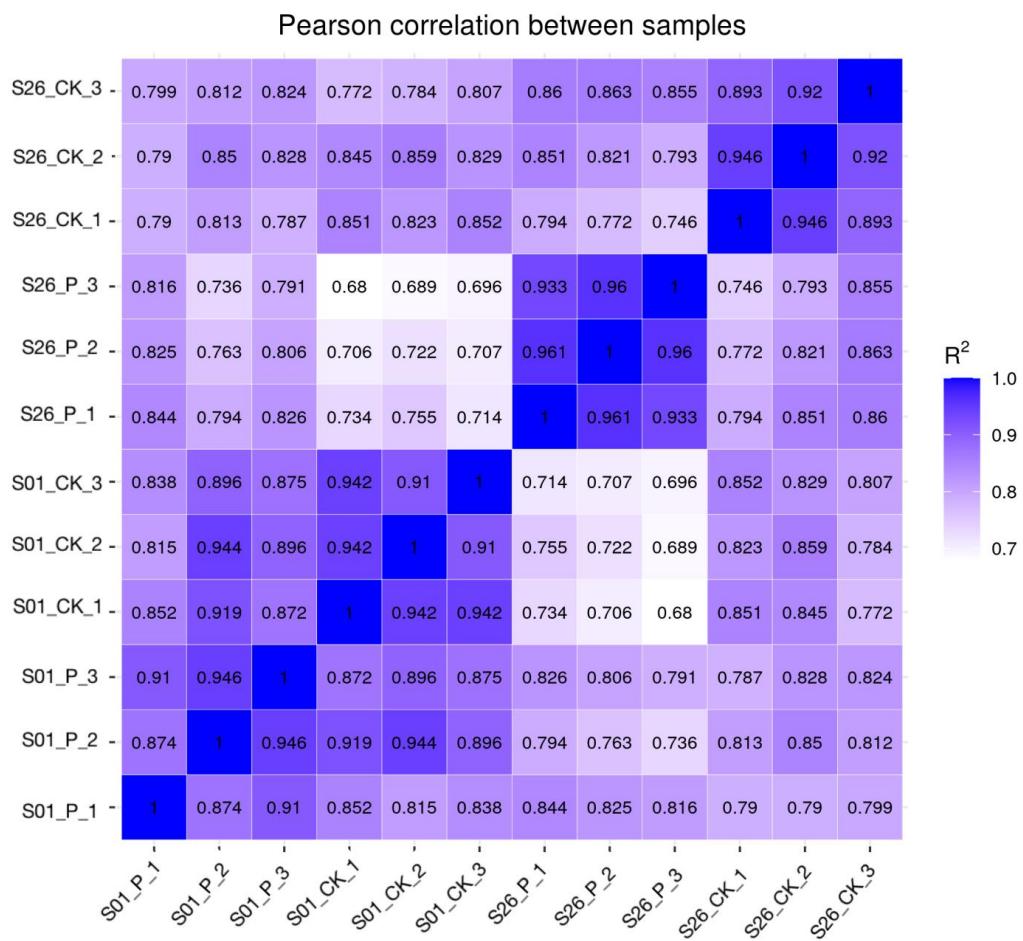
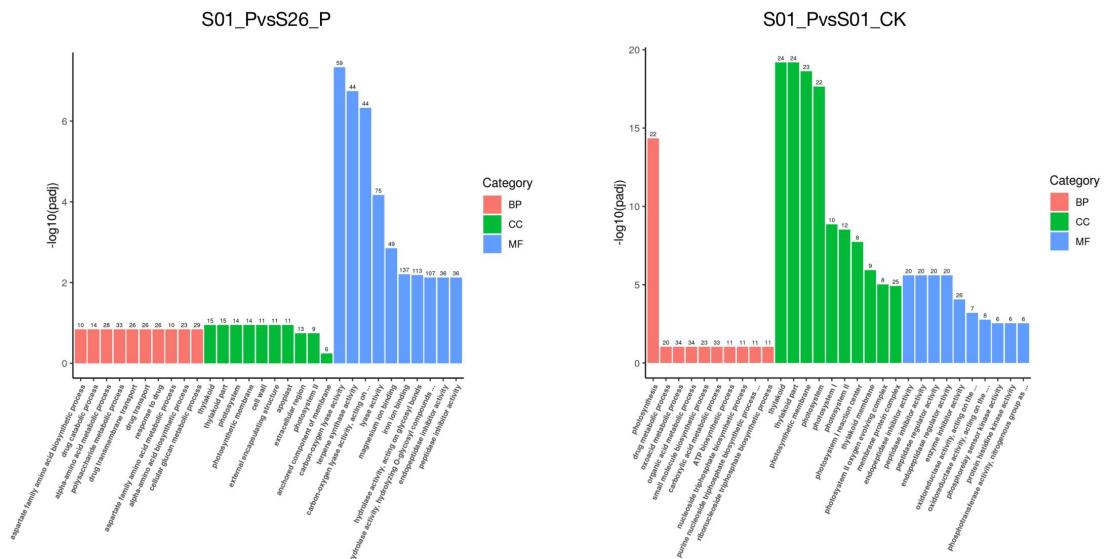




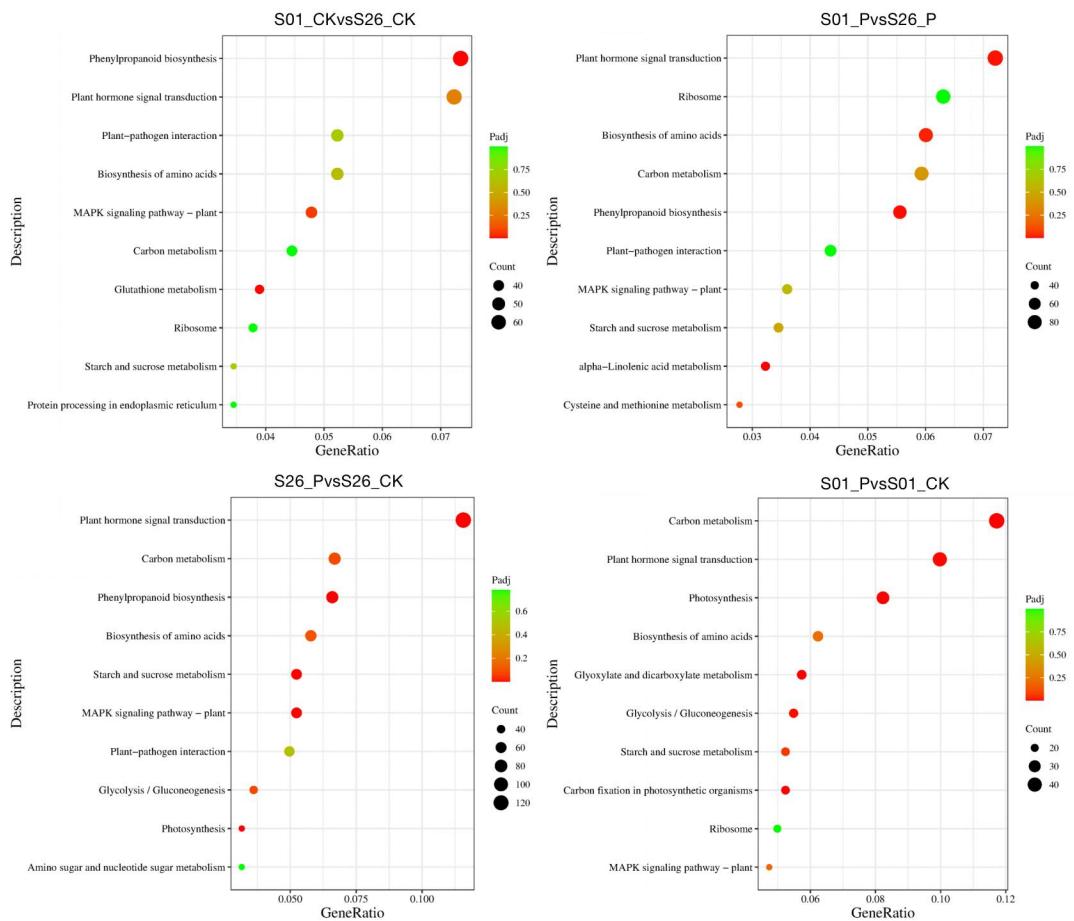
**Figure S1.** Phenotype changes of S01 and S26 drought treatment groups and control groups



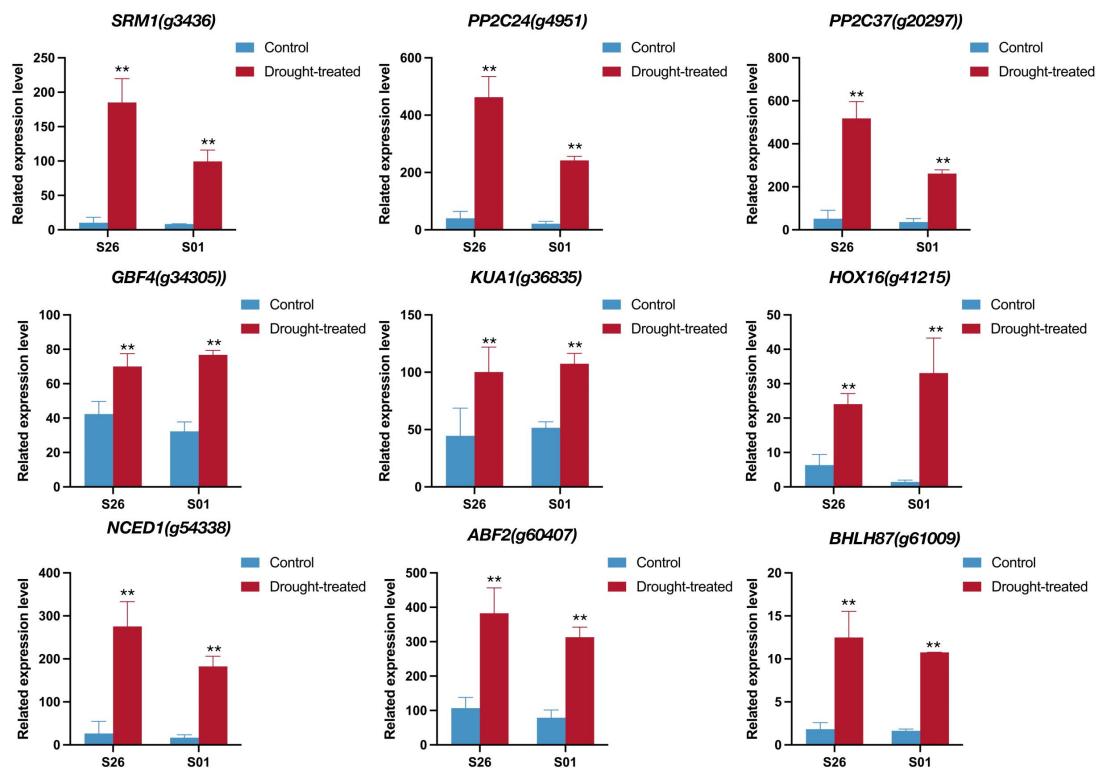
**Figure S2.** Correlation analysis of sample gene expression levels



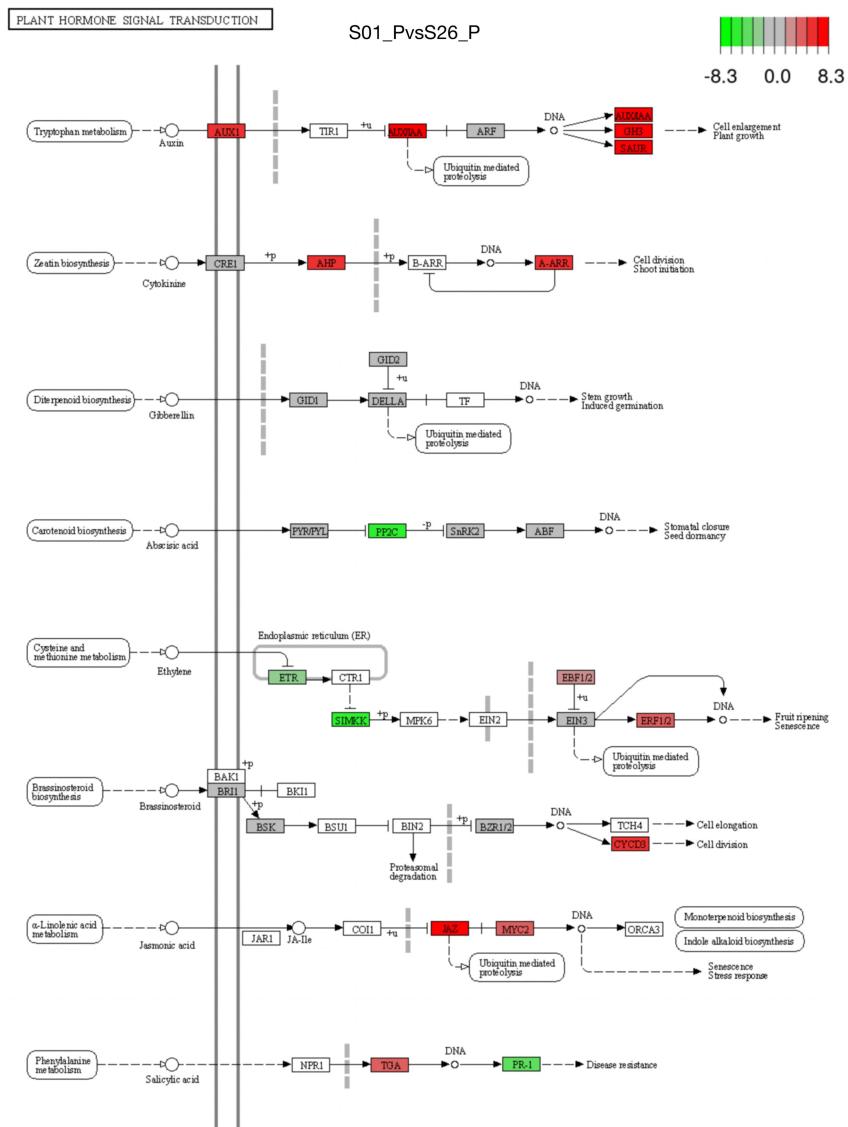
**Figure S3.** Differential gene GO enrichment analysis results. BP=biological process, CC=cellular component; MF=molecular function



**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