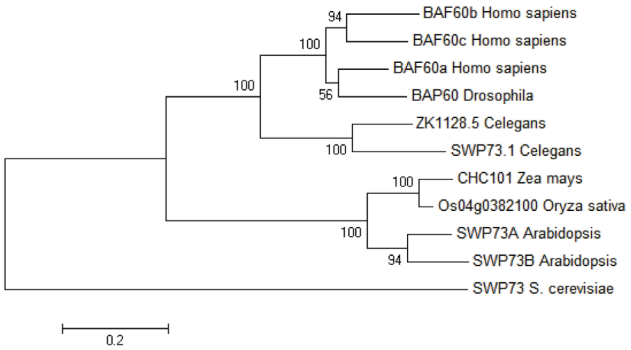
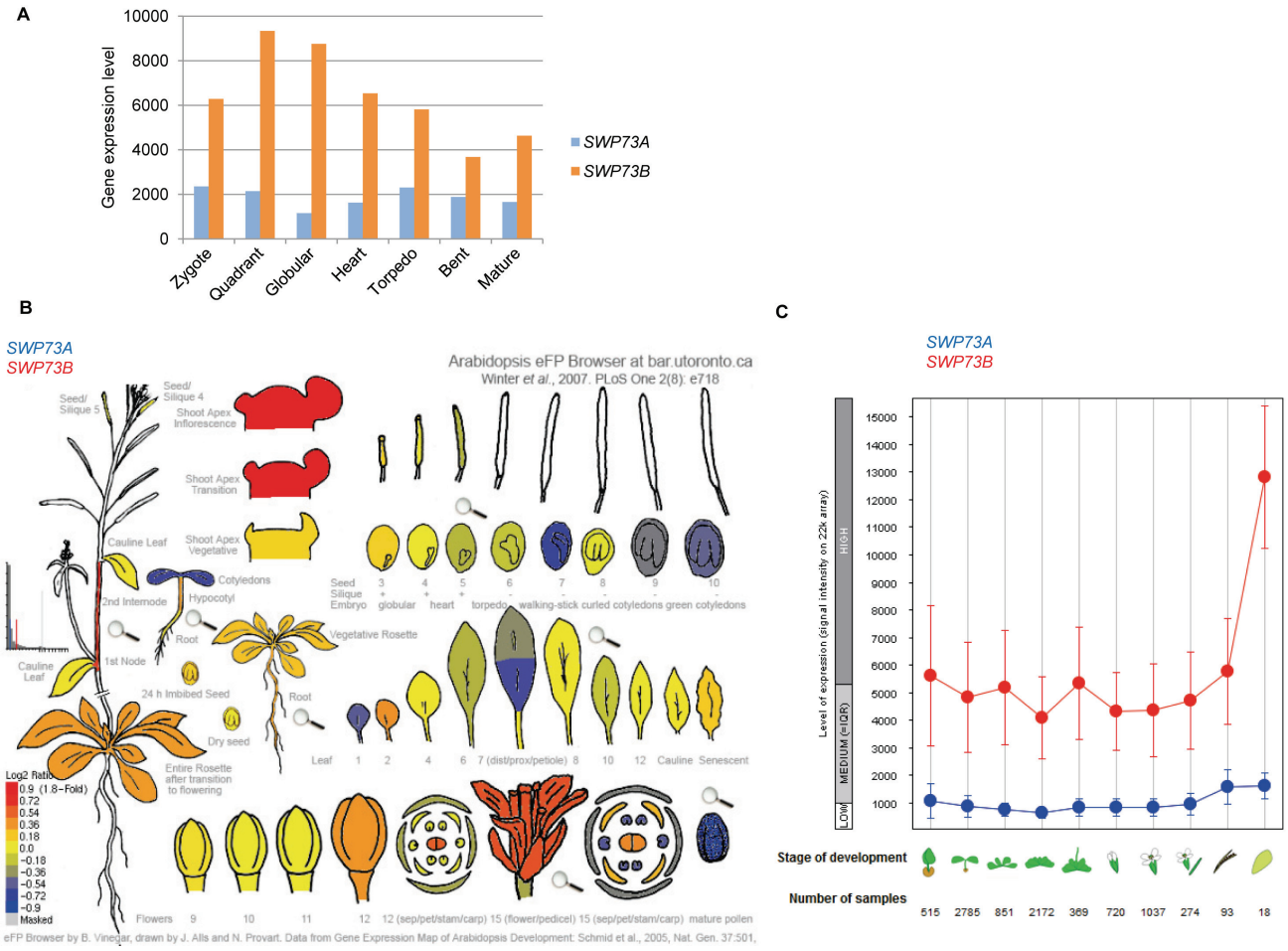



**Supplemental Figure 1.** Arabidopsis SWP73 Proteins are Evolutionarily Conserved. Phylogenetic tree of SWP73 homologues. Alignment was generated by ClustalW, the phylogenetic tree was constructed using the software MEGA6 (Tamura et al., 2013). Numbers at each branch point represent bootstrap probability values obtained using 1000 reiterations. The scale bar corresponds to an evolutionary distance of 0.2 substitution per amino acid position.

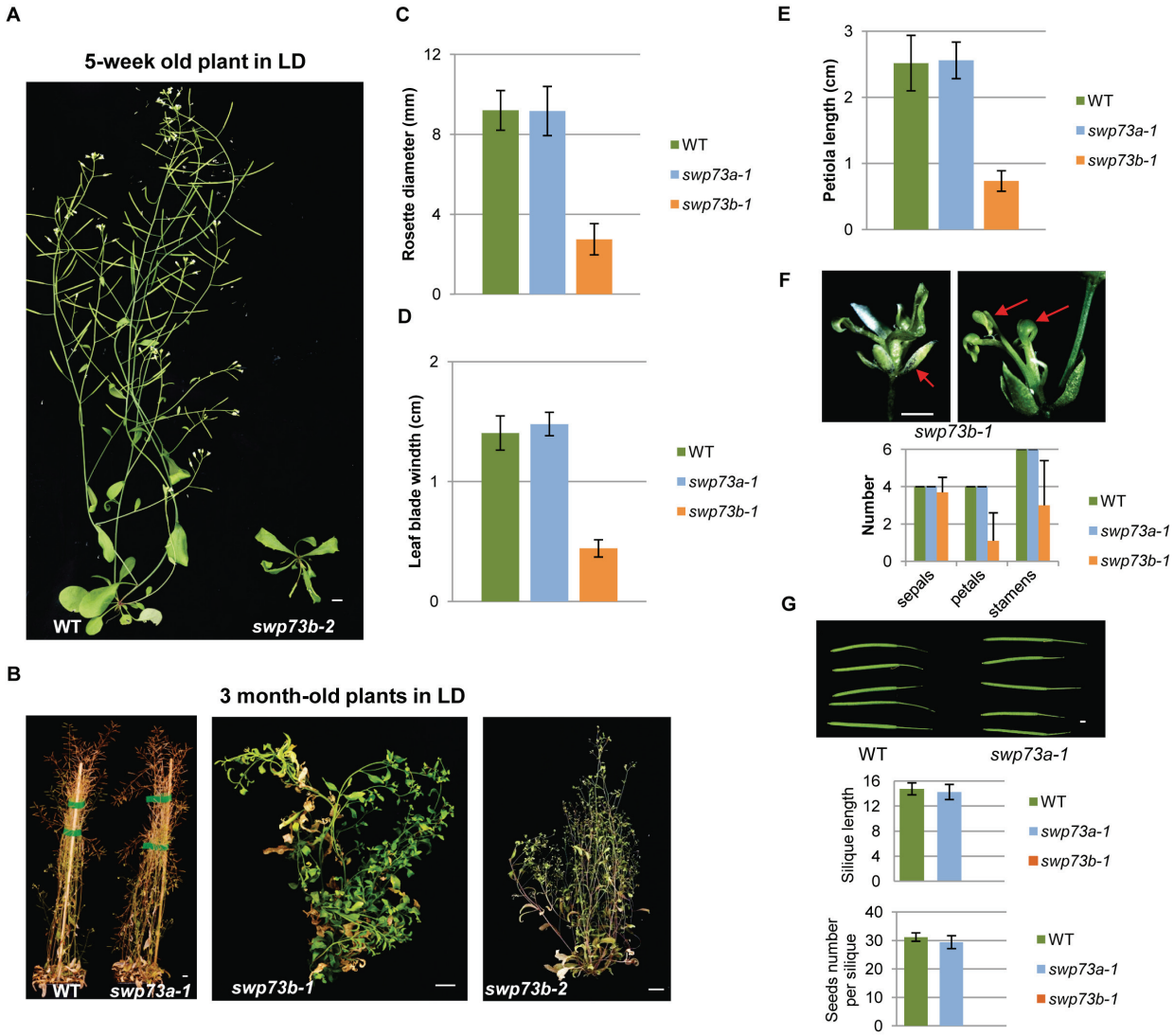



**Supplemental Figure 2.** Expression Patterns of Arabidopsis *SWP73* Genes Presented in Public Databases.

**(A)** Changes of *SWP73A* and *SWP73B* expression levels during different phases of embryonic development (Xiang et al., 2011).

**(B)** *SWP73A* and *SWP73B* expression patterns in different plant organs (eFP browse u-Toronto).

**(C)** Comparison of *SWP73A* and *SWP73B* transcript levels (Genevestigator database) indicate *SWP73B* is expressed at higher levels compared to SWP73A throughout plant development. Error bars refer to standard deviation.




**Supplemental Figure 3**. Inactivation of *SWP73B* Gene Causes Severe Developmental Defects.

**(A)** 5-week-old wild type (WT) and *swp73b-2* plants grown in LD conditions.

**(B)** 3-month-old *swp73a-1*, *swp73b-1, swp73b-2* and WT plants grown in LD conditions. The life span of *swp73b* mutants exceeded 3 months, whereas wild-type and *swp73a* plants exhibited 2-month-long life cycle. Scale bar: 1cm.

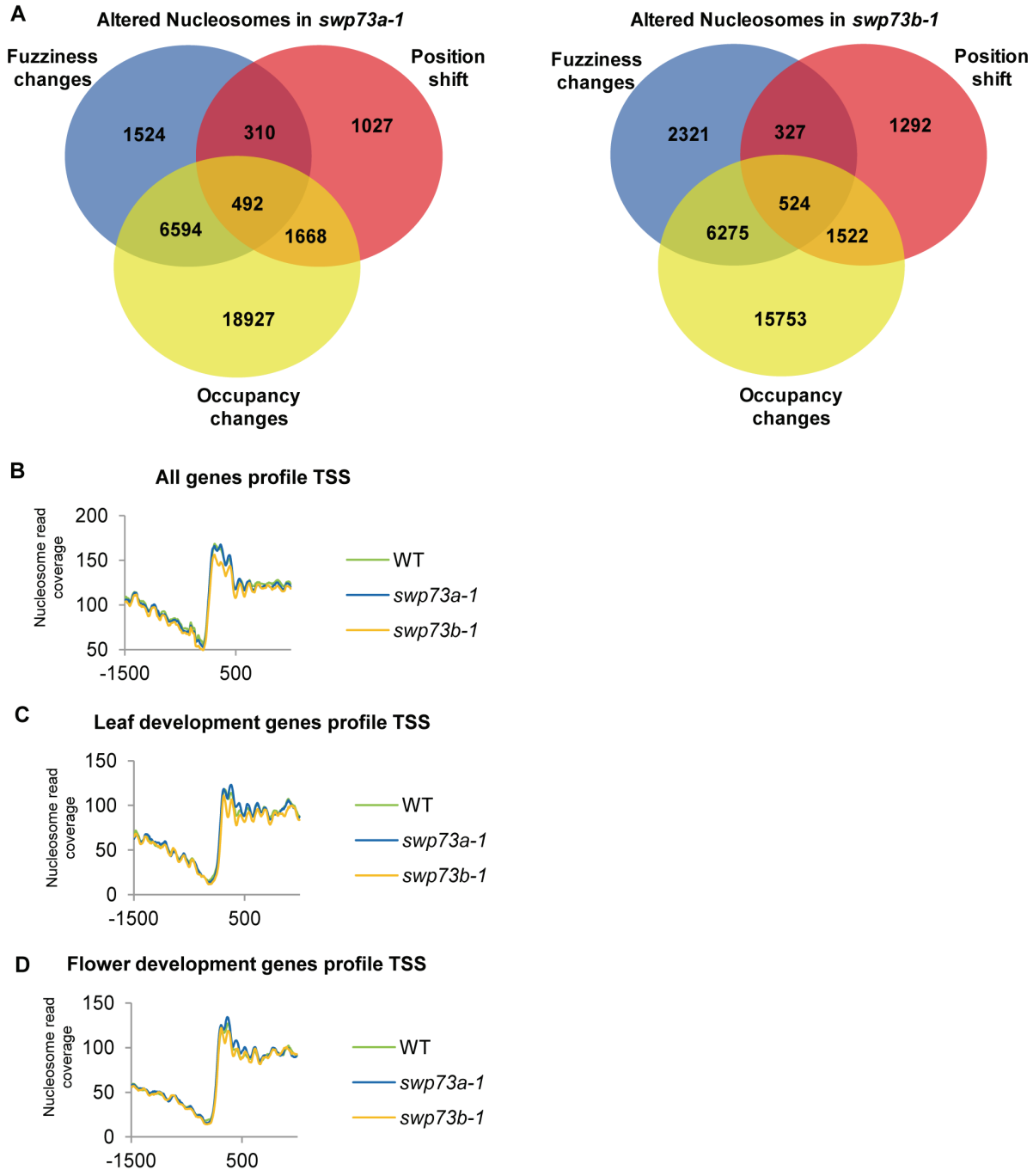
**(C)** *swp73b* mutant plants exhibit characteristically reduced rosette diameter at least 12 rosettes for each genotype were measured, error bars refer to standard deviation.

**(D)** Inactivation of *swp73b* causes reduced width of leaf blade. 24 leaves were measured for each genotype, error bars refer to standard deviation.

**(E)** Petiole length depends on functionality of SWP73B. 24 leaves were measured for each genotype, error bars refer to standard deviation.

**(F)** Comparison of number of flower organs in wild type, *swp73a-1* and *swp73b-1* plants. At least 12 flowers for each genotype were analyzed, error bars refer to standard deviation. Scale bar: 1mm.

**(G)** Inactivation of *SWP73A* does not Influence Silique Length and Seed Production while Functional *SWP73B* is Essential for Arabidopsis Fertility. At least 12 siliques for each genotype were measured, error bars refer to standard deviation. Scale bar: 1mm.




**Supplemental Figure 4**. Comparison of Genome-wide Nucleosome Distribution in WT, *swp73a-1* and *swp73b-1* Lines.

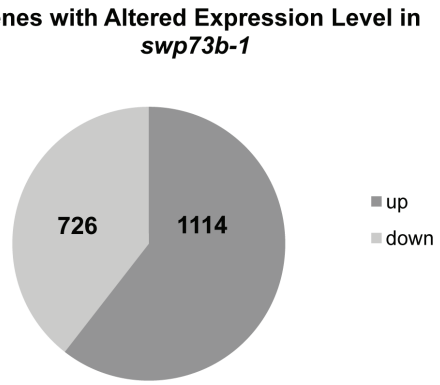
**(A)** Venn diagrams indicating the global changes in the nucleosome occupancy caused by inactivation of *swp73a* and *swp73b*.

**(B)** Genome-wide nucleosome distribution patterns surrounding the transcription start site (TSS) of genes.

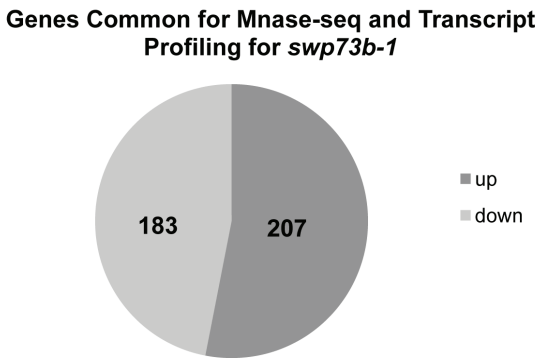
**(C)** Genome-wide nucleosome distribution patterns surrounding the transcription start site (TSS) of genes involved in leaf development.

**(D)** Genome-wide nucleosome distribution patterns surrounding the transcription start site (TSS) of genes involved in flower development.

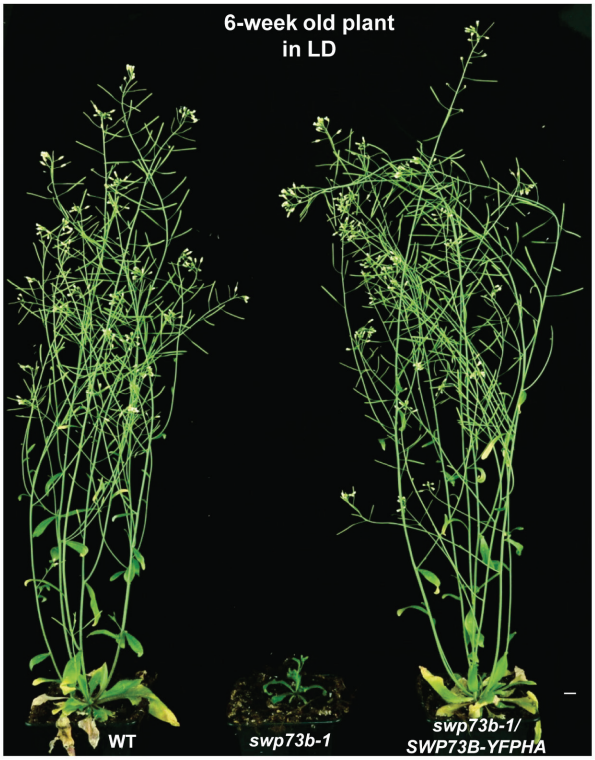
A




B

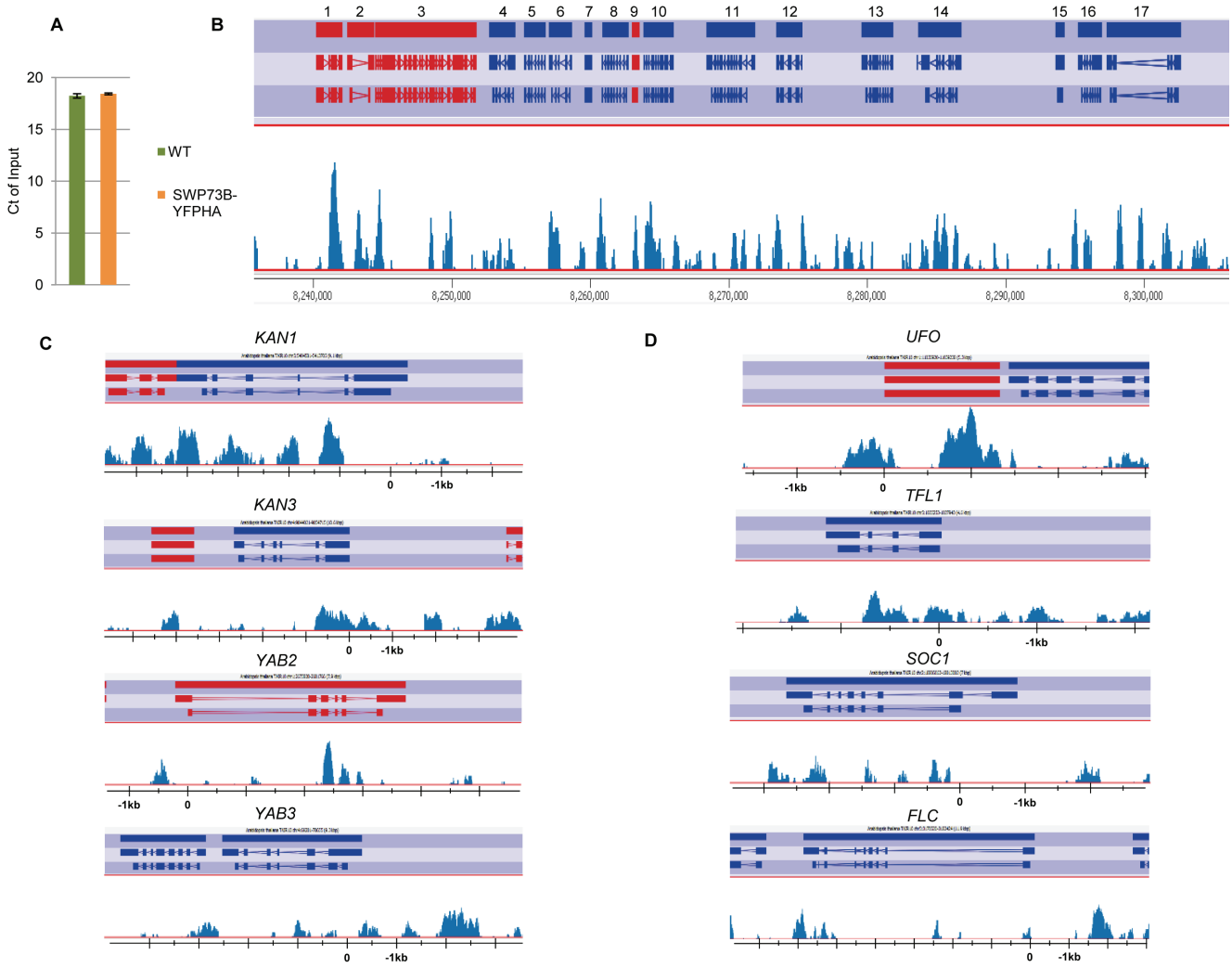



**Supplemental Figure 5.** Transcriptional Profiling of *swp73b-1* Mutant.
**(A)** Genes showing altered transcript levels in the *swp73b-1* mutant.
**(B)** Proportion of genes up- and down-regulated in *swp73b-1* that show altered nucleosome arrangement by MNase-seq analysis in their 5'-UTRs.






**Supplemental Figure 6.** Genetic Complementation of *swp73b-1* by the SWP73B-YFP-HA Construct Restores the Mutant Phenotype to Wild type. Picture of 6-week-old plants grown in LD conditions. Scale bar: 1cm.



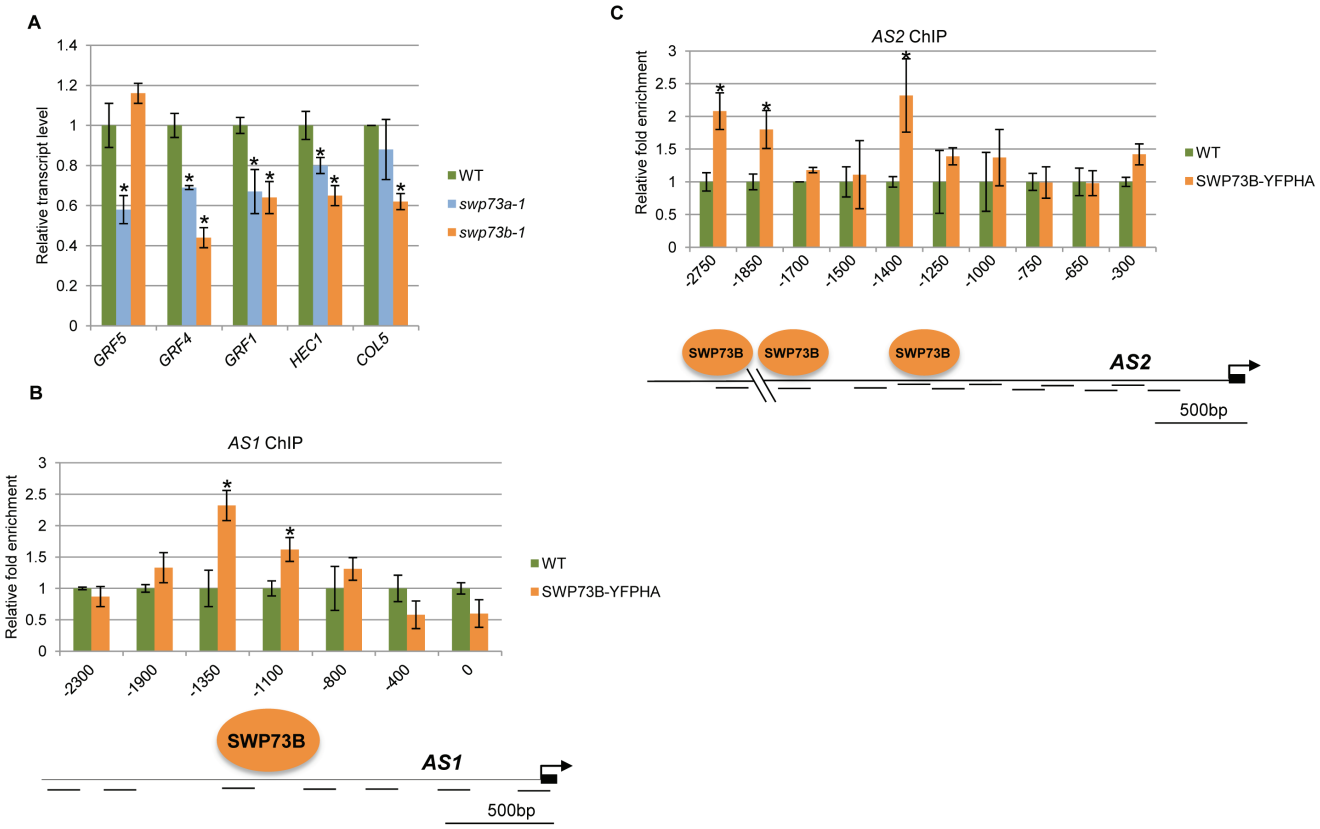

**Supplemental Figure 7.** Analysis of SWP73B-YFP-HA Distribution in the Genome by ChIP-Seq.

**(A)** Validation of ChIP-Seq input abundance by qPCR. Three technical replicates were used, error bars refer to standard deviation.

**(B)** Genome Browser snapshot of ChIP-Seq profile of SWP73B in a segment of chromosome I. The upper track of the figure shows open reading frames (ORFs) and their orientations Numbers correspond to gene *loci*- 1- AtGH9B6, 2-AT1G23220, 3-AT1G23230, 4-AT1G23240, 5-AT1G23250, 6-*MMZ1*, 7- AT1G23270, 8- AT1G23280, 9- *RPL27*, 10-AT1G23300, 11- *GGT1*, 12-*TAR1*, 13- AT1G23330, 14- AT1G23340, 15-AT1G23350, 16-*MENG*, and 17- *KNAT6*.

**(C)** ChIP-Seq peaks of SWP73B enrichment for genes involved in the regulation of leaf development.

**(D)** Localization of regions of SWP73B enrichment for genes involved in the regulation of flower development.



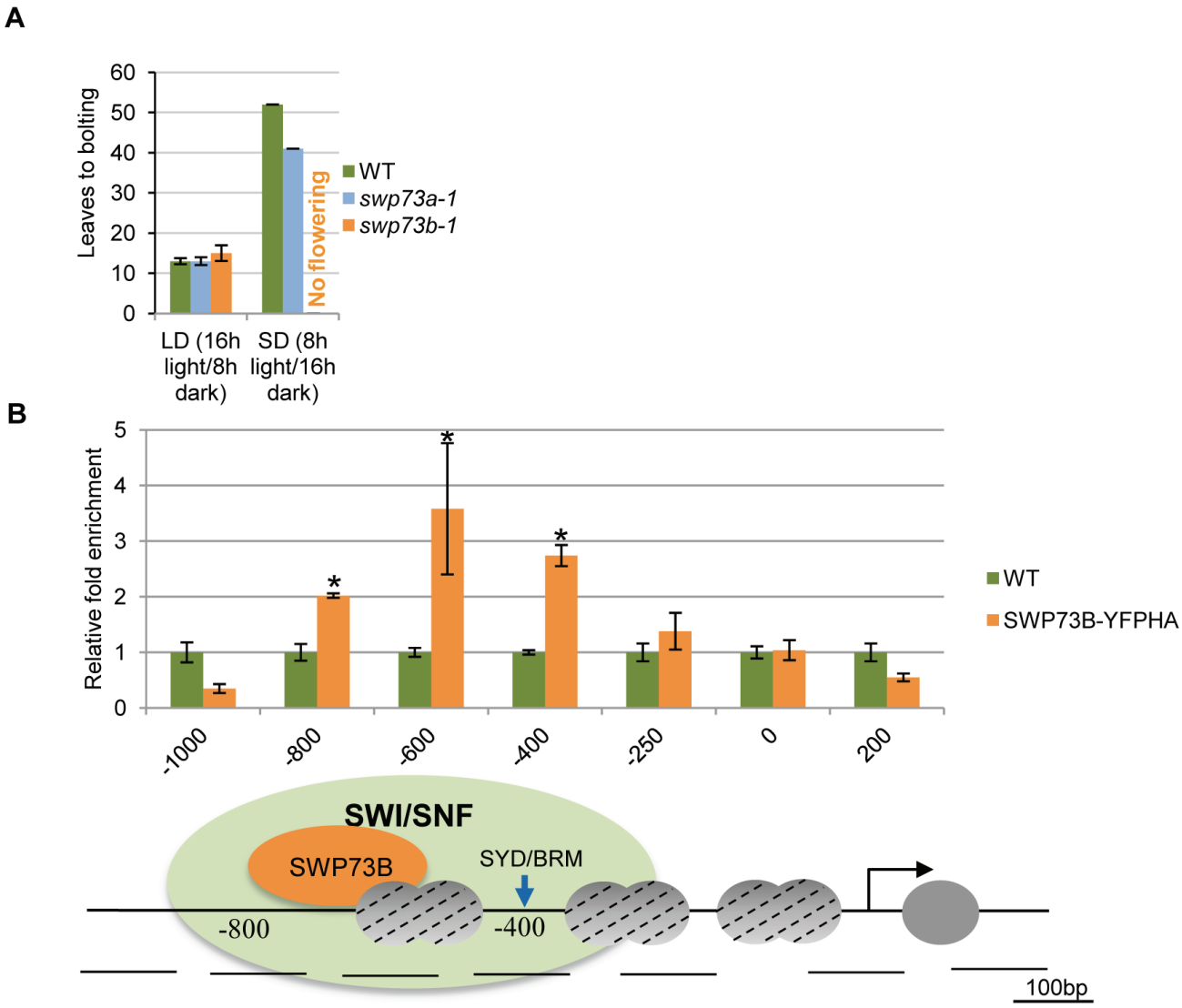

**Supplemental Figure 8.** qRT-PCR Measurement of Transcript Levels of AN3 Target Genes in the *swp73b* mutant and Detailed ChIP-qPCR Mapping of SWP73B in the Promoter Regions of *AS1* and *AS2*.

**(A)** qRT-PCR Analysis of Transcript Levels of AN3 Target Genes in the *swp73a* and *swp73b* Mutants.

**(B)** Results of ChIP-qPCR mapping of cross-linked SWP73B in the *AS1* promoter region (Upper panel) using the *TA3* retrotransposon as reference. Lower panel: Schematic presentation of SWP73B position in the *AS1* promoter. Lines indicate the location of primers used in ChIP-qPCR assays.

**(C)** ChIP-qPCR mapping of cross-linked SWP73B in the *AS2* promoter (Upper panel) using the *TA3* retrotransposon as reference. Lower panel: Schematic presentation of SWP73B location in the *AS2* promoter. Lines indicate the location of primers used in ChIP-qPCR assays.

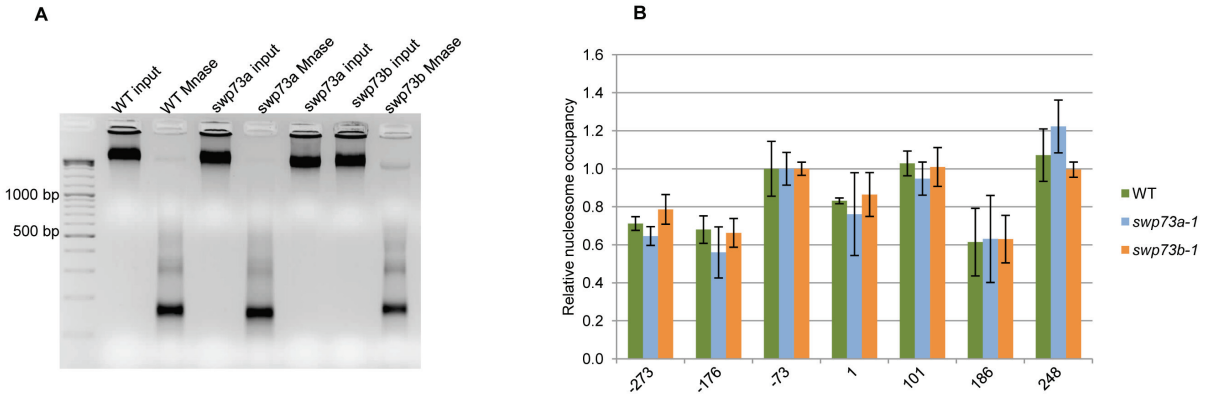
Three technical and three biological replicates were used, error bars refer to standard deviation, asterisks $P<0.05$.




**Supplemental Figure 9.** Flowering Time of *swp73a* and *swp73b* Mutants and Detailed SWP73B-YFP-HA ChIP Analysis of the *AP3* Gene.

**(A)** Flowering time as number of leaves at bolting of WT, *swp73a-1* and *swp73b-1* plants under LD and SD conditions At least 12 plants from each genotype were analyzed, error bars refer to standard deviation.

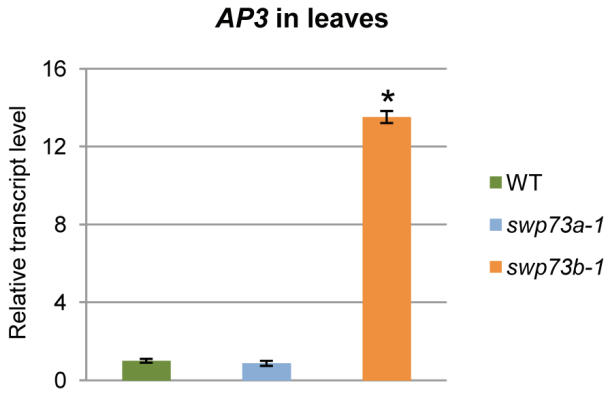
**(B)** Results of ChIP-qPCR mapping of cross-linked SWP73B in the *AP3* promoter region (Upper panel) using the *TA3* retrotransposon as reference. Three technical and three biological replicates were used, error bars refer to standard deviation, asterisk $P<0.05$. Lower panel: Schematic illustration of SWP73B (this work) and SYD/BRM (Wu et al. 2012) occupancy of *AP3* promoter. Lines indicate positions of primer pairs used for ChIP-qPCR.




**Supplemental Figure 10.** Controls for MNase Protection Assay of the *AP3* Promoter.

**(A)** Picture of agarose gel MNase digested DNA from MNase protection assay with the *AP3* promoter.

**(B)** The gypsy like retrotransposon (AT4G07700) (Kumar and Wigge, 2010) was used as the control in all MNase protection assays with the same DNA samples shown in Figure 5. The -73 region was used for normalization.



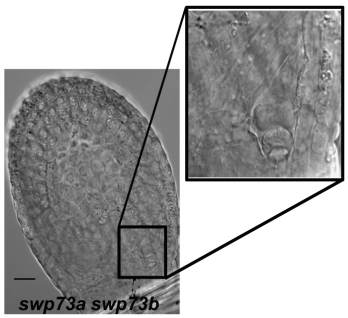

**Supplemental Figure 11**. Ectopic expression of AP3 in the *swp73b-1* mutant.
qRT-PCR analysis of *AP3* transcript levels in leaves of 2-weeks-old LD grown plants. Three technical and three biological replicates were used, error bars refer to standard deviation, asterisk $P<0.05$.

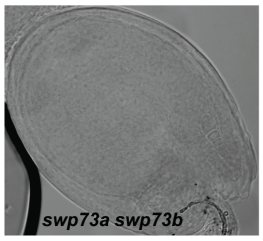
**A**

F2 progeny of self pollinated *swp73a/+ swp73b/+*

| Genotype | white aborted seeds (%) | arrested ovules (%) | n |
|---|---|---|---|
| **AABB** | 1.4 | 0.3 | 730 |
| **AABb** | 0.7 | 0.0 | 672 |
| **AaBB** | 1.6 | 0.0 | 495 |
| aa**BB** | 1.5 | 0.3 | 677 |
| **AaBb** | 6.3 | 2.4 | 891 |
| aa**Bb** | 17.1 | 7.0 | 1016 |
| **AA**bb | N/A | | |
| **A**abb | | | |
| aabb | | | |

**B**




**C**

| ♂ \ ♀ | **AB** |
|---|---|
| **AB** | 26% |
| **aB** | 39% |
| **Ab** | 29% |
| ab | 6% |

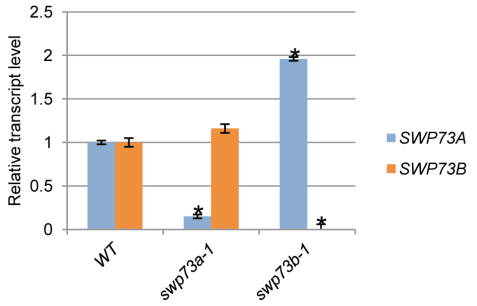
| ♂ \ ♀ | **aB** |
|---|---|
| **aB** | 65% |
| ab | 35% |

| ♂ \ ♀ | **aB** | **ab** |
|---|---|---|
| aB | 61% | 39% |

**D**

| Genotype | Expected segregation | Observed segregation | Phenotype |
|---|---|---|---|
| **AABB** | 6.25% | 12% | wt |
| **AABb** | 12.50% | 11% | |
| **AaBB** | 12.50% | 25% | |
| aa**BB** | 6.25% | 11% | |
| **AaBb** | 25% | 26% | |
| aa**Bb** | 12.50% | 9% | |
| **AA**bb | 6.25% | 3% | dwarfism |
| **A**abb | 12.50% | 3% | extreme dwarfism |
| aabb | 6.25% | | N/A |
| TOTAL | 100% | 100% | |

**E**




**Supplemental Figure 12**. SWP73A and *SWP73B* are Involved in Gametogenesis and Embryogenesis.

**(A)** Classification of progeny obtained by self pollination of *swp73a/+ swp73b/+* plants.

**(B)** Aborted embryos corresponding to double *swp73a swp73b* plants.

**(C)** Results of reciprocal crosses of *swp73a/+swp73b/+* with WT plants (left panel) and *swp73a swp73b/+* plant with *swp73a* plant (middle and right panel).

**(D)** Segregation of progeny of *swp73a/+ swp73b/+* plants indicates reduced *swp73a* and *swp73b* transmission.

**(E)** Inactivation of *SWP73A* does not influence the *SWP73B* expression but inactivation of *SWP73B* causes up-regulation of *SWP73A*. Three technical and three biological replicates were used, error bars refer to standard deviation, asterisks $P<0.05$.