



**Supplementary Figure 3. KEGG pathway enrichment analysis of differentially expressed genes (DEGs) between control (CK) and melatonin + drought (MD) conditions.** The bar graph illustrates the top KEGG pathways enriched among DEGs identified in CK vs. MD comparison. Pathways are grouped into categories such as Cellular processes, environmental information processing, genetic information processing and metabolism. The x-axis represents the percentage of genes annotated to each pathway, while numbers at the end of each bar indicate the gene count and proportion.