

## Supplementary Materials

**Table S1.** Primers used in this study.

Primer name	Primers sequences (5'-3')
DFaesPIF	ATGGGGAGAGGGAAGATTGAAATCAAG
DFaesPIR	ATCATAGAGTTCAGTTCACACACCCATAG
D1pPISP1	CGTGGTATTAGGGCTACAATACTCA
D1pPISP2	CCAGAACTCGCAAAGATAACCAGAG
D1pPISP3	TGCATCACACAGAACAGTAATCTCC
D2pPI_2SP1	AAATGGGTCGGGTCAAAGGAAGAA
D2pPI_2SP2	TGCAGTCTCCCACCACATCCACATG
D2pPI_2SP3	GATACAAGGGTAAGCGAAGTGGT
5RPI_1GSP1	TCTTGCTTATGGCGGTG
5RPI_1GSP2	GGAGAGAAGTGATGTCTTCTCTTAGATGT
5RPI_1GSP3	GCATCCCACAATCTCTGACC
5RPI_2GSP1	TCTCGCTTATGGCGGTA
5RPI_2GSP2	AATCTGTAAGTCACCATTTCTTTCTTCACTC
5RPI_2GSP3	GCATCCCACAATCTCTGACC
TpFaesPI_1F1	ATGATTACGAATT <u>CGAGCTC</u> CAGAAATCCTTAACTCCTTCCTTC
TpFaesPI_1F2	ATGATTACGAATT <u>CGAGCTC</u> GACCCTTGGCTAGTATCAAA
TpFaesPI_1F3	ATGATTACGAATT <u>CGAGCTC</u> CTCGAATAGATGCAGGAAC
TpFaesPI_1F4	ATGATTACGAATT <u>CGAGCTC</u> TTTTGTAGAGAGAAACATGTACG
TpFaesPI_2F1	ATGATTACGAATT <u>CGAGCTC</u> CTCGAAGGTATGAAGGAATA
TpFaesPI_2F2	ATGATTACGAATT <u>CGAGCTC</u> GACGATGAATAAGCGGTTAC
TpFaesPI_2F3	ATGATTACGAATT <u>CGAGCTC</u> TGACAACCTTACGCTAATCA
TpFaesPI_2F4	ATGATTACGAATT <u>CGAGCTC</u> TTTTGTAGAGAGAAACATGTACG
TpFaesPI_1/2R	TCTGCAGGTCGACT <u>CTAGACT</u> CCAAAAACAAACCCTAGT
Tp1DFaesPI_1F	ATGATTACGAATT <u>CGAGCTC</u> CAGAAATCCTTAACTCCTTCCTTC
Tp2DFaesPI_2F	ATGATTACGAATT <u>CGAGCTC</u> GAAAGGTATGAAGGAATATGAC
TpDFaesPIR	TCTGCAGGTCGACT <u>CTAGA</u> ATCATAGAGTTCAGTTCACACACC
qGUSF	GTTCTGCGACGCTCACACCGATA
qGUSR	CAGCCATGCACACTGATACTCTTC
qFaesPI_1F	AACCAACAGACAAGTTACTTATA
qFaesPI_1R	ATGCATCCTGCCAGAACTCG
qFaesPI_2F	AACCAACAGACAAGTTACTTATT
qFaesPI_2R	ACATCCTGCCAGAACTCC
qFaesactinF	ACCTTGCTGGACGTGACCTTAC

qFaesactinR	CCATCAGGAAGCTCATAGTTC
qTFaesPI_1F	GGAGATTACTGTTCTGTGTGATGC
qTFaesPI_1R	TGTCCAGAACATCAACAACCGTG
qTFaesPI_2F	TGGTTATCTTTGGGAGTTCTGGC
qTFaesPI_2R	CTTTGCATCCCACAATCTCTGAC
qActinF	GACCGTATGAGCAAAGAGATC
qActinR	CACATCTGTTGGAAGGTGCT

**Table S2.** Information on Sequences selected for alignments and phylogenetic analyses from NCBI GenBank.

Taxon and species	Protein name	Accession numbers	Lineage
Aristolochiaceae			
<i>Aristolochia fimbriata</i>	AfimPI	ALV83436.1	PI/GLO
	AfimAP3	ALV83437.1	AP3/DEF
Magnoliaceae			
<i>Liriodendron tulipifera</i>	LtPI	AIE44761.1	PI/GLO
	LtAP3	AIE44760.1	AP3/DEF
<i>Magnolia wufengensis</i>	MAwuPI	AFM75882.1	PI/GLO
	MAwuAP3_1	AFM75880.1	AP3/DEF
	MAwuAP3_2	AFM75881.1	AP3/DEF
Chloranthaceae			
<i>Hedyosmum orientale</i>	HoPI_1	AFP17796.1	PI/GLO
	HoPI_2	AFP17799.1	PI/GLO
	HoPI_3	AFP17800.1	PI/GLO
	HoAP3_1	AFP17801.1	AP3/DEF
	HoAP3_2	AFP17802.1	AP3/DEF
Liliaceae			
<i>Lilium longiflorum</i>	LMADS8	AEI88009.1	PI/GLO
	LMADS9	AEI88010.1	PI/GLO
	LMADS1	AAM27456.1	AP3/DEF
Orchidaceae			
<i>Cymbidium faberi</i>	CyfaPI	QEO60647.1	PI/GLO
	CyfaAP3_1	ADI58467.1	AP3/DEF
	CyfaAP3_2	QLJ83030.1	AP3/DEF
<i>Oncidium gower ramsey</i>	OPI	ADJ67236.1	PI/GLO
	OAP3-1	ADJ67234.1	AP3/DEF
	OAP3-2	ADJ67235.1	AP3/DEF
<i>Phalaenopsis equestris</i>	PeMADS6	AAV83997.1	PI/GLO
	PeMADS2	AAR26628.1	AP3/DEF

	PeMADS3	AAR26629.1	AP3/DEF
Zingiberaceae			
<i>Alpinia oblongifolia</i>	AoPI	ABB92623.1	PI/GLO
	AoAP3	ABS83561.1	AP3/DEF
Eupteleaceae			
<i>Euptelea pleiosperma</i>			
	EupPI	ADC79697.1	PI/GLO
	EupAP3-1	AEG25813.1	AP3/DEF
	EupAP3-2	ADC79696.1	AP3/DEF
Papaveraceae			
<i>Eschscholzia californica</i>	EscaGLO	ABN55897.1	PI/GLO
	EscaDEF1	ABN55895.1	AP3/DEF
	EscaDEF2	ABN55896.1	AP3/DEF
	EscaDEF3	CCC54332.1	AP3/DEF
Ranunculaceae			
<i>Nigella damascena</i>	NdPI1	ALM95515.1	AP3/DEF
	NdPI2	ALM95516.1	PI/GLO
	NdAP3-1	ALM95512.1	AP3/DEF
	NdAP3-2	ALM95513.1	AP3/DEF
	NdAP3-3	ALM95514.1	AP3/DEF
Paeoniaceae			
<i>Paeonia lactiflora</i>	PLPI1	AQM56615.1	PI/GLO
	PLPI2	AQM56626.1	PI/GLO
	PLAP3-1	AQM56588.1	AP3/DEF
	PLAP3-2	AQM56599.1	AP3/DEF
Vitaceae			
<i>Vitis vinifera</i>	VvPI	ABK59993.1	PI/GLO
	VvAP3	ABN71371.1	AP3/DEF
	VvTM6	ABI98021.1	AP3/DEF
Fabaceae			
<i>Medicago truncatula</i>	MtPI	ACJ36228.1	PI/GLO
	MtNGL9	ACJ36229.1	PI/GLO
	MtNMH7	AEW43601.1	AP3/DEF
	MtTM6	AEW43602.1	AP3/DEF
<i>Lotus japonicus</i>	LjPIa	AAX13299.1	PI/GLO
	LjPIb	AAX13300.1	PI/GLO
	LjAP3	AAX13301.1	AP3/DEF
Rosaceae			
<i>Kerria japonica</i>	KjPI	AXR86369.1	PI/GLO
	KjAP3	AXR86368.1	AP3/DEF
<i>Eriobotrya japonica</i>	EjPI	QGR27129.1	PI/GLO

<i>Malus domestica</i>	EjAP3	QGR27127.1	AP3/DEF
	MdPI	CAC28021.1	PI/GLO
	MdMADS13	CAC80856.1	AP3/DEF
	MdTM6	BAC11907.1	AP3/DEF
Violaceae			
<i>Viola philippica</i>	VpPI	APQ46145.1	PI/GLO
	VpTM6-1	APQ46143.1	AP3/DEF
	VpTM6-2	APQ46144.1	AP3/DEF
Brassicaceae			
<i>Arabidopsis thaliana</i>	AtPI	BAA06465.1	PI/GLO
	AtAP3	P35632.1	AP3/DEF
Polygonaceae			
<i>Fagopyrum esculentum</i>	FaesPI_1	OM032616.1	PI/GLO
	FaesPI_2	OM032617.1	PI/GLO
	FaesAP3_1	AFO83616.1	AP3/DEF
	FaesAP3_2	QLJ83023.1	AP3/DEF
Primulaceae			
<i>Primula vulgaris</i>	PvGLO1	AQT19636.1	PI/GLO
	PvGLO2	AQT19638.1	PI/GLO
	PvDEF1	ABD78317.1	AP3/DEF
	PvTM6	AZZ09244.1	AP3/DEF
Sapotaceae			
<i>Argania spinosa</i>	AsPI	UDH08096.1	PI/GLO
Actinidiaceae			
<i>Actinidia chinensis</i>	AcPI	ADU15475.1	AP3/DEF
	AcAP3-1	ADU15473.1	AP3/DEF
	AcAP3-2	ADU15474.1	AP3/DEF
Gentianaceae			
<i>Gentiana scabra</i>	GsPI1	BAS04475.1	PI/GLO
	GsPI2	BAS04476.1	PI/GLO
	GsPI3	BAS04478.1	PI/GLO
	GsAP3a	BAS04474.1	AP3/DEF
	GsAP3b	BAS04479.1	AP3/DEF
	GsTM6	BAS04472.1	AP3/DEF
Solanaceae			
<i>Physalis pubescens</i>	PFGLO1	AGN54427.1	PI/GLO
	PFGLO2	AGN54426.1	PI/GLO
	PFDEF	AGN54423.1	AP3/DEF
	PFTM6	AGN54424.1	AP3/DEF
<i>Lycopersicon esculentum</i>	TPI	ABG73411.1	PI/GLO
	TAP3	ABG73412.1	AP3/DEF

	TDR6	NP_001311309.1	AP3/DEF
Oleaceae			
<i>Osmanthus fragrans</i>	OfGLO1	QCS90129.1	PI/GL
Scrophulariaceae			
<i>Antirrhinum majus</i>	GLO	CAA48725.1	PI/GLO
	DEF	BAI68389.1	AP3/DEF
Bignoniaceae			
<i>Catalpa bungei</i>	CabuPI	AJY60427.1	PI/GLO
Asteraceae			
<i>Gerbera hybrid</i>	GGLO1	CAA08804.1	PI/GLO
	GDEF1	CAA08802.1	AP3/DEF
	GDEF2	CAA08803.1	AP3/DEF
	GDEF3	ACV53813.1	AP3/DEF

> *pFaesPI\_1*

-2186 CAGAAATCCT TAACTCCTTC CTTCCCAGCC TACTAACAA ATGTAGCTGA GATCTCCTTC  
POLLEN1LELAT52 CACTFTPPCA1 MYCCONSENSUSAT

-2126 CAATTGTAAG TTTGCTTGCT TCCGTTTTTC TTTTGAAAGT CATTAAAAAT TGACACTAGA  
CCAATBOX1 WRKY71OS

-2066 AGTTTAACTA GTTCAAAAGT CCAAGGAAAA TTTGGACCCC TACACTTTTG TGAGAGATTA  
CACTFTPPCA1 GTGANTG10

-2006 TTATTGTCCA TCTACAAGCT CAAAACAATA TAACATATGT TTAGTACAAA CAAAACACCA  
CAATBOX1 MYCCONSENSUSAT AACAAA motif

-1946 CAAAATGAAA AATAAAAAAT GTATAAGATT AGGTACACTG GAAGCATTCT AAAAATCAGA  
CACTFTPPCA1

-1886 TTGGGTACAC TGCAAGCATT TATACTGGTA TAAGAATAGA GAAGTTTCTC AAACATATCGA  
CACTFTPPCA1 CACTFTPPCA1

-1826 TGGATCATAC ATACAAAACCT GCAGCAATAA ATTCTTAACT TCAATCTCAA ACTATCGATG  
CAATBOX1 CAATBOX1

-1766 AATATAAAAC CTAACAGTTT ATTTGAAGTT TAGCAGCAGT TCCACAAATA TCAGACCACA  
MYBPLANT TATABOX5

-1706 CAAGAACAAA GATTAAATGG AGCTTAAATG GACACAATTG CAAGAGTATG AAGAAGTTTC  
AACAAA motif MYCCONSENSUSAT

-1646 AGCAACAGTC TAACTTTAAC AAAGATTATA AATGGACACA ATTGCAACCC ATAAATTACA  
MYBGAHV TATABOX2 MYCCONSENSUSAT

-1586 GAAGTCAATA GTCACAAAAT TACAACCTCTG AAGAGAAGAG TAAATTACAT CAGTTTGGAA  
CAATBOX1

-1526 ATAAAATGTA ATAAAGGAAG CAACCCGAAG CACAATTGCT CAACAATCAA GCAAACGCAG  
MYCCONSENSUSAT CAATBOX1

-1466 CAACTACAAC CTTATGGTAA GAATAATCAT ACCAATTTCA GTAGATAGAA CATGTATACA  
CCAATBOX1

-1406 GACTGACCCT TGGCTAGTAT CAAATTCAAA ATGGAAGCAT TATATATTAA ACATGAACTC

WRKY71OS

-1346 AGATTCTGAAC AGAGCAGTCA ATAACTCACT GCAAATTATA AACTCAGATT CGAAAAGCAA  
CAATBOX1 CACTFTPPCA1

-1286 CCCGAAGCAA CTACAAGTTT CCACATTCAT TTTAGGTGATA ACAAGTTTCC ACATTCATTI  
GTGANTG10 CArG-box

-1226 TTTAGTGATA ACAACATGTA TACAGACTAA CCCTTGGCTA GTATCAAATT CGAAATGGAA

-1166 GCATTATATT AAACATGAAC TCAGATTCGA ACAGAGCAGT CAATAACTCA CTGCAAATTA  
CAATBOX1 CACTFTPPCA1

-1106 TAAACTCAGA TTCGTTTAAT CTGAATAGAT GCAGGAAGAC TCAGATTATTA CTACAAAATC  
CACTFTPPCA1

-1046 TAATAACTCA CTGCAGCCAA GTTATTGACTC AGATTCTGAAA AGCAAAATAG ATGCAGGAAC  
WRKY71OS

-986 TCAAATTATA AACTCAGATT TGAGCAATCA CCACCATCAG ATTCGAATTG GAAAGAACAG  
CAATBOX1

-926 TCACCACCAT CAGATTCGAA TTCGAAAAGC AAAACAGATT CGAACAAAAC AGATTCTGAAC  
AACAAA motif

-866 AGAGCAGTCA CCACCGTCAG ATTCGAACAG ATTCGAATAG ATGCAGGAAC TCGAATAGAT

-806 GCAGGAACTT CAAAATGCATT GCAATCACAA ACACGGTTTA AGGGTTTTGA TGAGAATATI  
MYCONSENSUSAT CAATBOX1 CANBNNAPA

-746 ACTGTAATGC AGCAATCCGA AACGTACCTC AACTTGTCTG CCTTTTCTCG TCCTCTTGCC  
CACTFTPPCA1 CAATBOX1 PYRIMIDINEBOXOSRAMY1A

-686 GCCGTCAGTT TCTCTTTGCC GTTGCCGTCG CAGGGTTGCT CCAGATCGGG GAAGAAGATA  
MYBCORE

-626 GCAAGGTTTG ATGAGAGAGG GTGTTAATTA TATACCCGGT TAATGCGTAA TTCTTGTTAA  
MYBCORE

-566 TAGATGAGGGA TTTTTGGGT ATTTTGCACG GAGAAACCCT AGTGTAAACC CAAAACTCTT  
MYBST1 POLLEN1LELAT52

-506 GCTCAGATGG GAGTTTCACA AACAATCGGA GAAACACTAA TCACCACTGT TTCTCTCCGT  
MYCONSENSUSAT CAATBOX1 POLLEN1LELAT52

-446 GCCAAACACT CGTAAAAACG AGATACACTA CAAACAATA AAAAACAATA GTAGTATCCG  
CANBNNAPA CACTFTPPCA1 CAATBOX1 CAATBOX1

-386 TGTGCCCAAAC ACAACCTTAG CTTTTGTAG AGGAGAAACAT GTACGAATAG GTAGCTAAGT  
CANBNNAPA POLLEN1LELAT52

-326 TAACCTAGAA ATGTGTCTAG AGGAAAACCTC AGACTTGTAT GAATCTCATA TACAGCTAGC  
POLLEN1LELAT52

-266 TAGCTATGGA GGATAGAAAGG GACCAACCGGT TAACAAGGTG CAATAGCATT TTCTCATACA  
MYBST1 MYBCORE CAATBOX1

-206 AAGCAATGTT TTTTGGTGAA AATTCAGCAA GGTAATAATTG AAAAGACAAT TTCAAAACAA  
CAATBOX1 GTGANTG10 ERELEE4

-146 AGAGAGAAA AAACCCATTT AAAACCAACC TTTTGTCACT CTCTTAGAAA GTCTATTGTCTC  
POLLEN1LELAT52 MYBPLANT CACTFTPPCA1 POLLEN1LELAT52 ARFAT

-86 TCTTAAACCC TATATAGTAA GCATCTCACT GTACTCATCT TCTTCCCCCA CTCCACTTTA  
UP2ATMSD CACTFTPPCA1 CACTFTPPCA1 CACTFTPPCA1

+1

-26      ATTTTCACAT CCACCCCACTT CTTTTC**A**TTT GTCTTCTTCA CCTTCTTCCA TTATAATTTA  
    CACTFTPPCA1

+35      CAACACAGAG AAAAACTAGG TTTGTTTTT GGAG**ATG**  
                                  POLLEN1LELAT52      TTTGTT motif

**Supplementary Figure S1.** *pFaesPI\_1* 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 underlined.

> *pFaesPI\_2*

-2057      CTCGAAGGTA TGAAGGAATA TGACACGAAG GTTGCTGCTG CTTGCTACCA TGGCCTCCAG  
    WRKY71OS

-1997      ATCCAATGTT GATGTCGGCT GCAGAGGAGG AACGAGGCTA GACTCAACTG GAGGGGTTCG  
                                  LEAFYATAG      MYCONSENSUSAT

-1937      AGTGTTTCCT GAAGAGATCG ACGCAGATGG CCTGGGGACG GGGCTGTAGT GACTTGCTAG  
                                  MYCONSENSUSAT      GTGANTG10

-1877      CGCTATCCAT GGCTGAGGAC GAGGCTGGAG TGACCTGCTA GCGCCATCCA TGGCTGAGGA  
                                  GTGANTG10

-1817      CGAGGCTGGA GTGACCTGCT AGCGCCATCC ATGGCTGAGA ACAGGGCTGG AGTGAACTGC  
                                  GTGANTG10      GTGANTG10

-1757      TAGCGCCATC CATGGCAGAG TGCAGAAGCC GCGTCCAAG GAGGAGGTCC AGTCCAGGTA

-1697      GACGGCTGCT ATTGTGAGCC CTCACACGTG AAGAACGCTT GTTGCTGCTT GAGTAGAGGG  
                                  GTGANTG10      GTGANTG10

-1637      CTGGAAGTTC CGACTGTGCA GATCAGGAGG GGGAAAAGAG ATAGGTTGTA GGTAGAAGGT  
                                  LTRECOREATCOR15

-1577      TGTGTAGTAT ACCATGGATT AAATGTTTGA GTAAGTTCAG AAGGTGACGTA TGAATAAGCG  
                                  GTGANTG10

-1517      GTTACGAAAA GGGGAGGTGT GTGATTCTG TACGGGTTTT AGAAGGAAAG AGAGGTATTT  
                                  MYBCORE

-1457      GATAGGATCT ATTTATTCCC TGAATATACG GTAGGCTGGA ATGCTTCATT GCTGGCTGGT

-1397      AGAACCTGGC AGCTTGGGCT GAAGCATAAG GGTGCTAGAT CTTGGGCTTTT GTCATTGGGCT  
                                  SITEIIATCYTC      SITEIIATCYTC      SITEIIATCYTC

-1337      AGTCATGAGC TTGTCAAGGA TTTGTCATGG GCTTGTCAAA TGGCTTATT GCCTTGTCAA  
                                  SITEIIATCYTC      MYCONSENSUSAT

-1277      AAGGTCCATC AAATTCTACA TTTTCAAAAG TGTGTTATAA GTAGTATTTT ATTTGATCAA  
                                  TATABOX5

-1217      AACTCCACAT AAAATCATAA AAGTTTTGTAA AGATCATTTT ATGTGTTTAA TTCATCACAT  
                                  -300CORE

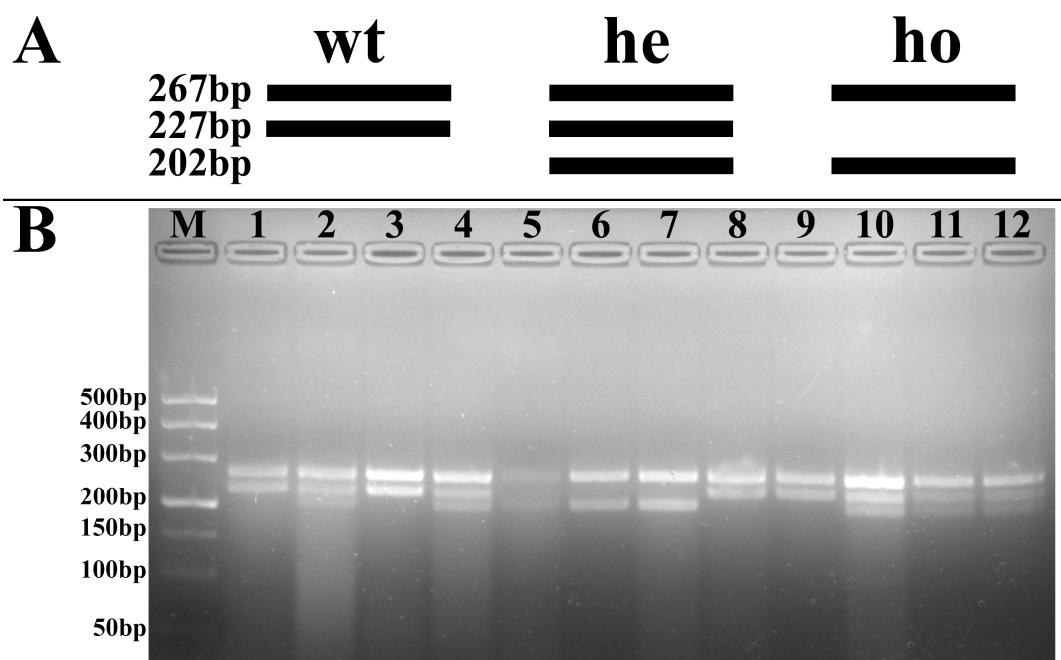
-1157      AAAATACCAA GATTTATTTT GACTTGTAAG TGAACGAAA GAAAAAAAAAT TTCCGGTTAT  
                                  TATABOX5      POLLEN1LELAT52      MYBCORE

-1097 TACCATTTGGC CTACGAGAGG GCCTCCAAAA GGCCGCCAAC ATTGGTATTC TATCCATATT  
 MYCONSENSUSAT  
 -1037 GAAGGTGACA ACCTTACGCT AATCAATGTA GTTAACCAAC TATGGAAGGC ACCATGGGGA  
 GTGANTG10 CAATBOX1 MYB1AT  
 -977 TGGATATGAT CATCTCGGAC ATCTCCACCT TGATATCCAG TTTTGAGCGG TTCTACGCTC  
 MYBST1  
 -917 AACATATATT TAGAGAAATC AACGTCGTAG CAGACAGACT TGCATTGCAT GATTTTTGACC  
 POLLEN1LELAT52 WRKY71OS  
 -857 CGGCAATAAA GACGAAGTGC TACCGGATTGA CTTTGGATGC TGTGAGAATG ACGGTTTTTA  
 CAATBOX1 WRKY71OS GTGANTG10 WRKY71OS  
 -797 GGAACATAACC TTACCACTTC GCTTACCCTT GTATCAAAAA GAAAAAGAAA AAAAAAAAAA  
 CACTFTPPCA1 POLLEN1LELAT52 POLLEN1LELAT52  
 -737 TTTGGTTGCA GCCAAACAAG CCCTAGGGAT TGGAAGTATT CTTCATTTTT GACAGCAGCT  
 WRKY71OS  
 -677 TTTGACCATG TGGATGTGGT GGGAGACTGC AGTAATTTCC TGAACCCATT TTCTTCCTTT  
 WRKY71OS  
 -617 GACCCGACC ATTTCCAAAA CCATGTAAAA AAAAAAGAAA AAAAAATAAAC GTCGCCCCACA  
 LTRECOREATCOR15 MYB1AT POLLEN1LELAT52 ABREOSRAB21  
 -557 TATATGTCTA TCCTTTGCTG ATCGTACAAG AAACAATAA ACTTGAGTTG ATATATTGAT  
 POLLEN1LELAT52 CAATBOX1  
 -497 TTGATGGTTA GGATCATGTG TATATTGCTG TGTCTCCTTC AGATTTCCCT CCAAACCCTA  
 MYCONSENSUSAT TELOBOXATEEF1AA1  
 -437 ATTGACATTT TGACATGACC CATTTTATCT CTCAGTCAGC TACCACTACAA ACTTCTTTTC  
 WRKY71OS WRKY71OS WRKY71OS CACTFTPPCA1  
 -377 ATTTACATC TCCTTATTAG ACTATAATTC TCTATTTATC ACTCTCATAA CAAAAATCTTC  
 CACTFTPPCA1 AACAAA motif  
 -317 ATCATCTTAA AATTACTCGAA TACTAAAATT AAAAACTCAG TAATTAACTC AATATATCAA  
 CACTFTPPCA1 CAATBOX1  
 -257 CTCAAGTTTT TTGTAGAGAG AAACATGTAC GAATAGGTAG CTAGGTTAAC CTAGAAATAT  
 POLLEN1LELAT52 POLLEN1LELAT52  
 -197 GTCTAGAGGA AAACCTCAGCA AGGTAAAATT GAAAAGACAA TTTCAAAAATA AAGAGAAGA  
 CAATBOX1 CArG-box  
 -137 AAAACCCATT TAAAACCAAC CTTTTTGCAC TCTCTTAGAA AGTCTATTGT CTCTTAAACC  
 POLLEN1LELAT52 MYBPLANT CACTFTPPCA1 POLLEN1LELAT52  
 -77 CTATATAGTA AGCATCTCAA TGTACTCATC TTCTTCCCCC ACTCCCACTTT AATTTTCACA  
 UP2ATMSD CAATBOX1 CACTFTPPCA1 CACTFTPPCA1 CACTFTPPCA1  
 +1  
 -17 TCCACCCCACT TCTTTTTATT TGTCTTCTTC TCGTTCTTCC ATTACCAATTT ACAACACAGA  
 CACTFTPPCA1 CAATBOX1  
 +44 GAAAAACTAG GGTTTGTTTT TGGAGATG  
 POLLEN1LELAT52 TTTGTT motif

Supplementary Figure S2. *pFaesPI\_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 underlined.



**Supplementary Figure S3.** Genotyping of wildtype, heterozygous and homozygous *pi-1* mutant *A. thaliana* by dCAPS.

The amplicons from transgenic lines in wild-type background *Arabidopsis* were cleaved by *BspHI* to produce 267 bp and 227 bp fragment, and the amplicon from heterozygous *PI/pi-1* background plants were cleaved by *BspHI* to produce 267 bp, 227 bp and 207 bp; the amplicon from transgenic lines.