

Supplementary Figure S1

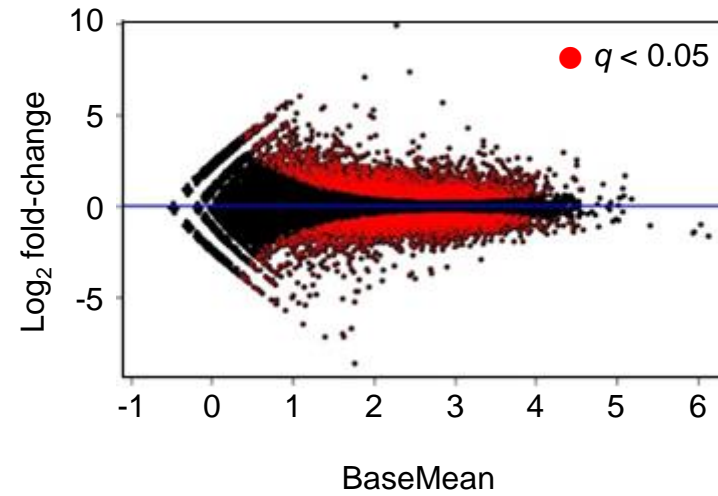


Figure S1. MA plot of differential expression between DMSO- and GA-treated samples. Red dots represent the either up- (2,805) and down- (2,916) regulated genes with $q < 0.05$ and $\geq |1.5|$ -fold change.

Supplementary Figure S2

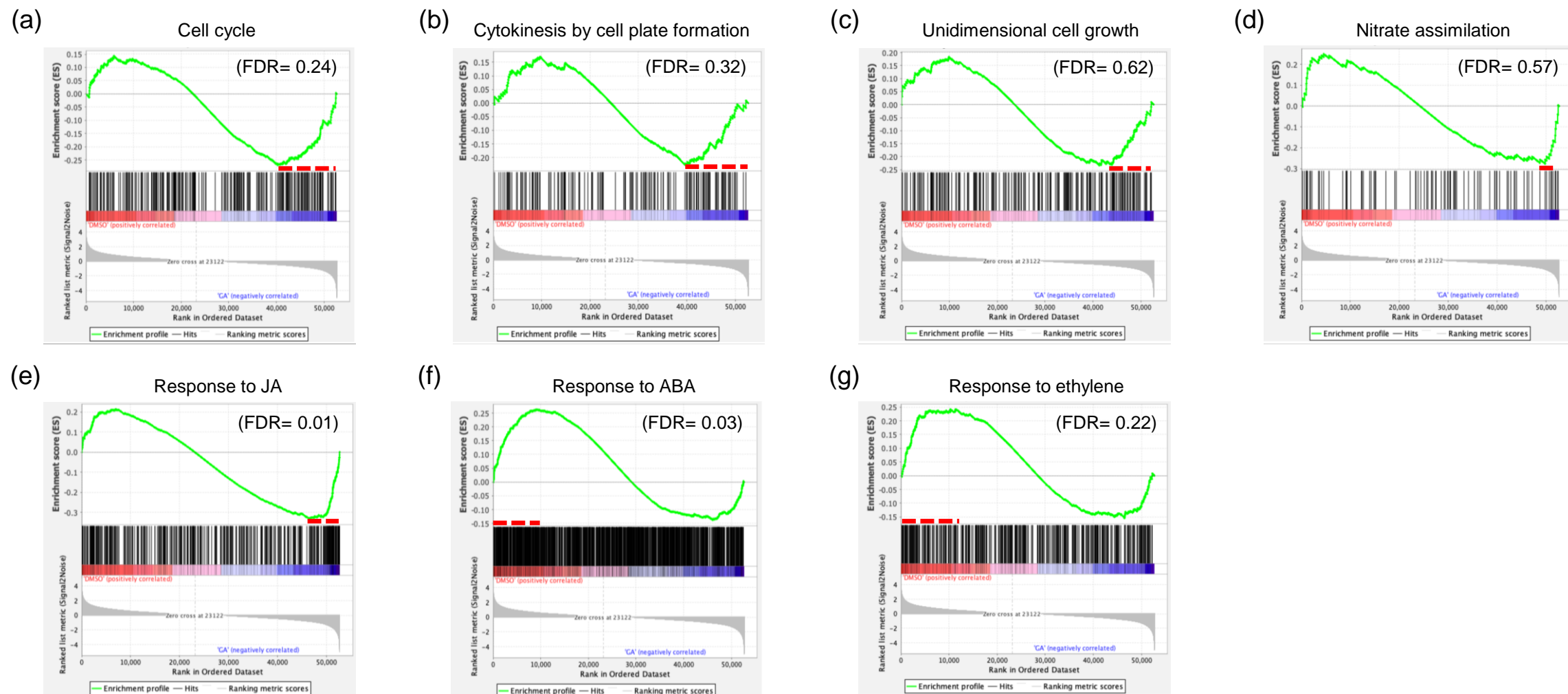


Figure S2. Enrichment plot for cell cycle, cytokinesis, cell growth, nitrate assimilation, and response to plant hormones using GSEA. In the plot, red dot line (---) indicates a leading-edge subset of the enriched gene set group leading to enrichment scores with respect to expression changes.

Supplementary Figure S3

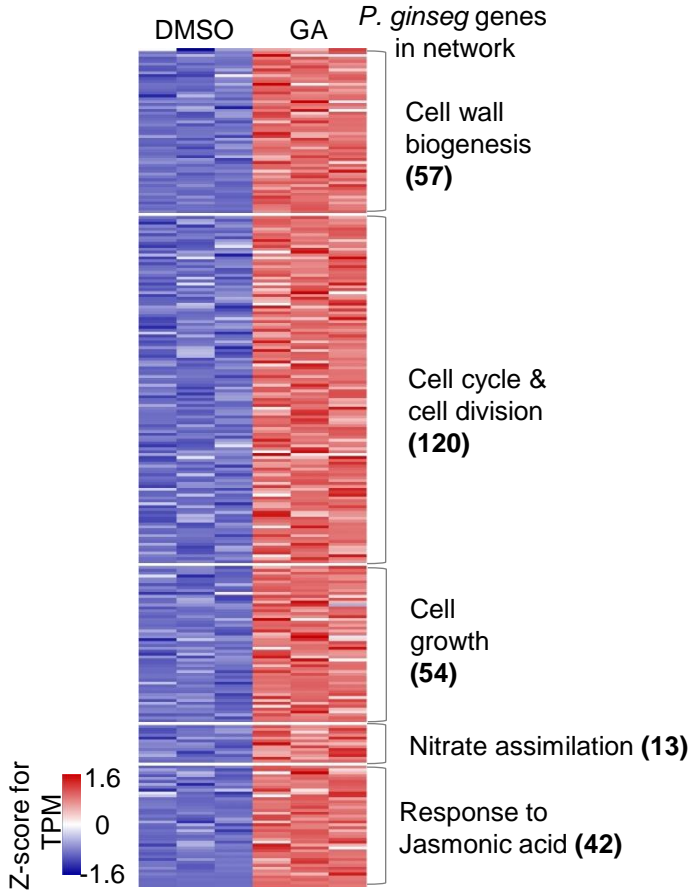


Figure S3. Expression heatmap of up-regulated genes contained in GA-induced transcriptional network.