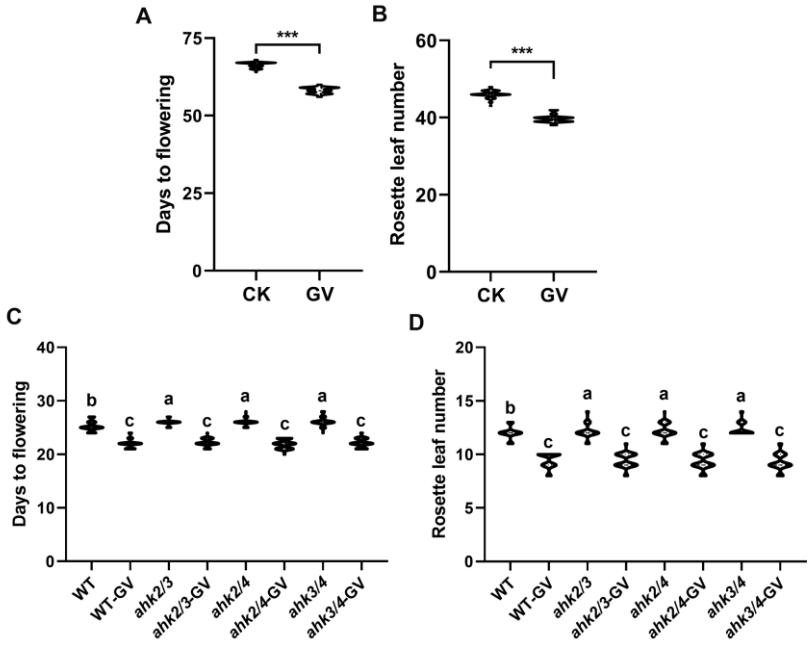
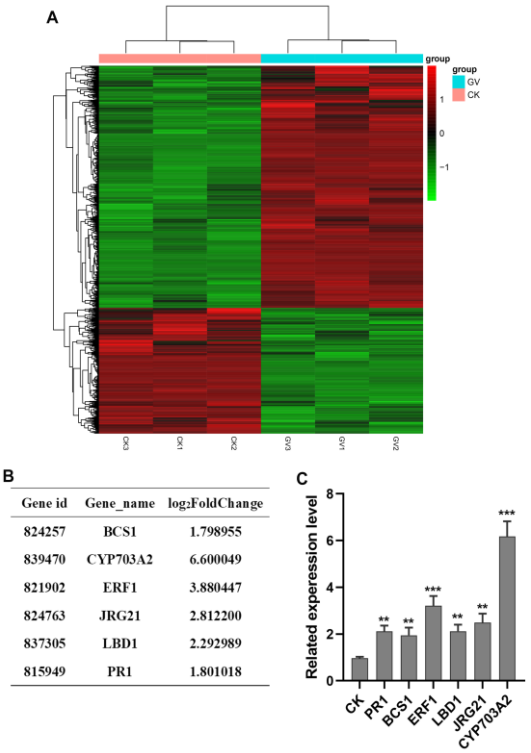


Figure S1 GV accelerates flowering in *Arabidopsis*. (A, B) Flowering phenotypes associated with GV treatment and CK as assessed by DTF (A) and RLN (B) grown under short day conditions. 7-week-old plants were sprayed with 50 mg L^{-1} GV and CK (0 mg L^{-1} GV). A significant difference analysis was Student's t-test (***, $p < 0.001$). (C, D) Flowering phenotypes of WT and three cytokinin receptor mutants ahk2/3, ahk2/4, and ahk3/4 associated with GV treatment as assessed by DTF (C) and RLN (D) grown under long day conditions. 2-week-old plants were sprayed with 50 mg l-1 GV and 0 mg L^{-1} GV treatment was used as a control. CK, control (treated with 0 mg L^{-1} GV). GV, 50 mg L^{-1} GV treatment. Different letters above the bars indicate statistically significant differences (adjusted $P < 0.05$, one-way ANOVA). Three biological replicates were counted with similar results. Values are expressed as means ± SD (n=15).



B

Gene id	Gene_name	log2FoldChange
824257	BCS1	1.798955
839470	CYP703A2	6.600049
821902	ERF1	3.880447
824763	JRG21	2.812200
837305	LBD1	2.292989
815949	PR1	1.801018

Figure S2 Analysis and validation of transcriptome data. (A) Clustering heat map of differentially expressed genes induced by GV. (B) The genes induced significantly by GV in our RNA-seq data. (C) Transcripts detection of genes in (A) by RT-qPCR. A significant difference analysis was Student's *t*-test (**, $p < 0.01$; ***, $p < 0.001$)

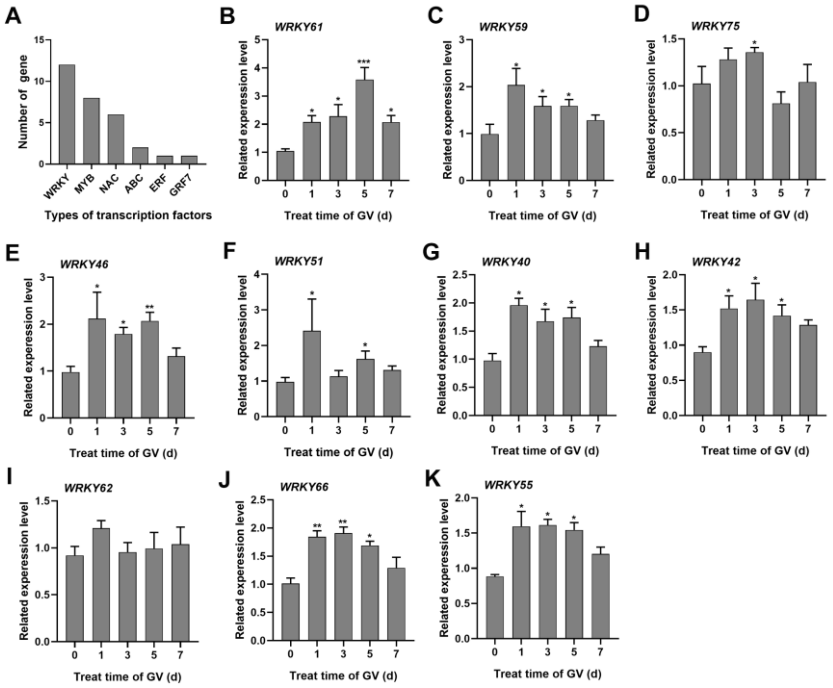


Figure S3 WRKY TFs were induced by GV. (A) The number of major transcription factor genes induced by GV. (B-K) The related transcript levels of *WRKY61* (B), *WRKY59* (C), *WRKY75* (D), *WRKY46* (E), *WRKY51* (F), *WRKY40* (G), *WRKY42* (H), *WRKY62* (I), *WRKY66* (J), and *WRKY55* (K) at 0, 1, 3, 5, and 7 d after 50 mg L^{-1} and 0 mg L^{-1} GV treatment. The WRKY TFs induced by GV at log_2FoldChange ≥ 1.5 were included in this analysis. Each experiment was repeated three times with similar results. Values are expressed as means ± SD (n=3). A significant difference analysis was Student's *t*-test (*, $p < 0.05$; **, $p < 0.01$, ***, $p < 0.001$).

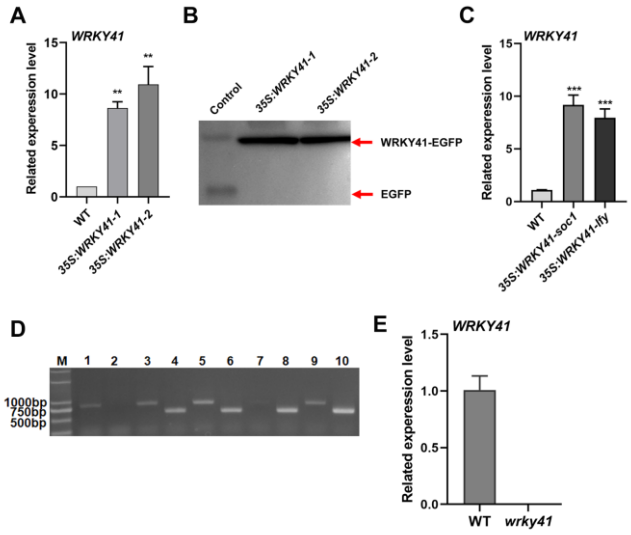


Figure S4 Validation of *WRKY41* transgenic lines and T-DNA insertion mutants. (A) The related transcript levels of *WRKY41* in two *35S:WRKY41* lines. Similar results were obtained from three replicates. (B) Western blot analysis of two *35S:WRKY41*-GFP lines. Control, EGFP protein. (C) The related transcript levels of *WRKY41* in two *35S:WRKY41-soc1* and *35S:WRKY41-lfy* lines. (D) Validation of *WRKY41* T-DNA insertion mutants using the three primers. LP+BP included 1, 3, 5, 7, and 9 Lanes. BP+RP included 2, 4, 6, 8, and 10 Lanes. LP, RP: Left, Right genomic primer. BP: T-DNA border primer. M, DNA marker. 1-2, WT. 3-10, *wrky41* lines. Lanes 7 and 8 represent the homozygous lines; lanes 3 4, 5 6, 9 10 represent the heterozygous lines. (E) The related transcript levels of *WRKY41* in *wrky41* lines. Values are expressed as means ± SD (n=3). A significant difference analysis was Student's *t*-test (**, $p < 0.01$, ***, $p < 0.01$).

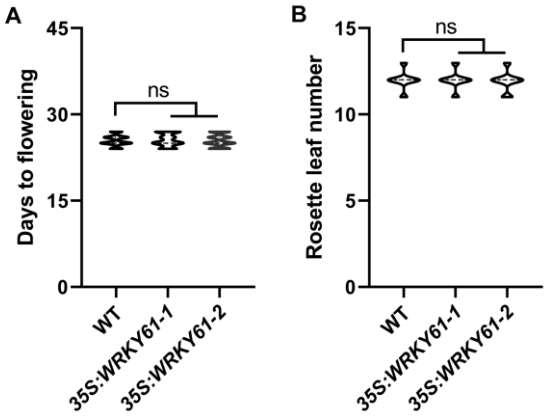


Figure S5 The flowering phenotype of *35S:WRKY61*. (A, B) The flowering phenotypes of *35S:WRKY61* were assessed by DTF (A) and RLN (B), respectively. Three biological replicates were counted with similar results, respectively. Values are expressed as means ± SD (n=15). A significant difference analysis was Student's *t*-test (ns, not significant).

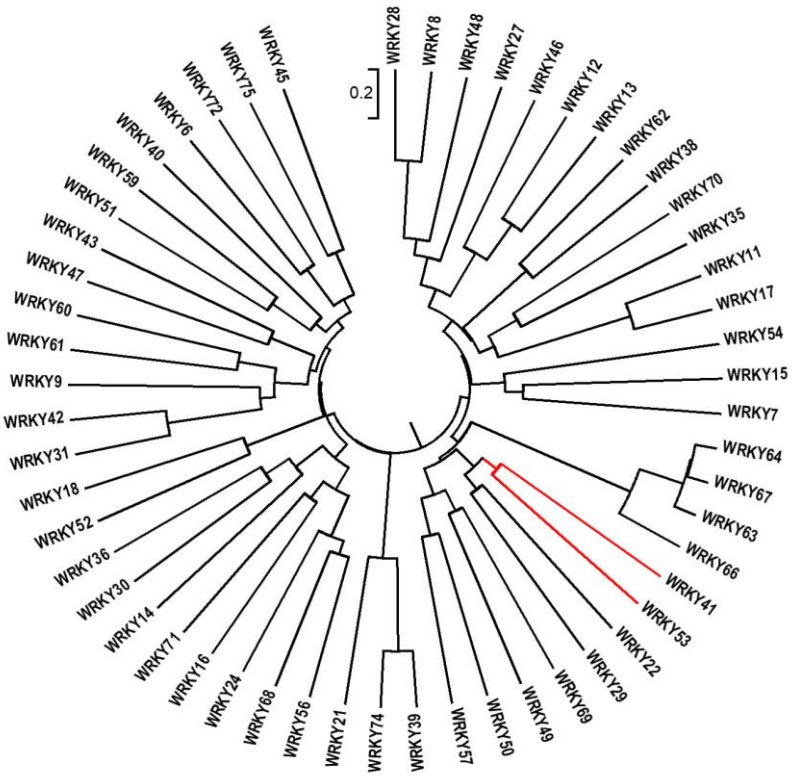


Figure S6 Phylogenetic tree of *Arabidopsis* WRKY TFs. The *Arabidopsis* WRKY genes were obtained in NCBI GenBank (https://www.ncbi.nlm.nih.gov/gene/). Then the phylogenetic tree was constructed using MEGA6 Software. Distance scale = 0.2. The red branch represents *WRKY41* and *WRKY53*.

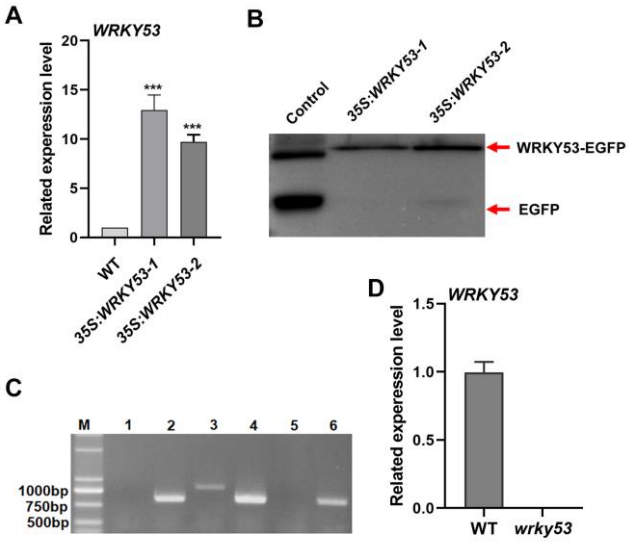


Figure S7 Validation of *WRKY53* transgenic lines and T-DNA insertion mutants. (A) The related transcript levels of *WRKY53* in two *35S:WRKY53* lines. Values are expressed as means ± SD (n=3). Similar results were obtained from three replicates. (B) Western blot analysis of two *35S:WRKY53*-GFP lines. Control, EGFP protein. (C) Validation of *WRKY53* T-DNA insertion mutants using the three primers. LP+BP included 1, 3, and 5 Lanes. BP+RP included 2, 4, and 6 Lanes. LP, RP: Left, Right genomic primer. BP: T-DNA border primer. M, DNA marker. 1-2, WT. 3-6, *wrky53* lines. Lanes 1-2, and 5-6 represent the homozygous lines; lanes 3-4 represent the heterozygous lines. (D) The related transcript levels of *WRKY53* in *wrky53* lines. A significant difference analysis was Student's *t*-test (***, $p < 0.01$).

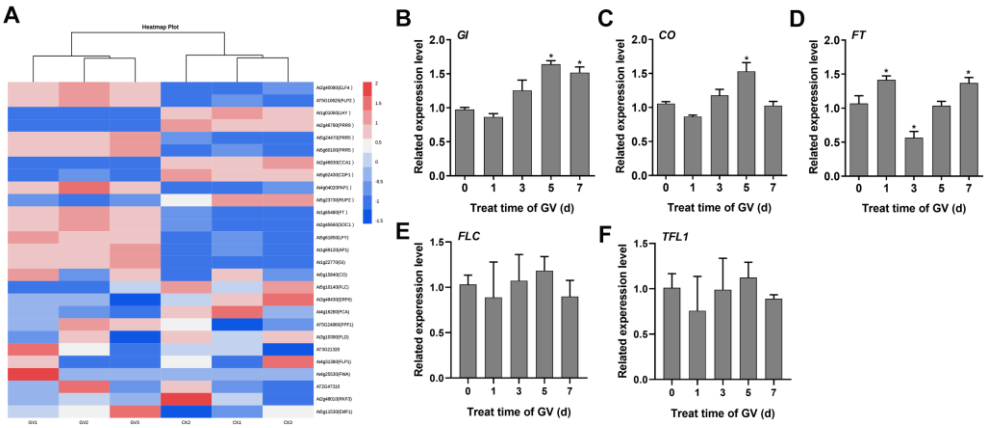


Figure S8 Analysis and validation of flowering regulatory gene expression induced by GV. (A) Clustering heat map of differentially expressed flowering-related genes induced by GV. (B-F) The relative expression level of the key flowering regulatory genes *GI* (B), *CO* (C), *FT* (D), *FLC* (E), and *TFL1* (F). Samples were collected at 0, 1, 3, 5, and 7 d after the treatment of 50 mg l^{-1} GV and control (treated with 0 mg L^{-1} GV). Each experiment was repeated three times with similar results. Values are expressed as means ± SD (n=3). A significant difference analysis was Student's *t*-test (*, $p < 0.05$).

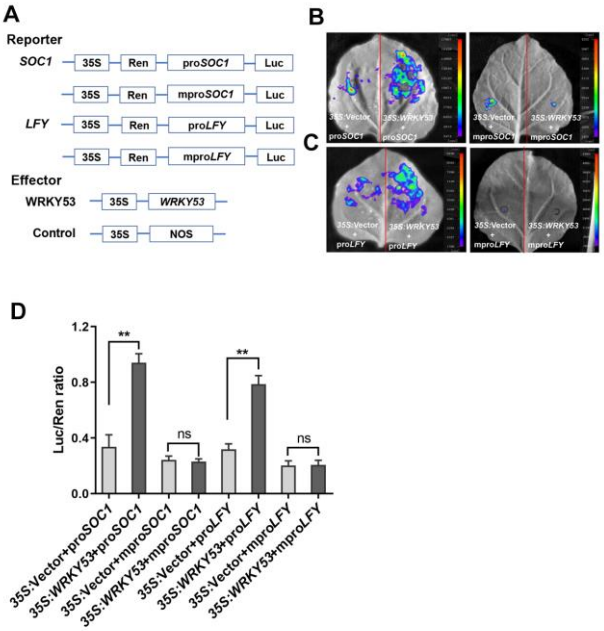


Figure S9 WRKY53 directly activates the transcription of *SOC1* and *LFY*. (A) The constructs were used for the transient transcriptional activity assay. The native and mutant promoters of *SOC1* and *LFY* were used as reporters, respectively. WRKY53 was used as an effector. (B) Transcription activation detection between WRKY53 and the pro*SOC1* (B left) and mpro*SOC1* (B right). (C) Transcription activation detection between WRKY53 and pro*LFY* (C left) and mpro*LFY* (C right). WRKY53 activated the expression of luciferase driven by the *SOC1* and *LFY* promoters. (D) Luc:Ren ratio after WRKY53 activated the transcription of *SOC1* and *LFY*. pro*SOC1*/pro*LFY*, the native promoter of *SOC1*/*LFY*. mpro*SOC1*/mpro*LFY*, the mutant promoter of *SOC1*/*LFY*. All experiments were repeated three times with similar results. Values are expressed as means ± SD (n=3). A significant difference analysis was Student's *t*-test (**, $p < 0.01$, ns, not significant).

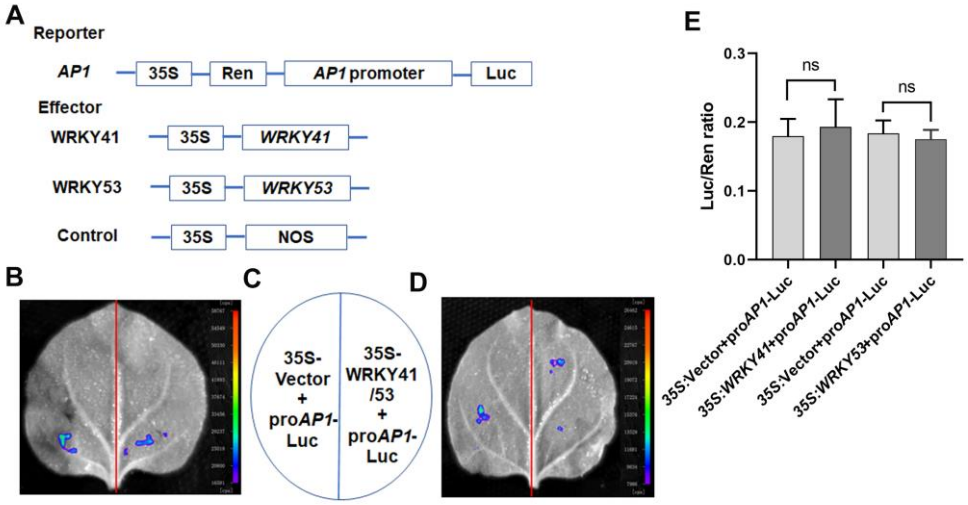


Figure S10 WRKY41 and WRKY53 do not activate the transcription of *AP1*. (A) The constructs were used for the transient transcriptional activity assay. The promoters of *AP1* were used as reporters. WRKY41 and WRKY53 were used as the effectors. (B, D) Transcription activation detection between WRKY41 (B) and WRKY53 (D) and *AP1* promoter by transient expression in *Nicotiana benthamiana*, respectively. (C) Distribution map of each treatment on *Nicotiana benthamiana* leaves. (E) Luc:Ren ratio detection after WRKY41 and WRKY53 acting on *AP1* promoter, respectively. All experiments were repeated three times with similar results. Values are expressed as means ± SD (n=3). A significant difference analysis was Student's *t*-test (ns, not significant).

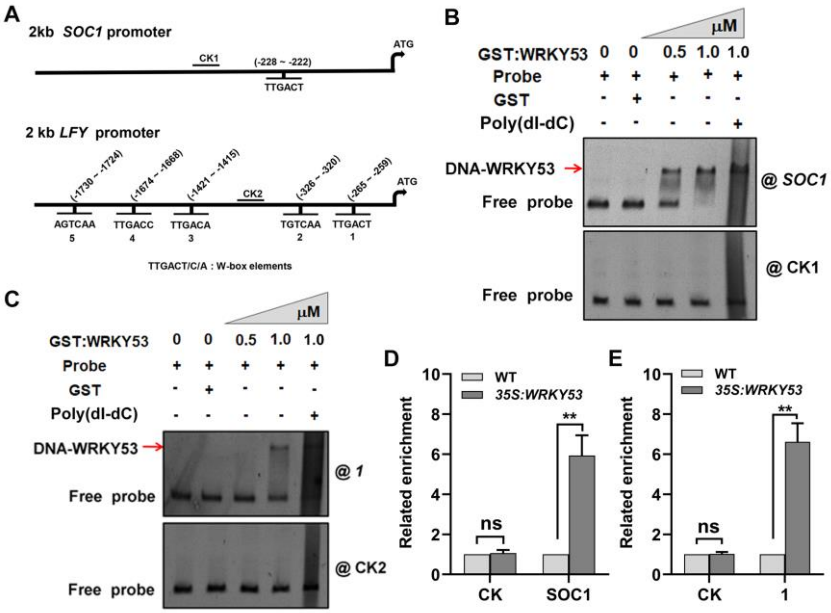


Figure S11 WRKY53 directly binds to the *SOC1* and *LFY* promoters. (A) The 2-kb promoters and *SOC1* and *LFY* fragments were used in EMSA. (-228~ -222), The position of the W-box in the *SOC1* promoter. 1, 2, 3, 4, and 5 represent the W-boxes located at (-265 ~ -259), (-326 ~ -320), (1421 ~ -1415), (-1674 ~ -1668), and (-1730 ~ -1724) bp in the *LFY* promoter. (B, C) GST-WRKY53 directly bound the W-box at (-228~ -222) bp in the *SOC1* promoter (B) and (-265 ~ -259) bp in the *LFY* promoter (C). 100-fold non-specific poly(dI-dC) was used to exclude non-specific binding between protein and probes. CK1 and CK2, negative control. (D, E) Enrichment of the W-box in the *SOC1* promoter (D) and 1 in the *LFY* promoter (E) as demonstrated by ChIP-qPCR. Samples were collected from three-week-old *35S:WRKY53* plants. The plus (+) and minus (-) symbols indicate the presence and absence of the indicated components. Arrows indicate band shifts. The triangle symbol indicates an increased concentration of GST-WRKY53. All experiments were repeated three times with similar results. Values are expressed as means ± SD (n=3). A significant difference analysis was Student's *t*-test (ns, not significant; **, $p < 0.01$).

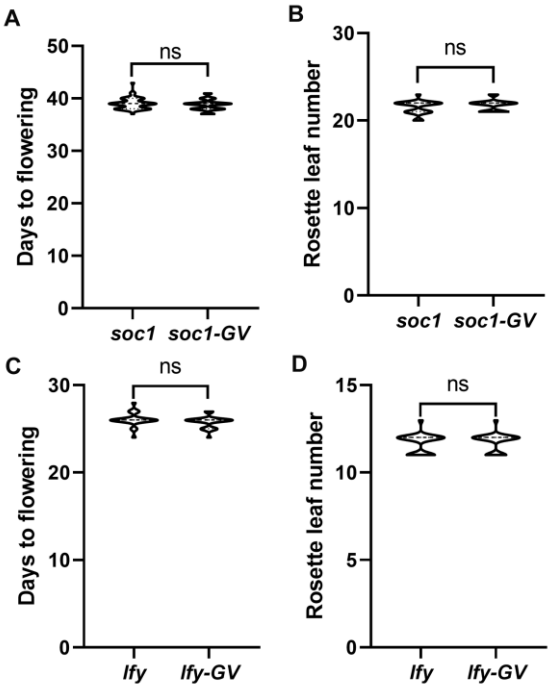


Figure S12 The flowering phenotype of *soc1* and *lfy* mutants induced by GV. (A, B) The flowering phenotypes of *soc1* treated without and with 50 mg L^{-1} GV were assessed by DTF (A) and RLN (B), respectively. (C, D) The flowering phenotypes of *lfy* were assessed by DTF (C) and RLN (D) after 50 mg l^{-1} GV-treated. 0 mg L^{-1} GV treatment was used as a control. Three biological replicates were counted with similar results. Values are expressed as means ± SD (n=15). A significant difference analysis was Student's t-test (ns, not significant).