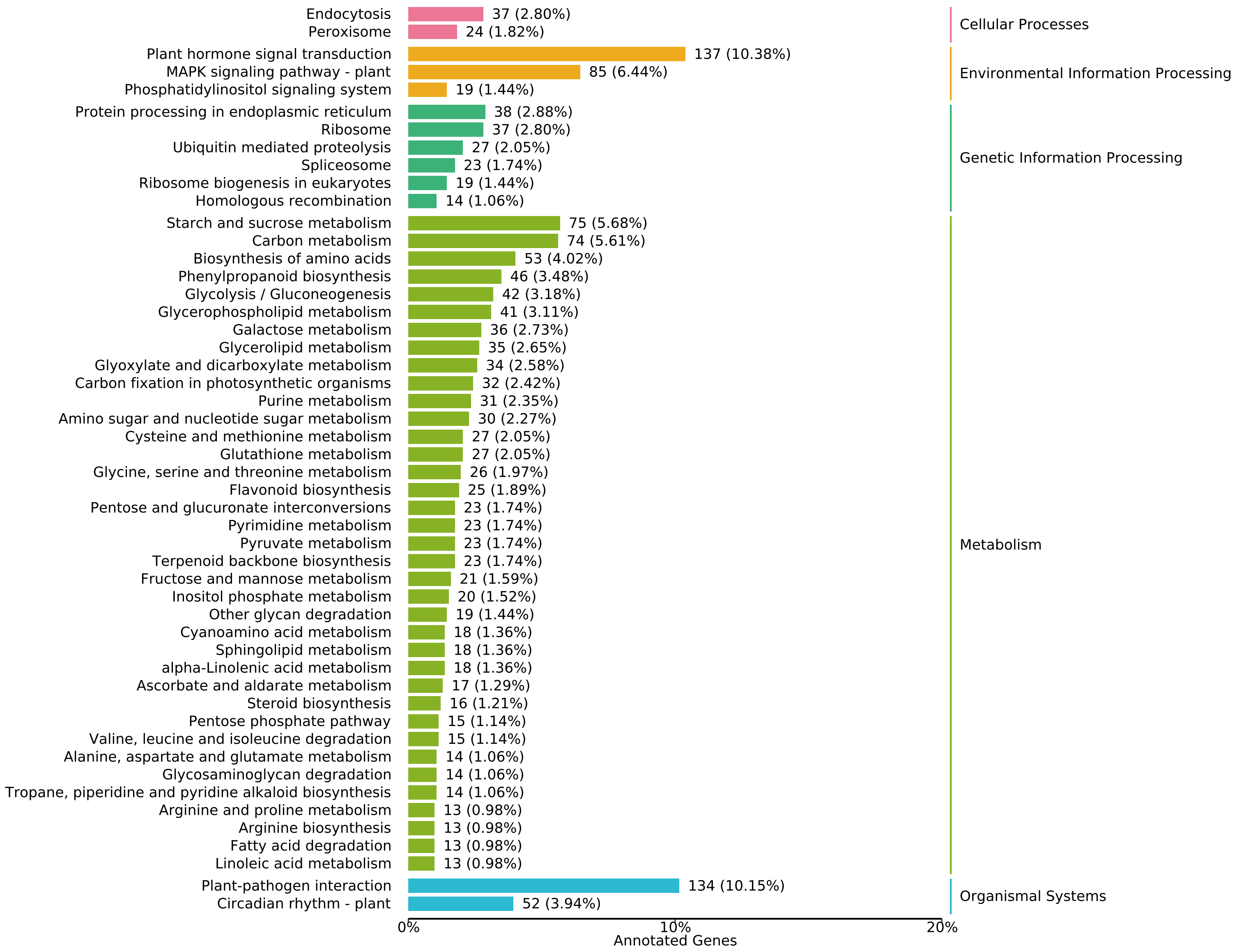

Supplementary Figure 4. KEGG pathway enrichment analysis of differentially expressed genes (DEGs) between drought (D) and melatonin + drought (MD) conditions. The bar graph illustrates the top KEGG pathways enriched among DEGs identified in D vs. MD comparison. Pathways are grouped into categories such 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.