

Supplementary Figures

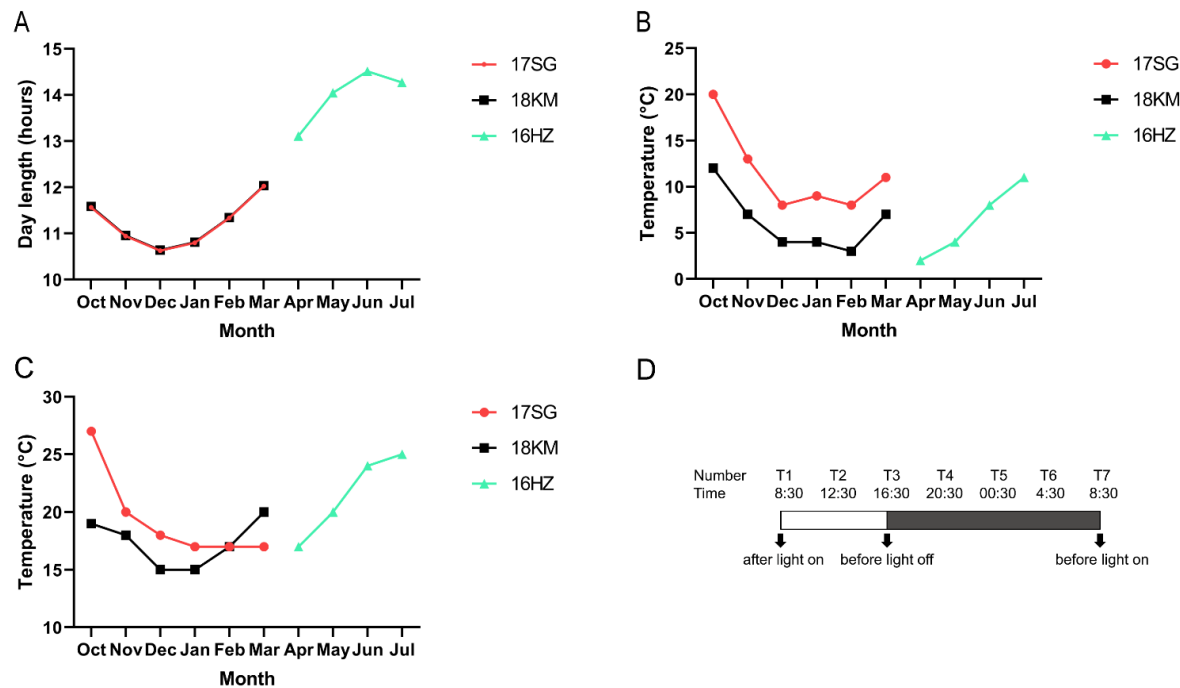


Figure S1. Average day length, temperature, and RNA-seq sampling diagram. Monthly average day length (A) and monthly average minimum (B) and maximum (C) temperature in three environments, and RNA-seq sampling diagram (D). Day length data was obtained from <https://richurimo.51240.com/>, and temperature data from <http://www.tianqi.com/>. T1-T7 represents seven sampling time-points during a day.

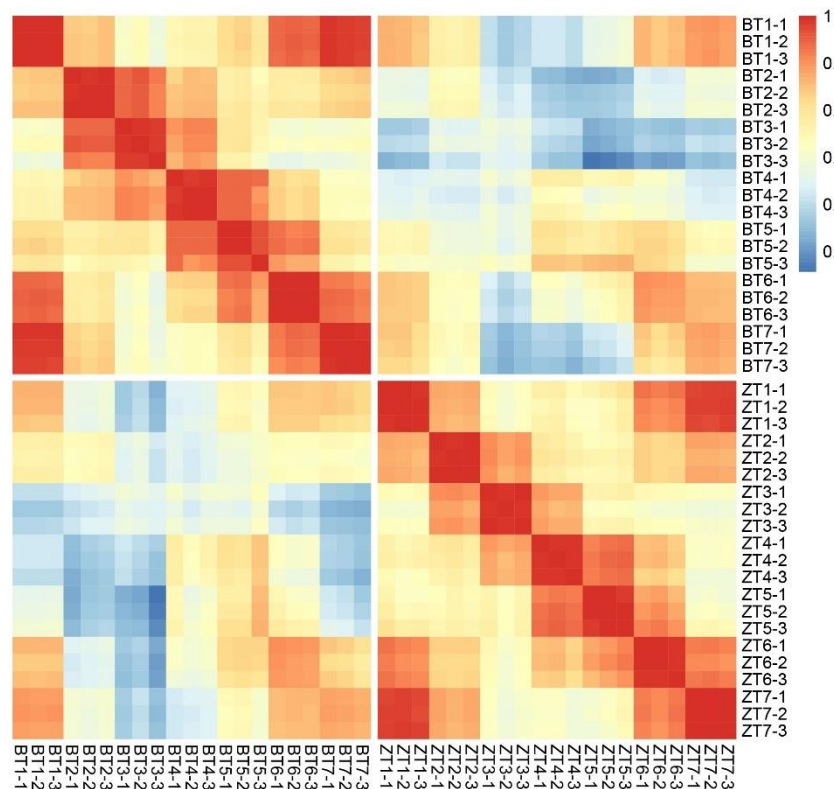


Figure S2. Heat map for correlation between RNA sequencing samples. Redder color indicates higher correlation between samples. B represents B409; Z represents ZS8; T1-T7 represent sampling time-points, -1, -2, -3 represent three biological replicates at each time-point.

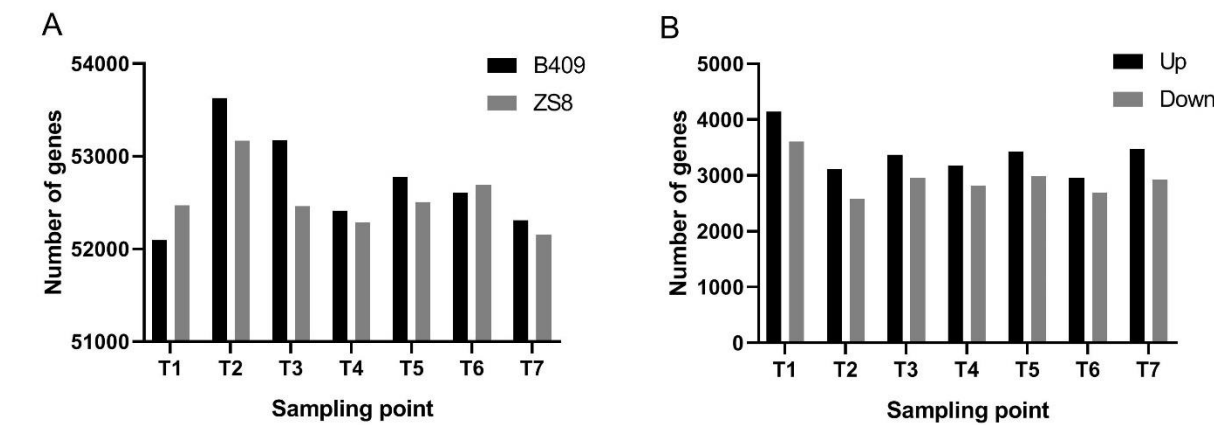


Figure S3. Column chart of gene expression. Number of genes expressed (A) and differentially expressed (B) at each time-point in RNA-seq data.

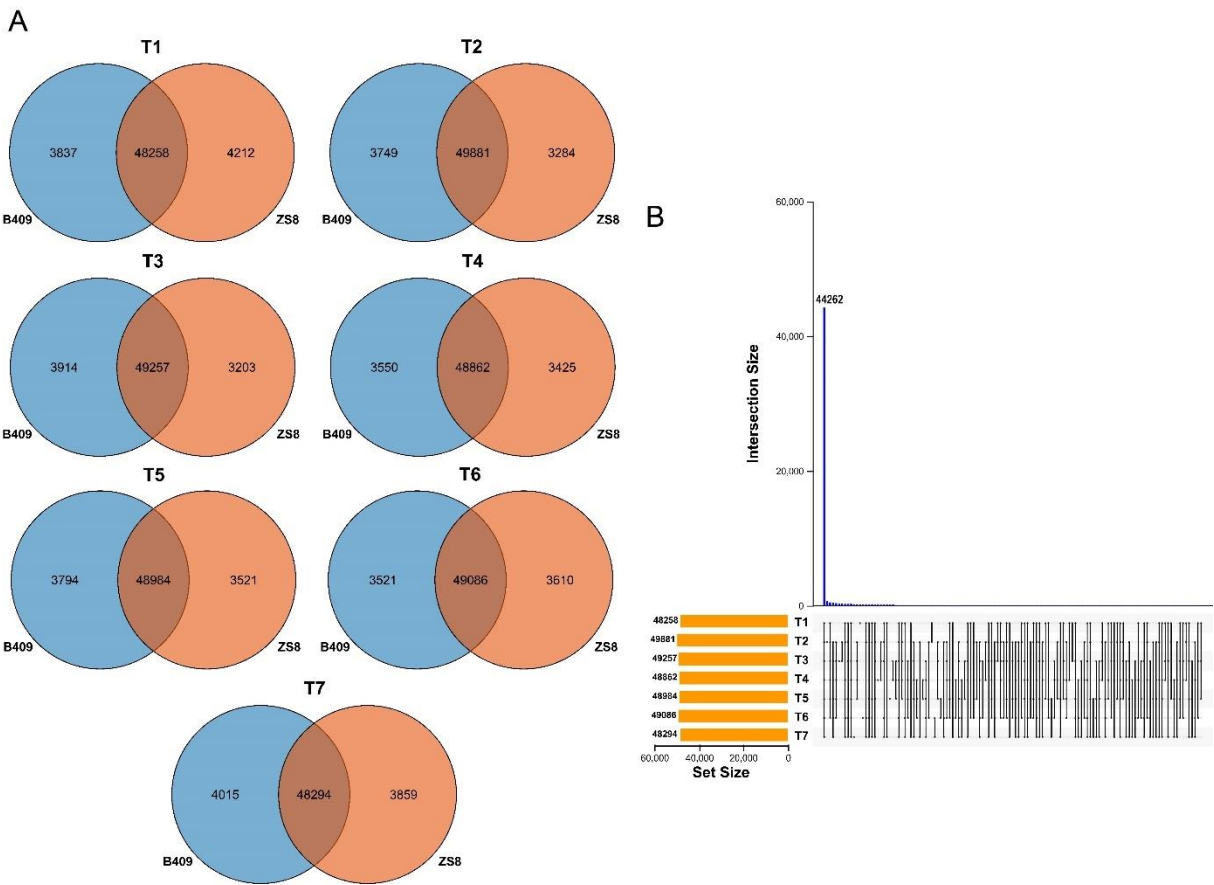


Figure S4. Venn diagram of expressed genes in B409 and ZS8. (A)Venn diagram of genes expressed in B409 and ZS8 at each time-point, and (B) UpSet Venn diagram of commonly expressed genes in B409 and ZS8 at each time-point.

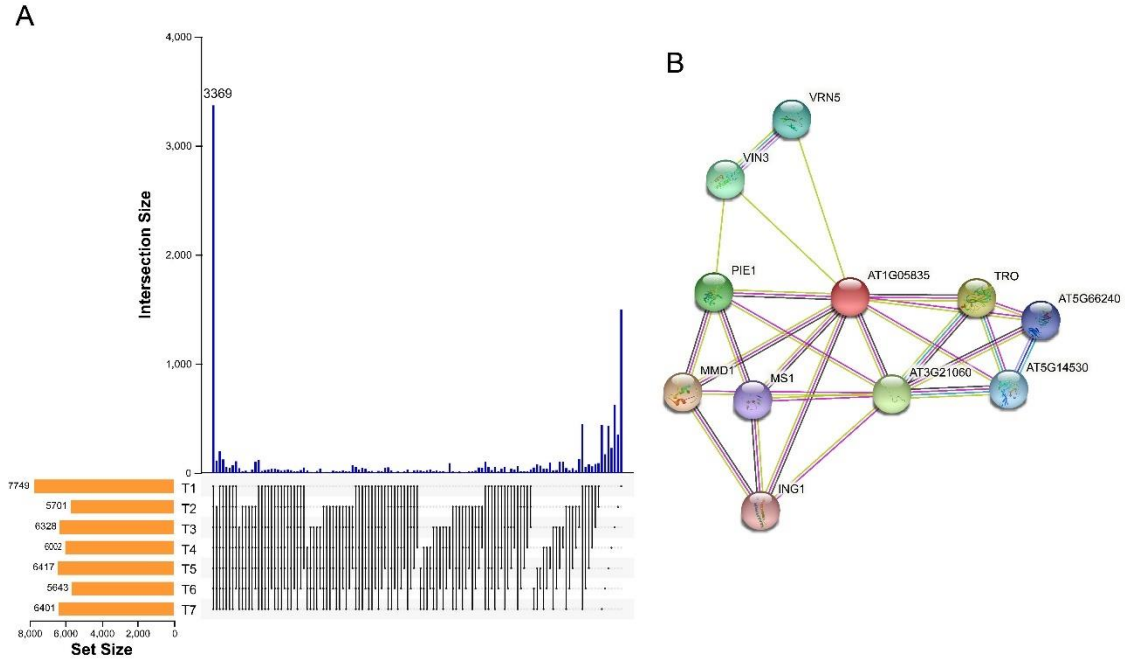


Figure S5. UpSet Venn of DEGs and protein interaction network diagrams. (A) UpSet Venn diagram of DEGs for B409 compared to ZS8, and (B) AT1G05835 protein interaction network diagram using STRING website (<https://stringdb.org/cgi/input.pl>, last accessed date 9 February 2021).

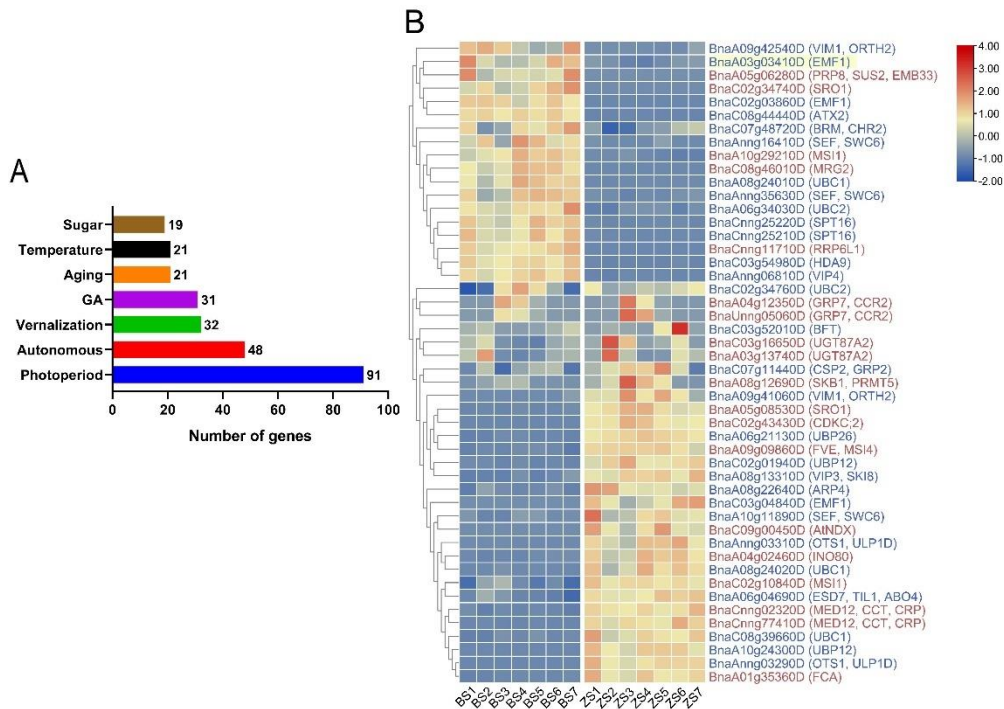


Figure S6. Histogram and heat map of differentially expressed flowering-time genes. (A) Histogram of number of differentially expressed flowering-time genes in seven pathways. (B) Heat map of differential expression of autonomous pathway flowering-time genes. Red and blue gene names indicate genes that are positive and negative flowering-time regulators, respectively. Gene name with yellow background are candidate genes in QTL intervals.

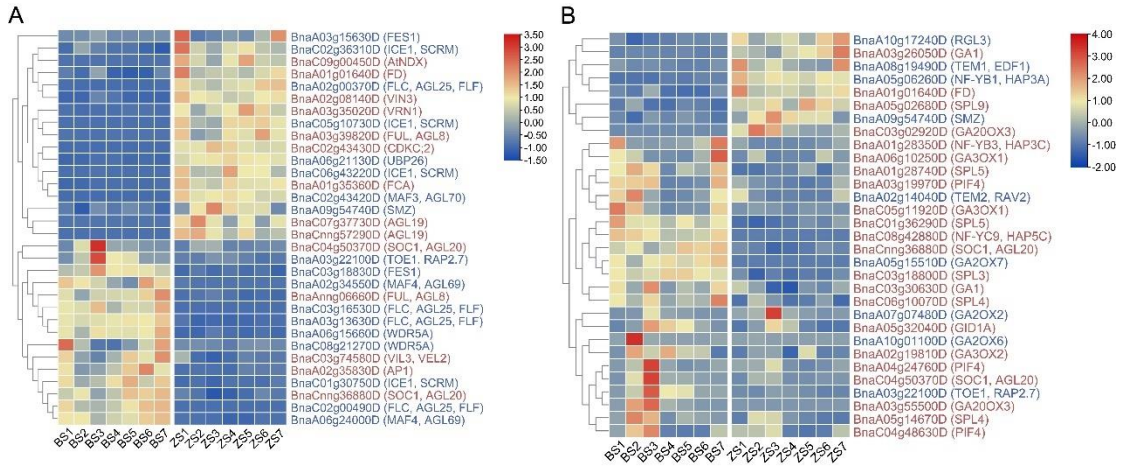


Figure S7. Heat map of differential expression of flowering-time genes in vernalization and GA pathways. Heat map of differential expression of flowering-time genes in vernalization (**A**) and GA pathways (**B**). Red and blue gene names indicate positive and negative flowering-time gene regulators, respectively. Gene names with yellow background indicate candidate genes in QTL interval.

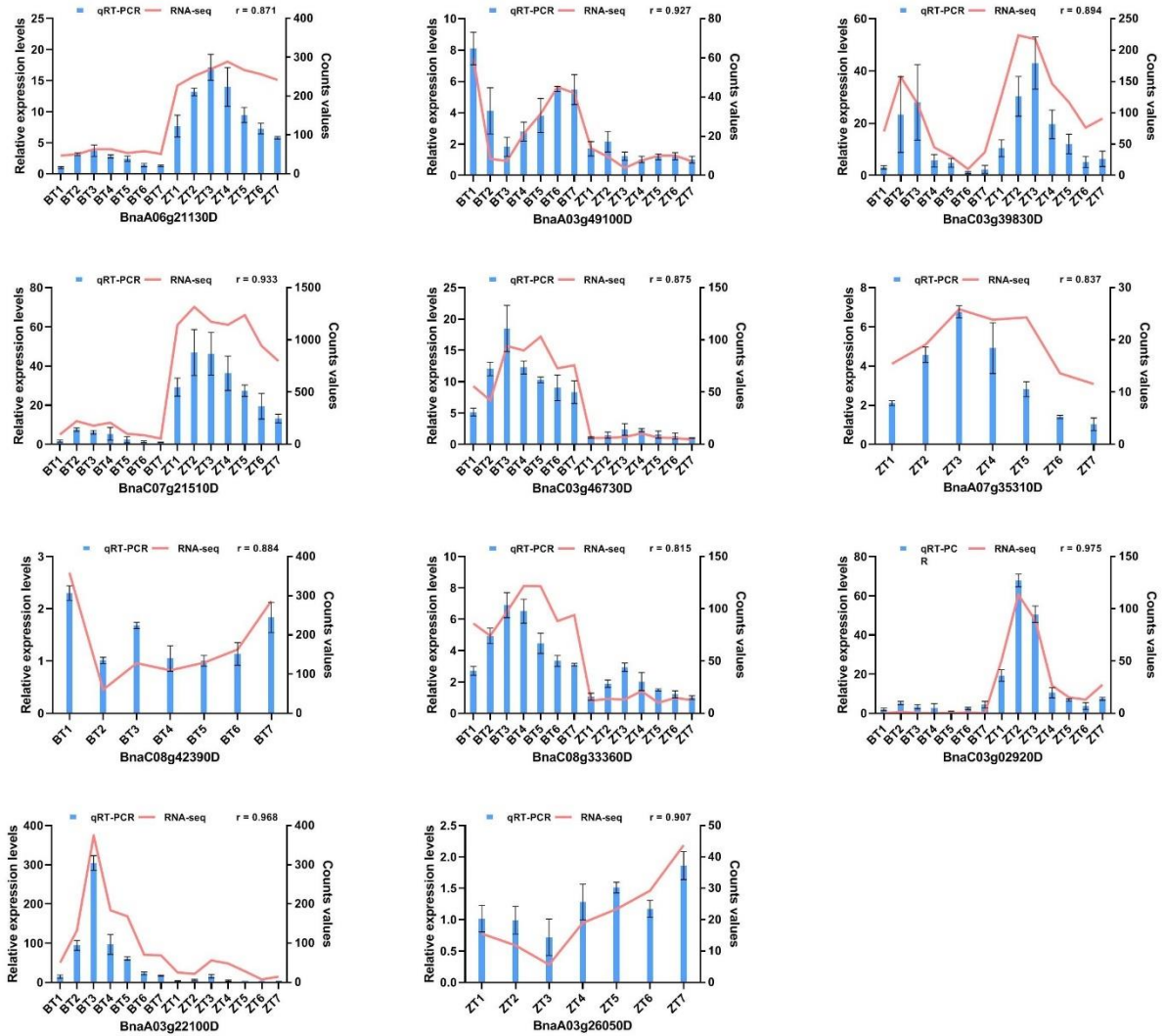


Figure S8. qRT-PCR validation of eleven randomly selected DEGs. Column charts illustrate relative gene expression levels (mean \pm SE) determined via qRT-PCR. Line charts illustrate gene expression counts values obtained via RNA-seq. r represents the Pearson correlation coefficient of gene expression determined via qRT-PCR and RNA-seq.