UNIVERSIDADE FEDERAL DE UBERLÂNDIA
INSTITUTO DE BIOTECNOLOGIA
PROGRAMA DE PÓS-GRADUAÇÃO EM BIOTECNOLOGIA

RAPHAEL RODRIGUES PORTO

IDENTIFICAÇÃO, CARACTERIZAÇÃO DE miRNAs E SUA VIA DE PROCESSAMENTO EM *Lanistes nyassanus E Marisa cornuarietis*

PATOS DE MINAS – MG

AGOSTO DE 2021

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Dissertação de mestrado apresentada ao Programa de Pós-graduação em Biotecnologia como requisito parcial para obtenção do título de Mestre.

Orientador Prof. Dr. Matheus de Souza Gomes
Co-orientador Prof. Dr. Fábio Ribeiro Queiroz

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Ficha Catalográfica Online do Sistema de Bibliotecas da UFU com dados informados pelo(a) próprio(a) autor(a).

P894
2021

Pôrto, Raphael Rodrigues, 1986-
IDENTIFICAÇÃO, CARACTERIZAÇÃO DE miRNAs E SUA VIA DE PROCESSAMENTO EM Lanistes nyassanus E Marisa cornuarietis [recurso eletrônico] / Raphael Rodrigues Pôrto. - 2021.

Orientador: Matheus de Souza Gomes.
Dissertação (Mestrado) - Universidade Federal de Uberlândia, Pós-graduação em Biotecnologia.
Modo de acesso: Internet.
Disponível em: http://doi.org/10.14393/ufu.di.2021.443
Inclui bibliografia.
Inclui ilustrações.

1. Biotecnologia. I. Gomes, Matheus de Souza,1981-, (Orient.). II. Universidade Federal de Uberlândia. Pós-graduação em Biotecnologia. III. Título.

CDU: 60

Bibliotecários responsáveis pela estrutura de acordo com o AACR2: Gizele Cristine Nunes do Couto - CRB6/2091

UNIVERSIDADE FEDERAL DE UBERLÂNDIA
Coordenação do Programa de Pós-Graduação em Biotecnologia
Av. Getúlio Vargas, 230, 3° andar, Sala 308 - Bairro Centro, Patos de Minas-MG, CEP 38700-128
Telefone: (34) 3823-3714 - Ramal 39 - www.ppgbiotec.ibtec.ufu.br - ppgbiotec@ibtec.ufu.br

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Programa de Pós-Graduação em:	Biotecnologia				
Defesa de:	Dissertação de Mestrado Acadêmico				
Data:	20 de agosto de 2021	Hora de início:	14:30	Hora de encerramento:	17:00
Matrícula do Discente:	41912BTC001				
Nome do Discente:	Raphael Rodrigues Pôrto				
Título do Trabalho:	Identificação, caracterização de miRNAs e sua via de processamento em *Lanistes nyassanus* e *Marisa cornuarietis*				
Área de concentração:	Biociência				
Linha de pesquisa:	Bioinformática e Biologia Molecular aplicada à genômica, transcritômica e proteômica				
Projeto de Pesquisa de vinculação:	Bioinformática e Biologia Molecular aplicada à genômica, transcritômica e proteômica				

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Referência: Processo n° 23117.053895/2021-14

SEI n° 2974977

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Aprovação: 20/08/2021

BANCA EXAMINADORA

Prof. Dr. Matheus de Souza Gomes
Universidade Federal de Uberlândia

Profa. Dra. Enyara Rezende Morais
Universidade Federal de Uberlândia

Profa. Dra. Fernanda Janku Cabral
Universidade Estadual de Campinas

PATOS DE MINAS – MG
AGOSTO DE 2021

AGRADECIMENTOS

Agradeço a minha esposa Nathália por cobrir com luz e inspiração minha vida. Minha companheira de jornada, oferecendo sempre carinho, compreensão, paciência e amor, na construção de nossa vida. Agradeço também aos meus filhotes Pedro Raphael e Bento por serem a materialização do nosso amor e ternura.

Ao meu pai Edson e minha mãe Lourdes por sempre estarem ao meu lado, serem exemplo, e suporte para que possa buscar minhas realizações, sou profundamente grato ao amor incondicional devotado a nossa família. Agradeço também a minha irmã Bethânia e seu esposo Felipe, e meu irmão Bernardo e sua esposa Bruna, pelos momentos de uma vida compartilhados e o carinho que se estende a nossa família

À Lusmaene, Gabriella , Gabriel e ao Roberto (*in memorian),* por me acolherem tão bem em sua família e por toda a colaboração e atenção despendida a mim.

Agradeço aos meus tios, em especial a tia Chrsitina, por despertar o interesse pela pesquisa e produção acadêmica e colaborar durante a realização do trabalho, como revisora e também babá.

À Hilda por estar tão presente e colaborando desde o início do curso, sempre pronta para o que foi necessário.

Agradeço aos meus colegas de trabalho da Superintendência Regional de Saúde de Patos de Minas, da Farmácia e Assessoria de Governaça, em especial a diretora Noemi Portilho pelo apoio e compreensão tão necessários para realização do mestrado.

Agradeço ao professor Dr. Matheus de Souza Gomes por sua compreensão e paciência e por me orientar e confiar durante o desenvolvimento do trabalho em uma área nova e desafiadora para mim.

RESUMO

Os micro RNAs (miRNAs) são pequenas sequências de RNA conservadas entre as espécies durante a evolução que possuem atividades de regulação gênica. Os Ampularídeos são uma família de moluscos que derivaram do clado Caenogastropoda e que devido a características como a origem durante a Gondwana e a presença em regiões tropicais da África e América são interessantes fontes de pesquisa para estudos evolutivos. As espécies *Lanistes nyassanus* e *Marisa cornuarietis* são ampularídeos do velho e novo mundo, respectivamente, que apresentam entre si variabilidade adaptativa. Mesmo sendo provavelmente o segundo filo em número de espécies, o número de genomas sequenciados de moluscos não tem acompanhado de maneira proporcional o de outros filos, prejudicando, por consequência análises *in silico*, as quais poderiam buscar por reguladores gênicos como os miRNAs. O presente estudo identificou, caracterizou e analisou os miRNAs (maduros e precursores) e as prováveis proteínas envolvidas na via de processamento dos miRNAs nos genomas e proteomas preditos das espécies *L. nyassanus* e *M. cornuarietis* utilizando ferramentas de bioinformática e o banco de dados público *National Center for Biotechnology Information* (NCBI). A análise revelou 141 precursores de miRNAs e 162 miRNAs maduros no genoma de *L. nyassanus*, e 279 precursores de miRNAs e 297 miRNAs maduros no genoma de *M. cornuarietis*, incluindo miRNAs Mollusca específicos. Também foi possível identificar e caracterizar as prováveis proteínas da via de biogênese de miRNAs destacando as proteínas Argonauta, DROSHA, Dicer e Exportina no proteoma predito das duas espécies. Os resultados obtidos neste trabalho abrem grandes possibilidades de estudo da especiação e fatores que levaram a diversidade de espécies na família Ampullariidae.

Palavras-chave: Análise computacional. Caramujo. Regulação gênica. Genoma.

ABSTRACT

miRNAs (micro RNAs) are small RNA sequences conserved among species during evolution that have gene regulatory activities. The Ampullariidae are a family of molluscs that derived from the Caenogastropodaclade and that, due to characteristics such as their origin during Gondwana and their presence in tropical regions of Africa and America, are interesting sources of research for evolutionary studies. The species *Lanistes nyassanus* and *Marisa cornuarietis* are Old and Newworld snails, which show adaptive variability to each other. Even though it is probably the second phylum in number of species, the number of genomes sequenced from molluscs has not been proportionally following that of other phyla, consequently impairing in silico analysis, which could search for gene regulators such as miRNAs. The present study identified, characterized and analysed the miRNAs (mature and precursors) and the probable proteins involved in the miRNA processing pathway in the predicted genomes and proteomes of *L. nyassanus* and *M. cornuarietis* species using bioinformatics tools and the public database NCBI (National Center for Biotechnology Information). The analysis revealed 141 precursors of miRNAs and 162 mature miRNAs in the genome of *L. nyassanus*, and 279 precursors of miRNAs and 297 mature miRNAs in the genome of *M. cornuarietis*, including Mollusca-specific miRNAs. It was also possible to identify and characterize the probable proteins of the miRNA biogenesis pathway, highlighting the Argonaute, DROSHA, Dicer and Exportin proteins in the predicted proteome of the two species. The results obtained in this work open great possibilities for the study of speciation and factors that lead to species diversity in the Ampullariidae family

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Keywords: Computational analysis. Apple snails. Gene regulation. Genome.

LISTA DE FIGURAS

LISTA DE TABELAS

SUMÁRIO

1 INTRODUÇÃO

1.1 PROBLEMA DE PESQUISA

Os miRNAs são importantes reguladores da expressão gênica que podem interferir no desenvolvimento de espécies e atuar como resposta a alterações ambientais. Considerando entre os ampularídeos as espécies *Lanistes nyassanus* e *Marisa cornuarietis,* têm-se as seguintes perguntas: quais são os miRNAs que podem ser preditos a partir de seus genomas? Quais são os prováveis genes envolvidos na via de miRNAs nas duas espécies? A presença de miRNAs podem garantir vantagens evolutivas as espécies?

1.2 HIPÓTESE

Os miRNAs, precursores e maduros, bem como os prováveis genes envolvidos na via de processamento de miRNAs estão presentes no genoma e transcritoma das espécies *L. nyassanus* e *M. cornuarietis.*

1.3 OBJETIVOS

1.3.1 Objetivo geral

Identificar e caracterizar os miRNAs e os prováveis genes responsáveis pelo processamento destes miRNAs no genoma e transcritoma de *L. nyassanus* e *M. cornuarietis.*

1.3.2 Objetivos específicos

- (i) Identificar as regiões que formam estruturas de “hairpin” condizentes com precursores de miRNAs nos genomas de *L. nyassanus* e *M. cornuarietis.*
- (ii) Caracterizar a estrutura secundária dos precursores de miRNAs de *L. nyassanus* e *M. cornuarietis.*
- (iii) Identificar os prováveis genes envolvidos na via de miRNAs nas espécies *L. nyassanus* e *M. cornuarietis.*

(iv) Caracterizar os domínios conservados e os sítios ativos das principais proteínas envolvidas na via de processamento de miRNAs nas duas espécies.

1.3.3 Justificativa

Nos últimos anos o conhecimento sobre os RNAs interferentes, assim como pequenos RNAs não codificadores de proteínas, como os miRNAs, e a sua presença em moluscos avançaram de forma muito lenta em comparação com outras espécies. O conhecimento sobre a presença e ação destes pequenos RNAs e sua via de processamento em espécies do Filo Mollusca se torna essencial para o melhor entendimento da biologia das espécies pertencentes a este Filo.

A elucidação da presença da maquinaria de processamento bem como dos pequenos RNAs podem ser o início de um estudo para o estabelecimento da relação dos miRNAs frente aos processos evolutivos que possam ter garantido a algumas espécies se estabelecerem melhor em diversos territórios, bem como a suscetibilidade das mesmas a parasitas. Há, portanto, um caminho promissor na consolidação de conhecimentos sobre a maquinaria de miRNAs presentes em outros moluscos da família ampularídeos.

2 REFERENCIAL TEÓRICO

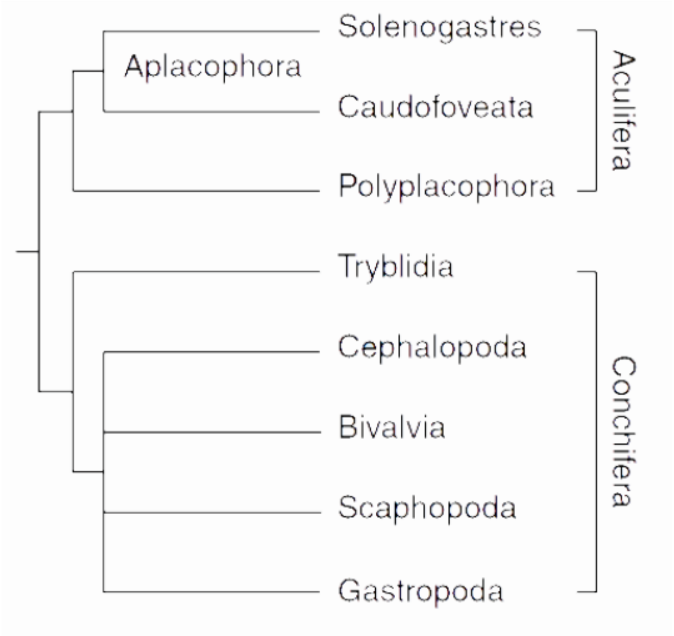
2.1 MOLUSCOS

Moluscos são um grupo de animais de corpo não segmentados, mole e com uma constituição de estrutural que pode ter um pé, base de apoio, desenvolvido através dos músculos da parede ventral, massa visceral dorsal, uma dobra da epiderme chamada de manto, formadora de conchas ou espículas calcáreas e a rádula que é uma estrutura de alimentação comum ao filo (ausente nos bivalves) (APPELTANS *et al.*, 2012; PYRON; BROWN, 2015; ROSENBERG, 2014).

A base de dados MolluscaBase (www.molluscabase.org) identifica 90.502 espécies pertencentes ao filo, e embora o mesmo dispute em quantidade de espécies reconhecidas recentemente com o filo dos Cordados, os Moluscos possuem a mais vasta diversidade entre as espécies ainda não descritas (ROSENBERG, 2014). Moluscos foram considerados durante um longo tempo como o filo com maior número de espécies marinhas; contudo, buscas recentes no banco de dados WoRMS demonstram que o maior número de espécies marinhas é atualmente creditado aos artrópodes (HORTON *et al.*, 2017).

A diversidade entre espécies de moluscos, como por exemplo, mexilhões, lulas gigantes e caramujos são exemplos da ampla plasticidade e adaptabilidade do filo. A proximidade do filo Mollusca com humanos pode ser devido a seu sucesso no domínio de ambientes, e também a capacidade de se estabelecer em várias condições de temperatura e disponibilidade de gases diferentes. O filo molusca (Figura 1; Quadro 1) é composto por oito classes e subdivisões taxonômicas que são bivalvia, scaphopoda, gastropoda, cephalopoda, monoplacophora, poliplacophora e aplacophora (solenogastes e caudofoveata) (SANMARTÍN; ROBERTS; FIGUERAS, 2016; SANTOS *et al.*, 2020).

Figura 1 – Distribuição das classes no filo Molusca.



Fonte: Adaptado de Haszprunar e Wanninger, (2012); Sanmartín; Roberts e Figueras, (2016)

Quadro 1 – Classes e Subdivisões de Moluscos.

Classes e Subdivisões de Moluscos

Solenogastres: 280 Espécies, grupo marinho de animais vermiformes de 1 mm a 30 cm. Extensão corpórea coberta por uma cutícula quitinosa com espiculas e escamas aragoníticas.

Caudofoveata: 180 Espécies, grupo marinho de animais vermiformes de 2 mm a 15 cm Extensão corpórea coberta por uma cutícula quitinosa com espículas ou escamas.

Polyplacophora: 1000 Espécies marinhas de 3 mm a 30 cm de extensão corporal. Estrutura como uma ventosa recoberta por uma manta que também abriga as guelras. A superfície dorsal é protegida por oito placas seriais, rodeadas por um cinto de escamas ou espículas aragoníticas. Utilizam a rádula para alimentação.

Monoplacophora (Tryblidia): Menos que 30 espécies existentes conhecidas. Possuem de 1 a 40 mm de comprimento e vivem de 200 m até 7000 m de profundidade.

Bivalvia: 20.000 Espécies com tamanho de 1 mm a 150 cm vivendo em ambientes aquáticos. Possuem concha bivalve e ausência de aparato bucal, tem pronunciada diversidade e se alimentam só por filtração.

Scaphopoda: 800 Espécies marinhas de 2 mm a 20 cm. Possuem concha em forma de presa de elefante.

Gastropoda: Cerca de 100.000 Espécies de 0,5 mm a 100 cm que habitam os ambientes terrestre e aquático. Grande variabilidade no formato de concha e presença de cabeça móvel e olhos

Cephalopoda: 1000 Espécies vivas exclusivamente marinhas com comprimento de 3 cm a 18 m com os tentáculos abertos. Todos são predadores.

Fonte: Adaptado de Haszprunar e Wanninger, (2012)

A variabilidade entre as classes de moluscos reflete-se em vários fatores, dentre os quais seu ciclo de vida que pode ser de alguns meses até 150 anos, a velocidade de locomoção que pode variar de um arrasto lento de alguns gastrópodes ao rápido deslocamento de maneira bípede de alguns cefalópodes. Questões de alimentação também evidenciam a variabilidade, uma vez que existem representantes sésseis, que nesse caso podem ser animais filtradores com a utilização de mecanismos de simbiose com bactérias, e existem também espécimes predadoras (HASZPRUNAR; WANNINGER, 2012; SANTOS *et al.*, 2020).

A relação dos moluscos com os seres humanos iniciou-se na alimentação, na utilização das espécies como fonte de proteínas, sendo atualmente o consumo de Gastropoda (escargots), Bivalvia (ostras), Cefalopodes (lula) bastante difundido. Pérolas, madrepérola e conchas podem ser utilizadas como joias ou decoração (SANTOS *et al.*, 2020). Moluscos também podem ser importantes modelos para estudo da organização cerebral. A relação com moluscos também pode incorrer em prejuízos para as outras espécies, devido a possibilidade de causarem prejuízos na agricultura, serem hospedeiros de patógenos humanos e possuírem veneno como alguns polvos (KOCOT *et al.*, 2011).

2.1.1.1 L. nyassanus e M. cornuarietis

L. nyassanus e *M. cornuarietis* são integrantes da família *Ampullariidae*, que é composta por caramujos de água doce. Os ampularídeos pertencem a super ordem *Caenogastropoda,* a que compreende cerca de 50.000 espécies e aproximadamente 60% das espécies dos Gastrópodes (STRONG *et al.*, 2008).

Como são uma família que derivou da super ordem *Caenogastropoda* no início da evolução (COWIE, 2015), os ampularídeos são um modelo para estudar a especiação e adaptação (HAYES *et al.*, 2009). Os ampularídeos vivem em áreas tropicais e possuem nove gêneros e cerca de 180 espécies. A família se originou há mais de 150 milhões de anos, e conquistou ambientes na África e América (JOKAT *et al.*, 2003; SUN *et al.*, 2019).

A espécie *L. nyassanus* foi descrita primariamente por Dohrn em 1865 e *M. cornuarietis* por Linné, Linné e Salvius em1758. Análises filogenéticas realizadas por Sun *et al.* (2019) estimam que as linhagens do novo mundo (América) e do velho mundo (África) podem ter se separado há 92,3 milhões de anos, período condizente com a cisão da Gondwana.

L. nyassanus e M. cornuarietis possuem divergências quanto a sua adaptabilidade. Enquanto *M. cornuarietis* apresenta uma melhor condição a resistir a fatores como baixa temperatura e hipóxia (MATSUKURA *et al.*, 2016; MU *et al.*, 2018), tendo ampla presença no continente americano, *L.* nyassanus possui uma baixa adaptabilidade, sendo endêmico do Lago

Nyassa, ou Malauí, geograficamente situado entre Malaui, Tanzânia e Moçambique (COWIE, 2015; DOHRN, 1865; VAN BOCXLAER, 2017). Diante das situações levantadas, seria também a maquinaria de miRNA corresponsável por diferenças na adaptabilidade entre as espécies?

2.1.2 Sequenciamento do genoma de moluscos e das espécies *L. nyassanus e M. cornuarietis*

O sequenciamento de DNA possibilitado pelo desenvolvimento da técnica de Sanger (SANGER; COULSON, 1975) representou um salto para a biologia. A técnica com sua acurácia e amplo uso foi utilizada por décadas, até o surgimento das novas tecnologias de sequenciamento de nova geração (NGS - *Next Generation Sequencing*), que geraram possibilidades ainda mais vantajosas de estudos em genômica de animais (GHOSH *et al.*, 2018; SANTOS *et al.*, 2020). A grande quantidade de dados gerada pelas técnicas de NGS necessitou de desenvolvimento em paralelo de ferramentas e análises de bioinformática (ZHANG *et al.*, 2011). Nesse contexto, o primeiro sequenciamento no filo Mollusca, e também no grupo Lophotrocozoa, foi realizado no ano de 2009, para a espécie *Aplysia californica* (SANTOS *et al.*, 2020)

Os sequenciamentos das espécies de estudo, *L. nyassanus* e *M. cornuarietis* foram realizados por Sun *et al.* (2019), em conjunto com duas outras espécies, a fim de possibilitar a comparação evolucional e relacionar características que podem ter garantido vantagens adaptativas.

O sequenciamento do genoma da espécie *L. nyassanus* foi publicado na biblioteca de genomas do NCBI (https://www.ncbi.nlm.nih.gov/genome/) sob o registro de Bio project PRJNA523095, enquanto *M. cornuarietis* foi registrado como PRJNA445755. O dados de sequenciamento dos genomas da espécie obtidos por Sun *et al.* (2019) estão demonstrados na Tabela 1.

Tabela 1 – Estatísticas da montagem do genoma de *L. nyassanus* e *M. cornuarietis*

Espécie	**Conteúdo de GC %**	**Tamanho da montagem**	**Número de Scaffolds**	**Maior Scaffold**	**Scaffold N50**	**Contig N50**
M. cornuarietis	41%	535,5 Mb	665	24,67 Mb	4,4 Mb	4,4 Mb
L. nyassanus	42%	510,0 Mb	34.401	1,79 Mb	316,6 kb	33,9 kb

Fonte: Adaptado de Sun *et al.* (2019)

2.2 PEQUENOS RNA INTERFERENTES E miRNAs

2.2.1 Histórico

O papel da regulação gênica desempenhados por pequenos RNAs, suas vias de processamento e sua atuação a nível celular têm sua importância demonstrada na literatura (MOAZED, 2009). Pequenos RNAs são definidos pelo seu tamanho, de 20-30 nucleotídeos (nt) e a sua associação com proteínas da família argonauta (HA; KIM, 2014). Os pequenos RNAs classificados como RNAs de interferência (RNAi) se destacam em três grupos: miRNA, siRNA e piRNA, respectivamente *micro* RNAs, *small interference* RNAs e *piwi* RNAs (Tabela 2). Os processos de regulação gênica são orquestrados por uma fina e específica regulação ao nível de genoma e/ou transcriptoma (KIM; HAN; SIOMI, 2009).

Tabela 2 – Principais características dos componentes da família dos RNAi.

Característica	**miRNA**	**siRNA**	**piRNA**
Tamanho aproximado	18~25 nt	19~23 nt	24~30 nt
Origem do pequeno RNA	Fita simples de RNA	Fita dupla de RNA	Fita simples de RNA
Enzimas de processamento	Drosha e Dicer	Dicer	Zucchini
Proteínas Argonauta	Argonauta	Argonauta	Aubergine e Piwi
Mecanismo de ação	Inibição da tradução; Clivagem do mRNA alvo	Clivagem do mRNA alvo	Clivagem do RNA alvo
Função	Regulação de genes codificadores de proteínas	Regulação de genes codificadores de proteínas; - Defesa antiviral	Regulação de elementos transponíveis; - Defesa antiviral

Fonte: Adaptado de Ha e Kim (2014)

Os primeiros miRNAs foram descritos após análises do controle temporal do estágio larval do verme *Caenorhabditis elegans*. Durante as primeiras análises acreditava-se que os miRNAs estariam envolvidos apenas no controle de desenvolvimento larval, a despeito de suas outras atividades regulatórias, assim sendo foram denominados de pequenos RNA temporais (stRNAs). Estudos posteriores permitiram a elucidação de outras atividades destes pequenos

RNAs endógenos, de fita simples, que possuem aproximadamente 18 a 24 nucleotídeos, como a função de regulação pós-transcricional de RNAs mensageiros (mRNAs), mediante complementariedade de sequência do tipo Watson-Crick (ADEMA *et al.*, 2017; HA; KIM, 2014; LECLERCQ; DIALLO; BLANCHETTE, 2013; LEE; FEINBAUM; AMBROS, 1993; WIGHTMAN *et al.*, 1991).

A evolução dos estudos possibilitou o conhecimento de novos papéis desempenhados pelos miRNAs, como regulador metabólico (ZAMBRANO *et al.*, 2015), controlador da senescência de células tronco mesenquimais (TOMÉ *et al.*, 2014), modulador da resposta imune (TSITSIOU; LINDSAY, 2009), e sua estreita relação com o controle do crescimento celular estimulando-o ou suprimindo-o em condições de distúrbios na homeostase ocasionados por cânceres (RUPAIMOOLE; SLACK, 2017), entre outras atividades. Alguns miRNAs podem ter ação diferente da postura clássica de silenciamento da tradução gênica ocasionando na regulação positiva da ação dos genes (ORANG; SAFARALIZADEH; KAZEMZADEH-BAVILI, 2014).

2.2.2 Biogênese dos miRNAs

2.2.2.1 Via Canônica

Os miRNAs são transcritos primeiramente em um longo RNA denominado miRNA primário ou pri-miRNA, com tamanho que pode superar 1000 nucleotídeos pela RNA polimerase II (RNA pol. II) e eventualmente regulado pela RNA polimerase III (RNA pol. III) (KOO *et al.*, 2015; LEE *et al.*, 2004). O seguimento transcrito possui a capacidade de se dobrar em uma estrutura que lembra um grampo de cabelo, e por isso denominada *hairpin*. Características comuns às sequências transcritas pela RNA pol. II, como a presença de cauda poli adeninas na extremidade 3’ e um grupo 7-metilguanosina na extremidade 5’, colaboraram para inferência dessa enzima polimerase como responsável pela transcrição (LEE *et al.*, 2004).

A via canônica de gênese dos miRNAs corresponde ao processamento dos pri-miRNAs pela endonuclease do tipo III (RNase III), DROSHA, e o processamento dos pré-miRNAs pela Dicer, outra endonuclease do tipo III (O’BRIEN *et al.*, 2018). Os pri-miRNAs dessa via podem ser transcritos a partir de localidades diversas do genoma, sejam elas intergênicas, exônicas ou intrônicas (KIM; HAN; SIOMI, 2009). Unidades de transcrição independentes pode ser transcritas individualmente, de maneira monocistrônica, ou em clusters, de maneira policistrônica, às vezes com centenas de miRNAs, que posteriormente serão processados de forma individual (BEREZIKOV, 2011; TREIBER; TREIBER; MEISTER, 2019). Regiões intrônicas de transcritos também são uma importante fonte de miRNAs, uma vez que 40% dos genes codificadores de proteínas para algumas espécies de mamíferos podem gerar em suas regiões intrônicas miRNAs (RODRIGUEZ, 2004).

A RNase III, Drosha, é o núcleo do complexo enzimático efetor da clivagem, responsável na via canônica pelo o processamento do pri-miRNA no núcleo celular a uma molécula com aproximadamente 70 nucleotídeos, o pré-miRNA (LEE *et al.*, 2002, 2003). O complexo enzimático é denominado “Microprocessador” e é composto pela DROSHA, pela proteína de ligação ao RNA de fita dupla (DiGeorge Syndrome Critical Region 8 - DGCR8), entre outros constituintes. A ausência de algum dos constituintes citados do complexo Microprocessador, principalmente a DROSHA e a DGCR8 pode prejudicar a gênese de miRNAs a partir de pri-miRNAs (GREGORY *et al.*, 2004; LANDTHALER; YALCIN; TUSCHL, 2004).

A proteína DGCR8 é responsável por se ligar a dupla fita do pri-miRNA no local devido para realização da clivagem. A identificação do local de ligação é possível devido a um radical metil que é ligado a uma adenosina precisamente a 11 pares de base de distância do ponto que as fitas do RNA se iniciam em seu pareamento para formação do *stem loop*, ou a alça do grampo (ALARCÓN *et al.*, 2015; HAN *et al.*, 2006). Ao complexo pri-miRNA e DGCR8 é unida a enzima DROSHA que forma um dímero intramolecular e cliva as fitas 3’ e 5’ do *stem loop*, sendo que a extremidade 3’ é dois nucleotídeos maior que a 5’, característica que recebe o nome de *overhang* (HAN *et al.*, 2004).

O produto da reação do complexo microprocessador no núcleo celular é o pré-miRNA, e as etapas posteriores de maturação serão realizadas no espaço citoplasmático. As proteínas Exportina 5 (XPO-5) e Exportina 1 (XPO-1) são corresponsáveis juntamente com a proteína RanGTP, um cofator, por enviar com gasto energético os pré-miRNA para o citoplasma (BÜSSING *et al.*, 2010). O complexo XPO-5/pré-miRNA/RanGTP mede cerca de 2.9 angstrom, e possui uma ligação forte nos 2 nucleotídeos, *overhang*, da extremidade 3’ do pré-miRNA, além de criar uma bolsa de interações fracas que incorporarão de maneira irreversível o seguimento de dupla fita (OKADA *et al.*, 2009).

No citoplasma, os pré-miRNAs que mantém a estrutura de grampo com seguimento de fita dupla de RNA passam por outro processo de clivagem; dessa vez, efetuado pela também RNase do tipo III de nome Dicer-1 (GRISHOK *et al.*, 2001; NICHOLSON, 2014). A enzima foi identificada e caracterizada primeiramente em pesquisas envolvendo o organismo modelo *Drosophila melanogaster* (BERNSTEIN *et al.*, 2001). Embora codificada por um só gene nos mamíferos, a enzima possui um complexo de multissubunidades, iniciando pela extremidade N-terminal: DEAD-like (DExD), helicase, um domínio de função desconhecida (DUF283), o domínio Piwi/Argonaute/Zwille (PAZ), os domínios das RNase IIIa e RNase IIIb, e o domínio de ligação ao dsRNA na porção C-terminal (SVOBODOVA; KUBIKOVA; SVOBODA, 2016). A clivagem pela Dicer também resulta em um *overhang* em 3', compensando a diferença entre número de nucleotídeos gerados pela clivagem da DROSHA, podendo ser direcionada através de conteúdo em nucleotídeos presentes na cadeia, resultando na produção de um duplex de RNA após a segregação da alça do grampo terminal, e por fim nos miRNAs 3p e 5p maduros (STAREGA-ROSLAN; GALKA-MARCINIAK; KRZYZOSIAK, 2015; ZHANG *et al.*, 2004).

2.2.2.2 Via Não Canônica

As vias "Não Canônicas" de geração dos miRNAs fogem do processamento sequencial por DROSHA e Dicer. Os miRNA das referidas vias podem ser processados utilizando as proteínas DROSHA, Dicer ou Argonauta 2 (AGO2) (O'BRIEN *et al.*, 2018).

As vias não canônicas podem ser divididas em três, sendo que primeiramente os miRNAs podem ser gerados a partir de curtos fragmentos intrônicos que assumem uma estrutura secundária em forma de grampo de cabelo semelhante ao pré-miRNA, sem passarem pelo processamento da DROSHA, são exportados ao citoplasma pela XPO-5/RanGTP e tem sua alça clivada por uma proteína Argonauta. O mecanismo de formação de miRNAs independente da Dicer utiliza o núcleo catalítico da proteína AGO2 para realizar a clivagem do pré-miRNA, devido a características como o tamanho do grampo formado. Estudos observaram a ausência do miR-451, que é conservado entre os mamíferos, em organismos que possuíam alelos com a AGO2 inativa (CHELOUFI *et al.*, 2010; YANG *et al.*, 2010).

Em uma segunda forma, os miRNAs não canônicos podem ser gerados devido a possuírem terminais coincidentes com os sítios de clivagem do processo de splicing (RUBY; JAN; BARTEL, 2007). Estes miRNAs são também exportados pela XPO-5/RanGTP e tem sua alça clivada na fase citoplasmática pela Dicer. Aos miRNAs que possuem essa via de processamento foi dado o nome de mirtrons. A nova via tem seu descobrimento computacional favorecido sem a utilização de genoma comparativo, diferentemente da via canônica (ORANG; SAFARALIZADEH; KAZEMZADEH-BAVILI, 2014).

A terceira variação é a partir de curtos transcritos que são "capeados" com um grupo na extremidade 5' com um grupamento 7-metilguanosina e são exportados pelo XPO-1 dependente de PHAX (Adaptador fosforilado para exportação de RNA) para serem processados pela Dicer. A presença do capeamento na extremidade 5' impossibilita a utilização do seguimento 5' do duplex miRNA, resultando essa via apenas no miRNA-3p funcional (XIE *et al.*, 2013).

2.2.3 Mecanismos de regulação gênica desenvolvidos por miRNAs

Os miRNAs pareiam suas bases com os RNAs alvo segundo uma relação do tipo Watson-Crick, não necessariamente por toda sua extensão, sendo comum a falta de pareamento entre algumas bases gerando *mismatches*. O primordial para a ação, entretanto, é a possibilidade de pareamento da região dos nucleotídeos 2 a 7 da porção 5' do miRNA, região conhecida como *seed*, sendo que estes seguimentos conservados delimitam miRNAs originários de um ancestral comum pertencentes a uma mesma família (GRIFFITHS-JONES, 2003). Inicialmente, creditava-se a ação de regulação gênica, repressão da tradução dos miRNAs, à sua ligação com regiões 3' UTR, atualmente a possibilidade de ligação a regiões 5' UTR e a sequência codificante já foram descritas (HUNTZINGER; IZAURRALDE, 2011; XU *et al.*, 2014)

Os miRNAs podem efetivar sua ação através do complexo miRISC (miRNA-*induced silencing complex*), no qual uma proteína da família AGO é carregada com uma fita guia de miRNA que direciona o complexo através do pareamento de bases que pode silenciar por uma variedade de vias de reações como a clivagem do alvo, ligação estável com o alvo, ligação transiente com o alvo, e por último, a ligação da fita guia com o alvo e deslocamento da fita do complexo miRISC (IPSARO; JOSHUA-TOR, 2015; JO *et al.*, 2015). A proteína AGO-2 possui ação endonucleolítica e o nível de complementariedade formado entre o complexo miRISC e o mRNA alvo é indicativo da ação do complexo. Sendo que, uma alta complementariedade favorece a clivagem, na qual os complexos miRISC que clivam os alvos passam por um acelerado processo de reciclagem, provavelmente devido a desestabilização da ligação do miRNA com a proteína AGO-2 (JO *et al.*, 2015). O silenciamento também pode se dar por alterações na porção 5' "Capeada" do mRNA e/ou em sua cauda poliadenilada, expondo o RNA a ação de degradação de exonucleases, como a enzima Xrn1p (BRAUN *et al.*, 2012; CHRISTIE *et al.*, 2013; ORANG; SAFARALIZADEH; KAZEMZADEH-BAVILI, 2014).

Os miRNAs também podem ser responsáveis por estimularem a expressão gênica através da ligação a porção 5’ UTR do mRNA com um complexo de proteínas. Entre as quais, a AGO-2, que pode se dar também em uma fase específica do ciclo celular, como no caso do miRNA let-7 (VASUDEVAN; STEITZ, 2007), ou a presença de fatores específicos, como por exemplo ausência da cauda poliadenilada (ORANG; SAFARALIZADEH; KAZEMZADEH-BAVILI, 2014).

A proteína AGO-2 consegue se deslocar para dentro do núcleo pela ação dos transportadores Importina-8 ou Exportina-1, com interação com uma proteína da família GW182, presente também nos complexos do miRISC, onde pode agir na degradação do mRNA nuclear, de maneira ainda não totalmente esclarecida, bem como na exposição de sítios para transcrição devido a alterações na cromatina (BOTTINI *et al.*, 2017; O’BRIEN *et al.*, 2018; PITCHIAYA *et al.*, 2017).

2.3 miRNAs EM MOLUSCOS E NAS ESPÉCIES *L. nyassanus* E *M. cornuarietis*

Os miRNAs possuem uma baixa homoplasia, isto é, sua presença em duas espécies diferentes tem uma maior probabilidade de estar vinculada a uma ancestralidade comum, correlacionando assim a distribuição de miRNAs em relações evolutivas das espécies (KENNY *et al.*, 2015).

Os registros de miRNAs disponíveis na base de dados miRBase, (www.mirbase.org) em sua última versão, (release 22.1, outubro de 2018) contam com a anotação de aproximadamente 48,885 miRNAs maduros, com alguns outros a serem identificados. O filo Molusca tem na base de dados apenas 245 miRNAs maduros identificados para as espécies *Lottia gigantea* (64 miRNAs maduros)*, Haliotis rufescens* (5 miRNAs maduros) *e Melibe leonina* (176 miRNAs maduros).

O intervalo temporal de atualizações das versões da base de dados miRBase, entre outros fatores, leva também em conta a necessidade de que a pesquisa por miRNAs seja realizada também em outras fontes de dados. Desse modo, buscas na literatura pela identificação de miRNAs em moluscos foram realizadas a fim de obter registros mais recentes ou outros que não foram contemplados nas atualizações do miRBase.

Para a espécie *Biomphalaria glabrata,* Adema *et al.* (2017) identificaram 95 precursores e 102 miRNAs, utilizando a predição a partir do genoma. O trabalho de Queiroz *et al.* (2020) através de uma estratégia de sequenciamento de pequenos RNAs resultou em 68 pré-miRNAs e 89 miRNA maduros também para *B. glabrata*. O estudo de Yu *et al.* (2020) encontrou para a espécie *Mytilus galloprovincialis* 137 miRNAs maduros, sendo desses 34 inéditos. Estudos realizados anteriormente como o de Picone, Rhode e Roodt-Wilding (2017), para a espécie de *Haliotis midae,* através do transcritoma, identificaram 105 miRNAs maduros. Para a espécie *Hyriopsis cumingii* foram identificados em exossomas de espécimes variantes de mantos branco e roxo respectivamente 136 e 159 miRNAs maduros, sendo que desses 125 são compartilhados entre as variantes (CHEN; BAI; LI, 2019). A busca por miRNA nas gônadas de *Crassostrea hongkongensis* identificou 50 miRNAs maduros conhecidos e 53 inéditos (WEI *et al.*, 2019).

Os miRNAs desempenham como reguladores gênicos relação com diversos processos biológicos em moluscos. Na espécie *Haliotis discus hannai* um total de 205 miRNAs, incluindo 200 inéditos foram identificados, e quando analisados observou-se a correlação de alguns dos miRNAs com processos metabólicos celulares, uma vez que em espécies menores apresentavam um padrão de expressão de miRNAs diferente de um grupo controle com tamanho de espécies maior (HUANG *et al.*, 2018).

Na espécie *Dosidicus gigas*, a pesquisa pelos níveis de expressão de 39 miRNAs conservados frente à hipóxia resultou na alteração de expressão de 16 miRNAs, quando comparado ao grupo controle exposto a condições normais de oxigenação (HADJ-MOUSSA *et al.*, 2018). No estudo de Walker *et al.*, (2018), 482 miRNAs em *Lymnaea stagnalis* foram identificados por sequenciamento, dos quais 263 conservados, sendo que 38 destes apresentaram alteração na expressão quando o sistema nervoso central da espécie foi exposto a ácido retinóico. Zhao *et al.* (2016) identificaram 202 e 87 miRNAs, respectivamente, em *Crassostrea gigas* e *C. hongkongensis*, dos quais, 6 em *C. gigas* e 2 em *C. hongkongensis* alteraram a expressão durante estresse osmótico.

Os miRNAs em moluscos também podem alterar seu perfil de expressão quando as espécies estão frente a processos infeciosos. Chen *et al.* (2016) identificaram em *C. gigas* o cgi-miR-92d que tem como alvo a região de codificação de TNF-α induzido por lipopolissacarídeos (CgLITAF3). O miRNA cgi-miR-92d diminui sua expressão quando o organismo é desafiado por lipopolissacarídeos ou pela bactéria gram negativa *Vibrio splendidus* enquanto CgLITAF3 é alterado de maneira oposta. A via de processamento também pode diferenciar sua expressão quando a espécie é sujeita a uma infecção. Queiroz *et al.* (2017) demonstraram a expressão diferencial de genes das proteínas Argonauta, Drosha, Piwi, Exportina-5 e Tudor, ligados a via de processamento de miRNAs em diferentes estágios evolutivos do caramujo *B. glabrata* e durante a infecção por *Schistossoma mansoni*.

3 MATERIAL E MÉTODOS

3.1 PREDIÇÃO DE PROTEÍNAS ENVOLVIDOS NA BIOGÊNESE DE miRNAs EM *L. nyassanus* E *M. cornuarietis*

Para a identificação de genes e suas prováveis proteínas envolvidas na via de miRNAs em *L. nyassanus* e *M. cornuarietis* foram utilizadas a ferramenta de alinhamento BLAST (Basic Local Alignment Search Tool- https://blast.ncbi.nlm.nih.gov/Blast.cgi) e bancos de dados de referência de proteínas (refseq-protein) e Nucleotídeos (nt_nr), disponibilizados no NCBI (National Center for Biotechnology Information) (http://www.ncbi.nlm.nih.gov/). Para a busca foram utilizadas sequências de aminoácidos das proteínas envolvidas na via de miRNA em organismos modelos como *D. melanogaster* e *C. elegans,* (Tabela 3) frente as sequências de aminoácidos dos proteomas preditos das espécies *L. nyassanus* e *M. cornuarietis*.

Tabela 3 – Proteínas ortólogas utilizadas para pesquisa nos bancos de dados.

Organismo modelo	**Proteína**	**Código de Acesso NCBI**
C. elegans	Argonaute	CCD73272.1
C. elegans	Drosha	O01326.2
C. elegans	Dicer	CDK13387.1
C. elegans	Exportin-T	NP_001294153.1
C. elegans	Exportin-1	NP_001368720.1
D. melanogaster	Exportin-1	NP_001303316.1
D. melanogaster	Drosha	NP_477436.1
D. melanogaster	TSN	NP_001261195.1
D. melanogaster	Argonaute-1	NP_001246314.1
D. melanogaster	Argonaute 2	NP_730054.1
D. melanogaster	Dicer-1	NP_524453.1
D. melanogaster	Argonaute 3	NP_001163498.1

Fonte: Dados do autor

3.2 ANÁLISE DOS DOMÍNIOS E DOS SÍTIOS ATIVOS E ANÁLISE FILOGENÉTICA DAS PROVÁVEIS PROTEÍNAS ENVOLVIDAS NA VIA DE MIRNAS EM *L. nyassanus* E *M. cornuarietis*

As prováveis proteínas envolvidas na via de miRNAs de *L. nyassanus* e *M. cornuarietis* foram submetidas ao BLAST (Basic Local Alignment Search Tool- https://blast.ncbi.nlm.nih.gov/Blast.cgi) para criação de um conjunto de proteína ortólogas. Para cada conjunto de proteínas dos organismos estudados e ortólogas realizou-se a busca por famílias de domínios e motivos conservados utilizando o "NCBI Conserved Domains" , banco de dados versão CDD v3.19 -58235 PSSMs (LU *et al.*, 2020; MARCHLER-BAUER *et al.*, 2011, 2015, 2017; MARCHLER-BAUER; BRYANT, 2004).

Para as proteínas Argonauta, Drosha e Dicer, foram realizadas buscas no NCBI Conserved Domains (https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi) pelos prováveis sítios ativos e os resíduos de aminoácidos que ocupavam as posições. Após encontrados, os sítios ativos, o conjunto de prováveis proteínas e ortólogas foram alinhadas com o programa ClustalX2.1 (LARKIN *et al.*, 2007), para posterior análise de conservação dos resíduos de aminoácidos dos sítios ativos e de áreas próximas.

As sequências de aminoácidos das proteínas também foram alinhadas utilizando os parâmetros padrão no ClustalX 2.1, e os alinhamentos foram utilizados para construção de árvores filogenéticas no programa MEGA X. A distribuição filogenética foi realizada utilizando o método Neighbor-Joining (SAITOU; NEI, 1987) aplicando o modelo "Kimura-two parameters", para estimar a divergência entre as sequências de aminoácidos foi utilizado o método JTT. Tanto o método quanto o modelo foram aplicados utilizando a ferramenta MEGA X (KUMAR *et al.*, 2018). A confiabilidade estatística de cada ramo na árvore gerada foi avaliada utilizando *bootstrap* com 2000 réplicas

3.3 PREDIÇÃO DE miRNAs PRECURSORES E MADUROS

Após a obtenção do genoma e transcritoma de *L. nyassanus* e *M. cornuarietis* do banco de dados do NCBI (https://www.ncbi.nlm.nih.gov/genome), as sequências foram processadas seguindo a metodologia estabelecida por Gomes *et al.* (2011) para predição de miRNAs maduros e seus precursores. As sequências passaram por uma seleção inicial, buscando segmentos que formassem estruturas semelhantes a *hairpins* e depois por uma série de filtros, selecionando, conforme parâmetros desejados, aquelas que correspondessem a prováveis precursores de miRNAs.

Os parâmetros determinados foram primeiramente, a Energia Mínima Livre (MFE) estabelecida após o dobramento da sequência do miRNA a partir do programa RNAfold (GRUBER *et al.*, 2008; HOFACKER, 2009), o valor de energia mínima livre de -18,00 kcal/mol é indicativo que a molécula é estável e está apta às etapas subsequentes do processo de maturação. O próximo passo foi selecionar as sequências que possuíam o conteúdo de CG (citosina e guanina) entre 30% e 70% (ZHOU *et al.*, 2009). Posteriormente, o alinhamento com miRNAs maduros do miRBase, no qual foram aceitos os candidatos que não possuíam *mismatches* na região *seed* (2 a 8 nt) e no máximo 4 *mismatches* no restante da sequência do miRNA maduro. Por fim, as sequências foram pesquisadas no Rfam microRNA Registry (version 14) (GRIFFITHS-JONES, 2003) sendo descartadas as sequências com alta similaridade a genes codificadores de proteínas e RNAs não codificantes e elementos repetitivos.

3.4 ALINHAMENTO, ANÁLISE DA ESTRUTURA SECUNDÁRIA E ANÁLISE FILOGENÉTICA DOS miRNAs DE *L. nyassanus* E *M. cornuarietis*

A sequência de nucleotídeos dos pré-miRNAs preditos foram utilizadas para busca de ortólogos nos bancos de dados do miRBase, (www.mirbase.org) em sua última versão, (release 22.1, outubro de 2018) (GRIFFITHS-JONES, 2004; GRIFFITHS-JONES *et al.*, 2008; KOZOMARA; BIRGAOANU; GRIFFITHS-JONES, 2019; KOZOMARA; GRIFFITHS-JONES, 2011, 2014), e em artigos publicados em periódicos (ADEMA *et al.*, 2017; HUANG *et al.*, 2021). Foram realizados alinhamentos múltiplos para os miRNAs através do programa ClustalX2.1 (LARKIN *et al.*, 2007), utilizando parâmetros ajustados de acordo com o tamanho e complexidade das sequências (gap opening: 22.50; gap extension: 0.83). As imagens do alinhamento da sequência de nucleotídeos dos precursores de miRNAs e seus ortólogos foi obtida utilizando o RNAalifold (http://rna.tbi.univie.ac.at/cgi-bin/RNAalifold.cgi) (BERNHART *et al.*, 2008). Posteriormente, as estruturas secundárias foram obtidas através da plataforma RNAfold (GRUBER *et al.*, 2008; HOFACKER, 2009). A nomenclatura dos precursores de miRNAs propostos foi baseada em sua similaridade, entre suas regiões maduras com os miRNAs com a de ortólogos registrados no miRBase.

A distribuição filogenética foi realizada utilizando o método Neighbor-Joining (SAITOU; NEI, 1987) aplicando o modelo “Kimura-two parameters” para estimar a divergência entre as sequências de miRNA. Tanto o método quanto o modelo foram aplicados utilizando a ferramenta MEGA X (KUMAR *et al.*, 2018). A confiabilidade estatística de cada ramo na árvore gerada foi avaliada utilizando *bootstrap* com 5000 réplicas.

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4 RESULTADOS E DISCUSSÃO

4.1 PREDIÇÃO DE PROTEÍNAS ENVOLVIDAS NA BIOGÊNESE DE PEQUENOS RNAS EM *L. nyassanus* E *M. cornuarietis*

A análise realizada identificou prováveis proteínas da via de miRNA nas duas espécies de estudo (Tabela 4), alinhamentos da sequência de aminoácidos de miRNA, presença de domínios descritos na literatura para as respectivas proteínas e conservação de aminoácidos que garantiram a conservação da localização de sítios ativos e vizinhança, além da distribuição das espécies nas árvores filogenéticas.

Tabela 4 – Resultados do Blastp do proteoma predito de *L. nyassanus* e *M. cornuarietis* frente as proteínas conhecidas de organismos modelo

Organismo modelo	**Proteína**	**Código de Acesso NCBI**	**Resultado do BlastP para *L. nyassanus***	**Resultado do BlastP para *M. cornuarietis***
C. elegans	Argonaute	CCD73272.1	Lny23421_c0_g1	Mco26370_c0_g1
C. elegans	Drosha	O01326.2	Lny18581_c0_g2	Mco22837_c2_g1
C. elegans	Dicer	CDK13387.1	Lny22963_c1_g2	Mco25637_c0_g1
C. elegans	Exportin-T	NP_001294153.1	Lny29270_c0_g1	Mco34551_c0_g1
C. elegans	Exportin-1	NP_001368720.1	Lny29270_c0_g1	Mco1704_c0_g1
D. melanogaster	Exportin-1	NP_001303316.1	Lny12572_c0_g1	Mco24030_c0_g2
D. melanogaster	Drosha	NP_477436.1	Lny18581_c0_g2	Mco22837_c2_g1
D. melanogaster	TSN	NP_001261195.1	Lny22624_c0_g1	Mco51286_c0_g1
D. melanogaster	Argonaute-1	NP_001246314.1	Lny23421_c0_g1	Mco26370_c0_g1
D. melanogaster	Argonaute 2	NP_730054.1	Lny23421_c0_g1	Mco26370_c0_g1
D. melanogaster	Dicer-1	NP_524453.1	Lny28171_c0_g1	Mco53856_c0_g1
D. melanogaster	Argonaute 3	NP_001163498.1	Lny28936_c7_g7	Mco25093_c0_g2

Fonte: Dados do autor

Análises anteriores de nosso grupo de estudos identificaram a presença das proteínas pertencentes a via de miRNAs em Moluscos (ADEMA *et al.*, 2017; QUEIROZ *et al.*, 2017) e Platelmintos (CARDOSO *et al.*, 2020). Proteína da via de miRNA também estão presentes e conservadas em plantas (KRISHNATREYA *et al.*, 2021).

4.1.1 Argonauta

Foram encontradas 3 possíveis proteínas AGO no genoma de *L. nyassanus,* Lny23421_c0_g1, Lny25187_c0_g1 e Lny28936_c7_g7 e 3 prováveis proteínas no genoma de *M. cornuarietis,* Mco25093_c0_g2, Mco26370_c0_g1, Mco27042_c1_g1. Entre as prováveis proteínas apenas Lny23421_c0_g1 e Mco26370_c0_g1. foram utilizadas como *query* em um blast afim de recuperar as ortólogas mais próximas.

O conjunto de prováveis proteínas da espécie e suas ortólogas foram submetidas à busca por domínios conservados no NCBI CD Search. Os domínios recuperados estão apresentados na Tabela 5 e suas posições de ocorrência ao longo da provável proteína na Figura 2. A proteína argonauta é caracterizada pela presença dos domínios PAZ e PIWI, apresentando também em sua construção os domínios Argo L1 e ArgoN (SONG *et al.*, 2004).

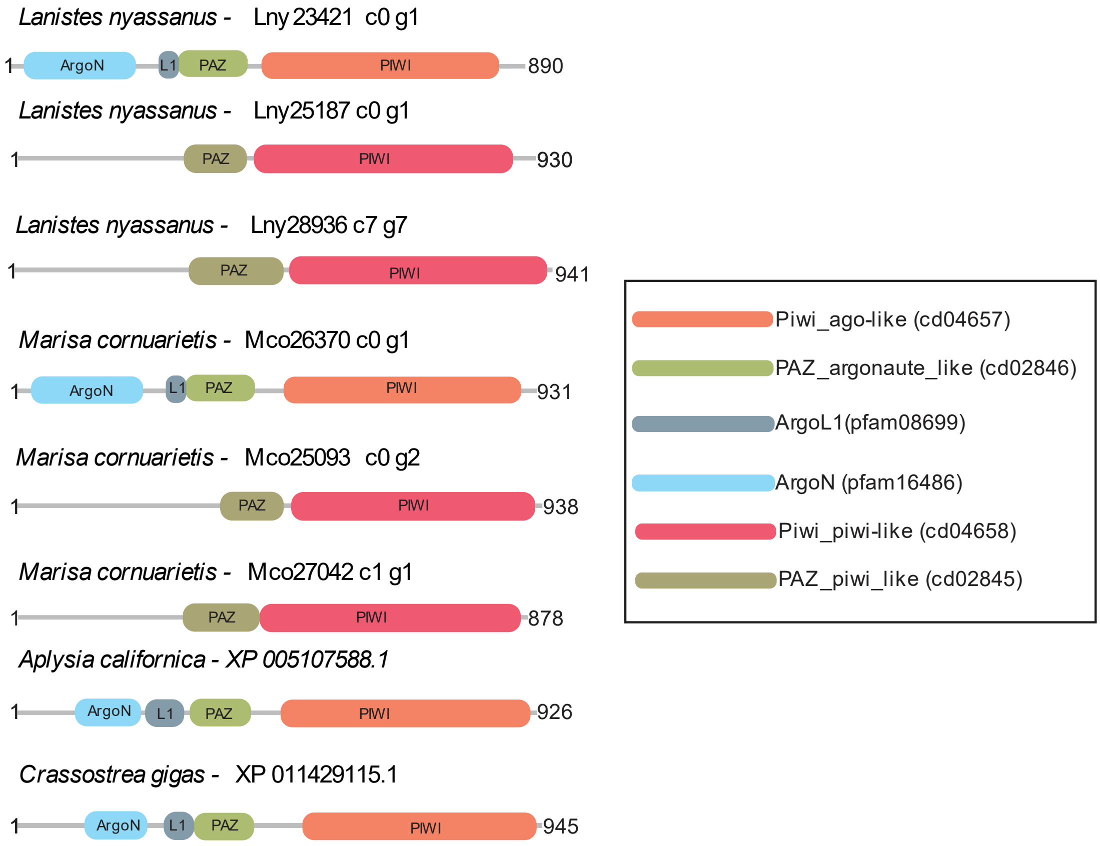
Tabela 5 – Domínios presentes nas prováveis proteínas Argonautas de *L. nyassanus* e *M. cornuarietis.*

Organismo	**Identificação / (Extensão)**	**Domínio**	**Início**	**Fim**	**E-Value**	**ID NCBI**
Lanistes nyassanus	Lny23421 c0 g1 (890)	Piwi_ago-like	422	847	0	cd04657
		PAZ_argonaute_like	257	377	1,80e^{-35}	cd02846
		ArgoL1	206	256	2,90e^{-17}	pfam08699
		ArgoN	66	196	4,11e^{-17}	pfam16486
	Lny25187 c0 g1 (880)	Piwi_piwi-like_Euk	417	862	0	cd04658
		PAZ_piwi_like	296	408	3,10e^{-46}	cd02845
	Lny28936 c7 g7(941)	Piwi_piwi-like_Euk	478	923	0	cd04658
		PAZ_piwi_like	352	470	1,94e^{-45}	cd02845
Marisa cornuarietis	Mco26370 c0 g1 (931)	Piwi_ago-like	457	888	0	cd04657
		PAZ_argonaute_like	292	412	2,73e^{-35}	cd02846
		ArgoL1	241	291	3,55e^{-16}	pfam08699
		ArgoN	101	231	5,08e^{-17}	pfam16486
	Mco25093 c0 g2 (938)	Piwi_piwi-like_Euk	475	920	0	cd04658
		PAZ_piwi_like	349	467	1,38e^{-43}	cd02845
	Mco27042 c1 g1 (878)	Piwi_piwi-like_Euk	415	860	0	cd04658
		PAZ	292	428	1,26e^{-44}	smart00949
Aplysia californica	XP 005107588.1 (926)	Piwi_ago-like	459	884	0	cd04657
		PAZ_argonaute_like	294	414	5,41e^{-36}	cd02846

		ArgoL1	243	293	$1,09e^{-16}$	pfam08699
		ArgoN	103	233	$8,20e^{-18}$	pfam16486
C. gigas	XP 011429115.1 (945)	Piwi_ago-like	478	903	0	cd04657
		PAZ_argonaute_like	313	433	$3,52e^{-36}$	cd02846
		ArgoL1	262	312	$1,86e^{-16}$	pfam08699
		ArgoN	122	252	$7,33e^{-17}$	pfam16486

Fonte: Dados do autor

Figura 2 – Distribuição dos domínios conservados nas prováveis proteínas Argonauta de *L. nyassanus, M. cornuarietis, A. californica* e *C. gigas.*



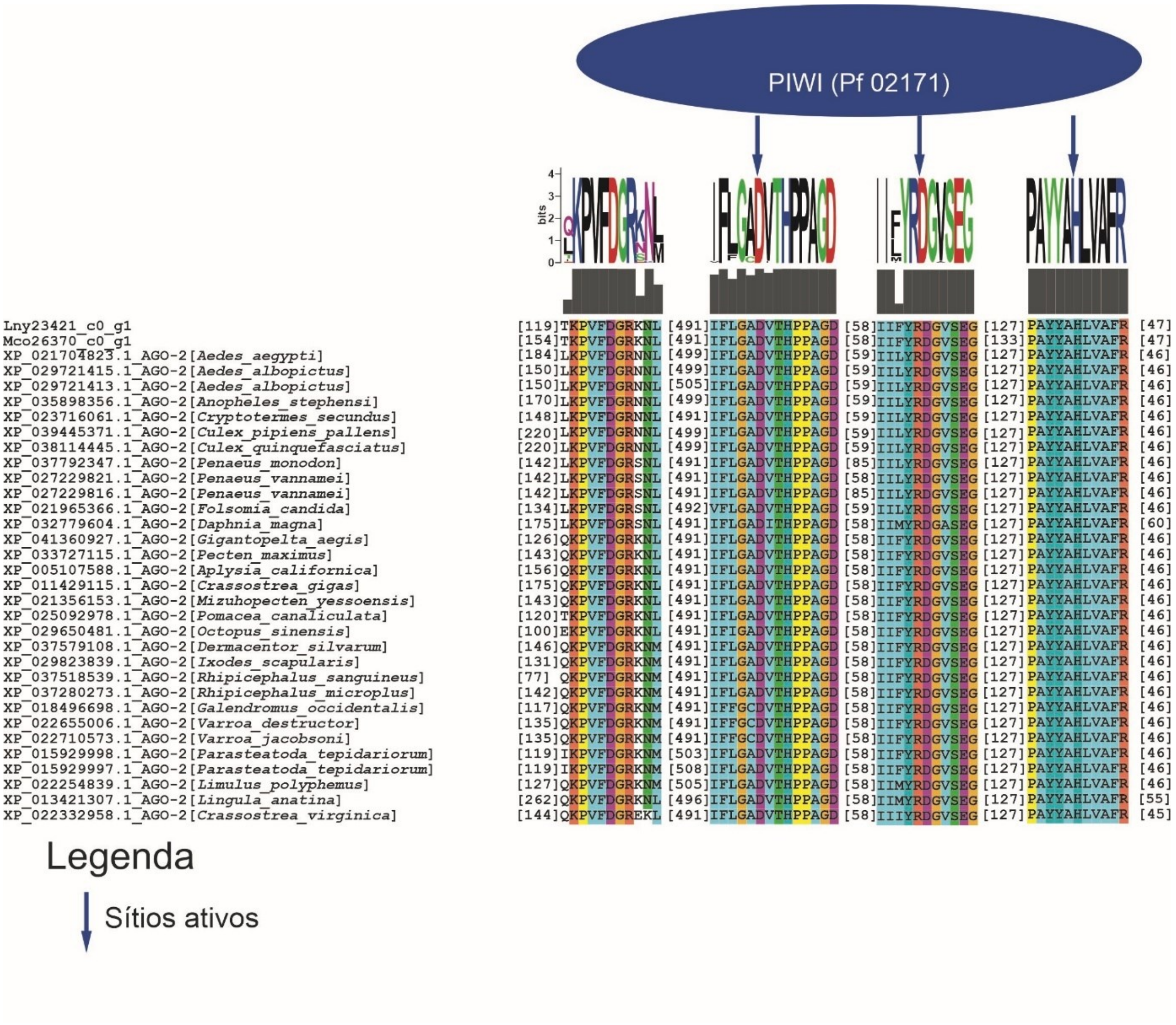
Fonte: Dados do autor

A análise de domínios revelou conservação entre os domínios das prováveis proteínas Lny23421_c0_g1 e Mco26370_c0_g1 com os das proteínas ortólogas. As demais prováveis proteínas citadas acima possuem os domínios PAZ e PIWI que se assemelham a proteínas PIWIs, uma subfamília da classe Argonautas.Com relação às prováveis proteínas Argonautas preditas os domínios PAZ apresentam sítios para fixação dos dois nucleotídeos do *overhang* dos miRNAs gerados a partir da clivagem pela DICER (YAN *et al.*, 2003). Os domínios PIWI guardam homologia funcional com a RNase H, que é conhecida por possibilitar a fragmentação de sequências de RNA (PARKER; ROE; BARFORD, 2004).

A atividade de endonuclease desempenhada pela proteína argonauta é possibilitada pela presença de aminoácido específico em sítios catalíticos (LIU *et al.*, 2004). A análise do alinhamento da sequência de aminoácidos dos domínios PIWI das prováveis proteínas frente às suas ortólogas comprovou a manutenção dos aminoácidos DDH (ácido aspártico, ácido aspártico e histidina) (

Figura 3) nas posições adequadas para atividade desempenhada.

Figura 3 – Análise Weblogo dos sítios ativos e os seus resíduos de aminoácidos que flanqueiam o domínio conservado PIWI (Pf 02171)das proteínas Argonauta de L. nyassanus e M. cornuarietis. A altura de cada símbolo de aminoácidos indica a conservação dos resíduos naquela posição.



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Lny23421_c0_g1                                  [119]TKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [47]
Mco26370_c0_g1                                  [154]TKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [133]PAYYAHLVAFR [47]
XP_021704823.1_AGO-2[Aedes_aegypti]             [184]LKPVFDGRNNL [499]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_029721415.1_AGO-2[Aedes_albopictus]          [150]LKPVFDGRNNL [499]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_029721413.1_AGO-2[Aedes_albopictus]          [150]LKPVFDGRNNL [505]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_035898356.1_AGO-2[Anopheles_stephensi]       [170]LKPVFDGRNNL [499]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_023716061.1_AGO-2[Cryptotermes_secundus]     [148]LKPVFDGRNNL [491]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_039445371.1_AGO-2[Culex_pipiens_pallens]     [220]LKPVFDGRNNL [499]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_038114445.1_AGO-2[Culex_quinquefasciatus]    [220]LKPVFDGRNNL [499]IFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_037792347.1_AGO-2[Penaeus_monodon]           [142]LKPVFDGRSNL [491]IFLGADVTHPPAGD [85]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_027229821.1_AGO-2[Penaeus_vannamei]          [142]LKPVFDGRSNL [491]IFLGADVTHPPAGD [58]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_027229816.1_AGO-2[Penaeus_vannamei]          [142]LKPVFDGRSNL [491]IFLGADVTHPPAGD [85]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_021965366.1_AGO-2[Folsomia_candida]          [134]LKPVFDGRSNL [492]VFLGADVTHPPAGD [59]IILYRDGVSEG [127]PAYYAHLVAFR [46]
XP_032779604.1_AGO-2[Daphnia_magna]             [175]LKPVFDGRSNL [491]IFLGADITHPPAGD [58]IIMYRDGASEG [127]PAYYAHLVAFR [60]
XP_041360927.1_AGO-2[Gigantopelta_aegis]        [126]QKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_033727115.1_AGO-2[Pecten_maximus]            [143]QKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_005107588.1_AGO-2[Aplysia_californica]       [156]QKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_011429115.1_AGO-2[Crassostrea_gigas]         [175]QKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_021356153.1_AGO-2[Mizuhopecten_yessoensis]   [143]QKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_025092978.1_AGO-2[Pomacea_canaliculata]      [120]TKPVFDGRKNL [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_029650481.1_AGO-2[Octopus_sinensis]          [100]EKPVFDGRKNL [491]IFIGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_037579108.1_AGO-2[Dermacentor_silvarum]      [146]QKPVFDGRKNM [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_029823839.1_AGO-2[Ixodes_scapularis]         [131]QKPVFDGRKNM [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_037518539.1_AGO-2[Rhipicephalus_sanguineus]  [77] QKPVFDGRKNM [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_037280273.1_AGO-2[Rhipicephalus_microplus]   [142]QKPVFDGRKNM [491]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_018496698.1_AGO-2[Galendromus_occidentalis]  [117]QKPVFDGRKNM [491]IFFGCDVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_022655006.1_AGO-2[Varroa_destructor]         [135]QKPVFDGRKNM [491]IFFGCDVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_022710573.1_AGO-2[Varroa_jacobsoni]          [135]QKPVFDGRKNM [491]IFFGCDVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_015929998.1_AGO-2[Parasteatoda_tepidariorum] [119]IKPVFDGRKNM [503]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_015929997.1_AGO-2[Parasteatoda_tepidariorum] [119]IKPVFDGRKNM [508]IFLGADVTHPPAGD [58]IIFYRDGVSEG [127]PAYYAHLVAFR [46]
XP_022254839.1_AGO-2[Limulus_polyphemus]        [127]QKPVFDGRKNM [505]IFLGADVTHPPAGD [58]IIMYRDGVSEG [127]PAYYAHLVAFR [46]
XP_013421307.1_AGO-2[Lingula_anatina]           [262]QKPVFDGRKNL [496]IFLGADVTHPPAGD [58]IIMYRDGVSEG [127]PAYYAHLVAFR [55]
XP_022332958.1_AGO-2[Crassostrea_virginica]     [144]QKPVFDGREKL [491]IFLGADVTHPPAGD [58]IIIYRDGVSEG [127]PAYYAHLVAFR [45]
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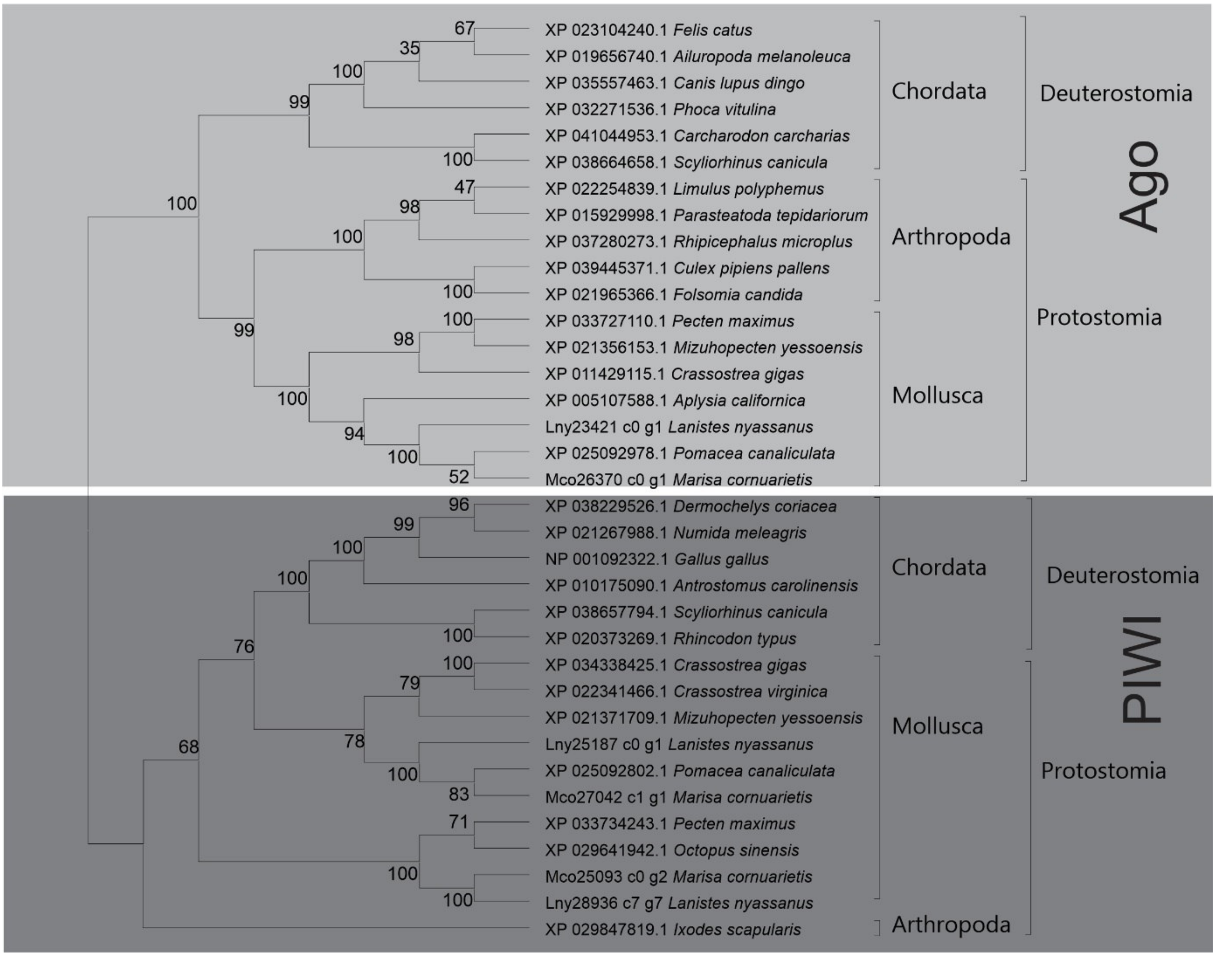
Fonte: Dados do autor

A distribuição filogenética das proteínas AGO corroborou com a árvore da vida. As candidatas a proteínas AGO Lny23421_c0_g1 e Mco26370_c0_g1 ficaram próximas as proteínas AGO de outras espécies de moluscos no clado Protostômios Figura 4, corroborando com os resultados obtidos para *B. glabrata* (QUEIROZ *et al.*, 2017). As prováveis proteínas Lny25187_c0_g1 e Lny28936_c7_g7*,* Mco25093_c0_g2, e Mco27042_c1_g1 se agruparam juntos com as proteínas PIWI, resultado que também foi obtido na pesquisa pelos domínios das referidas proteínas no NCBI e CDD.

Figura 4 – Distribuição filogenética das prováveis proteínas AGO identificadas em *L. nyassanus, M. cornuarietis* e suas ortólogas.



Fonte: Dados do autor

4.1.2 Dicer/DROSHA

Dicers e DROSHA são proteínas RNase III responsáveis pela atividade de clivagem das fitas de pri-miRNA e pré-miRNA, respectivamente. A atividade das enzimas se concentram em domínios RIBOc, que possuem sítios ativos compostos pelos seguintes aminoácidos EDDE (ácido glutâmico, ácido aspártico, ácido aspártico e ácido glutâmico) (HAN *et al.*, 2004; ZHANG *et al.*, 2004). Desse modo, a análise de domínios e sítios ativos foi realizada em paralelo para as duas proteínas, enquanto a análise filogenética foram realizadas de maneira conjunta.

4.1.2.1 Dicer

As Dicers são RNase de classe III compostas por vários domínios, tipicamente incluindo DExH RNA helicase/ATPase, um domínio PAZ, duas RNases III vizinhas e um sítio de ligação de fitas duplas de RNA (dsRBD). Para as espécies *L. nyassanus* e *M. cornuarietis* foram preditas as seguintes candidatas a proteína DICER: Lny28171_c0_g1, Lny22963_c1_g2, Mco25637_c0_g1, Mco16057_c0_g2, Mco53856_c0_g1. As proteínas preditas tiveram um tamanho significativamente menor do que as ortólogas utilizadas como query, como representado na Tabela 6.

Tabela 6 – Prováveis Dicer de *L. nyassanus* e *M. cornuarietis,* cobertura frente a NP_524453.1 Dicer-1 [*D. melanogaster*], E-Value, % de identidade e comprimento da sequência.

Código	Cobertura da *query*	E Value	Identidade %	Comprimento da sequência
NP_524453.1 Dicer-1 [*D. melanogaster*]	100%	0.0	100%	2249
Lny28171_c0_g1	38%	2,00e^{-162}	53,32%	1434
Mco53856_c0_g1	11%	6,00e^{-84}	55,38%	250
Lny22963_c1_g2	4%	2,00e^{-12}	33,02%	1135
Mco25637_c0_g1	10%	7,00e^{-12}	36,62%	1049
Mco16057_c0_g2	13%	6,00e^{-10}	22,%78	1063

Fonte: Dados do autor

O fato de as proteínas terem uma sequência de aminoácidos significativamente menor que a sequência, provavelmente, se deve por falta de cobertura em uma das extremidades da proteína. A falta de cobertura prejudica a identificação de domínios para todas as prováveis proteínas, possibilitando a análise de domínios conservados, ainda que de maneira incompleta, apenas para a proteína Lny28171_c0_g1(Tabela 7).

Tabela 7 – Domínios conservados das proteínas Dicer de *L. nyassanus* e ortólogas

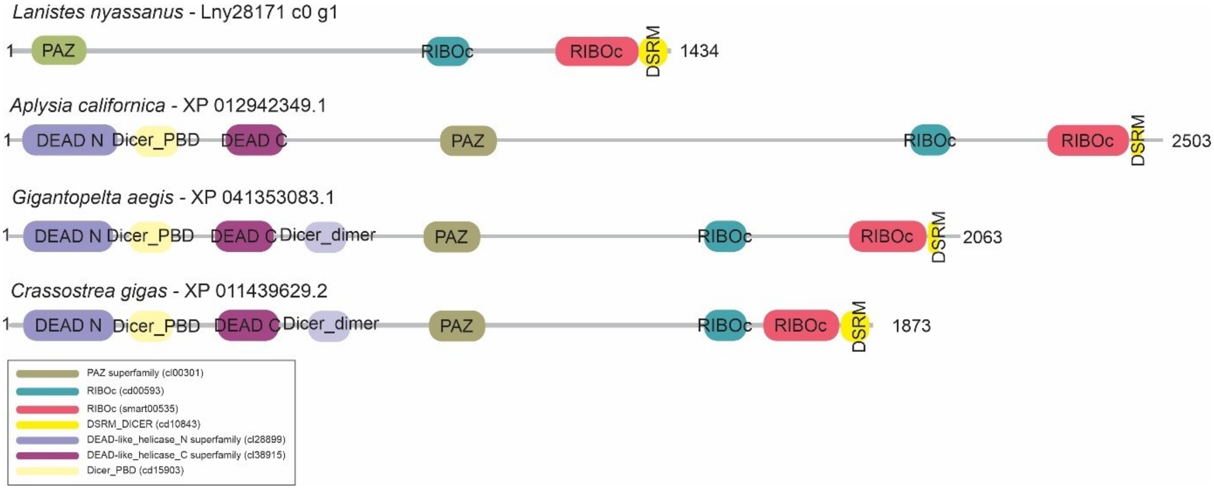
Organismo	Identificação / Extensão	Domínio	Início	Fim	E-Value	ID NCBI
Lanistes nyassanus	Lny28171_c0_g1 (1434)	PAZ superfamily	44	163	4,43e^{-44}	cl00301
		RIBOc	1183	1360	8,86e^{-34}	cd00593
		DSRM_DICER	1364	1426	1,79e^{-26}	cd10843
		RIBOc	902	996	5,51e^{-19}	smart00535
Aplysia californica	XP 012942349.1 (2503)	PAZ superfamily	932	1055	1,87e^{-47}	cl00301
		RIBOc	2252	2429	2,66e^{-34}	cd00593
		DEAD-like_helicase_N superfamily	24	231	7,40e^{-35}	cl28899
		DEAD-like_helicase_C superfamily	466	592	2,57e^{-30}	cl38915
		Dicer_dimer	676	766	1,61e^{-26}	pfam03368
		DSRM_DICER	2433	2495	4,43e^{-23}	cd10843
		RIBOc	1954	2042	1,39e^{-17}	smart00535
		Dicer_PBD	267	363	2,82e^{-15}	cd15903
Gigantopelta aegis	XP 041353083.1 (2063)	DEAD-like_helicase_N superfamily	26	221	5,73e^{-49}	cl28899
		PAZ superfamily	896	1019	7,11e^{-44}	cl00301
		RIBOc	1821	1989	2,24e^{-34}	cd00593
		DEAD-like_helicase_C superfamily	442	570	4,18e^{-33}	cl38915
		Dicer_dimer	637	728	2,89e^{-28}	pfam03368
		DSRM_DICER	1993	2055	1,86e^{-24}	cd10843
		RIBOc	1506	1598	2,69e$_{-19}$	smart00535
		Dicer_PBD	256	350	1,97e^{-11}	cd15903
		MSCRAMM_ClfA superfamily	1110	1469	5,32e^{-01}	cl41352
C. gigas	XP 011439629.2 (1873)	PAZ superfamily	908	1030	9,49e^{-46}	cl00301
		DEAD-like_helicase_N superfamily	26	223	4,48e^{-36}	cl28899
		RIBOc	1635	1799	3,03e^{-35}	cd00593
		DEAD-like_helicase_C superfamily	448	581	4,57e^{-34}	cl38915
		Dicer_dimer	645	736	1,42e^{-29}	pfam03368

	DSRM_DICER	1803	1865	1,30e^{-23}	cd10843
	RIBOc	1332	1426	2,49e^{-20}	smart00535
	Dicer_PBD	255	350	5,37e^{-15}	cd15903

Fonte: Dados do autor

A distribuição dos domínios (Figura 5) ressalta a manutenção de uma estrutura comum da proteína e leva a possível inferência da lacuna na porção N terminal da proteína predita para *L. nyassanus* .

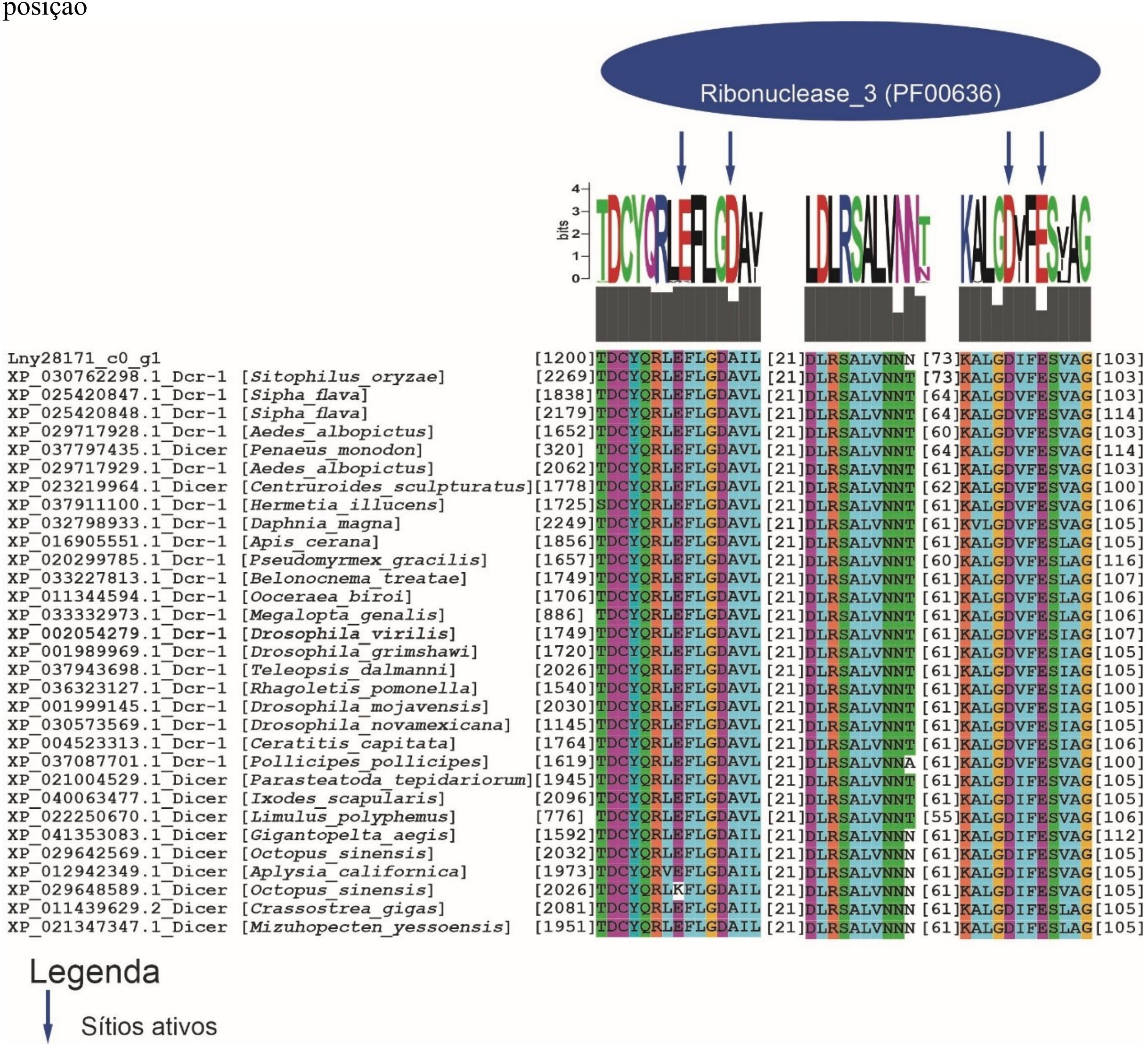
Figura 5 – Distribuição dos domínios conservados nas prováveis proteínas Dicer de *L. nyassanus, Aplysia californica, Gigantopelta aegis* e *C. gigas*



Fonte: Dados do autor

Com relação aos sítios ativos, a análise demonstrou conservação da estrutura EDDE (ácido glutâmico, ácido aspártico, ácido aspártico e ácido glutâmico), da vizinhança dos sítios e da distância entre eles (Figura 6), da candidata à Dicer – Lny28171_c0_g1 – e das proteínas ortólogas. A posição desses resíduos de aminoácidos é primordial para clivagem das fitas de RNA (ZHANG *et al.*, 2004).

Figura 6 – Análise Weblogo dos sítios ativos e os seus resíduos de aminoácidos que flanqueiam o domínio conservado Ribonuclease_3 (cd00593) das proteínas Dicer de *L. nyassanus, M. cornuarietis* e suas ortólogas. A altura de cada símbolo de aminoácidos indica a conservação dos resíduos naquela posição



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Lny28171_c0_g1                                          [1200]TDCYQRLEFLGDAIL [21]DLRSALVNNN [73]KALGDIFESVAG[103]
XP_030762298.1_Dcr-1 [Sitophilus_oryzae]                [2269]TDCYQRLEFLGDAVL [21]DLRSALVNNT [73]KALGDVFESVAG[103]
XP_025420847.1_Dcr-1 [Sipha_flava]                      [1838]TDCYQRLEFLGDAVL [21]DLRSALVNNT [64]KALGDVFESVAG[103]
XP_025420848.1_Dcr-1 [Sipha_flava]                      [2179]TDCYQRLEFLGDAVL [21]DLRSALVNNT [64]KALGDVFESVAG[114]
XP_029717928.1_Dcr-1 [Aedes_albopictus]                 [1652]TDCYQRLEFLGDAVL [21]DLRSALVNNT [60]KALGDVFESVAG[103]
XP_037797435.1_Dicer [Penaeus_monodon]                  [320] TDCYQRLEFLGDAVL [21]DLRSALVNNT [64]KALGDVFESVAG[114]
XP_029717929.1_Dcr-1 [Aedes_albopictus]                 [2062]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESVAG[103]
XP_023219964.1_Dicer [Centruroides_sculpturatus]        [1778]TDCYQRLEFLGDAVL [21]DLRSALVNNT [62]KALGDVFESVAG[100]
XP_037911100.1_Dcr-1 [Hermetia_illucens]                [1725]SDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESVAG[106]
XP_032798933.1_Dcr-1 [Daphnia_magna]                    [2249]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KVLGDVFESVAG[105]
XP_016905551.1_Dcr-1 [Apis_cerana]                      [1856]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESLAG[105]
XP_020299785.1_Dcr-1 [Pseudomyrmex_gracilis]            [1657]TDCYQRLEFLGDAVL [21]DLRSALVNNT [60]KALGDVFESLAG[116]
XP_033227813.1_Dcr-1 [Belonocnema_treatae]              [1749]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESLAG[107]
XP_011344594.1_Dcr-1 [Ooceraea_biroi]                   [1706]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESLAG[106]
XP_033332973.1_Dcr-1 [Megalopta_genalis]                [886] TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESLAG[106]
XP_002054279.1_Dcr-1 [Drosophila_virilis]               [1749]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[107]
XP_001989969.1_Dcr-1 [Drosophila_grimshawi]             [1720]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[105]
XP_037943698.1_Dcr-1 [Teleopsis_dalmanni]               [2026]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[105]
XP_036323127.1_Dcr-1 [Rhagoletis_pomonella]             [1540]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[100]
XP_001999145.1_Dcr-1 [Drosophila_mojavensis]            [2030]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[105]
XP_030573569.1_Dcr-1 [Drosophila_novamexicana]          [1145]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[105]
XP_004523313.1_Dcr-1 [Ceratitis_capitata]               [1764]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDVFESIAG[106]
XP_037087701.1_Dcr-1 [Pollicipes_pollicipes]            [1619]TDCYQRLEFLGDAVL [21]DLRSALVNNA [61]KALGDVFESVAG[100]
XP_021004529.1_Dicer [Parasteatoda_tepidariorum]        [1945]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDIFESVAG[105]
XP_040063477.1_Dicer [Ixodes_scapularis]                [2096]TDCYQRLEFLGDAVL [21]DLRSALVNNT [61]KALGDIFESVAG[105]
XP_022250670.1_Dicer [Limulus_polyphemus]               [776] TDCYQRLEFLGDAVL [21]DLRSALVNNT [55]KALGDIFESVAG[106]
XP_041353083.1_Dicer [Gigantopelta_aegis]               [1592]TDCYQRLEFLGDAIL [21]DLRSALVNNN [61]KALGDIFESVAG[112]
XP_029642569.1_Dicer [Octopus_sinensis]                 [2032]TDCYQRLEFLGDAIL [21]DLRSALVNNN [61]KALGDIFESVAG[105]
XP_012942349.1_Dicer [Aplysia_californica]              [1973]TDCYQRVEFLGDAIL [21]DLRSALVNNN [61]KALGDIFESVAG[105]
XP_029648589.1_Dicer [Octopus_sinensis]                 [2026]TDCYQRLKFLGDAIL [21]DLRSALVNNN [61]KALGDIFESVAG[105]
XP_011439629.2_Dicer [Crassostrea_gigas]                [2081]TDCYQRLEFLGDAIL [21]DLRSALVNNN [61]KALGDIFESLAG[105]
XP_021347347.1_Dicer [Mizuhopecten_yessoensis]          [1951]TDCYQRLEFLGDAIL [21]DLRSALVNNN [61]KALGDIFESLAG[105]
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Fonte: Dados do autor

4.1.2.2 DROSHA

As proteínas DROSHA são RNase III de classe II compostas por dois domínios RIBOc e um domínio de ligação do RNA de fita dupla. Para as espécies *L. nyassanus* e *M. cornuarietis*, a predição de proteínas através do genoma, identificou as seguintes candidatas a proteína DROSHA, Lny18581_c0_g2, Lny10158_c0_g1, Lny14351_c0_g1, Mco22837_c2_g1 e Mco14003_c0_g3. Assim como aconteceu para as proteínas Dicer, as proteínas DROSHA preditas tiveram um tamanho significativamente menor que as proteínas ortólogas utilizadas para busca (Tabela 8).

Tabela 8 – Prováveis DROSHA de *L. nyassanus* e *M. cornuarietis,* cobertura frente a NP_477436.1 DROSHA [*D. melanogaster*], E-Value, % de identidade e comprimento da sequência

Código	**Cobertura da *query***	**E Value**	**Identidade %**	**Comprimento da sequência**
NP_477436.1 Drosha [*D. melanogaster*]	100%	0.0	100,00	1327
O01326.2|drosha [*C. elegans*]	62%	0.0	39,53	1086
Mco22837_c2_g1	56%	0.0	60,96	760
Lny18581_c0_g2	27%	$7,00e^{-150}$	69,57	317
Lny14351_c0_g1	36%	$5,00e^{-142}$	49,59	724
Lny10158_c0_g1	12%	$2,00e^{-68}$	61,40	190
Mco14003_c0_g3	4%	$8,00e^{-26}$	63,49	101

Fonte: Dados do autor

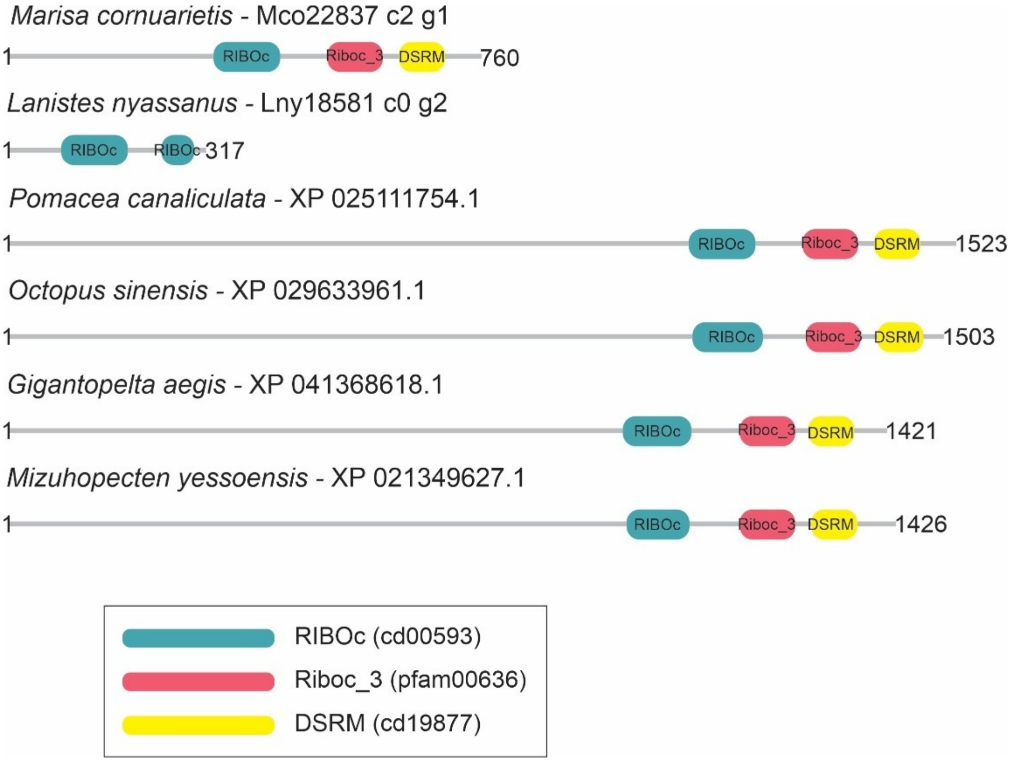
A falta de cobertura na predição da proteína, diferentemente do que aconteceu para proteína Dicer, não prejudicou a predição de domínios conservados para a proteína Mco22837 c2 g1, uma vez que ela se deu, provavelmente, na porção N terminal da proteína, a qual para DROSHA ainda não foram identificados domínios conservados funcionais. A proteína Drosha é marcada por ter dois domínios RIBOc e um domínio de ligação de RNA de fita dupla (BERNSTEIN *et al.*, 2001). Com relação às outras candidatas, Lny18581_c0_g2 apresentou um domínio RIBOc e um fragmento do segundo domínio RIBOc Para as outras proteínas propostas, Lny14351_c0_g1, Lny10158_c0_g1 e Mco14003_c0_g3, a busca por domínios conservados foi infrutífera (Tabela 9, Figura 7).

Tabela 9 – Domínios conservados das proteínas DROSHA de *L. nyassanus* e *M. cornuarietis* e ortólogas.

Organismo	**Identificação / Extensão**	**Domínio**	**Início**	**Fim**	**E-Value**	**ID NCBI**
Marisa cornuarietis	Mco22837 c2 g1 (760)	DSRM_RNAse_III_meta_like	627	701	$2,24e^{-40}$	cd19877
		RIBOc	329	436	$1,32e^{-31}$	cd00593
		Ribonuclease_3	512	601	$8,52e^{-19}$	pfam00636
Lanistes nyassanus	Lny18581 c0 g2 (317)	RIBOc	84	191	$1,46e^{-32}$	cd00593
		RIBOc	245	298	$1,88e^{-13}$	cd00593
Pomacea canaliculata	XP 025111754.1 (1523)	DSRM_RNAse_III_meta_like	1391	1465	$6,76e^{-41}$	cd19877
		RIBOc	1093	1200	$1,09e^{-31}$	cd00593
		Ribonuclease_3	1276	1365	$7,13e^{-21}$	pfam00636
Octopus sinensis		DSRM_RNAse_III_meta_like	1396	1470	$3,31e^{-39}$	cd19877
		RIBOc	1099	1212	$1,84e^{-32}$	cd00593

	XP 029633961.1 (1503)	Ribonuclease_3	1281	1369	3,6e^{-20}	pfam00636
Gigantopelta aegis	XP 041368618.1 (1412)	DSRM_RNAse_III_meta_like	1285	1356	4,09e^{-36}	cd19877
		RIBOc	987	1097	1,28e^{-34}	cd00593
		Ribonuclease_3	1170	1259	7,07e^{-17}	pfam00636
Mizuhopecten yessoensis	XP 021349627.1 (1426)	DSRM_RNAse_III_meta_like	1290	1364	6,58e^{-36}	cd19877
		RIBOc	993	1094	2,29e^{-32}	cd00593
		Ribonuclease_3	1175	1264	9,54e^{-21}	pfam00636

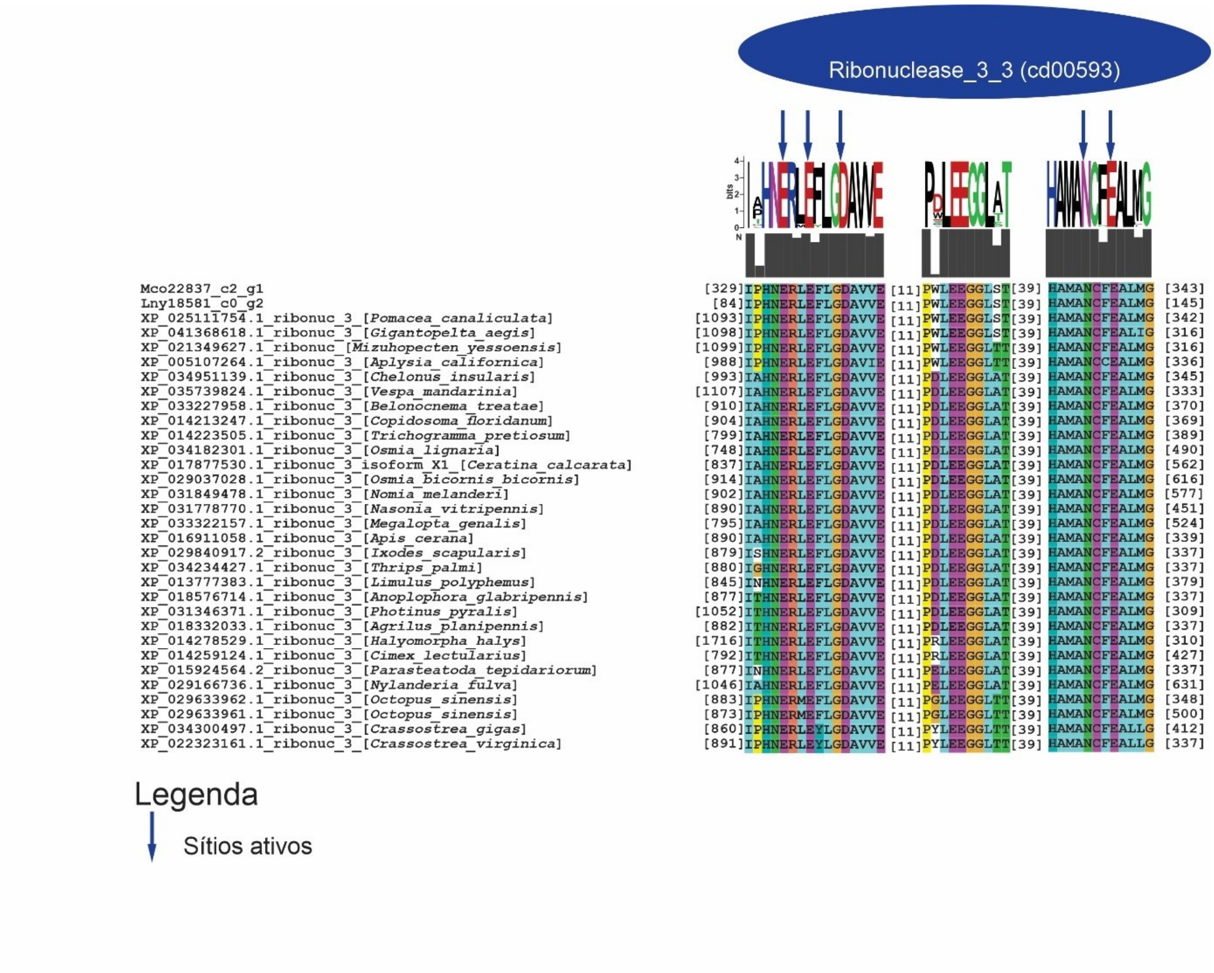
Figura 7 – Distribuição dos domínios conservados nas prováveis proteínas DROSHA de *M. cornuarietis L. nyassanus, P. canaliculata, Octopus sinensis, Gigantopelta aegis* e *Mizuhopecten yessoensis*



Fonte: Dados do autor

O resultado da busca por sítios ativos do domínio Ribonuclease_3 (pfam00636) foi realizada para os domínios de Mco22837 c2 g1 e Lny18581 c0 g2 (317). Os resultados demonstraram conservação dos resíduos EEDENE (ácido glutâmico, ácido glutâmico, ácido aspártico, ácido glutâmico, asparagina e ácido glutâmico) Figura 8, todos esses possuidores de grupos carboxila. A presença desses aminoácidos negativos, que possibilitam a ligação a íons magnésio e catalisam a clivagem das fitas de RNA, provavelmente forma os prováveis sítios ativos para esse domínios da proteína DROSHA, uma das classes de RNase III já reportada (BLASZCZYK *et al.*, 2001)

Figura 8 – Análise Weblogo dos sítios ativos e os seus resíduos de aminoácidos que flanqueiam o domínio conservado Ribonuclease_3 (cd00593) das proteínas DROSHA de *L. nyassanus*, *M. cornuarietis* e suas ortólogas. A altura de cada símbolo de aminoácidos indica a conservação dos resíduos naquela posição.

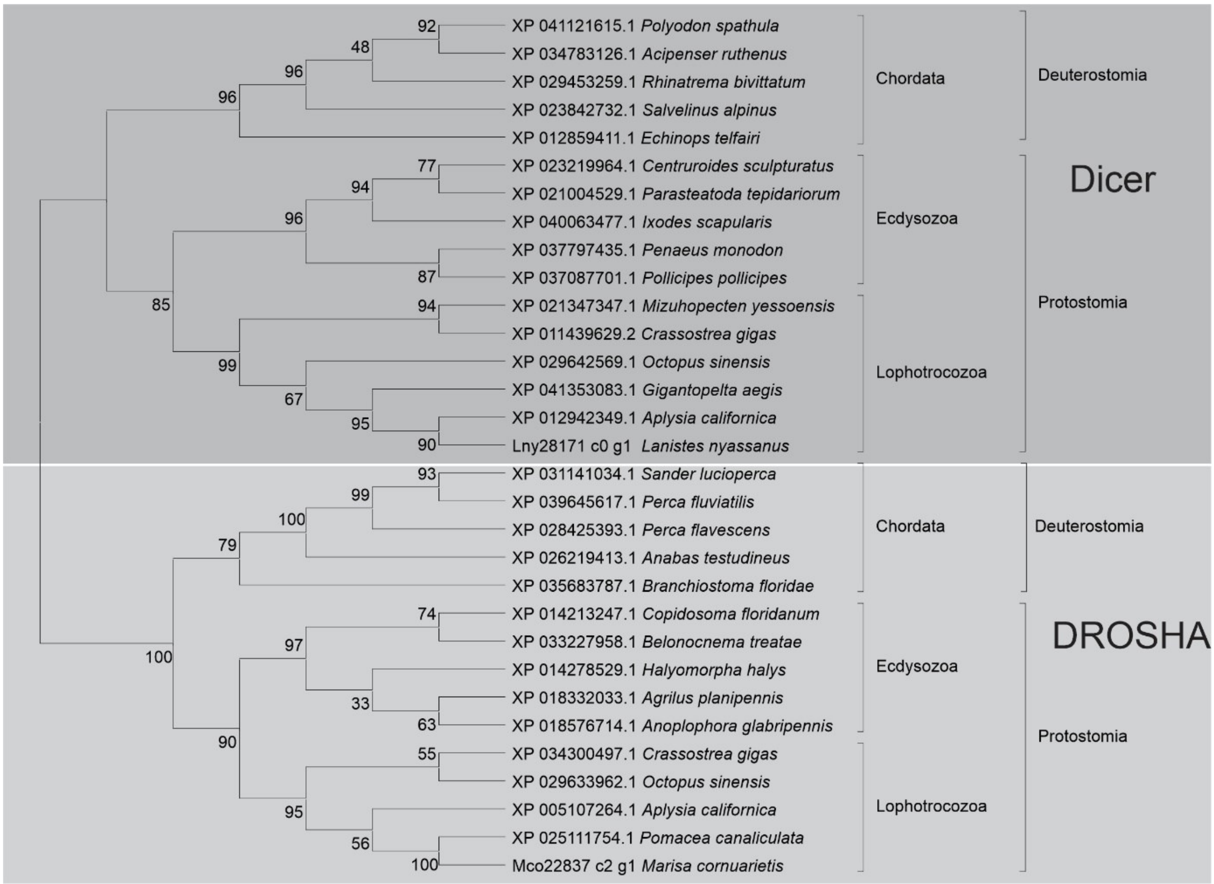


Fonte: Dados do autor

4.1.2.3 Árvore filogenética das proteínas Dicer e DROSHA

As proteínas Dicer e DROSHA pertencem a mesma classe de RNase III (BERNSTEIN *et al.*, 2001; BLASZCZYK *et al.*, 2001) e foram buscadas ortólogas semelhantes às proteínas Lny28171 c0 g1 e Mco22837 c2 g1 para construção da árvore filogenética (Figura 9). A disposição das ortólogas das prováveis DICER e DROSHA nos clados na árvore corroboraram com a árvore da vida, com visível distinção entre Deuterostômios e Protostômios para as duas classes de RNase.

Figura 9 – Distribuição filogenética das prováveis proteínas Dicer e DROSHA identificadas em *L. nyassanus, M. cornuarietis* e suas ortólogas.



Fonte: Dados do autor

4.1.3 Exportina

A busca pelas proteínas Exportinas (XPO1 e XPOT) utilizando como *query* as proteínas de *C. elegans* NP_001294153.1, NP_001368720.1 e de *D. melanogaster* NP_001303316.1, resultou nas prováveis proteínas traduzidas pelos genes: Mco1704_c0_g1, Mco24030_c0_g2, Lny29270_c0_g1 e Lny27692_c0_g2. O transporte de pré-miRNAs tem sido executado pelas proteína Exportinas com gasto de GTP (RUBY; JAN; BARTEL, 2007), e há menos tempo foram descrita também proteína XPO-1, como responsáveis por importar miRNAs aos núcleos.

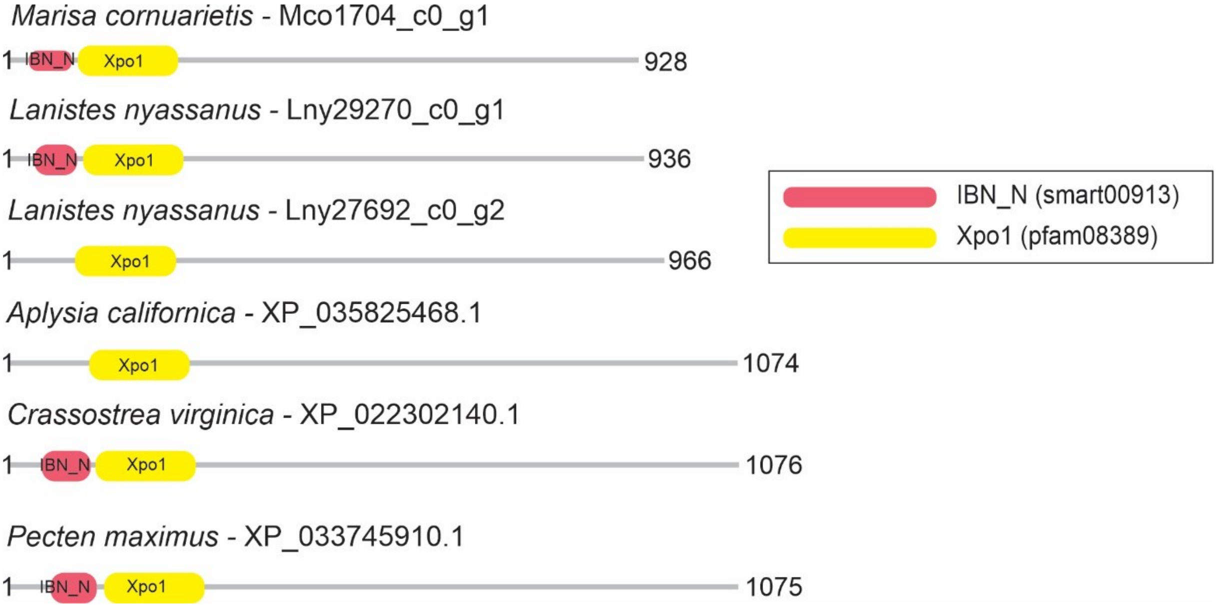
A análise dos domínios consensos, das candidatas a proteínas com relação às proteínas ortólogas presentes no banco de dados de NCBI CDD, a presença de domínios semelhantes entre as prováveis proteínas preditas para as espécies *L. nyassanus* e *M. cornuarietis* Tabela 10 e Figura 10. Nesse sentido, a presença do domínio conservado e seus resíduos de aminoácidos em posições definidas na proteína foram considerados relevantes para a determinação da conservação das proteínas analisadas. Além disso, as disposições dos domínios conservados, das representantes XPO-1 (IBN_N, XPO1 e CRM1_C), e XPO-t (XPO1), revelaram alto grau de similaridade entre as proteínas identificadas e suas ortólogas em *C. elegans*, *D. melanogaster*

Tabela 10 – Domínios conservados das proteínas DROSHA de *L. nyassanus* e *M. cornuarietis* e ortólogas.

Organismo	**Identificação / Extensão**	**Domínio**	**Início**	**Fim**	**E-Value**	**ID NCBI**
Marisa cornuarietis	Mco1704_c0_g1 (928)	Xpo1	101	249	1,89e^{-15}	pfam08389
		IBN_N	29	92	1,00e^{-04}	smart00913
Lanistes nyassanus	Lny29270_c0_g1 (936)	Xpo1	109	257	7,25e^{-15}	pfam08389
		IBN_N	37	100	1,15e^{-05}	smart00913
	Lny27692_c0_g2 (966)	Xpo1	97	246	1,25e^{-33}	pfam08389
Aplysia californica	XP_035825468.1 (1074)	Xpo1	118	266	2,19e^{-35}	pfam08389
Crassostrea virginica	XP_022302140.1 (1076)	Xpo1	127	275	7,06e^{-36}	pfam08389
		IBN_N	48	120	0.000607849	smart00913
Pecten maximus	XP_033745910.1 (1075)	Xpo1	140	288	2,47e^{-38}	pfam08389
		IBN_N	61	129	0.000828167	smart00913

Fonte: Dados do autor

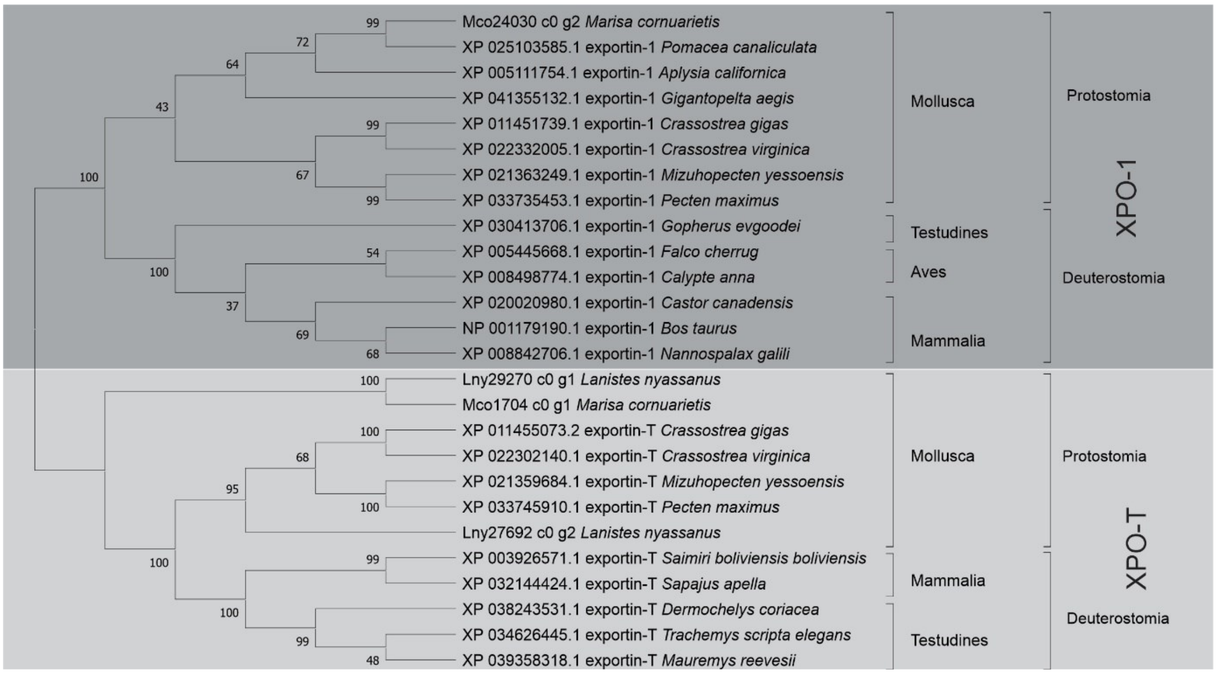
Figura 10 – Distribuição dos domínios conservados nas prováveis proteínas XPO de *M. cornuarietis L. nyassanus, A. californica, C. virginica* e *P. maximus.*



Fonte: Dados do autor

A árvore filogenética corroborou com a árvores da vida, agrupando em clados diferentes as proteínas XPO1 e XPOT, bem como as espécies pertencentes aos grupos Protostômios e Deuterostômios (Figura 11).

Figura 11 – Distribuição filogenética das prováveis proteínas XPO-1 e XPO-T identificadas em *L. nyassanus, M. cornuarietis* e suas ortólogas.



Fonte: Dados do autor

4.2 PREDIÇÃO DE miRNAS PERCURSORES E MADUROS

O genoma e transcritoma de *L. nyassanus* e *M. cornuarietis* foram processados de modo a buscar seguimentos em que suas estruturas secundárias formassem *hairpins*, conformação tomada pelos regiões que contém pré-miRNAs, e uma importante característica para a identificação dos miRNAs em genomas (HUANG *et al.*, 2007). A formação do *hairpin* ocasiona a variação negativa do valor de energia mínima livre (MFE).

O valor de energia mínima livre (MFE) menor que -20 kcal/mol para formação dos *hairpins*, é a primeira etapa de filtragem das sequências candidatas. Os pré-miRNAs identificados para *L. nyassanus* tiveram a média de suas MFE de -30,30 kcal/mol, sendo os valores máximo e mínimo encontrados respectivamente -18,50 e -50,90 kcal/mol. Para *M. cornuarietis* a média de MFE de -28,05 kcal/mol, sendo os valores máximo e mínimo encontrados respectivamente -18,50 e -67,10 kcal/mol (Tabela Suplementar 1, Tabela Suplementar 2).

Dentre os pré-miRNAs registrados no miRBase (release 19) aproximadamente 75% possuem valores de energia mínimas livre inferiores a -18,50 kcal/mol (LECLERCQ; DIALLO; BLANCHETTE, 2013). Trabalhos anteriores encontraram valores de energia mínimas livre entre -21,26 kcal/mol a -70,70 kcal/mol para o organismo *B. glabrata* (ADEMA *et al.*, 2017), dados semelhantes aos encontrados para este trabalho para os pré-miRNAs das duas espécies.

A etapa seguinte selecionou sequências com o conteúdo de citosina e guanina (CG) Os valores médios encontrados para *L. nyassanus* e *M. cornuarietis* foram respectivamente 41,26% e 41,64%. Os valores máximo e mínimo foram respectivamente 69,05 e 20,25% para *L. nyassanus* e 67,03% e 20,20% para *M. cornuarietis*.

Os valores encontrados para *L. nyassanus* e *M. cornuarietis* corroboram com os encontrados para *B. glabrata*, onde o máximo e mínimo foram respectivamente 60 e 31%, enquanto o valor médio foi de 44,35% (ADEMA *et al.*, 2017). O percentual de pré-miRNAs presentes no miRBase (versão 19) que possuíam conteúdo CG acima de 20% e inferior a 65% foi de 80% (LECLERCQ; DIALLO; BLANCHETTE, 2013).

Ao final dessas etapas foram identificados 142 precursores e 163 miRNAs maduros para a espécie *L. nyassanus* 279 precursores e 297 miRNAs maduros para *M. cornuarietis* (Tabela Suplementar 1, Tabela Suplementar 2). A predição de miRNAs a partir do genoma, similar ao trabalho, foram realizadas também para a espécie *B. glabrata,* sendo identificados 95 precursores e 102 miRNAs maduros (ADEMA *et al.*, 2017). O estudo de Huang *et al.* (2021) buscou através de Blast com os miRNAs disponíveis no miRBase os prováveis miRNAs de 35 espécies de moluscos, sendo encontrados no máximo 155 e 159 precursores e miRNAs maduros, respectivamente, no organismo *Conus tribblei,* e no mínimo 70 e 72 precursores e miRNAs maduros, respectivamente, para o organismo *L. gigantea.* A utilização de uma estratégia semelhante a deste trabalho, *in sílico,* para a busca de miRNAs identificou 149 miRNAs maduros e 131 precursores no platelminto *Schistosoma haematobium* (CARDOSO *et al.*, 2020).

A busca de miRNAs pode ser realizada também através de uma estratégia de sequenciamento de pequenos RNAs, diferente da utilizada em nosso trabalho. Utilizando do sequenciamento, Queiroz *et al.* (2020) identificaram em *B. glabrata* 68 pré-miRNAs e 89 miRNAs maduros. As diferenças nas quantidades de miRNAs encontrados provavelmente são devidos à variação na expressão de algum dos miRNAs em alguma fase da vida do animal, ou condição à qual ele foi submetido, problema não enfrentado na identificação através do genoma. Cada técnica deve ser empregada devido aos objetivos propostos, uma vez que através do genoma pode-se predizer a totalidade de miRNAs de uma espécie, e o sequenciamento pode identificar a expressão diferencial dos miRNAs durante o clico de vida e situações a que o organismo foi exposto.

Outros estudos que utilizaram a metodologia de sequenciamento de RNAs como o de Yu *et al.* (2020) relataram a identificação 137 miRNAs maduros para a espécie de molusco *Mytilus galloprovincialis*, sendo desses 34 inéditos. Picone; Rhode; Roodt-Wilding (2017), através do transcriptoma, identificaram 105 miRNAs maduros para a espécie de *H. midae*. A variação de número de miRNAs pode ser encontrada até em uma mesma espécie como por exemplo *H. cumingii* no qual foram identificados em exossomas de espécimes variantes de mantos branco e roxo respectivamente 136 e 159 miRNAs maduros, sendo que desses 125 são compartilhados entre as variantes (CHEN; BAI; LI, 2019).

4.3 ALINHAMENTO, ANÁLISE DA ESTRUTURA SECUNDÁRIA E ANÁLISE FILOGENÉTICA DOS miRNAS DE *L. nyassanus* E *M. cornuarietis*

Os miRNAs são estruturas que guardam alto índice de conservação entre espécies durante a evolução, e os miRNAs identificados em *L. nyassanus* e *M. cornuarietis* foram separados por sua presença exclusiva em clados filogenéticos. Os táxons que foram utilizados como parâmetro de seleção de espécies específicas são Bilatéria, Protostômios, Lophotrocozoa e Mollusca. Foram selecionados miRNAs comuns as duas espécies, e estes foram divididos devido a sua ocorrência em táxons específicos (Tabela 11).

Tabela 11 – Pré-miRNAs selecionados por táxon em *L. nyassanus* e *M. cornuarietis.*

Táxon	Espécie	Pré-miRNAs
Bilatéria	*L. nyassanus*	lny-mir-33, lny-mir-190, lny-mir-252a, lny-mir-281 e lny-mir-981
	M. cornuarietis	mcr-mir-33, mcr-mir-190, mcr-mir-252a, mcr-mir-281 e mcr-mir-981
Protostômios	*L. nyassanus*	lny-bantam, lny-mir-2a, lny-mir-67 e lny-mir-750
	M. cornuarietis	mcr-bantam, mcr-mir-2a, mcr-mir-67 e mcr-mir-750
Lophotrocozoa	*L. nyassanus*	lny-mir-96b, lny-mir-1990 e lny-mir-1994
	M. cornuarietis	mcr-mir-96b, mcr-mir-1990 e mcr-mir-1994
Moluscos	*L. nyassanus*	lny-mir-1985 e lny-mir-12096b
	M. cornuarietis	mcr-mir-1985 e mcr-mir-12096b

Fonte: Dados do autor

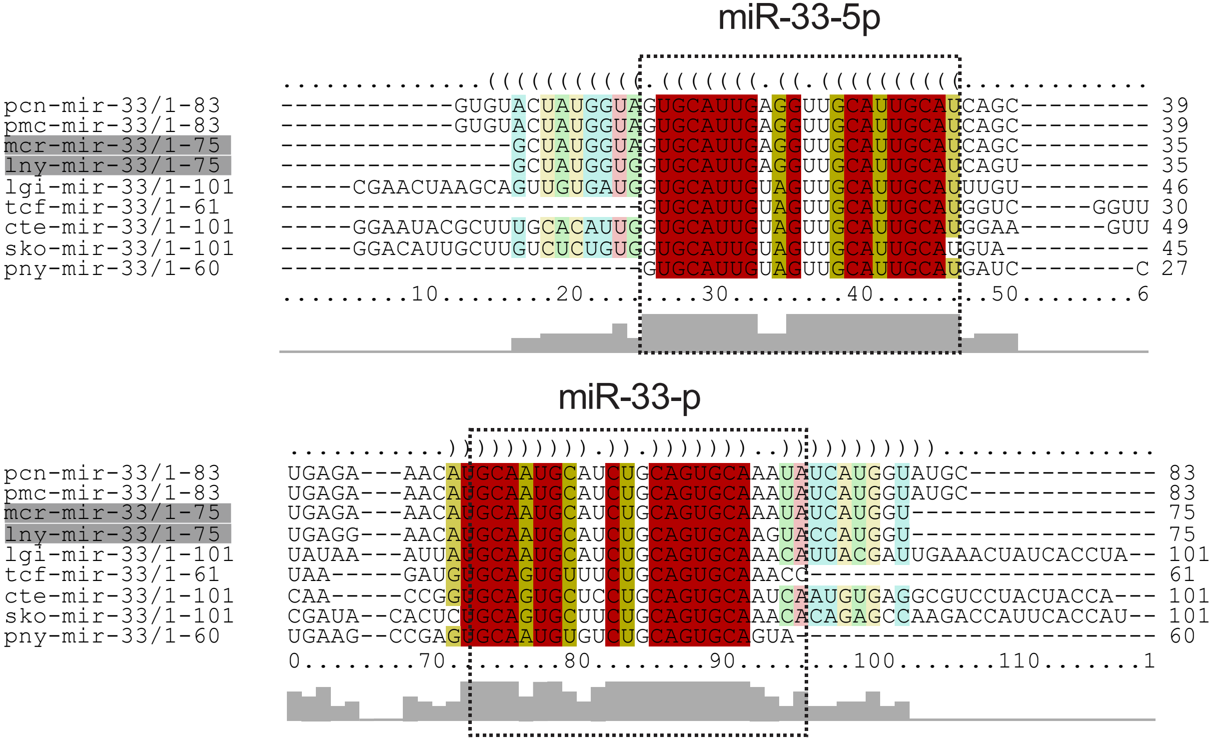
4.3.1 miRNAs Bilatéria específicos

O mais amplo clado filogenético selecionado para análise foi o grupo dos bilatérias, classificação pertencente ao reino metazoa. A divisão abriga os clados Protostômios e Deuterostômios. Os miRNAs precursores comum às duas espécies que também têm sua ocorrência em outras espécies do clado e possibilitaram sua análise filogenética foram o mir-33, mir-190, mir-252a, mir-281 e mir-981.

4.3.1.1 mir-33

A busca *in silico* de miRNAs nas espécies resultou em um precursor da família do mir-33 na espécie *L. nyassanus*, lny-mir-33 e em dois precursores da família em *M. cornuarietis*, mcr-mir-33 e mcr-mir-33b. Foi realizado o alinhamento dos precursores lny-mir-33 e mcr-mir-33 com ortólogos sendo identificado para duas espécies os miRNAs maduros miR-33-5p e miR-33-3p (Figura 12). e também foi realizada a predição das estruturas secundárias dos pré-miRNAs e seus ortólogos (Figura 13).

Figura 12 – Alinhamento do mir-33 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



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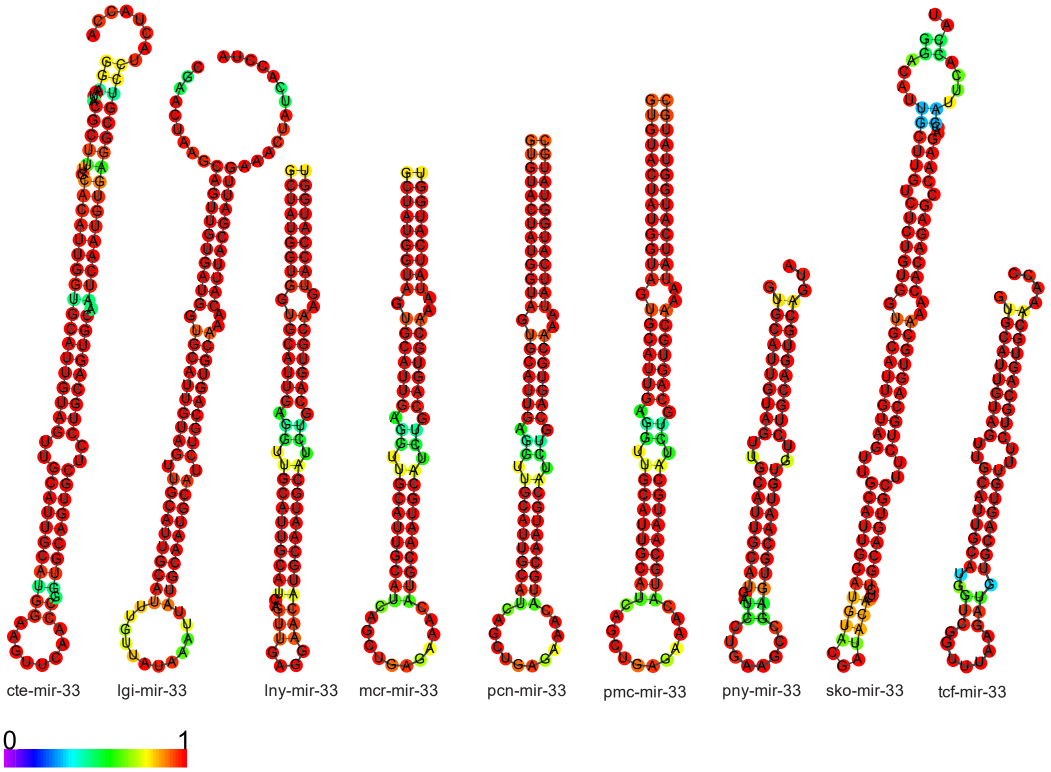
                    ..............(((((((((((.(((((((.((.((((((((((.............
pcn-mir-33/1-83     ------------GUGUACUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGC--------- 39
pmc-mir-33/1-83     ------------GUGUACUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGC--------- 39
mcr-mir-33/1-75     ----------------GCUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGC--------- 35
lny-mir-33/1-75     ----------------GCUAUGGUGGUGCAUUGAGGUUGCAUUGCAUCAGU--------- 35
lgi-mir-33/1-101    -----CGAACUAAGCAGUUGUGAUGGUGCAUUGUAGUUGCAUUGCAUUUGU--------- 46
tcf-mir-33/1-61     -------------------------GUGCAUUGUAGUUGCAUUGCAUGGUC-----GGUU 30
cte-mir-33/1-101    -----GGAAUACGCUUUGCACAUUGGUGCAUUGUAGUUGCAUUGCAUGGAA------GUU 49
sko-mir-33/1-101    -----GGACAUUGCUUGUCUCUGUGGUGCAUUGUAGUUGCAUUGCAUGUA---------- 45
pny-mir-33/1-60     -------------------------GUGCAUUGUAGUUGCAUUGCAUGAUC--------C 27
                    ........10........20........30........40........50........6

                    ...........)))))))))).)).)))))))..))))))))))).............. 
pcn-mir-33/1-83     UGAGA---AACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGUAUGC------------- 83
pmc-mir-33/1-83     UGAGA---AACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGUAUGC------------- 83
mcr-mir-33/1-75     UGAGA---AACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGU----------------- 75
lny-mir-33/1-75     UGAGG---AACAUGCAAUGCAUCUGCAGUGCAAGUACCAUGGU----------------- 75
lgi-mir-33/1-101    UAUAA---AUUAUGCAAUGCAUCUGCAGUGCAAACAUUACGAUUGAAACUAUCACCUA-- 101
tcf-mir-33/1-61     UAA-----GAUGUGCAGUGUUUCUGCAGUGCAAACC------------------------ 61
cte-mir-33/1-101    CAA-----CCGGUGCAGUGCUCCUGCAGUGCAAUCAAUGUGAGGCGUCCUACUACCA--- 101
sko-mir-33/1-101    CGAUA--CACUCUGCAGUGCUUCUGCAGUGCAAACACAGAGCCAAGACCAUUCACCAU-- 101
pny-mir-33/1-60     UGAAG--CCGAGUGCAAUGUGUCUGCAGUGCAGUA------------------------- 60
                    0........70........80........90........100.......110.......1
```

pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, lgi - *L. gigantea*, tcf - *Triops cancriformis*, cte - *Capitella teleta*, sko - *Saccoglossus kowalevskii*, pny - *Pundamilia nyererei.*

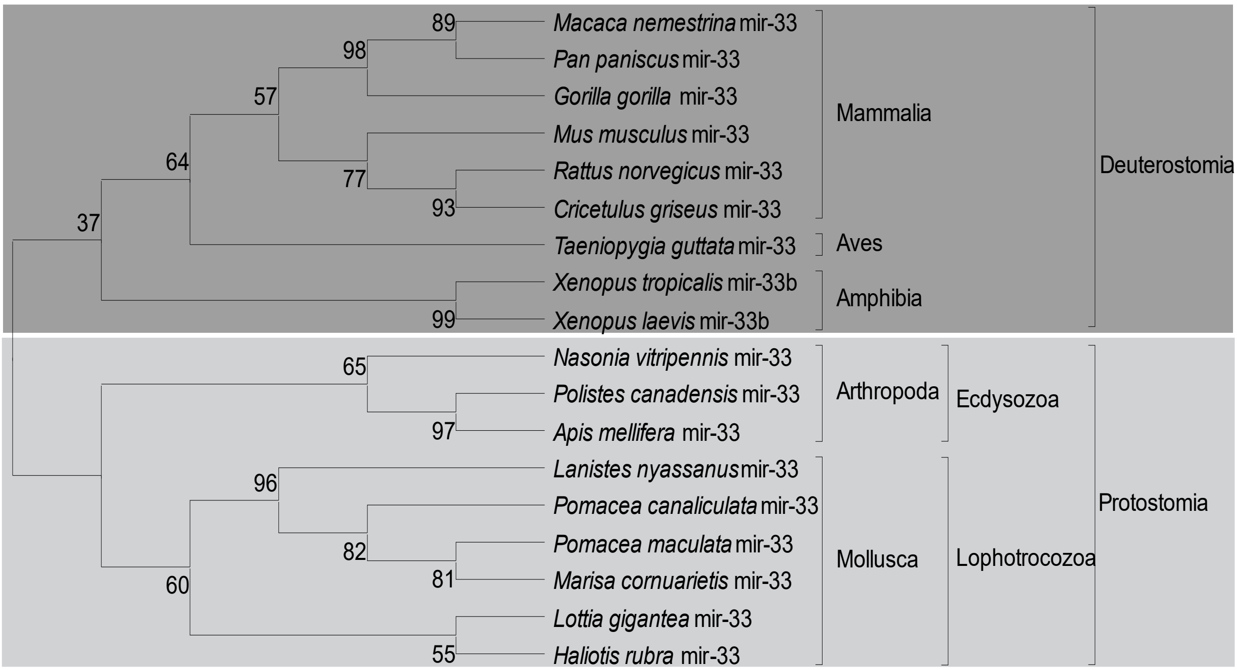
Figura 13 – Estrutura secundária do mir-33 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, lgi - *L. gigantea*, tcf - *Triops cancriformis*, cte - *C. teleta*, sko - *Saccoglossus kowalevskii*, pny - *Pundamilia nyererei.*

Variações na expressão do lgi-miR-33-5p, junto com outros miRNAs, podem estar relacionadas com variações nas cores de conchas de *C. gigas* (FENG *et al.*, 2020). A árvore filogenética mostrou a ocorrência do miRNA em Deuterostômios (mamíferos, aves e anfíbios), bem como em Protostômios (*Ecdysozoa* e *Lophotrocozoa*) (Figura 14).

Figura 14 – Distribuição filogenética mir-33 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



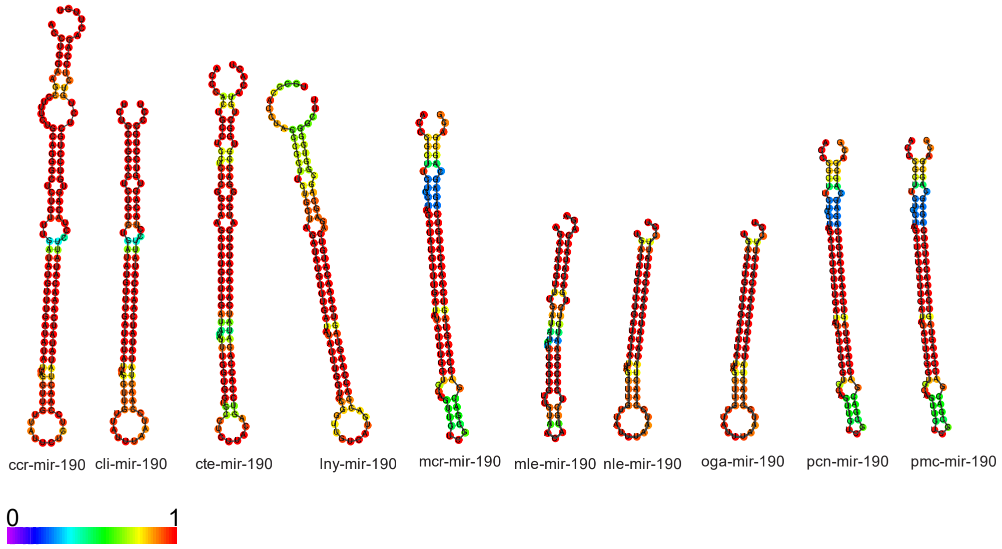
Fonte: Dados do autor

4.3.1.2 mir-190

A família do mir-190 apresentou apenas um precursor para cada uma das espécies, lny-mir-190 e mcr-mir-190, respectivamente. Apenas um miRNA maduro foi identificado para cada uma das espécies lny-miR-190-5p e mcr-miR-190-5p (

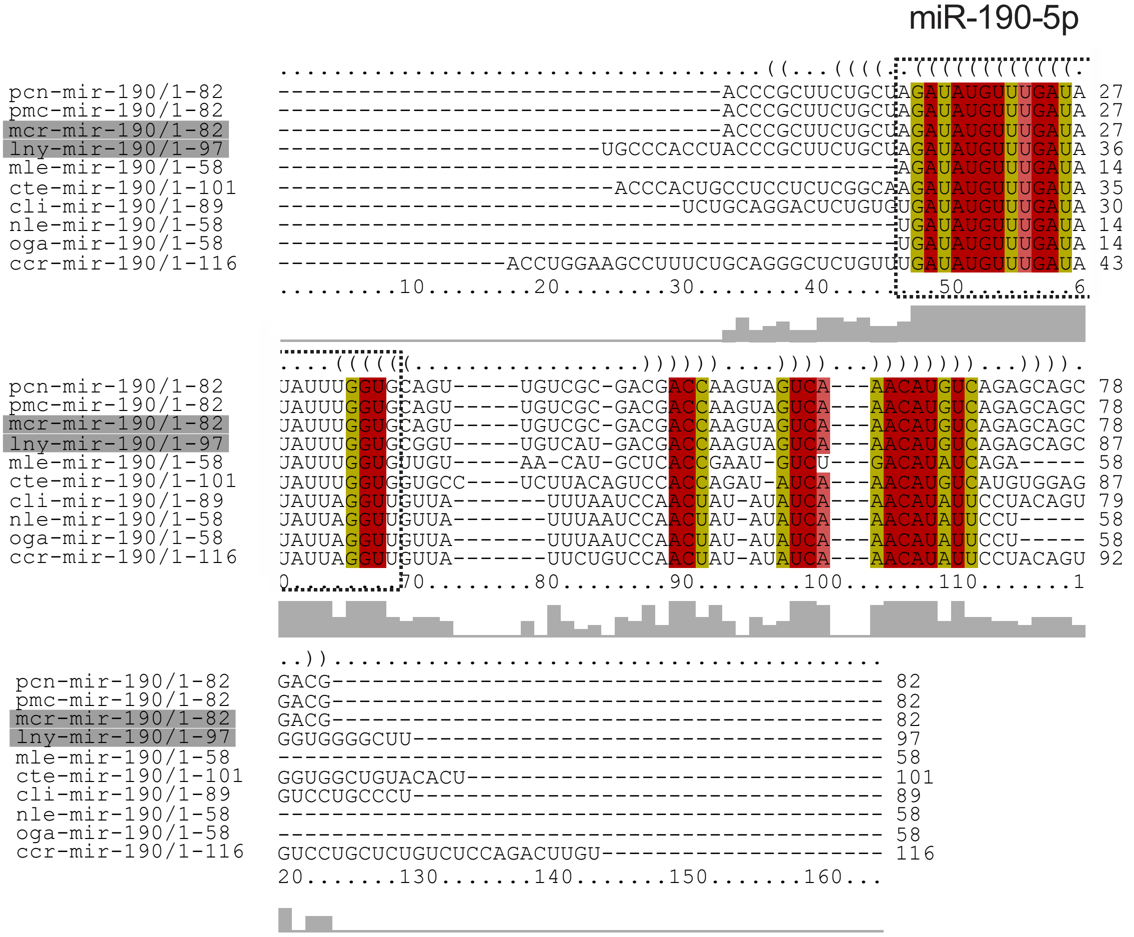
Figura 15, Figura 16).

Figura 15 – Estrutura secundária dos mir-190 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, mle - *M. leonina*, cte - *C. teleta*, cli - *Columba livia*, nle -*Nomascus leucogenys*, oga - *Otolemur garnettii*, ccr - *Cyprinus carpio*

Figura 16 – Alinhamento mir-190 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



```
                    ....................................((...((((.(((((((((((((.
pcn-mir-190/1-82    ---------------------------------ACCCGCUUCUGCUAGAUAUGUUUGAUA 27
pmc-mir-190/1-82    ---------------------------------ACCCGCUUCUGCUAGAUAUGUUUGAUA 27
mcr-mir-190/1-82    ---------------------------------ACCCGCUUCUGCUAGAUAUGUUUGAUA 27
lny-mir-190/1-97    ------------------------UGCCCACCUACCCGCUUCUGCUAGAUAUGUUUGAUA 36
mle-mir-190/1-58    ----------------------------------------------AGAUAUGUUUGAUA 14
cte-mir-190/1-101   -------------------------ACCCACUGCCUCCUCUCGGCAAGAUAUGUUUGAUA 35
cli-mir-190/1-89    ------------------------------UCUGCAGGACUCUGUGUGAUAUGUUUGAUA 30
nle-mir-190/1-58    ----------------------------------------------UGAUAUGUUUGAUA 14
oga-mir-190/1-58    ----------------------------------------------UGAUAUGUUUGAUA 14
ccr-mir-190/1-116   -----------------ACCUGGAAGCCUUUCUGCAGGGCUCUGUUUGAUAUGUUUGAUA 43
                    .........10........20........30........40........50........6

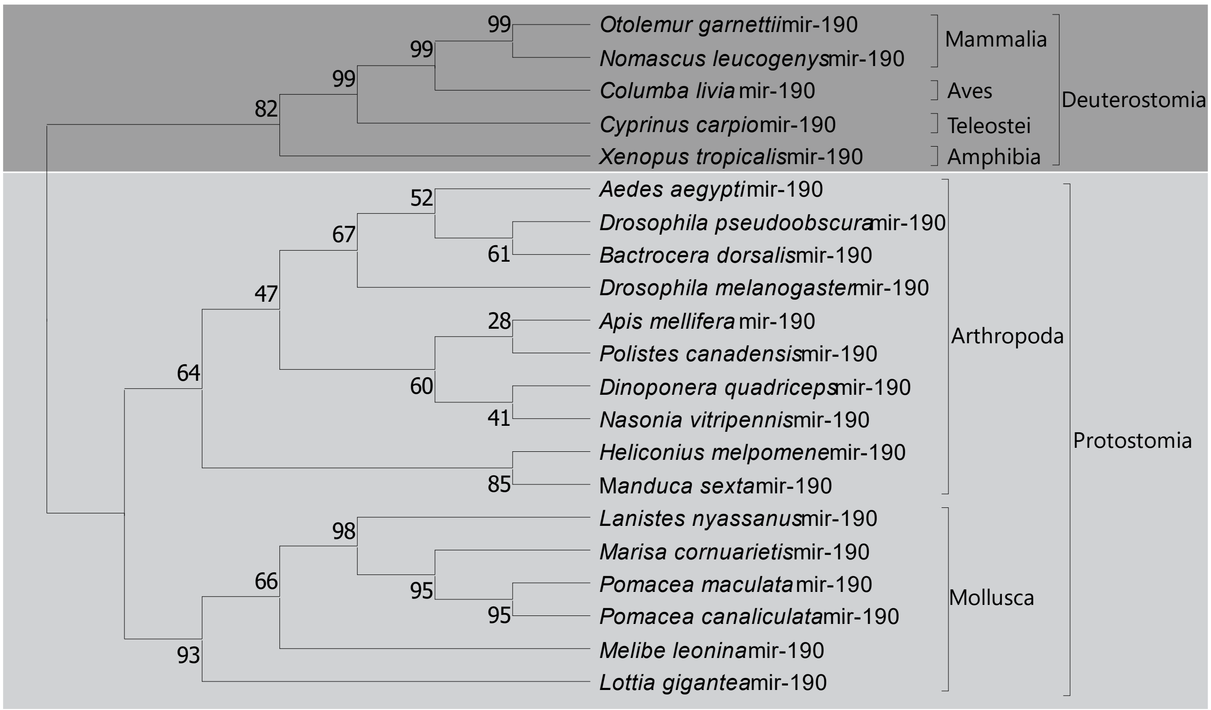
                    ....((((((................))))))....))))...))))))))...))))).
pcn-mir-190/1-82    UAUUUGGUGCAGU-----UGUCGC-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 78
pmc-mir-190/1-82    UAUUUGGUGCAGU-----UGUCGC-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 78
mcr-mir-190/1-82    UAUUUGGUGCAGU-----UGUCGC-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 78
lny-mir-190/1-97    UAUUUGGUGCGGU-----UGUCAU-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 87
mle-mir-190/1-58    UAUUUGGUGUUGU-----AA-CAU-GCUCACCGAAU-GUCU---GACAUAUCAGA----- 58
cte-mir-190/1-101   UAUUUGGUGGUGCC----UCUUACAGUCCACCAGAU-AUCA---AACAUGUCAUGUGGAG 87
cli-mir-190/1-89    UAUUAGGUUGUUA-------UUUAAUCCAACUAU-AUAUCA---AACAUAUUCCUACAGU 79
nle-mir-190/1-58    UAUUAGGUUGUUA-------UUUAAUCCAACUAU-AUAUCA---AACAUAUUCCU----- 58
oga-mir-190/1-58    UAUUAGGUUGUUA-------UUUAAUCCAACUAU-AUAUCA---AACAUAUUCCU----- 58
ccr-mir-190/1-116   UAUUAGGUUGUUA-------UUCUGUCCAACUAU-AUAUCA---AACAUAUUCCUACAGU 92
                    0........70........80........90........100.......110.......1

                    ..)).......................................
pcn-mir-190/1-82    GACG--------------------------------------- 82
pmc-mir-190/1-82    GACG--------------------------------------- 82
mcr-mir-190/1-82    GACG--------------------------------------- 82
lny-mir-190/1-97    GGUGGGGCUU--------------------------------- 97
mle-mir-190/1-58    ------------------------------------------- 58
cte-mir-190/1-101   GGUGGCUGUACACU----------------------------- 101
cli-mir-190/1-89    GUCCUGCCCU--------------------------------- 89
nle-mir-190/1-58    ------------------------------------------- 58
oga-mir-190/1-58    ------------------------------------------- 58
ccr-mir-190/1-116   GUCCUGCUCUGUCUCCAGACUUGU------------------- 116
                    20.......130.......140.......150.......160...
```

pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, mle - *M. leonina*, cte - *C. teleta*, cli - *Columba livia*, nle -*Nomascus leucogenys*, oga - *Otolemur garnettii*, ccr - *Cyprinus carpio*

O mir-190 foi encontrado ao longo da cadeia evolutiva sendo classificado como um miRNA bilatéria específico. Desse modo, representantes dos grupos Lophotrocozoa, Ecdysozoa e Deuterostômios estão presentes na árvore filogenética (Figura 17).

Figura 17 – Distribuição filogenética do mir-190 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



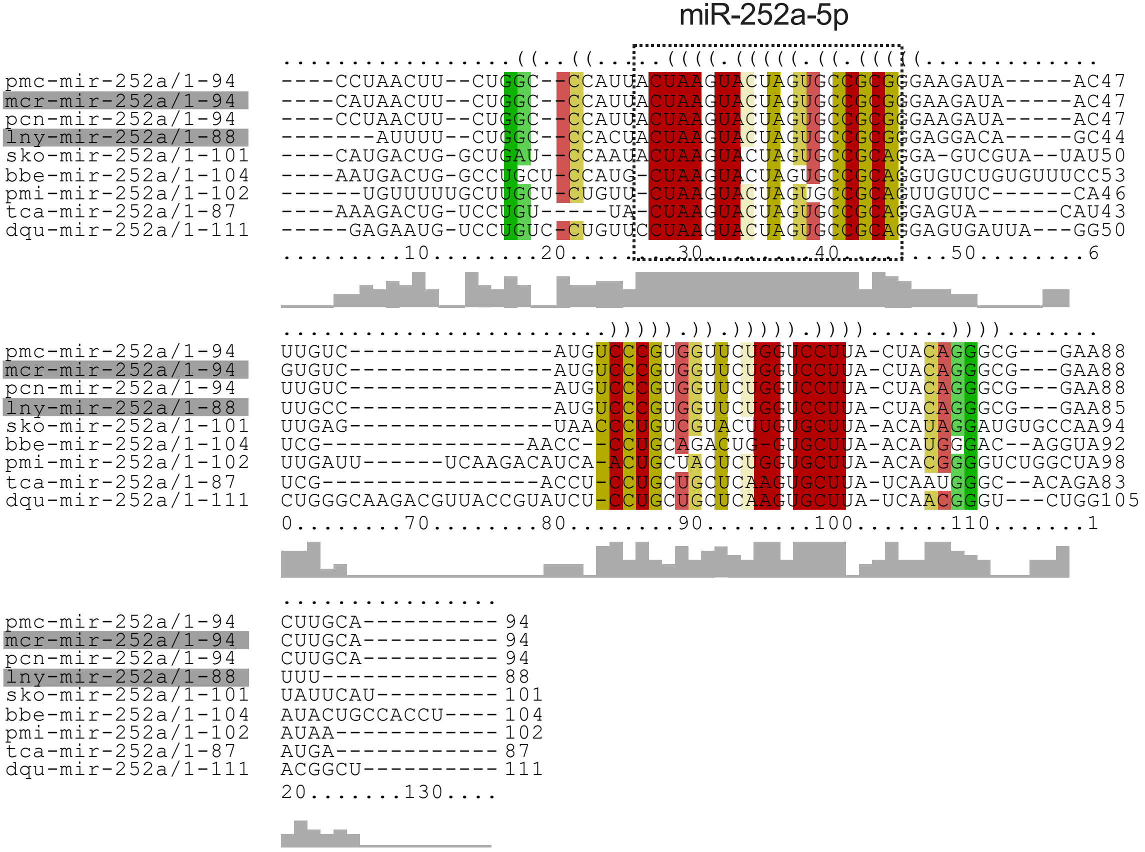
Fonte: Dados do autor

Variações da expressão do miRNA-190 podem estar relacionadas à indução ou inibição de apoptose (YANG *et al.*, 2012). A exposição de espécies ao inseticida diclorodifeniltricloroetano (DDT) pode levar a alterações na expressão com o aumento dos níveis de miRNA-190 circulantes (KALININA *et al.*, 2018).

4.3.1.3 mir-252a

A família do mir-252 foi identificada nas espécies *L. nyassanus,* representado pelo mir 252a, e em *M. cornuarietis,* representadas pelos mcr-mir-252a e mcr-mir-252. Com relação aos miRNAs maduros, foram identificados nas duas espécies apenas o miR-252a-5p. As sequências da espécie foram alinhadas com ortólogos e através do RNAfold foram preditas as estruturas secundárias (Figura 18 e Figura 19).

Figura 18 – Alinhamento mir-252a com seus ortólogos em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



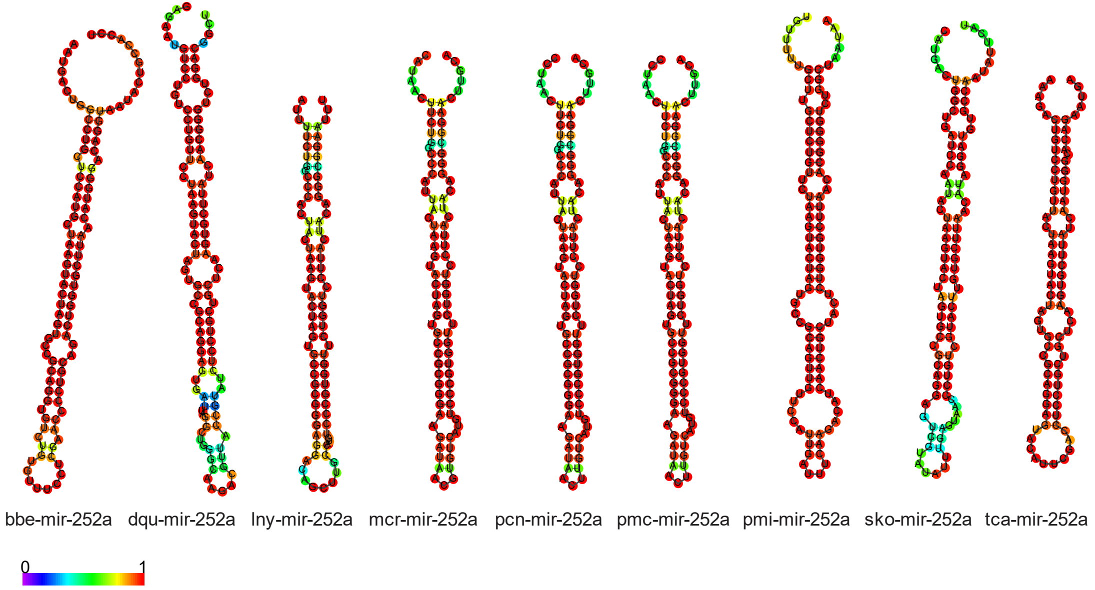
```
                                          miR-252a-5p
                      .................((..((......((((.(((((.((.(((((..............
pmc-mir-252a/1-94     ----CCUAACUU--CUGGC--CCAUUACUAAGUACUAGUGCCGCGGGAAGAUA-----AC47
mcr-mir-252a/1-94     ----CAUAACUU--CUGGC--CCAUUACUAAGUACUAGUGCCGCGGGAAGAUA-----AC47
pcn-mir-252a/1-94     ----CCUAACUU--CUGGC--CCAUUACUAAGUACUAGUGCCGCGGGAAGAUA-----AC47
lny-mir-252a/1-88     -------AUUUU--CUGGC--CCACUACUAAGUACUAGUGCCGCGGGAGGACA-----GC44
sko-mir-252a/1-101    ----CAUGACUG-GCUGAU--CCAAUACUAAGUACUAGUGCCGCAGGA-GUCGUA--UAU50
bbe-mir-252a/1-104    ----AAUGACUG-GCCUGCU-CCAUG-CUAAGUACUAGUGCCGCAGGUGUCUGUGUUUCC53
pmi-mir-252a/1-102    ------UGUUUUUGCUUGCU-CUGUU-CUAAGUACUAGUGCCGCAGUUGUUC------CA46
tca-mir-252a/1-87     ----AAAGACUG-UCCUGU-----UA-CUAAGUACUAGUGCCGCAGGAGUA------CAU43
dqu-mir-252a/1-111    -----GAGAAUG-UCCUGUC-CUGUUCCUAAGUACUAGUGCCGCAGGAGUGAUUA---GG50
                      .........10........20........30........40........50........6

                      .........................)))))).)).)))))).)))).......)))).......
pmc-mir-252a/1-94     UUGUC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA88
mcr-mir-252a/1-94     GUGUC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA88
pcn-mir-252a/1-94     UUGUC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA88
lny-mir-252a/1-88     UUGCC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA85
sko-mir-252a/1-101    UUGAG---------------UAACCCUGUCGUACUUGUGCUUA-ACAUAGGAUGUGCCAA94
bbe-mir-252a/1-104    UCG---------------AACC--CCUGCAGACUG-GUGCUUA-ACAUGGGAC--AGGUA92
pmi-mir-252a/1-102    UUGAUU------UCAAGACAUCA-ACUGCUACUCUGGUGCUUA-ACACGGGGUCUGGCUA98
tca-mir-252a/1-87     UCG-----------------ACCU-CCUGCUGCUCAAGUGCUUA-UCAAUGGGC--ACAGA83
dqu-mir-252a/1-111    CUGGGCAAGACGUUACCGUAUCU-CCUGCUGCUCAAGUGCUUA-UCAACGGGU---CUGG105
                      0........70........80........90........100.......110.......1

                      ..................
pmc-mir-252a/1-94     CUUGCA----------94
mcr-mir-252a/1-94     CUUGCA----------94
pcn-mir-252a/1-94     CUUGCA----------94
lny-mir-252a/1-88     UUU-------------88
sko-mir-252a/1-101    UAUUCAU---------101
bbe-mir-252a/1-104    AUACUGCCACCU----104
pmi-mir-252a/1-102    AUAA------------102
tca-mir-252a/1-87     AUGA------------87
dqu-mir-252a/1-111    ACGGCU----------111
                      20.......130....
```

pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, sko - *Saccoglossus kowalevskii,* bbe - *Branchiostoma belcherimle*, dqu -*Dinoponera quadríceps*, pmi - *Patiria miniatacte,* cte - *C. teleta*, tca - *Tribolium castaneumcli.*

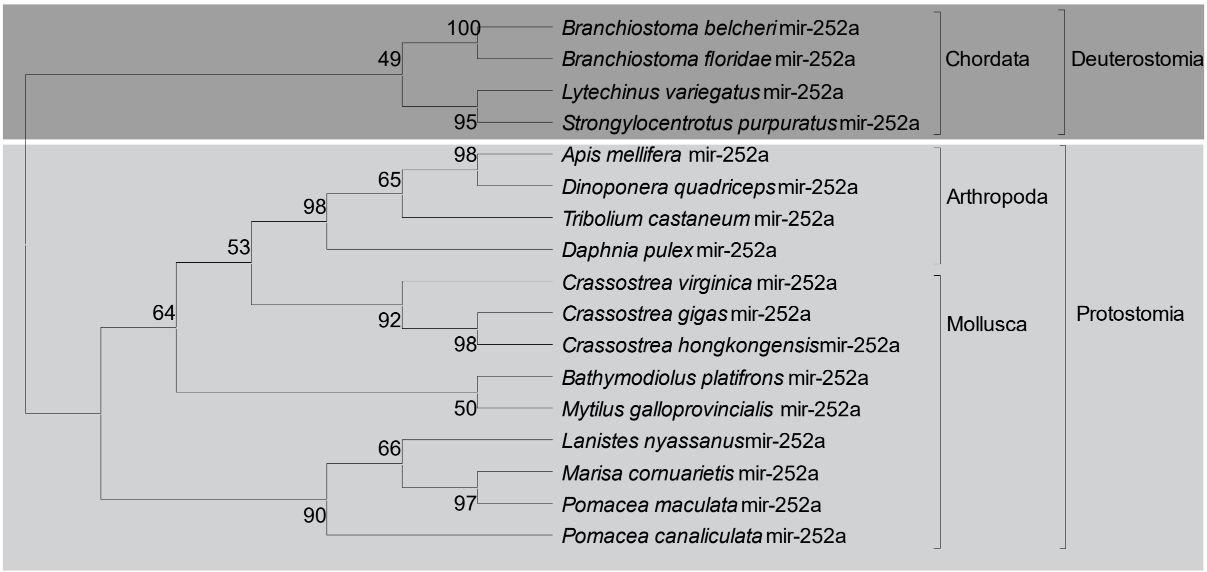
Figura 19 – Estrutura secundária dos mir-252a em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, sko - *Saccoglossus kowalevskii,* bbe - *Branchiostoma belcherimle*, dqu -*Dinoponera quadríceps*, pmi - *Patiria miniatacte,* cte - *C. teleta*, tca - *Tribolium castaneumcli.*

O mir 252a se encontra distribuído pelos clados protostômio (artrópodes e moluscos) e deuterostômio (equinodermas, cordados e nematoda), com maior número de representantes entre os protostômios (Figura 20), sendo expresso frente a situações de estivação em *Apostichopus japonicus* (CHEN *et al.*, 2013).

Figura 20– Distribuição filogenética do mir-252a em L. nyassanus e M. cornuarietis e seus ortólogos.

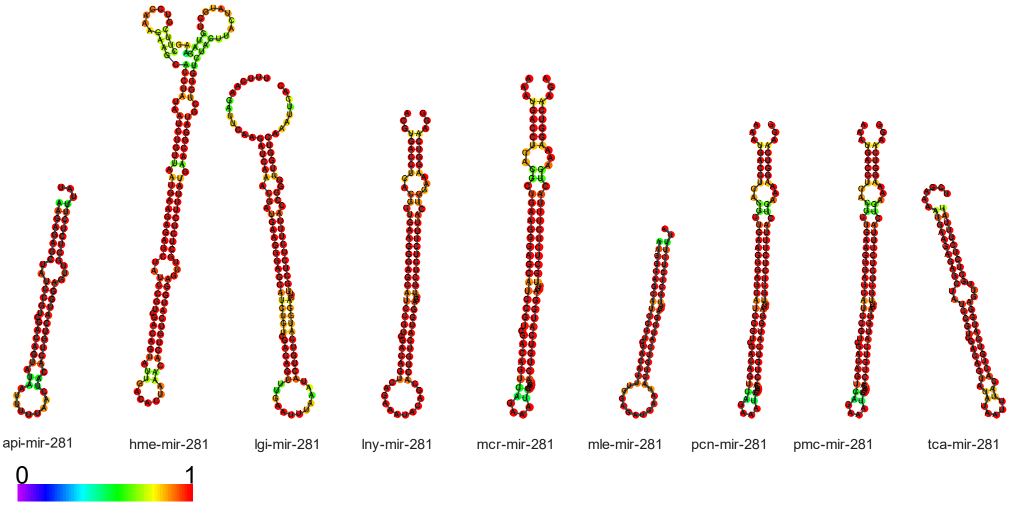


Fonte: Dados do autor

4.3.1.4 mir-281

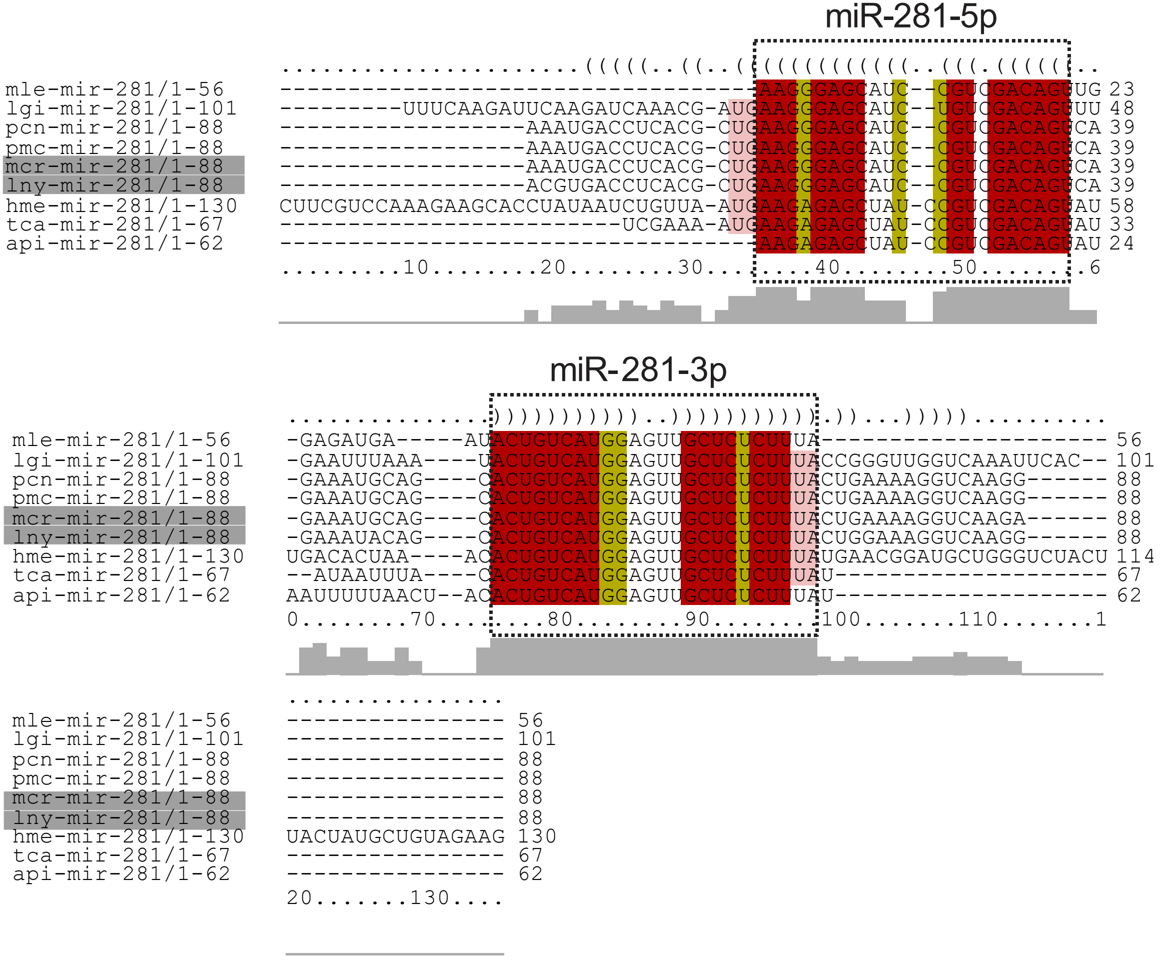
Foram identificados em *L. nyassanus* e *M. cornuarietis* a presença do mir-281. Este miRNA pertencente a família do mir46 e apresentou dois miRNAs maduros, conforme alinhamento com ortólogos para as duas espécies, miR-281-5p e miR-281-3p (Figura 21, Figura 22)

Figura 21 – Estrutura secundária dos mir-281 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



api - *Acyrthosiphon pisum*, hme - *Heliconius melpomene*, lny - *L. nyassanus*, lgi -*L. gigantea,* mcr - *M. cornuarietis*, mle - *M. leonina,* pcn - *P. canaliculata*, pmc - *P. maculata*, tca - *Tribolium castaneum.*

Figura 22 – Alinhamento mir-281 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



```
                     ......................(((((..((..(((((((((((((..(((.(((((..
mle-mir-281/1-56     -----------------------------------AAGGAGCAUC--CGUCGACAGUUG 23
lgi-mir-281/1-101    ---------UUUCAAGAUUCAAGAUCAAACG-AUGAAGGAGCAUC--UGUCGACAGUUU 48
pcn-mir-281/1-88     ------------------AAAUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
pmc-mir-281/1-88     ------------------AAAUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
mcr-mir-281/1-88     ------------------AAAUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
lny-mir-281/1-88     ------------------ACGUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
hme-mir-281/1-130    CUUCGUCCAAAGAAGCACCUAUAAUCUGUUA-AUGAAGAGAGCUAU-CCGUCGACAGUAU 58
tca-mir-281/1-67     --------------------------UCGAAA-AUGAAGAGAGCUAU-CCGUCGACAGUAU 33
api-mir-281/1-62     -----------------------------------AAGAGAGCUAU-CCGUCGACAGUAU 24
                     .........10........20........30........40........50........6

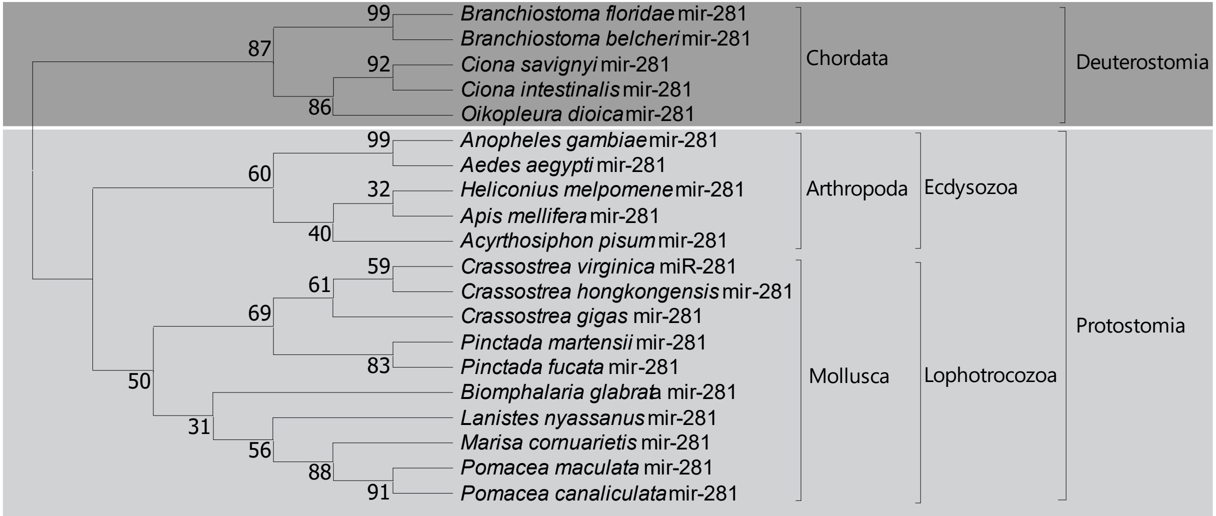
                     ..............)))))))))))..))))))))))).))...))))).........
mle-mir-281/1-56     -GAGAUGA-----AUACUGUCAUGGAGUUGCUCUCUUUA-------------------- 56
lgi-mir-281/1-101    -GAAUUUAAA----UACUGUCAUGGAGUUGCUCUCUUUACCGGGUUGGUCAAAUUCAC-- 101
pcn-mir-281/1-88     -GAAAUGCAG----CACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGG------ 88
pmc-mir-281/1-88     -GAAAUGCAG----CACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGG------ 88
mcr-mir-281/1-88     -GAAAUGCAG----CACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGA------ 88
lny-mir-281/1-88     -GAAAUACAG----CACUGUCAUGGAGUUGCUCUCUUUACUGGAAAGGUCAAGG------ 88
hme-mir-281/1-130    UGACACUAA----ACACUGUCAUGGAGUUGCUCUCUUUAUGAACGGAUGCUGGGUCUACU 114
tca-mir-281/1-67     --AUAAUUUA----CACUGUCAUGGAGUUGCUCUCUUUAU-------------------- 67
api-mir-281/1-62     AAUUUUUAACU--ACACUGUCAUGGAGUUGCUCUCUUUAU-------------------- 62
                     0........70........80........90........100.......110.......1

                     ................
mle-mir-281/1-56     ---------------- 56
lgi-mir-281/1-101    ---------------- 101
pcn-mir-281/1-88     ---------------- 88
pmc-mir-281/1-88     ---------------- 88
mcr-mir-281/1-88     ---------------- 88
lny-mir-281/1-88     ---------------- 88
hme-mir-281/1-130    UACUAUGCUGUAGAAG 130
tca-mir-281/1-67     ---------------- 67
api-mir-281/1-62     ---------------- 62
                     20.......130....
```

api - *Acyrthosiphon pisum*, hme - *Heliconius melpomene*, lny - *L. nyassanus*, lgi -*L. gigantea,* mcr - *M. cornuarietis*, mle - *M. leonina,* pcn - *P. canaliculata*, pmc - *P. maculata*, tca - *Tribolium castaneum.*

O mir-281 teve maior presença no clado Protostômios (Figura 23). A abundância desse miRNA em intestinos de *Aedes albopictus* favorece a replicação dos vírus da dengue (ZHOU *et al*., 2014a).

Figura 23 – Distribuição filogenética do mir-281 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.

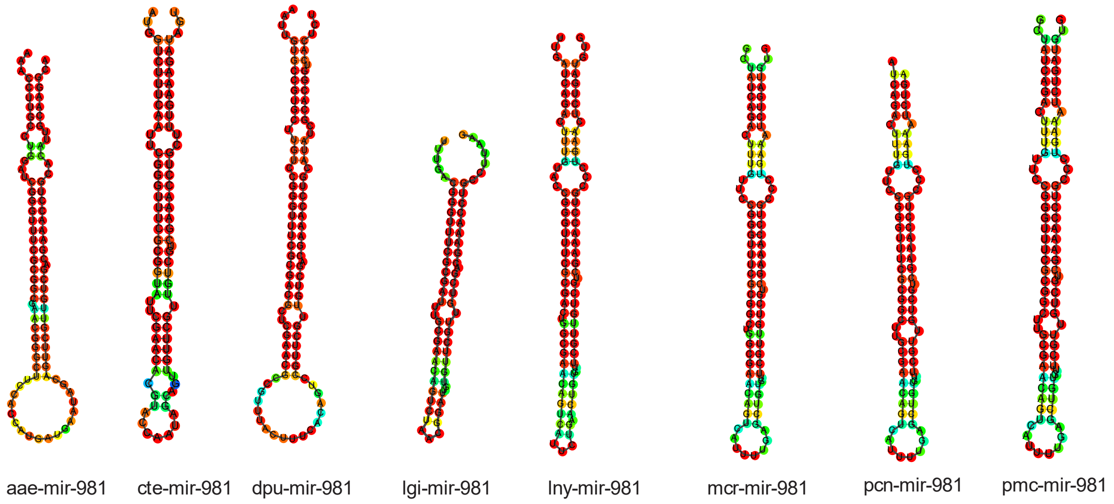


Fonte: Dados do autor

4.3.1.5 mir-981

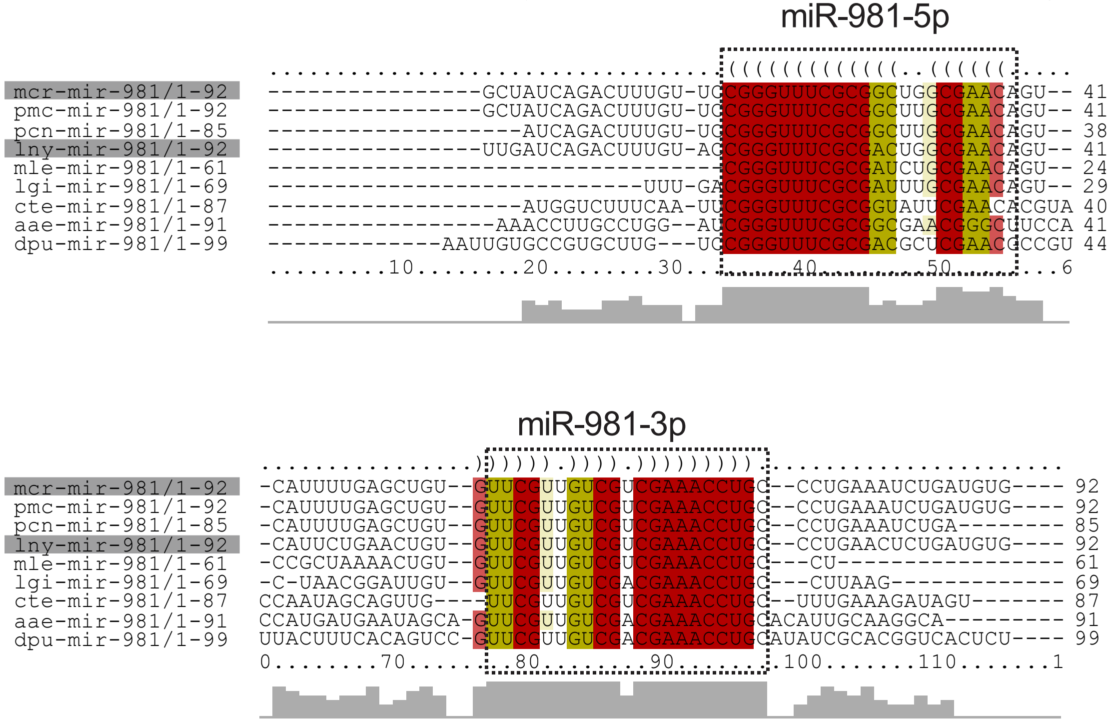
O precursor mir-981 apresentou dois miRNAs maduros nas espécies *L. nyassanus* e *M. cornuarietis,* miR-981-5p e miR-981-3p. O alinhamento com ortólogos, bem como suas estruturas secundárias confirmam uma conservação entre ortólogos (Figura 24, Figura 25).

Figura 24 – Estrutura secundária dos mir-981 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



aae - *Aedes aegypti,* dpu - *Daphnia pulex,* dme - *D. melanogaster* , lny - *L. nyassanus,* lgi - *L. gigantea,* mcr - *M. cornuarietis,* pcn - *P. canaliculata,* pmc - *P. maculata*

Figura 25 – Alinhamento mir-981 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



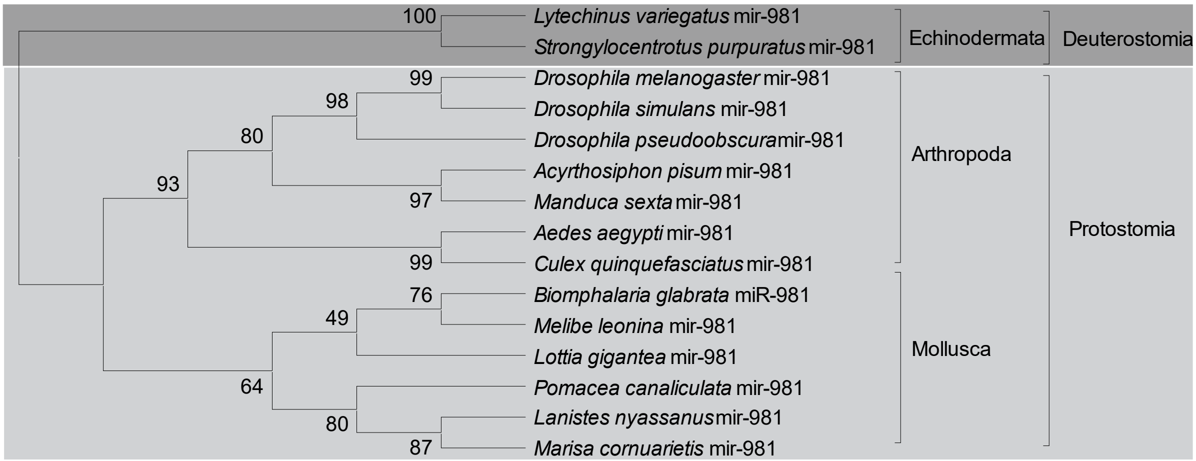
```
                  .................................(((((((((((((..((((((......
mcr-mir-981/1-92  ----------------GCUAUCAGACUUUGU-UCCGGGUUUCGCGGCUGGCGAACAGU-- 41
pmc-mir-981/1-92  ----------------GCUAUCAGACUUUGU-UCCGGGUUUCGCGGCUUGCGAACAGU-- 41
pcn-mir-981/1-85  -------------------AUCAGACUUUGU-UCCGGGUUUCGCGGCUUGCGAACAGU-- 38
lny-mir-981/1-92  ----------------UUGAUCAGACUUUGU-ACCGGGUUUCGCGACUGGCGAACAGU-- 41
mle-mir-981/1-61  ----------------------------------CGGGUUUCGCGAUCUGCGAACAGU-- 24
lgi-mir-981/1-69  ----------------------------UUU-GACGGGUUUCGCGAUUUGCGAACAGU-- 29
cte-mir-981/1-87  -------------------AUGGUCUUUCAA-UUCGGGUUUCGCGGUAUUCGAACACGUA 40
aae-mir-981/1-91  -----------------AAACCUUGCCUGG--AUCGGGUUUCGCGGCGAACGGGCUUCCA 41
dpu-mir-981/1-99  -------------AAUUGUGCCGUGCUUG---UCCGGGUUUCGCGACGCUCGAACGCCGU 44
                  .........10........20........30.........40.........50.........6

                  ................)))))).)))).))))))))).......................
mcr-mir-981/1-92  -CAUUUUGAGCUGU--GUUCGUUGUCGUCGAAACCUGC--CCUGAAAUCUGAUGUG---- 92
pmc-mir-981/1-92  -CAUUUUGAGCUGU--GUUCGUUGUCGUCGAAACCUGC--CCUGAAAUCUGAUGUG---- 92
pcn-mir-981/1-85  -CAUUUUGAGCUGU--GUUCGUUGUCGUCGAAACCUGC--CCUGAAAUCUGA-------- 85
lny-mir-981/1-92  -CAUUCUGAACUGU--GUUCGUUGUCGUCGAAACCUGC--CCUGAACUCUGAUGUG---- 92
mle-mir-981/1-61  -CCGCUAAAACUGU--GUUCGUUGUCGUCGAAACCUGC---CU----------------- 61
lgi-mir-981/1-69  -C-UAACGGAUUGU--GUUCGUUGUCGACGAAACCUGC---CUUAAG------------- 69
cte-mir-981/1-87  CCAAUAGCAGUUG----UUCGUUGUCGUCGAAACCUGC--UUUGAAAGAUAGU------- 87
aae-mir-981/1-91  CCAUGAUGAAUAGCA-GUUCGUUGUCGACGAAACCUGCACAUUGCAAGGCA--------- 91
dpu-mir-981/1-99  UUACUUUCACAGUCC-GUUCGUUGUCGACGAAACCUGCAUAUCGCACGGUCACUCU---- 99
                  0........70........80........90........100.......110.......1
```

aae - *Aedes aegypti*, dpu - *Daphnia pulex*, dme - *D. melanogaster* , lny - *L. nyassanus*, lgi - *L. gigantea*, mcr - *M. cornuarietis*, pcn - *P. canaliculata*, pmc - *P. maculata*

Há no miRBase poucos registros para o miR-981 entre Deuterostômios, o que é demonstrado pela distribuição filogenética. Entre Ecdysozoa o mir-981 pode reduzir a expressão da inportina beta4 e por consequência reduzir a distribuição de Argonauta-1 (HUSSAIN; O'NEILL; ASGARI, 2013).

Figura 26 – Distribuição filogenética do mir-981 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos



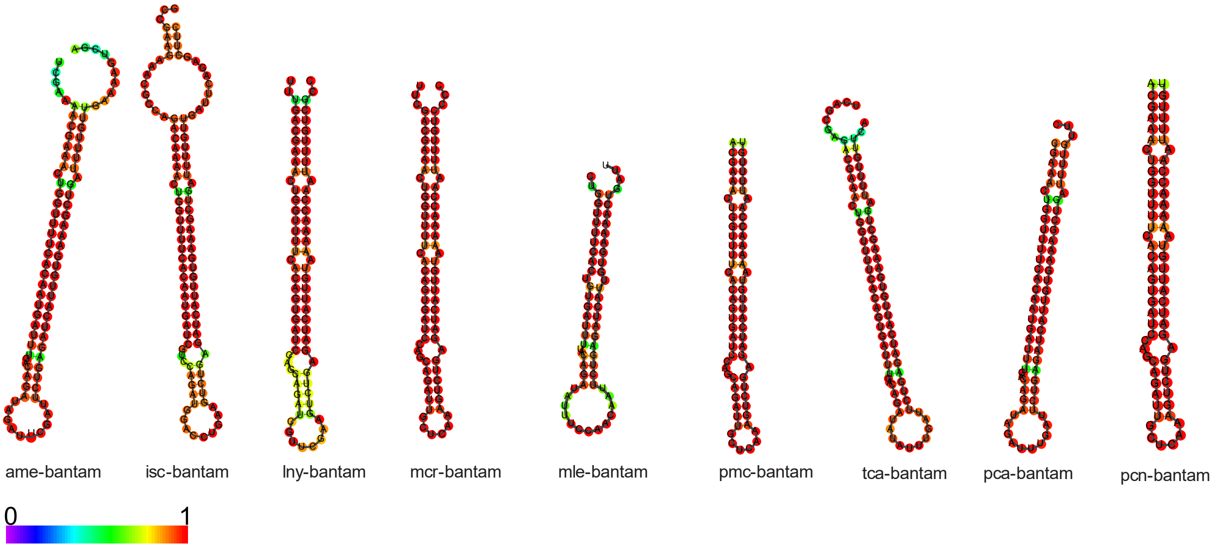
Fonte: Dados do autor

4.3.2 miRNAs Protostômios específicos

4.3.2.1 mir-bantam

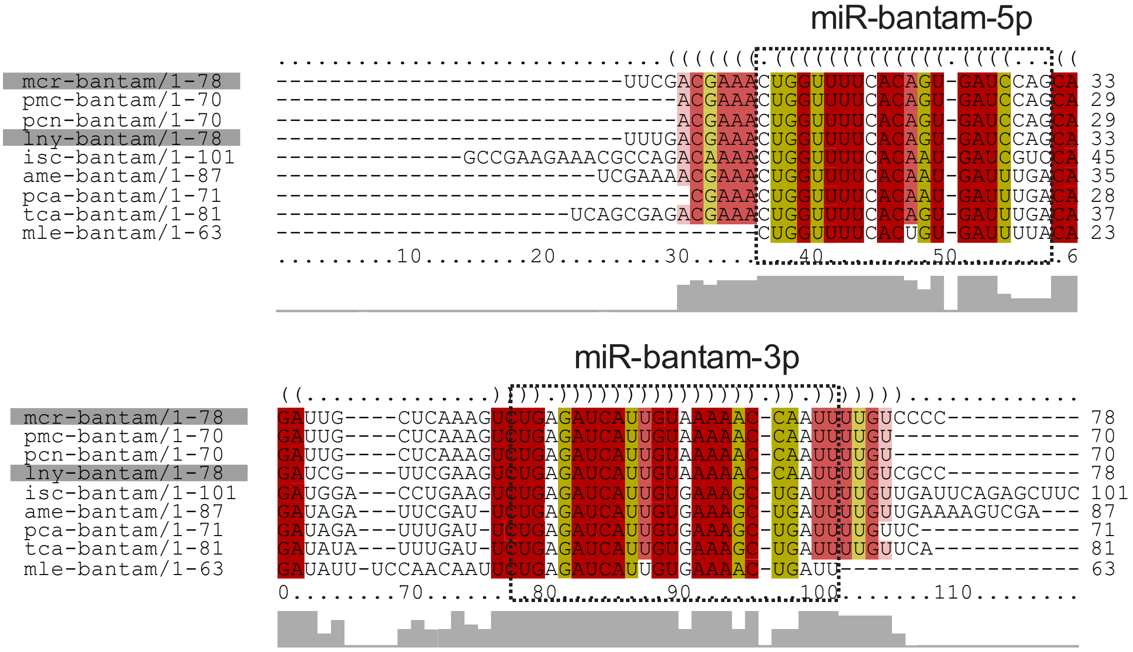
O precursor mir-Bantam e suas formas maduras miR-Bantam-5p e miR-Bantam-3p estão presentes nas espécies *L. nyassanus* e *M. cornuarietis.* Há uma grande conservação de nucleotídeos no alinhamento bem como uma similaridade entre as estruturas secundárias do miRNA (Figura 27, Figura 28).

Figura 27 – Estrutura secundária dos mir-Bantam em os *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



ame - *Apis melífera,* isc - *Ixodes scapularis,* lny - *L. nyassanus,* mcr - *M. cornuarietis,* pca - *Polistes canadenses,* pcn - *P. canaliculata,* pmc - *P. maculata*, tca - *Tribolium castaneum*

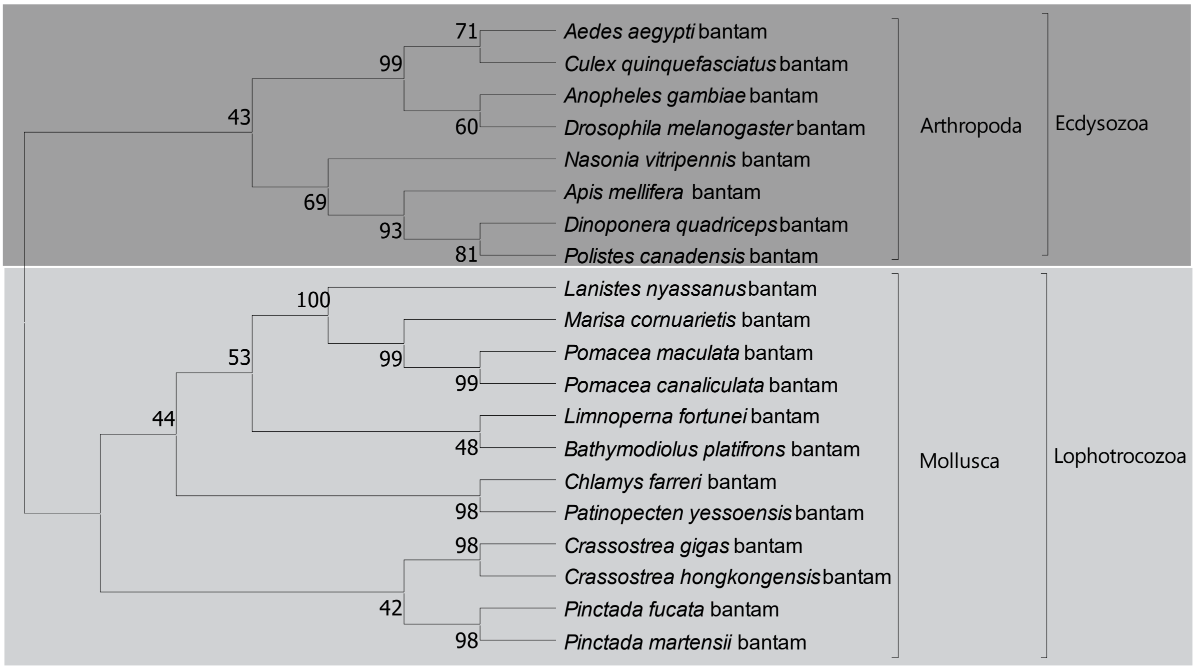
Figura 28 – Alinhamento mir-Bantam em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



ame - *Apis melífera,* isc - *Ixodes scapularis,* lny - *L. nyassanus,* mcr - *M. cornuarietis,* pca - *Polistes canadenses,* pcn - *P. canaliculata,* pmc - *P. maculata*, tca - *Tribolium castaneum*

O mir-Bantam está presente no organismo *B. glabrata* (ADEMA *et al.*, 2017; QUEIROZ *et al.*, 2020) e tem uma provável atuação neuronal pelo silenciamento de genes associados a sinapses (WU *et al.*, 2017), além do que os alvos gênicos preditos sugerem que ele pode estar também associado ao metabolismo do caramujo (QUEIROZ *et al.*, 2017).

Figura 29 – Distribuição filogenética do mir-Bantam *L. nyassanus* e *M. cornuarietis* e seus ortólogos

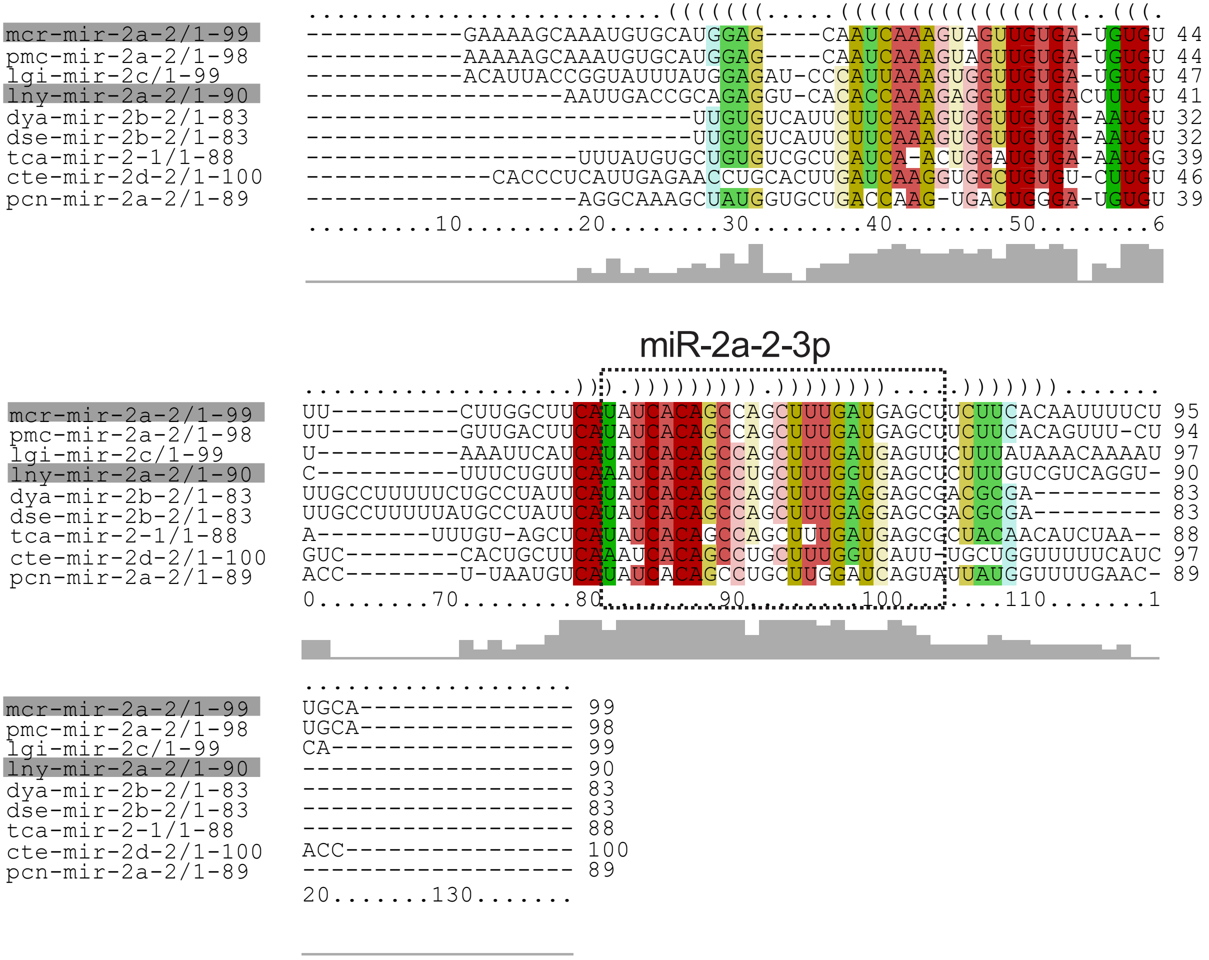


Fonte: Dados do autor

4.3.2.2 mir-2a-2

Foram identificados nas espécies *L. nyassanus* os seguintes miRNAs da família do miR-2: mir-2b-1, mir-2a-1, mir-2b-2, mir-2d e mir-2a-2. Na espécie *M. cornuarietis* foram identificados os seguintes miRNAs pertencentes à família: mir-2c, mir-2b-1, mir-2b-2, mir-2a-1, mir-2a-2 e mir-2a-3. Nas espécies foi identificado. O alinhamento do mir-2a das duas espécies revelou a presença de apenas um miRNA maduro o miR-2a-3p (Figura 30, Figura 31).

Figura 30 – Alinhamento mir-2a-2 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



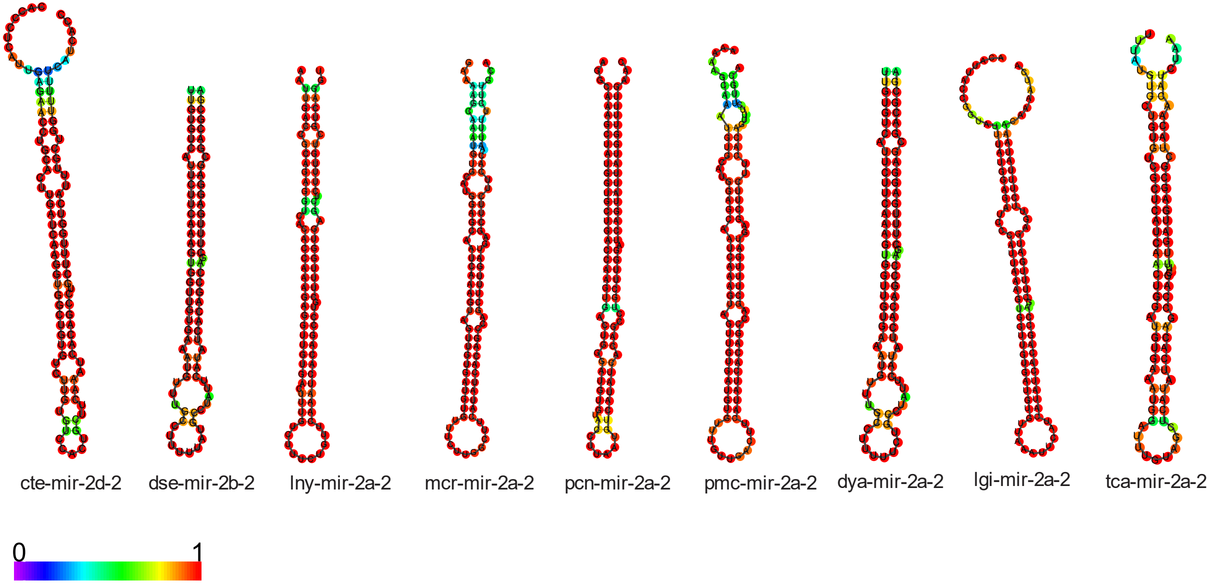
```
                      .........................((((((.....((((((((((((((((((..(((.
mcr-mir-2a-2/1-99     -----------GAAAAGCAAAUGUGCAUGGAG----CAAUCAAAGUAGUUGUGA-UGUGU 44
pmc-mir-2a-2/1-98     -----------AAAAAGCAAAUGUGCAUGGAG----CAAUCAAAGUAGUUGUGA-UGUGU 44
lgi-mir-2c/1-99       -----------ACAUUACCGGUAUUUAUGGAGAU-CCCAUUAAAGUGGUUGUGA-UGUGU 47
lny-mir-2a-2/1-90     ------------------AAUUGACCGCAGAGGU-CACACCAAAGAGGUUGUGACUUUGU 41
dya-mir-2b-2/1-83     ---------------------------UUGUGUCAUUCUUCAAAGUGGUUGUGA-AAUGU 32
dse-mir-2b-2/1-83     ---------------------------UUGUGUCAUUCUUCAAAGUGGUUGUGA-AAUGU 32
tca-mir-2-1/1-88      -------------------UUUAUGUGCUGUGUCGCUCAUCA-ACUGGAUGUGA-AAUGG 39
cte-mir-2d-2/1-100    -------------CACCCUCAUUGAGAACCUGCACUUGAUCAAGGUGGCUGUGU-CUUGU 46
pcn-mir-2a-2/1-89     -------------------AGGCAAAGCUAUGGUGCUGACCAAG-UGACUGGGA-UGUGU 39
                      ........10........20........30........40........50.........6

                      ...................)).)))))))))).))))))))......)))))))).......
mcr-mir-2a-2/1-99     UU---------CUUGGCUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAAUUUUCU 95
pmc-mir-2a-2/1-98     UU---------GUUGACUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAGUUU-CU 94
lgi-mir-2c/1-99       U----------AAAUUCAUCAUAUCACAGCCAGCUUUGAUGAGUUCUUUAUAAACAAAAU 97
lny-mir-2a-2/1-90     C----------UUUCUGUUCAAAUCACAGCCUGCUUUGGUGAGCUCUUUGUCGUCAGGU- 90
dya-mir-2b-2/1-83     UUGCCUUUUUCUGCCUAUUCAUAUCACAGCCAGCUUUGAGGAGCGACGCGA--------- 83
dse-mir-2b-2/1-83     UUGCCUUUUUAUGCCUAUUCAUAUCACAGCCAGCUUUGAGGAGCGACGCGA--------- 83
tca-mir-2-1/1-88      A--------UUUGU-AGCUCAUAUCACAGCCAGCUUUGAUGAGCGCUACAACAUCUAA-- 88
cte-mir-2d-2/1-100    GUC--------CACUGCUUCAAAUCACAGCCUGCUUUGGUCAUU-UGCUGGUUUUUCAUC 97
pcn-mir-2a-2/1-89     ACC--------U-UAAUGUCAUAUCACAGCCUGCUUGGAUCAGUAUUAUGGUUUUGAAC- 89
                      0.......70........80........90.......100.......110.........1

                      ....................
mcr-mir-2a-2/1-99     UGCA---------------- 99
pmc-mir-2a-2/1-98     UGCA---------------- 98
lgi-mir-2c/1-99       CA------------------ 99
lny-mir-2a-2/1-90     -------------------- 90
dya-mir-2b-2/1-83     -------------------- 83
dse-mir-2b-2/1-83     -------------------- 83
tca-mir-2-1/1-88      -------------------- 88
cte-mir-2d-2/1-100    ACC----------------- 100
pcn-mir-2a-2/1-89     -------------------- 89
                      20.......130.......
```

cte - *C. teleta*, dse - *Drosophila sechellia*, lny - *L. nyassanus,* mcr - *M. cornuarietis,* pcn - *P. canaliculata,* pmc - *P. maculata*, dya - *Drosophila yakuba*, lgi - *L. gigantea,* tca - *Tribolium castaneum*

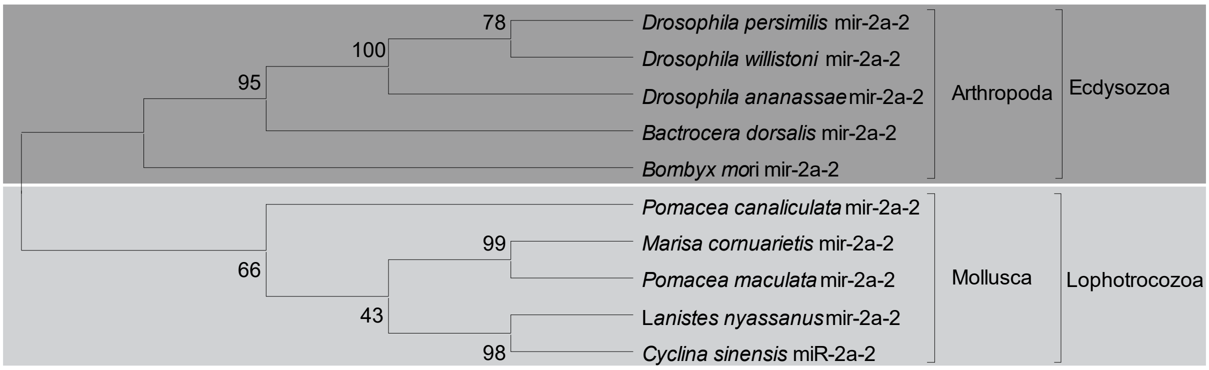
Figura 31 – Estrutura secundária dos mir-2a-2 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



cte - *C. teleta*, dse - *Drosophila sechellia*, lny - *L. nyassanus,* mcr - *M. cornuarietis,* pcn - *P. canaliculata,* pmc - *P. maculata*, dya - *Drosophila yakuba*, lgi - *L. gigantea,* tca - *Tribolium castaneum*

O mir-2a pode estar relacionado com a expressão de Ciclínas durante os ciclos de divisões celulares através da complementariedade a regiões in 3′-UTR da ciclína B (SONG *et al.*, 2014), além de poderem em conjunto com outros miRNAs estarem ligados as respostas de moluscos ao stress induzido pela exposição aos metais pesados (BAO *et al.*, 2014). A distribuição filogenética do miRNA mostra um maior número de artrópodes (Figura 32).

Figura 32 – Distribuição filogenética do mir-2a-2 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.

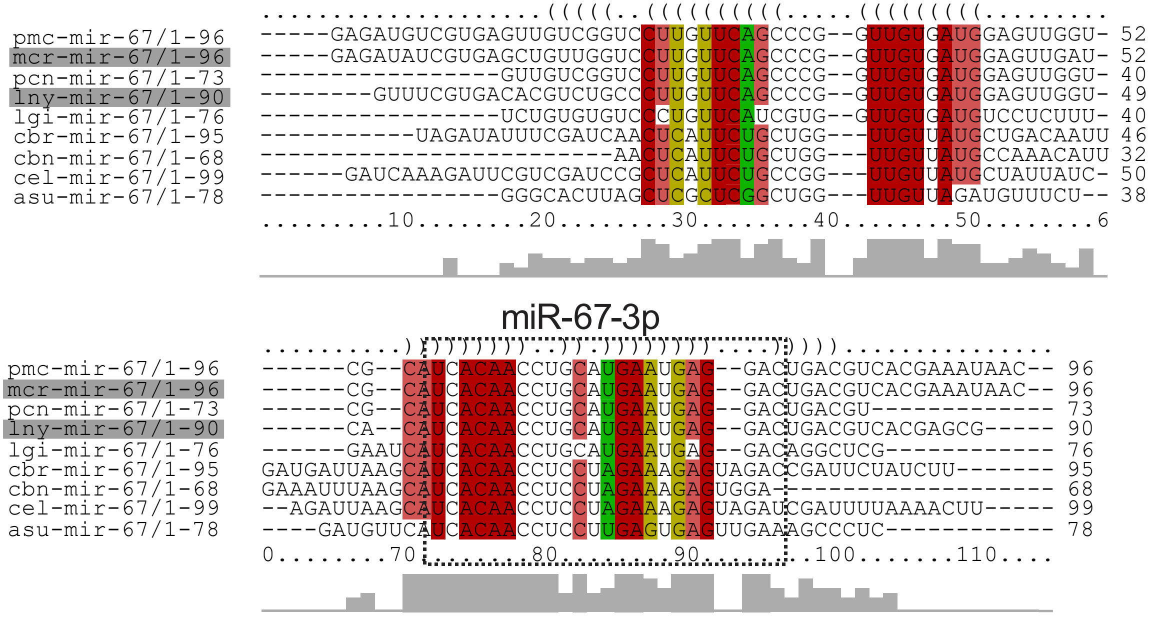


Fonte: Dados do autor

4.3.2.3 mir-67

Foram encontrados em *L. nyassanus* e *M. cornuarietis* apenas o precursor mir-67 como representante da família mir-67. Para estas duas espécies foi encontrado apenas o maduro miR-67-3p (Figura 33, Figura 34).

Figura 33 – Alinhamento mir-67 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.

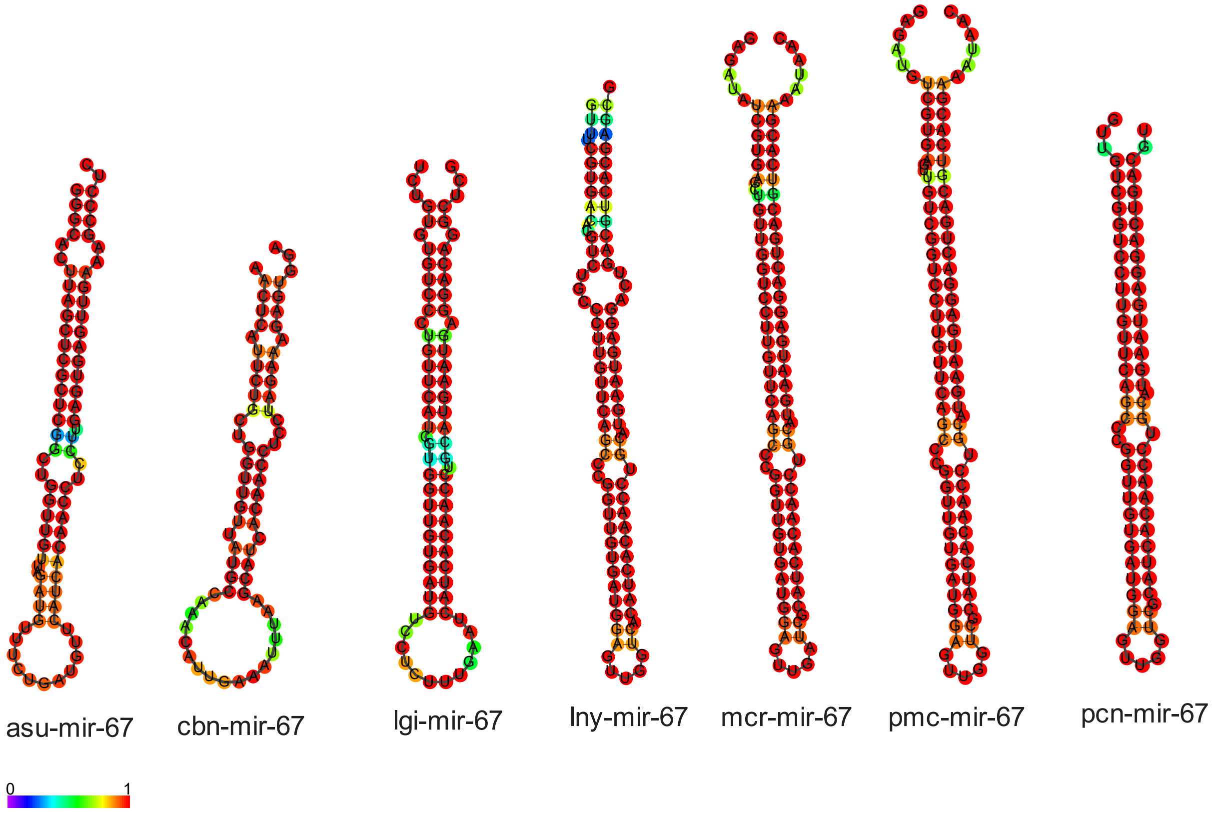


```
                    ....................(((((..(((((((((.....(((((((((..........
pmc-mir-67/1-96     -----GAGAUGUCGUGAGUUGUCGGUCCUUGUUCAGCCCG--GUUGUGAUGGAGUUGGU- 52
mcr-mir-67/1-96     -----GAGAUAUCGUGAGCUGUUGGUCCUUGUUCAGCCCG--GUUGUGAUGGAGUUGAU- 52
pcn-mir-67/1-73     ----------------GUUGUCGGUCCUUGUUCAGCCCG--GUUGUGAUGGAGUUGGU- 40
lny-mir-67/1-90     --------GUUUCGUGACACGUCUGCCCUUGUUCAGCCCG--GUUGUGAUGGAGUUGGU- 49
lgi-mir-67/1-76     ----------------UCUGUGUGUCCCUGUUCAUCGUG--GUUGUGAUGUCCUCUUU- 40
cbr-mir-67/1-95     -----------UAGAUAUUUCGAUCAACUCAUUCUGCUGG---UUGUUAUGCUGACAAUU 46
cbn-mir-67/1-68     ------------------------AACUCAUUCUGCUGG---UUGUUAUGCCAAACAUU 32
cel-mir-67/1-99     ------GAUCAAAGAUUCGUCGAUCCGCUCAUUCUGCCGG---UUGUUAUGCUAUUAUC- 50
asu-mir-67/1-78     ----------------GGGCACUUAGCUCGCUCGGCUGG---UUGUUAGAUGUUUCU-- 38
                    .........10........20........30........40........50........6

                    ..........)))))))))..)).))))))))....)))))...............
pmc-mir-67/1-96     ------CG--CAUCACAACCUGCAUGAAUGAG--GACUGACGUCACGAAAUAAC-- 96
mcr-mir-67/1-96     ------CG--CAUCACAACCUGCAUGAAUGAG--GACUGACGUCACGAAAUAAC-- 96
pcn-mir-67/1-73     ------CG--CAUCACAACCUGCAUGAAUGAG--GACUGACGU------------- 73
lny-mir-67/1-90     ------CA--CAUCACAACCUGCAUGAAUGAG--GACUGACGUCACGAGCG----- 90
lgi-mir-67/1-76     ------GAAUCAUCACAACCUGCAUGAAUGAG--GACAGGCUCG------------ 76
cbr-mir-67/1-95     GAUGAUUAAGCAUCACAACCUCCUAGAAAGAGUAGACCGAUUCUAUCUU------- 95
cbn-mir-67/1-68     GAAAUUUAAGCAUCACAACCUCCUAGAAAGAGUGGA-------------------- 68
cel-mir-67/1-99     --AGAUUAAGCAUCACAACCUCCUAGAAAGAGUAGAUCGAUUUUAAACUU------ 99
asu-mir-67/1-78     ----GAUGUUCAUCACAACCUCCUUGAGUGAGUUGAAAGCCCUC------------ 78
                    0........70........80........90........100.......110....
```

asu - *Ascaris suum*, cbn - *Caenorhabditis brenneri*, cbr - *Caenorhabditis briggsae*, cel - *C. elegans*, lny – *L. nyassanus* , lgi - *L. gigantea*, mcr-*M. cornuarietis* , pcn - *P. canaliculata*, pmc - *P. maculata*

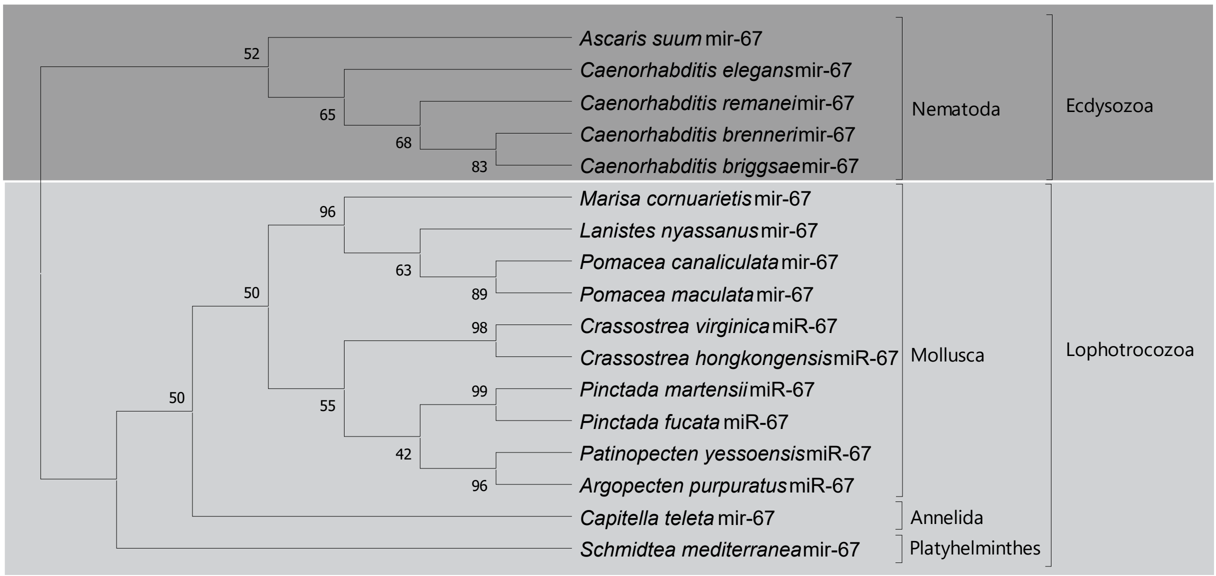
Figura 34 – Estrutura secundária dos mir-67 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



asu - *Ascaris suum*, cbn - *Caenorhabditis brenneri*, cbr - *Caenorhabditis briggsae*, cel - *C. elegans*, lny – *L. nyassanus* , lgi - *L. gigantea*, mcr-*M. cornuarietis* , pcn - *P. canaliculata*, pmc - *P. maculata*

O mir-67 está presente em Ecdysozoas (nematódeas) e Lophotrocozoas (anelídeos, moluscos e platelmintos). Zhou *et al.*, (2014b), identificaram altos níveis do miR-67a em células de defesa de um grupo controle de *C. gigas* em um experimento em que os moluscos seriam desafiados frente a infecção bacteriana.

Figura 35 – Distribuição filogenética do mir-67 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.

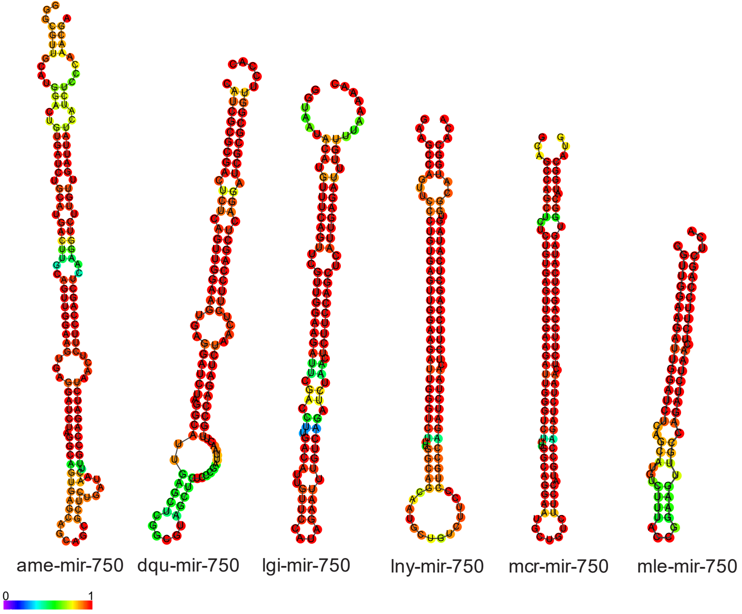


Fonte: Dados do autor

4.3.2.4 mir-750

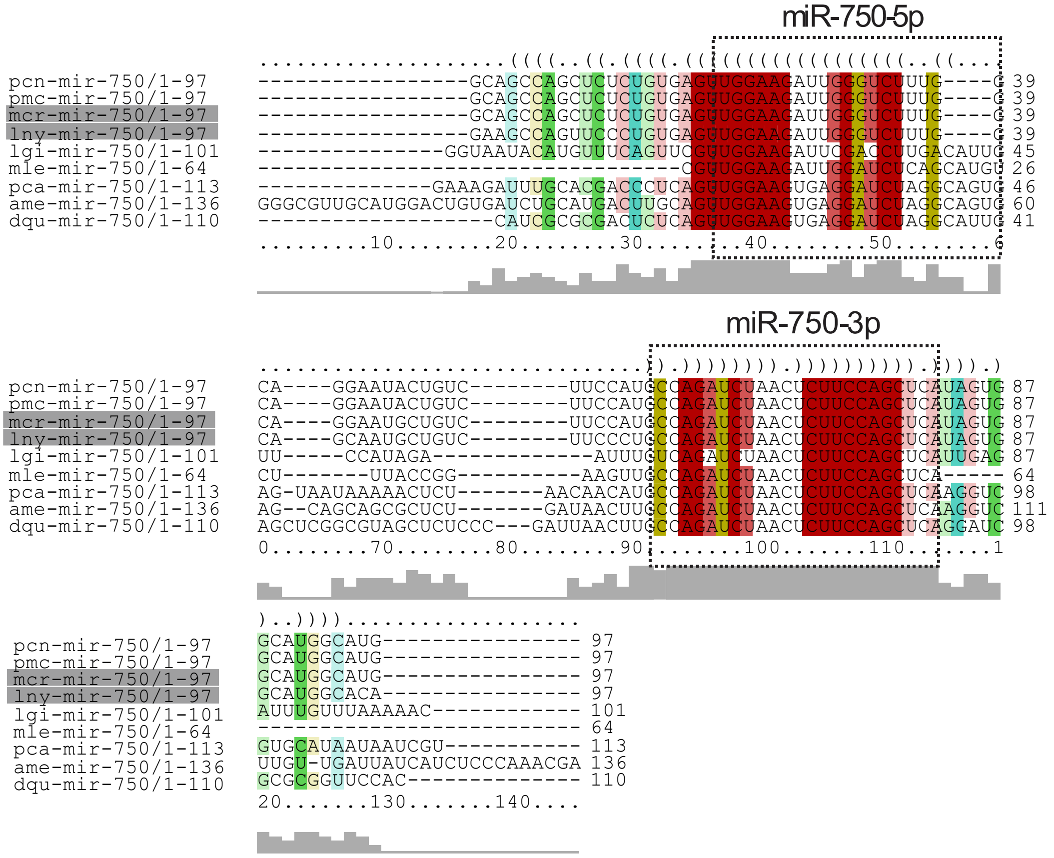
A família do mir-750 apresentou o precursor mir-750 nas espécies *M. cornuarietis* e *L. nyassanus* e os maduros miR-750-5p e miR-750-3p. O alinhamento com ortólogos e a análise de estruturas secundárias revelaram a conservação entre as espécies (Figura 36 e Figura 37)

Figura 36 – Estrutura secundária dos mir-750 com seus ortólogos.



pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata*, ame - *Apis melífera,* dqu - *Dinoponera quadríceps,* pca - Polistes canadenses, lgi - *L. gigantea*, mle - *M. leonina*.

Figura 37 – Alinhamento mir-750 *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



miR-750-5p

```
                      ....................((((..((.((((.((((((((((((((((..((.....
pcn-mir-750/1-97      -----------------GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
pmc-mir-750/1-97      -----------------GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
mcr-mir-750/1-97      -----------------GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
lny-mir-750/1-97      -----------------GAAGCCAGUUCCCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
lgi-mir-750/1-101     ---------------GGUAAUACAUGUUUCAGUUCGUUGGAAGAUUCGACCUUGACAUUG 45
mle-mir-750/1-64      ----------------------------------CGUUGGAAGAUUGGAUCUCAGCAUGU 26
pca-mir-750/1-113     --------------GAAAGAUUUGCACGACCCUCAGUUGGAAGUGAGGAUCUAGGCAGUG 46
ame-mir-750/1-136     GGGCGUUGCAUGGACUGUGAUCUGCAUGACUUGCAGUUGGAAGUGAGGAUCUAGGCAGUG 60
dqu-mir-750/1-110     -------------------CAUCGCGCGACUCUCAGUUGGAAGUGAGGAUCUAGGCAUUG 41
                      .........10........20........30.......40........50.........6
```

miR-750-3p

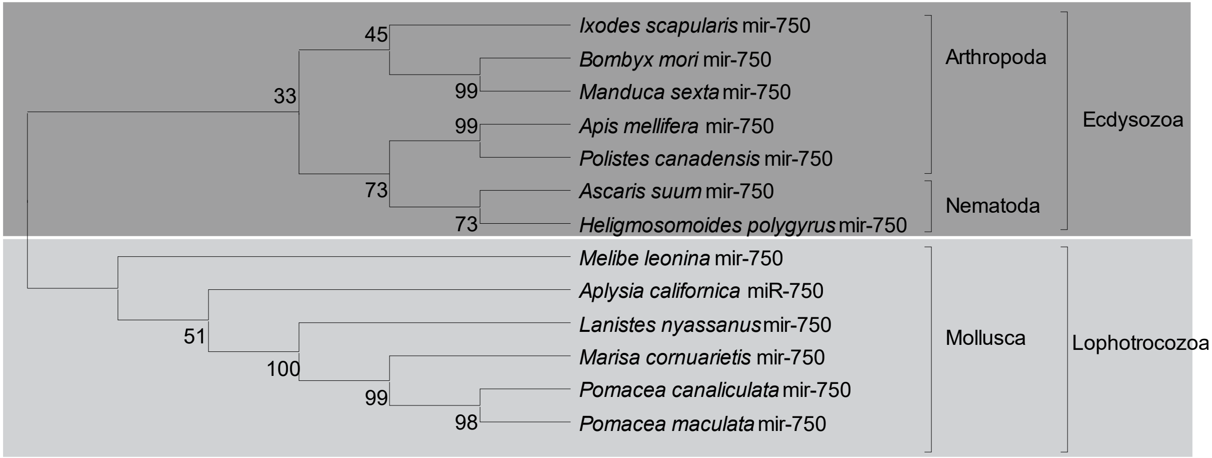
```
                      ...............................)).)))))))).)))))))))).)))).)
pcn-mir-750/1-97      CA----GGAAUACUGUC--------UUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
pmc-mir-750/1-97      CA----GGAAUACUGUC--------UUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
mcr-mir-750/1-97      CA----GGAAUGCUGUC--------UUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
lny-mir-750/1-97      CA----GCAAUGCUGUC--------UUCCCUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
lgi-mir-750/1-101     UU-----CCAUAGA-------------AUUUGUCAGAUCUAACUCUUCCAGCUCAUUGAG 87
mle-mir-750/1-64      CU-------UUACCGG----------AAGUUGCCAGAUCUAACUCUUCCAGCUCA----- 64
pca-mir-750/1-113     AG-UAAUAAAAACUCU-------AACAACAUGCCAGAUCUAACUCUUCCAGCUCAAGGUC 98
ame-mir-750/1-136     AG--CAGCAGCGCUCU-------GAUAACUUGCCAGAUCUAACUCUUCCAGCUCAAGGUC 111
dqu-mir-750/1-110     AGCUCGGCGUAGCUCUCCC---GAUUAACUUGCCAGAUCUAACUCUUCCAGCUCAGGAUC 98
                      0........70........80........90........100.......110.......1
```

```
                      )..)))).....................
pcn-mir-750/1-97      GCAUGGCAUG------------------ 97
pmc-mir-750/1-97      GCAUGGCAUG------------------ 97
mcr-mir-750/1-97      GCAUGGCAUG------------------ 97
lny-mir-750/1-97      GCAUGGCACA------------------ 97
lgi-mir-750/1-101     AUUUGUUUAAAAAC-------------- 101
mle-mir-750/1-64      ---------------------------- 64
pca-mir-750/1-113     GUGCAUAAUAAUCGU------------- 113
ame-mir-750/1-136     UUGU-UGAUUAUCAUCUCCCAAACGA   136
dqu-mir-750/1-110     GCGCGGUUCCAC---------------- 110
                      20.......130.......140....
```

pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* ame - *Apis melífera,* dqu - *Dinoponera quadríceps,* pca - Polistes canadenses, lgi - *L. gigantea*, mle - *M. leonina*.

O mir-750 foi encontrado em vesículas extracelulares de *Schistossoma japonicum,* e os resultados levam os autores do estudo a sugerir que este miRNA pode estar relacionado com desenvolvimento ovariano no parasito (DU *et al.*, 2020). O mir-750 foi encontrado na espécie *B. glabrata* (ADEMA *et al.*, 2017; QUEIROZ *et al.*, 2020)*,* e também em 33 espécies das analisadas por Huang *et al.*, (2021), além disso possui registros em 17 espécies no miRBase, com distribuição pelo clado Lophotrocozoa, como demonstrado por sua árvore filogenética (Figura 38).

Figura 38 – Distribuição filogenética do mir-750 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



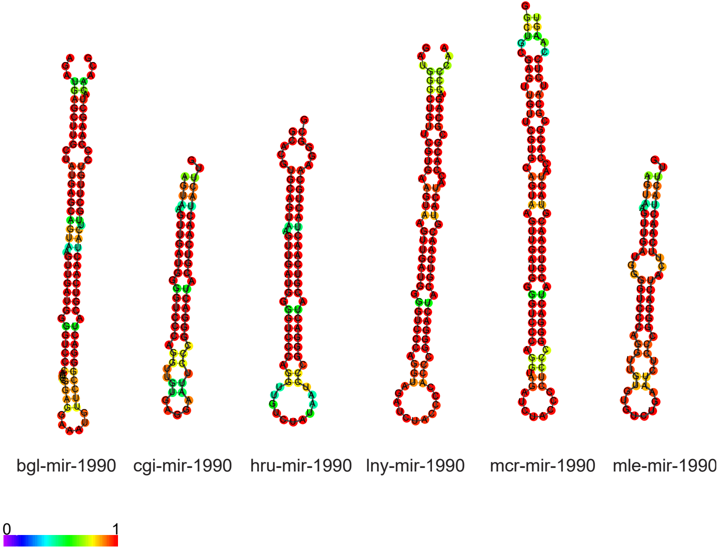
Fonte: Dados do autor

4.3.3 miRNAs Lophotrocozoa específicos

4.3.3.1 mir-1990

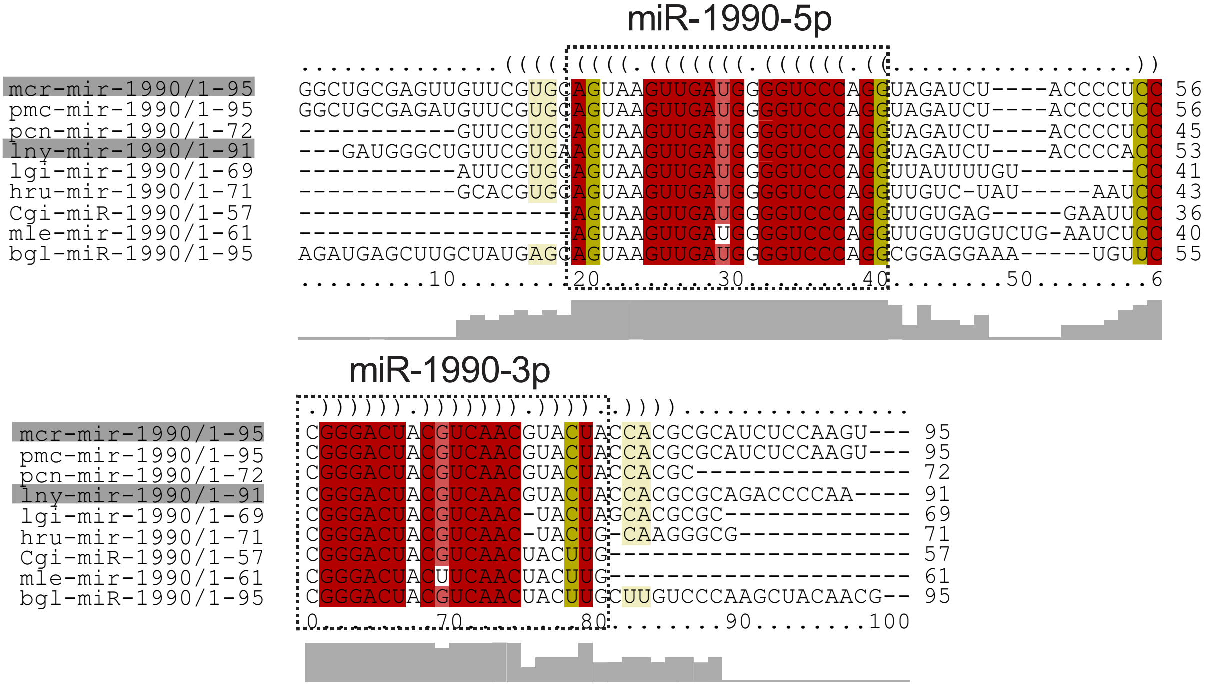
A família do mir-1990 predita para as espécies L. nyassanus e M. cornuarietis é composta pelos precursores lny-mir-1990, mco-mir-1990 e pelos miRNAs maduros lny-miR-1990-5p e mcr- miR-1990-3p os alinhamentos com ortólogos, bem como estruturas secundárias demonstram conservação entre os ortólogos (Figura 39, Figura 40).

Figura 39 – Estrutura secundária do mir-1990 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



pcn - *P. canaliculata*, lny - *L. nyassanus*, mcr - *M. cornuarietis*, pmc - *P. maculata*, lgi - *L. gigantea*, mle - *M. leonina*, cgi - *C. gigas* , bgl – *B. glabrata*, hru - *H. rufescens*

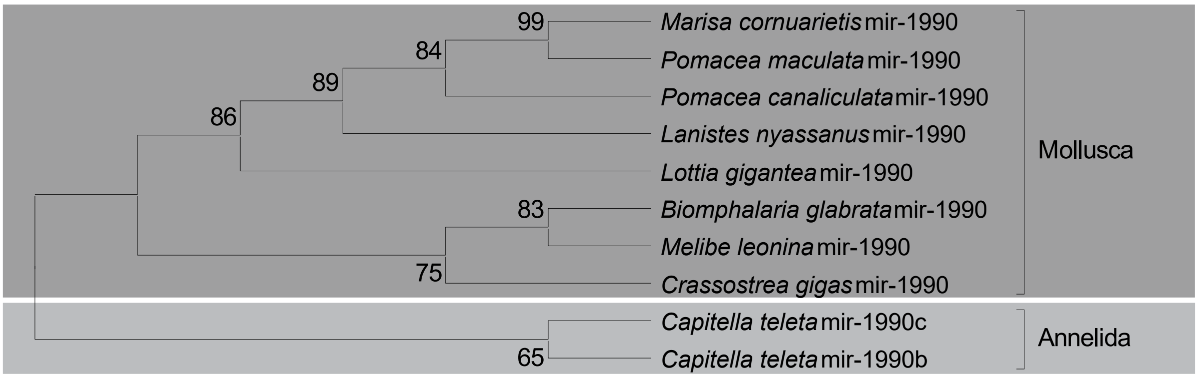
Figura 40 – Alinhamento mir-1990 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



pcn - *P. canaliculata*, lny - *L. nyassanus*, mcr - *M. cornuarietis*, pmc - *P. maculata*, lgi - *L. gigantea*, mle - *M. leonina*, cgi - *C. gigas* , bgl – *B. glabrata*, hru - *H. rufescens*

Para essa família foi observada a conservação e uma grande similaridade da estrutura primária, bem como a manutenção das estruturas secundárias em formato de grampo e um predomínio de ocorrência em gastrópodes, bem como uma papel chave no processo de biomineralização de *P. martensii* (HUANG *et al.*, 2019).

Figura 41 - Distribuição filogenética do mir-1990 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



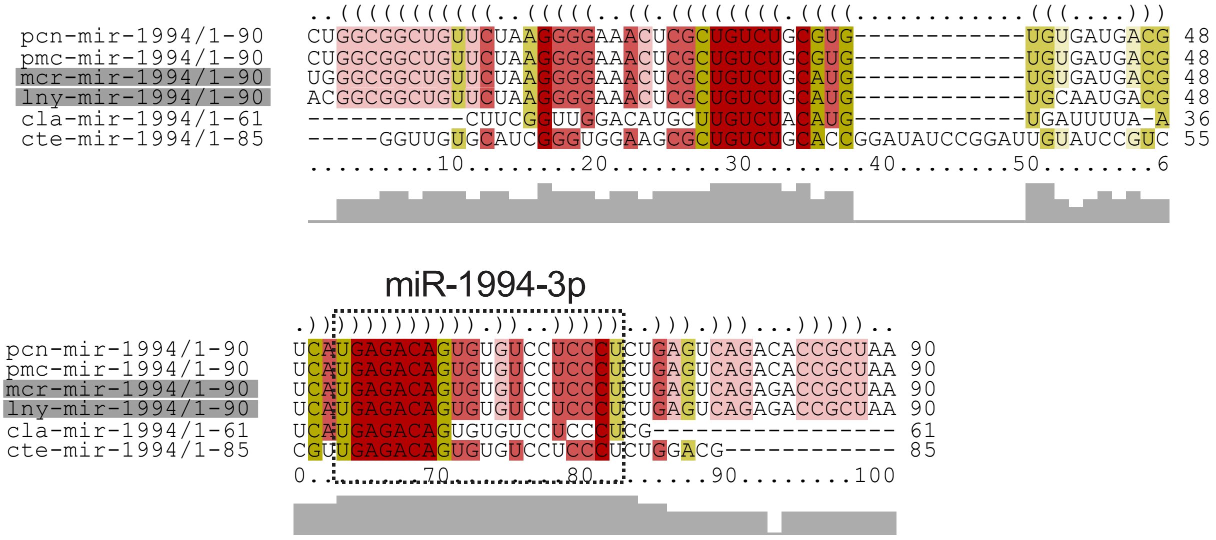
Fonte: Dados do autor

4.3.3.2 mir-1994

A família do mir-1994 é composta pelos precursores mir-1994, mir-1994a e mir-1994b foi predita nas espécies *L. nyassanus* e *M. cornuarietis* com os precursores lny-mir-1994 mcr-mir-1994a mcr-mir-1994 lny-miR-1994-3p. Frente aos seus ortólogos houve conservação da sequência de nucleotídeos bem como da estrutura secundária (

Figura 42, Figura 43).

Figura 42 – Alinhamento do mir-1994 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.

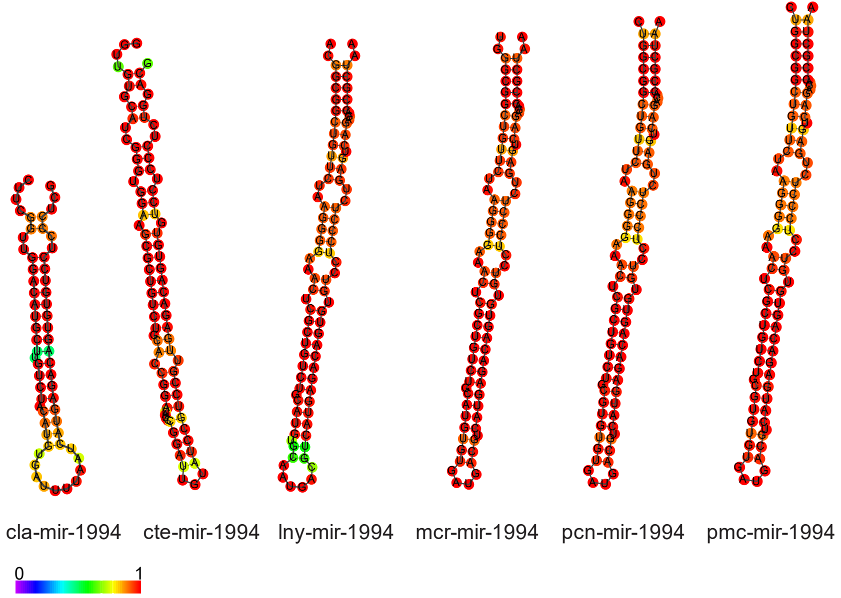


```
                  ..((((((((((..(((((..((.((((((((.((((............(((....)))
pcn-mir-1994/1-90 CUGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCGUG------------UGUGAUGACG 48
pmc-mir-1994/1-90 CUGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCGUG------------UGUGAUGACG 48
mcr-mir-1994/1-90 UGGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCAUG------------UGUGAUGACG 48
lny-mir-1994/1-90 ACGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCAUG------------UGCAAUGACG 48
cla-mir-1994/1-61 -----------CUUCGGUUGGACAUGCUUGUCUACAUG------------UGAUUUUA-A 36
cte-mir-1994/1-85 -----GGUUGUGCAUCGGGUGGAAGCGCUGUCUGCACCGGAUAUCCGGAUUGUAUCCGUC 55
                  .........10........20........30........40........50........6
```

```
                  .))))))))))))).))..))))))..))).)))...))))))..
pcn-mir-1994/1-90 UCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGACACCGCUAA 90
pmc-mir-1994/1-90 UCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGACACCGCUAA 90
mcr-mir-1994/1-90 UCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGAGACCGCUAA 90
lny-mir-1994/1-90 UCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGAGACCGCUAA 90
cla-mir-1994/1-61 UCAUGAGACAGUGUGUCCUCCCUCG----------------- 61
cte-mir-1994/1-85 CGUUGAGACAGUGUGUCCUCCCUCUGGACG------------ 85
                  0.........70.........80.........90........100
```

pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* cte - *C. teleta,* cla - *Cerebratulus lacteus*

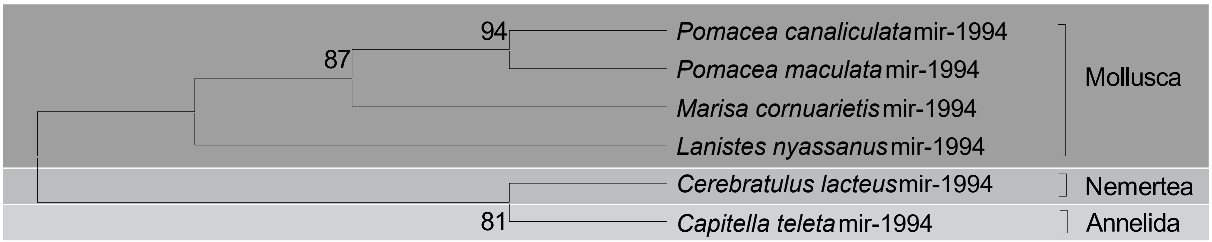
Figura 43 – Estrutura secundária do mir-1994 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* cte - *C. teleta,* cla - *Cerebratulus lacteus*

O precursor foi encontrado em B. glabrata (QUEIROZ *et al.*, 2020), *C. hongkongensis* (WEI *et al.*, 2019), *M. galloprovincialis* (YU *et al.*, 2020). A árvore filogenética foi construída através de uma pesquisa que revelou ortólogos dos filos Nemertea, Anelídeos e Moluscos (Figura 44). O mir-1994 foi, portanto, encontrado apenas em espécies pertencentes ao grupo Lophotrocozoa. O alinhamento com ortólogos demonstrou a conservação da região "*seed*" do miRNA maduro, bem como a manutenção de similaridade na estrutura secundária.

Figura 44 – Distribuição filogenética do mir-1994 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



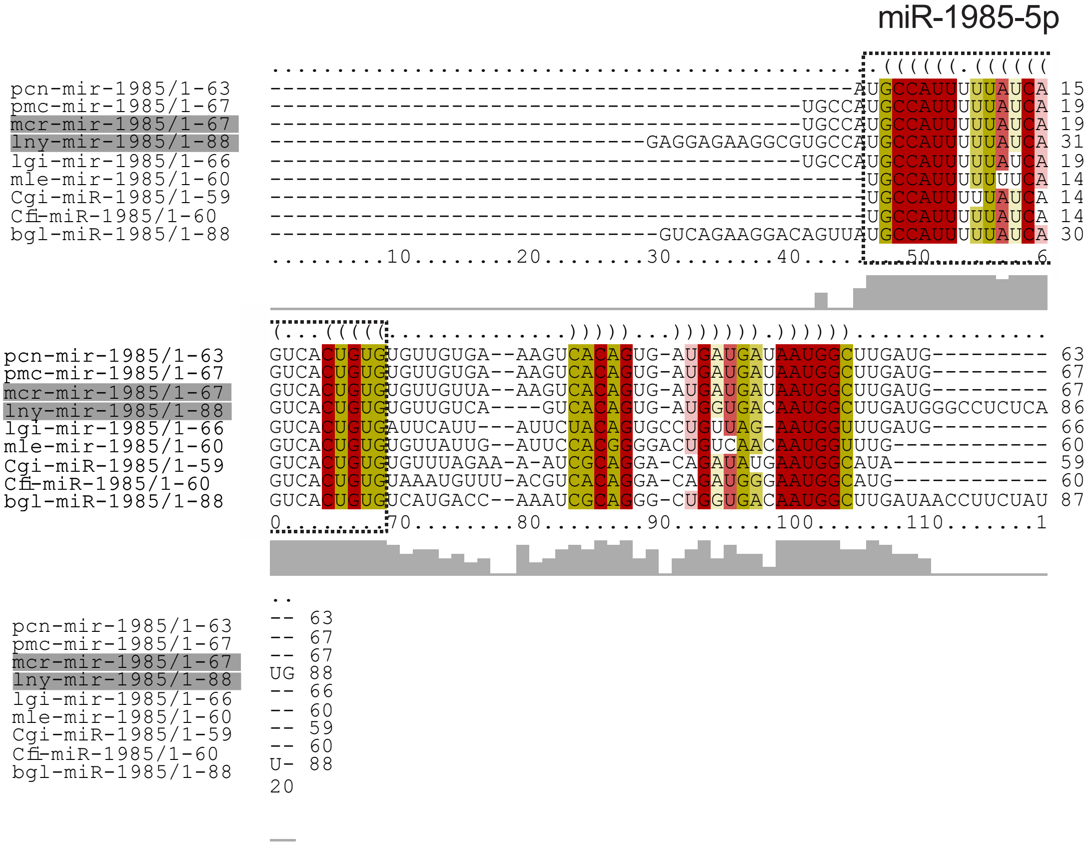
Fonte: Dados do autor

4.3.4 miRNA Molusco específicos

4.3.4.1 mir-1985

A família do mir-1985 predita para a espécie *L. nyassanus* e *M. cornuarietis* é composta pelos precursores lny-mir-1985 e mcr-mir-1985 e pelos miRNAs maduros lny-miR-1985-5p e mcr-miR-1985-5p. Este miRNA tem uma ampla distribuição entre o filo Mollusca sendo identificados também em *H. rufescens* (WHEELER *et al.*, 2009)*, B. glabrata* (QUEIROZ *et al.*, 2020)*, M. leonina e L. gigantea,* miRBase, *Patella vulgate* (KENNY *et al.*, 2015). Foi observado para esse miRNA grande identidade entre as estruturas ortólogas, bem como similaridade entre as estruturas secundárias (Figura 45, Figura 46).

Figura 45 – Alinhamento mir-1985 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



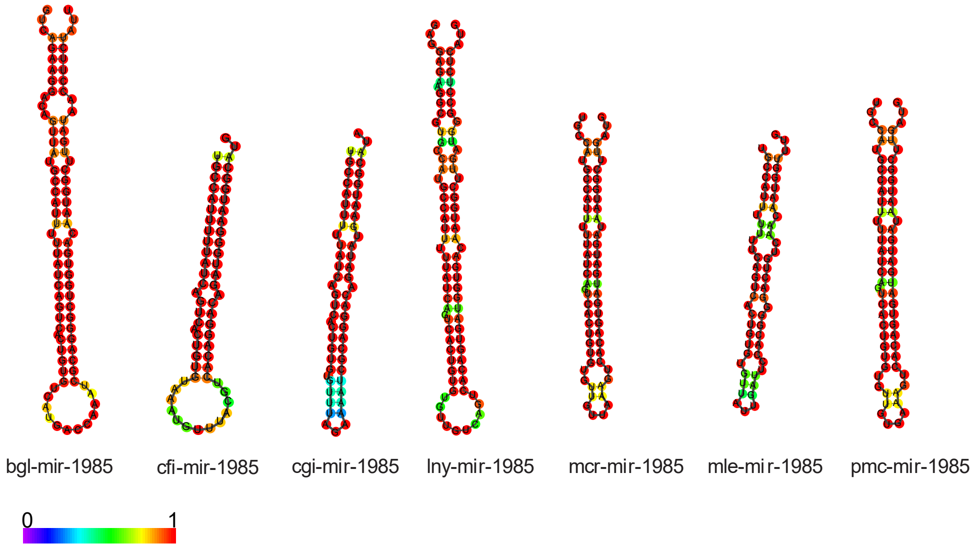
```
                    .............................................(((((((.((((((
pcn-mir-1985/1-63   ---------------------------------------------AUGCCAUUUUUAUCA 15
pmc-mir-1985/1-67   -----------------------------------------UGCCAUGCCAUUUUUAUCA 19
mcr-mir-1985/1-67   -----------------------------------------UGCCAUGCCAUUUUUAUCA 19
lny-mir-1985/1-88   -----------------------------GAGGAGAAGGCGUGCCAUGCCAUUUUUAUCA 31
lgi-mir-1985/1-66   -----------------------------------------UGCCAUGCCAUUUUUAUCA 19
mle-mir-1985/1-60   ----------------------------------------------UGCCAUUUUUUUCA 14
Cgi-miR-1985/1-59   ----------------------------------------------UGCCAUUUUUAUCA 14
Cfi-miR-1985/1-60   ----------------------------------------------UGCCAUUUUUAUCA 14
bgl-miR-1985/1-88   ------------------------------GUCAGAAGGACAGUUAUGCCAUUUUUAUCA 30
                    .........10........20........30........40.......50.........6

                    (...((((((..............)))))...))))))).)))))).............
pcn-mir-1985/1-63   GUCACUGUGUGUUGUGA--AAGUCACAGUG-AUGAUGAUAAUGGCUUGAUG--------- 63
pmc-mir-1985/1-67   GUCACUGUGUGUUGUGA--AAGUCACAGUG-AUGAUGAUAAUGGCUUGAUG--------- 67
mcr-mir-1985/1-67   GUCACUGUGUGUUGUUA--AAGUCACAGUG-AUGAUGAUAAUGGCUUGAUG--------- 67
lny-mir-1985/1-88   GUCACUGUGUGUUGUCA----GUCACAGUG-AUGGUGACAAUGGCUUGAUGGGCCUCUCA 86
lgi-mir-1985/1-66   GUCACUGUGAUUCAUU---AUUCUACAGUGCCUGUUAG-AAUGGUUUGAUG--------- 66
mle-mir-1985/1-60   GUCACUGUGUGUUAUUG--AUUCCACGGGGACUGUCAACAAUGGUUUG------------ 60
Cgi-miR-1985/1-59   GUCACUGUGUGUUUAGAA-A-AUCGCAGGA-CAGAUAUGAAUGGCAUA------------ 59
Cfi-miR-1985/1-60   GUCACUGUGUAAAUGUUU-ACGUCACAGGA-CAGAUGGGAAUGGCAUG------------ 60
bgl-miR-1985/1-88   GUCACUGUGUCAUGACC--AAAUCGCAGGG-CUGGUGACAAUGGCUUGAUAACCUUCUAU 87
                    0........70........80........90.......100.......110.......1

                    ..
pcn-mir-1985/1-63   -- 63
pmc-mir-1985/1-67   -- 67
mcr-mir-1985/1-67   -- 67
lny-mir-1985/1-88   UG 88
lgi-mir-1985/1-66   -- 66
mle-mir-1985/1-60   -- 60
Cgi-miR-1985/1-59   -- 59
Cfi-miR-1985/1-60   -- 60
bgl-miR-1985/1-88   U- 88
                    20
```

pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* lgi - *L. gigantea,* mle - *M. leonina,* cgi - *C. gigas* , cfi - *Chlamys farreri,* bgl – *B. glabrata*

Figura 46 – Estrutura secundária do mir-1985 em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.

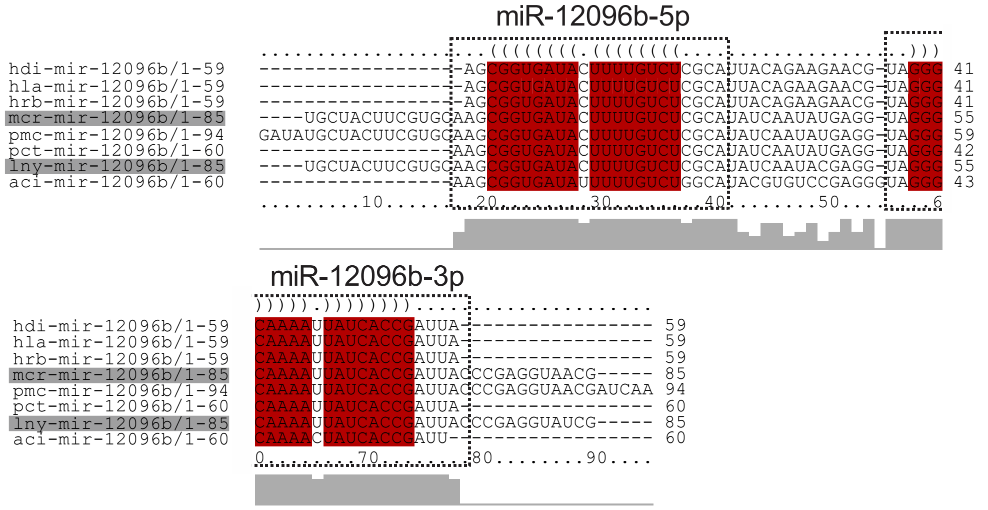


pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* lgi - *L. gigantea,* mle - *M. leonina,* cgi - *C. gigas* , cfi - *Chlamys farreri,* bgl – *B. glabrata*

4.3.4.2 mir-12096b

A família do mir-12096a predita para a espécie *L. nyassanus* e *M. cornuarietis* é composta pelos precursores lny-mir-12096a e mco-mir-12096a, e pelos miRNAs maduros lny-miR-12096-5p, miR-12096-5p, mcr- miR-12096-5p e mcr- miR-12096-3p (Figura 47, Figura 48). Este miRNA foi encontrado na plataforma miRBase para a espécie *M. leonina*. Para a família desse miRNA foram observadas a conservação do alinhamento, bem como das estruturas secundárias.

Figura 47 – Alinhamento do mir-12096b em *L. nyassanus* e *M. cornuarietis* seus ortólogos.



miR-12096b-5p

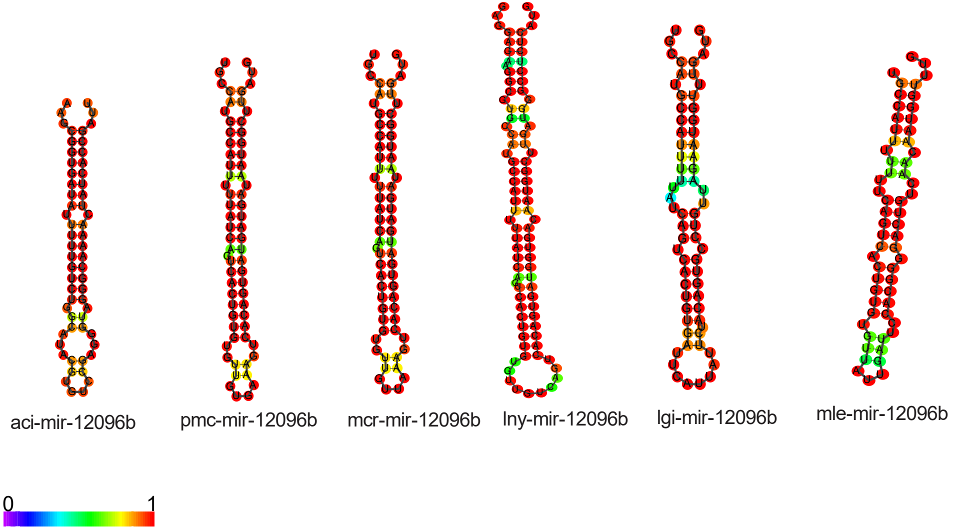
```
                      ....................((((((((.((((((((.................)))
hdi-mir-12096b/1-59   ------------------AGCGGUGAUACUUUUGUCUCGCAUUACAGAAGAACG-UAGGG 41
hla-mir-12096b/1-59   ------------------AGCGGUGAUACUUUUGUCUCGCAUUACAGAAGAACG-UAGGG 41
hrb-mir-12096b/1-59   ------------------AGCGGUGAUACUUUUGUCUCGCAUUACAGAAGAACG-UAGGG 41
mcr-mir-12096b/1-85   ----UGCUACUUCGUGGAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUAUGAGG-UAGGG 55
pmc-mir-12096b/1-94   GAUAUGCUACUUCGUGGAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUAUGAGG-UAGGG 59
pct-mir-12096b/1-60   -----------------AAGCGGUGAUACUUUUGUCUCGCAUAUCAAUAUGAGG-UAGGG 42
lny-mir-12096b/1-85   ----UGCUACUUCGUGGAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUACGAGG-UAGGG 55
aci-mir-12096b/1-60   -----------------AAGCGGUGAUAUUUUUGUCUGGCAUACGUGUCCGAGGGUAGGG 43
                      .........10.........20........30.........40.........50.....6
```

miR-12096b-3p

```
                      ))))).))))))))...........................
hdi-mir-12096b/1-59   CAAAAUUAUCACCGAUUA----------------------- 59
hla-mir-12096b/1-59   CAAAAUUAUCACCGAUUA----------------------- 59
hrb-mir-12096b/1-59   CAAAAUUAUCACCGAUUA----------------------- 59
mcr-mir-12096b/1-85   CAAAAUUAUCACCGAUUACCCGAGGUAACG----- 85
pmc-mir-12096b/1-94   CAAAAUUAUCACCGAUUACCCGAGGUAACGAUCAA 94
pct-mir-12096b/1-60   CAAAAUUAUCACCGAUUA----------------- 60
lny-mir-12096b/1-85   CAAAAUUAUCACCGAUUACCCGAGGUAUCG----- 85
aci-mir-12096b/1-60   CAAAACUAUCACCGAUU------------------ 60
                      0.........70.........80........90....
```

Aci - *Aplysia californica,* pmc - *P. maculata,* mcr - *M. cornuarietis,* lny - *L. nyassanus,* lgi - *L. gigantea,* hdi - *H. discus hannai,* hla - *Haliotis laevigata,* hrb - *Haliotis rubra*

Figura 48 – Estrutura secundária do mir-12096b em *L. nyassanus* e *M. cornuarietis* e seus ortólogos.



Aci - *Aplysia californica,* pmc - *P. maculata,* mcr - *M. cornuarietis,* lny - *L. nyassanus,* lgi - *L. gigantea,* hdi - *H. discus hannai,* hla - *Haliotis laevigata,* hrb - *Haliotis rubra*

5 CONCLUSÃO

A pesquisa por miRNAs nos moluscos *L. nyassanus* e *M. cornuarietis* resultou na busca de sequência de RNA que atendiam aos critérios estabelecidos de Energia Mínima Livre, Conteúdo CG e homologia com miRNAs já identificados, disponíveis em bacos de dados e na literatura. Estes miRNAs apresentam estruturas primárias e secundárias que guardam grande conservação com ortólogos.

As estruturas preditas como miRNAs quando analisadas em sua distribuição filogenética constitui-se em agrupamentos que corroboram com a árvore da vida. Foram encontrados nas espécies miRNAs específicos para as divisões taxonômicas nas quais as espécies selecionadas participam, demonstrando a conservação dos miRNAs bem como a especificidade de alguns.

Foram encontradas nos genomas das espécies *L. nyassanus* e *M. cornuarietis* prováveis proteínas da via de biogênese de miRNAs como argonautas, Dicer e DROSHA. A análise de domínios, de sítios ativos permitiram observar que as proteínas preditas guardam grande similaridade com ortólogas já caracterizadas, e a análise filogenética das proteínas preditas e suas ortólogas corroborou também com a árvore da vida.

Assim, a pesquisa por miRNAs e suas vias de processamento nas espécies *L. nyassanus* e *M. cornuarietis* foi capaz de predizer estruturas que atendiam aos critérios estabelecidos, complementando resultados anteriores de nosso grupo de estudo, bem como criando a necessidade de se estabelecer possíveis novos genes alvos para o miRNAs identificados.

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ANEXO A

Tabela Suplementar 1– Caracterização estrutural e termodinâmica dos precursores de miRNAs em *L. nyassanus*. Tamanho (Tam), conteúdo de G, conteúdo de A, conteúdo de C, conteúdo de U, conteúdo de GC, conteúdo de AU, razão de AU (R-AU), razão de GC (R-GC), Energia Mínima Livre (MFE), Energia Mínima Livre do Conjunto (MFEE), Frequência da estrutura do MFE no Conjunto (Freq), Diversidade do Conjunto (Div), Energia Mínima Livre Ajustada (AMFE), Índice de Energia Mínima Livre (MFEI).

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-316	UAGUUGUUAAACUGUAGGAAAACGUCUCUUAUUCCUAUCGGCUCAAUAUAUUUAUGAGCCUAGGCAACAAAUAUACUGUCUUUUUCCGCUUACAAAUG	98	15,30612	29,59184	19,38776	35,71429	34,69388	65,30612	1,206897	0,789474	-18,9	-14,1	0,015799	21,7	-19,2857	-0,55588
lny-mir-7965	AUGCAUCGAAGAAACCUCAAAUGACACGUUUUAAUUAGAAAUGGUGAGGGAAUGAAUUUUGUAUGCUAAAACAUAAAAUUGUCAGCAUUCUUGGAUGAUU	100	20	37	12	31	32	68	0,837838	1,666667	-20	-16,2	0,094567	7,12	-20	-0,625
lny-mir-2064	GACCAGUAUGGUCAGAGUUGAUGCUUAAGGCGCCAUUCCGUGGCUUAGCACAGCUUUUGACAAAUAAGCAGCACUGUGCAACUGCAA	87	25,28736	27,58621	22,98851	24,13793	48,27586	51,72414	0,875	1,1	-27,2	-26,8	0,071601	11,7	-31,2644	-0,64762
lny-mir-3484	aauacaaacagCUAAACUAGGAAAAGGAUAUGCUGUGCUUUCCACAUGGUGUUCCUACACAGAUUUUUCUAGUUACcuguuuguggu	87	13,7931	20,68966	14,94253	25,28736	28,73563	45,97701	1,222222	0,923077	-26,7	-26,3	0,091839	12,31	-30,6897	-1,068
lny-mir-10a	GGGGUGAGACCUACCCUGUAGAUCCGAAUUUGUGUGACAUUCGUGACGACAAAUUCGUGUUUGCACGGUAAGGCCUCACUGC	82	28,04878	21,95122	23,17073	26,82927	51,21951	48,78049	1,222222	1,210526	-38,9	-38,9	0,039205	2,67	-47,439	-0,92619
lny-mir-11	GACCCUAUGGCAAUGUGUCGAGGCUCAUCACAGGCAGAGUUCCagaccugucugucugcugacaUCUCUCUCAGACUGCCAUGGCCA	87	18,3908	16,09195	24,13793	17,24138	42,52874	33,33333	1,071429	0,761905	-29,4	-20,8	0,07357	22,9	-33,7931	-0,79459

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-2b-1	GAUCUGCUCAUCAAAGCUGGCUGUGAUAUGACUUACAAAAACACAUCCCAGCAGCUUUGAUGAGAAGGCC	70	21,42857	31,42857	24,28571	22,85714	45,71429	54,28571	0,727273	0,882353	-27,6	-27,6	0,092458	3,86	-39,4286	-0,8625
lny-mir-745a	AUUUGUCGGCUGGAGGCGGCUUUUCAACAGGCUGCCUUGCUUGGGAGGACACAAGCUGCCUGAUGAAGAGCUGUCCUGUAGCGGGCAGUA	90	34,44444	18,88889	22,22222	24,44444	56,66667	43,33333	1,294118	1,55	-46,8	-40,8	0,132252	8,07	-52	-0,91765
lny-mir-7c	GUGAUCUGGAAGACUAGUGAUUUUGUUGUUCUGAUGCUGACUAACAAUAAAUCACAUUCUUCCCCGAUUGC	71	19,71831	25,35211	19,71831	35,21127	39,43662	60,56338	1,388889	1	-21,1	-18,6	0,131089	9,74	-29,7183	-0,75357
lny-mir-9319	UCUCCUUCCCACUCACAGUCACUAGCAGAGCUAGUGGCCUCACCCCCACUACUUGCACUGGCUGCUUCAGGUGAAGGGGG	80	23,75	18,75	35	22,5	58,75	41,25	1,2	0,678571	-30,4	-30,4	0,219681	2,97	-38	-0,64681
lny-mir-466q-1	AUGGUCUGGUCAUGACAGAcaggcgcgcgcgugcacacacacacauacacacagacgugUAAAUGUCUGCUCGCGCGUCGUCUGACGUAAUACAUACAGA	100	15	16	13	16	28	32	1	1,153846	-34,9	-33,3	0,065729	20,26	-34,9	-1,24643
lny-mir-3297	UAAGCAAGGGUCACAAAACGCCGCUUUCAAGAUAGUGCAGAGAUUCAGCAGAGCACAUCUAGUCAAAACCAAGGUUUGUGACGAUCUUGCAGC	93	23,65591	33,33333	22,58065	20,43011	46,23656	53,76344	0,612903	1,047619	-22,6	-22	0,137599	8,48	-24,3011	-0,52558
lny-mir-7460	AUCAGCAUUCAGCCUGGCACCAUCCUCUUCACAAACAACAUCUGCCUGACUGAGCUCUGCUAGGGCUGUUUUGAGGGCCUGUGCGUGUCGAAUGCUGUC	99	24,24242	19,19192	29,29293	27,27273	53,53535	46,46465	1,421053	0,827586	-28,3	-17,6	0,013885	26,75	-28,5859	-0,53396
lny-mir-96b	CAUGGCUGUUCAAUUAUUUGGCACUUGUGGAAUAAUCGUUGCAUCUGAAGUCGAUUAUACAUCGGUGCCAAGUCAUCAGAAAGGCCGGA	89	24,7191	26,96629	19,10112	29,21348	43,82022	56,17978	1,083333	1,294118	-30,3	-28,8	0,042265	5,05	-34,0449	-0,77692

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-564	UGAGGUGAACAUUGUACGUGCCAACAAGACUGAAGGCACGGUGGCAGCAGAAGGGCAGGagauagguagguaauuuuuggCAGACAGUUAUUCCACCUUA	100	24	24	17	14	41	38	0,583333	1,411765	-22,3	-14,12	0,009426	22,56	-22,3	-0,5439
lny-mir-6632	CUUAUCGUCAGUGCUCAUCUCAGUCCgauagaaaagagagagaugagaggagUGCUGAACCAUUCC	66	9,090909	10,60606	21,21212	19,69697	30,30303	30,30303	1,857143	0,428571	-18,9	-17,8	0,132348	11,84	-28,6364	-0,945
lny-mir-6504	guuuguggguguaacCAUUACAGCACAGCCAUGUUUGCGGUGUAACCAUUACAGCACAGCUAUGUUUAUGGUGUAACCAUUACAGCACAGUU	91	16,48352	24,17582	19,78022	24,17582	36,26374	48,35165	1	0,833333	-26,5	-21	0,034382	27,18	-29,1209	-0,80303
lny-mir-4262	UAAAUGCCCAGCAGCUGGGACAACGUCGACAGGCCGACAUUCAGACUACCUGUCGACGUCGCCUUGAAUGCUGGGAUAAU	80	26,25	26,25	27,5	20	53,75	46,25	0,761905	0,954545	-36,8	-35,1	0,460005	2,87	-46	-0,85581
lny-mir-133c	UAACUACAGCUGGUUGAAGGGGACCAAAUGAAAGCCUCUUCAACAAUUUGGCCCGAGUUCAACCAGCUAUAGAAG	75	22,66667	33,33333	22,66667	21,33333	45,33333	54,66667	0,64	1	-30,4	-27,8	0,231076	4,17	-40,5333	-0,89412
lny-mir-10b	AGAGAGUGUGGGUGGCUUUACCCUGGAGAACCGAGCGUGUgugaucaugacgucacagcucguUUCUGAGGGUCAAGUCGCGAUACUCGCG	91	27,47253	14,28571	15,38462	17,58242	42,85714	31,86813	1,230769	1,785714	-41,7	-41,6	0,288526	9,6	-45,8242	-1,06923
lny-mir-8908i	cucaagaaagaaagaaauuugcaaUCCCCGAUAAACCCAAUGUAAUAGCAACUACCCGGUAAGGUAGUUGCCaagaaugucuuuuuuuuuuuacc	94	9,574468	15,95745	14,89362	10,6383	24,46809	26,59574	0,666667	0,642857	-21,2	-18,84	0,113508	8,17	-22,5532	-0,92174
lny-mir-1993	AGGAAGGCCCUGUAAUUUUCGGGAAUAUCGGCAUAAUGCAGUUGACUUGAGAUUCGUAUUAUGCUGCUAUUCACGAGAUGGAAGGGCUUGGA	92	29,34783	26,08696	15,21739	29,34783	44,56522	55,43478	1,125	1,928571	-36,7	-36,7	0,374278	3,58	-39,8913	-0,89512

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-466m	gugugugugugacugugugugcaugugcaugugugugguuugcaugcaugcacaauaaGGCCCUCCAGUCCCAGACAGGC	79	7,594937	5,063291	12,65823	2,531646	20,25316	7,594937	0,5	0,6	-33,8	-30,8	0,291201	4,92	-42,7848	-2,1125
lny-mir-8279	GAAACAGUUGAAGAACAGAGCUGAGAGAUUCAUGUCAAUCUGACAUUUGCAGUAGGUCUGCUagcuacauguauuuucaagUGUAGA	87	20,68966	25,28736	11,49425	20,68966	32,18391	45,97701	0,818182	1,8	-23,3	-21	0,095311	11,78	-26,7816	-0,83214
lny-mir-7661	CAAGCAGAUGUUGAAGGAAGUUCGUGUuucuacaaaagaaagaaaccuggAUAAACUAGACACUUCCAUCAAAGCGUGCAUC	82	15,85366	24,39024	14,63415	17,07317	30,4878	41,46341	0,7	1,083333	-19,2	-19,2	0,214952	11,41	-23,4146	-0,768
lny-mir-87a	AAAUCUUUGUUAAACACUUGGUAAUUUGCAAAUgaacaugcaaauaaaaggaacacaugacugGCACAUGGAAAUAAACCCAAGUUAACAACAGAUGA	99	10,10101	29,29293	11,11111	18,18182	21,21212	47,47475	0,62069	0,909091	-19,3	-19,3	0,407153	3,9	-19,4949	-0,91905
lny-mir-466b	CauagagagaauuacauauacauacacacauacuacUCACGCCAGAUAUGUGUCUACAUGUAAUUCUCUCUGUU	74	8,108108	10,81081	13,51351	20,27027	21,62162	31,08108	1,875	0,6	-24,6	-22,9	0,096333	7,47	-33,2432	-1,5375
lny-mir-10349	CACUGAGCACCAAUAAGCAGCAAUAAGCGGCGAUAGCUCACGACCAGUGAUCACGUGGUCGUUAUCAGCGGGGUUAUAUCCCUUGACUGGUAAUCACUG	99	25,25253	27,27273	25,25253	22,22222	50,50505	49,49495	0,814815	1	-28,4	-25,9	0,020752	14,01	-28,6869	-0,568
lny-mir-2049	AACUGUAUGUAGCACAGCAAUGACGUGAAAUUUUGUGCAUGUACGUGgauucaugugcaugcauucauga	70	17,14286	20	10	20	27,14286	40	1	1,714286	-23,5	-23,5	0,409874	4,97	-33,5714	-1,23684
lny-mir-5920	UCAGUGGGUGCCUGUAGCCUGCCGUUUUGUCAUUCGUAUACAAAACAGUAGGCCACUGCCCCACAUA	67	22,38806	22,38806	28,35821	26,86567	50,74627	49,25373	1,2	0,789474	-29,7	-29,7	0,51133	1,3	-44,3284	-0,87353
lny-mir-5600	AGUUGUAGUUAACUAAAUAGGACAUUUUGAAAAGAAGUGUUCUUGCUUCGUAAAUGCACUUAAUACAUGAGUGGaauguuuuguuucaguacuACAGAG	99	18,18182	28,28283	9,090909	25,25253	27,27273	53,53535	0,892857	2	-25,7	-25,7	0,154731	5,98	-25,9596	-0,95185

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-12096b	UGCUACUUCGUGCAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUACGAGGUAGGGCAAAAUUAUCACCGAUUACCCGAGGUAUCG	85	23,52941	25,88235	22,35294	28,23529	45,88235	54,11765	1,090909	1,052632	-29	-29	0,105265	6,21	-34,1176	-0,74359
lny-mir-263a-1	ACUUUCAAGAGUUGGCCAUGCUUAAUGGCACUGGUAGAAUAGCACACACCAUAGAGAUUAGUGCUGCAGUCAAGAGAGUGGUCAAUAUUGAACGU	95	25,26316	31,57895	17,89474	25,26316	43,15789	56,84211	0,8	1,411765	-24,2	-20,6	0,027018	17,04	-25,4737	-0,59024
lny-mir-124c	AAAUGAUGGUCUUCCCCUUGGCAUUCACCGCGUGCCUUAAUAGUGUGUCAAUCACCAAGGCCAACGCAgugaacacaaacagguaagCCCGGUCACAC	98	16,32653	19,38776	26,53061	18,36735	42,85714	37,7551	0,947368	0,615385	-26,5	-26,3	0,051306	9,68	-27,0408	-0,63095
lny-mir-4024	GUCUUUUUUACCUGUCCAAAGCCGUUUUUGAAUAGCUGUGCUACCGACUUUACUGUCUGUUAUUUGUAGGAUGAAAAGGUUAUUGGAAGUGAAAAAUUA	99	21,21212	26,26263	14,14141	38,38384	35,35354	64,64646	1,461538	1,5	-18,8	-16,9	0,025084	15,96	-18,9899	-0,53714
lny-mir-216a	guguuugucUAAUCUCAGCUGGUAAUUCUGAGUGGAGUUGUGUACACCUCAAGUUACUCGCCGAGAUUACAUAAAUAU	78	17,94872	25,64103	16,66667	28,20513	34,61538	53,84615	1,1	1,076923	-26,2	-26,2	0,262819	2,61	-33,5897	-0,97037
lny-mir-12	UUGAAUGGUCAGACUGUGAGUAUUACAUCAGGUACUGAGAAAACAGCAUGCUUCAGUACCUUUUGUGAUAUUCUUAGUCUGCCAUUUUG	89	21,34831	25,8427	16,85393	35,95506	38,20225	61,79775	1,391304	1,266667	-42,9	-42,9	0,38245	2,26	-48,2022	-1,26176
lny-mir-8335-1	ucuuguuguuguuguuguuuugguccuuGCAAAAAGUUUGAACCUCUCAACACUUUUUGAGGUACUUCAAAGCAAAUUACACAAACaggc	90	7,777778	25,55556	14,44444	16,66667	22,22222	42,22222	0,652174	0,538462	-24,3	-24,3	0,033164	11,07	-27	-1,215
lny-mir-9-1	CAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUACUUCAAUCAUACAGCUAGAUAACCAAAGACAAAACCG	76	11,84211	32,89474	22,36842	32,89474	34,21053	65,78947	1	0,529412	-24,2	-24,2	0,496783	1,38	-31,8421	-0,93077

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-8335-2	GUACACAAGCAAAAGUACAAUUGACAAAUGUUCCAGAACAGCCCAGCGUCUUUugacacuguuguuguuguuguuuuguuuuguggag	88	10,22727	22,72727	14,77273	12,5	25	35,22727	0,55	0,692308	-21	-18,9	0,011022	19,33	-23,8636	-0,95455
lny-mir-228	AGGCAUCAUGUGAAAAGAGCAUCAAUUGUAUAAUGGCACUGCAUgaauaaaaaauuauguuugCCAGAAAGAAUUGUGUCUUUGCUAAAUGACUGGUU	98	18,36735	26,53061	12,2449	23,46939	30,61224	50	0,884615	1,5	-22,7	-22,5	0,078762	7	-23,1633	-0,75667
lny-mir-2987	CGACCUGAGACUUGUCUGAUUGUUCAGGAAAGUCUGGAUCUCGCACACUACGUUAGCUGCUUGAAGACUUCAGAGCAAGGCUGAGGCUU	89	26,96629	23,59551	22,47191	26,96629	49,4382	50,5618	1,142857	1,2	-24,9	-16,6	0,027121	27,97	-27,9775	-0,56591
lny-mir-252b-1	GAGAGUAAGUACUCUCGACAGGGGGCGCUUCCUCCAACUUGCUGCGCAGAUGGUGUCCUUGGAGGUACGUGUCCCUGCGCAGUCCUACUGGG	92	32,6087	16,30435	27,17391	23,91304	59,78261	40,21739	1,466667	1,2	-34,9	-26,6	0,007771	20,62	-37,9348	-0,63455
lny-mir-9701a-1	GUGACAGCaggcugugugacuguguaccACCAUCAACCCGCGACGUGUGACCACAGUCGUAUUUUACUGGAGGUACAGGACAAAUGUCAGCUGUGUU	97	20,61856	20,61856	19,58763	18,5567	40,20619	39,17526	0,9	1,052632	-30,9	-30,1	0,097108	9,96	-31,8557	-0,79231
lny-mir-281	ACGUGACCUCACGCUGAAGGGAGCAUCCGUCGACAGUCAGAAAUACAGCACUGUCAUGGAGUUGCUCUCUUUACUGGAAAGGUCAAGG	88	27,27273	27,27273	23,86364	21,59091	51,13636	48,86364	0,791667	1,142857	-36,5	-36,1	0,381583	2,16	-41,4773	-0,81111
lny-mir-466i-1	GUUUGACAAGUCUGCuagcugacugugugugugugugagugugugugugacgcacAAAGACAUACAAACCACCGUCCCAGUCUGAACUGGUCAGAU	100	11	18	15	12	26	30	0,666667	0,733333	-35,6	-34,2	0,076901	11,8	-35,6	-1,36923
lny-mir-3128	GAaugguuuuucuuauuucagacUUGGAUUUGAAGAUGAAUGGUCAUGUGAUCCAUGGCACAUCCAUUGCA	100	18	24	14	23	32	47	0,958333	1,285714	-26,1	-23,4	0,009444	10,94	-26,1	-0,81563

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	GUUGAUUUCUGGCAAGUAAAAAACCAUCC															
lny-mir-279	GUCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACAAGGCCAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAAGACGG	91	25,27473	24,17582	25,27473	25,27473	50,54945	49,45055	1,045455	1	-40,2	-39,7	0,065907	7,67	-44,1758	-0,87391
lny-mir-36b	cuGGGGUGCGGUGGGUGUACGCCCUGGUUGGUGGGCGUCGGUAACAUCACCGGGUAUACAUUCAUCCGCACCCUGA	76	35,52632	14,47368	25	22,36842	60,52632	36,84211	1,545455	1,421053	-43,9	-41,1	0,167581	3,38	-57,7632	-0,95435
lny-mir-1662	GUAUAUUGUGUUGCAGAAAUUUGACAUCACCAUACUUUAUGUCGUCAGUUUGACAUCAUCAUACUUUAUGUCAUAAGUUUGACAUCACCAUACUU	95	13,68421	28,42105	18,94737	38,94737	32,63158	67,36842	1,37037	0,722222	-19,6	-19,6	0,371187	6,34	-20,6316	-0,63226
lny-mir-9a	ggaagggaaggagacGCAGUCCUUAAGCCCGCAGUUCUGUAACUGUCGAUAAGAAAUAAAGCUAGGCGACUGUCCGUCCUCGUUGCCUAAU	91	18,68132	20,87912	21,97802	21,97802	40,65934	42,85714	1,052632	0,85	-26,4	-17,7	0,034951	9	-29,011	-0,71351
lny-mir-8335-3	UGGCAUCGUUAGAACUUGAUUAAAGCAGGCUUGACucaugcuuuguuguuguuguuguuuugaagccaGAUUAAUCAUCUAAUGUGGCU	92	14,13043	17,3913	9,782609	19,56522	23,91304	36,95652	1,125	1,444444	-20	-18,3	0,054089	28,71	-21,7391	-0,90909
lny-mir-2001	GCUGCCAUUUUGUGACCGUUACAAUGGGCauugacagaaagacaaaugcuCCAUGUGAUGUUCACAAGAUGGCGGU	76	21,05263	14,47368	15,78947	21,05263	36,84211	35,52632	1,454545	1,333333	-39,7	-39,7	0,259527	3,56	-52,2368	-1,41786
lny-mir-252b-2	GGGGAUAGUGCCGGCGAUAAGUAGUGGUGCCGCAGGUAUGGCUCGUCAACUACCUGCUCAUCUCUGCUUAAUGUUGCUCUAUCAUU	86	27,90698	18,60465	23,25581	30,23256	51,16279	48,83721	1,625	1,2	-33,5	-33,5	0,133838	3,27	-38,9535	-0,76136
lny-mir-252a	AUUUUCUGGCCCACUACUAAGUACUAGUGCCGCGGGAGGACAGCU	88	27,27273	18,18182	26,13636	28,40909	53,40909	46,59091	1,5625	1,043478	-37,2	-36,8	0,059207	5,64	-42,2727	-0,79149

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UGCCAUGUCCCGUGGUUCUGGUCCUUACUACAGGGCGGAAUUU															
lny-mir-7371d	ACUGUAGGCAGCAGAGAGAACUUCCAGUAAAUGCAGUUCGCAAUCAUGGAAACACCAUUCACCAUAUUUGUACCAGAUGCUCUCUCUGGUGCCCACAGA	99	20,20202	30,30303	26,26263	23,23232	46,46465	53,53535	0,766667	0,769231	-33,9	-33,1	0,261583	12,77	-34,2424	-0,73696
lny-mir-190	UGCCCACCUACCCGCUUCUGCUAGAUAUGUUUGAUAUAUUUGGUGCGGUUGUCAUGACGACCAAGUAGUCAAACAUGUCAGAGCAGCGGUGGGGCUU	97	26,80412	21,64948	22,68041	28,86598	49,48454	50,51546	1,333333	1,181818	-44,3	-44,3	0,312382	10,4	-45,6701	-0,92292
lny-mir-92b-1	GACAGUCAGGGUUGUGUAGACCGGUACAGGGGCAAUGCAGUGAGUCGCUUGUAUUGCACUCGUCCCGGCCUAUACAGUCUGACUCGG	87	32,18391	19,54023	24,13793	24,13793	56,32184	43,67816	1,235294	1,333333	-41,1	-41,1	0,171444	4,85	-47,2414	-0,83878
lny-mir-92a	GCAUUAGCAUUAGGUCUUGAUGGGUGCAAUACUGGUGAGCCUGAUGGCAGAUUGCACUCGUCCCGGCCUUCUGCUAAAAG	80	28,75	21,25	22,5	27,5	51,25	48,75	1,294118	1,277778	-36,4	-36,4	0,391022	2,84	-45,5	-0,8878
lny-mir-92b-2	UAGCAUAGGGAGGUUGUGACCUGUGCAAUGAUUGGAGGAAUAUGAGCCAAUUGCACUUGUCCCGGCCUGCCCUGUGUGC	79	31,64557	20,25316	21,51899	26,58228	53,16456	46,83544	1,3125	1,470588	-35,3	-35,1	0,232461	3,35	-44,6835	-0,84048
lny-mir-184b	ACCCACAAGCCCUUAUCAGUUCUCCGUCCAGUGCUUGAGAACAGACGGGGCGGGGGAGUGAUAAGGAAAUGUGAAA	76	30,26316	28,94737	22,36842	18,42105	52,63158	47,36842	0,636364	1,352941	-35	-33,4	0,17411	3,39	-46,0526	-0,875
lny-mir-306	CAGCACCGAGACCGGCCAAUUUUGUCUUUCGAAAGAUCUUCCAGUUAAGAACACCAGCCUUGACACCUGUGACAAAUUUUGGUCAGGUACUGAGUGACU	99	21,21212	27,27273	25,25253	26,26263	46,46465	53,53535	0,962963	0,84	-24,1	-22,8	0,10238	6,82	-24,3434	-0,52391
lny-mir-1a	GCCCGGCACAUACUUCUUUGCUAUCCCAUAUGUUCUUCCAAAGCUA	73	19,17808	26,0274	23,28767	31,50685	42,46575	57,53425	1,210526	0,823529	-29,2	-29,2	0,14159	5,1	-40	-0,94194

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UGGAAUGUAAAGAAGUAUGUACCGUGU															
lny-mir-4690	UCACCUCCCGCUCAUCUCCUGGUCUGACCAGCACCGGCAGUCCGCGAUCGGGUGUGCUGGGGAGCAGGCGAGGCUGGGAGGGCU	84	36,90476	13,09524	32,14286	17,85714	69,04762	30,95238	1,363636	1,148148	-40,6	-39,2	0,073847	8,43	-48,3333	-0,7
lny-mir-8075	gcuUGACUGCUGAUGGCAGAUGUGUGUUGGCUGUUCAAUAAACAGAGCCCCACUGCCACACUCAGAUCAUGU	72	23,61111	23,61111	23,61111	25	47,22222	48,61111	1,058824	1	-19,8	-10,6	0,03638	15,58	-27,5	-0,58235
lny-mir-669k	UUUCUCUCGUACACUGAAGUCCAUAUCUUCAAGAGUGUUUAgaugugcaugucuguuuacuugugugugcauguauggacGUGCAUGUGUAUCAGAGAGG	100	14	15	11	21	25	36	1,4	1,272727	-32,7	-32,3	0,067561	17,27	-32,7	-1,308
lny-mir-9708c	GGGAAGUUGAGGGCUAGAAAAAUUUGUGUAGCACCAGACAUUUGugagcacagcuaaacauuuucuCUGCUGAGAUAAUUUUGUGGCGCCUCAACUUCCC	100	21	20	15	22	36	42	1,1	1,4	-39	-31,9	0,079272	20,93	-39	-1,08333
lny-mir-1731	uuauuuacuugacUGCAGGCACUACAGAUUAGUGAUAAUGCUGUUCCAGUCAGUCGAAAUCUGUAUUGAUUCGGUGUAAGUAAACGC	87	20,68966	24,13793	14,94253	25,28736	35,63218	49,42529	1,047619	1,384615	-21,8	-21,7	0,069971	9,58	-25,0575	-0,70323
lny-mir-8066	GauucccgcccccuccccuucucccacacaucGACCUUCCCAUGGUCCGAGGGGCCGAUGCAAUGUGAUCUUUUGGAGaacauggagaugggggaugU	98	16,32653	8,163265	11,22449	13,26531	27,55102	21,42857	1,625	1,454545	-34,7	-29,6	0,27164	13,85	-35,4082	-1,28519
lny-mir-5100	CGGGCACGUGACACCUACGUCAUGGCUGUUGUCGAAUCCCAGCGGUGCCCGAGAGCUGGUUCCAGUAACAGCUCACCUCGUCCUGGAGCCACGUGCGUC	99	29,29293	17,17172	33,33333	20,20202	62,62626	37,37374	1,176471	0,878788	-36,8	-36,7	0,095799	8,39	-37,1717	-0,59355
lny-mir-3906	agGGGCAAUGCUCUUGCAAGUUUUUUAUCCAAUAGUUGGAGCAGG	94	20,21277	31,91489	18,08511	27,65957	38,29787	59,57447	0,866667	1,117647	-20,6	-16,8	0,091919	20,31	-21,9149	-0,57222

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	AAGAAAAGCAUUUUGAAUGCAUAAAAAGCAUUCCAUAGACCACUCCUGU															
lny-mir-7062	GAUAAAAAGCUGCACAGCUGAUGGCCAUCCUGUUCGUGGAGGCCAGCUUGUGUCCAGGUUAUUGCA	66	28,78788	22,72727	22,72727	25,75758	51,51515	48,48485	1,133333	1,266667	-20,8	-18,1	0,025013	10,43	-31,5152	-0,61176
lny-mir-8485-1	UUugugguacacacacacacacacacacacacacguacuuaAAAUUUAGACUGCAGGGUGUUCGUGCGUUAAUUUCUAUGUGUGGGGGUACCACCAA	97	16,49485	13,40206	9,278351	20,61856	25,7732	34,02062	1,538462	1,777778	-25,5	-18,6	0,096418	19,61	-26,2887	-1,02
lny-mir-6756	ucccCCCACUUCUUGCCCCUCCCUCGCGCAUGGAUAUUACAUAUAUGAAAAUAUUACUUUUUGACUAGGGUGGGGCUGGAGGUGGGGAUA	90	24,44444	21,11111	21,11111	28,88889	45,55556	50	1,368421	1,157895	-39	-37,9	0,064711	9,53	-43,3333	-0,95122
lny-mir-10790	uuggauacAGAAAGCAGACUAACGGACGUCAGCAAGCAGGUGACACUGUCUGGCUgcucucuuuauuucucucucuguucguc	83	16,86747	18,07229	13,25301	8,433735	30,12048	26,50602	0,466667	1,272727	-21,7	-18,1	0,055432	16,72	-26,1446	-0,868
lny-mir-153	ACACCCCCUUCCCAGGCAGCUUUUGUGAUUCAGCAAUUGUACAGCUAUCAAAUUGCAUAGUCACAAAAGUGAUCGGGAGGCGGGGACU	88	23,86364	27,27273	25	23,86364	48,86364	51,13636	0,875	0,954545	-40,2	-40,2	0,334594	4,07	-45,6818	-0,93488
lny-mir-124	GUGUGACCGGGcuuaccuguuuguguucacUGCGUUGGCCUUGGUGAUUGACACACUAUUAAGGCACGCGGUGAAUGCCAAGGGGAAGACCAUCAUUU	98	26,53061	18,36735	16,32653	19,38776	42,85714	37,7551	1,055556	1,625	-40,2	-38,8	0,093576	10,13	-41,0204	-0,95714
lny-mir-133	CUUCUAUAGCUGGUUGAACUCGGGCCAAAUUGUUGAAGAGGCUUUCAUUUGGUCCCCUUCAACCAGCUGUAGUUA	75	22,66667	21,33333	22,66667	33,33333	45,33333	54,66667	1,5625	1	-35,5	-35,1	0,187007	6,7	-47,3333	-1,04412
lny-mir-10365	uuguGCCCGCAGUCCAUUAGAAUGUGGAAUCUAUGCUUUAAUGGUUGUGACAGAUUCUACUUUAAAAGACAUCUGGCAACC	81	19,75309	27,16049	19,75309	28,39506	39,50617	55,55556	1,045455	1	-20,4	-20,4	0,113197	12,46	-25,1852	-0,6375

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-466h	CCUGCuucgcacacacgcauacgcacgcacacacacacaucuccucGGCGACACGUGAAGAUGCACGUGGGAGGGUGUUCAUGUGUGCGAAUGCCUG	97	22,68041	10,30928	12,37113	12,37113	35,05155	22,68041	1,2	1,833333	-34,7	-33,9	0,086928	14,95	-35,7732	-1,02059
lny-mir-981	UUGAUCAGACUUUGUACCGGGUUUCGCGACUGGCGAACAGUCAUUCUGAACUGUGUUCGUUGUCGUCGAAACCUGCCCUGAACUCUGAUGUG	92	26,08696	18,47826	23,91304	31,52174	50	50	1,705882	1,090909	-35,3	-34,1	0,018788	7,48	-38,3696	-0,76739
lny-mir-7398y	AUGAGAUGUCGGAUGCAAAUGUGAUGGAGUGGGUGGUUUAaccuucccuucucucuuucucucucucaacaacUCGAUCUUUGUCAGGCAACAUCUCAA	99	20,20202	17,17172	9,090909	20,20202	29,29293	37,37374	1,176471	2,222222	-24,9	-23,9	0,214701	12,35	-25,1515	-0,85862
lny-bantam	uuugacgAAACUGGUUUUCACAGUGAUCCAGCAGAUCGUUCGAAGUCUGAGAUCAUUGUAAAAACCAAUUUUGUCGCC	78	17,94872	26,92308	19,23077	26,92308	37,17949	53,84615	1	0,933333	-31,9	-31,9	0,266041	5,12	-40,8974	-1,1
lny-mir-7006	GGUCACAGGUGAGUGGGGGUGUUCAAGAccccccaguuuucugugggccagcaucauagGGGUGAUGCACAUCGCCUCUCCCUUGCUG	88	23,86364	10,22727	14,77273	15,90909	38,63636	26,13636	1,555556	1,615385	-44,5	-43,9	0,07812	5,45	-50,5682	-1,30882
lny-mir-2a-1	GUGCCAAAGCUGUGAUGCUGACCAAGUGACUGGGAUGUGUGUUUGUUGUCAUAUCACAGCCUGCUUGGAUC	71	29,57746	19,71831	19,71831	30,98592	49,29577	50,70423	1,571429	1,5	-20,8	-17,8	0,088092	9,24	-29,2958	-0,59429
lny-mir-2b-2	GGCCUUCUCAUCAAAGCUGCUGGGAUGUGUUUUUGUAAGUCAUAUCACAGCCAGCUUUGAUGAGCAGAUC	70	24,28571	22,85714	21,42857	31,42857	45,71429	54,28571	1,375	1,133333	-32,9	-32,9	0,167727	4,14	-47	-1,02813
lny-mir-2d	GUAAGCAUGAAUGGAGGGCCAGCCAAAGUGGCGGUGAUCUGAUGUUCAGAGCAAAUCACAGCCUGCUUUGGUGAGCCUUCUGUCAUUCUGAG	92	30,43478	23,91304	20,65217	25	51,08696	48,91304	1,045455	1,473684	-40,6	-40,6	0,14781	5,41	-44,1304	-0,86383

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-2a-2	AAUUGACCGCAGAGGUCACACCAAAGAGGUUGugacuuugucuuucuguucaaaUCACAGCCUGCUUUGGUGAGCUCUUUGUCGUCAGGU	90	21,11111	16,66667	17,77778	20	38,88889	36,66667	1,2	1,1875	-39,5	-39,1	0,224362	3,21	-43,8889	-1,12857
lny-mir-6868	GUAUUCCUUCUGUUGUCUGUAAACUGCUUucgggaaaaaaacccauuguuCCUCCUUUGAGUUCUCAGGUAACAAGAGGAAAAG	84	15,47619	17,85714	15,47619	26,19048	30,95238	44,04762	1,466667	1	-23	-22,2	0,132737	4,31	-27,381	-0,88462
lny-mir-67	GUUUCGUGACACGUCUGCCCUUGUUCAGCCCGGUUGUGAUGGAGUUGGUCACAUCACAACCUGCAUGAAUGAGGACUGACGUCACGAGCG	90	28,88889	20	25,55556	25,55556	54,44444	45,55556	1,277778	1,130435	-43,9	-40,8	0,079095	4,8	-48,7778	-0,89592
lny-mir-8	UGCGCGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUCUGCUGG	94	24,46809	23,40426	21,2766	30,85106	45,74468	54,25532	1,318182	1,15	-46	-46	0,192059	3,37	-48,9362	-1,06977
lny-mir-6544	AAGUUGUAUUUCUUUUCGCAAACGCCUUGCUUGGUGAGGCUGACCGAAACACUAAGCACGUGUAGAUAUAUGCGGcguauuaaaagaaaaacaauug	97	19,58763	19,58763	15,46392	22,68041	35,05155	42,26804	1,157895	1,266667	-29,2	-29,2	0,173343	6,85	-30,1031	-0,85882
lny-mir-359	CGGAAAGAGGGAAGCCAGAUUUUCAUCUGUGUUCCCCCGUCACAAAAUGGAUGGUUCCAGGUGAACGUCAGAACUUGAUCACUGGUUUUCCUCUGUUGCG	100	26	23	23	28	49	51	1,217391	1,130435	-38,9	-38,3	0,123112	6,16	-38,9	-0,79388
lny-mir-184	UUUCACAUUUCCUUAUCACUCCCCCGCCCCGUCUGUUCUCAAGCACUGGACGGAGAACUGAUAAGGGCUUGUGGGU	76	22,36842	18,42105	30,26316	28,94737	52,63158	47,36842	1,571429	0,73913	-24,6	-24,3	0,091486	9,76	-32,3684	-0,615
lny-mir-4931	GGCCCAGCUGUCUUCAAACAGUCGUGAUACAUUUCUAACGUUUGCUCAUCGCUGAUUGGUUGAGCAGCCGGAAG	74	25,67568	21,62162	24,32432	28,37838	50	50	1,3125	1,055556	-21,3	-21,3	0,196775	4,36	-28,7838	-0,57568

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-750	GAAGCCAGUUCCCUGUGAGUUGGAAGAUUGGGUCUUUGGCAGCAAUGCUGUCUUCCCUGCCAGAUCUAACUCUUCCAGCUCAUAGUGGCAUGGCACA	97	25,7732	20,61856	25,7732	27,83505	51,54639	48,45361	1,35	1	-48,9	-47,3	0,207948	5,04	-50,4124	-0,978
lny-mir-1175	UGAUCAGGUGUGUUAUGUAGUGGAGAGAGUUUUAUCUCAUCAUGAGCCGUAAGCAGGUGAGAUUCAACUCCUCCAACUGCAGGCUACACCUGAAAC	96	25	27,08333	20,83333	27,08333	45,83333	54,16667	1	1,2	-44,8	-40,7	0,088251	5,34	-46,6667	-1,01818
lny-mir-137b	CUACCAGUCGGUUACGGGUAUUCUUGGGUAAAUAAUACAUUGAACCGCUGUUAUUGCUUGAGAAUACACGUAACUGACUGGGUG	84	25	26,19048	17,85714	30,95238	42,85714	57,14286	1,181818	1,4	-40	-39,2	0,16289	4,49	-47,619	-1,11111
lny-mir-2580	uguccguaAGUGUACucacgugucuguguguauguuucuaCAUAGACAUAUACAUGUGUACGGCUUCGGUUA	72	12,5	15,27778	9,722222	16,66667	22,22222	31,94444	1,090909	1,285714	-27,3	-27,2	0,115281	4,2	-37,9167	-1,70625
lny-mir-11976	gggcggcggcggcggcgccGGCGUGGGNNNNNNNNNNNNNNNNNNNNNGGGgggggcggcggcggcggcgccGGCGUGG	79	17,72152	0	2,531646	2,531646	20,25316	2,531646	0	7	-38,07	-38,07	0,922324	0,51	-48,1899	-2,37938
lny-mir-9-2	CGGUUUUGUCUUUGGUUAUCUAGCUGUAUGAUUGAAGUAGAAAUAUCAUAAAGCUAGGUUACCAAAGGCAAAAAUG	76	22,36842	32,89474	11,84211	32,89474	34,21053	65,78947	1	1,888889	-33,1	-33,1	0,29717	2,88	-43,5526	-1,27308
lny-mir-7290	ACUCUGCAAUCAGAGAUUUCUGGCUCUGUUUGCAGCAAAUCACUAGUCGUUGGCUCUGUUUGCAGCAAAUCACUAGUCGUUGGCUCUGUUUGCAGCAA	98	22,44898	21,42857	23,46939	32,65306	45,91837	54,08163	1,52381	0,956522	-31,6	-28,2	0,065716	6,74	-32,2449	-0,70222
lny-mir-4265	AGCUUCUGAGGAGACCUGUGGGCUCAGCUCUGCAUUUAUAUUAGGAGGCAAAUGUCCCUCAGAAAUA	67	25,37313	26,86567	20,89552	26,86567	46,26866	53,73134	1	1,214286	-18,8	-11,8	0,102899	12,25	-28,0597	-0,60645
lny-mir-9701a-2	CGCCAUAGUAACCACUAGCCGUGAGACACACAACAGGCCGUGUGAC	99	20,20202	22,22222	26,26263	13,13131	46,46465	35,35354	0,590909	0,769231	-31,4	-31,3	0,319797	5,61	-31,7172	-0,68261

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UGUGUACCACCAUCAAGGCGUGACGUGUGACCCCAaggugugugacuguguac															
lny-mir-451	GACAGUACCCAGCCCAAAGAACAAACUUUCGUUUGUAGUAAUGGUAAGGGUUUGAAUCUUAGGGUGGGGUGCUAAG	76	28,94737	28,94737	15,78947	26,31579	44,73684	55,26316	0,909091	1,833333	-29	-29	0,334254	2,61	-38,1579	-0,85294
lny-mir-33	GCUAUGGUGGUGCAUUGAGGUUGCAUUGCAUCAGUUGAGGAACAUGCAAUGCAUCUGCAGUGCAAGUACCAUGGU	75	30,66667	24	17,33333	28	48	52	1,166667	1,769231	-38,2	-37,2	0,235986	4,29	-50,9333	-1,06111
lny-mir-653	AAGCUAGGAAAGCCGAGCUGCAGUAGAGAUUGAGACAAUCUCUACUGCAACAACGGGUUCCUAGGUC	67	26,86567	31,34328	22,38806	19,40299	49,25373	50,74627	0,619048	1,2	-35	-33,2	0,416654	2,33	-52,2388	-1,06061
lny-mir-8485-2	CAUUGCAAGCAUGGCGCCUGUGUGGCUCUGCGCGCAugcaacgcacacacacacacacacguacaugcacgcacuc	76	15,78947	6,578947	14,47368	10,52632	30,26316	17,10526	1,6	1,090909	-25,8	-25,8	0,527609	3,34	-33,9474	-1,12174
lny-mir-11225	AACUACAGGGCAGUGGACUACAGCAGAUUGUACGUAAAACUGUACGUAAAACUGUUCUUAAGUCAUGGCCUGUACGA	77	23,37662	32,46753	19,48052	24,67532	42,85714	57,14286	0,76	1,2	-23,7	-23,7	0,093776	6,64	-30,7792	-0,71818
lny-mir-466i-2	CACCUCCUGGUUCGCGAAACAUGGCCAUcuauaaauauuauaaauauuauauauacacacacacacacacacaugaccaCUUUCAGCGAAACGGGAGAUG	100	13	12	14	10	27	22	0,833333	0,928571	-20,7	-18,07	0,038561	14,52	-20,7	-0,76667
lny-mir-7195	uauccuccccucucccccccccuccaccacacgAGUCAUACGAUUGACGUCAUGGGAAGUGGGGGAGCGGAAAAGGACAGGUGA	84	25	19,04762	7,142857	9,52381	32,14286	28,57143	0,5	3,5	-29,8	-23,2	0,107685	18,49	-35,4762	-1,1037
lny-mir-29b-1	CAUUGGGGCAGCGGGGCACUGGUCUCGACUGGUGGGUAGAUGGCGCUGUUAGUCUAGCACCAUUUGAAAUCAGUGCUCGCGCAUGUCUCCAGCA	94	32,97872	18,08511	24,46809	24,46809	57,44681	42,55319	1,352941	1,347826	-44,5	-44,5	0,069593	6,31	-47,3404	-0,82407

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
lny-mir-29a	AGAUGGCGAGAUGGAUGCUGGUCUCUUUUGGUGCUUAGAGUCAUAUCGCCUGUCUAGCACCAUUUGAAAUCAGUUUCCUGACCUGGCCACAG	92	26,08696	20,65217	22,82609	30,43478	48,91304	51,08696	1,473684	1,142857	-34	-34	0,158187	4,7	-36,9565	-0,75556
lny-mir-734	CAGGUGGAACUAUUCUGCAACAUUCAUGCUGAACCUGAGCCAGCCAUUAUGUGGUCAACACCUUGGGGCCAUGAGUUUGCUGACAUUUCGCACAUG	96	23,95833	23,95833	25	27,08333	48,95833	51,04167	1,130435	0,958333	-23,7	-22,5	0,102	11,88	-24,6875	-0,50426
lny-mir-9235b	ACGGAGAUAGUUCUAAUGGGACUUGUCUUCUCCGACAAAGGCAUGUUUGAGAAAUUAAUUUUGAUGUGGCUUGAGAACAGUACCAUAAAUUGUCUCCCC	99	22,22222	28,28283	18,18182	31,31313	40,40404	59,59596	1,107143	1,222222	-26,8	-24,1	0,009236	11,43	-27,0707	-0,67
lny-mir-263a-2	CUUAGUUCCCCUGCUAAUCAAUGGCACUGGUAGAAUUCACGGGUGCUUUCAAAAUCCCGUGGUCUUUCAGUGCCAUCUAUGGGCAAAGGGUGACCUGCA	99	24,24242	22,22222	25,25253	28,28283	49,49495	50,50505	1,272727	0,96	-40,8	-39,7	0,053135	7,61	-41,2121	-0,83265
lny-mir-1c	ACACGGUACAUACUUCUUUACAUUCCAUAGCUUUGGAAGAACAUAUGGGAUAGCAAAGAAGUAUGUGCCGGGC	73	23,28767	31,50685	19,17808	26,0274	42,46575	57,53425	0,826087	1,214286	-33,4	-32,3	0,415163	2,78	-45,7534	-1,07742
lny-mir-1990	GAUGGGCUGUUCGUGAAGUAAGUUGAUGGGGUCCCAGGUAGAUCUACCCCACCCGGGACUACGUCAACGUACUACCACGCGCAGACCCCAA	91	27,47253	24,17582	29,67033	18,68132	57,14286	42,85714	0,772727	0,925926	-42,4	-41,8	0,25783	4,43	-46,5934	-0,81538
lny-mir-466q-2	caugugcacacacacacauacaugcuugCACAUGCAGCCUCACGUGCAAGCUUAAGUUUauagugcacaug	71	8,450704	11,26761	12,67606	11,26761	21,12676	22,53521	1	0,666667	-24,9	-24,7	0,237339	3,05	-35,0704	-1,66
lny-mir-1947	AAAUGCUCAGAUAAGCUGUCAGGCGAAUCAAGGAUUUUGAAAACAGUUAACUAGCUGCUUUGUUUU	92	21,73913	29,34783	19,56522	29,34783	41,30435	58,69565	1	1,111111	-22,3	-21,5	0,091223	6,88	-24,2391	-0,58684

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	AGCACUGAGCUAGCUCUCUAGCAGUC															
lny-mir-2491	UCCUAUUGGCAUGUAGUCAAAACUGCUCAGUuccuaacaacaacagcagcagcagugaccUCACACCAAUAUAG	74	9,459459	18,91892	14,86486	17,56757	24,32432	36,48649	0,928571	0,636364	-18,7	-17,1	0,17106	10,72	-25,2703	-1,03889
lny-mir-1985	GAGGAGAAGGCGUGCCAUGCCAUUUUUAUCAGUCACUGUGUGUUGUCAGUCACAGUGAUGGUGACAAUGGCUUGAUGGGCCUCUCAUG	88	30,68182	20,45455	19,31818	29,54545	50	50	1,444444	1,588235	-38,3	-38,3	0,063273	5,09	-43,5227	-0,87045
lny-mir-1307	AGAUCGCGACUUCGCCACUCGGCGUGGCGUCGGUGCAAAGGUCGAAAUGCGUUCGGGGCGGCGGAGUGGGGAGGACACGAGCC	83	42,16867	18,07229	25,3012	14,45783	67,46988	32,53012	0,8	1,666667	-34,9	-33,3	0,314815	4,28	-42,0482	-0,62321
lny-mir-2944a	GUACAGGAGACAUUUCUCUGUGAAAAAGAGUAUAGGUGAUAUUUUCUCUUGCUGUCAUUUAGGGGGGCGAAGAUUUUCAGAAGGAACUUCUGCUGAUC	98	26,53061	26,53061	14,28571	32,65306	40,81633	59,18367	1,230769	1,857143	-22,4	-11,8	0,008713	30,59	-22,8571	-0,56
lny-mir-5397	agaaaacaaacuacgCAGAAGUUUGCUUCUGuaucauuuucccucccucgGAAUGUUUGCACAUGCGCAGCAAACGUCUCUGACAUUUAUUUCAG	95	13,68421	15,78947	13,68421	21,05263	27,36842	36,84211	1,333333	1	-20,9	-20,9	0,2969	5,73	-22	-0,80385
lny-mir-7045	acucucccccucccccgccccacuuUUCUUCUGCGAGGGACGCCGAUCAGACGACGCCCGGAGAAAGGUggaggcugggugggugggaggga	92	16,30435	10,86957	13,04348	7,608696	29,34783	18,47826	0,7	1,25	-50,9	-50,9	0,357037	6,43	-55,3261	-1,88519
lny-mir-106a	UUUUAUUAUCAGCCCUGCUACUGCAAUGCAAGCACAUUGACUGAAUUUUGCUCAGAGAACGUGCAGUUGGAGCUUGCUUUUCAUUGGCUGAUAAUAGCG	99	22,22222	24,24242	20,20202	33,33333	42,42424	57,57576	1,375	1,1	-30,3	-28,6	0,089339	10,78	-30,6061	-0,72143
lny-mir-3238	AGUGACUGAAAUGAAUCAUGCAUUUGGCAUGUAAACCUGUGGUGAAAUAGUGUguaacauugguguuug	98	18,36735	24,4898	9,183673	27,55102	27,55102	52,04082	1,125	2	-18,5	-18,5	0,036449	18	-18,8776	-0,68519

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	uguaAAUAUUCUGAUAAUUUCUAGUCGUG															
lny-mir-2361	CAUGCUgaguuguguuguuuuuuuuucaauacagcAGAUGAACUAACAAUACUGCAUCCAAAGUGCUAGCAUUAACAAGAAAUAUCAUAGCUUCAGCACA	100	10	29	16	16	26	45	0,551724	0,625	-23	-22,9	0,046036	12,62	-23	-0,88462
lny-mir-2493	AGCCUCUAUCACUCCUCUGAUCCUGUCGUCAGUGUAGUAAGAAAUUUUGGCGAAAGUAgcugcucacacacacacacagacgagagagagagagagaga	99	12,12121	15,15152	13,13131	18,18182	25,25253	33,33333	1,2	0,923077	-26,4	-18,6	0,022709	25,98	-26,6667	-1,056
lny-mir-9032	GUGAUGUUUGUUGCCAGUGAAUUAAUCAAAUUCUGCCAAUAUGCACUGCAGAUUCCGUUGAUGCAAUCCAAUGGUCAUCAUCAUGAG	87	20,68966	27,58621	19,54023	32,18391	40,22989	59,77011	1,166667	1,058824	-19	-19	0,117129	13,25	-21,8391	-0,54286
lny-mir-3963	GUACACACAGUCAAAUAAAGUAUUGUAUCCCACUUCUGACGCACAAUAUUUGUCGUUUGCCACAGAAAAAAUACCUGGGUUGACGGUGUGCAU	93	19,35484	31,1828	21,50538	27,95699	40,86022	59,13978	0,896552	0,9	-21,7	-21	0,161914	20,42	-23,3333	-0,57105
lny-mir-1994	ACGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCAUGUGCAAUGACGUCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGAGACCGCUAA	90	28,88889	22,22222	25,55556	23,33333	54,44444	45,55556	1,05	1,130435	-38,4	-38,4	0,344812	5,28	-42,6667	-0,78367
lny-mir-51	CUCCCAUCAUGUAUGCGUGCAUGGAAGCAGGUACAGUCACCUGUCCUGACUUAUCCAGCGAACAGUGUGGCCU	73	24,65753	21,91781	28,76712	24,65753	53,42466	46,57534	1,125	0,857143	-21,7	-17,1	0,160663	16,95	-29,726	-0,55641
lny-mir-9229d	UAGGGAUAAGGGGGAGGUUAAGAUAAGGAAAGGAUACUGUUAUCUGAGUCUUCCCCUUGAGCCUGU	66	31,81818	27,27273	13,63636	27,27273	45,45455	54,54545	1	2,333333	-25,9	-25,4	0,059825	5,61	-39,2424	-0,86333
lny-mir-4968	GCUCUUCUgcugguuuguuguuguguuguuguuaguaaCGAAGCUGUA	100	10	7	11	10	21	17	1,428571	0,909091	-45,8	-45,8	0,189807	22,44	-45,8	-2,18095

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	AUAGUUCCCCGUGGCAGCAGcaauaacagcagcaacagcagcagcagcag															
lny-mir-239b	CUCagccaucccccucccccccagaguGGGUCAGAUGGCACUUUUGUGGUGUGCAGGUUGGAUGGCUUGU	69	26,08696	7,246377	10,14493	23,18841	36,23188	30,43478	3,2	2,571429	-25,2	-13,05	0,115483	18,21	-36,5217	-1,008
lny-mir-466i-3	ACUCGCUCAAACACUGUCACUCACUCAAACACAUGGACGCAUUCGCgugcauucugugugugugugugugugugugugugugcgugc	88	6,818182	15,90909	19,31818	10,22727	26,13636	26,13636	0,642857	0,352941	-35,9	-35,4	0,211217	10,98	-40,7955	-1,56087
lny-mir-277a	UGUUCUUCGGGCAAGGAAACGCGAUCACACGGAgccauuucuuugugugcuuccUUGGCCGCCAAGAUCG	70	21,42857	17,14286	18,57143	12,85714	40	30	0,75	1,153846	-25,5	-25,4	0,03184	11,31	-36,4286	-0,91071
lny-mir-29b-2	UGUAAAGUGAUGUAUCGUAUCCUUUGGGAACGCCAGCUGGUUUCACAUGGACAGAUAACAACACUUUGUC	70	22,85714	27,14286	20	30	42,85714	57,14286	1,105263	1,142857	-19,1	-16,4	0,131874	6,17	-27,2857	-0,63667
lny-mir-466i-4	AUUACACGCUCUCGACCACACCCGGACCcucaaaccaacaaaaaacguUGGugagggaagugugugugugugugugugugug	82	7,317073	8,536585	15,85366	6,097561	23,17073	14,63415	0,714286	0,461538	-32,4	-31,1	0,058041	17,93	-39,5122	-1,70526

Tabela Suplementar 2 – Caracterização estrutural e termodinâmica dos precursores de miRNAs em *M. cornuarietis* . Tamanho (Tam), conteúdo de G, conteúdo de A, conteúdo de C, conteúdo de U, conteúdo de GC, conteúdo de AU, razão de AU (R-AU), razão de GC (R-GC), Energia Mínima Livre (MFE), Energia Mínima Livre do Conjunto (MFEE), Frequência da estrutura do MFE no Conjunto (Freq), Diversidade do Conjunto (Div), Energia Mínima Livre Ajustada (AMFE), Índice de Energia Mínima Livre (MFEI).

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-bantam	UUCGACGAAACUGGUUUUCACAGUGAUCCAGCAGAUUGCUCAAAGUCUGAGAUCAUUGUAAAAACCAAUUUUGUCCCC	78	17,94872	29,48718	23,07692	29,48718	41,02564	58,97436	1	0,777778	-33,4	-33,4	0,687059	0,82	-42,8205	-1,04375
mcr-mir-1002	UcguacaccaacaccugucaccucuUGUAGUCUGGUAUCUUUGUCUAAGUAGUUGAUACAUGAGUUGCAGAGGGUAUGGAGUAGUA	86	22,09302	17,44186	5,813953	26,74419	27,90698	44,18605	1,533333	3,8	-20,5	-18,9	0,106705	9,05	-23,8372	-0,85417
mcr-mir-10080	UCUGUCUCGUCUUUUCUCAGGUUGUCUCAAUCUUGCUUCAGUUUUGUCUGAAGACGUACAGACCagugagacaaaaagaaaccGU	85	15,29412	11,76471	18,82353	31,76471	34,11765	43,52941	2,7	0,8125	-19,1	-13,9	0,073241	20,99	-22,4706	-0,65862
mcr-mir-10089	UAUCAGCUCCCGAAGCAAAAUCAUGCCAAACAUAAUACAGGACGGUACUCGUGCAGGGAGAUAAUUUGCUGUUUUGGGAUGCUGCUG	87	25,28736	28,73563	20,68966	25,28736	45,97701	54,02299	0,88	1,222222	-22,8	-16,84	0,043074	18,63	-26,2069	-0,57
mcr-mir-10141	agcccGCAGCCUUGUGCAGUACagaggaaauaaaagaagaaacacgCAUUCGGUCUUCUUCAGUCAGCAUAUGGCUCGGAAA	82	15,85366	13,41463	17,07317	18,29268	32,92683	31,70732	1,363636	0,928571	-23,7	-22,7	0,301246	7,68	-28,9024	-0,87778
mcr-mir-10228	CAUUAGUACUGUGAUAUGUCAGUACACACGACAAUGAGUAUUGUACCAUGUCAGCACAUUAUUAGUC	94	19,14894	28,7234	18,08511	34,04255	37,23404	62,76596	1,185185	1,058824	-27,3	-27,3	0,173696	5,07	-29,0426	-0,78

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UUGUACUGUGUGUCAACAUUAGUACUG															
mcr-mir-10237	UCCAUUGUUAGUUUUGAGUGAGCUAGAAAGGGGUUAAAACUUCUUGCAGCAGGGACUGGUUUGUGGCACAUAUUUCAGCCUCucgacuaauaauaau	97	22,68041	19,58763	14,43299	27,83505	37,1134	47,42268	1,421053	1,571429	-23,8	-23,8	0,115043	18,95	-24,5361	-0,66111
mcr-mir-10325	AAAAUUAUCAUCGUCUUCUAUACAAGUGGCAUUCUCCUCGCCAUUAUUAUCAGCAGCAAAGGCGUUUUGCUAACUUGUCAAACAUGUGAUAAUAUA	96	14,58333	31,25	20,83333	33,33333	35,41667	64,58333	1,066667	0,7	-18,7	-18,7	0,080867	8,79	-19,4792	-0,55
mcr-mir-10379	AGUAACACAGUUAUUUUUCAAACAACUCAAACCAGGAAUAACAGACUGUUUUGUUCGUUGAACUAUGAUUGUGUUGCA	78	16,66667	33,33333	16,66667	33,33333	33,33333	66,66667	1	1	-24,4	-24,4	0,273807	6,43	-31,2821	-0,93846
mcr-mir-10456	UUUCUGUCAUACUAGAUGCAGGAUAUUUCUGUCAUACUAGAUGCAGGAUAUUUAUGACAUACUAGAUGCAGGAUAUUUCUGUCAUACUAGAUGCAGGAU	99	20,20202	29,29293	15,15152	35,35354	35,35354	64,64646	1,206897	1,333333	-32,6	-32,6	0,295291	5,75	-32,9293	-0,93143
mcr-mir-10457	AAGCAAAGAGUUUUUGACUACCAaucaaaauaguauuuuaacAAGUUUGCaauuauucuuuguuuguuguguqucuACACGACUCUUUGGCA	92	9,782609	16,30435	10,86957	14,13043	20,65217	30,43478	0,866667	0,9	-19,7	-18,9	0,188376	10,01	-21,413	-1,03684
mcr-mir-10698	uuuuaggaGAGGAAUUGCUGAGUUCAUGCAUGGCUUCUUUAGUAACGAGGUUCAUAUUCAUGAUAAGCUGACAUUCAUCUUCUAUCC	87	18,3908	22,98851	17,24138	32,18391	35,63218	55,17241	1,4	1,066667	-20,4	-20,4	0,075656	7,96	-23,4483	-0,65806

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-106b	CAGAGCGGGUAUCCUCUGUGGGUACCCCUUGUCACUGGCAGGACCGCACUGUGGGUACCCCUGUC	65	30,76923	13,84615	32,30769	23,07692	63,07692	36,92308	1,666667	0,952381	-27	-22,5	0,153722	17,97	-41,5385	-0,65854
mcr-mir-10717	GCGACACGGAUGCACACACACCUGCGCGCGCCAAGAGCAGUGGAGGUGAAAUAUUGUUUCGGUUAACAAAGGGCACAGCUCAGUGUGUUGCUGUGUGUU	99	31,31313	24,24242	22,22222	22,22222	53,53535	46,46465	0,916667	1,409091	-36,3	-35	0,209813	4,21	-36,6667	-0,68491
mcr-mir-10738	GUCCCAGUAACUGACCACUCUGACGUCUCUCCGCCCUUCCGGGUGCUGCUGUCUGCUUUGUAACUGAUGACGUCAGUGGGUCACGUGUAGCUGGUGU	97	27,83505	13,40206	28,86598	29,89691	56,70103	43,29897	2,230769	0,964286	-36,5	-35,1	0,181441	6,85	-37,6289	-0,66364
mcr-mir-10761	CUGGUCUGUGCAGACUACUAGUACGGUGACGAUGGUUGAAUUUGUUCUUGUCACCAUUGUGACAGAUUCUGAGCGCACAGUACUAC	86	25,5814	22,09302	20,93023	31,39535	46,51163	53,48837	1,421053	1,222222	-24,9	-19,7	0,050962	23,36	-28,9535	-0,6225
mcr-mir-10863	UCGAUAUACAACCCUACGAACAUCCCCAUGACCAAGUGAUAUCACCUUUGACUUCUUUGUGGGCACGAUGAUGCUUGUAAGAUUGUUUAUAUG	93	18,27957	26,88172	22,58065	32,25806	40,86022	59,13978	1,2	0,809524	-19,7	-17,9	0,1266	11,6	-21,1828	-0,51842
mcr-mir-10903-1	CUGCCACUUGAACGCUCAACAGCUCAUCUUCCGACUCGCUUGUGUCGGCCUCAGACCCACUGGCCUCACUGCUGUCUGCUGCGUUCCUGUGGUGG	95	24,21053	12,63158	35,78947	27,36842	60	40	2,166667	0,676471	-34,4	-34,4	0,328396	6,79	-36,2105	-0,60351
mcr-mir-10903-2	CUGCCACUUGAACGCCCAACAGCUCAUCUUCCGACUCGCUUGUGUCGGCCUCAGACCCACUGGCCUCA	95	24,21053	12,63158	36,84211	26,31579	61,05263	38,94737	2,083333	0,657143	-33,6	-33,6	0,309438	7,34	-35,3684	-0,57931

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	CUGCUGUCUGCUGCGUUCCUGUGGUGG															
mcr-mir-10903-3	CUGCCACUUGAACGCCCAACAGCUCAUCUUCCGACUCGCUUGUGUCGGCCUCAGACCCACUAGCCUCACUGCUGUCUGCUGCGUUCCUGUGGUGG	95	23,15789	13,68421	36,84211	26,31579	60	40	1,923077	0,628571	-30,3	-30,2	0,116672	10,54	-31,8947	-0,53158
mcr-mir-10918	GACAGGACAGAGAUUAAGGAguguuaaaauaguuugaagUAUUGGAAACUGGGUGUUCACAUAUAAGCUAUGUUACUCGAUAAUGCUCUUCCUUGC	96	18,75	23,95833	13,54167	23,95833	32,29167	47,91667	1	1,384615	-23,2	-20,8	0,051911	9,44	-24,1667	-0,74839
mcr-mir-10967	AACUGUACACUGCAUACUGUACAAUGUAGCUUGUCGGAUGAACUGUGAACUGCAUACUGUACAAUGUAGCUUGUCGGAUGAACUGUACACUG	92	22,82609	28,26087	19,56522	29,34783	42,3913	57,6087	1,038462	1,166667	-21,6	-20,2	0,048588	15,84	-23,4783	-0,55385
mcr-mir-10a	CGGUGCAAGACCUACCCUGUAGAUCCGaauuuguguaauauuuuaacUACAAAUUCGUGUUUGCACGGUAAGGCCUCGCAUCU	83	18,07229	16,86747	21,68675	19,27711	39,75904	36,14458	1,142857	0,833333	-33	-29,9	0,107106	4,44	-39,759	-1
mcr-mir-10b	AUGAGAGUGUGAGUGGCUUUACCCUGGAGAACCGAGCGUGUGUGAUCAUGACGUCACAGUUCGUUUCUGAGGGUCAAGUCGCGAUACUCUGUU	93	31,1828	20,43011	19,35484	29,03226	50,53763	49,46237	1,421053	1,611111	-40,6	-40,6	0,254812	9,91	-43,6559	-0,86383
mcr-mir-11	GACCUGGGAGAGCCGUGGCCAGCUGGAGACAUCCCUGGAGCUCUGGCUGUGCCGGGUGGAUUUCGUG	91	35,16484	15,38462	28,57143	20,87912	63,73626	36,26374	1,357143	1,230769	-35,2	-21,3	0,010022	23,33	-38,6813	-0,6069

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	CCAUGCAGUCAGCCUCUCCAGAUG															
mcr-mir-11591	uuuucGGGUACGUGAAACACCUUUACGAUUCGUUAUCCUUAGGCUGUGCUGUAAGUGUACUUUGAUAACGGUUCGGCAACAGGUUGAUUGUACCCGACAU	100	24	22	19	30	43	52	1,363636	1,263158	-33	-31	0,123962	9,74	-33	-0,76744
mcr-mir-1175	UGAUCAGGUGUGUUAUGUAGUGGAGAGAGUUUUAUCUCAUCAUGAGCCUCAGAAGCAGGUGAGAUUCAACUCCUCCAACUGCAGGCUAUACCUGAAAC	98	24,4898	27,55102	20,40816	27,55102	44,89796	55,10204	1	1,2	-42,7	-38,6	0,079856	5,62	-43,5714	-0,97045
mcr-mir-12	UGUUUCUACAUAUCUGUGGAAUCUUGCAGCAUCAUGUGCAUGUUGGUGGUGGUCAGACUGUGAGUAUUACAUCAGGUACUGAGAAUCU	88	26,13636	22,72727	15,90909	35,22727	42,04545	57,95455	1,55	1,642857	-21,2	-14,6	0,061401	34,13	-24,0909	-0,57297
mcr-mir-12037	UGGUAACUCAUUCUGUCUUCUCUUCCAAAAACCAGCAAAUGUGAAAUUGUGUAUGAGCAGUGGGUAUAUCUUUUUUGGUGGGACAAAUGAGUUAAAA	97	21,64948	29,89691	14,43299	34,02062	36,08247	63,91753	1,137931	1,5	-22,2	-21,7	0,076697	11,37	-22,8866	-0,63429
mcr-mir-12093	UACGGUCAAUAGCUAUCCCCAGGGUaauguuauuuuugcuuuauugCUUCUAACUUCAGCCCCUGGGGUAGCCUUACCUUU	81	14,81481	13,58025	23,45679	22,22222	38,2716	35,80247	1,636364	0,631579	-26,4	-26,4	0,139195	7,63	-32,5926	-0,85161
mcr-mir-12096b	UGCUACUUCGUGCAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUAUGAGGUAGGGCAAAAUUAUCACCGAUUACCCGAGGUAACG	85	23,52941	27,05882	21,17647	28,23529	44,70588	55,29412	1,043478	1,111111	-29,6	-29,2	0,079903	7,54	-34,8235	-0,77895

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-12193	UUUAAAGAAUUCAUCUUUAGAUCAUAACUGUUUAAGCAGUACAGACCAGUUUUAAACCGGUCCUUUCUGUCUAAUGUUCUGGAAAAGAUCUUUCUUUGUC	100	15	28	18	39	33	67	1,392857	0,833333	-20	-18,8	0,080489	17,54	-20	-0,60606
mcr-mir-12265	AGAUUCAGCCGUCUUGCAGCUGAAGCCAUACCACGUGAGACUUAGACUGAGGACACGCUGAAGCA	65	26,15385	29,23077	26,15385	18,46154	52,30769	47,69231	0,631579	1	-20	-17,1	0,213126	4,96	-30,7692	-0,58824
mcr-mir-12293	gcugccgUCUCCCUUCUACAUCCGCCUCUUGAUCUACUACAACUACGAGCACGAGGAGAUGUUACAGAGGAGAUCGGCCAU	81	18,51852	23,45679	27,16049	22,22222	45,67901	45,67901	0,947368	0,681818	-27,4	-27,4	0,349688	3,61	-33,8272	-0,74054
mcr-mir-12313	uaggucacgugacauguuAGCAUCUUGACAUAAAGGAAGUCAGUGUGUCUGUAAUGUGUAACAUGUCUCAUUACGAA	77	16,88312	24,67532	11,68831	23,37662	28,57143	48,05195	0,947368	1,444444	-19,1	-18,7	0,051013	5,78	-24,8052	-0,86818
mcr-mir-12322	agaagaaaagagaaguuGAUCAAACAGCCAACUGGGUUAUCCCGUGUGUUGGGACUCGCCUGUUCUCuggucauuucucuuucucac	87	14,94253	10,34483	16,09195	16,09195	31,03448	26,43678	1,555556	0,928571	-27,7	-27,5	0,020633	17,77	-31,8391	-1,02593
mcr-mir-12352	UUAUUGCUGUUAUGGUGUUAGUUCAGGUGAUUCUUAUGCAUGAGAAGUUAUGAGUUAACACCAUUACCACAacuu	75	20	25,33333	13,33333	36	33,33333	61,33333	1,421053	1,5	-21,8	-21,8	0,14281	5,72	-29,0667	-0,872
mcr-mir-1250	gaugacgacgguGCUGGAUGUGGAUAUGGAAUACGGACAGCUCCGUUUCUGAACAACAUCAGAACCUGUAGGUCCCA	77	22,07792	23,37662	19,48052	19,48052	41,55844	42,85714	0,833333	1,133333	-22,1	-19,8	0,186986	22,97	-28,7013	-0,69062

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-1256	cucuggccacugaGGCAUUGACUUCUCUUCAUGGCAUCUCAAAGGACAAGUCAAGUCAUGUGGUCAAAC	69	17,3913	23,18841	18,84058	21,73913	36,23188	44,92754	0,9375	0,923077	-22,5	-22,5	0,137838	3,93	-32,6087	-0,9
mcr-mir-1277	CACGUGCAGAUGUAUUGACAguuucuguguauauauauauauauauguacgauGCAACAGCACAUCUGCACUAC	74	10,81081	17,56757	16,21622	10,81081	27,02703	28,37838	0,615385	0,666667	-24,9	-21,6	0,120471	14,07	-33,6486	-1,245
mcr-mir-1278	AUUAAUCAGGAGCAGGUUUAUUGCAUGAGGUGUAGUAUUGACUGUAGUACUGUGCAUAUCAGCACCACAAAUCAUGCAGGAUGAAGACUGUUCGauugug	100	24	28	15	27	39	55	0,964286	1,6	-29,4	-28,6	0,050476	16,75	-29,4	-0,75385
mcr-mir-1304	CUUCAGGUCGUCACGGAAUGAAUUCUCACUGUAGCCUCGGCUCAGCGUGAUUUCAAACACGUCACAGCCUGCUG	74	22,97297	21,62162	29,72973	25,67568	52,7027	47,2973	1,1875	0,772727	-24,6	-22,7	0,479157	2,33	-33,2432	-0,63077
mcr-mir-130a	AUCCCUCCCUGCUCUGUUCCUUGUAUCUGCUCAUAGUGCAAUGUUAAAAGAGUACCUUUUGAGUUCUCUUGAGGUGACAAUGGAAAAGCAGGAGGGCU	99	23,23232	24,24242	21,21212	31,31313	44,44444	55,55556	1,291667	1,095238	-31	-29,3	0,028824	19,37	-31,3131	-0,70455
mcr-mir-133	CUUCUAUAGCUGGUUGAACUCGGGCCAAAUUGUUGAAGAGCCUUUCAUUUGGUCCCCUUCAACCAGCUGUAGUUA	75	21,33333	21,33333	24	33,33333	45,33333	54,66667	1,5625	0,888889	-35,5	-35,1	0,186674	6,73	-47,3333	-1,04412
mcr-mir-133c	UAACUACAGCUGGUUGAAGGGGACCAAAUGAAAGGCUCUUCAACAAUUUGGCCCGAGUUCAACCAGCUAUAGAAG	75	24	33,33333	21,33333	21,33333	45,33333	54,66667	0,64	1,125	-30,4	-28,9	0,184949	4,61	-40,5333	-0,89412

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-137b	AGUUCCAGUCGGUUACGGGUAUUCUUGGGUAAAUAAUACAUUGAACAGUUGUUAUUGCUUGAGAAUACACGUAACUACCUGGACGU	86	23,25581	27,90698	16,27907	32,55814	39,53488	60,46512	1,166667	1,428571	-33,1	-33,1	0,033251	6,83	-38,4884	-0,97353
mcr-mir-14	UAUAAAGGGAAGACAAUGAUCUGAGAGGUGCUGGCUGUACGCUGCUGAACUGAUCUCACUCucagucuuuuucucucucuuuuuu	85	20	20	14,11765	17,64706	34,11765	37,64706	0,882353	1,416667	-21,6	-18,47	0,04849	12,49	-25,4118	-0,74483
mcr-mir-1421ai	UUGUAGUCAGCAGGUCAGGUGUGGAAGCACUUUGCCAGGUUUUCCCCAUGGGUCCUGCGACUAGUG	66	31,81818	16,66667	22,72727	28,78788	54,54545	45,45455	1,727273	1,4	-24,4	-23,1	0,219346	4,86	-36,9697	-0,67778
mcr-mir-143	AUGUGUGAGCAUGACAGGAAUGAAAACUGUGCAAACCUCUGUGUGUGCAGUGCUGCAUCUCACAUUA	67	25,37313	28,35821	19,40299	26,86567	44,77612	55,22388	0,947368	1,307692	-20,7	-20,5	0,448845	1,84	-30,8955	-0,69
mcr-mir-146b	UUUAGGAACACGUUCUCAGAUGGAAGUUUCAGACCCUGUAUUCUGGAGGUUGAGAACUGGUUUUGAGCAAGUGCUUCCUUUU	82	25,60976	21,95122	17,07317	35,36585	42,68293	57,31707	1,611111	1,5	-24,2	-24,2	0,193626	6,98	-29,5122	-0,69143
mcr-mir-153-1	AACCAAAGCCUUAGCGUAGGUCAAGAAGAGUGUUAUAACCAAAUCAUCGUGCUGucauuuuugugauuuugagCUGACAGCUAGAUGCGUUGAAU	95	18,94737	26,31579	15,78947	18,94737	34,73684	45,26316	0,72	1,2	-21	-14,1	0,097127	11,84	-22,1053	-0,63636
mcr-mir-153-2	AUACCCUCUUCCCAGGCAGCUUUUGUGAUUCAGCAAUUGUACAGCUAUCAAAUUGCAUAGUCACAAAAGUGAUCGGGAGGCGGGGAC	87	24,13793	27,58621	22,98851	25,28736	47,12644	52,87356	0,916667	1,05	-37,9	-37,9	0,256161	6,4	-43,5632	-0,92439

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-1599	ACAUUACUCGCUCUCUGAGAAUcuggagggaggaaaaaaaaacgcuuAUUUUUUAAGCUCCAGAUGUUGACAGCAGGCGUAACCA	85	12,94118	20	16,47059	21,17647	29,41176	41,17647	1,058824	0,785714	-20,8	-16,6	0,027501	14,66	-24,4706	-0,832
mcr-mir-15a	aaauguuuauccuagcagcacagaauggcAAAAAUAUAGGGGUCCCUUUAAGAAGGAUAUUGGACGCCUGUGUUUUGUGCUGCUAGGGUAAGCAAUU	97	19,58763	19,58763	9,278351	21,64948	28,86598	41,23711	1,105263	2,111111	-47	-47	0,037871	8,59	-48,4536	-1,67857
mcr-mir-1610	ACGAAAAUAAUAUCAGCACUUUGCUGUGGCUUGUGGUGGAACGACAAACCAcuuucaacccccccccccccaauacaUUAAAGUGCCCAUAUAUGUUUCA	100	15	24	14	21	29	45	0,875	1,071429	-21,3	-17,3	0,147086	14,93	-21,3	-0,73448
mcr-mir-1621	GCGGUACGUGCGAGCGGGCUCUCAACCGGCUGCCUCGGUGGUAAGCGGUGUUGGAGGCUGCUGACCUACUGG	72	40,27778	12,5	26,38889	20,83333	66,66667	33,33333	1,666667	1,526316	-32,6	-32,1	0,106716	4,49	-45,2778	-0,67917
mcr-mir-1628	AAUUAACUUGAAUUAACGCGAAGAAGAUGUCUUUACACUACUUUGUUUCCUUCCUUUUGUAAGAGCUCUUCCUGUUCGUGUGUGAGAAUCACGCUUACAA	100	17	26	20	37	37	63	1,423077	0,85	-19,3	-19,3	0,079518	10,73	-19,3	-0,52162
mcr-mir-1693	ACCUUUAAGUGGCUAUUGAUGUCACCAAGAAAUGGUGCAAAGGAUGAAGCUGUAGCUGUGUUUCCUAAUGGCUGCACAAUAUGUUAUUUAAAAGU	95	23,15789	30,52632	14,73684	31,57895	37,89474	62,10526	1,034483	1,571429	-25,5	-25,5	0,09906	5,04	-26,8421	-0,70833
mcr-mir-1710	GAUCUGUUUCUCAUCUGCUGCAUAACCGUGUGUGACACAGGACAC	72	25	30,55556	23,61111	20,83333	48,61111	51,38889	0,681818	1,058824	-21,5	-21,5	0,221235	4,85	-29,8611	-0,61429

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	AGCGGUAGCACACAGAUACAAAAGGGA															
mcr-mir-1761	GACCAAGCAUAACAUAACGACGGAGGACAAUGGAGGACAGGGGUCACUUUUUUCCCCUGACCUUCACUUUUUCUUAUGUGAUCUUGUGG	89	23,59551	24,7191	22,47191	29,21348	46,06742	53,93258	1,181818	1,05	-28,5	-22,9	0,114468	11,78	-32,0225	-0,69512
mcr-mir-187	GAAAAUUAGAUGAUGUGCUGGUUGCUACAACACAGGACAAUUCUAAACUGAUUCGUAUUCUGCCUGUGCAAUUGCAAGCCCACAACAGAGAAUUGGU	97	21,64948	31,95876	19,58763	26,80412	41,23711	58,76289	0,83871	1,105263	-22,1	-19	0,108197	9,61	-22,7835	-0,5525
mcr-mir-190	ACCCGCUUCUGCUAGAUAUGUUUGAUAUAUUUGGUGCAGUUGUCGCGACGACCAAGUAGUCAAACAUGUCAGAGCAGCGACG	82	25,60976	25,60976	21,95122	26,82927	47,56098	52,43902	1,047619	1,166667	-32,5	-32,3	0,080048	9,84	-39,6341	-0,83333
mcr-mir-193-1	UUCUAAUAUCAUGGUAUCAGCAUGACUCGUAUGUGAUAUACUGGCCAGCACAAUUAGUGUCUAAUAUCAUGGUAUCACCAUGACUAGUAUGU	92	18,47826	29,34783	18,47826	33,69565	36,95652	63,04348	1,148148	1	-20,8	-20,8	0,129928	10,37	-22,6087	-0,61176
mcr-mir-193-2	GCCAGCACACUUACUGUCUGGUAUCAUGGUAUCAGCAUGACUCGUAUGUGAUAUACUGGCCAGCACAAUUAGUGUCUAAU	80	21,25	26,25	22,5	30	43,75	56,25	1,142857	0,944444	-21,7	-21,7	0,239175	6,47	-27,125	-0,62
mcr-mir-193-3	CUAAUAUCAUGGUAUCAGCAUGACUAGUAUGUGAUAUACUGGCCAGCACAAUUAGUGUCUAAUAUCAUGGUAUCAA	76	18,42105	32,89474	17,10526	31,57895	35,52632	64,47368	0,96	1,076923	-19,8	-19,8	0,11962	11,25	-26,0526	-0,73333

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-194	GUUUGGUCAUCUUCAGUUCCAUGCCAGCCCCACCUGGCAGCCAGUGGAGGUGGUGUAGaagguggucacgugaccagcc	78	23,07692	11,53846	20,51282	19,23077	43,58974	30,76923	1,666667	1,125	-32,8	-32,8	0,088541	4,32	-42,0513	-0,96471
mcr-mir-1947	AUCUGAAUGAAGGCUAGUGCACUGAGCUAGCUCUCUGCGUCAUCAACUGCAAUGAAGCAUAGAGGGAGGCAGCGGUGGAGUACAAUUCUUCAUAA	95	27,36842	29,47368	20	23,15789	47,36842	52,63158	0,785714	1,368421	-27,3	-11,2	0,050373	20,57	-28,7368	-0,60667
mcr-mir-194b	GUACUGCAUCAGCCACGCGCUGCGUUGUAACAGCAUCUCCAACUGCGGCGACCACGACGACAGCGACGAGCGCAAAUGUAGGUC	84	27,38095	25	32,14286	15,47619	59,52381	40,47619	0,619048	0,851852	-28,7	-27	0,178572	5,44	-34,1667	-0,574
mcr-mir-196c	GGUGUGUUGCUGACAACAACAUCAAACCACCUGCCGAACAUCUGGCCCAGGUGCUGGUGUUUCAUGCUCCAUCAACACGGG	81	24,69136	23,45679	29,62963	22,22222	54,32099	45,67901	0,947368	0,833333	-24,7	-24,7	0,061423	10,88	-30,4938	-0,56136
mcr-mir-1970	UUGUUAUACCCUGUGAUAAACUCUUUGGGUUGGGGGCUUAAAUAUCUUUCUUCUCAGAUUGUGUCACUGGGGAUAAUUA	79	22,78481	21,51899	15,18987	40,50633	37,97468	62,02532	1,882353	1,5	-22,3	-22,1	0,116729	7,91	-28,2278	-0,74333
mcr-mir-1984	UGUCGCCGUGCCCUAUCCGUCAGGAACUGUGAUCUCGCGAAACACAGGGUCUGGCGGUUGGGCCUCGGCGCUG	73	34,24658	13,69863	30,13699	21,91781	64,38356	35,61644	1,6	1,136364	-37,9	-37,9	0,133827	2,65	-51,9178	-0,80638
mcr-mir-1985	UGCCAUGCCAUUUUUAUCAGUCACUGUGUGUUGUUAAAGUcacagugaugaugauaauggcuUGAUG	67	14,92537	13,43284	10,44776	28,35821	25,37313	41,79104	2,111111	1,428571	-28,6	-28,6	0,286882	2,78	-42,6866	-1,68235

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-1990	GGCUGCGAGUUGUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCUACCCCUCCCGGGACUACGUCAACGUACUACCACGCGCAUCUCCAAGU	95	27,36842	20	29,47368	23,15789	56,84211	43,15789	1,157895	0,928571	-39,9	-39,5	0,101035	5,08	-42	-0,73889
mcr-mir-1992	CUAAGGGCAUGUGUCUAGUCAGUGGUUGACUGCUUGGUAUUCUAAAUGUAUCAGCAGUUGUACCACUGAUUUGCUACGUGCACCUCAC	88	23,86364	21,59091	21,59091	32,95455	45,45455	54,54545	1,526316	1,105263	-41,8	-41,4	0,125422	3,52	-47,5	-1,045
mcr-mir-1994	UGGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCAUGUGUGAUGACGUCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGAGACCGCUAA	90	31,11111	20	23,33333	25,55556	54,44444	45,55556	1,277778	1,333333	-40,6	-40,6	0,538688	3,53	-45,1111	-0,82857
mcr-mir-1994a	CAAAAGCUAUUUCUCAGGGGCGGUCACUCUGAUCUCCAUGUGCUCGCACCAGCAUGAGACAGUGUGUCCUCCCUUGAGGGAUGGGCUUAUA	91	26,37363	20,87912	26,37363	26,37363	52,74725	47,25275	1,263158	1	-44,3	-44,3	0,178398	5,12	-48,6813	-0,92292
mcr-mir-1c	AGUACAUACUUCUUUACAUUCCAUAGCUUUGCAAGAACAUAUGGGAUAGCAAAGAAGUAUGUGCC	65	18,46154	33,84615	18,46154	29,23077	36,92308	63,07692	0,863636	1	-27,1	-26	0,4687	2,23	-41,6923	-1,12917
mcr-mir-2	AAGGCGAAUGAAUGCUCUGUCUGUUGGUAUGCGAUAGGACCCAGUUUUUCAAAAGACUGUGUUGCUAUGUCCCAGACAUGUUCUACUUUCGCUAA	95	23,15789	24,21053	20	32,63158	43,15789	56,84211	1,347826	1,157895	-26,9	-26,9	0,129077	12,83	-28,3158	-0,6561
mcr-mir-2001	AAAGGAGAACUGUGUUGCUCUUGAUCGGAUGCUGCCAUUUUGUG	85	21,17647	16,47059	15,29412	22,35294	36,47059	38,82353	1,357143	1,384615	-20,5	-20,5	0,029997	7,42	-24,1176	-0,66129

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	ACCGUUACAAUGGGCauugacagaaaaacaaaugcuCCAUG															
mcr-mir-202	CAGAGGCauagggcaugugcggggccuCGACCAUAGCCAUAUUAAUCAAACACGCGGGGCCCUAGGUAGAUGCCUCGUCUGCCUGCCCCUAGGCCUAAG	99	20,20202	19,19192	26,26263	14,14141	46,46465	33,33333	0,736842	0,769231	-39,3	-39,3	0,05055	8,37	-39,697	-0,85435
mcr-mir-204	CCACUCACCAGUCGCUGGCAAUGGACGCUGGGAAGGCAAAGGGAACCUCGCGCGUGCGUUCGagcgaagggagagagu	78	26,92308	16,66667	24,35897	11,53846	51,28205	28,20513	0,692308	1,105263	-30,4	-24,1	0,011827	6,78	-38,9744	-0,76
mcr-mir-2040b	AGAGCAAGAGUCAGGUCAGCUACGACUGUAACACUAACUAUUUAUGAUAAGGUAUCGUGUGUAGCUAGAGUCUUAGCUGUGAUGACUAAUGCAAA	95	24,21053	32,63158	15,78947	27,36842	40	60	0,83871	1,533333	-32,6	-32,6	0,506504	3,85	-34,3158	-0,85789
mcr-mir-216a	GUGUUUGUCUAAUCUCAGCUGGUAAUUCUGAGUGGAGUUCUGCACACCUCAAGUUACUAGCCGAGAUUACAUAAAUAU	78	20,51282	26,92308	19,23077	33,33333	39,74359	60,25641	1,238095	1,066667	-30,5	-30,5	0,146188	3,64	-39,1026	-0,98387
mcr-mir-216b-1	CGUAGGAAGAUGAGCCAGGAUUACAAGAUGGUUGGGCCUGCGGCCCUAAUAUCAGCUGGUAAUCCUGAGUGAGCUUGCCUCAG	83	31,3253	24,09639	21,68675	22,89157	53,01205	46,98795	0,95	1,444444	-31,3	-30	0,152237	7,92	-37,7108	-0,71136
mcr-mir-216b-2	UGUCACUGUGCAUGACACUUACCUAUAGAGAUGUGUAUUGUCACUGUGCAUGGCACCCAGUAUGGUACCUAUAGAGAUGUGUAUUGUCACUGUGCAU	97	23,71134	23,71134	19,58763	32,98969	43,29897	56,70103	1,391304	1,210526	-26,6	-16,37	0,100351	18,69	-27,4227	-0,63333

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-216b-3	UACCUAUAGAGAUGUGUAUUGUCACUGUGCAUGACACUUACCUAUAGAGAUGUGUAUUGUCACUGUGCAUGACACUCACCUAUAGAGA	88	20,45455	28,40909	19,31818	31,81818	39,77273	60,22727	1,12	1,058824	-26,2	-26,2	0,289845	6,27	-29,7727	-0,74857
mcr-mir-2238k	CGGCUUGGAUGACAGGUUAGAUGCGAAAUCUUCAAUGACUGAACAGUGCAAUGCAGUUUUCGUGUCUAAACGUGGUUUgcaagugu	86	24,4186	23,25581	15,11628	27,90698	39,53488	51,16279	1,2	1,615385	-27	-26,2	0,149473	4,18	-31,3953	-0,79412
mcr-mir-2253a	GGAUAAACAGCUUGCACGCAUGGCACUGCUGAAGGUUCAUGCAUGUAUAGCAGCAACAUGUGUCAAGUGCCUUUAAGC	78	25,64103	28,20513	21,79487	24,35897	47,4359	52,5641	0,863636	1,176471	-22,7	-22,2	0,18444	5,69	-29,1026	-0,61351
mcr-mir-2254	ACAUUAUAAUUCUCGGCAGUCUUGCGGUUUGUACUAUGCAAAGUAAGUACUGCCGACCAUAUAUGAAGAA	70	20	31,42857	18,57143	30	38,57143	61,42857	0,954545	1,076923	-21,8	-21,4	0,07388	7,52	-31,1429	-0,80741
mcr-mir-2288	cccaccccaccccacgcCCUCAUCCACCUUCGACUUCUGAGCUCGAUCGUCGUUGCCUACAGCAGguaguaggugugugugugugggggggaguaGG	99	11,11111	8,080808	18,18182	13,13131	29,29293	21,21212	1,625	0,611111	-43,8	-42,9	0,179465	5,79	-44,2424	-1,51034
mcr-mir-22b	AUUAGCCUCAUCAUAGUUUACUGGACUGUGGUGUGGACAGCAGCGUUUGCAGCCUCACCUACAGUUCUUCAACUGGACUGAGCUCGC	87	24,13793	20,68966	26,43678	28,73563	50,57471	49,42529	1,388889	0,913043	-29,4	-28,1	0,059837	13,38	-33,7931	-0,66818
mcr-mir-2304-1	AGAACACAAACGAGAAUCCUAGGUAUAUGUGUUUUGUAUUGUGAAGACACAACACGUGUGGACGUAGUgguugugugguugugugug	87	19,54023	26,43678	11,49425	20,68966	31,03448	47,12644	0,782609	1,7	-24,4	-21	0,020111	11,06	-28,046	-0,9037

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-2304-2	AUACGCUgguuguguggguugugugugcaauuuuuauuuuuaucaucguGUAAAACUUUGCCAAAAAAAGUCACAUUCCACAAUCCAGCGGUC	93	7,526882	20,43011	15,05376	11,82796	22,58065	32,25806	0,578947	0,5	-30,4	-26,3	0,226556	12,43	-32,6882	-1,44762
mcr-mir-2325c	CUGUACUGUGCAAUuuuuuuggguuguuuuuuuucuuuugcuugaagCAGACGAACUUGUAAUAACGAAAAAAACCCAAGAGAAAUAACUACAUAAAU	98	9,183673	31,63265	12,2449	13,26531	21,42857	44,89796	0,419355	0,75	-20,8	-14,6	0,057963	16,12	-21,2245	-0,99048
mcr-mir-234	ACUCCGGCACUUCCGACAUGCAAUAAUUAAAGAUUCUUAAUcaguuuuuuccuguuuugauUAUUGCUCGAGAAUGACGGCUG	83	14,45783	22,89157	16,86747	21,68675	31,3253	44,57831	0,947368	0,857143	-18,5	-17,5	0,15476	7,04	-22,2892	-0,71154
mcr-mir-2390	aauuuuccugAUUUUUCUACACCUGCAUCCCAACACAAGUGGGAUCUACUAAAUCCUUGGGUCUUGuaguugugugguuuuuguugaaaaacaagaaaaua	100	9	14	15	18	24	32	1,285714	0,6	-24,1	-24,1	0,203585	18,05	-24,1	-1,00417
mcr-mir-242	AAUUUGUUAUGAACAAAUGCUGUAAGUUGAAUCUUGCCUUUUUUCAAGGGCAAGGAUUUGCGUAGGCACUUUGCAUGACAAUGU	84	22,61905	27,38095	14,28571	35,71429	36,90476	63,09524	1,304348	1,583333	-27	-25,4	0,060999	11,38	-32,1429	-0,87097
mcr-mir-2434-1	UUGCCUACAAUGCCCUCAAAUCUGAGaguuuguugggguuuuuuuugaaaaaauguccGAACAUAUCACGUGAUAUAAGGUGACAUGUUGGACA	94	13,82979	21,2766	13,82979	17,02128	27,65957	38,29787	0,8	1	-26,6	-20,5	0,012933	15,5	-28,2979	-1,02308
mcr-mir-2434-2	GCCUUCAAGGCCUAUGAGGCUCuugcuaaauuuuaaaauaaaagccaguuguugggguuuuuuuaaucAGCAUGUGCCCCAUGGGCCUUGAAAGU	95	14,73684	10,52632	14,73684	11,57895	29,47368	22,10526	1,1	1	-37,6	-29,5	0,042743	12,24	-39,5789	-1,34286

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-2444	UGGUCAAAACUAACUUCAACAACAAUAUAUCGUUGUUUCUUUUACCAUGGCACUAAGCCGugaaggugu uuguguuguuuuuuguuuugaaaa	93	8,602151	20,43011	15,05376	20,43011	23,65591	40,86022	1	0,571429	-21,7	-18,9	0,098683	7,42	-23,3333	-0,98636
mcr-mir-247	gagggggaaacagAUAAACAAGUUGUACGGUUUGUCUUCGAGAGGGAGAAAAUCACUAGAGAAAAGUUUCUACCGACAACUUGAAGUUAUUUCCCCCCU	99	17,17172	28,28283	17,17172	24,24242	34,34343	52,52525	0,857143	1	-32,3	-30,6	0,021058	14,61	-32,6263	-0,95
mcr-mir-2470	GCCAGAAAAACCUAAGCAUGACAAAAUAUCAUGCUUGUGUGGUUUUGGAUACUUGGAUUUUUCUCUC	67	19,40299	28,35821	17,91045	34,32836	37,31343	62,68657	1,210526	1,083333	-18,6	-18,5	0,281925	3,5	-27,7612	-0,744
mcr-mir-2491	GCUGCCaugaaacaacaacagcagcagcaacagcaacagcaagagGGAGCUGCUGAUGUGGAGAUUUUUCUGGCAGA	77	18,18182	7,792208	9,090909	14,28571	27,27273	22,07792	1,833333	2	-27,8	-25	0,10123	15,43	-36,1039	-1,32381
mcr-mir-250	CACUUGUCCCUGUGUACAGCACUUUAGUGAAUCACAGUCACCUGAGUAAAGAUGACUGCGCAGGGGCAACAC	72	23,61111	27,77778	26,38889	22,22222	50	50	0,8	0,894737	-26,4	-26,4	0,33034	11,12	-36,6667	-0,73333
mcr-mir-252	CCCAUAUCUCAGCAGCAACGGGUAGAUUUUUGUGCAACUAUCAAAAUAGUCUCGGUUGUAAAUUCACCUGCUCCCUGCUGCUGCCUUGCGAUAUAUC	97	18,5567	23,71134	26,80412	30,92784	45,36082	54,63918	1,304348	0,692308	-26,9	-26,9	0,313291	8,87	-27,732	-0,61136
mcr-mir-252a	CAUAACUUCUGGCCCAUUACUAAGUACUAGUGCCGCGGGAAGAUAACGUGUCAUGUCCCGUGGUUCUGGUCCUUACUACAGGGCGGAACUUGCA	94	25,53191	22,34043	25,53191	26,59574	51,06383	48,93617	1,190476	1	-37,6	-37,6	0,061669	5,2	-40	-0,78333

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-2582a	GUGACAGCCUGUAUUUCACAGUGUUCAUAAUAUUUCAGCUCCGUUUUGCCUUUGUAGCGAUGUCCCUAGCAAGACUGCUGAAACACUgacuuguaaa	97	17,52577	20,61856	21,64948	29,89691	39,17526	50,51546	1,45	0,809524	-19,7	-13,6	0,037527	15,34	-20,3093	-0,51842
mcr-mir-2699	UUUUGAGCUGUUUGUGAUAUUCGGCAUUCUUUACUCccugucucuguuucucucucccccaucccCCUCACACCGAGAUAUCGAGAAAAAGACUCAGGU	100	14	18	15	23	29	41	1,277778	0,933333	-19,4	-16,9	0,099228	8,03	-19,4	-0,66897
mcr-mir-277-1	CAACAGACAAAUGUGUCAACCGUAAAUGCAUuuucugcugcauuuuauugACACGAAAUGUCUGGAU	67	13,43284	28,35821	14,92537	14,92537	28,35821	43,28358	0,526316	0,9	-23,1	-23,1	0,480593	2,17	-34,4776	-1,21579
mcr-mir-277-2	cuccccccucccacacacacacucaucugCCCGUUCAGUAAAUGCAUUAUUUGGGGAGGUAAUGCUGGGUGAAGGAAGGGGUUC	84	23,80952	15,47619	8,333333	17,85714	32,14286	33,33333	1,153846	2,857143	-25,5	-13,7	0,072633	12,27	-30,3571	-0,94444
mcr-mir-279	CUCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACACUGCAAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAGGACGU	91	23,07692	23,07692	26,37363	27,47253	49,45055	50,54945	1,190476	0,875	-39,9	-39,4	0,157559	5,72	-43,8462	-0,88667
mcr-mir-281	AAAUGACCUCACGCUGAAGGGAGCAUCCGUCGACAGUCAGAAAUGCAGCACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGA	88	25	30,68182	22,72727	21,59091	47,72727	52,27273	0,703704	1,1	-35,2	-35,1	0,187538	3,76	-40	-0,8381
mcr-mir-283	GCUAAAUCGUGAUCCGUGCUAUAUUUAUCCUUGCUGGAAGAAAGUUAUCGGAAGGGGGCAUCUCCG	95	25,26316	30,52632	16,84211	27,36842	42,10526	57,89474	0,896552	1,5	-25,4	-24,2	0,095817	6,58	-26,7368	-0,635

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	AUAAAAUAUCAGCUGGUAAACGAAUUGGA															
mcr-mir-285	UUGUGUACGACGCUCUGUCCAUCAGUCAACUGGCUUCCAAAGGUCUCGAAAGCUCUGUUACUGCUGUAGGGAGGCGUCAUCAUUA	85	24,70588	21,17647	24,70588	29,41176	49,41176	50,58824	1,388889	1	-22,3	-15,9	0,018167	14,62	-26,2353	-0,53095
mcr-mir-2970-1	cgaAAUGCGGGUGGUGGACAAGGAUGUUCccugcacacagagacacaugAGUCGGUCGACCGAUCAGAUCAUCUCUUGAUCAACCUACAGCAUUCAG	97	20,61856	19,58763	17,52577	18,5567	38,14433	38,14433	0,947368	1,176471	-25,4	-16,4	0,010574	31,19	-26,1856	-0,68649
mcr-mir-2970-2	AGCAGGAGCCGGCCGGAGACGGCAAGCCUGGGUCCCGACAGUCAGCAGUUGGCUCCCCAUGGGUCUCUUGCCGGAUCAACCCGCUCCUACC	91	30,76923	17,58242	36,26374	15,38462	67,03297	32,96703	0,875	0,848485	-41,1	-41,1	0,129828	8,12	-45,1648	-0,67377
mcr-mir-297b	aaauauguaugugugcaugaacAUGCUUUAAAAUGUGUCAGUUGUAAGCUGUACAACUGAACAAGCUUUAAGAACAGAACUAUGAAAAAUCAUAGCA	97	13,40206	31,95876	11,34021	20,61856	24,74227	52,57732	0,645161	1,181818	-23,8	-23,8	0,133853	5,73	-24,5361	-0,99167
mcr-mir-29b	UUAAGAAUCUUGCAACAUAGCACCAUUAGAAAUGUUAGUUGUUGAGUAGAGUAGAUGGCUAAAUAUUUCUUACGGUAUUUUGCGGACUCUCAU	93	20,43011	30,10753	13,97849	35,48387	34,4086	65,5914	1,178571	1,461538	-19,8	-19,8	0,035107	6,69	-21,2903	-0,61875
mcr-mir-2a-1	UGCAAAGCUAUAGUGCUGACCAAGUGACUGGGAUGUGUACCUAAGUGUCAUAUCACAGCCUGCUUGGAUCAGUAUUGUGGUUUUUAA	87	25,28736	25,28736	17,24138	32,18391	42,52874	57,47126	1,272727	1,466667	-38	-37,6	0,220043	3,11	-43,6782	-1,02703

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-2a-2	GAAAAGCAAAUGUGCAUGGAGCAAUCAAAGUAGUUGUGAUGUGUUUCUUGGCUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAAUUUUCUUGCA	99	21,21212	27,27273	18,18182	33,33333	39,39394	60,60606	1,222222	1,166667	-33,6	-31	0,110768	7,68	-33,9394	-0,86154
mcr-mir-2a-3	UACGACUGCUGAGUCCACAUCAAAGAGGCUGUGACUUUGUGAUGCUGUAUCAAAUCACAGCCUGCUUUGGUGAGCUCUUUGCUGUCCAA	89	23,59551	22,47191	23,59551	30,33708	47,19101	52,80899	1,35	1	-36,2	-35,9	0,18632	8,53	-40,6742	-0,8619
mcr-mir-2b-1	UGCAAGAAAAUUGUGAAGAAGCUCAUCAAAGCUGGCUGUGAUAUGAAGCCAAGAAACACAUCACAACUACUUUGAUUGCUCCAUGCACAUUUGCUUUUC	99	18,18182	33,33333	21,21212	27,27273	39,39394	60,60606	0,818182	0,857143	-24,4	-24,4	0,305458	6,72	-24,6465	-0,62564
mcr-mir-2b-2	GAAGCGAGGCCAGCUCAUCAAAGCUGGCUGUGAUAUGACUGAACUCAACACAUCACAGCAUCUUUGAUGGACAGGUCCUAGCACU	85	23,52941	29,41176	25,88235	21,17647	49,41176	50,58824	0,72	0,909091	-31,5	-30,9	0,181124	5,11	-37,0588	-0,75
mcr-mir-2c	aaaagagaUUCGUCAACAUUGCCUGCUGCUUAUAAGACCUUUUAGCUUCAAUGUUUUAUGACAAGGUGCAAACAUGUUGACUuaagaaucucucuc	96	13,54167	19,79167	15,625	28,125	29,16667	47,91667	1,421053	0,866667	-27,8	-27,8	0,136659	7,8	-28,9583	-0,99286
mcr-mir-3131	UCUUAGCCAAUCAGAAAACAUUCCAUCAAGAAAGUGUGGUGUGGGAUGAGCACACACCUGACUCGAGGACUGGUGGAAUUUUCCAUGAAGUUGGUAACC	99	25,25253	30,30303	20,20202	24,24242	45,45455	54,54545	0,8	1,25	-27,7	-27,5	0,063458	7,98	-27,9798	-0,61556
mcr-mir-315b	UUUGCAGACUGCACUGAUAUAACAAUACCGCCGGAGGUCUCUUUUCUGCUUUGUGGACAUUUUGAUU	90	21,11111	17,77778	22,22222	38,88889	43,33333	56,66667	2,1875	0,95	-24,6	-24,6	0,280807	8,3	-27,3333	-0,63077

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	GUUGUACAGUCCGCUUCUGCUUU															
mcr-mir-317	GGGAAGGAUACCAUUGCUUGUUCACAGUAAAUUGGACAUGUGAACACAGCUGGUGGUAUCUUUUUU	66	25,75758	25,75758	15,15152	33,33333	40,90909	59,09091	1,294118	1,7	-29,1	-29,1	0,162636	2,6	-44,0909	-1,07778
mcr-mir-3223	ugaaaagguuaugggaugaccuuuaccuuuuaccuuuaccuuacagAAGGGUCAACCGGUCAAGCUCAUUCAUGCAUCUUUCCC	84	8,333333	10,71429	14,28571	11,90476	22,61905	22,61905	1,111111	0,583333	-18,5	-18,2	0,011779	13,83	-22,0238	-0,97368
mcr-mir-324	uugAACUCGAUUGUGACGUCUACAUCACAUGGCuucuuuccccacugccccaGGUGUCUUGUGAAGCACAUCGAGUUUGC	80	18,75	16,25	16,25	21,25	35	37,5	1,307692	1,153846	-23	-21,4	0,113698	17,15	-28,75	-0,82143
mcr-mir-3299	ACCUUGGGGGUUUUGGAAGCUUAAGCUCCAGGUUGUUUCUUUCUGCUCUAACUUGCAGGAGAUCGUUCAUUGUUAAAGUCUGCAUAACCCCCAACCU	97	21,64948	20,61856	23,71134	34,02062	45,36082	54,63918	1,65	0,913043	-31,4	-30,2	0,042103	13,35	-32,3711	-0,71364
mcr-mir-33	GCUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGCUGAGAAACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGU	75	26,66667	28	17,33333	28	44	56	1	1,538462	-33,6	-32,6	0,179681	5,16	-44,8	-1,01818
mcr-mir-33b	AGUGACAUGUACUUAAGUUACUGAAAGUACUCAAAUGUGUUUUAUGCAAUGUACCUGCAGUGCUuucagaaaagcaaaaacuuGUCUAU	89	15,73034	22,47191	12,35955	28,08989	28,08989	50,5618	1,25	1,272727	-19,3	-16,7	0,024573	11,69	-21,6854	-0,772
mcr-mir-34	UGAUCCCGUGGCAGUGUGGUUAGCUGGUUGUGGUCCGGCCGGUU	78	34,61538	12,82051	23,07692	29,48718	57,69231	42,30769	2,3	1,5	-36,4	-36,4	0,283704	3,17	-46,6667	-0,80889

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UGUGACAACCACUAUCUGCAGUGCCGCGUGAUUG															
mcr-mir-3529	UGUGGCUGCAGCAAUCAGGGAAGAAUGUGAUUUAUUGUUAGUCAGCAUCAGAACAACAAAAUCACUAGUCUUCCAGAUCACGGCAGCCugg	91	21,97802	30,76923	20,87912	23,07692	42,85714	53,84615	0,75	1,052632	-30,8	-29,7	0,103281	5,67	-33,8462	-0,78974
mcr-mir-3530	AGAGACAAGGUAGGCCUCCGGUGAAGAGAACAAUGGUGUGAGCUGGACAUGACUUGAUUAGCGAACGACAUCGAUCUCCCCGGCGCCACCUUUUCGGC	98	29,59184	25,5102	25,5102	19,38776	55,10204	44,89796	0,76	1,16	-31,7	-30,2	0,121532	8,78	-32,3469	-0,58704
mcr-mir-3671	AGUCACAUAGGUCGUAAGUUGAUCAUUACCUGUAACGUUUUUUAAAGUGAUCAAAUAAGGACUAGUGGCA	70	21,42857	32,85714	14,28571	31,42857	35,71429	64,28571	0,956522	1,5	-18,7	-18,5	0,348559	4,37	-26,7143	-0,748
mcr-mir-371b	AGUGUACGGCACGUGCUCCCCGCCGCUAGCGCACUCAAAAGAUGGCGGCAAGGGGGUGACGGGGGAGUCGCACGUUGCCGAACCGU	86	37,2093	19,76744	29,06977	13,95349	66,27907	33,72093	0,705882	1,28	-38,5	-35	0,126533	11,61	-44,7674	-0,67544
mcr-mir-372	GGAUGAUGUUCGAAAGUGCUGCGACAUUAUUACCGACGCUUAUGGUGGCCUCAGGUAUCGUACACGGCUUCUGUGUCGAAAUCCUUUCGUUCAUCAUUA	99	24,24242	21,21212	22,22222	32,32323	46,46465	53,53535	1,52381	1,090909	-32	-29,1	0,23008	11,94	-32,3232	-0,69565
mcr-mir-373	acggaugauAUAAAGGUGAUGUUCAUUAUGCCCAACUUGAUGGGCUUGGGCAGAAGGAUUCUCAAGCAUAAAAGUGCUUCCCUUUUAUUAUCAuu	95	18,94737	25,26316	15,78947	28,42105	34,73684	53,68421	1,125	1,2	-26,2	-25,2	0,010522	20,57	-27,5789	-0,79394

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-375-1	UUUAGCUGCCCAAUGACCCGAGCCGCUCGUAGCAAGGCGUCUUCACAAGUUUUGUUCGUUCGGCUCGCGUUACCAUGGUGGCACUGAC	88	26,13636	17,04545	29,54545	27,27273	55,68182	44,31818	1,6	0,884615	-35,3	-35,3	0,510508	5,41	-40,1136	-0,72041
mcr-mir-375-2	GGCUCUCCGUUUGUUCGUUUUGCUUGCUCAUGGGGUGGGUGGUGUGGGGGAGAAGGGAGCGAGUAAUAGAGCAAAAUACUAAACUACGGAGACAG	96	37,5	22,91667	14,58333	25	52,08333	47,91667	1,090909	2,571429	-26,5	-26,5	0,439668	2,92	-27,6042	-0,53
mcr-mir-376c	AGGUGCAAACACUGCCGUGUCAUGUUCAACAUAGAGGAAAAUCACCGAGGAAGUUGUGACAGUGCACCUGACACGGUCACACGUUGCAUCG	91	26,37363	29,67033	24,17582	19,78022	50,54945	49,45055	0,666667	1,090909	-27,4	-27,4	0,263715	8,34	-30,1099	-0,59565
mcr-mir-376d	UUUCAGGUGUAGAUUUUCCUUCUACAACUUAAUUGCUUCUCGCCGCAGGUGAAGUGAGGUCGAGGAAGAAGGAAACGUCUCCACCUGUGG	90	26,66667	23,33333	21,11111	28,88889	47,77778	52,22222	1,238095	1,263158	-32,7	-22,97	0,106712	16,3	-36,3333	-0,76047
mcr-mir-3834	UACGUCAGGUCGAUCUCUCUGAUGUUAUUUUCGACAAAUAAGCGAAAAGGCAUCUUGACCUGACUGC	67	20,89552	26,86567	22,38806	29,85075	43,28358	56,71642	1,111111	0,933333	-24,4	-23,6	0,406778	1,27	-36,4179	-0,84138
mcr-mir-3890	UCAGUUCGAACAGUGUUUCUAGACUCUGAAGAGCCGGUUAUGUACGGCUGUUCAAAGGUGGAUAGCUGUCAACCCA	76	26,31579	25	21,05263	27,63158	47,36842	52,63158	1,105263	1,25	-25,4	-24,2	0,10708	10,57	-33,4211	-0,70556
mcr-mir-39	UAAAUGUGAACUUUCACAAUCCCCUAUCAUGUCUUUAGUCACCUGGCUAAAGCUGAUUUCGUCUUGGGAGUUCUCAUAAU	80	16,25	25	22,5	36,25	38,75	61,25	1,45	0,722222	-22,5	-22,5	0,059743	2,98	-28,125	-0,72581

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-4000i	GACAAAGAAAGCUUUUCUUGAAGUUUUUAAGACAGGUUGACACAGUAAGUCUUAAAGUAGGGAAAUCUGAAACUUGCAAGGAACUGCUUUCUUUAUA	97	20,61856	35,05155	13,40206	30,92784	34,02062	65,97938	0,882353	1,538462	-24,9	-21	0,02901	8,86	-25,6701	-0,75455
mcr-mir-4003d	GGAUUUGUUGACACUCGUGACAACUUGCAGAGAAAGGUGCAUAUUAAGUUUACACCUAUUCCGCAGCCUGUCACUGAGAAUGGUAACCAAAAAA	94	21,2766	32,97872	20,21277	25,53191	41,48936	58,51064	0,774194	1,052632	-22,7	-22,7	0,028311	9,4	-24,1489	-0,58205
mcr-mir-4027	CUACCAUCACCUCACCAUUUAACACAUUCUGUGCCUCUGGUGCACUUGAAUUAAAACACUAUGUAUAUUACUUUUAUGUUAAUGAGUGAGACGAAGGUGA	100	16	30	21	33	37	63	1,1	0,761905	-20,8	-18,1	0,009559	16,79	-20,8	-0,56216
mcr-mir-4029	ACCCACACGUGAGGAUCAAUUCCUGUUUGUUUACAUUGCAUGCAUCGCUAGUGUAGUAACUACGAGAAAUAGACACUCACACGUGUGCGC	90	21,11111	27,77778	24,44444	26,66667	45,55556	54,44444	0,96	0,863636	-23	-17,1	0,03183	24,52	-25,5556	-0,56098
mcr-mir-4034	GCCAUUAUUUUUGCAAGGUGAAGGUGAGCAGGGAUCUUUUCUCUGGCACUGAGGACCAAAAUAUCCGUAUUCACACgugcaacugaaaaaaaauuaa	98	18,36735	20,40816	16,32653	22,44898	34,69388	42,85714	1,1	1,125	-21	-19,9	0,119554	9,47	-21,4286	-0,61765
mcr-mir-4040	AACUAGGGACUAGAUUUCAUGUUUACAAACUGAUGUAAUUUAACCCAUAGCACAAAAUACAACCAGAUCAGAAAGGUGAUAAGCUAGUUUCUACAC	96	15,625	39,58333	18,75	26,04167	34,375	65,625	0,657895	0,833333	-18,9	-18,5	0,175394	6,72	-19,6875	-0,57273

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-4048	UCAUUCCCUUUCCAGCACCUUGGUCACCAUAGUGACCCAUAGUGACCAAGGGGGAUGACGGGAAACC	67	23,8806	25,37313	29,85075	20,89552	53,73134	46,26866	0,823529	0,8	-25,9	-21,3	0,109726	8,22	-38,6567	-0,71944
mcr-mir-41	aagucUUGUCACCGGGUGAAAAACUGACGCCUGCAUAUCAUGGUUGAAUGUGGAGUCUGUGCAGUUGCUUGCGCGUGUGAACAAAGAAAA	90	27,77778	25,55556	16,66667	24,44444	44,44444	50	0,956522	1,666667	-28,1	-28,1	0,033067	9,16	-31,2222	-0,7025
mcr-mir-4127	AGGCAGCUGUGAGAGAGCCCUGUAUAUUAUAAUACCGCUAUAUAAGCCAGCUGUGAUUGAGCCCUGUAUAUUAUAAUACCGCUAUCUAAGCCAGCUGUGA	100	22	29	21	28	43	57	0,965517	1,047619	-22	-15,21	0,013453	23,23	-22	-0,51163
mcr-mir-4130	AUCGAACUCCCUCCGCUGCCCAGACAGCUGCGUGUCUUUAAGAUGGCGGCGCUUCUGCUUGGGUGACGAGAGGAGAGUCUCCCG	84	30,95238	16,66667	29,7619	22,61905	60,71429	39,28571	1,357143	1,04	-36	-35,6	0,091309	4,96	-42,8571	-0,70588
mcr-mir-427	UAGGUGACGGCCAUGUGAucgaaaagaaacagagaaagugCUUUCUGUUACUUCUUCUCAUAUCUGUCGGCACUUG	76	15,78947	10,52632	17,10526	27,63158	32,89474	38,15789	2,625	0,923077	-24	-24	0,200072	3,94	-31,5789	-0,96
mcr-mir-44-1	CGCAGGCGGGAGGUUGAAAUGCCGUUGUCGUGGUCAUCAGAUGACAGGACUGACAGCUGGAUGUGCUCGUUAACGUCGUUCUCCUGCAGCCUAAG	95	32,63158	20	23,15789	24,21053	55,78947	44,21053	1,210526	1,409091	-29,5	-21,4	0,033769	23,95	-31,0526	-0,5566
mcr-mir-44-2	GCUCAGUGCCUGUAUCCCUCAGUGACUGUGGGUUCGCACGACAGUGACUAGAUGAUCACAAGACAUUGUCA	71	25,35211	23,94366	25,35211	25,35211	50,70423	49,29577	1,058824	1	-19,8	-18,5	0,203176	16,29	-27,8873	-0,55

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-449a	UCACCUUUGCUUGUCCACUCCUCACAGUUGUAUAAAAUGGAGGUGGCAGUGCGUGUUAGUGAUGGAGAUGGUAAGGCACAGGAGG	85	31,76471	23,52941	17,64706	27,05882	49,41176	50,58824	1,15	1,8	-25,8	-25,6	0,084124	7,48	-30,3529	-0,61429
mcr-mir-4502	AcaaguugcugcugcugaugaugauggugauuggAAGUGCAGUCACAACAGACAGCGGCACACUGAC	67	11,9403	19,40299	14,92537	4,477612	26,86567	23,8806	0,230769	0,8	-25,2	-25,2	0,397491	8,17	-37,6119	-1,4
mcr-mir-452	CGGACCAUAUUAUCAAAUGUGACUGUUCGuuguuuuauuaucuuuugGUCAUAUAAACUGUUUGCAGAGGACAGUCACAUAUGUCCGAUAAGAAGGUCCU	100	18	25	16	23	34	48	0,92	1,125	-32,4	-32,4	0,183463	8,17	-32,4	-0,95294
mcr-mir-4552	CAUCAACUAACCAGCGUGAACAAGAGCGAGACCACCUCCCACUUGAUCACUGACAUUCUGGUAUGACCCGGGGUUAGUuggga	83	20,48193	26,50602	27,71084	19,27711	48,19277	45,78313	0,727273	0,73913	-26,2	-25,6	0,350856	1,8	-31,5663	-0,655
mcr-mir-466h	UcuugaguguuugugugucaugGCGCCCUUAUGUUAAAGUCGGUUCACGCACUCAGACACguauacgcacgcacacacacacacacacac	90	8,888889	10	13,33333	11,11111	22,22222	21,11111	1,111111	0,666667	-24,9	-24,9	0,117884	19,03	-27,6667	-1,245
mcr-mir-466i-1	auacacacacacauacacacgcgcacgcgcgcuaAAUGGCCUGUAUACAAACUCAUCAGAGCCUUUGCGCCAUAUUAUGAUGGUGUGGUC	90	14,44444	15,55556	13,33333	18,88889	27,77778	34,44444	1,214286	1,083333	-23	-17,8	0,062769	25,13	-25,5556	-0,92
mcr-mir-466i-2	ugugugugugugugugugugucucaauUGUUCUCUCCUAGUAGGUCAUCGUCUGAGACAUCUGUAGACAUAUUAAUCACUACAUCACCCU	90	10	17,77778	18,88889	23,33333	28,88889	41,11111	1,3125	0,529412	-23,3	-18,7	0,058678	13,27	-25,8889	-0,89615

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-467c	AAAAAUCUGUGUGUCUAAGUGCGUGCAUGUAUGCAGGAACAUUUUGAUCACAUGCAUGCAGGAACACAGAUUGAA	75	24	33,33333	16	26,66667	40	60	0,8	1,5	-31,1	-31,1	0,307267	3,37	-41,4667	-1,03667
mcr-mir-4760	UGAUGAUCUCAUGAUGAUUUCUUAGCAAAGAAUUCAUUUUCUUGUGUCCCUUUUAGAUUGAACAUGAAUGUUUAAAACAGGAUAUGAGGUCAGAU	95	18,94737	30,52632	12,63158	37,89474	31,57895	68,42105	1,241379	1,5	-22,4	-18,9	0,059494	17,85	-23,5789	-0,74667
mcr-mir-4810b	UUCCACAUGUAGGUUCAUGAGUAGACUUUUCAGAGGCUGAAGUGAGUUUAAGCAAUACUCUGAGGGUGUAUGAUGUACAUAAUGCUGCAU	90	25,55556	27,77778	14,44444	32,22222	40	60	1,16	1,769231	-18,6	-16,1	0,008321	19,96	-20,6667	-0,51667
mcr-mir-4865	UACAUGCAAGGCAGGCAACUCACACUACACACGGUAUGUAGAGAGAGUGACGCCGCUUUGUAUCGA	66	25,75758	30,30303	24,24242	19,69697	50	50	0,65	1,0625	-22,8	-22,6	0,613718	1,85	-34,5455	-0,69091
mcr-mir-4968-1	UCAGAGCAGUGCUGCUCAGcagagcagcagcaacagcagcagcagcagcagcacacuCCGCAGGCUGACUCUCAGAGCAACAUGUCUCAGC	91	15,38462	13,18681	18,68132	10,98901	34,06593	24,17582	0,833333	0,823529	-29,8	-28,8	0,303196	26,91	-32,7473	-0,96129
mcr-mir-4968-2	UAGGCAACAGGUCAGCACAacuaagcagcagcagcaacagcagcagcagcagcagcagcuguugUAGUGCCACUCUUGCUGG	82	12,19512	10,97561	12,19512	9,756098	24,39024	20,73171	0,888889	1	-26,6	-18,9	0,141152	31,1	-32,439	-1,33
mcr-mir-4968-3	CCGGCGUGACGUGCAGAuuaccagcaacaacagcagcagcagccgccgACGCUGACUCGCCGAAGCUGCUUGAUGAUGCAAGUGCCGCCACGCGCC	96	21,875	12,5	22,91667	10,41667	44,79167	22,91667	0,833333	0,954545	-29,2	-26,5	0,033415	18,93	-30,4167	-0,67907

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-4975	AUCAGGACUCAGCUGUCAAACCCAAAAUAUGCUUCUUUUUUACUUGGGUUUUCUUUcaggaagaaacaaauauugGUUCUGCUGAgccuuua	92	11,95652	15,21739	15,21739	29,34783	27,17391	44,56522	1,928571	0,785714	-22	-13,18	0,037553	24,75	-23,913	-0,88
mcr-mir-50	CGAGUAAUAUUAGACAGCGGAUUAUUCUUcaauauuauauuuaauaauauguauauauuaucuaUAAUAUAGAGUAACCCGUAGUCUUUUAUAACCUU	98	10,20408	20,40816	10,20408	23,46939	20,40816	43,87755	1,15	1	-24	-24	0,151437	7,98	-24,4898	-1,2
mcr-mir-5009	AGAAGUCAUACUGCAACAGCUCCUUCUCUUCGGUGGCCGAACUUCGGGAGUUGGACUUUUUCAGAUGGACUAGU	74	25,67568	21,62162	22,97297	29,72973	48,64865	51,35135	1,375	1,117647	-20,6	-20,6	0,124	9,33	-27,8378	-0,57222
mcr-mir-5101	GCGAuguugaugacuuuuguuuguuuugcuguauGAGUCUUUGUUGUAGAGCACGUGGAGCUGUUUACAAACUAAUUAGUCCGUcgacauuaa	93	16,12903	13,97849	9,677419	18,27957	25,80645	32,25806	1,307692	1,666667	-27,9	-27,4	0,018271	6,78	-30	-1,1625
mcr-mir-542	AUAAUCUUUACAACUGUGCUUUGAUGAUGUGCUCUCAUAAUAAAAUUGAUGUGACAGAUUGAUAAAGACGCACUUGGGAAAGAUGCA	87	20,68966	34,48276	13,7931	31,03448	34,48276	65,51724	0,9	1,5	-18,8	-18,8	0,137277	8,15	-21,6092	-0,62667
mcr-mir-5429	ccaggaaccuccgGCAUGACUAUUCCUCAAGGCACAUUUACUACGGCGuugacuacccuccaaggugccuugaggAAUAGUCAUGCUGGAGGUUCCUAG	99	14,14141	15,15152	14,14141	16,16162	28,28283	31,31313	1,066667	1	-67,1	-67,1	0,328258	3,51	-67,7778	-2,39643
mcr-mir-548d	CACUGAGGGGAGUAUACUCCUUCAGUCAACACAGUUUUAUUACCCUgugagaagaacaaaaaaaacugcaguUACUUGAAAAUAAACUACCCUCAUUc	98	9,183673	22,44898	18,36735	22,44898	27,55102	44,89796	1	0,5	-18,9	-17,7	0,01295	10,68	-19,2857	-0,7

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-550	CAAGUGCCUGAGGGAGUAGUGCCUUCUACAGGGAAAACAAUGACUGUAUGGAGCACGAUCUCCACCUUCAGAGGACACC	79	26,58228	29,11392	25,31646	18,98734	51,89873	48,10127	0,652174	1,05	-25,3	-22,1	0,053345	9,46	-32,0253	-0,61707
mcr-mir-5552	CUGCAGUCUAUAGAUAUAGCCUGUAGUCUGUUACAUUCUACCAAGUGAUCGCUACAGUUAUGUAGUUUGUAGUCUAUAGAUAUAUCCUGUAGUCUGUUA	99	19,19192	25,25253	17,17172	38,38384	36,36364	63,63636	1,52	1,117647	-28,8	-26,6	0,061307	13,22	-29,0909	-0,8
mcr-mir-5582	auuuguuGUAAUUUAAAACUUUAAGUGUGUCAGACAACUUUUCUUGCAAAAGCUAUGUGACCACAUAAGUUUAUAGUUUAUACAACAGGC	90	14,44444	32,22222	14,44444	31,11111	28,88889	63,33333	0,965517	1	-19	-18,7	0,032948	11,44	-21,1111	-0,73077
mcr-mir-5698	CAUACUGACCGCCCAACUGUGCACUGAAGUGGAUUUUAUUUAUCAGUGCgacacaccccucccccuuucuuuGUCCCAGUGUGGGGGAGUGCAGUGAA	99	22,22222	17,17172	16,16162	20,20202	38,38384	37,37374	1,176471	1,375	-28,3	-21	0,011177	15,74	-28,5859	-0,74474
mcr-mir-586	CUCCAUGUUGAUGGUAUGCAUAUUGUAUUUUGUACUUGUAGUUCCCUGGGUACAGUCACCAGUACCAAUGAUGCCAACACUUUACAUGCAU	91	18,68132	24,17582	21,97802	35,16484	40,65934	59,34066	1,454545	0,85	-19,1	-15,9	0,059302	17,12	-20,989	-0,51622
mcr-mir-5890c	CUCCAGACUAGUUUCAUUCCCUGUGCAGUUCAGGUCAUUGACCCAGACGCUGCCAUAUAACUGAACUGUCUGUGG	75	21,33333	21,33333	28	29,33333	49,33333	50,66667	1,375	0,761905	-21,4	-18,9	0,044239	9,08	-28,5333	-0,57838
mcr-mir-592	CCUGACGGUGAACAAGAACUCGGUCCUCGCAUAGCGACGUGACGUCAUCACGUGGUGACGUGUUCUAC	97	26,80412	17,52577	29,89691	25,7732	56,70103	43,29897	1,470588	0,896552	-31	-28,5	0,039975	20,27	-31,9588	-0,56364

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	GCGCCAUCUAGGUCUUUUUGCCCGUCGUC															
mcr-mir-6013	UUGUCCACGGCUGCUGACGACCGCCUCAAACGUCAGAAGUUGAAGGAAAACAGAGAGAGCUUGAGCGAGUCGCUGGCGCAGUGGAAGC	88	32,95455	27,27273	23,86364	15,90909	56,81818	43,18182	0,583333	1,380952	-27,3	-26,6	0,063669	7,38	-31,0227	-0,546
mcr-mir-6058	GGAGAAGAACUGGACAUUACUCAGCUGAUGACAAUGGUGAUGAAUCAGAUGGGUUACAAUAUGUAGUUGUCCUCUGCUGAUUUAUGGACGUCUUCCAU	98	25,5102	27,55102	16,32653	30,61224	41,83673	58,16327	1,111111	1,5625	-26,2	-26,2	0,10919	8,67	-26,7347	-0,63902
mcr-mir-6340	GCGGUGCUGGGUUUGCUCAGCUGGUGGAAGAUCAACAGACGUCAGCAGCAGCUUCGAUACCCAACACGAC	70	30	24,28571	27,14286	18,57143	57,14286	42,85714	0,764706	1,105263	-22,1	-22,1	0,286043	7,87	-31,5714	-0,5525
mcr-mir-6552	CCCAUCAUUCGACUUCAGCAGGGAAGACUUUCGCGAUCCUUUUCUAAAGCAACAAGAAGUGGACACGGUCUAUUUCCUGCAGGUGUCUGAAAUGAUUCA	99	21,21212	27,27273	24,24242	27,27273	45,45455	54,54545	1	0,875	-28,3	-23,2	0,012686	10,87	-28,5859	-0,62889
mcr-mir-6560	CGCUGUGUUGCUCCAUACUGCUGAAGAAGUGUCUGCACUUCUGUUUCAGUCAUACUGAGCAGCUCAUCA	69	21,73913	20,28986	26,08696	31,88406	47,82609	52,17391	1,571429	0,833333	-24,8	-24,8	0,250515	3,95	-35,942	-0,75152
mcr-mir-669f	CCUGCGAACCAUUAUGCUGGaauucucucucuauauauauauauauacacacacacacacauaagaauUUCAUUUAAUGGUUUCGCGUG	89	11,23596	7,865169	10,11236	16,85393	21,34831	24,7191	2,142857	1,111111	-19,4	-18,5	0,056046	7,7	-21,7978	-1,02105

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-67	GAGAUAUCGUGAGCUGUUGGUCCUUGUUCAGCCCGGUUGUGAUGGAGUUGAUCGCAUCACAACCUGCAUGAAUGAGGACUGACGUCAcgaaauaac	96	27,08333	19,79167	18,75	25	45,83333	44,79167	1,263158	1,444444	-47,7	-47,7	0,225173	3,14	-49,6875	-1,08409
mcr-mir-676	CUCUUCAACUUCAGGAUCGUUAAGACAAAAUCAUAGUUGCUGAUAUAGCAGAGCCUGGAuauguccuugucuuggccuugaCGAUGCUGAAUUUAAAGUG	100	17	25	14	22	31	47	0,88	1,214286	-30,9	-30,9	0,08456	5,13	-30,9	-0,99677
mcr-mir-6769b	UGAUGGUGGGUGAGGAGGAGAAAGCAAUUAGCAAUAGUUUUCGAAAGACUUUCUGGAAACUCGAUCGAuuauuucacucacucacucacucacucacuc	99	21,21212	22,22222	8,080808	17,17172	29,29293	39,39394	0,772727	2,625	-29,4	-23,1	0,04736	29,05	-29,697	-1,01379
mcr-mir-6780a	AAGCUCGUGUAGAAAAGCUCcuccucuguuuucuuuucaaaaugcaUGUCAGGUGCAACAUAGACGUGUAGUAGGAUGAAUCUUGACACACGAGGCC	97	20,61856	22,68041	14,43299	15,46392	35,05155	38,14433	0,681818	1,428571	-23,6	-23,3	0,05752	17,22	-24,3299	-0,69412
mcr-mir-6796	GGAGUACAAAGUUUCCGUCCUGAUUUUCUUGUGGGGUUGGAGAGUAUGGCUCCAUGCAAAGUCUAGAAACGUaaacuuggacaau	85	24,70588	20	14,11765	25,88235	38,82353	45,88235	1,294118	1,75	-24,9	-23,7	0,22456	3,8	-29,2941	-0,75455
mcr-mir-6800	CUGUAGUAGGUGACAGUCAGGCCUGGUCUCUUCUUGUCACCAAGGCCACAUUAUAGGGCUAAGAGGAGGCACUAGUAGUUCACUACUAUAU	91	25,27473	25,27473	21,97802	27,47253	47,25275	52,74725	1,086957	1,15	-26,7	-19	0,021509	23,54	-29,3407	-0,62093

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-6803	CUACACGCACCGCUGCCAGCACCGCCACGCGCCGAGGGCAGGUGUAAACGGAGCUGUCACGUGACCccgagggugggggugggggcugggAGAGUGGCU	100	24	16	26	9	50	25	0,5625	0,923077	-43,7	-40,7	0,072188	21,19	-43,7	-0,874
mcr-mir-6826	CACCUUACUGAUUCGUUUCACAACAGGACUGGUAUGUUCUGUGUCAAUAGGAAAGAGGUCUGUGAUUUGUCCUGUUUGUGAAUUGAUCAUACAGUAC	97	22,68041	24,74227	17,52577	35,05155	40,20619	59,79381	1,416667	1,294118	-25,9	-25,1	0,012492	20,76	-26,701	-0,6641
mcr-mir-6830	AGGAACAGGUGCGAUACGAUCGAGAGAGACAAGCGGGUCCUCAGAAAAUCCUCUUGAAAugcuuucuugucuuucuucucucccccaucuguuuuu	96	17,70833	21,875	12,5	9,375	30,20833	31,25	0,428571	1,416667	-29,9	-29,5	0,041352	6,82	-31,1458	-1,03103
mcr-mir-6864	GCAGUCGGAGGGUUAAAGUGAAAACAAAGGCAGUACUUGAAGGGACAAGUCAGACUUUAAUGACGCCAUGGGUAUUUCCUGUUACCCCGACAAU	94	26,59574	31,91489	19,14894	22,34043	45,74468	54,25532	0,7	1,388889	-23,6	-23,2	0,154259	11,86	-25,1064	-0,54884
mcr-mir-6873	CCUUGCAUGUGUCACAUGAGCAAAGAUUCAGAUAUAUGCACACACUUGCAUauguucucucugucuuucucucaugugcacUUGCAUGA	89	12,35955	20,22472	14,60674	19,10112	26,96629	39,32584	0,944444	0,846154	-35,2	-34,8	0,118812	5,2	-39,5506	-1,46667
mcr-mir-6925	ACAACACCUGAAGACUuuucuucaaggcaccuuggaggguagucgaugcUCAGUUGCAAGAGGAAGAAAUGGCUUACAAAUGUcag	86	12,7907	23,25581	10,46512	11,62791	23,25581	34,88372	0,5	1,222222	-20,5	-19,9	0,218392	9,52	-23,8372	-1,025
mcr-mir-6955	GCCCACAAGAGACAGCAAGUAGGAGGCACAUCCAGACACGAGUGCC	86	23,25581	22,09302	30,23256	24,4186	53,48837	46,51163	1,105263	0,769231	-24	-23,1	0,092411	15,34	-27,907	-0,52174

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UGGCAUUCUACACCUGUCUCCUUUGUCGUGUCCUUUGCUU															
mcr-mir-6975	AUCGCGAGGGGAAAGGCUGAGCACCGCUCAGCAUACUUUAGUUGCUGUUGGCUCUCUCCUUUCUCCUCCGCCUC	74	24,32432	14,86486	32,43243	28,37838	56,75676	43,24324	1,909091	0,75	-33,1	-33,1	0,158058	5,02	-44,7297	-0,7881
mcr-mir-6988	ggguggggugagagcUGAGUUACACGCAGUGAGCACUGCUCAUCCUCAGGCACUGCCUACAACUACGCUCCGCCUCAUCG	81	16,04938	17,28395	29,62963	17,28395	45,67901	34,5679	1	0,541667	-33,4	-33,4	0,234622	9,97	-41,2346	-0,9027
mcr-mir-7	AAUGCAAAUACUAGGGACAGGGUUUUCUUUUACACAGACGGGCUGAAUCGCUGACUGGUUACAAAAGCCAACAAGUCCCAGUCUUGGCGGA	91	25,27473	29,67033	21,97802	23,07692	47,25275	52,74725	0,777778	1,15	-22,6	-19,7	0,032478	10,33	-24,8352	-0,52558
mcr-mir-7042	AAGGGAGAAUUCAGUGGGAUCAUGUGGGGCUUGGAAGGGGAAGUAAUUUCAUGUUGAAGCCACCUAGUGACAGAUGUcccuuuguuuucuccaca	95	28,42105	23,15789	9,473684	20	37,89474	43,15789	0,863636	3	-36,4	-36,4	0,334669	3,58	-38,3158	-1,01111
mcr-mir-7051	AUGUUUAAAAGUUAUGUAGCUAAGUAUAAUGUUCACCAGGAGGAGGUGUGCACGUCCUAacuaaucauuauuauuauugcauaacAUUGUAAAGCG	96	18,75	22,91667	9,375	21,875	28,125	44,79167	0,954545	2	-21,7	-19,9	0,057538	7,51	-22,6042	-0,8037
mcr-mir-71	aaauuccuuuUGGUGUGAAAGACAUGGGUAGUGAGAUGUCGGUCCUGAAGAUUCACCUUAUUACCCUGUCUUUUGCAUCAAGGGGAAACC	90	24,44444	22,22222	16,66667	25,55556	41,11111	47,77778	1,15	1,466667	-44,2	-44,2	0,187606	4,57	-49,1111	-1,19459

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-7186	UGACAGUAGAAUAGCGAGUUGGCGUGUGCAUUAAGAGCUGUGGUUCCUGUAUGUUCGGGAAGCACAGUCACGCUCAGCCGAUGCAUUUCACUGGAU	96	30,20833	22,91667	19,79167	27,08333	50	50	1,181818	1,526316	-38	-38	0,237347	14,88	-39,5833	-0,79167
mcr-mir-7234	ACUGUCAGAGUUUCGGGCUUUCUGUGGUCCCCUAAAGACAUGUUUUAAUCGUGUAGCUUGUUUUCUCCAAAGAACACCAUAAACUUCGACUGA	93	19,35484	24,73118	22,58065	33,33333	41,93548	58,06452	1,347826	0,857143	-21,5	-21,5	0,443504	4,24	-23,1183	-0,55128
mcr-mir-7241	GUGUUUGUUAGGGUAGUAGAUACUCAUGGUGAGUAACCCAAAACCCGGGGUUACGGAUGUaucugcuucauaacuacgaccccagAGCAAAUUC	94	21,2766	20,21277	11,70213	20,21277	32,97872	40,42553	1	1,818182	-28,1	-27,8	0,130969	8,02	-29,8936	-0,90645
mcr-mir-7260	CGCAGCUGUUUUAAAGCCAGUAAUCAAGUCAUCCAGUACAAGGAGAAACAGUGCUGACAGUGCCUUUUACCGACUUUAGUGAUGGCUAAAACAACUGAC	99	21,21212	32,32323	22,22222	24,24242	43,43434	56,56566	0,75	0,954545	-22,8	-16,37	0,04421	16,66	-23,0303	-0,53023
mcr-mir-7371b	UCGAGCAACUUGAUGAUAUCGCUUAUUAUCUUCUCUUGAGUUGUAGAGAUGGACGGAGGAUAAGAUGCUUUGUAUCAGAUGCUUGC	86	25,5814	24,4186	15,11628	34,88372	40,69767	59,30233	1,428571	1,692308	-22,4	-20,5	0,034701	13,15	-26,0465	-0,64
mcr-mir-742	auuaucuGUGAUCUAGAGAGAAAGCCACCAUGCUGUUAUAUCACGUCUAUUGUUGAAUCGACUUCUUCGGUGGUGUCUUUUUCUACAUAACUACAUCAG	99	18,18182	23,23232	19,19192	32,32323	37,37374	55,55556	1,391304	0,947368	-19,2	-11,69	0,033442	29,11	-19,3939	-0,51892
mcr-mir-7456	UGCUGUUCGCCUGGCGAUCGCAUGGUAGCGUCUGGUUCAGGGAG	71	32,39437	18,30986	25,35211	23,94366	57,74648	42,25352	1,307692	1,277778	-24,5	-21,8	0,048336	5,34	-34,507	-0,59756

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	AUGUACCUGCUGCCAGCUGAAACAACG															
mcr-mir-7461	ACAUGCUCUUUGAUGACCAGCAUGGCUGGAAUGUGGCUGAGCAACAGUUCCCGGACGUUCUGGUUGAAUCAGAAGGCAAGC	81	29,62963	24,69136	22,22222	23,45679	51,85185	48,14815	0,95	1,333333	-26,8	-26,5	0,04965	8,31	-33,0864	-0,6381
mcr-mir-7462	UAUUAUGGCCUGCUCCAGGUACUGCGGUGUGUGAUGAGCGAUGAUAGGAUGCAACAGAAUAGCCACUGACACAACCUCAUUUCUAGCAGACCAUACAG	98	24,4898	28,57143	23,46939	23,46939	47,95918	52,04082	0,821429	1,043478	-23,7	-17	0,032162	19,67	-24,1837	-0,50426
mcr-mir-7465	CACcaggaauuauuuuuaaacacucaGUUACAAAUCAGCUCAAAUCUGGUAAAACUGCUUCAGAUAGCUGAUACUCAUUUUUAGAACAAUAUUUCUGCAG	100	11	26	16	24	27	50	0,923077	0,6875	-19,7	-19,7	0,176123	6,74	-19,7	-0,72963
mcr-mir-750	GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUGGCAGGAAUGCUGUCUUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUGGCAUGGCAUG	97	27,83505	19,58763	23,71134	28,86598	51,54639	48,45361	1,473684	1,173913	-52,7	-51,6	0,157091	3,48	-54,3299	-1,054
mcr-mir-7589	AUGUGCUUAAUUGAGCCCCCUUCGUCAGUUUCUCAUUCUGGAUGGAUUUCUGGAAAUGGAGAAAUCAGCCGAUGCGGAGGCUAACAGAGCAGUG	94	27,65957	24,46809	20,21277	27,65957	47,87234	52,12766	1,130435	1,368421	-29,8	-24,4	0,024214	13,36	-31,7021	-0,66222
mcr-mir-765	UGGUGCAGAAGGGAGUUCAGCUUACCAAAUACUGAGGACAUGGAGGAGAAGGAAGGUGUGGUCAGCUGAUCCUCACUUCCUGACAUUC	88	30,68182	27,27273	19,31818	22,72727	50	50	0,833333	1,588235	-24,1	-24,1	0,047094	9,07	-27,3864	-0,54773

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-7683	ACUUGGAAAGGUGGAACACUAACCAUACUGGCACUGUGGACCUUGGAAACCUGGAGGACAGGCGCAGGAUGGAUAGUAGCCUCCUCUGCACUG	93	30,10753	26,88172	23,65591	19,35484	53,76344	46,23656	0,72	1,272727	-28,7	-24,8	0,044924	9,43	-30,8602	-0,574
mcr-mir-770	GGUCACAUUCAAUCACGUUACAGGUGCAGAUCGAACCUCGUGCCAGUCACGAUCAGCACCACGUGUCUGGAAUCUGUUU	79	22,78481	24,05063	27,8481	25,31646	50,63291	49,36709	1,052632	0,818182	-22,2	-22,2	0,116359	8,08	-28,1013	-0,555
mcr-mir-7789	CUAUGAGCGAGUAGACUGCUGUGUUCCUcugagaagaggaagaagaugaaacGAUUCAGCAGAGCAGACGUCCAGCAGUCGAUGAUCGCUCACUU	95	20	16,84211	18,94737	18,94737	38,94737	35,78947	1,125	1,055556	-35,1	-32,4	0,057006	10,22	-36,9474	-0,94865
mcr-mir-7795	AGGAGACACGUGAUGCUUACAAUAUGACACCAGCAUCUAAUCUCUUAUCGGUAUAGGUGUGAAGUGUCAGAUGAUCGGUCUUGA	84	25	28,57143	17,85714	28,57143	42,85714	57,14286	1	1,4	-19,9	-19,9	0,054929	9,78	-23,6905	-0,55278
mcr-mir-789b	CCAUCCUGGUACACCACCAGCACAUCUCUCCAUUCCAGGUAUGAUGGCGUCGUGCUUCCGCUGCUGGAGAUGGCGGUCGCAGAUGCAGCAGGAAUC	96	27,08333	19,79167	31,25	21,875	58,33333	41,66667	1,105263	0,866667	-29,6	-23,8	0,110276	11,46	-30,8333	-0,52857
mcr-mir-7950b	UUUGGCAGGCCGGCGAAAGAGUUGCGCCAGACUCACCCAUCAAAGCAACCCGCAGGUCUGGCGCCUGCCUCCCUCG	76	27,63158	19,73684	36,84211	15,78947	64,47368	35,52632	0,8	0,75	-28	-24,8	0,1728	20,48	-36,8421	-0,57143
mcr-mir-7964a	CGCUCUAGGAUGCAGUGCGUAGUGCAAUCAAGCGGAGCGGAUGGGGAUGGUCAACCACUCGCUGCAUAUAGAUAA	75	32	26,66667	21,33333	20	53,33333	46,66667	0,75	1,5	-20,8	-17,3	0,208513	17,37	-27,7333	-0,52

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-8	CGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUUUG	86	22,09302	25,5814	19,76744	32,55814	41,86047	58,13953	1,272727	1,117647	-38,5	-38,5	0,175975	3,55	-44,7674	-1,06944
mcr-mir-802	uuaccuuuguaCCCAUUCCAUAGUUUGUCAGUAACAAAGAUUCUGUUACACAAGUGACUUGGACCUUGGUGACAAGGAUU	80	17,5	25	17,5	26,25	35	51,25	1,05	1	-20,1	-20,1	0,088615	9,87	-25,125	-0,71786
mcr-mir-81b	CCUGCAAAAACUCAUGGGCCCUAUUUCGGCCCUAUAUGGGCUUAAAAUAGGCCCUGCAUGGUGAAACGAUCAUGGGCCUAUGUGUGUUUUGCCCA	95	24,21053	23,15789	25,26316	27,36842	49,47368	50,52632	1,181818	0,958333	-38,4	-35,6	0,107415	11,5	-40,4211	-0,81702
mcr-mir-8234	GAACAGGAUAUUGGCAUGGAGAAGCAACACCACUCUUUGCCUUCUCCAUCCCAUCUUCUCCUGCCU	66	16,66667	22,72727	33,33333	27,27273	50	50	1,2	0,5	-23,7	-23,7	0,285672	2,31	-35,9091	-0,71818
mcr-mir-8293	AGGAGUGAUAGGUAGCUGAUUUAUCAUGAAAGAUAAAAGUGGAUGAAUACAUUCCCUGUCCUAGACAUGAUAAACCACUCACAGUUCACUGua	93	20,43011	34,4086	17,2043	25,80645	37,63441	60,21505	0,75	1,1875	-21,3	-20,8	0,146917	10,11	-22,9032	-0,60857
mcr-mir-83	AUGUAGCACCAUAUAAAUUCCUGCUGCUGAGCUGCUGCUAACUAAUGCAUUGAUAGUUUUAAGGAAUGUGGAGCAGCAUAGUUACUGUGUUGCUAUAC	98	22,44898	27,55102	17,34694	32,65306	39,79592	60,20408	1,185185	1,294118	-26,9	-26,9	0,117633	12,41	-27,449	-0,68974
mcr-mir-8319	AACAAUGCAGCAAGAGGCUCAUUGCCAUagauuuugguuguuuuuuucugagcuGUUCAAAUUAGCAAGUGAGGUCAGGCUGCCUUUAG	89	17,97753	21,34831	14,60674	16,85393	32,58427	38,20225	0,789474	1,230769	-21	-10,6	0,048695	25,91	-23,5955	-0,72414

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-8335-1	uuguuguuguuguuguuuugcucaUGGCUGGUCAUUAAGACCAAACUGACAAAACUGCUUACAGACAAUUU	71	11,26761	23,94366	14,08451	16,90141	25,35211	40,84507	0,705882	0,8	-21,2	-18,8	0,146315	6,81	-29,8592	-1,17778
mcr-mir-8335-2	GCGCUGCAGAGguguauauauaauguuugccauguuguuguuguuguuuuuuuuuuuuuagcuuacaGACGAUUAUUAUAUUGAUACACUUGUGAGGCC	99	12,12121	11,11111	8,080808	12,12121	20,20202	23,23232	1,090909	1,5	-23,4	-20,9	0,130829	15,27	-23,6364	-1,17
mcr-mir-8364j	UCGGGGCGACUGCGUGAUCUCACGUGugagcaugcaugugugucuuCAUUUCUCACGUGAAUGCGCGCGcccgag	75	21,33333	9,333333	18,66667	16	40	25,33333	1,714286	1,142857	-28,6	-24,2	0,014357	24,88	-38,1333	-0,95333
mcr-mir-8485-1	cacacacacacacacacaaaagucacAAUGUAACUGCAGUGUGUUUUUACACAUGGUCAGCAGUGACAGUGUGAUAUAUUGAAGUGAGAGAGUGUUUU	98	20,40816	20,40816	7,142857	25,5102	27,55102	45,91837	1,25	2,857143	-25,6	-20,8	0,086901	11,94	-26,1224	-0,94815
mcr-mir-8485-2	gaguuugcacacacacacacacacguaugauACAUUUCGUACUCCGCAAGCUCAGGUGAAUAUGGCAGGAGUGUGUGUUUCAUGAUGCUGGCAAAAAU	98	18,36735	18,36735	12,2449	19,38776	30,61224	37,7551	1,055556	1,5	-24,8	-19,4	0,065813	22,98	-25,3061	-0,82667
mcr-mir-8485-3	cacacacacacacacacacacgucacauuCAAGAGGGGAGCAAUCUAGAUCCCUGACAGAUUAGGUAUAUGCAugugauguguguauguuuuuuguaAG	99	13,13131	16,16162	8,080808	9,090909	21,21212	25,25253	0,5625	1,625	-26,8	-24,6	0,07266	13,36	-27,0707	-1,27619
mcr-mir-8881	CUGGUUUUUAAACCAAGAAAGGAAGAUAAAUUAUACAGAAUAUAAAUGCAGCCGUUGCUUUGUUUUCUCUGGUUCUUCUCUUUCAAAACUUU	92	15,21739	30,43478	16,30435	38,04348	31,52174	68,47826	1,25	0,933333	-20,4	-20,4	0,106037	7,86	-22,1739	-0,70345

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-8956	GCAGAUUCUGUUGACACAGCAUCCAACACAUCAGUGUGAAGGUGUGUUUCUUUGCCUGCAAAGCCCCUACAUUGACUUGGAUCUUUGCAACGUAUCGGU	99	22,22222	23,23232	24,24242	30,30303	46,46465	53,53535	1,304348	0,916667	-25,5	-24,6	0,178773	11,53	-25,7576	-0,55435
mcr-mir-8993	GUCAUGACCUUGACCUUUGACCAAGUGCAGCGCCUCUCGUGCUGACAUGAAUGAAGCAAAGGCCAGACUUGCUCCUGGCCAAGUGGCAUUGG	92	27,17391	22,82609	27,17391	22,82609	54,34783	45,65217	1	1	-28,9	-27	0,19811	10,01	-31,413	-0,578
mcr-mir-9077	UGUCUCAAAUUAUCUGAGGGCUUUUGCACUGCUGCUGAAAAUUUCUGCUGAUAUGCAGAAGUCAUAAAUAAAUGaguga	79	18,98734	27,8481	15,18987	31,64557	34,17722	59,49367	1,136364	1,25	-18,7	-18,3	0,09631	8,26	-23,6709	-0,69259
mcr-mir-9093	GCUGUCACGUAGAACCUGAUGGAUGUCACCUACGACUGUAGUCCAUGUCCCGGACCAGUGUGUGUCACAAUAGUUUCAAGUUCUUACAGGUGACUUU	97	23,71134	22,68041	23,71134	29,89691	47,42268	52,57732	1,318182	1	-25,6	-25,3	0,077213	8,56	-26,3918	-0,55652
mcr-mir-9-1	GGCGGCUCCGGUUUUGUCUUUGGUUAUCUAGCUGUAUGAUUGGGGCAGAAAUAUCAUAAAGCUAGGUUACCAAAGGCAAAAAUGGACGCCAAA	93	26,88172	29,03226	17,2043	26,88172	44,08602	55,91398	0,925926	1,5625	-45,5	-45,5	0,314517	3,87	-48,9247	-1,10976
mcr-mir-9186o	UGACUAAGAGGUGGCAUGGCUGGUGUUGGCAACAUUCCCUGACCUCUCUGAAAGCCUUGUGGUAUCCCCCCUGACCCAGGCAUGCCUUCUUCUAGCGA	98	25,5102	18,36735	29,59184	26,53061	55,10204	44,89796	1,444444	0,862069	-29,1	-25,24	0,012852	15,39	-29,6939	-0,53889

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-9-2	uugaacagcacaggugacagGGGACAACCUUAACGUAUGCUUACUGUAaugcaaaaguaagcuccucUUUGGUUAUCCAGUAGUAUUGUGCUUGUUGAG	99	15,15152	13,13131	9,090909	23,23232	24,24242	36,36364	1,769231	1,666667	-27,4	-24,7	0,019343	8,03	-27,6768	-1,14167
mcr-mir-92a-1	cUGGCAUUAGCAGUAGGUCUUGAUAAGUGCAAUUCUGGUGAAUUAGAUAACAGAUUGCACUUGUCCCGGCCUUCUGCUAAUAGCUAA	87	22,98851	26,43678	18,3908	31,03448	41,37931	57,47126	1,173913	1,25	-43,2	-43,2	0,272477	2,43	-49,6552	-1,2
mcr-mir-92a-2	AUUUGUGUGCUCAGGAAAGGUUGUGACUUGGGCAAUUCUGUGAUGUCCUGUCAGAUUGCACUUGUCCCGGCCUUGUCUUGGCUUACACUU	90	26,66667	15,55556	21,11111	36,66667	47,77778	52,22222	2,357143	1,263158	-31,5	-29,1	0,036643	11,93	-35	-0,73256
mcr-mir-92b	CACCGAUCAGGGUUGUGUAGACCGGAACAGGGGCAAUGCAUUUUGAGUCGUCUGUAUUGCACUCGUCCCGGCCUAUCCAAUCUGACUCGUAG	92	27,17391	20,65217	26,08696	26,08696	53,26087	46,73913	1,263158	1,041667	-33,5	-31,7	0,067381	6,55	-36,413	-0,68367
mcr-mir-92e	ACCAAGCAUUUCAAAGAUCcacgugggugugugcgugcgugugcgugggcggugugggugggugcaugGCACACACACGUGGAUCUUUGAACUGCUUGAU	100	9	16	13	13	22	29	0,8125	0,692308	-55,5	-54,6	0,151057	12,27	-55,5	-2,52273
mcr-mir-9-3	UUUGGCGUCCAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUGCCCCAAUCAUACAGCUAGAUAACCAAAGACAAAACCGGAGCCGCC	93	17,2043	26,88172	26,88172	29,03226	44,08602	55,91398	1,08	0,64	-34,1	-34	0,28369	3,42	-36,6667	-0,83171
mcr-mir-9358	UGAGGUACCCCGAGACAACUUUUUCGCUUUGACUAUUCGUUUGACAUGCUUGUUCCUGCAUUUUUUC	99	21,21212	19,19192	24,24242	35,35354	45,45455	54,54545	1,842105	0,875	-26	-26	0,127101	8,99	-26,2626	-0,57778

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UUCAAACGAGAACGAUGGCCCUGGGUACCUGU															
mcr-mir-936	CAGCUCGCUGGAcaggagagggaggaaggggacUGGAACCUUCCUUUCCUCAACAUCUCUCCAGUUGAGGCC	72	13,88889	12,5	25	19,44444	38,88889	31,94444	1,555556	0,555556	-31,6	-29,2	0,090386	19,4	-43,8889	-1,12857
mcr-mir-9392	AAACACUGGCUUUCCUUCAUAUUAUGACUAGAUGAAAuucauuaaauguuuuucuagUCACAUUAAUUCACUGAAAGAAGUGGCA	85	11,76471	28,23529	14,11765	22,35294	25,88235	50,58824	0,791667	0,833333	-18,6	-18,6	0,301505	7,56	-21,8824	-0,84545
mcr-mir-943	ACUACAAGACAGGGAGAGAAUGUCAGACGACAAUGAAAUAUCUUUCGAAAUGUCUGCCAGUGAUUCUUUCUGACUGUUGCUGUCCGUUUUUUGUCUG	97	22,68041	25,7732	18,5567	32,98969	41,23711	58,76289	1,28	1,222222	-21,5	-12,9	0,033141	29,31	-22,1649	-0,5375
mcr-mir-9438	AGCCUGGCUACACAUCAUACUACACAAGUGUCUAGUGUGGCUACAAACAUUGCAAGCACCCCCCACUUGUCUACUCUGGGUGCAGUGCAGGGG	93	23,65591	24,73118	29,03226	22,58065	52,68817	47,31183	0,913043	0,814815	-28,8	-28,3	0,192015	6,09	-30,9677	-0,58776
mcr-mir-9505	UGGAUGAUGUCUGUCAAAAUCCAAUGGAGACAUAAGAGGCCAGCAAGCACACUGCCUGCUGACCUGCUCUUGGACUACAUGAUUACAGACACUAAUGUG	99	23,23232	30,30303	23,23232	23,23232	46,46465	53,53535	0,766667	1	-27,7	-27,5	0,050009	11,15	-27,9798	-0,60217
mcr-mir-9542a	CGACUGACAAAACGGCUCACGACAUGGCCUGGCACUUUCUAAUUUCUGGCCAAGUUAGGCGCCUGUUUGUCGAGGGC	77	27,27273	20,77922	27,27273	24,67532	54,54545	45,45455	1,1875	1	-23,6	-19,5	0,032476	12,94	-30,6494	-0,5619

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-9573	agaaaaaauaucaaaacuaGGAUUGUGAGGCUGUUGGUCCAGCCCUGCCAUCAUGGUGUUGGUUUUUUACC	71	22,53521	8,450704	15,49296	26,76056	38,02817	35,21127	3,166667	1,454545	-19,6	-17,5	0,079399	19,85	-27,6056	-0,72593
mcr-mir-9592	GGAUUGCUUUGCUGUUUGGGGCUGAUGCAAGGUUCCUUGCAGUGACGACCUUAUUCAGACAAAGAAACGG	70	30	22,85714	18,57143	28,57143	48,57143	51,42857	1,25	1,615385	-20,9	-20,4	0,264055	3,01	-29,8571	-0,61471
mcr-mir-9598	GAUAUUAUUGAUAUAAAACUGUCAGUGCUUAUUAGUACUAGGAUUUUGAUUAGCUGUUGUAAUUAGUGCUACAGCUUAUAUCAAGGUAAUCGU	93	19,35484	30,10753	10,75269	39,78495	30,10753	69,89247	1,321429	1,8	-21,6	-20,9	0,026556	30,6	-23,2258	-0,77143
mcr-mir-9640	UUCACAUGUCUAAGCAUGCUUUCGUGUUUCAGAUGGCAGAGCUGGACAAGGUGUCGCACCCUGAGAAGCCCUACCCGUACAGCAUGGCUGACAUGUUCA	99	25,25253	23,23232	26,26263	25,25253	51,51515	48,48485	1,086957	0,961538	-27,2	-22,7	0,044766	14,41	-27,4747	-0,53333
mcr-mir-965	GGGGGAGAAGUUAUUGCUGCGAAGCCUCAGCUUCUGCAAGCAGGAguuggucuucagcaugucacGAAUGUGCUCGCAGCUAGCGUCUCCAAC	93	24,73118	18,27957	19,35484	16,12903	44,08602	34,4086	0,882353	1,277778	-38	-36,4	0,037571	7,54	-40,8602	-0,92683
mcr-mir-96b	CGACUGCUGGCUGUUCAAUUAUUUGGCACUUGUGGAAUAAUCGGUGUAUCUGAAAGUCGAUUAUACACCGGUGCCAAGUCAUCAGAAAUGCCUGAAGCAC	100	24	27	21	28	45	55	1,037037	1,142857	-33,2	-33,2	0,110762	3,59	-33,2	-0,73778
mcr-mir-9771g	CAAAACAGAGAACUACAUAUUUUACAUGCAAUGCUUCUAUUGCACUGGGcugucggaaaagucaugacgcAUU	98	13,26531	23,46939	14,28571	27,55102	27,55102	51,02041	1,173913	0,928571	-19,7	-19,7	0,07496	11,01	-20,102	-0,72963

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
	UUUGCAAUAUAUGGUGCUCGUUCAU															
mcr-mir-981	GCUAUCAGACUUUGUUCCGGGUUUCGCGGCUGGCGAACAGUCAUUUUGAGCUGUGUUCGUUGUCGUCGAAACCUGCCCUGAAAUCUGAUGUG	92	28,26087	16,30435	22,82609	32,6087	51,08696	48,91304	2	1,238095	-35,5	-31	0,014511	9,61	-38,587	-0,75532
mcr-mir-9896	GACCUGAUGGAACAGACUAUAGAGCGAGUGCUAAUGAAGGCCAUUACAAUAAUCGGACACACCGCCAGGCCACUCGCACUGCACGUGCUCAAUCAGUCC	99	23,23232	30,30303	29,29293	17,17172	52,52525	47,47475	0,566667	0,793103	-26,4	-26,4	0,216116	8,18	-26,6667	-0,50769
mcr-mir-99	CUGGUGGGUCUUCACCCUCCUCAUCCUCUCCGUCUACACGGCCAAGCUCGCCUCUGUGCUGACGGUGGAGGUGCAGGGCGCGAAGAUCGACUCU	94	28,7234	13,82979	34,04255	23,40426	62,76596	37,23404	1,692308	0,84375	-40,8	-40,8	0,362029	6,15	-43,4043	-0,69153
mcr-mir-9934	UUGCUUAUCAGCGAUGCAUCUGAUGGUCUUGAUAUGUCCAUUUCUAUAUCAGAUCCUUAGGCUUCGUCUGGUUAAGGGA	79	22,78481	20,25316	18,98734	37,97468	41,77215	58,22785	1,875	1,2	-24,6	-22	0,079099	4,85	-31,1392	-0,74545
mcr-mir-994	UUGUUCAGUAAUGCCAUAAUuucuaagaaagaaaaaguaaauucuUGUAGCUACAUAAUCACAGUUGCUGUUUCUUAGUUUGUUACUGGUACUGAAUAU	99	13,13131	19,19192	11,11111	31,31313	24,24242	50,50505	1,631579	1,181818	-23	-20,7	0,065496	12,27	-23,2323	-0,95833
mcr-mir-9945	cccccucccccaguugACCACCUGUCCACCUGAGCCCAUAGACAUAGAGGGUUGGACAAGGUCAGGUAGCAAUGGAGAGGAAA	83	24,09639	26,50602	18,07229	12,04819	42,16867	38,55422	0,454545	1,333333	-27,9	-21,9	0,019816	14,79	-33,6145	-0,79714

miRNA	Sequence	Tam	G	A	C	U	GC	AU	R-AU	R-GC	MFE	MFEE	Freq	Div	AMFE	MFEI
mcr-mir-9b	UUGUGUUAUGAGUUAACAUAAAGGCUGUUAUGCUGUAAGAACUGCGACUAAAGCUGAAGCAACUAUUGUUAAGUCUUAACAUAU	84	20,2381	33,33333	13,09524	33,33333	33,33333	66,66667	1	1,545455	-19,9	-17,3	0,08065	9,04	-23,6905	-0,71071

CROSSTALK OF CONSERVATION OF SEQUENCES OF miRNAs AND ENZYMATIC MACHINERY OF miRNAs PRODUCTION IN AMPULLARIIDAE

Raphael Rodrigues Porto[1*], Flávio César Thiago[1*], Carlos Bruno de Araújo[1], Tamires Caixeta Alves[1], Laurence Rodrigues do Amaral[1], Fabio Ribeiro Queiroz[2], Matheus de Souza Gomes[1**]

[1]Federal University of Uberlândia, Laboratory of Bioinformatics and Molecular Analysis, Patos de Minas, MG, Brazil
[2]Mário Penna Institute, Laboratory of Translational Research, Belo Horizonte, MG, Brazil

* These authors contributed equally to this work.
**Corresponding author
Corresponding Author: Matheus de Souza Gomes, Federal University of Uberlandia, Institute of Genetics and Biochemistry, Laboratory of Bioinformatics and Molecular Analysis, GetúlioVargas Avenue, 230, Patos de Minas, MG, Brazil. Phone: +55 34 38233714 matheusgomes@ufu.br.

ABSTRACT:

BACKGROUND: The Ampullariidae family of molluscs is an emerging model for evolutionary studies due to its high diversity, ancient history and wide geographic distribution. miRNAs are essential for the development of the organism, as they help and act in the control of gene expression. The analysis of miRNAs in molluscs, especially in the family Ampullariidae, is especially important due to the low representativeness of analyzed species and the possibility of analyzing the conservation of miRNAs among ampullariids species. **OBJECTIVE:** Identification and characterization of miRNAs (precursors and matures) and their processing pathway genes. **METHODS:** Computational prediction and characterization of miRNAs and genes involved in the miRNA pathway were performed using public database of *Lanistes nyassanus*, *Marisa cornuarietis*, *Pomacea canaliculata* and *Pomacea maculata*. The *in silico* analysis was performed using a robust algorithm to identify and characterize miRNAs and their precursors in genome of ampullariids species. To search for the putative proteins involved in the miRNA biogenesis the putative proteomes from 4 Ampullariids species and Blastp tool were used. Characterization of conserved protein domains was performed using the PFAM and CDD. Phylogenetic analyzes were performed for the ampullariids miRNA precursors and their orthologs and also for the putative ampullariids proteins involved in the miRNA pathway and their orthologs using MEGA program. **FINDINGS:** 141 pre-miRNAs and 162 mature miRNAs were identified in the genome of *L. nyassanus*, 279 pre-miRNAs and 297 mature miRNAs in the genome of *M. cornuarietis*, 269 pre-miRNAs and 296 mature miRNAs in the genome of *P. canaliculata* and 299 pre-miRNAs and 316 mature miRNAs in the genome of *P. maculata*. We identified and characterized 24 putative key proteins involved in the miRNA pathway including Argonaute, DICER, DROSHA and EXPORTIN protein families in the predicted proteome of the 4 ampullariids. The data obtained in this work will support studies of phylogeny, population divergence, speciation and patterns of diversity in the Ampullariidae Family. **MAIN CONCLUSIONS**: The searching for novel miRNAs and their processing pathway genes in 4 species of ampullariids was able to predict new structures expanding the study of miRNAs in molluscs and in Ampullariidae family, as well as open an avenue to study the roles of miRNAs in the organisms.

Keyword: miRNAs. Computational Analysis. Snails. Ampullariidae. Genome

INTRODUCTION

Molluscs of the Ampullariidae family are freshwater snails found in tropical and subtropical regions of Africa, Asia and the Americas. The animals belong to the subclass Caenogastropoda, which comprises about 50,000 species and approximately 60% of Gastropod species (Hayes et al., 2009; Strong et al., 2008). As they are a family that derived from the subclass Caenogastropoda in early evolution (Cowie, 2015) ampullariids are an excellent model to study speciation and adaptation (Hayes et al., 2009).

The scarcity of sequenced molluscs genomes was identified by the Global Invertebrate Genomics Alliance as a problem for species characterization (Voolstra et al., 2017). There are four ampullariids with sequenced genomes including the Old World (*Lanistes nyassanus*) and New World (*Pomacea canaliculata*, *Pomacea maculata* and *Marisa cornuarietis*) clades that can be the object of comparative genomic studies. The division between New and Old World lineages is consistent with the time of separation from Gondwana, around 120 million years ago (Jokat et al., 2003; Sun et al., 2019). The availability of the genome and transcriptome of the cited species makes it promising to study gene regulation, intrinsically the post-transcriptional regulation mediated by miRNAs. Almost all biological processes, including cell differentiation, tissue development and cell metabolism can be modulated by miRNAs. This regulation of gene expression is carried out through a fine control, where miRNAs and their silencing pathways carry out a specific regulation of gene expression and maintenance of genome integrity (Bartel, 2009). This may help to better understand the biology of the ampullariids studied and their adaptive properties. miRNAs have a low homoplasy, that is, their presence in two different species is more likely to be linked to a common ancestry, thus correlating the distribution of miRNAs in evolutionary relationships of the species (Kenny et al., 2015). This will allow a better understanding of the biology of the Ampullariidae family in molluscs, particularly its medical and economic importance for the humanity of ampullariids species.

P. canaliculata is involved in the transmission of the helminth *Angiostrongylus cantonensis* that causes eosinophilic meningitis in humans. Molluscs are the intermediate hosts when they are contaminated by ingestion of Larva L1. The infecting larva lodges in the Central Nervous System in humans, causing eosinophilic meningitis or ocular angiostrongyliasis in the eye ball (Luessi et al., 2009; Wang et al., 2012, 2008). Despite eosinophilic meningitis usually course in humans with low severity there may be some severe cases of the disease with severe neurological sequelae, coma and death (especially in children) (Chen et al., 2014; Lindo et al., 2002; Tsai et al., 2001). miRNAs are able to modulate the immune system of molluscs in response to stress caused by infectious processes (Picone et al., 2017).

P. canaliculata is used as a source of dietary protein in Southeast Asia. Ingestion of undercooked animals can transmit *A. cantonensis* causing eosinophilic meningitis in humans. In the Nueva Ecija region of the Philippines, the prevalence of *P. canaliculata* contaminated with nematodes was 17.75% (Cawas et al., 2020). The lack of awareness of the population is notorious, being considered a neglected disease and an important public health problem in the region (Dalton et al., 2017).

In mainland China, eosinophilic meningitis caused by *A. cantonensis* is considered an emerging infectious disease (Lv et al., 2008). Epidemiological evidence indicates that *P. canaliculata* is becoming the most prevalent intermediate host of *A. cantonensis* in this country, due to its high susceptibility to the parasite and its wide environmental tolerance (Yang et al., 2013). A major outbreak occurred in Beijing in 2006 with 160 cases of human angiostrongyliasis causing eosinophilic meningitis. The fact occurred due to the consumption of contaminated *P. canaliculata* imported from regions in southern China (Wang et al., 2008). Thus, we note the extreme importance of more epidemiological studies in the country regarding this serious public health problem. The study of the biology and adaptability of *P. canaliculata* has the same degree of importance for better management and control of eosinophilic meningitis.

P. canaliculata is described as an invasive species and was ranked among the top 100 pests worldwide. The species is resistant to elevated temperatures and drought (Matsukura et al., 2009; Yusa et al., 2006) . *P. maculata* has physiological and adaptive characteristics similar to *P. canaliculata*, both species being recognized for their rapid propagation and population increase, constituting a serious threat to the balance of an ecosystem. The economic costs of damage, control and repair can be immense (Pimentel et al., 2005).

P. canaliculata is considered an agricultural pest in many parts of Asia (Wang et al., 2020). In Indonesia, when introduced into rice plantations, it causes a 15% drop in production (Novarino, 2011). The dispersion of *P. canaliculata* in crops planted in humid regions causes serious damage in Southeast Asia (Carlsson et al., 2016) in Japan (Yusa, 1999) and also in China (Yang et al., 2013).

In 2003, China's State Department of the Environment ranked *P. canaliculata* in a list of 16 invasive pests. Since the mollusc was introduced to China around 1980, there is no accurate data on the spread of *P. canaliculata* in agriculture. Over the next twenty years, the molluscs spread widely in the country and as the snails moved into agriculture, control measures against *P. canaliculata* were implemented (Yang et al., 2013). More epidemiological studies are needed regarding the impact of *P. canaliculata* on agriculture in China. Work on the biology of the snail such as adaptability and environmental plasticity is also needed. The study of miRNAs in the species is an important step towards understanding part of the physiology of *P. canaliculata*, for possible mechanisms of population control of the species in agriculture.

The inherent skills of *P. canaliculata* and *P. maculata* referring to the invasive aspect could be confirmed by mapping characteristics by gene locus. The ability of *P. canaliculata* and *P. maculata* species to colonize and occupy new territories is attributed in part to genes that encode the G protein family (GRL101) (Sun et al., 2019), highly expressed in tentacles and cephalic palps (chemoreception in aquatic snails) (Schultz and Adema, 2017) . Still referring to invasiveness, studies have suggested that the voracious appetite of *P. canaliculata* and *P. maculata* species are attributed to the expansion of gene families related to cellulose digestion (Sun et al., 2019).

L. nyassanus and *M. cornuarietis* are snails related to freshwater (Strong et al., 2008) and have divergences regarding their adaptability. While *M. cornuarietis* is better able to resist factors such as low temperature and hypoxia (Matsukura et al., 2016; Mu et al., 2018) *L. nyassanus* has a low adaptability and is endemic to Lake Nyasa, or Malawi, geographically located between Malawi, Tanzania and Mozambique (Cowie, 2015; Dohrn, 1865; Van Bocxlaer, 2017).

Since miRNA-mediated post-transcriptional silencing performs several regulatory aspects in animals, it is necessary to understand the processing mechanisms of the miRNA pathway and their respective genes. The identification of major miRNA biogenesis factors including, AGO2, DGCR8, DICER, DROSHA, RAN and XPO5 was elucidated based on homologous sequence search in several molluscs (Huang et al., 2021) and in *Biomphalaria Glabrata* by researchers from our group (Queiroz et al., 2017).

Sun et al., published in 2019 the sequencing of the total genome of four species of Ampullariidae, *L. nyassanus*, *P. canaliculata*, *P. maculata* and *M. cornuarietis*. From then on, it was putative to carry out the mapping of characteristics by gene locus. Given the relevant regulatory aspect of non-protein coding RNAs in gene expression, specifically miRNAs, it is necessary to study mature and precursor miRNAs, as well as the genes involved in the miRNA processing pathway. In this work, mature and precursor miRNAs and the genes involved in miRNA pathway were identified and characterized using the genome of *L. nyassanus, P. canaliculata*, *P. maculata* and *M. cornuarietis*.

MATERIALS AND METHODS

PREDICTION AND CHARACTERIZATION OF MATURE AND PRECURSOR MIRNAS

The genomes of *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* were retrieved from the NCBI database (https://www.ncbi.nlm.nih.gov/genome). A robust algorithm was used to predict miRNAs, precursor and mature forms. The sequences were processed for identification and characterization of predicted mature miRNAs and their precursors, following the methodology established by Gomes *et al.* (2011).

Genome sequences with potential tendency to formation of hairpin structures or similarity to precursor miRNAs were obtained using the Einverted program (EMBOSS tool) and the BLASTn program (NCBI), for identification of homologous miRNAs from miRBase (http: //www.mirbase.org/). Then, the sequences were submitted through a series of filters, selecting, according to the desired parameters, those that corresponded to putative-putative precursors of miRNAs. These filters were based on conserved characteristics of precursor miRNAs and unwanted sequences were discarded. The filters used were the Minimum Free Energy (MFE) (Gruber et al., 2008; Hofacker, 2009), GC content (Zhou et al., 2009), homology with mature miRNAs already identified. Finally, sequences with high similarity to genes encoding proteins, repetitive elements and non-coding RNAs, except miRNAs, were discarded.

The putative precursors of miRNAs were compared to their orthologs at various levels. The sequences of pre-miRNAs and their respective miRNAs were submitted to multiple alignment, using the tools ClustalX 2.1(Larkin et al., 2007) and RNAalifold (Bernhart et al., 2008). Alignment patterns for ClustalX 2.1 were based on adjusted parameters (gap opening: 22.50; gap extension: 0.83). Secondary structures were obtained using the RNAfold platform (Gruber et al., 2008; Hofacker, 2009). The phylogenetic analysis of the putative pre-miRNAs of *L. nyassanus, M. cornuarietis, P. canaliculata* and *P. maculata* was carried out using MEGA program version X (Tamura et al., 2007) and the Neighbor-joining method applying the Kimura two-parameters model ("Kimura-twoparameters"), to stimulate the divergence between the sequences (N Saitou and Nei, 1987). Consensus trees were obtained using a bootstrap of 5000 replicates.

PREDICTION AND CHARACTERIZATION OF PROTEINS INVOLVED IN MIRNAS BIOGENESIS

In silico identification and characterization of putative miRNA pathway proteins were performed using the amino acid sequences of the proteins from the model organisms *Biomphalaria glabrata, Drosophila melanogaster* and *C. elegans* and the Blastp tool on the ampubase website (https://www.comp.hkbu.edu.hk/~db/AmpuBase/index.php#&panel1-2). Using PFAM (31.0) (Mistry et al., 2021) and conserved Domains CDD (Marchler-Bauer et al., 2017, 2015, 2011; Marchler-Bauer and Bryant, 2004; Shennan Lu et al., 2020) the putative domain architectures of the ampullariids proteins were established. Analysis of the active sites were used for the proteins Argonaut, Dicer and Drosha using Clustal X 2.1 and Weblogo.

Phylogenetic analysis was performed using the MEGA version X program (Kumar et al., 2018), after alignment in default parameters, using the Neighbor-Joining method (Naruya Saitou and Nei, 1987) and the JTT model. The statistical reliability of each branch in the generated tree was evaluated using a 2000-replica bootstrap.

RESULTS

IDENTIFICATION AND CHARACTERIZATION OF PUTATIVE PROTEINS INVOLVED IN MIRNA PATHWAY IN AMPULLARIIDS SPECIES

The predicted proteome of the species *L. nyassanus*. *M. cornuarietis*, *P. canaliculata* and *P. maculata* were retrieved from the NCBI database (National Center for Biotechnology Information - http://.ncbi.nlm.nih.gov/) to identify and characterize the putative proteins responsible for the biogenesis of the miRNAs. The identification was based on conservation, using as parameters protein length, conserved domains, active sites conservation and phylogeny analysis. Lny23421, Lny25187,Lny28936, Lny28171, Lny18581, Lny14710, Lny12572, Lny27692, Lny22624, Lny12572, Lny29643, Lny27624, Lny9931, Mco26370, Mco27042, Mco25093, Mco22837, Mco24030, Mco81614, Mco51286, Mco13761, Mco21592, Mco12258, Pca61914, Pca59652, Pca69814, Pca67531, Pca67887,Pca62316, Pca65193, Pca60969, Pca65193, Pca65324, Pca59979, Pca69254, Pma35144, Pma60501, Pma63715, Pma65850, Pma51393, Pma59467, Pma63331, Pma32975, Pma62419, Pma51302 and Pma61707 putative proteins involved in miRNA pathway were identified in predicted proteome of *L. nyassanus*, *M. cornuarietis*, *P. canaliculate* and *P. maculate*, respectively [Supplementary data I – (Supplementary Tables 1,2,3 and 4)]. The key proteins of the miRNA pathway were selected, Argonaute, DICER, DROSHA and Exportin, and thus used for further analysis.

Ten putative Argonaute proteins were identified in the predicted proteome of the ampullariids species, being 3 sequences for *L. nyassanus* (Lny23421_c0_g1, Lny25187_c0_g1 and Lny28936_c7_g7), 3 sequences for *M.* cornuarietis (Mco25093_c0_g2, Mco26370_c0_g1, Mco27042_c1_g1), 2 sequences for *P. canaliculata* (Pca69814_c1_g2, Pca61914_c0_g1) and 2 sequences for *P. maculata* (Pma63715_c0_g1_, Pma60501_c2_g16). The sequences Lny23421_c0_g1, Mco26370_c0_g, Pca69814_c1_g2 and Pma63715_c0_g1 exhibited six conserved domains, while the protein sequences Lny25187_c0_g1, Lny28936_c7_g7, Mco25093_c0_g2, Mco27042_c1_g1, Pca61914_c0_g1 e Pma60501_c2_g16 displayed only the PAZ and PIWI domains (Figure 1).

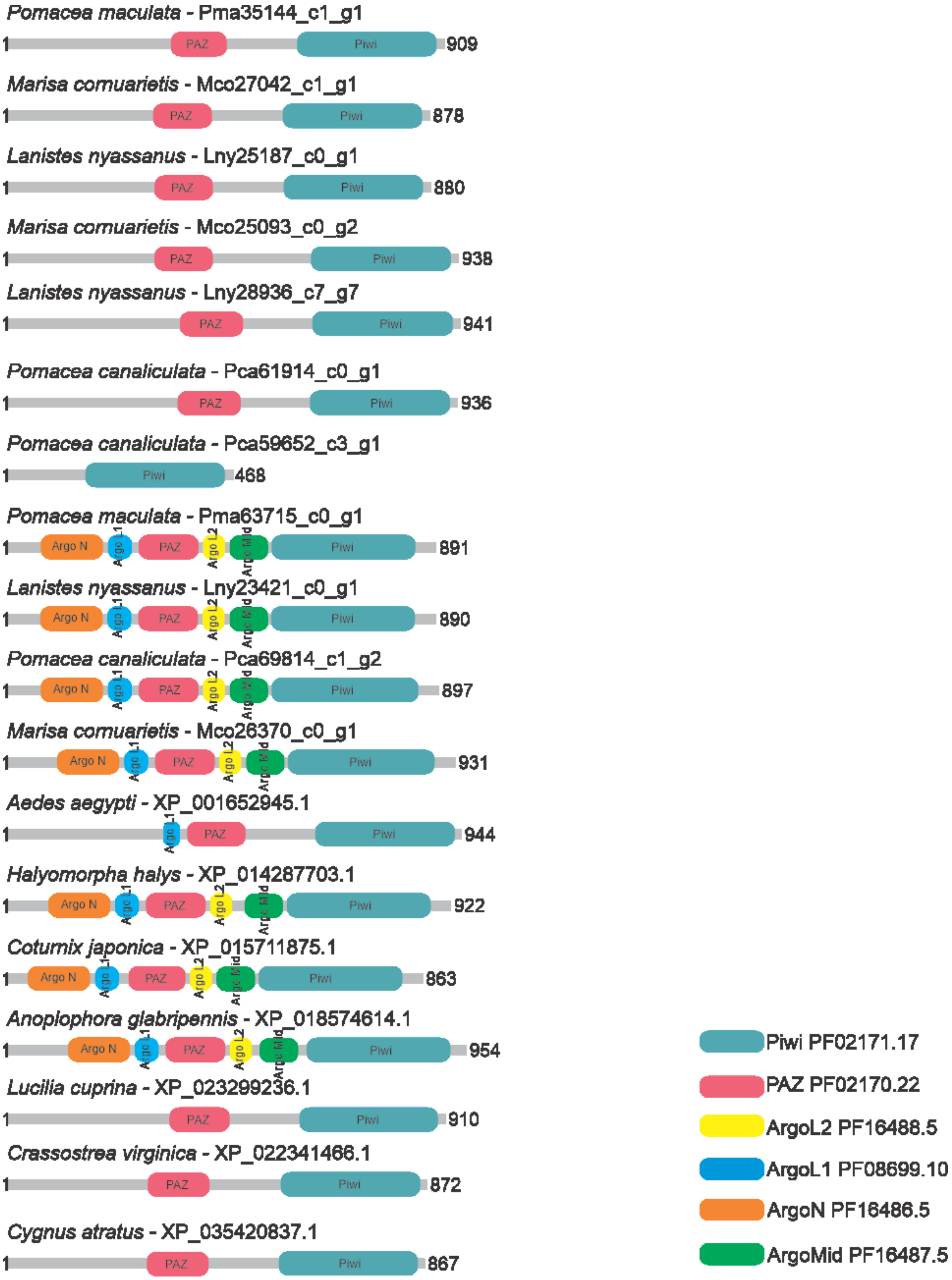


Figure 1: Argonaute's Conserved Domains, *L. nyassanus. M. cornuarietis, P. canaliculata, P. maculata* and orthologs.

The PIWI domain of these proteins presented a catalytic triad formed by DDH (aspartic acid, aspartic acid and histidine). The global alignment of the PIWI domains of the ampullariids

Argonaute proteins and their orthologs showed a conservation of amino acid sequences, being accentuated in the surroundings of the catalytic sites (Figure 2).

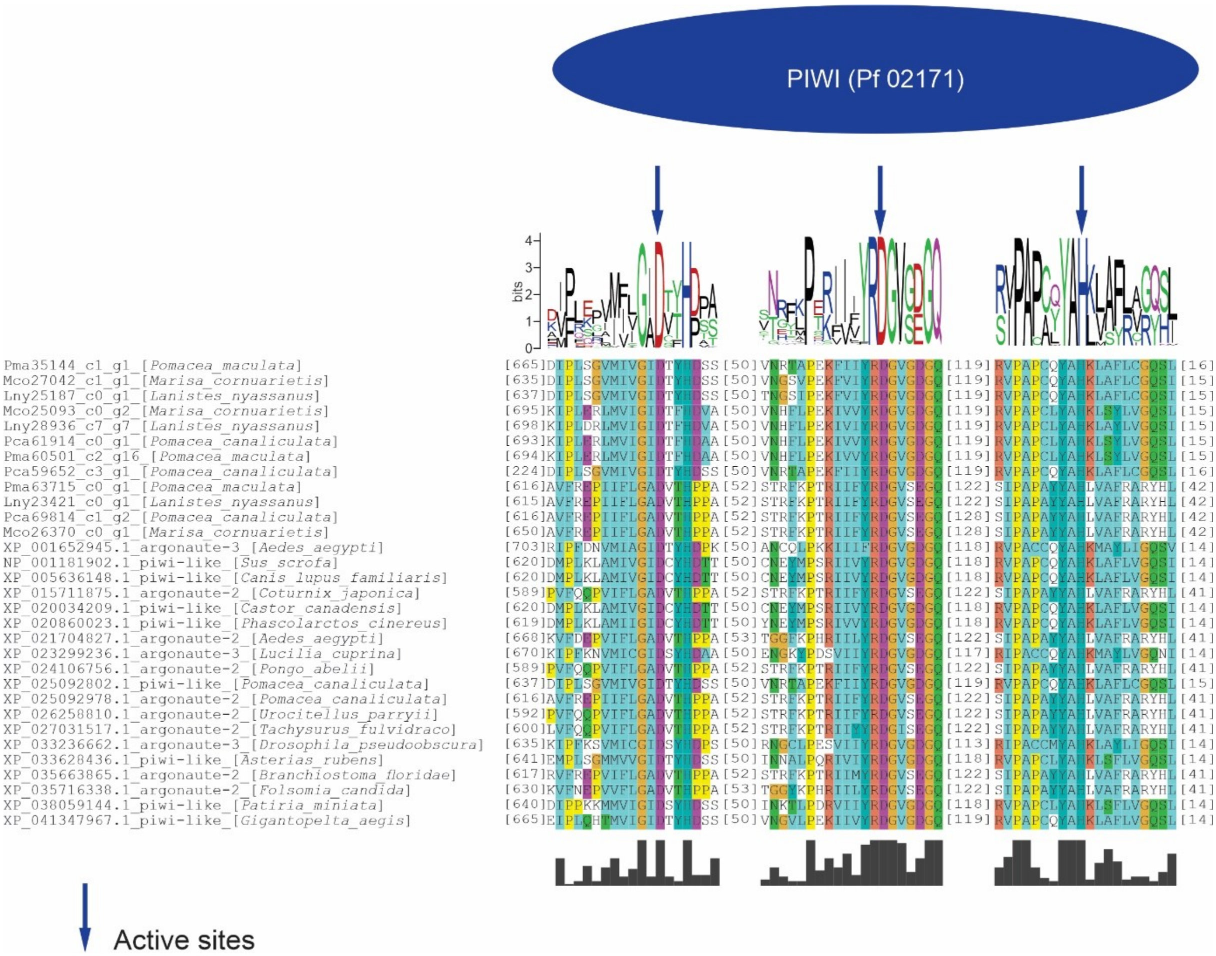


Figure 2: Global alignment analysis of the PIWI domain of Argonaute proteins de *L. nyassanus, M. cornuarietis, P. canaliculata* and *P. maculata*

The two subfamilies, AGO and PIWI compose the AGO protein family. The predicted sequences of *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* were used in the phylogenetic tree and their orthologs, in order to emphasize the conservation of these putative proteins identified in the Ampullariids species and wide distribution among deuterostomes and protostomes species. The distribution of Argonaute and PIWI proteins corroborated the distribution of species in the tree of life. As expected, the ampullariids species grouped together with the phylum Molluscs. The evolutionary proximity of species ampullariids*, L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* is represented in the tree (Figure 3).

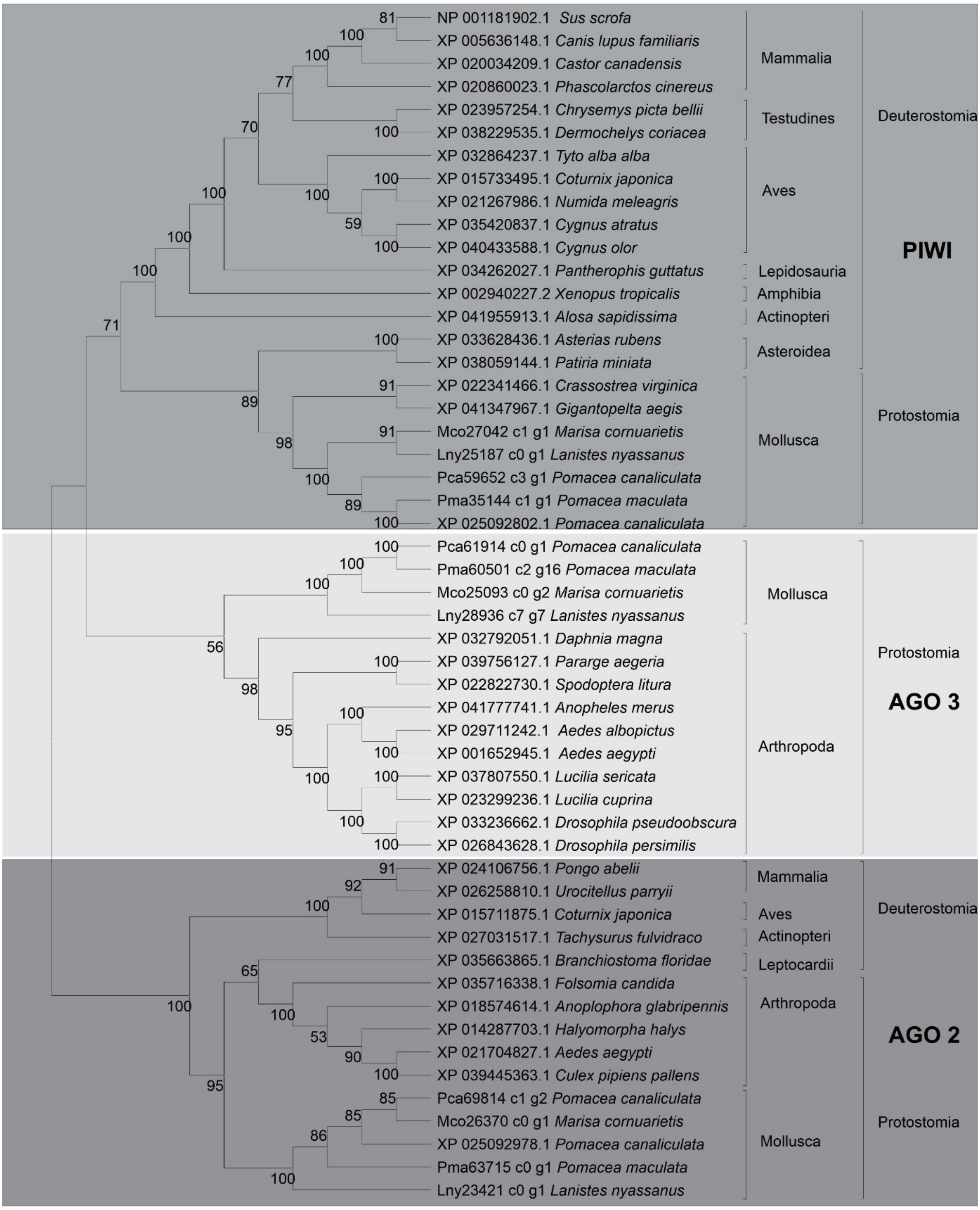


Figure 3: Phylogenetic analysis of AGO proteins, *L. nyassanus, M. cornuarietis, P. canaliculata* e *P. maculata* and their orthologs.

Five putative Drosha and two putative Dicer proteins were identified and characterized in the ampullariids species. For Drosha, 1 sequence for *L. nyassanus* (Lny18581_c0_g2), 1 sequence for *M. cornuarietis* (Mco22837_c2_g1), 1 sequence for *P. canaliculata* (Pca67887_c3_g1) and 2 sequences for *P. maculata* (Pma51393_c0-g1 and Pma65850_c2g4) were identified. The amino acid sequences of Pca67887_c3_g1 and Mco22837_c2_g1 had three conserved domains, Lny18581_c0_g2 and Pma65850_c2_g4 had two conserved domains, while the protein sequence Pma51393_c0_g1 had only one conserved domain. For Dicer 1 amino acid sequence were found for *P. canaliculata* (Pca67531_c1_g2), showing 4 conserved domains and for *L. nyassanus* (Lny28171_c0_g1) showing only 3 conserved domains (Figure 4 and Figure 5).

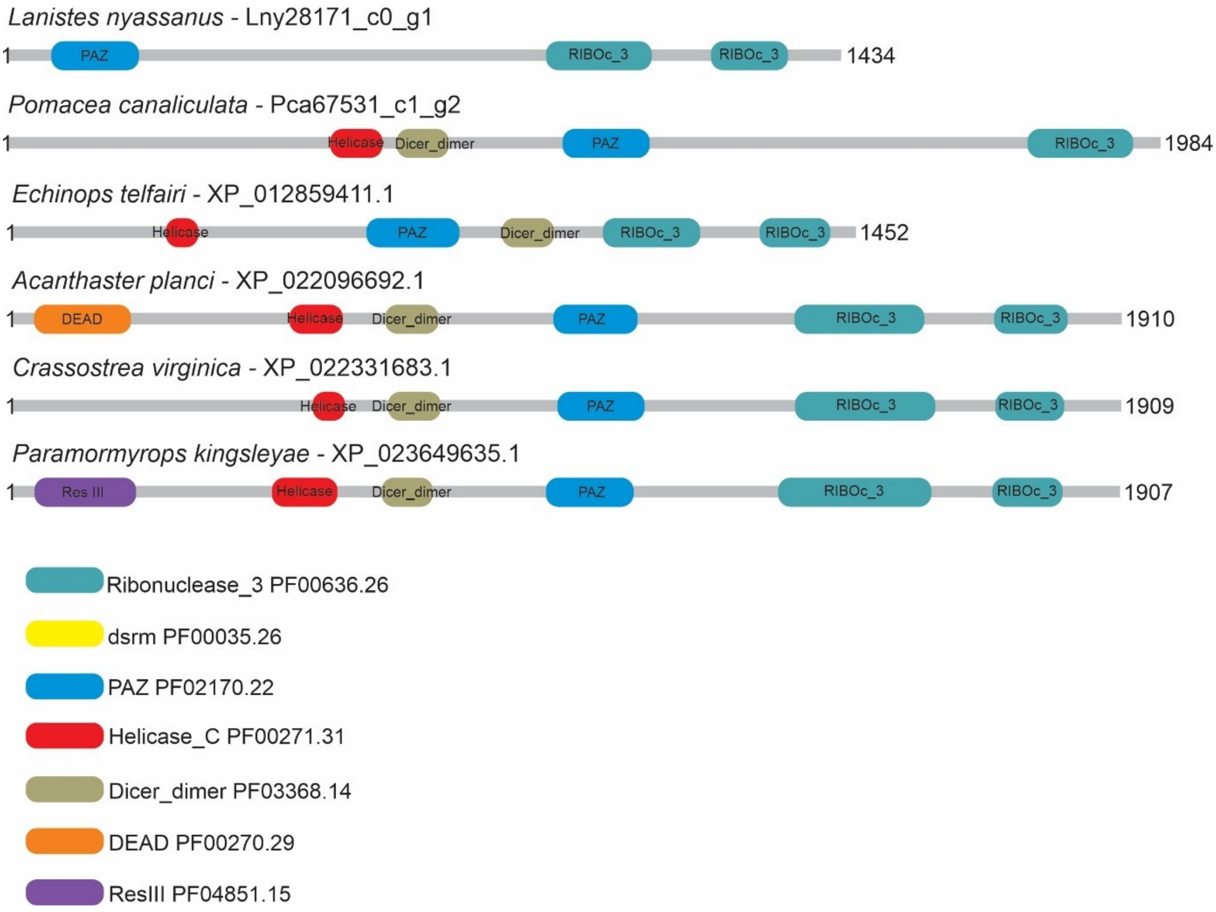


Figure 4: Analysis of conserved domains Dicer for *L. nyassanus, M. cornuarietis, P.* canaliculata, *P. maculata* and their orthologs.

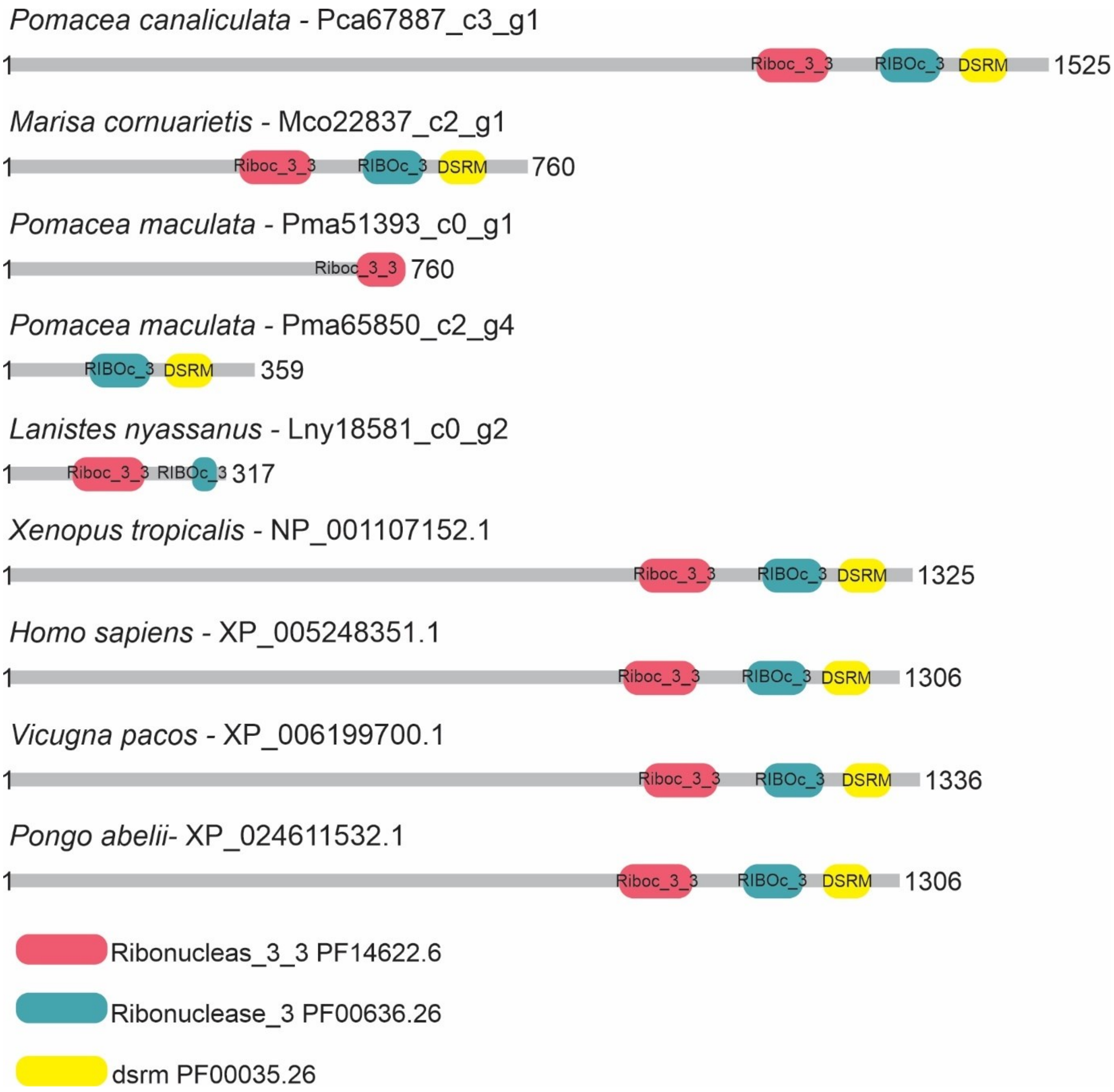


Figure 5: Analysis of conserved domains Drosha for *L. nyassanus*, *M. cornuarietis*, *P. canaliculata*, *P. maculata* and their orthologs.

In the analysis of the Drosha/Dicer proteins, only one conserved domain of Ribonuclease III was identified in the ampullariids studied. The Riboc I domains presented the catalytic amino acids in the conserved site regions (EDDE): glutamic acid (E), aspartate (D), aspartate (D) and glutamic acid (E). This was verified in the sequences Drosha, Lny18581_c0_g2, Mco22837_c2_g1, Pca67887_c3_g1 and Dicer, Lny28171_c0_g1. Note the conservation of amino acids in the active site itself and in the surroundings of the region (Figure 6).

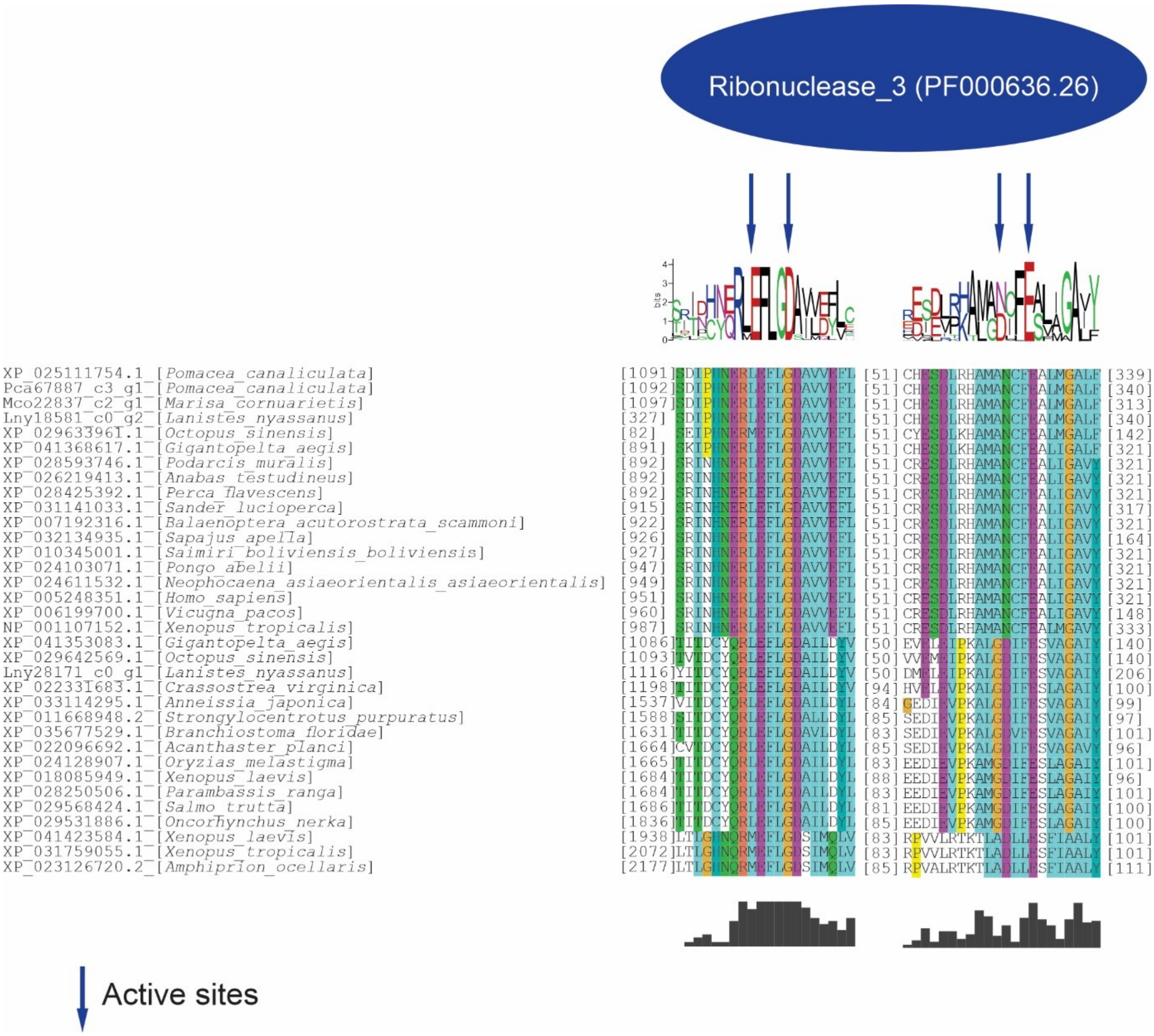


Figure 6: Analysis of the conserved domains of Ribonuclease III (Riboc) of the Drosha and Dicer proteins from ampullariids species.

Phylogenetic analysis of the predicted proteins DROSHA and DICER showed the evolutionary relationship with their orthologs. Proteins from *L. nyassanus*, *M. cornuarietis*, *P. canaliculata*, *P. maculata* grouped in the Molluscs clade, revealing close similarity among the ampullariids studied. The disposition of the orthologs of the putative DICER and DROSHA in the clades in the tree corroborated with the tree of life, with a visible distinction between Deuterostomes and Protostomes for the two classes of RNase (Figure 7).

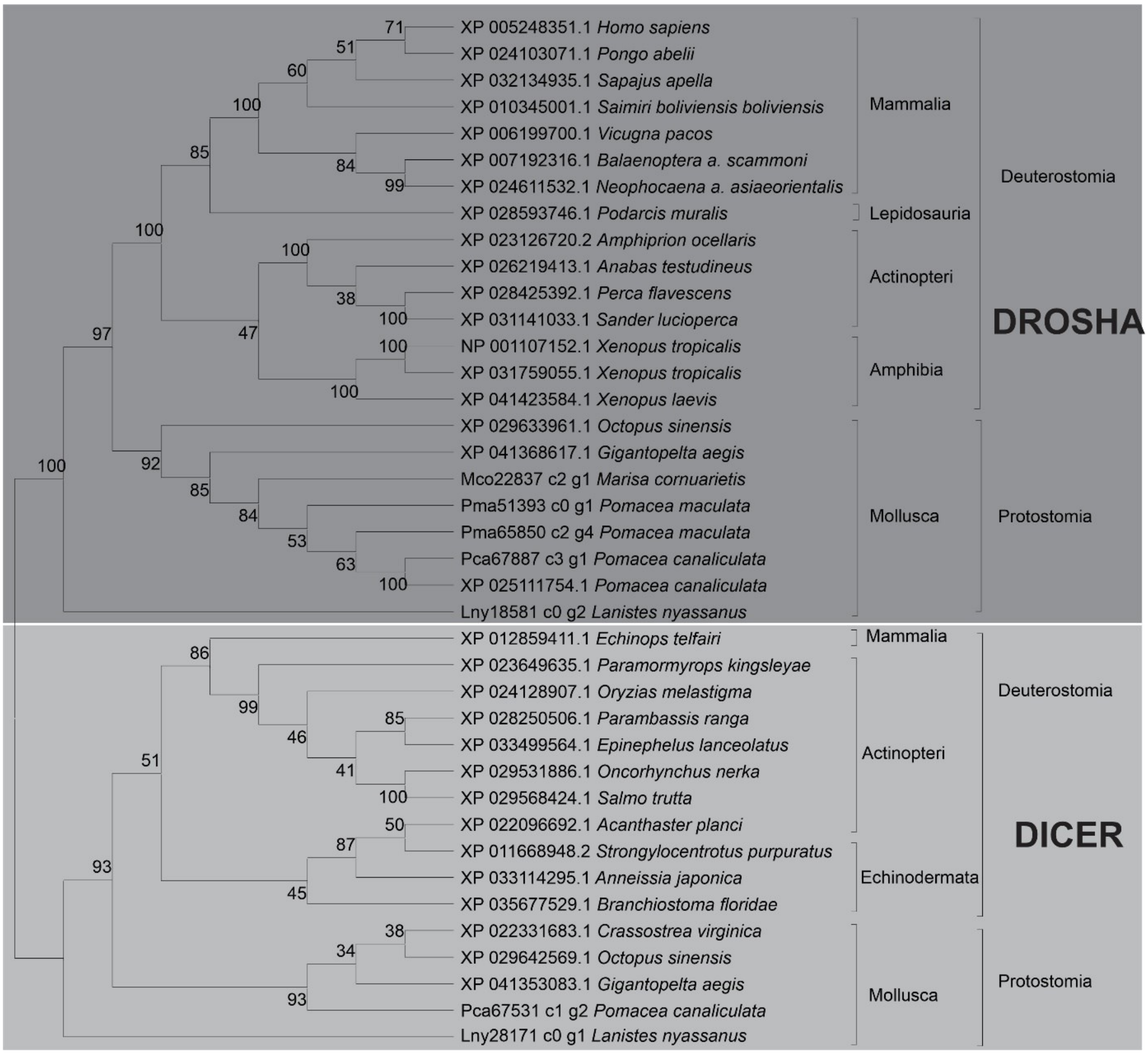


Figure 7: Phylogenetic analysis of DICER and DROSHA proteins from ampullariids and their orthologs.

Similarity of the predicted protein Drosha from *L. nyassanus*, *M. cornuarietis* and *P. canaliculata* with model organism *D. melanogaster* and evolutionarily close organisms. The percent identity, query coverage, length of the predicted protein Drosha from *P. canaliculata* are similar among closely related organisms (Table 1).

Code	**Query coverage**	**E Value**	**Identity %**	**Length of string**
NP_477436.1 Drosha [*D. melanogaster*]	100%	0.0	100,00	1327
XP_013069067.1 (*B. glabrata*)	73%	0.0	54,91	1469
XP_005107264.1 (*Aplysia californica*)	72%	0.0	54,81	1528
XP_041368618.1 (*G. aegis*)	72%	0,0	59,09	1412
Pca67887_c3_g1 (*P.canaliculata)*	66%	0.0	57,75	1525
Mco22837_c2_g1 (*M. cornuarietis*)	56%	0.0	60,96	760

Lny18581_c0_g2 (*L. yassanus*)	27%	$7e^{-150}$	69,57	317

Table 1: Putative DROSHA of *L. nyassanus*, *M. cornuarietis* and *P. canaliculata* cover against NP_477436.1 DROSHA [D. melanogaster], E-Value, % of String Identity and Length.

Comparison of the Dicer protein from the model organism *D. melanogaster* with the putative Dicer protein in *L. nyassanus* and *P. canaliculata* and evolutionarily close organisms. Once again, the predicted protein Dicer of *P. canaliculata* showed greater similarity with its orthologs when compared to the other Ampullariidae (Table 2).

Código	**Cobertura da *query***	**E Value**	**Identidade %**	**Comprimento da sequência**
NP_524453.1 Dicer-1 [*D. melanogaster*]	100%	0.0	100%	2249
XP_012942349.1 (*A. californica*)	77%	$2e^{-141}$	50%	2503
XP_013067888.1 *(B. glabrata*)	74%	$2e^{-148}$	51,90%	2332
XP_021347347.1 (*M. yessoensis*)	72%	$7e^{-152}$	52,87%	2284
XP_041353083.1 *(G. aegis*)	70%	$2e^{-150}$	50,26%	2063
Pca67531_c1_g2 (*P. canaliculata*)	71%	$7e^{-140}$	45.10%	1985
Lny28171_c0_g1 (*L. nyassanus*)	38%	$2e^{-162}$	53,32%	1434

Table 2: Putative Dicer *L. nyassanus* e *P. canaliculata*, coverage against NP_524453.1 Dicer-1 [D. melanogaster], E-Value, % identity and string length

Nine putative protein sequences belonging to the Exportin protein family (XPO-5, XPO-1, XPO-T) were identified and characterized in the predicted proteome of ampullariid species; XPO-5: *L. nyassanus* (Lny14170_c0_g1), *P. canaliculata* (Pca62316_c0_g2); XPO-1: *L. nyassanus* (Lny12572_c0_g1), *M. cornuarietis* (Mco24030_c0_g2), *P. canaliculata* (Pca65193_c2_g1) and *P. maculata* (Pma59467_c0_g1), XPO-T: *L. nyassanus* (Lny27692_c0_g2), *M. cornuarietis* (Mco81614_c0_g2) *P. maculata* (Pma63331_c0_g1). The sequences of XPO-5, Lny14170_c0_g1 and Pca62316_c0_g2, exhibited 2 domains. For the XPO-1 protein sequences, the putative proteins Lny12572_c0_g1, Mco24030_c0_g2 and Pma59467_c0_g1 displayed six conserved domains, except for the Pca65193_c2_g1, which exhibited only five conserved domains. Likewise, XPO-T putative proteins Lny27692_c0_g2, Mco81614_c0_g2 and Pma63331_c0_g1 showed one conserved domain (Figure 8).

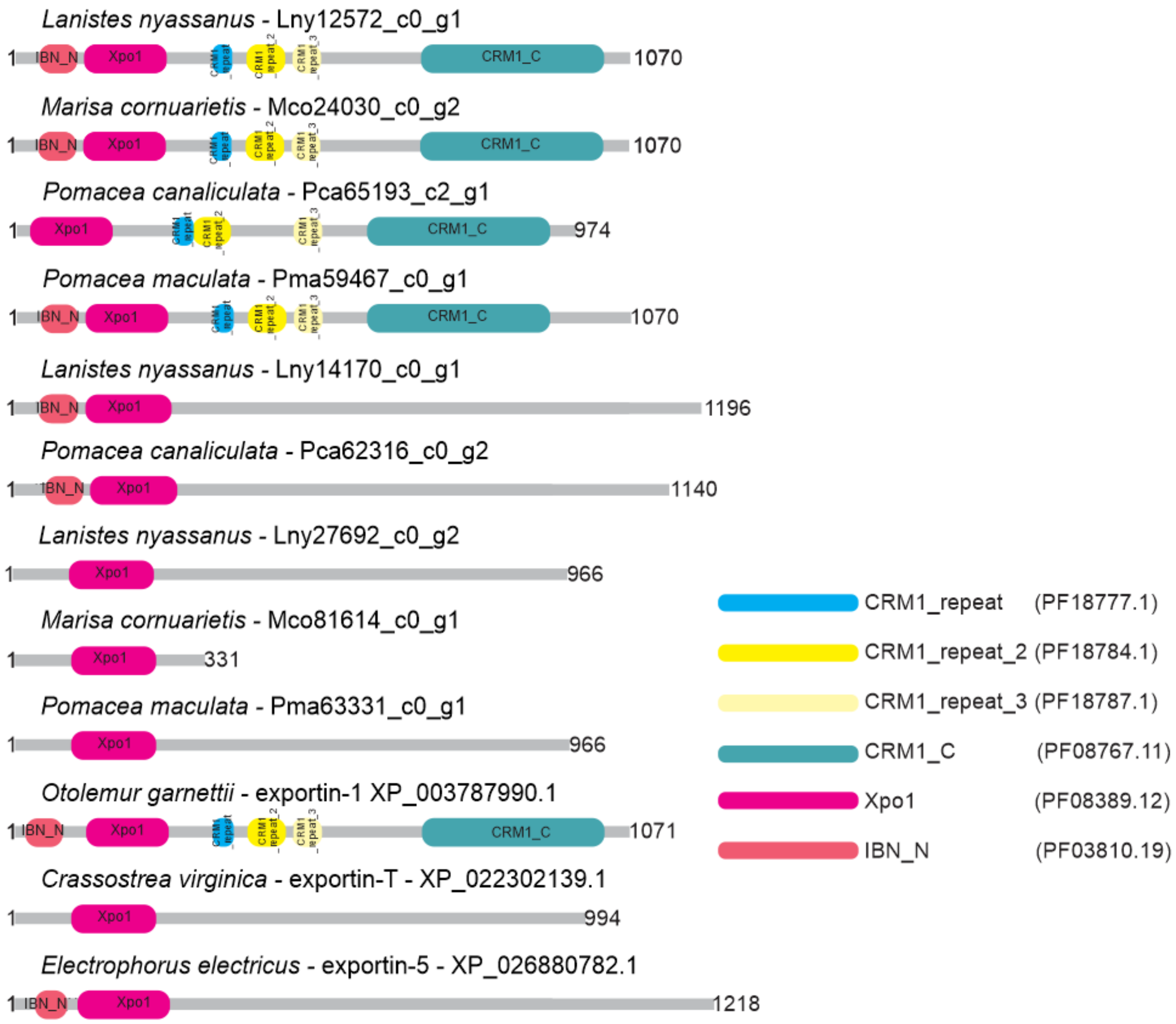


Figure 8: Distribution of conserved domains in putative proteins of the Exportin family in ampullariids species and orthologs.

In the phylogenetic analysis of putative proteins of the Exportin family (XPO-5, XPO-1 and XPO-T) the evolutionary relationship with their orthologs was verified. Protein sequences from *L. nyassanus*. *M. cornuarietis*, *P. canaliculata* and *P. maculata* were grouped in the phylum Molluscs, confirming once again a close proximity between the ampullariids species, as expected by the degree of relatedness of the species. The phylogenetic tree presented three distinct clades (XPO-5, XPO-1 and XPO-T clades), as well as species belonging to the Protostome and Deuterostome groups, corroborating with the literature (Figure 9).

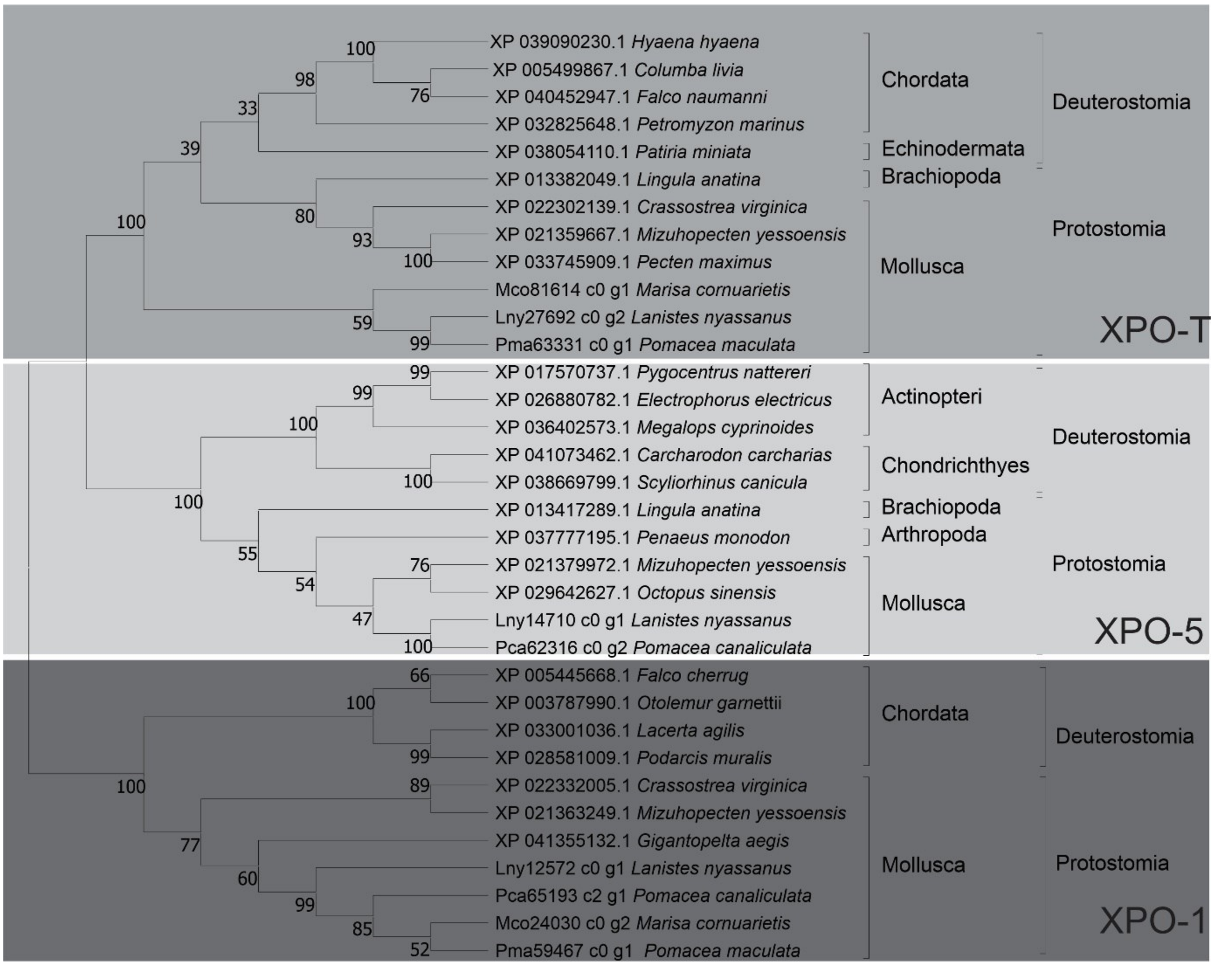


Figure 9: Phylogenetic distribution of putative proteins, XPO-5 XPO-1 and XPO-T identified in *L. nyassanus*. *M. cornuarietis, P. canaliculata* e *P. maculata* and their orthologs.

PREDICTION AND CHARACTERIZATION OF PERCURSOR AND MATURE MIRNAS.

A robust algorithm was applied to the genome sequences of the four ampullariids species to identify mature miRNAs and their precursors. 141 pre-miRNAs and 162 miRNAs of *L. nyassanus*, 279 pre-miRNAs and 297 miRNAs of *M. cornuarietis*, 269 pre-miRNAs and 296 miRNAs of *P. canaliculata*; 299 pre-miRNAs and 316 miRNAs of *P. maculata* were predicted [Supplementary data II – (Supplementary Tables 5,6,7,8 and 9)].

An accurate and stringent structural and thermodynamic analysis were used to identify and characterize conserved miRNAs(Y. Q. Zhang et al., 2009). All pre-miRNAs identified were analyzed for these particular characteristics [Supplementary data II - (Supplementary Tables 5,6,7 and 8)].The pre-miRNAs for *L. nyassanus* exhibited MFE (minimum free energy) with a mean of -30.30 kcal/mol, with values between -18.50 and -50.90 kcal/mol; for *M. cornuarietis* the mean MFE of -28.05 kcal/mol, with values between -18.50 and -67.10 kcal/mol; for *P. canaliculata* the mean of MFE -28.70 kcal/mol, with values between -18.70 and -48.4 kcal/mol; for *P. maculata* the mean of -27.55 kcal/mol, with values between -18.50 and -52.7 kcal/mol (Table 3).

Species	**Average size of precursors (nucleotides)**	**Precursor size variation (nucleotides)**	**Mean value MFE - Kcal/mol**	**Variation MFE - Kcal/mol**
L. nyassanus	87.04	66 to 100	-30,3	(-50.90 to -18.50)
M. cornuarietis	88.16	65 to 100	-28,05	(-67.10 to -18.50)
P. canaliculata	89,55	63 to 144	-28,7	(-48.40 to -18.70)
P. maculata	89.27	65 to 100	-27,55	(-52.70 to 18.50)

Table 3: Average size and size variation of precursors, average minimum free energy (MFE) and MFE variation of precursors in 4 species Ampullariidae

The precursors showed mean values for the guanine-cytosine (GC) content for *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata*; 41.26%, 41.64%, 41.70%, 40.74%, respectively. The maximum and minimum values were respectively 69.05 and 20.25% for *L. nyassanus*, 67.03% and 20.20% for *M. cornuarietis*, 68.29% and 20.83% for *P. canaliculata*, 68, 75% and 20.40% for *P. maculata*. In this study, the average size of miRNA precursors for *L. nyassanus*, *M. cornuarietis*, *P. canaliculata*, *P. maculata* were respectively; 87.04 nucleotides, 88.16 nucleotides, 89.55 nucleotides and 89.27 nucleotides. Size range of pre-miRNAs for *L. nyassanus* (66 to 100 nucleotides), *M. cornuarietis* (65 to 100 nucleotides), *P. canaliculata* (63 to 144 nucleotides), *P. maculata* (65 to 100 nucleotides).

The sequences of miRNAs have been shown to be evolutionarily conserved (De Wit et al., 2009). This conservation is accentuated in the seed region of the mature miRNAs, being considered important for recognition of their mRNA targets (Lewis et al., 2005). All mature miRNAs identified in this work showed 100% identity in the seed regions (position 2 to 8 nucleotides) with the structure of their respective ortholog deposited in miRBase, on which the homology comparison was based.

The mature miRNAs identified in this work had an average of 22.22 nucleotides in *L. nyassanus*, 21.92 nucleotides in *M. cornuarietis*, *21.86 nucleotides* in *P. canaliculata* and 21.77 nucleotides for *P. maculata*, ranging in size from 17 to 25 nucleotides for all species analyzed.

The Argonaute protein has a preference for the uracil nucleotide in the first position of the miRNA sequence at the 5' end to be loaded, to be inserted into the RISC complex (Seitz et al., 2011). In this work mature miRNAs from L. nyassanus, M. cornuarietis. P. canaliculata and

P. maculata respectively presented uracil as the main nucleotides in the first position; 41.97%, 44.44%, 41.2% and 42.40% (uracil), 17.28%, 17.84%, 20.9% and 17.8% (cytosine), 26.54%, 22.56%, 20.4% and 24.5% (adenine) and 14.19%, 15.15%, 17.5% and 15.3% (guanine) [Supplementary data II - (Supplementary table 9)].

The presence of miRNAs in two different species is more likely to be linked to a common ancestry, thus correlating the distribution of miRNAs in evolutionary relationships of species (Kenny et al., 2015). In order to emphasize the conservation of these putative miRNAs identified in the ampullariid species, phylogenetic trees were constructed. The global alignment and secondary structure characterization of the precursors of miRNAs was performed, to show the similarity of the sequences with their orthologs already identified. The taxa that were used as a parameter for the selection of specific are Bilateria, Protostomes, Lophotrocozoa and Molluscs. The selection of pre-miRNAs based on these taxons was performed having as parameter the miRNAs prevalent simultaneously in the 4 ampullariids species (Table 4). The characterization of miRNAs by taxons was shown in figures 1 to 11 and Supplementary data III - supplementary figures 1 to 34

Tax	Species	Pre-miRNAs
Bilateria	*L. nyassanus*	lny-mir-33, lny-mir-190, lny-mir-252a, lny-mir-281, lny-mir-981
	M. cornuarietis	mcr-mir-33, mcr-mir-190, mcr-mir-252a, mcr-mir-281, mcr-mir-981
	P. canaliculata	pcn-mir-33, pcn-mir-190, pcn -mir-252a, pcn-mir-281, pcn-mir-981
	P. maculata	pmc -mir-33, pmc-mir-190, pmc-mir-252a, pmc-mir-281, pmc-mir-981
Protostomies	*L. nyassanus*	lny-bantam, lny-mir-2a, lny-mir-67, lny-mir-750
	M. cornuarietis	mcr-bantam, mcr-mir-2a, mcr-mir-67, mcr-mir-750
	P. canaliculata	pcn-bantam, pcn-mir-750
	P. maculata	pcr-bantam, pcr-mir-2a, pcr-mir-67, pcr-mir-750
Lophotrocozoa	*L. nyassanus*	lny-mir-1990, lny-mir-745a, lny-mir-96b, lny-mir-1994
	M. cornuarietis	mcr-mir-1990, mcr-mir-96b, mcr-mir-1994
	P. canaliculata	pcn-mir-1990, pcn-mir-745a, pcn-mir-1992, pcn-mir-96b, pcn-mir-1994
	P. maculata	pmc-mir-1990, pmc-mir-745a, pmc-mir-1992, pmc-mir-96b, pmc-mir-1994
Molluscs	*L. nyassanus*	lny-mir-1985, lny-mir-12096b
	M. cornuarietis	mcr-mir-1985, mcr-mir-12096b
	P. canaliculata	pcn-mir-1985, pcn-mir-12096b

	P. maculata	Pmc-mir-1985, Pmc-mir-12096b

Table 4: miRNAs selected by taxon

The precursors of miR-33, Bilateria-specific-miRNA, were found in this study: lny-miR-33, mcr-miR-33, pcn-miR-33, pmc-miR-33. All precursors found the 4 species showed two mature miRNAs, 3p and 5p. The sequences of the precursors showed high conservation in the primary and secondary structures. The similarity of the ampullariids miRNA structures were found to be highly conserved each other (Figure 10 and 11).

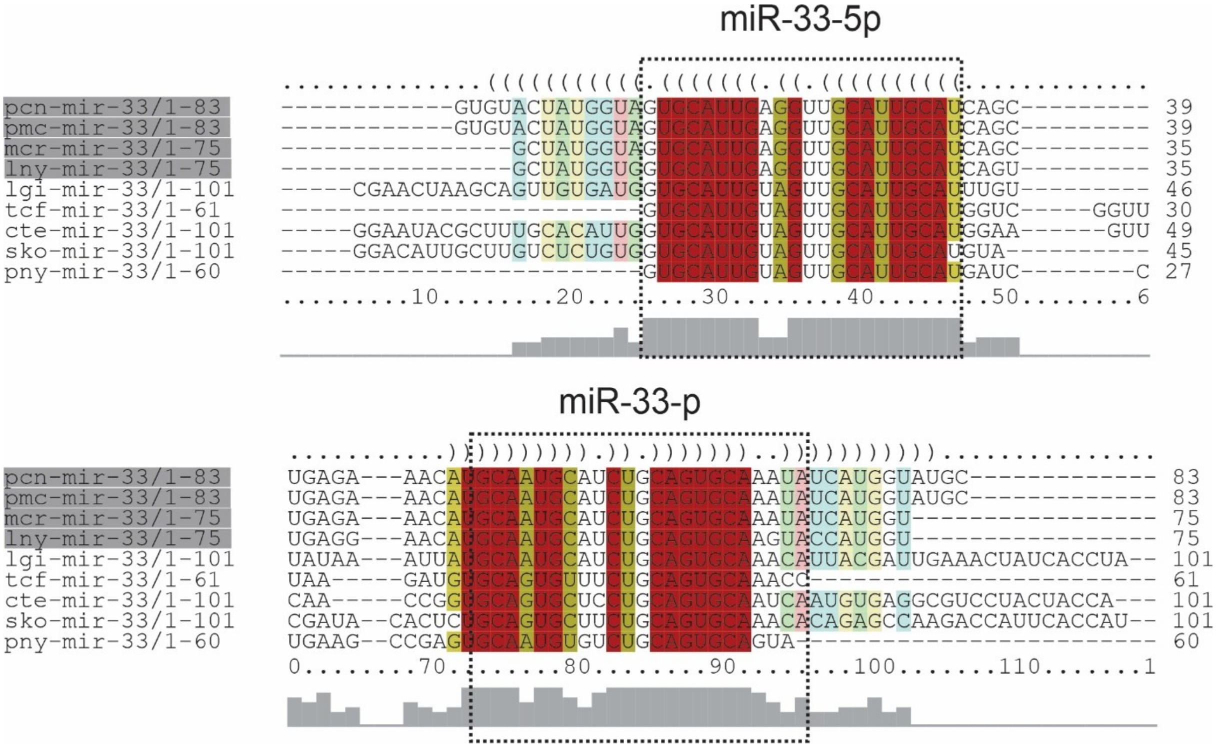


Figure 10: Alignment of mir-33 in *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* and their orthologs; pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny- *L. nyassanus*, lgi - *L. gigantea*, tcf - *Triops cancriformis*, cte - *Capitella teleta*, sko - *Saccoglossus kowalevskii*, pny - *Pundamilia nyererei*.

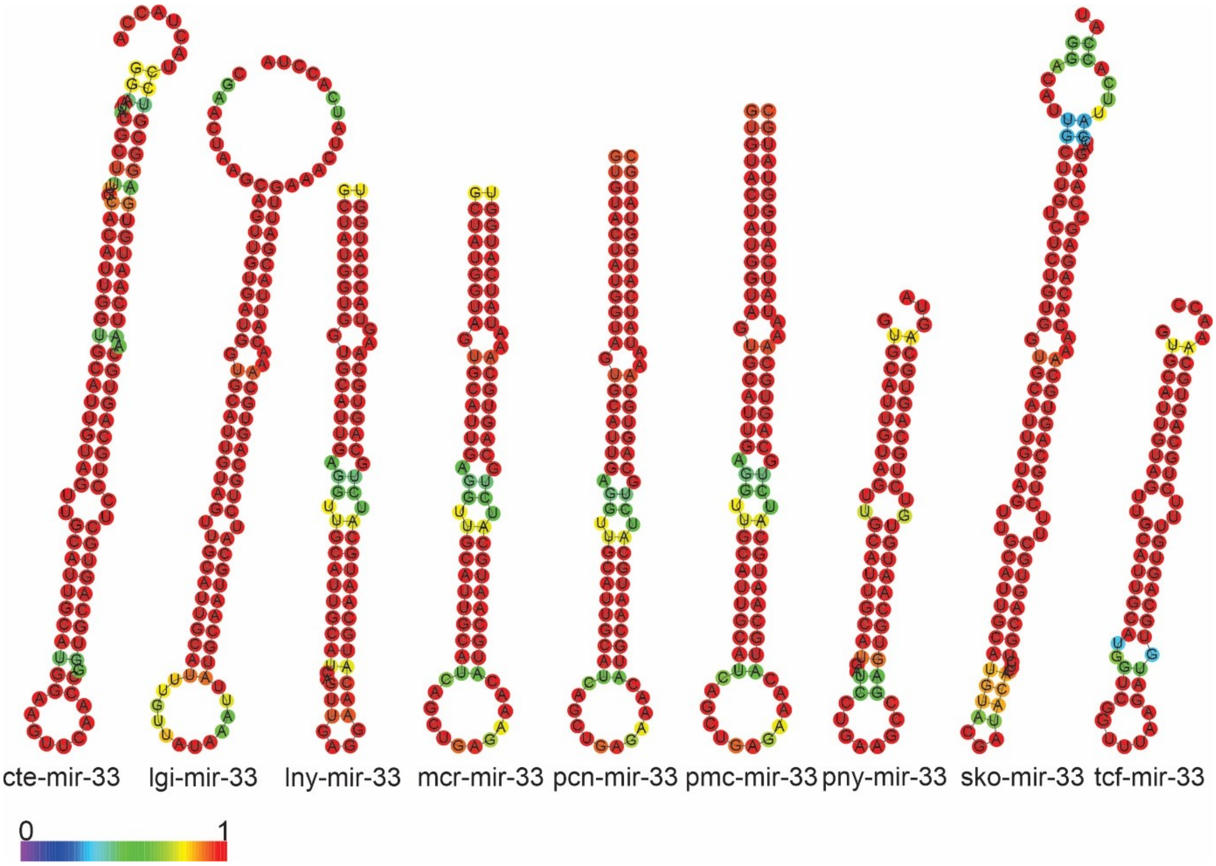


Figure 11: Secondary structure of mir-33 in *L. Nyassanus, M. cornuarietis*, *P. canaliculata*, *P. maculata* and their orthologs; pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, lgi - *L. gigantea*, tcf - *Triops cancriformis*, cte - *C. teleta*, sko - *Saccoglossus kowalevskii*, pny - *Pundamilia nyererei.*

The Protostome and Deuterostome clades were observed in the phylogenetic. The first clade was subdivided into Lophotrochozoa and Ecdysozoa, being represented respectively by molluscs and arthropods. In the phylum Molluscs, the presence of gastropods was observed, where the ampullariids species were grouped. Deuterostome organisms were represented by clades; mammals, birds and amphibians, verifying wide distribution in phylogenetic clades. This distribution corroborated with the tree of life (Figure 12).

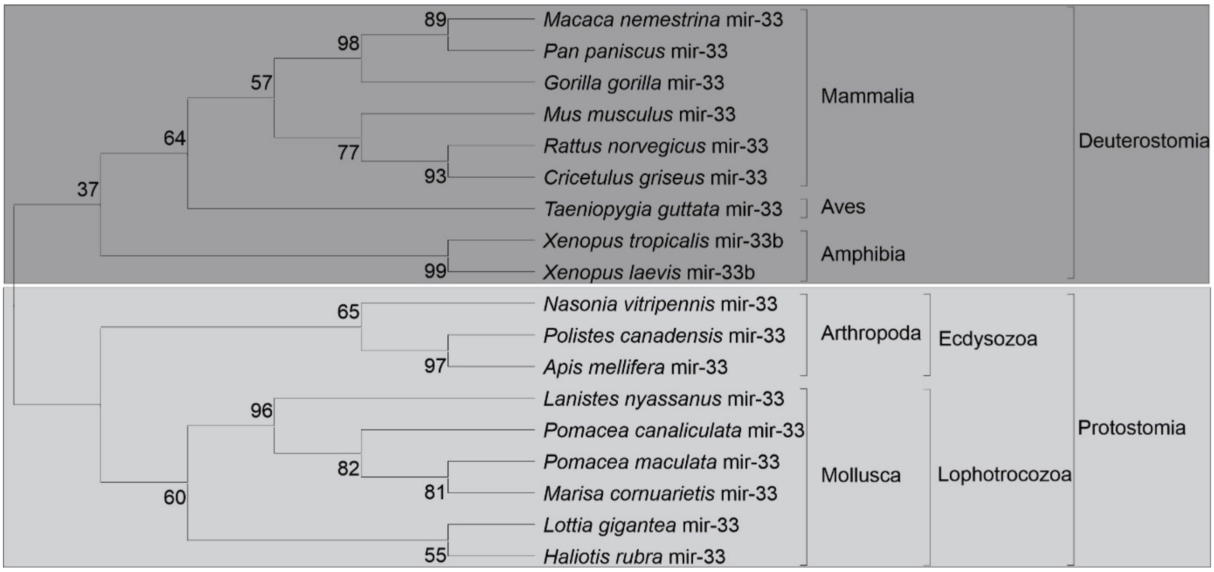


Figure 12: mir-33 phylogenetic distribution for *L. Nyassanus, M. cornuarietis P. canaliculata*, *P. maculata* and their orthologs.

The precursors of miRNAs (protostomes specific) lny-miR-67, mcr-miR-67, pcn-miR-67, pmc-miR-67 and a mature miRNA were identified for each Ampullariidae species analyzed. The primary structures of the mi-67 family in *L. nyassanus*, *M. cornuarietis*. *P. canaliculata* and *P. maculata* were highly conserved between themselves and their orthologs, especially in the region of mature miRNAs. Note the extreme similarity in the secondary structures of the precursors in *M. cornuarietis* and *P. maculata* (Figure 13 andFigure 14).

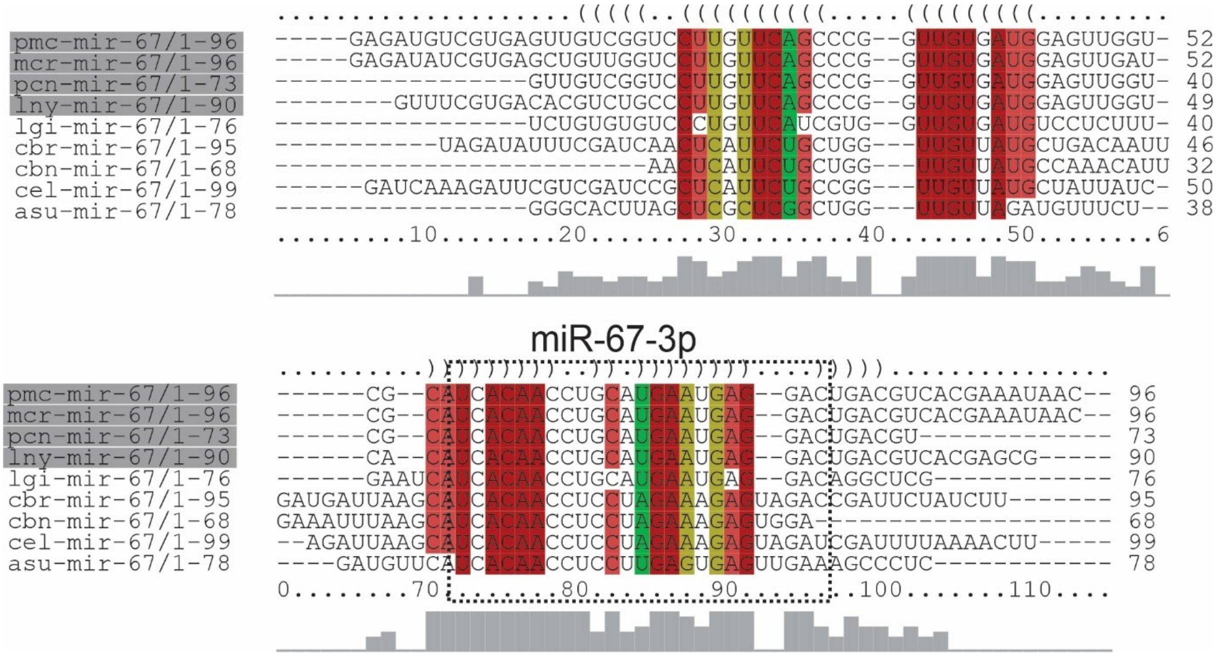


Figure 13: mir-67 alignment to *L. nyassanus*, *M. cornuarietis*. *P. canaliculata* e *P. maculata* and their orthologs; asu - *Ascaris suum*, cbn - *Caenorhabditis brenneri*, cbr - *Caenorhabditis briggsae*, cel - *C. elegans*, lny - *L. nyassanus*, lgi - *L. gigantea*, mcr - *M. cornuarietis*, pcn - *P. canaliculata*, pmc - *P. maculata*.

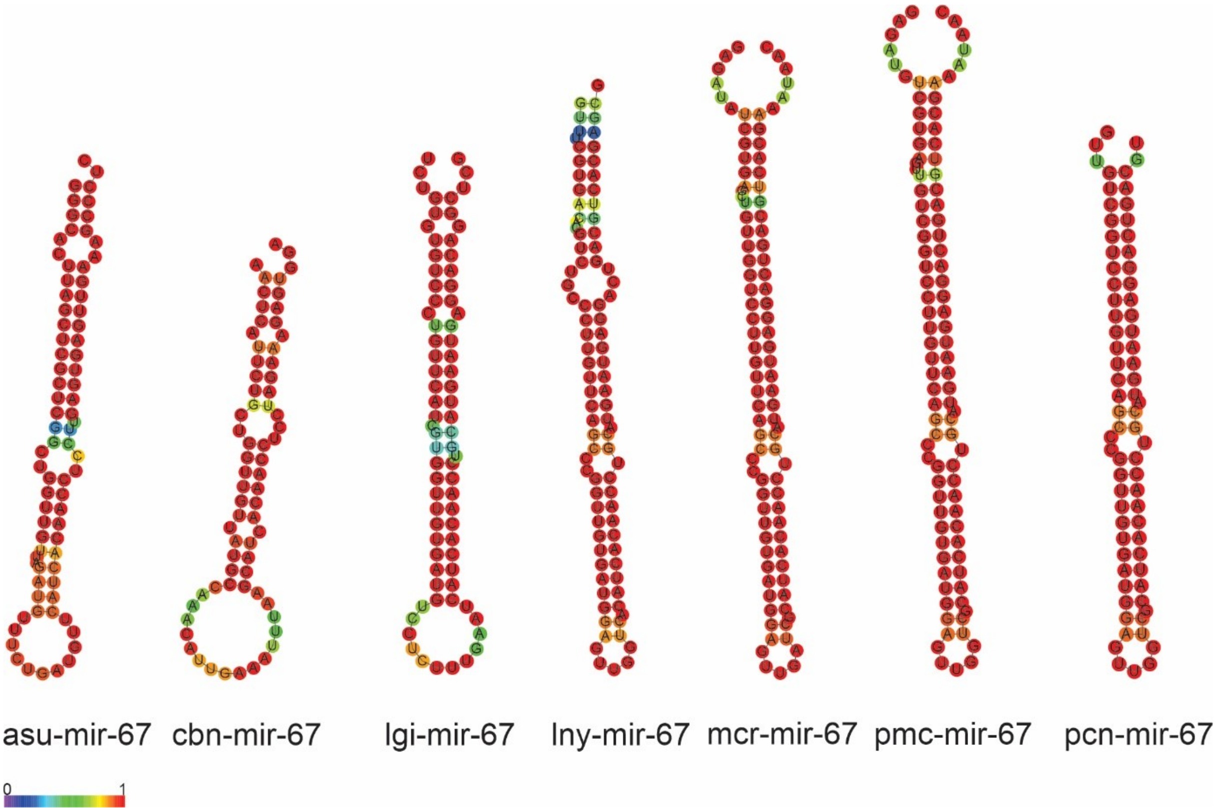


Figure 14: Secondary structure of mir-67 in *L. nyassanus, M. cornuarietis, P. maculata and their orthologs*; asu - *Ascaris suum*, cbn - *Caenorhabditis brenneri*, lny – *L. nyassanus*, lgi - *L. gigantea*, mcr-*M. cornuarietis*, pmc - *P. maculata*.

The Lophotrochozoa clade was subdivided into molluscs, annelids and flatworms. In the phylum Molluscs the presence of bivalves and gastropods was observed. For the first class of molluscs it was represented by the species: *Crassostrea virginica*, *Crassostrea hongkongensis*, *Pinctada martensii*, *Pinctada Fucata*, *Patinopecten yessoensis* and *Argopecten purpuratus*. The gastropod animals were represented exclusively by the analyzed Ampullariidae species: *L. nyassanus*, *M. cornuarietis*. *P. canaliculata* and *P. maculata*. This distribution is consistent with the tree of life, where a wide distribution was found in the phylogenetic clades (Figure 15).

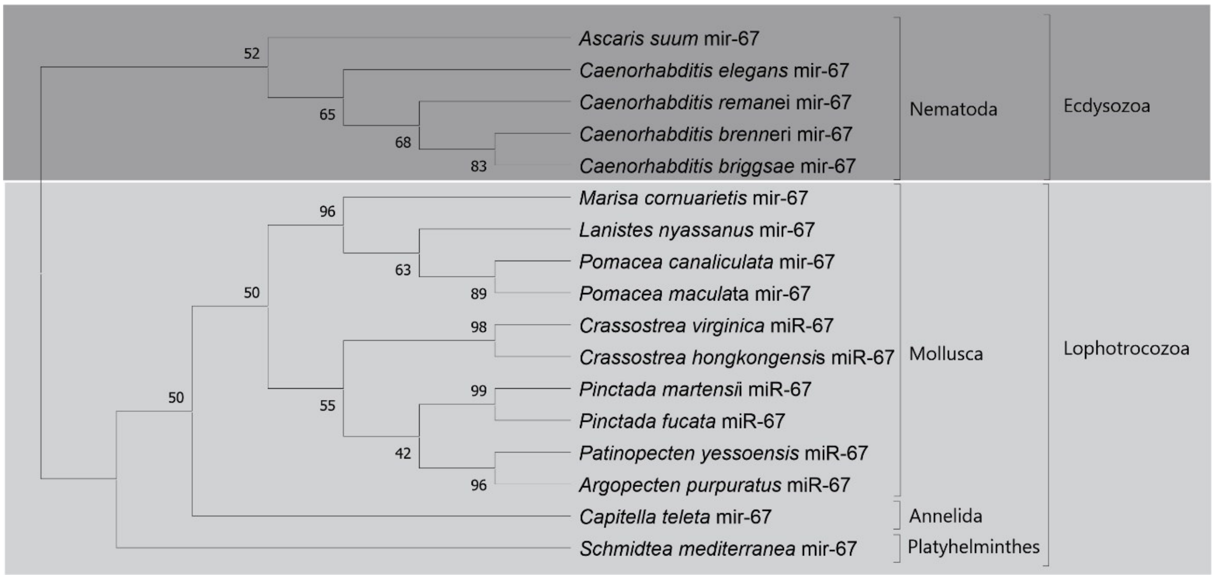


Figure 15: Phylogenetic distribution of mir-67 in *L. nyassanus, M. cornuarietis. P. canaliculata* e *P. maculata* and their orthologs.

Alignment of mir-96b precursors from Ampullariidae species and their orthologs demonstrated the presence of two mature miRNAs (5p and 3p strands) in *L. nyassanus*, *M. cornuarietis*. *P. canaliculata* and *P. maculata*. The 3p strand of mature miRNAs from the analyzed Ampullariidae species showed 100% identity to each other and high similarity with orthologs. The sequence of the precursors of miR-96b, specific Lophochotrozoa, demonstrated high similarity in secondary structure in the gastropod organisms *L.nyassanus*, *M. cornuarietis* and *B.glabrata* (Figure 16 and Figure 17).

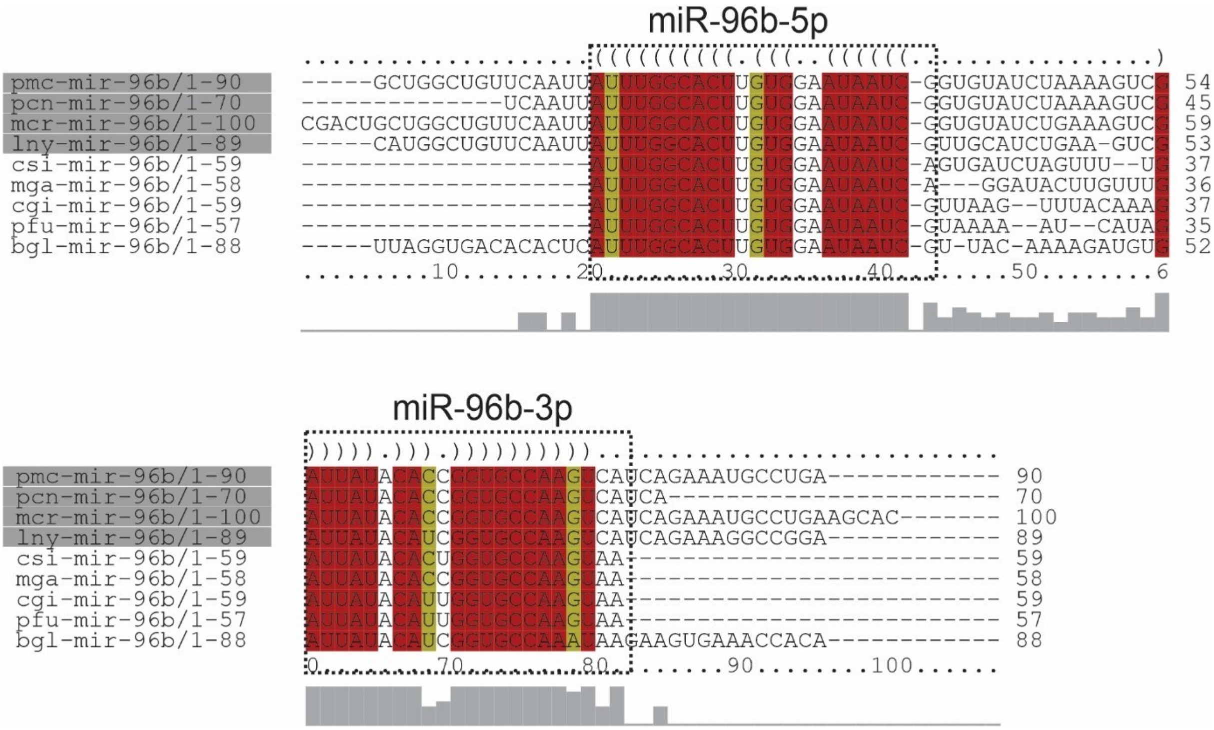


Figure 16: Alignment of miRNA-96b precursors of *L. nyassanus*. *M. cornuarietis, P. canaliculata* e *P. maculata* and their orthologs. bgl: *B. glabrata*, csi: *Cyclina sinensis*, lny*: Lanistes nyassanus,* mcr: *Marisa cornuarietis,* pfu: *Pinctada fucata*

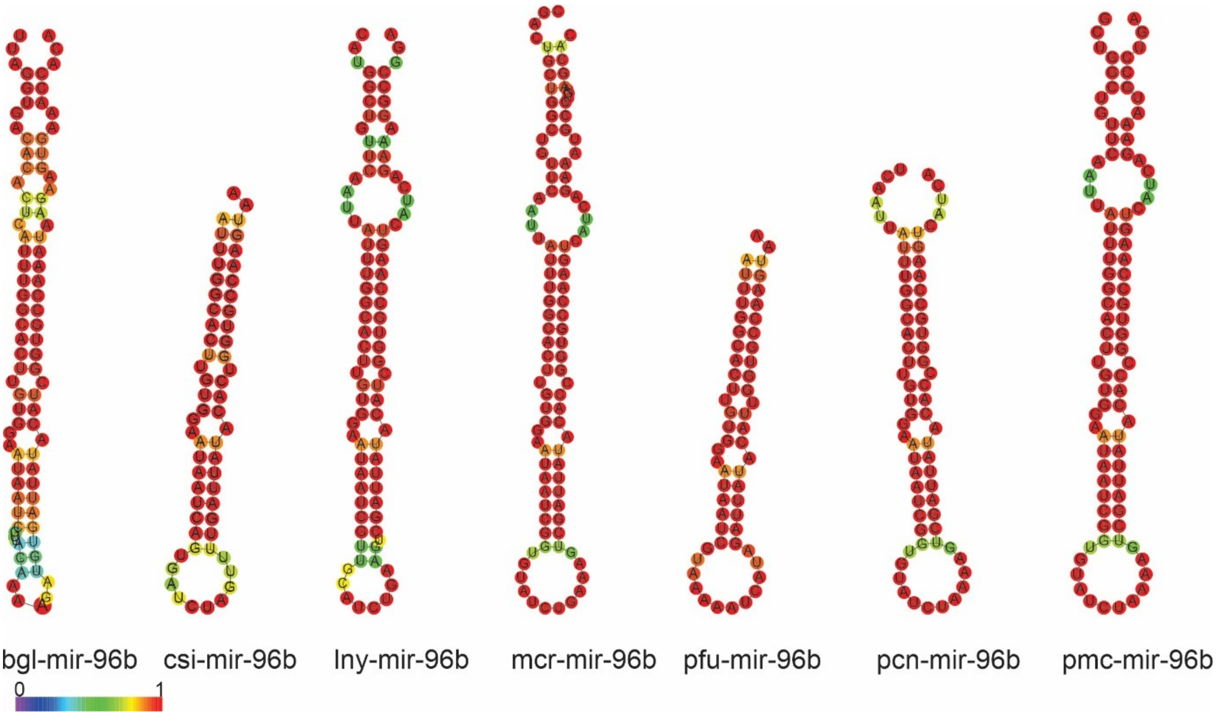


Figure 17: Secondary structure of ampullariids miRNA-96b precursors studied with their orthologs; bgl: *B. glabrata*, csi: *Cyclina sinensis*, lny*: Lanistes nyassanus,* mcr: *Marisa cornuarietis,* pfu: *Pinctada fucata*

The phylogenetic analysis of the precursors of mir-96b (Lophotrochozoa- specific) was verified the distribution among the species in three phyla (Molluscs, Anelideos and

Platelmiltos). A wide distribution was observed in the phylum Molluscs, where the presence of cephalopods, bivalves and gastropods was verified. The first class of molluscs was represented by *Architeuthis dux*. The bivalve class was represented by *Crassostrea gigas*, *C. virginica*, *C. hongkongensis*, *P. Fucata* and *P. martensii*. The presence of snails of the Ampullariidae family analyzed once again appeared grouped together, as expected. In addition, ampullariids appear segregated in the gastropod class with molluscs of the genus *Haliotis* and *Radix auricularia* species. A wide distribution was observed in the Lophotrochozoa clade, being constructed a phylogenetic tree consistent with the tree of life. (Figure 18).

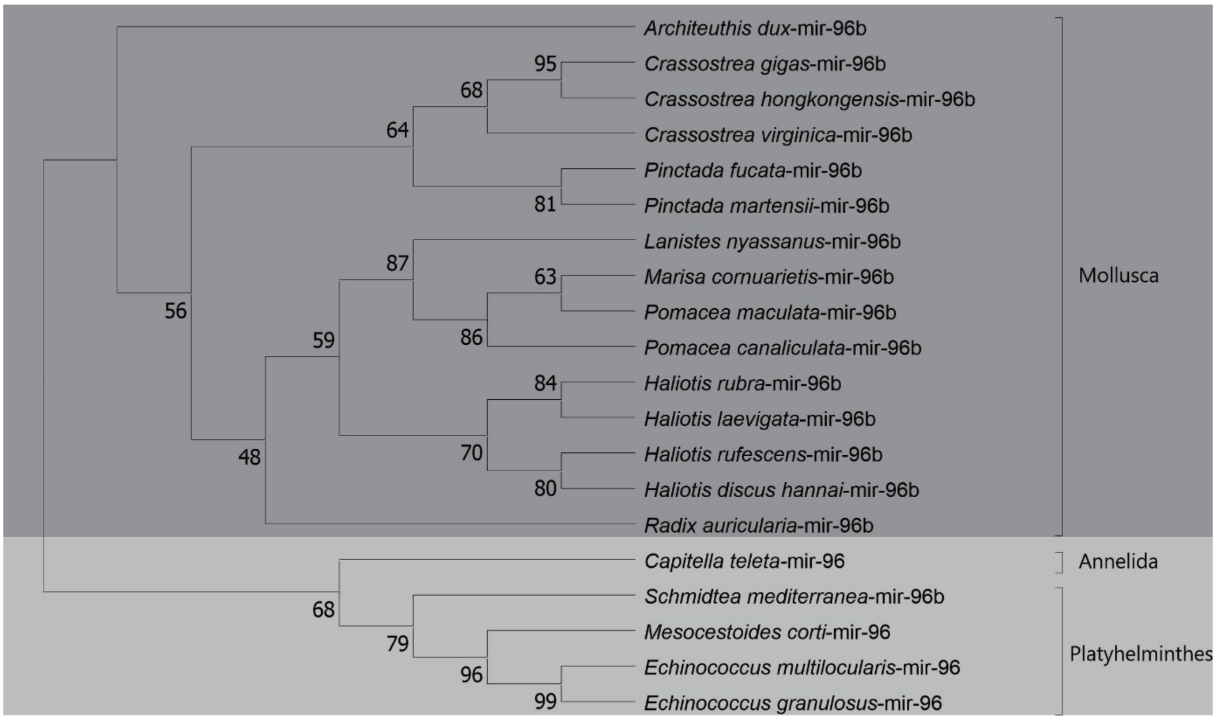
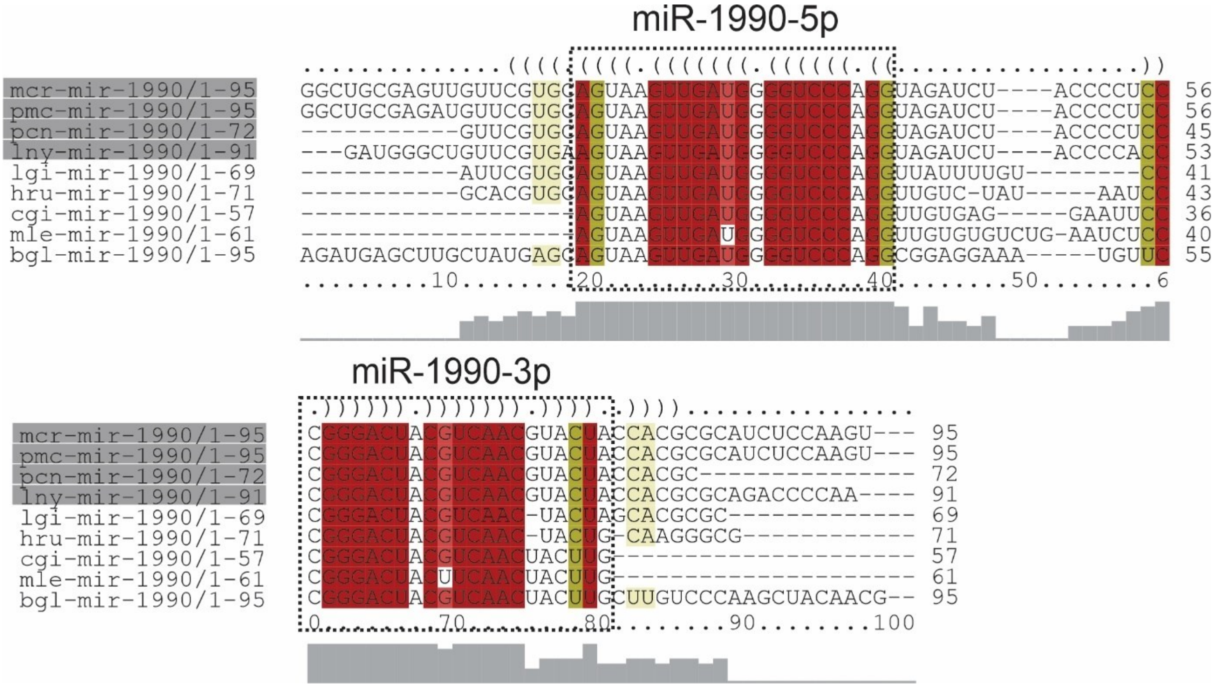


Figure 18: Phylogenetic analysis of miR-96b (Lophotrochozoa-specific) for *L. nyassanus. M. cornuarietis, P. canaliculata* e *P. maculata* and their orthologs.

The mir-1990 family predicted for species *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* is composed of the precursors lny-mir-1990, mcr-mir-1990, pcn-mir-1990 pcm-mir-1990 and the mature miRNAs, 3p and 5p, in each species ampullariids. For this family, the conservation and great similarity of the primary structure was observed, as well as secondary structures demonstrate conservation among orthologs (Figure 19 and Figure 20).



```
                   ...............((((((((.(((((((.((((((.((.................))
mcr-mir-1990/1-95  GGCUGCGAGUUGUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCU----ACCCCUCC 56
pmc-mir-1990/1-95  GGCUGCGAGAUGUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCU----ACCCCUCC 56
pcn-mir-1990/1-72  -----------GUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCU----ACCCCUCC 45
lny-mir-1990/1-91  ---GAUGGGCUGUUCGUGAAGUAAGUUGAUGGGGUCCCAGGUAGAUCU----ACCCCACC 53
lgi-mir-1990/1-69  -----------AUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUUAUUUUGU--------CC 41
hru-mir-1990/1-71  -----------GCACGUGCAGUAAGUUGAUGGGGUCCCAGGUUGUC-UAU-----AAUCC 43
cgi-mir-1990/1-57  -------------------AGUAAGUUGAUGGGGUCCCAGGUUGUGAG-----GAAUUCC 36
mle-mir-1990/1-61  -------------------AGUAAGUUGAUUGGGUCCCAGGUUGUGUGUCUG-AAUCUCC 40
bgl-mir-1990/1-95  AGAUGAGCUUGCUAUGAGCAGUAAGUUGAUGGGGUCCCAGGCGGAGGAAA-----UGUUC 55
                   .........10.......20.........30.........40.........50.......6

                   .)))))).))))))).)))).)))).................
mcr-mir-1990/1-95  CGGGACUACGUCAACGUACUACCACGCGCAUCUCCAAGU--- 95
pmc-mir-1990/1-95  CGGGACUACGUCAACGUACUACCACGCGCAUCUCCAAGU--- 95
pcn-mir-1990/1-72  CGGGACUACGUCAACGUACUACCACGC--------------- 72
lny-mir-1990/1-91  CGGGACUACGUCAACGUACUACCACGCGCAGACCCCAA---- 91
lgi-mir-1990/1-69  CGGGACUACGUCAAC-UACUAGCACGCGC------------- 69
hru-mir-1990/1-71  CGGGACUACGUCAAC-UACUG-CAAGGGCG------------ 71
cgi-mir-1990/1-57  CGGGACUACGUCAACUACUUG--------------------- 57
mle-mir-1990/1-61  CGGGACUACUUCAACUACUUG--------------------- 61
bgl-mir-1990/1-95  CGGGACUACGUCAACUACUUGCUUGUCCCAAGCUACAACG-- 95
                   0........70........80........90........100
```

Figure 19: mir-1990 alignment for *L. nyassanus, M. cornuarietis*. *P. canaliculata* e *P. maculata* and their orthologs; pcn - *P. canaliculata*, lny - *L. nyassanus*, mcr - *M. cornuarietis*, pmc - *P. maculata*, lgi- *L. gigantea*, mle- *M. leonina*, cgi - *C. gigas*, bgl – *B. glabrata*, hru- *H. rufescens*

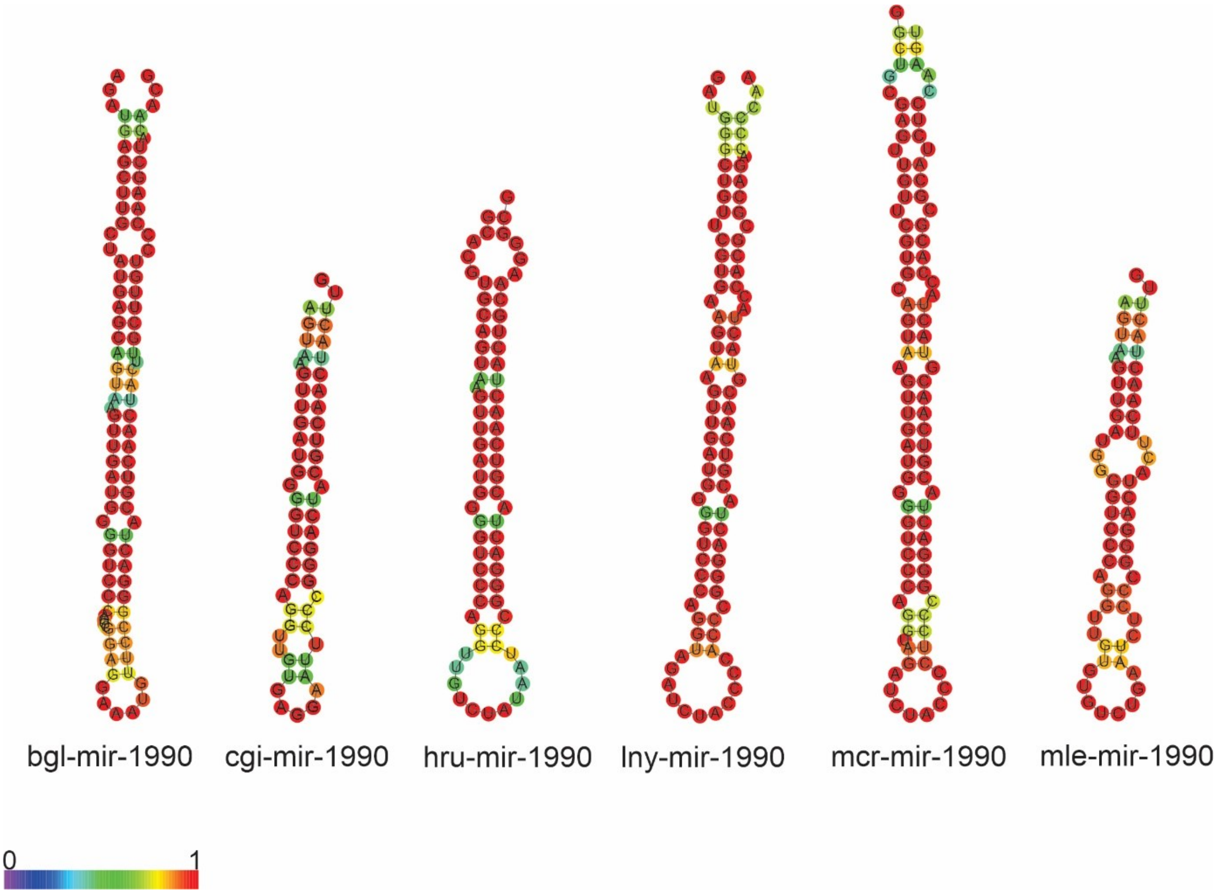


Figure 20: Secondary structure of the mir-1990 in *L. nyassanus, M. cornuarietis*. *P. canaliculata* e *P. maculata* and their orthologs

DISCUSSION OF RESULTS

In this study, three putative Argonaute proteins were found in *L. nyassanus* (Lny23421_c0_g1, Lny25187_c0_g1 and Lny28936_c7_g7). The same number encountered in *M.* cornuarietis (Mco25093_c0_g2, Mco26370_c0_g1, Mco27042_c1_g1). For each specie of the genus pomacea, two probable piwi protein were found, in orders *P. canaliculata* (Pca69814_c1_g2, Pca61914_c0_g1) and *P. maculata* (Pma63715_c0_g1_, Pma60501_c2_g16). The Argonaute protein is characterized by the presence of the PIWI and PAZ domains (PIWI-Argonaute-Zwille) (Song et al., 2004). The phylogenetic tree presented these two clades in a distinct way (figure 14). The argonaute proteins of eukaryotes can present in addition to these the following domains, N (N-terminal), and MID, together with two domain ligands L1 and L2 (Swarts et al., 2014). The PIWI domain in Argonaute contains three conserved catalytic residues composed of two aspartates and a histidine, called ‘DDH’ (Yang and Steitz, 1995). It was confirmed the presence of these conserved domains in Argonaute putative proteins identified. The analysis of the amino acid sequence of the PIWI domains confirmed the maintenance of the DDH amino acids (aspartic acid, aspartic acid and histidine) in the proper positions for the activity performed. The PIWI domains have great functional homology with RNase H, which is known for enabling the fragmentation of RNA sequences (Parker et al., 2004). The size of the predicted proteins was compatible with the average size of evolutionarily close organisms.

In this study, Lny28171_c0_g1 and Pca67531_c1_g2 DICER proteins were found in *L. nyassanus* and *P. canaliculata* respectively. Lny18581_c0_g2, Mco22837_c2_g1 and Pca67887_c3_g1 DROSHA proteins were found in *L. nyassanus*, *M. cornuarietis* and *P. canaliculata* respectively. The DROSHA and DICER proteins belong to the family of endoribonucleases, ribonuclease III (RNase III) that have specificity for cleavage of double-stranded RNA (dsRNA). The DROSHA protein is a class II RNAase III containing two endonuclease domains and a dsRBD. Dicer is a class III RNAase III that has two endonuclease domains, a dsRBD, an N-terminal helicase domain and a PAZ domain. Functionally class III enzymes produce single-stranded RNA (ssRNA) products of approximately 22 nucleotides in length from long dsRNA substrates (Bernstein et al., 2001; Blaszczyk et al., 2001; Filippov et al., 2000). The canonical pathway of miRNA biogenesis is the dominant pathway in which miRNAs are processed by class II (Drosha) and class III (Dicer) RNAases consecutively. These RNases III contain two catalytic centers with amino acids important for function. The Riboc I domain is composed of the amino acids; E (Glutamic acid), E (Glutamic acid), D (Aspartic acid) D (Aspartic acid); and the Riboc II domain is formed by E (Glutamic acid), Q (Glutamine), E (Glutamic acid), D (Aspartic acid), D (Aspartic acid), E (Glutamic acid); responsible for the cleavage of diester bonds (Blaszczyk et al., 2001).

The DROSHA protein predicted from *P. canaliculata* (Pca67887_c3_g1) showed compatible length and similarity with its orthologs (Table 1). The analysis of conserved domains showed the two endonuclease domains and one dsrm, characteristic of class II RNAases III. In the search for catalytic sites, he presented the first set composed of amino acids E-E-D-D in the Riboc I domain (figure 16). The 1525 amino acid length was compatible with the 1523 amino acid *P. canaliculata* protein (ID: XP_025111754.1) registered at the NCBI (National Center for Biotechnology Information — http://.ncbi.nlm.nih.gov/). These data corroborated the identification of the putative Drosha protein in *P. canaliculata*. On the other hand, in the DROSHA protein of *M. cornuarietis* (Mco22837 c2 g1), despite having a relatively smaller size than its orthologs (figure 15), the lack of coverage in the prediction of the protein did not affect the prediction of conserved domains, since it occurred, probably in the N-terminal portion of the protein, which, for DROSHA, functional conserved domains have not yet been identified. This predicted Drosha protein had two RIBOc domains and a double-stranded RNA binding domain and the presence of complete catalytic amino acid sequence in the Riboc I domain. These data support the identification for the putative Drosha protein in *M. cornuarietis* (Mco22837 c2 g1). Regarding another DROSHA candidate, *L. nyassanus* (Lny18581_c0_g2) presented a Riboc domain, a fragment of the second Riboc domain and the presence of a complete catalytic amino acid sequence in the Riboc I domain. The regions in the genome predicted for this gene are probably in error of annotation leading to the truncation of the protein sequences, consequently the size of the amino acid sequences for these genes were underestimated in size and structure. Further versions of the genome may solve this problem.

The putative DICER protein of *P. canaliculata* (Pca67531_c1_g2) was shorter in length (1984 aa) than the evolutionarily close organisms *A. californica* (2503 aa) and *B. glabrata* (2332 aa) (Table 2). Only conserved domains were identified; Ribonucleas_3_3, PAZ, Dicer dimer and Helicase_C; not showing the second Riboc domain. When verifying the starting position of the second Riboc domain of closely related organisms, *A. californica* (2273 aa) and *B. glabrata* (2100 aa), corroborated the fact that the second ribonuclease was not identified in the probable putative sequence. In Dicer, probably due to the lack of coverage in the sequencing of this region of the genome of *P. maculata*, it was not putative to evidence the presence of the second catalytic domain Riboc. The *P. canaliculata* Dicer protein (XP_025104500) identified at the NCBI with a length 2249 amino acids was orthologous to Pca67531_c1_g2, with a query coverage of 99% and a percentage of identification of 98.83%. The protein sequence Pca67531_c1_g2 using the BLASTp tool against the genome of *P. canaliculata* in the AmbuBase database (Department of Computer Science HKBU - https://www.comp.hkbu.edu.hk/~db/AmpuBase/#&panel1- 4) presented a percentage of identification and coverage of 100% (1984/1984 amino acids). Part of the first catalytic site of amino acids (ED) was observed in Riboc in the candidate protein cited (Pca67531_c1_g2) When performing the search for catalytic residues having as query NP_524453.1 Dicer-1 *D. melanogaster* the orthologous molluscs presented only the amino acids in the first domain Riboc catalysts (ED), with the exception of *Pectem maximus* (EDDE) NCBI (National Center for Biotechnology Information — http://.ncbi.nlm.nih.gov/). The data presented corroborated the identification of the putative protein. On the other hand, the putative DICER protein from *L. nyassanus* (Lny28171_c0_g1), despite having a relatively smaller size than its orthologs (figure 15), the lack of coverage in the protein prediction did not affect the prediction of the two conserved Riboc domains and a PAZ domain, since it was probably in the N-terminal portion of the protein, which for DICER the catalytic domains lie at the C-terminal end. This predicted DICER protein showed the presence of the complete catalytic amino acid sequence in the Riboc I domain. The data support the identification of the putative DICER protein in *L. nyassanus*. The regions in the genome predicted for this gene are likely to have annotation error leading to the truncation of the protein sequences. Consequently, the size of the amino acid sequences for these genes are underestimated in size and structure (Queiroz et al., 2017).

In this study, Lny14170_c0_g1, Lny12572_c0_g1, Lny27692_c0_g2, Mco24030_c0_g2, Mco81614_c0_g2, Pca62316_c0_g2, Pca65193_c2_g1, Pma59467_c0_g1, and Pma63331_c0_g1 Exportin protein family (XPO-5, XPO1 and XPO-T) were found *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* respectively. Intrinsically, the transport of miRNA precursors is performed by the XPO-5 protein. Occasionally the transport of pre-miRNAs can be accomplished by XPO-1 entering the non-canonical miRNA processing pathway without Drosha cleavage. Displacement of pre-miRNAs is also performed by exportin T (XPOT) in a Ran-GTP-dependent manner (Ruby et al., 2007). The search for Exportins proteins (XPO-5, XPO-1 and XPO-T) using the methodology of this work, resulted in the putative proteins found.

In order to emphasize the conservation of these putative proteins identified in the ampullariids species, a phylogenetic tree and studies of conserved domains were constructed. The phylogenetic analysis revealed a distribution of the studied amino acid sequences, in the genes of the Exportin protein family (XPO-5, XPO1 and XPO-T), grouped close to the Deuterostomes clade. Putative proteins from *L. nyassanus*. *M. cornuarietis*, *P. canaliculata* and *P. maculata* aggregated with their respective orthologs close to the phylum Molluscs and the clade Deuterostomes. The similarity of the identified Exportins of the Ampullariidae species was verified together with their orthologs, observing the level of preservation of the conserved domains and protein length. For Exportin 5 the putative proteins (Lny14170_c0_g1, Pca62316_c0_g2) presented the two conserved domains (Xpo1 and IBN_N) characteristic of the XPO-5 protein and a size compatible with the average dimension of its orthologs, confirming the identification of the putative Exportin 5 proteins. Exportin 1 putative proteins (Lny12572_c0_g1, Mco24030_c0_g2, Pca65193_c2_g1, Pma59467_c0_g1) showed six conserved domains characteristic of XPO-1 (IBN_N, Xpo1, CRM1_repeat, CRM1_repeat_2, CRM1_repeat_3 and only five domains except for the CRM1_cc1. The Pca65193_c2 did not show the conserved IBN_N domain. The lack of protein sequence prediction in the N-terminal region was already reported in this work for *P. canaliculata*, resulting in a relatively smaller size when compared to the analyzed species. Even the length of the protein sequences analyzed for XPO-1 (Lny12572_c0_g1, Mco24030_c0_g2, Pca65193_c2_g1, Pma59467_c0_g1) were strictly the same (1070 aa). This dimension also matched to the average size of the Exportin 1 protein for orthologous organisms. All these factors corroborated the identification of putative XPO-1 proteins in the analyzed species. Likewise, Exportin T in genes (Lny27692_c0_g2, Mco81614_c0_g2 and Pma63331_c0_g1) showed a characteristic conserved domain for all protein sequences (Xpo1). This time, lack of protein sequence prediction was verified in the N-terminal region for M. cornuarietis (Mco81614_c0_g2), presenting a smaller size (331 aa) than the analyzed species. Interestingly, the protein sequences (Lny27692_c0_g2 and Pma63331_c0_g1) also had the same size (966 aa) and matched the average size of XOP-T proteins from orthologous organisms. They were convincing evidence for the identification of putative Exportin T in the analyzed species.

The genomes of four ampullariids (Old World - Lanistes nyassanus and New World - Pomacea canaliculata, P. maculata, and Marisa cornuarietis) were published by Sun et al., 2019, in order to understand the genomic basis underlying the diversity of the Ampullariidae species and also their behavioral, morphological, and physiological adaptations. In our study we were able to apply a robust analysis to identify and characterize miRNAs and the putative proteins involved in miRNA pathway using the genome and predicted proteome from four Ampullariidae species. Either miRNAs or proteins of their biosynthetic pathway were described in several organisms, including several kingdoms such as plants and animals. In model species such as *D. melanogaster* and *C. elegans* mature and precursor miRNAs and also their pathway proteins have been extensively studied. Even though Mollusca is a phylum containing many species, little has been studied about miRNAs and their processing pathway in this phylum.

Sun et al., 2019, sequenced and analyzed the four genomes of ampullariids species, P. canaliculata, P. maculata, and L. nyassanus. The genomes were assembled in 535.5 Mb million base pairs (Mb) in total length or smaller and produced thousands of scaffolds anchored or not to chromosomes. Automatic annotation analyses of the four genomes displayed around 20 thousand gene models (Sun et al., 2019). So far, no study on miRNAs and their processing pathway in ampullariids species has been reported in the literature. In order to improve and increase the annotation of non-protein coding genes, such as miRNAs, and also of protein-coding genes of small RNA processing pathways, this work proposed an in-depth study of mature and precursory miRNAs and their pathway processing in the genome of the four species of ampullariids.

In our study, we were able to identify conserved miRNAs in four species, being 162 mature miRNAs and 141 miRNA precursors in *L. nyassanus*, 297 mature miRNAs and 279 miRNA precursors in *M. cornuarietis*, 296 mature miRNAs and 269 miRNA precursors in *P. canaliculata* and 316 mature miRNAs and 299 miRNA precursors in *P. maculata*. Two miRNAs found in all species was Mollusca-specific.

The minimum free energy value, -18 kcal/mol, in general, is the value necessary for a miRNA precursor to be stable and generates miRNAs (Gomes et al., 2011; Hofacker, 2009). The sequences of pre-miRNAs presented in this work MFE mean of (minimum free energy) and variation of values (Table 3). The mean value of the studied precursors was similar to the mean value of pre-miRNAs of lophotrochozoan species (-31.27 kcal/mol) (Gomes et al., 2011). Of the pre-miRNAs deposited in miRBase approximately 75% of those had minimum free energy values below -18.50 kcal/mol (Leclercq et al., 2013).

The size of the precursors of the lophotrochozoan species is between 57 and 153 nucleotides, with an average of 90 nucleotides per sequence(Gomes et al., 2011). In this study, the average size of the precursors and the length variation were showed in Table 3. The size of pre-miRNAs in animal species ranges from 47 to 177 nucleotides with a mean of 87 ± 29 nucleotides (Zhou et al., 2009). The data from this study corroborated with the average size of pre-miRNAs and the reference range for the size of lophotrochozoan species and metazoans in general.

GC content is one of the main parameters for the identification of pre-miRNAs and is very important for the stability of the secondary structure of precursors. The percentage of pre-miRNAs present in miRBase that had GC content above 20% and below 65% was 80% (Leclercq et al., 2013). In this work, the variation of GC content and the percentage of miRNAs in the range between 20% and 65% were respectively; *L. nyassanus* (20.25% to 69.05%) and 98.5%, *M. cornuarietis* (20.20% to 67.03%) and 98%, *P. canaliculata* (20.83% and 68.29 %) and 99.25%, *P. maculata* (20.40% and 68.75%) and 98.66%. The precursors presented mean values for the guanine-cytosine (GC) content for *L. nyassanus*, *M. cornuarietis, P. canaliculata* and *P. maculata*; 41.26%, 41.64%, 41.70%, 40.74% respectively. The mean value of the GC content of the studied ampullariids precursors was similar to the mean of the lophotrochozoan species (40.49%) (Gomes et al., 2011). Comparatively the GC content of the miRNA precursors were not observed statistical differences ($p > 0.05$) between the Ampullariidae analyzed and lophotrochozoan species.

Mature miRNAs were identified in the genome of 4 ampullariids species: 162 miRNAs for *L. nyassanus*, 297 miRNAs for *M. cornuarietis*, 296 miRNAs for *P. canaliculata* and 316 miRNAs for *P. maculata*. The number of miRNAs identified in *L. nyassanus* genome was similar to the gastropod species *Conus tribblei* (159 miRNAs) (Huang et al., 2021). The number of miRNAs found in *M. cornuarietis* (297 miRNAs), *P. canaliculata* (296 miRNAs), *P. maculata* (316 miRNAs) corroborated with the number of miRNAs identified for *Lymnaea stagnalis* (freshwater gastropod molluscs), 264 conserved mature miRNAs (Walker et al., 2018). There are plausible justifications for the smaller quantitative number of miRNAs for *L. nyassanus* compared to other ampullariids under study. *L. nyassanus* has fewer adaptive and functional properties when compared to other ampullariids under study (Sun et al., 2019). *L. nyassanus* is endemic to Lake Nyasa in Africa (Cowie, 2015; Dohrn, 1865; Van Bocxlaer, 2017), while *P. canaliculata* and *P. maculata* are geographically distributed on almost every continent, fast growing, high reproduction rate, tolerance and adaptation to environmental stress (Liu et al., 2018; Pimentel et al., 2005). Species of the genus *Pomacea* have the adaptive property of terrestrial egg laying, while *L. nyassanus* does egg laying in the aquatic environment (Sun et al., 2019). In addition, *M. cornuarietis* is better able to resist factors such as low temperature and hypoxia (Matsukura et al., 2016; Mu et al., 2018). As reported in previous studies, there is a significant increase in the number of miRNAs as the morphological complexity of the species increases (Heimberg et al., 2008), thus, justifying a lower number of miRNAs in *L. nyassanus*, when compared to other ampullariids in study.

The data presented corroborated the identification of miRNAs with the literature (Ha and Kim, 2014; Rachagani et al., 2010). The number of nucleotides in the mature miRNAs from ampullariids species had an arithmetic mean of 21.94 nucleotides/miRNA, with a size range from 17 to 25 nucleotides.

The Argonaute protein prefers the uracil nucleotide in the first position of the miRNA sequence, to be inserted in the RISC complex (Seitz et al., 2011). In this work mature miRNAs from *L. nyassanus, M. cornuarietis*. *P. canaliculata* and *P. maculata* presented, respectively, quantitative uracil nucleotides in the first position; 41.97%, 44.44%, 41.2% and 42.40%. Mostly presented this nucleotide in the first position in the miRNA sequence.

The structural and thermodynamic characteristics of pre-miRNAs were more similar among *M. cornuarietis*, *P. canaliculata* and *P. maculata* species. *L. nyassanus* had more dissimilar values, however it is the organism that most diverges with reference to the three species mentioned. The justifications for this probably in phylogeny. The division between the New World (*M. cornuarietis*, *P. canaliculata* and *P. maculata*) and Old World (*L. nyassanus*) lineages may have occurred at the time of the separation from Gondwana, around 120 million years ago (Jokat et al., 2003; Sun et al., 2019).

miR-33, Bilateria-specific, was found in the genomes of *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* and had two mature miRNAs (3p and 5p chains), corroborating studies observed in bivalve molluscs and *D. melanogaster* (Bao et al., 2014; Clerbaux et al., 2021). Mir-33-5p supposedly regulates genes involved in the heavy metal-induced stress response in the mollusc *Tegillarca granosa* (Bao et al., 2014). Likewise, *P. canaliculata* is able to survive in environments with heavy metals, where there is a high concentration of these metals in the gills (Kruatrachue et al., 2011), probably regulated by this micro-RNA. In this study, miR-33-5p showed 100% similarity between the ampullariid and orthologous species (figure 1). Furthermore, miR -33 is a pleiotropic regulator of metabolic and developmental processes in *D. melanogaster*. It is suggested that mir-33 is a conserved regulator of lipid homeostasis (Clerbaux et al., 2021).

The family of precursors of mir-67, protostomes specific, was found in the genome of the 4 species Ampullariidae with the presence of mature miR-67-3p for each species, corroborating the wide distribution of this miRNA in molluscs and *C. elegans* (Huang et al., 2021; Ma et al., 2017). Like miRNA-33, miRNA-67 is potentially associated with gene regulation when exposed to toxic levels of cadmium (Cd) in the bivalve *T. granosa* (Bao et al., 2014). Regulation of the immune system is also performed by mi-67 in *C. elegans* when exposed to pathogenic bacteria *Pseudomonas aeruginosa*. miRNA-67 inhibits the expression of the SAX-7 protein in the worm, that induces pathogen avoidance behavior (Ma et al., 2017). Furthermore, mir-67 was identified in 34 species of molluscs (Huang et al., 2021).

The sequences of the precursors of miR-96b presented two mature miRNAs, 3p and 5p, in the genomes of the species: *L. nyassanus*, *M. cornuarietis*. *P. canaliculata* and *P. maculata*. The mir-96b, Lophotrochozoa-specific, regulates genes post-transcriptionally in flatworms and molluscs. In the freshwater worm: *Schmidtea mediterranea* may have functions in wound healing, neoblast proliferation (mainly responsible for regeneration in planarians) and blastema differentiation (Sasidharan et al., 2013). In molluscs, miR-96b is involved together with other miRNAs in the pigmentation of the shells of *C. gigas*, inducing the synthesis of melanin, carotenoid or tetrapyrrole (Feng et al., 2020). The miR-96b was also found in the genome of gastropods evolutionarily close to the 4 species Ampullariidae, *B. glabrata* (Queiroz et al., 2020) and *A. californica* (Huang et al., 2021). Findings in the scientific literature corroborate the data of this work.

The family of mir-1990, Lophotrochozoa-specific miRNA, presented two mature miRNAs, 3p and 5p. A wide distribution of mir-1990 in molluscs was verified, mainly in 15 bivalve animals, 10 gastropods and 1 cephalopod (Huang et al., 2021). Few studies describe the role of miRNAs in molluscs development. However, mir-1990-3p may play a vital role in the shell biomineralization process in *P. fucata*, as it is highly expressed in mantle tissues (Huang et al., 2021). mir-1990 was found only in molluscs, however the mir-1990 family is Lophotrochozoa-specific as cte-miR-1990c-3p, cte-miR-1990a and cte-miR-1990b have been identified in *Capitella teleta* (http: //www.mirbase.org/). The wide distribution of mir-1990 in molluscs and the likely mechanism of gene control in the species corroborated the data in this study.

The functional form of a miRNA is generally 22 nucleotides in length, with a size range from 17 to 25 nucleotides (Ha and Kim, 2014; Rachagani et al., 2010). These small RNAs are generated by two cleavage reactions in which miRNAs are processed by RNAases III Drosha and Dicer consecutively (Lee et al., 2002; Tanzer and Stadler, 2004; Y. F. Zhang et al., 2009), in canonical miRNA processing pathway. The microprocessor complex, composed of a protein (DGCR8) and a ribonuclease III enzyme (Drosha), performs the cleavage of pri-miRNA in pre-miRNA in the cell nucleus. DGCR8 binds to a structure in pri-miRNA while Drosha performs the duplex scission. After the pre-miRNAs are generated, they are transported to the cytoplasm through the exportin 5 (XPO5) / RanGTP complex (Alarcón et al., 2015; Denli et al., 2004; Han et al., 2004; Okada et al., 2009). In the cytoplasm, pre-miRNAs are cleaved by Dicer into mature. The miRNAs can effect their action through the miRISC complex, in which a protein from the AGO family is loaded with a miRNA guide strand that directs the complex to base pairing, which by different mechanisms induces the silencing of gene expression (Ipsaro and

Joshua-Tor, 2015; Jo et al., 2015). The AGO-2 protein has endonucleolytic action and the level of complementarity formed between the miRISC complex and the target mRNA is indicative of the complex's action (Jo et al., 2015). All these factors in our analysis were of great relevance.

CONCLUSION

The search for miRNAs in *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* was able to predict 162 mature forms of miRNAs for *L. nyassanus*, 297 miRNAs for *M. cornuarietis*, 296 miRNAs for *P. canaliculata* and 316 miRNAs for *P. maculata*.

It was possible to identify the biogenesis pathway of miRNAs in species of the Ampullariidae family, highlighting several putative key pathway proteins; Argonaute, DROSHA, DICER, XPOs, among others. The prediction of some proteins of the miRNA pathway was not verified in some species, probably due to annotation error in the part of the sequenced gene specific to each organism.

Our results expand the study of miRNAs in molluscs, bringing new challenges to the understanding of the essential processes related to the invasiveness of *P. canaliculata* and *P. maculata* species and supposed advances in the control of these molluscs considered agricultural pests for humanity.

Thus, the search for miRNAs and their processing pathways in the species *L. nyassanus*, *M. cornuarietis*, *P. canaliculata* and *P. maculata* were able to predict structures that found the established criteria, also complementing previous results from our study group as well, as creating the need to establish putative new target genes for the discovered miRNAs.

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SUPPLEMENTARY DATA I

Supplementary Table 1 Id Protein, putative name, length, ID protein Ortholog, Ortholog species, Ortholog length and E-value of *L. nyassanus* proteins

ID protein	Putative name	Length (AA)	ID protein Ortholog	Ortholog Species	Length (AA)	E-value
Lny23421	Argonaute 1.1	890	NP_493837.1	*Caenorhabditis elegans*	891	0.0
			NP_001163498.1	*Drosophila melanogaster*	866	$7e^{-35}$
			XP_013068463.1	*Biomphalaria glabrata*	895	0.0
Lny25187	Argonaute 1.2	880	NP_493837.1	*Caenorhabditis elegans*	891	$9e^{-44}$
			NP_001163498.1	*Drosophila melanogaster*	866	$8e^{-180}$
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Lny28936	Argonaute 1.3	941	NP_493837.1	*Caenorhabditis elegans*	891	$3e^{-43}$
			NP_001163498.1	*Drosophila melanogaster*	866	0.0
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Lny28171	Dicer	1434	NP_498761.2	*Caenorhabditis elegans*	1910	$9e^{-124}$
			NP_524453.1	*Drosophila melanogaster*	2249	$2e^{-159}$
			XP_013067888.1	*Biomphalaria glabrata*	2332	$2e^{-159}$
Lny18581	Drosha	317	NP_492599.1	*Caenorhabditis elegans*	1086	$4e^{-87}$
			NP_477436.1	*Drosophila melanogaster*	1327	$1e^{-146}$
			XP_013069067.1	*Biomphalaria glabrata*	1469	$2e^{-171}$
Lny14710	Exportin 5	1196	NP_741567.1	*Caenorhabditis elegans*	1080	$1e^{-11}$
			NP_001285453.1	*Drosophila melanogaster*	1241	0.0
			XP_013087907.1	*Biomphalaria glabrata*	1193	0.0
Lny12572	Exportin 1	1070	NP_741567.1	*Caenorhabditis elegans*	1080	0.0
			NP_001303316.1	*Drosophila melanogaster*	1063	0.0
			XP_013069551.1	*Biomphalaria glabrata*	1996	0.0
Lny27692	Exportin T	966	NP_501320.2	*Caenorhabditis elegans*	950	$3e^{-101}$

			XP_013079973.1	*Biomphalaria glabrata*	963	0.0
Lny22624	Tudor - SN	897	NP_494839.1	*Caenorhabditis elegans*	914	0.0
			NP_001261195.1	*Drosophila melanogaster*	926	0.0
Lny29643	Loquacious	338	NP_723813.1	*Drosophila melanogaster*	419	$8e^{-43}$
Lny27624	PASHA	701	NP_001293461.1	*Caenorhabditis elegans*	751	$1e^{-28}$
			NP_651879.1	*Drosophila melanogaster*	642	$1e^{-137}$
Lny9931	VIG	312	NP_001367502.1	*Caenorhabditis elegans*	378	$3e^{-09}$
			NP_723898.1	*Drosophila melanogaster*	490	$1e^{-26}$

Supplementary Table 2 Id Protein, putative name, length, ID protein Ortholog, Ortholog Species, Ortholog Length and E-value of *M. cornuarietis* proteins

ID protein	Putative name	Length (AA)	ID protein Ortholog	Ortholog Species	Length (AA)	E-value
Mco26370	Argonaute 1.1	931	NP_493837.1	*Caenorhabditis elegans*	891	0.0
			NP_001163498.1	*Drosophila melanogaster*	866	$1e^{-32}$
			XP_013068463.1	*Biomphalaria glabrata*	895	0.0
Mco27042	Argonaute 1.2	878	NP_493837.1	*Caenorhabditis elegans*	891	$3e^{-44}$
			NP_001163498.1	*Drosophila melanogaster*	866	$3e^{-178}$
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Mco25093	Argonaute 1.3	938	NP_493837.1	*Caenorhabditis elegans*	891	$1e^{-41}$
			NP_001163498.1	*Drosophila melanogaster*	866	0.0
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Mco22837	Drosha	760	NP_492599.1	*Caenorhabditis elegans*	1086	$6e^{-157}$
			NP_477436.1	*Drosophila melanogaster*	1327	0.0
			XP_013069067.1	*Biomphalaria glabrata*	1469	0.0
Mco24030	Exportin 1	1070	NP_741567.1	*Caenorhabditis elegans*	1080	0.0
			NP_001285453.1	*Drosophila melanogaster*	1241	$3e^{-10}$
			XP_013069551.1	*Biomphalaria glabrata*	1076	0.0
Mco81614	Exportin T	331	NP_001294153.1	*Caenorhabditis elegans*	952	$4e^{-43}$
			NP_001294153.1	*Biomphalaria glabrata*	963	$2e^{-122}$
Mco51286	Tudor - SN	926	NP_494839.1	*Caenorhabditis elegans*	914	0.0
			NP_001261195.1	*Drosophila melanogaster*	926	0.0
Mco13761	Loquacious	316	NP_723813.1	*Drosophila melanogaster*	419	$1e^{-44}$
Mco21592	PASHA	709	NP_001293461.1	*Caenorhabditis elegans*	751	$2e^{-28}$
			NP_651879.1	*Drosophila melanogaster*	642	$8e^{-135}$
Mco12258	VIG	414	NP_001367502.1	*Caenorhabditis elegans*	378	$4e^{-09}$

			NP_723898.1	*Drosophila melanogaster*	490	$2e^{-24}$

Supplementary Table 3 Id Protein, putative name, length, ID protein Ortholog, Ortholog Species, Ortholog Length and E-value of *P. canaliculata* proteins

ID protein	Putative name	Length (AA)	ID protein Ortholog	*Ortholog Species*	Length (AA)	E-value
Pca61914	Argonaute 1.1	936	NP_493837.1	*Caenorhabditis elegans*	891	$7e^{-44}$
			NP_001163498.1	*Drosophila melanogaster*	866	0.0
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Pca59652	Argonaute 1.2	468	NP_493837.1	*Caenorhabditis elegans*	891	$3e^{-36}$
			NP_001163498.1	*Drosophila melanogaster*	866	$6e^{-111}$
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Pca69814	Argonaute 1.3	897	NP_493837.1	*Caenorhabditis elegans*	891	0.0
			NP_001163498.1	*Drosophila melanogaster*	866	$1e^{-32}$
			XP_013068463.1	*Biomphalaria glabrata*	895	0.0
Pca67531	Dicer	1984	NP_498761.2	*Caenorhabditis elegans*	1910	$1e^{-12}$
			NP_524453.1	*Drosophila melanogaster*	2249	$3e^{-48}$
			XP_013067888.1	*Biomphalaria glabrata*	2332	0.0
Pca67887	Drosha	1525	NP_492599.1	*Caenorhabditis elegans*	1086	$5e^{-171}$
			NP_477436.1	*Drosophila melanogaster*	1327	0.0
			XP_013069067.1	*Biomphalaria glabrata*	1469	0.0
Pca62316	Exportin 5	1140	NP_741567.1	*Caenorhabditis elegans*	1080	$1e^{-11}$
			NP_001285453.1	*Drosophila melanogaster*	1241	0.0
			XP_013069067.1	*Biomphalaria glabrata*	1469	0.0
Pca65193	Exportin 1	974	NP_741567.1	*Caenorhabditis elegans*	1080	0.0
			NP_001303316.1	*Drosophila melanogaster*	1063	0.0
			XP_013069067.1	*Biomphalaria glabrata*	1469	0.0
Pca60969	Tudor - SN	898	NP_494839.1	*Caenorhabditis elegans*	914	0.0
			NP_001261195.1	*Drosophila melanogaster*	926	0.0
Pca65324	Loquacious	258	NP_723813.1	*Drosophila melanogaster*	419	$3e^{-25}$

Pca59979	PASHA	731	NP_001293461.1	*Caenorhabditis elegans*	751	$4e^{-28}$
			NP_651879.1	*Drosophila melanogaster*	642	$2e^{-132}$
Pca69254	VIG	390	NP_723898.1	*Drosophila melanogaster*	490	$8e^{-10}$

Supplementary Table 4 Id Protein, putative name, length, ID protein Ortholog, Ortholog Species, Ortholog Length and E-value of *P. maculata* proteins

ID protein	Putative name	Length (AA)	ID protein Ortholog	Ortholog Species	Length (AA)	E-value
Pma35144	Argonaute 1.1	909	NP_493837.1	*Caenorhabditis elegans*	891	$8e^{-41}$
			NP_001163498.1	*Drosophila melanogaster*	866	$2e^{-179}$
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Pma60501	Argonaute 1.2	937	NP_493837.1	*Caenorhabditis elegans*	891	$1e^{-43}$
			NP_001163498.1	*Drosophila melanogaster*	866	0.0
			XP_013089248.1	*Biomphalaria glabrata*	897	0.0
Pma63715	Argonaute 1.3	891	NP_493837.1	*Caenorhabditis elegans*	891	0.0
			NP_001163498.1	*Drosophila melanogaster*	866	$1e^{-34}$
			XP_013068463.1	*Biomphalaria glabrata*	895	0.0
Pma65850	Drosha	359	NP_492599.1	*Caenorhabditis elegans*	1086	$2e^{-96}$
			NP_477436.1	*Drosophila melanogaster*	1327	$2e^{-96}$
			XP_013069067.1	*Biomphalaria glabrata*	1469	$8e^{-178}$
Pma51393	Drosha	580	NP_492599.1	*Caenorhabditis elegans*	1080	$4e^{-77}$
			NP_477436.1	*Drosophila melanogaster*	1241	0.0
			XP_013069067.1	*Biomphalaria glabrata*	1469	0.0
Pma59467	Exportin 1	1070	NP_741567.1	*Caenorhabditis elegans*	1080	0.0
			NP_001303316.1	*Drosophila melanogaster*	1063	0.0
			XP_013069551.1	*Biomphalaria glabrata*	1076	0.0
Pma63331	Exportin T	966	NP_501320.2	*Caenorhabditis elegans*	950	$1e^{-97}$
			XP_013079973.1	*Biomphalaria glabrata*		0.0
Pma32975	Tudor - SN	603	NP_494839.1	*Caenorhabditis elegans*	914	0.0
			NP_001261195.1	*Drosophila melanogaster*	926	0.0
Pma62419	PASHA	709	NP_001293461.1	*Caenorhabditis elegans*	751	$2e^{-28}$

			NP_651879.1	*Drosophila melanogaster*	642	$2e^{-135}$
Pma51302	VIG	414	NP_001367502.1	*Caenorhabditis elegans*	378	$3e^{-10}$
			NP_723898.1	*Drosophila melanogaster*	490	$8e_{-25}$
Pma61707	Loquacious	316	NP_723813.1	*Drosophila melanogaster*	419	$4e^{-45}$

SUPPLEMENTARY DATA II

Supplementary Table 1– Structural and thermodynamic characterization of miRNA precursors in *L. nyassanus*. Size (Tam), G content, A content, C content, U content, GC content, AU content, AU ratio (R-AU), GC ratio (R-GC), Minimum Free Energy (MFE), Minimum Free Energy of the Pool (MFEE), Frequency of the MFE Structure in the Pool (Freq), Diversity of the Pool (Div), Minimum Adjusted Free Energy (AMFE), Minimum Free Energy Index (MFEI).

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-316	UAGUUGUUAAACUGUAGGAAAACGUCUCUUAUUCCUAUCGGCUCAAUAUAUUUAUGAGCCUAGGCAACAAAUAUACUGUCUUUUUCCGCUUACAAAUG	98	15,30612	29,59184	19,38776	35,71429	34,69388	65,30612	1,206897	0,789474	-18,9	-14,1	0,015799	21,7	-19,2857	-0,55588
lny-mir-7965	AUGCAUCGAAGAAACCUCAAAUGACACGUUUUAAUUAGAAAUGGUGAGGGAAUGAAUUUUGUAUGCUAAAACAUAAAAUUGUCAGCAUUCUUGGAUGAUU	100	20	37	12	31	32	68	0,837838	1,666667	-20	-16,2	0,094567	7,12	-20	-0,625
lny-mir-2064	GACCAGUAUGGUCAGAGUUGAUGCUUAAGGCGCCAUUCCGUGGCUUAGCACAGCUUUUGACAAAUAAGCAGCACUGUGCAACUGCAA	87	25,28736	27,58621	22,98851	24,13793	48,27586	51,72414	0,875	1,1	-27,2	-26,8	0,071601	11,7	-31,2644	-0,64762
lny-mir-3484	aauacaaacagCUAAACUAGGAAAAGGAUAUGCUGUGCUUUCCACAUGGUGUUCCUACACAGAUUUUUCUAGUUACcuguuuguggu	87	13,7931	20,68966	14,94253	25,28736	28,73563	45,97701	1,222222	0,923077	-26,7	-26,3	0,091839	12,31	-30,6897	-1,068
lny-mir-10a	GGGGUGAGACCUACCCUGUAGAUCCGAAUUUGUGUGACAUUCGU	82	28,04878	21,95122	23,17073	26,82927	51,21951	48,78049	1,222222	1,210526	-38,9	-38,9	0,039205	2,67	-47,439	-0,92619

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GACGACAAAUUCGUGUUUGCACGGUAAGGCCUCACUGC															
lny-mir-11	GACCCUAUGGCAAUGUGUCGAGGCUCAUCACAGGCAGAGUUCCagaccugucugucugcugacaUCUCUCUCAGACUGCCAUGGCCA	87	18,3908	16,09195	24,13793	17,24138	42,52874	33,33333	1,071429	0,761905	-29,4	-20,8	0,07357	22,9	-33,7931	-0,79459
lny-mir-2b-1	GAUCUGCUCAUCAAAGCUGGCUGUGAUAUGACUUACAAAAACACAUCCCAGCAGCUUUGAUGAGAAGGCC	70	21,42857	31,42857	24,28571	22,85714	45,71429	54,28571	0,727273	0,882353	-27,6	-27,6	0,092458	3,86	-39,4286	-0,8625
lny-mir-745a	AUUUGUCGGCUGGAGGCGGCUUUUCAACAGGCUGCCUUGCUUGGGAGGACACAAGCUGCCUGAUGAAGAGCUGUCCUGUAGCGGGCAGUA	90	34,44444	18,88889	22,22222	24,44444	56,66667	43,33333	1,294118	1,55	-46,8	-40,8	0,132252	8,07	-52	-0,91765
lny-mir-7c	GUGAUCUGGAAGACUAGUGAUUUUGUUGUUCUGAUGCUGACUAACAAUAAAUCACAUUCUUCCCCGAUUGC	71	19,71831	25,35211	19,71831	35,21127	39,43662	60,56338	1,388889	1	-21,1	-18,6	0,131089	9,74	-29,7183	-0,75357
lny-mir-9319	UCUCCUUCCCACUCACAGUCACUAGCAGAGCUAGUGGCCUCACCCCCACUACUUGCACUGGCUGCUUCAGGUGAAGGGGG	80	23,75	18,75	35	22,5	58,75	41,25	1,2	0,678571	-30,4	-30,4	0,219681	2,97	-38	-0,64681
lny-mir-466q-1	AUGGUCUGGUCAUGACAGAcaggcgcgcgcgugcacacacacacauacacacagacgugUAAAUGUCUGCUCGCGCGUCGUCUGACGUAAUACAUACAGA	100	15	16	13	16	28	32	1	1,153846	-34,9	-33,3	0,065729	20,26	-34,9	-1,24643
lny-mir-3297	UAAGCAAGGGUCACAAAACGCCGCUUUCAAGAUAGUGCAGAGAUUCAGCAGAGCACAUCUAGUCAAAA	93	23,65591	33,33333	22,58065	20,43011	46,23656	53,76344	0,612903	1,047619	-22,6	-22	0,137599	8,48	-24,3011	-0,52558

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CCAAGGUUUGUGACGAUCUUGCAGC															
lny-mir-7460	AUCAGCAUUCAGCCUGGCACCAUCCUCUUCACAAACAACAUCUGCCUGACUGAGCUCUGCUAGGGCUGUUUUGAGGGCCUGUGCGUGUCGAAUGCUGUC	99	24,24242	19,19192	29,29293	27,27273	53,53535	46,46465	1,421053	0,827586	-28,3	-17,6	0,013885	26,75	-28,5859	-0,53396
lny-mir-96b	CAUGGCUGUUCAAUUAUUUGGCACUUGUGGAAUAAUCGUUGCAUCUGAAGUCGAUUAUACAUCGGUGCCAAGUCAUCAGAAAGGCCGGA	89	24,7191	26,96629	19,10112	29,21348	43,82022	56,17978	1,083333	1,294118	-30,3	-28,8	0,042265	5,05	-34,0449	-0,77692
lny-mir-564	UGAGGUGAACAUUGUACGUGCCAACAAGACUGAAGGCACGGUGGCAGCAGAAGGGCAGGagauagguagguaauuuuuggCAGACAGUUAUUCCACCUUA	100	24	24	17	14	41	38	0,583333	1,411765	-22,3	-14,12	0,009426	22,56	-22,3	-0,5439
lny-mir-6632	CUUAUCGUCAGUGCUCAUCUCAGUCCgauagaaaagagagagaugagaggagUGCUGAACCAUUCC	66	9,090909	10,60606	21,21212	19,69697	30,30303	30,30303	1,857143	0,428571	-18,9	-17,8	0,132348	11,84	-28,6364	-0,945
lny-mir-6504	guuugugguguaacCAUUACAGCACAGCCAUGUUUGCGGUGUAACCAUUACAGCACAGCUAUGUUUAUGGUGUAACCAUUACAGCACAGUU	91	16,48352	24,17582	19,78022	24,17582	36,26374	48,35165	1	0,833333	-26,5	-21	0,034382	27,18	-29,1209	-0,80303
lny-mir-4262	UAAAUGCCCAGCAGCUGGGACAACGUCGACAGGCCGACAUUCAGACUACCUGUCGACGUCGCCUUGAAUGCUGGGAUAAU	80	26,25	26,25	27,5	20	53,75	46,25	0,761905	0,954545	-36,8	-35,1	0,460005	2,87	-46	-0,85581
lny-mir-133c	UAACUACAGCUGGUUGAAGGGGACCAAAUGAAAGCCUCUUCAACA	75	22,66667	33,33333	22,66667	21,33333	45,33333	54,66667	0,64	1	-30,4	-27,8	0,231076	4,17	-40,5333	-0,89412

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AUUUGGCCCGAGUUCAACCAGCUAUAGAAG															
lny-mir-10b	AGAGAGUGUGGGUGGCUUUACCCUGGAGAACCGAGCGUGUgugaucaugacgucacagcucguUUCUGAGGGUCAAGUCGCGAUACUCGCG	91	27,47253	14,28571	15,38462	17,58242	42,85714	31,86813	1,230769	1,785714	-41,7	-41,6	0,288526	9,6	-45,8242	-1,06923
lny-mir-8908i	cucaagaaagaaagaaauuugcaaUCCCCGAUAAACCCAAUGUAAUAGCAACUACCCGGUAAGGUAGUUGCCaagaaugucuuuuuuuuuuacc	94	9,574468	15,95745	14,89362	10,6383	24,46809	26,59574	0,666667	0,642857	-21,2	-18,84	0,113508	8,17	-22,5532	-0,92174
lny-mir-1993	AGGAAGGCCCUGUAAUUUUCGGGAAUAUCGGCAUAAUGCAGUUGACUUGAGAUUCGUAUUAUGCUGCUAUUCACGAGAUGGAAGGGCUUGGA	92	29,34783	26,08696	15,21739	29,34783	44,56522	55,43478	1,125	1,928571	-36,7	-36,7	0,374278	3,58	-39,8913	-0,89512
lny-mir-466m	gugugugugugacugugugugcaugugcaugugugguuugcaugcaugcacaauaaGGCCCUCCAGUCCCAGACAGGC	79	7,594937	5,063291	12,65823	2,531646	20,25316	7,594937	0,5	0,6	-33,8	-30,8	0,291201	4,92	-42,7848	-2,1125
lny-mir-8279	GAAACAGUUGAAGAACAGAGCUGAGAGAUUCAUGUCAAUCUGACAUUUGCAGUAGGUCUGCUagcuacauguauuuucaagUGUAGA	87	20,68966	25,28736	11,49425	20,68966	32,18391	45,97701	0,818182	1,8	-23,3	-21	0,095311	11,78	-26,7816	-0,83214
lny-mir-7661	CAAGCAGAUGUUGAAGGAAGUUCGUGUuucuacaaaagaaagaaaccuggAUAAACUAGACACUUCCAUCAAAGCGUGCAUC	82	15,85366	24,39024	14,63415	17,07317	30,4878	41,46341	0,7	1,083333	-19,2	-19,2	0,214952	11,41	-23,4146	-0,768
lny-mir-87a	AAAUCUUUGUUAAACACUUGGUAAUUUGCAAAUgaacaugcaaauaaaaggaacacaugacugGCACAUGGA	99	10,10101	29,29293	11,11111	18,18182	21,21212	47,47475	0,62069	0,909091	-19,3	-19,3	0,407153	3,9	-19,4949	-0,91905

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AAUAAACCCAAGUUAACAACAGAUGA															
lny-mir-466b	CauagagagaauuacauauacauacacacauacuacUCACGCCAGAUAUGUGUCUACAUGUAAUUCUCUCUGUU	74	8,108108	10,81081	13,51351	20,27027	21,62162	31,08108	1,875	0,6	-24,6	-22,9	0,096333	7,47	-33,2432	-1,5375
lny-mir-10349	CACUGAGCACCAAUAAGCAGCAAUAAGCGGCGAUAGCUCACGACCAGUGAUCACGUGGUCGUUAUCAGCGGGGUUAUAUCCCUUGACUGGUAAUCACUG	99	25,25253	27,27273	25,25253	22,22222	50,50505	49,49495	0,814815	1	-28,4	-25,9	0,020752	14,01	-28,6869	-0,568
lny-mir-2049	AACUGUAUGUAGCACAGCAAUGACGUGAAAUUUUGUGCAUGUACGUGgauucaugugcaugcauucauga	70	17,14286	20	10	20	27,14286	40	1	1,714286	-23,5	-23,5	0,409874	4,97	-33,5714	-1,23684
lny-mir-5920	UCAGUGGGUGCCUGUAGCCUGCCGUUUUGUCAUUCGUAUACAAAACAGUAGGCCACUGCCCCACAUA	67	22,38806	22,38806	28,35821	26,86567	50,74627	49,25373	1,2	0,789474	-29,7	-29,7	0,51133	1,3	-44,3284	-0,87353
lny-mir-5600	AGUUGUAGUUAACUAAAUAGGACAUUUUGAAAAGAAGUGUUCUUGCUUCGUAAAUGCACUUAAUACAUGAGUGGaauguuuuguuucaguacuACAGAG	99	18,18182	28,28283	9,090909	25,25253	27,27273	53,53535	0,892857	2	-25,7	-25,7	0,154731	5,98	-25,9596	-0,95185
lny-mir-12096b	UGCUACUUCGUGCAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUACGAGGUAGGGCAAAAUUAUCACCGAUUACCCGAGGUAUCG	85	23,52941	25,88235	22,35294	28,23529	45,88235	54,11765	1,090909	1,052632	-29	-29	0,105265	6,21	-34,1176	-0,74359
lny-mir-263a-1	ACUUUCAAGAGUUGGCCAUGCUUAAUGGCACUGGUAGAAUAGCACACACCAUAGAGAUUAGUGCUGC	95	25,26316	31,57895	17,89474	25,26316	43,15789	56,84211	0,8	1,411765	-24,2	-20,6	0,027018	17,04	-25,4737	-0,59024

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AGUCAAGAGAGUGGUCAAUAUUGAACGU															
lny-mir-124c	AAAUGAUGGUCUUCCCCUUGGCAUUCACCGCGUGCCUUAAUAGUGUGUCAAUCACCAAGGCCAACGCAgugaacacaaacagguaagCCCGGUCACAC	98	16,32653	19,38776	26,53061	18,36735	42,85714	37,7551	0,947368	0,615385	-26,5	-26,3	0,051306	9,68	-27,0408	-0,63095
lny-mir-4024	GUCUUUUUUACCUGUCCAAAGCCGUUUUUGAAUAGCUGUGCUACCGACUUUACUGUCUGUUAUUUGUAGGAUGAAAAGGUUAUUGGAAGUGAAAAAUUA	99	21,21212	26,26263	14,14141	38,38384	35,35354	64,64646	1,461538	1,5	-18,8	-16,9	0,025084	15,96	-18,9899	-0,53714
lny-mir-216a	guguuugucUAAUCUCAGCUGGUAAUUCUGAGUGGAGUUGUGUACACCUCAAGUUACUCGCCGAGAUUACAUAAAUAU	78	17,94872	25,64103	16,66667	28,20513	34,61538	53,84615	1,1	1,076923	-26,2	-26,2	0,262819	2,61	-33,5897	-0,97037
lny-mir-12	UUGAAUGGUCAGACUGUGAGUAUUACAUCAGGUACUGAGAAAACAGCAUGCUUCAGUACCUUUUGUGAUAUUCUUAGUCUGCCAUUUUG	89	21,34831	25,8427	16,85393	35,95506	38,20225	61,79775	1,391304	1,266667	-42,9	-42,9	0,38245	2,26	-48,2022	-1,26176
lny-mir-8335-1	ucuuguuguuguuguuguuuugguccuuGCAAAAAGUUUGAACCUCUCAACACUUUUUGAGGUACUUCAAAGCAAAUUACACAAACaggc	90	7,777778	25,55556	14,44444	16,66667	22,22222	42,22222	0,652174	0,538462	-24,3	-24,3	0,033164	11,07	-27	-1,215
lny-mir-9-1	CAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUACUUCAAUCAUACAGCUAGAUAACCAAAGACAAAACCG	76	11,84211	32,89474	22,36842	32,89474	34,21053	65,78947	1	0,529412	-24,2	-24,2	0,496783	1,38	-31,8421	-0,93077

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-8335-2	GUACACAAGCAAAAGUACAAUUGACAAAUGUUCCAGAACAGCCCAGCGUCUUUugacacuguuguuguuguuguuuuguuuuguggag	88	10,22727	22,72727	14,77273	12,5	25	35,22727	0,55	0,692308	-21	-18,9	0,011022	19,33	-23,8636	-0,95455
lny-mir-228	AGGCAUCAUGUGAAAAGAGCAUCAAUUGUAUAAUGGCACUGCAUgaauaaaaaauuauguuugCCAGAAAGAAUUGUGUCUUUGCUAAAUGACUGGUU	98	18,36735	26,53061	12,2449	23,46939	30,61224	50	0,884615	1,5	-22,7	-22,5	0,078762	7	-23,1633	-0,75667
lny-mir-2987	CGACCUGAGACUUGUCUGAUUGUUCAGGAAAGUCUGGAUCUCGCACACUACGUUAGCUGCUUGAAGACUUCAGAGCAAGGCUGAGGCUU	89	26,96629	23,59551	22,47191	26,96629	49,4382	50,5618	1,142857	1,2	-24,9	-16,6	0,027121	27,97	-27,9775	-0,56591
lny-mir-252b-1	GAGAGUAAGUACUCUCGACAGGGGGCGCUUCCUCCAACUUGCUGCGCAGAUGGUGUCCUUGGAGGUACGUGUCCCUGCGCAGUCCUACUGGG	92	32,6087	16,30435	27,17391	23,91304	59,78261	40,21739	1,466667	1,2	-34,9	-26,6	0,007771	20,62	-37,9348	-0,63455
lny-mir-9701a-1	GUGACAGCaggcugugugacuguguaccACCAUCAACCCGCGACGUGUGACCACAGUCGUAUUUUACUGGAGGUACAGGACAAAUGUCAGCUGUGUU	97	20,61856	20,61856	19,58763	18,5567	40,20619	39,17526	0,9	1,052632	-30,9	-30,1	0,097108	9,96	-31,8557	-0,79231
lny-mir-281	ACGUGACCUCACGCUGAAGGGAGCAUCCGUCGACAGUCAGAAAUACAGCACUGUCAUGGAGUUGCUCUCUUUACUGGAAAGGUCAAGG	88	27,27273	27,27273	23,86364	21,59091	51,13636	48,86364	0,791667	1,142857	-36,5	-36,1	0,381583	2,16	-41,4773	-0,81111
lny-mir-466i-1	GUUUGACAAGUCUGCuagcugacugugugugugugugagugugugugug	100	11	18	15	12	26	30	0,666667	0,733333	-35,6	-34,2	0,076901	11,8	-35,6	-1,36923

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	ugacgcacAAAGACAUACAAACCACCGUCCCAGUCUGAACUGGUCAGAU															
lny-mir-3128	GAaugguuuuucuuauuucagacUUGGAUUUGAAGAUGAAUGGUCAUGUGAUCCAUGGCACAUCCAUUGCAGUUGAUUUCUGGCAAGUAAAAAACCAUCC	100	18	24	14	23	32	47	0,958333	1,285714	-26,1	-23,4	0,009444	10,94	-26,1	-0,81563
lny-mir-279	GUCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACAAGGCCAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAAGACGG	91	25,27473	24,17582	25,27473	25,27473	50,54945	49,45055	1,045455	1	-40,2	-39,7	0,065907	7,67	-44,1758	-0,87391
lny-mir-36b	cuGGGGUGCGGUGGGUGUACGCCCUGGUUGGUGGGCGUCGGUAACAUCACCGGGUAUACAUUCAUCCGCACCCUGA	76	35,52632	14,47368	25	22,36842	60,52632	36,84211	1,545455	1,421053	-43,9	-41,1	0,167581	3,38	-57,7632	-0,95435
lny-mir-1662	GUAUAUUGUGUUGCAGAAAUUUGACAUCACCAUACUUUAUGUCGUCAGUUUGACAUCAUCAUACUUUAUGUCAUAAGUUUGACAUCACCAUACUU	95	13,68421	28,42105	18,94737	38,94737	32,63158	67,36842	1,37037	0,722222	-19,6	-19,6	0,371187	6,34	-20,6316	-0,63226
lny-mir-9a	ggaagggaaggagacGCAGUCCUUAAGCCCGCAGUUCUGUAACUGUCGAUAAGAAAUAAAGCUAGGCGACUGUCCGUCCUCGUUGCCUAAU	91	18,68132	20,87912	21,97802	21,97802	40,65934	42,85714	1,052632	0,85	-26,4	-17,7	0,034951	9	-29,011	-0,71351
lny-mir-8335-3	UGGCAUCGUUAGAACUUGAUUAAAGCAGGCUUGACucaugcuuuguuguuguuguuguuuugaagccaGAUUAAUCAUCUAAUGUGGCU	92	14,13043	17,3913	9,782609	19,56522	23,91304	36,95652	1,125	1,444444	-20	-18,3	0,054089	28,71	-21,7391	-0,90909

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-2001	GCUGCCAUUUUGUGACCGUUACAAUGGGCauugacagaaagacaaaugcuCCAUGUGAUGUUCACAAGAUGGCGGU	76	21,05263	14,47368	15,78947	21,05263	36,84211	35,52632	1,454545	1,333333	-39,7	-39,7	0,259527	3,56	-52,2368	-1,41786
lny-mir-252b-2	GGGGAUAGUGCCGGCGAUAAGUAGUGGUGCCGCAGGUAUGGCUCGUCAACUACCUGCUCAUCUCUGCUUAAUGUUGCUCUAUCAUU	86	27,90698	18,60465	23,25581	30,23256	51,16279	48,83721	1,625	1,2	-33,5	-33,5	0,133838	3,27	-38,9535	-0,76136
lny-mir-252a	AUUUUCUGGCCCACUACUAAGUACUAGUGCCGCGGGAGGACAGCUUGCCAUGUCCCGUGGUUCUGGUCCUUACUACAGGGCGGAAUUU	88	27,27273	18,18182	26,13636	28,40909	53,40909	46,59091	1,5625	1,043478	-37,2	-36,8	0,059207	5,64	-42,2727	-0,79149
lny-mir-7371d	ACUGUAGGCAGCAGAGAGAACUUCCAGUAAAUGCAGUUCGCAAUCAUGGAAACACCAUUCACCAUAUUUGUACCAGAUGCUCUCUCUGGUGCCCACAGA	99	20,20202	30,30303	26,26263	23,23232	46,46465	53,53535	0,766667	0,769231	-33,9	-33,1	0,261583	12,77	-34,2424	-0,73696
lny-mir-190	UGCCCACCUACCCGCUUCUGCUAGAUAUGUUUGAUAUAUUUGGUGCGGUUGUCAUGACGACCAAGUAGUCAAACAUGUCAGAGCAGCGGUGGGGCUU	97	26,80412	21,64948	22,68041	28,86598	49,48454	50,51546	1,333333	1,181818	-44,3	-44,3	0,312382	10,4	-45,6701	-0,92292
lny-mir-92b-1	GACAGUCAGGGUUGUGUAGACCGGUACAGGGGCAAUGCAGUGAGUCGCUUGUAUUGCACUCGUCCCGGCCUAUACAGUCUGACUCGG	87	32,18391	19,54023	24,13793	24,13793	56,32184	43,67816	1,235294	1,333333	-41,1	-41,1	0,171444	4,85	-47,2414	-0,83878
lny-mir-92a	GCAUUAGCAUUAGGUCUUGAUGGGUGCAAUACUGGUGAGCCUGAUGGCAGAUUGCACUCGUCCCGGCCUUCUGCUAAAAG	80	28,75	21,25	22,5	27,5	51,25	48,75	1,294118	1,277778	-36,4	-36,4	0,391022	2,84	-45,5	-0,8878

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-92b-2	UAGCAUAGGGAGGUUGUGACCUGUGCAAUGAUUGGAGGAAUAUGAGCCAAUUGCACUUGUCCCGGCCUGCCCUGUGUGC	79	31,64557	20,25316	21,51899	26,58228	53,16456	46,83544	1,3125	1,470588	-35,3	-35,1	0,232461	3,35	-44,6835	-0,84048
lny-mir-184b	ACCCACAAGCCCUUAUCAGUUCUCCGUCCAGUGCUUGAGAACAGACGGGGCGGGGGAGUGAUAAGGAAAUGUGAAA	76	30,26316	28,94737	22,36842	18,42105	52,63158	47,36842	0,636364	1,352941	-35	-33,4	0,17411	3,39	-46,0526	-0,875
lny-mir-306	CAGCACCGAGACCGGCCAAUUUUGUCUUUCGAAAGAUCUUCCAGUUAAGAACACCAGCCUUGACACCUGUGACAAAUUUUGGUCAGGUACUGAGUGACU	99	21,21212	27,27273	25,25253	26,26263	46,46465	53,53535	0,962963	0,84	-24,1	-22,8	0,10238	6,82	-24,3434	-0,52391
lny-mir-1a	GCCCGGCACAUACUUCUUUGCUAUCCCAUAUGUUCUUCCAAAGCUAUGGAAUGUAAAGAAGUAUGUACCGUGU	73	19,17808	26,0274	23,28767	31,50685	42,46575	57,53425	1,210526	0,823529	-29,2	-29,2	0,14159	5,1	-40	-0,94194
lny-mir-4690	UCACCUCCCGCUCAUCUCCUGGUCUGACCAGCACCGGCAGUCCGCGAUCGGGUGUGCUGGGGAGCAGGCGAGGCUGGGAGGGCU	84	36,90476	13,09524	32,14286	17,85714	69,04762	30,95238	1,363636	1,148148	-40,6	-39,2	0,073847	8,43	-48,3333	-0,7
lny-mir-8075	gcuUGACUGCUGAUGGCAGAUGUGUGUUGGCUGUUCAAUAAACAGAGCCCCACUGCCACACUCAGAUCAUGU	72	23,61111	23,61111	23,61111	25	47,22222	48,61111	1,058824	1	-19,8	-10,6	0,03638	15,58	-27,5	-0,58235
lny-mir-669k	UUUCUCUCGUACACUGAAGUCCAUAUCUUCAAGAGUGUUUAgaugugcaugucuguuuacuugugugugcauguauggacGUGCAUGUGUAUCAGAGAGG	100	14	15	11	21	25	36	1,4	1,272727	-32,7	-32,3	0,067561	17,27	-32,7	-1,308

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-9708c	GGGAAGUUGAGGGCUAGAAAAAUUUGUGUAGCACCAGACAUUUGugagcacagcuaaacauuuucuCUGCUGAGAUAAUUUUGUGGCGCCUCAACUUCCC	100	21	20	15	22	36	42	1,1	1,4	-39	-31,9	0,079272	20,93	-39	-1,08333
lny-mir-1731	uuauuuacuugacUGCAGGCACUACAGAUUAGUGAUAAUGCUGUUCCAGUCAGUCGAAAUCUGUAUUGAUUCGGUGUAAGUAAACGC	87	20,68966	24,13793	14,94253	25,28736	35,63218	49,42529	1,047619	1,384615	-21,8	-21,7	0,069971	9,58	-25,0575	-0,70323
lny-mir-8066	GauucccgcccccuccccuucucccacacaucGACCUUCCCAUGGUCCGAGGGGCCGAUGCAAUGUGAUCUUUUGGAGaacauggagaugggggaugU	98	16,32653	8,163265	11,22449	13,26531	27,55102	21,42857	1,625	1,454545	-34,7	-29,6	0,27164	13,85	-35,4082	-1,28519
lny-mir-5100	CGGGCACGUGACACCUACGUCAUGGCUGUUGUCGAAUCCCAGCGGUGCCCGAGAGCUGGUUCCAGUAACAGCUCACCUCGUCCUGGAGCCACGUGCGUC	99	29,29293	17,17172	33,33333	20,20202	62,62626	37,37374	1,176471	0,878788	-36,8	-36,7	0,095799	8,39	-37,1717	-0,59355
lny-mir-3906	agGGGCAAUGCUCUUGCAAGUUUUUUAUCCAAUAGUUGGAGCAGGAAGAAAAGCAUUUUGAAUGCAUAAAAAGCAUUCCAUAGACCACUCCUGU	94	20,21277	31,91489	18,08511	27,65957	38,29787	59,57447	0,866667	1,117647	-20,6	-16,8	0,091919	20,31	-21,9149	-0,57222
lny-mir-7062	GAUAAAAAGCUGCACAGCUGAUGGCCAUCCUGUUCGUGGAGGCCAGCUUGUGUCCAGGUUAUUGCA	66	28,78788	22,72727	22,72727	25,75758	51,51515	48,48485	1,133333	1,266667	-20,8	-18,1	0,025013	10,43	-31,5152	-0,61176
lny-mir-8485-1	UUugugguacacacacacacacacacacacacacguacuuaAAAUUUAGACUGCAGGGUGUUCGUGCGUUAAUUUCUAUGUGUGGGGGUACCACCAA	97	16,49485	13,40206	9,278351	20,61856	25,7732	34,02062	1,538462	1,777778	-25,5	-18,6	0,096418	19,61	-26,2887	-1,02

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-6756	ucccCCCACUUCUUGCCCCUCCCUCGCGCAUGGAUAUUACAUAUAUGAAAAUAUUACUUUUUGACUAGGGUGGGGCUGGAGGUGGGGAUA	90	24,44444	21,11111	21,11111	28,88889	45,55556	50	1,368421	1,157895	-39	-37,9	0,064711	9,53	-43,3333	-0,95122
lny-mir-10790	uuggauacAGAAAGCAGACUAACGGACGUCAGCAAGCAGGUGACACUGUCUGGCUgcucucuuuauuucucucucuguucguc	83	16,86747	18,07229	13,25301	8,433735	30,12048	26,50602	0,466667	1,272727	-21,7	-18,1	0,055432	16,72	-26,1446	-0,868
lny-mir-153	ACACCCCCUUCCCAGGCAGCUUUUGUGAUUCAGCAAUUGUACAGCUAUCAAAUUGCAUAGUCACAAAAGUGAUCGGGAGGCGGGGACU	88	23,86364	27,27273	25	23,86364	48,86364	51,13636	0,875	0,954545	-40,2	-40,2	0,334594	4,07	-45,6818	-0,93488
lny-mir-124	GUGUGACCGGGcuuaccuguuuguguucacUGCGUUGGCCUUGGUGAUUGACACACUAUUAAGGCACGCGGUGAAUGCCAAGGGGAAGACCAUCAUUU	98	26,53061	18,36735	16,32653	19,38776	42,85714	37,7551	1,055556	1,625	-40,2	-38,8	0,093576	10,13	-41,0204	-0,95714
lny-mir-133	CUUCUAUAGCUGGUUGAACUCGGGCCAAAUUGUUGAAGAGGCUUUCAUUUGGUCCCCUUCAACCAGCUGUAGUUA	75	22,66667	21,33333	22,66667	33,33333	45,33333	54,66667	1,5625	1	-35,5	-35,1	0,187007	6,7	-47,3333	-1,04412
lny-mir-10365	uuguGCCCGCAGUCCAUUAGAAUGUGGAAUCUAUGCUUUAAUGGUUGUGACAGAUUCUACUUUAAAAGACAUCUGGCAACC	81	19,75309	27,16049	19,75309	28,39506	39,50617	55,55556	1,045455	1	-20,4	-20,4	0,113197	12,46	-25,1852	-0,6375
lny-mir-466h	CCUGCuucgcacacacgcauacgcacgcacacacacacaucuccucGGCGACACGUGAAGAUGCACGUGGGAGGGUGUUCAUGUGUGCGAAUGCCUG	97	22,68041	10,30928	12,37113	12,37113	35,05155	22,68041	1,2	1,833333	-34,7	-33,9	0,086928	14,95	-35,7732	-1,02059

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-981	UUGAUCAGACUUUGUACCGGGUUUCGCGACUGGCGAACAGUCAUUCUGAACUGUGUUCGUUGUCGUCGAAACCUGCCCUGAACUCUGAUGUG	92	26,08696	18,47826	23,91304	31,52174	50	50	1,705882	1,090909	-35,3	-34,1	0,018788	7,48	-38,3696	-0,76739
lny-mir-7398y	AUGAGAUGUCGGAUGCAAAUGUGAUGGAGUGGGUGGUUUAaccuucccuucucucuuucucucucucaacaacUCGAUCUUUGUCAGGCAACAUCUCAA	99	20,20202	17,17172	9,090909	20,20202	29,29293	37,37374	1,176471	2,222222	-24,9	-23,9	0,214701	12,35	-25,1515	-0,85862
lny-bantam	uuugacgAAACUGGUUUUCACAGUGAUCCAGCAGAUCGUUCGAAGUCUGAGAUCAUUGUAAAAACCAAUUUUGUCGCC	78	17,94872	26,92308	19,23077	26,92308	37,17949	53,84615	1	0,933333	-31,9	-31,9	0,266041	5,12	-40,8974	-1,1
lny-mir-7006	GGUCACAGGUGAGUGGGGGUGUUCAAGAcccccccaguuuucugugggccagcaucauagGGGUGAUGCACAUCGCCUCUCCCUUGCUG	88	23,86364	10,22727	14,77273	15,90909	38,63636	26,13636	1,555556	1,615385	-44,5	-43,9	0,07812	5,45	-50,5682	-1,30882
lny-mir-2a-1	GUGCCAAAGCUGUGAUGCUGACCAAGUGACUGGGAUGUGUGUUUGUUGUCAUAUCACAGCCUGCUUGGAUC	71	29,57746	19,71831	19,71831	30,98592	49,29577	50,70423	1,571429	1,5	-20,8	-17,8	0,088092	9,24	-29,2958	-0,59429
lny-mir-2b-2	GGCCUUCUCAUCAAAGCUGCUGGGAUGUGUUUUUGUAAGUCAUAUCACAGCCAGCUUUGAUGAGCAGAUC	70	24,28571	22,85714	21,42857	31,42857	45,71429	54,28571	1,375	1,133333	-32,9	-32,9	0,167727	4,14	-47	-1,02813
lny-mir-2d	GUAAGCAUGAAUGGAGGGCCAGCCAAAGUGGCGGUGAUCUGAUGUUCAGAGCAAAUCACAGCCUGCU	92	30,43478	23,91304	20,65217	25	51,08696	48,91304	1,045455	1,473684	-40,6	-40,6	0,14781	5,41	-44,1304	-0,86383

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UUGGUGAGCCUUCUGUCAUUCUGAG															
lny-mir-2a-2	AAUUGACCGCAGAGGUCACACCAAAGAGGUUGugacuuugucuuucuguucaaaUCACAGCCUGCUUUGGUGAGCUCUUUGUCGUCAGGU	90	21,11111	16,66667	17,77778	20	38,88889	36,66667	1,2	1,1875	-39,5	-39,1	0,224362	3,21	-43,8889	-1,12857
lny-mir-6868	GUAUUCCUUCUGUUGUCUGUAAACUGCUUucgggaaaaaaacccauuguuCCUCCUUUGAGUUCUCAGGUAACAAGAGGAAAAG	84	15,47619	17,85714	15,47619	26,19048	30,95238	44,04762	1,466667	1	-23	-22,2	0,132737	4,31	-27,381	-0,88462
lny-mir-67	GUUUCGUGACACGUCUGCCCUUGUUCAGCCCGGUUGUGAUGGAGUUGGUCACAUCACAACCUGCAUGAAUGAGGACUGACGUCACGAGCG	90	28,88889	20	25,55556	25,55556	54,44444	45,55556	1,277778	1,130435	-43,9	-40,8	0,079095	4,8	-48,7778	-0,89592
lny-mir-8	UGCGCGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUCUGCUGG	94	24,46809	23,40426	21,2766	30,85106	45,74468	54,25532	1,318182	1,15	-46	-46	0,192059	3,37	-48,9362	-1,06977
lny-mir-6544	AAGUUGUAUUUCUUUUCGCAAACGCCUUGCUUGGUGAGGCUGACCGAAACACUAAGCACGUGUAGAUAUAUGCGGcguauuaaaagaaaaacaauug	97	19,58763	19,58763	15,46392	22,68041	35,05155	42,26804	1,157895	1,266667	-29,2	-29,2	0,173343	6,85	-30,1031	-0,85882
lny-mir-359	CGGAAAGAGGGAAGCCAGAUUUUCAUCUGUGUUCCCCCGUCACAAAAUGGAUGGUUCCAGGUGAACGUCAGAACUUGAUCACUGGUUUUCCUCUGUUGCG	100	26	23	23	28	49	51	1,217391	1,130435	-38,9	-38,3	0,123112	6,16	-38,9	-0,79388

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-184	UUUCACAUUUCCUUAUCACUCCCCCGCCCCGUCUGUUCUCAAGCACUGGACGGAGAACUGAUAAGGGCUUGUGGGU	76	22,36842	18,42105	30,26316	28,94737	52,63158	47,36842	1,571429	0,73913	-24,6	-24,3	0,091486	9,76	-32,3684	-0,615
lny-mir-4931	GGCCCAGCUGUCUUCAAACAGUCGUGAUACAUUUCUAACGUUUGCUCAUCGCUGAUUGGUUGAGCAGCCGGAAG	74	25,67568	21,62162	24,32432	28,37838	50	50	1,3125	1,055556	-21,3	-21,3	0,196775	4,36	-28,7838	-0,57568
lny-mir-750	GAAGCCAGUUCCCUGUGAGUUGGAAGAUUGGGUCUUUGGCAGCAAUGCUGUCUUCCCUGCCAGAUCUAACUCUUCCAGCUCAUAGUGGCAUGGCACA	97	25,7732	20,61856	25,7732	27,83505	51,54639	48,45361	1,35	1	-48,9	-47,3	0,207948	5,04	-50,4124	-0,978
lny-mir-1175	UGAUCAGGUGUGUUAUGUAGUGGAGAGAGUUUUAUCUCAUCAUGAGCCGUAAGCAGGUGAGAUUCAACUCCUCCAACUGCAGGCUACACCUGAAAC	96	25	27,08333	20,83333	27,08333	45,83333	54,16667	1	1,2	-44,8	-40,7	0,088251	5,34	-46,6667	-1,01818
lny-mir-137b	CUACCAGUCGGUUACGGGUAUUCUUGGGUAAAUAAUACAUUGAACCGCUGUUAUUGCUUGAGAAUACACGUAACUGACUGGGUG	84	25	26,19048	17,85714	30,95238	42,85714	57,14286	1,181818	1,4	-40	-39,2	0,16289	4,49	-47,619	-1,11111
lny-mir-2580	uguccguaAGUGUACucacgugucuguguguauguuucuaCAUAGACAUAUACAUGUGUACGGCUUCGGUUA	72	12,5	15,27778	9,722222	16,66667	22,22222	31,94444	1,090909	1,285714	-27,3	-27,2	0,115281	4,2	-37,9167	-1,70625
lny-mir-11976	gggcggcggcggcggcgccGGCGUGGGNNNNNNNNNNNNNNNNNNNNNGGGgggggcggcggcggcggcgccGGCGUGG	79	17,72152	0	2,531646	2,531646	20,25316	2,531646	0	7	-38,07	-38,07	0,922324	0,51	-48,1899	-2,37938

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-9-2	CGGUUUUGUCUUUGGUUAUCUAGCUGUAUGAUUGAAGUAGAAAUAUCAUAAAGCUAGGUUACCAAAGGCAAAAAUG	76	22,36842	32,89474	11,84211	32,89474	34,21053	65,78947	1	1,888889	-33,1	-33,1	0,29717	2,88	-43,5526	-1,27308
lny-mir-7290	ACUCUGCAAUCAGAGAUUUCUGGCUCUGUUUGCAGCAAAUCACUAGUCGUUGGCUCUGUUUGCAGCAAAUCACUAGUCGUUGGCUCUGUUUGCAGCAA	98	22,44898	21,42857	23,46939	32,65306	45,91837	54,08163	1,52381	0,956522	-31,6	-28,2	0,065716	6,74	-32,2449	-0,70222
lny-mir-4265	AGCUUCUGAGGAGACCUGUGGGCUCAGCUCUGCAUUUAUAUUAGGAGGCAAAUGUCCCUCAGAAAUA	67	25,37313	26,86567	20,89552	26,86567	46,26866	53,73134	1	1,214286	-18,8	-11,8	0,102899	12,25	-28,0597	-0,60645
lny-mir-9701a-2	CGCCAUAGUAACCACUAGCCGUGAGACACACAACAGGCCGUGUGACUGUGUACCACCAUCAAGGCGUGACGUGUGACCCCAaggugugugacuguguac	99	20,20202	22,22222	26,26263	13,13131	46,46465	35,35354	0,590909	0,769231	-31,4	-31,3	0,319797	5,61	-31,7172	-0,68261
lny-mir-451	GACAGUACCCAGCCCAAAGAACAAACUUUCGUUUGUAGUAAUGGUAAGGGUUUGAAUCUUAGGGUGGGGUGCUAAG	76	28,94737	28,94737	15,78947	26,31579	44,73684	55,26316	0,909091	1,833333	-29	-29	0,334254	2,61	-38,1579	-0,85294
lny-mir-33	GCUAUGGUGGUGCAUUGAGGUUGCAUUGCAUCAGUUGAGGAACAUGCAAUGCAUCUGCAGUGCAAGUACCAUGGU	75	30,66667	24	17,33333	28	48	52	1,166667	1,769231	-38,2	-37,2	0,235986	4,29	-50,9333	-1,06111
lny-mir-653	AAGCUAGGAAAGCCGAGCUGCAGUAGAGAUUGAGACAAUCUCUACUGCAACAACGGGUUCCUAGGUC	67	26,86567	31,34328	22,38806	19,40299	49,25373	50,74627	0,619048	1,2	-35	-33,2	0,416654	2,33	-52,2388	-1,06061

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-8485-2	CAUUGCAAGCAUGGCGCCUGUGUGGCUCUGCGCGCAugcaacgcacacacacacacacacguacaugcacgcacuc	76	15,78947	6,578947	14,47368	10,52632	30,26316	17,10526	1,6	1,090909	-25,8	-25,8	0,527609	3,34	-33,9474	-1,12174
lny-mir-11225	AACUACAGGGCAGUGGACUACAGCAGAUUGUACGUAAAACUGUACGUAAAACUGUUCUUAAGUCAUGGCCUGUACGA	77	23,37662	32,46753	19,48052	24,67532	42,85714	57,14286	0,76	1,2	-23,7	-23,7	0,093776	6,64	-30,7792	-0,71818
lny-mir-466i-2	CACCUCCUGGUUCGCGAAACAUGGCCAUcuauaaauauuauaaauauuauauacacacacacacacacaugaccaCUUUCAGCGAAACGGGAGAUG	100	13	12	14	10	27	22	0,833333	0,928571	-20,7	-18,07	0,038561	14,52	-20,7	-0,76667
lny-mir-7195	uauccuccccucucccccccccuccaccacacgAGUCAUACGAUUGACGUCAUGGGAAGUGGGGGAGCGGAAAAGGACAGGUGA	84	25	19,04762	7,142857	9,52381	32,14286	28,57143	0,5	3,5	-29,8	-23,2	0,107685	18,49	-35,4762	-1,1037
lny-mir-29b-1	CAUUGGGGCAGCGGGGCACUGGUCUCGACUGGUGGGUAGAUGGCGCUGUUAGUCUAGCACCAUUUGAAAUCAGUGCUCGCGCAUGUCUCCAGCA	94	32,97872	18,08511	24,46809	24,46809	57,44681	42,55319	1,352941	1,347826	-44,5	-44,5	0,069593	6,31	-47,3404	-0,82407
lny-mir-29a	AGAUGGCGAGAUGGAUGCUGGUCUCUUUUGGUGCUUAGAGUCAUAUCGCCUGUCUAGCACCAUUUGAAAUCAGUUUCCUGACCUGGCCACAG	92	26,08696	20,65217	22,82609	30,43478	48,91304	51,08696	1,473684	1,142857	-34	-34	0,158187	4,7	-36,9565	-0,75556
lny-mir-734	CAGGUGGAACUAUUCUGCAACAUUCAUGCUGAACCUGAGCCAGCCAUUAUGUGGUCAACACCUUGGGGCCAUGAGUUUGCUGACAUUUCGCACAUG	96	23,95833	23,95833	25	27,08333	48,95833	51,04167	1,130435	0,958333	-23,7	-22,5	0,102	11,88	-24,6875	-0,50426

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-9235b	ACGGAGAUAGUUCUAAUGGGACUUGUCUUCUCCGACAAAGGCAUGUUUGAGAAAUUAAUUUUGAUGUGGCUUGAGAACAGUACCAUAAAUUGUCUCCCC	99	22,22222	28,28283	18,18182	31,31313	40,40404	59,59596	1,107143	1,222222	-26,8	-24,1	0,009236	11,43	-27,0707	-0,67
lny-mir-263a-2	CUUAGUUCCCCUGCUAAUCAAUGGCACUGGUAGAAUUCACGGGUGCUUUCAAAAUCCCGUGGUCUUUCAGUGCCAUCUAUGGGCAAAGGGUGACCUGCA	99	24,24242	22,22222	25,25253	28,28283	49,49495	50,50505	1,272727	0,96	-40,8	-39,7	0,053135	7,61	-41,2121	-0,83265
lny-mir-1c	ACACGGUACAUACUUCUUUACAUUCCAUAGCUUUGGAAGAACAUAUGGGAUAGCAAAGAAGUAUGUGCCGGGC	73	23,28767	31,50685	19,17808	26,0274	42,46575	57,53425	0,826087	1,214286	-33,4	-32,3	0,415163	2,78	-45,7534	-1,07742
lny-mir-1990	GAUGGGCUGUUCGUGAAGUAAGUUGAUGGGGUCCCAGGUAGAUCUACCCCACCCGGGACUACGUCAACGUACUACCACGCGCAGACCCCAA	91	27,47253	24,17582	29,67033	18,68132	57,14286	42,85714	0,772727	0,925926	-42,4	-41,8	0,25783	4,43	-46,5934	-0,81538
lny-mir-466q-2	caugugcacacacacacauacaugcuugCACAUGCAGCCUCACGUGCAAGCUUAAGUUUauagugcacaug	71	8,450704	11,26761	12,67606	11,26761	21,12676	22,53521	1	0,666667	-24,9	-24,7	0,237339	3,05	-35,0704	-1,66
lny-mir-1947	AAAUGCUCAGAUAAGCUGUCAGGCGAAUCAAGGAUUUUGAAAACAGUUAACUAGCUGCUUUGUUUUAGCACUGAGCUAGCUCUCUAGCAGUC	92	21,73913	29,34783	19,56522	29,34783	41,30435	58,69565	1	1,111111	-22,3	-21,5	0,091223	6,88	-24,2391	-0,58684
lny-mir-2491	UCCUAUUGGCAUGUAGUCAAAACUGCUCAGUuccuaacaacaacagcagcagcagugaccUCACACCAAUAUAG	74	9,459459	18,91892	14,86486	17,56757	24,32432	36,48649	0,928571	0,636364	-18,7	-17,1	0,17106	10,72	-25,2703	-1,03889

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-1985	GAGGAGAAGGCGUGCCAUGCCAUUUUUAUCAGUCACUGUGUGUUGUCAGUCACAGUGAUGGUGACAAUGGCUUGAUGGGCCUCUCAUG	88	30,68182	20,45455	19,31818	29,54545	50	50	1,444444	1,588235	-38,3	-38,3	0,063273	5,09	-43,5227	-0,87045
lny-mir-1307	AGAUCGCGACUUCGCCACUCGGCGUGGCGUCGGUGCAAAGGUCGAAAUGCGUUCGGGGCGGCGGAGUGGGGAGGACACGAGCC	83	42,16867	18,07229	25,3012	14,45783	67,46988	32,53012	0,8	1,666667	-34,9	-33,3	0,314815	4,28	-42,0482	-0,62321
lny-mir-2944a	GUACAGGAGACAUUUCUCUGUGAAAAAGAGUAUAGGUGAUAUUUUCUCUUGCUGUCAUUUAGGGGGGCGAAGAUUUUCAGAAGGAACUUCUGCUGAUC	98	26,53061	26,53061	14,28571	32,65306	40,81633	59,18367	1,230769	1,857143	-22,4	-11,8	0,008713	30,59	-22,8571	-0,56
lny-mir-5397	agaaaacaaacuacgCAGAAGUUUGCUUCUGuaucauuuucccucccucgGAAUGUUUGCACAUGCGCAGCAAACGUCUCUGACAUUUAUUUCAG	95	13,68421	15,78947	13,68421	21,05263	27,36842	36,84211	1,333333	1	-20,9	-20,9	0,2969	5,73	-22	-0,80385
lny-mir-7045	acucucccccucccccgccccacuuUUCUUCUGCGAGGGACGCCGAUCAGACGACGCCCGGAGAAAGGUggaggcugggugggguggaggga	92	16,30435	10,86957	13,04348	7,608696	29,34783	18,47826	0,7	1,25	-50,9	-50,9	0,357037	6,43	-55,3261	-1,88519
lny-mir-106a	UUUUAUUAUCAGCCCUGCUACUGCAAUGCAAGCACAUUGACUGAAUUUUGCUCAGAGAACGUGCAGUUGGAGCUUGCUUUUCAUUGGCUGAUAAUAGCG	99	22,22222	24,24242	20,20202	33,33333	42,42424	57,57576	1,375	1,1	-30,3	-28,6	0,089339	10,78	-30,6061	-0,72143
lny-mir-3238	AGUGACUGAAAUGAAUCAUGCAUUUGGCAUGUAAACCUGUGGUGAAAUAGUGUguaacauugguguuug	98	18,36735	24,4898	9,183673	27,55102	27,55102	52,04082	1,125	2	-18,5	-18,5	0,036449	18	-18,8776	-0,68519

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	uguaAAUAUUCUGAUAAUUUCUAGUCGUG															
lny-mir-2361	CAUGCUgaguuguguuguuuuuuuuucaauacagcAGAUGAACUAACAAUACUGCAUCCAAAGUGCUAGCAUUAACAAGAAAUAUCAUAGCUUCAGCACA	100	10	29	16	16	26	45	0,551724	0,625	-23	-22,9	0,046036	12,62	-23	-0,88462
lny-mir-2493	AGCCUCUAUCACUCCUCUGAUCCUGUCGUCAGUGUAGUAAGAAAUUUUGGCGAAAGUAgcugcucacacacacacacagacgagagagagagagagaga	99	12,12121	15,15152	13,13131	18,18182	25,25253	33,33333	1,2	0,923077	-26,4	-18,6	0,022709	25,98	-26,6667	-1,056
lny-mir-9032	GUGAUGUUUGUUGCCAGUGAAUUAAUCAAAUUCUGCCAAUAUGCACUGCAGAUUCCGUUGAUGCAAUCCAAUGGUCAUCAUCAUGAG	87	20,68966	27,58621	19,54023	32,18391	40,22989	59,77011	1,166667	1,058824	-19	-19	0,117129	13,25	-21,8391	-0,54286
lny-mir-3963	GUACACACAGUCAAAUAAAGUAUUGUAUCCCACUUCUGACGCACAAUAUUUGUCGUUUGCCACAGAAAAAAUACCUGGGUUGACGGUGUGCAU	93	19,35484	31,1828	21,50538	27,95699	40,86022	59,13978	0,896552	0,9	-21,7	-21	0,161914	20,42	-23,3333	-0,57105
lny-mir-1994	ACGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCAUGUGCAAUGACGUCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGAGACCGCUAA	90	28,88889	22,22222	25,55556	23,33333	54,44444	45,55556	1,05	1,130435	-38,4	-38,4	0,344812	5,28	-42,6667	-0,78367
lny-mir-51	CUCCCAUCAUGUAUGCGUGCAUGGAAGCAGGUACAGUCACCUGUCCUGACUUAUCCAGCGAACAGUGUGGCCU	73	24,65753	21,91781	28,76712	24,65753	53,42466	46,57534	1,125	0,857143	-21,7	-17,1	0,160663	16,95	-29,726	-0,55641

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
lny-mir-9229d	UAGGGAUAAGGGGGAGGUUAAGAUAAGGAAAGGAUACUGUUAUCUGAGUCUUCCCCUUGAGCCUGU	66	31,81818	27,27273	13,63636	27,27273	45,45455	54,54545	1	2,333333	-25,9	-25,4	0,059825	5,61	-39,2424	-0,86333
lny-mir-4968	GCUCUUCUgcuggguuuguuguuguuguuguuguuaguaaCGAAGCUGUAAUAGUUCCCCGUGGCAGCAGcaauaacagcagcaacagcagcagcagcag	100	10	7	11	10	21	17	1,428571	0,909091	-45,8	-45,8	0,189807	22,44	-45,8	-2,18095
lny-mir-239b	CUCagccaucccccucccccagaguGGGUCAGAUGGCACUUUUGUGGUGUGCAGGUUGGAUGGCUUGU	69	26,08696	7,246377	10,14493	23,18841	36,23188	30,43478	3,2	2,571429	-25,2	-13,05	0,115483	18,21	-36,5217	-1,008
lny-mir-466i-3	ACUCGCUCAAACACUGUCACUCACUCAAACACAUGGACGCAUUCGCgugcauucuguguguguguguguguggugugugugcgugc	88	6,818182	15,90909	19,31818	10,22727	26,13636	26,13636	0,642857	0,352941	-35,9	-35,4	0,211217	10,98	-40,7955	-1,56087
lny-mir-277a	UGUUCUUCGGGCAAGGAAACGCGAUCACACGGAgccauuucuuugugugcuuccUUGGCCGCCAAGAUCG	70	21,42857	17,14286	18,57143	12,85714	40	30	0,75	1,153846	-25,5	-25,4	0,03184	11,31	-36,4286	-0,91071
lny-mir-29b-2	UGUAAAGUGAUGUAUCGUAUCCUUUGGGAACGCCAGCUGGUUUCACAUGGACAGAUAACAACACUUUGUC	70	22,85714	27,14286	20	30	42,85714	57,14286	1,105263	1,142857	-19,1	-16,4	0,131874	6,17	-27,2857	-0,63667
lny-mir-466i-4	AUUACACGCUCUCGACCACACCCGGACCcucaaaccaacaaaaaacguUGGugagggaagugugugugugugugugugugug	82	7,317073	8,536585	15,85366	6,097561	23,17073	14,63415	0,714286	0,461538	-32,4	-31,1	0,058041	17,93	-39,5122	-1,70526

Supplementary Table 2 – Structural and thermodynamic characterization of miRNA precursors in *M. cornuarietis*. Size (Tam), G content, A content, C content, U content, GC content, AU content, AU ratio (R-AU), GC ratio (R-GC), Minimum Free Energy (MFE), Minimum Free Energy of the Pool (MFEE), Frequency of the MFE Structure in the Pool (Freq), Diversity of the Pool (Div), Minimum Adjusted Free Energy (AMFE), Minimum Free Energy Index (MFEI).

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-bantam	UUCGACGAAACUGGUUUUCACAGUGAUCCAGCAGAUUGCUCAAAGUCUGAGAUCAUUGUAAAAACCAAUUUUGUCCCC	78	17,94872	29,48718	23,07692	29,48718	41,02564	58,97436	1	0,777778	-33,4	-33,4	0,687059	0,82	-42,8205	-1,04375
mcr-mir-1002	UcguacaccaacaccugucaccucuUGUAGUCUGGUAUCUUUGUCUAAGUAGUUGAUACAUGAGUUGCAGAGGGUAUGGAGUAGUA	86	22,09302	17,44186	5,813953	26,74419	27,90698	44,18605	1,533333	3,8	-20,5	-18,9	0,106705	9,05	-23,8372	-0,85417
mcr-mir-10080	UCUGUCUCGUCUUUUCUCAGGUUGUCUCAAUCUUGCUUCAGUUUUGUCUGAAGACGUACAGACCagugagacaaaaagaaaccGU	85	15,29412	11,76471	18,82353	31,76471	34,11765	43,52941	2,7	0,8125	-19,1	-13,9	0,073241	20,99	-22,4706	-0,65862
mcr-mir-10089	UAUCAGCUCCCGAAGCAAAAUCAUGCCAAACAUAAUACAGGACGGUACUCGUGCAGGGAGAUAAUUUGCUGUUUUGGGAUGCUGCUG	87	25,28736	28,73563	20,68966	25,28736	45,97701	54,02299	0,88	1,222222	-22,8	-16,84	0,043074	18,63	-26,2069	-0,57
mcr-mir-10141	agcccGCAGCCUUGUGCAGUACagaggaaauaaaagaagaaacacgCAUUCGGUCUUCUUCAGUCAGCAUAUGGCUCGGAAA	82	15,85366	13,41463	17,07317	18,29268	32,92683	31,70732	1,363636	0,928571	-23,7	-22,7	0,301246	7,68	-28,9024	-0,87778
mcr-mir-10228	CAUUAGUACUGUGAUAUGUCAGUACACACGACAAUGAGUAUUGUACCAUGUCAGCACAUUAUUAGUC	94	19,14894	28,7234	18,08511	34,04255	37,23404	62,76596	1,185185	1,058824	-27,3	-27,3	0,173696	5,07	-29,0426	-0,78

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UUGUACUGUGUGUCAACAUUAGUACUG															
mcr-mir-10237	UCCAUUGUUAGUUUUGAGUGAGCUAGAAAGGGGUUAAAACUUCUUGCAGCAGGGACUGGUUUGUGGCACAUAUUUCAGCCUCucgacuaauaauaau	97	22,68041	19,58763	14,43299	27,83505	37,1134	47,42268	1,421053	1,571429	-23,8	-23,8	0,115043	18,95	-24,5361	-0,66111
mcr-mir-10325	AAAAUUAUCAUCGUCUUCUAUACAAGUGGCAUUCUCCUCGCCAUUAUUAUCAGCAGCAAAGGCGUUUUGCUAACUUGUCAAACAUGUGAUAAUAUA	96	14,58333	31,25	20,83333	33,33333	35,41667	64,58333	1,066667	0,7	-18,7	-18,7	0,080867	8,79	-19,4792	-0,55
mcr-mir-10379	AGUAACACAGUUAUUUUUCAAACAACUCAAACCAGGAAUAACAGACUGUUUUGUUCGUUGAACUAUGAUUGUGUUGCA	78	16,66667	33,33333	16,66667	33,33333	33,33333	66,66667	1	1	-24,4	-24,4	0,273807	6,43	-31,2821	-0,93846
mcr-mir-10456	UUUCUGUCAUACUAGAUGCAGGAUAUUUCUGUCAUACUAGAUGCAGGAUAUUUAUGACAUACUAGAUGCAGGAUAUUUCUGUCAUACUAGAUGCAGGAU	99	20,20202	29,29293	15,15152	35,35354	35,35354	64,64646	1,206897	1,333333	-32,6	-32,6	0,295291	5,75	-32,9293	-0,93143
mcr-mir-10457	AAGCAAAGAGUUUUUGACUACCAaucaaaauaguauuuuaacAAGUUUGCaauuauucuuuguuuguuguguguc uACACGACUCUUUGGCA	92	9,782609	16,30435	10,86957	14,13043	20,65217	30,43478	0,866667	0,9	-19,7	-18,9	0,188376	10,01	-21,413	-1,03684
mcr-mir-10698	uuuuaggaGAGGAAUUGCUGAGUUCAUGCAUGGCUUCUUUAGUAA	87	18,3908	22,98851	17,24138	32,18391	35,63218	55,17241	1,4	1,066667	-20,4	-20,4	0,075656	7,96	-23,4483	-0,65806

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CGAGGUUCAUAUUCAUGAUAAGCUGACAUUCAUCUUCUAUCC															
mcr-mir-106b	CAGAGCGGGUAUCCUCUGUGGGUACCCCUUGUCACUGGCAGGACCGCACUGUGGGUACCCCUGUC	65	30,76923	13,84615	32,30769	23,07692	63,07692	36,92308	1,666667	0,952381	-27	-22,5	0,153722	17,97	-41,5385	-0,65854
mcr-mir-10717	GCGACACGGAUGCACACACACCUGCGCGCGCCAAGAGCAGUGGAGGUGAAAUAUUGUUUCGGUUAACAAAGGGCACAGCUCAGUGUGUUGCUGUGUGUU	99	31,31313	24,24242	22,22222	22,22222	53,53535	46,46465	0,916667	1,409091	-36,3	-35	0,209813	4,21	-36,6667	-0,68491
mcr-mir-10738	GUCCCAGUAACUGACCACUCUGACGUCUCUCCGCCCUUCCGGGUGCUGCUGUCUGCUUUGUAACUGAUGACGUCAGUGGGUCACGUGUAGCUGGUGU	97	27,83505	13,40206	28,86598	29,89691	56,70103	43,29897	2,230769	0,964286	-36,5	-35,1	0,181441	6,85	-37,6289	-0,66364
mcr-mir-10761	CUGGUCUGUGCAGACUACUAGUACGGUGACGAUGGUUGAAUUUGUUCUUGUCACCAUUGUGACAGAUUCUGAGCGCACAGUACUAC	86	25,5814	22,09302	20,93023	31,39535	46,51163	53,48837	1,421053	1,222222	-24,9	-19,7	0,050962	23,36	-28,9535	-0,6225
mcr-mir-10863	UCGAUAUACAACCCUACGAACAUCCCCAUGACCAAGUGAUAUCACCUUUGACUUCUUUGUGGGCACGAUGAUGCUUGUAAGAUUGUUUAUAUG	93	18,27957	26,88172	22,58065	32,25806	40,86022	59,13978	1,2	0,809524	-19,7	-17,9	0,1266	11,6	-21,1828	-0,51842
mcr-mir-10903-1	CUGCCACUUGAACGCUCAACAGCUCAUCUUCCGACUCGCUUGUGUCGGCCUCAGACCCACUGGCCUCA	95	24,21053	12,63158	35,78947	27,36842	60	40	2,166667	0,676471	-34,4	-34,4	0,328396	6,79	-36,2105	-0,60351

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CUGCUGUCUGCUGCGUUCCUGUGGUGG															
mcr-mir-10903-2	CUGCCACUUGAACGCCCAACAGCUCAUCUUCCGACUCGCUUGUGUCGGCCUCAGACCCACUGGCCUCACUGCUGUCUGCUGCGUUCCUGUGGUGG	95	24,21053	12,63158	36,84211	26,31579	61,05263	38,94737	2,083333	0,657143	-33,6	-33,6	0,309438	7,34	-35,3684	-0,57931
mcr-mir-10903-3	CUGCCACUUGAACGCCCAACAGCUCAUCUUCCGACUCGCUUGUGUCGGCCUCAGACCCACUAGCCUCACUGCUGUCUGCUGCGUUCCUGUGGUGG	95	23,15789	13,68421	36,84211	26,31579	60	40	1,923077	0,628571	-30,3	-30,2	0,116672	10,54	-31,8947	-0,53158
mcr-mir-10918	GACAGGACAGAGAUUAAGGAguguuaaaauaguuugaagUAUUGGAAACUGGGUGUUCACAUAUAAGCUAUGUUACUCGAUAAUGCUCUUCCUUGC	96	18,75	23,95833	13,54167	23,95833	32,29167	47,91667	1	1,384615	-23,2	-20,8	0,051911	9,44	-24,1667	-0,74839
mcr-mir-10967	AACUGUACACUGCAUACUGUACAAUGUAGCUUGUCGGAUGAACUGUGAACUGCAUACUGUACAAUGUAGCUUGUCGGAUGAACUGUACACUG	92	22,82609	28,26087	19,56522	29,34783	42,3913	57,6087	1,038462	1,166667	-21,6	-20,2	0,048588	15,84	-23,4783	-0,55385
mcr-mir-10a	CGGUGCAAGACCUACCCUGUAGAUCCGaauuuguguaauauuuuaacUACAAAUUCGUGUUUGCACGGUAAGGCCUCGCAUCU	83	18,07229	16,86747	21,68675	19,27711	39,75904	36,14458	1,142857	0,833333	-33	-29,9	0,107106	4,44	-39,759	-1
mcr-mir-10b	AUGAGAGUGUGAGUGGCUUUACCCUGGAGAACCGAGCGUGUGUGAUCAUGACGUCACAGUUCGUUU	93	31,1828	20,43011	19,35484	29,03226	50,53763	49,46237	1,421053	1,611111	-40,6	-40,6	0,254812	9,91	-43,6559	-0,86383

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CUGAGGGUCAAGUCGCGAUACUCUGUU															
mcr-mir-11	GACCUGGGAGAGCCGUGGCCAGCUGGAGACAUCCCUGGAGCUCUGGCUGUGCCGGGUGGAUUUCGUGCCAUGCAGUCAGCCUCUCCAGAUG	91	35,16484	15,38462	28,57143	20,87912	63,73626	36,26374	1,357143	1,230769	-35,2	-21,3	0,010022	23,33	-38,6813	-0,6069
mcr-mir-11591	uuuucGGGUACGUGAAACACCUUUACGAUUCGUUAUCCUUAGGCUGUGCUGUAAGUGUACUUUGAUAACGGUUCGGCAACAGGUUGAUUGUACCCGACAU	100	24	22	19	30	43	52	1,363636	1,263158	-33	-31	0,123962	9,74	-33	-0,76744
mcr-mir-1175	UGAUCAGGUGUGUUAUGUAGUGGAGAGAGUUUUAUCUCAUCAUGAGCCUCAGAAGCAGGUGAGAUUCAACUCCUCCAACUGCAGGCUAUACCUGAAAC	98	24,4898	27,55102	20,40816	27,55102	44,89796	55,10204	1	1,2	-42,7	-38,6	0,079856	5,62	-43,5714	-0,97045
mcr-mir-12	UGUUUCUACAUAUCUGUGGAAUCUUGCAGCAUCAUGUGCAUGUUGGUGGUGGUCAGACUGUGAGUAUUACAUCAGGUACUGAGAAUCU	88	26,13636	22,72727	15,90909	35,22727	42,04545	57,95455	1,55	1,642857	-21,2	-14,6	0,061401	34,13	-24,0909	-0,57297
mcr-mir-12037	UGGUAACUCAUUCUGUCUUCUCUUCCAAAAACCAGCAAAUGUGAAAUUGUGUAUGAGCAGUGGGUAUAUCUUUUUUGGUGGGACAAAUGAGUUAAAA	97	21,64948	29,89691	14,43299	34,02062	36,08247	63,91753	1,137931	1,5	-22,2	-21,7	0,076697	11,37	-22,8866	-0,63429
mcr-mir-12093	UACGGUCAAUAGCUAUCCCCAGGGUaauguuauuuuugcuuuauugCUU	81	14,81481	13,58025	23,45679	22,22222	38,2716	35,80247	1,636364	0,631579	-26,4	-26,4	0,139195	7,63	-32,5926	-0,85161

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CUAACUUCAGCCCCUGGGGUAGCCUUACCUUU															
mcr-mir-12096b	UGCUACUUCGUGCAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUAUGAGGUAGGGCAAAAUUAUCACCGAUUACCCGAGGUAACG	85	23,52941	27,05882	21,17647	28,23529	44,70588	55,29412	1,043478	1,111111	-29,6	-29,2	0,079903	7,54	-34,8235	-0,77895
mcr-mir-12193	UUUAAAGAAUUCAUCUUUAGAUCAUAACUGUUUAAGCAGUACAGACCAGUUUUAAACCGGUCCUUUCUGUCUAAUGUUCUGGAAAAGAUCUUUCUUUGUC	100	15	28	18	39	33	67	1,392857	0,833333	-20	-18,8	0,080489	17,54	-20	-0,60606
mcr-mir-12265	AGAUUCAGCCGUCUUGCAGCUGAAGCCAUACCACGUGAGACUUAGACUGAGGACACGCUGAAGCA	65	26,15385	29,23077	26,15385	18,46154	52,30769	47,69231	0,631579	1	-20	-17,1	0,213126	4,96	-30,7692	-0,58824
mcr-mir-12293	gcugccgUCUCCCUUCUACAUCCGCCUCUUGAUCUACUACAACUACGAGCACGAGGAGAUGUUACAGAGGAGAUCGGCCAU	81	18,51852	23,45679	27,16049	22,22222	45,67901	45,67901	0,947368	0,681818	-27,4	-27,4	0,349688	3,61	-33,8272	-0,74054
mcr-mir-12313	uaggucacgugacauguuAGCAUCUUGACAUAAAGGAAGUCAGUGUGUCUGUAAUGUGUAACAUGUCUCAUUACGAA	77	16,88312	24,67532	11,68831	23,37662	28,57143	48,05195	0,947368	1,444444	-19,1	-18,7	0,051013	5,78	-24,8052	-0,86818
mcr-mir-12322	agaagaaaagagaaguuGAUCAAACAGCCAACUGGGUUAUCCCGUGUGUUGGGACUCGCCUGUUCUCugguCAUUUCUCUUUCUCAC	87	14,94253	10,34483	16,09195	16,09195	31,03448	26,43678	1,555556	0,928571	-27,7	-27,5	0,020633	17,77	-31,8391	-1,02593

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-12352	UUAUUGCUGUUAUGGUGUUAGUUCAGGUGAUUCUUAUGCAUGAGAAGUUAUGAGUUAACACCAUUACCACAacuu	75	20	25,33333	13,33333	36	33,33333	61,33333	1,421053	1,5	-21,8	-21,8	0,14281	5,72	-29,0667	-0,872
mcr-mir-1250	gaugacgacgguGCUGGAUGUGGAUAUGGAAUACGGACAGCUCCGUUUCUGAACAACAUCAGAACCUGUAGGUCCCA	77	22,07792	23,37662	19,48052	19,48052	41,55844	42,85714	0,833333	1,133333	-22,1	-19,8	0,186986	22,97	-28,7013	-0,69062
mcr-mir-1256	cucuggccacugaGGCAUUGACUUCUCUUCAUGGCAUCUCAAAGGACAAGUCAAGUCAUGUGGUCAAAC	69	17,3913	23,18841	18,84058	21,73913	36,23188	44,92754	0,9375	0,923077	-22,5	-22,5	0,137838	3,93	-32,6087	-0,9
mcr-mir-1277	CACGUGCAGAUGUAUUGACAguuucuguguauauauauauauauauguacgauGCAACAGCACAUCUGCACUAC	74	10,81081	17,56757	16,21622	10,81081	27,02703	28,37838	0,615385	0,666667	-24,9	-21,6	0,120471	14,07	-33,6486	-1,245
mcr-mir-1278	AUUAAUCAGGAGCAGGUUUAUUGCAUGAGGUGUAGUAUUGACUGUAGUACUGUGCAUAUCAGCACCACAAAUCAUGCAGGAUGAAGACUGUUCGauugug	100	24	28	15	27	39	55	0,964286	1,6	-29,4	-28,6	0,050476	16,75	-29,4	-0,75385
mcr-mir-1304	CUUCAGGUCGUCACGGAAUGAAUUCUCACUGUAGCCUCGGCUCAGCGUGAUUUCAAACACGUCACAGCCUGCUG	74	22,97297	21,62162	29,72973	25,67568	52,7027	47,2973	1,1875	0,772727	-24,6	-22,7	0,479157	2,33	-33,2432	-0,63077
mcr-mir-130a	AUCCCUCCCUGCUCUGUUCCUUGUAUCUGCUCAUAGUGCAAUGUUAAAAGAGUACCUUUUGAGUUCUCUUGAGGUGACAAUGGAAAAAGCAGGAGGGCU	99	23,23232	24,24242	21,21212	31,31313	44,44444	55,55556	1,291667	1,095238	-31	-29,3	0,028824	19,37	-31,3131	-0,70455

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/ mol)	MFEE(kcal/m ol)	Freq	Div	AMFE (kcal/ mol)	MFEI (kcal/ mol)
mcr-mir-133	CUUCUAUAGCUGGUUGAACUCGGGCCAAAUUGUUGAAGAGCCUUUCAUUUGGUCCCCUUCAACCAGCUGUAGUUA	75	21,33333	21,33333	24	33,33333	45,33333	54,66667	1,5625	0,888889	-35,5	-35,1	0,186674	6,73	-47,3333	-1,04412
mcr-mir-133c	UAACUACAGCUGGUUGAAGGGGACCAAAUGAAAGGCUCUUCAACAAUUUGGCCCGAGUUCAACCAGCUAUAGAAG	75	24	33,33333	21,33333	21,33333	45,33333	54,66667	0,64	1,125	-30,4	-28,9	0,184949	4,61	-40,5333	-0,89412
mcr-mir-137b	AGUUCCAGUCGGUUACGGGUAUUCUUGGGUAAAUAAUACAUUGAACAGUUGUUAUUGCUUGAGAAUACACGUAACUACCUGGACGU	86	23,25581	27,90698	16,27907	32,55814	39,53488	60,46512	1,166667	1,428571	-33,1	-33,1	0,033251	6,83	-38,4884	-0,97353
mcr-mir-14	UAUAAAGGGAAGACAAUGAUCUGAGAGGUGCUGGCUGUACGCUGCUGAACUGAUCUCACUCucagucuuuucucucucuuuuuu	85	20	20	14,11765	17,64706	34,11765	37,64706	0,882353	1,416667	-21,6	-18,47	0,04849	12,49	-25,4118	-0,74483
mcr-mir-1421ai	UUGUAGUCAGCAGGUCAGGUGUGGAAGCACUUUGCCAGGUUUUCCCCAUGGGUCCUGCGACUAGUG	66	31,81818	16,66667	22,72727	28,78788	54,54545	45,45455	1,727273	1,4	-24,4	-23,1	0,219346	4,86	-36,9697	-0,67778
mcr-mir-143	AUGUGUGAGCAUGACAGGAAUGAAAACUGUGCAAACCUCUGUGUGUGCAGUGCUGCAUCUCACAUUA	67	25,37313	28,35821	19,40299	26,86567	44,77612	55,22388	0,947368	1,307692	-20,7	-20,5	0,448845	1,84	-30,8955	-0,69
mcr-mir-146b	UUUAGGAACACGUUCUCAGAUGGAAGUUUCAGACCCUGUAUUCUGGAGGUUGAGAACUGGUUUUGAGCAAGUGCUUCCUUUU	82	25,60976	21,95122	17,07317	35,36585	42,68293	57,31707	1,611111	1,5	-24,2	-24,2	0,193626	6,98	-29,5122	-0,69143

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-153-1	AACCAAAGCCUUAGCGUAGGUCAAGAAGAGUGUUAUAACCAAAUCAUCGUGCUGucauuuuugugauuuugagCUGACAGCUAGAUGCGUUGAAU	95	18,94737	26,31579	15,78947	18,94737	34,73684	45,26316	0,72	1,2	-21	-14,1	0,097127	11,84	-22,1053	-0,63636
mcr-mir-153-2	AUACCCUCUUCCCAGGCAGCUUUUGUGAUUCAGCAAUUGUACAGCUAUCAAAUUGCAUAGUCACAAAAGUGAUCGGGAGGCGGGGAC	87	24,13793	27,58621	22,98851	25,28736	47,12644	52,87356	0,916667	1,05	-37,9	-37,9	0,256161	6,4	-43,5632	-0,92439
mcr-mir-1599	ACAUUACUCGCUCUCUGAGAAUcuggagggaggaaaaaaaaacgcuuAUUUUUUAAGCUCCAGAUGUUGACAGCAGGCGUAACCA	85	12,94118	20	16,47059	21,17647	29,41176	41,17647	1,058824	0,785714	-20,8	-16,6	0,027501	14,66	-24,4706	-0,832
mcr-mir-15a	aaauguuuauccuagcagcacagaauggcAAAAAUAUAGGGGUCCCUUUAAGAAGGAUAUUGGACGCCUGUGUUUUGUGCUGCUAGGGUAAGCAAUU	97	19,58763	19,58763	9,278351	21,64948	28,86598	41,23711	1,105263	2,111111	-47	-47	0,037871	8,59	-48,4536	-1,67857
mcr-mir-1610	ACGAAAAUAAUAUCAGCACUUUGCUGUGGCUUGUGGUGGAACGACAAACCAcuuucaacccccccccccccaauacaUUAAAGUGCCCAUAUAUGUUUCA	100	15	24	14	21	29	45	0,875	1,071429	-21,3	-17,3	0,147086	14,93	-21,3	-0,73448
mcr-mir-1621	GCGGUACGUGCGAGCGGGCUCUCAACCGGCUGCCUCGGUGGUAAGCGGUGUUGGAGGCUGCUGACCUACUGG	72	40,27778	12,5	26,38889	20,83333	66,66667	33,33333	1,666667	1,526316	-32,6	-32,1	0,106716	4,49	-45,2778	-0,67917

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-1628	AAUUAACUUGAAUUAACGCGAAGAAGAUGUCUUUACACUACUUUGUUUCCUUCCUUUUGUAAGAGCUCUUCCUGUUCGUGUGUGAGAAUCACGCUUACAA	100	17	26	20	37	37	63	1,423077	0,85	-19,3	-19,3	0,079518	10,73	-19,3	-0,52162
mcr-mir-1693	ACCUUUAAGUGGCUAUUGAUGUCACCAAGAAAUGGUGCAAAGGAUGAAGCUGUAGCUGUGUUUCCUAAUGGCUGCACAAUAUGUUAUUUAAAAGU	95	23,15789	30,52632	14,73684	31,57895	37,89474	62,10526	1,034483	1,571429	-25,5	-25,5	0,09906	5,04	-26,8421	-0,70833
mcr-mir-1710	GAUCUGUUUCUCAUCUGCUGCAUAACCGUGUGUGACACAGGACACAGCGGUAGCACACAGAUACAAAAGGGA	72	25	30,55556	23,61111	20,83333	48,61111	51,38889	0,681818	1,058824	-21,5	-21,5	0,221235	4,85	-29,8611	-0,61429
mcr-mir-1761	GACCAAGCAUAACAUAACGACGGAGGACAAUGGAGGACAGGGGUCACUUUUUUCCCCUGACCUUCACUUUUUCUUAUGUGAUCUUGUGG	89	23,59551	24,7191	22,47191	29,21348	46,06742	53,93258	1,181818	1,05	-28,5	-22,9	0,114468	11,78	-32,0225	-0,69512
mcr-mir-187	GAAAAUUAGAUGAUGUGCUGGUUGCUACAACACAGGACAAUUCUAAACUGAUUCGUAUUCUGCCUGUGCAAUUGCAAGCCCACAACAGAGAAUUGGU	97	21,64948	31,95876	19,58763	26,80412	41,23711	58,76289	0,83871	1,105263	-22,1	-19	0,108197	9,61	-22,7835	-0,5525
mcr-mir-190	ACCCGCUUCUGCUAGAUAUGUUUGAUAUAUUUGGUGCAGUUGUCGCGACGACCAAGUAGUCAAACAUGUCAGAGCAGCGACG	82	25,60976	25,60976	21,95122	26,82927	47,56098	52,43902	1,047619	1,166667	-32,5	-32,3	0,080048	9,84	-39,6341	-0,83333

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-193-1	UUCUAAUAUCAUGGUAUCAGCAUGACUCGUAUGUGAUAUACUGGCCAGCACAAUUAGUGUCUAAUAUCAUGGUAUCACCAUGACUAGUAUGU	92	18,47826	29,34783	18,47826	33,69565	36,95652	63,04348	1,148148	1	-20,8	-20,8	0,129928	10,37	-22,6087	-0,61176
mcr-mir-193-2	GCCAGCACACUUACUGUCUGGUAUCAUGGUAUCAGCAUGACUCGUAUGUGAUAUACUGGCCAGCACAAUUAGUGUCUAAU	80	21,25	26,25	22,5	30	43,75	56,25	1,142857	0,944444	-21,7	-21,7	0,239175	6,47	-27,125	-0,62
mcr-mir-193-3	CUAAUAUCAUGGUAUCAGCAUGACUAGUAUGUGAUAUACUGGCCAGCACAAUUAGUGUCUAAUAUCAUGGUAUCAA	76	18,42105	32,89474	17,10526	31,57895	35,52632	64,47368	0,96	1,076923	-19,8	-19,8	0,11962	11,25	-26,0526	-0,73333
mcr-mir-194	GUUUGGUCAUCUUCAGUUCCAUGCCAGCCCCACCUGGCAGCCAGUGGAGGUGGUGUAGaaguggucacgugaccagcc	78	23,07692	11,53846	20,51282	19,23077	43,58974	30,76923	1,666667	1,125	-32,8	-32,8	0,088541	4,32	-42,0513	-0,96471
mcr-mir-1947	AUCUGAAUGAAGGCUAGUGCACUGAGCUAGCUCUCUGCGUCAUCAACUGCAAUGAAGCAUAGAGGGAGGCAGCGGUGGAGUACAAUUCUUCAUAA	95	27,36842	29,47368	20	23,15789	47,36842	52,63158	0,785714	1,368421	-27,3	-11,2	0,050373	20,57	-28,7368	-0,60667
mcr-mir-194b	GUACUGCAUCAGCCACGCGCUGCGUUGUAACAGCAUCUCCAACUGCGGCGACCACGACGACAGCGACGAGCGCAAAUGUAGGUC	84	27,38095	25	32,14286	15,47619	59,52381	40,47619	0,619048	0,851852	-28,7	-27	0,178572	5,44	-34,1667	-0,574
mcr-mir-196c	GGUGUGUUGCUGACAACAACAUCAAACCACCUGCCGAACAUCUGG	81	24,69136	23,45679	29,62963	22,22222	54,32099	45,67901	0,947368	0,833333	-24,7	-24,7	0,061423	10,88	-30,4938	-0,56136

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CCCAGGUGCUGGUGUUUCAUGCUCCAUCAACACGGG															
mcr-mir-1970	UUGUUAUACCCUGUGAUAAACUCUUUGGGUUGGGGGCUUAAAUAUCUUUCUUCUCAGAUUGUGUCACUGGGGAUAAUUA	79	22,78481	21,51899	15,18987	40,50633	37,97468	62,02532	1,882353	1,5	-22,3	-22,1	0,116729	7,91	-28,2278	-0,74333
mcr-mir-1984	UGUCGCCGUGCCCUAUCCGUCAGGAACUGUGAUCUCGCGAAACACAGGGUCUGGCGGUUGGGCCUCGGCGCUG	73	34,24658	13,69863	30,13699	21,91781	64,38356	35,61644	1,6	1,136364	-37,9	-37,9	0,133827	2,65	-51,9178	-0,80638
mcr-mir-1985	UGCCAUGCCAUUUUUAUCAGUCACUGUGUGUUGUUAAAGUcacagugaugaugauaauggcuUGAUG	67	14,92537	13,43284	10,44776	28,35821	25,37313	41,79104	2,111111	1,428571	-28,6	-28,6	0,286882	2,78	-42,6866	-1,68235
mcr-mir-1990	GGCUGCGAGUUGUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCUACCCCUCCCGGGACUACGUCAACGUACUACCACGCGCAUCUCCAAGU	95	27,36842	20	29,47368	23,15789	56,84211	43,15789	1,157895	0,928571	-39,9	-39,5	0,101035	5,08	-42	-0,73889
mcr-mir-1992	CUAAGGGCAUGUGUCUAGUCAGUGGUUGACUGCUUGGUAUUCUAAAUGUAUCAGCAGUUGUACCACUGAUUUGCUACGUGCACCUCAC	88	23,86364	21,59091	21,59091	32,95455	45,45455	54,54545	1,526316	1,105263	-41,8	-41,4	0,125422	3,52	-47,5	-1,045
mcr-mir-1994	UGGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCAUGUGUGAUGACGUCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGAGACCGCUAA	90	31,11111	20	23,33333	25,55556	54,44444	45,55556	1,277778	1,333333	-40,6	-40,6	0,538688	3,53	-45,1111	-0,82857

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-1994a	CAAAAGCUAUUUCUCAGGGGCGGUCACUCUGAUCUCCAUGUGCUCGCACCAGCAUGAGACAGUGUGUCCUCCCUUGAGGGAUGGGCUUAUA	91	26,37363	20,87912	26,37363	26,37363	52,74725	47,25275	1,263158	1	-44,3	-44,3	0,178398	5,12	-48,6813	-0,92292
mcr-mir-1c	AGUACAUACUUCUUUACAUUCCAUAGCUUUGCAAGAACAUAUGGGAUAGCAAAGAAGUAUGUGCC	65	18,46154	33,84615	18,46154	29,23077	36,92308	63,07692	0,863636	1	-27,1	-26	0,4687	2,23	-41,6923	-1,12917
mcr-mir-2	AAGGCGAAUGAAUGCUCUGUCUGUUGGUAUGCGAUAGGACCCAGUUUUUCAAAAGACUGUGUUGCUAUGUCCCAGACAUGUUCUACUUUCGCUAA	95	23,15789	24,21053	20	32,63158	43,15789	56,84211	1,347826	1,157895	-26,9	-26,9	0,129077	12,83	-28,3158	-0,6561
mcr-mir-2001	AAAGGAGAACUGUGUUGCUCUUGAUCGGAUGCUGCCAUUUUGUGACCGUUACAAUGGGCauugacagaaaaacaaaugcuCCAUG	85	21,17647	16,47059	15,29412	22,35294	36,47059	38,82353	1,357143	1,384615	-20,5	-20,5	0,029997	7,42	-24,1176	-0,66129
mcr-mir-202	CAGAGGCauagggcaugugcggggccuCGACCAUAGCCAUAUUAAUCAAACACGCGGGGCCCUAGGUAGAUGCCUCGUCUGCCUGCCCCUAGGCCUAAG	99	20,20202	19,19192	26,26263	14,14141	46,46465	33,33333	0,736842	0,769231	-39,3	-39,3	0,05055	8,37	-39,697	-0,85435
mcr-mir-204	CCACUCACCAGUCGCUGGCAAUGGACGCUGGGAAGGCAAAGGGAACCUCGCGCGUGCGUUCGagcgaagggagagagu	78	26,92308	16,66667	24,35897	11,53846	51,28205	28,20513	0,692308	1,105263	-30,4	-24,1	0,011827	6,78	-38,9744	-0,76
mcr-mir-2040b	AGAGCAAGAGUCAGGUCAGCUACGACUGUAACACUAACUAUUUAUGAUAAGGUAUCGUGUGUAGCUA	95	24,21053	32,63158	15,78947	27,36842	40	60	0,83871	1,533333	-32,6	-32,6	0,506504	3,85	-34,3158	-0,85789

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GAGUCUUAGCUGUGAUGACUAAUGCAAA															
mcr-mir-216a	GUGUUUGUCUAAUCUCAGCUGGUAAUUCUGAGUGGAGUUCUGCACACCUCAAGUUACUAGCCGAGAUUACAUAAAUAU	78	20,51282	26,92308	19,23077	33,33333	39,74359	60,25641	1,238095	1,066667	-30,5	-30,5	0,146188	3,64	-39,1026	-0,98387
mcr-mir-216b-1	CGUAGGAAGAUGAGCCAGGAUUACAAGAUGGUUGGGCCUGCGGCCCUAAUAUCAGCUGGUAAUCCUGAGUGAGCUUGCCUCAG	83	31,3253	24,09639	21,68675	22,89157	53,01205	46,98795	0,95	1,444444	-31,3	-30	0,152237	7,92	-37,7108	-0,71136
mcr-mir-216b-2	UGUCACUGUGCAUGACACUUACCUAUAGAGAUGUGUAUUGUCACUGUGCAUGGCACCCAGUAUGGUACCUAUAGAGAUGUGUAUUGUCACUGUGCAU	97	23,71134	23,71134	19,58763	32,98969	43,29897	56,70103	1,391304	1,210526	-26,6	-16,37	0,100351	18,69	-27,4227	-0,63333
mcr-mir-216b-3	UACCUAUAGAGAUGUGUAUUGUCACUGUGCAUGACACUUACCUAUAGAGAUGUGUAUUGUCACUGUGCAUGACACUCACCUAUAGAGA	88	20,45455	28,40909	19,31818	31,81818	39,77273	60,22727	1,12	1,058824	-26,2	-26,2	0,289845	6,27	-29,7727	-0,74857
mcr-mir-2238k	CGGCUUGGAUGACAGGUUAGAUGCGAAAUCUUCAAUGACUGAACAGUGCAAUGCAGUUUUCGUGUCUAAACGUGGUUUgcaagugu	86	24,4186	23,25581	15,11628	27,90698	39,53488	51,16279	1,2	1,615385	-27	-26,2	0,149473	4,18	-31,3953	-0,79412
mcr-mir-2253a	GGAUAAACAGCUUGCACGCAUGGCACUGCUGAAGGUUCAUGCAUGUAUAGCAGCAACAUGUGUCAAGUGCCUUUAAGC	78	25,64103	28,20513	21,79487	24,35897	47,4359	52,5641	0,863636	1,176471	-22,7	-22,2	0,18444	5,69	-29,1026	-0,61351

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-2254	ACAUUAUAAUUCUCGGCAGUCUUGCGGUUUGUACUAUGCAAAGUAAGUACUGCCGACCAUAUAUGAAGAA	70	20	31,42857	18,57143	30	38,57143	61,42857	0,954545	1,076923	-21,8	-21,4	0,07388	7,52	-31,1429	-0,80741
mcr-mir-2288	cccaccccaccccacgcCCUCAUCCACCUUCGACUUCUGAGCUCGAUCGUCGUUGCCUACAGCAGguaguaggugugugugugugggggggaguaGG	99	11,11111	8,080808	18,18182	13,13131	29,29293	21,21212	1,625	0,611111	-43,8	-42,9	0,179465	5,79	-44,2424	-1,51034
mcr-mir-22b	AUUAGCCUCAUCAUAGUUUACUGGACUGUGGUGUGGACAGCAGCGUUUGCAGCCUCACCUACAGUUCUUCAACUGGACUGAGCUCGC	87	24,13793	20,68966	26,43678	28,73563	50,57471	49,42529	1,388889	0,913043	-29,4	-28,1	0,059837	13,38	-33,7931	-0,66818
mcr-mir-2304-1	AGAACACAAACGAGAAUCCUAGGUAUAUGUGUUUUGUAUUGUGAAGACACAACACGUGUGGACGUAGUgguugugugguugugugug	87	19,54023	26,43678	11,49425	20,68966	31,03448	47,12644	0,782609	1,7	-24,4	-21	0,020111	11,06	-28,046	-0,9037
mcr-mir-2304-2	AUACGCUgguuguguggguugugugggcaauuuuuauuuuuaucaucguGUAAAACUUUGCCAAAAAAAGUCACAUUCCACAAUCCAGCGGUC	93	7,526882	20,43011	15,05376	11,82796	22,58065	32,25806	0,578947	0,5	-30,4	-26,3	0,226556	12,43	-32,6882	-1,44762
mcr-mir-2325c	CUGUACUGUGCAAUuuuuuuggguuguuuuuuuucuuuugcuugaagCAGACGAACUUGUAAUAACGAAAAAAACCCAAGAGAAAUAACUACAUAAAU	98	9,183673	31,63265	12,2449	13,26531	21,42857	44,89796	0,419355	0,75	-20,8	-14,6	0,057963	16,12	-21,2245	-0,99048
mcr-mir-234	ACUCCGGCACUUCCGACAUGCAAUAAUUAAAGAUUCUUAAUcaguu	83	14,45783	22,89157	16,86747	21,68675	31,3253	44,57831	0,947368	0,857143	-18,5	-17,5	0,15476	7,04	-22,2892	-0,71154

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	uuuuccuguuuugauUAUUGCUCGAGAAUGACGGCUG															
mcr-mir-2390	aauuuuccugAUUUUUCUACACCUGCAUCCCAACACAAGUGGGAUCUACUAAAUCCUUGGGUCUUGuaguugugugguuuuuguugaaaaacaagaaaaua	100	9	14	15	18	24	32	1,285714	0,6	-24,1	-24,1	0,203585	18,05	-24,1	-1,00417
mcr-mir-242	AAUUUGUUAUGAACAAAUGCUGUAAGUUGAAUCUUGCCUUUUUUCAAGGGCAAGGAUUUGCGUAGGCACUUUGCAUGACAAUGU	84	22,61905	27,38095	14,28571	35,71429	36,90476	63,09524	1,304348	1,583333	-27	-25,4	0,060999	11,38	-32,1429	-0,87097
mcr-mir-2434-1	UUGCCUACAAUGCCCUCAAAUCUGAGaguuuguugggguuuuuuuugaaaaaauguccGAACAUAUCACGUGAUAUAAGGUGACAUGUUGGACA	94	13,82979	21,2766	13,82979	17,02128	27,65957	38,29787	0,8	1	-26,6	-20,5	0,012933	15,5	-28,2979	-1,02308
mcr-mir-2434-2	GCCUUCAAGGCCUAUGAGGCUCuugcuaaauuuuaaaauaaaagccaguuguuggggguuuuuuuuaaucAGCAUGUGCCCCAUGGGCCUUGAAAGU	95	14,73684	10,52632	14,73684	11,57895	29,47368	22,10526	1,1	1	-37,6	-29,5	0,042743	12,24	-39,5789	-1,34286
mcr-mir-2444	UGGUCAAAACUAACUUCAACAACAAUAUAUCGUUGUUUCUUUUACCAUGGCACUAAGCCGugaaggugguuguguuguuuuuuguuuugaaaa	93	8,602151	20,43011	15,05376	20,43011	23,65591	40,86022	1	0,571429	-21,7	-18,9	0,098683	7,42	-23,3333	-0,98636
mcr-mir-247	gagggggaaacagAUAAACAAGUUGUACGGUUUGUCUUCGAGAGGGAGAAAAUCACUAGAGAAAAGUUUCUACCGACAACUUGAAGUUAUUUCCCCCCU	99	17,17172	28,28283	17,17172	24,24242	34,34343	52,52525	0,857143	1	-32,3	-30,6	0,021058	14,61	-32,6263	-0,95

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-2470	GCCAGAAAAACCUAAGCAUGACAAAAUAUCAUGCUUGUGUGGUUUUGGAUACUUGGAUUUUUCUCUC	67	19,40299	28,35821	17,91045	34,32836	37,31343	62,68657	1,210526	1,083333	-18,6	-18,5	0,281925	3,5	-27,7612	-0,744
mcr-mir-2491	GCUGCCaugaaacaacaacagcagcagcaacagcaacagcaagagGGAGCUGCUGAUGUGGAGAUUUUUCUGGCAGA	77	18,18182	7,792208	9,090909	14,28571	27,27273	22,07792	1,833333	2	-27,8	-25	0,10123	15,43	-36,1039	-1,32381
mcr-mir-250	CACUUGUCCCUGUGUACAGCACUUUAGUGAAUCACAGUCACCUGAGUAAAGAUGACUGCGCAGGGGCAACAC	72	23,61111	27,77778	26,38889	22,22222	50	50	0,8	0,894737	-26,4	-26,4	0,33034	11,12	-36,6667	-0,73333
mcr-mir-252	CCCAUAUCUCAGCAGCAACGGGUAGAUUUUUGUGCAACUAUCAAAAUAGUCUCGGUUGUAAAUUCACCUGCUCCCUGCUGCUGCCUUGCGAUAUAUC	97	18,5567	23,71134	26,80412	30,92784	45,36082	54,63918	1,304348	0,692308	-26,9	-26,9	0,313291	8,87	-27,732	-0,61136
mcr-mir-252a	CAUAACUUCUGGCCCAUUACUAAGUACUAGUGCCGCGGGAAGAUAACGUGUCAUGUCCCGUGGUUCUGGUCCUUACUACAGGGCGGAACUUGCA	94	25,53191	22,34043	25,53191	26,59574	51,06383	48,93617	1,190476	1	-37,6	-37,6	0,061669	5,2	-40	-0,78333
mcr-mir-2582a	GUGACAGCCUGUAUUUCACAGUGUUCAUAAUAUUUCAGCUCCGUUUUGCCUUUGUAGCGAUGUCCCUAGCAAGACUGCUGAAACACUGacuuguaaa	97	17,52577	20,61856	21,64948	29,89691	39,17526	50,51546	1,45	0,809524	-19,7	-13,6	0,037527	15,34	-20,3093	-0,51842
mcr-mir-2699	UUUUGAGCUGUUUGUGAUAUUCGGCAUUCUUUACUCccugucucuguuucucucucuccccaucccCCUCACAC	100	14	18	15	23	29	41	1,277778	0,933333	-19,4	-16,9	0,099228	8,03	-19,4	-0,66897

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CGAGAUAUCGAGAAAAAGACUCAGGU															
mcr-mir-277-1	CAACAGACAAAUGUGUCAACCGUAAAUGCAUuuucugcugcauuuuauugACACGAAAUGUCUGGAU	67	13,43284	28,35821	14,92537	14,92537	28,35821	43,28358	0,526316	0,9	-23,1	-23,1	0,480593	2,17	-34,4776	-1,21579
mcr-mir-277-2	cucccccucccacacacacacucaucugCCCGUUCAGUAAAUGCAUUAUUUGGGGAGGUAAUGCUGGGUGAAGGAAGGGGUUC	84	23,80952	15,47619	8,333333	17,85714	32,14286	33,33333	1,153846	2,857143	-25,5	-13,7	0,072633	12,27	-30,3571	-0,94444
mcr-mir-279	CUCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACACUGCAAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAGGACGU	91	23,07692	23,07692	26,37363	27,47253	49,45055	50,54945	1,190476	0,875	-39,9	-39,4	0,157559	5,72	-43,8462	-0,88667
mcr-mir-281	AAAUGACCUCACGCUGAAGGGAGCAUCCGUCGACAGUCAGAAAUGCAGCACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGA	88	25	30,68182	22,72727	21,59091	47,72727	52,27273	0,703704	1,1	-35,2	-35,1	0,187538	3,76	-40	-0,8381
mcr-mir-283	GCUAAAUCGUGAUCCGUGCUAUAUUUAUCCUUGCUGGAAGAAAGUUAUCGGAAGGGGGCAUCUCCGAUAAAAUAUCAGCUGGUAAACGAAUUGGA	95	25,26316	30,52632	16,84211	27,36842	42,10526	57,89474	0,896552	1,5	-25,4	-24,2	0,095817	6,58	-26,7368	-0,635
mcr-mir-285	UUGUGUACGACGCUCUGUCCAUCAGUCAACUGGCUUCCAAAGGUCUCGAAAGCUCUGUUACUGCUGUAGGGAGGCGUCAUCAUUA	85	24,70588	21,17647	24,70588	29,41176	49,41176	50,58824	1,388889	1	-22,3	-15,9	0,018167	14,62	-26,2353	-0,53095

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-2970-1	cgaAAUGCGGGUGGUGGACAAGGAUGUUCccugcacacagagacacaugAGUCGGUCGACCGAUCAGAUCAUCUCUUGAUCAACCUACAGCAUUCAG	97	20,61856	19,58763	17,52577	18,5567	38,14433	38,14433	0,947368	1,176471	-25,4	-16,4	0,010574	31,19	-26,1856	-0,68649
mcr-mir-2970-2	AGCAGGAGCCGGCCGGAGACGGCAAGCCUGGGUCCCGACAGUCAGCAGUUGGCUCCCCAUGGGUCUCUUGCCGGAUCAACCCGCUCCUACC	91	30,76923	17,58242	36,26374	15,38462	67,03297	32,96703	0,875	0,848485	-41,1	-41,1	0,129828	8,12	-45,1648	-0,67377
mcr-mir-297b	aaauauguaugugugcaugaacAUGCUUUAAAAUGUGUCAGUUGUAAGCUGUACAACUGAACAAGCUUUAAGAACAGAACUAUGAAAAAUCAUAGCA	97	13,40206	31,95876	11,34021	20,61856	24,74227	52,57732	0,645161	1,181818	-23,8	-23,8	0,133853	5,73	-24,5361	-0,99167
mcr-mir-29b	UUAAGAAUCUUGCAACAUAGCACCAUUAGAAAUGUUAGUUGUUGAGUAGAGUAGAUGGCUAAAUAUUUCUUACGGUAUUUUGCGGACUCUCAU	93	20,43011	30,10753	13,97849	35,48387	34,4086	65,5914	1,178571	1,461538	-19,8	-19,8	0,035107	6,69	-21,2903	-0,61875
mcr-mir-2a-1	UGCAAAGCUAUAGUGCUGACCAAGUGACUGGGAUGUGUACCUAAGUGUCAUAUCACAGCCUGCUUGGAUCAGUAUUGUGGUUUUUAA	87	25,28736	25,28736	17,24138	32,18391	42,52874	57,47126	1,272727	1,466667	-38	-37,6	0,220043	3,11	-43,6782	-1,02703
mcr-mir-2a-2	GAAAAGCAAAUGUGCAUGGAGCAAUCAAAGUAGUUGUGAUGUGUUUCUUGGCUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAAUUUUCUUGCA	99	21,21212	27,27273	18,18182	33,33333	39,39394	60,60606	1,222222	1,166667	-33,6	-31	0,110768	7,68	-33,9394	-0,86154

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-2a-3	UACGACUGCUGAGUCCACAUCAAAGAGGCUGUGACUUUGUGAUGCUGUAUCAAAUCACAGCCUGCUUUGGUGAGCUCUUUGCUGUCCAA	89	23,59551	22,47191	23,59551	30,33708	47,19101	52,80899	1,35	1	-36,2	-35,9	0,18632	8,53	-40,6742	-0,8619
mcr-mir-2b-1	UGCAAGAAAAUUGUGAAGAAGCUCAUCAAAGCUGGCUGUGAUAUGAAGCCAAGAAACACAUCACAACUACUUUGAUUGCUCCAUGCACAUUUGCUUUUC	99	18,18182	33,33333	21,21212	27,27273	39,39394	60,60606	0,818182	0,857143	-24,4	-24,4	0,305458	6,72	-24,6465	-0,62564
mcr-mir-2b-2	GAAGCGAGGCCAGCUCAUCAAAGCUGGCUGUGAUAUGACUGAACUCAACACAUCACAGCAUCUUUGAUGGACAGGUCCUAGCACU	85	23,52941	29,41176	25,88235	21,17647	49,41176	50,58824	0,72	0,909091	-31,5	-30,9	0,181124	5,11	-37,0588	-0,75
mcr-mir-2c	aaaagagaUUCGUCAACAUUGCCUGCUGCUUAUAAGACCUUUUAGCUUCAAUGUUUUAUGACAAGGUGCAAACAUGUUGACUuaagaaucucucuc	96	13,54167	19,79167	15,625	28,125	29,16667	47,91667	1,421053	0,866667	-27,8	-27,8	0,136659	7,8	-28,9583	-0,99286
mcr-mir-3131	UCUUAGCCAAUCAGAAAACAUUCCAUCAAGAAAGUGUGGUGUGGGAUGAGCACACACCUGACUCGAGGACUGGUGGAAUUUUCCAUGAAGUUGGUAACC	99	25,25253	30,30303	20,20202	24,24242	45,45455	54,54545	0,8	1,25	-27,7	-27,5	0,063458	7,98	-27,9798	-0,61556
mcr-mir-315b	UUUGCAGACUGCACUGAUAUAACAAUACCGCCGGAGGUCUCUUUUCUGCUUUGUGGACAUUUUGAUUGUUGUACAGUCCGCUUCUGCUUU	90	21,11111	17,77778	22,22222	38,88889	43,33333	56,66667	2,1875	0,95	-24,6	-24,6	0,280807	8,3	-27,3333	-0,63077

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-317	GGGAAGGAUACCAUUGCUUGUUCACAGUAAAUUGGACAUGUGAACACAGCUGGUGGUAUCUUUUUU	66	25,75758	25,75758	15,15152	33,33333	40,90909	59,09091	1,294118	1,7	-29,1	-29,1	0,162636	2,6	-44,0909	-1,07778
mcr-mir-3223	ugaaaagguuaugggaugaccuuuaccuuuuaccuuuaccuuacagAAGGGUCAACCGGUCAAGCUCAUUCAUGCAUCUUUCCC	84	8,333333	10,71429	14,28571	11,90476	22,61905	22,61905	1,111111	0,583333	-18,5	-18,2	0,011779	13,83	-22,0238	-0,97368
mcr-mir-324	uugAACUCGAUUGUGACGUCUACAUCACAUGGCuucuuuccccacugccccaGGUGUCUUGUGAAGCACAUCGAGUUUGC	80	18,75	16,25	16,25	21,25	35	37,5	1,307692	1,153846	-23	-21,4	0,113698	17,15	-28,75	-0,82143
mcr-mir-3299	ACCUUGGGGGUUUUGGAAGCUUAAGCUCCAGGUUGUUUCUUUCUGCUCUAACUUGCAGGAGAUCGUUCAUUGUUAAAGUCUGCAUAACCCCCAACCU	97	21,64948	20,61856	23,71134	34,02062	45,36082	54,63918	1,65	0,913043	-31,4	-30,2	0,042103	13,35	-32,3711	-0,71364
mcr-mir-33	GCUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGCUGAGAAACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGU	75	26,66667	28	17,33333	28	44	56	1	1,538462	-33,6	-32,6	0,179681	5,16	-44,8	-1,01818
mcr-mir-33b	AGUGACAUGUACUUAAGUUACUGAAAGUACUCAAAUGUGUUUUAUGCAAUGUACCUGCAGUGCUuucagaaaagcaaaaacuuGUCUAU	89	15,73034	22,47191	12,35955	28,08989	28,08989	50,5618	1,25	1,272727	-19,3	-16,7	0,024573	11,69	-21,6854	-0,772
mcr-mir-34	UGAUCCCGUGGCAGUGUGGUUAGCUGGUUGUGGUCCGGCCGGUUUGUGACAACCACUAUCUGCAGUGCCGCGUGAUUG	78	34,61538	12,82051	23,07692	29,48718	57,69231	42,30769	2,3	1,5	-36,4	-36,4	0,283704	3,17	-46,6667	-0,80889

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-3529	UGUGGCUGCAGCAAUCAGGGAAGAAUGUGAUUUAUUGUUAGUCAGCAUCAGAACAACAAAAUCACUAGUCUUCCAGAUCACGGCAGCCugg	91	21,97802	30,76923	20,87912	23,07692	42,85714	53,84615	0,75	1,052632	-30,8	-29,7	0,103281	5,67	-33,8462	-0,78974
mcr-mir-3530	AGAGACAAGGUAGGCCUCCGGUGAAGAGAACAAUGGUGUGAGCUGGACAUGACUUGAUUAGCGAACGACAUCGAUCUCCCCGGCGCCACCUUUUCGGC	98	29,59184	25,5102	25,5102	19,38776	55,10204	44,89796	0,76	1,16	-31,7	-30,2	0,121532	8,78	-32,3469	-0,58704
mcr-mir-3671	AGUCACAUAGGUCGUAAGUUGAUCAUUACCUGUAACGUUUUUUAAAGUGAUCAAAUAAGGACUAGUGGCA	70	21,42857	32,85714	14,28571	31,42857	35,71429	64,28571	0,956522	1,5	-18,7	-18,5	0,348559	4,37	-26,7143	-0,748
mcr-mir-371b	AGUGUACGGCACGUGCUCCCCGCCGCUAGCGCACUCAAAAGAUGGCGGCAAGGGGGUGACGGGGGAGUCGCACGUUGCCGAACCGU	86	37,2093	19,76744	29,06977	13,95349	66,27907	33,72093	0,705882	1,28	-38,5	-35	0,126533	11,61	-44,7674	-0,67544
mcr-mir-372	GGAUGAUGUUCGAAAGUGCUGCGACAUUAUUACCGACGCUUAUGGUGGCCUCAGGUAUCGUACACGGCUUCUGUGUCGAAAUCCUUUCGUUCAUCAUUA	99	24,24242	21,21212	22,22222	32,32323	46,46465	53,53535	1,52381	1,090909	-32	-29,1	0,23008	11,94	-32,3232	-0,69565
mcr-mir-373	acggaugauAUAAAGGUGAUGUUCAUUAUGCCCAACUUGAUGGGCUUGGGCAGAAGGAUUCUCAAGCAUAAAAGUGCUUCCCUUUUAUUAUCAuu	95	18,94737	25,26316	15,78947	28,42105	34,73684	53,68421	1,125	1,2	-26,2	-25,2	0,010522	20,57	-27,5789	-0,79394

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-375-1	UUUAGCUGCCCAAUGACCCGAGCCGCUCGUAGCAAGGCGUCUUCACAAGUUUUGUUCGUUCGGCUCGCGUUACCAUGGUGGCACUGAC	88	26,13636	17,04545	29,54545	27,27273	55,68182	44,31818	1,6	0,884615	-35,3	-35,3	0,510508	5,41	-40,1136	-0,72041
mcr-mir-375-2	GGCUCUCCGUUUGUUCGUUUUGCUUGCUCAUGGGGUGGGUGGUGUGGGGGGAGAAGGGAGCGAGUAAUAGAGCAAAAUACUAAACUACGGAGACAG	96	37,5	22,91667	14,58333	25	52,08333	47,91667	1,090909	2,571429	-26,5	-26,5	0,439668	2,92	-27,6042	-0,53
mcr-mir-376c	AGGUGCAAACACUGCCGUGUCAUGUUCAACAUAGAGGAAAAUCACCGAGGAAGUUGUGACAGUGCACCUGACACGGUCACACGUUGCAUCG	91	26,37363	29,67033	24,17582	19,78022	50,54945	49,45055	0,666667	1,090909	-27,4	-27,4	0,263715	8,34	-30,1099	-0,59565
mcr-mir-376d	UUUCAGGUGUAGAUUUUCCUUCUACAACUUAAUUGCUUCUCGCCGCAGGUGAAGUGAGGUCGAGGAAGAAGGAAACGUCUCCACCUGUGG	90	26,66667	23,33333	21,11111	28,88889	47,77778	52,22222	1,238095	1,263158	-32,7	-22,97	0,106712	16,3	-36,3333	-0,76047
mcr-mir-3834	UACGUCAGGUCGAUCUCUCUGAUGUUAUUUUCGACAAAUAAGCGAAAAGGCAUCUUGACCUGACUGC	67	20,89552	26,86567	22,38806	29,85075	43,28358	56,71642	1,111111	0,933333	-24,4	-23,6	0,406778	1,27	-36,4179	-0,84138
mcr-mir-3890	UCAGUUCGAACAGUGUUUCUAGACUCUGAAGAGCCGGUUAUGUACGGCUGUUCAAAGGUGGAUAGCUGUCAACCCA	76	26,31579	25	21,05263	27,63158	47,36842	52,63158	1,105263	1,25	-25,4	-24,2	0,10708	10,57	-33,4211	-0,70556
mcr-mir-39	UAAAUGUGAACUUUCACAAUCCCCUAUCAUGUCUUUAGUCACCUGGCUAAAGCUGAUUUCGUCUUGGGAGUUCUCAUAAU	80	16,25	25	22,5	36,25	38,75	61,25	1,45	0,722222	-22,5	-22,5	0,059743	2,98	-28,125	-0,72581

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-4000i	GACAAAGAAAGCUUUUCUUGAAGUUUUUAAGACAGGUUGACACAGUAAGUCUUAAAGUAGGGAAAUCUGAAACUUGCAAGGAACUGCUUUCUUUAUA	97	20,61856	35,05155	13,40206	30,92784	34,02062	65,97938	0,882353	1,538462	-24,9	-21	0,02901	8,86	-25,6701	-0,75455
mcr-mir-4003d	GGAUUUGUUGACACUCGUGACAACUUGCAGAGAAAGGUGCAUAUUAAGUUUACACCUAUUCCGCAGCCUGUCACUGAGAAUGGUAACCAAAAAA	94	21,2766	32,97872	20,21277	25,53191	41,48936	58,51064	0,774194	1,052632	-22,7	-22,7	0,028311	9,4	-24,1489	-0,58205
mcr-mir-4027	CUACCAUCACCUCACCAUUUAACACAUUCUGUGCCUCUGGUGCACUUGAAUUAAAACACUAUGUAUAUUACUUUUAUGUUAAUGAGUGAGACGAAGGUGA	100	16	30	21	33	37	63	1,1	0,761905	-20,8	-18,1	0,009559	16,79	-20,8	-0,56216
mcr-mir-4029	ACCCACACGUGAGGAUCAAUUCCUGUUUGUUUACAUUGCAUGCAUCGCUAGUGUAGUAACUACGAGAAAUAGACACUCACACGUGUGCGC	90	21,11111	27,77778	24,44444	26,66667	45,55556	54,44444	0,96	0,863636	-23	-17,1	0,03183	24,52	-25,5556	-0,56098
mcr-mir-4034	GCCAUUAUUUUUGCAAGGUGAAGGUGAGCAGGGAUCUUUUCUCUGGCACUGAGGACCAAAAUAUCCGUAUUCACACgugcaacugaaaaaaaaauuaa	98	18,36735	20,40816	16,32653	22,44898	34,69388	42,85714	1,1	1,125	-21	-19,9	0,119554	9,47	-21,4286	-0,61765
mcr-mir-4040	AACUAGGGACUAGAUUUCAUGUUUACAAACUGAUGUAAUUUAACCCAUAGCACAAAAUACAACCAGAUCAGAAAGGUGAUAAGCUAGUUUCUACAC	96	15,625	39,58333	18,75	26,04167	34,375	65,625	0,657895	0,833333	-18,9	-18,5	0,175394	6,72	-19,6875	-0,57273

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-4048	UCAUUCCCUUUCCAGCACCUUGGUCACCAUAGUGACCCAUAGUGACCAAGGGGGAUGACGGGAAACC	67	23,8806	25,37313	29,85075	20,89552	53,73134	46,26866	0,823529	0,8	-25,9	-21,3	0,109726	8,22	-38,6567	-0,71944
mcr-mir-41	aagucUUGUCACCGGGUGAAAAACUGACGCCUGCAUAUCAUGGUUGAAUGUGGAGUCUGUGCAGUUGCUUGCGCGUGUGAACAAAGAAAA	90	27,77778	25,55556	16,66667	24,44444	44,44444	50	0,956522	1,666667	-28,1	-28,1	0,033067	9,16	-31,2222	-0,7025
mcr-mir-4127	AGGCAGCUGUGAGAGAGCCCUGUAUAUUAUAAUACCGCUAUAUAAGCCAGCUGUGAUUGAGCCCUGUAUAUUAUAAUACCGCUAUCUAAGCCAGCUGUGA	100	22	29	21	28	43	57	0,965517	1,047619	-22	-15,21	0,013453	23,23	-22	-0,51163
mcr-mir-4130	AUCGAACUCCCUCCGCUGCCCAGACAGCUGCGUGUCUUUAAGAUGGCGGCGCUUCUGCUUGGGUGACGAGAGGAGAGUCUCCCG	84	30,95238	16,66667	29,7619	22,61905	60,71429	39,28571	1,357143	1,04	-36	-35,6	0,091309	4,96	-42,8571	-0,70588
mcr-mir-427	UAGGUGACGGCCAUGUGAucgaaaagaaacagagaaagugCUUUCUGUUACUUCUUCUCAUAUCUGUCGGCACUUG	76	15,78947	10,52632	17,10526	27,63158	32,89474	38,15789	2,625	0,923077	-24	-24	0,200072	3,94	-31,5789	-0,96
mcr-mir-44-1	CGCAGGCGGGAGGUUGAAAUGCCGUUGUCGUGGUCAUCAGAUGACAGGACUGACAGCUGGAUGUGCUCGUUAACGUCGUUCUCCUGCAGCCUAAG	95	32,63158	20	23,15789	24,21053	55,78947	44,21053	1,210526	1,409091	-29,5	-21,4	0,033769	23,95	-31,0526	-0,5566
mcr-mir-44-2	GCUCAGUGCCUGUAUCCCUCAGUGACUGUGGGUUCGCACGACAGU	71	25,35211	23,94366	25,35211	25,35211	50,70423	49,29577	1,058824	1	-19,8	-18,5	0,203176	16,29	-27,8873	-0,55

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GACUAGAUGAUCACAAGACAUUGUCA															
mcr-mir-449a	UCACCUUUGCUUGUCCACUCCUCACAGUUGUAUAAAAUGGAGGUGGCAGUGCGUGUUAGUGAUGGAGAUGGUAAGGCACAGGAGG	85	31,76471	23,52941	17,64706	27,05882	49,41176	50,58824	1,15	1,8	-25,8	-25,6	0,084124	7,48	-30,3529	-0,61429
mcr-mir-4502	AcaaguugcugcugcugaugaugaugguGauuggAAGUGCAGUCACAACAGACAGCGGCACACUGAC	67	11,9403	19,40299	14,92537	4,477612	26,86567	23,8806	0,230769	0,8	-25,2	-25,2	0,397491	8,17	-37,6119	-1,4
mcr-mir-452	CGGACCAUAUUAUCAAAUGUGACUGUUCGuuguuuuauuaucuuuugGUCAUAUAAACUGUUUGCAGAGGACAGUCACAUAUGUCCGAUAAGAAGGUCCU	100	18	25	16	23	34	48	0,92	1,125	-32,4	-32,4	0,183463	8,17	-32,4	-0,95294
mcr-mir-4552	CAUCAACUAACCAGCGUGAACAAGAGCGAGACCACCUCCCACUUGAUCACUGACAUUCUGGUAUGACCCGGGGUUAGUuggga	83	20,48193	26,50602	27,71084	19,27711	48,19277	45,78313	0,727273	0,73913	-26,2	-25,6	0,350856	1,8	-31,5663	-0,655
mcr-mir-466h	UcuugaguguuugugugucaugGCGCCCUUAUGUUAAAGUCGGUUCACGCACUCAGACACguauacgcacgcacacacacacacacac	90	8,888889	10	13,33333	11,11111	22,22222	21,11111	1,111111	0,666667	-24,9	-24,9	0,117884	19,03	-27,6667	-1,245
mcr-mir-466i-1	auacacacacacauacacacgcgcacgcgcgcuaAAUGGCCUGUAUACAAACUCAUCAGAGCCUUUGCGCCAUAUUAUGAUGGUGUGGUC	90	14,44444	15,55556	13,33333	18,88889	27,77778	34,44444	1,214286	1,083333	-23	-17,8	0,062769	25,13	-25,5556	-0,92

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-466i-2	ugugugugugugugugugugucucaauUGUUCUCUCCUAGUAGGUCAUCGUCUGAGACAUCUGUAGACAUAUUAAUCACUACAUCACCCU	90	10	17,77778	18,88889	23,33333	28,88889	41,11111	1,3125	0,529412	-23,3	-18,7	0,058678	13,27	-25,8889	-0,89615
mcr-mir-467c	AAAAAUCUGUGUGUCUAAGUGCGUGCAUGUAUGCAGGAACAUUUUGAUCACAUGCAUGCAGGAACACAGAUUGAA	75	24	33,33333	16	26,66667	40	60	0,8	1,5	-31,1	-31,1	0,307267	3,37	-41,4667	-1,03667
mcr-mir-4760	UGAUGAUCUCAUGAUGAUUUCUUAGCAAAGAAUUCAUUUUCUUGUGUCCCUUUUAGAUUGAACAUGAAUGUUUAAAACAGGAUAUGAGGUCAGAU	95	18,94737	30,52632	12,63158	37,89474	31,57895	68,42105	1,241379	1,5	-22,4	-18,9	0,059494	17,85	-23,5789	-0,74667
mcr-mir-4810b	UUCCACAUGUAGGUUCAUGAGUAGACUUUUCAGAGGCUGAAGUGAGUUUAAGCAAUACUCUGAGGGUGUAUGAUGUACAUAAUGCUGCAU	90	25,55556	27,77778	14,44444	32,22222	40	60	1,16	1,769231	-18,6	-16,1	0,008321	19,96	-20,6667	-0,51667
mcr-mir-4865	UACAUGCAAGGCAGGCAACUCACACUACACACGGUAUGUAGAGAGAGUGACGCCGCUUUGUAUCGA	66	25,75758	30,30303	24,24242	19,69697	50	50	0,65	1,0625	-22,8	-22,6	0,613718	1,85	-34,5455	-0,69091
mcr-mir-4968-1	UCAGAGCAGUGCUGCUCAGcagagcagcagcaacagcagcagcagcagcagcacacuCCGCAGGCUGACUCUCAGAGCAACAUGUCUCAGC	91	15,38462	13,18681	18,68132	10,98901	34,06593	24,17582	0,833333	0,823529	-29,8	-28,8	0,303196	26,91	-32,7473	-0,96129
mcr-mir-4968-2	UAGGCAACAGGUCAGCACAacuaagcagcagcagcaacagcagcagcagcagc	82	12,19512	10,97561	12,19512	9,756098	24,39024	20,73171	0,888889	1	-26,6	-18,9	0,141152	31,1	-32,439	-1,33

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	agcagcuguugUAGUGCCACUCUUGCUGG															
mcr-mir-4968-3	CCGGCGUGACGUGCAGAuuaccagcaacaacagcagcagcagccgccgACGCUGACUCGCCGAAGCUGCUUGAUGAUGCAAGUGCCGCCACGCGCC	96	21,875	12,5	22,91667	10,41667	44,79167	22,91667	0,833333	0,954545	-29,2	-26,5	0,033415	18,93	-30,4167	-0,67907
mcr-mir-4975	AUCAGGACUCAGCUGUCAAACCCAAAAUAUGCUUCUUUUUUACUUGGGUUUUCUUUcaggaagaaacaaauauugGUUCUGCUGAgccuuua	92	11,95652	15,21739	15,21739	29,34783	27,17391	44,56522	1,928571	0,785714	-22	-13,18	0,037553	24,75	-23,913	-0,88
mcr-mir-50	CGAGUAAUAUUAGACAGCGGAUUAUUCUUcaauauuauauuuaauaauauguauauauuaucuaUAAUAUAGAGUAACCCGUAGUCUUUUAUAACCUU	98	10,20408	20,40816	10,20408	23,46939	20,40816	43,87755	1,15	1	-24	-24	0,151437	7,98	-24,4898	-1,2
mcr-mir-5009	AGAAGUCAUACUGCAACAGCUCCUUCUCUUCGGUGGCCGAACUUCGGGAGUUGGACUUUUUCAGAUGGACUAGU	74	25,67568	21,62162	22,97297	29,72973	48,64865	51,35135	1,375	1,117647	-20,6	-20,6	0,124	9,33	-27,8378	-0,57222
mcr-mir-5101	GCGAuguugaugacuuuuguuuguuuugcuguauGAGUCUUUGUUGUAGAGCACGUGGAGCUGUUUACAAACUAAUUAGUCCGUcgacauuaa	93	16,12903	13,97849	9,677419	18,27957	25,80645	32,25806	1,307692	1,666667	-27,9	-27,4	0,018271	6,78	-30	-1,1625
mcr-mir-542	AUAAUCUUUACAACUGUGCUUUGAUGAUGUGCUCUCAUAAUAAAAUUGAUGUGACAGAUUGAUAAAGACGCACUUGGGAAAGAUGCA	87	20,68966	34,48276	13,7931	31,03448	34,48276	65,51724	0,9	1,5	-18,8	-18,8	0,137277	8,15	-21,6092	-0,62667

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-5429	ccaggaaccuccgGCAUGACUAUUCCUCAAGGCACAUUUACUACGGCGuugacuacccuccaaggugccuugaggAAUAGUCAUGCUGGAGGUUCCUAG	99	14,14141	15,15152	14,14141	16,16162	28,28283	31,31313	1,066667	1	-67,1	-67,1	0,328258	3,51	-67,7778	-2,39643
mcr-mir-548d	CACUGAGGGGAGUAUACUCCUUCAGUCAACACAGUUUUAUUACCCUgugagaagaacaaaaaaaacugcaguUACUUGAAAAUAAACUACCCUCAUUc	98	9,183673	22,44898	18,36735	22,44898	27,55102	44,89796	1	0,5	-18,9	-17,7	0,01295	10,68	-19,2857	-0,7
mcr-mir-550	CAAGUGCCUGAGGGAGUAGUGCCUUCUACAGGGAAAACAAUGACUGUAUGGAGCACGAUCUCCACCUUCAGAGGACACC	79	26,58228	29,11392	25,31646	18,98734	51,89873	48,10127	0,652174	1,05	-25,3	-22,1	0,053345	9,46	-32,0253	-0,61707
mcr-mir-5552	CUGCAGUCUAUAGAUAUAGCCUGUAGUCUGUUACAUUCUACCAAGUGAUCGCUACAGUUAUGUAGUUUGUAGUCUAUAGAUAUAUCCUGUAGUCUGUUA	99	19,19192	25,25253	17,17172	38,38384	36,36364	63,63636	1,52	1,117647	-28,8	-26,6	0,061307	13,22	-29,0909	-0,8
mcr-mir-5582	auuuguuGUAAUUUAAAACUUUAAGUGUGUCAGACAACUUUUCUUGCAAAAGCUAUGUGACCACAUAAGUUUAUAGUUUAUACAACAGGC	90	14,44444	32,22222	14,44444	31,11111	28,88889	63,33333	0,965517	1	-19	-18,7	0,032948	11,44	-21,1111	-0,73077
mcr-mir-5698	CAUACUGACCGCCCAACUGUGCACUGAAGUGGAUUUUAUUUAUCAGUGCgacacacccccucccccuuucuuuGUCCCAGUGUGGGGGAGUGCAGUGAA	99	22,22222	17,17172	16,16162	20,20202	38,38384	37,37374	1,176471	1,375	-28,3	-21	0,011177	15,74	-28,5859	-0,74474

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-586	CUCCAUGUUGAUGGUAUGCAUAUUGUAUUUUGUACUUGUAGUUCCCUGGGUACAGUCACCAGUACCAAUGAUGCCAACACUUUACAUGCAU	91	18,68132	24,17582	21,97802	35,16484	40,65934	59,34066	1,454545	0,85	-19,1	-15,9	0,059302	17,12	-20,989	-0,51622
mcr-mir-5890c	CUCCAGACUAGUUUCAUUCCCUGUGCAGUUCAGGUCAUUGACCCAGACGCUGCCAUAUAACUGAACUGUCUGUGG	75	21,33333	21,33333	28	29,33333	49,33333	50,66667	1,375	0,761905	-21,4	-18,9	0,044239	9,08	-28,5333	-0,57838
mcr-mir-592	CCUGACGGUGAACAAGAACUCGGUCCUCGCAUAGCGACGUGACGUCAUCACGUGGUGACGUGUUCUACGCGCCAUCUAGGUCUUUUUGCCCGUCGUC	97	26,80412	17,52577	29,89691	25,7732	56,70103	43,29897	1,470588	0,896552	-31	-28,5	0,039975	20,27	-31,9588	-0,56364
mcr-mir-6013	UUGUCCACGGCUGCUGACGACCGCCUCAAACGUCAGAAGUUGAAGGAAAACAGAGAGAGCUUGAGCGAGUCGCUGGCGCAGUGGAAGC	88	32,95455	27,27273	23,86364	15,90909	56,81818	43,18182	0,583333	1,380952	-27,3	-26,6	0,063669	7,38	-31,0227	-0,546
mcr-mir-6058	GGAGAAGAACUGGACAUUACUCAGCUGAUGACAAUGGUGAUGAAUCAGAUGGGUUACAAUAUGUAGUUGUCCUCUGCUGAUUUAUGGACGUCUUCCAU	98	25,5102	27,55102	16,32653	30,61224	41,83673	58,16327	1,111111	1,5625	-26,2	-26,2	0,10919	8,67	-26,7347	-0,63902
mcr-mir-6340	GCGGUGCUGGGUUUGCUCAGCUGGUGGAAGAUCAACAGACGUCAGCAGCAGCUUCGAUACCCAACACGAC	70	30	24,28571	27,14286	18,57143	57,14286	42,85714	0,764706	1,105263	-22,1	-22,1	0,286043	7,87	-31,5714	-0,5525

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-6552	CCCAUCAUUCGACUUCAGCAGGGAAGACUUUCGCGAUCCUUUUCUAAAGCAACAAGAAGUGGACACGGUCUAUUUCCUGCAGGUGUCUGAAAUGAUUCA	99	21,21212	27,27273	24,24242	27,27273	45,45455	54,54545	1	0,875	-28,3	-23,2	0,012686	10,87	-28,5859	-0,62889
mcr-mir-6560	CGCUGUGUUGCUCCAUACUGCUGAAGAAGUGUCUGCACUUCUGUUUCAGUCAUACUGAGCAGCUCAUCA	69	21,73913	20,28986	26,08696	31,88406	47,82609	52,17391	1,571429	0,833333	-24,8	-24,8	0,250515	3,95	-35,942	-0,75152
mcr-mir-669f	CCUGCGAACCAUUAUGCUGGaauucucucucuauauauauauauauacacacacacacacauaagaauUUCAUUUAAUGGUUUCGCGUG	89	11,23596	7,865169	10,11236	16,85393	21,34831	24,7191	2,142857	1,111111	-19,4	-18,5	0,056046	7,7	-21,7978	-1,02105
mcr-mir-67	GAGAUAUCGUGAGCUGUUGGUCCUUGUUCAGCCCGGUUGUGAUGGAGUUGAUCGCAUCACAACCUGCAUGAAUGAGGACUGACGUCAcgaaauaac	96	27,08333	19,79167	18,75	25	45,83333	44,79167	1,263158	1,444444	-47,7	-47,7	0,225173	3,14	-49,6875	-1,08409
mcr-mir-676	CUCUUCAACUUCAGGAUCGUUAAGACAAAAUCAUAGUUGCUGAUAUAGCAGAGCCUGGAuauguccuugucuuggccuugaCGAUGCUGAAUUUAAAGUG	100	17	25	14	22	31	47	0,88	1,214286	-30,9	-30,9	0,08456	5,13	-30,9	-0,99677
mcr-mir-6769b	UGAUGGUGGGUGAGGAGGAGAAAGCAAUUAGCAAUAGUUUUCGAAAGACUUUCUGGAAACUCGAUCGAuuauuucacucacucacucacucacucacuc	99	21,21212	22,22222	8,080808	17,17172	29,29293	39,39394	0,772727	2,625	-29,4	-23,1	0,04736	29,05	-29,697	-1,01379

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-6780a	AAGCUCGUGUAGAAAAGCUCcuccucuguuuucuuuucaaaaugcaUGUCAGGUGCAACAUAGACGUGUAGUAGGAUGAAUCUUGACACACGAGGCC	97	20,61856	22,68041	14,43299	15,46392	35,05155	38,14433	0,681818	1,428571	-23,6	-23,3	0,05752	17,22	-24,3299	-0,69412
mcr-mir-6796	GGAGUACAAAGUUUCCGUCCUGAUUUUCUUGUGGGGUUGGAGAGUAUGGCUCCAUGCAAAGUCUAGAAACGUaaacuuggacaau	85	24,70588	20	14,11765	25,88235	38,82353	45,88235	1,294118	1,75	-24,9	-23,7	0,22456	3,8	-29,2941	-0,75455
mcr-mir-6800	CUGUAGUAGGUGACAGUCAGGCCUGGUCUCUUCUUGUCACCAAGGCCACAUUAUAGGGCUAAGAGGAGGCACUAGUAGUUCACUACUAUAU	91	25,27473	25,27473	21,97802	27,47253	47,25275	52,74725	1,086957	1,15	-26,7	-19	0,021509	23,54	-29,3407	-0,62093
mcr-mir-6803	CUACACGCACCGCUGCCAGCACCGCCACGCGCCGAGGGCAGGUGUAAACGGAGCUGUCACGUGACCccgagggugggggugggggcugggAGAGUGGCU	100	24	16	26	9	50	25	0,5625	0,923077	-43,7	-40,7	0,072188	21,19	-43,7	-0,874
mcr-mir-6826	CACCUUACUGAUUCGUUUCACAACAGGACUGGUAUGUUCUGUGUCAAUAGGAAAGAGGUCUGUGAUUUGUCCUGUUUGUGAAUUGAUCAUACAGUAC	97	22,68041	24,74227	17,52577	35,05155	40,20619	59,79381	1,416667	1,294118	-25,9	-25,1	0,012492	20,76	-26,701	-0,6641
mcr-mir-6830	AGGAACAGGUGCGAUACGAUCGAGAGAGACAAGCGGGUCCUCAGAAAAUCCUCUUGAAAugcuuucuugucuuucuucucuccccaucuguuuuu	96	17,70833	21,875	12,5	9,375	30,20833	31,25	0,428571	1,416667	-29,9	-29,5	0,041352	6,82	-31,1458	-1,03103

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-6864	GCAGUCGGAGGGUUAAAGUGAAAACAAAGGCAGUACUUGAAGGGACAAGUCAGACUUUAAUGACGCCAUGGGUAUUUCCUGUUACCCCGACAAU	94	26,59574	31,91489	19,14894	22,34043	45,74468	54,25532	0,7	1,388889	-23,6	-23,2	0,154259	11,86	-25,1064	-0,54884
mcr-mir-6873	CCUUGCAUGUGUCACAUGAGCAAAGAUUCAGAUAUAUGCACACACUUGCAUauguucucucugucuuucucucaugugcacUUGCAUGA	89	12,35955	20,22472	14,60674	19,10112	26,96629	39,32584	0,944444	0,846154	-35,2	-34,8	0,118812	5,2	-39,5506	-1,46667
mcr-mir-6925	ACAACACCUGAAGACUuuucuucaaggcaccuuggaggguagucgaugcUCAGUUGCAAGAGGAAGAAAUGGCUUACAAAUGUcag	86	12,7907	23,25581	10,46512	11,62791	23,25581	34,88372	0,5	1,222222	-20,5	-19,9	0,218392	9,52	-23,8372	-1,025
mcr-mir-6955	GCCCACAAGAGACAGCAAGUAGGAGGCACAUCCAGACACGAGUGCCUGGCAUUCUACACCUGUCUCCUUUGUCGUGUCCUUUGCUU	86	23,25581	22,09302	30,23256	24,4186	53,48837	46,51163	1,105263	0,769231	-24	-23,1	0,092411	15,34	-27,907	-0,52174
mcr-mir-6975	AUCGCGAGGGGAAAGGCUGAGCACCGCUCAGCAUACUUUAGUUGCUGUUGGCUCUCUCCUUUCUCCUCCGCCUC	74	24,32432	14,86486	32,43243	28,37838	56,75676	43,24324	1,909091	0,75	-33,1	-33,1	0,158058	5,02	-44,7297	-0,7881
mcr-mir-6988	ggguggggugggagagcUGAGUUACACGCAGUGAGCACUGCUCAUCCUCAGGCACUGCCUACAACUACGCUCCGCCUCAUCG	81	16,04938	17,28395	29,62963	17,28395	45,67901	34,5679	1	0,541667	-33,4	-33,4	0,234622	9,97	-41,2346	-0,9027
mcr-mir-7	AAUGCAAAUACUAGGGACAGGGUUUUCUUUUACACAGACGGGCUGAAUCGCUGACUGGUUACAAAA	91	25,27473	29,67033	21,97802	23,07692	47,25275	52,74725	0,777778	1,15	-22,6	-19,7	0,032478	10,33	-24,8352	-0,52558

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GCCAACAAGUCCCAGUCUUGGCGGA															
mcr-mir-7042	AAGGGAGAAUUCAGUGGGAUCAUGUGGGGCUUGGAAGGGGAAGUAAUUUCAUGUUGAAGCCACCUAGUGACAGAUGUcccuuuguuuucuccaca	95	28,42105	23,15789	9,473684	20	37,89474	43,15789	0,863636	3	-36,4	-36,4	0,334669	3,58	-38,3158	-1,01111
mcr-mir-7051	AUGUUUAAAAGUUAUGUAGCUAAGUAUAAUGUUCACCAGGAGGAGGUGUGCACGUCCUAacuaaucauuauuauuauugcauaacAUUGUAAAGCG	96	18,75	22,91667	9,375	21,875	28,125	44,79167	0,954545	2	-21,7	-19,9	0,057538	7,51	-22,6042	-0,8037
mcr-mir-71	aaauuccuuuUGGUGUGAAAGACAUGGGUAGUGAGAUGUCGGUCCUGAAGAUUCACCUUAUUACCCUGUCUUUUGCAUCAAGGGGAAACC	90	24,44444	22,22222	16,66667	25,55556	41,11111	47,77778	1,15	1,466667	-44,2	-44,2	0,187606	4,57	-49,1111	-1,19459
mcr-mir-7186	UGACAGUAGAAUAGCGAGUUGGCGUGUGCAUUAAGAGCUGUGGUUCCUGUAUGUUCGGGAAGCACAGUCACGCUCAGCCGAUGCAUUUCACUGGAU	96	30,20833	22,91667	19,79167	27,08333	50	50	1,181818	1,526316	-38	-38	0,237347	14,88	-39,5833	-0,79167
mcr-mir-7234	ACUGUCAGAGUUUCGGGCUUUCUGUGGUCCCCUAAAGACAUGUUUUAAUCGUGUAGCUUGUUUUCUCCAAAGAACACCAUAAACUUCGACUGA	93	19,35484	24,73118	22,58065	33,33333	41,93548	58,06452	1,347826	0,857143	-21,5	-21,5	0,443504	4,24	-23,1183	-0,55128
mcr-mir-7241	GUGUUUGUUAGGGUAGUAGAUACUCAUGGUGAGUAACCCAAAAC	94	21,2766	20,21277	11,70213	20,21277	32,97872	40,42553	1	1,818182	-28,1	-27,8	0,130969	8,02	-29,8936	-0,90645

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CCGGGGUUACGGAUGUaucugcuu cauaacuacgaccccagAGCAAAUUC															
mcr-mir-7260	CGCAGCUGUUUUAAAGCCAGUA AUCAAGUCAUCCAGUACAAGGAG AAACAGUGCUGACAGUGCCUUU UACCGACUUUAGUGAUGGCUAA AACAACUGAC	99	21,21212	32,32323	22,22222	24,24242	43,43434	56,56566	0,75	0,954545	-22,8	-16,37	0,04421	16,66	-23,0303	-0,53023
mcr-mir-7371b	UCGAGCAACUUGAUGAUAUCGC UUAUUAUCUUCUCUUGAGUUGU AGAGAUGGACGGAGGAUAAGAU GCUUUGUAUCAGAUGCUUGC	86	25,5814	24,4186	15,11628	34,88372	40,69767	59,30233	1,428571	1,692308	-22,4	-20,5	0,034701	13,15	-26,0465	-0,64
mcr-mir-742	auuaucuGUGAUCUAGAGAGAAA GCCACCAUGCUGUUAUAUCACGU CUAUUGUUGAAUCGACUUCUUC GGUGGUGUCUUUUUCUACAUAA CUACAUCAG	99	18,18182	23,23232	19,19192	32,32323	37,37374	55,55556	1,391304	0,947368	-19,2	-11,69	0,033442	29,11	-19,3939	-0,51892
mcr-mir-7456	UGCUGUUCGCCUGGCGAUCGCA UGGUAGCGUCUGGUUCAGGGAG AUGUACCUGCUGCCAGCUGAAAC AACG	71	32,39437	18,30986	25,35211	23,94366	57,74648	42,25352	1,307692	1,277778	-24,5	-21,8	0,048336	5,34	-34,507	-0,59756
mcr-mir-7461	ACAUGCUCUUUGAUGACCAGCAU GGCUGGAAUGUGGCUGAGCAAC AGUUCCCGGACGUUCUGGUUGA AUCAGAAGGCAAGC	81	29,62963	24,69136	22,22222	23,45679	51,85185	48,14815	0,95	1,333333	-26,8	-26,5	0,04965	8,31	-33,0864	-0,6381
mcr-mir-7462	UAUUAUGGCCUGCUCCAGGUAC UGCGGUGUGUGAUGAGCGAUGA UAGGAUGCAACAGAAUAGCCACU	98	24,4898	28,57143	23,46939	23,46939	47,95918	52,04082	0,821429	1,043478	-23,7	-17	0,032162	19,67	-24,1837	-0,50426

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GACACAACCUCAUUUCUAGCAGACCAUACAG															
mcr-mir-7465	CACcaggaauuauuuuuaaacacucaGUUACAAAUCAGCUCAAAUCUGGUAAAACUGCUUCAGAUAGCUGAUACUCAUUUUUAGAACAAUAUUUCUGCAG	100	11	26	16	24	27	50	0,923077	0,6875	-19,7	-19,7	0,176123	6,74	-19,7	-0,72963
mcr-mir-750	GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUGGCAGGAAUGCUGUCUUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUGGCAUGGCAUG	97	27,83505	19,58763	23,71134	28,86598	51,54639	48,45361	1,473684	1,173913	-52,7	-51,6	0,157091	3,48	-54,3299	-1,054
mcr-mir-7589	AUGUGCUUAAUUGAGCCCCCUUCGUCAGUUUCUCAUUCUGGAUGGAUUUCUGGAAAUGGAGAAAUCAGCCGAUGCGGAGGCUAACAGAGCAGUG	94	27,65957	24,46809	20,21277	27,65957	47,87234	52,12766	1,130435	1,368421	-29,8	-24,4	0,024214	13,36	-31,7021	-0,66222
mcr-mir-765	UGGUGCAGAAGGGAGUUCAGCUUACCAAAUACUGAGGACAUGGAGGAGAAGGAAGGUGUGGUCAGCUGAUCCUCACUUCCUGACAUUC	88	30,68182	27,27273	19,31818	22,72727	50	50	0,833333	1,588235	-24,1	-24,1	0,047094	9,07	-27,3864	-0,54773
mcr-mir-7683	ACUUGGAAAGGUGGAACACUAACCAUACUGGCACUGUGGACCUUGGAAACCUGGAGGACAGGCGCAGGAUGGAUAGUAGCCUCCUCUGCACUG	93	30,10753	26,88172	23,65591	19,35484	53,76344	46,23656	0,72	1,272727	-28,7	-24,8	0,044924	9,43	-30,8602	-0,574
mcr-mir-770	GGUCACAUUCAAUCACGUUACAGGUGCAGAUCGAACCUCGUGCCAG	79	22,78481	24,05063	27,8481	25,31646	50,63291	49,36709	1,052632	0,818182	-22,2	-22,2	0,116359	8,08	-28,1013	-0,555

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UCACGAUCAGCACCACGUGUCUGGAAUCUGUUU															
mcr-mir-7789	CUAUGAGCGAGUAGACUGCUGUGUUCCUcugagaagaggaagaagaugaaacGAUUCAGCAGAGCAGACGUCCAGCAGUCGAUGAUCGCUCACUU	95	20	16,84211	18,94737	18,94737	38,94737	35,78947	1,125	1,055556	-35,1	-32,4	0,057006	10,22	-36,9474	-0,94865
mcr-mir-7795	AGGAGACACGUGAUGCUUACAAUAUGACACCAGCAUCUAAUCUCUUAUCGGUAUAGGUGUGAAGUGUCAGAUGAUCGGUCUUGA	84	25	28,57143	17,85714	28,57143	42,85714	57,14286	1	1,4	-19,9	-19,9	0,054929	9,78	-23,6905	-0,55278
mcr-mir-789b	CCAUCCUGGUACACCACCAGCACAUCUCUCCAUUCCAGGUAUGAUGGCGUCGUGCUUCCGCUGCUGGAGAUGGCGGUCGCAGAUGCAGCAGGAAUC	96	27,08333	19,79167	31,25	21,875	58,33333	41,66667	1,105263	0,866667	-29,6	-23,8	0,110276	11,46	-30,8333	-0,52857
mcr-mir-7950b	UUUGGCAGGCCGGCGAAAGAGUUGCGCCAGACUCACCCAUCAAAGCAACCCGCAGGUCUGGCGCCUGCCUCCCUCG	76	27,63158	19,73684	36,84211	15,78947	64,47368	35,52632	0,8	0,75	-28	-24,8	0,1728	20,48	-36,8421	-0,57143
mcr-mir-7964a	CGCUCUAGGAUGCAGUGCGUAGUGCAAUCAAGCGGAGCGGAUGGGGAUGGUCAACCACUCGCUGCAUAUAGAUAA	75	32	26,66667	21,33333	20	53,33333	46,66667	0,75	1,5	-20,8	-17,3	0,208513	17,37	-27,7333	-0,52
mcr-mir-8	CGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUUUG	86	22,09302	25,5814	19,76744	32,55814	41,86047	58,13953	1,272727	1,117647	-38,5	-38,5	0,175975	3,55	-44,7674	-1,06944

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-802	uuaccuuuguaCCCAUUCCAUAGUUUGUCAGUAACAAAGAUUCUGUUACACAAGUGACUUGGACCUUGGUGACAAGGAUU	80	17,5	25	17,5	26,25	35	51,25	1,05	1	-20,1	-20,1	0,088615	9,87	-25,125	-0,71786
mcr-mir-81b	CCUGCAAAAACUCAUGGGCCCUAUUUCGGCCCUAUAUGGGCUUAAAAUAGGCCCUGCAUGGUGAAACGAUCAUGGGCCUAUGUGUGUUUUGCCCA	95	24,21053	23,15789	25,26316	27,36842	49,47368	50,52632	1,181818	0,958333	-38,4	-35,6	0,107415	11,5	-40,4211	-0,81702
mcr-mir-8234	GAACAGGAUAUUGGCAUGGAGAAGCAACACCACUCUUUGCCUUCUCCAUCCCAUCUUCUCCUGCCU	66	16,66667	22,72727	33,33333	27,27273	50	50	1,2	0,5	-23,7	-23,7	0,285672	2,31	-35,9091	-0,71818
mcr-mir-8293	AGGAGUGAUAGGUAGCUGAUUUAUCAUGAAAGAUAAAAGUGGAUGAAUACAUUCCCUGUCCUAGACAUGAUAAACCACUCACAGUUCACUGua	93	20,43011	34,4086	17,2043	25,80645	37,63441	60,21505	0,75	1,1875	-21,3	-20,8	0,146917	10,11	-22,9032	-0,60857
mcr-mir-83	AUGUAGCACCAUAUAAAUUCCUGCUGCUGAGCUGCUGCUAACUAAUGCAUUGAUAGUUUUAAGGAAUGUGGAGCAGCAUAGUUACUGUGUUGCUAUAC	98	22,44898	27,55102	17,34694	32,65306	39,79592	60,20408	1,185185	1,294118	-26,9	-26,9	0,117633	12,41	-27,449	-0,68974
mcr-mir-8319	AACAAUGCAGCAAGAGGCUCAUUGCCAUagauuuugguuguuuuuuucugagcuGUUCAAAUUAGCAAGUGAGGUCAGGCUGCCUUUAG	89	17,97753	21,34831	14,60674	16,85393	32,58427	38,20225	0,789474	1,230769	-21	-10,6	0,048695	25,91	-23,5955	-0,72414

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-8335-1	uuguuguuguuguuguuuugcucaUGGCUGGUCAUUAAGACCAAACUGACAAAACUGCUUACAGACAAUUU	71	11,26761	23,94366	14,08451	16,90141	25,35211	40,84507	0,705882	0,8	-21,2	-18,8	0,146315	6,81	-29,8592	-1,17778
mcr-mir-8335-2	GCGCUGCAGAGguguauauauaauguuugccauguuguuguuguuguuuuuuuuuuuuuagcuuacaGACGAUUAUUAUAUUGAUACACUUGUGAGGCC	99	12,12121	11,11111	8,080808	12,12121	20,20202	23,23232	1,090909	1,5	-23,4	-20,9	0,130829	15,27	-23,6364	-1,17
mcr-mir-8364j	UCGGGGCGACUGCGUGAUCUCACGUGugagcaugcaugugugucuuCAUUUCUCACGUGAAUGCGCGCGcccgag	75	21,33333	9,333333	18,66667	16	40	25,33333	1,714286	1,142857	-28,6	-24,2	0,014357	24,88	-38,1333	-0,95333
mcr-mir-8485-1	cacacacacacacacacaaaagucacAAUGUAACUGCAGUGUGUUUUUACACAUGGUCAGCAGUGACAGUGUGAUAUAUUGAAGUGAGAGAGUGUUUU	98	20,40816	20,40816	7,142857	25,5102	27,55102	45,91837	1,25	2,857143	-25,6	-20,8	0,086901	11,94	-26,1224	-0,94815
mcr-mir-8485-2	gaguuugcacacacacacacacacguaugauACAUUUCGUACUCCGCAAGCUCAGGUGAAUAUGGCAGGAGUGUGUGUUUCAUGAUGCUGGCAAAAAU	98	18,36735	18,36735	12,2449	19,38776	30,61224	37,7551	1,055556	1,5	-24,8	-19,4	0,065813	22,98	-25,3061	-0,82667
mcr-mir-8485-3	cacacacacacacacacacacgucacauuCAAGAGGGGAGCAAUCUAGAUCCCUGACAGAUUAGGUAUAUGCAugugauguguguauguuuuuuguaAG	99	13,13131	16,16162	8,080808	9,090909	21,21212	25,25253	0,5625	1,625	-26,8	-24,6	0,07266	13,36	-27,0707	-1,27619
mcr-mir-8881	CUGGUUUUUAAACCAAGAAAGGAAGAUAAAUUAUACAGAAUAUAAAUGCAGCCGUUGCUUUGUUUU	92	15,21739	30,43478	16,30435	38,04348	31,52174	68,47826	1,25	0,933333	-20,4	-20,4	0,106037	7,86	-22,1739	-0,70345

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CUCUGGUUCUUCUCUUUCAAAACUUU															
mcr-mir-8956	GCAGAUUCUGUUGACACAGCAUCCAACACAUCAGUGUGAAGGUGUGUUUCUUUGCCUGCAAAGCCCCUACAUUGACUUGGAUCUUUGCAACGUAUCGGU	99	22,22222	23,23232	24,24242	30,30303	46,46465	53,53535	1,304348	0,916667	-25,5	-24,6	0,178773	11,53	-25,7576	-0,55435
mcr-mir-8993	GUCAUGACCUUGACCUUUGACCAAGUGCAGCGCCUCUCGUGCUGACAUGAAUGAAGCAAAGGCCAGACUUGCUCCUGGCCAAGUGGCAUUGG	92	27,17391	22,82609	27,17391	22,82609	54,34783	45,65217	1	1	-28,9	-27	0,19811	10,01	-31,413	-0,578
mcr-mir-9077	UGUCUCAAAUUAUCUGAGGGCUUUUGCACUGCUGCUGAAAAUUUCUGCUGAUAUGCAGAAGUCAUAAAUAAAUGaguga	79	18,98734	27,8481	15,18987	31,64557	34,17722	59,49367	1,136364	1,25	-18,7	-18,3	0,09631	8,26	-23,6709	-0,69259
mcr-mir-9093	GCUGUCACGUAGAACCUGAUGGAUGUCACCUACGACUGUAGUCCAUGUCCCGGACCAGUGUGUGUCACAAUAGUUUCAAGUUCUUACAGGUGACUUU	97	23,71134	22,68041	23,71134	29,89691	47,42268	52,57732	1,318182	1	-25,6	-25,3	0,077213	8,56	-26,3918	-0,55652
mcr-mir-9-1	GGCGGCUCCGGUUUUGUCUUUGGUUAUCUAGCUGUAUGAUUGGGGCAGAAAUAUCAUAAAGCUAGGUUACCAAAGGCAAAAAUGGACGCCAAA	93	26,88172	29,03226	17,2043	26,88172	44,08602	55,91398	0,925926	1,5625	-45,5	-45,5	0,314517	3,87	-48,9247	-1,10976
mcr-mir-9186o	UGACUAAGAGGUGGCAUGGCUGGUGUUGGCAACAUUCCCUGACCUCUCUGAAAGCCUUGUGGUAUCCC	98	25,5102	18,36735	29,59184	26,53061	55,10204	44,89796	1,444444	0,862069	-29,1	-25,24	0,012852	15,39	-29,6939	-0,53889

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CCCUGACCCAGGCAUGCCUUCUUCUAGCGA															
mcr-mir-9-2	uugaacagcacaggugacagGGGACAACCUUAACGUAUGCUUACUGUAaugcaaaaguaagcuccucUUUGGUUAUCCAGUAGUAUUGUGCUUGUUGAG	99	15,15152	13,13131	9,090909	23,23232	24,24242	36,36364	1,769231	1,666667	-27,4	-24,7	0,019343	8,03	-27,6768	-1,14167
mcr-mir-92a-1	cUGGCAUUAGCAGUAGGUCUUGAUAAGUGCAAUUCUGGUGAAUUAGAUAACAGAUUGCACUUGUCCCGGCCUUCUGCUAAUAGCUAA	87	22,98851	26,43678	18,3908	31,03448	41,37931	57,47126	1,173913	1,25	-43,2	-43,2	0,272477	2,43	-49,6552	-1,2
mcr-mir-92a-2	AUUUGUGUGCUCAGGAAAGGUUGUGACUUGGGCAAUUCUGUGAUGUCCUGUCAGAUUGCACUUGUCCCGGCCUUGUCUUGGCUUACACUU	90	26,66667	15,55556	21,11111	36,66667	47,77778	52,22222	2,357143	1,263158	-31,5	-29,1	0,036643	11,93	-35	-0,73256
mcr-mir-92b	CACCGAUCAGGGUUGUGUAGACCGGAACAGGGGCAAUGCAUUUUGAGUCGUCUGUAUUGCACUCGUCCCGGCCUAUCCAAUCUGACUCGUAG	92	27,17391	20,65217	26,08696	26,08696	53,26087	46,73913	1,263158	1,041667	-33,5	-31,7	0,067381	6,55	-36,413	-0,68367
mcr-mir-92e	ACCAAGCAUUUCAAAGAUCcacgugggugugugcgugcgugugcgugggcggugugggugggugcaugGCACACACACGUGGAUCUUUGAACUGCUUGAU	100	9	16	13	13	22	29	0,8125	0,692308	-55,5	-54,6	0,151057	12,27	-55,5	-2,52273
mcr-mir-9-3	UUUGGCGUCCAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUGCCCCAAUCAUACAGCUAGA	93	17,2043	26,88172	26,88172	29,03226	44,08602	55,91398	1,08	0,64	-34,1	-34	0,28369	3,42	-36,6667	-0,83171

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UAACCAAAGACAAAACCGGAGCCGCC															
mcr-mir-9358	UGAGGUACCCCGAGACAACUUUUUCGCUUUGACUAUUCGUUUGACAUGCUUGUUCCUGCAUUUUUUCUUCAAACGAGAACGAUGGCCCUGGGUACCUGU	99	21,21212	19,19192	24,24242	35,35354	45,45455	54,54545	1,842105	0,875	-26	-26	0,127101	8,99	-26,2626	-0,57778
mcr-mir-936	CAGCUCGCUGGAcaggagagggaggaaggggacUGGAACCUUCCUUUCCUCAACAUCUCUCCAGUUGAGGCC	72	13,88889	12,5	25	19,44444	38,88889	31,94444	1,555556	0,555556	-31,6	-29,2	0,090386	19,4	-43,8889	-1,12857
mcr-mir-9392	AAACACUGGCUUUCCUUCAUAUUAUGACUAGAUGAAAuucauuaaauguuuuucuagUCACAUUAAUUCACUGAAAGAAGUGGCA	85	11,76471	28,23529	14,11765	22,35294	25,88235	50,58824	0,791667	0,833333	-18,6	-18,6	0,301505	7,56	-21,8824	-0,84545
mcr-mir-943	ACUACAAGACAGGGAGAGAAUGUCAGACGACAAUGAAAUAUCUUUCGAAAUGUCUGCCAGUGAUUCUUUCUGACUGUUGCUGUCCGUUUUUUGUCUG	97	22,68041	25,7732	18,5567	32,98969	41,23711	58,76289	1,28	1,222222	-21,5	-12,9	0,033141	29,31	-22,1649	-0,5375
mcr-mir-9438	AGCCUGGCUACACAUCAUACUACACAAGUGUCUAGUGUGGCUACAAACAUUGCAAGCACCCCCCACUUGUCUACUCUGGGUGCAGUGCAGGGG	93	23,65591	24,73118	29,03226	22,58065	52,68817	47,31183	0,913043	0,814815	-28,8	-28,3	0,192015	6,09	-30,9677	-0,58776
mcr-mir-9505	UGGAUGAUGUCUGUCAAAAUCCAAUGGAGACAUAAGAGGCCAGCAAGCACACUGCCUGCUGACCUGCU	99	23,23232	30,30303	23,23232	23,23232	46,46465	53,53535	0,766667	1	-27,7	-27,5	0,050009	11,15	-27,9798	-0,60217

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CUUGGACUACAUGAUUACAGACACUAAUGUG															
mcr-mir-9542a	CGACUGACAAAACGGCUCACGACAUGGCCUGGCACUUUCUAAUUUCUGGCCAAGUUAGGCGCCUGUUUGUCGAGGGC	77	27,27273	20,77922	27,27273	24,67532	54,54545	45,45455	1,1875	1	-23,6	-19,5	0,032476	12,94	-30,6494	-0,5619
mcr-mir-9573	agaaaaaauaucaaaacuaGGAUUGUGAGGCUGUUGGUCCAGCCCUGCCAUCAUGGUGUUGGUUUUUUACC	71	22,53521	8,450704	15,49296	26,76056	38,02817	35,21127	3,166667	1,454545	-19,6	-17,5	0,079399	19,85	-27,6056	-0,72593
mcr-mir-9592	GGAUUGCUUUGCUGUUUGGGGCUGAUGCAAGGUUCCUUGCAGUGACGACCUUAUUCAGACAAAGAAACGG	70	30	22,85714	18,57143	28,57143	48,57143	51,42857	1,25	1,615385	-20,9	-20,4	0,264055	3,01	-29,8571	-0,61471
mcr-mir-9598	GAUAUUAUUGAUAUAAAACUGUCAGUGCUUAUUAGUACUAGGAUUUUGAUUAGCUGUUGUAAUUAGUGCUACAGCUUAUAUCAAGGUAAUCGU	93	19,35484	30,10753	10,75269	39,78495	30,10753	69,89247	1,321429	1,8	-21,6	-20,9	0,026556	30,6	-23,2258	-0,77143
mcr-mir-9640	UUCACAUGUCUAAGCAUGCUUUCGUGUUUCAGAUGGCAGAGCUGGACAAGGUGUCGCACCCUGAGAAGCCCUACCCGUACAGCAUGGCUGACAUGUUCA	99	25,25253	23,23232	26,26263	25,25253	51,51515	48,48485	1,086957	0,961538	-27,2	-22,7	0,044766	14,41	-27,4747	-0,53333
mcr-mir-965	GGGGGAGAAGUUAUUGCUGCGAAGCCUCAGCUUCUGCAAGCAGGAguuggucuucagcaugucacGAAUGUGCUCGCAGCUAGCGUCUCCAAC	93	24,73118	18,27957	19,35484	16,12903	44,08602	34,4086	0,882353	1,277778	-38	-36,4	0,037571	7,54	-40,8602	-0,92683

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-96b	CGACUGCUGGCUGUUCAAUUAUUUGGCACUUGUGGAAUAAUCGGUGUAUCUGAAAGUCGAUUAUACACCGGUGCCAAGUCAUCAGAAAUGCCUGAAGCAC	100	24	27	21	28	45	55	1,037037	1,142857	-33,2	-33,2	0,110762	3,59	-33,2	-0,73778
mcr-mir-9771g	CAAAACAGAGAACUACAUAUUUUACAUGCAAUGCUUCUAUUGCACUGGGcugucggaaaagucaugacgcAUUUUUGCAAUAUAUGGUGCUCGUUCAU	98	13,26531	23,46939	14,28571	27,55102	27,55102	51,02041	1,173913	0,928571	-19,7	-19,7	0,07496	11,01	-20,102	-0,72963
mcr-mir-981	GCUAUCAGACUUUGUUCCGGGUUUCGCGGCUGGCGAACAGUCAUUUUGAGCUGUGUUCGUUGUCGUCGAAACCUGCCCUGAAAUCUGAUGUG	92	28,26087	16,30435	22,82609	32,6087	51,08696	48,91304	2	1,238095	-35,5	-31	0,014511	9,61	-38,587	-0,75532
mcr-mir-9896	GACCUGAUGGAACAGACUAUAGAGCGAGUGCUAAUGAAGGCCAUUACAAUAAUCGGACACACCGCCAGGCCACUCGCACUGCACGUGCUCAAUCAGUCC	99	23,23232	30,30303	29,29293	17,17172	52,52525	47,47475	0,566667	0,793103	-26,4	-26,4	0,216116	8,18	-26,6667	-0,50769
mcr-mir-99	CUGGUGGGUCUUCACCCUCCUCAUCCUCUCCGUCUACACGGCCAAGCUCGCCUCUGUGCUGACGGUGGAGGUGCAGGGCGCGAAGAUCGACUCU	94	28,7234	13,82979	34,04255	23,40426	62,76596	37,23404	1,692308	0,84375	-40,8	-40,8	0,362029	6,15	-43,4043	-0,69153
mcr-mir-9934	UUGCUUAUCAGCGAUGCAUCUGAUGGUCUUGAUAUGUCCAUUUCUAUAUCAGAUCCUUAGGCUUCGUCUGGUUAAGGGA	79	22,78481	20,25316	18,98734	37,97468	41,77215	58,22785	1,875	1,2	-24,6	-22	0,079099	4,85	-31,1392	-0,74545

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
mcr-mir-994	UUGUUCAGUAAUGCCAUAAUuucuaagaaagaaaaaguaaauucuUGUAGCUACAUAAUCACAGUUGCUGUUUCUUAGUUUGUUACUGGUACUGAAUAU	99	13,13131	19,19192	11,11111	31,31313	24,24242	50,50505	1,631579	1,181818	-23	-20,7	0,065496	12,27	-23,2323	-0,95833
mcr-mir-9945	cccccucccccaguugACCACCUGUCCACCUGAGCCCAUAGACAUAGAGGGUUGGACAAGGUCAGGUAGCAAUGGAGAGGAAA	83	24,09639	26,50602	18,07229	12,04819	42,16867	38,55422	0,454545	1,333333	-27,9	-21,9	0,019816	14,79	-33,6145	-0,79714
mcr-mir-9b	UUGUGUUAUGAGUUAACAUAAAGGCUGUUAUGCUGUAAGAACUGCGACUAAAGCUGAAGCAACUAUUGUUAAGUCUUAACAUAU	84	20,2381	33,33333	13,09524	33,33333	33,33333	66,66667	1	1,545455	-19,9	-17,3	0,08065	9,04	-23,6905	-0,71071

Supplementary Table 3 – Structural and thermodynamic characterization of miRNA precursors in *P. canaliculata*. Size (Tam), G content, A content, C content, U content, GC content, AU content, AU ratio (R-AU), GC ratio (R-GC), Minimum Free Energy (MFE), Minimum Free Energy of the Pool (MFEE), Frequency of the MFE Structure in the Pool (Freq), Diversity of the Pool (Div), Minimum Adjusted Free Energy (AMFE), Minimum Free Energy Index (MFEI).

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-bantam	ACGAAACUGGUUUUCACAGUGAUCCAGCAGAUUGCUCAAAGUCUGAGAUCAUUGUAAAAACCAAUUUUGU	70	18,57143	32,85714	18,57143	30	37,14286	62,85714	0,913043	1	-29,4	-29,4	0,496236	1,25	-42	-1,13077
pcn-let-7b	UCAUACUGUGACUAGAUCAUAUCUCAUUGAGGUAGUGGUUGUAUCGUAUUACUCUCUGUAAUCAGUUGUCAGUCACAUAAAG	84	19,04762	26,19048	17,85714	36,90476	36,90476	63,09524	1,409091	1,066667	-18,7	-18,7	0,092975	12,14	-22,2619	-0,60323
pcn-let-7d	cugcugcugcugcuguaugUGCCCAGAGAAGACGUCUGCCUCAGACGUUGUGGCUGCACUAUACAACCUGCUGCGGCAGGCA	85	21,17647	16,47059	22,35294	14,11765	43,52941	30,58824	0,857143	0,947368	-35,8	-29,3	0,041106	14,27	-42,1176	-0,96757
pcn-let-7f	GGUCUGCACAUUCCACCAUCCAUUACUGUAGGUAAUAUUGUGUCCUCUUUGAGAGCCUAUAUCAGCAAAGCUACGGUAAUUGCUGGUAGUGGCAGUCA	98	22,44898	24,4898	22,44898	30,61224	44,89796	55,10204	1,25	1	-28	-20,9	0,057504	32,52	-28,5714	-0,63636
pcn-mir-1	AUUAUUACAUAUCUGGUAUGUUUGUGGAGUUGAUGUGUUCAUGCUUCUUUAUAGUUUGACCUUUUCCCUCacacaacauaaagaugagaaaUUCU	95	13,68421	12,63158	12,63158	38,94737	26,31579	51,57895	3,083333	1,083333	-18,5	-17,2	0,045655	8,13	-19,4737	-0,74
pcn-mir-1002	CACUGCAGGUGUAAAGGUUAUGUACAGGUCAGUGCCGAGACUGAGAAUAUUGUACAGCUAAGUAGU	92	22,82609	29,34783	13,04348	21,73913	35,86957	51,08696	0,740741	1,75	-21,4	-20,5	0,064133	16,07	-23,2609	-0,64848

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UGAUACAAACAGUAacaccagcaaaa															
pcn-mir-10a	CAUGUCGGUGCAAGACCUACCCUGUAGAUCCGAAUUUGUGuaauauuauuaacaacaaauuCGUGUUUGCACGGUAAGGCCUCGCACGUGACGCU	95	22,10526	14,73684	21,05263	20	43,15789	34,73684	1,357143	1,05	-36,3	-36,2	0,024951	6,41	-38,2105	-0,88537
pcn-mir-11	CAAACACCAUUCAGCAUCAUGUUCAUCACAGUCAGAGUUCACUGACUAACUGUGAGCAAAGCUCUGCUGGUGUCGA	76	19,73684	28,94737	26,31579	25	46,05263	53,94737	0,863636	0,75	-23,7	-23,7	0,279042	5,58	-31,1842	-0,67714
pcn-mir-1175	UGAUCAGGUGUGUUAUGUAGUGGAGAGAGUUUUAUCUCAUCAUGAGCCUCAGAAGCAGGUGAGAUUCAACUCCUCCAACUGCAGGCUAUACCUGAAAC	98	24,4898	27,55102	20,40816	27,55102	44,89796	55,10204	1	1,2	-42,7	-38,6	0,079856	5,62	-43,5714	-0,97045
pcn-mir-1187	GCGACUACAACACCACCUUAGUCAACACACUGCACCAGCCCCGGGGUGGCUGGGGGACGUAGGGUGggaguuuauauauaugugugugugUaugugugug	100	21	15	21	9	42	24	0,6	1	-30,8	-25,4	0,029578	28,62	-30,8	-0,73333
pcn-mir-12	UGGUGGUCAGACUGUGAGUAUUACAUCAGGUACUGAGAAUCUAACAAGCUUCAGUACCUUUUGUGAUAUUCUUAGUCUGCCAUUU	85	21,17647	24,70588	17,64706	36,47059	38,82353	61,17647	1,47619	1,2	-41,7	-40,3	0,196235	2,83	-49,0588	-1,26364
pcn-mir-122b	GGUCAACAGUAGUGUGACACUGGUGUGACAGUCGUGCCUGUCGUCACACAGGCCAGGGCCUAUACCC	91	26,37363	21,97802	29,67033	21,97802	56,04396	43,95604	1	0,888889	-27,9	-27,4	0,053765	26,46	-30,6593	-0,54706

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UGUCAUCACACAAUCCGCUUGCAG															
pcn-mir-1238	GACAGGGCGCGAGGGCCAUCGACUGGGUGUCUUCCUCGUCUGUCUGAAGCAGUGAUGCUGCGGGGAAGUCUGGUCAGUCGGAGGCUCUCUCUGGCCUUUA	100	36	14	25	25	61	39	1,785714	1,44	-49,3	-47,6	0,09807	9,54	-49,3	-0,8082
pcn-mir-124	UACCUGUUUGUGUUCACUGCGUUGGCCUUGGUGAUUUACACACUAUUAAGGCACGCGGUGAAUGCCAAGGGGAA	74	28,37838	21,62162	20,27027	29,72973	48,64865	51,35135	1,375	1,4	-33,9	-32,5	0,275153	6,77	-45,8108	-0,94167
pcn-mir-124c	UCCCCUUGGCAUUCACCGCGUGCCUUAAUAGUGUGUAAAUCACCAAGGCCAACGCAGUGAACACAAACAGGUA	73	20,54795	30,13699	28,76712	20,54795	49,31507	50,68493	0,681818	0,714286	-19,3	-17,4	0,083313	8,41	-26,4384	-0,53611
pcn-mir-1277-1	AAGACUCUAUGGUUAAACUAcgaugguauauauauauauguacguCUAUACGUUUCUACAAUGUAUAUUUGCCUUGUUCAUCCAUGCGUGAC	92	10,86957	19,56522	15,21739	27,17391	26,08696	46,73913	1,388889	0,714286	-19,4	-19,4	0,182954	5,41	-21,087	-0,80833
pcn-mir-1277-2	UGUAUAGAUAGUGUAUUUAUCUGUAUUUCUGCGUGUGUUCUUGAGUCUUUGCCUCUUUUaggcaaaaaaaauauauauauauauguaugau	91	13,18681	8,791209	8,791209	34,06593	21,97802	42,85714	3,875	1,5	-21,1	-21,1	0,15848	5,1	-23,1868	-1,055
pcn-mir-1322	UCUCUUACCUGcgaugaugcugcugaugacaaGGGGUAGAAUGGCAGCAUUCAUCAUCCGCAUGUACAGCUC	72	16,66667	15,27778	19,44444	19,44444	36,11111	34,72222	1,272727	0,857143	-19,5	-15,5	0,030502	11,17	-27,0833	-0,75

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-1328	gagagagagagaaaugagaaacaaauauuucgCUAGAGCUACAACAGUUUUACGAGUGCUGCUAUUUGCUGUUCACAUUGUCUCCUCUUAU	91	10,98901	13,18681	15,38462	25,27473	26,37363	38,46154	1,916667	0,714286	-22,2	-17,7	0,038242	22,78	-24,3956	-0,925
pcn-mir-133	AAUGCUCUUCUAUAGCUGGUUGAACUCGGGCCAAAUUGUUGAAGAGCCUUUCAUUUGGUCCCCUUCAACCAGCUGUAGUUAGCAGU	86	22,09302	22,09302	23,25581	32,55814	45,34884	54,65116	1,473684	0,95	-39,7	-39,3	0,1295	7,69	-46,1628	-1,01795
pcn-mir-133c	UAACUACAGCUGGUUGAAGGGGACCAAAUGAAAGGCUCUUCAACAAUUUGGCCCGAGUUCAACCAGCUAUAGAAG	75	24	33,33333	21,33333	21,33333	45,33333	54,66667	0,64	1,125	-30,4	-28,9	0,184949	4,61	-40,5333	-0,89412
pcn-mir-137b	AGUUCCAGUCGGUUACGGGUAUUCUUGGGUAAAUAAUACAUUGAGUAGUUGUUAUUGCUUGAGAAUACACGUAACUACCUGGAC	84	23,80952	27,38095	15,47619	33,33333	39,28571	60,71429	1,217391	1,538462	-33,1	-29,3	0,039071	10	-39,4048	-1,00303
pcn-mir-13b	uaaaauacacuuuaacUGACGUGUGGCUUCUGAUGUCUCUGAAGGGUGCGAGAGUUUGUUGUUCAGACUCAUCAAGCCUcguuaaaauguuugug	95	20	11,57895	12,63158	22,10526	32,63158	33,68421	1,909091	1,583333	-24,2	-23,8	0,019635	15,65	-25,4737	-0,78065
pcn-mir-1421a	CUCCUUCAGCAGUGAUUCAGUCUCACGCUGCAUCCCUUGUGACGGUGGCUGCGAGACUGAGACACAUGGCAUAAAGACA	79	25,31646	24,05063	27,8481	22,78481	53,16456	46,83544	0,947368	0,909091	-23,9	-23,9	0,016513	12,42	-30,2532	-0,56905
pcn-mir-1421am	GGUGCGUCAAGGCGGUCAGUAAGACGUCCGCCACCUUAGGCGUUCAAACGGAUUUCGAGGAGGUCGU	96	34,375	19,79167	23,95833	21,875	58,33333	41,66667	1,105263	1,434783	-31,8	-26,1	0,047723	21,41	-33,125	-0,56786

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AGGUCAUCCUGUAGACGACUUGGCGCUGG															
pcn-mir-143	ACGACAGAGGGCCUCAUCAGUCUGGCUGAACACAAGAAGUAGAAAGUGUUGCACACAGUCUGAGAUGAAGCACUCGUUUG	80	27,5	31,25	21,25	20	48,75	51,25	0,64	1,294118	-22,9	-21,7	0,179141	6,12	-28,625	-0,58718
pcn-mir-153-1	CUGUUGAUCACAACACCAGAUAAAUUACAGGAAACAGAACAUGUAACACGAGUAACAUGUUUACGCAUAUCAUUUUUGUGAUGUUAUCAAUAA	93	15,05376	38,70968	17,2043	29,03226	32,25806	67,74194	0,75	0,875	-19,2	-19,2	0,260282	8,93	-20,6452	-0,64
pcn-mir-153-2	AUACCCUCUUCCCAGGCAGCUUUUGUGAUUCAGCAAUUGUACAGCUAUCAAAUUGCAUAGUCACAAAAGUGAUCGGGAGGCGGGGAC	87	24,13793	27,58621	22,98851	25,28736	47,12644	52,87356	0,916667	1,05	-37,9	-37,9	0,256161	6,4	-43,5632	-0,92439
pcn-mir-1584	GAGUUACAAUCAUAACCGGGUGGGGCUGGGCCAUAUAAGgguagaucacgugaccacucGGUGAUUAGUUAGUAAGCA	78	24,35897	21,79487	10,25641	17,94872	34,61538	39,74359	0,823529	2,375	-20,5	-16	0,070486	11,15	-26,2821	-0,75926
pcn-mir-15c	UUGAAGAAUAUCUCUUAUCCCAUAGGACAGAUAUUUCAAGGAAUCAUGUGACCAGCAGACCAUUCUGGGCUAUGGGGUCAGAGCUAUUCUUUUU	94	21,2766	27,65957	19,14894	31,91489	40,42553	59,57447	1,153846	1,111111	-32	-28,3	0,131794	8,15	-34,0426	-0,84211
pcn-mir-1602	AUCCUAUAUCCAUGUAUCUAUCCUGUAAUGGGCUCUGCAUCACCAGCAGUCUAAUCUGUCUUCAGUA	96	18,75	27,08333	23,95833	30,20833	42,70833	57,29167	1,115385	0,782609	-25,3	-25,2	0,141519	11,45	-26,3542	-0,61707

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CAUGGCAGGUUAGACAUGAAUCUGAGCAA															
pcn-mir-1603	AUAGCAGAAAUCAAAACAGCCCACAUUUUAUGUCAAACUUAUUACACAGAGAUAUUAAAGCAAuggguuuguuuuguguugcgCA	86	8,139535	34,88372	15,11628	17,44186	23,25581	52,32558	0,5	0,538462	-20,1	-20,1	0,033978	10,39	-23,3721	-1,005
pcn-mir-1632	GAUGGCUGUUGACACACUCGAGUGACAAGACAAAGGUCUGAUUUCCUUGCUUGUUUUUGGAUGAAAUUAUUUUGCGACGCAGCUGUUCACAGCCUCU	97	23,71134	22,68041	20,61856	32,98969	44,3299	55,6701	1,454545	1,15	-26	-26	0,016941	14,04	-26,8041	-0,60465
pcn-mir-1677	UGACCAUCACCUUUAUCUCUCUGCCGUCGAGGUAGCGCGACACGAACUCCACUCCAUUCUGUGCGUUGACUUCAAUAGGAGAGACAGGAGUGAUGGUGA	99	25,25253	23,23232	26,26263	25,25253	51,51515	48,48485	1,086957	0,961538	-36,2	-35,3	0,026404	8,83	-36,5657	-0,7098
pcn-mir-1744-1	UUUGAGAAGAGGUACUUCAACAGGAGCAAGUCAAGGCAUGCUUCUUUUUAACACCAGUCUUCUCUGC	67	20,89552	26,86567	22,38806	29,85075	43,28358	56,71642	1,111111	0,933333	-19,2	-19,2	0,273743	3	-28,6567	-0,66207
pcn-mir-1744-2	CCACACACUUCAACAGGAGCAAAGUGUAAGAUGAUAAUGCUGUGCCUACAUGUUAGCCUCUUACAUCAUGUGGGCUAUCUGAUACUAAGUGUGGCC	96	21,875	28,125	22,91667	27,08333	44,79167	55,20833	0,962963	0,954545	-27,6	-27,6	0,347188	6,28	-28,75	-0,64186
pcn-mir-184	CAGUUCACCUUUUUCACGUUUCCUUGUCACUCCUCCGCCCCGUCUGUGAACAAGCACUGGACGGAGAAC	97	23,71134	20,61856	26,80412	28,86598	50,51546	49,48454	1,4	0,884615	-33,8	-33,8	0,131517	7,97	-34,8454	-0,6898

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UGAUAAGGGCUUGUGGGUGAUUUGACAA															
pcn-mir-190	ACCCGCUUCUGCUAGAUAUGUUUGAUAUAUUUGGUGCAGUUGUCGCGACGACCAAGUAGUCAAACAUGUCAGAGCAGCGACG	82	25,60976	25,60976	21,95122	26,82927	47,56098	52,43902	1,047619	1,166667	-32,5	-32,3	0,080048	9,84	-39,6341	-0,83333
pcn-mir-1905c	UGUAGGUGUGUGUCUGUUGCUGGAUGCGCUUGAUGGUCGCCCCCUUGGGUCCCACCACCAGCCCCACCACGCGGUAUGGCACAGCCACCC	90	28,88889	13,33333	35,55556	22,22222	64,44444	35,55556	1,666667	0,8125	-31,8	-31,7	0,089456	8,15	-35,3333	-0,54828
pcn-mir-1951	UUAGUUUUGCGCAUCAAUCACCAUCAUUUGUGUAAACGUCUUCCCUGACUUAUUUGGAGCCCCCAAAUGUAGUGGAGACUGGUGGCGAAACCUU	94	21,2766	23,40426	23,40426	31,91489	44,68085	55,31915	1,363636	0,909091	-26,2	-17,5	0,079573	16,28	-27,8723	-0,62381
pcn-mir-1976	ACUCUCCUGCCCUCCUUGCCCAGACAGGGGCAGCGUGUCCAUGACCUGUCUGUGCGAUCAGCUGCACGAGGGC	73	28,76712	15,06849	35,61644	20,54795	64,38356	35,61644	1,363636	0,807692	-28,7	-28,7	0,157786	6,45	-39,3151	-0,61064
pcn-mir-1984	ACACUGGCACUGUCGCCGUGCCCUAUCCGUCAGGAACUGUGAUCUCGCGAAACACAGGGUCUGGCGGUUGGGCCUCGGCGCUGGUGGUCcagacg	95	31,57895	13,68421	28,42105	20	60	33,68421	1,461538	1,111111	-47,8	-47,8	0,195263	3,22	-50,3158	-0,8386
pcn-mir-1985	AUGCCAUUUUUAUCAGUCACUGUGUGUUGUGAAAGucacagugaugaugauaauggcuUGAUG	63	15,87302	14,28571	7,936508	25,39683	23,80952	39,68254	1,777778	2	-27	-27	0,311248	2,46	-42,8571	-1,8

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-1986	CGUUUGUGGCCGCGGGUCAUGGGAGCGCCACGUACAAUCAAAGCGGUGGAUUUCCCAAGAUCCGUGAUCGCACUAC	76	30,26316	21,05263	27,63158	21,05263	57,89474	42,10526	1	1,095238	-33,4	-33,1	0,171582	3,66	-43,9474	-0,75909
pcn-mir-1990	GUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCUACCCCUCCCGGGACUACGUCAACGUACUACCACGC	72	26,38889	20,83333	30,55556	22,22222	56,94444	43,05556	1,066667	0,863636	-30,6	-30,6	0,28064	3,02	-42,5	-0,74634
pcn-mir-1992	GCAUGUGUCCAGUCAGUGGUUGACUGCUCGGUAUUCUAAACGUAUCAGCAGUUGUACCACUGAUUUGCUACGUG	74	25,67568	20,27027	21,62162	32,43243	47,2973	52,7027	1,6	1,1875	-32,7	-31,7	0,194317	3,34	-44,1892	-0,93429
pcn-mir-1994	CUGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCGUGUGUGAUGACGUCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGACACCGCUAA	90	30	18,88889	25,55556	25,55556	55,55556	44,44444	1,352941	1,173913	-41,1	-41,1	0,501637	4,6	-45,6667	-0,822
pcn-mir-1994a	UUUCUCAGGGGCGGUCACUCUGAUCUCCAUGUGCUCGCACCAGCAUGAGACAGUGUGUCCUCCCUUGAGGGA	72	27,77778	16,66667	29,16667	26,38889	56,94444	43,05556	1,583333	0,952381	-36,5	-36,2	0,349274	3,61	-50,6944	-0,89024
pcn-mir-1996b	UAUUCUGACCUUAUUUGAUAAUGACCAGUAUUUCCUUUCGUCGUCCUCUUGUAGACUGAUGCUGAUGCUUAACUGUCAUUAUCAAGUGAGGUCAGAAUA	99	18,18182	24,24242	19,19192	38,38384	37,37374	62,62626	1,583333	0,947368	-42,2	-42,2	0,071127	11,72	-42,6263	-1,14054

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-1a	GGCACAUACUUCUUUGCUAUCCCAUAUGUUCUUGCAAAGCUAUGGAAUGUAAAGAAGUAUGUACU	65	18,46154	29,23077	18,46154	33,84615	36,92308	63,07692	1,157895	1	-23,7	-22,1	0,075024	6,51	-36,4615	-0,9875
pcn-mir-1c	AGUACAUACUUCUUUACAUUCCAUAGCUUUGCAAGAACAUAUGGGAUAGCAAAGAAGUAUGUGCC	65	18,46154	33,84615	18,46154	29,23077	36,92308	63,07692	0,863636	1	-27,1	-26	0,4687	2,23	-41,6923	-1,12917
pcn-mir-2001	GCUGCCAUUUUGUGACCGUUACAAUGGGcauugacagaaaaacaaaugcuCCAUGUGGUGUUCACAAGAUGGCGGU	76	22,36842	13,15789	14,47368	21,05263	36,84211	34,21053	1,6	1,545455	-36,2	-36,2	0,193282	4,14	-47,6316	-1,29286
pcn-mir-2008	AGGUUAAUUAUAGUUUGUGUCCUCACUUGAAGGCACACUUCCAGUGUGAGAGUAUUAACAAUGUGGCUACAGUGAUGUGACAAAUAUUGUUAAUAC	96	21,875	30,20833	14,58333	33,33333	36,45833	63,54167	1,103448	1,5	-24,3	-24,3	0,153115	8,97	-25,3125	-0,69429
pcn-mir-203b	ACUUGUGAAGUUACCACCCAACAAAUAUUAGUUUGGGUCAAAGAAUUGAAUAUUUGAACUGUUAAGAACAGUAAAUUAGUUGCUAAUGGAACUUCCAUUU	100	17	36	14	33	31	69	0,916667	1,214286	-20,1	-18,9	0,016531	14,54	-20,1	-0,64839
pcn-mir-204	GUUCUUUGUGUCACCUCACUUCCACUUCCGGUGAAAUCCGGAUUGGUAAUGCAAGGACAGCAAAGGGA	68	25	25	23,52941	26,47059	48,52941	51,47059	1,058824	1,0625	-21,9	-21,9	0,137453	4,4	-32,2059	-0,66364
pcn-mir-2047	CCAAAGCCUAUGUCACGUCUCUCAGAGAUAAAGGACGUCAGCAGUGUAUUACGCCCUUUCGCCGAGCAGAUGUGUGAAGGUUAAG	85	25,88235	27,05882	23,52941	23,52941	49,41176	50,58824	0,869565	1,1	-23,3	-22,2	0,082417	6,14	-27,4118	-0,55476

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-2155	GUGUGCUCUGGUGCUCUGUGAAUGUAAGUUCUUUGUGGUAGAAUGAAGUGACACUGUUUUACACUCUACUGGAGCCUCAAGCAAAG	86	26,74419	23,25581	17,44186	32,55814	44,18605	55,81395	1,4	1,533333	-20,5	-17,1	0,059402	25,69	-23,8372	-0,53947
pcn-mir-216a	uguugguguuugucUAAUCUCAGCUGGUAAUUCUGAGUGGAGUUCUGCACACCUCAAGUUACUAGCCGAGAUUACAUAAAUAUCGUA	87	16,09195	25,28736	17,24138	25,28736	33,33333	50,57471	1	0,933333	-34	-34	0,097375	3,66	-39,0805	-1,17241
pcn-mir-216b-1	GCGGGACCACUUGCCCUGUGGAGCGAGGAUGCUCUGGAGGACGGCUGGACCUUUAUUAAAACUCGCCUCUACACAGUGGCUACUGGGUCCACA	93	30,10753	20,43011	27,95699	21,50538	58,06452	41,93548	1,052632	1,076923	-34,9	-29	0,081319	17,93	-37,5269	-0,6463
pcn-mir-216b-2	CGUAGGAAGAUGAGCCAGGAUUACAAGAUUGUUGGGCCUGCGGCCCUAAUAUCAGCUGGUAAUCCUGAGUGAGCUUGCCUCAG	83	30,12048	24,09639	21,68675	24,09639	51,80723	48,19277	1	1,388889	-31	-30,7	0,290814	5,92	-37,3494	-0,72093
pcn-mir-219-1	GUUGUCUGGCUGUGAUUGUCCAAACGCAAUUCUUGUGAAGUUUAAAUCAAGAACUGUGUGUGGACAUCAGUGCUUGA	77	25,97403	24,67532	15,58442	33,76623	41,55844	58,44156	1,368421	1,666667	-27,4	-27,4	0,170426	3,13	-35,5844	-0,85625
pcn-mir-219-2	GUGAUUGUCCAAACGCAAUUCUUGUGAAGUUUAAAUCAAGAACUGUGUGUGGACAUCAGUGCUUGAG	67	25,37313	28,35821	14,92537	31,34328	40,29851	59,70149	1,105263	1,7	-21,9	-21,9	0,222542	3,22	-32,6866	-0,81111
pcn-mir-2196	CAAGGUCAACUGCAAGAAUUUGCCUCUCUGUGCUGCCAGCAAAAAU	88	20,45455	32,95455	25	21,59091	45,45455	54,54545	0,655172	0,818182	-21,1	-14,7	0,0689	11,59	-23,9773	-0,5275

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UCUGAGCGCUCUGCAAGACAAAUACAAGCAUGUUGAACCAAG															
pcn-mir-2218b	aaaaauaauaauaaaguacauaUUUGGGUGGAGGCAUGGUCUAGCGCCUUGGGUUGGCGUGGGAACAUUUGGGAAAAAUUUGUAGUUUGUAUUCUUCGG	99	28,28283	13,13131	9,090909	27,27273	37,37374	40,40404	2,076923	3,111111	-21,1	-19,4	0,05187	8,22	-21,3131	-0,57027
pcn-mir-2284c	uaaugauaagCUGUACAUGAAACAGCUAAAAAUCUAAGUGAACUGUGACGGUGGAAAAUUUUACAUGUUGCACAGUCAUCUUGCUCAGCA	90	17,77778	30	16,66667	24,44444	34,44444	54,44444	0,814815	1,066667	-19,4	-19,4	0,041642	12,72	-21,5556	-0,62581
pcn-mir-2284t	UCUCUUUGAUUGAAAUCCCUCUUGAUCCAUGUCAAUAAAACUCGAAUGAAUGUAGUUCGUAGGACAGGCUCACUGUCAAAGAAAGUUACAAUCUAAGACC	100	17	33	21	29	38	62	0,878788	0,809524	-19,3	-17,8	0,046921	9,84	-19,3	-0,50789
pcn-mir-2324	AAACACGUGACUAACGUCGUUGACCUGGGGUUGGGGCAGUGACCAGCAGGUGUCGUCUGCUAGGCUUCAAAGCCGUUAGACCGACGUGGGC	91	34,06593	20,87912	24,17582	20,87912	58,24176	41,75824	1	1,409091	-29,7	-20,7	0,058231	28,39	-32,6374	-0,56038
pcn-mir-2392	AUCCCCUCUCACUCCCGGCCCUCGUUACGCCUUAUGUUAGCAUCCUGUCUCCUCUUUGCCUACAGGACUUAGUGAACGAUGGAUGGGGGUGAGGGGGAUG	100	27	16	29	28	56	44	1,75	0,931034	-43,6	-43,1	0,044553	14,74	-43,6	-0,77857
pcn-mir-2405	UUGCAGAAAACUGCAACAACACACAAGGCUUGUAUAUAUAUGGggu	74	10,81081	22,97297	10,81081	13,51351	21,62162	36,48649	0,588235	1	-20,3	-20,3	0,060748	10,16	-27,4324	-1,26875

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	agauugugugugugguuuguuuggu u															
pcn-mir-2464	GAAUGUUGUCUGGCGUCCucgacaucaacaucaacaucaacaucagcuUCAUCAGCUAUUGACUUCUGCUGCAGACCUCAAGGAUGCcagaaacaaga	98	14,28571	11,22449	15,30612	17,34694	29,59184	28,57143	1,545455	0,933333	-27,8	-26,8	0,142155	8,83	-28,3673	-0,95862
pcn-mir-2470	GCCAGAAAAACCUAAGCAUGACAAAAUAUCAUGCUUGUGUGGUUUUGGAUACUUGGAUUUUUCUCCC	67	19,40299	28,35821	19,40299	32,83582	38,80597	61,19403	1,157895	1	-19,9	-19,9	0,542669	2,57	-29,7015	-0,76538
pcn-mir-2491-1	GCAGUUGUCUUCUUUUGCAUGUUCUGUGUUCGUAAAAUCGCUUAUCAAUGAUGUAGUCGGUagccaacaacagcagcagcaacaacaacaacggc	95	14,73684	11,57895	10,52632	27,36842	25,26316	38,94737	2,363636	1,4	-23,2	-23,2	0,178642	4,92	-24,4211	-0,96667
pcn-mir-2491-2	GAUGGCGGCGAAGAAGUCCACGCcugaagaagaacaacaacagcagcagcaacaacaaggGUGGCGAGGGCUGCUUCGUCACCUGU	86	22,09302	9,302326	15,11628	10,46512	37,2093	19,76744	1,125	1,461538	-27,25	-26,3	0,182896	6,2	-31,686	-0,85156
pcn-mir-2491-3	agcagcagcagcagcagcaacaacaacagcagcagcagaacaGGCAAGGUAAUGGUGAUUGCUCUGCAUUUUUGUGUACUUCUGAUCUCCUAAA	94	12,76596	11,70213	9,574468	21,2766	22,34043	32,97872	1,818182	1,333333	-19	-15,7	0,14487	14,83	-20,2128	-0,90476
pcn-mir-2500	GAUCAUACAUUAAAGUGUUCAUAUGUAAUGUAAAGGGAAAAGGUGUAAUGUCUUCCCUUAACAGACAAGAGGAUUUUGUGUGUGGAC	87	24,13793	33,33333	11,49425	31,03448	35,63218	64,36782	0,931034	2,1	-24,7	-24,1	0,053178	5,65	-28,3908	-0,79677
pcn-mir-252a	CCUAACUUCUGGCCCAUUACUAAGUACUAGUGCCGCGGGAAGAUAACUUGUCAUGUCCCGUGGUUCU	94	24,46809	21,2766	26,59574	27,65957	51,06383	48,93617	1,3	0,92	-37,6	-37,6	0,059589	5,1	-40	-0,78333

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GGUCCUUACUACAGGGCGGAACUUGCA															
pcn-mir-254	GUGUGUGCAAAUCUUUUGCAACAGACUUUUAAACUAUGGGUGUUUGGUGUUUGAGUGUGCAGAGUUGUUUGCAAACUCUUUGCUACAGAA	90	25,55556	23,33333	13,33333	37,77778	38,88889	61,11111	1,619048	1,916667	-21,5	-16,1	0,016973	23,25	-23,8889	-0,61429
pcn-mir-279-1	UCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACACGUCAAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAGGACGUUCAC	94	22,34043	23,40426	26,59574	27,65957	48,93617	51,06383	1,181818	0,84	-39,9	-38,8	0,123884	5,39	-42,4468	-0,86739
pcn-mir-279-2	CUCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACACGUCAAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAGGACGU	91	23,07692	23,07692	26,37363	27,47253	49,45055	50,54945	1,190476	0,875	-39,9	-38,8	0,126379	5,36	-43,8462	-0,88667
pcn-mir-279b	AAGGGGACCAACCACUAGAGUGACUAGACUGAUAACCCCUAGAGAUGUUGUGCUUCAGUUAUCACUAACCAUGGUGGUGGAUCCCUGA	88	25	28,40909	22,72727	23,86364	47,72727	52,27273	0,84	1,1	-27,8	-27,3	0,031686	14,17	-31,5909	-0,6619
pcn-mir-2804	UUUUUAAACCACAGUAACAGAUGACAUGGUGAACCAUGAUGAAGGGUAGUGUAUUACAAUACUGACCAAGUUUUCAGCUGUUUGCUGUGUUUGUAAAUA	99	21,21212	31,31313	14,14141	33,33333	35,35354	64,64646	1,064516	1,5	-25,6	-25,4	0,006063	12,93	-25,8586	-0,73143
pcn-mir-281	AAAUGACCUCACGCUGAAGGGAGCAUCCGUCGACAGUCAGAAAUGC	88	26,13636	29,54545	22,72727	21,59091	48,86364	51,13636	0,730769	1,15	-35,2	-35,1	0,187538	3,76	-40	-0,8186

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AGCACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGG															
pcn-mir-2962	UCGUGCAGUGAGUCAGGUGCUCGUGACAGGGAUGCUGUGGCAGGUGUUGUGGGGCGUGACACAGGUCACUGUGCAUCCCCUGCCUCUCUCAUAC	94	34,04255	14,89362	25,53191	25,53191	59,57447	40,42553	1,714286	1,333333	-36	-36	0,402579	13,67	-38,2979	-0,64286
pcn-mir-297	AUGAACGAAUGAAUGUCUACAGUACUGUguacguguauguaugugugcauguauggaGCCUGGCAGGUAGAGAGAUGUAUAGAUGCAUUCAUUUUG	96	18,75	20,83333	9,375	20,83333	28,125	41,66667	1	2	-23,6	-19,07	0,041644	16,8	-24,5833	-0,87407
pcn-mir-29a	GACUGGGCCGGGAUGGAUGCUGGUCUCUUUUGGUGCUUAGAGUCAUUCCCUGUCUAGCACCAUUUGAAAUCAGUUUCUUGAACUGGCCA	89	26,96629	17,97753	22,47191	32,58427	49,4382	50,5618	1,8125	1,2	-36,3	-36,3	0,263044	3,27	-40,7865	-0,825
pcn-mir-29b	GGGAGGAGAGUGGGAGGCAGCGGGACACUGGUCUCGACUGGUGGAUAGAUGGCUGCUAUUCUAGCACCAUUUGAAAUCAGUGCUCUCGCUUGUUU	95	34,73684	20	18,94737	26,31579	53,68421	46,31579	1,315789	1,833333	-35,8	-30,9	0,043188	34,86	-37,6842	-0,70196
pcn-mir-2a-1	CAUCAGUUAUGACUGCUGAGUUCACAUCAAAGAGGCUGUGACUUUGUGAUGCUGUUUCAAAUCACAGCCUGCUUUGGUGAGCUCUUUGCUGUCAGAUUC	99	23,23232	21,21212	21,21212	34,34343	44,44444	55,55556	1,619048	1,095238	-40,8	-39,5	0,13114	5,78	-41,2121	-0,92727
pcn-mir-2a-2	AGGCAAAGCUAUGGUGCUGACCAAGUGACUGGGAUGUGUACCUUA	89	25,8427	25,8427	17,97753	30,33708	43,82022	56,17978	1,173913	1,4375	-39,8	-39,4	0,329351	1,72	-44,7191	-1,02051

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AUGUCAUAUCACAGCCUGCUUGGAUCAGUAUUAUGGUUUUGAAC															
pcn-mir-2a-3	AGUGCUAGGAUCUGCCCAUCAAAGAUGCUGUGAUGUGUUGAGUUCAGUCAUAUCACAGCCAGCUUUGAUGAGCUGGUCUAGCUUC	85	25,88235	22,35294	21,17647	30,58824	47,05882	52,94118	1,368421	1,222222	-40,5	-40,2	0,12355	3,87	-47,6471	-1,0125
pcn-mir-2a-4	ACAAAGCAAAUGUGCAUGGAGCAAUCAAAGUAGUUGUGAUGUGUUUGUUGACUUCAUAUCACAGCCAGCUUUGAUGAGCUUUUUCACAGUUUCUUGCA	98	21,42857	27,55102	17,34694	33,67347	38,77551	61,22449	1,222222	1,235294	-32,4	-30,6	0,111894	7,44	-33,0612	-0,85263
pcn-mir-2b-1	UGCAAGAAACUGUGAAAAAGCUCAUCAAAGCUGGCUGUGAUAUGAAGUCAACAAACACAUCACAACUACUUUGAUUGCUCCAUGCACAUUUGCUUUGU	98	17,34694	33,67347	21,42857	27,55102	38,77551	61,22449	0,818182	0,809524	-24,8	-24,8	0,336462	7,7	-25,3061	-0,65263
pcn-mir-2b-2	GAAGCUAGACCAGCUCAUCAAAGCUGGCUGUGAUAUGACUGAACUCAACACAUCACAGCAUCUUUGAUGGGCAGAUCCUAGCACU	85	21,17647	30,58824	25,88235	22,35294	47,05882	52,94118	0,730769	0,818182	-34,5	-34,5	0,219013	4,37	-40,5882	-0,8625
pcn-mir-2e	CUACUGGUAUAACUCAAUUAUCAAUCUCUUGAAUUCAGAGAUACCAACUUUGACUGAUGAGAUCUGAUACUGAAUAGCCAGAAA	84	15,47619	35,71429	19,04762	29,7619	34,52381	65,47619	0,833333	0,8125	-19,3	-19,3	0,294993	3,58	-22,9762	-0,66552
pcn-mir-2f	UCGGGUAGAUAAGCCAGCGAUGUGAGACUCAGACGAUGGUGUGACUGAGAGUUAGCAGACCAGUGU	96	27,08333	27,08333	20,83333	25	47,91667	52,08333	0,923077	1,3	-28,6	-28,6	0,066397	6,92	-29,7917	-0,62174

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/ mol)	MFEE(kcal/m ol)	Freq	Div	AMFE (kcal/ mol)	MFEI (kcal/ mol)
	AUGUAUAUCACAGCCAUGCUAAUCUCCUCU															
pcn-mir-3027	UCCAGGCCCCAGUCUUGCAUUUAUGAAACAUCAUUAGGAUUAUGCCUGGGUUAGUGGUGGAAUAUGAAAUGCAAGCUUUGUGCCUAAG	88	25	26,13636	18,18182	30,68182	43,18182	56,81818	1,173913	1,375	-25,5	-23,3	0,022525	10,35	-28,9773	-0,67105
pcn-mir-3050	AAUGAUCAGAUAUGAGAUCUUGAUAAACAUCAACUGACUGCUAAUUGGUCAUCAGGUCGAUGUAUGACCCAGUCCAAGAUGUGAUCUCU	89	20,22472	31,46067	19,10112	29,21348	39,32584	60,67416	0,928571	1,058824	-23,6	-23,6	0,62089	5,09	-26,5169	-0,67429
pcn-mir-3057	agagugacUGGCUGUUCUUGAGAGAUGUUAGCAAGUUAGUUCAAAAUGUUAUGGCGCGAACCAACAUCCCACAGGCCCAGCUGUCACAAA	90	21,11111	26,66667	21,11111	22,22222	42,22222	48,88889	0,833333	1	-24,5	-23	0,146061	9,33	-27,2222	-0,64474
pcn-mir-3071	AuaucaucaaaacaaauguGCAUAGUGUUACACAGAUACCAGGAUCAUGGAUUCAGCUGAUUUAGUGACUGaaacacuuucauuucuugAUGAAGC	96	15,625	19,79167	10,41667	16,66667	26,04167	36,45833	0,842105	1,5	-20,1	-19,8	0,178747	6,13	-20,9375	-0,804
pcn-mir-308	CGAGUGCGCAUGACAGCGCGCGCAGGAUUUGCUUGUUUUGAGCAACUCGGGUGGCGAUGUCCAUGACGCACAGC	74	33,78378	18,91892	25,67568	21,62162	59,45946	40,54054	1,142857	1,315789	-32,3	-32,3	0,25533	2,19	-43,6486	-0,73409
pcn-mir-3084a	UAUAUGUAUUGAAGGUUCAUUAGCCUUGUGGUCAGAGCACUCCAAUUUGGAGCAAAAGGUUACUGGUUCAAGGUCUGCUUGAACCUAUGACUAAAUaau	99	22,22222	27,27273	16,16162	31,31313	38,38384	58,58586	1,148148	1,375	-27,5	-22,4	0,08872	12,04	-27,7778	-0,72368

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-31	UCAAGGUGUGAAUCCAGGUUAGGCAAGAUGUUGGCAUAGCUGAGUGAACUCUAACAUCAGCUGUGUCGCAUGGUGCCACCAUUUGGGUUCUUGUGAAC	98	28,57143	23,46939	19,38776	28,57143	47,95918	52,04082	1,217391	1,473684	-39,3	-36,9	0,095943	6,94	-40,102	-0,83617
pcn-mir-315	UUGGCUCAUUUUUUGAUUGUUGCUCAGAAAGCCGGUGACUCAGCUGCGGCACUCGAGUAACAAUCAAAGCGUGACGCU	78	25,64103	23,07692	23,07692	28,20513	48,71795	51,28205	1,222222	1,111111	-33,4	-33,4	0,276248	3,37	-42,8205	-0,87895
pcn-mir-317-1	AAUAUGUGCACUGUGGGAAGGAUACCAUUGCUUGUUCACAGUGAAUUGGACAUGUGAACACAGCUGGUGGUAUCUUUUUUAAUGUGAACAUGAC	94	25,53191	27,65957	14,89362	31,91489	40,42553	59,57447	1,153846	1,714286	-40,1	-40,1	0,224017	2,93	-42,6596	-1,05526
pcn-mir-317-2	UCACUUAUUGGCAUGUACAGUGAACACAGCUGGUCACAACAUCCUCACAUACAGUUGUACAGUGAACACAGCUGGUCACAACAUCCUCACAUACAGUUG	99	17,17172	31,31313	27,27273	24,24242	44,44444	55,55556	0,774194	0,62963	-22,1	-22,1	0,047361	10,2	-22,3232	-0,50227
pcn-mir-3173	ACAUGUACUGUUUCUAGCUGAGCACAGAUACCUUUAAGCCAGAGUGCUCGGAGUGUUCUGAUGCUGAAGGAGGAAACAGGCUACAGAU	88	27,27273	28,40909	19,31818	25	46,59091	53,40909	0,88	1,411765	-29	-29	0,195168	5,51	-32,9545	-0,70732
pcn-mir-33	GUGUACUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGCUGAGAAACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGUAUGC	83	26,50602	27,71084	16,86747	28,91566	43,37349	56,62651	1,043478	1,571429	-38,7	-37,7	0,204831	5,09	-46,6265	-1,075

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-340	GAAUAAACAUAUAAAACGUCUGUGGGAUUAUAAAGCAAUGAGAGUUUCCGUUGUGUGUUGUUUAGAAAAUCCCACAUGUUGCAGuuuguuuaaau	95	20	29,47368	11,57895	27,36842	31,57895	56,84211	0,928571	1,727273	-21,5	-20,6	0,012485	17,74	-22,6316	-0,71667
pcn-mir-345	UCAGCGGCUCGUGGUGCAACAUUUGUUACCUGCACCUUUCUGCACUCGGCGGAGAUGAAGAACACGUGACGAGAACGUGCUGACCCCUAGUCCGCCUC	98	26,53061	20,40816	30,61224	22,44898	57,14286	42,85714	1,1	0,866667	-28,8	-28,8	0,301092	13,36	-29,3878	-0,51429
pcn-mir-3529	UGUGGCUGCAGCAAUCAGGGAAGAAUGUGAUUUAUUGUUAGUCAGCAUCAGAACAACAAAAUCACUAGUCUUCCAGAUCACGGCAGCCugg	91	21,97802	30,76923	20,87912	23,07692	42,85714	53,84615	0,75	1,052632	-30,8	-29,7	0,103281	5,67	-33,8462	-0,78974
pcn-mir-3547	ACAAUUAAUAGAAGCUAGACAAUGAUAGCGGGUGGCCAAGUGGGAAGAGGGGUGGAGGUGAAGCCACCGCAUACACACCCUGUCaacuuuuuaauauc	98	27,55102	27,55102	17,34694	13,26531	44,89796	40,81633	0,481481	1,588235	-22,6	-22,6	0,156123	13,36	-23,0612	-0,51364
pcn-mir-355	UGAcugauuuaucuguuuauuuguuuuagccUGAGUCGCCAGAGGAAAUGGAUGAUGAAUCUGAACAACCUAAAACAGCUGGCAAGAUAAUUCAGGCA	98	18,36735	27,55102	12,2449	13,26531	30,61224	40,81633	0,481481	1,5	-22,1	-22,1	0,017425	13,25	-22,551	-0,73667
pcn-mir-3609	CAAAGUGAUGAGUAAUUAAGGCGCAUUUGAAUUAUGGCUACCUCCAAUGAGAUUUAUAACACUAUA	92	16,30435	34,78261	17,3913	31,52174	33,69565	66,30435	0,90625	0,9375	-18,5	-17	0,066153	14,65	-20,1087	-0,59677

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AAUGCCAUAAAUUGUGCAUCUCUCAU															
pcn-mir-3680	GAAUGUCUUGCUCCUGGUGUGGGUGACUCACUCACAGGAUGUGGUGAGGACCUCGGGCAGCUAGCUUCUGCCgaucacacacaccaacaacacaaaa	97	24,74227	11,34021	18,5567	19,58763	43,29897	30,92784	1,727273	1,333333	-32,3	-32	0,065042	7,8	-33,299	-0,76905
pcn-mir-36b	UGAUGCGGUGAGUGUAAACCCUGGUCGGUGCUCACCAGCAACAUCACCGGGUAUACAUUCAUCCGCACCC	70	24,28571	22,85714	31,42857	21,42857	55,71429	44,28571	0,9375	0,772727	-30,8	-30,8	0,109108	5,78	-44	-0,78974
pcn-mir-3716b	CUCAUCAGUCGGCUAUUCGAUUCGAUGUUAUUUGAAAUAUCAAACAUUCGAUUUGAAGUGUCGCUGUAUAUC	72	18,05556	26,38889	18,05556	37,5	36,11111	63,88889	1,421053	1	-20,4	-20,4	0,086216	4,88	-28,3333	-0,78462
pcn-mir-3739	CAGUCCCCCUUUCCAUGUCGACCUCUGCAAGUUCAUUGCCAUGAAGGCAACGAAAGGUGcuugggaggggggagagaguggAAAGGUGAGGAGGG	94	22,34043	20,21277	19,14894	15,95745	41,48936	36,17021	0,789474	1,166667	-39,3	-38	0,332678	4,7	-41,8085	-1,00769
pcn-mir-375-1	ACAGAACAUUUCGCUGCCCAAUGACCCGAGCCGCUCGUAGCAAGGCAUCUUCACAAGUUUUGUUCGUUCGGCUCGCGUUACCAUGGUGGCACUUGCAG	98	24,4898	20,40816	29,59184	25,5102	54,08163	45,91837	1,25	0,827586	-34,5	-34,5	0,452928	2,76	-35,2041	-0,65094
pcn-mir-375-2	GGGACUUAAUUCAUCGCGAGCAGAAAAGAACGCAACAUCUUGUUCGUUCGGCUCGUUCUGAAAAAGUGAC	70	24,28571	30	21,42857	24,28571	45,71429	54,28571	0,809524	1,133333	-20,3	-20,3	0,298895	4,19	-29	-0,63438

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-377	UUUCCAGAUUAACUAGAGGUUGCCUUUGGUGAGAGAAGUCAUAGCCGAUGUCUUCAUCCUAGGAAUUAGCUAGUCUGGUAG	81	25,92593	24,69136	17,28395	32,09877	43,20988	56,79012	1,3	1,5	-24	-24	0,093863	9,2	-29,6296	-0,68571
pcn-mir-3776	UCGAGCACGCUUCACCUUUGCUUUCUCUAUGCCUGAAAAGGAGGGGGGGAGAGAGauuuauaaacacauauauaagcagauaugagugAGCGUCUGUG	98	22,44898	13,26531	14,28571	16,32653	36,73469	29,59184	1,230769	1,571429	-25,2	-24,8	0,072592	27,27	-25,7143	-0,7
pcn-mir-3809	UUACUACUUCAACUUUUCGGUUAGUCGGUCGGUCAGUUGGUUAGAUGACUUUUUGUCAUUUAGCAACUCGGCACAGAUAAAGAGAUAGAUGAAUAGAUA	99	22,22222	28,28283	15,15152	34,34343	37,37374	62,62626	1,214286	1,466667	-24,9	-24,7	0,021265	13,08	-25,1515	-0,67297
pcn-mir-3831	CAGCUUGUGUGUCUCAGAGCAAACAUUGCUAUUUUUCAUAUCCAAUGUGGCUCCGAGAUGCAAAAGGUA	69	21,73913	27,53623	20,28986	30,43478	42,02899	57,97101	1,105263	1,071429	-23,4	-23,4	0,214068	5,17	-33,913	-0,8069
pcn-mir-3928	ACCAAGCAACUUUGUCUCAGACCUAUCAUUGAGAUUCACUAUGAAAUCAGUAUAUGAAGCUCUAAGGUUCAUCCCAGACAAGGCUGCAUUUUA	93	16,12903	32,25806	22,58065	29,03226	38,70968	61,29032	0,9	0,714286	-21,1	-19,7	0,138205	13,46	-22,6882	-0,58611
pcn-mir-3957	guugguguugguguuggugcugguguugguguugguccCAUAUCCAGAAGACGCACAGCACCUCACACUGACGCCGUU	78	8,974359	15,38462	19,23077	7,692308	28,20513	23,07692	0,5	0,466667	-39,7	-39,7	0,412668	1,21	-50,8974	-1,80455

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-3965	UGCUUAUCAGCCUGAUUCUGCUAACGCUGCAUCGUUGAAGUCAGCUAGCUGUGAUAGAAGGAAUAACAGGCUUGAUAAAAA	81	23,45679	30,8642	18,51852	27,16049	41,97531	58,02469	0,88	1,266667	-26,4	-26,4	0,24589	2,99	-32,5926	-0,77647
pcn-mir-4057	GGUCGGCAACUGACCUCCUGCAUCUCCAGGGUGUAGGAGAUGGGGGUGGCUUGGCGACUGUAGUAGGGCAGUUCCGCUG	79	39,24051	15,18987	22,78481	22,78481	62,02532	37,97468	1,5	1,722222	-33,5	-28,4	0,21803	20,3	-42,4051	-0,68367
pcn-mir-4066	aacccaucauGCAGAACAUGCCUUUAUCAUGUGUUAGCUAAACACUUGGUUAUCGUGCUCACACGAAGACAGUGUUAAACCAGUGUUUUUCAUGUGGGGA	100	21	24	17	28	38	52	1,166667	1,235294	-29,1	-22,3	0,120404	15,88	-29,1	-0,76579
pcn-mir-4070	GCAAGCAGGUUGUGAGCGACCACCacgcgucacgugacaccuaGUGACAGCUGUGUUGACGUCACAGGCAGCUGUC	76	25	15,78947	19,73684	14,47368	44,73684	30,26316	0,916667	1,266667	-25,8	-25,2	0,153161	8,62	-33,9474	-0,75882
pcn-mir-4185	CAUAAAGUAUCUAUGUUUAAUGCGCUAUUGUGUGAGUCUCCUUCUUUGUAUUCAUACUGUCUGUUACAAGCAAGCGGAUUAUUCAAAGAAUACUUUGCA	99	17,17172	27,27273	17,17172	38,38384	34,34343	65,65657	1,407407	1	-24	-18,6	0,091273	7,49	-24,2424	-0,70588
pcn-mir-4187	CUAGUGUGGUCAAUUAACAACUGUUUUGGUGUUGUGCUGUUUAACUUCACGUCGAAGUAAACAguauauuuucacacacacauc	84	16,66667	19,04762	11,90476	27,38095	28,57143	46,42857	1,4375	1,4	-21	-15,37	0,010024	18,73	-25	-0,875
pcn-mir-4195	ACCCUAGUUACAUGUAAUACAUUGUACCUUGGUUACAUGUAAUAC	85	12,94118	32,94118	20	34,11765	32,94118	67,05882	1,035714	0,647059	-22,2	-22,2	0,043533	6,38	-26,1176	-0,79286

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AUUGUACCCUAGUUACAUGUAAUACAUUGUACCCUAGAAA															
pcn-mir-4271	UACAGGUCACCUAACAUCAUUUGCCACAGUUUUUCUCUUAGAACUGUGGGGAGAGGUGGUAGGGGGAAGAAAAGGUGGCAGGUGUGGCAUGUGUCCUAAA	100	32	26	16	26	48	52	1	2	-35,9	-32,3	0,296371	32,35	-35,9	-0,74792
pcn-mir-4323	AUCUGCGGCUUCCUGCACUUAGAGGGGAGCGAUUUGCUUUUGACAGCCCCACAGCCUCAGGAGCAGAAAGCUGCAUAG	78	28,20513	23,07692	26,92308	21,79487	55,12821	44,87179	0,944444	1,047619	-28,2	-24,9	0,122046	7,91	-36,1538	-0,65581
pcn-mir-4472	UGCUCUGCAGCAACAAUCGACUAUUCCCACCCUCCUUUUUuacuggggggggggugggggguguuGUUGAUCAGAAAU	79	8,860759	16,4557	20,25316	21,51899	29,11392	37,97468	1,307692	0,4375	-38,6	-38,6	0,308719	10,28	-48,8608	-1,67826
pcn-mir-449a	ACAACUGUACAGACUUUAGUCCAAUCAUCUAUACUGGCUUGUAUGUUUGACACCAGCUGACAUUCAGUCCAGAUGAUAAGCAGAUCUUGACAGUGUC	97	18,5567	28,86598	22,68041	29,89691	41,23711	58,76289	1,035714	0,818182	-22,3	-19,2	0,020241	9,91	-22,9897	-0,5575
pcn-mir-449d	CCUAUCAACCAUUGUCAGCAGUGAAACUAAUGGUAUUCAUUUGUCUUGAAGGCUGUGUGCUGUAAAGAUAAUGCUCACUGCUGCCCUCGUGGAUCUG	97	22,68041	23,71134	21,64948	31,95876	44,3299	55,6701	1,347826	1,047619	-25,6	-22,8	0,037152	9,97	-26,3918	-0,59535
pcn-mir-4525	AGUGCAUGCCAGAUAUCCCACCACGUCAUGCGCAGGGUGUGCCUG	70	35,71429	18,57143	27,14286	18,57143	62,85714	37,14286	1	1,315789	-31	-30,8	0,214837	9,25	-44,2857	-0,70455

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GACCUGGGGGGGAUGUGCAUGCCAG															
pcn-mir-4617	CCAGGUGUAGACGGGUGUGACAAGUCcucaacacacagacacuggUUAGUGGGGUCUUCUGUGGCUGUCACACCUAAACACCCGC	85	23,52941	15,29412	20	18,82353	43,52941	34,11765	1,230769	1,176471	-30,3	-19,95	0,101687	17,71	-35,6471	-0,81892
pcn-mir-4654	GGCUGAUACGCCAGGUGAUGUGGGAUCUGGAGGCAGACUUCGGCUUCCGCAUCGGCCCGUGGAACCAGGCCUACAUGUACGACACCCUGCCGAUCAGUC	99	31,31313	19,19192	30,30303	19,19192	61,61616	38,38384	1	1,033333	-41,7	-40,2	0,172557	4,86	-42,1212	-0,68361
pcn-mir-466i-1	CAUAACCACAAGCUACACACGACUAUUCAGAUAUGCAUUGACACCUAUCUACACUUGUGUcaguauguguaucugugugugugugugugugugugu uugu	98	7,142857	20,40816	17,34694	16,32653	24,4898	36,73469	0,8	0,411765	-36,4	-36,4	0,12872	16,86	-37,1429	-1,51667
pcn-mir-466i-2	gugugugugugugugugugugugugugugugugugaugguuuaucACUCACCAUCUCAAUCUUUUAUGUGCACAAACACACCCCCAGCACACACAGAACAAGC	100	5	21	22	10	27	31	0,47619	0,227273	-34,8	-12,3	0,119059	30,37	-34,8	-1,28889
pcn-mir-466i-3	GUGUgcauagcugugugugugugugugugugcgugcgcgcgcccCACGUCUCGUGAUGAGCCAGUACACACCACAGAACUCGUGCAGCG	89	14,60674	13,48315	16,85393	10,11236	31,46067	23,59551	0,75	0,866667	-31,6	-16,94	0,020806	35,43	-35,5056	-1,12857
pcn-mir-466i-4	ggugugugugugugugugugagaagugUCCUCUUAAUUCAGACAGAAGAG	94	13,82979	12,76596	10,6383	12,76596	24,46809	25,53191	1	1,3	-36,9	-36	0,067742	18,68	-39,2553	-1,60435

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUGUGCUCGUGAGGACAGACUGCuaaacacacaucacacacuaU															
pcn-mir-466m	CAUAGUAUGUUCuucucggugugugugugugcaugugcaugugugcuugcauguaaGUGAACAAGCAACCGAGUCAGCAAAUGCUCGG	88	12,5	15,90909	11,36364	10,22727	23,86364	26,13636	0,642857	1,1	-26,9	-24,4	0,033755	13,99	-30,5682	-1,28095
pcn-mir-466n	uuuuauauuACUUCAUGCUCAcgaaugugugcacacacacacaugggugCAUAGGAGACAGGUGUGUGCGUACAUGUACUCAUGUAUAUACAU	95	12,63158	16,84211	11,57895	17,89474	24,21053	34,73684	1,0625	1,090909	-27,2	-25,5	0,120489	14,18	-28,6316	-1,18261
pcn-mir-466p	UGCUGUUUAUCCCUUCACUAUCUUCCACACUUCCUAUCUCACUGAAUGAGUGAAuuauaauaugugugugUacaugugaagAGAGAAUCACUC	93	8,602151	18,27957	20,43011	23,65591	29,03226	41,93548	1,294118	0,421053	-19,9	-15,6	0,079044	7,09	-21,3978	-0,73704
pcn-mir-466q	UCGAUGAGGUAGUGGUGCACAAAUGAGAGAAUUAUUUUUGAGAGAAGAAUUCAGAUUUUGAGGCAGUAAAUACUGCaucaugugcacacacacacauacg	100	21	26	7	22	28	48	0,846154	3	-25,7	-22,5	0,021246	16,27	-25,7	-0,91786
pcn-mir-467f	UAUGCCAACGUCUCCCUCCCGCUGAaaaauuuauauacacacacacaccuuucaaGUGGGAGGAGAUGGACAAUGGCCCA	80	18,75	13,75	18,75	11,25	37,5	25	0,818182	1	-26,5	-26,5	0,059461	8,5	-33,125	-0,88333
pcn-mir-4715	CGCCACGCUGAUCACGUGCCAACGUGCCACCUUAACUGCACGGACCGCGGAAGAUGGUUUGGCCGUGGAAAGUGAGAGGUGAGU	84	33,33333	22,61905	26,19048	17,85714	59,52381	40,47619	0,789474	1,272727	-31,6	-31,6	0,443187	3,44	-37,619	-0,632

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-4757	aaaaaaaaccaaaacucaAGCGUCUCAGUAAAGGGUCUACAUUUUACACCUGUCAUUUCCAUGACGUCACAGAGGCGAGGUUUGGCUUUUGGA	93	20,43011	18,27957	17,2043	24,73118	37,63441	43,01075	1,352941	1,1875	-22,4	-21,8	0,139005	15,42	-24,086	-0,64
pcn-mir-4801	AAAGGUCUUCCUCUGUGUGUCUCCAGGAACCGGUCAAUAUUUCCAGCUGAUCAACACCGUUCUGAACGAAAUACACAAGAAAACCAAA	89	16,85393	33,70787	25,8427	23,59551	42,69663	57,30337	0,7	0,652174	-19,8	-19,8	0,127971	8,44	-22,2472	-0,52105
pcn-mir-4860	GGUGCACAUGCUUGUUUAGAAGUUACAAGCUUUGCUAGAAAAUGAUUGUAAGUUAUGUUGUAGAGAUUGUGUGAACUGCUAGACACAUCACUGAUGCUCU	100	24	28	14	34	38	62	1,214286	1,714286	-21	-15	0,009321	18,79	-21	-0,55263
pcn-mir-49	aacaaaagaaaccaaaaaggGCAUCUUCCCAUGAUGCAAAUAGACUAAGGGAAGCACCAUGUGAAGCACUUUUCUGGUUUCUUUUCCa	88	14,77273	19,31818	18,18182	23,86364	32,95455	43,18182	1,235294	0,8125	-26	-26	0,306727	8,11	-29,5455	-0,89655
pcn-mir-4918	AGCAACGAACCGAUGGGAGCUGUGAGCACGAUGGCCAGCACUGCCAGUGUCAGAACCUGCCCACAGUCACCGUUUGCGuucaa	83	27,71084	22,89157	28,91566	14,45783	56,62651	37,3494	0,631579	0,958333	-25,6	-24,9	0,031622	11,38	-30,8434	-0,54468
pcn-mir-4968-1	agcaucagcaucagcaacagcagcagcagcagaggaCCAGCCCAGAAGAUUCUGGUAGCCAGACCGCUGCACGCGCUGGUCCUGCGCAGAUCGA	94	18,08511	12,76596	21,2766	9,574468	39,3617	22,34043	0,75	0,85	-30,8	-28,6	0,049334	13,84	-32,766	-0,83243
pcn-mir-4968-2	CGACAGCGcacuggcagcagcaacagcagcagcagcagcagcagcacucgGCGGA	96	21,875	6,25	15,625	12,5	37,5	18,75	2	1,4	-34,7	-33,6	0,230058	16,55	-36,1458	-0,96389

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UGUGCAGCUUCCCUCGGUGGUUGCUGGCAGGGCCACUGGUU															
pcn-mir-4968-3	ACUUGCGCAUGCUUCGAGGUGUGGCUGCGCCCUCUCUUAGACAAGGUUGAGcgcacagcaacagcagcagcagcagcagca	81	19,75309	9,876543	16,04938	17,28395	35,80247	27,16049	1,75	1,230769	-27,9	-24	0,074193	12,7	-34,4444	-0,96207
pcn-mir-4968-4	uugugugugugugugagacuggcAUCAUUAUGCUAAGUACUCAUCAGCCUCGACUGUAGCCACUAAGGAUguacagcaacagcagcagcagcagcg	96	8,333333	14,58333	12,5	13,54167	20,83333	28,125	0,928571	0,666667	-21,1	-16,1	0,014202	21,15	-21,9792	-1,055
pcn-mir-5317a	GGGCCAGGGCCACAUCCCUAGCUACGGUccguuucuugucucuguguaCCUCUUGUGCUGCCAGACCGAGUGGUGAUCGGUGACCGCUGGAAC	93	25,80645	12,90323	24,73118	15,05376	50,53763	27,95699	1,166667	1,043478	-29,1	-29,1	0,378556	7,01	-31,2903	-0,61915
pcn-mir-5391	uuccugcaaGGUACCUUAUGAGGUAACUUGUUUGGACAGUUAUGAAGAAGUGGAAUUUAAUGUCCAACAGUUUAGAAUCAAACAGGCUAUCAUUCAGACc	100	20	30	13	27	33	57	0,9	1,538462	-18,8	-15,1	0,010656	34,01	-18,8	-0,5697
pcn-mir-5392	AAGUGAUUUUGCUCCAUGUGUGCAAUAAACUGGGAAAGAACGAUCUUUUUAGGUUUUAUUUGGCACAAUAUGUGUUACUugacauuuugagaaaacagUG	100	18	22	10	31	28	53	1,409091	1,8	-18,9	-12,7	0,006717	26,01	-18,9	-0,675
pcn-mir-5440	aaaaaauuugcgAAUGCUUUUUAGUUUAUCAGGAGGACUGAAGGGUGGAUGUGAAUACCACAUCCuuaac	98	15,30612	19,38776	11,22449	21,42857	26,53061	40,81633	1,105263	1,363636	-20,2	-18,8	0,104707	19,27	-20,6122	-0,77692

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	aaacuaaaaauaaccUCACUAAUUUGAC															
pcn-mir-5549	CCccaaaauaucaaaauagaaUAAUAAGAGGAGGGUGGGACUUCUUUAACAUUACACAGAUAUCCUAUUAUUCUUCAUGUUGGUUUUUUGAAU	93	15,05376	21,50538	11,82796	31,1828	26,88172	52,68817	1,45	1,272727	-19,5	-19,3	0,091982	11,56	-20,9677	-0,78
pcn-mir-559	AUCUGUCAAAGUACACAAACUAAUGAUGCUCAAAAUGUUAGCCAUUUGCGUUUAUAUGAUAAAGUAAAUAAGCACAGACUAUGUGUGGUUGUGACAGUU	99	19,19192	35,35354	14,14141	31,31313	33,33333	66,66667	0,885714	1,357143	-20,1	-16,59	0,039207	24,4	-20,303	-0,60909
pcn-mir-5594	GCAGUAAAGAAGGAAGACACGGUAUUUGCUGUUACAGACCUCGCAUAGCUAAGAGUACUGUAGUUUUUCCAAAGACCGUUCUCGCUCUCCGUUUACUCA	99	21,21212	27,27273	23,23232	28,28283	44,44444	55,55556	1,037037	0,913043	-22,2	-20	0,015865	13,26	-22,4242	-0,50455
pcn-mir-5595	UAGUGUCACGUGCUUUAAAAAAGGUGCAGGCUCUCUUUUUUCUCGCAGUCCCGCACUGACCUGAGAGAGUCACCAUCUUAUGUCAAACACAUGGACAAGA	100	21	27	25	27	46	54	1	0,84	-26,5	-26,5	0,090708	10,96	-26,5	-0,57609
pcn-mir-574-1	UCUAGACCUCAGUGCACGCGcggcgugagugugugugugagugugugugcgugugugugugcagagcuGAACGCAGGAGCACGAGCGGAGCUCCCCCCUCAACACCCCAGUGCUGUCGUCAUGGACCAUGCUACCUCC	140	15,71429	13,57143	25	10	40,71429	23,57143	0,736842	0,628571	-42,8	-36,9	0,005974	29,56	-30,5714	-0,75088

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-574-2	AAAGCGCCACACUCUAGACCUCAGUGCACGCGcggcgugagugugugugugagugugugugcgug	67	10,44776	13,43284	17,91045	5,970149	28,35821	19,40299	0,444444	0,583333	-29,2	-15,45	0,069833	22,63	-43,5821	-1,53684
pcn-mir-5965	AUCUUGGGUGAUGACAAUUCUGACAUUUUGCAAGGUUUCAUCCUUGUCUGUUUCAUUCUUCAAACUGCGAAGUCGCGCAUCACCAAUGG	89	20,22472	22,47191	22,47191	34,83146	42,69663	57,30337	1,55	0,9	-20,4	-19,7	0,042628	9,27	-22,9213	-0,53684
pcn-mir-6	CCGCCAGUCGGACUAAAGCAGUCCGUUUUGUUGGCAGGAGggaacugcugcugcagcgacugggcc	66	19,69697	12,12121	15,15152	13,63636	34,84848	25,75758	1,125	1,3	-29	-25,9	0,187241	5,82	-43,9394	-1,26087
pcn-mir-6013	GGCGCCCUGGCCUACGAGCGGAGGAACAGCAUGGCGACCCUGUCCUCGGCUGCUGACGACCGCCUCAAACGCCAGAGGCUGA	82	32,92683	19,5122	35,36585	12,19512	68,29268	31,70732	0,625	0,931034	-33,6	-22,8	0,076623	17,71	-40,9756	-0,6
pcn-mir-6037-1	GGAAUCUUAUACACUAUACUGUGUGUACUUUAGUGUAACAUGGAAUCUUAUGCACUAAGCUCUGUGUACUUUAGUGUAACAUAGUAUGUGGACAGAUAUG	100	21	29	14	36	35	65	1,241379	1,5	-27,2	-27,2	0,192392	10,82	-27,2	-0,77714
pcn-mir-6037-2	AACUCUGUGUACUUUAGUGUAACAUAGUCAUGGAGUCUUAUACACUAAGCUCUGUGUACUUUAGUGUAACACAGUCACGGAAUG	84	20,2381	28,57143	17,85714	33,33333	38,09524	61,90476	1,166667	1,133333	-27,2	-27,2	0,62986	1,19	-32,381	-0,85
pcn-mir-6076	GCUGACACCCUUCCCUCAGGUCGUCCUCCUCUAAGAAGCAAACAGAAGCAUGACAGAGGAGAGGAGAAAACCCAAAGGGAGGGCUCUCUGU	91	26,37363	30,76923	27,47253	15,38462	53,84615	46,15385	0,5	0,96	-30,3	-29,9	0,158352	9,81	-33,2967	-0,61837

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-6098	GUGCUCGUCAUAGUGAUUGUGUGUUUCUAGAAGACAAGACCGUGUUCUGUUCAGAACACAAACAACAUGCUGAUUGUCGAGUAA	84	23,80952	28,57143	17,85714	29,7619	41,66667	58,33333	1,041667	1,333333	-22	-19,4	0,02079	16,09	-26,1905	-0,62857
pcn-mir-6132-1	gaaagcagggcuggggauucuggcauggcaccguuCCCCCAUCGGCCAGGUGCCAGAGCACCAAACCUGACUGAa	75	12	13,33333	21,33333	5,333333	33,33333	18,66667	0,4	0,5625	-29,7	-28,6	0,15428	5,96	-39,6	-1,188
pcn-mir-6132-2	CCCUGCAagagcagggcuggggauucuggcaaugGCGCCUCCUCCCUUCGCCAUGGUCCAGAGCcaaccacccuggcugcaaga	84	9,52381	4,761905	21,42857	8,333333	30,95238	13,09524	1,75	0,444444	-34,2	-34,2	0,026095	5,82	-40,7143	-1,31538
pcn-mir-6132-3	ggaagcagggcuggggauucuggcaugggcacGCGCCCCGCCACGUCCAGAGCUACACCCUGCUGGA	67	13,43284	8,955224	23,8806	5,970149	37,31343	14,92537	0,666667	0,5625	-30,2	-21,3	0,185778	16,57	-45,0746	-1,208
pcn-mir-6335	AUAGACAUUCAAGCCAAUCACUGCAUACACAGUGAUGCAGGUCAUUCGACAACUUUACUGCACCACUGUUUGAGCAUAUGUCUUGUGUCAGU	92	18,47826	28,26087	23,91304	29,34783	42,3913	57,6087	1,038462	0,772727	-25,4	-25,4	0,193109	5,21	-27,6087	-0,65128
pcn-mir-6416	AGCAAAUUGCUUGAUCAUAGUGAGCGUAUCAUGGCAGCACAUCCUCAUGGGUUUGCGUCUCCGUAUCAUCUGCUAGCUACUGAGAACAAUUUUUU	95	21,05263	24,21053	22,10526	32,63158	43,15789	56,84211	1,347826	0,952381	-21,2	-20,6	0,052561	13,18	-22,3158	-0,51707
pcn-mir-64c	uaauuaguccagugUUGAUGUCACACCAGUGUUAAUUGUCUCCAUGUCCAGCUGCUCGUUGGCAUGACACACUGGCUGAACCA	83	18,07229	18,07229	22,89157	24,09639	40,96386	42,16867	1,333333	0,789474	-23,4	-23,3	0,067275	11,61	-28,1928	-0,68824

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-6505	UUUAGCUCCAUCUGACUUCUACCUGUUCCCUAAACUCAAAUCCCACCUAGUUGGUCAccauuuuggaaacaaugauGAAGUCAUAUGAGCUGUG	94	12,76596	19,14894	22,34043	25,53191	35,10638	44,68085	1,333333	0,571429	-21,1	-19,17	0,013409	12,71	-22,4468	-0,63939
pcn-mir-6516	CGGUCUUAUUCUAACUGGUUUCAUGAAUGCAGUAACAGGUGUCUCCACCUCUGCAUUGCUCAAACCACAUUACAUCAGAAAG	82	17,07317	28,04878	25,60976	29,26829	42,68293	57,31707	1,043478	0,666667	-19,7	-19,7	0,160405	4,33	-24,0244	-0,56286
pcn-mir-6560	CGCUGUGUUGCUCCAUACUGCUGAAGUAGUGUCUGUACUUCUGUUUCAGUCAUAAUGAGCAGCUCAUCA	69	21,73913	20,28986	23,18841	34,78261	44,92754	55,07246	1,714286	0,9375	-19,8	-18,8	0,070623	8,29	-28,6957	-0,63871
pcn-mir-6575	GAACUCCAAACGGUGGGCCUGGGAAGAGGACAGGAGCAUCUGUCGAGUUUUCCCAGGCUGAUGUGUGGAGCAG	73	36,9863	23,28767	20,54795	19,17808	57,53425	42,46575	0,823529	1,8	-37,7	-37,7	0,136478	3,17	-51,6438	-0,89762
pcn-mir-6587	guuuuuuuuugguuuuuuguuuuuuguuuauugcuuugcUGGAAGUGGUGCUAUAUGUCGCUUCUUCGUAGAAACCAUAGGACCAAAGAAACUG	94	14,89362	18,08511	10,6383	14,89362	25,53191	32,97872	0,823529	1,4	-20,8	-14,3	0,005082	23,66	-22,1277	-0,86667
pcn-mir-6603	acacacagugagauCAAGUUAAAGGACAAGAGGAAAUAACUUGAGCAGCUUUGUCAUUUUCAGCUCGUAUUUUAUUUUGAUCCAUCAGUGAUU	93	16,12903	25,80645	12,90323	30,10753	29,03226	55,91398	1,166667	1,25	-18,6	-16,4	0,03366	16,97	-20	-0,68889
pcn-mir-6680	CCACAAAACACACUAAAGCGGAUGUUGCUGAUGAAGAUAAAUCGUGGACCUAAGGUAUCAGCGGACAU	93	22,58065	31,1828	22,58065	23,65591	45,16129	54,83871	0,758621	1	-24	-24	0,03754	8,12	-25,8065	-0,57143

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	CCAAGCUCUAGUAUUGUCUCUGGUC															
pcn-mir-669f	acacacauauacauacacacacacguguuguUUCACAAGUAGUACAACAGGCGUGUGAGAUGUUUAUGUGAGG	73	17,80822	16,43836	6,849315	16,43836	24,65753	32,87671	1	2,6	-25,6	-20,3	0,138486	10,86	-35,0685	-1,42222
pcn-mir-67	GUUGUCGGUCCUUGUUCAGCCCGGUUGUGAUGGAGUUGGUCGCAUCACAACCUGCAUGAAUGAGGACUGACGU	73	31,50685	17,80822	21,91781	28,76712	53,42466	46,57534	1,615385	1,4375	-42,5	-42,5	0,387173	1,28	-58,2192	-1,08974
pcn-mir-6816	UCCUGCACGUCGCUCCCGUCGUUGAUCAGGGCGUUCCCAAAUUGAAGGACCUGCACCUUGCAUGGAACGCCAUAUCCAGCCUCGAGGACAAUGCACUC	98	23,46939	21,42857	33,67347	21,42857	57,14286	42,85714	1	0,69697	-29,7	-29,4	0,03583	9,47	-30,3061	-0,53036
pcn-mir-6852	CUAAAGAUUUGUCCUCUGUUCCUCAUCGUUCGUGAUCACAAAGCCAAACGCUUUGCUUUCAGUGAACAAAAUUGUCAAAACAGUUGGAUAAUCUUCAC	98	15,30612	29,59184	23,46939	31,63265	38,77551	61,22449	1,068966	0,652174	-24,8	-24,8	0,119887	4,49	-25,3061	-0,65263
pcn-mir-6894	CCGCUUGGUGGUAAUGUCAAGGAGGAUGGAGAGCUGUUACAGCAUCUUCGCCAUCUUACAUCCUAGCAAGUAG	73	27,39726	24,65753	21,91781	26,0274	49,31507	50,68493	1,055556	1,25	-25,9	-25,9	0,400909	2,89	-35,4795	-0,71944
pcn-mir-6951	UUGUUGUAUUUGUGUGAUUCCCGACACUGUUCCUUGUACUGUAUAUACAGCGAACAGGACCUUUAUCACACCUACAAUGG	80	18,75	23,75	22,5	35	41,25	58,75	1,473684	0,833333	-23,5	-23,4	0,272799	2,62	-29,375	-0,71212

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-6974	UCAACCACAACGACGACGGUGGACAAGGGGUGGACCUCGAUGCCAGCAUGGUGUCCACCAGCUACAUUGCGCUCUUCUCCACUCUCUUCUGUGUCGUGGG	100	27	19	31	23	58	42	1,210526	0,870968	-34,3	-27,1	0,01583	24,28	-34,3	-0,59138
pcn-mir-6977	CCUCGUGCGUGGAGAAAACAUUGAUUGUGAGGCGCUGUGGGCAGGUGAGCCAGACUGUCACUAAUGUAUGACUUCUGCUCACUCACGGCU	90	30	21,11111	23,33333	25,55556	53,33333	46,66667	1,210526	1,285714	-29,4	-28,7	0,036666	9,79	-32,6667	-0,6125
pcn-mir-6999	CACACGUGCACUGCACGCCAUCUCGCCUCCAUCCCAUCAUCUcaggagaaggaaggagagucAGGAGCGUGAAUGUCUUGCAGAUGCCCCGUCAC	95	15,78947	15,78947	30,52632	16,84211	46,31579	32,63158	1,066667	0,517241	-27,3	-17,3	0,084758	25,48	-28,7368	-0,62045
pcn-mir-7000	CAAACAGUGCCCACCCACCUGCCUGUCACAGUgugauuuauuuacauuguaaCUGGAUGCUCAUGGCUGGUGGCCCAGCACUGUAUA	87	18,3908	16,09195	26,43678	16,09195	44,82759	32,18391	1	0,695652	-32,8	-32,5	0,12354	7,83	-37,7011	-0,84103
pcn-mir-7072	UGAGGAUACAAAGGAGGGGCAGGUCUAGCUUCUCUUCUUCCAGUUCCUGCUGGUCUCUUUGUCUCCAGA	69	26,08696	17,3913	24,63768	31,88406	50,72464	49,27536	1,833333	1,058824	-22,9	-22,9	0,435548	12,1	-33,1884	-0,65429
pcn-mir-71-1	AAGAAAUCCUUUUGGUGUGAAAGACAUGGGUAGUGAGAUGUCGGUCCUUCAGAUUCACCUUAUUACCCUGUCUUUUGCAUCAAGGGGAAACCAUGCGUCAA	101	23,76238	26,73267	19,80198	29,70297	43,56436	56,43564	1,111111	1,2	-43,3	-43,3	0,1969	5,13	-42,8713	-0,98409

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-71-2	gcacagacacaucUGCAUUCACAUUACACUUACUUGCACCCGUACCCUAGUCUGGUGAAAGACACAGGUAGAAUGUAAUUCGUGUUGUUCUGCUG	95	17,89474	21,05263	20	27,36842	37,89474	48,42105	1,3	0,894737	-19,9	-10,75	0,038952	25,08	-20,9474	-0,55278
pcn-mir-7151	UUGUUGACACUGAGAAAAGUGACAGGAUCCAUCUCUGCCUGCUCACCUUCACUUUUGUGGUGAGCAGcugucauuucucucuuugCAAGAU	91	18,68132	19,78022	18,68132	23,07692	37,36264	42,85714	1,166667	1	-33,5	-32,8	0,126184	5,54	-36,8132	-0,98529
pcn-mir-7307	AGUCAGGAGAAUGCCAUUGAGUUAUUAACUUGGUGUGGUGGACAUUGUUUCAGUCACAUCAGCGAUGAAGAUGAUAAUCAAAUGGUCAUUUCUGCGA	97	25,7732	28,86598	14,43299	30,92784	40,20619	59,79381	1,071429	1,785714	-26,8	-23,4	0,005514	16,02	-27,6289	-0,68718
pcn-mir-7314	GUCACAGGGACCCUGGUUGGCCUGCACAAGCCCCAGUAAUACUGGUGUCAAGGAUAGACGAAACUCCUUGAAGAUUGUCAGAAACAGUGUCUCUGUGCa	99	26,26263	26,26263	24,24242	22,22222	50,50505	48,48485	0,846154	1,083333	-32,6	-28,7	0,010541	12,05	-32,9293	-0,652
pcn-mir-7386e	UGUAAAGUAGUAAACACUUUACCCGUUUGACUGUUUGCCCUUGUUCUUGAACAGUGUGGGUGAACCUCUUGACUGGUGUAAAGUUGUAUAACUUUUUA	98	21,42857	23,46939	16,32653	38,77551	37,7551	62,2449	1,652174	1,3125	-24,7	-24,1	0,025944	13,11	-25,2041	-0,66757
pcn-mir-7389	GUUGGGAAGAAGCUGCGGUCACAGCUGUUGGUGAGGGUGAGCCCUUGCUGUACUUGAAGCAAGAGAGACCUCCUGACUGUUACCUCCAgcuucucccccu	100	28	19	20	21	48	40	1,105263	1,4	-40,8	-39,7	0,083977	10,1	-40,8	-0,85

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-7398h	CGUACAGGUACACGGGACUCAACAGUCACCUUGUCGUAACCCUCCCUUCUUUAUGAUAGCCCUUCAAGAUGCUUUACCGCAGUGACCUGUGGG	93	21,50538	21,50538	30,10753	26,88172	51,6129	48,3871	1,25	0,714286	-24,3	-24,3	0,03188	3,28	-26,129	-0,50625
pcn-mir-7399	AGGACUUCAAUGUAGCACUUAUacgcauguauauguauauacaugaaUGUAUUUAUGAAUGUACACAUGUAUCUCUCAUAGGUACUUUGAAGUAUU	96	12,5	21,875	10,41667	29,16667	22,91667	51,04167	1,333333	1,2	-23,9	-23,9	0,118362	17,65	-24,8958	-1,08636
pcn-mir-743b	AGUAGACACUUCUGAACGAGCUUCUUGUACUAACCUUGCUGUAAACCCCAGGACGAAGCUGUUCAGACUGGUGUCUGGU	79	24,05063	24,05063	24,05063	27,8481	48,10127	51,89873	1,157895	1	-26,2	-25,6	0,030673	10,47	-33,1646	-0,68947
pcn-mir-745a	GAGGCGGCUUUUCAACAGGCUGCCUUGCGUUCUUAAUACAAGCUGCCUGAUGAAGAGCUGUCCU	64	26,5625	20,3125	25	28,125	51,5625	48,4375	1,384615	1,0625	-30,5	-30,5	0,08838	5,12	-47,6563	-0,92424
pcn-mir-745b	AGCCUAUUUCCCUCCGCUCUUCCUUUGGACAGCUAUCGUGCCGACAAGGAGAGCUGCCAAAUGAAGGGCUGUGGUGGACGGGC	83	30,12048	19,27711	27,71084	22,89157	57,83133	42,16867	1,1875	1,086957	-35,7	-31,3	0,025365	10,13	-43,012	-0,74375
pcn-mir-7472	GCAUUCCGGGGAGAACAUUUCAUAUGAGAUGUGCUGGAGAUGAAAACUCUUCCUCCCCAGAACAU	65	23,07692	29,23077	23,07692	24,61538	46,15385	53,84615	0,842105	1	-20,8	-20,8	0,342745	5,01	-32	-0,69333
pcn-mir-750	GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUGGCAGGAAUACUGUCUUCCAUGCCAGAUCU	97	26,80412	20,61856	23,71134	28,86598	50,51546	49,48454	1,4	1,130435	-52,7	-51,6	0,157091	3,48	-54,3299	-1,07551

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AACUCUUCCAGCUCAUAGUGGCAUGGCAUG															
pcn-mir-751	CUUGGCUCUGUGUGAUUGGUUUCUGUUCUCCAAGauuaaaacauguuugaauGGCCACCACUUUGGCACAGUAAACAUCAUCCAUAGAGCCCUU	94	17,02128	15,95745	22,34043	25,53191	39,3617	41,48936	1,6	0,761905	-27,8	-22,8	0,051558	21,54	-29,5745	-0,75135
pcn-mir-753d	AGAAGAUCAUUAUUCAAGCGAUUGCAGAGAGAAAAACUAUUCGCAUGCAUGAAUGCAUAGGUAUGAGUGUGCACGUGCCUGCAUAUGAUCUCAC	94	23,40426	32,97872	18,08511	25,53191	41,48936	58,51064	0,774194	1,294118	-22,8	-18,7	0,009746	21,51	-24,2553	-0,58462
pcn-mir-760	GAGCAAGUGACUGACACAGAAAAGCUGAUCAUGAAGAUCGGCUCUGGGUCUGUGAAGUCAGUUGGCA	67	31,34328	29,85075	17,91045	20,89552	49,25373	50,74627	0,7	1,75	-29,1	-28,8	0,330018	2,01	-43,4328	-0,88182
pcn-mir-7643	aguuuguuuuucaguGAACAUUGAAUACUGUCGACAUCUGUUUCUCAGUAAUUUUUACUUAGUAUCACAGAUUCAACUGAACACUGAUACAGAACGA	97	12,37113	28,86598	16,49485	26,80412	28,86598	55,6701	0,928571	0,75	-20,4	-15,3	0,02611	14,6	-21,0309	-0,72857
pcn-mir-7649	GAGAUCAUAGUAAUGACAGCAGUGCUGUAUCUAUGUAUGCCAACAAAGUGAAUCAUUGUUGUACUUUAUUUAUGAUUUG	79	20,25316	30,37975	12,65823	36,70886	32,91139	67,08861	1,208333	1,6	-19,5	-18,5	0,065763	5,47	-24,6835	-0,75
pcn-mir-76b-1	ACAUCCAAGCCUCACCCAUAGUUGAGAAAAGCCAUAGUUGUGGUAAcaaacugucuuguuuuuuucaacucccugggugaggcuuagaaca	90	10	17,77778	12,22222	11,11111	22,22222	28,88889	0,625	0,818182	-43,4	-43,4	0,140211	4,23	-48,2222	-2,17

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-76b-2	UACACUGCUGCCAAAUUGUUGAUAGAAAUGGUAGUUCCGCAAUUGCAGgugucuuguuuuuuucaacUGCGUUUGCACUACAAUUUUGAACAGUUGU	97	17,52577	21,64948	14,43299	26,80412	31,95876	48,45361	1,238095	1,214286	-21	-14,9	0,029354	18,5	-21,6495	-0,67742
pcn-mir-770	UGUUGAUUGGACUGUACAUGUAUGUACCAGCAGUUGGGGCAGCACCACGUGUCUGGUAAAUCUGAGUGUCAACAUGG	77	29,87013	23,37662	18,18182	28,57143	48,05195	51,94805	1,222222	1,642857	-19,8	-19,4	0,075721	9,14	-25,7143	-0,53514
pcn-mir-7880k	AAACGUCACAGUCCUGAGCUCUGCCAAACCCgaggucacgaggucagaaAUGGUUGCUGAGCUCCACGUGACGCCG	76	18,42105	17,10526	26,31579	14,47368	44,73684	31,57895	0,846154	0,7	-22,8	-18,67	0,085099	18,19	-30	-0,67059
pcn-mir-7880q	UCAAUGACAUUUACAUACUCUUGGAAGAGGGUCAUGCCUACCAUGCAGUUUGCGACCAaaaucacucucucuuucaaguACUAUUGCUUACAUGCAUUCA	100	14	22	19	24	33	46	1,090909	0,736842	-19,6	-19,6	0,125227	11,54	-19,6	-0,59394
pcn-mir-79	GGUUGGUAUUAUAUcuguauuauauuauauuagUCAGUUGCUGUAGCCACUGUAACUCUGUAGCUCUUUUAUAAUGUAAAGCUAAAUUACCAGUG	95	15,78947	21,05263	12,63158	30,52632	28,42105	51,57895	1,45	1,25	-18,8	-18,8	0,098286	9,53	-19,7895	-0,6963
pcn-mir-7901	CGUCGUCAUUUCUGAAAGUGAUUGUUUGUCUUUAUGAUUACUGUAGUUGAAGCGCUAUUGGUUCAACUUGAAAAACAGUGACUUCUCUGUUCUGACGACU	100	21	23	17	39	38	62	1,695652	1,235294	-28,4	-28	0,058835	13,99	-28,4	-0,74737

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-7c	aaaaaaaaacuaacccaGGCUGCCGUGAUCUGGAAGACUAGUGAUUUUGUUGUUCUGAUGCUGACUAACAAUAAAUCACAUUCUUCCCUGAUUGCUGCAGCCACAUGCU	109	18,34862	19,26606	19,26606	27,52294	37,61468	46,78899	1,428571	0,952381	-37,2	-34,7	0,144483	9,32	-34,1284	-0,90732
pcn-mir-8-1	GCGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUCU	86	22,09302	25,5814	20,93023	31,39535	43,02326	56,97674	1,227273	1,055556	-39,6	-39,6	0,178161	3,42	-46,0465	-1,07027
pcn-mir-8196b	UGCAAGAAAUUUACGaugcuguuuuaaaauguaacggGUUACAAGUCCGUUCUGGCAUUUUGACACCAGuaguuaauuuuucuu	84	11,90476	15,47619	11,90476	16,66667	23,80952	32,14286	1,076923	1	-19,6	-19,4	0,052609	9,33	-23,3333	-0,98
pcn-mir-8-2	UGCGCGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUCUGCUGG	94	24,46809	23,40426	21,2766	30,85106	45,74468	54,25532	1,318182	1,15	-46	-46	0,192059	3,37	-48,9362	-1,06977
pcn-mir-8296	UGAGACCUCGAGAUGAUGGAGAGCACACUUGACUUACUCUGGCUGAGAGUCCGUGAUGUGUCUCUCGUCUUCUCCUGGUCAGA	83	27,71084	19,27711	24,09639	28,91566	51,80723	48,19277	1,5	1,15	-35,3	-34,3	0,251447	8,1	-42,5301	-0,82093
pcn-mir-8332	UCCAUUUAUCUGCACAUCUCUUGAUGAAGUCAGUAAAGACCACAGAUCCUCCGggauguuucuuucuuugcucuucUCGACAUGCGUGCACAAAAUAAG	99	13,13131	24,24242	20,20202	19,19192	33,33333	43,43434	0,791667	0,65	-24,6	-24,5	0,280827	4,23	-24,8485	-0,74545

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-8335-1	uuuuguuguuguuguuguuuugccaACUGGAUUGUAGAUGCGGCACGCAGAGGCAGUAAAUAUGCUAACCACugguuaaauaaaauaacaacagac	96	13,54167	15,625	10,41667	9,375	23,95833	25	0,6	1,3	-27,7	-27,7	0,191059	9,75	-28,8542	-1,20435
pcn-mir-8335-2	uaccuguuguuguuguuguuguuuugguuuuuuuugcugCAAGGCUGUUAGCUUAUCUUCACCCGCAAGCACAAGCAUUACAACGAACAGACA	93	9,677419	20,43011	17,2043	10,75269	26,88172	31,1828	0,526316	0,5625	-21	-18	0,029125	12,45	-22,5806	-0,84
pcn-mir-8364g	GCCCACCUUCCCUUUCUGCUUACCAAACGGAAAAAGGAUGCUACGCAGAGAGUGUGgaaaaggggagagggaggugcAG	79	17,72152	20,25316	20,25316	15,18987	37,97468	35,44304	0,75	0,875	-29	-29	0,217216	5,42	-36,7089	-0,96667
pcn-mir-8416	uaugauugGUCACAUAGUUUAUCAGAUGAUAAAUGGAGUGAACAUAGUAUUUACUUCCCCUGCUGAUAAGUUAAGUAUCCAUUCUUG	87	16,09195	27,58621	14,94253	32,18391	31,03448	59,77011	1,166667	1,076923	-18,7	-18,7	0,245232	4,5	-21,4943	-0,69259
pcn-mir-8422	AGGAAAAGAUCAUCAGAACUUGCAAUUAAAAGUAgcacaaacaagaaagcaagaCCAAGUGUUAGUAAAAUGCAUGUUGAGGAUGAUUCUUUUUCA	96	15,625	30,20833	9,375	23,95833	25	54,16667	0,793103	1,666667	-23,6	-23,1	0,141217	4,11	-24,5833	-0,98333
pcn-mir-8462-1	AAUCCCAGGUGCAGAUAGGCAAAAAUCAUAAGAAUGAUCAAAUAAUUGUCCUUGUGAUUUGACACUCACUGGGGUG	76	22,36842	34,21053	17,10526	26,31579	39,47368	60,52632	0,769231	1,307692	-21,6	-18,9	0,11733	10,16	-28,4211	-0,72
pcn-mir-8462-2	aaacugucaagcAUCUUUCUUUUGGAAACAAGUAAAUCAUAUGCCACCUGUCAGUGACAUGAUGAUUAAU	100	16	30	14	28	30	58	0,933333	1,142857	-19,5	-18	0,090701	10,52	-19,5	-0,65

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UUGAUAAGAUGAAAUGGUCUUCAACAGCAG															
pcn-mir-8485-1	UGUACAGGCAGCCCAUACCUGUCAUUUCUGUUUGGUAGAguguacgcgcgcgcacacacacacacacguauucaUAGAGUAuguuuugcgugugug	98	11,22449	11,22449	9,183673	15,30612	20,40816	26,53061	1,363636	1,222222	-28,9	-25,3	0,086631	28,22	-29,4898	-1,445
pcn-mir-8485-2	acacacacacacacacacguacucacacacacacauguucauuCAGGCUCGCGCCACAGGAAACAUCAGGUGAGAGACAugucgcugcuguugcugugg	99	11,11111	12,12121	10,10101	3,030303	21,21212	15,15152	0,25	1,1	-20,6	-10,9	0,017176	20,99	-20,8081	-0,98095
pcn-mir-87	UUUUAAAAGUGCGGAACUGGCCUGCCUGAAAUUUAUGCUCAAACCUAUCUUGUGAUAAGGUGAGCAAAGUUUCAGGUGUGUUAGAUCUGUACCUGAUC	98	23,46939	26,53061	17,34694	32,65306	40,81633	59,18367	1,230769	1,352941	-42	-38,2	0,120168	3,71	-42,8571	-1,05
pcn-mir-8834a	UUGCUGCCGGGCCUGGAGGCCAGCUGUACCACACAUCUGCUGCCCCUCCACACCUGCGGCAGGUG	65	29,23077	13,84615	38,46154	18,46154	67,69231	32,30769	1,333333	0,76	-28,3	-28,3	0,089597	7	-43,5385	-0,64318
pcn-mir-888	UCAAAGGACUGACACCUCUUUGUCCAGCUCAUGACAGGCUGCACAGAUGAGCCGGACAAGUGUUGUUAGUGGCUUCAU	78	25,64103	24,35897	24,35897	25,64103	50	50	1,052632	1,052632	-25,5	-24,5	0,08259	6,42	-32,6923	-0,65385
pcn-mir-8915-1	UAUUUGCCACCGCUUGGCGGCUUCUGGGUUUUCUUCGGGAGCAGGACGGCCUGGAUGUUGGGCAGCACACCACCUUGCGCGAUGGUGACGCCAGACAGAAGCUUGUUCAACU	144	32,63889	15,97222	27,08333	24,30556	59,72222	40,27778	1,521739	1,205128	-48,1	-38,5	0,009336	30,97	-33,4028	-0,5593

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/ mol)	MFEE(kcal/m ol)	Freq	Div	AMFE (kcal/ mol)	MFEI (kcal/ mol)
	CCUCGUCGUUGCGGAUGGCCAGCUGCAGGUGA															
pcn-mir-8915-2	GCUUAUUUGCCGCCGCUUGGCGGCUUCUGGAUUUUCUUGGGGAGGACGGCUUGGAUGUUGGGCAGCACACCACCGUGUGCGAUGGUGACGCCAGACAGAAGCUUGUUCAACUCCUUGUCGUUGCGGAUGGCCAGCUGCAGGUGA	144	34,02778	15,27778	24,30556	26,38889	58,33333	41,66667	1,727273	1,4	-51,5	-47,1	0,029851	26,76	-35,7639	-0,6131
pcn-mir-8915-3	ACGGCCUGGAUGUUGGGCAGCACACCACCUUGCGCGAUGGUGACGCCGGACAGAAGCUUGUUCAACUCCUCGUCGUUGCGGAUGGCCAGCUGCAGGUGACGGGGGAUGAUUCUCGUCUUCUUGUUGUCGCGAGCGGCGUU	140	34,28571	15	26,42857	24,28571	60,71429	39,28571	1,619048	1,297297	-50,2	-44,5	0,009254	28,93	-35,8571	-0,59059
pcn-mir-8915-4	GACGGCCUGGAUGUUGGGCAGCACACCACCUUGCGCGAUGGUGACGCCAGACAGAAGCUUGUUCAACUCCUCGUCGUUGCGGAUGGCCAGCUGCAGGUGACGGGGGAUGAUUCUCGUCUUCUUGUUGUCGCGAGCGGCGUUG	142	34,50704	15,49296	26,05634	23,94366	60,56338	39,43662	1,545455	1,324324	-51,2	-50,3	0,023929	15,77	-36,0563	-0,59535
pcn-mir-8915-5	GACGGCUUGGAUGUUGGGCAGCACACCACCGUGUGCGAUGGUGACGCCAGACAGAAGCUUGUUCAACUCCUUGUCGUUGCGGAUGGCCAGCUGCAGGUGACAGGUUACUGCAAACCCUAGAAAGGAUUUGAGAUUUGUAGCU	142	30,98592	22,53521	22,53521	23,94366	53,52113	46,47887	1,0625	1,375	-48,4	-48,4	0,094252	13,02	-34,0845	-0,63684

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-9015	CGAGGAGUGUCACGAUGGUCCCAGAGGAGACGAGAAAGUUGUUUGGCUUCCAUCACUCCGAUCUCCUAAUCGACUGUUGUGACAUUCCGCU	91	26,37363	21,97802	25,27473	26,37363	51,64835	48,35165	1,2	1,043478	-38,6	-36,5	0,087379	7,6	-42,4176	-0,82128
pcn-mir-9-1	GUCCAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUGCCCCAAUCAUACAGCUAGAUAACCAAAGACAAAACCGGAGCCGCCG	88	17,04545	28,40909	27,27273	27,27273	44,31818	55,68182	0,96	0,625	-27,8	-27,8	0,435416	2,15	-31,5909	-0,71282
pcn-mir-9120	CCUCUUCUACACAACAAUCUCACUGGGGAGAGGUACACUCGUGACUCAGUCUCCCUCUCUCGCUAUCUCGCGCACAGAGAUGGUUAGAAgcac	93	19,35484	22,58065	30,10753	23,65591	49,46237	46,23656	1,047619	0,642857	-26,6	-26,6	0,320862	10,09	-28,6022	-0,57826
pcn-mir-9-2	UUGGCGUCCAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUGCCCCAAUCAUACAGCUAGAUAACCAAAGACAAA	80	15	28,75	23,75	32,5	38,75	61,25	1,130435	0,631579	-23,1	-20	0,134445	5,8	-28,875	-0,74516
pcn-mir-92a-1	AUUUGUGUGCUCAGGAAAGGUUGUGACUUGGGCAAUUCUGUGAUGUCCUGUCAGAUUGCACUUGUCCCGGCCUUGUCUUGGCUUAcacuu	90	26,66667	14,44444	18,88889	34,44444	45,55556	48,88889	2,384615	1,411765	-31,5	-29,1	0,036643	11,93	-35	-0,76829
pcn-mir-92a-2	CUGGCAUUAGCAGUAGGUCUUGAUGGGUGCAAUUCUGAUGCAUUAAAUAACAGAUUGCACUUGUCCCGGCCUUCUGCCAAUAGCUAA	87	22,98851	25,28736	21,83908	29,88506	44,82759	55,17241	1,181818	1,052632	-35,5	-35,5	0,137395	3,64	-40,8046	-0,91026

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pcn-mir-92b	AGCGAUCAGGGUUGUGUAGACCGGAACAGGGGCAAUGCAUUUGAGUCGUCUGUAUUGCACUCGUCCCGGCCUAUCCAAUCUGACUCAUA	89	26,96629	22,47191	24,7191	25,8427	51,68539	48,31461	1,15	1,090909	-32	-32	0,072274	6,85	-35,9551	-0,69565
pcn-mir-92c	AUUAUGUGUUAUUGUAAAAGGUUGGGAUGUGGGCUCUGUCGCGCAAUAGAUAACUUUCUUUGACAAGCAUUCGCCCACACCUUAUUACAACACAAUCAC	99	19,19192	28,28283	21,21212	31,31313	40,40404	59,59596	1,107143	0,904762	-26,6	-26,6	0,055246	15,72	-26,8687	-0,665
pcn-mir-9-3	UUUGGCGUCCAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUGCCCCAAUCAUACAGCUAGAUAACCAAAGACAAAACCGGAGCCGCC	93	17,2043	26,88172	26,88172	29,03226	44,08602	55,91398	1,08	0,64	-34,1	-34	0,28369	3,42	-36,6667	-0,83171
pcn-mir-9341-1	ACCUGAUUGUUAGUUAAAAGGGCCGAGGAUAGUCAGGCAUAUCGACAAGUUUGUGUAUCGCUUCUCGGCCUUUUGGCUAAGAUCAAAG	88	26,13636	26,13636	18,18182	29,54545	44,31818	55,68182	1,130435	1,4375	-31,8	-28,3	0,01871	14,65	-36,1364	-0,81538
pcn-mir-9341-2	caauucugacauuuuuacugugCCAUGGAUGAGACUUGUUGUCAAAAUGGACAUCGCUUCUCGGCCUUUUGGCUAAGAucaaagugugagaaaaa	95	14,73684	13,68421	12,63158	17,89474	27,36842	31,57895	1,307692	1,166667	-29,5	-29,5	0,182004	3,22	-31,0526	-1,13462
pcn-mir-9388	UUAUGUGCacguauguauguauguacauauaauaUUUAUCAGUGGGUGUGAGCACCAAAACAUUUAUGAAUGCAUGAUAAGCACAGUC	88	15,90909	21,59091	11,36364	21,59091	27,27273	43,18182	1	1,4	-19	-17	0,162177	22,34	-21,5909	-0,79167
pcn-mir-9-4	GGCGGCUCCGGUUUUGUCUUUGGUUAUCUAGCUGUAUGAUUGGGGCAGAAAUAUCAUAAAGCUAGG	93	26,88172	29,03226	17,2043	26,88172	44,08602	55,91398	0,925926	1,5625	-45,5	-45,5	0,314517	3,87	-48,9247	-1,10976

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UUACCAAAGGCAAAAAUGGACGCCAAA															
pcn-mir-9543a	GAGAAACUAGCAAGUUCAUUAUAUGUCAGUAUGCAGAUUGCAAUGGUUUACUUUCCAUUGCACUGCACUGGAGUAAAUAUUgcuuguuuauu	92	17,3913	27,17391	14,13043	29,34783	31,52174	56,52174	1,08	1,230769	-28	-26,4	0,033319	14,41	-30,4348	-0,96552
pcn-mir-96	ACAUgguauuuauuuacaaucauguGCAGUGCAGUUCUUUAUAUAACUAAUCAUACUGCAAAAAGUACAUGACUGCAAUAUGCAAAAAACAUAUCACAC	99	9,090909	33,33333	16,16162	20,20202	25,25253	53,53535	0,606061	0,5625	-19,7	-17,9	0,056255	11,21	-19,899	-0,788
pcn-mir-969	AAGAAGCGCGAAUCUUCUUCUCCUGGAucaggaaaauaaauuauuuaagaGUUCCACUAAGCAAGUUAUCUUGCAGGAGCUAGAAAAUCGCCCUUAGA	98	16,32653	22,44898	18,36735	19,38776	34,69388	41,83673	0,863636	0,888889	-22,7	-22,7	0,05101	17,67	-23,1633	-0,66765
pcn-mir-96b	UCAAUUAUUUGGCACUUGUGGAAUAAUCGGUGUAUCUAAAAGUCGAUUAUACACCGGUGCCAAGUCAUCA	70	20	30	18,57143	31,42857	38,57143	61,42857	1,047619	1,076923	-23,4	-23,4	0,19695	2,59	-33,4286	-0,86667
pcn-mir-972	CUCUGGGAUGUAGGGGGAAAACUGUCaguaauguaaauauuuuuuuugucaacuGAUAUAUGAGAAUUAUGUGGCUACUUUAACCCCUUCACCCACAC	98	16,32653	19,38776	16,32653	19,38776	32,65306	38,77551	1	1	-23,7	-19,6	0,044018	24,34	-24,1837	-0,74063
pcn-mir-981	AUCAGACUUUGUUCCGGGUUUCGCGGCUUGCGAACAGUCAUUUU	85	25,88235	17,64706	23,52941	32,94118	49,41176	50,58824	1,866667	1,1	-32,6	-28,1	0,035045	8	-38,3529	-0,77619

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GAGCUGUGUUCGUUGUCGUCGAAACCUGCCCUGAAAUCUGA															
pcn-mir-9891	CUCCACCUGGCGGCCGACCGAUGGUUCGGGAUGCGCGUUGACCUCAUCGGCUUCGUCCUCGUCUUGGCCACGACACUCGGCUCGGCACUUCAUGGUGCAC	100	29	12	36	23	65	35	1,916667	0,805556	-37,2	-28,7	0,102885	18,05	-37,2	-0,57231
pcn-mir-995	CUGACCGCCAGGAGCAGACGAGAACUAACCAGAGCCCGGAUACUGUGUGUGGCUCAUGAUUGACUGUCACACCUUCUCGCUGGAUGGUAAA	91	27,47253	25,27473	26,37363	20,87912	53,84615	46,15385	0,826087	1,041667	-25,2	-20,28	0,073074	27,75	-27,6923	-0,51429

Supplementary Table 4– Structural and thermodynamic characterization of miRNA precursors in P. maculata. Size (Tam), G content, A content, C content, U content, GC content, AU content, AU ratio (R-AU), GC ratio (R-GC), Minimum Free Energy (MFE), Minimum Free Energy of the Pool (MFEE), Frequency of the MFE Structure in the Pool (Freq), Diversity of the Pool (Div), Minimum Adjusted Free Energy (AMFE), Minimum Free Energy Index (MFEI).

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-bantam	ACGAAACUGGUUUUCACAGUGAUCCAGCAGAUUGCUCAAAGUCUGAGAUCAUUGUAAAAACCAAUUUUGU	70	18,57143	32,85714	18,57143	30	37,14286	62,85714	0,913043	1	-29,4	-29,4	0,496236	1,25	-42	-1,13077
pmc-mir-1	AUUAUUACAUAUCUGGUAUGUUUGUGGAGUUGAUGUGUUCAUGCUUCUUUAUAGUUUGACCUUUUCCCUCacacaacauaaagaugagaaaUUCU	95	13,68421	12,63158	12,63158	38,94737	26,31579	51,57895	3,083333	1,083333	-18,5	-17,2	0,045655	8,13	-19,4737	-0,74
pmc-mir-1000	ACUACAGAUGUGGACUGGCUGGUGUGAUGGGACAAGACUUCAUCACUCUCUCUGCCGGUUUCAUCAUCUGUCAA	74	24,32432	21,62162	24,32432	29,72973	48,64865	51,35135	1,375	1	-28	-27,1	0,031686	6,94	-37,8378	-0,77778
pmc-mir-10031c	UUACUGAUGUUAUUACUCGUCCAUGUCUUCCUCUUCGUCCUUAUGAUCCCUAACAUAGGUAUGUGCACACCUGACACUGUGAGGAGUUUUAACGCAGGUA	100	19	22	24	35	43	57	1,590909	0,791667	-27,5	-27,5	0,437289	4,9	-27,5	-0,63953
pmc-mir-10046	CGCCGUCCUGCGAGAUCUCACCUGUCUAACGCGCAUGCGCCUCUCAUCACCACGCGCAACGGUUCCGCCUGACAGGGCGACUUGUCGCAGUGACGACA	98	25,5102	18,36735	37,7551	18,36735	63,26531	36,73469	1	0,675676	-37,2	-35,3	0,365188	5,25	-37,9592	-0,6

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-10055	UUGCUCCUGCAUCUGCAAGCCUGGGCCAGGGUACCccgggugggagggagggaggacuuuuuuuuuccucagguAGCGAUGACUGGAGACG	91	18,68132	10,98901	16,48352	10,98901	35,16484	21,97802	1	1,133333	-33,1	-29,2	0,094013	18,78	-36,3736	-1,03437
pmc-mir-10089	UCCAGCAUAAUUUGCUGUUUUGGUGAUAUACUCGUGUACAAUGAAAAUGAGCAAGACUAUGAUAUCAUCAUGAAAGCGAGAAAUGUUAGCUCAG	94	21,2766	34,04255	14,89362	29,78723	36,17021	63,82979	0,875	1,428571	-19	-17,9	0,02445	17,13	-20,2128	-0,55882
pmc-mir-10173	UAGAACUUUUUUCUUCCCACCAUUCCUACACGCCUACUUCUUGCGGAAGGAAGugaggaaggaaaacaaauuaaa	75	10,66667	16	21,33333	22,66667	32	38,66667	1,416667	0,5	-22,1	-21,7	0,383116	2,01	-29,4667	-0,92083
pmc-mir-10249-1	UGAAGAAGUGACUAACGCUGAUAACAGUCGAUGGACGAGGUAGAguugguggugggcgguggguguugCCAGCGGAGCAGUUCUGAC	85	23,52941	23,52941	14,11765	12,94118	37,64706	36,47059	0,55	1,666667	-23,1	-18,2	0,173316	22,89	-27,1765	-0,72188
pmc-mir-10249-2	AGAAGUGAACAAGAAGUGACUAACGCUGAUAACAGUUGGUGGACGAGGUGGAguugguggugggcgguggguugCCAGCGGAGCAGUUCUGACACUUGU	99	25,25253	24,24242	13,13131	15,15152	38,38384	39,39394	0,625	1,923077	-27,2	-13,3	0,036951	27,09	-27,4747	-0,71579
pmc-mir-10256	UAGCCAGUAUAGAACAGUAGCCAGGCAUGUGAGCACCACAAGCUAUGUAUAUAAAACUUAUGGUACCCCUAUCACAUGUCUGCUAUGGCCUUCCUGGUAU	100	20	29	24	27	44	56	0,931034	0,833333	-30,5	-29	0,074934	11,46	-30,5	-0,69318

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-10267	AGAGCUUUGUCGGUUUUUGGCUGUGAGGGAGACCAGAUCAAACCAccgcccccacacacaccaaaaaagcAAGGCAAU	78	20,51282	19,23077	11,53846	16,66667	32,05128	35,89744	0,866667	1,777778	-21,7	-15,8	0,291539	8,02	-27,8205	-0,868
pmc-mir-10492a	gucauugucauugucaucgcugucgucaucgucgucguuuaGCUCUCUGAUUUAUGUAGCAGACGAGAGGCAUGAGAGACGAAUUGGACAGAAAUUCU	98	16,32653	18,36735	9,183673	14,28571	25,5102	32,65306	0,777778	1,777778	-22,8	-11,64	0,059506	28,54	-23,2653	-0,912
pmc-mir-10508b	agagagagauauguaaAAUGUCAGGAAAGGUAAACAGGUGUAAUCAUUCAAUACCUCUGAACAGCAUUUCGUGACUUCUUUAAAUAUCUUCAGU	94	13,82979	27,65957	14,89362	26,59574	28,7234	54,25532	0,961538	0,928571	-19,8	-16,4	0,034776	12,65	-21,0638	-0,73333
pmc-mir-10509	CUGUGUCACGUACAGUAACACUGAUCGUCACGACUCCACCGUGACAUGACGAUGUACAGUGAGUGACGUGACAUGA	76	25	27,63158	25	22,36842	50	50	0,809524	1	-27,4	-24,3	0,170278	7,05	-36,0526	-0,72105
pmc-mir-10578	CUCCUUCAGCAGUGAGUCAGUCUCACGCUGCAUCCCUUGUGACGGUGGCUGCGAGACUGAGACACAUGGCAUAAAGACA	79	26,58228	24,05063	27,8481	21,51899	54,43038	45,56962	0,894737	0,954545	-24,8	-24,8	0,024862	11,14	-31,3924	-0,57674
pmc-mir-10611	GUCAUGAUGAUUAGCUUUCACUGAUUUCUAAGGGUUCUAAUAGCAUCACCACUCUUGAUUUCCCUUUUUCACACAGUGGGaaauuuaaucuucauuuu	98	14,28571	18,36735	18,36735	30,61224	32,65306	48,97959	1,666667	0,777778	-20,3	-19,5	0,141481	6,16	-20,7143	-0,63438

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-10639	GAUAAGCUUAUCAUACGUAACCCAUACAAAGGUUAUGGAAGUGAGGAGAAGAACAAGAAGUUCUCUCCCAUGGGUAUUUGCCAUGAUAGCUUUGG	95	24,21053	32,63158	16,84211	26,31579	41,05263	58,94737	0,806452	1,4375	-29,6	-26,6	0,069014	9,88	-31,1579	-0,75897
pmc-mir-10770-1	GCGAAACCACAGAACACGACUGACUGAUACGAUCUCAAAGGGCUUUCUGCUAAAAAGCAUCCUUgaguuguugauguuguuguuguuguuuuguu	98	12,2449	22,44898	17,34694	13,26531	29,59184	35,71429	0,590909	0,705882	-26,4	-25	0,014385	16,81	-26,9388	-0,91034
pmc-mir-10770-2	cuuguugaugcuguuguuguuucccGCAGCCUCAAAGAUGCGGACCUUGUCAAGUAAGGGGGAGACAAAAAUACAGUAUCUAACCUC	87	17,24138	25,28736	16,09195	12,64368	33,33333	37,93103	0,5	1,071429	-28,5	-28,5	0,138113	8,95	-32,7586	-0,98276
pmc-mir-10892	GCCACGAAAAAAGACCAGUGGACAACCAUCGGUGAAUAAUGGAUGAAUAACAUCCUGUUUCUAUCAUCCGAUGGGCGAGCUGUGUUUGUUGUCGUCUU	98	24,4898	27,55102	20,40816	27,55102	44,89796	55,10204	1	1,2	-30,8	-30,8	0,239683	4,62	-31,4286	-0,7
pmc-mir-10972	CCGGUAGUGAUGACAACGAUGAGAACAAUGAUGAUUCAUCAACGAUGAUUUGCUAUGGUCAUCAUAUAUGUGUCUCAUAUAGUUUGCACAAUACAGG	97	21,64948	31,95876	16,49485	29,89691	38,14433	61,85567	0,935484	1,3125	-23,3	-23,3	0,070908	15,83	-24,0206	-0,62973
pmc-mir-10b-1	UGCCAAGUCGACCACGGCACCCGGUGUGUCCCUCCCACUGACCAGUCAUCUCGGUACUCGGGAGGUCAAAUCGACUGAGGUCAGGGGUCGAAUUGACU	98	28,57143	20,40816	30,61224	20,40816	59,18367	40,81633	1	0,933333	-34	-32,9	0,060236	18,2	-34,6939	-0,58621

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-10b-2	GUGAGAGUGUGAGUGGCUUUACCCUGGAGAACCGAGCGUGUGUgaucaugacgucacaguucGUUUCUGAGGGUCAAGUCGCGAUACUCUGUU	93	27,95699	13,97849	13,97849	23,65591	41,93548	37,63441	1,692308	2	-40,6	-40,6	0,262649	9,81	-43,6559	-1,04103
pmc-mir-11054	uguuuguaguguuuguUGCCAGAGAUUUAGCAGAUAUGAUGGAAAcugcauuuucuuguuuucacacaUUAGAAUCUAAGAGAAACAGCACUAUCAACCA	100	12	26	10	13	22	39	0,5	1,2	-21,4	-15,8	0,089496	35,03	-21,4	-0,97273
pmc-mir-11280	AGAUACAGAUGUGUGACAUACaugucuaacccuaacccugaaugAGAGAAGAUCCGUGUGUGAGGUUGGAUGUAGGUGUAAACAUCUUACAC	92	21,73913	23,91304	9,782609	19,56522	31,52174	43,47826	0,818182	2,222222	-21,9	-21,2	0,135428	13,09	-23,8043	-0,75517
pmc-mir-1175-1	UGAUCAGGUGUGUUAUGUAGUGGAGAGAGUUUUAUCUCAUCAUGAGCCUCAGAAGCAGGUGAGAUUCAACUCCUCCAACUGCAGGCUAUACCUGAAAC	98	24,4898	27,55102	20,40816	27,55102	44,89796	55,10204	1	1,2	-42,7	-38,6	0,079856	5,62	-43,5714	-0,97045
pmc-mir-1175-2	CACACGGAAGUGAAGAGAAGAAUGAAGAAGGAGGCUAUAGCGAAAUUAUagguauuucuuuuuuaucaucaucaucaucaucucaucaucgucgucgu	98	15,30612	22,44898	5,102041	7,142857	20,40816	29,59184	0,318182	3	-20,9	-20	0,079297	13,02	-21,3265	-1,045
pmc-mir-1187	UGACUCAGGUAUCAAAUGuucuuuuauguguguaugugugugugaugugugauacgugugguugCUAGCGGCUAAAAGCAAUAUGUGAGAGCGAGUGU	99	15,15152	17,17172	8,080808	12,12121	23,23232	29,29293	0,705882	1,875	-20,3	-19,5	0,064187	14,27	-20,5051	-0,88261

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-11922	CGUUUCGACCUGACAGAUGCAGUUGGAUCGUUGAUCUUUUCAGGAGAUCAUCGAUAUGUUCAUCGUUCAGGGUGAAGGA	79	27,8481	22,78481	17,72152	31,64557	45,56962	54,43038	1,388889	1,571429	-25,9	-25,9	0,042274	4,91	-32,7848	-0,71944
pmc-mir-12	UGGUGGUCAGACUGUGAGUAUUACAUCAGGUACUGAGAAUCUAACAAGCUUCAGUACCUUUUGUGAUAUUCUUAGUCUGCCAUUU	85	21,17647	24,70588	17,64706	36,47059	38,82353	61,17647	1,47619	1,2	-41,7	-40,3	0,196235	2,83	-49,0588	-1,26364
pmc-mir-12096b	GAUAUGCUACUUCGUGCAAGCGGUGAUACUUUUGUCUCGCAUAUCAAUAUGAGGUAGGGCAAAAUUAUCACCGAUUACCCGAGGUAACGAUCAA	94	22,34043	29,78723	20,21277	27,65957	42,55319	57,44681	0,928571	1,105263	-32	-31,6	0,104639	7,62	-34,0426	-0,8
pmc-mir-12228	UCCCCACUGCUCCCCCAACAUCCCCCCACCAGCGCCGgcuaccccacccacccugcUGCGGGGGACGAGCUCGGAGGAGUCGUGGUCU	88	22,72727	11,36364	32,95455	11,36364	55,68182	22,72727	1	0,689655	-33,2	-19,6	0,075853	14,44	-37,7273	-0,67755
pmc-mir-1224	uugaucuucaccuccucucucuccucccuucaaCUAAUAUGUCUGAGGUGUCAAUCAUGGGCUGUUUGAAGUUAGCGAAAGAGUUGACGAAGAUAUU	95	18,94737	20	7,368421	21,05263	26,31579	41,05263	1,052632	2,571429	-24,7	-21,1	0,129321	12,41	-26	-0,988
pmc-mir-12245	CCUUCCCCCGCCCCGCCCGGCUCAAGGUCAGCGCGCCAGAGAGCAAUUCGUCCAGGUAGACCAGGUGCUUGAACCCGAGAGGCGCGGUGGCGACAG	96	32,29167	18,75	36,45833	12,5	68,75	31,25	0,666667	0,885714	-33,6	-33,1	0,051978	10,23	-35	-0,50909
pmc-mir-12286	ACGCUGCUCAGCACGUCACUCUAUCAUUUCACAGUCUCGUGGGGC	80	31,25	18,75	25	25	56,25	43,75	1,333333	1,25	-28,6	-19,19	0,08512	19,63	-35,75	-0,63556

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UGCAGGGCUGAGUAAGCUGAGUGGCUGAGUAGGCU															
pmc-mir-12287	GGCUGUGGGGGUGCAGGUGGGCACACAUUCAUGGGAGGGGGCCCCCCCAUCAUAGGAGGCCAAGGUGCCGGCCCCAUCAUAG	82	39,02439	18,29268	28,04878	14,63415	67,07317	32,92683	0,8	1,391304	-31,7	-15,9	0,099725	26,92	-38,6585	-0,57636
pmc-mir-12292	GUUUCUGACGAUAUGGGGUCUUGGGGUCAUGCAGGAAGAGAUCUACGCGCUCGUGAACGACCCCAACCACCGCGAGCAUCAGAUUC	86	29,06977	23,25581	26,74419	20,93023	55,81395	44,18605	0,9	1,086957	-26,4	-25,2	0,09755	8,86	-30,6977	-0,55
pmc-mir-12293	gcugcuggugcugccGUCUCCUUUCUACAUCCGCCUCUUGAUCUACUAUAACUACGAGCACGAGGAGAUGAUAGAGAGGAGAUCGGCCAUCUCCCGCCUG	100	19	20	25	21	44	41	1,05	0,76	-39,4	-30,9	0,181223	7,86	-39,4	-0,89545
pmc-mir-12296	ACUGCAGUGCCCUGUGUGGUGUGGGGAGUgaggggcaggggcaggggcaggggCACACGACAUUACGGGCACAGCGGG	79	26,58228	12,65823	16,4557	12,65823	43,03797	25,31646	1	1,615385	-33,3	-33,3	0,678283	1,48	-42,1519	-0,97941
pmc-mir-12321	AAUGCGCCCUgcccucccuuccccucuccuccacccucaCACCGUUACUACCGAUUGUGAGAACGGGACCACAAGGAGGAACAACGGUAGGGCGCGAC	98	21,42857	20,40816	19,38776	9,183673	40,81633	29,59184	0,45	1,105263	-38,7	-38,7	0,150689	6,68	-39,4898	-0,9675
pmc-mir-12327	caacuucuuuucucucuuucccucucucuuugcUUUAGUGUUCAAAUGUACACAAGGUAUAAAGAAAGAGGAUUGGUGAGCGAGCAGGGAAGcaa	95	20	23,15789	5,263158	13,68421	25,26316	36,84211	0,590909	3,8	-29	-28,1	0,068017	8,35	-30,5263	-1,20833

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-12339	uuccaucuuuuucugcCAUGUUUAUCUUCACUGCUGGAAAGAUUGUUCUGGAUUGCCACUGGAGUGCAGUGCAGAGAAACAUGGCAUAGAAAGAUGGAA	99	23,23232	25,25253	13,13131	22,22222	36,36364	47,47475	0,88	1,769231	-43,9	-41,47	0,037169	11,26	-44,3434	-1,21944
pmc-mir-12358	CCCCAUCUCCUCCCUUCUACCUAAUCAUCUUAAAAUCAUCUCACUGUCAUCCGCUUUAUCUAUGAUUUCAUCGGGUAagguaaagggagguaauguaa	98	6,122449	17,34694	26,53061	28,57143	32,65306	45,91837	1,647059	0,230769	-26,7	-26,7	0,382757	2,63	-27,2449	-0,83438
pmc-mir-12396	CCGCGCAGUGUGAGUGACUGAAAAGAGAGACACAGACAAGAAAGAUAUUCUUUAAAACCUCUCCUUUCGUCAGCUCGCACUGCGAAG	87	22,98851	32,18391	24,13793	20,68966	47,12644	52,87356	0,642857	0,952381	-35,8	-35,8	0,255939	5,41	-41,1494	-0,87317
pmc-mir-124	cuaUCGCUUUCAUCCGUGACGACACCGUGUCCUCCCGGCAAGUGACGUUCCCGcgacuguugcugcugucgcCAGGAGUCAAGGCGAACA	90	20	15,55556	25,55556	14,44444	45,55556	30	0,928571	0,782609	-27,7	-19,2	0,073181	30,63	-30,7778	-0,67561
pmc-mir-12410	GUCCAUCGUAAAcgguugcuguuuuuuuuuuucuucguggaACUAAAGAAACCcgggaagaaggaagaaaggaaacuGAGAUCCGGUCACGUGACG	96	10,41667	15,625	11,45833	7,291667	21,875	22,91667	0,466667	0,909091	-25,7	-23,6	0,044841	16,09	-26,7708	-1,22381
pmc-mir-1273h	GUGCUGGGUGAGUACUCGGUGCGCGUGCUGUGGGACACAGGUGUAGAGAGCACGUGCAGAGCAGGGCGGGACUGCAGACUCGACCUCAGGAU	92	41,30435	19,56522	21,73913	17,3913	63,04348	36,95652	0,888889	1,9	-37,1	-12,11	0,089734	23,69	-40,3261	-0,63966

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-1277	GACGUACUGCAAGGAucccuguauauauauauauguacucuaCAAGGGAGUCGAUGUACGUACAGA	66	19,69697	19,69697	10,60606	9,090909	30,30303	28,78788	0,461538	1,857143	-19,3	-18,4	0,217022	13,76	-29,2424	-0,965
pmc-mir-130b	AAUUCUGAUAAGCGAAACAUAUGUUUCAUCUAUGUUGGUAUAACCGAUUACUAAACAUAUGCAAAACAGUGCaauaaugaaaguauuuuuguucaGACGA	100	13	29	13	22	26	51	0,758621	1	-19,9	-19,9	0,042179	8,59	-19,9	-0,76538
pmc-mir-1322	GGAAUAUCUGGUCGUAGCUCAgagcugaugcugcugcugauggcuaUCAAGUAAAUGAUGCUGGUCAACAGAUGAAAUAUGGCACACCAAGAUAUCUG	98	17,34694	25,5102	13,26531	18,36735	30,61224	43,87755	0,72	1,307692	-24,5	-22,2	0,016132	23,72	-25	-0,81667
pmc-mir-133c	UAACUACAGCUGGUUGAAGGGGACCAAAUGAAAGGCUCUUCAACAAUUUGGCCCGAGUUCAACCAGCUAUAGAAG	75	24	33,33333	21,33333	21,33333	45,33333	54,66667	0,64	1,125	-30,4	-28,9	0,184949	4,61	-40,5333	-0,89412
pmc-mir-1376	CUCAGCUGCAACAGACUCUGACAUUAGCAGAUCUCAAGCUCAGCAGCACUCUUUGAGCUUGGAGGAUGUUAGUCAUGAUGCUUUGCAGACUCUG	94	23,40426	24,46809	24,46809	27,65957	47,87234	52,12766	1,130435	0,956522	-31,4	-26,8	0,072951	8,03	-33,4043	-0,69778
pmc-mir-137b	AGUUCCAGUCGGUUACGGGUAUUCUUGGGUAAAUAAUACAUUGAGUAGUUGUUAUUGCUUGAGAAUACACGUAACUACCUGGACGU	86	24,4186	26,74419	15,11628	33,72093	39,53488	60,46512	1,26087	1,615385	-33,1	-29,3	0,022171	10,78	-38,4884	-0,97353
pmc-mir-13b	uaaaauacacuuuaacUGACGUCUGGCUUCUGAUGUCUCUGAAGGGU	95	18,94737	11,57895	13,68421	22,10526	32,63158	33,68421	1,909091	1,384615	-25,4	-18,3	0,096917	31,5	-26,7368	-0,81935

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GCGAGAGUUUGUUGUUCAGACUCAUCAAGCCUcguuaaaauguuugug															
pmc-mir-1421am	GGUGCGUCAAGGCGGUCAGUAAGACGUCCGCCACCUUAGGCGUUCAAACGGAUUUCGAGGAGGUCGUAGGUCAUCCUGUAGACGACUUGGCGCUGG	96	34,375	19,79167	23,95833	21,875	58,33333	41,66667	1,105263	1,434783	-31,8	-26,1	0,047723	21,41	-33,125	-0,56786
pmc-mir-1422j	UGGGUGUUCUACUGUUUCAUGAUUUAUCAUAGGGAGAUGACACAUAAUCGAAAACUGCAUCUGGAUUAUGAUAUCAAGUGAAAUAUAUCAGAAAACUAA	99	19,19192	36,36364	13,13131	31,31313	32,32323	67,67677	0,861111	1,461538	-22,3	-22,3	0,232835	3,91	-22,5253	-0,69688
pmc-mir-143	GCACAUGACAGAGGGCCUCAUCGGUCUGGCUGAACACAAGAAGUAGAAAGUGUUGCACACAGUCUGAGAUGAAGCACUCGUUUGCAUGAUA	91	27,47253	30,76923	20,87912	20,87912	48,35165	51,64835	0,678571	1,315789	-25,3	-24,9	0,120125	12,48	-27,8022	-0,575
pmc-mir-149	acaugaaucgucucccccccccccaccaccgcAAUACAUGGCGCAGUGCAAAGGUCACACCGCUAGUGCUGAGAGGGAGGGACGGGGGAUUCAAGA	96	25	19,79167	12,5	9,375	37,5	29,16667	0,473684	2	-33	-12,4	0,017431	29,49	-34,375	-0,91667
pmc-mir-150	ACAUGUCACCACAUGCGUGUGCACGCACAUAAAUAUGUCAGCUUAUCUCACAGAUACAUGUUGCUGGUACAGGCCUGGGGGAGACAAAU	89	23,59551	29,21348	23,59551	23,59551	47,19101	52,80899	0,807692	1	-25,1	-25,1	0,081451	10,2	-28,2022	-0,59762
pmc-mir-153	AUACCCUCUUCCCAGGCAGCUUUUGUGAUUCAGCAAUUGUACAGC	87	24,13793	27,58621	22,98851	25,28736	47,12644	52,87356	0,916667	1,05	-37,9	-37,9	0,256161	6,4	-43,5632	-0,92439

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UAUCAAAUUGCAUAGUCACAAAAGUGAUCGGGAGGCGGGGAC															
pmc-mir-1551	CUUUUGAUCUUAAUGUGGUAAAACGCAUUUCAGGUUUAUGAGUUUGUGUUGCUGGGACAAUGACUGUUUUAGGCCAUCUGUACAUCAACCA	91	21,97802	24,17582	16,48352	37,36264	38,46154	61,53846	1,545455	1,333333	-19,4	-19,4	0,255295	14,12	-21,3187	-0,55429
pmc-mir-15c	UUGAAGAAUAUCUCUUAUCCCAUAGGACAGCUAUUUCAAGGAAUCAUGUGACCAGCAGACCAUUCUGGGCUAUGGGGUCAGAGCUAUUCUUUUU	94	21,2766	26,59574	20,21277	31,91489	41,48936	58,51064	1,2	1,052632	-29,6	-28,4	0,088206	10,15	-31,4894	-0,75897
pmc-mir-1603-1	AUAGCAGAAAUCAAAACAGCCCACAUUUUAUGUCAAACUUAUUACACAGAGAUAUUAAAGCaauggugguuguuuuguguugcgCA	86	8,139535	32,55814	15,11628	17,44186	23,25581	50	0,535714	0,538462	-20,1	-20,1	0,033978	10,39	-23,3721	-1,005
pmc-mir-1603-2	GGGUUAGUGUUUGACAGAGGAUUGCAGCUUGCAauguugguuugguuuguuuuuuuucuaaacacagCGACAAUAUCUUGUGAAAUAGUAAGUU	94	18,08511	18,08511	7,446809	20,21277	25,53191	38,29787	1,117647	2,428571	-20,1	-19,5	0,022965	9,06	-21,383	-0,8375
pmc-mir-1632	GAUGGCUGUUGACACACUCGAGUGACAAGACAAAGGUCUGAUUUCCUUGCUUGUUUUUGGAUGAAAUUAUUUUGCGACGCAGCUGUUCACAGCCUCU	97	23,71134	22,68041	20,61856	32,98969	44,3299	55,6701	1,454545	1,15	-26	-26	0,016941	14,04	-26,8041	-0,60465
pmc-mir-1642	GUGAACACUUAAAUAACUGCUUGUCCCCUCUACCCUGAUAGAGGG	83	25,3012	27,71084	16,86747	30,12048	42,16867	57,83133	1,086957	1,5	-20,1	-14,7	0,16303	24,29	-24,2169	-0,57429

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AAAGUGGUGAGAGGCUGUCAGUUUUGUAAGAUAUUUAG															
pmc-mir-1677	UGACCAUCACCUUUAUCUCUCUGCCGUCGAGGUAGCGCGACACGAACUCCACUCCAUUCUGUGCGUUGACUUCAAUAGGAGAGACAGGAGUGAUGGUGA	99	25,25253	23,23232	26,26263	25,25253	51,51515	48,48485	1,086957	0,961538	-36,2	-35,3	0,026404	8,83	-36,5657	-0,7098
pmc-mir-17	CACGGCGAUGACUGGAGUCAUUAGGGAGGCGCACGCGCGGCACUAGACCUUAACUGCACUGCAAGCACCGCCACA	75	29,33333	25,33333	32	13,33333	61,33333	38,66667	0,526316	0,916667	-24,1	-19,8	0,261623	4,23	-32,1333	-0,52391
pmc-mir-1728	UGUGACUGUUCUGCAGUGACUGUAUGCGUCCCAUGAAUCAUUGGUUGAUCCAUUGGAAGAAACAUGACUGGGUACAUCCUG	81	25,92593	23,45679	19,75309	30,8642	45,67901	54,32099	1,315789	1,3125	-18,9	-18,9	0,107603	12,57	-23,3333	-0,51081
pmc-mir-1744	UUUGAGAAGAGGUACUUCAACAGGAGCAAGUCAAGGCAUGCUUCUUUUUAACACCAGUCUUCUCUGC	67	20,89552	26,86567	22,38806	29,85075	43,28358	56,71642	1,111111	0,933333	-19,2	-19,2	0,273743	3	-28,6567	-0,66207
pmc-mir-1775	guaaaaauuaaggCAAAGAAAUCCUGUAGCCAGAAGACAGCGGAGGACCAGAGUUGUCUGUGCAGCCUGGCUACAUGUUUCUCUGUCCAAGAUUUUGAG	99	23,23232	23,23232	19,19192	21,21212	42,42424	44,44444	0,913043	1,210526	-34,9	-34,9	0,331788	5,38	-35,2525	-0,83095
pmc-mir-1781-1	GUUUGAAAGGAUUUAAAUCAUCCAGCUGCCUUUUUGACUGUUUAGCAGUCUCCAACAGGAGUGGAUUAAUUUGAGUAAUUUUCAUUC	87	19,54023	26,43678	16,09195	37,93103	35,63218	64,36782	1,434783	1,214286	-23,1	-23,1	0,071767	5,41	-26,5517	-0,74516

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-1781-2	GUUUGAAAAGAUUUAAAUCAUCCAGCUGCCUUUUUGACUGUUUAGCAGUCUCCAACAGGAGUGGAUUAAUUUGAGUAAUUUUCAUUC	87	18,3908	27,58621	16,09195	37,93103	34,48276	65,51724	1,375	1,142857	-23,4	-23,4	0,079721	4,68	-26,8966	-0,78
pmc-mir-1896	CAUUCUUCCUCAAACCAAGUGUGUAUUAGAGAUAAAUGGGGUCUCAAAGGACAUAGACACCGAGUGUAUCCACUCAUACGGUGGugggugaggaggagga	100	19	26	18	21	37	47	0,807692	1,055556	-32,2	-31,6	0,027684	15,11	-32,2	-0,87027
pmc-mir-190	ACCCGCUUCUGCUAGAUAUGUUUGAUAUAUUUGGUGCAGUUGUCGCGACGACCAAGUAGUCAAACAUGUCAGAGCAGCGACG	82	25,60976	25,60976	21,95122	26,82927	47,56098	52,43902	1,047619	1,166667	-32,5	-32,3	0,080048	9,84	-39,6341	-0,83333
pmc-mir-1951	UUAGUUUUGUGCAUCAAUCACCAUCAUUUGUGUAAACGUCUUCCCUGACUUAUUUGGAGCCCCCAAAUGUAGUGGAGACUGGUGGCGAAACCUU	94	21,2766	23,40426	22,34043	32,97872	43,61702	56,38298	1,409091	0,952381	-23,5	-14,8	0,063911	17,89	-25	-0,57317
pmc-mir-1955	GGAGGAGCAUUGCAUGCUGGACGCGCGUGAUCAGGUCCUGGCGGUGUCAGUGACAGUCAUUGCCAUGACAGCAGCGUGCACAGGUCAUGUGACUCCACC	99	33,33333	20,20202	26,26263	20,20202	59,59596	40,40404	1	1,269231	-40,3	-34,2	0,115974	33,97	-40,7071	-0,68305
pmc-mir-196a	AAACAUCCUUUUUGCACACGACAAUGACCUGGUGGCCGACGGCAACAAGAAACUGUGACUGAGCCACAGUGUAUUGAUAUUGAAUGCAGACAGGAUGCCA	100	24	32	23	21	47	53	0,65625	1,043478	-31,3	-31,3	0,07221	6,07	-31,3	-0,66596

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-1984	UGUCGCCGUGCCCUAUCCGUCAGGAACUGUGAUCUCGCGAAACACAGGGUCUGGCGGUUGGGCCUCGGCGCUG	73	34,24658	13,69863	30,13699	21,91781	64,38356	35,61644	1,6	1,136364	-37,9	-37,9	0,133827	2,65	-51,9178	-0,80638
pmc-mir-1985	UGCCAUGCCAUUUUUAUCAGUCACUGUGUGUUGUGAAAGUcacagugaugaugauaauggcuUGAUG	67	16,41791	13,43284	10,44776	26,86567	26,86567	40,29851	2	1,571429	-28,6	-28,6	0,287364	2,77	-42,6866	-1,58889
pmc-mir-199	CAUUGCAUGUCAAAACUAAGGGAUGUUUACCUAUAUUUGUAGAGACACACAUGACAGUAGUCUGCACAUGCUAUAGAUUUUGGGGAUGCAGCA	93	22,58065	31,1828	17,2043	29,03226	39,78495	60,21505	0,931034	1,3125	-20,3	-17,4	0,056275	14,69	-21,828	-0,54865
pmc-mir-1990	GGCUGCGAGAUGUUCGUGCAGUAAGUUGAUGGGGUCCCAGGUAGAUCUACCCCUCCCGGGACUACGUCAACGUACUACCACGCGCAUCUCCAAGU	95	27,36842	21,05263	29,47368	22,10526	56,84211	43,15789	1,05	0,928571	-44,2	-43,8	0,106149	4,96	-46,5263	-0,81852
pmc-mir-1994	CUGGCGGCUGUUCUAAGGGGAAACUCGCUGUCUGCGUGUGUGAUGACGUCAUGAGACAGUGUGUCCUCCCUCUGAGUCAGACACCGCUAA	90	30	18,88889	25,55556	25,55556	55,55556	44,44444	1,352941	1,173913	-41,1	-41,1	0,501637	4,6	-45,6667	-0,822
pmc-mir-1994a	CAAAAGCUAUUUCUCAGGGGCGGUCACUCUGAUCUCCAUGUGCUCGCACCAGCAUGAGACAGUGUGUCCUCCCUUGAGGGAUGGGCUUAUA	91	26,37363	20,87912	26,37363	26,37363	52,74725	47,25275	1,263158	1	-44,3	-44,3	0,178398	5,12	-48,6813	-0,92292

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-1a	GGCACAUACUUCUUUGCUAUCCCAUAUGUUCUUGCAAAGCUAUGGAAUGUAAAGAAGUAUGUACU	65	18,46154	29,23077	18,46154	33,84615	36,92308	63,07692	1,157895	1	-23,7	-22,1	0,075024	6,51	-36,4615	-0,9875
pmc-mir-1b	CCAGUAGAGACAAGUGAUGUUACACAGGUUAUGCGUAUAAACAAAGGUAUGGUCGCAUUAUAUUACGUGUCCUAAUCAUACUUCUUUACAUU	92	18,47826	31,52174	17,3913	32,6087	35,86957	64,13043	1,034483	1,0625	-19,8	-19,2	0,145182	8,89	-21,5217	-0,6
pmc-mir-1c	AGUACAUACUUCUUUACAUUCCAUAGCUUUGCAAGAACAUAUGGGAUAGCAAAGAAGUAUGUGCC	65	18,46154	33,84615	18,46154	29,23077	36,92308	63,07692	0,863636	1	-27,1	-26	0,4687	2,23	-41,6923	-1,12917
pmc-mir-2001	GCUGCCAUUUUGUGACCGUUACAAUGGGCauugacagaaaaacaaaugcucCAUGUGGUGUUCACAAGAUGGCGGU	76	22,36842	13,15789	14,47368	21,05263	36,84211	34,21053	1,6	1,545455	-36,2	-36,2	0,193282	4,14	-47,6316	-1,29286
pmc-mir-200b	AAUUUCAUACGUCAUCUUACCUGACAGUCAACAGCAAACAAAGUUGCUCCUUUGGUCUUAUUGACACAGGUGAUGAGAUUGAAGGU	86	19,76744	30,23256	19,76744	30,23256	39,53488	60,46512	1	1	-21,8	-21,6	0,126933	11,76	-25,3488	-0,64118
pmc-mir-201	AGUUGCUGGAAGAGCUGCAGGCCACUUCCUAUGAACAGCGCCUUUCUCACGUGCGGUGUCCUCAGCACCUCGCCCAGCACGA	82	25,60976	19,5122	34,14634	20,73171	59,7561	40,2439	1,0625	0,75	-25,8	-25,8	0,163281	11,03	-31,4634	-0,52653
pmc-mir-2017	GAAGUGCACGUGGUGUUGACAGUUACCUGUGCACCUGUGCACGUGGUGUUGACAAUGACCUGUGCACGUG	70	32,85714	18,57143	21,42857	27,14286	54,28571	45,71429	1,461538	1,533333	-29	-29	0,16383	21,21	-41,4286	-0,76316

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-204	GUUCUUUGUGUCACCUCACUUCCACUUCCGGUGAAAUCCGGAUUGGUAAUGCAAGGACAGCAAAGGGA	68	25	25	23,52941	26,47059	48,52941	51,47059	1,058824	1,0625	-21,9	-21,9	0,137453	4,4	-32,2059	-0,66364
pmc-mir-2064	AUGAGAUUCAGAAACAUGUCCAUCACAAGCUGCUGAAAGAAGCAGCACUGUGCAAGAUACUUUUUCCCCGAAUCUGGG	78	21,79487	32,05128	23,07692	23,07692	44,87179	55,12821	0,72	0,944444	-23	-22,9	0,480687	3,28	-29,4872	-0,65714
pmc-mir-2155	GUGUGCUCUGGUGCUCUGUGAAUGUAAGUUCUUUGUGGUAGAAUGAAGUGACACUGUUUUACACUCUACUGGAGCCUCAAGCAAAG	86	26,74419	23,25581	17,44186	32,55814	44,18605	55,81395	1,4	1,533333	-20,5	-17,1	0,059402	25,69	-23,8372	-0,53947
pmc-mir-216a	guguuugucUAAUCUCAGCUGGUAAUUCUGAGUGGAGUUCUGCACACCUCAAGUUACUAGCCGAGAUUACAUAAAUAU	78	16,66667	26,92308	17,94872	26,92308	34,61538	53,84615	1	0,928571	-30,5	-30,5	0,146188	3,64	-39,1026	-1,12963
pmc-mir-216b-1	CGUAGGAAGAUGAGCCAGGAUUACAAGAUUGUUGGGCCUGCGGCCCUAAUAUCAGCUGGUAAUCCUGAGUGAGCUUGCCUCAG	83	30,12048	24,09639	21,68675	24,09639	51,80723	48,19277	1	1,388889	-31	-30,7	0,290814	5,92	-37,3494	-0,72093
pmc-mir-216b-2	GCGGGACCACUUGCCCUGUGGAGCGAGGAUGCUCUGGAGGACGGCUGGACCUUUAUUAAAACUCGCCGCUACACAGUGGCUACUGGGUCCACA	93	31,1828	20,43011	27,95699	20,43011	59,13978	40,86022	1	1,115385	-34,1	-34	0,183887	24,97	-36,6667	-0,62
pmc-mir-216b-3	ACACAGUUACCUGUAGAUUGUGUCACUGACUAGUAACACAGUUACCUGUAGAUUGUCACUGACUAGU	91	17,58242	29,67033	21,97802	30,76923	39,56044	60,43956	1,037037	0,8	-20,7	-20,6	0,056424	15,43	-22,7473	-0,575

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AACACACUUACCUGUAGACUGUUA															
pmc-mir-2223	AAGUGUUUGUAACAAACAUCCUGUGUCUGUACUGUACACAUGACGUGCUACAGUAUUUGUACUCAUGUAAGUAUUUGUAACAAACAUCC	89	16,85393	30,33708	19,10112	33,70787	35,95506	64,04494	1,111111	0,882353	-23,8	-18,8	0,195676	11,23	-26,7416	-0,74375
pmc-mir-2238i	GUACCCGCACGUGGUCAUCACCAAGUUCCGGUCCAAGGAAGGCCGUUCACUCAUCUCGGAGCUGAUCAUCGAGCGGGGCC	80	28,75	20	32,5	18,75	61,25	38,75	0,9375	0,884615	-27,6	-25,2	0,123572	5,73	-34,5	-0,56327
pmc-mir-2284c	AUAUGAUGAUAAGGUGUACAUGAAACAGCUAAAAAUCUAAGUGAACUGUCAAGGUGGAAAAUUUUACAUGUUGCACAGUCACCUUGCUCAGCAGGA	96	21,875	36,45833	15,625	26,04167	37,5	62,5	0,714286	1,4	-22,9	-19,8	0,195896	4,07	-23,8542	-0,63611
pmc-mir-2298	CUACCUGCUGGGUUGGUCAGGGUAGUGGGAUACAGAACGAUGACUGAUGUUGUUGUUCAAGAACCAAACCCUGACCAUGGAGCGAGCAGGCGC	93	32,25806	24,73118	21,50538	21,50538	53,76344	46,23656	0,869565	1,5	-44,5	-41,7	0,259982	2,97	-47,8495	-0,89
pmc-mir-2304	AGUUCAGCGGUUGGUAGUGGAAGUGGUGUGUAGGUGuggguugugugguugugugGCGGUCAGUGUGCUCCUGCACUUCACACGACAAACACGUUGACAA	100	27	18	16	20	43	38	1,111111	1,6875	-32,8	-27,8	0,059196	33,54	-32,8	-0,76279
pmc-mir-2361	CAUUCAAUGGAAGGUCGUUAUUCAUUAUCGUAAACAAAACACAUGGAAGacaguuuguguuguuuuguuuu	100	12	30	10	18	22	48	0,6	1,2	-25,8	-25,8	0,03599	8,11	-25,8	-1,17273

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	gcauaguaACAAAAUGAAUACAUUGAAUG															
pmc-mir-2371	AUGUUAUGUAUAGUUUUGUGUGGUGUAUAAGUuguauaaauuuuacagaaacaaCUUGUCCACCACUAAAAAAAGAUACUAAUGA	85	14,11765	24,70588	8,235294	27,05882	22,35294	51,76471	1,095238	1,714286	-23,4	-20,9	0,161131	8,21	-27,5294	-1,23158
pmc-mir-2470	GCCAGAAAAACCUAAGCAUGACAAAAUAUCAUGCUUGUGUGGUUUUGGAUACUUGGAUUUUUCUCCC	67	19,40299	28,35821	19,40299	32,83582	38,80597	61,19403	1,157895	1	-19,9	-19,9	0,542669	2,57	-29,7015	-0,76538
pmc-mir-2491-1	CAGUGUUGCAAAGUUUACCUGCUGCUAUUGUGACUCAGACAUCUCAAGGGCaccugcaacaacaacagcagcagcaacaacaacagcaacaaca	94	12,76596	12,76596	12,76596	15,95745	25,53191	28,7234	1,25	1	-25,1	-23,1	0,06655	7,31	-26,7021	-1,04583
pmc-mir-2491-2	GAAUGUUAAUGACGAUGACUGCUGUUGUUCCCUUGAAAUAGGCUAAGGUCUacuuaacaacaacagcagcagcaacaacaacaaca	86	15,11628	15,11628	9,302326	19,76744	24,4186	34,88372	1,307692	1,625	-24,4	-24,2	0,192125	18,27	-28,3721	-1,1619
pmc-mir-2491-3	GAUGGCGGCGAAGAAGUCCACGCcugaagaagaacaacaacagcagcagcaacaacaaggGUGGCGAGGGCUGCUUCGUCACCUGU	86	22,09302	9,302326	15,11628	10,46512	37,2093	19,76744	1,125	1,461538	-27,25	-26,3	0,182896	6,2	-31,686	-0,85156
pmc-mir-2493	AUCGCUGUGUGGGACUCGUGUUGAUCAUCGCGGUGCACUAAAUGUCAUCCGGCCAGACAUCAGACCAucgugcucacacacacacacagccag	93	19,35484	16,12903	19,35484	17,2043	38,70968	33,33333	1,066667	1	-28,2	-25,4	0,239172	8,2	-30,3226	-0,78333

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-2505	GACCGUGUAUUCUCGcucucgugcacacacacacauacacacgcgcgcgcgcgagcaGACAUACCCGCUG	70	10	7,142857	12,85714	10	22,85714	17,14286	1,4	0,777778	-20	-18,8	0,634526	4,68	-28,5714	-1,25
pmc-mir-252a	CCUAACUUCUGGCCCAUUACUAAGUACUAGUGCCGCGGGAAGAUAACUUGUCAUGUCCCGUGGUUCUGGUCCUUACUACAGGGCGGAACUUGCA	94	24,46809	21,2766	26,59574	27,65957	51,06383	48,93617	1,3	0,92	-37,6	-37,6	0,059589	5,1	-40	-0,78333
pmc-mir-254	GUGUGUGCAAAUCUUUUGCAACAGACUUUUAAACUAUGGGUGUUUGGUGUUUGAGUGUGCAGAGUUGUUUGCAAACUCUUUGCUACAGAA	90	25,55556	23,33333	13,33333	37,77778	38,88889	61,11111	1,619048	1,916667	-21,5	-16,1	0,016973	23,25	-23,8889	-0,61429
pmc-mir-2571	UCCUUCUGCAUGGCCACUUCGCUGGUGUGAGUGGUGAUGAUGUUUACCACUCAGGACGAAGUCAAAGAGGCGAUCAGCAACAA	83	27,71084	25,3012	22,89157	24,09639	50,60241	49,39759	0,952381	1,210526	-29,2	-29,2	0,309071	7,4	-35,1807	-0,69524
pmc-mir-279	CUCUCUUAUCUUUGCGGGUGGCUGUGAGUCUAGUCCAUGUGACACUGCAAGCUCAUGACUAGAUCCACACUCAUCCACAAGGAUAGGACGU	91	23,07692	23,07692	26,37363	27,47253	49,45055	50,54945	1,190476	0,875	-39,9	-39,4	0,157559	5,72	-43,8462	-0,88667
pmc-mir-279b	AAGGGGACCAACCACUAGAGUGACUAGACUGAUAACCCCUAGAGAUGUUGUGCUUCAGUUAUCACUAACCAUUGUGGUGGAUCCCUGA	88	23,86364	28,40909	22,72727	25	46,59091	53,40909	0,88	1,05	-25,9	-23	0,049529	18,81	-29,4318	-0,63171
pmc-mir-279c	GUUUCUGCCGGAACAUGACCAGCAUCGUUCUGGAAGGAGGCACUCGGCUGGCGGGUGUUCGUUUCGA	100	36	18	24	22	60	40	1,222222	1,5	-38,8	-38,3	0,103385	8,74	-38,8	-0,64667

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUACGAGGGCGGGAUCAUCAGCUUCGGCGACAG															
pmc-mir-281	AAAUGACCUCACGCUGAAGGGAGCAUCCGUCGACAGUCAGAAAUGCAGCACUGUCAUGGAGUUGCUCUCUUUAcugaaaaggucaagg	88	20,45455	22,72727	20,45455	19,31818	40,90909	42,04545	0,85	1	-35,2	-35,1	0,187538	3,76	-40	-0,97778
pmc-mir-282	uaauauguuuuuugugguuguuuuuggCAGUCCUGUAGACAUCAAUACUAGACAUAGCCUAAAAGAGGCACCAAGAAUGAUAaca	85	11,76471	27,05882	14,11765	11,76471	25,88235	38,82353	0,434783	0,833333	-20,6	-20,6	0,141364	11,91	-24,2353	-0,93636
pmc-mir-2953	AGACCAUGCCUCAGACACUGUGCUGCUCCUGAACUUGUUCCUUCAUGCUACAGAAGUGUUCGUGGGGGAUGGAAA	75	26,66667	22,66667	24	26,66667	50,66667	49,33333	1,176471	1,111111	-23,8	-23,8	0,296458	3,88	-31,7333	-0,62632
pmc-mir-2a-1	AGGCAAAGCUAUGGUGCUGACCAAGUGACUGGGAUGUGUACCUAAAUAUCAUAUCACAGCCUGCUUGGAUCAGUAUUAUGGUUUUGAAC	89	24,7191	28,08989	17,97753	29,21348	42,69663	57,30337	1,04	1,375	-38,6	-38,2	0,276363	1,97	-43,3708	-1,01579
pmc-mir-2a-2	AAAAAGCAAAUGUGCAUGGAGCAAUCAAAGUAGUUGUGAUGUGUUUGUUGACUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAGUUUCUUGCA	98	21,42857	28,57143	17,34694	32,65306	38,77551	61,22449	1,142857	1,235294	-34,2	-33,9	0,160179	6,48	-34,898	-0,9
pmc-mir-2a-3	UUAUGACUGCUGAGUUCACAUCAAAGAGGCUGUGACUUUGUGAUGCUGUUUCAAAUCACAGCCUGCUUUGGUGAGCUCUUUGCUGUCAGAU	91	24,17582	20,87912	19,78022	35,16484	43,95604	56,04396	1,684211	1,222222	-40,8	-40,8	0,328315	3,78	-44,8352	-1,02

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-2b-1	UGCAAGAAACUGUGAAGAAGCUCAUCAAAGCUGGCUGUGAUAUGAAGUCAACAAACACAUCACAACUACUUUGAUUGCUCCAUGCACAUUUGCUUUUU	98	17,34694	32,65306	21,42857	28,57143	38,77551	61,22449	0,875	0,809524	-24,8	-24,8	0,342782	4,57	-25,3061	-0,65263
pmc-mir-2b-2	GAAGCUAGACCAGCUCAUCAAAGCUGGCUGUGAUAUGACUGAACUCAACACAUCACAGCAUCUUUGAUGGGCAGAUCCUAGCAAU	85	21,17647	31,76471	24,70588	22,35294	45,88235	54,11765	0,703704	0,857143	-34,5	-34,5	0,221463	4,35	-40,5882	-0,88462
pmc-mir-2f	UCGGGUAGAUAAGCCAGCGAUGUGAGACUCCAGACGAUGGUGUGACUGAGGAGUUAGCAGACCAGUGUAUGUAUAUCACAGCCAUGCUAAUCUCCUCU	98	27,55102	26,53061	21,42857	24,4898	48,97959	51,02041	0,923077	1,285714	-28,7	-28,7	0,071984	7,94	-29,2857	-0,59792
pmc-mir-300	AGCGCUCGGUGGAUUAAGCGUGUCUUGCCCAUGUAUCUAUACAAGGGCAGACUCCAUCCCCAAGCCAC	68	23,52941	23,52941	30,88235	22,05882	54,41176	45,58824	0,9375	0,761905	-24,8	-23,9	0,250391	4,52	-36,4706	-0,67027
pmc-mir-302a	CUACACCCGUGGACCACUCCAUUUAUUUGAUaacaggaaagugcuuccuuUUAUUGGUGAUUUCACACUAUUAUUGAGAGGAACACCGGGUGGUG	95	17,89474	18,94737	16,84211	26,31579	34,73684	45,26316	1,388889	1,0625	-26,3	-26,3	0,019986	22,21	-27,6842	-0,79697
pmc-mir-302b	GAAACUAGCUUGACAGCCAAUGCAUAGCCAUCAGACAAAGUGCUUCCAUGUUUAAUUCAGUCCAUGGCUUUGUAUUAGCCUUAAAGCUGUAUA	93	18,27957	30,10753	21,50538	30,10753	39,78495	60,21505	1	0,85	-25,2	-25,2	0,130818	5,39	-27,0968	-0,68108

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-3057	agagugacUGGCUGUUCUUGAGAGAUGUUAGCAAGUUCAAAAUGUUAUGGCGCGAACCAACAUCCCACAGGCCCAGCUGUCACAAA	86	20,93023	26,74419	22,09302	20,93023	43,02326	47,67442	0,782609	0,947368	-24,4	-20,9	0,20764	8,46	-28,3721	-0,65946
pmc-mir-3071	AuaucaucaaaacaaauguGCAUAGUGUUACACAGAUACCAGGAUCAUGGAUUCAGCUGAUUUAGUGACUGaaacacuuucauuucuugauGAAGC	96	15,625	18,75	10,41667	15,625	26,04167	34,375	0,833333	1,5	-20,1	-19,8	0,178747	6,13	-20,9375	-0,804
pmc-mir-308	CGAGUGCGCAUGACAGCGCGCGCAGGAUUUGCUUGUUUUGAGCAACUCGGGUGGCGAUGUCCAUGACGCACAGC	74	33,78378	18,91892	25,67568	21,62162	59,45946	40,54054	1,142857	1,315789	-32,3	-32,3	0,25533	2,19	-43,6486	-0,73409
pmc-mir-3084a	UAUAUGUAUUGAAGGUUCAUUAGCCUUGUGGUCAGAGCACUCCAAUUUGGAGCAAAAGGUUACUGGUUCAAGGUCUGCUUGAACCUAUGACUAAAUaau	99	22,22222	27,27273	16,16162	31,31313	38,38384	58,58586	1,148148	1,375	-27,5	-22,4	0,08872	12,04	-27,7778	-0,72368
pmc-mir-31	GUCUGUGCUGGUCuacauuuuguaucuguuugaaCUGUCUGUUGGCAAGAUGUUGGCACAGCGUAGUGAGAUUGACAGAAAGUGAAAACCGGCCACAGAA	100	25	21	15	18	40	39	0,857143	1,666667	-31,6	-26,5	0,025901	18,56	-31,6	-0,79
pmc-mir-315	UGAUGUGAAGUUCUUAGCAGAGGGGUCAAUGUAAGUUAAUUUUGAUUGUUGCUCUAGAAAUUAGAGCUCUUUGUAAAAGUUUACAGAG	88	25	29,54545	9,090909	36,36364	34,09091	65,90909	1,230769	2,75	-18,6	-18,6	0,01829	11,85	-21,1364	-0,62
pmc-mir-317	AAUAUGUGCACUGUGGGAAGGAUACCAUUGCUUGUUCACAGUGAAUUGGACAUGUGAACACAGCUG	94	25,53191	27,65957	14,89362	31,91489	40,42553	59,57447	1,153846	1,714286	-40,1	-40,1	0,224017	2,93	-42,6596	-1,05526

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUGGUAUCUUUUUUAAUGUGAACAUGAC															
pmc-mir-33	GUGUACUAUGGUAGUGCAUUGAGGUUGCAUUGCAUCAGCUGAGAAACAUGCAAUGCAUCUGCAGUGCAAAUAUCAUGGUAUGC	83	26,50602	27,71084	16,86747	28,91566	43,37349	56,62651	1,043478	1,571429	-38,7	-37,7	0,204831	5,09	-46,6265	-1,075
pmc-mir-336	UGACAGAGUACUUGAUUUGCUAUGUCACCCUUCCAUAUCUUUUGGUUUACUUUGUAUGAUGUGAAGUGUAUGUGAGCAAAGCUGAACAUCUGGAA	95	22,10526	25,26316	15,78947	36,84211	37,89474	62,10526	1,458333	1,4	-18,9	-14,5	0,043153	12,58	-19,8947	-0,525
pmc-mir-33b	CAUUGACUACUAUAAUCCAUCUGUCAAGCAGACACGUUUCAGUGCCUCUGCAGUGGAUGUAUGGUGGCAUCU	72	22,22222	23,61111	23,61111	30,55556	45,83333	54,16667	1,294118	0,941176	-23,6	-23,6	0,187831	6,78	-32,7778	-0,71515
pmc-mir-345	UCAGCGGCUCGUGGUGCAACAUUUGUUACCUGCACCUUUCUGCACUCGGCGGAGAUGAAGAACACGUGACGAGAACGUGCUGACCCCUAGUCCGCCUC	98	26,53061	20,40816	30,61224	22,44898	57,14286	42,85714	1,1	0,866667	-28,8	-28,8	0,301092	13,36	-29,3878	-0,51429
pmc-mir-3529	UGUGGCUGCAGCAAUCAGGGAAGAAUGUGAUUUAUUGUUAGUCAGCAUCAGAACAACAAAAUCACUAGUCUUCCAGAUCACGGCAGCCugg	91	21,97802	30,76923	20,87912	23,07692	42,85714	53,84615	0,75	1,052632	-30,8	-29,7	0,103281	5,67	-33,8462	-0,78974
pmc-mir-3532	CACGCUCGACGGACUUCACGAGAGCUGUUUUACACUCAUACACAAGCUCGGGUCUUGGAGGCUGCAGU	99	27,27273	19,19192	29,29293	24,24242	56,56566	43,43434	1,263158	0,931034	-40,6	-30,6	0,036618	11,77	-41,0101	-0,725

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUGACCUCAGCCUCGUGUCUGUCGCAGCAGU															
pmc-mir-355	UGACugauuuaucuguuuauuuguuuuagccUGAGUCGCCAGAGGAAAUGGAUGAUGAAUCUGAACAACCUAAAACAGCUGGCAAGAUAAUUCAGGCA	98	18,36735	27,55102	13,26531	13,26531	31,63265	40,81633	0,481481	1,384615	-22,1	-22,1	0,017425	13,25	-22,551	-0,7129
pmc-mir-36	UGAGACUCUUGUCAAUAAAGUACGUGUCGUUCUUGUCACCGGGUGGAAAUUCGUCUUUAAGACCUCCUUCAGUAUUUUGUGAGAAGGGUCAUA	93	23,65591	23,65591	18,27957	34,4086	41,93548	58,06452	1,454545	1,294118	-25,6	-18,64	0,051427	15,9	-27,5269	-0,65641
pmc-mir-3620	GGGUGGGCUGGGCUGGGCUGGGCUGAAAUAGGAAAAGAAUUAAUCCUCUUUCUGCUCCACAGUACAGCACAUCA	74	29,72973	25,67568	21,62162	22,97297	51,35135	48,64865	0,894737	1,375	-27,3	-24,8	0,167443	4,41	-36,8919	-0,71842
pmc-mir-3643	GGUCGAGAAUCACGGCAACUGGCUUGAGAUGUGAGUUUAUCUAAAUUCAGGAAAUGAGGAGCAGACAAGCUCGCUGGGUGAUUUCGUUG	89	31,46067	26,96629	15,73034	25,8427	47,19101	52,80899	0,958333	2	-21,4	-13,5	0,040157	24,56	-24,0449	-0,50952
pmc-mir-36b	UGAUGCGGUGAGUGUAAACCCUGGUCGGUGCACACCAGCAACAUCACCGGGUAUACAUUCAUCCGCACCC	70	24,28571	24,28571	31,42857	20	55,71429	44,28571	0,823529	0,772727	-30,6	-27,6	0,171958	5,87	-43,7143	-0,78462
pmc-mir-3724	AACUGCAUUGUAGUAAUUGGCAGGAAUCCCCCAGAAUCGUGGUAAACUUUGUCCUCGCCCUACAUUCUUACAGUGCACUC	80	18,75	25	27,5	28,75	46,25	53,75	1,15	0,681818	-20,3	-19,1	0,192073	5,28	-25,375	-0,54865

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-375-1	CGCCGCCAGACGACAUCACAGAACAUGUAGCUGCCCAAUGACCCGAGCCGCUCGUAGCAAGGCAUCUUCACAAGUUUUGUUCGUUCGGCUCGCGUUA	97	23,71134	22,68041	31,95876	21,64948	55,6701	44,3299	0,954545	0,741935	-30,9	-30,9	0,454586	4,38	-31,8557	-0,57222
pmc-mir-375-2	GGGACUUAAUUCAUCGCGAGCAGAAAAGAACGCAACAUCUUGUUCGUUCGGCUCGUUCUGAAAAAGUGAC	70	24,28571	30	21,42857	24,28571	45,71429	54,28571	0,809524	1,133333	-20,3	-20,3	0,298895	4,19	-29	-0,63438
pmc-mir-3782	AGGAGAGGAUCGGGGCCAGCCAAGGAGGCUUACAGAGGCACUUGGGUGGCGCGCCAUUCCACUUGA	66	37,87879	22,72727	24,24242	15,15152	62,12121	37,87879	0,666667	1,5625	-27,1	-26,3	0,354302	7,68	-41,0606	-0,66098
pmc-mir-3792	CUUAUCUUUCUGGGCCUCGUGUUAUGUAAGUCAUCAGACACUAACGACugaggaaagagagauguu	66	13,63636	16,66667	18,18182	24,24242	31,81818	40,90909	1,454545	0,75	-19,9	-17,6	0,1503	5,43	-30,1515	-0,94762
pmc-mir-3821	AAGCUUACUAUUGAGAGGGUCAguacuuuuuucauuugaguUCAUUUCUAGUGAGUGAGGGUACUUUGUAGCUGAUGUUCUCAAUGUUAGUAG	93	21,50538	19,35484	9,677419	29,03226	31,1828	48,3871	1,5	2,222222	-28,6	-28,6	0,072168	9,75	-30,7527	-0,98621
pmc-mir-4009c	CUUGCAUgcagcacagacacagauagUGCAGCCUCUCAUUAUUGCACUUUUACUGGUCGUGGCUCCAGGCUCC	73	15,06849	9,589041	23,28767	26,0274	38,35616	35,61644	2,714286	0,647059	-20,8	-20,7	0,16755	3,74	-28,4932	-0,74286
pmc-mir-4013b	auuugauuuugcuuACUUGCUUUAACAGCUUACUUACAGGUACAAAGUAGGCUUUUAACCUGUGUACCUG	99	17,17172	25,25253	19,19192	24,24242	36,36364	49,49495	0,96	0,894737	-30,2	-30,2	0,107048	16,44	-30,5051	-0,83889

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UUAGAGACGGGUACACACACAAGUCACGU															
pmc-mir-4057	GGUCGGCAACUGACCUCCUGCAUCUCCAGGGUGUAGGAGAUGGGGGUGGCUUGGCGACUGUAGUAGGGCAGUUCCGCUG	79	39,24051	15,18987	22,78481	22,78481	62,02532	37,97468	1,5	1,722222	-33,5	-28,4	0,21803	20,3	-42,4051	-0,68367
pmc-mir-4070	CUCACAAGCAGGUUGUGAGCGACCACCacgcgucacgugacaccuagUGACAGCUGUGUUGACGUCACAGGCAGCUGUCUC	81	20,98765	16,04938	22,22222	16,04938	43,20988	32,09877	1	0,944444	-27,1	-20,9	0,082254	16,72	-33,4568	-0,77429
pmc-mir-4133	aaaccauguuguguuuuuguaugcAGGAUUAGCUGCAAGUGACAAGGAAAAUUACUGUCACAAGAUAAUCCUUCCAUCAGGAAACUCAAAUGGGAC	96	15,625	29,16667	14,58333	15,625	30,20833	44,79167	0,535714	1,071429	-26,4	-26,4	0,07692	7,8	-27,5	-0,91034
pmc-mir-4140	UCAAUUAUAUAAAAUCAACUGGUGCAAGAUGCUUUGCUGGAGAUUUCAUGGUAAUACUUCAGUAACCAGAUGAUUAUGACACAAUAAA	88	17,04545	37,5	14,77273	30,68182	31,81818	68,18182	0,818182	1,153846	-18,9	-18,9	0,163592	6,36	-21,4773	-0,675
pmc-mir-4177	UUACAGGGUGUUUACAUAAUUGcuguuuuaaacaguuuucaggUUAUAUACCAGGAUCAAACAGACUCUAGUCAUAAUACCCUGGGU	87	13,7931	24,13793	13,7931	24,13793	27,58621	48,27586	1	1	-20,5	-19,4	0,131475	8,3	-23,5632	-0,85417
pmc-mir-4185	CAUAAAGUAUCUAUGUUUAAUGCGCUGUUGUGUGAGUCUCCUUCUUUGUAUUCAUACUGUCUGUUACAAGCAAGCGGAUUAUUCAAAGAAUACUUUGCA	99	18,18182	26,26263	17,17172	38,38384	35,35354	64,64646	1,461538	1,058824	-24,4	-20,7	0,040505	9,56	-24,6465	-0,69714

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-4323	AUCUGCGGCUUCCUGCACUUAGAGGGGAGAGAUUUGCUUUUGACAGCCCCACAGCCUCAGGAGCAGAAAGCUGCAUAG	78	28,20513	24,35897	25,64103	21,79487	53,84615	46,15385	0,894737	1,1	-26,3	-25	0,219804	12,73	-33,7179	-0,62619
pmc-mir-4472	UGCUCUGCAGCAACAAUCGACUAUUCCCACCCUCCUUUUUUUACUGGGGUGGGGGGUGUUGUUGAUCAGAAAU	73	24,65753	19,17808	23,28767	32,87671	47,94521	52,05479	1,714286	1,058824	-25,5	-22,6	0,074609	17,51	-34,9315	-0,72857
pmc-mir-449d	CCUAUCAACCAUUGUCAGCAGUGAAACUAAUGGUAUUCAUUUGUCUUGAAGGCUGUGUGCUGUAAAGAUAAUGCUCACUGCUGCCCUCGUGGAUCUA	97	21,64948	24,74227	21,64948	31,95876	43,29897	56,70103	1,291667	1	-25,6	-22,8	0,038963	9,81	-26,3918	-0,60952
pmc-mir-4629	AACGAGGCUCACGUGUGUGAUGACGUGGCAGUGUCACGGCGAGGAUCCUGUCCCAAUGACUGGACGUUCAUCGCCGACAGCGAUGGCUCUCCCU	94	30,85106	19,14894	28,7234	21,2766	59,57447	40,42553	1,111111	1,074074	-30,5	-25,9	0,016318	28,06	-32,4468	-0,54464
pmc-mir-4654	GGCUGAUACGCCAGGUGAUGUGGGAUCUGGAGGCAGACUUCGGCUUCCGCAUCGGCCCGUGGAACCAGGCCUACAUGUACGACACCCUGCCGAUCAGUC	99	31,31313	19,19192	30,30303	19,19192	61,61616	38,38384	1	1,033333	-41,7	-40,2	0,172557	4,86	-42,1212	-0,68361
pmc-mir-466-1	AUACAGUCUGUGGCGUGUUUUGUAUGauguauaauauauacacacacacauauauauauauacacacauacacauacaaggCCUAGAGUCUGCGG	95	13,68421	6,315789	7,368421	14,73684	21,05263	21,05263	2,333333	1,857143	-24,1	-24,1	0,035265	12,2	-25,3684	-1,205

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-466-2	uauauauauacacacacacaaccauggAGUCUCCACAUGAGUGAGACAAGUGACCCUGAAAUGAGUGACUCAGCACCCAAGUUUUUGUguauaaauagc	99	14,14141	18,18182	14,14141	15,15152	28,28283	33,33333	0,833333	1	-19	-10,61	0,024059	19,5	-19,1919	-0,67857
pmc-mir-466-3	CAGGUGAUACAGAGCGAACUGUAAUAUUcauacuguguauauauauacacacacacauauacauauaaugaaCAUUAUGUGUGCACUGUAUUACUAG	97	12,37113	16,49485	8,247423	17,52577	20,61856	34,02062	1,0625	1,5	-29,3	-29,3	0,326455	3,38	-30,2062	-1,465
pmc-mir-466h	AGCUGAUCGGCCAGGAUUCUCGCGCGUGcgcguacgcacgcacacacacacacacgcacgcacgccugGCCAAACAACa	79	13,92405	11,39241	15,18987	7,594937	29,11392	18,98734	0,666667	0,916667	-29,5	-29,5	0,500936	3,9	-37,3418	-1,28261
pmc-mir-466i-1	gugugugugugugugugugugugugugugugaucauaaCAUAUGCCAUCUCCUGAUCACAGGCAUUCACACUAAACAACACCAGGA	86	6,976744	19,76744	18,60465	10,46512	25,5814	30,23256	0,529412	0,375	-30,8	-24,1	0,099618	12,29	-35,814	-1,4
pmc-mir-466i-2	ugugugugugugugugugugguucauucuAGUcuauccucugugugugugugcaucaAGAAGCCUCUCAAUGAACCACCAGAACAGCACGGG	94	9,574468	14,89362	11,70213	4,255319	21,2766	19,14894	0,285714	0,818182	-20,1	-12,9	0,014359	21,92	-21,383	-1,005
pmc-mir-466m	aaauugugugcaugugcaugugaaugugugugcaugcuuacCUGCUUUAGAGAUAUCAGAGCAGAGAACAUCUACCAUGCAUGACCAUGCCAAACCU	97	10,30928	19,58763	15,46392	12,37113	25,7732	31,95876	0,631579	0,666667	-27,1	-26,2	0,171386	21,7	-27,9381	-1,084
pmc-mir-466n	uuuuguauUACUUCAUGCUCAcgaaugugugcacacacacacacaugggugCA	97	12,37113	11,34021	10,30928	13,40206	22,68041	24,74227	1,181818	1,2	-28,3	-28,2	0,049412	16,07	-29,1753	-1,28636

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UAGGGGACAGGUGUGUGCGUACAUGUACUCAuguauauacauag															
pmc-mir-466q	CCGCGAGCUGUaacgugcacacagacacacagacuguugCGUGCUGuaacgugugcacacacacacauacacugguGCGUGCUGUAACGUACUGCCGCGU	100	15	4	13	10	28	14	2,5	1,153846	-33,1	-14,84	0,013848	33,92	-33,1	-1,18214
pmc-mir-467d	GAGGGUUGUAAGUGCGCGCAUGUAUUUAUGUUGCAUUCGUAUGUAGUUAUGCAUGUAUAAAUACAUGCACUCGAUAAAAACCAGA	85	23,52941	30,58824	14,11765	31,76471	37,64706	62,35294	1,038462	1,666667	-25,9	-23,2	0,094769	13,72	-30,4706	-0,80938
pmc-mir-467f	GUAGGCCAACGUCUCCCUCCCGCUGAaaaauuuauauacacacacacaccuuucaagUGGGAGGAGAUGGACAAUGGCCCAU	82	19,5122	13,41463	18,29268	10,97561	37,80488	24,39024	0,818182	1,066667	-30	-30	0,050335	8,93	-36,5854	-0,96774
pmc-mir-4715	CGCCACGCUGAUCACGUGCCAACGUGCCACCUUAACUGCACGGACCGCGGAAGAUGGUUUGGCCGUGGAAAGUGAGCGGUGAGU	84	33,33333	21,42857	27,38095	17,85714	60,71429	39,28571	0,833333	1,217391	-31,6	-31,6	0,33988	8,09	-37,619	-0,61961
pmc-mir-4750	CCUUCAAUGUCUCACGUGCACGAUGGGGGGAAGGGGCUGUGAACACAUGGACUGACACCUGACCCACCCCCUCCCUACUCUGACCGUGACAGUGACAA	98	25,5102	23,46939	32,65306	18,36735	58,16327	41,83673	0,782609	0,78125	-29,8	-19,7	0,066962	29,71	-30,4082	-0,52281
pmc-mir-4757	aaaaaaaaccaaaacucaAGCGUCUCAGUAAAGGGUCUACAUUUUACACCUGUCAUUUCCAUGACGUCACAGAGGCGAGGUUUGGCUUUUGGA	93	20,43011	18,27957	17,2043	24,73118	37,63441	43,01075	1,352941	1,1875	-22,4	-21,8	0,139005	15,42	-24,086	-0,64

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-4769	AUUGCUGGCUUCACUCUUCUGCCAUCCUCCCUCUCGUCUGUCGACAUGGCUGACCCCAAGAUGGUCAGAAGAGUGAACAAGCGAG	85	23,52941	21,17647	30,58824	24,70588	54,11765	45,88235	1,166667	0,769231	-34,6	-34,5	0,204288	8,13	-40,7059	-0,75217
pmc-mir-487a	GGGAUUGUGCACUAGUGGCUAUCCCUGCUGUCAUCCCACCGAUAUCACGGCCAUAGCACGGUCACCACUAUUACAAUAGU	80	21,25	23,75	30	25	51,25	48,75	1,052632	0,708333	-22,7	-22,7	0,227369	6,98	-28,375	-0,55366
pmc-mir-49	aacaaaagaaaccaaaaaggGCAUCUUCCCAUGAUGCAAAUAGACUAAGGGAAGCACCAUGUGAAGCACUUUUCUGGUUUCUUUUCCa	88	14,77273	19,31818	18,18182	23,86364	32,95455	43,18182	1,235294	0,8125	-26	-26	0,306727	8,11	-29,5455	-0,89655
pmc-mir-4938	UUUCUgcauauuauuauaaucaucaugcaucaucauuauugaCCAUGCAGGUGCAUGAUCGAUCCUUAAUUGUAUGAGGAU	81	12,34568	12,34568	9,876543	19,75309	22,22222	32,09877	1,6	1,25	-23,1	-20,9	0,193135	5,48	-28,5185	-1,28333
pmc-mir-4949	AUUAGCAUUCAUGAUACGGAUUUUAAGGAaguggugugcgugugugugugugcccacuUAUGACAAAGUCCACAUCAUGUAACGCUGUU	89	12,35955	22,47191	11,23596	21,34831	23,59551	43,82022	0,95	1,1	-28	-28	0,194482	3,14	-31,4607	-1,33333
pmc-mir-4968-1	gaCGUUGCUGCCGAGCUCGGCUGUGCGUCGUGCUGgacggcagcagcagcaacagcagcagcagcagcaacauu	74	17,56757	1,351351	13,51351	12,16216	31,08108	13,51351	9	1,3	-35,3	-30,4	0,160289	15,99	-47,7027	-1,53478
pmc-mir-4968-2	CGACAGCGCAcuggcagcaacagcagcagcagcagcagcacucgGCGGAUGUGCAGCUUCCCUCGGUGGUUGCUGGCAGGGCCACUGGUU	90	23,33333	7,777778	17,77778	13,33333	41,11111	21,11111	1,714286	1,3125	-33,6	-22,2	0,144928	16,86	-37,3333	-0,90811

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-4968-3	ACACGACAGCCCGCAUCUGAUGCACUGCUUCCUCAGUUUCauccagcaacaacagcagcagcaacagcagcagcagcaaugccGAGAUGCCGGGA	95	13,68421	11,57895	17,89474	11,57895	31,57895	23,15789	1	0,764706	-24,8	-24,1	0,103418	14,12	-26,1053	-0,82667
pmc-mir-4968-4	CUACACCCUGGGCUGCGGCGGUUGUGUCCAGcaucacagcagcaacagcagcagcagcagcagccucaaCCAGCGCAGCAGCUGCAGCGGUGCGA	98	21,42857	8,163265	19,38776	9,183673	40,81633	17,34694	1,125	1,105263	-38,8	-38,8	0,480796	14,61	-39,5918	-0,97
pmc-mir-4999	GACGCAUUGACCAACAAUAUGAUACACUGAUGGCUUUCCUAUUGCUGUAUUGUCAGGUUUGUAGAUAUUGUAAUAGGUUAACUGCCAU	88	20,45455	27,27273	17,04545	35,22727	37,5	62,5	1,291667	1,2	-20,3	-20,2	0,098	21,47	-23,0682	-0,61515
pmc-mir-501	AAUGCACCCGGGCAAGUCAGAGGACACAUUAAGAGCCCCAUUAGAGUAAAACGGGAAUGGAGUUCCGUUAACUGACGUCAUUUGUUUCCAGGGGUGCCAG	100	28	29	22	21	50	50	0,724138	1,272727	-28,4	-28,4	0,207312	9,5	-28,4	-0,568
pmc-mir-5101-1	uuuguuuguuuguuuguuuguuuguuuugcugucugACGUUUGCGGAAAACCACAGCUCAGUCUGUCAGCAGACAACCAgaugaaaugaaagauaacaug	100	9	14	13	7	22	21	0,5	0,692308	-26,2	-19,3	0,014197	18,79	-26,2	-1,19091
pmc-mir-5101-2	UCGACCGAAGGAUAGUGACGGuccuauuuguuuguuuugcugugugcUUAUUUGUGUUAGGUUUGGUCUUAGGACUGUUUUaccuuugguuuu	93	18,27957	10,75269	6,451613	23,65591	24,73118	34,4086	2,2	2,833333	-26,8	-26,2	0,065192	10,31	-28,8172	-1,16522
pmc-mir-519f	GUGCGCAUAUUUCUUGCUGAAAAUUGUCAUGUUUAAUUUGGAGGAUAAAGUGCAUCCUUUUAUGGC	97	24,74227	27,83505	13,40206	34,02062	38,14433	61,85567	1,222222	1,846154	-23,4	-22,1	0,126706	9,47	-24,1237	-0,63243

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GAAACAUCAAUUCGGAAUGUAAUGUGCGGGA															
pmc-mir-5317a	GGGCCAGGGCCACAUCCCUAGCUCUGGUCCGUUUCUUGUCUCUGUGUACCUCUCGUGCUGCCAGACCAAGUGGUGAUCGGUGACCGCUGGAAC	93	29,03226	13,97849	31,1828	25,80645	60,21505	39,78495	1,846154	0,931034	-33,8	-33,8	0,197453	11,33	-36,3441	-0,60357
pmc-mir-539	AUGGUGAUGACUCAUCAUACAAGGACAAUUUGUCACCAGCGAAGAUGUUAUUUAUACCAUGACAGAAUGUGUCUUGUAUUUGUUCACACGAA	92	19,56522	31,52174	17,3913	31,52174	36,95652	63,04348	1	1,125	-20,4	-20,2	0,064375	14,18	-22,1739	-0,6
pmc-mir-5391	uuccugcaagGUACCUUAUGAGGUAACUUGUUUGGACAGUUAUGAAGAAGUGGAAUCUAAUGUCCAACAGUUUAGAAUCAAACAGGCUAUCAUUCAGACC	100	19	30	15	26	34	56	0,866667	1,266667	-18,8	-12,3	0,005609	35,95	-18,8	-0,55294
pmc-mir-5396b	GAAGAGGAAUCCCCCACACAACCAGCAAGAUUUGCUGCUGCGGAAGGAACAUCCCGGCAUUCGUUGACUGCCUCUGGUGGGUGGAGUCCUCGUG	94	29,78723	22,34043	27,65957	20,21277	57,44681	42,55319	0,904762	1,076923	-34,1	-26,1	0,0206	19,14	-36,2766	-0,63148
pmc-mir-5549	CcccaaaauaucaaaauagaaUAAUAAGAGGAGGGUGGGACUUCUUUAACAUUACACAGAUAUCCUAUUAUUCUUCAUGUUGGUUUUUUGAAU	93	15,05376	21,50538	10,75269	31,1828	25,80645	52,68817	1,45	1,4	-19,5	-19,3	0,091982	11,56	-20,9677	-0,8125
pmc-mir-5552	gucuguagucuauagucuguagucuguagucuaUAGUCUGUGGUCUGUAGU	85	15,29412	12,94118	9,411765	23,52941	24,70588	36,47059	1,818182	1,625	-23	-20,4	0,065706	32,41	-27,0588	-1,09524

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	UUGUAGUCUAAAGUCUGCAGCAAUGAGUUCAUCU															
pmc-mir-5595	UAGUGUCACGUGCUUUAAAAAAGGUGCAGGCUCUCUUUUUUCUCGCAGUCCCGCACUGACCUGAGAGAGUCACCAUCUUAUGUCAAAGACAUGGACAAGA	100	22	27	24	27	46	54	1	0,916667	-30,6	-30,6	0,243502	5,31	-30,6	-0,66522
pmc-mir-5600	UGAGGUCUUUGACAGUAAGUACAGAGUUUGCUCAGACAAGUAAGGAAUCAGuggaauguuuuguuucaguaGUUGUCUAUCUUCUGUACCAAUGACCAUC	100	18	23	15	24	33	47	1,043478	1,2	-24,6	-24,6	0,137757	6,7	-24,6	-0,74545
pmc-mir-5612	ACAGGUGUCUAUAUGCUACAUCACCUGAAUAAUAGCUAUUGUGUCUAUACAUCACCAGUUGACAUGUUAGGUAUGGUAUUUAUACACCACC	91	16,48352	29,67033	20,87912	32,96703	37,36264	62,63736	1,111111	0,789474	-20,8	-15,6	0,041563	12,19	-22,8571	-0,61176
pmc-mir-574-1	CAGCUCACAGAAACCAUCAGCCACAGGCUUCAAGAAAAAUACUCUAAUGACAGCUCGCGCCAUUGAGAGUCGUggaggugagugugugugugagugc	99	14,14141	25,25253	21,21212	13,13131	35,35354	38,38384	0,52	0,666667	-26	-18,3	0,019862	27,93	-26,2626	-0,74286
pmc-mir-574-2	AUUUUCCGCCAUUACUCAUCUUCCACCCAGCAUCACGUUAGUUAAUAGUCAGGcggagugugagugugugugugagugugugguaaggGGGAAUAC	97	10,30928	16,49485	17,52577	18,5567	27,83505	35,05155	1,125	0,588235	-27,6	-27,5	0,03265	10,86	-28,4536	-1,02222
pmc-mir-5918b	UUCUCAUGGUUGUGUGUUAUUAUGUUCGCUCUACAUCGUGUGGUCAGAGAUggugagagagggaagagaga	100	15	10	10	24	25	34	2,4	1,5	-22,4	-14	0,095221	25,67	-22,4	-0,896

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	gugagagaaagaaugacaagaCAUGAUGC															
pmc-mir-5965	CAACCUUGGGUGAUGACAAUUCUGACAUUUUGCAAGGUUUCAUCCUUGUCUGUUUCAUUCUUCAAACUGCGAAGUCGCGCAUCACCAAUGGGUA	94	20,21277	23,40426	23,40426	32,97872	43,61702	56,38298	1,409091	0,863636	-24,6	-23,9	0,068188	8,99	-26,1702	-0,6
pmc-mir-6056	UCUCUGUCGACUUCAUUUCCUCCUCGGCCCAGUCUUCCUCUCUCUGGUGAUGAUAGGGGUGAGGUGAGGGacgaggagggaggaggaagacgAGAGAGC	99	23,23232	11,11111	20,20202	23,23232	43,43434	34,34343	2,090909	1,15	-50,2	-46,8	0,12691	12,98	-50,7071	-1,16744
pmc-mir-6076	AAGGCUGACACCCUUCCCUCAGGUCGUCCUCCUCUAAGAAGCAAACAGAAGCAUGACAGAGGAGAGGAGAAAACCCAAAGGGAAGGCUCUCUGCAUG	97	25,7732	32,98969	26,80412	14,43299	52,57732	47,42268	0,4375	0,961538	-33,4	-33,4	0,461099	5,24	-34,433	-0,6549
pmc-mir-6098	GUGCUCGUCAUAGUGAUUGUGUGUUUCUAGAAGACAAGACCGUGUUCUGUUCAGAACACAAACAACAUGCUGAUUGUCGAGUAA	84	23,80952	28,57143	17,85714	29,7619	41,66667	58,33333	1,041667	1,333333	-22	-19,4	0,02079	16,09	-26,1905	-0,62857
pmc-mir-623	UAACAUACCUGUUCCGCCAUGGUGAACGAGUGAGGAAAAGACCGGAACGGGGUUCACACGUUUCCCUUGCAGGGGCUGAGGUAUGAGA	88	31,81818	26,13636	21,59091	20,45455	53,40909	46,59091	0,782609	1,473684	-29,8	-29,8	0,153312	7,64	-33,8636	-0,63404
pmc-mir-626	UGACACUGUGUCACACCAGCAAGcugucugaaaauguuugcaugaaaacau	96	14,58333	10,41667	10,41667	6,25	25	16,66667	0,6	1,4	-22,1	-10,23	0,039265	24,65	-23,0208	-0,92083

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	gaagacauuaaaacauuuauaaaaagugCGGGUGGGGAAGUGCAC															
pmc-mir-6302	GGAUGAGUCACUCgagauauuugauauuuuucaucaaUGAAACCAUGUUCCUGUGAUGAAGAUAGAUAAUGCACCAAACUCAUCGUCAGCCACUCACGA	99	15,15152	24,24242	19,19192	17,17172	34,34343	41,41414	0,708333	0,789474	-18,9	-17,1	0,135467	11,6	-19,0909	-0,55588
pmc-mir-6416	AGCAAAUUGCUUGAUCAUAGUGAGCGUAUCAUGGCAGCACAUCCUCAUGGGUUUGCGUCUCCGUAUCAUCUGCUAGCUACUGAGAACAAUUUUUU	95	21,05263	24,21053	22,10526	32,63158	43,15789	56,84211	1,347826	0,952381	-21,2	-20,6	0,052561	13,18	-22,3158	-0,51707
pmc-mir-6505	CUUAGCUCCAUCUGACUUCUACCUGUUCCCUAAACUCAAAUCCCACCUAGUUGGUCAccauuuuggaaacaaugauGAAGUCAUAUGAGCUGUG	94	12,76596	19,14894	23,40426	24,46809	36,17021	43,61702	1,277778	0,545455	-21,1	-19,17	0,012139	12,86	-22,4468	-0,62059
pmc-mir-651	CAUGAUAUUUUAAGUGAUAAAGGCUUUUACCUGCAAAAGAUAUGGAGUUUUAUGCUCGAUAUAAAAUUUUAGGAUAAGUUUGAACACGUAAAGCAUCAAU	100	18	37	11	34	29	71	0,918919	1,636364	-21,6	-21,5	0,14346	4,59	-21,6	-0,74483
pmc-mir-6516	GAGUCUUAUUCUAACUGGUUUCAUGAAUGCAGUAACAGGUGUCUCCACCUCUGCAUUGCUCAAACCACAUUACAUCAGAAAG	82	17,07317	29,26829	24,39024	29,26829	41,46341	58,53659	1	0,7	-19,7	-19,6	0,151242	5,16	-24,0244	-0,57941
pmc-mir-6528	GGUGGGuaggagagagggaagagggaagAAAGCAAGAUGAAAGUGUCGCCUCUGGGAGAGCUUUCGGUGGU	97	23,71134	14,43299	18,5567	20,61856	42,26804	35,05155	1,428571	1,277778	-32,8	-27	0,029155	15,05	-33,8144	-0,8

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	AUUCUCCUCCCUGUCACGUAGCCUCU															
pmc-mir-6548	CCGUUCACACAGAGAUUUGAGAGGGGGAGGGGCAGAAAAGAGAGGUGCCCCGCUGUCUGUUCUCUGGUGAAAAG	74	36,48649	25,67568	18,91892	18,91892	55,40541	44,59459	0,736842	1,928571	-31	-31	0,103929	5,12	-41,8919	-0,7561
pmc-mir-6560	CGCUGUGUUGCUCCAUACUGCUGAAGUAGUGUCUGUACUUCUGUUUCAGUCAUAAUGAGCAGCUCAUCA	69	21,73913	20,28986	23,18841	34,78261	44,92754	55,07246	1,714286	0,9375	-19,8	-18,8	0,070623	8,29	-28,6957	-0,63871
pmc-mir-6562	AGGCAUAUGAGGGGAAAGGAAUGUGCAGGUAAUGGUACUUGUAGUUUCCUAGUUUGUAAACAUUAACACUGGACACUUGUCUCCCUCGGUUCAuaugcaa	100	24	25	16	28	40	53	1,12	1,5	-31,7	-31,3	0,048803	12	-31,7	-0,7925
pmc-mir-6568	CUGAGCCUGACGAUGCCGGGCGCCAUAAUGGCCACGAGCUAACUGUCGCACGGCGGCCGCCAUCUUGCGGAGCUGUG	77	33,76623	16,88312	32,46753	16,88312	66,23377	33,76623	1	1,04	-27,4	-27	0,220859	16,73	-35,5844	-0,53725
pmc-mir-669f	acacacauauacauacacacacacguguuguUUCACAAGUAGUACAACAGGCGUGUGAGAUGUUUAUGUGAGG	73	17,80822	16,43836	6,849315	16,43836	24,65753	32,87671	1	2,6	-25,6	-20,3	0,138486	10,86	-35,0685	-1,42222
pmc-mir-669j	CUUUGACAUGACAGUUUUUGAUUUGUGGAUCguauaaaagacaaauacaucCACAGGCAUGCAUAUACUCACAUGUGCACAC	82	14,63415	19,5122	17,07317	24,39024	31,70732	43,90244	1,25	0,857143	-18,5	-17,6	0,121983	11,36	-22,561	-0,71154

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-67	GAGAUGUCGUGAGUUGUCGGUCCUUGUUCAGCCCGGUUGUGAUGGAGUUGGUCGCAUCACAACCUGCAUGAAUGAGGACUGACGUCACGAAAUAAC	96	30,20833	22,91667	20,83333	26,04167	51,04167	48,95833	1,136364	1,45	-50,4	-50,4	0,287211	2,51	-52,5	-1,02857
pmc-mir-6701	CCUAUCAUUAUGGAGUUGCUUUGUUGUUAUCUGACAGCCCAGGAAAAAUAUUCUGAUUAUUUUACAGACAGCAACUAUGAAUCCAAAACUGGAUGAU	97	17,52577	31,95876	17,52577	32,98969	35,05155	64,94845	1,032258	1	-19,2	-18,9	0,066024	11,85	-19,7938	-0,56471
pmc-mir-6876	CUUUCACUUCAGCUGUCUGUGUUUUCCCAGAUGCAGAAAUAAGUAUAUUGUGGUUUAUUGUGUUCUAGUCUGUAAACAAUGCAGUGaagcgaugu	95	18,94737	21,05263	14,73684	35,78947	33,68421	56,84211	1,7	1,285714	-22,5	-22	0,114242	8,28	-23,6842	-0,70312
pmc-mir-6891	CACCCUcaucuuccccuccccucuccaucccacccccaccucGGCGAGCGGACUGCGAAACGGAGAGGAAAUGGGAAG	78	21,79487	16,66667	11,53846	3,846154	33,33333	20,51282	0,230769	1,888889	-24,9	-24,9	0,700959	2,36	-31,9231	-0,95769
pmc-mir-6971	CGCCCGUUUCCCUAGAGAAGAAGCGUGUCAUCUGCGACAGCCUCUGCUUCUUCAGCUAGUGUCACGGAAG	70	25,71429	20	30	24,28571	55,71429	44,28571	1,214286	0,857143	-24,5	-23,2	0,750631	1,04	-35	-0,62821
pmc-mir-6974	ACAACGACGACGGUGGACAGGGGGUGGACCUCGAUGCCAGCAUGGUGUCCACCAGCUACAUUGCGCUCUUCUCCACUCUCUUCUGUGUCGUGGG	94	29,78723	17,02128	29,78723	23,40426	59,57447	40,42553	1,375	1	-35,8	-34,3	0,187738	13,56	-38,0851	-0,63929

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-7000	CAAACAGUGCCCACCCACCUGCCUGUCACAcugugauuuauuuacauuguaaCUGGAUGCUCAUGGCUGGUGGCCCAGCACUGUAUA	87	17,24138	16,09195	26,43678	14,94253	43,67816	31,03448	0,928571	0,652174	-28,9	-28,6	0,111346	9,33	-33,2184	-0,76053
pmc-mir-7046	GGUGUAGGGUGAGGCUGGUGGGUUAGUUGGGUGGCUGGUCGGGUGAAGAAAGGGAAGUAAGUCAAAUUUAAACGUGACACCACCACCCACCUACCCU	97	35,05155	24,74227	18,5567	21,64948	53,60825	46,39175	0,875	1,888889	-32,6	-28	0,059458	25,01	-33,6082	-0,62692
pmc-mir-71	CACCCGUACCCUAGUCUGGUGAAAGACACAGGUAGAAUGUAAUUCUACUGUUCACUUUUAAACGAGGGAUGCGGACU	77	23,37662	28,57143	22,07792	25,97403	45,45455	54,54545	0,909091	1,058824	-24,6	-24,6	0,07754	10,03	-31,9481	-0,70286
pmc-mir-7-1	UACUGUUCUCCAGAUUGACUUCCUCUAAGUACUGAUAGUUGUUGUUACCAACAAAUCGUAGCCUCAGAGGUAAGGCAGGUCAUUGaacaacacau	95	18,94737	23,15789	18,94737	28,42105	37,89474	51,57895	1,227273	1	-23,3	-21,3	0,085299	10,39	-24,5263	-0,64722
pmc-mir-7151	UUGUUGACACUGAGAAAAGUGACAGGAUCCAUCUCUGCCUGCUCACCUUCACGUUUGUGGUGAGCAgcugucauuuuucucuuugcAAGAU	91	18,68132	19,78022	17,58242	21,97802	36,26374	41,75824	1,111111	1,0625	-37,2	-36,5	0,178864	4,62	-40,8791	-1,12727
pmc-mir-7-2	AAUGCAAAUACUAGGGACAggguucuuuuuaaaaaaaaaaaugcagacggCUGAAUCGCUGACUGGUUACAAAAGCCAACAAGUCCCAGUCUUGGCGGA	98	16,32653	23,46939	16,32653	13,26531	32,65306	36,73469	0,565217	1	-20,7	-16,47	0,006838	17,31	-21,1224	-0,64688

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-7207	AGUUGAGGAAAUGAAAGuugcuuucaucuuuuaaaauacaggGUGUUGACAGUCAUUUCACCAGAUGAAUAAACACGUGGCUCAAUUCCUCAUUC	95	15,78947	24,21053	13,68421	20	29,47368	44,21053	0,826087	1,153846	-20,6	-19,9	0,070254	20,54	-21,6842	-0,73571
pmc-mir-722	UAUAAGGUAGAAUUUUGCAGAAACGUUUACAGUUUACUACUCUUUGGAGUUGGCUGGUGUAUAUGUUACAAGUAUAUUUCCUACCUUUUG	90	20	25,55556	13,33333	41,11111	33,33333	66,66667	1,608696	1,5	-20,7	-19,6	0,061494	7,79	-23	-0,69
pmc-mir-7241	CACCUGUUGUGAAAAUGCUUUGAACUUAGGUGUAUGCAUGUUGGAUCCUGACUCCUACUUGCAUGAGUUAAUGAUUUGUCAGGUCAACAGAGG	93	24,73118	24,73118	17,2043	33,33333	41,93548	58,06452	1,347826	1,4375	-20,3	-17,7	0,029323	17,26	-21,828	-0,52051
pmc-mir-7314	GUCACAGGGACCCUGGUUGGCCUGCACAAGCCCCAGUAAUACUGGUGUCAAGGAUAGACGAAACUCCUUGAAGAUUGUCAGAAACAGUGUCUCUGUGCa	99	26,26263	26,26263	24,24242	22,22222	50,50505	48,48485	0,846154	1,083333	-32,6	-28,7	0,010541	12,05	-32,9293	-0,652
pmc-mir-7323	UUUUUCCGAAAUAGCUUUGUGCUUUGACAAGUGCACUCUGCAAGUUACAGAAUUGUGUGAUCAACGUCAAUUCUAAUUUCCGGAAUAU	88	18,18182	27,27273	18,18182	36,36364	36,36364	63,63636	1,333333	1	-20	-20	0,049302	14,06	-22,7273	-0,625
pmc-mir-7386e	UGUAAAGUAGUAAACACUUUACCCGUUUGACUGUUUGCCCUUGUUCUUGAACAGUGUGGGUGAACCUCUUGACUGGUGUAAAGUUGUAUAacuuuuua	98	21,42857	21,42857	15,30612	33,67347	36,73469	55,10204	1,571429	1,4	-24,7	-24,1	0,025944	13,11	-25,2041	-0,68611

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-7388c	UGGUCCUUCAAGUGUGGCGUCAGUUACCUGCCCCUGUUCUACCUGCACAAGGUGCACAGACGUGACAUCGUUGAGGAAGU	80	27,5	20	26,25	26,25	53,75	46,25	1,3125	1,047619	-24,4	-24,4	0,084225	8,96	-30,5	-0,56744
pmc-mir-7398a	aaagagaacuUCCGUAACCUGUAACAUUCACAUGAUGAUUUGUUAAUUUGGAGCUUAUGAGCUCACCGUAUGUGUAGAGGUGAGAAAGUUGUCGCU	96	21,875	22,91667	14,58333	30,20833	36,45833	53,125	1,318182	1,5	-21,1	-15,38	0,110809	24,91	-21,9792	-0,60286
pmc-mir-743b	AGUAGACACUUCUGAACGAGCUUCUUGUACUAACCUUGCUGUAAACCCCAGGACGAAGCUGUUCAGACUGGUGUCUGGU	79	24,05063	24,05063	24,05063	27,8481	48,10127	51,89873	1,157895	1	-26,2	-25,6	0,030673	10,47	-33,1646	-0,68947
pmc-mir-7448	ACAACUUGAGUCUCGAAGAAGCGAACUGUUGUAGAACAGUUCCGAUCAAUCGAUAAUCGAGUAUU	65	21,53846	33,84615	18,46154	26,15385	40	60	0,772727	1,166667	-20,4	-19,3	0,340793	2,64	-31,3846	-0,78462
pmc-mir-745a	AGCUUGCUGGCUGGAGGCGGCUUUUCAACAGGCUGCCUUGCGUUCUAAAUACAAGCUGCCUGAUGAAGAGCUGUCCUGUGGCGAGCAAUGU	91	30,76923	19,78022	23,07692	26,37363	53,84615	46,15385	1,333333	1,333333	-46,9	-46,9	0,097683	4,24	-51,5385	-0,95714
pmc-mir-745b	UUCCCUCCGCUCUUCCUUUGGACAGCUAUCGUGCCGACAAGGAGAGCUGCCAAAUGAAGGGCUGUGGUGG	70	30	18,57143	27,14286	24,28571	57,14286	42,85714	1,307692	1,105263	-29	-25,7	0,096995	8,37	-41,4286	-0,725
pmc-mir-7472	CCUGUGCCUGCUGAUUGUGCAUUCCGGGGAGAACAUUUCAUAUGAGAUGUGCUGGAGAUGAAAACU	97	24,74227	24,74227	24,74227	25,7732	49,48454	50,51546	1,041667	1	-30,5	-27,9	0,050851	8,11	-31,4433	-0,63542

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUUCCUCCCCAGAACAUAAAUCUGGCACCGC															
pmc-mir-750	GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUGGCAGGAAUACUGUCUUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUGGCAUGGCAUG	97	26,80412	20,61856	23,71134	28,86598	50,51546	49,48454	1,4	1,130435	-52,7	-51,6	0,157091	3,48	-54,3299	-1,07551
pmc-mir-751	CUUGGCUCUGUGUGAUUGGUUUCUGUUCUCCAAGauuaaaacauguuugaaugGCCACCACUUUGGCACAGUAAACAUCAUCCAUAGAGCCCUU	94	15,95745	15,95745	22,34043	25,53191	38,29787	41,48936	1,6	0,714286	-27,8	-22,8	0,051558	21,54	-29,5745	-0,77222
pmc-mir-7562	cacacaccccgacacacacacacacauucauggaCACGCAUGCCUGCACUAAAAGUUUGGUUGGGAAUUGUGAGAGAUAUGUCGCGCAUGUUUA	95	17,89474	15,78947	10,52632	18,94737	28,42105	34,73684	1,2	1,7	-20,2	-20,2	0,122747	10,51	-21,2632	-0,74815
pmc-mir-7575	AGCACAAAAAGUUAGCAUGGUCAUGAUCAUGACACAAUGGGACAAUUAUGCACCAUAUGGCUGAUUAUUUGUUUA	75	20	34,66667	16	29,33333	36	64	0,846154	1,25	-19,1	-16,7	0,188578	11,02	-25,4667	-0,70741
pmc-mir-7643	aguuuguuuuucagugaACAUUGAAUACUGUCGACAUCUGUUUCUCAGUAAUUCUUACUUAGUAUCACAGAUUCAACUGAACACUGAUACAGAACGA	97	11,34021	27,83505	17,52577	25,7732	28,86598	53,60825	0,925926	0,647059	-20,4	-15,3	0,025588	14,82	-21,0309	-0,72857
pmc-mir-785a	AAUCUCGGACUUAUGAAAAUAAGUGAAUACUCUGUUAUGUCGUUAUUGUCCAgguguuuugaaaaaagaa	99	12,12121	17,17172	9,090909	20,20202	21,21212	37,37374	1,176471	1,333333	-19,4	-19,4	0,222469	10,6	-19,596	-0,92381

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	uuucauuuauuguucuuuuguccUAGCGG															
pmc-mir-7880b	uggcagacagacaacugucaaccuauacacguccaugguuggAUGGUUGGUUAUUUUGGUUUAUAGUUGGUUGGAUCAGUUUGGUUUGGCUGGUA	95	18,94737	7,368421	2,105263	27,36842	21,05263	34,73684	3,714286	9	-27,3	-24,5	0,144234	12,84	-28,7368	-1,365
pmc-mir-7880q	UCAAUGACAUUUACAUACUCUUGGAAGAGGGUCAUGCCUACCAUGCAGUUUGCGACCAaaaucacucucucuuucaaguACUAUUGguuacaugcauaca	100	13	18	15	19	28	37	1,055556	0,866667	-18,6	-17	0,048677	12,83	-18,6	-0,66429
pmc-mir-79	GGUUGGUAUUAUAAcuguauuauauuauauuagUCAGUUGCUGUAGCCACUGUAACUCUGUAGCUCUUUUAUAAUGUAAAGCUAAAUUACCAGUG	95	15,78947	22,10526	12,63158	29,47368	28,42105	51,57895	1,333333	1,25	-18,8	-18,8	0,097081	11,62	-19,7895	-0,6963
pmc-mir-8	UGCGCGGACUCUGGGUUCAUCUUACCUAACAGCAUUAGAUGUGUGUCAGCAUUUUCUAAUACUGUCAGGUAAAGAUGUCCACAGAGUCUGCUGG	94	24,46809	23,40426	21,2766	30,85106	45,74468	54,25532	1,318182	1,15	-46	-46	0,192059	3,37	-48,9362	-1,06977
pmc-mir-8250d	CAGGCUGCAAACGUUCCAAUCCACACAAGUCCAGUCAUAGAACAGAUCUUAUAGACAGAAGUCCUUUAUUUGUCUGGGUGGAGGGUUUGGCUGCUUA	97	23,71134	26,80412	21,64948	27,83505	45,36082	54,63918	1,038462	1,095238	-26,2	-23,38	0,012202	14,09	-27,0103	-0,59545
pmc-mir-8265	CAUGAAGCUCAGCGAACAGCACCUAGCAUUAUCUACAUGCCAUCAGUUAAUGAACUGUGGGCUGUAGU	96	18,75	23,95833	28,125	29,16667	46,875	53,125	1,217391	0,666667	-25,5	-25,5	0,101749	8,96	-26,5625	-0,56667

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUCUGAUACUCUUCGCUCCACCUUCCUU															
pmc-mir-8293	AUCUUAGAUGAAAGAUAAAAGUGUCUCGUGAGUGCUUGUUGCAGUUUCGCAUCUGUGGUGCAGAUAAGUAAGCAgcaucuguuuauuuuccucCUAAUAC	100	20	24	12	25	32	49	1,041667	1,666667	-21,5	-13,1	0,030404	22,6	-21,5	-0,67188
pmc-mir-8311	UGUUUACUAGAAGAGAGAACUCCUACAAGGGAAAAACCACCAUCAGUGAUUGUGAGAUUCCCCCACCUAGCCACUAGAAGUUCUCUUUCGUAGUAAAGU	99	19,19192	32,32323	23,23232	25,25253	42,42424	57,57576	0,78125	0,826087	-28,4	-28,4	0,262782	6,39	-28,6869	-0,67619
pmc-mir-8335	UCCGACAUAACAACCACGACUACAGUCAACAGAUGGCCACUgaacucucauucucucuccaCUGcuccauguuguuguuguuguuuugucagu	96	7,291667	15,625	15,625	7,291667	22,91667	22,91667	0,466667	0,466667	-24,4	-20,9	0,125649	19,36	-25,4167	-1,10909
pmc-mir-8398	UGCUUGCACUGAUCUagaagacagaagugaaaaCACUUUUCUAAAUGAAGUGAAUCUGAACAAAUGAUcacaguucuuucuuuuuagcauGCAAAGU	97	10,30928	19,58763	10,30928	18,5567	20,61856	38,14433	0,947368	1	-18,6	-15,1	0,018215	22,4	-19,1753	-0,93
pmc-mir-8422	AGGAAAAGAUCAUCAGAACUUGCAAUUAAAAGUAgcacaaacaagaaagcaagaCCAAGUGUUAGUAAAAUGCAUGUUGAGGAUGAUUCUUUUUCA	96	15,625	30,20833	9,375	23,95833	25	54,16667	0,793103	1,666667	-23,6	-23,1	0,141217	4,11	-24,5833	-0,98333
pmc-mir-8443	ACCAGAUUGGUGGUACUUUGCAUUCAUAUUUGAGUUUCGUAACAUUCUUUUCAGCUGGGUGAUAUG	92	21,73913	28,26087	14,13043	35,86957	35,86957	64,13043	1,269231	1,538462	-18,7	-18,6	0,076444	11,42	-20,3261	-0,56667

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
	GUAGGUAAUAGUACUACAAAACUAAG															
pmc-mir-8460	AAGGUCAGCUAUAGUUUCCUUGUCACAcuaauuauauuauauuugcuUUCUAGGGAAUUAUAGGACGAGGCAGUCACUAAGCUGACGGG	89	21,34831	21,34831	14,60674	20,22472	35,95506	41,57303	0,947368	1,461538	-23,7	-20,9	0,049028	10,23	-26,6292	-0,74062
pmc-mir-8462	aaacugucaagcAUCUUUCUUUUGGAAACAAGUAAAUCAUAUGCCACCUGUCAGUGACAUUAUGAUUAAUUUGAUAAGAUGAAAUGGUCUUCAACAGCAG	100	15	30	14	29	29	59	0,966667	1,071429	-19,5	-18	0,088648	10,6	-19,5	-0,67241
pmc-mir-8470	AAAUUAAAACUAUAUAUUGUGAUGCAAUAGCUAGGAUGGCAAAAUUUUGUGCCUGAAAGCUGAGCAUAAGAAUAUGUucuuuaacau	87	18,3908	34,48276	9,195402	26,43678	27,58621	60,91954	0,766667	2	-19,4	-18,4	0,195062	6,64	-22,2989	-0,80833
pmc-mir-84f	uuguauugucaUGUUUCACAAGAGAUGAGGUAGUUUUAAAUGAAGCUUGAUAUUUAAAGCACCAUCUGGUGCUGAAAAUGGAUAGAUAGUU	91	20,87912	29,67033	8,791209	28,57143	29,67033	58,24176	0,962963	2,375	-21,2	-20,2	0,110814	22,46	-23,2967	-0,78519
pmc-mir-85	AGGUGACAAGGGAUCUGGGUGUCAGUGGGUGGGUGACCUCAGGACCUCAUCAAGUCCCGGGUACAAAGUAUUUGAAACCACAGAGUCGCUAGUGCAAGA	99	32,32323	27,27273	20,20202	20,20202	52,52525	47,47475	0,740741	1,6	-26,6	-24,3	0,014883	18,45	-26,8687	-0,51154
pmc-mir-8834a	UUGCUGCCGGGCCUGGAGGCCAGCUGUACCACACAUCUGCUGCCCCUCCACACCUGCGGCAGGUG	65	29,23077	13,84615	38,46154	18,46154	67,69231	32,30769	1,333333	0,76	-28,3	-28,3	0,089597	7	-43,5385	-0,64318

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-888	UCAAAGGACUGACACCUCUUUGUCCAGCUCAUGACAGGCUGCACAGAUGAGCCGGACAAGUGUUGUUAGUGGCUUCAU	78	25,64103	24,35897	24,35897	25,64103	50	50	1,052632	1,052632	-25,5	-24,5	0,08259	6,42	-32,6923	-0,65385
pmc-mir-8993	aucgCAGAACGUGACCUCUAUUacagggucaagggucaaaCAUGGUUAUGUCCGCCAUCUUGCUGGUGACCCUGUGGAGAAUUUACGugaucugcuuu	98	16,32653	13,26531	16,32653	20,40816	32,65306	33,67347	1,538462	1	-39,4	-39,4	0,233529	5,01	-40,2041	-1,23125
pmc-mir-9-1	UUUGGCGUCCAUUUUUGCCUUUGGUAACCUAGCUUUAUGAUAUUUCUGCCCCAAUCAUACAGCUAGAUAACCAAAGACAAAACCGGAGCCGCC	93	17,2043	26,88172	26,88172	29,03226	44,08602	55,91398	1,08	0,64	-34,1	-34	0,28369	3,42	-36,6667	-0,83171
pmc-mir-9120	CACUUACAUUCAUAUAUACACUCUUGUUcagucucccucucucacacacacaagcagcagCAAAGAGGUUGUAACACGAGAGAAGAUGAGAAAGUAAGGA	100	14	27	10	17	24	44	0,62963	1,4	-19,1	-18,3	0,095566	17,68	-19,1	-0,79583
pmc-mir-9170	AUAGCUCUUAAGAGCCUGAAUAGCCGGCGAGUCACCAGAGUCAAGUGUUGAAGGUGAUGUUUGCAUCCUGGCUCUGCUAUCUACAGUAUUAAGUGCUAU	99	25,25253	25,25253	20,20202	29,29293	45,45455	54,54545	1,16	1,25	-25,6	-23,2	0,013327	17,12	-25,8586	-0,56889
pmc-mir-9-2	GGCGGCUCCGGUUUUGUCUUUGGUUAUCUAGCUGUAUGAUUGGGGCAGAAAUAUCAUAAAGCUAGGUUACCAAAGGCAAAAAUGGACGCCAAA	93	26,88172	29,03226	17,2043	26,88172	44,08602	55,91398	0,925926	1,5625	-45,5	-45,5	0,314517	3,87	-48,9247	-1,10976

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-9256b	GGGGUGGGCGGCUACCCGCGGUGAGGUCUCACGAGGUGUAAUAAUCAGGCCACUACCUCUUACCGAGACCUCACAGGGGGCCGCUUCACAUU	92	31,52174	19,56522	29,34783	19,56522	60,86957	39,13043	1	1,074074	-43,8	-42,6	0,14803	4,74	-47,6087	-0,78214
pmc-mir-92a-1	CUGGCAUUAGCAGUAGGUCUUGAUGGGUGCAAUUCUGAUGAAUUAAAUAACAGAUUGCACUUGUCCCGGCCUUCUGCCAAUAGCUAA	87	22,98851	26,43678	20,68966	29,88506	43,67816	56,32184	1,130435	1,111111	-35,5	-35,5	0,154162	3,54	-40,8046	-0,93421
pmc-mir-92a-2	AUUUGUGUGCUCAGGAAAGGUUGUGACUUGGGCAAUUCUGUGAUGUCCUGUCAGAUUGCACUUGUCCCGGCCUUGUCUUGGCUUAcacuu	90	26,66667	14,44444	18,88889	34,44444	45,55556	48,88889	2,384615	1,411765	-31,5	-29,1	0,036643	11,93	-35	-0,76829
pmc-mir-92b	AGCGAUCAGAGUUGUGUAGACCGGAACAGGGGCAAUGCAUUUGAGUCGUCUGUAUUGCACUCGUCCCGGCCUAUCCAAUCUGACUCAUA	89	25,8427	23,59551	24,7191	25,8427	50,5618	49,4382	1,095238	1,045455	-32,6	-32,6	0,172648	4,96	-36,6292	-0,72444
pmc-mir-92c	AUUAUGUGUUAUUGUAAAAGGUUGGGAUGUGGGCUCUGUCGCGCAAUAGAUAACUUUCUUUGACAAGCAUUCGCCCACACCUUAUUACAACACAAUCAC	99	19,19192	28,28283	21,21212	31,31313	40,40404	59,59596	1,107143	0,904762	-26,6	-26,6	0,055246	15,72	-26,8687	-0,665
pmc-mir-9341	ACCUGAUUGUUAGUUAAAAGGGCCGAGGAUAGUCAGGCAUAUCGACAAGCUGUAGUAUCGCUUCUCGGCCUUUUGGCUAAGAUCAAAG	88	26,13636	27,27273	19,31818	27,27273	45,45455	54,54545	1	1,352941	-31,1	-21,81	0,019761	18,12	-35,3409	-0,7775

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-9369	CCAACAGGCCUGACCAGAAUACAUAUUCUUCUUUCCAUUUCCUUACAGUGUUGCUGAUUGUUUGAUAAGAUUUGUCAGUCUUAGUGCCUGUCAU	94	17,02128	22,34043	22,34043	38,29787	39,3617	60,6383	1,714286	0,761905	-18,9	-18,8	0,083295	15,62	-20,1064	-0,51081
pmc-mir-9382	GAUGUUGACCAUCGGAAUAUCACAGUGUGGCUGAAAUAUGCUGAGAUGGAAAUGAAGUAaguauuaauaaauuuucugugaUAUUCAUGCUAAACCAA	98	18,36735	27,55102	11,22449	20,40816	29,59184	47,95918	0,740741	1,636364	-19,3	-15,05	0,237583	13,37	-19,6939	-0,66552
pmc-mir-9434	UAGUCAGUGAGCAGACUUUCUGUCGUUGGUUAUGUAACGGCUCGCAGCUCUGACAGGAAUUCUGAACCCUGAUGU	75	26,66667	21,33333	21,33333	30,66667	48	52	1,4375	1,25	-23	-19,2	0,186112	9,2	-30,6667	-0,63889
pmc-mir-9505	UCUUGAAGUUAGGUUUAUGAUGUCUGUCAAAAUGUGAUCUCUCACGAAGGCAGACACCGUGACCCUUUCUUCAUGC	76	21,05263	23,68421	22,36842	32,89474	43,42105	56,57895	1,388889	0,941176	-29,4	-29,4	0,503167	1,22	-38,6842	-0,89091
pmc-mir-9542a	CACCGACUGACAGAACGCCUCACGACAUGGCCUGGCACUUUCUAAUUUCUGGCCAAGUUAGGCGCCUGUUUGUCGAGG	78	25,64103	20,51282	29,48718	24,35897	55,12821	44,87179	1,1875	0,869565	-29,2	-29,2	0,234782	2,71	-37,4359	-0,67907
pmc-mir-9543a	GAGAAACUAGCAAGUUCAUUAUAUGUCAGUAUGCAGAUUGCAAUGGUUUACUUUCCAUUGCACUGCACUGGAGUAAAUAUugcuuguuuauu	92	17,3913	27,17391	14,13043	28,26087	31,52174	55,43478	1,04	1,230769	-28	-26,4	0,033319	14,41	-30,4348	-0,96552

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-96	UACAUaguauuuauuuacaaucaugUGCAGUGCAGUUCUUUAUAUAACUAAUCAUACUGCAAAAAGUACAUGACUGCAAUAUGCAAAAAACAUAUCAC	98	9,183673	32,65306	15,30612	22,44898	24,4898	55,10204	0,6875	0,6	-19,5	-19,1	0,124316	9,09	-19,898	-0,8125
pmc-mir-969	AAGAAGCGCGAAUCUUCUUCUCCUGGaucaggaaaauaaauuauuuaagaGUUCCACUAAGCAAGUUAUCUUGCAGGAGCUAGAAAAUCGCCCUUAGA	98	16,32653	21,42857	18,36735	19,38776	34,69388	40,81633	0,904762	0,888889	-22,7	-22,7	0,05101	17,67	-23,1633	-0,66765
pmc-mir-96b	GCUGGCUGUUCAAUUAUUUGGCACUUGUGGAAUAAUCGGUGUAUCUAAAAGUCGAUUAUACACCGGUGCCAAGUCAUCAGAAAUGCCUGA	90	23,33333	27,77778	18,88889	30	42,22222	57,77778	1,08	1,235294	-30,3	-30,3	0,149015	2,78	-33,6667	-0,79737
pmc-mir-970	AAGAGAAGCCUUGCAUGAGCUCUAGGUgucuccagauguuuguacagaguauucaGCAGGAACAGCUUGGAUCAUCUACACCUCUCCCAGCUCUAUA	97	15,46392	19,58763	19,58763	16,49485	35,05155	36,08247	0,842105	0,789474	-20,4	-15,2	0,030264	26,39	-21,0309	-0,6
pmc-mir-971	UGCUGAUGAAAGUGAAAUGAUCUCGAUGGUGUUCUAGCCUCCAUCGACAUAGAAAAAACACCAUCAUGCAGAUACAUGCCUUUAUCAUGU	90	18,88889	32,22222	21,11111	27,77778	40	60	0,862069	0,894737	-21,2	-20,1	0,039445	9,59	-23,5556	-0,58889
pmc-mir-981	GCUAUCAGACUUUGUUCCGGGUUUCGCGGCUUGCGAACAGUCAUUUUGAGCUGUGUUCGUUGUCGUCGAAACCUGCCCUGAAAUCUGAUGUG	92	27,17391	16,30435	22,82609	33,69565	50	50	2,066667	1,190476	-35,2	-30,7	0,023194	9,17	-38,2609	-0,76522

Pre-miRNA	Sequence	Length (AA)	G (%)	A (%)	C (%)	U (%)	GC (%)	AU (%)	R-AU	R-GC	MFE (kcal/mol)	MFEE(kcal/mol)	Freq	Div	AMFE (kcal/mol)	MFEI (kcal/mol)
pmc-mir-9851	AUGACAACAGCAGCUCAACUGUUACUGUGGAUGGCACCAGCACUGGCACUGCCAUGGAUCAGAGCAGUGAUGUCAGUUGUUUU	83	26,50602	25,3012	22,89157	25,3012	49,39759	50,60241	1	1,157895	-26,3	-24,6	0,066358	12,72	-31,6867	-0,64146

Supplementary Table 5: – Structural characterization of miRNAs in Apullariidae species, lny - *L. nyassanus*, mcr - *M. cornuarietis*, pcn - *P. canaliculata*, pmc - *P. maculata*.

Mature miRNA	Mature miRNA sequence	miRNA length	Mature miRNA	Mature miRNA sequence	miRNA length	Mature miRNA	Mature miRNA sequence	miRNA length	Mature miRNA	Mature miRNA sequence	miRNA length
pmc-bantam-3p	UGAGAUCAUUGUAAAAACCAAUU	23	pcn-bantam-3p	UGAGAUCAUUGUAAAAACCAAUU	23	mcr-bantam-3p	UGAGAUCAUUGUAAAAACCAAUU	23	lny-bantam-3p	UGAGAUCAUUGUAAAAACCAAUU	23
pmc-bantam-5p	CUGGUUUUCACAGUGAUCCAGCAG	24	pcn-bantam-5p	CUGGUUUUCACAGUGAUCCAGCAG	24	mcr-bantam-5p	CUGGUUUUCACAGUGAUCCAGCAG	24	lny-bantam-5p	CUGGUUUUCACAGUGAUCCAGCAG	24
pmc-miR-1000-5p	CUGGUGUGAUGGGACAAGACUU	22	pcn-let-7b-3p	UGAGGUAGUGGUUGUAUCGUAU	22	mcr-miR-1002-3p	CUAAGUAGUUGAUACAUGAGUUG	23	lny-miR-10349-5p	UGAGCACCAAUAAGCAGCAAUAAG	24
pmc-miR-10031c-5p	CUCGUCCAUGUCUUCCUCUUCG	22	pcn-let-7d-3p	CUAUACAACCUGCUGCGGCAGG	22	mcr-miR-10080-5p	UUUCUCAGGUUGUCUCAAUC	20	lny-miR-10365-5p	AUUAGAAUGUGGAAUCUAUGCUU	23
pmc-miR-10046-3p	ACUUGUCGCAGUGACGACA	19	pcn-let-7f-5p	CUGCACAUUCCACCAUCCAUU	21	mcr-miR-10089-3p	UAAUUUGCUGUUUUGGGAUGCU	22	lny-miR-106a-5p	UACUGCAAUGCAAGCACAUUGA	22
pmc-miR-10055-3p	GUGGGAGGGAGGGAGGACUUU	21	pcn-miR-1002-3p	CUAAGUAGUUGAUACAAACAGUA	23	mcr-miR-10141-3p	AGAAGAAACACGCAUUCGGUCU	22	lny-miR-10790-3p	UUUAUUUCUCUCUCUGUUCGUC	22
pmc-miR-10089-5p	UAAUUUGCUGUUUUGGUGAUAU	22	pcn-miR-10a-5p	ACCCUGUAGAUCCGAAUUUGUGUA	24	mcr-miR-10228-3p	UGAGUAUUGUACCAUGUCAGCA	22	lny-miR-10a-5p	UACCCUGUAGAUCCGAAUUUGUGU	24
pmc-miR-10173-3p	AGGAAGUGAGGAAGGAAAACAA	22	pcn-miR-11-3p	CAUCACAGUCAGAGUUCACUGA	22	mcr-miR-10237-3p	AGCAGGGACUGGUUUGUGGCAC	22	lny-miR-10b-5p	UUACCCUGGAGAACCGAGCGUGUG	24
pmc-miR-10249-1-3p	GUGGUGGCGGUGGUGUUGCCAG	22	pcn-miR-1175-3p	UGAGAUUCAACUCCUCCAACUGC	23	mcr-miR-10325-5p	UAUCAUCGUCUUCUAUACAAGUGG	24	lny-miR-11225-3p	AAAACUGUUCUUAAGUCAUGGC	22
pmc-miR-10249-2-3p	GUGGUGGCGGUGGUGUUGCCAG	22	pcn-miR-1175-5p	AGUGGAGAGAGUUUUAUCUCAUC	23	mcr-miR-10379-3p	ACUGUUUUGUUCGUUGAACUAU	22	lny-miR-11-3p	CAUCACAGGCAGAGUUCCAGA	21
pmc-miR-10256-3p	CAUGUCUGCUAUGGCCUUCC	20	pcn-miR-1187-3p	UAUGUGUGUGUGUAUGUGUGUG	22	mcr-miR-10456-3p	GAUGCAGGAUAUUUAUGACA	20	lny-miR-11-5p	CAUCACAGGCAGAGUUCCAGAC	22
pmc-miR-10267-3p	CAGAUCAAACCACCGCCCCC	20	pcn-miR-122b-5p	AGUGUGACACUGGUGUGACA	20	mcr-miR-10457-3p	UUUGUUUGUUGUGUGUCUAC	20	lny-miR-1175-3p	UGAGAUUCAACUCCUCCAACUGC	23

pmc-miR-10492c-3p	GUUUAGCUCUCUGAUUUAUG	20	pcn-miR-1238-5p	CUUCCUCGUCUGUCUGAAGC	20	mcr-miR-10698-5p	UCAUGCAUGGCUUCUUUAGUA	21	lny-miR-1175-5p	AGUGGAGAGAGUUUUAUCUCAUC	23
pmc-miR-10508b-3p	AACAGCAUUUCGUGACUUCUU	21	pcn-miR-12-3p	AGUACCUUUUGUGAUAUUCUUA	22	mcr-miR-106b-3p	GACCGCACUGUGGGUACCCCUG	22	lny-miR-11976-5p	GGCGGCGGCGGCGCCGGCGUG	21
pmc-miR-10509-5p	UGUGUCACGUACAGUAACACUGA	23	pcn-miR-124-3p	UUAAGGCACGCGGUGAAUGCCAA	23	mcr-miR-10717-5p	CACGGAUGCACACACACCUGCG	22	lny-miR-12096b-3p	UAGGGCAAAAUUAUCACCGAUUAC	24
pmc-miR-10578-5p	AGCAGUGAGUCAGUCUCACGCU	22	pcn-miR-124-5p	GUGUUCACUGCGUUGGCCUUGGU	23	mcr-miR-10738-3p	CGGGUGCUGCUGUCUGCUUUG	21	lny-miR-12096b-5p	AAGCGGUGAUACUUUUGUCUCGCA	24
pmc-miR-10611-3p	UUUCCCUUUUUCACACAGUGGG	22	pcn-miR-124c-5p	CAUUCACCGCGUGCCUUAAUA	21	mcr-miR-10761-3p	UUGAAUUUGUUCUUGUCACCAU	22	lny-miR-12-3p	AGUACCUUUUGUGAUAUUCUUA	22
pmc-miR-10639-3p	UUGCCAUGAUAGCUUUGG	18	pcn-miR-12-5p	UGAGUAUUACAUCAGGUACUGA	22	mcr-miR-10863-3p	UGACUUCUUUGUGGGCACGAUG	22	lny-miR-124-3p	UUAAGGCACGCGGUGAAUGCCAA	23
pmc-miR-10770-1-3p	UUGUUGAUGUUGUUGUUGUUGU	22	pcn-miR-1277-1-3p	UAUAUAUAUAUAUGUACGUCUA	22	mcr-miR-10903-1-3p	GACUCGCUUGUGUCGGCCUC	20	lny-miR-124-5p	GUGUUCACUGCGUUGGCCUUGGU	23
pmc-miR-10770-2-5p	UUGUUGAUGCUGUUGUUGUUUC	22	pcn-miR-1277-2-3p	AAAUAUAUAUAUAUAUGUAUGAU	23	mcr-miR-10903-2-3p	GACUCGCUUGUGUCGGCCUC	20	lny-miR-124c-5p	CAUUCACCGCGUGCCUUAAUA	21
pmc-miR-10892-3p	UGAAUAAUGGAUGAAUAACAUC	22	pcn-miR-1322-5p	GAUGAUGCUGCUGAUGACA	19	mcr-miR-10903-3-3p	GACUCGCUUGUGUCGGCCUC	20	lny-miR-12-5p	UGAGUAUUACAUCAGGUACUGA	22
pmc-miR-10972-3p	UUUGCUAUGGUCAUCAUAUAUG	22	pcn-miR-1328-5p	GAGAGAGAAAUGAGAAAC	18	mcr-miR-10918-3p	CAUAUAAGCUAUGUUACUCGAU	22	lny-miR-1307-5p	ACUCGGCGUGGCGUCGGUGCAAA	23
pmc-miR-10b-1-3p	CAUCUCGGUACUCGGGAGGUCA	22	pcn-miR-133-3p	UUUGGUCCCCUUCAACCAGCUGUA	24	mcr-miR-10967-3p	UGAACUGUGAACUGCAUACUG	21	lny-miR-133-3p	UUUGGUCCCCUUCAACCAGCUGUA	24
pmc-miR-10b-2-5p	UUACCCUGGAGAACCGAGCGUGUG	24	pcn-miR-133-5p	AGCUGGUUGAACUCGGGCCAAAU	23	mcr-miR-10a-5p	ACCCUGUAGAUCCGAAUUUGUGUA	24	lny-miR-133-5p	AGCUGGUUGAACUCGGGCCAAAU	23
pmc-miR-11054-5p	AGUGUUUGUUGCCAGAGAUUUA	22	pcn-miR-133c-5p	CAGCUGGUUGAAGGGGACCAA	21	mcr-miR-10b-5p	UUACCCUGGAGAACCGAGCGUGUG	24	lny-miR-133c-5p	CAGCUGGUUGAAGGGGACCAA	21
pmc-miR-11280-3p	AUGAGAGAAGAUCCGUGUGUGA	22	pcn-miR-137b-3p	UUAUUGCUUGAGAAUACACGUAA	23	mcr-miR-11-3p	GGAGCUCUGGCUGUGCCGGGUG	22	lny-miR-137b-3p	UUAUUGCUUGAGAAUACACGUAA	23
pmc-miR-1175-1-3p	UGAGAUUCAACUCCUCCAACUGC	23	pcn-miR-137b-5p	ACGGGUAUUCUUGGGUAAAUAAUA	24	mcr-miR-11591-3p	GGCUGUGCUGUAAGUGUACUUU	22	lny-miR-137b-5p	ACGGGUAUUCUUGGGUAAAUAAUA	24
pmc-miR-1175-1-5p	AGUGGAGAGAGUUUUAUCUCAUC	23	pcn-miR-13b-3p	UCGUUAAAAUGUUUGUG	17	mcr-miR-1175-3p	UGAGAUUCAACUCCUCCAACUGC	23	lny-miR-153-3p	UUGCAUAGUCACAAAAGUGAUCG	23
pmc-miR-1175-2-5p	AAGUGAAGAGAAGAAUGAAGAA	22	pcn-miR-1-3p	CAUGCUUCUUUAUAGUUUGACC	22	mcr-miR-1175-5p	AGUGGAGAGAGUUUUAUCUCAUC	23	lny-miR-1662-3p	UUGACAUCAUCAUACUUUAUGU	22
pmc-miR-1187-3p	UAUGUGUGUGUGUAUGUGUGUAU	23	pcn-miR-1421a-3p	CUGCAUCCCUUGUGACGGUGGC	22	mcr-miR-12037-5p	CAUUCUGUCUUCUCUUCCAA	20	lny-miR-1731-5p	ACUUGACUGCAGGCACUACAGAU	23
pmc-miR-11922-3p	UUCAGGAGAUCAUCGAUAUGUU	22	pcn-miR-1421am-3p	AGGAGGUCGUAGGUCAUCCUGU	22	mcr-miR-12093-3p	UCAGCCCCUGGGGUAGCCUUAC	22	lny-miR-184-3p	ACUGGACGGAGAACUGAUAAGGGC	24
pmc-miR-12096b-3p	UAGGGCAAAAUUAUCACCGAUUAC	24	pcn-miR-143-3p	GUCUGAGAUGAAGCACUCGUUUG	23	mcr-miR-12096b-3p	UAGGGCAAAAUUAUCACCGAUUAC	24	lny-miR-184-5p	CCUUAUCACUCCCCCGCCCCGU	22
pmc-miR-12096b-5p	AAGCGGUGAUACUUUUGUCUCGCA	24	pcn-miR-153-1-3p	UCAUUUUUGUGAUGUUAUCAAUA	23	mcr-miR-12096b-5p	AAGCGGUGAUACUUUUGUCUCGCA	24	lny-miR-184b-5p	CCUUAUCAGUUCUCCGUCCAGU	22
pmc-miR-12228-5p	UCCCCACUGCUCCCCCAACA	20	pcn-miR-153-2-3p	UUGCAUAGUCACAAAAGUGAUCG	23	mcr-miR-12193-3p	ACCGGUCCUUUCUGUCUAAUG	21	lny-miR-190-5p	AGAUAUGUUUGAUAUAUUUGGUG	23

pmc-miR-12245-5p	CCCCGCCCCGCCCGGCUCAAGG	22	pcn-miR-1584-5p	CCGGGUGGGGCUGGGCCAUA	20	mcr-miR-12265-5p	UCAGCCGUCUUGCAGCUGAAG	21	lny-miR-1947-3p	GCACUGAGCUAGCUCUCUAGCA	22
pmc-miR-1224-5p	UCACCUCCUCUCUCCUCCCUU	21	pcn-miR-15c-3p	CAGACCAUUCUGGGCUAUGGGG	22	mcr-miR-12293-5p	CGCCUCUUGAUCUACUACAACUA	23	lny-miR-1985-5p	UGCCAUUUUUAUCAGUCACUGUGU	24
pmc-miR-12286-3p	UGGGGCUGCAGGGCUGAGUAAGC	23	pcn-miR-1602-5p	UGGGCUCUGCAUCACCAGCAGU	22	mcr-miR-12313-5p	ACAUGUUAGCAUCUUGACAUAA	22	lny-miR-1990-3p	CGGGACUACGUCAACGUACUA	21
pmc-miR-12287-5p	UGGGGGUGCAGGUGGGCACAC	21	pcn-miR-1603-3p	GUGGUUUGUUUUGUGUUGCG	20	mcr-miR-12322-3p	UCUGGUCAUUUCUCUUUCUCAC	22	lny-miR-1990-5p	AGUAAGUUGAUGGGGUCCCAGG	22
pmc-miR-12292-5p	AUGGGGUCUUGGGGUCAUG	19	pcn-miR-1632-3p	UGCUUGUUUUUGGAUGAAAUUAU	23	mcr-miR-12352-5p	UAUUGCUGUUAUGGUGUUAGUU	22	lny-miR-1993-3p	UAUUAUGCUGCUAUUCACGAGA	22
pmc-miR-12293-5p	CGCCUCUUGAUCUACUAUAACUA	23	pcn-miR-1677-3p	UUGACUUCAAUAGGAGAGACAGG	23	mcr-miR-12-3p	UGAGUAUUACAUCAGGUACUGA	22	lny-miR-1993-5p	UCGGGAAUAUCGGCAUAAUGCA	22
pmc-miR-12296-3p	GGGCAGGGGCAGGGGGCA	18	pcn-miR-1744-1-5p	ACUUCAACAGGAGCAAGUCAAG	22	mcr-miR-1250-5p	ACGGUGCUGGAUGUGGAUAU	20	lny-miR-1994-3p	UGAGACAGUGUGUCCUCCCUCU	22
pmc-miR-12321-5p	GCCCUGCCCUCCCUUCCCCUCUC	23	pcn-miR-1744-2-5p	ACUUCAACAGGAGCAAAGUGUA	22	mcr-miR-1256-5p	AGGCAUUGACUUCUCUUCAUGG	22	lny-miR-1a-3p	UGGAAUGUAAAGAAGUAUGUAC	22
pmc-miR-12327-5p	UUUCUCUCUUUCCCUCUCUCU	21	pcn-miR-184-3p	ACUGGACGGAGAACUGAUAAGGGC	24	mcr-miR-1277-3p	UAUAUAUAUAUAUGUACGAUGC	22	lny-miR-1a-5p	ACAUACUUCUUUGCUAUCCCAUAU	24
pmc-miR-12339-3p	AGAUUGUUCUGGAUUGCCACUG	22	pcn-miR-184-5p	CCUUGUCACUCCUCCGCCCCGU	22	mcr-miR-1278-3p	UAGUACUGUGCAUAUCAGCAC	21	lny-miR-1c-5p	GUACAUACUUCUUUACAUUCCA	22
pmc-miR-12358-3p	AUCUAUGAUUUCAUCGGGUAAG	22	pcn-miR-1905c-3p	CACCACCAGCCCCACCACGCGGUAU	25	mcr-miR-1304-3p	UCUCACUGUAGCCUCGGCUCAG	22	lny-miR-2001-5p	UUGUGACCGUUACAAUGGGCAUU	23
pmc-miR-12396-5p	AGAGAGACACAGACAAGAAAGAU	23	pcn-miR-190-5p	AGAUAUGUUUGAUAUAUUUGGUG	23	mcr-miR-130a-3p	UAGUGCAAUGUUAAAAGAGUAC	22	lny-miR-2049-3p	GAUUCAUGUGCAUGCAUUCAUG	22
pmc-miR-12-3p	AGUACCUUUUGUGAUAUUCUUA	22	pcn-miR-1951-3p	GUAGUGGAGACUGGUGGCGAAA	22	mcr-miR-133-3p	UUUGGUCCCCUUCAACCAGCUGUA	24	lny-miR-2064-3p	AAGCAGCACUGUGCAACUGCAA	22
pmc-miR-12410-3p	AAGGAAACUGAGAUCCGGUCAC	22	pcn-miR-1976-5p	CUCCUGCCCUCCUUGCCCAGA	21	mcr-miR-133-5p	AGCUGGUUGAACUCGGGCCAAAU	23	lny-miR-216a-3p	CAAGUUACUCGCCGAGAUUACA	22
pmc-miR-124-5p	CGCUUUCAUCCGUGACGACACC	22	pcn-miR-1984-5p	UGCCCUAUCCGUCAGGAACUGUG	23	mcr-miR-133c-5p	CAGCUGGUUGAAGGGGACCAA	21	lny-miR-216a-5p	UAAUCUCAGCUGGUAAUUCUGAG	23
pmc-miR-12-5p	UGAGUAUUACAUCAGGUACUGA	22	pcn-miR-1985-5p	UGCCAUUUUUAUCAGUCACUGUGU	24	mcr-miR-137b-3p	UUAUUGCUUGAGAAUACACGUAA	23	lny-miR-228-5p	AAUGGCACUGCAUGAAUAAAAAA	23
pmc-miR-1273h-3p	CUGCAGACUCGACCUCAGGAU	21	pcn-miR-1986-3p	UGGAUUUCCCAAGAUCCGUGAU	22	mcr-miR-137b-5p	ACGGGUAUUCUUGGGUAAAUAAUA	24	lny-miR-2361-5p	GUUGUGUUGUUUUUUUUUCA	20
pmc-miR-1277-3p	UAUAUAUAUAUAUGUACUCUAC	22	pcn-miR-1990-3p	CGGGACUACGUCAACGUACUA	21	mcr-miR-1421ai-5p	AGCAGGUCAGGUGUGGAAGCAC	22	lny-miR-239b-3p	GCACUUUUGUGGUGUGCAGGUU	22
pmc-miR-130b-3p	CAGUGCAAUAAUGAAAGUAUUUU	23	pcn-miR-1990-5p	AGUAAGUUGAUGGGGUCCCAGG	22	mcr-miR-143-3p	UGUGCAGUGCUGCAUCUCACA	21	lny-miR-2491-3p	CAACAACAGCAGCAGCAG	18
pmc-miR-1322-5p	GAUGCUGCUGCUGAUGGC	18	pcn-miR-1992-3p	UCAGCAGUUGUACCACUGAUUUG	23	mcr-miR-14-3p	UCAGUCUUUUUCUCUCUCUUUU	22	lny-miR-2493-3p	GCUCACACACACACACAGACG	21
pmc-miR-133c-5p	CAGCUGGUUGAAGGGGACCAA	21	pcn-miR-1992-5p	AGUCAGUGGUUGACUGCUCGGU	22	mcr-miR-146b-3p	UGAGAACUGGUUUUGAGCAAGU	22	lny-miR-252a-5p	CUAAGUACUAGUGCCGCGGGAG	22
pmc-miR-1376-3p	GCUCAGCAGCACUCUUUGAGC	21	pcn-miR-1994-3p	UGAGACAGUGUGUCCUCCCUCU	22	mcr-miR-153-1-3p	GUCAUUUUUGUGAUUUUGAGCU	22	lny-miR-252b-1-3p	CCCUGCGCAGUCCUACUGGG	20

pmc-miR-137b-3p	UUAUUGCUUGAGAAUACACGUAA	23	pcn-miR-1994a-3p	UGAGACAGUGUGUCCUCCCUUG	22	mcr-miR-153-2-3p	UUGCAUAGUCACAAAAGUGAUCG	23	lny-miR-252b-2-5p	AUAAGUAGUGGUGCCGCAGGUA	22
pmc-miR-137b-5p	ACGGGUAUUCUUGGGUAAAUAAUA	24	pcn-miR-1996b-3p	AUCAAGUGAGGUCAGAAUA	19	mcr-miR-1599-5p	GGAGGGAGGAAAAAAAACG	20	lny-miR-2580-3p	CGUGUCUGUGUGUAUGUUUCUA	22
pmc-miR-13b-3p	UCGUUAAAAUGUUUGUG	17	pcn-miR-1a-3p	UGGAAUGUAAAGAAGUAUGUAC	22	mcr-miR-15a-5p	UAGCAGCACAGAAUGGCAAAA	21	lny-miR-263a-1-5p	CUUAAUGGCACUGGUAGAAUAGCA	24
pmc-miR-1-3p	CAUGCUUCUUUAUAGUUUGACC	22	pcn-miR-1a-5p	ACAUACUUCUUUGCUAUCCCAUAU	24	mcr-miR-1610-5p	UGGCUUGUGGUGGAACGACAA	21	lny-miR-263a-2-5p	AAUGGCACUGGUAGAAUUCACGG	23
pmc-miR-1421am-3p	AGGAGGUCGUAGGUCAUCCUGU	22	pcn-miR-1c-5p	GUACAUACUUCUUUACAUUCCA	22	mcr-miR-1621-3p	ACCGGCUGCCUCGGUGGUAA	20	lny-miR-277a-3p	GAGCCAUUUCUUUGUGUGCU	20
pmc-miR-1422j-3p	AAAACUGCAUCUGGAUUAUGA	21	pcn-miR-2001-5p	UUGUGACCGUUACAAUGGGCAUU	23	mcr-miR-1628-3p	AAGAGCUCUUCCUGUUCGUGUG	22	lny-miR-279-3p	UGACUAGAUCCACACUCAUCCA	22
pmc-miR-143-3p	GUCUGAGAUGAAGCACUCGUUUGC	24	pcn-miR-2008-3p	GUAUUAACAAUGUGGCUACAGU	22	mcr-miR-1693-3p	GCAAAGGAUGAAGCUGUAGCU	21	lny-miR-281-3p	UGUCAUGGAGUUGCUCUCUUUA	22
pmc-miR-149-3p	GAGGGAGGGACGGGGGAUUCAAG	23	pcn-miR-203b-3p	UUGAACUGUUAAGAACAGUAAA	22	mcr-miR-1710-5p	UCAUCUGCUGCAUAACCGUGUG	22	lny-miR-281-5p	AAGGGAGCAUCCGUCGACAGU	21
pmc-miR-150-3p	CUGGUACAGGCCUGGGGGAGA	21	pcn-miR-204-3p	UGCAAGGACAGCAAAGGGA	19	mcr-miR-1761-3p	CAGGGGUCACUUUUUUCCCC	20	lny-miR-2944a-3p	GAAGGAACUUCUGCUGAUC	19
pmc-miR-153-3p	UUGCAUAGUCACAAAAGUGAUCG	23	pcn-miR-2047-3p	UUCGCCGAGCAGAUGUGUGAAG	22	mcr-miR-187-5p	GCUACAACACAGGACAAUUCUA	22	lny-miR-2987-3p	AGAGCAAGGCUGAGGCUU	18
pmc-miR-1551-3p	UGAGUUUGUGUUGCUGGGACAA	22	pcn-miR-2155-3p	GACACUGUUUUACACUCUACUGG	23	mcr-miR-190-5p	AGAUAUGUUUGAUAUAUUUGGUG	23	lny-miR-29a-3p	UAGCACCAUUUGAAAUCAGUUU	22
pmc-miR-15c-3p	CAGACCAUUCUGGGCUAUGGGG	22	pcn-miR-216a-3p	CAAGUUACUAGCCGAGAUUACA	22	mcr-miR-193-1-3p	UACUGGCCAGCACAAUUAGUGU	22	lny-miR-29b-1-3p	UAGCACCAUUUGAAAUCAGUGCU	23
pmc-miR-1603-1-3p	GUGGUUUGUUUUGUGUUGCG	20	pcn-miR-216a-5p	UAAUCUCAGCUGGUAAUUCUGAG	23	mcr-miR-193-2-3p	UACUGGCCAGCACAAUUAGUGU	22	lny-miR-29b-2-3p	AGCUGGUUUCACAUGGACAGAUAAC	25
pmc-miR-1603-2-3p	UUGGUUUGGUUUGUUUUUUU	20	pcn-miR-216b-1-3p	CACAGUGGCUACUGGGUCCACA	22	mcr-miR-193-3-3p	UACUGGCCAGCACAAUUAGUGU	22	lny-miR-2a-1-3p	UAUCACAGCCUGCUUGGAUC	20
pmc-miR-1632-3p	UGCUUGUUUUUGGAUGAAAUUAU	23	pcn-miR-216b-2-3p	UAAUAUCAGCUGGUAAUCCUGAG	23	mcr-miR-194-3p	CCAGUGGAGGUGGUGUAGAAGU	22	lny-miR-2a-2-3p	AAUCACAGCCUGCUUUGGUGAGCU	24
pmc-miR-1642-3p	UGAGAGGCUGUCAGUUUUGUAAG	23	pcn-miR-219-1-3p	AGAACUGUGUGUGGACAUCAGU	22	mcr-miR-1947-5p	GCACUGAGCUAGCUCUCUGCGU	22	lny-miR-2b-1-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24
pmc-miR-1677-3p	UUGACUUCAAUAGGAGAGACAGG	23	pcn-miR-219-1-5p	UGAUUGUCCAAACGCAAUUCUUG	23	mcr-miR-194b-3p	UGUAACAGCAUCUCCAACUGCGG	23	lny-miR-2b-2-3p	UAUCACAGCCAGCUUUGAUGAGC	23
pmc-miR-1728-3p	UGGUUGAUCCAUUGGAAGAAACA	23	pcn-miR-219-2-3p	AGAACUGUGUGUGGACAUCAGU	22	mcr-miR-196c-5p	ACAACAACAUCAAACCACCUGC	22	lny-miR-2d-3p	AAUCACAGCCUGCUUUGGUGAG	22
pmc-miR-17-3p	ACUGCACUGCAAGCACCGCCACA	23	pcn-miR-219-2-5p	UGAUUGUCCAAACGCAAUUCUUG	23	mcr-miR-1970-3p	UGUGUCACUGGGGAUAAUUA	20	lny-miR-306-3p	UCAGGUACUGAGUGACU	17
pmc-miR-1744-5p	ACUUCAACAGGAGCAAGUCAAG	22	pcn-miR-2196-5p	CCUCUCUGUGCUGCCAGCAAAAAU	24	mcr-miR-1984-5p	UGCCCUAUCCGUCAGGAACUGUG	23	lny-miR-3128-3p	UCUGGCAAGUAAAAAACCAUCC	22
pmc-miR-1775-5p	UCCUGUAGCCAGAAGACAGCGG	22	pcn-miR-2218b-3p	AAAUUUGUAGUUUGUAUUCUUC	22	mcr-miR-1985-5p	UGCCAUUUUUAUCAGUCACUGUGU	24	lny-miR-316-3p	UGUCUUUUUCCGCUUACAAAUG	22
pmc-miR-1781-1-5p	UUUAAAUCAUCCAGCUGCCUU	21	pcn-miR-2284c-3p	AAAAUCUAAGUGAACUGUGACG	22	mcr-miR-1990-3p	CGGGACUACGUCAACGUACUA	21	lny-miR-3238-5p	AAAUGAAUCAUGCAUUUGGCAUGUA	25

pmc-miR-1781-2-5p	UUUAAAUCAUCCAGCUGCCUU	21	pcn-miR-2284t-3p	AAACUCGAAUGAAUGUAGUUCG	22	mcr-miR-1990-5p	AGUAAGUUGAUGGGGUCCCAGG	22	lny-miR-3297-3p	GCACAUCUAGUCAAAACCAAGGUUU	25
pmc-miR-1896-3p	UGGUGGGUGAGGAGGAGG	18	pcn-miR-2324-5p	UGGGGUUGGGGCAGUGACCAGCA	23	mcr-miR-1992-3p	UCAGCAGUUGUACCACUGAUUUG	23	lny-miR-33-3p	GCAAUGCAUCUGCAGUGCAAGUA	23
pmc-miR-190-5p	AGAUAUGUUUGAUAUAUUUGGUG	23	pcn-miR-2392-3p	AUGGAUGGGGGUGAGGGGGAUG	22	mcr-miR-1994-3p	UGAGACAGUGUGUCCUCCCUCU	22	lny-miR-33-5p	GUGCAUUGAGGUUGCAUUGCAU	22
pmc-miR-1951-3p	GUAGUGGAGACUGGUGGCGAAA	22	pcn-miR-2405-3p	UGUGUGGUUUGUUUGGUU	18	mcr-miR-1994a-3p	UGAGACAGUGUGUCCUCCCUUG	22	lny-miR-3484-5p	AUACAAACAGCUAAACUAGG	20
pmc-miR-1955-5p	GAGCAUUGCAUGCUGGACGCG	21	pcn-miR-2464-3p	ACUUCUGCUGCAGACCUCAAGGAU	24	mcr-miR-1c-5p	GUACAUACUUCUUUACAUUCCA	22	lny-miR-359-3p	UCACUGGUUUUCCUCUGUUGCG	22
pmc-miR-196a-3p	ACGGCAACAAGAAACUGUGACU	22	pcn-miR-2470-3p	UUGUGUGGUUUUGGAUACUUG	21	mcr-miR-2001-3p	UUGUGACCGUUACAAUGGGCAUU	23	lny-miR-36b-3p	UCACCGGGUAUACAUUCAUCCGC	23
pmc-miR-1984-5p	UGCCCUAUCCGUCAGGAACUGUG	23	pcn-miR-2491-1-3p	CAACAACAGCAGCAGCAA	18	mcr-miR-202-5p	AGAGGCAUAGGGCAUGUGCGGG	22	lny-miR-3906-3p	AAAAGCAUUUUGAAUGCAUAAAA	23
pmc-miR-1985-5p	UGCCAUUUUUAUCAGUCACUGUGU	24	pcn-miR-2491-2-3p	CAACAACAGCAGCAGCAA	18	mcr-miR-2040b-5p	UCAGGUCAGCUACGACUGUAACA	23	lny-miR-3963-5p	UGUAUCCCACUUCUGACGC	19
pmc-miR-1990-3p	CGGGACUACGUCAACGUACUA	21	pcn-miR-2491-3-5p	CAACAACAGCAGCAGCAG	18	mcr-miR-204-3p	GCUGGGAAGGCAAAGGGAACC	21	lny-miR-4024-3p	UUUGUAGGAUGAAAAGGUU	19
pmc-miR-1990-5p	AGUAAGUUGAUGGGGUCCCAGG	22	pcn-miR-2500-3p	GGAUUUUGUGUGUGGAC	17	mcr-miR-216a-3p	CAAGUUACUAGCCGAGAUUACA	22	lny-miR-4262-3p	GACAUUCAGACUACCUG	17
pmc-miR-199-3p	ACAGUAGUCUGCACAUGCUAU	21	pcn-miR-252a-5p	CUAAGUACUAGUGCCGCGGGAA	22	mcr-miR-216a-5p	UAAUCUCAGCUGGUAAUUCUGAG	23	lny-miR-4265-5p	CUGUGGGCUCAGCUCUGCA	19
pmc-miR-1994-3p	UGAGACAGUGUGUCCUCCCUCU	22	pcn-miR-254-5p	UGCAAAUCUUUUGCAACAGACUU	23	mcr-miR-216b-1-3p	UAAUAUCAGCUGGUAAUCCUGAG	23	lny-miR-451-3p	UAGUAAUGGUAAGGGUUUG	19
pmc-miR-1994a-3p	UGAGACAGUGUGUCCUCCCUUG	22	pcn-miR-279-1-3p	UGACUAGAUCCACACUCAUCCA	22	mcr-miR-216b-2-5p	ACACUUACCUAUAGAGAUGUGU	22	lny-miR-466b-5p	AUAUACAUACACACAUACUAC	21
pmc-miR-1a-3p	UGGAAUGUAAAGAAGUAUGUAC	22	pcn-miR-279-2-3p	UGACUAGAUCCACACUCAUCCA	22	mcr-miR-216b-3-3p	ACACUUACCUAUAGAGAUGUGU	22	lny-miR-466h-5p	UACGCACGCACACACACAC	19
pmc-miR-1a-5p	ACAUACUUCUUUGCUAUCCCAUAU	24	pcn-miR-279b-5p	UGACUAGACUGAUAACCCCUAG	22	mcr-miR-2238k-3p	AAUGACUGAACAGUGCAAUGCA	22	lny-miR-466i-1-5p	UGUGUGUGUGUGUGAGUG	20
pmc-miR-1b-3p	UCAUACUUCUUUACAUU	17	pcn-miR-2804-3p	GUAGUGUAUUACAAUACUGACC	22	mcr-miR-2253a-5p	CAUGGCACUGCUGAAGGUUCA	21	lny-miR-466i-2-3p	AUACACACACACACACACACAU	22
pmc-miR-1c-5p	GUACAUACUUCUUUACAUUCCA	22	pcn-miR-281-3p	UGUCAUGGAGUUGCUCUCUUUA	22	mcr-miR-2254-3p	UUUGUACUAUGCAAAGUAAGUAC	23	lny-miR-466i-3-3p	UGUGUGUGUGUGUGUGUG	20
pmc-miR-2001-5p	UUGUGACCGUUACAAUGGGCAUU	23	pcn-miR-281-5p	AAGGGAGCAUCCGUCGACAGU	21	mcr-miR-2288-3p	AGGUAGUAGGUGUGUGUGUG	20	lny-miR-466i-4-3p	UGUGUGUGUGUGUGUGUG	20
pmc-miR-200b-5p	CAUCUUACCUGACAGUCAACAG	22	pcn-miR-2962-3p	CAUCCCCUGCCUCUCUCAUAC	21	mcr-miR-22b-3p	ACAGUUCUUCAACUGGACUGAG	22	lny-miR-466m-5p	UGUGUGCAUGUGCAUGUGUGUGU	23
pmc-miR-201-3p	UGAACAGCGCCUUUCUCACGUG	22	pcn-miR-297-3p	AUGUAUGUGUGCAUGUAUGGAGC	23	mcr-miR-2304-1-3p	GGUUGUGUGGUUGUGUGUG	19	lny-miR-466q-1-5p	GUGCACACACACACAUACAC	20
pmc-miR-2017-3p	UACCUGUGCACCUGUGCACGUG	22	pcn-miR-29a-3p	UAGCACCAUUUGAAAUCAGUUU	22	mcr-miR-2304-2-5p	GGUUGUGUGGUUGUGUGUGG	20	lny-miR-466q-2-5p	GUGCACACACACACAUACAU	20
pmc-miR-204-3p	UGCAAGGACAGCAAAGGGA	19	pcn-miR-29b-3p	UAGCACCAUUUGAAAUCAGUGCU	23	mcr-miR-2325c-5p	GGUUGUUUUUUUUCUUUUGC	20	lny-miR-4690-3p	GAGCAGGCGAGGCUGGGAGGGC	22

pmc-miR-2064-3p	AAGCAGCACUGUGCAAGAUACU	22	pcn-miR-2a-1-3p	AAUCACAGCCUGCUUUGGUGAGCU	24	mcr-miR-234-3p	AUUAUUGCUCGAGAAUGACGGC	22	lny-miR-4931-3p	UCGCUGAUUGGUUGAGCAGC	20
pmc-miR-2155-3p	GACACUGUUUUACACUCUACUGG	23	pcn-miR-2a-2-3p	UAUCACAGCCUGCUUGGAUCAGUA	24	mcr-miR-2390-3p	GUUGUGUGUUUUUGUUGAAA	20	lny-miR-4968-3p	CAGCAACAGCAGCAGCAGCAG	21
pmc-miR-216a-3p	CAAGUUACUAGCCGAGAUUACA	22	pcn-miR-2a-3-3p	UAUCACAGCCAGCUUUGAUGAGCU	24	mcr-miR-2-3p	UUCAAAAGACUGUGUUGCUAUG	22	lny-miR-5100-5p	UCGAAUCCCAGCGGUGCCCGA	21
pmc-miR-216a-5p	UAAUCUCAGCUGGUAAUUCUGAG	23	pcn-miR-2a-4-3p	UAUCACAGCCAGCUUUGAUGAGCU	24	mcr-miR-242-3p	UUGCGUAGGCACUUUGCAUGAC	22	lny-miR-51-5p	CAUGGAAGCAGGUACAGUCACC	22
pmc-miR-216b-1-3p	UAAUAUCAGCUGGUAAUCCUGAG	23	pcn-miR-2b-1-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24	mcr-miR-2434-1-5p	UUGUUGGGGUUUUUUUUGAA	20	lny-miR-5397-5p	UACGCAGAAGUUUGCUUCUGUA	22
pmc-miR-216b-2-3p	CACAGUGGCUACUGGGUCCACA	22	pcn-miR-2b-2-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24	mcr-miR-2434-2-3p	UUGUUGGGGUUUUUUUAAUC	20	lny-miR-5600-3p	AGUGGAAUGUUUUGUUUCAGUA	22
pmc-miR-216b-3-3p	CACACUUACCUGUAGACUGUUA	22	pcn-miR-2e-3p	UACCAACUUUGACUGAUGAGA	21	mcr-miR-2444-3p	UUUGUGUUGUUUUUUGUUUU	20	lny-miR-564-5p	AGGCACGGUGGCAGCAGAA	19
pmc-miR-216b-3-5p	ACAGUUACCUGUAGAUUGUGU	21	pcn-miR-2f-3p	UAUCACAGCCAUGCUAAUCUCCU	23	mcr-miR-2470-3p	UUGUGUGGUUUUGGAUACUUG	21	lny-miR-5920-3p	GUUUUGUCAUUCGUAUACAAAACA	24
pmc-miR-2223-3p	UUUGUACUCAUGUAAGUAUUU	21	pcn-miR-3027-5p	CCAGUCUUGCAUUUAUGAAACA	22	mcr-miR-247-3p	UAGAGAAAAGUUUCUACCGACA	22	lny-miR-6504-5p	CAUUACAGCACAGCCAUGUU	20
pmc-miR-2238i-3p	CCGUUCACUCAUCUCGGAGCUGA	23	pcn-miR-3050-5p	UGAGAUCUUGAUAAACAUCAAC	22	mcr-miR-2491-5p	CAACAACAGCAGCAGCAA	18	lny-miR-653-3p	UUGAGACAAUCUCUACUGCAAC	22
pmc-miR-2284c-3p	AAAAUCUAAGUGAACUGUCAAG	22	pcn-miR-3057-3p	UCCCACAGGCCCAGCUGUCACA	22	mcr-miR-250-3p	AAUCACAGUCACCUGAGUAA	20	lny-miR-6544-5p	AAGUUGUAUUUCUUUUCGCAAACG	24
pmc-miR-2298-3p	GACUGAUGUUGUUGUUCAAG	20	pcn-miR-3071-5p	AUCAUCAAAACAAAUGUGCAUA	22	mcr-miR-252-3p	ACCUGCUCCCUGCUGCUGCCUU	22	lny-miR-6632-3p	AGAGAUGAGAGGAGUGCUGAACCAU	25
pmc-miR-2304-3p	GGUUGUGUGGUUGUGUGGGC	20	pcn-miR-3084a-5p	UUGAAGGUUCAUUAGCCUUGUG	22	mcr-miR-252a-5p	CUAAGUACUAGUGCCGCGGGAA	22	lny-miR-669k-3p	UGUGCAUGUCUGUUUACUUGUGUGU	25
pmc-miR-2361-3p	UUUGUGUUGUUUUGUUUUGC	20	pcn-miR-308-5p	CGCAGGAUUUGCUUGUUUUGAG	22	mcr-miR-2582a-5p	UUCACAGUGUUCAUAAUAUUUCAG	24	lny-miR-67-3p	UCACAACCUGCAUGAAUGAGGAC	23
pmc-miR-2371-5p	UAUAGUUUUGUGUGGUGUAU	20	pcn-miR-31-3p	AGCUGUGUCGCAUGGUGCCACC	22	mcr-miR-2699-5p	GUUUGUGAUAUUCGGCAUUCUU	22	lny-miR-6756-3p	AGGGUGGGGCUGGAGGUGGGGAU	23
pmc-miR-2470-3p	UUGUGUGGUUUUGGAUACUUG	21	pcn-miR-315-5p	UUUUGAUUGUUGCUCAGAAAGCC	23	mcr-miR-277-1-3p	GUAAAUGCAUUUUCUGCUGCA	21	lny-miR-6868-5p	UUCCUUCUGUUGUCUGUAAAC	21
pmc-miR-2491-1-3p	CAACAACAGCAGCAGCAA	18	pcn-miR-31-5p	AGGCAAGAUGUUGGCAUAGCUGA	23	mcr-miR-277-2-3p	UAAAUGCAUUAUUUGGGGAGGUA	23	lny-miR-7006-5p	UGGGGGUGUUCAAGACCCCCCAGUU	25
pmc-miR-2491-2-3p	CAACAACAGCAGCAGCAA	18	pcn-miR-317-1-3p	UGAACACAGCUGGUGGUAUCUUUUU	25	mcr-miR-279-3p	UGACUAGAUCCACACUCAUCCA	22	lny-miR-7045-5p	UCUCCCCCCUCCCCCGCCCCA	21
pmc-miR-2491-3-3p	CAACAACAGCAGCAGCAA	18	pcn-miR-317-2-5p	AGUGAACACAGCUGGUCACAAC	22	mcr-miR-281-3p	UGUCAUGGAGUUGCUCUCUUUA	22	lny-miR-7062-3p	UGGAGGCCAGCUUGUGUCCAGGUU	24
pmc-miR-2493-3p	GCUCACACACACACACAGCCA	21	pcn-miR-3173-3p	GAAGGAGGAAACAGGCUACAGAU	23	mcr-miR-281-5p	AAGGGAGCAUCCGUCGACAGU	21	lny-miR-7195-5p	UAUCCUCCCCUCUCCCCCCCCCU	23
pmc-miR-2505-3p	UCGUGCACACACACACAUACAC	22	pcn-miR-33-3p	GCAAUGCAUCUGCAGUGCAAAUA	23	mcr-miR-283-3p	AAAUAUCAGCUGGUAAACGAAU	22	lny-miR-7290-5p	UCUGGCUCUGUUUGCAGCAA	20
pmc-miR-252c-5p	CUAAGUACUAGUGCCGCGGGAA	22	pcn-miR-33-5p	GUGCAUUGAGGUUGCAUUGCAU	22	mcr-miR-285-3p	ACUGGCUUCCAAAGGUCUCGAAA	23	lny-miR-734-5p	GAACUAUUCUGCAACAUUCAUG	22

pmc-miR-254-5p	UGCAAAUCUUUUGCAACAGACUU	23	pcn-miR-340-5p	UUAUAAAGCAAUGAGAGUUUCC	22	mcr-miR-2970-1-3p	UCAGAUCAUCUCUUGAUCAAC	21	lny-miR-7371d-3p	UAUUUGUACCAGAUGCUCUCUCUGG	25
pmc-miR-2571-3p	GUGAGUGGUGAUGAUGUUUACCACU	25	pcn-miR-345-3p	UGCUGACCCCUAGUCCGCCUC	21	mcr-miR-2970-2-3p	GACAGUCAGCAGUUGGCUCCCC	22	lny-miR-7398y-3p	UAACCUUCCCUUCUCUCUUUCU	22
pmc-miR-279-3p	UGACUAGAUCCACACUCAUCCA	22	pcn-miR-3529-3p	AACAACAAAAUCACUAGUCUUCCA	24	mcr-miR-297b-5p	AUGUAUGUGUGCAUGAACAUGC	22	lny-miR-745a-3p	AGCUGCCUGAUGAAGAGCUGUCC	23
pmc-miR-279b-5p	UGACUAGACUGAUAACCCCUAG	22	pcn-miR-3547-3p	GUGGGAAGAGGGGUGGAGGUGAAGC	25	mcr-miR-29b-5p	UAGCACCAUUAGAAAUGUUAGU	22	lny-miR-7460-3p	CCUGACUGAGCUCUGCUAGGGC	22
pmc-miR-279c-3p	CGGGUGUUCGUUUCGAGUACGA	22	pcn-miR-355-5p	UUUGUUUUAGCCUGAGUCGCC	21	mcr-miR-2a-1-3p	UAUCACAGCCUGCUUGGAUCAGUA	24	lny-miR-750-3p	CCAGAUCUAACUCUUCCAGCUCA	23
pmc-miR-281-3p	UGUCAUGGAGUUGCUCUCUUUA	22	pcn-miR-3609-5p	CAAAGUGAUGAGUAAUUAAGGCGC	24	mcr-miR-2a-2-3p	UAUCACAGCCAGCUUUGAUGAGCU	24	lny-miR-750-5p	AGUUGGAAGAUUGGGUCUUUGGC	23
pmc-miR-281-5p	AAGGGAGCAUCCGUCGACAGU	21	pcn-miR-3680-5p	GACUCACUCACAGGAUGUGGUG	22	mcr-miR-2a-3-3p	AAUCACAGCCUGCUUUGGUGAGCU	24	lny-miR-7661-3p	AAGAAAGAAACCUGGAUAAACUAGA	25
pmc-miR-282-3p	ACAUAGCCUAAAAGAGGCACCA	22	pcn-miR-36b-3p	UCACCGGGUAUACAUUCAUCCGC	23	mcr-miR-2b-1-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24	lny-miR-7965-3p	UUUUGUAUGCUAAAACAUAAAAU	23
pmc-miR-2953-3p	UACAGAAGUGUUCGUGGGGGA	21	pcn-miR-3716b-3p	CGAUGUUAUUUGAAAUAUCAAAC	23	mcr-miR-2b-2-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24	lny-miR-7c-5p	UGGAAGACUAGUGAUUUUGUUGUUC	25
pmc-miR-2c-1-3p	UAUCACAGCCUGCUUGGAUCAGUA	24	pcn-miR-3739-3p	UUGGGAGGGGGAGAGAGUGGAA	22	mcr-miR-2c-5p	UCGUCAACAUUGCCUGCUGCUU	22	lny-miR-8066-3p	CAAUGUGAUCUUUUGGAGAAC	21
pmc-miR-2c-2-3p	UAUCACAGCCAGCUUUGAUGAGCU	24	pcn-miR-375-1-3p	UUUGUUCGUUCGGCUCGCGUUA	22	mcr-miR-3131-3p	UCGAGGACUGGUGGAAUUUUCCA	23	lny-miR-8075-5p	UGCUGAUGGCAGAUGUGUGUUGGC	24
pmc-miR-2c-3-3p	AAUCACAGCCUGCUUUGGUGAGCU	24	pcn-miR-375-2-3p	CUUGUUCGUUCGGCUCGUUC	20	mcr-miR-315b-3p	UUUUGAUUGUUGUACAGUCCGC	22	lny-miR-8279-5p	AGAUUCAUGUCAAUCUGACAUU	22
pmc-miR-2b-1-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24	pcn-miR-377-5p	AGAGGUUGCCUUUGGUGAGAGA	22	mcr-miR-317-3p	UGAACACAGCUGGUGGUAUCUUUUU	25	lny-miR-8335-1-5p	GUUGUUGUUGUUGUUUUGGUCCUUG	25
pmc-miR-2b-2-5p	UCAUCAAAGCUGGCUGUGAUAUGA	24	pcn-miR-3776-3p	AGGAGGGGGGGAGAGAGAUUUA	22	mcr-miR-3223-5p	UACCUUUUACCUUUACCUUACA	22	lny-miR-8335-2-3p	GUUGUUGUUGUUGUUUUGUUUUGUG	25
pmc-miR-2f-3p	UAUCACAGCCAUGCUAAUCUCCU	23	pcn-miR-3809-5p	GUCGGUCAGUUGGUUAGAUG	20	mcr-miR-324-3p	CCCACUGCCCCAGGUGUCUUGUG	23	lny-miR-8335-3-3p	GUUGUUGUUGUUGUUUUGAAGCCAG	25
pmc-miR-300-3p	UAUACAAGGGCAGACUCCAUCC	22	pcn-miR-3831-3p	CAAACAUUGCUAUUUUUCAUAUCCAA	26	mcr-miR-3299-3p	UCAUUGUUAAAGUCUGCAUAACC	23	lny-miR-8-3p	UAAUACUGUCAGGUAAAGAUGUC	23
pmc-miR-302a-3p	AAGUGCUUCCUUUUAUUGGUGAU	23	pcn-miR-3928-3p	UGAAGCUCUAAGGUUCAUCCCAG	23	mcr-miR-33-3p	GCAAUGCAUCUGCAGUGCAAAUA	23	lny-miR-8485-1-5p	CACACACACACACACACGUAC	21
pmc-miR-302b-3p	AAAGUGCUUCCAUGUUUAAUUCA	23	pcn-miR-3957-3p	ACGCACAGCACCUCACACUGAC	22	mcr-miR-33-5p	GUGCAUUGAGGUUGCAUUGCAU	22	lny-miR-8485-2-3p	CACACACACACACACACGUAC	21
pmc-miR-3057-3p	UCCCACAGGCCCAGCUGUCACA	22	pcn-miR-3965-5p	UGCUUAUCAGCCUGAUUCU	19	mcr-miR-33b-3p	CAAUGUACCUGCAGUGCUUUC	21	lny-miR-8-5p	CAUCUUACCUAACAGCAUUAGA	22
pmc-miR-3071-5p	AUCAUCAAAACAAAUGUGCAUA	22	pcn-miR-4057-3p	GGCUUGGCGACUGUAGUAGG	20	mcr-miR-34-3p	CAACCACUAUCUGCAGUGCCGCG	23	lny-miR-87a-5p	AACACUUGGUAAUUUGCAAAUGAA	24
pmc-miR-3084a-5p	UUGAAGGUUCAUUAGCCUUGUG	22	pcn-miR-4066-5p	CAUGCCUUUAUCAUGUGUU	19	mcr-miR-34-5p	UGGCAGUGUGGUUAGCUGGUUGUG	24	lny-miR-8908i-3p	UACCCGGUAAGGUAGUUGCCAAGAA	25
pmc-miR-308-5p	CGCAGGAUUUGCUUGUUUUGAG	22	pcn-miR-4070-3p	CACGCGUCACGUGACACCU	19	mcr-miR-3529-3p	AACAACAAAAUCACUAGUCUUCCA	24	lny-miR-9032-3p	UGCAGAUUCCGUUGAUGCAAUCCAA	25

pmc-miR-31-3p	UGGCAAGAUGUUGGCACAGCG	21	pcn-miR-4185-3p	UGUAUUCAUACUGUCUGUUACA	22	mcr-miR-3530-5p	CAAUGGUGUGAGCUGGACAUG	21	lny-miR-9-1-3p	UCAUACAGCUAGAUAACCAAAGA	23
pmc-miR-315-3p	UUUUGAUUGUUGCUCUAGAAAUU	23	pcn-miR-4187-3p	UUUGGUGUUGUGCUGUUUAA	20	mcr-miR-3671-3p	AUCAAAUAAGGACUAGUGGCA	21	lny-miR-9-1-5p	CCUUUGGUAACCUAGCUUUAUGA	23
pmc-miR-317-3p	UGAACACAGCUGGUGGUAUCUUUUU	25	pcn-miR-4195-5p	UACAUGUAAUACAUUGUACC	20	mcr-miR-371b-3p	ACUCAAAAGAUGGCGGCAAGG	21	lny-miR-9229d-3p	UGAGUCUUCCCCUUGAG	17
pmc-miR-33-3p	GCAAUGCAUCUGCAGUGCAAAUA	23	pcn-miR-4271-3p	GGGGGAAGAAAAGGUGGCA	19	mcr-miR-372-5p	AAAGUGCUGCGACAUUAUUACCG	23	lny-miR-9235b-3p	UAAUUUUGAUGUGGCUUGAGAACA	24
pmc-miR-33-5p	GUGCAUUGAGGUUGCAUUGCAU	22	pcn-miR-4323-3p	CAGCCCCACAGCCUCAGG	18	mcr-miR-373-3p	AAAGUGCUUCCCUUUUAUUAUC	22	lny-miR-9-2-3p	AUAAAGCUAGGUUACCAAAGGCA	23
pmc-miR-336-5p	UCACCCUUCCAUAUCUUUUGG	21	pcn-miR-4472-3p	GGUGGGGGGUGUUGUUGA	18	mcr-miR-375-1-3p	UUUGUUCGUUCGGCUCGCGUUA	22	lny-miR-9-2-5p	UCUUUGGUUAUCUAGCUGUAUGAUU	25
pmc-miR-33b-3p	CAGUGCCUCUGCAGUGGAUGU	21	pcn-miR-449a-3p	ACCAGCUGACAUUCAGUCCAGA	22	mcr-miR-375-2-5p	UUUGUUCGUUUUGCUUGCUCAUG	23	lny-miR-92a-3p	GAUUGCACUCGUCCCGGCCUUC	22
pmc-miR-345-3p	UGCUGACCCCUAGUCCGCCUC	21	pcn-miR-449d-3p	GAAGGCUGUGUGCUGUAAAG	20	mcr-miR-376c-3p	AACAUAGAGGAAAAUCACCGA	21	lny-miR-92b-1-3p	UAUUGCACUCGUCCCGGCCUA	21
pmc-miR-3529-3p	AACAACAAAAUCACUAGUCUUCCA	24	pcn-miR-4525-3p	GGGGGGAUGUGCAUGCCAG	19	mcr-miR-376c-5p	AACAUAGAGGAAAAUCACCGA	21	lny-miR-92b-2-3p	AAUUGCACUUGUCCCGGCCUGC	22
pmc-miR-3532-3p	UUGGAGGCUGCAGUGUGACCUC	22	pcn-miR-4617-3p	UGUGGCUGUCACACCUAAACAC	22	mcr-miR-376d-5p	GUAGAUUUUCCUUCUACAACUU	22	lny-miR-9319-3p	AGCAGAGCUAGUGGCCUCACCCC	23
pmc-miR-355-5p	UUUGUUUUAGCCUGAGUCGCC	21	pcn-miR-4654-5p	UGUGGGAUCUGGAGGCAGACUUC	23	mcr-miR-3834-3p	UGAUGUUAUUUUCGACAAAU	20	lny-miR-96b-3p	AUUAUACAUCGGUGCCAAGUCA	22
pmc-miR-3620-5p	GUGGGCUGGGCUGGGCUGGGCU	22	pcn-miR-466i-1-3p	UGUGUGUGUGUGUGUGUG	20	mcr-miR-3890-3p	AGCCGGUUAUGUACGGCUG	19	lny-miR-96b-5p	AUUUGGCACUUGUGGAAUAAUCG	23
pmc-miR-36-3p	UCACCGGGUGGAAAUUCGUCUUU	23	pcn-miR-466i-2-5p	UGUGUGUGUGUGUGUGUG	20	mcr-miR-39-3p	AGCUGAUUUCGUCUUGGGAGUU	22	lny-miR-9701a-1-5p	CUGUGUACCACCAUCAACCCGCG	23
pmc-miR-3643-3p	GUGAGUUUAUCUAAAUUCAGGA	22	pcn-miR-466i-3-5p	UGUGUGUGUGUGUGUGUG	20	mcr-miR-4000i-3p	UGAAACUUGCAAGGAACUGC	20	lny-miR-9701a-2-3p	CUGUGUACCACCAUCAAGGCGUG	23
pmc-miR-36b-3p	UCACCGGGUAUACAUUCAUCCGC	23	pcn-miR-466i-4-5p	GGUGUGUGUGUGUGUGUG	20	mcr-miR-4003d-3p	UGAGAAUGGUAACCAAAAAA	20	lny-miR-9708c-3p	UGAGCACAGCUAAACAUUUUCU	22
pmc-miR-3724-3p	AUCGUGGUAAACUUUGUCCUCG	22	pcn-miR-466m-3p	UGUGUGCAUGUGCAUGUGUGCUU	23	mcr-miR-4027-3p	UAUAUUACUUUUAUGUUAAU	20	lny-miR-981-3p	UUCGUUGUCGUCGAAACCUGCCC	23
pmc-miR-375-1-3p	UUUGUUCGUUCGGCUCGCGUUA	22	pcn-miR-466n-3p	GUGUGUGCGUACAUGUACUCAU	22	mcr-miR-4029-5p	GUUUACAUUGCAUGCAUCGC	20	lny-miR-981-5p	CGGGUUUCGCGACUGGCGAACA	22
pmc-miR-375-2-3p	CUUGUUCGUUCGGCUCGUUC	20	pcn-miR-466p-3p	UAUGUGUGUGUACAUGUGAAG	21	mcr-miR-4034-3p	CUUUUCUCUGGCACUGAGGA	20	lny-miR-9a-3p	AUAAAGCUAGGCGACUGUCCGU	22
pmc-miR-3782-3p	CUUACAGAGGCACUUGGGUGGCGC	24	pcn-miR-466q-3p	GUGCACACACACACAUACG	19	mcr-miR-4040-3p	CAACCAGAUCAGAAAGGUGA	20			
pmc-miR-3792-3p	GACUGAGGAAAGAGAGAUGUU	21	pcn-miR-467f-3p	AUAUACACACACACACCUUUC	21	mcr-miR-4048-5p	GCACCUUGGUCACCAUAGUGAC	22			
pmc-miR-3821-3p	AUUUCUAGUGAGUGAGGGUACUU	23	pcn-miR-4715-5p	GUGCCACCUUAACUGCACGGACC	23	mcr-miR-4127-5p	AGGCAGCUGUGAGAGAGCCCU	21			
pmc-miR-4009c-3p	UAUUGCACUUUUACUGGUCG	20	pcn-miR-4757-3p	CAUGACGUCACAGAGGCGAGGU	22	mcr-miR-4130-5p	CAGACAGCUGCGUGUCUUUA	20			

pmc-miR-4013b-5p	UUACUUGCUUUAACAGCUUA	20	pcn-miR-4801-3p	UACACAAGAAAACCAAA	17	mcr-miR-41-5p	UCACCGGGUGAAAAACUGAC	20			
pmc-miR-4057-3p	GGCUUGGCGACUGUAGUAGG	20	pcn-miR-4860-3p	UGUAGAGAUUGUGUGAACUGCUAG	24	mcr-miR-427-3p	GAAAGUGCUUUCUGUUACUUCUU	23			
pmc-miR-4070-3p	CACGCGUCACGUGACACCU	19	pcn-miR-4918-5p	GUGAGCACGAUGGCCAGCACUGCC	24	mcr-miR-44-1-3p	CUGGAUGUGCUCGUUAACGUC	21			
pmc-miR-4133-5p	CAUGUUGUGUUUUUGUAUG	19	pcn-miR-49-3p	AAGCACCAUGUGAAGCACUUUU	22	mcr-miR-44-2-3p	UGACUAGAUGAUCACAAGACAU	22			
pmc-miR-4140-3p	ACCAGAUGAUUAUGACACAA	20	pcn-miR-4968-1-5p	CAGCAACAGCAGCAGCAGCAGA	22	mcr-miR-449a-3p	UGGCAGUGCGUGUUAGUGAUG	21			
pmc-miR-4177-5p	UAAUUGCUGUUUUAAACAGU	20	pcn-miR-4968-2-5p	CAGCAACAGCAGCAGCAGCAGC	22	mcr-miR-4502-5p	GCUGAUGAUGAUGGUGAUUGGA	22			
pmc-miR-4185-3p	UGUAUUCAUACUGUCUGUUACA	22	pcn-miR-4968-3-3p	CAGCAACAGCAGCAGCAGCAGC	22	mcr-miR-452-3p	AACUGUUUGCAGAGGACAGUCACA	24			
pmc-miR-4323-3p	CAGCCCCACAGCCUCAGG	18	pcn-miR-4968-4-3p	CAGCAACAGCAGCAGCAGCAGC	22	mcr-miR-4552-3p	UCCCACUUGAUCACUGACAUUCU	23			
pmc-miR-4472-3p	GGUGGGGGGUGUUGUUGA	18	pcn-miR-5317a-3p	UUUCUUGUCUCUGUGUACCUCUUG	24	mcr-miR-466h-3p	UACGCACGCACACACACAC	19			
pmc-miR-449d-3p	GAAGGCUGUGUGCUGUAAAG	20	pcn-miR-5391-5p	UGGACAGUUAUGAAGAAGUG	20	mcr-miR-466i-1-5p	AUACACACACACAUACACACGC	22			
pmc-miR-4629-3p	UGACUGGACGUUCAUCGCCG	20	pcn-miR-5392-3p	UGUUACUUGACAUUUUGAGA	20	mcr-miR-466i-2-5p	UGUGUGUGUGUGUGUGUG	20			
pmc-miR-4654-5p	UGUGGGAUCUGGAGGCAGACUUC	23	pcn-miR-5440-5p	UCAGGAGGACUGAAGGGUGGA	21	mcr-miR-467c-5p	UAAGUGCGUGCAUGUAUGCAGG	22			
pmc-miR-466-1-3p	AUAUAUACACACACACAUAUAUA	23	pcn-miR-5549-3p	UCAUGUUGGUUUUUUGAAU	19	mcr-miR-4760-3p	UUUAGAUUGAACAUGAAUGUUU	22			
pmc-miR-466-2-5p	AUAUAUACACACACACAACCAUG	23	pcn-miR-559-3p	UAAAGUAAAUAAGCACAGACU	21	mcr-miR-4810b-5p	GUAGGUUCAUGAGUAGACUUUU	22			
pmc-miR-466-3-3p	AUAUAUACACACACACAUAUACA	23	pcn-miR-5594-3p	AAGAGUACUGUAGUUUUUCCAA	22	mcr-miR-4865-3p	AUGUAGAGAGAGUGACGCCGCUU	23			
pmc-miR-466h-3p	UACGCACGCACACACACAC	19	pcn-miR-5595-3p	UCUCUUUUUUCUCGCAGUCCCGCA	24	mcr-miR-4968-1-3p	CAGCAACAGCAGCAGCAGCAGC	22			
pmc-miR-466i-1-5p	UGUGUGUGUGUGUGUGUG	20	pcn-miR-574-1-5p	UGAGUGUGUGUGUGUGAGUGUGUG	24	mcr-miR-4968-2-3p	CAGCAACAGCAGCAGCAGCAGC	22			
pmc-miR-466i-2-5p	UGUGUGUGUGUGUGUGUG	20	pcn-miR-574-2-3p	UGAGUGUGUGUGUGUGAGUGUGUG	24	mcr-miR-4968-3-5p	CAGCAACAACAGCAGCAGCAGC	22			
pmc-miR-466m-5p	UGUGUGCAUGUGCAUGUGAAUGU	23	pcn-miR-5965-5p	GACAAUUCUGACAUUUUGCA	20	mcr-miR-4975-3p	UUUACUUGGGUUUUCUUUCAG	21			
pmc-miR-466n-3p	GUGUGUGCGUACAUGUACUCAU	22	pcn-miR-6013-3p	GCUGCUGACGACCGCCUCA	19	mcr-miR-5009-3p	UUGGACUUUUUCAGAUGGACUAGU	24			
pmc-miR-466q-3p	GUGCACACACACACAUACAC	20	pcn-miR-6037-1-3p	UAAGCUCUGUGUACUUUAGUG	21	mcr-miR-50-5p	CGAGUAAUAUUAGACAGCGGAUU	23			
pmc-miR-467d-5p	UAAGUGCGCGCAUGUAUUUAUG	22	pcn-miR-6037-2-3p	UAAGCUCUGUGUACUUUAGUG	21	mcr-miR-5101-5p	UUUGUUUGUUUUGCUGUAUGAG	22			

pmc-miR-467f-3p	AUAUACACACACACACCUUUC	21	pcn-miR-6076-3p	AGCAUGACAGAGGAGAGGAGA	21	mcr-miR-542-3p	UGUGACAGAUUGAUAAAGACGC	22			
pmc-miR-4715-5p	GUGCCACCUUAACUGCACGGACC	23	pcn-miR-6098-5p	AUAGUGAUUGUGUGUUUCUA	20	mcr-miR-5429-3p	AUAGUCAUGCUGGAGGUUCCUA	22			
pmc-miR-4750-3p	CCUGACCCACCCCCUCCCUACU	22	pcn-miR-6132-1-5p	AGCAGGGCUGGGGAUUCUG	19	mcr-miR-548d-3p	AAAAAACUGCAGUUACUUGAA	21			
pmc-miR-4757-3p	CAUGACGUCACAGAGGCGAGGU	22	pcn-miR-6132-2-5p	AGCAGGGCUGGGGAUUCUG	19	mcr-miR-550-5p	AGUGCCUGAGGGAGUAGUGCCUU	23			
pmc-miR-4769-5p	UCUGCCAUCCUCCCUCUCGUCU	22	pcn-miR-6132-3-5p	AGCAGGGCUGGGGAUUCUG	19	mcr-miR-5552-3p	UGUAGUUUGUAGUCUAUAGAUAU	23			
pmc-miR-487c-5p	GUGGCUAUCCCUGCUGUCAUCC	22	pcn-miR-6335-5p	CUGCAUACACAGUGAUGCAGGU	22	mcr-miR-5582-5p	UAAAACUUUAAGUGUGUCAGAC	22			
pmc-miR-4938-5p	AUCAUCAUGCAUCAUCAUUAUUG	23	pcn-miR-6-3p	AGGGAACUGCUGCUGCAGCGACU	23	mcr-miR-5698-3p	UGGGGGAGUGCAGUGAA	17			
pmc-miR-49-3p	AAGCACCAUGUGAAGCACUUUU	22	pcn-miR-6416-3p	CUCCGUAUCAUCUGCUAGCUA	21	mcr-miR-586-5p	UAUGCAUAUUGUAUUUUGUACUUG	24			
pmc-miR-4949-3p	AGUGGUGUGCGUGUGUGUGUGU	22	pcn-miR-64c-3p	CAUGACACACUGGCUGAACCA	21	mcr-miR-5890c-3p	CAUAUAACUGAACUGUCUGUG	21			
pmc-miR-4968-1-3p	CAGCAACAGCAGCAGCAGCAGC	22	pcn-miR-6505-5p	UGACUUCUACCUGUUCCCUAA	21	mcr-miR-592-3p	UCAUCACGUGGUGACGUGUUC	21			
pmc-miR-4968-2-5p	CAGCAACAGCAGCAGCAGCAGC	22	pcn-miR-6516-3p	AUGCAGUAACAGGUGUCUCCAC	22	mcr-miR-6013-5p	GCUGCUGACGACCGCCUCA	19			
pmc-miR-4968-3-3p	CAGCAACAGCAGCAGCAGCAAU	22	pcn-miR-6560-5p	UGUGUUGCUCCAUACUGCUGAAG	23	mcr-miR-6058-5p	AUGACAAUGGUGAUGAAUCAG	21			
pmc-miR-4968-4-3p	CAGCAACAGCAGCAGCAGCAGC	22	pcn-miR-6575-3p	GAGUUUUCCCAGGCUGAUGUGU	22	mcr-miR-6340-3p	GUCAGCAGCAGCUUCGAUACCCA	23			
pmc-miR-4999-3p	UGCUGUAUUGUCAGGUUUGUA	21	pcn-miR-6587-3p	UGCUGGAAGUGGUGCUAUAUGUC	23	mcr-miR-6552-3p	CAACAAGAAGUGGACACGGUC	21			
pmc-miR-501-5p	AAUGCACCCGGGCAAGUCAGA	21	pcn-miR-6603-5p	AAGGACAAGAGGAAAUAACUUGA	23	mcr-miR-6560-5p	UGUGUUGCUCCAUACUGCUGAAG	23			
pmc-miR-5101-1-5p	UUUGUUUGUUUUGCUGUCUGAC	22	pcn-miR-6680-5p	GUUGCUGAUGAAGAUAAAUCGU	22	mcr-miR-669f-3p	UAUAUACACACACACACACAUAA	23			
pmc-miR-5101-2-5p	UUUGUUUGUUUUGCUGUGUGCU	22	pcn-miR-669f-5p	CAUAUACAUACACACACACGUGU	23	mcr-miR-67-3p	UCACAACCUGCAUGAAUGAGGAC	23			
pmc-miR-519f-3p	AAAGUGCAUCCUUUUAUGGCGA	22	pcn-miR-67-3p	UCACAACCUGCAUGAAUGAGGAC	23	mcr-miR-676-5p	CUCUUCAACUUCAGGAUCGUUA	22			
pmc-miR-5317a-3p	UUUCUUGUCUCUGUGUACCUCUCG	24	pcn-miR-6816-3p	GAAGGACCUGCACCUUGC	18	mcr-miR-6769b-5p	UGGUGGGUGAGGAGGAGAAAGCA	23			
pmc-miR-5391-5p	UGGACAGUUAUGAAGAAGUG	20	pcn-miR-6852-5p	UGUCCUCUGUUCCUCAU	17	mcr-miR-6780a-5p	CUCCUCUGUUUUCUUUUCAAA	21			
pmc-miR-539-5p	AUCAUACAAGGACAAUUUGUCA	22	pcn-miR-6894-3p	AGGAGGAUGGAGAGCUGUUACAGC	24	mcr-miR-6796-3p	UUGUGGGGUUGGAGAGUAUGGCU	23			
pmc-miR-5396b-5p	CCACACAACCAGCAAGAUUUGC	22	pcn-miR-6951-5p	UUGUAUUUGUGUGAUUCCCGA	21	mcr-miR-6800-5p	GUAGGUGACAGUCAGGCCUGG	21			

pmc-miR-5549-3p	UCAUGUUGGUUUUUUGAAU	19	pcn-miR-6974-3p	UCUCCACUCUCUUCUGUGUCGU	22	mcr-miR-6803-3p	GUGGGGGUGGGGGGCUGGGAGA	22			
pmc-miR-5552-3p	UGUAGUUUGUAGUCUAAAGUCUG	23	pcn-miR-6977-5p	GUGAGGCGCUGUGGGCAGGUGAGCC	25	mcr-miR-6826-3p	UCAAUAGGAAAGAGGUCUGUGAU	23			
pmc-miR-5595-3p	UCUCUUUUUUCUCGCAGUCCCGCA	24	pcn-miR-6999-3p	AAGGAAGGAGAGUCAGGAGCGUG	23	mcr-miR-6830-3p	UGUCUUUCUUCUCUCCCCCAUCU	23			
pmc-miR-5600-3p	AGUGGAAUGUUUUGUUUCAGUA	22	pcn-miR-7000-5p	CACCCACCUGCCUGUCACAGUG	22	mcr-miR-6864-3p	UUGAAGGGACAAGUCAGACUUUAA	24			
pmc-miR-5612-3p	UAUACAUCACCAGUUGACAUGU	22	pcn-miR-7072-3p	CUAGCUUCUCUUCUUCCAGUU	21	mcr-miR-6873-3p	UUCUCUCUGUCUUUCUCUCAUGU	23			
pmc-miR-574-1-3p	UGAGUGUGUGUGUGAGUGC	21	pcn-miR-71-1-5p	UGAAAGACAUGGGUAGUGAGAUG	23	mcr-miR-6925-3p	AGAGGAAGAAAUGGCUUACAAA	22			
pmc-miR-574-2-3p	UGAGUGUGUGUGUGAGUGUGUG	24	pcn-miR-71-2-3p	UGAAAGACACAGGUAGAAUGUA	22	mcr-miR-6955-3p	ACACCUGUCUCCUUUGUCGUGU	22			
pmc-miR-5918b-5p	UCGCUCUACAUCGUGUGGUCAG	22	pcn-miR-7151-5p	GAUCCAUCUCUGCCUGCUCACCU	23	mcr-miR-6975-3p	UCUCUCCUUUCUCCUCCGCC	20			
pmc-miR-5965-5p	GACAAUUCUGACAUUUUGCA	20	pcn-miR-7307-3p	CAAAUGGUCAUUUCUGCGA	19	mcr-miR-6988-5p	GGGGUGGAGAGCUGAGUUACA	21			
pmc-miR-6056-3p	GAGGGACGAGGAGGGAGGAG	20	pcn-miR-7314-3p	UCAGAAACAGUGUCUCUG	18	mcr-miR-7042-3p	UGUCCCUUUGUUUUCUCCACA	21			
pmc-miR-6076-3p	AGCAUGACAGAGGAGAGGAGA	21	pcn-miR-7386e-5p	GUAAACACUUUACCCGUUUGA	21	mcr-miR-7051-5p	UCACCAGGAGGAGGUGUGCACG	22			
pmc-miR-6098-5p	AUAGUGAUUGUGUGUUUCUA	20	pcn-miR-7389-3p	GCUGUACUUGAAGCAAGAGAGA	22	mcr-miR-71-5p	UGAAAGACAUGGGUAGUGAGAUG	23			
pmc-miR-623-3p	UUCCCUUGCAGGGGCUGAGGUAU	23	pcn-miR-7398h-3p	UAACCCUCCCUUCUUUAUGAUA	22	mcr-miR-7186-3p	CUGUGGUUCCUGUAUGUUCGGG	22			
pmc-miR-626-5p	AGCUGUCUGAAAAUGUUUG	19	pcn-miR-7399-5p	UACGCAUGUAUAUGUAUAUACA	22	mcr-miR-7234-3p	UUGUUUUCUCCAAAGAACACCAU	23			
pmc-miR-6302-3p	CAAACUCAUCGUCAGCCACUCA	22	pcn-miR-743b-3p	UGUUCAGACUGGUGUCUGGU	20	mcr-miR-7241-5p	UAGUAGAUACUCAUGGUGAGUA	22			
pmc-miR-6416-3p	CUCCGUAUCAUCUGCUAGCUA	21	pcn-miR-745a-3p	AGCUGCCUGAUGAAGAGCUGUCC	23	mcr-miR-7260-3p	AUGGCUAAAACAACUGAC	18			
pmc-miR-6505-5p	UGACUUCUACCUGUUCCCUAA	21	pcn-miR-745b-3p	GAGCUGCCAAAUGAAGGGCUGU	22	mcr-miR-7371b-3p	UUUGUAUCAGAUGCUUGC	18			
pmc-miR-651-3p	UUUAGGAUAAGUUUGAACACGU	22	pcn-miR-7472-3p	AUGUGCUGGAGAUGAAAACUCU	22	mcr-miR-7-3p	CAACAAGUCCCAGUCUUGGCGG	22			
pmc-miR-6516-3p	AUGCAGUAACAGGUGUCUCCAC	22	pcn-miR-750-3p	CCAGAUCUAACUCUUCCAGCUCA	23	mcr-miR-742-5p	GAAAGCCACCAUGCUGUUAUAU	22			
pmc-miR-6528-5p	AGAGGGAAGAGGGAAGAAAG	20	pcn-miR-750-5p	AGUUGGAAGAUUGGGUCUUUGGC	23	mcr-miR-7456-3p	CAGGGAGAUGUACCUGCUGCCA	22			
pmc-miR-6548-3p	AGAGGUGCCCCGCUGUCUGUUC	22	pcn-miR-751-3p	CAUGUUUGAAUGGCCACCACU	21	mcr-miR-7461-5p	CAUGGCUGGAAUGUGGCUGAGCAAC	25			
pmc-miR-6560-5p	UGUGUUGCUCCAUACUGCUGAAG	23	pcn-miR-753d-5p	AGAUCAUUAUUCAAGCGAUUG	21	mcr-miR-7462-3p	CAACCUCAUUUCUAGCAGACCA	22			

pmc-miR-6562-5p	AGGGGAAAGGAAUGUGCAGGUA	22	pcn-miR-760-3p	CGGCUCUGGGUCUGUGAAGUCA	22	mcr-miR-7465-3p	UCAGAUAGCUGAUACUCAUU	20			
pmc-miR-6568-3p	GCGGCCGCCAUCUUGCGGAGC	21	pcn-miR-7643-3p	GACAUCUGUUUCUCAGUAAUUU	22	mcr-miR-750-3p	CCAGAUCUAACUCUUCCAGCUCA	23			
pmc-miR-669f-5p	CAUAUACAUACACACACACGUGU	23	pcn-miR-7649-5p	UGACAGCAGUGCUGUAUCUAUG	22	mcr-miR-750-5p	AGUUGGAAGAUUGGGUCUUUGGC	23			
pmc-miR-669j-3p	UGCAUAUACUCACAUGUGCACA	22	pcn-miR-76b-1-3p	UCUUGUUUUUUUCAACUCCUGG	22	mcr-miR-7589-3p	UGGAAAUGGAGAAAUCAGCCGA	22			
pmc-miR-6701-3p	AUUAUUUUACAGACAGCAACU	21	pcn-miR-76b-2-3p	UCUUGUUUUUUUCAACUGCGUU	22	mcr-miR-765-3p	UGGAGGAGAAGGAAGGUGUGG	21			
pmc-miR-67-3p	UCACAACCUGCAUGAAUGAGGAC	23	pcn-miR-770-3p	AGCACCACGUGUCUGGUAAAUC	22	mcr-miR-7683-5p	UGGAAAGGUGGAACACUAACC	21			
pmc-miR-6876-5p	AGCUGUCUGUGUUUUCCCAGAUGC	24	pcn-miR-7880k-3p	GGUCAGAAAUGGUUGCUGAGCUCCAC	26	mcr-miR-770-3p	AGCACCACGUGUCUGGAAUCUG	22			
pmc-miR-6891-5p	CCCUCAUCUUCCCCUCCCCUC	21	pcn-miR-7880q-3p	UUUGCGACCAAAAUCACUCUCU	22	mcr-miR-7789-3p	CAGCAGAGCAGACGUCCAGCA	21			
pmc-miR-6971-3p	ACAGCCUCUGCUUCUUCAGCU	21	pcn-miR-7901-3p	UACUGUAGUUGAAGCGCUAUU	21	mcr-miR-7795-5p	AGGAGACACGUGAUGCUUAC	20			
pmc-miR-6974-3p	UCUCCACUCUCUUCUGUGUCGU	22	pcn-miR-79-3p	GUAAAGCUAAAUUACCAGUG	20	mcr-miR-789b-5p	CCAUCCUGGUACACCACCAGCA	22			
pmc-miR-7000-5p	CACCCACCUGCCUGUCACACUG	22	pcn-miR-7c-3p	UGGAAGACUAGUGAUUUUGUUGUUC	25	mcr-miR-7950b-5p	GCCGGCGAAAGAGUUGCGCCA	21			
pmc-miR-7046-5p	UGUAGGGUGAGGCUGGUGGGUUAG	24	pcn-miR-7c-5p	UGGAAGACUAGUGAUUUUGUUGU	23	mcr-miR-7964a-3p	GUCAACCACUCGCUGCAUAU	20			
pmc-miR-7-1-3p	CAACAAAUCGUAGCCUCAGAG	21	pcn-miR-8-1-3p	UAAUACUGUCAGGUAAAGAUGUC	23	mcr-miR-802-3p	UCAGUAACAAAGAUUCUGUUACAC	24			
pmc-miR-7151-5p	GAUCCAUCUCUGCCUGCUCACCU	23	pcn-miR-8-1-5p	CAUCUUACCUAACAGCAUUAGA	22	mcr-miR-81b-3p	AUGGGCCUAUGUGUGUUUUGCC	22			
pmc-miR-71-5p	UGAAAGACACAGGUAGAAUGUA	22	pcn-miR-8196b-3p	AGUAGUUAAUUUUUCUU	17	mcr-miR-8234-3p	CUCCAUCCCAUCUUCUCCUGCC	22			
pmc-miR-7207-5p	AUCUUUUAAAAUACAGGGUG	20	pcn-miR-8-2-3p	UAAUACUGUCAGGUAAAGAUGUC	23	mcr-miR-8293-5p	AUGAAAGAUAAAAGUGGAUGAAU	23			
pmc-miR-722-5p	UUUUGCAGAAACGUUUACAGUU	22	pcn-miR-8-2-5p	CAUCUUACCUAACAGCAUUAGA	22	mcr-miR-8319-3p	AAAUUAGCAAGUGAGGUCAGGCU	23			
pmc-miR-7-2-3p	CAACAAGUCCCAGUCUUGGCGG	22	pcn-miR-8296-5p	UCGAGAUGAUGGAGAGCACACU	22	mcr-miR-8319-5p	AGAGGCUCAUUGCCAUAG	18			
pmc-miR-7241-3p	ACUUGCAUGAGUUAAUGAUUUGU	23	pcn-miR-8332-3p	UUCUUUGCUCUUCUCGACAUGCG	23	mcr-miR-8335-1-5p	GUUGUUGUUGUUGUUUUGCUCAUGG	25			
pmc-miR-7314-3p	UCAGAAACAGUGUCUCUG	18	pcn-miR-8335-1-5p	GUUGUUGUUGUUGUUUUGCCAACUG	25	mcr-miR-8335-2-3p	GUUGUUGUUGUUGUUUUUUUUUUUU	25			
pmc-miR-7323-3p	UUACAGAAUUGUGUGAUCAAC	21	pcn-miR-8335-2-5p	GUUGUUGUUGUUGUUUUGGUUUUUU	25	mcr-miR-83-5p	UAGCACCAUAUAAAUUCCUGCU	22			
pmc-miR-7386e-5p	GUAAACACUUUACCCGUUUGA	21	pcn-miR-8364g-3p	AGAGAGUGUGGAAAAGGGGAGAG	23	mcr-miR-8364j-3p	UCUUCAUUUCUCACGUGAAUGCG	23			

pmc-miR-7388c-3p	UGCACAGACGUGACAUCGUU	20	pcn-miR-8416-5p	UGAUUGGUCACAUAGUUUA	19	mcr-miR-8-3p	UAAUACUGUCAGGUAAAGAUGUC	23			
pmc-miR-7398c-3p	UGUGUAGAGGUGAGAAAGUUGUC	23	pcn-miR-8422-5p	GCAAUUAAAAGUAGCACAA	19	mcr-miR-8485-1-5p	CACACACACACACACACAAAA	21			
pmc-miR-743b-3p	UGUUCAGACUGGUGUCUGGU	20	pcn-miR-8462-1-3p	GAAUGAUCAAAUAAUUGUC	19	mcr-miR-8485-2-5p	CACACACACACACACACGUAU	21			
pmc-miR-7448-3p	AACUGUUGUAGAACAGUUCCGAU	23	pcn-miR-8462-2-3p	UGAUUAAUUUGAUAAGAUGA	20	mcr-miR-8485-3-5p	CACACACACACACACACGUCA	21			
pmc-miR-745c-3p	AGCUGCCUGAUGAAGAGCUGUCC	23	pcn-miR-8485-1-3p	CACACACACACACACACGUAU	21	mcr-miR-8-5p	CAUCUUACCUAACAGCAUUAGA	22			
pmc-miR-745b-3p	GAGCUGCCAAAUGAAGGGCUGU	22	pcn-miR-8485-2-5p	CACACACACACACACACGUAC	21	mcr-miR-8881-3p	UUUGUUUUCUCUGGUUCUUCUCU	23			
pmc-miR-7472-3p	AUGUGCUGGAGAUGAAAACUGU	22	pcn-miR-87-3p	GUGAGCAAAGUUUCAGGUGUGU	22	mcr-miR-8956-3p	UUGACUUGGAUCUUUGCAACGUAUC	25			
pmc-miR-750-3p	CCAGAUCUAACUCUUCCAGCUCA	23	pcn-miR-87-5p	CUGCCUGAAAUUUAUGCUCAAACCU	25	mcr-miR-8993-5p	UGACCUUGACCUUUGACCAAGUG	23			
pmc-miR-750-5p	AGUUGGAAGAUUGGGUCUUUGGC	23	pcn-miR-8834n-5p	UGCCGGGCCUGGAGGCCAGCUGU	23	mcr-miR-9077-5p	UCUGAGGGCUUUUGCACUGCUGCU	24			
pmc-miR-751-3p	CAUGUUUGAAUGGCCACCACU	21	pcn-miR-888-5p	GACUGACACCUCUUUGUCCAGC	22	mcr-miR-9093-3p	CUGUAGUCCAUGUCCCGGACCAG	23			
pmc-miR-7562-5p	CACACACAUUCAUGGACACGCA	22	pcn-miR-8915-1-3p	CGGAUGGCCAGCUGCAGGUGA	21	mcr-miR-9-1-3p	AUAAAGCUAGGUUACCAAAGGCA	23			
pmc-miR-7575-5p	GCAUGGUCAUGAUCAUGACA	20	pcn-miR-8915-2-3p	CGGAUGGCCAGCUGCAGGUGA	21	mcr-miR-9-1-5p	UCUUUGGUUAUCUAGCUGUAUGAUU	25			
pmc-miR-7643-3p	GACAUCUGUUUCUCAGUAAUUC	22	pcn-miR-8915-3-3p	CGGAUGGCCAGCUGCAGGUGACG	23	mcr-miR-9186r-5p	GAGGUGGCAUGGCUGGUGUUGGC	23			
pmc-miR-785c-5p	UAAGUGAAUACUCUGUUAUGU	21	pcn-miR-8915-4-3p	CGGAUGGCCAGCUGCAGGUGACG	23	mcr-miR-9-2-3p	UCUUUGGUUAUCCAGUAGUAUU	22			
pmc-miR-7880b-3p	UGGUUGGAUCAGUUUGGUUUGG	22	pcn-miR-8915-5-3p	CGGAUGGCCAGCUGCAGGUGACA	23	mcr-miR-92a-1-3p	GAUUGCACUUGUCCCGGCCUUCU	23			
pmc-miR-7880q-3p	UUUGCGACCAAAAUCACUCUCU	22	pcn-miR-9015-5p	UCCCAGAGGAGACGAGAAAGUUG	23	mcr-miR-92a-2-3p	GAUUGCACUUGUCCCGGCCUUG	22			
pmc-miR-79-3p	GUAAAGCUAAAUUACCAGUG	20	pcn-miR-9120-3p	UCAGUCUCCCUCUCUCGCUAU	21	mcr-miR-92b-3p	UAUUGCACUCGUCCCGGCCUA	21			
pmc-miR-8250d-3p	UCCUUUAUUUGUCUGGGUGGAGGGU	25	pcn-miR-9-1-3p	UCAUACAGCUAGAUAACCAAAGA	23	mcr-miR-92e-3p	CGGUGUGGGUGGGUGCAUGG	20			
pmc-miR-8265-3p	UCUGAUACUCUUCGCUCCACCUUC	24	pcn-miR-9-1-5p	CCUUUGGUAACCUAGCUUUAUGA	23	mcr-miR-9-3-3p	UCAUACAGCUAGAUAACCAAAGA	23			
pmc-miR-8293-5p	AUGAAAGAUAAAAGUGUCUCGUG	23	pcn-miR-9-2-3p	UCAUACAGCUAGAUAACCAAAGA	23	mcr-miR-9358-3p	UUUGACAUGCUUGUUCCUGCAU	22			
pmc-miR-8311-3p	UGAUUGUGAGAUUCCCCCACCU	22	pcn-miR-9-2-5p	CCUUUGGUAACCUAGCUUUAUGA	23	mcr-miR-9-3-5p	CCUUUGGUAACCUAGCUUUAUGA	23			
pmc-miR-8335-3p	GUUGUUGUUGUUGUUUUGUCAGU	23	pcn-miR-92a-1-3p	GAUUGCACUUGUCCCGGCCUUG	22	mcr-miR-936-5p	ACAGGAGAGGGAGGAAGGGGAC	22			

pmc-miR-8398-3p	AGUUCUUUCUUUUUAGCAUGCA	22	pcn-miR-92a-2-3p	GAUUGCACUUGUCCCGGCCUUCU	23	mcr-miR-9392-3p	AUUAAAUGUUUUUCUAGUCAC	21			
pmc-miR-8-3p	UAAUACUGUCAGGUAAAGAUGUC	23	pcn-miR-92b-3p	UAUUGCACUCGUCCCGGCCUA	21	mcr-miR-943-3p	CUGACUGUUGCUGUCCGUUUU	21			
pmc-miR-8422-5p	GCAAUUAAAAGUAGCACAA	19	pcn-miR-92c-5p	AGGUUGGGAUGUGGGCUCUGUCGC	24	mcr-miR-9438-5p	AUACUACACAAGUGUCUAGUGU	22			
pmc-miR-8443-5p	ACUUUGCAUUCAUAUUUGA	19	pcn-miR-9-3-3p	UCAUACAGCUAGAUAACCAAAGA	23	mcr-miR-9505-5p	UGAUGUCUGUCAAAAUCCAAU	21			
pmc-miR-8460-5p	UAAUUAUAUUAUAUUUGCUU	20	pcn-miR-9341-1-3p	UCUCGGCCUUUUGGCUAAGAU	21	mcr-miR-9542a-3p	CCUGGCACUUUCUAAUUUCUGG	22			
pmc-miR-8462-3p	UGAUUAAUUUGAUAAGAUGA	20	pcn-miR-9341-2-3p	UCUCGGCCUUUUGGCUAAGAU	21	mcr-miR-9573-5p	UCAAAACUAGGAUUGUGAGGCU	22			
pmc-miR-8470-3p	CUGAGCAUAAGAAUAUGUUC	20	pcn-miR-9-3-5p	CCUUUGGUAACCUAGCUUUAUGA	23	mcr-miR-9592-3p	GACCUUAUUCAGACAAAGAAAC	22			
pmc-miR-84f-5p	UGAGGUAGUUUUAAAUGAAGCUU	23	pcn-miR-9388-5p	GUAUGUAUGUAUGUACAUAUAAU	23	mcr-miR-9598-3p	UAGUACUAGGAUUUUGAUUAGCU	23			
pmc-miR-85-3p	UACAAAGUAUUUGAAACCACAGAG	24	pcn-miR-9-4-3p	AUAAAGCUAGGUUACCAAAGGCA	23	mcr-miR-9640-5p	UCAGAUGGCAGAGCUGGACAAGG	23			
pmc-miR-8-5p	CAUCUUACCUAACAGCAUUAGA	22	pcn-miR-9-4-5p	UCUUUGGUUAUCUAGCUGUAUGAUU	25	mcr-miR-965-5p	GGGGAGAAGUUAUUGCUGCGAAG	23			
pmc-miR-8834a-5p	UGCCGGGCCUGGAGGCCAGCUGU	23	pcn-miR-9543a-3p	AAAUAUUGCUUGUUUAUU	18	mcr-miR-96b-3p	AUUAUACACCGGUGCCAAGUCA	22			
pmc-miR-888-5p	GACUGACACCUCUUUGUCCAGC	22	pcn-miR-96-5p	CAAUCAUGUGCAGUGCAGUUCU	22	mcr-miR-96b-5p	AUUUGGCACUUGUGGAAUAAUCG	23			
pmc-miR-8993-5p	CAGGGUCAAGGGUCAAACAUGGU	23	pcn-miR-969-3p	GAGUUCCACUAAGCAAGUUAU	21	mcr-miR-9771g-3p	GAAAAGUCAUGACGCAUUUUU	21			
pmc-miR-9120-5p	UCAGUCUCCCUCUCUCACACA	21	pcn-miR-96b-3p	AUUAUACACCGGUGCCAAGUCA	22	mcr-miR-981-3p	UUCGUUGUCGUCGAAACCUGCCC	23			
pmc-miR-9-1-3p	UCAUACAGCUAGAUAACCAAAGA	23	pcn-miR-96b-5p	AUUUGGCACUUGUGGAAUAAUCG	23	mcr-miR-981-5p	CGGGUUUCGCGGCUGGCGAACA	22			
pmc-miR-9-1-5p	CCUUUGGUAACCUAGCUUUAUGA	23	pcn-miR-972-5p	UAAAUAUUUUUUUUGUCAACU	21	mcr-miR-9896-3p	ACAAUAAUCGGACACACCGCCA	22			
pmc-miR-9170-3p	UUUGCAUCCUGGCUCUGCUAUCU	23	pcn-miR-981-3p	UUCGUUGUCGUCGAAACCUGCCC	23	mcr-miR-9934-5p	AUGGUCUUGAUAUGUCCAUUUC	22			
pmc-miR-9-2-3p	AUAAAGCUAGGUUACCAAAGGCA	23	pcn-miR-981-5p	CGGGUUUCGCGGCUUGCGAACA	22	mcr-miR-99-3p	CAAGCUCGCCUCUGUGCUGACGG	23			
pmc-miR-9256b-3p	UAAUAAUCAGGCCACUACCUCU	22	pcn-miR-9891-3p	UCGGCUUCGUCCUCGUCUUGG	21	mcr-miR-994-3p	CACAGUUGCUGUUUCUUAGUUUG	23			
pmc-miR-9-2-5p	UCUUUGGUUAUCUAGCUGUAUGAUU	25	pcn-miR-995-3p	GCCCGGAUACUGUGUGUGGCUCA	23	mcr-miR-9945-5p	CUGUCCACCUGAGCCCAUAGAC	22			
pmc-miR-92c-1-3p	GAUUGCACUUGUCCCGGCCUUCU	23				mcr-miR-9b-3p	UAAAGCUGAAGCAACUAUUGUU	22			
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pmc-miR-92b-3p	UAUUGCACUCGUCCCGGCCUA	21									
pmc-miR-92c-5p	AGGUUGGGAUGUGGGCUCUGUCGC	24									
pmc-miR-9341-3p	UCUCGGCCUUUUGGCUAAGAU	21									
pmc-miR-9369-5p	AUACAUAUUCUUCUUUCCAUUU	22									
pmc-miR-9382-5p	AUCACAGUGUGGCUGAAAUAU	21									
pmc-miR-9434-3p	UCUGACAGGAAUUCUGAACCCUG	23									
pmc-miR-9505-5p	UGAUGUCUGUCAAAAUGUGAU	21									
pmc-miR-9542a-3p	CCUGGCACUUUCUAAUUUCUGG	22									
pmc-miR-9543a-3p	AAAUAUUGCUUGUUUAUU	18									
pmc-miR-96-5p	CAAUCAUGUGCAGUGCAGUUCU	22									
pmc-miR-969-3p	GAGUUCCACUAAGCAAGUUAU	21									
pmc-miR-96b-3p	AUUAUACACCGGUGCCAAGUCA	22									
pmc-miR-96b-5p	AUUUGGCACUUGUGGAAUAAUCG	23									
pmc-miR-970-5p	AGCCUUGCAUGAGCUCUAGGUGUCU	25									
pmc-miR-971-3p	AUGGUGUUCUAGCCUCCAUCGA	22									
pmc-miR-981-3p	UUCGUUGUCGUCGAAACCUGCCC	23									
pmc-miR-981-5p	CGGGUUUCGCGGCUUGCGAACA	22									
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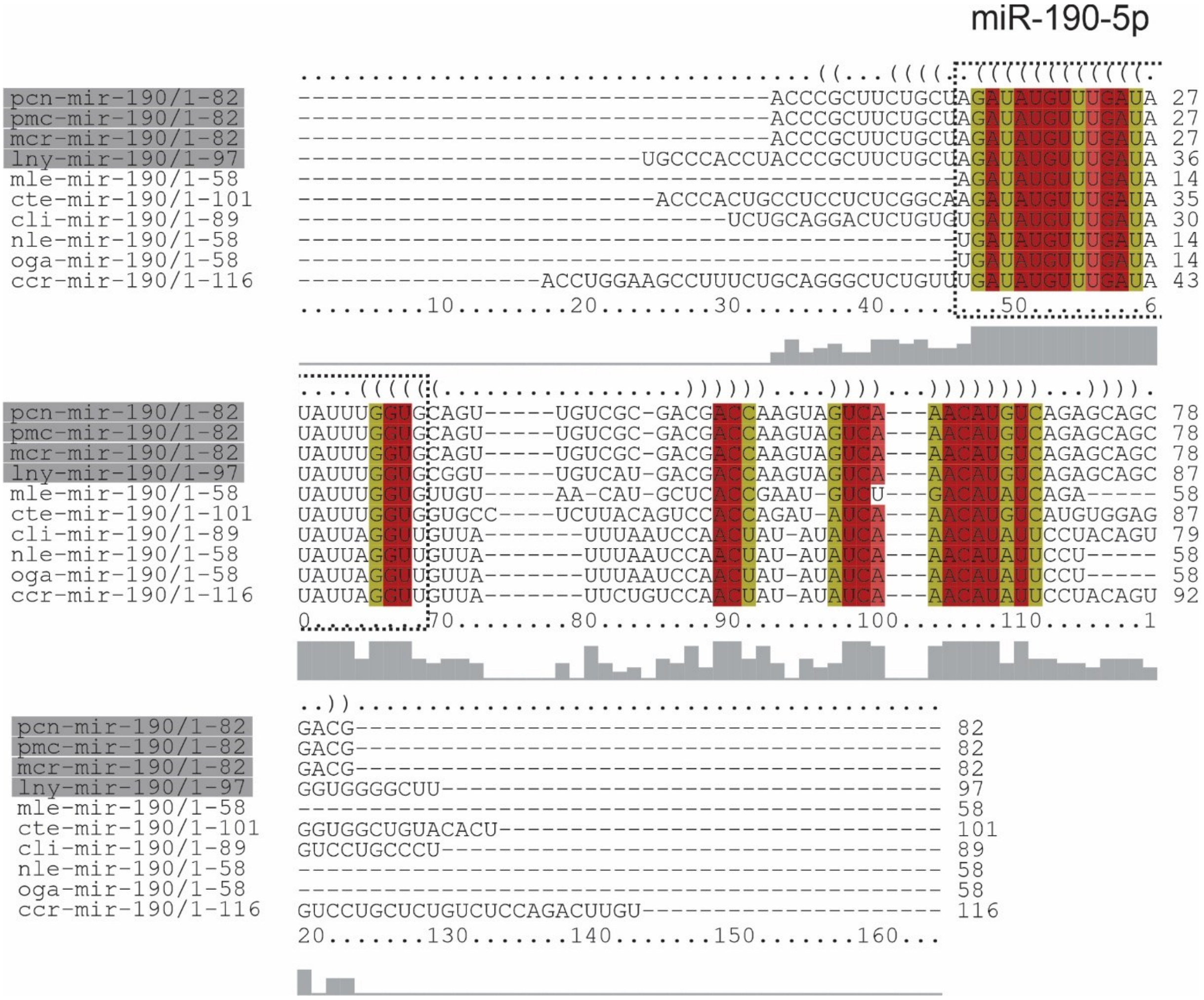
SUPPLEMENTARY DATA III

Bilaterial specific miRNAs

mir-190



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pmc-mir-190/1-82    ---------------------------------ACCCGCUUCUGCUAGAUAUGUUUGAUA 27
mcr-mir-190/1-82    ---------------------------------ACCCGCUUCUGCUAGAUAUGUUUGAUA 27
lny-mir-190/1-97    ------------------------UGCCCACCUACCCGCUUCUGCUAGAUAUGUUUGAUA 36
mle-mir-190/1-58    ----------------------------------------------AGAUAUGUUUGAUA 14
cte-mir-190/1-101   -------------------------ACCCACUGCCUCCUCUCGGCAAGAUAUGUUUGAUA 35
cli-mir-190/1-89    ------------------------------UCUGCAGGACUCUGUGUGAUAUGUUUGAUA 30
nle-mir-190/1-58    ----------------------------------------------UGAUAUGUUUGAUA 14
oga-mir-190/1-58    ----------------------------------------------UGAUAUGUUUGAUA 14
ccr-mir-190/1-116   -----------------ACCUGGAAGCCUUUCUGCAGGGCUCUGUUUGAUAUGUUUGAUA 43
                    .........10........20........30........40........50........6

                    ....((((((.................))))))....))))...))))))))...)))).
pcn-mir-190/1-82    UAUUUGGUGCAGU-----UGUCGC-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 78
pmc-mir-190/1-82    UAUUUGGUGCAGU-----UGUCGC-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 78
mcr-mir-190/1-82    UAUUUGGUGCAGU-----UGUCGC-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 78
lny-mir-190/1-97    UAUUUGGUGCGGU-----UGUCAU-GACGACCAAGUAGUCA---AACAUGUCAGAGCAGC 87
mle-mir-190/1-58    UAUUUGGUGUUGU-----AA-CAU-GCUCACCGAAU-GUCU---GACAUAUCAGA----- 58
cte-mir-190/1-101   UAUUUGGUGGUGCC----UCUUACAGUCCACCAGAU-AUCA---AACAUGUCAUGUGGAG 87
cli-mir-190/1-89    UAUUAGGUUGUUA-------UUUAAUCCAACUAU-AUAUCA---AACAUAUUCCUACAGU 79
nle-mir-190/1-58    UAUUAGGUUGUUA-------UUUAAUCCAACUAU-AUAUCA---AACAUAUUCCU----- 58
oga-mir-190/1-58    UAUUAGGUUGUUA-------UUUAAUCCAACUAU-AUAUCA---AACAUAUUCCU----- 58
ccr-mir-190/1-116   UAUUAGGUUGUUA-------UUCUGUCCAACUAU-AUAUCA---AACAUAUUCCUACAGU 92
                    0........70........80........90........100.......110.......1

                    ..)).........................................
pcn-mir-190/1-82    GACG----------------------------------------- 82
pmc-mir-190/1-82    GACG----------------------------------------- 82
mcr-mir-190/1-82    GACG----------------------------------------- 82
lny-mir-190/1-97    GGUGGGGCUU----------------------------------- 97
mle-mir-190/1-58    --------------------------------------------- 58
cte-mir-190/1-101   GGUGGCUGUACACU------------------------------- 101
cli-mir-190/1-89    GUCCUGCCCU----------------------------------- 89
nle-mir-190/1-58    --------------------------------------------- 58
oga-mir-190/1-58    --------------------------------------------- 58
ccr-mir-190/1-116   GUCCUGCUCUGUCUCCAGACUUGU--------------------- 116
                    20.......130.......140.......150.......160...
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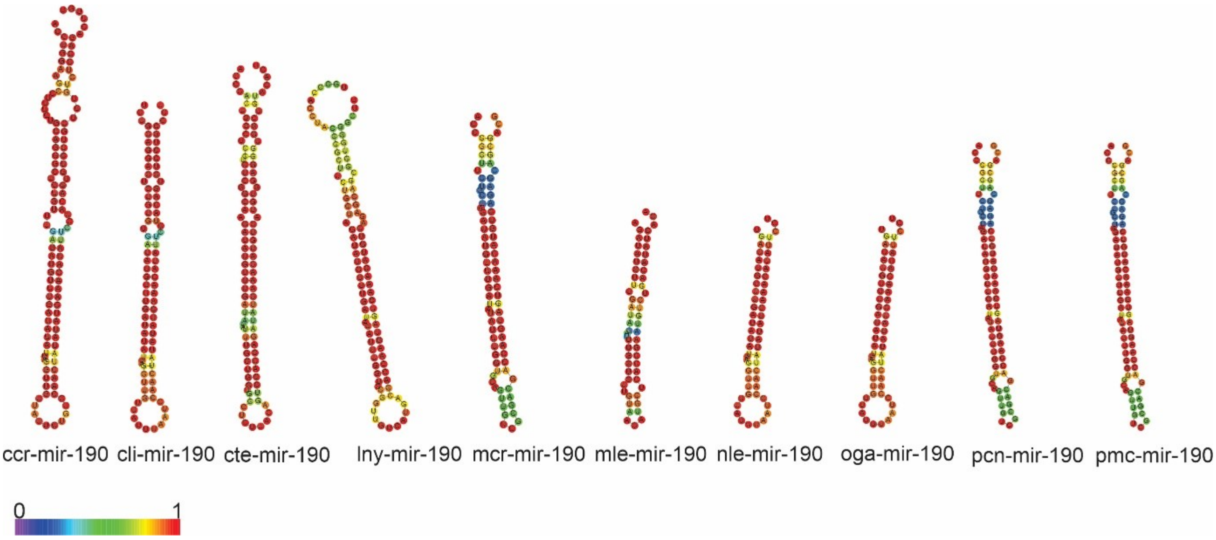
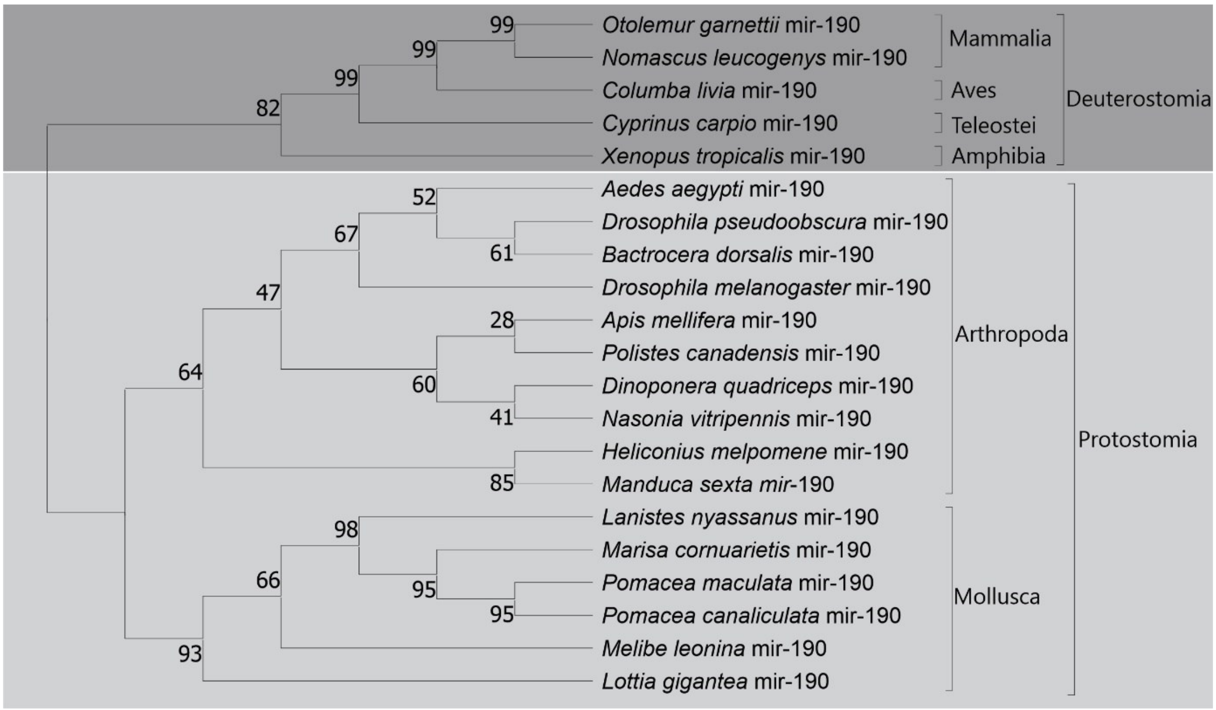
Supplementary figure 1: Alignment of mi-190 in Ampullariidae species and their orthologs; pcn - *P. canaliculata*, pmc - *P. maculala*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, mle – *M. leonina*, cte - C. teleta, cli - *Columba livia*, nle - *Nomascus leucogenys*, oga - *Otolemur garnettii*, ccr - *Cyprinus carpio*.

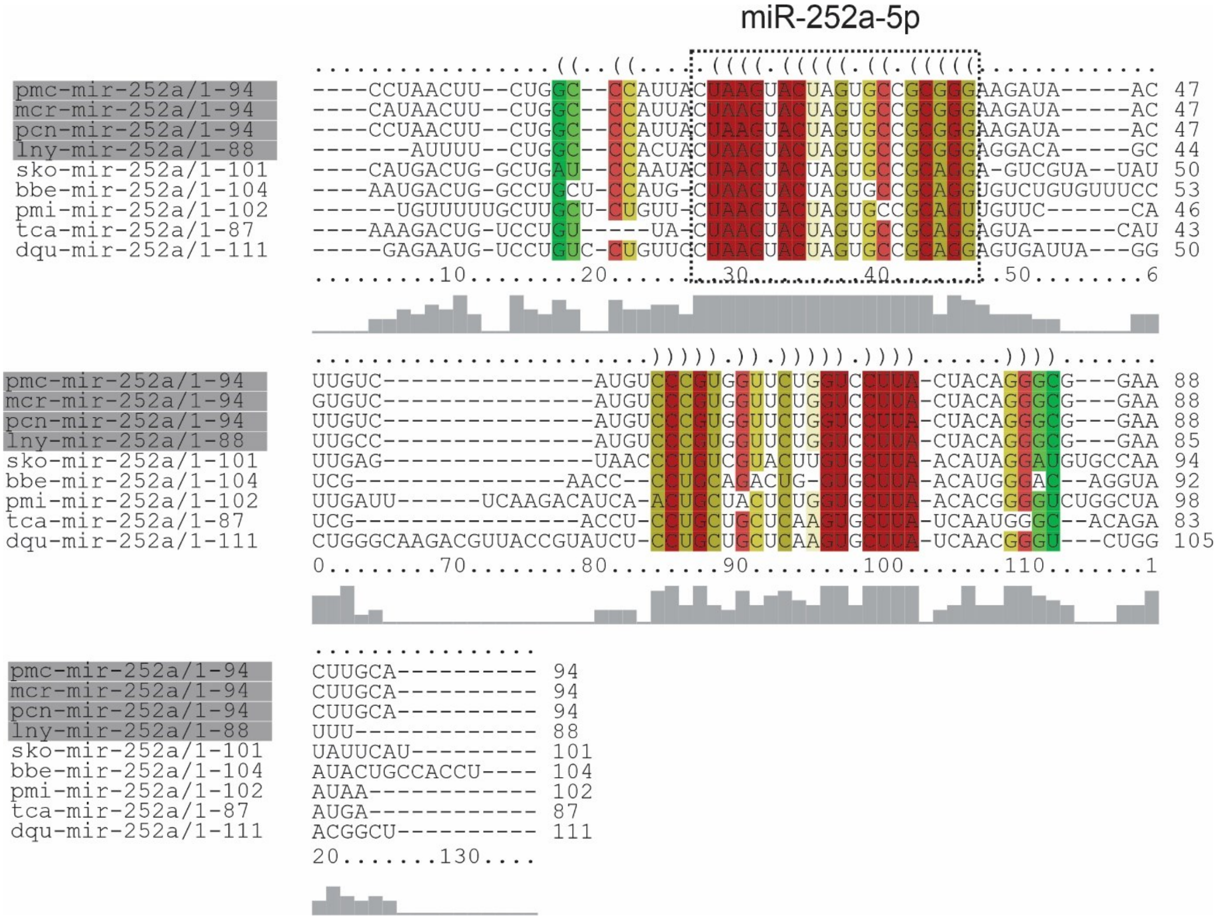


Supplementary figure 2: Secondary structure of mir-190 in Ampullariidae species and their orthologs; pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuaritis*, lny - *L. nyassanus*, mle - *M. leonina*, cte - *C. teleta*, cli - *Columba livia*, nle - *Nomascus leucogenys*, oga - *Otolemur garnettii*, ccr - *Cyprinus carpio*.



Supplementary figure 3: Phylogenetic distribution of mir- in Ampullariidae species and their orthologs.

mir-252a



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                                              miR-252a-5p
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mcr-mir-252a/1-94       ----CAUAACUU--CUGGC--CCAUUACUAAGUACUAGUGCCGCGGGAAGAUA-----AC 47
pcn-mir-252a/1-94       ----CCUAACUU--CUGGC--CCAUUACUAAGUACUAGUGCCGCGGGAAGAUA-----AC 47
lny-mir-252a/1-88       -------AUUUU--CUGGC--CCACUACUAAGUACUAGUGCCGCGGGAGGACA-----GC 44
sko-mir-252a/1-101      ----CAUGACUG-GCUGAU--CCAAUACUAAGUACUAGUGCCGCAGGA-GUCGUA--UAU 50
bbe-mir-252a/1-104      ----AAUGACUG-GCCUGCU-CCAUG-CUAAGUACUAGUGCCGCAGGUGUCUGUGUUUCC 53
pmi-mir-252a/1-102      ------UGUUUUUGCUUGCU-CUGUU-CUAAGUACUAGUGCCGCAGUUGUUC------CA 46
tca-mir-252a/1-87       ----AAAGACUG-UCCUGU-----UA-CUAAGUACUAGUGCCGCAGGAGUA------CAU 43
dqu-mir-252a/1-111      -----GAGAAUG-UCCUGUC-CUGUUCCUAAGUACUAGUGCCGCAGGAGUGAUUA---GG 50
                        .........10........20........30........40........50........6

                        ........................))))).)).))))).)))).....))))).......
pmc-mir-252a/1-94       UUGUC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA 88
mcr-mir-252a/1-94       GUGUC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA 88
pcn-mir-252a/1-94       UUGUC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA 88
lny-mir-252a/1-88       UUGCC---------------AUGUCCCGUGGUUCUGGUCCUUA-CUACAGGGCG---GAA 85
sko-mir-252a/1-101      UUGAG---------------UAACCCUGUCGUACUUGUGCUUA-ACAUAGGAUGUGCCAA 94
bbe-mir-252a/1-104      UCG---------------AACC--CCUGCAGACUG-GUGCUUA-ACAUGGGAC--AGGUA 92
pmi-mir-252a/1-102      UUGAUU------UCAAGACAUCA-ACUGCUACUCUGGUGCUUA-ACACGGGGUCUGGCUA 98
tca-mir-252a/1-87       UCG----------------ACCU-CCUGCUGCUCAAGUGCUUA-UCAAUGGGC--ACAGA 83
dqu-mir-252a/1-111      CUGGGCAAGACGUUACCGUAUCU-CCUGCUGCUCAAGUGCUUA-UCAACGGGU---CUGG 105
                        0........70........80........90........100.......110.......1

                        ................
pmc-mir-252a/1-94       CUUGCA---------- 94
mcr-mir-252a/1-94       CUUGCA---------- 94
pcn-mir-252a/1-94       CUUGCA---------- 94
lny-mir-252a/1-88       UUU------------- 88
sko-mir-252a/1-101      UAUUCAU--------- 101
bbe-mir-252a/1-104      AUACUGCCACCU---- 104
pmi-mir-252a/1-102      AUAA------------ 102
tca-mir-252a/1-87       AUGA------------ 87
dqu-mir-252a/1-111      ACGGCU---------- 111
                        20.......130....
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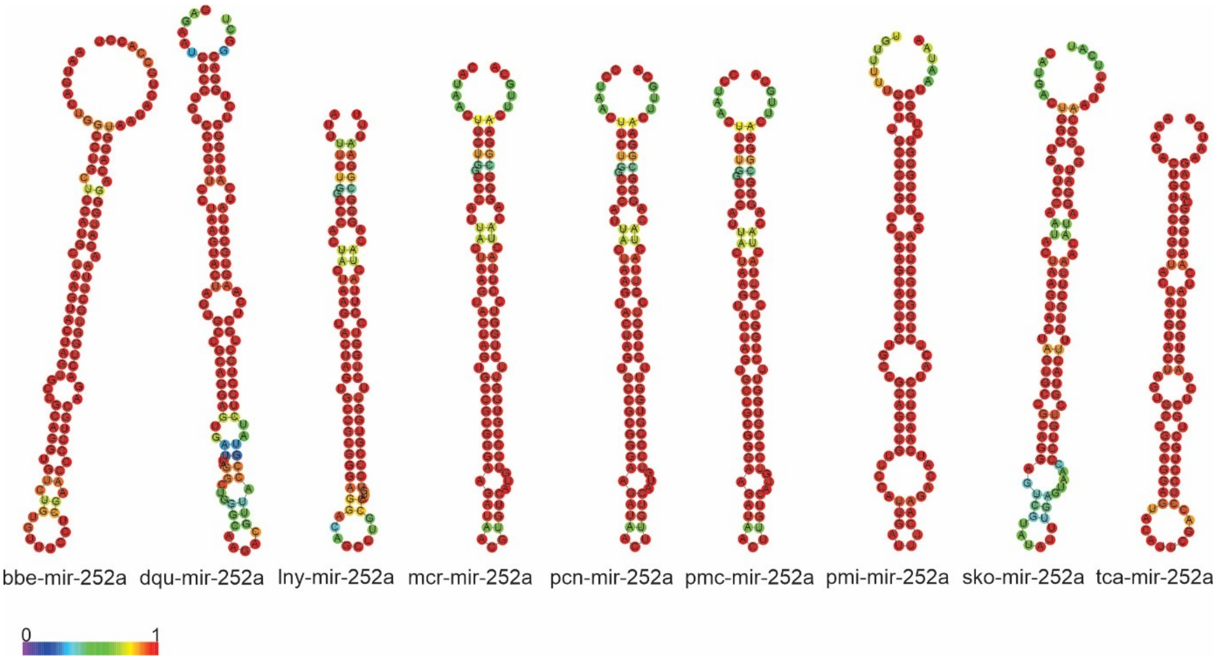
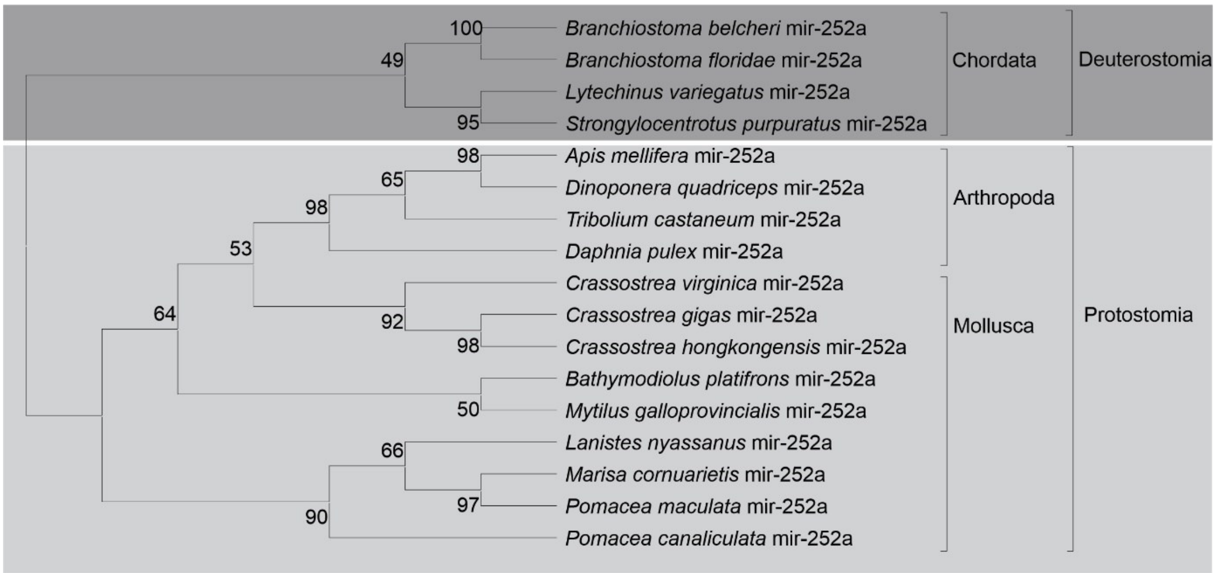
Supplementary figure 4: Alignment of mir-252a in Ampullariidae species and their orthologs; pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, sko - *Saccoglossus kowalevskii*, bbe - *Branchiostoma belcherimle*, dqu - *Dinoponera quadríceps*, pmi - *Patiria miniata*, tca - *Tribolium castaneum*

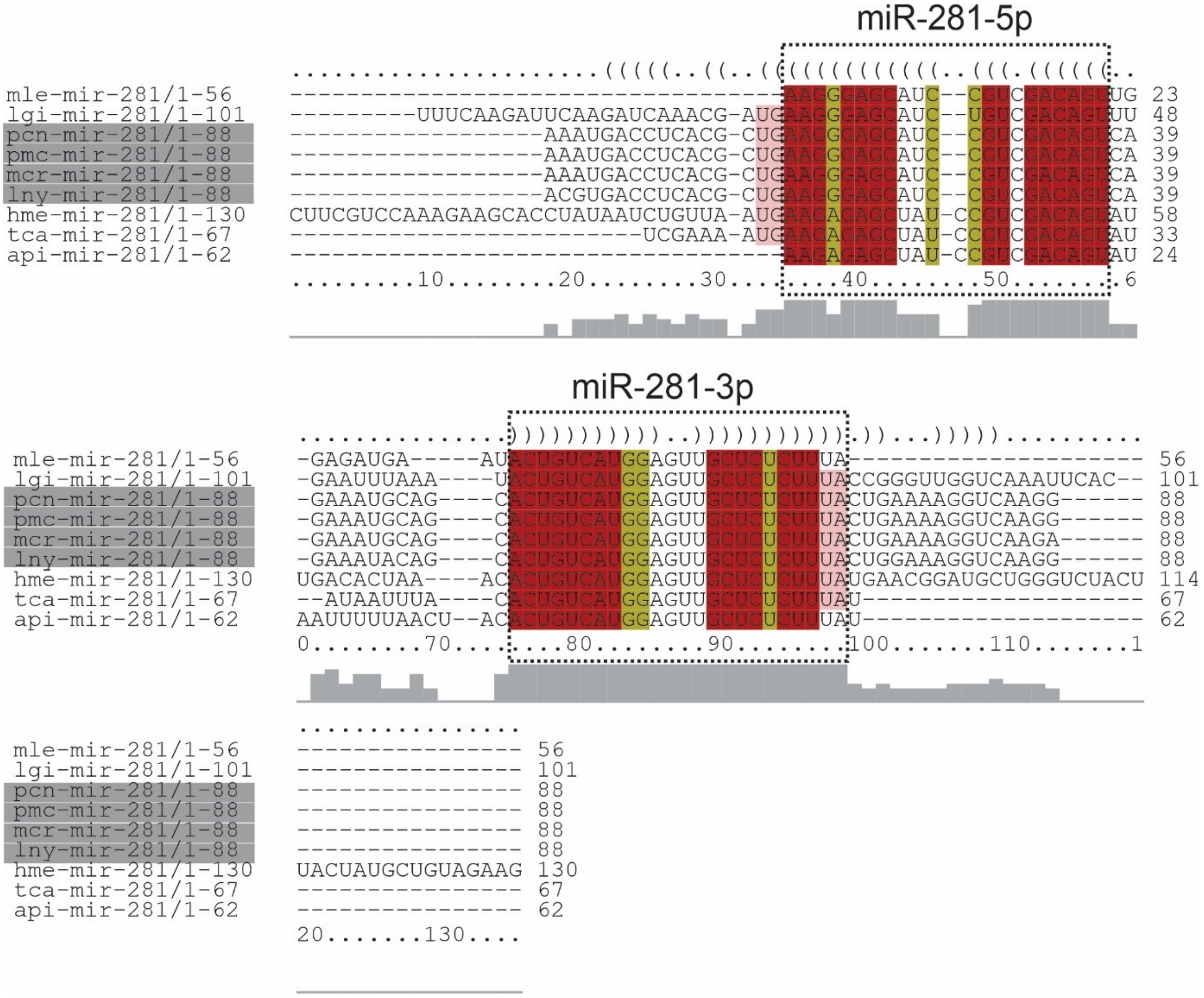


Supplementary figure 5: Secondary structure of mir-252a in Ampullariidae species and their orthologs; pcn - *P. canaliculata*, pmc - *P. maculata*, mcr - *M. cornuarietis*, lny - *L. nyassanus*, sko - *Saccoglossus kowalevskii,* bbe - *Branchiostoma belcherimle*, dqu - *Dinoponera quadríceps*, pmi - *Patiria miniata*, tca - *Tribolium castaneum.*



Supplementary figure 6: Phylogenetic distribution of mir-252a in Ampullariidae species and their orthologs.

mir-281



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                 ......................(((((..((..((((((((((((((..(((.((((((..
mle-mir-281/1-56  -----------------------------------AAGGGAGCAUC--CGUCGACAGUUG 23
lgi-mir-281/1-101 ---------UUUCAAGAUUCAAGAUCAAACG-AUGAAGGGAGCAUC--UGUCGACAGUUU 48
pcn-mir-281/1-88  ------------------AAAUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
pmc-mir-281/1-88  ------------------AAAUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
mcr-mir-281/1-88  ------------------AAAUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
lny-mir-281/1-88  ------------------ACGUGACCUCACG-CUGAAGGGAGCAUC--CGUCGACAGUCA 39
hme-mir-281/1-130 CUUCGUCCAAAGAAGCACCUAUAAUCUGUUA-AUGAACAGAGCUAU-CCGUCGACAGUAU 58
tca-mir-281/1-67  -------------------------UCGAAA-AUGAACAGAGCUAU-CCGUCGACAGUAU 33
api-mir-281/1-62  -----------------------------------AAGAGAGCUAU-CCGUCGACAGUAU 24
                  ........10........20........30........40........50........6

                  ...............))))))))))).))))))))))).))...)))))..........
mle-mir-281/1-56  -GAGAUGA-----AUACUGUCAUGGAGUUGCUCUCUUUA--------------------- 56
lgi-mir-281/1-101 -GAAUUUAAA----UACUGUCAUGGAGUUGCUCUCUUUACCGGGUUGGUCAAAUUCAC-- 101
pcn-mir-281/1-88  -GAAAUGCAG----CACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGG------ 88
pmc-mir-281/1-88  -GAAAUGCAG----CACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGG------ 88
mcr-mir-281/1-88  -GAAAUGCAG----CACUGUCAUGGAGUUGCUCUCUUUACUGAAAAGGUCAAGA------ 88
lny-mir-281/1-88  -GAAAUACAG----CACUGUCAUGGAGUUGCUCUCUUUACUGGAAAGGUCAAGG------ 88
hme-mir-281/1-130 UGACACUAA----ACACUGUCAUGGAGUUGCUCUCUUUAUGAACGGAUGCUGGGUCUACU 114
tca-mir-281/1-67  --AUAAUUUA----CACUGUCAUGGAGUUGCUCUCUUUAU-------------------- 67
api-mir-281/1-62  AAUUUUUAACU--ACACUGUCAUGGAGUUGCUCUCUUUAU-------------------- 62
                  0........70........80........90........100.......110.......1

                  ................
mle-mir-281/1-56  ---------------- 56
lgi-mir-281/1-101 ---------------- 101
pcn-mir-281/1-88  ---------------- 88
pmc-mir-281/1-88  ---------------- 88
mcr-mir-281/1-88  ---------------- 88
lny-mir-281/1-88  ---------------- 88
hme-mir-281/1-130 UACUAUGCUGUAGAAG 130
tca-mir-281/1-67  ---------------- 67
api-mir-281/1-62  ---------------- 62
                  20.......130....
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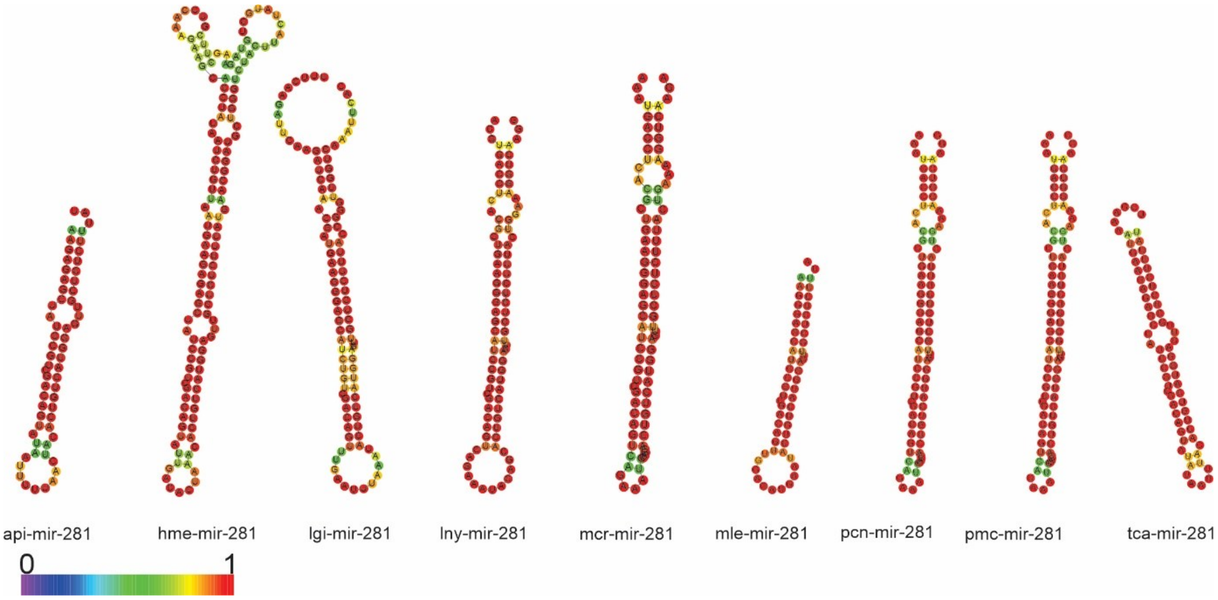
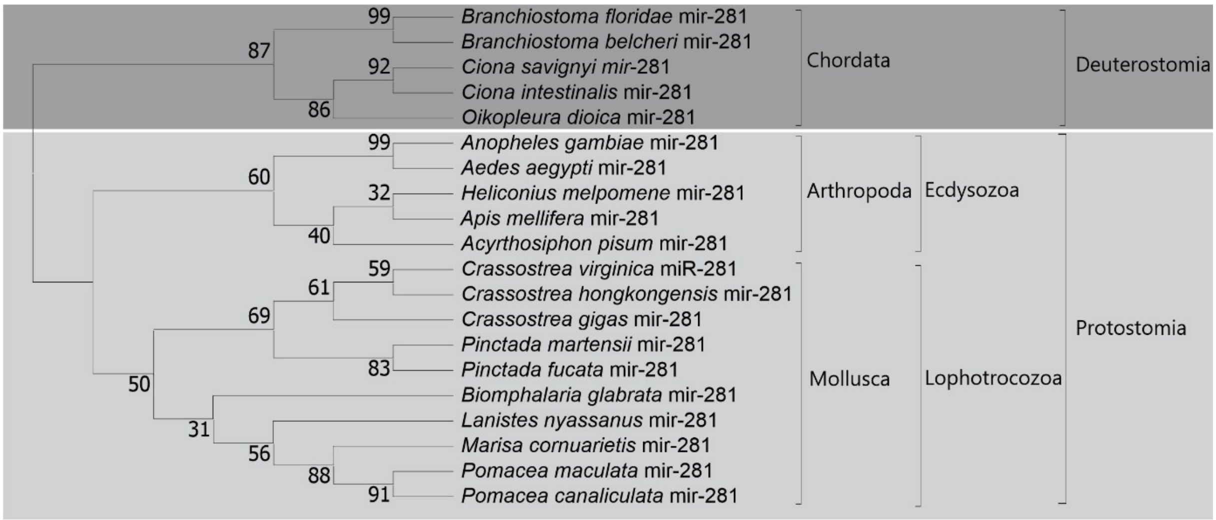
Supplementary figure 7: Alignment of mir-281 in Ampullariidae species and their orthologs; api - *Acyrthosiphon pisum*, hme - *Heliconius melpomene*, lny - *L. nyassanus*, lgi - *L. gigantea,* mcr - *M. cornuarietis*, mle - *M. leonina,* pcn - *P. canaliculata*, pmc - *P. maculata*, tca - *Tribolium castaneum*.

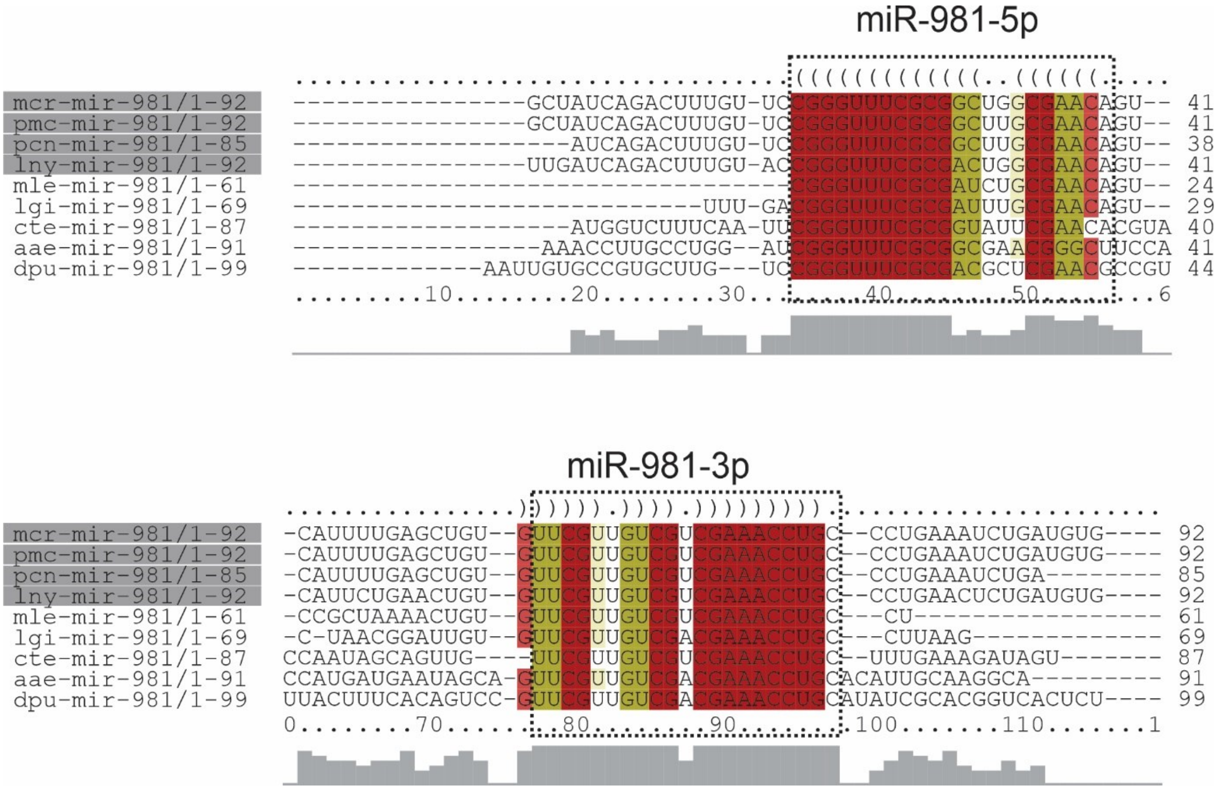


Supplementary figure 8: Secondary structure of mir-281 in Ampullariidae species and their orthologs; api - *Acyrthosiphon pisum*, hme - *Heliconius melpomene*, lny - *L. nyassanus*, lgi - *L. gigantea,* mcr - *M. cornuarietis*, mle - *M. leonina,* pcn - *P. canaliculata*, pmc - *P. maculata*, tca - *Tribolium castaneum.*

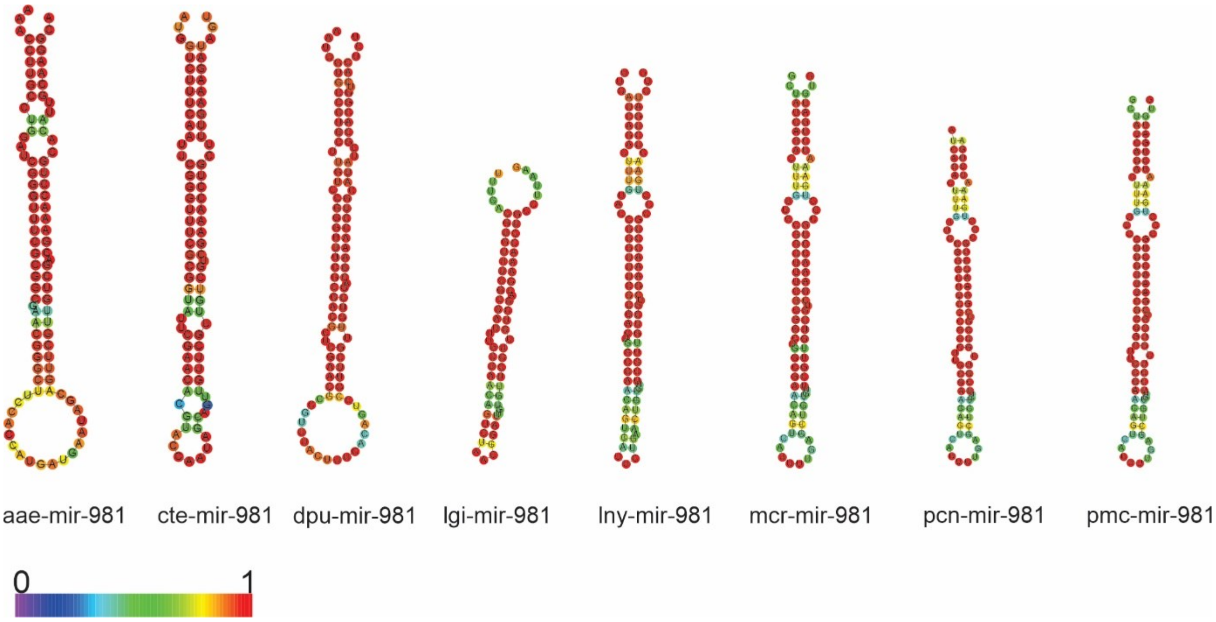


Supplementary figure 9: Phylogenetic distribution of mir-281 in Ampullariidae species and their orthologs.

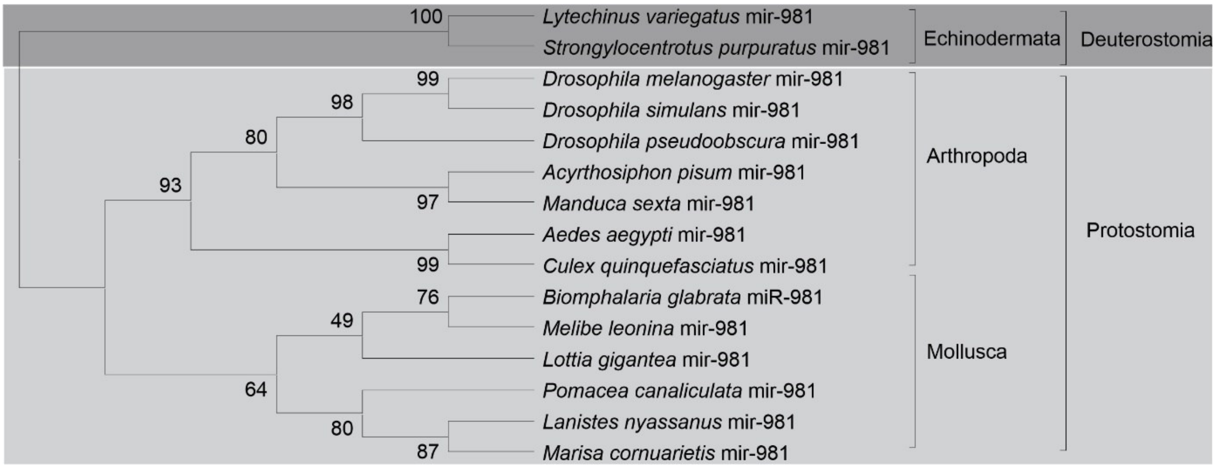
mir-981



Supplementary figure 10: Alignment of mir-981 in Ampullariidae species and their orthologs; aae - Aedes aegypti, dpu - Daphnia pulex, mle – M. leonina, lny - L. nyassanus, lgi - L. gigantea, mcr - M. cornuarietis, pcn - P. canaliculata, pmc - P. maculata, cte - C. teleta.



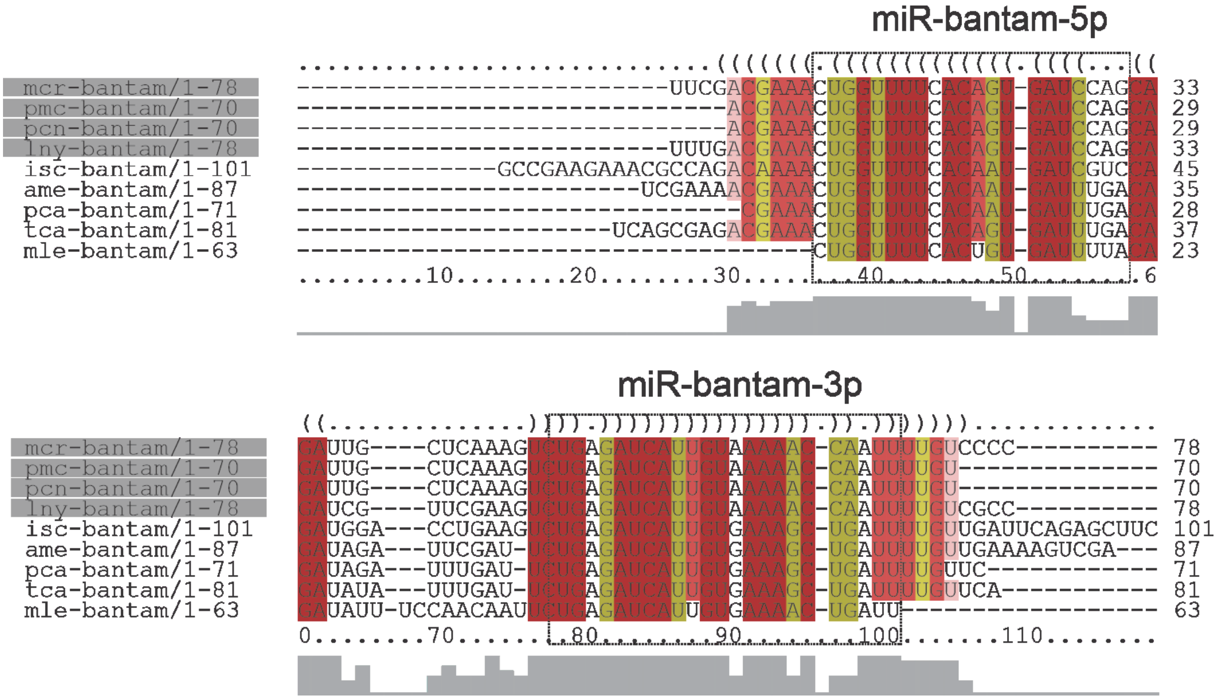
Supplementary figure 11: Secondary structure of mir-981 in Ampullariidae species and their orthologs; aae - *Aedes aegypti,* dpu - *Daphnia pulex,* cte - *C. teleta,* lny - *L. nyassanus,* lgi - *L. gigantea,* mcr - *M. cornuarietis,* pcn - *P. canaliculata,* pmc - *P. maculata.*



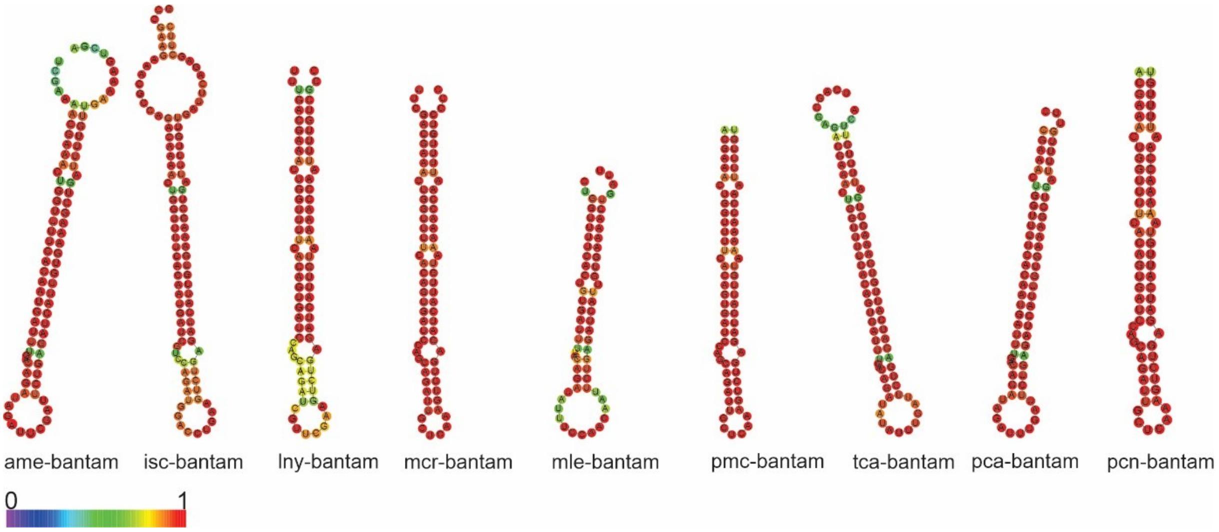
Supplementary figure 12: Phylogenetic distribution of mir-981 in Ampullariidae species and their orthologs.

Protostome specific miRNAs

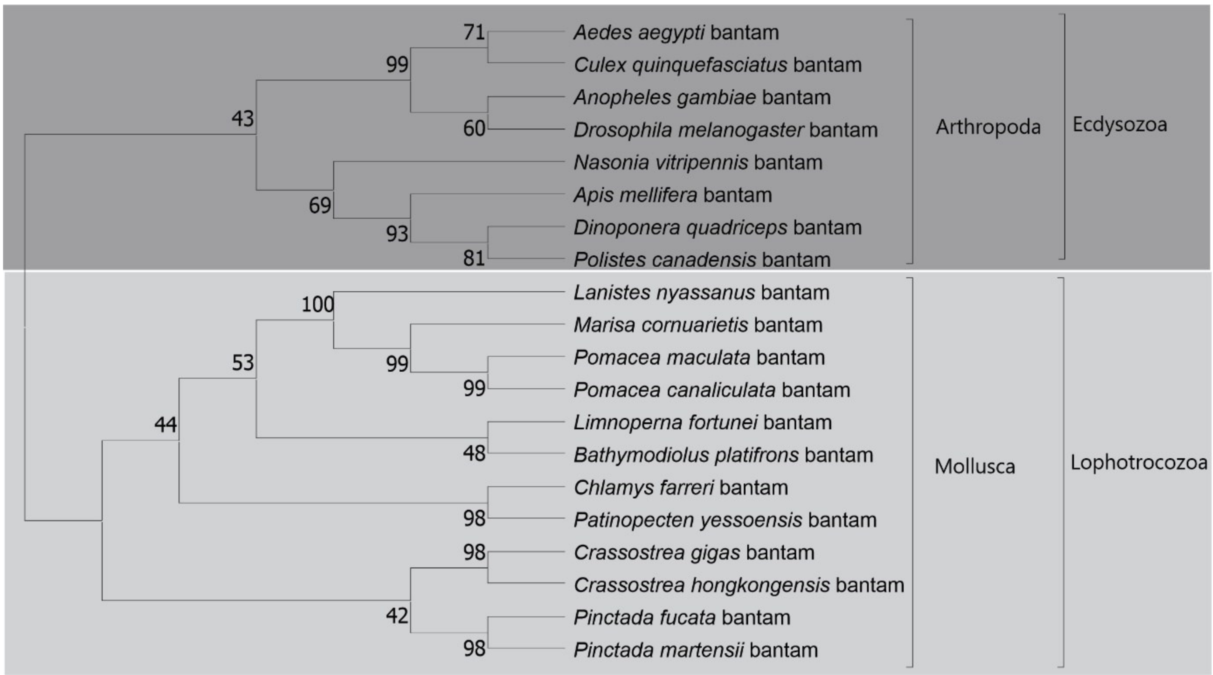
mir-bantam



Supplementary figure 13: Alignment of mi-bantam in Ampullariidae species and their orthologs; ame - *Apis melífera,* isc - *Ixodes scapularis,* lny - *L. nyassanus,* mcr - *M. cornuarietis,* pca - *Polistes canadenses,* pcn - *P. canaliculata,* pmc - *P. maculata*, tca - *Tribolium castaneum*, mle - *M. leonina.*

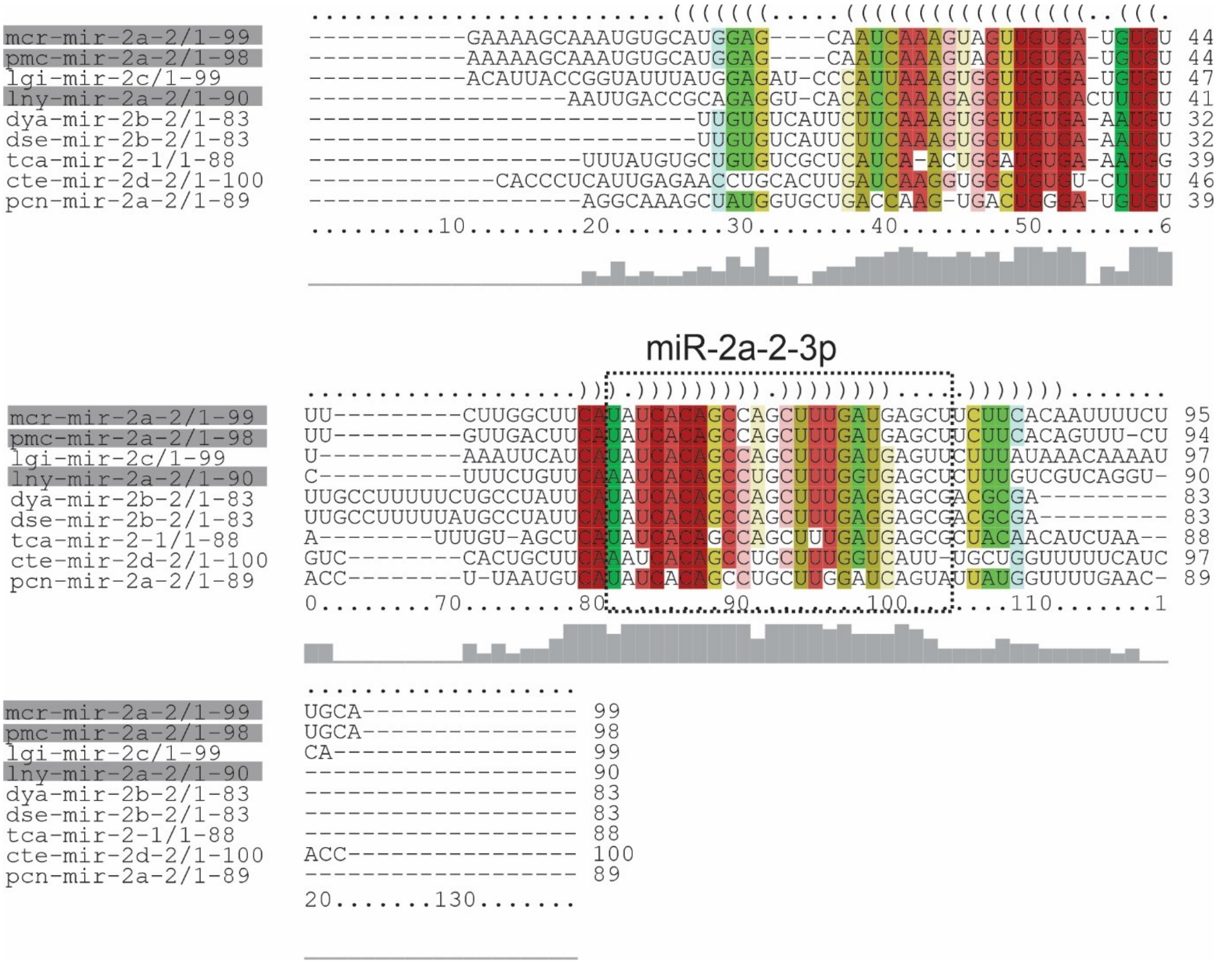


Supplementary figure 14: Secondary structure of mir-bantam in Ampullariidae species and their orthologs; ame – *Apis melífera,* isc - *Ixodes scapularis,* lny - *L. nyassanus,* mcr - *M. cornuarietis,* pca - *Polistes canadenses,* pcn - *P. canaliculata,* pmc - *P. maculata*, tca - *Tribolium castaneum*, mle – *M. leonina.*



Supplementary figure 15: Phylogenetic distribution of mir-bantam in Ampullariidae species and their orthologs.

mir- 2a-2



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                       .........................(((((((.....(((((((((((((((((..(((.
mcr-mir-2a-2/1-99      -----------GAAAAGCAAAUGUGCAUGGAG----CAAUCAAAGUAGUUGUGA-UGUGU 44
pmc-mir-2a-2/1-98      -----------AAAAAGCAAAUGUGCAUGGAG----CAAUCAAAGUAGUUGUGA-UGUGU 44
lgi-mir-2c/1-99        -----------ACAUUACCGGUAUUUAUGGAGAU-CCCAUUAAAGUGGUUGUGA-UGUGU 47
lny-mir-2a-2/1-90      ------------------AAUUGACCGCAGAGGU-CACACCAAAGAGGUUGUGACUUUGU 41
dya-mir-2b-2/1-83      ----------------------------UUGUGUCAUUCUUCAAAGUGGUUGUGA-AAUGU 32
dse-mir-2b-2/1-83      ----------------------------UUGUGUCAUUCUUCAAAGUGGUUGUGA-AAUGU 32
tca-mir-2-1/1-88       --------------------UUUAUGUGCUGUGUCGCUCAUCA-ACUGGAUGUGA-AAUGG 39
cte-mir-2d-2/1-100     -------------CACCCUCAUUGAGAACCUGCACUUGAUCAAGGUGGCUGUGU-CUUGU 46
pcn-mir-2a-2/1-89      --------------------AGGCAAAGCUAUGGUGCUGACCAAG-UGACUGGGA-UGUGU 39
                       .........10........20........30........40........50........6

                       ...................))).))))))))).))))))))......)))))))......
mcr-mir-2a-2/1-99      UU---------CUUGGCUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAAUUUUCU 95
pmc-mir-2a-2/1-98      UU---------GUUGACUUCAUAUCACAGCCAGCUUUGAUGAGCUUCUUCACAGUUU-CU 94
lgi-mir-2c/1-99        U----------AAAUUCAUCAUAUCACAGCCAGCUUUGAUGAGUUCUUUAUAAACAAAAU 97
lny-mir-2a-2/1-90      C----------UUUCUGUUCAAAUCACAGCCUGCUUUGGUGAGCUCUUUGUCGUCAGGU- 90
dya-mir-2b-2/1-83      UUGCCUUUUUCUGCCUAUUCAUAUCACAGCCAGCUUUGAGGAGCGACGCGA--------- 83
dse-mir-2b-2/1-83      UUGCCUUUUUAUGCCUAUUCAUAUCACAGCCAGCUUUGAGGAGCGACGCGA--------- 83
tca-mir-2-1/1-88       A--------UUUGU-AGCUCAUAUCACAGCCAGCUUUGAUGAGCGCUACAACAUCUAA-- 88
cte-mir-2d-2/1-100     GUC--------CACUGCUUCAAAUCACAGCCUGCUUUGGUCAUU-UGCUGGUUUUUCAUC 97
pcn-mir-2a-2/1-89      ACC--------U-UAAUGUCAUAUCACAGCCUGCUUGGAUCAGUAUUAUGGUUUUGAAC- 89
                       0........70........80........90........100.......110.......1

                       ...................
mcr-mir-2a-2/1-99      UGCA--------------- 99
pmc-mir-2a-2/1-98      UGCA--------------- 98
lgi-mir-2c/1-99        CA----------------- 99
lny-mir-2a-2/1-90      ------------------- 90
dya-mir-2b-2/1-83      ------------------- 83
dse-mir-2b-2/1-83      ------------------- 83
tca-mir-2-1/1-88       ------------------- 88
cte-mir-2d-2/1-100     ACC---------------- 100
pcn-mir-2a-2/1-89      ------------------- 89
                       20.......130.......
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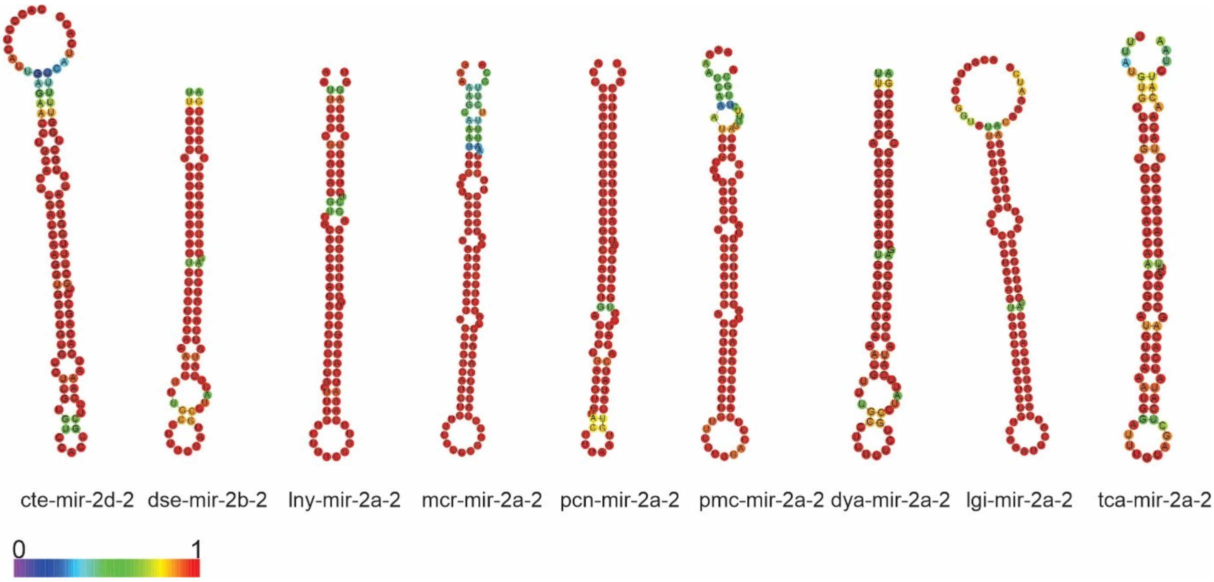
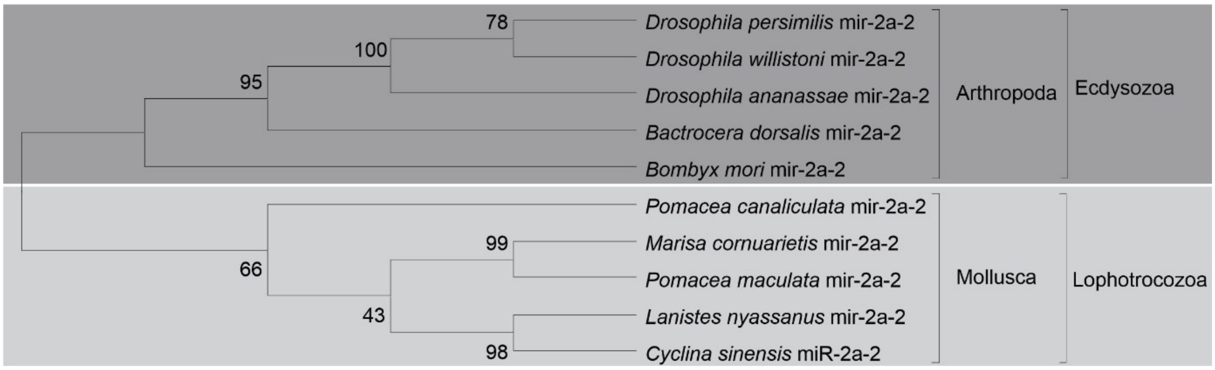
Supplementary figure 16: Alignment of mir-2a-2 in Ampullariidae species and their orthologs; cte - *C. teleta*, dse - *Drosophila sechellia*, lny - *L. nyassanus,* mcr - *M. cornuarietis,* pcn - *P. canaliculata,* pmc - *P. maculata*, dya - *Drosophila yakuba*, lgi- *L. gigantea,* tca - *Tribolium castaneum.*

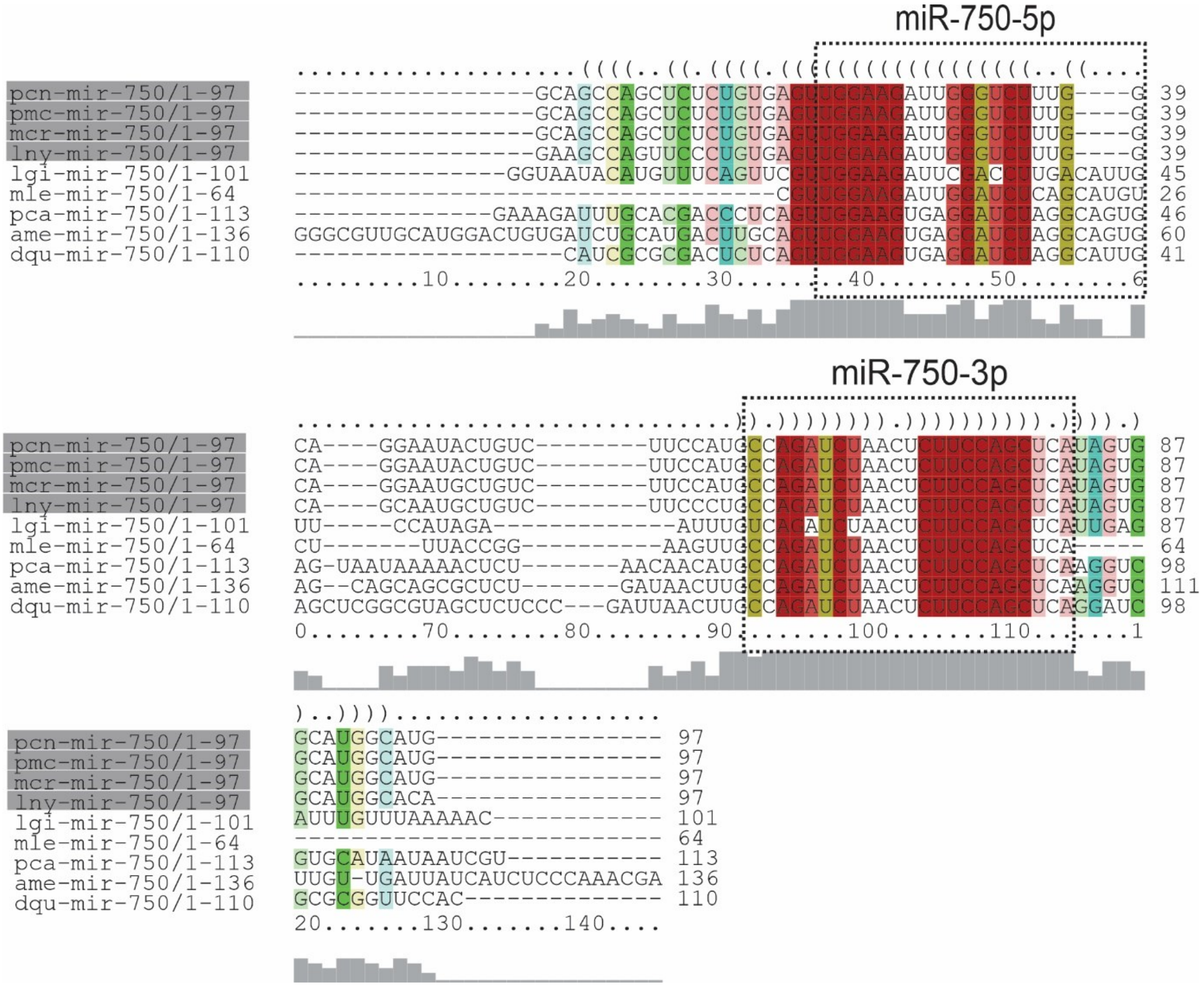


Supplementary figure 17: Secondary structure of mir-2a-2 in Ampullariidae species and their orthologs; cte - *C. teleta*, dse - *Drosophila sechellia*, lny - *L. nyassanus,* mcr - *M. cornuarietis,* pcn - *P. canaliculata,* pmc - *P. maculata*, dya - *Drosophila yakuba*, lgi- *L. gigantea,* tca - *Tribolium castaneum*



Supplementary figure 18: Phylogenetic distribution of mir-2a-2 in Ampullariidae species and their orthologs

mir-750



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                    ....................((((..((.((((.((((((((((((((((((..((....
pcn-mir-750/1-97    -----------------GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
pmc-mir-750/1-97    -----------------GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
mcr-mir-750/1-97    -----------------GCAGCCAGCUCUCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
lny-mir-750/1-97    -----------------GAAGCCAGUUCCCUGUGAGUUGGAAGAUUGGGUCUUUG----G 39
lgi-mir-750/1-101   ---------------GGUAAUACAUGUUUCAGUUCGUUGGAAGAUUCGACCUUGACAUUG 45
mle-mir-750/1-64    ----------------------------------CGUUGGAAGAUUGGAUCUCAGCAUGU 26
pca-mir-750/1-113   --------------GAAAGAUUUGCACGACCCUCAGUUGGAAGUGAGGAUCUAGGCAGUG 46
ame-mir-750/1-136   GGGCGUUGCAUGGACUGUGAUCUGCAUGACUUGCAGUUGGAAGUGAGGAUCUAGGCAGUG 60
dqu-mir-750/1-110   -------------------CAUCGCGCGACUCUCAGUUGGAAGUGAGGAUCUAGGCAUUG 41
                    .........10........20........30........40........50.........6

                    ...............................)).)))))))).)))))))))).)))).)
pcn-mir-750/1-97    CA----GGAAUACUGUC--------UUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
pmc-mir-750/1-97    CA----GGAAUACUGUC--------UUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
mcr-mir-750/1-97    CA----GGAAUGCUGUC--------UUCCAUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
lny-mir-750/1-97    CA----GCAAUGCUGUC--------UUCCCUGCCAGAUCUAACUCUUCCAGCUCAUAGUG 87
lgi-mir-750/1-101   UU-----CCAUAGA-------------AUUUGUCAGAUCUAACUCUUCCAGCUCAUUGAG 87
mle-mir-750/1-64    CU-------UUACCGG----------AAGUUGCCAGAUCUAACUCUUCCAGCUCA----- 64
pca-mir-750/1-113   AG-UAAUAAAAACUCU-------AACAACAUGCCAGAUCUAACUCUUCCAGCUCAAGGUC 98
ame-mir-750/1-136   AG--CAGCAGCGCUCU-------GAUAACUUGCCAGAUCUAACUCUUCCAGCUCAAGGUC 111
dqu-mir-750/1-110   AGCUCGGCGUAGCUCUCCC---GAUUAACUUGCCAGAUCUAACUCUUCCAGCUCAGGAUC 98
                    0........70........80........90.......100.......110.........1

                    )..)))))...................
pcn-mir-750/1-97    GCAUGGCAUG---------------- 97
pmc-mir-750/1-97    GCAUGGCAUG---------------- 97
mcr-mir-750/1-97    GCAUGGCAUG---------------- 97
lny-mir-750/1-97    GCAUGGCACA---------------- 97
lgi-mir-750/1-101   AUUUGUUUAAAAAC------------ 101
mle-mir-750/1-64    -------------------------- 64
pca-mir-750/1-113   GUGCAUAAUAAUCGU----------- 113
ame-mir-750/1-136   UUGU-UGAUUAUCAUCUCCCAAACGA 136
dqu-mir-750/1-110   GCGCGGUUCCAC-------------- 110
                    20.......130.......140....
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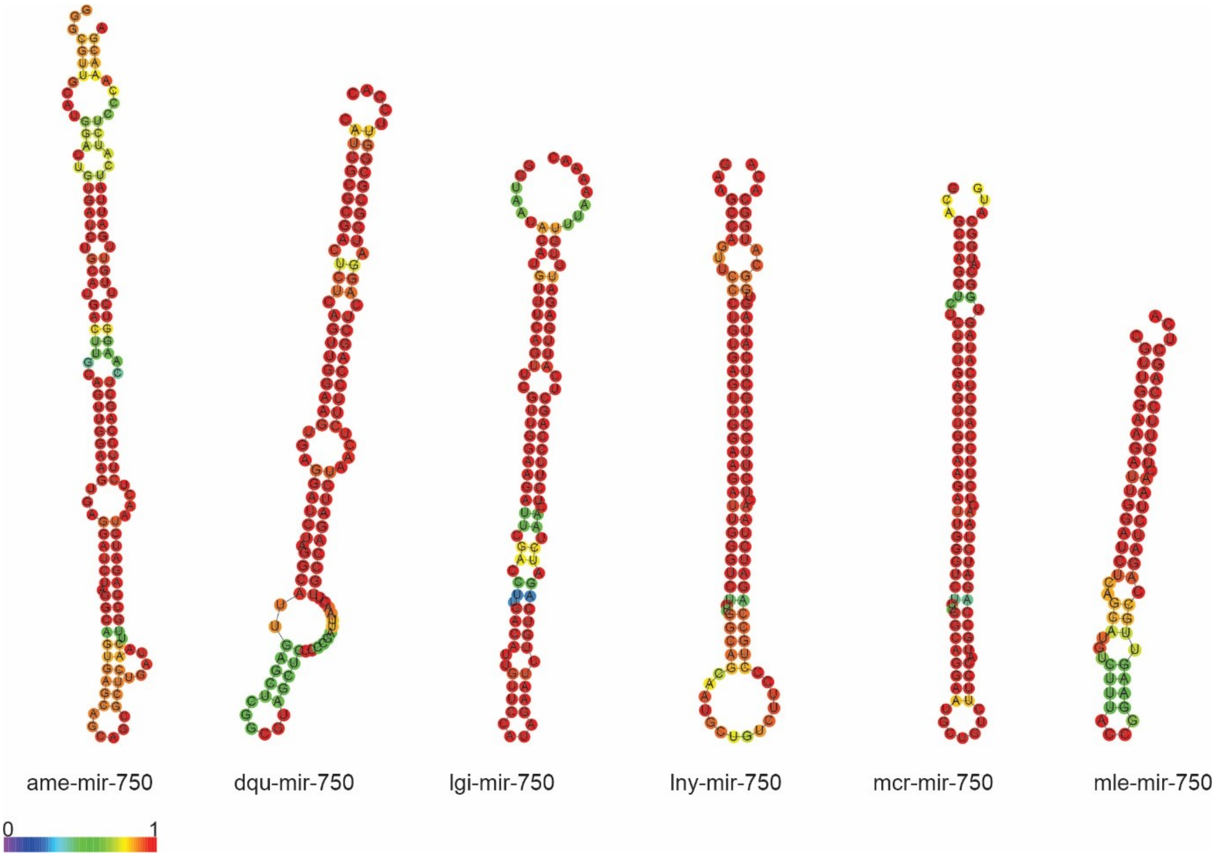
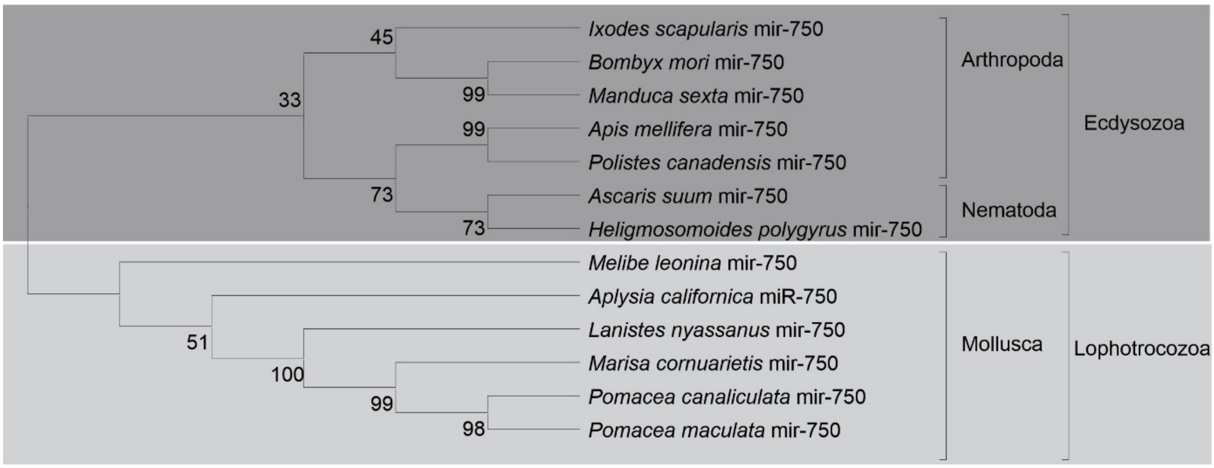
Supplementary figure 19: Alignment of mi-750 in Ampullariidae species and their orthologs; pcn - *P. canaliculata*, lny - *L. nyassanus*, mcr - *M. cornuarietis*, pmc - *P. maculata*, ame – *Apis melífera*, dqu - *Dinoponera quadríceps*, pca - *Polistes canadenses*, lgi - *L. gigantea*, mle - *M. leonina*.



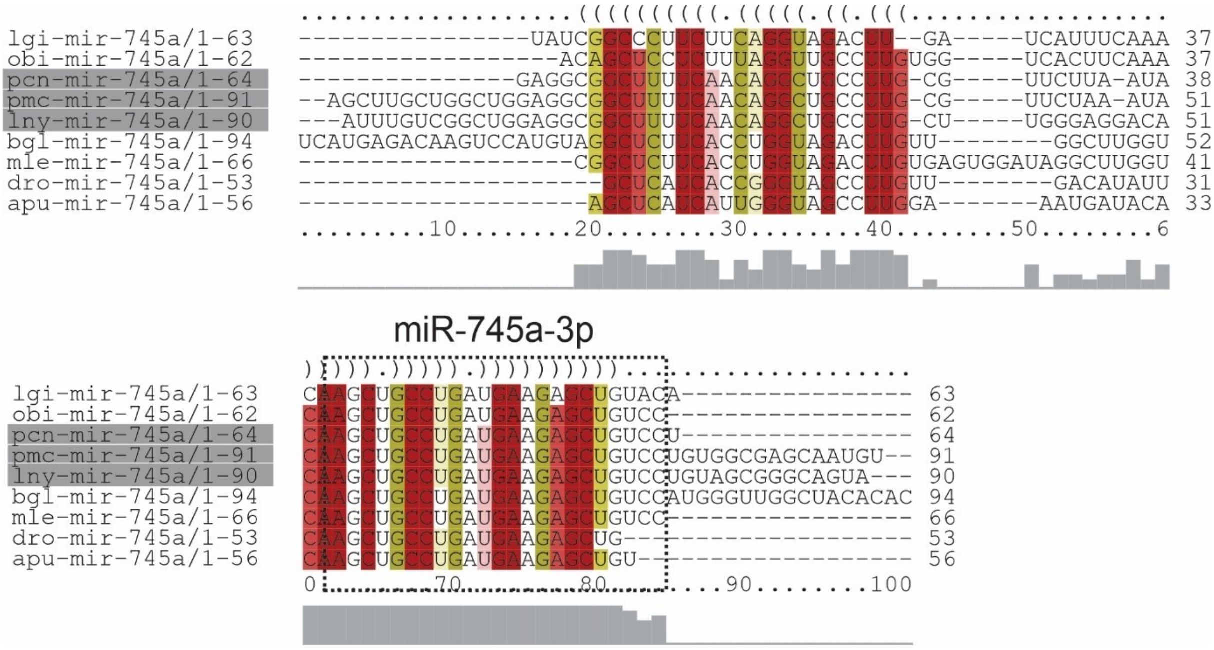
Supplementary figure 20: Secondary structure of mir-750 in Ampullariidae species and their orthologs; lny - *L. nyassanus,* mcr - *M. cornuarietis*, ame - *Apis melífera*, dqu - *Dinoponera quadriceps*, lgi - *L. gigantea*, mle - *M. leonina.*



Supplementary figure 21: Phylogenetic distribution of mir-750 in Ampullariidae species and their orthologs.

Lophotrochozoa specific miRNAs

mir-745[a]



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                    ...................((((((((((.(((((.((.(((..................
lgi-mir-745a/1-63   ----------------UAUCGGCCCUUCUUCAGGUAGACUU--GA-----UCAUUUCAAA 37
obi-mir-745a/1-62   ------------------ACAGCUCCUCUUUAGGUUGCCUUGUGG-----UCACUUCAAA 37
pcn-mir-745a/1-64   ---------------GAGGCGGCUUUUCAACAGGCUGCCUUG-CG-----UUCUUA-AUA 38
pmc-mir-745a/1-91   --AGCUUGCUGGCUGGAGGCGGCUUUUCAACAGGCUGCCUUG-CG-----UUCUAA-AUA 51
lny-mir-745a/1-90   ---AUUUGUCGGCUGGAGGCGGCUUUUCAACAGGCUGCCUUG-CU-----UGGGAGGACA 51
bgl-mir-745a/1-94   UCAUGAGACAAGUCCAUGUAGGCUCUUCACCUGGUAGACUUGUU--------GGCUUGGU 52
mle-mir-745a/1-66   -------------------CGGCUCUUCACCUGGUAGACUUGUGAGUGGAUAGGCUUGGU 41
dro-mir-745a/1-53   ---------------------GCUCAUCACCGGGUAGCCUUGUU--------GACAUAUU 31
apu-mir-745a/1-56   --------------------AGCUCAUCAUUGGGUAGCCUUGGA-------AAUGAUACA 33
                    ........10........20........30........40........50........6

                    ))))).))))).))))))))))....................
lgi-mir-745a/1-63   CAAGCUGCCUGAUGAAGAGCUGUACA---------------- 63
obi-mir-745a/1-62   CAAGCUGCCUGAUGAAGAGCUGUCC----------------- 62
pcn-mir-745a/1-64   CAAGCUGCCUGAUGAAGAGCUGUCCU---------------- 64
pmc-mir-745a/1-91   CAAGCUGCCUGAUGAAGAGCUGUCCUGUGGCGAGCAAUGU-- 91
lny-mir-745a/1-90   CAAGCUGCCUGAUGAAGAGCUGUCCUGUAGCGGGCAGUA--- 90
bgl-mir-745a/1-94   CAAGCUGCCUGAUGAAGAGCUGUCCAUGGGUUGGCUACACAC 94
mle-mir-745a/1-66   CAAGCUGCCUGAUGAAGAGCUGUCC----------------- 66
dro-mir-745a/1-53   CAAGCUGCCUGAUGAAGAGCUG-------------------- 53
apu-mir-745a/1-56   CAAGCUGCCUGAUGAAGAGCUGU------------------- 56
                    0.......70........80........90........100
```
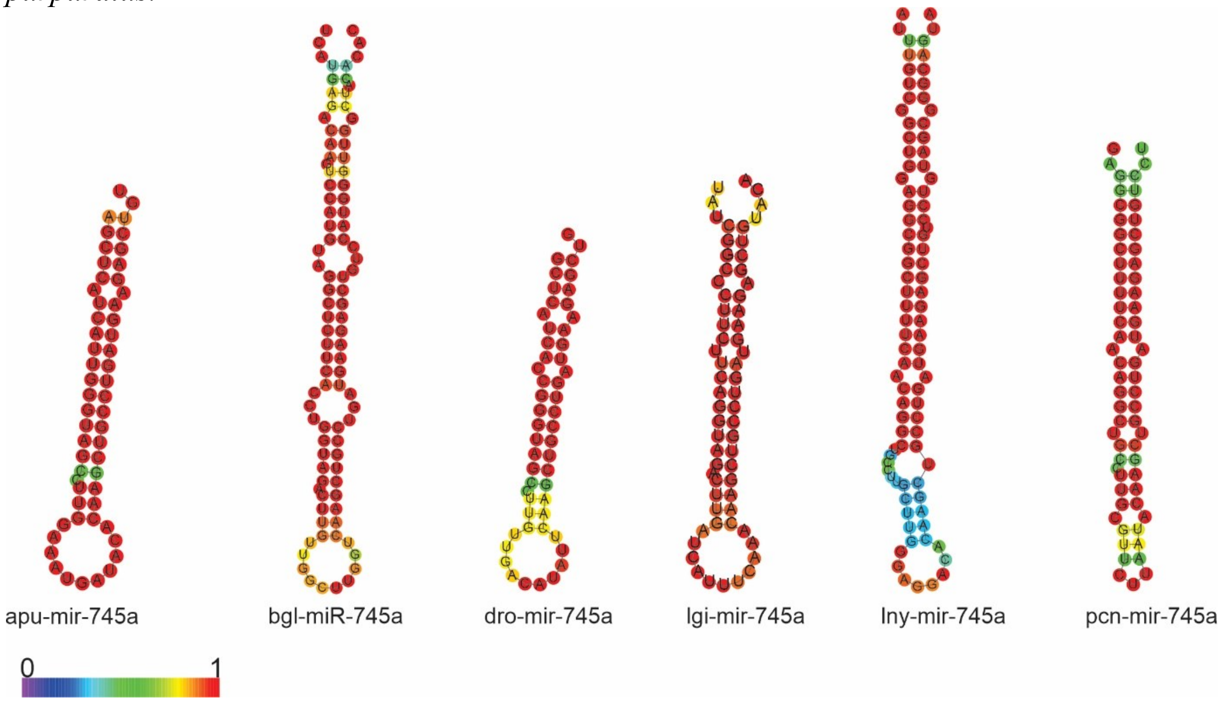
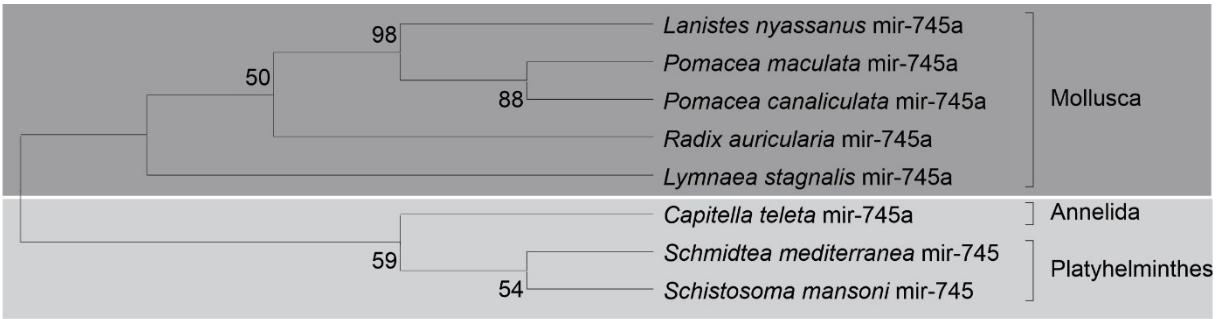

Supplementary figure 22: Alignment of mir-745a in Ampullariidae species and their orthologs; pcn - *P. canaliculata,* lny - *L. nyassanus*, pmc - *P. maculata*, lgi - *L. gigantea*, mle - *M. leonina*, obi – *Octopus bimaculoides*, bgl – *B. glabrata*, dro - *Dreissena rostriformis*, apu - *Argopecten purpuratus.*

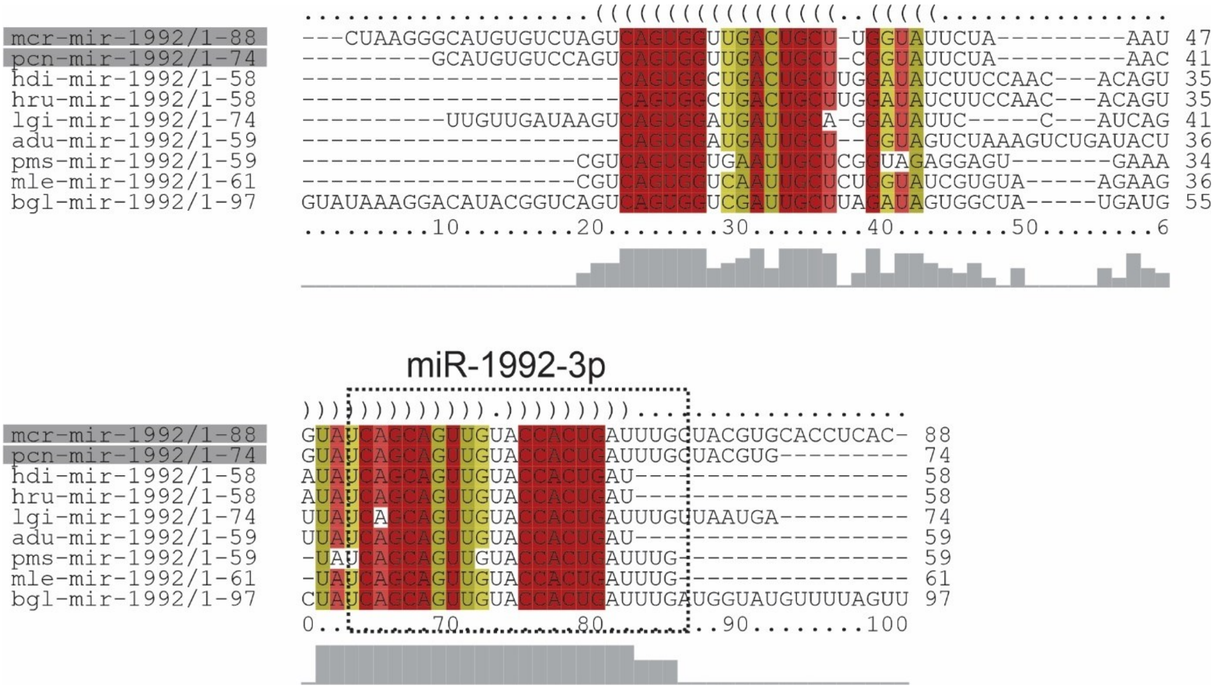


Supplementary figure 23: Secondary structure of mir-745a in Ampullariidae species and their orthologs; pcn - *P. canaliculata,* lny - *L. nyassanus*, lgi - *L. gigantea*, bgl – *B. glabrata*, dro - *Dreissena rostriformis*, apu - *Argopecten purpuratus.*



Supplementary figure 24: Phylogenetic distribution of mir-745a in Ampullariidae species and their orthologs.

mir-1992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                     .....................((((((((((((((((..(((((................
mcr-mir-1992/1-88    ---CUAAGGGCAUGUGUCUAGUCAGUGGUUGACUGCU-UGGUAUUCUA---------AAU 47
pcn-mir-1992/1-74    ---------GCAUGUGUCCAGUCAGUGGUUGACUGCU-CGGUAUUCUA---------AAC 41
hdi-mir-1992/1-58    ----------------------CAGUGGCUGACUGCUUGGAUAUCUUCCAAC---ACAGU 35
hru-mir-1992/1-58    ----------------------CAGUGGCUGACUGCUUGGAUAUCUUCCAAC---ACAGU 35
lgi-mir-1992/1-74    ----------UUGUUGAUAAGUCAGUGGAUGAUUGCA-GGAUAUUC-----C---AUCAG 41
adu-mir-1992/1-59    ----------------------CAGUGGAUGAUUGCU--GGUAGUCUAAAGUCUGAUACU 36
pms-mir-1992/1-59    -------------------CGUCAGUGGUGAAUUGCUCGGUAGAGGAGU-------GAAA 34
mle-mir-1992/1-61    -------------------CGUCAGUGGUCAAUUGCUCUGGUAUCGUGUA-----AGAAG 36
bgl-mir-1992/1-97    GUAUAAAGGACAUACGGUCAGUCAGUGGUCGAUUGCUUAGAUAGUGGCUA-----UGAUG 55
                     .........10........20........30........40........50........6
```

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                     ))))))))))))).)))))))))...................
mcr-mir-1992/1-88    GUAUCAGCAGUUGUACCACUGAUUUGGUACGUGCACCUCAC- 88
pcn-mir-1992/1-74    GUAUCAGCAGUUGUACCACUGAUUUGGUACGUG--------- 74
hdi-mir-1992/1-58    AUAUCAGCAGUUGUACCACUGAU------------------- 58
hru-mir-1992/1-58    AUAUCAGCAGUUGUACCACUGAU------------------- 58
lgi-mir-1992/1-74    UUAUCAGCAGUUGUACCACUGAUUUGUUAAUGA--------- 74
adu-mir-1992/1-59    UUAUCAGCAGUUGUACCACUGAU------------------- 59
pms-mir-1992/1-59    -UAUCAGCAGUUGUACCACUGAUUUG---------------- 59
mle-mir-1992/1-61    -UAUCAGCAGUUGUACCACUGAUUUG---------------- 61
bgl-mir-1992/1-97    CUAUCAGCAGUUGUACCACUGAUUUGAUGGUAUGUUUUAGUU 97
                     0.........70........80........90.......100
```
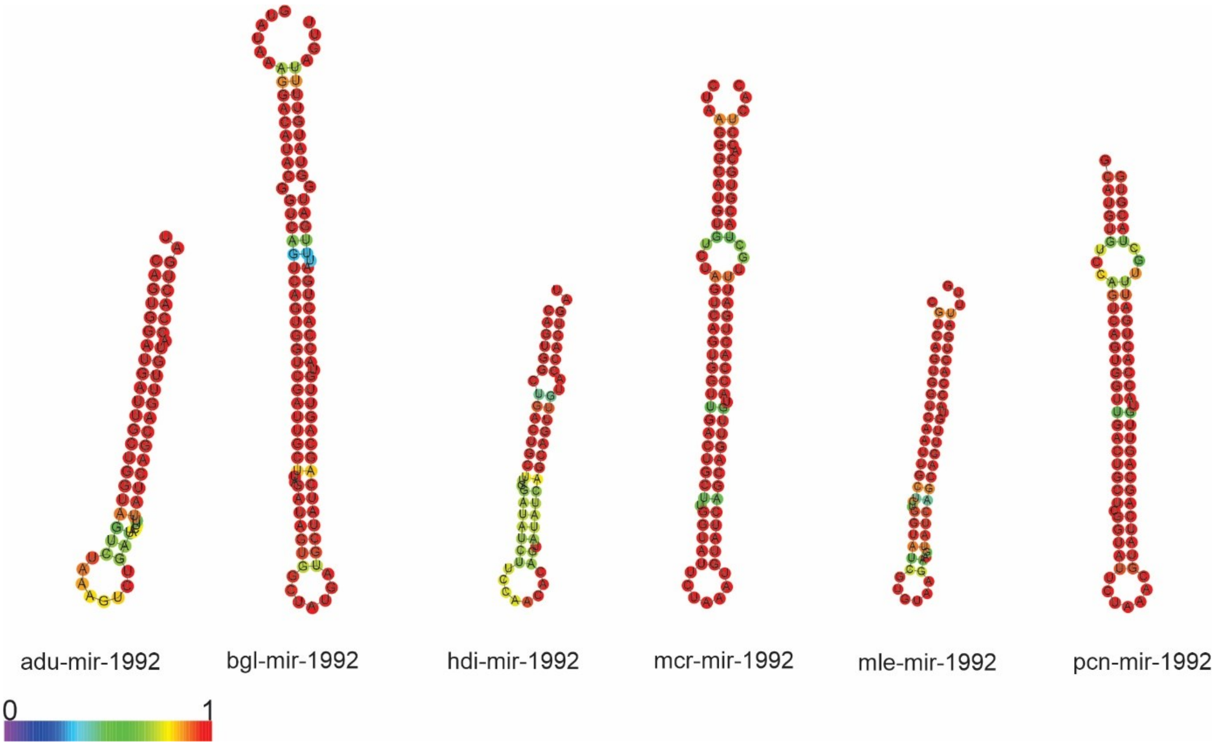
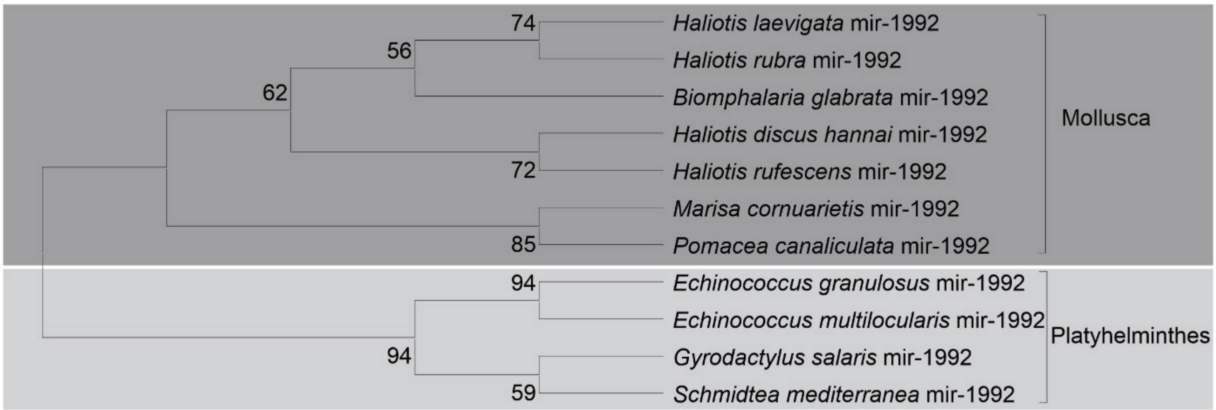

Supplementary figure 25: Alignment of mi-1992 in Ampullariidae species and their orthologs; mcr - *M. cornuarietis*, pcn- *P. canaliculata,* hdi - *Haliotis discus hannai*, hru – *Haliotis rufescens*, lgi - *L. gigantea*, adu - *Architeuthis dux*, pms - *Pinctada martensii*, mle - *M. leonina*, bgl – *B. glabrata.*

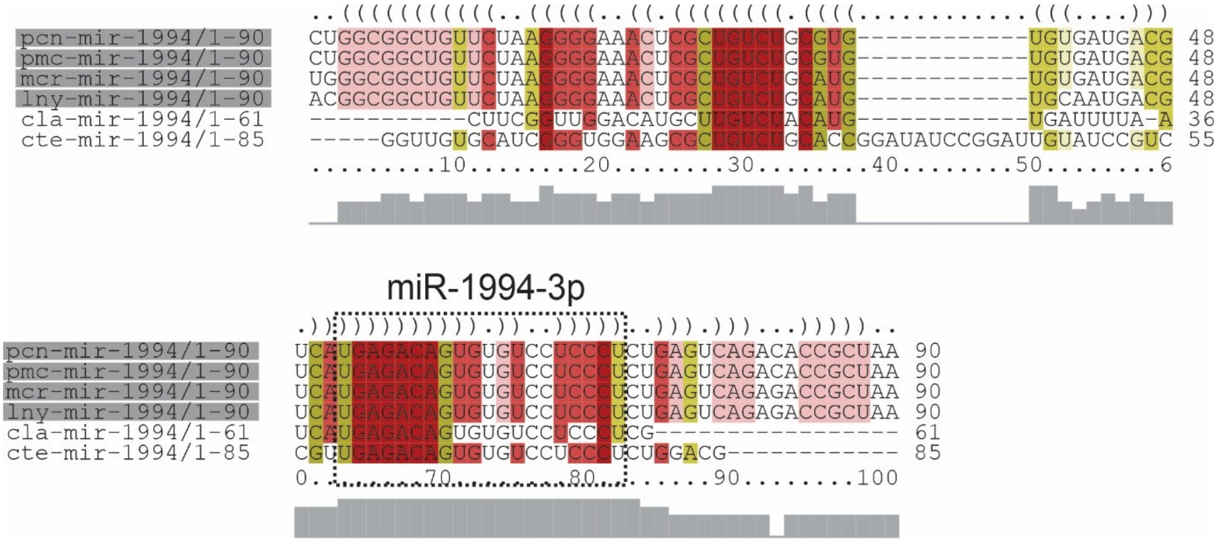


Supplementary figure 26: Secondary structure of mir-1992 in Ampullariidae species and their orthologs; mcr -*M. cornuarietis*, pcn- *P. canaliculata,* hdi - *Haliotis discus hannai*, lgi - *L. gigantea*, adu - *Architeuthis dux*, mle - *M. leonina*, bgl - *B. glabrata.*

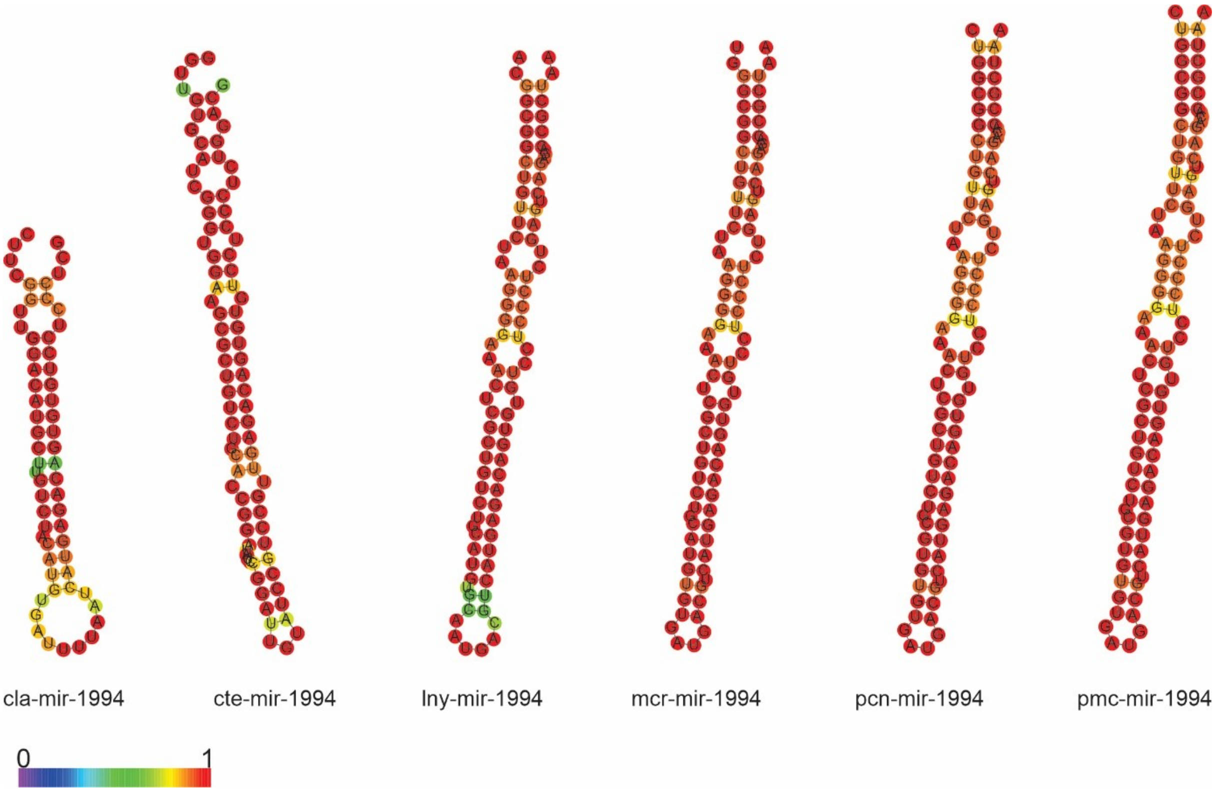


Supplementary figure 27: Phylogenetic distribution of mir-1992 in Ampullariidae species and their orthologs.

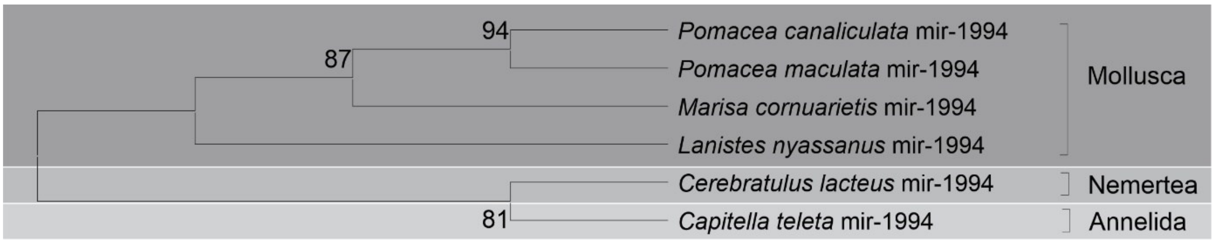
mir-1994



Supplementary figure 28: Alignment of mi-1994 in Ampullariidae species and their orthologs; pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* cte - *C. teleta,* cla - *Cerebratulus lacteus.*



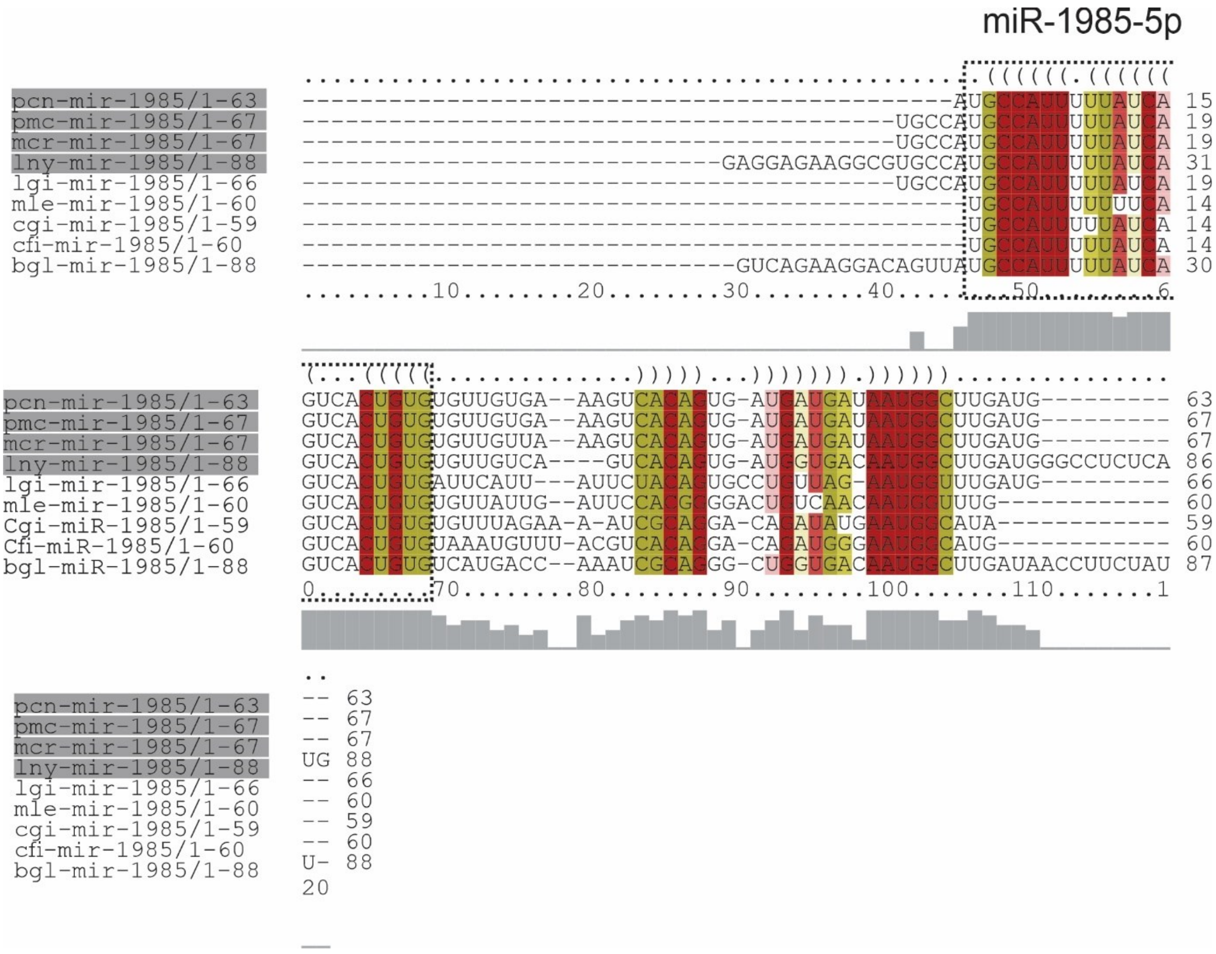
Supplementary figure 29: Secondary structure of mir-1994 in Ampullariidae species and their orthologs; pcn - *P. canaliculata,* lny - *L. nyassanus,* mcr - *M. cornuarietis*, pmc - *P. maculata,* cte - *C. teleta,* cla - *Cerebratulus lacteus.*



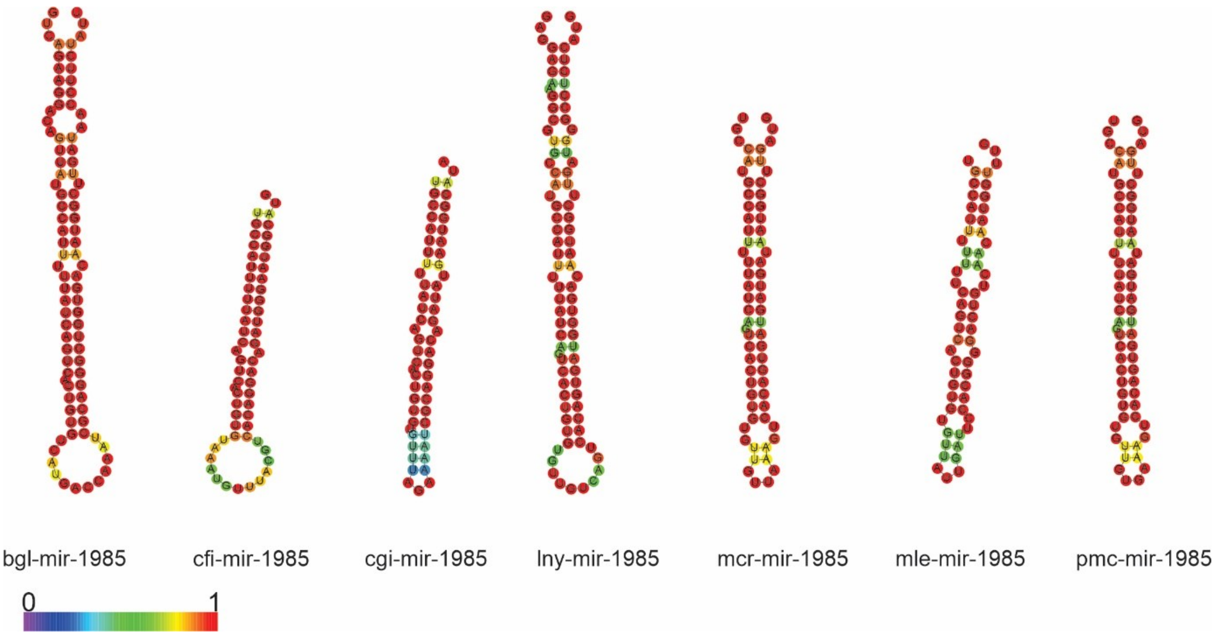
Supplementary figure 30: Phylogenetic distribution of mir-1994 in Ampullariidae species and their orthologs.

Mollusc-specific miRNAs

mir-1985

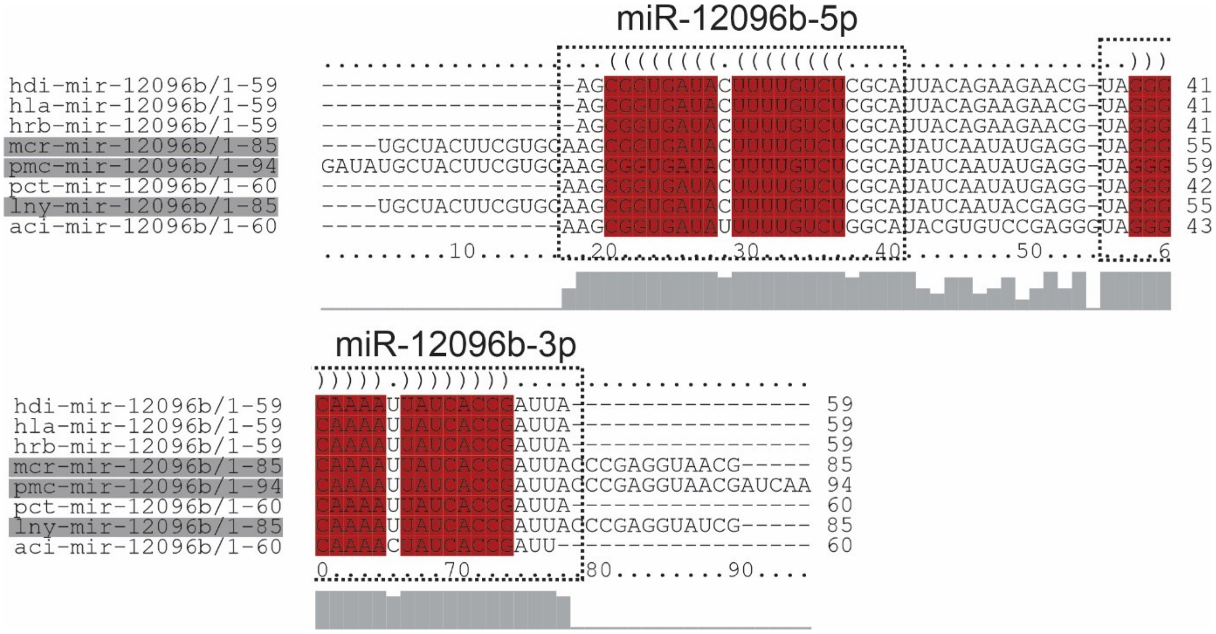


Supplementary figure 31: Alignment of mi- in Ampullariidae species and their orthologs; pcn- *P. canaliculata,* lny - *L. nyassanus,* mcr -*M. cornuarietis*, pmc - *P. maculata,* lgi - *L. gigantea,* mle - *M. leonina,* cgi - *C. gigas,* cfi - *Chlamys farreri,* bgl – *B. glabrata.*

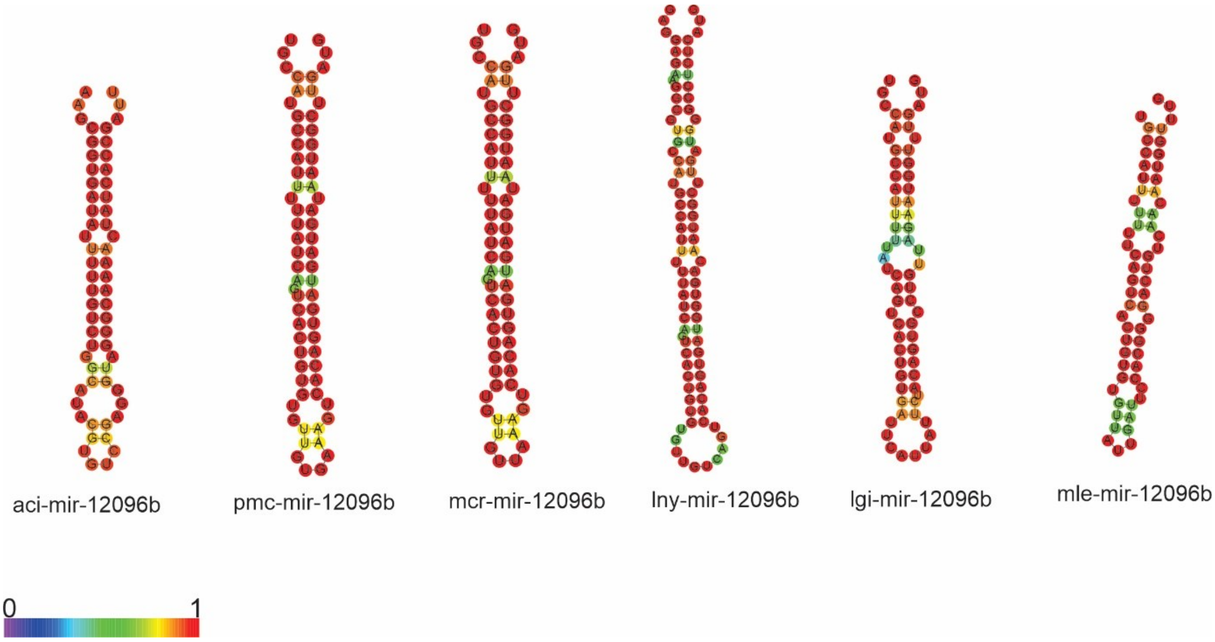


Supplementary figure 32: Secondary structure of mir- in Ampullariidae species and their orthologs; lny - *L. nyassanus,* mcr -*M. cornuarietis*, pmc - *P. maculata,* mle - *M. leonina,* cgi - *C. gigas,* cfi - *Chlamys farreri,* bgl – *B. glabrata*

mir-12096b



Supplementary figure 33: Alignment of mir-12096b in Ampullariidae species and their orthologs; Aci- *Aplysia californica,* pmc - *P. maculata,* mcr - *M. cornuarietis,* lny - *L. nyassanus,* lgi - *L. gigantea,* hdi - *H. discushannai,* hla - *Haliotis laevigata,* hrb - *Haliotis rubra*



Supplementary figure 34: Secondary structure of mir-12096b in Ampullariidae species and their orthologs; Aci- *Aplysia californica,* pmc - *P. maculata,* mcr - *M. cornuarietis,* lny - *L. nyassanus,* lgi - *L. gigantea,* mle – *M. leonina.*