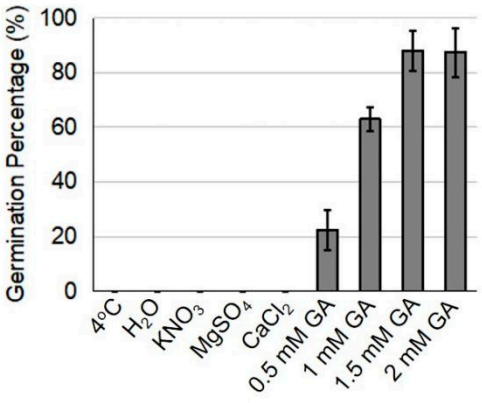

Figure S1. Germination percentage of *S. torvum* seeds under different pre-treatments. The seeds were treated at low temperature (4ºC) or pre-soaked in KNO_3 (20 g/L), $MgSO_4$ (20 g/L), $CaCl_2$ (20 g/L) or various concentration of GA (0.5, 1, 1.5, and 2mM). The data was collected at day 14 and calculated based on three independent experiments.

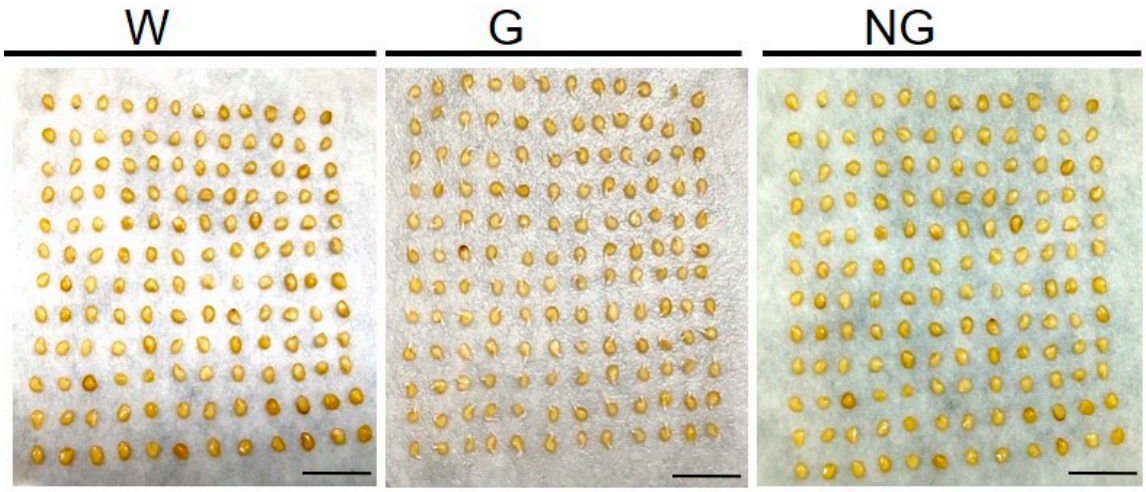

Figure S2. Seed samples collected for RNA-seq analysis. G, germinated GA-treated seeds; NG, ungerminated GA-treated seeds; W, control seeds treated by ddH_2O. Scale bar, 1 cm.

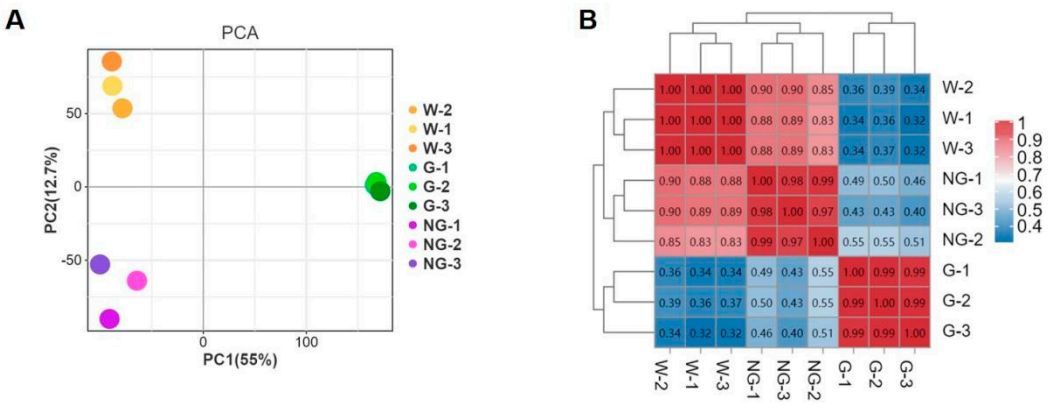

Figure S3. Transcriptome analysis of germinated and ungerminated *S. torvum* seeds. (A) Principal component analysis (PCA) of RNA-seq data. G, germinated GA-treated seeds; NG, ungerminated GA-treated seeds; W, control seeds treated by ddH_2O. (B) Pearson's correlation analysis of RNA-seq data between each sample.

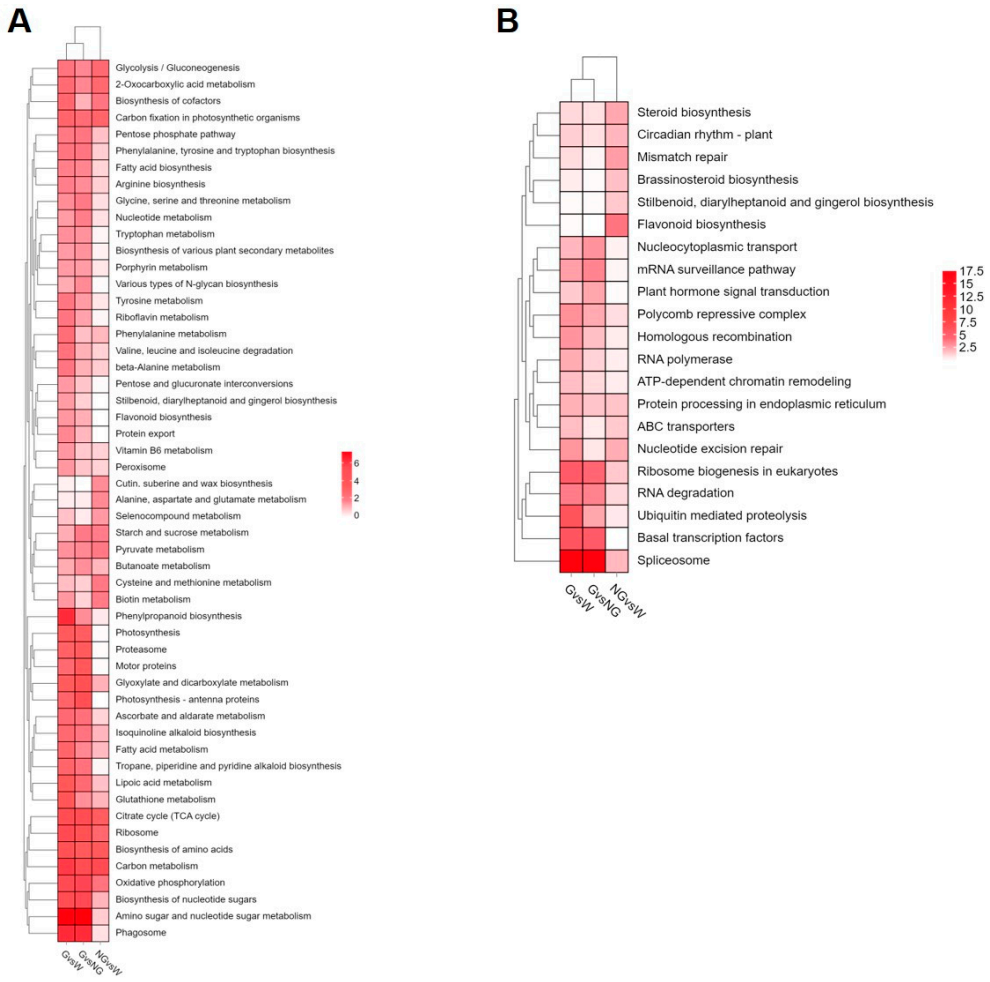

Figure S4. KEGG pathways enriched in DEGs identified in each comparison group. (A) KEGG pathways enriched in the up-regulated DEGs. (B) KEGG pathways enriched in the down-regulated DEGs.

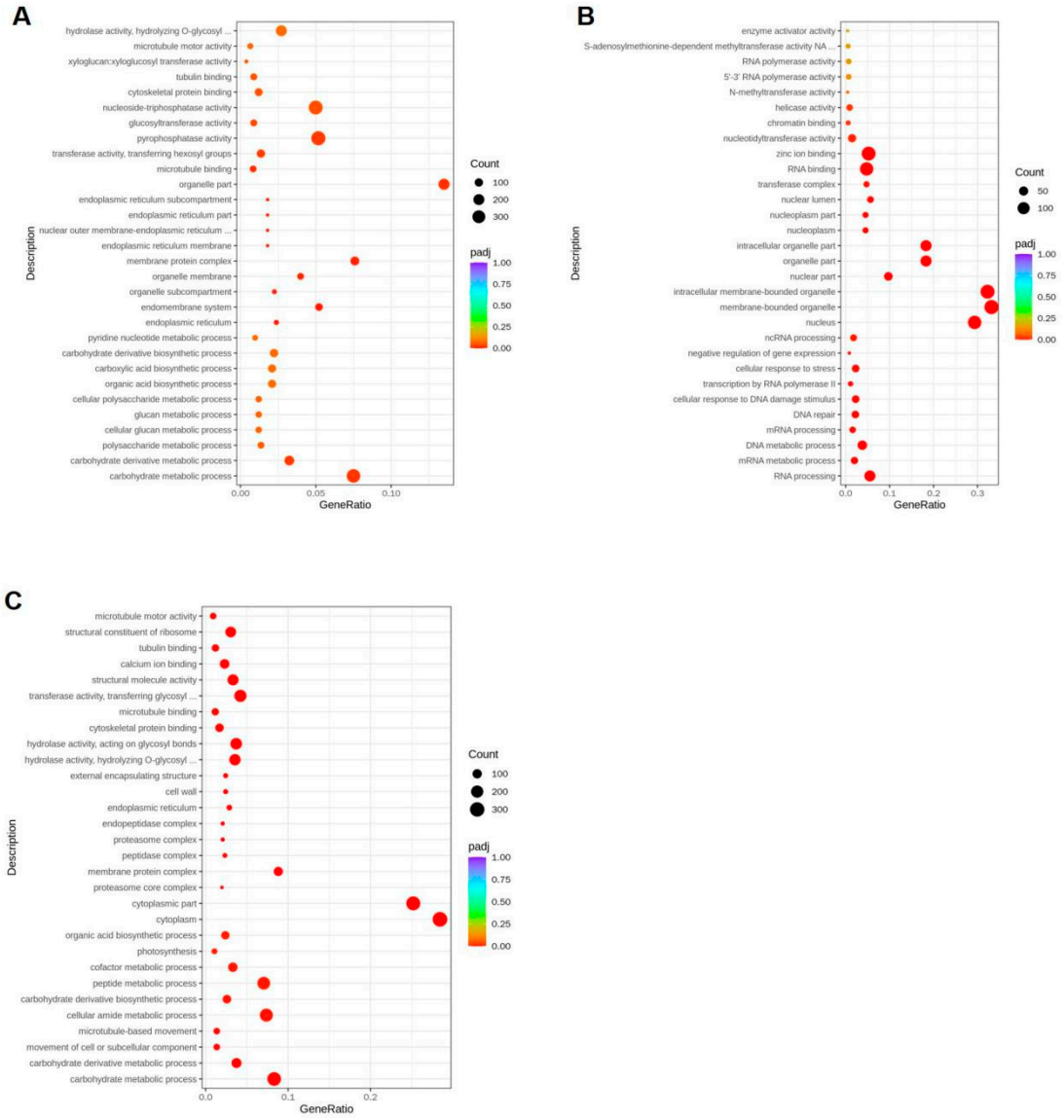

Figure S5. Top 20 GO terms enriched in the DEGs in G group compared to W group. (A) The top 20 GO enrichment terms of all the DEGs in G group compared to W group. (B) The top 20 GO enrichment terms of the down-regulated DEGs in G group compared to W group. (C) The top 20 GO enrichment terms of the common up-regulated DEGs in G group compared to W group.

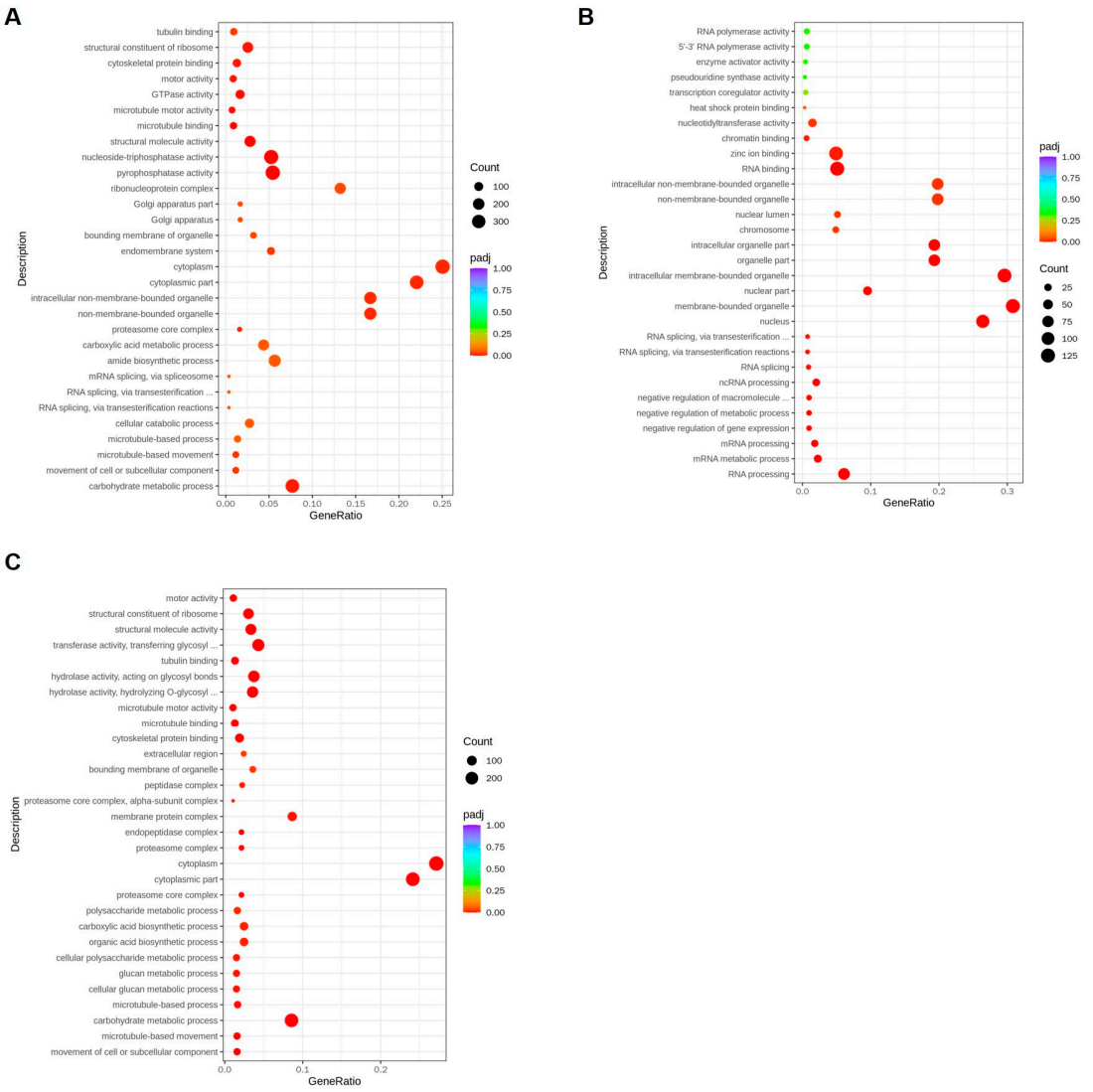

Figure S6. Top 20 GO terms enriched in the DEGs in G group compared to NG group. (A) The top 20 GO enrichment terms of all the DEGs in G group compared to NG group. (B) The top 20 GO enrichment terms of the down-regulated DEGs in G group compared to NG group. (C) The top 20 GO enrichment terms of the common up-regulated DEGs in G group compared to NG group.

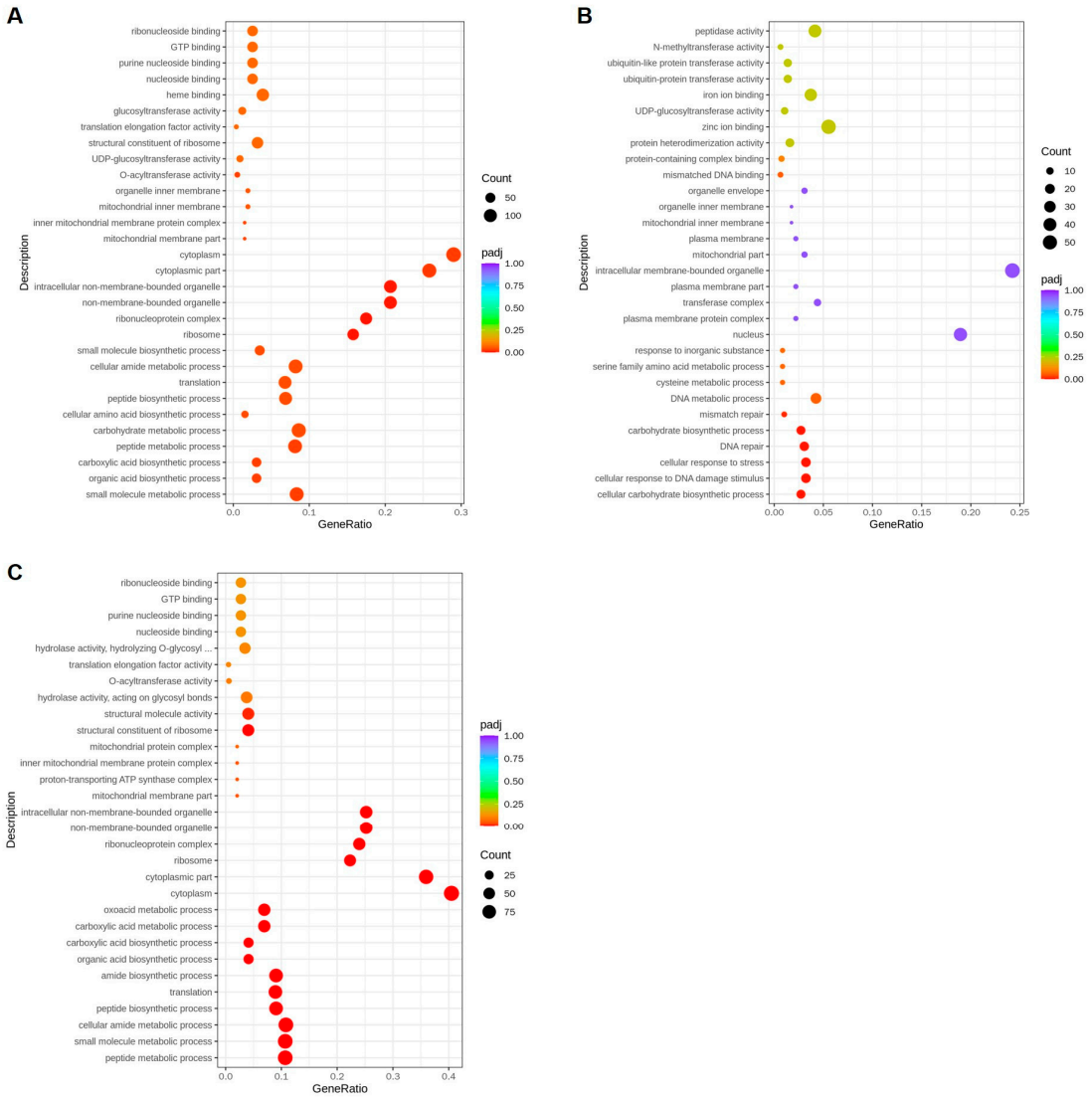

Figure S7. Top 20 GO terms enriched in the DEGs in NG group compared to W group. (A) The top 20 GO enrichment terms of all the DEGs in NG group compared to W group. (B) The top 20 GO enrichment terms of the down-regulated DEGs in NG group compared to W group. (C) The top 20 GO enrichment terms of the common up-regulated DEGs in NG group compared to W group.

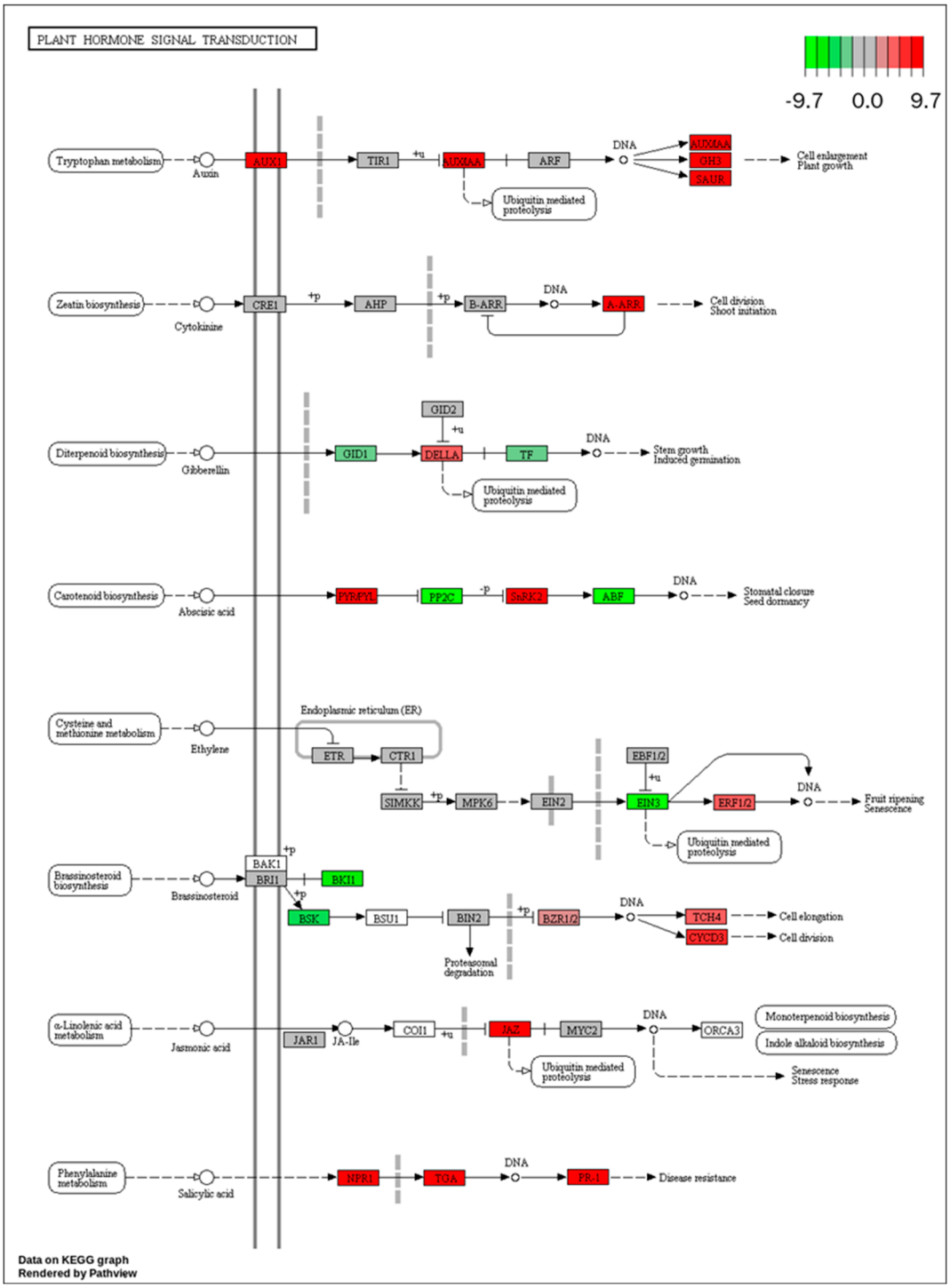

Figure S8. Overview of plant hormone signaling transduction pathway via KEGG analysis. Red and green colored boxes indicated the key factors significantly enriched in GRGs.