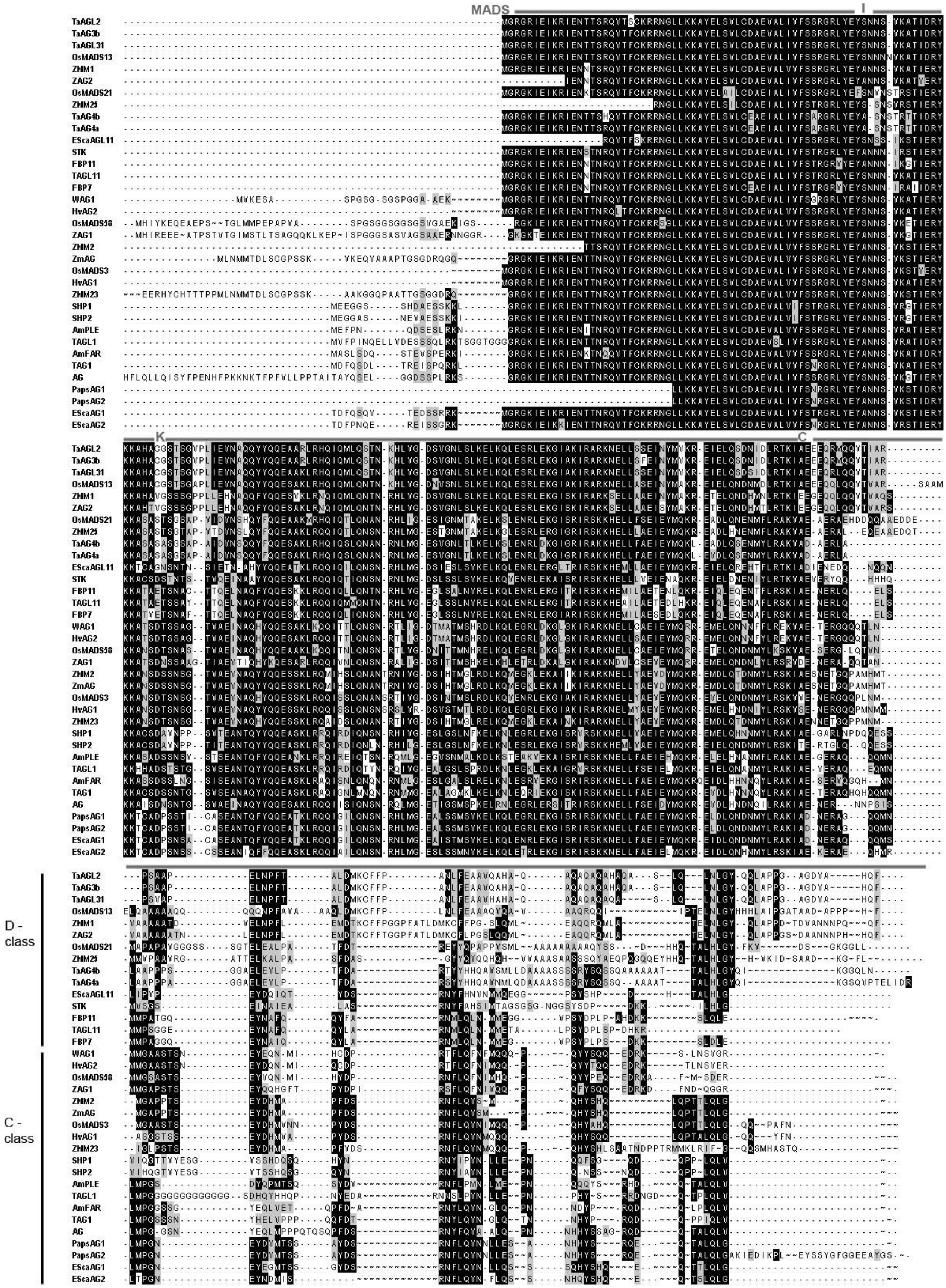
SUPPLEMENTARY DATA

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.



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

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

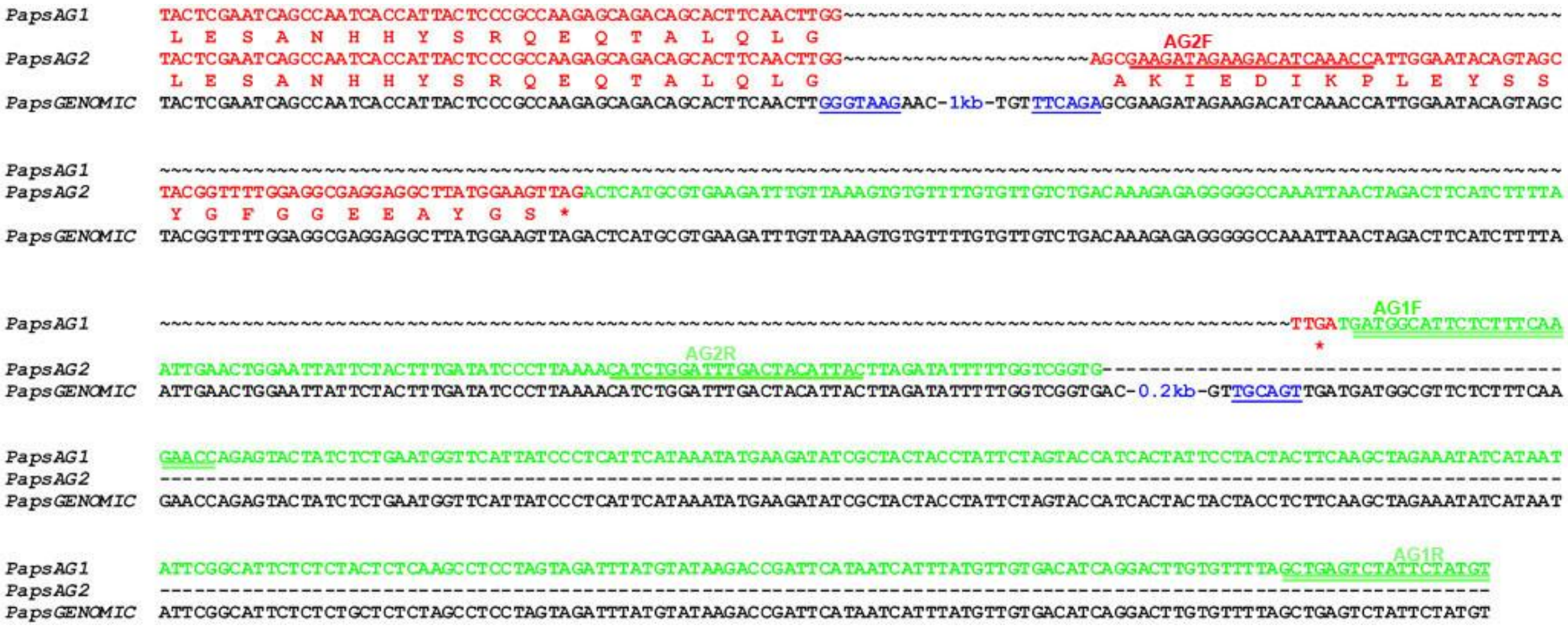


Fig. S3. mRNA ISH of (A) *PapsAG-1*and (B–D) *PapsAG-2* at stages P5 (A, B), P6 (C) and P7 (D). Other than *PapsAG-2* expression in the petal at stage P5 there were no differences in expression observed between the two transcripts. Abbreviations: pe, petals; se, septae. Scale bars = 200 µm.

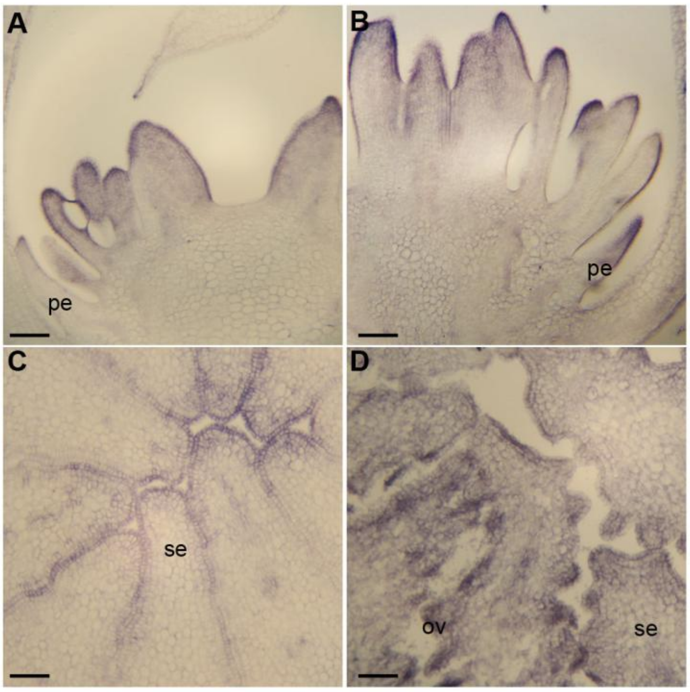


FIG. S4. mRNA ISH with *PapsH4-1* (A, B) and with sense probes for *PapsAG-1* (C) and *PapsAG-2* (D). Scale bars = 200 μm.

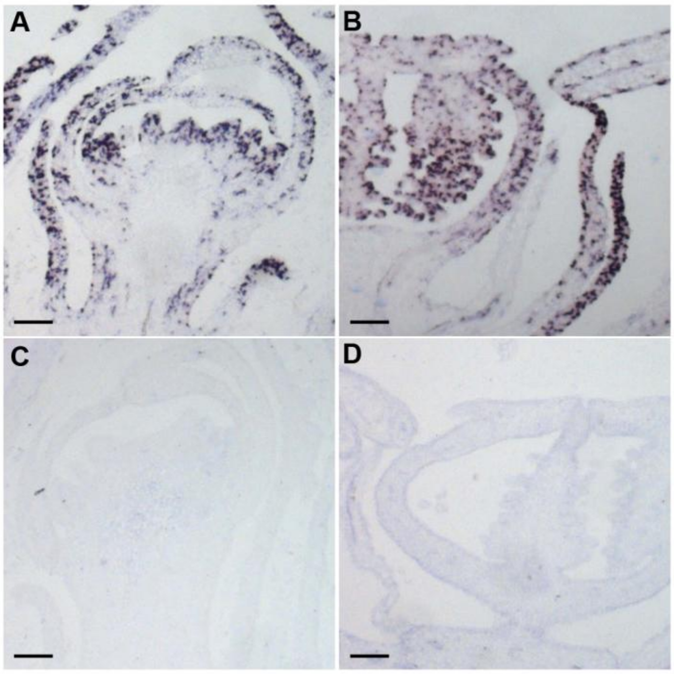


FIG. S5. Empty TRV2 vector control results at pendant (A) and mature flower stages (B, C); scale bars = 2 mm. RT-PCR expression analysis of four lines (D).