	-0,7714286
sga-MIR9679-2	132	15,1515152	36,3636364	15,9090909	32,5757576	31,0606061	68,9393939	0,89583333	0,95238095	-36,7	-36,7	0,102047	6,17	-27,80303	-0,895122
sga-MIR9679-3	132	15,9090909	36,3636364	16,6666667	31,0606061	32,5757576	67,4242424	0,85416667	0,95454545	-36,7	-36,7	0,090004	6,56	-27,80303	-0,8534884
sga-MIR9726	102	15,6862745	33,3333333	14,7058824	36,2745098	30,3921569	69,6078431	1,08823529	1,06666667	-31,1	-28,1	0,0100907	13,41	-30,490196	-1,0032258
sga-MIR9736	331	25,3776435	31,4199396	13,897281	29,305136	39,2749245	60,7250755	0,93269231	1,82608696	-91,3	-88,8	0,00018568	26,83	-27,583082	-0,7023077
sga-MIR9750	226	19,4690265	29,2035398	17,2566372	34,0707965	36,7256637	63,2743363	1,16666667	1,12820513	-59,5	-56,1	0,00049044	42,05	-26,327434	-0,7168675
sga-MIR9751	331	16,0120846	32,0241692	16,918429	35,0453172	32,9305136	67,0694864	1,09433962	0,94642857	-82,5	-78,5	0,00041839	37,65	-24,924471	-0,7568807
sga-MIR9760	115	27,826087	27,826087	9,56521739	34,7826087	37,3913043	62,6086957	1,25	2,90909091	-30,6	-25,7	0,0255981	26,25	-26,608696	-0,7116279
sga-MIR9761	197	23,3502538	31,4720812	15,7360406	29,4416244	39,0862944	60,9137056	0,93548387	1,48387097	-56,6	-43,11	0,00352777	39,04	-28,730964	-0,7350649
sga-MIR9773-1	179	14,5251397	35,1955307	15,6424581	34,6368715	30,1675978	69,8324022	0,98412698	0,92857143	-43,6	-38,3	0,0239983	25,9	-24,357542	-0,8074074
sga-MIR9773-2	279	19,7132616	31,1827957	11,1111111	37,9928315	30,8243728	69,1756272	1,2183908	1,77419355	-61,6	-30,13	0,00013436	89,27	-22,078853	-0,7162791

Supplementary Table S17. Thermodynamic and structural characterization of *Solanum chilense* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Size	G content	A content	C content	U content	GC content	AU content	UA-ratio	GC-ratio	MFE	MFEE	Freq	Div	AMFE	MFEI
sch-MIR10189-1	180	27,2222222	28,8888889	20	23,8888889	47,2222222	52,7777778	0,82692308	1,36111111	-65,3	-58,7	0,00860048	24,22	-36,277778	-0,7682353
sch-MIR10189-2	333	20,1201201	36,3363363	13,5135135	30,03003	33,6336336	66,3663664	0,82644628	1,48888889	-88,6	-72,2	4,61E-05	61,57	-26,606607	-0,7910714
sch-MIR10197	157	14,0127389	30,5732484	17,8343949	37,5796178	31,8471338	68,1528662	1,22916667	0,78571429	-48,4	-48	0,0198108	13,41	-30,828025	-0,968
sch-MIR10211b	223	15,6950673	40,8071749	15,2466368	28,2511211	30,941704	69,058296	0,69230769	1,02941176	-48,5	-46,6	0,0053387	37,41	-21,748879	-0,7028986
sch-MIR10215-1	66	22,7272727	36,3636364	13,6363636	27,2727273	36,3636364	63,6363636	0,75	1,66666667	-29,9	-29,9	0,317938	2,15	-45,30303	-1,2458333
sch-MIR1028b	312	15,0641026	33,0128205	16,6666667	35,2564103	31,7307692	68,2692308	1,06796117	0,90384615	-77,5	-74,5	4,96E-05	47,3	-24,839744	-0,7828283
sch-MIR1033e	224	21,4285714	27,2321429	16,9642857	34,375	38,3928571	61,6071429	1,26229508	1,26315789	-67,6	-64,6	0,00033376	31,43	-30,178571	-0,7860465
sch-MIR10405d-1	284	14,7887324	37,3239437	15,8450704	32,0422535	30,6338028	69,3661972	0,85849057	0,93333333	-67,3	-61,3	8,64E-05	36,16	-23,697183	-0,7735632
sch-MIR10405d-2	287	19,8606272	33,7979094	11,8466899	34,4947735	31,7073171	68,2926829	1,02061856	1,67647059	-76,9	-73,1	0,00088132	41,65	-26,794425	-0,8450549
sch-MIR10405d-3	136	16,9117647	35,2941176	16,1764706	31,6176471	33,0882353	66,9117647	0,89583333	1,04545455	-35	-34,6	0,0561197	13,99	-25,735294	-0,7777778
sch-MIR10419-1	220	20,9090909	30,4545455	10,4545455	38,1818182	31,3636364	68,6363636	1,25373134	2	-53,3	-42,77	4,35E-05	47	-24,227273	-0,7724638
sch-MIR10419-2	184	17,3913043	34,7826087	17,9347826	29,8913043	35,326087	64,673913	0,859375	0,96969697	-64,2	-63	0,0284231	11,82	-34,891304	-0,9876923
sch-MIR10427b	143	22,3776224	31,4685315	11,1888112	34,965035	33,5664336	66,4335664	1,11111111	2	-43,8	-42,9	0,0144713	12,57	-30,629371	-0,9125
sch-MIR1043-1	260	15	36,9230769	16,9230769	31,1538462	31,9230769	68,0769231	0,84375	0,88636364	-78,2	-76,2	0,00091099	33,74	-30,076923	-0,9421687
sch-MIR1043-2	198	20,2020202	29,2929293	14,1414141	36,3636364	34,3434343	65,6565657	1,24137931	1,42857143	-63	-61,6	0,00063865	19,49	-31,818182	-0,9264706
sch-MIR1043-3	206	16,0194175	38,8349515	15,5339806	29,6116505	31,5533981	68,4466019	0,7625	1,03125	-79,7	-79,7	0,0227596	8,27	-38,68932	-1,2261538
sch-MIR1044	275	17,0909091	34,1818182	15,6363636	33,0909091	32,7272727	67,2727273	0,96808511	1,09302326	-80,4	-79,9	0,0202105	13,86	-29,236364	-0,8933333
sch-MIR1046	110	16,3636364	30	15,4545455	38,1818182	31,8181818	68,1818182	1,27272727	1,05882353	-36,5	-32,1	0,0415481	16,2	-33,181818	-1,0428571
sch-MIR10519-4	315	17,7777778	30,1587302	12,6984127	39,3650794	30,4761905	69,5238095	1,30526316	1,4	-77,1	-65,1	1,57E-05	78,87	-24,47619	-0,803125
sch-MIR10521	243	18,9300412	21,8106996	16,0493827	43,2098765	34,9794239	65,0205761	1,98113208	1,17948718	-59,6	-47,5	7,00E-05	60,84	-24,526749	-0,7011765
sch-MIR10528	97	18,556701	35,0515464	17,5257732	28,8659794	36,0824742	63,9175258	0,82352941	1,05882353	-42,3	-42,3	0,0530642	7,51	-43,608247	-1,2085714
sch-MIR10531	300	19,6666667	27	14,3333333	39	34	66	1,44444444	1,37209302	-72,9	-66	0,00072119	38,15	-24,3	-0,7147059
sch-MIR10532-1	192	22,9166667	28,6458333	12,5	35,9375	35,4166667	64,5833333	1,25454545	1,83333333	-48,7	-44,4	0,00236393	28,99	-25,364583	-0,7161765
sch-MIR10532-2	245	17,9591837	35,1020408	14,6938776	32,244898	32,6530612	67,3469388	0,91860465	1,22222222	-72,8	-58,78	0,00209918	43,59	-29,714286	-0,91
sch-MIR10532-3	274	19,3430657	31,3868613	15,3284672	33,9416058	34,6715328	65,3284672	1,08139535	1,26190476	-68,8	-56,14	0,00123667	42,12	-25,109489	-0,7242105
sch-MIR10533-1	193	18,134715	29,015544	17,6165803	35,2331606	35,7512953	64,2487047	1,21428571	1,02941176	-89,4	-88,4	0,0477334	8,75	-46,321244	-1,2956522
sch-MIR10533-2	129	24,8062016	30,2325581	10,0775194	34,8837209	34,8837209	65,1162791	1,15384615	2,46153846	-34,3	-31,1	0,00479314	28,27	-26,589147	-0,7622222
sch-MIR10535a	119	18,487395	31,9327731	15,1260504	34,4537815	33,6134454	66,3865546	1,07894737	1,22222222	-60,1	-60,1	0,0544645	5,86	-50,504202	-1,5025
sch-MIR10538-1	183	18,579235	30,0546448	16,3934426	34,9726776	34,9726776	65,0273224	1,16363636	1,13333333	-90,7	-90,1	0,0996593	19,08	-49,562842	-1,4171875
sch-MIR10538-10	138	15,2173913	36,2318841	15,942029	32,6086957	31,1594203	68,8405797	0,9	0,95454545	-72	-72	0,343421	4,58	-52,173913	-1,6744186
sch-MIR10538-11	86	19,7674419	33,7209302	15,1162791	31,3953488	34,8837209	65,1162791	0,93103448	1,30769231	-39,6	-39,6	0,816292	0,46	-46,046512	-1,32
sch-MIR10538-12	143	16,0839161	34,2657343	17,4825175	32,1678322	33,5664336	66,4335664	0,93877551	0,92	-74,6	-74,4	0,272698	2,23	-52,167832	-1,5541667
sch-MIR10538-13	100	17	30	19	34	36	64	1,13333333	0,89473684	-48,5	-48	0,12194	9,44	-48,5	-1,3472222
sch-MIR10538-14	287	13,9372822	34,8432056	19,8606272	31,358885	33,7979094	66,2020906	0,9	0,70175439	-85,8	-78,17	0,00013838	37,32	-29,89547	-0,8845361
sch-MIR10538-15	155	19,3548387	32,2580645	12,2580645	36,1290323	31,6129032	68,3870968	1,12	1,57894737	-78	-78	0,406304	8,37	-50,322581	-1,5918367
sch-MIR10538-2	202	15,3465347	36,1386139	14,8514851	33,6633663	30,1980198	69,8019802	0,93150685	1,03333333	-72,7	-55,66	0,0060521	47,09	-35,990099	-1,1918033
sch-MIR10538-3	169	13,6094675	35,5029586	16,5680473	34,3195266	30,1775148	69,8224852	0,96666667	0,82142857	-85,6	-85,6	0,233572	5,76	-50,650888	-1,6784314
sch-MIR10538-4	148	16,2162162	32,4324324	16,2162162	35,1351351	32,4324324	67,5675676	1,08333333	1	-78	-78	0,436489	29,03	-52,702703	-1,625
sch-MIR10538-5	174	17,816092	35,0574713	12,6436782	34,4827586	30,4597701	69,5402299	0,98360656	1,40909091	-74,3	-73,3	0,060386	8,54	-42,701149	-1,4018868
sch-MIR10538-6	172	13,9534884	32,5581395	17,4418605	36,0465116	31,3953488	68,6046512	1,10714286	0,8	-80,5	-80,5	0,309214	3,88	-46,802326	-1,4907407
sch-MIR10538-7	161	16,7701863	34,7826087	13,6645963	34,7826087	30,4347826	69,5652174	1	1,22727273	-66,7	-66,7	0,175784	2,96	-41,428571	-1,3612245
sch-MIR10538-8	233	18,0257511	30,9012876	14,1630901	36,9098712	32,1888412	67,8111588	1,19444444	1,27272727	-57,9	-56,1	0,00057099	29,5	-24,849785	-0,772
sch-MIR10538-9	172	15,6976744	36,627907	15,1162791	32,5581395	30,8139535	69,1860465	0,88888889	1,03846154	-77,7	-77,7	0,0948812	6,9	-45,174419	-1,4660377
sch-MIR1054	161	14,2857143	32,9192547	17,3913043	35,4037267	31,6770186	68,3229814	1,0754717	0,82142857	-92	-92	0,0243433	8,44	-57,142857	-1,8039216
sch-MIR10540-1	142	14,7887324	32,3943662	19,7183099	33,0985915	34,5070423	65,4929577	1,02173913	0,75	-61,2	-58,7	0,0509118	5,87	-43,098592	-1,2489796
sch-MIR10540-2	100	15	37	16	32	31	69	0,86486486	0,9375	-24,7	-23,9	0,092496	17,6	-24,7	-0,7967742
sch-MIR10540-3	149	18,7919463	34,2281879	12,7516779	34,2281879	31,5436242	68,4563758	1	1,47368421	-58,8	-53,57	0,0490579	16,3	-39,463087	-1,2510638
sch-MIR10542-1	237	18,5654008	37,5527426	12,6582278	31,2236287	31,2236287	68,7763713	0,83146067	1,46666667	-59,7	-48,3	0,00254926	66,65	-25,189873	-0,8067568
sch-MIR10542-2	268	18,6567164	35,8208955	13,4328358	32,0895522	32,0895522	67,9104478	0,89583333	1,38888889	-67,8	-55,5	0,00029746	69,27	-25,298507	-0,7883721
sch-MIR10542-3	302	15,8940397	36,0927152	14,5695364	33,4437086	30,4635762	69,5364238	0,9266055	1,09090909	-69,2	-55,2	0,00063106	52,26	-22,913907	-0,7521739
sch-MIR10542-4	257	17,8988327	37,3540856	12,4513619	32,2957198	30,3501946	69,6498054	0,86458333	1,4375	-61,1	-45,5	0,00039856	55,29	-23,774319	-0,7833333
sch-MIR1078-1	142	17,6056338	30,2816901	14,084507	38,028169	31,6901408	68,3098592	1,25581395	1,25	-33,3	-33,3	0,0133111	15,96	-23,450704	-0,74
sch-MIR1078-2	129	12,4031008	37,9844961	19,379845	30,2325581	31,7829457	68,2170543	0,79591837	0,64	-28,8	-28	0,0595491	11,38	-22,325581	-0,702439
sch-MIR1085	291	16,1512027	31,6151203	15,8075601	36,4261168	31,9587629	68,0412371	1,15217391	1,02173913	-85	-77,6	7,31E-05	45,55	-29,209622	-0,9139785
sch-MIR10992	329	16,7173252	35,2583587	13,9817629	34,0425532	30,6990881	69,3009119	0,96551724	1,19565217	-74,4	-61,9	0,00010818	42,6	-22,613982	-0,7366337
sch-MIR11008	236	21,1864407	32,2033898	15,2542373	31,3559322	36,440678	63,559322	0,97368421	1,38888889	-83,9	-80,4	0,00104208	34,44	-35,550847	-0,9755814
sch-MIR11011a	122	17,2131148	34,4262295	18,0327869	30,3278689	35,2459016	64,7540984	0,88095238	0,95454545	-63,1	-63,1	0,216836	2,51	-51,721311	-1,4674419
sch-MIR11018-1	279	16,4874552	43,0107527	14,6953405	25,8064516	31,1827957	68,8172043	0,6	1,12195122	-82,4	-73,2	0,00152977	27,59	-29,53405	-0,9471264

sch-MIR11018-2	112	16,9642857	38,3928571	15,1785714	29,4642857	32,1428571	67,8571429	0,76744186	1,11764706	-27,2	-27,37	0,0505265	7,73	-24,285714	-0,7555556
sch-MIR1106-1	151	14,5695364	38,410596	15,8940397	31,1258278	30,4635762	69,5364238	0,81034483	0,91666667	-59,4	-58,5	0,148849	10,1	-39,337748	-1,2913043
sch-MIR1106-2	154	15,5844156	33,7662338	14,9350649	35,7142857	30,5194805	69,4805195	1,05769231	1,04347826	-82,7	-82,6	0,0997272	8,84	-53,701299	-1,7595745
sch-MIR11066	126	21,4285714	30,1587302	20,6349206	27,7777778	42,0634921	57,9365079	0,92105263	1,03846154	-42,3	-40,2	0,0225739	8,75	-33,571429	-0,7981132
sch-MIR11068f	236	14,4067797	32,6271186	16,9491525	36,0169492	31,3559322	68,6440678	1,1038961	0,85	-98,8	-98,8	0,0540296	5,81	-41,864407	-1,3351351
sch-MIR11076-1	72	23,6111111	27,7777778	19,4444444	29,1666667	43,0555556	56,9444444	1,05	1,21428571	-29,2	-28,9	0,384663	3,57	-40,555556	-0,9419355
sch-MIR11076-2	115	20	29,5652174	20	30,4347826	40	60	1,02941176	1	-37,4	-35,2	0,0264569	15,91	-32,521739	-0,8130435
sch-MIR11077a	209	16,2679426	31,1004785	16,7464115	35,8851675	33,0143541	66,9856459	1,15384615	0,97142857	-49	-41,5	0,00173226	35,17	-23,444976	-0,7101449
sch-MIR11079	243	26,7489712	23,8683128	11,5226337	37,8600823	38,2716049	61,7283951	1,5862069	2,32142857	-69,5	-66,4	0,00024198	48,68	-28,600823	-0,7473118
sch-MIR11085-1	168	15,4761905	33,9285714	17,8571429	32,7380952	33,3333333	66,6666667	0,96491228	0,86666667	-95,5	-93,8	0,0875329	4,86	-56,845238	-1,7053571
sch-MIR11085-2	195	17,4358974	32,8205128	14,3589744	35,3846154	31,7948718	68,2051282	1,078125	1,21428571	-78	-74,9	0,0548267	9,21	-40	-1,2580645
sch-MIR11088a	100	23	29	19	29	42	58	1	1,21052632	-36,1	-36,1	0,201089	5,45	-36,1	-0,8595238
sch-MIR11093	171	16,9590643	35,0877193	16,9590643	30,994152	33,9181287	66,0818713	0,88333333	1	-70,4	-70,4	0,0663898	9,1	-41,169591	-1,2137931
sch-MIR11107c	189	20,6349206	22,7513228	12,1693122	44,4444444	32,8042328	67,1957672	1,95348837	1,69565217	-47,5	-41,1	0,0241171	22,4	-25,132275	-0,766129
sch-MIR11108a	298	18,7919463	33,557047	13,7583893	33,8926174	32,5503356	67,4496644	1,01	1,36585366	-68,7	-40,6	0,00079949	77,72	-23,053691	-0,7082474
sch-MIR11108e	119	20,1680672	33,6134454	10,0840336	36,1344538	30,2521008	69,7478992	1,075	2	-28,9	-25,3	0,0142752	20,76	-24,285714	-0,8027778
sch-MIR11108h	278	25,1798561	25,8992806	17,9856115	30,9352518	43,1654676	56,8345324	1,19444444	1,4	-88,7	-80	8,12E-05	48,88	-31,906475	-0,7391667
sch-MIR11114	268	14,5522388	35,8208955	15,6716418	33,9552239	30,2238806	69,7761194	0,94791667	0,92857143	-59,1	-48,3	0,00018937	60,32	-22,052239	-0,7296296
sch-MIR11122	294	14,6258503	35,0340136	17,0068027	33,3333333	31,6326531	68,3673469	0,95145631	0,86	-65,8	-62,3	0,00021752	53,94	-22,380952	-0,7075269
sch-MIR11131	143	13,986014	33,5664336	18,1818182	34,2657343	32,1678322	67,8321678	1,02083333	0,76923077	-78,9	-78,9	0,236719	2,98	-55,174825	-1,7152174
sch-MIR11144-1	272	18,75	34,9264706	13,2352941	33,0882353	31,9852941	68,0147059	0,94736842	1,41666667	-83,5	-79,6	0,0011195	35,44	-30,698529	-0,9597701
sch-MIR11144-2	271	17,7121771	35,7933579	12,5461255	33,9483395	30,2583026	69,7416974	0,94845361	1,41176471	-79,6	-79,2	0,00087355	27,87	-29,372694	-0,9707317
sch-MIR1122	299	19,3979933	37,458194	11,7056856	31,4381271	31,1036789	68,8963211	0,83928571	1,65714286	-68,3	-54,8	0,00015782	60,06	-22,842809	-0,7344086
sch-MIR1127-1	75	20	30,6666667	18,6666667	30,6666667	38,6666667	61,3333333	1	1,07142857	-37,3	-37,3	0,651992	0,76	-49,733333	-1,2862069
sch-MIR1127-2	249	18,4738956	29,7188755	17,6706827	34,1365462	36,1445783	63,8554217	1,14864865	1,04545455	-82,4	-76,14	0,00064086	57,55	-33,092369	-0,9155556
sch-MIR1127b-1	131	20,610687	29,0076336	16,7938931	33,5877863	37,4045802	62,5954198	1,15789474	1,22727273	-75,2	-75,1	0,0472192	5,66	-57,40458	-1,5346939
sch-MIR1128-1	275	21,0909091	33,8181818	13,8181818	31,2727273	34,9090909	65,0909091	0,92473118	1,52631579	-75,3	-58,3	0,00142643	57,3	-27,381818	-0,784375
sch-MIR1128-2	269	15,6133829	34,2007435	15,2416357	34,9442379	30,8550186	69,1449814	1,02173913	1,02439024	-99,5	-95,9	0,00833592	30,26	-36,988848	-1,1987952
sch-MIR1128-3	236	22,0338983	33,8983051	10,1694915	33,8983051	32,2033898	67,7966102	1	2,16666667	-56	-52,7	0,00014848	51,81	-23,728814	-0,7368421
sch-MIR1128-4	226	14,159292	33,1858407	22,5663717	30,0884956	36,7256637	63,2743363	0,90666667	0,62745098	-60,9	-51,8	0,00028657	33,45	-26,946903	-0,7337349
sch-MIR1128-5	226	22,5663717	30,0884956	14,159292	33,1858407	36,7256637	63,2743363	1,10294118	1,59375	-74,8	-62,9	9,78E-05	53,23	-33,097345	-0,9012048
sch-MIR11314	155	24,516129	28,3870968	8,38709677	38,7096774	32,9032258	67,0967742	1,36363636	2,92307692	-56,7	-55,6	0,00069425	24,01	-36,580645	-1,1117647
sch-MIR11330	145	17,9310345	33,7931034	15,1724138	33,1034483	33,1034483	66,8965517	0,97959184	1,18181818	-83,2	-83,2	0,193414	3,92	-57,37931	-1,7333333
sch-MIR1133-1	311	16,3987138	30,5466238	15,755627	37,2990354	32,1543408	67,8456592	1,22105263	1,04081633	-94,1	-91,9	0,00036775	27,97	-30,257235	-0,941
sch-MIR1133-2	288	15,9722222	37,8472222	16,3194444	29,8611111	32,2916667	67,7083333	0,78899083	0,9787234	-79,5	-78,2	0,00096028	25,39	-27,604167	-0,8548387
sch-MIR1134	126	19,047619	33,3333333	18,2539683	29,3650794	37,3015873	62,6984127	0,88095238	1,04347826	-40,8	-40,2	0,0425385	7,12	-32,380952	-0,8680851
sch-MIR11409d	252	14,6825397	31,7460317	16,6666667	36,9047619	31,3492063	68,6507937	1,1625	0,88095238	-67,3	-61,8	0,00748501	34,26	-26,706349	-0,8518987
sch-MIR11424	190	20,5263158	25,2631579	15,7894737	38,4210526	36,3157895	63,6842105	1,52083333	1,3	-67,8	-66,8	0,0543577	7,52	-35,684211	-0,9826087
sch-MIR11425f	127	18,1102362	32,2834646	13,3858268	36,2204724	31,496063	68,503937	1,12195122	1,35294118	-28,6	-25,64	0,0140747	23,16	-22,519685	-0,715
sch-MIR11426b	217	13,3640553	28,1105991	24,8847926	33,640553	38,2488479	61,7511521	1,19672131	0,53703704	-63,1	-61,07	0,016225	24,26	-29,069124	-0,76
sch-MIR11444	160	19,375	33,125	11,25	36,25	30,625	69,375	1,09433962	1,72222222	-41	-36,6	0,0105549	32,79	-25,625	-0,8367347
sch-MIR11466b	160	18,125	35,625	20,625	25,625	38,75	61,25	0,71929825	0,87878788	-60,2	-58,5	0,00871408	14,41	-37,625	-0,9709677
sch-MIR11466c	157	17,1974522	30,5732484	13,3757962	38,8535032	30,5732484	69,4267516	1,27083333	1,28571429	-38	-38	0,0334132	14,02	-24,203822	-0,7916667
sch-MIR11497-1	95	20	37,8947368	10,5263158	31,5789474	30,5263158	69,4736842	0,83333333	1,9	-21,7	-21,7	0,240206	5	-22,842105	-0,7482759
sch-MIR11497-2	95	22,1052632	37,8947368	8,42105263	31,5789474	30,5263158	69,4736842	0,83333333	2,625	-30,9	-30,9	0,309377	2,66	-32,526316	-1,0655172
sch-MIR11498c	121	22,3140496	31,4049587	13,2231405	33,0578512	35,5371901	64,4628099	1,05263158	1,6875	-31	-23,9	0,0168902	29,05	-25,619835	-0,7209302
sch-MIR11509	104	18,2692308	29,8076923	16,3461538	35,5769231	34,6153846	65,3846154	1,19354839	1,11764706	-29,5	-28,6	0,0246643	10,62	-28,365385	-0,8194444
sch-MIR11576	204	26,9607843	26,4705882	11,2745098	35,2941176	38,2352941	61,7647059	1,33333333	2,39130435	-81,3	-79,8	0,0457344	5,89	-39,852941	-1,0423077
sch-MIR11583b-1	265	18,490566	32,4528302	13,5849057	35,4716981	32,0754717	67,9245283	1,09302326	1,36111111	-67,2	-44,9	6,24E-05	68,51	-25,358491	-0,7905882
sch-MIR11583b-2	315	17,4603175	34,6031746	13,968254	33,968254	31,4285714	68,5714286	0,98165138	1,25	-76,3	-67	0,00010206	67,63	-24,222222	-0,7707071
sch-MIR11583b-3	212	21,6981132	34,4339623	14,1509434	29,7169811	35,8490566	64,1509434	0,8630137	1,53333333	-65	-61,62	0,00037097	28,73	-30,660377	-0,8552632
sch-MIR11592-1	82	20,7317073	29,2682927	21,9512195	28,0487805	42,6829268	57,3170732	0,95833333	0,94444444	-37,1	-36,7	0,0606463	6,98	-45,243902	-1,06
sch-MIR11592-2	77	20,7792208	36,3636364	18,1818182	24,6753247	38,961039	61,038961	0,67857143	1,14285714	-23,8	-23,8	0,414198	9,39	-30,909091	-0,7933333
sch-MIR1167	254	16,1417323	35,0393701	14,1732283	34,6456693	30,3149606	69,6850394	0,98876404	1,13888889	-84,7	-81,5	3,45E-05	28,34	-33,346457	-1,1
sch-MIR1170	333	15,6156156	33,6336336	17,1171171	33,6336336	32,7327327	67,2672673	1	0,9122807	-80,2	-66,7	4,06E-05	58,01	-24,084084	-0,7357798
sch-MIR11891-1	135	20,7407407	31,8518519	14,0740741	33,3333333	34,8148148	65,1851852	1,04651163	1,47368421	-61,4	-57,8	0,0971327	10,03	-45,481481	-1,306383
sch-MIR11891-2	135	20,7407407	32,5925926	14,8148148	31,8518519	35,5555556	64,4444444	0,97727273	1,4	-54,1	-50,7	0,120094	11,98	-40,074074	-1,1270833
sch-MIR12142	285	17,1929825	30,877193	17,8947368	34,0350877	35,0877193	64,9122807	1,10227273	0,96078431	-97,7	-97	0,00074432	28,18	-34,280702	-0,977
sch-MIR12168	99	19,1919192	34,3434343	11,1111111	35,3535354	30,3030303	69,6969697	1,02941176	1,72727273	-25,7	-24,8	0,111067	6,69	-25,959596	-0,8566667
sch-MIR1222d	266	27,8195489	28,9473684	15,7894737	27,443609	43,6090226	56,3909774	0,94805195	1,76190476	-84,5	-77,1	0,0025034	56,14	-31,766917	-0,7284483
sch-MIR1309	292	16,7808219	33,5616438	15,7534247	33,9041096	32,5342466	67,4657534	1,01020408	1,06521739	-79,4	-75,6	0,0001098	39	-27,191781	-0,8357895
sch-MIR1312a	198	16,1616162	33,3333333	16,1616162	34,3434343	32,3232323	67,6767677	1,03030303	1	-71,5	-71,5	0,167329	7,19	-36,111111	-1,1171875
sch-MIR1428a	177	15,2542373	36,7231638	20,9039548	27,1186441	36,1581921	63,8418079	0,73846154	0,72972973	-82,9	-82,9	0,114574	8,01	-46,836158	-1,2953125
sch-MIR1432	99	30,3030303	21,2121212	22,2222222	26,2626263	52,5252525	47,4747475	1,23809524	1,36363636	-37,6	-37,2	0,304974	4,01	-37,979798	-0,7230769
sch-MIR1440a	120	22,5	29,1666667	16,6666667	31,6666667	39,1666667	60,8333333	1,08571429	1,35	-36,3	-30,6	0,0182668	20,81	-30,25	-0,7723404
sch-MIR1446	108	18,5185185	25,9259259	19,4444444	36,1111111	37,962963	62,037037	1,39285714	0,95238095	-44,8	-44,8	0,107092	4,57	-41,481481	-1,0926829

sch-MIR1511	231	16,8831169	37,2294372	15,5844156	30,3030303	32,4675325	67,5324675	0,81395349	1,08333333	-53,8	-45,5	0,00727098	35,88	-23,290043	-0,7173333
sch-MIR1513b	107	15,8878505	29,9065421	14,953271	39,2523364	30,8411215	69,1588785	1,3125	1,0625	-45,2	-44	0,0683076	8,26	-42,242991	-1,369697
sch-MIR1514b-1	168	17,8571429	33,3333333	12,5	36,3095238	30,3571429	69,6428571	1,08928571	1,42857143	-37,5	-21,2	0,00121152	49,18	-22,321429	-0,7352941
sch-MIR1514b-2	143	17,4825175	40,5594406	13,986014	27,972028	31,4685315	68,5314685	0,68965517	1,25	-62,1	-61,5	0,0415543	7,14	-43,426573	-1,38
sch-MIR1521b	292	15,4109589	33,2191781	18,4931507	32,8767123	33,9041096	66,0958904	0,98969072	0,83333333	-89,9	-85,3	0,00057494	31,91	-30,787671	-0,9080808
sch-MIR1525	285	26,3157895	26,3157895	17,1929825	30,1754386	43,5087719	56,4912281	1,14666667	1,53061224	-88,9	-80,4	0,00043133	61,91	-31,192982	-0,7169355
sch-MIR1530-1	181	15,4696133	35,9116022	17,679558	30,9392265	33,1491713	66,8508287	0,86153846	0,875	-48,4	-50,35	0,014492	14,14	-26,740331	-0,8066667
sch-MIR1530-2	253	13,8339921	37,5494071	18,5770751	30,0395257	32,4110672	67,5889328	0,8	0,74468085	-78,4	-78,4	0,0124396	10,95	-30,988142	-0,9560976
sch-MIR1530-3	175	15,4285714	38,8571429	17,1428571	28,5714286	32,5714286	67,4285714	0,73529412	0,9	-41,3	-37,02	0,0277402	33,51	-23,6	-0,7245614
sch-MIR1533-1	185	20,5405405	31,3513514	23,2432432	24,8648649	43,7837838	56,2162162	0,79310345	0,88372093	-81,6	-81,5	0,0199351	9,06	-44,108108	-1,0074074
sch-MIR1533-2	182	21,4285714	31,8681319	21,4285714	25,2747253	42,8571429	57,1428571	0,79310345	1	-79	-78	0,00811608	10,92	-43,406593	-1,0128205
sch-MIR1533-3	178	16,2921348	32,5842697	14,0449438	37,0786517	30,3370787	69,6629213	1,13793103	1,16	-70,3	-64,24	0,00416265	36,62	-39,494382	-1,3018519
sch-MIR1533-4	219	16,4383562	41,5525114	14,1552511	27,8538813	30,5936073	69,4063927	0,67032967	1,16129032	-63,3	-61,74	0,00067115	30,16	-28,90411	-0,9447761
sch-MIR156aa	341	17,3020528	29,6187683	19,0615836	34,0175953	36,3636364	63,6363636	1,14851485	0,90769231	-92	-81,7	0,00010166	59,47	-26,979472	-0,7419355
sch-MIR156b-1	92	20,6521739	26,0869565	19,5652174	33,6956522	40,2173913	59,7826087	1,29166667	1,05555556	-43,8	-43,8	0,200633	3,88	-47,608696	-1,1837838
sch-MIR156b-10	181	19,8895028	29,8342541	17,679558	32,5966851	37,5690608	62,4309392	1,09259259	1,125	-72,4	-72,4	0,0452775	13,59	-40	-1,0647059
sch-MIR156b-11	106	24,5283019	24,5283019	22,6415094	28,3018868	47,1698113	52,8301887	1,15384615	1,08333333	-67,7	-67,7	0,510729	2,13	-63,867925	-1,354
sch-MIR156b-12	108	22,2222222	25,9259259	17,5925926	34,2592593	39,8148148	60,1851852	1,32142857	1,26315789	-51,4	-51	0,00718945	10,31	-47,592593	-1,1953488
sch-MIR156b-13	140	18,5714286	28,5714286	15	37,8571429	33,5714286	66,4285714	1,325	1,23809524	-55	-54	0,037706	9,95	-39,285714	-1,1702128
sch-MIR156b-14	138	18,8405797	33,3333333	18,115942	29,7101449	36,9565217	63,0434783	0,89130435	1,04	-55,1	-55	0,0398162	7,48	-39,927536	-1,0803922
sch-MIR156b-15	108	26,8518519	23,1481481	21,2962963	28,7037037	48,1481481	51,8518519	1,24	1,26086957	-60,2	-60,2	0,0982525	7,8	-55,740741	-1,1576923
sch-MIR156b-16	132	16,6666667	31,8181818	13,6363636	37,8787879	30,3030303	69,6969697	1,19047619	1,22222222	-44,9	-40,4	0,00735677	20,27	-34,015152	-1,1225
sch-MIR156b-17	102	24,5098039	25,4901961	23,5294118	26,4705882	48,0392157	51,9607843	1,03846154	1,04166667	-66,2	-66,2	0,642287	1,78	-64,901961	-1,3510204
sch-MIR156b-18	237	16,0337553	25,3164557	16,4556962	42,1940928	32,4894515	67,5105485	1,66666667	0,97435897	-62,1	-57,3	0,0105293	15,01	-26,202532	-0,8064935
sch-MIR156b-2	99	23,2323232	24,2424242	17,1717172	35,3535354	40,4040404	59,5959596	1,45833333	1,35294118	-58,3	-58,3	0,310263	5,29	-58,888889	-1,4575
sch-MIR156b-3	183	25,136612	32,7868852	13,6612022	28,4153005	38,7978142	61,2021858	0,86666667	1,84	-50	-48,1	0,0175681	23,12	-27,322404	-0,7042254
sch-MIR156b-4	183	14,2076503	26,2295082	21,8579235	37,704918	36,0655738	63,9344262	1,4375	0,65	-48,8	-48,8	0,0832006	9,26	-26,666667	-0,7393939
sch-MIR156b-5	101	17,8217822	29,7029703	18,8118812	33,6633663	36,6336634	63,3663366	1,13333333	0,94736842	-43,5	-42,2	0,119446	6,96	-43,069307	-1,1756757
sch-MIR156b-6	88	21,5909091	25	23,8636364	29,5454545	45,4545455	54,5454545	1,18181818	0,9047619	-44,1	-44,1	0,312754	2,54	-50,113636	-1,1025
sch-MIR156b-7	98	20,4081633	30,6122449	18,3673469	30,6122449	38,7755102	61,2244898	1	1,11111111	-48	-40,4	0,0363143	5,83	-48,979592	-1,2631579
sch-MIR156b-8	100	24	24	18	34	42	58	1,41666667	1,33333333	-35,9	-35,8	0,0665494	8,93	-35,9	-0,8547619
sch-MIR156b-9	103	21,3592233	27,184466	16,5048544	34,9514563	37,8640777	62,1359223	1,28571429	1,29411765	-49,8	-45,2	0,00660707	10,63	-48,349515	-1,2769231
sch-MIR156f-1	89	20,2247191	29,2134831	17,9775281	32,5842697	38,2022472	61,7977528	1,11538462	1,125	-32,9	-32,3	0,122664	4,36	-36,966292	-0,9676471
sch-MIR156f-2	88	21,5909091	27,2727273	17,0454545	34,0909091	38,6363636	61,3636364	1,25	1,26666667	-39,1	-39,1	0,385297	2,11	-44,431818	-1,15
sch-MIR156g-1	119	19,3277311	26,0504202	19,3277311	35,2941176	38,6554622	61,3445378	1,35483871	1	-74,5	-74,5	0,171813	3,48	-62,605042	-1,6195652
sch-MIR156g-2	113	19,4690265	30,0884956	19,4690265	30,9734513	38,9380531	61,0619469	1,02941176	1	-42,3	-40,47	0,0124657	15,64	-37,433628	-0,9613636
sch-MIR156h-1	334	15,2694611	30,239521	24,5508982	29,9401198	39,8203593	60,1796407	0,99009901	0,62195122	-94,4	-80,42	0,00010886	58,53	-28,269461	-0,7099248
sch-MIR156h-2	191	12,0418848	30,3664921	23,5602094	34,0314136	35,6020942	64,3979058	1,12068966	0,51111111	-52,7	-31,87	0,0019158	58,12	-27,591623	-0,775
sch-MIR156i	178	19,1011236	27,5280899	17,4157303	35,9550562	36,5168539	63,4831461	1,30612245	1,09677419	-89,7	-86,5	0,00771836	17,74	-50,393258	-1,38
sch-MIR156j	118	20,3389831	31,3559322	17,7966102	30,5084746	38,1355932	61,8644068	0,97297297	1,14285714	-42,5	-42,5	0,0777663	10,23	-36,016949	-0,9444444
sch-MIR158a-1	70	21,4285714	35,7142857	11,4285714	31,4285714	32,8571429	67,1428571	0,88	1,875	-26,2	-22	0,172064	5,71	-37,428571	-1,1391304
sch-MIR158a-2	169	16,5680473	33,7278107	18,3431953	31,3609467	34,9112426	65,0887574	0,92982456	0,90322581	-46,7	-38,3	0,00115083	33,94	-27,633136	-0,7915254
sch-MIR158b	248	16,5322581	29,0322581	15,3225806	39,1129032	31,8548387	68,1451613	1,34722222	1,07894737	-87,4	-82,5	0,00072455	44,85	-35,241935	-1,1063291
sch-MIR159	137	16,0583942	32,8467153	15,3284672	35,7664234	31,3868613	68,6131387	1,08888889	1,04761905	-65	-65	0,107585	10,34	-47,445255	-1,5116279
sch-MIR159a-1	186	22,5806452	24,7311828	16,6666667	36,0215054	39,2473118	60,7526882	1,45652174	1,35483871	-83,4	-80,8	0,0195527	12,3	-44,83871	-1,1424658
sch-MIR159a-2	112	16,9642857	39,2857143	16,0714286	27,6785714	33,0357143	66,9642857	0,70454545	1,05555556	-40,1	-40,1	0,0837877	4,17	-35,803571	-1,0837838
sch-MIR159a-3	103	24,2718447	21,3592233	25,2427184	29,1262136	49,5145631	50,4854369	1,36363636	0,96153846	-53,3	-50,4	0,0465054	8,48	-51,747573	-1,045098
sch-MIR159b-1	180	21,1111111	28,3333333	16,1111111	34,4444444	37,2222222	62,7777778	1,21568627	1,31034483	-76,2	-74,1	0,011904	9,17	-42,333333	-1,1373134
sch-MIR159b-2	214	21,4953271	28,9719626	16,3551402	33,1775701	37,8504673	62,1495327	1,14516129	1,31428571	-91,3	-88,4	0,00611142	12,64	-42,663551	-1,1271605
sch-MIR159b-3	216	20,8333333	31,0185185	16,6666667	31,4814815	37,5	62,5	1,01492537	1,25	-79,6	-77,6	0,00175442	19,22	-36,851852	-0,982716
sch-MIR159b-4	186	19,8924731	33,8709677	15,5913978	30,6451613	35,483871	64,516129	0,9047619	1,27586207	-86,2	-86,2	0,0632615	8,37	-46,344086	-1,3060606
sch-MIR159c	174	23,5632184	27,5862069	22,4137931	26,4367816	45,9770115	54,0229885	0,95833333	1,05128205	-77,2	-72,5	0,0172515	25,58	-44,367816	-0,965
sch-MIR160-1	104	23,0769231	24,0384615	21,1538462	31,7307692	44,2307692	55,7692308	1,32	1,09090909	-52,3	-51,4	0,100504	4,55	-50,288462	-1,1369565
sch-MIR160-2	95	26,3157895	23,1578947	24,2105263	26,3157895	50,5263158	49,4736842	1,13636364	1,08695652	-41,9	-37,9	0,0750999	10,38	-44,105263	-0,8729167
sch-MIR160-3	257	19,0661479	30,7392996	16,3424125	33,8521401	35,4085603	64,5914397	1,10126582	1,16666667	-91,1	-87,2	0,00059055	27,62	-35,447471	-1,0010989
sch-MIR160c	81	23,4567901	24,691358	25,9259259	25,9259259	49,382716	50,617284	1,05	0,9047619	-38,8	-38,8	0,437357	3,28	-47,901235	-0,97
sch-MIR160e	92	22,826087	31,5217391	20,6521739	25	43,4782609	56,5217391	0,79310345	1,10526316	-40,2	-39,2	0,253019	2,43	-43,695652	-1,005
sch-MIR160g	97	21,6494845	29,8969072	23,7113402	24,742268	45,3608247	54,6391753	0,82758621	0,91304348	-48,9	-48,9	0,183973	3,15	-50,412371	-1,1113636
sch-MIR160h-1	90	24,4444444	24,4444444	21,1111111	30	45,5555556	54,4444444	1,22727273	1,15789474	-44,3	-44,3	0,126198	3,12	-49,222222	-1,0804878
sch-MIR160h-2	95	23,1578947	29,4736842	24,2105263	23,1578947	47,3684211	52,6315789	0,78571429	0,95652174	-43,8	-43,8	0,356827	2,2	-46,105263	-0,9733333
sch-MIR160h-3	92	20,6521739	25	22,826087	31,5217391	43,4782609	56,5217391	1,26086957	0,9047619	-39,4	-39,2	0,372634	3,25	-42,826087	-0,985
sch-MIR162-1	135	22,962963	31,1111111	20	25,9259259	42,962963	57,037037	0,83333333	1,14814815	-50,3	-49,9	0,0103044	10,28	-37,259259	-0,8672414
sch-MIR162-2	110	26,3636364	20	24,5454545	29,0909091	50,9090909	49,0909091	1,45454545	1,07407407	-56,4	-56,4	0,16867	8,36	-51,272727	-1,0071429
sch-MIR162-3	93	23,655914	31,1827957	24,7311828	20,4301075	48,3870968	51,6129032	0,65517241	0,95652174	-42	-42	0,347985	4,29	-45,16129	-0,9333333
sch-MIR162-4	135	20	25,9259259	22,962963	31,1111111	42,962963	57,037037	1,2	0,87096774	-53,8	-52,1	0,120578	6,65	-39,851852	-0,9275862
sch-MIR163	243	27,1604938	31,6872428	17,2839506	23,8683128	44,4444444	55,5555556	0,75324675	1,57142857	-76,8	-76,8	0,0370098	13,84	-31,604938	-0,7111111

sch-MIR164	169	20,1183432	28,4023669	16,5680473	34,9112426	36,6863905	63,3136095	1,22916667	1,21428571	-60,3	-58,2	0,00285138	17,43	-35,680473	-0,9725806
sch-MIR164a	228	21,4912281	25,877193	15,7894737	36,8421053	37,2807018	62,7192982	1,42372881	1,36111111	-68,1	-59,8	0,00145801	56,1	-29,868421	-0,8011765
sch-MIR164c-1	107	22,4299065	24,2990654	27,1028037	26,1682243	49,5327103	50,4672897	1,07692308	0,82758621	-53,5	-49,7	0,14001	7,12	-50	-1,009434
sch-MIR164c-2	93	19,3548387	25,8064516	19,3548387	35,483871	38,7096774	61,2903226	1,375	1	-51,4	-48,1	0,112296	4,98	-55,268817	-1,4277778
sch-MIR164e-1	131	21,3740458	23,6641221	22,1374046	32,8244275	43,5114504	56,4885496	1,38709677	0,96551724	-59,3	-56,9	0,0100087	11,99	-45,267176	-1,0403509
sch-MIR164e-2	96	21,875	26,0416667	17,7083333	34,375	39,5833333	60,4166667	1,32	1,23529412	-44,7	-42,7	0,020444	10,47	-46,5625	-1,1763158
sch-MIR166-1	118	16,9491525	29,6610169	20,3389831	33,0508475	37,2881356	62,7118644	1,11428571	0,83333333	-33,4	-32,2	0,0225194	10,33	-28,305085	-0,7590909
sch-MIR166-2	146	17,1232877	33,5616438	17,8082192	31,5068493	34,9315068	65,0684932	0,93877551	0,96153846	-50	-47	0,0643619	9,47	-34,246575	-0,9803922
sch-MIR166a-1	165	21,8181818	28,4848485	18,7878788	30,9090909	40,6060606	59,3939394	1,08510638	1,16129032	-60,1	-59,8	0,0553121	12,59	-36,424242	-0,8970149
sch-MIR166a-2	158	21,5189873	25,9493671	15,8227848	36,7088608	37,3417722	62,6582278	1,41463415	1,36	-71,6	-71,6	0,220409	5,17	-45,316456	-1,2135593
sch-MIR166b	98	22,4489796	21,4285714	23,4693878	32,6530612	45,9183673	54,0816327	1,52380952	0,95652174	-36,5	-34	0,0526194	9,72	-37,244898	-0,8111111
sch-MIR166c	189	21,1640212	30,6878307	15,3439153	32,8042328	36,5079365	63,4920635	1,06896552	1,37931034	-79,8	-77	0,0152093	14,18	-42,222222	-1,1565217
sch-MIR166d	114	21,0526316	28,0701754	16,6666667	34,2105263	37,7192982	62,2807018	1,21875	1,26315789	-49,5	-48,3	0,149845	12,39	-43,421053	-1,1511628
sch-MIR167b-1	95	16,8421053	29,4736842	20	33,6842105	36,8421053	63,1578947	1,14285714	0,84210526	-35,3	-35,3	0,064061	5,85	-37,157895	-1,0085714
sch-MIR167b-2	84	25	29,7619048	20,2380952	25	45,2380952	54,7619048	0,84	1,23529412	-41,7	-41,7	0,476326	3,16	-49,642857	-1,0973684
sch-MIR167b-3	80	17,5	33,75	20	28,75	37,5	62,5	0,85185185	0,875	-29,3	-28,6	0,0365419	8,45	-36,625	-0,9766667
sch-MIR167b-4	112	24,1071429	26,7857143	22,3214286	26,7857143	46,4285714	53,5714286	1	1,08	-53,8	-53,8	0,0810847	4,39	-48,035714	-1,0346154
sch-MIR167b-5	107	20,5607477	29,9065421	23,364486	26,1682243	43,9252336	56,0747664	0,875	0,88	-43,5	-43,5	0,19246	5,26	-40,654206	-0,9255319
sch-MIR167d-1	90	17,7777778	34,4444444	17,7777778	30	35,5555556	64,4444444	0,87096774	1	-38,9	-38,4	0,174373	4,55	-43,222222	-1,215625
sch-MIR167d-2	93	20,4301075	29,0322581	18,2795699	32,2580645	38,7096774	61,2903226	1,11111111	1,11764706	-43	-42,9	0,0891337	5,81	-46,236559	-1,1944444
sch-MIR167d-3	113	22,1238938	26,5486726	23,8938053	27,4336283	46,0176991	53,9823009	1,03333333	0,92592593	-49,5	-49,5	0,0256038	9,19	-43,80531	-0,9519231
sch-MIR167h	119	20,1680672	26,8907563	24,3697479	28,5714286	44,5378151	55,4621849	1,0625	0,82758621	-49,4	-49,4	0,0393334	8,91	-41,512605	-0,9320755
sch-MIR168c-1	154	27,9220779	22,7272727	22,7272727	26,6233766	50,6493506	49,3506494	1,17142857	1,22857143	-70,3	-69	0,0384443	16,8	-45,649351	-0,9012821
sch-MIR168c-2	157	29,9363057	19,7452229	24,2038217	26,1146497	54,1401274	45,8598726	1,32258065	1,23684211	-76,1	-70,8	0,0250534	14,91	-48,471338	-0,8952941
sch-MIR168c-3	175	30,2857143	20,5714286	24	25,1428571	54,2857143	45,7142857	1,22222222	1,26190476	-77,8	-77	0,0157525	18,91	-44,457143	-0,8189474
sch-MIR169a-1	182	20,3296703	22,5274725	15,9340659	41,2087912	36,2637363	63,7362637	1,82926829	1,27586207	-75,2	-72,8	0,0168998	13,35	-41,318681	-1,1393939
sch-MIR169a-2	157	22,9299363	22,9299363	17,1974522	36,9426752	40,1273885	59,8726115	1,61111111	1,33333333	-74,1	-72,8	0,0474389	10,37	-47,197452	-1,1761905
sch-MIR169a-3	158	24,6835443	27,8481013	15,1898734	32,278481	39,8734177	60,1265823	1,15909091	1,625	-80,1	-80,1	0,0532798	5	-50,696203	-1,2714286
sch-MIR169c-1	177	20,3389831	28,2485876	13,559322	37,8531073	33,8983051	66,1016949	1,34	1,5	-78,7	-76	0,00881749	14,1	-44,463277	-1,3116667
sch-MIR169c-2	205	13,6585366	29,2682927	17,0731707	40	30,7317073	69,2682927	1,36666667	0,8	-69,3	-66,3	0,015257	14,13	-33,804878	-1,1
sch-MIR169c-3	179	14,5251397	27,9329609	17,877095	39,6648045	32,4022346	67,5977654	1,42	0,8125	-62,3	-59,3	0,0492383	6,15	-34,804469	-1,0741379
sch-MIR169c-4	212	19,3396226	31,6037736	15,0943396	33,9622642	34,4339623	65,5660377	1,07462687	1,28125	-85,9	-83,1	0,00297299	13,72	-40,518868	-1,1767123
sch-MIR169c-5	185	21,0810811	20	23,7837838	35,1351351	44,8648649	55,1351351	1,75675676	0,88636364	-82,1	-70,3	0,00270742	19,26	-44,378378	-0,9891566
sch-MIR169e-1	193	20,7253886	26,9430052	16,5803109	35,7512953	37,3056995	62,6943005	1,32692308	1,25	-76,2	-70,61	0,00127045	22,93	-39,481865	-1,0583333
sch-MIR169e-2	169	17,1597633	35,5029586	18,9349112	28,4023669	36,0946746	63,9053254	0,8	0,90625	-69,6	-66,9	0,151292	3,99	-41,183432	-1,1409836
sch-MIR169e-3	144	18,75	36,1111111	18,75	26,3888889	37,5	62,5	0,73076923	1	-65,9	-63,2	0,0411438	7,66	-45,763889	-1,2203704
sch-MIR169f	218	21,559633	33,0275229	10,5504587	34,8623853	32,1100917	67,8899083	1,05555556	2,04347826	-56,7	-47,6	0,00093264	31,6	-26,009174	-0,81
sch-MIR169h	250	14,8	28,8	16,8	39,6	31,6	68,4	1,375	0,88095238	-91,5	-84	0,0032225	17,09	-36,6	-1,1582278
sch-MIR169j-1	163	17,791411	25,7668712	20,8588957	35,5828221	38,6503067	61,3496933	1,38095238	0,85294118	-55,4	-55,4	0,0265359	12,48	-33,98773	-0,8793651
sch-MIR169j-2	155	20	23,2258065	22,5806452	34,1935484	42,5806452	57,4193548	1,47222222	0,88571429	-57,1	-57,1	0,0213211	8,11	-36,83871	-0,8651515
sch-MIR169j-3	144	18,75	26,3888889	18,75	36,1111111	37,5	62,5	1,36842105	1	-68,7	-68,7	0,0187684	9,11	-47,708333	-1,2722222
sch-MIR169j-4	164	21,3414634	25	21,3414634	32,3170732	42,6829268	57,3170732	1,29268293	1	-70,3	-70,3	0,00635806	10,05	-42,865854	-1,0042857
sch-MIR169j-5	212	20,754717	25	18,3962264	35,8490566	39,1509434	60,8490566	1,43396226	1,12820513	-80,2	-73,3	0,0050148	19,35	-37,830189	-0,9662651
sch-MIR169j-6	169	18,9349112	28,4023669	17,1597633	35,5029586	36,0946746	63,9053254	1,25	1,10344828	-75,4	-75,4	0,00917106	9,92	-44,615385	-1,2360656
sch-MIR169j-7	178	20,2247191	25,2808989	19,1011236	35,3932584	39,3258427	60,6741573	1,4	1,05882353	-76,9	-72,9	0,007653	9,84	-43,202247	-1,0985714
sch-MIR169k	260	29,6153846	23,4615385	19,2307692	27,6923077	48,8461538	51,1538462	1,18032787	1,54	-90,3	-66,05	0,00159846	57,1	-34,730769	-0,7110236
sch-MIR169l	184	18,4782609	36,4130435	20,6521739	24,4565217	39,1304348	60,8695652	0,67164179	0,89473684	-59,9	-55,6	0,0322699	17,82	-32,554348	-0,8319444
sch-MIR169n	104	25	26,9230769	19,2307692	28,8461538	44,2307692	55,7692308	1,07142857	1,3	-33,1	-33,1	0,055723	12,25	-31,826923	-0,7195652
sch-MIR169r-1	285	19,6491228	26,6666667	17,8947368	35,7894737	37,5438596	62,4561404	1,34210526	1,09803922	-99,5	-94,67	0,00027811	37,19	-34,912281	-0,9299065
sch-MIR169r-2	184	21,7391304	26,6304348	18,4782609	33,1521739	40,2173913	59,7826087	1,24489796	1,17647059	-72,2	-72,2	0,00968743	10,72	-39,23913	-0,9756757
sch-MIR169r-3	184	20,6521739	24,4565217	18,4782609	36,4130435	39,1304348	60,8695652	1,48888889	1,11764706	-74,8	-69,4	0,0213931	18,97	-40,652174	-1,0388889
sch-MIR169r-4	202	19,8019802	25,7425743	18,3168317	36,1386139	38,1188119	61,8811881	1,40384615	1,08108108	-76,6	-76,54	0,00055589	21,21	-37,920792	-0,9948052
sch-MIR169r-5	74	24,3243243	24,3243243	18,9189189	32,4324324	43,2432432	56,7567568	1,33333333	1,28571429	-37,1	-37,1	0,436513	2,79	-50,135135	-1,159375
sch-MIR171a-1	94	24,4680851	24,4680851	17,0212766	34,0425532	41,4893617	58,5106383	1,39130435	1,4375	-44,7	-44,7	0,654507	1,08	-47,553191	-1,1461538
sch-MIR171a-2	94	23,4042553	29,787234	17,0212766	29,787234	40,4255319	59,5744681	1	1,375	-53,9	-53,9	0,509078	1,19	-57,340426	-1,4184211
sch-MIR171b-1	136	15,4411765	34,5588235	20,5882353	29,4117647	36,0294118	63,9705882	0,85106383	0,75	-36,6	-34,1	0,0501205	8,45	-26,911765	-0,7469388
sch-MIR171b-2	98	17,3469388	29,5918367	23,4693878	29,5918367	40,8163265	59,1836735	1	0,73913043	-40,1	-40	0,217095	2,66	-40,918367	-1,0025
sch-MIR171b-3	112	19,6428571	30,3571429	21,4285714	28,5714286	41,0714286	58,9285714	0,94117647	0,91666667	-46,2	-44,7	0,0821287	10,9	-41,25	-1,0043478
sch-MIR171b-4	127	17,3228346	33,8582677	22,0472441	26,7716535	39,3700787	60,6299213	0,79069767	0,78571429	-44	-37,4	0,0487887	14,11	-34,645669	-0,88
sch-MIR171b-5	89	21,3483146	28,0898876	15,7303371	34,8314607	37,0786517	62,9213483	1,24	1,35714286	-48,1	-48,1	0,487955	1,75	-54,044944	-1,4575758
sch-MIR171c-1	99	16,1616162	31,3131313	14,1414141	38,3838384	30,3030303	69,6969697	1,22580645	1,14285714	-46,6	-46,6	0,250493	2,08	-47,070707	-1,5533333
sch-MIR171c-2	89	21,3483146	28,0898876	15,7303371	34,8314607	37,0786517	62,9213483	1,24	1,35714286	-45,3	-45,3	0,496565	1,73	-50,898876	-1,3727273
sch-MIR171d	92	18,4782609	29,3478261	17,3913043	34,7826087	35,8695652	64,1304348	1,18518519	1,0625	-42,2	-42,2	0,652436	0,91	-45,869565	-1,2787879
sch-MIR171f-1	87	17,2413793	28,7356322	16,091954	37,9310345	33,3333333	66,6666667	1,32	1,07142857	-37,1	-37,1	0,181408	3,43	-42,643678	-1,2793103
sch-MIR171f-2	115	24,3478261	28,6956522	16,5217391	30,4347826	40,8695652	59,1304348	1,06060606	1,47368421	-44,8	-39,5	0,0823715	15,38	-38,956522	-0,9531915
sch-MIR171f-3	110	22,7272727	27,2727273	19,0909091	30,9090909	41,8181818	58,1818182	1,13333333	1,19047619	-45,2	-41,9	0,0564017	15,27	-41,090909	-0,9826087

sch-MIR171f-4	128	17,1875	26,5625	17,96875	38,28125	35,15625	64,84375	1,44117647	0,95652174	-50,5	-50,5	0,232889	2,78	-39,453125	-1,1222222
sch-MIR171f-5	136	20,5882353	29,4117647	15,4411765	34,5588235	36,0294118	63,9705882	1,175	1,33333333	-50,8	-50,8	0,211228	9,25	-37,352941	-1,0367347
sch-MIR171f-6	67	16,4179104	25,3731343	19,4029851	38,8059701	35,8208955	64,1791045	1,52941176	0,84615385	-24,5	-24,5	0,515537	2,21	-36,567164	-1,0208333
sch-MIR171h-1	177	14,6892655	35,0282486	16,9491525	33,3333333	31,6384181	68,3615819	0,9516129	0,86666667	-98,1	-97,6	0,145596	6,44	-55,423729	-1,7517857
sch-MIR171h-2	186	19,8924731	29,5698925	12,9032258	37,6344086	32,7956989	67,2043011	1,27272727	1,54166667	-49,5	-49,4	0,00935422	27,47	-26,612903	-0,8114754
sch-MIR171o-1	101	20,7920792	38,6138614	13,8613861	26,7326733	34,6534653	65,3465347	0,69230769	1,5	-27,2	-23,9	0,0999463	5,68	-26,930693	-0,7771429
sch-MIR171o-2	99	21,2121212	30,3030303	15,1515152	33,3333333	36,3636364	63,6363636	1,1	1,4	-43,6	-43,6	0,30538	2,17	-44,040404	-1,2111111
sch-MIR172a-1	123	19,5121951	34,9593496	18,699187	26,8292683	38,2113821	61,7886179	0,76744186	1,04347826	-55,5	-55,5	0,208451	3,24	-45,121951	-1,1808511
sch-MIR172a-2	123	18,699187	26,8292683	19,5121951	34,9593496	38,2113821	61,7886179	1,3030303	0,95833333	-69,5	-69,5	0,659562	1,24	-56,504065	-1,4787234
sch-MIR172b-1	110	14,5454545	37,2727273	17,2727273	30,9090909	31,8181818	68,1818182	0,82926829	0,84210526	-38,8	-38,8	0,424607	4,49	-35,272727	-1,1085714
sch-MIR172b-2	110	17,2727273	30,9090909	14,5454545	37,2727273	31,8181818	68,1818182	1,20588235	1,1875	-38,5	-38,5	0,111657	8,4	-35	-1,1
sch-MIR172c-1	188	18,0851064	37,2340426	12,7659574	31,9148936	30,8510638	69,1489362	0,85714286	1,41666667	-68,4	-66,5	0,0212146	14,14	-36,382979	-1,1793103
sch-MIR172c-2	94	23,4042553	29,787234	13,8297872	32,9787234	37,2340426	62,7659574	1,10714286	1,69230769	-42,8	-39,3	0,069746	9,2	-45,531915	-1,2228571
sch-MIR172c-3	149	16,7785235	30,2013423	16,1073826	36,9127517	32,885906	67,114094	1,22222222	1,04166667	-39,6	-38,8	0,0440202	12,35	-26,577181	-0,8081633
sch-MIR172d-1	130	24,6153846	27,6923077	13,8461538	33,8461538	38,4615385	61,5384615	1,22222222	1,77777778	-57,3	-50,3	0,0176622	11,68	-44,076923	-1,146
sch-MIR172d-2	99	17,1717172	35,3535354	15,1515152	32,3232323	32,3232323	67,6767677	0,91428571	1,13333333	-44,9	-44,9	0,0871318	8	-45,353535	-1,403125
sch-MIR172d-3	188	18,6170213	35,6382979	13,2978723	32,4468085	31,9148936	68,0851064	0,91044776	1,4	-56,4	-56,4	0,027277	28,89	-30	-0,94
sch-MIR172j	92	14,1304348	33,6956522	22,826087	29,3478261	36,9565217	63,0434783	0,87096774	0,61904762	-35,9	-35,9	0,0919534	4,45	-39,021739	-1,0558824
sch-MIR1847	83	21,686747	32,5301205	24,0963855	21,686747	45,7831325	54,2168675	0,66666667	0,9	-36,2	-35,6	0,232108	5,77	-43,614458	-0,9526316
sch-MIR1866	87	18,3908046	35,6321839	16,091954	29,8850575	34,4827586	65,5172414	0,83870968	1,14285714	-38,4	-38,4	0,110701	5,06	-44,137931	-1,28
sch-MIR1886f-1	131	18,3206107	31,2977099	16,7938931	33,5877863	35,1145038	64,8854962	1,07317073	1,09090909	-47,6	-46,4	0,0713639	8,81	-36,335878	-1,0347826
sch-MIR1886f-2	108	16,6666667	33,3333333	20,3703704	29,6296296	37,037037	62,962963	0,88888889	0,81818182	-47,3	-47,3	0,173657	5,31	-43,796296	-1,1825
sch-MIR1886f-3	114	18,4210526	29,8245614	19,2982456	32,4561404	37,7192982	62,2807018	1,08823529	0,95454545	-53,2	-53,2	0,151332	7,15	-46,666667	-1,2372093
sch-MIR1886f-4	97	17,5257732	30,9278351	15,4639175	36,0824742	32,9896907	67,0103093	1,16666667	1,13333333	-38,7	-38,7	0,0501627	13,4	-39,896907	-1,209375
sch-MIR1886f-5	114	19,2982456	28,0701754	17,5438596	35,0877193	36,8421053	63,1578947	1,25	1,1	-48,4	-48,4	0,132662	8,15	-42,45614	-1,152381
sch-MIR1886i-1	116	16,3793103	29,3103448	19,8275862	34,4827586	36,2068966	63,7931034	1,17647059	0,82608696	-39,9	-32,7	0,0250331	18,72	-34,396552	-0,95
sch-MIR1886i-2	296	16,2162162	34,4594595	14,8648649	34,4594595	31,0810811	68,9189189	1	1,09090909	-67,3	-61,5	0,00040128	42,5	-22,736486	-0,7315217
sch-MIR1888a	289	23,183391	30,7958478	13,4948097	32,5259516	36,6782007	63,3217993	1,05617978	1,71794872	-79,3	-68,3	0,00038786	48,38	-27,439446	-0,7481132
sch-MIR1888b-1	317	20,1892744	33,4384858	13,2492114	33,1230284	33,4384858	66,5615142	0,99056604	1,52380952	-78	-71,2	1,62E-05	60,64	-24,605678	-0,7358491
sch-MIR1888b-2	288	18,75	30,5555556	14,5833333	36,1111111	33,3333333	66,6666667	1,18181818	1,28571429	-74,8	-65,6	3,25E-05	67,27	-25,972222	-0,7791667
sch-MIR1916-1	112	10,7142857	32,1428571	19,6428571	37,5	30,3571429	69,6428571	1,16666667	0,54545455	-30,9	-29,6	0,0293422	8,23	-27,589286	-0,9088235
sch-MIR1916-2	225	16	31,1111111	14,6666667	38,2222222	30,6666667	69,3333333	1,22857143	1,09090909	-48,7	-46,2	0,00037998	38,34	-21,644444	-0,7057971
sch-MIR1917-1	216	16,2037037	36,5740741	16,2037037	31,0185185	32,4074074	67,5925926	0,84810127	1	-57,3	-54,9	0,00051798	42,13	-26,527778	-0,8185714
sch-MIR1917-2	223	16,5919283	37,2197309	13,9013453	32,2869955	30,4932735	69,5067265	0,86746988	1,19354839	-76,3	-76	0,00848511	16,1	-34,215247	-1,1220588
sch-MIR1918-1	127	17,3228346	29,1338583	21,2598425	32,2834646	38,5826772	61,4173228	1,10810811	0,81481481	-38,2	-37	0,0743782	16,03	-30,07874	-0,7795918
sch-MIR1918-2	186	18,2795699	33,3333333	16,1290323	32,2580645	34,4086022	65,5913978	0,96774194	1,13333333	-70,7	-70	0,0136242	12,33	-38,010753	-1,1046875
sch-MIR1919-1	160	21,875	26,875	20	31,25	41,875	58,125	1,1627907	1,09375	-69,3	-65,7	0,0393909	17,78	-43,3125	-1,0343284
sch-MIR1919-2	163	21,4723926	25,7668712	20,8588957	31,9018405	42,3312883	57,6687117	1,23809524	1,02941176	-71,7	-65,3	0,0175014	19,4	-43,98773	-1,0391304
sch-MIR1919-3	187	22,459893	23,5294118	21,3903743	32,6203209	43,8502674	56,1497326	1,38636364	1,05	-91,5	-91,5	0,0642815	10,8	-48,930481	-1,1158537
sch-MIR1919-4	122	23,7704918	26,2295082	18,0327869	31,9672131	41,8032787	58,1967213	1,21875	1,31818182	-59,7	-59,7	0,124949	8,4	-48,934426	-1,1705882
sch-MIR2077	165	16,3636364	32,7272727	19,3939394	31,5151515	35,7575758	64,2424242	0,96296296	0,84375	-72,4	-72,4	0,0369005	10,88	-43,878788	-1,2271186
sch-MIR2099	213	13,1455399	32,8638498	18,3098592	35,6807512	31,4553991	68,5446009	1,08571429	0,71794872	-47,7	-42,4	0,00012202	30,1	-22,394366	-0,7119403
sch-MIR2111d-1	106	19,8113208	26,4150943	16,0377358	37,7358491	35,8490566	64,1509434	1,42857143	1,23529412	-44,7	-44,7	0,043837	7,51	-42,169811	-1,1763158
sch-MIR2111d-2	109	19,266055	27,5229358	16,5137615	36,6972477	35,7798165	64,2201835	1,33333333	1,16666667	-48,7	-48,7	0,02898	6,52	-44,678899	-1,2487179
sch-MIR2111d-3	109	19,266055	27,5229358	15,5963303	37,6146789	34,8623853	65,1376147	1,36666667	1,23529412	-50,5	-50,5	0,0352007	6,28	-46,330275	-1,3289474
sch-MIR2118a	173	13,2947977	33,5260116	17,9190751	35,2601156	31,2138728	68,7861272	1,05172414	0,74193548	-70,7	-66,34	0,011207	14,48	-40,867052	-1,3092593
sch-MIR2118b	109	26,6055046	16,5137615	30,2752294	26,6055046	56,8807339	43,1192661	1,61111111	0,87878788	-54	-52,6	0,122194	8,85	-49,541284	-0,8709677
sch-MIR2119	225	15,1111111	33,3333333	16	35,5555556	31,1111111	68,8888889	1,06666667	0,94444444	-61,8	-37,8	0,00157453	59,78	-27,466667	-0,8828571
sch-MIR2122	255	21,1764706	39,6078431	9,80392157	29,4117647	30,9803922	69,0196078	0,74257426	2,16	-64,6	-60,5	0,00653869	24,18	-25,333333	-0,8177215
sch-MIR2275c	222	14,8648649	32,4324324	15,3153153	37,3873874	30,1801802	69,8198198	1,15277778	0,97058824	-74,5	-73,8	0,0103145	17,47	-33,558559	-1,1119403
sch-MIR2595	295	21,0169492	34,2372881	12,2033898	32,5423729	33,220339	66,779661	0,95049505	1,72222222	-78,5	-69,7	0,00037944	52,87	-26,610169	-0,8010204
sch-MIR2604	270	17,037037	37,4074074	14,8148148	30,7407407	31,8518519	68,1481481	0,82178218	1,15	-68,4	-52,4	0,00022807	53,1	-25,333333	-0,7953488
sch-MIR2605	174	24,7126437	32,183908	14,9425287	28,1609195	39,6551724	60,3448276	0,875	1,65384615	-54,3	-52,4	0,026363	19,98	-31,206897	-0,7869565
sch-MIR2642	122	18,852459	29,5081967	17,2131148	34,4262295	36,0655738	63,9344262	1,16666667	1,0952381	-49	-49	0,195495	2,91	-40,163934	-1,1136364
sch-MIR2645	223	19,2825112	32,735426	14,3497758	33,632287	33,632287	66,367713	1,02739726	1,34375	-58,3	-52,6	0,00033403	39,65	-26,143498	-0,7773333
sch-MIR2655o	203	18,226601	31,0344828	14,7783251	35,9605911	33,0049261	66,9950739	1,15873016	1,23333333	-74,6	-73,3	0,0164191	13,14	-36,748768	-1,1134328
sch-MIR2667b	270	21,1111111	25,5555556	14,0740741	39,2592593	35,1851852	64,8148148	1,53623188	1,5	-69	-60,5	0,00020751	64,33	-25,555556	-0,7263158
sch-MIR2670g	115	28,6956522	21,7391304	21,7391304	27,826087	50,4347826	49,5652174	1,28	1,32	-41,6	-32,17	0,0159288	26,2	-36,173913	-0,7172414
sch-MIR2673b-1	285	12,2807018	23,8596491	25,6140351	38,245614	37,8947368	62,1052632	1,60294118	0,47945205	-99,6	-94,75	0,00258666	20,26	-34,947368	-0,9222222
sch-MIR2673b-2	207	18,8405797	25,1207729	21,7391304	34,2995169	40,5797101	59,4202899	1,36538462	0,86666667	-60,8	-47,3	0,00057637	55,26	-29,371981	-0,7238095
sch-MIR2675	74	31,0810811	27,027027	18,9189189	22,972973	50	50	0,85	1,64285714	-27,4	-22,5	0,0387604	14,63	-37,027027	-0,7405405
sch-MIR2678	238	27,3109244	23,1092437	22,6890756	26,8907563	50	50	1,16363636	1,2037037	-89,7	-76,9	0,00568028	45,33	-37,689076	-0,7537815
sch-MIR2863a	166	16,8674699	36,746988	13,8554217	32,5301205	30,7228916	69,2771084	0,8852459	1,2173913	-99,5	-99,4	0,0357384	5,96	-59,939759	-1,9509804
sch-MIR2867	210	16,6666667	36,6666667	19,047619	27,6190476	35,7142857	64,2857143	0,75324675	0,875	-55,7	-54,8	0,00557246	14,77	-26,52381	-0,7426667
sch-MIR2868-1	283	16,9611307	32,8621908	14,8409894	35,335689	31,8021201	68,1978799	1,07526882	1,14285714	-70,3	-63,39	0,00057358	44,61	-24,840989	-0,7811111
sch-MIR2868-2	161	19,2546584	30,4347826	13,0434783	37,2670807	32,2981366	67,7018634	1,2244898	1,47619048	-36,6	-35,1	0,0176631	23,63	-22,732919	-0,7038462

sch-MIR2928	235	14,4680851	28,9361702	16,1702128	40,4255319	30,6382979	69,3617021	1,39705882	0,89473684	-59,4	-42,71	0,00033231	49,13	-25,276596	-0,825
sch-MIR2931	112	14,2857143	28,5714286	22,3214286	34,8214286	36,6071429	63,3928571	1,21875	0,64	-38,9	-38,9	0,35949	2,39	-34,732143	-0,9487805
sch-MIR319	213	23,0046948	31,4553991	19,7183099	25,8215962	42,7230047	57,2769953	0,82089552	1,16666667	-85,6	-84,8	0,0115224	14,81	-40,187793	-0,9406593
sch-MIR319a	187	22,459893	29,9465241	21,3903743	26,2032086	43,8502674	56,1497326	0,875	1,05	-80,6	-75,9	0,0407605	23,38	-43,101604	-0,9829268
sch-MIR319b-1	173	21,3872832	27,7456647	18,4971098	32,3699422	39,8843931	60,1156069	1,16666667	1,15625	-85,9	-85,2	0,0165425	10,02	-49,653179	-1,2449275
sch-MIR319b-2	180	25	28,8888889	21,1111111	25	46,1111111	53,8888889	0,86538462	1,18421053	-88,5	-87,7	0,0415991	9,06	-49,166667	-1,0662651
sch-MIR319b-3	171	25,7309942	25,7309942	21,6374269	26,9005848	47,3684211	52,6315789	1,04545455	1,18918919	-77,3	-67,6	0,0234881	14,34	-45,204678	-0,954321
sch-MIR319b-4	213	21,1267606	31,4553991	19,2488263	28,1690141	40,3755869	59,6244131	0,89552239	1,09756098	-89,9	-89,1	0,0139626	12,12	-42,206573	-1,0453488
sch-MIR319c	176	25,5681818	23,8636364	21,5909091	28,9772727	47,1590909	52,8409091	1,21428571	1,18421053	-76,5	-65,1	0,0169927	17,33	-43,465909	-0,9216867
sch-MIR319d	202	24,2574257	23,7623762	21,7821782	30,1980198	46,039604	53,960396	1,27083333	1,11363636	-96,5	-95,7	0,0354537	8,59	-47,772277	-1,0376344
sch-MIR319g	149	22,147651	28,1879195	20,1342282	29,5302013	42,2818792	57,7181208	1,04761905	1,1	-59,2	-56,9	0,013989	10,9	-39,731544	-0,9396825
sch-MIR319h	71	25,3521127	21,1267606	28,1690141	25,3521127	53,5211268	46,4788732	1,2	0,9	-27,7	-27,3	0,0693612	6,15	-39,014085	-0,7289474
sch-MIR319j	155	19,3548387	30,9677419	24,516129	25,1612903	43,8709677	56,1290323	0,8125	0,78947368	-82,5	-81,9	0,0670381	6,46	-53,225806	-1,2132353
sch-MIR3434	232	20,6896552	34,0517241	12,9310345	32,3275862	33,6206897	66,3793103	0,94936709	1,6	-57,3	-40,6	0,00100953	55,47	-24,698276	-0,7346154
sch-MIR3438	101	26,7326733	21,7821782	19,8019802	31,6831683	46,5346535	53,4653465	1,45454545	1,35	-41,1	-40,6	0,0828942	5,5	-40,693069	-0,8744681
sch-MIR3447	92	19,5652174	32,6086957	11,9565217	35,8695652	31,5217391	68,4782609	1,1	1,63636364	-24,6	-22	0,094301	33,59	-26,73913	-0,8482759
sch-MIR3448	104	23,0769231	34,6153846	13,4615385	28,8461538	36,5384615	63,4615385	0,83333333	1,71428571	-29	-29	0,201646	6,65	-27,884615	-0,7631579
sch-MIR3627	125	22,4	28	20	29,6	42,4	57,6	1,05714286	1,12	-51	-51	0,181166	4,18	-40,8	-0,9622642
sch-MIR3628	159	19,4968553	38,3647799	11,9496855	30,1886792	31,4465409	68,5534591	0,78688525	1,63157895	-35,9	-29,5	0,00591844	19,46	-22,578616	-0,718
sch-MIR3635	246	15,8536585	31,300813	16,6666667	36,1788618	32,5203252	67,4796748	1,15584416	0,95121951	-57,1	-46,2	0,0003756	64,36	-23,211382	-0,71375
sch-MIR3700	209	15,7894737	36,3636364	21,0526316	26,7942584	36,8421053	63,1578947	0,73684211	0,75	-61,4	-60,2	0,00286449	15,37	-29,37799	-0,7974026
sch-MIR3706-1	80	22,5	30	8,75	38,75	31,25	68,75	1,29166667	2,57142857	-21,1	-21,1	0,0232569	14,07	-26,375	-0,844
sch-MIR3706-2	68	19,1176471	26,4705882	25	29,4117647	44,1176471	55,8823529	1,11111111	0,76470588	-34,4	-34,4	0,579292	2,06	-50,588235	-1,1466667
sch-MIR3706-3	222	21,6216216	31,5315315	14,4144144	32,4324324	36,036036	63,963964	1,02857143	1,5	-85,4	-85,4	0,0109862	22,57	-38,468468	-1,0675
sch-MIR3706-4	70	27,1428571	30	17,1428571	25,7142857	44,2857143	55,7142857	0,85714286	1,58333333	-35,7	-35,7	0,543871	0,99	-51	-1,1516129
sch-MIR3707	152	19,7368421	25,6578947	19,0789474	35,5263158	38,8157895	61,1842105	1,38461538	1,03448276	-70,4	-67,9	0,0184635	12,32	-46,315789	-1,1932203
sch-MIR390-1	119	20,1680672	23,5294118	20,1680672	36,1344538	40,3361345	59,6638655	1,53571429	1	-54,1	-54,1	0,361379	2,35	-45,462185	-1,1270833
sch-MIR390-2	106	19,8113208	31,1320755	22,6415094	26,4150943	42,4528302	57,5471698	0,84848485	0,875	-40,8	-40,2	0,101168	6,63	-38,490566	-0,9066667
sch-MIR390-3	182	15,3846154	40,1098901	16,4835165	28,021978	31,8681319	68,1318681	0,69863014	0,93333333	-48,6	-46,74	0,00861087	12,53	-26,703297	-0,837931
sch-MIR390a	106	22,6415094	26,4150943	19,8113208	31,1320755	42,4528302	57,5471698	1,17857143	1,14285714	-48,8	-46,1	0,101334	6,7	-46,037736	-1,0844444
sch-MIR391	96	23,9583333	34,375	16,6666667	25	40,625	59,375	0,72727273	1,4375	-46,7	-46,7	0,336484	3,38	-48,645833	-1,1974359
sch-MIR391i	115	28,6956522	22,6086957	21,7391304	26,9565217	50,4347826	49,5652174	1,19230769	1,32	-44,5	-41,1	0,072184	9,98	-38,695652	-0,7672414
sch-MIR393	170	19,4117647	31,1764706	15,2941176	34,1176471	34,7058824	65,2941176	1,09433962	1,26923077	-44	-43,1	0,00148024	21,04	-25,882353	-0,7457627
sch-MIR393b-1	86	19,7674419	26,744186	22,0930233	31,3953488	41,8604651	58,1395349	1,17391304	0,89473684	-43,8	-43,8	0,225096	2,63	-50,930233	-1,2166667
sch-MIR393b-2	173	18,4971098	31,7919075	17,9190751	31,7919075	36,416185	63,583815	1	1,03225806	-63,2	-61,6	0,0181433	18,63	-36,531792	-1,0031746
sch-MIR393b-3	182	19,2307692	32,4175824	15,3846154	32,967033	34,6153846	65,3846154	1,01694915	1,25	-97,4	-96,6	0,125511	6,01	-53,516484	-1,5460317
sch-MIR394	61	29,5081967	21,3114754	27,8688525	21,3114754	57,3770492	42,6229508	1	1,05882353	-31,2	-30,9	0,175055	3,56	-51,147541	-0,8914286
sch-MIR394b-1	171	18,7134503	30,4093567	17,5438596	33,3333333	36,2573099	63,7426901	1,09615385	1,06666667	-83,7	-83,7	0,0803388	7,51	-48,947368	-1,35
sch-MIR394b-2	86	18,6046512	32,5581395	12,7906977	36,0465116	31,3953488	68,6046512	1,10714286	1,45454545	-41,3	-40,6	0,0249794	11,37	-48,023256	-1,5296296
sch-MIR394c	197	25,8883249	26,9035533	16,2436548	30,964467	42,1319797	57,8680203	1,1509434	1,59375	-75,9	-71,4	0,00717553	19,77	-38,527919	-0,9144578
sch-MIR395	200	19,5	33	16	31,5	35,5	64,5	0,95454545	1,21875	-52	-46,3	0,00852396	26,57	-26	-0,7323944
sch-MIR3951a	156	17,9487179	32,6923077	14,7435897	34,6153846	32,6923077	67,3076923	1,05882353	1,2173913	-96	-96	0,305187	2,75	-61,538462	-1,8823529
sch-MIR395a-1	165	21,8181818	30,3030303	17,5757576	30,3030303	39,3939394	60,6060606	1	1,24137931	-66,4	-66,4	0,117171	9,68	-40,242424	-1,0215385
sch-MIR395a-2	169	23,6686391	28,4023669	17,1597633	30,7692308	40,8284024	59,1715976	1,08333333	1,37931034	-69,5	-69,5	0,0731107	10,28	-41,12426	-1,0072464
sch-MIR395a-3	263	23,5741445	24,3346008	18,2509506	33,8403042	41,8250951	58,1749049	1,390625	1,29166667	-95,5	-95,4	0,00565355	18,31	-36,311787	-0,8681818
sch-MIR395b-1	121	23,9669421	21,4876033	19,0082645	35,5371901	42,9752066	57,0247934	1,65384615	1,26086957	-44,9	-41,2	0,0543083	11,24	-37,107438	-0,8634615
sch-MIR395b-2	128	21,875	21,875	22,65625	33,59375	44,53125	55,46875	1,53571429	0,96551724	-45,4	-45,4	0,104474	12,83	-35,46875	-0,7964912
sch-MIR395b-3	107	25,2336449	16,8224299	23,364486	34,5794393	48,5981308	51,4018692	2,05555556	1,08	-54,2	-54,2	0,463403	2,39	-50,654206	-1,0423077
sch-MIR395c-1	208	21,1538462	30,2884615	14,9038462	33,6538462	36,0576923	63,9423077	1,11111111	1,41935484	-57,2	-49,3	0,00016846	38,32	-27,5	-0,7626667
sch-MIR395c-2	243	24,2798354	26,7489712	16,0493827	32,9218107	40,3292181	59,6707819	1,23076923	1,51282051	-82,8	-76,6	0,00121129	46,06	-34,074074	-0,844898
sch-MIR395c-3	199	24,6231156	28,6432161	15,0753769	31,6582915	39,6984925	60,3015075	1,10526316	1,63333333	-63,5	-53,1	0,00146166	33,67	-31,909548	-0,8037975
sch-MIR395j-1	92	27,173913	14,1304348	23,9130435	34,7826087	51,0869565	48,9130435	2,46153846	1,13636364	-45,1	-45,1	0,335661	3,1	-49,021739	-0,9595745
sch-MIR395j-2	122	19,6721311	25,4098361	18,852459	36,0655738	38,5245902	61,4754098	1,41935484	1,04347826	-51,6	-51,6	0,354634	4,55	-42,295082	-1,0978723
sch-MIR396a-1	144	15,9722222	34,7222222	20,1388889	29,1666667	36,1111111	63,8888889	0,84	0,79310345	-51,6	-50,2	0,0388467	9,35	-35,833333	-0,9923077
sch-MIR396a-2	99	17,1717172	28,2828283	19,1919192	35,3535354	36,3636364	63,6363636	1,25	0,89473684	-25,5	-20,8	0,0179685	16,37	-25,757576	-0,7083333
sch-MIR396b-1	134	18,6567164	31,3432836	14,1791045	35,8208955	32,8358209	67,1641791	1,14285714	1,31578947	-55,8	-53,48	0,035831	15,33	-41,641791	-1,2681818
sch-MIR396b-2	161	18,6335404	33,5403727	12,4223602	35,4037267	31,0559006	68,9440994	1,05555556	1,5	-52,7	-49,98	0,0105893	21,23	-32,732919	-1,054
sch-MIR396c	118	27,1186441	24,5762712	11,0169492	37,2881356	38,1355932	61,8644068	1,51724138	2,46153846	-33,6	-33,6	0,0325119	11,11	-28,474576	-0,7466667
sch-MIR396e	92	18,4782609	30,4347826	18,4782609	32,6086957	36,9565217	63,0434783	1,07142857	1	-29	-27,7	0,0826923	6,22	-31,521739	-0,8529412
sch-MIR396f	134	19,4029851	29,8507463	14,9253731	35,8208955	34,3283582	65,6716418	1,2	1,3	-49,7	-46	0,00504672	19,12	-37,089552	-1,0804348
sch-MIR396h	96	20,8333333	29,1666667	22,9166667	27,0833333	43,75	56,25	0,92857143	0,90909091	-40,4	-38,7	0,0643073	12,44	-42,083333	-0,9619048
sch-MIR397	179	21,7877095	28,4916201	20,1117318	29,6089385	41,8994413	58,1005587	1,03921569	1,08333333	-55,4	-55,4	0,020543	12,07	-30,949721	-0,7386667
sch-MIR397b-1	118	16,1016949	26,2711864	21,1864407	36,440678	37,2881356	62,7118644	1,38709677	0,76	-45,7	-45,5	0,076355	5,37	-38,728814	-1,0386364
sch-MIR397b-2	127	19,6850394	37,007874	17,3228346	25,984252	37,007874	62,992126	0,70212766	1,13636364	-49,6	-49,6	0,0681703	8,3	-39,055118	-1,0553191
sch-MIR397b-3	126	19,047619	30,1587302	20,6349206	30,1587302	39,6825397	60,3174603	1	0,92307692	-45,3	-45,3	0,272877	3,49	-35,952381	-0,906
sch-MIR398-1	106	19,8113208	21,6981132	17,9245283	40,5660377	37,7358491	62,2641509	1,86956522	1,10526316	-50,6	-50,6	0,361861	4,65	-47,735849	-1,265

sch-MIR398-2	68	23,5294118	35,2941176	13,2352941	27,9411765	36,7647059	63,2352941	0,79166667	1,77777778	-20,6	-20,6	0,083811	4,85	-30,294118	-0,824
sch-MIR398a-1	90	20	25,5555556	14,4444444	40	34,4444444	65,5555556	1,56521739	1,38461538	-33,8	-27,6	0,0162507	17,38	-37,555556	-1,0903226
sch-MIR398a-2	100	20	27	16	37	36	64	1,37037037	1,25	-37,9	-36,7	0,0661613	10,29	-37,9	-1,0527778
sch-MIR398a-3	166	18,0722892	32,5301205	16,8674699	32,5301205	34,939759	65,060241	1	1,07142857	-56,8	-51,4	0,0101275	24,73	-34,216867	-0,9793103
sch-MIR398b-1	124	23,3870968	20,1612903	22,5806452	33,8709677	45,9677419	54,0322581	1,68	1,03571429	-63,9	-63,8	0,088157	7,49	-51,532258	-1,1210526
sch-MIR398b-2	126	23,8095238	20,6349206	20,6349206	34,9206349	44,4444444	55,5555556	1,69230769	1,15384615	-65,3	-65,3	0,0914687	5,14	-51,825397	-1,1660714
sch-MIR399a	188	17,0212766	34,5744681	17,0212766	31,3829787	34,0425532	65,9574468	0,90769231	1	-55,5	-50,3	0,00331823	27,61	-29,521277	-0,8671875
sch-MIR399b-1	258	22,8682171	30,2325581	16,6666667	30,2325581	39,5348837	60,4651163	1	1,37209302	-81,1	-71,5	0,00040649	46,1	-31,434109	-0,795098
sch-MIR399b-2	223	22,4215247	30,941704	16,1434978	30,4932735	38,5650224	61,4349776	0,98550725	1,38888889	-72	-66,5	0,00110666	30,24	-32,286996	-0,8372093
sch-MIR399b-3	103	21,3592233	28,1553398	19,4174757	31,0679612	40,776699	59,223301	1,10344828	1,1	-47,6	-47,6	0,203168	6,7	-46,213592	-1,1333333
sch-MIR399b-4	103	24,2718447	27,184466	18,4466019	30,0970874	42,7184466	57,2815534	1,10714286	1,31578947	-52	-52	0,228858	4,89	-50,485437	-1,1818182
sch-MIR399b-5	187	20,3208556	32,0855615	18,7165775	28,8770053	39,0374332	60,9625668	0,9	1,08571429	-63,6	-62,9	0,0179119	13	-34,010695	-0,8712329
sch-MIR399f-1	120	18,3333333	26,6666667	16,6666667	38,3333333	35	65	1,4375	1,1	-47,8	-46,1	0,0771278	14,72	-39,833333	-1,1380952
sch-MIR399f-2	140	14,2857143	34,2857143	17,8571429	33,5714286	32,1428571	67,8571429	0,97916667	0,8	-63,2	-61,7	0,0211659	10,46	-45,142857	-1,4044444
sch-MIR399f-3	131	14,5038168	29,7709924	19,0839695	36,6412214	33,5877863	66,4122137	1,23076923	0,76	-50,8	-48,9	0,046938	9,66	-38,778626	-1,1545455
sch-MIR399f-4	119	17,6470588	27,7310924	19,3277311	35,2941176	36,9747899	63,0252101	1,27272727	0,91304348	-47,5	-45,1	0,0311447	9,9	-39,915966	-1,0795455
sch-MIR399i-1	96	23,9583333	26,0416667	20,8333333	29,1666667	44,7916667	55,2083333	1,12	1,15	-40,3	-36,2	0,184114	5,44	-41,979167	-0,9372093
sch-MIR399i-2	107	22,4299065	26,1682243	14,953271	36,4485981	37,3831776	62,6168224	1,39285714	1,5	-57,8	-55,5	0,188535	3	-54,018692	-1,445
sch-MIR399i-3	107	21,4953271	28,0373832	16,8224299	33,6448598	38,317757	61,682243	1,2	1,27777778	-55,3	-55,3	0,18202	3,38	-51,682243	-1,3487805
sch-MIR399j	71	19,7183099	30,9859155	21,1267606	28,1690141	40,8450704	59,1549296	0,90909091	0,93333333	-29,2	-26,5	0,125645	6,1	-41,126761	-1,0068966
sch-MIR400	194	16,4948454	36,0824742	15,9793814	31,443299	32,4742268	67,5257732	0,87142857	1,03225806	-48,3	-45,9	0,00318545	17,27	-24,896907	-0,7666667
sch-MIR403	127	18,8976378	29,1338583	18,8976378	33,0708661	37,7952756	62,2047244	1,13513514	1	-44	-44	0,0241739	12,34	-34,645669	-0,9166667
sch-MIR403b	127	18,8976378	33,0708661	18,8976378	29,1338583	37,7952756	62,2047244	0,88095238	1	-41,7	-40,4	0,00991442	17	-32,834646	-0,86875
sch-MIR408-1	71	25,3521127	18,3098592	28,1690141	28,1690141	53,5211268	46,4788732	1,53846154	0,9	-32	-32	0,704395	1,32	-45,070423	-0,8421053
sch-MIR408-2	128	25,78125	32,03125	22,65625	19,53125	48,4375	51,5625	0,6097561	1,13793103	-46,6	-41,4	0,0291793	9,07	-36,40625	-0,7516129
sch-MIR408a	72	22,2222222	25	29,1666667	23,6111111	51,3888889	48,6111111	0,94444444	0,76190476	-35,5	-34	0,759969	0,83	-49,305556	-0,9594595
sch-MIR415	271	23,2472325	35,7933579	12,9151292	28,0442804	36,1623616	63,8376384	0,78350515	1,8	-70,8	-47,7	0,00704457	63,25	-26,125461	-0,722449
sch-MIR4223	165	15,7575758	34,5454545	15,7575758	33,9393939	31,5151515	68,4848485	0,98245614	1	-36,4	-34,6	0,00710878	37,45	-22,060606	-0,7
sch-MIR4235	147	19,047619	33,3333333	13,6054422	34,0136054	32,6530612	67,3469388	1,02040816	1,4	-49,5	-46,8	0,0265279	22,16	-33,673469	-1,03125
sch-MIR4243-1	272	20,2205882	37,5	10,6617647	31,6176471	30,8823529	69,1176471	0,84313725	1,89655172	-69,9	-68	0,00016663	31,79	-25,698529	-0,8321429
sch-MIR4243-2	198	22,7272727	27,2727273	17,1717172	32,8282828	39,8989899	60,1010101	1,2037037	1,32352941	-57,2	-56,3	0,00674562	27,74	-28,888889	-0,7240506
sch-MIR4248c	161	19,2546584	30,4347826	19,8757764	30,4347826	39,1304348	60,8695652	1	0,96875	-53,9	-52,8	0,00443014	20,54	-33,478261	-0,8555556
sch-MIR426	142	16,1971831	29,5774648	19,7183099	34,5070423	35,915493	64,084507	1,16666667	0,82142857	-56,8	-54,2	0,107671	5,53	-40	-1,1137255
sch-MIR444a	162	16,6666667	32,0987654	16,0493827	35,1851852	32,7160494	67,2839506	1,09615385	1,03846154	-66,2	-66	0,0479193	15,98	-40,864198	-1,2490566
sch-MIR444b-1	146	20,5479452	33,5616438	11,6438356	34,2465753	32,1917808	67,8082192	1,02040816	1,76470588	-43,3	-42,4	0,0123587	16,92	-29,657534	-0,9212766
sch-MIR444b-2	221	22,1719457	29,8642534	9,95475113	38,0090498	32,1266968	67,8733032	1,27272727	2,22727273	-79	-76,9	0,00010601	37,7	-35,746606	-1,1126761
sch-MIR444b-3	97	22,6804124	32,9896907	9,27835052	35,0515464	31,9587629	68,0412371	1,0625	2,44444444	-32,7	-32,7	0,114563	3,79	-33,71134	-1,0548387
sch-MIR477-1	134	21,641791	28,358209	21,641791	28,358209	43,2835821	56,7164179	1	1	-51,5	-48,6	0,0209643	14,73	-38,432836	-0,887931
sch-MIR477-2	116	25	27,5862069	20,6896552	26,7241379	45,6896552	54,3103448	0,96875	1,20833333	-58,4	-57,9	0,114479	7,54	-50,344828	-1,1018868
sch-MIR477a	68	25	19,1176471	27,9411765	27,9411765	52,9411765	47,0588235	1,46153846	0,89473684	-35,4	-34	0,219683	2,56	-52,058824	-0,9833333
sch-MIR477b-1	90	21,1111111	21,1111111	20	37,7777778	41,1111111	58,8888889	1,78947368	1,05555556	-37,2	-33,9	0,0605207	7,71	-41,333333	-1,0054054
sch-MIR477b-2	70	25,7142857	20	21,4285714	32,8571429	47,1428571	52,8571429	1,64285714	1,2	-31,4	-28,1	0,265145	5,59	-44,857143	-0,9515152
sch-MIR477b-3	105	22,8571429	21,9047619	20	35,2380952	42,8571429	57,1428571	1,60869565	1,14285714	-42,1	-37,9	0,0782346	8,87	-40,095238	-0,9355556
sch-MIR477g	322	18,0124224	24,2236025	17,0807453	40,6832298	35,0931677	64,9068323	1,67948718	1,05454545	-81	-78,87	0,00022139	36,93	-25,15528	-0,7168142
sch-MIR479-1	104	20,1923077	28,8461538	19,2307692	31,7307692	39,4230769	60,5769231	1,1	1,05	-46,2	-44,2	0,0945518	9,72	-44,423077	-1,1268293
sch-MIR479-2	112	21,4285714	28,5714286	19,6428571	30,3571429	41,0714286	58,9285714	1,0625	1,09090909	-52,6	-51,4	0,154084	9,5	-46,964286	-1,1434783
sch-MIR479-3	92	17,3913043	34,7826087	18,4782609	29,3478261	35,8695652	64,1304348	0,84375	0,94117647	-28,2	-27,8	0,480796	1,93	-30,652174	-0,8545455
sch-MIR482a-1	95	14,7368421	18,9473684	21,0526316	45,2631579	35,7894737	64,2105263	2,38888889	0,7	-34,7	-34,7	0,107497	4,99	-36,526316	-1,0205882
sch-MIR482a-2	153	19,6078431	20,9150327	16,9934641	42,4836601	36,6013072	63,3986928	2,03125	1,15384615	-63	-63	0,144761	4,39	-41,176471	-1,125
sch-MIR482b-1	121	17,3553719	29,7520661	18,1818182	34,7107438	35,5371901	64,4628099	1,16666667	0,95454545	-50,1	-49,7	0,125402	5,38	-41,404959	-1,1651163
sch-MIR482b-2	141	19,858156	28,3687943	17,7304965	34,0425532	37,5886525	62,4113475	1,2	1,12	-61,5	-56,6	0,0147759	18,34	-43,617021	-1,1603774
sch-MIR482b-3	221	25,3393665	21,2669683	22,6244344	30,7692308	47,9638009	52,0361991	1,44680851	1,12	-89,8	-77,1	0,00019598	52,95	-40,633484	-0,8471698
sch-MIR482b-4	160	26,25	28,75	21,25	23,75	47,5	52,5	0,82608696	1,23529412	-56,4	-47,4	0,00461101	20,82	-35,25	-0,7421053
sch-MIR482d-1	238	21,4285714	24,789916	12,605042	41,1764706	34,0336134	65,9663866	1,66101695	1,7	-59,3	-51	0,00063593	49,76	-24,915966	-0,7320988
sch-MIR482d-2	158	20,8860759	27,2151899	18,9873418	32,9113924	39,8734177	60,1265823	1,20930233	1,1	-73,8	-73,3	0,0166407	9,34	-46,708861	-1,1714286
sch-MIR482d-3	115	22,6086957	27,826087	12,173913	37,3913043	34,7826087	65,2173913	1,34375	1,85714286	-46,5	-44,3	0,0529635	15,77	-40,434783	-1,1625
sch-MIR482e	213	21,1267606	28,1690141	15,4929577	35,2112676	36,6197183	63,3802817	1,25	1,36363636	-82,4	-82,3	0,0109571	15,31	-38,685446	-1,0564103
sch-MIR482h	247	16,194332	35,6275304	14,1700405	34,0080972	30,3643725	69,6356275	0,95454545	1,14285714	-73,2	-65,6	0,00080536	30,85	-29,635628	-0,976
sch-MIR4994	152	22,3684211	25	22,3684211	30,2631579	44,7368421	55,2631579	1,21052632	1	-71,1	-68,7	0,0177172	11,79	-46,776316	-1,0455882
sch-MIR5012	147	19,047619	28,5714286	17,6870748	34,6938776	36,7346939	63,2653061	1,21428571	1,07692308	-59,3	-54,48	0,00818976	23,17	-40,340136	-1,0981481
sch-MIR5014a-1	251	15,5378486	31,4741036	17,1314741	35,8565737	32,6693227	67,3306773	1,13924051	0,90697674	-58,4	-58	0,00051553	19,92	-23,266932	-0,7121951
sch-MIR5014a-2	274	19,7080292	35,7664234	11,3138686	33,2116788	31,0218978	68,9781022	0,92857143	1,74193548	-84	-63,8	0,00094554	58,64	-30,656934	-0,9882353
sch-MIR5014a-3	205	13,1707317	37,5609756	20	29,2682927	33,1707317	66,8292683	0,77922078	0,65853659	-52,6	-47,1	0,00620534	17,92	-25,658537	-0,7735294
sch-MIR5014a-4	304	18,0921053	36,1842105	12,1710526	33,5526316	30,2631579	69,7368421	0,92727273	1,48648649	-71	-49,4	0,00012053	65,69	-23,355263	-0,7717391
sch-MIR5014a-5	170	18,8235294	34,7058824	15,8823529	30,5882353	34,7058824	65,2941176	0,88135593	1,18518519	-77,3	-61,64	0,0400131	23,39	-45,470588	-1,3101695
sch-MIR5014a-6	145	15,1724138	35,862069	17,2413793	31,7241379	32,4137931	67,5862069	0,88461538	0,88	-51,1	-51,1	0,104061	4,68	-35,241379	-1,087234

sch-MIR5015	180	21,1111111	25,5555556	18,8888889	34,4444444	40	60	1,34782609	1,11764706	-50,4	-48,8	0,0197474	15,23	-28	-0,7
sch-MIR5020b	177	16,9491525	33,3333333	14,6892655	35,0282486	31,6384181	68,3615819	1,05084746	1,15384615	-95,6	-91,5	0,0208434	15,69	-54,011299	-1,7071429
sch-MIR5021-1	129	17,0542636	24,0310078	24,8062016	34,1085271	41,8604651	58,1395349	1,41935484	0,6875	-39,2	-33,3	0,0596834	21,62	-30,387597	-0,7259259
sch-MIR5021-2	248	20,5645161	35,0806452	16,9354839	27,4193548	37,5	62,5	0,7816092	1,21428571	-65,3	-61,34	0,00082264	42,57	-26,330645	-0,7021505
sch-MIR5021-3	128	25	35,15625	17,96875	21,875	42,96875	57,03125	0,62222222	1,39130435	-40,8	-39,1	0,0862032	5,21	-31,875	-0,7418182
sch-MIR5026-1	89	23,5955056	31,4606742	16,8539326	28,0898876	40,4494382	59,5505618	0,89285714	1,4	-31,9	-29	0,0635026	9,86	-35,842697	-0,8861111
sch-MIR5026-2	78	24,3589744	34,6153846	20,5128205	20,5128205	44,8717949	55,1282051	0,59259259	1,1875	-36,7	-31	0,0329293	7,23	-47,051282	-1,0485714
sch-MIR5026-3	70	22,8571429	30	25,7142857	21,4285714	48,5714286	51,4285714	0,71428571	0,88888889	-33,7	-33,7	0,501308	1,62	-48,142857	-0,9911765
sch-MIR5026-4	91	23,0769231	32,967033	23,0769231	20,8791209	46,1538462	53,8461538	0,63333333	1	-34,7	-34	0,188897	5,44	-38,131868	-0,8261905
sch-MIR5026-5	210	17,1428571	34,2857143	15,7142857	32,8571429	32,8571429	67,1428571	0,95833333	1,09090909	-88,3	-88,1	0,0257735	9,96	-42,047619	-1,2797101
sch-MIR5026-6	195	21,025641	27,1794872	9,23076923	42,5641026	30,2564103	69,7435897	1,56603774	2,27777778	-47,6	-45,8	0,00128107	30,07	-24,410256	-0,8067797
sch-MIR5026-7	185	15,6756757	36,7567568	19,4594595	28,1081081	35,1351351	64,8648649	0,76470588	0,80555556	-96,7	-96,67	0,1772	3,1	-52,254054	-1,4872308
sch-MIR5029	185	13,5135135	31,8918919	22,7027027	31,8918919	36,2162162	63,7837838	1	0,5952381	-64	-62,4	0,0715927	53,8	-34,594595	-0,9552239
sch-MIR5035	148	16,2162162	33,1081081	16,8918919	33,7837838	33,1081081	66,8918919	1,02040816	0,96	-74,9	-73,7	0,0418216	9,23	-50,608108	-1,5285714
sch-MIR5051-1	324	18,2098765	33,9506173	13,5802469	34,2592593	31,7901235	68,2098765	1,00909091	1,34090909	-82,5	-77,5	2,69E-05	42,1	-25,462963	-0,8009709
sch-MIR5051-2	286	17,4825175	36,3636364	12,9370629	33,2167832	30,4195804	69,5804196	0,91346154	1,35135135	-67,7	-62,8	8,70E-05	46,62	-23,671329	-0,7781609
sch-MIR5070-1	257	17,5097276	28,0155642	14,0077821	40,4669261	31,5175097	68,4824903	1,44444444	1,25	-58,3	-51,6	0,0002611	56,02	-22,684825	-0,7197531
sch-MIR5070-2	112	16,0714286	33,9285714	15,1785714	34,8214286	31,25	68,75	1,02631579	1,05882353	-30,3	-23,22	0,0593952	15,69	-27,053571	-0,8657143
sch-MIR5083	84	15,4761905	33,3333333	15,4761905	35,7142857	30,952381	69,047619	1,07142857	1	-31,1	-31	0,189007	4,02	-37,02381	-1,1961538
sch-MIR5142-1	318	21,0691824	27,0440252	9,74842767	42,1383648	30,8176101	69,1823899	1,55813953	2,16129032	-75,3	-22,3	0,00010759	129,89	-23,679245	-0,7683673
sch-MIR5142-2	108	21,2962963	30,5555556	11,1111111	37,037037	32,4074074	67,5925926	1,21212121	1,91666667	-31,9	-31,1	0,060254	12,97	-29,537037	-0,9114286
sch-MIR5163a	153	16,3398693	33,3333333	15,6862745	34,6405229	32,0261438	67,9738562	1,03921569	1,04166667	-67,3	-55,1	0,151088	14,58	-43,986928	-1,3734694
sch-MIR5163b	95	18,9473684	33,6842105	20	27,3684211	38,9473684	61,0526316	0,8125	0,94736842	-28,8	-24	0,131066	9,06	-30,315789	-0,7783784
sch-MIR5174d-1	267	17,9775281	37,4531835	13,8576779	30,7116105	31,835206	68,164794	0,82	1,2972973	-69	-48,6	0,00014018	71,95	-25,842697	-0,8117647
sch-MIR5174d-2	259	20,0772201	36,2934363	14,2857143	29,3436293	34,3629344	65,6370656	0,80851064	1,40540541	-82,2	-72,3	0,00162563	40,17	-31,737452	-0,9235955
sch-MIR5176	145	15,1724138	39,3103448	15,862069	29,6551724	31,0344828	68,9655172	0,75438596	0,95652174	-51,7	-51,7	0,098835	7,01	-35,655172	-1,1488889
sch-MIR5181b	212	17,9245283	33,490566	16,9811321	31,6037736	34,9056604	65,0943396	0,94366197	1,05555556	-66,1	-56,64	0,00110468	35,17	-31,179245	-0,8932432
sch-MIR5181c	248	21,7741935	30,6451613	16,9354839	30,6451613	38,7096774	61,2903226	1	1,28571429	-78,4	-59,3	0,00011147	72,8	-31,612903	-0,8166667
sch-MIR5185m	221	20,361991	34,841629	12,6696833	32,1266968	33,0316742	66,9683258	0,92207792	1,60714286	-58,3	-58	0,00038735	26,42	-26,38009	-0,7986301
sch-MIR5205a	142	14,7887324	33,0985915	16,1971831	35,915493	30,9859155	69,0140845	1,08510638	0,91304348	-47,4	-36,57	0,0250853	23,68	-33,380282	-1,0772727
sch-MIR5205b	73	16,4383562	31,5068493	19,1780822	32,8767123	35,6164384	64,3835616	1,04347826	0,85714286	-21,4	-21,1	0,0324222	7,96	-29,315068	-0,8230769
sch-MIR5205d	189	13,7566138	30,6878307	17,4603175	38,0952381	31,2169312	68,7830688	1,24137931	0,78787879	-41,9	-37,9	0,00133338	26,79	-22,169312	-0,7101695
sch-MIR5213	231	21,2121212	27,2727273	19,4805195	32,034632	40,6926407	59,3073593	1,17460317	1,08888889	-92,4	-89,5	0,0164108	18,86	-40	-0,9829787
sch-MIR5214	208	13,4615385	34,6153846	16,8269231	35,0961538	30,2884615	69,7115385	1,01388889	0,8	-73,2	-73	0,0143968	10,53	-35,192308	-1,1619048
sch-MIR5238	180	16,6666667	35	13,8888889	34,4444444	30,5555556	69,4444444	0,98412698	1,2	-46,1	-43,5	0,00599858	27,56	-25,611111	-0,8381818
sch-MIR5248	236	17,7966102	37,2881356	14,4067797	30,5084746	32,2033898	67,7966102	0,81818182	1,23529412	-61,6	-46,54	0,00058053	49,48	-26,101695	-0,8105263
sch-MIR5251	194	23,1958763	27,3195876	14,9484536	34,5360825	38,1443299	61,8556701	1,26415094	1,55172414	-58,1	-54,6	0,0269387	13,67	-29,948454	-0,7851351
sch-MIR5256-1	283	12,7208481	30,7420495	18,7279152	37,8091873	31,4487633	68,5512367	1,22988506	0,67924528	-66,1	-61,6	0,00114164	35,47	-23,35689	-0,7426966
sch-MIR5256-2	321	12,7725857	32,3987539	18,3800623	36,4485981	31,152648	68,847352	1,125	0,69491525	-75,5	-73,9	0,00158842	28,62	-23,520249	-0,755
sch-MIR5262	247	21,8623482	25,9109312	13,3603239	38,8663968	35,2226721	64,7773279	1,5	1,63636364	-60,9	-56,2	0,00088624	34,16	-24,65587	-0,7
sch-MIR5265	169	15,9763314	33,7278107	17,1597633	33,1360947	33,1360947	66,8639053	0,98245614	0,93103448	-97,8	-97,8	0,0671128	4,46	-57,869822	-1,7464286
sch-MIR529	245	18,3673469	36,3265306	13,877551	31,4285714	32,244898	67,755102	0,86516854	1,32352941	-68,7	-56,62	0,0003186	48,91	-28,040816	-0,8696203
sch-MIR530	88	22,7272727	27,2727273	18,1818182	31,8181818	40,9090909	59,0909091	1,16666667	1,25	-41	-40,1	0,0599492	5,96	-46,590909	-1,1388889
sch-MIR5300	265	19,6226415	29,0566038	16,6037736	34,7169811	36,2264151	63,7735849	1,19480519	1,18181818	-89,7	-89,1	0,00152504	19,48	-33,849057	-0,934375
sch-MIR5303-1	265	13,9622642	31,6981132	23,7735849	30,5660377	37,7358491	62,2641509	0,96428571	0,58730159	-70,5	-67,41	0,00280788	17,17	-26,603774	-0,705
sch-MIR5303-3	117	19,6581197	30,7692308	21,3675214	28,2051282	41,025641	58,974359	0,91666667	0,92	-41,6	-41,6	0,2282	3,99	-35,555556	-0,8666667
sch-MIR5303d	127	18,1102362	26,7716535	30,7086614	24,4094488	48,8188976	51,1811024	0,91176471	0,58974359	-48,9	-47,2	0,0780195	9,24	-38,503937	-0,7887097
sch-MIR5303f-1	113	29,2035398	24,7787611	15,9292035	30,0884956	45,1327434	54,8672566	1,21428571	1,83333333	-47,9	-47,9	0,153292	5,17	-42,389381	-0,9392157
sch-MIR5303h	126	18,2539683	25,3968254	28,5714286	27,7777778	46,8253968	53,1746032	1,09375	0,63888889	-50	-49,6	0,0675859	5,41	-39,68254	-0,8474576
sch-MIR5303i-1	116	20,6896552	28,4482759	19,8275862	31,0344828	40,5172414	59,4827586	1,09090909	1,04347826	-42,8	-42,7	0,00341967	17,71	-36,896552	-0,9106383
sch-MIR5339	312	17,6282051	36,2179487	17,6282051	28,525641	35,2564103	64,7435897	0,78761062	1	-83,5	-70,8	0,00083212	36,48	-26,762821	-0,7590909
sch-MIR535f	107	22,4299065	30,8411215	17,7570093	28,9719626	40,1869159	59,8130841	0,93939394	1,26315789	-67,6	-67,4	0,250673	2,03	-63,17757	-1,572093
sch-MIR5368	83	28,9156627	25,3012048	25,3012048	20,4819277	54,2168675	45,7831325	0,80952381	1,14285714	-33	-33	0,448662	1,92	-39,759036	-0,7333333
sch-MIR5370	187	19,7860963	37,4331551	13,368984	29,4117647	33,1550802	66,8449198	0,78571429	1,48	-61	-60,7	0,0115881	11,81	-32,620321	-0,983871
sch-MIR5376	162	22,8395062	31,4814815	18,5185185	27,1604938	41,3580247	58,6419753	0,8627451	1,23333333	-47	-39,47	0,00776109	23,42	-29,012346	-0,7014925
sch-MIR5379	286	19,2307692	36,013986	11,1888112	33,5664336	30,4195804	69,5804196	0,93203883	1,71875	-69,4	-65,4	0,00032108	43,06	-24,265734	-0,7977011
sch-MIR5498	202	16,8316832	35,6435644	13,3663366	34,1584158	30,1980198	69,8019802	0,95833333	1,25925926	-48,3	-42,9	0,00637879	32,15	-23,910891	-0,7918033
sch-MIR5499	189	21,6931217	29,6296296	11,1111111	37,5661376	32,8042328	67,1957672	1,26785714	1,95238095	-43,6	-26,45	0,00057207	40,69	-23,068783	-0,7032258
sch-MIR5543	312	20,8333333	36,2179487	10,2564103	32,6923077	31,0897436	68,9102564	0,90265487	2,03125	-72,1	-45,6	0,00023103	86,04	-23,108974	-0,743299
sch-MIR5556	210	25,7142857	25,2380952	20,4761905	28,5714286	46,1904762	53,8095238	1,13207547	1,25581395	-70,3	-68,4	0,0192117	31,47	-33,47619	-0,7247423
sch-MIR5568b	280	18,5714286	31,0714286	14,6428571	35,7142857	33,2142857	66,7857143	1,14942529	1,26829268	-89	-80,2	0,00027312	43,25	-31,785714	-0,9569892
sch-MIR5568d	179	19,5530726	36,8715084	11,7318436	31,8435754	31,2849162	68,7150838	0,86363636	1,66666667	-39,3	-33,5	0,00016445	26,83	-21,955307	-0,7017857
sch-MIR5628-1	118	20,3389831	31,3559322	16,1016949	32,2033898	36,440678	63,559322	1,02702703	1,26315789	-51,8	-49,3	0,0294021	12,76	-43,898305	-1,2046512
sch-MIR5628-2	103	20,3883495	32,038835	15,5339806	32,038835	35,9223301	64,0776699	1	1,3125	-43,5	-43,5	0,125184	6,67	-42,23301	-1,1756757
sch-MIR5640	222	16,6666667	38,2882883	15,3153153	29,7297297	31,981982	68,018018	0,77647059	1,08823529	-72,3	-57,8	0,00596249	42,22	-32,567568	-1,0183099
sch-MIR5654	253	15,8102767	30,8300395	19,7628458	33,5968379	35,5731225	64,4268775	1,08974359	0,8	-73	-71,2	0,00255705	38,59	-28,853755	-0,8111111

sch-MIR5658-1	298	23,4899329	29,8657718	10,738255	35,9060403	34,2281879	65,7718121	1,20224719	2,1875	-73,4	-50,6	1,92E-05	78,39	-24,630872	-0,7196078
sch-MIR5658-2	219	20,0913242	28,7671233	12,7853881	38,3561644	32,8767123	67,1232877	1,33333333	1,57142857	-64,6	-64,2	0,0121599	13,83	-29,497717	-0,8972222
sch-MIR5662	255	14,5098039	37,6470588	15,6862745	32,1568627	30,1960784	69,8039216	0,85416667	0,925	-88,9	-84,2	0,0125872	16,69	-34,862745	-1,1545455
sch-MIR5669	178	16,8539326	34,2696629	18,5393258	30,3370787	35,3932584	64,6067416	0,8852459	0,90909091	-76,5	-76,5	0,0287754	7,73	-42,977528	-1,2142857
sch-MIR5720	316	18,6708861	28,164557	12,0253165	41,1392405	30,6962025	69,3037975	1,46067416	1,55263158	-93,6	-89,5	6,57E-05	63,12	-29,620253	-0,9649485
sch-MIR5721	327	22,0183486	35,4740061	12,2324159	30,2752294	34,2507645	65,7492355	0,85344828	1,8	-80,7	-71	9,81E-05	49,31	-24,678899	-0,7205357
sch-MIR5759	233	19,7424893	31,3304721	18,4549356	30,472103	38,1974249	61,8025751	0,97260274	1,06976744	-97,9	-90,27	0,00153197	20,01	-42,004292	-1,0996629
sch-MIR5770b	138	27,5362319	26,0869565	13,0434783	33,3333333	40,5797101	59,4202899	1,27777778	2,11111111	-45,2	-45,2	0,0870391	6,94	-32,753623	-0,8071429
sch-MIR5773-1	152	17,1052632	33,5526316	13,8157895	35,5263158	30,9210526	69,0789474	1,05882353	1,23809524	-86,2	-85,4	0,0893978	8,58	-56,710526	-1,8340426
sch-MIR5773-2	161	17,3913043	35,4037267	14,2857143	32,9192547	31,6770186	68,3229814	0,92982456	1,2173913	-90,2	-86	0,0166419	12,7	-56,024845	-1,7686275
sch-MIR5796	88	22,7272727	32,9545455	17,0454545	27,2727273	39,7727273	60,2272727	0,82758621	1,33333333	-31,6	-31,6	0,270234	5,69	-35,909091	-0,9028571
sch-MIR5997	79	17,721519	36,7088608	17,721519	27,8481013	35,443038	64,556962	0,75862069	1	-35,6	-35,6	0,250439	4,64	-45,063291	-1,2714286
sch-MIR6020a	281	16,0142349	33,8078292	16,3701068	33,8078292	32,3843416	67,6156584	1	0,97826087	-64,3	-54,9	2,25E-05	35,07	-22,882562	-0,7065934
sch-MIR6022	236	19,4915254	30,5084746	19,0677966	30,9322034	38,559322	61,440678	1,01388889	1,02222222	-75	-54,06	0,00364512	50,21	-31,779661	-0,8241758
sch-MIR6023	198	19,1919192	30,8080808	18,1818182	31,8181818	37,3737374	62,6262626	1,03278689	1,05555556	-87,1	-84,3	0,00766523	13,76	-43,989899	-1,177027
sch-MIR6024-1	118	19,4915254	23,7288136	21,1864407	35,5932203	40,6779661	59,3220339	1,5	0,92	-50,6	-50,6	0,290393	5,37	-42,881356	-1,0541667
sch-MIR6024-2	116	20,6896552	24,137931	19,8275862	35,3448276	40,5172414	59,4827586	1,46428571	1,04347826	-47,1	-46,7	0,0467391	12,82	-40,603448	-1,0021277
sch-MIR6024-3	157	19,1082803	22,9299363	19,1082803	38,8535032	38,2165605	61,7834395	1,69444444	1	-52,9	-51,4	0,0389198	26,93	-33,694268	-0,8816667
sch-MIR6024-4	117	19,6581197	23,9316239	21,3675214	35,042735	41,025641	58,974359	1,46428571	0,92	-48,5	-48,5	0,248244	10,22	-41,452991	-1,0104167
sch-MIR6024-5	287	20,5574913	32,7526132	14,6341463	32,0557491	35,1916376	64,8083624	0,9787234	1,4047619	-74,3	-58,37	0,00031184	48,61	-25,888502	-0,7356436
sch-MIR6025e-1	164	20,7317073	27,4390244	11,5853659	40,2439024	32,3170732	67,6829268	1,46666667	1,78947368	-53,5	-50,3	0,0088117	22,53	-32,621951	-1,009434
sch-MIR6025e-2	164	24,3902439	26,2195122	12,804878	36,5853659	37,195122	62,804878	1,39534884	1,9047619	-58,7	-54	0,0078616	19,98	-35,792683	-0,9622951
sch-MIR6026	244	18,442623	27,0491803	13,9344262	40,5737705	32,3770492	67,6229508	1,5	1,32352941	-91,3	-88,87	0,00824316	23,65	-37,418033	-1,1556962
sch-MIR6027-1	166	19,2771084	30,7228916	13,8554217	36,1445783	33,1325301	66,8674699	1,17647059	1,39130435	-57,3	-56,8	0,0298837	14,94	-34,518072	-1,0418182
sch-MIR6027-2	165	19,3939394	32,1212121	13,9393939	34,5454545	33,3333333	66,6666667	1,0754717	1,39130435	-54,8	-54,3	0,0107929	16,47	-33,212121	-0,9963636
sch-MIR6108e	93	22,5806452	27,9569892	11,827957	37,6344086	34,4086022	65,5913978	1,34615385	1,90909091	-24,1	-24,1	0,0630788	7,99	-25,913978	-0,753125
sch-MIR6108f	83	31,3253012	13,253012	30,1204819	25,3012048	61,4457831	38,5542169	1,90909091	1,04	-36,1	-36,1	0,333067	6,42	-43,493976	-0,7078431
sch-MIR6111	172	21,5116279	33,7209302	12,7906977	31,9767442	34,3023256	65,6976744	0,94827586	1,68181818	-45,6	-41,97	0,00756989	33,6	-26,511628	-0,7728814
sch-MIR6116	87	16,091954	32,183908	18,3908046	33,3333333	34,4827586	65,5172414	1,03571429	0,875	-36	-36	0,262563	3,47	-41,37931	-1,2
sch-MIR6137b	200	14	30	19	37	33	67	1,23333333	0,73684211	-61,9	-52	0,00190871	64,07	-30,95	-0,9378788
sch-MIR6145b-1	91	25,2747253	30,7692308	21,978022	21,978022	47,2527473	52,7472527	0,71428571	1,15	-41,7	-41,7	0,270278	4,97	-45,824176	-0,9697674
sch-MIR6145b-2	72	29,1666667	25	15,2777778	30,5555556	44,4444444	55,5555556	1,22222222	1,90909091	-33,3	-33,3	0,649993	0,88	-46,25	-1,040625
sch-MIR6145c	292	14,7260274	30,4794521	15,4109589	39,3835616	30,1369863	69,8630137	1,29213483	0,95555556	-73,4	-71	0,00601282	46,71	-25,136986	-0,8340909
sch-MIR6145e	77	19,4805195	20,7792208	22,0779221	37,6623377	41,5584416	58,4415584	1,8125	0,88235294	-24,2	-22,5	0,166111	9,49	-31,428571	-0,75625
sch-MIR6149	118	16,1016949	39,8305085	17,7966102	26,2711864	33,8983051	66,1016949	0,65957447	0,9047619	-34	-31,1	0,0720996	35,54	-28,813559	-0,85
sch-MIR6149b	175	15,4285714	34,2857143	17,1428571	33,1428571	32,5714286	67,4285714	0,96666667	0,9	-63,7	-59,8	0,00592442	17,98	-36,4	-1,1175439
sch-MIR6157	256	17,578125	35,15625	16,015625	31,25	33,59375	66,40625	0,88888889	1,09756098	-87	-84,3	0,0074953	16,69	-33,984375	-1,0116279
sch-MIR6160	219	18,7214612	31,9634703	14,1552511	35,1598174	32,8767123	67,1232877	1,1	1,32258065	-52,9	-37,7	0,00123117	54,08	-24,155251	-0,7347222
sch-MIR6164b-1	297	15,8249158	32,996633	16,1616162	35,016835	31,986532	68,013468	1,06122449	0,97916667	-71,1	-70,6	0,00039259	37,43	-23,939394	-0,7484211
sch-MIR6164b-2	231	16,4502165	30,7359307	17,7489177	35,0649351	34,1991342	65,8008658	1,14084507	0,92682927	-58,2	-58,2	0,00265988	23,38	-25,194805	-0,7367089
sch-MIR6191	72	26,3888889	25	18,0555556	30,5555556	44,4444444	55,5555556	1,22222222	1,46153846	-28,4	-27,2	0,155449	4,7	-39,444444	-0,8875
sch-MIR6196-1	279	20,0716846	32,2580645	13,6200717	34,0501792	33,6917563	66,3082437	1,05555556	1,47368421	-73,2	-67,8	8,91E-05	38,39	-26,236559	-0,7787234
sch-MIR6196-2	195	20	36,4102564	12,3076923	31,2820513	32,3076923	67,6923077	0,85915493	1,625	-45,7	-29,38	0,00139484	56,59	-23,435897	-0,7253968
sch-MIR6222	192	14,0625	34,375	18,75	32,8125	32,8125	67,1875	0,95454545	0,75	-48,8	-40,9	0,00061384	40,69	-25,416667	-0,7746032
sch-MIR6230	204	20,5882353	28,9215686	20,5882353	29,9019608	41,1764706	58,8235294	1,03389831	1	-82,9	-81,8	0,00299972	19,35	-40,637255	-0,9869048
sch-MIR6231	217	19,8156682	34,562212	14,7465438	30,875576	34,562212	65,437788	0,89333333	1,34375	-92,9	-55,38	0,00199903	44,8	-42,81106	-1,2386667
sch-MIR6232b-1	307	16,6123779	30,2931596	21,1726384	31,9218241	37,7850163	62,2149837	1,05376344	0,78461538	-88	-85	0,00094277	34,04	-28,664495	-0,7586207
sch-MIR6232b-2	112	20,5357143	33,0357143	16,9642857	29,4642857	37,5	62,5	0,89189189	1,21052632	-74,2	-73,9	0,180751	4,04	-66,25	-1,7666667
sch-MIR6254	176	15,9090909	30,6818182	18,75	34,6590909	34,6590909	65,3409091	1,12962963	0,84848485	-60,7	-60,7	0,0448872	9,29	-34,488636	-0,995082
sch-MIR6272	209	14,8325359	33,0143541	16,2679426	35,8851675	31,1004785	68,8995215	1,08695652	0,91176471	-49	-46,7	0,0300027	15,35	-23,444976	-0,7538462
sch-MIR6273-2	179	15,0837989	38,547486	15,6424581	30,726257	30,726257	69,273743	0,79710145	0,96428571	-84,5	-83,7	0,0132747	36,38	-47,206704	-1,5363636
sch-MIR6273-4	84	19,047619	26,1904762	14,2857143	40,4761905	33,3333333	66,6666667	1,54545455	1,33333333	-21,4	-21,4	0,179606	6,74	-25,47619	-0,7642857
sch-MIR6283	89	22,4719101	29,2134831	14,6067416	33,7078652	37,0786517	62,9213483	1,15384615	1,53846154	-34,5	-33,7	0,114464	6,21	-38,764045	-1,0454545
sch-MIR6287	204	20,0980392	32,3529412	13,2352941	34,3137255	33,3333333	66,6666667	1,06060606	1,51851852	-48,2	-41	0,00744508	37,45	-23,627451	-0,7088235
sch-MIR6288c-1	84	16,6666667	29,7619048	15,4761905	38,0952381	32,1428571	67,8571429	1,28	1,07692308	-25,7	-23,4	0,0950196	5,44	-30,595238	-0,9518519
sch-MIR6288c-2	231	20,3463203	31,1688312	9,95670996	38,5281385	30,3030303	69,6969697	1,23611111	2,04347826	-53,6	-46	0,00048874	69,71	-23,203463	-0,7657143
sch-MIR6288c-3	239	17,9916318	28,0334728	13,3891213	40,5857741	31,3807531	68,6192469	1,44776119	1,34375	-53,4	-44,5	0,00336489	32,65	-22,343096	-0,712
sch-MIR6299	281	20,2846975	35,5871886	14,9466192	29,1814947	35,2313167	64,7686833	0,82	1,35714286	-73,3	-66,3	0,00074176	29,74	-26,085409	-0,740404
sch-MIR6300	241	17,4273859	34,0248963	13,2780083	35,2697095	30,7053942	69,2946058	1,03658537	1,3125	-66,1	-51,2	0,00010333	54,88	-27,427386	-0,8932432
sch-MIR6427	193	19,1709845	34,1968912	17,6165803	29,015544	36,7875648	63,2124352	0,84848485	1,08823529	-64,1	-49,65	0,0102687	39,06	-33,212435	-0,9028169
sch-MIR6430	203	18,7192118	31,5270936	18,7192118	31,0344828	37,4384236	62,5615764	0,984375	1	-57,6	-57,3	0,031243	17,64	-28,374384	-0,7578947
sch-MIR6439a	83	18,0722892	28,9156627	22,8915663	30,1204819	40,9638554	59,0361446	1,04166667	0,78947368	-27	-27	0,18612	5,93	-32,53012	-0,7941176
sch-MIR6457b-1	143	21,6783217	22,3776224	26,5734266	29,3706294	48,2517483	51,7482517	1,3125	0,81578947	-54,1	-53,6	0,0151938	8,68	-37,832168	-0,784058
sch-MIR6457b-2	140	19,2857143	25,7142857	26,4285714	28,5714286	45,7142857	54,2857143	1,11111111	0,72972973	-46,2	-45,3	0,0315555	13,89	-33	-0,721875
sch-MIR6462c	314	18,4713376	26,433121	12,4203822	42,6751592	30,8917197	69,1082803	1,61445783	1,48717949	-73,9	-58	2,43E-05	55,53	-23,535032	-0,7618557
sch-MIR6464	223	18,3856502	30,4932735	20,1793722	30,941704	38,5650224	61,4349776	1,01470588	0,91111111	-95,7	-89,3	0,018421	23,09	-42,914798	-1,1127907

sch-MIR6472	118	16,1016949	29,6610169	18,6440678	35,5932203	34,7457627	65,2542373	1,2	0,86363636	-31,2	-24,5	0,0231628	28,38	-26,440678	-0,7609756
sch-MIR6475	87	21,8390805	29,8850575	13,7931034	34,4827586	35,6321839	64,3678161	1,15384615	1,58333333	-35,8	-35,8	0,479073	2,53	-41,149425	-1,1548387
sch-MIR7122	78	16,6666667	29,4871795	20,5128205	33,3333333	37,1794872	62,8205128	1,13043478	0,8125	-31,5	-31,5	0,154352	3,65	-40,384615	-1,0862069
sch-MIR7122a	137	15,3284672	38,6861314	16,0583942	29,9270073	31,3868613	68,6131387	0,77358491	0,95454545	-70,4	-70,4	0,312446	4,05	-51,386861	-1,6372093
sch-MIR7484e	194	18,0412371	35,5670103	13,4020619	32,9896907	31,443299	68,556701	0,92753623	1,34615385	-44,1	-36,1	0,00092609	27,77	-22,731959	-0,7229508
sch-MIR7484j	170	17,6470588	28,2352941	18,2352941	35,8823529	35,8823529	64,1176471	1,27083333	0,96774194	-77,6	-73,6	0,00185927	20,16	-45,647059	-1,2721311
sch-MIR7484m	158	14,556962	32,278481	16,4556962	36,7088608	31,0126582	68,9873418	1,1372549	0,88461538	-38	-37,3	0,0093737	21,22	-24,050633	-0,7755102
sch-MIR7488	336	19,047619	35,7142857	11,6071429	33,6309524	30,6547619	69,3452381	0,94166667	1,64102564	-83,6	-73,2	0,000105	69,07	-24,880952	-0,8116505
sch-MIR7490	188	14,893617	32,4468085	17,0212766	35,6382979	31,9148936	68,0851064	1,09836066	0,875	-42,7	-42,7	0,0148065	14,8	-22,712766	-0,7116667
sch-MIR7492c	237	16,4556962	33,7552743	14,3459916	35,443038	30,8016878	69,1983122	1,05	1,14705882	-67,5	-63,7	0,00048903	39,47	-28,481013	-0,9246575
sch-MIR7492f-1	217	15,6682028	29,4930876	17,5115207	37,3271889	33,1797235	66,8202765	1,265625	0,89473684	-74,7	-70,6	0,00492614	21,41	-34,423963	-1,0375
sch-MIR7492f-2	200	16,5	30	17,5	36	34	66	1,2	0,94285714	-52,2	-47,7	0,00186856	24,42	-26,1	-0,7676471
sch-MIR7501	154	24,025974	31,8181818	17,5324675	26,6233766	41,5584416	58,4415584	0,83673469	1,37037037	-47,7	-47,5	0,00494701	10,46	-30,974026	-0,7453125
sch-MIR7502c-1	206	15,5339806	30,5825243	18,4466019	35,4368932	33,9805825	66,0194175	1,15873016	0,84210526	-49	-45,1	0,00110627	29,42	-23,786408	-0,7
sch-MIR7502c-2	280	17,8571429	34,2857143	15	32,8571429	32,8571429	67,1428571	0,95833333	1,19047619	-79,7	-77,6	0,00608786	16,38	-28,464286	-0,8663043
sch-MIR7512	248	21,3709677	24,5967742	17,3387097	36,6935484	38,7096774	61,2903226	1,49180328	1,23255814	-69,3	-53,27	0,00116797	44,09	-27,943548	-0,721875
sch-MIR7517	258	21,7054264	29,0697674	16,2790698	32,9457364	37,9844961	62,0155039	1,13333333	1,33333333	-94,1	-89,1	0,00444481	30,66	-36,472868	-0,9602041
sch-MIR7519	190	18,9473684	35,2631579	13,1578947	32,6315789	32,1052632	67,8947368	0,92537313	1,44	-56,9	-53,7	0,0145699	16,7	-29,947368	-0,9327869
sch-MIR7525	238	12,1848739	31,092437	18,0672269	38,6554622	30,2521008	69,7478992	1,24324324	0,6744186	-53,1	-37,8	0,00048091	64,39	-22,310924	-0,7375
sch-MIR7528	214	20,0934579	26,1682243	14,4859813	39,2523364	34,5794393	65,4205607	1,5	1,38709677	-52,7	-49,1	0,00753413	31,56	-24,626168	-0,7121622
sch-MIR7533c	275	21,4545455	33,4545455	14,1818182	30,9090909	35,6363636	64,3636364	0,92391304	1,51282051	-73,4	-66,8	0,0001134	36,03	-26,690909	-0,7489796
sch-MIR7535-1	196	23,4693878	28,0612245	12,244898	36,2244898	35,7142857	64,2857143	1,29090909	1,91666667	-51,5	-51,4	0,00227255	30,78	-26,27551	-0,7357143
sch-MIR7535-2	125	28,8	24	14,4	32,8	43,2	56,8	1,36666667	2	-38,9	-36,7	0,0389861	27,35	-31,12	-0,7203704
sch-MIR7696b-1	177	25,9887006	29,3785311	11,299435	33,3333333	37,2881356	62,7118644	1,13461538	2,3	-48,2	-48,2	0,00244141	28,25	-27,231638	-0,730303
sch-MIR7696b-2	165	16,969697	33,3333333	15,7575758	33,9393939	32,7272727	67,2727273	1,01818182	1,07692308	-85	-85	0,05126	11,15	-51,515152	-1,5740741
sch-MIR7696d	148	14,1891892	38,5135135	16,8918919	30,4054054	31,0810811	68,9189189	0,78947368	0,84	-33,3	-33,3	0,0272183	10,57	-22,5	-0,723913
sch-MIR7698	210	18,5714286	28,5714286	17,1428571	35,7142857	35,7142857	64,2857143	1,25	1,08333333	-86,1	-86,1	0,00966934	14,4	-41	-1,148
sch-MIR7699-1	327	15,9021407	38,2262997	14,9847095	30,8868502	30,8868502	69,1131498	0,808	1,06122449	-77,3	-53,8	6,92E-05	64,17	-23,639144	-0,7653465
sch-MIR7699-2	81	16,0493827	28,3950617	16,0493827	39,5061728	32,0987654	67,9012346	1,39130435	1	-24,4	-23	0,187885	3,78	-30,123457	-0,9384615
sch-MIR7701	131	20,610687	32,8244275	12,2137405	34,351145	32,8244275	67,1755725	1,04651163	1,6875	-36	-35,9	0,0166007	10,96	-27,480916	-0,8372093
sch-MIR7719	314	20,7006369	38,8535032	11,1464968	29,2993631	31,8471338	68,1528662	0,75409836	1,85714286	-70,2	-58,21	0,00031687	79,49	-22,356688	-0,702
sch-MIR773b	99	30,3030303	23,2323232	19,1919192	27,2727273	49,4949495	50,5050505	1,17391304	1,57894737	-36,6	-36,6	0,102963	12,09	-36,969697	-0,7469388
sch-MIR7757-1	85	24,7058824	21,1764706	18,8235294	35,2941176	43,5294118	56,4705882	1,66666667	1,3125	-37,1	-37,1	0,174871	4,85	-43,647059	-1,0027027
sch-MIR7757-2	97	16,4948454	25,7731959	14,4329897	43,2989691	30,9278351	69,0721649	1,68	1,14285714	-27,1	-27,1	0,155273	6,07	-27,938144	-0,9033333
sch-MIR7776	118	18,6440678	31,3559322	15,2542373	34,7457627	33,8983051	66,1016949	1,10810811	1,22222222	-36,4	-33,6	0,0266182	15,37	-30,847458	-0,91
sch-MIR780	238	18,0672269	30,2521008	14,2857143	37,394958	32,3529412	67,6470588	1,23611111	1,26470588	-88,7	-85,8	0,00319236	18,38	-37,268908	-1,1519481
sch-MIR7803b	78	17,9487179	30,7692308	21,7948718	29,4871795	39,7435897	60,2564103	0,95833333	0,82352941	-26,2	-26	0,277758	4,03	-33,589744	-0,8451613
sch-MIR7808	71	28,1690141	25,3521127	25,3521127	21,1267606	53,5211268	46,4788732	0,83333333	1,11111111	-34	-34	0,115047	4,7	-47,887324	-0,8947368
sch-MIR7816	95	8,42105263	31,5789474	22,1052632	37,8947368	30,5263158	69,4736842	1,2	0,38095238	-22,7	-22,7	0,236631	3,8	-23,894737	-0,7827586
sch-MIR782	196	16,3265306	33,6734694	20,9183673	29,0816327	37,244898	62,755102	0,86363636	0,7804878	-52,8	-51,5	0,0131712	15,55	-26,938776	-0,7232877
sch-MIR7822-1	213	15,4929577	37,5586854	15,0234742	31,9248826	30,5164319	69,4835681	0,85	1,03125	-66,7	-66,7	0,042965	15,22	-31,314554	-1,0261538
sch-MIR7822-2	209	15,7894737	33,492823	14,354067	36,3636364	30,1435407	69,8564593	1,08571429	1,1	-89,6	-87,9	0,0368767	16,8	-42,870813	-1,4222222
sch-MIR7822-3	196	17,8571429	29,5918367	14,7959184	37,755102	32,6530612	67,3469388	1,27586207	1,20689655	-76,1	-75,2	0,0354761	8,74	-38,826531	-1,1890625
sch-MIR7822-4	157	17,8343949	32,4840764	13,3757962	36,3057325	31,2101911	68,7898089	1,11764706	1,33333333	-54	-51,6	0,00393687	19,99	-34,394904	-1,1020408
sch-MIR7822-5	252	18,2539683	30,952381	14,2857143	36,5079365	32,5396825	67,4603175	1,17948718	1,27777778	-70,7	-66,29	0,00029787	47,74	-28,055556	-0,8621951
sch-MIR7828	247	21,0526316	31,9838057	17,8137652	29,1497976	38,8663968	61,1336032	0,91139241	1,18181818	-81,1	-78,4	0,00544098	39,64	-32,834008	-0,8447917
sch-MIR7831	239	23,4309623	25,5230126	20,5020921	30,5439331	43,9330544	56,0669456	1,19672131	1,14285714	-90,4	-82,05	0,00714557	40,88	-37,824268	-0,8609524
sch-MIR7980b-1	66	24,2424242	24,2424242	13,6363636	37,8787879	37,8787879	62,1212121	1,5625	1,77777778	-27,8	-27,8	0,340918	3,01	-42,121212	-1,112
sch-MIR7980b-2	114	21,9298246	27,1929825	18,4210526	32,4561404	40,3508772	59,6491228	1,19354839	1,19047619	-44	-39,8	0,0411657	14,6	-38,596491	-0,9565217
sch-MIR7980b-3	142	18,3098592	30,9859155	16,9014085	33,8028169	35,2112676	64,7887324	1,09090909	1,08333333	-55,7	-55,7	0,0936954	8,03	-39,225352	-1,114
sch-MIR7980b-4	117	17,0940171	29,0598291	17,9487179	35,8974359	35,042735	64,957265	1,23529412	0,95238095	-45,1	-42,1	0,103766	10,84	-38,547009	-1,1
sch-MIR7980b-5	208	13,9423077	37,0192308	18,2692308	30,7692308	32,2115385	67,7884615	0,83116883	0,76315789	-59,5	-55,7	0,00138272	30,58	-28,605769	-0,8880597
sch-MIR7981-1	216	17,1296296	34,2592593	15,2777778	33,3333333	32,4074074	67,5925926	0,97297297	1,12121212	-72,1	-70,2	0,00230686	20,07	-33,37963	-1,03
sch-MIR7981-12	228	17,5438596	31,1403509	14,4736842	36,8421053	32,0175439	67,9824561	1,18309859	1,21212121	-68,2	-61,2	0,00080882	30,11	-29,912281	-0,9342466
sch-MIR7981-13	200	16	32,5	17	34,5	33	67	1,06153846	0,94117647	-80,2	-77,2	0,0165739	19,77	-40,1	-1,2151515
sch-MIR7981-14	266	18,4210526	32,7067669	21,4285714	27,443609	39,8496241	60,1503759	0,83908046	0,85964912	-91,6	-88,1	0,00035483	29,48	-34,43609	-0,8641509
sch-MIR7981-18	258	18,2170543	34,496124	16,6666667	30,620155	34,8837209	65,1162791	0,88764045	1,09302326	-84,2	-78,5	0,00101062	41,69	-32,635659	-0,9355556
sch-MIR7981-2	244	18,852459	31,9672131	22,1311475	27,0491803	40,9836066	59,0163934	0,84615385	0,85185185	-95	-83,39	0,0009154	28,03	-38,934426	-0,95
sch-MIR7981-6	258	16,6666667	30,620155	18,2170543	34,496124	34,8837209	65,1162791	1,12658228	0,91489362	-96,9	-86,52	0,00654492	36,19	-37,55814	-1,0766667
sch-MIR7981-7	304	16,1184211	34,2105263	21,7105263	27,9605263	37,8289474	62,1710526	0,81730769	0,74242424	-87,5	-81,37	0,00016053	32,27	-28,782895	-0,7608696
sch-MIR7981-8	253	13,8339921	34,7826087	16,6007905	34,7826087	30,4347826	69,5652174	1	0,83333333	-94,3	-92,9	0,00029052	21,07	-37,272727	-1,2246753
sch-MIR7981a-14	196	15,8163265	37,755102	17,3469388	29,0816327	33,1632653	66,8367347	0,77027027	0,91176471	-77	-75,7	0,016042	13,13	-39,285714	-1,1846154
sch-MIR7981a-2	180	16,1111111	38,3333333	15	30,5555556	31,1111111	68,8888889	0,79710145	1,07407407	-76,2	-75,6	0,0384991	10,58	-42,333333	-1,3607143
sch-MIR7981a-33	193	17,6165803	35,7512953	19,6891192	26,9430052	37,3056995	62,6943005	0,75362319	0,89473684	-87,9	-84	0,00419675	20,03	-45,544041	-1,2208333
sch-MIR7981a-57	312	20,1923077	32,6923077	13,4615385	33,6538462	33,6538462	66,3461538	1,02941176	1,5	-87,6	-77,9	3,40E-05	57,83	-28,076923	-0,8342857
sch-MIR7981a-64	241	15,3526971	35,6846473	14,9377593	34,0248963	30,2904564	69,7095436	0,95348837	1,02777778	-88,1	-88,1	0,0179301	11,77	-36,556017	-1,2068493

sch-MIR7981b-27	238	15,5462185	36,9747899	17,2268908	30,2521008	32,7731092	67,2268908	0,81818182	0,90243902	-99,1	-93,5	0,00271292	19,58	-41,638655	-1,2705128
sch-MIR7981b-8	205	14,6341463	35,1219512	16,5853659	33,6585366	31,2195122	68,7804878	0,95833333	0,88235294	-84,5	-82,3	0,00232161	22,75	-41,219512	-1,3203125
sch-MIR7981d-11	233	18,8841202	30,9012876	14,1630901	36,0515021	33,0472103	66,9527897	1,16666667	1,33333333	-99,8	-97,3	0,00532464	16,8	-42,832618	-1,2961039
sch-MIR7981d-4	246	15,8536585	36,9918699	17,8861789	29,2682927	33,7398374	66,2601626	0,79120879	0,88636364	-99,9	-99,2	0,00760898	17,33	-40,609756	-1,2036145
sch-MIR7981d-6	264	15,530303	33,7121212	20,0757576	30,6818182	35,6060606	64,3939394	0,91011236	0,77358491	-88,7	-84,9	0,00128854	22,72	-33,598485	-0,943617
sch-MIR7981d-8	226	19,0265487	30,5309735	19,9115044	30,5309735	38,9380531	61,0619469	1	0,95555556	-86	-84,3	0,00999699	30,07	-38,053097	-0,9772727
sch-MIR7981d-9	212	16,9811321	37,2641509	16,9811321	28,7735849	33,9622642	66,0377358	0,7721519	1	-72,5	-66,4	0,00447711	28,34	-34,198113	-1,0069444
sch-MIR7983-1	216	15,7407407	37,5	17,5925926	29,1666667	33,3333333	66,6666667	0,77777778	0,89473684	-62	-51,44	0,00186827	31,76	-28,703704	-0,8611111
sch-MIR7983-10	66	24,2424242	28,7878788	18,1818182	28,7878788	42,4242424	57,5757576	1	1,33333333	-23,5	-22,9	0,236892	3,96	-35,606061	-0,8392857
sch-MIR7983-11	206	14,5631068	30,0970874	16,5048544	37,3786408	31,0679612	67,4757282	1,24193548	0,88235294	-49,2	-43,4	0,00134121	30,26	-23,883495	-0,76875
sch-MIR7983-12	182	13,1868132	33,5164835	18,1318681	35,1648352	31,3186813	68,6813187	1,04918033	0,72727273	-52,2	-51,6	0,0107526	19,2	-28,681319	-0,9157895
sch-MIR7983-13	209	14,354067	29,6650718	16,7464115	39,2344498	31,1004785	68,8995215	1,32258065	0,85714286	-53,9	-49,5	0,00288777	33,04	-25,789474	-0,8292308
sch-MIR7983-2	181	13,8121547	32,5966851	16,5745856	37,0165746	30,3867403	69,6132597	1,13559322	0,83333333	-42	-41,7	0,00825239	18,33	-23,20442	-0,7636364
sch-MIR7983-3	66	19,6969697	27,2727273	21,2121212	31,8181818	40,9090909	59,0909091	1,16666667	0,92857143	-22,1	-20,9	0,239663	3,8	-33,484848	-0,8185185
sch-MIR7983-4	216	13,4259259	29,6296296	17,1296296	39,8148148	30,5555556	69,4444444	1,34375	0,78378378	-48,7	-41,1	0,00116114	47,74	-22,546296	-0,7378788
sch-MIR7983-5	214	16,3551402	38,7850467	15,4205607	29,4392523	31,7757009	68,2242991	0,75903614	1,06060606	-55,4	-51,3	0,0106641	12,46	-25,88785	-0,8147059
sch-MIR7983-6	72	18,0555556	29,1666667	18,0555556	34,7222222	36,1111111	63,8888889	1,19047619	1	-30,2	-30,2	0,232648	3,63	-41,944444	-1,1615385
sch-MIR7983-7	228	16,2280702	30,2631579	16,2280702	37,2807018	32,4561404	67,5438596	1,23188406	1	-72,6	-62,3	0,00188075	38,92	-31,842105	-0,9810811
sch-MIR7983-8	215	17,2093023	27,4418605	17,6744186	37,6744186	34,8837209	65,1162791	1,37288136	0,97368421	-78,3	-78,3	0,0127369	14,6	-36,418605	-1,044
sch-MIR7983-9	214	14,0186916	31,7757009	16,3551402	37,8504673	30,3738318	69,6261682	1,19117647	0,85714286	-61,1	-59,5	0,00668842	21,19	-28,551402	-0,94
sch-MIR7984b-1	188	18,6170213	32,4468085	15,9574468	32,9787234	34,5744681	65,4255319	1,01639344	1,16666667	-61,4	-57,09	0,00927461	33,19	-32,659574	-0,9446154
sch-MIR7984b-2	197	15,2284264	34,5177665	16,2436548	34,0101523	31,4720812	68,5279188	0,98529412	0,9375	-64,4	-64,4	0,0244475	14,25	-32,690355	-1,0387097
sch-MIR7984b-3	215	16,2790698	34,8837209	15,3488372	33,4883721	31,627907	68,372093	0,96	1,06060606	-88,4	-86,97	0,00090803	20,22	-41,116279	-1,3
sch-MIR7984b-4	88	18,1818182	28,4090909	21,5909091	31,8181818	39,7727273	60,2272727	1,12	0,84210526	-49,8	-49,8	0,204618	2,96	-56,590909	-1,4228571
sch-MIR7984b-5	258	14,7286822	34,496124	16,6666667	34,1085271	31,3953488	68,6046512	0,98876404	0,88372093	-74,2	-67,74	0,00083611	28,17	-28,75969	-0,9160494
sch-MIR7984c-1	204	17,1568627	30,8823529	18,1372549	33,8235294	35,2941176	64,7058824	1,0952381	0,94594595	-76,4	-72	0,00975156	17,72	-37,45098	-1,0611111
sch-MIR7984c-2	239	16,7364017	30,9623431	16,3179916	35,9832636	33,0543933	66,9456067	1,16216216	1,02564103	-81,4	-71,36	0,00175716	35,97	-34,058577	-1,0303797
sch-MIR7984c-3	218	14,6788991	34,4036697	16,5137615	34,4036697	31,1926606	68,8073394	1	0,88888889	-91,6	-89,3	0,00547638	15,84	-42,018349	-1,3470588
sch-MIR7984d-1	278	15,1079137	34,8920863	15,8273381	34,1726619	30,9352518	69,0647482	0,97938144	0,95454545	-93,4	-90,2	0,00390735	19,47	-33,597122	-1,0860465
sch-MIR7984d-2	242	15,2892562	33,0578512	17,768595	33,8842975	33,0578512	66,9421488	1,025	0,86046512	-60,3	-47,82	0,00209084	58,84	-24,917355	-0,75375
sch-MIR7985-1	187	31,0160428	18,1818182	24,0641711	26,7379679	55,0802139	44,9197861	1,47058824	1,28888889	-76,8	-54,2	0,00631812	60,56	-41,069519	-0,7456311
sch-MIR7985-2	212	29,7169811	17,4528302	23,1132075	29,7169811	52,8301887	47,1698113	1,7027027	1,28571429	-92	-82,7	0,00330692	33,78	-43,396226	-0,8214286
sch-MIR7986	148	17,5675676	31,7567568	14,8648649	35,8108108	32,4324324	67,5675676	1,12765957	1,18181818	-84,4	-84,4	0,626332	1,38	-57,027027	-1,7583333
sch-MIR7987	201	13,4328358	31,840796	17,4129353	37,3134328	30,8457711	69,1542289	1,171875	0,77142857	-48,7	-47,6	0,00249064	26,79	-24,228856	-0,7854839
sch-MIR7988	272	19,8529412	31,9852941	13,2352941	34,9264706	33,0882353	66,9117647	1,09195402	1,5	-83,8	-60,2	0,00013238	53,17	-30,808824	-0,9311111
sch-MIR7990a	133	15,7894737	27,8195489	15,7894737	40,6015038	31,5789474	68,4210526	1,45945946	1	-40	-38,9	0,0277241	15,54	-30,075188	-0,952381
sch-MIR7992-1	138	18,115942	33,3333333	15,942029	32,6086957	34,057971	65,942029	0,97826087	1,13636364	-43	-43	0,0741663	14,27	-31,15942	-0,9148936
sch-MIR7992-10	210	20	33,3333333	15,7142857	30,952381	35,7142857	64,2857143	0,92857143	1,27272727	-85,6	-85,6	0,0219549	9,85	-40,761905	-1,1413333
sch-MIR7992-11	167	20,3592814	27,5449102	20,9580838	31,1377246	41,3173653	58,6826347	1,13043478	0,97142857	-60,6	-60,3	0,0091918	23,33	-36,287425	-0,8782609
sch-MIR7992-12	195	18,974359	31,7948718	17,4358974	31,7948718	36,4102564	63,5897436	1	1,08823529	-91,5	-90,8	0,0624168	9,46	-46,923077	-1,2887324
sch-MIR7992-13	194	15,4639175	38,1443299	18,556701	27,8350515	34,0206186	65,9793814	0,72972973	0,83333333	-65,4	-64,6	0,0080883	13,4	-33,71134	-0,9909091
sch-MIR7992-14	254	12,5984252	39,3700787	18,503937	29,5275591	31,1023622	68,8976378	0,75	0,68085106	-59,4	-56,7	0,00207429	21,57	-23,385827	-0,7518987
sch-MIR7992-15	175	14,8571429	36	16,5714286	32,5714286	31,4285714	68,5714286	0,9047619	0,89655172	-46,3	-43,6	0,00226817	18,09	-26,457143	-0,8418182
sch-MIR7992-2	155	21,2903226	30,3225806	20,6451613	27,7419355	41,9354839	58,0645161	0,91489362	1,03125	-88,4	-88,4	0,144852	4,05	-57,032258	-1,36
sch-MIR7992-3	233	14,1630901	33,9055794	18,4549356	33,4763948	32,6180258	67,3819742	0,98734177	0,76744186	-95	-86,94	0,0118586	21,63	-40,772532	-1,25
sch-MIR7992-4	233	19,7424893	30,0429185	21,4592275	28,7553648	41,2017167	58,7982833	0,95714286	0,92	-85,4	-70,72	0,00355999	40,94	-36,652361	-0,8895833
sch-MIR7992-5	182	22,5274725	27,4725275	19,7802198	30,2197802	42,3076923	57,6923077	1,1	1,13888889	-62,7	-60,4	0,00619793	21,65	-34,450549	-0,8142857
sch-MIR7992-6	206	18,9320388	26,6990291	25,2427184	29,1262136	44,1747573	55,8252427	1,09090909	0,75	-77,6	-76,2	0,0214085	15,48	-37,669903	-0,8527473
sch-MIR7992-7	223	16,1434978	35,8744395	18,8340807	29,1479821	34,9775785	65,0224215	0,8125	0,85714286	-61,6	-60,4	0,0119254	24,32	-27,623318	-0,7897436
sch-MIR7992-8	151	19,205298	32,4503311	21,192053	27,1523179	40,397351	59,602649	0,83673469	0,90625	-51,3	-45,43	0,0216655	21,02	-33,97351	-0,8409836
sch-MIR7992-9	158	22,1518987	30,3797468	20,2531646	27,2151899	42,4050633	57,5949367	0,89583333	1,09375	-48	-43,2	0,0034878	18,01	-30,379747	-0,7164179
sch-MIR7993b	276	18,8405797	28,2608696	17,3913043	35,5072464	36,2318841	63,7681159	1,25641026	1,08333333	-90	-80,62	0,00014751	33,78	-32,608696	-0,9
sch-MIR7997b-1	235	22,5531915	26,8085106	18,2978723	32,3404255	40,8510638	59,1489362	1,20634921	1,23255814	-69,8	-65,7	0,00125823	25,96	-29,702128	-0,7270833
sch-MIR7997b-10	142	22,5352113	30,9859155	22,5352113	23,943662	45,0704225	54,9295775	0,77272727	1	-72,7	-67,2	0,102034	4,79	-51,197183	-1,1359375
sch-MIR7997b-11	129	17,8294574	26,3565891	28,6821705	27,1317829	46,5116279	53,4883721	1,02941176	0,62162162	-53,4	-53,4	0,183688	4,55	-41,395349	-0,89
sch-MIR7997b-12	142	21,8309859	28,8732394	19,0140845	30,2816901	40,8450704	59,1549296	1,04878049	1,14814815	-52,2	-49,6	0,0215494	14,05	-36,760563	-0,9
sch-MIR7997b-13	101	20,7920792	29,7029703	25,7425743	23,7623762	46,5346535	53,4653465	0,8	0,80769231	-36,9	-36,9	0,336482	6,21	-36,534653	-0,7851064
sch-MIR7997b-14	118	16,9491525	27,1186441	21,1864407	34,7457627	38,1355932	61,8644068	1,28125	0,8	-34,5	-33,6	0,0290643	11,38	-29,237288	-0,7666667
sch-MIR7997b-15	114	14,9122807	33,3333333	21,9298246	29,8245614	36,8421053	63,1578947	0,89473684	0,68	-35,1	-35,1	0,156243	7,88	-30,789474	-0,8357143
sch-MIR7997b-16	114	22,8070175	25,4385965	22,8070175	28,9473684	45,6140351	54,3859649	1,13793103	1	-52	-49,4	0,040081	9,22	-45,614035	-1
sch-MIR7997b-17	104	16,3461538	28,8461538	22,1153846	32,6923077	38,4615385	61,5384615	1,13333333	0,73913043	-32,8	-32,8	0,0922036	8,47	-31,538462	-0,82
sch-MIR7997b-18	125	24	28	18,4	29,6	42,4	57,6	1,05714286	1,30434783	-52	-52	0,280037	3,19	-41,6	-0,9811321
sch-MIR7997b-19	136	20,5882353	27,9411765	23,5294118	27,9411765	44,1176471	55,8823529	1	0,875	-47,7	-46,7	0,0101114	12,51	-35,073529	-0,795
sch-MIR7997b-2	173	19,0751445	30,0578035	24,8554913	26,0115607	43,9306358	56,0693642	0,86538462	0,76744186	-82,3	-82,3	0,100325	7,25	-47,572254	-1,0828947
sch-MIR7997b-20	127	19,6850394	26,7716535	26,7716535	26,7716535	46,4566929	53,5433071	1	0,73529412	-58,5	-57,6	0,337661	3,8	-46,062992	-0,9915254
sch-MIR7997b-3	135	20,7407407	25,1851852	28,1481481	25,9259259	48,8888889	51,1111111	1,02941176	0,73684211	-72,4	-71,14	0,073204	8,07	-53,62963	-1,0969697

sch-MIR7997b-4	119	18,487395	28,5714286	27,7310924	25,210084	46,2184874	53,7815126	0,88235294	0,66666667	-55,6	-55,6	0,369826	2,22	-46,722689	-1,0109091
sch-MIR7997b-5	146	21,9178082	23,9726027	23,2876712	30,8219178	45,2054795	54,7945205	1,28571429	0,94117647	-60,4	-59,6	0,048431	10,63	-41,369863	-0,9151515
sch-MIR7997b-6	127	26,7716535	24,4094488	19,6850394	29,1338583	46,4566929	53,5433071	1,19354839	1,36	-54,2	-51,5	0,115842	6,59	-42,677165	-0,9186441
sch-MIR7997b-7	129	20,9302326	31,7829457	20,1550388	27,1317829	41,0852713	58,9147287	0,85365854	1,03846154	-50,1	-46,8	0,0585886	11,84	-38,837209	-0,945283
sch-MIR7997b-8	127	19,6850394	25,984252	26,7716535	27,5590551	46,4566929	53,5433071	1,06060606	0,73529412	-54,2	-54,2	0,0811027	6,69	-42,677165	-0,9186441
sch-MIR7997b-9	127	15,7480315	28,3464567	22,0472441	33,8582677	37,7952756	62,2047244	1,19444444	0,71428571	-39,6	-36,4	0,0377646	8,91	-31,181102	-0,825
sch-MIR7997c-1	109	20,1834862	29,3577982	20,1834862	30,2752294	40,3669725	59,6330275	1,03125	1	-39,2	-36,3	0,0962386	10,29	-35,963303	-0,8909091
sch-MIR7997c-10	130	20	28,4615385	19,2307692	32,3076923	39,2307692	60,7692308	1,13513514	1,04	-49,3	-42,04	0,031076	17,95	-37,923077	-0,9666667
sch-MIR7997c-11	118	27,1186441	26,2711864	19,4915254	27,1186441	46,6101695	53,3898305	1,03225806	1,39130435	-50,8	-50,5	0,0277408	9,93	-43,050847	-0,9236364
sch-MIR7997c-12	159	22,0125786	32,7044025	20,1257862	25,1572327	42,1383648	57,8616352	0,76923077	1,09375	-51,8	-51,8	0,0432085	10,2	-32,578616	-0,7731343
sch-MIR7997c-13	122	17,2131148	36,0655738	18,852459	27,8688525	36,0655738	63,9344262	0,77272727	0,91304348	-37,8	-37,8	0,051233	6,71	-30,983607	-0,8590909
sch-MIR7997c-14	111	18,9189189	30,6306306	17,1171171	33,3333333	36,036036	63,963964	1,08823529	1,10526316	-45,3	-42,2	0,0813712	13,87	-40,810811	-1,1325
sch-MIR7997c-15	123	21,9512195	30,0813008	16,2601626	31,7073171	38,2113821	61,7886179	1,05405405	1,35	-54,8	-53,7	0,0503228	6,56	-44,552846	-1,1659574
sch-MIR7997c-16	123	21,1382114	32,5203252	19,5121951	26,8292683	40,6504065	59,3495935	0,825	1,08333333	-58,4	-58,4	0,12641	7,31	-47,479675	-1,168
sch-MIR7997c-17	130	20	24,6153846	22,3076923	33,0769231	42,3076923	57,6923077	1,34375	0,89655172	-61,5	-60,9	0,169921	4,14	-47,307692	-1,1181818
sch-MIR7997c-18	120	25,8333333	27,5	15	31,6666667	40,8333333	59,1666667	1,15151515	1,72222222	-44,7	-44,7	0,0368765	8,89	-37,25	-0,9122449
sch-MIR7997c-19	329	19,4528875	31,0030395	12,1580547	37,3860182	31,6109422	68,3890578	1,20588235	1,6	-85,2	-79,3	3,26E-05	40,31	-25,896657	-0,8192308
sch-MIR7997c-2	100	18	34	18	30	36	64	0,88235294	1	-36,2	-36,2	0,28359	9,39	-36,2	-1,0055556
sch-MIR7997c-20	128	19,53125	26,5625	25	28,90625	44,53125	55,46875	1,08823529	0,78125	-56,9	-56,5	0,100028	5,91	-44,453125	-0,9982456
sch-MIR7997c-21	133	26,3157895	31,5789474	17,2932331	24,8120301	43,6090226	56,3909774	0,78571429	1,52173913	-51,7	-51,7	0,155739	9,53	-38,87218	-0,8913793
sch-MIR7997c-22	242	20,2479339	30,5785124	19,0082645	30,1652893	39,2561983	60,7438017	0,98648649	1,06521739	-91,7	-89,1	0,00581445	24,02	-37,892562	-0,9652632
sch-MIR7997c-23	104	17,3076923	30,7692308	25	26,9230769	42,3076923	57,6923077	0,875	0,69230769	-39,6	-38,21	0,0974548	7,42	-38,076923	-0,9
sch-MIR7997c-24	160	19,375	33,125	19,375	28,125	38,75	61,25	0,8490566	1	-57,7	-56,5	0,0968793	8,49	-36,0625	-0,9306452
sch-MIR7997c-25	129	20,9302326	28,6821705	18,6046512	31,7829457	39,5348837	60,4651163	1,10810811	1,125	-43,3	-43	0,0367644	7,11	-33,565891	-0,8490196
sch-MIR7997c-26	120	29,1666667	23,3333333	15	32,5	44,1666667	55,8333333	1,39285714	1,94444444	-57,8	-57,8	0,204935	8,01	-48,166667	-1,090566
sch-MIR7997c-27	116	21,5517241	28,4482759	17,2413793	32,7586207	38,7931034	61,2068966	1,15151515	1,25	-48,3	-48,3	0,281239	4,59	-41,637931	-1,0733333
sch-MIR7997c-28	185	20	32,4324324	19,4594595	28,1081081	39,4594595	60,5405405	0,86666667	1,02777778	-58	-58	0,0460947	10,65	-31,351351	-0,7945205
sch-MIR7997c-29	149	20,8053691	28,8590604	22,147651	28,1879195	42,9530201	57,0469799	0,97674419	0,93939394	-70,7	-70,7	0,133173	8,37	-47,449664	-1,1046875
sch-MIR7997c-3	112	19,6428571	29,4642857	19,6428571	31,25	39,2857143	60,7142857	1,06060606	1	-41,8	-39,8	0,0631614	10,38	-37,321429	-0,95
sch-MIR7997c-30	140	22,8571429	27,1428571	20	30	42,8571429	57,1428571	1,10526316	1,14285714	-65,4	-64,7	0,214726	6,78	-46,714286	-1,09
sch-MIR7997c-31	133	24,8120301	26,3157895	18,7969925	30,075188	43,6090226	56,3909774	1,14285714	1,32	-53,9	-49,5	0,0706655	10,8	-40,526316	-0,9293103
sch-MIR7997c-32	129	27,1317829	27,9069767	20,1550388	24,8062016	47,2868217	52,7131783	0,88888889	1,34615385	-50	-47,7	0,0295146	12,92	-38,75969	-0,8196721
sch-MIR7997c-33	135	28,1481481	25,9259259	20,7407407	25,1851852	48,8888889	51,1111111	0,97142857	1,35714286	-79,7	-79,7	0,288205	3,27	-59,037037	-1,2075758
sch-MIR7997c-34	124	19,3548387	36,2903226	17,7419355	26,6129032	37,0967742	62,9032258	0,73333333	1,09090909	-40,4	-40,4	0,26275	14,55	-32,580645	-0,8782609
sch-MIR7997c-35	114	24,5614035	28,9473684	13,1578947	33,3333333	37,7192982	62,2807018	1,15151515	1,86666667	-43,9	-43,9	0,049252	5,78	-38,508772	-1,0209302
sch-MIR7997c-36	260	19,6153846	32,3076923	16,1538462	31,9230769	35,7692308	64,2307692	0,98809524	1,21428571	-72,3	-63,14	0,0001121	38,71	-27,807692	-0,7774194
sch-MIR7997c-37	146	22,6027397	26,0273973	19,8630137	31,5068493	42,4657534	57,5342466	1,21052632	1,13793103	-54,1	-52,5	0,00391958	16,62	-37,054795	-0,8725806
sch-MIR7997c-4	106	25,4716981	28,3018868	15,0943396	31,1320755	40,5660377	59,4339623	1,1	1,6875	-49,5	-49,5	0,10552	8,23	-46,698113	-1,1511628
sch-MIR7997c-5	125	17,6	32	24,8	25,6	42,4	57,6	0,8	0,70967742	-46,8	-46,8	0,0942293	7,8	-37,44	-0,8830189
sch-MIR7997c-6	133	26,3157895	26,3157895	16,5413534	30,8270677	42,8571429	57,1428571	1,17142857	1,59090909	-58,8	-58,8	0,219153	3,13	-44,210526	-1,0315789
sch-MIR7997c-7	124	25,8064516	29,8387097	16,9354839	27,4193548	42,7419355	57,2580645	0,91891892	1,52380952	-52,1	-42,1	0,0153074	17,93	-42,016129	-0,9830189
sch-MIR7997c-8	143	19,5804196	32,8671329	16,0839161	31,4685315	35,6643357	64,3356643	0,95744681	1,2173913	-63,2	-63,2	0,0384998	9,58	-44,195804	-1,2392157
sch-MIR7997c-9	146	18,4931507	30,8219178	23,9726027	26,7123288	42,4657534	57,5342466	0,86666667	0,77142857	-57,9	-57,9	0,128707	7,87	-39,657534	-0,933871
sch-MIR8001a	176	15,3409091	32,9545455	18,1818182	33,5227273	33,5227273	66,4772727	1,01724138	0,84375	-69,8	-69,4	0,0309319	23,94	-39,659091	-1,1830508
sch-MIR8001b-1	143	16,0839161	35,6643357	15,3846154	32,8671329	31,4685315	68,5314685	0,92156863	1,04545455	-65,7	-64,5	0,152633	3,79	-45,944056	-1,46
sch-MIR8001b-2	154	17,5324675	33,7662338	14,2857143	34,4155844	31,8181818	68,1818182	1,01923077	1,22727273	-61,4	-61,4	0,0960631	8,67	-39,87013	-1,2530612
sch-MIR8001b-3	162	16,6666667	33,9506173	14,1975309	35,1851852	30,8641975	69,1358025	1,03636364	1,17391304	-60,6	-60,2	0,00959078	14,68	-37,407407	-1,212
sch-MIR8001b-4	92	17,3913043	31,5217391	15,2173913	35,8695652	32,6086957	67,3913043	1,13793103	1,14285714	-40,6	-39,7	0,0765879	6,99	-44,130435	-1,3533333
sch-MIR8001b-5	91	19,7802198	36,2637363	13,1868132	30,7692308	32,967033	67,032967	0,84848485	1,5	-28,6	-28,6	0,156502	7,54	-31,428571	-0,9533333
sch-MIR8001b-6	96	20,8333333	34,375	12,5	32,2916667	33,3333333	66,6666667	0,93939394	1,66666667	-38,9	-38,9	0,0375793	8,53	-40,520833	-1,215625
sch-MIR8003	126	19,047619	26,984127	12,6984127	41,2698413	31,7460317	68,2539683	1,52941176	1,5	-32,5	-32,5	0,0788555	7,75	-25,793651	-0,8125
sch-MIR8005c	184	19,0217391	32,0652174	13,0434783	35,8695652	32,0652174	67,9347826	1,11864407	1,45833333	-47,8	-42,8	3,29E-05	36,26	-25,978261	-0,8101695
sch-MIR8006-1	325	16	30,4615385	18,7692308	34,7692308	34,7692308	65,2307692	1,14141414	0,85245902	-89,5	-85,99	1,52E-05	48	-27,538462	-0,7920354
sch-MIR8006-2	209	16,7464115	29,6650718	20,5741627	33,0143541	37,3205742	62,6794258	1,11290323	0,81395349	-83,9	-83,9	0,0522789	14,47	-40,143541	-1,075641
sch-MIR8006-3	78	25,6410256	30,7692308	20,5128205	23,0769231	46,1538462	53,8461538	0,75	1,25	-33	-32,6	0,240065	2,04	-42,307692	-0,9166667
sch-MIR8006-4	209	19,138756	29,1866029	17,7033493	33,9712919	36,8421053	63,1578947	1,16393443	1,08108108	-85,4	-83,9	0,0188249	14,9	-40,861244	-1,1090909
sch-MIR8006-5	289	16,9550173	33,9100346	17,6470588	31,4878893	34,6020761	65,3979239	0,92857143	0,96078431	-80,2	-77,3	0,00019002	27,34	-27,750865	-0,802
sch-MIR8006-6	225	16	33,3333333	19,5555556	31,1111111	35,5555556	64,4444444	0,93333333	0,81818182	-83,6	-76,94	0,00087531	27,03	-37,155556	-1,045
sch-MIR8006-7	166	24,0963855	29,5180723	18,0722892	28,313253	42,1686747	57,8313253	0,95918367	1,33333333	-80,9	-76,7	0,00633245	15,39	-48,73494	-1,1557143
sch-MIR8006-8	217	20,2764977	34,1013825	15,2073733	30,4147465	35,483871	64,516129	0,89189189	1,33333333	-64,6	-53,89	0,0002163	48,96	-29,769585	-0,838961
sch-MIR8008b-1	67	19,4029851	25,3731343	14,9253731	40,2985075	34,3283582	65,6716418	1,58823529	1,3	-37,9	-37,5	0,249103	2,92	-56,567164	-1,6478261
sch-MIR8008b-2	74	18,9189189	31,0810811	12,1621622	37,8378378	31,0810811	68,9189189	1,2173913	1,55555556	-20,6	-20,6	0,0262956	12,06	-27,837838	-0,8956522
sch-MIR8008b-3	177	16,9491525	30,5084746	20,9039548	31,6384181	37,8531073	62,1468927	1,03703704	0,81081081	-53,5	-43,3	0,0110531	54,59	-30,225989	-0,7985075
sch-MIR8008b-4	191	16,7539267	29,3193717	18,8481675	35,078534	35,6020942	64,3979058	1,19642857	0,88888889	-58,7	-43,03	0,00408526	69,71	-30,732984	-0,8632353
sch-MIR8009-1	126	16,6666667	30,952381	18,2539683	34,1269841	34,9206349	65,0793651	1,1025641	0,91304348	-46,4	-44,7	0,0382957	13,09	-36,825397	-1,0545455
sch-MIR8009-2	107	24,2990654	27,1028037	18,6915888	29,9065421	42,9906542	57,0093458	1,10344828	1,3	-52,7	-50,9	0,054982	12,34	-49,252336	-1,1456522

sch-MIR8011a-1	99	18,1818182	30,3030303	23,2323232	28,2828283	41,4141414	58,5858586	0,93333333	0,7826087	-50,2	-50,2	0,400147	1,79	-50,707071	-1,2243902
sch-MIR8011a-2	97	22,6804124	27,8350515	18,556701	30,9278351	41,2371134	58,7628866	1,11111111	1,22222222	-50,9	-50,9	0,274503	3,31	-52,474227	-1,2725
sch-MIR8011a-3	135	20	31,1111111	20	28,8888889	40	60	0,92857143	1	-49,7	-46,9	0,0443706	9,17	-36,814815	-0,9203704
sch-MIR8011a-4	288	20,8333333	33,6805556	14,5833333	30,9027778	35,4166667	64,5833333	0,91752577	1,42857143	-71,6	-62,45	0,00016189	56,52	-24,861111	-0,7019608
sch-MIR8011a-5	171	21,6374269	28,6549708	16,374269	33,3333333	38,0116959	61,9883041	1,16326531	1,32142857	-85	-79,5	0,0317615	15,81	-49,707602	-1,3076923
sch-MIR8013-1	175	20	30,2857143	17,7142857	32	37,7142857	62,2857143	1,05660377	1,12903226	-78,7	-62,45	0,0023853	69,89	-44,971429	-1,1924242
sch-MIR8013-2	189	19,5767196	29,6296296	16,4021164	34,3915344	35,978836	64,021164	1,16071429	1,19354839	-84,9	-81,5	0,00390039	21,96	-44,920635	-1,2485294
sch-MIR8014	205	18,0487805	37,5609756	13,1707317	31,2195122	31,2195122	68,7804878	0,83116883	1,37037037	-60	-58,8	0,00382286	28,89	-29,268293	-0,9375
sch-MIR8018	73	19,1780822	27,3972603	23,2876712	30,1369863	42,4657534	57,5342466	1,1	0,82352941	-33,9	-33,9	0,268682	3,95	-46,438356	-1,0935484
sch-MIR8020	121	19,0082645	35,5371901	17,3553719	28,0991736	36,3636364	63,6363636	0,79069767	1,0952381	-55,2	-55,2	0,102968	4,64	-45,619835	-1,2545455
sch-MIR8021-1	221	15,8371041	31,2217195	15,3846154	37,5565611	31,2217195	68,7782805	1,20289855	1,02941176	-58,3	-53,2	0,00290399	32,77	-26,38009	-0,8449275
sch-MIR8021-2	242	21,4876033	33,0578512	14,8760331	30,5785124	36,3636364	63,6363636	0,925	1,44444444	-71,6	-63,9	0,00065548	32,7	-29,586777	-0,8136364
sch-MIR8022-1	235	22,5531915	28,5106383	16,1702128	32,7659574	38,7234043	61,2765957	1,14925373	1,39473684	-65,5	-49,9	0,00116465	51,54	-27,87234	-0,7197802
sch-MIR8022-2	231	22,0779221	30,3030303	16,017316	31,6017316	38,0952381	61,9047619	1,04285714	1,37837838	-67,4	-54,4	0,00602765	50,8	-29,177489	-0,7659091
sch-MIR8025-1	215	14,4186047	33,4883721	15,8139535	36,2790698	30,2325581	69,7674419	1,08333333	0,91176471	-87,6	-87,6	0,0796043	9,35	-40,744186	-1,3476923
sch-MIR8025-2	208	15,8653846	36,0576923	14,9038462	33,1730769	30,7692308	69,2307692	0,92	1,06451613	-79,8	-79,6	0,0248841	11,11	-38,365385	-1,246875
sch-MIR8026-1	203	22,6600985	33,0049261	14,7783251	29,5566502	37,4384236	62,5615764	0,89552239	1,53333333	-59	-48,4	0,00360806	45,12	-29,064039	-0,7763158
sch-MIR8026-2	115	22,6086957	29,5652174	19,1304348	28,6956522	41,7391304	58,2608696	0,97058824	1,18181818	-37,3	-37,1	0,0278083	9,53	-32,434783	-0,7770833
sch-MIR8030-1	119	19,3277311	35,2941176	13,4453782	31,9327731	32,7731092	67,2268908	0,9047619	1,4375	-29,6	-24,2	0,0273194	32,12	-24,87395	-0,7589744
sch-MIR8030-2	105	14,2857143	31,4285714	22,8571429	31,4285714	37,1428571	62,8571429	1	0,625	-28,2	-28,2	0,238247	3,8	-26,857143	-0,7230769
sch-MIR8030-3	124	19,3548387	34,6774194	12,9032258	33,0645161	32,2580645	67,7419355	0,95348837	1,5	-30	-25,4	0,00960944	28,66	-24,193548	-0,75
sch-MIR8030-4	73	20,5479452	28,7671233	15,0684932	35,6164384	35,6164384	64,3835616	1,23809524	1,36363636	-24,1	-23,9	0,0694209	8,6	-33,013699	-0,9269231
sch-MIR8030-5	108	16,6666667	30,5555556	22,2222222	30,5555556	38,8888889	61,1111111	1	0,75	-33,8	-33,8	0,100817	7,53	-31,296296	-0,8047619
sch-MIR8032e	285	17,8947368	31,5789474	13,3333333	36,8421053	31,2280702	68,4210526	1,16666667	1,34210526	-66	-64,8	0,00036518	40,13	-23,157895	-0,741573
sch-MIR8033	72	16,6666667	31,9444444	16,6666667	34,7222222	33,3333333	66,6666667	1,08695652	1	-36,3	-36,3	0,152784	4,21	-50,416667	-1,5125
sch-MIR8038b-1	98	17,3469388	28,5714286	21,4285714	32,6530612	38,7755102	61,2244898	1,14285714	0,80952381	-27,2	-27,2	0,200082	4,53	-27,755102	-0,7157895
sch-MIR8038b-2	180	20	30	14,4444444	35,5555556	34,4444444	65,5555556	1,18518519	1,38461538	-51,1	-50,6	0,0216371	9,3	-28,388889	-0,8241935
sch-MIR8038b-3	136	19,1176471	30,1470588	18,3823529	32,3529412	37,5	62,5	1,07317073	1,04	-60,4	-60,4	0,0512838	8,29	-44,411765	-1,1843137
sch-MIR8039-1	208	22,5961538	31,7307692	12,9807692	32,6923077	35,5769231	64,4230769	1,03030303	1,74074074	-61,3	-50,12	0,00061397	39,58	-29,471154	-0,8283784
sch-MIR8039-2	142	24,6478873	32,3943662	12,6760563	30,2816901	37,3239437	62,6760563	0,93478261	1,94444444	-51,9	-47	0,0126501	17,32	-36,549296	-0,9792453
sch-MIR8039-3	142	21,8309859	35,2112676	13,3802817	29,5774648	35,2112676	64,7887324	0,84	1,63157895	-47,6	-45,2	0,241762	10,17	-33,521127	-0,952
sch-MIR8040	245	17,9591837	30,2040816	15,5102041	36,3265306	33,4693878	66,5306122	1,2027027	1,15789474	-83,8	-73,8	0,00012796	48,44	-34,204082	-1,0219512
sch-MIR8042	99	20,2020202	35,3535354	17,1717172	27,2727273	37,3737374	62,6262626	0,77142857	1,17647059	-33,3	-33,1	0,140233	6,51	-33,636364	-0,9
sch-MIR8045	236	23,3050847	30,9322034	13,1355932	32,6271186	36,440678	63,559322	1,05479452	1,77419355	-69,1	-60,8	0,00082127	46,67	-29,279661	-0,8034884
sch-MIR8046-1	136	22,0588235	30,8823529	16,9117647	30,1470588	38,9705882	61,0294118	0,97619048	1,30434783	-70,5	-70,5	0,427839	1,71	-51,838235	-1,3301887
sch-MIR8046-2	122	18,852459	26,2295082	18,0327869	36,8852459	36,8852459	63,1147541	1,40625	1,04545455	-33,5	-33,3	0,189634	7,83	-27,459016	-0,7444444
sch-MIR8047	208	16,3461538	32,2115385	19,2307692	32,2115385	35,5769231	64,4230769	1	0,85	-60,5	-50,4	0,00067703	26,73	-29,086538	-0,8175676
sch-MIR812f	217	19,8156682	31,3364055	17,9723502	30,875576	37,7880184	62,2119816	0,98529412	1,1025641	-99,2	-99,2	0,0553984	7,52	-45,714286	-1,2097561
sch-MIR812o	160	20,625	25,625	18,125	35,625	38,75	61,25	1,3902439	1,13793103	-66,5	-60,8	0,00171829	19,78	-41,5625	-1,0725806
sch-MIR8132	203	20,1970443	27,5862069	16,2561576	35,9605911	36,453202	63,546798	1,30357143	1,24242424	-80,9	-80,4	0,0562191	9,8	-39,852217	-1,0932432
sch-MIR8138-1	171	17,5438596	33,3333333	18,7134503	30,4093567	36,2573099	63,7426901	0,9122807	0,9375	-81	-79,8	0,0964599	8,57	-47,368421	-1,3064516
sch-MIR8138-2	171	18,128655	32,748538	18,128655	30,994152	36,2573099	63,7426901	0,94642857	1	-81,3	-80	0,0399073	9,28	-47,54386	-1,3112903
sch-MIR8151	216	15,2777778	36,5740741	15,2777778	32,8703704	30,5555556	69,4444444	0,89873418	1	-70,4	-64,57	0,0039358	25,46	-32,592593	-1,0666667
sch-MIR827	111	26,1261261	20,7207207	16,2162162	36,9369369	42,3423423	57,6576577	1,7826087	1,61111111	-37,6	-34,7	0,0380954	32,01	-33,873874	-0,8
sch-MIR828b	119	17,6470588	29,4117647	17,6470588	35,2941176	35,2941176	64,7058824	1,2	1	-50,2	-50,2	0,0903238	5,37	-42,184874	-1,1952381
sch-MIR829	113	15,9292035	28,3185841	16,8141593	38,9380531	32,7433628	67,2566372	1,375	0,94736842	-30	-29,6	0,103738	9,56	-26,548673	-0,8108108
sch-MIR830	78	20,5128205	32,0512821	11,5384615	35,8974359	32,0512821	67,9487179	1,12	1,77777778	-23	-23	0,0479318	6,27	-29,487179	-0,92
sch-MIR837	219	23,7442922	25,1141553	15,5251142	35,6164384	39,2694064	60,7305936	1,41818182	1,52941176	-60,3	-59	0,0032809	24,1	-27,534247	-0,7011628
sch-MIR838	309	17,4757282	32,6860841	18,4466019	31,3915858	35,9223301	64,0776699	0,96039604	0,94736842	-81,7	-68,8	0,00081616	45,32	-26,440129	-0,736036
sch-MIR844-1	253	18,972332	28,458498	16,2055336	35,9683794	35,1778656	64,4268775	1,26388889	1,17073171	-79,3	-75,6	0,00054351	33,03	-31,343874	-0,8910112
sch-MIR844-2	211	19,9052133	27,014218	16,5876777	36,492891	36,492891	63,507109	1,35087719	1,2	-80	-80	0,0164053	10,87	-37,914692	-1,038961
sch-MIR845e	124	20,9677419	38,7096774	11,2903226	29,0322581	32,2580645	67,7419355	0,75	1,85714286	-36,7	-32,6	0,0175781	18,76	-29,596774	-0,9175
sch-MIR857-1	172	18,0232558	32,5581395	17,4418605	31,9767442	35,4651163	64,5348837	0,98214286	1,03333333	-54	-51,8	0,0142775	25,63	-31,395349	-0,8852459
sch-MIR857-2	199	18,0904523	31,6582915	14,0703518	36,1809045	32,160804	67,839196	1,14285714	1,28571429	-46,4	-45,3	0,0133553	19,22	-23,316583	-0,725
sch-MIR857-3	275	15,6363636	36	16,7272727	31,6363636	32,3636364	67,6363636	0,87878788	0,93478261	-82	-77,2	0,00308674	36,58	-29,818182	-0,9213483
sch-MIR8578	214	17,7570093	28,9719626	15,8878505	37,3831776	33,6448598	66,3551402	1,29032258	1,11764706	-52,5	-30,9	0,00290595	55,58	-24,53271	-0,7291667
sch-MIR8586	167	16,7664671	41,9161677	14,3712575	26,9461078	31,1377246	68,8622754	0,64285714	1,16666667	-44,7	-42	0,00803506	22,82	-26,766467	-0,8596154
sch-MIR860	246	21,9512195	31,7073171	12,601626	33,7398374	34,5528455	65,4471545	1,06410256	1,74193548	-70,4	-66,6	0,00372891	46,45	-28,617886	-0,8282353
sch-MIR8601	232	17,2413793	21,9827586	17,6724138	43,1034483	34,9137931	65,0862069	1,96078431	0,97560976	-60	-46,1	0,00482723	41,69	-25,862069	-0,7407407
sch-MIR8610	146	26,7123288	22,6027397	23,2876712	27,3972603	50	50	1,21212121	1,14705882	-54,3	-54,3	0,0647695	19,4	-37,191781	-0,7438356
sch-MIR863-1	203	18,226601	37,4384236	14,2857143	30,0492611	32,5123153	67,4876847	0,80263158	1,27586207	-73,9	-73,92	0,0897604	8,7	-36,413793	-1,12
sch-MIR863-2	135	14,0740741	31,8518519	16,2962963	37,7777778	30,3703704	69,6296296	1,18604651	0,86363636	-31,9	-27,7	0,0133857	18,43	-23,62963	-0,7780488
sch-MIR863-3	249	18,4738956	30,5220884	12,4497992	38,5542169	30,9236948	69,0763052	1,26315789	1,48387097	-61,4	-42,8	9,58E-05	71,25	-24,658635	-0,7974026
sch-MIR8634	287	27,5261324	25,4355401	14,2857143	32,4041812	41,8118467	57,8397213	1,2739726	1,92682927	-88,3	-78,4	0,00034011	38,43	-30,766551	-0,7358333
sch-MIR865-1	165	13,9393939	38,7878788	17,5757576	29,6969697	31,5151515	68,4848485	0,765625	0,79310345	-41,5	-35,02	0,0161857	33,69	-25,151515	-0,7980769
sch-MIR865-2	185	18,9189189	31,3513514	14,5945946	35,1351351	33,5135135	66,4864865	1,12068966	1,2962963	-90,7	-90,7	0,105372	4,88	-49,027027	-1,4629032

sch-MIR865-3	270	17,4074074	35,1851852	13,3333333	34,0740741	30,7407407	69,2592593	0,96842105	1,30555556	-60,6	-49	0,00073087	53	-22,444444	-0,7301205
sch-MIR8666	286	18,8811189	33,5664336	12,2377622	35,3146853	31,1188811	68,8811189	1,05208333	1,54285714	-64,7	-58	0,00013063	71,31	-22,622378	-0,7269663
sch-MIR8668	86	25,5813953	31,3953488	11,627907	31,3953488	37,2093023	62,7906977	1	2,2	-24,5	-24,3	0,486608	5,02	-28,488372	-0,765625
sch-MIR867	175	17,1428571	37,1428571	14,8571429	30,8571429	32	68	0,83076923	1,15384615	-75,2	-74,6	0,0534158	9,49	-42,971429	-1,3428571
sch-MIR8724	191	25,1308901	25,1308901	20,4188482	29,3193717	45,5497382	54,4502618	1,16666667	1,23076923	-62,5	-58,5	0,00289409	31,35	-32,722513	-0,7183908
sch-MIR8727	124	16,9354839	29,8387097	26,6129032	26,6129032	43,5483871	56,4516129	0,89189189	0,63636364	-45,8	-45,3	0,0391571	12,43	-36,935484	-0,8481481
sch-MIR8739	223	21,0762332	30,044843	17,9372197	30,941704	39,0134529	60,9865471	1,02985075	1,175	-90,4	-90,3	0,0130373	18,69	-40,538117	-1,0390805
sch-MIR8740	241	20,3319502	37,7593361	12,4481328	29,4605809	32,780083	67,219917	0,78021978	1,63333333	-57,7	-40,3	8,75E-05	69,4	-23,941909	-0,7303797
sch-MIR8743e	142	19,7183099	33,8028169	12,6760563	33,8028169	32,3943662	67,6056338	1	1,55555556	-54,1	-53,4	0,0367162	15,11	-38,098592	-1,176087
sch-MIR8762c	86	24,4186047	32,5581395	11,627907	31,3953488	36,0465116	63,9534884	0,96428571	2,1	-23,7	-23,7	0,457726	5,52	-27,55814	-0,7645161
sch-MIR902a	111	14,4144144	40,5405405	16,2162162	28,8288288	30,6306306	69,3693694	0,71111111	0,88888889	-32,7	-32,7	0,0570209	5,39	-29,459459	-0,9617647
sch-MIR902j	321	17,4454829	32,0872274	14,3302181	36,1370717	31,7757009	68,2242991	1,12621359	1,2173913	-85,8	-79,8	0,00013326	46,25	-26,728972	-0,8411765
sch-MIR917	209	17,2248804	25,8373206	18,1818182	38,7559809	35,4066986	64,5933014	1,5	0,94736842	-80,2	-80,2	0,013951	11,1	-38,373206	-1,0837838
sch-MIR9469-1	141	20,5673759	27,6595745	24,1134752	27,6595745	44,6808511	55,3191489	1	0,85294118	-89	-88,3	0,130135	5,67	-63,120567	-1,4126984
sch-MIR9469-2	143	23,7762238	27,2727273	21,6783217	27,2727273	45,4545455	54,5454545	1	1,09677419	-94,7	-94,7	0,267161	2,59	-66,223776	-1,4569231
sch-MIR9471a-1	181	24,3093923	32,0441989	10,4972376	33,1491713	34,8066298	65,1933702	1,03448276	2,31578947	-59,6	-57,19	0,015869	19,25	-32,928177	-0,9460317
sch-MIR9471a-2	142	19,7183099	33,0985915	14,7887324	32,3943662	34,5070423	65,4929577	0,9787234	1,33333333	-58,2	-58,2	0,0478358	6,41	-40,985915	-1,1877551
sch-MIR9471a-3	150	20	32,6666667	14	33,3333333	34	66	1,02040816	1,42857143	-57,5	-57,5	0,117983	12,97	-38,333333	-1,127451
sch-MIR9471b	147	25,8503401	29,2517007	14,2857143	30,6122449	40,1360544	59,8639456	1,04651163	1,80952381	-69,5	-69,5	0,0546444	8,31	-47,278912	-1,1779661
sch-MIR9473	120	18,3333333	33,3333333	17,5	30,8333333	35,8333333	64,1666667	0,925	1,04761905	-52,4	-51	0,215142	6,05	-43,666667	-1,2186047
sch-MIR9474-1	187	16,0427807	37,4331551	14,973262	31,5508021	31,0160428	68,9839572	0,84285714	1,07142857	-78,4	-78,4	0,0268638	18,04	-41,925134	-1,3517241
sch-MIR9474-2	259	20,0772201	38,6100386	11,969112	29,3436293	32,046332	67,953668	0,76	1,67741935	-61,4	-54,2	0,00028169	52,24	-23,706564	-0,739759
sch-MIR9476-1	109	16,5137615	33,0275229	16,5137615	33,9449541	33,0275229	66,9724771	1,02777778	1	-64,3	-62,6	0,0663692	6,4	-58,990826	-1,7861111
sch-MIR9476-2	111	16,2162162	34,2342342	17,1171171	32,4324324	33,3333333	66,6666667	0,94736842	0,94736842	-63,5	-63,5	0,0754442	7,05	-57,207207	-1,7162162
sch-MIR9477	119	20,1680672	28,5714286	18,487395	32,7731092	38,6554622	61,3445378	1,14705882	1,09090909	-72,9	-68,6	0,175858	6,61	-61,260504	-1,5847826
sch-MIR9478-1	301	17,9401993	32,5581395	16,9435216	32,5581395	34,8837209	65,1162791	1	1,05882353	-94,4	-90,1	0,00050444	49,33	-31,362126	-0,8990476
sch-MIR9478-2	118	19,4915254	33,0508475	15,2542373	32,2033898	34,7457627	65,2542373	0,97435897	1,27777778	-31,8	-27,4	0,0246224	16,12	-26,949153	-0,7756098
sch-MIR9555b-1	291	20,6185567	31,2714777	14,4329897	33,6769759	35,0515464	64,9484536	1,07692308	1,42857143	-72,9	-58,7	0,00010456	58,41	-25,051546	-0,7147059
sch-MIR9555b-2	222	16,6666667	28,3783784	13,963964	40,990991	30,6306306	69,3693694	1,44444444	1,19354839	-54,2	-47,8	0,00029299	44,06	-24,414414	-0,7970588
sch-MIR9562-1	314	15,2866242	29,6178344	15,6050955	39,4904459	30,8917197	69,1082803	1,33333333	0,97959184	-73	-66,7	4,02E-05	57,57	-23,248408	-0,7525773
sch-MIR9562-2	225	15,5555556	28,4444444	20,8888889	35,1111111	36,4444444	63,5555556	1,234375	0,74468085	-57,5	-56,7	0,00849735	16,13	-25,555556	-0,7012195
sch-MIR9563a	139	23,0215827	24,4604317	23,0215827	29,4964029	46,0431655	53,9568345	1,20588235	1	-53,8	-53,8	0,0230631	8,02	-38,705036	-0,840625
sch-MIR9563b	201	19,4029851	33,8308458	17,4129353	29,3532338	36,8159204	63,1840796	0,86764706	1,11428571	-75,8	-62,2	0,00312937	28,45	-37,711443	-1,0243243
sch-MIR9652	268	19,4029851	30,5970149	13,8059701	36,1940299	33,2089552	66,7910448	1,18292683	1,40540541	-64	-60,8	0,0001299	47,67	-23,880597	-0,7191011
sch-MIR9736	152	13,8157895	35,5263158	17,1052632	33,5526316	30,9210526	69,0789474	0,94444444	0,80769231	-82,4	-82,4	0,255213	3,38	-54,210526	-1,7531915
sch-MIR9749-1	135	22,2222222	34,0740741	15,5555556	28,1481481	37,7777778	62,2222222	0,82608696	1,42857143	-38,3	-38,1	0,0519476	8,36	-28,37037	-0,7509804
sch-MIR9749-2	266	13,9097744	35,3383459	18,0451128	32,7067669	31,9548872	68,0451128	0,92553191	0,77083333	-73,1	-70,5	0,00259751	38,83	-27,481203	-0,86
sch-MIR9760-1	137	20,4379562	26,2773723	11,6788321	41,6058394	32,1167883	67,8832117	1,58333333	1,75	-42,7	-42,5	0,0520996	16,09	-31,167883	-0,9704545
sch-MIR9760-2	112	29,4642857	26,7857143	6,25	37,5	35,7142857	64,2857143	1,4	4,71428571	-29,4	-29,4	0,338178	6,72	-26,25	-0,735
sch-MIR9762	287	18,1184669	35,5400697	13,5888502	32,7526132	31,7073171	68,2926829	0,92156863	1,33333333	-72	-66,2	0,00049711	37,89	-25,087108	-0,7912088
sch-MIR9773-1	182	19,2307692	29,6703297	17,032967	34,0659341	36,2637363	63,7362637	1,14814815	1,12903226	-89,9	-89,5	0,00429514	20,54	-49,395604	-1,3621212

Supplementary Table S18. Thermodynamic and structural characterization of *Solanum peruvianum* pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Size	G content	A content	C content	U content	GC content	AU content	UA-ratio	GC-ratio	MFE	MFEE	Freq	Div	AMFE	MFEI
spr-MIR10528-1	97	18,556701	35,0515464	17,5257732	28,8659794	36,0824742	63,9175258	0,82352941	1,05882353	-42	-42,3	0,0530642	7,51	-43,608247	-1,2085714
spr-MIR10528-2	95	18,9473684	28,4210526	17,8947368	34,7368421	36,8421053	63,1578947	1,22222222	1,05882353	-48	-48,1	0,17202	2,69	-50,631579	-1,3742857
spr-MIR11091	117	20,5128205	40,1709402	15,3846154	23,9316239	35,8974359	64,1025641	0,59574468	1,33333333	-34	-24,9	0,0144489	33,35	-29,316239	-0,8166667
spr-MIR1511	196	23,9795918	24,4897959	20,4081633	31,122449	44,3877551	55,6122449	1,27083333	1,175	-65	-63	0,0194193	13,44	-33,010204	-0,7436782
spr-MIR1520a	213	21,5962441	24,4131455	16,9014085	37,0892019	38,4976526	61,5023474	1,51923077	1,27777778	-59	-42,8	0,00215505	74,95	-27,699531	-0,7195122
spr-MIR1521a	77	15,5844156	33,7662338	18,1818182	32,4675325	33,7662338	66,2337662	0,96153846	0,85714286	-20	-20,1	0,662899	2,81	-26,103896	-0,7730769
spr-MIR166k	157	20,3821656	28,6624204	18,4713376	32,4840764	38,8535032	61,1464968	1,13333333	1,10344828	-59	-58,3	0,101382	9,47	-37,324841	-0,9606557
spr-MIR1886f	106	16,0377359	34,9056604	15,0943396	33,9622642	31,1320755	68,8679245	0,97297297	1,0625	-26	-25,6	0,0104879	11,91	-24,150943	-0,7206107
spr-MIR1918	222	20,7207207	22,0720721	13,5135135	43,6936937	34,2342342	65,7657658	1,97959184	1,53333333	-58	-57,8	0,0106143	14,79	-26,126126	-0,7631579
spr-MIR3448	104	23,0769231	34,6153846	13,4615385	28,8461539	36,5384615	63,4615385	0,83333333	1,71428571	-29	-29	0,201646	6,65	-27,884615	-0,7631579
spr-MIR3710h	260	26,1538462	23,8461539	19,2307692	30,7692308	45,3846154	54,6153846	1,29032258	1,36	-86	-77	0,00130243	45,24	-32,961538	-0,7757576
spr-MIR393	290	21,7241379	22,7586207	24,137931	31,3793103	45,862069	54,137931	1,37878788	0,9	-100	-98,4	0,00087651	30,95	-34,448276	-0,7511278
spr-MIR482b	227	25,1101322	28,6343612	18,5022026	27,753304	43,6123348	56,3876652	0,96923077	1,35714286	-72	-64,4	0,00904893	13,4	-31,718062	-0,7272727
spr-MIR5016	179	19,5530726	33,5195531	15,6424581	31,2849162	35,1955307	64,8044693	0,93333333	1,25	-47	-40,4	0,00088811	27,54	-25,977654	-0,7380952
spr-MIR5021-1	162	19,7530864	35,8024691	10,4938272	33,9506173	30,2469136	69,7530864	0,94827586	1,88235294	-38	-26,8	0,00338954	49,73	-23,518519	-0,7225
spr-MIR5021-2	137	18,2481752	32,8467153	16,0583942	32,8467153	34,3065693	65,6934307	1	1,13636364	-36	-34,6	0,00787538	13,61	-26,20438	-0,7638298
spr-MIR5303	146	22,6027397	26,7123288	17,8082192	32,8767123	40,4109589	59,5890411	1,23076923	1,26923077	-63	-63,1	0,121448	7,94	-43,287671	-1,0711864
spr-MIR5303d-1	126	23,015873	24,6031746	23,8095238	28,5714286	46,8253968	53,1746032	1,16129032	0,96666667	-66	-66,1	0,183568	4,24	-52,460317	-1,120339
spr-MIR5303f-1	120	27,5	26,6666667	18,3333333	27,5	45,8333333	54,1666667	1,03125	1,5	-56	-55,9	0,252072	4,39	-46,583333	-0,956
spr-MIR5303f-2	127	25,984252	28,3464567	18,8976378	26,7716535	44,8818898	55,1181102	0,94444444	1,375	-68	-67,6	0,199084	2,29	-53,228346	-0,7262712
spr-MIR5303h-1	110	19,0909091	27,2727273	27,2727273	26,3636364	46,3636364	53,6363636	0,96666667	0,7	-55	-55,2	0,348255	3,55	-50,181818	-0,8870588
spr-MIR5303h-3	116	22,4137931	25	24,137931	28,4482759	46,5517241	53,4482759	1,13793103	0,92857143	-53	-53,4	0,07251	5,56	-46,034483	-0,9888889
spr-MIR5303h-4	130	16,1538462	33,8461539	24,6153846	25,3846154	40,7692308	59,2307692	0,75	0,65625	-43	-42,2	0,231471	6,32	-32,923077	-0,8075472
spr-MIR5303h-5	159	17,6100629	35,2201258	18,8679245	28,3018868	36,4779874	63,5220126	0,80357143	0,93333333	-55	-54,5	0,0396588	8	-34,339623	-0,9413793
spr-MIR5303h-6	136	21,3235294	32,3529412	17,6470588	28,6764706	38,9705882	61,0294118	0,88636364	1,20833333	-48	-46,3	0,0486362	8,21	-35	-0,8981132
spr-MIR5303i-1	121	15,7024793	34,7107438	20,661157	28,9256198	36,3636364	63,6363636	0,83333333	0,76	-39	-39,1	0,42596	2,38	-32,31405	-0,8886364
spr-MIR5303i-2	162	17,9012346	27,7777778	21,6049383	32,7160494	39,5061728	60,4938272	1,17777778	0,82857143	-49	-49,3	0,0316103	15,21	-30,432099	-0,7703125
spr-MIR5368-1	171	32,1637427	20,4678363	25,7309942	21,6374269	57,8947368	42,1052632	1,05714286	1,25	-73	-50,4	0,0121474	38	-42,807018	-0,955102
spr-MIR5368-2	83	28,9156627	25,3012048	25,3012048	20,4819277	54,2168675	45,7831325	0,80952381	1,14285714	-33	-33	0,448662	1,92	-39,759036	-0,7333333
spr-MIR5566	96	22,9166667	29,1666667	22,9166667	25	45,8333333	54,1666667	0,85714286	1	-32	-31,8	0,138675	3,1	-33,229167	-0,725
spr-MIR5633	214	24,2990654	30,8411215	19,1588785	25,7009346	43,4579439	56,5420561	0,83333333	1,26829268	-67	-62,5	0,0045882	15,33	-31,214953	-0,7182796
spr-MIR5658	232	19,8275862	31,8965517	18,1034483	30,1724138	37,9310345	62,0689655	0,94594595	1,0952381	-63	-51,7	0,00043405	44,69	-27,327586	-0,7204545
spr-MIR6022-1	238	18,907563	32,3529412	19,3277311	29,4117647	38,2352941	61,7647059	0,90909091	0,97826087	-79	-72,2	0,00763077	37,14	-33,361345	-0,7674419
spr-MIR6022-2	238	19,7478992	30,6722689	18,907563	30,6722689	38,6554622	61,3445378	1	1,04444444	-80	-72,4	0,00792575	37,4	-33,445378	-0,8375
spr-MIR6034	173	26,0115607	28,3236994	19,0751445	26,5895954	45,0867052	54,9132948	0,93877551	1,36363636	-61	-60,8	0,0312204	9,85	-35,202312	-0,7807692
spr-MIR6284	126	22,2222222	29,3650794	20,6349206	27,7777778	42,8571429	57,1428571	0,94594595	1,07692308	-39	-36,9	0,015598	11,35	-31,031746	-0,7240741
spr-MIR7822	160	18,125	28,125	16,25	37,5	34,375	65,625	1,33333333	1,11538462	-48	-47,2	0,0117547	20,63	-30,1875	-0,9896104
spr-MIR7981a	100	25	22	23	30	48	52	1,36363636	1,08695652	-48	-47,8	0,0959116	12,91	-47,8	-0,9958333
spr-MIR7981b	100	23	30	25	22	48	52	0,73333333	0,92	-47	-46,8	0,0705881	8,38	-46,8	-0,975
spr-MIR7983-1	132	19,6969697	35,6060606	12,8787879	31,8181818	32,5757576	67,4242424	0,89361702	1,52941177	-33	-33,6	0,0134425	21,66	-25	-1,0163636
spr-MIR7983-2	103	18,4466019	35,9223301	12,6213592	33,0097087	31,0679612	68,9320388	0,91891892	1,46153846	-25	-25,2	0,0295328	9,31	-24,466019	-0,7875
spr-MIR7992	216	18,5185185	35,6481482	15,7407407	30,0925926	34,2592593	65,7407407	0,84415584	1,17647059	-56	-45,84	0,0160928	32,84	-25,972222	-0,9333333
spr-MIR7997c-1	136	17,6470588	28,6764706	21,3235294	32,3529412	38,9705882	61,0294118	1,12820513	0,82758621	-50	-49,6	0,0225853	9,03	-36,985294	-0,9490566
spr-MIR7997c-2	97	21,6494845	29,8969072	19,5876289	28,8659794	41,2371134	58,7628866	0,96551724	1,10526316	-29	-28,9	0,0648285	10,02	-29,793814	-0,85
spr-MIR7997c-3	264	20,0757576	31,0606061	11,3636364	37,5	31,4393939	68,5606061	1,20731707	1,76666667	-61	-54,8	0,00040188	50,29	-23,106061	-0,7349398
spr-MIR7997c-4	98	25,5102041	29,5918367	17,3469388	27,5510204	42,8571429	57,1428571	0,93103448	1,47058824	-33	-27	0,0608648	15,93	-33,979592	-0,7928571
spr-MIR7997c-5	97	19,5876289	28,8659794	21,6494845	29,8969072	41,2371134	58,7628866	1,03571429	0,90476191	-31	-30,6	0,145566	5,45	-31,85567	-0,7725
spr-MIR8011a	135	20	31,1111111	20	28,8888889	40	60	0,92857143	1	-50	-46,9	0,042841	9,32	-36,814815	-0,9203704
spr-MIR8047	234	16,2393162	35,4700855	20,0854701	28,2051282	36,3247863	63,6752137	0,79518072	0,80851064	-67	-55,6	0,00020295	29,21	-28,632479	-0,7882353
spr-MIR8718	332	23,1927711	25	16,2650602	35,5421687	39,4578313	60,5421687	1,42168675	1,42592593	-94	-93,6	5,74E-05	38,38	-28,433735	-0,8969697
spr-MIR8767c	137	24,8175183	26,2773723	18,9781022	29,9270073	43,7956204	56,2043796	1,13888889	1,30769231	-43	-37,7	0,0159635	16,26	-31,021898	-0,7083333
spr-MIR9478	77	18,1818182	32,4675325	15,5844156	33,7662338	33,7662338	66,2337662	1,04	1,16666667	-22	-21,4	0,330649	3	-28,831169	-0,8781818

Supplementary Table S19. Thermodynamic and structural characterization of *Solanum pimpinellifollium* LA0480 pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Sequence	Len	G	A	C	U	GC	AU	UA-ratio	GC-ratio	MFE	MFE-ensemble	frequency	diversity	AMFE	MFEI
spiLA0480-MIR10197	UGGUUCAAUUUUUAUGUGAACUUACUUUCGUUUAAUGGUUAAACAAAAGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAUUUCUUAAUUUUGUUUUUCUGUUUUCGGUCAGAUUUUUAUUUUUUCAUGUUGGUUAAAAUUUUAAAAAUAUUUUUUCUUUAGAAAAAGUAAGUUACCUAAAAAAUGAAUUA	**232**	18,534483	27,155172	14,224138	40,086207	32,758621	67,241379	1,4761905	1,3030303	-57,8	-53,6	0,0011966	44	-24,913793	-0,7605263
spiLA0480-MIR10199	UUUAUUUUCUCAUAUACCAAGCAUGGUAUGAUUUUAUACAGUUGGCUCGACUACUACAACUGGUAUGAUACUAGAGUUGGGUUAAGUUUUAUUAGAGGAAAUUAAUUUUAAGAAUAUUCAUUUAAAAUAGUGGUCAAAAUUGAUUGUCAACAAUAUAGCUGAGAGACAACGGGUGUGUAUCAUUAGGUCAGACAUGCAUCAUUAUACUUGACAUUGCAUUCCAUUGCAUUGCACGUACUUAUUAUUAGUGAACUUGAUAUCGUGUUUUGCUGAUCUUCUGAUUUCCUCCUGUGGAACUUGUAAUAGAUCAAUAUUGAGCUUGUUAUUGUGAAUAUGUACUCCGUGAAAAGUUGCGACUUUUAUGAAGAGUUGCGACUUUCAUAAAGAAUUGCGACUUGUAUGAAAAGUUGUGACUUUUAUGAAAUAUUGUGUUCUUUUAG	**338**	18,639053	29,585799	13,609467	38,16568	32,248521	67,751479	1,29	1,3695652	-77,6	-63,57	1,57E-05	67	-22,95858	-0,7119266
spiLA0480-MIR10203	AAGGAUUGUAACUUUUCCAAAGAGUUGUGACCUUUCCGAUA	**143**	20,979021	28,671329	13,286713	37,062937	34,265734	65,734266	1,2926829	1,5789474	-46,9	-44,4	0,0213085	16	-32,797203	-0,9571429
spiLA0480-MIR10205	CACACACAAUACACAAGAGAAAAAAACAUAAAGUGAAAGUGUUAGUCUAAAAGAGAGUUCUUAUUACUUGAAUGGAGGUGUUUUUUUUUUUUGUGGAGCUUUGGACUCAACUCUUGUCCAGAGUUGUUGAGUUAUACUUUGUGAAGGUUGUUGUAUCAUGGAGGGGACAAGUCAAAGAGGACUACUGUUGGACCGGUGAAAACAUUUGCUACAGUAGACUUGAAUCUCUUUAAAGAGAGCGAGAUAUCCGCGCCUCAGCCUUGAAGAGAUUUAUUUUCUUCAUUUUUUAUUUUCAAUUGUAAUUAUGUAUU	**311**	21,543408	29,903537	13,826367	34,726688	35,369775	64,630225	1,1612903	1,5581395	-78,7	-56,2	4,27E-05	73	-25,305466	-0,7154545
spiLA0480-MIR10215-1	AUAAUAACCUUGAAUCAAUAAUUCAAAUUCAAGUUAGAUUGAAGAGUUAAAUUUUGAGAAUUCUUUCCAAAAUUCUAAGAAAGUCCCUUUUGACACAUUCGAGAGUUCGAGUUAGCUAUGGUGAGUCUCCUUGCUUCCAUAGGAUUUCAUUUACUUUUCAGUUUAGUCAGGAUCUCAUGGGUCGUAUCCCGACUUCCAUAUUUCUCUGUUAGAGGCUUCAUCGAUUGUUAGUAUAGUUGAGGAGUCUGUAUUAAUCUUUUAUUUUAUUAAAUGUUAUAAA	**280**	16,785714	28,571429	15,357143	39,285714	32,142857	67,857143	1,375	1,0930233	-65,2	-63,7	0,0009063	45	-23,285714	-0,7244444
spiLA0480-MIR10215-2	AAUUAGUAACGUAAUAGAAAUAACAUUGUAAUAAUCAAAAAGUAAAAUAGAGAUGUGAAUCAUAGUUCUCCAAAUUGGAGAACUACUAUCCACCUCUUUAUAAUUGCAGAAUAGAGAGUUAAAUAGAGAGUGGUCUAUUUUACUUUCCAAAUAUAGAGAAUGGAGAGUAAAAUAGAGAUGGAUUGGAGAUGGUCUAAGGGGUACGAGAGCCACUCAUACUAUGUCACUUACUCAUAACUCAUGCCCAAGAGCUCGUCACAUAGCUACAGUUUCUAUAAUGAUAGAUGAAGCUUUGGGUACUUACAUUAUUUUUCUUGUUACUAGGC	**326**	19,018405	35,889571	14,723926	30,368098	33,742331	66,257669	0,8461538	1,2916667	-90,6	-88	4,39E-05	42	-27,791411	-0,8236364
spiLA0480-MIR1027c	UGUGCCACAUCCAUCAUUGCUCUUGCAUACAUCUCUUAGAGAAGAUAGGUGGAUGCACCAGGUAUCCCUUCAAUUACAUAUCAUUUCUAUCUUCUCUAGGAGAUGUAUGCAAGAGCAAUGAUGGAUGUGGCGCC	**134**	20,895522	26,119403	22,38806	30,597015	43,283582	56,716418	1,1714286	0,9333333	-93,1	-93,1	0,416422	3,8	-69,477612	-1,6051724
spiLA0480-	GGAUUAUUCAUAUAGAGAUGUCAAAUCUGAAUCA	**145**	18,62069	36,551724	17,241379	27,586207	35,862069	64,137931	0,754717	1,08	-	-34,3	0,0133052	20	-	-

MIR10407b	UCCUAGUUCGAGAAAUACGCCACUAACGGCCCUC GAAUCAUGGAUAAAUCAUCUUAGAGAGUAGAAUC AAGGGAUGAACGGAUUUGUACUCACAAUCUUUAU GAAUAAAAU UUGCUUAGGAUGGAUGAAAGAGAUGUGAGGCAAA CGAAAUUGACAAAUCCAAUUUGGUCCGACCAUUA AUUCAUUUUCUCCUAAAUGAAAUUGCCUCUCCCA									37,4				25,793103	0,7192308
spiLA0480-MIR10410c	CAUCGUUUCUCAAACAAUUUUCAAUUUUACAAUAG UCUCACAUCGGUAUUUCAUCCUUUUUGAGGAU UAAUUUUAUGCACCUUUUGGCUUACGUAACAUCU	**169**	15,384615	30,177515	20,118343	34,319527	35,502959	64,497041	1,1372549	0,7647059	-42,7	-41,9	0,0177465	17	-25,266272	-0,7116667
spiLA0480-MIR10429	AAAUAUCUCGCACGGGUCUCAAUUUCGUGGAGUU ACGGAGUGUGUUACGUAAGACAAAAGAUGUACAA AAUUA	**107**	19,626168	30,841121	16,82243	32,71028	36,448598	63,551402	1,0606061	1,1666667	-38,9	-38,9	0,149652	3,6	-36,35514	-0,9974359
spiLA0480-MIR10434	GAUAAAUAUAUAUUAGAAAAUGUGUAGUGAGUAC UAAUUAUAGAGUUAAUACCUCAGAUGGUCACUCA AUUAUGCACUCUUAUUCAAAGUUAAGUGACUUUC UGAGAAAGAAAGCAAUAGUUGAGUGACUUUUGAG UGAAAAUUGAAAGUUGAGUGACUUUCUGAGAAAG AAAGCAAUAGUUGAGUGACUUUUGAGUGAAAAUU AAAAGUUGAGUGACUUUCUGAGAGAAGAGUGCAU AGUUGAGUGGUAUUAACUCACUAAUUAUAUACAAA AGAUACAAAAACACACAUGUUUGGCAGCUAUUAUU UUGA	**312**	20,512821	37,5	10,25641	31,730769	30,769231	69,230769	0,8461538	2	-79,4	-63,9	2,52E-05	76	-25,448718	-0,8270833
spiLA0480-MIR10436	UUGUAAAAAGAUAUGUAGGACUACUAGACAACUCA AGCUUUAACACUCUAACUUGUCUACCAGUUGAUU CAGUUCCCUUUGGUUAGGGACUGUCUUCAUUGG UUAUGGUGGUCAACUGGUAGGCAAGUUAGAGUUU UUAAGCUUGAGCUGUCUAGUAGUCUUAUAUACCG UUUUAACG	**178**	21,348315	25,842697	16,853933	35,955056	38,202247	61,797753	1,3913043	1,2666667	-93,7	-88,6	0,0058755	14	-52,640449	-1,3779412
spiLA0480-MIR10445	AUGAAACCGUUGCCUUGGCAGCGAUUUGUAAGAA GCAAAAUUUUGAAAUAAAAUUUUUUUUGGCAAAAU CGCUGCUGAGGCAGCGAUUUUAC	**92**	21,73913	31,521739	15,217391	31,521739	36,956522	63,043478	1	1,4285714	-41,4	-39,1	0,0353232	11	-45	-1,2176471
spiLA0480-MIR10448	UUAUAUCUUUUUUAGACUUAGUUAAUGAAUACACA AACAAGUUAGGCUUUGUGGGUGUGCAAGAACUAA UUGUUCUUGCUCCAAGCGAAUUUUUUUUUUUUGA AAUAAUAGGUGAUGAGGGGGUUAGGACCUUAGCA UCUUUUGUAUCUAGUGAGUAUAAUCAAUUCACUU GUUUGCUACGGAUUAAUGUGACUUGUCUGUUAAA GUAACU	**211**	20,379147	27,488152	12,322275	39,810427	32,701422	67,298578	1,4482759	1,6538462	-53,6	-53,1	0,015746	15	-25,402844	-0,7768116
spiLA0480-MIR1046-1	UGCCUUGGAAGGUGAGAAGGCAAGUGAGAGGAU GAUUUGAAAAUGAACUAAGAGCCACCUAUUUAUA GGAAUAAAUUCAUCCUAUUAAUGUCAUCCAUGACA UCACUAUGUGUCAAAAAUGCCAAGGUUAAGAAUA UGAAAUAAUUUUAUGGUUUGCCUAAAUUUCACCU ACCAAGAUA	**179**	18,994413	36,871508	15,083799	29,050279	34,078212	65,921788	0,7878788	1,2592593	-44,5	-40,47	0,0067003	36	-24,860335	-0,7295082
spiLA0480-MIR1046-2	AAAAAUAAUAUCAAAUCGCUGCCCUGGCAGCGAU UUGUAAGAAGAAAAAUUUUGAAAUCGCUGCUUGA GCAGCGAUUUCAUUUUUUAU	**88**	18,181818	34,090909	15,909091	31,818182	34,090909	65,909091	0,9333333	1,1428571	-36,7	-35,8	0,160185	9,6	-41,704545	-1,2233333
spiLA0480-MIR1046-3	GGGGUCGUUUGGUAGAGUGUAUAAAAGUAAUGCU AAAUAUAGUGUAUUAGCAAUACUGGCAUUAGUAA UUUUUGCAUUAGUUAUACUUGCAUUAGUUGUACA UACAUUAUUUCUUAUGCAUUGUUUGGUUUGGUGU AUUAAAAUUAACAUGUAUUGUACAAAAGUAUCCUU CACAUUAUGGUGAAAAAGAUGAAAAAGUGUUUUU GAGGGGUGUUUGUAUCUUUUAAGUGCUAAUGCAU GCAUUAAAUCCCUUUGCAUUACUAAUACCUAGAAA UCCAUGGUAUUAGUAAUGUACUCUCCAAUACACA AU	**310**	18,387097	31,290323	11,935484	38,387097	30,322581	69,677419	1,2268041	1,5405405	-77,3	-41,2	0,0001629	99	-24,935484	-0,8223404
spiLA0480-MIR10519	AUGUGCAUAAAUAGACACUUAAACUUGUAUAAAGU UGACAAAUAGACACACAUGUCCUACAUGUCAUCC UACAUAUCAUUUUUUUUCUUACGUGAUGUCGUAC GUGUAUUGUGUCAUGUAGAACUCAUGUAUUUAUU UAUUCAAAAGUUGGAUAAUUAAAGUGUCUGUUUG UGCAUUA	**178**	15,730337	30,898876	14,606742	38,764045	30,337079	69,662921	1,2545455	1,0769231	-53,6	-52,3	0,0107316	13	-30,11236	-0,9925926
spiLA0480-MIR10528-1	UAAUGAAUGCAAUGUCAUAUACCAUCAACACUCG GAAACUCAAAUUGAGGUUAAAUCUCGGAGUGAUG	**95**	17,894737	34,736842	17,894737	29,473684	35,789474	64,210526	0,8484848	1	-41,7	-41,7	0,0516862	7,1	-43,894737	-1,2264706

spiLA0480-MIR10528-2	AUGGUAUAUGACCUUGCAAUUCACUAUUUUUAAGUUCCAAGUGAUUAAAGAAAUAUUAGGCAAGGAUGUUAAUUCCAAAUGUGGUAUUAAGUAUGAUUUGGCUAACGUAACUGCCAUUAACUUUAAGUUAGAGAUUAAUUAGUGGCUGAUUAGGAUUAAAUUAAUCUAGUGGGCCCCACCACUCAAGGCAAAUUAAAAGGAAUCAGAUUAGGAGCUGGCCUUAGUGGGACACGUGUAGAGGGGGGUUGCCUCCACUUCAUAUUAUAAAUGGGUGGUGAAAUGCAUUGCAACAUACCAUCUUCUUUACCACUUGGCUUAGGC	**294**	22,789116	30,952381	15,646259	30,612245	38,435374	61,564626	0,989011	1,4565217	-81	-80,1	0,0003598	37	-27,55102	-0,7168142
spiLA0480-MIR10529	AACAUAACGAGUGAGACUUGCUCAGUUGGUAAAACACCUCCACGGUCUAACCAAUUAUCUUGGUCGAGGGUUCAAGUCAUGUUGGAAGCAAUGUGGGGGCGUCCAGCUUAGCAAGCCUCAUCCGUUUUGCUU	**132**	25	25	22,727273	27,272727	47,727273	52,272727	1,0909091	1,1	-52,4	-52,4	0,30337	2,8	-39,69697	-0,831746
spiLA0480-MIR10530	AACAUGUUGAAUGUUGGGGAACGAACGUCUAAGGUUUGGGUCAACGAUCUCAAUGUUGAUGCGUCCGCUUGUUGUUGAUGCUGCUCCAAAAGGUUCAACAUUGGGAUUUUAGCCCAAACAUCAGACGUCCCUUCCCCAUCGUUCAACAUCGUU	**153**	22,875817	24,183007	22,875817	30,065359	45,751634	54,248366	1,2432432	1	-71,3	-70,1	0,0484994	6,7	-46,601307	-1,0185714
spiLA0480-MIR10531-1	AUAUCUGGGGUCCUAGUAGAGUCGGUUCUACAUUGGGUGUUAAGUGUUUUGAGUAAUCAUCAUUGAAAGUAACAUACUUAAAACCCAAUGUUGAAUUGACUCUACUCGGAUCCCAAAUAUC	**121**	19,834711	29,752066	17,355372	33,057851	37,190083	62,809917	1,1111111	1,1428571	-60,6	-60,6	0,158264	5,9	-50,082645	-1,3466667
spiLA0480-MIR10531-2	UACUCAUGCUACAUUUUCUCGUAGUACUGAGGGUUGUUAAGAGUCUAUUUUUUCAUUAGUUCAUUCUGAUAUUUGGGGUCCUAGUAGAGUCAGUUCUACUUUAGGAUUUCGUUAUUUUGUUAGUUUCAUUGAUGAUUAUUCGAGAUGCACUUGGGUUUUCUUAAUGAAAGAUUGUUCUGAGUUACUUUCUAUUUUCAAAAGUUCCUUUGCUGAAAUGCAAAAUCAGUUUGGUGUUUCCAUUCAUACUUUCAGUAGUGAUCAACAAAAAGGUGUAGCUGAAAG	**282**	19,503546	24,822695	13,829787	41,843972	33,333333	66,666667	1,6857143	1,4102564	-67,6	-56,4	6,95E-05	47	-23,971631	-0,7191489
spiLA0480-MIR10532-1	GCUCUAUACCCGAAAUUUCAGAGACACACUUAUAUUAUACUAAGGUCACUUUUUUCGGUCUACGUGACACUAGCUUGAAAAAAUGUCAAAACGCGCUGAGCCCAGAAAAUAGUGUCACGUAGGCCAAAAACGGGUAGAAAAUUCUUUUUAUAAAAUAAGUUAUGGAGAGUAAUAAGACCUUAGUAUAAUAUAAGUGUGUCUCUGAGAUUUCGAGCAUAGCUU	**222**	18,918919	34,684685	17,117117	29,279279	36,036036	63,963964	0,8441558	1,1052632	-98,5	-94	0,0055439	24	-44,369369	-1,23125
spiLA0480-MIR10532-10	GUACCCCCUCAACCUAUGCCUGAAAUUCCAGAGACUCACUUGUACUUUACUAAGGUCCUAUAAUUUAAAAUUUGUCAAUACACGCUGGGUCCACAAGAUAGUGCUACGUAAGUCGAAAAGGGAUAAAAAUUAUUUAUAAAAUAAGUUCGGGGGGAGNAAGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAUGAGGGGGGGGGGGUAAUAGGACCUUAGUAUAGUAGAAGUGUGUCUCUAAGAUUUCGGGCAUAGUUCAGGGGGGUA	**265**	24,90566	33,207547	14,339623	27,169811	39,245283	60,377358	0,8181818	1,7368421	-93,1	-80,72	0,0017595	41	-35,132075	-0,8951923
spiLA0480-MIR10532-11	UUUAUUGAAUCAUUGAACCACACAUAAGUGUGUCUCUGAGAUUUCGAGCACAGGUUGAGGAGGUACUUGUGCAUUAUCCCAAGUUAAAUUGGUGAAUAUCAUGUUGGAAUUAAGUUAAAACUAAACUAAUUAGACUUAGAAAGUUCUUAAGUUCUUCAAAUUAGCUAAUGUGAUUAAGUUGGUUAAUAUAGUGUUGGAAUUGAGUUAAAACUAAACUAAUUAGACAUGGGAAGUUGUUAAGUUGUUCAAUGAGUUAAAUUGG	**262**	20,610687	33,969466	10,305344	35,114504	30,916031	69,083969	1,0337079	2	-59,7	-58,3	0,0011483	47	-22,78626	-0,737037
spiLA0480-MIR10532-12	AUGAAUUCAAAGAAAUUAAAUAUAGAUUUAUAAAUCCCCCUGAACUUAUUUUAUAUGUAUUUUUCUACCCCUUUUUAGCCUACAUGGCACUAGUUCGAAAAAAAAAGUCAACCAUCGUUGGGCCCACAAGAUAGUGCCACGUAAGCUAAAAAUGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAGGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUCG	**232**	17,241379	36,206897	15,517241	31,034483	32,758621	67,241379	0,8571429	1,1111111	-76,1	-72,8	0,0015099	30	-32,801724	-1,0013158
spiLA0480-MIR10532-13	UAAAACAAGUUCAGGGGGUAAUAGGACCUUAGUAUAGUAUAAGUGUGUCUCUGAGAUUUCGAGCAUAGGUUGGGGGGUACUUGUACAUUUUUCCAUUAAAAAGAUAAUCUAACAUAACUUGUUACAUCAUUAAUAAA	**227**	15,859031	33,480176	15,418502	35,242291	31,277533	68,722467	1,0526316	1,0285714	-65,1	-62,6	0,0185354	17	-28,678414	-0,9169014

spiLA0480-MIR10532-14	AUGCAUAAAUUUCCCCUUUAACUUGUAUUGAAAAGUCAGUUACACACUUCAAUUAUUAUGAUGACCUAUUACACACUUAUUCUUGUUCAAUUAUAAUUUUUUUGAGAAAUUACCUAACCGACAACUUUUCGGCCUACGUGACACUAUCUUGUGGGCCCAACGCUGGUUGACUUUUUUCUUCAAGCUAGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUUAGGGGGUAAUAGGACCUUAGUAUAGUAUAAAUGUGUCUCUGAGAUUUCGGGCAUAGAUUGACGGGGUACUUGUGCAUUUUCCCCCGUUCAUUAUAACAGUAAUAUUAUUAAAAACAAUUAUUUUGGGGAAAAUGCACAAGUACCCCCUCAACCUAUGUCUUAAAUCAUAGAGGCACACUUAUACUAUUACCUAUUAAGUGGGGUAAUAGGACCUUAGUAUAAUAUAAAUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGGGUACUUGUGCAUCGUUCCUAUACUUAAACUAUGACUGAAAUUUCAAAGAUACACUUUAACGAAUUAAAUUCCUAUUACCCCCCUAAGCUUACUUUUUUUUUUUGCAUUUUCAUACACCUUUUUCGCUUAUGUGGCAUCAAAAAAUAUCUUCAACGUGCCACAAUUGUAUGGAGUCAUGAAGUCUGCUACGUUAAAAAAAAAGAUGUACGAAAUUACAAAAAAAUAAAAGUUCAAGGGUAAUAGGACCUUAGUUUAUGAAGGUGUGUCUCUGAGAUUUCGGUCAUAGUCUAGGGGACUGAAAUUUCAAAGAUACACUUUAACGAAUUAAAUUCCUAUUACCCCCCUAAGCUUACUUUUUUUUUUUGCAUUUUCAUACACCUUUUUCGCUUAUGUGGCAUCAAAAAAUAUCUUCAACGUGCCACAAUUGUAUGGAGUCAUGAAGUCUGCUACGUUAAAAAAAAAGAUGUACGAAAUUACAAAAAAAUAAAAGUUCAAGGGUAAUAGGACCUUAGUUUAUGAAGGUGUGUCUCUGAGAUUUCGGUCAUAGUCUAGUAUACUUGUAUCUUAUCCCAAAUAUAUCCUCUAAACUAUUAAAUGUACUUAUAUUCUCAAUC	**269**	19,702602	29,739777	16,728625	33,828996	36,431227	63,568773	1,1375	1,1777778	-71,6	-58,4	0,0004376	45	-26,6171	-0,7306122
spiLA0480-MIR10532-2	AUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGGGUACUUGUGCAUCGUUCCUAUACUUAAACUAUGACUGAAAUUUCAAAGAUACACUUUAACGAAUUAAAUUCCUAUUACCCCCCUAAGCUUACUUUUUUUUUUUGCAUUUUCAUACACCUUUUUCGCUUAUGUGGCAUCAAAAAAUAUCUUCAACGUGCCACAAUUGUAUGGAGUCAUGAAGUCUGCUACGUUAAAAAAAAAGAUGUACGAAAUUACAAAAAAAUAAAAGUUCAAGGGUAAUAGGACCUUAGUUUAUGAAGGUGUGUCUCUGAGAUUUCGGUCAUAGUCUAGUAUACUUGUAUCUUAUCCCAAAUAUAUCCUCUAAACUAUUAAAUGUACUUAUAUUCUCAAUC	**160**	22,5	28,75	18,125	30,625	40,625	59,375	1,0652174	1,2413793	-95,3	-95,3	0,27076	10	-59,5625	-1,4661538
spiLA0480-MIR10532-3	CAAGUAUAGAGAUUAUUGUCGGGAUAAGGAACAAGUACCCUAUAGACUAUAAACAAAAUUUGAAAGGCACACAUAAGCUUAACUAGGGUCUUAUCCCCGGCCCAACGAUGGUUGACUUUUUUUUUCAAACUAGUGUCACGUAGGCUAAAAAGGGGUAGAAAAUUACUUAUAAAACAAGUUCAGGGGAGUAAUAGGACCUUAGUAUAGUAUGAGUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAAGGGUACUUGUGCAUUUUCCCUAAAAUCUAUAUACAAA	**273**	15,750916	33,699634	16,849817	33,699634	32,600733	67,399267	1	0,9347826	-97,5	-92,8	0,0587331	15	-35,714286	-1,0955056
spiLA0480-MIR10532-4	AGGGAAAAUGCACAAGUACCCCCUCAAUCUAUGUCCGAAAUCCCAAAAACACACAAGAUAGUGCCACGUAGGCUAAAAGGGGUAAAAAAUUAUUAAUAAAAUAAGUUCAGGGGUAAUAGGACCUUAAUAUAGUAUAACUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGAUACUUGAGCAUUAUCUCAACGUGGCACUAGUUUGAAAAAAAAAAGCCAACCAUCGUUGGGCCACAGGAUAGUGCCACGUAGGCUAAAUGGGAUAAAAAAUUAUUAAUUAAAUAAGUUCAGGGAGGUAAUAGGACGUUAGUAUAGUAUAAGUGUGUCUCUAAGAUUUCAGGCAUAGGUUGAGGGGGUACUUGGGCAUUAUCCCCCGAGGGCCCUAAAUCUUAUAUAGCGUGUUCAAUAAAAAUUAGUCACGUAAAACUAAACUUGACUUCAUAGGCACCUCCCUCAAUAAUAAUUAUUAUUGUAUCUUUUUCUUGUUUUUUUUUUUUUUUCAUAUUUGUGUCCAUCUAAAAUAAGUUCAGGGGGGUAAUAGUACCUUAGUAUAGUAUAAGUGUGUUUCUGAGAUUUCGAGCAUAGGUUGAGGGGGUACUUGGGCUUUAUCCCUAAGAACAACUAUAAAUGAGUAAAGACAAAAUUCCCUCUUGAACUUGUACCGAAAAGUUAGUUACACGCUUAAACUAUCACAGUAACAUAUUACACACCUAUAUUAUUCAG	**323**	13,931889	33,436533	17,647059	34,98452	31,578947	68,421053	1,0462963	0,7894737	-96,4	-91,7	0,0165417	22	-29,845201	-0,945098
spiLA0480-MIR10532-5	GUUGAAGGGUACUUGUGCAUUUUCCCUAAAAUCUAUAUACAAA	**281**	21,708185	33,807829	15,658363	28,825623	37,366548	62,633452	0,8526316	1,3863636	-89,1	-76,36	0,0016151	38	-31,708185	-0,8485714
spiLA0480-MIR10532-6	GUUCAGGGGUAAUAGGACCUUAAUAUAGUAUAACUGUGUCUCUGAGAUUUCGGGCAUAGGUUGAGGGAUACUUGAGCAUUAUCUCA	**190**	21,052632	36,842105	17,368421	24,736842	38,421053	61,578947	0,6714286	1,2121212	-67,1	-61,1	0,004577	29	-35,315789	-0,9191781
spiLA0480-MIR10532-7	UGGGCAUUAUCCCCCGAGGGCCCUAAAUCUUAUAUAGCGUGUUCAAUAAAAAUUAGUCACGUAAAACUAAACUUGACUUCAUAGGCACCUCCCUCAAUAAUAAUUAUUAUUGUAUCUUUUUCUUGUUUUUUUUUUUUUUUCAUAUUUGUGUCCAUCUAAAAUAAGUUCAGGGGGGUAAUAGUACCUUAGUAUAGUAUAAGUGUGUUUCUGAGAUUUCGAGCAUAGGUUGAGGGGGUACUUGGGCUUUAUCCCUAAGAACAACUAUAAAUGAGUAAAGACAAAAUUCCCUCUUGAACUUGUACCGAAAAGUUAGUUACACGCUUAAACUAUCACAGUAACAUAUUACACACCUAUAUUAUUCAG	**328**	19,512195	31,097561	16,158537	33,231707	35,670732	64,329268	1,0686275	1,2075472	-82,6	-59,9	1,04E-05	90	-25,182927	-0,7059829
spiLA0480-MIR10532-8		**207**	19,323671	34,299517	15,942029	30,434783	35,2657	64,7343	0,8873239	1,2121212	-55,9	-51,97	0,0020451	33	-27,004831	-0,7657534

spiLA0480-MIR10532-9	AAUGCACAAGUACCCCUCAACAUAUCCUGAAAUUUCAGAGACAAACUUAUAUUAUACUAAGAUCCUUUGUAUAGUAUAAGUGUGUCUCUGAGAUUUCAGGCAUAUGUUGAGGAGGUACUGGUGCAUU	**127**	18,897638	31,496063	17,322835	32,283465	36,220472	63,779528	1,025	1,0909091	-81,7	-81,7	0,186874	2,8	-64,330709	-1,776087
spiLA0480-MIR10533	AAAAACUCUAAGAACCAAUGCAAACCAUGCAAUCUUAGUUUUGACUAUUUUAUGGAUUAAGCGAUUGUGUCUCAAUGCUUAUGAAUUCUAGUGUAGUUUUCUUUGGGCUAUUGAAUGAUAUAAGAAUUGUAUUGGAUUGAUGCAUAGGCUGUCUUAGAUUGAU	**163**	19,631902	30,06135	12,269939	38,03681	31,90184	68,09816	1,2653061	1,6	-37	-30,34	0,0067247	27	-22,699387	-0,7115385
spiLA0480-MIR10534-1	UGGCUCCAAAAUACCCUUGUCAUCCAACAUUGGAUUCAAAAUUGACCACUUAUUUAACGGUCCAUUUUGAACAAAAAGGUGGAUGACAAGGGUAUUUUGGAGCCAA	**106**	18,867925	33,018868	19,811321	28,301887	38,679245	61,320755	0,8571429	0,952381	-60,8	-60,8	0,200477	3,8	-57,358491	-1,4829268
spiLA0480-MIR10534-2	GGCUCCAAAAUACCCUUGUCAUCCACCUUUUUGUUCAAAAUGGACCGUUAAAUAAGUGGUCAAUUUUGAAUCCAAUGUUGGAUGACAAGGGUAUUUUGGAGCCA	**104**	20,192308	28,846154	19,230769	31,730769	39,423077	60,576923	1,1	1,05	-61,9	-61	0,0925874	4,9	-59,519231	-1,5097561
spiLA0480-MIR10535a	AAAGGGUUGGCAUAAGUUUGUGAAAGCCGGAGAUUUAGGAGUAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUUG	**121**	19,008264	30,578512	14,876033	35,53719	33,884298	66,115702	1,1621622	1,2777778	-63,4	-62,1	0,078587	5,3	-52,396694	-1,5463415
spiLA0480-MIR10535b	AAAGGGUUGGCAUGAGUUUGUGAAAGCCGGAGGUUUAGGAGCAAAGUACAAUUAUUUUCGCAAAUAAUUGUAUCUUUUGCUCUUAAACCUUUAGCUUUAACAAAUUUGUGCCAACCCUUUG	**121**	20,661157	28,92562	15,702479	34,710744	36,363636	63,636364	1,2	1,3157895	-71,2	-69,9	0,087176	5,1	-58,842975	-1,6181818
spiLA0480-MIR10536-1	UUGAAUAAGAAGGAAAUUGAAGAUUAAAACAUGUCAAAGGAACUGGUCCGAUGUAGUAGAUUGACUUGUCUACAACAAGUGUUGAUGAAGAAGGAAGCUGAGGAUCAUAACAUGUUGUUGGACCUUUCUUCAUCAUCACUCGUUAUAGAUAAGUCAAUUAACUGCGUUGUCCUUUGACAUGUUCUAAUCGUUAGUUUUCUUUUUUUUUUU	**210**	20	30	13,809524	36,190476	33,809524	66,190476	1,2063492	1,4482759	-93,3	-91	0,0364465	12	-44,428571	-1,3140845
spiLA0480-MIR10536-2	CAGCAAGUGUUGAUGAAGAAGGAAGCUGACGAUAGGAACAGGUCCAACAAAGCUGACUGGCGAGUUUACAGCACUUGCUUCAGACACGUCAGCCAGCUUCGUUGGACAUGUUUCUUUGACAUGUCCUAAUCGUCAAUUUCCUUCUUCAUCAACAGUUGUCC	**161**	22,360248	26,708075	23,602484	27,329193	45,962733	54,037267	1,0232558	0,9473684	-85,1	-85	0,057812	9,2	-52,857143	-1,15
spiLA0480-MIR10537	GUUGCACGUACAAGGAUGUUCUACAACGUACGUAGGGUAAGUGGAUGGCUGAAAUUCGUUAGCCUAACCGUGGCCCUGGAAAUACUUCUUUGCAGGACAAGCUUCAUUUCCAUUACCGGAUAUCAACAGAAAGGUUGAAAAAGACAACAAUGUAGAGGAUUUGGUGGAGUGUGGAAAGAUUUGAAUGCAAACUUAUCGAAGAUUGAUCAUCAUGGAUUUAAGCCAUCCAUUUACCCCAAGUUCGUUGUCAAACGCCUUUGUAAGUGCGCG	**270**	24,074074	30	18,518519	27,407407	42,592593	57,407407	0,9135802	1,3	-96,2	-95	0,0021153	27	-35,62963	-0,8365217
spiLA0480-MIR10538-1	UUAUUGUUUAAAAGUUGACGACGUUAGAUUGAUAUACAUUACUCACAGUAACGUUGUACUCACAUUUUAGUAGUAAAACGGUACUCAAAAUAACGUUUUAGGAGUAAAACGCUACUUACAGUAAUGUAUAUCAACCUAACGCUGUUCGUUUUUAAAAAAUGA	**162**	15,432099	35,802469	14,814815	33,950617	30,246914	69,753086	0,9482759	1,0416667	-49,7	-49,1	0,017443	10	-30,679012	-1,0142857
spiLA0480-MIR10538-10	AUGGCGUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUAGGAGUAAAACGUUACUGAAAAUAACGUUUUAAAAGUAAAACGUUACUUACAGUGACGUAUAUCAACCUAAUGCUGU	**117**	17,948718	35,897436	15,384615	30,769231	33,333333	66,666667	0,8571429	1,1666667	-50,6	-50,6	0,277456	10	-43,247863	-1,2974359
spiLA0480-MIR10538-11	GACAUACAGCUAGAUAUCACAUACCCUUUGAACUUCCCAAACAGACCAUAGAGUGAUUUACGUAAUUAACAUACAAGGCUACUAAACAACCCCAAGAAACAAAUUAGGUGGUUGCUCAGGGGUAGUCUUGUAUGUCGUUUAUGUAUGUAUGGUCUGGAACAGUCUUUGCACGCUUGGGUUGGGAAGUUCAACUGUAAUUUUAUUAGUGUAUUUU	**215**	20,465116	30,232558	17,674419	31,627907	38,139535	61,860465	1,0461538	1,1578947	-67,8	-65,4	0,0030249	17	-31,534884	-0,8268293
spiLA0480-MIR10538-12	GUCAGAUUGAUAUACGUUACUCACAGUAACAUUUUACUCCUAAAACGUUACUCACAGUAACGUUUUAGGAGUAAAACGUUAUUGAAAAUAACGUUUUAAAAGUAAAACGUUACUUGCAGUAACGUAUAUCAACCUAAU	**138**	13,768116	37,681159	16,666667	31,884058	30,434783	69,565217	0,8461538	0,826087	-62,7	-62,7	0,144417	5,9	-45,434783	-1,4928571
spiLA0480-	ACAGCAUUAGGUUGAUAUACGUUAUUGUAAGUAG	**148**	16,891892	32,432432	15,540541	35,135135	32,432432	67,567568	1,0833333	1,0869565	-	-73	0,16221	6,6	-	-1,55625

MIR10538-13	CGUUUUACUCCUAAAACAUUAUAUUCAGUAACGUUUUACUCCUAAAACGUUACUAUGAGUAACGUUUUAGGAGUAAAAUGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAU									74,7				50,472973	
spiLA0480-MIR10538-14	GUCAGAUUGAUAUACGUUACUCACAGUAACGUUUUACUCCUAAAACGUUACUCACAGUAAAACGUUACUGAAAAUAACGUUUUAAAAGUGAAACGUUACUUACAGUAACGUAUAUCAACCUAAU	**124**	12,903226	37,903226	18,548387	30,645161	31,451613	68,548387	0,8085106	0,6956522	-54,1	-54,1	0,298684	2,4	-43,629032	-1,3871795
spiLA0480-MIR10538-2	UCGUAAAACUAACAGCAUUAGGUUGAUGUACGUUACUGUAAGUAUCAGUAACGUUUUAGGAGUAAAAUGUUACUGUGAGUAACGUAUAUCAACUCUGACGCCAUCAACUUUUAAA	**140**	15,714286	34,285714	15,714286	34,285714	31,428571	68,571429	1	1	-63,5	-63,5	0,312678	3,2	-45,357143	-1,4431818
spiLA0480-MIR10538-3	AACAGCAUUAGGUUGAUAUACGUUACUGUAAGUAACAUUUUACUCCUAAAACGUUACUGUGAGUAACGUAUUUUAGGAGUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGACGCUAUC	**119**	17,647059	33,613445	15,12605	33,613445	32,773109	67,226891	1	1,1666667	-67,2	-67,2	0,632394	0,8	-56,470588	-1,7230769
spiLA0480-MIR10538-4	UUUAAAAGUUGAUGGCGUCAGAUUGAUAUGCGUUACUGUAAAUAACGUUUUACUCCUAAAACGUUACUCAAAGUAACGUUUUAGGAGUAAAACGUUACUUACAGUGACGAAUAUCAACCUAAUGCUGUUAAUUUUUUAA	**139**	16,546763	33,81295	14,388489	35,251799	30,935252	69,064748	1,0425532	1,15	-76,3	-76,3	0,145677	4,9	-54,892086	-1,7744186
spiLA0480-MIR10538-5	ACAGCAUUAGGUUGAUAUACGUAACUGUAAGUAACGUUUUACUUUUAAAACGUUAUUUUGAAUAACGUUUUACUCCUAAAAUGUUACUGUGAGUAACGUUUUAGGAGUAAAACAUUAUUGUGAGUAACGUAUAUCAAUCUGACGCCAU	**148**	16,891892	33,108108	13,513514	36,486486	30,405405	69,594595	1,1020408	1,25	-66,1	-66,1	0,254781	4,1	-44,662162	-1,4688889
spiLA0480-MIR10538-6	UAAAAGCUGACGGCAUUAUAUUGAUAUACGUUACUCAUUGUAACGUUUUACUCCUAAAACGUUACCCAAAAAAUGUUUUACGCCUAAAACGUUACUCACAGUAAUGCAUAUCAACCUAACACCGUCAACUUAUG	**135**	11,851852	35,555556	22,222222	30,37037	34,074074	65,925926	0,8541667	0,5333333	-43,9	-43,1	0,36883	2,6	-32,518519	-0,9543478
spiLA0480-MIR10538-7	AUUAGGUUGAUAUACGUUACUGUAAGUAACGUUUUACUCUUAAAACGUUAUUUUCAGUAACGUUUUACUCCUAAAACGUUACUGUGAGUAACGUUUUAGGAGUAAAACGUUACUGUGAGUAACAUCUAUCAAUCUGAC	**138**	16,666667	31,15942	15,217391	36,956522	31,884058	68,115942	1,1860465	1,0952381	-76,1	-76,1	0,471927	1,4	-55,144928	-1,7295455
spiLA0480-MIR10538-8	AUUAGGUUGAUAUACGUUACUGUAAGUGACGUUUUACUUUUAAAACGUUAUUUUCAGUAACGUUUUAUUACUCCUGUGAGUAACGUAUAUCAAUCUGAC	**130**	16,153846	29,230769	15,384615	39,230769	31,538462	68,461538	1,3421053	1,05	-54,1	-53,6	0,0429749	25	-41,615385	-1,3195122
spiLA0480-MIR10538-9	AAAAGCUGACGGUGUUAGGUUGAUAUACGUUACUACAGGUAACGUUUUCAUCCUAAAACGUUACUAUGAGUAACGUUUUAGCAGUAAAACGUUACUGUGAGUAACAUAUAUCAAUGUAACACCGUCAGCUUUU	**133**	18,796992	32,330827	16,541353	32,330827	35,338346	64,661654	1	1,1363636	-75,6	-75,2	0,0776365	5,9	-56,842105	-1,6085106
spiLA0480-MIR10540-1	UGCGGGGUUGAAUUCUCAAAUGGUUACUCAACUUAUAGUUAUUAUCUCAGAAAAUCUCUUUUCGUUCUUGAUUCUGAUGCAAAGAAAGUCACUUUGUUAGAUAUAAACUAUUAGUUGAGUGACCAUCUGUGAAAUCAACUCCUGU	**145**	17,241379	28,965517	16,551724	37,241379	33,793103	66,206897	1,2857143	1,0416667	-53,5	-51,3	0,0245621	16	-36,896552	-1,0918367
spiLA0480-MIR10540-2	CGUAUGGCUCUUGAAUUGUCGGAGUUGAUUUCUCAUAUAGUCACUUAAUUAACUGUUAUUAUCUUGUAAAAUUAUUUUUCUUUAUUGACUUUCUAAGCUAAUAACUGUUAGUUGAGUGAUCAUCUGAGAAAUCAACCUGAAUUGAUGGCAAUCUU	**155**	16,129032	27,741935	14,193548	41,935484	30,322581	69,677419	1,5116279	1,1363636	-49,8	-48,6	0,0391249	9,6	-32,129032	-1,0595745
spiLA0480-MIR10540-3	AGUCACUCAACUACUUGCUAGUAUCUCAGAAAAUCACUUUUUUUGUUGAAGAAAAUAGGAAUCACGAAGAAAGCCGUCUUUCUGAGAUAAUAACUAUUAGUUGAAUGUUC	**110**	16,363636	34,545455	16,363636	32,727273	32,727273	67,272727	0,9473684	1	-29,2	-28,5	0,0697882	5,6	-26,545455	-0,8111111
spiLA0480-MIR10542-1	AAAUAUACCUUGAACUUUGAUUGAAGAAUCGUAUAUACCCCUAAAUAAUAUUUUUAAAAAAAAAUAGAAGUAAUAAAUAUAAAUUUAAAACUAAUUUUUCAACUUCCGCUAAAUGAAGGGUAUAUGUGAGCCAUUUUGUAACGGCAGGGGUAUAUGUGAGCCGUUUGUAUAACGGUAGCGAGGGGUAUAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAUAUGAGCCACUUUUAUAACGAGGGGUAUAUCAGCUCCAAAUGACAAAGUUGAAGGGUAUA	**278**	20,143885	36,330935	12,94964	30,57554	33,093525	66,906475	0,8415842	1,5555556	-69,7	-52,3	0,000242	83	-25,071942	-0,7576087

spiLA0480-MIR10542-2	UCA AAAACAUACCUUGAACUUUGAUAGAAGAAUCAUAU AUACCCAUAAAUAAUUUAAAAAAAUUAAAAGUACA AAUAUAAACUUAAAACUGUUUUUUAACUUCCGUU AAAUGAAGGAUAUGUGUGAGCUCAUUUUGUAACG GCAGGGGUAUAUGUGAGCCAUUUGUAUAACGGUA AGGACAUAUAUGAGUCACUUUCAUAACGAGGGGU AUAUCAGCUCCAAGUGACAAAGUUGAGGGGUAUG UCAA	**245**	18,77551	37,959184	13,061224	30,204082	31,836735	68,163265	0,7956989	1,4375	-58,1	-52,6	0,0003895	39	-23,714286	-0,7448718
spiLA0480-MIR10542-3	UUUGAUAGAAGAAUCAUAUAUACCCCUAAAUAAUU UUUUUUAAAAAAAAUUAGAAGUAAUAAAUAUAAAUU UAAAACUAAUUUUUUAACUUCCGUCAAAUGAAGG GUAUAUCUGAGCCAUUUUGUAACGGCAGGGGUAU AUAUGAGCCGUUUGUAUAACGGUAAGGGCAUAUA UGAGCCACUUUUAUAACGAGUGAGUAUAUCAGCU CUAAAUGACAAAGUUAAGGGGUAUAUCAGACCCU UUACCCUU	**248**	16,935484	36,290323	13,709677	33,064516	30,645161	69,354839	0,9111111	1,2352941	-60	-46,7	0,0007643	59	-24,193548	-0,7894737
spiLA0480-MIR10542-4	UUGAACUUUGAUAGAAGAAUCAUAUAUACCCCUAA AUAGUUUUUUUAAAAAAACUAGAAGUAAUAAAUAU AAAUUUAAAACUAAUUUUUUAAUUUCCGUUAAAUG AAGGGUAUAUGUGAGUCAUUUGGUAACUACAGGG GUAUAUGUGUGCCGUUUGUAUAAUGGUAAGGGCA UAUAUGAGCCACUUUUAUAACGAGGGAUAUAUCA GCUCCAAAUGACAAAGUUGAGGGGUAUAUCAGAC CCUUUUCCCAAGUUUUA	**258**	18,217054	35,271318	12,403101	34,108527	30,620155	69,379845	0,967033	1,46875	-61,1	-51,18	0,0006791	83	-23,682171	-0,7734177
spiLA0480-MIR10542-5	AACUUUUAUAGAAGAAUCAUAUAUACCCCUAAAUA AUUUCUUUAAAAAAAUUAGAAGUAAUAAAUAUAAA UUUAAAACUAAUUUUUUAACUUCCGUUAAAUGAAG GGUAUAUGUGAGUCUUGUUGUAACGGCAGAGGUA UAUGUGAGCCGUUUGUAUAACGGUAAGGGCAUAU AUGAGCCACUUUUAUAACGAGGGGUAUAUUAGCU UCAAAUGACAGAGUUGAGGGGUAUAUCAGACCUU UUUCCCAUAAAACAA	**256**	17,96875	36,71875	12,5	32,8125	30,46875	69,53125	0,893617	1,4375	-63,4	-59,5	0,002399	28	-24,765625	-0,8128205
spiLA0480-MIR1062	UGACCACACGUGGGGUUUGGGGAGGGUGGUGUG UACGCAAACCUUGCCCCUAACUUAUGCAGGUAGA GUUAAGGUAUGCGUACAUCCUACCCUCCCCAGAC CCUAUUUGUGGGAU	**115**	28,695652	20,869565	24,347826	26,086957	53,043478	46,956522	1,25	1,1785714	-74,2	-70,3	0,0990653	6,3	-64,521739	-1,2163934
spiLA0480-MIR1072	UUGGGUGGUCGUCUUAUGUAGCACCUUUAUAUCC UGCAGGUUUCUGAUCUUCACAUUGUCAUAUUUGA AUCUUACUCCCCAGCAGUCCCGAAAUCUGUGUUA GGGAGUAUGAUUCAAAUCUGACAACGUGAACAGC UGAAACCCUACAGGGUACAACAGGUGCUUCAUAA GACGAUGACCUGU	**183**	21,311475	25,68306	22,404372	30,601093	43,715847	56,284153	1,1914894	0,9512195	-92,3	-91,7	0,035276	8,5	-50,437158	-1,15375
spiLA0480-MIR1078	CUCAAAAGUCAACGGAUGAUUGUUUAAAUGUUGA UGCAUCUACAACGUCAAAAUCAAAACCACCAACAU UGGACGAUUAUCCUGAUUUUACC	**92**	14,130435	35,869565	21,73913	28,26087	35,869565	64,130435	0,7878788	0,65	-23,1	-23,1	0,100261	5,3	-25,108696	-0,7
spiLA0480-MIR1088	UAUGAAAGAGGUGAAGGUGAUGACAGAAGCAUAG AGAGCACAAAUGAAUUGAGAUGCUUUUGCUGCCC AAAUUGAAUGAAAUUAGCAUAUCAUCAUUAGUGCU CUCUAUCUUCUGUCAACAAUAAUCACUCUUUCUU C	**138**	18,84058	33,333333	17,391304	30,434783	36,231884	63,768116	0,9130435	1,0833333	-54,9	-54,8	0,039747	7,5	-39,782609	-1,098
spiLA0480-MIR1098	AACGAAGCUGAUGACGUGUCUGCAGCAAGUGUUG AUGAAGAAGGAAGCUGACGAUAGGAACAGGUCCA ACAAAGCUGACUGGCGAGUUUACAGCACUUGCUU CAGACACGUCAGCCAGCUUCGUU	**125**	28	29,6	21,6	20,8	49,6	50,4	0,7027027	1,2962963	-62	-62	0,301946	4,4	-49,6	-1
spiLA0480-MIR10999b	ACAGGUGCGUGUUUUUCUUGCGACCGUCAGGGU CAUACUAUGAGGAAAUGUAACCUUAGAGGUAGUG CAGGUGGUAUGGCUCAGCCUACUGGGUCCGUGG AUGGUUCAUCUUCUUCUGUGGUUAUGCACCCUAC GGGGCAGGGUAUUCAGGCACCAAC	**158**	30,379747	19,620253	21,518987	28,481013	51,898734	48,101266	1,4516129	1,4117647	-61,5	-51,69	0,020735	25	-38,924051	-0,75
spiLA0480-MIR11028	UCCCUCCGUUUCAAUUUGUUUGUUUUACUUUUCU UGUUGGUCUGUUUCAAAAAGAAUGUUUUUUCCCC UUUUUGACGAUACAUAGAGCAUAAUAUCAUAAGAU UCAAAUGUUUUAUAUACUUUCUCAAACUCUGUGU CAAGUCAAAACCAGACAAACAAAUUGAAAUGGAGU GU	**174**	13,793103	29,310345	17,241379	39,655172	31,034483	68,965517	1,3529412	0,8	-49,1	-49,1	0,0239275	9,3	-28,218391	-0,9092593

spiLA0480-MIR11032	UGGUGGCUGCCGAAAAGCAGCAAGAGAAGGCUGCAACGCAAAUCGAAAGUUCUGCCGGGGAGCAACGAGGGCAGAAUAGCGGGACAGACAAGGGCAAGAACGUUGUUGUUGGCAUGUUCAAUCACAUGGCGUUGAUCAACCAUAUUUCUAUUGCUGCUUUGGCUGCCAAAC	**171**	29,824561	28,654971	21,052632	20,467836	50,877193	49,122807	0,7142857	1,4166667	-61,7	-60,2	0,0139721	19	-36,081871	-0,7091954
spiLA0480-MIR11036	AUCCAUUAUUCUUCUGAAUUGUUUAUCUUCUGCUUUGAUAUGACAGCUUUAUUGUAUUCAUUCAGGAAUGUGAGGAGUAUGAAGAUUUGGAUGAAUAUGAGGAAGAAAGCGGUGCAGAGGAAUAUGAGG	**129**	25,581395	29,457364	10,077519	34,883721	35,658915	64,341085	1,1842105	2,5384615	-34,1	-28,74	0,0044519	29	-26,434109	-0,7413043
spiLA0480-MIR11039-1	UUCUCUACUUGUUAUGAGGAUAUGCAUGGUAUGUGUCUAUAUGAUGUAGUCUUAUUCUUAUGUGAACUAUGUGAGUCUUAGUGACUAUAGGAUGGAAAUUGUUGAUAGUAAUUGAGUUGUACUUAUGCAUUAUGUUGAUGUAUGAAGUGUUAAGAUUUGUGGUGUCGUGAAGGGUUUACAGAAUGUAUGGAGUUAUGGGGCUUCAUAUGUUCAUUGAACUAGUAGACUA	**229**	25,764192	25,764192	8,2969432	40,174672	34,061135	65,938865	1,559322	3,1052632	-58,1	-39,8	0,0011052	55	-25,371179	-0,7448718
spiLA0480-MIR11039-2	AUGCAAGUUUAGAUCUAAUUUUCAACGAUUUAUCUCUAUUCGUUGGAUCAUAUUUCUUCUUCGCUCGUGAAAAUGUUUAACUAGAAUAAAAUUUGAUCGCUCUUAUUGAAUUUCUCUAUUGAGAAGUUCGUUUUUAUCUUCUAUUUGAAGAAAUUGUUGCUCGAAAAUGAUGGGUUGUUGUGGUGAACAAAUCUACGUGAAUUGAUAAAGGUGAAAUGGAGAUGAAGAGUUAAUAUUUGGUGAAAAUGGUGGGUCAACUUGAGU	**264**	20,833333	29,545455	10,984848	38,636364	31,818182	68,181818	1,3076923	1,8965517	-59	-48,3	9,18E-05	53	-22,348485	-0,702381
spiLA0480-MIR11042	UUUAAAAACUACAGCAUAUAUACCAUUUAUAUUAACAAAUAUACACGUGUCAUAAUCUUAUCGACCGACCUCACAUUUAUCAAAUAUCGAAUCGACGGAUAAGAUUGUGCCAUAUGUUCCUAUUAAGUCUUCUGUUAGAGUGAAGGGCAUGUAUACUCUAGUUUUUGGAUAGAUAAGUAUUUUUUAGUUUGUAUGUAAAAUUAUUAAUAUGAAAUAAAAAGUGAGUUUUUAUAUCAUUCUUCUUAAAACUCCAUAUAUAGUCGAAAGUGAAGGUUGCGAUCUUCAGCCUUAAGGAGGAACAGUAACAAAGUAGCCAAAGACUGCGGUCGCCAGGGUGAAACACUGUUCAUGGCCUGAAAGGAGAAAUACUGCGG	**169**	14,792899	33,136095	17,751479	34,319527	32,544379	67,455621	1,0357143	0,8333333	-40,1	-38,1	0,022226	13	-23,727811	-0,7290909
spiLA0480-MIR11044	CAUUGAUAGAGACUAUUCAUCGACAAAAGAGAAGAAAGGUAUACACACAAACUUUUUAUUACAUACUAUAUAAUUUUACAGAUAUACUAUAUACACUUAUUUU	**308**	17,532468	37,337662	13,961039	31,168831	31,493506	68,506494	0,8347826	1,255814	-80,7	-78,1	0,0031126	15	-26,201299	-0,8319588
spiLA0480-MIR11045	UCCGCAAUGUAUUUAGUUCAUUAUGUUUGAAAUGAUGGGGUUUAGAUUGGUUGGUUCGCUCACAUAGGAGGAUAAAUGUAGAUGCCACUCACGGCCCGAUUUGGGUCGUGACAUUAACCCAAUCCGACUCGAAUCUGCGCGCGAUCUGUUUUAUUUAAAAAGAUAUUUCAUCAUUUUGGAAAUGACUGUUCUGAAAGAUUGCAAC	**205**	22,439024	26,829268	17,560976	33,170732	40	60	1,2363636	1,2777778	-58,5	-57,4	0,0177494	14	-28,536585	-0,7134146
spiLA0480-MIR1106-1	AAUCCCCAUGCACUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGCCCACGUGGACACACUACUAUUUAUAAUUAUGAAAUAUUUAUGAUGUCCACGUGGACACAUAUAUACCUUCAAAAGACACACUAUUAAGUAGUGUGUGUGGGGUG	**151**	17,880795	32,450331	16,556291	33,112583	34,437086	65,562914	1,0204082	1,08	-77,4	-69,2	0,0362544	16	-51,258278	-1,4884615
spiLA0480-MIR1106-2	UUACCCCAGCAUUAUUUAAUAGUGUAUUUUAAAGGUAUAUAUGUGCGCAUGUGGACAUCAAAGAUAUUGCAUAAUUAUGAAUAGUAAUGUGUCCACGUGGACACAUAUAUACCUUUAAAAUACAGUUUUAAAUAGUUCAGGGGGUG	**146**	19,178082	33,561644	13,013699	34,246575	32,191781	67,808219	1,0204082	1,4736842	-69	-66,1	0,134117	7,3	-47,260274	-1,4680851
spiLA0480-MIR1106-3	CACCCCCUGAACUAUUUAAAACUGUAUUUUAAAGGUAUAUAUGUGUCCACGUGGACACAUUACUAUUCAUAAUUAUGCAAUAUCUUUGAUGUCCACAUGCGCACAUAUAUACCUUUAAAAUACACUAUUAAAUAAUGCUGGGGUAA	**146**	13,013699	34,246575	19,178082	33,561644	32,191781	67,808219	0,98	0,6785714	-59,4	-58,9	0,228449	6,3	-40,684932	-1,2638298
spiLA0480-MIR11068c	UAUUCUAAUUCAUGGAUUAGUUAUACCUCAUACAAAAUCUUAUUUUAUUCCUAGAAAAGGGUGGGAUAACUAAUCCAAGGUUUAACAAUCCUUGGAUUAGACCC	**104**	14,423077	33,653846	17,307692	34,615385	31,730769	68,269231	1,0285714	0,8333333	-29	-20,58	0,143131	24	-27,884615	-0,8787879
spiLA0480-	UUCUUCAUCUUCUUAAAGCUCAUUGAUAGAGCUU	**137**	17,518248	31,386861	17,518248	33,576642	35,036496	64,963504	1,0697674	1	-	-25,6	0,0171327	21	-24,59854	-

MIR11068e	UUCUUCACAUGGUAUCAGAGCACAGGAGAAUUUG										33,7					0,7020833
spiLA0480-MIR11068f	AAACUCUCUGUUGAGCUCUUCAUAAUCUGAAGAC AAGAGUCUAAAGAAUCUUGAAUUGAAGAUCAAUU G UUUGAGGUGUAGUAGUAGUUGGUUAUAUUUAUAG UGGUGGAGCAUGUGGUUUAAUUCGAUGCAAAGCU AAGAACCUUACCAGGGCUUGACAUUAUAUGUUUU CUUUGCAUUAAGUAACAAUUGAGCAAAAAGUCUA GUAGAGACCGAACCAACUUUUACUGUACAUCGAU GAUCAAGGCUUACUUCGAGCGAAUAUCAACCAGA UCUUGAUGAUGAGGCUAUAGUAGCAAAUAUCGAA AACAUUUUAACAUUAGAUUGUCUUGGUAAUUAACA AGAACAUGAACAACAAUAAUAUGUAAUUUUAUUUC UCAAGUUUAAUUGAUGAAUUAAGAAUAUGUAAAG GCCUACAAGACACUAUUACAAACUUCACUUUGUUA	**170**	22,352941	30	13,529412	34,117647	35,882353	64,117647	1,1372549	1,6521739	-45,7	-44,6	0,0300315	9,8	-26,882353	-0,7491803
spiLA0480-MIR11077b	UAUUAAUCAAGCAAUACAUUGAUGAAAUGUAAGAU CUUUGCUUCAUUUUGCCUCUUUCAUCAUGAGGAC UAUAGUUUCAUCUAGUCGAGUUAGCUUGCAC AAGUGCUAUUCUUAUUUUUGCUUAUCUGGAGUUA CAAGUUGAGGAUCUUAUUGGUUAACGAUAGUUAU UAUCCCACUGUAAUAAAUACUUCUAACCAUGAAGA	**307**	15,309446	35,179153	15,635179	33,876221	30,944625	69,055375	0,962963	0,9791667	-66,5	-57,3	0,0001111	44	-21,661238	-0,7
spiLA0480-MIR11078d	UCCUCAACUUGUCGCUUCAGAUAAGAAAAUUAGU CAUUGCAUGG UGAUCCACCCACCUAACCCGACCCAUUUAAAAAAU AUGAUAUGACCCAUUUUAUUUUCUCUUUAAUCCU AAGUUAUUCCCUCCUUAAACCUUGAAUUAUGAUU	**147**	17,006803	29,931973	16,326531	36,734694	33,333333	66,666667	1,2272727	1,0416667	-60,1	-57,7	0,0396981	12	-40,884354	-1,2265306
spiLA0480-MIR11078e	AAAGACAAAAUAAAAUGGUUCAUAUCAUAUUUUUU AAAUGGGUCGGGUUAGGUAGGUGGAUCA GAUUUCAAUAAGUAUUUGCAAUAAAGACAGAGAUU UGGGUCUUCAAGUUAUCUGAGGCUGUUUUGCGU AAAAAAAAAUGCUUCAUUCCAGGCAAUGGAUUGG UUGCUGGUGUCAAAAGCUUCACUUAGAGGAAUGC CACAUGAUUACCGAGGCUGGACUUUUUGGCAUAG UUUUGAACUGUGGUAAGAACCUGAAGCCGAGGCU	**166**	13,253012	32,53012	19,277108	34,939759	32,53012	67,46988	1,0740741	0,6875	-95	-95	0,178707	4,5	-57,228916	-1,7592593
spiLA0480-MIR11078f	GGAUAUUUUGGCAUAGUUUUGAACUGUGGUAAGA AACUGAAGCCCGAGGCUGGAUUUUUUGGCAUAGU UUUGAACUG AUAAUAAUAAGGGAGAAGUGUUGAAAACACCCCUA AACUCGGUUUUCUAUUAAGAGACCCAUACUCCUA CAAGAGUUUGAGACCACUUGCAAUUUCACGUAGU AGAUCAAAGGUGUAUCUAAGUUUAGUUAGUCAAG UAGAGGGGUGUUUUUAAGGUUGUCAAUAGUUUG	**281**	25,978648	27,758007	14,590747	31,672598	40,569395	59,430605	1,1410256	1,7804878	-79,9	-53,1	0,0001285	74	-28,434164	-0,7008772
spiLA0480-MIR11083c	GGGAUGAAAAUGAUAAUUAUGCCAAGUUCAGGGG UGUUUUCAAUACUAUUCUCUAUGAUAAA ACUAGUGAACUUCAUCUUUGUAAUGAGUUCCAAU UCCCUACCAUAUUGCCAAAUAUUUGCCUUUAUCU UUGUGUUCAUCUAGCUAAAGACAAAUGUUUGGCA	**232**	21,551724	32,758621	13,793103	31,896552	35,344828	64,655172	0,9736842	1,5625	-67,1	-50,6	0,0006364	60	-28,922414	-0,8182927
spiLA0480-MIR11085	AUAUGGUAGGGGAUUCUGGUCUUCUGUACACAGG GAAAAGUUGACUUCU GUUAAAAUUGAAAAUAUUUAAAUGGGUUGAAUAGA AAUUGGGUUGGGUCUUGACCUGCCCAAGUUUACU	**151**	18,543046	26,490066	18,543046	36,423841	37,086093	62,913907	1,375	1	-64,1	-63,9	0,0414341	12	-42,450331	-1,1446429
spiLA0480-MIR11088b-1	UUGGACUCAAAUGGGGGCUAAAAUAUGUGUUGGG UCUUGACCCACCCAAUUUGACUUGAUUAAUUUCA AUAAUUUAACAUAUUGAU UAGUGGUUUGGUUUGACUUGAUUUGGUGUUGGG	**155**	20,645161	30,967742	12,903226	35,483871	33,548387	66,451613	1,1458333	1,6	-45,5	-39,9	0,0179728	27	-29,354839	-0,875
spiLA0480-MIR11088b-2	AAAAAAACCCGACUAUAUUUGGGUUGGGUUGAUU UCAACUAAAAUAAACCAACCCGAGACCAAACCAAC C AUUUAGGAGAGAAGAGAUGAAGGGCAAAUCUGGU CCCACUGGGCGUGCCAAUUUUGCAACAAAUUUUA AAGUGAUUAAAAAUAAACUGCAAUCACAAAUAAAA UCUGGAGAAACAUGAUUUUAUUGAUAAAUAUUGC	**103**	22,330097	31,067961	17,475728	29,126214	39,805825	60,194175	0,9375	1,2777778	-36	-33,6	0,029739	24	-34,951456	-0,8780488
spiLA0480-MIR11089a	GGGUACAAUUCUGUUGAUCCCUUGAUUCUACUCU CCUAGGC	**178**	19,662921	34,831461	16,292135	29,213483	35,955056	64,044944	0,8387097	1,2068966	-49,2	-47,6	0,0053513	22	-27,640449	-0,76875
spiLA0480-MIR11091	CGACUGACUUGUCUACUUCAAGUGUUGAUGAAGA AGGAAGCUGAGUAUUGGAGCAUGUCGAAGGAACA	**124**	26,612903	31,451613	15,322581	26,612903	41,935484	58,064516	0,8461538	1,7368421	-40	-40	0,055982	8,2	-32,258065	-0,7692308

spiLA0480-MIR11092	UGUUCAACGAAGCUGACUGACGAGUUACAACACU GUUGAAGAUUUAGAGUCAGAUU ACUUCAGCUGACAAGUAAGCCACUCCAACUUUGA GAGUGAAUAUCUAAACGCCUCAACUUGGUCUCAA CAUUCAAUUUGUCCUCGUGCCACAUAAAUUUUGC AUGUGUGUAUAGAUGAUCAUUUUGUAACUGACAC AGAGGAGACGAGUUGAAGUGUUUAGAUGUACAUA CUCAAAGCUGGAGUGUUUAAUUGUUAGCUGAGAC UGUGGAGUAUUCGUGGUCUUGAUCUCUUUGUGG AUUUUUCGAGAUGCCUUUUAAGGGAAUUUAAUAG	**204**	20,588235	29,901961	18,627451	30,882353	39,215686	60,784314	1,0327869	1,1052632	-83,5	-83,2	0,007636	20	-40,931373	-1,04375
spiLA0480-MIR11103c-1	CCUUUAUAUAGGCAUAAAGUAGGGUUUAGGGUUG AGUAGCAUUCAAGAAUCCUAAUCUGAAUUGAACAC AAUUUGUAGAGUCCCAACUCGAAUUGAACGCAUC UUCUAGAAUUCCACAAAAUUUCAAUGUCUACAAAU GCCCCCUG	**213**	20,187793	28,638498	17,370892	33,802817	37,558685	62,441315	1,1803279	1,1621622	-56,8	-42,8	0,000524	42	-26,666667	-0,71
spiLA0480-MIR11103c-2	UCAAUUUGUAGAUUAUUCGAGAUCUUGAUCUCUU UAAUCUUUAUAGAAUUUCUGAGAUGCCUUUUAAG GGAAUUUAGUACCCUUUAUAUAGGCAUAAACUAG GGUUUAGGGUUGAGUAGCAUCCAAGAAUCCUAGA AUUGAACACAAUUUGUAGUGUCCCAACUCGAAUU GAACGCAUCUUCUAGAGUUCCACAAAAUUUCAAU GUCUACAAAUGCC	**217**	17,050691	30,875576	17,511521	34,562212	34,562212	65,437788	1,119403	0,9736842	-54,1	-52	0,0010136	32	-24,930876	-0,7213333
spiLA0480-MIR11108h	UGUAGGGAGGAUAGUGUUAAAGUAUGACAAAAGU CUCACAUCGGUGAUUAAUGAGAUGGGUGGACUCU UUAUAAGGCUUGGACAAUUCUCCUCCCUUUG	**99**	26,262626	27,272727	15,151515	31,313131	41,414141	58,585859	1,1481481	1,7333333	-28,7	-26,7	0,0286074	15	-28,989899	-0,7
spiLA0480-MIR11108s	GCCAGUGGGCCACCCCAAAGGAUAUAUAUUGCUA CUUUUGAGGAUAUGUAAGUCGGCUAAUCCUCAAA AGUAGAAAUAUAUAUCCUUUGGGGUGGCCCACUU GA	**104**	23,076923	28,846154	20,192308	27,884615	43,269231	56,730769	0,9666667	1,1428571	-73,4	-73,1	0,161245	2,5	-70,576923	-1,6311111
spiLA0480-MIR11110b	AGUGAUUCUGAACAUGGCAGAAUUAUACUCAUGU AUAGACUUAAAUUCUUGUAGCCUUAGAUGCAUCC AAUCAUAUCGUGCAUUUAGAUGUAUGACCAUCUU CAAGUGGUCAAAUCUUUCUUUUAGGUUUUUCCAC AAAACAAGUGGAUCCUUAACUGUCAGAUAUUUGA UUUUCAGAAUCUUG	**184**	16,304348	29,347826	17,391304	36,956522	33,695652	66,304348	1,2592593	0,9375	-45,6	-42,2	0,0059938	24	-24,782609	-0,7354839
spiLA0480-MIR11114	CCCUCUGUCCCUAUUUAGUUGUCCGCUUUAGAAG UGACACACAUAUUAAGGCACCAAUUAUCAUCAUAG GUUAGCUACAAUUUUAUCCUUAACUUAAAAGAUUA UGCAUAUCCACAAGUAUAAUAAAUGUAUUUCUGG UUCCAAAAAGCAUGCAUUACAACUUAGUAGUACUA GAAAUUUUCUAGAAUUAAAUAAGGGCAUAUUAGG GAAAAAAAUGUUGUCCUUCCUUGAUUUGUUAAAA UGAACAAGUAAAUAGGGACAGAUAU	**266**	15,037594	36,090226	16,165414	32,706767	31,203008	68,796992	0,90625	0,9302326	-64,4	-64	0,0013052	35	-24,210526	-0,7759036
spiLA0480-MIR11124	UGAUCUGAAAUUUGGGUAAGAUUCAACAAAACAG GACACAACAUUGUUUGCUUAGAGGCUUCUUUGUC AUCUUGGUGCUUGAUCGGAGCCUGAAGCUCCAAU AGAUGGAGCGGUGGGCAUACCAUUUGUUGAUCCA UUUUCAAGUGGUGGAGGGACUCCCCAUUUGCCUU CAGAUUCAAGUGGUUCAAAAACAUGAACACUACCA UCUGACAGACCUAAUGCAAACUGGUUUGGAUCUU GUGGAUGUGCUGCAACUACGACUGGGUGGAUGU UUGAAUUGCUGCAGAAAAAUGACAAGGUUUUAUG AAAAAUUACAUCAAAUAUCAGAAAU	**331**	23,26284	29,607251	17,824773	29,305136	41,087613	58,912387	0,9897959	1,3050847	-96,5	-74,5	0,0010334	89	-29,154079	-0,7095588
spiLA0480-MIR11136-1	UGUAAAAAUCGAACCGACCAAUAAAUCGAACCGAU AAAAUGUUAUUGGGUUAUUGUAAUUGGGUUAUUG GGUUUUUAAUGGGUUUAGAAAAAAUAAUUAUUGG GUUAUUGGGUCGGUUUCGGUUUUUCCU	**130**	23,076923	29,230769	9,2307692	38,461538	32,307692	67,692308	1,3157895	2,5	-32,7	-28,8	0,0028012	30	-25,153846	-0,7785714
spiLA0480-MIR11136-2	UCUUAGAUAACAGAAUGGUUGGGAGUUUGAGCCC CCACGACCCCUUAGAUUUUUAGAGUUAAAUUCGA UACAAUAUGGAGGUUGUGGGCUCAAACACCCACA ACCCCCCUUAUAUUUUUUUUAAAUUUCGCUUAGG AGGCUGUGAGGUGGUGGGUUCAAAUCCCACAGC CCCUCUAUCAUUUAUUU	**186**	20,430108	25,268817	22,043011	32,258065	42,473118	57,526882	1,2765957	0,9268293	-61,2	-48	0,0021679	38	-32,903226	-0,7746835
spiLA0480-MIR11156	UUCCAUUAAGAUUAAGAGGUCUGAAUCUGAAUAC ACAUCUGAUAUUAAGAGUUGCAGUAAGAUUGGAU GUUUCAAUCUGAAUACACAUCUGAAUAUUAAGAU	**137**	17,518248	36,49635	13,868613	32,116788	31,386861	68,613139	0,88	1,2631579	-30,6	-27,8	0,0090613	13	-22,335766	-0,7116279

spiLA0480-MIR11175	GUAGUCUCCAAAUCAGAGCACUAAAUAUAAUGUUG GAGAUAGCUUUCAACAAGAGAAAAGGAGAGAAAG AACAGGGUUCUUUUGCUGCAGUCUUUUCUACGAC CAGUCACGUUCAGAUCAUGUUUCCUGAUUAACUA ACCGUUGGAUCGGACUGAAAUUUGGAGAGAGUGU CCCUGACAUCUUGGUGGUUGAUUUGAACGAUGGA GAUCGGAUUCAGAGGUUAGAAAGAUCCUGUUUUA GGUCCCGUACAAAAGUUGGGUUUGGGUGGUGUU UCUUUCUAUUUAUCUUUUGUUGGUGUAGCUAUUGU	**272**	26,470588	24,632353	15,073529	33,823529	41,544118	58,455882	1,3731343	1,7560976	-80,2	-74,8	0,0005079	52	-29,485294	-0,7097345
spiLA0480-MIR1127	GUGUAGUGGACAAGUAAAGGUGGAUGGAAGAAUUACUUCCUCCGUCCACUUUUAUUUGUUCACUAUACAACAUUUCAGUUGAUCUUGAUCCCAUUUACUCCCUCUCCCUUUGCCGGACAAUAGUUGUCCACUAUUGACUUGGUACAGGGAUUAAGAAGCAGUAAAUGAUAGGGGUAAUUUUACCAAAUCACCCUUAUUAAAAGUAAGUCACAUAAACAUCGAAAAAUAAAUAGUAUUUAAUAGCAAGGUAAAAACGACACAACAUGCUAAAUGACUCAUUGAUUUAAUAAGCUGGACAAGUAUUGUUGGACGUCUCAAAAUAGUAUAGUGGACAAGUAAAGAUGGACAGAGGGAGAGGGAGUAGCUUAGACUCAUAGCAGCAAAGAAAUUAU	**68**	22,058824	26,470588	17,647059	33,823529	39,705882	60,294118	1,2777778	1,25	-43,4	-43,4	0,597752	0,9	-63,823529	-1,6074074
spiLA0480-MIR1127b	UAUUACUCCCUCCGUCCCAAUUUAUAUGAGUUAGUUUGACUUGUCAUGGAGUGUAUGAAAGAAGAAAAGACUUUUGAAACUUGUGGUCUAAAAUAAGUCCUAUAUAUUGUAAGGCUAGAGCCUAGAAAUAAUUUCAUUAAGGGUAACAUGAACAUUUUAAAGUUAAAUCGUUAUUAAUUAUAGAAAUAUGUCAUUCUUUUUGGGACUGAGUAAAAAGGAAAGUAAGUCAUAUAAAGUGGGACAGAGGGAGUAGUU	**324**	19,444444	37,345679	16,358025	26,851852	35,802469	64,197531	0,7190083	1,1886792	-88,1	-76,1	0,000286	52	-27,191358	-0,7594828
spiLA0480-MIR1128-1	CGCUACUCCCUUCGUCCCUAAUUACUUGUCCACUUUUCCUUUUAUAGUUGUCCGUAAUUACUUGUCCAUUUUGACAAAUUAAGAAAGGACGAAUUUUUUUUACCUAUUCUAUUAAAUGACUAAUUACUUUGAAAAAUGUAGAACUUUUCAUCCAUUUUAAAAUUAAUAGGGGUAAAAUGAUAAAACUCACUACGUCAUUAAUUAUUUUCUUAAUAGGUGUGCCAAUUCAAAAGUGGAAAAGUAAAACGGGAUGGAGGGAAUAUUA	**256**	20,3125	35,546875	10,9375	33,203125	31,25	68,75	0,9340659	1,8571429	-74,2	-72,2	0,0043251	43	-28,984375	-0,9275
spiLA0480-MIR1128-10	AAUUACUCCCUCCGUCCCAAUUUAAGUGUUUUAGUUCGAUUGGACACAAAGUUUAAGAAAUAAAGGGAGACUUUGAAUCUUGUGGUCUUCAAUUAAAGAUGUGUGUAGUCCUUUAAAUCUUGUGGUCUCAAAACUUUCCAUGUAUAAUGUUGGAAUUGGAGAACUUAUUAAAUAUUGAAAGAGGCAGUCUUGCUGGGACAGACUAAAUGGGAAGACACUUAAAUUGGGAUGGAGGGAGUAGUA	**265**	14,339623	33,207547	15,849057	36,603774	30,188679	69,811321	1,1022727	0,9047619	-64,4	-50,79	0,0001037	69	-24,301887	-0,805
spiLA0480-MIR1128-2	GGCUAAUAAUGUACUACUCCCUCCGUCCCAUUUUAUGUGGCACCAUUUCCUUUUUGGUCAGUCCCAAAAAGAAUGUCACAUUUUCUUAUAUGGUAAGUAUUUAAAGGUACAAUUCCUCUUUUACCCUUGUUGGUCCCACUUAAGUACUCUAAUACAUUUAUGAGGAGAGAGAAAAGGCGAGUUUACUUUUUUGAAGGGCAAUUUGGUAAACAUUUCAAAGUCUUCAUUAUUUCUUAAACUCCGUGCCGGGUCAAAUGUUGCCACAUAAAAUGGGACAGAGGGAGUAUUAUUUUAUCUAUUA	**243**	23,045267	31,687243	13,168724	32,098765	36,213992	63,786008	1,012987	1,75	-81,5	-74	0,0004101	57	-33,539095	-0,9261364
spiLA0480-MIR1128-3	UACUACUCCCUCCGUCCCAAAAUAAGUGUCACUUUAGCAAUAAUCAUACUCACUAAGAAAAAUAAUAAAUAGAAAGGUAUAGUUCACCAAGUUACCCCUAUUUAUUAGUUGUUUCUUGACAAUUGAGCAUGAUUGAUAAGUAGUUCUUUAGUACAAAGGUAUACUUGGAAAAACACAUACUAAUUUCUGUCUUAAGUUCCUAUGGUGACACUUAUUUUGGAAAAAAAUUUAUUGCUAAAGUGACACUUAUUUUGGGACGGAUGGAGUAUUU	**300**	17,666667	28	18,666667	35,666667	36,333333	63,666667	1,2738095	0,9464286	-97,7	-97,7	0,0069308	18	-32,566667	-0,8963303
spiLA0480-MIR1128-4	UGACUUUCCUGAAAAGUUGUGACUUUUAUGGAAAGUUGUGACUUUUAUG	**269**	15,613383	34,200743	15,613383	34,572491	31,226766	68,773234	1,0108696	1	-98,5	-97	0,0031694	27	-36,6171	-1,172619
spiLA0480-MIR11285		**113**	22,123894	30,088496	9,7345133	38,053097	31,858407	68,141593	1,2647059	2,2727273	-40,9	-39,5	0,0019822	15	-36,19469	-1,1361111

spiLA0480-MIR1128-5	AAGAGUUGCGACUUCUAUGAAAAGUUAUGACUUUUAUGAAAGGUUUUCUACUCCCUCCGUCCCAUAUUAGUGGUCCACCUUACUAUAAAUAGUUGUUCCACAUUACGGAAGUGGACAACUAAUAUGGGAUGGAGGGAGUACUUGGCUAAUGUUUAUUACUCCCUCCGUCCCAAUGUGAGGUAGUUUGACUUGGCAGUUUAAGAAAACAGUCUAAAAUAAGUUAUAGAUGUUGGUGUAGCUGUAGAUCAUUUUAUUAAGGGUAAAAUAGGCACUUUAAAGUUAGAUUGUUACUGAAUAUUGAAAUGCGUCAUUC	**98**	20,408163	26,530612	22,44898	30,612245	42,857143	57,142857	1,1538462	0,9090909	-54,4	-54,4	0,26242	4,4	-55,510204	-1,2952381
spiLA0480-MIR1128-6	UUUUUGGGCUGACUUAAAAGAAAAGUGAGCAUAUAAAUUGGGACAGGGAGUAUAUAGAAAGUAAAUUACUACUCCCUCCAUCCCAAUUUAAGUGUCUUCCCAUUUAGUCUGUCCCAGCAAGACUGCCUCUUUCAAUAUUUAAUAAGUUCUCCAAUUCCAACAUUAUACAUGGAAAGUUUUGAGACCACAAGAUUUAAAGGACU	**236**	22,457627	33,474576	11,016949	33,050847	33,474576	66,525424	0,9873418	2,0384615	-57,6	-52,7	0,0003112	52	-24,40678	-0,7291139
spiLA0480-MIR1128-7	ACACACAUCUUUAAUUGAAGACCACAAGAUUCAAAGUCUCCCUUUAUUUCUUAAACUUUGUGUCCAAUCGAACUAAAACACUUAAAUUGGGACGGAGGGAGUAAUU	**243**	13,168724	32,098765	23,045267	31,687243	36,213992	63,786008	0,9871795	0,5714286	-66,1	-59	0,0012488	34	-27,201646	-0,7511364
spiLA0480-MIR1128-8	UAAUUUGUUGACUUCCAAGAAAGCUAUUACUCCCUCCGUCCAACAAUACUUGUCCACUUCAUGAAAUCCAUGAAUAAUUUUACACUUAGUUCCUAAUUUACCCUUAUCAUAAAUUAUAGUCAUUUCACUCAUUUCCCUAUUUCCCUAUUAUAUUUUUCAAGACAUUGUAUUUAUUAUAUUCAAAGGGUGAUAUAAUAAAAUUACCCAUCUAUAAGAAGUGUACCAAGUCAAUAGUGGACAACUAUUGUUGGACAGAGGGAGUAUAAAAGUUUUGAAAGACACCAAAAUG	**289**	12,110727	34,256055	18,685121	34,948097	30,795848	69,204152	1,020202	0,6481481	-72,5	-65,6	0,0005726	41	-25,093426	-0,8148315
spiLA0480-MIR11288c	ACUACAGGAAUCUAUUGAUUUAGGAUUUGUCAAACUAUACCGUUAUCAAGAACAGAGGAGAUGUGACCAUUACUCAUCUCCUCUGUUCUUGAAUAGUUUGACAAAUCAUAAAUCAAUAGAUUCCUGUGAA	**130**	16,153846	33,846154	17,692308	32,307692	33,846154	66,153846	0,9545455	0,9130435	-78,2	-78	0,554057	1,9	-60,153846	-1,7772727
spiLA0480-MIR1128-9	AAAUAAUACUCCCUCCGUCCCAUUUUAUGAGGCAAAAUUUGACCGGGCACGGAGUUUAAGAAAUAAUGAAGACUUUGAAAUGUUUAUCAAAUUGUCCUUCAAAAAGUAAAUUCACUUUUCUCUCUCCUCAUAAAUGUAUUAGAGUACUAUGUUUAAAAUUAAGUGGGACCAACAAGAGUAAAAGAGGAAUUGUACCUUUAAAGACUUACCAUAUAAGGAAACAUGACAUUCUUAUUGAGACUGACCAAAAAGGAAAUGGUGCCACAUAAAAUGGAACGGGGGGAGUAGUACAU	**294**	18,367347	37,755102	15,986395	27,891156	34,353741	65,646259	0,7387387	1,1489362	-74,2	-62,3	0,0002272	67	-25,238095	-0,7346535
spiLA0480-MIR1130b-1	AUGUAUAAAAUUGAACAAUUAGACAUAUUUGUCCGACAUGUCGUCCUUGCACCCUACAUAUAUUAUGUCACGUAGGACACAUAUAUCUUCUUGUUCAAUUUUAUAUAA	**108**	12,037037	32,407407	18,518519	37,037037	30,555556	69,444444	1,1428571	0,65	-32,6	-28,49	0,142363	12	-30,185185	-0,9878788
spiLA0480-MIR1130b-2	GAAAACUAGUACUUACUUCCAAUGUCCAACAAUAGUUGUCCAUUAUUGACUUGACACAUGAAUUAGAAACAGUUAAUGAUAAGAGUAAUUUUACCAAAUCACCCUUAUUAAGUACAAGUCAUCUAACAUUAUAAAAUGGGACAGAGGAAGAAGUAUUUAAUAGCAAGGGUAAAAUAGACAUAACAUGGUAAACUAUUCAUUGCUUUUAUGAACUUCACAAGUAUUGUUAACAUUCCAAAGUAAUAUGAUGGACAAGUAAAGAUGGACGAAAGGAGUAAUUAACUGUUAUG	**290**	16,551724	40,344828	13,793103	29,310345	30,344828	69,655172	0,7264957	1,2	-62,5	-60,07	0,0003097	36	-21,551724	-0,7102273
spiLA0480-MIR11330	UCUCCCUACUGUUAAAACGAAGUUAUUUUUACCCCUACCGUUACUAAUUUCAUCAUUUUAACAUUGGGUUUGAAAUGGGAAAUGUAUAAAUGAUGAAAUUAGUAACGGUAGGGAUAAAAAUAACUUCAUUUUGACGGUAGGGGCA	**145**	18,62069	33,103448	14,482759	33,793103	33,103448	66,896552	1,0208333	1,2857143	-81,1	-81,1	0,193063	3,9	-55,931034	-1,6895833
spiLA0480-MIR1134-1	UUGAAACUUUAUGCACAAAAAUUGCAGCUUCCUCUCCGGUUUGAUCAACAACUAGAAGCAAAAGAAGGUUGUCGAAUUUCCACCAAAAAAAAAUAGCCUUCCUUUGCUUCUAGAAAUUCAGAGUGUUGAUCAAACCCGAGAGGAAUCUGCAGUUUUUGUGCAUAAAGUUUCAA	**173**	17,34104	34,104046	19,653179	28,901734	36,99422	63,00578	0,8474576	0,8823529	-96,9	-96,9	0,0981255	4,8	-56,011561	-1,5140625

spiLA0480-MIR1134-2	GAUAAAAUCAUUGAUGAUCUUCUCAUGAAUUACU UUCUGCAAGGAUCACAAUUUGCUGAUCUUUCCCU AGCUGAUGAUAGUUGGGAAUUGGAUAUUGAAGGA UAUUUAUAUGAUUACUAAUCUAUUUGUUAUAUCU UUGCAGAAUGGCAGGCGGAGAUGAGCCUCCGCCA UGGUCGCAUAUUCGUGGCCGUGGAGGAAAAACUA GAGGAAGAGGAAGAUCAUCCUCUUCACAGACCAG AAGAUCGUCAUACGAUUCUUCCU	**261**	22,222222	28,735632	18,007663	31,034483	40,229885	59,770115	1,08	1,2340426	-85,1	-78,5	0,0002475	43	-32,605364	-0,8104762
spiLA0480-MIR1134-3	GUUUCAAUAUUUCUCUUUGUAUUGGCUAUCAACA ACAACAAGAAGAAGAAUGCCGCAUAUACGUAUUU GUAGAAAUCAGUUCUGAUGUGGCUGAAUGCCACG UUAGAGUUGAGAUGAAUAAAAAUAAAGUAUUGACU A	**138**	19,565217	35,507246	13,768116	31,15942	33,333333	66,666667	0,877551	1,4210526	-33,3	-24,1	0,0064761	27	-24,130435	-0,723913
spiLA0480-MIR11409d	CUGAACUUUAUUCACUAUAACAGUAUGGUCACAAA ACUAUCUUUUGUUGCGUUAAAGUACGUGUUAAUU GCUCAAACAAUGACUAGAAGGUUAAAUAUUCUUU UAAUAUUAUUUUGAGCCAGAAAUUUAACCUUUGG GCCAUUUGUCUCAUUUGAGCAAUCCACACCCCUA GUUCAGUUACUUUAAUGUGACAAAAAUUAGUUCU GUGAUUCUACCGUUACCGAGGAUAAAAUUAAA	**237**	14,767932	32,067511	17,299578	35,864979	32,067511	67,932489	1,1184211	0,8536585	-71,6	-71,3	0,0055749	12	-30,21097	-0,9421053
spiLA0480-MIR11414	GUUGGAUCCAAGUUGGACGAGGGGAAAUAUAUUG GAGGCCUCGCAUCAACAAAAUUAGGGCCGAAUUC GGGUGGAGGCGUGUCCUGCCUUCGCUGGAUCUC GACCCUCAUAUCUUCUAUCAGCUGCAUCAGGUGU GCAAUUAAUUCAUUUUGUUCUGCCACGGUGGGCU GAGCCCCCACAACAUUUGUGAGGCUAACUUCAUC AUUGUUGUCUCCCAUGGCUGUAUUUCCUCUGUCU AAGUUUGGUCCGGG	**251**	25,896414	19,920319	23,904382	30,278884	49,800797	50,199203	1,52	1,0833333	-92,2	-77,2	0,0006746	55	-36,733068	-0,7376
spiLA0480-MIR11451	GAGUUAGGGGUCGUUUGGUAGAGUUUCUUAGAAA AAAUAAUGCAUGCAUUAGCCUUGUGUAUUACUAG UACCUUGUUUGGUACUCUUUUCCAACCUAUGUAU AACACUCUAUAGUGUAUUACGAUGUAUAUUGCUA AUACCAUUGAUUUCUAGAUAUGAUUUUAAUGCAU GCAUUAGCAUGAUUAAAGACCAAUUGCAUCUUAAA ACCUUUUUUUACAUCCUUUCCACCAUAAUAGUGG AGGUUAUCUUUGUAAAUUAAAUUUAUUAUGCAAU GCAUGCUAUUUUUUUAUGCAUCAAACCAAAUGAU GCAUAAAAA	**316**	15,189873	31,012658	15,189873	38,607595	30,379747	69,620253	1,244898	1	-76,9	-76,7	0,0004187	36	-24,335443	-0,8010417
spiLA0480-MIR11464a-1	UAGACACAUUCGUCCUACAUAACAUCCUACAUGG CGAUUUUUUGUCCUACUUGGCGUCCUACAUGUAU UAUGUCAUGUAGGACACGUGUGUGCA	**94**	19,148936	23,404255	23,404255	34,042553	42,553191	57,446809	1,4545455	0,8181818	-32,3	-27,5	0,143356	7,1	-34,361702	-0,8075
spiLA0480-MIR11464a-2	GCCCUUCAACUUAGGAUGUGCACAAGUAGACACU UAAACUUGUAUAAAGUUGAAUAAACGGACACACAU AUCUUAAAUGUCAUCCUACAUGUCAUUUAUUGUC AUAUGUGGUGUCCUACGUAUAUUGCGCCAUGUAG GACUCAUGUUUUAAUUUAUUUAAAAGUUGGAUAG UUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUGGA GAUA	**209**	19,138756	30,62201	14,832536	35,406699	33,971292	66,028708	1,15625	1,2903226	-67,1	-58,3	0,0305374	29	-32,105263	-0,9450704
spiLA0480-MIR11466a	NNNAACCUCUUAAUGGAUUAUACUUAUUUAUUAU GAAAUAAUAAUGAUUUAAUAAUCAUCUUGUCUAGU CACUACUACAGCUUUCUUCUUUGGUUAGUUACCC UAACAGCGCCUCAACUUUGUUUACUCCCCUAAAC GGCUUUCUUGCCUACCGGUUUCAACCUUAGGAUG ACAUAGUCUGGGCAUACUUAUCCAGAGAAUAUUU CUGUAGCAAACCUUCUAGAGAUGUUUAUUAAAGC AUUAUUAAGUCAUGAUAAACAAUUAUAAUCAACAA GAGAUUUUC	**283**	13,074205	30,388693	19,434629	36,042403	32,508834	66,431095	1,1860465	0,6727273	-75,3	-72,8	0,0033449	22	-26,607774	-0,8184783
spiLA0480-MIR11499b	CUUAGUAUGUGAUGCACCUACUUUGUCCUUUUGG UUGGCCAAUAAGUCAAAGUUUGUUAUGCACCUAC AUGGUCUUUUGAGUUGGUCAAUAAGUCAAAGUAG GUGAUGCAACUACUUGU	**119**	21,848739	24,369748	16,806723	36,97479	38,655462	61,344538	1,5172414	1,3	-35,8	-33,1	0,0239431	17	-30,084034	-0,7782609
spiLA0480-MIR11504-1	CGUUGUGGCUUGUGCUUGAGUAGUAAUGGCUUG GUCCAUUUUAGAAGGAAUUACCCUCAUCUCCGCC UCCAUCAUAGGUGGAGGGUUAUCCGGGUCUUGA UCAACACUAGCAUUCUCCUCAUGUGGAGGAACUU GAUCAACAUGGGGAGGAGCUCAUGCUUUAGCAAC	**196**	23,979592	21,938776	23,469388	30,612245	47,44898	52,55102	1,3953488	1,0217391	-68,2	-58,3	0,000862	37	-34,795918	-0,7333333

spiLA0480-MIR11504-2	UUUCUCCUCAAGUAUUCGAGCCACAUUCAUAUUGUUCAGCUGAAUCAACAGGAGGAAGAGGUUGCAGUUCUGGAUAAGUGGCCGGCGGUGGAACAGCCGCUGGCAAAGGAAAAGGUCCAGCUGCUAAUGCUGGAACUUGCACACCAGCUGGCUGUGGAUGGUUAAAUUUACAGGUGAUACCAAAUUUACAGUGCCCUGUUUUCAUAUAGUGUGCACAUUCCUUUUCAUUCUGUGAAACAAACU	**215**	26,046512	27,44186	19,534884	26,976744	45,581395	54,418605	0,9830508	1,3333333	-70,7	-52,7	0,0074866	51	-32,883721	-0,7214286
spiLA0480-MIR11514-1	UGCCCCUACCGUCAAAAUGAAGUUAUUUUUAUCCCUACCGUUACUAAUUUCAUCAUUUAUACAUUUCCCAUUUCAAACCCAAUGUUAAAAUGAUGAAAUUAGUAACGGUAGGGGUAAAAAUAACUUCGUUUUAACAGUAGGGAGA	**145**	14,482759	33,793103	18,62069	33,103448	33,103448	66,896552	0,9795918	0,7777778	-79,4	-79,4	0,448539	1,8	-54,758621	-1,6541667
spiLA0480-MIR11514-2	AUAUUAGUACUUAAGUUCACUUAUGCCCUUACCGUCAAAUACUUGGUCCAAAUACUAUGCGCAAUUGAGCAGAAUAAGGGUGUAUGUGGGCCAAGUAUUUGAUGCUAAGGGCUUAAGUACAUUGAAGUAUAAACGUGGUAAGGUUAUAUGUAUGUUGAAGUCAAAAGCC	**135**	21,481481	31,851852	16,296296	30,37037	37,777778	62,222222	0,9534884	1,3181818	-56,4	-55,5	0,0742568	13	-41,777778	-1,1058824
spiLA0480-MIR11519	GUAAUGGUAUACUUCAAGUAAAGGAAUGAUGGAAUUAAGGUUGAUUGACUGGAAUGACAUCAUAUCAAACCUUAGUA	**111**	23,423423	36,036036	9,9099099	30,630631	33,333333	66,666667	0,85	2,3636364	-27,4	-27,4	0,075049	17	-24,684685	-0,7405405
spiLA0480-MIR11525b	CGCUAUAGGAAAAGGGUAUAUGUGAGCCAUUUGUUUACAAAUAAGGGUAUAUAUGAGCCACUUUCAUAACUAGGGGUAUAUAAGCUCUAAAUGACAAAGUAGAGGGCUUUAUCAGACCCUUUUCCCUUUAUGU	**133**	21,052632	31,578947	15,789474	31,578947	36,842105	63,157895	1	1,3333333	-35,7	-34,8	0,020834	26	-26,842105	-0,7285714
spiLA0480-MIR11546e	UAAAAUGGAUGAUUUAGCUAUGGAUUGAAGUAGUGAGAAUGGAUUGGUGGUACACUGCCCUAUUCUCCUUAUUUUAUCUAAUGUAAAUCUUGAAUUACG	**99**	21,212121	29,292929	12,121212	37,373737	33,333333	66,666667	1,2758621	1,75	-25,3	-25	0,0371092	11	-25,555556	-0,7666667
spiLA0480-MIR11551b-1	ACCAUUUAUUUGACAAAUUUCCAUGUCAGCGCGAGUGUGCUACACUCAUUUUAUAUUUUUAGCUGAUUGUCAAAAAAAUGCUCAAAUGGUUAUAAUUCAACUCGGUAGAGGUGUUUAAUAGGUACAUGUUAUAGUUAAGGUGUUUAAAUGAAAUAUGCGAACAACUUUAAUGGGCUGUAAAUGACUUAAGUCGUAAUGCAAAUGAUUUAAUGCAUGCAUUGAUAUGAUUAAAGACUCAAUUACCCCUCAAAAGUACUUUUACAUCUUUUCCACCAUAAUUGUGACUGAUAUUUUAGUAAAUAAAUAUUAAAAAAACUAACAGCAUUAGGUUGAUAUACUAGAA	**308**	15,909091	33,766234	14,285714	36,038961	30,194805	69,805195	1,0673077	1,1136364	-66,1	-63,3	0,0009017	24	-21,461039	-0,7107527
spiLA0480-MIR11551b-2	UGUAAGUAACGUUGUACUCCUAAAACGUUACUGUGAGCAGUAACGUUUUACUCCUAAAACGUUACUGUGAGUAACGUAUAUCAAUCUGACGCCAUCAAUUUUUUUU	**137**	13,868613	35,036496	16,788321	34,306569	30,656934	69,343066	0,9791667	0,826087	-43,6	-43,4	0,103234	10	-31,824818	-1,0380952
spiLA0480-MIR11553-1	AACAAAAUUAUUAAAAAUGGGUCGGAUAACGUAUUUAAAAGGAGUUGAUUUAUGGGUUGGAUUAGGUGUUUAUGAGUCCGGAUAUCUUUUCAUUUUCAUAUAAAUGUCACGUGGUAAGGUCAAAAUGACAUAGCAAUUCCAUGUGGCAUUUUAAAAAAUGAAAAAUGAGUUGGAUAUGUCCAACAUGAAAACUAACGUCCAUAAGGGCAUAUUGGACCAAAAGUUGGACGGCGAGGGCAUGAGACCUUUUCGAAUAGUUUAGGAGCAUAUUUGAUCCUUUUCCC	**316**	21,835443	34,177215	13,291139	30,696203	35,126582	64,873418	0,8981481	1,6428571	-80,1	-69,6	3,16E-05	59	-25,348101	-0,7216216
spiLA0480-MIR11553-2	GAUUUAUGGGCCGGAUUAGUUGUUUAUGAGUUCGAAUAUCUUUCCAUUUUCAUAUAAAUGUCAUGUUUUAAGGUCAAAAUUACAUGUCAAUUCCAUGUGGCAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUAUCCAACAUGACAACUAACGCUCAUAAGGG	**161**	18,63354	33,540373	13,664596	34,161491	32,298137	67,701863	1,0185185	1,3636364	-37,2	-30,8	0,0013084	36	-23,10559	-0,7153846
spiLA0480-MIR11553-3	UGACAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUACCCAACAUGGCAACUAACGCUCAUUAGGGCAUAUUUGGACCAAAAGUUGGACGGCGAGGGCAUGAGUGAACCAAUCUUUAAACGGAGAAUAUAUCUAAACUUUUUCGAAUAGUUUAGAGGCAUAUUUGACUCUUUUCCUUUCUUUAAAUGAAA	**188**	19,680851	35,106383	15,425532	29,787234	35,106383	64,893617	0,8484848	1,2758621	-47	-45,3	0,0075659	24	-25	-0,7121212
spiLA0480-MIR11563	GAAGAGAUAGUACUAUCUAUACAUUUCAUUAAAAUGAUUUUCUGGGAUUUUGUGGCGAUUGUUGUCCCCGCUAAUGGUCUAAUUCUUUUGUAGUGAAUCCUAGUUGGCAACGCUUAGGUGGAAGAAUUAGUCCCAC	**239**	22,175732	27,615063	16,317992	33,891213	38,493724	61,506276	1,2272727	1,3589744	-66,3	-65,5	0,0005112	27	-27,740586	-0,7206522

spiLA0480-MIR11574	AUUGUCUUGCCAUGUCACGAAAACUUGGGGAUUAACCUUAGAAUAACGGCAGGGCAUUUUUUAUCCCAAAAUGUAAUGAAGGGUAUAAGUGGUCUAUUUCGCAAACUUUAUGGAAGAUCUUUUACCCCUAAGCUAUUUAAUAGUGUUAAAGGUAUAUAUGUGCCCACGUGUACACGUCACUAUUUAUCAUUAUGCAGUAUUUUUAUGCUCAUGUGAACACAUAUUUACCUUUAAAAUACACUAUUAAAUAGUACACGGGAUGAAAGGUCCUUCCCAAAGUUU	**181**	14,364641	32,044199	17,679558	35,911602	32,044199	67,955801	1,1206897	0,8125	-64,4	-60,7	0,0087752	20	-35,58011	-1,1103448
spiLA0480-MIR11578	GCAUGAACACGAUAUGAGUUGAAGCCUUUAACUAUAUCAUUGUUUAGGCUGCUUCUGUUGAAGUUGAUAAGUUGUUUCUGGAUUUGGAACCACAAGUGAUCAUUGUUGUAAUUCAACUUUAAUUCAUAUUUUAUUCAACU	**140**	17,857143	27,857143	14,285714	40	32,142857	67,857143	1,4358974	1,25	-32,9	-32,5	0,0599136	10	-23,5	-0,7311111
spiLA0480-MIR11592	GAUGUACCGGUACCGGUCCAGUACCUUCCGAUUUGUUUCGGUUCGUCCCGAUUCGGUUGCCUACGAGACGAAAUGGGACAUCCUGAAUCGGGACACGGAACGGAACGAAACCGAAGUUUGGUACCGGUGUACUGGUACCGA	**141**	29,078014	22,695035	24,822695	23,404255	53,900709	46,099291	1,03125	1,1714286	-64,5	-63	0,0105917	13	-45,744681	-0,8486842
spiLA0480-MIR11602	UUAUUUUAUAAGUAAUUUUCUGCCCCUUUUUAGCCUACGUGGCACUAAUUUUUUUAAAAAAGCUAACCAUCGUUGGCCCACAAGAUAGUGCUAUGUAGGUCGAUCUUUCCAUUCUAAUACUCUAUCCGAGAGUUAUCAGUAUUUAUCAAAUCUGUUCUUAUCUAACGGAACGCUAUUGGAUCAAAUGCCAAAGACAUUGUUGAAAAAAGAUGGCUUUUCCCGGAUGAAAUGAAAAUUGGAUUCAUGUAACAGGAGAAAGAUUUCCCAUUCCUUAGCCGGAAAGAUAUGUGGCCAUGAAAGAGGGAAAAGGGGUAAAAAAUUAUUAAUAAAAUAA	**335**	18,208955	34,029851	16,41791	31,343284	34,626866	65,373134	0,9210526	1,1090909	-93,6	-86,1	4,45E-05	59	-27,940299	-0,8068966
spiLA0480-MIR11605	UGAAUAGUUUAGGGGGCAUAUUUGACAUUUUUUCCUUUAAAGAAUUAUCAAUGUAUUAAAAAGGGUCAAGACAAGUACCCCCAGACUAUGAU	**92**	18,478261	34,782609	14,130435	32,608696	32,608696	67,391304	0,9375	1,3076923	-21,8	-20,1	0,0357829	17	-23,695652	-0,7266667
spiLA0480-MIR11891	AUGUUAGUACUUUAGUUCAUAUAUGCCCUUACCGUCAAAUACUUGGUCUAAAUACUAUGCGCAAUUGAGCAGAAUAAGGGCGUAUUUGGAUCAAGUAUUUGAUGCUAAGGGCUUAAGUAAAUUGAAGUAUAAACG	**135**	20,740741	32,592593	14,074074	32,592593	34,814815	65,185185	1	1,4736842	-58,1	-54,5	0,0915536	11	-43,037037	-1,2361702
spiLA0480-MIR12156	UCCCCUGCACGUCGCAAGGCUGAGCGCGGGGGAGAAAGCUGGCCUCCCGUGCGCCCGGCCUAAAUGUGAGUCCACGUCGACGGACGUCGCGGCAAGGGGUUGUUGAAACUCAAUUCUCUCUAGUUGUCGCGACUACAGCCCGUUGCGCGUCUGGACU	**157**	31,847134	17,197452	30,573248	20,382166	62,420382	37,579618	1,1851852	1,0416667	-71,8	-63,7	0,0238889	16	-45,732484	-0,7326531
spiLA0480-MIR12162	UGAUGAAGAGAUUUCUUUUGAAAAUGUAUUUUUGGAUGACUGAGUCAGUCUCCAAGUGGGAGAACUGUUAGGUAGUGGAGCCUGAUUAAUUUUAGGUUUUCCUAUUUAUUCUCUAUUUUAGGCUUUCCUAUUUAUUCUCUAUUUUAGGUUUUCCUAUUUAUUAUCUGUAACCAAAAAUACUCUGAUUUAUUAAUAUAAAUAUACCUCACCG	**211**	16,113744	26,540284	14,218009	43,127962	30,331754	69,668246	1,625	1,1333333	-48,5	-46,7	0,016799	39	-22,985782	-0,7578125
spiLA0480-MIR12168	AGGCAUUCAAUCAAUUAGUGACAUCCAAAAAAUAAAGGAAUGUAGUGGGAUGGUAAGUAUUGUACUCAACCUUAAUUAAAAGUUUGGGGUUCAAAUAUUGGAUUGAUGUCA	**111**	21,621622	36,936937	10,810811	30,630631	32,432432	67,567568	0,8292683	2	-25,7	-25,5	0,0097252	14	-23,153153	-0,7138889
spiLA0480-MIR12169	CACAUACCGACACAAGAGAAAUAAUAGUUAUUGAAUUGGUUUUUAUUAAUGAGUUAAGUCUUCCGCAUUACUUUAUGUUUAUAUUACAUUGAAAUGUUAAGGCUUAGAUUGAUUGGUUCGCUCACAUAGGAGGGUAAGUGUGGGUGUCAGUCGCGGCUCGGUUUUGGGUCGUGACAAACUUGGUAUCUCAUCACACAAGAACGAGUCUAGUAGAGUCUUAAGGAACGGUAGGGGGACGCCUUUACUUUUCUUUGAGAGGCUAUAAGACUUUAGGAAAAUUCCAUUCUUUCUUUCUUUCUUUCGUGCUAUUAC	**312**	22,435897	26,282051	16,025641	35,25641	38,461538	61,538462	1,3414634	1,4	-90,5	-86,3	0,0010221	25	-29,00641	-0,7541667
spiLA0480-MIR1312c	UAAUAAUUUUCUAUUUUUUUUCGGUCUACGUGGUACUAUCAUAUGGGUCCAACGCUGAUUAUUUUUUUUUUUCAAGCUAGUGCCACGUAGGUCGAAAAGGAAU	**114**	17,54386	27,192982	15,789474	39,473684	33,333333	66,666667	1,4516129	1,1111111	-45,5	-45	0,102304	5,5	-39,912281	-1,1973684

spiLA0480-MIR1313d	AGAAAAUUACCUUACUAUAAAACUCUCUCAGACCGUCUUCUAAGCAUAUAAUGUCAUACUGGCUUCAAAAAAACCACUGAAAAUCUUUUGCAACCACAAAGAGAAAUAUAUAUAUAUAUAUAUGCUUAGAGGACGGUCUGAGAGAGUUUUAUACAA	**148**	13,513514	39,189189	17,567568	29,72973	31,081081	68,918919	0,7586207	0,7692308	-63,8	-61,8	0,0236466	20	-43,108108	-1,3869565
spiLA0480-MIR1432	UAAAUUCACGAGGUUGUCAUUUCUCUUGUAUUCACGUGUGUGUGUGUAUAUAUAUAUACACACACACACAUGAAUACAAGAGAAAUGACAACCUCGGGAAUUUA	**104**	17,307692	33,653846	17,307692	31,730769	34,615385	65,384615	0,9428571	1	-74,2	-74,2	0,445523	1,3	-71,346154	-2,0611111
spiLA0480-MIR1435	UGAUUUUCGUGUGCUAUAGUCCAUGGAUUUUUUGUGAUUCAGGAUUACAGAUUUUCUUUUGUCAAAAUUUUUCAUGAUAGAUUGGCUCCUAAAUAUAAAAAAUGGACUCUCGAAUUGGUGACUGUACAUAUUACUCCUCCAACUCCCUACAGAGAGUUCUCUAAUGGUUUCAAAUUGAAAUCGUUUGAAAGCAAUAUGACCAAAAUAUUCAUGGGCUAACACACACAAAAAAUU	**234**	15,811966	32,051282	17,094017	35,042735	32,905983	67,094017	1,0933333	0,925	-54,8	-46,9	0,0002763	50	-23,418803	-0,7116883
spiLA0480-MIR1512c	GAGGUAAAGCAGAAACUCUUUCAAAUAGAGCCAAAUAGUUCUAAGAAUUCUAAGUUGAUCCUCACUAGCACCACAAAGAUUUUUUUUAGUUUCAAAAAACAUAUUCUGUGUGGUGCUGAUGACGAUUAACUUAGAAUUCUUGGAGCAUUUUGCUCUACUUGAAGGAGUUUUUGGUUUACACA	**182**	18,131868	31,868132	15,934066	34,065934	34,065934	65,934066	1,0689655	1,137931	-92,8	-90,5	0,102169	11	-50,989011	-1,4967742
spiLA0480-MIR1513a	UGUAUAAUUAUAUGUGUAUAAGACGGAGAUAUAUGUAUUUACAUGUGUAUAUACAAUUUUCUCUCGCUUUAUACAAUUAGAAACACAAUUUAUACAAUUCUAUUGUAUAAAGCGAGAGAGGCAAGCGAAGGAAGCGAGCGAGAGAGGGAGAGUGGCGAGCGAGAAUAUGAGGAAUAGAGAGACUGACAAAUAGUUUGCUAUGAAACAGAAAUAAAUCAAAUGAUAGCUACUAUAAUUAUUUU	**242**	21,900826	38,842975	10,743802	28,512397	32,644628	67,355372	0,7340426	2,0384615	-56,5	-55,27	0,001022	38	-23,347107	-0,7151899
spiLA0480-MIR1514a	AAGGGUAUAAUUAUAUAUUAUGCCUAUUACAUAAUGCACACGGGACACCACAUAGAACACAGAUUGUCAUGUAGGAUGUCAUGUAGAACAUGUGUGUCUAUUUGUUCAAUUUUAUACAAAUUUGAGAGUCUACUUAUGCAUUUUCAAAAUAGGAGAGCAUAAAUAUUAAAUGAGACCAAGUUAGAAGGCAUAUUUAUAUAUUAUGCCUAA	**210**	17,142857	36,666667	13,333333	32,857143	30,47619	69,52381	0,8961039	1,2857143	-48	-32,9	0,0002911	49	-22,857143	-0,75
spiLA0480-MIR1514b	AUCAAAUCGCUGCCCUGGCAGCGAUUUGUAAGAAGAAAAAUUUUGAAAUCACUGCUUGAGCAGCGAUUUCAUUUUUUUAUUAAACAAAAUUUUUUUGGCAAAAUCGCUGCCUCAGUAGCGAUUUUAC	**128**	17,1875	30,46875	17,96875	34,375	35,15625	64,84375	1,1282051	0,9565217	-51,1	-49,6	0,0499996	19	-39,921875	-1,1355556
spiLA0480-MIR1518-1	AGUUGAAUUCACUUCACAGCACUCAACCACAUUAGUUCCUAUGACAUCAUAGGAACUAAUGUGAUUGAGUGCUGUGAAGUGAAUACACAA	**90**	17,777778	34,444444	20	27,777778	37,777778	62,222222	0,8064516	0,8888889	-60,8	-60	0,250098	2,5	-67,555556	-1,7882353
spiLA0480-MIR1518-2	GUAUUCACUUCACAGCACUCAAUCACAUUAGUUCCUAUGAUGUCAUAGGAACUAAUGUGGUUGAGUGCUGUGAAGUGAAUUC	**82**	20,731707	28,04878	18,292683	32,926829	39,02439	60,97561	1,173913	1,1333333	-63,8	-63,8	0,654612	0,8	-77,804878	-1,99375
spiLA0480-MIR1520b	AUUCGGUUUUUGUAUUUUGGACUUAGGGAUUUGAGUUUGUGGUGUAUAAGAGUCAAGUUACUGUGUAAAUAGUAAGAGUCAAGUAACUGUGUAAAUAGUAAAGGCCAAUCAUCCUUUAACAAGGAUGAAAGGUCAUUAUGUAUGUCUAUAUAAGGGGCAUUUGCCUUCAUAAAUAAAAUAUCCUUCUUCCAACAAUCUUCUCUCUACUCUAAAAUAACAAAACCGCUU	**228**	17,982456	32,45614	14,912281	34,649123	32,894737	67,105263	1,0675676	1,2058824	-61,3	-60,8	0,0028043	18	-26,885965	-0,8173333
spiLA0480-MIR1520f	CUACUACCAAGAGAAGGGUUACAAGAAGGUUCUCUUACCUUGCUCUUGUCACGUUUCUUGGAAGGAUCAAAAAUUAGAGCAUAAAUGCUCUUCACUCUAAGCGAAGACUAAAUAGGGACACACGGGCGUUAUCUUAUCCGUCAAUAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACAUAUGUUCUAGUUUUUG	**67**	22,38806	25,373134	20,895522	31,343284	43,283582	56,716418	1,2352941	1,0714286	-21,1	-20,4	0,204799	6,3	-31,492537	-0,7275862
spiLA0480-MIR1520k-1	UAAAUAGGGACAUGUGGCGCAAUCUUAUCCGUCGACAAAUGUCGGAUCGGUGGAUAAGAUUAUGACACAUGUCCGUUAUAAA	**154**	22,077922	32,467532	15,584416	29,87013	37,662338	62,337662	0,92	1,4166667	-54,9	-51,4	0,0238332	11	-35,649351	-0,9465517
spiLA0480-MIR1520k-2		**82**	24,390244	31,707317	17,073171	26,829268	41,463415	58,536585	0,8461538	1,4285714	-34,6	-34,6	0,172718	6,8	-42,195122	-1,0176471
spiLA0480-	AAGACUAAACAUGGACACGUGACGCGAUCUUAUC	**92**	23,913043	31,521739	16,304348	28,26087	40,217391	59,782609	0,8965517	1,4666667	-	-31,3	0,0864158	8,5	-	-

MIR1520l-1	CGUCAAUAAAUGUCGGAUUGGUGGAUAAGAUUAU GACACGUGUAUGUCCGUUAGUAUA										32,1				34,891304	0,8675676
spiLA0480-MIR1520l-2	GGGACACAUGGCACAAUCUUAUCCAUCAAUUCAA UAUCGUGUCGAUGGAUAAGAUUAUGACACGUGUA UG	**70**	21,428571	31,428571	18,571429	28,571429	40	60	0,9090909	1,1538462	-24,4	-23,3	0,214599	3,3	-34,857143	-0,8714286
spiLA0480-MIR1520l-3	CACCUGUCGUUCAUAAAUUAGAUUAUAUAUGUCC UUUACUCUUACGGAAGACUAAAUAGGAACACGUA GUGCAAUAUUAUCCGUUGAUAAAUGUCGAGAUCG AUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAG UAUAAAGGGUGUAUAUGCUCUGUUUUUUAGACGA UAGAGA	**176**	21,022727	31,25	14,204545	33,522727	35,227273	64,772727	1,0727273	1,48	-55,3	-55,3	0,0288117	9,2	-31,420455	-0,8919355
spiLA0480-MIR1521b	AAUUAAUGAUAUACAAAUAUUUUUCGUCAUACUUU GGGAUAUUGGUGCUCUUGUCGUUAAAAAAUUAAA AUGUAUAUACCCUUUAUACUAAGAGACAUACACAU GUCAUAAUCUUAUCUACUGAUUUGAUUUUUAAUC AACGGAUAACGUGUUCCUUUUUAGUCUUCCGUUA CAGUUAGAGUAAAGGGCAUAUAUGCUCAAGUUUU GGAACGGAAAGGACACCAAUGUCCCAAAAGUAUG ACGAAGGUAUCUGCAUACCAUGUACGA	**267**	16,853933	32,958801	16,104869	34,082397	32,958801	67,041199	1,0340909	1,0465116	-87,7	-81,6	0,0003226	32	-32,846442	-0,9965909
spiLA0480-MIR1525	UGAAAAAAUCGAACCGACUGAUAAAUCGAAUCGAA AAAAAUGUUAUUGGGUUAUUGGGUUUUCAAUGGG UUUAUAAAUUUUUUUAUUGGGUUAUGGGUUCGGU AUCGGUUUUUACU	**116**	22,413793	29,310345	8,6206897	39,655172	31,034483	68,965517	1,3529412	2,6	-30,6	-29,8	0,0098947	14	-26,37931	-0,85
spiLA0480-MIR1530	AAUGGAGUUUGAGUGGUUAGGAGGAAGGUUGAU GGUGGAUGCUUUGAGAAGAUGGUGGUUUCACUA UUUUGAAAUAAAUUAAUAUUUUAUUUUAAAAUAGA UAAUACAUAAUUAUGACGUGGUAUUAAUGUGAGU GACAUGGAUUUGACUUGUCAUCUAUGCAAGAGAG AGUGAGGUACUCACAUGGUUAGAGUGGUUUAGCA AUCAUUUUUUUAUUGAGUUCAGGGGUCUAGAUGA CAAAAGGGUAAGUAGAAGGAUUCACACUUUAAAC GCAUACAAGUACAAGGGUCCACCAGACCAUUCCA CCUAAAUUCUAAUCCUGA	**323**	23,839009	32,198142	11,764706	32,198142	35,603715	64,396285	1	2,0263158	-84,6	-75,6	6,38E-05	58	-26,19195	-0,7356522
spiLA0480-MIR1531	CAUAACACAUGCCUAAAUAAUUAAUUGUUCAGCUC UUCCUCCACAUCCAUUCAAAUGGUUUGAAUGGCC AUGGAGGAAGAGCUGAGUAAUUAAUUAUUAAUGU UGUUGUUGUU	**113**	17,699115	30,088496	16,814159	35,39823	34,513274	65,486726	1,1764706	1,0526316	-53,7	-53,7	0,0532811	8,8	-47,522124	-1,3769231
spiLA0480-MIR1534-1	GAACCCAAUAGGUCUUUAAGAAUGUGUAUUGGGG GUACAUAGGCAUCCCAAUGCUCAAAAUUGAGAAU UAUUGGGUAG	**78**	25,641026	32,051282	14,102564	28,205128	39,74359	60,25641	0,88	1,8181818	-29,1	-28,8	0,131155	4,7	-37,307692	-0,9387097
spiLA0480-MIR1534-2	AGAGCCCAAUAGGUCUUUAAGAAUGUGUAUUGGG GGUACAUAGGCAUCCAAUUCCAAAUAUUGAGAAA UAUUGGGCAUA	**79**	24,050633	34,177215	13,924051	27,848101	37,974684	62,025316	0,8148148	1,7272727	-24	-23	0,0890542	6,9	-30,379747	-0,8
spiLA0480-MIR156b-1	GUGAUAUUGUUGACAGAAGAUAGAGAGCACAUAU GAUGGAAUGCUGCUGCUGCUGCUGCUAAAUCUG GAGAGUCUUAACAAUAAAAAAAAGCAUUUCACUUC AUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCA UCCUCUUCUCCUUCUAUUUUUCUCUUUUCUCUCC CUAAAUCUAUA	**181**	14,917127	24,861878	23,20442	37,016575	38,121547	61,878453	1,4888889	0,6428571	-48,7	-45,3	0,118032	8,6	-26,906077	-0,7057971
spiLA0480-MIR156b-2	UUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUG CUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCU CAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUC	**101**	17,821782	29,70297	18,811881	33,663366	36,633663	63,366337	1,1333333	0,9473684	-43,5	-42,2	0,119446	7	-43,069307	-1,1756757
spiLA0480-MIR156b-3	GUGACAGAAGAGAGUGAGCACACAUGGUUCUUUC AUGGAUUAUUCCCCAUGUUUAAAAGCUCUGCGUG CUCACGCUCUAUCUGUCACA	**88**	21,590909	25	23,863636	29,545455	45,454545	54,545455	1,1818182	0,9047619	-44,1	-44,1	0,312754	2,5	-50,113636	-1,1025
spiLA0480-MIR156b-4	AAAGGGCGGUGACAGAAGAGAGUGAGCACAUAUG GUCUUUUCAAGCAUGAUGUUUACAUGCUUGAAGC UAUGCGUGCUCACUUCUCUAUCUGUCACCCCCCC CC	**104**	23,076923	24,038462	25,961538	26,923077	49,038462	50,961538	1,12	0,8888889	-62	-56	0,151205	6	-59,615385	-1,2156863
spiLA0480-MIR156b-5	UAUUGUUGACAGAAGAUAGAGAGCACGAAUAAUG AGGUGCUAAUUGGAAGCUGCACCUUAAUUCUUUG UGCUCUCUAUUCUUCUGUCAUCAUCU	**94**	20,212766	26,595745	18,085106	35,106383	38,297872	61,702128	1,32	1,1176471	-48,4	-48,4	0,0852724	4,2	-51,489362	-1,3444444
spiLA0480-MIR156b-6	AUUGAUUUGUGUAAAAUGUAGGGAGGAAAAAAAA AGAGGGGAAAAUGGAAUGGGUGAUAUUGUUGACA GAAGAUAGAGAGCACAUAUGAUGGAAUGCUGCUG CUGCUGCUGCUAAAUCUGGAGAGUCUUAACAAUA	**246**	18,699187	29,674797	18,292683	33,333333	36,99187	63,00813	1,1232877	1,0222222	-85,1	-81,7	0,0086171	28	-34,593496	-0,9351648

spiLA0480-MIR156c-1	AAAAAAAGCAUUUCACUUCAUUUGUGCUCUCUAUGCUUCCGUCAUCCCUUUCAUCCUCUUCUCCUUCUAUUUUUCUCUUUUCUCUCCCUAAAUCUAUACAAUAACUCGUUGCGCGUUUUCUGGCAUGAUGUUUAUAUAUAUAUAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCUCCCACCAA	**115**	23,478261	26,956522	20,869565	28,695652	44,347826	55,652174	1,0645161	1,125	-63,9	-63,9	0,217754	8,5	-55,565217	-1,2529412
spiLA0480-MIR156c-2	AAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUUAAAAGGGCGGUGACAGAAGAGAGUGAGCACAUAUGGUCUUUUCAAGCAUGAUGUUUACAUGCUUGAAGCUAUGCGUGCUCACUUCUCUAUCUGUCACCCCCCCCCCC	**107**	22,429907	24,299065	26,168224	27,102804	48,598131	51,401869	1,1153846	0,8571429	-62	-56	0,150886	6	-57,943925	-1,1923077
spiLA0480-MIR156c-3	AGAUAAUUGAAUCGAAGAGGUAAAAUAAAAGGGGCGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUAGCAUGAUGUUUUACAUGCUUGAAACUAUGUGUGCUCACUGCUCUAUCUGUCACCCCCCAUCGCUUUCUAUAUCUCUCUCUAGAUUUUAUUAGAG	**166**	21,686747	28,313253	18,674699	31,325301	40,361446	59,638554	1,106383	1,1612903	-75,5	-75,1	0,0316798	15	-45,481928	-1,1268657
spiLA0480-MIR156d	UAUAAUUGAAAUUGAUAGGAAGAAAGAGUGAUUAUUGUUGACAGAAGAUAGAGAGCACUAAUGAUGAUAUGCUAAUUUCAUUCAAUUUGGGCAGCAAAAGCAUCUCAAUUCAUUUGUGCUCUCUAUGCUUCUGUCAUCAC	**140**	19,285714	33,571429	14,285714	32,857143	33,571429	66,428571	0,9787234	1,35	-44,7	-43,4	0,023105	15	-31,928571	-0,9510638
spiLA0480-MIR156f-1	AAUUCUAUUGACAGAAGAGAGAGAGUACAAUCUGUCAUCAGCAAAAUGAUAUUGUUGUUUGUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUGGAAAC	**97**	21,649485	29,896907	16,494845	31,958763	38,14433	61,85567	1,0689655	1,3125	-45,8	-45,8	0,37245	2	-47,216495	-1,2378378
spiLA0480-MIR156f-2	UUCUGUUGACAGAAGAGAGAAAGCACAGUCUGUCAUCAACAAAAUGGUAUUUGUUGUUUGUUUGGAAUGUGCUCUCUCUGCUUCUGCCAAUAGA	**94**	22,340426	26,595745	17,021277	34,042553	39,361702	60,638298	1,28	1,3125	-40,3	-40,3	0,201346	3	-42,87234	-1,0891892
spiLA0480-MIR156g	GUGUCAAUAACAGCUGUGAAGGAAUAUCUGGGCCCAAAGAUGUAUUGACAUAGCUUUCUCUUUUUUUGUGUCAGUACAUCUUUGGGCCCAGACAUAUUCCUUCAUAGCUGUCAUGAUUA	**119**	20,168067	25,210084	19,327731	35,294118	39,495798	60,504202	1,4	1,0434783	-74,5	-74,5	0,171764	3,5	-62,605042	-1,5851064
spiLA0480-MIR156i-1	AAAAGAGGUGACAGAAGAGCGUGAGCACAUGUGUGUUUUCUAGCAUGAUGUUUAUAUGCUUGAAUCUAUGCGUGCUCACUGCUCUAUCUUUCAUCCUCAUCG	**102**	22,54902	24,509804	19,607843	33,333333	42,156863	57,843137	1,36	1,15	-42,4	-42,4	0,328673	4,2	-41,568627	-0,9860465
spiLA0480-MIR156i-2	CAAAAGGGAGGUGACAGAAGAGAGUGAGCACGUAUGGUAUUUUCUCGCAUGCUUGAAACUAUGUCUGCUCACUUCUCUAUCUGUCAUCCCUACCAU	**96**	21,875	26,041667	22,916667	29,166667	44,791667	55,208333	1,12	0,9545455	-39,5	-39,5	0,0670787	10	-41,145833	-0,9186047
spiLA0480-MIR156k	UGGUGACAGAAGAGAGUGAGCACACAUGGUGUUUUCUUGCAUGAUGUUUAUAUAUAUAUGCUUGAAACUAUGUGUGCUUACUCUCUAUCUGUCACC	**96**	21,875	25	16,666667	36,458333	38,541667	61,458333	1,4583333	1,3125	-57,5	-57,5	0,335821	5,1	-59,895833	-1,5540541
spiLA0480-MIR156t	GGGAUUAUUUGUCUUCCUAGUCUUUGACACAAGAAAGGGGUGUAGAAAAAUCCUUUUUUCUUGUGUCGAAACAAAAGAGUAAUGAUUCU	**89**	21,348315	30,337079	13,483146	34,831461	34,831461	65,168539	1,1481481	1,5833333	-31,4	-30,6	0,119342	6	-35,280899	-1,0129032
spiLA0480-MIR158	CUUAUUAGCAUCUAGCCAAGCUUUUUAAAGAGUCCGGAGCCUAAAGGGUACAAAAUAUUAACAAAAAUUUCAAAACGUCUGCAGCGAUUUUGCUUUUUCCGGUGGAGUAAAUCGCUGUUGAUGCAACGAUUUUAUCGUUUUUGUUAAUAUAAAAUUUUAUAUAUCGUUUUGAAUUUUUCAUUAAUAUUUUAUACCCUUUAGGCUCCGGACUCGCUUUUUAAAAGUGUUUGGGGAGGAAACUAAUUUU	**247**	17,408907	29,149798	14,979757	38,461538	32,388664	67,611336	1,3194444	1,1621622	-98,6	-96,9	0,0015253	22	-39,919028	-1,2325
spiLA0480-MIR159	UUUAUGUGUUAUGGGAGUGGAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAUUGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAGCUUUAUUUUCACUUUUUGGAUUGAAGGGAGCUCUACAUUCAUUUC	**205**	21,95122	23,902439	16,585366	37,560976	38,536585	61,463415	1,5714286	1,3235294	-84,5	-81,9	0,0065703	13	-41,219512	-1,0696203
spiLA0480-MIR159a-1	GAGCUCCUUGAAGUCCAACAGAAGAUCUAACAGGUUAGAUUGAGCUGCUGACCUAUGGAUUCCUCAGCCCUAUCUAUUUAUGAUUUCAAACAUAUAGAUAGGUUUGUGGGUUUGCAUAUGUCAGGAGCUUUAUUUUACCCUUUGUUUGAUCACUUUUUGGAUUGAAGGGAGCUC	**174**	21,83908	24,712644	17,816092	35,632184	39,655172	60,344828	1,4418605	1,2258065	-74,6	-72	0,013088	12	-42,873563	-1,0811594
spiLA0480-	UCCAAAGCAGAGAAGUUAUGAUUUAUUAUUUGAU	**266**	16,165414	36,090226	16,165414	31,578947	32,330827	67,669173	0,875	1	-	-48,87	9,86E-05	72	-	-

MIR159a-2	AACUUAUCGAAUGAGUCUGAAUGUUGUUAAGGGU CUCCCACAUAUAUGAUUCGUUCAUACCUCUUCAG ACUCAUUAAGAGAUUUUUUAAAAAAAUAAAACAAA UGAACUUAAUGGGCUCAUUUAGAUUCAGACCUAA AAAUCAAACGUACUUAAUGGGGUGAAUCUGAAAAA UUAAGAUUCAGACCUCCAUUAAGUGCAAACAAAUG AGGCCUAAGCUUCGUUUGCUUUCAA UGGAUACUCUGUUUGUGGAUUACACUAAUAUUCA UAUAGUUGAUUUUAACUUGUUCGAGGAAGAUUAG AGUUCUGAAUGUAGAGCUUUUCUGAAUUUCAAAG AGGAUCUGAGAGGGAAAAUCGAGCUGCUAAUCUA UGGAUCCCUCAAACCUAUCUAUUCUCAAAAUAAUU UUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGAGC										71,5				26,879699	0,8313953
spiLA0480-MIR159b-1	UUCAUUUACUCUUCUAGGAUCCUUAUUGGAAUGA AGGGAGCUCUACGUU UUUUAACUGUUCGAAAAAGACCAGAGUUUUGAAG GUAGAGCUCUUCUGAAUUCCAAAAAGGAUCUGAG AGGGAAAAUUGAGCUGCUAAUCUAUGGAUCCCUC AAUCCUAUCUAUUCUCAAAUUAAUUUUAGAUAGGU UUGUGGUUUGCAUAUAUCAGGAGCUGCAUUUACU	**254**	20,866142	28,346457	14,566929	36,220472	35,433071	64,566929	1,2777778	1,4324324	-88,2	-82,1	7,39E-05	33	-34,724409	-0,98
spiLA0480-MIR159b-2	CUUCUAGGAUCCUUAUUGGAAAGAAGGGAGCUCU A UUUAACUUGUUCGAGGAAGAUUAGAGUUCUGAAU GUAGAGCUUUUCUGAAUUUCAAAGAGGAUCUGAG AGGGAAAAUCGAGCUGCUAAUCUAUGGAUCCCUC AAACCUAUCUAUUCUCAAAAUAAUUUUAGAUAGGU UUGUGGUUUGCAUAUAUCAGGAGCUUCAUUUACU	**206**	20,873786	30,097087	16,019417	33,009709	36,893204	63,106796	1,0967742	1,3030303	-72,7	-70,8	0,0020569	23	-35,291262	-0,9565789
spiLA0480-MIR159b-3	CUUCUAGGAUCCUUAUUGGAAUGAAGGGAGCUCU A AAGGUAGAGCUCUUCUGAAUUCCAAAAAGGAUCU GAGAGGGAAAAUUGAGCUGCUAAUCUAUGGAUCC CUCAAUCCUAUCUAUUCUCAAAUUAAUUUUAGAUA GGUUUGUGGUUUGCAUAUAUCAGGAGCUGCAUUU	**206**	21,359223	29,126214	15,048544	34,466019	36,407767	63,592233	1,1833333	1,4193548	-74,6	-69,8	0,0015612	21	-36,213592	-0,9946667
spiLA0480-MIR159b-4	ACUCUUCUAGGAUCCUUAUUGGAAAGAAGGGAGC UCUACACUU AAUGUAGAGCUUUUCUGAAUUUCAAAGAGGAUCU GAGAGGGAAAAUCGAGCUGCUAAUCUAUGGAUCC CUCAAACCUAUCUAUUCUCAAAAUAAUUUUAGAUA GGUUUGUGGUUUGCAUAUAUCAGGAGCUUCAUUU	**180**	20,555556	29,444444	17,222222	32,777778	37,777778	62,222222	1,1132075	1,1935484	-73,8	-71,7	0,0046981	14	-41	-1,0852941
spiLA0480-MIR159b-5	ACUCUUCUAGGAUCCUUAUUGGAAUGAAGGGAGC UCUACGUUU UACUCUGCUUGUGGAUUAUACUGAUAUUCAUAUA GUUGAUUUUAACUUGUUCGGGGAAGACCAGAGUU UUGAAGGUAGAGCUCUUCUGAAUUCCAAAGAGGA UCUAAGAGGGAAAAUCGAGCUGCUAAUCUAUGGA UCCCUCAAUCCUAUCUAUUCUCAAAAUAAUUUUAG AUAGGUUUGUGGUUUGCAUAUAUCAGGAGCUGUA	**180**	20,555556	28,888889	16,111111	34,444444	36,666667	63,333333	1,1923077	1,2758621	-77,2	-75,3	0,0053671	12	-42,888889	-1,169697
spiLA0480-MIR159b-6	UUUACUCUUCUAGGAUCCUUAUUGGAAAGAAGGG AGCUCUACACUUGAUAACUUUUUUUUUUCUA AGAGUUUUGAAUGUAGAGCUCUUCUGAAUUCCAA AGAGGAUCUAAGAGGGAAAAUCGAGCUGCUAAUC UAUGGAUCCCUCAAUCCUAUCUAUUCUCAAAAUAA UUUUAGAUAGGUUUGUGGUUUGCAUAUAUCAGGA	**270**	20	27,777778	15,555556	36,666667	35,555556	64,444444	1,32	1,2857143	-93,2	-90,3	0,0022068	28	-34,518519	-0,9708333
spiLA0480-MIR159b-7	GCUGCAUUUACUCUUCUAGGAUCCUUAUUGGAAA GAAGGGAGCUCUACACUUGAUAACCUG AGGAAGAUCAGAGUUUUGAAGGUAGAGCUCUUCU GAAUUCCAAAGAGGAUCUAAGAGGGAAAAUUGAG CUGCUGAUCUAUGGAUCCCUCAAUCCUAUCUAUU UUCAGAUUAAUUUUAGAUAGGUUUGUGGUUUGCA UAUAUCAGGAGCUGCAUUUACUCUUCUAGGAUCU	**198**	20,707071	29,79798	17,171717	32,323232	37,878788	62,121212	1,0847458	1,2058824	-76,7	-74,8	0,0059664	14	-38,737374	-1,0226667
spiLA0480-MIR159b-8	UUAUUGGAAAGAAGGGAGCUCUACACUUGAUAAC CUGGUUUUUUU CCAAGUUUACUUUGGGCUAAAAUGGAUUGGGUUA	**215**	22,325581	27,906977	14,883721	34,883721	37,209302	62,790698	1,25	1,5	-92,1	-89,2	0,0058915	14	-42,837209	-1,15125
spiLA0480-MIR159c	AAGUGAGCUAACCCAAUUCAAUUUGACCCGAUUA AUCUCAA	**75**	18,666667	32	18,666667	30,666667	37,333333	62,666667	0,9583333	1	-24,7	-24,7	0,28393	4	-32,933333	-0,8821429
spiLA0480-	GGUAACUUUAUAUGACGAGAUGGUUACAUAUUUC	**206**	17,475728	32,524272	19,902913	30,097087	37,378641	62,621359	0,9253731	0,8780488	-	-61,2	0,0128627	28	-	-

MIR160-1	AACAUCAUAUACACGAUAUCGGAAUAUGCUUGGCUCCUCAUACGCCAUUCAACAAGGCCCAUCGAUAUAUUACGGUGAGCUUUGCAAAUGGCAUACAGGGAGCCAGGCAUAUACGUGUACACGACUUGUAUCAGUACAUAUAUACACACUCAUAUGUAUAUAUAAAAUUUUU										64,9				31,504854	0,8428571
spiLA0480-MIR160-2	GGUGGUAUGCUUGGCUCCUUAUACGCCACCCACUGAUCAGUCAAUCAAAGAAUUGGUGAAUGUGUGGGCAUACAGGGAGCCAGGCACAUCCUUC	**95**	26,315789	24,210526	24,210526	25,263158	50,526316	49,473684	1,0434783	1,0869565	-42,1	-38,1	0,0541257	13	-44,315789	-0,8770833
spiLA0480-MIR160-3	UUGAUGGAUCUGCCUGUCUCCUCUGGUACCAACUAGGAAGAGUGUCAAUUUUUUUGACAAUACUGUUCUUAGUUGGCAUCCAGGGAGCCAGGCAGAACAAUUUC	**104**	23,076923	24,038462	21,153846	31,730769	44,230769	55,769231	1,32	1,0909091	-52,3	-51,4	0,100504	4,6	-50,288462	-1,1369565
spiLA0480-MIR160-4	GACAUGAAACUCUAUACAUGCUUAGCUCCUAGAAUGCCAUCUGAAAAGGCCAUCAAUUCUUGGUGGAACAAUGCAAAUGGCAUACAAGGAGCCAGGCAUGUUGUGUUAUCGAUCAC	**116**	21,551724	31,896552	21,551724	25	43,103448	56,896552	0,7837838	1	-41,7	-40,3	0,0514112	9,2	-35,948276	-0,834
spiLA0480-MIR160c	AUGUGCCUGGCUCCCUGUAUGCCACACACAUUCACCAAUUCUUUGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGCAUA	**85**	23,529412	24,705882	24,705882	27,058824	48,235294	51,764706	1,0952381	0,952381	-41,5	-41,5	0,340971	2,9	-48,823529	-1,0121951
spiLA0480-MIR160g	AAUUGUUCUGCCUGGCUCCCUGGAUGCCAACUAAGAACAGUAUUGUCAAAAAAAAUUGACACUCUUCCUAGUUGGUACCAGAGGAGACAGGCAGAUCCAU	**99**	21,212121	30,30303	23,232323	25,252525	44,444444	55,555556	0,8333333	0,9130435	-48,9	-48,9	0,136739	3,4	-49,393939	-1,1113636
spiLA0480-MIR160h-1	AUGCCUGGCUCCUUGUAUGCCAUUUGCAUUGUUCCACCAAGAAUUGAUGGCCUUUUCAGAUGGCAUUCUAGGAGCUAAGCAUG	**83**	22,891566	21,686747	22,891566	32,53012	45,783133	54,216867	1,5	1	-34,8	-34,6	0,337929	3,5	-41,927711	-0,9157895
spiLA0480-MIR160h-2	UAUAUGCCUGGCUCCCUGUAUGCCAUUUGCAAAGCUCACCGUAAUAUAUCGAUGGGCCUUGUUGAAUGGCGUAUGAGGAGCCAAGCAUAU	**90**	24,444444	24,444444	22,222222	28,888889	46,666667	53,333333	1,1818182	1,1	-46,8	-46,8	0,126945	3,1	-52	-1,1142857
spiLA0480-MIR162-1	ACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGGAAGCUGAAUAUAUAUAUACGCAAAAAUACAGCAAAAGGAAUCGGUCGAUAAACCUCUGCAUCCAGUG	**103**	22,330097	33,009709	22,330097	22,330097	44,660194	55,339806	0,6764706	1	-41,3	-40,9	0,116727	5,5	-40,097087	-0,8978261
spiLA0480-MIR162-2	GAACACUGGAGGCAGCGGUUCAUCGAUCUGUUCCCUGAAAAGCGAUAAAUACAGCAACAGGAAGCGAUCGAUAAACCUCUGCAUCCAGUGCUU	**93**	23,655914	31,182796	24,731183	20,430108	48,387097	51,612903	0,6551724	0,9565217	-42	-42	0,347985	4,3	-45,16129	-0,9333333
spiLA0480-MIR162b-1	GAAAAGAAAAAAAAAUCCUUCGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUGCGUAUAUAUAUAUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUC	**137**	21,89781	27,737226	20,437956	29,927007	42,335766	57,664234	1,0789474	1,0714286	-50,2	-46,9	0,0624806	8,3	-36,642336	-0,8655172
spiLA0480-MIR162b-2	CGGGGUUAAGCACUGGAUGCAGAGGUUUAUCGACCGAUUCCUUUUGCUGUAUUUUGCGUAUAUAUAUUCAGCUUCCAGGGAACAGAUCGAUGAACCGCUGCCUCCAGUGUCUUCAACCAAC	**124**	22,580645	23,387097	23,387097	30,645161	45,967742	54,032258	1,3103448	0,9655172	-51,5	-49,8	0,144055	6,7	-41,532258	-0,9035088
spiLA0480-MIR164-1	GAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUGAC	**169**	19,526627	28,994083	16,568047	34,911243	36,094675	63,905325	1,2040816	1,1785714	-60,9	-58,8	0,0028583	17	-36,035503	-0,9983607
spiLA0480-MIR164-2	UCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUG	**171**	19,883041	28,654971	16,374269	35,087719	36,25731	63,74269	1,2244898	1,2142857	-60,7	-58,6	0,0019808	18	-35,497076	-0,9790323
spiLA0480-MIR164-3	UAGGUGAGUGACGAUCGAGAUGGAGAAGCAGGGCACGUGCAUUACUAACUCAUACGCAAGAUUUAUCGAUGUUUCGAAAAUUCUGCUAUCAUAGUACUGUAUUUUACAGCAAAUAGUGUUUGUACUUUACAUGUAUGUGAUAAAAUGAUGAGUUAGUUAUUCAUGUGCCUGUUUUCCCCAUCAUG	**185**	21,621622	28,648649	15,675676	34,054054	37,297297	62,702703	1,1886792	1,3793103	-61	-58,6	0,0009532	21	-32,972973	-0,884058
spiLA0480-MIR164c	UAUUUAAGCUGGAGAAGCAGGGCACGUGCAUUACUAACUUGAAACUUUGACUUUUCAAGAAUUUUGCAUGUGCUCUAGCUCUCCAGCUUAAUUC	**93**	19,354839	26,88172	19,354839	34,408602	38,709677	61,290323	1,28	1	-51,1	-48,1	0,249809	2,2	-54,946237	-1,4194444
spiLA0480-MIR164e	UGUUGGAGAAGCAGGGCACGUGCAAAUUCUUGUAUUCGACGAUAUAUGCAUUACUAAUGGUAAUGCAU	**97**	21,649485	25,773196	19,587629	32,989691	41,237113	58,762887	1,28	1,1052632	-48	-47,2	0,0328079	9,8	-49,484536	-1,2

spiLA0480-MIR166-1	GAAUUUUGCACGUGUUCUCCUUCUCCAACGGAAUGUUGUUUGGCUCGAAGUCAUUAUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUAAAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUCAUUCCCCCCAAUUUGGAAACAAAAAUUACAUUCCGUAAUUCUCUCUCCGUCUCUGGU	**185**	15,675676	29,72973	19,459459	35,135135	35,135135	64,864865	1,1818182	0,8055556	-56,6	-51,9	0,0793912	17	-30,594595	-0,8707692
spiLA0480-MIR166-2	AUAUUGUUGAGGAGAAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGCAUAUAUGUAUCGUGAAUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUG	**120**	21,666667	28,333333	16,666667	33,333333	38,333333	61,666667	1,1764706	1,3	-52,7	-51,5	0,335949	5,5	-43,916667	-1,1456522
spiLA0480-MIR166-4	AAUGUCGUCUGGUUCGAGAUCUUUCAUAAGAAAGGUAAAUGAAUGACAAGUUUUCAUAUAUGUAUCGUGAAUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCUGAUC	**109**	19,266055	28,440367	19,266055	33,027523	38,53211	61,46789	1,1612903	1	-36	-34,8	0,118666	7,3	-33,027523	-0,8571429
spiLA0480-MIR166-5	ACGGUUGGGGAGAAUGUUGUCUGGUUCGAAAUCUUUCUAUAGAAAAAUCAGUGGCGGAUUCAGUCAUGGAUUUCAAAAUCGUUAAAUCUUAUAUAUGUACAAAAACAAGUACAAUAUAUAUUUUUAGACCCUAAAAAUGUUGAAUAUAUAUUCUGAAUCCGUCAUAGAUUAGAUCGUUUGAUCAAUCAAAUUAUUGAGUGAUUUCGGACCAGGCUUCAUUCCCCUCAACUCU	**232**	17,241379	32,758621	15,948276	34,051724	33,189655	66,810345	1,0394737	1,0810811	-82,7	-82,1	0,001321	32	-35,646552	-1,074026
spiLA0480-MIR166-6	UAAACUAAACAAGAUCAUGUUAAGGAGAAUGUUGUCUGGUUCGUGACCAUAUAUCUUUCUUCACAUAAAUGAUCUCGGACCAGGCUUCAUUCCCCUCAACUCAUCAAGGUUAUGUCAU	**118**	16,101695	29,661017	22,033898	32,20339	38,135593	61,864407	1,0857143	0,7307692	-33	-31,7	0,0408643	10	-27,966102	-0,7333333
spiLA0480-MIR166a	UGCGGGGAAUGUUGUCUGGCUCGAGGAAUCAAAAAUUGUUUCUUAUAGAUAGAUCUGUAUAUUUUGUUUAUAGAUCUAUAAUGUUUUUGAUGUCGUCGGACCAGGCUUCAUUCCC	**115**	22,608696	23,478261	14,782609	39,130435	37,391304	62,608696	1,6666667	1,5294118	-46,9	-46,9	0,242124	4,6	-40,782609	-1,0906977
spiLA0480-MIR166b	CAGAUUUGAGGGGAAUGUUGUUUGGCUCGAAGUCAUUAUCUCAUUAUAGAUCGAACCAAUCCAAUUUUAUAUAUUCAAUCUAGUUUAAAAUAUAUGUAAAUUACGAUGAUGAUGAGAUAGUGUCUUCGGACCAGGCUUCA	**140**	19,285714	31,428571	14,285714	35	33,571429	66,428571	1,1136364	1,35	-40,3	-35,6	0,0644504	17	-28,785714	-0,8574468
spiLA0480-MIR166f-1	AUGAAGAAAAACAAGAAAAGUGAUGCUAGAAGGGAAGGAAGAAUAAACAUUUUUUGUUUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAA	**158**	23,417722	31,64557	16,455696	28,481013	39,873418	60,126582	0,9	1,4230769	-47	-43,7	0,0042127	20	-29,746835	-0,7460317
spiLA0480-MIR166f-2	UUAAUUUUGAGGGGAAUGUUGUUUGGCUCGAGGCCACCAACUUCAUCUAAUGUGAGCAAACUCUUUGUUAGUGUCGUCGGACCAGGCUUCAUUCCCCUCAAAAUCUC	**107**	21,495327	22,429907	23,364486	32,71028	44,859813	55,140187	1,4583333	0,92	-44,2	-41	0,0417107	13	-41,308411	-0,9208333
spiLA0480-MIR166k	AGGAAGUUCUCUCAGUUGAGGGGAAUGUUGUCUGGCUCGAGGUCACCAAUUAGAUCCAUAAUCCCUAUAUAUACCAUGCUUUUCAAAAAAAGAUUUAUAAUAUGAAAAGGGGUUAUGAAUCAUGUGUUAGUGUUGUCGGACCAGGCUUCAUUCCCCCCAAUUG	**163**	21,472393	28,834356	18,404908	31,288344	39,877301	60,122699	1,0851064	1,1666667	-58	-57,7	0,048518	12	-35,582822	-0,8923077
spiLA0480-MIR167a	UUCAGACUACGUGGCAGUAUCUUGUGGGCCCAACACUGGUUUAUUUUUUUUCAAGCUAGUGCCACGUAGGCUAAA	**75**	22,666667	22,666667	21,333333	33,333333	44	56	1,4705882	1,0625	-26,3	-26,3	0,255505	4,3	-35,066667	-0,7969697
spiLA0480-MIR167b-1	UACUAUCAGUUGAAGCUGCCAGCAUGAUCUAAACUUACCUAUAAAUUUAUAUUAAGGCAAGAUCAGAUCAUGUGGUUGCUUCACCUGUUAGUU	**93**	17,204301	30,107527	18,27957	34,408602	35,483871	64,516129	1,1428571	0,9411765	-35,3	-35,3	0,0640059	5,9	-37,956989	-1,069697
spiLA0480-MIR167b-2	UGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAUCAGAUCAUGUGGCAGCCUCAC	**80**	18,75	31,25	21,25	28,75	40	60	0,92	0,8823529	-34,9	-34,7	0,120167	5,2	-43,625	-1,090625
spiLA0480-MIR167b-3	GCUAUCAAAUUAAAAACAGAUGCCUAAUCUGAACUCAUCUACCCCAAAUAAAGCAAGCAGUUUUACUAGGUCCUAGUAAAGCUGCUUGCUUUAUUUGGGGUAGAUGAGCUCAGGUUGGUGUUUUUAUUUGAUUCU	**135**	19,259259	28,888889	17,777778	34,074074	37,037037	62,962963	1,1794872	1,0833333	-82,1	-79,8	0,156678	5,8	-60,814815	-1,642
spiLA0480-MIR167b-4	GGAAGUUUGUUUUAGUUAUUGAAUGUGCUAAGUACGAACGGAAACCAUAAUCGGAUUAUUAGUGGUGUCAUGUUGGUGCUUGGGCUGUUUUGAUUAAAUCAAACUGUG	**108**	26,851852	25,925926	10,185185	37,037037	37,037037	62,962963	1,4285714	2,6363636	-33,4	-33,4	0,0291746	8,6	-30,925926	-0,835

spiLA0480-MIR167c-1	UCGUGCAGCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUCCUUUUAGUUCAAAUAUAAUUCGAGGAAAGAUCAGAUCAUGUGGCAGCCUCACCUGUCAAUGCCAUCACGAAUUAUUAAA	**125**	18,4	31,2	22,4	28	40,8	59,2	0,8974359	0,8214286	-49,3	-49,1	0,127357	5,2	-39,44	-0,9666667
spiLA0480-MIR167c-2	AUCGUGAACCACUAGCAGUUGAAGCUGCCAGCAUGAUCUAAACUUUUCUAUUGCUCCGUACGAGGAAAGAUCAGAUCAUGUGGCAGCAUCACCUGUUGAUGGUUUCGCGG	**110**	24,545455	25,454545	22,727273	27,272727	47,272727	52,727273	1,0714286	1,08	-53,5	-53,5	0,0801293	4,4	-48,636364	-1,0288462
spiLA0480-MIR167c-3	CCAUAGGCCUAAAAAAGUUUUGAGAAUGUGAAGAACUAACUGAAUUCUAGUAAACUAAUGGGUGAAAGGAAACCCACUAGUGAACUCCCACAUACAUGGUGACAAAAUAUACGAAGAAAUCCUUUUAAAUUUAGGACUAAAAUUUGAAGAACACUUCUUCUUAUUCUUGAGAGGACAUGUUGAUAGUUUCCUCUUGUAUUUGGUCAAAGUAGGAUUAUUUUUCGAGAAUGAGGGAGUUGGUAGAUUCUUACUAUAUUGUUAGGCUUAGAC	**271**	20,295203	33,948339	14,02214	31,734317	34,317343	65,682657	0,9347826	1,4473684	-69,3	-65,7	0,0005391	50	-25,571956	-0,7451613
spiLA0480-MIR167d	ACGAGAAAGAAUUGCUUACGUGGCUAAUAUCUCUAAAUCCUACCAUUAUCGGUUCGAGUCACCGAGCAAUGGAAGCUCCCAGGAAGGUGUUAGCCACUUGAGCAACUCUUUCUUUU	**116**	20,689655	27,586207	23,275862	28,448276	43,965517	56,034483	1,03125	0,8888889	-49,5	-49,5	0,172191	5,2	-42,672414	-0,9705882
spiLA0480-MIR167e	UGGACCUUCAAUCGUACGCUUAAUCUUCAUCCUCUUACAGCCUUACCUGGGAAUGACUAAUGAGCAAUUUAGAUUUGUUAUUAUCAGGAGCUACUUGGAUUGCAUGGUUCGUCAAGAAAAAAGCUUUCAUAAUAUGGUCGGGAGUUGAAACUUUUAUAGUACAAAUCCAAUGAUGUUACAACAUUCCUUGCAAGGGUUAUUUGUUAAUGAGAGUGAUGAUACAUUCAAAGAACUUAACCAUCUUUUGAUAAUAACAAAUUCAAAUCUCUUAGUGAACCAUCCUCAGACCAUGCUGCUUAGGGGAAGAAGAUUAAGAAUACUGAUGAAGGUUGA	**333**	18,918919	32,432432	16,816817	31,831832	35,735736	64,264264	0,9814815	1,125	-98,9	-93,3	0,000283	33	-29,6997	-0,8310924
spiLA0480-MIR167h-1	UAACAGGUGAAGCAACCACAUGAUCUGAUCUUGCCUUAAUAUAAAUUUAUAGGUAAGUUUAGAUCAUGCUGGCAGCUUCAACUGAU	**86**	18,604651	32,55814	17,44186	31,395349	36,046512	63,953488	0,9642857	1,0666667	-38,9	-38,4	0,194618	4,2	-45,232558	-1,2548387
spiLA0480-MIR167h-2	AAUUCGUGAUGGCAUUGACAGGUGAGGCUGCCACAUGAUCUGAUCUUUCCUCGAAUUAUAUUUGAACUAAAAGGAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGCUGCACGAUGU	**122**	23,770492	27,04918	18,852459	30,327869	42,622951	57,377049	1,1212121	1,2608696	-62,7	-62,7	0,159834	4,7	-51,393443	-1,2057692
spiLA0480-MIR167h-3	UUCCGCGAAACCAUCAACAGGUGAUGCUGCCACAUGAUCUGAUCUUUCCUCGUACGGAGCAAUAGAAAAGUUUAGAUCAUGCUGGCAGCUUCAACUGCUAGUGGUUCACGAUC	**113**	22,123894	26,548673	24,778761	26,548673	46,902655	53,097345	1	0,8928571	-46,1	-46,1	0,0248159	9,3	-40,79646	-0,8698113
spiLA0480-MIR168	GUUUCUCAUUCGCUUGGUGCAGGUCGGGACCUACCUCGCCGGCAACAAUGGCGGUAGCUGACGGCGACGGCAGCGUACCGGUAAAAAAGAAUCUUAUUUUACAUGUUGUUGCGUAGUUUGGGUCCCGCCUUGCAUCAACUGAAUAGGAGACUG	**154**	28,571429	21,428571	23,376623	26,623377	51,948052	48,051948	1,2424242	1,2222222	-70,3	-69	0,0138865	15	-45,649351	-0,87875
spiLA0480-MIR168b	AUGCUUGGCCCGCAAGGCUUGGGCCAGGUAGGGCUGGACCAACCCUUUUUGACAACUCUAGAUACAUCAAAAGUAGAGUUGUCAAAACGUGUCGAUCCAGUCUCACCCGGCCCAAGCCUGGCGGGCCAAGGAACUCUUAUUCGCUUGGUGCAGGUCGGGACCUCAU	**133**	27,067669	25,56391	27,819549	19,548872	54,887218	45,112782	0,7647059	0,972973	-85,8	-83,6	0,296536	3,1	-64,511278	-1,1753425
spiLA0480-MIR168c	UCGCCGGCGCCGGGAAUAAUGCCGGACGAACGACGGCGGUGUUAAUUCUACUAAAGCUGUCACCGACGGAUAGAUGUUUGAUUAGCGGCGAAAUUUGGGUCCUGCCUUGCAUCAACUGAAUUGGA	**158**	29,113924	21,518987	23,417722	25,949367	52,531646	47,468354	1,2058824	1,2432432	-63,1	-58,8	0,0104247	20	-39,936709	-0,760241
spiLA0480-MIR169a-1	AUAGAAAUGGAGAGUGGAUUGCAGCCAGGGAUGACUUGCCGAUGAUUUCUUUCCUAGUUUUCCUAUUAAAGAUUAUGUAUCGGCAAGUUGUCCCUGGCUACCUUUCGCUCUCUUCUUCU	**119**	21,848739	21,008403	21,008403	36,134454	42,857143	57,142857	1,72	1,04	-62,6	-61,7	0,352304	2,8	-52,605042	-1,227451
spiLA0480-MIR169a-2	UGUCUAGAGAGUUAUUGUAUGAAGAGGUAGGGAGUGGAGUGCAGCCAAGGAUGACUUGCCGAGAUGUUGUAGCCUAAUGCAAUGACAUAUCGGCAGGUCAUCUUUGGCUACAUUUUAUUCUCUCCUAUUCAUGUAAAACUUUAUAGACGUAUAUGUA	**157**	24,840764	27,388535	15,286624	32,484076	40,127389	59,872611	1,1860465	1,625	-82	-82	0,062004	4,1	-52,229299	-1,3015873
spiLA0480-MIR169ad	UGGAAAAGGGAGGUUGUGGGUUCGAACCCCCACAACCUCCUUAUUUUAAUUUAAAUUCGCUAGAGGCU	**110**	23,636364	22,727273	22,727273	30,909091	46,363636	53,636364	1,36	1,04	-52	-52	0,341621	5	-47,272727	-1,0196078

spiLA0480-MIR169c-1	GUGAGGUGGUGGGUUCAAACCCCCACAGCCUCCUAUUUUUUUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAUUUAUAUUAAUCUCAUCUCGGAUUUA	**205**	14,146341	27,804878	18,04878	40	32,195122	67,804878	1,4385965	0,7837838	-66	-63	0,0045299	17	-32,195122	-1
spiLA0480-MIR169c-2	GUUUUACAUGAAGUUGAGAGUAUUGUUUAGUAGCCAAGGAUGACUUGCCUACUUCAUUUGAUAUAUAGUUUAAAAUAAUAAUAUUGACAAUAUUUGUCAUUUGGUCGUAGGCAAGUUAUCCUGGCUAUCUUGACAUGCUCGUAAUUUUUCAUGUAAGA	**158**	18,987342	29,113924	12,658228	39,240506	31,64557	68,35443	1,3478261	1,5	-67	-64,3	0,0063161	14	-42,405063	-1,34
spiLA0480-MIR169c-3	UUAGGAAGAGAGGUCUUACAUGAAAAGAAAAACCUUUGUUAAUUAGCCAAGGAUGACUUGCCUAAUGUACCCACUAUUUAUUUUCCUCCUAUUUUUUAUGGAGUAUUUAAUAGUAUACUAGGCAGUCGUCUUUAGCUAUAUUGACACAUUUUUCUUUAUCAUGCUAGUUCUCUUCUUCCCAU	**182**	14,835165	27,472527	18,131868	39,56044	32,967033	67,032967	1,44	0,8181818	-64,8	-61,8	0,0091554	15	-35,604396	-1,08
spiLA0480-MIR169c-4	GUUGAAGAGAGGUAUUGCAUGAAGAUAAAGUGCCUGCUCUGAUAGCCAAGGAUGACUUGCCUAAAAUCAUUUUUAUGAAGGGUCUUAACUAAUUAAACUUUAGUUACUAAAAUUAAAGUUUAUAUUAUAUGAUCUUAAAAUUGGGAUUUUAGGCGUUGUCUGAGGCUAAUUGAGAGACACUUAUCUUUCAUGAAACACCUUCAUUCUCU	**209**	18,660287	32,057416	13,875598	35,406699	32,535885	67,464115	1,1044776	1,3448276	-69,2	-64,9	0,0010146	17	-33,110048	-1,0176471
spiLA0480-MIR169e-1	UAGGAGGAGAGGCCUUACAUGAAUUAGAAGAGUUUCUAUUUGUUUAGUAGCCAAGGAUGACUUGCCUUUCAUCAAUGCCUUUUGUAAAAUGGAAAUUGAUUACAACACUUUCUAUGGUAUUGGGAAAAUGAGUGGCAAGCAUCUUUGGCGACUUGACAAACUCUUCUUUGUCAUGUUAGUCCAUCUUCUUCCU	**193**	20,725389	26,943005	17,098446	35,233161	37,823834	62,176166	1,3076923	1,2121212	-78,5	-74,8	0,006646	15	-40,673575	-1,0753425
spiLA0480-MIR169e-2	UUUAAAAAAGAUAUCUUGCAUAAAAGAAAAGAGCAUGUCAAGAUAGCCAAGGAGACUGCCUGAAACCAAAUUAAAAUGUGAUUAAACACAUUUUAGACUAUGGAGCAGGCAAGUCAUCCUUGGCUACUAAACAAUAUGACUCUCCUCUUCAUGUAAGACUUCUCUUCUUUUUC	**172**	15,697674	36,046512	19,186047	29,069767	34,883721	65,116279	0,8064516	0,8181818	-63	-60,3	0,0486431	9,3	-36,627907	-1,05
spiLA0480-MIR169j-1	AUAGCCAAGGAUGACUUGCCUGCAUCAUUAGUUCUUGAGGUUUGUGAUAUAUAUCAUGUAUAUGACAUGUAUACAAGCAUUCUUCUUUGAUGGCCAGGCAGUCUCCUUGGCUACU	**115**	20,869565	24,347826	19,130435	35,652174	40	60	1,4642857	1,0909091	-48,7	-48,7	0,0458276	11	-42,347826	-1,0586957
spiLA0480-MIR169j-2	GUCUUAUUUAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCGUACUUGAAAAGGUCUUUCAUAUGUCCAUCAACAAGAAGAACCUGAGUCAAGUGAUCAGCCGUCUUUUAUAAUCCCUAUGUCAUCUGCCCAUAGAGAAAACAAUGCUACUACUCCUCCAGUUUUUGGGGUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUCUUCUUUUCAUGCAAGGCUUUCUCUC	**265**	19,245283	28,301887	21,509434	30,943396	40,754717	59,245283	1,0933333	0,8947368	-83,3	-82,4	0,0003092	30	-31,433962	-0,7712963
spiLA0480-MIR169j-3	GAAAAAGAAGAGAAGUCUUACAUGAAGAGGAGAGUCAUAUUGUUUAGUAGCCAAGGAUGACUUGCCUGCUCCAUAGUCUAAAAUGUGUUUAAUCACAUUUUAAUUUGGUUUCAGGCAGUCUCCUUGGCUAUCUUGACAUGCUCUUUUCUUUUAUGCAAGAUAUCUUUUUAAA	**172**	19,186047	29,069767	15,697674	36,046512	34,883721	65,116279	1,24	1,2222222	-72,7	-72,7	0,010282	11	-42,267442	-1,2116667
spiLA0480-MIR169j-4	UUAAAAGAAGAGAAGUCUAGCAUGAUGAGAAGAGUCUUAUUUGGUAGCCAAGGAUGACUUGCCUGCACCGUACUUGAAAAGGUCUUUCAUAUGUCCAUCAACAAGAAGAACCUGAGUCAAGUGAUCAGCCGUCUUUUAUAAUCCCUAUGUCAUCUGCCCAUAGAGAAAACAAUGCUACUACUCCUCCAGUUUUUGGGGUCAAGCAGGUCAUCUUUAGCUAACUUGACAAGCUCUUCUUUUUCAUGCAAGGCUUUCUCUUCUUUCGU	**266**	19,172932	27,819549	21,804511	31,203008	40,977444	59,022556	1,1216216	0,8793103	-90,1	-89,2	0,000464	29	-33,87218	-0,8266055
spiLA0480-	UAAAUUAAUGGUAUUAUUGGAUCGGAGUGUCACG	**194**	23,71134	26,28866	18,041237	31,958763	41,752577	58,247423	1,2156863	1,3142857	-	-32,7	0,0106225	47	-	-

MIR169j-5	UUCCAAUACAGUAUUCUUGGAUCAGAGUGUCACG										57,9				29,845361	0,7148148
spiLA0480-MIR169l	UUCCGACACGGUAAUUUUGGAUCGGAGUAUCACG UUUCGACACGAUAUUCUUGGAUCAGAGUGUCACA UUUCGACACGGUAUUCUUGGAUCGGAGUGUCACG UUCCGACACGAUAAUAUUAAUGGA AACAACAACAGCUGUUUCAUAAAAAAUCUGGCAUG AGAAAAUGAGGCAGAUAUGUAGCCAAAAAUGACU UGCCAGACAUGAAGCAGAAUUGAUCGAGCUUGCC GGCAAGUCAUCCUUGGCUGCAAUUCAAUAACCUU GUUCCCUCAUGCAAGACUUUAACAUGAAUAAAGA CAUGUCUAUUCAA	**184**	18,478261	36,413043	20,652174	24,456522	39,130435	60,869565	0,6716418	0,8947368	-57,5	-49,6	0,0085437	19	-31,25	-0,7986111
spiLA0480-MIR169r-1	CAUCCAAUGAGCUUCUCACAAGUUGUGUUUUGUU AGAUGAAGUAGGAAACUGCUAAUUCUAUUUGCCA UAGGGAAUGUUGGAUUUUCUUCUUCAGGAAACUA CACUUCCCUAUAAUUGAAUAGACAUGUCUUUAUU CAUGUUAAAGUCUUGCAUGAGGGAACAAGGUUAU UGAAUUGCAGCCAAGGAUGACUUGCCGGCAAGCU CGAUCAAUUCUGCUUCAUGUCUGGCAAGUCAUUU UUGGCUACAUAUCUGCCUCAUUUUCUCAUGCCAG AUUUUUUAUGAAA	**285**	19,298246	26,666667	18,596491	35,438596	37,894737	62,105263	1,3289474	1,0377358	-98,2	-93,37	0,0004296	33	-34,45614	-0,9092593
spiLA0480-MIR169r-2	AAAGUCUUGCAUGAGGGAACAAGGUUAUUGAAUU GCAGCCAAGGAUGACUUGCCGGCAAGCUCGAUCA AUUCUGCUUCAUGUCUGGCAAGUCAUUUUGGCU ACAUAUCUGCCUCAUUUUCUCAUGCCAGAUUUUU UAUGAAACAGCUGUUGUUGUUAAUUGUCAAAUCA GGAAUUGUGGACAA	**184**	21,73913	26,630435	18,478261	33,152174	40,217391	59,782609	1,244898	1,1764706	-70,9	-70,9	0,0109624	10	-38,532609	-0,9581081
spiLA0480-MIR169r-3	UGCAGCCAAGGAUGACUUGCCGGACCAUAAAUUG CUAGGGUUUUAUAGUUUCGGCAAGUUGUUCUUG GCUAUA	**73**	26,027397	23,287671	17,808219	32,876712	43,835616	56,164384	1,4117647	1,4615385	-34,7	-34,7	0,0847862	7,3	-47,534247	-1,084375
spiLA0480-MIR169r-4	UUGAAUAGACAUGUCUUUAUUCAUGUUAAAGUCU UGCAUGAGGGAACAAGGUUAUUGAAUUGCAGCCA AGGAUGACUUGCCGGCAAGCUCGAUCAAUUCUGC UUCAUGUCUGGCAAGUCAUUUUUGGCUACAUAUC UGCCUCAUUUUCUCAUGCCAGAUUUUUUAUGAAA CAGCUGUUGUUGUU	**184**	20,652174	24,456522	18,478261	36,413043	39,130435	60,869565	1,4888889	1,1176471	-73,5	-68,1	0,0261518	17	-39,945652	-1,0208333
spiLA0480-MIR171a-1	UGAUGUUGGAAUGGCUCAAUCUAAUGAAAGUUUC CAAACAUUUUUGGUCAUUUUAAUUUGAUUGAGCC GUGCCAAUAUCAUAUCGUC	**87**	18,390805	27,586207	16,091954	37,931034	34,482759	65,517241	1,375	1,1428571	-37,1	-37,1	0,108205	3,6	-42,643678	-1,2366667
spiLA0480-MIR171a-2	GAUCAACUUGCGAUGUUGGUGUGGUUCAAUUAGA UAACAAUCUCCACGUAAAAUUAUAGAGUUUGUUAU UUGAUUGAGCCGUGCCAAUAUCACAUGUAAAGAA AAUAA	**108**	19,444444	34,259259	13,888889	32,407407	33,333333	66,666667	0,9459459	1,4	-42,8	-42,8	0,175856	3,7	-39,62963	-1,1888889
spiLA0480-MIR171a-3	CUGUCGCAGAUGACUUUCGCCCUUCUAAGGAACC ACACUUUCUGUAAAUCUAAUUAAUUUGAAUUCAAU GUGGCAGGACGAGAGUCAUCUGUGACAGG	**98**	21,428571	27,55102	21,428571	29,591837	42,857143	57,142857	1,0740741	1	-40,3	-40,3	0,125815	10	-41,122449	-0,9595238
spiLA0480-MIR171a-4	UUGAUCAACUUGCGAUGUUGGUGUGGUUCAAUUA GAUAACAAUCUCCACGUAAAAUUAUAGAGUUUGU UAUUUGAUUGAGCCGUGCCAAUAUCACAUGUAAA GAAAAU	**108**	19,444444	32,407407	13,888889	34,259259	33,333333	66,666667	1,0571429	1,4	-42,8	-42,8	0,16246	4	-39,62963	-1,1888889
spiLA0480-MIR171a-5	AUACACGAGAUAUUGGUGCGGUUCAAUGAGAAAG CAGUACUUAAGAACAUUUUUGAGUCUACUUUUUG AUUGAGCCGCGCCAAUAUCACGUGUA	**94**	22,340426	29,787234	17,021277	30,851064	39,361702	60,638298	1,0357143	1,3125	-54,2	-54,2	0,535341	1,2	-57,659574	-1,4648649
spiLA0480-MIR171a-6	CUAUGAAACAGUAACUUUGAUAUUGGCCUGGUUC ACUCAGACAACAAAAUGUAAACUAUAUUUGAAUGG UUGAGUUUUCGUUUUUCGUUUGAUUGAGCCGUG CCAAUAUCUCAGUUUCUCUUUCACUU	**128**	17,1875	25,78125	17,96875	39,0625	35,15625	64,84375	1,5151515	0,9565217	-46	-46	0,136677	6,9	-35,9375	-1,0222222
spiLA0480-MIR171a-7	GUGUGAUGUUGGAAUGGCUCAAUCUAAUGAAAGU UUCCAAACAUUUUUGGUCAUUUUAAUUUGAUUGA GCCGUGCCAAUAUCAUAU	**86**	19,767442	27,906977	13,953488	38,372093	33,72093	66,27907	1,375	1,4166667	-40,3	-40,3	0,105416	3,8	-46,860465	-1,3896552
spiLA0480-MIR171b-1	AUUUUGGGAUUAAAAUGGAAGAAGCGAUGUUGGU GAGGUUCAAUCCGAAGACGAAUUUAUGCUUAUUU UCGUAAAGAACGAUCUCAGAUUGAGCCGCGCCAA UAUCACUUCUUAU	**115**	22,608696	30,434783	15,652174	31,304348	38,26087	61,73913	1,0285714	1,4444444	-43	-37,7	0,131277	7	-37,391304	-0,9772727
spiLA0480-MIR171b-2	GAAGAAGCGAUGUUGGUGAGGUUCAAUCCGAAGA CGAAUUUAUGCUUAUUUUCGUAAAGAACGAUCUC AGAUUGAGCCGCGCCAAUAUCACUUCUUA	**97**	22,680412	29,896907	18,556701	28,865979	41,237113	58,762887	0,9655172	1,2222222	-43	-40	0,320459	3,8	-44,329897	-1,075

spiLA0480-MIR171b-3	AGCUACACGUGAUAUUGGCGCGGCUCAAUCAAAAGUAGACUCAAAAAUGUUCUUAAGUACUGCUUUCUCAUUGAACCGCACCAAUAUCUCGUGUAUUC	**99**	17,171717	30,30303	23,232323	29,292929	40,40404	59,59596	0,9666667	0,7391304	-40,6	-40,6	0,313587	2,5	-41,010101	-1,015
spiLA0480-MIR171b-4	AACGGAAUGAAAAUAAGAAGUGAUAUUGGCGCGGCUCAAUCUGAGAUCGUUCUUUACGAAAAUAAGCAUAAAUUCGUCUUCGGAUUGAACCUCACCAACAUCGCUUCUUCCAUUUUAAUCCCAAA	**125**	16,8	33,6	21,6	28	38,4	61,6	0,8333333	0,7777778	-38,9	-33,7	0,0464737	13	-31,12	-0,8104167
spiLA0480-MIR171c-1	AGAUAUUGAUGCGGUUCAAUCUGAAAGACAUGGUUAGAUAUGUAAUUAGCCUUGUAAUUUUGGAUUGAGCCGCGUUAAUAUCUC	**84**	22,619048	28,571429	13,095238	35,714286	35,714286	64,285714	1,25	1,7272727	-43,1	-43,1	0,429404	1,9	-51,309524	-1,4366667
spiLA0480-MIR171c-2	AAUACGUGAUAUUGGCACGGCUCAAUUAAAUAACGAAGUUCUAUAUAUAAAGAAGUGCGCUUUCUAAUUGAACCGCACCAAUAUCUCGUUAG	**92**	17,391304	34,782609	18,478261	29,347826	35,869565	64,130435	0,84375	0,9411765	-28,2	-27,8	0,480796	1,9	-30,652174	-0,8545455
spiLA0480-MIR171c-3	CUAACGAGAUAUUGGUGCGGUUCAAUUAGAAAGCGCACUUCUUUAUAUAUAGAACUUCGUUAUUUAAUUGAGCCGUGCCAAUAUCACGUAUU	**92**	18,478261	29,347826	17,391304	34,782609	35,869565	64,130435	1,1851852	1,0625	-42,2	-42,2	0,652436	0,9	-45,869565	-1,2787879
spiLA0480-MIR171f-1	CUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAGU	**81**	17,283951	22,222222	18,518519	41,975309	35,802469	64,197531	1,8888889	0,9333333	-24,6	-24,6	0,271433	6	-30,37037	-0,8482759
spiLA0480-MIR171f-2	ACUCUGAUAUUGGCCUGGUUCACUCAGACACAUAUUAUUUUGAUUGAUUUUACUUUUGAUUGAGCCGUGUCAAUAUCUCAG	**81**	17,283951	23,45679	18,518519	40,740741	35,802469	64,197531	1,7368421	0,9333333	-24,5	-24,5	0,269034	5,6	-30,246914	-0,8448276
spiLA0480-MIR171t	AAUCCGGGCUCUGCAACUAUGUUGAACUGCGUGACUAUCUCAUUUAAAAGGUUUAGAUGAGAUAGUCAGACACUUCAACAUUGUAUCAAGCCAGGCCC	**98**	20,408163	29,591837	22,44898	27,55102	42,857143	57,142857	0,9310345	0,9090909	-42,6	-40,9	0,111429	11	-43,469388	-1,0142857
spiLA0480-MIR172-1	UUCAUCAUCAGUCAAUGUUUGAGGAUGCAACAUCAUCAAGAUUCACAAAACUUGAAGGGAGAAGUAUUUAAUUAUAUAUUUAGGGUGAAUAUUGGAUAUAUAAUAUAGUUCAAAGUCUCUUAUUUUCUCUCUUUGGGAAUCUUGAUGAUGCUGCAUCAUCUAACAUAUGACUCUAU	**176**	16,477273	32,386364	14,204545	36,931818	30,681818	69,318182	1,1403509	1,16	-58,4	-53,07	0,015918	22	-33,181818	-1,0814815
spiLA0480-MIR172-2	UGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUUCAAAAAUGAGAAUCUUGAUGAUGCUGCAUCGACAAAUUAUGACUUUUUCCCCUCGAAUUAAAAGAAUUCAGGAUGAUCUCGACUUUACUAUUUAUUUUUGGUAAGUAUGCAAUUUGGACUUUGACU	**246**	15,447154	34,146341	15,04065	35,365854	30,487805	69,512195	1,0357143	1,027027	-68,6	-60,2	0,0001992	36	-27,886179	-0,9146667
spiLA0480-MIR172-3	GUGUACACAGUUGUUGUUUGCAAAUGCAGCACUAUUAAGAUUCUCAAAUAUUCUGACAUUUAAAAUGCAAUUAAAUGUGAAUCUUGAUGAUGCUGCAUUAGCAAUAAA	**108**	16,666667	35,185185	13,888889	34,259259	30,555556	69,444444	0,9736842	1,2	-33,1	-33,1	0,034275	16	-30,648148	-1,0030303
spiLA0480-MIR172-4	CUUACAGUCGUUGUUUGCAUAUGUGGCAUAAUCAAGAUUCACGUGAAAAGUUGCAAAUUGGUUAUAUAAUUGAUGAAAUUAAUGGCUGGCUAUUUGAAACUCACGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAACGAC	**140**	20,714286	32,857143	15	31,428571	35,714286	64,285714	0,9565217	1,3809524	-53,2	-52,3	0,0268638	15	-38	-1,064
spiLA0480-MIR172-5	UGGUUGACACAUGUACAGUCGUUAUUUGCAGCUGCAGCAUCAUCAAGAUUCACAUAAAAUAGAAAUAAUAUGGAGUAGGAAAAAAAAAUCAAGUUGCUUCUAAAUUCCAUAUUAUUAUUUUUUUUCAAAAAUGAGAAUCUUGAUGAUGCUGCAUCGACAAAU	**161**	16,149068	37,267081	14,285714	32,298137	30,434783	69,565217	0,8666667	1,1304348	-51,6	-43,8	0,0058017	28	-32,049689	-1,0530612
spiLA0480-MIR172-6	GCAGAUGCAGCAUCUUCAAGAUUCACAUAGAUUUAUAUAAAAUAUAGAGUUCCAUGUUUGGGGUGAAAGUAAUUAAUUAAUUAAUUUUCUCCUAUAUAUUGGCUCUAUUGAUUAUUAUUUGUUGUGAGAAUCUUGAUGAUGCUGCAGCGGCA	**156**	18,589744	30,769231	12,179487	38,461538	30,769231	69,230769	1,25	1,5263158	-58,2	-57,4	0,0167833	14	-37,307692	-1,2125
spiLA0480-MIR172-7	UACAGUCGUUGUUUGCAUAUGUGGCAUAAUCAAGAUUCACGUGAAAAGUUGCAAAUUGGUUAUAUAAUUGAUGAAAUUAAUGGCUGGCUAUUUGAAACUCACGAGAAUCUUGAUGAUGCUGCAUCAGCAAUAAACGACUAUU	**142**	20,422535	33,098592	14,084507	32,394366	34,507042	65,492958	0,9787234	1,45	-55,4	-54,5	0,0249561	15	-39,014085	-1,1306122
spiLA0480-MIR172a-1	AAACACUGUCUCAAAUGUAAAUCUUCAGGUCGCCAAAGUCUAUAUCCUCCAAAAAGUAGUGCAUUUUUGGAGUAGAACAACAUAGACAUUGACGACAUGAAG	**124**	17,741935	36,290323	19,354839	26,612903	37,096774	62,903226	0,7333333	0,9166667	-57,6	-57,6	0,248658	2,9	-46,451613	-1,2521739

spiLA0480-MIR172a-2	AUUUACAUCUGAGACAGUGCAUAUGAAGAAUUAGGUGAAUAUGCUGAGGAGAUGGAGUUGAUAAAUGUUCCUUUGACUCUGGUAUAAGCGACAAAGAAACACUGCCAUCCUCAAUCUUCUCAUCAUAAGCAUCUUUUUUUUAAAUUUAGUCGUUUAUUGCUAAUGCAGCAUCAUCAAG	**122**	18,852459	32,786885	16,393443	31,967213	35,245902	64,754098	0,975	1,15	-35,2	-29,5	0,0580515	11	-28,852459	-0,8186047
spiLA0480-MIR172b	AUUCACAUUUAAUUGCAUUUUAAAUGUCAGAAUAUUUGAGAAUCUUAAUAGUGCUGCAUUUGCAAACAACAACUGUG	**111**	15,315315	32,432432	15,315315	36,936937	30,630631	69,369369	1,1388889	1	-34,6	-32,8	0,0365855	13	-31,171171	-1,0176471
spiLA0480-MIR172c	GGAGCAUCAUCAAGAUUCACAUAGCUAUAUUAGGGCUUUUAUAAUUUUUAAAAACCCUAUGGGCGAUGUGUGGGAAUCUUGAUGAUGCUGCA	**92**	22,826087	29,347826	15,217391	32,608696	38,043478	61,956522	1,1111111	1,5	-42,1	-38,6	0,0016633	9	-45,76087	-1,2028571
spiLA0480-MIR172d-1	AUUCAGACCUAAAAAUCAAACGUACUGAAUAGGCUGAAUCUGAAUGAUUAAGAUUCACACCUCCAUUGAGUGCAAACAAAUGAGGCCUUAGUUGUCAUUUGUUUUCAUUAAGAUUAAGAGGUCUGAAUCUGAAUAAACAUCUGAAUAUUAAGAUUUGCAUUAAGAUUUGAGUGCUUUAAUCUGAGU	**186**	17,741935	34,946237	14,516129	32,795699	32,258065	67,741935	0,9384615	1,2222222	-47,1	-47,1	0,0180475	22	-25,322581	-0,785
spiLA0480-MIR172d-2	CAAACUUAAUGGGCUAAAUCUAAAUUAUUCAAAUUCAGACCUAAAAACCAAACGUACUUAAUAGGCUGAAUCUGAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCA	**106**	13,207547	40,566038	18,867925	27,358491	32,075472	67,924528	0,6744186	0,7	-34,1	-34,1	0,197494	4,4	-32,169811	-1,0029412
spiLA0480-MIR172d-3	AAAUGAACUUAAUGGAUUUAAUCUGAAUGAUUCAGAUCCAAACCUAAAAAUCAUACGUACUUAAUAGGUUGAAUCUGAAUGAUUAAGAUUCAGACCUCCAUUAAGUGCAAAC	**112**	14,285714	40,178571	16,071429	29,464286	30,357143	69,642857	0,7333333	0,8888889	-32,6	-30,4	0,0225799	8	-29,107143	-0,9588235
spiLA0480-MIR172e	UAAAAAAAUAAGGUAUAUCGCUGCCAGGGAAGCGAUUUAAAAUAAAAAAUAAAAAAUUUAUAAAACGCUGCCCAGGCAGCGACGUUUAUGAAAAUUUUUUUUUUUAUAAAAUAAAUCGCUGCCAAGGCAGCGAUUUAUAGAAUUUUUUUUUUUCUAAACGCUGCCCAGGCAGCGACAUUAUGAUUUUUCUU	**189**	15,873016	36,507937	15,343915	32,275132	31,216931	68,783069	0,884058	1,0344828	-71,8	-64,9	0,0071803	29	-37,989418	-1,2169492
spiLA0480-MIR172j	UGCAGCAUCAUCAAGAUUCCCACACAUCGCCCAUAGGGUUUUUAAAAAUUAUAAAAGCCCUAAUAUAGCUAUGUGAAUCUUGAUGAUGCUCCAC	**94**	14,893617	32,978723	23,404255	28,723404	38,297872	61,702128	0,8709677	0,6363636	-40,2	-40,2	0,227698	3,3	-42,765957	-1,1166667
spiLA0480-MIR1847-1	UUUGGCCUACGUGACACUAACUUGAAAAAAAGUCAACCAGCGUUGUGCCCACAAGAUAGUGCCACGUAGACCGAA	**75**	21,333333	33,333333	25,333333	20	46,666667	53,333333	0,6	0,8421053	-26	-26	0,264209	2,1	-34,666667	-0,7428571
spiLA0480-MIR1847-2	AACUUAUUUUAUAAAUGAUUUUUUACCCCUUUUUAAGCAUAAUGGAACUAUCUUGAAAAACAUAUGUCAACACGCACUUGGCCGACAAGAUAGUGUCACGUAGGCCAAAAAGGGGUAGAGUAUUAUUUAUAAUAUAACUG	**140**	16,428571	35,714286	15,714286	32,142857	32,142857	67,857143	0,9	1,0454545	-45	-44,4	0,050251	7,3	-32,142857	-1
spiLA0480-MIR1847-3	AUUCCUUUUCAGCCUACCUAGCACUAACUUGAAAAAAAAAGGCAAUCAGUGUUGGGCCCACAAGAUAGUGUCACGUAGGCCGAAAAGGAGU	**93**	21,505376	35,483871	21,505376	21,505376	43,010753	56,989247	0,6060606	1	-33,7	-32,3	0,17009	6	-36,236559	-0,8425
spiLA0480-MIR1850	UGAUUACUUCCGGUUCUUCCCAUAGCUUGUCAAUACUAUUUUGAUUAGUUCACAUUUAAAAUGAAUAAAGAGCCUCGAAUGCACCAAACAAUGCUGUAAGACAUGGGAAGAAACAUUAACAAAACUUGACUUCGUCCGAAUAUUGACAAGCGAUGGGAAGAAUUGGAAGUAAGUU	**175**	18,857143	35,428571	17,142857	28,571429	36	64	0,8064516	1,1	-56	-52,4	0,0078454	23	-32	-0,8888889
spiLA0480-MIR1863	CGUCAAAGUCAAUACCCUUUCUUUGACCGAAUUUCUUAUUAAGGUCAGUAGUCGAUUGCAACAAAGGUGUGCCCAAUUUGCUGCAAAUCUUGCCAAAAAGAUUUUCUUCCUUUAAAGAUGGGAUUUGGACCCCAUAACUUGAAGCUCAGGUACAAAGUUAGAUUGGUUGUUAAGCUAUUUGGCCGAAGGAAGGGUAUUGACUUUGAAG	**208**	21,634615	28,846154	17,788462	31,730769	39,423077	60,576923	1,1	1,2162162	-72,6	-69,5	0,005693	34	-34,903846	-0,8853659
spiLA0480-MIR1863a-1	AAUUGUGAAAUUAGGUCCUAGAGCUAACUCACACUUCAAAAGCUAGCUCAAAGAGAGGAUGAUUUUUCAAGUCUUAUAAGGAGUCCACCCAUCUUAUUUAUCACCGAUGUGGACUUUUUGUCAUUCUUUAACACUCCACCUCACGCCCAGUGCUUACCAUCUGGUGCGUGGGCAAUUUUGAUUUUGGGGGUCCCAACAUCGGGUGAGAUGGGCCCUGCUCUGAUACCAUGUAAAAUU	**261**	20,306513	26,05364	23,371648	30,268199	43,678161	56,321839	1,1617647	0,8688525	-82,6	-69,65	0,0003152	67	-31,64751	-0,7245614

spiLA0480-MIR1863a-2	AGGUAUUAGGCCUAAUUCACACCC UUAAUAUAGAAAUUAGGUUUUAGGCCUAACUCAC ACCUCAAAAGUUAACUUAAAGGGAGGAAGAAUACA CAAUUCUUAUAAAAAGUCCACUCAUCUCAUUAACC ACCGAUUUAGACUUUUGUCAUUCUUUAACAUCCC ACCUCAAGUACAGUGCUUAGCAUCGGGUGAGACG AACCUGCUCUGAUACCAUCUGAAAUUAGGUUUUA GGCCUAAUUCAAACCCCAAAAGCUAGCUUUUCGG GUGUGAGUUAAGCCUAAAAUAUUUCACAUAAA AUGUUUAUGUCUUUCAGUUUUGAGUUUGCAUAAG UAAACACUUAAAAUUGAACAAAUAGAUACAUUCGU CCUACGUAAUAAUUUUGUAUCCUGGUGGUGUGCU	**272**	15,441176	33,823529	21,323529	29,411765	36,764706	63,235294	0,8695652	0,7241379	-71,6	-54,7	0,0001293	52	-26,323529	-0,716
spiLA0480-MIR1881	ACGUGUAUUAUGUUGUGAAGGAUGCGUGUGAUUA CUUGUUCAAUUUUAUACAAGUUUAAAUGUUUGAU UGUGCAUACAAAAAGUUGGAUGACGUAGAAAGG GUCAUGCAAUACCAUAUCAUGAUAUGGUAUCGUG	**204**	21,078431	29,901961	10,784314	38,235294	31,862745	68,137255	1,2786885	1,9545455	-61,2	-61,2	0,040164	10	-30	-0,9415385
spiLA0480-MIR1886f-1	AGAUGAAAUCAGCGUUUGGACAUGCGAUUUUACG CUGAUUCCAUCUCAUGAUUCUAUAUCAUGAGAUG UGAUUCCAUAUU	**114**	19,298246	28,070175	17,54386	35,087719	36,842105	63,157895	1,25	1,1	-48,4	-48,4	0,132662	8,2	-42,45614	-1,152381
spiLA0480-MIR1886f-2	CGGUGAUAUGGUAUCGUGAGAUGAAAUCAGCGUU UGAAUAUAUGAUUUUACCCUAAUUUCAUCUCAUG AUUUCAUAACAUGA	**82**	18,292683	30,487805	14,634146	36,585366	32,926829	67,073171	1,2	1,25	-27,8	-27,8	0,244148	5,5	-33,902439	-1,0296296
spiLA0480-MIR1886f-3	GAUAUGGUAUCGUGAGAUGAAAUCAGCAUUUGGA CAUUUGAUUUCACGUUGAUUCCAUCUCAUGAUUC CAUGAG	**74**	21,621622	27,027027	16,216216	35,135135	37,837838	62,162162	1,3	1,3333333	-29,6	-29,6	0,372615	1,8	-40	-1,0571429
spiLA0480-MIR1886h-1	CGUGAGAUGAAAUCAGCAUUUGGAUAUGCAAUUU UACGUUGAUUUCAUCUCAUGA	**55**	20	29,090909	14,545455	36,363636	34,545455	65,454545	1,25	1,375	-24,5	-23,3	0,420644	4,7	-44,545455	-1,2894737
spiLA0480-MIR1886h-2	GCCAUGAGAUACCGUAUCGUGGCCUUUGGCCAUG AGAUAUCAUAUCACGAUAUGAAAUCGUGAGAUUG AAUUCGUGUUUGGACAUAUAAUUUUACGUUGAUU UCAUCUCAUGAUUUUAUAUAAUGAGAUGUGAUUU CGUAUUCUCCAAAAAUCAUGAUAUGGGAAUUUCA UAUC	**174**	18,965517	29,310345	14,942529	36,781609	33,908046	66,091954	1,254902	1,2692308	-59,7	-55,67	0,0106782	23	-34,310345	-1,0118644
spiLA0480-MIR1886h-3	ACCAUAUCACGAUAUGGAAUUAUGAGAUGGAAUC AUCGUUUGGACAUCUAAUUUUACGUUGAUUCCAU CUCAUGAUUCCAUAUCAUGAUAUAUG	**94**	15,957447	30,851064	17,021277	36,170213	32,978723	67,021277	1,1724138	0,9375	-49,7	-49,7	0,602118	2,3	-52,87234	-1,6032258
spiLA0480-MIR1886i	GGCGAUACGGUAUCAUGAGAUGGAAUUAGCGUUU GGACAUGCGAUUUUGUGCUGAUUCAGUCUGAUGA UUCCAUAUCAUG	**80**	27,5	23,75	15	33,75	42,5	57,5	1,4210526	1,8333333	-26,6	-25,9	0,100283	5,2	-33,25	-0,7823529
spiLA0480-MIR1888b-1	CUAGGCCCAUUGGGCCGGCCUGGCCUAACCCGG GAUUUAAUAGGGUUGGGCUAAGAUUUUUGGAGCC CAUUUAAGGAAAAGGCUUUUUAGCCCGACCUAAU UAAGUCUGUUGAUUUAAGGGGCUUGAGAAAUAUA GGUAUGGCCGGCCCGUGGGCCAAU	**159**	29,559748	23,27044	20,125786	27,044025	49,685535	50,314465	1,1621622	1,46875	-80,9	-78,6	0,0984503	20	-50,880503	-1,0240506
spiLA0480-MIR1888b-2	CUGAGAUUUAAUAGGGUUGGGCUAAGGUUUUUGA AGCCUAUUUAAGAAAAGGGCUUUUUAGCCCGACC UGAAUAAGUCUGUU	**82**	25,609756	26,829268	13,414634	34,146341	39,02439	60,97561	1,2727273	1,9090909	-33,1	-33	0,143768	4,7	-40,365854	-1,034375
spiLA0480-MIR1917-1	GGAAUCAAUACAACAAAAAUAACUUUUAGCGGCAU UAAAUAUUGACAUUAAUAAAGAGUGUUAAAGUCUU UACCGGCAUUAGUAAGUGCCAUUAGAAUCAAUGU CUCUAAAGACUUUAGGGACAUAUACAACCAGUGA CAAUUGCCACUAAAAAUCCAUAUUUUGCGACAAUU AAGAAUUAAUUGUCGCUAAUGAUCAUUUUUGUUG UAGUGGAUAAU	**218**	16,055046	37,614679	14,678899	31,651376	30,733945	69,266055	0,8414634	1,09375	-60,4	-52,3	0,0010364	28	-27,706422	-0,9014925
spiLA0480-MIR1917-2	AUAACACUACAAUAAAAAUGACUUUUAGCGGCAUU AAAUAUUGACAUUAAUAAAGAGUGCUAAAGCCUUU ACCGACAUUGGUUAAGUGCCAUUAGAACCAAUGU CGCUAAAGGCUUUAGGGACAUAUACAAAGAGUGU CAAUUGCCGCUAAAUAUACAUAUUUAGCUACAAUU GAGAAUUAAUUGCCUCUAUUAAUCAUUUUUGUUG UAGUGUAAC	**216**	16,203704	36,111111	15,740741	31,944444	31,944444	68,055556	0,8846154	1,0294118	-79,7	-69,1	0,0047835	34	-36,898148	-1,1550725
spiLA0480-MIR1917-3	AGAUAUAUAUAUGCUCACGUGGACAUGAAUUAUU UAUAAUUAUUACUACAAAAAAAUAACUUUUAGCGG CAUUAAAUAUGACACUAAUAAAGAGUGCUAAAGUC UUUACCGGCAUUAGUUAAGUGUCAUUAGAACCAA UGUCGCUAAAGGCUUUAGGGACAUAUACAAAGAG	**271**	16,236162	36,162362	14,02214	33,579336	30,258303	69,741697	0,9285714	1,1578947	-78,6	-76,1	7,83E-05	37	-29,00369	-0,9585366

spiLA0480-MIR1917-4	UGACAAUUGCCUCUAAAAUUACAUAUUUAGCGGGCUAAUAGUUAUUUUUGUUGUAAUGUAUACAAUAUUUAUGAUGCUUACGUGAGCACAUAUAUACCUUCUCUACAAUAAAAAUAACUUUUAGCGGCAAUAAAUAGAUACAUUAAUAAAGAGUGCUAAAGUCUUUACCGGCAUUAGUUAAGUGUCAUUAGAUCCAAUGUCGCUAAAGCCUUUAGUGACACAUACAAAGAGUGCUAAUUGCCACUAAAACCAUAUAUUUAGCGGCAAUUGCUAAUUAAUUGCCGCUAAAGCUCAUUUUUAAUGUAGUGU	**210**	15,714286	35,714286	17,142857	31,428571	32,857143	67,142857	0,88	0,9166667	-61	-58	0,0032374	32	-29,047619	-0,884058
spiLA0480-MIR1918	GUAGCUCAGUUGGUUUAAUUAGUUGAAUUGUCAUUUUGUUGGUGAGAGUUCGAUUCUCCAUUACGCAAUCUCCUCUUUAAUUUAAGAGAAAAAGAUAUGCUACAAGGUGGAGAAUCGAACUACCGCUAACAGAAUGGAAGUUCAAAUACUUAAUCAAUUAAGCUAC	**166**	19,277108	32,53012	15,662651	32,53012	34,939759	65,060241	1	1,2307692	-70,5	-69,8	0,0387501	9,8	-42,46988	-1,2155172
spiLA0480-MIR1919-1	GCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUUCUUUUAAUUUGAAUCCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGG	**143**	23,076923	25,174825	19,58042	32,167832	42,657343	57,342657	1,2777778	1,1785714	-68,1	-64,6	0,0350805	14	-47,622378	-1,1163934
spiLA0480-MIR1919-2	CCGGUAGUCCUGUCGCAGAUGACUUUCGCCCAUUUAUGGAACCACACUUUCUUUAAUUUGAAUUCUAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUAAUGGAAGAUCGAGUUAUCAAAGGCUUAUUGGGCGUUUCCUUUUUCAU	**147**	23,129252	23,809524	19,047619	34,013605	42,176871	57,823129	1,4285714	1,2142857	-54,1	-49,4	0,0125193	23	-36,802721	-0,8725806
spiLA0480-MIR1919-3	GACGCCUUUGAUGUUCACAUCUUCCGGUAGUCCUGUCGCAGAUGACUCUCGCCAAGCCCCUUUCUCUAAGUCUAAUUAAUUUGAAUUCAAUGUGGUAGGACGAGAGUCAUCUGUGACAGGAUUAUGGAAGAUCGAGUUAUCAAAGGCUUA	**150**	22,666667	25,333333	21,333333	30,666667	44	56	1,2105263	1,0625	-73,5	-72,64	0,0141312	14	-48,98	-1,1131818
spiLA0480-MIR1919-4	UAGUCCUGUCGCAGAUGACUUUCGCCCUUCUAAGGAACCACACUUUCUGUAAAUCUAAUUAAUUUGAAUUCAAUGUGGCAGGACGAGAGUCAUCUGUGACAGGAUAA	**107**	20,560748	28,971963	20,560748	29,906542	41,121495	58,878505	1,0322581	1	-46,6	-46,6	0,116525	11	-43,551402	-1,0590909
spiLA0480-MIR2083	GGCAGACUGACGAGGGCAAGUAAAACAUGACUGACAGACUUCUAAACAGACAAAUUUUUGAAACAGAAGUGCAUAUGAUAUAUCAGACGAAUCUCAUAUCUCCAUGAGGGAGGAAAGUGAAUUUAUUAUGCACACUUCUGUUUCAGAAGCUUGUCAAUUUAGAAGUCUGUCAAUCCUGCUUGACCUGCCCUCAUCAGUCUAGA	**203**	20,197044	33,004926	19,704433	27,093596	39,901478	60,098522	0,8208955	1,025	-91,1	-81,94	0,016452	22	-44,876847	-1,1246914
spiLA0480-MIR2089	UCUGAUCUGUAUAGCAUGCAUUAAGGUUUGAUCGUACUUCUGCAAUAAGUAAAGAAAUGCUCAAAACCAAUAUCUUUUCUUUUUUGAGAUAAAAAAAAAAGUUAUAUUGGUUUUGAGCAUUUCUUUACCUAUUGCACAAGUACGAUCACAAUUUAGUAUGACGCUAUAAAGGUCUUC	**177**	15,254237	33,333333	15,254237	36,158192	30,508475	69,491525	1,0847458	1	-79,7	-74	0,0432896	18	-45,028249	-1,4759259
spiLA0480-MIR2099	GCCUCUCUCACUUUAUAUACAAACACAAAUGUACAAAUGUGUUUGUACAAAAGUGAUAUAAAAUGCAUACAUACAUCUCUUUUCGUCUGCCUCUCCCCUAGAGAAUCUCGUUUGCCUCUCUCACUCACCUCUCUCACUUUAUACAAACACAUAUAUAUUGUCUCUGUGUUUGUAUAAAGCGAGAGAAAA	**189**	11,640212	30,687831	24,338624	33,333333	35,978836	64,021164	1,0862069	0,4782609	-51,3	-51,3	0,121185	27	-27,142857	-0,7544118
spiLA0480-MIR2101-1	UUCAUUUCAUUAUGUGCAUCACUUGAGGCUGACCUCAUUCUUUCAUUGGGAAAUUUAACUCAAGUGAGCAUCAUGAAAUCCA	**82**	15,853659	28,04878	20,731707	35,365854	36,585366	63,414634	1,2608696	0,7647059	-24,1	-23,8	0,209963	8,4	-29,390244	-0,8033333
spiLA0480-MIR2101-2	AUGUGAUUAAUGAUUAAGGAUUGUGGAGUUGCCCUCAUGUUUAUAAGUUGACAGUUGGUCCACUUAAUUAAAUGAAGGGUAAAAGGGUAAUUUCACAAUACCUAAUUUAACCAACU	**116**	19,827586	33,62069	12,931034	33,62069	32,758621	67,241379	1	1,5333333	-32,2	-29,3	0,0321742	12	-27,758621	-0,8473684
spiLA0480-MIR2108a	AUGUAUUUGUAUACUCUGGCGAAUUAUACAUAUACAAACGUGACUAAUUAUACAAACUUGAAGUCAACCAACGUAAUUAAUGUAUAAUGUUAGUCGCGAGUGACAAUUAUAG	**112**	16,071429	37,5	14,285714	32,142857	30,357143	69,642857	0,8571429	1,125	-24,7	-20,2	0,0367328	30	-22,053571	-0,7264706
spiLA0480-MIR2111	ACUCAUCUGAAUAUUCAGAUUUGCUUUAAGAUUUGAGUGCUUUGAUCUGAAUACACAUCUGAAUAUUAAGAUGUGG	**76**	18,421053	30,263158	13,157895	38,157895	31,578947	68,421053	1,2608696	1,4	-22,6	-21,3	0,045092	14	-29,736842	-0,9416667

spiLA0480-MIR2111d	UGGUAAUCUGCAUCCUGAGGUUUAGAUCAAUUUAUAACUUACUGGAUCUAGUCCUUGGGAUGCAGAUUAUC	**71**	21,126761	25,352113	16,901408	36,619718	38,028169	61,971831	1,4444444	1,25	-36,4	-36,4	0,232791	2,1	-51,267606	-1,3481481
spiLA0480-MIR2118a	AUAUUCCGUAGAAUUUAGAAACGAUUUCACUGAAUUACAUAGAACCCCUUUUCCUCAUUUCUCCAUUUCCUUAGAACGAUUUCACAAAAUACAUAAGUUCUAAGGGAAAGGGGUUUUAUGUUCUUCAGUGAAGUCGUUUCUAAAUUCUAAGGGAAAGA	**158**	15,822785	32,278481	17,721519	34,177215	33,544304	66,455696	1,0588235	0,8928571	-76,1	-74,6	0,0664005	9,7	-48,164557	-1,4358491
spiLA0480-MIR2118b	CUAGGGAAACGCAUCAUGACCAACCAAGGUAAAGAAUUCUAAAUAGAACUCUUUACCUUGCCUUGGUUGGUCCCGAUGCGUUCCCUUU	**88**	19,318182	27,272727	25	28,409091	44,318182	55,681818	1,0416667	0,7727273	-47	-46,9	0,0417533	8,3	-53,409091	-1,2051282
spiLA0480-MIR2275b	UCAUGAGUCGAUUUAAUCAAUUUUAUACGAUUUAAGUAAUUAUUUGUGUGCAUUUUAAAUUGGAAGGCAUAGGCGUAAGAUAAGGCUAAGUUUAAAAAAAUGUUGUAUUAAGCGUAAUGCAUAAUAUGUCAUCUAACUUGGUUUGAGCUCAUAUUGUUGUCCUCCAAUUUUUGGUGUGCACAAGUAGACACUUAAAUUUCUAUAGAGUUGAACAAAUAGACACACGC	**227**	18,502203	33,039648	12,77533	35,682819	31,277533	68,722467	1,08	1,4482759	-68,5	-67,2	0,0115438	22	-30,176211	-0,9647887
spiLA0480-MIR2607-1	UCUGUUUUAGAAAACAUUAUACAUGUCAUUAUUUGUUAACUGAAAACAGUUCUAACUUUGCAAAAUUGUUUUAUACGCGGUCAGUUAUGAUUGGGGCACGUCAUUAAUUAAAUUAUUUUUUAAAAAGUGAAAAAUGUUCAAAUAUGCCAACGAACUUAUAGAAUAGGCUCAUCUAUGCUAUCCGUUAAGAGUUUUCCUCAUCCGUGUCAUUUUAGUUAGGAAAUGCUGACAUGGAUAAGUCUUUUCUCAAACAAA	**254**	15,748031	33,070866	14,96063	36,220472	30,708661	69,291339	1,0952381	1,0526316	-57,4	-53,9	0,0011817	38	-22,598425	-0,7358974
spiLA0480-MIR2607-2	UGGACAUACCCAUUUAAGGGAAAAUUACAUGGGAUGUCAAACAUCCCCAUGUAAUUAGUUAAUAAGGGUAUAGUUUA	**77**	19,480519	36,363636	14,285714	29,87013	33,766234	66,233766	0,8214286	1,3636364	-26,2	-25	0,0298097	8,4	-34,025974	-1,0076923
spiLA0480-MIR2608	AAUAAAAGUUUGUUUAUAUACCAAUAUUCUUCAAAAUUGAUAAGUAGUUCAAAGUGGAAGUUGCGAUUUCCAGCCUUUAGGAGGAAUAGCGAAAAAAGUAGCCGUAAGAGUGGAGAAGGCGAAAAAAGCUAUUCAUGGCCGAAGAGGAGAAAUGUUGAGGCAUUGAUAGGACUAAUUAUCAACUAGAGGAAGAAGGUAUAAAAACUAUCUUUUAUU	**216**	23,148148	38,888889	11,111111	26,851852	34,259259	65,740741	0,6904762	2,0833333	-57,9	-57,9	0,044163	22	-26,805556	-0,7824324
spiLA0480-MIR2619b	CGUGGUGGAGCUUCCAGUUCUAGCGGUCCCUCAAACCGUAUAUAUGCUUUGAGUAAUAGGCAAGAUCAGGAGGCGUCACCUAA	**83**	26,506024	25,301205	22,891566	25,301205	49,39759	50,60241	1	1,1578947	-30,1	-29,7	0,337259	3,7	-36,26506	-0,7341463
spiLA0480-MIR2622-1	UUUUCCAGAAGUUCAGGAUGAAGCACGUUCCACAUGUAGAACAAAUUUAUCUACACGUUGAAUGUGCUUCAUCCUGAACUUUGGACCU	**88**	18,181818	28,409091	21,590909	31,818182	39,772727	60,227273	1,12	0,8421053	-49,8	-49,8	0,204618	3	-56,590909	-1,4228571
spiLA0480-MIR2622-2	AUGCCCUCGGAACUAUUUAAAACUGUAUUUUAAAGAUAUAUAUGUGCCCACGUGGACUUUUCAUAUCCACGUGGACACAUAUAUACGUUUAACAUACUCUACUAAAAAUUGUAGGAGGGUGG	**122**	18,032787	31,967213	18,032787	31,967213	36,065574	63,934426	1	1	-46,5	-46,5	0,376403	2,7	-38,114754	-1,0568182
spiLA0480-MIR2622-3	UAUCAAUCUAGCAAGGAACCAGAUCCUUGUUAUUGAAACUGCUGACAGUGAGAUGAAUGACAAACUCAGUGUGAGGUAUAUUUGUGUGCUAUCAUCAAAAAGGGAAAAAAUGUUAUAUUCUAGGUGUUUUGAUGAUCCUCACAAAUGCAAGGACCUGGUCCCUGUCAGAGUGCUC	**175**	22,285714	31,428571	17,142857	29,142857	39,428571	60,571429	0,9272727	1,3	-50,5	-50,2	0,0124769	14	-28,857143	-0,7318841
spiLA0480-MIR2650	CGUGUUAAAAUUAAAAAUAUUUAAUGGGUUGAAUAGAAAUUGGGUUGGGUCUUGACGUGCCCAAGUUUACUUUGGACUCAAAUGGGGGCUAAAAUAUGUGUUCGGUCUUGACCCACCCAAUUUGACUUGAUUAAUCUCAAUAAUUUAACAUAUUGAUAUUUAACUUUUUGUGAAAUGACUUGAGAGGUGUAGUAUAAGUGGGAGCCGAAAGGCGAAAGUGAAAUACCACUACUUUUAACGUUAUUUUACUUA	**167**	19,161677	30,538922	13,772455	36,526946	32,934132	67,065868	1,1960784	1,3913043	-42	-30,9	0,0030131	43	-25,149701	-0,7636364
spiLA0480-MIR2662	UCUUCUCUUCAUCCGACAAUGAUGAUGCAAGUGAUGCAGGGCCUGAUGGGUGAAUAAUGGAUUUCUACCAAAGUUCUAGGAAUUUCAUCAGUUCAGUCAUCAUGGAAGCCCUACAUCACUACCAUCAACAAUGUUAGAUGGUGAGACAA	**86**	24,418605	32,55814	11,627907	31,395349	36,046512	63,953488	0,9642857	2,1	-23,7	-23,7	0,457726	5,5	-27,55814	-0,7645161
spiLA0480-MIR2669b		**149**	20,805369	30,201342	20,805369	28,187919	41,610738	58,389262	0,9333333	1	-57,5	-57,5	0,0207298	9,3	-38,590604	-0,9274194
spiLA0480-	GUCCAGUCCUCUUCCUCUUCCUCUACCACCGCUG	**158**	19,620253	33,544304	17,721519	29,113924	37,341772	62,658228	0,8679245	1,1071429	-	-48,2	0,0216246	12	-	-

MIR2673b	UCAUUGAUUCAAAAUCAAAAUUUUCAAUUAAAGAU										48,7				30,822785	0,8254237
spiLA0480-MIR2864	UGAAAUCAACAAUAAAGAAGAUUUUUCGUUUUACC UCCUAUUGGAAUGAGAAAAGGCAGAGUAGGAUGA GGAUGAGGAUGAGGAUGAAG CAUUGCACCUAUGGACGUGUUCGAUAUCAUUUUA GGGCUGGAGUUUUGGUACGAGGUUAACGCGUUU AUUUCACCGCGUCACAACCAGAUGCACAUCAGCG ACACCGGAGGUUCAUGCGUGGUACCCCUUAUUCA GGUACCACAAAACGGGAUGCACUUAUCGGUGAUG CAAAUUGUUAAGGUUUUUAAGAGAGGUGAACCAA CCUUUCUUGCUGCCCUUGUUGCUUUUCUGAGGC AGUUCCAUUUUCUCAUUGCAUUGAGCACGUCCUU AGUGACAAUA	**280**	23,214286	23,214286	22,5	31,071429	45,714286	54,285714	1,3384615	1,031746	-91,1	-83,7	0,0005911	49	-32,535714	-0,7117188
spiLA0480-MIR2868-1	GAAAUAAUGCAUGCAUUAGCUUUGUGUAUUAGUA GUACCUUGUUUGGUACACUUUUUGAACCUAUGUA UAGCUAAUGAUUGCAUUAGUUAUACAUUCUAUUG UGUAUUGAGUGUAUUUUCCUACGAAUACAUGGAA AUUCAUGGUAUUAGUAAUGCAAGAGGGUUCAAUG UAUGCAUUAUCAU	**183**	19,125683	28,961749	12,021858	39,89071	31,147541	68,852459	1,3773585	1,5909091	-64,8	-63,5	0,0415548	20	-35,409836	-1,1368421
spiLA0480-MIR2868-2	AGUACUCUAUUUGGGGUCGUUUGGUAGGGCGUA UACGAAUAGUGUUGAAUAUGGUGUAUUGGUAUUG UUGCCUUUAGUAAUGGUGGUAUUAAUUAUUUUUU AUGCAUUGUUUGGUUUGGUGUAUUAAAAAUAGCA UGUAUAUCACAACUUUCAAUAAAAAAAAAAUUGUU AACAAAAGUACCCUCUACAAAUAUGGUGGAAAUGA UGCGGAAAAGGUUUUGAGGGACAAUUGUGGCUUU AACCAUGCUAAUGCAUGCAUUAAAAACCCUUGUAU UGCUAAUAACAUAGUUUGCUAUGUACUAGUUAUG CAUACCAUAAUACCAAAUAGAGUGCA	**334**	20,658683	32,035928	11,976048	35,329341	32,634731	67,365269	1,1028037	1,725	-82,2	-74,84	4,17E-05	78	-24,610778	-0,7541284
spiLA0480-MIR2873b	CCUACGGGACGGGACAUCCUGAAUCUGGACACGA AACUAAAUGGAAUCGAGGUUUGGUACCGGUGUAC CGAUACCUAUUUCAUCCCGGUUUAUUCCGAUUCU GGUUCGGUCUGGUCCGGUUUG	**123**	26,829268	20,325203	23,577236	29,268293	50,406504	49,593496	1,44	1,137931	-45,9	-45,9	0,268102	3,2	-37,317073	-0,7403226
spiLA0480-MIR2875	CGUUAAUUUUAGGUAUGGACAAGUAAACAUUUAA ACUUGUAUAAAAUUGAACAAAUAGACACAUUUGUC CUACAUGACACCCUACAUGAAAAUUGUGUCCUAC GCGGCGUCCGAUACAUAUUAUGUCAUGUAGAACA CGUGUGUUUACUUGUUCAGUUAUAUACAGUUUUA AGUGCCUACUUGUGUACACUCAAAGUUAGAG	**202**	17,326733	32,178218	17,326733	33,168317	34,653465	65,346535	1,0307692	1	-74,1	-74,1	0,0244233	11	-36,683168	-1,0585714
spiLA0480-MIR2921	AUGAGAUGGCUCUGAGGUUGAGUUUGAUCCACAU UCAUUUCAUUACACGAUAGUAUAGCAAAAUCUAUG UAUGUACUACCUUGUAGUGAAAUGGAUGUUGAAU CUAAUUUAACCUUAGAGCUUUCUUUU	**129**	18,604651	28,682171	14,728682	37,984496	33,333333	66,666667	1,3243243	1,2631579	-59,9	-58,9	0,0712501	4,9	-46,434109	-1,3930233
spiLA0480-MIR2923	UGGCCUAAGAUUUUCUAAGUCUGAUGCAUCACUU ACAUUUUUUUCUCAUUCUCCGUUGUUGGUGCCUC UCCAAAAAGAAAGUUGAAUGGAGAAUGAAAAAGAA AAAUGUAAAGAAUAAAUAGAGCGAAUAAUUUAGGA UG	**140**	19,285714	35,714286	13,571429	31,428571	32,857143	67,142857	0,88	1,4210526	-32,7	-30,7	0,0188247	15	-23,357143	-0,7108696
spiLA0480-MIR2931	AAGGGGGUAAAACUUACCCGCAUCGGGUGUUUAC ACCAAGUCAAUACAUGCAUGCCAUGUGUUUAAGU UUAUUGUUCAUGUCAUGUUACUUCAUUAAAUCAC AUAAUAAUGAAAAUUGUAUUGACUUGGUGUAAACA CAAAGUGCAGGUAGUUUUUUCCCAAG	**163**	19,018405	31,288344	16,564417	33,128834	35,582822	64,417178	1,0588235	1,1481481	-65,2	-61,5	0,0369165	11	-40	-1,1241379
spiLA0480-MIR2949a	CCAAAUGGCAAAUCGAGUCAAACGAAAAAAAAACG ACUAGUGAUUUGGUUUGACUUGAUUUGGUAUUGA A	**70**	21,428571	38,571429	12,857143	27,142857	34,285714	65,714286	0,7037037	1,6666667	-25,6	-25,6	0,306331	3,5	-36,571429	-1,0666667
spiLA0480-MIR319a-1	AAAUAAGGAGCUCUCUCCGGUCCAGUCCGAGGCA CUCAAAGGCUAAAAACACAGCUGACGACUCGUUG AUUCUCAAACAUAUCAAGAAGCAUUUUUUGAAAUU GGUGUGUUUAAGAUUCAACGAUGCGUGAGCUAUG UUUGGCUAGCGUUGUCACGUCUUGGACUGAAGG GAGCUCCCUAUUAA	**184**	23,369565	28,26087	20,652174	27,717391	44,021739	55,978261	0,9807692	1,1315789	-82,5	-77,3	0,0450054	22	-44,836957	-1,0185185
spiLA0480-MIR319a-2	UGGUAUAAGAGAGCUUCCUUUAGUCCACUCAUAG GUAGACGAAGGAUUUGAAUUAUCUCCCGACUCAU UCAUUCAAACGCAAUAGGAAGUAUGUAAUCUUAUA CUAUUGUGAAUGUGUGAAUGAUGCGGGAGAUAAA	**185**	21,081081	27,027027	18,378378	33,513514	39,459459	60,540541	1,24	1,1470588	-92,3	-91,6	0,0174515	9,7	-49,891892	-1,2643836

spiLA0480-MIR319a-3	UUCUCUCCUUUUUAUCUGUGCUUGGACUGAAGGGAGCUCCCUUUUACCAGAGAGCUUUCUUUAGUCCACUAGGGUUCAAUUUGCUGCCGACUCAUUCAUCCAAAUGUUGAGGUCUUGAUAAUCGAAUGCCACCUCAGCAACUGAGUGAAUGAAGCGGGAGUACAAGUUGAGUCUUGAGCUUCCUGUACUUGGACUGAAGGGAGCUCCCU	**174**	24,712644	26,436782	21,264368	27,586207	45,977011	54,022989	1,0434783	1,1621622	-79,7	-75,9	0,0254984	9,7	-45,804598	-0,99625
spiLA0480-MIR319a-4	GUAUAAUAUAUGUAGAGAGCUUUCUUUAGUCCACAUAAAGGGGGCAGUAUGGUUCAAUUAGCUGCUGACUCAUUCACACAAAUGCUAAGGCUUUGAGAAUUAUUAGGAGGAAAAACCUUAGUAACUGAGUGAAUGAUGCGGUAGGCUGACUGAAUCUUAAGCUUUUUUUGCUUGGACUGAAGGGAGCUCCCUCUUCGUAAUUACUU	**206**	23,300971	28,640777	16,019417	32,038835	39,320388	60,679612	1,1186441	1,4545455	-78,8	-73,4	0,0037409	16	-38,252427	-0,9728395
spiLA0480-MIR319b-1	UUAGAUGUAAGUAGAAGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCGGACUGAAGGGAGCUCCCUAUCCAUUUAU	**198**	23,232323	29,79798	20,20202	26,767677	43,434343	56,565657	0,8983051	1,15	-90,9	-90,9	0,107999	5,5	-45,909091	-1,0569767
spiLA0480-MIR319b-2	AGCUCCUUUCAGGCCAAGACCGAGGGACGAGGAGCGGCAAGAGCUGCCUAGUCAUGCAUAUUGGUUAACCUUAACAAACAAAUUAUGUAUAGUGUUAAGAUUAACCAGUUGCAUGGCAAGGGAGCAACUACUUCCGCUAACUUGUCUCACUUAUUGGACUGAAGGGAGCUCCUAUCCAUUUAUAUAUAGUUAAGUUAACUAUAUAAAAUAU	**211**	20,853081	31,753555	19,43128	27,962085	40,28436	59,71564	0,880597	1,0731707	-90,2	-90,2	0,0273192	8,5	-42,748815	-1,0611765
spiLA0480-MIR319b-3	AGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUC	**122**	25,409836	25,409836	18,032787	31,147541	43,442623	56,557377	1,2258065	1,4090909	-42,4	-31,2	0,0597266	14	-34,754098	-0,8
spiLA0480-MIR319c	AAGAGAGCUUCCUUCAGCCCACUCACGGAGGAGAAAUGGGGUUGAAUUAGCUGCCGACUCAUUCAUCCAACCACUCAGUAGAAAGGAUAGGUUUUGUGCUACUGUGAUUGAGUGAAUGAUGCGGGAGAUAGUUUUCUAUCCCUCUCUUUCCUUGCUUGGACUGAAGGGAGCUCCUU	**176**	25,568182	23,863636	21,590909	28,977273	47,159091	52,840909	1,2142857	1,1842105	-76,5	-65,1	0,0169927	17	-43,465909	-0,9216867
spiLA0480-MIR319d	AGCAGAGGAGAGAAGGAAACUGUUUAGUCCAACCCAAGGUGGGGUAUUGGAACUGAUCUUUGCUGCUGAAUCAUUGGCUCAUGAGCAUGUCAAAGAAGAUGAUUGAACAUUCUGGACAUGUUCUUGCUCCAAUGAUGCAGGAGCUGAGCUCGGUUUUUCACCGCCUUUCUUGGACUGAAGGGUUCCCUUCCCUUCUCUUUA	**202**	25,247525	23,762376	20,792079	30,19802	46,039604	53,960396	1,2708333	1,2142857	-96,4	-95,6	0,0428561	6,6	-47,722772	-1,0365591
spiLA0480-MIR319h	UUGUGUCGCUUCUUCAUCUGAAGCGAGCGCCUUUUUCAGAUCGCAUCGCCUCAGGAGAAAGAAGCGCAGUG	**71**	26,760563	21,126761	25,352113	26,760563	52,112676	47,887324	1,2666667	1,0555556	-27,6	-27,2	0,078875	5,8	-38,873239	-0,7459459
spiLA0480-MIR319n	AGAGGCGGAGUCAGAAUUUUCAAUAAGGGGUUCAAAAUCUGUAGAUAUAGAUAGUCAAAGAGGGUUCGACAUCUACUAUAAACUUAUUUUAACCAUGUACAAUUAAUAUAAUUUUCCUCCGAAGGGAACCCCUUGUAUGAAGGUAGCUCCUCCGCCCCU	**159**	19,496855	32,075472	19,496855	28,930818	38,993711	61,006289	0,9019608	1	-45,3	-44,1	0,0111482	22	-28,490566	-0,7306452
spiLA0480-MIR3434	GUUCAAGACAACAUUUCUAGAGAGAUUCUUCCCCAGAGAGAUGAGGGAGGACAAGGUUGAGGAGUUCAUCAACCUUAAGGCCCUAUGACGGUCAGGGAGUAUUCCCAGAAGUUUGUUAAGCUAUCAAGGUAUGUUACUUCCCUUAAUAUUUAAUAACAAGAAUGAGAAGAUUACUUAGUUGGUUGUAAUUAUCCAGGUAUGCUAAUUCCCUGGUUUUGAAUAGUAGGGGUGAGAUGAGCAGGUUCCUCACAGAAUCAAUGGAGACCUAGAGGAGGAGUGUCGAUAUGCGAUGCUCCAUGAUAAUAUGGAUCUUUCUAGGUUAAUGGUGCUUGUCC	**335**	25,373134	28,955224	16,119403	29,552239	41,492537	58,507463	1,0206186	1,5740741	-97,3	-79,12	2,26E-05	64	-29,044776	-0,7
spiLA0480-MIR3444b	CCAAAUAUGAUUAAUGUAACAUUCUGAAAAAUUACAUGUCUAAUGAAGAUCCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGAUACAUAGGCAUAUCAAUUCCGAAUAUUGAGAAAUACUGGGCAUAGUAUAGUUGCU	**233**	18,88412	36,051502	12,017167	33,04721	30,901288	69,098712	0,9166667	1,5714286	-53	-45,6	0,0065455	42	-22,746781	-0,7361111

spiLA0480-MIR3448	UAAGGGGUAUUAGCCAAUUUCUAUAUAAUACCCAAAUAAGCAGAAUAUUGGCUUAAAGGGUGUUAGACAAUUUUUCUAAGUAUUAAUGAGAUUGUUUAAAAGAAGGAGUCAAGAACGCACCAUACAGGAAAACAUCUUGAUAAGAAGUGUUACUAUGUUUAGACAAUUGUAUGGUUCGGGUAUUGACUUCUGUACUUGGA	**104**	23,076923	34,615385	13,461538	28,846154	36,538462	63,461538	0,8333333	1,7142857	-29	-29	0,201646	6,7	-27,884615	-0,7631579
spiLA0480-MIR3513	AUAGGGCUUGAGUUGACACUUGUAAAGCAAGAGAUGGAGCGAGAGAGGGAGAGUGGCGAGCGAGAGUUUGAGGGAGAGAGGUGACUGGCAAACAGUUUGCUAAAAGGUACAAUUAAAUCAAAGUGUAGUUAUAAAAUUUAAUUUAAUUUAUUAGUUUGUUAUUAUAUAAUUUUCCGAUAUUAAAAAGCACAAACUCAUUUGAAGGUCAUACCUCAAAAGGCCGGCCCAAAUGCUUUACAGGUGUCAACUCAAGCCCAAA	**261**	23,754789	35,632184	13,793103	26,819923	37,547893	62,452107	0,7526882	1,7222222	-81,5	-70,1	0,0009696	54	-31,226054	-0,8316327
spiLA0480-MIR3515	UCGAAUCCUUAUUAAUUUGGAUGUCAAUCAAAAUAUAUUGUUUCAUGUUUAAUAUCUACAUUCAUAUGUUUUUGAGGUUAUCACGGGCCGAUGACCCCUACCCUUGGGUAGGUCCAGAGGCGGACCGACAUGGUGUUCGCCGGGUGCUUGAGUACCUAUUAACUUCGUUACGGAAUAUAUAUCUAUGUAGAAAUUGAUAGGUAUUUGUAUAAAAUUAACAUAGAGCACCCAAUGAAUAAAUGAUUUAG	**250**	20	29,6	16,4	34	36,4	63,6	1,1486486	1,2195122	-67,2	-55,7	0,0001176	44	-26,88	-0,7384615
spiLA0480-MIR3520	CUGUCUUAUCACUCUUCUCUUUGAAGGGAGAGGCUUUAAUCAGUGUACCUGCAAUAGGAAUAUUGAUUCCUUCAAGAGGAGGAGUGGUAGAUUC	**94**	24,468085	25,531915	17,021277	32,978723	41,489362	58,510638	1,2916667	1,4375	-37,8	-37,6	0,04708	10	-40,212766	-0,9692308
spiLA0480-MIR3627	GAGAGAGAUUGAGGGAAUCUUGUCGCAGGAGAGAUGGCACUUGCCAUUCCUUUUAAUUGGUACAAUGCCUAAAUGGAACCAAUUAAGUGCCUCUGUCUUUCGACACGAUGCUCACAAUUUCUAUU	**125**	22,4	27,2	20	30,4	42,4	57,6	1,1176471	1,12	-47,6	-47,6	0,149706	5,1	-38,08	-0,8981132
spiLA0480-MIR3636	GUGUGUGUGUGUGUGUGUAUAUGUAUGUGUAUAUAUAUGUAUUUCGGGUUGGUUUGAGUUCGGUUUGAUUCUUUGUUUAAAUACCAAACCAAAUCAAGAGUGGUCCGAUUUUUUUAUCAAUUGCCAAACCAAUCAAACCAAAUCACAAUUGAGGUUUUGUUCGGUUUGAUUUGGUUCGUCGGUUUGGUUUACUUAAUGGUUCGGUGUAUACACCCCUAAUCAUAAACAAAGACAUAUUAUUGUAGAGUCAAGUUAACAUUUCAUAUCAAUAGAUUAUAUAAACAUAAUAUACAAAACACUUACAAAU	**307**	17,915309	30,618893	13,680782	37,785016	31,596091	68,403909	1,2340426	1,3095238	-76,7	-51	0,0001359	95	-24,983713	-0,7907216
spiLA0480-MIR3637	UUAAUGAACUCUGUAACUCUAUAUUUUUAUCUUGUGUUUUGUCUCUUCCAAACCAAAUGAAGACCAUCACUAUUUAUACUAGAAGAAGUCUUCCUAGCAAGGAAUAGGAAGAUAAUGGAGUAGUAAAAUGAAGAUAAUGGUCUUAGGAGUUACAUAUGUUUCAUAGG	**167**	17,964072	34,131737	13,772455	34,131737	31,736527	68,263473	1	1,3043478	-38,8	-25,79	0,0008129	39	-23,233533	-0,7320755
spiLA0480-MIR3693	AACGUAGAUAUGAAAGGUUCUGAUAGAUGGAUCCACCUAAGUUUCAGGGUGGGAAGAGUGAGGAUGCUCAUGACUUUCUGACAACAUGUCGAGACUUGCUAGAUGUUGUUGGAUUAGCUGAGUCACAUAAGUUUCGAUAUGCUACAAU	**148**	26,351351	29,054054	14,864865	29,72973	41,216216	58,783784	1,0232558	1,7727273	-43,5	-43,5	0,256178	10	-29,391892	-0,7131148
spiLA0480-MIR3706-1	AUAUUUUUAAGAGAAAGUGGAUAAAUAAAUUUCGAACUAUCGUAAAUGUUAUGAAGAUAUUUUCGUCUUAUUUUAUGAACAUUGAUAUUAAUGAAAAUACACGUGUCAUAAUUUUAUCCACCGACCAAACAUCGGAUGGAUGGAUAAGACUACGUCACGUGUCCAUAUUUGGUCUCUCGUUAGAACAAAAGGGCAUAUAUGCUCUAGUUUUUUUAGGAUAGAGGCAUCAAUUUUCCAAAAAUAUGACGAAGGAUAUCUGCAUAUCAUUACGAUAGUUCGAAGAUAUACUUAUUCUUUUCACUAUUUUUUUAAAAAGGC	**318**	16,352201	34,27673	14,150943	35,220126	30,503145	69,496855	1,0275229	1,1555556	-99,6	-93,8	1,38E-05	34	-31,320755	-1,0268041
spiLA0480-MIR3706-2	AAGACACGUGGCACAAUCUUAUCCAUCUAUCCGAUGUCGGGUCAGUGGAUAAGAUUAUGACACAUGUAUU	**70**	21,428571	30	20	28,571429	41,428571	58,571429	0,952381	1,0714286	-28,7	-28,7	0,428936	2,8	-41	-0,9896552
spiLA0480-MIR390	CGAGCAUGAAGAAGCCAUAAAACUCAGGAUGGAUAGCGCUAUAGAUAGCCAUUAAGAUGUAUUCAUGGUGCUAUCCCUCCUGAGCUUUAUAGAUUCCCCAUG	**106**	20,754717	30,188679	22,641509	26,415094	43,396226	56,603774	0,875	0,9166667	-43,7	-43,7	0,157079	5,7	-41,226415	-0,95

spiLA0480-MIR390a	CCAUAUGGCAUGGGGAAUCUAUAAAGCUCAGGAGGGAUAGCACCAUGAAUACAUCUUAAUGGCUAUCUAUAGCGCUAUCCAUCCUGAGUUUUAUGGCUUCUUCAUGCUCG	**106**	22,641509	26,415094	20,754717	30,188679	43,396226	56,603774	1,1428571	1,0909091	-51,5	-48,8	0,102755	6,7	-48,584906	-1,1195652
spiLA0480-MIR391	AAAAGGCUUGCUACGCAGGAGAGAUGAUGCUGGACGAUAGAGAAAAUGGGAUUUAAUUUAUUGGCCAGCAUCAUACUCCUGCAUAUUAAGCCUAAA	**96**	23,958333	34,375	16,666667	25	40,625	59,375	0,7272727	1,4375	-46,7	-46,7	0,336484	3,4	-48,645833	-1,1974359
spiLA0480-MIR393b	CUUUAAGAGCUCGUUUGGUUGGGAACAAGUUAUCCCAGGACAAGUUAUCCUGAGGUUAGUUAUCUUGGAAUAGCUUAUCACAUACACUAUGAUAUAAAUGGUGGGAUAAGCUAUCCCAAACAUGGCAACCAAACAAGAUAUAAAAACCGUAUCCCAUCAUUAUUUUUCUAUCCCAUUACUAUUUAUUUUUAUCCCUCACACCAAACGACCUCUUAUUA	**218**	14,220183	32,110092	21,559633	32,110092	35,779817	64,220183	1	0,6595745	-59,1	-56	0,0253873	23	-27,110092	-0,7576923
spiLA0480-MIR393d	AUCCAAAAGAAUUGGAUUAAUUGUUUUGUUAGCAUUGUAAAGACGUCUCAAAGUUCUUGUGUAUUUUAUGAACACUAGGUCAUGUUGAGGUGCUUCAGGGUUCUCUUCCUCAAUGACCAAGUGUUCAAAAAUAUAAUAGAAUAUCAAGGCGUCCUUGCAAUGCUCACAAUGGAUUGAUCCACUUCUUUUGCAU	**193**	18,65285	29,015544	17,098446	35,233161	35,751295	64,248705	1,2142857	1,0909091	-82,6	-81,6	0,0456835	8,8	-42,797927	-1,1971014
spiLA0480-MIR394-1	UUGGCAUUCUGUCCACCUCCCAGCUUGCUGAGGACUGAGGAGGGGGCCAAAGUGCCAAA	**59**	30,508475	22,033898	27,118644	20,338983	57,627119	42,372881	0,9230769	1,125	-30,6	-30,3	0,212308	3,4	-51,864407	-0,9
spiLA0480-MIR394-2	UUUUCAUGAAGAUUUCUCAAAGGGUUCCUUACAUAGUUCUUUGGCAUUCUGUCCACCUCCUUUACCUUCAUAAUCUUCUAUUUUUUUAGAAAAAUAAUUUUUGUUAUUCUUUUUAAAAAAAAAUGGAGGUGGGCAUACUGUCAACAGAUUUGUGUUAGUUUCUCUUUGUGAAAUCUUCUUGAUGU	**185**	14,594595	25,405405	15,675676	44,324324	30,27027	69,72973	1,7446809	0,9310345	-66	-65,9	0,0833134	6,6	-35,675676	-1,1785714
spiLA0480-MIR394b	GAUGAAGAAAAAAAAUAUGAAGAUUAAUUAGUUUCACGGAGGUUUGACAAAGGGUUUCUUACAGAGUUCAUUGGCAUUCUGUCCACCUCCUUCGUUCUUUUUUCGAGAAAAAAAGAAGAAGGGGGGAAGCAAGAUUUAGUGUGGAGGUGGGCAUACUGCCAAUAGAGCUGUGUUGGUUUCUCUUUGUAAAACCCUCGUGAUACACGUCAAGUAAGAUAGAGAGUGAUUUGAUC	**233**	25,321888	30,901288	14,16309	29,613734	39,484979	60,515021	0,9583333	1,7878788	-81,8	-80,4	0,0292371	19	-35,107296	-0,8891304
spiLA0480-MIR3951a-1	GUGCGCUUCUUUCUCCUGAGGCGAUGCGAUCUGAAAAAGGCGCUCGCUUCAGAUAAAGAAGCGAGA	**66**	28,787879	25,757576	22,727273	22,727273	51,515152	48,484848	0,8823529	1,2666667	-32,8	-32,8	0,246537	2	-49,69697	-0,9647059
spiLA0480-MIR3951a-2	GUGCGCUUCUUUCUCCUGAUGCGAUGCGAUCUGAAAAAGGCGCUCGCUUCAGAUAAAGAAGCGAGA	**66**	27,272727	25,757576	22,727273	24,242424	50	50	0,9411765	1,2	-29,3	-29,3	0,233455	2,1	-44,393939	-0,8878788
spiLA0480-MIR3951b-1	UAAGUACAAUCUCUCGCUAUUUCUUUUAUUUUUUAUCUAACAAUAAUUAGUUUCACCCCAGGGGAUCUUGUUGUCCCUAUAAAGGGGUAGUAGUUAUUGUUGUUGUGGUGUAUGAGCAUGAAAUCUUUAUAUCAACCUUAAAUAGGAAAGCUUAAAGAACUCAAGUGAGCAUUGUGACAUG	**181**	18,78453	29,281768	14,917127	37,016575	33,701657	66,298343	1,2641509	1,2592593	-44,4	-41,9	0,0109911	26	-24,530387	-0,7278689
spiLA0480-MIR3951b-2	CAUGAGAACAUAAGAGAGGUUUUCAACAAGAGAAAAGAGAGAAAGAAAAAGGUUCUUUUGCUGCAGUCUUUUUCUCCGACCAGCAACAUUCAGAUCGUCUUUCUUGCUUAACUAACCGUUGGAUCGGGUUGAAAUUCGGACUGAGUGUUCCUGACAUUUUGUUGGUUGAUUUUAACGGUGGAGAUUGAAUUGAAGGUCAUAAAGAUCCUGUUGUUAGUCCCGAACAGAAAUUGGGUUUGAGUAGUGUUUCUUUCUAUUAUCUUUUGUUGGUGUAGCUAUUGUUUGUUCUCUUU	**293**	23,208191	25,59727	14,675768	36,518771	37,883959	62,116041	1,4266667	1,5813953	-79,7	-72,8	0,0005005	63	-27,201365	-0,718018
spiLA0480-MIR395a-1	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUUUGGGCUUACUUCAUUGUUUGAUGCCCUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAU	**107**	22,429907	18,691589	22,429907	36,448598	44,859813	55,140187	1,95	1	-50,3	-50,3	0,188576	5,7	-47,009346	-1,0479167
spiLA0480-MIR395a-2	AUGCCCUAUUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAUAGAAGUGUAUGAAUCCUGGCUGUGGAUGAUGAACAUAAUAGUUCACGUAUAAAUCUAUUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUCAUGAGGGCUU	**163**	21,472393	28,834356	17,791411	31,90184	39,263804	60,736196	1,106383	1,2068966	-62,4	-62,4	0,0650395	16	-38,282209	-0,975
spiLA0480-MIR395a-3	UGUUUGAUGCCUUGCUGAAGUGUUUGGGGGAACUCUUGGACUCACUUUGAAAUUUUACACAAACAAAU	**174**	22,988506	27,586207	15,517241	33,908046	38,505747	61,494253	1,2291667	1,4814815	-61,5	-60,4	0,0209354	15	-35,344828	-0,9179104

spiLA0480-MIR395b-1	AGAAGUGUAGGAGUCCUGGCUAUGGAUGAUGAAC AUGAUAGUUCAUGUUUAAAUCUAUUAAGGUGAUC CCUAGAGUUCACUUGACCACUUCAUGAGGGCUUA AUUU UUAAGGUGUUCCCUAGAGUUCCCUUGACCACUUC AUGAGGGCUUACUUUGAUGUUAGAAGCGUUGCUG AAGUGUUUGGGGGAACUCCUGGGUUGACUUUA	**100**	28	19	18	35	46	54	1,8421053	1,5555556	-46,3	-46,3	0,479123	2,5	-46,3	-1,0065217
spiLA0480-MIR395b-2	GGUGUUCCCUAGAGUUCCCUUGACCACUUCAUUA GGGAUUACUUCGUUGUUUGAUGCCCUGCUGAAG UGUUUGGGGGAACUCCUGGGCUCAC	**92**	27,173913	15,217391	23,913043	33,695652	51,086957	48,913043	2,2142857	1,1363636	-45	-45	0,256744	3,9	-48,913043	-0,9574468
spiLA0480-MIR395b-3	GAUGCCCUGCUGAAGUGUUUGGGGGAACUCCUG GGCUCACUCUGAAAUUUUAUGCAAAUUAAACCAAU AGAAGUGUUGGAGUGCUGGUUGUGGAUGAUAAAC AUGAUAGUUCACGUAGAAAUCUAUCAAGGUGUUC CCUAGAGUUUCCUUGACCACUUCAUGAGGGCUUA	**170**	25,294118	26,470588	17,647059	30,588235	42,941176	57,058824	1,1555556	1,4333333	-61,3	-54,9	0,0395845	24	-36,058824	-0,839726
spiLA0480-MIR395b-4	CUAUCAAGGUGUUCCCUAGAGUUCCCUUGACCGC UUCAUUAGGGCUUACUUCAUUGUUUGAUGCCCUG UUGAAGUGUAUGGGGGAACUCUUGGACUCACUUU GAAAU	**107**	23,364486	19,626168	21,495327	35,514019	44,859813	55,140187	1,8095238	1,0869565	-51,4	-51,4	0,0793298	6,7	-48,037383	-1,0708333
spiLA0480-MIR395c	UUGAAGUGUUUGAGGGAACUCCUGGGUUGACAUU GAAAAUUACGCAAACAAGUAUAUAUAAAUGCAUGA UGAGUACGUAUUAGCUAGAGAUGAUGAAUACAAU AUUGAUUCACGUAUAAAACUACCUCUGGAGUUUC CUUGACCACUUUAU	**151**	19,86755	33,774834	14,569536	31,788079	34,437086	65,562914	0,9411765	1,3636364	-37,8	-34,1	0,0211106	25	-25,033113	-0,7269231
spiLA0480-MIR395g-1	CUAUCAAGGUGUUCCCUAAAGUUCCCUUGACCUC UUCAUUAGGGUUUAGUUCAUUGUUUGAUGUCUUG CUGAAGUGUUUGGGGGAACUUUUGGACUCACAUU GAAAU	**107**	22,429907	20,560748	17,757009	39,252336	40,186916	59,813084	1,9090909	1,2631579	-34,8	-32,8	0,0635288	11	-32,523364	-0,8093023
spiLA0480-MIR395g-2	UUGAAGUGUUGAGGAGAAUUUCCAAGCUCACUUU GAAAUUUACACAAACAAAUAGAAGUGUUAGAGUAU UAAUGGGAGACUGAUUCCCGAGAGUUUCCUUGAC CACUUCGUGAGGAUUUAAUUACUUUGUUGUUUUA UGCCUUUCUGAAGUGUUUGGGGGAACUUUAGGG UUCACUUUAAAAUUUACACAAAUAAGUAGAAGUAA AUGAGUACUAAUGGAAGAUGAUAGAUGAAUGCAA CGAUUUAUUUUAUAUCUAUCAAGGUGUUUUCGAG AUUUCCCUUGACCACUUAAU	**293**	20,477816	31,05802	13,31058	35,153584	33,788396	66,211604	1,1318681	1,5384615	-74,1	-66,3	4,47E-05	49	-25,290102	-0,7484848
spiLA0480-MIR395m	UUUGUUAUUGCAUACUUUUCUUCAGAUGAUAAGA AAUUAUCCCACCAUCCUCUGAGUUGACCUGUAAA UCCUGCUAUAAUCAUUUUACAUAUAGCAUGAUCA CUAUUCUGAUUCGUAUGACGACAAAUUGAUGAGU ACAUCAACAUCCGAUGUACCAUAAUGGAAACCUG CCUUUCAGUCAAGGCAUCCAAAUUCCAUUCAUAC ACCUCAUUACCACUGUAAGAUGUGUUAGUUUGAU UCCAAUCUCUUUCUUCGACUAACACAUCUUGGGG AGUAGGACGAGGAUAAUAAUAAGUCAUCAUUGAA GGGAGAGUUGCAUAACCCC	**325**	16	30,461538	21,538462	32	37,538462	62,461538	1,0505051	0,7428571	-90,4	-89,7	0,0001771	34	-27,815385	-0,7409836
spiLA0480-MIR395n-1	GACAAGUCUAGUAGAGUCUUGAGGAACGGUAUGG GGACGCCUUUACUUUUCUUCGAGAGGCUAUAGGA CUUUAG	**74**	29,72973	24,324324	16,216216	29,72973	45,945946	54,054054	1,2222222	1,8333333	-32,1	-32,1	0,500115	1,4	-43,378378	-0,9441176
spiLA0480-MIR395n-2	AACAAGUCUAGUAGAGUCUUGAGGAACGGUAUGG GGACGCCUUUACUUUUCUUCGAGAGGCUAUAAGA CUUUAG	**74**	27,027027	27,027027	16,216216	29,72973	43,243243	56,756757	1,1	1,6666667	-32,1	-32,1	0,512835	1,4	-43,378378	-1,003125
spiLA0480-MIR396a-1	UGGCACUACAAGAAAACUGUGAAUUACAUGGGAU UUUCCUAAGAUUAGUAUGAAAAUACGUAGGAAAC UUAUUUUCCUGCAAAAAUUCAUCCUGAUUUUCAG GAAAAUCUCAAUGUAAUUCAUACUUUUCUUGUAG UGUGG	**141**	17,021277	33,333333	14,893617	34,751773	31,914894	68,085106	1,0425532	1,1428571	-68,9	-66,5	0,116068	3,1	-48,865248	-1,5311111
spiLA0480-MIR396a-2	AGUCCAAAGCUUGCCAUCUUUUCCCACAGCUUUC UUGGACUUUCAUAGCUUCAAAUCUCAUCUCAAAA UUAUCAAUUUAGAGAUCAAAAUUUAGCAAGAAGAA GUUCAAGAAAGCUGUGGAAAAGCAUGACUAGGAC UUGGUCA	**144**	16,666667	34,027778	20,138889	29,166667	36,805556	63,194444	0,8571429	0,8275862	-51,6	-50,2	0,0321931	10	-35,833333	-0,9735849
spiLA0480-MIR396a-3	GUCAUCUAGAAAAACUAGGUUUUCUAGUCCUUUU UGGAUUAGGAAGAAAUCUCUAUAUAUAGGGAUUC UUCUAACAUAGAAAAUAGAUGAUUAGUUUUCUAUU	**185**	18,378378	31,351351	15,675676	34,594595	34,054054	65,945946	1,1034483	1,1724138	-46,3	-42	0,0009094	26	-25,027027	-0,7349206

spiLA0480-MIR396b	CAUACUUGCCCACCCAAGUAUUGAGAGAGUUCGGAUGUGACUUGAGAUCACUAUAGAAGACCAUAGCUAUCUUGUAGAUUCU	**219**	20,091324	30,136986	16,894977	32,876712	36,986301	63,013699	1,0909091	1,1891892	-60,8	-47,4	0,0009614	43	-27,762557	-0,7506173
spiLA0480-MIR396f-1	UUUUCUUUCUAGAUUAGCUUUCCUCACCCUUUCAUAAUUUAGUGUCAGAUCCGCCACAUUCUAGUUAAAUUUGGCAUCCGUAUAGAGGCGGAAGUGUCUAGAGUUGUGGAGAGGUUUGCGAAAAAAUCUAGAACCUUCUAGAUCAAUCAAGAAUGCUUGGAAUUCUCUAGAAUAACUUAGACUUUUUAAGAAAGGCUUUGGAAGAUCCUAGAAAGAGUA	**152**	21,710526	33,552632	14,473684	30,263158	36,184211	63,815789	0,9019608	1,5	-44,8	-40,1	0,0050352	30	-29,473684	-0,8145455
spiLA0480-MIR396f-2	GGGUCUAGAGUUGUGGAGAGGUUUACGGAGAACUCUAGAACCUUCUAGAUUAAUCAAGAAGGCUAGAGAAUUCCUUAGAAUUCUCUAGAAUAACUUAGGCAUUUCAAGAAAGUCUUUGGAAGAUCUUCGAAAGUAUACACUUUUCUAGAAUAUGACCAAGUCCUAGUCAUGCUUUUCCACAGCUUUCUUGAACUUCUUCUUGCUAAAUUUUGAUCUCUAAAUUGAUAAUUUUGAGAUGAGAUUUGAAGCUAUGAAAGUCCAAGAAAGCUGUGGGAAAAGAUGGCAAGCUUUGGACU	**144**	20,138889	29,166667	16,666667	34,027778	36,805556	63,194444	1,1666667	1,2083333	-53,8	-49,5	0,0035876	24	-37,361111	-1,0150943
spiLA0480-MIR396g	CCUUGGAAAUAGGUGGUCUUGAACUUUUGCUACAUGGUUAAACCUUUGACGCCAAAAGUCGAUACUUGAUGUUCUGUUCAUGGGGCGCAAGAUUAAAAGUUCAAGAUCAUCCACCUCCAAAG	**122**	21,311475	28,688525	20,491803	29,508197	41,803279	58,196721	1,0285714	1,04	-39,9	-39,9	0,148352	6,9	-32,704918	-0,7823529
spiLA0480-MIR397b-1	CAGAGUACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGAA	**118**	16,949153	26,271186	21,186441	35,59322	38,135593	61,864407	1,3548387	0,8	-49,1	-48,9	0,132646	4,3	-41,610169	-1,0911111
spiLA0480-MIR397b-2	UACUUAGAAACAUCAUUGAGUGCAGCGUUGAUGACAUAUUUGAGAAUUCCUGCAUUUGGGCCUUCCUCAUUUUUCAUCAACGCUACACUCGAUCAUGUUUUUAAUUCUCUGAAGGGACAUU	**121**	17,355372	25,619835	20,661157	36,363636	38,016529	61,983471	1,4193548	0,84	-44,2	-44	0,0867621	6,6	-36,528926	-0,9608696
spiLA0480-MIR397b-3	AAUUAUCUUACUUAAUUAUUUUUUAUAGUUUAUUUGGCAACCUUAUUCGGAAGAUGUUAUUAUUGGAUUGUCUGAGUGGUGUCGGUUAGGACAACAUGUCUGGAUGACACAGGUGCCACUUAUUUAUGAAAUUUAUCGUGAGUGGCACAUGGUUAAUCGUGUUGUGAGACAGUUUGGUUAUUUACAACAUAUUCUUAGACCGUGUACCCAAUUUUUCGAAUAUCAUUUUAAACGUGAUAAACGAGCCAAAAUAAAACAAGAAGAUAUAG	**269**	19,702602	30,483271	13,3829	36,431227	33,085502	66,914498	1,195122	1,4722222	-69,5	-63,5	8,29E-05	45	-25,836431	-0,7808989
spiLA0480-MIR397b-4	CCCUUCAGAGAAUUAAAAACAUGAUCGAGUGUAGCGUUGAUGAAAAAUGAGGAAGGCCCAAAUGCAGGAAUUCUCAAAUAUGUCAUCAACGCUGCACUCAAUGAUGUUUCUAAGUACUCUGCAAUAA	**127**	19,685039	36,220472	18,897638	25,19685	38,582677	61,417323	0,6956522	1,0416667	-49,6	-49,6	0,0660774	8,3	-39,055118	-1,0122449
spiLA0480-MIR398-1	UAUUCAACAGGGGCAACUUGAGAUCACAUGUUGUCAUUUUUUUCUUUUUGGUUUGAUUCGAUGAAUCAGUAUCUCAACAUGUGUUCUCAGGUUACCCCUGUUGAAUUA	**108**	18,518519	23,148148	17,592593	40,740741	36,111111	63,888889	1,76	1,0526316	-49,7	-49,4	0,150203	9	-46,018519	-1,274359
spiLA0480-MIR398-2	AUGAACAAUGGUGCAUCCCAGAGGAGUGUGCCUAAGAACACAGGUGUAUUUUGGUCUUCUCCUGUUUUGGACCCAAAGUAUGCUUGUGUUCUCAGGUCACCCCUUUGGGAUCACCUUGCUUUUU	**124**	23,387097	20,16129	22,580645	33,870968	45,967742	54,032258	1,68	1,0357143	-63,9	-63,8	0,088157	7,5	-51,532258	-1,1210526
spiLA0480-MIR398a	UCAAUAGGGUUGAUUUGAGAACAUAUGUAUGUGCAUAUUUUGUUUGUAACAAUUUACCGUUUAUAAAUAUGACACAUAUGUUCUCAGGUCGCCCCUGUAGAC	**102**	18,627451	28,431373	15,686275	37,254902	34,313725	65,686275	1,3103448	1,1875	-39,3	-37,7	0,0412401	13	-38,529412	-1,1228571
spiLA0480-MIR399a-1	UACAAGAAUCGCAGGUUAUUCUCCUUUGGCAAGAACAACUAUGUCAUGCAUAAAUCUUUCCUUGCCAAGGGAGAAUUGCCCUACGUUUCUUCAU	**94**	17,021277	27,659574	23,404255	31,914894	40,425532	59,574468	1,1538462	0,7272727	-35,3	-34,9	0,031615	6,7	-37,553191	-0,9289474
spiLA0480-MIR399a-2	AGCAAGAAUCGCAGGUUAUUCUUCUCUGGCAAGAAAACUAUGGUUAUGCAUAAAUUAUUUCUUGCCAAGGGAGAAUUGCCCUACGUUUCUUUAU	**94**	19,148936	28,723404	18,085106	34,042553	37,234043	62,765957	1,1851852	1,0588235	-32,9	-32,6	0,0741787	7,2	-35	-0,94
spiLA0480-MIR399a-3	ACUACUCAAAAGAAUUUGAAGAAUUGGAGAGGACAAGAAACGCAGGGUAUUCUCCCUUAGCAAGAUUGCUUUAUGCAUGAAUUAAAUUCUUUCUUGCCAAGGGAGAAUUGCCCUGCGUUUCUUCAUUUCCACAAAAGUCUAAUUCAUCUGGUGUC	**155**	19,354839	30,322581	19,354839	30,967742	38,709677	61,290323	1,0212766	1	-60,8	-59,2	0,0094212	14	-39,225806	-1,0133333

spiLA0480-MIR399b-1	UUAUAAGAGAAACAGUGGUAGGGCUACUCUCUAUUGGCAUGCACUUAUAUAUUUAAACUGACAUGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUG	**103**	21,359223	28,15534	19,417476	31,067961	40,776699	59,223301	1,1034483	1,1	-47,6	-47,6	0,203168	6,7	-46,213592	-1,1333333
spiLA0480-MIR399b-2	UGAUGAAGCGGAAGCAUGAGAAAGGAAGUCGUUGGUGAAUGAAAAUAAGGGAAAUAGUGAUAGGGCUACUCUCUAUUGGCAUGCACUCCAAUUCACUGUAUCGCAUAUUUUAACCGAUACGCCAAAGGAGAGCUGCCCUGCUACUGUCUCUGCUUAAUAUAAUAACUCAAAGGUCCAUUCUUAAUACUCCGAUGCAGAA	**217**	22,119816	32,258065	18,43318	27,18894	40,552995	59,447005	0,8428571	1,2	-70,1	-68,8	0,0014428	16	-32,304147	-0,7965909
spiLA0480-MIR399b-3	GAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUC	**86**	23,255814	25,581395	23,255814	27,906977	46,511628	53,488372	1,0909091	1	-43,5	-43,5	0,369104	2,1	-50,581395	-1,0875
spiLA0480-MIR399b-4	UUGUAAGGGAAACAGUGAUAGGGCUACUCUCUAUUGGCAUGCAAUUGUAUAUUUCAGCUGACACGCCAAAGGAGAGCUGCCCUGUUACUGUCUCUGCUUAAUC	**103**	23,300971	25,242718	21,359223	30,097087	44,660194	55,339806	1,1923077	1,0909091	-47,9	-47,9	0,296977	6,8	-46,504854	-1,0413043
spiLA0480-MIR399i-1	UUCGUGAACGAUAGUAAUUGUAAGGGAAACAGUGAUAGGGCUACACUCUAUUGGCAUGCAACUUGAUCAAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUAUUACUGUCUC	**116**	23,275862	31,034483	17,241379	28,448276	40,517241	59,482759	0,9166667	1,35	-46,9	-43,8	0,124095	8,1	-40,431034	-0,9978723
spiLA0480-MIR399i-2	UAGUAAUUGUAAGGGAAACAGUGAUAGGGCUACACUCUAUUGGCAUGCAACUUGAUCAAAUAUUUGAGCUGAAAUGCCAAAGGAGAGUUGCCCUA	**95**	24,210526	33,684211	15,789474	26,315789	40	60	0,78125	1,5333333	-31,4	-31,4	0,325008	3,6	-33,052632	-0,8263158
spiLA0480-MIR399i-3	AAGAUUAUACUAAAUAUGUUAUUGUUGGUGUGCUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCCUCUGCUUAAUU	**137**	21,89781	28,467153	13,138686	36,49635	35,036496	64,963504	1,2820513	1,6666667	-60	-57,7	0,017822	8,4	-43,79562	-1,25
spiLA0480-MIR399i-4	CUUAUUAAGUGAAACAGUUGUAGGGCAAUUCUCCGUUUGGCAGAUAUAUGAUUAUGAAUGUAAUCUGCCAAAGGAGAGUUGCCCUAUGAUUGCCUCUGCUUAAUUAU	**107**	21,495327	28,037383	15,88785	34,579439	37,383178	62,616822	1,2333333	1,3529412	-55,8	-53,5	0,237852	2,8	-52,149533	-1,395
spiLA0480-MIR399o	AACAGUGAUAGGGCUACUCUCUAUAGGCAUAUGCCGUUUAUCACACAUUACAGCUGACACGCCAAAGGAGAGCUGCCCUAUUACUGUCU	**89**	20,224719	28,089888	25,842697	25,842697	46,067416	53,932584	0,92	0,7826087	-36,6	-36,6	0,510615	4,6	-41,123596	-0,8926829
spiLA0480-MIR399r	AGUUAUGUGUGGAUGCAUUACUGGGCUAAUCUUCUUUGGCAAAUAAUUUCACUAUUAUUUGGUGCAAAUUUGGUCAUUUAUUGCCAAAGAAGAUUUGCCCCGUAAAUCAUUCAUACAAUAUUA	**123**	17,073171	29,268293	15,447154	38,211382	32,520325	67,479675	1,3055556	1,1052632	-50,2	-48,5	0,0626769	16	-40,813008	-1,255
spiLA0480-MIR403	UCAGGAAGAGGCAUAUUUCACGUUUGUGCGUGAAUCUAACAACUCUUUUCAUCAGAAAAACUGUUAUUGUUUGCUAGAUUCACGCACAAGCUCGUAAUAUGGCUUUUCCAAU	**112**	17,857143	28,571429	19,642857	33,928571	37,5	62,5	1,1875	0,9090909	-45,7	-42,7	0,101296	10	-40,803571	1,0880952
spiLA0480-MIR403b	AUUGGAAAAGCCAUAUUACGAGCUUGUGCGUGAAUCUAGCAAACAAUAACAGUUUUUCUGAUGAAAAGAGUUGUUAGAUUCACGCACAAACGUGAAAUAUGCCUCUUCCUGA	**112**	19,642857	33,928571	17,857143	28,571429	37,5	62,5	0,8421053	1,1	-43,6	-42,3	0,0948255	9,2	-38,928571	1,0380952
spiLA0480-MIR405d	UCGGAUUAGGUGUUUAUGAGUCCGAAAAUCUUUCCAUUUUCAUAUAAAUGUUAUGUGGUAAGGUCAAAAUGACAUGACAAUUCCAUGUGGCAUUUAAAGAAAUGAAAAAUGAGUUGGAUAUAAUGCACAAAUCAUC	**136**	19,117647	36,029412	12,5	32,352941	31,617647	68,382353	0,8979592	1,5294118	-34,8	-34,3	0,022635	15	-25,588235	-0,8093023
spiLA0480-MIR408-1	ACGGGGACGAGCCAGAGCAUGAGAUGUGCAAUUUUUGCUUUGCCUAUUCCAUGCACUGCCUCUUCCCUGGC	**71**	25,352113	18,309859	28,169014	28,169014	53,521127	46,478873	1,5384615	0,9	-32	-32	0,704395	1,3	-45,070423	-0,8421053
spiLA0480-MIR408-2	AAAAGGAAGGAUUGUGGGGAGAGGAGAGCCAGGGAAGAGGCAGUGCAUGGAAUAGGCAAAGCAAAAAUUGCACAUCUCAUGCUCUGGCUCGUCCCCGUCUAUCCAUACCACACCAAUUUUUACCUCAA	**128**	25,78125	32,03125	22,65625	19,53125	48,4375	51,5625	0,6097561	1,137931	-46,6	-41,4	0,0291793	9,1	-36,40625	-0,7516129
spiLA0480-MIR408a	AAGUGGAGAGGAUAGACAGGGACGAGGCAGCGCAUGAGAUGUACAAUUUUAUUAGUUGUCCAUUCCAUGCACAGCCUCUUCCCUGGCUUUCCUCCCCAAAAAUUACUAAUCUAUUUGUAAUACUUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUUCGUGGUCGUGGAGGAAGAAGUAGAGGAAGGGGA	**101**	23,762376	26,732673	24,752475	24,752475	48,514851	51,485149	0,9259259	0,96	-51,6	-50,1	0,410187	2,2	-51,089109	-1,0530612
spiLA0480-MIR414-1		**257**	19,455253	30,350195	19,066148	31,128405	38,521401	61,478599	1,025641	1,0204082	-73,3	-64,2	0,0001569	51	-28,521401	-0,740404

spiLA0480-MIR414-2	AGAUCAUCCUCUUCCAAGUCUAGAAGAUCAUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAACUCAAAGAUUAAUGAAGCAUCUUCAUCAGCUUCGUCCUUUGUAAAUUUAAAGGAUAUUCCCAAUGAUAGUUCAUUCAUUACAAAGUUCUAUCAUCCUGAUCCUCCUUCUCCUUUCAUGCCUCCUCUUCUCUAGUUAAAUCUUCUGAUCGUACUUAUUAACAAUCUAGAGCUUCUAAAUUGUUAGCAGGAUCGAAAAAUUUAACUAAAGAGAGGAAUCCAUGAAGGAAGAACGGGGAUUUGGAUUAGAGAACUUUAUAAUUUU	**190**	15,263158	31,052632	18,947368	34,736842	34,210526	65,789474	1,1186441	0,8055556	-66,1	-64,5	0,0045414	16	-34,789474	-1,0169231
spiLA0480-MIR417	AACAAAAACACUUAAAUUGUUCCAAUUUGUUGAGUUUCAUAGCUAAACUAUCAAGUGUGUGUGAGUUUUCUGUCUGUACUAGUAUCAAAUGCUUCGCGAAGCAAACCUGAUUGUUCAGGUAGGAAAAGUGAACAACUUGUAGUUCAUUUGUGUUUCCGUAAACAUUUGGUGAUAGUACAGGUAGGAAACUCACACACCUGAUAGUUCAUGUAUGAAACUCAAAAAUGAAAAAAUGUAAUGAAUUUGUU	**248**	18,951613	33,870968	14,516129	32,66129	33,467742	66,532258	0,9642857	1,3055556	-96,7	-96,7	0,0013888	17	-38,991935	-1,1650602
spiLA0480-MIR419	AAAUAGUAAAGGCCAAUCGUCCUUUAACAAGGAUGAAAGGUCAUUAUGUAUGUCUAUAUAAGGGGCAUUUGCCUUCAUAAAU	**82**	19,512195	35,365854	14,634146	30,487805	34,146341	65,853659	0,862069	1,3333333	-22,6	-20,8	0,140292	9,7	-27,560976	-0,8071429
spiLA0480-MIR4405	AUGAUAUUAUUGGAUCGGAGUGUCACGUUCUGACACGGUAUUAUGGGAUCGGAGUGUCACAUUCCGACACGGAAUACGGGAUCGGAGUGUCACGUCCCGACACAUAACAUUAA	**114**	26,315789	28,070175	20,175439	25,438596	46,491228	53,508772	0,90625	1,3043478	-43,4	-38,3	0,0953935	12	-38,070175	-0,8188679
spiLA0480-MIR4412	AUAAUGCAUGCAUUAGCUUUGUGUAUUAGUAGUACCUUGUUUGGUACACUUUUUGAACCUAUGUAUAGCUAAUGAUUGCAUUAGUUAUACAUUCUAUUGUGUAUUGAGUGUAUUUUCCUACGAAUACAUGGAAAUUCAUGGUAUUAGUAAUGCAAGAGGGUUCAAUGUAUGCAUUAUCAUGGUUAAAGACCCAAUCGCCCCUCAACUUUUUUUUACAUGUUAUCACCAUACUUGUGGAGGGUAUCUUUGUAAAUAAUUUUUUUUUAAAAACUAUACAAUACAUACUAUAUUUAAUACACCAAACAAAACAACGCAUAAG	**319**	15,047022	31,974922	15,360502	37,617555	30,407524	69,592476	1,1764706	0,9795918	-75,3	-62,5	0,0001782	51	-23,605016	-0,7762887
spiLA0480-MIR444b	CUUUCAUGAAAAGAUGUGACUCUUAUGAAAAAUUGCAACUUUAAUGAAGAGUUGCGACUUUAUGAAAGGUUGUGACUUUUAUGAAAGAUUGUGAACUUUAUGAAAGGUUGCACCUUUUCCAAUUAGUUGUAUCAUUUCUGAUAC	**144**	18,75	31,25	12,5	37,5	31,25	68,75	1,2	1,5	-39,7	-35	0,0228768	51	-27,569444	-0,8822222
spiLA0480-MIR475b	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGUCUAUGGCUUUGCUCUUAAAGUCCCCAUUGAUUUAGGAGAGUGGACGGGGCAGACUGACUUCACUA	**99**	22,222222	25,252525	26,262626	26,262626	48,484848	51,515152	1,04	0,8461538	-34	-32,3	0,0549769	7,9	-34,343434	-0,7083333
spiLA0480-MIR477a-1	CCUCUCCCUCAAGGGCUUCUCUCCUGCAUGCUUUUUGUGUUGGGAAAGAAGCUCUAGCAGGGAGAGCCAUUAAAUUUAUGUAAGUUAUUAUACACUAGAAAUAUUUGAAUCAUGAAUUCUAGUUUGCUAGUAAACGGGAAACAGGGAGAAAACUGCUAGACUAUGCCAUCCCAUAGUGGAAACAGGUAGGCGAGGGAUGCCGUUAGGGGAGUACACAAGGUUGAGGCGCUGAUAAGCAAUAAUUAUACGCUAAAGUAUGAUGCUAGUGGUAACCAGAAAACAUGAUAACAAUACUCUAGUUUAUAAUAAACUAAUAUGAAUUUAAU	**68**	26,470588	17,647059	27,941176	27,941176	54,411765	45,588235	1,5833333	0,9473684	-35,5	-31,5	0,291438	5,9	-52,205882	-0,9594595
spiLA0480-MIR477a-2	AUAUAUUCCUGAAUAUCAUAUAUAUGAUUGAUUAAAUUUAUGUUAGUUAUUAUACACUAGAAAUAUUUGAAUCAUGAAUUCUAGUUUGCUAGUAAACGGGAAACAGGGAGAAAACUGCUAGACUAUGCCAUCCCACAGUGGAAAUCGGUAGGUGAGGGAUGCCGUUAGGGGAGUACACAAGGUUGAGGCGCUGAUAAGCAGUAAUUAUCCGCUAAAGUACGAUGCUAGUAGUGACCGGAAAACAUGAUAACGAUACUCUAGUUUAUAAUAAACUAAUAUGAAUUUAAUUAGAUUAUGAUAUGAUAGGAAGGAAUAACU	**258**	21,317829	37,984496	13,178295	27,51938	34,496124	65,503876	0,7244898	1,6176471	-62,6	-52	6,40E-05	47	-24,263566	-0,7033708
spiLA0480-MIR477a-3	GUCUUUUUUCACUCUCCCUCAAAGGCUUCUGGCUUAAAAUGCCUUUUGUGCUAAUGCUAGAGGUCUUU	**318**	21,383648	36,477987	12,578616	29,559748	33,962264	66,037736	0,8103448	1,7	-94,4	-84,11	0,0001225	35	-29,685535	-0,8740741
spiLA0480-MIR477b		**90**	20	22,222222	20	37,777778	40	60	1,7	1	-37,2	-32	0,0386397	6,9	-41,333333	-1,0333333

spiLA0480-MIR477c	CGAGUGAGAGUGAAUAAAUUCU CAUAACAAACUAGUUCUUGAGGUUGAGUUAGGCG CAUGUGUCAUAUCUUUACAUGGUCUGAUAUCUGA GACCAUGUAAGGAUAUGACACAUGAGCCCAACUC AUCCCCAAGAGUUAGUUUUUGCC GUCACAAAAAAGGCGCAGCUUAAUUGGUGAAAGG CGAUCCCCUUGGGAGGGAUGUAAAAGAGUCAUAA GUCACGGGUUCGAUUCUCCCUUGAGGCUGCAUG CUAAUAAGAGGGGAUUAAAAGAGCGAAUGGCCGC	**125**	20,8	28	20,8	30,4	41,6	58,4	1,0857143	1	-73	-73	0,293418	3,4	-58,4	-1,4038462
spiLA0480-MIR477j	CCAUGGCAGAGACAAUACCUGAGUAUGUGGAUCC CGAGGGGGUUGUCACAAAAAAGGCGCCUUUUUUG UGAC	**207**	29,951691	28,985507	19,323671	21,73913	49,275362	50,724638	0,75	1,55	-80,3	-67,52	0,0056652	39	-38,792271	-0,7872549
spiLA0480-MIR479-1	GAAGACAUGGCGUGAUAUUGGUUUGGCUCACUAA UUUCUGAUUCGCGAAACAGAUAAGAGAUGAGCCG AACCAAUAUCACUCUUGUAUUCUU	**92**	21,73913	29,347826	18,478261	30,434783	40,217391	59,782609	1,037037	1,1764706	-40,9	-39,7	0,0909347	7,8	-44,456522	-1,1054054
spiLA0480-MIR479-2	AUGAUGGAGAAGAAGACAUGGCGUGAUAUUGGUU UGGCUCACUAAUUUCUGAUUCGCGAAACAGAUAA GAGAUGAGCCGAACCAAUAUCACUCUUGUAUUCU UCUUCAUACC	**112**	21,428571	30,357143	18,75	29,464286	40,178571	59,821429	0,9705882	1,1428571	-53,8	-52,6	0,084803	7,8	-48,035714	-1,1955556
spiLA0480-MIR482	CUUGGGUAGUGUCAUCCUUGAGAUGUGCCACAGA CUUGGUGCAAAAUGUGGCGAGAUAGUCGUGUCCU AGGAGGGGUGCCAGUCACCUGGGAGCUGUUCAA GACAACAUUUUUGGAAAGGUUCUUCCCUAGGGAG AUGAAGGAGGCCAAGGUUGAGGAGUUCAUCAACC UUAACCAAGGGUCUAUGACGGUCAGGGAGCAUUC UCUGAAGUUUGUGAAGCUAUCAAGGUAUGUUACU UCCCUUG	**244**	29,918033	24,180328	18,852459	27,04918	48,770492	51,229508	1,1186441	1,5869565	-84	-82,8	0,0006619	36	-34,42623	-0,7058824
spiLA0480-MIR482b-1	UAUUCAUAAAAAAAAAAAAAUUCAGAAAUUGGGAAA GGGAUGAAGAUUUUUGGGAAGCUUUUGGCGUGA GCGGUGGGGAAAGAUAGAUCUAUCAUAUUAGUAU GAUAUGAUAAAUCUUGCCUACACCGCCCAUGCCC AUGGCUUCCAAUGAUUUCUUCCUUUCCAUACAAU UUCUUCAUGUUAUUUUUUUU	**190**	18,947368	30,526316	15,789474	34,736842	34,736842	65,263158	1,137931	1,2	-73,6	-70,8	0,0020091	25	-38,736842	-1,1151515
spiLA0480-MIR482b-2	AUUUUUCAGGAAGCUUUUGGAGUGGGUGGCAUG GUAAGAUAUCAUAUCUUGUUUUUCAUAAAAAAAAA AUGAAAUUGAAAUCUUACCGAUUCCCCCCAUUCC AAUGGCUUCCAGUUAUAAC	**121**	17,355372	31,404959	17,355372	33,884298	34,710744	65,289256	1,0789474	1	-47,5	-47,1	0,0757122	8,8	-39,256198	-1,1309524
spiLA0480-MIR482b-3	UUCUGCUUAAGUUGGUGUCUUAACUUGUAAUUCA CUUCUAUCGUGGAUCGCUUCUGCUUUUGAAGUAC CAUAGAAGUGAAUUGCAAGGUAAGACACCAACUU AAGCAGAA	**110**	20	28,181818	18,181818	33,636364	38,181818	61,818182	1,1935484	1,1	-67,6	-67,5	0,111525	3,9	-61,454545	-1,6095238
spiLA0480-MIR482b-4	UCUUCUAAAAUAACUAGGUUUUCUAGUCCUUUUU GGAUUAGGAAGAAAUCUCUAUAUAUAGGGAUUCU UCUAACCUAGAAAUAGAUUAUUAGUUUUCUAUUCA UACUUUUCCACCCAAGUAUUGAGAGAGUUCGGAU GUGACUUGGGAUCACUGUAGAAGACCAUAGAUAU CUUGUAGAUUU	**182**	17,582418	29,67033	14,835165	37,912088	32,417582	67,582418	1,2777778	1,1851852	-44,3	-34,4	0,0012176	41	-24,340659	-0,7508475
spiLA0480-MIR482c-1	GAGUUUUUCGAAAAUCUAUGGGGAUUGGUGAGUU GGAAAGCUUUUCUUUUUCUUCUCUUGUGAUUAGC UUUCCAAUUCCACCCAUUCCUAUGGUUUUUCGGU AUUCUCU	**109**	19,266055	17,431193	18,348624	44,954128	37,614679	62,385321	2,5789474	1,05	-48,7	-48,5	0,323046	2,5	-44,678899	-1,1878049
spiLA0480-MIR482c-2	GUGUUUCGAGGAGGUGUUGGAGUGGGUGGUGUG GUAAGAUUUCAUAUUUAUUUUCCAUAAAAAUUGAG AUCUUGCCAAUACCGCCCAUUCCUAUGGCUUCUG AUCAUUUC	**110**	24,545455	21,818182	16,363636	37,272727	40,909091	59,090909	1,7083333	1,5	-51	-51	0,0344304	12	-46,363636	-1,1333333
spiLA0480-MIR482c-3	AACUGAAGACAGUCAAUGCCACUCCCACUUCCGU CCAUGGCUUUGCUCCUUAAGUCCCCAUUGAUUUA GGAGAGUGGACGGGGCAGACUGACUUCACGA	**99**	23,232323	24,242424	28,282828	24,242424	51,515152	48,484848	1	0,8214286	-35,9	-34,7	0,111243	9,7	-36,262626	-0,7039216
spiLA0480-MIR482c-4	CCAACAAAAACUUUUGGGAAUGGGUGGGUUGGUA AGCUUUUCCUUUUUUAUAUGUGUGUUCCCUUAGC UUACCAAUUCCACCCAUUCCUAUGGGUUUUUGUG CU	**104**	20,192308	19,230769	20,192308	40,384615	40,384615	59,615385	2,1	1	-49,6	-49,6	0,208714	3,1	-47,692308	-1,1809524
spiLA0480-MIR482d	UGGAAAGGGAGGAGGGAUUUGGGAAUCUUUUGG AGUGGGUGGGAUGGAAAAAUAUUGUAUUUUUUUU UCUAACGGAAAAAAAGAUGAGAAUUGAGAUUUUU CCUAUUCCACCCAUGCCAAUGGCUUCCAGUCAUU	**147**	24,489796	27,210884	14,285714	34,013605	38,77551	61,22449	1,25	1,7142857	-62,2	-57,6	0,0085388	15	-42,312925	-1,0912281

spiLA0480-MIR5014a-1	UACUCCUUUUCC AUUUUUCAUUUUAGGUGUGCACAAGUAGGCACUU AAACUUGUAUAAACUUGAACAAAUAGACACAUUUG UUCUACAUGACACCCUACAUGAAACUUUUGUGUC CUAUUUUAUUAUGUCAUGUAGAACAUGAGCGUGU ACUUAUUCAAUUUUAUACAAAUUUAAGGGUCUAAU UAUGCAUACUCAAAGUUGAAAGAC	**196**	14,795918	33,163265	15,816327	36,22449	30,612245	69,387755	1,0923077	0,9354839	-63,1	-60,1	0,0009663	20	-32,193878	-1,0516667
spiLA0480-MIR5014a-10	CAUUUAUGCCCUUCAACUUUGGAUGUGCACAAAU AAACACUUAAAUUUGUAUAAAAUUGAACAAAUAGA CACAUAUGUCCUACAUGUCAUCUUACAUAUCAUAU UUUGUCCUAUGUGGUGUCCUACGUGUAUUGUGU CAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGU UGAAUAGUUAAAGUGUCUAUUUGUGCAUUGUGAA AGUUGGAGGUCAAAGUU	**222**	17,567568	30,18018	13,963964	38,288288	31,531532	68,468468	1,2686567	1,2580645	-82,7	-82,6	0,0284664	12	-37,252252	-1,1814286
spiLA0480-MIR5014a-11	GAUAACUAUGCCCUUCAACUUUGAGUGUGCACAA AUAGACACCUAAACUAAUAUAAAUUAAAUAAGUAG ACACAAUAUCCUACAUGGCAUAAUACACGUAGGAC GCCACAUAAGACAUAAAAUUUGUUAUAUAGGGUG UCAUGAAGGACGAAUAUGUCUAAUUAUUUGAUUU UGUACAAGUUUAAGUGUCUACUUAUGCACAUUCA AAGUUAAAGGUCAUAUUUGUU	**227**	15,859031	37,004405	15,418502	31,718062	31,277533	68,722467	0,8571429	1,0285714	-79,7	-74,6	0,0028498	22	-35,110132	-1,1225352
spiLA0480-MIR5014a-12	AAUUUUAACUUUGACCUCGAACUUUCAUAAUGCA UAAACAAGCACUUUAACUAUCCAACUUUUAUAAAC ACAUGAGUCCUACAUGACACAAUACACGUAGGAC AAAAAAUGACAUGUAGGACAUGUGUGUCUAUUUG UUCAACUUUAUACAAAUUUAAGCAUCUACUUAUGC ACACCCAAAGUUGAAGAGCAUAAAUGUAAUUCGAA GUCAAGUUAAAGAG	**221**	13,574661	38,461538	18,552036	29,411765	32,126697	67,873303	0,7647059	0,7317073	-49,9	-47,2	0,0003989	27	-22,579186	-0,7028169
spiLA0480-MIR5014a-2	ACCCUUUAAUUUUAAAUGUGCACAAAUAGACACUU AAACUAUUAUAAAAUUGAACAAGUAAACACAAUUA UCCUACAUGACAUAAUACAUGUAAGAUGCCAUAUA GGAUACAAAAUUGCCAUGCAGGGUGCCACGUAGG ACAAUGUGUUUAUUUGUUUAAUUUUGUACAAAUU UAAGUGUCUACUCGUGCACACUCAAAAUAAAGCA U	**208**	13,942308	38,461538	16,826923	30,769231	30,769231	69,230769	0,8	0,8285714	-69,4	-69,4	0,0083138	12	-33,365385	-1,084375
spiLA0480-MIR5014a-3	GAUGUGCGCAAGUAGGCACUUAAAUUGUAUAAAA UUGAACAAGUAGACACAUGUGUCCUACAUGACAU GAUACACGUAACACACCACGUUAGACACAACUUUU UCAUGUAGGGUGUCAUAUAGGAUGAAUGUAUAGA CUUGUUUAAUUUUAUACAAGUUUAAGUGUCUAUU UGUGCACAUC	**181**	18,78453	33,149171	16,022099	32,044199	34,80663	65,19337	0,9666667	1,1724138	-82	-81,8	0,0311961	9	-45,303867	-1,3015873
spiLA0480-MIR5014a-4	UUCAAAUUUUAACUUUGACCUCCAAUUUUCUUAAU GCACAAACAAACACUUUAGCUAUCCAACUUUUAAA UAAAUAGACACAUGAGUCCUACAUGACGCAACAC GUGUAAGACACCACCUAGGACAAAAAAUGAUAUG UAGGACAUGUGUGUCUAUUUAUUCAACUUUAUAC AAGUUUAAGUGUCUAUUUGUUCACAUCCAAAAUU AAAGGGCAUAAAUAUAAUUUAAA	**229**	11,790393	37,991266	18,340611	31,877729	30,131004	69,868996	0,8390805	0,6428571	-52,9	-52,9	0,0048574	18	-23,100437	-0,7666667
spiLA0480-MIR5014a-5	UAGUUUGCAACUAUGAUCCUUAACUUUGGAUGUG CACAAGUAGGGACUUAAAGCUUGUAUAAAAUUGA ACAAGUAGACACAUGUGUCUUAGAUGGAAUGAUA CUUGUAGGACGCCACAUAGGACACAAAAUUUUCA UGUAGGAUGCCAUGUAGCAUGAAUGUGUCAAUUU GCUCAAUUUUACACAAAUUUAGGUGCCAAUUGUG CAAAUUUAAAGUUACGGAUCAUAAUUGCCAAAUGA	**239**	20,083682	33,891213	15,062762	30,962343	35,146444	64,853556	0,9135802	1,3333333	-89,7	-88,4	0,0040274	14	-37,531381	-1,0678571
spiLA0480-MIR5014a-6	AUUUACGUCCUUCAACUUUGGGUGUGCAUAAGUA GACACUUAACAUUGUAUAAAAUUGAACAAGUAGAC ACAUGAGUCAUAUGUAUACACGUGGACACAAAUU GUCAUGUAGGAUGUCACGUAGUACGUGUGUAUCU AUUUAUUCAAUUUUAUACAAAUUUAAGUAUUGAUU UGUGCAUGCUCAAGUUGAGGGCAUAAAU	**200**	19	32,5	14	34,5	33	67	1,0615385	1,3571429	-75,1	-69,2	0,001036	29	-37,55	-1,1378788
spiLA0480-MIR5014a-7	UAAUGCAUAAAUAGACACUUUAACUAUCCAACUUU UAAAUAAAUAAACGCAUGAGUCCCACAUGGCACAA ACCACGUAGGACAAAAAAUGACAUGUAGGACAUAU GUGUCUAUUUGUUCAACUUUAUACAAGUUUAAGU GUCUACUUGUGCACAC	**155**	14,193548	37,419355	19,354839	29,032258	33,548387	66,451613	0,7758621	0,7333333	-47,5	-47,5	0,0476145	5,4	-30,645161	-0,9134615

spiLA0480-MIR5014a-8	AUGAUAUUUAGCGUGCACAAGUAGAAACUCAAACUUGUAUAAAAUUGAACAAAUAGAAACAUUUAUUCUACAUGACAAAAUUUGUAUCCUACGUGGCGUCUCAUGUGUAUUAUGUCAUGUAGAACACAUGUGUCUACUUAUUCAAUUUUAUGCAAAUUUAAGUGUCUACUUGUGCACACUCAAAAUUGA	**189**	14,814815	34,920635	15,873016	34,391534	30,687831	69,312169	0,9848485	0,9333333	-68,5	-67,6	0,0026827	13	-36,243386	-1,1810345
spiLA0480-MIR5014a-9	GAUUAUGACCUUUAACUUUAGAUGUGUACAAGUAGACAGUUAAACUUGUAUAAAAUUGAGCAAAUGAACGCAUUUGUCAUACAUGAUACCGCUACAUGACAACUUUGUCUCCUACAUGACAUUCUACGCGUAUUAUGUCAUUUAGGACACUUGUGUCUACUUUUUCAAUCUUGUACAAAUUUAAGUGUAUACUUGUGUACAUUCAAAGUUGAAGGACAUAGUU	**223**	16,143498	31,390135	16,591928	35,874439	32,735426	67,264574	1,1428571	0,972973	-75,2	-67,07	0,0017623	33	-33,721973	-1,030137
spiLA0480-MIR5016	UACAACCCAUUGCGAUACUAGAAGUUUUAUGUUUUAUUGAGUGACUCAAGAUUGGAGUCGUGCAGGCGGAGAUCCUUUUGUCGAUUCCUUGGGUUAAAUGUUGUUCCACUGUAGUUUGGGUUAUAGAUGAUACAUGAUACUUCUAUGUUCUUAUUGGUUCCC	**162**	22,839506	22,222222	16,049383	38,888889	38,888889	61,111111	1,75	1,4230769	-47	-44,9	0,0164632	14	-29,012346	-0,7460317
spiLA0480-MIR5017	UAUAAAUUUGCAGGUAACGGUAACAUUCUGAAAAGUUGUUACUCUUUUCGAAAAGUCGUUACUUUCCGAAAAGUCGUUACUUUCCUAACAGACACAAUUUUCUGAAAAGUUGUUAUUUUUUCCAAAAGACACAACUCUCUGGAUAAAAUGGGUCUGAACAGAUUUCACUGAACAGACACGUUCCUUGCUGAAAAUGGCUAUAAAAGGAAGUCAAUUUUCAAUUUUUCAAACCCUGAAAUUUUUUU	**244**	15,163934	33,196721	17,622951	34,016393	32,786885	67,213115	1,0246914	0,8604651	-57,2	-54,8	0,0048939	16	-23,442623	-0,715
spiLA0480-MIR5026-1	CGCCUUUUCGGCCUACGUGACACUAGCUUAAAAAAUCAACUAGUCUUGAGCUCACAAGAUAGUGCCACGUAAGCCAAAAAGAAA	**85**	17,647059	36,470588	24,705882	21,176471	42,352941	57,647059	0,5806452	0,7142857	-26,2	-26,2	0,276839	6,6	-30,823529	-0,7277778
spiLA0480-MIR5026-2	CCUUUUCGGCCUACGUAGCACUAGCUUGAAACAAAAAGUCAACCGGCGUUGGACCCACAAGAUAGUGUUACGUAGGCCAAAGAA	**84**	22,619048	32,142857	25	20,238095	47,619048	52,380952	0,6296296	0,9047619	-35,4	-34,8	0,0579671	9,7	-42,142857	-0,885
spiLA0480-MIR5026-3	UGUAUUCCUUUUCGGCCUACGUGAUACUAGCUUGAAAAAGAAGUCAAUCAGAGUUGGACCCACAAGAUAGUGUCACGUAGGCCGAAAAGGGAUAGA	**96**	25	32,291667	18,75	23,958333	43,75	56,25	0,7419355	1,3333333	-51,7	-51,7	0,280212	3,7	-53,854167	-1,2309524
spiLA0480-MIR5030-1	AUGUAUAUCGCUGCCCAGGCAGCGACUUUAUGAAAAACAAUUUGUUUUUUAUAAAACGCUGCACAGGCAGCGACUUUAUGAAAAACAAUUUUUUUUUAUUUUAUGAAACGCUGCCCAGGCAGCGACUUUAUGA	**133**	18,045113	30,827068	18,796992	32,330827	36,842105	63,157895	1,0487805	0,96	-55,8	-54	0,0176748	13	-41,954887	-1,1387755
spiLA0480-MIR5030-2	GACAUUCAAGGGGAGUGUUAUAAACAAUUUGUAUUAUAGUGAAUGUCUAAUUAUGUGGAGUCCUUGUAGGAUAUGGUUAGGAAUCCUACUUGGGGACCAAGUAAGGUUUUCCUUAUAAAUAAAGGGUUUUCCUUCAUUGUAAACAAGAUUUGUAAAAGAUCUCUGAAUCCU	**171**	21,637427	30,994152	12,280702	35,087719	33,918129	66,081871	1,1320755	1,7619048	-41,9	-23,1	0,0024407	40	-24,502924	-0,7224138
spiLA0480-MIR5035	UUUACCAAAUGCCUAGAUAAGCCAAAAAAUUGCUUAUAAGCUAGUUUGACCAGCUUAUAAGCUUAGAGGGUGUUUGACUAAGCUUAUAAGCUGGUCAAAUUGGCUUAUUAACACUUUUUAGCUUAUCUACUCAUUUGGUAAA	**142**	16,901408	31,690141	16,197183	35,211268	33,098592	66,901408	1,1111111	1,0434783	-74,2	-73	0,0279829	9,4	-52,253521	-1,5787234
spiLA0480-MIR5039	UUGUUAUUGGAUUGUCAUUUACUUCCGCACUUUGUUAGAUAUUGGGUUUUAGGCUGACUUGUCUUGGUGGGAUAAGACGAGUGCCAUUCACGUCCAUUUUUGAAUCGUGACAUUAGACCUAAGACCUAAUUUCACAAAUGAAAAAGUCAAAAUUUCAUUAAUAAGGUUGUCAAAUCAUAAAUAGACAAGUAAUUAGGGACAGAAGGAGUACUAUCUAUCAUGAACACACAUAUAUUUAUUUUUUUAAAAAAAAUUGUGUAUGUGUGUGGUGGUGGUGGUGAUAGGGUGGGGGUGGUGGUUAAAAAUGUGGGAAGUCGUAAUUCGUAUCCUCACCUACAAAAAUUUAGAUAGUCAACCAACUGAGCUAGCUAAUGAGAUCCGAAAAUAAUUUUCUAUAUAUUUUUUGCUU	**167**	19,760479	28,143713	15,568862	36,526946	35,329341	64,670659	1,2978723	1,2692308	-43,7	-43	0,009786	26	-26,167665	-0,740678
spiLA0480-MIR5049b	ACCAUGACAAUUAAAAGUGGACGGAGGGAGUAAUUUACGCACUUCUUAAGAAAUUAUAGGUAGAAAACUAAUUUUACUAUAUUACCCUUUGAAUAUACUCCCUU	**243**	21,8107	33,744856	11,522634	32,921811	33,333333	66,666667	0,9756098	1,8928571	-58	-56,5	0,0003185	28	-23,868313	-0,7160494
spiLA0480-MIR5049c		**127**	14,173228	34,645669	16,535433	34,645669	30,708661	69,291339	1	0,8571429	-32,9	-32,9	0,0052944	17	-25,905512	-0,8435897

spiLA0480-MIR5083-1	AGUUCAUUUUAAUAUGUCAUCCUUCACAAGGAUAUCAAAAAUUAUUGCAAUUCUCUGAUCAAGCAACGUGGAGAAAAACUAAUCUGUUGGAUGGAUGUUGUAUCCACGUUGCUUGAUCAGAGAAUUGCAGUAAUUCUCCACGUUGCUUGAUCAGAGAAUUGCAAUAAUUGUUGAUAUCCUUGUGA	**153**	20,261438	29,411765	15,686275	34,640523	35,947712	64,052288	1,1777778	1,2916667	-95,9	-94,2	0,0216119	11	-62,679739	-1,7436364
spiLA0480-MIR5083-2	UCACAAGGAUAUCAACAAUUACUGCAAUUCUCUGAUCAAGCAACGUGGAGAAAAAACUUAUCAAGCAACGUGGAUACAACAUCCAUCCAACAGAUUAGUUUUUCUCCACGUUGCUUGAUCAGAGAAUUGCAAUAAUUUUUGAUAUCCUUGUGA	**153**	15,686275	34,640523	20,261438	29,411765	35,947712	64,052288	0,8490566	0,7741935	-91,1	-89,4	0,0485835	5,9	-59,542484	-1,6563636
spiLA0480-MIR5157b-1	UAAAUUUAUAAUGUUAUCUAAGUCAACACCAAGGGUUGUAGGCGAGAUGGAUAAUGAUGCCUUUAUGUUUAACCAGAAGUCUCGGGUUCGAAUCUCAAGAAUGAAAAUAAUUCUUGUAGGUAGUUCUGUACCUUAUUUAGACUCAAAUCCGAGAUCUCUGGUUAUGGAUAAAAGUAUUCCAUUCAUCCCGUCACAUCCUUAAUUUUUAUUAGCUAUGAAUUCAGUAUAUAUCGA	**234**	17,521368	31,196581	16,239316	35,042735	33,760684	66,239316	1,1232877	1,0789474	-68,1	-66,1	0,0113503	21	-29,102564	-0,8620253
spiLA0480-MIR5157b-2	UUGUGAUUUUUAUGAAAAGUUGCGACUUUUAUGAAGGGUUGCGACUUUAACGAAGAGUCAUGACUUUUAUGAGAAGUUGUGACUUUUAUGAAGAGUUGCGUCUUUUAUGAAAAGUUGUGAAUUUUAUGAUAGGGUGUGACUUUUCCGAAGGAUUGUAACUUUUCCAAAGAGUCGUGACCUUUUCAAUAAAGAACAGUG	**198**	23,737374	28,282828	10,606061	37,373737	34,343434	65,656566	1,3214286	2,2380952	-68,7	-64,3	0,0016361	25	-34,69697	-1,0102941
spiLA0480-MIR5157b-3	GAGUUGUGACUUUUUUGAAGAGUUGCGACUUUUUUGAAAAGUUGUGGCUUUUAUAAAAAAAUUGCAACUUUAAUGAUUAGUUGUAAAUUUUAUGAAAGAUUGUGACCUUUCAUAAGGGUUGUCAGUUUUCCAAAUAGUUGUGACUUUUCCGAAGGGUUGCAACUUUUCCAAUAGUUGUAUCCUUUUCGAUAAGGCACAAUAA	**203**	19,704433	29,064039	11,82266	39,408867	31,527094	68,472906	1,3559322	1,6666667	-66,4	-61,2	0,0293255	49	-32,70936	-1,0375
spiLA0480-MIR5160	AUCUAAAACAUGGUUGUGGUCAGAGAAUGUAUCAUUUCGAGGGUAGUAUCGCACGUCGUGAUGGAUAUUAUAUUUCGAGGGACAUAUCGCGUGCCUUGAUUGUUUCUAUUAUCGAGUAUCGUGUCGUGCGCCGCGACAGAUGCAUUGACAGAUAUGUCCCCCAUGGGUGUGUAUCGUUAGGGAAGACAUGCAUUACUAUUCUUGACAUUGCAUCUCAUGGCAUUACACAUUUUUUAUUA	**239**	23,849372	24,267782	17,991632	33,891213	41,841004	58,158996	1,3965517	1,3255814	-74,7	-68,1	0,0008607	41	-31,25523	-0,747
spiLA0480-MIR5167b-1	UGCCCUUACUUUAAAUGGUCAAACUAGCCGUUAACUAGUCGUUGUAGAGUUUUAGGAGCUUUAAUAAAGAACUAGUUUAGGUAUAAUAACCAUAAAUCGUAAGGUUU	**107**	18,691589	32,71028	14,018692	34,579439	32,71028	67,28972	1,0571429	1,3333333	-26,9	-26,9	0,0390296	7,6	-25,140187	-0,7685714
spiLA0480-MIR5167b-2	UUGUGGAGCUUUGGACUCUUCAACUAAUCCGGAGUUGCUUGAGUUAUACACUGUUGUUGGGCUGUUGUAUCCUGGAAGAGACAAGUCUAGAGUAUUACUGCUGGAUCGGUGUAGAUUAUGCCGCAGUUGGCUUGAAUCUCCUUAAAGAGAGCGAGAUAUCCGUGCUUCAGCCUAAAGAUUUAUUUCUUCAUUAUAUUUUCAAUUAUAAUCUUACAAUUUUAUUAUAUUGUAAGUUUUCUUUAACACAAAUUUUAGGGUUAAAGAAUCCAAAUCAUCGCAAGA	**282**	19,858156	27,659574	15,957447	36,524823	35,815603	64,184397	1,3205128	1,2444444	-71,9	-66,6	0,0005639	46	-25,496454	-0,7118812
spiLA0480-MIR5173	UUGCAUGUGUAUAUACAAUUUUCUCACACUUUAUACAAAUAGAAACGCAAUUUAUACAUUUCGCUUCUGUUUGUAUAAAUGAGAAAAGCGAGGGUGGCGAGCGAGAUUUGAGAGAGUGGCGAGCGAGAUCUGAAAGAGGGGAGAGAGGGGAACAAAAAUAUAUGUAUUUAUAUAAUUUUCUCUGCUUUAUACAAUUAGAAACAUUUUUUAUACACUUGUGU	**221**	21,719457	33,484163	12,217195	32,579186	33,936652	66,063348	0,972973	1,7777778	-53,4	-52,3	0,0058843	33	-24,162896	-0,712
spiLA0480-MIR5174d-1	AUGCUACUCUCCAGCUUCGUGGAACAGCGAGAGACUGGUGGAGGACUUAUUUUGGAUGUUUGCCAGUUGGAUCUCCUCCAGUGAAUUGGGAGCAGUUUGCUAGUGCAUUCCAAGAUCGUUUUAUCCCAUGGAGCGUGAGAGAGGAGAGU	**149**	30,201342	22,147651	18,791946	28,85906	48,993289	51,006711	1,3030303	1,6071429	-52	-50,6	0,0229681	14	-34,899329	-0,7123288
spiLA0480-MIR5174d-2	AGAUAUACUCCCUCCGUUUAAAAAAGAAUGACCCUGUUUUCUUGUUAGUAUAAAAAAAUGGCCCCUUUCCUUUUUUGACAACACUUUAACUUUAACUUUCCAC	**256**	13,671875	31,25	18,75	36,328125	32,421875	67,578125	1,1625	0,7291667	-59,3	-49,66	0,0001475	45	-23,164063	-0,7144578

spiLA0480-MIR5174e-1	GUGGCAUGUUUAAGACCACAAGAUUAAAGGGCAUUUUGGUACAUUUGACAUAACUUUAAUUUUGAACCACAAGAUUAAAAAGUUUUCUUUCUUUUCUUAACUCUGUUCCAAGUCAAACUAGGUCAUCCUUUUUGAAACGGAUGGAGUAUAAUAAACUGUAUGGUACUCCCUCUGUUUCAAUUUGUUUGUCUGGCUUUGACAUGACACAAAGUUUAGGAAAGUAAAAAAUACUUUUGAAUCUUGUGAUCUUAAACAUGUCACGUGAAAAGUUGAAAUUAAAGAGUUGCAAAAAAGGAAAGUAAGACAAGCAAAUUGAAACGGACUGGAUGUAUCAUGCAAAG	**188**	20,212766	37,234043	13,297872	29,255319	33,510638	66,489362	0,7857143	1,52	-62,8	-60,2	0,0079949	16	-33,404255	-0,9968254
spiLA0480-MIR5174e-2	GUACUCCCUCCAUCCCAUAUUAGUUGUCCACUUCCGUAAUGUGGAACAACUAUUUAUAGUAAGGUGGACCACUAAUAUGGGACGGAGGGAGUAG	**94**	23,404255	27,659574	21,276596	27,659574	44,680851	55,319149	1	1,1	-52,1	-48,2	0,0898871	10	-55,425532	-1,2404762
spiLA0480-MIR5185m	AAUAUUAUUAAAAAUUAAACUAAAAAAAAUUUCACUUCAGUUAGAGAAAAGGGUAUAUAUGAGUGAUUCCUAUACCGGUAUAGGUAUAUAUGAGUCACUUUCAUAGCGAGGGAUAUAUCAACUCUAAAUGACAAAGUUAGGAGAUAUAUCAGACCUUCGCCUCAGCUAUGAAAGAAGAAUGAGACUCGAAUCGAUCUUGUAAAAAAUAAUUAGGGGGUUCCUAAAAAUGUGGCUAAUUUGUUCUUUUACCACUUAGCCACACUCUCAAUAUAGUUGAUCUAGAUAGUCUGAAUACAAAUUUAUUUUCUUUUAUGUGUUACAAUUCU	**326**	16,257669	36,196319	14,417178	33,128834	30,674847	69,325153	0,9152542	1,1276596	-74,6	-67,2	0,0002299	40	-22,883436	-0,746
spiLA0480-MIR5205a	GUAGUCUAAAUUAUUACUCCCACCGUCCUAUUUUAUGUGUCAUCAUUUCCUUUUUGGUCCGUCCCAAAAAGAAUGUCACAUUUUCUUAUAUGUUAAAUAUUUAAAGGUACAAUUUCUCUUUUACCAUUGUUGGUCCCACUUAAUUUUAAAUAAUACUCUAAUACAUUUAUGAGGAGAGAGAAAAGUGAGUCUACUUUUAAAGGACAAUUUGAUAAACAAUUCAAAGUCUUCAUUUAUUUCCUUAACUCCGUGUCGGGUCAAAUGAUGCCACAUAAAAUAGGACGGAGGGAGUAUUAUUUUAACAAU	**306**	14,379085	31,699346	16,993464	36,928105	31,372549	68,627451	1,1649485	0,8461538	-88,3	-87,2	0,0003503	32	-28,856209	-0,9197917
spiLA0480-MIR5214	UAAGAAUUCAAGUAUUCAAGUUUAAGAAUUCAAGUAUUCAAGAUAAAGUUAAGAACGAUCAAGAUAAAGUUAAGUUCAAGAACGAUCAAAAGAUCAAGACCAUCGGAUUCAUGAUCAAGCUUGAAGCCCUUGAAUUCAAC	**141**	16,312057	42,553191	15,602837	25,531915	31,914894	68,085106	0,6	1,0454545	-32,8	-26	0,109331	16	-23,262411	-0,7288889
spiLA0480-MIR5240	ACCUAACUUCAAAAGGUCAUAUCUCACUCAUCCAAACUUGAAACUUAGAAAAAUUGGUUGAUUUGGAAAGAUGAUUCAAACGUCUUUCCUAUGGUAUCUUGUAUCACACCUAGAUCAUCAUGUUCUAGGAGUUAUGAUCGUUUGAAGUUAACC	**153**	15,686275	32,026144	18,954248	33,333333	34,640523	65,359477	1,0408163	0,8275862	-44,5	-44,4	0,0258992	9,2	-29,084967	-0,8396226
spiLA0480-MIR5253	AAAAUUCUUUUUCCUUUAACUAACUAAAAGGUAUGAGGCAUCCAAGUGUCAAGCCUAGAUAUGAUGUCACAUGAUCAAUUAAAAUGAUUAUGUAGAGUAAGCAGUGCCCAAGGACAUAGCGAGGAUCCUUGGGACAAUUAGUAAACAUUCCCAAAGGAACCAUAAAUAAUAGUUACUUAGGAAAUUACAACCAACCCAUGUGCAAGCACAUGUACAACACAUGUGAAUAAGCACCAAAGGAGGGGACCACCCUAACCGAAUUCGGUUAGGUUAGUUAAGGGGAAAAAAAUGUG	**293**	20,136519	38,225256	18,088737	23,549488	38,225256	61,774744	0,6160714	1,1132075	-88,2	-85,4	0,000481	35	-30,102389	-0,7875
spiLA0480-MIR5256	UAAGGGGUAAUAGGAAAGGGGGUAGGGAAGGGGGGGGGAAAAUUUCAUAUAUGGCAAACUUAAUUGAUUAAAUAACAUUAUAUGGGUAUAGUUUACCUAAUUACAUUCUAUGCGUAUAGUUUGGUUAUUAAAAUAGACGCUACCCGACAAAGGGAGAAUAUUCUAACGGGCAUUUAAGUAAUAUAUUCAAAGUUAGCAAUAAAAAUAAAAUAAAUAAAAUUAGCGAUUGUUUCUUCCCGGCAUACUGUACGACACAUUUUGUCGUCCUCCCCUUCCCUUCCCUUCCCUUCCCUUCCCCAAC	**301**	18,936877	32,890365	17,940199	30,232558	36,877076	63,122924	0,9191919	1,0555556	-84,6	-65,37	0,0001648	69	-28,106312	-0,7621622
spiLA0480-MIR5272e	UUUCUCUCGCUUUAUACAAAUAGAAACGCAAUUUAUACAAUUCGUUUCUGUUUGUAUAAGCGAUAUAGGUGAGGGUGGCGAGCAAGAUCUGAGAGGGGAUAAAGGAGAGAGGGGAACAAAAAUAUAUGUAUAUAUACAAUUUUUCUCGUUUUAUACAAACACAAACACAUUU	**205**	21,463415	35,121951	12,195122	31,219512	33,658537	66,341463	0,8888889	1,76	-59	-48,6	0,0017041	41	-28,780488	-0,8550725

spiLA0480-MIR5278	UAUACACUUGUGUUUGUAUAAAAGUGAGAGGGACAUACUUGUUGAAAUUAUUAGCCACAAAUGUGAAAAUUGGUAGACACCAAUGUGAAAGUUAGUAGCCACAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAGAGUUAGGAAACCAAUUUUUUGUUGAAAUCGGUUACCACAUUAUGUCAUUAAUGAUGUAAACAAGUGUU	**169**	21,301775	34,319527	11,83432	32,544379	33,136095	66,863905	0,9482759	1,8	-40,2	-33,9	0,0050197	34	-23,786982	-0,7178571
spiLA0480-MIR5290	UGGCAUAAUAGAUAUAUGCCCUUUAACUUGACUUCAAAUCAUACUUAUGCUCUUCAACUUUGUGUGCGUAGAAACUUAAACUUGUAUAAAGUUGGAGAAAUAGACACACAUAUCCUACAUGUCAUUUUUUGUCCUACGUGAUGUCCUACAUGUAUUUUGCCGUGUAGUACUCAUGUAUUUAUUUAUUUAAAAGUUGAAAUGUUAAAGUGUCUGUUUGUGCAUUAUGAAAAUUGGAGGUCAAAAUUAAAAUUUGAAGCCAAGUUUAGAAUCCAAUAUAUGUAUUAUGAUU	**289**	16,262976	31,83391	13,84083	38,062284	30,103806	69,896194	1,1956522	1,175	-70	-59,8	9,46E-05	63	-24,221453	-0,8045977
spiLA0480-MIR5293-1	CCAUGAUAAUGUUGCAGAAUGGGUUCGAGCCAAUUUUCAGAUUGGGAAGAGAUUCACAAGGAAUUAUUGGGCCUGUUCCGGUCCUUCCUAAAGAGUCCAAAUAUGGUUUGGGGUAUACCCCCACAGAUGACGAUAUGAAGAUGAAGAAGAAAAAGGAUCAAGAGUUGGCUAAACCGAUCCUGCAUCUGUAUCAAUC	**196**	24,489796	31,632653	18,367347	25,510204	42,857143	57,142857	0,8064516	1,3333333	-59,5	-56,3	0,0387998	24	-30,357143	-0,7083333
spiLA0480-MIR5293-2	AUGGGUUCGAGCCAGGUUUUGGAUUUGGAAGAGAUUCCCAAGGAAUUAUCGAACCUGUUCCGAUCCUUGAUAAGGGAUCCAAAUAUGGUUUGGGGUAUACCCCCACAGAUGACGAUAUGAAGAUGAAGAAGAAAAAGGAUCAAGAGUUGGCUAAACCGAUACCGCAUCUGUAUCAAUCCUUUCCAAUCCAAGAGUGCGUCGAGCCUGA	**208**	25	30,769231	19,711538	24,519231	44,711538	55,288462	0,796875	1,2682927	-67,8	-67,1	0,0053108	21	-32,596154	-0,7290323
spiLA0480-MIR5298c	GGCGCCACAUCCAUCAUUGCUCUUGCAUACAUCUCCUAGAGAAGAUAGAAAUGAUAUGUAAUUGAAGGGAUACCUGGUGCAUCCACCUAUCUUCUCUAAGAGAUGUAUGCAAGAGCAAUGAUGGAUGUGGCACA	**134**	22,38806	30,597015	20,895522	26,119403	43,283582	56,716418	0,8536585	1,0714286	-87,3	-87	0,407195	3,3	-65,149254	-1,5051724
spiLA0480-MIR530	UUUAUCUGCAUUUGCACCUGCACCUUAGUGAACGAAUUAGUUCGCGUAUAAUUCGUGCAGAAAGGUGUAGGUGUUCAUGCAGACAAAA	**88**	22,727273	28,409091	18,181818	30,681818	40,909091	59,090909	1,08	1,25	-42,8	-42,1	0,204281	3	-48,636364	-1,1888889
spiLA0480-MIR5300	UUGACCAAAAUUCUUCUUCUCCAGUCCAGGCAUUCCAACAGUUGAUAACAUCUAGAUCUGCCAAUACUUUGUAUUUUUGUUCUUCUAUUUUUCACAUGACAUCUUCAAAAUCUACUAUGAGCUUCAUCAUAAGCUAAGAAAUGGUGAGUUUUGAUGAUGUGAUGCCUAAAAUAGGAUUAAAUGAAAGUACUAGUAAAAAGGUGUUCAGAUCUGGAGGUUAUGUUAAGCUGGUGGUAUGCUUUGAUUGGGAAAGAUGACUUAGGUCA	**266**	19,548872	30,075188	15,413534	34,962406	34,962406	65,037594	1,1625	1,2682927	-95,7	-93,3	0,0019998	16	-35,977444	-1,0290323
spiLA0480-MIR5303-20	ACCCUAUGUUACUCGGACUCUCCUAAAAUGCUUUUGCACCCGGCUCGGAUCUUCAAUAAAUGCACUUAUUUGGAGGUUCUGACACGCACCUAUAAACAUUUUUGAAGAGUUCGAGCAACAUAGUCG	**126**	18,253968	26,984127	24,603175	30,15873	42,857143	57,142857	1,1176471	0,7419355	-40	-37,7	0,007413	12	-31,746032	-0,7407407
spiLA0480-MIR5303-21	GAGCUAUGUUGCUCGGACUAUUCUAAAAUAUUGACAGGUACAUGUUGGGUACUCUAGAAAUAGUGCAUGUUUGGAGGAUCCGACAUGGGUAUGACAACAUUUUUGAAGAGUUCGAGCAACUAGGCG	**126**	26,984127	28,571429	15,079365	29,365079	42,063492	57,936508	1,0277778	1,7894737	-52	-51,9	0,0483959	6,9	-41,269841	-0,9811321
spiLA0480-MIR5303-23	CCCCUAUGUUUUCGGACUUUCCAAAAAUGUUAUCAUACCUAUGUCGGAUCCUUCAAAAUAGUGUAAUUUUGGAGGACACGACACGCAGGCAUCAGCAAUUUUGAAGAGUUCGAGCAACAUAGCUU	**125**	19,2	29,6	21,6	29,6	40,8	59,2	1	0,8888889	-47,9	-47,9	0,324352	2,5	-38,32	-0,9392157
spiLA0480-MIR5303-7	AGUACCUACCUGCUAAGUUGCUCGGAGUUUCUAAAAUUGUUGGUGCACGCAUGUUGGAUCCUCCAAAAUUGCCUACUUUUGAAGGAUCGACCAGGCACCUGAUCACAUUUUUUAAGAGUUCGAGCAACAUAGCCUUGUAGUGUGUC	**146**	21,917808	24,657534	21,917808	31,506849	43,835616	56,164384	1,2777778	1	-50,6	-49,9	0,0616115	12	-34,657534	-0,790625
spiLA0480-MIR5303d-3	UCAUAAGUUUAAGUUGCGCGGACUCUUCAAUGUAGAUGCUGCACUCGUGCCUGAUCUCCAAAAAUAUGCUACUUUUGGAGAAUCCGACACGCACCCACUGACAUUUUUGAAGAGUCCGAGCAACAUAACUAUAGGU	**136**	19,852941	28,676471	23,529412	27,941176	43,382353	56,617647	0,974359	0,84375	-46,1	-40,2	0,0034067	18	-33,897059	-0,7813559
spiLA0480-MIR5303d-4	AACCUAUGUUGCUCAUACUCUCCAAAAAUGUUGCUGCACCCCUGUCGGAUUCUCCAAAAGUGCAGUAC	**126**	18,253968	28,571429	29,365079	23,809524	47,619048	52,380952	0,8333333	0,6216216	-55,8	-55,2	0,0801491	6,3	-44,285714	-0,93

spiLA0480-MIR5303f-6	UUUUGGAGAAUCCGACACGCACCCGCCGACAUUUCUGAAGAGUCCAAGCAACAAGACUGAAUUAUGUUGCUCGGACUCUUCAAAAAUGUCAAAGGGUGCGUGUCGGAUUCGCCAAAAGUAGUGUAUUUUUGGAGAAUCUGACACGGGUGCGGCAUCAAAAGUGAAGAGUCCGCGCAACUAAGCUAAGCAGUAUGCUGCUCAGACUCUCCAAAAAUAUU	**126**	27,777778	28,571429	18,253968	25,396825	46,031746	53,968254	0,8888889	1,5217391	-60	-58,2	0,0778704	5,6	-47,619048	-1,0344828
spiLA0480-MIR5303h-6	GCCACACCUGUAUCGUAUCCUUCGGACAGGCACUACUUUUGGAGGAUCGAACAAGCACCUGACAACAUUUUUGAAGAGUCUGAGCAACAUAGUGAAG	**131**	20,610687	31,29771	23,664122	24,427481	44,274809	55,725191	0,7804878	0,8709677	-52	-49,3	0,114148	4,7	-39,694656	-0,8965517
spiLA0480-MIR5303i-2	ACCUAUGUUGCUCGGACUAUGCAAAAUGCUCCCGAACUAGAGCGUUGGAUUUUCCAAAAAAAUAUGCUGCUUUUGGAGGAUCCACCACGCACCUGACAAUAUUUUUGAAGAGUCUGAGCAACAUAAUC	**128**	19,53125	30,46875	22,65625	27,34375	42,1875	57,8125	0,8974359	0,862069	-47,3	-47,3	0,0823415	9,8	-36,953125	-0,8759259
spiLA0480-MIR5303i-4	AUCAUGUUGUUCGGACUCACCAAAAAUGUCGAUGCAUCCAUGUCGGAUCCUCCAAAAAUGCACUAUUGUUGGAGUAUCCGACACACGCCUGUUGAUAUUUUUGAAGAGUCUGAGCAACAUAAA	**123**	19,512195	30,081301	21,95122	28,455285	41,463415	58,536585	0,9459459	0,8888889	-58,1	-57,9	0,0997352	4,1	-47,235772	-1,1392157
spiLA0480-MIR5304	UCAAUGCUACAUACUCAUCCCCACAACUUUCAUCUCACGUUCAAAAGAUGAAAGUUAUAGAGAUGAGUAUGGUGCAUUGGA	**81**	17,283951	33,333333	20,987654	28,395062	38,271605	61,728395	0,8518519	0,8235294	-35,5	-35,3	0,456836	1,1	-43,82716	-1,1451613
spiLA0480-MIR5340	AUGGUUUUGCAAAGCCAUUUUUGACACGUGGUCAAUUAUAAUUUGGUCAUGUCAUCAAUUUUUUAAUUAAAAAAUUCAAAAAAAUUGAUGACGUGGCCGAAUUACAAUUGGUCACGUCUCAAAAAUGGUUUUACAAAACUAC	**142**	15,492958	35,211268	14,788732	34,507042	30,28169	69,71831	0,98	1,047619	-72,2	-72,2	0,141693	4,4	-50,84507	-1,6790698
spiLA0480-MIR535	CCCUAUGCAUAAUUUCGGUGGAGCUUACAACAGCAAGACAGUGAGAGAGAUUUUUGCUCUCUCUCAUUUUCUUGCUGUUGUAAGCUCCACCGGAAUCAUGCGUAAUA	**107**	20,560748	25,233645	22,429907	31,775701	42,990654	57,009346	1,2592593	0,9166667	-74,5	-74,5	0,602335	0,9	-69,626168	-1,6195652
spiLA0480-MIR5368	CUAACCUUGUGUCAGGACCUACGGGCCAAGGGACAGUCUCAGGUAGACAGUUUCUAUGGGGCGUAGGCCUCCCAAAAGGUAAC	**83**	28,915663	25,301205	25,301205	20,481928	54,216867	45,783133	0,8095238	1,1428571	-33	-33	0,448662	1,9	-39,759036	-0,7333333
spiLA0480-MIR5379	AAAGAAAAGAGAGAAUAUGAAAAGUGAGGGAACUACUUUGGAAGGAAAAUUAAAAGUCAUUUGCAAAGUGCAAAUGAAAGUCAUUUCUUAUAAAUUUGCAGGUAACGGUAACAUUCUGAAAAGUUGUUACUCUUUUCGAAAAGUCGUUACUUUUCGAA	**158**	20,253165	39,873418	10,759494	29,113924	31,012658	68,987342	0,7301587	1,8823529	-34,5	-25,3	0,0060181	37	-21,835443	-0,7040816
spiLA0480-MIR5380b	AAAUGAAUUUAAUGGGUUGAAUCUGAAUGAUUCAGUUUCAGACCUAAAAAUCAAACGUACUUAAUAGGCUGAAUCUGAAUGAUGAAGAUUUGGACCUCCAUUAAGUGCAAAC	**112**	18,75	37,5	14,285714	29,464286	33,035714	66,964286	0,7857143	1,3125	-34	-32,2	0,0542414	20	-30,357143	-0,9189189
spiLA0480-MIR5499	ACACAACCUGUGUACAAUUAAGCCGAUGCUCCGGACAUUUAAAAAUGAAGGCAGCAUGGUUAUGUGCACAGAGAUUGAAU	**80**	22,5	35	18,75	23,75	41,25	58,75	0,6785714	1,2	-25,6	-25,1	0,104881	5,5	-32	-0,7757576
spiLA0480-MIR5532-1	ACCCUUAUUGGAUGAUAUAUAUGCCAAAUAUGAUUAAUGUAACAUUCUGAAAAAUUACAUGUCUAAUGAAGAUCCCAAUAGGUCUUUAAGAAUGUGUAUUGGGGAUACAUAGGCAUAUCAAUUCCGAAUAUUGAGAAAUACUGGGCAUAGUAUAGUUGCUUAAGGGGUAUUAGCCAAUUUCUAUAUAAUACCCAAAUAAGCAG	**203**	18,226601	36,453202	13,793103	31,527094	32,019704	67,980296	0,8648649	1,3214286	-45,8	-30,89	0,0007559	51	-22,561576	-0,7046154
spiLA0480-MIR5532-2	UAUUCCAUGAAUAUGAUAUCUAUCUAGUGUGAUGUAUGGAAUAUAUGACAAAGGUGGAUCUAUUGAUCGGUCAUGUCAUAUAGGCCCGAGUUGGACAUCCAAUUGCUUCGAUUUGAAUUAUCCGGAGAAUGCAAUGCCUGAUAUAUAUCAAAAAGAUGGACAA	**163**	21,472393	32,515337	14,723926	31,288344	36,196319	63,803681	0,9622642	1,4583333	-46,4	-46,2	0,0434157	11	-28,466258	-0,7864407
spiLA0480-MIR5558	GAAGAUAUUUCAUGUGAUAAAUUUUAAUUCCGCACUACUUUUCAUACAUACAUGUAUGCAAUGAAUGAUGUCAAAGGGCUUGUACAAGACCUCCGUGAGGUCAAGUACGCCAUGUCGCACUCCGAGAGUGUCAUAUCUUCUAGUGUGUGCUCUCGGGGUGUGACAUAUACACAAUGGAAUUAUCAACCUUGAUGAUACAAAUACAAUAUAUGAUACAGAUUUAGAAUUAGUUAAGCAAAUAUGAUCAGUCUUAAUGAUACAAAUACAAUAUAUGAUAUUAAUUUAAUAUUAGUUAAACAAAAAUUAUCAGUCAUAAUAAUAUCAAG	**326**	16,257669	36,503067	15,337423	31,90184	31,595092	68,404908	0,8739496	1,06	-82,1	-67,2	0,0002268	72	-25,184049	-0,7970874

spiLA0480-MIR5559	GUUGGAAGCACAACGAAAAGGAAAGGCUCAAGUCUCAUAGUGAUUGUUAAACUAUUUGAGGCAAGUGGAUUUCUAAACUCUUGUUAAGCGUAUGAAAUUCGUGUAUCCUUGUGUGGUGUUGAGAAUGACUUGGAGACUUGUUGCUUAUUUGUUGGUGUUGUAUUCCUUG	**170**	25,882353	25,294118	12,352941	36,470588	38,235294	61,764706	1,4418605	2,0952381	-52,9	-52,9	0,0312154	8,1	-31,117647	-0,8138462
spiLA0480-MIR5565d	AAAUUCCCGAGGUUGUCAUUUCUCUUGUAUUCAUGUGUGUGUGUGUAUAUAUAUAUACACACACACACGUGAAUACAAGAGAAAUGACAACCUCGUGAAUUUUUAUACUCCCUCCGUCCCAAUUUAAGUGUCCUAG	**102**	17,647059	31,372549	17,647059	33,333333	35,294118	64,705882	1,0625	1	-76,8	-76,8	0,39682	1,2	-75,294118	-2,1333333
spiLA0480-MIR5567	UUUAACUGUGCACUAAGUUUAUGAAAGGGGAGACACUGACUCUUUUAGUCUUAAAUUAAAGAUGCAUGUGUGUAUCCCUUUGAUUUUUGGUCUUAGACCUGCCAUGUAGAAUGUUGGAACUGGAAAGGUUACUAAAUAUAGAAAGACGCUCUUUUUGGGACAGAUCAAAAGGAAAAUAAGACAACUUAAACUUGGGACGGAGGGAGUACCA	**245**	21,632653	31,020408	16,734694	30,612245	38,367347	61,632653	0,9868421	1,2926829	-80,8	-64,5	0,0001258	58	-32,979592	-0,8595745
spiLA0480-MIR5569	CCUAUGGACCGUAGGUGGCCUCCGUAGUUUGUGAUUGAGGCUGAGUUUUGCCUUCCUAUUGCAUGCUUGAAUUAUGGAGGAAGACCUAAGGUGCAUCAU	**99**	28,282828	20,20202	19,191919	32,323232	47,474747	52,525253	1,6	1,4736842	-37,6	-37,6	0,205842	5	-37,979798	-0,8
spiLA0480-MIR5628-1	CUGGAGAAAUAUGGAAGAGAUGAUCGGAGAAAUAUUAUGUUCUAAUGAGCUAAUGCCACAAGAAAAGUAAUGAUGUCUAUAACUUUAAAGCUCUGAAGUAAUAUCUCUCCAGUCACCUCAUCCCUAU	**135**	17,777778	35,555556	17,777778	28,888889	35,555556	64,444444	0,8125	1	-39,7	-36,6	0,053902	22	-29,407407	-0,8270833
spiLA0480-MIR5628-2	UGAAGUAAUAUCUCUCCAGUCACCUCAUCCCUAUUUCUCGAAUAGGUUGCUAAUUCAAGCAUUAGAGAAAUAUGGAAGAGGUGAUUGGAGAAAUAUUUCUAGG	**103**	20,38835	32,038835	16,504854	31,067961	36,893204	63,106796	0,969697	1,2352941	-45,7	-45,1	0,124302	7,2	-44,368932	-1,2026316
spiLA0480-MIR5637-1	ACAAAACUGUAUAAUUCGCUAUACAUAUACAAUUGUACAAUUCGCUGGCCUAAAUUGUAUAAUUUGCUGGCCUAUUUCGCUGCAAUUGUAUAAUUCGCUAUCCUAUUUCACUGCAAUUGUAUAAUGCACAAUUGUAUAGUUUGCU	**145**	13,793103	29,655172	18,62069	37,931034	32,413793	67,586207	1,2790698	0,7407407	-37,3	-36,7	0,0112921	11	-25,724138	-0,793617
spiLA0480-MIR5637-2	AAUAUAUAACUAUAUAAUUCGCCAUACAUAUACAAUGGUAUAAUUCGCUGGCCAAAAUUGUAUAAUUCGGUAGUCUCGCUAUACAUAUACAAUUGUAUGAUUCGCUGGCCUAUUUCGUUGCAAUUGUAUAAUUCGCUGGCCUAUUUCACUGCAAUUGUAUAAUGCGCAAUUGUAUAUUUCGCUGGCCUAUUUCGCCGCAAUAUGUGUAUAAAAUUUGCUUUGCGAUCAAAGUAAAAUGUUUGUAUAUUGUAUAAUUAAGAGUAUAUGAA	**269**	16,356877	30,855019	15,613383	37,174721	31,97026	68,02974	1,2048193	1,047619	-62,2	-48,04	0,0010077	75	-23,122677	-0,7232558
spiLA0480-MIR5650-1	ACACUAGAUGCAUGUAUCUGAUGUAAUUCACAUAUAUAUGAGAUAUAAGAUACAUAGGAGAGUGACGAGAGCUGGGAGAGAGGCGAGCCAGAUAGGUAAGGAGGCAAAUAAGAUUUGUUAUGUAGCUCAGAUACAUGUGAAUCUACUUGGAUACAAUGUAUCUAGAAC	**168**	25,595238	36,309524	12,5	25,595238	38,095238	61,904762	0,704918	2,047619	-45,9	-42,9	0,0144327	20	-27,321429	-0,7171875
spiLA0480-MIR5650-2	CAACCGCAACUCUAGCCAGUCUUCAUCACACCAGAUUUCAGGGUGAGCUAAAGCUUNCUAGCUUGGACUGGAUCUUCUUCUUCAUGUCUUGAUGCCUUGAAGUUCUGGCAUAGACUAGCUAUUAUUUAUGUUUAGUUUCUUAGAUACUCUUAGCUUUAAUAAUUUGAGGAUAGAUGUUCUUGUGAUGAUGACUUCCAGAUUUUGGGGAUA	**210**	20	23,809524	18,571429	37,142857	38,571429	60,952381	1,56	1,0769231	-57,2	-54,5	0,0016177	27	-27,238095	-0,7061728
spiLA0480-MIR5652	AAAUGAACUUAAUGAGUUGAAUCUGAAUGAUUCAGAUUCAGACUUAAAAAUCAAACGUAGUUAAUAGGCUGAAUCUGAAUUAUUAAGAUUCAGACCUCCAUUAAGUGCAAAC	**112**	16,071429	40,178571	14,285714	29,464286	30,357143	69,642857	0,7333333	1,125	-40,6	-40,6	0,0418379	6,4	-36,25	-1,1941176
spiLA0480-MIR5658-1	UGCGGUGCGGUAAAGAUGUUGAUGAUGAAGAGAUUUUUUUUGAGAAUGUAUUUUUUGGAUGACGGAAUCAGUCUCCAAAUCGGAGAAUUGUUAGGUAGUGGAUCCUGAUUAAUAGUUGAUGUACUUUAACAAAAAUACUCUGAUUUAUUAAUAUAUGUACCCAACCUCCGUUGCGGUGCGGUAAAGAUGUUGAUGAUGAAGAGAUUUUUUUUAGAAUGUAUUUUUUGAAUGAUUGAAUCAGUCUCCAAGUGGGAAAAUUGUUAGGUUGUGGAGUCUGAUUAAUAUUUGAUGUAUUGUCAUAUAU	**171**	21,637427	30,409357	12,280702	35,672515	33,918129	66,081871	1,1730769	1,7619048	-42,6	-33,5	0,0159618	38	-24,912281	-0,7344828
spiLA0480-MIR5658-2		**231**	19,91342	26,839827	12,554113	40,692641	32,467532	67,532468	1,516129	1,5862069	-55,9	-42,8	0,0075225	49	-24,199134	-0,7453333

spiLA0480-MIR5670a	UACUGUUUACGCGGUUUAGGCUGUACUAUUUAUUCUCCAUUUAUUCUCUGUAACCAAAAAUACUCUGAUUUAUUAAUAUAUAUACCCCACUGCCGUUGCAAUAUUUGAAGUAAAAUGUUUGUAAAUUGUAUAAUUAAGUGUAUAACACGAAGAUAUAUAUAUUUUUACAUGUGUAUAUACAAUUUUCUCUCGCUUUUUACAAAACAGAAACAGAAUUUAUACACUUCUGUGUAUAAAGCGAGAAUGGAGAGUGGCGAGCGCGAUUUUUGGGAGAGAGACGCCUGGCAAACUUUAGUUAACAUUUGCUAUGGAGCACAAUUAAAUCAAACCCUAUCUACUUCAUUUAUUUUA	**255**	17,254902	34,509804	13,72549	34,509804	30,980392	69,019608	1	1,2571429	-61,3	-46,4	0,0018339	50	-24,039216	-0,7759494
spiLA0480-MIR5716	AACAAGGUUAAUAUAUAUUUAUAUAUACUGAUGAGGAAUGAAUACAACAAAAUGGUAUGUAAUAAUAUUCUAUUUUAUAGUUGUAAUUUAAAUAAUAACAAUUAGCAAAUUGGGGAUGUAGCUCAAAUGGUAGAGCGCUCGCUUUGCAUGCGAGAGGCACGGGGUUCGAUCCCCCGCAUCUCCAUUUUUUUCCCUCUGAAAUAUGGAUCUUUGUAUAUAUAAAUGCAUAUAUUUUCGUCGAUCUUUGUAUAUAUAAAUGCAUAUAUUUUCGUCUUAUA	**279**	17,204301	32,258065	13,978495	36,55914	31,182796	68,817204	1,1333333	1,2307692	-66,2	-47,7	8,31E-05	63	-23,727599	-0,7609195
spiLA0480-MIR5720	GCUUGUGGUUUGGUUUGAUUGGUUUGGCGAUUGAAAAAAAAAAUCGACCACUCUUGGUUUGGUAUGGUAUUAGAAAAAAAGAAUCAAACUGAACUCAAACCAAACCGACACAC	**113**	21,238938	35,39823	15,929204	27,433628	37,168142	62,831858	0,775	1,3333333	-32,5	-20,81	0,0413664	23	-28,761062	-0,7738095
spiLA0480-MIR5752b	UAGAAUGUAUUAGUAAUGUUUGCAUUAAUUAAACAUAGAUGAUUUCUUAUGCAUUGUUUGGUUUGGUGUAUUUUAUAUUUUUUUUAGUUUCCCACCCUGUGUCUGGAGCCCAUGUUGGAGCUCCGUCUAAAUCCGAAUCGCGCUCUGCAGGGGCCCAUUCGGGGGUGACACUCCCAAAAGGUUUUCUCCAUAUCGAGGGACCUCUGAUUAAGGAUGAAACACUCCACCAAUGCACCACAACCCAUGUUGGUGGUUUGGUGAAUUAUUAAUAGCAUACAUUGCAUAAAAUAUUUAC	**295**	20,338983	25,762712	19,661017	34,237288	40	60	1,3289474	1,0344828	-82,9	-69,8	5,15E-05	64	-28,101695	-0,7025424
spiLA0480-MIR5773-1	GAUCCAUCCAUCUAACCCGAUCCAUUAAAAAAUAUAAUAUGAUCCAUUUUAUUUUGUCUUUAAUCCUAAAUUAAUCCCUCUCUUUAAACCUUGAAUUAGGAUUAAAGACGAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGUGUGGAUC	**164**	14,634146	32,317073	16,463415	36,585366	31,097561	68,902439	1,1320755	0,8888889	-95,5	-95,5	0,45389	2,1	-58,231707	-1,872549
spiLA0480-MIR5773-2	UGAUCCACCCACUUAAUCCGACCCAUUUAAAAAAUAUGAUAUGACCCAUUUUAUUUUCUCUUUAAUCCUAAAUUAUUCCCUCUUUAAACCUUGAAUUAGGAUUAAAGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAAUGGGUCAGGUUAGGUCGGUGGAUCA	**166**	13,253012	33,13253	18,072289	35,542169	31,325301	68,674699	1,0727273	0,7333333	-96,8	-96,8	0,277025	3,4	-58,313253	-1,8615385
spiLA0480-MIR5773-3	ACCCACCUAACCCGACCAAUUAAAAAAAUAUGAUAUGACCCAUUUUAUUUUGUCUUUAAUCCUAAUUUCAGGUUUAAAGAGAGGGAUUAAUUUAGGAUCGAAGACAAAAUAAAAUGGGUCAUAUCAUAUUUUUUAAUGGGUCGGGUUAGGUGUAU	**155**	17,419355	34,83871	14,193548	33,548387	31,612903	68,387097	0,962963	1,2272727	-85,5	-84,6	0,011893	12	-55,16129	-1,744898
spiLA0480-MIR5781	UGCACCACUAUCCUGAAUUAGAGACUGCAUGAUGCGUAGAAAAAUUUUCCUUCUUCUAAUCUUAUCGUGCCUUCUCUAAUGUCGGAUUUAUUGGUAUU	**98**	16,326531	24,489796	20,408163	38,77551	36,734694	63,265306	1,5833333	0,8	-29	-28,2	0,0965677	5,1	-29,591837	-0,8055556
spiLA0480-MIR5826	ACAUAACUCACAUCUCAAAACUAGCCCAAAGGGAGGAGCAUUGUCCAUGCACCCAAAUCUCAUUAACCACAAUUCUUAAAGAAUGACAAAGUCCUGCAUCGGUGGUUAAUGAGAUGGGUGGACUCCUUAUAAGGCUUGAGCAAUCCUUCUCCGUUUGAGCUAGCUUUUGGGGUGUGAAUUAGGC	**184**	21,73913	29,347826	22,282609	26,630435	44,021739	55,978261	0,9074074	0,9756098	-75,9	-75,8	0,019793	12	-41,25	-0,937037
spiLA0480-MIR6022-1	AAUACCAUCCUGGAUAUUCUCCCUUCCAUCACUAAGUUAUUUAGACCGAGUUUUAACCAAUUGCACGGUCCUCUACCCAAGAUUGAGGUUUCGUAAAAUGUAACUUAAGAUCAAGUCGCGUUAGGUUCAUGAAGUUUUGAAUUGACUUAGGAAGAGUACCUUGCAACUUAAAACUUUGAGGCGAAAUAAGUUAGUGAUGGAAAGGAUAAUAUCCAGGAUCGUAUUGUUCCGUUCAGGG	**238**	20,588235	30,252101	18,067227	31,092437	38,655462	61,344538	1,0277778	1,1395349	-85,8	-80,1	0,0086902	31	-36,05042	-0,9326087
spiLA0480-MIR6022-2	AACAAUACGAUCCUGGAUAUUAUCCUUUCCAUCACUAACUUAUUUCGCCUCAAAGUUUUAAGUUGCAA	**231**	17,748918	31,168831	19,480519	31,601732	37,229437	62,770563	1,0138889	0,9111111	-90,7	-90,7	0,0062484	14	-39,264069	-1,0546512

spiLA0480-MIR6024-1	GGUACUCUUCCUAAGUCAAUUCAAAACUUCAUGA ACCUAACGCGACUUGAUCUUAAGUUACAUUUUAC GAAACCUCAAUCUUGGGUAGAGGACCGUGCAAUU GGUUAAAACUCGGUCUAAAUAACUUAGUGAUGGA AGGGAGAAUAUCCAGGAUGGUAUUGUU AACUGGAAAUGGGGAAGUGGAGAAACAACACUUG CUAAAGGAAGUUCACCAGUCAUCUCUUUUCUUUU GGAGUUUUUUUAGCAAGAGUUGUUUUACCUCUUC UCAAUUCCGUCUCU CAUGAAAAGUUGUGACAUUUAUGAAAAGUUGCAA CUUUUAUGAAGAGUUGUUACUUUUAUGAAGAAUU	**116**	19,827586	25,862069	18,965517	35,344828	38,793103	61,206897	1,3666667	1,0454545	-43	-42,8	0,0913448	6,7	-37,068966	-0,9555556
spiLA0480-MIR6024-2	GUGACUUUUACGAAAUGUUGUGUCCUUUCCGAAG GGUUGUAACUCUUUCAAAGAGUUGUAUCCUUAUG GAUAAGUGACAAUAAUCAUUUUCUAC UGUAUAGUUAUUUCAUGUACACUUGCACAAAAAUA UUAUUGAACCUUGAUGUUAUCUCAGUGUUGGCAU	**162**	19,135802	30,246914	12,345679	38,271605	31,481481	68,518519	1,2653061	1,55	-46,3	-42,6	0,0005508	36	-28,580247	-0,9078431
spiLA0480-MIR6025b-1	GCAUAAAUUGGGUAAAUUUAUGAUUGAAUGUGUA UUUUGGUGUUGUACCAAAUCCAGGCAUGCCAACU AUUGGGAUGGCAUCUCGGUUUGUUA AAAAUAUUAUUGAACCUUGAUGUUAUCUCAGUGU UGGCAUGCAUAAAUUGGGUAAAUUUAUGAUUGAA	**162**	20,987654	27,160494	13,580247	38,271605	34,567901	65,432099	1,4090909	1,5454545	-52,9	-50,2	0,021433	25	-32,654321	-0,9446429
spiLA0480-MIR6025b-2	UGUGUAUUUUGGUGUUGUACCAAAUCCAGGCAUG CCAACUAUUGGGAUGGCAUCUCGGUUUGUUAGUU GCUGUGCAGUAUGAUCACUGUGGCAG GUAAUUUUACAUGAUUAUGGGUAGCACAAGGAUU	**162**	24,691358	25,308642	13,580247	36,419753	38,271605	61,728395	1,4390244	1,8181818	-59,7	-59,7	0,0307663	17	-36,851852	-0,9629032
spiLA0480-MIR6027	AAUGUGAAACAGAAAAGUGAUAUGCAAAGAAGAUG GAGAUUCAAUUGUUUAUUGUUACGAAGAAAACAC UUUUGUGUUUCUCGUGAAUCCUUCGGCUAUCCAU AAUCAUGUUGAAUGUG	**153**	21,568627	33,333333	11,764706	33,333333	33,333333	66,666667	1	1,8333333	-57,7	-52	0,0615353	16	-37,712418	-1,1313725
spiLA0480-MIR6108c	AGGUCUGAAUCUGAAUCAUUCAGAUUCAGCCCAA UAAGUACGUUUGAUUUUUAGGUCUGAAUGUGAAU CAUUCAGAUUCAGCCCAUUAAGUUAAUUUGUUUU AAUUUUUAGAAAACCUCUUAAUGGGUCUGAAGAG AUCUGAACGAAUAAGAUCUGUAGGA UGUAUAGGGAAAAAUACUCAAAUAUGCUAUCGAAC UUUCAGAAAAGACUCAUUUAUGCCAUUCGUUAAAA GUUUGACUCAUCUAUGCCAUUACCGUUCAAGAAA AGACUCAUUUAUGCCAUUAUUUUUUAAUAGUGAU	**161**	19,254658	31,677019	14,285714	34,782609	33,540373	66,459627	1,0980392	1,3478261	-51,1	-44,9	0,0112601	42	-31,73913	-0,9462963
spiLA0480-MIR6110-1	UUUGCAAAACCAUUUUUGACACGUGAUCAAUUAU AAUUCGGCCACGUCAUCAAUUUUUAAAAUAAAAAA AAUGUAACUGAUGGCAUAAAUGAGCCUUUUCUGG AAGUUCAAUGGUAUAUUUAUGUCUUUUCCCAUUU G UUUUUGACACGUGGCCAAUUAUAAUUCGGCCACG	**276**	14,130435	33,695652	16,304348	35,869565	30,434783	69,565217	1,0645161	0,8666667	-79,7	-75	0,0002505	40	-28,876812	-0,9488095
spiLA0480-MIR6110-2	UCAUCAAUUUUUUUAAGAAAAUAAAAUUAUUUUAA AAUUGAUGACGUGGCCAAUUGUAAUUCGUCCACG UCAUCAAUUU	**113**	14,159292	31,858407	16,814159	37,168142	30,973451	69,026549	1,1666667	0,8421053	-48,7	-47,7	0,0094363	11	-43,097345	-1,3914286
spiLA0480-MIR6112	AAAUUUAUUUAAUAAAACUUUGGUUCUUCGGUGC ACCGUAGUUUCGGGACUCUUGCACCAAACUUCGA ACCGAAGUUUCAAAAAUAAAAAA	**91**	15,384615	35,164835	18,681319	30,769231	34,065934	65,934066	0,875	0,8235294	-26,4	-26,4	0,215984	4,9	-29,010989	-0,8516129
spiLA0480-MIR6116	CGCCUCUGUGUGCAUUCAACAUUAGAGGAUUCAU CAUUAUUGUUAGAAAAUGAUGGAUCCUCUAAUAC UAAAUUCACAUCAGAGAUU	**87**	16,091954	32,183908	18,390805	33,333333	34,482759	65,517241	1,0357143	0,875	-36	-36	0,262563	3,5	-41,37931	-1,2
spiLA0480-MIR6139	AUUAACAGUAAGUACCCCAAUGACACAUCCGAUUU CAACAAGAGAAGUUUGAAGGACAUGCAUUUAGUG UAAUCCAACUAUCCCUUGCACCUAACCUUCUUUG UGAAGUGAGUAAAAGUACUGAAGAGGUGACCAAA UAACUUUGGGAAGGGAUGGAAGGACUUUACUGGG ACUAAUUGGUGACAAGAAGGAUGUUGUUUCAACA ACGUCUUUACACAUUUAAGAUGUAGUCGGGUACU UUGUUGCA	**247**	22,267206	32,388664	17,004049	28,340081	39,271255	60,728745	0,875	1,3095238	-68,4	-57,8	0,0010276	49	-27,692308	-0,7051546
spiLA0480-MIR6140b	UAUCUCUCUCUCUCUCUCUCCCUCGCUUUAUACA AACAUAAAAUAUGCAAUGUAUUUUGUAUAAUUUGU AUUUGUAUAAAGCGAGAAAGAAAGAACGGAAAAGA GAACUGGGCAAGGGUAUAUUUGUAUUGUAUAAUU ACGAGUAUAUAAGACGAAGAUAUAUGUAUUUGCA	**261**	19,157088	34,482759	13,409962	32,950192	32,56705	67,43295	0,9555556	1,4285714	-90,3	-87,8	0,0153028	23	-34,597701	-1,0623529

spiLA0480-MIR6145b-1	UGUGUCUAUACAAUUUUUUCUCGUUUUAUACAAUAAAGCCGCAAUUUAUACUGAUUGUAUAAAGUGAGAGAGGCGAGCGACAGAGGGAAUUUCUAUCCUUUUUACGUACGUGGCACUAUCUUGUGGGUUCAACGAUGUUUGACUUUUUUUUAAGCUAGUGUAACGUAGGCCGAAAAGGGGUAGAAAAUCCCUUUUGGCCUACGUGGCACUAGCUUGAAGAAA	**101**	22,772277	24,752475	14,851485	37,623762	37,623762	62,376238	1,52	1,5333333	-34,4	-26,6	0,0384798	9,8	-34,059406	-0,9052632
spiLA0480-MIR6145b-2	AAUUUAACCAACGUUGGGCCCACAAAAUAGUGUCACGUAGGCCAAAAAAG	**84**	21,428571	33,333333	23,809524	21,428571	45,238095	54,761905	0,6428571	0,9	-36,1	-36,1	0,199956	8	-42,97619	-0,95
spiLA0480-MIR6149b	UUAUAGCCUUUGUAUGUCAAAGCUUCGAUACGCACCUGAAUCGACAAAUACAUAUAUUAUUCAGACUUUUUAAGAAUAUCACGCGUUUAUUAUUUUUAUAAGUCUGAAUAACAUAAAUCAUAUAUAACAUAUAUGUCGAUUCGGGUUCGUAUGAAAACUAUGGCAUACCUCAAAGGGUAACG	**182**	14,835165	34,615385	16,483516	34,065934	31,318681	68,681319	0,984127	0,9	-60,9	-57,9	0,0114551	19	-33,461538	-1,0684211
spiLA0480-MIR6155	GAAGGAUGUGCCUGGCUCCCUGUAUGCCACACACAUUCACCAAUUCUUUGAUUGACUGAUCAGUGGGUGGCGUAUAAGGAGCCAAGCAUACCACC	**95**	24,210526	25,263158	26,315789	24,210526	50,526316	49,473684	0,9583333	0,92	-44,9	-44,9	0,474049	2,6	-47,263158	-0,9354167
spiLA0480-MIR6160	AUUAUAUUUUUUUUCAUUUCCGUUAGAGGAAAAGGGUAUAUGUGAGCCAUUUGUUUACAAGUAAGGGUAUAUGUGCCACUUUCAUAACAAUGGGUAUAUCAGCUCUAAAUGACAAAGUUGAGGGGUAGAUCAGACCCCUUUUCCCUUUAACUUAAUUCGAAUAAUAUAUUCA	**173**	17,919075	31,213873	14,450867	36,416185	32,369942	67,630058	1,1666667	1,24	-39,7	-27,8	0,0013013	57	-22,947977	-0,7089286
spiLA0480-MIR6162	UUGUUGAUAUUACUAGUCACAAAUGUGAAAAUUGGUAGCCAUCAAUGUGAAAGUUGGUAGCUACAUUUGUGGAAGUAGGUAGUCAAAGUUUGGUAUAAGUUUGAUAGAGUUAGGCAACCAAUUUUUUUGUUGAAAUUGGCUACCAUAUAUGUCAUUAAUGAUGUAAACAAGUG	**173**	22,543353	32,369942	9,8265896	35,260116	32,369942	67,630058	1,0892857	2,2941176	-48,2	-46,5	0,0069082	19	-27,861272	-0,8607143
spiLA0480-MIR6197-1	AAUUUUCUCACGCUUUAUACAAAUAGAAACGCAAUUUAUACAUUUCGCUUCUGUUUGUAUAUGUGAGAAAGGC	**73**	15,068493	31,506849	16,438356	36,986301	31,506849	68,493151	1,173913	0,9166667	-25,2	-25,2	0,25399	3,2	-34,520548	-1,0956522
spiLA0480-MIR6197-2	AAGAUUAAACGGGGACACACGUCGUAAUCUUAUCUGUCAAUAAAUGUCGGAUCGAUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAAUAUA	**92**	21,73913	33,695652	15,217391	29,347826	36,956522	63,043478	0,8709677	1,4285714	-34,4	-32,8	0,0706673	9	-37,391304	-1,0117647
spiLA0480-MIR6198	GUUUACAAAGGAAAUGCCUCUGGACCAACCAGAGUAAAGAGUUCUAUUUAGAAGUCUUUACCUUGGUUGGUCAUGAUGCAUUUCCCUAGUAAAC	**94**	20,212766	29,787234	19,148936	30,851064	39,361702	60,638298	1,0357143	1,0555556	-49,8	-49,8	0,56076	1,6	-52,978723	-1,3459459
spiLA0480-MIR6204	AUCAACCGUAAAGAAGGAUCUAUGACGGUCAGGGAGUAUUUUCUGAAGUUUGUGAAGCUAUCAAGGUAUGUUACUUCCCUUGAUAUUUAAUAGAAAGAAUGAGGAGAGUACUUAGAUUUGUUGAAAUUAUCCAGGUAUGCUACUUCCCUGGUUUCGAACAACAGGGAUGAGAUGCGAAGGUUCCUCACAGGAAUCAAUGGAGACCUGGAGGAUGAGUGUCGGUCUGCGAUGCUCCAUGAUAAUAUUGACCUUUCUAGGUUAAU	**263**	25,095057	29,277567	15,589354	30,038023	40,684411	59,315589	1,025974	1,6097561	-76,2	-67,8	0,0017789	42	-28,973384	-0,7121495
spiLA0480-MIR6228	CAUGACACCUUUAAACUGGUCCAUGGCAGUAAAAAUAAUGCAUGACACGCCUCAUGUGCGUAGUAACAACUCAGACUAGGAAAUGGGUCAAAAUUGUCCAUUUACAAAGAAAUUAAAUAGUUCUGUGGGGUGAUAGAACACUUUAAAAAUUAAGGUGUCUUAAUACAAAUACAGGACAACUUUGAUGGUGUCUUU	**195**	19,487179	35,897436	16,410256	28,205128	35,897436	64,102564	0,7857143	1,1875	-51,3	-44,6	0,006958	21	-26,307692	-0,7328571
spiLA0480-MIR6230-2	AGCGCACAUCGAGACACCUCAACUUGGUAUCAAAUGAACACUAAACACUUCAACUAGACCCCACUGUGUUUCAUGGACACCCUGCGUUGACAUGGCACAUAAAUUUUGGAGAUGUCUAGAUGAUCAUAUUUGUAAGUUGGAGUGUUCAUCCGAUACAGUGGAGACAAGUUGAGGUGUCUAGAUGUGCAUU	**190**	22,105263	29,473684	20,526316	27,894737	42,631579	57,368421	0,9464286	1,0769231	-70,5	-65,95	0,0107426	39	-37,105263	-0,8703704
spiLA0480-MIR6232b	GAGCUCUACAGUGCAACUUCAGCAUAAUAAAGAGUAGAGACUAAUUAAUGCCUACAUAUGUAGGGAUUAAUGAGUCUACUCUUUGCUAUACUGAAGUUGCACUGUAGAGAUA	**112**	20,535714	33,928571	16,071429	29,464286	36,607143	63,392857	0,8684211	1,2777778	-63,6	-63,3	0,161277	4,3	-56,785714	-1,5512195
spiLA0480-MIR6234b	CUUUUAAAUAAAUAAACACAUGAGUCCUACACGGCACAAUAAACGUAGGUUACCACGUAGGACAAAAAAUGACAUGUAGGACACGUGUGUUUAUUUAUUUAACU	**105**	16,190476	38,095238	17,142857	28,571429	33,333333	66,666667	0,75	0,9444444	-35,7	-30,44	0,151156	9	-34	-1,02

spiLA0480-MIR6235-1	U AAAUAUAAGUAUGUAGUUGAAAAUCAUAUAAUUAA AGCUGUUAAAAUGGGUCGGUCCAACUCAACCCAA UCCUAACGGGCUAGAGAGUUAAAUGGGUUGGGAC GGGCUGAUCCUUUUAAUUAAAGGACCUGUAAAAU AGCAAUCCAACCAAGCCCUAAGCGGGCCACGGGU UGGGAUGGGUUGACCCUUCAACGAAAAACGGACA ACAUUUUUCUCUUUGAAAGAACACGAACGUUGAU GAAUUACACAUACUUUAGUGAAUAUUUACAAAAUA AAUACAUAAUAGCC	**288**	20,138889	36,111111	18,055556	25,694444	38,194444	61,805556	0,7115385	1,1153846	-77	-69,3	0,0014187	50	-26,736111	-0,7
spiLA0480-MIR6235-2	AACAUAUUCAGUAUUUGGGUUGUUGGUUUGUAGU GUGACACUACAUGUCAGACGUCUCCGGUUCGAAC CGAAGGUCCAAAAUGGACAGUGAAAUAAAAAUAAU GUUGUCACUCAUGCUCGAACUGGAGACCCGUGAU AUGUAGUGUCAAACUCCAACCAACAGCCCAAGUA GCUAAAUAUACA	**183**	21,311475	32,240437	20,218579	26,229508	41,530055	58,469945	0,8135593	1,0540541	-87	-86,7	0,0238561	7,6	-47,540984	-1,1447368
spiLA0480-MIR6271-1	AAAUAUAUAGUUCAUGUUCAAGCUAUUGACAACCU UGAAACUAUCGUUAUAUUUGGCUAAUUAAACUUAA AUACACUCUUAAUCUUGCAACAUGCCUGAAAUACA AUUCAAAAAUUCUCGCCUAGUUUAGGAGUGUUUU CAACACUUUACUCGGCUUAGUAUUAAGAGUCACA UGCUCCUACGAGACUACUUCCGAUGUCAUGUGAC AGAACAUAGAUGUAUCUAAGUUAAUUAUUCAAGUA AAUUAAUAUUUUUAAGACUGUCAAUAGUGAGAGA UAAAACUAAUAAUU	**290**	13,793103	35,517241	16,551724	34,137931	30,344828	69,655172	0,961165	0,8333333	-67,5	-64,4	0,0001099	30	-23,275862	-0,7670455
spiLA0480-MIR6271-2	AAGUAAUGAAGCCAAGUACCUAUUUUUGCUUUGU UCCUUGUUCGAGGAAGAUAGAGAUAUAUAAUUAC UUUGGAUAUGGAAGUGGGUUUCACAUCUUUCCGG GCAUUGAAAAUUUAGAACAAGCAAGAGAUAGGGC GUGUCUUCUGUUAGAA	**152**	23,684211	30,263158	13,157895	32,894737	36,842105	63,157895	1,0869565	1,8	-39,9	-39,8	0,0089113	12	-26,25	-0,7125
spiLA0480-MIR6273	UAAUUUUCUACCCCUUUUGGUCUAUGUGGCAUUA UCUUGUGGGCCCAACGCUGUUUGACUUUUUUUUU CAAACUAGUGUCACGUAGGCAGAAAAGGGGUAGA AAAUUA	**108**	21,296296	24,074074	17,592593	37,037037	38,888889	61,111111	1,5384615	1,2105263	-49	-49	0,219407	5,7	-45,37037	-1,1666667
spiLA0480-MIR6281	UACAUUUAUGUUUGUACUCCCUCUAUCCCUACUU ACUUGUCCAUAUUUUCUCUUUUAAAUGUCCCCAU UUGCUUGUCCAUUUUGACAAAUUAAGAAAGGAAA AAAUUGUUUUUCCUAUUAUACCCUCAUUUAAACUU AUUGAAAAUUUCUAAGUUUUAAUUCAUCCUUUCU GAAACCAUAUUUAAUAAAGGUAAAACUGUAAUUAC UAUGUUAAUUAUUGUUAUCUUAAGAUGUGUCCCU UUUCUAAAGUGGACAACUAAAUAGGGACAGAUGG AGUAUUAAGUGAGAGAGAGAGAGAGUGACGAACA AGAUCAG	**315**	14,285714	32,380952	15,873016	37,460317	30,15873	69,84127	1,1568627	0,9	-75,1	-64,8	1,30E-05	59	-23,84127	-0,7905263
spiLA0480-MIR6293	GACGACAACAGCAAUAACAUAUCCAGUGAAAUCCC ACAAGUGGGAUCAGGGGCUGCGAGAAUAAGGCAG ACAAUAGAAAAGGUUACCUAGUAUUUUUAUGUUA CUGUUGGGAUUUGAACCUUGGUUUUCAAGAUUUG CACUCACAUUACUGAUUUUUUUUUUUGAGUCGAG UAUCUGUUGGAAACAACCUCUCUAUCCCGUAAGA GGUAGAUGACUAGAGAUAAAGUCUGCGGUACAUC CUACCUUCCCUAAACCGCACUUGUAGGAUCACAC UAGGUAUAUAUUAUUGUUGCAGUCCAC	**300**	20,666667	29,666667	19,666667	30	40,333333	59,666667	1,011236	1,0508475	-87,7	-83,5	0,0002776	42	-29,233333	-0,7247934
spiLA0480-MIR6299	GAGAUUUUGGCAGGGAAGUAAUUUUAUUGUAUAA UCAUAAGUGUAUAAGACGGAGAUAUAUGUAUUUG CAUAUGUAUAUACAAUUUUCUCUCACUUUAUACAA UUAGAAACACACUUUAUACAAUUCUAUUGUAUGAA GCGAGAGAGGCGAGCGAAGAAAGCGAGCGAGAGU GGCAAGUGAAAAUAUGCGGGAGAGAGGGACUGAC AAACAGUUUGCUAUGAAACACAAAAUAAAUUAAAC GGUAGCUACUAUAUUUAUUUUAUAUUAUUAGUUU GUCAUUAUUUAUAUAUAAUUAUCCCUUAAUCAAAA UGAU	**314**	19,10828	36,942675	11,464968	32,484076	30,573248	69,426752	0,8793103	1,6666667	-67,3	-55,96	3,73E-05	62	-21,433121	-0,7010417
spiLA0480-MIR6429	AAUCUUGAUUGCGUGUUUUUACUUGUGAGUUCCU UUCUACUGCUACAUAAGCUGAAGAAGUAGCUAUU GUGUUACAGAUCAAACCACACAUUCUAUCGUCAAA	**157**	15,923567	35,031847	19,745223	29,299363	35,66879	64,33121	0,8363636	0,8064516	-67,9	-67,9	0,152976	12	-43,248408	-1,2125

spiLA0480-MIR6447	UUUAAACAGUAGUAGUAGAAAGGAACUCACAAGUAAAAACACCCAAUCCAGCAAUAUGAAGAGUUCUGACUUUUAUGAAAGGUUGUGACUUUUAUGAAAGUUGCGACUUUUAUGAAAAGUUGUGACUUUUAUGGAAAGUUGAACUUUUAUGAAAGAUGACGACUAUUCCGAAAGAAUUUAUGGACUUCUUCUUC	**161**	21,118012	29,813665	10,559006	38,509317	31,677019	68,322981	1,2916667	2	-60	-58	0,0163106	16	-37,267081	-1,1764706
spiLA0480-MIR6458	UGACAAUUAUGUGAUUAAUGAUUAAGGAUUGUGGAGUUGCCCUCAAGUUUAUAAGUUGACAGUUUGGUCCACUGAAUUAAAUAAAGGAUAAAAGGGUAACUUCACAAUGCCUAAUUUAACCAACUAUUGGUG	**132**	20,454545	34,090909	12,878788	32,575758	33,333333	66,666667	0,9555556	1,5882353	-35,5	-30,9	0,0119964	26	-26,893939	-0,8068182
spiLA0480-MIR6459a	UAUAUUUCGGAAACAAAAAAAUCGAAAAAUAAGUUACCUUGUUGAAAUGACUGGGAUCAACAUUGUCAUCGAGGGAAUGAACAGCCUCAAGCAAAAAUCUGAUCCCAGUCAUUUCGACAAGGUAACUUAUUUUUUGAUUUUUUUUUGUUUCCGAAAUGUA	**160**	16,875	35	15,625	32,5	32,5	67,5	0,9285714	1,08	-89,5	-89,5	0,0359536	8,3	-55,9375	-1,7211538
spiLA0480-MIR6464	UAACAUAAUACAAAAGUGCCCGAAGUCAUUACCUUAACCGCAAGGAGGGGGAUGCCGAAGGCAGGGCUAGUGACUGGAGUGAAGUCGUAACAAGGUAGCCGUACUGGAAGGUGCGGCUGGAUCACCUCCUUUUCAGGGAGAGCUAAUGCUUGUUGGGUAUUUUGAUUUGACA	**172**	30,232558	27,325581	18,604651	23,837209	48,837209	51,162791	0,8723404	1,625	-58,9	-54	0,0073321	23	-34,244186	-0,7011905
spiLA0480-MIR6469	GGCUAAUGUAAGUGCCAUUAACUUUAAGCGAGAGAUUAAUUAGUGGCUGAUUAGUGGGCCCCACCACUUAUAAUUAGUGGCUGAUUAGGAUUAAUU	**112**	22,321429	30,357143	14,285714	33,035714	36,607143	63,392857	1,0882353	1,5625	-31,7	-31	0,123597	9,8	-28,303571	-0,7731707
spiLA0480-MIR6483	UUUAUCCAUGUGUCAAUUAAUCAAUGGAGGGUCACCCAACUAUUGUUGGUUGGACCUCUCCCAUUGUAAAUUUUUUCAUGAGAUGCA	**87**	18,390805	25,287356	19,54023	36,781609	37,931034	62,068966	1,4545455	0,9411765	-27,5	-27,5	0,0376586	8,6	-31,609195	-0,8333333
spiLA0480-MIR7122	UAUAUACAGAGAAACCGCUGUCGAUUAUAAUGAGAAAUUCGGUGUUUCUCAUACUCCACAGCGUUUUUCUGUAUAACC	**78**	16,666667	29,487179	20,512821	33,333333	37,179487	62,820513	1,1304348	0,8125	-31,5	-31,5	0,154352	3,7	-40,384615	-1,0862069
spiLA0480-MIR7130	UUUGUUGGGACUCUACAAGAUGCGUUCAAUUUGAGUUGGGAAUCUACAAAUUGUGUUCAACUCAAAUUAGGAUUCUUAGAGUCUACUCAACCCC	**94**	19,148936	27,659574	19,148936	34,042553	38,297872	61,702128	1,2307692	1	-28,3	-28,3	0,0792231	8,7	-30,106383	-0,7861111
spiLA0480-MIR7484k	UUCAAACCAAAGCCUAUAAUUCCUCCUCUUGCCAUUUACAAUUAAGACCUUUUCCAUCAAUCUCAAGAGAGGUAUGUUUCUAUGUAUUUGGCGUUAAUUUUUCUUGAAUCAUUUAUGUGAGAUAUCACAUUUAGAAUAAACAAAAUUUCUAAAUGAAAUCAAAGACCAGUGUUGCAUAUUGGUCGGUUUGGUUCGGUUUUGAAAUUUAUUGGGUUGACUUAUUGGUUAUCGAUUUGUAGAGAUGCUAAAAAGUUGUAGAACGACUAAGAUCUUGACUUAUCGGUUAUUGGUUUAUC	**297**	17,508418	29,62963	14,478114	38,383838	31,986532	68,013468	1,2954545	1,2093023	-70	-65	0,0001145	57	-23,569024	-0,7368421
spiLA0480-MIR7486b	CACCCCACACACACUACUUAAUAGUGUGUCUUUUGAAGGUAUAUAUGUGUCCACGUGGACAUCAUAAAUAUUUCAUAAUUAUAAAUAGUAGUGUGUCCACGUGGGCACAUAUAUACCUUUAAAAUACACUAUUAAAUAGUGCAUGGGGAUU	**151**	16,556291	33,112583	17,880795	32,450331	34,437086	65,562914	0,98	0,9259259	-79,5	-79,5	0,108194	7,8	-52,649007	-1,5288462
spiLA0480-MIR7486c	CCACCCUCCUACAAUUUUUAGUAGAGUAUGUUAAACGUAUAUAUGUGUCCACGUGGAUAUGAAAAGUCCACGUGGGCACAUAUAUAUCUUUAAAAUACAGUUUUAAAAUAGUUCCGAGGGCAU	**122**	18,032787	31,967213	18,032787	31,967213	36,065574	63,934426	1	1	-51	-51	0,32761	6,6	-41,803279	-1,1590909
spiLA0480-MIR7504b	AUGUAAAUAACAAAAGAAUUUACACAUAUAUGAGUCGGAUUAGGGGCAUAAUUGAACCAUUUAAAAGACGGUCGUAUAUGUGUUUUAAAAUUGGGUCGGAUAGUUAGGGCAUAAGUGACCCCUUUCCCUUUUAAUGUAAAUGUCAAAUGAUAAUAUAUAUAAAUGAUGUGAAAUCUCAUUUGGCAUUUAAAG	**192**	19,270833	36,458333	11,458333	32,8125	30,729167	69,270833	0,9	1,6818182	-43,5	-42,6	0,0025344	31	-22,65625	-0,7372881
spiLA0480-MIR7504c	CCUCUCUCACUUUAUGUACAGACACAAAUGUAUAAAAUGUGUUUGUAUUUGUAUAAAAUGAGAGAAAAUUGUAUUUAUACAUCUCUUUUCGUUUGCCUAUCUGUCCUAAAAAUCUCGCUCGUUACUCUCACUCGUCUCUCUCACUUUAUACAAACACAAAUGUAUAAAAUUACGUUUAUGUUUGUAUAAAGCGAGAGUAA	**200**	12,5	31,5	18,5	37,5	31	69	1,1904762	0,6756757	-53,4	-53,4	0,0678458	12	-26,7	-0,8612903
spiLA0480-	AUAAAGUUGAACAAGUAAACACAUGAGUCCUACAU	**125**	16	42,4	15,2	26,4	31,2	68,8	0,6226415	1,0526316	-	-41,44	0,0448591	8,6	-33,776	-

MIR7504f	GACAUUAUACACGUAAGACACCACUAGGAUAAAAA AAAAUGACAUAUAAGAUGUCAUGAAGGACAUGUG UGUCUAUAUGUUCAACUUUAU										42,2					1,0825641
spiLA0480-MIR7504g	GUUCUAGUUUGCCUUUCGGGGAAGAAAUUUGAUU UUCCAUCUUGAAGGUUUACCAUGAAAUAGUCAUU CUUGUCUUGAAUGUUUGACUGACCUCUGCUUAUU UCAUGGGCAAACUUUCAAGACGAAAAAACAAGUUU CUUUUCCAAGAGGCAAACAAGGUC	**161**	19,254658	27,950311	18,012422	34,782609	37,267081	62,732919	1,2444444	1,0689655	-64,5	-62,3	0,016799	15	-40,062112	-1,075
spiLA0480-MIR7504j	AAAGCCCCCUAACCUAUAUCCGGAUUUCCAACAAC UUCACUUGAGUCUUAUCACCCUGUGAACUAUUUA AAACUGAAAUUCCAUCUCCCUGGAGGUGAUAGGA CUCAAGUGAAGUUGAAGAGUGUGGUUGAAAAUCC GGAUAUAAGUUAGGGGGCUUU	**158**	20,886076	29,746835	20,886076	28,481013	41,772152	58,227848	0,9574468	1	-83,9	-80	0,0423929	9	-53,101266	-1,2712121
spiLA0480-MIR7508	AAUAAAAGUUUGUUUAUAUACCAAUAUUCUUCAAA AUUGAUAAGUAGUUCAAAGUGGAAGUUGCGCUUU CCAACCUUUAGGAGGAAUAGCAAAAAAAGUAGCC GUAAGAGUGAAGAAGGCGAAAAAAGCUAUUCAUG GCCAAAGAGGAGAAAUGGUGAAGCAUUGAUAGGA AUAAUUAUCAACAAGAGGAAGAAGGUAUAAAAAUA UCUUUUAUU	**215**	21,395349	41,860465	10,697674	26,046512	32,093023	67,906977	0,6222222	2	-50	-48,9	0,0113724	21	-23,255814	-0,7246377
spiLA0480-MIR7531	CAUCCUAAAUUAUUCGCUCUAUUUAUUCUUUACA UUUUUCUUUUUCAUUCUCCAUUCAACUUUCUUUU UGGAGAGGCACCAACAACGGAGAAUGAGAAAAAA AUGUAAGUGAUGCAUCAGACUUAGAAAAUCUUAG GCCA	**140**	13,571429	31,428571	19,285714	35,714286	32,857143	67,142857	1,1363636	0,7037037	-34	-32,9	0,0289558	9,6	-24,285714	-0,7391304
spiLA0480-MIR7533b	UCAACUUGUCUUACUCUAUUUUCCUAAAAAAAGAG UAGAAGAGAAAAGCUUAUUGUCUGUUUCUCCAUU GAUCUCUUGGGCUUAUCGAAGCUUCUUGAGGAG GUUAUGGAAAGAAGGUUGAGUGCUUGUAGUAAAA AAGUAUAGCAAGUCAU	**152**	21,710526	30,921053	13,815789	33,552632	35,526316	64,473684	1,0851064	1,5714286	-38,3	-33,3	0,0019567	24	-25,197368	-0,7092593
spiLA0480-MIR7533c	UUGAAAAUCGUCGGAUAAUUUAUUUAAAAGGGGG UUGAUUUAUGGGUCGGAUUAGGUGUUUAUGAGU CCGAAUAUCUUUUCAUUUUCAUAUAAAUGUCAUG UGGUUAGGUCAAAAUGACAUGGCAAAUCCAUGUG GCAUUUACAAAAAUUAAAAAUGAGUUGAAUAUGUC CAACAUGACAUCUAACGCCCAUAAGGGCAUAUUU GGACCAAAAGUUGGAUGGCGAGGGCAUGAGUGAA CCAAACUUUAAACGGAGGGUACAUUUAGACCUUU UUGAAUAGUUUAGGGGCAUAUUUGACCCUUUUCC CAUUAAAUAAUUGGACUUUUUACC	**330**	21,515152	31,515152	14,242424	32,727273	35,757576	64,242424	1,0384615	1,5106383	-87,5	-43,04	0,0002317	98	-26,515152	-0,7415254
spiLA0480-MIR7539	AUUCUCUCUCUCUCUCUCUCUCUCGCUUUACACAAA CCUAAAUUAUACAUUGUAUUUUGUAUAAUUUGUG UUUGUAUAAAACGAGAAAGAGAGAAAGACAAAAGA GAACUGGGAAGGGGUAAUGUUUGUAUUGUAUAAU UAUAAGGAUAUCGGACGAAAAUAUAUGUAUUUGC AUGUUUGUAAUAAUUUUCUCUCGCUUUAUACAAA CAGAAACACAAUUUAUAAAUUUCUGAUUGUAUAAA GCGAGAGAGACAGCGACAAAGGGA	**264**	17,80303	35,984848	13,257576	32,954545	31,060606	68,939394	0,9157895	1,3428571	-83,8	-72,4	0,0015536	38	-31,742424	-1,0219512
spiLA0480-MIR7695	CCAUUUCCUUAGAACGAUUUCACAAAAUACAUAAG UUCUAAGGGAAAGGGGUUUUAUGUUCUUCAGUGA AGUCGUUUCUAAAUUCUAAGGGAAAGAGGAAAUU GGGGGAAAUUAGGGGUAAGUUUAUUAGUCUACGU GGCAUGAGUGGAACUCUAUUGGCUUAUGUGGCAU GUCAUGUGACAUUCACAUGGCAUUUAAGUGAUAU UUAACCGAUUCUGUUAAUAAAAAGAGUAUUUUUG ACCCUAUAGUUUAAGGAAAAAG	**261**	22,988506	31,800766	12,260536	32,950192	35,249042	64,750958	1,0361446	1,875	-69,4	-48,9	0,0001745	61	-26,590038	-0,7543478
spiLA0480-MIR7696b	AAUUGGCUUCAAACCACAUUUAUGUCCUUCAACU UUGGAUGUGCACAAAUAGACACUUAAACCUGUAU AGAGUUGAACAAAUAGACACACAUGUCCUACAUAU CAUUUUUCGUCCUACGUGGUGUCCUACGUGUAUU GUGUCAUGUAGGACUUAUGUGUUUAUUUAUUUAA AAAUUGGAUAGUUAAAGUGUCUGUUUGUGCAUUA UGAAAAAUUGAAGGUCUAAGUUUUGAAGCCAGGU UUUUGAUGGUUUAAGGCUUUCAAGUUUCGUUGUG	**239**	18,828452	29,707113	15,481172	35,983264	34,309623	65,690377	1,2112676	1,2162162	-89,9	-88	0,0025641	15	-37,615063	-1,0963415
spiLA0480-MIR7696d-1	UGCAUCGUCUCCUAAAGGUCCAUUUUAUGUUUUA AUUGGGUUGAUUUAUAGCCAGUGAAUUAUGAAUU	**240**	18,333333	27,5	14,583333	39,583333	32,916667	67,083333	1,4393939	1,2571429	-58,5	-53,5	0,0009084	41	-24,375	-0,7405063

spiLA0480-MIR7696d-2	GUGACUUCCAAGGAAGGAGCUUUUUUUAUUCUAAUACCAUACAAGUCAAUGGUAGAGGUUCUCUCUUUUUUGAAUUAUGAGUACUUGAAACUCAAAUAGCUUCCAACGGAAUUUGGAAAACUAUUUAUAACAUCAUUC	**98**	17,346939	34,693878	15,306122	32,653061	32,653061	67,346939	0,9411765	1,1333333	-30,5	-29,7	0,0335336	9,5	-31,122449	-0,953125
spiLA0480-MIR7697	AGCACAUGAUACAUGUGUGUUACGUUACCCAAAAUAUACAUUUGUGUUUUGAAUUAAAAGCACAUGAUACAUUGGCUAAAGCAUAUGUAUCAUGUACG	**127**	19,685039	29,92126	22,834646	27,559055	42,519685	57,480315	0,9210526	0,862069	-78,2	-78,2	0,113012	5,7	-61,574803	-1,4481481
spiLA0480-MIR7699	UAUAUUCAGCCCAUACAAAUCCGAUCAAAUCCAAUGUACAAGCAUAGCACAGGAAAUAGGCGUAUGACCCAAUCUCCUGUGCUAUGCUUGUACAUUCGAUUUGAUCGGAUUUGCAUGGGCGUAUGAC	**88**	15,909091	36,363636	17,045455	30,681818	32,954545	67,045455	0,84375	0,9333333	-24,9	-24,9	0,337585	4	-28,295455	-0,8586207
spiLA0480-MIR7708a	UAACUUAAUCCAUGGAUUAGUUAUACCUCAUACAAAGUCUUAUUUUAUCCCUAGGAAAGGGAAGGAUAGCUAAUCCAAGAUUUAGCAA	**92**	20,652174	29,347826	14,130435	35,869565	34,782609	65,217391	1,2222222	1,4615385	-23	-23	0,294942	4,7	-25	-0,71875
spiLA0480-MIR7710	AGCCCACGACUCUUAAGAUAAUGGUAUUGUACUAAGGCGAAUUUCAAUUUUCUAUUGAAACAAUUUCUUAGUCAUUAAGUUAGUGGUGGUGG	**206**	13,592233	33,495146	19,902913	33,009709	33,495146	66,504854	0,9855072	0,6829268	-63,4	-63,4	0,0254407	15	-30,776699	-0,9188406
spiLA0480-MIR7711-1	CAGUCCUAGAGUUUAAAUUAAAGAUGUUGGUGUCAACUCAUAAAAUUUGGGAUUAAAUCUAUCCUAUAUUUGGUUGAGGGUAUUCCCUAAUACCAUGAUAAAUCCUGGAUAACCUGACUUUGACACCUUAACUCCAUACUCCUUCAUAACCCACAAACUUAAUUUAAAAUUUGACAUCAACAUCUUUAAUUUAAACGCUAGGAGCGAAUAUAGAAAUCGCUGCCUCAGCAACGAUUUAUAAAUUAUUAUUUUUUUUAAUAAAUCGCUGCCCUGGUAAGGUUAUCCUUGCUGCUGACGAGUCUACUGGUACAAUUGGCAAGCAUCUAUCCAGCAUUAAUGUUGAGAAUGUCGAGUCAAACAGGAGGACUCUUCGAGAGUUGCUCUUCUGCGCACCUGGUGCUCUUCAGUACCUUAGUGAAAUCAUCUUGUUCGAGGAAACCCUUUAUCAGAAGACAACAACUGGUACGUUUAUAUGAAUUCUAAUGUCUAAUUUUUUUUUUAAAAAAAAUUGCUGUCUCAGCAGCGAUUUCUAUAUU	**329**	18,237082	28,571429	19,148936	34,042553	37,386018	62,613982	1,1914894	0,952381	-93,4	-81,8	7,18E-05	84	-28,389058	-0,7593496
spiLA0480-MIR7711-2	AAGUGUUAAUAAGCCAAUUUGACCAGCUUAUAAGCUUAGUCAAACACCCUCUAAGCUUAUAAGCUGGUCAAACUAGCUUAUAAGCAAUU	**89**	14,606742	35,955056	20,224719	29,213483	34,831461	65,168539	0,8125	0,7222222	-43,6	-43,6	0,49261	1,5	-48,988764	-1,4064516
spiLA0480-MIR7722	ACAAAAAAGAAAAAAAGGAUACGUGUGAGGAGGAUCAAAUAUACCCACUAUAUGGAUUUUUAUUUUUUCACGUCCGUUAGAGGAAAAAGGUAUAUAUGAGCCAUUUGUAUAAUAGUUGGGGUAUAUAUGAACCACUUUCAUAACGAGAGAUAUAUCAACUCUAAAUGACAAAGUGGAGGGGAAUGUUAGGCCCUUUUCCCUAUUAAUUAUACUUAAUAAAAUAUUUCAGUUCGAUUGAUUCGGUUGUAUUGCCUCCUCCCCGUACUUUUCUUGGUUUUCAC	**281**	18,505338	32,384342	15,658363	33,451957	34,163701	65,836299	1,032967	1,1818182	-68,1	-64,8	0,0024724	46	-24,234875	-0,709375
spiLA0480-MIR7725b	GAUUAAGUCAUUAAGGUUGACCCUAAAAUCUUAUCCACCAUCCCUUAGCUUAAUGAACAAGCUAUUCUUUAAUUAGGGAAUCGAAAACCAAUUUCCUAUUUAAAGAAUAGUUGGCUCAUUAGGUUAAAGGGUGGUGGAUAAGAUUUUAGGAGUAAUUUUCAGAUAUUUAGUG	**172**	18,604651	33,139535	13,953488	34,302326	32,55814	67,44186	1,0350877	1,3333333	-80,6	-78,5	0,0375707	10	-46,860465	-1,4392857
spiLA0480-MIR7727	GUACAAAACCAAACCAAAAUGCAAACCGAGUCAGAUCGAAAAAAACCCGACUAGUGGUUUAGUUUGACUUGGUUUGGUGUUGGAA	**85**	22,352941	36,470588	17,647059	23,529412	40	60	0,6451613	1,2666667	-26,9	-24,9	0,2419	9,6	-31,647059	-0,7911765
spiLA0480-MIR7732	AUUUCUUUGUACAAGGAUCACAAUUUUCUGAUCUUUCCCUAGCUGAUGAUAACUGGGAACUAGAUAUUGAAGGAUAUUGAUUACUAAUCUAUUUGUAAUACUUUUUGCAGUAUGGCAGGCGACGAGCCUCCGCCAUGGUCACAUAUUCGUGGUCGUGGAGGAAGAAGUAGAGGAAGGGGAAGAUCAUCCUCUUCCAAGUCUAGAAGAUCAUCAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCAACUCAAAGAUUA	**274**	20,437956	29,927007	17,883212	31,751825	38,321168	61,678832	1,0609756	1,1428571	-79,3	-73,9	0,0001701	48	-28,941606	-0,7552381
spiLA0480-MIR7745	CUGUGAGUAACAUUUUACUCCUAAAACGUUACUGUGAGUAACGUCUUACUCUUAAAACGUUACUCACA	**131**	16,030534	35,114504	16,793893	32,061069	32,824427	67,175573	0,9130435	0,9545455	-75,3	-75,3	0,41652	1,5	-57,480916	-1,7511628

spiLA0480-MIR7748a	GUAAGGUUUUAGGAGUAAAACGUUACUCAAAAAAACGUUUUAGGAGUAAAACGUUACUCAUAUCGGUGGAUAUGUUGCUGAGAAAAGAGAAAAGCACAUGAAUAUUUUUUCACCUUUUGGAUGAAGCAGUAAUCAUGGUGAUUGUUUUUAGUUCUGCUUAACAUUUCACAUACUUUGUGAUACUGUGGAUAUGUUACUGAGAAAAGAGAAAAGGACAUGAAUAUUUUUUCACCUUUUGGAUGAAGCAGUAAUCAUGGUGAUUGUUUUUGUUCUGCUUAACAUUUCACAUAC	**227**	20,704846	29,955947	12,77533	36,563877	33,480176	66,519824	1,2205882	1,6206897	-56,7	-34,87	0,0018042	86	-24,977974	-0,7460526
spiLA0480-MIR7755	UUCAUAUAAUGAACUGUCUUUAGGAUUAUCCUUUAUAUUUAUAGAGGAUGAAGCUAAUGAAGAGGCUUCGCCAAUCUUUGAAUUAAUCAAAGUUUUACUUCCUAACUGUAUAACAGGAAAGGAAGAGUCAUAUGACGACCUUGUAGAUUGUAAAGAGGACGAUCUUCCCCUUCCUCGUUGAUUUUUUUCCAACGACUACGAACAUGUUGACAUGGCGGAGGGUCAGUACCUCCAUACUGCAAAAUGAAUAACUCUAAUCAUAAAAACAUCCUGAUAUAUC	**280**	17,5	32,5	18,571429	31,428571	36,071429	63,928571	0,967033	0,9423077	-71,1	-70,5	0,0006428	25	-25,392857	-0,7039604
spiLA0480-MIR7756	UUUUUGGCAUAGUUUUGAACUGUGAUAAGAAACUGAAGCCAAGGCUGGAUAUUUUGGCAUAGUUUUGAACUGUGGUAAGAAACUGAAGCCAAGGC	**95**	26,315789	30,526316	12,631579	30,526316	38,947368	61,052632	1	2,0833333	-27,7	-24,3	0,0672969	33	-29,157895	-0,7486486
spiLA0480-MIR7764	UGUUAAUUCUUUAGAAUACCUUUGUUAAUUAUCCAUUAAUAUUAAGAAGGGGGUGUGACCAGUAGCUUAGGAAGUUUGUUUUAGUUAUUGAAUGUGCUAAGUAUGAACGAAAACCAUAAUCGGAUUAUUAGUGGUGUCGUGUUGGUGCUUGGGCUGUUUUGAUUAAAGCAAACUGCGGGAAAAUUCUAUUUUGGCGUUAUGUAUAUGUUAAAUAUGUAUGAGUAUAUACUCCAAAGGAUGAAUACGAUAAGGUAGAUGUGUUGAGAAUUAUAA	**273**	23,443223	30,769231	9,1575092	36,630037	32,600733	67,399267	1,1904762	2,56	-66,1	-52,9	7,33E-05	51	-24,212454	-0,7426966
spiLA0480-MIR7774	UGAGCAGAAAAAUGGAUUUCGAAAAUAAUUUUUCACGAAUUAGUCCUCUUUUUUUAUGGUGAGAAUUAUCAACUAUGGUCUGUGAGAAUGGAAACUUACUUGGAGGUUCUUGAUCUUUGAGAAGUCGUGGAAGAGGAUUAUGAAAUCAAUUUACUGCGAA	**160**	22,5	31,875	11,25	34,375	33,75	66,25	1,0784314	2	-41	-40,7	0,0118321	25	-25,625	-0,7592593
spiLA0480-MIR779	GUUAAGCUUAUCUGCAUCGAGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUGAAACUUGUUGUUCAUUUUACUUCAUUAAAUCACAUAAUAAUGGAAAUUGCAUUGGCUUGGUGUAAACAUUCGAUGCGGGUAAGUUGUU	**146**	19,863014	28,082192	15,753425	36,30137	35,616438	64,383562	1,2926829	1,2608696	-64,5	-61,5	0,0497348	10	-44,178082	-1,2403846
spiLA0480-MIR7803b	CAUACACGUGUCAUAAUCUUAUCCACCGACCUGACAUUGGAUCGAUGGAUAAGAUUGUAUCACGUGUCCC	**70**	18,571429	27,142857	25,714286	28,571429	44,285714	55,714286	1,0526316	0,7222222	-33,5	-33,5	0,736678	1	-47,857143	-1,0806452
spiLA0480-MIR7804-1	GAUAUUUGUAUGAUUACUAAUCUAUUUGUUAUAUCUUUUGUAGUAUGGAAGGCGACGAGCCUCCGCCAUGGUCACAUAUUUGUGGUCGUGGGGGAAGAGGUAGAGGAAGGGGAAGAUCAUCCUCUUCACAGUCUAGAAGAUUAUUAUACGAUUCUUCCUUUCCUGUUAUACAGUUAGGAAGUAAAACUUUAAUCGAAUCAACGAUUGGCGAAGCCUCCUAAUCAGCUUCAUCCUCUGUAAAUUUAAAAGAUAUUCCUAAGGACAGUUCAUUAUAUGAACAAAUUUA	**286**	20,27972	30,06993	16,783217	32,867133	37,062937	62,937063	1,0930233	1,2083333	-77	-48,3	0,0003561	75	-26,923077	-0,7264151
spiLA0480-MIR7804-2	CUCGAGUUGAUUUCUCAGAUGGUCACUCGACUAAUAGCUGUAUUAUCUUAGAAAGUCACUUUUUUGGUUGAAGAAAAGCGGAAUCAAGAAGAGAAGUGACUUUUUUUAUAUAAUGACUAUUAAUCGAGUGAACAUCUGAGCAAUCAAUUCCGU	**154**	19,480519	31,818182	14,935065	33,766234	34,415584	65,584416	1,0612245	1,3043478	-62,9	-62,9	0,12587	10	-40,844156	-1,1867925
spiLA0480-MIR7805	GCCCUGGUAAUUGGAUUUGGUGUAAUUACAUUGUCUGUCCUAUUUAGUUUGACAGGGUAAUUACAUGGUCAGCAGGUAUUUGGUGUAAUUGACAGUGAGUAAUUACACUCUCCAAUUCACAGUCA	**125**	22,4	25,6	16	36	38,4	61,6	1,40625	1,4	-35,5	-27,25	0,0138822	27	-28,4	-0,7395833
spiLA0480-MIR7813	CAUUAAUUCAGGGAUUAGUAAUGCAUGGAUUGGUAAUGCAAGGAUUAGUAAUGCAGAUAUUAUUU	**95**	25,263158	33,684211	7,3684211	33,684211	32,631579	67,368421	1	3,4285714	-25,2	-22	0,458311	4,9	-26,526316	-0,8129032
spiLA0480-MIR7816	UGUAUAACUAAUACCCACAUAACUUUUUCCACCUUCUACCCUGCAUAUCUGUAUACAUAGAUUCCCUCA	**95**	9,4736842	29,473684	22,105263	38,947368	31,578947	68,421053	1,3214286	0,4285714	-22,9	-22,9	0,255038	2,9	-24,105263	-0,7633333

spiLA0480-MIR781b	UAAGUUAUGUUGGUAUUAAUUAUGUACGUGAAAAGGGAAAAAUAGAAGAAAGAGAUGUUAGAGUUAUGUGGAUAAUUUGGAGAUUGUAUAAAAAUAUUAAGGGCAAAAAGGUAAAAAUGUGGUCAACUUAAAACAGCUUAUAAGCUGGAAAAAAAAAAGCACCCCUACCCCAGCUUUUAACUUUUAGCUUAAAAUAAGUUUUUUUUUAACUUAAAAUAAGUUGUUUUGAGUAUUGCCAAACAGGUAAAUAAGUCAAAAAUCAGCUUUUAAGUCAGUUUGACCAGCUUUUAAGCUGAGCCAAAUAUGCUCUUAAUCCCUUCUUCUCUUUUUUUUCUAU	**312**	16,666667	37,179487	13,461538	32,692308	30,128205	69,871795	0,8793103	1,2380952	-74,2	-66,6	0,00058	55	-23,782051	-0,7893617
spiLA0480-MIR7822-1	GGGACACGUGACACAAUCUUAUUCGUCGAUUUGAUAUUUAAUAAAUGUCGAGUCGAUGGAUAAGAUUAUGACACAUGUAUG	**81**	22,222222	32,098765	13,580247	32,098765	35,802469	64,197531	1	1,6363636	-36,5	-36,5	0,451545	2	-45,061728	-1,2586207
spiLA0480-MIR7822-2	UCAAAUGGGCGGAGUAGGUUUGAAAUUGAAAAUAUUAAAAUGGGUUUAAUAUAAAUCGGAUUGGGUCUUGACCUAUCCAAAUUUAUUUUGGGCUCGAAUGGGCUAAAAAACGGGUUGGGUCUUGACCUGUUCAGUUUAACCCGAUUAAUCUCAAUAAUUUAACAUAUUGAUAUUUAACUUUUUAUAAUCACAAUUUGAAUUUCCGCUCAUUAAU	**214**	18,224299	31,775701	13,551402	36,448598	31,775701	68,224299	1,1470588	1,3448276	-54,6	-38,3	9,56E-05	54	-25,514019	-0,8029412
spiLA0480-MIR7823	AAAUAAUGCAUGCAUUAGCUUGAUGUAUUAGUAGUACCUUGUUUGGUACACUUUUCUAACCUAUGCAUCACCAAUGCUUGUAUUAGUA	**88**	15,909091	28,409091	17,045455	38,636364	32,954545	67,045455	1,36	0,9333333	-25	-23,9	0,203199	5,5	-28,409091	-0,862069
spiLA0480-MIR7825	UAUUAUAGUCUGUAUGUAAAACUAAAAAUAUGAAAUAAACAGUUGAUUUUUAUAUCCUUUUUCUUAAAACUUCAUUAAUAGUCGUAAGUGAAGGUUGCAAUCUUCAGCCUCAGGGAGGAACAGUAACAGAGUAGCCAAAGACUGAGGUCGUUAGGGUGAAACAUUGUUCAUGGCCUAUAGGGAGAACUACUGCGGUAGUGAUAAAGACUAUUGAUCGACAAAAGAGAAGAAAGGUAUACACGCAAACUUUUUUUAAAAUAUUAUUAAAUUUACAAAUAUACUAUAUGU	**288**	18,75	37,5	12,847222	30,902778	31,597222	68,402778	0,8240741	1,4594595	-64,4	-57,6	0,0011705	40	-22,361111	-0,7076923
spiLA0480-MIR7840	GGCAAUGGAAUAGGUGGUCACUAGAAUGCAUUAAUUGCACUCCAAUUAUAGGAGUAAUUAAUGUCAUUGGAAUUGUCUAAACAAUUAAUUGACUUUUUAAAAAAAUGAAAACAAACGGUCGUAUAUGUGUUUUAAAAUUGGGUCGGAUAAUUAGGGCAUAAGUGACCCCUUUCUCUUUUAA	**181**	19,337017	34,80663	12,707182	33,149171	32,044199	67,955801	0,952381	1,5217391	-41,5	-39,7	0,0027548	35	-22,928177	-0,7155172
spiLA0480-MIR7980b-1	AUAUGGUAUCACAUCUCAUUAUAUGAAAUCAUGAGACGGAAUUAACGUAAAAUCGAAUGUCCAAACGCUGAUUUCAUCUCAUAUCACAA	**110**	15,454545	36,363636	16,363636	31,818182	31,818182	68,181818	0,875	0,9444444	-32,8	-32,8	0,207741	5,3	-29,818182	-0,9371429
spiLA0480-MIR7980b-2	UCUCAUGAUAUGAAAUCAUGAGAUGGAAUUAACGUGAAAUUAUAUGUCCAAACGCUGAUUUCAUCUCAUGAUUUCAUAUUGCAUGUCC	**88**	15,909091	31,818182	17,045455	35,227273	32,954545	67,045455	1,1071429	0,9333333	-36,4	-36,4	0,375896	3,3	-41,363636	-1,2551724
spiLA0480-MIR7980b-3	CACAUCUCAUGAGAUGGAAUCAGCGUGAAAUCGCAUGUCCAAACGCUGAUUCCAUCUCAUGAUAUCAUAUAUAUAAUAUUAGGGGUAAGAUAUAAGUACCUCUUAGAUUAUGAUCGAAAUUUGAGAUAUCUUAAUUAAACUAAAUUCAUAUUAUCUCCUCACGCAGUUGAGGCGCGUGAGAGAUAUUUUGAUGCCAUGUAAAAGCCAAAAAGGUCUACGAAAUAACAAAACAAAUUGGUUCGGGGGUAAUAGAACCUUAAUAUAGUUAAGGUGUGUCUCUAAGUUUCAGUCAUAGUCUAGAGGAUAUUUACACCUUAUCCCUAUAAUAUUGUAGAC	**68**	17,647059	30,882353	25	26,470588	42,647059	57,352941	0,8571429	0,7058824	-34,9	-34,9	0,596211	1,4	-51,323529	-1,2034483
spiLA0480-MIR7981-10	CUAUGACCGAAAUCUCAGAGACACACCUUAACUUAACUAAGGUUCUAUUAAUCUCAACUCAUUUGUUUUGUAAUUUUGUACUGGUACACUCCGUGACUCGAGGCGCGUGAGAGAUGUUUGGAUGUCAGUGUACAGAAUUACAAAAAAAAAUGGAUUCGGGGGUAAUAGGACUUUAGUUUAGUUAAGGUCUGUCGCUCGAAUUUCGAUCAUAC	**268**	18,283582	35,447761	14,179104	32,089552	32,462687	67,537313	0,9052632	1,2894737	-86,9	-78	0,0005287	35	-32,425373	-0,9988506
spiLA0480-MIR7981-11	ACCUUAACUAAACUAAGUUUUUAUUACCCCUGAAUUUAUUUUUAGAUAAUUUUGUACACCUUUUUAGC	**211**	21,327014	28,909953	17,535545	32,227488	38,862559	61,137441	1,1147541	1,2162162	-85	-77,5	0,007145	24	-40,28436	-1,0365854
spiLA0480-MIR7981-12	UACGUGGCAUCCAAAAAUCUCCCACGCGUCUCAA	**204**	18,137255	33,823529	16,176471	31,862745	34,313725	65,686275	0,942029	1,1212121	-80,7	-80,2	0,0756256	17	-39,558824	-1,1528571

spiLA0480-MIR7981-13	UUGCGUGUAGUCACGGAGUGUGUCAAGUAACACGAAAGGUGUAUAAAAUUGGGGAAAAAAAAUAAGUUCAGGGGAUAAUAGGACCUUAGUUUAGUAAAAAUCAGAUAUUGCUGUUCUAUCAUGCAAAGUUUAGUUUCAUUUUUUAUAUGUCUUAUGUGGCACACUCCGUGACUCCACACAAUUGAUGCGUGUGGGAGAUACUUGAAAUCCAUGUAAGCUAUAAAGGUGUAUAAAUUAUAAAAAAUAAGUUCAGGGGUAAUAGGACCUUAGUUUAGUUAAGAUGUGUCUUUGAGAUUUCGGUCAUAGUCUAGCGAGGUACUUGUGCAUUUUCCCUUUACUUAUUAAAGAAGAUCUAUAGUUCUUUCUUAUGCAUUUUGCCUGAGAAUGAUAAGCAAUAUGCA	**300**	19,666667	29,333333	14,666667	36,333333	34,333333	65,666667	1,2386364	1,3409091	-75,7	-74,7	3,51E-05	36	-25,233333	-0,7349515
spiLA0480-MIR7981-14	AUUAAAUGUCAGAGAGGCACACCUUAAUUAAACUAAGGUCAUAUUACCACCUAAAUCUUUUUUUGGUAAUUUUGUGCACCUUUAUCUUAUGUGGCACGCUCCGUGACUUUAUGUAAUUGAGGCGCGUGAGAUAUUUUGAUAUCACGUAAGUAAAAAAGGUACACAAAAUGGCAAAAAAAAAAGUUCAGGGGAUAAUAGGACCUUAGUAUGGUUAAGGUGUCUCUGGAAUUUCGG	**234**	20,940171	32,478632	14,957265	31,623932	35,897436	64,102564	0,9736842	1,4	-85,5	-80,2	0,0031478	26	-36,538462	-1,0178571
spiLA0480-MIR7981-4	CUUAACUAAAGUAAGGUCCUAUUAUUCUUGAACUUAUUUUUUUUUUAAUUUUGUAAACCUUUUAUCUUACGUGGCACACUUCGUGACUUCACACAAUUGAGACGCGUGAGAGAUAUUUGGAUGCCACGUAAGCCAAAAGUGCACAAAAUUACAAAAAAUAGGUUUAGGUAAUAUGAUCUUAGUUUAGUUAAA	**193**	16,062176	32,642487	15,025907	36,26943	31,088083	68,911917	1,1111111	1,0689655	-65,6	-59	0,0027898	22	-33,989637	-1,0933333
spiLA0480-MIR7981-5	UCGAGCGACAGACCUUAACUAAACUAAAGUCCUAUUACCCCCGAAUCCAUUUUUUUUGUAAUUCUGUACACUGACAUCCAAACAUCUCUCACGCGCCUCGAGUCACGGAGUGUACCAGUACAAAAUUACAAAACAAAUGAGUUGAGAUUAAUAGAACCUUAGUUAAGUUAAGGUGUGUCUCUGAG	**185**	16,756757	32,432432	22,702703	28,108108	39,459459	60,540541	0,8666667	0,7380952	-56,5	-56,5	0,0278245	14	-30,540541	-0,7739726
spiLA0480-MIR7981-6	AUUUUAACUAAACUAAUGCCCUAUUACCACACCCCACAAACUUAUUUUUUUGUAAUUUUAUACACAUUUUUUUACGUGGCACACUGUGUGACUUCACGCAAUUGAGGCGCGUGAGAGAUAUUUGGAUGCCAUGUAAGUCAAAAAGGUGCAAAUUUUUUUCAAAUAAAGUAUUCAAGGGUAAUAGGACCUUAGUUUAAUUAAGGU	**204**	16,666667	31,862745	16,666667	34,803922	33,333333	66,666667	1,0923077	1	-53	-41,71	0,0016557	47	-25,980392	-0,7794118
spiLA0480-MIR7981-7	ACAAACAUCCCAAAGACACAUUAACUAAACUAAAGUCCUAUUACUCCCCUGAACUUUUUUUUUGUAAUUUUAUACACCUUUUGUCUUACGUGGCACACUCCAUGACUCCACACAAUUGAGGAAUGUGACAGAUAUUUGAAGGUCACGUAAGCCAAGAAGUUGCACAAAAUUACAAAAAAAAAAAGAAGUUCAGGAGGUAAUAGGACCUUAGAAUAGUUAAGGUGUGUCUUUGGGAUUUCGG	**241**	17,427386	35,26971	18,672199	28,630705	36,099585	63,900415	0,8117647	0,9333333	-93,8	-89,2	0,0002803	28	-38,921162	-1,0781609
spiLA0480-MIR7981-8	CUUAAUUAAACUAAGGUCCUAUUAUCACACCGAACUCAAUAAUUUUGUAAUUUUGUACACCUUUUAUUGGCUUACGUGACAUCCAAACAUCUUCCACACGUCUUAACUAUAUGGAGUCACAGAGUGUGCAACGUAAGCCAAAAUGUGUAUAAAAUUACAAAAGAAAAUGAGUUCAACGGGUUAAUAGGAUCUUAGUUUAGUUAAG	**205**	15,609756	35,121951	17,560976	31,707317	33,170732	66,829268	0,9027778	0,8888889	-81,3	-73,59	0,0099401	22	-39,658537	-1,1955882
spiLA0480-MIR7981-9	ACAUUUAGGAAAAAGCACAAGUACUUCCUACACUAUGAAUGAUAUCCUAGAGACAUACCUUAACUAAACUAAAGUCCUAUUCCCCCCCCCCCCAAAAAAAAGGUUUGUUUGUAAUUCGAUACACCUUUUGGCUUACAUGACACACUCCAUGACUACACACAACUAAGAUUUAUUGGAUAUGUUUGGAUGCCACAAGUGGAAAAGGUGAACAAAAUUAUAAAAAAUGGGAUCACGGGGUAUUAGGAUCUAAGUUUAGUUAACACAUGUAUAUGGGGUUUCGGUCAUAAUCUAGGUAGUACUUGUACUUUAUCUCGCUAAAAUU	**322**	16,770186	34,47205	19,254658	29,503106	36,024845	63,975155	0,8558559	0,8709677	-90,9	-68,76	0,0005698	45	-28,229814	-0,7836207
spiLA0480-MIR7981a-37	AUAUCCCUUCUCGGCCUACGUGGCACUACCUUGAAGAAAAAAGUCAACCAGCGUUGGGCCCACAAGAUAGUGUCACGUAGGCUGAAAAGGGAGAG	**95**	26,315789	30,526316	24,210526	18,947368	50,526316	49,473684	0,6206897	1,0869565	-47,5	-47,5	0,378897	4,8	-50	-0,9895833
spiLA0480-MIR7981a-	UAAUUUUCUACUCCUUUUUCGGCCUACGUGACACUAGCUUAAAAAAAGUCAACCAACGUUGGUACCACA	**107**	16,82243	35,514019	21,495327	26,168224	38,317757	61,682243	0,7368421	0,7826087	-36,6	-36,6	0,0848654	15	-34,205607	-0,8926829

38	AGAUAGUGCCACGUAGGUCAAAAAGGGACAUAAAAUUA															
spiLA0480-MIR7981a-39	UUAUAAGUAAUUUUCUACCCCUUUUCGGCUUAUGUGGCACUAGCUUGAAGAAAAAAGUAAACCAGCGUUGGGCCCACAAGAUACUGUCAUGUAGGCCGAAAAGGGGUAGAAAAUUAUUAACA	**122**	21,311475	33,606557	18,032787	27,04918	39,344262	60,655738	0,804878	1,1818182	-55,8	-54,2	0,107172	7,5	-45,737705	-1,1625
spiLA0480-MIR7981a-40	AAUUUCAGAGACACACUUAUAGUAUACUAAGGUCCUAUUACCCUCCUGAACUUAUUUUAUAAGUAAUUUUCCACCUCUUUUCGGUCUACGUGGCACUAACUUGAAGAAAAAAAGUCAAUCAACGUUGGGUCCACAAGAUAAUGCCACGUAAGUCGAAAAGGGAUAGAAAAUUAUUAAAAUAACUUUAGUAGAUAAUAGGACCUUAGUAUAGUAUAAAUAUGUCUCUGAAAAU	**234**	15,384615	37,179487	16,666667	30,769231	32,051282	67,948718	0,8275862	0,9230769	-98,3	-96,4	0,0115898	17	-42,008547	-1,3106667
spiLA0480-MIR7981a-41	UUUCCCUUUUUGGCCUACGUGGCACUACUUUGAAAAAAAAAGUCAACAAGCAUUGGGCUCACAAGAUAGUGUCACGUAGGCCGAAAAGGGGUA	**94**	23,404255	31,914894	20,212766	24,468085	43,617021	56,382979	0,7666667	1,1578947	-46,2	-42	0,0289424	12	-49,148936	-1,1268293
spiLA0480-MIR7981a-42	UUACCCCCUGAACUUAUUUUAUAAAUAAUUUUCUACCCCUUUUCGGCCUACGUGGCACUAGCUUGAAAAAAAAGUCAAUCAGCGUUGGGCCCACAAGAUAGUGUCACAUAGGUCCAAAAGAGAUAGAAAAUUAUUAUAAAACAAGUUUAGGGGGGUA	**158**	18,35443	34,810127	18,987342	27,848101	37,341772	62,658228	0,8	0,9666667	-66,1	-63,6	0,027678	12	-41,835443	-1,120339
spiLA0480-MIR7981a-43	UCCAAGGUCCUAUUACCUCCUGAACUUAUUUUAUUAAUAAUUUUAUAUCCCUUUUCGACAUACGUGGCACUAUCGUGUGGGUCCAAUACUGGUUGACUUUUUUUCAAGUUAGUACCACGUAGAUCGAAAAAGGGUAGAAAAUUACUUAUAAAAUAAGUUCAGGAGGUAAUAGGACCUUAAU	**181**	17,127072	30,939227	17,127072	34,80663	34,254144	65,745856	1,125	1	-86,6	-82	0,0140485	21	-47,845304	-1,3967742
spiLA0480-MIR7981a-44	AGUAAUUUUCUACCCCUUUUCGGCCUACAUGGUACUAGCUUGAAAAAAAAGUCAACCAGUGUCGGGCCUACAAGAUAGUGUCAUGUAGGCCGAAAAGGGGUAGAAAAUUAUU	**112**	22,321429	32,142857	18,75	26,785714	41,071429	58,928571	0,8333333	1,1904762	-61,5	-60,2	0,0901105	7,7	-54,910714	-1,3369565
spiLA0480-MIR7981a-45	UAGAUUUUUACCCCUUUUCGACCUACGUGGCACUAUCUUGUGGGCCCAACGAAGGUUGACUUUUUUUUUCAAACUAGUGUCACGUAGGCUAAAAAGGGGUAUAAAAUUAC	**110**	20	26,363636	20	33,636364	40	60	1,2758621	1	-43,5	-40,1	0,103168	13	-39,545455	-0,9886364
spiLA0480-MIR7981a-46	UGUAGGUCCUAUUAUUCCCUGAACUUAUUUUGUAAGUAAUUUUUUACUCCUUCUCGGCCUACAUGACACUAACUUGAAAAAAAAAGUCAACCAACGUUGAACCCACAAAAUAGUGUCACGUAGGCCGAAAAGGGAUAGAAAAUUAUUAAUAAAAUAAGUUCAGGGGUAAUAGGACCUUAG	**180**	17,222222	36,111111	17,777778	28,888889	35	65	0,8	0,96875	-90,5	-86,7	0,0577197	8,4	-50,277778	-1,4365079
spiLA0480-MIR7981a-47	UAUUAUUUAUCUGAACUUAUUUUAUAAGUAAUUUUUACUUCUUUUCGGCUUACGUGACACUAGUUUAAAAGAAAAAGUCAACCAGCGUUGAACCCACAAGAUAGUGCCACGUAGGCCAAAAAGGGUAGAAAAUUAUUAAUAAAAUAAGUUCAGAGAUAAUAGGA	**164**	16,463415	38,414634	14,02439	31,097561	30,487805	69,512195	0,8095238	1,173913	-60,2	-60,1	0,0117775	13	-36,707317	-1,204
spiLA0480-MIR7981a-48	AAAAUCUCAGAGACACGCUUAUAUUAUACUAAGAUCCUAUUAUCCAUGAAUCCCUUUUCGGCUUACGCGGCACUAGUUUGAAAGAAAAAGUCAACCAGCAUUGGGCCUACAAGAUAGUUUCACGUAGGCCGAAAAGGGAUAGAAUACUAUCAAUAAAAUAAGUUCAGGGGUAAUCGAACCUUAGUAUAGUAUAAAUGUGUCUCUGAGAUUUC	**212**	18,867925	34,90566	18,396226	27,830189	37,264151	62,735849	0,7972973	1,025641	-87,4	-86,1	0,0077958	17	-41,226415	-1,1063291
spiLA0480-MIR7981a-49	CUAAGGUCCUAUUACCCCCCUGAAGUUAUUUUAUAAGUAAUUUUCUACCCCUUUUAGGCCUACGUGGCACUAGUUUGAAAGAAAAAGUCAACCAGUGUUGGGCCCACAAGAUAGUGCCACGUAAGUCAAAAAGGGGUAGAAUAUUACUAAUAAAAUAAGUUCAGGGGGUAAUAAGACCUUUG	**182**	20,32967	32,967033	18,681319	28,021978	39,010989	60,989011	0,85	1,0882353	-94,5	-94,4	0,0132111	12	-51,923077	-1,3309859
spiLA0480-MIR7981a-50	CUCUACUAAAGUUCAAUUACCCUCCUAAAUUUAUUUUAAAUAUUUUUCUACCCCUUUUCGGCCUACGUGGCACUAGUUUGAAAAAUAAUGUGAACACACGUUGGACCCACAAUAUAGUCUCUCAUAAGAGGAAAAGUGGUAAAAAUUUAUUUAUAAAAUAAGUUUUAGGGGGUUAUAAAACCUUAGUAUAC	**194**	13,917526	34,536082	17,010309	34,536082	30,927835	69,072165	1	0,8181818	-59,6	-59,2	0,0080243	16	-30,721649	-0,9933333
spiLA0480-	AUUAUUUUCUACUCCUUUUCGGUCUACGUGACAC	**109**	21,100917	24,770642	19,266055	34,862385	40,366972	59,633028	1,4074074	1,0952381	-	-41,6	0,0713803	8,9	-	-

MIR7981a-51	UAUAUUGUGGGCUCAACGCUGGUUGAUUUUUUUUCAAGCUAGUGCCACGUAGGUCGAAAAGGGACAGAAAAUUAC									41,6				38,165138	0,9454545
spiLA0480-MIR7981a-52	AAGUAAUUUUCUACCCCUUUUCGACCUACGUGACACUAGGUUGAAAGAAAAAGUCAAUCAGAAUUGGGCACAAGAUAGUGCUAUGUAGGCCGAAAAGGGGUAGAAAAUUAUUA	**113**	22,123894	36,283186	15,929204	25,663717	38,053097	61,946903	0,7073171	1,3888889	-52,3	-51,6	0,221408	11	-46,283186	-1,2162791
spiLA0480-MIR7981a-53	UUAUAAUUUUUUACCCCUUUUCGGCCUACGUGGCACUAUCUUGUAGGCCCAACGAUGGUUGACUUUUUUUUCCAAACCAGUGUCACGUAGGCUAAAAAGGGAUAGAAAAUUAGUU	**115**	19,130435	26,086957	20	34,782609	39,130435	60,869565	1,3333333	0,9565217	-46,2	-41,9	0,107703	13	-40,173913	-1,0266667
spiLA0480-MIR7981a-54	AUUUAUCCCUUUUCGACCUACGUGACACUAUCUUGUGGGUCCAAUGAUGAUUGAUUUUUUUUUCAAACUAGUGUCACGUAGAUUAAAAAGGGGUAGAA	**98**	19,387755	27,55102	16,326531	36,734694	35,714286	64,285714	1,3333333	1,1875	-37	-33,5	0,0343982	11	-37,755102	-1,0571429
spiLA0480-MIR7981a-55	UUACCCUCCUGAACUUAUUUUAUUAAUAAUUUUCUACCCUUUUUUGGCCUACGUGGCACUAUCUUGUGGGCCCAAUGCUGAUUGACUUUUUUUUUUCAAGCUAGUGCCACGUAGGCUUAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUCAUGGGGGUAA	**162**	18,518519	25,925926	17,901235	37,654321	36,419753	63,580247	1,452381	1,0344828	-87,2	-87,1	0,0567597	8,6	-53,82716	-1,4779661
spiLA0480-MIR7981a-56	UAUUAUAAUUUUUUUGAGAAAUUACCUAACCGACAACUUUUCGGCCUACGUGACACUAUCUUGUGGGCCCAACGCUGGUUGACUUUUUUCUUCAAGCUAGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUACUUAUAAAUAAGUUUAGGG	**152**	19,736842	29,605263	18,421053	32,236842	38,157895	61,842105	1,0888889	1,0714286	-45,9	-45,7	0,0685278	11	-30,197368	-0,7913793
spiLA0480-MIR7981a-57	CUACCCCCUUUCCGUCUACGUUGCACUAUUUUGAGAAAAAAGUCAAUCAGCAUUGUGCCCACAAAAUAGUGCCACGUAGGCUGAAAAUGGGUAG	**94**	20,212766	29,787234	24,468085	25,531915	44,680851	55,319149	0,8571429	0,826087	-38	-37,5	0,113297	6,4	-40,425532	-0,9047619
spiLA0480-MIR7981a-58	UUUUCUACCCCUUUUCGGCCUACAUGGCACUAUCUUAUGGGCUCAGCGCGUGUUGACAAUUUUUUCAAUGAUAGUGUCACGUAGGUUGAAAAGUGGUAGAAAA	**103**	22,330097	24,271845	19,417476	33,980583	41,747573	58,252427	1,4	1,15	-49,3	-49,3	0,206231	5,4	-47,864078	-1,1465116
spiLA0480-MIR7981a-59	UGGACUUAUUUUAUAAGUAAUUUUCAACCCCUUUUCGGCCUACGUGGCACUAGCUUGAAAAAAAAGUCAACCAACAUUGGGCCCAAAAUAUACUGCCACGUGGGCCGAAAAGAGGUAGAAAAUUAUUUAUAAAAUAAGUGUA	**142**	18,309859	35,915493	18,309859	27,464789	36,619718	63,380282	0,7647059	1	-67,6	-67,4	0,102413	7,2	-47,605634	-1,3
spiLA0480-MIR7981b-22	GUCCUAUUACCUCCCUGAACUUAUUUUAUUAAUAAUUUUUUACCCCUUUUUGAGCUUACGUGACACUAUAUUGUGGGCCCAACGAUGAUUAACUUUUUUUUCGAACUAGUGCCACAUAGGCUAAAAAGGGAUAGAAAAUUACAUAUAAAAUAAGUUCAGGGGGUAAUAGAAC	**171**	15,789474	32,163743	17,54386	34,502924	33,333333	66,666667	1,0727273	0,9	-74,5	-74,5	0,238672	6,3	-43,567251	-1,3070175
spiLA0480-MIR7981b-23	AUCAACUUAUUUUAUUAAUAAUUUUUUACCCCUUUUUAGCCUACGUGACACUAUCUUGUGGGUCCAACGAUGGAUGGUUGACUUUUUUUUUCAAACUAGUGCCACGUAAGCUAAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUCAA	**149**	15,436242	31,543624	16,107383	36,912752	31,543624	68,456376	1,1702128	0,9583333	-61	-56,5	0,0742531	7	-40,939597	-1,2978723
spiLA0480-MIR7981b-24	GAACUUAUUUUAUCAAUAACUUUCUACUCCUUUUCUGCUUACGUGACACUAUCUAGUGGGUAUGACGCUGGUUGACUUUUUUUUCAAGCUAGUGUCACGUAGGUCGAAAAGGGGUAACAAAUUACUUAUAAAAUAAGAAA	**140**	17,857143	30	16,428571	35,714286	34,285714	65,714286	1,1904762	1,0869565	-51,3	-51	0,0900453	6,7	-36,642857	-1,06875
spiLA0480-MIR7981b-25	GUAAUUUUCUACCCCUUUUUUGGCUACGUGGCACUAGUUUGAAAAAAAAGUCAACCAUCGUUGGGCCCACAAGAUAGUGCCACGUAGGACGAAAAGGGGUAACAAAUGAU	**110**	22,727273	31,818182	20	25,454545	42,727273	57,272727	0,8	1,1363636	-44,3	-44,2	0,109691	9,4	-40,272727	-0,9425532
spiLA0480-MIR7981b-26	NNCGAACUUAUUUUAUAAAUAAUUUUCUACCCCUUUUUAGCCUACGUGGCACUAGUUUGAAAAAAAAGUCAACCUUCGUUGGGCCCACAAGAUAGUGCCACGUAGGUCGAAAAGGGGUAAAAAAAUAUUAACAAAAUAAGUUCAGG	**145**	17,931034	35,172414	17,931034	27,586207	35,862069	62,758621	0,7843137	1	-62,1	-62	0,0575061	9,1	-42,827586	-1,1942308
spiLA0480-MIR7981b-27	UAUCCCUUUUUAGCUUACGUGGCACUAUCUUGUGGGCCCACGCCCAACGAUGAUUGACUUUUUUUUCCGAACUAGUGCCACGUAGGCUAAAAAGAGGUAG	**100**	22	23	24	31	46	54	1,3478261	0,9166667	-46,8	-46,8	0,0870994	8,4	-46,8	-1,0173913
spiLA0480-MIR7981b-28	CUACCCCUUUUUAGCCUACGUGGCACUAGUUCGAAAGAAAAAGUCAACUAUCGUUGGGCCCACAAGAUAGUGCCACGUAAGCUAAAAAGGGGUAA	**95**	22,105263	32,631579	23,157895	22,105263	45,263158	54,736842	0,6774194	0,9545455	-47,3	-46,3	0,153914	14	-49,789474	-1,1

spiLA0480-MIR7981b-29	ACCCCCCUGAACUUAUUUUAUUAAUAAUUUUUUAC CCCUUUUUAGCCUACGUGGCACUAUCUUGUGGGC CCGACGAUGGUUGACUUUUUUUUCAAACUAGUGC CACGUAAGCUAAAAAGGGGUAGAAAACUACUUAUA AAAUAAGUUCAGGGGGGU	**156**	19,230769	27,564103	19,871795	33,333333	39,102564	60,897436	1,2093023	0,9677419	-86,4	-86,4	0,0419471	11	-55,576923	-1,4213115
spiLA0480-MIR7981b-30	UUUUACCCCUUUUUAGCUUACGUGGCACUAUCUU GUGGGACCAACGAUGGUUGACUUUUCUUUUCGAG UCACGUAGGCUAAAAAGAGGUAGAA	**93**	22,580645	23,655914	19,354839	34,408602	41,935484	58,064516	1,4545455	1,1666667	-38,1	-31,77	0,0629199	15	-40,967742	-0,9769231
spiLA0480-MIR7981b-31	ACACCUAUUAUCCCCCUGAACUUAUUUUAUAAGUA AUUUUCUACCCCUUUUUAGCCUACGUGGCACUAG UUUAAAAAAAUAAGUCAACCAUCGUUCGAGCCAUA AGAUAGUGCCACAUAGGCUAAAAAGGGGUAAAAA AUUAUUAAUAAAAUAAGUUCAAGGGGGUAAUAGG ACC	**175**	16	36,571429	18,857143	28,571429	34,857143	65,142857	0,78125	0,8484848	-89	-88,9	0,0788989	9,2	-50,857143	-1,4590164
spiLA0480-MIR7981b-32	UAUACUAUCCUAAGGUCCUAUUACCCCCUGAACA UAUUUUAUAUGUAAUUUUCUACCCCUUUUUAGCC UAUGUGGCACUAGUUCAGAAAAAAAAGUCAACCAC UGUUGGGCCCACAAGAUAGUGCCACGUAAGCAAA AAAGGGGUACAAAAUUAUUAAUAAAAUAAGUUCAG GGGAAUUAAAAGAACAAUUCUAGAAUAGUGUC	**204**	16,176471	36,764706	18,627451	28,431373	34,803922	65,196078	0,7733333	0,8684211	-74,8	-74,8	0,0241643	15	-36,666667	-1,0535211
spiLA0480-MIR7981b-33	UGCUUGCCCCCAGAUCAUUAUUAAUAAUUUUUUA CCCCUUUUUAGCUUACGUGGCACUAUCUUGUGGG CCCAACGAUGAAUGACUUUUUUUUUUAACUAGUG CCACAUAGGUUAAAAAGGGGUAGCAAAUUACAUA UAAAAUAAGUUCAGGGGGUAAUAG	**160**	18,75	29,375	17,5	34,375	36,25	63,75	1,1702128	1,0714286	-57,7	-53,4	0,0371036	14	-36,0625	-0,9948276
spiLA0480-MIR7981b-34	AACCCCCUGAACUUCUUUUAUUAAUAAUUUUUUAC CCCUUUUUAGCUUACGUGGCACUAUCUUGUGGGU CCAACGAUGGUUGACUUUUUUUCUGAACUAGUGC CACAUAGGCUAAAAAGGGGUAGAAAAUUACAUAUA AAAUAAGUUCAGGGGAUA	**156**	17,948718	29,487179	17,948718	34,615385	35,897436	64,102564	1,173913	1	-79,9	-75,5	0,17024	4	-51,217949	-1,4267857
spiLA0480-MIR7981d-10	CUCCUAGACUAUUGACUGAAAUUUCAGAGACACA CUUUAACUAAACUAAGAUCCUAUUUAUAAUUUUAU ACACCUUUUAUCUUAUGUGGCUCUCUCCGUGACU CUGCGCAAUUAAUGUGCGUGUGAGAUAUUUGGAU UUCACGUAAGCUAAAAAUGUGCACAAAAUAACAAA ACAAAAUGAAUUCUGCAGGUAAUAAGAUCUUAGU UUAGUUAAAGCGUGCCUCUGAAAUUUCGAUCAUA GUAUAGAAA	**249**	15,662651	34,136546	17,269076	32,931727	32,931727	67,068273	0,9647059	0,9069767	-80,3	-77,7	0,0011776	22	-32,248996	-0,9792683
spiLA0480-MIR7981d-11	GCCCGAAAUCUCAUAGAUAUACUUAUACUAUACUA AGAUCCUAGUGCCACGUAGACCGAAAAGGGGUAG AAAAUUUACUUAUAAAAUAAGUUCAGAGAGGGUAA UAGGACCUUAGUAUAGUAUAAGUGUGACUCUCUG AUUUCGAAU	**147**	19,727891	36,054422	15,646259	28,571429	35,37415	64,62585	0,7924528	1,2608696	-50,1	-45,81	0,0376396	14	-34,081633	-0,9634615
spiLA0480-MIR7981d-7	UGCACAAGUAUCCCCUCAACAUAUACUCGAAAAUC CAGCGACACACCUAUACGAUAAUAAAGUACUAUUA CCCCCUGAACUUAUAUUAUAAGUUAUUGUAGGCC GAAAAUGGGUAGAAAAUUAUUAGUAAAAUAAAUUC AGGGGGGUAAUAGGACCUUGGUAUAUUAUAAGUG UUUCCUAAGAUUUCGUUCAUAGGUUGAGGGGGUA CUUGUACA	**215**	19,069767	34,418605	16,744186	29,767442	35,813953	64,186047	0,8648649	1,1388889	-76,8	-76,7	0,0004245	18	-35,72093	-0,9974026
spiLA0480-MIR7981d-8	AAAUAAUUCUGAGGGAAAAUGCACAGGUACCCCC UCAACCUAUGUCCGAAAUUUCAGAGACACACUUA UACAACACUAAGGUCCUAUUACCCCCUCAACUUAU UUUAUAAGUAAUUUUCUAUCUCUUUUCGACCUAU CGGACAUAGGUUGAGGGGUACUUGUGCAUUUUU UCCCUGAACUUAUUU	**185**	14,594595	28,648649	23,243243	33,513514	37,837838	62,162162	1,1698113	0,627907	-71,2	-66,54	0,000716	29	-38,486486	-1,0171429
spiLA0480-MIR7981d-9	UGUGUCUCUGGGAUUUCGGGCGUAGGUUGAGGG GCUACUUGUGCAUUUUCCCUUUUUAUAUACUCUU AAAGUUAAGGUUAAUAUUAACACUCCACACAUAAU GUUUUUUUAUUUUUAGGGAUAAUGCAUAAGUACC CUCUCAACCUAUGCCCGAAAUUUCAGAGACAUA	**169**	18,343195	26,035503	18,343195	37,278107	36,686391	63,313609	1,4318182	1	-86,7	-83,7	0,0077548	21	-51,301775	-1,3983871
spiLA0480-MIR7981f-15	UGUUUUGUUAAAAAGGGAUAAUGCACAAGUAGAA AAUUACUUAUCUAAUAAGUUCAGGGGGUAAUAGG ACCUUAGUAUAGUAUAAGUGUGUCUCUGGGAUUU CGGCCAUAGGUUGAGGGGGUACUUGUGCAUUUU CCCUUUUUAAAAAUUU	**151**	23,84106	29,139073	11,258278	35,761589	35,099338	64,900662	1,2272727	2,1176471	-45,4	-33,35	0,0012987	34	-30,066225	-0,8566038

spiLA0480-MIR7981f-16	GCUUUUAUUAAAGGGAUAAUGCACAAAUACCCCUCAAUCUACGCCCGAAAUUACUUAUAAAAUAAGUUCAAAAGGGUAAUAAGACCUUAGUAUAUUAUAAGUGUGUCUCUGGACUUGUGCAUUUUCCCUUUAUUAAAUUUUUGAAAUUUUGGGCAUAAAUUGAAGGGGUACUUCGGGCAUAGGUUGAGGGGAUACUUGUGCUUGUUUAAAAGGGAUAAUGCACAAGUACCCAGGCACUAUCUUGUGGGUCCAAUGUUGGUUGACUUUUUUUUCAUGAUAGUGCCAUGUAGGCCGAAAAGGGGUAGAAAAUUACUUAUAAAAUAAGUUUAGGGGGGCAAUAAGACCUUAGUAUAAUAUAAGUGUGUCUCUGGGAUUUCGGGCAUAGGUUGAGGGGAUACUUGUGCAUUUUCCCUAUAUAAAAUG	**165**	16,363636	33,939394	15,151515	34,545455	31,515152	68,484848	1,0178571	1,08	-62,4	-59,3	0,0169805	20	-37,818182	-1,2
spiLA0480-MIR7981f-17		**222**	25,225225	29,279279	13,063063	32,432432	38,288288	61,711712	1,1076923	1,9310345	-70,5	-62	0,0010552	30	-31,756757	-0,8294118
spiLA0480-MIR7983-1	UCCCUAAAGCCUUUAGCGACAUUGGUUUUAAUGACAGUUAACUAAUGCCGGUAAAGACUUUAGCACAUCAUAUACACUACAUCAAAAAUGAGCUUUAGCGGCUAUUAACACUUUCUGUAUGUGUCUCUAACGGCUUUAGCAACAUUGGAUCUAGUGACAGUUAACUAAUGCCGGUAAAGACUUUAACACUCUAUAUGAAUGUCUUUUAUUGUCGCUAAAAAUUAUUUUUGUUGUAGUGACAUCAA	**66**	18,181818	30,30303	21,212121	30,30303	39,393939	60,606061	1	0,8571429	-20,5	-20,1	0,267845	3	-31,060606	-0,7884615
spiLA0480-MIR7983-10		**182**	14,835165	31,868132	15,934066	37,362637	30,769231	69,230769	1,1724138	0,9310345	-46,4	-43,85	0,0310341	16	-25,494505	-0,8285714
spiLA0480-MIR7983-11	GAACACUACAUCAAAAAUGAGUUUUAGUCGUAAUUAAUUAGUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUAACACUCUUUGUAUAUGUCCCUAAAGGUUUCAGCGACAUUGAAUCUAAGGACACUUAACUAAUGCCGGUAAAGACUUUAACACUCUAUAUGAAUGUGUCUUUUAUUGUCGCUAAAAGUUAUUUUUGUUGUAGUGAAA	**213**	16,431925	32,394366	15,023474	36,150235	31,455399	68,544601	1,115942	1,09375	-62	-60,3	0,0002108	28	-29,107981	-0,9253731
spiLA0480-MIR7983-2	UAAUAAAUAGCAAAUCACAUUACAACAAAAAUAACUUUUAGCGUCAUUAAAUAUUGACACUAAUAAAGAGUGCUAAAGUCUUUACCGACAUUAGUUAAGUGUCAUUAGAACCAAUGUCGCUAAAGGCUUUAGAGACAUAUACAAAGAGUAACAACUGCCGCUAAAAAUACAUAUUUAGCGGCAAUUAAGAAUUAAAUGUCGCUAAUGGUCAUUUUUGUUGUAGUGUCAUGGUAUGUAAUCUUGCAACAAAAAUGAUCAUUAGCGGCAUUUAAUUUUUAAUUGUCGCUAAAUAUGUAUUUUUAGCGACAAUUAUCACUUUGUAUAUGUCCUCAAAGCCUUUAGCGACAUUGGUUCUAAUGGCACUUAACUACUGUCGGUAAAGACUUUAGCGCUCUUUAUUAAUGUCAAUAUUUUAGCGCUAAAAGUUGUUUUUGUUGUAGUGGCACUAUGACAAAAAUGAUCAUUAGCGACAAUUAAUUCUUAAUUGCUAUUAAAUAUGUAUUUUUAGCGGCAAUUGUCACUCUUUGUAUAUGUCCCUAAAGCCUUUAGCGACAUUGGUUCUUAUGAAUCUUAACUAAUGCCGGUAAAAACUUUAACACUCUUUAUUAGUGUCAAUAUUUAAUGUCGCUAAAAGUUAUUUUUGUUGUAGUGUGA	**240**	15,833333	38,75	15	30,416667	30,833333	69,166667	0,7849462	1,0555556	-76,2	-74,4	0,0026446	21	-31,75	-1,0297297
spiLA0480-MIR7983-3		**202**	16,336634	28,712871	15,841584	39,108911	32,178218	67,821782	1,362069	1,03125	-67,2	-67,2	0,0057088	17	-33,267327	-1,0338462
spiLA0480-MIR7983-4		**214**	15,420561	30,373832	14,953271	39,252336	30,373832	69,626168	1,2923077	1,03125	-60,5	-55,7	0,0012314	47	-28,271028	-0,9307692
spiLA0480-MIR7983-5	UUCCUAAAGUCUUUAGCGACAUUGGUUCUAACAACACUUAACUAAUGUCAGUAAAGACGUUAGCACUAUGUUUCUAGAGUCUUUAGCGACAUUGGUUCUAAUAACACUUAACUAAUGCCGGUAAAGACUUUAACACUCU	**66**	15,151515	33,333333	21,212121	30,30303	36,363636	63,636364	0,9090909	0,7142857	-21,2	-21,2	0,365306	2,3	-32,121212	-0,8833333
spiLA0480-MIR7983-6		**73**	15,068493	30,136986	19,178082	35,616438	34,246575	65,753425	1,1818182	0,7857143	-22,5	-22,5	0,197498	4,2	-30,821918	-0,9
spiLA0480-MIR7983-7	UCUCACUACAACAAAAAUGAUCAUUAGCGGCAUUUAAUAUGUAUUUUUAGCGCCAAUUGUCAUUCUUUAUAUAUGUCCCUAAAGCCUUUAGACAUUGGUUCUAAUGACACUUAACUAAUGCCGAUAAAGACUUUAGCACUCUUUAUUAGUGUCAAUAUUUAAUGCCGCUAAAAAUUGCUUUUGUUGCGGUGUCU	**194**	14,43299	29,381443	18,556701	37,628866	32,989691	67,010309	1,2807018	0,7777778	-53,6	-53,6	0,0336111	12	-27,628866	-0,8375
spiLA0480-MIR7983-8	UUGCACUACAACAAAAAUAACCAUUAGCGGCAUUUAAUUCUUAAUUGCCGCUAAAUAUGUAUUUUUAGCGGCAAUUGUCACACUUUGUAUAUGUACCUAAAGCUUUUAGCGACAUUGGUUCUACUGACACUUAACUAAUGCCGGUAAAGACUUUAGCACUCUUUAUUAGUGUCAAUAUUUAAUGCCGCUAAAAGUUGUUUUUGUUGUAGUGUUG	**214**	16,35514	28,971963	17,28972	37,383178	33,64486	66,35514	1,2903226	0,9459459	-83,1	-82,1	0,0123376	11	-38,831776	-1,1541667
spiLA0480-	UAUGUCCUUAAAGUCUUUAGCGACAUUGGUUCUA	**73**	17,808219	28,767123	17,808219	35,616438	35,616438	64,383562	1,2380952	1	-	-20,4	0,0621775	6,8	-30	-

MIR7983-9	AUGACAGUUAACUAAUGCUGGUAAAGACUUUAGCACUCU										21,9						0,8423077
spiLA0480-MIR7984b	UACGAUACCAAACGUUGGAAAUGACUUUUUACCCAUGCACUAUUUAAAAGUCCCACGUGGACAUAAAAAUAUUGCAUAACUAUAAAUAGUAAUAUGUCCAGGUGGACACAUAUAUACCUUUAAAAUAUACUAUUAAUAGUUGAGGAGGGUAAAAGCUCCUCCAUAAACUUUGGUAUCAUA	**181**	14,917127	38,121547	17,127072	29,834254	32,044199	67,955801	0,7826087	0,8709677	-50,5	-48,2	0,020155	29	-27,900552	-0,8706897
spiLA0480-MIR7984c	CUUACUUAGUGAAAAGAGUGAAAAAAAUUUCAACGUUGAUCAAAAUUGUUAUGAUACCAAAGUUUAUGGAGGAGCUUUUACCCUCCUCAACUAUUAAUAGUAUAUUUUAAAGGUAUAUAUGUGUCCACCUGGACAUAUUACUAUUUAUAGUUAUGCAAUAUUUUUUAUGUCCACGUGGGACUUUUAAAUAGUGCAUGGGUAAAAAGUCAUUUCCAACGUUUGGUAUCGUAGCAACAAAUUUUGAUUGAAGUUCGGAUAUAUUUCGGAUCUUCUUCUCAUUUAGUUAU	**287**	16,724739	31,358885	13,937282	37,979094	30,662021	69,337979	1,2111111	1,2	-85,9	-84,1	0,0002649	29	-29,930314	-0,9761364
spiLA0480-MIR7984d-1	UUUGGGAAAAAGUGUGAAAUAUAUUUGAAUUUUGAUUGAAAUUGCCGUUACGAUACCAAACUUUGAGAAUGACACGUGGACAUAAAUUUUUUUGCCGAAUUAUCAAUAAUAAUGUCCUCCAUAAAGUUUGAUACGUAACAACAAUUUCGGUCAAAGUUUGAGUAUUUUUUUAGACCCUUUUCCCUAU	**187**	16,042781	32,620321	14,438503	36,898396	30,481283	69,518717	1,1311475	1,1111111	-57,2	-49,83	0,0130212	20	-30,588235	-1,0035088
spiLA0480-MIR7984d-2	CACGGUAAAUUUAUGGAAAAAGGGUCUGAAAUAUAUCUGAACUUUAACCCAAAUUAUUGUAACAAUCUCCAGCUUUUGGGAGGACCUUUUACUCCGUACCUUAUAAAUACAUUAUUAAAUAGUGCAGAGGGUAAUAGGUCCUCCCCAAAGUUAGGAUUGUUACCACAAUUUCGAUCAAAGUUCGAAUAUAUUUAAAACCCUUUUCCCCUAAAUUUAUCCUUU	**222**	14,414414	32,882883	19,369369	33,333333	33,783784	66,216216	1,0136986	0,744186	-83,3	-82,3	0,0080447	16	-37,522523	-1,1106667
spiLA0480-MIR7985-1	GGACUUCCAUGUUGGAGGUCUCAAGUUUGAAACCCCUUGUCAGUGAAAGCAAAGUGUUUGCCUUCUGGGUCGAGCUUGUCGCACCGGGCUUGCCUAGUGCGGGUUACCACUCCUAUGUGGUUGUGAGUUAUUGCAUAGGAGCGGGGGUUUUACCCUGUGCGCAUCCAAAGGGUAGCGG	**178**	31,460674	17,977528	21,910112	28,651685	53,370787	46,629213	1,59375	1,4358974	-67,8	-58,7	0,0030071	45	-38,089888	-0,7136842
spiLA0480-MIR7985-2	CUACUAUCCUUCGGGGUGGCCCAGUGGUUUGGGCUUGGGACUUCCAUGUUGGAGGUCUCAAGUUUGAAACGGGUUUUGACUUCUGGGUCGAGCUUGUUGCUCCGGGCUUGCCUAGUGCGGGUUACCUCUCCUAUGAGGUUAGCGAGCUUAUCGCAUAGGAGGGGGUUUUUACCCUGUGCGCACCCAAAGGGUAGCGG	**197**	32,994924	14,720812	22,335025	29,949239	55,329949	44,670051	2,0344828	1,4772727	-94	-91,7	0,0083668	15	-47,715736	-0,8623853
spiLA0480-MIR7986	ACAGCAUUAGGUUGAUAUACGUCACUGUAAGUAACGUUUUACUUUUAAAACGUUAUUUUCAGUAACGUUUUAAAACGUUACUGUGAGUAACGUUUAAGGAGUAAAACGUUACUGUAAGUAACGUAUAUCAAUCUGACGCCAA	**142**	17,605634	33,802817	14,788732	33,802817	32,394366	67,605634	1	1,1904762	-74,9	-74,9	0,420654	1,8	-52,746479	-1,6282609
spiLA0480-MIR7987-1	CACAAGUACCAACACUAGCUGAUGCUAUUGAUGACAAAAAUUGGUUUUCUUGCAAGAUCAAUUUGUGUCAAUCUAGUGUUGAUACUUAUAAAUGUUUGUUGAUUGUAAGGACCAACACUAGUUGAUCUUAUUGAUGACAAAAAUUAAUGUUCUUGCAAGAUCGAGUUGUGUCCAUCUAGUGUUGAUACUUAGC	**208**	19,230769	30,288462	13,942308	36,538462	33,173077	66,826923	1,2063492	1,3793103	-59,2	-50,5	0,003571	47	-28,461538	-0,857971
spiLA0480-MIR7987-2	AAGAUCAAUUUGUGUCAAUCUAGUGUUGAUACUUAGUUUUAGUUUAGGAAUAAAUGUUUGUUGAUUGUAAGGACCAACACUAGUUGAUCUUAUUGAUGACAAAAAUUAAUGUUCUUGCAAGAUCGAGUUGUGUCCAUCUAGUGUUGAUACUUAGCUUUAAUUUAGUAAUAAUGGUGUUUGUUAGGCAUAAGUACCAACACUAGUUGAUCCUAUUGAUGAA	**220**	19,545455	30,454545	11,363636	38,636364	30,909091	69,090909	1,2686567	1,72	-53,4	-22,4	0,0010897	91	-24,272727	-0,7852941
spiLA0480-MIR7987-3	UAGGAAUAAUGUAUCUGUUAAGCAUAAGUACCAACAGUAGUUGAUCCUAUUGAUGACAAAAUUGAUUUUCUUGCAAGAUCGACUCGUGUCCAUCUAGUGUUGAUACUAAGUUUUAUUUAGGAAUAAUAUGUUUGUUAAGCAUAAGUAUCAACACUAGUUGAUCUUAUUGA	**189**	17,460317	31,746032	12,698413	38,095238	30,15873	69,84127	1,2	1,375	-41,8	-33,3	0,0007928	58	-22,116402	-0,7333333

spiLA0480-MIR7988-1	UGACAAAUUGAUUUUCUUG UUUUAAGGGAAAAGGGACAAACAUACUUCGAUAC UAACAUAAAUGGUACGCAGAUAAUCUUUCGUCAU ACUUUUGAGAUAUUAGUACCACCGUCGUCCAAAA ACUAGAGUAUAUAUAUCCUUUGUACUAACGGACA UACACGUGUCAUAAUUUUAUCCACCGAUUGUAUA UCGAAUACGGAUAAAAUUGUGUCAUGAUGGAGAG UAUUUGCAUAUCAUUUACUAAUAUUAUAGAGAUAU AUUUAUCGUUUUCCCUAUAUUU	**261**	15,32567	33,716475	16,091954	34,8659	31,417625	68,582375	1,0340909	0,952381	-62,2	-58,9	5,50E-05	37	-23,831418	-0,7585366
spiLA0480-MIR7988-2	CACUCCCGUUAGAACAAAAUGGUAUAUUUUAGAA UAUUUAUGUAAUAAUAUGAGUGUAUGUAAGCCAC UUUUUUAAUAAGGGAAAAGGCUCAAAUAUGCCGU UGAACUUUUAGAAAAGACUCAUUUAUGUCAUCCG UUAAAAGUUUGACUCGUUCAUGUUAUUACCAUUU AGGAAAAGACUCAUUCAUGCCAUUAGUUUUUAAC GGCGAUUU	**212**	16,509434	33,018868	14,622642	35,849057	31,132075	68,867925	1,0857143	1,1290323	-51,6	-42,98	0,0038801	28	-24,339623	-0,7818182
spiLA0480-MIR7990a-1	GCAAAAGUUAUGACCAUUUGAAGUGUCACAAAUU UACAACUACUUUUUUUGAGUUAUACUCUUUAAUU UGGUGAAACUUCAAAUGAUCGUAACUUUGGCC	**100**	15	31	16	38	31	69	1,2258065	0,9375	-32,6	-32,6	0,100323	7,6	-32,6	-1,0516129
spiLA0480-MIR7990a-2	CGCAUAGAUCUCAAAAAAGUAACCGAAUUGAAAAA AAAAUCGCCUCAAUCGGACAACAGAGACAAAAGUC AUUACCACUUGAAUUUUCAAAACUUUACAACUACU UUUAUUGAGUUACACUCUUCAAUUUGGUGAAACU UCAAAUGAUCGUAACUUUGGCAUCUAAUAUCCGU UUGAGACGAUUUUUUUUCAAUUUGGUUAUUUUUU UGAGAUCUAUAUG	**220**	13,636364	34,545455	17,272727	34,545455	30,909091	69,090909	1	0,7894737	-73,1	-62,2	0,0003453	37	-33,227273	-1,075
spiLA0480-MIR7990a-3	UGUGUAUAUCUCGAAAAAAUAACCAAUUGGAAAUA AAAAAUCGCCUCGAUCGGACAUCAAAGACAAAAGU UAUGACCGUUUUAAGUUUCACAAAUUUACAACUAC CUUUUUUUGAGUUACACUCCUUAAUUUGGUGAAA CUUCAAAUGAUCGUAACUUUGACCUUGAAUAUCU GUUUGAGGCGAUUAUUUUUCAAUGAGGUUAUCUU CUGAGAUCUACGUG	**221**	15,837104	32,579186	16,742081	34,841629	32,579186	67,420814	1,0694444	0,9459459	-70,4	-69,17	0,0026263	21	-31,855204	-0,9777778
spiLA0480-MIR7990a-4	AAGAUCUCGAAAAAUUAUCAGAUUGAAAAAGAUUG CCUCAAUCACACAUCCAAGGCAAAAAAAUUUACCA UUUGAAGUUUCACAAAUUUACAACUACUUUUUCU GAGUUGCACUCUUUAUUUUUUGUGAAUCUUCAAA UGAUCGUAACUUUGGCCUCGAAUAUCCGUUUGAG GCGAUUUCUUUUUCAAUUGCACUAUUUUCUCGAG AUAUA	**211**	13,270142	31,753555	18,483412	36,492891	31,753555	68,246445	1,1492537	0,7179487	-62,1	-60,7	0,0093892	23	-29,43128	-0,9268657
spiLA0480-MIR7990a-5	CGUGUAGAUCUCUAAAAAAUAAUCAAAUUGAAGGA AAAAUUGCCUCAAUAAAACAUCUGGGGGGGAAAG UAAGAUCGUAUGAAAUUUCAAAAAUUUACAACUAC UUUUAUUGAGUAACACUCUUUAAUUUGGUGAAAC UUCAAAUGAUCGUAACUUUGACCUCGAAUAUCCU UUUUAGGCUAUUUCAUUUUUCAAUGAUGUUAUAU UUUCGAGAUCUACGUG	**222**	15,765766	34,684685	14,414414	35,135135	30,18018	69,81982	1,012987	1,09375	-57,4	-49,7	0,002339	25	-25,855856	-0,8567164
spiLA0480-MIR7990b	GAGUUGUGACUUUUAUGAAGAGUUACGACUUUUA UAAAGAGUUGCGACUUCUAUGAAAAGUUGUGACU UUUAUGAAAAGUUGCGAUUUUAAUGAAGAGUUGU AACUUUUAUGAAAAAAUUGUUACUUUUAUGAAAGA UUGUGACUUUUUCGAAGUGUUGCAACUUUUCCAA GUAGUUUUGACCUUUAAUAAGGGUUGCAACUUUU CAAAUAGUUGUAACCUUUCCGAUAAGGCACAAUA U	**240**	19,166667	30,833333	11,25	38,75	30,416667	69,583333	1,2567568	1,7037037	-79,7	-26	0,0036489	112	-33,208333	-1,0917808
spiLA0480-MIR7991c-1	AUCAAAUUUUAGAAUAUCGACCUCCGGAAGUUGG UAUUUUUAUUUUCUAUUUUUUAGAUUUUGACCUC UGGAGGUCGGUAUUUUCAUUUCUUAUUUUUUUGA UUCUGAUCUCUGGAGGUCGGUAUUUCUAUUUCUU AUUUUUUAGAUUCCGACCUCCAGAGGUCGGUAUU UCUAUUUCUUAAUUCUUUAGAUUCCGACUUUCGG AGGUCGGUAUUUAUAUUUCCU	**225**	16,888889	19,111111	16	48	32,888889	67,111111	2,5116279	1,0555556	-84,9	-81,4	0,0075996	24	-37,733333	-1,1472973
spiLA0480-MIR7991c-2	CAUCUUCCGUAGGUCAGAAUUUUUAAUUAUCAAA UUUUAGAAACCAACCUCCGGAAGUUGGUAUUUUU AUUUCUUAUUUUUUUAGAUUCUUACCUCUGGAGG UCGGUAUUUUCAUUUCUUAUUUUUUUAAUUCCGA	**192**	15,625	21,354167	17,1875	45,833333	32,8125	67,1875	2,1463415	0,9090909	-53,3	-51,7	0,0058935	28	-27,760417	-0,8460317

spiLA0480-MIR7992-1	UCUCUGGAGGUCGGUAUUUCUAUUUCUUAUUGUU UAGAUUCCGACCUCCGAAGGUU GUGCCCUUUCACUUGACUUUAAAUCACAAUUAUG CUCUUCAACUUUGGAUGUGCACAAAUAGACACUU AAACUUAUAUAAAGUUGAAAAAAUAGACACAUCUG UCCUAAUUUUUUUUUUGUCCUACGUGGUGUCCUA CAUUUAUUGUGCCAUGUAGUGCUCAUGUGUAUAU UUAUUUAAAAGUUAGAUAGUUGAAGUGUUUCUCU GUGCAUUAAUAAGGUUGGAGGUUAAGGUUAAAAU UUGAAGCCAAGUGUAGGGUAA	**260**	18,461538	29,615385	14,230769	37,692308	32,692308	67,307692	1,2727273	1,2972973	-80,1	-78,2	0,0032866	21	-30,807692	-0,9423529
spiLA0480-MIR7992-10	CUUCAAUUUUGGGUAUACACAAGUAGACACUUAA ACCUGUAUAAACUUGAACAAGUAGACACAUGAGU UCUACGUAGCACAAUACACGUAAAAUACCACAUAU GACGAAAAAUGAUAUACAUGAUGUCAUGUAGAACA UGUGUGUCUAUUUGUUCAACCUUCUAUAAGUUUA AGUGUCUAUUUGUACACACUCAAAGUUGAAG	**203**	15,763547	36,453202	17,241379	30,541872	33,004926	66,995074	0,8378378	0,9142857	-83,2	-83	0,0297799	16	-40,985222	-1,241791
spiLA0480-MIR7992-11	UUAUGCCCUUUAACUUUGAGUGUGCACAAGUAGA CACUUAAACUUGUAUAAAGUUGAACAAAUAGACAC ACAUGUCCUACAUGUCAUCCUACAUGUCAUUUUU UGUCCUACGUGGUGUUUUACGUGUAUUGUGUCA UGUAUGACUCAUGUGUUUAUUUAUUUAAAAGCUG GAUAGUAAAGUGUUUAUUUGUGCAUUAUGACAGU UGGAGGUCAAAG	**216**	19,444444	27,777778	14,814815	37,962963	34,259259	65,740741	1,3666667	1,3125	-72,3	-68,3	0,0135915	17	-33,472222	-0,977027
spiLA0480-MIR7992-12	AAUUGGUAUUUACGUACUCAAACUUUGAGUGUGC ACAAGUAGACACUUAAAAACUUGUAUAAAAUUGAA UAAUUAAAUGCACACGUCUUAUGUGACAUAUUACA CGUAGGAUACCACAUGUAUGAUGCAAAUUGUCCA CAUAAGACGUCAUGUAAGAGGUAUAUAUGUAUCU GUUUGUUCAAUUUUGAACAAGUUUGAAUGACUAC UUAUAUACAUCUGAAUUUAAAGGACAUAGAUAUCA CUC	**244**	15,983607	36,065574	14,754098	33,196721	30,737705	69,262295	0,9204545	1,0833333	-63,3	-53,2	0,0001185	40	-25,942623	-0,844
spiLA0480-MIR7992-13	CCUCUUUACUUGACCUCAUUUUACAUUUAUUUUG GGUAUGCACAAGUAGAUACUUAAACUUGUAUAAA CUUGAACAAGUAGACACAUGAGUCCUACGUGACA CAACACACACAUAGGGCAAAAAUGACAUGUAGGAC AUGUGCGUCUAUUUGUUCAACUUUAUAUAAGUUU AAGUGUCUACUUGGACACAUCCAAAGCUGAAAGG CAUAAACAUAAUUUGAAGCCAAGUUA	**231**	16,450216	34,632035	18,614719	30,30303	35,064935	64,935065	0,875	0,8837209	-93,6	-92	0,10426	6,2	-40,519481	-1,1555556
spiLA0480-MIR7992-14	UGUACUCCAGCUUCGAGAGUGAACAUCUACACAC CUCAAUUGGACACUCCAACUCGUCCCUAGUGUGA UGCUGACAUGGCAUAUAAAUUUUGGAGACGAGUU GAGGUGUCUAGAUGUGCAUACUCAAAGUUGGAGU GCU	**139**	23,741007	26,618705	21,582734	28,057554	45,323741	54,676259	1,0540541	1,1	-66,4	-65,4	0,0335415	12	-47,769784	-1,0539683
spiLA0480-MIR7992-15	CUUCAACUUUAGUAGCGUACAUCCAGACACCUCA ACAACUCAUCCCUACCGAGUCUCGUGGACACCCA AUUCUAACGUGACACAUAAAUUUUGAAGAUAUGU GAAUGAUCAUUUUGUAAGGUGGAGUGUUCAACUA ACACACUAGAACGAGCUGAGGUGUCUAGAUGUGC AUUCUCAAAGUUGGAG	**186**	19,892473	30,645161	22,043011	27,419355	41,935484	58,064516	0,8947368	0,902439	-58,4	-57,7	0,0076555	20	-31,397849	-0,7487179
spiLA0480-MIR7992-16	UGGUAAGUAAGUAAUACCACGUAACUUUGAGAGU GCACAUCUAGAUACCUCAACUAGACCCUCCAACU CGUGCCCGCUGUGUCUUGUAGACACUUGACAUUA AAGUAGCAGAUAAACUUUAGAGGUGUCUCAAUGA UGAUUUUGUAGAUGUUGGAGUAUUUAACUAACAC AUUGGAGACGAGUUGAGGUGUCUAGAUGUGCAUA CUCAAAGUUUAAGUGUUUGUUUCUGUAUUAUGC	**237**	21,940928	28,691983	16,877637	32,489451	38,818565	61,181435	1,1323529	1,3	-84,1	-80,9	0,0038903	26	-35,485232	-0,9141304
spiLA0480-MIR7992-17	AAGUGUCUAUUUGUGCACAUCCAAAGUUGAAGGA CAUAAAUGUAAUUUGAAGCCAAGUUAAAAGACACA UUUAAGUAUCGUAUAAUACAUAAAUAUAUCCUUUA ACUUGGCUUCGAAUCACAUUUAUGCCCUUCAACU UUGGGUGUGCACAAGUAGACACUU	**162**	16,049383	34,567901	17,283951	32,098765	33,333333	66,666667	0,9285714	0,9285714	-97,6	-97,6	0,281439	2,2	-60,246914	-1,8074074
spiLA0480-MIR7992-18	UUUAACUUGGCUUCAAAUCACAUUUAUGCCUUUC AACUUUGGAUGUGCACAAAUAGACACUUAAACUU GUAUGAAGUUAAAUAAAUACACACGUGUCCUACAU GUCAUUUCUUGUCCUAUUUAGUGUCCUACGUGUA CUGUUUCAUGUAGGACCCAUGUGUUUAUUUAUUU	**247**	17,004049	29,959514	14,574899	38,461538	31,578947	68,421053	1,2837838	1,1666667	-75,5	-69,77	0,0023169	32	-30,566802	-0,9679487

spiLA0480-MIR7992-19	AAAAGGUGGAUAUUUAAAGUAUCUGUUUAUGCAUUAUGAAAGUUGGGUCAAAGUUAAAAUUUGAAGUCAAGUUUAGCCUUCAACUUUGGGUGUGCACAAGUAGACACUUAAACUUGUAGAAAGUUGAACAAAUAGACACUCAUGUCCUACAUGUCAUUUUUCAUCCUACGUGGUGUCUUACAUGUAUUUUGCCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUAGAUAGUUAAAGUGUCUGUUUGUGCAUUAUGAAAGUUAGAGGU	**194**	19,587629	28,350515	14,948454	37,113402	34,536082	65,463918	1,3090909	1,3103448	-72,7	-71,9	0,0667135	9,4	-37,474227	-1,0850746
spiLA0480-MIR7992-2	UCCAAUCAUUACUCCAACUUUGGAGUGCACAUCCAGACACUUCAAAUCAUGUCCACUAUAUCAAUUGAACACUCAACAGUCCAACUUACAAUAUGAACGUGUAGACACCACCAAAAUUUACGUGUCACGUCAAUGUUGAGUUCCCACAAGAUCAGUGGGACUGAGUUGAGAUGUCUAGAUGUGCACUCCAAAGUUGGAGAGUAUUAUC	**208**	17,307692	32,211538	23,557692	26,923077	40,865385	59,134615	0,8358209	0,7346939	-78,7	-76	0,0010701	21	-37,836538	-0,9258824
spiLA0480-MIR7992-20	GCAUAAUAUAUAGAUAGACACCUUAAAUUGGCCUUAACGAGCAAGUAAAGACCCAAACUAACACGGGGCCAACUUAAACCAAGUUCAUGUGUCUAGAUGUGCAUUCUCAAAGUGUAGGUCUUUACAUGUCAGUUAAGUCCAAGUUAAGGUGUCUAUCUACGUGUUACAAAUAAUGCACAUAUAGACACUUUAACUAUCCAACUUUUAAGUAAAUAAAUAAAUGUGUCCUACGUGACAUAAUACAUGUAGGACACCACGUAGGACAAAAAAUGACAUGUAGGAUGAUAUGUAGGUCAUGUGUGUCUAUUUGUUCAACUUUAAACAAGUUUAAAUGUCUAUUUGUGCAUAUC	**169**	18,934911	33,727811	19,526627	27,810651	38,461538	61,538462	0,8245614	0,969697	-64,2	-64,2	0,0596601	12	-37,988166	-0,9876923
spiLA0480-MIR7992-21	AACCUUAACUUGGACUCAAUUGACAGCUAGCCAACCUAACUCUGAAAAUGCACAUCUAGACCCCUUAACUUGAUCUAACUUUCCCCCUUUAAGACCUCAACUUUGAGAAUGCACAUCUAGAAUUCACAAUUUGAGAAUGCACAUCCGGAAAAGUGUAUUUAGGGGGCCAACUUACACCAGGUUAAGAUGUCUAGAUGUGUCUUUUCAAAGUUGGGGUGUCCAAUUGUCAGUUGAGACCAAGUUAAGAUG	**181**	16,022099	36,464088	14,917127	32,596685	30,939227	69,060773	0,8939394	1,0740741	-53,8	-46,1	0,0101278	32	-29,723757	-0,9607143
spiLA0480-MIR7992-3	CUGGCAAGUAAGCGCUCCAACUUUGUGUAUGCACAUCUAGACGCCAAGUUGAGGUGUCUAGAUGUGCACUCUCAAAGUUGGAGUGCGUACUUGCUAG	**249**	18,473896	30,923695	22,088353	28,514056	40,562249	59,437751	0,9220779	0,8363636	-98,9	-96,9	0,0362719	20	-39,718876	-0,9792079
spiLA0480-MIR7992-4	UUUAUACAAAUUUAAGUGUCUACCAACUUUGGAAAUGCACAAGUAGACACUUAAACAUGUAUAAAGUUGAAUAAGUAGACGCAUGAGUCCUAUGUGACAAAAUACACGUAGGACAAAAAAAUGAUAUGUAGGACAUGUGUGUUUAUUUGUUCAACUUUAUACAACUAUAAGUGAGCAAAUCCAAAGUUGAAAAACAUAAAUGUGAUUUG	**97**	26,804124	23,71134	21,649485	27,835052	48,453608	51,546392	1,173913	1,2380952	-69,7	-68,1	0,703449	0,7	-71,85567	-1,4829787
spiLA0480-MIR7992-5	AGUAAGCACUCAAACUUUGAGAGUGCACAUCUAGAUACCUCAACUUGGUCAUAACCGACUACUAAACAAUCCACGACCACUCGUCUCCACUUUGUCUCAUGCACACUAGACUCUGACAUGACACAUAAAUUUUGGAGGUGUCUAGAUGAUCAUUUUGUAAGUUGAAGUGUUCUGUCUAGAUAUACAUUCUCAAAGUUGGAGUGCUUGAG	**209**	17,22488	40,191388	12,91866	29,665072	30,143541	69,856459	0,7380952	1,3333333	-71,5	-71,5	0,100086	16	-34,210526	-1,1349206
spiLA0480-MIR7992-6	UCUUUUAUUCCAUUCCAAUUUGGGUAUGCACAAGUAGACUCUUAAACUUGAACAAGUAGACACAUGAGUCUUACGUGGUACGAUACAUAUAGUUAUCACAUAGGAUAAAAAAUGACAUGUGGGAGGUCAUGUUAUACAUGUAUGUCUAUUUUUUAAGCUUUUAUACAAGUUUAAUAGUCUACUUGUGCACACGCAAAGUUUAAGGGCAUAAACGU	**209**	18,181818	29,665072	22,009569	30,143541	40,191388	59,808612	1,016129	0,826087	-66,5	-48,2	0,0036919	48	-31,818182	-0,7916667
spiLA0480-MIR7992-7	UAAUCAAGCUUGAUCUCAGUUGAGCAGUAAACACUCCAACUUAGAAGAUGCACAUCUAGACAGCUCAACUCAAAUCCACUGUGUCAAUUGAGGUGUCUAGAUGUGCAUUCUCAAAGUUGGAGUGCUUACUUGCCAAUUGAGGUCAAGUUUGAGUG	**215**	18,139535	32,55814	15,348837	33,953488	33,488372	66,511628	1,0428571	1,1818182	-68,1	-66,6	0,0108214	12	-31,674419	-0,9458333
spiLA0480-MIR7992-8	AAAGCAUAAUACAUAGACAAGACCCUUUAACUUGGCCUUCACCGGCACCUGAACAUCAAUCCCAGCUCU	**155**	21,290323	29,677419	20	29,032258	41,290323	58,709677	0,9782609	1,0645161	-89,2	-88,7	0,0713096	6,4	-57,548387	-1,39375
spiLA0480-MIR7992-9		**249**	20,080321	28,11245	19,277108	32,53012	39,35743	60,64257	1,1571429	1,0416667	-92,9	-90,3	0,0103655	22	-37,309237	-0,9479592

spiLA0480-MIR7993b	AAUUGUGAUCAUCUUGACACAGGUGUGUCUCGCAAACAUCUUAACUUUGAUAAUGCACACUUUUGAGAACGUGUCUAGAUGUGCAUUUUCAAAGUUAGGCUGUUUACGGGGUUUUCAAAGUUGGAGUGUUUAGUUACCUGUUGAGGUAAAGUUAAGAUGUCUAUCUAUGUAUUGUGCCAAUGUGUGUUCCCAUUUGUAUGUGAGGUAGUUAAGUUAACCACAUAAAAUAUAUUGUCAUCUCCUUUAAUUCUAUGCAUUCGCCUUACCAAGUCGUAAACACCCAAGAUGUUUUCUACAAAGGUUGAUGUAUAUAAUUAAAGGAGACAGCAUAUUUUUAUAUAGUUAACUUAACUACAUAAUAGACAAAUGAAAACACGCU	**199**	14,572864	34,673367	16,582915	34,170854	31,155779	68,844221	0,9855072	0,8787879	-70,4	-67,1	0,0183485	17	-35,376884	-1,1354839
spiLA0480-MIR7993d-1	GUGUAUUCUCAAGUGCUCAUACGUAGAUAAGCUAACCACAUAGAUUAUGUACUUUAAUUAUUCACAUCAGACUAAACUGGAACAUGCUUGAGCCUUUACUUGAUGUGUAUAACUAAAGGAGGUGACAUAUUUUUAGUGGUUAACUUAUCUAGGUAACGGAUACUUGAGAAUAUGU	**175**	18,857143	32	14,857143	34,285714	33,714286	66,285714	1,0714286	1,2692308	-60,9	-60,9	0,0096291	16	-34,8	-1,0322034
spiLA0480-MIR7993d-2	AACUUUUUGCGUGUGUUUUCAUUCGUCUAUUAGUUAGUGAAGUUAAUUACAUGAAAUGUAUCAUCUUUUUUAACCGUACACAUUAACUUCAAGUAAAAAAUGCUUGAGGUUUUAAGGCGUAUUGAGGCGCAAGCGUAUAAUUAAAGGAGAUAGAGAUAUUUUAUGUUGUUAACUUAACUACAUCGUAGAUAAAUGAGUGAGCACAAACCAGAAAAAAA	**218**	18,348624	35,321101	12,385321	33,944954	30,733945	69,266055	0,961039	1,4814815	-68,8	-67,9	0,0132785	15	-31,559633	-1,0268657
spiLA0480-MIR7997b-1	ACAAUUAAAACAGCAGACUUCAUAUAAUUUAUGCUGCUCGGACUCUUCAAAAAUAUCAAGGGGUGUGUGUCGGAACUCGGAUCCUCCAAAAGUUGUGCAUUUUUGGGGGAUCUGGCAUCGGCGGAACAACAUUUUGAAGAGCCUGAGCAACAUAAAACAUAAUUAUAAAGUAACACCUCCUUUUAAUAUU	**190**	19,473684	33,157895	18,947368	28,421053	38,421053	61,578947	0,8571429	1,0277778	-58,4	-58,1	0,0042147	19	-30,736842	-0,8
spiLA0480-MIR7997b-2	AAGAAACUAUGCUGCUCGGACUCUUCAAAGAUAUUGGUGGGUUUGUGUAGCAUCAGCUAUACAUUUUUGGAGAUCUAACACAGGUGCAGCAACAUCUUUAGAGAGUUCGAGCAACAUAGGUUAGC	**125**	24	29,6	17,6	28,8	41,6	58,4	0,972973	1,3636364	-50,6	-50,6	0,121895	5,2	-40,48	-0,9730769
spiLA0480-MIR7997b-3	AUGGCAUGCUGCUCGGACUCUUCAAAAAUGUUGCUAGGUCUGUGUUGGAUCCUCCAAAAGUAGUGCAUAUUUGAAGGAUCCGACAUGAGUGCGGCAACAUUGUUGGAGAGUCUGAGCAACAUAGCAGA	**128**	27,34375	27,34375	18,75	26,5625	46,09375	53,90625	0,9714286	1,4583333	-66,4	-63,8	0,025604	10	-51,875	-1,1254237
spiLA0480-MIR7997b-4	CUUUUGAAACCAUUGUUUGUACCUAAGUUGCUCGGACUCUUCAAAAAUGUCAGUGGGUGUGUGUCGGAUUCUCCAAAAGUAGUCUGACACGGGUGUGGCAACAAUGUGAAGAGUCCGCAACUUAGGUUUGUACAAGGUGCAAUUU	**145**	25,517241	25,517241	17,931034	31,034483	43,448276	56,551724	1,2162162	1,4230769	-59,2	-59,2	0,0599793	6	-40,827586	-0,9396825
spiLA0480-MIR7997b-5	GAAUCCUCCAAAAGUAGUGUAUUUUUUGAGGAUCCAAAACACGAGUGCGGCAACAUUUUAGGAGAGUACAAGCAACCAUUUUUCUCUUUUUGGAUUGAUUGAUUUGGUAAUGUAUGUGAUUCUAAAUCUCUCUCAUUCUCAAUAAUGGCUGUGAAUAUUUCUUAAUAAAGAUUGUUAAUUUGGAGUAAGAAUCUUAUUAUUUCCUCCUACGUUGCUUGGACUCUUCAAAAAUGUUGAAGGGUGUGUGUCGGAUCCUCCAAAAGUAGUGUAUUUUUGGAGGAUCC	**284**	20,070423	27,816901	15,140845	36,971831	35,211268	64,788732	1,3291139	1,3255814	-93,5	-75,84	0,0001774	46	-32,922535	-0,935
spiLA0480-MIR7997c-1	UCGCUAUGUUGCUCGGAUUCUCCAAAAUGUUGUCGCACGGAUCCUUAAGAAAUGCACUACAUUUGGAGGAUUGGACACUCGCCUAUCUGCAUUCUGAAAGAGUCCGAACAGCAUAGGUU	**119**	22,689076	26,05042	22,689076	28,571429	45,378151	54,621849	1,0967742	1	-37,8	-35,4	0,180913	7,4	-31,764706	-0,7
spiLA0480-MIR7997c-10	CUUCUAUGUUGCUCGGACUCUUUAAAGAUGUUUACGGGUGCAUGUCUAUUUCUUCCAAACUAGUGCAUGUUUGAAGGAACCGACACAGGUGCAACAGCAUCUUAGGAGAGUCUGAACAACAUAGGUU	**127**	22,834646	26,771654	19,685039	30,708661	42,519685	57,480315	1,1470588	1,16	-52,1	-52,1	0,061159	8,4	-41,023622	-0,9648148
spiLA0480-MIR7997c-11	AUUAUUUUAGUCUAUAUUGCUCGGACUCUUCAAAAAUGUCAAUGGUAGUGUAUUUUUGAAGAAUCUCAGACGGGUGCGGCAUCAAAAGUGAAGAGUCCGUGCAACUAAGAUUUUAAUUGC	**120**	21,666667	30	15	33,333333	36,666667	63,333333	1,1111111	1,4444444	-34	-33	0,0425875	15	-28,333333	-0,7727273
spiLA0480-	AGGCUAUGUUGCUCGAACUCUUCAAAAUGUUGUG	**80**	25	27,5	11,25	36,25	36,25	63,75	1,3181818	2,2222222	-	-31,8	0,159294	3,5	-39,75	-

MIR7997c-12	AAACUUGUAGAAGUGGUGUUUUUGAAGAUUUCGAGCAAUAUAGGUU										31,8						1,0965517
spiLA0480-MIR7997c-13	CUUCUAUGUUGCUCAGACUCUUCAAAAAUGUCGCCAUGUGCAUGUUGGAUCCUUCAAAAGCAGUACGUCUUUUUAUGGAUACCACAGGUGUGGCGACAUUAUUGGAGAGUCCGAGCAACAUAGCUG	**126**	23,015873	25,396825	21,428571	30,15873	44,444444	55,555556	1,1875	1,0740741	-63	-63	0,0493363	4,5	-50	-1,125
spiLA0480-MIR7997c-14	AGAAGCUAUGUUUCUCGGACUCUCCAAAAAUGCUACAUAAUUCACUAUUUUUGAUGGAUCCGACAUGCAACCCAUAGUGUUUUUGAAGAGUUCGAGAAGCAUAGCUGAG	**109**	20,183486	30,275229	19,266055	30,275229	39,449541	60,550459	1	1,047619	-42,8	-41,22	0,0727514	13	-39,266055	-0,9953488
spiLA0480-MIR7997c-15	CUACUAUGAUAUUGCUCAGACUCUUUAAAAAUAUCACUAGCUGCGUGUUGGAGGUGUUGGAUCCUCCAAAGUAAGUGCAUUUCUAGAUGAUUUGAUAUAGGUGCAACAAUGUUUUUGAAGAGUUCGAGAAUUUUCCUAGCAC	**143**	20,979021	28,671329	16,083916	34,265734	37,062937	62,937063	1,195122	1,3043478	-37,8	-34,9	0,0069025	17	-26,433566	-0,7132075
spiLA0480-MIR7997c-16	GGAUCCUAUGUUGCUCGGACUCUUCAAAAAAGUCGAGGGGUGUUUGUCAGGUCCUCCGAAAGCAGUGUGCUUUUGAAGGAUCUGACACGGGUGGGGCAACAUACUUGGAGAGUCCGAGCAACAUAGGAGGG	**131**	32,824427	24,427481	19,083969	23,664122	51,908397	48,091603	0,96875	1,72	-70,8	-69,77	0,0350722	11	-54,045802	-1,0411765
spiLA0480-MIR7997c-17	CCUAUGUUGCUCGGACUCUCCAAAAAUAAGGAUCAGAUACACAACCAUCGAUAUUUUUGACGAGUUCGAGCAACAUUAA	**79**	16,455696	34,177215	22,78481	26,582278	39,240506	60,759494	0,7777778	0,7222222	-31,5	-31,5	0,498324	3	-39,873418	-1,016129
spiLA0480-MIR7997c-18	UGACAUAUAUGUUAUGUUGCUCGGACUCUUCAAAAAUGUUGUAACAUUCAUGUUAGAUCCUCUGAAAAUGUACAACUUUUGAAGAAUCUGACAUGUAUUGACGAUAUUUUUGAAGAGCUCGAGCAACAUAGCAUAGAGUGAAA	**143**	18,881119	33,566434	14,685315	32,867133	33,566434	66,433566	0,9791667	1,2857143	-64,1	-64,1	0,0905617	11	-44,825175	-1,3354167
spiLA0480-MIR7997c-19	AAGACCUAUGUUGCUCGGACUCUCCAAAAAUCAACUACUUUUGAAGAGUCCUAUACACGUGUUGACAUUUUCAGAGAGUCCGACCAACAUAGGUAAA	**97**	17,525773	32,989691	22,680412	26,804124	40,206186	59,793814	0,8125	0,7727273	-38,5	-38,5	0,0847405	8,4	-39,690722	-0,9871795
spiLA0480-MIR7997c-2	UGGAAAAUUUCUAUGUUGCUCGGACUCUUUAAAAAUGUUGAUGAGUGUGUGUUGGAUACUCCAAAAGUAGUGCAUUUUGGAGGAUACGACACGGGUGUGGUGAUAAUUUUGAGAGUUUGAGUAACGUAGGCAAAAUUUAUU	**141**	26,950355	28,368794	9,929078	34,751773	36,879433	63,120567	1,225	2,7142857	-51,2	-49,9	0,0034051	12	-36,312057	-0,9846154
spiLA0480-MIR7997c-20	AUAUUGCUCGGACUCUUCAAAAAUGUGGACGGGUGUGUGUCGGAUGAUCCUCCAAAAGUAGUGCAUUUUUGGAGGAUCUGGCUUAGGUGCGGCAACAAUUUUGGAGAGUCCGGGUAAGUU	**120**	30,833333	23,333333	15,833333	30	46,666667	53,333333	1,2857143	1,9473684	-58,2	-58,2	0,114642	5	-48,5	-1,0392857
spiLA0480-MIR7997c-21	AGAGGCUAUGUUGCUCGGACUCUUUCAAAAUGUGGAAGGUUGUGUCAGACCCUCCAAAAAUAGUGUAUUUUUGAAGGAUCCGACACGGGCGAGGCAUCAUUUUGGAGAGUCCGAGCAACUUAGCCCAG	**128**	27,34375	26,5625	20,3125	25,78125	47,65625	52,34375	0,9705882	1,3461538	-66,4	-64,1	0,044684	5,3	-51,875	-1,0885246
spiLA0480-MIR7997c-3	CGACUAUAUUGCUCGUACUUUUCAAAAAUGUUGUCAGACCUGUAUGUAUGUACUUUUGGACGAUCUGACACACACCUGACAGUACUUUUGAAGAGCUCGAGCAACAUAGAAA	**112**	18,75	30,357143	20,535714	30,357143	39,285714	60,714286	1	0,9130435	-36,5	-35,2	0,0688978	9,1	-32,589286	-0,8295455
spiLA0480-MIR7997c-4	UACUAUGUUGUUCGGACUCUUCAAAAAUGUUGCUGCGCCCAUGUCAGAUCCUCCAAAAAAUGUACUAAUUUUUGAGGAUCCAAUGUGCACUCGGUGCCUUCUUUGAAGAGUUCGAGCAACAUAAUU	**126**	19,047619	26,984127	21,428571	32,539683	40,47619	59,52381	1,2058824	0,8888889	-52,6	-50,8	0,0718719	16	-41,746032	-1,0313725
spiLA0480-MIR7997c-5	UGAAUUAAUAUUAUGUUGCUUGGACUCUUCAAAAAUGCUGAUGGCUGAGAAUUGGAUCCUUCGAAAAUAGUGCAGUUUUCGAGGAUCUGAUACGGGUGCAGCAGCAUUUUCGAAGAGUCAAAGCAACAUAGAAUUAAUGUA	**141**	23,404255	31,914894	14,184397	30,496454	37,588652	62,411348	0,9555556	1,65	-64,5	-64,5	0,054351	6,5	-45,744681	-1,2169811
spiLA0480-MIR7997c-6	AUUCUAUGUUGCUCGGACUCUUAAAAGAUGUCGAUGAGUGUGAGUCCAAUCCUCCAAAAAUAUUAAAUUAUUGAAGAUCUGACAUGUGUGACAAUAUUUUCGGGAAGUUUGAGCAACAUAGUCU	**124**	20,16129	31,451613	15,322581	33,064516	35,483871	64,516129	1,0512821	1,3157895	-36	-29,5	0,0194592	18	-29,032258	-0,8181818
spiLA0480-MIR7997c-7	GGUUAUAUUGCUCCGACUCUUCAAAAGUGGUCACACCCAUGUUGAAUCCUCCAAAAAGGCAAUACUUUUGGUGGAUCCAACAUGCACCUGUUGACAUUUCUGAAGAGUUCGAGCAACAUAGUU	**123**	19,512195	28,455285	22,764228	29,268293	42,276423	57,723577	1,0285714	0,8571429	-48,2	-45,4	0,0079312	9,3	-39,186992	-0,9269231
spiLA0480-MIR7997c-8	AAGCUAUGUUGCUCGGACUCUUCAAAAAUGUCGCUGGUAGUGCAUUUUUUUGGAGGAUCCGAUAAGG	**106**	24,528302	28,301887	16,037736	31,132075	40,566038	59,433962	1,1	1,5294118	-49,5	-49,5	0,0779466	10	-46,698113	-1,1511628

spiLA0480-MIR7997c-9	GUGCUGCAACAUUUUUAAAGAGUUCGAGCAACAUAGAUAUGGACUAUAUUGCUUAUACUCUUCAAAAAUAACGACGGAUGCAUAUCGGAUACUCCAAAAAUAGUGUACUUUUGGAGAAUUCGAUAUGGAUGUGACAACACUUUUGGAGAGUUCGAGCAACAUAGUUUU	**129**	20,155039	32,55814	15,503876	31,782946	35,658915	64,341085	0,9761905	1,3	-51,7	-51,7	0,166614	3,5	-40,077519	-1,123913
spiLA0480-MIR7998-1	AUUGUAGGUCCAGUCACGGUCCAUCAGUGGGUAGACCUAGAUUUCUCAUCUAGGAUGUUUGAGUAUGUGUCGAACUACCGAGGCUAGUGACGGACCGUAGAUCAAUCCACGGUCCAUACUGCAAGUUUAACAAUGAUCACUUAGAGUUAAAUUUCAAAGUCUGGAUGAAAAAUUCUAAGUGUGGACCCACAGAGGACCCAUGGAACAUGGAUCGACCCA	**219**	23,744292	29,680365	21,004566	25,570776	44,748858	55,251142	0,8615385	1,1304348	-72,7	-72	0,0001018	24	-33,196347	-0,7418367
spiLA0480-MIR7998-2	ACCACCGACAGACCGUAGGGUGACCUACGGUCCAUAGGUAGGGUCUAUAGAUGGUCACCUGCAACUCUCCCCGGAAAAGUCCAAAAAAUUGUUCACGGUCGAACCCACGGACCGUAGGUCAAUCCACGGUUGUGGUCCU	**139**	25,179856	25,899281	28,776978	20,143885	53,956835	46,043165	0,7777778	0,875	-54,3	-51,5	0,0251781	27	-39,064748	-0,724
spiLA0480-MIR8001a-1	GUGCACUACAAGAAAACUAUGAAUUAUAUGGGCAUUUUUCUGGGGAUUAGUAUGAAAAUUCGCAGAAAACUUAUAUUCCUGCAAAUUUUCAUACUAAUUCCUCGAAAAAUCCCCAUGUAAUUCACAGUUUUCUUGUAGUGGGA	**143**	16,783217	32,867133	16,783217	33,566434	33,566434	66,433566	1,0212766	1	-78,3	-78	0,265716	3,3	-54,755245	-1,63125
spiLA0480-MIR8001a-2	UCCUGGGGAUUAGUAUGAAAAUUCAAAAGAAACUUAUUUUCCUGCAAAUUUUCACACUAAUUCCCAUGA	**69**	13,043478	34,782609	18,84058	33,333333	31,884058	68,115942	0,9583333	0,6923077	-22,6	-22,2	0,160219	5,2	-32,753623	-1,0272727
spiLA0480-MIR8001a-3	AUGGGGAUUUUCCUGGGGAUUAGUAUGAAAAUUCGUACCAAACUUAUUUUUCUGCAAAUUUUCAUACUAAUUCCAGGAAAAUCCCCUU	**88**	15,909091	29,545455	18,181818	36,363636	34,090909	65,909091	1,2307692	0,875	-44,7	-44,3	0,0664815	6,2	-50,795455	-1,49
spiLA0480-MIR8001a-4	UUUUCCUGGGGAUUAGUAUGAAAGUUCGCAGGAAACUUAUUUUCCUGCAAAUUUUCAUAUAAAUUUCCAGGAAAA	**75**	17,333333	32	14,666667	36	32	68	1,125	1,1818182	-40,3	-40,3	0,261995	1,8	-53,733333	-1,6791667
spiLA0480-MIR8001b-1	GGGAAUUACAUGGGGAUUAGUAUGAAAUUUGCAGGAAAAAUAAUUUUUUGCGGAUUUUCAUACUAAUUCCUAGGAAAAUUUCU	**82**	20,731707	32,926829	9,7560976	36,585366	30,487805	69,512195	1,1111111	2,125	-34,6	-34,6	0,0822065	4,9	-42,195122	-1,384
spiLA0480-MIR8001b-2	CCACACUACAAGAAAAGUAUGAAUUACAUUGAGAUUUUCCUGAAAAUCAGGAUGAAUUUUUGCAGGAAAAUAAGUUUCCUACGUAUUUUCAUACUAAUCUUAGGAAAAUCCCAUGUAAUUCACAGUUUUCUUGUAGUGCCA	**141**	14,893617	34,751773	17,021277	33,333333	31,914894	68,085106	0,9591837	0,875	-54,1	-52,3	0,0391154	6,5	-38,368794	-1,2022222
spiLA0480-MIR8001b-3	UUCUUUUUGGUGGCAAUUGGUUCGAAUUUGCCACGCGAUAUAUCUAGUAUACAUGGUAUAUUCAAACUAAUUCCCACGAAAAAAUC	**86**	16,27907	30,232558	18,604651	34,883721	34,883721	65,116279	1,1538462	0,875	-27,1	-26,9	0,320398	4	-31,511628	-0,9033333
spiLA0480-MIR8001b-4	UCCCACUACAAGAAAACUGUGAAUUACAUGGGGAUUUUUCGAGGAAUUAGUAUGAAAAUUUGCAGGAAUAUAAGUUUUCUGCGAAUUUUCAUACUAAUCCCCAGAAAAAUGCCCAUAUAAUUCAUAGUUUUCUUGUAGUGCAC	**143**	16,783217	33,566434	16,783217	32,867133	33,566434	66,433566	0,9791667	1	-82,9	-82,9	0,567608	2,4	-57,972028	-1,7270833
spiLA0480-MIR8001b-5	UAAACUACUCCUAGAAAACUGUGAAUUACAUAGGGAUAGGAAAACUAAUUCCUAGGAAAAUCCCCAUGUAAUUCAUAGUUUUCUUGUAGUGUGCA	**95**	16,842105	35,789474	16,842105	30,526316	33,684211	66,315789	0,8529412	1	-39,2	-39,2	0,208816	5,3	-41,263158	-1,225
spiLA0480-MIR8003	AGGUAGGUUCUUCAUUAUUUCGAUAUACAAAUGGGUCCUGUAUUUUUUUCGGUAUACAAUGGAUCCUGCAUUUGUAUAUUUCAGUAUAUAAACGGGUUCUGCAUUUGAAUAUUUCGGUCUAAUUGUAUAUUUUGAUAUACAAAUGGGUCCUACAUUUGUAUAUUUCGGUAUACAAAUGGGAUGACAAAAAAUAUGGAAUGUUUGCUACGAAUUACAAAUAGAAGAAACUAUGG	**233**	18,88412	31,330472	12,017167	37,76824	30,901288	69,098712	1,2054795	1,5714286	-59,5	-58,2	0,0026651	36	-25,536481	-0,8263889
spiLA0480-MIR8004	AUAAGUGGGGUCUUGAGAGGGUAGAGUGUAUGCAAAUCUUACCCCUGCCUCUUUAUCUUUACGAGGUAGGGGUAAAGUAUGCGUAUAACCUACCCUCCCCAGACCCCACUUGU	**113**	23,893805	23,893805	23,893805	28,318584	47,787611	52,212389	1,1851852	1	-71,8	-70,6	0,187101	4,4	-63,539823	-1,3296296
spiLA0480-MIR8005b-1	GUGAACUGAAAAUUGAAAAUAUUAAAUCGAGUUGAGAUAGAAGUCGGGUUGGGUAUUGACCCACCCAAGUUUAAUUUGGGCUCGAAUGGACAUAAAAACGGGUUGGAUCUUGACCCGUCAAUUUGAUCCGAUUAAUC	**245**	16,734694	32,653061	13,877551	36,734694	30,612245	69,387755	1,125	1,2058824	-53,9	-36,5	1,78E-05	75	-22	-0,7186667

spiLA0480-MIR8005b-2	UAACAUACCACACAUAUUGAUAUUUAACUUUUAUA AUCACAAUUUGAAUUUUAGCUCGAAAUUAUAUAUA UAUUAGCUUAUGAUUUAAGUUUUUCUUUUUCAUU UUGA UCUAUAAUUAUAGACAUAAACAUUUUGUGGAGCU CUACAAGACUUGUUUAAUUUGUGUUGGGAUUCCA CAAAUUGUGAUCAACUCAAAUUAGGAUUCUUGGA GACUAGUCAACUCUAAAUUCUAAUUUAUGCC	**133**	15,789474	31,578947	15,789474	36,842105	31,578947	68,421053	1,1666667	1	-31,8	-31	0,0451105	12	-23,909774	-0,7571429
spiLA0480-MIR8005c	UGUACCUUACAAAUCAAAAUCUUCUUUUUAAACUC AUUCAAAUUCUCAUCCUCAAAUUGGUUGGCCUUG AUCUCUUUAAUGAAUUUGGCCCUCAAUUCAAUAC UAGAUAGUUUUAGGUUUAGGGUUUAGGAUUUAGG GUUUGGAUAUAGGGUUUAGAGUUUAGGGUUUUG AGUUUAGGGUUUU	**183**	19,672131	25,136612	13,114754	42,076503	32,786885	67,213115	1,673913	1,5	-49,4	-33,02	0,0076779	34	-26,994536	-0,8233333
spiLA0480-MIR8006-1	UGCGUUCCUGCCGUCCAAGAACUAGAACAUGUAU AUCCUUUAUACUAACGGACAUACAUGUCAUAUUC UUAUCCGCUGAUUCGACACUUAUUGACGAAUAAG AUUGUGUCAUCUGUCCCUAUUUAGUCUUAUGUUA UAGUGAAGGGCAUAUAUACUCUAGUUUUUGGACG ACAGGGACACC	**181**	18,232044	27,071823	20,994475	33,701657	39,226519	60,773481	1,244898	0,8684211	-67,3	-66,9	0,0920172	11	-37,18232	-0,9478873
spiLA0480-MIR8006-10	UAUCCUCUGUCAUAUUUUGGAGACAUUGCAUAUA UGCCUUUUACUCUGACGAAAGACUAAACAGGAAC ACAUGGUGCAAUCUUAUCUGUCGAUUCAAUAUUU AAUAAAUGUUGGAUCGGUGAAUAAGAUUAUGACA CGUGAAUGUCAGUUAGUAUAAAAGGUAUGUAUGC UCUAAUUUUUUGACGACAUGGGUACCAAUGUCCC AAAAGUAUGACGGAGGAUA	**223**	20,179372	32,286996	15,246637	32,286996	35,426009	64,573991	1	1,3235294	-81,4	-74,09	8,33E-05	30	-36,502242	-1,0303797
spiLA0480-MIR8006-11	AUAUAUUCUCGAAUUAUUAUGACUAAUAUCCUCG UCAUAUUUUUGAGACAUUAAUGUUUUUUUGUCCA AAAACUAGAACAUAUAUACCAUUUAUAUUAAUGGA UAUACAUGUGACGUAAUCUUGUUCCUAUUUAGUC UUCCGUUAGAGUAAAGGAAAUAUAUACUCUAGUU UUUGGACGGCAAGGGAACCAAUGUCCCAAAAGUA UGACGGAGGAGGGUAUGCGCAUAUCAUUAUAAUA GUC	**242**	16,942149	32,644628	14,876033	35,53719	31,818182	68,181818	1,0886076	1,1388889	-74,3	-72,8	0,0013465	47	-30,702479	-0,9649351
spiLA0480-MIR8006-12	AUCUUAGUGCCCCUGUCGUCCAAAACUAGAGCAU AUAUACUUUUUAUACUAACGGACAUACAUGUGUC AUAAUCUUAUCCACUGACCCGACAUCAGAUCGAU GGAUAAGAUUGACCACGUGACUCUAUUUUGUCAA GGGCAUAUACAUUCUAGUUUUUGGACGACAGGGG CACCAAUGU	**179**	18,435754	29,050279	22,346369	30,167598	40,782123	59,217877	1,0384615	0,825	-72,6	-71	0,0045106	17	-40,558659	-0,9945205
spiLA0480-MIR8006-13	GUUUCCCUAUUUAGUCUUUUGUUAGAGUGAAGGA CAUAUAUACUCUAGUUUUUGGAUGGCAGGUGCAC CAGUGUUCCAAAAGUAUGACAGAGGUAUCUGCAU ACCAUUUACGAUAGUUCAGGGCUAUAUUUGUCCU UUUUCUAUAUAUUAUUAUAUAUUUACUGCUUAAGA GUUUACUACGUAUCUUACACUUAGAUACAUAUAU UUUUGCUACAGAUACACAUAAAUAGGGAGCU	**236**	17,372881	28,389831	15,677966	38,559322	33,050847	66,949153	1,358209	1,1081081	-59,5	-51,4	0,0002457	32	-25,211864	-0,7628205
spiLA0480-MIR8006-14	GAACUAUCGUAAAUGGUAUGCAGAUAUCCUUCCU CAUACUUUAGGGACGUUGGUGCCUCUGCUAUCCA AAAAACUAAAGCAUAUAUACCUUUUACACCAACAA ACAUACACGUGUCAUAAUUUUAUACCGACCUGAC AUCGGAUCGAUGAAUAAGAUUGUAUCACGUGUCC CUAUUUAGUCUUCCGCUACACUCUAGUUUUUGAA CGACAAUGGCACCAAUAUGUUCCAAAAGUAUGAC CGAGAGUAUCUGCAUAUCAUUUACUAUAGCUC	**271**	15,498155	30,99631	22,878229	30,627306	38,376384	61,623616	0,9880952	0,6774194	-92,5	-92	0,0074345	16	-34,132841	-0,8894231
spiLA0480-MIR8006-2	CAUAUACCCUCCGUCAUACUUUUAGGGCAGUGGU GAACAUAUAUGUCAUUCACUCUAACGAAAGACUAA AUAGGGUCACGUGACACAAUCUUAUUCAUCGAUA AUAUUUAAUAAAUAUCGGGUCAGUCGAUGAGAUU AUGUCAUGUAUAUGUCCGUAUUCAUAAAGGGUAU AUAUGCUCUAAUUUUUGGACGGCAUGAGCACCAA UGUCUCAAAAGUAUGACGGCAGAUAUUUU	**234**	18,803419	31,623932	17,521368	32,051282	36,324786	63,675214	1,0135135	1,0731707	-71,5	-68,7	0,0034414	36	-30,555556	-0,8411765
spiLA0480-MIR8006-3	UUUUGGGACAUUGGUGCUCCUACCGUCCAAAAAC UGGAGCAUAUUCGUAGAUAAAUGUCGGAUCAGUG GAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAU	**155**	23,225806	30,967742	16,129032	29,677419	39,354839	60,645161	0,9583333	1,44	-58,5	-48,07	0,01007	26	-37,741935	-0,9590164

spiLA0480-MIR8006-4	AAAGGGUAUAUAUGCUUUAAUUUUUAGACGACAG GAGCAACGAUGUCCCAAAA AGAUUCGUCAUAUUUUUUGGAUAUAUUUAUCUUA GUCGUCCAAAAACUAGAGCAUAUAUACCCUUUAUA CUAACGGACAUGCACGUAUUAUAAUCUUAUUAAC CGACCCGACAUUUAUUAAAUAUCAGAUCGACGGA UAAGGUUGUGUUACGUGUCCUUAUUUAGUCUUUC GUUAGAAUAAAUGACAUAUAUGACCUAGGUUUUG GACGACAGGGCACCAAUGUCCCAAAAGUAUGACG AAGAG	**244**	17,622951	31,967213	17,622951	32,786885	35,245902	64,754098	1,025641	1	-87,3	-85,6	0,0170707	14	-35,778689	-1,0151163
spiLA0480-MIR8006-5	UGCUUUUGGGACAUUGGUACCCCUACCGUCCAAA GACUAGAGCAUAUACCAUUUAUAUUAAUUGACAUA CACGUUUCAUAAUUUUAUCCACCAACCUGACAUCA GAUCAAUGGAUAAGAUUGUGUCACGUGUCCCUAU UUAGUCUUUCUUUAGAGUGAAAGAUAUAUACGCU CAAAUUUUUGAAUGACAGGAGCACUAAUGUCCCA AAAAAG	**212**	16,037736	32,075472	20,283019	31,603774	36,320755	63,679245	0,9852941	0,7906977	-70,2	-69	0,069176	11	-33,113208	-0,9116883
spiLA0480-MIR8006-6	CAUAUAUAUACUCUAGUUUUUGGAUUACAGAGAC ACCAAUGUCCCAAAAAUAUGACAGAGAGUAUUUAC CUAUCAUUUACCAUAAUGACAAUUUUUUUGGUAAA ACAAUAAACUCUACAAAAUGUAUAUUUUUAAGGAA AAAGGACAAAUAUAUCUCAAGCUAUCGUAAAUGGU AUGCAGAUACCCUCCGUCAUAUUUUUGGAACAUU AGUGCCCUGCCGUCCAAAAACUAGAGCAAUAUGC C	**243**	13,99177	37,037037	18,518519	30,452675	32,510288	67,489712	0,8222222	0,7555556	-73,6	-62,91	0,0010512	34	-30,288066	-0,9316456
spiLA0480-MIR8006-7	CUAAACAAAUGUGAACACAUCAUUGGUCCGAUGU CGGGUCGGUGGAUAAGAUUAUGACACGUGUAUAU CCGUUAGUAUAAAGGGUAUAUAUGCUCUAGUUUU UGGAUGACAGGGGCACCUAUGUCACAAAAGCAUG AUGGAGGGUAUUAUAAUACCAUUAAUGAUAGUUC GGGGGUAUAUUUGUCCUUUUUCCCUAUUUAUAAC GAGUGAGUGCUCUUUACAUUUGUUACG	**231**	23,376623	27,705628	15,151515	33,766234	38,528139	61,471861	1,21875	1,5428571	-63,7	-50,6	0,0002553	53	-27,575758	-0,7157303
spiLA0480-MIR8006-8	UUUGUCAUAUUUUUAGUAUGUGUCUUUAUCAUUA AAAAAUAAAGCAUAUAUUAUGUCCUUUAAUCUAAC AGAAGACUAAAUAUUGACAUACAUGUGCGUAAUC UUCUCCAUCGAUUCGAUGUCGGAUCGGUGGAUAA GAUUAUGACCACGUGUAUGUCUGUUAGUAUAAAG CGUAUAUAUGCUCUAGUUUUUGGACGGCAGAAAC ACCAAUAUCUCUAAUAUAUGACGGA	**230**	17,391304	31,73913	15,217391	35,652174	32,608696	67,391304	1,1232877	1,1428571	-78,1	-68,5	0,000606	33	-33,956522	-1,0413333
spiLA0480-MIR8006-9	UGGGACAUUGGUGUCCCUACCAUCUAAAAACUAG UAUAUACCCUUUAUACUAACGCACAUACACAUGUC AUAAUCUAAUCCACCGACCCGACAUUUAUUAAAUA UUGGAUCGAUGGUUAAUAUUGUGUCACGUGUGUC UAUUUAGUCCUCCGUUAGAGUGAAGGGUAUAUAU ACUCUAGUUUUUGGACAUCAAGGGCACCAUGUCU CA	**208**	17,307692	28,846154	21,153846	32,692308	38,461538	61,538462	1,1333333	0,8181818	-80,9	-70,9	0,0073482	19	-38,894231	-1,01125
spiLA0480-MIR8007a-1	AUGUAUUUAUACUAAGUUUAUGGUCACUGUCACA AGUAUCAACCAGUGUAAUGGUACUUCCUCUGUGC CAUUUUAUGUGGCACUUUUCGGAUUUCGAGUAAA CAUUUUGAAUUAUUAAUUAUUGUGACCAAUACUU UUUAUAAAUAGUU	**149**	15,436242	28,187919	14,765101	41,610738	30,201342	69,798658	1,4761905	1,0454545	-37,1	-35,9	0,0309072	17	-24,899329	-0,8244444
spiLA0480-MIR8007a-2	UAAUACUUCCUCUGUUCCAAUUUAUGUGGCAUAU UUCGGAUUUUGAGAUUCUAACAAGUUUAAGUGGU UAAUACUUCCUCCAUUCCAAUUUAUGUGCACAUU UUGAAUCUCGAAAUCUGAACUGUACCAUACAAAUU GGGACAAAGGUAGUAACA	**155**	15,483871	30,322581	18,064516	36,129032	33,548387	66,451613	1,1914894	0,8571429	-54,5	-54,5	0,126561	7,4	-35,16129	-1,0480769
spiLA0480-MIR8007b-1	AAAUUUUCUUACAUAGAGGUGGAUCCCGAAUCUU GAGUUUAUGGAUUUAGAUUCUAGAAAAGGUUACA UUUUCAAAACCCAACAAGUUACAUUUUUAGAAUUU CGUAUCCACAAACUCAAAAUUCUGGAUUCACCUC UACGUAAGCGAAAAGAG	**154**	15,584416	35,064935	17,532468	31,818182	33,116883	66,883117	0,9074074	0,8888889	-57,1	-56,3	0,0549398	9,3	-37,077922	-1,1196078
spiLA0480-MIR8007b-2	CGGGGACUUUCUUAAAGAGGAACCUCAUGUAAAU ACCAUGGAAUAAGGUUUGAUCCUAUUCAUGGAGA UUCCGUAACUAUUCCAAAAAUGGAAAGUUCGACA CAAUUGGUAUUUUUUUUUUGAAAUUGGAAGCAGU UACUAAUUCAUGAUCUGGCAUGUACAGAAUGAAA	**211**	18,483412	32,227488	15,63981	33,649289	34,123223	65,876777	1,0441176	1,1818182	-50,9	-40,7	0,0021715	43	-24,123223	-0,7069444

spiLA0480-MIR8007b-3	ACUUCAUUCUCGAUUCUACGAGAAUUUUUAUGAAAGCCUUUAUGCUAACAUGAUACUCCCUCUGUCCCAUUUUAUGUGACACUUUUUGUUUUUCGAGAGUCAAACGAUUUAACUUUGAUCAGACAUUUGCGCAUGGAAUCUUCAAUUUUUUUUUGAAAUGAAAUUUAUAUAUUUGUAACUACGUAAAGAGUUACUAAUGAGUCACAGUAAUUGAUAAUUCAAAAUGUUAAAAGGAUCUAUGAAAAACUUACGGUCAAAAAUAGACUUAUUUAAAUCUCGAAAUGCGAAAAGUGCAACGUAAAAUGGGACGGAGGGAGUAUUUAUUUAGUCG	**290**	17,241379	34,482759	13,793103	34,482759	31,034483	68,965517	1	1,25	-95,3	-88,07	0,0002958	38	-32,862069	-1,0588889
spiLA0480-MIR8007b-4	ACUGUUAAAUAAAUAAACACAUGAGUCCUAUAUGGCACAAUACAUGUAGGACAACACAUAGGACAAAAAAUGACAUGUAGGACAUAUGUGUCUAUUUGUUCAACUUU	**107**	15,88785	40,186916	15,88785	28,037383	31,775701	68,224299	0,6976744	1	-30,4	-29,52	0,0803746	12	-28,411215	-0,8941176
spiLA0480-MIR8007b-5	CUCCCUCUCUCCCAUUUUAUGUGACACUUUUCGGAUUUCGAGAUUCAAACAAGUCUAUCUUUGACCGUAAAUUUUUCAUAGAUCUUUUAAACAUUUUAAAUUAUCAAUUGUGGUGACUUAUAGUACUUUUUAUGUAGUUUACAAAUAUAUAAAUUCAUUCAAAAGAAUUAAAGAUUCCAUGCGCAAAUUUUCGGUCAAACUUAAACUACUUGACUCUUGGAAAACGAAAAGUGCCACAUAAAUUGGGACAAAGGGAG	**257**	14,007782	33,463035	17,120623	35,40856	31,128405	68,871595	1,0581395	0,8181818	-81,2	-66,49	0,0055432	44	-31,595331	-1,015
spiLA0480-MIR8007b-6	UAUAAAUAAACACAUGAGUCUUACAUGGCACAAUACACGUAGGACACCACGUAGGACAAAAAAUGACAUGUAGGACAUGUGUGUCUAUUUGUU	**93**	19,354839	37,634409	17,204301	25,806452	36,55914	63,44086	0,6857143	1,125	-27,8	-26,8	0,207973	4,3	-29,892473	-0,8176471
spiLA0480-MIR8008b-1	UUUUCCAUCACUUUUUUGCAUAAUUCUUUCAAAUAAACCCAGAAAAGCGACAGACAGGGUCCUUUAGUGCGUCGCGUUUCUGGGUUUUUCAAAAAAAUAAUUUUCAGAAAAGAUGGAUAG	**120**	17,5	31,666667	17,5	33,333333	35	65	1,0526316	1	-34,7	-31,8	0,0092715	14	-28,916667	-0,8261905
spiLA0480-MIR8008b-2	UUUGUCCGUCGCUUUUUUGCUUUAUUUAUUUCAAAUAAACCCAGAAAAGCGACGGACAAGGUUCUUUGGUCCGUCACUUCUCUAGGUAUUUUAAAAAAUUAAUUUCAAGGAAACCGACAGACAUUGUCCUUUAGUCGUCCCUCGCUUUUCUGGAAUUUUCAAAAUAUAAAUUUAAAGAAAGGCGACGGACUGC	**193**	17,098446	29,015544	19,689119	34,196891	36,787565	63,212435	1,1785714	0,8684211	-63,6	-54,18	0,0121722	45	-32,953368	-0,8957746
spiLA0480-MIR8009	AAUUUCCAGAAAAGCGACGGACAGGGUCCUUUAAUCUGUCGCUAUUCUGGGAUUUU	**56**	23,214286	25	19,642857	32,142857	42,857143	57,142857	1,2857143	1,1818182	-24	-23,7	0,138185	4,8	-42,857143	-1
spiLA0480-MIR8011a-1	ACAUGAACUUUGUUUUGUGUCUCACACAACUGAUGUAAGUUGUGUGAGGUCUCUUUUUGUUUUACAAGUCAGUGCGACCCAAAUCGUUGGACUCACCAACUCGUGAAAUAAAAAGAAGUCUCACGCAACUUGUGUUAAUUCUGUGAGUCGCAAAGUAAAUUUUCAAAU	**168**	19,047619	29,166667	18,452381	33,333333	37,5	62,5	1,1428571	1,0322581	-64,5	-64,1	0,0153601	11	-38,392857	-1,0238095
spiLA0480-MIR8011a-2	AAAUUAAUUAUCAAUCCGUAACUGUCAAUUGAAUGAGGUCUCUUUUUAUUUCACAAGUAGUUAGAAACUUAAAUCUUACAAAAAGUCCACAUUACUUUGUGUCCUGUCCACUUGUGAGAUAAAAAAGAGGUUCUGACAAAUAUUGUUAGCUUGUGGCACAUGUCAUCAAGGGCGGAGUCACUUUGUAGGUAGGGGUUCAUCUGAACCUCAUUCAACGGAAAAUUAUAUUAUUUAAACA	**238**	17,647059	32,773109	16,386555	33,193277	34,033613	65,966387	1,0128205	1,0769231	-59,9	-52,3	0,0010532	35	-25,168067	-0,7395062
spiLA0480-MIR8011a-3	GACACUAGUCAAGUGAGACUCAUUUUUGCCUCACAAAAAAUUAAGCCCAUUUGAGUCUACUUUUAUGUGAGACAAAAAGAAGCCUCACACAACUAGUAUUUUCUUUAUGACAACACGAAUACUAGUUGUGUGAG	**100**	15	36	21	28	36	64	0,7777778	0,7142857	-29,3	-29,2	0,345427	3,7	-29,3	-0,8138889
spiLA0480-MIR8011a-4	GCUUCUUUUUGUCUCACAUAAAAGUAGACUCAAAUGGGCUUAAUUUUUUGUGAGGCAAAAAUGAGUCUCACUUGACUAGUGUCAGAUGUGUGAGUCACAAAAUA	**138**	20,289855	30,434783	15,217391	34,057971	35,507246	64,492754	1,1190476	1,3333333	-55	-52,8	0,0207479	11	-39,855072	-1,122449
spiLA0480-MIR8011a-5	GUCUCACACAGCUGACACUAAUUAUGUAGGGCUUCUUUUUGUCCCACAAGUUAAUGAACCCAAAUUAUUACACUUCUGGGUCCACCGACUUGUAAAAUAAAAAGAAGCCUCAAAGAACUGGUGUUAGUUGUGUGAAGG	**138**	19,565217	31,15942	20,289855	28,985507	39,855072	60,144928	0,9302326	0,9642857	-59,2	-59,2	0,11776	4,7	-42,898551	-1,0763636
spiLA0480-MIR8011b	CCUUCACACAACUAACACCAGUUCUUUGAGGCUUCUUUUUAUUUUACAAGUCGGUGGACCCAGAAGUGUAAUAAUUUGGGUUCAUUAACUUGUGGGACAAAA	**138**	20,289855	28,985507	19,565217	31,15942	39,855072	60,144928	1,075	1,037037	-58,2	-58,2	0,0502544	7,3	-42,173913	-1,0581818

spiLA0480-MIR8013	AGAAGCCCUACAUAAUUAGUGUCAGCUGUGUGAGAC ACACAGCAGCAAUUUUUGUGUUUUUUAAAAAAAUUAACAAGUCAAUUUUGUCAGAAGAAAAUCGCUCCGUCAGAAGCGAUUUAGCCCUUUUGAUUAAAAAAAUAAUUAUAGCAGCUAUUUCCUUUUUCCUUAAAUAGAGGCAGGCAUUUUGGUCCUAACAUUUGGUCUGCCCAGCAACAUUUGUUAAUUUUUUUUUUUUGACAAAAUCGCUGCUGGAA	**218**	15,59633	31,192661	16,972477	36,238532	32,568807	67,431193	1,1617647	0,9189189	-57,9	-53,2	0,0050554	26	-26,559633	-0,815493
spiLA0480-MIR8014-1	UUUUACUCCCUCUGUCCAACAAUUCUUGUUCACUAUUGAAUAUAAUAAAUAUAAUGUGUUGAAAAAUGUCACAGAGAAAUGAUUAUAAGUAGGUAAAUUAGAAAAGAAGUGUAAAAUAAUCCACUGAUUUCAUAAAGUGGACAAGUAUUGUUGGACAUCCCAAAUUAGUAUAGUGGACAACUAUUGUUGGACAAAGGGAGUAGUUACAAUAUGAUACAUUAUGAAUCAAUACGUAACAACCAUCUAAACAGAGUGUAAUUAAGCACAACUGAGCUUCUCUCGUAAGUGUUGCAUUAGCUUUAUUUUGUAGCAAUUCAGUAGAAUUUAGAGCUUAAAAAUAAUAUAAUUGAGAAAGAAAAAAUGUAGCAAUCCUUUAAGCAAAGCUAAGCUUUUCACCAAACUAUGGUAUAUCAACCAUCACAGUCCUAACAAGGUAGUGUCCUUUUGGUUCCAAAAUGAGACAGAGUAUGGGGUGACUUCU	**205**	18,04878	38,04878	12,195122	31,707317	30,243902	69,756098	0,8333333	1,48	-59,1	-57,9	0,0088869	31	-28,829268	-0,9532258
spiLA0480-MIR8014-2	UUCUGAUCCCCUAACACUUUGUUUGGAUCAUUGUUACCCAUUGUUUCAUAAUGUAUUGUAUUGU	**340**	16,176471	33,823529	17,058824	32,941176	33,235294	66,764706	0,973913	0,9482759	-96,2	-94,5	0,001366	51	-28,294118	-0,8513274
spiLA0480-MIR8016	GGUAUUUCAUCCUUUUUGAGGAUUUUUUGGUUUCUAUAUAAAUCCACUUCAUUCACUAUUUUUAGAGGAGGAUUUUUGAGGGGAAGACCAAAGAGUACCCAUAAAAUUUUGAGAAUUCU	**119**	18,487395	28,571429	13,445378	39,495798	31,932773	68,067227	1,3823529	1,375	-26,8	-23,9	0,0069998	19	-22,521008	-0,7052632
spiLA0480-MIR8019	CCCCCCCCCGUUUUAAAAAGAAUAAUCUAGUUUGACUUGACAAGGAGUUUAAAAAAAGAAAGAAGACUUUUUAAUCUUGUGGUUCUAUAUUAAAUUUAUGUCAAAUGUAUCAAAAUGCCCUUCAAUCUUGUGGUCUUAAACAUGCCACGUGGAAAGUUAAGGUUAAAGUGUUGCCAAAAAAAGAAAAGGUCAUUCUUUUUUAAACAGACUAACAAGGAAACAAGGUCAUUCUUUUUUAGACGGAGGGAGU	**250**	18	36	15,2	30,8	33,2	66,8	0,8555556	1,1842105	-59,2	-53,7	0,0002369	43	-23,68	-0,713253
spiLA0480-MIR8020-1	CUCUCCUCAGACCUCACUUAGUAGAAUUUCAUUGAGUAUGUUGUUGUUGUAAAGCAUACUGAAUUAAUGCAAGUACACAAGUUACAACAACAACAUACUUACUGAAAUGCCACAAAAAGGGGUCUAGGAAGG	**132**	18,181818	35,606061	18,939394	27,272727	37,121212	62,878788	0,7659574	0,96	-49,9	-49,9	0,0474005	7,1	-37,80303	-1,0183673
spiLA0480-MIR8020-2	CAAGAUAUAGCUAAUUAGUUGAGUGACCAUCUGAGAAAUCAAUUCGAUUGAAGUCUGUAUACACUCUAUCCAUCCCAGACUUCACUAAUGUAAUUAUGCUGAAUAUGUUGUUGUUAUACACAAAGUAGGGGCAAAGUUGAGUUGAUUUCUCAUAUCGUCACUUGACUAAUAGAUAUUAUCCUA	**183**	16,939891	32,240437	16,939891	33,879781	33,879781	66,120219	1,0508475	1	-58,6	-58,6	0,0032995	14	-32,021858	-0,9451613
spiLA0480-MIR8021-1	AUAUUCAAGGCUCAAACUCGAGACCUCUAGUUAAGGAUCGAUGUUUCAUAUACAUCCCUUCAUAACUAUUGUUGGUUCUAAUAAUAACUUAAUUCACUCUCUCUUUUAUAUAAAUAGAAAUACGUUAAUAUUAUUGAGUUCUACCAACAAUAUUGUGUUGGUGAAGAAGUUAAUAUUACUUCAUCCUUAACUAGAAGUGUCAAGUUUGAGUCUUGGAAAUG	**221**	14,479638	32,579186	15,837104	37,104072	30,316742	69,683258	1,1388889	0,9142857	-73,8	-72,4	0,0228995	23	-33,393665	-1,1014925
spiLA0480-MIR8021-2	UCUUCAUAUUCAAGGCUCAAACUCGAGACCUCUGGUUAAGGAUAGAUGGAUCAUAUACAACCCACCACAACUUUUAUGGUACUAAUAAUGACUUGAUUUACUUUCUCUUAAAUAUUUGACAAUAUGUUGGAUUUAUUUGUUGUAUUCUACCAACAAAUAUUUUGAUUGAGUGAAAGUUAGUAUUUAUUUAUCCUUAGCCAGAAGUGUCAGGUUCGAAUCUUAGACAUGAGUU	**232**	15,948276	30,603448	15,948276	37,5	31,896552	68,103448	1,2253521	1	-61,6	-60,3	0,0018956	30	-26,551724	-0,8324324
spiLA0480-MIR8024a	AAACCAAGAACAAGAAAUGGAAGAAUGAAAGUCGUAUGGGUUCACAAAGACUCUGUGGCUAAAAAGUAAAAAAGAUAUAUUGAAGUUGUUUUGAUGAUUCAAGAAUCUUAUUACUUCAAUCUGAAGUUCUUAGUUACUUCGACUGGAUGAGUCCUAGUGAGGGAAUAAUUA	**222**	19,369369	34,684685	12,162162	33,783784	31,531532	68,468468	0,974026	1,5925926	-55,2	-30,7	0,001081	57	-24,864865	-0,7885714

spiLA0480-MIR8025-1	AGUCAUAAUUCAUUGGUUGAUUGUAUCAUUAACCAUUUCUUUUUUUGGUACCACACACUACACAUGCAAUUAAAUUAGUAUAAGUCGCCAUUAUGUUUUUCUUAACCAAGCUGAAUCAUAUAAUGGUGACUUAUACUAAUUUAAUUGCAUGCCGACUGUGUGUAUUUUCCGCAUGUGUGUAACUACUCUAU	**140**	14,285714	30	19,285714	36,428571	33,571429	66,428571	1,2142857	0,7407407	-58,4	-50	0,26536	14	-41,714286	-1,2425532
spiLA0480-MIR8025-2	GUCAAACAUCAUAAAGAAAUAUUUUACCACACACUACACAUGCAAUUAAAUUAGUAUAAGUCGCCAUUAUGUUUUUCUUAACCAAGCUGAAUCAUAUAAUGGUGACUUAUACUAAUUUAAUUGCAUGCCGACUGUGUGU	**139**	12,94964	35,251799	17,985612	33,81295	30,935252	69,064748	0,9591837	0,72	-57,4	-57,4	0,428416	6,2	-41,294964	-1,3348837
spiLA0480-MIR8025-3	UACUUAAUUAACUAAUUAAACUUAAAAACACCCCGAUCUUGCCAGUUCAACUUGAGUGCAAUACACUUUUAAAUUCUUGCCAAGUUUAGGGUUGUUUUCAACAUUUCUUUCGGCGUUUUAUUAAAAGCCUCAUGUUCCUACCUGAGUAUAAGACCACUUCUUAUGUUAUGUGGCAGAUCGGGAGUGUAUCUAAGUUUAGUUAGUUAAAUAACGA	**214**	15,88785	29,439252	18,224299	36,448598	34,11215	65,88785	1,2380952	0,8717949	-63,3	-55,2	0,0016574	28	-29,579439	-0,8671233
spiLA0480-MIR8027	UGUCUGAGCCAGCUUAUGAGCUGCUUGAAUCGUUUCAAGUAUCAAGUAACUCAGCCAAAUUAUAAGAUAUAAUAAUCCAGGAUAAAAUGCAGGAUUAUUUUAUAGUAUGUUUAGUUGGAGGUAUUAGGUAAUGCUUGGAUUGUUUAUUCCACUAUUUAUACCUUAGUGAUAAUAUAAGUUUAUCUCAUAUACAUGGUGGAAUAACUUAUAACGGCAUAAUUAAUCUCGAGAUAACUUGUUUCCAACCAAACGACUCAUAAGUGUCUUAGUUUAUCUAUUUCUAUUUGUAUAAAGCGAGAUGAAAUUGUAUAAAUACAUAUAUUUUUGUUCACCUCUCUCCCUAAUCUCGCUCGUCACCCUCACCUCUCUCGCUUAUACAAACAGAAACGAAGUGUAUAAAUUGUGUUUGUGUUUGUAUAAAGCGAGAGAAAAUUGUAUAUACACAUGCAAAUACAUAUAUUUUCAUCCUAUACACUUAUAAUUAUACAAUAAAGAUACUC	**272**	17,279412	32,352941	14,338235	36,029412	31,617647	68,382353	1,1136364	1,2051282	-65,8	-57,4	0,0001992	62	-24,191176	-0,7651163
spiLA0480-MIR8028	GUACAAAACUGAACCGAAAAUCAAACCAAAUCGCAAAUCGAGUCAACCCAAAAAAAAUCCGACUAGUGAUUUGGUUUGACUUGGUUUGGUAUUGGAA	**228**	11,403509	34,210526	18,859649	35,526316	30,263158	69,736842	1,0384615	0,6046512	-54,5	-52,02	0,0014547	30	-23,903509	-0,7898551
spiLA0480-MIR8030-1	UAGUGGUUUGGUUUGACUUGGUUUGGUAUUGGACAAAAAUACCCGACUAUAUUUGGGUUGGUUUAGUUUUAGCUAAAAAAAACAAACUCGAGACCAAACCAACC	**97**	18,556701	39,175258	18,556701	23,71134	37,113402	62,886598	0,6052632	1	-32,9	-32,9	0,421455	3,2	-33,917526	-0,9138889
spiLA0480-MIR8030-2	GGCAUGUAAUAAGGUUGAAUAACACAAUUAACUAAACUGAAAGUAGCGGUGUACAAAACCAAACCAAACCGCACACCGAGUCAAACCGAAAAGAAACCCGACUAGUAGCUUGGUUUGACUUGGUUUGGUAUUGGGAAAACCCCCCCACUAUAUUUGGGUUGGUUUGUUUUUAACUAAAAAAAAAUCAACCCGAGACCAGACCAACCC	**103**	21,359223	31,067961	15,533981	32,038835	36,893204	63,106796	1,03125	1,375	-30,1	-28,6	0,0151681	19	-29,223301	-0,7921053
spiLA0480-MIR8030-3	GACUUCAUUUUUGUAAUUUUGAAAUAUAAUUUUAUACAUAAA	**248**	16,935484	36,693548	19,758065	26,612903	36,693548	63,306452	0,7252747	0,8571429	-64,1	-54,4	0,0001633	42	-25,846774	-0,7043956
spiLA0480-MIR8032e	GAAUGAUCAUUUUUUAUCAAAAAGUUCAAGAAGAUGACAUCAGAAUCAAAUUCUGACGAUUCCAUCAGUUUCGGAAGGGUCAUUUUAGGCUAGUAGCAUUGUCACCCUGACUCCCAAAGUUUUCAGUGUGAGUUGGUGUGAUUAGGCGUUUUUACUUUAAGAUAAAGGCAAAGUUUGAAUUUAGUCAACAUUCUGAGUAAACGCGCUCGGAUGAGAAUUUCGUCAGCGCGACUUGCUCCGGAAUGUCGAGUUUUGUCUAGUUUGAUCCUUCUUUUGGGUUUUGAGGUUUUUGAUAUUUUUCCAAGCCCUUUUGUGGUUUUUGACUUAAAAUGACCAAAGGCAUUAGCUGGAGUACAAGCUUCCAAAGCUGCAG	**339**	21,828909	25,958702	16,224189	35,988201	38,053097	61,946903	1,3863636	1,3454545	-98,8	-96,5	0,0004187	34	-29,144543	-0,7658915
spiLA0480-MIR8033	AAAUGAGUUUUUUUUUUAACUGAAAAAGAAAAACUAUUUCUGCAGCUUUGGAAUUUUUUACUCCAGCUAAGUU	**108**	17,592593	31,481481	15,740741	35,185185	33,333333	66,666667	1,1176471	1,1176471	-60,1	-59,1	0,115534	5,4	-55,648148	-1,6694444
spiLA0480-MIR8034	UUUAAAUACUGAAUUAAGAAAAAGUAAAAUCAGAUUGUUGUUCUUAACUAAUUAAUUAAUGGGGCGGUUUGGGUCGGGUUGACCUUGAGGGACCCGUUUUUG	**309**	18,446602	32,038835	12,621359	36,893204	31,067961	68,932039	1,1515152	1,4615385	-73,2	-60,95	0,0002261	46	-23,68932	-0,7625

spiLA0480-MIR8037	CGAUGGGGACAUCACGGGUUAGAACCCGAUGGAAGAAACAUUUAAGUGGAUGAAAUUGAGGUUUAUAAUCUAAUUUAUAAAUUAAUUAACUUUAUUAUGUUAACAGCUUUUAAGGGUAUUUCAGACAUUUUGAUUUAAAAAGCUGUUUAUAAGCACUUAUUUGCCAAACACAUCAACAACUUUUUUUUUUACUUCAGCACUUUUAU	**159**	20,125786	38,36478	11,320755	30,188679	31,446541	68,553459	0,7868852	1,7777778	-37,2	-35,9	0,0321117	19	-23,396226	-0,744
spiLA0480-MIR8038b	UAAAAAUGCAUUUAUUUGGAAUAAUAGUAACCAUGAAUAGUAAGAGUCAAGUUACUGUGUAAAUAGUAAGAGUCAAGUAACUGUGUAAAUAGUAAAGGCCAAUCGUCCUUUAGCAAGGAUGAAAGGUCAUUAUGUAUGUCUAUAUAAGAGGCAUUUACC	**136**	19,117647	30,147059	19,117647	31,617647	38,235294	61,764706	1,0487805	1	-62,8	-62,1	0,0861435	6,2	-46,176471	-1,2076923
spiLA0480-MIR8039-1	UAUUUUUCAAGUCAAAACAGUUUCUCCUUGUGAGUAAGUUGAAUCUCGUGCUCGUUAAACCGCAAGAGACGUAGAAUGCGUCCCAACAUGAGAUUCAACUUACUCACUUGGAAAAAUUGUUUUUGCUUGAGAAGCACUUGUUUCAUAUCUCUACUAUCCAUGGUUCUAUUUACCUAUCUAAACUAUCACUCCCUUUGUAUUAAAGACAAAUGAGCGCUGAGCUAGCCAAUAUGUAUUUGACCAACUCAGCUUCGAGGUGCCUUUUAAUAAAAACUGAGUGAUAGUUUAGCUAAGUACAGAGAACAAUAGAUAGUUGAGGUAAGAAACUAU	**194**	16,494845	32,474227	18,556701	32,474227	35,051546	64,948454	1	0,8888889	-63	-63	0,0072132	10	-32,474227	-0,9264706
spiLA0480-MIR8039-2	UAGAACUAUCAGAAGUUACGUUUUCCUAUCUGAACUAUCACCAUCGUUCAGGAAAGAAGAGGAAACAAUUGACAGUUGACUUGUGUUUUAAUACAUGGAUGGUGAUAGUUCAAGUAAGAAAGGGGAACAACUGAUAGUUGGA	**142**	23,239437	35,211268	13,380282	28,169014	36,619718	63,380282	0,8	1,7368421	-51,9	-49,3	0,249552	12	-36,549296	-0,9980769
spiLA0480-MIR8039-3	UUAAUAGUCAAAAACACAUUUGAACUGUUACUUUUUCGGUAGUUUCACACUUUAACUACCGGUUAUUCCUUUUUCCUAUCUGAACUAUGACCAUCGUUCAGGUAGGAAAAGGAAACAACUGAUAGUUGAAAUGUGAAACUGACGAGAGAACAAUAGUUCAUUUGAGUUUUUGAGCUAUGCU	**181**	17,679558	31,491713	16,574586	34,254144	34,254144	65,745856	1,0877193	1,0666667	-81,9	-81,9	0,0158656	8,6	-45,248619	-1,3209677
spiLA0480-MIR8040	AGCAUGGAUGAAUAAAUUGUCAACAUUAUAAUUCAGUUUAUAAUGUUAAUUGUGAAAAGUUUGCACAGCGUCGCUUUGGCCGAGUGGUUAAGGCGCUUGCCUGCUAAGUAAGUGGGGUUUCCCCGCGUGAGUUCGAAUCUCACAGGCGACGUUGCAUAUGUUUUUGUCGAUACUGUUAUCGACAAUUUUUUACACCUAUUUAUACCUAUAUAGUAUGUUAAACCACCAGAUAAGCACUUCCAUCUAAUUUCUAAAAGGUGGUCAAGGGAAC	**202**	22,772277	25,247525	17,326733	34,653465	40,09901	59,90099	1,372549	1,3142857	-64,9	-59,9	0,0043538	30	-32,128713	-0,8012346
spiLA0480-MIR8042	GAGGUGGUGAAACACAUGUAACUUGACACAACUUUCAGAAAUUAGACUGAAAUGCUGAUCUGGUUUCUUAUAUACAUUAUACAUAGUUU	**158**	17,088608	34,810127	17,088608	31,012658	34,177215	65,822785	0,8909091	1	-51,1	-51,1	0,0483277	13	-32,341772	-0,9462963
spiLA0480-MIR8045	ACACACCUAGGAUAUACCCAUUUUUUGAGUUUCAUAUAGGAAAUAUCAUCAUCGUUCAGGUAGGAAAAGUAAACAAUUGAUAGUUGAGGUGUGUUUUGAUGAAUAACGGUGAUAGUUUAGGUAGGAAAUUCGCACACAUGAUAGUUUAGGUUUGAAACUCGAAAAAUCGGAGUACUUUAGGUGUGU	**186**	23,11828	32,795699	11,827957	32,258065	34,946237	65,053763	0,9836066	1,9545455	-48	-37,63	0,0004667	40	-25,806452	-0,7384615
spiLA0480-MIR8046	GGAGGUAAUAGGACCUUAGUAUAAUAUAAGUGUCUCUGAAAUUUCGAGCAUAGUUUGAGGGGUAAUUGUGCAUUAUCCCUUAUUUUUAUUAAAAACAUAGAGAAAAUGGUCUAAACUCACCCUAAACUAUACCUGAAAUUCACCUACACACUCUUAUUUCACAGGUCCUAUUACCCUC	**178**	15,168539	32,58427	19,662921	32,58427	34,831461	65,168539	1	0,7714286	-50,9	-48,2	0,0013052	24	-28,595506	-0,8209677
spiLA0480-MIR8051	UAUGCAAAUUCCUUCUGCCAUACUAUUGGGGCAAUGAUACCCCUGCUAUCUAAAAGCUAGAGCAUAUACACCCUCUACUUUAACAGAAGACUAAUAGGGAUACAUAACACAAUCUUAUCUGUCAUCAGAUAUUUAAUCAGUGGAUAAAAUUACGACAAUAUAUAUCCGUUAGUAUAAAGGACGUAUAUGCUUUAAUUUUUGGACGGCAUGAACAUCAAUGUUCAAAAAAUAUGACGAAAAAUAUUUGCUCA	**251**	14,741036	36,653386	18,326693	30,278884	33,067729	66,932271	0,826087	0,8043478	-59,7	-47,63	0,0003195	40	-23,784861	-0,7192771
spiLA0480-MIR8121	UUUCACUUUACCCGCUCAAAAGGCGUGCCUAAACGACAGGUGACAAGUCAGUCAGGUGUGUUUGAUAG	**96**	26,041667	23,958333	18,75	31,25	44,791667	55,208333	1,3043478	1,3888889	-36,6	-33,8	0,0899723	8,2	-38,125	-0,8511628

spiLA0480-MIR812f	GUACACUUGUUGAGUGGUUUAAGUGUUC AAUAUCGUAAUGGUAAGUAAAUACCCUCUGUCAC ACUUUUGGAAUAUUAAGUCUAUGAUGUUUAAAAA UUAGAGUUAUAUGUCCGUCAUUUUAACGGAAGAU UAAAUAUUGACACGUGCCGCAAUUUUAUUUAUCG CUCUGAUGUCGGAUCAGUGGAUAAGAUUAUGAUA CGUGAAUGUCCGUUAGUAUAUAAAGGGUAUAUAG GCUCUAGUUUUUGAACAAUAGGGAACCUAUGUCC CAAAAGUAUGACGGAGGUUAUCUGCAUAACAUUU AUGAUGGU	**280**	20,357143	31,785714	13,571429	34,285714	33,928571	66,071429	1,0786517	1,5	-94	-92,1	0,0004867	23	-33,571429	-0,9894737
spiLA0480-MIR812q	AACUUUUUUUUUGUAAUUAUUUGUACCUCUUUGG CUUACGUGGCAUCCAAAUAUCUCCGGCGCGCCUC AAUUGCGUGGAGUCAAAUAGAGUGCCACAUAAGA CAAAAGGUGUAUAAAAUUACAAAAAAAAAAAA	**134**	17,164179	35,074627	17,910448	29,850746	35,074627	64,925373	0,8510638	0,9583333	-45,4	-39,9	0,0112749	14	-33,880597	-0,9659574
spiLA0480-MIR8130	ACAUCACAAAUGCAGAUUAUGCCAUCACUGGAGC UGGUAGAAAAGGCAUUAUUGUUUCGCUGAUCAAC AUCAUGUAAUGGACCUGAUGGGGUUGUAUAUACA UAAGAGAACCCUAGGCCCGUUUAUGUGGAGCCAC CACAAACAAGGAUUUCCUUUUAAUUUAUUUAUUUC AAAAUUUAGUCUUUACCUUUAAUGGAAAGUUGUG ACUUUUAUGAAUUGCUGUAACAUUUAUGAAAGGU UGUGACAUUUUUAAAGUGUUGUGACUUUUCCAAA AAGUUAUGGCCUUUCCAGUAAAGCACAAUAAGCA UUUGUGACAU	**317**	18,927445	30,914826	16,088328	34,069401	35,015773	64,984227	1,1020408	1,1764706	-81,8	-66,1	2,17E-05	62	-25,804416	-0,7369369
spiLA0480-MIR8132-1	UACCCCCCUGAACUUAUUUUAUUAGUAAUUUUUU UACCCGUUUUAGCCUAUGUGACACUAUCUGGUGG GCCCAACGAUGGUUGACUUCUUUUUUUUCAAACU AGUGCCACGUAGGCCAAAAAGGGGUAGAAAAUUA CUUAUAAAAUAGGUUCAGGGGGUAA	**161**	19,875776	27,329193	18,63354	34,161491	38,509317	61,490683	1,25	1,0666667	-75,8	-74,6	0,019215	19	-47,080745	-1,2225806
spiLA0480-MIR8132-2	UCUCACUUCACGCGCUCAAAAGGCGUGCUUCAAA CGAUAGGUGACAAGUCAGUCACGUGUGUUUGAUA GGUACACUUUUUAAGUGGUUUAAGUGUUC	**97**	23,71134	24,742268	19,587629	31,958763	43,298969	56,701031	1,2916667	1,2105263	-35,5	-33,7	0,213875	2,8	-36,597938	-0,8452381
spiLA0480-MIR814c	AUUUUUUGUAGCUCAUCGAGCAUCUAGGGUGGCA AGUUGUACUAUGAACUGCUCAUAUCUUGAUAUAC CUUUUAAGCACCUCCAUACCUUUUCAGAAUAAGC AGUUCAUAGUACAACUUGCCACCCUAGAUGCUAG AUGAGCUACAAAAUCA	**152**	16,447368	29,605263	22,368421	31,578947	38,815789	61,184211	1,0666667	0,7352941	-90,4	-89,7	0,100476	7,3	-59,473684	-1,5322034
spiLA0480-MIR8170	GCUAUAUCGGCUUCUCUGGCUAAAGAGGCAUAGG UAUUACCUUGCUCUUUUUUAUGCAGAUAUGCUUG AAUCUGUUCAUAUACUGAACUAUCUUUUGGGAUA UCUUUUAUAUUCAGAGAGGAUGAAACUGAUGAAG AAGCUUCGCCAAUCUUUGAAUUGAUUAAAGUUUU UCUUCCUAACUGUAUAACAGGAAAGGAAGAAUCG UAUGACGAUCUUCUGGUCUGUGAAGAGGAUGAUC UU	**240**	20,833333	27,916667	15,416667	35,833333	36,25	63,75	1,2835821	1,3513514	-61,3	-42,2	0,0001989	71	-25,541667	-0,7045977
spiLA0480-MIR8175-1	CUAUAGUAAAAAGUUCAAGUUAAUCUAAAAUCUAU GAUCCCCGGCAACGGCGCCAAAAUUUGAUACACU CAAACUUACUUCUCAAAUAAGAAGUAAAGCGGUC GUGUCAAGUAAAUAACCCAACUAGUGAGGUUGGG AUCGUUCCCACGAGGAAAAUAGUCUAGACUUAAC UUCAACGUGUUAUUACUAUUA	**192**	17,1875	35,9375	19,791667	27,083333	36,979167	63,020833	0,7536232	0,8684211	-51,8	-51,8	0,0324484	16	-26,979167	-0,7295775
spiLA0480-MIR8175-2	UAAGUUCAAGUUAAUCUUAAAGCUAUGAUCCCCG GCAACGGCGCCAAAAUUUGAUACGCUCAAACUUA CUUCUCAAAUAAGAAGUAAAGCAGUCGUGUCAAG UAAAUAACCCAACUAGUGAGGUUGGGAUCGUUCC AACGAGGAAAAUAGUCUAGACUUAACUUCAACCU G	**171**	18,71345	35,087719	21,052632	25,146199	39,766082	60,233918	0,7166667	0,8888889	-49,9	-49,9	0,0831043	9,2	-29,181287	-0,7338235
spiLA0480-MIR8179	CUUGCAUUAGUUAUACAUGACAUGAAAAAGUGUA CCAAACAAGGUACUACUAAUACACACCUAAUGCAU GCAUUAUAAUGUUUGGUAGAGUGUAUUAGAGAAA CUAAUGUUUGCAUUAGCUUGAUGUAUUAGUAGUA CCUUAUUUGGUACACUUUUCUAACUCAUGCAUAA CUAAUGCUUG	**181**	16,574586	33,149171	15,469613	34,80663	32,044199	67,955801	1,05	1,0714286	-84,9	-84,3	0,0988032	6,2	-46,906077	-1,4637931
spiLA0480-MIR8182	CAAAUAUGUCGUUCACUCUAAUGGAAGACUAAAAU GUCACAAUCUUAUCCGUCAAUCCGAUAGUGGAUA AGAUUGUGAUACGUGUAUGUUUGUUAGCAUAAAA	**113**	18,584071	34,513274	15,044248	31,858407	33,628319	66,371681	0,9230769	1,2352941	-36	-36	0,0978592	6,1	-31,858407	-0,9473684

spiLA0480-MIR818e	GAUAUAUACG CAAGAGCAUAUAUAUCCUUUAUAUUAACGGAAUCU UAUUCAUCGACUCAACAUCGAAUCAAUAGAUAAGA UUGUGUCACGUGUCCCUAUUUAAUCUUCCGUUAG UGUGAAGGGGCAUAUACGCUCUAG	**128**	17,1875	30,46875	19,53125	32,8125	36,71875	63,28125	1,0769231	0,88	-39,6	-32,34	0,0662609	19	-30,9375	-0,8425532
spiLA0480-MIR821e-1	UUUAGUUAUCUUUAACACUUGUAAGGAUAUGAUC UAUGGAAAUAAAUCUUGGCAACAAUUAAUUUGGC AGUCAUACUUGUCGAAAUUACAAGUCACAAAUGU GAAAAUUGAUAGUCAUCAAUGUGAAAGUUGGUAG CCACAUUUGUGGAAGUAGGUAGUCAAAGUUUAGU AGAGUUAGACAGCCAAAUUUUUGUUGAAAUUUGC UACCACAUUAUGUCAUUGAUGAUGUAAACAAGUG UUCAAAAAAACUCUA	**253**	18,577075	35,573123	12,648221	33,201581	31,225296	68,774704	0,9333333	1,46875	-60,2	-56,4	0,001834	38	-23,794466	-0,7620253
spiLA0480-MIR821e-2	ACAAAUGUGAAAAUUGGUAGCCAUCAAUAUGAAAG UUGGUAGCCAAAUUUGUGGAAGUAGGUAGUCAAA GUUUGGUAUAAGUUUGAUAGAGUUAGGCAGCCAA UUUUUUUGUUGAAAUUGGCUACCAUAUUUUUUCA UUACU	**142**	21,830986	31,690141	10,56338	35,915493	32,394366	67,605634	1,1333333	2,0666667	-48,1	-47,5	0,0366222	13	-33,873239	-1,0456522
spiLA0480-MIR823	CAUCUCCUCAUUAGGUAUUAUGUUCAUCCUCUUG UAACCAGAUGAUUCAAUACAAAGUGUAUAUGUAUA AUUCUGAAUGUACGUACAAUACUUUUAGCUUAAA GACACUUCCUUGAGGAAAUGCAGAUAUUGAAGUA GAUGUGUGAUCAUAUAGCAACAAUAUGAUUAGAA AUGAAGAUAUCUGAAAUAAGGUGGGACUGAUCUC CACGUUGGAGUGAGACUGAGAUGAUUUGGACAUG UGAAUAGGAGAUGCAUAGACGCACCAAUGAGGAG GUG	**276**	22,463768	33,695652	14,130435	29,710145	36,594203	63,405797	0,8817204	1,5897436	-73,6	-59,8	0,0005234	44	-26,666667	-0,7287129
spiLA0480-MIR825	GGUUUCCAUGGUCAGUUUAUGCUUAUCCAGAAGG UGCAGGGGUUGGUUUCUGGUAGAACGAGCUUAU CUUAAACAUGUUUUGUUGAAGAAGCUAUGGUUUC GAUCUGAUUUGCCUGCACCUUAUGUUUGAGCAUG CGCUACCAUGAACUA	**150**	25,333333	22	17,333333	35,333333	42,666667	57,333333	1,6060606	1,4615385	-54,2	-47,1	0,0045766	20	-36,133333	-0,846875
spiLA0480-MIR827-1	AGUGAUGAAGAUGUUUGUUGAUGUUCAUCUAAUC AUGGCAUAUUAAUGGUUCCAAAAACUAUGCCAAAU GAUAUGAUGAAUAGAUGACCAUCAACAAACAAAUU CAUAACUACACAAU	**118**	15,254237	39,830508	15,254237	29,661017	30,508475	69,491525	0,7446809	1	-43,5	-43,5	0,258698	5,7	-36,864407	-1,2083333
spiLA0480-MIR827-2	CUAGCCUGACCAGUGAGGACUUGCUAUUUUACUU UCUAGAUGGCCUUCAAAACUGGGCCAAGCAAGAU CUUCAAAGACGUCAAGUUCACGACGUGGAUGAGG CGAU	**106**	24,528302	27,358491	22,641509	25,471698	47,169811	52,830189	0,9310345	1,0833333	-35,5	-33,8	0,270248	6,6	-33,490566	-0,71
spiLA0480-MIR827-3	ACAUGAAGUGAUGAAGAUGUUUGUUGAUGUUCAU CUAAUCAUGGCAUAUUAAUGGUUCCAAAAACUAU GCCAAAUGAUAUGAUGAAUAGAUGACCAUCAACAA ACAAAUUCAUAACUACACAA	**123**	15,447154	40,650407	15,447154	28,455285	30,894309	69,105691	0,7	1	-44,3	-44,3	0,16497	5,9	-36,01626	-1,1657895
spiLA0480-MIR827-4	UUGUGUAGUUAUGAAUUUGUUUGUUGAUGGUCAU CUAUUCAUCAUAUCAUUUGGCAUAGUUUUUGGAA CCAUUAAUAUGCCAUGAUUAGAUGAACAUCAACAA ACAUCUUCAUCACUUCAUGU	**123**	15,447154	28,455285	15,447154	40,650407	30,894309	69,105691	1,4285714	1	-45,3	-45,3	0,0457494	7,2	-36,829268	-1,1921053
spiLA0480-MIR827-5	UAACAACUUUUUUUUUGGUGGCAAUUUGUUCGAA CUUACCAUGUGAUAUAUCUACUAUACAUGGUAUA UUCGAACUAGUUCCCACGAAAAAGAAUAAUUGCAC AUUUACAUUCACUUCUUUGGGAAAGCCUCUUGCU	**103**	14,563107	32,038835	17,475728	35,92233	32,038835	67,961165	1,1212121	0,8333333	-34,6	-33,9	0,0472286	7,1	-33,592233	-1,0484848
spiLA0480-MIR828b	CAAAUGAGUAUUCCAACAAAUGUCUAAUUGACAUA CUUUUGAGAUACUCAUUUGGGUAAGAAGUUUUAC CAGGAAGGUUGUACUU	**119**	17,647059	29,411765	16,806723	36,134454	34,453782	65,546218	1,2285714	1,05	-48,2	-48,2	0,0901791	5,4	-40,504202	-1,1756098
spiLA0480-MIR835	CGCUUUGCCCUCAUGUUUGCUUCACCUACCACCC UAUUUUAUAUACUUUUAUGCAUUGGGGACAAUUG UAUGUCUUUUUGUUGGGGUGGGGUAAAUGGAAA GUAAGUGUUAGGGUGAAGUUUGAGUAUCCCAACU CACGAUCCUCUCUUGGGGUUUUCUUGCAUGUGU UCUUUAUCCCCAAGAGACUGGUUAUUUUAUUGUU GAAACGGCAUGUUGGUAUCUUUUGUACAUAGUAU AGAAAUGGAAUCUAAAGCAUGAUGGCUAAACAA	**269**	22,304833	23,791822	16,728625	37,174721	39,033457	60,966543	1,5625	1,3333333	-74,8	-67,5	0,0002958	46	-27,806691	-0,712381
spiLA0480-MIR838	AAUUAUUUGGUCCCUAUAGUGCCCAUAUUUAACU AGAACUCAGAAUCCUAUUUCUAUGCAAAAAGGAAG AAUAAUAUGGAUUUUUUUCUAGUCUUCUAGAAAAA	**266**	16,541353	33,082707	16,541353	33,834586	33,082707	66,917293	1,0227273	1	-69,2	-58,9	0,0001022	30	-26,015038	-0,7863636

spiLA0480-MIR840-1	UUAGGUUUUCUAGUUCUUUUUGGAUUAGGAAGACAUCUCUAUAAACAGGGAUUCUCCUAACCUAGCAAAUAGAGGAAUUAGUAUUAUAUUCAUGCUUACCCACCCAAGUAUUGAGAGAGUUCAGAUAUGACUUGGGAUCACUGUAGAAGACCAUAACUAUCUGUAUACCCUAAGAUUAUCCUAUUAGGGGUACAUAGGCACCCCAAUGCCCAAUAUUGAGAAAUAUUGGGCAUCAAAUAGAAAAAUUGGCUAAGAUAUAUUAGCUAAUUUUCUAUAUACGAAUAAUUAAAUAUACUUUUUGGACGUUCAUACCGCAAUCCAAGAUUGUUGUUCAAUAAAUGUACCUUCAAUGAAGACCCUAAACUAAAAUUGUUUUUACUUUAACUCACAAAAAGGUAUGAGGCAUCCAAGUGUCAAGCCUAGAUACCAUGUCAUAUGAUCAAUUAAAAUGAUAAUGUAGAGUAAGC	**305**	15,409836	37,377049	16,721311	30,491803	32,131148	67,868852	0,8157895	0,9215686	-74,4	-55,6	7,97E-05	66	-24,393443	-0,7591837
spiLA0480-MIR840-2	CCAAUAGGUCUUUAAGAAUGUGUAUUGGGGUACAUAGGCAUCCCAAUGCCCAAUAUUUUGAAAUAUUGGGCAUAGUAUAGAAAAUUGGCUAAGAUGUAUUAGCCAAUUUCUAUAUAAUACCCAAAUAAGCAAAUAUUGGCAUAUUAGAAAAUAUUGGCUUAAAGGGUGUUAGCCAAUUUUCUAGCAUUAAUGAGCUUGUUUAAGAAAUGCACUUGCAAUGAAGACCCUAAUCUAAAAACAUUUAUUCACAACUUAGCACUUUAGAUACGAGGCACCCAAGUGUCAAGCCUAGGUACCAUUCCACAUGACCAUUUAAAAUGAUCAUGUA	**328**	17,073171	35,670732	17,073171	30,182927	34,146341	65,853659	0,8461538	1	-95,1	-87,1	8,50E-05	61	-28,993902	-0,8491071
spiLA0480-MIR841a	CCAAACCGACGAACCAAAUCAAACUGAAAAAAAAAAUCGGCUUGUGGUUUGGUUUGAUUGGUUUGGCGAUUGAA	**74**	22,972973	35,135135	16,216216	25,675676	39,189189	60,810811	0,7307692	1,4166667	-28,9	-28,9	0,494871	1,7	-39,054054	-0,9965517
spiLA0480-MIR846	UGGCUAAGAUUUUUGGAGCCCAUCUAAGAAAAGGACUUUUUAGUCCGGCCUGAAUAAGCCUGUUGAUUUGAUGGGCUUGAGAAAUAUAGGUA	**92**	26,086957	28,26087	14,130435	31,521739	40,217391	59,782609	1,1153846	1,8461538	-32,1	-31,9	0,0696503	13	-34,891304	-0,8675676
spiLA0480-MIR852-1	AUAAUAAGGGUGCUAAUUCCUCAAAAAUUUCCCUCCUCUUGAAAAAAAAGGAAACAAAGUCAAAUAUCUUAUUACCUUUAUUUUCCUUUUCCAGAAGAGGGAAAUUUUUGAGGAUUUGACCCCCUUAUGUU	**131**	13,740458	33,587786	18,320611	34,351145	32,061069	67,938931	1,0227273	0,75	-49,4	-46,7	0,0185586	11	-37,709924	-1,1761905
spiLA0480-MIR852-2	UUCCUCAAAAAUUUCCCUCUUCUUGAAAAAAAAGGAAAACGAAGUCAAAUAUCUUAUUACCUUUGUUUUCCUUUUCCAGAAGAGGGAACUUUUUGAGGAU	**100**	14	33	18	35	32	68	1,0606061	0,7777778	-47,1	-47	0,0489448	6,6	-47,1	-1,471875
spiLA0480-MIR855	UAAGACUAUAAAUAUGAGAUUAGGUCCCUCUCCUAGCUUAAGAAAAAGAUGUAUUCCCAUAAGGUGGAUACGUCAUAAGCUAAAGGAGAGGAAGACUCAGCCUAGCUUAUAUUCAGU	**117**	20,512821	35,897436	17,094017	26,495726	37,606838	62,393162	0,7380952	1,2	-40,7	-40,7	0,14275	4,9	-34,786325	-0,925
spiLA0480-MIR8562c	GGCACAAGGAUUAGUUGAGGUGUCUAAAUGAAUUAUGCGGACAACUUUGAGUGGCUGCAGAUGACUUAAGCCUAAGAAUAAAAUGAAAUUUGUAGUAAAAGUGGAUGCCACGUAAGCUUCACAUUAUGGCAAAUUAAUGACCAAAGUAAAAUUAUGGGAGAAAGGAUAAAAAUUACCUCUCAACUUGGUUUAUAGUUGCCAUAAGUCAUAUGUGAUCCCUUUAAAUUAUCCGUAUAAUUUAUUUAGACAUUUUAAUUAGUACUAGUACC	**269**	19,330855	35,687732	13,754647	31,226766	33,085502	66,914498	0,875	1,4054054	-81,1	-71,7	8,71E-05	41	-30,148699	-0,911236
spiLA0480-MIR8564-1	CGACUGAGAAUUGCAAAGGUAAAGUGAAAGCGACUAAUGCUAAGGAGGAAGUUUUGCACAUAACCUUAGCAUUACUGUUGGUUUCAUAUUUUCCUUUCUUUCUUAGGUA	**109**	21,100917	29,357798	15,59633	33,944954	36,697248	63,302752	1,15625	1,3529412	-35,6	-34,8	0,0767203	5,8	-32,66055	-0,89
spiLA0480-MIR8564-2	GCCCUUCAACUUUGGAUGUGCACAAGUAGACACUUAAACUUAUAUAAAGUUGAACAAACAGACACACAUGUCUUACAUGUCAUCCUACAUGUCAUUUUGUUGCCAUAUGUGAUGCCCUACGUGUAUUGUGCCCUGUUGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAACGUGUCUGUUUGUACAUUAUGAAAGUUGGAGAUC	**210**	19,047619	27,619048	17,619048	35,714286	36,666667	63,333333	1,2931034	1,0810811	-56,4	-45,9	0,002758	32	-26,857143	-0,7324675
spiLA0480-MIR8567	AUGCACUGUCUCAGAUGUAAAUCUUCAUGUCGUCAAUGUCUAUGUUGUUCUACUCCAAAAAUGCACUACUUUUUGGAGGAUAUAGACUUUGGCGACCUGAAGAUUUACAUUUGAGACAGUGUUU	**124**	19,354839	26,612903	17,741935	36,290323	37,096774	62,903226	1,3636364	1,0909091	-71,8	-71,8	0,592873	1,3	-57,903226	-1,5608696
spiLA0480-MIR8573	UAUUAUUUAGUUUAGAUAAGUUCUUAUAUCAUUAUAAGUGUGACUGUUGUCUUCUGUUGAGUUAUGUA	**340**	21,176471	25,882353	13,823529	39,117647	35	65	1,5113636	1,5319149	-90,6	-80,3	0,0004505	28	-26,647059	-0,7613445

spiLA0480-MIR8575	AGCUAGGUCAAGGGCCCGCUCGAGGCCAGCAAUGGUCAUCGAGUUCCAGUCUGGCGCAAGGUGUAGGCUCGGAGCGUGAGAUGGAGAUUGAGGAUUAGAGUAGAAGGUUAGUAGGUAGUUAAAAUUUAUCUAGUUUUUCUUGUUAAUGUUCUUUUUAUCAUUACGGACUAUCUUGUUUCAUAAUUCUUUUAUUACAUUUUUUUUCUUUUAUUCAAUAACCGUAUUACAUAUGGUUGUUACUGAGACAAGGGUCUAUCUAAAACAACAUAUCU	**104**	20,192308	33,653846	14,423077	31,730769	34,615385	65,384615	0,9428571	1,4	-26,5	-26,5	0,081745	7,3	-25,480769	-0,7361111
spiLA0480-MIR8577	AAGUUGUGACUUAUGAAAAGUUGUGACAUUUGUGAAAGGUAGUAACCUCUUCGAAGCGUUGAAACCUUUCAAAUAGUUGUAACCUUUCCGAUGAGACAUAAUAA	**97**	17,525773	31,958763	14,43299	36,082474	31,958763	68,041237	1,1290323	1,2142857	-37,6	-36,4	0,121899	7,1	-38,762887	-1,2129032
spiLA0480-MIR8580	CGGACUAUUUGCCAUGUCUGAGAUCAUCUUAAGCUAUUCUUUUUAUUUCUCAAAAAAUGAAUAGGUGAUGAUGAUUCCAGAUAUGGAAAAUAGUAUCUGGUAAAUAGCGUCUUGAUGUGAAGCGAAGACACUUUACGCGAUGUAUCGGUCAAAUAUAUCACUUUAUGCUAUGUAUUAAUAGGUUGAAUGAUGUAUCUUAAAUUGAGACGCGAUAUAUCAGGACGUUGAGUGAUGUAUUCGACAUCAGGACGCAAUAUAUUG	**164**	23,170732	31,097561	13,414634	32,317073	36,585366	63,414634	1,0392157	1,7272727	-51,3	-50,1	0,0110199	14	-31,280488	-0,855
spiLA0480-MIR859-1	AGAUUUCAUUGAUUUUACAAAAAAUAGGAUUGAAUUUCUCAAAUGUUCUCCAGUUUAUACUUUCCAUUAUGUUGGUGGUAGAUACGGUAGAGUGGCAUGGAUCAUGUGAGAAUCAAGUUACUCUUAAACUUGUAUUGGAAUGUGGUUUGCAUGUGUGCAUUGUUGCAAUUAUGAAAUGUUUAGUGCAUGGGAGCUGGGGACCAUAUGGAAAUUGAUAUGUAGUGAUGUCCAAUUGCAGUAACUAAGGUUUUCUGAGAAAACAAAUAGUUUUUUUUUCUUCUUUUUAAAGUCAAUAAAAAAA	**302**	21,192053	30,463576	10,927152	37,417219	32,119205	67,880795	1,2282609	1,9393939	-70,4	-60,3	8,04E-05	62	-23,311258	-0,7257732
spiLA0480-MIR859-2	UUUUUUAUAAUUUUGUGCAACUUUUUAGCUUACGUGACAUCCAAAUAUAUCCCACACGCCUCAAUUGUGUGAAGUCACAGAGUGUGCCACGUAAGACAAAAGGUGUACAAAAUUACUAAAGUC	**123**	16,260163	32,520325	19,512195	31,707317	35,772358	64,227642	0,975	0,8333333	-36,3	-36,1	0,0316986	15	-29,512195	-0,825
spiLA0480-MIR8594	ACAAUACCCUCCAUCAUACUUUUGGGACAUUGGUACACAUCCCGUCAAAAAACUAGAGCAUAUAUGUCAUUCACUCUAACAGAUCAAUCUUAUCUAUCGAUAUGAUAUUUACUAAAUAUCGGGUCAGUGGAUAAGAUUAUGACACGUGUAUGUUUGUUAGUAUAAAGGUUAUAUAUGCUCUAAUUUUGGAUGGUAGGGGCACCAAUGUCACAAAAAUAUGACAGAGGGUAUCUG	**234**	18,376068	32,905983	17,094017	31,623932	35,470085	64,529915	0,961039	1,075	-87,1	-86,4	0,0104412	14	-37,222222	-1,0493976
spiLA0480-MIR8599-1	AAACUAAAGAUAUUAAAAUGAGUUGAAAUAGAAUCGGGUUGGGUCUUGACCUGCCCAAGUUUACUUUGGGCUAAAAUGGGUUGGGUUCAAAUGGGCUAAGAACGGGUUGGGUUUUGAACCACCUAAUUUGACCCGAUUAAUAUCAACAAUUCUAACAUAGUGAUAUUUAACUUUUAUAAUCACAAUUCGAAUUUCAGCUUUAAUAUUUUUAAAGA	**215**	19,069767	33,488372	13,953488	33,488372	33,023256	66,976744	1	1,3666667	-56,4	-56	0,0002589	42	-26,232558	-0,7943662
spiLA0480-MIR8599-2	UUCUUUUUCCAAAAGAAAUAAAACUUGUGGGAUCGUUUGACAUAGGGGUGUCAAAUAGGCGGGUUGAGUUGAAAUUGAAACUGUUAAAAUGAGUUAAACUAUAAAUCGGGUUGGGUCUUGACCCGCCUAAAUUUACUUUGGGAUCAAAUGGGUUGGGUUAAAUGGACUACAAAAUGGGUUGGGUCUUGACCCAUCCAAUUUGAUUCAAUUAAUCUCAAUAAUUUUAACAUAGUGAUAUUUAAAUUUUAUAAUUACAAUUCGAAUUUCGGCUCAAGUUUUUUUUUAUAUAUAAAAUGU	**297**	19,52862	31,986532	12,121212	36,363636	31,649832	68,350168	1,1368421	1,6111111	-72,9	-66,4	1,76E-05	60	-24,545455	-0,7755319
spiLA0480-MIR860	UCCUAACACACGUGUCAUAAUCUUAUUUACUGAUCCGAUAUUUAUCAAUAGAUAAGAUUGUGUCACGUGUCUCUAUUU	**78**	12,820513	28,205128	19,230769	39,74359	32,051282	67,948718	1,4090909	0,6666667	-28,7	-28,7	0,633967	1	-36,794872	-1,148
spiLA0480-MIR8610	UUGACGGUCACAAACUACGGAUUGUAGGUUCGUCCAUCAAUCAGGACUUAACCAAAUUUUCCUGGGCUGAGAUUUGGGGUUUUUGACCCCAUUGAUGGAUGUGCAGGACGGACUGUGGGUCAGGCUACGAUCCGUCGAUAGCCACCGUUUG	**151**	27,81457	21,854305	21,854305	28,476821	49,668874	50,331126	1,3030303	1,2727273	-53,4	-53,2	0,0210505	28	-35,364238	-0,712
spiLA0480-	AUGACUCAGUUGGUUUGGAGGGUGGUUAUCCACA	**76**	27,631579	21,052632	22,368421	28,947368	50	50	1,375	1,2352941	-35	-35	0,441141	9,5	-	-

MIR8613	CGGAUGACCUGGGAUCAAUCCCCUCAAUGCCUUCUGAGUUGA														46,052632	0,9210526
spiLA0480-MIR8614	UGCACAAGUAGACACUUAAACUUAUAUAAAAGUUGAAUAAAUAGAUACACAUGUCCUGCAUGUCAUUUUUUUGUCUUACAUGGUGUCCUACGUGUAUUGUGUCAUGUAGGACUCAUGUGUUUAUUUAUUUAAAAGUUGGAUAGUUAAAGUGAUUGUUUGUACA	**163**	18,404908	30,06135	12,269939	39,263804	30,674847	69,325153	1,3061224	1,5	-52,4	-52,3	0,0472745	7,1	-32,147239	-1,048
spiLA0480-MIR8639e-1	CAACUACGCCCUUCAACUUUGAAUGUGCACAAAUAAACACGUAAACUUGUAUAAAAUUGAACAAGUAGACGCAAGUGCCCUACAUGGCAUAAUACACGUUGGCAUGUAGGACACAAAAUUGUCAUGUAGGAUGAAUGUGUAUAUUUGCUCAAUUUUAUAGAAGUUUAAGUACCUACUUGUGCACACCCAAAGUUAAAGGUCAUAGUUA	**208**	17,788462	35,576923	18,269231	28,365385	36,057692	63,942308	0,7972973	0,9736842	-78,4	-75,8	0,0349959	12	-37,692308	-1,0453333
spiLA0480-MIR8639e-2	GCAUCAGCUGACAACUAUGACCUUUAACUUUGGAUGUGCACAAGUAGACACUUAAACUUGUAUAAAAUUAAACAAAUAGACACAUUCGUCCUACAUGGCACCCUAGAUGAAAAAUUUAUGUCAUAUGUGUGUCUACUUGUUCAAUUUUAUAUAAGUUCAAAUGACUACUUGUGCAGAAUCAAAGUUGAAGGGCAUAAUUAUCCGCUGAAAG	**211**	16,587678	35,07109	17,535545	30,805687	34,123223	65,876777	0,8783784	0,9459459	-84	-82,8	0,0425927	8	-39,810427	-1,1666667
spiLA0480-MIR8639e-3	CUACAUUUUUAGGCAUAAUACAUAAACAUGACAUUUAACUUACAUUUAGCGGACAACUGUAACCUCCUACUUUGAGUGUACACAAGUAGACACUUAAAUUUUUAUAAAAUUAAACAAGUAGACAUAUGUGUUCUACAUGACAUAACGCAUGUAGGAUGUCGUGUAGGACACAAAUUGUCAUGUAUGGUGCCAUGUAAAAUGGAU	**205**	16,585366	36,097561	16,097561	31,219512	32,682927	67,317073	0,8648649	1,030303	-53,7	-50,2	0,0006756	24	-26,195122	-0,8014925
spiLA0480-MIR8643b	AUACACAUCUGAAUAUUAAGAUCUGCAUUAAUAUCCAUGUGUUUCGAUCUGAAUGCACAUCUACAUAUUAAGAUGUGGUC	**80**	15	32,5	17,5	35	32,5	67,5	1,0769231	0,8571429	-22,1	-22,1	0,316526	2,7	-27,625	-0,85
spiLA0480-MIR8648	CGGUAUAAUUUACUAUACAUAUACAAUUAUAUAAGUUGCUGGCCUAAAUUGUAUAAUUCGCUGGCUUCGCUAUACAUAUACAAUUGUAUGAUUCGCUAGUCUAUUUUGCUGCAAUUGUAUAAUUCGGUGGCCUAUUUCAGCGCAAUUGUAUAAUUCGCUGGCCUAUUUCGCUGCAAUAUCUGUAUAAAAUUUGCUUUGUAUACAAUUGAAUCGAAGUAAAAUGUUUGUAUAUUGUAUAAUUAUAAAU	**247**	15,789474	29,959514	14,574899	39,676113	30,364372	69,635628	1,3243243	1,0833333	-62,9	-56	0,0025591	44	-25,465587	-0,8386667
spiLA0480-MIR8651	GCAUUAUUUAUUAAUUAGGUCUAUUAAUUGAAAAGAAAAAAGAUCAUUUCAAAUGGUUUCACGCGCUUGGGGACCGUGAAAUACACAUUUUUUGCCACAUAAGUCAUUUGUGUCCAAUAGGAACUGUUUUUGAACACAUAAGGUGUUCAAUAGGUAUGAGGCUAAAUUGAGGUGUCUAAGUGAAAUAUACGGACAACUUUAAGGGGCCGCAUAUGACUUAAGCCUUUUGGGAAGUUUAAUUUGUCUCAUCUCAUGUUGAUGUUUAAUCCUUAAUUAAUGGAUAAUAACAAUAUAAAAA	**298**	19,127517	33,557047	13,422819	33,892617	32,550336	67,449664	1,01	1,425	-69,1	-54,5	2,12E-05	63	-23,187919	-0,7123711
spiLA0480-MIR8657b-1	ACAAAGAUCCUAUUACCCCCCUAUACUUAUUAUAUAAGUAAUUUUCUAUCCCUUUUGGCCUACGUGACACUAGCUUGAAAAAAUAAUCAACCAGCGUUGAGCCCACAAGAUAGUGUCACGUAGAUCGAAAAGGAUAGAAAAUUAUUAAUAAAAGAAAUUCAGGGAGGUAAUAAAACCUUAGC	**182**	15,384615	38,461538	19,230769	26,923077	34,615385	65,384615	0,7	0,8	-66	-64,4	0,0599258	8,2	-36,263736	-1,047619
spiLA0480-MIR8657b-2	UAUAGGUUUUAUUACCCUCUGAAUUUAUAUUAUAAAUAAUUUUCUACUCUUUUUCGGUCGAUGUGACACUAGCUUGAAAAAAAAGUCAACAAGCAUUGAACCCACAAGAUAGUGUUACGUAGGUCAAAAUGGGGUAGAAAAUUAUUAAUAGAAUAAGUUCAGGGGGUAAUAGGACCUUAG	**180**	18,888889	35,555556	13,333333	32,222222	32,222222	67,777778	0,90625	1,4166667	-76,2	-75,6	0,0642091	9,7	-42,333333	-1,3137931
spiLA0480-MIR8660-1	UAAUGCACAAACAGAAACUUUAACUAUCCAACUUUUAAAUAAAUAAACACAUGAAUCCUACAUGGCACAAUACAUGUAGGACACCAUGUAGGACAAAAAAUGAUAUGGAGGACAUGUGUGUCUAUUUGUUUAACUUUAUACAAGUUUAAGUUGAUAUUUGUGCACAU	**167**	14,97006	38,922156	15,568862	30,538922	30,538922	69,461078	0,7846154	0,9615385	-47,1	-46,8	0,0936699	11	-28,203593	-0,9235294
spiLA0480-MIR8660-2	AAAUAAACACAUGAGUCCUACAUGGCAAAAUACACGUAGAACACCACGUAGGACGAAAAAUGACAUGUA	**87**	19,54023	40,229885	19,54023	20,689655	39,08046	60,91954	0,5142857	1	-28,1	-28,1	0,15777	5,1	-32,298851	-0,8264706

spiLA0480-MIR8665	GGACACGUGUGUCUAUUUAAAGGAAAUUUUUAGAUUUCGGUUAAGACAUAAAAGGGACAACCUAGUACCUAACCUAGGAUGGUCCGAAGAGUUAGUUAAGAUACUAAAUACUUAAGGGUACUCUAGUAAUUACCCUAGGAUACUUAAUUAAUAAAUAUAUCAACAUAAUUAAUUAAUUUAAAGGUGCAAAACCGAAAUCAGAAAGCAAUAUCCAGA	**198**	16,161616	42,424242	14,141414	27,272727	30,30303	69,69697	0,6428571	1,1428571	-43,3	-39,1	0,0088726	35	-21,868687	-0,7216667
spiLA0480-MIR8668-1	UGGUCGCCUUGGCUUACAGAAACAUUUUGGAAUGAUGACUAUAACGAGUGGGAUAAUCUGAGAAAUGUUUUUGUACAAGGAGAUAU	**86**	25,581395	31,395349	11,627907	31,395349	37,209302	62,790698	1	2,2	-25,3	-25,3	0,458373	5,9	-29,418605	-0,790625
spiLA0480-MIR8668-2	AGUUUGAUUUCUCAGAUGAUCACUCGACUAAUUGUUAUCAUCUCAGGAAGUCACUUUCUUUGUUGAAAGUUUUGGAAUCAAGAAGAAAGGGGACUUUCGAGAUAAUAACUAUUAAUCAAGUGACUAUAUGAGAAAUCAACCG	**142**	19,014085	33,802817	14,788732	32,394366	33,802817	66,197183	0,9583333	1,2857143	-52	-52	0,0438196	6,6	-36,619718	-1,0833333
spiLA0480-MIR8672	UGGAAAUGGAAAUAAUGUUAAAAUAACUAUAACUAUAAUUAAAAAGAAUGUUGAAAUAAAUAAAGAAUGAAAAAGGAAUCUUAAAGCAACUCAAGAAUGAGAAAUAAUUAGAUGAAAAAGGGGUCUGACAGCACCUGUAAGGCGCAGAAUAUCAGGCACCUUUUUUUUUAAUGCAAGGCAAAAGCCAUCAUGUGCCUUCCUCUUUUCAUCGGUUGACGCCGUUAACGGCGUAUAGGGGAAGGCACGUGGGCCCCUGUGCCUUUAGCGUUUUGGUUUCCUGAAUAAAUUGUUUGCCCUUUUUGGAACUUUUAGACAAUUAUGUUGCCCUUUUGG	**333**	21,321321	33,033033	15,915916	29,72973	37,237237	62,762763	0,9	1,3396226	-88,4	-74,6	2,37E-05	70	-26,546547	-0,7129032
spiLA0480-MIR8675b	GUUAUUGGUGCUUCUGCUGUUCAAAAACUAGAGCAUAUAUUGUCACUCACUCUAACGGAAAACUAAGUGGGAACAUGUGGCACAAUCUCAUCCGUCGAUUUGAUAUUUAAUAAAUGUCAGGUUAGUGGAUAAGAUUGUGACACGUGUAUGUAUGUUAGCAUAAAAGGUAUAUAUGCUCUAUUUUUUUGACUGCAGAAACACCAAUGUU	**208**	20,192308	30,769231	15,384615	33,653846	35,576923	64,423077	1,09375	1,3125	-79,7	-72,6	0,0039065	17	-38,317308	-1,077027
spiLA0480-MIR8678	ACACCGUUUCAUAUUUAUACUCUUCAACUUUGAGUGUAUACAAGUAGACACUUAAACUUGUAUAAAAUUGCACAAGUACACAUGAGUCCAAUGUGACAUAAUACAAGUAGGACACAAAUUGUCAUGUAGAAUGUCACGUAGGACAUGUAUGUAUUUGUUCAACUUUAUACAAGUUUAUAUGUUUAUUGUGCACGCCCAAAAUUAAAGAGCAUAUAUGUGAAAUGGGAC	**228**	16,666667	35,526316	15,789474	32,017544	32,45614	67,54386	0,9012346	1,0555556	-90,4	-90,4	0,027772	8,4	-39,649123	-1,2216216
spiLA0480-MIR868	UAUAAAUGAUAUGCAGAUAUCUUCAUCAUACUUUUGGGACAUUUAGUGCCCCUGCUGUAAAAAACUAGAGCAUAUAUAUACCCUUUAUAUUAACGGAUAUAUGCGUGUCGUAAUCUUAUUCACUAACCGAAUAUUUAUUAAAUAUCAGAUCAACGGAUAAGAUUUCACCAUGUAUCCCAAUUUAGGUUUCUCUUAGAGUGAAAGACAUAUAUGCUCUAACACGAUAACACAUAUAUCCCAAAAAUAUGACGGAGGAUAUAUCUAUAUCAUUUUUUUUUGGUCUUGCCUCAAUGCUCAUGAAUUCUAGUGUAGUUUUAUAUGGGCUAUUGAAUGAUGUAAUAAUUGUAUUGAAUUGAUGUGUAGGCCAUCUUAUAUUGAUAAGUUUAUAUUGAAUUGACCUAGAUUCAUUGAGUAUUAUGAUUUUUGUAUUGAAUUGAUGAUCAUGACCAUGGGUAAGAGCCUUU	**275**	13,454545	34,909091	17,454545	34,181818	30,909091	69,090909	0,9791667	0,7708333	-72,5	-71	0,0040639	23	-26,363636	-0,8529412
spiLA0480-MIR8706b-1	ACGGGUAAAACUUAUCUGCACAUGGUGUUUACACCAAGUCAAUACAUGCAUGCCAUGUGUUCAAAUUUAUAGUUCAUUUUACUUCUUUAAAUAUCGUAAUAAUAUUUUUUGCAUUUACUUGAUGUAAACACCCGGUACGAAUAAGUUUUUCCUUU	**189**	20,634921	26,984127	10,05291	42,328042	30,687831	69,312169	1,5686275	2,0526316	-43,7	-35,2	9,44E-05	38	-23,121693	-0,7534483
spiLA0480-MIR8706b-2	AAAGACGUUUUACCCCUGCACUGUUUAAUAAUGUAUUUUAAAGGUAUAUAUGUGCUUACAUGGGCAUAAAAAUAUUGCAUAAUUAUAAAUAGUAAUGUGUCCACGUGGACACAUAUAUACCUUUAAAAUACACUAUUAAGUAGUUCAGGGGCUAAAUGGUCCUC	**155**	13,548387	29,677419	17,419355	39,354839	30,967742	69,032258	1,326087	0,7777778	-38,6	-38,6	0,0361932	15	-24,903226	-0,8041667
spiLA0480-MIR8709a	GGAGAAAUAAUGAAUUAACCCUACACUUGAAAUUUAGGAAACAUGUAAUUAGACCUAUUGGUUGGAAUCAAUAUUUAGGAACUUUAUUAUACAUUUGAGUGAG	**295**	21,016949	31,525424	9,8305085	37,627119	30,847458	69,152542	1,1935484	2,137931	-69	-57,4	1,76E-05	61	-23,389831	-0,7582418

spiLA0480-MIR8713	UUUUGGGUCUAAGCUAGACAUAUGAGUGUUGUUAGUUACGAAAUUUUUUUGUGAUUAUUAAUAUGAAUAGAUUUCUUUGAGUUGGAAGUACAACGAAAAGGAAAGGCUCAAGUCUUAGAGUGAUUGUUCGACUAUUUGAGGCAAGUUGAUUUCUAAACUUUUGUUAUGGGUAUGAAAUUCGUGUAUUUCCUUACUAUUAGUGUACAGUCAGACCUCUUUAUAACAGUGUCGUUUGUCUGGAUAUGUUUUGGUUGCUAUAACGAGAUGGUGUUAUAGAUAACAUAUAUUAAAGUCGAUUCCAAAAGAUCUAACUAGGCCGUUAAAGUGAAAUUUUGUUAUAAAGGAUGACUGUUAUAGAGAGGUUUGACUGUAAAUUGAUCUC	**190**	21,052632	31,052632	12,105263	35,789474	33,157895	66,842105	1,1525424	1,7391304	-61,7	-58,1	0,0133126	30	-32,473684	-0,9793651
spiLA0480-MIR8714	CAACAAGUGAUAUCACAUUCGACGAGAUGAACAUAGAGGUAACUGAGUUACAAUAUAUGACUUGCUUUACUAUGUUUAUCAUGUCAAGGUAACUUGAAAUGUUCACUCUCCUUUUUUGUUUAAACUCACAUAUUAUUUAUUUUAGGAUAAAUUUGAGAGUGUUAACUUUAAUGAUCACCAUGAUCAUACAUUUGGAUGGAUGAAUGAGUUAUGGAACAAAUUGAGAGGAUACUUGUAUGCUACUUAUGUGAAGAAUAAGCCUAUUAUUCCAGCUCUUAAGAAUAAUCCAAAGGGAGUAGAAACAAGGAAUGGGAGUGAUUA	**99**	18,181818	36,363636	15,151515	30,30303	33,333333	66,666667	0,8333333	1,2	-24,5	-24,3	0,043187	13	-24,747475	-0,7424242
spiLA0480-MIR8738b	CGCAAAUUGUAUGUAAAUAUCCCCAUCAUACUUUUGAGAUAUUGUUGUCCCUGCCGUCAGAAAGCUAGAGCACGUACUUCCUUCACUCUAACGGAAGACUAAAUAGGGACAUGUGGCGCAAUCUUAUCGGUCGAUAUGAUAUUUAAUAAGUUGUUGUUAGUGGAUAAGAUUAUGACACGUGUAUGUCCGUUAGUAUAAACGGUAUGUAUAUUCUAGUUUUUGAACGGCAUGGCACCAAUGUUUUAAAAGUAUAACGGAGGAUAUCCGCAUAUACCAUUUACA	**222**	19,369369	33,783784	12,162162	34,684685	31,531532	68,468468	1,0266667	1,5925926	-54,7	-42,7	0,005026	58	-24,63964	-0,7814286
spiLA0480-MIR8739-1	UUGGGUGUCCCUGCUGUUAAAAAAUUAGAGCAUAUAUGUUCUUCACUCUACGGGAGACUAAAUAGGAACAUGUGGCACAAUCUUAUUCGUUGAUCCGAUAUUUAAUAAAUGUCGGGUCGGUGGAUAAGAUUAUGAUACGUGUAUGUUCGUUAGUAUAAAUGGUAUAUUUGCUCUAGUUUUUUUUACGGUAGGAUCACCAAU	**282**	20,212766	30,141844	17,375887	32,269504	37,588652	62,411348	1,0705882	1,1632653	-98,1	-94,97	0,0028285	24	-34,787234	-0,9254717
spiLA0480-MIR8739-2	CCAAACUAUCAUAAAUGGUAUGCAAAUACCUUUCGUCAUACUUUUGGGACAUUGAUAUUCCUGCCGUUCAUAAACUGGAGCAUAUAUGUCCUUCACUCUAAGGAAGACUAAAUAGGGACACAUGACGCAAUCUUAUCCGUCGAUAGAUGUCGGAUCAAUGAAUAAGAUUAUGACACAUAUAUGUCCGUCAGUAUAAAGGAUAUAUAUACUCUUUUUCUAAAAUUACAUAUGCAAUUAAUAUUCUAAAAAUAUGAUAGAAAUUAUUUACAUUCCAUUUACGAUAGUUCAA	**201**	21,890547	27,860697	13,930348	36,318408	35,820896	64,179104	1,3035714	1,5714286	-78,6	-75,1	0,0048545	22	-39,104478	-1,0916667
spiLA0480-MIR8739-3	AAGACUAAAUAGGGACACGUGAUGUGAUCUUAUCCGUUAAGUCGGUGGAUAAGAUUAUGACACGUGUACGUUCAUUAGUAUA	**289**	14,186851	35,640138	17,301038	32,871972	31,487889	68,512111	0,9223301	0,82	-67,4	-52,47	0,0001923	47	-23,321799	-0,7406593
spiLA0480-MIR8739-4	AGUAUAAAUAUAUCCACUUAAACUAUCGUAAAUAAUAUACAGAUACCUUUCGUCAUACUUUAAGAAUAUUGAUGUCUCCGUCGUCCAAAAAACUAGAGUAUGCCUUUUAGUCCAACGGAAGACUUAAUAGGGACACAUGUCACAAUCUCAUCCAUCGAUCUGAUCGAUGUCGAGUCAAUGGAUAAGAUUAUGAUACGUGUAUGUCUGUUUGUAUAAAGUGUAUAUAUAUUCUAAUUUUUGGACGGCAAAGAAACCAACAUUCCUAAAAUAUGACAAAAAAUAUCUACCUACCGUUUAUGAUAGUUCAAGGGUAUAUUUAUUUU	**82**	24,390244	31,707317	13,414634	30,487805	37,804878	62,195122	0,9615385	1,8181818	-29,8	-27,6	0,0755047	4,4	-36,341463	-0,9612903
spiLA0480-MIR8739-5	CUACAUUUGAAGAACAGAGAGUAACAUAGAGAUGGAUUGAAGUGUUUAUUCUCUAUUUUACUCUCCAAAUAUAGAGAAUAGAGAGUAAAUAGAGGUGGGGUGGAGAUGGUCAAAAUGAUAAUGAUUAGUAAUUAAAUCGAAGACUAUGAAGGGAAAUUGGACUCCCUUGGA	**323**	15,170279	34,98452	16,718266	33,126935	31,888545	68,111455	0,9469027	0,9074074	-99,3	-97,4	0,000574	31	-30,743034	-0,9640777
spiLA0480-MIR8748	CUAUCUAAUUGUCCUAUUCUUCAAUUGGUC	**201**	22,38806	34,825871	11,940299	30,845771	34,328358	65,671642	0,8857143	1,875	-51,2	-40,8	0,0099508	45	-25,472637	-0,742029
spiLA0480-	UGGUUGAAUUUGAAUAUUAUAUUGACCGCUAGAU	**140**	16,428571	30,714286	17,142857	35,714286	33,571429	66,428571	1,1627907	0,9583333	-	-51,1	0,170251	4,4	-36,5	-1,087234

MIR8751a	UUGUAGAUUCAAGACGUUCAUUGAUAGGGAGUAC ACUUGUACUCCUUAUCAAUGAAUUUCCUGAUUUC UACAACUCUCACGACCACUAUAAGAUCGAAAGUAA UUU										51,1					
spiLA0480-MIR8763-1	UUUUAUGUAAGACUAUUAAUAGUGUUGGACUUGU UCGUCCUCAUGCCUUUCGUCUAAAUUCAGUCAAC AAUAGUUAUGCUUAGUCAACAAUAUGGUUCAUGU GACUUUUUUAGGAUAAAACCCUAAACAUAAUUUUU GUCGGCUAAAUUUAGAUGUAGGGCGUAAGUACGA ACUAGUCCAACACUAUGAAUAGCCUUACAUACCU UCCAUUCAUACACCUCAUUACCACUGUAAGAUGU	**205**	16,585366	30,243902	17,560976	35,609756	34,146341	65,853659	1,1774194	0,9444444	-85,4	-84,3	0,0131708	8,8	-41,658537	-1,22
spiLA0480-MIR8763-2	GUUAGUUUGAUUUCAAUCUCUUUCUUCAACUAGC ACAUCUUGAGGAGUAGGACGAGGAUAAUAAU GUAUAACUAAUACCCACAUAACUUAUUUCACUUUC	**99**	16,161616	29,292929	20,20202	34,343434	36,363636	63,636364	1,1724138	0,8	-28,8	-28,8	0,139918	11	-29,090909	-0,8
spiLA0480-MIR8766	UACCCUGCAUAACUUUAUACAUAGAUUCCCUCAUA AGUUAUGUUGGUAUUAGUUAGGU UAACUUGGCUUUGAAUCAUAUUUAUGCCCUUCAA	**93**	10,752688	30,107527	20,430108	38,709677	31,182796	68,817204	1,2857143	0,5263158	-27	-27	0,407838	2,7	-29,032258	-0,9310345
spiLA0480-MIR8771f	CUUUGGAUGUGCACAAGUAGACACUUAAACUUGU AUAAAGUUGAACAACCAGACACACAUGUCUUACAU GUCAUUUUUUGUCAUAUGUGGUGUCCUACGUGUA UUGUGCCAUGUAGGACUCAUGUGUUUAUUUAUUU AAAAGUUGGAUAGUUAACGUGUCUAUUCGUGCAU UAUGGAAGUUGGAGAUCAAAGUUAAAAUUUGAAG UCAAGUUU	**247**	19,433198	28,744939	14,574899	37,246964	34,008097	65,991903	1,2957746	1,3333333	-80,9	-68,3	0,000972	53	-32,753036	-0,9630952
spiLA0480-MIR8781a-1	UUUAACUUGGGUUCGAAUUACAUUUACGCCCUUC AACUUUAGAUGUGCACAAGUAGACACUUAAACUU GUAUAAAAUUGAACAAAUAAACAUGUGUCCUACAU GUCAUUUUUUGUCCUACAUGAUGUCUUACGUGUA UUGUGCCAUGUAGGACUCAUGUAUUUAUUUAUUU AAAAGUUGGAUAGUUAAAGUGUGUUUGUGCAUUA UGAAAGUUGGAGGUCAAAGUUAAAAUUUGAAAUC AAGUUUAG	**247**	18,218623	31,174089	12,955466	37,651822	31,174089	68,825911	1,2077922	1,40625	-78,2	-78,2	0,0042813	18	-31,659919	-1,0155844
spiLA0480-MIR8781a-2	UUUCAAAUUUGGAUGUGCACAAAUAGACGCUCAA ACUUGUACAAAAUUGAAUAAAUAGACACACAUGUC AUUUUUUGUCCUACGUGGUGUCCUACGUGUAUUG UGUCAUGUAGGACUCAUGUAUUUAUUUAUUUAAA AGUUGGAUAGUUAAAGUGUCUUUUUGUGAAUUAU AAAAGUUGGAG	**182**	19,230769	30,769231	12,087912	37,912088	31,318681	68,681319	1,2321429	1,5909091	-54,2	-51,8	0,0034541	17	-29,78022	-0,9508772
spiLA0480-MIR9386	GUCCUCCAACUUUGGGUAUGCACAAAUACACUUA GUUUAAAAUUGAACAAGUAGACACAUGAGUCCUA UGUGGCAUGAUACAUGUAGGAAAUCACAUAGGAC ACAAAUUGAUAUGUAGGAUGCCGCGUGGUACGUG UGUUUUUUAAGUGCCCAUUUUUGCACUUCCAAAG UUGGAGGGU	**179**	22,905028	29,608939	17,318436	30,167598	40,223464	59,776536	1,0188679	1,3225806	-66,8	-64,6	0,0091517	23	-37,318436	-0,9277778
spiLA0480-MIR9471a-1	GAUCUUUGACGGAUUUGGGGUUCUGAGAUUCAG UUGAUUUCUCAGGUGCUCACUCAGCUAAUAGUUA UUAUUUAAGAAACUCAAUAAUAUUGGCAGCAAGGA GAAUGGUGACUUUCAGGAUGAUAACUAUUGGCUG AGUGAGCAUCACGGAAAUCAACGUGAUUCUGAGA GGAAAAUGAU	**180**	25	30,555556	13,888889	30,555556	38,888889	61,111111	1	1,8	-73,7	-70,3	0,048521	14	-40,944444	-1,0528571
spiLA0480-MIR9471a-2	GGUUCUGAGAUUUAGUUGAUUUCUCUGGUGCUUA CUCAACUAAUAGUUAUUAUUUAAGAAAAUCAAUAA UAUUGGAAGCAAGGAGAAUGGAGACUAUCAGGAU GAUAACUAUUGGUUGAGCAGCAUUAGAGAAAUUG ACAUGAUUCUGAGAGGA	**154**	23,376623	34,415584	10,38961	31,818182	33,766234	66,233766	0,9245283	2,25	-58,5	-58,5	0,120957	6,7	-37,987013	-1,125
spiLA0480-MIR9471b	UUGAGAUUCAGUUGAUUUCUGAGGUGCUCACUCA GCUAAUAGUUAUUGUUUAAGAAACUCAAUAAUAUU GGCAGCAAGGAGAAUGGUGACUUUCAGGAUGAUA ACUAUUGGCUGAGUGAGCAUCACUGAAAUCGACA UGAUUCUGAG	**147**	23,809524	30,612245	14,285714	31,292517	38,095238	61,904762	1,0222222	1,6666667	-65,2	-65,1	0,0700697	7,9	-44,353741	-1,1642857
spiLA0480-MIR9472	AUGGGUUUCAAUUAUAGCUACAGAUCUUCCCAUA GAUCUACUCGAUUUAUUUUUCAGUAGACGUUGUG AAUAAUUGAUAAAUACAGGUAUACAGAGGUCUUAA UAUAGUCAGAACCUAGAAAUAUGUGUAACUAGAU UCAGACCUUUGUACACUUGUAUUCUGUUGCUAUU CACAAUCUCUGCUGAAAAAUGAUUGACUAGAUCU	**232**	16,37931	32,327586	16,37931	34,913793	32,758621	67,241379	1,08	1	-81,1	-79,2	0,001364	16	-34,956897	-1,0671053

spiLA0480-MIR9473-1	ACGAAUAAUCUAGAUUAUUAAUGCCCG CUAGCAGAUAUUGGCUGUAAAUCUAAACUCGUUC UACUCCACUAGUCAUCAUGUAAUGACAUUUACUA GAAGAAGAGACUAUUGGGGUAAAACGAGUUCAGA UUUACAGCCAAUAUUGUU	**120**	18,333333	33,333333	17,5	30,833333	35,833333	64,166667	0,925	1,047619	-54,5	-53	0,0353033	8,6	-45,416667	-1,2674419
spiLA0480-MIR9473-2	AAAACAAUAUUGGCUGUAAAUCUGAACUCGUUUU ACCCCAAUAGUCUCUUCUUCUAGUAAAUGUCAUU ACAUGAUGACUAGUGGAGUAGAACGAGUUUAGAU UUACAGCCAAUAUCUG	**118**	16,949153	32,20339	17,79661	33,050847	34,745763	65,254237	1,0263158	0,952381	-55,9	-55	0,0591018	9	-47,372881	-1,3634146
spiLA0480-MIR9476-1	AUCCUGCUAUUGGUCUAGUCCUGCAUCUUUUUUU AUAUUUUUUGAUAACGGAAAAAAUGUAAAAAAAGA UGCAGGACUAGACCAAUAGCAGUU	**94**	17,021277	32,978723	14,893617	35,106383	31,914894	68,085106	1,0645161	1,1428571	-63,4	-63,4	0,890285	0,5	-67,446809	-2,1133333
spiLA0480-MIR9476-2	CGUUAAAACGGUAUAUAAGACUACUAGACAGCUC AAGCUUAAAAACUCUAACUUGCCUACCAGUUGAC CACCAUAACCAAUGAAGACAGUCCCUAACCAAAGG GAACUGAAUCAACUGGUAGACAAGUUAGAGUGUU AAAGCUUGAGUUGUCUAGUAGUCCUACAUAUCUU UUUACAA	**178**	16,853933	35,955056	21,348315	25,842697	38,202247	61,797753	0,71875	0,7894737	-86,7	-80,6	0,0179975	10	-48,707865	-1,275
spiLA0480-MIR9476-3	AAACUGCUAUUGGUCUAGUCCUGCAUCUUUUUUU ACAUUUUUUCCGUUAUCAAAAAAUAUAAAAAAAGA UGCAGGACUAGACCAAUAGCAGGAU	**94**	14,893617	35,106383	17,021277	32,978723	31,914894	68,085106	0,9393939	0,875	-58,3	-58,3	0,77138	0,6	-62,021277	-1,9433333
spiLA0480-MIR9477-1	CUACCUGAUCUAUCACCAUCUAUGUAUUAAAAAAC ACCUCGAAGAUGACAAGUCCAACUAUCAAUUGUU UCCUUUUUCAACCUGAACUAUCAUACCAUCUACU CAACUAGGUGUGUCUUAAUAUAUAGAUGGUGAUA CUCCAGGUAG	**147**	12,92517	31,972789	23,129252	31,972789	36,054422	63,945578	1	0,5588235	-46,9	-41,02	0,0303478	17	-31,904762	-0,8849057
spiLA0480-MIR9477-2	AUGUUUAUCGACACACACACCUCAACUAUUAGUU GUUCUCUUUUCCUACCUGAAUGAUGGUGAUAUUC UAGGUUGGGAAAGGGAACAACUGAUAGUUGAGGU AUGUUUCGAUAAACAU	**118**	20,338983	28,813559	16,949153	33,898305	37,288136	62,711864	1,1764706	1,2	-67,3	-63	0,0789966	7,1	-57,033898	-1,5295455
spiLA0480-MIR9477-3	GUGAAUGUAUCCGGUUUUUCAAAUUUUAUAUCUA AACUAACACUAAAUGUUUAUCGACAUACACACCUC AACUAUCAGUUGUUCUCUUUUCCUACCUGAAUGA UGGUGAUAUUCUAGGUUGGGAAAGGGAACAACUG AUAGUUGAGGUAUGUUUCUAUAAACAUUUGGUGA UAGUUCAGGUUGGGAACUCGGAAAAAGGAAUACU UGAU	**209**	20,095694	30,62201	14,832536	34,449761	34,92823	65,07177	1,125	1,3548387	-90,7	-84,7	0,0070104	25	-43,397129	-1,2424658
spiLA0480-MIR9477-4	AAGCCAACUAUCCGUUGUUCACUUUUCCUACCUA AACACUCUGUGUUUUCUAUAUAGACGGUGAUAGU UCAGGUACAAGAGGGAACAACAAAUAGUUGGGAU UUAUAAAAGGGAUAAGGCUUAAAUAUGUCGAUCG	**102**	19,607843	30,392157	19,607843	30,392157	39,215686	60,784314	1	1	-34,8	-33,2	0,118973	12	-34,117647	-0,87
spiLA0480-MIR9478	AACUUUGAGAAAAGACUCAUCUAUGUCAUCUGGU AAAGUUUGGUGUGUAAUGGUUUGAAUGAGCCUUU UCUCGAACGAAAAUGGUGUAGAUGAGUUAAAUUU UUAACGGAUUACAUAAUUGAGUCUUUUCUCAUAG UUCGAUGACAUAUUUGAGCGUUUUCCCAAUUAUA	**204**	20,588235	30,882353	12,254902	36,27451	32,843137	67,156863	1,1746032	1,68	-82	-74,63	0,0053936	27	-40,196078	-1,2238806
spiLA0480-MIR950	UCAUGCCUUGGGCCACGGUCGUUUCUAUGACAAA CUUGGGUUUGGCAAGAGUCUUCGAGGGCACCAA GGCAACA	**74**	28,378378	22,972973	24,324324	24,324324	52,702703	47,297297	1,0588235	1,1666667	-28,9	-28,9	0,43351	5,9	-39,054054	-0,7410256
spiLA0480-MIR9555b	UAAAAUUUGCAUUUCUAUACAAUUGAAUCGAAGUA AAAUAUUUGUAAAUUGUAUAAUUAAGUGUAUAGCA CGAAGAUGUAUGUUUUUGCAUGUGUAUAUAUAAU UUUCUCUCGCUUUAUACAAAACAGAAACACAAUAU AUACAAUUCUGUUAUAUAAAGCGAGAGAGGCGAA CAGAGGGAGAAUGGCGAGCGAGAAUGCGAGAGUU GCGAGCGAGAGUUUCGGGAGAGAGGCGACUGAC AAACUUUGGCAAAUGUUUGCUUUGGUGCACAAUU AAAUCAAACAGUAACUACUCCAUUUAUUUUAGGUU AUUAAUUUGCUAUUAUAUACAAUUAUC	**336**	19,940476	35,119048	12,797619	32,142857	32,738095	67,261905	0,9152542	1,5581395	-84,6	-68,8	0,0005192	51	-25,178571	-0,7690909
spiLA0480-MIR9556	UGUACUUAAGCCCUUAGCAUCAAAUACUUGGCCC ACAUACACCCUUAUUCUGCUCAAUUGCGCAUAGU AUUUGGACCAAGUAUUUGACGGUAAGGGCAUAAG UGAA	**106**	18,867925	29,245283	22,641509	29,245283	41,509434	58,490566	1	0,8333333	-43,7	-41,1	0,189229	6,2	-41,226415	-0,9931818
spiLA0480-MIR9560	CGACUUUUAUGAAGAGUUGUGACAUAUAUGAAAU GUUGCGACUUUUAUGAAAAAUUGCGACUUUUAUG AAAAGUUGUGACAUUUAUGGAAAGUGUGACCACC	**115**	20,869565	32,173913	11,304348	35,652174	32,173913	67,826087	1,1081081	1,8461538	-31,6	-26,4	0,023348	34	-27,478261	-0,8540541

spiLA0480-MIR9562-1	UUUCUGAAAGAUU CAUAAUUGCGUUCCAUAGCAAACAUAUAACUGUAU AAUUCGCUAUACAUAUACAAUUGUAUAAUUCGCU GGCCUAAAUUGUAUAAUUCGCUGGUCUCGCUAUG CAUAUACAAUUGUAUUAUUCGCUGGCCUAAAUUG UAUAAUUUGUUGGCCUAUUCGGCUGCAAUUGUA UGUAUGCUAUAGCAAAGUUUGCAUAAUUGCGCUC CAUAGCGAACAUAAAACUGUAUAAUUCGCUAUACA UAUACAAUUGUAUAAUUUGCUGGCCUAAAUUGUA UAAUUCGCUGGCCUAUUUCGCUGUAAUUGUAUAA UUUGCUAUCCUAUUUAACUGCAAUUGUAUAAUGC	**170**	15,882353	28,823529	18,235294	37,058824	34,117647	65,882353	1,2857143	0,8709677	-42,7	-41,2	0,0237052	35	-25,117647	-0,7362069
spiLA0480-MIR9562-2	ACAAUUGAAUAAUUCGCUGCCUAUUUCGCUGCAA UUUUUAUAUAAAAUUUGCUUUGCAUACA CAUACACGUCUCAUAAUCUUAUCCACUGAUCCGC	**233**	14,16309	30,472103	17,167382	38,197425	31,330472	68,669528	1,2535211	0,825	-54	-44,7	5,77E-05	41	-23,175966	-0,739726
spiLA0480-MIR9563a-1	ACAUUAUAUCGAUGGAUAAGAUUGUGUCACGUGU CCC	**71**	15,492958	26,760563	26,760563	30,985915	42,253521	57,746479	1,1578947	0,5789474	-28,5	-28,5	0,650482	0,8	-40,140845	-0,95
spiLA0480-MIR9563a-2	AUACUACAAGACUAUUUGUUGUUGAAGCUUCUGC UUAAGUUGGUGUCUUACCUUGCAAUUCACUUCUA UGGUACUUCAAAAGCAGAAGCGAUCCACGAUAGA AGUGAAUUACAAGUUAAGACACCAACUUAAGCAGA AGCUUCAACAACAAAUAGUCUGGAGAGG	**165**	19,393939	33,939394	18,787879	27,878788	38,181818	61,818182	0,8214286	1,0322581	-98,8	-97,8	0,0876142	9,9	-59,878788	-1,568254
spiLA0480-MIR9668	CACCAUUUUUGGGGUGAUCCGGAUUACGACGUCA AAAAUGUCAAAUAUUUUCGUGGACAUCUCUCAAG ACCUUGUCUAUGCAUGCGGUUGGCCAUCACGGCU UUUCCGGCCCAUUUAGAGGGUCAAACAAGCGUAG AAGCGAGCAUACGCCUCAUUUCGACGAUUUUCGU GUGCUAUAGCACACCAUUUUUUGGGUGAUCCGGA UUCCGACGUUAAAAAUGUCA	**224**	22,767857	24,553571	23,214286	29,464286	45,982143	54,017857	1,2	0,9807692	-72,2	-66,8	0,0037063	32	-32,232143	-0,7009709
spiLA0480-MIR9679-1	GACUUAUAAAACCCUCUAAAUCUCAUGGUCUUGU ACUGCAUUUUAUGUUAAUAAAGCUGCAGAACAAG AAAGAGGUGUUCCCAGGUUUGUAAUAAAUU	**98**	17,346939	33,673469	16,326531	32,653061	33,673469	66,326531	0,969697	1,0625	-26,1	-24,4	0,094145	6,7	-26,632653	-0,7909091
spiLA0480-MIR9679-2	AAAUUGAUAAUUUAUUAUCAAAGGGACUUAUAAAA CCCUCUAAAUCUCCAUGGUCUUGUACUGCAUUUU AUGUUAAUAAAGUUGCAGAACAAGAAAGAGGUGU UCCCAGUUUGGUAAUAAAUUACAAGCC	**130**	16,153846	36,153846	15,384615	32,307692	31,538462	68,461538	0,893617	1,05	-39,1	-39,1	0,0431227	7,5	-30,076923	-0,9536585
spiLA0480-MIR9726-1	UCCUUCUAUAAAUAGAGCAUUGUUGCUCAUUUGG UAAGAUUUACAACCAUUUUUGACUUUGCUAUAUU UACCUAUGUCAUUAGUGACAUAAGCAUGAUUUUA UCCUUCUAUAAAUAGAGCAUUCUUGCUCAUUUGU AGAACAC	**143**	13,286713	28,671329	17,482517	40,559441	30,769231	69,230769	1,4146341	0,76	-34	-27,2	0,0067136	44	-23,776224	-0,7727273
spiLA0480-MIR9726-2	AUAAGGAGUGUCCAUAAAUAACUCUUUUCAAAAAG UAGAACUAGUGAAAUUCGAACACACAAGCACUACC UCAUCCUAAGGAGGUAAAACCACUGGAGUACAGU AGCUUGUUGUGUUAAGGGUGUUAAAAAUAUGUUA UUUAAUUAUUUUGUGUAUUAUAUUACUUGUAUAC ACAAUAUUUUUUUCUGACGAAGGGUAUUCAAUUG GACACCCUAAC	**217**	17,050691	34,562212	15,207373	33,179724	32,258065	67,741935	0,96	1,1212121	-54,8	-48,7	0,0004141	30	-25,253456	-0,7828571
spiLA0480-MIR9726-3	UUUAUCAUUAUAAGUGUAAUUUUUUUCUUCAAUU GAUUUAAGUAAGUUAGGCCAAGGGUCCGCUCGAG GCCAGUAAUGGUCAUCGAGUAUCAGUCUCAUCCA GGAUGUAGGAUCGCGAUGUGAAAUUUUUAGCGUC AAACUAUAAAAACUUUGACCAAUAUUUUACGAUGU AUAUUUUCAUCAUAUUGAUAUGAAAAAAGAUUACA AUUUAUAGUAUUUU	**220**	17,272727	31,818182	13,636364	37,272727	30,909091	69,090909	1,1714286	1,2666667	-51,3	-48,8	0,000726	32	-23,318182	-0,7544118
spiLA0480-MIR9728	AUGGAAAGAGUUUACUUUGUGUCUCACACAACUG ACACAAGUUGUGGGGAUUCUUUUUGUUUCACAAA UUUGUGGACCAAAAGUGUAAGACUAGGGUCCAGU AAUUUGUAGAUCAAAGCCUCACACAACCUGUGUC UGUUGUGUGAGACACAAAAUGAAGUUUCUCUUG CGCUUGCCAAGUUUGCACACUGCAAGGACUUGGC	**169**	21,893491	28,994083	17,159763	31,952663	39,053254	60,946746	1,1020408	1,2758621	-75,5	-72,1	0,0379878	18	-44,674556	-1,1439394
spiLA0480-MIR9736	GGGAAUAUGAUGCAACUCUAAGAGAACAACUGCU AGGUGGAGCUGGUAUGUUCAACAAAGGUUUGAUU CUUCUUGUUUCUUACAAUGGGAUUGCCCAGUAAG CUUAGAAGUUUUGGCCGGAGUUGUUUAUACGCAU GCUUGGAACACAAACCAAGGUGGAGAUUGAAAGA GUUGGUUUUGGUUCUUGUGGAAUCAAACUAAAUG	**331**	25,377644	31,41994	13,897281	29,305136	39,274924	60,725076	0,9326923	1,826087	-91,3	-88,8	0,0001857	27	-27,583082	-0,7023077

spiLA0480-MIR9739	GAAGAUGAAUUAAUAUGAAUAUUUGGUAGGAAGA UAAUUAGUACAAAAUACAAGUCAAAGAUUGUAUCU UGGUAGGUGAAAGUUAGGCAAACC GUUUUCAUGGGUAAGAUAUAGUGUAUAGUGAGUU GAGAAUUUAUUUAUUAUCACGGAUUGGGAUUUCU AGGGACGUUAGUGUGGUUAUUAGGUGAUAGUCUA UUAAAAUCCUUACUCGCUUAGGGAUUUCUAGGGA CGUUAGUGAGUGAGUUUAGGGUCUAUGAUAUACC UAUAAUAAUUUGAAUGUCCACAAACUUGCUUACUU AUGAAUAU	**213**	23,474178	27,699531	10,328638	38,497653	33,802817	66,197183	1,3898305	2,2727273	-53,8	-50	0,0007975	40	-25,258216	-0,7472222
spiLA0480-MIR9742	UUGCUGGAUUGGGUGUUUUUACUUGUGAGUUCC UUUCUACUACUACUGUUUAAAUUUGACGAUAGAA UGUGUGGUUUGAUCUGUAACACAAUAGCUACUUC UUCAGCUUAUGUAGCAGUAGAAAGGAACUCACAA GUAAAAACACGCAAUCAAGAUU	**157**	19,745223	29,299363	15,923567	35,031847	35,66879	64,33121	1,1956522	1,24	-67,8	-61,28	0,0298622	23	-43,184713	-1,2107143
spiLA0480-MIR9746i-1	UACCCUUUAACUUGGCUUCGAAUCACAUUUAUGC CCUUCAACUUUGAGUGUGCAUAAAUAGACACUUA AACUUGUAGAAAGUUGAACAAAUAGACACACAUGU CCUAUAUGUCAUUUUUUGUCCUACGUGUAUUUUG UCAUGUAGGACUCACGUGUUUAAUUAUUUAAAAG GUGGAUAGUUAAAGUGUUUGUUUGUCCAUUAUGA AAGUUGGAUAGUUAAAGUAUUUGUUUGUGCAUAA UGAAAGUUGGAGGUCAAAGUUAAAAUUUGAGUCA AGUUUAGGAUC	**284**	19,366197	30,28169	13,028169	37,323944	32,394366	67,605634	1,2325581	1,4864865	-92,5	-87,5	0,0017401	43	-32,570423	-1,0054348
spiLA0480-MIR9746i-2	UCUUUCUCAACAAAACUAAAUGGUAGCUCGUCAA CAAUUAUCGUUUUGGCUAAAGCUUUCCUACUUUG UACUUGGUCAAAUUUCCAAGUGCUAAUGACCCCU UCCUGUGAUCCCGUUGAAGAUGGUAGAAAAUUAA UUAGAUUUUGAUAUCUACGGUGUCACGAGGAAAU UUAGGACAUAUUCUCAAAUGAGUAUUCAUUGAUG ACGUACCAUUAGAUGAUGUAGAAGUU	**230**	18,26087	30	17,391304	34,347826	35,652174	64,347826	1,1449275	1,05	-60,7	-55,8	0,0008013	30	-26,391304	-0,7402439
spiLA0480-MIR9748	ACGAGUCUAGUAGAGUCUUAAGGAACGGUAGGGG GACGCCAUUACUUUUCUUUGAGAGGCUAUAAGAC UUUA	**72**	27,777778	27,777778	15,277778	29,166667	43,055556	56,944444	1,05	1,8181818	-29,5	-29,5	0,312541	2,7	-40,972222	-0,9516129
spiLA0480-MIR9751	UUGGAUUAUUCCGUUAAAUGGGGGCUGAUUUUG GUGAAAUUAGUAACGGGAGGGGUAAAAUUAACUC CAUUUUAACGGAGAGGAUAAAUUUAAACAAUAAAU UAAAGUCGAGGGUAUUUUUAACCCUUAUCCCUUU AAAUAACUAAAUAUAGCCAUGGUUUAAUAAUCAAU CAUU	**175**	18,857143	35,428571	12	33,714286	30,857143	69,142857	0,9516129	1,5714286	-39,1	-38,7	0,0266531	28	-22,342857	-0,7240741
spiLA0480-MIR9760-1	UUGAAGAAACAUAAUUUUAUUGAUUAAGAUAGCG GGUACAAUUCUGUUGAUCCCUUGAUUCUACUCUC UUCGGAUUUAUCCAUGAUUCGAGAGACGCUAGUA GCGUAUUUCUCGAACUAGGAUGAUUUAGAUUUGA UCUUUCUAUGUGAAUAAUCCAUCAAUUUGUGGAG UAUUCGAGAUCUUGAUGUCUUUAAGAAAUUUUUG AGAUGCCUUUUAAGAGAAUUUAGUACCCUUUAUA UAGGCAUAAAUUAGAUUUUUAUG	**261**	18,390805	28,735632	13,409962	39,463602	31,800766	68,199234	1,3733333	1,3714286	-59,5	-51,4	1,95E-05	63	-22,796935	-0,7168675
spiLA0480-MIR9760-2	UCUUUCUCUCAUGAAAUUGAUGAGAAAUUGGAGG AUUUAGUAUUGACUGUUGAGGAUGAUUUGGGGAU GAAGAUGGUUGGAUGGGUCAUCCUCUCAUGAAAU UCAUGAGAAAUUG	**115**	27,826087	27,826087	9,5652174	34,782609	37,391304	62,608696	1,25	2,9090909	-30,6	-25,7	0,0255981	26	-26,608696	-0,7116279
spiLA0480-MIR9761	AAAAGGGCCUAAAACGCCCUUAAAUUAUGAGAUUA UGUACACUAUUACGCACCAACUACUUAAUGAGUG UGAUCCGUUGGGCAUAAGGUAUUUUUGAGUCGAA AGGUAAAUGUCAAGGAUAUUUUAAGACCGAUAGG UGGAUGGAGGAUAAUUUUAUACCAAUUCAAAUAC UUGAGGGGCAUGUUAGGCCCUUCU	**195**	22,564103	32,307692	15,384615	29,74359	37,948718	62,051282	0,9206349	1,4666667	-55,8	-42,31	0,0115833	37	-28,615385	-0,7540541
spiLA0480-MIR9767	UCCUAGGUUAGUAGUUAAGAUAGUUAGUUAGGGC CUAGAGUUAUUUAGGAAGUUAGGCCCCACAUCGA GGGACCCGUACACCAUGCUGCCCCUUAACUACCC UAACCGAAUUUGGUUAGGGUGGUCCCCUCCUUUG GUCGAUUCUCACUUGCUUUGCCCAUGUUCAUGCA CAUGGGCGGGUUGUACUUUUCUAACUAACUAUUU GGAAUAGUUACUUAUCG	**221**	22,624434	21,719457	23,076923	32,579186	45,701357	54,298643	1,5	0,9803922	-76,9	-72,9	0,0024923	35	-34,79638	-0,7613861
spiLA0480-	UCAUCAGAAAUUUCUUUUAUCCUCAAGACUUAAAC	**199**	15,075377	30,653266	15,075377	39,19598	30,150754	69,849246	1,2786885	1	-43	-32,4	0,0021732	27	-21,60804	-

MIR9773	GCGAUAUAUCUACUUAAGAAUGAAGGGAUUUUAU UCAUUUCAUCAGUACCCCUUGAUAAAGCGUAUGG UUUAUUAAAAUCGAACUACCAUAAAUGUGUAGUUU AACUUUCUUUGGCUUAGAUAUUUGUUUUUAUAUU UUUAGGACCAUUAGAGAUUUCGGACAG ACUAAGGAAUGAGUCAAAAUGACCCAUUUACAAAG AUAUUAAAUAGUUCUGUGGGGUGAUAGGACACUU UGAAAGUUAAAGUGUCUUUAUACAAAUACUGGAC															0,7166667
spiLA0480-MIR9774	AACUUUGAUGGUGUCUUUAUGUCUUUUCUCUUUU U GCAUUCCACUUUCAUGAAAAGAUGUGACUUUUAU GAAAUUUUGCUACUUUAACGAGGAGGUGCGACUU UAAUCAAAAGUUGUAACUUUUAUGAAAAGUUGUG ACUCUAAUGAAGAGUUACGAUUUUUAUGAAAAAUU GUGACUUUUGUGAAGAGUUGCGACUUUAAUGAAG	**138**	18,84058	31,15942	13,043478	36,956522	31,884058	68,115942	1,1860465	1,4444444	-32,1	-29,3	0,0104784	26	-23,26087	-0,7295455
spiLA0480-MIR9776	AGUUGCGACUUUAUGAAAAGUUGUAACUUUUACG AAAGGUUGUGAACUU AAAUUGAACAAGUAGACACAUGUGUCCUACAUGU CAUCCCACAUGUCAUUUUUUGUCAUACAUGGUGU	**220**	20,909091	31,818182	10,909091	36,363636	31,818182	68,181818	1,1428571	1,9166667	-75,5	-75,4	0,0018279	20	-34,318182	-1,0785714
spiLA0480-MIR9781	CCUACGUGUAUUUUGUCAUAUAGAACUCAUGUGU UUAUUUAUUUAAAAG UGCGUUGAGACAGUUGUAGUGUCUAAAUCUUGUU AAUUGAGGCCAAGUUUGAGAGUGUUUAUAGCGGC AAUUUAUUGUGUAUACAAUUUGACAUAAUACAUAA AUAGUUUCUUUAACUUGGGUAUGAAUUACGUUUA	**117**	15,384615	29,059829	17,094017	38,461538	32,478632	67,521368	1,3235294	0,9	-29,7	-27,6	0,0736138	17	-25,384615	-0,7815789
spiLA0480-MIR9782	UACCCUUCAAUUUUGGGUGUGCACAAGUAGACAC UUAAACUAGUAUAAAGUUGGACAAAUAGACACACA UGUCCUACAUG	**217**	19,815668	31,336406	13,824885	35,023041	33,640553	66,359447	1,1176471	1,4333333	-51,9	-43,6	0,0020695	69	-23,917051	-0,7109589

Supplementary Table S20. Thermodynamic and structural characterization of *Solanum pimpinellifolium* LA1589 pre-miRNAs (Size, G content, A content, C content, U content, GC content, AU content, AU ratio, GC ratio, Minimum Free Energy (MFE), Minimal Free Energy of the thermodynamic ensemble (MFEE), MFE structure Frequency in the ensemble (Freq), Ensemble Diversity (Div), Adjusted Minimum Free Energy (AMFE), Minimum Free Energy Index (MFEI)).

Precursor name	Len	G	A	C	U	GC	AU	UA-ratio	GC-ratio	MFE	MFE-ensemble	frequency	diversity	AMFE	MFEI
spiLA1589-mir171d-1	**85**	20	29,411765	16,470588	34,117647	36,470588	63,529412	1,16	1,2142857	-34,4	-34,4	0,265713	2,11	-40,470588	-1,1096774
spiLA1589-mir171d-2	**81**	18,518519	29,62963	16,049383	35,802469	34,567901	65,432099	1,2083333	1,1538462	-33,9	-33,9	0,413811	1,24	-41,851852	-1,2107143
spiLA1589-mir5304	**141**	21,276596	27,659574	19,148936	31,914894	40,425532	59,574468	1,1538462	1,1111111	-60,3	-60	0,106114	3,77	-42,765957	-1,0578947
spiLA1589-mir482d-2	**145**	24,137931	27,586207	15,172414	33,103448	39,310345	60,689655	1,2	1,5909091	-65	-61,7	0,0248161	9,65	-44,827586	-1,1403509
spiLA1589-mir482d-1	**111**	24,324324	25,225225	18,918919	31,531532	43,243243	56,756757	1,25	1,2857143	-50,4	-49,2	0,0372456	9,02	-45,405405	-1,05
spiLA1589-mir477-1	**132**	21,212121	28,787879	22,727273	27,272727	43,939394	56,060606	0,9473684	0,9333333	-53,2	-50,1	0,054659	9,94	-40,30303	-0,9172414
spiLA1589-mir477-2	**114**	25,438596	27,192982	21,052632	26,315789	46,491228	53,508772	0,9677419	1,2083333	-56,7	-56,2	0,136212	7,34	-49,736842	-1,0698113
spiLA1589-mir166b-1	**138**	19,565217	31,15942	13,768116	35,507246	33,333333	66,666667	1,1395349	1,4210526	-39	-34,3	0,0610093	17,07	-28,26087	-0,8478261
spiLA1589-mir10528	**97**	18,556701	35,051546	17,525773	28,865979	36,082474	63,917526	0,8235294	1,0588235	-42,3	-42,3	0,0530642	7,51	-43,608247	-1,2085714
spiLA1589-mir169r-1	**285**	19,298246	26,666667	18,596491	35,438596	37,894737	62,105263	1,3289474	1,0377358	-98,2	-93,37	0,0004296	33,32	-34,45614	-0,9092593
spiLA1589-mir169r-2	**184**	21,73913	26,630435	18,478261	33,152174	40,217391	59,782609	1,244898	1,1764706	-70,9	-70,9	0,0109624	10,12	-38,532609	-0,9581081
spiLA1589-mir482e-1	**189**	22,222222	24,338624	17,460317	35,978836	39,68254	60,31746	1,4782609	1,2727273	-76	-75,9	0,0196879	12,81	-40,21164	-1,0133333
spiLA1589-mir169a	**159**	24,528302	27,044025	15,09434	33,333333	39,622642	60,377358	1,2325581	1,625	-82	-82	0,0608701	4,2	-51,572327	-1,3015873
spiLA1589-mir162-2	**137**	21,89781	28,467153	19,708029	29,927007	41,605839	58,394161	1,0512821	1,1111111	-50,4	-47,1	0,0627452	8,25	-36,788321	-0,8842105
spiLA1589-mir162-1	**103**	22,330097	33,009709	22,330097	22,330097	44,660194	55,339806	0,6764706	1	-41,3	-40,9	0,116727	5,53	-40,097087	-0,8978261
spiLA1589-mir164e	**97**	20,618557	25,773196	19,587629	34,020619	40,206186	59,793814	1,32	1,0526316	-44,1	-42,4	0,0243927	13,08	-45,463918	-1,1307692
spiLA1589-mir167b-4	**110**	24,545455	25,454545	22,727273	27,272727	47,272727	52,727273	1,0714286	1,08	-53,5	-53,5	0,0801293	4,39	-48,636364	-1,0288462
spiLA1589-mir8038b-1	**100**	18	27	20	35	38	62	1,2962963	0,9	-27,8	-27,8	0,248004	4,94	-27,8	-0,7315789
spiLA1589-mir319b-3	**171**	24,561404	26,315789	21,637427	27,48538	46,19883	53,80117	1,0444444	1,1351351	-79,4	-75,6	0,0508234	8,78	-46,432749	-1,0050633
spiLA1589-mir172b-2	**156**	19,230769	30,128205	12,179487	38,461538	31,410256	68,589744	1,2765957	1,5789474	-56,8	-56	0,0081088	16,19	-36,410256	-1,1591837
spiLA1589-mir172	**125**	21,6	27,2	10,4	40,8	32	68	1,5	2,0769231	-28,6	-24,9	0,0016041	17,63	-22,88	-0,715
spiLA1589-mir172d-2	**99**	18,181818	34,343434	15,151515	32,323232	33,333333	66,666667	0,9411765	1,2	-45,7	-45,7	0,10629	7,47	-46,161616	-1,3848485
spiLA1589-mir166c-1	**187**	20,855615	31,016043	14,438503	33,68984	35,294118	64,705882	1,0862069	1,4444444	-74,5	-66,9	0,0155504	14,38	-39,839572	-1,1287879
spiLA1589-mir408a	**72**	22,222222	23,611111	27,777778	26,388889	50	50	1,1176471	0,8	-26,6	-25,6	0,192474	5,48	-36,944444	-0,7388889
spiLA1589-mir8009-1	**54**	24,074074	24,074074	20,37037	31,481481	44,444444	55,555556	1,3076923	1,1818182	-24	-23,7	0,181087	4,08	-44,444444	-1
spiLA1589-mir6024	**118**	19,491525	25,423729	19,491525	35,59322	38,983051	61,016949	1,4	1	-43	-42,8	0,0914477	6,75	-36,440678	-0,9347826
spiLA1589-mir160h-2	**92**	25	23,913043	21,73913	29,347826	46,73913	53,26087	1,2272727	1,15	-47,1	-47,1	0,140918	2,99	-51,195652	-1,0953488
spiLA1589-mir172d-1	**126**	24,603175	27,777778	15,079365	32,539683	39,68254	60,31746	1,1714286	1,6315789	-57	-50	0,0133231	11,75	-45,238095	-1,14
spiLA1589-mir172j-1	**102**	15,686275	30,392157	27,45098	26,470588	43,137255	56,862745	0,8709677	0,5714286	-40,4	-40,4	0,113589	4,54	-39,607843	-0,9181818
spiLA1589-mir172e-1	**162**	17,283951	33,333333	12,962963	36,419753	30,246914	69,753086	1,0925926	1,3333333	-52,9	-47,57	0,0177217	21,69	-32,654321	-1,0795918
spiLA1589-mir319b-4	**211**	20,853081	31,753555	19,43128	27,962085	40,28436	59,71564	0,880597	1,0731707	-90,2	-90,2	0,0273192	8,53	-42,748815	-1,0611765
spiLA1589-mir319b-2	**198**	23,737374	29,292929	20,20202	26,767677	43,939394	56,060606	0,9137931	1,175	-97,8	-97,8	0,114249	5,34	-49,393939	-1,1241379
spiLA1589-mir477a	**70**	27,142857	18,571429	27,142857	27,142857	54,285714	45,714286	1,4615385	1	-36	-32	0,0660925	7,18	-51,428571	-0,9473684
spiLA1589-mir477b	**72**	23,611111	22,222222	22,222222	31,944444	45,833333	54,166667	1,4375	1,0625	-34,4	-29,2	0,188148	4,56	-47,777778	-1,0424242
spiLA1589-mir319a	**182**	23,626374	27,472527	20,879121	28,021978	44,505495	55,494505	1,02	1,1315789	-82,2	-77	0,0402093	22,69	-45,164835	-1,0148148
spiLA1589-mir156b-7	**142**	19,014085	33,802817	14,788732	32,394366	33,802817	66,197183	0,9583333	1,2857143	-45,3	-44	0,0371928	14,76	-31,901408	-0,94375
spiLA1589-mir156b-8	**142**	14,084507	30,28169	19,014085	36,619718	33,098592	66,901408	1,2093023	0,7407407	-44,7	-43,4	0,0792376	8,53	-31,478873	-0,9510638
spiLA1589-mir156b-2	**122**	18,032787	33,606557	13,934426	34,42623	31,967213	68,032787	1,0243902	1,2941176	-31,8	-30,3	0,0201607	17,38	-26,065574	-0,8153846
spiLA1589-mir167b-3	**86**	17,44186	30,232558	18,604651	33,72093	36,046512	63,953488	1,1153846	0,9375	-31,2	-31,2	0,0737315	5,66	-36,27907	-1,0064516
spiLA1589-mir172c	**190**	17,894737	38,421053	12,631579	31,052632	30,526316	69,473684	0,8082192	1,4166667	-63,9	-57,4	0,0063425	21,29	-33,631579	-1,1017241
spiLA1589-mir6025b-2	**162**	24,691358	25,308642	13,580247	36,419753	38,271605	61,728395	1,4390244	1,8181818	-59,7	-59,7	0,0307663	16,86	-36,851852	-0,9629032
spiLA1589-mir6025b-1	**162**	20,987654	27,160494	13,580247	38,271605	34,567901	65,432099	1,4090909	1,5454545	-52,9	-50,2	0,021433	24,61	-32,654321	-0,9446429
spiLA1589-mir5300	**266**	19,548872	29,699248	15,413534	35,338346	34,962406	65,037594	1,1898734	1,2682927	-91,7	-89,3	0,0018507	16,24	-34,473684	-0,9860215
spiLA1589-mir394c	**233**	25,321888	30,901288	14,592275	29,184549	39,914163	60,085837	0,9444444	1,7352941	-81,2	-79,7	0,0100066	25,35	-34,849785	-0,8731183
spiLA1589-mir396b-2	**159**	17,610063	32,075472	13,207547	37,106918	30,81761	69,18239	1,1568627	1,3333333	-57	-52,51	0,0083291	21,99	-35,849057	-1,1632653
spiLA1589-mir396b-1	**131**	19,083969	29,007634	14,503817	37,40458	33,587786	66,412214	1,2894737	1,3157895	-54,9	-51,51	0,0184962	15,27	-41,908397	-1,2477273
spiLA1589-mir396b-3	**133**	17,293233	33,082707	13,533835	36,090226	30,827068	69,172932	1,0909091	1,2777778	-49,6	-46,31	0,0304801	15,85	-37,293233	-1,2097561
spiLA1589-mir167b-1	**84**	25	29,761905	20,238095	25	45,238095	54,761905	0,84	1,2352941	-41,7	-41,7	0,476326	3,16	-49,642857	-1,0973684
spiLA1589-mir398a	**92**	18,478261	28,26087	15,217391	38,043478	33,695652	66,304348	1,3461538	1,2142857	-35,9	-34,3	0,0503768	13,81	-39,021739	-1,1580645
spiLA1589-mir319b-1	**171**	21,637427	27,48538	18,71345	32,163743	40,350877	59,649123	1,1702128	1,15625	-85,3	-84,6	0,0228358	9,44	-49,883041	-1,2362319
spiLA1589-mir166d-1	**122**	21,311475	29,508197	16,393443	32,786885	37,704918	62,295082	1,1111111	1,3	-52,7	-51,5	0,334282	5,48	-43,196721	-1,1456522
spiLA1589-mir171a	**94**	22,340426	30,851064	17,021277	29,787234	39,361702	60,638298	0,9655172	1,3125	-52,4	-52,4	0,317948	1,36	-55,744681	-1,4162162
spiLA1589-mir1446	**108**	18,518519	25,925926	20,37037	35,185185	38,888889	61,111111	1,3571429	0,9090909	-51	-51	0,177923	3,7	-47,222222	-1,2142857
spiLA1589-mir167b-2	**110**	20	30	22,727273	27,272727	42,727273	57,272727	0,9090909	0,88	-41,6	-41,6	0,133137	5,88	-37,818182	-0,8851064
spiLA1589-mir397b-1	**118**	16,949153	26,271186	21,186441	35,59322	38,135593	61,864407	1,3548387	0,8	-49,1	-48,9	0,132646	4,34	-41,610169	-1,0911111
spiLA1589-mir397b-2	**121**	17,355372	25,619835	20,661157	36,363636	38,016529	61,983471	1,4193548	0,84	-44,2	-44	0,0867621	6,62	-36,528926	-0,9608696
spiLA1589-mir166f	**156**	23,076923	31,410256	16,666667	28,846154	39,74359	60,25641	0,9183673	1,3846154	-46,1	-42,6	0,0040479	21,93	-29,551282	-0,7435484

spiLA1589-mir2111d-1	**93**	19,354839	25,806452	16,129032	38,709677	35,483871	64,516129	1,5	1,2	-43,9	-43,9	0,0320415	5,17	-47,204301	-1,330303
spiLA1589-mir171c-1	**86**	22,093023	27,906977	12,790698	37,209302	34,883721	65,116279	1,3333333	1,7272727	-43,5	-43,5	0,485905	1,76	-50,581395	-1,45
spiLA1589-mir479a-1	**92**	21,73913	29,347826	18,478261	30,434783	40,217391	59,782609	1,037037	1,1764706	-40,9	-39,7	0,0909347	7,81	-44,456522	-1,1054054
spiLA1589-mir160g	**87**	22,988506	31,034483	24,137931	21,83908	47,126437	52,873563	0,7037037	0,952381	-47,3	-47,3	0,308681	2,21	-54,367816	-1,0673913
spiLA1589-mir159-1	**206**	22,815534	28,15534	14,563107	34,466019	37,378641	62,621359	1,2241379	1,5666667	-76,6	-74,1	0,0019981	18,7	-37,184466	-1,1536585
spiLA1589-mir9478	**207**	19,806763	32,36715	12,560386	35,2657	32,36715	67,63285	1,0895522	1,5769231	-85	-84	0,0034901	14,83	-41,062802	-0,9948052
spiLA1589-mir159a-1	**233**	21,030043	23,60515	15,450644	39,914163	36,480687	63,519313	1,6909091	1,3611111	-87,8	-84	0,0034801	17,97	-37,682403	-0,9702703
spiLA1589-mir9471a-1	**125**	22,4	31,2	15,2	31,2	37,6	62,4	1	1,4736842	-53,7	-53,7	0,177426	8,3	-42,96	-1,1612245
spiLA1589-mir169j-4	**153**	20,261438	22,222222	23,529412	33,986928	43,79085	56,20915	1,5294118	0,8611111	-59,7	-59,7	0,0190951	8,48	-39,019608	-1,0396825
spiLA1589-mir169j-2	**148**	16,891892	24,324324	19,594595	39,189189	36,486486	63,513514	1,6111111	0,862069	-53,5	-51,7	0,0548572	12,68	-36,148649	-0,979661
spiLA1589-mir169j-3	**154**	16,883117	24,675325	18,181818	40,25974	35,064935	64,935065	1,6315789	0,9285714	-53,5	-51,7	0,0484976	15,51	-34,74026	-0,8910448
spiLA1589-mir156b-4	**97**	21,649485	24,742268	17,525773	36,082474	39,175258	60,824742	1,4583333	1,2352941	-58,3	-58,3	0,350584	5,07	-60,103093	-1,2018519
spiLA1589-mir394-1	**81**	28,395062	22,222222	27,160494	22,222222	55,555556	44,444444	1	1,0454545	-43,7	-43,4	0,247506	3,21	-53,950617	-1,0802632
spiLA1589-mir394-2	**61**	29,508197	21,311475	27,868852	21,311475	57,377049	42,622951	1	1,0588235	-31,2	-30,9	0,175055	3,56	-51,147541	-0,8538462
spiLA1589-mir164-2	**173**	19,653179	29,479769	16,184971	34,682081	35,83815	64,16185	1,1764706	1,2142857	-62,2	-60,1	0,0019867	17,99	-35,953757	-0,8885714
spiLA1589-mir164-1	**165**	19,393939	29,090909	16,363636	35,151515	35,757576	64,242424	1,2083333	1,1851852	-59,4	-57,3	0,0027898	17,41	-36	-0,8957143
spiLA1589-mir7981d-1	**253**	15,41502	36,363636	17,391304	30,83004	32,806324	67,193676	0,8478261	0,8863636	-98,3	-95,54	0,0060935	17,9	-38,853755	-1,0032258
spiLA1589-mir171f-6	**108**	21,296296	28,703704	17,592593	32,407407	38,888889	61,111111	1,1290323	1,2105263	-43	-35,8	0,144237	6,97	-39,814815	-1,1794872
spiLA1589-mir171f-4	**113**	23,00885	30,088496	15,929204	30,973451	38,938053	61,061947	1,0294118	1,4444444	-43	-40	0,242291	5,41	-38,053097	-1,0238095
spiLA1589-mir7990a	**102**	14,705882	30,392157	15,686275	39,215686	30,392157	69,607843	1,2903226	0,9375	-32,6	-32,6	0,100386	7,6	-31,960784	-0,9772727
spiLA1589-mir171f-5	**110**	19,090909	33,636364	13,636364	33,636364	32,727273	67,272727	1	1,4	-42,8	-42,8	0,148276	4,48	-38,909091	-1,0170213
spiLA1589-mir171f-1	**110**	19,090909	33,636364	14,545455	32,727273	33,636364	66,363636	0,972973	1,3125	-42,8	-42,8	0,171206	3,8	-38,909091	-1,1888889
spiLA1589-mir319c	**176**	25,568182	23,863636	21,590909	28,977273	47,159091	52,840909	1,2142857	1,1842105	-76,5	-65,1	0,0169927	17,33	-43,465909	-0,8591398
spiLA1589-mir530	**86**	23,255814	27,906977	18,604651	30,232558	41,860465	58,139535	1,0833333	1,25	-42,7	-42,7	0,345573	2,23	-49,651163	-1,0753846
spiLA1589-mir169c-2	**158**	18,987342	29,113924	12,658228	39,240506	31,64557	68,35443	1,3478261	1,5	-67	-64,3	0,0063161	14,4	-42,405063	-1,1833333
spiLA1589-mir6023-1	**235**	19,148936	30,212766	18,297872	32,340426	37,446809	62,553191	1,0704225	1,0465116	-94,5	-89,3	0,0017158	29,94	-40,212766	-1,2
spiLA1589-mir6023-2	**237**	20,675105	28,270042	17,299578	33,755274	37,974684	62,025316	1,1940299	1,195122	-69	-68,07	0,0016912	21,06	-29,113924	-1,0738636
spiLA1589-mir395j-1	**90**	24,444444	15,555556	23,333333	36,666667	47,777778	52,222222	2,3571429	1,047619	-40,1	-36,3	0,0393152	7,91	-44,555556	-0,7666667
spiLA1589-mir9470-1	**237**	23,206751	31,223629	18,565401	27,004219	41,772152	58,227848	0,8648649	1,25	-77,5	-76,2	0,0077949	26,37	-32,700422	-0,9311111
spiLA1589-mir408-1	**71**	25,352113	18,309859	28,169014	28,169014	53,521127	46,478873	1,5384615	0,9	-32	-32	0,704395	1,32	-45,070423	-0,7708333
spiLA1589-mir169e-1	**191**	20,942408	27,225131	17,277487	34,554974	38,219895	61,780105	1,2692308	1,2121212	-78,4	-78,4	0,0268458	13,22	-41,04712	-0,7744186
spiLA1589-mir6231-1	**198**	14,646465	34,343434	15,656566	35,353535	30,30303	69,69697	1,0294118	0,9354839	-91,2	-85,5	0,0071425	17,35	-46,060606	-0,9926829
spiLA1589-mir827-2	**116**	15,517241	39,655172	15,517241	29,310345	31,034483	68,965517	0,7391304	1	-42,4	-41,5	0,156744	7,07	-36,551724	-1,453125
spiLA1589-mir827-1	**88**	15,909091	31,818182	15,909091	36,363636	31,818182	68,181818	1,1428571	1	-34,9	-34,9	0,0956756	6,03	-39,659091	-0,9222222
spiLA1589-mir6022-1	**238**	20,588235	30,252101	18,487395	30,672269	39,07563	60,92437	1,0138889	1,1136364	-86,7	-71,97	0,0090202	31,9	-36,428571	-1,1866667
spiLA1589-mir171f-8	**101**	22,772277	25,742574	13,861386	37,623762	36,633663	63,366337	1,4615385	1,6428571	-45,5	-44,5	0,0487507	7,11	-45,049505	-1,1333333
spiLA1589-mir482a-1	**109**	19,266055	17,431193	18,348624	44,954128	37,614679	62,385321	2,5789474	1,05	-48,7	-48,5	0,323046	2,47	-44,678899	-1,2297297
spiLA1589-mir169c-1	**203**	14,285714	27,093596	18,226601	40,394089	32,512315	67,487685	1,4909091	0,7837838	-65,8	-62,8	0,0048882	16,4	-32,413793	-1,1878049
spiLA1589-mir156f-2	**146**	21,917808	33,561644	14,383562	30,136986	36,30137	63,69863	0,8979592	1,5238095	-63,6	-63,6	0,0980466	6,13	-43,561644	-1,1484848
spiLA1589-mir399j-1	**116**	24,137931	31,034483	16,37931	28,448276	40,517241	59,482759	0,9166667	1,4736842	-46,9	-44,2	0,20809	5,51	-40,431034	-1,2
spiLA1589-mir1886i-1	**55**	20	29,090909	14,545455	36,363636	34,545455	65,454545	1,25	1,375	-24,5	-23,3	0,420644	4,7	-44,545455	-0,9978723
spiLA1589-mir398	**106**	18,867925	22,641509	17,924528	40,566038	36,792453	63,207547	1,7916667	1,0526316	-49,3	-49	0,126228	9,17	-46,509434	-0,7894737
spiLA1589-mir171f-2	**131**	12,977099	26,717557	19,847328	40,458015	32,824427	67,175573	1,5142857	0,6538462	-31,5	-31,5	0,160306	10,28	-24,045802	-1,2894737
spiLA1589-mir171f-3	**79**	17,721519	22,78481	17,721519	41,772152	35,443038	64,556962	1,8333333	1	-24,3	-24,3	0,435288	5,09	-30,759494	-1,2641026
spiLA1589-mir171f-7	**79**	16,455696	22,78481	18,987342	41,772152	35,443038	64,556962	1,8333333	0,8666667	-24,3	-24,3	0,494065	4,21	-30,759494	-0,7325581
spiLA1589-mir399b-1	**75**	24	24	22,666667	29,333333	46,666667	53,333333	1,2222222	1,0588235	-37,8	-37,8	0,6764	0,97	-50,4	-0,8678571
spiLA1589-mir399b-2	**73**	23,287671	27,39726	20,547945	28,767123	43,835616	56,164384	1,05	1,1333333	-36,5	-36,2	0,171685	3,73	-50	-0,8678571
spiLA1589-mir156b-6	**90**	23,333333	24,444444	23,333333	28,888889	46,666667	53,333333	1,1818182	1	-43,8	-43,8	0,312135	2,55	-48,666667	-1,0042553
spiLA1589-mir8020-1	**88**	15,909091	37,5	15,909091	30,681818	31,818182	68,181818	0,8181818	1	-33,4	-33,4	0,323498	3,18	-37,954545	-0,9723404
spiLA1589-mir10531	**122**	21,311475	29,508197	16,393443	32,786885	37,704918	62,295082	1,1111111	1,3	-58,8	-58,8	0,126282	7,15	-48,196721	-1,0428571
spiLA1589-mir159b-1	**219**	21,004566	28,767123	15,525114	34,703196	36,52968	63,47032	1,2063492	1,3529412	-84,6	-82,7	0,000706	16,15	-38,630137	-1,2782609
spiLA1589-mir159b-2	**254**	21,259843	27,952756	14,173228	36,614173	35,433071	64,566929	1,3098592	1,5	-87,4	-84,5	0,0002388	35,69	-34,409449	-0,9879121
spiLA1589-mir172b-1	**161**	16,149068	37,267081	14,285714	32,298137	30,434783	69,565217	0,8666667	1,1304348	-51,6	-43,8	0,0058017	28,38	-32,049689	-1,2242424
spiLA1589-mir156f-1	**92**	22,826087	26,086957	17,391304	33,695652	40,217391	59,782609	1,2916667	1,3125	-38,3	-38,3	0,259233	2,69	-41,630435	-0,9728814
spiLA1589-mir8039-1	**146**	19,863014	26,712329	18,493151	34,931507	38,356164	61,643836	1,3076923	1,0740741	-42,3	-37,25	0,0046302	25,71	-28,972603	-1,0351351
spiLA1589-mir9473-2	**120**	16,666667	31,666667	19,166667	32,5	35,833333	64,166667	1,0263158	0,8695652	-56	-55,1	0,0470197	9,14	-46,666667	-0,9942857
spiLA1589-mir9473-1	**118**	18,644068	33,898305	16,949153	30,508475	35,59322	64,40678	0,9	1,1	-54	-52,6	0,0496702	8,58	-45,762712	-0,7553571
spiLA1589-mir10529	**134**	24,626866	25,373134	23,134328	26,865672	47,761194	52,238806	1,0588235	1,0645161	-52,4	-52,4	0,270923	3,11	-39,104478	-1,3023256
spiLA1589-mir169j-1	**266**	19,924812	29,323308	16,165414	34,586466	36,090226	63,909774	1,1794872	1,2325581	-90,3	-83,9	0,0005558	30,17	-33,947368	-1,2857143
spiLA1589-mir156b-5	**110**	24,545455	24,545455	22,727273	28,181818	47,272727	52,727273	1,1481481	1,08	-67,7	-67,7	0,510596	2,13	-61,545455	-0,8822581
spiLA1589-mir160h-1	**81**	22,222222	20,987654	23,45679	33,333333	45,679012	54,320988	1,5882353	0,9473684	-33,6	-33,4	0,303642	3,48	-41,481481	-0,8070175
spiLA1589-mir156b-3	**104**	22,115385	25	20,192308	32,692308	42,307692	57,692308	1,3076923	1,0952381	-42,4	-42,4	0,328687	4,15	-40,769231	-0,9081081
spiLA1589-mir156a	**76**	19,736842	25	19,736842	35,526316	39,473684	60,526316	1,4210526	1	-31,7	-31,7	0,172323	4,55	-41,710526	-0,9057143
spiLA1589-mir10534-1	**104**	19,230769	32,692308	20,192308	27,884615	39,423077	60,576923	0,8529412	0,952381	-60,1	-60,1	0,246862	3,53	-57,788462	-0,9975
spiLA1589-mir10534-2	**106**	19,811321	28,301887	18,867925	33,018868	38,679245	61,320755	1,1666667	1,05	-62,4	-61,5	0,0701495	5,27	-58,867925	-1,0566667
spiLA1589-mir156b-1	**92**	20,652174	26,086957	18,478261	34,782609	39,130435	60,869565	1,3333333	1,1176471	-43,1	-42,7	0,0993213	5,52	-46,847826	-1,0962264

spiLA1589-mir9760-1	**257**	22,568093	27,626459	14,396887	35,40856	36,964981	63,035019	1,2816901	1,5675676	-66,8	-44,5	0,0002285	59,52	-25,992218	-1,0510638
spiLA1589-mir3512-1	**208**	21,634615	28,846154	17,788462	31,730769	39,423077	60,576923	1,1	1,2162162	-72,6	-69,5	0,005693	33,88	-34,903846	-1,1972222
spiLA1589-mir7997c-1	**131**	32,824427	24,427481	19,083969	23,664122	51,908397	48,091603	0,96875	1,72	-70,8	-69,77	0,0350722	10,95	-54,045802	-0,7031579
spiLA1589-mir8011a-1	**238**	17,647059	32,773109	16,386555	33,193277	34,033613	65,966387	1,0128205	1,0769231	-59,9	-52,3	0,0010532	35,43	-25,168067	-1,0411765
spiLA1589-mir6273-1	**178**	18,539326	32,022472	12,921348	36,516854	31,460674	68,539326	1,1403509	1,4347826	-46,6	-32,7	0,0040891	61,33	-26,179775	-0,8578947
spiLA1589-mir167d-1	**113**	22,123894	26,548673	24,778761	26,548673	46,902655	53,097345	1	0,8928571	-46,1	-46,1	0,0248159	9,32	-40,79646	-0,7395062
spiLA1589-mir156e	**152**	24,342105	35,526316	10,526316	29,605263	34,868421	65,131579	0,8333333	2,3125	-38,3	-32,8	0,0039314	18,14	-25,197368	-0,8698113
spiLA1589-mir7981f-1	**170**	21,176471	37,058824	15,882353	25,882353	37,058824	62,941176	0,6984127	1,3333333	-69,6	-67,4	0,0114353	14,83	-40,941176	-0,8576923
spiLA1589-mir9675	**107**	19,626168	26,168224	22,429907	31,775701	42,056075	57,943925	1,2142857	0,875	-74,9	-74,9	0,602081	0,94	-70	-1,1047619
spiLA1589-mir5568f	**125**	21,6	26,4	16,8	35,2	38,4	61,6	1,3333333	1,2857143	-38,2	-32	0,0208671	13,49	-30,56	-1,6644444
spiLA1589-mir8030-1	**78**	16,666667	33,333333	14,102564	35,897436	30,769231	69,230769	1,0769231	1,1818182	-22,6	-22,6	0,369863	4,05	-28,974359	-1,1372549
spiLA1589-mir6463	**217**	17,97235	29,493088	17,97235	34,562212	35,9447	64,0553	1,171875	1	-80,8	-78,1	0,0051837	17,34	-37,235023	-0,7958333
spiLA1589-mir5057-1	**206**	19,902913	33,009709	12,135922	34,951456	32,038835	67,961165	1,0588235	1,64	-57,6	-57,2	0,0058086	20,97	-27,961165	-0,9416667
spiLA1589-mir319h	**71**	26,760563	21,126761	25,352113	26,760563	52,112676	47,887324	1,2666667	1,0555556	-27,6	-27,2	0,078875	5,83	-38,873239	-1,0358974
spiLA1589-mir8001b-1	**82**	20,731707	32,926829	9,7560976	36,585366	30,487805	69,512195	1,1111111	2,125	-34,6	-34,6	0,0822065	4,92	-42,195122	-0,8727273
spiLA1589-mir5725-1	**82**	24,390244	31,707317	17,073171	26,829268	41,463415	58,536585	0,8461538	1,4285714	-34,6	-34,6	0,172718	6,82	-42,195122	-0,7459459
spiLA1589-mir8011a-2	**138**	20,289855	30,434783	15,217391	34,057971	35,507246	64,492754	1,1190476	1,3333333	-55	-52,8	0,0207479	11,31	-39,855072	-1,384
spiLA1589-mir8710b	**113**	18,584071	37,168142	14,159292	30,088496	32,743363	67,256637	0,8095238	1,3125	-54	-54	0,19076	3,55	-47,787611	-1,0176471
spiLA1589-mir7981f-2	**306**	18,627451	33,660131	13,72549	33,986928	32,352941	67,647059	1,0097087	1,3571429	-71,4	-48,3	1,25E-05	74,01	-23,333333	-1,122449
spiLA1589-mir479	**92**	16,304348	35,869565	18,478261	29,347826	34,782609	65,217391	0,8181818	0,8823529	-23,9	-23,5	0,473419	1,97	-25,978261	-1,4594595
spiLA1589-mir5337a	**145**	17,241379	28,965517	16,551724	37,241379	33,793103	66,206897	1,2857143	1,0416667	-53,5	-51,3	0,0245621	15,52	-36,896552	-0,7212121
spiLA1589-mir5051	**310**	19,032258	37,419355	12,903226	30,645161	31,935484	68,064516	0,8189655	1,475	-77,4	-72,8	4,69E-05	40,31	-24,967742	-0,746875
spiLA1589-mir6271	**152**	23,684211	30,263158	13,157895	32,894737	36,842105	63,157895	1,0869565	1,8	-39,9	-39,8	0,0089113	12,28	-26,25	-0,7818182
spiLA1589-mir7981a-1	**136**	16,911765	30,147059	18,382353	34,558824	35,294118	64,705882	1,1463415	0,92	-56,7	-47,9	0,0532244	17,96	-41,691176	-0,7125
spiLA1589-mir11484	**237**	14,767932	32,067511	17,299578	35,864979	32,067511	67,932489	1,1184211	0,8536585	-71,6	-71,3	0,0055749	11,9	-30,21097	-1,1921053
spiLA1589-mir5083-1	**153**	20,261438	29,411765	15,686275	34,640523	35,947712	64,052288	1,1777778	1,2916667	-95,9	-94,2	0,0216119	10,7	-62,679739	-1,18125
spiLA1589-mir7992-1	**249**	18,473896	30,923695	22,088353	28,514056	40,562249	59,437751	0,9220779	0,8363636	-98,9	-96,9	0,0362719	19,69	-39,718876	-0,9421053
spiLA1589-mir11330	**145**	18,62069	33,103448	14,482759	33,793103	33,103448	66,896552	1,0208333	1,2857143	-81,1	-81,1	0,193063	3,93	-55,931034	-1,7436364
spiLA1589-mir395a-1	**174**	22,988506	27,586207	15,517241	33,908046	38,505747	61,494253	1,2291667	1,4814815	-61,5	-60,4	0,0209354	15,39	-35,344828	-0,9792079
spiLA1589-mir172d-3	**186**	17,741935	34,946237	14,516129	32,795699	32,258065	67,741935	0,9384615	1,2222222	-47,1	-47,1	0,0180475	21,67	-25,322581	-1,6895833
spiLA1589-mir7980b-1	**88**	15,909091	31,818182	17,045455	35,227273	32,954545	67,045455	1,1071429	0,9333333	-36,4	-36,4	0,375896	3,29	-41,363636	-0,9179104
spiLA1589-mir447a	**152**	25	21,710526	23,684211	29,605263	48,684211	51,315789	1,3636364	1,0555556	-82,8	-82,8	0,1954	8,56	-54,473684	-0,785
spiLA1589-mir171b-1	**125**	16,8	33,6	21,6	28	38,4	61,6	0,8333333	0,7777778	-38,9	-33,7	0,0464737	13,27	-31,12	-1,1189189
spiLA1589-mir167a-1	**191**	14,659686	36,125654	16,230366	32,984293	30,890052	69,109948	0,9130435	0,9032258	-54,1	-50,65	0,0019304	27,55	-28,324607	-0,9571429
spiLA1589-mir11304	**85**	22,352941	36,470588	17,647059	23,529412	40	60	0,6451613	1,2666667	-26,9	-24,9	0,2419	9,6	-31,647059	-0,8104167
spiLA1589-mir827b-1	**227**	14,096916	32,15859	16,740088	37,004405	30,837004	69,162996	1,1506849	0,8421053	-54,9	-52,8	0,0006656	26,79	-24,185022	-0,9169492
spiLA1589-mir835-1	**269**	22,304833	23,791822	17,100372	36,802974	39,405204	60,594796	1,546875	1,3043478	-75,3	-66,8	0,0003245	47,45	-27,992565	-0,7911765
spiLA1589-mir7997c-2	**140**	22,857143	27,142857	20	30	42,857143	57,142857	1,1052632	1,1428571	-65,4	-64,7	0,214726	6,78	-46,714286	-0,7842857
spiLA1589-mir1074	**203**	20,197044	27,586207	12,315271	39,901478	32,512315	67,487685	1,4464286	1,64	-46,3	-44,1	0,0001111	25,92	-22,807882	-0,7103774
spiLA1589-mir8127	**331**	23,26284	29,607251	17,824773	29,305136	41,087613	58,912387	0,9897959	1,3050847	-96,5	-74,5	0,0010334	88,54	-29,154079	-0,7015152
spiLA1589-mir1521a-1	**133**	19,548872	28,571429	15,037594	36,842105	34,586466	65,413534	1,2894737	1,3	-35,6	-33,1	0,0256473	20,03	-26,766917	-0,7095588
spiLA1589-mir7997c-3	**112**	18,75	30,357143	20,535714	30,357143	39,285714	60,714286	1	0,9130435	-36,5	-35,2	0,0688978	9,08	-32,589286	-1,1064516
spiLA1589-mir6145b-1	**86**	24,418605	22,093023	18,604651	34,883721	43,023256	56,976744	1,5789474	1,3125	-29,5	-27,9	0,0317685	15,4	-34,302326	-0,7
spiLA1589-mir7980b-2	**174**	18,965517	29,310345	13,793103	37,931034	32,758621	67,241379	1,2941176	1,375	-58,1	-49,67	0,0106201	28,99	-33,390805	-0,8295455
spiLA1589-mir7981d-2	**267**	18,35206	37,078652	15,355805	29,213483	33,707865	66,292135	0,7878788	1,195122	-92,9	-80,9	0,0002768	31,06	-34,794007	-0,7972973
spiLA1589-mir7822-1	**202**	17,326733	32,178218	17,326733	33,168317	34,653465	65,346535	1,0307692	1	-74,1	-74,1	0,0244233	10,98	-36,683168	-1,0322222
spiLA1589-mir7992-2	**97**	26,804124	23,71134	21,649485	27,835052	48,453608	51,546392	1,173913	1,2380952	-69,7	-68,1	0,703449	0,66	-71,85567	-1,2449275
spiLA1589-mir5274b	**317**	16,719243	34,069401	17,350158	31,861199	34,069401	65,930599	0,9351852	0,9636364	-93,7	-85,1	0,000254	43,65	-29,55836	-1,0585714
spiLA1589-mir1069-1	**82**	19,512195	30,487805	15,853659	34,146341	35,365854	64,634146	1,12	1,2307692	-22,2	-22,2	0,0657563	8,68	-27,073171	-0,8675926
spiLA1589-mir7983-1	**252**	15,873016	31,746032	16,666667	35,714286	32,539683	67,460317	1,125	0,952381	-65,4	-61,9	0,0008058	28	-25,952381	-0,9166667
spiLA1589-mir1046-1	**281**	18,505338	32,384342	15,658363	33,451957	34,163701	65,836299	1,032967	1,1818182	-68,1	-64,8	0,0024724	45,96	-24,234875	-0,797561
spiLA1589-mir7981a-2	**105**	20,952381	35,238095	22,857143	20,952381	43,809524	56,190476	0,5945946	0,9166667	-37	-34,6	0,289378	4,87	-35,238095	-0,7178082
spiLA1589-mir8048	**307**	15,309446	35,179153	15,635179	33,876221	30,944625	69,055375	0,962963	0,9791667	-66,5	-57,3	0,0001111	44,42	-21,661238	-0,709375
spiLA1589-mir5658-1	**171**	21,637427	30,409357	12,280702	35,672515	33,918129	66,081871	1,1730769	1,7619048	-42,6	-33,5	0,0159618	37,8	-24,912281	-0,8043478
spiLA1589-mir159c	**75**	18,666667	32	18,666667	30,666667	37,333333	62,666667	0,9583333	1	-24,7	-24,7	0,28393	3,96	-32,933333	-0,7
spiLA1589-mir7823-1	**88**	15,909091	28,409091	15,909091	39,772727	31,818182	68,181818	1,4	1	-29,6	-28,6	0,211438	5,37	-33,636364	-0,7344828
spiLA1589-mir5014a-1	**192**	17,708333	35,416667	15,625	31,25	33,333333	66,666667	0,8823529	1,1333333	-81,2	-81,2	0,0758102	5,72	-42,291667	-0,8821429
spiLA1589-mir169j-5	**172**	19,186047	29,069767	15,697674	36,046512	34,883721	65,116279	1,24	1,2222222	-72,7	-72,7	0,010282	10,64	-42,267442	-1,0571429
spiLA1589-mir169j-6	**178**	21,348315	24,157303	19,101124	35,393258	40,449438	59,550562	1,4651163	1,1176471	-77,9	-75,6	0,0049241	12,82	-43,764045	-1,26875
spiLA1589-mir395g-1	**293**	20,819113	30,716724	13,651877	34,812287	34,47099	65,52901	1,1333333	1,525	-82,5	-77,4	0,0001536	40,41	-28,156997	-1,0819444
spiLA1589-mir5181c	**245**	21,632653	31,020408	16,734694	30,612245	38,367347	61,632653	0,9868421	1,2926829	-80,8	-64,5	0,0001258	58,21	-32,979592	-0,745
spiLA1589-mir167c-1	**265**	20,377358	34,339623	12,830189	32,45283	33,207547	66,792453	0,9450549	1,5882353	-67,9	-65,2	0,0001803	26,69	-25,622642	-0,8595745
spiLA1589-mir5773	**160**	16,875	31,875	18,125	33,125	35	65	1,0392157	0,9310345	-91,8	-91,8	0,0466966	9,02	-57,375	-0,7220339
spiLA1589-mir5568g	**94**	17,021277	34,042553	13,829787	35,106383	30,851064	69,148936	1,03125	1,2307692	-22,3	-22,3	0,301335	7,95	-23,723404	-0,7715909
spiLA1589-mir390-1	**115**	21,73913	23,478261	20,869565	33,913043	42,608696	57,391304	1,4444444	1,0416667	-56,9	-56,9	0,591975	1,35	-49,478261	-1,6392857
spiLA1589-mir477-3	**242**	16,115702	34,297521	14,876033	34,710744	30,991736	69,008264	1,0120482	1,0833333	-56	-54,4	0,0034309	23,16	-23,140496	-0,7689655

spiLA1589-mir7981b-1	**134**	15,671642	36,567164	15,671642	32,089552	31,343284	68,656716	0,877551	1	-47,8	-47,7	0,126107	6,2	-35,671642	-0,7466667
spiLA1589-mir8001b-2	**90**	21,111111	37,777778	12,222222	28,888889	33,333333	66,666667	0,7647059	1,7272727	-29	-27,9	0,0376156	14,82	-32,222222	-0,7362637
spiLA1589-mir169r-3	**184**	20,652174	24,456522	18,478261	36,413043	39,130435	60,869565	1,4888889	1,1176471	-73,5	-68,1	0,0261518	16,53	-39,945652	-1,1380952
spiLA1589-mir9472-1	**180**	16,666667	32,777778	16,111111	34,444444	32,777778	67,222222	1,0508475	1,0344828	-73,2	-73	0,0209188	8,16	-40,666667	-1,0208333
spiLA1589-mir11039	**229**	25,764192	25,764192	8,2969432	40,174672	34,061135	65,938865	1,559322	3,1052632	-58,1	-39,8	0,0011052	55,29	-25,371179	-0,86
spiLA1589-mir5165	**117**	20,512821	35,897436	17,094017	26,495726	37,606838	62,393162	0,7380952	1,2	-40,7	-40,7	0,14275	4,9	-34,786325	-1,240678
spiLA1589-mir10542-1	**245**	18,77551	37,959184	13,061224	30,204082	31,836735	68,163265	0,7956989	1,4375	-58,1	-52,6	0,0003895	38,87	-23,714286	-0,7448718
spiLA1589-mir8006-1	**243**	13,99177	37,037037	18,518519	30,452675	32,510288	67,489712	0,8222222	0,7555556	-73,6	-62,91	0,0010512	34,42	-30,288066	-0,925
spiLA1589-mir10542-2	**211**	17,535545	36,966825	12,796209	32,701422	30,331754	69,668246	0,8846154	1,3703704	-54,2	-50	0,0039508	35,45	-25,687204	-0,7448718
spiLA1589-mir867-1	**313**	16,613419	36,102236	15,335463	31,948882	31,948882	68,051118	0,8849558	1,0833333	-71,1	-64,6	2,12E-05	54,87	-22,715655	-0,9316456
spiLA1589-mir10519-1	**254**	20,07874	29,527559	10,629921	39,76378	30,708661	69,291339	1,3466667	1,8888889	-58,9	-51,5	0,0005031	51,2	-23,188976	-0,846875
spiLA1589-mir5021-1	**168**	19,642857	34,52381	10,714286	35,119048	30,357143	69,642857	1,0172414	1,8333333	-39,3	-38	0,0083973	20,66	-23,392857	-0,711
spiLA1589-mir11106	**290**	16,551724	40,689655	13,793103	28,965517	30,344828	69,655172	0,7118644	1,2	-64,3	-63,1	0,0015561	21,76	-22,172414	-0,7551282
spiLA1589-mir11115	**122**	22,95082	22,95082	18,032787	36,065574	40,983607	59,016393	1,5714286	1,2727273	-62,9	-61,1	0,027588	8,37	-51,557377	-0,7306818
spiLA1589-mir5303-1	**124**	20,967742	29,032258	21,774194	28,225806	42,741935	57,258065	0,9722222	0,962963	-41,3	-37,4	0,0308588	13,77	-33,306452	-1,6607143
spiLA1589-mir160e-1	**245**	15,918367	35,510204	14,693878	33,877551	30,612245	69,387755	0,954023	1,0833333	-64,7	-64	0,0061964	29,86	-26,408163	-1,225
spiLA1589-mir11295	**264**	20,833333	29,545455	10,984848	38,636364	31,818182	68,181818	1,3076923	1,8965517	-59	-48,3	9,18E-05	53,47	-22,348485	-0,7491803
spiLA1589-mir399b-3	**217**	22,580645	31,797235	18,43318	27,18894	41,013825	58,986175	0,8550725	1,225	-70,1	-68,8	0,0011332	16,52	-32,304147	-0,702381
spiLA1589-mir11563-1	**295**	17,627119	26,440678	13,898305	42,033898	31,525424	68,474576	1,5897436	1,2682927	-68,4	-40,5	0,0001656	81,81	-23,186441	-0,7212121
spiLA1589-mir5574	**173**	17,34104	34,104046	19,653179	28,901734	36,99422	63,00578	0,8474576	0,8823529	-96,9	-96,9	0,0981255	4,78	-56,011561	-0,7876404
spiLA1589-mir7987-1	**324**	18,518519	30,246914	13,271605	37,962963	31,790123	68,209877	1,255102	1,3953488	-87,2	-76,7	5,54E-05	72,82	-26,91358	-0,7354839
spiLA1589-mir2083	**203**	20,197044	33,004926	19,704433	27,093596	39,901478	60,098522	0,8208955	1,025	-91,1	-81,94	0,016452	21,69	-44,876847	-0,8466019
spiLA1589-mir1106	**190**	14,736842	34,736842	17,368421	33,157895	32,105263	67,894737	0,9545455	0,8484848	-75,5	-75,5	0,0075343	17,86	-39,736842	-0,9416667
spiLA1589-mir7997c-4	**141**	26,950355	28,368794	9,929078	34,751773	36,879433	63,120567	1,225	2,7142857	-51,2	-49,9	0,0034051	12,21	-36,312057	-1,1246914
spiLA1589-mir11068c-1	**104**	14,423077	33,653846	17,307692	34,615385	31,730769	68,269231	1,0285714	0,8333333	-29	-20,58	0,143131	23,98	-27,884615	-0,9846154
spiLA1589-mir8668	**86**	25,581395	31,395349	10,465116	32,55814	36,046512	63,953488	1,037037	2,4444444	-25,3	-25,3	0,458091	5,92	-29,418605	-1,3930233
spiLA1589-mir7997c-5	**95**	18,947368	29,473684	22,105263	29,473684	41,052632	58,947368	1	0,8571429	-33,1	-33,1	0,0923641	8,16	-34,842105	-0,816129
spiLA1589-mir399f-1	**138**	15,217391	31,884058	18,115942	34,782609	33,333333	66,666667	1,0909091	0,84	-61,7	-58,4	0,0274829	17,2	-44,710145	-1,4145833
spiLA1589-mir1521b-1	**267**	16,853933	32,958801	16,479401	33,707865	33,333333	66,666667	1,0227273	1,0227273	-86,4	-80,3	0,0002455	36,81	-32,359551	-0,8487179
spiLA1589-mir399a-1	**94**	19,148936	28,723404	18,085106	34,042553	37,234043	62,765957	1,1851852	1,0588235	-32,9	-32,6	0,0741787	7,24	-35	-1,0275862
spiLA1589-mir1888b-1	**113**	27,433628	28,318584	15,044248	29,20354	42,477876	57,522124	1,03125	1,8235294	-41,5	-38,9	0,0262816	8,74	-36,725664	-0,7441176
spiLA1589-mir9744	**189**	11,640212	31,216931	24,338624	32,804233	35,978836	64,021164	1,0508475	0,4782609	-51,5	-51,5	0,169832	7,61	-27,248677	-0,94
spiLA1589-mir11078d	**147**	17,006803	29,931973	16,326531	36,734694	33,333333	66,666667	1,2272727	1,0416667	-60,1	-57,7	0,0396981	12	-40,884354	-0,8645833
spiLA1589-mir7993b	**199**	14,572864	34,673367	16,582915	34,170854	31,155779	68,844221	0,9855072	0,8787879	-70,4	-67,1	0,0183485	17,26	-35,376884	-0,7573529
spiLA1589-mir390-2	**194**	17,010309	28,865979	14,43299	39,690722	31,443299	68,556701	1,375	1,1785714	-66,6	-62,8	0,0057862	28,31	-34,329897	-1,2265306
spiLA1589-mir172a-1	**124**	17,741935	36,290323	19,354839	26,612903	37,096774	62,903226	0,7333333	0,9166667	-57,6	-57,6	0,248658	2,91	-46,451613	-0,84
spiLA1589-mir7997c-6	**126**	23,015873	25,396825	21,428571	30,15873	44,444444	55,555556	1,1875	1,0740741	-63	-63	0,0493363	4,5	-50	-1,3418919
spiLA1589-mir9760-2	**219**	19,634703	28,767123	15,068493	36,52968	34,703196	65,296804	1,2698413	1,3030303	-57,4	-54,3	0,0011433	32,36	-26,210046	-1,2521739
spiLA1589-mir8643b	**80**	15	32,5	17,5	35	32,5	67,5	1,0769231	0,8571429	-22,1	-22,1	0,316526	2,69	-27,625	-1,125
spiLA1589-mir1128-1	**236**	22,457627	33,474576	10,59322	33,474576	33,050847	66,949153	1	2,12	-57,5	-56	0,0001297	53,9	-24,364407	-0,7552632
spiLA1589-mir5182	**249**	20,080321	28,11245	19,277108	32,53012	39,35743	60,64257	1,1571429	1,0416667	-92,9	-90,3	0,0103655	21,95	-37,309237	-0,85
spiLA1589-mir166e	**144**	22,916667	28,472222	11,805556	36,805556	34,722222	65,277778	1,2926829	1,9411765	-36,8	-28,4	0,0017133	30,28	-25,555556	-0,9479592
spiLA1589-mir1217	**294**	21,088435	36,054422	13,605442	29,251701	34,693878	65,306122	0,8113208	1,55	-81	-65,6	7,53E-05	57,39	-27,55102	-0,9931818
spiLA1589-mir848	**138**	15,217391	34,057971	16,666667	34,057971	31,884058	68,115942	1	0,9130435	-31,5	-30,8	0,0911364	19,77	-22,826087	-0,727451
spiLA1589-mir7981a-3	**103**	22,330097	23,300971	20,38835	33,980583	42,718447	57,281553	1,4583333	1,0952381	-46,7	-46,6	0,0756953	4,79	-45,339806	-0,7941176
spiLA1589-mir7981f-3	**102**	22,54902	27,45098	10,784314	39,215686	33,333333	66,666667	1,4285714	2,0909091	-25,3	-24,3	0,0880289	12,97	-24,803922	-1,4392857
spiLA1589-mir7981a-4	**152**	18,421053	26,973684	18,421053	36,184211	36,842105	63,157895	1,3414634	1	-70,5	-68	0,0163726	9,45	-46,381579	-0,925
spiLA1589-mir7997b-1	**127**	16,535433	25,984252	22,834646	34,645669	39,370079	60,629921	1,3333333	0,7241379	-44,5	-44,2	0,0437971	5,8	-35,03937	-0,7441176
spiLA1589-mir11066	**122**	21,311475	28,688525	20,491803	29,508197	41,803279	58,196721	1,0285714	1,04	-39,9	-39,9	0,148352	6,86	-32,704918	-0,89
spiLA1589-mir857-1	**185**	15,675676	34,054054	14,594595	35,675676	30,27027	69,72973	1,047619	1,0740741	-59,5	-55,7	0,0076506	19,06	-32,162162	-0,75
spiLA1589-mir8011a-3	**168**	19,047619	29,166667	19,047619	32,738095	38,095238	61,904762	1,122449	1	-70	-69,6	0,0268794	10,2	-41,666667	-1,0625
spiLA1589-mir5014a-2	**148**	16,216216	30,405405	15,540541	37,837838	31,756757	68,243243	1,2444444	1,0434783	-73,3	-73,3	0,143015	4,4	-49,527027	-1,568254
spiLA1589-mir11314-1	**335**	20,895522	30,149254	15,522388	33,432836	36,41791	63,58209	1,1089109	1,3461538	-95,4	-92,8	0,0004458	43,78	-28,477612	-1,09375
spiLA1589-mir8006-2	**259**	16,216216	32,046332	20,849421	30,888031	37,065637	62,934363	0,9638554	0,7777778	-94	-91,6	0,0181467	13,87	-36,293436	-1,5595745
spiLA1589-mir7715	**276**	11,594203	34,057971	19,202899	35,144928	30,797101	69,202899	1,0319149	0,6037736	-68,1	-66,8	0,001404	30,7	-24,673913	-0,9791667
spiLA1589-mir5532	**263**	18,631179	29,657795	19,771863	31,939163	38,403042	61,596958	1,0769231	0,9423077	-75,8	-74,9	0,0010517	20,74	-28,821293	-0,9428571
spiLA1589-mir773b-1	**89**	17,977528	39,325843	21,348315	21,348315	39,325843	60,674157	0,5428571	0,8421053	-28,5	-28,5	0,527315	1,65	-32,022472	-0,8011765
spiLA1589-mir1127-1	**131**	18,320611	28,244275	18,320611	35,114504	36,641221	63,358779	1,2432432	1	-63,8	-63,8	0,107937	4,17	-48,70229	-0,750495
spiLA1589-mir5752b	**310**	18,387097	31,290323	11,935484	38,387097	30,322581	69,677419	1,2268041	1,5405405	-77,3	-41,2	0,0001629	99,05	-24,935484	-0,8142857
spiLA1589-mir1512c	**182**	18,131868	31,868132	15,934066	34,065934	34,065934	65,934066	1,0689655	1,137931	-92,8	-90,5	0,102169	10,72	-50,989011	-1,3291667
spiLA1589-mir5066	**119**	14,285714	30,252101	15,966387	39,495798	30,252101	69,747899	1,3055556	0,8947368	-33	-33	0,109048	6,76	-27,731092	-0,8223404
spiLA1589-mir5185l	**190**	16,842105	34,736842	14,210526	34,210526	31,052632	68,947368	0,9848485	1,1851852	-48,2	-40,1	0,0013727	45,4	-25,368421	-0,7666667
spiLA1589-mir774a	**196**	23,979592	22,44898	22,959184	30,612245	46,938776	53,061224	1,3636364	1,0444444	-70,4	-68,3	0,0025993	26,07	-35,918367	-0,7577778
spiLA1589-mir7981d-3	**209**	17,22488	33,492823	15,311005	33,971292	32,535885	67,464115	1,0142857	1,125	-77,1	-61,82	0,0017907	46,67	-36,889952	-0,8169492
spiLA1589-mir8008b-1	**194**	14,948454	38,659794	19,072165	27,319588	34,020619	65,979381	0,7066667	0,7837838	-58	-56,9	0,0089631	32,72	-29,896907	-0,7652174
spiLA1589-mir399i	**107**	21,495327	28,037383	15,88785	34,579439	37,383178	62,616822	1,2333333	1,3529412	-55,8	-53,5	0,237852	2,78	-52,149533	-1,1338235

spiLA1589-mir156b-10	**132**	16,666667	32,575758	14,393939	36,363636	31,060606	68,939394	1,1162791	1,1578947	-51,8	-47,8	0,0213025	14,18	-39,242424	-0,8787879
spiLA1589-mir156b-9	**138**	17,391304	30,434783	18,84058	33,333333	36,231884	63,768116	1,0952381	0,9230769	-56,2	-54,9	0,0574866	8,31	-40,724638	-1,395
spiLA1589-mir7997c-7	**97**	17,525773	32,989691	22,680412	26,804124	40,206186	59,793814	0,8125	0,7727273	-38,5	-38,5	0,0847405	8,39	-39,690722	-1,2634146
spiLA1589-mir3700	**208**	17,788462	35,576923	18,269231	28,365385	36,057692	63,942308	0,7972973	0,9736842	-78,4	-75,8	0,0349959	11,81	-37,692308	-0,9871795
spiLA1589-mir6149b	**182**	14,835165	34,615385	16,483516	34,065934	31,318681	68,681319	0,984127	0,9	-60,9	-57,9	0,0114551	19,3	-33,461538	-1,1268657
spiLA1589-mir7997c-8	**135**	25,925926	25,185185	20,740741	28,148148	46,666667	53,333333	1,1176471	1,25	-51,2	-49,1	0,0721081	9,96	-37,925926	-1,0684211
spiLA1589-mir5303-2	**146**	21,917808	25,342466	21,232877	31,506849	43,150685	56,849315	1,2432432	1,0322581	-48,4	-47,7	0,047362	13,33	-33,150685	-0,8333333
spiLA1589-mir172j-2	**169**	13,609467	36,094675	17,159763	33,136095	30,769231	69,230769	0,9180328	0,7931034	-54,4	-54,4	0,131028	13,83	-32,189349	-0,8126984
spiLA1589-mir6027	**153**	21,568627	33,333333	11,764706	33,333333	33,333333	66,666667	1	1,8333333	-57,7	-52	0,0615353	15,59	-37,712418	-0,768254
spiLA1589-mir11068c-2	**192**	19,791667	29,166667	12,5	38,541667	32,291667	67,708333	1,3214286	1,5833333	-56,9	-55,45	0,0037947	36,28	-29,635417	-1,0461538
spiLA1589-mir9781-1	**117**	15,384615	29,059829	17,094017	38,461538	32,478632	67,521368	1,3235294	0,9	-29,7	-27,6	0,0736138	17,11	-25,384615	-0,7107692
spiLA1589-mir1435	**234**	15,811966	32,051282	17,094017	35,042735	32,905983	67,094017	1,0933333	0,925	-54,8	-46,9	0,0002763	50,38	-23,418803	-0,8567568
spiLA1589-mir390a	**106**	22,641509	26,415094	20,754717	30,188679	43,396226	56,603774	1,1428571	1,0909091	-51,5	-48,8	0,102755	6,65	-48,584906	-0,7815789
spiLA1589-mir11085-1	**151**	18,543046	26,490066	18,543046	36,423841	37,086093	62,913907	1,375	1	-64,1	-63,9	0,0414341	11,75	-42,450331	-1,1195652
spiLA1589-mir7981a-5	**95**	22,105263	32,631579	22,105263	23,157895	44,210526	55,789474	0,7096774	1	-43,5	-43,5	0,519233	1,98	-45,789474	-1,3705882
spiLA1589-mir11078f	**281**	26,33452	27,402135	14,590747	31,672598	40,925267	59,074733	1,1558442	1,804878	-82,5	-72,2	7,05E-05	50,84	-29,359431	-1,1446429
spiLA1589-mir8739-1	**268**	16,41791	33,208955	17,910448	32,462687	34,328358	65,671642	0,9775281	0,9166667	-80,9	-76,8	0,0004662	32,96	-30,186567	-0,7173913
spiLA1589-mir10540-1	**159**	13,836478	33,962264	16,352201	35,849057	30,188679	69,811321	1,0555556	0,8461538	-41	-40,5	0,0162367	14,67	-25,786164	-0,8793478
spiLA1589-mir5168	**150**	25,333333	22	17,333333	35,333333	42,666667	57,333333	1,6060606	1,4615385	-54,2	-47,1	0,0045766	20,36	-36,133333	-0,747619
spiLA1589-mir8020-2	**139**	20,143885	30,935252	14,388489	34,532374	34,532374	65,467626	1,1162791	1,4	-36,4	-34,4	0,0016485	29,71	-26,18705	-0,8541667
spiLA1589-mir7997c-9	**143**	18,881119	33,566434	15,384615	32,167832	34,265734	65,734266	0,9583333	1,2272727	-63,4	-57,5	0,0833743	12,43	-44,335664	-0,846875
spiLA1589-mir823-1	**286**	19,93007	30,41958	16,783217	32,867133	36,713287	63,286713	1,0804598	1,1875	-76,3	-63,5	0,0004845	67,26	-26,678322	-0,7583333
spiLA1589-mir9479	**169**	21,893491	30,769231	23,076923	24,260355	44,970414	55,029586	0,7884615	0,9487179	-64,4	-53,24	0,0197494	29,82	-38,106509	-1,2938776
spiLA1589-mir10533	**129**	25,581395	29,457364	10,077519	34,883721	35,658915	64,341085	1,1842105	2,5384615	-34,1	-28,74	0,0044519	28,73	-26,434109	-0,7266667
spiLA1589-mir8039-2	**194**	16,494845	32,474227	18,556701	32,474227	35,051546	64,948454	1	0,8888889	-63	-63	0,0072132	10,05	-32,474227	-0,7413043
spiLA1589-mir8039-3	**277**	19,133574	35,018051	15,523466	30,32491	34,65704	65,34296	0,8659794	1,2325581	-95,1	-88,4	0,000921	33,76	-34,33213	-0,7481481
spiLA1589-mir8001a-1	**69**	13,043478	34,782609	18,84058	33,333333	31,884058	68,115942	0,9583333	0,6923077	-22,6	-22,2	0,160219	5,15	-32,753623	-1,1285714
spiLA1589-mir167d-2	**109**	23,853211	26,605505	20,183486	29,357798	44,036697	55,963303	1,1034483	1,1818182	-57,5	-57,2	0,0498655	4,96	-52,752294	-0,8586207
spiLA1589-mir7997c-10	**135**	25,185185	32,592593	17,037037	25,185185	42,222222	57,777778	0,7727273	1,4782609	-47	-47	0,155276	8,59	-34,814815	-1,0272727
spiLA1589-mir169c-3	**209**	18,660287	31,578947	13,875598	35,885167	32,535885	67,464115	1,1363636	1,3448276	-73,9	-69,6	0,0029696	16,47	-35,358852	-0,7884615
spiLA1589-mir7504j	**158**	20,886076	29,746835	20,886076	28,481013	41,772152	58,227848	0,9574468	1	-83,9	-80	0,0423929	9	-53,101266	-0,8342857
spiLA1589-mir7997b-2	**117**	21,367521	29,91453	19,65812	29,059829	41,025641	58,974359	0,9714286	1,0869565	-51,3	-49,4	0,0602199	8,24	-43,846154	-1,0867647
spiLA1589-mir3513	**118**	19,491525	33,050847	19,491525	27,966102	38,983051	61,016949	0,8461538	1	-66,3	-66,3	0,493159	3,06	-56,186441	-1,2712121
spiLA1589-mir7981a-6	**121**	18,181818	27,272727	15,702479	38,842975	33,884298	66,115702	1,4242424	1,1578947	-35,9	-33,6	0,0478921	7,8	-29,669421	-1,4413043
spiLA1589-mir1514a	**209**	20,574163	31,100478	16,267943	32,057416	36,842105	63,157895	1,0307692	1,2647059	-54,2	-52,4	0,0012344	36,22	-25,933014	-0,9584416
spiLA1589-mir7817a	**324**	18,518519	32,098765	16,975309	32,407407	35,493827	64,506173	1,0096154	1,0909091	-83,1	-78,4	2,44E-05	46,3	-25,648148	-0,9188406
spiLA1589-mir1044-1	**237**	16,033755	30,801688	14,767932	38,396624	30,801688	69,198312	1,2465753	1,0857143	-66,2	-61,6	0,0004113	36,94	-27,932489	-0,7038961
spiLA1589-mir396d	**130**	14,615385	36,923077	19,230769	29,230769	33,846154	66,153846	0,7916667	0,76	-35,8	-30,61	0,0207255	16,47	-27,538462	-0,7226087
spiLA1589-mir5303i-1	**126**	22,222222	29,365079	18,253968	30,15873	40,47619	59,52381	1,027027	1,2173913	-46,3	-44,3	0,0012604	23,1	-36,746032	-0,9068493
spiLA1589-mir1130b	**108**	12,037037	32,407407	18,518519	37,037037	30,555556	69,444444	1,1428571	0,65	-32,6	-28,49	0,142363	11,53	-30,185185	-0,8136364
spiLA1589-mir7981b-2	**124**	17,741935	28,225806	16,129032	37,903226	33,870968	66,129032	1,3428571	1,1	-49,8	-49,2	0,0067422	16,96	-40,16129	-1,7574074
spiLA1589-mir1886i-2	**80**	27,5	23,75	15	33,75	42,5	57,5	1,4210526	1,8333333	-26,6	-25,9	0,100283	5,19	-33,25	-1,1719298
spiLA1589-mir902a	**128**	20,3125	32,8125	16,40625	30,46875	36,71875	63,28125	0,9285714	1,2380952	-43,5	-41,2	0,0084579	13,76	-33,984375	-1,1857143
spiLA1589-mir5049	**94**	23,404255	27,659574	21,276596	27,659574	44,680851	55,319149	1	1,1	-52,1	-48,2	0,0898871	10,09	-55,425532	-0,7823529
spiLA1589-mir7504f	**85**	15,294118	30,588235	17,647059	36,470588	32,941176	67,058824	1,1923077	0,8666667	-26,5	-25,7	0,0962127	4,91	-31,176471	-1,2404762
spiLA1589-mir7981a-7	**222**	18,918919	31,081081	13,063063	36,936937	31,981982	68,018018	1,1884058	1,4482759	-77	-73,9	0,0006743	24,07	-34,684685	-1,13
spiLA1589-mir11419-1	**161**	16,770186	32,298137	19,254658	31,677019	36,024845	63,975155	0,9807692	0,8709677	-58,8	-58,2	0,104838	10,44	-36,521739	-1,0636364
spiLA1589-mir7981a-8	**119**	16,806723	36,134454	21,848739	25,210084	38,655462	61,344538	0,6976744	0,7692308	-46,4	-46,4	0,0502363	7,86	-38,991597	-1,084507
spiLA1589-mir827-3	**106**	24,528302	27,358491	22,641509	25,471698	47,169811	52,830189	0,9310345	1,0833333	-35,5	-33,8	0,270248	6,6	-33,490566	-1,0137931
spiLA1589-mir6283-1	**199**	17,085427	35,678392	15,577889	31,658291	32,663317	67,336683	0,8873239	1,0967742	-45,6	-39,7	0,0021879	32,81	-22,914573	-1,0086957
spiLA1589-mir7981b-3	**96**	23,958333	21,875	19,791667	34,375	43,75	56,25	1,5714286	1,2105263	-42,9	-42,5	0,0063745	10,67	-44,6875	-0,71
spiLA1589-mir159-2	**181**	14,364641	33,149171	16,022099	36,464088	30,38674	69,61326	1,1	0,8965517	-80	-80	0,0534396	12,69	-44,198895	-0,7015385
spiLA1589-mir7997c-11	**127**	22,834646	26,771654	19,685039	30,708661	42,519685	57,480315	1,1470588	1,16	-52,1	-52,1	0,061159	8,41	-41,023622	-1,0214286
spiLA1589-mir396a	**144**	16,666667	34,027778	20,138889	29,166667	36,805556	63,194444	0,8571429	0,8275862	-51,6	-50,2	0,0321931	10,38	-35,833333	-0,9648148
spiLA1589-mir8011a-4	**138**	20,289855	28,985507	19,565217	31,15942	39,855072	60,144928	1,075	1,037037	-58,2	-58,2	0,0502544	7,29	-42,173913	-0,756044
spiLA1589-mir7981a-9	**103**	25,242718	21,359223	19,417476	33,980583	44,660194	55,339806	1,5909091	1,3	-50,4	-50,3	0,146189	4,58	-48,932039	-0,9735849
spiLA1589-mir8002	**188**	17,021277	37,234043	15,957447	29,787234	32,978723	67,021277	0,8	1,0666667	-63,1	-60,8	0,0052864	15,31	-33,56383	-1,0581818
spiLA1589-mir7981a-10	**192**	15,625	32,8125	17,1875	34,375	32,8125	67,1875	1,047619	0,9090909	-69,1	-64,5	0,0018214	14,52	-35,989583	-1,0956522
spiLA1589-mir837	**261**	19,157088	34,482759	13,409962	32,950192	32,56705	67,43295	0,9555556	1,4285714	-90,3	-87,8	0,0153028	22,53	-34,597701	-1,0177419
spiLA1589-mir7992-3	**237**	21,940928	28,691983	16,877637	32,489451	38,818565	61,181435	1,1323529	1,3	-84,1	-80,9	0,0038903	26,45	-35,485232	-1,0968254
spiLA1589-mir7981d-4	**211**	21,327014	28,909953	17,535545	32,227488	38,862559	61,137441	1,1147541	1,2162162	-85	-77,5	0,007145	24,26	-40,28436	-1,0623529
spiLA1589-mir7997c-12	**210**	15,238095	32,857143	22,857143	29,047619	38,095238	61,904762	0,884058	0,6666667	-60,5	-58,2	0,0015374	31,65	-28,809524	-0,9141304
spiLA1589-mir7981d-5	**259**	20,849421	30,501931	16,988417	31,660232	37,837838	62,162162	1,0379747	1,2272727	-98,7	-93,6	0,0008741	28,22	-38,108108	-1,0365854
spiLA1589-mir166l	**160**	21,875	38,125	13,75	26,25	35,625	64,375	0,6885246	1,5909091	-41,4	-41	0,0521344	13,04	-25,875	-0,75625
spiLA1589-mir160e-2	**116**	21,551724	31,896552	21,551724	25	43,103448	56,896552	0,7837838	1	-41,7	-40,3	0,0514112	9,2	-35,948276	-1,0071429
spiLA1589-mir7984d	**222**	14,414414	32,882883	19,369369	33,333333	33,783784	66,216216	1,0136986	0,744186	-83,3	-82,3	0,0080447	15,7	-37,522523	-0,7263158

spiLA1589-mir8038b-2	**136**	20,588235	28,676471	19,117647	31,617647	39,705882	60,294118	1,1025641	1,0769231	-64	-64	0,243902	7,11	-47,058824	-1,1106667
spiLA1589-mir5162	**139**	17,266187	35,971223	13,669065	33,093525	30,935252	69,064748	0,92	1,2631579	-33,5	-27,17	0,0231865	15,62	-24,100719	-1,36
spiLA1589-mir9760-3	**243**	15,63786	33,744856	17,695473	32,921811	33,333333	66,666667	0,9756098	0,8837209	-57,5	-53,6	0,0007985	25,66	-23,662551	-1,1851852
spiLA1589-mir2607-1	**185**	22,702703	31,351351	9,1891892	36,756757	31,891892	68,108108	1,1724138	2,4705882	-43,9	-38,5	0,0059417	30,72	-23,72973	-0,7790698
spiLA1589-mir408-2	**128**	25,78125	32,03125	22,65625	19,53125	48,4375	51,5625	0,6097561	1,137931	-46,6	-41,4	0,0291793	9,07	-36,40625	-0,7098765
spiLA1589-mir159b-3	**304**	16,776316	31,578947	13,486842	38,157895	30,263158	69,736842	1,2083333	1,2439024	-78,5	-73,3	6,14E-05	50,56	-25,822368	-0,7440678
spiLA1589-mir950	**74**	28,378378	22,972973	24,324324	24,324324	52,702703	47,297297	1,0588235	1,1666667	-28,9	-28,9	0,43351	5,92	-39,054054	-0,7516129
spiLA1589-mir5837	**247**	22,267206	32,388664	17,004049	28,340081	39,271255	60,728745	0,875	1,3095238	-68,4	-57,8	0,0010276	49,41	-27,692308	-0,8532609
spiLA1589-mir7981a-11	**169**	17,159763	35,502959	17,751479	29,585799	34,911243	65,088757	0,8333333	0,9666667	-72	-72	0,0824363	11,31	-42,60355	-0,7410256
spiLA1589-mir11575-1	**183**	21,311475	25,68306	22,404372	30,601093	43,715847	56,284153	1,1914894	0,9512195	-92,3	-91,7	0,035276	8,51	-50,437158	-0,9565789
spiLA1589-mir8006-3	**271**	15,867159	30,627306	22,878229	30,627306	38,745387	61,254613	1	0,6935484	-95,1	-94,6	0,0025815	15,16	-35,092251	-0,7395833
spiLA1589-mir7997b-3	**127**	21,259843	33,858268	18,110236	26,771654	39,370079	60,629921	0,7906977	1,173913	-45,7	-38,7	0,0389538	11,13	-35,984252	-1,15375
spiLA1589-mir9742	**157**	19,10828	29,299363	15,923567	35,66879	35,031847	64,968153	1,2173913	1,2	-72	-65,48	0,0440633	22,66	-45,859873	-0,9057143
spiLA1589-mir7696d	**241**	17,842324	36,514523	14,107884	31,53527	31,950207	68,049793	0,8636364	1,2647059	-80	-75,2	0,0006204	27,42	-33,195021	-0,914
spiLA1589-mir479a-2	**112**	21,428571	30,357143	18,75	29,464286	40,178571	59,821429	0,9705882	1,1428571	-53,8	-52,6	0,084803	7,75	-48,035714	-1,038961
spiLA1589-mir7981f-4	**165**	16,363636	33,939394	15,151515	34,545455	31,515152	68,484848	1,0178571	1,08	-62,4	-59,3	0,0169805	20,32	-37,818182	-1,0102941
spiLA1589-mir10532-1	**155**	20	33,548387	10,322581	36,129032	30,322581	69,677419	1,0769231	1,9375	-33,2	-25	0,0077022	30,5	-21,419355	-1,2
spiLA1589-mir9472-2	**218**	22,477064	30,733945	16,055046	30,733945	38,53211	61,46789	1	1,4	-59,5	-58,6	0,017138	16,2	-27,293578	-0,706383
spiLA1589-mir5035	**142**	16,197183	30,985915	16,901408	35,915493	33,098592	66,901408	1,1590909	0,9583333	-65,4	-64,2	0,0277947	9,42	-46,056338	-0,7516129
spiLA1589-mir11342	**307**	17,589577	34,201954	17,263844	30,944625	34,85342	65,14658	0,9047619	1,0188679	-80,6	-73,3	0,0009931	61,76	-26,254072	-0,7083333
spiLA1589-mir8748	**115**	21,73913	30,434783	14,782609	33,043478	36,521739	63,478261	1,0857143	1,4705882	-40,4	-39,5	0,263651	5,17	-35,130435	-1,3914894
spiLA1589-mir10192	**264**	23,484848	27,272727	9,469697	39,772727	32,954545	67,045455	1,4583333	2,48	-61,2	-57,2	0,0001053	50,58	-23,181818	-0,9619048
spiLA1589-mir1048	**242**	15,702479	35,53719	17,768595	30,991736	33,471074	66,528926	0,872093	0,8837209	-79,4	-77	0,0065662	29,71	-32,809917	-1,0061224
spiLA1589-mir7981d-6	**213**	21,596244	29,577465	21,126761	27,699531	42,723005	57,276995	0,9365079	1,0222222	-93,4	-92,9	0,0323884	18,37	-43,849765	-0,7034483
spiLA1589-mir1128-2	**289**	12,110727	34,256055	18,685121	34,948097	30,795848	69,204152	1,020202	0,6481481	-72,5	-65,6	0,0005726	41,23	-25,093426	-0,9802469
spiLA1589-mir7981b-4	**328**	15,853659	35,97561	15,853659	32,317073	31,707317	68,292683	0,8983051	1	-74,6	-70,4	5,38E-05	62,26	-22,743902	-1,0263736
spiLA1589-mir828b-1	**105**	19,047619	29,52381	18,095238	33,333333	37,142857	62,857143	1,1290323	1,0526316	-46,3	-46,3	0,116572	4,85	-44,095238	-0,8148315
spiLA1589-mir7992-4	**209**	17,22488	40,191388	12,91866	29,665072	30,143541	69,856459	0,7380952	1,3333333	-71,5	-71,5	0,100086	15,58	-34,210526	-0,7173077
spiLA1589-mir6191	**263**	17,870722	30,798479	15,969582	35,361217	33,840304	66,159696	1,1481481	1,1190476	-93,4	-91,4	0,000379	30,17	-35,513308	-1,1871795
spiLA1589-mir868-1	**275**	13,454545	34,909091	17,454545	34,181818	30,909091	69,090909	0,9791667	0,7708333	-72,5	-71	0,0040639	23,36	-26,363636	-1,1349206
spiLA1589-mir5725-2	**201**	21,890547	27,860697	13,930348	36,318408	35,820896	64,179104	1,3035714	1,5714286	-78,6	-75,1	0,0048545	21,66	-39,104478	-1,0494382
spiLA1589-mir391	**96**	23,958333	34,375	16,666667	25	40,625	59,375	0,7272727	1,4375	-46,7	-46,7	0,336484	3,38	-48,645833	-1,0916667
spiLA1589-mir7981a-12	**210**	14,285714	38,571429	16,190476	30,952381	30,47619	69,52381	0,8024691	0,8823529	-69,4	-67,6	0,040025	8,29	-33,047619	-0,7588235
spiLA1589-mir6232b-1	**112**	21,428571	33,035714	16,071429	29,464286	37,5	62,5	0,8918919	1,3333333	-70,1	-69,8	0,178559	4,07	-62,589286	-1,084375
spiLA1589-mir156h	**334**	15,269461	30,239521	24,550898	29,94012	39,820359	60,179641	0,990099	0,6219512	-98,2	-93,82	0,0001358	47,34	-29,401198	-1,6690476
spiLA1589-mir5014a-3	**188**	14,893617	30,319149	15,957447	38,829787	30,851064	69,148936	1,2807018	0,9333333	-79,5	-79,5	0,0371622	6,73	-42,287234	-0,7013333
spiLA1589-mir7983-2	**213**	15,023474	31,455399	17,370892	36,150235	32,394366	67,605634	1,1492537	0,8648649	-65,5	-64,1	0,0019913	17,9	-30,751174	-0,7383459
spiLA1589-mir6288b	**300**	19,666667	29,333333	14,666667	36,333333	34,333333	65,666667	1,2386364	1,3409091	-75,7	-74,7	3,51E-05	35,91	-25,233333	-1,3706897
spiLA1589-mir2673b-1	**196**	21,938776	28,571429	19,897959	29,591837	41,836735	58,163265	1,0357143	1,1025641	-57,7	-31,2	0,0131078	53,51	-29,438776	-0,9492754
spiLA1589-mir867-2	**161**	19,875776	27,329193	18,63354	34,161491	38,509317	61,490683	1,25	1,0666667	-75,8	-74,6	0,019215	19,23	-47,080745	-0,7036585
spiLA1589-mir7997c-13	**126**	19,047619	26,984127	21,428571	32,539683	40,47619	59,52381	1,2058824	0,8888889	-52,6	-50,8	0,0718719	15,85	-41,746032	-0,7771429
spiLA1589-mir9497	**276**	18,84058	24,637681	13,405797	43,115942	32,246377	67,753623	1,75	1,4054054	-65,4	-58,9	0,0011933	65,52	-23,695652	-1,2225806
spiLA1589-mir11146	**142**	21,126761	34,507042	10,56338	33,802817	31,690141	68,309859	0,9795918	2	-33	-24,2	0,0170243	18,93	-23,239437	-1,0313725
spiLA1589-mir399b-4	**101**	22,772277	26,732673	20,792079	29,70297	43,564356	56,435644	1,1111111	1,0952381	-47,9	-47,9	0,377241	3,59	-47,425743	-0,7348315
spiLA1589-mir1533-1	**183**	21,311475	31,693989	20,765027	26,229508	42,076503	57,923497	0,8275862	1,0263158	-89,7	-89,4	0,0253445	7,41	-49,016393	-1,0886364
spiLA1589-mir9471a-2	**149**	20,134228	36,241611	13,422819	30,201342	33,557047	66,442953	0,8333333	1,5	-36,6	-31,1	0,0037908	40,03	-24,563758	-0,7443299
spiLA1589-mir9470-2	**338**	19,230769	35,502959	15,680473	29,585799	34,911243	65,088757	0,8333333	1,2264151	-97	-88,6	0,0014659	36,87	-28,698225	-1,1649351
spiLA1589-mir7981b-5	**240**	15	33,333333	17,083333	34,583333	32,083333	67,916667	1,0375	0,8780488	-94,8	-94,4	0,0254794	20,75	-39,5	-0,732
spiLA1589-mir835-2	**90**	17,777778	31,111111	14,444444	36,666667	32,222222	67,777778	1,1785714	1,2307692	-22,1	-22,1	0,0971727	5,82	-24,555556	-0,8220339
spiLA1589-mir1046-2	**141**	17,021277	33,333333	14,893617	34,751773	31,914894	68,085106	1,0425532	1,1428571	-68,9	-66,5	0,116068	3,1	-48,865248	-1,2311688
spiLA1589-mir11498a	**313**	24,28115	33,226837	11,501597	30,990415	35,782748	64,217252	0,9326923	2,1111111	-91,8	-79,7	0,0004036	54,33	-29,329073	-0,762069
spiLA1589-mir169r-4	**72**	25	23,611111	18,055556	33,333333	43,055556	56,944444	1,4117647	1,3846154	-34,8	-34,8	0,116017	6,52	-48,333333	-0,8196429
spiLA1589-mir169m	**175**	24	24,571429	24	27,428571	48	52	1,1162791	1	-88,2	-88,2	0,0896404	13,01	-50,4	-0,8941176
spiLA1589-mir821b	**99**	18,181818	34,343434	20,20202	27,272727	38,383838	61,616162	0,7941176	0,9	-30	-23,4	0,0773011	13,36	-30,30303	-1,05
spiLA1589-mir7122	**79**	17,721519	29,113924	20,253165	32,911392	37,974684	62,025316	1,1304348	0,875	-30,6	-30,6	0,154815	3,66	-38,734177	-0,7403226
spiLA1589-mir3693i	**145**	17,241379	33,103448	15,172414	34,482759	32,413793	67,586207	1,0416667	1,1363636	-98,1	-98,1	0,0780953	4,99	-67,655172	-1,02
spiLA1589-mir3951b	**181**	18,78453	29,281768	14,917127	37,016575	33,701657	66,298343	1,2641509	1,2592593	-44,4	-41,9	0,0109911	26,13	-24,530387	-2,087234
spiLA1589-mir6273-2	**272**	17,647059	31,985294	13,970588	36,397059	31,617647	68,382353	1,137931	1,2631579	-62,8	-43	8,27E-05	74,28	-23,088235	-1,3225
spiLA1589-mir2868	**183**	19,125683	28,961749	12,021858	39,89071	31,147541	68,852459	1,3773585	1,5909091	-64,8	-63,5	0,0415548	20,1	-35,409836	-0,7278689
spiLA1589-mir477c	**125**	20,8	28	20,8	30,4	41,6	58,4	1,0857143	1	-73	-73	0,293418	3,39	-58,4	-0,7302326
spiLA1589-mir171f-9	**128**	17,1875	25,78125	17,96875	39,0625	35,15625	64,84375	1,5151515	0,9565217	-46	-46	0,136677	6,85	-35,9375	-1,1368421
spiLA1589-mir1098	**125**	28	30,4	21,6	20	49,6	50,4	0,6578947	1,2962963	-62,1	-62,1	0,508383	3,94	-49,68	-1,4038462
spiLA1589-mir5174d	**97**	18,556701	31,958763	12,371134	37,113402	30,927835	69,072165	1,1612903	1,5	-24,4	-24,4	0,0580429	12,59	-25,154639	-1,0222222
spiLA1589-mir7492f-1	**219**	15,981735	29,223744	16,438356	38,356164	32,420091	67,579909	1,3125	0,9722222	-67,7	-63,8	0,0015086	30,31	-30,913242	-1,0016129
spiLA1589-mir7997b-4	**190**	19,473684	33,157895	18,947368	28,421053	38,421053	61,578947	0,8571429	1,0277778	-58,4	-58,1	0,0042147	19,2	-30,736842	-0,8133333
spiLA1589-mir403	**112**	17,857143	28,571429	19,642857	33,928571	37,5	62,5	1,1875	0,9090909	-45,7	-42,7	0,101296	10,27	-40,803571	-0,9535211

spiLA1589-mir7997b-5	**136**	20,588235	27,941176	24,264706	27,205882	44,852941	55,147059	0,9736842	0,8484848	-45,9	-44,2	0,0057457	19,74	-33,75	-0,8
spiLA1589-mir7828	**250**	20,8	32,4	18,4	28,4	39,2	60,8	0,8765432	1,1304348	-91,9	-78,92	0,0024164	32,25	-36,76	-1,0880952
spiLA1589-mir4249-1	**90**	20	27,777778	17,777778	34,444444	37,777778	62,222222	1,24	1,125	-65	-64,1	0,277544	2,64	-72,222222	-0,752459
spiLA1589-mir7983-3	**249**	17,670683	31,726908	17,269076	33,333333	34,939759	65,060241	1,0506329	1,0232558	-89,8	-82,7	0,0002089	28,58	-36,064257	-1,9117647
spiLA1589-mir11583b-1	**67**	13,432836	38,80597	17,910448	29,850746	31,343284	68,656716	0,7692308	0,75	-26,4	-26,2	0,345131	1,49	-39,402985	-0,996875
spiLA1589-mir7981d-7	**285**	15,789474	31,929825	16,140351	36,140351	31,929825	68,070175	1,1318681	0,9782609	-99,4	-93,5	0,0030824	23,98	-34,877193	-1,0321839
spiLA1589-mir7997c-14	**83**	18,072289	36,144578	21,686747	24,096386	39,759036	60,240964	0,6666667	0,8333333	-36,4	-36,4	0,664314	2,37	-43,855422	-1,2571429
spiLA1589-mir9668-1	**66**	16,666667	30,30303	16,666667	36,363636	33,333333	66,666667	1,2	1	-34,3	-33	0,237973	3,71	-51,969697	-1,1030303
spiLA1589-mir9668-2	**71**	16,901408	29,577465	18,309859	35,211268	35,211268	64,788732	1,1904762	0,9230769	-33,9	-32,6	0,122739	6,44	-47,746479	-0,8955556
spiLA1589-mir5160	**163**	17,177914	29,447853	13,496933	39,877301	30,674847	69,325153	1,3541667	1,2727273	-35,4	-33,4	0,0055753	33,66	-21,717791	-1,5590909
spiLA1589-mir5026-1	**126**	19,84127	35,714286	17,460317	26,984127	37,301587	62,698413	0,7555556	1,1363636	-49,8	-49,8	0,297428	3,73	-39,52381	-1,356
spiLA1589-mir5371	**304**	20,394737	31,907895	13,157895	34,539474	33,552632	66,447368	1,0824742	1,55	-73,9	-72,34	0,0002454	36,13	-24,309211	-0,8507937
spiLA1589-mir11423i	**245**	28,979592	22,857143	19,591837	28,571429	48,571429	51,428571	1,25	1,4791667	-86	-77,3	1,27E-05	44,52	-35,102041	-0,7245098
spiLA1589-mir8003	**233**	18,88412	31,330472	12,017167	37,76824	30,901288	69,098712	1,2054795	1,5714286	-59,5	-58,2	0,0026651	35,79	-25,536481	-0,9295455
spiLA1589-mir7981a-13	**101**	20,792079	24,752475	20,792079	33,663366	41,584158	58,415842	1,36	1	-40,7	-40,5	0,0512124	8,32	-40,29703	-0,7226891
spiLA1589-mir7981f-5	**156**	19,871795	28,846154	17,307692	33,974359	37,179487	62,820513	1,1777778	1,1481481	-77,4	-77,4	0,009772	7,38	-49,615385	-0,8263889
spiLA1589-mir5180a	**190**	15,789474	32,631579	21,052632	30,526316	36,842105	63,157895	0,9354839	0,75	-69,6	-68,1	0,0438619	18,89	-36,631579	-0,9690476
spiLA1589-mir6230	**107**	23,364486	28,971963	19,626168	28,037383	42,990654	57,009346	0,9677419	1,1904762	-53,1	-50,8	0,162778	8,46	-49,626168	-0,9942857
spiLA1589-mir10532-2	**158**	20,886076	31,64557	17,088608	30,379747	37,974684	62,025316	0,96	1,2222222	-42,9	-40,47	0,0086324	24,65	-27,151899	-1,0103448
spiLA1589-mir6231-2	**151**	13,245033	37,086093	17,218543	32,450331	30,463576	69,536424	0,875	0,7692308	-33,1	-25,8	0,0034169	29,65	-21,92053	-1,1543478
spiLA1589-mir11563-2	**239**	22,175732	27,615063	16,317992	33,891213	38,493724	61,506276	1,2272727	1,3589744	-66,3	-65,5	0,0005112	26,54	-27,740586	-0,715
spiLA1589-mir5181b-1	**81**	22,222222	32,098765	14,814815	30,864198	37,037037	62,962963	0,9615385	1,5	-39,3	-39,3	0,453938	1,99	-48,518519	-0,7195652
spiLA1589-mir6145b-2	**114**	20,175439	28,947368	15,789474	35,087719	35,964912	64,035088	1,2121212	1,2777778	-44,3	-43,9	0,0899433	6,64	-38,859649	-1,31
spiLA1589-mir7981d-8	**194**	22,680412	32,474227	14,43299	30,412371	37,113402	62,886598	0,9365079	1,5714286	-70,3	-66,1	0,0022803	37,54	-36,237113	-0,8227273
spiLA1589-mir7993d-1	**199**	16,582915	34,170854	14,572864	34,673367	31,155779	68,844221	1,0147059	1,137931	-71	-64,8	0,0031524	19,77	-35,678392	-1,0804878
spiLA1589-mir10532-3	**290**	20	32,413793	13,448276	34,137931	33,448276	66,551724	1,0531915	1,4871795	-95,8	-90,4	0,0050077	29,77	-33,034483	-0,9763889
spiLA1589-mir7981e-1	**199**	14,572864	36,683417	17,58794	31,155779	32,160804	67,839196	0,8493151	0,8285714	-70,1	-69,28	0,0086533	18,55	-35,21608	-1,1451613
spiLA1589-mir403b	**112**	19,642857	33,928571	17,857143	28,571429	37,5	62,5	0,8421053	1,1	-43,6	-42,3	0,0948255	9,22	-38,928571	-0,9876289
spiLA1589-mir8047	**208**	16,346154	32,211538	19,230769	32,211538	35,576923	64,423077	1	0,85	-63,4	-61,8	0,0024767	20,89	-30,480769	-1,095
spiLA1589-mir7981-1	**255**	16,470588	32,156863	19,215686	32,156863	35,686275	64,313725	1	0,8571429	-98,4	-89,37	0,0032427	30,36	-38,588235	-1,0380952
spiLA1589-mir5183	**165**	16,363636	32,121212	20	31,515152	36,363636	63,636364	0,9811321	0,8181818	-88,8	-85,3	0,236648	10,82	-53,818182	-0,8567568
spiLA1589-mir865-1	**104**	18,269231	37,5	16,346154	27,884615	34,615385	65,384615	0,7435897	1,1176471	-27,6	-26,6	0,0343658	10,21	-26,538462	-1,0813187
spiLA1589-mir160h-3	**206**	17,475728	32,524272	19,902913	30,097087	37,378641	62,621359	0,9253731	0,8780488	-64,9	-61,2	0,0128627	27,85	-31,504854	-1,48
spiLA1589-mir10186e	**244**	19,672131	34,42623	13,934426	31,967213	33,606557	66,393443	0,9285714	1,4117647	-62,2	-60	0,0012082	31,21	-25,491803	-0,7666667
spiLA1589-mir8005c	**183**	19,672131	25,136612	13,114754	42,076503	32,786885	67,213115	1,673913	1,5	-49,4	-33,02	0,0076779	34,27	-26,994536	-0,8428571
spiLA1589-mir8766	**93**	10,752688	30,107527	20,430108	38,709677	31,182796	68,817204	1,2857143	0,5263158	-27	-27	0,407838	2,66	-29,032258	-0,7585366
spiLA1589-mir8021-1	**139**	13,669065	32,374101	17,266187	36,690647	30,935252	69,064748	1,1333333	0,7916667	-32,4	-29,3	0,0107712	13,86	-23,309353	-0,8233333
spiLA1589-mir5658-2	**339**	22,418879	23,893805	13,569322	40,117994	35,988201	64,011799	1,6790123	1,6521739	-96,9	-83,6	4,04E-05	48,98	-28,584071	-0,9310345
spiLA1589-mir11078e	**233**	18,454936	35,622318	12,875536	33,04721	31,330472	68,669528	0,9277108	1,4333333	-67,8	-58,1	0,0001316	46,11	-29,098712	-0,7954545
spiLA1589-mir7997c-15	**121**	19,008264	28,92562	23,140496	28,92562	42,14876	57,85124	1	0,8214286	-48,2	-45,4	0,0088954	9,07	-39,834711	-1,0222222
spiLA1589-mir11083c	**332**	23,493976	25,60241	12,650602	38,253012	36,144578	63,855422	1,4941176	1,8571429	-89	-77,8	1,94E-05	49,22	-26,807229	-0,945098
spiLA1589-mir161	**171**	30,994152	27,48538	21,052632	20,467836	52,046784	47,953216	0,7446809	1,4722222	-65,5	-62,8	0,0156106	15,1	-38,304094	-0,7657143
spiLA1589-mir475b	**99**	22,222222	25,252525	26,262626	26,262626	48,484848	51,515152	1,04	0,8461538	-34	-32,3	0,0549769	7,87	-34,343434	-0,7416667
spiLA1589-mir7981f-6	**236**	27,118644	22,457627	27,118644	23,305085	54,237288	45,762712	1,0377358	1	-89,8	-79,5	0,0008516	36,27	-38,050847	-0,7359551
spiLA1589-mir7981b-6	**141**	17,730496	38,297872	13,475177	30,496454	31,205674	68,794326	0,7962963	1,3157895	-62,9	-60,3	0,134343	6,21	-44,609929	-0,7083333
spiLA1589-mir395j-2	**326**	22,392638	28,834356	16,564417	32,208589	38,957055	61,042945	1,1170213	1,3518519	-92,8	-86,7	0,000698	49,83	-28,466258	-1,4295455
spiLA1589-mir11116	**94**	20,212766	32,978723	15,957447	30,851064	36,170213	63,829787	0,9354839	1,2666667	-33,5	-33,5	0,315283	2,77	-35,638298	-1,0949153
spiLA1589-mir7827	**203**	22,660099	28,571429	14,778325	33,990148	37,438424	62,561576	1,1896552	1,5333333	-58,1	-55,9	0,0008094	24,37	-28,62069	-0,7307087
spiLA1589-mir7981a-14	**234**	15,384615	37,179487	16,666667	30,769231	32,051282	67,948718	0,8275862	0,9230769	-98,3	-96,4	0,0115898	17,18	-42,008547	-0,7644737
spiLA1589-mir6145b-3	**111**	21,621622	32,432432	18,918919	27,027027	40,540541	59,459459	0,8333333	1,1428571	-44,9	-44,9	0,340345	4,18	-40,45045	-0,8034483
spiLA1589-mir156b-11	**94**	20,212766	26,595745	18,085106	35,106383	38,297872	61,702128	1,32	1,1176471	-48,4	-48,4	0,0852724	4,15	-51,489362	-1,3106667
spiLA1589-mir1128-3	**265**	14,339623	33,207547	15,849057	36,603774	30,188679	69,811321	1,1022727	0,9047619	-64,4	-50,79	0,0001037	69,26	-24,301887	-0,9977778
spiLA1589-mir171b-2	**136**	14,705882	35,294118	20,588235	29,411765	35,294118	64,705882	0,8333333	0,7142857	-35,8	-30,6	0,0232514	9,97	-26,323529	-1,3444444
spiLA1589-mir7997c-16	**126**	22,222222	28,571429	19,84127	29,365079	42,063492	57,936508	1,0277778	1,12	-50,6	-50,6	0,0375121	5,36	-40,15873	-0,805
spiLA1589-mir162-3	**135**	20,740741	25,185185	22,962963	31,111111	43,703704	56,296296	1,2352941	0,9032258	-53,8	-52,1	0,118759	6,73	-39,851852	-0,7458333
spiLA1589-mir5725-3	**208**	20,192308	30,769231	15,384615	33,653846	35,576923	64,423077	1,09375	1,3125	-79,7	-72,6	0,0039065	17,41	-38,317308	-0,954717
spiLA1589-mir7997b-6	**123**	21,95122	30,894309	20,325203	26,829268	42,276423	57,723577	0,8684211	1,08	-42,2	-39	0,0582534	14,83	-34,308943	-0,9118644
spiLA1589-mir167a-2	**319**	19,122257	27,899687	15,047022	37,931034	34,169279	65,830721	1,3595506	1,2708333	-87,5	-85	9,67E-05	50,42	-27,429467	-1,077027
spiLA1589-mir1069-2	**208**	18,269231	35,096154	13,942308	32,692308	32,211538	67,788462	0,9315068	1,3103448	-63,2	-58,7	0,0012699	31,22	-30,384615	-0,8115385
spiLA1589-mir1127-2	**258**	17,054264	31,007752	17,829457	34,108527	34,883721	65,116279	1,1	0,9565217	-78,6	-73,25	0,0003959	39,63	-30,465116	-0,8027523
spiLA1589-mir7997b-7	**101**	20,792079	29,70297	25,742574	23,762376	46,534653	53,465347	0,8	0,8076923	-36,9	-36,9	0,336482	6,21	-36,534653	-0,9432836
spiLA1589-mir167b-5	**109**	20,183486	29,357798	23,853211	26,605505	44,036697	55,963303	0,90625	0,8461538	-48	-48	0,23008	4,13	-44,036697	-0,8733333
spiLA1589-mir11419-2	**153**	17,647059	30,718954	28,104575	23,529412	45,751634	54,248366	0,7659574	0,627907	-49,3	-49,1	0,0698091	13,32	-32,222222	-0,7851064
spiLA1589-mir4994	**152**	23,026316	24,342105	21,710526	30,921053	44,736842	55,263158	1,2702703	1,0606061	-67,7	-66,7	0,0304524	7,48	-44,539474	-0,7042857
spiLA1589-mir3448	**104**	23,076923	34,615385	13,461538	28,846154	36,538462	63,461538	0,8333333	1,7142857	-29	-29	0,201646	6,65	-27,884615	-1,148
spiLA1589-mir8011b	**100**	15	36	21	28	36	64	0,7777778	0,7142857	-29,3	-29,2	0,345427	3,67	-29,3	-0,9955882

spiLA1589-mir7981f-7	**134**	21,641791	29,104478	16,41791	32,835821	38,059701	61,940299	1,1282051	1,3181818	-61	-61	0,104164	6,22	-45,522388	-0,7631579
spiLA1589-mir7997b-8	**91**	15,384615	27,472527	18,681319	38,461538	34,065934	65,934066	1,4	0,8235294	-26,7	-26,7	0,212688	5,39	-29,340659	-0,8138889
spiLA1589-mir11137	**173**	17,919075	31,213873	15,606936	35,260116	33,526012	66,473988	1,1296296	1,1481481	-68	-64,8	0,0198922	31,52	-39,306358	-1,1960784
spiLA1589-mir1886f-1	**80**	21,25	26,25	13,75	38,75	35	65	1,4761905	1,5454545	-33,4	-31,1	0,245499	6,36	-41,75	-0,8612903
spiLA1589-mir5014a-4	**232**	17,672414	30,172414	13,362069	38,793103	31,034483	68,965517	1,2857143	1,3225806	-97,1	-97,1	0,0418464	9,92	-41,853448	-1,1928571
spiLA1589-mir4348b	**119**	21,848739	24,369748	16,806723	36,97479	38,655462	61,344538	1,5172414	1,3	-35,8	-33,1	0,0239431	16,86	-30,084034	-1,1829787
spiLA1589-mir7981a-15	**94**	20,212766	29,787234	24,468085	25,531915	44,680851	55,319149	0,8571429	0,826087	-38	-37,5	0,113297	6,41	-40,425532	-1,3486111
spiLA1589-mir8674a	**99**	25,252525	20,20202	24,242424	30,30303	49,494949	50,505051	1,5	1,0416667	-38,9	-38,6	0,226296	3,53	-39,292929	-0,7782609
spiLA1589-mir390-3	**115**	20,869565	33,913043	21,73913	23,478261	42,608696	57,391304	0,6923077	0,96	-47,1	-46,5	0,331975	3,34	-40,956522	-0,9047619
spiLA1589-mir319b-5	**206**	23,300971	28,640777	16,019417	32,038835	39,320388	60,679612	1,1186441	1,4545455	-78,8	-73,4	0,0037409	15,75	-38,252427	-0,9612245
spiLA1589-mir10519-2	**178**	15,730337	30,898876	14,606742	38,764045	30,337079	69,662921	1,2545455	1,0769231	-53,6	-52,3	0,0107316	13,28	-30,11236	-0,9728395
spiLA1589-mir166-1	**143**	17,482517	32,867133	16,783217	32,867133	34,265734	65,734266	1	1,0416667	-53	-53	0,0299885	11,43	-37,062937	-0,8730769
spiLA1589-mir6145b-4	**84**	21,428571	33,333333	23,809524	21,428571	45,238095	54,761905	0,6428571	0,9	-36,1	-36,1	0,199956	8,02	-42,97619	-1,241791
spiLA1589-mir7981-2	**182**	14,835165	37,912088	17,032967	30,21978	31,868132	68,131868	0,7971014	0,8709677	-48,8	-47,57	0,0157237	27,49	-26,813187	-0,95
spiLA1589-mir390-4	**106**	20,754717	30,188679	22,641509	26,415094	43,396226	56,603774	0,875	0,9166667	-43,7	-43,7	0,157079	5,71	-41,226415	-0,75
spiLA1589-mir7981e-2	**111**	18,918919	28,828829	12,612613	39,63964	31,531532	68,468468	1,375	1,5	-28,5	-28,5	0,159668	4,93	-25,675676	-0,95
spiLA1589-mir10532-4	**175**	17,142857	32,571429	18,857143	31,428571	36	64	0,9649123	0,9090909	-74,3	-74,1	0,0450299	8,45	-42,457143	-0,9766667
spiLA1589-mir6441	**127**	14,173228	34,645669	16,535433	34,645669	30,708661	69,291339	1	0,8571429	-32,9	-32,9	0,0052944	17,32	-25,905512	-0,8142857
spiLA1589-mir7997c-17	**80**	25	26,25	11,25	37,5	36,25	63,75	1,4285714	2,2222222	-31,8	-31,8	0,144807	4	-39,75	-1,1793651
spiLA1589-mir11003	**95**	14,736842	40	15,789474	29,473684	30,526316	69,473684	0,7368421	0,9333333	-28,1	-25,7	0,0864284	4,98	-29,578947	-0,8435897
spiLA1589-mir7997c-18	**131**	23,664122	24,427481	21,374046	30,534351	45,038168	54,961832	1,25	1,1071429	-66,2	-66,2	0,0841551	4,52	-50,534351	-1,0965517
spiLA1589-mir172b-3	**111**	16,216216	31,531532	15,315315	36,936937	31,531532	68,468468	1,1714286	1,0588235	-40,6	-38,8	0,0382092	13,04	-36,576577	-0,9689655
spiLA1589-mir10197	**211**	13,270142	31,753555	18,483412	36,492891	31,753555	68,246445	1,1492537	0,7179487	-62,1	-60,7	0,0093892	22,57	-29,43128	-1,1220339
spiLA1589-mir10541	**156**	15,384615	33,974359	16,666667	33,974359	32,051282	67,948718	1	0,9230769	-35,6	-22,58	0,0085445	39,93	-22,820513	-0,9268657
spiLA1589-mir10540-2	**110**	16,363636	34,545455	16,363636	32,727273	32,727273	67,272727	0,9473684	1	-29,2	-28,5	0,0697882	5,6	-26,545455	-1,040625
spiLA1589-mir7980b-3	**110**	14,545455	36,363636	16,363636	32,727273	30,909091	69,090909	0,9	0,8888889	-28,8	-28,4	0,186838	3,87	-26,181818	-0,712
spiLA1589-mir7981a-16	**109**	20,183486	24,770642	17,431193	37,614679	37,614679	62,385321	1,5185185	1,1578947	-44,5	-43,9	0,0651591	8,83	-40,825688	-0,8111111
spiLA1589-mir7981d-9	**268**	14,925373	33,208955	17,164179	34,701493	32,089552	67,910448	1,0449438	0,8695652	-94	-85,5	0,0004705	38,94	-35,074627	-0,8470588
spiLA1589-mir823-2	**276**	22,463768	33,695652	14,130435	29,710145	36,594203	63,405797	0,8817204	1,5897436	-73,6	-59,8	0,0005234	43,59	-26,666667	-1,0853659
spiLA1589-mir167d-3	**189**	18,518519	33,862434	16,402116	31,216931	34,920635	65,079365	0,921875	1,1290323	-66	-64,4	0,0094346	14,9	-34,920635	-1,0930233
spiLA1589-mir9477-1	**98**	20,408163	27,55102	19,387755	32,653061	39,795918	60,204082	1,1851852	1,0526316	-56,3	-56,3	0,196998	6,17	-57,44898	-0,7287129
spiLA1589-mir8001a-2	**88**	17,045455	28,409091	18,181818	36,363636	35,227273	64,772727	1,28	0,9375	-44,1	-43,7	0,0662309	6,24	-50,113636	-1
spiLA1589-mir7981d-10	**127**	18,897638	31,496063	17,322835	32,283465	36,220472	63,779528	1,025	1,0909091	-81,7	-81,7	0,186874	2,8	-64,330709	-1,4435897
spiLA1589-mir5725-4	**282**	20,212766	30,141844	17,375887	32,269504	37,588652	62,411348	1,0705882	1,1632653	-98,1	-94,97	0,0028285	23,56	-34,787234	-1,4225806
spiLA1589-mir9760-4	**115**	27,826087	27,826087	9,5652174	34,782609	37,391304	62,608696	1,25	2,9090909	-30,6	-25,7	0,0255981	26,25	-26,608696	-1,776087
spiLA1589-mir1530-1	**230**	15,652174	33,043478	17,391304	33,913043	33,043478	66,956522	1,0263158	0,9	-56,4	-51,3	0,0011698	36,1	-24,521739	-0,9254717
spiLA1589-mir7981a-17	**194**	16,494845	34,020619	13,917526	35,56701	30,412371	69,587629	1,0454545	1,1851852	-43,6	-34,8	0,0025355	29,98	-22,474227	-0,7116279
spiLA1589-mir7981a-18	**141**	14,893617	37,588652	20,567376	26,950355	35,460993	64,539007	0,7169811	0,7241379	-49,3	-48,4	0,175174	4,03	-34,964539	-0,7421053
spiLA1589-mir8184	**231**	19,91342	33,333333	13,419913	33,333333	33,333333	66,666667	1	1,483871	-62,3	-55,4	0,0034743	28,32	-26,969697	-0,986
spiLA1589-mir8030-2	**107**	23,364486	29,906542	12,149533	34,579439	35,514019	64,485981	1,15625	1,9230769	-28	-24,6	0,0388986	18,84	-26,168224	-0,9705882
spiLA1589-mir2609b	**144**	20,138889	31,944444	11,111111	36,805556	31,25	68,75	1,1521739	1,8125	-31,8	-25,2	0,0337485	18,87	-22,083333	-0,852
spiLA1589-mir1862e	**118**	17,79661	34,745763	16,949153	30,508475	34,745763	65,254237	0,8780488	1,05	-34,4	-34,2	0,0589896	7,59	-29,152542	-0,925
spiLA1589-mir1128-4	**256**	20,3125	35,546875	10,9375	33,203125	31,25	68,75	0,9340659	1,8571429	-74,2	-72,2	0,0043251	42,98	-28,984375	-0,7066667
spiLA1589-mir6145b-5	**87**	22,988506	24,137931	18,390805	34,482759	41,37931	58,62069	1,4285714	1,25	-36,2	-36,2	0,0961154	9,31	-41,609195	-0,8390244
spiLA1589-mir1530-2	**218**	14,220183	32,110092	21,559633	32,110092	35,779817	64,220183	1	0,6595745	-59,1	-56	0,0253873	23,32	-27,110092	-0,9275
spiLA1589-mir11299	**283**	16,607774	33,215548	17,667845	32,508834	34,275618	65,724382	0,9787234	0,94	-72,8	-64,8	5,66E-05	41,17	-25,724382	-1,0055556
spiLA1589-mir164c	**93**	19,354839	26,88172	20,430108	33,333333	39,784946	60,215054	1,24	0,9473684	-51,1	-48,1	0,25053	2,22	-54,946237	-0,7576923
spiLA1589-mir171f-10	**125**	21,6	28	16,8	33,6	38,4	61,6	1,2	1,2857143	-49,3	-45,4	0,0539825	6,28	-39,44	-0,7505155
spiLA1589-mir2672	**139**	17,266187	35,251799	12,94964	34,532374	30,215827	69,784173	0,9795918	1,3333333	-30,7	-30,7	0,0302041	13,22	-22,086331	-1,3810811
spiLA1589-mir1888b-2	**165**	30,909091	23,030303	20	26,060606	50,909091	49,090909	1,1315789	1,5454545	-82,5	-80,2	0,0582495	22,33	-50	-1,0270833
spiLA1589-mir7539	**270**	18,148148	35,185185	13,333333	33,333333	31,481481	68,518519	0,9473684	1,3611111	-87	-82,3	0,0007623	37,21	-32,222222	-0,7309524
spiLA1589-mir159-3	**215**	22,325581	27,906977	14,883721	34,883721	37,209302	62,790698	1,25	1,5	-92,1	-89,2	0,0058915	13,96	-42,837209	-0,9821429
spiLA1589-mir159b-4	**101**	19,80198	27,722772	15,841584	36,633663	35,643564	64,356436	1,3214286	1,25	-29,2	-27,3	0,2274	5,62	-28,910891	-1,0235294
spiLA1589-mir11451	**316**	15,189873	31,012658	15,189873	38,607595	30,379747	69,620253	1,244898	1	-76,9	-76,7	0,0004187	35,81	-24,335443	-1,15125
spiLA1589-mir9781-2	**124**	20,967742	29,032258	15,322581	34,677419	36,290323	63,709677	1,1944444	1,3684211	-42,5	-38,7	0,010076	12,49	-34,274194	-0,8111111
spiLA1589-mir856	**128**	17,96875	32,03125	15,625	34,375	33,59375	66,40625	1,0731707	1,15	-32,4	-31,8	0,0036575	17,32	-25,3125	-0,7861111
spiLA1589-mir8040-1	**338**	20,710059	26,035503	14,792899	38,461538	35,502959	64,497041	1,4772727	1,4	-95,1	-91,2	1,19E-05	45,03	-28,136095	-0,75
spiLA1589-mir9556	**119**	16,806723	34,453782	22,689076	26,05042	39,495798	60,504202	0,7560976	0,7407407	-39	-38,2	0,0162546	11,55	-32,773109	-0,7534884
spiLA1589-mir4243-1	**116**	20,689655	30,172414	13,793103	35,344828	34,482759	65,517241	1,1714286	1,5	-29,4	-27,1	0,0297858	12,19	-25,344828	-0,7925
spiLA1589-mir1525-1	**101**	18,811881	33,663366	13,861386	33,663366	32,673267	67,326733	1	1,3571429	-26	-22,1	0,0415104	23,33	-25,742574	-0,8297872
spiLA1589-mir10204	**107**	22,429907	31,775701	19,626168	26,168224	42,056075	57,943925	0,8235294	1,1428571	-73,5	-73,5	0,411599	1,15	-68,691589	-0,7878788
spiLA1589-mir172e-2	**169**	17,159763	33,136095	13,609467	36,094675	30,769231	69,230769	1,0892857	1,2608696	-58,4	-53,07	0,0160855	21,81	-34,556213	-0,9098039
spiLA1589-mir7997c-20	**143**	20,979021	28,671329	16,083916	34,265734	37,062937	62,937063	1,195122	1,3043478	-37,8	-34,9	0,0069025	16,51	-26,433566	-1,6333333
spiLA1589-mir164b	**300**	21,666667	32,666667	17,666667	28	39,333333	60,666667	0,8571429	1,2264151	-85,1	-72,9	4,79E-05	51,51	-28,366667	-1,1230769
spiLA1589-mir7997c-19	**120**	21,666667	30	15	33,333333	36,666667	63,333333	1,1111111	1,4444444	-34	-33	0,0425875	15,1	-28,333333	-0,7132075
spiLA1589-mir2118-1	**124**	22,580645	33,870968	12,903226	30,645161	35,483871	64,516129	0,9047619	1,75	-30,9	-29,6	0,0332672	16,42	-24,919355	-0,7727273

spiLA1589-mir171c-2	**215**	19,069767	33,488372	13,953488	33,488372	33,023256	66,976744	1	1,3666667	-56,4	-56	0,0002589	41,68	-26,232558	-1,112069
spiLA1589-mir7981-3	**210**	18,571429	32,857143	14,761905	33,809524	33,333333	66,666667	1,0289855	1,2580645	-91,4	-91,4	0,0956785	5,13	-43,52381	-0,7366667
spiLA1589-mir9761	**195**	23,076923	31,794872	15,384615	29,74359	38,461538	61,538462	0,9354839	1,5	-56,3	-42,81	0,0058455	37,86	-28,871795	-1,1058824
spiLA1589-mir2118b	**296**	24,324324	31,418919	13,513514	30,743243	37,837838	62,162162	0,9784946	1,8	-88,4	-74,1	1,74E-05	51,87	-29,864865	-0,7147059
spiLA1589-mir2607-2	**254**	15,748031	33,070866	15,354331	35,826772	31,102362	68,897638	1,0833333	1,025641	-60,4	-60,1	0,0005229	35,56	-23,779528	-0,7892857
spiLA1589-mir1530-3	**323**	23,839009	32,198142	11,764706	32,198142	35,603715	64,396285	1	2,0263158	-84,6	-75,6	6,38E-05	58,29	-26,19195	-1,0541667
spiLA1589-mir11533a	**149**	21,47651	31,543624	10,738255	36,241611	32,214765	67,785235	1,1489362	2	-35,5	-35,2	0,0160272	23,27	-23,825503	-0,764557
spiLA1589-mir8583	**289**	21,453287	33,217993	14,878893	30,449827	36,33218	63,66782	0,9166667	1,4418605	-76	-54	5,66E-05	98,47	-26,297578	-0,7356522
spiLA1589-mir7981a-19	**152**	17,763158	36,184211	13,815789	32,236842	31,578947	68,421053	0,8909091	1,2857143	-61,3	-59,3	0,0924459	10,81	-40,328947	-0,7395833
spiLA1589-mir11123	**307**	18,892508	30,618893	17,915309	32,57329	36,807818	63,192182	1,0638298	1,0545455	-83,7	-79,3	0,0007471	32,07	-27,263844	-0,7238095
spiLA1589-mir3627	**125**	22,4	27,2	20	30,4	42,4	57,6	1,1176471	1,12	-47,6	-47,6	0,149706	5,08	-38,08	-1,2770833
spiLA1589-mir7981d-11	**217**	16,129032	29,953917	16,589862	37,327189	32,718894	67,281106	1,2461538	0,9722222	-53,8	-46,19	0,0010966	37,81	-24,792627	-0,740708
spiLA1589-mir6429	**157**	15,923567	35,66879	19,10828	29,299363	35,031847	64,968153	0,8214286	0,8333333	-72,1	-72,1	0,225024	10,57	-45,923567	-0,8981132
spiLA1589-mir10419	**185**	14,054054	38,918919	18,378378	28,648649	32,432432	67,567568	0,7361111	0,7647059	-44	-42,1	0,024981	24,05	-23,783784	-0,7577465
spiLA1589-mir4243-2	**242**	21,487603	31,404959	9,5041322	37,603306	30,991736	69,008264	1,1973684	2,2608696	-57,9	-55,2	0,0036671	22,42	-23,92562	-1,3109091
spiLA1589-mir7981b-7	**116**	19,827586	27,586207	17,241379	35,344828	37,068966	62,931034	1,28125	1,15	-58,7	-58,7	0,221222	7,57	-50,603448	-0,772
spiLA1589-mir10538-1	**162**	16,049383	32,716049	15,432099	35,802469	31,481481	68,518519	1,0943396	1,04	-70,1	-69,7	0,0702312	5,03	-43,271605	-0,75625
spiLA1589-mir2922	**338**	17,159763	35,502959	14,201183	33,136095	31,360947	68,639053	0,9333333	1,2083333	-79	-70,84	8,60E-05	48,53	-23,372781	-0,9327273
spiLA1589-mir156b-12	**101**	21,782178	26,732673	21,782178	29,70297	43,564356	56,435644	1,1111111	1	-47,4	-47,4	0,368348	2,98	-46,930693	-1,3745098
spiLA1589-mir156b-13	**114**	21,052632	26,315789	24,561404	28,070175	45,614035	54,385965	1,0666667	0,8571429	-51,7	-45	0,0301645	10,31	-45,350877	-0,745283
spiLA1589-mir156i-1	**239**	15,062762	25,941423	17,154812	41,841004	32,217573	67,782427	1,6129032	0,8780488	-64,4	-59,7	0,0242852	32,98	-26,945607	-0,8866667
spiLA1589-mir7981f-8	**239**	17,991632	27,196653	15,481172	39,330544	33,472803	66,527197	1,4461538	1,1621622	-56	-44,9	0,0028366	32,01	-23,430962	-1,0806452
spiLA1589-mir160e-3	**162**	22,839506	22,222222	16,049383	38,888889	38,888889	61,111111	1,75	1,4230769	-47	-44,9	0,0164632	13,81	-29,012346	-0,7568627
spiLA1589-mir5303i-2	**240**	17,083333	34,166667	14,166667	34,583333	31,25	68,75	1,0121951	1,2058824	-70,1	-65,5	0,0071818	25,65	-29,208333	-0,7
spiLA1589-mir1886f-2	**114**	16,666667	35,964912	18,421053	28,947368	35,087719	64,912281	0,804878	0,9047619	-30,6	-29,6	0,0196201	23,18	-26,842105	-0,9346667
spiLA1589-mir7822-2	**219**	15,525114	36,073059	15,525114	32,876712	31,050228	68,949772	0,9113924	1	-86,6	-82,64	0,0196376	22,82	-39,543379	-0,8387097
spiLA1589-mir8714	**99**	18,181818	36,363636	15,151515	30,30303	33,333333	66,666667	0,8333333	1,2	-24,5	-24,3	0,043187	12,53	-24,747475	-1,2735294
spiLA1589-mir166b-2	**107**	21,495327	22,429907	23,364486	32,71028	44,859813	55,140187	1,4583333	0,92	-44,2	-41	0,0417107	13,02	-41,308411	-1,1096774
spiLA1589-mir397b-3	**127**	19,685039	36,220472	18,897638	25,19685	38,582677	61,417323	0,6956522	1,0416667	-49,6	-49,6	0,0660774	8,29	-39,055118	-0,7424242
spiLA1589-mir5014a-5	**239**	20,083682	33,891213	15,062762	30,962343	35,146444	64,853556	0,9135802	1,3333333	-89,7	-88,4	0,0040274	13,68	-37,531381	-0,9208333
spiLA1589-mir7997c-21	**132**	21,969697	29,545455	17,424242	31,060606	39,393939	60,606061	1,0512821	1,2608696	-49,6	-49,6	0,159053	6,48	-37,575758	-1,0122449
spiLA1589-mir8764	**155**	13,548387	29,677419	17,419355	39,354839	30,967742	69,032258	1,326087	0,7777778	-38,6	-38,6	0,0361932	14,92	-24,903226	-1,0678571
spiLA1589-mir482a-2	**104**	20,192308	19,230769	19,230769	41,346154	39,423077	60,576923	2,15	1,05	-46,7	-46,7	0,208174	3,07	-44,903846	-0,9538462
spiLA1589-mir10215	**66**	22,727273	36,363636	12,121212	28,787879	34,848485	65,151515	0,7916667	1,875	-33,2	-33,2	0,34445	1,69	-50,30303	-1,1390244
spiLA1589-mir1886f-3	**125**	20,8	25,6	20,8	32,8	41,6	58,4	1,28125	1	-51	-51	0,217335	13,39	-40,8	-0,8289474
spiLA1589-mir6147	**154**	15,584416	35,064935	16,883117	32,467532	32,467532	67,532468	0,9259259	0,9230769	-54,2	-53,4	0,0545559	9,35	-35,194805	-1,4434783
spiLA1589-mir7997c-22	**137**	25,547445	29,19708	16,788321	28,467153	42,335766	57,664234	0,975	1,5217391	-68,4	-65,6	0,11475	3,83	-49,927007	-1,084
spiLA1589-mir5174e	**149**	15,436242	27,516779	16,778523	40,268456	32,214765	67,785235	1,4634146	0,92	-34,4	-25,72	0,008733	30,71	-23,087248	-0,735
spiLA1589-mir398b	**124**	23,387097	20,16129	22,580645	33,870968	45,967742	54,032258	1,68	1,0357143	-63,9	-63,8	0,088157	7,49	-51,532258	-1,1793103
spiLA1589-mir4240	**241**	24,896266	28,215768	9,9585062	36,929461	34,854772	65,145228	1,3088235	2,5	-83,9	-81,8	0,0009708	24,91	-34,813278	-0,7166667
spiLA1589-mir7981a-20	**260**	17,307692	36,153846	15	31,538462	32,307692	67,692308	0,8723404	1,1538462	-68,6	-62,4	0,0004428	36,9	-26,384615	-1,1210526
spiLA1589-mir169j-7	**205**	18,04878	30,731707	19,512195	31,707317	37,560976	62,439024	1,031746	0,925	-74	-70,6	0,0175537	15,34	-36,097561	-0,9988095
spiLA1589-mir1128-5	**98**	20,408163	26,530612	22,44898	30,612245	42,857143	57,142857	1,1538462	0,9090909	-54,4	-54,4	0,26242	4,44	-55,510204	-0,8166667
spiLA1589-mir10538-2	**148**	16,216216	36,486486	14,189189	33,108108	30,405405	69,594595	0,9074074	1,1428571	-72,1	-72,1	0,205991	2,85	-48,716216	-0,961039
spiLA1589-mir8001a-3	**137**	15,328467	32,846715	16,058394	35,766423	31,386861	68,613139	1,0888889	0,9545455	-71,3	-71,3	0,235509	2,66	-52,043796	-1,2952381
spiLA1589-mir5568a	**208**	17,307692	32,211538	23,557692	26,923077	40,865385	59,134615	0,8358209	0,7346939	-78,7	-76	0,0010701	20,52	-37,836538	-1,6022222
spiLA1589-mir7981f-9	**146**	18,493151	39,041096	12,328767	30,136986	30,821918	69,178082	0,7719298	1,5	-33,6	-28,31	0,0110153	16,55	-23,013699	-1,6581395
spiLA1589-mir7997b-9	**173**	18,49711	30,057803	25,433526	26,011561	43,930636	56,069364	0,8653846	0,7272727	-78,5	-78,5	0,0889947	8,92	-45,375723	-0,9258824
spiLA1589-mir9470-3	**115**	21,73913	24,347826	8,6956522	45,217391	30,434783	69,565217	1,8571429	2,5	-34,8	-32,4	0,0649658	15,66	-30,26087	-0,7466667
spiLA1589-mir6025c	**133**	24,06015	29,323308	17,293233	29,323308	41,353383	58,646617	1	1,3913043	-42,4	-42,4	0,0314193	12,9	-31,879699	-1,4181818
spiLA1589-mir1435b	**246**	16,666667	32,113821	17,073171	34,146341	33,739837	66,260163	1,0632911	0,9761905	-65,8	-64	0,0032497	42,41	-26,747967	-0,7754839
spiLA1589-mir7981b-8	**184**	20,108696	28,26087	16,847826	34,782609	36,956522	63,043478	1,2307692	1,1935484	-92,8	-92,8	0,0069181	14,16	-50,434783	-0,7709091
spiLA1589-mir6151i	**215**	24,651163	27,906977	16,27907	31,162791	40,930233	59,069767	1,1166667	1,5142857	-73,4	-61,41	0,003069	38,88	-34,139535	-0,7927711
spiLA1589-mir1520d	**77**	19,480519	32,467532	14,285714	33,766234	33,766234	66,233766	1,04	1,3636364	-26	-25,4	0,374877	2,53	-33,766234	-1,3647059
spiLA1589-mir7543-1	**70**	22,857143	28,571429	18,571429	30	41,428571	58,571429	1,05	1,2307692	-30,7	-30,7	0,668782	0,89	-43,857143	-0,8340909
spiLA1589-mir171t	**98**	20,408163	29,591837	22,44898	27,55102	42,857143	57,142857	0,9310345	0,9090909	-42,6	-40,9	0,111429	11,49	-43,469388	-1
spiLA1589-mir7981e-3	**223**	19,282511	32,286996	16,143498	32,286996	35,426009	64,573991	1	1,1944444	-93,3	-87,6	0,0015967	26,62	-41,838565	-1,0586207
spiLA1589-mir7980b-4	**122**	20,491803	25,409836	17,213115	36,885246	37,704918	62,295082	1,4516129	1,1904762	-52,1	-49,1	0,136651	18,78	-42,704918	-1,1810127
spiLA1589-mir868-2	**254**	25,590551	25,19685	18,110236	31,102362	43,700787	56,299213	1,234375	1,4130435	-79,8	-77	0,0125333	26,29	-31,417323	-1,1326087
spiLA1589-mir773b-2	**98**	22,44898	32,653061	19,387755	25,510204	41,836735	58,163265	0,78125	1,1578947	-35,4	-35,4	0,12568	5,45	-36,122449	-0,925
spiLA1589-mir4229	**76**	27,631579	21,052632	22,368421	28,947368	50	50	1,375	1,2352941	-35	-35	0,441141	9,52	-46,052632	-0,7189189
spiLA1589-mir7823-2	**88**	15,909091	28,409091	17,045455	38,636364	32,954545	67,045455	1,36	0,9333333	-25	-23,9	0,203199	5,48	-28,409091	-0,8634146
spiLA1589-mir7543-2	**321**	14,641745	34,579439	18,068536	32,71028	32,71028	67,28972	0,9459459	0,8103448	-73,9	-64,7	0,0002698	51,3	-23,021807	-0,9210526
spiLA1589-mir171b-3	**112**	18,75	29,464286	21,428571	30,357143	40,178571	59,821429	1,030303	0,875	-43,5	-38,6	0,0246346	18,25	-38,839286	-0,862069
spiLA1589-mir156i-2	**169**	14,201183	39,053254	15,976331	30,769231	30,177515	69,822485	0,7878788	0,8888889	-44,9	-44,9	0,0482921	6,07	-26,568047	-0,9666667
spiLA1589-mir9471a-3	**154**	19,480519	31,818182	14,935065	33,766234	34,415584	65,584416	1,0612245	1,3043478	-62,9	-62,9	0,12587	10,48	-40,844156	-1,3078431

spiLA1589-mir1159	**178**	17,977528	32,58427	13,483146	35,955056	31,460674	68,539326	1,1034483	1,3333333	-53,1	-53,1	0,0322733	13,25	-29,831461	-0,8803922
spiLA1589-mir7981b-9	**142**	14,788732	30,985915	16,901408	37,323944	31,690141	68,309859	1,2045455	0,875	-48,4	-45,3	0,0315598	16,58	-34,084507	-1,1867925
spiLA1589-mir7997c-23	**205**	19,512195	31,707317	19,02439	29,756098	38,536585	61,463415	0,9384615	1,025641	-65,4	-58	0,0039741	22,96	-31,902439	-0,9482143
spiLA1589-mir391a	**118**	19,491525	27,966102	19,491525	33,050847	38,983051	61,016949	1,1818182	1	-70,2	-69,9	0,404923	3,87	-59,491525	-1,0755556
spiLA1589-mir2673b-2	**245**	21,22449	35,918367	16,326531	26,530612	37,55102	62,44898	0,7386364	1,3	-64,7	-53,9	0,0026364	30,57	-26,408163	-0,8278481
spiLA1589-mir393b	**99**	21,212121	26,262626	21,212121	31,313131	42,424242	57,575758	1,1923077	1	-50,6	-50,6	0,278714	2,42	-51,111111	-1,526087
spiLA1589-mir1879	**89**	17,977528	30,337079	15,730337	35,955056	33,707865	66,292135	1,1851852	1,1428571	-23,7	-23,7	0,0450309	10,74	-26,629213	-0,7032609
spiLA1589-mir169c-4	**182**	14,835165	27,472527	18,131868	39,56044	32,967033	67,032967	1,44	0,8181818	-64,8	-61,8	0,0091554	14,95	-35,604396	-0,79
spiLA1589-mir419	**113**	17,699115	30,088496	16,814159	35,39823	34,513274	65,486726	1,1764706	1,0526316	-53,7	-53,7	0,0532811	8,75	-47,522124	-0,7116279
spiLA1589-mir7981a-21	**118**	21,186441	29,661017	22,881356	26,271186	44,067797	55,932203	0,8857143	0,9259259	-84,8	-84,8	0,381904	1,98	-71,864407	-1,08
spiLA1589-mir6231-3	**106**	15,09434	34,90566	17,924528	32,075472	33,018868	66,981132	0,9189189	0,8421053	-40,2	-40,2	0,306319	5,67	-37,924528	-1,6307692
spiLA1589-mir10211a	**83**	20,481928	26,506024	21,686747	31,325301	42,168675	57,831325	1,1818182	0,9444444	-28,3	-28,1	0,107074	6,12	-34,096386	-1,055814
spiLA1589-mir7980b-5	**114**	20,175439	27,192982	18,421053	34,210526	38,596491	61,403509	1,2580645	1,0952381	-44,4	-44,4	0,0964784	13,75	-38,947368	-1,1485714
spiLA1589-mir1313	**204**	18,627451	33,333333	16,176471	31,862745	34,803922	65,196078	0,9558824	1,1515152	-80,8	-80,3	0,0707303	16,96	-39,607843	-0,8085714
spiLA1589-mir6288c-1	**240**	18,333333	27,5	14,583333	39,583333	32,916667	67,083333	1,4393939	1,2571429	-58,5	-53,5	0,0009084	41,21	-24,375	-1,0090909
spiLA1589-mir11444	**190**	21,052632	31,052632	12,105263	35,789474	33,157895	66,842105	1,1525424	1,7391304	-61,7	-58,1	0,0133126	30,49	-32,473684	-1,1380282
spiLA1589-mir10542-3	**237**	18,14346	38,396624	13,080169	30,379747	31,223629	68,776371	0,7912088	1,3870968	-54	-43,57	0,0019109	41,43	-22,78481	-0,7405063
spiLA1589-mir10424d	**229**	14,847162	32,751092	18,777293	33,624454	33,624454	66,375546	1,0266667	0,7906977	-54,4	-50,3	0,0137052	38,14	-23,755459	-0,9793651
spiLA1589-mir1428e	**170**	18,823529	32,352941	14,705882	34,117647	33,529412	66,470588	1,0545455	1,28	-41,5	-41	0,0169126	25,69	-24,411765	-0,7297297
spiLA1589-mir7502c-1	**276**	14,130435	33,695652	16,304348	35,869565	30,434783	69,565217	1,0645161	0,8666667	-79,7	-75	0,0002505	40,37	-28,876812	-0,7280702
spiLA1589-mir11592-1	**141**	29,078014	22,695035	24,822695	23,404255	53,900709	46,099291	1,03125	1,1714286	-64,5	-63	0,0105917	13,06	-45,744681	-0,9794118
spiLA1589-mir8021-2	**243**	14,814815	32,510288	16,872428	35,802469	31,687243	68,312757	1,1012658	0,8780488	-80,6	-75,2	0,0043382	28,04	-33,168724	-0,9488095
spiLA1589-mir5303h-1	**131**	17,557252	30,534351	22,137405	29,770992	39,694656	60,305344	0,975	0,7931034	-47,9	-46,6	0,0972115	6,15	-36,564885	-1,0467532
spiLA1589-mir7981d-12	**187**	13,368984	29,946524	18,181818	38,502674	31,550802	68,449198	1,2857143	0,7352941	-50,5	-50,49	0,02977	15,81	-27,005348	-0,731746
spiLA1589-mir7981-4	**256**	16,015625	30,46875	22,65625	30,859375	38,671875	61,328125	1,0128205	0,7068966	-90,1	-89,6	0,0002754	27,66	-35,195313	-0,9211538
spiLA1589-mir7997c-24	**127**	19,685039	27,559055	21,259843	31,496063	40,944882	59,055118	1,1428571	0,9259259	-53,9	-53,9	0,0522291	5,73	-42,440945	-0,8559322
spiLA1589-mir7992-5	**169**	18,934911	33,727811	19,526627	27,810651	38,461538	61,538462	0,8245614	0,969697	-64,2	-64,2	0,0596601	12,29	-37,988166	-0,910101
spiLA1589-mir6457b	**122**	14,754098	27,04918	15,57377	42,622951	30,327869	69,672131	1,5757576	0,9473684	-41,3	-41,3	0,128304	4,25	-33,852459	-1,026087
spiLA1589-mir7981d-13	**227**	20,704846	29,07489	16,740088	33,480176	37,444934	62,555066	1,1515152	1,2368421	-95,8	-94	0,0041923	16,77	-42,202643	-0,8
spiLA1589-mir9749	**168**	17,857143	24,404762	18,452381	39,285714	36,309524	63,690476	1,6097561	0,9677419	-42,7	-39,6	0,0071385	17,29	-25,416667	-1,1162162
spiLA1589-mir1173	**179**	19,553073	30,167598	16,759777	33,519553	36,312849	63,687151	1,1111111	1,1666667	-55,7	-53,6	0,0036353	24,4	-31,117318	-1,1270588
spiLA1589-mir8042	**158**	17,088608	34,810127	17,721519	30,379747	34,810127	65,189873	0,8727273	0,9642857	-50,2	-50,2	0,0728821	9,99	-31,772152	-0,7
spiLA1589-mir7981b-10	**174**	17,816092	34,482759	20,689655	27,011494	38,505747	61,494253	0,7833333	0,8611111	-73,3	-72,8	0,207429	6,26	-42,126437	-0,8569231
spiLA1589-mir162-4	**93**	23,655914	31,182796	24,731183	20,430108	48,387097	51,612903	0,6551724	0,9565217	-42	-42	0,347985	4,29	-45,16129	-0,9127273
spiLA1589-mir7997c-25	**120**	29,166667	24,166667	14,166667	32,5	43,333333	56,666667	1,3448276	2,0588235	-53,5	-53,4	0,0259672	7,79	-44,583333	-1,0940299
spiLA1589-mir8727	**123**	17,073171	29,268293	26,829268	26,829268	43,902439	56,097561	0,9166667	0,6363636	-41,1	-41,1	0,0316478	13,23	-33,414634	-0,9333333
spiLA1589-mir1054	**171**	29,824561	28,654971	21,052632	20,467836	50,877193	49,122807	0,7142857	1,4166667	-61,7	-60,2	0,0139721	19,25	-36,081871	-1,0288462
spiLA1589-mir11078c	**198**	28,787879	30,30303	20,20202	20,707071	48,989899	51,010101	0,6833333	1,425	-68,7	-59	0,0015687	26,62	-34,69697	-0,7611111
spiLA1589-mir1046-3	**139**	18,705036	36,690647	15,107914	29,496403	33,81295	66,18705	0,8039216	1,2380952	-35,2	-32,4	0,0097686	12,41	-25,323741	-0,7091954
spiLA1589-mir8040-2	**120**	16,666667	19,166667	16,666667	47,5	33,333333	66,666667	2,4782609	1	-32,7	-31,5	0,0257622	12,16	-27,25	-0,7082474
spiLA1589-mir7981b-11	**112**	19,642857	26,785714	16,964286	36,607143	36,607143	63,392857	1,3666667	1,1578947	-50,2	-50,2	0,158598	7,3	-44,821429	-0,8175
spiLA1589-mir7981a-22	**287**	16,027875	32,055749	15,33101	36,585366	31,358885	68,641115	1,1413043	1,0454545	-96,5	-92,6	0,0001198	45,26	-33,623693	-1,2243902
spiLA1589-mir11317	**97**	17,525773	31,958763	14,43299	36,082474	31,958763	68,041237	1,1290323	1,2142857	-37,6	-36,4	0,121899	7,14	-38,762887	-0,7757576
spiLA1589-mir9471a-4	**142**	19,014085	33,802817	14,788732	32,394366	33,802817	66,197183	0,9583333	1,2857143	-52	-52	0,0438196	6,62	-36,619718	-1,0722222
spiLA1589-mir7981f-10	**225**	16,888889	29,333333	18,222222	35,555556	35,111111	64,888889	1,2121212	0,9268293	-86,6	-85,1	0,0009166	18,37	-38,488889	-1,2129032
spiLA1589-mir7992-6	**209**	18,181818	29,665072	22,009569	30,143541	40,191388	59,808612	1,016129	0,826087	-66,5	-48,2	0,0036919	47,74	-31,818182	-1,0833333
spiLA1589-mir7980b-6	**74**	18,918919	35,135135	18,918919	27,027027	37,837838	62,162162	0,7692308	1	-29,5	-29,5	0,314845	2,99	-39,864865	-0,7916667
spiLA1589-mir1043-1	**200**	18	33	14	35	32	68	1,0606061	1,2857143	-73,2	-71,7	0,0024815	31,78	-36,6	-1,0535714
spiLA1589-mir5303j	**113**	19,469027	33,628319	15,044248	31,858407	34,513274	65,486726	0,9473684	1,2941176	-33	-33	0,0346219	10,28	-29,20354	-1,009434
spiLA1589-mir7981a-23	**202**	16,831683	36,138614	17,326733	29,70297	34,158416	65,841584	0,8219178	0,9714286	-83,9	-83,6	0,0071841	15,34	-41,534653	-1,14375
spiLA1589-mir3637-1	**252**	14,68254	31,746032	16,666667	36,904762	31,349206	68,650794	1,1625	0,8809524	-72,2	-72,2	0,0028649	21,06	-28,650794	-0,8461538
spiLA1589-mir7981b-12	**111**	21,621622	21,621622	22,522523	34,234234	44,144144	55,855856	1,5833333	0,96	-53,3	-51,5	0,0168385	10,88	-48,018018	-1,215942
spiLA1589-mir1917-1	**261**	16,858238	38,697318	15,708812	28,735632	32,56705	67,43295	0,7425743	1,0731707	-70,6	-65,9	0,0002761	33,93	-27,049808	-0,9139241
spiLA1589-mir5057-2	**192**	22,916667	28,645833	7,8125	40,625	30,729167	69,270833	1,4181818	2,9333333	-43,2	-40,7	0,0030968	37,96	-22,5	-1,0877551
spiLA1589-mir11553	**188**	19,680851	35,106383	15,425532	29,787234	35,106383	64,893617	0,8484848	1,2758621	-47	-45,3	0,0075659	23,62	-25	-0,8305882
spiLA1589-mir7699	**305**	21,639344	31,803279	15,409836	31,147541	37,04918	62,95082	0,9793814	1,4042553	-79,7	-75,2	0,0005395	32,88	-26,131148	-0,7322034
spiLA1589-mir437a	**200**	13	31,5	19	36,5	32	68	1,1587302	0,6842105	-62,8	-54,3	0,0044487	59,08	-31,4	-0,7121212
spiLA1589-mir7981-5	**156**	25,641026	29,487179	11,538462	33,333333	37,179487	62,820513	1,1304348	2,2222222	-40,8	-39,3	0,0205761	13,36	-26,153846	-0,98125
spiLA1589-mir4223	**247**	17,004049	29,959514	14,574899	38,461538	31,578947	68,421053	1,2837838	1,1666667	-75,5	-69,77	0,0023169	31,94	-30,566802	-0,7148148
spiLA1589-mir1525-2	**116**	22,413793	29,310345	8,6206897	39,655172	31,034483	68,965517	1,3529412	2,6	-30,6	-29,8	0,0098947	14,34	-26,37931	-0,7034483
spiLA1589-mir7502c-2	**183**	19,672131	32,786885	12,568306	34,972678	32,240437	67,759563	1,0666667	1,5652174	-57,6	-52,5	0,0080831	18,97	-31,47541	-0,9679487
spiLA1589-mir160	**104**	23,076923	24,038462	21,153846	31,730769	44,230769	55,769231	1,32	1,0909091	-52,3	-51,4	0,100504	4,55	-50,288462	-0,85
spiLA1589-mir8573	**340**	21,176471	25,882353	13,823529	39,117647	35	65	1,5113636	1,5319149	-90,6	-80,3	0,0004505	28,02	-26,647059	-1,1369565
spiLA1589-mir7981a-24	**198**	15,656566	29,79798	17,676768	36,868687	33,333333	66,666667	1,2372881	0,8857143	-75,4	-74,3	0,0414721	12,19	-38,080808	-0,7254237
spiLA1589-mir5029	**189**	12,698413	31,746032	24,338624	31,216931	37,037037	62,962963	0,9833333	0,5217391	-62,3	-61,7	0,171476	27,62	-32,962963	-0,7613445
spiLA1589-mir158b	**203**	22,660099	31,527094	14,778325	31,034483	37,438424	62,561576	0,984375	1,5333333	-55,9	-49	0,0028238	28,06	-27,536946	-1,1424242

spiLA1589-mir7981a-25	**90**	21,111111	34,444444	24,444444	20	45,555556	54,444444	0,5806452	0,8636364	-36,1	-36,1	0,679712	1,45	-40,111111	-0,89
spiLA1589-mir169c-5	**181**	14,364641	35,359116	16,574586	33,701657	30,939227	69,060773	0,953125	0,8666667	-83,6	-83,2	0,173422	6,42	-46,187845	-0,7355263
spiLA1589-mir5302b	**151**	15,89404	33,774834	14,569536	35,761589	30,463576	69,536424	1,0588235	1,0909091	-33,2	-25,86	0,0072465	31,06	-21,986755	-0,7534483
spiLA1589-mir167a-3	**208**	14,423077	31,730769	15,865385	37,980769	30,288462	69,711538	1,1969697	0,9090909	-60,4	-59,2	0,0230477	9,47	-29,038462	-0,7736842
spiLA1589-mir159a-2	**174**	21,83908	24,712644	17,241379	36,206897	39,08046	60,91954	1,4651163	1,2666667	-76,6	-74	0,0215353	12,01	-44,022989	-0,7217391
spiLA1589-mir7981-6	**185**	16,756757	32,432432	22,702703	28,108108	39,459459	60,540541	0,8666667	0,7380952	-56,5	-56,5	0,0278245	14,03	-30,540541	-0,9587302
spiLA1589-mir2093	**82**	20,731707	29,268293	19,512195	30,487805	40,243902	59,756098	1,0416667	1,0625	-29,4	-29,4	0,22484	2,89	-35,853659	-1,1264706
spiLA1589-mir7992-7	**236**	18,220339	30,508475	12,288136	38,983051	30,508475	69,491525	1,2777778	1,4827586	-73	-70,8	0,0062624	15,92	-30,932203	-0,7739726
spiLA1589-mir167c-2	**257**	28,404669	24,902724	20,233463	26,459144	48,638132	51,361868	1,0625	1,4038462	-88,8	-85	0,0103868	49,42	-34,552529	-0,8909091
spiLA1589-mir5026-2	**191**	20,942408	38,219895	16,753927	24,08377	37,696335	62,303665	0,630137	1,25	-60,4	-55,6	0,0027015	19,27	-31,623037	-1,0138889
spiLA1589-mir1521a-2	**137**	24,817518	31,386861	11,678832	32,116788	36,49635	63,50365	1,0232558	2,125	-39,7	-30,9	0,0011443	28,46	-28,978102	-0,7104
spiLA1589-mir7997c-26	**129**	20,155039	32,55814	15,503876	31,782946	35,658915	64,341085	0,9761905	1,3	-51,7	-51,7	0,166614	3,47	-40,077519	-0,794
spiLA1589-mir172d-4	**110**	15,454545	40	17,272727	27,272727	32,727273	67,272727	0,6818182	0,8947368	-37	-37	0,0645438	5,55	-33,636364	-0,8475
spiLA1589-mir7981-7	**268**	18,283582	35,447761	14,179104	32,089552	32,462687	67,537313	0,9052632	1,2894737	-86,9	-78	0,0005287	34,9	-32,425373	-1,123913
spiLA1589-mir1064	**181**	16,022099	36,464088	14,364641	33,149171	30,38674	69,61326	0,9090909	1,1153846	-78,7	-75,3	0,0802047	18,19	-43,480663	-1,0277778
spiLA1589-mir11425f	**338**	18,047337	28,402367	12,426036	41,12426	30,473373	69,526627	1,4479167	1,452381	-85,4	-79	0,000123	34,11	-25,266272	-0,9033333
spiLA1589-mir7981a-26	**106**	17,924528	36,792453	21,698113	23,584906	39,622642	60,377358	0,6410256	0,826087	-34,6	-32,65	0,0180474	14,05	-32,641509	-1,2758621
spiLA1589-mir8030-3	**78**	21,794872	29,487179	11,538462	37,179487	33,333333	66,666667	1,2608696	1,8888889	-26,4	-23,9	0,0358992	9,6	-33,846154	-0,8291262
spiLA1589-mir7741	**224**	20,089286	27,678571	16,964286	35,267857	37,053571	62,946429	1,2741935	1,1842105	-58,5	-56,5	0,0008201	34,18	-26,116071	-0,8238095
spiLA1589-mir7981f-11	**335**	18,507463	32,835821	12,537313	36,119403	31,044776	68,955224	1,1	1,4761905	-92,2	-86	4,89E-05	63,38	-27,522388	-1,0153846
spiLA1589-mir7993d-2	**218**	18,348624	35,321101	12,385321	33,944954	30,733945	69,266055	0,961039	1,4814815	-68,8	-67,9	0,0132785	15,4	-31,559633	-0,7048193
spiLA1589-mir7981a-27	**145**	14,482759	28,965517	20	36,551724	34,482759	65,517241	1,2619048	0,7241379	-42,9	-42,2	0,0274387	12,95	-29,586207	-0,8865385
spiLA1589-mir7981a-28	**169**	16,568047	29,585799	18,343195	35,502959	34,911243	65,088757	1,2	0,9032258	-67,1	-65,7	0,0242275	17,9	-39,704142	-1,0268657
spiLA1589-mir1128-6	**243**	13,168724	32,098765	23,045267	31,687243	36,213992	63,786008	0,9871795	0,5714286	-66,1	-59	0,0012488	33,76	-27,201646	-0,858
spiLA1589-mir166-2	**118**	16,101695	29,661017	22,033898	32,20339	38,135593	61,864407	1,0857143	0,7307692	-33	-31,7	0,0408643	10,37	-27,966102	-1,1372881
spiLA1589-mir7997c-27	**138**	22,463768	27,536232	15,217391	34,782609	37,681159	62,318841	1,2631579	1,4761905	-53,6	-53,1	0,0030524	15,41	-38,84058	-0,7333333
spiLA1589-mir8006-4	**177**	24,858757	28,248588	19,20904	27,683616	44,067797	55,932203	0,98	1,2941176	-82,2	-82,2	0,002635	14,32	-46,440678	-0,9063492
spiLA1589-mir7984c	**187**	16,042781	32,620321	14,438503	36,898396	30,481283	69,518717	1,1311475	1,1111111	-57,2	-49,83	0,0130212	20,45	-30,588235	-1,0307692
spiLA1589-mir169e-2	**172**	15,697674	36,046512	19,186047	29,069767	34,883721	65,116279	0,8064516	0,8181818	-63	-60,3	0,0486431	9,32	-36,627907	-1,0538462
spiLA1589-mir7840	**181**	19,337017	34,80663	12,707182	33,149171	32,044199	67,955801	0,952381	1,5217391	-41,5	-39,7	0,0027548	35,19	-22,928177	-1,05
spiLA1589-mir8014	**205**	18,04878	38,04878	12,682927	31,219512	30,731707	69,268293	0,8205128	1,4230769	-59,1	-57,9	0,0092321	30,26	-28,829268	-1,316129
spiLA1589-mir7981-8	**233**	20,600858	33,476395	15,450644	30,472103	36,051502	63,948498	0,9102564	1,3333333	-86,1	-63,71	0,0005619	37,8	-36,95279	-0,7155172
spiLA1589-mir169j-8	**164**	21,95122	23,780488	21,95122	32,317073	43,902439	56,097561	1,3589744	1	-76,3	-76,3	0,0075372	9,02	-46,52439	-0,9380952
spiLA1589-mir7981a-29	**98**	20,408163	23,469388	23,469388	32,653061	43,877551	56,122449	1,3913043	0,8695652	-43,4	-43,4	0,143851	5,66	-44,285714	-1,0597222
spiLA1589-mir8008b-2	**120**	17,5	31,666667	17,5	33,333333	35	65	1,0526316	1	-34,7	-31,8	0,0092715	14,13	-28,916667	-0,8387097
spiLA1589-mir10420	**139**	17,266187	33,093525	16,546763	33,093525	33,81295	66,18705	1	1,0434783	-41,5	-37,3	0,0133714	22,4	-29,856115	-0,8261905
spiLA1589-mir7981-9	**225**	17,333333	36,444444	16	30,222222	33,333333	66,666667	0,8292683	1,0833333	-77,4	-77,4	0,0639537	16,37	-34,4	-0,9931818
spiLA1589-mir4995	**290**	20	27,586207	15,862069	36,551724	35,862069	64,137931	1,325	1,2608696	-78,5	-65,9	0,000192	59,87	-27,068966	-0,8829787
spiLA1589-mir5205a	**290**	16,551724	29,655172	15,862069	37,931034	32,413793	67,586207	1,2790698	1,0434783	-74,6	-66	0,0002126	51,45	-25,724138	-1,032
spiLA1589-mir7981d-14	**93**	20,430108	27,956989	18,27957	33,333333	38,709677	61,290323	1,1923077	1,1176471	-37,5	-35,5	0,109725	6,86	-40,322581	-0,7548077
spiLA1589-mir8006-5	**212**	15,09434	32,54717	21,698113	30,660377	36,792453	63,207547	0,942029	0,6956522	-63,3	-61,7	0,0065847	18,02	-29,858491	-0,793617
spiLA1589-mir7983-4	**108**	14,814815	30,555556	15,740741	38,888889	30,555556	69,444444	1,2727273	0,9411765	-28,1	-28,1	0,0435357	8,33	-26,018519	-1,0416667
spiLA1589-mir8039-4	**142**	23,239437	35,211268	13,380282	28,169014	36,619718	63,380282	0,8	1,7368421	-51,9	-49,3	0,249552	11,56	-36,549296	-0,8115385
spiLA1589-mir10223	**207**	21,256039	31,400966	10,628019	36,714976	31,884058	68,115942	1,1692308	2	-56,7	-54,6	0,0050751	18,37	-27,391304	-0,8515152
spiLA1589-mir2118-2	**326**	15,95092	36,503067	14,417178	33,128834	30,368098	69,631902	0,907563	1,106383	-74,6	-72,3	0,0005417	36,64	-22,883436	-0,9980769
spiLA1589-mir821e	**260**	14,230769	31,538462	16,923077	37,307692	31,153846	68,846154	1,1829268	0,8409091	-58,9	-54,8	0,0001865	35,82	-22,653846	-0,7535354
spiLA1589-mir7985	**178**	31,460674	17,977528	21,910112	28,651685	53,370787	46,629213	1,59375	1,4358974	-67,8	-58,7	0,0030071	44,94	-38,089888	-1,0123077
spiLA1589-mir7997c-28	**126**	29,365079	26,984127	19,047619	24,603175	48,412698	51,587302	0,9117647	1,5416667	-56,7	-55,7	0,0553408	6,53	-45	-0,7271605
spiLA1589-mir839	**280**	23,214286	23,214286	22,5	31,071429	45,714286	54,285714	1,3384615	1,031746	-91,1	-83,7	0,0005911	48,63	-32,535714	-0,9295082
spiLA1589-mir172a-2	**124**	19,354839	26,612903	17,741935	36,290323	37,096774	62,903226	1,3636364	1,0909091	-71,8	-71,8	0,592873	1,25	-57,903226	-0,8666667
spiLA1589-mir11068f	**211**	16,587678	34,597156	18,009479	30,805687	34,597156	65,402844	0,890411	0,9210526	-85,6	-84,4	0,0339795	10,61	-40,56872	-0,7117188
spiLA1589-mir7981d-15	**152**	20,394737	29,605263	14,473684	35,526316	34,868421	65,131579	1,2	1,4090909	-98,8	-98,6	0,16976	7,69	-65	-1,1726027
spiLA1589-mir1886f-4	**101**	18,811881	26,732673	18,811881	35,643564	37,623762	62,376238	1,3333333	1	-40,2	-40,2	0,392178	3,05	-39,80198	-1,1103448
spiLA1589-mir1886i-3	**88**	17,045455	35,227273	15,909091	31,818182	32,954545	67,045455	0,9032258	1,0714286	-32,6	-32,6	0,16972	4,16	-37,045455	-1,8641509
spiLA1589-mir6112	**91**	15,384615	35,164835	18,681319	30,769231	34,065934	65,934066	0,875	0,8235294	-26,4	-26,4	0,215984	4,9	-29,010989	-1,0578947
spiLA1589-mir7981a-30	**175**	16,571429	37,142857	15,428571	30,857143	32	68	0,8307692	1,0740741	-61,4	-59,2	0,0160727	16,19	-35,085714	-1,1241379
spiLA1589-mir7981a-31	**178**	18,539326	33,707865	20,786517	26,966292	39,325843	60,674157	0,8	0,8918919	-90,1	-90,1	0,0142814	9,55	-50,617978	-0,8516129
spiLA1589-mir7997c-29	**119**	22,689076	26,05042	22,689076	28,571429	45,378151	54,621849	1,0967742	1	-37,8	-35,4	0,180913	7,43	-31,764706	-1,0964286
spiLA1589-mir7981b-13	**147**	15,646259	38,095238	16,326531	29,931973	31,972789	68,027211	0,7857143	0,9583333	-51,9	-51,9	0,182549	3,85	-35,306122	-1,2871429
spiLA1589-mir5185m	**131**	14,503817	31,29771	16,793893	37,40458	31,29771	68,70229	1,195122	0,8636364	-30,7	-27,8	0,0138189	16,54	-23,435115	-0,7
spiLA1589-mir1128-7	**260**	15,769231	33,076923	17,692308	33,461538	33,461538	66,538462	1,0116279	0,8913043	-66,7	-55,54	7,06E-05	59,18	-25,653846	-1,1042553
spiLA1589-mir7981a-32	**145**	16,551724	30,344828	16,551724	36,551724	33,103448	66,896552	1,2045455	1	-35,4	-35	0,0393196	14,67	-24,413793	-0,7487805
spiLA1589-mir11891	**200**	15	36,5	16	32,5	31	69	0,890411	0,9375	-47,9	-37,9	0,0019484	34,12	-23,95	-0,7666667
spiLA1589-mir399j-2	**108**	17,592593	29,62963	25,925926	26,851852	43,518519	56,481481	0,90625	0,6785714	-39,7	-39,7	0,338886	5,2	-36,759259	-0,7725806
spiLA1589-mir7981b-14	**337**	17,507418	35,905045	13,05638	33,531157	30,563798	69,436202	0,9338843	1,3409091	-85	-71,6	0,0001032	74,27	-25,222552	-0,7954545
spiLA1589-mir1027c	**307**	13,355049	34,527687	16,938111	35,179153	30,29316	69,70684	1,0188679	0,7884615	-78,8	-76,4	0,0002442	50,57	-25,667752	-0,8252427

spiLA1589-mir1044-2	**199**	15,075377	37,18593	20,603015	27,135678	35,678392	64,321608	0,7297297	0,7317073	-50,6	-50,6	0,0367407	13,94	-25,427136	-0,8473118
spiLA1589-mir6149	**196**	19,387755	27,040816	16,836735	36,734694	36,22449	63,77551	1,3584906	1,1515152	-52,1	-46,1	0,0007314	28,85	-26,581633	-0,7277228
spiLA1589-mir166a	**232**	17,241379	32,758621	15,948276	34,051724	33,189655	66,810345	1,0394737	1,0810811	-82,7	-82,1	0,001321	31,93	-35,646552	-0,7126761
spiLA1589-mir7997b-10	**145**	25,517241	25,517241	17,931034	31,034483	43,448276	56,551724	1,2162162	1,4230769	-59,2	-59,2	0,0599793	5,96	-40,827586	-1,074026
spiLA1589-mir9764	**186**	15,053763	33,333333	18,27957	33,333333	33,333333	66,666667	1	0,8235294	-45,4	-40,5	0,0034872	25,86	-24,408602	-0,9396825
spiLA1589-mir11068c-3	**200**	19	29	13	39	32	68	1,3448276	1,4615385	-66,5	-66,5	0,0601264	7,89	-33,25	-0,7930233
spiLA1589-mir2122	**174**	13,793103	29,310345	17,241379	39,655172	31,034483	68,965517	1,3529412	0,8	-49,1	-49,1	0,0239275	9,29	-28,218391	-0,7322581
spiLA1589-mir9387	**245**	15,102041	31,020408	16,326531	37,55102	31,428571	68,571429	1,2105263	0,925	-57,9	-54,2	0,001321	44,1	-23,632653	-1,0390625
spiLA1589-mir396f	**144**	20,138889	29,166667	16,666667	34,027778	36,805556	63,194444	1,1666667	1,2083333	-53,8	-49,5	0,0035876	23,57	-37,361111	-0,9092593
spiLA1589-mir8763	**205**	16,585366	30,243902	17,560976	35,609756	34,146341	65,853659	1,1774194	0,9444444	-85,4	-84,3	0,0131708	8,75	-41,658537	-0,7519481
spiLA1589-mir7997c-30	**146**	28,767123	27,39726	15,068493	28,767123	43,835616	56,164384	1,05	1,9090909	-48,9	-47,7	0,0133754	11,31	-33,493151	-1,0150943
spiLA1589-mir1917-2	**232**	16,810345	36,637931	14,224138	32,327586	31,034483	68,965517	0,8823529	1,1818182	-59,2	-50,11	0,0053871	25,84	-25,517241	-1,22
spiLA1589-mir1886f-5	**263**	14,068441	34,60076	17,490494	33,840304	31,558935	68,441065	0,978022	0,8043478	-86	-77,62	0,0004073	58,77	-32,69962	-0,7640625
spiLA1589-mir167h	**119**	20,168067	26,890756	24,369748	28,571429	44,537815	55,462185	1,0625	0,8275862	-49,4	-49,4	0,0393334	8,91	-41,512605	-0,8222222
spiLA1589-mir9553	**138**	19,565217	31,15942	20,289855	28,985507	39,855072	60,144928	0,9302326	0,9642857	-59,2	-59,2	0,11776	4,67	-42,898551	-1,0361446
spiLA1589-mir10538-3	**130**	15,384615	39,230769	16,153846	29,230769	31,538462	68,461538	0,745098	0,952381	-43,2	-40,6	0,144984	9,36	-33,230769	-0,9320755
spiLA1589-mir171c-3	**265**	20,377358	29,056604	19,245283	31,320755	39,622642	60,377358	1,0779221	1,0588235	-78,7	-65,7	0,0002669	50,88	-29,698113	-1,0763636
spiLA1589-mir399f-3	**126**	14,285714	28,571429	20,634921	36,507937	34,920635	65,079365	1,2777778	0,6923077	-47,6	-45,7	0,0813954	8,9	-37,777778	-1,0536585
spiLA1589-mir399f-2	**138**	18,115942	34,782609	15,217391	31,884058	33,333333	66,666667	0,9166667	1,1904762	-64,9	-64,7	0,0472321	8,71	-47,028986	-0,7495238
spiLA1589-mir5026-3	**85**	17,647059	36,470588	24,705882	21,176471	42,352941	57,647059	0,5806452	0,7142857	-26,2	-26,2	0,276839	6,57	-30,823529	-1,0818182
spiLA1589-mir397b-4	**126**	19,047619	30,15873	18,253968	32,539683	37,301587	62,698413	1,0789474	1,0434783	-49,6	-49,6	0,227047	3,27	-39,365079	-1,4108696
spiLA1589-mir7981b-15	**136**	18,382353	26,470588	16,176471	38,970588	34,558824	65,441176	1,4722222	1,1363636	-56	-52,2	0,0388909	10,96	-41,176471	-0,7277778
spiLA1589-mir6277	**247**	20,242915	32,388664	11,740891	35,62753	31,983806	68,016194	1,1	1,7241379	-62,9	-43,9	0,0001584	78,66	-25,465587	-1,0553191
spiLA1589-mir7981a-33	**149**	14,09396	35,57047	20,134228	30,201342	34,228188	65,771812	0,8490566	0,7	-45,8	-45,8	0,0906969	12,65	-30,738255	-1,1914894
spiLA1589-mir1917-3	**95**	18,947368	33,684211	11,578947	35,789474	30,526316	69,473684	1,0625	1,6363636	-22,3	-22,3	0,106891	19,13	-23,473684	-0,7962025
spiLA1589-mir7997c-31	**129**	27,131783	29,457364	18,604651	24,806202	45,736434	54,263566	0,8421053	1,4583333	-46,9	-46,97	0,0754675	9,23	-36,356589	-0,8980392
spiLA1589-mir399a-2	**176**	18,75	32,386364	17,613636	31,25	36,363636	63,636364	0,9649123	1,0645161	-62,4	-58,2	0,0027656	29,65	-35,454545	-0,7689655
spiLA1589-mir7981a-34	**128**	17,1875	28,125	14,84375	39,84375	32,03125	67,96875	1,4166667	1,1578947	-47	-43,6	0,0640242	10,84	-36,71875	-0,7949153
spiLA1589-mir8006-6	**181**	18,232044	27,071823	20,994475	33,701657	39,226519	60,773481	1,244898	0,8684211	-67,3	-66,9	0,0920172	11,21	-37,18232	-0,975
spiLA1589-mir7981b-16	**95**	23,157895	29,473684	21,052632	26,315789	44,210526	55,789474	0,8928571	1,1	-48	-45,4	0,260235	13,92	-50,526316	-1,1463415
spiLA1589-mir8006-7	**193**	17,61658	34,715026	20,725389	26,943005	38,341969	61,658031	0,7761194	0,85	-72,6	-64,4	0,0423944	24,11	-37,61658	-0,9478873
spiLA1589-mir7981a-35	**167**	14,371257	31,736527	18,562874	35,329341	32,934132	67,065868	1,1132075	0,7741935	-63,5	-63,5	0,103693	8,16	-38,023952	-0,9810811
spiLA1589-mir3515	**294**	19,047619	29,591837	17,006803	34,353741	36,054422	63,945578	1,1609195	1,12	-80,3	-66,5	0,0022594	47,15	-27,312925	-0,7394737
spiLA1589-mir5049b-1	**243**	21,8107	33,744856	11,522634	32,921811	33,333333	66,666667	0,9756098	1,8928571	-58	-56,5	0,0003185	27,56	-23,868313	-1,1545455
spiLA1589-mir7992-8	**155**	21,290323	29,677419	20	29,032258	41,290323	58,709677	0,9782609	1,0645161	-89,2	-88,7	0,0713096	6,39	-57,548387	-0,7575472
spiLA1589-mir10532-5	**111**	18,018018	33,333333	12,612613	36,036036	30,630631	69,369369	1,0810811	1,4285714	-45	-44,8	0,0437015	10,44	-40,540541	-0,7160494
spiLA1589-mir7981a-36	**181**	17,127072	34,80663	17,127072	30,939227	34,254144	65,745856	0,8888889	1	-94,8	-94,8	0,0710409	12,51	-52,375691	-1,39375
spiLA1589-mir7983-5	**227**	16,740088	37,004405	14,096916	32,15859	30,837004	69,162996	0,8690476	1,1875	-57	-53,1	0,0015462	48,99	-25,110132	-1,3235294
spiLA1589-mir6299	**285**	18,245614	37,54386	14,385965	29,824561	32,631579	67,368421	0,7943925	1,2682927	-75,5	-72,9	0,0048896	14,17	-26,491228	-1,5290323
spiLA1589-mir7981b-17	**224**	20,982143	30,803571	16,517857	31,696429	37,5	62,5	1,0289855	1,2702703	-63	-58,1	0,0001957	35,82	-28,125	-0,8142857
spiLA1589-mir5569	**99**	28,282828	20,20202	19,191919	32,323232	47,474747	52,525253	1,6	1,4736842	-37,6	-37,6	0,205842	5,02	-37,979798	-0,811828
spiLA1589-mir4249-2	**135**	19,259259	35,555556	11,111111	34,074074	30,37037	69,62963	0,9583333	1,7333333	-30,1	-20,5	0,0491195	26,35	-22,296296	-0,75
spiLA1589-mir5530	**170**	25,882353	25,294118	12,352941	36,470588	38,235294	61,764706	1,4418605	2,0952381	-52,9	-52,9	0,0312154	8,14	-31,117647	-0,8
spiLA1589-mir6135e	**213**	21,126761	34,741784	11,737089	32,394366	32,86385	67,13615	0,9324324	1,8	-53,5	-52,5	0,0056917	25,98	-25,117371	-0,7341463
spiLA1589-mir10532-6	**198**	19,69697	31,313131	12,626263	36,363636	32,323232	67,676768	1,1612903	1,56	-49,7	-49,7	0,0128262	30,86	-25,10101	-0,7642857
spiLA1589-mir6288c-2	**232**	18,965517	30,603448	12,5	37,931034	31,465517	68,534483	1,2394366	1,5172414	-63	-62	0,0129906	18,75	-27,155172	-0,74
spiLA1589-mir6293	**300**	20,666667	29,666667	19,666667	30	40,333333	59,666667	1,011236	1,0508475	-87,7	-83,5	0,0002776	42,22	-29,233333	-0,7765625
spiLA1589-mir9477-2	**147**	12,92517	31,972789	23,129252	31,972789	36,054422	63,945578	1	0,5588235	-46,9	-41,02	0,0303478	16,65	-31,904762	-0,8630137
spiLA1589-mir7822-3	**189**	14,814815	34,920635	15,873016	34,391534	30,687831	69,312169	0,9848485	0,9333333	-68,5	-67,6	0,0026827	13,38	-36,243386	-0,7247934
spiLA1589-mir1886i-4	**131**	16,793893	31,29771	17,557252	34,351145	34,351145	65,648855	1,097561	0,9565217	-42,7	-42,3	0,181523	7,68	-32,59542	-0,8849057
spiLA1589-mir5628-1	**135**	18,518519	35,555556	17,037037	28,888889	35,555556	64,444444	0,8125	1,0869565	-43,7	-40,6	0,055683	22,11	-32,37037	-1,1810345
spiLA1589-mir5628-2	**103**	21,359223	32,038835	15,533981	31,067961	36,893204	63,106796	0,969697	1,375	-49,7	-49,1	0,128409	7,13	-48,252427	-0,9488889
spiLA1589-mir1863	**99**	16,161616	32,323232	14,141414	37,373737	30,30303	69,69697	1,15625	1,1428571	-23,8	-23,8	0,406899	3,36	-24,040404	-1,3078947
spiLA1589-mir8006-8	**203**	15,270936	33,990148	17,241379	33,497537	32,512315	67,487685	0,9855072	0,8857143	-57,2	-57	0,0048855	24,87	-28,17734	-1
spiLA1589-mir482d-3	**129**	26,356589	30,232558	13,953488	29,457364	40,310078	59,689922	0,974359	1,8888889	-37,1	-21,19	0,0104492	32,49	-28,75969	-0,7933333
spiLA1589-mir5171b	**124**	17,741935	37,096774	16,129032	29,032258	33,870968	66,129032	0,7826087	1,1	-33,3	-28,1	0,0081116	16,83	-26,854839	-0,8666667
spiLA1589-mir7997c-32	**121**	24,793388	25,619835	14,049587	35,53719	38,842975	61,157025	1,3870968	1,7647059	-55,8	-52,1	0,0703448	8,27	-46,115702	-0,7134615
spiLA1589-mir390-5	**272**	15,441176	31,617647	15,073529	37,867647	30,514706	69,485294	1,1976744	1,0243902	-60,5	-49,2	0,0001519	76,92	-22,242647	-0,7928571
spiLA1589-mir11131	**82**	17,073171	35,365854	18,292683	29,268293	35,365854	64,634146	0,8275862	0,9333333	-32,2	-32,2	0,426762	1,53	-39,268293	-1,187234
spiLA1589-mir7981a-37	**143**	19,58042	37,762238	16,083916	26,573427	35,664336	64,335664	0,7037037	1,2173913	-49,8	-47,8	0,0209451	8,21	-34,825175	-1,1103448
spiLA1589-mir5049b-2	**324**	19,444444	37,345679	16,358025	26,851852	35,802469	64,197531	0,7190083	1,1886792	-88,1	-76,1	0,000286	51,78	-27,191358	-0,9764706
spiLA1589-mir2863a	**244**	24,590164	22,540984	17,213115	35,655738	41,803279	58,196721	1,5818182	1,4285714	-72,4	-63,2	0,0006825	53,46	-29,672131	-1,4134615
spiLA1589-mir11575-2	**202**	22,772277	25,247525	17,326733	34,653465	40,09901	59,90099	1,372549	1,3142857	-64,9	-59,9	0,0043538	29,89	-32,128713	-0,7594828
spiLA1589-mir1534	**89**	21,348315	33,707865	15,730337	29,213483	37,078652	62,921348	0,8666667	1,3571429	-23,7	-23,7	0,0684843	10,22	-26,629213	-0,7098039
spiLA1589-mir1533-2	**326**	19,018405	35,889571	14,723926	30,368098	33,742331	66,257669	0,8461538	1,2916667	-90,6	-88	4,39E-05	42,19	-27,791411	-0,8012346
spiLA1589-mir1886f-6	**112**	19,642857	28,571429	17,857143	33,928571	37,5	62,5	1,1875	1,1	-49,2	-49,2	0,139662	7,01	-43,928571	-0,7181818

spiLA1589-mir865-2	**168**	13,095238	39,285714	19,642857	27,97619	32,738095	67,261905	0,7121212	0,6666667	-40,1	-40,1	0,0830606	6,11	-23,869048	-1,1714286
spiLA1589-mir2111d-2	**153**	19,607843	30,065359	16,339869	33,986928	35,947712	64,052288	1,1304348	1,2	-38,8	-38,8	0,0077571	14,94	-25,359477	-0,8933333
spiLA1589-mir7984b-1	**197**	15,228426	34,517766	16,243655	34,010152	31,472081	68,527919	0,9852941	0,9375	-64,4	-64,4	0,0244475	14,25	-32,690355	-0,7054545
spiLA1589-mir7502c-3	**140**	15,714286	35	15,714286	33,571429	31,428571	68,571429	0,9591837	1	-45	-40,7	0,0340138	13,37	-32,142857	-0,7630435
spiLA1589-mir1127-3	**265**	16,981132	36,981132	15,09434	30,943396	32,075472	67,924528	0,8367347	1,125	-72	-68,7	0,0003574	31,18	-27,169811	-1,0387097
spiLA1589-mir7981a-38	**200**	15,5	30,5	17,5	36,5	33	67	1,1967213	0,8857143	-88,9	-86,68	0,0069318	15,61	-44,45	-1,0227273
spiLA1589-mir10532-7	**195**	17,948718	33,846154	19,487179	28,717949	37,435897	62,564103	0,8484848	0,9210526	-82,4	-80,4	0,0121632	11,84	-42,25641	-0,8470588
spiLA1589-mir156g	**185**	22,702703	32,432432	16,216216	28,648649	38,918919	61,081081	0,8833333	1,4	-51,9	-50,5	0,039732	9,27	-28,054054	-1,1287671
spiLA1589-mir1886f-7	**82**	18,292683	30,487805	14,634146	36,585366	32,926829	67,073171	1,2	1,25	-27,8	-27,8	0,244148	5,5	-33,902439	-0,7525424
spiLA1589-mir7981-10	**204**	16,666667	31,862745	16,666667	34,803922	33,333333	66,666667	1,0923077	1	-53	-41,71	0,0016557	47,47	-25,980392	-0,7208333
spiLA1589-mir8046-1	**263**	18,250951	29,277567	20,152091	32,319392	38,403042	61,596958	1,1038961	0,9056604	-89,6	-88,4	0,0034636	28,98	-34,068441	-1,0296296
spiLA1589-mir8009-2	**187**	18,181818	36,898396	16,57754	28,342246	34,759358	65,240642	0,7681159	1,0967742	-55	-44,4	0,002252	31,4	-29,411765	-0,8871287
spiLA1589-mir1886f-8	**87**	24,137931	25,287356	13,793103	36,781609	37,931034	62,068966	1,4545455	1,75	-34,8	-34,7	0,0456391	6,3	-40	-0,9656716
spiLA1589-mir7981a-39	**286**	17,482517	30,769231	15,034965	36,713287	32,517483	67,482517	1,1931818	1,1627907	-86	-82	0,0005455	27,62	-30,06993	-0,8461538
spiLA1589-mir5163a	**262**	16,793893	33,587786	14,885496	34,732824	31,679389	68,320611	1,0340909	1,1282051	-59,9	-59,5	0,0027014	35,78	-22,862595	-1,0545455
spiLA1589-mir5181b-2	**83**	19,277108	33,73494	14,457831	32,53012	33,73494	66,26506	0,9642857	1,3333333	-26,3	-26,3	0,144103	2,71	-31,686747	-0,9247312
spiLA1589-mir5382	**122**	18,032787	36,065574	22,95082	22,95082	40,983607	59,016393	0,6363636	0,7857143	-57,9	-54,8	0,0721108	4,92	-47,459016	-0,7216867
spiLA1589-mir166d-2	**75**	30,666667	17,333333	20	32	50,666667	49,333333	1,8461538	1,5333333	-35,8	-35,8	0,30084	2,07	-47,733333	-0,9392857
spiLA1589-mir5287a	**140**	17,142857	30,714286	17,142857	35	34,285714	65,714286	1,1395349	1	-51,1	-51,1	0,170251	4,43	-36,5	-1,158
spiLA1589-mir477-4	**79**	18,987342	31,64557	13,924051	35,443038	32,911392	67,088608	1,12	1,3636364	-22,4	-22,4	0,0660549	7,88	-28,35443	-1,0645833
spiLA1589-mir11463	**222**	20,27027	31,531532	16,666667	31,531532	36,936937	63,063063	1	1,2162162	-57,7	-48,07	0,005632	26,23	-25,990991	-0,8615385
spiLA1589-mir166c-2	**148**	20,945946	34,459459	12,162162	32,432432	33,108108	66,891892	0,9411765	1,7222222	-51,5	-44,5	0,0696188	22,24	-34,797297	-0,8222222
spiLA1589-mir7981b-18	**117**	19,65812	24,786325	20,512821	35,042735	40,17094	59,82906	1,4137931	0,9583333	-57,6	-57,6	0,0301727	11,7	-49,230769	-0,7036585
spiLA1589-mir11285	**113**	22,123894	30,088496	9,7345133	38,053097	31,858407	68,141593	1,2647059	2,2727273	-40,9	-39,5	0,0019822	15,35	-36,19469	-1,2255319
spiLA1589-mir6248	**206**	21,84466	31,553398	11,650485	34,951456	33,495146	66,504854	1,1076923	1,875	-48,5	-35,6	0,0016095	44,98	-23,543689	-1,0506667
spiLA1589-mir7981a-41	**115**	17,391304	24,347826	20,869565	37,391304	38,26087	61,73913	1,5357143	0,8333333	-52,6	-52,6	0,0787857	5,83	-45,73913	-1,1361111
spiLA1589-mir477d	**115**	20,869565	28,695652	12,173913	38,26087	33,043478	66,956522	1,3333333	1,7142857	-34,4	-34,4	0,153815	6,82	-29,913043	-0,7028986
spiLA1589-mir7981a-40	**228**	17,54386	35,087719	16,666667	30,701754	34,210526	65,789474	0,875	1,0526316	-98,5	-95,1	0,0143548	14,36	-43,201754	-1,1954545
spiLA1589-mir11409d	**127**	14,173228	33,858268	18,110236	33,858268	32,283465	67,716535	1	0,7826087	-44,1	-41,9	0,0208498	12,8	-34,724409	-0,9052632
spiLA1589-mir7997b-11	**176**	17,045455	30,681818	24,431818	27,840909	41,477273	58,522727	0,9074074	0,6976744	-70,8	-70,6	0,0821785	8,55	-40,227273	-1,2628205
spiLA1589-mir7981b-19	**110**	19,090909	25,454545	17,272727	38,181818	36,363636	63,636364	1,5	1,1052632	-49,9	-49,1	0,0991205	8,8	-45,363636	-1,0756098
spiLA1589-mir1917-4	**133**	16,541353	39,849624	15,789474	27,819549	32,330827	67,669173	0,6981132	1,047619	-31	-23,6	0,0571977	17,1	-23,308271	-0,969863
spiLA1589-mir6273-3	**167**	20,359281	28,742515	19,161677	31,736527	39,520958	60,479042	1,1041667	1,0625	-48	-43,3	0,0092226	21,33	-28,742515	-1,2475
spiLA1589-mir171b-4	**99**	17,171717	29,292929	23,232323	30,30303	40,40404	59,59596	1,0344828	0,7391304	-40,6	-40,6	0,320035	2,45	-41,010101	-0,7209302
spiLA1589-mir827b-2	**121**	14,049587	35,53719	20,661157	29,752066	34,710744	65,289256	0,8372093	0,68	-48,7	-48,7	0,247828	2,97	-40,247934	-0,7272727
spiLA1589-mir1917-5	**335**	16,41791	36,41791	14,029851	33,134328	30,447761	69,552239	0,9098361	1,1702128	-86,4	-78,6	0,0001812	55,85	-25,791045	-0,9891304
spiLA1589-mir1886f-9	**119**	17,647059	29,411765	18,487395	34,453782	36,134454	63,865546	1,1714286	0,9545455	-49,7	-46,2	0,0594033	13,52	-41,764706	-0,7809524
spiLA1589-mir159a-3	**112**	16,964286	38,392857	16,071429	28,571429	33,035714	66,964286	0,744186	1,0555556	-30,1	-30	0,0482024	5,93	-26,875	-1,1833333
spiLA1589-mir7981e-4	**158**	22,78481	27,21519	10,126582	39,873418	32,911392	67,088608	1,4651163	2,25	-36,6	-36,6	0,0084394	20,46	-23,164557	-0,8069767
spiLA1589-mir8046-2	**199**	16,080402	32,160804	18,090452	33,668342	34,170854	65,829146	1,046875	0,8888889	-62,2	-59,7	0,0044282	21,15	-31,256281	-0,7038462
spiLA1589-mir3706	**70**	27,142857	27,142857	18,571429	27,142857	45,714286	54,285714	1	1,4615385	-36,6	-36,6	0,664442	0,99	-52,285714	-0,9152542
spiLA1589-mir7981d-16	**222**	18,918919	34,684685	17,117117	29,279279	36,036036	63,963964	0,8441558	1,1052632	-98,5	-94	0,0055439	23,67	-44,369369	-0,9147059
spiLA1589-mir7701-1	**156**	24,358974	29,487179	15,384615	30,769231	39,74359	60,25641	1,0434783	1,5833333	-47	-43	0,0120827	36,68	-30,128205	-1,14375
spiLA1589-mir5303-3	**125**	17,6	25,6	24,8	32	42,4	57,6	1,25	0,7096774	-37,2	-34,6	0,0225732	14,94	-29,76	-1,23125
spiLA1589-mir156b-14	**243**	18,930041	29,62963	18,106996	33,333333	37,037037	62,962963	1,125	1,0454545	-83,9	-67,89	0,0021219	38,97	-34,526749	-0,7580645
spiLA1589-mir7981a-42	**269**	14,869888	32,342007	16,728625	36,05948	31,598513	68,401487	1,1149425	0,8888889	-97,4	-94,6	0,0033261	21,01	-36,208178	-0,7018868
spiLA1589-mir7981a-43	**147**	19,047619	38,77551	12,92517	29,251701	31,972789	68,027211	0,754386	1,4736842	-62,5	-62,5	0,10063	6,87	-42,517007	-0,9322222
spiLA1589-mir7997c-33	**126**	26,984127	25,396825	20,634921	26,984127	47,619048	52,380952	1,0625	1,3076923	-62	-61,4	0,102572	5,77	-49,206349	-1,1458824
spiLA1589-mir7981d-17	**280**	20	30	15,714286	34,285714	35,714286	64,285714	1,1428571	1,2727273	-99,6	-95,8	0,0042832	18,31	-35,571429	-1,3297872
spiLA1589-mir7981a-44	**190**	18,421053	28,947368	15,789474	36,842105	34,210526	65,789474	1,2727273	1,1666667	-94,1	-90,2	0,0070135	12,78	-49,526316	-1,0333333
spiLA1589-mir3512-2	**81**	19,753086	37,037037	16,049383	27,160494	35,802469	64,197531	0,7333333	1,2307692	-26,3	-26,3	0,2245	3,53	-32,469136	-0,996
spiLA1589-mir8672	**333**	21,321321	33,033033	15,915916	29,72973	37,237237	62,762763	0,9	1,3396226	-88,4	-74,6	2,37E-05	69,84	-26,546547	-0,9068966
spiLA1589-mir1886f-10	**111**	20,720721	27,927928	17,117117	34,234234	37,837838	62,162162	1,2258065	1,2105263	-51,4	-51,4	0,176018	5,34	-46,306306	-0,7223684
spiLA1589-mir1043-2	**221**	17,19457	29,864253	13,574661	39,366516	30,769231	69,230769	1,3181818	1,2666667	-74,7	-74,7	0,0073968	13,66	-33,800905	-0,7129032
spiLA1589-mir7997c-34	**131**	25,19084	26,717557	16,793893	31,29771	41,984733	58,015267	1,1714286	1,5	-43,2	-36,7	0,0067255	18,32	-32,977099	-1,2238095
spiLA1589-mir7492f-2	**210**	17,142857	31,428571	15,714286	35,714286	32,857143	67,142857	1,1363636	1,0909091	-69,4	-62,6	0,0081434	17,25	-33,047619	-1,0985294
spiLA1589-mir7981-11	**267**	18,35206	33,333333	18,35206	29,962547	36,70412	63,29588	0,8988764	1	-95	-87,6	0,0025836	30,86	-35,580524	-0,7854545
spiLA1589-mir8610	**151**	27,81457	21,854305	21,854305	28,476821	49,668874	50,331126	1,3030303	1,2727273	-53,4	-53,2	0,0210505	28,18	-35,364238	-1,0057971
spiLA1589-mir7997c-36	**109**	20,183486	30,275229	19,266055	30,275229	39,449541	60,550459	1	1,047619	-42,8	-41,22	0,0727514	12,91	-39,266055	-0,9693878
spiLA1589-mir7997c-35	**128**	27,34375	26,5625	20,3125	25,78125	47,65625	52,34375	0,9705882	1,3461538	-66,4	-64,1	0,044684	5,32	-51,875	-0,9953488
spiLA1589-mir9409	**230**	19,565217	31,73913	15,652174	33,043478	35,217391	64,782609	1,0410959	1,25	-56,7	-45,8	0,0006736	38,66	-24,652174	-0,7318841
spiLA1589-mir7981b-20	**112**	16,071429	29,464286	19,642857	34,821429	35,714286	64,285714	1,1818182	0,8181818	-41,1	-41,1	0,095439	7,74	-36,696429	-1,0885246
spiLA1589-mir8615	**226**	18,584071	27,876106	18,584071	34,955752	37,168142	62,831858	1,2539683	1	-67,1	-61,5	0,0034232	29,89	-29,690265	-0,7
spiLA1589-mir7984b-2	**248**	13,709677	37,096774	17,33871	31,854839	31,048387	68,951613	0,8586957	0,7906977	-59,8	-54,7	0,0001744	33,81	-24,112903	-1,0275
spiLA1589-mir5021-2	**99**	28,282828	38,383838	15,151515	18,181818	43,434343	56,565657	0,4736842	1,8666667	-33	-31,8	0,507801	2,2	-33,333333	-0,7988095
spiLA1589-mir6283-2	**89**	21,348315	30,337079	13,483146	34,831461	34,831461	65,168539	1,1481481	1,5833333	-31,4	-30,6	0,119342	5,96	-35,280899	-0,7674419

spiLA1589-mir5567	**70**	27,142857	24,285714	17,142857	31,428571	44,285714	55,714286	1,2941176	1,5833333	-28,7	-28,7	0,258827	4,75	-41	-0,9274603
spiLA1589-mir11085-2	**210**	14,285714	30,952381	17,142857	37,619048	31,428571	68,571429	1,2153846	0,8333333	-58	-55,9	0,0536059	28,11	-27,619048	-1,0129032
spiLA1589-mir11314-2	**317**	18,927445	30,914826	16,088328	34,069401	35,015773	64,984227	1,1020408	1,1764706	-81,8	-66,1	2,17E-05	62,41	-25,804416	-0,9258065
spiLA1589-mir482c-1	**288**	20,138889	36,111111	18,055556	25,694444	38,194444	61,805556	0,7115385	1,1153846	-77	-69,3	0,0014187	49,96	-26,736111	-0,8787879
spiLA1589-mir1513c	**182**	27,472527	26,923077	15,934066	29,67033	43,406593	56,593407	1,1020408	1,7241379	-55,7	-53	0,0011304	33,35	-30,604396	-0,7369369
spiLA1589-mir5026-4	**173**	17,34104	34,682081	19,653179	28,323699	36,99422	63,00578	0,8166667	0,8823529	-77,6	-75	0,045245	15,33	-44,855491	-0,7
spiLA1589-mir11580	**288**	16,319444	28,125	17,708333	37,847222	34,027778	65,972222	1,345679	0,9215686	-71,9	-42,17	3,84E-05	84,51	-24,965278	-0,7050633
spiLA1589-mir7997c-37	**126**	21,428571	29,365079	17,460317	31,746032	38,888889	61,111111	1,0810811	1,2272727	-52,7	-52,7	0,143485	5,85	-41,825397	-0,7336735
spiLA1589-mir7543-3	**81**	24,691358	29,62963	14,814815	30,864198	39,506173	60,493827	1,0416667	1,6666667	-31,5	-30,1	0,213416	7,51	-38,888889	-1,0755102
spiLA1589-mir7981a-45	**110**	17,272727	33,636364	19,090909	30	36,363636	63,636364	0,8918919	0,9047619	-41,2	-41,2	0,138227	6,41	-37,454545	-0,9388235
spiLA1589-mir7981a-46	**312**	17,948718	32,051282	17,948718	32,051282	35,897436	64,102564	1	1	-93,5	-86,8	0,0003718	49,72	-29,967949	-0,984375
spiLA1589-mir5014a-6	**196**	14,795918	33,163265	15,816327	36,22449	30,612245	69,387755	1,0923077	0,9354839	-63,1	-60,1	0,0009663	19,92	-32,193878	-1,03
spiLA1589-mir5057-3	**105**	20	34,285714	17,142857	28,571429	37,142857	62,857143	0,8333333	1,1666667	-28,3	-26,5	0,0706513	11,25	-26,952381	-0,8348214
spiLA1589-mir7997c-38	**174**	19,54023	31,034483	17,241379	32,183908	36,781609	63,218391	1,037037	1,1333333	-63,8	-62,4	0,0121098	12,66	-36,666667	-1,0516667
spiLA1589-mir1128-8	**108**	16,666667	36,111111	14,814815	32,407407	31,481481	68,518519	0,8974359	1,125	-25,5	-20,2	0,0117931	20,03	-23,611111	-0,725641
spiLA1589-mir7981a-47	**123**	18,699187	35,772358	19,512195	26,01626	38,211382	61,788618	0,7272727	0,9583333	-54	-53	0,079192	10,47	-43,902439	-0,996875
spiLA1589-mir7983-6	**221**	15,384615	38,00905	16,289593	30,316742	31,674208	68,325792	0,797619	0,9444444	-59,8	-58,9	0,0013464	24,97	-27,058824	-0,75
spiLA1589-mir8739-2	**248**	20,967742	29,83871	17,33871	31,854839	38,306452	61,693548	1,0675676	1,2093023	-93,2	-91,6	0,0019832	18,05	-37,580645	-1,1489362
spiLA1589-mir7701-2	**289**	24,567474	28,027682	13,148789	34,256055	37,716263	62,283737	1,2222222	1,8684211	-89,3	-79,8	0,0049778	26,15	-30,899654	-0,8542857
spiLA1589-mir7981d-18	**168**	12,5	32,738095	17,857143	36,904762	30,357143	69,642857	1,1272727	0,7	-37,8	-22,89	0,0039877	34,43	-22,5	-0,9810526
spiLA1589-mir482d-4	**171**	16,959064	34,502924	18,71345	29,824561	35,672515	64,327485	0,8644068	0,90625	-63,3	-53,9	0,0037445	23,43	-37,017544	-0,8192661
spiLA1589-mir7981a-48	**238**	17,647059	32,352941	15,546218	34,453782	33,193277	66,806723	1,0649351	1,1351351	-99,8	-99,5	0,0141195	13,41	-41,932773	-0,7411765
spiLA1589-mir395a-2	**163**	21,472393	28,834356	17,791411	31,90184	39,263804	60,736196	1,106383	1,2068966	-62,4	-62,4	0,0650395	16,34	-38,282209	-1,0377049
spiLA1589-mir7981a-49	**175**	17,142857	30,857143	21,142857	30,857143	38,285714	61,714286	1	0,8108108	-68,2	-64,4	0,0186173	28,84	-38,971429	-1,2632911
spiLA1589-mir9477-3	**186**	23,11828	32,795699	11,290323	32,795699	34,408602	65,591398	1	2,047619	-49	-45,12	0,0005356	39,58	-26,344086	-0,975
spiLA1589-mir1043-3	**297**	18,518519	30,976431	13,804714	36,700337	32,323232	67,676768	1,1847826	1,3414634	-71,6	-63,1	4,10E-05	57,52	-24,107744	-1,0179104
spiLA1589-mir7981a-50	**122**	21,311475	33,606557	18,032787	27,04918	39,344262	60,655738	0,804878	1,1818182	-55,8	-54,2	0,107172	7,54	-45,737705	-0,765625
spiLA1589-mir1040	**127**	28,346457	18,110236	23,622047	29,92126	51,968504	48,031496	1,6521739	1,2	-46,4	-35,34	0,029914	24,19	-36,535433	-0,7246914
spiLA1589-mir7981b-21	**129**	17,054264	32,55814	13,178295	37,209302	30,232558	69,767442	1,1428571	1,2941176	-50,2	-49,3	0,135803	4,95	-38,914729	-0,7394737
spiLA1589-mir319d	**202**	25,247525	23,267327	20,792079	30,693069	46,039604	53,960396	1,3191489	1,2142857	-92,4	-91,6	0,041103	6,71	-45,742574	-0,7030303
spiLA1589-mir7997c-39	**113**	20,353982	25,663717	17,699115	36,283186	38,053097	61,946903	1,4137931	1,15	-39,8	-39,8	0,181235	11,19	-35,221239	-1,2871795
spiLA1589-mir5303-4	**205**	21,95122	21,95122	20	36,097561	41,95122	58,04878	1,6444444	1,097561	-68,4	-49,5	0,0003501	49,5	-33,365854	-0,9935484
spiLA1589-mir8006-9	**218**	19,266055	33,944954	15,59633	31,192661	34,862385	65,137615	0,9189189	1,2352941	-86,1	-80,8	0,0037063	22,44	-39,495413	-0,9255814
spiLA1589-mir857-2	**161**	19,254658	27,950311	18,012422	34,782609	37,267081	62,732919	1,2444444	1,0689655	-64,5	-62,3	0,016799	14,97	-40,062112	-0,7953488
spiLA1589-mir6145e	**186**	17,204301	31,182796	14,516129	37,096774	31,72043	68,27957	1,1896552	1,1851852	-49,1	-40,4	0,0010979	39,43	-26,397849	-1,1328947
spiLA1589-mir7728	**176**	17,045455	34,090909	17,613636	31,25	34,659091	65,340909	0,9166667	0,9677419	-75,8	-75,8	0,17058	13,7	-43,068182	-1,075
spiLA1589-mir482e-2	**79**	21,518987	25,316456	16,455696	36,708861	37,974684	62,025316	1,45	1,3076923	-42,3	-42,3	0,125589	6,35	-53,544304	-0,8322034
spiLA1589-mir7997c-40	**156**	25	28,846154	18,589744	27,564103	43,589744	56,410256	0,9555556	1,3448276	-72,6	-70,4	0,0458824	6,78	-46,538462	-1,242623
spiLA1589-mir816	**215**	13,488372	30,697674	18,139535	37,674419	31,627907	68,372093	1,2272727	0,7435897	-47,8	-40,3	0,0054797	24,85	-22,232558	-1,41
spiLA1589-mir6022-2	**231**	18,181818	30,735931	19,480519	31,601732	37,662338	62,337662	1,028169	0,9333333	-91,6	-91,6	0,005125	14,56	-39,65368	-1,0676471
spiLA1589-mir396b-4	**280**	16,785714	28,571429	15,357143	39,285714	32,142857	67,857143	1,375	1,0930233	-65,2	-63,7	0,0009063	44,72	-23,285714	-1,0528736
spiLA1589-mir7997c-41	**122**	20,491803	29,508197	22,131148	27,868852	42,622951	57,377049	0,9444444	0,9259259	-50,2	-50,2	0,114311	6	-41,147541	-0,7863636
spiLA1589-mir3637-2	**89**	20,224719	31,460674	13,483146	34,831461	33,707865	66,292135	1,1071429	1,5	-22,3	-22,3	0,194488	10,41	-25,05618	-0,7244444
spiLA1589-mir7533c	**180**	18,888889	36,666667	16,111111	28,333333	35	65	0,7727273	1,1724138	-48,2	-43,2	0,0017025	28,4	-26,777778	-0,9653846
spiLA1589-mir482b	**110**	20	28,181818	18,181818	33,636364	38,181818	61,818182	1,1935484	1,1	-67,6	-67,5	0,111525	3,91	-61,454545	-0,7433333
spiLA1589-mir8138	**138**	21,014493	28,985507	19,565217	30,434783	40,57971	59,42029	1,05	1,0740741	-59,8	-54,3	0,0174319	16,34	-43,333333	-1,6095238
spiLA1589-mir8557	**150**	16,666667	28	17,333333	38	34	66	1,3571429	0,9615385	-36	-34,68	0,0134871	19,47	-24	-0,7927711
spiLA1589-mir7505b	**186**	19,892473	30,645161	22,043011	27,419355	41,935484	58,064516	0,8947368	0,902439	-58,4	-57,7	0,0076555	20,02	-31,397849	-1,0678571
spiLA1589-mir3434	**239**	23,849372	24,267782	17,991632	33,891213	41,841004	58,158996	1,3965517	1,3255814	-74,7	-68,1	0,0008607	40,76	-31,25523	-0,7058824
spiLA1589-mir7981-12	**298**	20,469799	30,536913	13,758389	35,234899	34,228188	65,771812	1,1538462	1,4878049	-72,4	-49	3,28E-05	49,84	-24,295302	-0,7487179
spiLA1589-mir11076	**109**	20,183486	36,697248	16,513761	26,605505	36,697248	63,302752	0,725	1,2222222	-33,2	-33,2	0,159309	7,65	-30,458716	-0,747
spiLA1589-mir8771f	**160**	13,75	33,125	17,5	35,625	31,25	68,75	1,0754717	0,7857143	-35,5	-35,5	0,0027966	15,4	-22,1875	-0,7098039
spiLA1589-mir7981a-51	**102**	20,588235	36,27451	23,529412	19,607843	44,117647	55,882353	0,5405405	0,875	-55	-55	0,581516	1,09	-53,921569	-0,83
spiLA1589-mir482c-2	**99**	23,232323	24,242424	28,282828	24,242424	51,515152	48,484848	1	0,8214286	-35,9	-34,7	0,111243	9,73	-36,262626	-0,71
spiLA1589-mir7997c-42	**130**	16,153846	35,384615	21,538462	26,923077	37,692308	62,307692	0,7608696	0,75	-38,3	-38,3	0,0330856	9,11	-29,461538	-0,7039216
spiLA1589-mir8594	**116**	20,689655	34,482759	14,655172	30,172414	35,344828	64,655172	0,875	1,4117647	-32	-30,2	0,046331	7,14	-27,586207	-0,7122449
spiLA1589-mir7981a-52	**187**	16,042781	35,294118	18,716578	29,946524	34,759358	65,240642	0,8484848	0,8571429	-73,5	-73,2	0,0240947	12,02	-39,28877	-0,7816327
spiLA1589-mir3950	**295**	21,016949	31,525424	9,8305085	37,627119	30,847458	69,152542	1,1935484	2,137931	-69	-57,4	1,76E-05	61,49	-23,389831	-1,1303077
spiLA1589-mir7997c-43	**97**	22,680412	26,804124	17,525773	32,989691	40,206186	59,793814	1,2307692	1,2941176	-47,2	-47,2	0,258028	3,95	-48,659794	-1,0142857
spiLA1589-mir156b-15	**138**	18,84058	33,333333	17,391304	30,434783	36,231884	63,768116	0,9130435	1,0833333	-54,9	-54,8	0,039747	7,49	-39,782609	-0,7582418
spiLA1589-mir394-3	**185**	14,594595	24,864865	15,675676	44,864865	30,27027	69,72973	1,8043478	0,9310345	-65	-64,2	0,0394065	10,19	-35,135135	-1,2102564
spiLA1589-mir9726	**220**	17,272727	32,272727	13,181818	37,272727	30,454545	69,545455	1,1549296	1,3103448	-51,9	-43,1	0,0013384	41,67	-23,590909	-1,098
spiLA1589-mir11592-2	**65**	23,076923	33,846154	18,461538	24,615385	41,538462	58,461538	0,7272727	1,25	-25,9	-25,9	0,163024	3,26	-39,846154	-1,1607143
spiLA1589-mir6020a	**135**	17,037037	34,814815	15,555556	32,592593	32,592593	67,407407	0,9361702	1,0952381	-49,3	-49,3	0,204405	5,78	-36,518519	-0,9592593
spiLA1589-mir7987-2	**118**	16,949153	30,508475	16,949153	35,59322	33,898305	66,101695	1,1666667	1	-32,5	-32,5	0,186562	4,41	-27,542373	-1,1204545
spiLA1589-mir1917-6	**136**	18,382353	37,5	15,441176	28,676471	33,823529	66,176471	0,7647059	1,1904762	-41,3	-40,1	0,0292818	10,44	-30,367647	-1,0804348

spiLA1589-mir828b-2	**138**	14,492754	33,333333	17,391304	34,782609	31,884058	68,115942	1,0434783	0,8333333	-37,6	-34	0,0288378	13,51	-27,246377	-0,8125
spiLA1589-mir859	**302**	21,192053	30,463576	11,258278	37,086093	32,450331	67,549669	1,2173913	1,8823529	-69,8	-61,8	4,54E-05	74,32	-23,112583	-0,8978261
spiLA1589-mir9477-4	**181**	17,679558	31,491713	16,022099	34,80663	33,701657	66,298343	1,1052632	1,1034483	-86,6	-86,6	0,016793	8,5	-47,845304	-0,8545455
spiLA1589-mir11136	**96**	21,875	29,166667	11,458333	37,5	33,333333	66,666667	1,2857143	1,9090909	-23	-20,3	0,0649264	11,49	-23,958333	-1,4196721
spiLA1589-mir8006-10	**180**	23,888889	27,777778	19,444444	28,888889	43,333333	56,666667	1,04	1,2285714	-96,5	-96,5	0,0811866	7,12	-53,611111	-0,71875
spiLA1589-mir7997c-44	**115**	31,304348	24,347826	18,26087	26,086957	49,565217	50,434783	1,0714286	1,7142857	-50,2	-50,2	0,0695107	10,69	-43,652174	-1,2371795
spiLA1589-mir10532-8	**205**	21,463415	23,902439	12,682927	41,95122	34,146341	65,853659	1,755102	1,6923077	-52,1	-48,1	0,0012961	21,99	-25,414634	-0,8807018
spiLA1589-mir1916	**228**	17,105263	33,77193	15,789474	33,333333	32,894737	67,105263	0,987013	1,0833333	-90,1	-90,1	0,0038152	11,81	-39,517544	-0,7816667
spiLA1589-mir865-3	**109**	16,513761	36,697248	17,431193	29,357798	33,944954	66,055046	0,8	0,9473684	-39,1	-31,1	0,129756	32,54	-35,87156	-0,7442857
spiLA1589-mir536	**199**	35,678392	16,080402	25,628141	22,613065	61,306533	38,693467	1,40625	1,3921569	-97	-97	0,0067583	12,31	-48,743719	-1,2013333
spiLA1589-mir10538-4	**135**	16,296296	32,592593	16,296296	34,814815	32,592593	67,407407	1,0681818	1	-60	-60	0,164913	5,46	-44,444444	-1,0567568
spiLA1589-mir7981a-53	**211**	17,535545	36,018957	17,061611	29,383886	34,597156	65,402844	0,8157895	1,0277778	-97,4	-91	0,007038	15,44	-46,161137	-0,795082
spiLA1589-mir7998	**219**	23,744292	29,223744	21,004566	26,027397	44,748858	55,251142	0,890625	1,1304348	-71,9	-66,3	0,0007424	40,84	-32,83105	-1,3636364
spiLA1589-mir6273-4	**178**	18,539326	26,966292	19,101124	35,393258	37,640449	62,359551	1,3125	0,9705882	-90,4	-88,7	0,218218	6	-50,786517	-1,3342466
spiLA1589-mir7120b	**125**	29,6	24	20,8	25,6	50,4	49,6	1,0666667	1,4230769	-46	-39,4	0,152644	8,51	-36,8	-0,7336735
spiLA1589-mir7981a-54	**166**	17,46988	36,144578	18,072289	28,313253	35,542169	64,457831	0,7833333	0,9666667	-84,4	-83,4	0,163248	11,15	-50,843373	-1,3492537
spiLA1589-mir5369	**124**	26,612903	31,451613	15,322581	26,612903	41,935484	58,064516	0,8461538	1,7368421	-40	-40	0,055982	8,23	-32,258065	-0,7301587
spiLA1589-mir395g-2	**150**	21,333333	30,666667	16,666667	31,333333	38	62	1,0217391	1,28	-43,3	-41,7	0,012021	20,92	-28,866667	-1,4305085
spiLA1589-mir7997c-45	**95**	18,947368	30,526316	23,157895	27,368421	42,105263	57,894737	0,8965517	0,8181818	-36,5	-36,18	0,0913363	6,35	-38,4	-0,7692308
spiLA1589-mir7981a-55	**115**	19,130435	25,217391	17,391304	38,26087	36,521739	63,478261	1,5172414	1,1	-49,3	-48,9	0,0844013	4,83	-42,869565	-0,7596491
spiLA1589-mir5014a-7	**199**	15,577889	34,170854	17,58794	32,663317	33,165829	66,834171	0,9558824	0,8857143	-46,6	-33,1	0,0025869	42,66	-23,417085	-0,912
spiLA1589-mir11085-3	**312**	16,025641	31,089744	18,910256	33,974359	34,935897	65,064103	1,0927835	0,8474576	-78,7	-64,6	1,89E-05	64,49	-25,224359	-1,1738095
spiLA1589-mir6160	**229**	19,213974	31,441048	15,720524	33,624454	34,934498	65,065502	1,0694444	1,2222222	-57,6	-54,7	0,0061061	33,89	-25,152838	-0,7060606
spiLA1589-mir5083-2	**274**	20,437956	29,927007	17,883212	31,751825	38,321168	61,678832	1,0609756	1,1428571	-79,3	-73,9	0,0001701	47,98	-28,941606	-0,7220183
spiLA1589-mir1147	**257**	19,455253	30,350195	19,066148	31,128405	38,521401	61,478599	1,025641	1,0204082	-73,3	-64,2	0,0001569	50,6	-28,521401	-0,72
spiLA1589-mir11088b	**211**	19,905213	32,227488	11,374408	36,492891	31,279621	68,720379	1,1323529	1,75	-48,8	-39,1	0,0006677	49,12	-23,127962	-0,7552381
spiLA1589-mir7981a-56	**166**	16,86747	34,939759	19,879518	28,313253	36,746988	63,253012	0,8103448	0,8484848	-74	-73,3	0,111292	7,67	-44,578313	-0,740404
spiLA1589-mir3693c	**327**	15,902141	24,159021	16,819572	43,119266	32,721713	67,278287	1,7848101	0,9454545	-82,7	-71,7	0,0002517	62,7	-25,29052	-0,7393939
spiLA1589-mir10532-9	**279**	17,921147	35,125448	13,978495	32,97491	31,899642	68,100358	0,9387755	1,2820513	-64,9	-61,4	0,0011429	35,38	-23,261649	-1,2131148
spiLA1589-mir10519-3	**266**	18,796992	29,323308	13,533835	38,345865	32,330827	67,669173	1,3076923	1,3888889	-70,1	-44	3,98E-05	99,09	-26,353383	-0,7728972
spiLA1589-mir395b-1	**170**	25,882353	26,470588	16,470588	31,176471	42,352941	57,647059	1,1777778	1,5714286	-64,3	-64,3	0,111808	14,13	-37,823529	-0,7292135
spiLA1589-mir395b-2	**170**	25,294118	26,470588	17,647059	30,588235	42,941176	57,058824	1,1555556	1,4333333	-61,3	-54,9	0,0395845	23,82	-36,058824	-0,8151163
spiLA1589-mir395j-3	**118**	24,576271	25,423729	16,949153	33,050847	41,525424	58,474576	1,3	1,45	-47,7	-47,7	0,219613	8,07	-40,423729	-0,8930556
spiLA1589-mir395c	**151**	19,86755	33,774834	14,569536	31,788079	34,437086	65,562914	0,9411765	1,3636364	-37,8	-34,1	0,0211106	25,22	-25,033113	-0,839726
spiLA1589-mir7981a-57	**233**	14,592275	37,339056	16,309013	31,759657	30,901288	69,098712	0,8505747	0,8947368	-83,8	-82,7	0,0048961	18,92	-35,965665	-0,9734694
spiLA1589-mir7997c-46	**131**	17,557252	32,061069	22,137405	28,244275	39,694656	60,305344	0,8809524	0,7931034	-54,8	-51,4	0,0217096	12,73	-41,832061	-0,7269231
spiLA1589-mir7981a-58	**182**	17,032967	32,967033	20,879121	29,120879	37,912088	62,087912	0,8833333	0,8157895	-97,3	-97,3	0,198808	3,96	-53,461538	-1,1638889
spiLA1589-mir7997b-12	**124**	16,935484	30,645161	23,387097	29,032258	40,322581	59,677419	0,9473684	0,7241379	-54,9	-54,9	0,297759	4,35	-44,274194	-1,0538462
spiLA1589-mir7981a-59	**122**	16,393443	38,52459	20,491803	24,590164	36,885246	63,114754	0,6382979	0,8	-41,7	-40,12	0,0484766	10,01	-34,180328	-1,4101449
spiLA1589-mir8124	**255**	19,607843	31,372549	12,941176	36,078431	32,54902	67,45098	1,15	1,5151515	-71,6	-71	0,0010816	21,3	-28,078431	-1,098
spiLA1589-mir7981-13	**241**	18,257261	35,26971	16,182573	30,290456	34,439834	65,560166	0,8588235	1,1282051	-77,1	-76,8	0,0032498	16,64	-31,991701	-0,8626506
spiLA1589-mir6430	**204**	18,627451	30,392157	19,117647	31,862745	37,745098	62,254902	1,0483871	0,974359	-55,3	-48,5	0,009611	24,02	-27,107843	-0,7634409
spiLA1589-mir7981a-60	**123**	18,699187	29,268293	17,886179	34,146341	36,585366	63,414634	1,1666667	1,0454545	-64,1	-63,4	0,155115	8,15	-52,113821	-0,94
spiLA1589-mir2597	**121**	19,008264	31,404959	13,22314	36,363636	32,231405	67,768595	1,1578947	1,4375	-28,9	-28,7	0,011422	9,52	-23,884298	-0,7181818
spiLA1589-mir8639e	**174**	15,517241	38,505747	15,517241	30,45977	31,034483	68,965517	0,7910448	1	-59,6	-58,8	0,0353122	10,18	-34,252874	-1,4244444
spiLA1589-mir7981b-22	**100**	23	27	18	32	41	59	1,1851852	1,2777778	-47,9	-45,4	0,178308	9,31	-47,9	-0,7410256
spiLA1589-mir7981a-61	**284**	18,309859	31,338028	15,140845	35,211268	33,450704	66,549296	1,1235955	1,2093023	-76,1	-66,5	0,0001809	56,85	-26,795775	-1,1682927
spiLA1589-mir7492f-3	**264**	15,151515	27,651515	16,666667	40,530303	31,818182	68,181818	1,4657534	0,9090909	-85,6	-82,3	0,0012729	21,43	-32,424242	-0,7294118
spiLA1589-mir5218	**175**	18,857143	35,428571	17,142857	28,571429	36	64	0,8064516	1,1	-56	-52,4	0,0078454	23,47	-32	-0,815873
spiLA1589-mir7983-7	**104**	14,423077	32,692308	17,307692	35,576923	31,730769	68,269231	1,0882353	0,8333333	-24	-24	0,111195	6,82	-23,076923	-1,0190476
spiLA1589-mir1044-3	**198**	14,141414	38,383838	20,707071	26,767677	34,848485	65,151515	0,6973684	0,6829268	-52,4	-53,16	0,0330451	11,66	-26,459596	-0,8888889
spiLA1589-mir7981b-23	**81**	19,753086	34,567901	19,753086	25,925926	39,506173	60,493827	0,75	1	-35,6	-35,6	0,447879	2,41	-43,950617	-0,7272727
spiLA1589-mir172a-3	**142**	20,422535	33,098592	14,084507	32,394366	34,507042	65,492958	0,9787234	1,45	-55,4	-54,5	0,0249561	15,23	-39,014085	-1,1125
spiLA1589-mir7997c-47	**123**	17,886179	30,894309	20,325203	30,894309	38,211382	61,788618	1	0,88	-49,7	-47,8	0,15839	10,27	-40,406504	-0,7794118
spiLA1589-mir8006-11	**224**	19,196429	31,696429	18,75	30,357143	37,946429	62,053571	0,9577465	1,0238095	-83,6	-81,2	0,0031293	18,47	-37,321429	-1,1306122
spiLA1589-mir169l	**184**	18,478261	36,413043	20,652174	24,456522	39,130435	60,869565	0,6716418	0,8947368	-57,5	-49,6	0,0085437	19,49	-31,25	-1,0574468
spiLA1589-mir2873b	**221**	19,909502	34,38914	15,384615	30,316742	35,294118	64,705882	0,8815789	1,2941176	-70,6	-69,8	0,0438028	13,74	-31,945701	-0,9835294
spiLA1589-mir1521b-2	**212**	17,924528	29,245283	17,924528	34,90566	35,849057	64,150943	1,1935484	1	-77,2	-68,05	0,0016151	28,58	-36,415094	-0,7986111
spiLA1589-mir11583b-2	**261**	22,988506	32,56705	13,409962	31,034483	36,398467	63,601533	0,9529412	1,7142857	-69,4	-67,7	0,0009113	47	-26,590038	-0,9051282
spiLA1589-mir6144	**202**	20,792079	22,772277	17,326733	39,108911	38,118812	61,881188	1,7173913	1,2	-56,1	-49,9	0,0021521	24,45	-27,772277	-1,0157895
spiLA1589-mir5026-5	**94**	20,212766	35,106383	26,595745	18,085106	46,808511	53,191489	0,5151515	0,76	-34	-34	0,263884	5,7	-36,170213	-0,7305263
spiLA1589-mir7997c-48	**106**	25,471698	28,301887	15,09434	31,132075	40,566038	59,433962	1,1	1,6875	-49,5	-49,5	0,10552	8,23	-46,698113	-0,7285714
spiLA1589-mir7981-14	**259**	18,532819	36,293436	13,899614	31,274131	32,432432	67,567568	0,8617021	1,3333333	-85	-83,3	0,0073421	19,78	-32,818533	-1,1511628
spiLA1589-mir10532-10	**94**	20,212766	29,787234	12,765957	37,234043	32,978723	67,021277	1,25	1,5833333	-22,5	-22,5	0,119698	13,88	-23,93617	-0,847619
spiLA1589-mir7981a-63	**182**	17,582418	28,571429	17,582418	36,263736	35,164835	64,835165	1,2692308	1	-80,8	-80,8	0,0694824	9,18	-44,395604	-1,0119048
spiLA1589-mir2607-3	**77**	19,480519	36,363636	14,285714	29,87013	33,766234	66,233766	0,8214286	1,3636364	-26,2	-25	0,0298097	8,43	-34,025974	-0,7258065

spiLA1589-mir7981b-24	**114**	17,54386	35,087719	19,298246	28,070175	36,842105	63,157895	0,8	0,9090909	-35,7	-29,4	0,010203	14,05	-31,315789	-1,2625
spiLA1589-mir6232b-2	**269**	19,330855	34,572491	14,869888	31,226766	34,200743	65,799257	0,9032258	1,3	-98,7	-95,2	0,0054902	31,67	-36,69145	-1,0076923
spiLA1589-mir7981a-64	**132**	21,212121	24,242424	15,909091	38,636364	37,121212	62,878788	1,59375	1,3333333	-49,9	-49,7	0,0150126	12,5	-37,80303	-0,85
spiLA1589-mir5303h-2	**192**	17,1875	28,125	14,583333	40,104167	31,770833	68,229167	1,4259259	1,1785714	-46,9	-32,34	0,0007668	38,69	-24,427083	-1,0728261
spiLA1589-mir7981a-62	**124**	18,548387	28,225806	20,16129	33,064516	38,709677	61,290323	1,1714286	0,92	-45	-44,1	0,0458089	9,37	-36,290323	-1,0183673
spiLA1589-mir7822-4	**179**	22,905028	29,608939	17,877095	29,608939	40,782123	59,217877	1	1,28125	-63	-60,5	0,0054074	22,09	-35,195531	-0,7688525
spiLA1589-mir7981a-65	**130**	16,153846	27,692308	18,461538	37,692308	34,615385	65,384615	1,3611111	0,875	-42,4	-39,2	0,0201586	13,91	-32,615385	-1,003125
spiLA1589-mir7981b-25	**96**	18,75	34,375	23,958333	22,916667	42,708333	57,291667	0,6666667	0,7826087	-47,4	-47,4	0,429864	3,58	-49,375	-0,7912088
spiLA1589-mir172d-5	**105**	14,285714	38,095238	17,142857	30,47619	31,428571	68,571429	0,8	0,8333333	-30,7	-30,7	0,169255	4,8	-29,238095	-0,9422222
spiLA1589-mir10540-3	**137**	18,248175	33,576642	13,868613	34,306569	32,116788	67,883212	1,0217391	1,3157895	-60,3	-58,5	0,0151148	12,91	-44,014599	-1,1560976
spiLA1589-mir11036	**141**	14,893617	34,751773	17,021277	33,333333	31,914894	68,085106	0,9591837	0,875	-54,1	-52,3	0,0391154	6,47	-38,368794	-0,930303
spiLA1589-mir7981a-66	**102**	23,529412	31,372549	23,529412	21,568627	47,058824	52,941176	0,6875	1	-41,1	-41,1	0,137924	8,13	-40,294118	-1,3704545
spiLA1589-mir7987-3	**296**	19,256757	34,459459	13,851351	32,432432	33,108108	66,891892	0,9411765	1,3902439	-73,7	-52,82	7,35E-05	78,14	-24,898649	-1,2022222
spiLA1589-mir2678	**277**	23,104693	24,187726	24,187726	28,519856	47,292419	52,707581	1,1791045	0,9552239	-94,9	-55,6	0,0001588	94,71	-34,259928	-1,0818182
spiLA1589-mir7981a-68	**195**	17,948718	24,615385	20,512821	36,923077	38,461538	61,538462	1,5	0,875	-89,4	-88,7	0,0256843	12,89	-45,846154	-0,94
spiLA1589-mir7981a-69	**175**	15,428571	32,571429	18,285714	33,714286	33,714286	66,285714	1,0350877	0,84375	-54,9	-52,6	0,0050661	18,21	-31,371429	-0,7244275
spiLA1589-mir5303d	**79**	21,518987	30,379747	21,518987	26,582278	43,037975	56,962025	0,875	1	-27,3	-27,3	0,115387	2,34	-34,556962	-1,192
spiLA1589-mir1309	**293**	16,723549	33,447099	16,040956	33,788396	32,764505	67,235495	1,0102041	1,0425532	-75,4	-51,1	6,23E-05	73,03	-25,733788	-0,9305085
spiLA1589-mir7981b-26	**181**	17,127072	35,911602	17,127072	29,834254	34,254144	65,745856	0,8307692	1	-77,1	-76,7	0,0210263	12,45	-42,596685	-0,7854167
spiLA1589-mir7981a-67	**104**	22,115385	33,653846	17,307692	26,923077	39,423077	60,576923	0,8	1,2777778	-49,8	-49,7	0,0164018	12,52	-47,884615	-0,8327586
spiLA1589-mir159-4	**111**	16,216216	27,027027	17,117117	39,63964	33,333333	66,666667	1,4666667	0,9473684	-29,9	-28,7	0,0074538	12,01	-26,936937	-1,2435484
spiLA1589-mir6267a	**261**	18,390805	28,735632	13,409962	39,463602	31,800766	68,199234	1,3733333	1,3714286	-59,5	-51,4	1,95E-05	63,37	-22,796935	-1,2146341
spiLA1589-mir7981a-71	**171**	23,391813	26,315789	17,54386	32,748538	40,935673	59,064327	1,2444444	1,3333333	-98,4	-98,4	0,0031825	17,32	-57,54386	-0,7168675
spiLA1589-mir7981a-70	**120**	14,166667	40	17,5	28,333333	31,666667	68,333333	0,7083333	0,8095238	-36,7	-36,7	0,164409	4,78	-30,583333	-0,95
spiLA1589-mir7981a-72	**244**	16,803279	34,42623	20,081967	28,688525	36,885246	63,114754	0,8333333	0,8367347	-69,5	-61,77	0,0044928	34,47	-28,483607	-1,4057143
spiLA1589-mir7981b-27	**108**	18,518519	33,333333	22,222222	25,925926	40,740741	59,259259	0,7777778	0,8333333	-52,7	-52,1	0,133066	7,74	-48,796296	-0,9657895
spiLA1589-mir7981b-28	**192**	17,1875	34,375	15,625	32,8125	32,8125	67,1875	0,9545455	1,1	-70	-64,1	0,0002729	26,36	-36,458333	-0,7722222