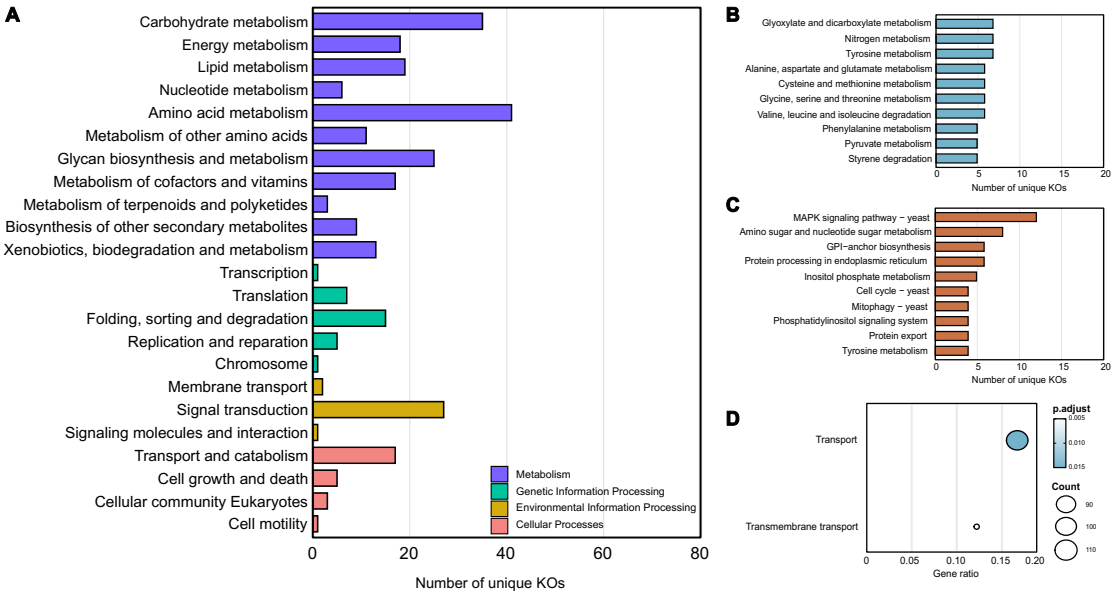


Figure S4. KEGG pathway and Gene Ontology enrichment from differentially expressed genes (DEGs) in *Trichoderma atroviride* mycelium during co-culture. (A) Bar plot showing KEGG gen-eral pathway categories enriched among *T. atroviride* DEGs. The x-axis represents the number of unique KOs per pathway, and the y-axis lists pathway categories. (B–C) Bar charts showing the most enriched KEGG pathways based on differential gene expression, highlighting those with the greatest numbers of up-regulated (red bars) (B), and down-regulated (blue bars) (C) genes in *T. atroviride* mycelium. (D) Balloon plots of Gene Ontology (GO) Biological Process enrichment for all *T. atroviride* DEGs. 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.