

Supplementary Material

Supplementary Table S1: Primers used in this study.

Primer name	Primers sequences (5'-3')
3RAP2GSP	ATACAACAGGGAAACACAGCT
3RTOEGSP	GCAAGCTCTTTTCCCTTTAACAG
3RAP1_2GSP	GGCCACACAACCTACACCAAAAATTG
DpAP1-2SP1	GATCTTCTCCATGCTTGAATCAGTAG
DpAP1-2SP2	GACAATAAGGGCAACTTCAGCATCAC
DpAP1-2SP3	GCTTTCTTCACTAAACCTCCTCTTCT
Y1HFaesTOEF	ATGGAGGCCAGTGAATTCGCAAGCTCTTTTCCCTTTAACAG
Y1HFaesTOER	ATTCATCTGCAGCTCGAGCTCCTCCTTAAACCTCACATCTCCAT
Y1HFaesAP2F	ATGGAGGCCAGTGAATTCATACAACAGGGAAACACAGC
Y1HFaesAP2R	ATTCATCTGCAGCTCGAGCTCAAGAGGATGATACCCATTGT
Y1HpAP1_1F	AAGCTTGAATTCGAGCTCACTATATACGTGCATTAAGCTGT
Y1HpAP1_1R	ACATGCCTCGAGGTCGACTGGTTCGTCTACACTTATTTGGG
Y1HpAP1_2F	AAGCTTGAATTCGAGCTCCTCATATCCACCCTAATGCAG
Y1HpAP1_2R	ACATGCCTCGAGGTCGACTGGTGTAGTTGTGTGGCCAAA
Y1HpFaesPI_1F	AAGCTTGAATTCGAGCTCCAACCCGAAGCAACTACAAG
Y1HpFaesPI_1R	ACATGCCTCGAGGTCGACGGCAAGAGGACGAGAAAAGG
Y1HpFaesPI_2F	AAGCTTGAATTCGAGCTCTCAGCTACACTACAACTTCTT
Y1HpFaesPI_2R	ACATGCCTCGAGGTCGACATTGTAATGGAAGAACGAGA
Y1HpFaesAP3_1F	AAGCTTGAATTCGAGCTCGCAACAAATGAGGAAGAGTGGTA
Y1HpFaesAP3_1R	ACATGCCTCGAGGTCGACGCAATCTCTCTAGTTCTTCCCTTG
Y1HpFaesAP3_2F	AAGCTTGAATTCGAGCTCCATTTTGAGATGTTTGTGA
Y1HpFaesAP3_2R	ACATGCCTCGAGGTCGACCATAACAAAGTAGGAAGAAAA
Y1HpFaesAG-F	AAGCTTGAATTCGAGCTCAGCATGTCTTTAACTTGACCT
Y1HpFaesAG-R	ACATGCCTCGAGGTCGACACTGAGTTGGGTAAGTTAGGG
Y1HpFaesELF3F	AAGCTTGAATTCGAGCTCGGAAACAGGAAAATCTAGCAT
Y1HpFaesELF3R	ACATGCCTCGAGGTCGACTCAACCTCTCTTAACAATCCA
Dual-FaesTOEF	CGCGGTGGCGGCCGCTCTAGAGCAAGCTCTTTTCCCTTTAACAG
Dual-FaesTOER	AAGCTTGATATCGAATTCCTCCTTAAACCTCACATCTCCAT
Dual-pFaesAP1_2F	GGGCCCCCCTCGAGGTCGACCTCATATCCACCCTAATGCAG
Dual-pFaesAP1_2R	CAGGAATTCGATATCAAGCTTGGTGTAGTTGTGTGGCCAAA
qFaesAP2F	GGTAAAGATGCTGTCACAAAC
qFaesAP2R	TGTTTCCTTGATTGAGCTAC
qFaesAP1_2F	CCATAGCTCAAGAAGTGCAG

qFaesAP1_2R	TTACCCGATGTTGAGAGAAG
qFaesTOEF	CCCAAGGAAGATCTTAGAGGT
qFaesTOER	CAATAGCAACCCTACCATAAT
qFaesactinF	ACCTTGCTGGACGTGACCTTAC
qFaesactinR	CCATCAGGAAGCTCATAGTTC
TRV2-FaesAP2F	GTTACCGAATTCTCTAGAGAACCATACTGCAACTTGAT
TRV2-FaesAP2R	CTCGAGACGCGTGAGCTCCATTCGAAGGTGAGGATGAG
TRV2-FaesTOEF	GTTACCGAATTCTCTAGATTGATGGCCCTACGAGTAAC
TRV2-FaesTOER	CTCGAGACGCGTGAGCTCCTGAAGCTGAGCCTGAGCGA
TRV2-FaesAP1_2F	GTTACCGAATTCTCTAGACAAAGAGAGGGAAAGATCCATAG
TRV2-FaesAP1_2R	CTCGAGACGCGTGAGCTCTTATTCGGAAACTCGTGCACTTC

Supplementary Table S2: The sequence information of APETALA2-like proteins used to construct phylogenetic tree was selected from NCBI Genbank.

Taxon and species		Protein name	Accession numbers	Lineage
Arecaceae	<i>Elaeis guineensis</i>	EgAP2	XP_010932035.1	AP2
Musaceae	<i>Musa acuminata</i>	MaAP2a	XP_009418515.1	AP2
	<i>Musa troglodytarum</i>	MutrAP2	URD92577.1	AP2
Zingiberaceae	<i>Zingiber officinale</i>	ZoTOE3	XP_042381587.1	AP2
Poaceae	<i>Triticum aestivum</i>	WANT-1	BAH57730.1	ANT
		TaTOE1-B1	ANW09544.1	TOE
		OsAP2	CAJ86049.1	AP2
	<i>Oryza sativa</i>	OsIDS1	Q84TB5.1	TOE
		SNB	Q8H443.1	TOE
		OsPLT7	XP_025879549.1	ANT
		OsPLT8	XP_025882595.1	ANT
		OsPLT9	XP_015629409.1	ANT
	<i>Zea mays</i>	ZmRAP2-7	ABR19870.1	TOE
		ZmAP2L	ABR19870.1	TOE
Paeoniaceae	<i>Paeonia lactiflora</i>	PIAP2	AGI61068.1	AP2
	<i>Paeonia suffruticosa</i>	PasuAP2	AEK33829	AP2
Vitaceae	<i>Vitis vinifera</i>	VvAP2	NP_001267881.1	AP2
Fabaceae	<i>Medicago truncatula</i>	MetrAP2	KEH31465.1	AP2
		MtANT1	XP_039688487.1	ANT
	<i>Glycine max</i>	GmTOE4b	XP_003542008.1	TOE
		GmTOE4a	XP_003547042.3	TOE
Rosaceae	<i>Malus domestica</i>	MaDoAP2	ADE41133.1	AP2
	<i>Kerria japonica</i>	KjAP2	AXR86367.1	AP2
	<i>Rosa chinensis</i>	RcAP2L	XP_024186592.1	TOE
		RcAP2	XP_024182693.1	AP2

	<i>Prunus persica</i>	PpTOE	XP_007205143.1	TOE
		PpANT	XP_020422785.1	ANT
		PpAP2	XP_007208004.1	AP2
	<i>Prunus mume</i>	PmAP2L	XP_008224982.1	TOE
		PmAP2	AJT39804.1	AP2
Fagaceae	<i>Castanea mollissima</i>	CmAP2	KAF3973429.1	AP2
Cucurbitaceae	<i>Cucumis sativus</i>	CsTOE3	XP_004141908.1	AP2
Sapindaceae	<i>Xanthoceras</i>	XsAP2	KAH7566610.1	AP2
	<i>sorbifolium</i>			
Brassicaceae	<i>Arabidopsis thaliana</i>	AtAP2	AAC13770.1	AP2
		AtTOE1	AAC49773.1	TOE
		AtTOE2	NP_200820.3	TOE
		AtTOE3	NP_201519.1	TOE
		AtSMZ	NP_191059.2	TOE
		AtSNZ	NP_850313.2	TOE
		AtANT	AAB17364.1	ANT
		AIL1	Q1PFE1.1	ANT
		AIL5	Q6PQQ3.2	ANT
		AIL6	Q52QU2.1	ANT
		AIL7	Q6J9N8.2	ANT
	<i>Brassica rapa</i>	BrAIL6	XP_009122044.2	ANT
		BrAIL7	XP_033129837.1	ANT
		BrANT-1	XP_009138530.2	ANT
	<i>Brassica napus</i>	BnAIL6	WFR93999.1	ANT
Polygonaceae	<i>Fagopyrum</i>	FaesAP2	AKI81900.1	AP2
	<i>esculentum</i>			
		FaesTOE	WWB03765	TOE
		FaesANT	WWB03766	ANT
Solanaceae	<i>Petunia hybrida</i>	PhROB1	AAD39439.1	AP2
		PhROB2	APG29273.1	AP2
		PhROB3	APG29274.1	AP2
		PhBEN	AAD39440.1	TOE
		PhBOB	APG29272.1	TOE
		PhANT	AHC98702.1	ANT
	<i>Solanum tuberosum</i>	SoyuAP2	CAR92295.1	TOE
	<i>Solanum lycopersicum</i>	SITOE1	XP_004246701.1	TOE
Acanthaceae	<i>Andrographis</i>	AnpaTOE3	XP_051114135.1	TOE
	<i>paniculata</i>			
Lamiaceae	<i>Salvia splendens</i>	SaspTOE3	XP_042016810.1	TOE

Supplementary Table S3: The sequence information of APETALA1-like proteins used to construct phylogenetic tree was selected from NCBI Genbank.

Taxon and species		Protein name	Accession numbers	Lineage	
Orchidaceae	<i>Dendrobium hybrid</i>	DOAP1	ARI44760.1	Ful-Like	
	<i>cultivar</i>				
	<i>Oncidium hybrid</i>	OAP1	ADJ67240.1	Ful-Like	
	<i>cultivar</i>				
		OSEP3	ADJ67238.1	SEP	
		OAGL6	ADJ67239.1	AGL6	
Poaceae	<i>Brachypodium</i>	BdFUL2	ADQ92357.1	Ful-Like	
	<i>distachyon</i>				
	<i>Oryza sativa</i>	OsMADS6	Q6EU39.1	AGL6	
Eupteleaceae	<i>Euptelea pleiosperma</i>	EpFUL-1	ABG49518.1	Ful-Like	
		EpFUL-2	ABG49519.1	Ful-Like	
		EuplSEP1	ADC79707.1	SEP	
		EuplSEP3	ADC79706.1	SEP	
Berberidaceae	<i>Epimedium</i>	EsFUL	AEX58637.1	Ful-Like	
	<i>sagittatum</i>				
		EsAGL2-1	AEX58639.1	SEP	
		EsAGL2-2	AEX58640.1	SEP	
		EsAGL6	AEX58638.1	AGL6	
Ranunculaceae	<i>Nigella damascena</i>	NdFL2	ALM95511.1	Ful-Like	
		NdFL1	ALM95510.1	Ful-Like	
		NdSEP2	ALM95518.1	SEP	
		NdSEP1	ALM95517.1	SEP	
		NdAGL6	ALM95509.1	AGL6	
	<i>Aquilegia coerulea</i>	AqFL1a	AGX01552.1	Ful-Like	
		AqFL1b	AGX01553.1	Ful-Like	
Cercidiphyllaceae	<i>Cercidiphyllum</i>	CejaFUL	ASY97766.1	AGL79	
	<i>japonicum</i>				
		CejaAGL6	ASY97761.1	AGL6	
Saxifragaceae	<i>Heuchera americana</i>	HeaFUL	AAP83374.1	euFUL	
Vitaceae	<i>Vitis vinifera</i>	VFUL-L	AAT07448.1	AGL79	
Fabaceae	<i>Glycine max</i>	GmAP1a	XP_003547792.1	euAP1	
		GmAP1c	XP_003516454.1	euAP1	
		GmAP1d	XP_006574961.1	euAP1	
		GmAP1b	XP_003531957.1	euAP1	
Rosaceae	<i>Malus domestica</i>	MdAP1	BAH10867.1	euAP1	
		MdAGL6	NP_001280892.1	AGL6	
	<i>Prunus persica</i>	PperFUL	CAJ28929.1	euFUL	
		PpAGL6-1	XP_020412713.1	AGL6	
		PpAGL6-2	XP_007220094.2	AGL6	
		<i>Prunus dulcis</i>	PdAGL6	BBG97451	AGL6
		<i>Rosa chinensis</i>	RcFUL	QIH54603.1	AGL79

Betulaceae	<i>Betula pendula</i>	BpMADS4	Q39400	AGL79
Passifloraceae	<i>Passiflora edulis</i>	PaedAP1	AQN67666.1	euAP1
		PeFUL	AQN67667.1	euFUL
		PaedSEP1	AET98846.1	SEP
Lythraceae	<i>Punica granatum</i>	PgSEP3a	WHA03959.1	SEP
		PgSEP3b	WHA03960.1	SEP
Malvaceae	<i>Gossypium hirsutum</i>	GhSEP1	AEL33631.1	SEP
Brassicaceae	<i>Arabidopsis thaliana</i>	AtAP1	CAA78909.1	euAP1
		AGL79	AAN52802.1	AGL79
		SEP1	P29382.2	SEP
		SEP2	P29384.1	SEP
		SEP3	NP_850953.1	SEP
		SEP4	P29383.2	SEP
		AGL6	AEC10582.1	AGL6
Polygonaceae	<i>Fagopyrum esculentum</i>	FaesAP1-1	AKI81897.1	euAP1
		FaesAP1-2	WWB03767	euAP1
Amaranthaceae	<i>Spinacia oleracea</i>	SpAP1-1	ACE75943.2	euAP1
		SpAP1-2	ACE75944.2	euAP1
Rubiaceae	<i>Coffea arabica</i>	CaAP1	AHW58038.1	euAP1
		CaFUL	AHW58040.1	euFUL
		CaSEP3	AHW58034.1	SEP
		CaSEP4	AHW58033.1	SEP
		CaAGL6	AHW58046.1	AGL6
Solanaceae	<i>Nicotiana tabacum</i>	NAP1-2	AAD01422.1	euAP1
		NFUL	ABF82231.1	euFUL
	<i>Petunia x hybrida</i>	Ph-FBP2	AAA86854.1	SEP
		Ph-FBP5	AAK21248.1	SEP
		Ph-FBP4	AAK21247.1	SEP
		pMADS4	BAA94287.1	AGL6
	<i>Solanum lycopersicum</i>	SlAGL6	NP_001348459.1	AGL6
Plantaginaceae	<i>Antirrhinum majus</i>	AmFUL	AAP83363.1	euFUL
		DEFH28	AAK72467.1	AGL79
Asteraceae	<i>Tagetes erecta</i>	TeAP1-1	QOJ53895.1	euAP1
		TeAP1-2	QOJ53896.1	euAP1
		TeFUL1	QOJ53897.1	euFUL
		TeFUL3	QOJ53899.1	euFUL
		TeFUL2	QOJ53898.1	AGL79
		TeSEP1	QOJ53900.1	SEP
		TeSEP4	QOJ53904.1	SEP
	<i>Chrysanthemum x morifolium</i>	CmAP1	AAO22979.1	euAP1
		CmeuFUL	AAO22981.1	euFUL

	CmAGL79	AAO22980.1	AGL79
<i>Gerbera hybrid</i>	GSQUA5	CAX65663.1	euFUL
<i>cultivar</i>	GSQUA6	CAX65664.1	euFUL
	GSQUA2	CAX65661.1	AGL79
	GRCD6	ASP44958.1	SEP
	GRCD8	ASP44960.1	SEP

Supplementary Figure S1:*FaesAPI_2* 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.

> *pFaesAPI_2*

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-593 GAAAAAAGAG AGTATATTTT AACTTTTAAA GGTGATTTTG TTTAAATTAA CCTATTAAAT
      GTGANTG10 TTTGTT/AACAAA motif
-533 AGTTATTTTAT AAGAAATAGT GGGACAAAAG AAAGATCAAG GAAAAGTAAC AGTAAGCTAG
      TATABOX5 POLLENILELAT5 POLLENILELAT5
-473 TCATGTGAGAG CTGAGAGCTA CATCTCATAT CCACCCTAAT GCAGTAAAAAT TCCGTACAGC
      GTGANTG10
-413 TCAAACTCAC ATCAACCAAT CAAAGACCGA CAACGCACCA ACTCTACAAA ACCAACCCGG
      CCAATBOX1 DRECRCTCOREAT MYBPLANT
-353 TTTTCGTAAA ACCACTAATT CTCCAAACCC CATACTTTCA CTCCTTTTCA GAAAAGTGA
      PYRIMIDINEBOXOSRAMY1A GTGANTG10
-293 AAAATAAAAT TATAAAAAAA GCACATATAT TTCCATTATT TCGTATGAGT ACCATAATAA
      TATABOX5
-233 CTATTCCTAG TAAAAAATTT ACAAACATCA CTCTGAGTAA AAACCCTTGA AAAAACCGTA

-173 AGATATTTAT CTGTGCCTAC AGCAAAAGGA GGAATAGTAC TATGTAACAA AATTCATTAT
      TTTGTT/AACAAA motif
-113 TTTCTTTCTT ATTTTTGGGA ATTTGTAAAT AAAAAGTTTA TTTAACAAT GGGTTATTCT
      CArG-BOX TATABOX5 CAATBOX1
      +1
-53 TGTTTTATT TTTTTTATAT TTTTGTGTT ACTGATATTG CTATAAATGC TAACTTTGCT
      TATABOX2
+8 TTCTTCTTTT GGCCACACAA CTACACCAA AATTGAAGAA A GAAAAGATAA AGAAAAAA
      POLLENILELAT5 POLLENILELAT5
+68 TG

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