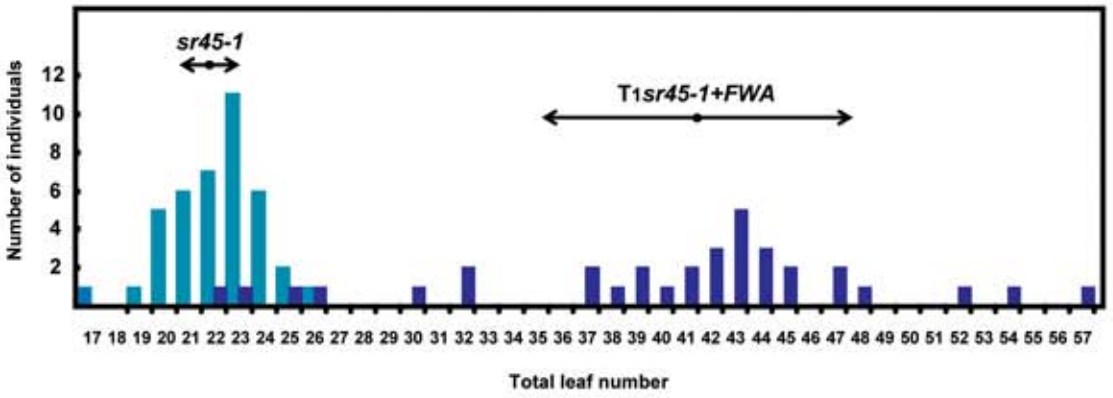
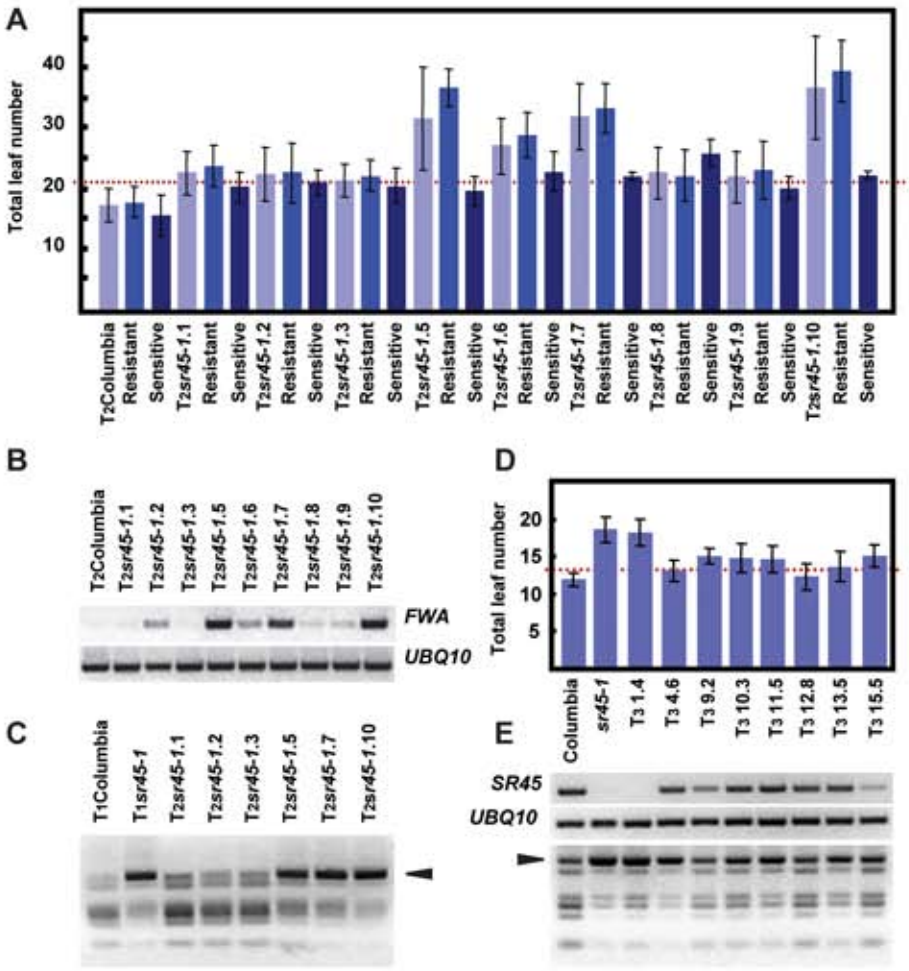
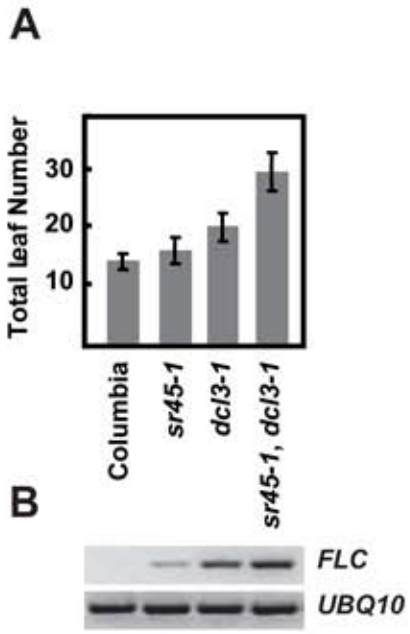


Supplementary Figure 1. Flowering time distribution of *sr45-1* versus *sr45-1+FWA*



Supplementary Figure 2. Confirmation of *sr45-1 de novo* phenotype. (A) Flowering time of randomly selected T_2 *sr45-1+FWA* transformants. *FWA* construct has a Basta® resistance gene as a selection marker that allows testing for the presence of *FWA* construct. Red-dotted line depicts the flowering time of untransformed *sr45-1* mutants grown under the same conditions. **(B)** RT-PCR showing *FWA* expression ofa selection of the above-mentioned lines. *UBQ10* expression is showed as a loading control. **(C)** Bisulfite cutting assay, showing *FWA* methylation status in the above-mentioned lines. Genomic DNA is digested with *BglII* to destroy the endogenous *FWA* gene before bisulfite treatment. DNA methylation of transgenic *FWA* was assayed by PCR from bisulfite-treated DNA followed by *ClaI* digestion. CG methylation protects the *ClaI* site from bisulfite conversion. Black arrow indicates the unmethylated size. **(D)** Flowering time of homozygous T_3 *sr45-1+SR45* complemented lines after *FWA* transformation. **(E)** RT-PCR and bisulfite cutting assay showing SR45 expression and partial restoration of methylation at *FWA*. *UBQ10* expression is showed as a loading control.



Supplementary Figure 3. *FLC* de-repression enhancement. (A) Flowering time of Columbia, *sr45-1*, *dcl3-1* and *sr45-1, dcl3-1* double mutant. **(B)** RT-PCR showing the expression of *FLC* in the above-mentioned lines. *UBQ10* expression is showed as a loading control.