

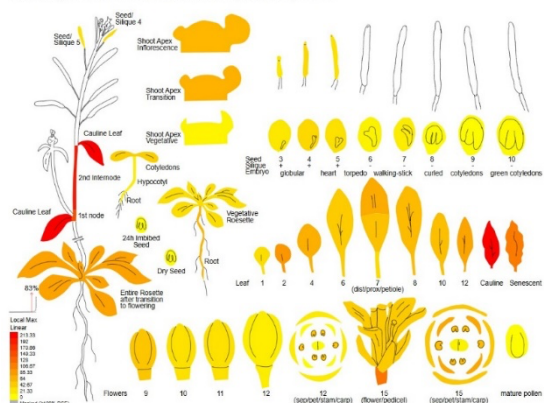
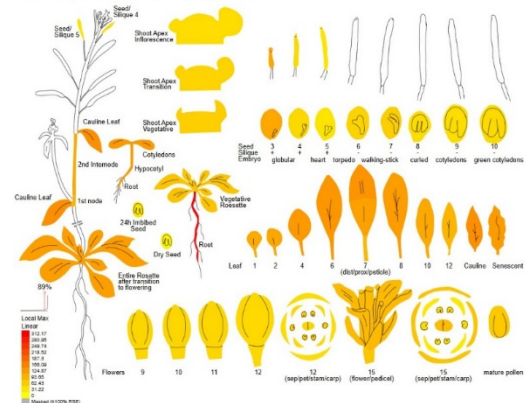
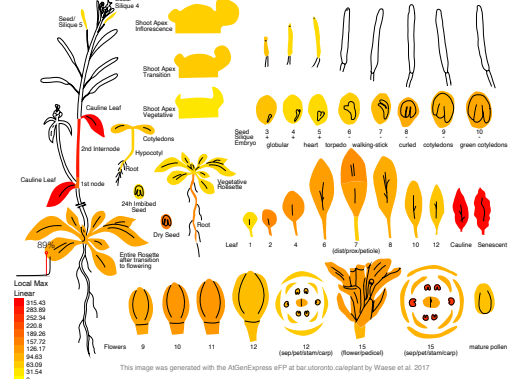
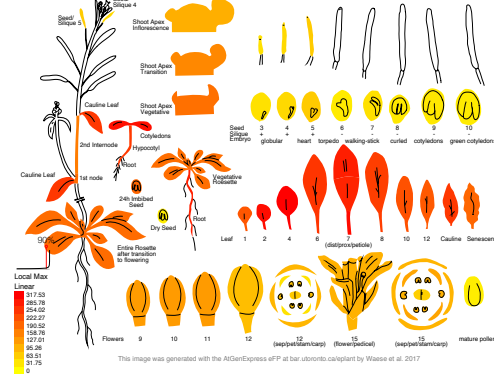


Figure S1. Expression patterns for *PYL8*, *PYL9*, *AGL16* and *SOC1* in *Arabidopsis*.

These data come from the Arabidopsis electronic fluorescent pictograph (eFP) browser (<http://bar.utoronto.ca/eplant/?ActiveSpecies>).

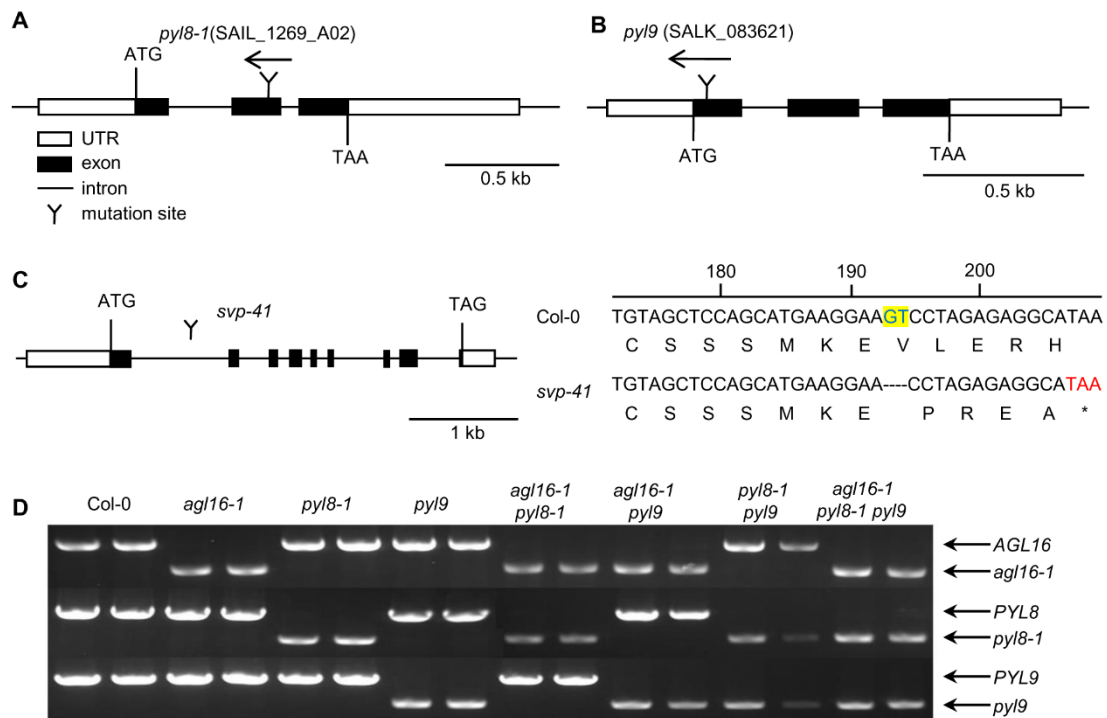


Figure S2. Genotyping of mutants used in this research.

(A) and (B) Schematic representation of T-DNA insertion sites in *pyl8-1* and *pyl9* mutants. (C) The structure of *SVP* gene and the amino acid sequence of *svp-41* mutant. The loss of two nucleotides in *svp-41* causes premature termination of the coding sequence. (D) PCR verification of homozygous T-DNA insertions in *agl16-1*, *pyl8-1*, and *pyl9* mutants.

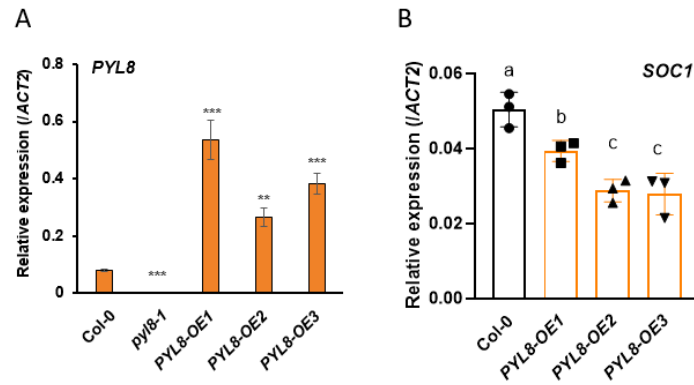


Figure S3. *PYL8* and *SOC1* expression in mutant or *35S:gPYL8* transgenic lines.

Seeds of Col-0, *pyl8-1*, and *35S:gPYL8* overexpression lines were germinated and grown on $\frac{1}{2}$ MS medium for 10 days, then the RNA was isolated and the transcript level of *PYL8* and *SOC1* were determined. Bars represent mean $\pm$ SD with 3 or 4 biological replicates. *ACT2* was used as a reference gene. Asterisks in A represent significant differences determined by Student's *t* test, ** $P < 0.01$, *** $P < 0.001$. Letters above columns in B indicate significant differences among lines (ANOVA with Tukey's HSD post-hoc test, $P < 0.05$).

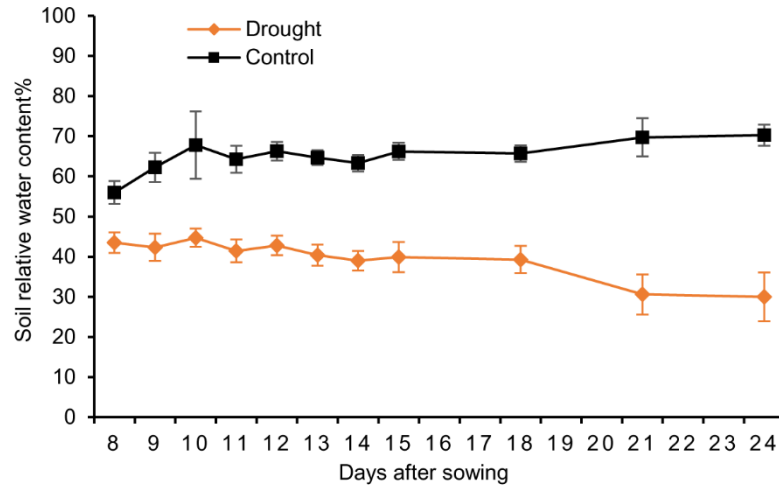


Figure S4. Soil relative water content measurements during the drought stress.

The experiment was performed in growth chambers. Three days after sowing, the relative humidity for the drought-stress group was set at 30%, while the control group maintained a humidity level of 60%. The drought-stress group was subjected to water withholding. Eight days after sowing, but before floral transition, relative water contents were recorded for each pot of soil. The relative water content percentage was calculated as total weight minus dry soil weight divided by saturation moisture content before drought. Soil relative water content of the control was maintained at 55-70% while that of drought stress was kept between 30-45%. Error bars indicate SD ($n \geq 13$).

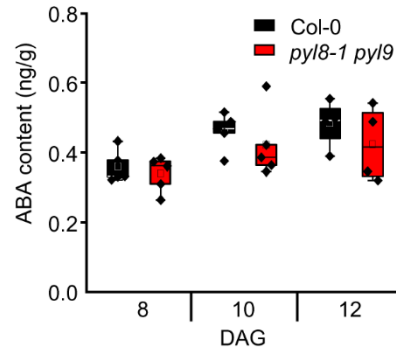


Figure S5. ABA content in the wild-type Col-0 and the *pyl8-1 pyl9* mutant.

The whole seedlings of 8-, 10-, and 12-day-old (DAG) *Arabidopsis* plants grown on $\frac{1}{2}$ MS were used to measure the ABA content. For each developmental stage and both lines, four to five biological replicates were used in each experiment. DAG, days after germination. No significant difference was observed between Col-0 and *pyl8-1 pyl9* at each time point.

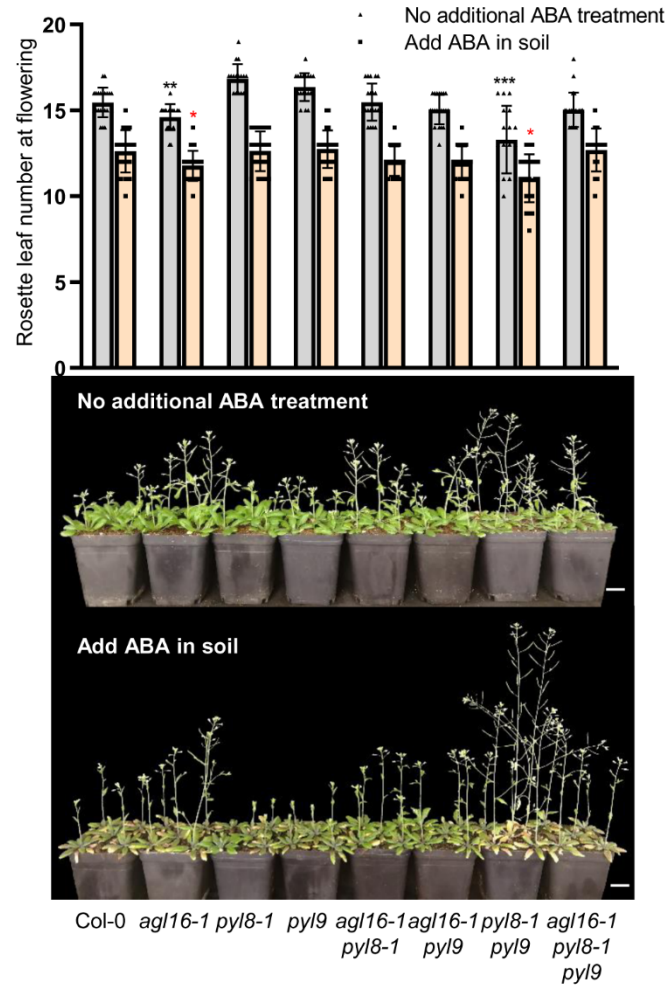


Figure S6. Leaf number at flowering and flowering phenotypes of the single, double, and triple mutants of *PYL8*, *PYL9*, and *AGL16* with or without additional ABA treatment.

A. Rosette leaf production upon flowering for the single, double, and triple mutants of *PYL8*, *PYL9*, and *AGL16* with or without additional ABA treatment. Black asterisks represent significant differences compared to Col-0 in the control experiment, while the red asterisks indicate significant differences compared to Col-0 under ABA treatment. Student's *t*-test, *, $P < 0.01$, **, $P < 0.01$, ***, $P < 0.001$.

B. Flowering phenotype of the single, double, and triple mutants of *PYL8*, *PYL9*, and *AGL16* with or without exogenous ABA. Scale bars, 2 cm.

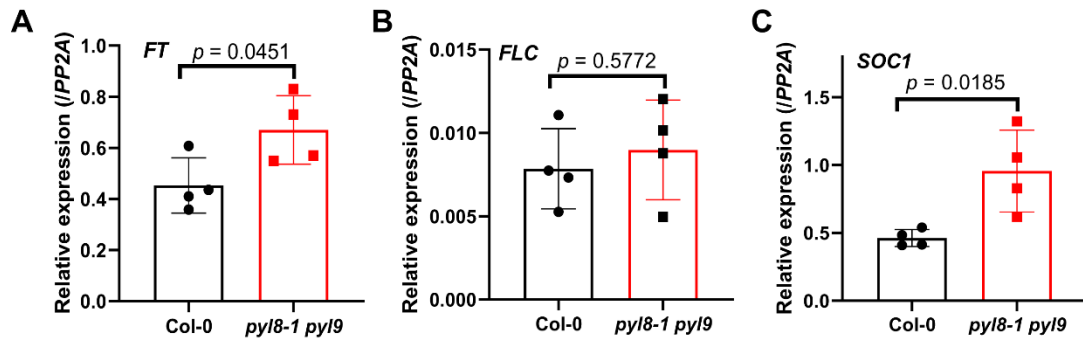


Figure S7. Relative expression of *FT* (A), *FLC* (B) and *SOC1* (C) in *pyl8-1 pyl9*.

LD-growing seedlings at 10-day-old were sampled at ZT16 for RT-qPCR analyses with *PP2A* as reference. P values indicate the significances between lines (Student's *t*-test).

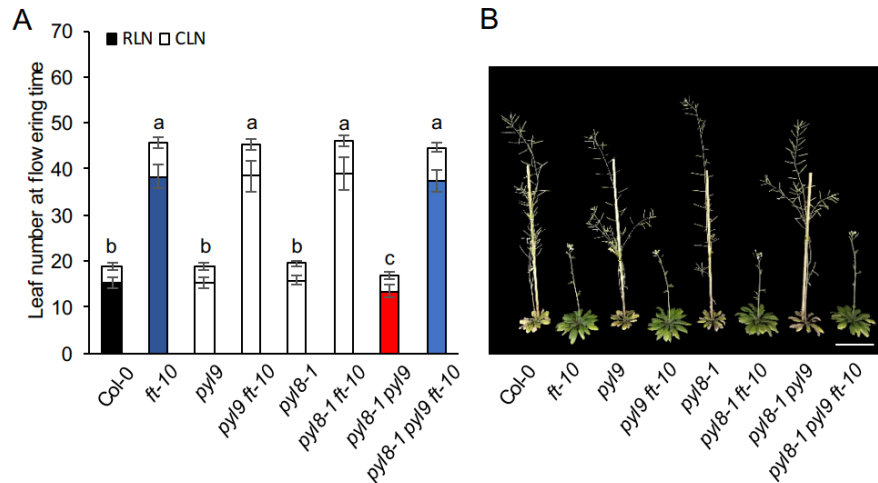


Figure S8. *FT* acts genetically downstream of *PYL8* and *PYL9* in the regulation of flowering time under LD conditions.

A. Flowering time in leaf (RLN and CLN) production for the *pyl8-1*, *pyl9*, and *ft-10* mutant sets compared to Col-0. Letters a to c above bars indicate significant differences of RLN among lines (minimum 19 replicates).

B. The growth phenotypes for **A**. Scale bars, 7 cm.

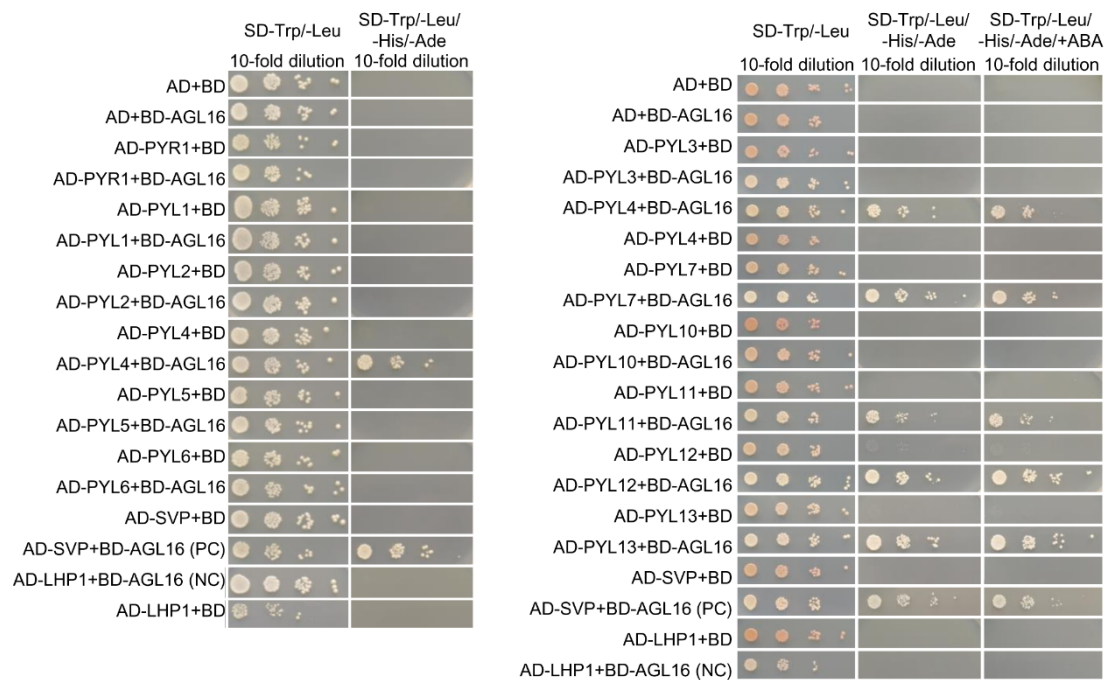


Figure S9. AGL16 interacts with a subset of PYLs as tested using the Y2H approach.

Y2H assays were used to test interactions between AD-PYLs and BD-AGL16 in yeast cells. Interactions were determined by growth assays on media lacking Trp/Leu/His/Ade in the absence and presence of 10 μ M ABA. Ten times dilution of cultures were spotted onto the plates and photographed after four days. Positive control (PC): AD-SVP and BD-AGL16; negative control (NC): AD-LHP1 and BD-AGL16. Empty vectors were used for no-interaction control. AD, Gal4 activation domain; BD, Gal4 DNA-binding domain.

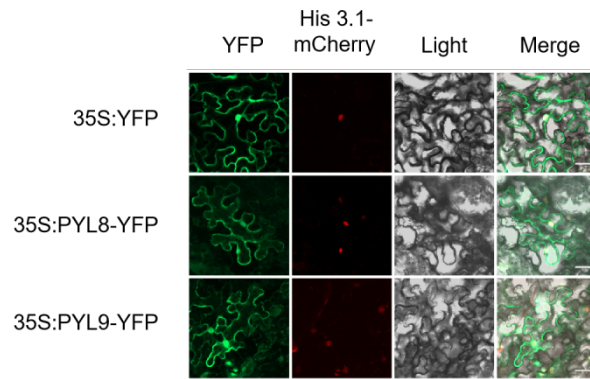


Figure S10. Sub-cellular localization of PYL8 and PYL9.

The empty vector *35S:YFP* was used as a control and His 3.1-mCherry was explored as nuclear marker. Confocal images were taken 36 hours after infiltration. Scale bars, 10 μ m.