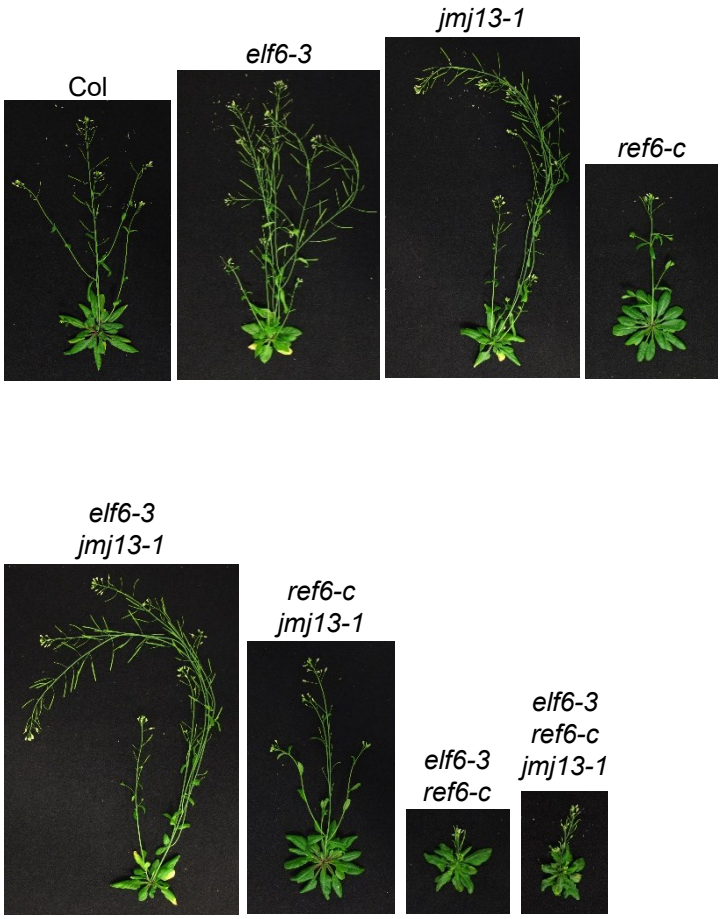

Figure S1. Pictures of histone demethylases mutant combination. Representative images of single, double, and triple mutant combinations of ELF6, JMJ13, and REF6. Photographs were taken of mature plants grown at 22°C under long-day conditions at the same developmental stage.

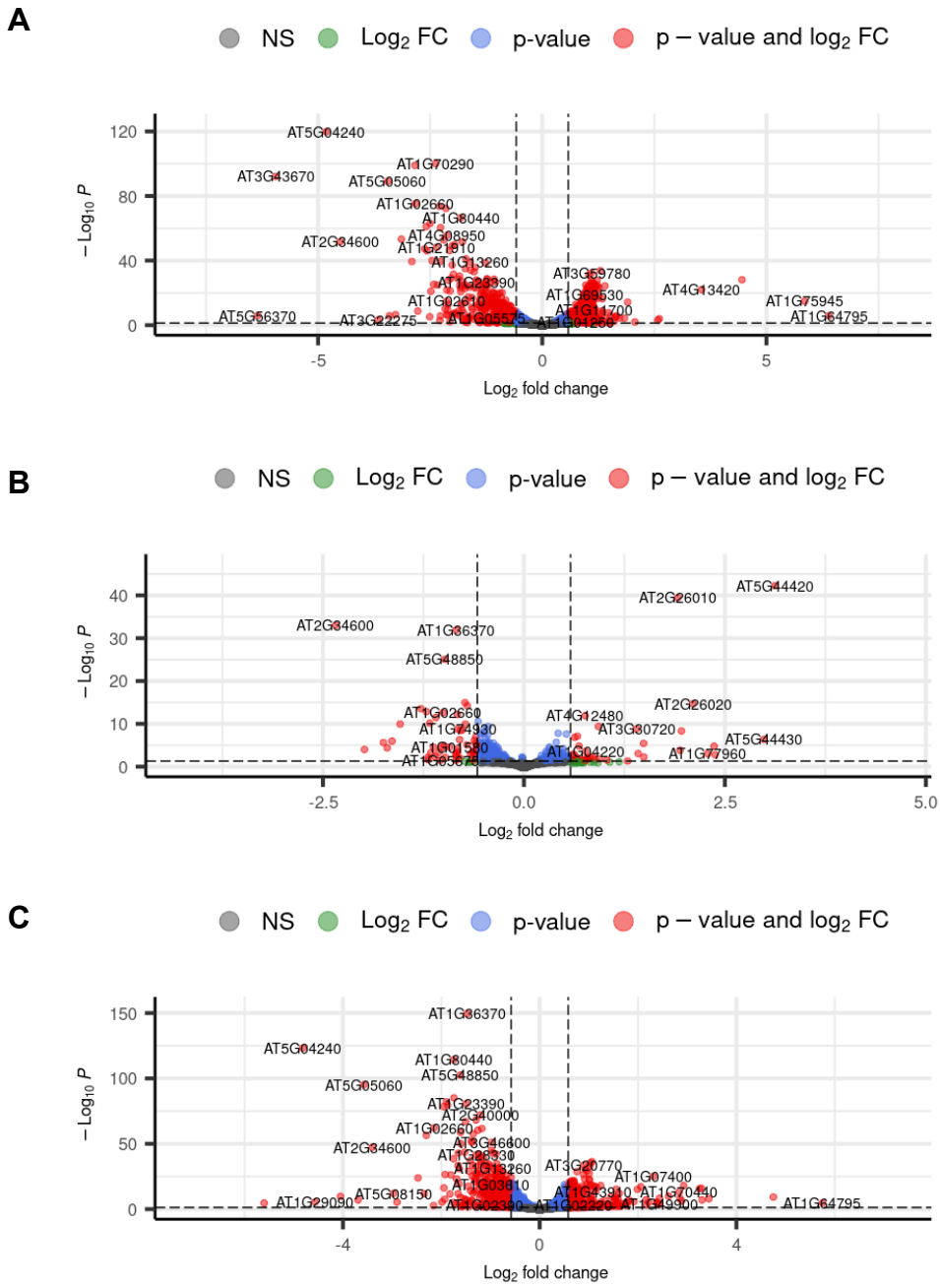

Figure S2. Transcriptomic analysis reveals ELF6's primary role and JMJ13's partial redundancy. **A-C**) Volcano plot showing the differentially expressed genes in *elf6-3* **(A)**, *jmj13-1* **(B)** and *elf6-3 jmj13-1* **(C)** compared to the wild type. Significantly misregulated genes (p-adj ≤ 0.1; $|\log_2 FC| \geq 0.5$) are highlighted in red.

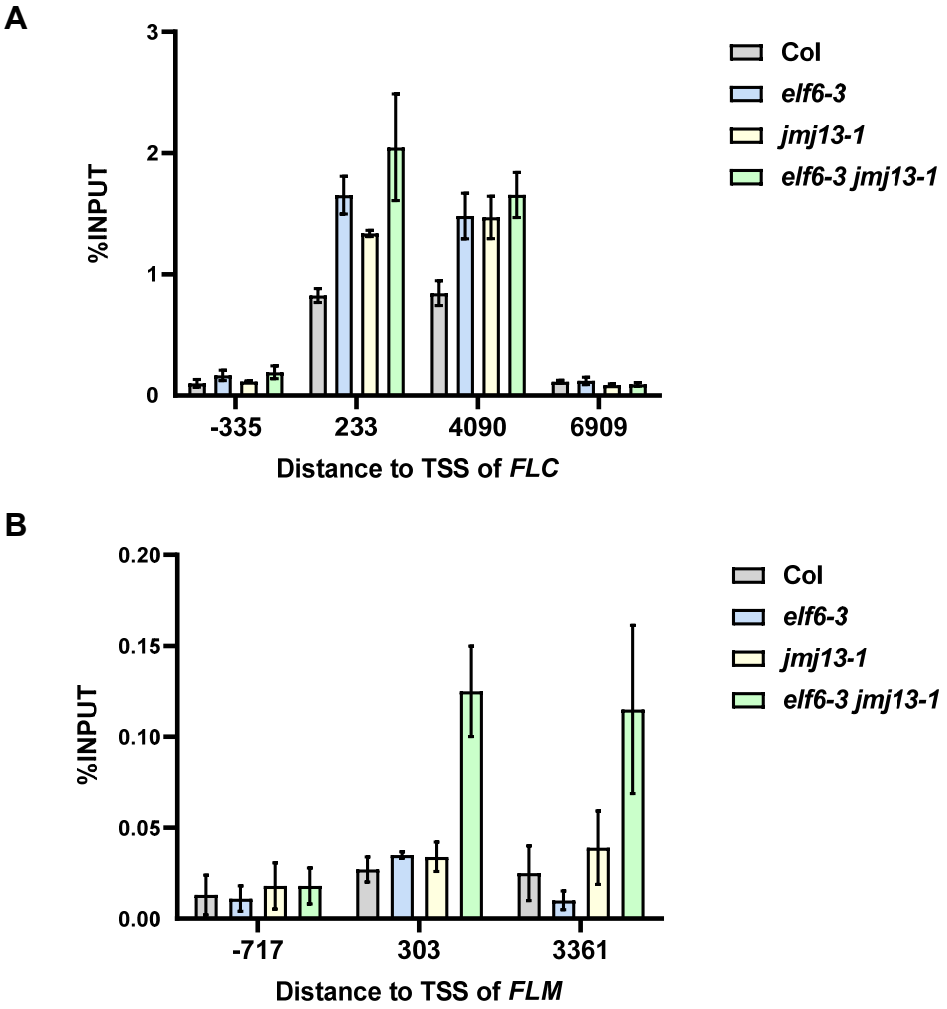

Figure S3. ELF6 and JMJ13 control H3K27me3 levels at *FLC*-clade genes. A-C) H3K27me3 ChIP data for *FLC* **(A)** and *FLM* **(B)** in Col, *elf6-3, jmj13-1* and *elf6-3 jmj13-1*. Seedlings were grown at standard conditions and harvested 9 days after sowing. Error bars indicate ± s.e.m. (n = 3 biological replicates).

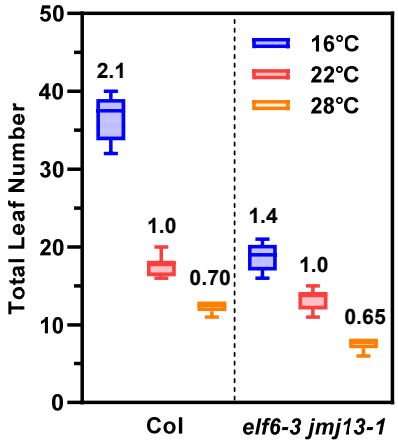

Figure S4. Flowering time of *elf6-3 jmj13-1* at different ambient temperatures. Flowering time experiments of wild-type (Col) and *elf6-3 jmj13-1* mutant plants growing at high ambient temperature (28°C) and low ambient temperature (16°C), compared to standard laboratory conditions (22°C). The numbers above each box plot represent the ratio of the average flowering time at 16°C or 28°C to the flowering time at 22°C.

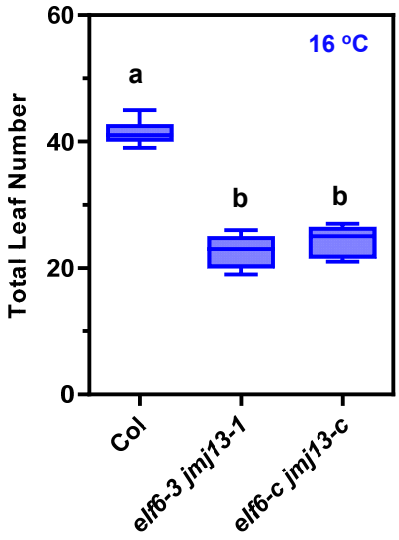

Figure S5. Flowering time of CRISPR/cas9 alleles. Flowering time of the *elf6-3 jmj13-1* double mutant and the independent CRISPR/Cas9 loss-of-function double mutant *elf6-c jmj13-c* grown at 16°C. Statistical significance was assessed using one-way ANOVA with Tukey's test for multiple comparisons (n = 12). Different letters indicate significant differences ($P < 0.05$), while the same letters denote no significant differences.

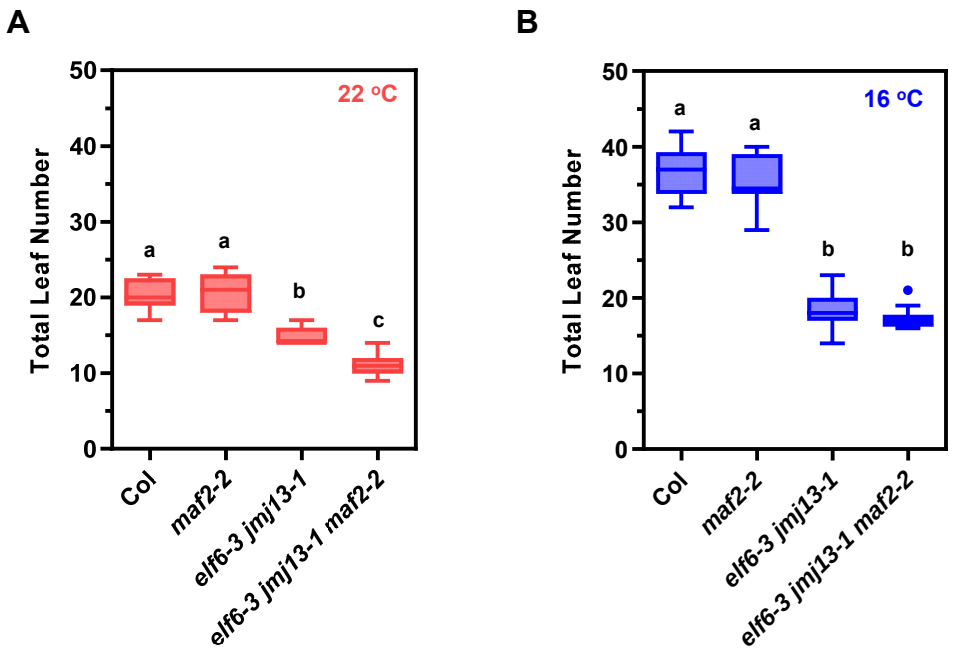

Figure S6. *MAF2* is dispensable for the low-temperature response of *elf6-3 jmj13-1*. Flowering time data for different genotypes including the *elf6-3 jmj13-1 maf2-2* triple mutant grown at 22°C **(A)** or 16°C **(B).** Statistical significance was assessed using one-way ANOVA with Tukey's test for multiple comparisons (n = 12). Different letters indicate significant differences ($P < 0.05$), while the same letters denote no significant differences.

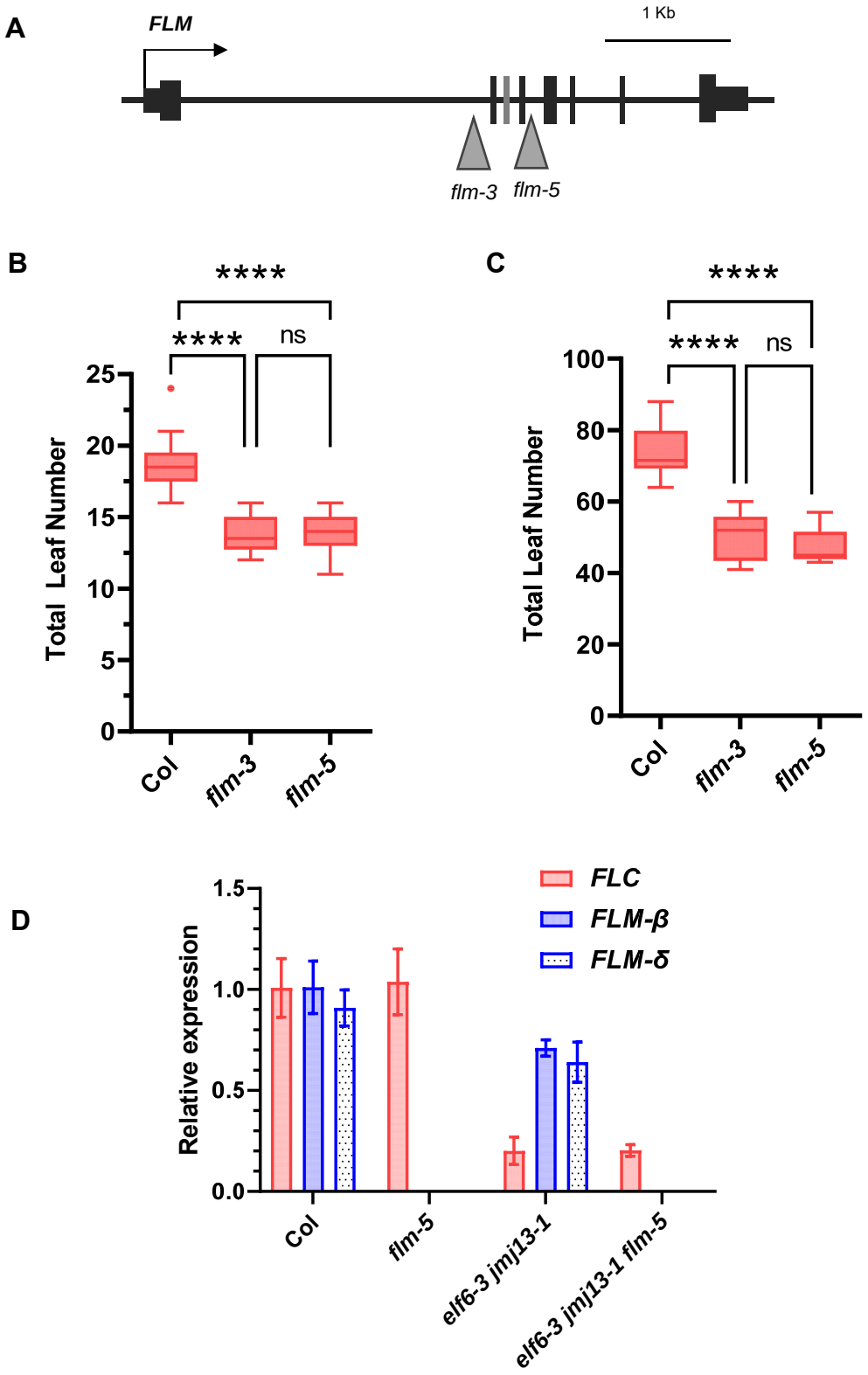

Figure S7. The mutant *flm-5* is a knockout allele. A) The *flm-5* allele carries a T-DNA insertion in the second exon that impairs *FLM* gene expression and affects flowering time. **C-D)** Flowering time data comparing *flm-3* and *flm-5* flowering time under long-day and standard temperature conditions **(C)** and short day **(D)** photoperiod conditions (n = 12). Statistical significance was assessed using a two-tailed t-test (*** P < 0.0001). **E)** RT-qPCR data for *FLC*, *FLM-β*, and *FLM-δ* in Col, *flm-5, elf6-3 jmj13-1,* and triple mutant *elf6-3 jmj13-1 flm-5*. Data for each gene was calculated relative to UBC and normalized to the value of Col. Error bars indicate ± s.e.m. (n = 3 biological replicates).

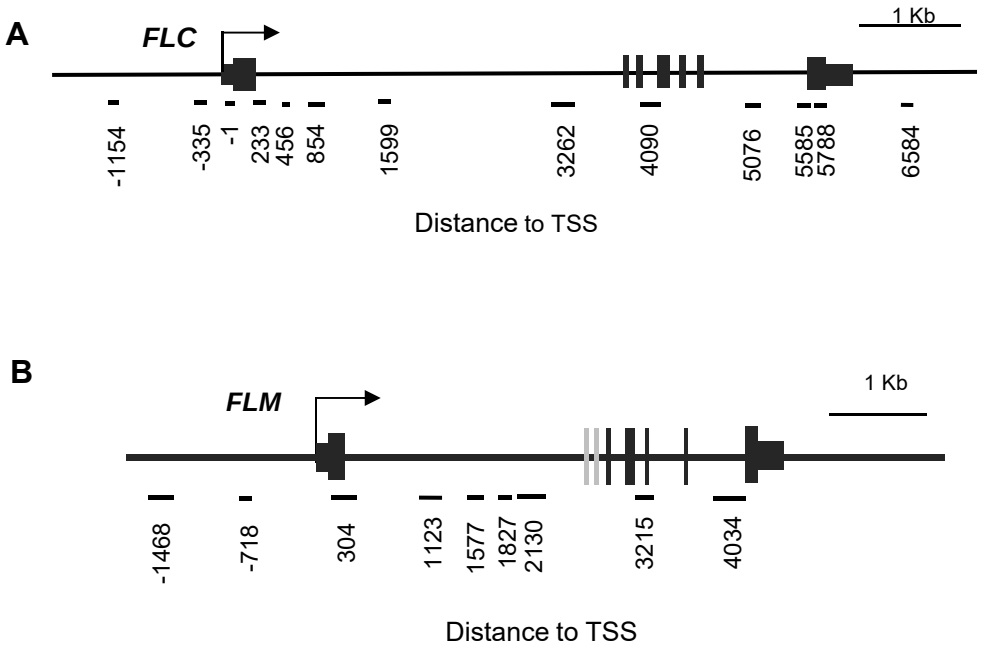

Figure S8. Schematic representation of *FLC* and *FLM* loci. A-B) Cartoon indicating the regions analyzed by ChIP at *FLC* **(A)** and *FLM* **(B)**. The numbers indicate the position of PCR amplicons analyzed relative to the transcriptional start site (TSS) the gene. Exons 2 and 3 of *FLM*, which determine the *FLM-β* and *FLM-δ* isoforms, respectively, are highlighted in light gray.

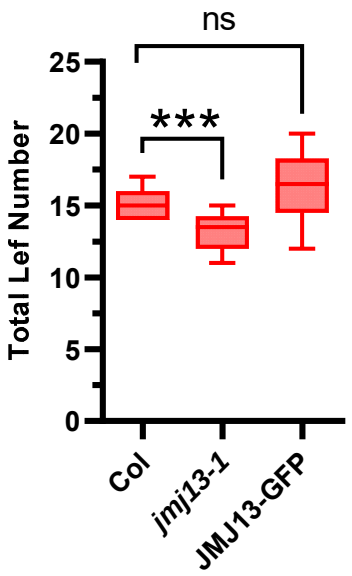

Figure S9. JMJ13-GFP is a functional complementing lines. A) Flowering time data of the transgenic line JMJ13-GFP compared to the wild type and the *elf6-3* and *jmj13*-1 single mutants (n = 12). Statistical significance was assessed using a two-tailed t-test (**** $P < 0.0001$, ns means not significant).

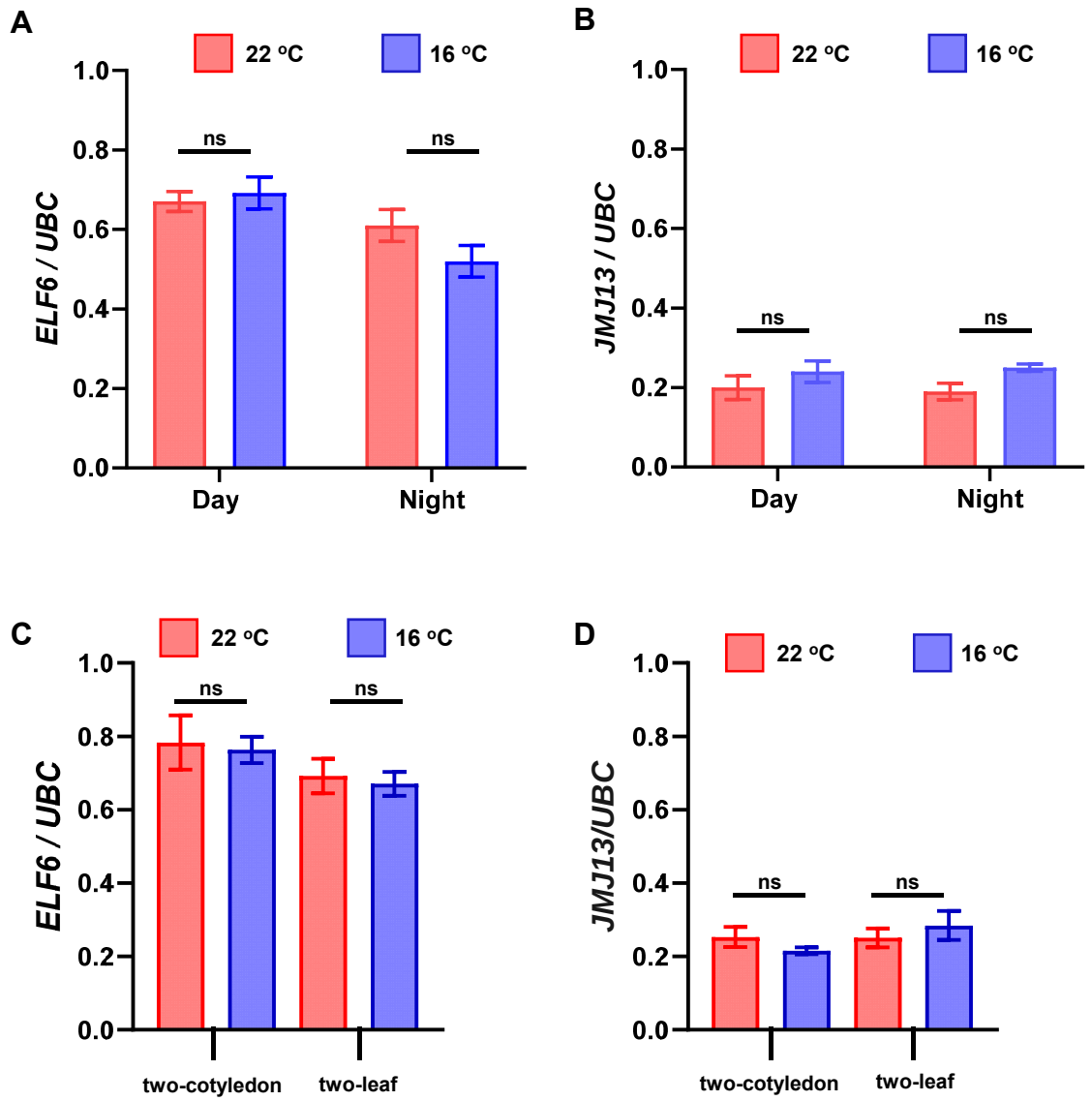

Figure S10. *ELF6* and *JMJ13* gene expression do not change in response to ambient temperature. RT-qPCR data for *ELF6* **(A, C)** and *JMJ13* **(B, D)** in Col seedlings. **A-B)** Plants were grown under long-day conditions at 16 °C or 22 °C and harvested at the two-leaf stage at the middle of the day or night period. Error bars indicate ± s.e.m. (n = 4 biological replicates) Statistical significance was assessed using a two-tailed t-test (ns means not significant). **C-D)** Plants were grown under long-day conditions at 16 °C or 22 °C and harvested at the end of the day at either the two-cotyledon or two-leaf stage Error bars indicate ± s.e.m. (n = 4 biological replicates) Statistical significance was assessed using a two-tailed t-test (ns means not significant).

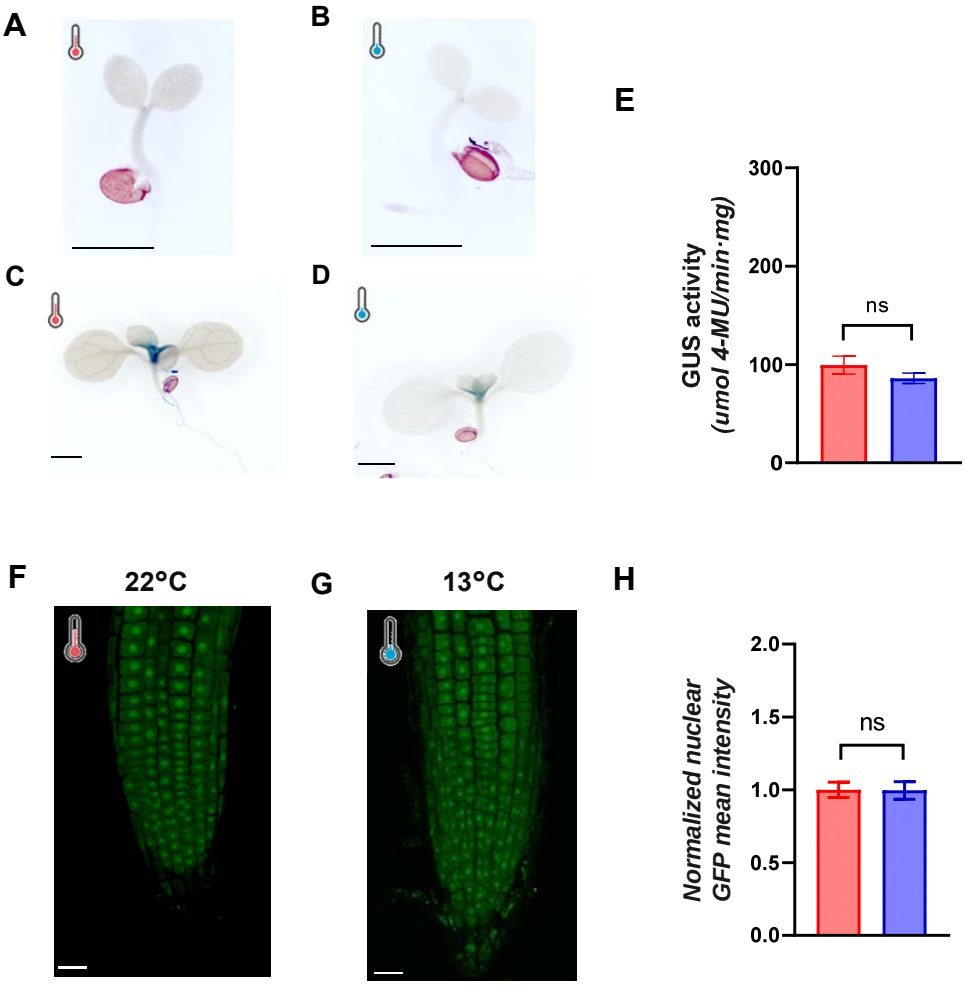

Figure S11. JMJ13 protein levels does not change in response to temperature. A-D) Histochemical staining of JMJ13-GUS seedlings at two-cotyledon **(A, B)** or two-leaf **(C-D)** developmental stage seedlings grown at 22ºC **(A, C)** or 16ºC **(B, D).** Scale bars = 10mm. **B)** Fluorometric GUS assay of two-cotyledon stage of JMJ13-GUS seedlings grown at 22ºC or 16ºC. Error bars indicate ± s.e.m. (n = 14 biological replicates). **F)-G)** Confocal images of JMJ13-GFP in roots of two-cotyledon stage seedlings grown at 22 °C **(F)** or 13ºC **(G)** Quantification of JMJ13–GFP nuclear mean fluorescence intensity in root epidermal cells. Mean signal per root was normalized to the 22 °C mean intensity. Error bars indicate ± s.e.m. (n = 6 biological replicates, ~100 nuclei per replicate). Statistical significance was assessed using a two-tailed t-test (*** $P < 0.0005$).