

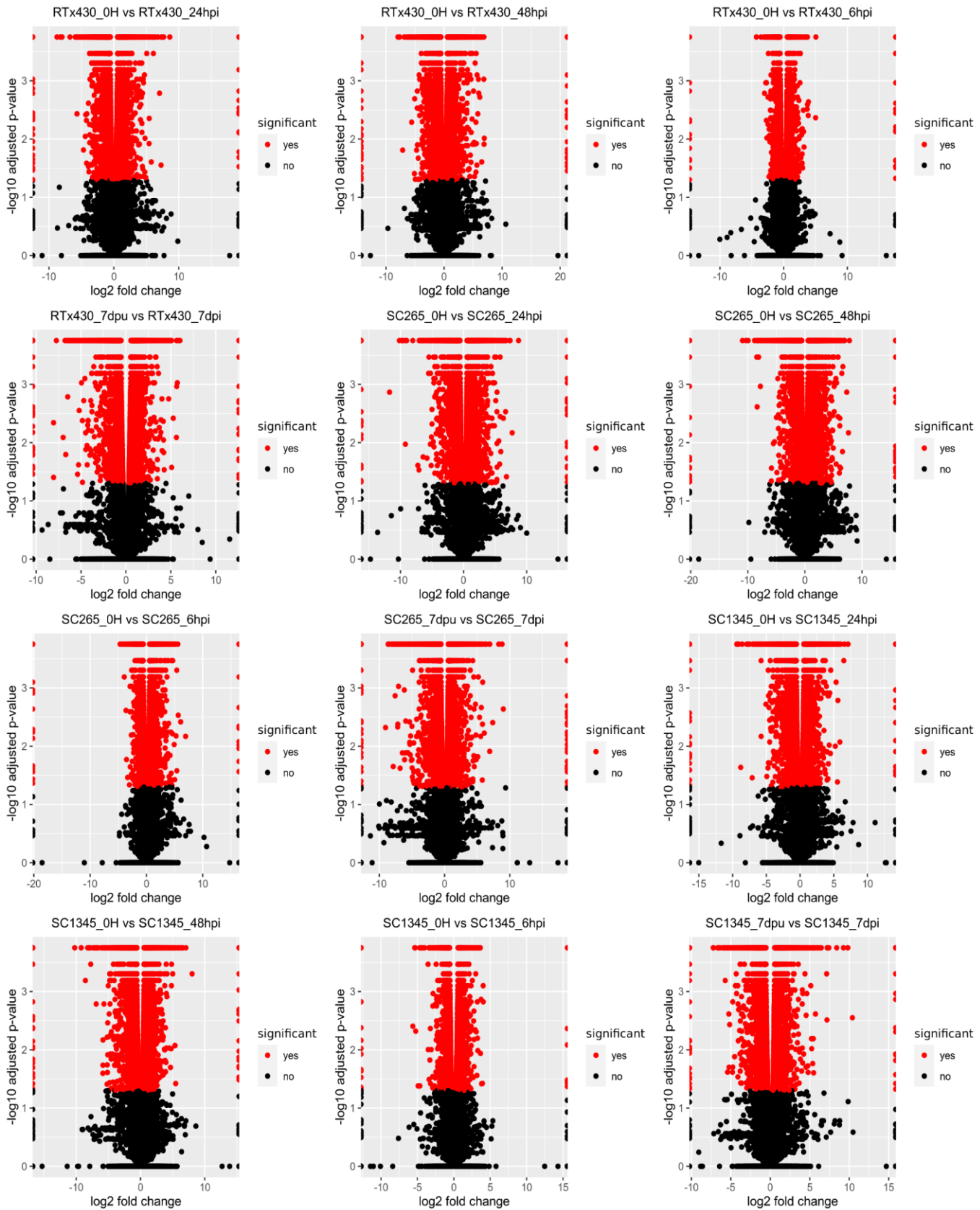


Figure S1. Volcano plots based on the RNA-seq data for each comparison. Red indicates a significant differential expression (adjusted P -value < 0.05 and $|\log_2(\text{FC})| \geq 1$).

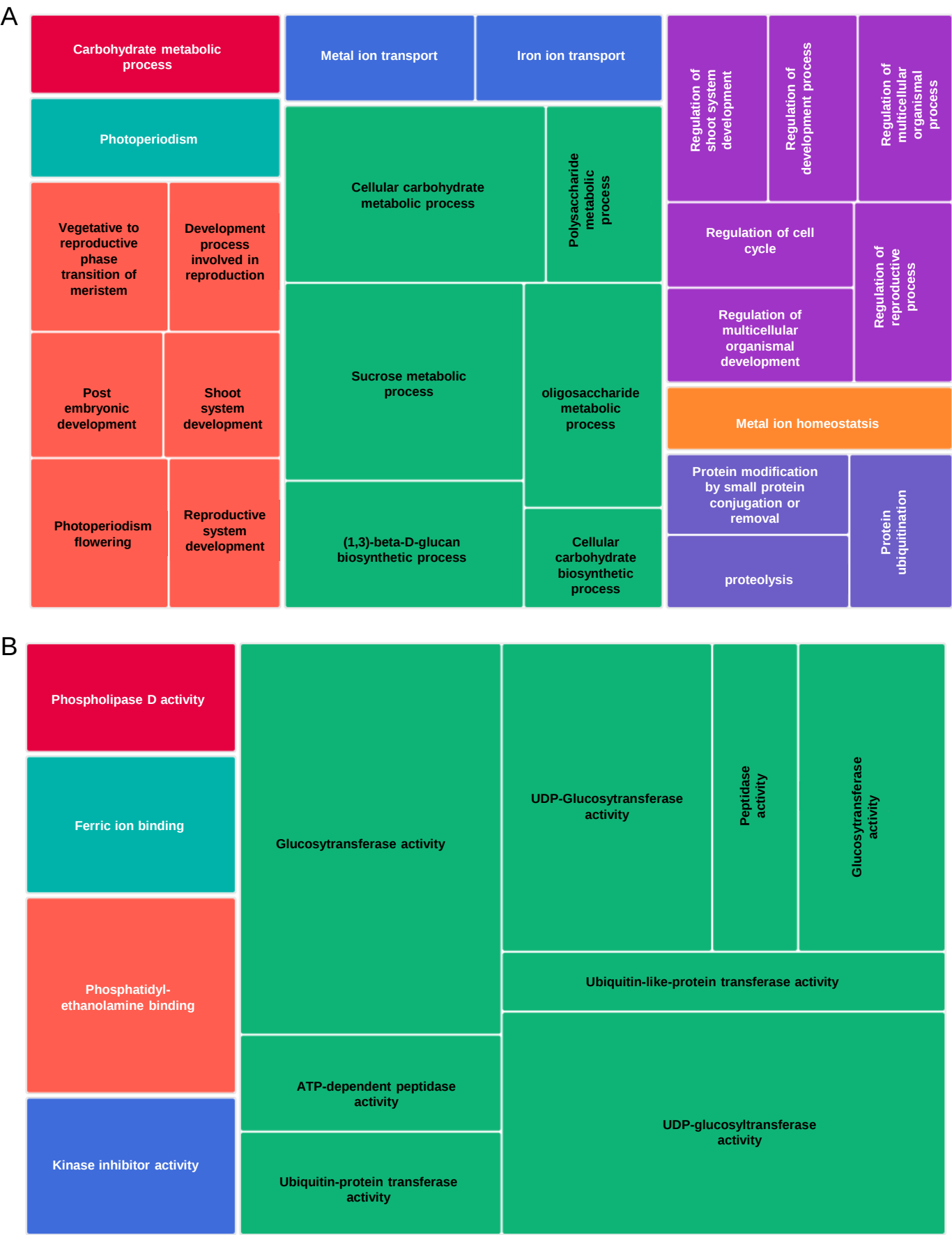
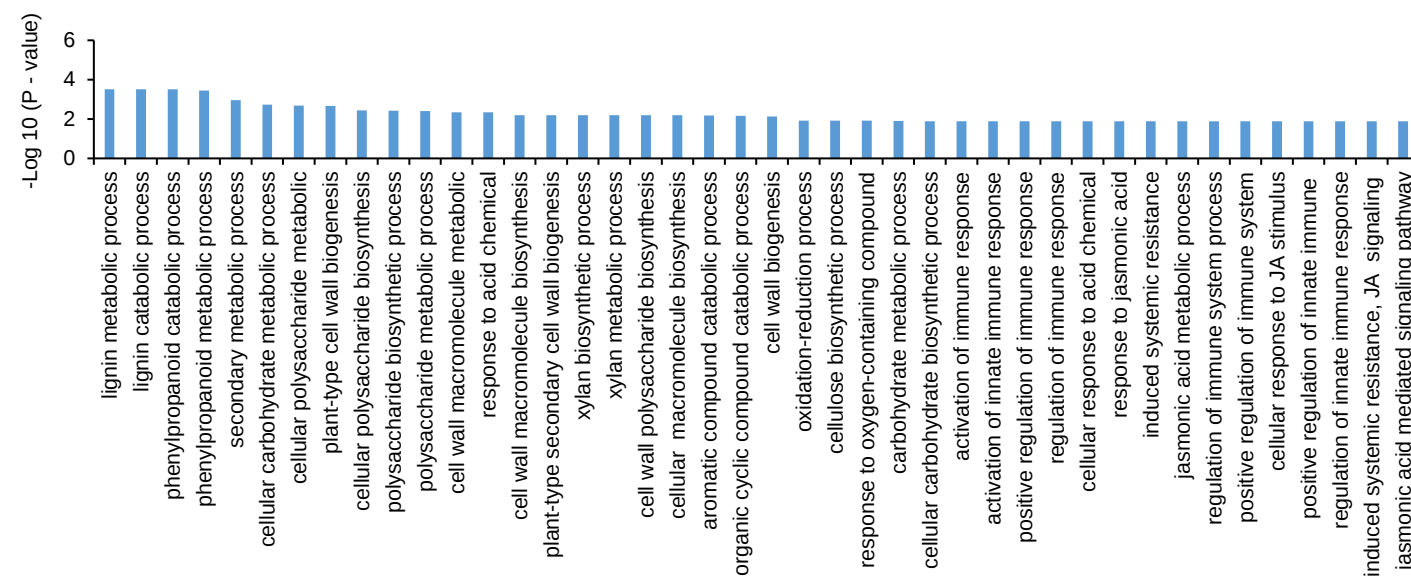


Figure S2. Gene ontology (GO) treemap of overrepresented GO terms in module 19 made by REVIGO program for A) Biological functions and B) Molecular functions. Each box represents the –log10 (*P*-value) of individual GO term and bigger size of the box reflects most significant GO terms. Similar functional categories with semantic similarity are represented in similar colored boxes.

A



B

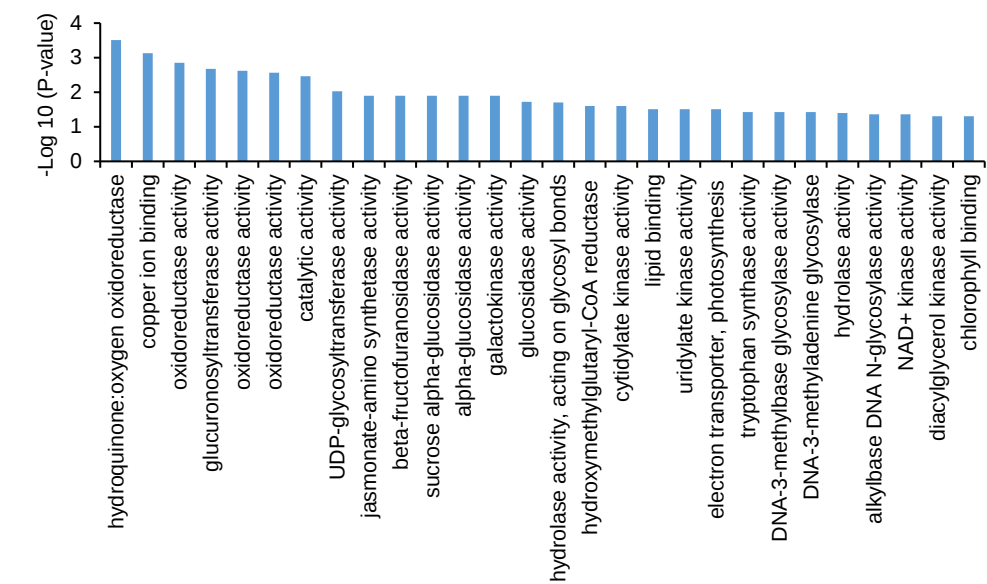
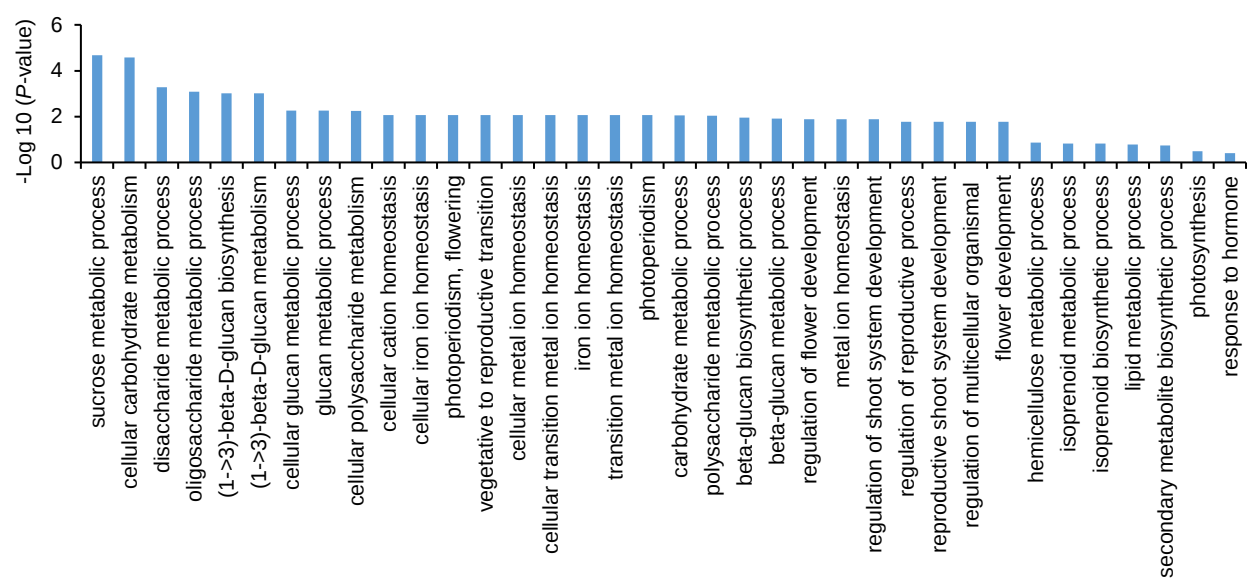


Figure S3. Gene enrichment analysis of differentially expressed genes (DEGs) in module M4. Significantly enriched genes of A) Biological functions and B) Molecular functions are plotted against the negative logarithm of *P*-value (*P*<0.05).

A



B

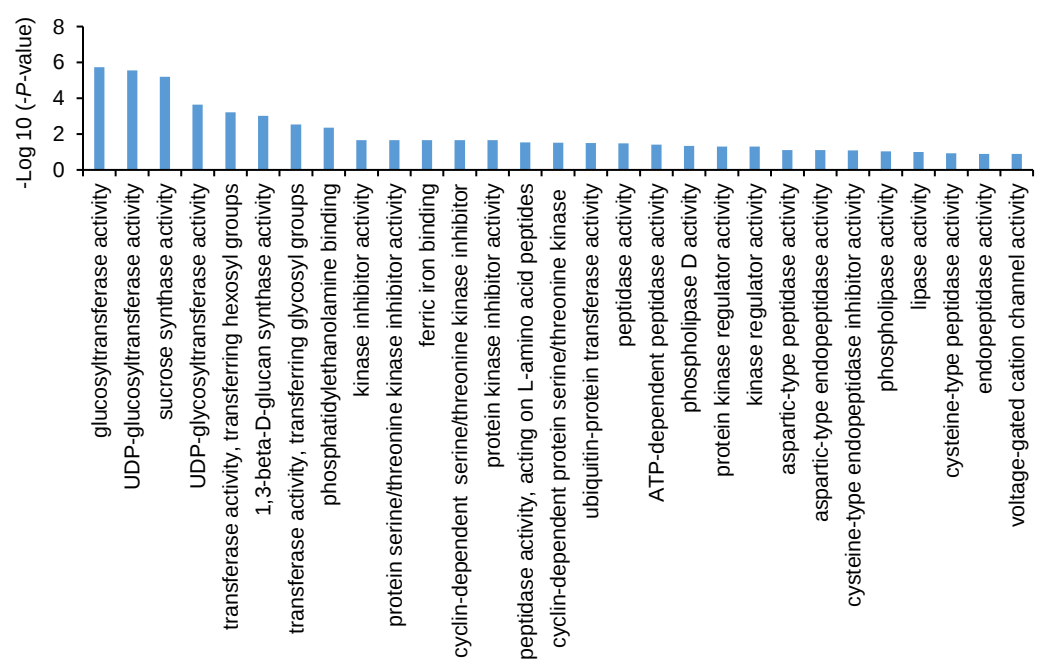


Figure S4. Gene enrichment analysis of differentially expressed genes (DEGs) in module M19. Significantly enriched genes of A) Biological functions and B) Molecular functions are plotted against the negative logarithm of *P*-value (*P*<0.05).