

Additional materials to the article

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FUNCTIONAL ENRICHMENT ANALYSIS OF DYSREGULATED GENES

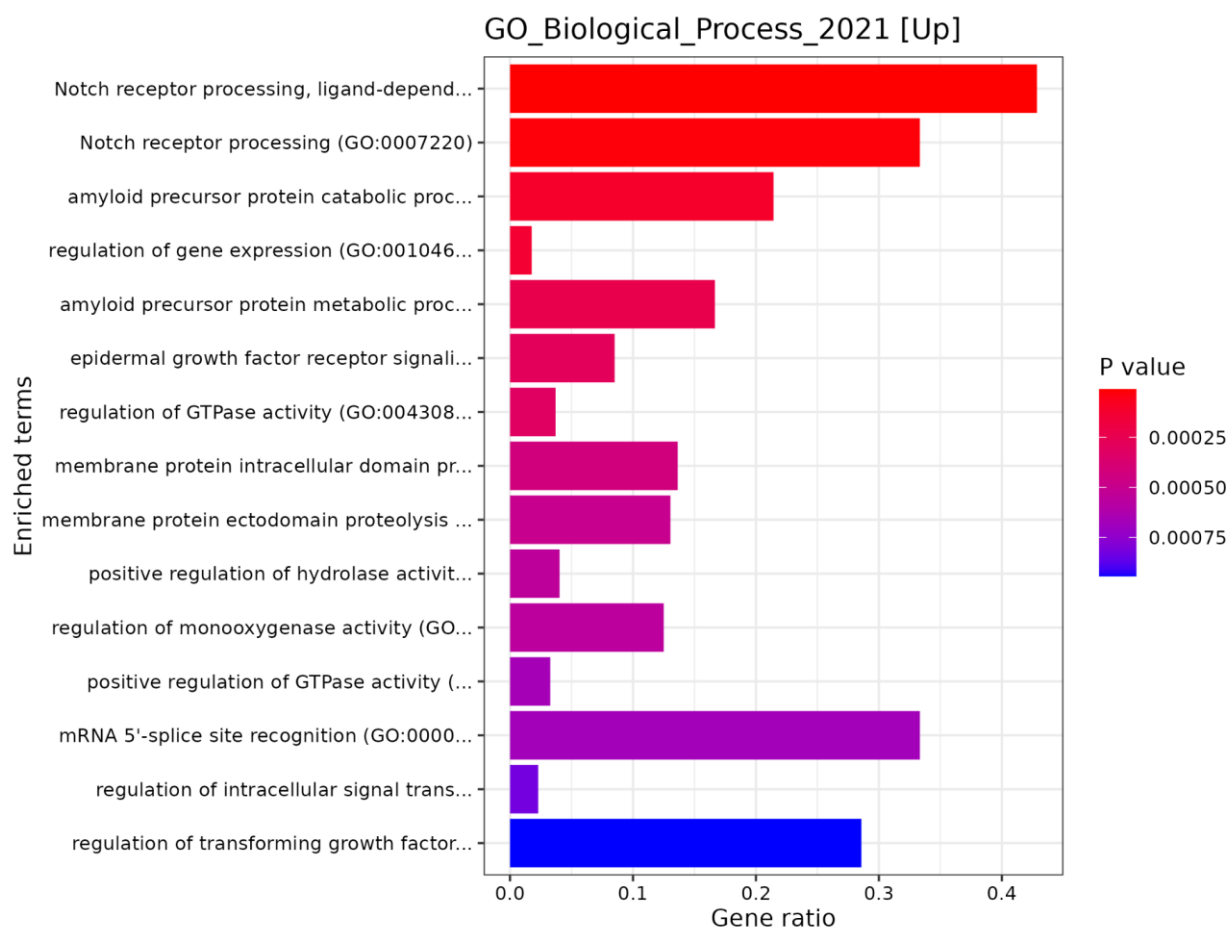


Figure S1. Go biological process of upregulated genes. Gene ratio represents how many genes are involved in BP. The larger bar in the bar chart plot represents the highest number of genes involved in BP.

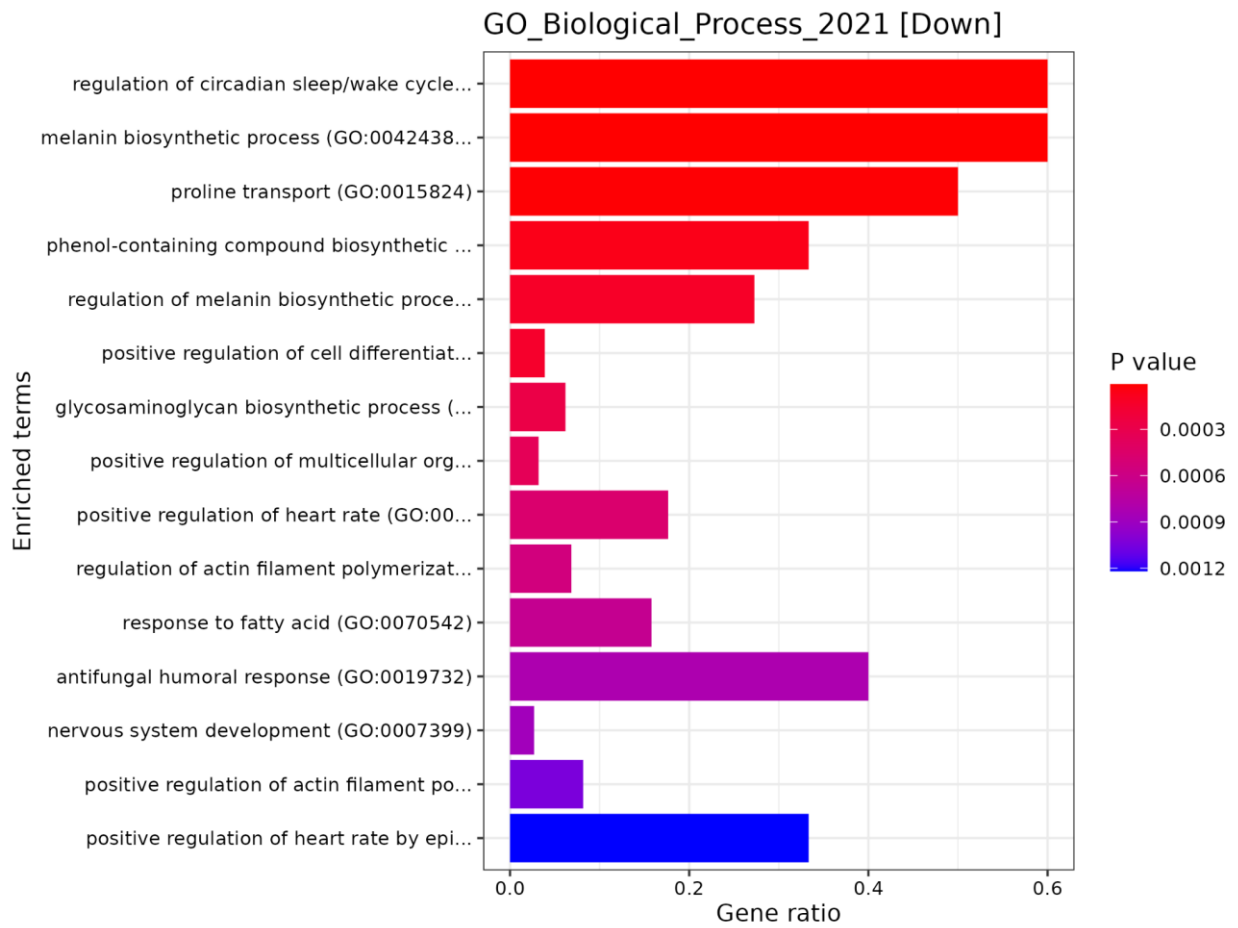


Figure S2. Go biological process of downregulated genes. Gene ratio represents how many genes are involved in BP. The larger bar in the bar chart plot represents the highest number of genes involved in BP.

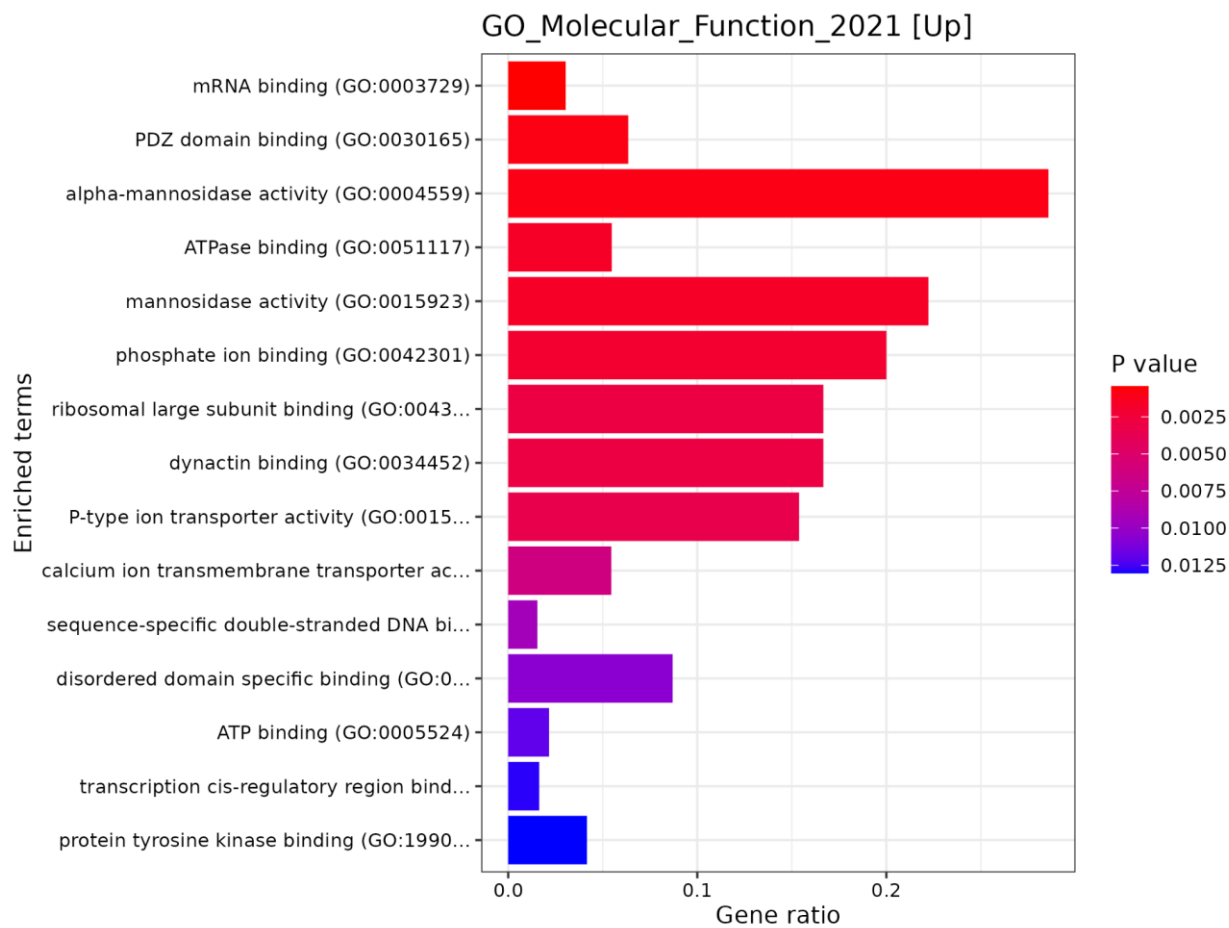


Figure S3. Go molecular function of upregulated genes. Gene ratio represents how many genes are involved in MF. The larger bar in the bar chart plot represents the highest number of genes involved in MF.

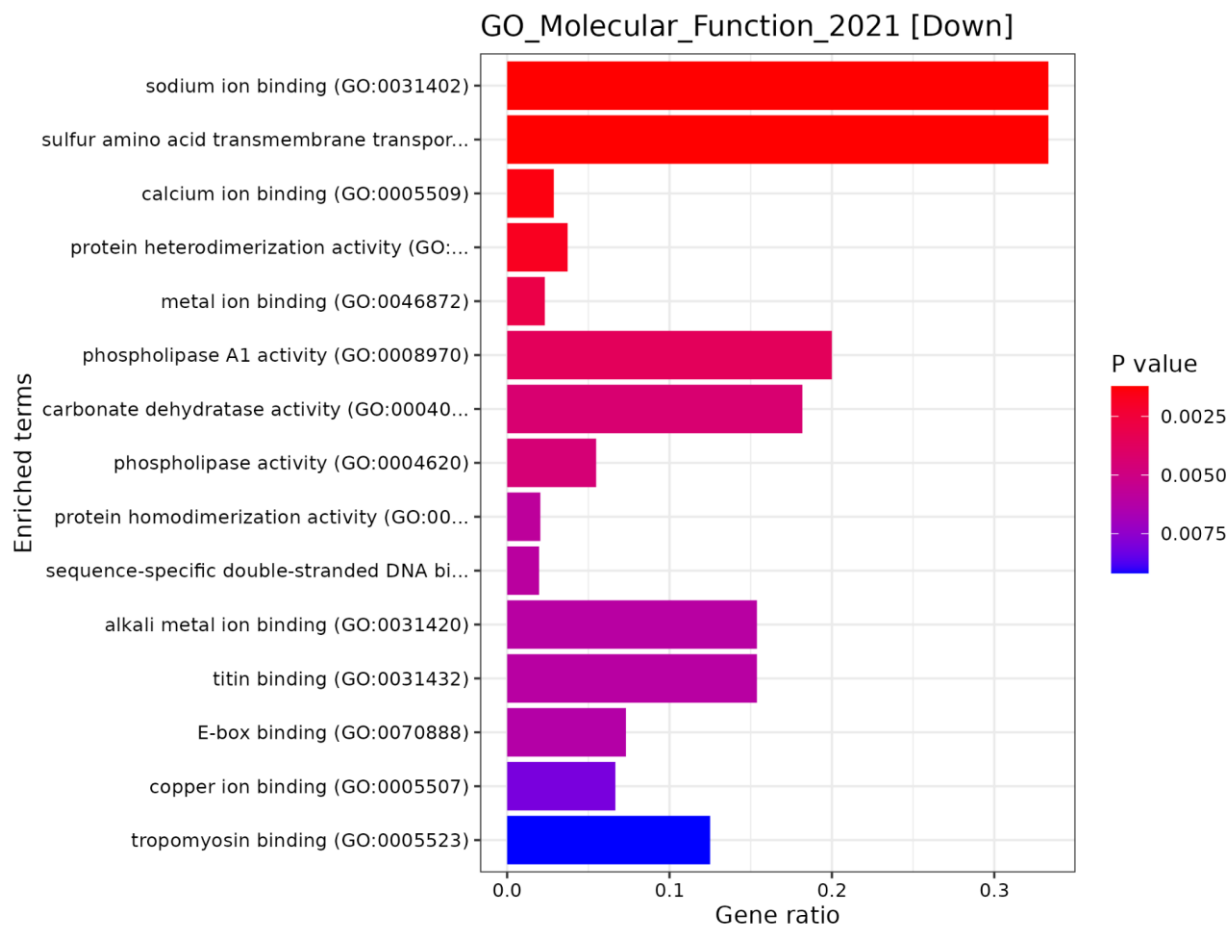


Figure S4. Go molecular function of downregulated genes. Gene ratio represents how many genes are involved in MF. The larger bar in the bar chart plot represents the highest number of genes involved in MF.

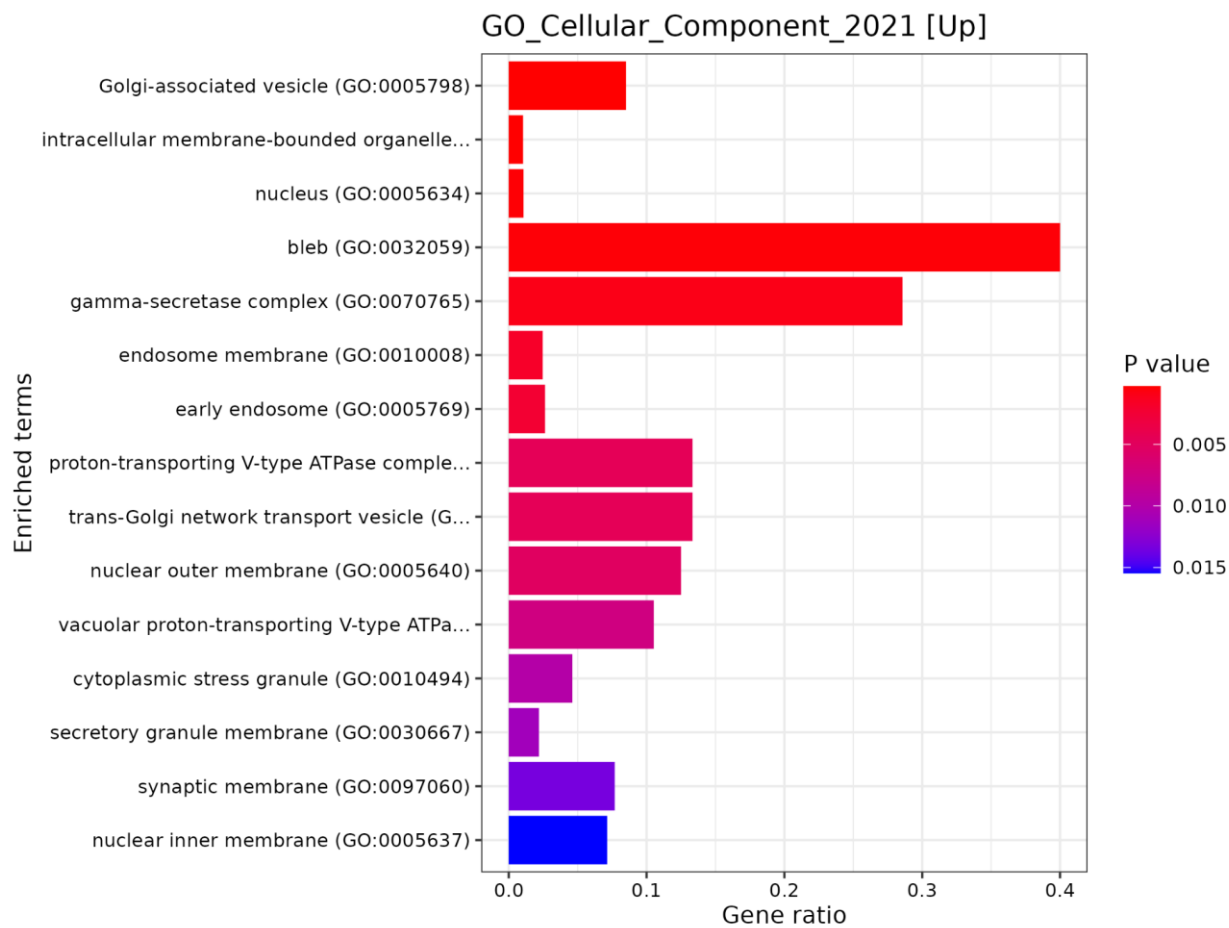


Figure S5. Go cellular component of upregulated genes. Gene ratio represents how many genes are involved in CC. The larger bar in the bar chart plot represents the highest number of genes involved in CC.

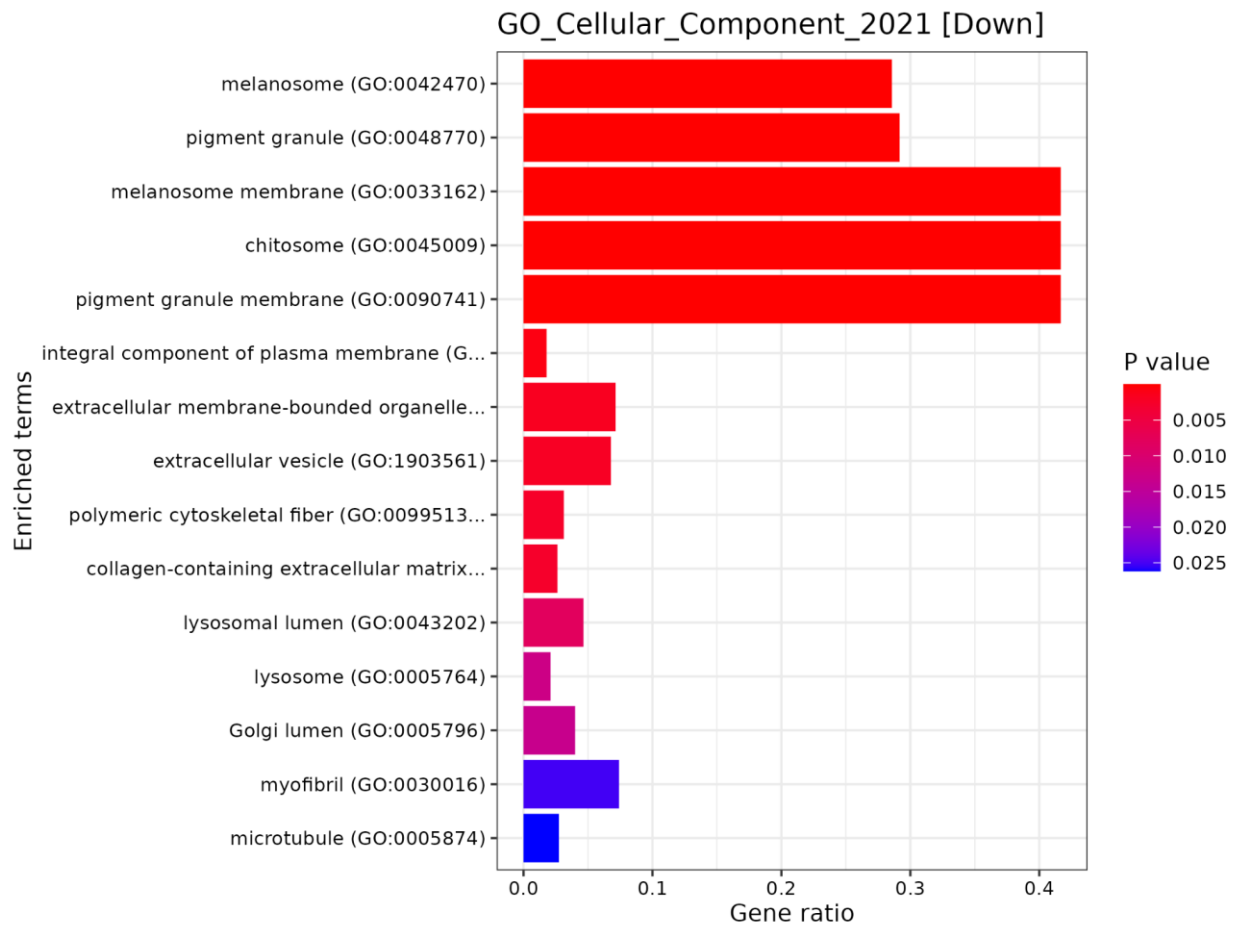


Figure S6. Go cellular component of upregulated genes. Gene ratio represents how many genes are involved in CC. The larger bar in the bar chart plot represents the highest number of genes involved in CC.

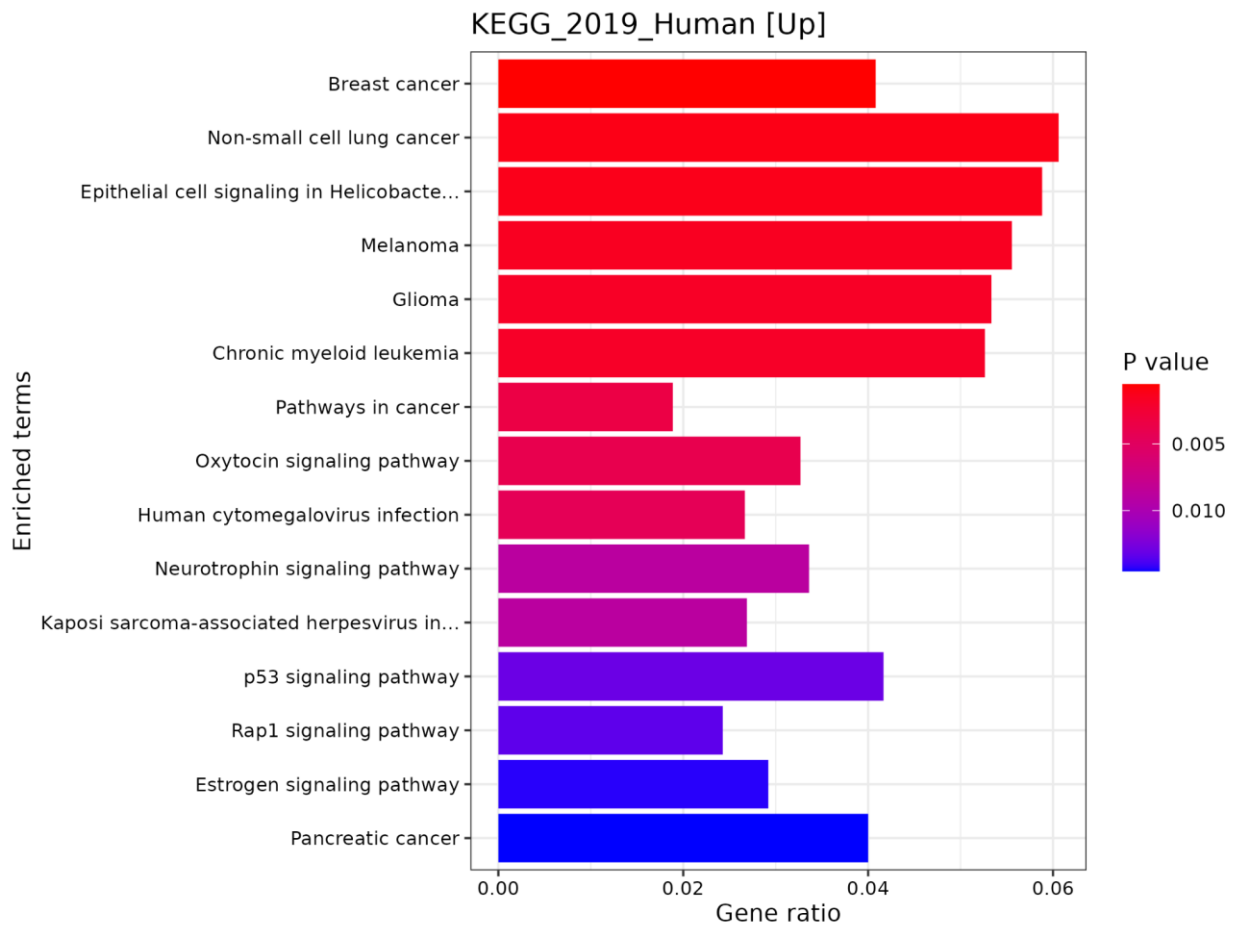


Figure S7. The bar chart represents KEGG pathways listed on the y-axis and the gene ratio displayed on the x-axis. Each bar corresponds to a specific KEGG pathway, and its length is proportional to the associated gene ratio, specifically representing the ratio of upregulated genes within each pathway. The gene ratio reflects the relative abundance of upregulated genes within each pathway among the differentially expressed genes.

PROTEIN-PROTEIN INTERACTIONS AND HUB GENES IDENTIFICATION

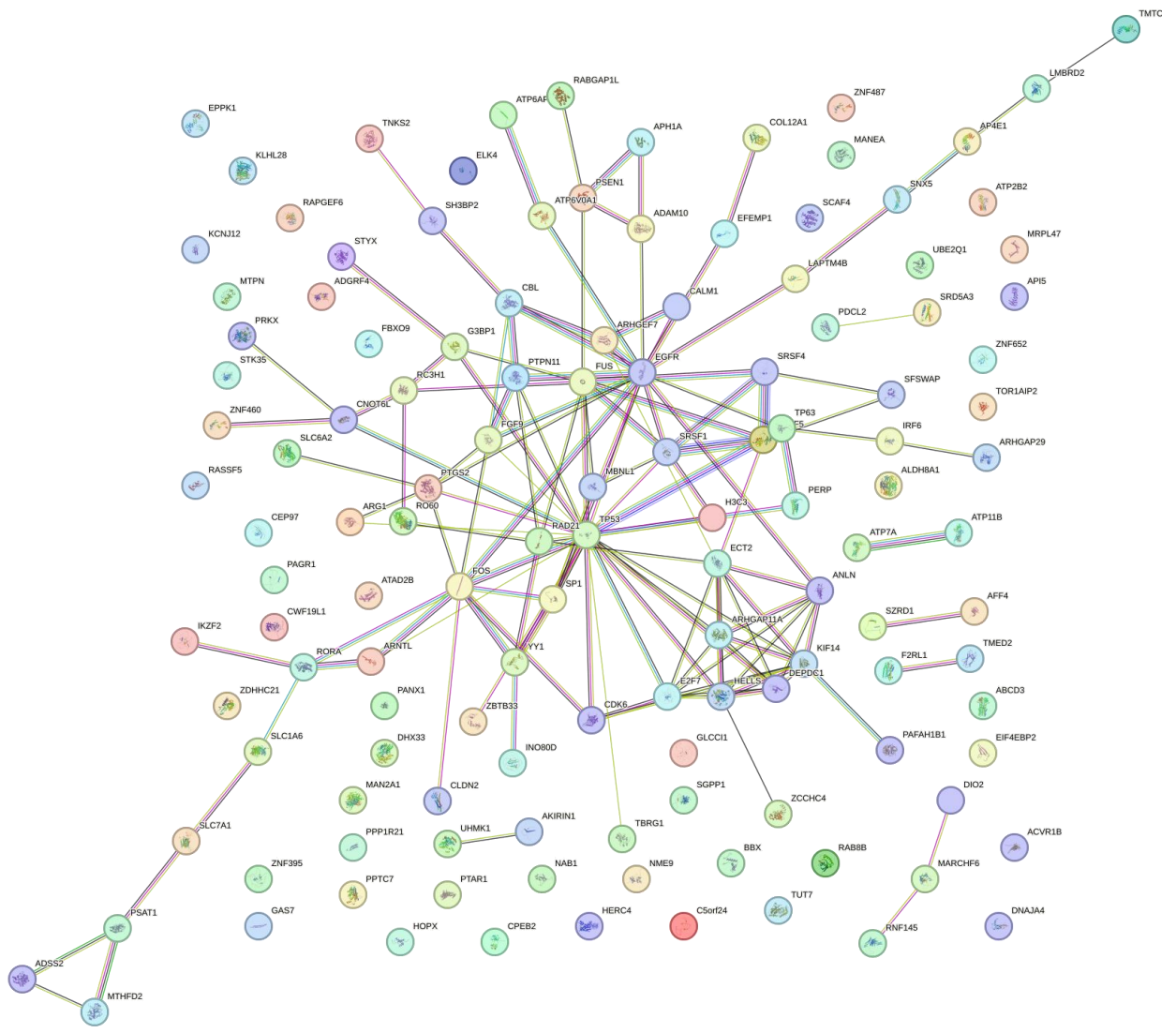


Figure S8. Visual representation of PPI network of upregulated genes.

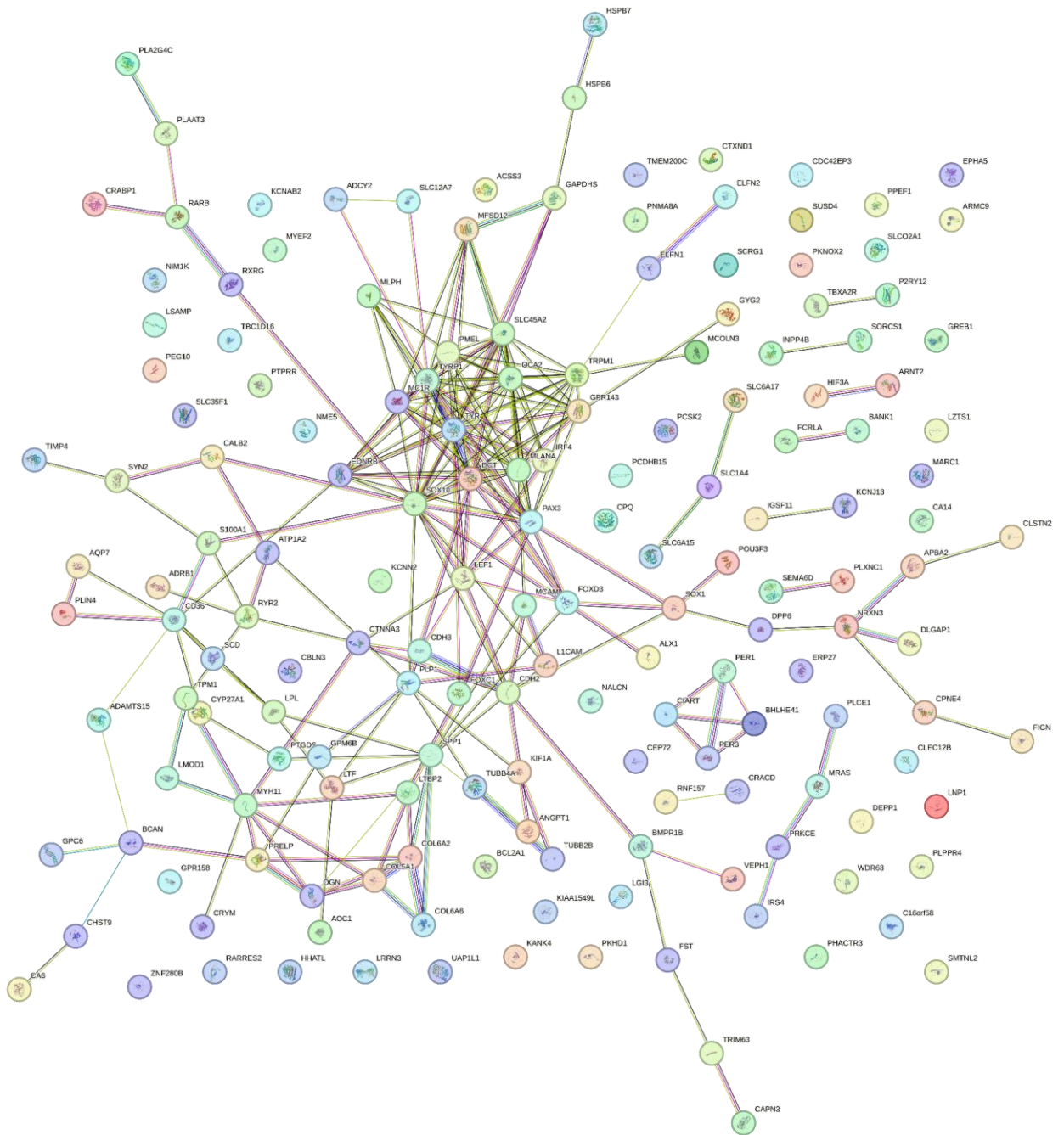


Figure S9. Visual representation of PPI network of downregulated genes.

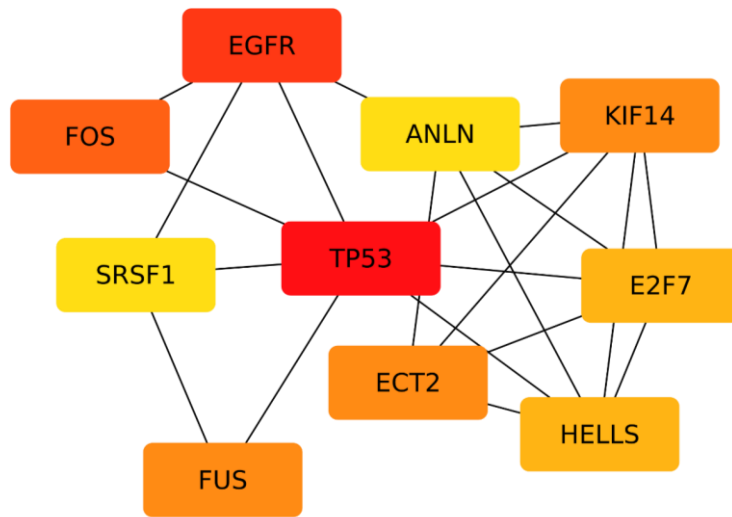


Figure S10. Visual representation of top 10 upregulated hub genes identified through CytoHubba plug-in within Cytoscape.