

> *pFaesAP1*

-1959 TTGTTTCACT G CAATAGGTT CACCTGTTCC A AGAAAAAACA AAACAAAACA AAACGAAACT
 CAATbox POLLEN1LELAT52
 -1899 TGTATAATCT CCAAGTAAG A TGCTTGCTGA AATATTC ATC ACATG TAATT TTG CATCTGC
 MYCCONSUSAT
 -1839 ATATAGCAAG TTTTTTCTG T AAGGATTAGG TTGA TACTTTG TATTCATCAT GATAGA TACT
 CACTFTPPCA1 CACTFTPPCA1
 -1779 TAGTACCCAT TTGGTTGGAA CAGTGGAATG G AATAAAATA AGGGCCCGTT TGGTTTAAAC
 MYCCONSUSAT
 -1719 TCCGGAATCG GAAACGAAT C TAGTCCATAC GTATAGTTTT ATTCATGAAA GTTTTGAAA
 SEF4MOTIFGM7S
 -1659 TCATTCCTTG TGCTTTGAA G TAATTGGAGT AGAGTTA AAT TACTTTTGAT ACTCTATAGG
 CACTFTPPCA1
 -1599 TAACGAAATG TGGGGAAAC A AGTGCATTTT GCATT AAACC AAAATGAATG CTTCCATAAA
 MYB1AT
 -1539 ATTTCACGAA TAAGGATACG TATATGGACT AAATTC GTTT CCATTCCATT TCCG TTTTCG
 RHERPATEXPA7 MYBST1
 -1479 TAGTTGGAAC TAAATGGGCC CTAAAATTGA ATAAACCATA AGAAAGGAA ATGGAATTGA
 MYB1AT POLLEN1LELAT52
 -1419 TGAGATTATT TTCTAGTATA AAATGACCTC TAAACAAACA TAGTTTTTGA TTAATTGGAA
 TATAbox MYBPLANT SEF4MOTIFGM7S
 -1359 TGATTCCTAG CGGTTCCAA A CGAACCTAA ATTTATG AAA CTTC TAACTG ATGAATTTGC
 MYB2AT
 -1299 AGGAAGCCTA CATATCCAAT TTGAAGAACA AATCAAAC CT TTAGTATCCT GAACC ACAAA
 CAATbox XYLAT
 -1239 GAACCATTGA TGCTGCTATA TTTGATCATC AAAC AGAAAG AACTTGTCAG ATTGAAG GCT
 POLLEN1LELAT52
 -1179 CATTTCGAAC TATATACGTG CATTAAGCTG TAAGCCC AAC AATCTGAACT TTTTC CATGA
 -1119 CTGCATACAA GCTAAGTAAG GATTTGT CAT CTGGGTTAGG GTAAAAAAA C TCC AGAAA
 MYCCONSUSAT
 -1059 TGAAATTGGG GCGAATCTTT TGAGATTG CA ATATTGAAAC CCT AGAAAGA ATGGAACAA
 CAATbox POLLEN1LELAT52
 -999 AGGCATGGAA TATGATAGTG CTGAAGTGAA AAAGCC ATGG GAATCTGAAT GAGATGTCAA
 -939 GTGCAC ACAA AGAAAAGAAA CAAAAGTAAA AAAGTAGAAT GAGGTGTTGT TCCACGGAAG
 XYLAT POLLEN1LELAT52
 -879 CTAGTTGGAA AACTAATTAC T CCGACTCTA TGATTTTGAC ATGG GTGGGG TTC CAACTGT
 LTRECOREATCOR15 MYCCONSUSAT
 -819 CGGCACTCAA ACTATTCAA A TCTT CAATCA AGAGTTCTTC TACTAG GGT TAAGTAATTT
 CAATbox
 -759 TGT CAATTAA GATAAACCTA CTTT CTACA TAATCCATA TCA GTAGGGC GCCGTCAGCA
 CAATbox
 -699 CAAGGATGAC GTCCGTACAA CCCAAATAAG TG TAGACGAA CCAGAAC ACG ACAGCACACC

Figure S1: FaesAP1 promoter sequence. The transcription start site (+1) is in bold and boxed. The start codon ATG is in bold and boxed. Putative cis-acting regulatory elements are in bold and underline.

Table S1: Information on Sequences selected for alignments and phylogenetic analyses from NCBI GenBank.

Taxon and species	Protein name	Accession numbers	lineage
Brassicaceae			
<i>Arabidopsis thaliana</i>	AP1	P35631.2	AP1/FUL
	euFUL	Q38876.1	AP1/FUL
	AGL79	AAN52802.1	AP1/FUL
	SEP1	P29382.2	SEP
	SEP2	P29384.1	SEP
	SEP3	NP_850953.1	SEP
	SEP4	P29383.2	SEP
	AGL6	AEC10582.1	AGL6
<i>Cardamine hirsuta</i>	CahiAP1	AQQ16907.1	AP1/FUL
Polygonaceae			
<i>Fagopyrum esculentum</i>	FaesAP1	AKI81897.1	AP1/FUL
Poaceae			
<i>Oryza sativa</i>	OsMADS14	Q10CQ1.2	AP1/FUL
	OsMADS15	Q6Q9I2.2	AP1/FUL
	OsMADS18	Q0D4T4.1	AP1/FUL
	OsMADS20	Q2QQA3.2	AP1/FUL
	OsMADS5	Q0DEB8.1	SEP
	OsMADS7	Q0J466.2	SEP
	OsMADS8	Q9SAR1.1	SEP
	OsMADS34	Q6Q9H6.2	SEP
	OsMADS6	Q6EU39.1	AGL6
Orchidaceae			
<i>Dendrobium</i> hybrid cultivar	DOAP1	ARI44760.1	AP1/FUL
<i>Oncidium</i> hybrid cultivar	OAP1	ADJ67240.1	AP1/FUL
	OSEP3	ADJ67238.1	SEP
	OSEP1/2	ADJ67241.1	SEP
	OAGL6	ADJ67239.1	AGL6
Liliaceae			
<i>Lilium longiflorum</i>	LMADS5	ADT78582.1	AP1/FUL
	LMADS6	ADT78583.1	AP1/FUL
	LMADS7	ADT78584.1	AP1/FUL
Chloranthaceae			
<i>Chloranthus spicatus</i>	CsAP1	AAQ83693.1	AP1/FUL
Ranunculaceae			
<i>Nigella damascena</i>	NdFL1	ALM95510.1	AP1/FUL
	NdFL2	ALM95511.1	AP1/FUL
	NdSEP3	ALM95519.1	SEP
	NdSEP2	ALM95518.1	SEP
	NdSEP1	ALM95517.1	SEP
	NdAGL6	ALM95509.1	AGL6
<i>Aquilegia coerulea</i>	AqFL1a	AGX01552.1	AP1/FUL
	AqFL1b	AGX01553.1	AP1/FUL
Berberidaceae			
<i>Epimedium sagittatum</i>	EsFUL	AEX58637.1	AP1/FUL
	EsAGL2-1	AEX58639.1	SEP
	EsAGL2-2	AEX58640.1	SEP
	EsAGL6	AEX58638.1	AGL6
Eupteleaceae			
<i>Euptelea pleiosperma</i>	EuplFL1	ABG49518.1	AP1/FUL
	EuplFL2	ABG49519.1	AP1/FUL
	EuplSEP1	ADC79707.1	SEP
	EuplSEP3	ADC79706.1	SEP
Cercidiphyllaceae			
<i>Cercidiphyllum japonicum</i>	CejaFUL	ASY97766.1	AP1/FUL
	CejaAP1	ASY97763.1	AP1/FUL
	CejaAGL6	ASY97761.1	AGL6
Vitaceae			
<i>Vitis vinifera</i>	VAP1	AAT07447.1	AP1/FUL
	VFUL	AAT07448.1	AP1/FUL
Rosaceae			
<i>Prunus persica</i>	PpMADS1	ABU63953.1	AP1/FUL

<i>Kerria japonica</i>	PperFUL	CAJ28929.1	AP1/FUL
	KejaAP1	AXR86366.1	AP1/FUL
	KejaSEP1	AXR86364.1	SEP
	KejaSEP3	AXR86365.1	SEP
Passifloraceae			
<i>Passiflora edulis</i>	PaedAP1	AQN67666.1	AP1/FUL
	PaedFUL	AQN67667.1	AP1/FUL
	PaedSEP1	AET98846.1	SEP
Euphorbiaceae			
<i>Jatropha curcas</i>	JcAP1	AKM06060.1	AP1/FUL
<i>Plukenetia volubilis</i>	PlvoAP1	ANA05340.1	AP1/FUL
Salicaceae			
<i>Salix discolor</i>	SAP1	AAAY82245.1	AP1/FUL
Chenopodiaceae			
<i>Spinacia oleracea</i>	SpAP1-1	ACE75943.2	AP1/FUL
	SpAP1-2	ACE75944.2	AP1/FUL
	SpFUL	ACE75945.2	AP1/FUL
Theaceae			
<i>Camellia japonica</i>	CjAPL1	AFW15783.1	AP1/FUL
	CjAPL2	AFX74875.1	AP1/FUL
	CjAGL6	AFW15784.1	SEP
Rubiaceae			
<i>Coffea arabica</i>	CaAP1	AHW58038.1	AP1/FUL
	CaFUL	AHW58040.1	AP1/FUL
	CaAGL6	AHW58046.1	AGL6
	CaSEP1/2	AHW58036.1	SEP
	CaSEP3	AHW58034.1	SEP
	CaSEP4	AHW58033.1	SEP
Solanaceae			
<i>Solanum lycopersicum</i>	MADS-MC	NP_001234665.1	AP1/FUL
	TDR4	CAA43169.1	AP1/FUL
	MBP7	NP_001294867.1	AP1/FUL
	SIAGL6	NP_001348459.1	AGL6
Scrophulariaceae			
<i>Antirrhinum majus</i>	SQUA	CAA45228.1	AP1/FUL
	DEFH28	AAK72467.1	AP1/FUL
Asteraceae			
<i>Gerbera</i> hybrid cultivar	GSQUA1	CAA08805.2	AP1/FUL
	GSQUA3	CAX65662.1	AP1/FUL
	GSQUA2	CAX65661.1	AP1/FUL
	GSQUA5	CAX65663.1	AP1/FUL
	GSQUA6	CAX65664.1	AP1/FUL
	GRCD6	ASP44958.1	SEP
	GRCD7	ASP44959.1	SEP
	GRCD8	ASP44960.1	SEP
	CDM8	AAO22981.1	AP1/FUL
	CDM41	AAO22980.1	AP1/FUL
	CDM111	AAO22979.1	AP1/FUL
<i>Chrysanthemum x morifolium</i>			