



Figure S1 Weighted gene co-expression network analysis in response to drought. (A) Statistical figure of the number of genes contained in each module of WGCNA analysis. The module is represented by abscissa (represented by the module color); the ordinate represents the number of members belonging to the module; (B) Analysis of the correlation between genes and phenotypes in WGCNA module. The upper part of the figure is the genetic hierarchical cluster tree, the middle is the module belonging to the gene and the lower part shows the heat map of the correlation between genes and traits in the module. Each row represents a phenotype, and each column represents a gene within the module. Color represents correlation. By default, red represents positive correlation and green represents negative correlation. SWC=soil relative water content, RWC =leaf relative water content.