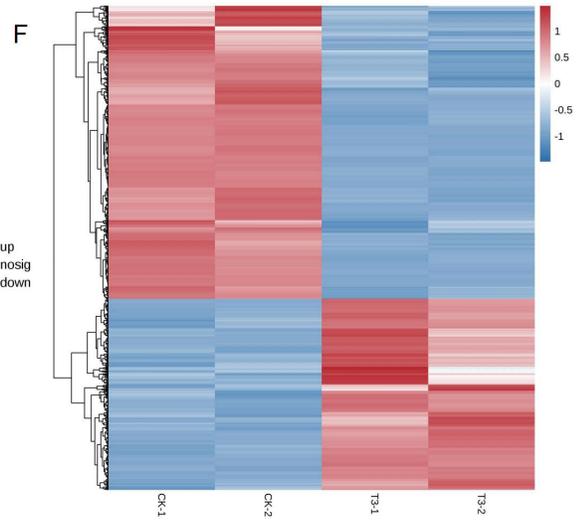
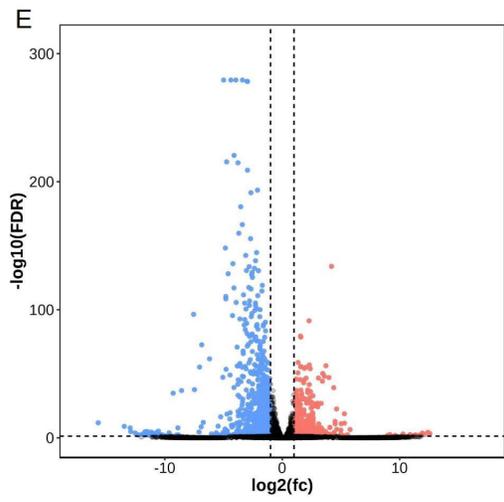
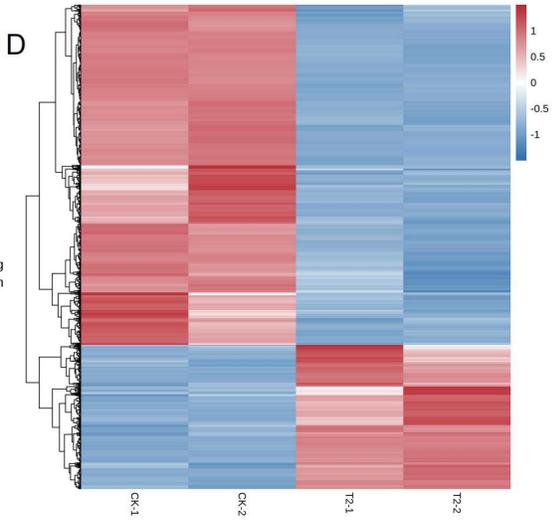
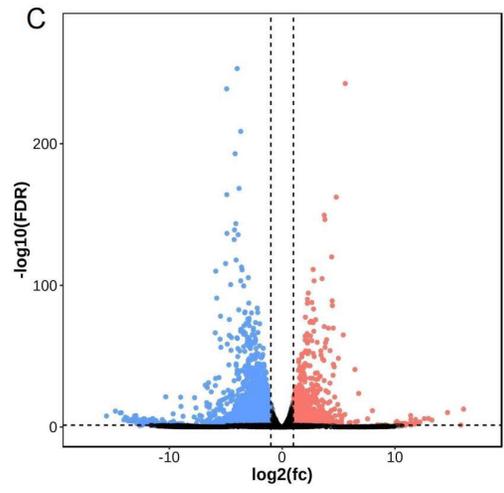
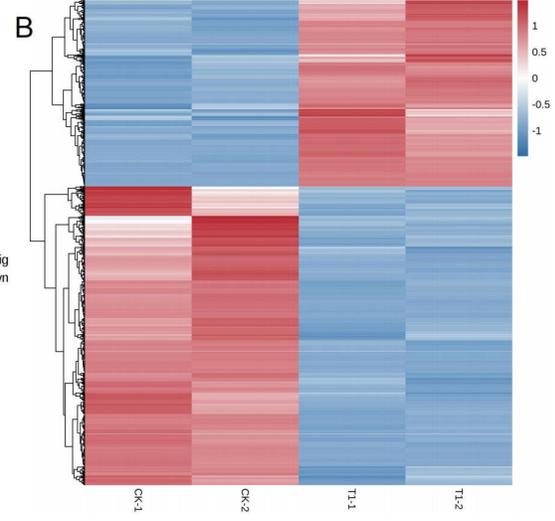
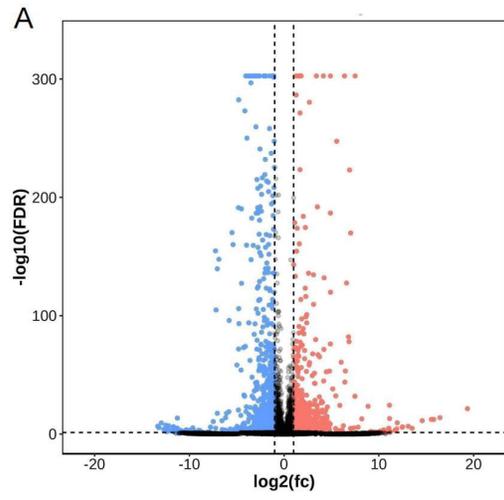
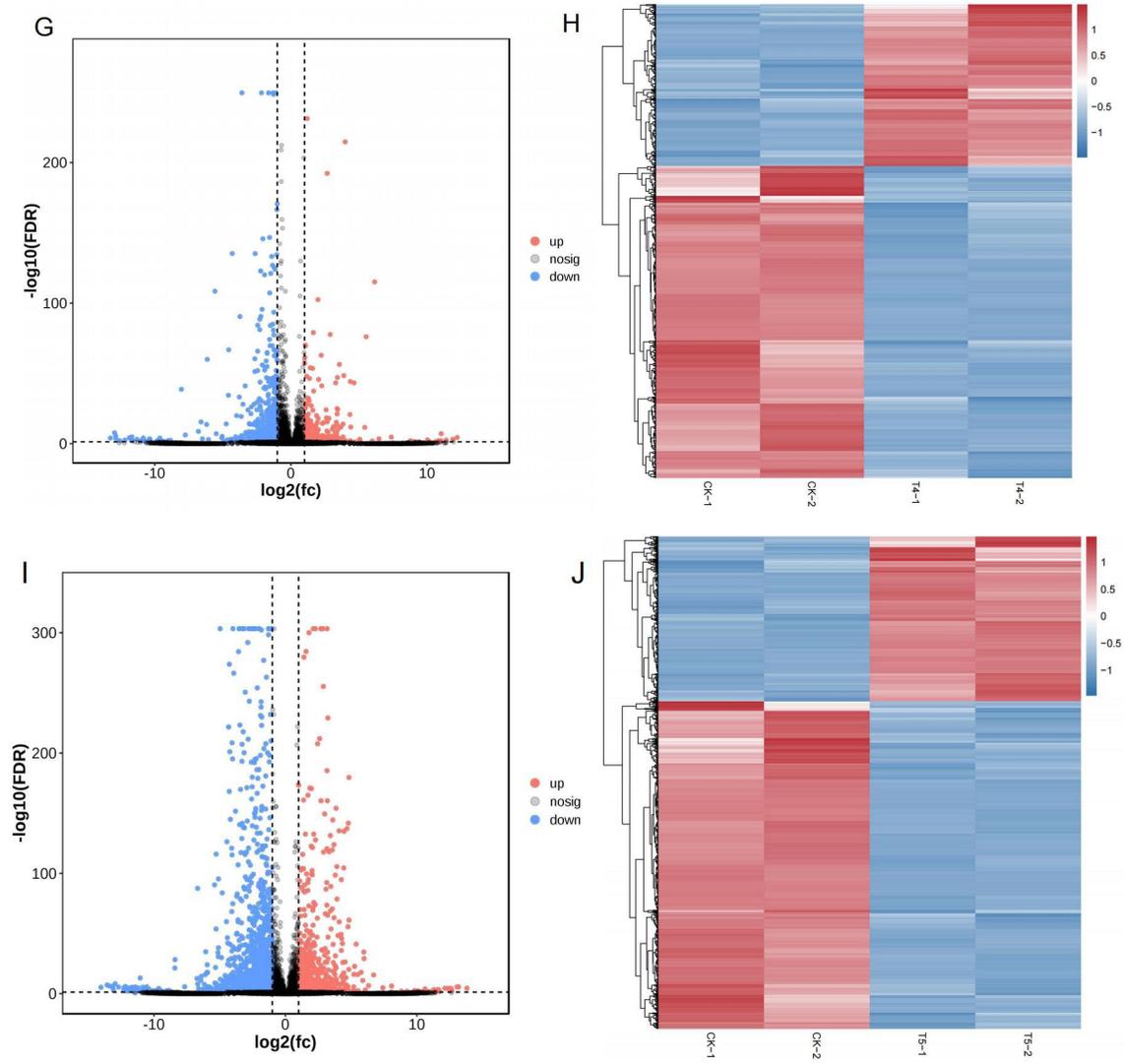
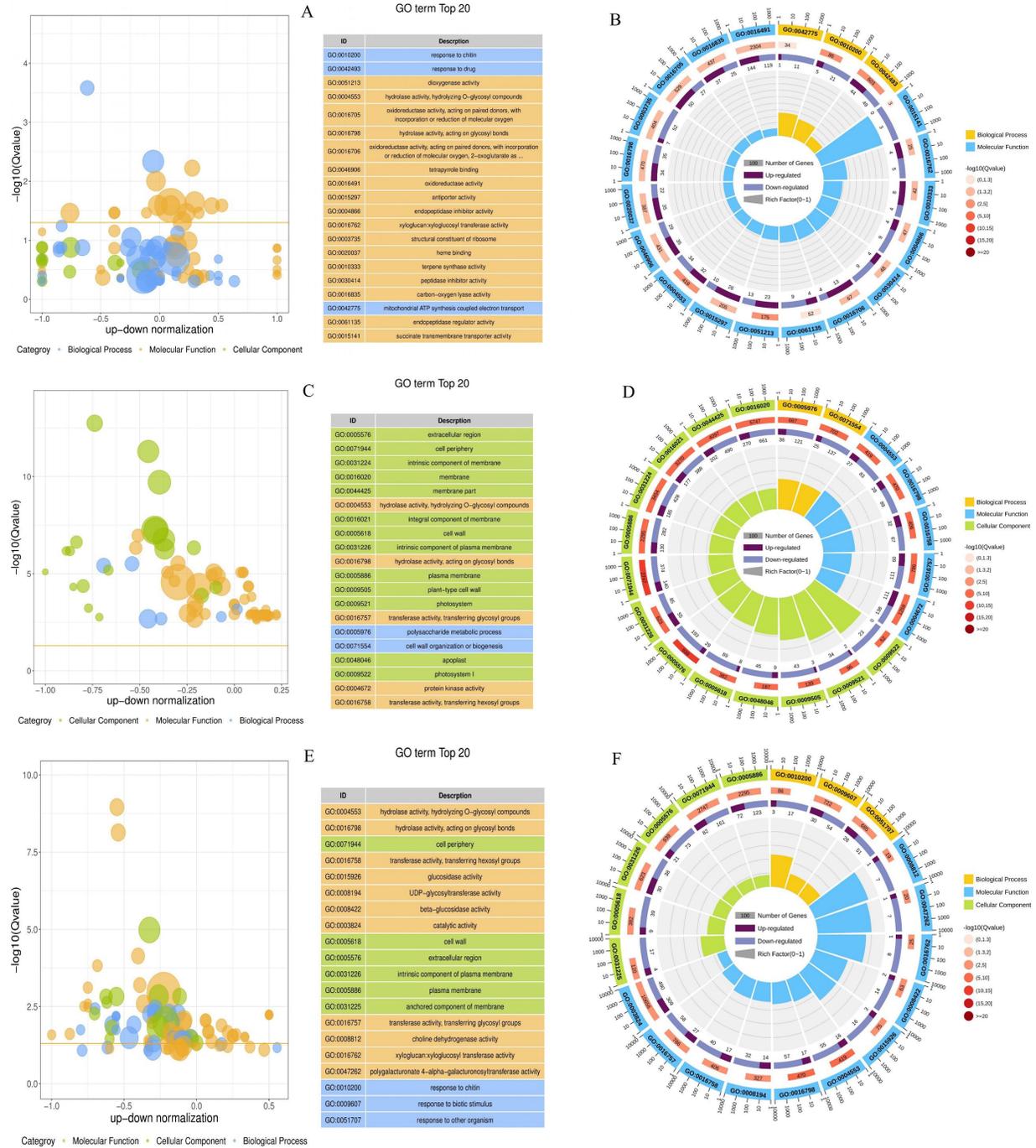


**Figure S1.** (A) alignment of the sample's clean reads to the reference genome. (B, C) genes coverage distribution in CK-1, CK-2. (D, E) genes coverage distribution in T1-1, T1-2. (F, G) genes coverage distribution in T2-1, T2-2. (H, I) genes coverage distribution in T3-1, T3-2. (J, K) genes coverage distribution in T4-1, T4-2. (L, M) genes coverage distribution in T5-1, T5-2. Mg sufficiency (CK; 3 mM), deficiency (T1; 0 mM), low (T2; 1 mM) moderate low (T3; 2 mM) toxicity (T4; 6 mM) and high toxicity (T5; 9 mM).



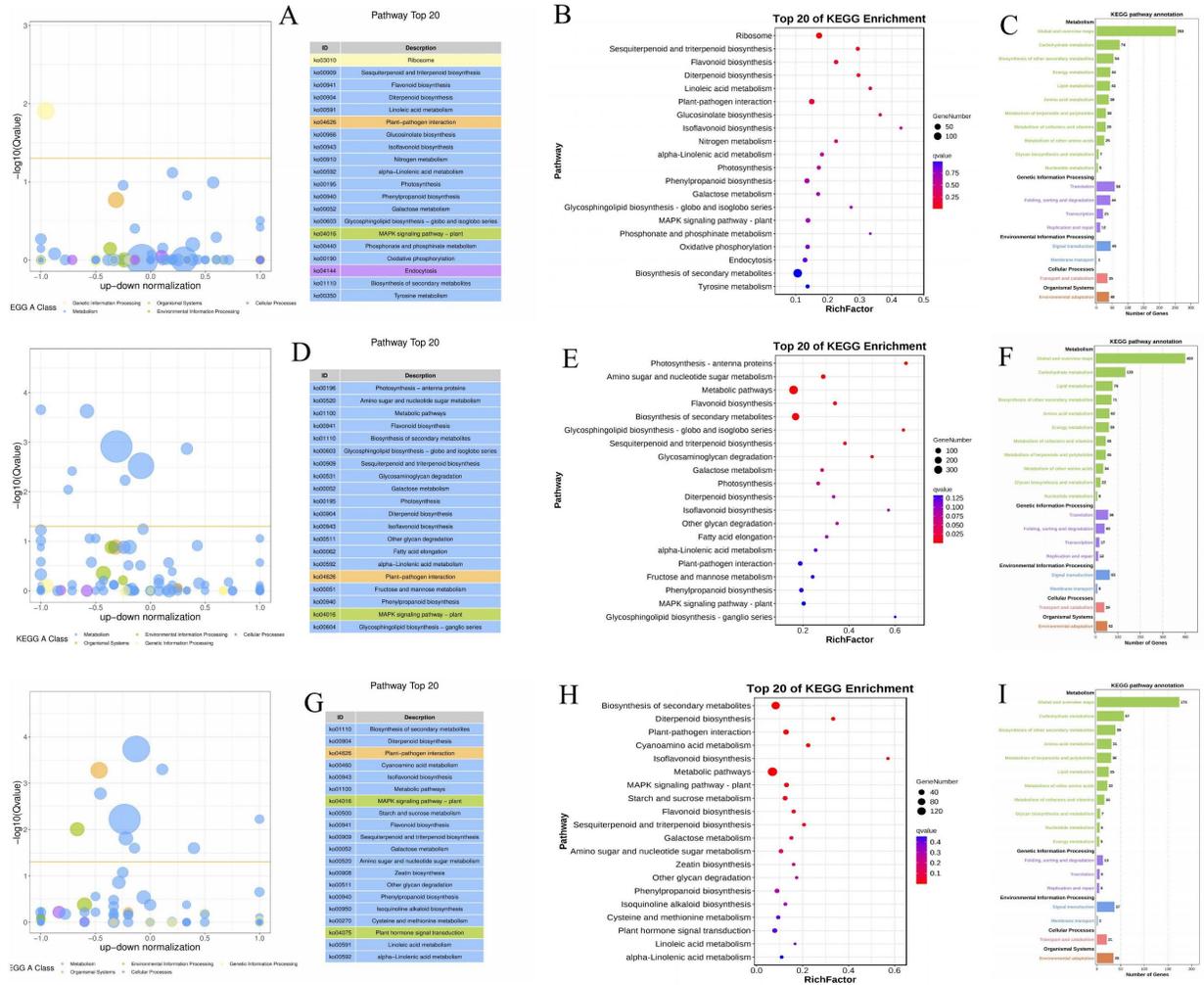


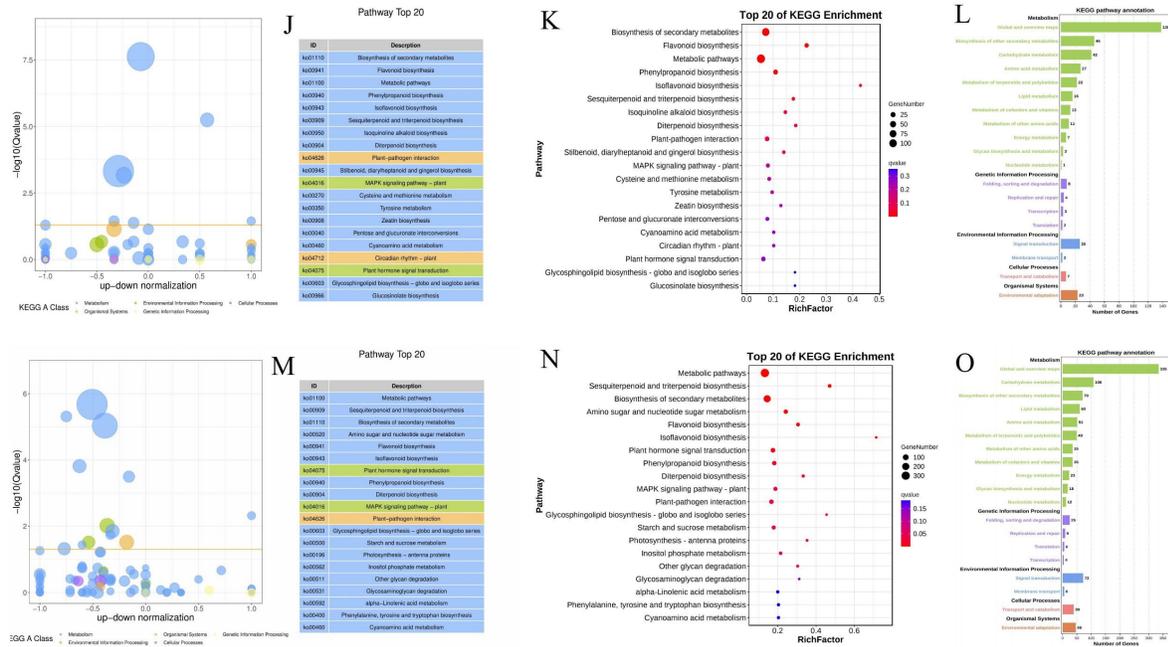
**Figure S2.** Volcano plot and heatmap showing the distribution of the differentially expressed genes (DEGs) in T1 (A, B), T2 (C, D), T3 (E, F), T4 (G, H) and T5 (I, J). Red and blue colors represent genes with higher and lower concentrations, respectively.





**Figure S4.** Gene Ontology (GO) enrichment results of the DEGs Mg toxicity treatments based on q-value <0.05. (b) and enrichment factor. (A, B) Top 20 GO enrichment in T4. (C, D) Top 20 GO enrichment in T5. (E) GO term secondary classification involving the DEGs





**Figure S5.** KEGG enrichment analysis of the DEGs across Mg-deficiency and Mg supply treatments. Rich Factor represents the ratio between the number of DEGs mapped to a certain pathway and total number of genes mapped to the corresponding KEGG pathway. (A-C) KEGG pathways that are significantly enriched based on q-value ( $FDR \leq 0.05$ ) in T1. (D-F) KEGG pathways in T2. (G-I) KEGG pathways in T3. (J-L) KEGG pathways in T4. (M-O) KEGG pathways in T5.