

Enrichment Analysis Figures

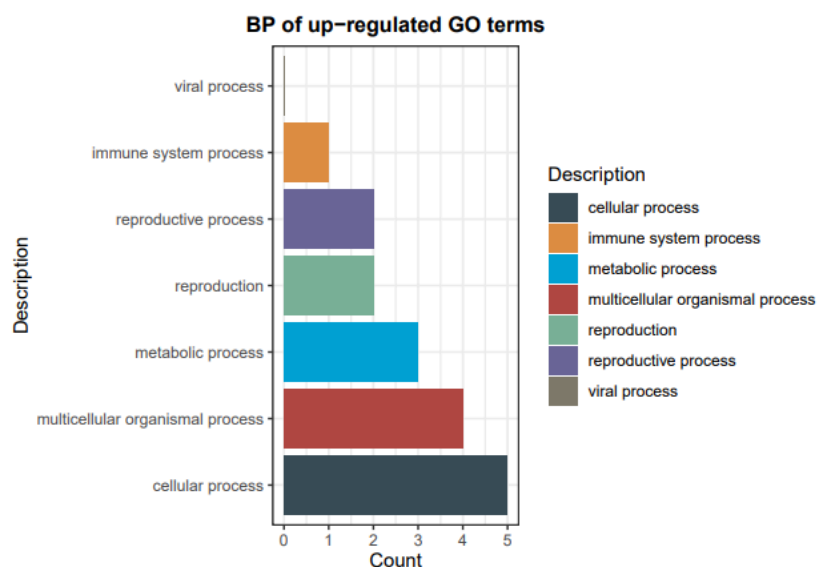


Figure 1

Barplot indicates how many up-regulated significant genes are annotated with a Biological process GO term (e.g. 5 up-regulated significant genes out of 10 are annotated with cellular process GO term).

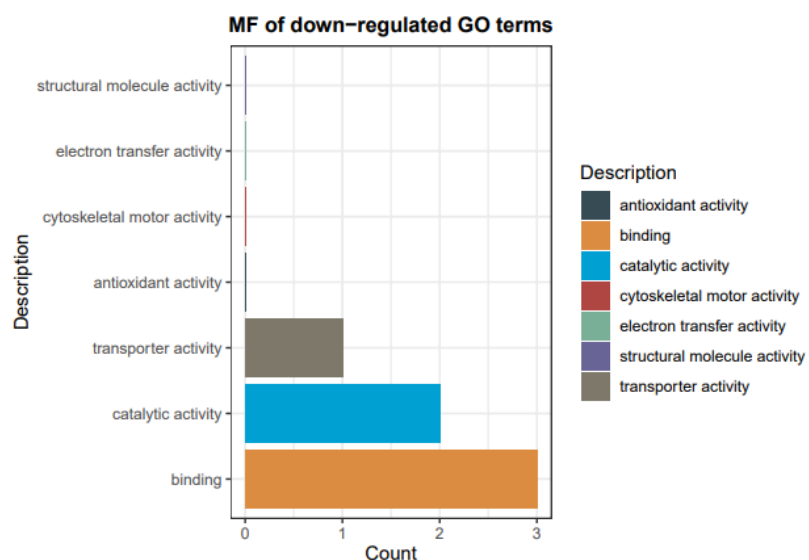


Figure 2

Barplot indicates how many down-regulated significant genes are annotated with a Molecular Function GO term (e.g. 3 down-regulated significant genes out of 6 are annotated with binding GO term).

Over-representation Analysis

☐ GO Enrichment Analysis:

1) Figures of enriched GO terms among up-regulated significant genes.

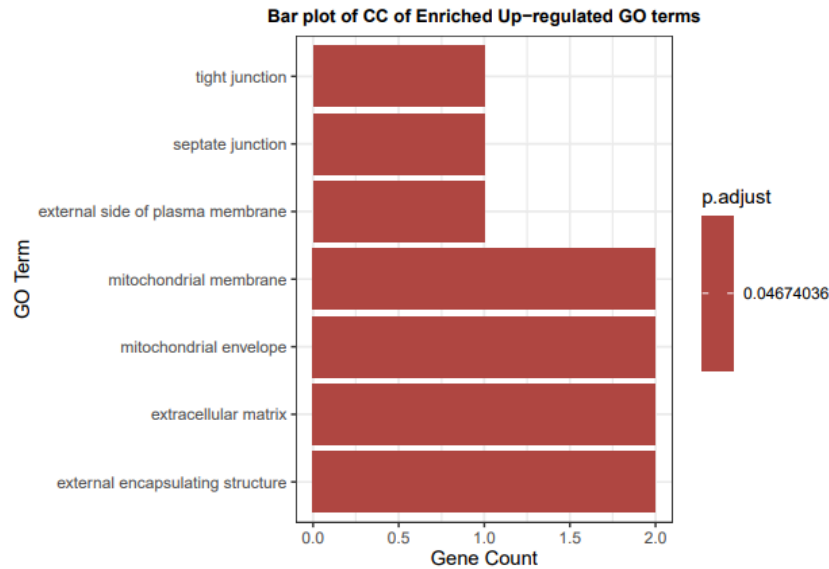


Figure 3

Barplot indicates significantly enriched Cellular Component GO terms among up-regulated significant genes (GO terms with lower p-values, p.adjust, and q-values are more significantly enriched).

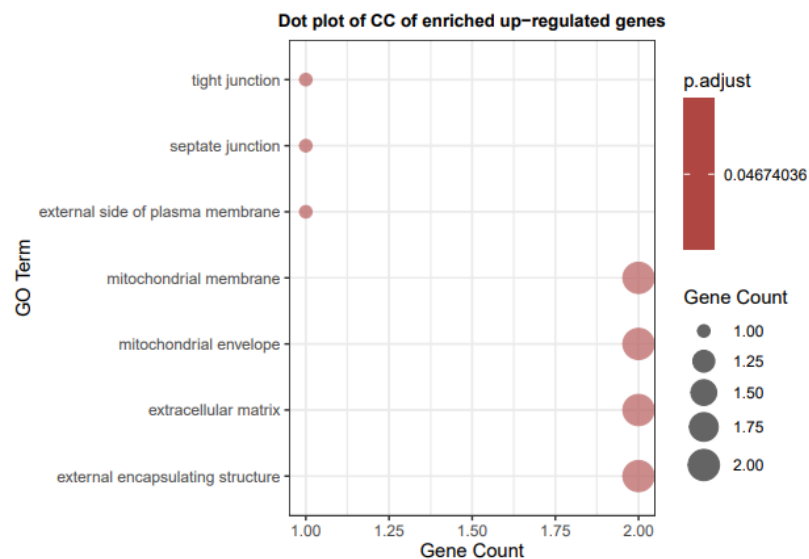


Figure 4

Dotplot indicates significantly enriched Cellular Component GO terms among up-regulated significant genes. the color indicates the significance of the Cellular Component GO terms and the size indicates how many genes are contributing to the enriched terms

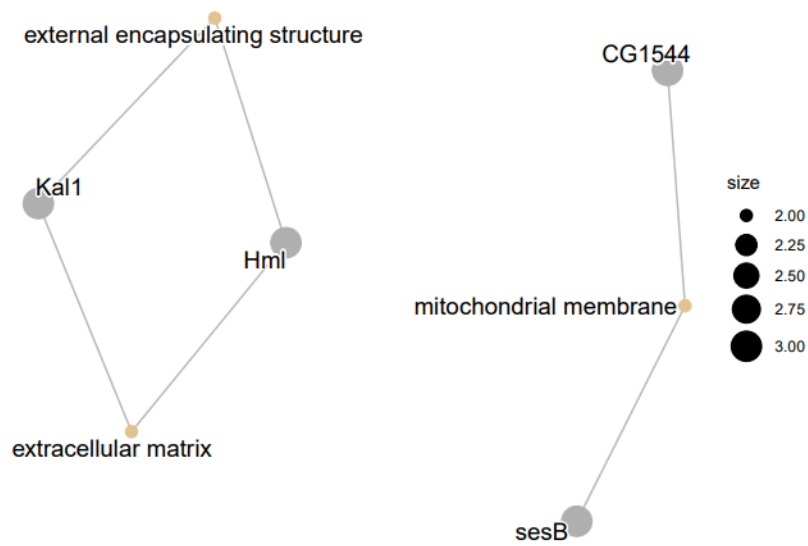


Figure 5

Network plot that represents three nodes of the top 3 enriched GO terms and up-regulated genes that are associated with these GO terms. The edges indicate which genes are involved in which Cellular Component.

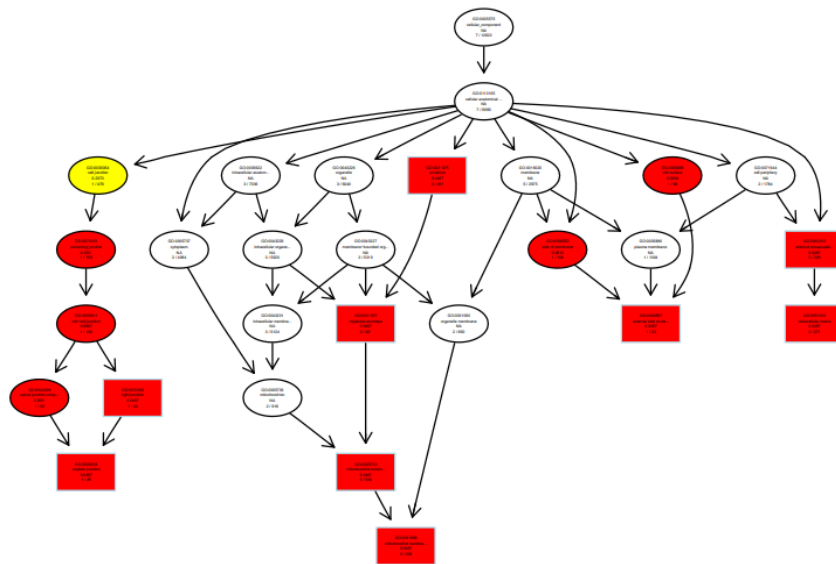


Figure 6

The GO graph visually represents the hierarchical relationships among enriched GO terms. Each node represents an enriched GO term. Edges represent the hierarchical relationships between GO terms, showing parent-child relationships.

2) Figures of enriched GO terms among down-regulated significant genes.

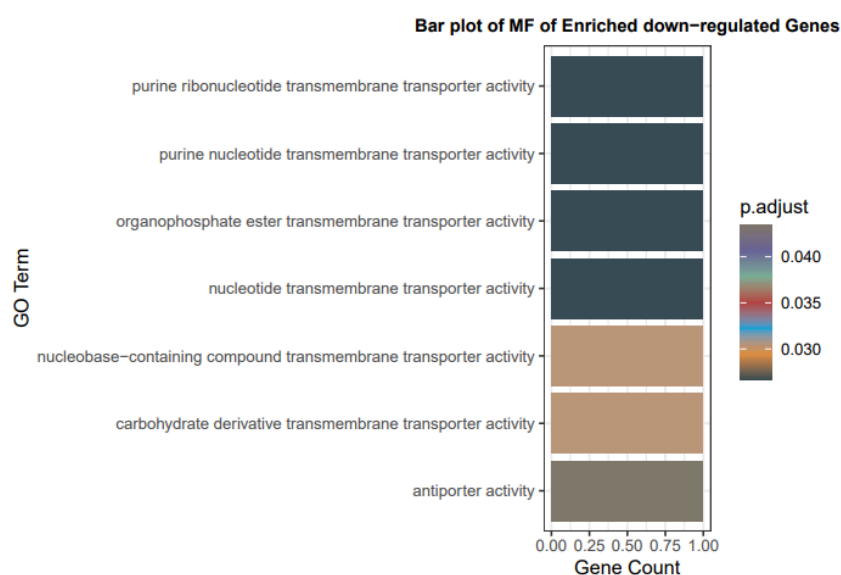


Figure 7

Barplot indicates significantly enriched Molecular Function GO terms among down-regulated significant genes (GO terms with lower p-values, p.adjust, and q-values are more significantly enriched).

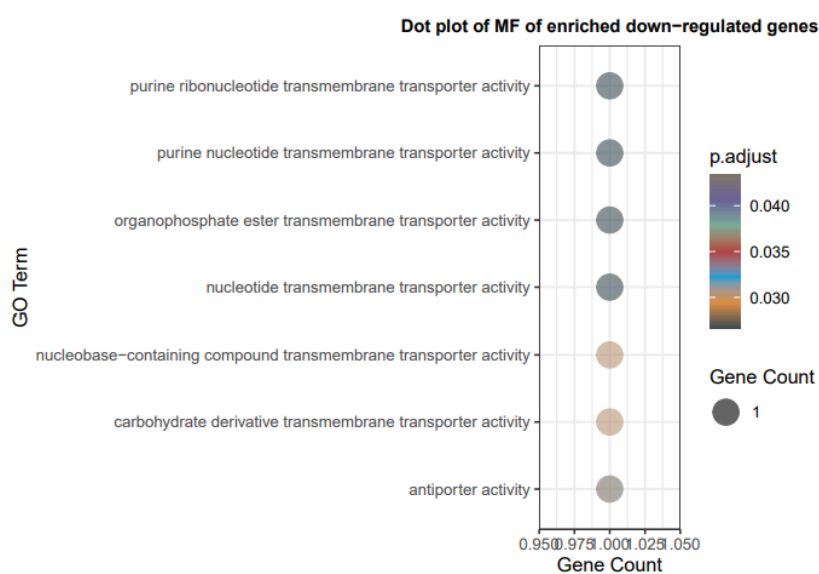


Figure 8

Dotplot indicates significantly enriched Molecular Function GO terms among down-regulated significant genes. the color indicates the significance of the GO terms and the size indicates how many genes are contributing to enriched MF.

☐ **Pathway Enrichment Analysis:**
1) **Figures of enriched KEGG pathways among up-regulated significant genes.**

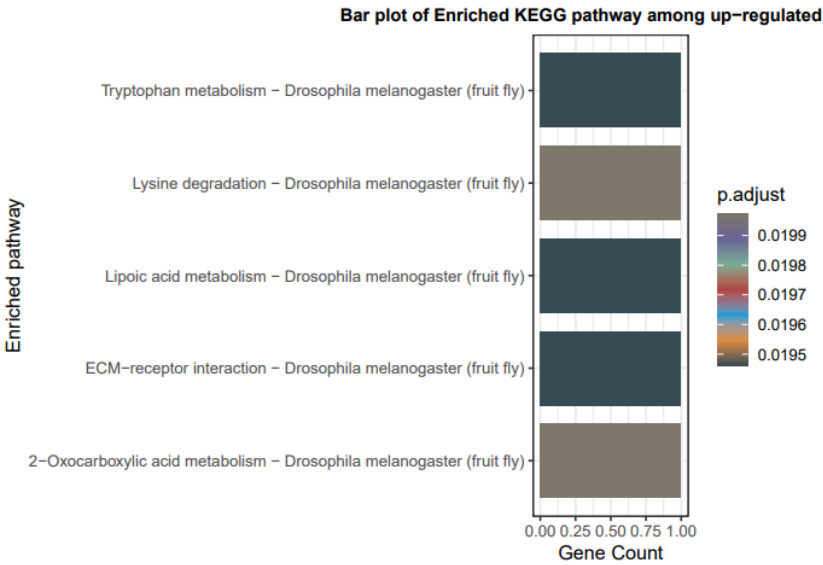


Figure 11

Barplot indicates significantly enriched KEGG pathways among up-regulated significant genes (pathways with lower p-values, p.adjust, and q-values are more significantly enriched).

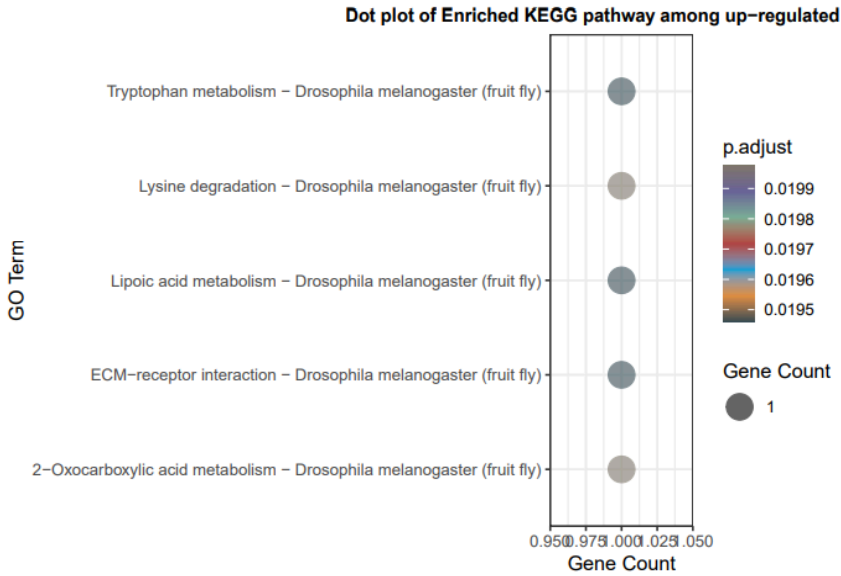


Figure 12

Dotplot indicates significantly enriched KEGG pathways among up-regulated significant genes. the color indicates the significance of the pathways and the size indicates how many genes are contributing to the enriched pathway.

2) Figures of enriched Reactome pathways among down-regulated significant genes.

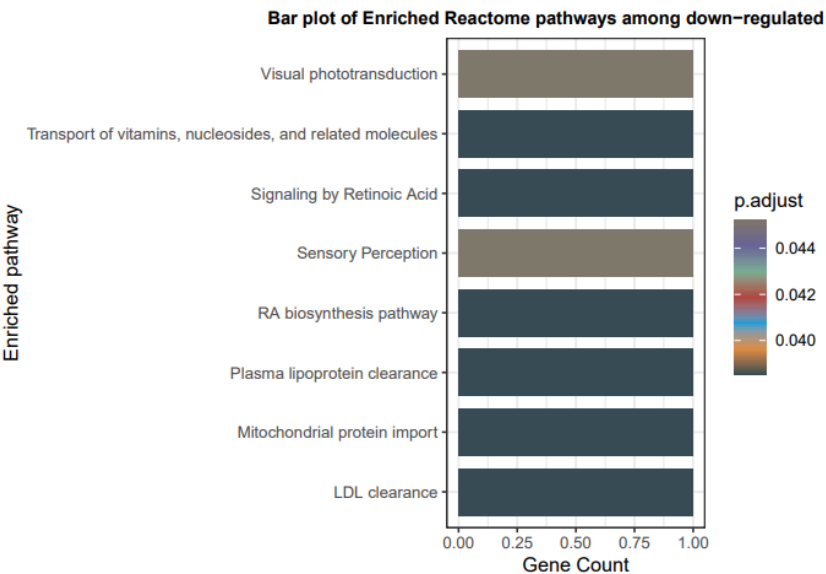


Figure 14

Barplot indicates significantly enriched Reactome pathways among down-regulated significant genes (pathways with lower p-values, p.adjust, and q-values are more significantly enriched).

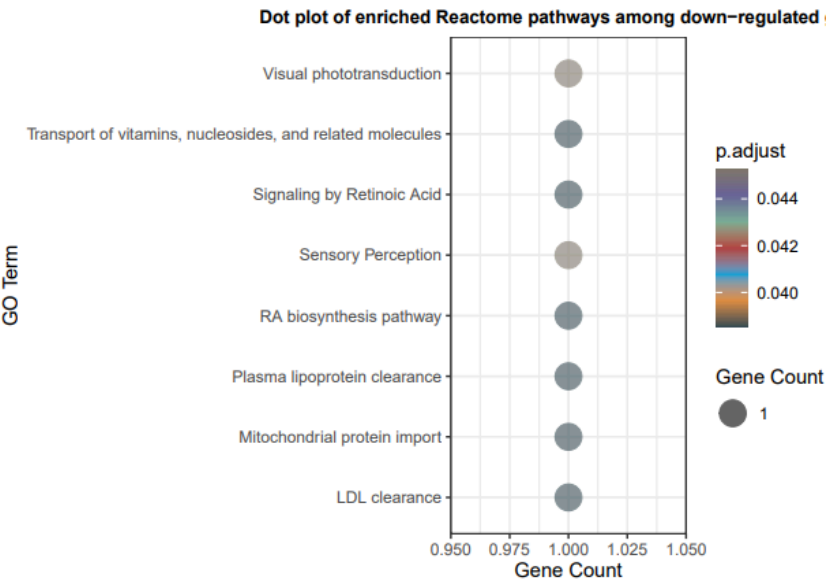


Figure 15

Dotplot indicates significantly enriched Reactome pathways among down-regulated significant genes. the color indicates the significance of the Reactome pathways and the size indicates how many genes are contributing to the enriched pathway.