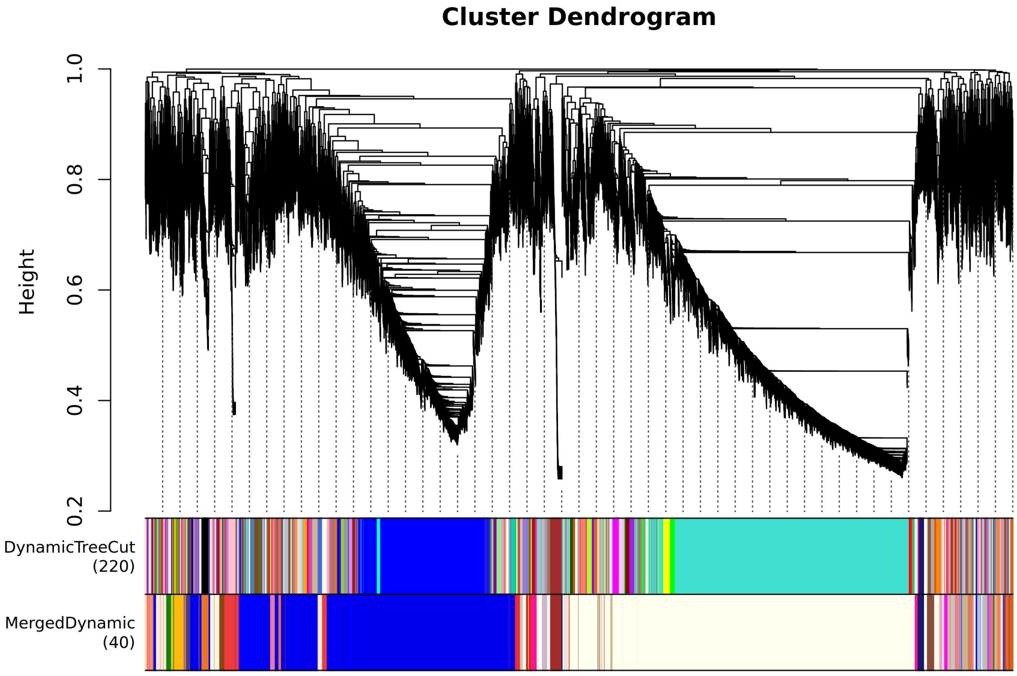
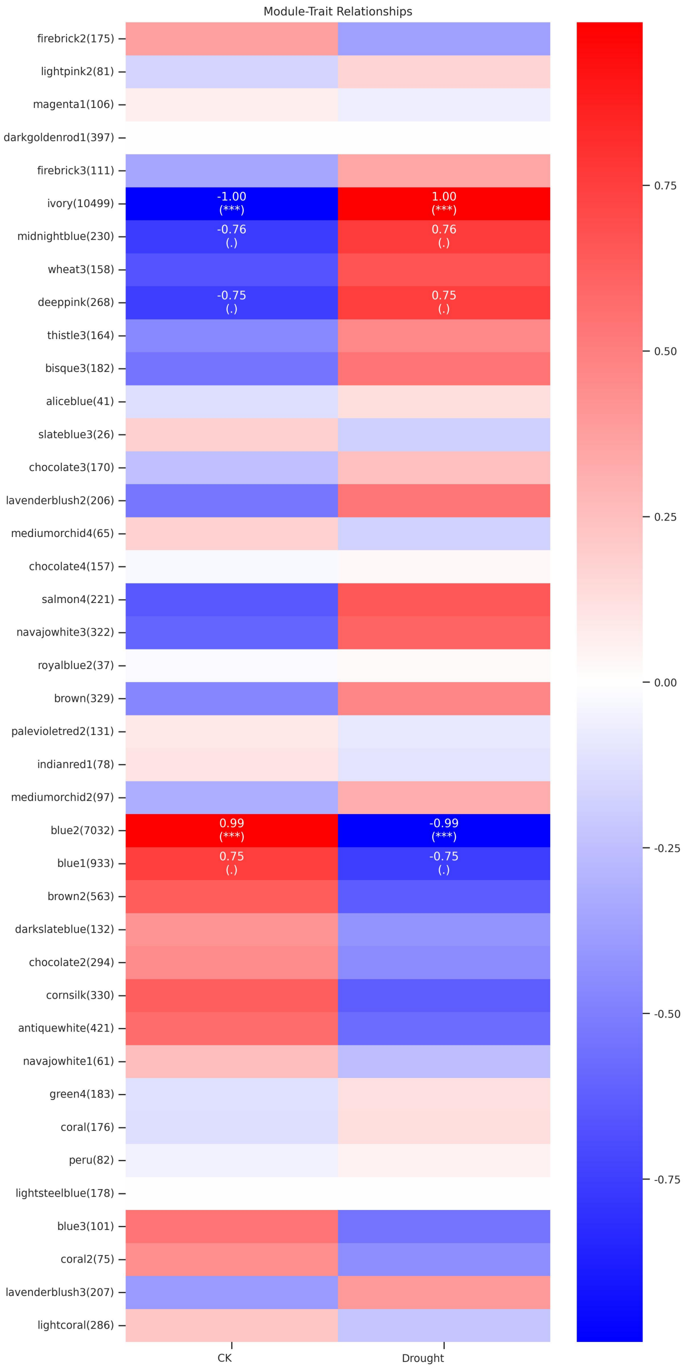
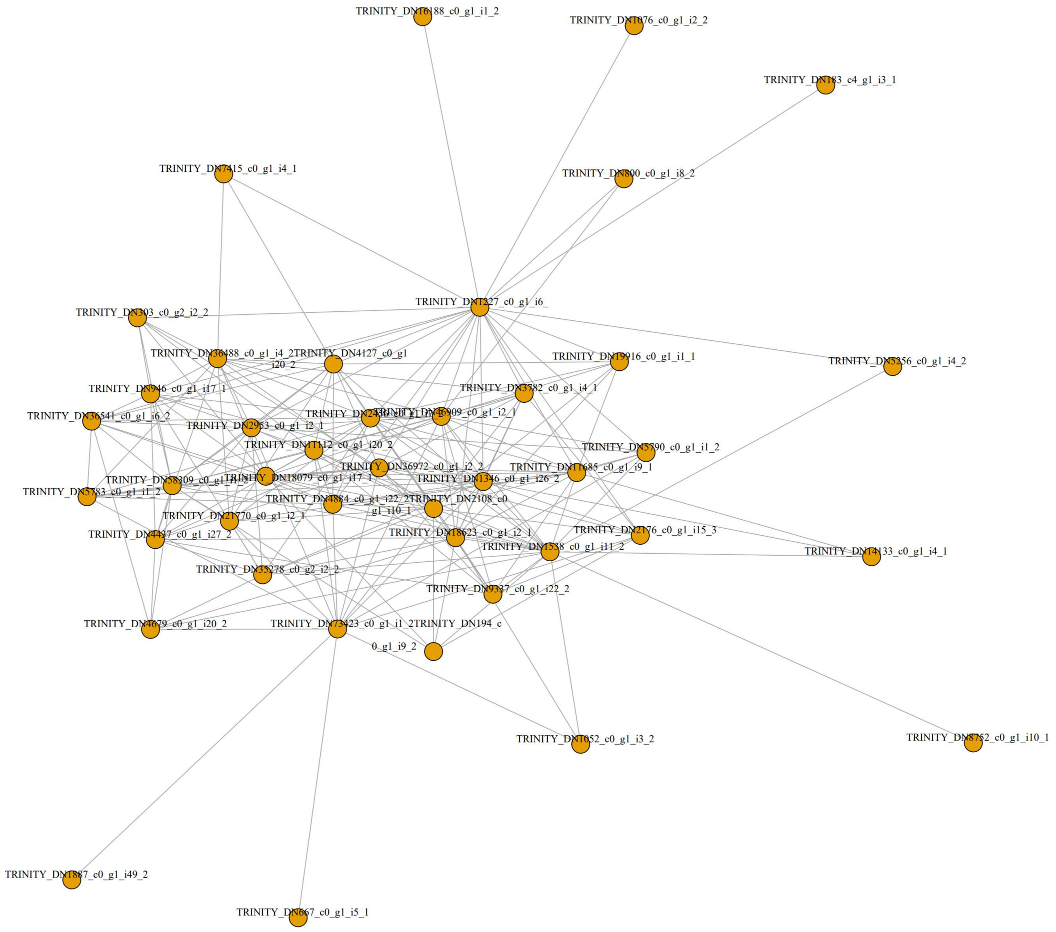


Supplementary Fig. S1a

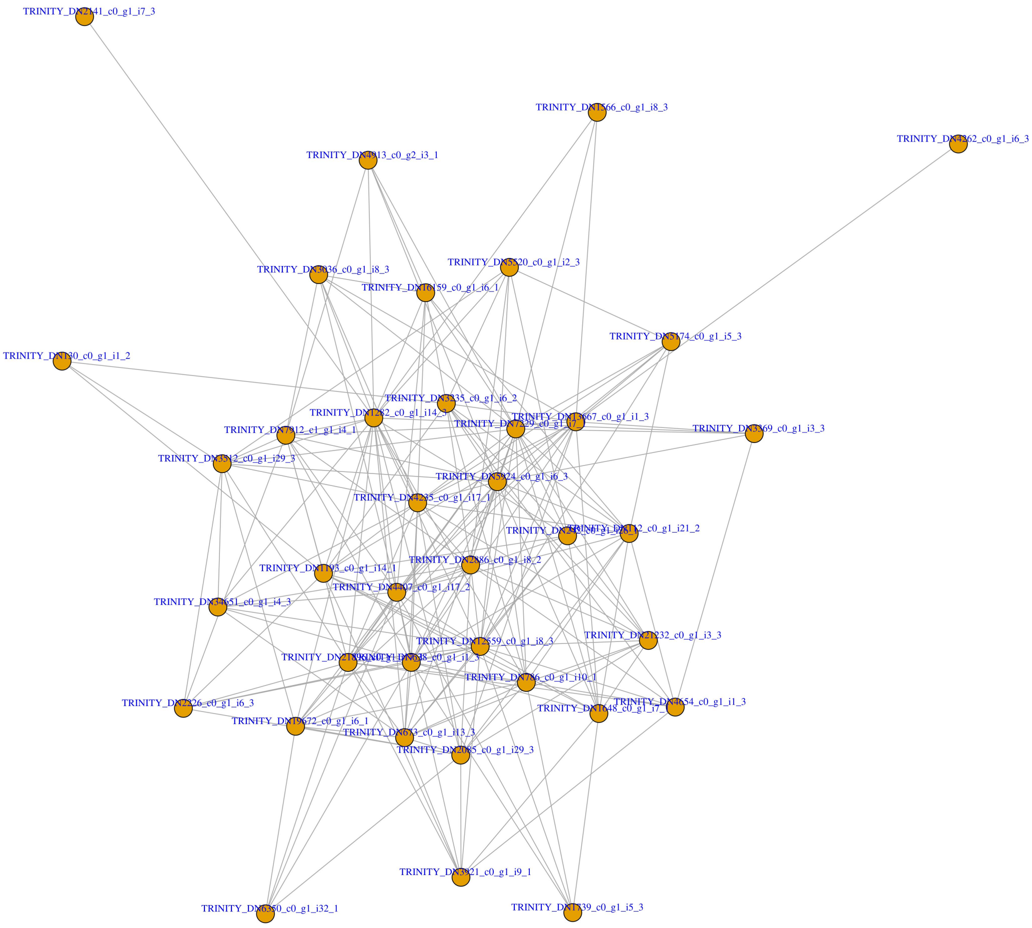
Identification and Analysis of WGCNA Modules. The upper panel ofthe figure shows the gene clustering tree (dendrogram) constructed based on the dissimilaritymatrix (dissTOM) derived from weighted correlation coefficients. The lower panel displays themodule assignment, where each color represents a distinct co-expression module.



Supplementary Fig. S1b WGCNA Module-Trait Relationship Heatmap. Modules associated with each trait were screened using a threshold of an absolute correlation coefficient ≥ 0.3 and a p-value < 0.05.



Supplementary Fig. S1c Analysis of Hub Genes in the Ivory Module. Hub genes within the ivory module were defined as the top 50 genes possessing the highest intramodular connectivity. Therelationships among these hub genes were subsequently visualized and analyzed.



Supplementary Fig. S1d Analysis of Hub Genes in the Blue2 Module. Hub genes within theblue2 module were defined as the top 50 genes possessing the highest intramodular connectivity.The relationships among these hub genes were subsequently visualized and analyzed.