



Figure S1. Phenotype changes of S01 and S26 drought treatment groups and control groups

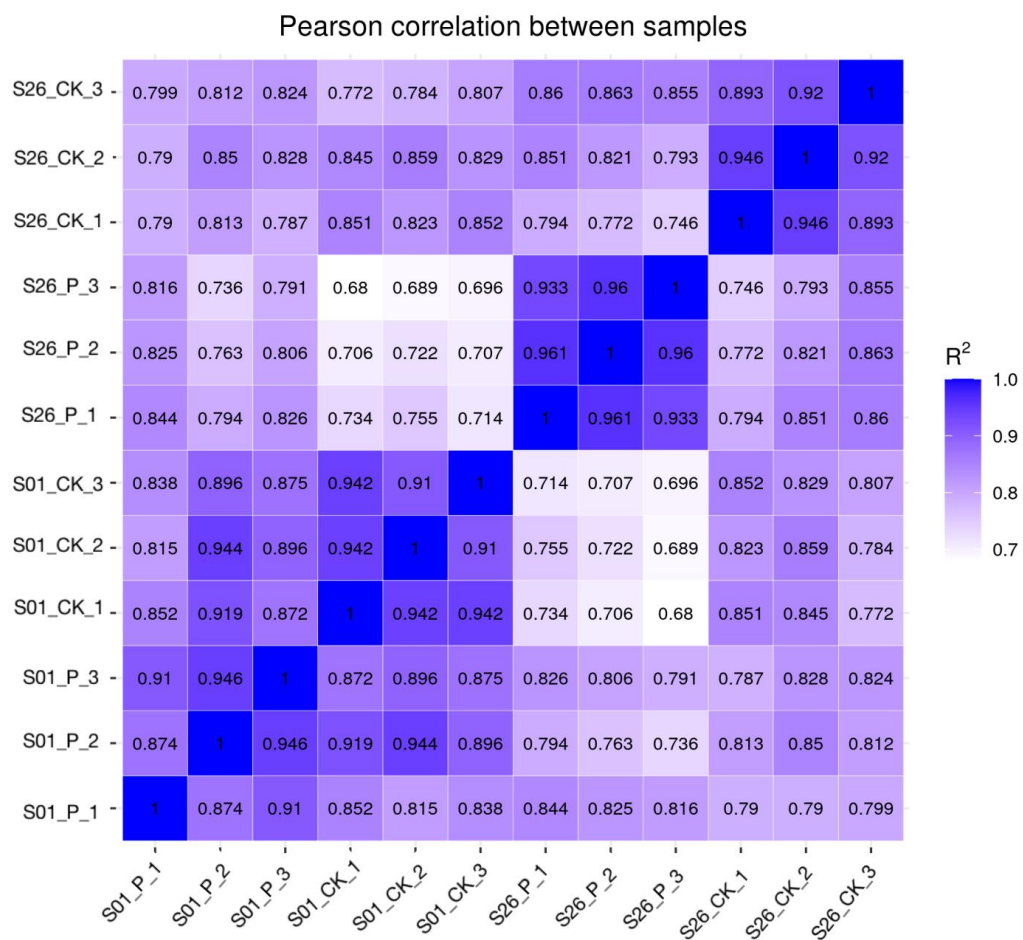


Figure S2. Correlation analysis of sample gene expression levels

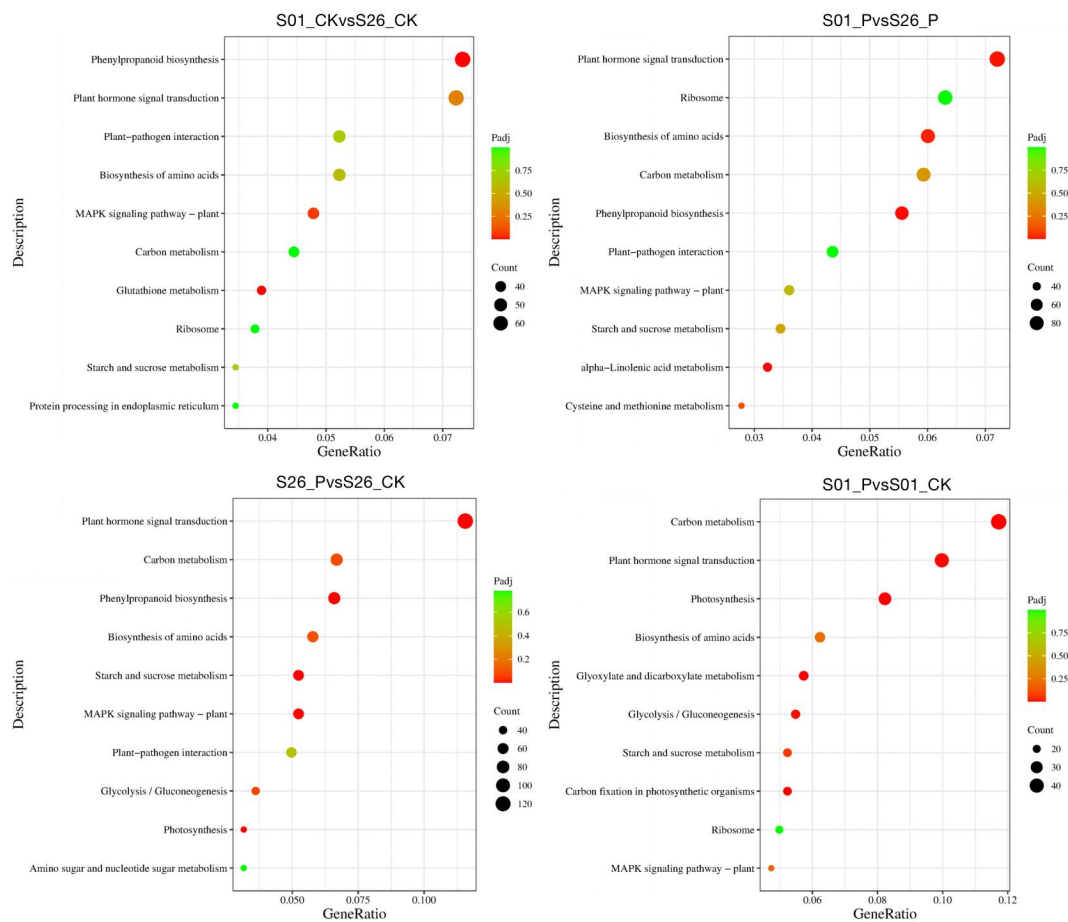


Figure S4. KEGG metabolic pathway analysis of DEGs. The size of the circles represents the number of genes annotated to this pathway

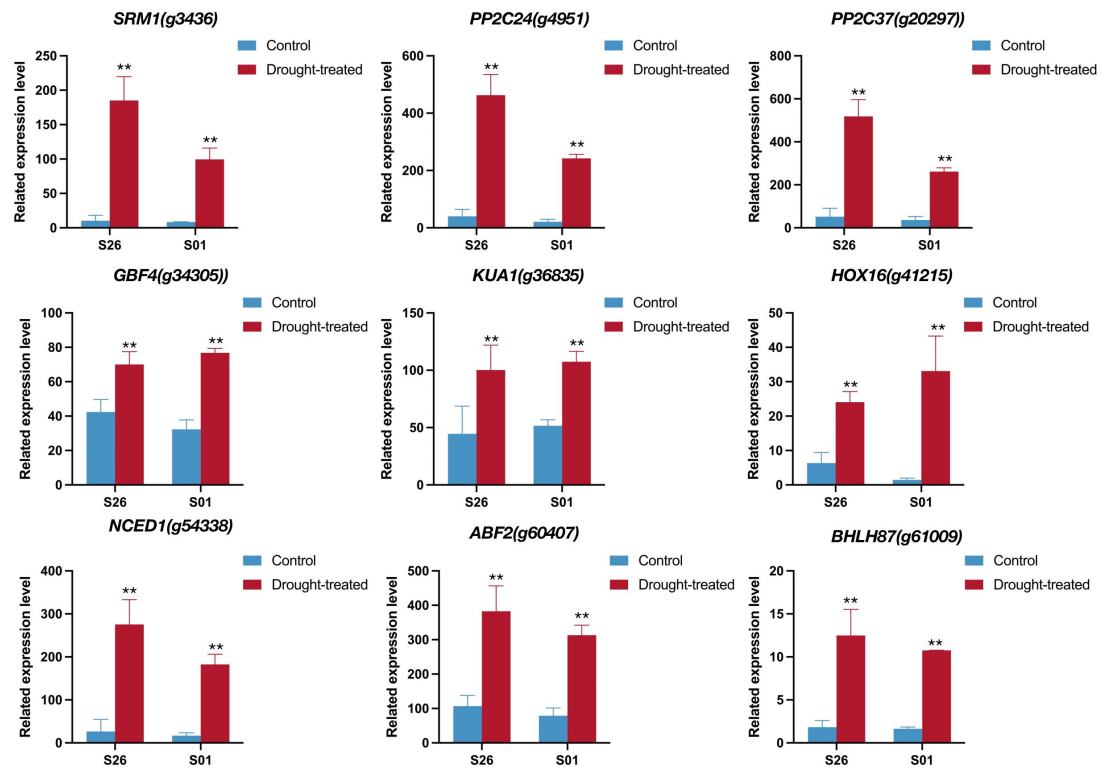


Figure S5. RNA seq data gene expression levels. ** indicates that the different physiological index between control group and experimental group was significant at P value < 0.01 .

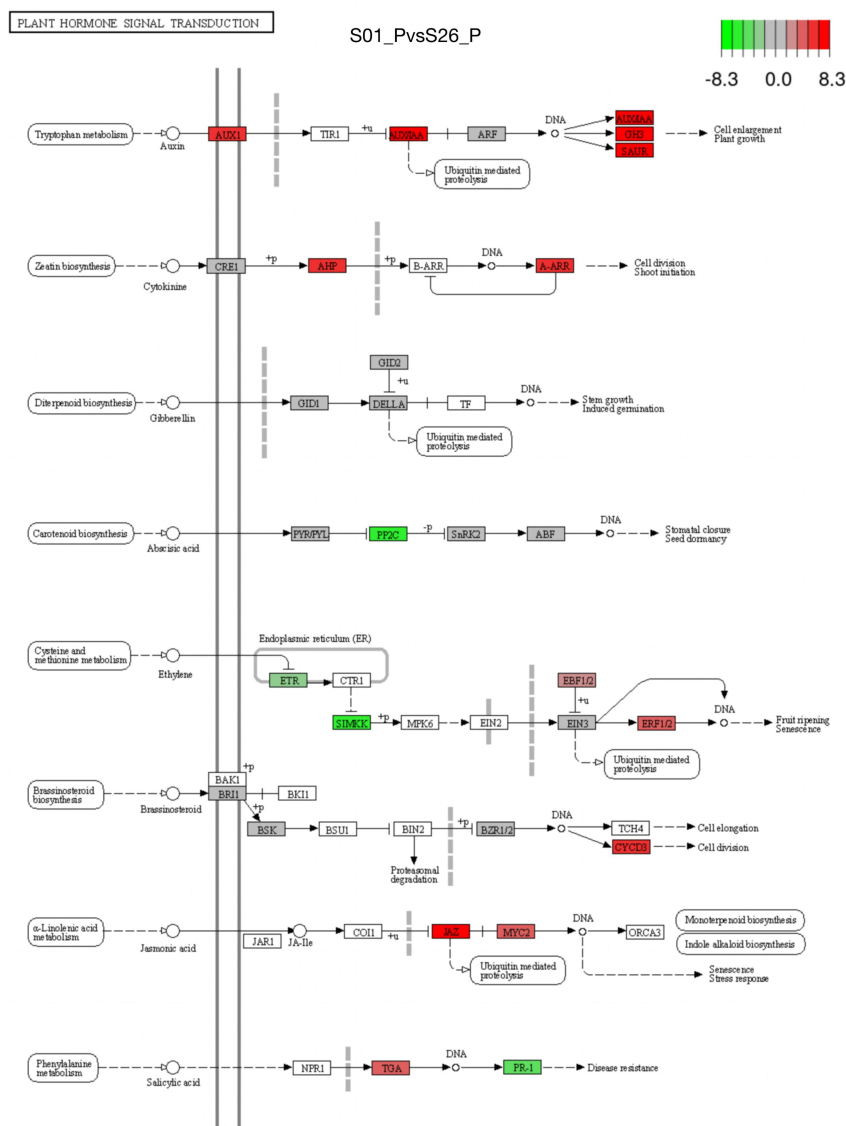


Figure S6. Plant hormone conduction pathway diagram