

Supplementary Materials

Table S1. Primers used in this study.

Primer name	Primers sequences (5'-3')
GSPAP3	GAAATAGAACAAGACGTGATGGC
DFaesAP3_2F	ATGGCGAGGGGAAAGATCCAGATAC
DFaesAP3_2R	GTGAGGAACCATATACAATCGGAGAC
qFaesAP3_2F	TGATGTGTTGAGGGAGGATC
qFaesAP3_2R	AATCGGAGACACGAACAGCT
qFaesAP3_2aF	CGTGGCACAGCATTCTTTT
qFaesAP3_2aR	GAGACACGAACAGCTGCTAC
qFaesactinF	ACCTTGCTGGACGTGACCTTAC
qFaesactinR	CCATCAGGAAGCTCATAGTTC
D1pAP3_1SP1	TCCTCTTGATCTTCTGTACATCGTC
D1pAP3_1SP2	GGAGTCGTACATCTGCTTGGTGCTAC
D1pAP3_1SP3	GTGGTGTTGGGAGTGATGAATTCGTG
D2pAP3_1SP1	GCGTTGATCGTCCCATTTGTTTATTC
D2pAP3_1SP2	TCTTCTGTAATCCATTTGTCTTGCC
D2pAP3_1SP3	CATCCACAACCACCATTTAAGTCCT
FLpAP3_2SP1	AGGATTACGTGGTGTTGGGACTGATG
FLpAP3_2SP2	ATCGCAGAGAACCGTGAGCTCAT
FLpAP3_2SP3	CTTGCTGTGGTTGCGTTCTCTATCC
5RAP3_2GSP1	GTGAGGAACCATATACAATC
5RAP3_2GSP2	TGGTATCCAGCGCAGTCCTAGAAC
5RAP3_2GSP3	GTATCAATCTGATTCGCGAGTAC
TpFaesAP3_1F	<u>GAGCTCCGATACGACTCCTACTACGGTTC</u>
TpFaesAP3_1R	<u>TCTAGATTTTGTTACTTGTTGTCCTTAGCAATC</u>
TpFaesAP3_2F	ATGATTACGAATTC <u>GAGCTCAGTTAAACCAGACACATTTACTCCC</u>
TpFaesAP3_2R	TCTGCAGGTCGACT <u>CTAGAAACAAAGTAGGAAGAAAACTAGGTGGAG</u>
TFaesAP3_2/2aF	AACACGGGGGACT <u>CTAGACCACCTTTACTCTCTCCACCTAG</u>
TFaesAP3_2/2aR	TCGGGGAAATTC <u>GAGCTCTCCTAAGTAGGAACACATGCAGC</u>
qTFaesAP3_2F	GATTTGGCATCACACTTTCTACAATG
qTFaesAP3_2R	GTATCCAGCGCAGTCCT
qUBQ5F	AAGACTTACACCAAGCCGAAGAAGATC
qUBQ5R	CCAGCTCCACAGGTTGCGTTAG

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

Taxon and species	Protein name	Accession numbers	Lineage
Amborellaceae			
<i>Amborella trichopoda</i>	AmAP3	BAD42444.1	AP3
	AmPI	BAD42443.1	PI
Nymphaeaceae			
<i>Nymphaea tetragona</i>	NtAP3	BAD42348.1	AP3
	NtPI	BAD42349.1	PI
Cabombaceae			
<i>Brasenia schreberi</i>	BsAP3	BAD42352.1	AP3
	BsPI	BAD42353.1	PI
Aristolochiaceae			
<i>Asarum caudigerum</i>	AcAP3	ACA62949.1	AP3
	AcAP3-D	AGO59776.1	AP3
Magnoliaceae			
<i>Magnolia wufengensis</i>	MAwuAP3-1	AFM75880.1	AP3
	MAwuAP3-2	AFM75881.1	AP3
	MAwuPI	AFM75882.1	PI
Calycanthaceae			

<i>Chimonanthus praecox</i>	CpAP3	ABK34952.1	AP3
Chloranthaceae			
<i>Hedyosmum orientale</i>	HoAP3-1	AFP17801.1	AP3
	HoAP3-2	AFP17802.1	AP3
	HoPI-1	AFP17796.1	PI
	HoPI-2	AFP17799.1	PI
	HoPI-3	AFP17800.1	PI
<i>Chloranthus spicatus</i>	CsAP3	AAR06664.1	AP3
Liliaceae			
<i>Lilium longiflorum</i>	LMADS1	AAM27456.1	AP3
	LMADS8	AEI88009.1	PI
	LMADS9	AEI88010.1	PI
Orchidaceae			
<i>Oncidium hybrid cultivar</i>	OMADS3	AAO45824.1	AP3
	OMADS5	ADJ67234.1	AP3
	OMADS9	ADJ67235.1	AP3
	OMADS8	ADJ67236.1	PI
<i>Cymbidium sinense</i>	CysiAP3-1	AUO28994.1	AP3
	CysiPI	AUO28996.1	PI
Iridaceae			
<i>Crocus sativus</i>	CsatAP3a	AAY24691.1	AP3
	CsatAP3b	AAY24692.1	AP3
	CsatPIc1	ABB22780.1	PI
	CsatPIc2	ABB22781.1	PI
Zingiberaceae			
<i>Alpinia oblongifolia</i>	AoAP3	ABS83561.1	AP3
	AoPI	ABB92623.1	PI
Poaceae			
<i>Zea mays</i>	silky 1	NP_001104951.1	AP3
	Zmm16	NP_001105136.1	PI
	Zmm18	CAC33849.1	PI
	Zmm29	CAC33850.1	PI
Papaveraceae			
<i>Bocconia frutescens</i>	BofrAP3-1	AOC50670.1	AP3
	BofrPI-1	AOC50677.1	PI
	BofrPI-2	AOC50678.1	PI
	BofrPI-3	AOC50679.1	PI
	BofrPI-4	AOC50680.1	PI
Lardizabalaceae			
<i>Akebia trifoliata</i>	AktAP3-1	AAT46097.1	AP3
	AktAP3-2	AAT46098.1	AP3
	AktAP3-3	ABC02398.1	AP3
	AktPI	AAT46101.1	PI
Ranunculaceae			
<i>Aquilegia vulgaris</i>	AqvAP3-1	ABP01804.1	AP3
	AqvAP3-2	ABP01803.1	AP3
	AqvAP3-3	ABP01802.1	AP3
	AqvPI	ABP01801.1	PI
<i>Thalictrum dioicum</i>	ThdAP3-1	AAW78033.1	AP3
	ThdAP3-2a	AAW78034.1	AP3
	ThdAP3-2b	AAW78035.1	AP3
	ThdPI-1	AAW78031.1	PI

<i>Nigella damascena</i>	ThdPI-2	AAW78032.1	PI
	NdAP3-1	ALM95512.1	AP3
	NdAP3-2	ALM95513.1	AP3
	NdAP3-3	AGH39931.1	AP3
	NdPI1	ALM95515.1	PI
	NdPI2	ALM95516.1	PI
Cercidiphyllaceae			
<i>Cercidiphyllum japonicum</i>	CejaAP3-1	ASY97764.1	AP3
	CejaAP3-2	ASY97765.1	AP3
	CejaPI	ASY97767.1	PI
Violaceae Batsch			
<i>Viola yedoensis Makino</i>	VpTM6-1	APQ46143.1	AP3
	VpTM6-2	APQ46144.1	AP3
	VpPI	APQ46145.1	PI
Cucurbitaceae			
<i>Cucumis sativus L.</i>	CsMADS1	AAX37273.1	AP3
Fabaceae			
<i>Medicago truncatula</i>	MtNMH7	AEW43601.1	AP3
	MtTM6	AEW43602.1	TM6
<i>Lotus japonicus</i>	LjAP3	AAX13301.1	AP3
	LjPIa	AAX13299.1	PI
	LjPIb	AAX13300.1	PI
Rosaceae			
<i>Eriobotrya japonica</i>	EjAP3	QGR27127.1	AP3
	EjPI	QGR27129.1	PI
Malvaceae			
<i>Gossypium hirsutum</i>	GhMADS53	AGW23355.1	AP3
	GhTM6	ADX60056.1	TM6
	GhMADS12	ACJ26767.1	PI
	GhMADS50	AGW23352.1	PI
Caricaceae			
<i>carica papaya</i>	CpTM6-1	ABQ51321.1	TM6
	CpTM6-2	ABQ51322.1	TM6
	CpPI	ABQ51323.1	PI
Brassicaceae			
<i>Arabidopsis thaliana</i>	AP3	AAD51903.1	AP3
	PI	BAA06465.1	PI
Polygonaceae			
<i>Fagopyrum esculentum</i>	FaesAP3-1	AFO83616.1	AP3
	FaesAP3-2	QLJ83023.1	AP3
	FaesPI	AFO83617.1	PI
Ericaceae			
<i>Rhododendron kaempferi</i>	RkAP3a	BBC77405.1	AP3
	RkPI1-1	BBA27230.1	PI
	RkPI1-2	BBA27231.1	PI
Pyrolaceae			
<i>Monotropa hypopitys</i>	MhyAP3	AQM52302.1	AP3
	MhyTM6	AQM52303.1	TM6
	MhyPI	AQM52304.1	PI
Rubiaceae			
<i>Coffea arabica</i>	CaAP3	AHW58039.1	AP3
	CaTM6	AHW58030.1	TM6

	CaPI	AHW58035.1	PI
Gentianaceae			
<i>Gentiana scabra</i> Bunge	GsAP3a	BAS04474.1	AP3
	GsAP3b	BAS04479.1	AP3
	GsTM6	BAS04472.1	TM6
	GsPI1	BAS04475.1	PI
	GsPI2	BAS04476.1	PI
	GsPI3	BAS04478.1	PI
Solanaceae			
<i>Petunia x hybrida</i>	PhDEF	AAQ72510.2	AP3
	PhTM6	AAS46017.1	TM6
	PhGLO1	AAS46018.1	GLO
<i>Solanum lycopersicum</i>	LDEF	NP_001234077.2	AP3
	TDR6	NP_001311309.1	TM6
	TPI	ABG73411.1	PI
<i>Physalis pubescens</i>	PFDEF	AGN54423.1	AP3
	PFTM6	AGN54424.1	TM6
	PFGLO1	AGN54427.1	PI
	PFGLO2	AGN54426.1	PI
<i>Nicotiana tabacum</i>	NTDEF	CAA65288.1	AP3
	NTGLO	CAA48142.1	GLO
Scrophulariaceae			
<i>Antirrhinum majus</i> L	DEF	BAI68389.1	AP3
	GLO	CAA48725.1	GLO
<i>Torenia fournieri</i>	TfDEF	BAG24492.1	AP3
	TfGLO	BAJ15423.1	GLO
Asteraceae			
<i>Gerbera hybrid</i>	GDEF2	CAA08803.1	AP3
	GDEF3	ACV53813.1	AP3
	GDEF1	CAA08802.1	TM6
	GGLO1	CAA08804.1	GLO

> pFaesAP3_1

-2295 CGATACGACT CCTACTACGG TTCGTGACCCT CCATGCTTCT GAACTGATCA TGTTTACGAT
CACTFTPPCA1 GTGANTG10

-2235 TATGTAAAAA ACATAATCAA CTCCACCGTG GTGGGGTTAG TCTTCCACGT AGACTAAGCC
CAREOSREP1 ACGTATERD1

-2175 AATACATAAG CGATGCATAT ATATGAACGT GACATGAGTA TAAGCATAAA TAATATCATA
CCAATBOX1 CArG-box ACGTATERD1

-2115 TGATCTTTGG TAATACTCAA AGGATTAAAT ATGCAACATG CTTTCAAAAT CATTATAAGT
MYCONSENSUSAT CACTFTPPCA1

-2055 CTCAAAATGT TCAAATCATC ATGTCTCAAT ACTTAAATA TCTCAAAAGG TTTCAAACCG
CAATBOX1

-1995 ATATCATCTC AAAAGTATTAC TCATAACCAT CAAGTGTTTA AAATCAATAT CATCTCGATA
CACTFTPPCA1 MYBIAT MYCONSENSUSAT CAATBOX1

-1935 ACTCGTAAAC ATCTCAAAAG AGTTCAAAGT CAATCTCATC CAATAACTC GTAATCCAAA
CAATBOX1 CAATBOX1

-1875 TCTAGTAACA CATCAAAATC AATCTCATCT CAATAACTCG TAATCCAAAT CATGTAACCTC

CAATBOX1 CAATBOX1
 -1815 ATCAATATCA TCTCAATAAC TCGTAATCCA AATTTATCAG TATAACATAT CTAATGGTCA
 CAATBOX1 CAATBOX1
 -1755 ATTGA~~CCGAA~~ATGGGGTAAC AAGGTCGATC CTTGCCCTT TCTCAAATCC ATCATAAAAA
 LTRE1HVBTL49
 -1695 TCATCCAAAT CACAATAACAA AATATGCTCG AGCATT~~TTTA~~CTTTATAAAT TGTATTCAAC
 CAATBOX1 CACTFTPPCA1 TATABOX2
 -1635 TCACGTGTTT GTATT~~TTATT~~TTAAAACATG TCCAACCCAT GTTGAACACG ATGATACCTC
 CAREOSREP1 TATABOX5
 -1575 CTAACCTTGA~~CC~~ATGAGATT CTCACAGCAA~~TC~~ACGGATCA~~AGTG~~CAGTCC TCGTCATCCA
 WRKY71OS CAATBOX1 MYCONSENSUSAT
 -1515 CAATGACCGG GCACAACTC GGCCACACA AACTAAGATT ACAACC~~ACTA~~GTGAGCATGA
 CAATBOX1 CACTFTPPCA1 GTGANTG10
 -1455 CCCGCCTAAA CCGAGGAGCA TAAAAATCAT GAAACAAAA CGGATGGAAA AT~~ACT~~TCGGT
 CACTFTPPCA1
 -1395 GTGGTCATAG ACCAACTCTT CTCTCAATAT AATAGGGCAA ATTGTCCGCT ATTGTCGTAG
 CAREOSREP1 CAATBOX1
 -1335 ACCAAATTAT CTCTGTGTC~~ACATA~~AGAAA~~AAAATGCCGC~~TTAAGTCAAA GACCAAATCA
 TGTACACMCUCUMISIN POLLEN1LELAT52
 -1275 TCTCAAATCC TCAATATCAA~~TA~~ACCCACTT CTTTCCAAA ATATTTCAAT AAAATTTCTT
 CAATBOX1 CAATBOX1 CACTFTPPCA1 CAATBOX1
 -1215 TAATGATCAC AATCAAAATT AACACTTCAC CGCCAATATT GTCAAATCAA CACAAGGCAA
 CACTFTPPCA1 CCAATBOX1
 -1155 GTATTCTCAA AGGCTTTTAC~~CA~~AATGACATA TCAAACTCAT~~TT~~CATATTCT CAAACCAAG
 CAATBOX1 INRNTPSADB MYBIAT
 -1095 ACAATATCAT TACACTTTCC ATAACTTTCA~~AT~~AACACTT ATCTTTAAAC ATAACAGCGT
 CAATBOX1 CACTFTPPCA1 CAATBOX1
 -1035 ATAAAGCATT ACAACTAAAG TGTTATGAAA~~AGT~~CATGACA AAATCAAATA ATATATGGGT
 -300ELEMENT WRKY71OS
 -975 TAAAATAGTA GGGGAAAAAT GCCTAAAATG TACTTGTATG~~TG~~AAAAATACA~~AATGT~~GAAAA
 CACTFTPPCA1 GTGANTG10 MYCONSENSUSAT
 -915 ACATATTATG GTAATGAAAA AAATAATTA AACTCAGAGA AGATTCGAA AAAAGGACTT
 -855 AAATGGTGGT TGTGGATGGT AAAACCA~~TTA~~ACTTCTGGCA AGACA~~AAATG~~GATTACAGAAG
 MYBIAT MYCONSENSUSAT
 -795 AACCTCAATA AAAATTTGAT CAACTCTACA AAATAATTA CCAACTACAT CATGAATAAA
 CAATBOX1
 -735 CAATGGGACG ATCAACGCAT TGATCACTAC ATACACTTTT ACCGATTGAT ATTGTTAAGA
 CAATBOX1 CACTFTPPCA1 CACTFTPPCA1
 -675 AAATTAATAA ACATAACCTT CCCATGAAGG AGATAAATGA TAGAATATAA TGGGCAACA
 POLLEN1LELAT52
 -615 ATGAGGAAGA GTGGTACTTA TCTTAGTGGC GGAAGCCTTC GCTCTTCGGG AGGGTCTACA
 MYCONSENSUSAT CACTFTPPCA1

-555 AAAGGCCGCT AGCATTGATG CCACATCCAT TGAGATTACA GGAGACAACT TAATATTCAT

-495 GAACTCGGCC AACCAAATTC AGAAGCCTCC ATGCTAGACA AACATTGACCA ACTCAAATAT
WRKY71OS

-435 TTCCACCAATG ATCCCGGGTT TTATGCATGA TAACGTGCAA CACATTTCG GGGAAATCAA
CAATBOX1 ACGTATERD1

-375 CACCGGTTGCT GATCGACTCG CGTTACATGA ACACCAATCCG AATGTTTGACG ACGTTATCAT
MYBCORE CAATBOX1 WRKY71OS

-315 TTCACATGAT GTTGATGACC TCATCCGAAA AAATGCTATA GGACCTACAA TTTGTAAAA
MYCONSENSUSAT LTRE1HVBLT49 CAATBOX1

-300ELEMENT

-255 TTGACCGTTT ACTCCTTACC TTGGTCAAAA AAATAAAATA AATAAAAATG TCATGTGTAA
MYCONSENSUSAT

-195 ACTTACTGCT GCGACATTAT CTAAGCAAAA TATCAGTTTT CCGTCACTGT CTGCCGTTTG
CACTFTPPCA1 CACTFTPPCA1

-135 ACCGCGAAAA CCATCAAACG GCGTTCCGTC CAATCAATCA AAGCGCTATT GACGACTTCC
MYB1AT CCAATBOX1

-75 ACTCTTTACA CAGTTAATTG ACGGAAAGTA AATGTGGGAG GGGTTTAAAT ATGGGACTCT
CACTFTPPCA1 +1

-15 GCAATTGAAA CTTTCATCAA TGCTTCGCAA GGCTTTATTTT TCCATTTGTA GTAACCTCTT
CAATBOX1 CAATBOX1 TATABOX5

+46 CCTTTTTCTC TCGTTGGAAC TTCAAAGGTG ATCTTGAGTT CAAGCCAAGG GAAGAACTAG
PYRIMIDINEBOXOSRAMY1A GTGANTG10

+106 AGAGATTGCT AAGGACAACA AGTAACAAA ATG
GAREAT

Figure S1: *FaesAP3_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.

> *pFaesAP3_2*

-1401 CAGTAAACCC AGACACATT **T ACT**CCCAAAT TTTTAT**CAAA TG**CCAGCTTC TGAATGGTTT
CACTFTPPCA1 MYCCONSENSUSAT

-1341 ATGAAGAACA **T TAACTG**CAA TATCGCCT**CA AT**TAAGGGAC TTCCATGGAA CACGATATTT
MYB2AT CAATBOX1

-1281 ACGTACT**CAA T**CTGGTGGTT GTGGAAGTGG CGGTGTAACC GT**CAAT**GGG GAAAGACAAT
CAATBOX1 CAATBOX1

-1221 ACTCCTCCCC AGAAGAGTGT AT**TTATCCTC AAT**CAAGCCT CTGA**ACATAT GAATGT****TATT**
SREATMSD CAATBOX1 MYCCONSENSUSAT TATABOX5

-1161 **T**CGACGGCAA GGAGACTGGG GACT**CAAT**CC CGGAAAGAAG AGGTTTGTAT **CAGCTG**GAGG
CAATBOX1 MYCCONSENSUSAT

-1101 AGACCACCTT CTGTTTGGGT TAAGTGGAAT TCT**TGAC**GGAG CTGTCAAACA AGGCTGCGGG
WRKY71OS

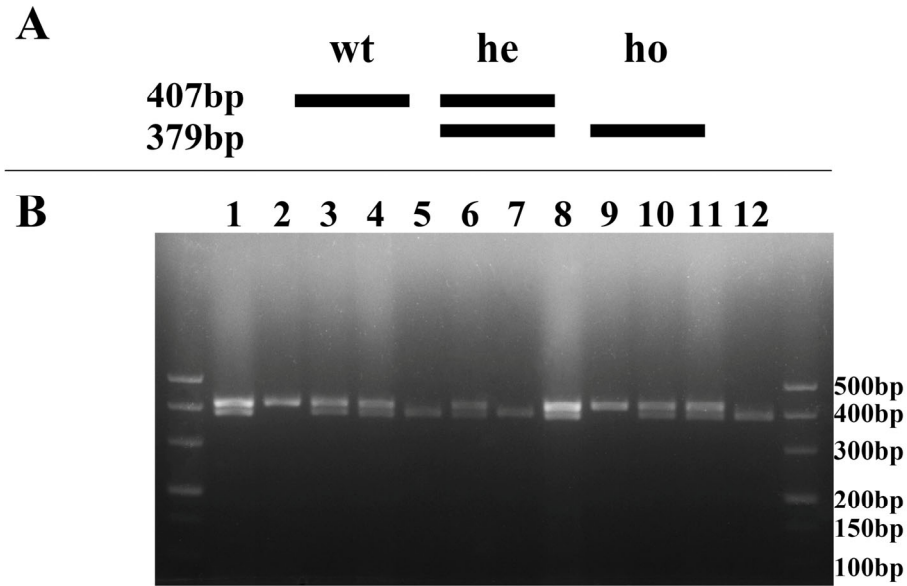


Figure S3. Genotyping of wild-type, heterozygous and homozygous *ap3-3* mutant *A. thaliana* by dCAPS. The amplicons from transgenic lines in wild-type background *Arabidopsis* were cleaved by *Cla*I to produce a 407 bp fragment, and the amplicon from heterozygous *AP3/ap3-3* background plants were cleaved by *Cla*I to produce 407 bp and 379 bp fragments; the amplicon from transgenic lines in homozygous *ap3-3* lines were cleaved by *Cla*I to produce a 379 bp fragment.

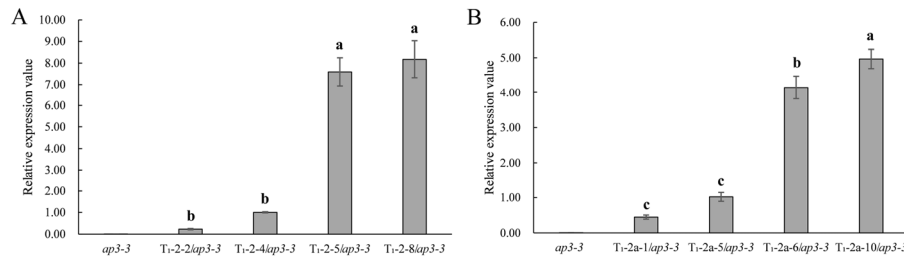


Figure S4. Expression of *FaesAP3_2* and *FaesAP3_2a* in transgenic *Arabidopsis ap3-3* mutant confirmed by qRT-PCR. (A) Expression of *FaesAP3_2* in transgenic *Arabidopsis ap3-3* mutant confirmed by qRT-PCR; (B) Expression of *FaesAP3_2a* in transgenic *Arabidopsis ap3-3* mutant confirmed by qRT-PCR. (*ap3-3*) *Arabidopsis ap3-3* mutant; (T₁-2-2/*ap3-3*) independent lines of 35S::*FaesAP3_2* transgenic *Arabidopsis ap3-3* mutant with no phenotype complementation; (T₁-2-4/*ap3-3*) independent lines of 35S::*FaesAP3_2* transgenic *Arabidopsis ap3-3* mutant with a weak complement phenotype; (T₁-2-5/*ap3-3*) independent lines 35S::*FaesAP3_2* transgenic *Arabidopsis ap3-3* mutant with a medium complement phenotype producing filament attached with carpeloid anther in whorl 3; (T₁-2-8/*ap3-3*) independent lines 35S::*FaesAP3_2* transgenic *Arabidopsis ap3-3* mutant with strong complement phenotype rescuing stamen-like organs in the 3rd whorl of flower; (T₁-2a-1/*ap3-3*) independent lines of 35S::*FaesAP3_2a* transgenic *Arabidopsis ap3-3* mutant with no phenotype complementation; (T₁-2a-5/*ap3-3*) independent lines of 35S::*FaesAP3_2a* transgenic *Arabidopsis ap3-3* mutant with a weak complement phenotype; (T₁-2a-6/*ap3-3*) independent lines 35S::*FaesAP3_2a* transgenic *Arabidopsis ap3-3* mutant with a medium complement phenotype producing flower with filament attached with stigmatic papillae or carpeloid anther in whorl 3; (T₁-2a-10/*ap3-3*) independent lines 35S::*FaesAP3_2a* transgenic *Arabidopsis ap3-3* mutant with strong complement phenotype rescuing stamen-like organs in the 3rd whorl of flower. Different letters indicate statistically significant differences.