

UNIVERSIDADE FEDERAL DE UBERLÂNDIA
INSTITUTO DE BIOTECNOLOGIA
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MICHELLE TEIXEIRA LIMA

**ANÁLISE EVOLUTIVA DOS FATORES DE TRANSCRIÇÃO AP2/ERF NO REINO
VEGETAL**

PATOS DE MINAS
DEZEMBRO 2019

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Monografia apresentada ao Instituto de Biotecnologia da Universidade Federal de Uberlândia como requisito final para a obtenção do título de Bacharel em Biotecnologia.

**Prof. Dr. Aulus Estevão Anjos de Deus
Barbosa.**

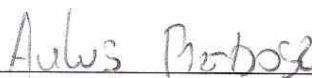
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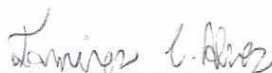
Análise evolutiva dos fatores de transcrição AP2/ERF no reino vegetal

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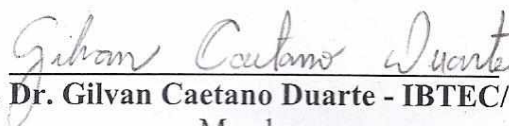
Banca examinadora:



Prof. Dr. Aulus Estevão de Deus Barbosa – IBTEC/UFU
Presidente



Me. Tamires Caixeta Alves - IBTEC/UFU
Membro



Prof. Dr. Gilvan Caetano Duarte - IBTEC/UFU
Membro

Patos de Minas, 09 de dezembro de 2019.

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RESUMO

Os fatores de transcrição são proteínas que ativam genes em resposta a diversos fatores bióticos e abióticos durante o desenvolvimento dos vegetais. Estes fatores de transcrição são capazes de se ligar a sequências de DNA nos promotores de genes alvo e ativar, ou reprimir, a expressão destes genes interagindo com a RNA polimerase e outras proteínas envolvidas na transcrição. Dentre os fatores ambientais que provocam respostas fisiológicas em plantas podemos citar a presença de elevados teores de sal, umidade excessiva, estresse hídrico, e defesa a ataque de patógenos. A classificação dos fatores de transcrição em subfamílias é sustentada pela presença do domínio AP2, sendo o motivo característico de cada subclasse. Estes domínios participam ativamente na regulação da expressão gênica em resposta aos mais diversos estresses. Devido a essa importância, o objetivo deste trabalho foi identificar a presença de fatores de transcrição AP2/ERF na linhagem vegetal, desde algas mais primitivas, o que permitiu visualizar a evolução destes genes. Utilizando a bioinformática e suas ferramentas de análise foi possível, identificar 483 prováveis sequências dos fatores de transcrição AP2/ERF sendo que 4 delas foram identificadas em duas espécies de algas, 134 sequências em espécies de Algas verdes, 165 sequências em espécies de Briófitas e 180 sequências em espécies de Pteridófitas. Em conclusão observou-se que os fatores de transcrição da subfamília AP2 estão presentes nas espécies vegetais desde algas mais primitivas até organismos mais complexos. Esta subfamília pode, portanto, ter originado os genes pertencentes às demais subfamílias, pois se mostrou ser a classe mais antiga dentre as classes analisadas.

Palavras-chave: Estresse. Evolução. Adaptação. Resistência. Fatores Bióticos.

ABSTRACT

Transcription factors are proteins that activate genes in response to various biotic and abiotic factors during plant development. These transcription factors are capable of connecting DNA sequences to target gene promoters and activating or suppressing an expression of these genes interacting with RNA polymerase and other transcriptional applications. Among the environmental factors that cause physiological responses in plants, we can mention the presence of high salt levels, excessive exposure, water stress and defense against pathogen attacks. The classification of transcription factors in subfamilies is supported by the presence of the AP2 domain, which is the characteristic reason for each subclass. These domains actively participate in the application of gene expression in response to various stresses. Considering this importance, or the objective of this study, was to identify the presence of transcription factors AP2 / ERF in the plant line, from more primitive algae, or to visualize the evolution of these genes. Using a bioinformatics and its analysis tools it was possible to identify 483 sequences of transcription factors AP2 / ERF, 4 of them identified in two species of algae, 134 sequences in green algae species, 165 sequences in fish species and 180 sequences in pteridophyte species. In conclusion, whether the transcription factors of subfamily AP2 are present in even more complex primitive algal plant species. This subfamily may therefore have originated the genes belonging to other subfamilies, as it has been shown to be an older class among the analyzed classes.

Keywords: Stress. Evolution. Adaptation. Resistance. Biotic factors.

SUMÁRIO

1 INTRODUÇÃO.....	8
2 REFERENCIAL TEÓRICO.....	9
2.1 Evolução das plantas	9
2.3 O controle da transcrição gênica dos vegetais sob estresse.....	10
2.4 Classificação dos fatores de transcrição AP2/ERF.....	10
2.2 Bioinformática no ramo da genômica	14
3 OBJETIVOS.....	15
3.1 Objetivo geral	15
3.2 Objetivos específicos.....	15
4 MATERIAL E MÉTODOS.....	15
4.1 Buscas pelas sequências transcricionais da família AP2/ERF em <i>Arabidopsis thaliana</i> em bancos de dados	15
4.2 Bancos de dados de genomas vegetais	16
4.3 Identificações das sequências dos fatores de transcrição AP2/ERF nas linhagens selecionadas.....	16
4.4 Análises dos domínios conservados da superfamília de TF's AP2/ERF	17
4.5 Alinhamentos dos fatores de transcrição AP2/ERF	17
4.6 Análises filogenéticas das sequencias de AP2/ERF	17
5 RESULTADOS E DISCUSSÃO	17
5.1 Identificação e classificação dos fatores de transcrição AP2/ERF nas linhagens vegetais	17
5.2 Alinhamentos do domínio conservado AP2/ERF.....	18
5.3 Análises filogenética dos fatores de transcrição AP2/ERF nas linhagens vegetais selecionadas.....	24
6 CONCLUSÃO.....	29
Referências	30

APÊNDICES	36
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1 INTRODUÇÃO

Como resultado da seleção natural ao longo da evolução, alguns vegetais conseguiram desenvolver mecanismos que permitissem o seu crescimento em condições adversas. Esse processo é conhecido como adaptação, e regulado em níveis moleculares, com o auxílio de fito-hormônios e fatores de transcrição responsivos a eles, desencadeiam mudanças em níveis fisiológicos e morfológicos nas plantas (NAKANO et al., 2006; NATH et al., 2019).

Estas mudanças proporcionam maior robustez e tolerância às plantas, induzindo muitas vezes respostas a múltiplos fatores, como a distribuição de nutrientes, ataque de patógenos, e resistência a elevadas temperaturas. Um dos principais mecanismos de regulação bioquímica e fisiológica nas plantas. A ligação dos fatores de transcrição da superfamília APETALA2/Ethylene Responsive Factor, se dá pela interação da região promotora dos genes alvo com as proteínas responsáveis pela ativação ou repressão da expressão gênica. A ligação ocorre de maneira específica a cada estímulo e também devido ao domínio conservado AP2/ERF, em que cada subfamília apresenta seu motivo específico (LI et al., 2018; SONG; LI; HOU, 2013).

Com a interação, dos fatores de transcrição AP2/ERF e os promotores gênicos ativam-se mecanismos que levam a adaptação das plantas aos estresses capacitando-as a sobreviver em condições diferentes das consideradas ideais para o seu crescimento. Os fatores de transcrição AP2/ERF são classificados de acordo com o número de cópias do domínio AP2 em que as subfamílias ERF, DREB, RAVe solista, apresentam uma cópia do domínio ligado aos motivos específicos de cada subclasse. Apenas a subfamília APETALA2 apresenta duas cópias do domínio AP2. A presença do domínio conservado junto ao motivo específico de cada subclasse está intimamente relacionada a especificidade da ligação ao gene expresso em condições de estresse, e o desencadeamento em resposta a determinado estímulo (FUJIMOTO et al., 2000; LI et al., 2013; XIE et al., 2019; OKAMURO et al., 1997). Entender a evolução desses fatores de transcrição e quando surgiram pode trazer informações bastante relevantes, visto que estes são utilizados em diversas aplicações na biotecnologia em áreas como a transgenia e o melhoramento genético vegetal.

2 REFERENCIAL TEÓRICO

2.1 Evolução das plantas

O estabelecimento em ambientes terrestres de organismos fotossintetizantes eucarióticos, como as algas vermelhas e verdes, só foi possível após uma série de adaptações (VRIES; ARCHIBALD, 2018). A partir da migração dos ambientes marinhos para os ambientes terrestres foram surgindo, ao longo do tempo, diversas características. Por exemplo, o desenvolvimento de sistemas condutores que permitissem melhor distribuição de água e nutrientes e consequentemente, organismos de tamanhos maiores (MENDÃO, 2007). No entanto, no ambiente marinho esta característica não é necessária. As algas possuem meios de realizar suas trocas metabólicas que não dependem de transporte vascular, pois estas possuem uma maior permeabilidade epidérmica, característica responsável por sua nutrição. Além disso, no início da história evolutiva, as algas utilizavam apenas recursos disponíveis de forma abundante, como oxigênio, luz solar, carbono e hidrogênio (MENDÃO, 2007).

À medida que recursos como se tornavam escassos, as plantas aquáticas tiveram de desenvolver sistemas teciduais para a conexão e a nutrição de locais onde os raios solares não estivessem ao alcance, o que impedia a realização do processo de fotossíntese. Com isto, os organismos aquáticos foram se tornando cada vez mais complexos, tanto fisiologicamente, quanto bioquimicamente (MENDÃO, 2007; RAVEN; EVERT; EICHHORN, 2013).

Assim, de maneira gradual, as plantas aquáticas conseguiram desenvolver estruturas de fixação às rochas e a terra firme, para isto produziram moléculas de enrijecimento celular, como a lignina e esporopolenina, que as protegem de danos físicos pelo atrito causado pela rebentação das ondas. (DELWICHE; GRAHAM; THOMSON, 1989; RAVEN; EVERT; EICHHORN, 2013). Evidências apontam que estas moléculas foram cruciais para a evolução das plantas, pois auxiliaram no processo de tolerância à dessecação e permitiram o início do desenvolvimento em diversas orientações de divisão celular, observadas hoje em grande parte das plantas verdes. Em algas o crescimento se dava apenas de maneira planar (GRAHAM; COOK; BUSSE, 2000; HARRISSON, 2017) até ocorrer de fato a regulação genética necessária para isto e, consequentemente, a regulação bioquímica deste processo. Algumas briófitas como os musgos também apresentam essa característica (SOUFFREAU et al., 2013; VRIES, ARCHIBALD, 2018).

Quando surgiram os tecidos vasculares houve um grande salto em relação à adaptação das plantas ao ambiente terrestre. O processo de diferenciação celular, desencadeado por fito-

hormônios aliados a fatores de transcrição, permitiu o surgimento de tecidos especializados (WAGAS, et al., 2019). O desenvolvimento de tecidos foi essencial para a passagem de estados vegetativos para os reprodutivos, dando origem a órgãos de maior complexidade, como os responsáveis pela reprodução das plantas, os tecidos gametofíticos. Esta característica permitiu às plantas, conhecidas como superiores, o sucesso na reprodução e consequentemente a conquista do espaço terrestre (GRAHAM; COOK; BUSSE, 2000).

2.3 O controle da transcrição gênica dos vegetais sob estresse

Considerando a grande variação de temperatura no globo terrestre, bem como a variação de disponibilidade hídrica e de nutrientes essenciais a sua sobrevivência, os vegetais se utilizam de mecanismos de controle transcricionais para se adaptarem a condições não ideais ao seu desenvolvimento e reprodução (NATH et al., 2019; WU et al., 2015; LI et al., 2014; LI et al., 2017; ELLIOTT et al., 1996). O mecanismo adaptativo destes vegetais é guiado por cascatas de sinalização. Em resposta a essas vias, ocorre no núcleo celular a ligação de proteínas específicas, a regiões gênicas conhecidas como promotores. Essas proteínas são denominadas fatores de transcrição e possuem duas porções. A primeira é responsável pelo reconhecimento e ligação a regiões próximas aos promotores gênicos, denominados elemento de ligação cis reguladores, como GCC-box. A segunda porção é responsável ativação ou repressão gênica mediada por sinalizações endógenas ou exógenas tendo por consequência o recrutamento de RNAs polimerase e iniciação da transcrição, ou o bloqueio total desta atividade (D'ALMEIDA, 2014).

Por sua vez a estas porções possuem afinidades de ligação diferenciais devido a especificidade de cada classe (GU et al., 2017), servindo também como requisito para a classificação destes fatores em superfamílias, como AP2/ERF, MYB entre outras (GONÇALVES, 2014;; MOORE; LOAKE; SPOEL, 2011; WU et al., 2015; NATH et al., 2019). Sendo assim, cada subfamília de fatores de transcrição possui uma assinatura característica, responsável por mudanças metabólicas e fisiológicas decorrentes de estímulos ambientais (NAKANO et al., 2006; RIECHMANN et al., 2000; BAILLO et al., 2019).

2.4 Classificação dos fatores de transcrição AP2/ERF

Apresentando cerca de 60 a 70 aminoácidos, a superfamília AP2/ERF é constituída por fatores de transcrição que possuem, como principal característica, a capacidade de ligação a regiões promotoras de genes expressos em condições de estresse. Esta ligação ocorre por meio da interação entre as sequências do domínio conservado desta superfamília (Figura 1) e seu respectivo domínio de ligação, garantindo a especificidade da resposta promovida (LI et al., 2018; NAKANO et al., 2006). Participando diretamente da regulação de vias como a do ácido jasmônico, etileno e ácido salicílico (FUJIMOTO et al., 2000; OÑATE-SÁNCHEZ; SINGH, 2002; MANTIRI et al., 2008) os membros da superfamília AP2/ERF desempenham papéis fundamentais na sobrevivência dos vegetais expostos a condições prejudiciais ao seu desenvolvimento. Tornando-os capazes de realizar adaptações bioquímicas em seu metabolismo, em condições de estresse hídrico, a regulação em nível transcricional destes fatores confere ao vegetal uma maior capacidade de adaptação, crescimento e desenvolvimento (SONG; LI; HOU, 2013; LI et al., 2013; HORSTMAN et al., 2014; KULUEV et al., 2015).

A caracterização da superfamília AP2/ERF, e os mecanismos pelos quais estes fatores de transcrição atuam, foram descritos em diversas espécies como *Arabidopsis Thaliana* (JOFUKU et al., 1994; XIE et al., 2019), *Camellia sinensis* (WU et al., 2015) e *Phyllostachys edulis* (HUANG et al., 2016). A descrição destes processos é de suma importância, pois estes genes conferem características bastante relevantes do ponto de vista econômico. Recentemente, tem surgido uma crescente demanda de utilização de plantas resistentes aos mais diversos fatores ambientais, sendo a seca um dos principais desafios encontrados na produção agrícola (ITO, et al., 2012).

Dentro da superfamília AP2/ERF, os fatores de transcrição foram classificados em subfamílias como AP2, ERF, DREB, RAV e Solista, que se diferem principalmente pela quantidade de domínios AP2 (Figuras 1 e 2) e o motivo característico de cada classe ligado a ele, além da resposta desencadeada. (LICAUSI et al., 2010; NAKANO, 2006; SAKUMA et al., 2002; ZHUANG et al., 2010; MIZOI et al., 2012; WU et al., 2015; RIECHMANN et al., 2000; ROMERO et al., 2016).

As proteínas da subfamília AP2 possuem, ao longo do seu sítio de ligação, duas cópias do domínio APETALA2 unidas por uma porção de 25 aminoácidos, que garantem a especificidade da ligação na região promotora do gene alvo, o motivo CAACA. (SALEH; PAGÉS, 2003). Dentre as suas funções está a capacidade de promover a diferenciação celular através da determinação de meristemas e órgão florais (JOFUKU et al., 1994). Estudos

genéticos comprovam que a existência de mutações no gene APETALA2 pode levar a má formação de óvulos e gametófitos. Essas mutações também podem causar desordem no desenvolvimento de meristemas apicais, afetando diretamente o desenvolvimento e a reprodução dos vegetais (CHUCK; MEELEY; HAKE, 1998). Apresentando resposta dependente do fito-hormônio etileno, os fatores de transcrição da subfamília ERF estão envolvidos em diferentes papéis na defesa das plantas e são classificados em ERF e DREB. No grupo ERF o desencadeamento das respostas ocorre por meio da ligação dos fatores de transcrição aos motivos AGCCGCC/ ERE regulando os genes codificantes de defensinas responsivas ao hormônio etileno (SOLANO et al., 1998; MULLER, MUNÉ-BOSCH, 2015). Estes fatores também são responsáveis pela obtenção de resistência ao ataque de patógenos e a estresses osmóticos (CHENG et al., 2013; MULLER; MUNÉ-BOSCH, 2015; BERROCAL-LOBO; MOLINA; SOLANO, 2002; LORENZO et al., 2002; CHENG et al., 2013; XIE et al., 2019). Os fatores DREB podem ainda ser divididos em 6 grupos, 1A, 2A, 3A, 4A, 5A E 6A e participam da regulação do crescimento e desenvolvimento das plantas por meio da ligação ao elemento regulatório *cis*-DRE/CRT. Com isso, medeiam a respostas a condições de seca, ataque de patógenos, além de promover a tolerância a grandes variações de temperatura, e altas concentrações de sais (REICHEL, 2016; LI et al., 2018; ECKARDT, 2019; AGARWAL et al., 2006; SAKUMA et al., 2002; KONZEN et al., 2019; NAKASHIMA; ITO; YAMAGUCHI-SHINOZAKI, 2009).

Participando ativamente de respostas a estresses abióticos a subfamília RAV tem como principal característica estrutural a presença de um motivo B3 C-terminal ligado ao domínio AP2, que reconhecem, respectivamente, as sequências de ligação CACCTG e CAACA (ROMANEL et al., 2009; KAGAYA; OHMIYA; HATTORI, 1999; XIE et al., 2019). Este motivo está relacionado à tolerância ao estresse osmótico e, assim como o domínio AP2, contém uma alta afinidade e especificidade de ligação às sequências alvo, graças a presença dos seus motivos característicos (ZHAO et al., 2019; KAGAYA, OHMIYA; HATTORI, 1999).

A subfamília solista possui também um único domínio AP2, porém o que se sabe é que estes divergem de maneira bastante significativa dos demais membros da superfamília AP2/ERF (NAKANO et al., 2006).

Figura 1. Alinhamento dos domínios conservados AP2/ERF de *A. thaliana*

Subfamília APETALA2

R1 (Repeat1)

		-----YRG-----	-----RAYD-----	
consensus		.S..YRGVT..R.TGR.E.H.WD.....G.QVYLGG.D....AARAYD.AA.K..G....NF....Y....		
AtAP2	1	SSYRGVTFRRRTGRREHHWD.....CGQVYLGGDTAHAAARAYDRAAARFCEVADINFNIDDDDDL	67	
Glossy15	1	SSYRGVTFRRRTGRREHHWD.....CGQVYLGGDTAQAAARAYDRAAARFCEVADINFNIDDDDDL	67	
ZmINSPIK1	1	SSYRGVTFRRRTGRREHHWD.....CGQVYLGGDTAHAAARAYDRAAARFCEVADINFNIDDDDDL	67	
ANT	1	SSYRGVTRRRRTGRREHHWDNSFKKEGHSRKGQVYLGGDMEEKAAARAYDLAAARFCEVADINFNIDDDDDL	77	
BnBBM2	1	SSYRGVTRRRRTGRREHHWDNSCKREGQTRKGQVYLGGDMEEKAAARAYDLAAARFCEVADINFNIDDDDDL	77	
AtBBM	1	SSYRGVTRRRRTGRREHHWDNSCKREGQTRKGQVYLGGDMEEKAAARAYDLAAARFCEVADINFNIDDDDDL	77	

Linker

Consensus		.M.....E.V...LRR...GF.RG
AtAP2	1	EMKHMTRDEIVASLRRSSGFSRG 25
Glossy15	1	EMKHMTRDEIVASLRRSSGFSRG 25
ZmINSPIK1	1	EMKHMTRDEIVASLRRSSGFSRG 25
ANT	1	EMKHMTRDEIVASLRRSSGFSRG 25
BnBBM2	1	EMKHMTRDEIVASLRRSSGFSRG 25
AtBBM	1	EMKHMTRDEIVASLRRSSGFSRG 25

R2 (Repeat2)

		-----YRG-----	-----RAYD-----	
Consensus		.S..RGVT..H..G.W.A.R.G...G.K..YLG.....EAA.AYD.AA....G..AVTNF....Y....		
AtAP2	1	SSRGVTFRRRTGRREHHWD.....CGQVYLGGDTAHAAARAYDRAAARFCEVADINFNIDDDDDL	68	
Glossy15	1	SSRGVTFRRRTGRREHHWD.....CGQVYLGGDTAHAAARAYDRAAARFCEVADINFNIDDDDDL	68	
ZmINSPIK1	1	SSRGVTFRRRTGRREHHWD.....CGQVYLGGDTAHAAARAYDRAAARFCEVADINFNIDDDDDL	68	
ANT	1	SSRGVTRRRRTGRREHHWDNSFKKEGHSRKGQVYLGGDMEEKAAARAYDLAAARFCEVADINFNIDDDDDL	69	
BnBBM2	1	SSRGVTRRRRTGRREHHWDNSCKREGQTRKGQVYLGGDMEEKAAARAYDLAAARFCEVADINFNIDDDDDL	69	
AtBBM	1	SSRGVTRRRRTGRREHHWDNSCKREGQTRKGQVYLGGDMEEKAAARAYDLAAARFCEVADINFNIDDDDDL	69	

Subfamília ERF

AtERF#100 (AtERF1)	(IX)	HYRGVRRQRP	SKFAAGIRDP	AKNGARVWLG	TFPTAEDDAL	AYDRAAFMR	GSRALLNEP
		***	**	**			
AtERF#001 (WIN1/SHN1)	(V)	KRYGVRRQRP	SKFAAGIRDP	LL-KRRINLG	TFPTAEDDAL	AYDRAAFMR	GSRALLNEP
AtERF#007 (RAP2.9)	(II)	KRYGVRRQRP	SKFAAGIRDP	NK-KRRINLG	TFPTAEDDAL	AYDRAAFMR	GSRALLNEP
AtERF#029 (CBF1/DREB1B)	(III)	KRYGVRRQRP	SKFAAGIRDP	NK-KRRINLG	TFPTAEDDAL	AYDRAAFMR	GSRALLNEP
AtERF#040 (TINY)	(III)	KRYGVRRQRP	SKFAAGIRDP	NK-KRRINLG	TFPTAEDDAL	AYDRAAFMR	GSRALLNEP
AtERF#045 (DREB2A)	(IV)	KRYGVRRQRP	SKFAAGIRDP	NK-KRRINLG	TFPTAEDDAL	AYDRAAFMR	GSRALLNEP

Subfamília DREB

AtDREB1A	1	PIIRGVRRR-NSGKVVCEIREP-NKKTRVWLG	FDTAEAAARADVAALALGRSACLNFD	60
AtDREB1B	1	PIIRGVRRR-NSGKVVCEIREP-NKKTRVWLG	FDTAEAAARADVAALALGRSACLNFD	60
AtDREB1C	1	PIIRGVRRR-NSGKVVCEIREP-NKKTRVWLG	FDTAEAAARADVAALALGRSACLNFD	60
AtDREB2A	1	CSIRGVRRR-IWGWVCEIREP-NRGRVWLG	FDTAEAAARADVAALALGRSACLNFD	60
AtDREB2B	1	CSIRGVRRR-IWGWVCEIREP-NRGRVWLG	FDTAEAAARADVAALALGRSACLNFD	60
OsDREB1A	1	PVERGVRRRGNAGKVVCEIREP-NRGRVWLG	FDTAEAAARADVAALALGRSACLNFD	62
OsDREB2A	1	CAIRGVRRR-TWGWVCEIREP-NRGRVWLG	FDTAEAAARADVAALALGRSACLNFD	60

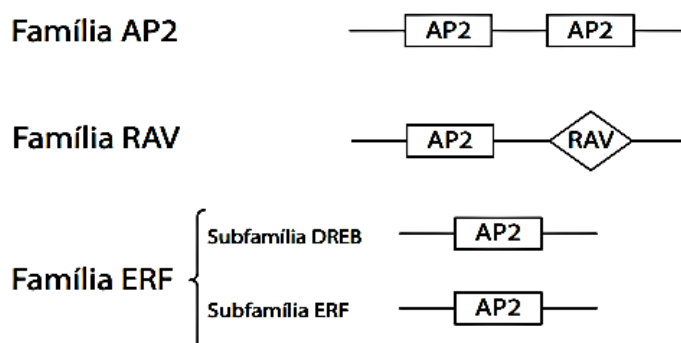
Subfamília RAV

			AP2 domain	
BNAVAV-1-HY15		MEVSCVDESTTS.....TCSEIYETPAITPAKTSVNLHRMGSG.SSVVLDABNGARABSRKLP.SSRKMGVYVQDNGRGAQIYKSRHNLWG		
RAV2_AT1G25560.1		MEVSCVDDSTTSSESISSTTPKPTTTTEKLSSPPATSMRLYRMGSGSSVLDSENGVETESRKLPS.SSRKMGVYVQDNGRGAQIYKSRHNLWG		
RAV1_AT1G50680.1		MRDDDEPENALVVS.....SRTVVASGN.....VRGRGVYVQDNGRGAQIYKSRHNLWG		
RAV1_AT1G51120.1		MDMSVAKTTSSESISSTTPKPTTTTEKLSSPPATSMRLYRMGSGSSVLDSENGVETESRKLPS.SSRKMGVYVQDNGRGAQIYKSRHNLWG		
RAV2_AT1G68840.1		MDSCIDEISSS.....TSSEFSATTAKLSPPPAALRLYRMGSGSSVLDSENGVETESRKLPS.SSRKMGVYVQDNGRGAQIYKSRHNLWG		
			YRG element	WLG motif
BNAVAV-1-HY15		FEDEEAAARSIVAVHREGRDAVTFNFKDARLD..DGEVSELSHSHKSGIVDLKSKHTYSRELEQSKRR.....RNGGNVAVRSTTQNDGVSTTE		
RAV2_AT1G25560.1		FEDEEAAARSIVAVHREGRDAVTFNFKDARLD..DGEVSELSHSHKSGIVDLKSKHTYSRELEQSKRR.....RNGGNVAVRSTTQNDGVSTTE		
RAV1_AT1G50680.1		FEDEEAAARSIVAVHREGRDAVTFNFKDARLD..DGEVSELSHSHKSGIVDLKSKHTYSRELEQSKRR.....RNGGNVAVRSTTQNDGVSTTE		
RAV1_AT1G51120.1		FEDEEAAARSIVAVHREGRDAVTFNFKDARLD..DGEVSELSHSHKSGIVDLKSKHTYSRELEQSKRR.....RNGGNVAVRSTTQNDGVSTTE		
RAV2_AT1G68840.1		FEDEEAAARSIVAVHREGRDAVTFNFKDARLD..DGEVSELSHSHKSGIVDLKSKHTYSRELEQSKRR.....RNGGNVAVRSTTQNDGVSTTE		
			B3 domain	
BNAVAV-1-HY15		FEAVSLEPRAVPSDVGKLNRLVPRHAKHFEPLSPS.....NVSVRGVNLNFEVAGKVFERYSYNSSQSVYDAGSRFVKEKNLRA		
RAV2_AT1G25560.1		FEAVSLEPRAVPSDVGKLNRLVPRHAKHFEPLSPS.....NVSVRGVNLNFEVAGKVFERYSYNSSQSVYDAGSRFVKEKNLRA		
RAV1_AT1G50680.1		FEAVSLEPRAVPSDVGKLNRLVPRHAKHFEPLSPS.....NVSVRGVNLNFEVAGKVFERYSYNSSQSVYDAGSRFVKEKNLRA		
RAV1_AT1G51120.1		FEAVSLEPRAVPSDVGKLNRLVPRHAKHFEPLSPS.....NVSVRGVNLNFEVAGKVFERYSYNSSQSVYDAGSRFVKEKNLRA		
RAV2_AT1G68840.1		FEAVSLEPRAVPSDVGKLNRLVPRHAKHFEPLSPS.....NVSVRGVNLNFEVAGKVFERYSYNSSQSVYDAGSRFVKEKNLRA		

Fonte: Adaptado de Saleh; Pagès, 2003; Zhuang et al., 2011; Nakano et al., 2006

Figura 2. Estrutura dos fatores de transcrição AP2/ERF.

Classificação da Família AP2/ERF



Fonte: ITO et al., 2012.

2.2 Bioinformática no ramo da genômica

Buscando a otimização do processamento e análise de dados biológicos, constantemente estão sendo desenvolvidas novas ferramentas de bioinformática. Para isto é preciso unir metodologias de biologia celular com tecnologias computacionais. Com os constantes avanços de projetos genômicos, os impactos por eles produzidos e diante da geração de grande quantidade de dados, percebeu-se a necessidade de decodificar e armazenar esses dados. A existência dos bancos de dados permite que eles sejam utilizados para desvendar a provável função de genes e demais características acerca do genoma estudado. A bioinformática, integrando distintas áreas do conhecimento, tem se mostrado essencial para pesquisas de base, como a predição de funções proteicas e também no diagnóstico de doenças e anomalias a partir de dados brutos, obtidos de sequenciamento (ARAÚJO et al., 2008). E tão importante quanto à decodificação de dados biológicos, são os bancos de dados onde estes são depositados.

Plataformas científicas, como o *National Center for Biotechnology Information-NCBI* (<https://www.ncbi.nlm.nih.gov/>) proporcionam o acesso a dados e informações sobre a pesquisa a serem realizadas. Em bancos de dados podemos encontrar sequências proteicas, muitas vezes utilizadas como base nas análises, e ferramentas de processamento de dados como o BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) (ALTSCHUL et al., 1990). A partir desta ferramenta são possíveis análises de comparação entre sequências por similaridade de sequências, uma das principais metodologias utilizadas no ramo da bioinformática. Com

outras ferramentas podem ser realizadas diversas outras análises, como a checagem de domínios conservados com o *The Protein Families Database*-Pfam (FINN et al., 2014), bem como alinhamentos e análises filogenéticas, que predizem a identidade de sequências, bem como a sua distância evolutiva.

Tendo em vista a gama de processos em que é aplicada, a bioinformática vem sendo cada vez mais utilizada graças à robustez das análises, aliadas ao uso de tecnologias computacionais para investigação e predição da função de genes e proteínas, envolvidos nos mais diversos mecanismos biológicos (ESPÍNDOLA et al., 2010).

3 OBJETIVOS

3.1 Objetivo geral

Caracterizar os genes que codificam os fatores de transcrição da família AP2/ERF na linhagem vegetal, desde algas até Pteridófitas.

3.2 Objetivos específicos

- Identificar os genes da família AP2/ERF nos genomas de algas, algas verdes, briófitas e pteridófitas;
- Classificar os genes encontrados em subfamílias AP2, DREB, ERF, RAV;
- Comparar com os genes já conhecidos em Angiospermas;
- Caracterizar a origem e a evolução de cada uma destas subfamílias.

4 MATERIAL E MÉTODOS

4.1 Buscas pelas sequências transcricionais da família AP2/ERF em *Arabidopsis thaliana* em bancos de dados

Inicialmente foram realizadas revisões na literatura para identificar os códigos de sequências gênicas que codificam fatores de transcrição das subfamílias: AP2, ERF, DREB, RAV e Solista em *Arabidopsis thaliana*. As buscas foram realizadas no banco de dados *The Universal Protein Resource*-UniProt (<https://www.uniprot.org/>) (APWEILER et al., 2004)

uma plataforma completa que disponibiliza sequências proteicas, bem como suas respectivas anotações e classificações. Os códigos de identificação das sequências usados como “query” foram obtidos através da publicação “*AP2/ERF family transcription factors in plant abiotic stress responses*” de Mizoi e colaboradores (Tabela 1).

Tabela 1. Códigos de identificação de TF's da superfamília AP2/ERF de *A. thaliana* na plataforma UniProt e NCBI.

Fator de transcrição	Número de acesso gene	Número de acesso proteína
RAP2.7 R1	AT2G28550	Q9SK03
WR11 R1	AT3G54320	Q6X5Y6
SOLIST	AT4G13040	Q56XP9
RAV1	AT1G13260	Q9ZWM9
RAP2.11	AT5G19790	Q6J9S1
DREB2D	AT1G75490	Q9LQZ2
DREB A-5	AT1G44830	Q9LPE8
DREB A-1	AT2G35700	Q9ZQP3

4.2 Bancos de dados de genomas vegetais

Foram obtidas do banco de dados *1000 plants* (<https://db.cngb.org/onekp/>), localizado no *China National GeneBank-CNGB*, sequências proteicas codificadas pelos genomas de espécies pertencentes as classes vegetais de algas, briófitas e pteridófitas (APÊNDICE 1). A partir das sequências FASTA das espécies foram construídos novos bancos de dados, um para cada grupo vegetal, que foram utilizados em todas as análises seguintes.

4.3 Identificações das sequências dos fatores de transcrição AP2/ERF nas linhagens selecionadas

As sequências primárias obtidas no item 4.1 foram usadas como “query” na ferramenta Blastp (ALTSCHUL et al., 1990) contra o banco de dados multifasta criado no item 4.2. Os resultados obtidos do Blastp foram salvos em formato FASTA.

4.4 Análises dos domínios conservados da superfamília de TF's AP2/ERF

Usando o software Blast2GO (versão 5.2.1) (CONESA; GOTZ, 2007) os arquivos FASTA obtidos anteriormente foram submetidos às análises de BLAST e InterProScan contra o banco de dados NCBI e The *protein families database*-Pfam (FINN et al., 2014). Esta análise permitiu a identificação dos domínios conservados dos membros da família AP2/ERF. As sequências que não apresentaram o domínio conservado característico da superfamília AP2/ERF foram descartadas e não participaram das análises seguintes.

4.5 Alinhamentos dos fatores de transcrição AP2/ERF

Após a verificação dos domínios conservados, as sequências “query” da família de fatores de transcrição AP2/ERF de *A. thaliana*, juntamente com as que se confirmaram possuir o domínio AP2/ERF foram submetidas aos alinhamentos múltiplos feitos através da ferramenta Muscle (EDGAR, 2004) e seus resultados foram exportados como FASTA.

4.6 Análises filogenéticas das sequências de AP2/ERF

A análise filogenética foi executada com o programa MEGA X (KUMAR et al., 2018) utilizando o método *Neighbor-Joining* (SAITOU, NEI, 1987), modelo JTT, com o teste filogenético Bootstrap 1000. Para a obtenção da árvore filogenética e identificação da distância evolutiva foram utilizadas as sequências das proteínas AP2/ERF de *A. thaliana*, descrita por Mizoi, Shinozaki e Yamaguchi-Shinozaki (2012), e as sequências de proteínas AP2/ERF identificadas nas linhagens vegetais analisadas.

5 RESULTADOS E DISCUSSÃO

5.1 Identificação e classificação dos fatores de transcrição AP2/ERF nas linhagens vegetais

Como resultado do Blastp, realizado com as sequências de referência, foi possível identificar 483 possíveis sequências codificantes dos fatores de transcrição da superfamília AP2/ERF dentre as espécies das linhagens vegetais analisadas (Tabela 2). As sequências que

não apresentavam o domínio conservado ou apresentavam estarem incompletas foram retiradas das análises subsequentes.

Tabela 2. Sequências dos fatores AP2/ERF encontradas em Algas, Algas Verdes, Briófitas e Pteridófitas.

Linhagem	Nº de sequências identificadas
Algas	4
Algas Verdes	134
Briófitas	165
Pteridófitas	180
TOTAL	483

5.2 Alinhamentos do domínio conservado AP2/ERF

Os alinhamentos demonstraram a presença do domínio conservado AP2/ERF, bem como os motivos característicos de cada subclasse de fatores de transcrição (FIGURAS 3, 4, 5 e 6). Segundo Okamuro e colaboradores (1997) este motivo inicial pode estar intimamente relacionado à ligação dos fatores de transcrição AP2/ERF aos promotores alvos por apresentar uma alta taxa de conservação em muitas outras espécies estudadas.

Figura 3. Alinhamento do domínio AP2/ERF das espécies de algas *Picochlorum atomus* (JQFK) e *Chroomonas* sp (ROZZ) com proteínas de *Arabidopsis* (sp). Em azul e vermelho estão destacadas as porções responsáveis pela formação de folhas Beta e Alfa-hélices descritas por Nakano e colaboradores (2006), respectivamente.

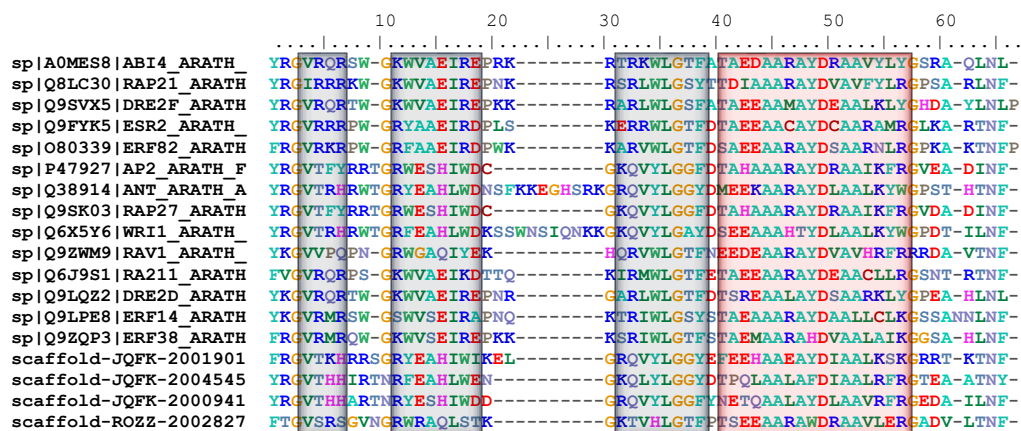


Figura 4. Alinhamento do domínio AP2/ERF de espécies de algas verdes (scaffolds) com proteínas de *Arabidopsis* (sp). Em azul e vermelho estão destacadas as porções responsáveis pela formação de folhas Beta e Alfa-hélices descritas por Nakano e colaboradores (2006), respectivamente.

	10	20	30	40	50	60	70	80	90
sp A0MES8 ABI4_ARATH	YRGV-RORSWQKWAEEI	R	EPKRRTRKWLGTFAEDAA	RAYDRAAVYL	YG-S	RA-Q	LNL		
sp Q8LC30 RAP21_ARATH	YRGI-RRRKWQKWAEEI	R	EPNKRSLRLWLGSYTTDIAAA	RAYDVAVFYLL	RG-P	SA-R	LNF		
sp Q9SVX5 DRE2F_ARATH	YRGV-RORTWQKWAEEI	R	EPKRRRLRLWLGSPTAEAAA	MAYDEAAKL	YG-H	DA-Y	LNL		
sp Q9FYK5 ESR2_ARATH	YRGV-RRRPWGRYAAEI	R	DPLSKERRRLWLGTDDAEAAA	CAYDCAARAM	RG-L	KA-R	TNF		
sp O80339 ERF82_ARATH	FRGV-RKRPPWGRFAAEI	NDPW	KARVWLGTDDAEAAA	RAYDSAAINL	RG-P	KA-K	TNF		
sp P47927 AP2_ARATH_F	YRGVTFYRRTGRWESHI	W	DCGQVYLGGLDFAHAAA	RAYDRAAIKF	RG-V	EA-D	LNF		
sp Q38914 ANT_ARATH_A	YRGVTRHRTGRYEAHL	W	DNSFKKEGHSRGRQVYLGGLDMEEKAA	RAYDLAALKY	WG-P	ST-H	TNF		
sp P47927 AP2_ARATH_F	YRGVTFYRRTGRWESHI	W	DCGQVYLGGLDFAHAAA	RAYDRAAIKF	RG-V	EA-D	LNF		
sp Q9SK03 RAP27_ARATH	YRGVTFYRRTGRWESHI	W	DCGQVYLGGLDFAHAAA	RAYDRAAIKF	RG-V	DA-D	LNF		
sp Q6X5Y6 WRI1_ARATH	YRGVTRHRTGRFEAHL	W	DKSSWNSIQNKKGQVYLGAYDEEAAA	HTYDLAALKY	WG-P	DT-I	LNF		
sp Q9ZWM9 RAV1_ARATH	YRGV-VQPNGRWGAQI	Y	EKGQVYLGGLTPNDEEAAA	RAYDVAVIRF	RR-R	DA-V	TNF		
sp Q6J9S1 RA211_ARATH	FRGV-RORPSGKWAEEI	K	DTTKIRMLWLGTTPAEAAA	RAYDEAACLL	RG-S	NT-R	TNF		
sp Q9LQ22 DRE2D_ARATH	YRGV-RORTWQKWAEEI	R	EPNRRRLWLGTDDSEAAA	LAYDAAIKL	YG-P	EA-H	LNL		
sp Q9LPE8 ERF14_ARATH	YRGV-RMRSGWSVSEI	R	APNKRIRLWLGSYSTAEAAA	RAYDAALLCL	KG-S	SANN	LNF		
scaffold-XJGM-2004684	YRGVTFYRRTGRWESHI	W	QDGKQVYLGGLYNDVAAA	RAYDKASIKF	RG-A	EA-E	LNF		
sp Q9ZQP3 ERF38_ARATH	FRGV-RMRQWGWVSEI	R	EPKKRSIRLWLGTSTAEAAA	RAHDVAALAI	KG-G	SA-H	LNF		
scaffold-XRT2-2006949	YRGVTFYRRTGRWESHI	W	DSGRQVYLGGLDFAVAAAYIAYDQAAIKF		RG-V	TA-E	TNF		
scaffold-XMCL-2002058	YRGVTFYRRTGRWESHI	W	DEGRQVYLGGLDFAEIAAA	RAYDKAAIKF	RG-Q	TA-D	TNF		
scaffold-NNHQ-2034102	YRGVTFYRRTGRWESHI	W	QDGKQVYLGGLDSEEA	RSYDRAALRL	RGPE	DA-E	LNF		
scaffold-MXE2-2005400	FRGVTKHRTGRWEAHV	W	DEGNQVYLGGLDTEERAG	RAYDIALKC	RG-R	DT-E	TNF		
scaffold-JMTE-2016560	FRGVTKHRTGRWEAHV	W	DEGNQVYLGGLDTEERAG	RAYDIALKC	RG-R	DT-E	TNF		
scaffold-TGNL-2001628	FRGVTHHCRTRGRWEAHI	W	EDGQVYLGGLDSEEQAA	LAYDIAAIKC	RG-S	KA-V	TNF		
scaffold-HYHN-2002914	FRGVYYRKTGRWDIAHI	W	HGGQVYLGGLDDEEKAA	RAYDQACLFK	RG-T	AA-E	LNF		
scaffold-XMCL-2003231	YRGVTKHRTGRWEAHV	W	DSGRQVYLGGLDDEEKAA	RAYDIISLKA	RG-D	NA-M	TNF		
scaffold-XJGM-2004017	FRGVTHHCRTRGRWEAHI	W	ESGQVYLGGLDSEEQAA	LAYDIAAIKC	RG-R	DA-Q	TNF		
scaffold-XJGM-2004775	YRGVTFHRTGRWEAHL	W	DGGKQVYLGGLDSETKAA	TAYDFMALKC	RE-K	DA-Q	LNF		
scaffold-XMCL-2003517	YRGVTFHRTGRWEAHL	W	DGGKQVYLGGLDSEAKAA	TAYDFMALKC	RG-E	DA-C	LNF		
scaffold-HKZ-2004193	YRGVTHHRTGRWEAHI	W	ESSKQVYLGGLDSEEQAA	LAYDMAAIKC	RG-P	SA-T	TNL		
scaffold-GJY-2018987	FRGVTHHCRTRGRYESHI	W	DSGQVYLGGLDTEEQAA	LAYDLAAIKC	RG-A	DA-T	TNF		
scaffold-CBNG-2005394	FRGVTHHCRTRGRYESHI	W	DCGQVYLGGLDTEEQAA	LAYDLAAIKC	RG-T	EA-T	TNF		
scaffold-JIWI-2039695	FRGVTHHCRTRGRYESHI	W	DCNQVYLGGLDTEEQAA	LAYDLAAIKC	RG-Q	EA-Y	TNF		
scaffold-OQON-2007511	YRGVTHHCRTRGRYESHI	W	DSGQVYLGGLDSEEQAA	LAYDLAAIKC	RG-E	EA-Q	TNF		
scaffold-XMCL-2016286	FRGVTHHCRTRGRWEAHI	W	ESKQVYLGGLDSEEQAA	LAYDIAAIKC	RG-K	EA-V	TNF		
scaffold-LETF-2022423	FRGVTHHCRTRGRYESHI	W	DCGQVYLGGLDTEEQAA	LAYDLAAIKC	RG-S	DA-T	TNF		
scaffold-VAZE-2007381	YRGVTHHRTGRWEAHI	W	EDSKQVYLGGLDTEQDAA	LAYDIAALKF	RG-R	DA-V	TNF		
scaffold-XMCL-2003047	YRGVAIHRLTGRWEAHI	W	KSGQVYLGGLDSEEA	RIYDQAAIKL	KG-T	SA-Q	LNF		
scaffold-HYHN-2016399	YRGVTRHRTGRFEAHL	W	DAGKQVYLGGLDSEEA	RAYDLMSLHC	RGQA	DA-Q	LNF		
scaffold-WDGV-2011669	FRGVTHHCRTRGRWEAHI	W	ESKQVYLGGLDSEDMAA	FAYDIAAIKRVFAGFRG	RG-S	DA-H	TNL		
scaffold-LSHT-2001918	YRGVTHHCRTRGRFESHI	W	DSGQVYLGGLDTEEQAA	LAYDLAAVKC	RG-H	SA-I	TNF		
scaffold-AJAU-2037420	YRGVTHHCRTRGRYESHI	W	DCGQVYLGGLDTEAQAA	LAYDLAAVKC	RG-P	SA-A	TNF		
scaffold-XJGM-2002730	FRGVTHHRTGRFEAHL	W	YGGQVYLGGLDDEVKAA	RAYDIALVLC	RG-E	SA-Q	TNF		
scaffold-KSFK-2004026	YRGVTHHCRSSRFESHI	W	DAGKQVYLGGLDSEEA	IAYDLAAIKF	RG-H	EA-S	TNF		
scaffold-MXE2-2001130	FRGVTHHCRTRGRWEAHI	W	EGGRQVYLGGLDSEEQAA	LAYDIAAIKC	RG-Q	HA-A	TNY		
scaffold-JMTE-2004735	FRGVTHHCRTRGRWEAHI	W	EGGRQVYLGGLDSEEQAA	LAYDIAAIKC	RG-Q	HA-A	TNY		
scaffold-OAE2-2004460	FRGVTHHCRTRGRYESHI	W	DSGQVYLGGLDTEEQAA	LAYDLAAVKC	RG-Q	TA-I	TNF		
scaffold-OAE2-2004461	YRGVTHHCRTRGRYESHI	W	DSGQVYLGGLDSEEQAA	LAYDLAAIKC	RG-E	DA-Q	TNF		
scaffold-TGNL-2008943	YRGVTHHCRSSRWEAHI	W	VKEGQVYLGGLDSEEHAA	EAYDVAAIKC	KG-S	TV-K	TNF		
scaffold-MXE2-2003601	FRGVTRHRSRGRWEAHL	W	CRETGKQVYLGGLDSEEHAA	EAFDVAAIKC	KGRE	KA-K	LNF		
scaffold-JMTE-2003979	FRGVTRHRSRGRWEAHL	W	CRETGKQVYLGGLDSEEHAA	EAFDVAAIKC	KGRE	KA-K	LNF		
scaffold-XJGM-2002731	YRGVTHHRTGRFEAHL	W	YGGQVYLGGLDDEVKAA	RAYDIALVLC	RG-E	SA-Q	TNF		
scaffold-XMCL-2000255	YRGVTHHRSRGRWEAHI	W	SARLKGQVYLGGLDTEEDAA	EADHIFSLKC	KK-D	KA-V	LNF		
scaffold-NQYP-2026622	FRGVTHHCRTRGRYESHI	W	DNGKQVYLGGLDTEEQAA	LAYDLMAVKC	RG-A	QA-I	TNF		
scaffold-BZSH-2002154	FRGVTHHCRTRGRWEAHI	W	VKEGQVYLGGLDSEEHAA	EAYDVAAIKC	KG-K	KV-K	TNF		
scaffold-KSFK-2004473	FRGVTHHCRTRGRFESHI	W	DSGQVYLGGLDTEEQAA	LAYDLAAIKC	RG-P	TA-I	TNF		
scaffold-GYBH-2000485	YRGVTHHRSRGRWEAHI	W	IKDIGRQVYLGGLDSEEHAA	EAYDVAAIKC	KG-R	RV-K	TNF		
scaffold-HYHN-2003812	YRGVTFHRTGRYESHI	W	SGGQVYLGGLDSEEA	TAFDFMALKC	RG-D	DA-Q	LNF		
scaffold-JIWI-2040818	YRGVSRHRLTRWEASV	W	SGRQVYLGGLDTEASAA	KAYDIASLVL	KG-G	SG-T	TNF		
scaffold-TGNL-2008788	FRGVTHHRTGRWEAHI	W	EIKKQVYLGGLDSEEA	RAYDVMAIKL	RGTR	EA-D	TNF		
scaffold-SNOX-2007103	FRGVTHHRTGRWEAHI	W	EEGKQVYLGGLDSEEQAA	LAYDIAAIKC	RG-R	EA-I	TNL		
scaffold-ZFXU-2007117	YRGVTRHRTGRYESHI	W	DSSAPRKSSSANGKGRTRGQVYLGGLDTEEEAA	RAYDRAAIKY	WG-Q	TA-Q	LNF		
scaffold-MNPL-2006997	FRGVTRHRTGRYESHI	W	DSSAPRKSSSANGKGRTRGQVYLGGLDTEEEAA	RAYDRAAIKY	WG-Q	TA-Q	LNF		
scaffold-NKUU-2001509	YRGVTHHRSRGRWEAHI	W	VREMGQVYLGGLDSEEHAA	EAYDVAAIKC	KG-F	KV-K	TNF		
scaffold-YOXI-2008251	YRGVTHHRTGRWEAHI	W	EDSKQVYLGGLDSEEA	LAYDIAALKF	RG-P	DA-V	TNF		
scaffold-KSFK-2023795	YRGVTHHRSRGRWEAHI	W	IGKQVYLGGLDSEEHAA	EAYDMAALKT	KG-F	ET-P	TNF		
scaffold-NQYP-2005716	YRGVTHHRSRGRYESHI	W	SEGKQVYLGGLDSEEHAA	IAYDLAAIKF	RG-S	SA-V	TNF		
scaffold-GYBH-2023467	YTGVSQKHKSRGRWEVHI	W	LSDLGRQVYLGGLDDVAAA	EAYDIVQLRS	RG-L	DA-K	TNF		
scaffold-ODXI-2018702	FRGVTHHRSRGRWEAHI	W	IKDIGRQVYLGGLDSEEHAA	EAYDVAAIKT	KG-L	KS-K	TNF		
scaffold-HHXJ-2002769	FRGVTRHRTGRFEAHL	W	DSSVERVVRNNVGRRRGQVYLGGLDSEEA	RAYDKAALKY	WG-K	NA-T	LNF		
scaffold-JIWI-2039799	YRGVTHHRSRGRWEAHI	W	IGGKQVYLGGLDSEEHAA	EAYDMAALKT	KG-F	DT-P	TNF		
scaffold-AKCR-2022107	YRGVSKHRLTRWEASL	W	LAGRQVYLGGLDPODDAA	RAYDIAALAC	KG-E	GA-D	TNF		
scaffold-BILC-2020016	FRGVTHHRLTRGRFEAHL	W	DASHKREVKGGKGRTRGQVYLGGLDTEEEAA	RAYDLAALAF	LG-S	AA-P	LNF		
scaffold-BILC-2000056	FRGVTHHRSRGRYESHI	W	VKDLGRQVYLGGLDSEEHAA	EAYDIAALKC	KGRR	GC-K	TNF		
scaffold-XMCL-2000957	YRGVSRHRLTRWEASL	W	IKRQVYLGGLDTEIKAA	RAYDVAAIKC	KG-P	GT-P	TNF		
scaffold-HYHN-2002847	YRGVAIHRTGRWEAHL	W	AGRGQVYLGGLDSEETA	RVFDRACRLR	RP-R	DA-AVKMLNF			
scaffold-GXBM-2015916	YRGVTHHRSRGRWEAHL	W	VREDGQVYLGGLDSEEA	EADHVAALKC	HG-L	KA-K	TNF		
scaffold-GJY-2019487	YRGVTHHRSRGRWEAHI	W	IGKQVYLGGLDSEEHAA	EAYDMAALKT	KG-F	DT-P	TNF		
scaffold-ZDOF-2035777	FRGVTHHRSRGRWEAHI	W	VKDLGRQVYLGGLDSEEHAA	EAYDVAAIKC	KG-M	KV-K	TNF		
scaffold-TGNL-2002590	FRGVTRHRTGRWEAHL	W	SGKQVYLGGLDSEAKAA	QAYDKAVLTL	RG-K	AA-V	TNF		
scaffold-QYXY-2046093	YRGVTHHRSRGRWEAHL	W	VKEGRQVYLGGLDSEEQAA	EAYDVAAIKC	KG-P	RA-A	TNL		
scaffold-EEJO-2009604	FRGVSRHRLTRWEASL	W	LGRQVYLGGLDSEEDAA	HAYDLAALAC	KG-L	DA-Q	LNF		
scaffold-AJAU-2034888	YRGVTHHRSRGRWEAHI	W	IGGKQVYLGGLDSEEHAA	EAYDMAALKT	KG-F	DT-P	TNF		
scaffold-TNAA-2078645	FRGVTRHRTGRFEAHL	W	DSSCIRDNKTGKGRTRGQVYLGGLDSEEA	RAYDRAAIKY	WG-D	KA-T	TNF		
scaffold-LETF-2022055	YRGVTHHRSRGRWEAHI	W	IGGKQVYLGGLDSEEHAA	EAYDMAALKT	KG-T	TA-T	TNF		
scaffold-LETF-2000971	FRGVTHHRTGRYESHI	W	DASAVNTSGARKTRGQVYLGGLDTEEA	RAYDRAAIKY	LG-D	KA-K	LNF		
scaffold-DXNY-2034656	FRGVTHHRSRGRWEAHI	W	VKDLGRQVYLGGLDSEEHAA	EAYDVAAIKC	KG-M	KV-K	TNF		
scaffold-NQYP-2001454	YRGVTHHRSRGRWEAHI	W	IGKQVYLGGLDSEEHAA	EAYDMAALKT	KG-F	AT-P	TNF		
scaffold-BZSH-2037682	YRGVTHHRTGRWEAHL	W	QDGKQVYLGGLDSEEQAA	FANDIAAIGM	KG-A	KA-V	TNF		
scaffold-XJGM-2023702	FRGVTRHRTGRWEAHL	W	DNERKDGTRGQVYLGGLDTEEAAG	KAYDRAAIKY	FGEE	RV-E	LNF		
scaffold-XOAL-2000596	FRGVTHHCRTRGRWEAHI	W	EDGKQVYLGGLDSEEQAA	LAYDIAAVKC	RG-R	DA-Q	LNF		
scaffold-HVNO-2006954	FRGVTRHRTGRYESHI	W	DPAAERACSSSSTGRRKGRQVYLGGLDTEEA	KAYDKAALAF	WG-D	KA-R	LNF		
scaffold-NNHQ-2004050	FRGVYDGRTRGRWEGYV	R	FNGKQVYLGGLDTEEEAA	LAYDLAAIKSS	RG-A	GA-V	TNF		

scaffold-CHJJ-2015669 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-BNCU-2017564 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-AWOI-2073679 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-NGTD-2008018 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TMAJ-2024209 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-VMXJ-2013364 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-RGKI-2006743 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-WSPM-2005726 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-WNGH-2090887 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-JADL-2010640 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ZACW-2015664 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-QMWB-2013075 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-QKQO-2012242 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-EEMJ-2009083 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-LNSF-2070298 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-FBMM-2004665 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-YEPO-2082282 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-IGUH-2021869 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TCBC-2014104 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-HERT-2009033 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-RDOO-2017995 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-NRWZ-2101123 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-DHWX-2069272 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-FFPD-2002776 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-CMEQ-2014630 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-BGXB-2082095 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TAVP-2011689 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-IRBN-2015009 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-YBQN-2013959 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-HPXA-2019593 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-LGOW-2105533 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-RTMU-2021445 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-WZYK-2016494 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TWUW-2009517 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-BSNI-2004871 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-FITN-2086600 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-AKXB-2011631 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-UCRN-2011439 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ZTHV-2015592 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-IRBT-2018690 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-OFTV-2002882 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-WEEQ-2013653 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-WJLO-2038118 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-KRUQ-2013358 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-UUHD-2017389 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-JHFI-2018921 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-LNSF-2010117 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-FTYI-2003310 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-YFGP-2018813 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ORKS-2058526 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-HVBQ-2019659 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-IHWO-2007265 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TXVB-2014377 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-JPYU-2004536 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-AWOI-2007087 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-IGUH-2017082 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ZACW-2007459 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-PIUF-2016506 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-QMWB-2008260 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TMAJ-2019624 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-WSPM-2046773 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-JADL-2006659 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-VBMM-2006013 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-EEMJ-2039276 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-TAVP-2007700 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ILBQ-2002531 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-BGXB-2081174 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-DHWX-2001234 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-SQD-2012843 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ZQRI-2005738 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-YEPO-2076662 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-RDOO-2009038 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-ZQRI-2005737 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-HVBQ-2131604 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-RGKI-2064441 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-VMXJ-2131054 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-FFPD-2013730 YRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGANT-TINF

scaffold-KEFD-2053122 YRGVTRHRWTGRYE¹⁰EAHLWDNS²⁰CRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPST-TINF

scaffold-IRBN-2013981 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKRYWGPST-LINF

scaffold-IHWO-2007267 FRGVTRHRWTGRYE¹⁰EAHLWDNS²⁰CRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPNT-TINF

scaffold-ABCO-2008193 YRGVTRHRWTGRFE¹⁰EAHLWDKSSW²⁰NDKQLKGRQVYLGGYDAEEAARAYDLAALKYWGAGT-VINF

scaffold-VBMM-2009296 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNEAQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-HVBQ-2007589 YRGVTRHRWTGRYE¹⁰EAHLWDNS²⁰CRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPST-TINF

scaffold-RDOO-2012594 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-NGTD-2013210 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-ABCD-2078166 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-GRKU-2021343 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQKKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-FFPD-2011359 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-JMXW-2010238 FRGVTRHRWTGRYE¹⁰EAHLWDKTCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-QMWB-2061497 FRGVTRHRWTGRYE¹⁰EAHLWDKSCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-CHJJ-2009253 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-VMXJ-2015109 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-ZTHV-2017512 YRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQKKGRQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-ANON-2008619 YRGVTRHRWTGRFE¹⁰EAHLWDKSAWNQSQNKKGQVYLGGYDEQAARAYDLAALKYWGPST-VINF

scaffold-RXRQ-2023776 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-WEEQ-2014813 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-HPXA-2011358 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-SKQD-2013275 YRGVTRHRWTGRYE¹⁰EAHLWDKTCW²⁰NDKQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-JHFI-2014632 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-BSNI-2009665 YRGVTRHRWTGRFE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-THW-2050471 YRGVTRHRWTGRFE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-BPSG-2020100 YRGVTRHRWTGRYE¹⁰EAHLWDNS²⁰CRKEGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPST-TINF

scaffold-UCRN-2051427 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-TFYI-2068150 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-IHWO-2011695 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-TXVB-2014057 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-JHFI-2113902 YRGVTRHRWTGRYE¹⁰EAHLWDKSCW²⁰NDKQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-PIUF-2092192 YRGVTRHRWTGRYE¹⁰EAHLWDKSCW²⁰NDKQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-DUHD-2150530 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-TCBC-2014529 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-QMWB-2008680 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-IRBN-2013980 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKRYWGPST-LINF

scaffold-RXRQ-2113920 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-2136366 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-FITN-2090607 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-FITN-2085763 YRGVTRHRWTGRYE¹⁰EAHLWDKSGSWNSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-DHXX-2070928 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-ANON-2034215 YRGVTRHRWTGRFE¹⁰EAHLWDKSSW²⁰NQAQKKKGQVYLGGYDEEEAARAYDLAALKYWGPST-TINF

scaffold-RXRQ-2124708 YRGVTRHRWTGRFE¹⁰EAHLWDKSTWNQTONKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-IGUH-2165053 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNEAQNKKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-NRWZ-2100444 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-RTMU-2013488 YRGVTRHRWTGRYE¹⁰EAHLWDKTCR²⁰NQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-BPSG-2013414 FRGVTRHRWTGRFE¹⁰EAHLWDKSCW²⁰NDKQLKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-BSNI-2009666 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-TWUW-2006424 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-IINF

scaffold-ZTHV-2013413 YRGVTRHRWTGRYE¹⁰EAHLWDKSSW²⁰NDKQHKGRQVYLGGYDEEEAARAYDLAALKYWGPST-VINF

scaffold-NRWZ-2002693 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNQSQNKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

scaffold-TMAJ-2018824 YRGVTRHRWTGRYE¹⁰EAHLWDKSTWNEAQNKKKGQVYLGGYDEEEAARAYDLAALKYWGPST-LINF

Figura 6. Alinhamento do domínio AP2/ERF de espécies de pteridófitas (scaffolds) com proteínas de *Arabidopsis* (sp). Em azul e vermelho estão destacadas as porções responsáveis pela formação de folhas Beta e Alfa-hélices descritas por Nakano e colaboradores (2006), respectivamente.

	10	20	30	40	50	60	70
sp A0MES8 ABI4_ARATH	YRGV	RRSW	GKWA	ETREPR	-----	KRTR	-----
sp Q8LC30 RAP21_ARATH	YRGV	RRRK	GKWA	ETREPN	-----	KRSR	-----
sp Q9SVX5 DRE2F_ARATH	YRGV	RQRT	GKWA	ETREPK	-----	KRAR	-----
sp Q9FYK5 ESR2_ARATH	YRGV	RRRP	GKWA	ETRDPL	-----	SKER	-----
sp O80339 ERF82_ARATH	FRGV	RKRP	GKWA	ETRDPL	-----	KKAR	-----
sp P47927 AP2_ARATH_F	YRGV	TFYR	RTGR	WESHID	-C-----	GKQ	-----
sp Q38914 ANT_ARATH_A	YRGV	TRHR	WTGR	FEAHLW	DNSF	FKKEGHSR	-KGRQ----
sp P47927 AP2_ARATH_F	YRGV	TFYR	RTGR	WESHID	-C-----	GKQ	-----
sp Q9SK03 RAP27_ARATH	YRGV	TFYR	RTGR	WESHID	-C-----	GKQ	-----
sp Q6X5Y6 WRI1_ARATH	YRGV	TRHR	WTGR	FEAHLW	DKSSWNSIQNK	-GKQ----	-----
sp Q9ZWM9 RAV1_ARATH	YKGV	VQPQ	NGRW	GQAQIE	-----	KHQR	-----
sp Q6J9S1 RA211_ARATH	FVGV	RQPS	GKWA	EIKDTTQKIR	-----	MW	-LGTEETAEEAARAYDEAACLLRGS-NTRTNF
sp Q38914 ANT_ARATH_A	YKGV	RQRT	GKWA	ETREPN	-----	RGAR	-----
sp Q9LPE8 ERF14_ARATH	YKGV	RMRS	WGSW	SEIRAPN	-----	QKTR	-----
sp Q9ZQP3 ERF38_ARATH	FRGV	RMRS	WGSW	SEIREPK	-----	KKSR	-----
scaffold-NWWI-2024501	YRGV	TFYR	RTGR	WESHID	-C-----	GKQ	-----
scaffold-NWWI-2006397	YRGV	TFYR	RTGR	WESHID	-C-----	GKQ	-----
scaffold-NWWI-2036201	MRGV	TRHR	WTGR	FEAHLW	DKSTWNQSQNK	-GKQ----	-----
scaffold-ALVQ-2008157	YRGV	TFYR	RTGR	WESHID	-C-----	GKQ	-----

scaffold-QVMR-2014896	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHTAARAYDRAALKFRGL	-DADINF	
scaffold-ZFGK-2006788	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-ZZOL-2002460	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-UPMJ-2019983	YRGVTFYRRTGRWESH	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-KJYC-2000129	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAQSAARAYDKAAIKFRGL	-DADINF	
scaffold-2006618	YRGVTFYRRTGRWESH	W	D	-	C	-----	CGKQ	----	VY--	LGGE	DTSHAAARAYDKAAIKFRGL	-DADINF	
scaffold-GTUO-2025514	YRGVTFYRRTGRWESH	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTSHTAARAYDKAAIKFRGL	-DADINF	
scaffold-GKAG-2010704	YRGVTFYRRTGRWESH	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTSHTAARAYDKAAIKFRGL	-DADINF	
scaffold-JVSZ-2131893	FRGVTFYRRTGRWEA	H	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAQTAARAYDRAAIKFRGL	-DADINF
scaffold-DFHO-2058448	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-EADINF	
scaffold-ABIJ-2008493	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-LGDQ-2003782	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-UGNK-2009040	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-GAON-2012197	YRGVTFYRRTGRWESH	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTSHNAARAYDKAAIKFRGL	-DADINF	
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scaffold-ZFGK-2000175	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-KUXM-2043901	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTSHSAARAYDKAAIKFRGL	-DADINF	
scaffold-DFHO-2009754	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
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scaffold-WCLG-2009145	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTSHSAARAYDRAAIKFRGL	-DADINF	
scaffold-JVSZ-2009599	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTSHSAARAYDRAAIKFRGL	-DADINF	
scaffold-BEGM-2000391	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-XDDT-2014872	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-EADINF	
scaffold-ENQF-2002028	YRGVTFYRRTGRWESH	W	D	-	C	-----	TGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
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scaffold-CAPN-2004389	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTSHSAARAYDRAAIKFRGL	-DADINF	
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scaffold-PYHZ-2076301	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTSHSAARAYDKAAIKFRGL	-DADINF	
scaffold-GTUO-2001943	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-EADINF	
scaffold-NYBX-2004406	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-EADINF	
scaffold-KUXM-2043751	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
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scaffold-XXHP-2003951	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-UPMJ-2016874	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-PKOX-2009486	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
scaffold-QHVS-2007795	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-QADINF	
scaffold-ULKI-2009010	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
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scaffold-YJJY-2016570	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
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scaffold-YOWV-2005126	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LG	DTALAAARAYDRAAIKFRGL	-DADINF	
scaffold-WTJG-2012311	FRGVTFYRRTGRWEA	H	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF
scaffold-JKAA-2178315	FRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTVHAARAYDKAAIKFRGL	-DADINF	
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scaffold-GTUO-2014774	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAAKAYDKAAIKFRGL	-DADINF	
scaffold-CAPN-2006565	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	YI--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-YIXP-2010510	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
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scaffold-WTJG-2012312	FRGVTFYRRTGRWESH	W	D	-	C	-----	VKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-KJYC-2008665	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
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scaffold-QVMR-2010385	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
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scaffold-PQTO-2082715	YRGVTFYRRTGRWESH	W	D	-	C	-----	TGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-EADINF	
scaffold-QVMR-2009765	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-EADINF	
scaffold-ALVQ-2007389	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-UPMJ-2082449	YRGVTFYRRTGRWESH	W	D	-	C	-----	SGKQ	----	VY--	LGGE	DTAHSAAARAYDKAAIKFRGL	-DADINF	
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scaffold-ALVQ-2007387	YRGVTFYRRTGRWESH	W	D	-	C	-----	GKQ	----	VY--	LGGE	DTAHSAAARAYDRAAIKFRGL	-DADINF	
scaffold-WGTU-2070826	YRGVTKHRTGRWEA	H	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTSHTAARAYDKAAIKFRGL	-DADINF
scaffold-NYBX-2123266	YRGVTFYRRTGRWESH	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTSHTAARAYDKAAIKFRGL	-DADINF	
scaffold-JVSZ-2131718	YRGVTRHRTGRWEA	H	W	D	-	C	-----	NGKQ	----	VY--	LGGE	DTEDKAARSYDLAALKYWG	-TTTINF

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scaffold-KJYC-2007474 YRGVTRHRWTGRYEEAHLWDNTCRKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-TTTINF
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scaffold-2104629 YRGVTRHRWTGRYEEAHLWDNSCRKEGGQTR-KGRQ-----VY--LGGYDREEKAARSYDLAALKYWGP-STHINF
scaffold-ZFGK-2008759 YRGVTRHRWTGRYEEAHLWDNTCRKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-STTTNF
scaffold-JVSG-2014406 YRGVTRHRWTGRYEEAHLWDNTCRKEGGQTR-KGRQ-----VY--LGGYDREDKAARSYDLAALKYWGP-SAHINF
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scaffold-WCLG-2008778 YRGVTRHRWTGRYEEAHLWDNSCRKEGGQTRRRKGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-STHTNF
scaffold-XDDT-2013649 YRGVTRHRWTGRYEEAHLWDKSNWNSQSK-KGRQ-----VY--LGAYDEDTAARSYDLAALKYWGP-DTILNF
scaffold-ALVQ-2001462 YRGVTRHRWTGRYEEAHLWDNSCRKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-TTHINF
scaffold-CAPN-2002949 YRGVTRHRWTGRYEEAHLWDNSCRKEGGQTR-KGRQ-----VY--LGGYDEKAARSYDLAALKYWGP-STHINF
scaffold-KUXM-2008976 YRGVTRHRWTGRYEEAHLWDNSCRKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-ATTINF
scaffold-GKAG-2001295 YRGVTFYRRTGRWESHIWD-----SGKQ-----VY--LGGFDTAHAARSYDKAII-----
scaffold-KJYC-2013663 YRGVTRHRWTGRYEEAHLWDKNTWNHTQNK-KGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF
scaffold-PYHZ-2073098 YRGVTRHRWTGRYEEAHLWDKSTWNHTQNK-KGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF
scaffold-PYHZ-2012844 YRGVTRHRWTGRYEEAHLWDKGSWNHSQNK-RGKQ-----VY--LGAYDEEEAARAYDLAALKYWGP-KSVLNF
scaffold-QHVS-2099240 YRGVTFYRRTGRWESHIWD-----CRKQ-----VY--LGGFDTADHARDYDRAIKF-----
scaffold-PKOK-2091976 YRGVTRHRWTGRYEEAHLWDKSTWNHTQNK-KGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF
scaffold-CBAE-2009147 YRGVTFYRRTGRWESHIWD-----NGKQ-----VY--LGGFDTSHNARSYDKAIKFRGL-DADI--
scaffold-ZFGK-2040624 YRGVTRHRWTGRYEEAHLWDKSTWNHSQNK-RGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF
scaffold-GTUO-2000602 FRGVTRHRWTSRYEEAHLWDKDAWNHTQKK-KGKQ-----VY--VGAYDEEEAARSYDLAALKYWGP-KTVLNF
scaffold-ULKT-2013401 YRGVTRHRWTGRYEEAHLWDNSCKKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-TTTINF
scaffold-EEAQ-2087743 YRGVTRHRWTGRYEEAHLWDKSTWNQNQNK-KGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF
scaffold-UGNK-2017092 YRGVTRHRWTGRYEEAHLWDKSTWNQNQNK-KGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF
scaffold-JVSG-2006493 YRGVTRHRWTGRYEEAHLWDKSTWNENQNK-RGKQ-----VY--LGAYDEEEAARSYDLAALKYWGPSTGTQINF
scaffold-ABIJ-2009206 YRGVTRHRWTGRYEEAHLWDKSTFLRSLSE-RRVC-----PFDLPGAYDEEEAARSYDLAALKYWGP-GTIL-L
scaffold-GAON-2055686 FRGVTRHRLTGRYEEAHLWDNSCKKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-TTTINF
scaffold-XDDT-2069201 YRGVTRHRWTGRYEEAHLWDNSCRKEGGQTR-KGRQ-----VY--LGGYDKEEKAARAYDLAALKYWGP-STHINF
scaffold-WGTU-2000067 YRGVTRHRWTGRYEEAHLWDKSTWNQNQNK-KGKQ-----VY--LGAYDEEEAARSYDLAALKYWGP-GTLINF

```

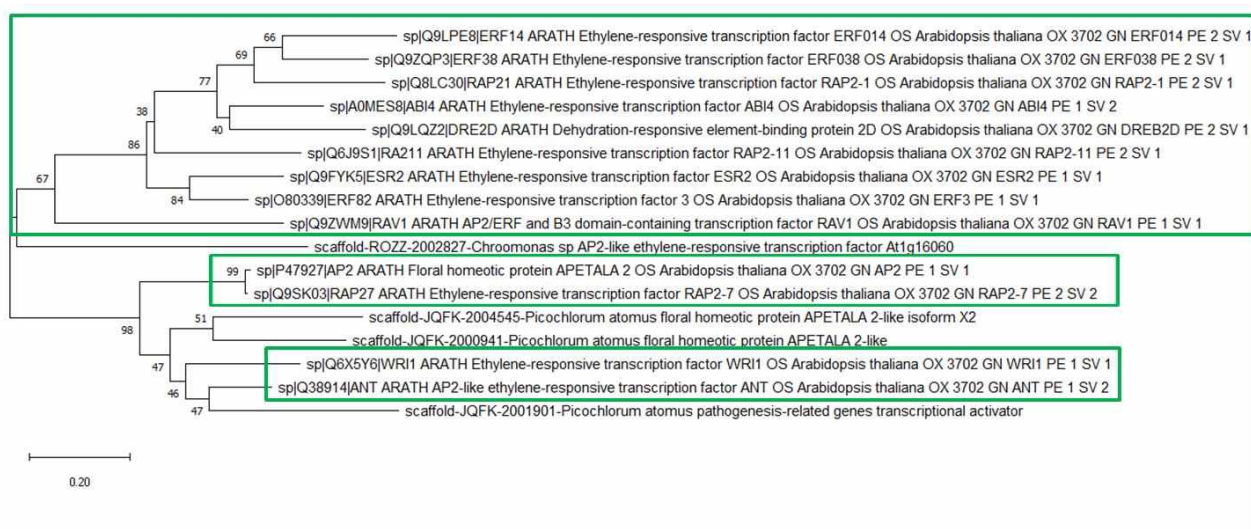
5.3 Análises filogenética dos fatores de transcrição AP2/ERF nas linhagens vegetais selecionadas

As árvores filogenéticas foram obtidas utilizando como parâmetros o método *Neighbor-Joining*, que realiza aproximações entre as sequências analisadas obtendo a relação de ancestralidade das mesmas pelo comprimento de suas ramificações. Este método agrupa as espécies de maneira que estatisticamente fiquem mais próximas e apresentem a menor distância evolutiva e consequentemente os menores comprimentos nas ramificações (SAITOU, NEI, 1987; CALDART, 2016).

As árvores filogenéticas mostram que boa parte das sequências referência apresentou maior similaridade entre si do que quando comparadas às sequências analisadas. Por este motivo encontram-se agrupadas em ramos separados. As sequências encontram-se mais próximos evolutivamente das sequências analisadas em algas, algas verdes, briófitas e pteridófitas foram às dos genes pertencentes à subclasse AP2 (Figuras 7, 8, 9 e 10). Possivelmente os demais genes das outras subfamílias podem ter evoluído a partir deles, pois se observou a presença dos mesmos desde os vegetais mais primitivos até as pteridófitas.

Sendo conhecida pela sua versatilidade para a produção de biomassa em condições adversas a espécie *Picochlorum atomus*, é bastante utilizada na biorremediação e na aquicultura, têm-se mostrado uma ótima alternativa para enriquecimentos alimentares (ALVENSLEBEN et al., 2013; BECKER, 2007). As microalgas são ainda conhecidas pelos seus fornecimentos de ácidos graxos e pigmentos como clorofila, β -caroteno e luteína essenciais para a prevenção de câncer e doenças cardiovasculares, graças às atividades anti-inflamatórias e antioxidantes. Nesta espécie identificamos possíveis sequências codificantes de fatores AP2/ERF, que podem estar associados à característica desta microalga de resistir a amplas variações de salinidade (SHARIFAH; EGUCHI, 2011).

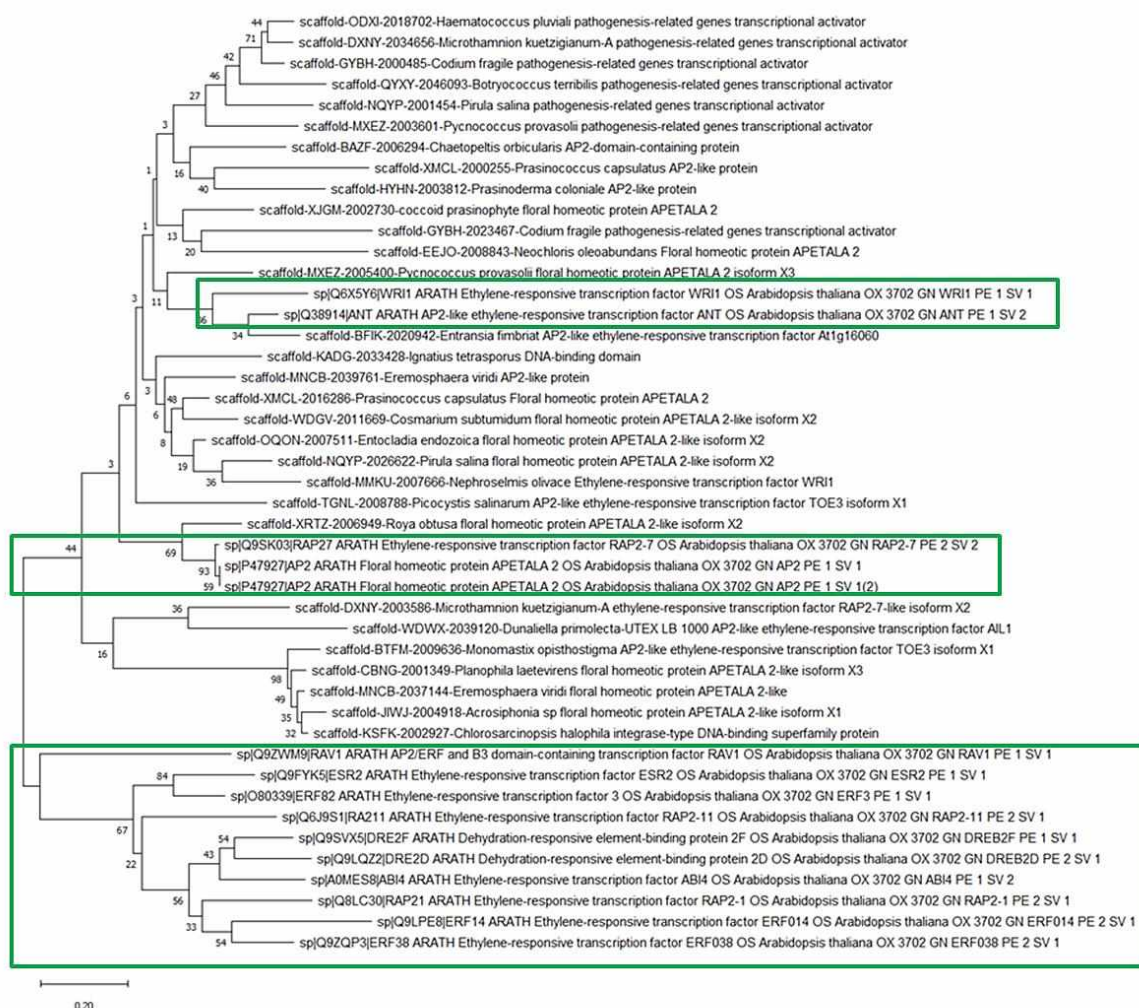
Figura 7. Arvore filogenética dos fatores de transcrição AP2/ERF de *A. thaliana* destacadas em verde e espécies de algas *Picochlorum atomus* (JQFK) e *Chroomonas sp* (ROZZ).



Em algas verdes, as funções dos genes AP2/ERF podem estar associadas com a proteção contra patógenos, e a necessidade de modulação fisiológica das plantas para a adaptação ao ambiente terrestre (WANG, 2015; LI et al., 2011). Este pode ser um indício de que podem ter surgido nas algas verdes, os fatores que mediarão a transição do

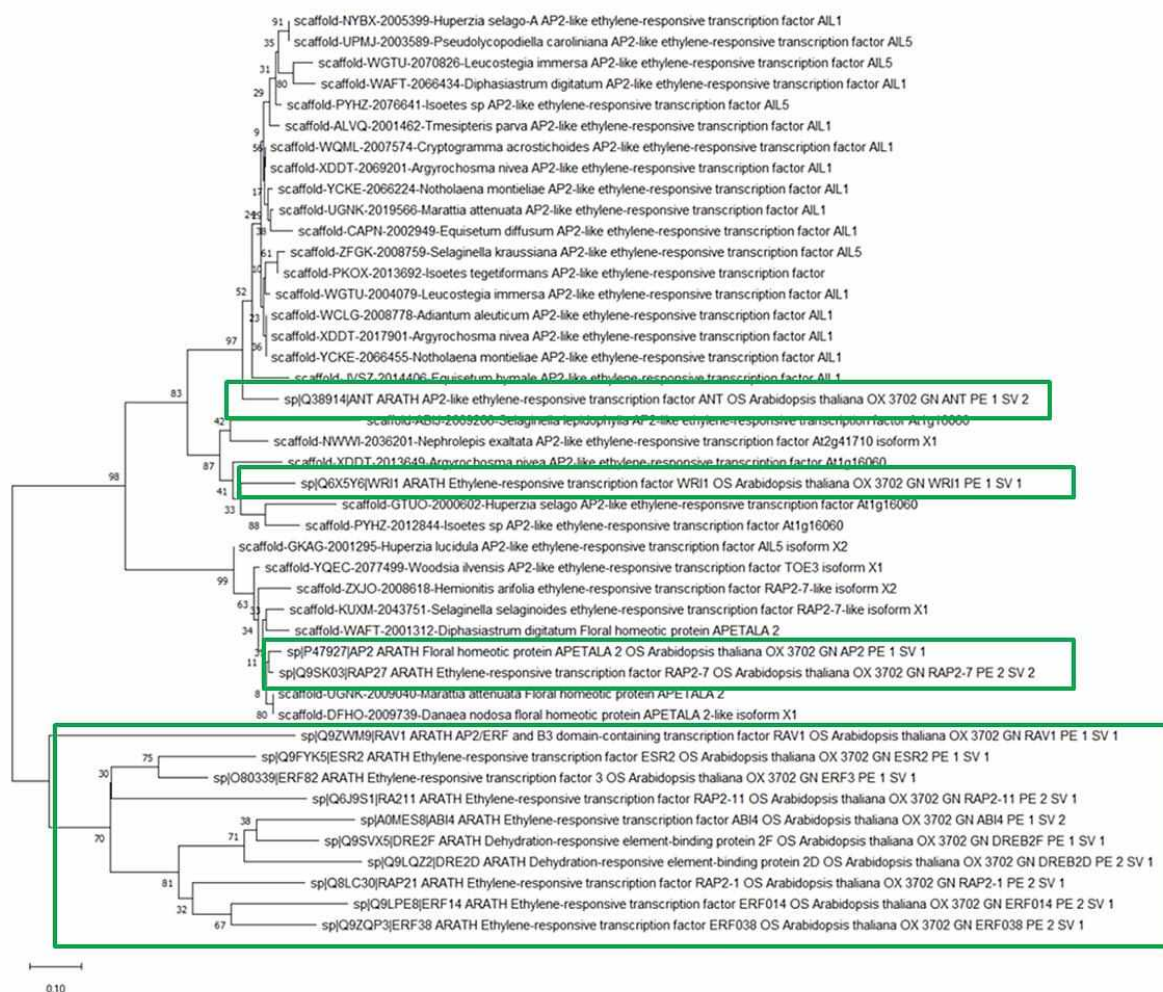
desenvolvimento vegetativo para o reprodutivo, estimulados pelas condições ambientais e sinalizações endógenas, garantindo a adaptação desses organismos em ambientes terrestres (PATIL et al., 2019; HUIJSER, SCHMID, 2011; AMASINO, 2010; POEL et al., 2016; MEHRNIA et al., 2013).

Figura 8. Arvore filogenética dos fatores de transcrição AP2/ERF de *A. thaliana* destacadas em verde e espécies de algas verdes.



Em briófitas, os genes AP2/ERF podem também ter participado das etapas de transição para o ambiente terrestre. Estando associado à tolerância a condições de sobrevivência, a presença do domínio AP2/ERF pode ter contribuído para a sobrevivência à dessecação de espécies pertencentes a essa classe (PROCTOR, LIGRONE, DUCKETT, 2007; QIU et al., 2006; OLIVER, VELTEN, MISHLER, 2005).

Figura 10. Árvore filogenética dos fatores de transcrição AP2/ERF de *A. thaliana* destacadas em verde e espécies de pteridófitas.



Quando comparadas as 145 sequências AP2/ERF presentes no genoma de *Arabidopsis* (SAKUMA et al., 2002; NAKANO et al., 2006) observamos que houve um aumento significativo no número de cópias dos fatores de transcrição AP2/ERF durante o processo evolutivo. Esse maior número de genes pode estar relacionando com a maior capacidade das plantas superiores em suportar uma maior variação de temperatura e maior resistência ao estresse hídrico, o que permitiu a dispersão das plantas pelos mais variados ambientes terrestres.

Para a investigação das características desta superfamília em cada grupo de plantas bem como os mecanismos de regulação da resposta aos estímulos bióticos e abióticos que em estas estão envolvidas, experimentos adicionais devem ser realizados para a confirmação das funções desempenhadas pelos mesmos desde os organismos primitivos até mais complexos.

6 CONCLUSÃO

Dentro das classes vegetais analisadas foi possível identificar *in silico* 3 possíveis sequências AP2/ERF em 2 espécies de algas, 134 sequências em 60 espécies de Algas Verdes, 165 sequências em 67 espécies de Briófitas e 180 sequências em 40 espécies de Pteridófitas. Com os resultados deste trabalho podemos inferir que os fatores de transcrição AP2/ERF da subclasse APETALA2 estão presentes desde espécies de algas mais primitivas, porém a classificação pôde ser aplicada apenas em algumas espécies dentro das classes analisadas. Uma hipótese levantada é que os demais genes da superfamília AP2/ERF observadas em plantas superiores e que o grande número de genes AP2/ERF, observados nas Angiospermas, deve ter ocorrido após eventos de duplicação recente. Portanto, experimentos adicionais devem ser feitos para a confirmação das funções do domínio conservado AP2/ERF nessas espécies de algas, briófitas e pteridófitas.

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APÊNDICES

Apêndice 1. Espécies utilizadas nas análises.

Cod.	Clado	Família	Especie
GAON	Lycophytes	Lycopodiaceae	Huperzia squarrosa
GKAG	Lycophytes	Lycopodiaceae	Huperzia lucidula
NYBX	Lycophytes	Lycopodiaceae	Huperzia selago
CBAE	Lycophytes	Huperziaceae	Huperzia myrsinites
GTUO	Lycophytes	Huperziaceae	Huperzia selago
ULKT	Lycophytes	Lycopodiaceae	Lycopodiella appressa
QTO	Lycophytes	Lycopodiaceae	Lycopodium deuterodensum
ENQF	Lycophytes	Lycopodiaceae	Lycopodium annotinum
UPMJ	Lycophytes	Lycopodiaceae	Pseudolycopodiella caroliniana
XNXF	Lycophytes	Lycopodiaceae	Dendrolycopodium obscurum
WAFI	Lycophytes	Lycopodiaceae	Diphasiastrum digitatum
PKOX	Lycophytes	Isoetaceae	Isoetes tegetiformans
PYHZ	Lycophytes	Isoetaceae	Isoetes sp.
LGDQ	Lycophytes	Selaginellaceae	Selaginella apoda
JKAA	Lycophytes	Selaginellaceae	Selaginella wallacei
ABIJ	Lycophytes	Selaginellaceae	Selaginella lepidophylla
ZZOL	Lycophytes	Selaginellaceae	Selaginella stauntoniana
KUXM	Lycophytes	Selaginellaceae	Selaginella selaginoides
ZFGK	Lycophytes	Selaginellaceae	Selaginella kraussiana
KJYC	Lycophytes	Selaginellaceae	Selaginella willdenowii
CAPN	Eusporangiate Monilophytes	Equisetaceae	Equisetum diffusum
JVSZ	Eusporangiate Monilophytes	Equisetaceae	Equisetum hyemale
UXCS	Eusporangiate Monilophytes	Marattiaceae	Marattia sp.
UGNK	Eusporangiate Monilophytes	Marattiaceae	Marattia attenuata
DFHO	Eusporangiate Monilophytes	Marattiaceae	Danaea nodosa
BEGM	Eusporangiate Monilophytes	Ophioglossaceae	Botrypus virginianus
WTJG	Eusporangiate Monilophytes	Ophioglossaceae	Ophioglossum petiolatum
QHVS	Eusporangiate Monilophytes	Ophioglossaceae	Ophioglossum vulgatum
EEAQ	Eusporangiate Monilophytes	Ophioglossaceae	Sceptridium dissectum
QVMR	Eusporangiate Monilophytes	Psilotaceae	Psilotum nudum
ALVQ	Eusporangiate Monilophytes	Psilotaceae	Tmesipteris parva
PNZO	Leptosporangiate Monilophytes	Culcitaceae	Culcita macrocarpa
GANB	Leptosporangiate Monilophytes	Cyatheaceae	Cyathea (Alsophila) spinulosa
EWXK	Leptosporangiate Monilophytes	Thyrsopteridaceae	Thyrsopteris elegans
XDVM	Leptosporangiate Monilophytes	Gleicheniaceae	Sticherus lobatus
MEKP	Leptosporangiate Monilophytes	Dipteridaceae	Dipteris conjugata
TWFZ	Leptosporangiate Monilophytes	Hymenophyllaceae	Crepidomanes venosum
QIAD	Leptosporangiate Monilophytes	Hymenophyllaceae	Hymenophyllum bivalve
TRPJ	Leptosporangiate Monilophytes	Hymenophyllaceae	Hymenophyllum cupressiforme
BIVQ	Leptosporangiate Monilophytes	Osmundaceae	Osmundastrum cinnamomeum

RFMZ	Leptosporangiate Monilophytes	Osmundaceae	<i>Osmundastrum cinnamomeum</i>
YKSS	Leptosporangiate Monilophytes	Osmundaceae	<i>Osmunda regalis</i>
UOMY	Leptosporangiate Monilophytes	Osmundaceae	<i>Osmunda</i> sp.
VIBO	Leptosporangiate Monilophytes	Osmundaceae	<i>Osmunda javanica</i>
UWOD	Leptosporangiate Monilophytes	Plagiogyriaceae	<i>Plagiogyria japonica</i>
IXLH	Leptosporangiate Monilophytes	Polypodiaceae	<i>Polypodium hesperium</i>
GYFU	Leptosporangiate Monilophytes	Polypodiaceae	<i>Polypodium hesperium</i>
YLJA	Leptosporangiate Monilophytes	Polypodiaceae	<i>Polypodium amorphum</i>
CJNT	Leptosporangiate Monilophytes	Polypodiaceae	<i>Polypodium glycyrrhiza</i>
ZQYU	Leptosporangiate Monilophytes	Polypodiaceae	<i>Phlebodium pseudoaureum</i>
UJWU	Leptosporangiate Monilophytes	Polypodiaceae	<i>Pleopeltis polypodioides</i>
ORJE	Leptosporangiate Monilophytes	Polypodiaceae	<i>Phymatosorus grossus</i>
OQWW	Leptosporangiate Monilophytes	Davalliaceae	<i>Davallia fejeensis</i>
NWWI	Leptosporangiate Monilophytes	Lomariopsidaceae	<i>Nephrolepis exaltata</i>
JBLI	Leptosporangiate Monilophytes	Elaphoglossaceae	<i>Bolbitis repanda</i>
FQGQ	Leptosporangiate Monilophytes	Dryopteridaceae	<i>Polystichum acrostichoides</i>
RFRB	Leptosporangiate Monilophytes	Hypodematiaceae	<i>Didymochlaena truncatula</i>
WGTU	Leptosporangiate Monilophytes	Hypodematiaceae	<i>Leucostegia immersa</i>
PSKY	Leptosporangiate Monilophytes	Aspleniaceae	<i>Asplenium nidus</i>
KJZG	Leptosporangiate Monilophytes	Aspleniaceae	<i>Asplenium platyneuron</i>
OCZL	Leptosporangiate Monilophytes	Diplaziopsidaceae	<i>Homalosorus pycnocarpus</i>
MROH	Leptosporangiate Monilophytes	Thelypteridaceae	<i>Thelypteris acuminata</i>
YJJY	Leptosporangiate Monilophytes	Woodsiaceae	<i>Woodsia scopulina</i>
YQEC	Leptosporangiate Monilophytes	Woodsiaceae	<i>Woodsia ilvensis</i>
HTFH	Leptosporangiate Monilophytes	Onocleaceae	<i>Onoclea sensibilis</i>
VITX	Leptosporangiate Monilophytes	Blechnaceae	<i>Blechnum spicant</i>
URCP	Leptosporangiate Monilophytes	Athyriaceae	<i>Athyrium filix-femina</i>
FCHS	Leptosporangiate Monilophytes	Athyriaceae	<i>Deparia lobato-crenata</i>
UFJN	Leptosporangiate Monilophytes	Athyriaceae	<i>Diplazium wichurae</i>
HNDZ	Leptosporangiate Monilophytes	Cystopteridaceae	<i>Cystopteris utahensis</i>
LHLE	Leptosporangiate Monilophytes	Cystopteridaceae	<i>Cystopteris fragilis</i>
XXHP	Leptosporangiate Monilophytes	Cystopteridaceae	<i>Cystopteris fragilis</i>
RICC	Leptosporangiate Monilophytes	Cystopteridaceae	<i>Cystopteris reevesiana</i>
YOWV	Leptosporangiate Monilophytes	Cystopteridaceae	<i>Cystopteris protrusa</i>
HEGQ	Leptosporangiate Monilophytes	Cystopteridaceae	<i>Gymnocarpium dryopteris</i>
MTGC	Leptosporangiate Monilophytes	Dennstaedtiaceae	<i>Dennstaedtia davallioides</i>
WCLG	Leptosporangiate Monilophytes	Pteridaceae	<i>Adiantum aleuticum</i>
BMJR	Leptosporangiate Monilophytes	Pteridaceae	<i>Adiantum raddianum</i>
DCDT	Leptosporangiate Monilophytes	Pteridaceae	<i>Gaga arizonica</i>
WQML	Leptosporangiate Monilophytes	Pteridaceae	<i>Cryptogramma acrostichoides</i>
ZXJO	Leptosporangiate Monilophytes	Pteridaceae	<i>Parahemionitis cordata</i>
POPJ	Leptosporangiate Monilophytes	Pteridaceae	<i>Pteris vittata</i>
FLTD	Leptosporangiate Monilophytes	Pteridaceae	<i>Pteris ensiformis</i>
UJTT	Leptosporangiate Monilophytes	Pteridaceae	<i>Pityrogramma trifoliata</i>
YCKE	Leptosporangiate Monilophytes	Pteridaceae	<i>Notholaena montieliae</i>
XDDT	Leptosporangiate Monilophytes	Pteridaceae	<i>Argyrochosma nivea</i>

GSXD	Leptosporangiate Monilophytes	Pteridaceae	<i>Myriopteris rufa</i>
SKYV	Leptosporangiate Monilophytes	Pteridaceae	<i>Vittaria lineata</i>
NDUV	Leptosporangiate Monilophytes	Pteridaceae	<i>Vittaria appalachiana</i>
PIVW	Leptosporangiate Monilophytes	Pteridaceae	<i>Ceratopteris thalictroides</i>
NOKI	Leptosporangiate Monilophytes	Lindsaeaceae	<i>Lindsaea linearis</i>
YIXP	Leptosporangiate Monilophytes	Lindsaeaceae	<i>Lindsaea microphylla</i>
BMIF	Leptosporangiate Monilophytes	Lindsaeaceae	<i>Asplenium</i> sp.
VVRN	Leptosporangiate Monilophytes	Lonchitidaceae	<i>Lonchitis hirsuta</i>
CVEG	Leptosporangiate Monilophytes	Salviniaceae	<i>Azolla</i> cf. <i>caroliniana</i>
KIIX	Leptosporangiate Monilophytes	Marsileaceae	<i>Pilularia globulifera</i>
CQPW	Leptosporangiate Monilophytes	Anemiaceae	<i>Anemia tomentosa</i>
PBUU	Leptosporangiate Monilophytes	Lygodiaceae	<i>Lygodium japonicum</i>
ORKS	Mosses	Bartramiaceae	<i>Philonotis fontana</i>
BGXB	Mosses	Mielichhoferiaceae	<i>Plagiomnium insigne</i>
JMXW	Mosses	Bryaceae	<i>Bryum argenteum</i>
WNGH	Mosses	Aulacomniaceae	<i>Aulacomnium heterostichum</i>
VBMM	Mosses	Brachytheciaceae	<i>Claopodium rostratum</i>
QMWB	Mosses	Myuriaceae	<i>Anomodon attenuatus</i>
ABCD	Mosses	Grimmiaceae	<i>Racomitrium elongatum</i>
RDOO	Mosses	Grimmiaceae	<i>Racomitrium varium</i>
BPSG	Mosses	Scouleriaceae	<i>Scouleria aquatica</i>
HRWG	Mosses	Buxbaumiaceae	<i>Buxbaumia aphylla</i>
NGTD	Mosses	Dicranaceae	<i>Dicranum scoparium</i>
VMXJ	Mosses	Leucobryaceae	<i>Leucobryum albidum</i>
RGKI	Mosses	Leucobryaceae	<i>Leucobryum glaucum</i>
FFPD	Mosses	Ditrichaceae	<i>Ceratodon purpureus</i>
AWOI	Mosses	Diphysciaceae	<i>Diphyscium foliosum</i>
KEFD	Mosses	Encalyptaceae	<i>Encalypta streptocarpa</i>
XWHK	Mosses	Bryaceae	<i>Rosulabryum</i> cf. <i>capillare</i>
YEPO	Mosses	Funariaceae	<i>Physcomitrium</i> sp.
YWNF	Mosses	Hedwigiaceae	<i>Hedwigia ciliata</i>
WSPM	Mosses	Hylocomiaceae	<i>Loeskeobryum brevirostre</i>
ZACW	Mosses	Leucodontaceae	<i>Leucodon brachypus</i>
LNSF	Mosses	Pylaisiaceae	<i>Stereodon subimponens</i>
QKQO	Mosses	Plagiotheciaceae	<i>Pseudotaxiphyllum elegans</i>
EEMJ	Mosses	Thuidiaceae	<i>Thuidium delicatulum</i>
JADL	Mosses	Brachytheciaceae	<i>Rhynchostegium serrulatum</i>
IGUH	Mosses	Leucodontaceae	<i>Leucodon julaceus</i>
TAVP	Mosses	Calliergonaceae	<i>Calliergon cordifolium</i>
MIRS	Mosses	Climaciaceae	<i>Climacium dendroides</i>
DHWX	Mosses	Fontinalaceae	<i>Fontinalis antipyretica</i>
TMAJ	Mosses	Neckeraceae	<i>Neckera douglasii</i>
CMEQ	Mosses	Orthotrichaceae	<i>Orthotrichum lyellii</i>
SZYG	Mosses	Polytrichaceae	<i>Polytrichum commune</i>
ZTHV	Mosses	Polytrichaceae	<i>Atrichum angustatum</i>
GRKU	Mosses	Pottiaceae	<i>Syntrichia princeps</i>

GOWD	Mosses	Sphagnaceae	<i>Sphagnum lescurii</i>
RCBT	Mosses	Sphagnaceae	<i>Sphagnum palustre</i>
UHLI	Mosses	Sphagnaceae	<i>Sphagnum recurvum</i>
SKQD	Mosses	Takakiaceae	<i>Takakia lepidozoides</i>
HVBQ	Mosses	Tetraphidaceae	<i>Tetraphis pellucida</i>
ZQRI	Mosses	Timmiaaceae	<i>Timmia austriaca</i>
FANS	Hornworts	Leiosporocerotaceae	<i>Leiosporoceros dussii</i>
ANON	Hornworts	Leiosporocerotaceae	<i>Leiosporoceros dussii</i>
IQJU	Hornworts	Anthoceroaceae	<i>Anthoceros angustus</i>
TWUW	Hornworts	Anthoceroaceae	<i>Anthoceros agrestis</i>
BSNI	Hornworts	Anthoceroaceae	<i>Anthoceros agrestis</i>
FAJB	Hornworts	Notothyladaceae	<i>Paraphymatoceros hallii</i>
WCZB	Hornworts	Notothyladaceae	<i>Phaeoceros carolinianus</i>
RXRQ	Hornworts	Notothyladaceae	<i>Phaeoceros carolinianus</i>
WEEQ	Hornworts	Notothyladaceae	<i>Phaeoceros carolinianus</i>
ZFRE	Hornworts	Notothyladaceae	<i>Phaeoceros carolinianus</i>
DXOU	Hornworts	Dendrocerotaceae	<i>Nothoceros aenigmaticus</i>
TCBC	Hornworts	Dendrocerotaceae	<i>Nothoceros vincentianus</i>
UCRN	Hornworts	Dendrocerotaceae	<i>Megaceros flagellaris</i>
AKXB	Hornworts	Dendrocerotaceae	<i>Phaeomegaceros coriaceus</i>
AEXY	Liverworts	Blasiaceae	<i>Blasia</i> sp.
YBQN	Liverworts	Cephaloziaceae	<i>Odontoschisma prostratum</i>
WZYK	Liverworts	Lepidoziaceae	<i>Bazzania trilobata</i>
RTMU	Liverworts	Calypogeiaceae	<i>Calypogeia fissa</i>
CHJJ	Liverworts	Frullaniaceae	<i>Frullania</i> spp.
IRBN	Liverworts	Scapaniaceae	<i>Scapania nemorosa</i>
OFTV	Liverworts	Scapaniaceae	<i>Barbilophozia barbata</i>
HPXA	Liverworts	Ptilidiaceae	<i>Ptilidium pulcherrimum</i>
LGOW	Liverworts	Schistochilaceae	<i>Schistochila</i> sp.
UUHD	Liverworts	Porellaceae	<i>Porella pinnata</i>
TGKW	Liverworts	Frullaniaceae	<i>Frullania</i> sp.
JPYU	Liverworts	Marchantiaceae	<i>Marchantia polymorpha</i>
TFYI	Liverworts	Marchantiaceae	<i>Marchantia emarginata</i>
HMHL	Liverworts	Marchantiaceae	<i>Marchantia paleacea</i>
IHOW	Liverworts	Marchantiaceae	<i>Marchantia paleacea</i>
ILBQ	Liverworts	Conocephalaceae	<i>Conocephalum conicum</i>
TXVB	Liverworts	Lunulariaceae	<i>Lunularia cruciata</i>
TFDQ	Liverworts	Monocleaceae	<i>Monoclea gottschei</i>
WJLO	Liverworts	Ricciaceae	<i>Ricciocarpos natans</i>
NRWZ	Liverworts	Metzgeriaceae	<i>Metzgeria crassipilis</i>
YFGP	Liverworts	Pallaviciniaceae	<i>Pallavicinia lyellii</i>
PIUF	Liverworts	Pelliaceae	<i>Pellia</i> sp. (cf <i>epiphylla</i> (L.) Corda)
JHFI	Liverworts	Pelliaceae	<i>Pellia neesiana</i>
YPSN	Liverworts	Pelliaceae	<i>Noteroclada confluens</i>
KRUQ	Liverworts	Porellaceae	<i>Porella navicularis</i>
BNCU	Liverworts	Radulaceae	<i>Radula lindenbergiana</i>

HERT	Liverworts	Sphaerocarpaceae	Sphaerocarpos texanus
FITN	Liverworts	Treubiaceae	Treubia lacunosa
XMCL	Green Algae	Prasinococcaceae	Prasinococcus capsulatus
XJGM	Green Algae	Prasinococcaceae	coccoid-prasinophyte
HYHN	Green Algae	Prasinococcaceae	Prasinoderma coloniale
MXEZ	Green Algae	Pycnococcaceae	Pycnococcus provasolii
JMTE	Green Algae	Pycnococcaceae	Pseudoscurfieldia marina
TNAW	Green Algae	Pyramimonadaceae	Pyramimonas parkeae
XIVI	Green Algae	Pyramimonadaceae	Cymbomonas sp.
MCPK	Green Algae	Mamiellaceae	Bathycoccus prasinus
QXSZ	Green Algae	Mamiellaceae	Mantoniella squamata
BTFM	Green Algae	Monomasticaceae	Monomastix opisthostigma
XOAL	Green Algae	Dolichomastigaceae	Dolichomastix tenuilepis
MMKU	Green Algae	Nephroselmidaceae	Nephroselmis olivacea
ISIM	Green Algae	Nephroselmidaceae	Nephroselmis pyriformis
FMVB	Green Algae	Chlorodendraceae	Scherffelia dubia
HVNO	Green Algae	Chlorodendraceae	Tetraselmis chui
DUMA	Green Algae	Chlorodendraceae	Tetraselmis cordiformis
HHXJ	Green Algae	Chlorodendraceae	Tetraselmis striata
BAZF	Green Algae	Chaetopeltidaceae	Chaetopeltis orbicularis
VFIV	Green Algae	Chaetophoraceae	Fritschiella tuberosa
AJAU	Green Algae	Chaetophoraceae	Helicodictyon planctonicum
NQYP	Green Algae	Chaetophoraceae	Pirula salina
JMUI	Green Algae	Chaetophoraceae	Stigeoclonium helveticum
RAWF	Green Algae	Chaetophoraceae	Uronema belkae
ISGT	Green Algae	Chaetophoraceae	Uronema sp.
IJMT	Green Algae	Aphanochaetaceae	Aphanochaete repens
GXBM	Green Algae	Coccomyaceae	Coccomyxa pringsheimii
BZSH	Green Algae	Golenkiniaceae	Golenkinia longispicula
XKWQ	Green Algae	Hydrodictyaceae	Pediastrum duplex CCAC 0012
NLOM	Green Algae	Hydrodictyaceae	Pediastrum duplex CCAC 0012
XTON	Green Algae	Hydrodictyaceae	Pediastrum duplex CCAC 0147
PZIF	Green Algae	Scenedesmaceae	Acutodesmus dimorphus
ALZF	Green Algae	Chlorocystidaceae	Halochlorococcum marinum
USIX	Green Algae	Chlorosarcinaceae	Neochlorosarcina sp.
FOYQ	Green Algae	Microsporaceae	Microspora cf. tumidula
DVYE	Green Algae	Oedogoniaceae	Oedogonium cardiacum
SDPC	Green Algae	Oedogoniaceae	Oedogonium foveolatum
KUJU	Green Algae	Goniaceae	Gonium pectorale
EEJO	Green Algae	incertae sedis	Neochloris oleoabundans
KSFK	Green Algae	Chlorosarcinaceae	Chlorosarcinopsis halophila
GJIY	Green Algae	Neochloridaceae	Neochloris sp.
OTQG	Green Algae	Ankistrodesmaceae	Ankistrodesmus sp.
JWGT	Green Algae	Volvocaceae	Volvox aureus
WRSL	Green Algae	Volvocaceae	Volvox aureus
ISPU	Green Algae	Volvocaceae	Volvox globator

RNAT	Green Algae	Volvocaceae	Eudorina elegans
RYJX	Green Algae	Volvocaceae	Pandorina morum
MNPL	Green Algae	Asteromonadaceae	Asteromonas gracilis
NTLE	Green Algae	Asteromonadaceae	Asteromonas gracilis
VIAU	Green Algae	Carteriaceae	Carteria crucifera
RUIF	Green Algae	Carteriaceae	Carteria obtusa
MULF	Green Algae	Chlamydomonadaceae	Chlamydomonas bilatus
OVHR	Green Algae	Chlamydomonadaceae	Chlamydomonas bilatus
BCYF	Green Algae	Chlamydomonadaceae	Chlamydomonas cribrum
JRGZ	Green Algae	Chlamydomonadaceae	Chlamydomonas moewusii
VALZ	Green Algae	Chlamydomonadaceae	Chlamydomonas noctigama
TSBQ	Green Algae	Chlamydomonadaceae	Chlamydomonas sp.
GUBD	Green Algae	Chlamydomonadaceae	Brachiomonas submarina
IHOI	Green Algae	Chlamydomonadaceae	Chloromonas oogama
QRTH	Green Algae	Chlamydomonadaceae	Chlorococcum microstigmaticum
LBPR	Green Algae	Chlamydomonadaceae	Chloromonas reticulata
GDUD	Green Algae	Chlamydomonadaceae	Chloromonas reticulata
AJUW	Green Algae	Chlamydomonadaceae	Chloromonas rosae v. psychrophila
GFUR	Green Algae	Chlamydomonadaceae	Chloromonas subdivisa
UTRE	Green Algae	Chlamydomonadaceae	Chloromonas tughillensis
IRYH	Green Algae	Chlamydomonadaceae	Heterochlamydomonas inaequalis
OFUE	Green Algae	Chlamydomonadaceae	Lobochlamys segnis
JKKI	Green Algae	Chlamydomonadaceae	Lobomonas rostrata
XDLL	Green Algae	Chlamydomonadaceae	Oogamochlamys gigantea
MXDS	Green Algae	Chlamydomonadaceae	Spermatozopsis exsultans
ENAU	Green Algae	Chlamydomonadaceae	Spermatozopsis similis
QWRA	Green Algae	Chlamydomonadaceae	Vitreochlamys sp.
WDWX	Green Algae	Dunaliellaceae	Dunaliella tertiolecta
RHVC	Green Algae	Dunaliellaceae	Dunaliella salina
SYJM	Green Algae	Dunaliellaceae	Dunaliella viridis dumsii
UKUC	Green Algae	Dunaliellaceae	Dunaliella salina
ZDIZ	Green Algae	Dunaliellaceae	Dunaliella tertiolecta
FXHG	Green Algae	Dunaliellaceae	Hafniomonas reticulata
ODXI	Green Algae	Haematococcaceae	Haematococcus pluvialis
AGIO	Green Algae	Haematococcaceae	Haematococcus pluvialis
ZLQE	Green Algae	Haematococcaceae	Stephanosphaera pluvialis
ZIVZ	Green Algae	Phacotaceae	Phacotus lenticularis
LNIL	Green Algae	Phacotaceae	Pteromonas angulosa
ACRY	Green Algae	Phacotaceae	Pteromonas sp.
NKXU	Green Algae	Trebouxiaceae	Trebouxia arboricola
ETGN	Green Algae	Botryococcaceae	Botryococcus braunii
VJDZ	Green Algae	Botryococcaceae	Botryococcus sudeticus
QYXY	Green Algae	Botryococcaceae	Botryococcus terrestris
MWAN	Green Algae	Chlorellaceae	Chlorella minutissima
PFUD	Green Algae	Chlorellaceae	Geminella sp.
MFYC	Green Algae	Chlorellaceae	Nannochloris atomus

AKCR	Green Algae	Chlorellaceae	Parachlorella kessleri
BILC	Green Algae	Chlorellaceae	Prototheca wickerhamii
ZNUM	Green Algae	Leptosiraceae	Leptosira obovata
MNCB	Green Algae	Oocystaceae	Eremosphaera viridis
DXNY	Green Algae	Microthamniaceae	Microthamnion kuetzingianum
ZDOF	Green Algae	Microthamniaceae	Microthamnion kuetzingianum
WCLV	Green Algae	Prasiolaceae	Prasiola crispa
WXRI	Green Algae	Prasiolaceae	Stichococcus bacillaris
CQQP	Green Algae	Ulvaceae	Ochlochaete sp.
OAEZ	Green Algae	Ulvaceae	Percursaria percura
LSHT	Green Algae	Bolbocoleonaceae	Bolbocoleon piliferum
PZBH	Green Algae	Oltmannsiellopsidaceae	Oltmannsiellopsis viridis
QJYX	Green Algae	Oltmannsiellopsidaceae	Oltmannsiellopsis viridis
OQON	Green Algae	Ulvellaceae	Entocladia endozoica
VLH	Green Algae	Cladophoraceae	Cladophora glomerata
NATT	Green Algae	Trentepohliaceae	Trentepohlia annulata
YDCQ	Green Algae	Trentepohliaceae	Cephaleuros virescens
CBNG	Green Algae	Borodinellaceae	Planophila laetevirens
LETG	Green Algae	Borodinellaceae	Planophila terrestris
DZPJ	Green Algae	Cylindrocapsaceae	Cylindrocapsa geminella
JIWJ	Green Algae	Ulotrichaceae	Acrosiphonia sp.
KADG	Green Algae	Ulotrichaceae	Ignatius tetrasporus
FPCO	Green Algae	Ulotrichaceae	Interfilum paradoxum
JTIG	Green Algae	Bryopsidaceae	Bryopsis plumosa
GYBH	Green Algae	Codiaceae	Codium fragile
VHIJ	Green Algae	Chaetosiphonaceae	Blastophysa cf. rhizopus
KYIO	Green Algae	Mesostigmataceae	Mesostigma viride
RRSV	Green Algae	Pedinomonadaceae	Pedinomonas minor
PUAN	Green Algae	Pedinomonadaceae	Pedinomonas tuberculata
EGNB	Green Algae	Scourfieldiaceae	Scourfieldia sp.
PRIQ	Green Algae	Pleurastraceae	Chlorococcum oleofaciens
TGNL	Green Algae	incertae sedis	Picocystis salinarum
MWXT	Green Algae	Characeae	Chara vulgaris
QPDY	Green Algae	Coleochaetaceae	Coleochaete irregularis
VQBJ	Green Algae	Coleochaetaceae	Coleochaete scutata
DRGY	Green Algae	Chaetosphaeridiaceae	Chaetosphaeridium globosum
FQLP	Green Algae	Klebsormidiaceae	Klebsormidium subtile
BFIK	Green Algae	Klebsormidiaceae	Entransia fimbriata
JOJQ	Green Algae	Zygnemataceae	Cylindrocystis cushleackae
ZRMT	Green Algae	Zygnemataceae	Mougeotia sp.
HAOX	Green Algae	Zygnemataceae	Spirogyra sp.
WGMD	Green Algae	Zygnemataceae	Zygnema sp.
MFZO	Green Algae	Zygnemataceae	Zygnemopsis sp.
DRFX	Green Algae	Closteriaceae	Closterium lunula
DFDS	Green Algae	Desmidiaceae	Desmidium aptogonum
QWV	Green Algae	Desmidiaceae	Bambusina borrieri

HIDG	Green Algae	Desmidiaceae	Cosmarium broomei
MNNM	Green Algae	Desmidiaceae	Cosmarium granatum
STKJ	Green Algae	Desmidiaceae	Cosmarium ochthodes
HJVM	Green Algae	Desmidiaceae	Cosmarium ochthodes
WDGV	Green Algae	Desmidiaceae	Cosmarium subtumidum
BHBK	Green Algae	Desmidiaceae	Cosmarium tinctum
RQFE	Green Algae	Desmidiaceae	Cosmocladium cf. constrictum
GYRP	Green Algae	Desmidiaceae	Euastrum affine
MCHJ	Green Algae	Desmidiaceae	Micrasterias fimbriata
GGWH	Green Algae	Desmidiaceae	Onychonema laeve
RPQV	Green Algae	Desmidiaceae	Phymatodocis nordstedtiana
MOYY	Green Algae	Desmidiaceae	Pleurotaenium trabecula
ISHC	Green Algae	Desmidiaceae	Staurostrum sebaldi
WCQU	Green Algae	Desmidiaceae	Staurodesmus convergens
RPRU	Green Algae	Desmidiaceae	Staurodesmus omearii
GBGT	Green Algae	Desmidiaceae	Xanthidium antilopaeum
WSJO	Green Algae	Mesotaeniaceae	Mesotaenium braunii
HKZW	Green Algae	Mesotaeniaceae	Mesotaenium caldariorum
WDCW	Green Algae	Mesotaeniaceae	Mesotaenium endlicherianum
NBYF	Green Algae	Mesotaeniaceae	Mesotaenium kramstae
YOXI	Green Algae	Mesotaeniaceae	Cylindrocystis brebissonii
RPGL	Green Algae	Mesotaeniaceae	Cylindrocystis brebissonii
VAZE	Green Algae	Mesotaeniaceae	Cylindrocystis sp.
FFGR	Green Algae	Mesotaeniaceae	Netrium digitus
KMNX	Green Algae	Mesotaeniaceae	Nucleotaenium eifelense
SNOX	Green Algae	Mesotaeniaceae	Planotaenium ohtanii
XRTZ	Green Algae	Mesotaeniaceae	Roya obtusa
NNHQ	Green Algae	Mesotaeniaceae	Spirotaenia minuta
TPHT	Green Algae	Mesotaeniaceae	Spirotaenia sp.
YSQT	Green Algae	Peniaceae	Penium exiguum
AEKF	Green Algae	Peniaceae	Penium margaritaceum
KEYW	Green Algae	Gonatozygaceae	Gonatozygon kinahanii
POOW	Glaucophyta (Algae)	Glaucocystaceae	Glaucocystis cf. nostochinearum
QFND	Glaucophyta (Algae)	Glaucocystaceae	Cyanophora paradoxa
YTYU	Glaucophyta (Algae)	Glaucocystaceae	Cyanophora paradoxa
PQED	Glaucophyta (Algae)	Glaucocystaceae	Gloeochaete wittrockiana
JKHA	Glaucophyta (Algae)	incertae sedis	Cyanoptycha gloecystis
OBUY	Red Algae	Porphyridiaceae	Porphyridium cruentum
PVGP	Red Algae	Porphyridiaceae	Porphyridium purpureum
RSOF	Red Algae	Glaucosphaeraceae	Glaucosphaera vacuolata
JJZR	Red Algae	Rhodochaetaceae	Rhodochaete parvula
LLXJ	Red Algae	Stylonemataceae	Chroodactylon ornatum
ZULJ	Red Algae	Bangiaceae	Pyropia yezoensis
VZWX	Red Algae	Ceramaceae	Ceramium kondoi
YSBD	Red Algae	Dasyaceae	Heterosiphonia pulchra
XAXW	Red Algae	Rhodomelaceae	Neosiphonia japonica

UYFR	Red Algae	Rhodomelaceae	Symphycladia latiuscula
IEHF	Red Algae	Dumontiaceae	Dumontia simplex
SBLT	Red Algae	Endocladaceae	Gloiopeltis furcata
UGPM	Red Algae	Gigartinaceae	Chondrus crispus
WEJN	Red Algae	Gigartinaceae	Mazzaella japonica
BWVJ	Red Algae	Solieriaceae	Betaphycus philippinensis
JEBK	Red Algae	Solieriaceae	Eucheuma denticulatum
IHJY	Red Algae	Solieriaceae	Kappaphycus alvarezii
FTRP	Red Algae	Gracilariaceae	Gracilaria chouae
VNAL	Red Algae	Gracilariaceae	Gracilaria vermiculophylla
LJPN	Red Algae	Gracilariaceae	Gracilaria blodgettii
IKWM	Red Algae	Gracilariaceae	Gracilaria lemaneiformis
ZJOJ	Red Algae	Halymeniaceae	Grateloupia filicina
IKIZ	Red Algae	Halymeniaceae	Grateloupia livida
URSB	Red Algae	Halymeniaceae	Grateloupia turuturu
PYDB	Red Algae	Halymeniaceae	Grateloupia catenata
PWKQ	Red Algae	Halymeniaceae	Gracilaria sp.
RTLC	Red Algae	Rhodellaceae	Rhodella violacea
BAKF	Chromista (Algae)	Cryptomonadaceae	Cryptomonas curvata
ROZZ	Chromista (Algae)	Chroomonadaceae	Chroomonas sp.
MJMQ	Chromista (Algae)	Chroomonadaceae	Hemiselmis virescens
IRZA	Chromista (Algae)	Geminigeraceae	Proteomonas sulcata
IAYV	Chromista (Algae)	Pyrenomonadaceae	Rhodomonas sp.
BAJW	Chromista (Algae)	Isochrysidaceae	Isochrysis sp.
APTP	Chromista (Algae)	Ishigeaceae	Ishige okamurae
LXRN	Chromista (Algae)	Prymnesiaceae	Prymnesium parvum
NMAK	Chromista (Algae)	Pavlovaceae	Pavlova lutheri
RFAD	Chromista (Algae)	Pavlovaceae	Pavlova lutheri CCAC 0028
LLEN	Chromista (Algae)	Pavlovaceae	Pavlova lutheri SAG 926-1
RAPY	Chromista (Algae)	Laminariaceae	Saccharina sculpera
OGZM	Chromista (Algae)	Laminariaceae	Saccharina japonica
QDTV	Chromista (Algae)	Laminariaceae	Saccharina japonica
FIDQ	Chromista (Algae)	Alariacea	Undaria pinnatifida
EBWI	Chromista (Algae)	Chromulinaceae	Ochromonas sp.
JQFK	Chromista (Algae)	Monodopsidaceae	Picochlorum atomus
BOGT	Chromista (Algae)	Mallomonadaceae	Mallomonas sp.
VKVG	Chromista (Algae)	Mallomonadaceae	Synura sp.
DBYD	Chromista (Algae)	Mallomonadaceae	Synura petersenii
FSQE	Chromista (Algae)	Desmarestiaceae	Desmarestia viridis
QLMZ	Chromista (Algae)	Scytosiphonaceae	Colpomenia sinuosa
JCXF	Chromista (Algae)	Scytosiphonaceae	Scytosiphon lomentaria
ASZK	Chromista (Algae)	Chordariacea	Punctaria latifolia
ULXR	Chromista (Algae)	Scytosiphonacea	Scytosiphon dotyi
VRGZ	Chromista (Algae)	Scytosiphonacea	Petalonia fascia
LDRY	Chromista (Algae)	Sargassaceae	Sargassum fusiforme
VYER	Chromista (Algae)	Sargassaceae	Sargassum hemiphyllum

FIKG	Chromista (Algae)	Sargassaceae	Sargassum henslowianum
RWXW	Chromista (Algae)	Sargassaceae	Sargassum horneri
FOMH	Chromista (Algae)	Sargassaceae	Sargassum integerrimum
YRMA	Chromista (Algae)	Sargassaceae	Sargassum thunbergii
HFIK	Chromista (Algae)	Sargassaceae	Sargassum vachellianum
JGGD	Chromista (Algae)	Sargassaceae	Sargassum muticum
TZJQ	Dinophyceae	Prorocentraceae	Prorocentrum micans
UNBZ	Euglenozoa	Euglenaceae	Euglena sp.

Apêndice 2A. Sequências AP2/ERF encontradas em Algas.

SeqName	Description	Length
scaffold-JQFK-2001901-Nannochloropsis_oculata	pathogenesis-related genes transcriptional activator	158
scaffold-JQFK-2004545-Nannochloropsis_oculata	floral homeotic protein APETALA 2-like isoform X2	157
scaffold-JQFK-2000941-Nannochloropsis_oculata	floral homeotic protein APETALA 2-like	167
scaffold-ROZZ-2002827-Chroomonas_sp	AP2-like ethylene-responsive transcription factor At1g16060	155

Apendice 2B. Sequências AP2/ERF encontradas em Algas Verdes

SeqName	Description	Length	e-Value	sim mean
scaffold-XRTZ-2006949-Roya_obtusa	floral homeotic protein APETALA 2-like	165	1,50E-53	80.53
scaffold-XMCL-2002058-Prasinococcus_capsulatus	floral homeotic protein APETALA 2-like	158	3,36E-67	81.01
scaffold-XMCL-2002057-Prasinococcus_capsulatus	floral homeotic protein APETALA 2-like	158	3,36E-67	81.01
scaffold-XJGM-2004684-coccoid_prasinophyte	floral homeotic protein APETALA 2-like isoform X1	175	1,03E-60	79.13
scaffold-NNHQ-2034102-Spirotaenia_minuta	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	166	1,35E-48	77.91
scaffold-MXEZ-2005400-Pycnococcus_provasolii	floral homeotic protein APETALA 2 isoform X3	168	4,92E-39	81.4
scaffold-JMTE-2016560-Pseudoscurfieldia_marina	floral homeotic protein APETALA 2 isoform X3	168	4,92E-39	81.4
scaffold-TGNL-2001628-Picocystis_salinarum	floral homeotic protein APETALA 2-like isoform X2	164	2,70E-76	80.54
scaffold-HYHN-2002914-Prasinoderma_coloniale	APETALA2-like transcriptional regulator	167	9,62E-43	75.51
scaffold-XMCL-2003231-Prasinococcus_capsulatus	floral homeotic protein APETALA 2	157	2,13E-58	81.13
scaffold-XJGM-2004017-coccoid_prasinophyte	AP2-like protein	182	4,35E-69	77.22
scaffold-XJGM-2004775-coccoid_prasinophyte	ethylene-responsive transcription factor RAP2-7 isoform X1	188	1,92E-51	72.5
scaffold-XMCL-2003517-Prasinococcus_capsulatus	floral homeotic protein APETALA 2-like isoform X2	162	6,07E-49	75.06
scaffold-HKZW-2004193-Mesotaenium_caldarium	floral homeotic protein APETALA 2-like isoform X2	160	2,50E-67	75.79
scaffold-GJIY-2018987-Neochloris_sp	DNA-binding domain	162	6,95E-72	77.57
scaffold-CBNG-2005394-Planophila_laetevirens	APETALA2-like transcriptional regulator	162	5,90E-60	76.87
scaffold-JIWI-2039695-Acrosiphonia_sp	AP2-like protein	182	8,36E-69	75.45
scaffold-OQON-2007511-Entocladia_endozoica	floral homeotic protein APETALA 2-like isoform X2	165	5,09E-65	77.59
scaffold-XMCL-2016286-Prasinococcus_capsulatus	Floral homeotic protein APETALA 2	160	9,28E-74	78.77
scaffold-LETF-2022423-Planophila_terrestris	floral homeotic protein APETALA 2-like	162	1,32E-59	77.41

scaffold-VAZE-2007381-Cylindrocystis_sp	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	160	7,12E-54	74.55
scaffold-XMCL-2003047-Prasinococcus_capsulatus	AP2-like ethylene-responsive transcription factor At1g16060	201	2,18E-40	68.39
scaffold-HYHN-2016399-Prasinoderma_coloniale	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	160	1,30E-52	73.75
scaffold-WDGV-2011669-Cosmarium_subtumidum	floral homeotic protein APETALA 2-like isoform X2	172	2,09E-72	72.52
scaffold-LSHT-2001918-Bolbocoleon_piliferum	predicted protein	177	6,92E-63	76.51
scaffold-LSHT-2001919-Bolbocoleon_piliferum	predicted protein	177	6,92E-63	76.51
scaffold-AJAU-2037420-Helicodictyon_planctonicum	DNA-binding domain	161	1,20E-59	76.26
scaffold-XJGM-2002730-coccoid_prasinophyte	floral homeotic protein APETALA 2	163	6,04E-32	76.5
scaffold-KSFK-2004026-Chlorosarcinopsis_halophila	DNA-binding domain	156	9,99E-62	75.77
scaffold-MXEZ-2001130-Pycnococcus_provasolii	floral homeotic protein APETALA 2-like	165	8,75E-65	78.02
scaffold-JMTE-2004735-Pseudoscurfieldia_marina	floral homeotic protein APETALA 2-like	165	8,78E-64	78.41
scaffold-OAEZ-2004460-Persursaria_percursa	AP2-like protein	160	2,66E-57	75.81
scaffold-OAEZ-2004461-Persursaria_percursa	DNA-binding domain	155	5,34E-55	71.39
scaffold-TGNL-2008943-Picocystis_salinarum	pathogenesis-related genes transcriptional activator	165	7,89E-77	87.0
scaffold-MXEZ-2003601-Pycnococcus_provasolii	pathogenesis-related genes transcriptional activator	166	5,26E-82	86.35
scaffold-JMTE-2003979-Pseudoscurfieldia_marina	pathogenesis-related genes transcriptional activator	166	5,26E-82	86.35
scaffold-XJGM-2002731-coccoid_prasinophyte	AP2/ERF domain-containing transcription factor	115	4,46E-23	77.3
scaffold-LFVP-2009993-LFVP-Marchantia_paleacea-2_samples_combined	AP2-like ethylene-responsive transcription factor	222	9,11E-149	90.47
scaffold-XMCL-2000255-Prasinococcus_capsulatus	AP2-like protein	169	4,26E-52	71.44
scaffold-NQYP-2026622-Pirula_salina	floral homeotic protein APETALA 2-like isoform X2	163	2,99E-66	74.01
scaffold-BZSH-2002154-Golenkinia_longispicula	pathogenesis-related genes transcriptional activator	164	4,23E-75	88.93
scaffold-KSFK-2004473-Chlorosarcinopsis_halophila	DNA-binding domain	165	4,34E-61	75.62
scaffold-GYBH-2000485-Codium_fragile	pathogenesis-related genes transcriptional activator	175	6,78E-94	87.69
scaffold-GYBH-2000486-Codium_fragile	pathogenesis-related genes transcriptional activator	175	6,78E-94	87.69
scaffold-HYHN-2003812-Prasinoderma_coloniale	AP2-like protein	164	4,97E-49	71.21
scaffold-JIWJ-2040818-Acrosiphonia_sp	AP2-like ethylene-responsive transcription factor	165	2,14E-54	71.63
scaffold-TGNL-2008788-Picocystis_salinarum	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	172	2,05E-43	72.08
scaffold-SNOX-2007103-Planotaenium_ohitanii	AP2-like protein	159	9,12E-65	75.01
scaffold-ZFXU-2007117-ZFXU-Asteromonas_gracilis-4_samples_combined	AP2-like ethylene-responsive transcription factor AIL1	172	1,30E-54	78.91
scaffold-MNPL-2006997-Asteromonas_gracilis-A	AP2-like ethylene-responsive transcription factor AIL1	172	1,30E-54	78.91
scaffold-NKXU-2001509-Trebouxia_arboricola	pathogenesis-related genes transcriptional activator	157	1,65E-63	84.45
scaffold-NKXU-2001508-Trebouxia_arboricola	pathogenesis-related genes transcriptional activator	157	1,65E-63	84.45
scaffold-YOXI-2008251-Cylindrocystis_breissonii-M2213	ethylene-responsive transcription factor RAP2-7-like isoform X1	122	2,33E-28	73.28
scaffold-KSFK-2023795-Chlorosarcinopsis_halophila	pathogenesis-related genes transcriptional activator	192	3,62E-67	81.37
scaffold-NQYP-2005716-Pirula_salina	floral homeotic protein APETALA 2-like	165	1,25E-50	68.34
scaffold-NQYP-2005715-Pirula_salina	floral homeotic protein APETALA 2-like	165	1,25E-50	68.34
scaffold-GYBH-2023467-Codium_fragile	pathogenesis-related genes transcriptional activator	186	8,18E-51	73.7
scaffold-ODXI-2018702-Haematococcus_pluviali	pathogenesis-related genes transcriptional activator	186	6,09E-74	84.79

scaffold-HHXJ-2002769-Tetraselmis_striata	ant-like protein	171	4,59E-52	77.38
scaffold-JIWI-2039799-Acrosiphonia_sp	pathogenesis-related genes transcriptional activator	179	1,82E-55	78.27
scaffold-AKCR-2022107-Parachlorella_kessleri	ethylene-responsive transcription factor RAP2-7 isoform X1	156	1,58E-69	74.84
scaffold-BILC-2020016-Prototheca_wickerhamii	AP2-like ethylene-responsive transcription factor ANT	172	3,63E-75	79.94
scaffold-BILC-2000056-Prototheca_wickerhamii	pathogenesis-related genes transcriptional activator	163	1,02E-85	88.36
scaffold-XMCL-2000957-Prasinococcus_capsulatus	AP2-like ethylene-responsive transcription factor PLT2	160	1,88E-56	71.07
scaffold-XMCL-2000956-Prasinococcus_capsulatus	AP2-like ethylene-responsive transcription factor PLT2	160	1,88E-56	71.07
scaffold-HYHN-2002847-Prasinoderma_coloniale	AP2-like ethylene-responsive transcription factor At1g16060	164	4,62E-37	68.71
scaffold-GXBM-2015916-Coccomyxa_pringsheimii	pathogenesis-related genes transcriptional activator	164	8,43E-85	77.55
scaffold-GJIY-2019487-Neochloris_sp	pathogenesis-related genes transcriptional activator	162	1,51E-66	80.7
scaffold-ZDOF-2035777-Microthamnion_kuetzigianum-B	pathogenesis-related genes transcriptional activator	162	1,35E-75	84.24
scaffold-TGNL-2002590-Picocystis_salinarum	floral homeotic protein APETALA 2-like isoform X1	159	5,13E-41	70.67
scaffold-QYXY-2046093-Botryococcus_terrabilis	pathogenesis-related genes transcriptional activator	164	4,47E-68	80.74
scaffold-LFVP-2009994-LFVP-Marchantia_paleacea-2_samples_combined	AP2-like ethylene-responsive transcription factor AIL5	130	1,22E-82	97.38
scaffold-EEJO-2009604-Neochloris_oleoabundans	AP2/ERF domain-containing transcription factor	156	7,37E-81	77.09
scaffold-AJAU-2034888-Helicodictyon_planctonicum	pathogenesis-related genes transcriptional activator	179	4,47E-59	78.71
scaffold-TNAW-2078645-Pyramimonas_parkeae	AP2-like ethylene-responsive transcription factor ANT	175	2,74E-69	82.52
scaffold-LETF-2022055-Planophila_terrestris	pathogenesis-related genes transcriptional activator	161	8,22E-59	79.99
scaffold-LETF-2000971-Planophila_terrestris	AP2-like ethylene-responsive transcription factor ANT	171	1,54E-48	69.87
scaffold-DXNY-2034656-Microthamnion_kuetzigianum-A	pathogenesis-related genes transcriptional activator	162	1,28E-74	83.65
scaffold-NQYP-2001454-Pirula_salina	pathogenesis-related genes transcriptional activator	162	1,58E-64	80.66
scaffold-BZSH-2037682-Golenkinia_longispicula	floral homeotic protein APETALA 2-like isoform X2	159	7,77E-37	69.45
scaffold-XJGM-2023702-coccoid_prasinophyte	AP2-like ethylene-responsive transcription factor AIL1	130	1,16E-49	82.71
scaffold-XOAL-2000596-Dolichomastix_tenuilepi	AP2-domain-containing protein	106	9,27E-46	76.34
scaffold-HVNO-2006954-Tetraselmis_chui	AP2-like ethylene-responsive transcription factor At1g79700	172	4,34E-37	73.16
scaffold-HVNO-2006955-Tetraselmis_chui	AP2-like ethylene-responsive transcription factor At1g79700	172	4,34E-37	73.16
scaffold-NNHQ-2004050-Spirotaenia_minuta	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	157	7,76E-23	66.95
scaffold-MNCB-2039761-Eremosphaera_viridi	AP2-like protein	157	5,72E-48	68.34
scaffold-AJAU-2033723-Helicodictyon_planctonicum	AP2-like ethylene-responsive transcription factor At1g79700	195	2,48E-37	62.76
scaffold-ZRMT-2006567-Mougeotia_sp	AP2-like ethylene-responsive transcription factor AIL5	151	1,61E-80	88.91
scaffold-BZSH-2002270-Golenkinia_longispicula	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	159	2,51E-37	68.99
scaffold-BZSH-2002271-Golenkinia_longispicula	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	159	2,51E-37	68.99
scaffold-WCLV-2013868-Prasiola_crispa	pathogenesis-related genes transcriptional activator	149	7,45E-86	86.64
scaffold-LFVP-2086018-LFVP-Marchantia_paleacea-2_samples_combined	AP2-like ethylene-responsive transcription factor At1g16060	198	1,41E-109	92.09
scaffold-OAEZ-2027632-Persusaria_percursa	pathogenesis-related genes transcriptional activator	162	1,16E-55	79.23
scaffold-AJAU-2008679-Helicodictyon_planctonicum	AP2-like ethylene-responsive transcription factor At1g16060	154	2,94E-42	71.1
scaffold-UKUC-2018312-Dunaliella_salina-UTEX_LB_200	AP2-like ethylene-responsive transcription factor AIL1	175	1,68E-50	73.99
scaffold-HVNO-2013718-Tetraselmis_chui	AP2-like ethylene-responsive transcription factor ANT	158	5,02E-58	70.02

scaffold-VJDZ-2035587-Botryococcus_sudeticus	AP2-like ethylene-responsive transcription factor AIL1	173	9,88E-18	69.03
scaffold-GYBH-2004484-Codium_fragile	pathogenesis-related genes transcriptional activator	166	5,80E-37	68.24
scaffold-HYHN-2000344-Prasinoderma_coloniale	floral homeotic protein APETALA 2-like	162	5,60E-43	65.63
scaffold-PFUD-2031672-Geminella_sp	floral homeotic protein APETALA 2-like isoform X2	163	6,27E-82	65.67
scaffold-EEJO-2008843-Neochloris_oleoabundans	Floral homeotic protein APETALA 2	166	6,74E-47	66.37
scaffold-MCHJ-2060647-Micrasterias_fimbriata	AP2-like ethylene-responsive transcription factor AIL5	132	4,12E-53	86.22
scaffold-GYBH-2004656-Codium_fragile	pathogenesis-related genes transcriptional activator	161	1,01E-47	68.51
scaffold-WXRI-2003961-Stichococcus_bacillaris	pathogenesis-related genes transcriptional activator	145	5,43E-78	86.83
scaffold-XJGM-2003910-coccoid_prasinophyte	floral homeotic protein APETALA 2-like isoform X1	200	1,91E-23	54.58
scaffold-MFYC-2030481-Nannochloris_atomus	predicted protein	164	1,18E-64	66.17
scaffold-NKXU-2006171-Trebouxia_arboricola	predicted protein	163	3,72E-50	64.3
scaffold-LETF-2024468-Planophila_terrestris	floral homeotic protein APETALA 2-like isoform X1	164	1,46E-61	65.99
scaffold-XJGM-2003802-coccoid_prasinophyte	floral homeotic protein APETALA 2-like	159	8,83E-32	68.1
scaffold-CBNG-2001349-Planophila_laetevirens	floral homeotic protein APETALA 2-like isoform X3	164	3,98E-60	66.75
scaffold-XOAL-2008429-Dolichomastix_tenuilepi	predicted protein	163	6,64E-68	66.14
scaffold-KADG-2033428-Ignatius_tetrasporus	DNA-binding domain	101	5,25E-28	71.65
scaffold-GYBH-2023346-Codium_fragile	AP2-like protein	162	1,22E-42	68.92
scaffold-ZNUM-2022477-Leptosira_obovata	predicted protein	163	2,57E-56	68.75
scaffold-POIR-2040606-POIR-Volvox_aureus-2_samples_combined	AP2-like ethylene-responsive transcription factor AIL7	128	5,91E-36	72.11
scaffold-VJDZ-2037095-Botryococcus_sudeticus	Ethylene-responsive transcription factor WR11	176	2,77E-36	74.18
scaffold-AKCR-2022369-Parachlorella_kessleri	floral homeotic protein APETALA 2-like isoform X1	175	2,83E-61	63.88
scaffold-KSFK-2002927-Chlorosarcinopsis_halophila	integrase-type DNA-binding superfamily protein	163	9,60E-65	64.72
scaffold-ISIM-2000393-Nephroselmis_pyriformis	predicted protein	181	1,10E-64	66.96
scaffold-AJAU-2035798-Helicodictyon_planctonicum	floral homeotic protein APETALA 2-like isoform X1	164	4,07E-60	64.02
scaffold-PZIF-2051399-Scenedesmus_dimorphus	AP2-domain-containing protein	102	2,45E-29	69.57
scaffold-XMCL-2016197-Prasinococcus_capsulatus	AP2-like ethylene-responsive transcription factor ANT	166	3,51E-51	81.46
scaffold-MNCB-2037144-Eremosphaera_viridi	floral homeotic protein APETALA 2-like	159	5,66E-63	64.52
scaffold-JIWI-2004918-Acrosiphonia_sp	floral homeotic protein APETALA 2-like isoform X1	164	3,88E-63	64.2
scaffold-BAZF-2006294-Chaetopeltis_orbicularis	AP2-domain-containing protein	95	1,44E-25	72.14
scaffold-TGNL-2008643-Picocystis_salinarum	ethylene-responsive transcription factor RAP2-7-like isoform X1	167	8,23E-32	64.7
scaffold-GJIY-2003369-Neochloris_sp	floral homeotic protein APETALA 2-like isoform X2	179	5,13E-63	63.29
scaffold-AGIO-2011802-Haematococcus_pluvialis	AP2-like ethylene-responsive transcription factor AIL1	154	2,09E-30	67.86
scaffold-KADG-2006474-Ignatius_tetrasporus	ethylene-responsive transcription factor RAP2-7-like isoform X2	93	1,38E-20	72.64
scaffold-WDWX-2006164-Dunaliella_primolecta-UTEX_LB_1000	AP2-like ethylene-responsive transcription factor AIL1	110	5,50E-18	76.33
scaffold-ZDIZ-2049714-Dunaliella_tertiolecta-CCMP_364	AP2-like ethylene-responsive transcription factor AIL1	110	5,50E-18	76.33
scaffold-MMKU-2007666-Nephroselmis_olivace	Ethylene-responsive transcription factor WR11	128	6,26E-46	73.21
scaffold-WDWX-2039120-Dunaliella_primolecta-UTEX_LB_1000	AP2-like ethylene-responsive transcription factor AIL1	115	2,46E-37	78.65
scaffold-NNHQ-2029250-Spirotaenia_minuta	RAP2-7 transcription factor	87	3,87E-32	74.8

scaffold-AJAU-2031675-Helicodictyon_planctonicum	AP2-like ethylene-responsive transcription factor At1g79700	161	1,04E-38	70.37
scaffold-BZSH-2004272-Golenkinia_longispicula	ethylene-responsive transcription factor rap2-7	80	9,01E-12	75.9
scaffold-CQQP-2075123-Ochlochaete_sp	predicted protein	164	7,08E-55	63.68
scaffold-XOAL-2004641-Dolichomastix_tenuilepi	ap2-like ethylene-responsive transcription factor ant-like protein	118	2,23E-47	83.86
scaffold-UKUC-2011311-Dunaliella_salina-UTEX_LB_200	AP2-like ethylene-responsive transcription factor AIL1	106	1,71E-16	75.68
scaffold-BFIK-2020942-Entransia_fimbriat	AP2-like ethylene-responsive transcription factor At1g16060	120	3,58E-43	81.29
scaffold-CQQP-2012218-Ochlochaete_sp	pathogenesis-related genes transcriptional activator	148	7,03E-41	68.06
scaffold-DXNY-2003586-Microthamnion_kuetzigianum-A	ethylene-responsive transcription factor RAP2-7-like isoform X2	105	3,13E-23	64.11
scaffold-ZDOF-2039921-Microthamnion_kuetzigianum-B	floral homeotic protein APETALA 2-like isoform X2	180	9,42E-60	63.87
scaffold-DXNY-2039622-Microthamnion_kuetzigianum-A	floral homeotic protein APETALA 2-like isoform X2	180	9,42E-60	63.87
scaffold-BTFM-2009636-Monomastix_opisthostigma	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	174	2,28E-60	65.61
scaffold-AJAU-2003925-Helicodictyon_planctonicum	pathogenesis-related genes transcriptional activator	105	6,61E-28	70.88
scaffold-AJAU-2003927-Helicodictyon_planctonicum	pathogenesis-related genes transcriptional activator	105	6,61E-28	70.88
scaffold-PFUD-2026757-Geminella_sp	AP2-like protein	96	1,12E-23	67.6

Apêndice 2C. Sequências AP2/ERF encontradas em Briófitas.

SeqName	Description	Length	e-Value	sim mean
scaffold-RXRQ-2022798-Phaeoceros_carolinianus-sporophyte	floral homeotic protein APETALA 2-like isoform X1	201	2,80E-103	93.73
scaffold-FITN-2004168-Treubia_lacunose	floral homeotic protein APETALA 2-like isoform X1	173	1,02E-89	97.07
scaffold-FITN-2091824-Treubia_lacunose	floral homeotic protein APETALA 2-like isoform X2	221	1,45E-68	81.72
scaffold-NWWI-2024501-Nephrolepis_exaltata	floral homeotic protein APETALA 2-like isoform X3	196	5,93E-74	89.56
scaffold-NWWI-2024499-Nephrolepis_exaltata	floral homeotic protein APETALA 2-like isoform X3	196	5,93E-74	89.56
scaffold-FITN-2004169-Treubia_lacunose	AP2-like ethylene-responsive transcription factor TOE3 isoform X3	210	1,27E-83	77.7
scaffold-NWWI-2006397-Nephrolepis_exaltata	ethylene-responsive transcription factor RAP2-7 isoform X2	119	1,36E-44	98.38
scaffold-BPSG-2090810-Scouleria_aquatica	AP2-like ethylene-responsive transcription factor	207	9,09E-131	96.17
scaffold-NGTD-2008017-Dicranum_scoparium	AP2-like ethylene-responsive transcription factor AIL1	168	2,79E-105	97.95
scaffold-GRKU-2005874-Syntrichia_princeps	AP2-like ethylene-responsive transcription factor AIL1	168	2,79E-105	97.95
scaffold-FFPD-2000775-Ceratodon_purpureus	AP2-like ethylene-responsive transcription factor	207	1,04E-132	96.48
scaffold-SKQD-2080074-Takakia_lepidozioides	AP2-like ethylene-responsive transcription factor	208	2,42E-113	94.26
scaffold-YWNF-2012996-Hedwigia_ciliata	AP2-like ethylene-responsive transcription factor	168	2,09E-106	97.92
scaffold-ORKS-2002573-Philonotis_fontana	AP2-like ethylene-responsive transcription factor	168	2,09E-106	97.92
scaffold-ORKS-2002572-Philonotis_fontana	AP2-like ethylene-responsive transcription factor	168	2,09E-106	97.92
scaffold-JMXW-2011544-Bryum_argenteum	AP2-like ethylene-responsive transcription factor	168	2,09E-106	97.92
scaffold-CHJJ-2015669-Lejeuneaceae_sp	AP2-like ethylene-responsive transcription factor AIL5	168	3,25E-106	97.41
scaffold-BNCU-2017564-Radula_lindenbergia	AP2-like ethylene-responsive transcription factor AIL5	168	3,25E-106	97.41
scaffold-AWOI-2073679-Diphyscium_foliosum	AP2-like ethylene-responsive transcription factor AIL5	168	7,72E-110	98.93
scaffold-NGTD-2008018-Dicranum_scoparium	AP2-like ethylene-responsive transcription factor	203	2,09E-	96.55

			127	
scaffold-TMAJ-2024209-Neckera_douglasii	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-VMXJ-2013364-Leucobryum_albidum	AP2-like ethylene-responsive transcription factor	203	1,23E-128	96.93
scaffold-VMXJ-2013366-Leucobryum_albidum	AP2-like ethylene-responsive transcription factor	203	1,23E-128	96.93
scaffold-RGKI-2006743-Leucobryum_glaucum	AP2-like ethylene-responsive transcription factor	203	1,23E-128	96.93
scaffold-RGKI-2006742-Leucobryum_glaucum	AP2-like ethylene-responsive transcription factor	203	1,23E-128	96.93
scaffold-VMXJ-2013365-Leucobryum_albidum	AP2-like ethylene-responsive transcription factor	203	1,23E-128	96.93
scaffold-WSPM-2005726-Rhytidiadelphus_loreus	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-WSPM-2005727-Rhytidiadelphus_loreus	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-WNGH-2090887-Aulacomnium_heterostichum	AP2-like ethylene-responsive transcription factor	168	2,09E-106	97.92
scaffold-JADL-2010640-Rhynchostegium_serrulatum	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-ZACW-2015664-Leucodon_sciuroides	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-QMWB-2013075-Anomodon_attenuatus	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-QKQO-2012242-Pseudotaxiphyllum_elegans	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-EEMJ-2009083-Thuidium_delicatulum	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-LNSF-2070298-Hypnum_subimponens	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-VBMM-2054665-Anomodon_rostratus	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-YEPO-2082282-cf._Physcomitrium_sp	AP2-like ethylene-responsive transcription factor	168	6,67E-112	98.42
scaffold-IGUH-2021869-Schwetschkeopsis_fabronia	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-TCBC-2014104-Megaceros_vincentianus	AP2-like ethylene-responsive transcription factor AIL5	171	1,09E-106	98.16
scaffold-HERT-2009033-Sphaerocarpos_texanus	AP2-like ethylene-responsive transcription factor AIL5	168	3,59E-106	97.38
scaffold-FFPD-2001182-Ceratodon_purpureus	AP2-like ethylene-responsive transcription factor	203	2,91E-129	96.95
scaffold-RDOO-2017995-Racomitrium_varium	AP2-like ethylene-responsive transcription factor	203	2,91E-129	96.95
scaffold-FFPD-2001183-Ceratodon_purpureus	AP2-like ethylene-responsive transcription factor	203	2,91E-129	96.95
scaffold-NRWZ-2101123-Metzgeria_crassipilis	AP2-like ethylene-responsive transcription factor AIL5	168	3,28E-105	97.41
scaffold-DHWX-2069272-Fontinalis_antipyretica	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-FFPD-2000776-Ceratodon_purpureus	AP2-like ethylene-responsive transcription factor	205	3,05E-131	96.45
scaffold-CMEQ-2014630-Orthotrichum_lyellii	AP2-like ethylene-responsive transcription factor	168	3,59E-105	98.33
scaffold-BGXB-2082095-Plagiomnium_insigne	AP2-like ethylene-responsive transcription factor	168	3,59E-105	98.33
scaffold-TAVP-2011689-Calliergon_cordifolium	AP2-like ethylene-responsive transcription factor AIL1	168	2,43E-105	97.74
scaffold-IRBN-2015009-Scapania_nemorosa	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-YBQN-2013959-Odontoschisma_prostratum	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-HPXA-2019593-Ptilidium_pulcherrimum	AP2-like ethylene-responsive transcription factor AIL5	168	8,41E-105	97.59
scaffold-LGOW-2105533-Schistochila_sp	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-GRKU-2021445-Syntrichia_princeps	AP2-like ethylene-responsive transcription factor	168	3,59E-105	98.33
scaffold-WZYK-2016494-Bazzania_trilobata	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-TWUW-2009517-Anthoceros_agrestis-A	AP2-like ethylene-responsive transcription factor AIL5	171	3,53E-107	98.22
scaffold-BSNI-2004871-Anthoceros_agrestis-B	AP2-like ethylene-responsive transcription factor AIL5	171	3,53E-107	98.22

scaffold-FITN-2086600-Treubia_lacunose	AP2-like ethylene-responsive transcription factor AIL5	168	4,44E-105	97.56
scaffold-AKXB-2011631-Phaeomegaceros_coriaceus	AP2-like ethylene-responsive transcription factor AIL5	168	6,61E-105	98.75
scaffold-UCRN-2011439-Megaceros_tosanus	AP2-like ethylene-responsive transcription factor AIL5	171	1,09E-106	98.16
scaffold-ZTHV-2015592-Atrichum_angustatum	AP2-like ethylene-responsive transcription factor AIL5	168	1,42E-88	98.36
scaffold-RTMU-2018690-Calypogeia_fissa	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-OFTV-2002882-Barbilophozia_barbata	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-WEEQ-2013653-Phaeoceros_carolinianus-gametophyte_1575	AP2-like ethylene-responsive transcription factor AIL5	168	6,61E-105	98.75
scaffold-WJLO-2038118-Riccia_berychiana	AP2-like ethylene-responsive transcription factor AIL5	168	6,83E-106	97.92
scaffold-KRUQ-2013358-Porella_navicularis	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-UUHD-2017389-Porella_pinnata	AP2-like ethylene-responsive transcription factor AIL5	168	8,54E-106	97.32
scaffold-JHFI-2018921-Pellia_neesiana	AP2-like ethylene-responsive transcription factor AIL5	168	3,92E-106	96.96
scaffold-LNSF-2010117-Hypnum_subimponens	AP2-like ethylene-responsive transcription factor At1g16060	169	1,21E-96	90.47
scaffold-TFYI-2003310-Marchantia_emarginata	AP2-like ethylene-responsive transcription factor AIL5	168	5,65E-107	97.98
scaffold-YFGP-2018813-Pallavicinia_lyellii	AP2-like ethylene-responsive transcription factor AIL5	168	5,65E-107	97.98
scaffold-ORKS-2058526-Philonotis_fontana	AP2-like ethylene-responsive transcription factor At1g16060	171	3,69E-97	90.03
scaffold-HVBQ-2019659-Tetraphis_pellucida	AP2-like ethylene-responsive transcription factor	168	3,70E-88	98.18
scaffold-IHWO-2007265-Marchantia_paleacea-mycorrhizal	AP2-like ethylene-responsive transcription factor AIL5	168	6,95E-108	98.04
scaffold-TXVB-2014377-Lunularia_cruciata	AP2-like ethylene-responsive transcription factor AIL5	168	6,95E-108	98.04
scaffold-JPYU-2004536-Marchantia_polymorpha	AP2-like ethylene-responsive transcription factor AIL5	168	6,95E-108	98.04
scaffold-AWOI-2007087-Diphyscium_foliosum	AP2-like ethylene-responsive transcription factor At1g79700	168	5,12E-78	88.88
scaffold-IGUH-2017082-Schwetschkeopsis_fabronia	AP2-like ethylene-responsive transcription factor At1g79700	169	5,71E-95	90.0
scaffold-ZACW-2007459-Leucodon_sciuroides	AP2-like ethylene-responsive transcription factor At1g79700	169	5,71E-95	90.0
scaffold-PIUF-2016506-Pellia_cf_Epiphylla	AP2-like ethylene-responsive transcription factor AIL5	168	1,70E-101	96.85
scaffold-QMWB-2008260-Anomodon_attenuatus	AP2-like ethylene-responsive transcription factor At1g16060	169	1,21E-96	90.47
scaffold-TMAJ-2019624-Neckera_douglasii	AP2-like ethylene-responsive transcription factor At1g16060	169	1,21E-96	90.47
scaffold-WSPM-2046773-Rhytidiadelphus_loreus	AP2-like ethylene-responsive transcription factor At1g16060	169	1,21E-96	90.47
scaffold-JADL-2006659-Rhynchostegium_serrulatum	AP2-like ethylene-responsive transcription factor At1g16060	168	4,71E-95	90.3
scaffold-JADL-2006660-Rhynchostegium_serrulatum	AP2-like ethylene-responsive transcription factor At1g16060	168	4,71E-95	90.3
scaffold-VBMM-2006013-Anomodon_rostratus	AP2-like ethylene-responsive transcription factor At1g16060	168	4,71E-95	90.3
scaffold-EEMJ-2039276-Thuidium_delicatulum	ethylene-responsive transcription factor WR11	169	1,83E-97	91.01
scaffold-TAVP-2007700-Calliergon_cordifolium	AP2-like ethylene-responsive transcription factor At1g16060	168	1,80E-94	90.3
scaffold-TAVP-2007699-Calliergon_cordifolium	AP2-like ethylene-responsive transcription factor At1g16060	168	1,80E-94	90.3
scaffold-ILBQ-2002531-Conocephalum_conicum	AP2-like ethylene-responsive transcription factor AIL5	168	5,54E-105	96.73
scaffold-BGXB-2081174-Plagiomnium_insigne	AP2-like ethylene-responsive transcription factor At1g16060	168	9,14E-83	88.97
scaffold-DHWX-2001234-Fontinalis_antipyretica	AP2-like ethylene-responsive transcription factor At1g16060	169	2,21E-95	90.41
scaffold-SKQD-2012843-Takakia_lepidozoides	AP2-like ethylene-responsive transcription factor At1g16060	186	5,28E-95	93.08
scaffold-ZQRI-2005738-Timmia_austriaca	AP2-like ethylene-responsive transcription factor	203	1,54E-122	94.7
scaffold-QKQO-2049720-Pseudotaxiphyllum_elegans	AP2-like ethylene-responsive transcription factor At1g16060	162	3,71E-91	90.34

scaffold-YEPO-2076662-cf._Physcomitrium_sp	ethylene-responsive transcription factor WR11-like	176	1,87E-119	89.73
scaffold-RDOO-2009038-Racomitrium_varium	AP2-like ethylene-responsive transcription factor At1g16060	180	2,04E-95	88.71
scaffold-ZQRI-2005737-Timmia_austriaca	AP2-like ethylene-responsive transcription factor	199	4,57E-123	92.64
scaffold-HVBQ-2131604-Tetraphis_pellucida	AP2-like ethylene-responsive transcription factor At1g16060	168	1,17E-84	91.01
scaffold-RGKI-2064441-Leucobryum_glaucum	ethylene-responsive transcription factor WR11-like	177	1,43E-92	89.69
scaffold-VMXJ-2131054-Leucobryum_albidum	ethylene-responsive transcription factor WR11-like	177	1,43E-92	89.69
scaffold-CMEQ-2013519-Orthotrichum_lyellii	AP2-like ethylene-responsive transcription factor At1g16060	162	2,89E-90	90.8
scaffold-FFPD-2013730-Ceratodon_purpureus	AP2-like ethylene-responsive transcription factor At1g16060	172	1,05E-89	89.85
scaffold-KEFD-2053122-Encalypta_streptocarpa	AP2-like ethylene-responsive transcription factor	130	1,01E-81	98.0
scaffold-IRBN-2013981-Scapania_nemorosa	AP2-like ethylene-responsive transcription factor At1g16060	198	2,61E-110	90.57
scaffold-IHWO-2007267-Marchantia_paleacea-mycorrizal	AP2-like ethylene-responsive transcription factor AIL5	130	1,22E-82	97.38
scaffold-YWNF-2008485-Hedwigia_ciliata	AP2-like ethylene-responsive transcription factor At1g16060	162	2,73E-90	90.46
scaffold-ABCD-2008193-Niphotrichum_elongatum	AP2-like ethylene-responsive transcription factor At1g16060	168	2,35E-92	89.88
scaffold-VBMM-2009296-Anomodon_rostratus	AP2-like ethylene-responsive transcription factor At1g16060	171	4,48E-90	90.61
scaffold-CMEQ-2008218-Orthotrichum_lyellii	AP2-like ethylene-responsive transcription factor At1g16060	172	1,83E-96	89.74
scaffold-CMEQ-2008217-Orthotrichum_lyellii	AP2-like ethylene-responsive transcription factor At1g16060	172	1,83E-96	89.74
scaffold-HVBQ-2007589-Tetraphis_pellucida	AP2-like ethylene-responsive transcription factor AIL5	130	5,06E-62	96.27
scaffold-RDOO-2012594-Racomitrium_varium	AP2-like ethylene-responsive transcription factor At1g16060	168	1,17E-91	90.33
scaffold-NGTD-2013210-Dicranum_scoparium	AP2-like ethylene-responsive transcription factor At1g16060	168	1,06E-91	91.49
scaffold-ABCD-2078166-Niphotrichum_elongatum	AP2-like ethylene-responsive transcription factor At1g16060	168	8,71E-93	89.79
scaffold-GRKU-2021343-Syntrichia_princeps	AP2-like ethylene-responsive transcription factor At1g79700	172	1,53E-93	90.16
scaffold-FFPD-2011359-Ceratodon_purpureus	AP2-like ethylene-responsive transcription factor At1g16060	168	3,71E-93	90.78
scaffold-JMXW-2010238-Bryum_argenteum	AP2-like ethylene-responsive transcription factor At1g16060	168	1,38E-98	90.09
scaffold-BPSG-2013413-Scouleria_aquatica	AP2-like ethylene-responsive transcription factor At1g16060	154	5,91E-74	78.01
scaffold-QMWB-2061497-Anomodon_attenuatus	AP2-like ethylene-responsive transcription factor At1g16060	168	3,63E-93	90.98
scaffold-CHJJ-2009253-Lejeuneaceae_sp	AP2-like ethylene-responsive transcription factor AIL1	168	2,68E-87	91.65
scaffold-BGXB-2079425-Plagiomnium_insigne	AP2-like ethylene-responsive transcription factor At1g16060	154	1,43E-81	88.83
scaffold-VMXJ-2015109-Leucobryum_albidum	AP2-like ethylene-responsive transcription factor At1g16060	168	1,95E-92	90.65
scaffold-GOWD-2008873-Sphagnum_lescurii	AP2-like ethylene-responsive transcription factor AIL5	134	9,28E-82	97.01
scaffold-ZTHV-2017512-Atrichum_angustatum	AP2-like ethylene-responsive transcription factor At2g41710	176	6,33E-65	84.72
scaffold-ANON-2008619-Leiosporoceros_dussii-B	AP2-like ethylene-responsive transcription factor At1g16060	168	3,37E-87	93.72
scaffold-RXRQ-2023776-Phaeoceros_carolinianus-sporophyte	AP2-like ethylene-responsive transcription factor At1g16060	168	6,60E-87	95.19
scaffold-WEEQ-2014813-Phaeoceros_carolinianus-gametophyte_1575	AP2-like ethylene-responsive transcription factor At1g16060	168	8,66E-87	95.25
scaffold-HPXA-2011358-Ptilidium_pulcherrimum	AP2-like ethylene-responsive transcription factor At1g16060	177	4,29E-78	84.73
scaffold-DHWX-2014203-Fontinalis_antipyretica	AP2-like ethylene-responsive transcription factor At1g16060	162	2,59E-89	90.93
scaffold-SKQD-2013275-Takakia_lepidozioides	AP2-like ethylene-responsive transcription factor At1g16060	198	6,93E-89	89.38
scaffold-JHFI-2014632-Pellia_neesiana	AP2-like ethylene-responsive transcription factor At1g16060	168	6,29E-86	95.43
scaffold-BSNI-2009665-Anthoceros_agrestis-B	AP2-like ethylene-responsive transcription factor At1g16060	168	1,50E-86	95.71

scaffold-TWUW-2050471-Anthoceros_agrestis-A	AP2-like ethylene-responsive transcription factor At1g16060	168	1,50E-86	95.71
scaffold-BPSG-2020100-Scouleria_aquatica	AP2-like ethylene-responsive transcription factor	113	1,38E-65	97.88
scaffold-IRBN-2002839-Scapania_nemorosa	AP2-like ethylene-responsive transcription factor At1g16060	179	3,63E-83	93.12
scaffold-BPSG-2018131-Scouleria_aquatica	AP2-like ethylene-responsive transcription factor At1g16060	162	5,15E-87	90.47
scaffold-WSPM-2047131-Rhytidiadelphus_loreus	AP2-like ethylene-responsive transcription factor At1g16060	162	8,05E-90	90.83
scaffold-VBMM-2009295-Anomodon_rostratus	AP2-like ethylene-responsive transcription factor At1g16060	162	8,05E-90	90.83
scaffold-VMXJ-2014379-Leucobryum_albidum	AP2-like ethylene-responsive transcription factor At1g16060	162	8,05E-90	90.83
scaffold-LNSF-2069537-Hypnum_subimponens	AP2-like ethylene-responsive transcription factor At1g16060	162	8,05E-90	90.83
scaffold-UCRN-2051427-Megaceros_tosanus	AP2-like ethylene-responsive transcription factor At1g16060	168	3,01E-86	95.33
scaffold-TFYI-2068150-Marchantia_emarginata	AP2-like ethylene-responsive transcription factor AIL1	168	1,91E-86	95.27
scaffold-IHWO-2011695-Marchantia_paleacea-mycorrizal	AP2-like ethylene-responsive transcription factor AIL1	168	1,91E-86	95.27
scaffold-TXVB-2014057-Lunularia_cruciata	AP2-like ethylene-responsive transcription factor At1g16060	168	7,48E-86	95.24
scaffold-YWNF-2051638-Hedwigia_ciliata	AP2-like ethylene-responsive transcription factor At1g16060	162	1,01E-90	90.93
scaffold-JHFI-2113902-Pellia_neesiana	AP2-like ethylene-responsive transcription factor At1g16060	171	6,65E-82	94.0
scaffold-PIUF-2092192-Pellia_cf_Epiphylla	AP2-like ethylene-responsive transcription factor At1g16060	171	1,66E-81	93.51
scaffold-ZACW-2011152-Leucodon_sciuroides	AP2-like ethylene-responsive transcription factor At1g16060	162	6,69E-89	90.31
scaffold-UUHD-2150530-Porella_pinnata	AP2-like ethylene-responsive transcription factor At1g16060	171	9,68E-81	93.74
scaffold-TCBC-2014529-Megaceros_vincentianus	AP2-like ethylene-responsive transcription factor AIL1	168	3,32E-86	94.55
scaffold-QMWB-2008680-Anomodon_attenuatus	AP2-like ethylene-responsive transcription factor At1g16060	175	1,42E-88	86.28
scaffold-QKQO-2050159-Pseudotaxiphyllum_elegans	AP2-like ethylene-responsive transcription factor At1g16060	162	1,29E-88	90.34
scaffold-IRBN-2013980-Scapania_nemorosa	AP2-like ethylene-responsive transcription factor AIL1	151	3,79E-77	94.56
scaffold-KRUQ-2113920-Porella_navicularis	AP2-like ethylene-responsive transcription factor At1g16060	171	3,94E-82	94.12
scaffold-RXRQ-2136366-Phaeoceros_carolinianus-sporophyte	AP2-like ethylene-responsive transcription factor AIL1	168	1,48E-83	95.0
scaffold-AWOI-2068371-Diphyscium_foliosum	AP2-like ethylene-responsive transcription factor At1g16060	162	1,31E-91	91.08
scaffold-TAVP-2018694-Calliergon_cordifolium	AP2-like ethylene-responsive transcription factor At1g16060	162	3,19E-88	90.77
scaffold-KRUQ-2002495-Porella_navicularis	AP2-like ethylene-responsive transcription factor At1g16060	168	2,25E-81	93.75
scaffold-KRUQ-2002496-Porella_navicularis	AP2-like ethylene-responsive transcription factor At1g16060	168	2,25E-81	93.75
scaffold-FITN-2090607-Treubia_lacunose	AP2-like ethylene-responsive transcription factor AIL1	169	1,04E-79	90.94
scaffold-FITN-2085763-Treubia_lacunose	AP2-like ethylene-responsive transcription factor At1g16060	168	1,92E-78	94.02
scaffold-DHWX-2070928-Fontinalis_antipyretica	AP2-like ethylene-responsive transcription factor At2g41710	133	1,12E-67	91.78
scaffold-ANON-2034215-Leiosporoceros_dussii-B	AP2-like ethylene-responsive transcription factor AIL1	168	1,26E-79	93.33
scaffold-RXRQ-2124708-Phaeoceros_carolinianus-sporophyte	AP2-like ethylene-responsive transcription factor AIL1	130	2,69E-65	94.54
scaffold-IGUH-2160503-Schwetschkeopsis_fabronia	AP2-like ethylene-responsive transcription factor At2g41710	130	2,43E-65	91.22
scaffold-NRWZ-2100444-Metzgeria_crassipilis	AP2-like ethylene-responsive transcription factor At1g16060	171	4,18E-82	93.53
scaffold-RTMU-2013488-Calypogeia_fissa	AP2-like ethylene-responsive transcription factor At1g16060	169	4,57E-72	89.82
scaffold-KRUQ-2003456-Porella_navicularis	ethylene-responsive transcription factor RAP2-7 isoform X3	93	5,41E-16	71.45
scaffold-BPSG-2013414-Scouleria_aquatica	AP2-like ethylene-responsive transcription factor At1g16060	130	2,90E-64	90.77
scaffold-FITN-2088454-Treubia_lacunose	AP2-like ethylene-responsive transcription factor AIL5	145	1,33E-75	90.9

scaffold-VBMM-2009297-Anomodon_rostratus	AP2-like ethylene-responsive transcription factor At1g16060	165	3,29E-76	81.67
scaffold-ORKS-2007155-Philonotis_fontana	AP2-like ethylene-responsive transcription factor At1g79700	134	1,80E-71	91.94
scaffold-CHJJ-2009252-Lejeuneaceae_sp	AP2-like ethylene-responsive transcription factor AIL1	134	2,13E-61	91.44
scaffold-BSNI-2009666-Anthoceros_agrestis-B	AP2-like ethylene-responsive transcription factor AIL1	120	8,15E-58	95.12
scaffold-WZYK-2086361-Bazzania_trilobata	AP2-like ethylene-responsive transcription factor At1g16060	134	4,04E-63	93.88
scaffold-GRKU-2008439-Syntrichia_princeps	AP2-like ethylene-responsive transcription factor At1g79700	142	1,96E-56	90.93
scaffold-GRKU-2008440-Syntrichia_princeps	AP2-like ethylene-responsive transcription factor At1g79700	142	1,96E-56	90.93
scaffold-TWUW-2006424-Anthoceros_agrestis-A	AP2-like ethylene-responsive transcription factor At2g41710	110	6,55E-51	99.54
scaffold-TMAJ-2015165-Neckera_douglasii	AP2-like ethylene-responsive transcription factor At1g79700	113	1,19E-65	91.05
scaffold-ABCD-2008192-Niphotrichum_elongatum	AP2-like ethylene-responsive transcription factor At1g79700	128	1,61E-63	90.95
scaffold-NWWI-2036201-Nephrolepis_exaltata	AP2-like ethylene-responsive transcription factor At2g41710 isoform X1	142	2,09E-53	83.41
scaffold-ZTHV-2013413-Atrichum_angustatum	AP2-like ethylene-responsive transcription factor At2g41710 isoform X2	109	1,64E-43	90.95
scaffold-NRWZ-2002693-Metzgeria_crassipilis	AP2-like ethylene-responsive transcription factor At2g41710	131	2,68E-57	94.02
scaffold-CMEQ-2081005-Orthotrichum_lyellii	AP2-like ethylene-responsive transcription factor At1g16060	128	2,94E-48	82.54
scaffold-NWWI-2031662-Nephrolepis_exaltata	ap2-like ethylene-responsive transcription factor ant-like protein	96	1,18E-18	78.81
scaffold-TMAJ-2018824-Neckera_douglasii	AP2-like ethylene-responsive transcription factor At2g41710 isoform X2	111	1,67E-50	96.84
scaffold-NRWZ-2096677-Metzgeria_crassipilis	AP2-like ethylene-responsive transcription factor At1g79700	111	9,52E-65	92.16

Apêndice 2D. Sequências AP2/ERF encontradas em Pteridófitas.

SeqName	Description	Length	e-Value	sim mean
scaffold-ALVQ-2008157-Tmesipteris_parva	floral homeotic protein APETALA 2-like isoform X1	195	1,81E-71	92.9
scaffold-QVMR-2014896-Psilotum_nudum	ethylene-responsive transcription factor RAP2-7-like isoform X1	197	1,08E-70	93.17
scaffold-ZFGK-2006788-Selaginella_kraussiana	ethylene-responsive transcription factor RAP2-7-like isoform X1	184	1,55E-108	92.35
scaffold-ZZOL-2002460-Selaginella_stauntoniana	homeotic APETALA2 protein	224	4,43E-140	91.5
scaffold-ZZOL-2002461-Selaginella_stauntoniana	homeotic APETALA2 protein	224	4,43E-140	91.5
scaffold-UPMJ-2019983-Pseudocyclopodiella_caroliniana	ethylene-responsive transcription factor RAP2-7 isoform X2	201	1,22E-88	91.38
scaffold-KJYC-2000129-Selaginella_willdenowii	ethylene-responsive transcription factor RAP2-7 isoform X1	200	3,45E-111	91.83
scaffold-KJYC-2000128-Selaginella_willdenowii	ethylene-responsive transcription factor RAP2-7 isoform X1	200	3,45E-111	91.83
scaffold-CAPN-2006618-Equisetum_diffusum	APETALA 2-like protein	225	2,68E-90	83.85
scaffold-GTUO-2025514-Huperzia_selago	ethylene-responsive transcription factor RAP2-7 isoform X1	166	9,47E-89	94.86
scaffold-GKAG-2010704-Huperzia_lucidula	ethylene-responsive transcription factor RAP2-7 isoform X1	166	9,47E-89	94.86
scaffold-GKAG-2010703-Huperzia_lucidula	ethylene-responsive transcription factor RAP2-7 isoform X1	166	9,47E-89	94.86
scaffold-JVSZ-2131893-Equisetum_hymale	ethylene-responsive transcription factor RAP2-7-like isoform X1	192	1,41E-84	89.3
scaffold-DFHO-2058448-Danaea_nodosa	Floral homeotic protein APETALA 2	251	6,19E-91	86.14
scaffold-ABII-2008493-Selaginella_lepidophylla	homeotic APETALA2 protein	189	1,07E-109	93.53
scaffold-LGDQ-2003782-Selaginella_apoda	ethylene-responsive transcription factor RAP2-7 isoform X1	176	1,13E-105	96.25
scaffold-UGNK-2009040-Marattia_attenuata	Floral homeotic protein APETALA 2	246	1,92E-	83.76

			92	
scaffold-GAON-2012197-Huperzia_squarrosa	target of EAT1-B1	182	3,73E-90	94.54
scaffold-WAFT-2001312-Diphasiastrum_digitatum	Floral homeotic protein APETALA 2	258	1,22E-93	76.7
scaffold-YIXP-2003618-Lindsaea_microphylla	ethylene-responsive transcription factor RAP2-7 isoform X2	160	3,79E-60	87.75
scaffold-ZFGK-2000175-Selaginella_kraussiana	ethylene-responsive transcription factor RAP2-7 isoform X1	219	1,67E-76	80.71
scaffold-KUXM-2043901-Selaginella_selaginoides	floral homeotic protein APETALA 2-like isoform X1	169	1,12E-81	97.4
scaffold-DFHO-2009754-Danaea_nodosa	AP2-like ethylene-responsive transcription factor TOE3	210	4,37E-85	88.62
scaffold-WAFT-2001313-Diphasiastrum_digitatum	ethylene-responsive transcription factor RAP2-7-like isoform X1	203	7,14E-82	92.32
scaffold-WCLG-2009145-Adiantum_aleuticum	ethylene-responsive transcription factor RAP2-7 isoform X2	175	8,38E-72	88.91
scaffold-JVSZ-2009599-Equisetum_hymale	floral homeotic protein APETALA 2-like	193	2,06E-89	91.58
scaffold-BEGM-2000391-Botrypus_virginianus	Floral homeotic protein APETALA 2	245	2,73E-100	85.99
scaffold-XDDT-2014872-Argyrochosma_nivea	floral homeotic protein APETALA 2 isoform X2	216	2,75E-87	88.37
scaffold-ENQF-2002028-Lycopodium_annotinum	ethylene-responsive transcription factor RAP2-7-like isoform X1	192	5,41E-91	91.69
scaffold-PKOX-2101181-Isoetes_tegetiformans	floral homeotic protein APETALA 2-like isoform X1	173	1,02E-89	97.07
scaffold-CAPN-2004389-Equisetum_diffusum	floral homeotic protein APETALA 2-like	193	6,28E-90	91.53
scaffold-UGNK-2009041-Marattia_attenuata	floral homeotic protein APETALA 2-like isoform X3	244	3,46E-102	83.53
scaffold-EEAQ-2016020-Sceptridium_dissectum	Floral homeotic protein APETALA 2	245	1,14E-99	85.5
scaffold-WCLG-2009422-Adiantum_aleuticum	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	215	9,35E-88	89.33
scaffold-YCKE-2002060-Notholaena_montieliae	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	217	1,27E-88	89.54
scaffold-PYHZ-2076301-Isoetes_sp	floral homeotic protein APETALA 2-like isoform X1	173	1,02E-89	97.07
scaffold-GTUO-2001943-Huperzia_selago	floral homeotic protein APETALA 2	201	9,62E-90	90.0
scaffold-NYBX-2004406-Huperzia_selago-A	floral homeotic protein APETALA 2	201	9,62E-90	90.0
scaffold-KUXM-2043751-Selaginella_selaginoides	ethylene-responsive transcription factor RAP2-7-like isoform X1	184	4,47E-85	96.59
scaffold-ZXJO-2073244-Hemionitis_arifolia	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	190	1,85E-84	94.92
scaffold-CBAE-2061689-Huperzia_myrsinites	ethylene-responsive transcription factor RAP2-7-like isoform X2	201	2,32E-89	90.29
scaffold-YLJA-2015535-Polypodium_amorphum	ethylene-responsive transcription factor RAP2-7-like isoform X1	200	1,89E-82	93.82
scaffold-XXHP-2015076-Cystopteris_fragilis-Stewart	ethylene-responsive transcription factor RAP2-7-like isoform X2	181	8,70E-71	87.51
scaffold-XDDT-2010892-Argyrochosma_nivea	ethylene-responsive transcription factor RAP2-7 isoform X2	176	9,24E-73	90.3
scaffold-GAON-2017079-Huperzia_squarrosa	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	191	4,15E-89	91.14
scaffold-WQML-2008276-Cryptogramma_acrostichoides	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	188	3,06E-82	95.06
scaffold-YQEC-2077499-Woodsia_ilvensis	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	215	1,25E-86	89.07
scaffold-YJJY-2007971-Woodsia_scopulina	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	188	1,26E-81	94.85
scaffold-PQTO-2009940-Lycopodium_deuterodensum	Floral homeotic protein APETALA 2	229	3,02E-89	81.81
scaffold-ULKT-2009011-Lycopodiella_apressa	ethylene-responsive transcription factor RAP2-7 isoform X1	194	1,82E-86	91.79
scaffold-ULKT-2009009-Lycopodiella_apressa	ethylene-responsive transcription factor RAP2-7 isoform X1	194	1,82E-86	91.79
scaffold-ULKT-2009007-Lycopodiella_apressa	ethylene-responsive transcription factor RAP2-7 isoform X1	194	1,82E-86	91.79
scaffold-DFHO-2009739-Danaea_nodosa	floral homeotic protein APETALA 2-like isoform X1	194	4,20E-94	92.51
scaffold-ZXJO-2008618-Hemionitis_arifolia	ethylene-responsive transcription factor RAP2-7-like isoform X2	152	1,84E-72	95.26

scaffold-WGTU-2008938-Leucostegia_immersa	ethylene-responsive transcription factor RAP2-7-like isoform X2	180	2,68E-60	87.85
scaffold-YOWV-2009307-Cystopteris_protrusa	floral homeotic protein APETALA 2-like isoform X1	176	2,81E-78	96.22
scaffold-WQML-2009876-Cryptogramma_acrostichoides	ethylene-responsive transcription factor RAP2-7-like isoform X2	174	4,63E-72	89.37
scaffold-XXHP-2003951-Cystopteris_fragilis-Stewart	floral homeotic protein APETALA 2-like isoform X1	176	2,40E-80	97.06
scaffold-UPMJ-2016874-Pseudolycopodiella_caroliniana	ethylene-responsive transcription factor RAP2-7-like isoform X5	178	1,77E-81	94.11
scaffold-PKOX-2009486-Isoetes_tegetiformans	floral homeotic protein apetala 2-like	221	7,67E-71	81.21
scaffold-QHVS-2007795-Ophioglossum_vulgatum-leaf	floral homeotic protein APETALA 2-like isoform X3	205	2,85E-85	84.69
scaffold-ULK1-2009010-Lycopodiella_apressa	ethylene-responsive transcription factor RAP2-7 isoform X1	197	6,86E-84	90.76
scaffold-ABIJ-2009941-Selaginella_lepidophylla	ethylene-responsive transcription factor RAP2-7-like isoform X1	154	1,78E-87	95.49
scaffold-PYHZ-2074748-Isoetes_sp	floral homeotic protein APETALA 2-like isoform X2	221	1,45E-68	81.72
scaffold-YLJA-2007377-Polypodium_amorphum	ethylene-responsive transcription factor RAP2-7-like isoform X2	189	2,20E-58	88.63
scaffold-ULK1-2009008-Lycopodiella_apressa	ethylene-responsive transcription factor RAP2-7-like isoform X1	201	4,36E-82	89.28
scaffold-YJJY-2016570-Woodsia_scopulina	ethylene-responsive transcription factor RAP2-7 isoform X2	174	1,98E-69	88.95
scaffold-YQEC-2003937-Woodsia_ilvensis	ethylene-responsive transcription factor RAP2-7-like isoform X2	148	6,43E-67	95.8
scaffold-YLJA-2007379-Polypodium_amorphum	ethylene-responsive transcription factor RAP2-7-like isoform X2	186	1,96E-58	87.96
scaffold-YLJA-2007378-Polypodium_amorphum	ethylene-responsive transcription factor RAP2-7-like isoform X2	186	1,96E-58	87.96
scaffold-JVSZ-2004279-Equisetum_hymale	ethylene-responsive transcription factor RAP2-7 isoform X2	200	9,01E-57	79.11
scaffold-ZZOL-2001082-Selaginella_stauntoniana	AP2-like ethylene-responsive transcription factor TOE3 isoform X3	178	2,23E-106	91.67
scaffold-YCKE-2009983-Notholaena_montieliae	ethylene-responsive transcription factor RAP2-7-like isoform X1	196	1,29E-81	89.04
scaffold-ULK1-2085573-Lycopodiella_apressa	AP2-like ethylene-responsive transcription factor AIL5 isoform X1	121	3,89E-58	95.09
scaffold-WGTU-2013071-Leucostegia_immersa	floral homeotic protein APETALA 2-like isoform X1	167	3,27E-78	98.53
scaffold-YOWV-2005126-Cystopteris_protrusa	ethylene-responsive transcription factor RAP2-7-like isoform X2	182	7,13E-65	85.08
scaffold-WTJG-2012311-Ophioglossum_vulgatum	floral homeotic protein APETALA 2-like isoform X3	153	1,62E-65	92.22
scaffold-JKAA-2178315-Selaginella_wallacei	floral homeotic protein apetala 2-like	169	4,22E-73	95.47
scaffold-JVSZ-2014313-Equisetum_hymale	floral homeotic protein APETALA 2-like isoform X1	191	1.7E-84	86.12
scaffold-GTUO-2014774-Huperzia_selago	ethylene-responsive transcription factor RAP2-7 isoform X1	184	3,47E-70	82.11
scaffold-CAPN-2006565-Equisetum_diffusum	floral homeotic protein APETALA 2-like isoform X1	190	1,15E-82	87.17
scaffold-YIXP-2010510-Lindsaea_microphylla	floral homeotic protein APETALA 2-like	199	1,76E-71	87.75
scaffold-GKAG-2001296-Huperzia_lucidula	ethylene-responsive transcription factor RAP2-7 isoform X1	179	1,39E-79	93.98
scaffold-EEAQ-2015184-Sceptridium_dissectum	ethylene-responsive transcription factor RAP2-7 isoform X1	155	2,68E-64	92.18
scaffold-WTJG-2012312-Ophioglossum_vulgatum	ethylene-responsive transcription factor RAP2-7 isoform X4	132	2,40E-55	95.63
scaffold-KJYC-2008665-Selaginella_willdenowii	Floral homeotic protein APETALA 2	157	1,14E-67	94.61
scaffold-JKAA-2174643-Selaginella_wallacei	floral homeotic protein APETALA 2	169	5,05E-56	91.08
scaffold-QVMR-2010385-Psilotum_nudum	AP2/ERF domain-containing transcription factor	184	1,16E-67	82.86
scaffold-EEAQ-2015129-Sceptridium_dissectum	floral homeotic protein apetala 2-like	186	3,64E-62	84.51
scaffold-PQTO-2082715-Lycopodium_deuterodensum	AP2-like ethylene-responsive transcription factor AIL5 isoform X1	138	9,70E-54	96.2
scaffold-QVMR-2009765-Psilotum_nudum	floral homeotic protein APETALA 2 isoform X3	183	7,43E-69	84.57
scaffold-ALVQ-2007389-Tmesipteris_parva	AP2/ERF domain-containing transcription factor	184	3,49E-60	81.09

scaffold-UPMJ-2082449-Pseudolycopodiella_caroliniana	ethylene-responsive transcription factor RAP2-7-like isoform X1	134	4,74E-39	92.54
scaffold-ALVQ-2007388-Tmesipteris_parva	AP2/ERF domain-containing transcription factor	182	1,82E-58	81.43
scaffold-XNXF-2004707-Dendrolycopodium_obscurum	ethylene-responsive transcription factor RAP2-7-like isoform X1	142	1,24E-60	90.55
scaffold-XNXF-2004706-Dendrolycopodium_obscurum	ethylene-responsive transcription factor RAP2-7-like isoform X1	142	1,24E-60	90.55
scaffold-ALVQ-2007387-Tmesipteris_parva	floral homeotic protein APETALA 2 isoform X1	178	5,36E-54	78.68
scaffold-GTUO-2001944-Huperzia_selago	floral homeotic protein APETALA 2	152	9,87E-71	87.46
scaffold-GKAG-2097660-Huperzia_lucidula	floral homeotic protein APETALA 2	152	9,87E-71	87.46
scaffold-NYBX-2004405-Huperzia_selago-A	floral homeotic protein APETALA 2	152	9,87E-71	87.46
scaffold-XNXF-2005304-Dendrolycopodium_obscurum	ethylene-responsive transcription factor RAP2-7-like isoform X5	156	1,10E-70	85.36
scaffold-ENQF-2001305-Lycopodium_annotinum	Floral homeotic protein APETALA 2	137	1,21E-58	90.5
scaffold-JVSZ-2014422-Equisetum_hymale	floral homeotic protein APETALA 2-like	133	1,38E-64	90.16
scaffold-UGNK-2009042-Marattia_attenuata	ethylene-responsive transcription factor RAP2-7 isoform X1	130	6,82E-58	93.4
scaffold-BEGM-2018587-Botrypus_virginianus	ethylene-responsive transcription factor RAP2-7-like isoform X1	131	2,86E-57	90.57
scaffold-ZFGK-2000174-Selaginella_kraussiana	ethylene-responsive transcription factor RAP2-7 isoform X1	133	1,05E-53	85.48
scaffold-WGTU-2070826-Leucostegia_immersa	AP2-like ethylene-responsive transcription factor AIL5	197	7,94E-121	95.9
scaffold-CAPN-2004213-Equisetum_diffusum	ethylene-responsive transcription factor RAP2-7 isoform X2	137	1,56E-31	75.54
scaffold-NYBX-2123266-Huperzia_selago-A	floral homeotic protein APETALA 2-like isoform X2	110	4,37E-40	92.17
scaffold-CAPN-2006566-Equisetum_diffusum	ethylene-responsive transcription factor RAP2-7 isoform X1	126	3,03E-58	87.58
scaffold-JVSZ-2131718-Equisetum_hymale	AP2-like ethylene-responsive transcription factor AIL1	172	2,64E-106	97.75
scaffold-KJYC-2014207-Selaginella_willdenowii	AP2-like ethylene-responsive transcription factor AIL5	168	2,73E-99	95.26
scaffold-GAON-2003584-Huperzia_squarrosa	AP2-like ethylene-responsive transcription factor AIL5	168	2,33E-106	97.08
scaffold-CAPN-2006567-Equisetum_diffusum	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	119	3,90E-59	86.08
scaffold-UPMJ-2011564-Pseudolycopodiella_caroliniana	AP2-like ethylene-responsive transcription factor AIL5	168	3,09E-103	97.62
scaffold-CBAE-2049377-Huperzia_myrsinites	floral homeotic protein APETALA 2	106	6,38E-56	93.11
scaffold-ZZOL-2009827-Selaginella_stauntoniana	AP2-like ethylene-responsive transcription factor AIL5	168	7,83E-107	98.54
scaffold-CAPN-2007863-Equisetum_diffusum	AP2-like ethylene-responsive transcription factor AIL1	173	3,59E-103	96.25
scaffold-WGTU-2077167-Leucostegia_immersa	AP2-like ethylene-responsive transcription factor AIL1	168	3,30E-105	98.24
scaffold-GAON-2008382-Huperzia_squarrosa	AP2-like ethylene-responsive transcription factor AIL5	189	2,97E-109	95.5
scaffold-PQTO-2011838-Lycopodium_deuterodensum	AP2-like ethylene-responsive transcription factor	194	2,10E-114	94.81
scaffold-WAFT-2066434-Diphasiastrum_digitatum	AP2-like ethylene-responsive transcription factor AIL1	168	9,62E-97	95.12
scaffold-XDDT-2017901-Argyrochosma_nivea	AP2-like ethylene-responsive transcription factor AIL1	184	2,97E-108	93.75
scaffold-YCKE-2066224-Notholaena_montieliae	AP2-like ethylene-responsive transcription factor AIL1	168	4,58E-103	97.23
scaffold-WQML-2007574-Cryptogramma_acrostichoides	AP2-like ethylene-responsive transcription factor AIL1	168	8,68E-105	98.27
scaffold-ABIJ-2002464-Selaginella_lepidophylla	AP2-like ethylene-responsive transcription factor AIL5	168	1,44E-105	98.54
scaffold-UPMJ-2003589-Pseudolycopodiella_caroliniana	AP2-like ethylene-responsive transcription factor AIL5	187	1,04E-110	95.47
scaffold-PYHZ-2076641-Isoetes_sp	AP2-like ethylene-responsive transcription factor AIL5	168	4,44E-105	97.56
scaffold-PKOX-2010530-Isoetes_tegetiformans	AP2-like ethylene-responsive transcription factor AIL5	168	4,44E-105	97.56
scaffold-GKAG-2014305-Huperzia_lucidula	AP2-like ethylene-responsive transcription factor AIL5	168	2,51E-102	98.6

scaffold-NYBX-2005399-Huperzia_selago-A	AP2-like ethylene-responsive transcription factor AIL1	200	1,09E-112	90.64
scaffold-JKAA-2174111-Selaginella_wallacei	AP2-like ethylene-responsive transcription factor AIL5	166	1,75E-103	97.95
scaffold-JVSZ-2013345-Equisetum_hymale	AP2-like ethylene-responsive transcription factor AIL1	177	4,90E-110	96.39
scaffold-DFHO-2007144-Danaea_nodosa	AP2-like ethylene-responsive transcription factor AIL1	168	1,11E-103	97.62
scaffold-PQTO-2011839-Lycopodium_deuterodensum	AP2-like ethylene-responsive transcription factor AIL5	194	9,50E-108	98.68
scaffold-JVSZ-2003654-Equisetum_hymale	AP2-like ethylene-responsive transcription factor AIL1	168	4,36E-101	96.34
scaffold-PQTO-2081807-Lycopodium_deuterodensum	AP2-like ethylene-responsive transcription factor AIL5	168	6,39E-104	96.1
scaffold-YCKE-2066455-Notholaena_montieliae	AP2-like ethylene-responsive transcription factor AIL1	184	3,02E-110	94.76
scaffold-PKOX-2013692-Isoetes_tegetiformans	AP2-like ethylene-responsive transcription factor	205	5,37E-115	91.51
scaffold-JKAA-2007692-Selaginella_wallacei	AP2-like ethylene-responsive transcription factor AIL5	168	6,32E-105	98.81
scaffold-WGTU-2004079-Leucostegia_immersa	AP2-like ethylene-responsive transcription factor AIL1	171	1,08E-87	94.88
scaffold-ZFGK-2008369-Selaginella_kraussiana	AP2-like ethylene-responsive transcription factor AIL5	168	6,26E-96	95.92
scaffold-KJYC-2007474-Selaginella_willdenowii	AP2-like ethylene-responsive transcription factor AIL5	168	9,79E-101	99.05
scaffold-PYHZ-2012953-Isoetes_sp	AP2-like ethylene-responsive transcription factor ANT	205	1,52E-116	91.5
scaffold-UGNK-2104629-Marattia_attenuata	AP2-like ethylene-responsive transcription factor AIL1	163	5,12E-100	97.12
scaffold-ZFGK-2008759-Selaginella_kraussiana	AP2-like ethylene-responsive transcription factor AIL5	168	4,65E-88	98.24
scaffold-YQEC-2070836-Woodsia_ilvensis	AP2-like ethylene-responsive transcription factor AIL1	161	1,17E-99	98.14
scaffold-JVSZ-2014406-Equisetum_hymale	AP2-like ethylene-responsive transcription factor AIL1	174	1,39E-92	95.86
scaffold-WCLG-2062313-Adiantum_aleuticum	AP2-like ethylene-responsive transcription factor AIL1	130	3,08E-82	99.54
scaffold-UGNK-2019566-Marattia_attenuata	AP2-like ethylene-responsive transcription factor AIL1	153	2,15E-93	98.5
scaffold-LGDQ-2010911-Selaginella_apoda	AP2-like ethylene-responsive transcription factor AIL5	153	1,37E-94	98.37
scaffold-KJYC-2005523-Selaginella_willdenowii	AP2-like ethylene-responsive transcription factor At1g16060	195	4,67E-119	91.79
scaffold-WCLG-2008778-Adiantum_aleuticum	AP2-like ethylene-responsive transcription factor AIL1	129	1,30E-75	96.67
scaffold-XDDT-2013649-Argyrochosma_nivea	AP2-like ethylene-responsive transcription factor At1g16060	180	2,32E-94	90.8
scaffold-ALVQ-2001462-Tmesipteris_parva	AP2-like ethylene-responsive transcription factor AIL1	142	1,43E-69	98.17
scaffold-ALVQ-2001461-Tmesipteris_parva	AP2-like ethylene-responsive transcription factor AIL1	124	9,53E-62	98.51
scaffold-ALVQ-2001460-Tmesipteris_parva	AP2-like ethylene-responsive transcription factor AIL1	124	9,53E-62	98.51
scaffold-ALVQ-2001459-Tmesipteris_parva	AP2-like ethylene-responsive transcription factor AIL1	124	9,53E-62	98.51
scaffold-CAPN-2002949-Equisetum_diffusum	AP2-like ethylene-responsive transcription factor AIL1	162	1,76E-95	92.08
scaffold-KUXM-2008976-Selaginella_selaginoides	AP2-like ethylene-responsive transcription factor AIL1	163	1,58E-82	89.14
scaffold-ZZOL-2004863-Selaginella_stauntoniana	AP2-like ethylene-responsive transcription factor AIL5	158	2,32E-100	93.89
scaffold-GKAG-2001295-Huperzia_lucidula	AP2-like ethylene-responsive transcription factor AIL5 isoform X2	58	1,67E-10	98.28
scaffold-GKAG-2089243-Huperzia_lucidula	AP2-like ethylene-responsive transcription factor AIL5	116	1,43E-62	92.59
scaffold-KJYC-2013663-Selaginella_willdenowii	AP2-like ethylene-responsive transcription factor At1g16060	206	3,82E-104	92.24
scaffold-PQTO-2006385-Lycopodium_deuterodensum	AP2-like ethylene-responsive transcription factor AIL1	148	2,68E-75	90.0
scaffold-PYHZ-2073098-Isoetes_sp	AP2-like ethylene-responsive transcription factor AIL1	169	1,04E-79	90.94
scaffold-PYHZ-2012844-Isoetes_sp	AP2-like ethylene-responsive transcription factor At1g16060	168	1,92E-78	94.02
scaffold-QHVS-2099240-Ophioglossum_vulgatum-leaf	ethylene-responsive transcription factor RAP2-7	68	3,56E-15	88.3

scaffold-PKOX-2091976-Isoetes_tegetiformans	AP2-like ethylene-responsive transcription factor AIL1	134	9,24E-65	93.45
scaffold-CBAE-2009147-Huperzia_myrsinites	floral homeotic protein APETALA 2-like	120	1,15E-22	64.42
scaffold-ZFGK-2040624-Selaginella_kraussiana	AP2-like ethylene-responsive transcription factor At1g16060	171	2,59E-88	93.79
scaffold-ZXJO-2068826-Hemionitis_arifolia	AP2-like ethylene-responsive transcription factor AIL5	134	1,41E-39	79.14
scaffold-GTUO-2000602-Huperzia_selago	AP2-like ethylene-responsive transcription factor At1g16060	168	2,17E-65	90.0
scaffold-ULKT-2013401-Lycopodiella_apressa	AP2-like ethylene-responsive transcription factor AIL5	104	6,59E-60	97.84
scaffold-YLJA-2015530-Polypodium_amorphum	AP2-like ethylene-responsive transcription factor AIL5	134	6,12E-32	79.95
scaffold-DFHO-2007143-Danaea_nodosa	AP2-like ethylene-responsive transcription factor AIL1	126	9,57E-69	95.79
scaffold-PQTO-2075168-Lycopodium_deuterodensum	ethylene-responsive transcription factor WR11	158	1,33E-71	92.97
scaffold-EEAQ-2087743-Sceptridium_dissectum	AP2-like ethylene-responsive transcription factor At2g41710	162	2,78E-57	80.22
scaffold-YJJY-2008560-Woodsia_scopulina	AP2-like ethylene-responsive transcription factor ANT isoform X3	134	1,98E-32	80.83
scaffold-UGNK-2017092-Marattia_attenuata	AP2-like ethylene-responsive transcription factor At2g41710	126	2,67E-55	93.65
scaffold-JVSZ-2006493-Equisetum_hymale	AP2-like ethylene-responsive transcription factor At2g41710 isoform X1	127	1,67E-51	92.6
scaffold-ABIJ-2009206-Selaginella_lepidophylla	AP2-like ethylene-responsive transcription factor At1g16060	173	6,44E-68	81.96
scaffold-CAPN-2033990-Equisetum_diffusum	AP2-like ethylene-responsive transcription factor AIL1	100	3,78E-55	95.6
scaffold-JVSZ-2122056-Equisetum_hymale	ethylene-responsive transcription factor RAP2-7-like isoform X2	94	3,43E-16	69.77
scaffold-UPMJ-2019757-Pseudolycopodiella_caroliniana	AP2-like ethylene-responsive transcription factor At1g79700	119	1,88E-58	94.42
scaffold-GAON-2055686-Huperzia_squarrosa	AP2-like ethylene-responsive transcription factor AIL5	111	1,24E-57	93.7
scaffold-XDDT-2069201-Argyrochosma_nivea	AP2-like ethylene-responsive transcription factor AIL1	96	7,24E-55	99.11
scaffold-WGTU-2000067-Leucostegia_immersa	AP2-like ethylene-responsive transcription factor At2g41710 isoform X2	110	1,27E-47	97.13
scaffold-JVSZ-2129064-Equisetum_hymale	AP2-like ethylene-responsive transcription factor AIL1	117	1,79E-61	95.08
scaffold-QVMR-2052399-Psilotum_nudum	AP2-like ethylene-responsive transcription factor At2g41710 isoform X2	101	4,85E-43	91.49