

Figure S1. Interactions between AFPs and ABI5 or DELLA proteins assayed by bimolecular fluorescence complementation. Agrobacteria carrying plasmids encoding the indicated pairs of fusions to the N-terminal (nYFP) or C-terminal (cYFP) portions of yellow fluorescent protein were co-infiltrated into *N. benthamiana* leaves. Micrographs of the lower epidermis were taken 2-3d after infiltration.

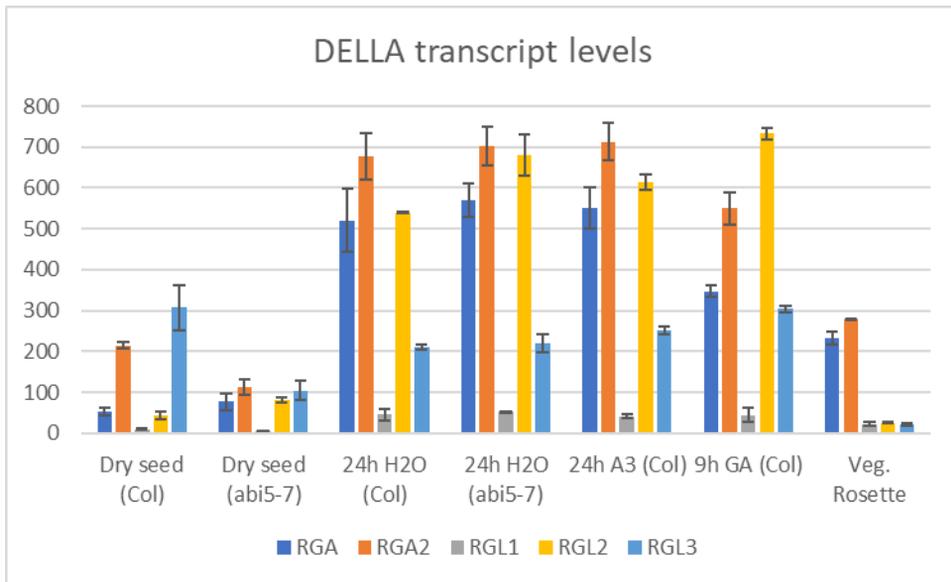


Figure S2. DELLA transcript levels in dry and imbibing seeds and vegetative rosettes. Transcriptome data from Nakabayashi et al 2005, the Yamaguchi lab, and Schmid et al 2005, present on the Arabidopsis eFP browser at ([bar.utoronto.ca](http://bar.utoronto.ca)) [22, 23].

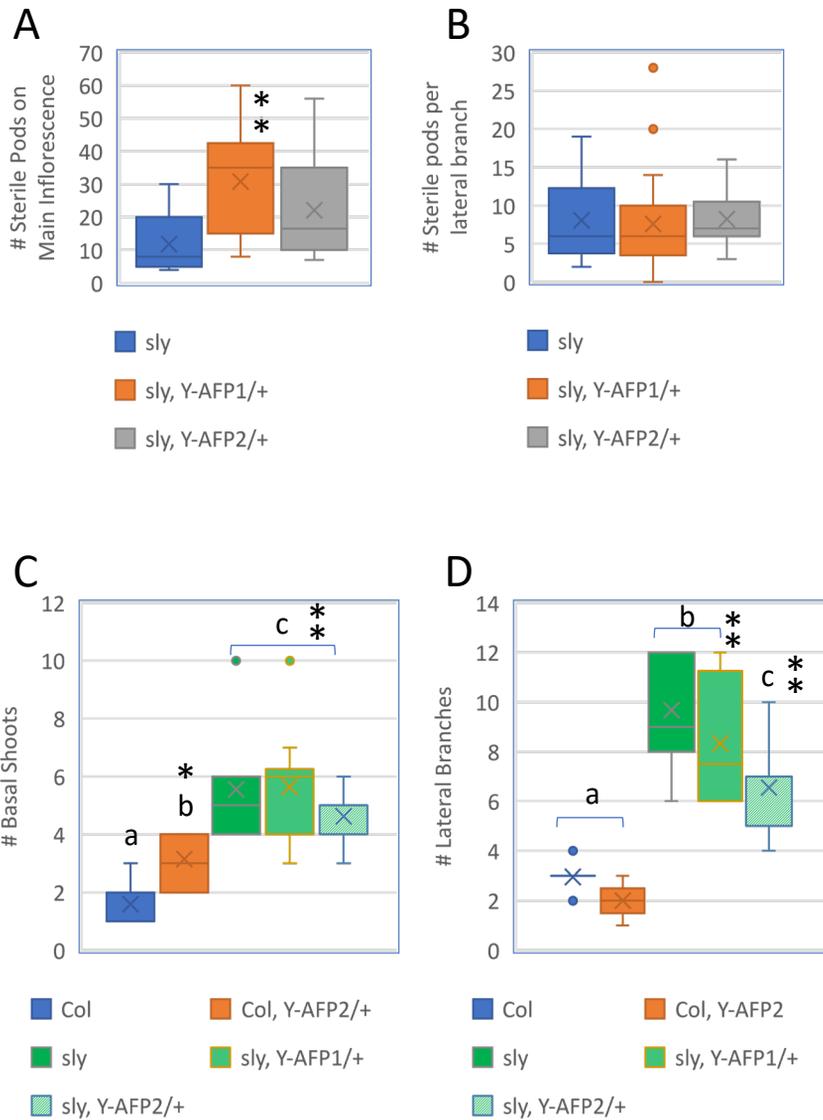


Figure S3. Reduced fertility and apical dominance of the *sly1* mutants, with or without the YFP-AFP transgenes. (A) Number of sterile pods in main inflorescence before production of fertile flowers. No sterility was observed in the Col-0 background. (B) Number of sterile pods per lateral branch. (C) Number of shoots originating from rosette. (D) Number of lateral shoots per plant. Graphs display data distribution with mean (X), first and third quartiles within the box. Statistical significance was determined by OneWay Anova with post-hoc Tukey HSD [52]. \* =  $P < 0.05$ , \*\* =  $P < 0.01$  relative to *sly1* (panels A & B) or Col (panels C & D).

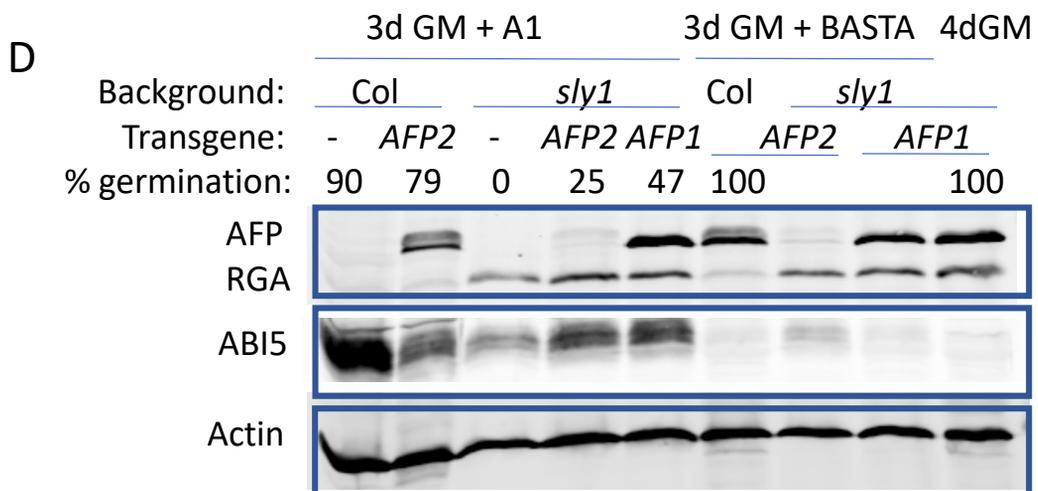
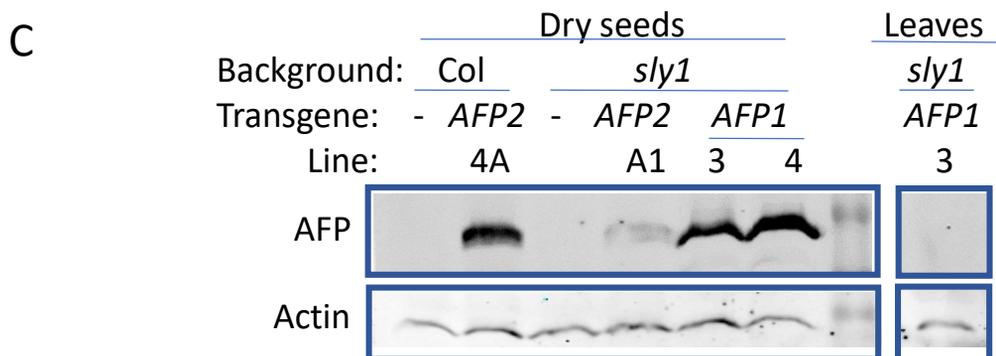
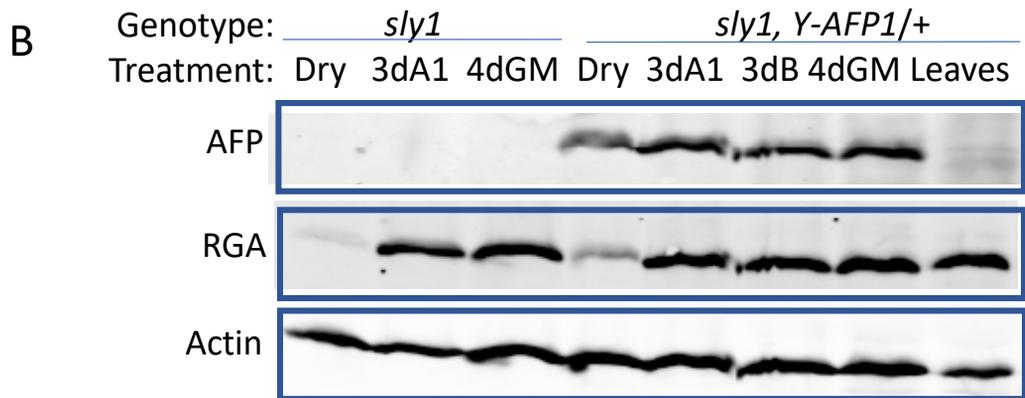
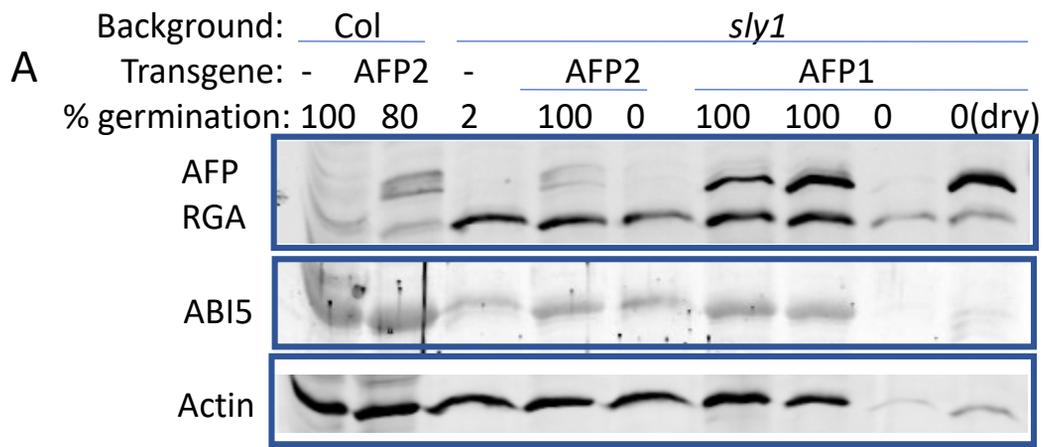


Figure S4. Immunoblot comparisons of AFP, RGA, and ABI5 accumulation in all genotypes at specific time points. Actin was used as a loading control. (A) Comparison of YFP-AFP, RGA, and ABI5 accumulation in seeds or seedlings after 4d incubation on GM or dry seeds (lane 10). The YFP-AFP transgenes are segregating in all backgrounds. For those in the *sly1* background, separate extracts were made from germinated and non-germinating seeds. YFP-AFP expression was limited to the germinating seeds. (B) Comparison of RGA and YFP-AFP1 accumulation in *sly1* mutants with or without the *YFP-AFP1* transgene in dry seeds, leaves or after 3d incubation on GM with either 1  $\mu$ M ABA (A1) or BASTA (B) or 4d on GM with no supplement. (C) Comparison of YFP-AFP fusion protein accumulation in dry seeds of the indicated lines or rosette leaves of *sly*, YFP-AFP1 #3. (D) Comparison of YFP-AFP, RGA, and ABI5 accumulation in seeds or seedlings after 3d incubation on GM with either 1  $\mu$ M ABA, BASTA or no supplement (lane 10)

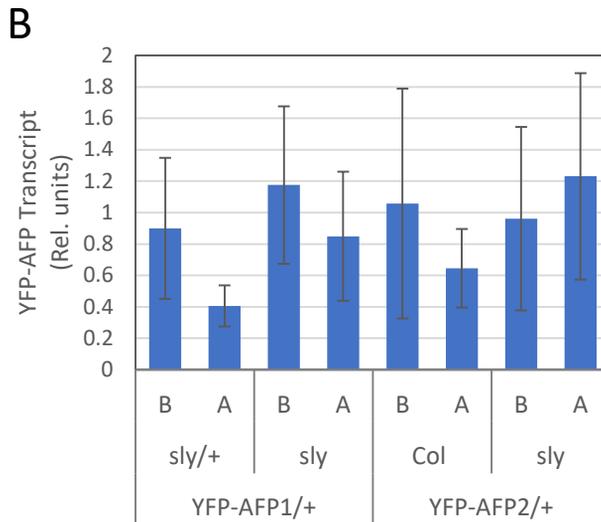
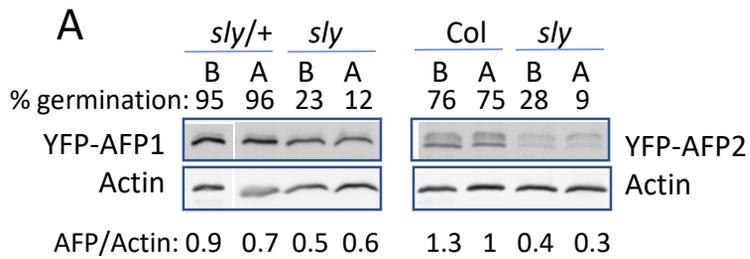


Figure S5. Comparison of YFP-AFP protein and transcript accumulation in wild-type and *sly1* backgrounds. Seeds and seedlings were harvested after 3d on GM with either 1  $\mu$ M ABA (A) or BASTA (B). (A) Immunoblot comparisons of representative samples. AFP:Actin ratios were determined from scans of replicate blots with duplicate samples and a standard dilution series. (B) Relative levels of YFP-AFP transcripts in samples harvested in parallel to those used for protein determination. YFP-fusion transcripts are expressed relative to PP2AA3 transcript, previously identified as relatively constant in seeds and seedlings. Differences in transcript levels were not statistically significant.

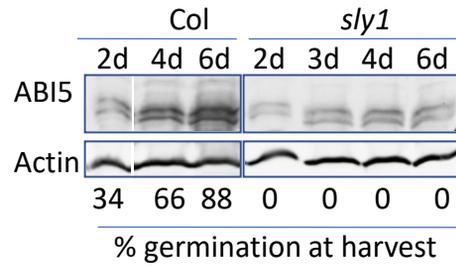


Figure S6. Timecourse of ABI5 accumulation post-stratification in wild-type (Col) and *sly1* mutants. Seeds were incubated on GM with 1  $\mu$ M ABA for the indicated days post-stratification before harvest and extraction.

Table S1. Primers used for construction of cDNA clones and subclones, and qRT-PCR.

Primer name	Sequence
BglIII-RGL2-F	G AAA <u>GAT CTT</u> ATGAAGAGAG GATACGGAGA AAC
BglIII-RGL2-R	G AAA <u>GAT CTCA</u> GGC GAG TTT CCA CGC C
BglIII-Stop-RGL2-DELLA-R	G AAA <u>GAT CT</u> <u>tca</u> CTCGTCAAAGACTTCCTCTTCC
BglIII-RGL2-GRAS-F	G AAA <u>GAT CTT</u> <u>GAAGAGGAAGTCTTTGACGAG</u>
Bam-stop-RGA2-DELLA-R	CGCGGATCC <u>tca</u> CGAAGAAGCCGAATCGATAG
EcoRI-RGA2-GRAS-F	CCGGA ATT <u>CCTATCGATT</u> CGGCTTCTTCGT
attL1-RGA2	GCT <u>tctgcagg</u> ACCATGAAGAGAG ATCATCATCA TCATC
attL2-RGA2	GAAAGCTGGGT <u>tctcgag</u> CTA ATT GGT GGA GAG TTT CCA AG
attL1-RGA1	GCT <u>tctgcagg</u> ACCATGAAGAGAG ATCATCACCA ATTC
attL2-RGA1	GAAAGCTGGGT <u>tctcgag</u> TCA GTA CGC CGC CGT C
YFPqRT-F	TCAAGATCCGCCACAACATC
YFPqRT-R	TGGTAGCTCAGGTAGTGGTT
PP2AA3qRT-F	TAACGTCCGCAAATGATGC
PP2AA3qRT-R	GTTCTCCACAACCGCTTGGT