

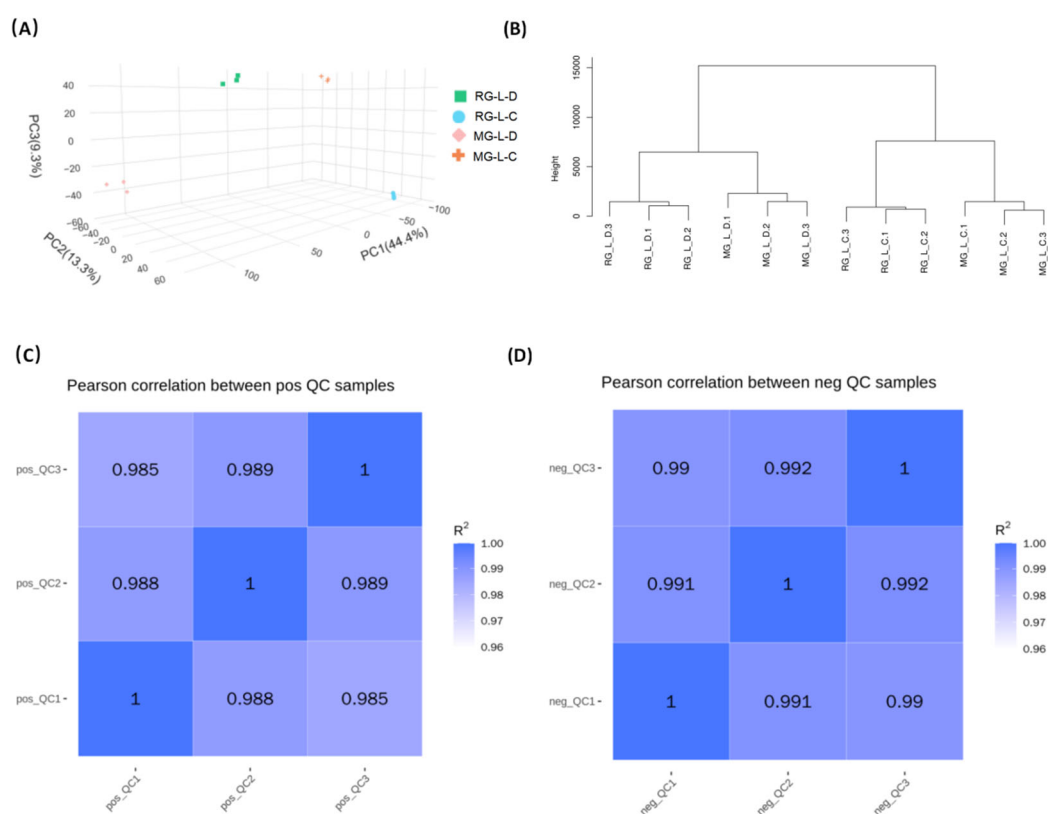


Figure S1 Quality assessment and clustering analyses of transcriptomic and metabolomic datasets. (A) Principal component analysis (PCA) of transcriptomic samples. (B) Hierarchical clustering analysis of transcriptomic samples. (C) Pearson correlation analysis of quality control (QC) samples acquired in positive ion mode for metabolomic analysis. (D) Pearson correlation analysis of quality control (QC) samples acquired in negative ion mode for metabolomic analysis.

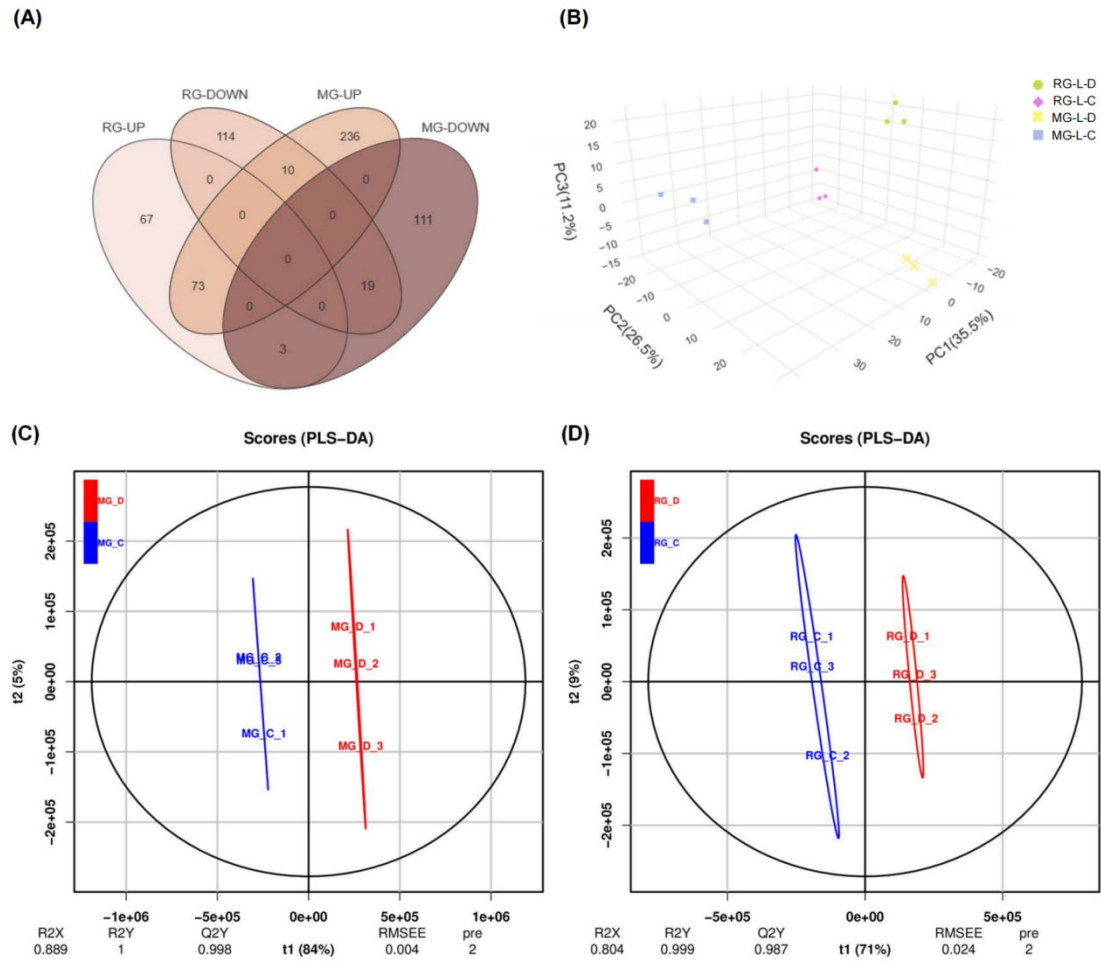


Figure S2 Multivariate statistical and clustering analysis of differential metabolites.

(A) Metabolite Venn diagram. (B) Metabolite PCA score plot. (C-D) OPLS-DA score plots of metabolites (C: 'MG'; D: 'RG').

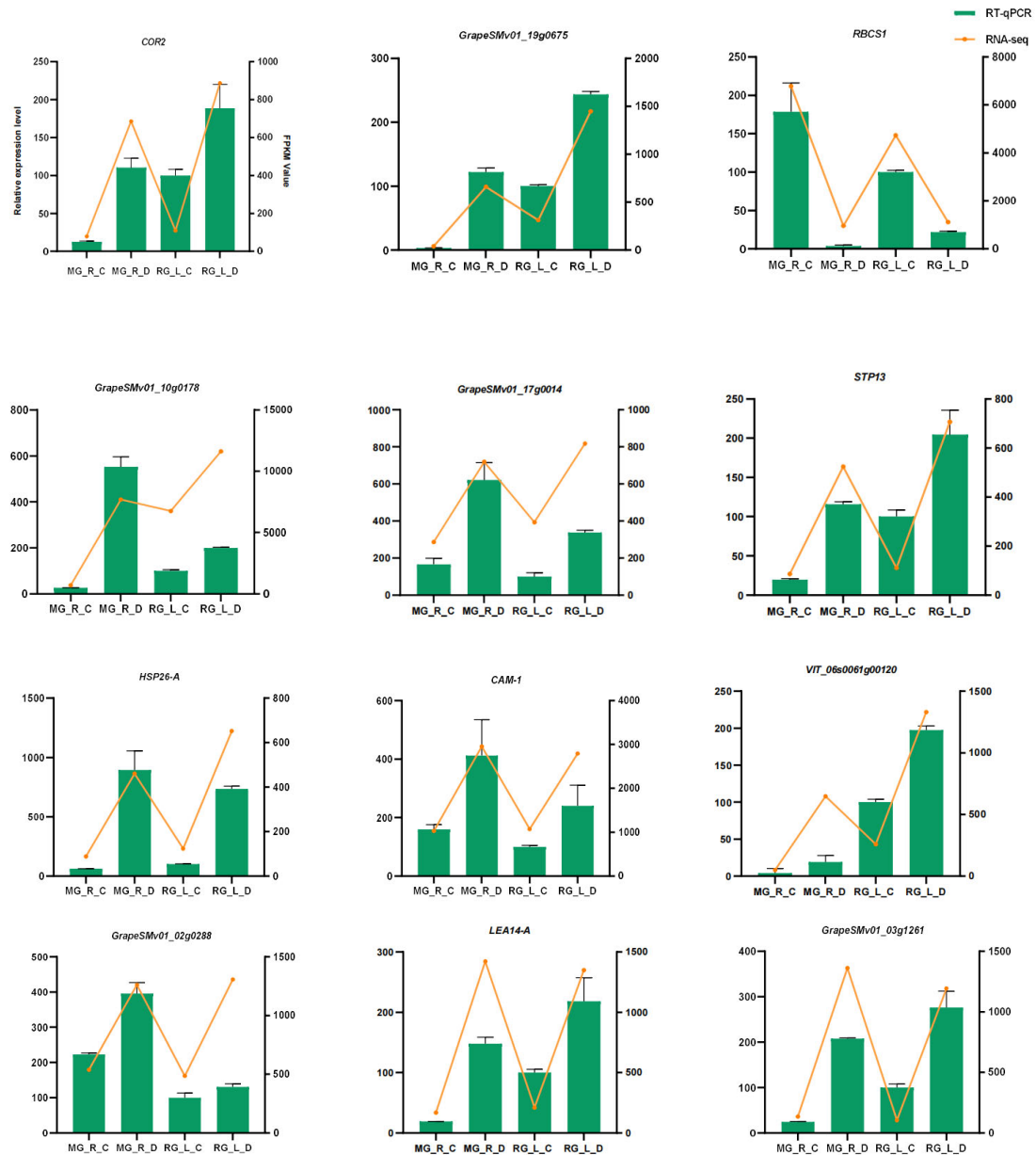


Figure S3 RT-qPCR validation of core gene expression levels. The bar chart with the primary vertical axis represents the relative expression levels measured by RT-qPCR (Real-Time Quantitative Polymerase Chain Reaction), while the line graph with the secondary vertical axis displays the FPKM values (Fragments Per Kilobase of exon model per Million mapped reads) from RNA-seq (Transcriptome Sequencing).

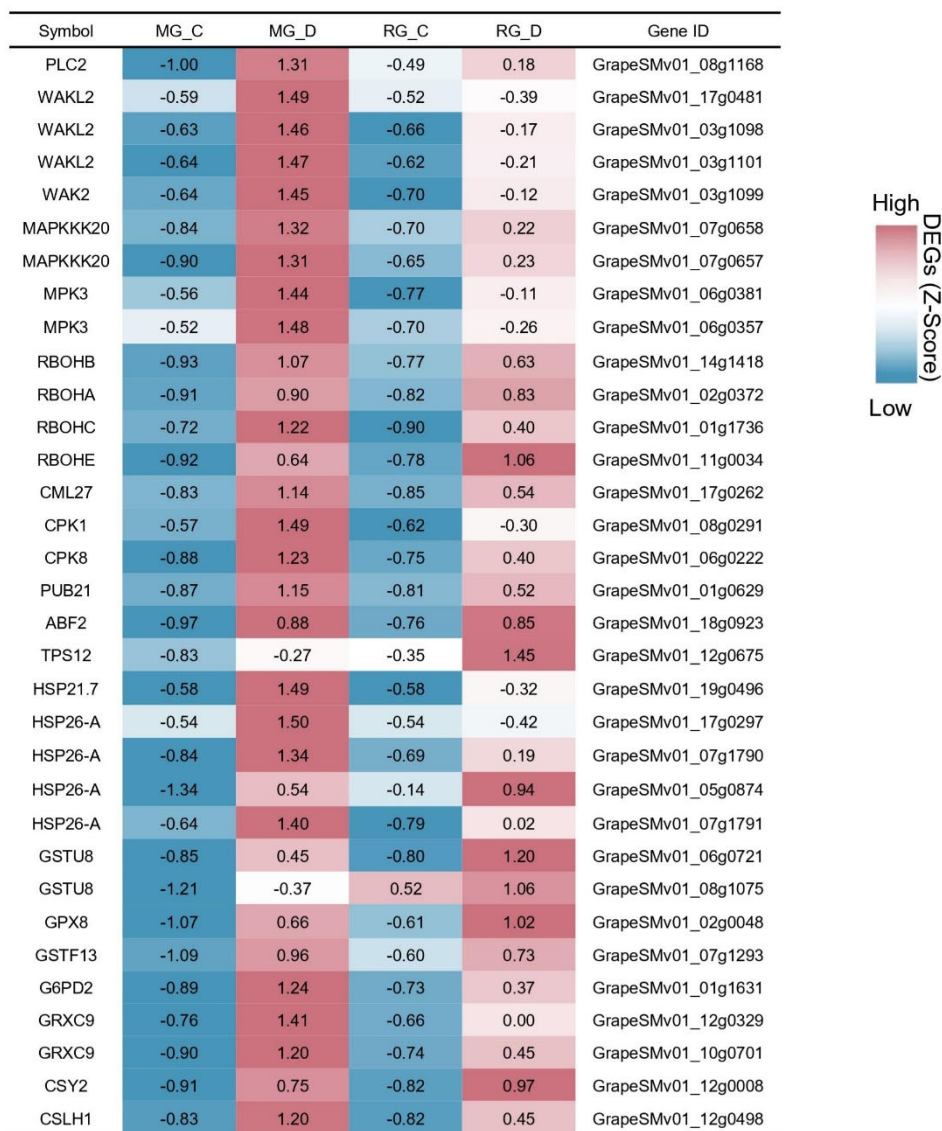


Figure S4 Heatmap of related gene expression in MG and RG under drought stress.

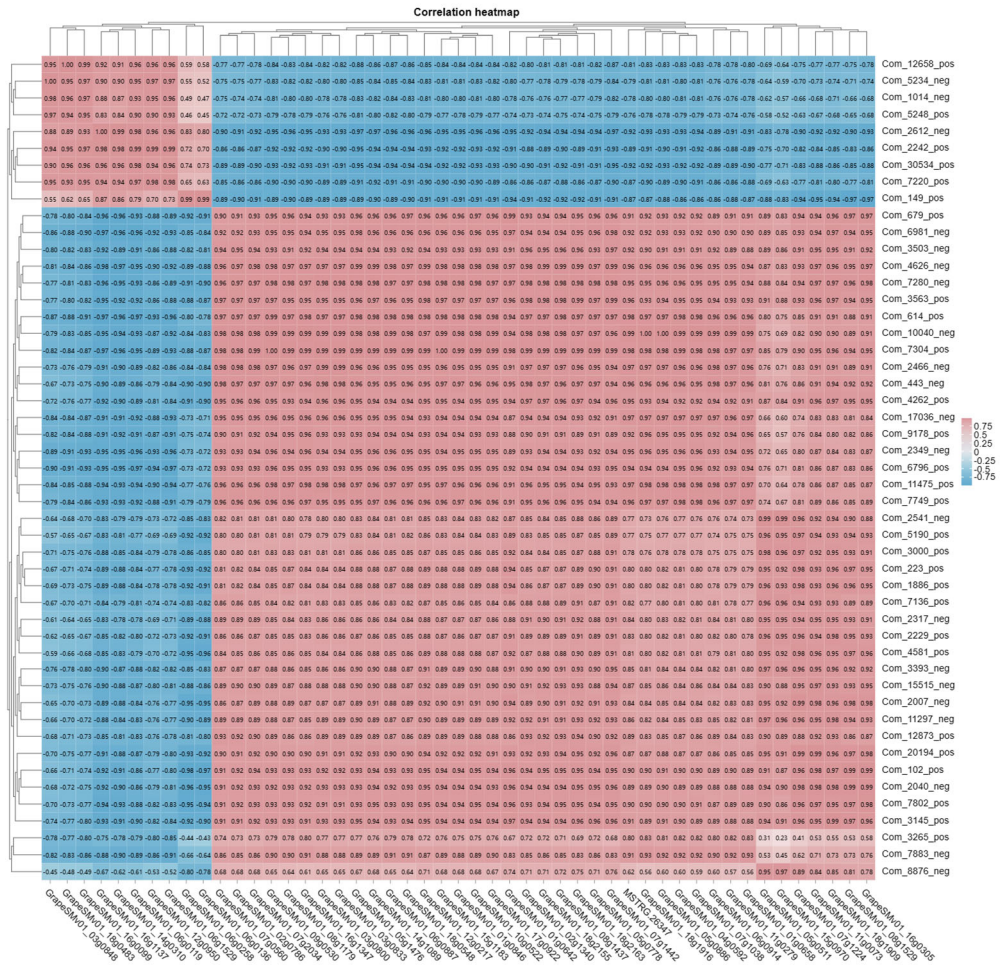


Figure S5 Correlation heatmap of core DEGs and DAMs. Based on the top 50 differentially expressed genes (DEGs) and differentially accumulated metabolites (DAMs), a correlation heatmap was generated to visualize the associations between these DEGs and DAMs across different comparison groups. Pearson correlation coefficient was used to evaluate the correlations between gene expression and metabolite abundance.

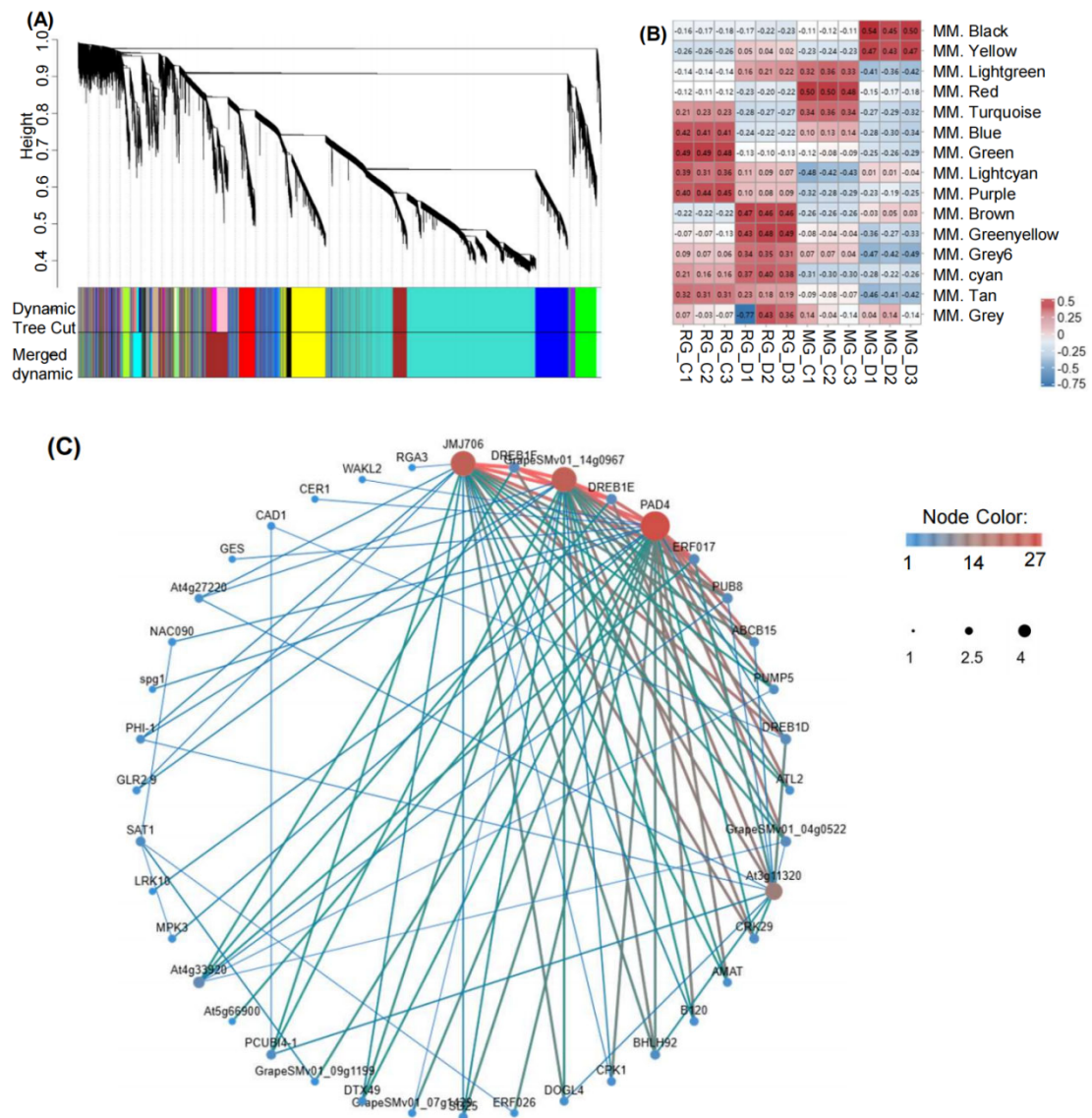


Figure S6 Weighted correlation network analysis of leaf response to drought stress. (A) Co-expression modules based on WGCNA. (B) Hierarchical clustering tree of module-sample expression patterns. Correlation coefficients are displayed at row and column junctions, with *p*-values color-coded. (C) Gene regulatory network. Network illustrating connections among hub genes within the drought-associated module MM.

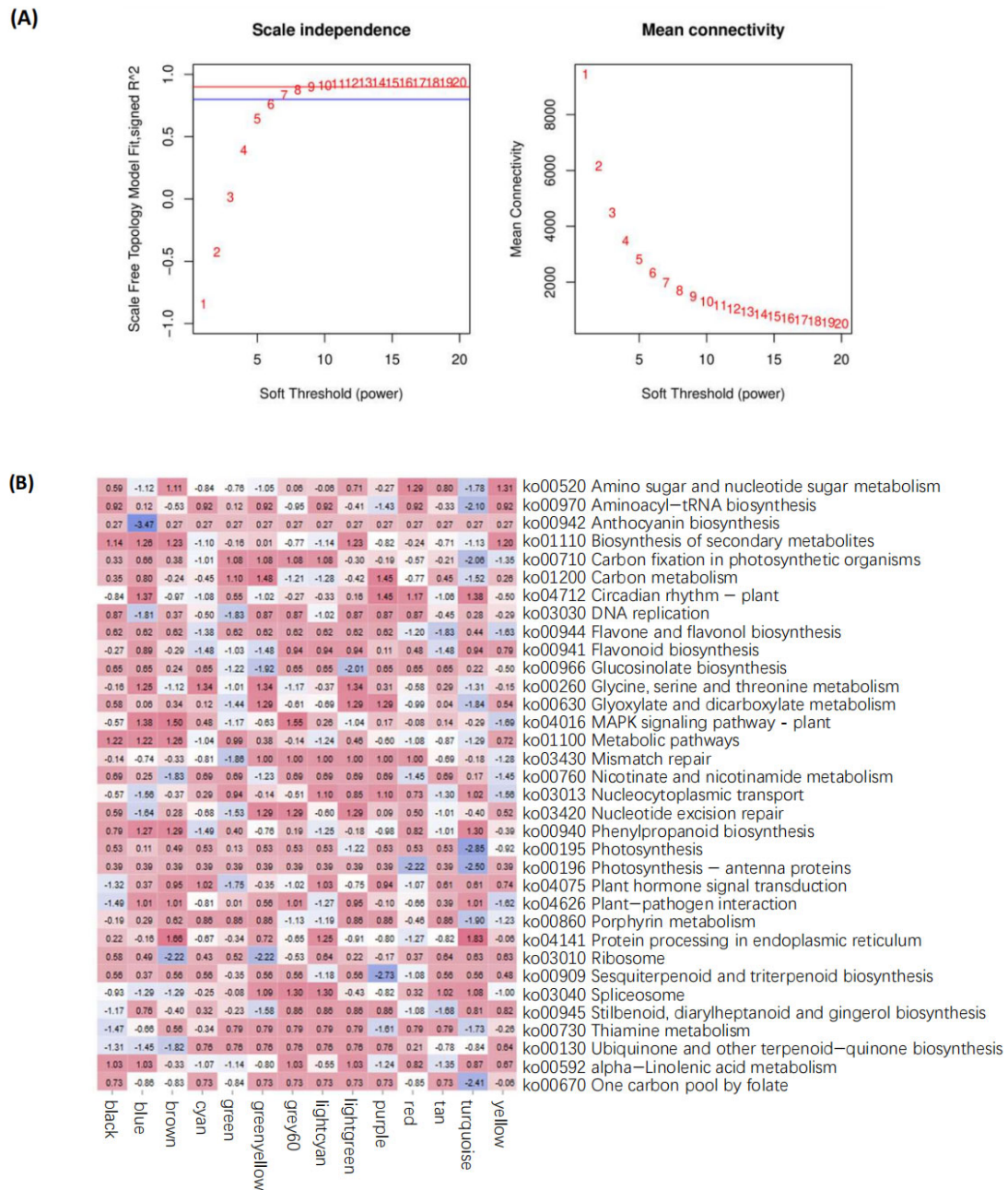


Figure S7 Determination of soft-threshold power and KEGG pathways in WGCNA. (A) Analysis of scale-free fit index and mean connectivity for various soft-threshold powers. (B) Enrichment of KEGG pathways by WGCNA.

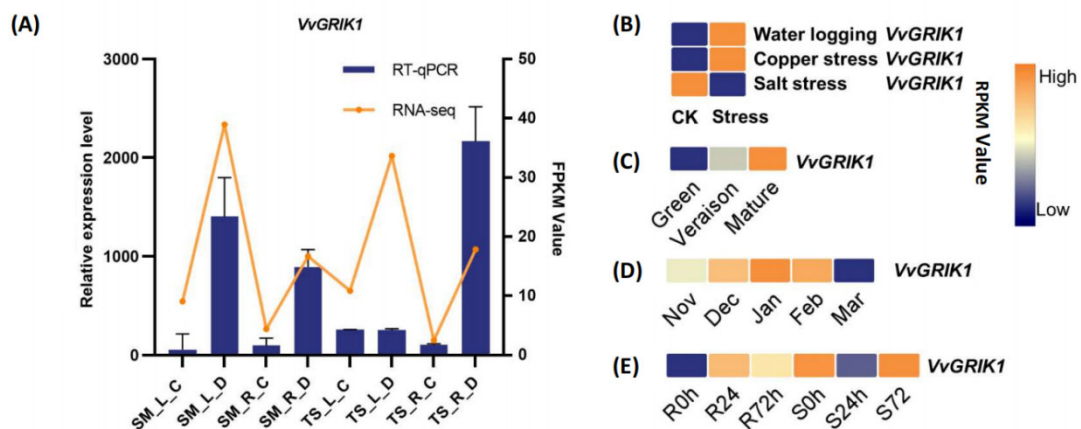


Figure S8 Analysis of VvGRIK1 gene expression patterns under different stress and different growth and development periods. (A) Drought stress. (B) Waterlogging stress, Copper stress, Salt stress. (C) different stages of fruit development (green, veraison, mature). (D) bud dormancy. (E) Downy mildew (R: Disease resistance, S susceptibility).

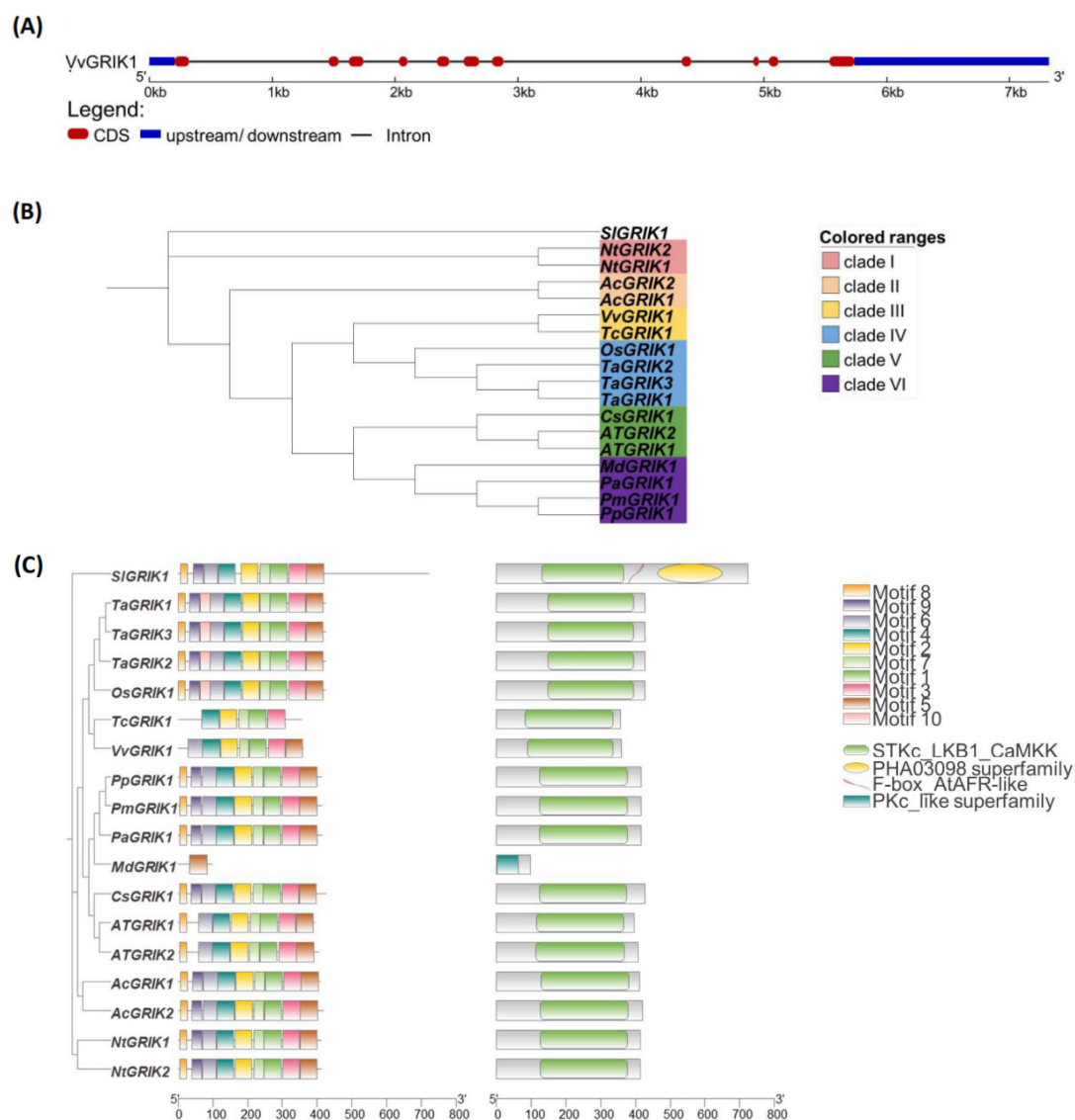


Figure S9 GRIKs bioinformatics analysis. (A) *VvGRIK1* gene structure analysis. (B) Phylogenetic tree analysis of GRIKs in 13 different species. (C) Analysis of conserved motif (left) and conserved domain (right) of GRIK protein.

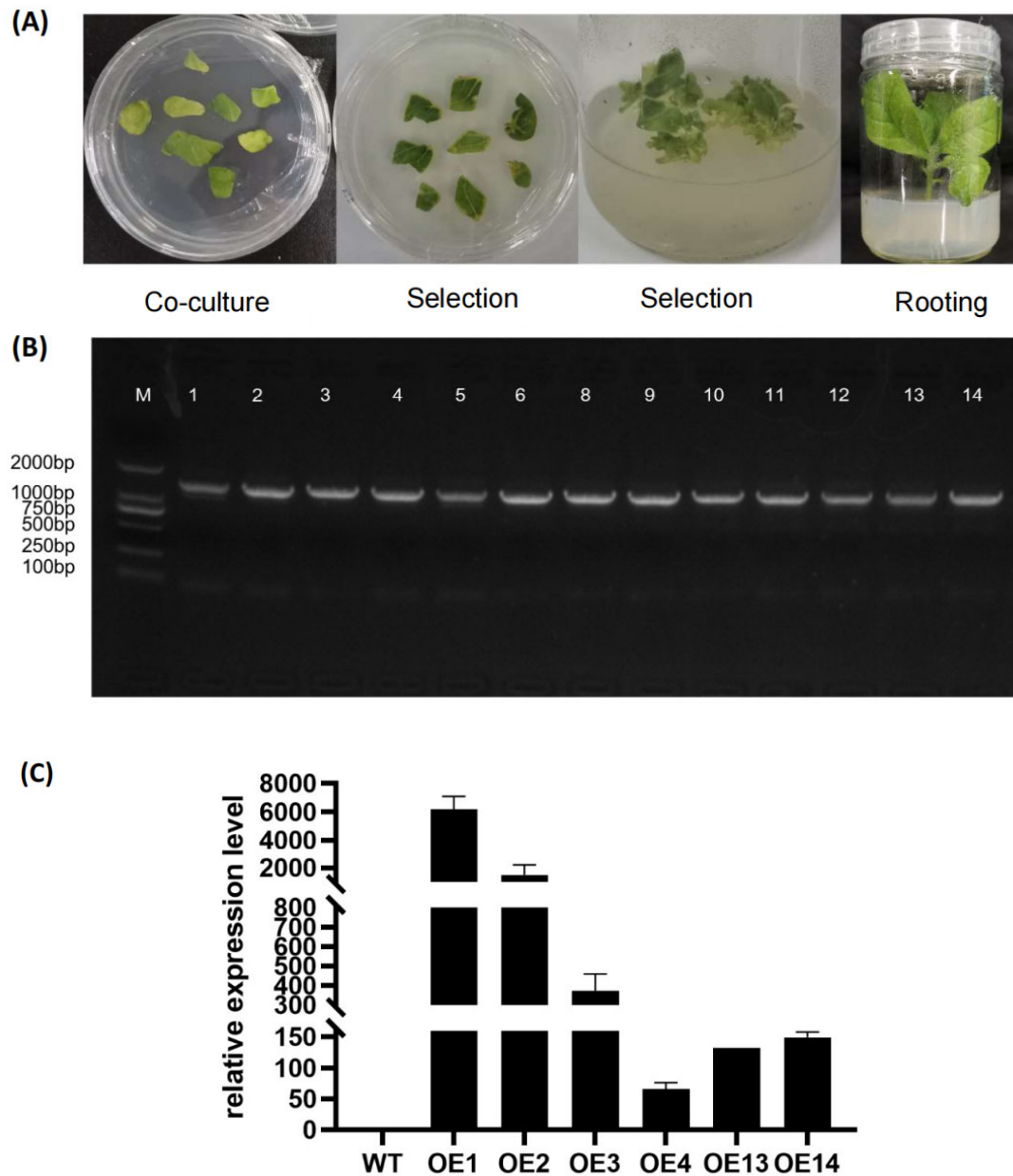


Figure S10 Genetic transformation and transgenic line identification of *VvGRIK1* transgenic Tobacco. (A) Genetic transformation system of transgenic tobacco. (B) PCR Identification of transgenic lines. (C) Quantitative analysis of transgenic lines.

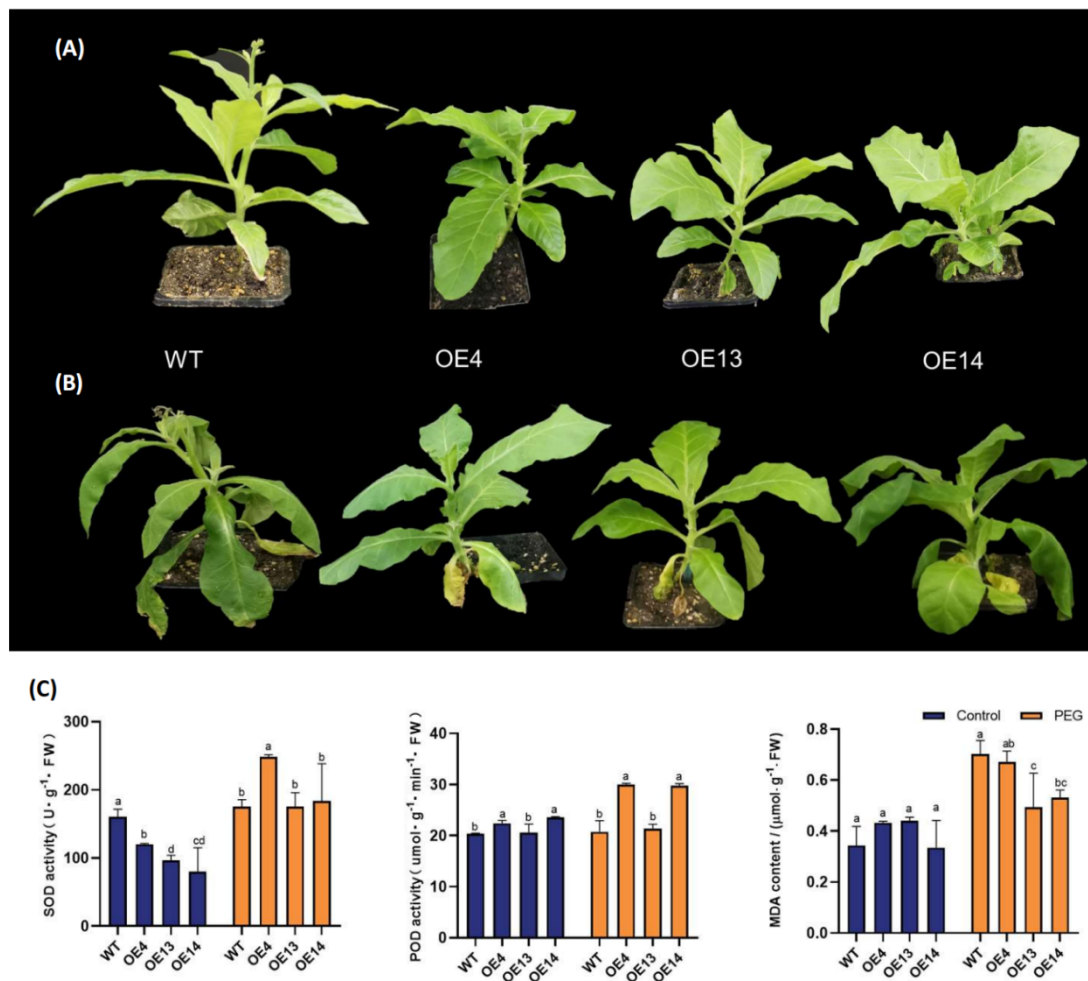


Figure S11 Growth of *VvGRIK1* transgenic tobacco after PEG treatment. (A) Phenotype on day 0 of PEG treatment. (B) Phenotype on day 10 of PEG treatment. (C) SOD(left); POD(middle); MDA(right). The different letters mean significant differences at $P < 0.05$.