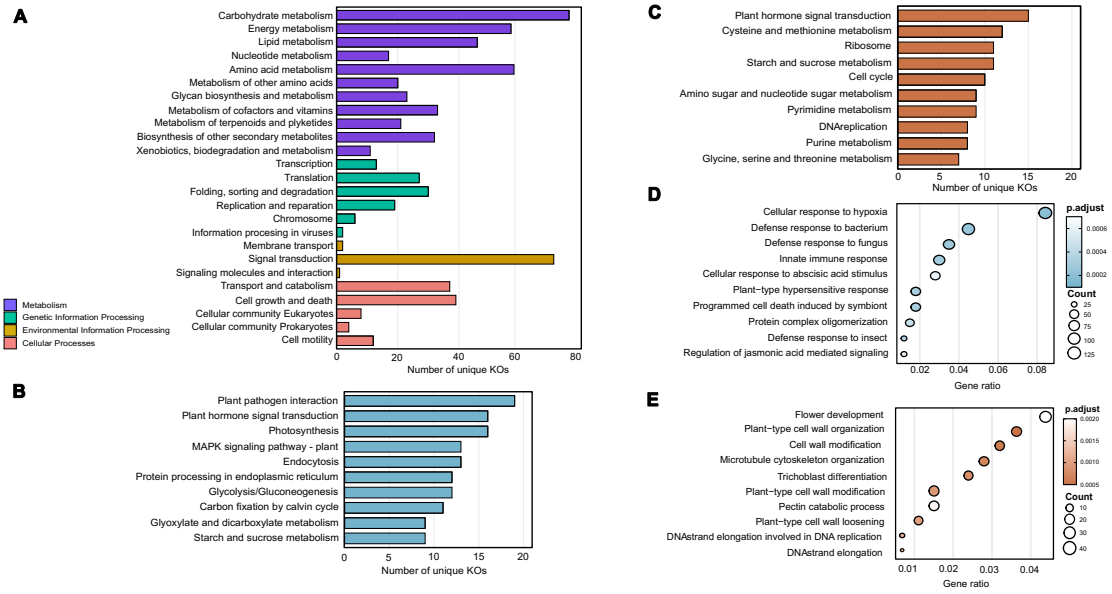



**Figure S2. KEGG pathway and Gene Ontology enrichment from differentially expressed genes (DEGs) in *Arabidopsis thaliana* roots during co-culture with *Trichoderma atroviride*.** (A) Bar plot showing KEGG general pathway categories present among *A. thaliana* DEGs; horizontal bars indicate the total number of unique KEGG orthologs. (B–C) Bar charts showing the most represented KEGG pathways. Bars represent the number of unique KEGG orthologs mapped for upregulated genes (cyan bars) (B), or down-regulated genes (orange bars) (C) in *A. thaliana* roots. (D–E) Balloon plots of Gene Ontology (GO) Biological Process enrichment for *A. thaliana* up-regulated (D) and down-regulated (E) genes. Dot size represents the number of genes per term, and color intensity indicates FDR-adjusted p-values; the x-axis represents the Gene ratio, and the y-axis lists GO terms.