

SUPPLEMENTARY DATA

FIG. S1. Amino acid alignment of AG orthologues from taxa across the angiosperms. Sequence names and accession numbers of protein sequences used in the alignment are given in the table below.

	MADS	I
TaAGL2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaAG3b	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaAGL31	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
OsMADS13	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZMH1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZAG2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
OsMADS21	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZMH29	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaAG4b	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaAG4a	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
EscaAGL11	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
STK	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
FBP11	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaGL11	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
FBP7	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
WAG1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
HuAG2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
OsMADS58	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZAG1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZMH2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZmAG	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
OsMADS3	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
ZMH23	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
SHP1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
SHP2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
AmPLE	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaGL1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
AmFAR	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
TaGL1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
AG	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
PapsAG1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
PapsAG2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
EscaAG1	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY
EscaAG2	MRGRLEIKRIENTTSRQYTFCKRRNGLLKKAYELSVLDCAEVALVFSSRGRLEYEYNNNS	VKATIDRY

	K	C
TaAGL2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaAG3b	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaAGL31	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
OsMADS13	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZMH1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZAG2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
OsMADS21	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZMH29	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaAG4b	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaAG4a	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
EscaAGL11	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
STK	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
FBP11	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaGL11	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
FBP7	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
WAG1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
HuAG2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
OsMADS58	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZAG1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZMH2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZmAG	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
OsMADS3	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
ZMH23	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
SHP1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
SHP2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
AmPLE	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaGL1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
AmFAR	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
TaGL1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
AG	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
PapsAG1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
PapsAG2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
EscaAG1	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR
EscaAG2	KKAAHAGDSTSGVPLIEVNAQYQOEAARLRHQIQMLQSTNKHLYGDSVGNLSLKEQLQESLRLEKGIARKRNELLSFEINMYMKREI	ELQSDNIDLRTKIAEERDQQQVIAAR

	D-class	C-class
TaAGL2	PSLAP	ELNPF
TaAG3b	PSLAP	ELNPF
TaAGL31	PSLAP	ELNPF
OsMADS13	ELNPF	ELNPF
ZMH1	ELNPF	ELNPF
ZAG2	ELNPF	ELNPF
OsMADS21	ELNPF	ELNPF
ZMH29	ELNPF	ELNPF
TaAG4b	ELNPF	ELNPF
TaAG4a	ELNPF	ELNPF
EscaAGL11	ELNPF	ELNPF
STK	ELNPF	ELNPF
FBP11	ELNPF	ELNPF
TaGL11	ELNPF	ELNPF
FBP7	ELNPF	ELNPF
WAG1	ELNPF	ELNPF
HuAG2	ELNPF	ELNPF
OsMADS58	ELNPF	ELNPF
ZAG1	ELNPF	ELNPF
ZMH2	ELNPF	ELNPF
ZmAG	ELNPF	ELNPF
OsMADS3	ELNPF	ELNPF
HuAG1	ELNPF	ELNPF
ZMH23	ELNPF	ELNPF
SHP1	ELNPF	ELNPF
SHP2	ELNPF	ELNPF
AmPLE	ELNPF	ELNPF
TaGL1	ELNPF	ELNPF
AmFAR	ELNPF	ELNPF
TaGL1	ELNPF	ELNPF
AG	ELNPF	ELNPF
PapsAG1	ELNPF	ELNPF
PapsAG2	ELNPF	ELNPF
EscaAG1	ELNPF	ELNPF
EscaAG2	ELNPF	ELNPF

Sequence name and accession numbers of protein sequences used in the alignment

Gene annotation	Source	Genbank Accession
TaAGL2	<i>Triticum aestivum</i>	DQ512337
TaAG3b	<i>Triticum aestivum</i>	AM502865
TaAGL31	<i>Triticum aestivum</i>	ABF57933
OsMADS13	<i>Oryza sativa</i>	AF151693
ZMM1	<i>Zea mays</i>	X81199
ZAG2	<i>Zea mays</i>	L18925
OsMADS21	<i>Oryza sativa</i>	Q8RU31
ZMM25	<i>Zea mays</i>	AJ430639
TaAG4b	<i>Triticum aestivum</i>	AM502895
TaAG4a	<i>Triticum aestivum</i>	AM502894
EScaAGL11	<i>Eschscholzia californica</i>	DQ088998
STK	<i>Arabidopsis thaliana</i>	U20182
FBP11	<i>Petunia hybrida</i>	X81852
TAGL11	<i>Solanum lycopersicum</i>	AY098736
FBP7	<i>Petunia hybrida</i>	X81651
WAG1	<i>Triticum aestivum</i>	AT1G53700
HvAG2	<i>Hordeum vulgare</i>	AF486649
OsMADS58	<i>Oryza sativa</i>	AB232157
ZAG1	<i>Zea mays</i>	L18924
ZMM2	<i>Zea mays</i>	X81200
ZmAG	<i>Zea mays</i>	L81162
OsMADS3	<i>Oryza sativa</i>	L37528
HvAG1	<i>Hordeum vulgare</i>	AF486648
ZmM23	<i>Zea mays</i>	AJ430637
SHP1	<i>Arabidopsis thaliana</i>	M55550
SHP2	<i>Arabidopsis thaliana</i>	M55553
AmPLE	<i>Antirrhinum majus</i>	S53900
TAGL1	<i>Solanum lycopersicum</i>	AY098735
AmFAR	<i>Antirrhinum majus</i>	AJ239057
TAG1	<i>Solanum lycopersicum</i>	L26295
AG	<i>Arabidopsis thaliana</i>	X53579
PapsAG1	<i>Papaver somniferum</i>	GU123602
PapsAG2	<i>Papaver somniferum</i>	GU123603
EScaAG1	<i>Eschscholzia californica</i>	DQ088996
EScaAG2	<i>Eschscholzia californica</i>	DQ088997

FIG. S2. Detailed view of the 3' end of the *PapsAG* transcripts aligned with the corresponding genomic sequence. The transcript sequence is in red, genomic sequence in black, 3'UTRs in green and consensus 5' and 3' splice sites are indicated in blue. The primers used to generate transcript-specific fragments for mRNA ISH and VIGS are shown by lines overlying the sequence.

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PapsAG1      TACTCGAATCAGCCAATCACCATTACTCCGCCAAGAGCAGACAGCACTTCAAATTGG~~~~~
                L E S A N H H Y S R Q E Q T A L Q L G                               AG2F
PapsAG2      TACTCGAATCAGCCAATCACCATTACTCCGCCAAGAGCAGACAGCACTTCAAATTGG~~~~~AGCGAAGATAGAAGACATCAAACCATTGGAATACAGTAGC
                L E S A N H H Y S R Q E Q T A L Q L G                               A K I E D I K P L E Y S S
PapsGENOMIC  TACTCGAATCAGCCAATCACCATTACTCCGCCAAGAGCAGACAGCACTTCAAATTGGGTAAGAAC-1kb-TGTTCAGAGCGAAGATAGAAGACATCAAACCATTGGAATACAGTAGC

PapsAG1      ~~~~~
PapsAG2      TACGGTTTTGGAGGCGAGGAGGC TTAGGAAGT TAGACTCATCGGTGAAGATTGTTAAAGTGTGTTTGTGTTGTCCTGACAAAGAGAGGGGGCCAAATTAAGTAGACTTCATCTTTTA
                Y G F G G E E A Y G S *
PapsGENOMIC  TACGGTTTTGGAGGCGAGGAGGC TTAGGAAGT TAGACTCATCGGTGAAGATTGTTAAAGTGTGTTTGTGTTGTCCTGACAAAGAGAGGGGGCCAAATTAAGTAGACTTCATCTTTTA

PapsAG1      ~~~~~
PapsAG2      AATTGAAC TGGAATTATCTACTTTGATATCCCTTAAACA TCTGGA TTTGACTACATTACTTAGATATTTTGGTCGGTG-----
                AG2R
PapsGENOMIC  AATTGAAC TGGAATTATCTACTTTGATATCCCTTAAACA TCTGGA TTTGACTACATTACTTAGATATTTTGGTCGGTGAC-0.2kb-GTGCAGTTGATGATGGCGTCTCTTTCAA
                *
                AG1F
                TTGATGATGGCATTCTCTTTCAA

PapsAG1      GAAACAGAGTACTATCTCTGAATGGTTCATTATCCCTCATTCATAAATATGAAGATATCGCTACTACCTATTCTAGTACCATCACTATTCCTACTACTTCAAGCTAGAAATATCATAAT
PapsAG2      -----
PapsGENOMIC  GAACAGAGTACTATCTCTGAATGGTTCATTATCCCTCATTCATAAATATGAAGATATCGCTACTACCTATTCTAGTACCATCACTACTACTACTTCAAGCTAGAAATATCATAAT

PapsAG1      ATTCGGCATCTCTCTACTCTCAAGCTCCTAGTAGATTTATGTATAGACCGATTCAATCATTTATGTTGTGACATCAGGACTTGTGTTT TAGCTGAGTCTATTCTATGT
                AG1R
PapsAG2      -----
PapsGENOMIC  ATTCGGCATCTCTCTGCTCTCTAGCTCCTAGTAGATTTATGTATAGACCGATTCAATCATTTATGTTGTGACATCAGGACTTGTGTTT TAGCTGAGTCTATTCTATGT

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FIG. S3. mRNA ISH of (A) *PapsAG-1* and (B–D) *PapsAG-2* at stages P5 (A, B), P6 (C) and P7 (D). Other than *PapsAG-2* expression in the petal at stage P5 there were no differences in expression observed between the two transcripts. Abbreviations: pe, petals; se, septae. Scale bars = 200 μ m.

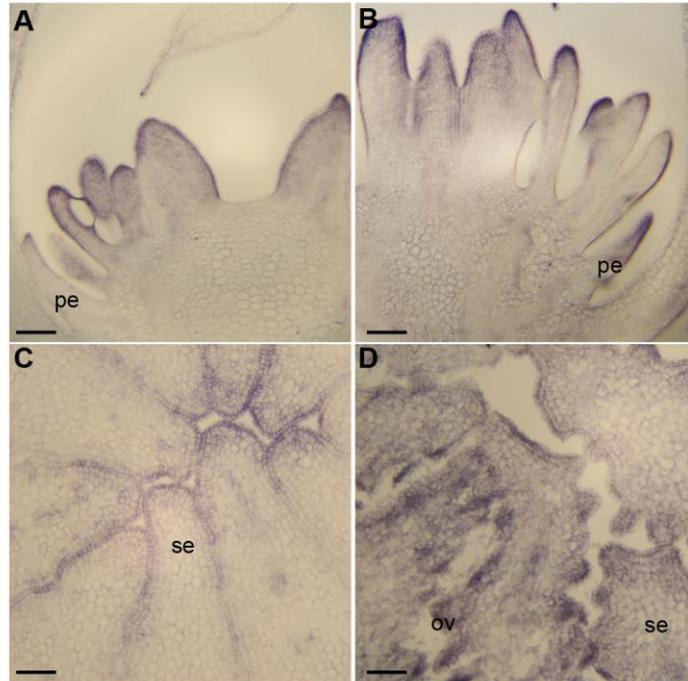


FIG. S4. mRNA ISH with *PapsH4-1* (A, B) and with sense probes for *PapsAG-1* (C) and *PapsAG-2* (D). Scale bars = 200 μ m.

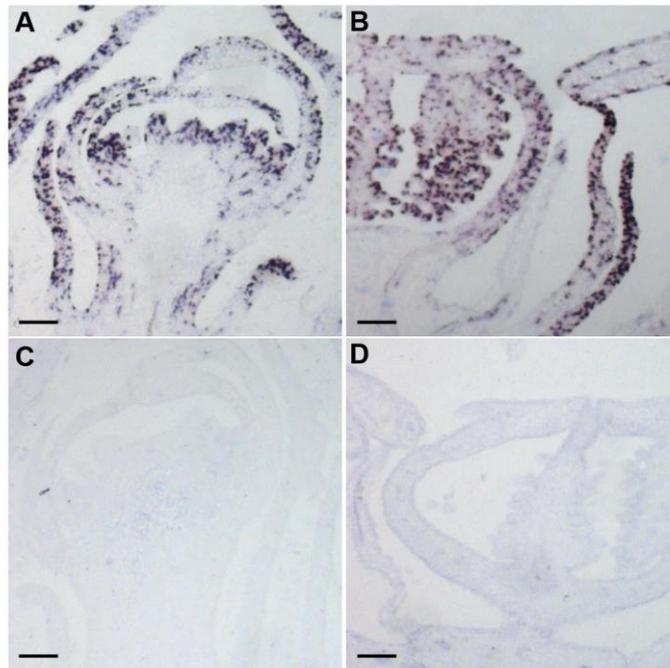


FIG. S5. Empty TRV2 vector control results at pendant (A) and mature flower stages (B, C); scale bars = 2 mm. RT-PCR expression analysis of four lines (D).

