**Supplemental Figure 1.** Diagram showing differences in first, second, and third order branching in California poppy wild type (left) and *escafl1fl2* plants (right). The terminal flower is yellow, first order flowers are green, second order branches are pink, third order branches are purple.

**Supplemental Figure 2.** Amino acid alignment of the opium poppy and California poppy FUL-like proteins. FUL-like motif is indicated by the box. Lines below indicate the locations of the primers used to amplify the regions for VIGS constructs from the *PapsFUL-like* genes from opium poppy and the *EscaFUL-like* genes from California poppy. *PapsFL1-PapsFL2* reverse primers are not shown because they bind to the 3'UTR. EcFL Fwd, forward *EscaFL* primer; EcFL Rev, reverse *EscaFL* primer; PapsFL Fwd, forward *PapsFL1- PapsFL2* primers.

**Supplemental Figure 3.** In situ hybridization controls.
**(A)** to **(C)** Controls for opium poppy. **(A)** *PapsFL1* sense probe. **(B)** *PapsFL2* sense probe. **(C)** Expression of *PapsPI* used to test the specificity of the technique in light of the broad expression of *PapsFL1*; results are similar to those obtained by Drea et al. (2007)
**(D)** to **(F)** Controls for California poppy **(D)** *EscaFL* sense probe. **(E)** and **(F)** Expression of *EscaAG* used to test the specificity of the technique in light of the broad expression of *EscaFUL-like* genes; results are similar to those of Zahn et al. (2006).
Scale bars: 50 µm

**Supplemental Figure 4.** Locus-specific RT-PCR and qRT-PCR using cDNA prepared from organs of VIGS-treated plants.
**(A), (C) and (E) RT-PCR** analysis of opium poppy plants transformed with **(A)** TRV2-*PapsFL1*, **(C)** TRV2-*PapsFL2* and **(E)** TRV2-*PapsFL1* and TRV2-*PapsFL2* simultaneously, showing preliminary categories of un-silenced (un), mildly (mild), moderately (mod), and strongly (str) silenced plants. Samples were extracted from leaves (l), leaf-like sepals (ls) or fruits (f) and screened for down-regulation of *PapsFL1* and *PapsFl2* as well as presence of the vector (TRV2). Note specific down-regulation of

*PapsFL1* in **(A)**, specific down-regulation of *PapsFL2* in **(C)** and down-regulation of both copies in **(E)**. Samples of wild type leaf (l), sepal (s) and fruit (f) were used for comparison and *ACTIN* was used as a control.
**(B)**, **(D)** and **(F)** qRT-PCR of a subset of leaf samples showing the range of silencing (from mildly to strongly down-regulated) of **(B)** *PapsFL1*, **(D)** *PapsFL2* and **(F)** *PapsFL1* and *PapsFL2* simultaneously. Fold change in *PapsFL1* (black bars) and *PapsFL2* (gray bars) expression in samples is shown relative to the wild type leaf gene expression. Error bars show ± SD among three technical replicates. *GADPH* was used as the endogenous control.
**(G)** RT-PCR analysis showing preliminary categories of un-silenced (un), mildly (mild), moderately (mod) and strongly (str) silenced tissue samples from California poppy plants transformed with TRV2-*EscaFL1* and TRV2-*EscaFL2*. Samples were collected from the same organs as opium poppy plants. Treated plants were screened for down-regulation of *EscaFL1* and *EscaFl2* and for presence of the vector (TRV2). Note down-regulation of both *EscaFL1* and *EscaFL2*. Similar wild type samples were used for comparison and *UBIQUITIN* was used as a control.
**(H)** qRT-PCR of a subset of leaf samples showing the range of silencing (from mildly to strongly down-regulated) of *EscaFL1* and *EscaFL2* simultaneously. Fold change in *EscaFL1* (black bars) and *EscaFL2* (gray bars) expression is shown relative to the wild type leaf gene expression. Error bars show ± SD among three technical replicates. *GADPH* was used as the endogenous control.

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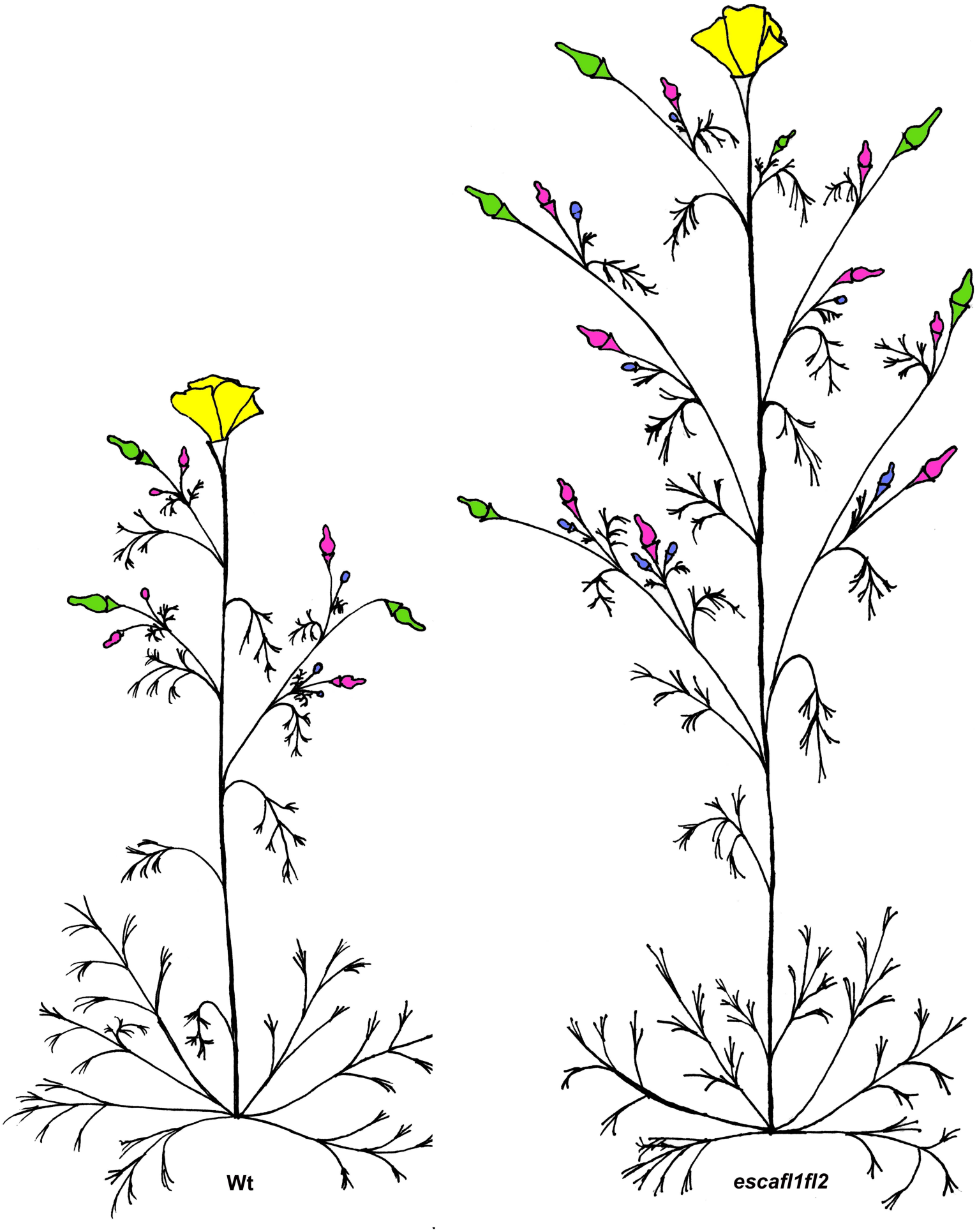
**Supplemental Figure 6.** Range of variation of the leaf-like sepal phenotype in *escafl1-fl2* California poppy plants.

**(A)** to **(C)** Slightly abnormal sepals, with leafy edges. In these flowers, floral organs remain trapped inside because sepals are largely fused but not deciduous. Floral cup is visible.

**(D)** to **(I)** Strongly abnormal, free (un-fused) sepals with highly dissected leaf-like edges that allow full or partial exposure of the remaining floral organs. Floral cup is present.

**(J)** to **(L)** Complete homeotic transformation of sepals into leaf- like organs, where no remnants of the floral cup are observed. Scale Bars: 0.5 cm

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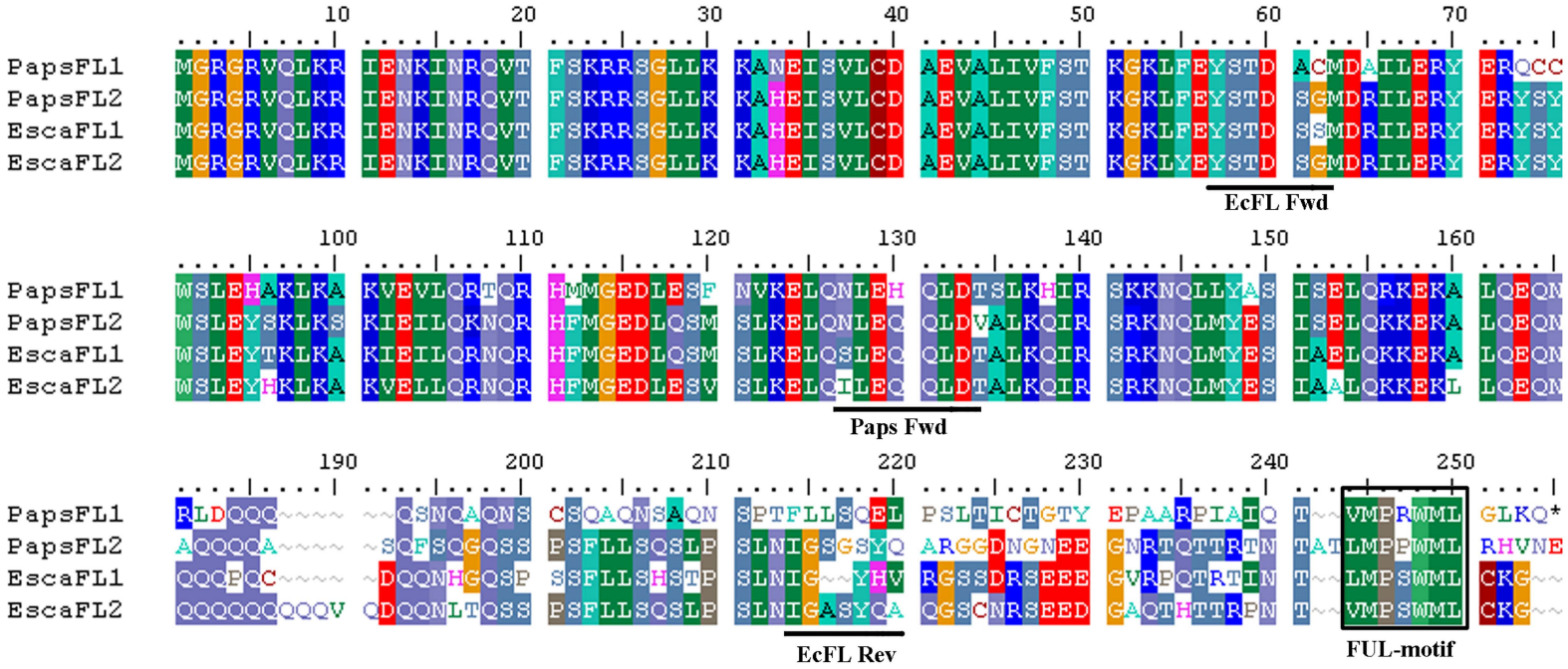


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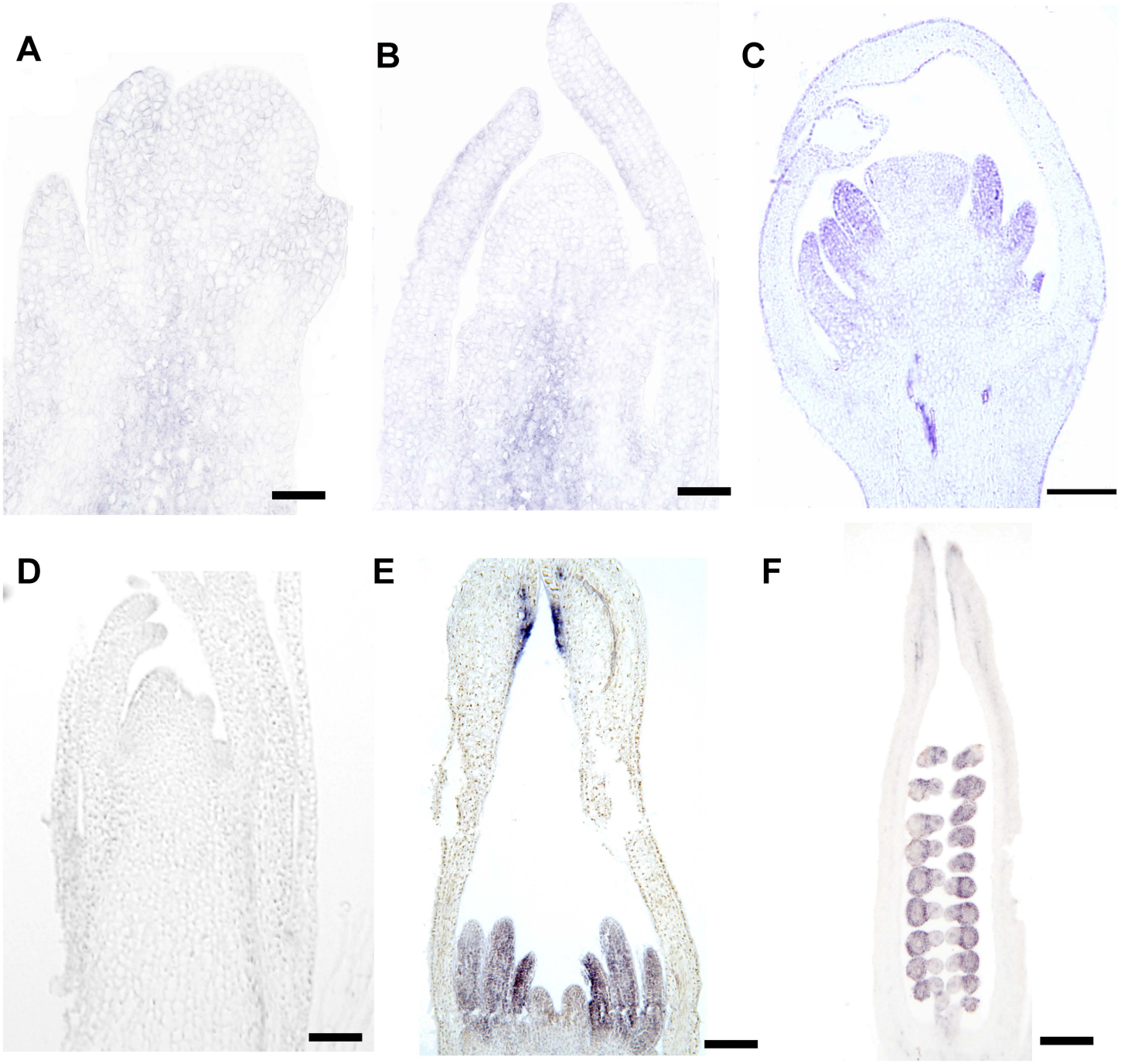


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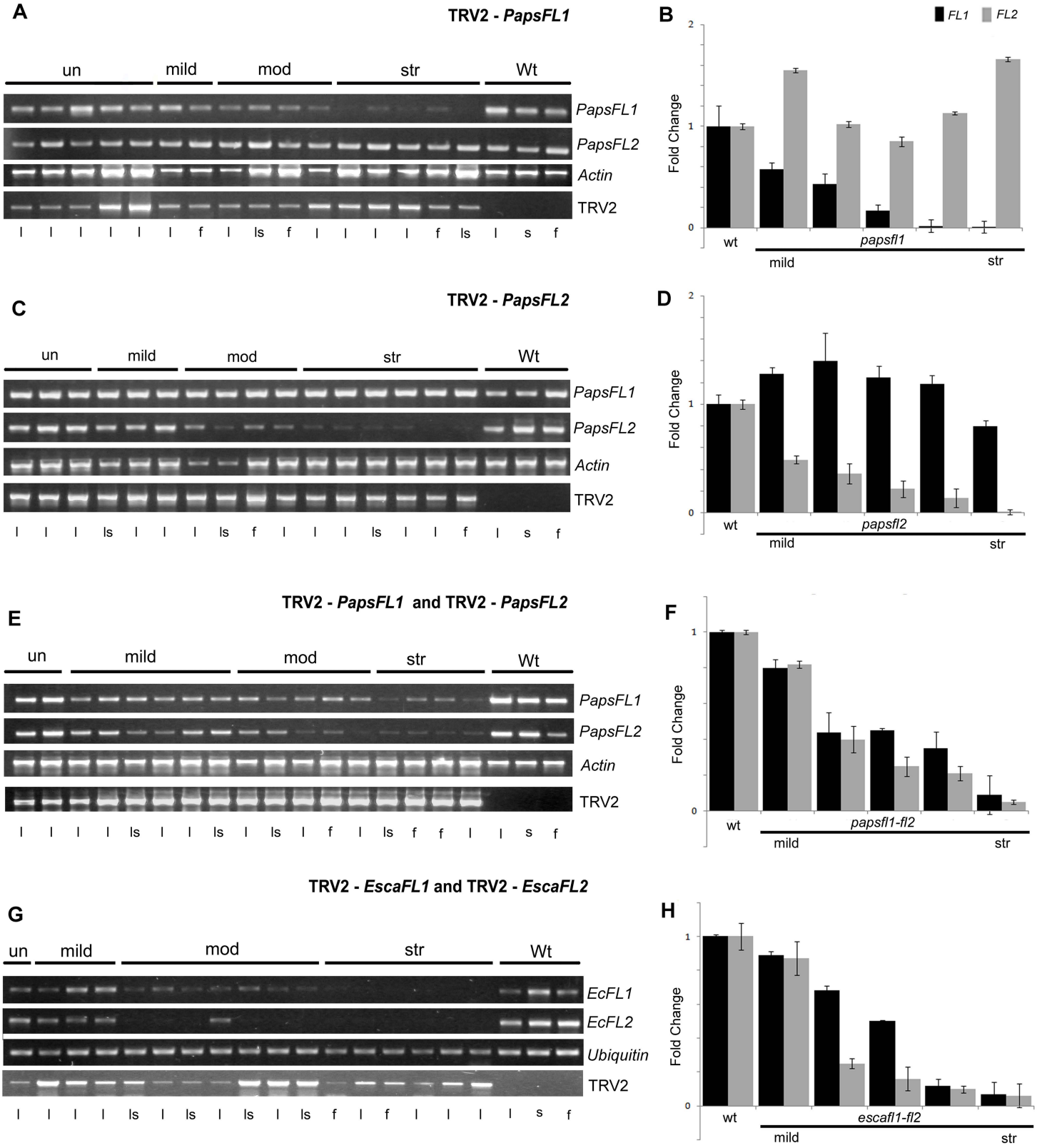


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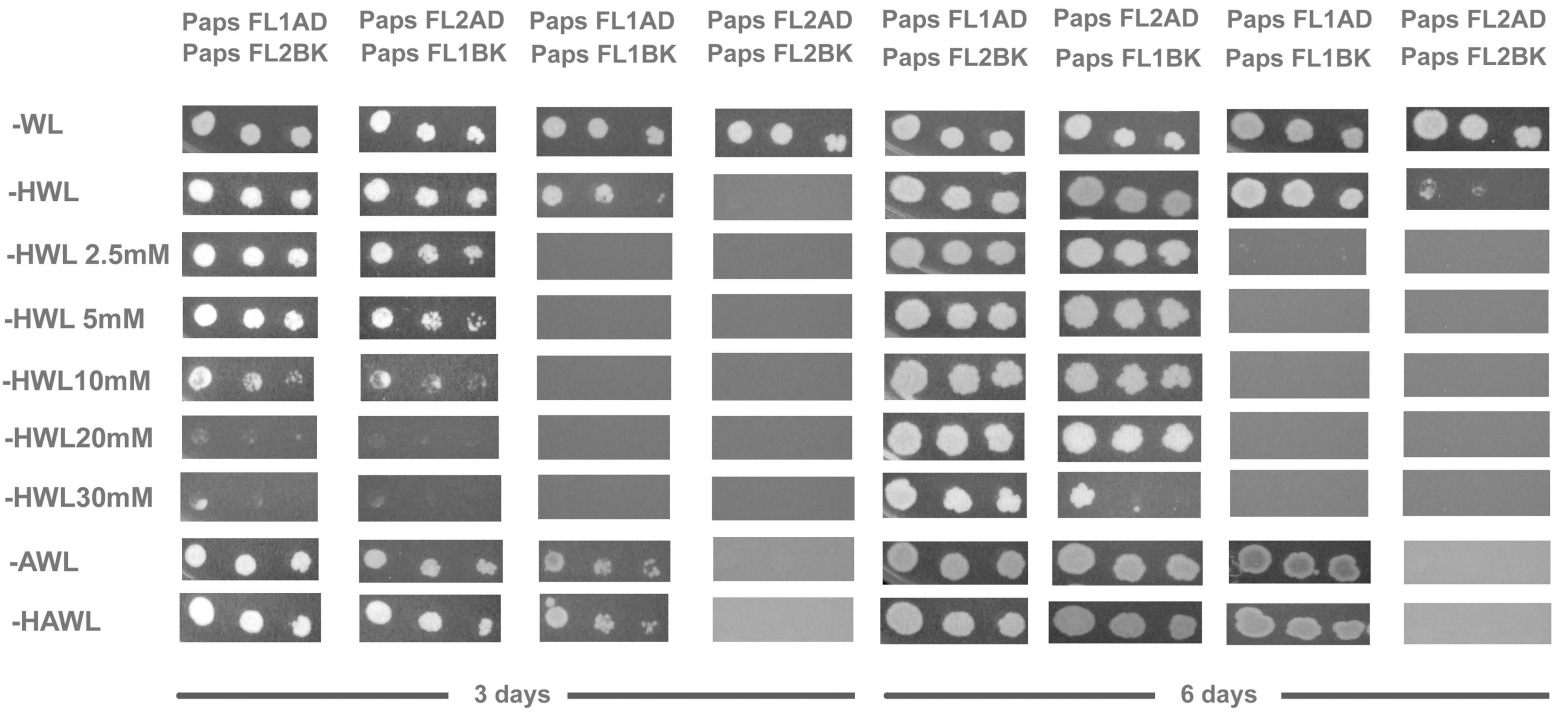


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**Supplemental Table 1.** Summary of phenotypes identified using VIGS to silence poppy *FUL-like* genes individually and simultaneously

| Construct /(effectiveness[a]) | Phenotypes | N°plants |
|---|---|---|
| TRV2-PapsFL1/ ( 27/100) | Branched inflorescences | 21 |
| | Overgrowth and shape defects in cauline leaves | 6 |
| | Leaf –like sepals | 8 |
| | Carpel defects /Premature fruit rupture | 4 |
| TRV2-PapsFL2/ (13/80) | Branched inflorescences | 10 |
| | Overgrowth and shape defects in cauline leaves | 5 |
| | Leaf –like sepals | 7 |
| | Carpel defects /Premature fruit rupture | 3 |
| TRV2-PapsFL1 and TRV2-PapsFL2/ (15/108) | Delay in reproductive transition | 12 |
| | Branched inflorescences | 7 |
| | Overgrowth and shape defects in cauline leaves | 5 |
| | Leaf –like sepals | 5 |
| | Mosaic green petals | 5 |
| | Carpel defects /Premature fruit rupture | 5 |
| TRV2-EscaFL[b] (40/120) | Branched inflorescences | 40 |
| | Leaf –like sepals | 40 |
| | Carpel defects /Premature fruit rupture | 4 |

[a]effectiveness: (Total number of plants down-regulated/ Total number of plants transformed)

[b]both constructs downregulated both gene copies therefore data are combined here.

**Supplemental Table 2.** Primers used for all the experiments

| | Primer name | Primer sequence |
|---|---|---|
| In Situ Hybridization | *PapsFL1*- F | GCACCAACTTGATACTTCC |
| | *PapsFL1*- R-T7 | CTTAATACGACTCACTATAGGGTGATCCCTGATTGCTTTCTT |
| | *PapsFL2*- F | AAGAGCTCCAAAATCTAG |
| | *PapsFL2*- R-T7 | CTTAATACGACTCACTATAGGGAGATACAACATTACATGCA |
| | *PapsPI* F | AGTGGAAATTCATGGAAGAGG |
| | *PapsPI* R T7 | CTTAATACGACTCACTATAGGGAGTTATAGTAGCAGCTATGATC |
| | *EcFL1*- F | GGAAAACTCTTTGAATACTCTACTGATTCCAGCA |
| | *EcFL1*- R-T7 | CTTAATACGACTCACTATAGGGTCGCTGCTGCCTCGAACATGGTA |
| | *EcFL2*- F | GCTCTATGAATACTCCACTGATTCTGGTA |
| | *EcFL2*- R-T7 | CTTAATACGACTCACTATAGGGTCCTTGCGCCTGATAACTTG |
| | *EcAG* F | GCAACCAAACTGCGTCAACAAATCG |
| | *EcAG* R T7 | CTTAATACGACTCACTATAGGGTGTCTGCTCCTGGTGGGAGTAATG |
| Yeast 2 Hybrid | *PapsFL1- Nde*I | CATATGGGAAGAGGTAGGGTTCAGCTGAAG |
| | *PapsFL1- Eco*RI | GAATTCCTATTGTTTGAGACCAAGCATCCA |
| | *PapsFL2- Nde*I | CATATGGGAAGAGGTAGGGTTCAGCTGAA |
| | *PapsFL2- Eco*RI | GAATTCTTCATTAACATGGCGAAGCATCCA |
| VIGS Insert | *EcFL1- Kpn*I F | GGTACCGGAAAACTCTTTGAATACTCTACTGATTCCAGCA |
| | *EcFL1- Sac*I R | GAGCTCTCGCTGCTGCCTCGAACATGGTAA |
| | *EcFL2- Kpn*I F | GGTACCGCTCTATGAATACTCCACTGATTCTGGTA |
| | *EcFL2- Sac*I R | GAGCTCCCTTGCGCCTGATAACTTGCACCAATG |
| | *PapsFL1-Eco*RI F | GAATTCTTGGAGCACCAACTTGATACTTCCT |
| | *PapsFL1-Xba*I R | TCTAGAAAGCACTGACCGTGTTCATG |
| | *PapsFL2*- F | AAGAGCTCCAAAATCTAGA |
| | *PapsFL2-Bam*HI R | GGATCCGAATAGAGATACAACATTACATGCATG |
| Locus specific RT-PCR | TRV2 - pYL156 F | GGTCAAGGTACGTAGTAGAG |
| | TRV2 - pYL156R | CGAGAATGTCAATCTCGTAGG |
| | *ACTIN* F | GATGGATCCTCCAATCCAGACACTGTA |
| | *ACTIN* R | GTATTGTGTTGGACTCTGGTGATGGTGT |
| | *PapsFL1* F | CAATAGAAAGATACTTACTTCCATGGT |
| | *PapsFL1* R | AAGCACTGACCGTGTTCATG |
| | *PapsFL2* F | GTAACCGAATAATCTCATATCTATCTC |
| | *PapsFL2* R | GAATAGAGATACAACATTACATGCATG |
| | *UBIQUITIN* F | AACCCTTGAGGTTGAATCATCC |
| | *UBIQUITIN* R | GTCCTTCTTTCTGGTAAACGT |
| | *EcFL1*- F | GGAAAACTCTTTGAATACTCTACTGATTCCAGCA |
| | *EcFL1*- R | TCGCTGCTGCCTCGAACATGGTAA |
| | *EcFL2*- F | GCTCTATGAATACTCCACTGATTCTGGTA |
| | *EcFL2*-R | TCCTTGCGCCTGATAACTTG |
| VIGS Down-regulation screen | *PapsFL1* F | GATTTAGAATCCTTCAATGTGA |
| | *PapsFL1* R | AAGCACTGACCGTGTTCATG |
| | *PapsFL2* F | GACTTACAATCCATGAGTCTTAAA |
| | *PapsFL2* R | GAATAGAGATACAACATTACATGCATG |
| | *EcFL1*- F | TCTCTGTTCTTTGTGATGCTGAAGT |
| | *EcFL1*- R | TTGATGGTTCTAGTCTGTGGTCGAA |
| | *EcFL2*- F | GAAGTTGCTTTAATTGTCTTCTCTA |
| | *EcFL2*-R | AGGCCTCGTCGTATGTGTTTGTGC |
| qRT-PCR | *PapsFL1* F | TTATGCCACGGTGGATGCT |
| | *PapsFL1* R | ACAGATCTATATGAAACATCCATCAACA |
| | *PapsFL2* F | GAAGAAGGGAATCGAACTCAGACT |
| | *PapsFL2* R | TGCGACGGATAGACACCCA |
| | *EcFL1*- F | ACAGCAGCAACCTCAGTGTGA |
| | *EcFL1*- R | TGCTGCCTCGAACATGGTAA |
| | *EcFL2*- F | ATAACCCAGCAGCAGCAGCAGCA |
| | *EcFL2*-R | GTATGTGTTTGTGCTCCATCTGTGTT |
| | *GADPH*-F | GCTTCCTTCAACATCATTCC |
| | *GADPH*-R | AGTTGCCTTCTTCTCAAGTC |