

Figure S1. Daily average temperature (°C) and relative humidity (%) of wheat during flowering-maturity period. Temperature (°C) and relative humidity (%) are recorded every hour, and the value is the average of 24 values every day. (Yellow: daily average relative humidity (%). Orange: Daily max-temperature (°C). Blue: Daily average temperature (°C). Grey: Daily min-temperature (°C) )

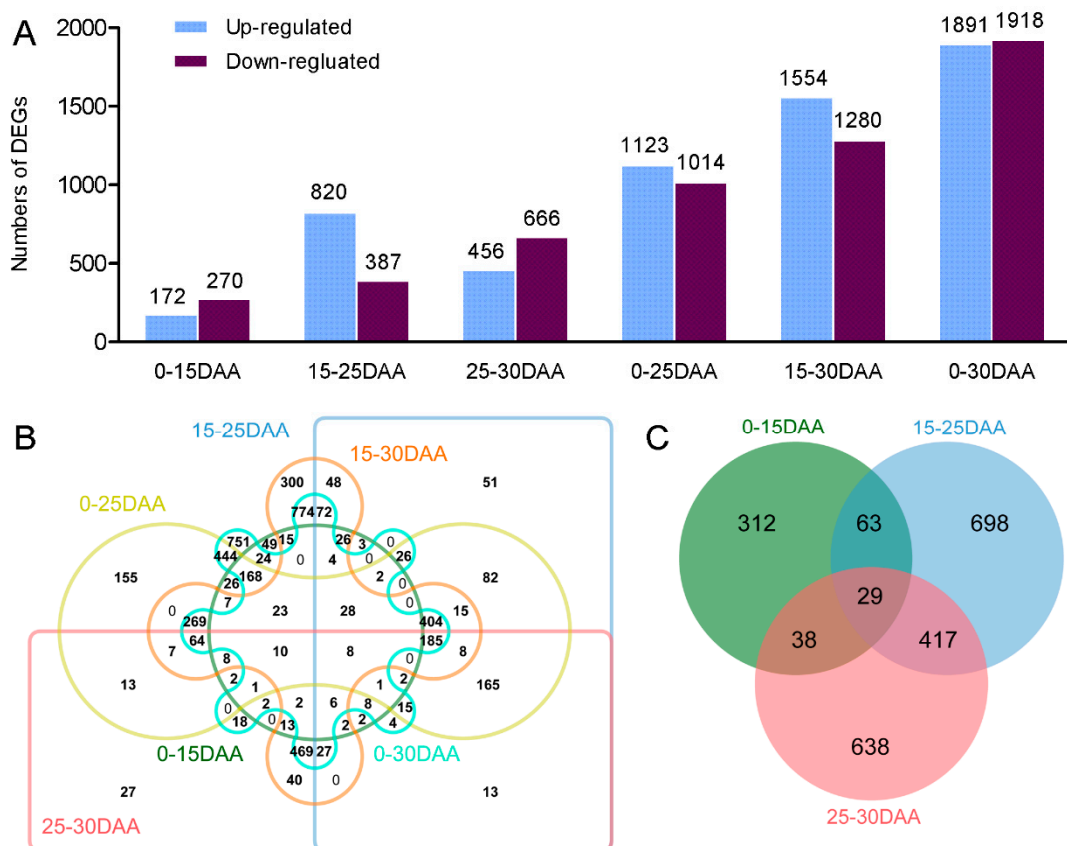


Figure S2. Number of DEGs per interval.

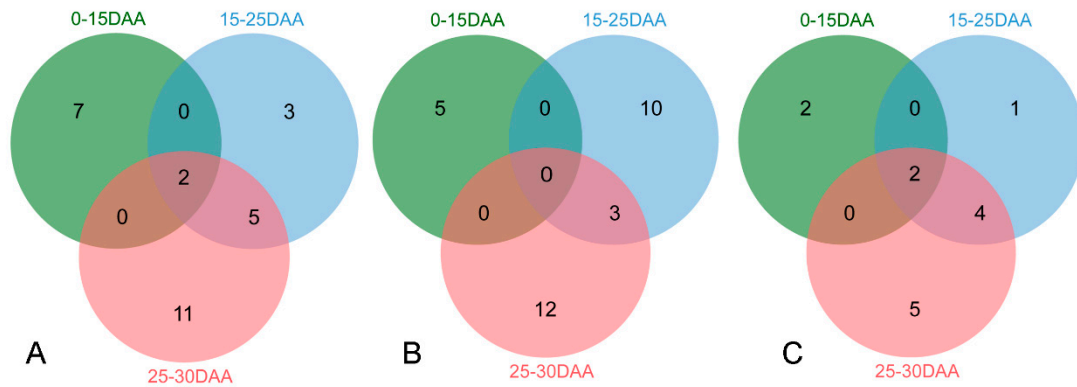
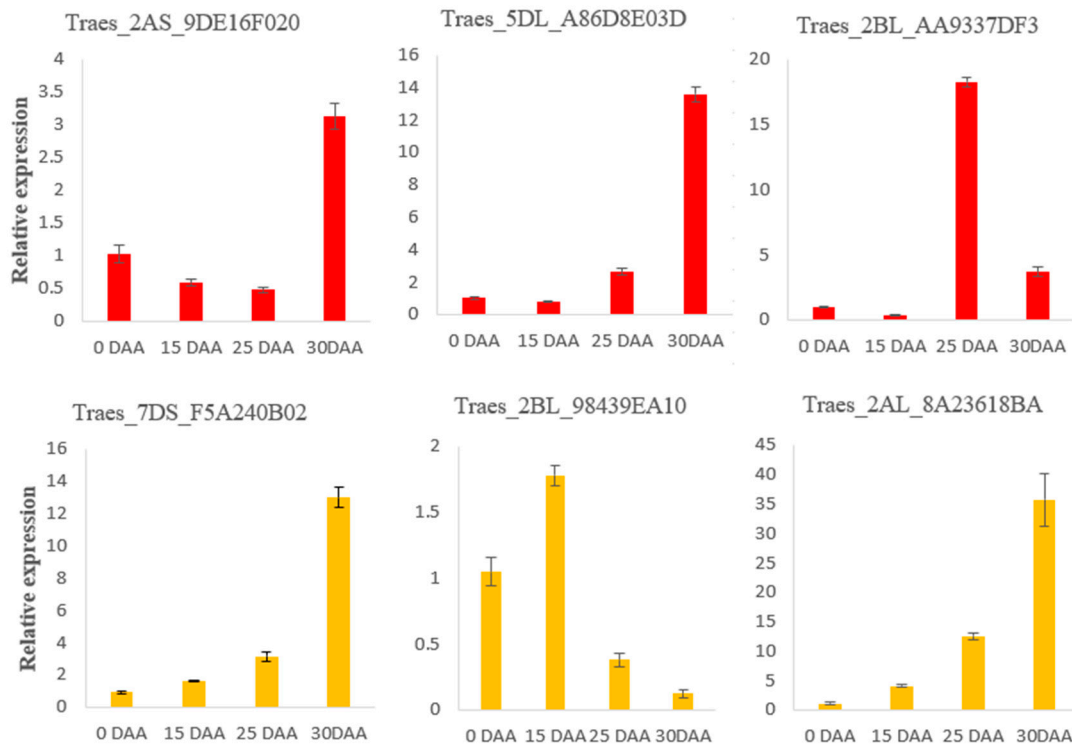


Figure S3. Metabolic pathways significantly enriched in each period. (A). All metabolic pathways significantly enriched. (B). Metabolic pathways with significant enrichment of up-regulated genes. (C). Metabolic pathways with significant enrichment of down-regulated expression genes.



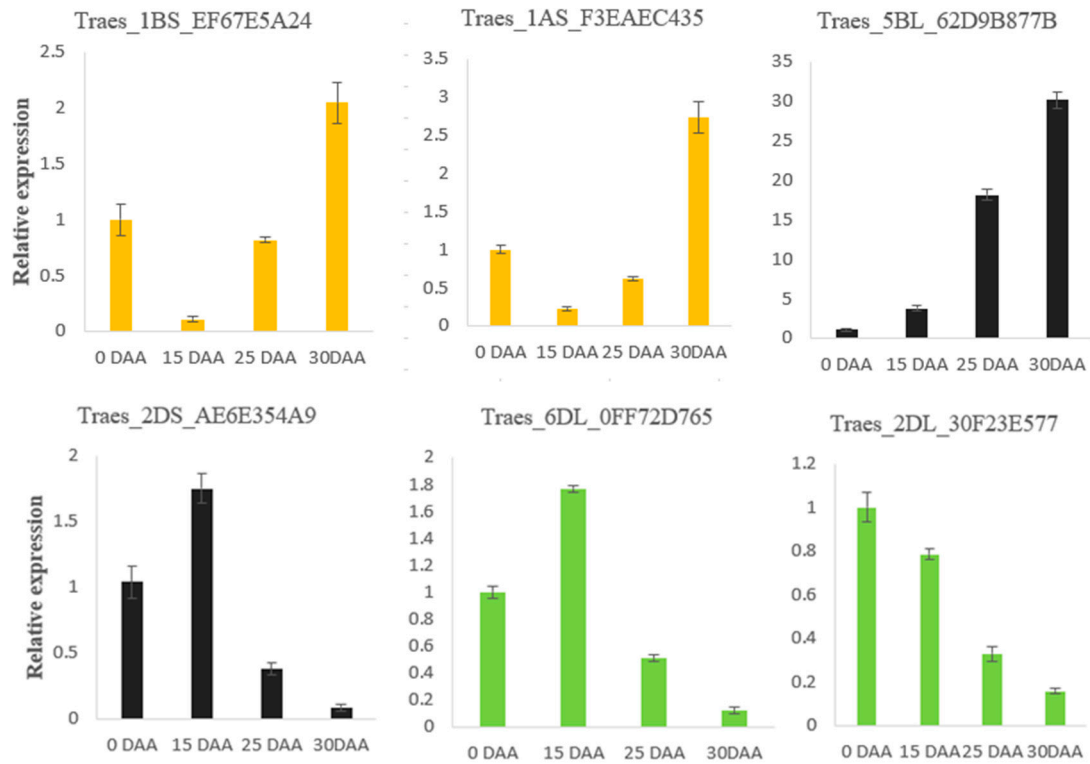


Figure S4. Analysis of relative expressions of different types of SAGs genes. Red: Transporter-related; Orange: Transcription factor-related; Black: Phytohormone-related; Green: Chlorophyll-related. The relative expression of each gene 0 DAA is '1.'

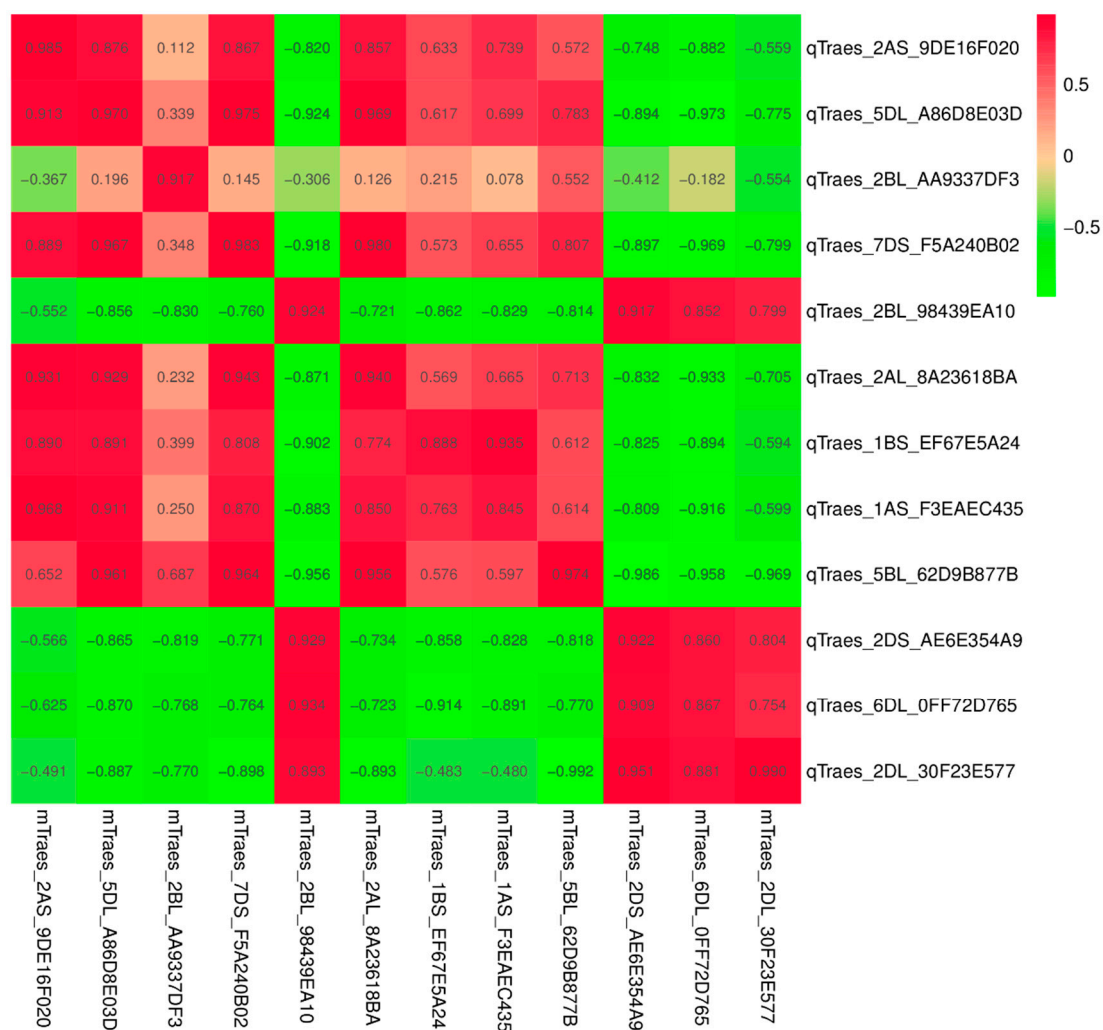


Figure S5: Heat map of RNA-seq and qRT-PCR correlation. q+gene represents qRT-PCR data; m+gene represents RNA-seq data.

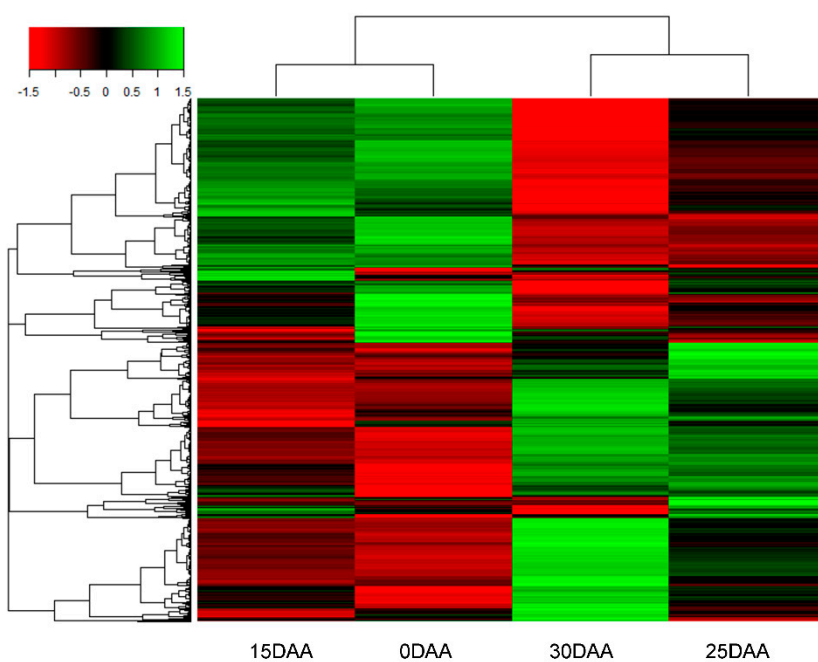


Figure S6. Clustering heat map of differentially expressed gene expression trends.

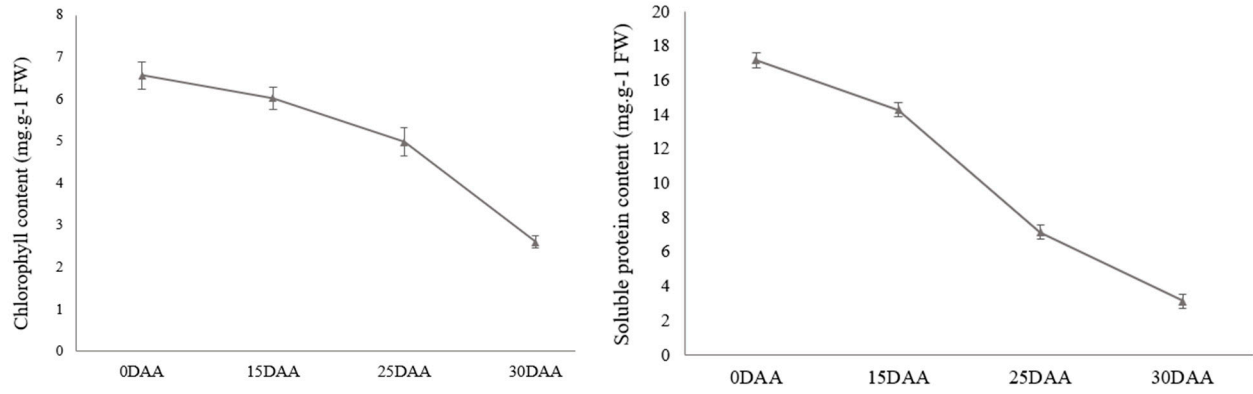


Figure S7: Changes in Chlorophyll content (a) and soluble protein content (b), after flowering in wheat flag leaves. For all values,  $n = 10$  and the data represent the mean  $\pm$  sd.