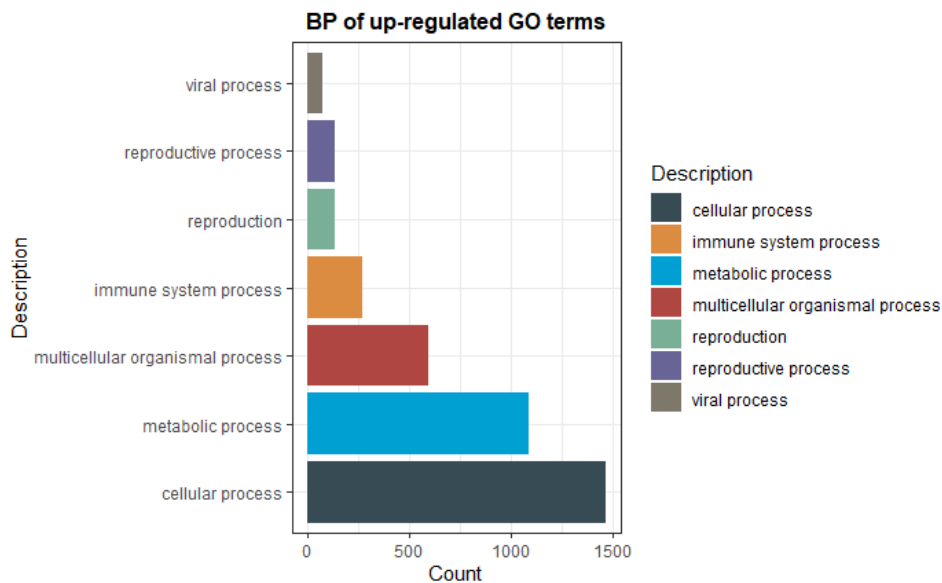
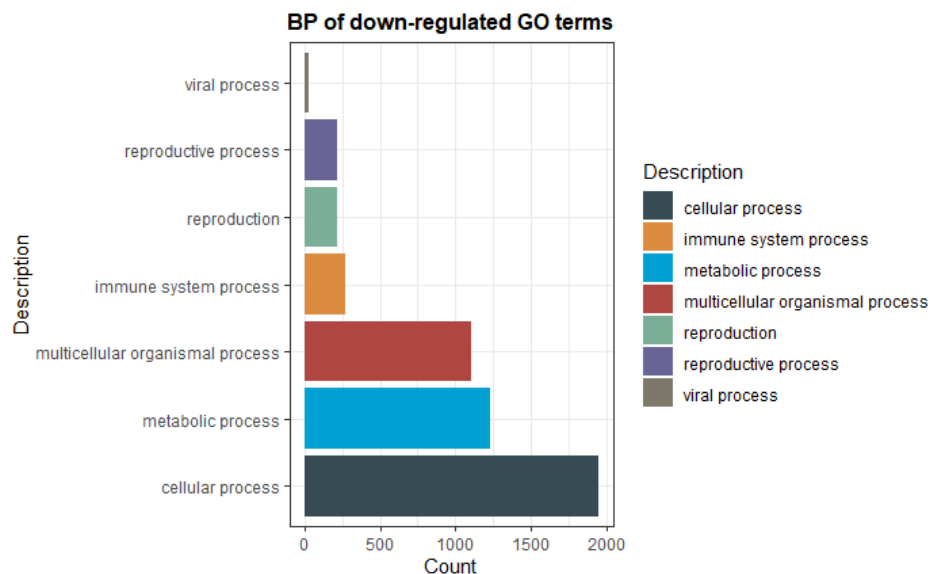


# Enrichment Analysis Figures



**Figure 1**

Barplot indicates how many up-regulated significant genes are annotated with a Biological process GO term (e.g. 75 up-regulated significant genes out of 1650 are annotated with viral process GO term).



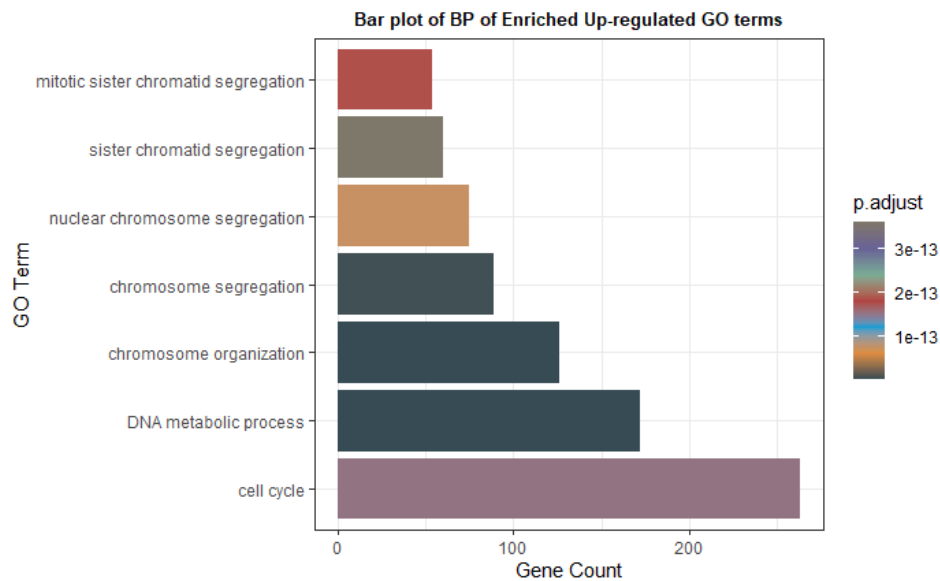
**Figure 2**

Barplot indicates how many down-regulated significant genes are annotated with a Biological process GO term (e.g. 1234 down-regulated significant genes out of 2336 are annotated with metabolic process GO term).

## Over-representation Analysis

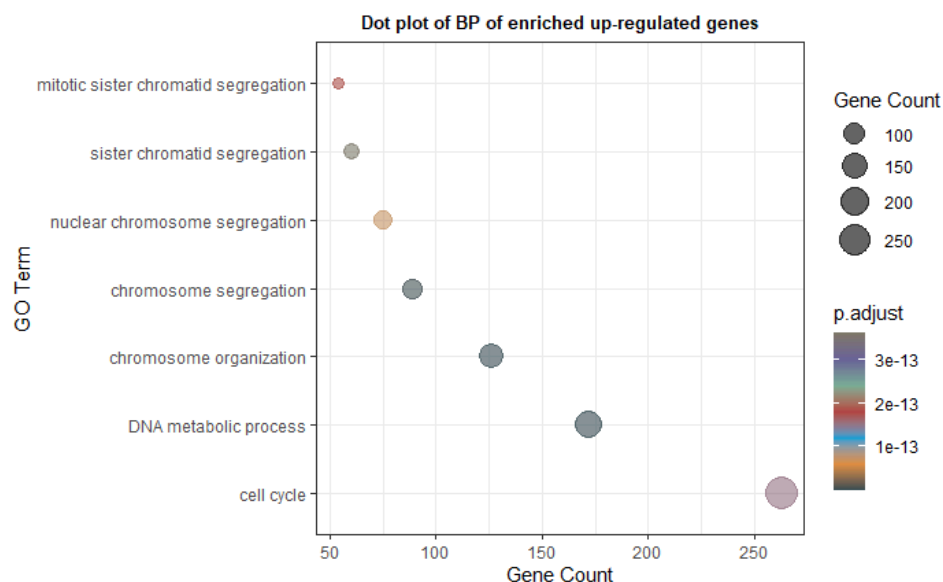
### ☐ GO Enrichment Analysis:

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



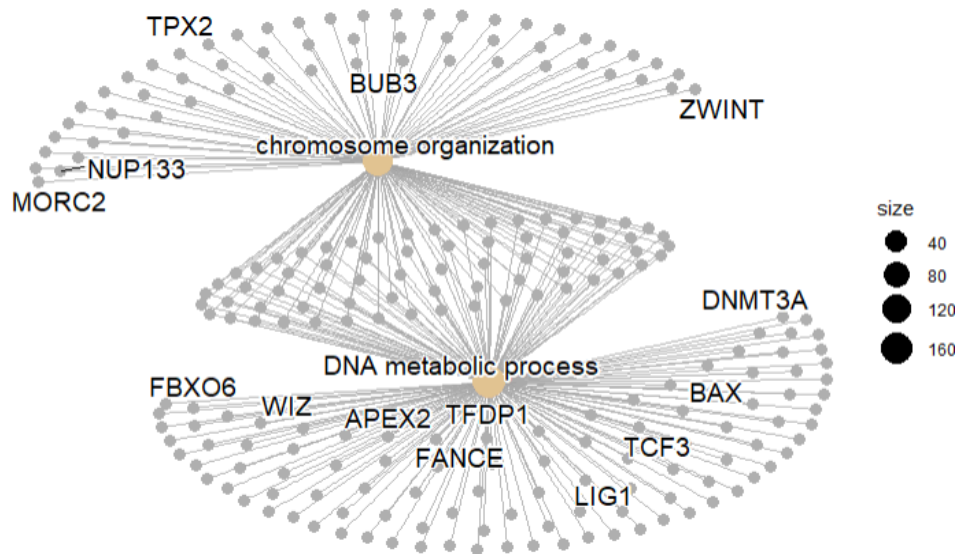
**Figure 3**

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



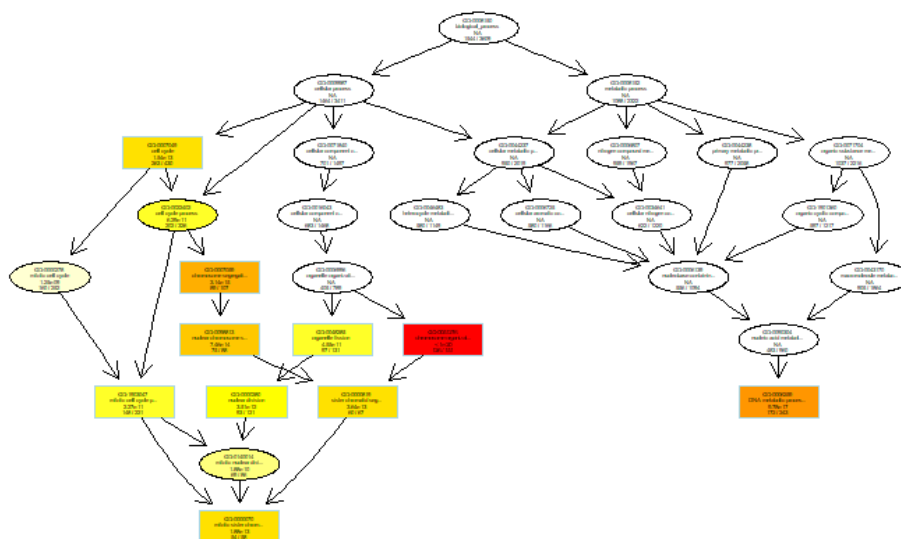
**Figure 4**

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



**Figure 5**

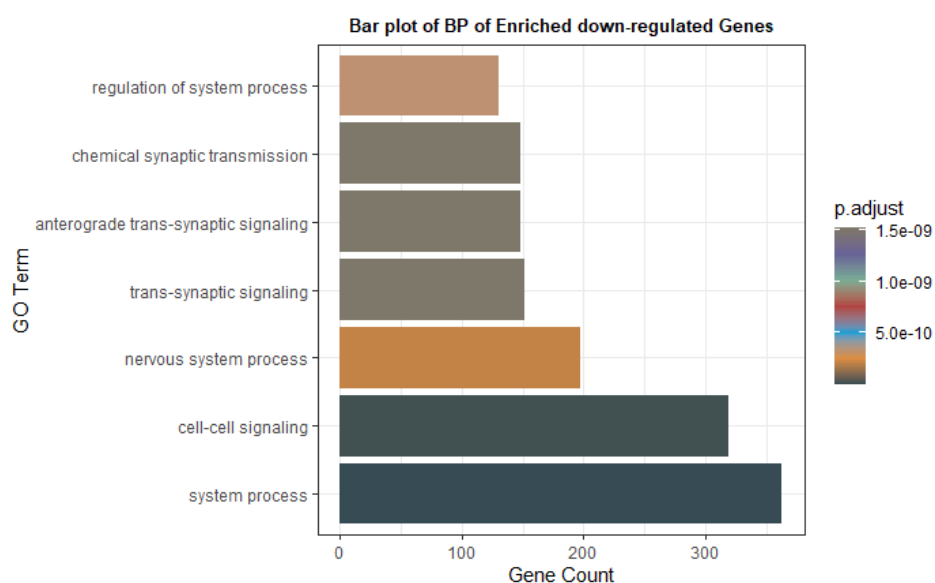
Network plot that represents two nodes of the top 2 enriched GO terms and up-regulated genes that are associated with these GO terms. The edges indicate which genes are involved in which biological processes.



**Figure 6**

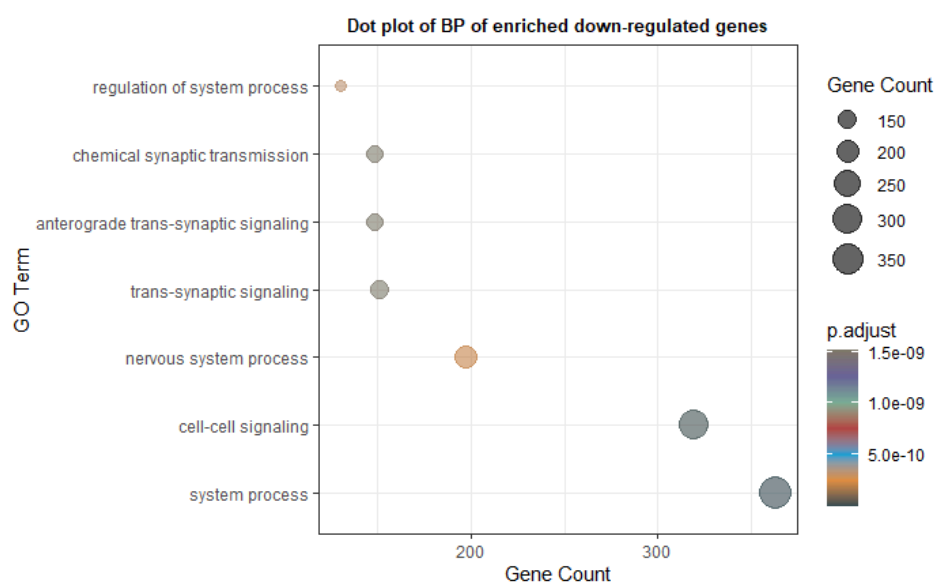
The GO graph visually represents the hierarchical relationships among enriched GO terms. Each node represents an enriched GO term. Edges represent the hierarchical relationships between GO terms, showing parent-child relationships.

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



**Figure 7**

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



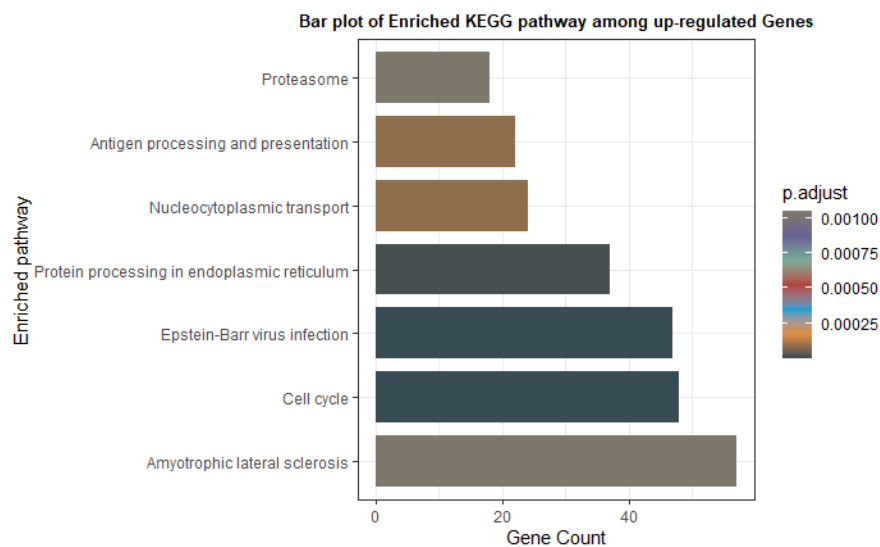
**Figure 8**

Dotplot that indicates significantly enriched biological process GO terms among down-regulated significant genes. the color indicates the significance of the biological process GO terms and the size indicates how many genes are contributing to enriched biological processes.



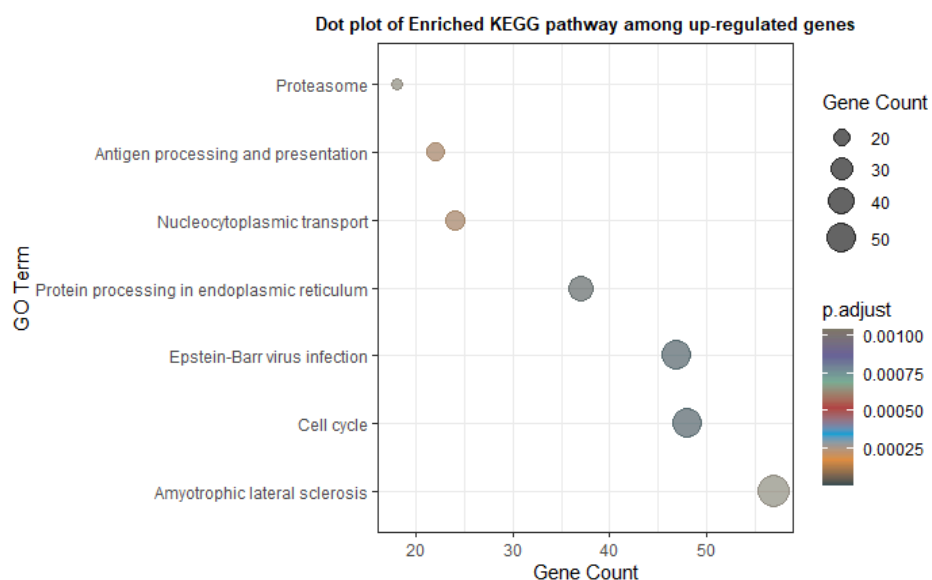
□ **Pathway Enrichment Analysis:**

**1) Figures of enriched KEGG pathways among up-regulated significant genes.**



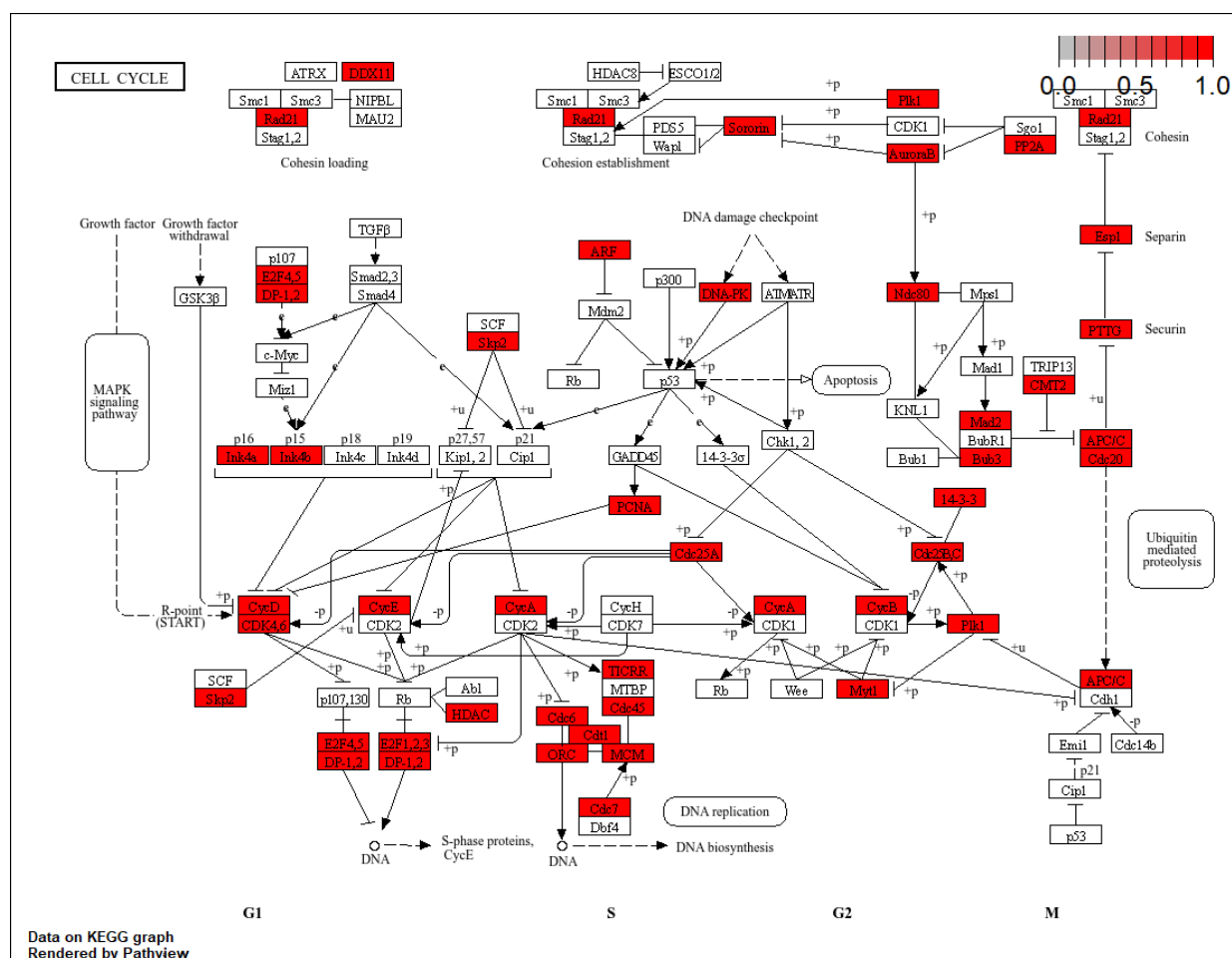
**Figure 10**

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



**Figure 11**

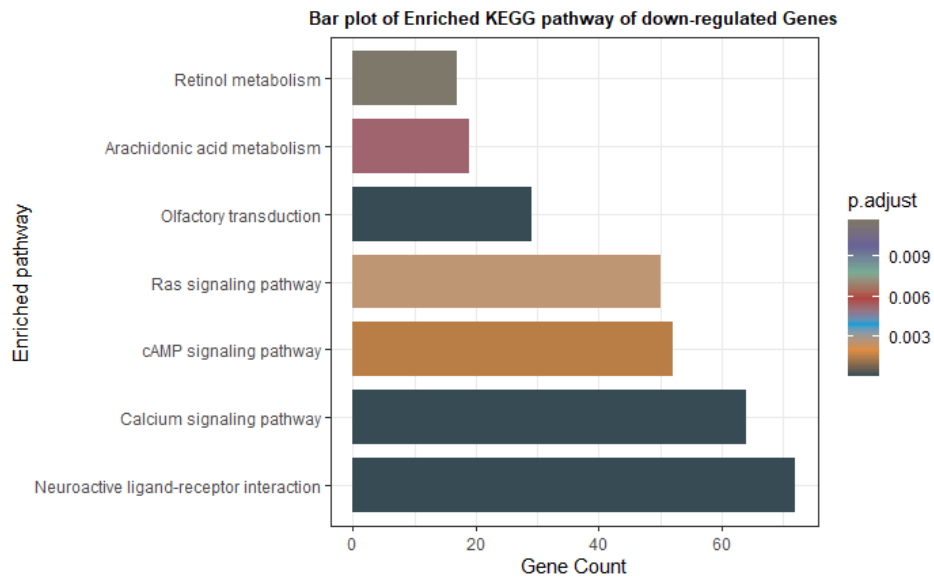
Dotplot that indicates significantly enriched biological process pathways among up-regulated significant genes. the color indicates the significance of the biological process pathways and the size indicates how many genes are contributing to the enriched pathway.



**Figure 12**

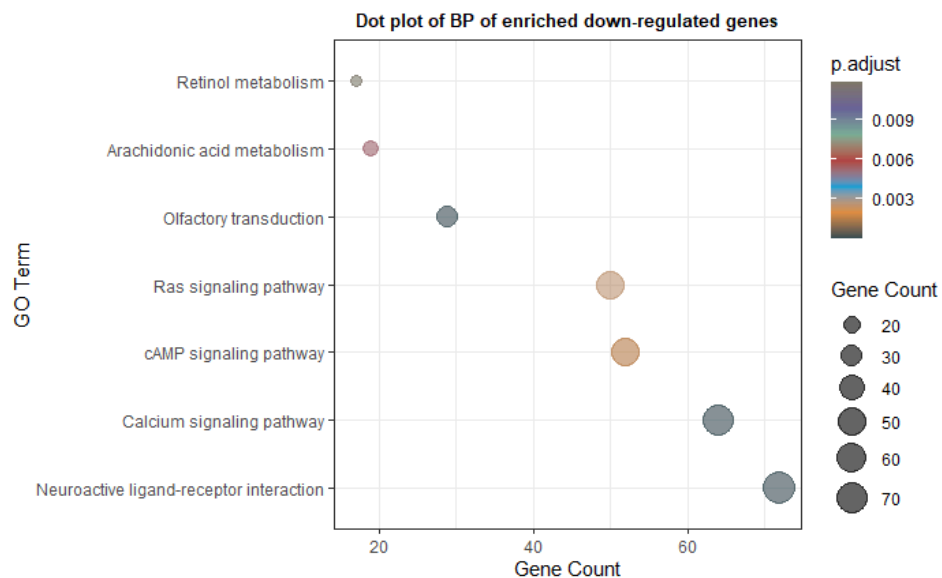
KEGG pathway map that visually represents the "Cell Cycle" pathway ( The top significant enriched pathway among up-regulated significant genes). Up-regulated genes are highlighted, indicating where they act within the pathway.

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



**Figure 13**

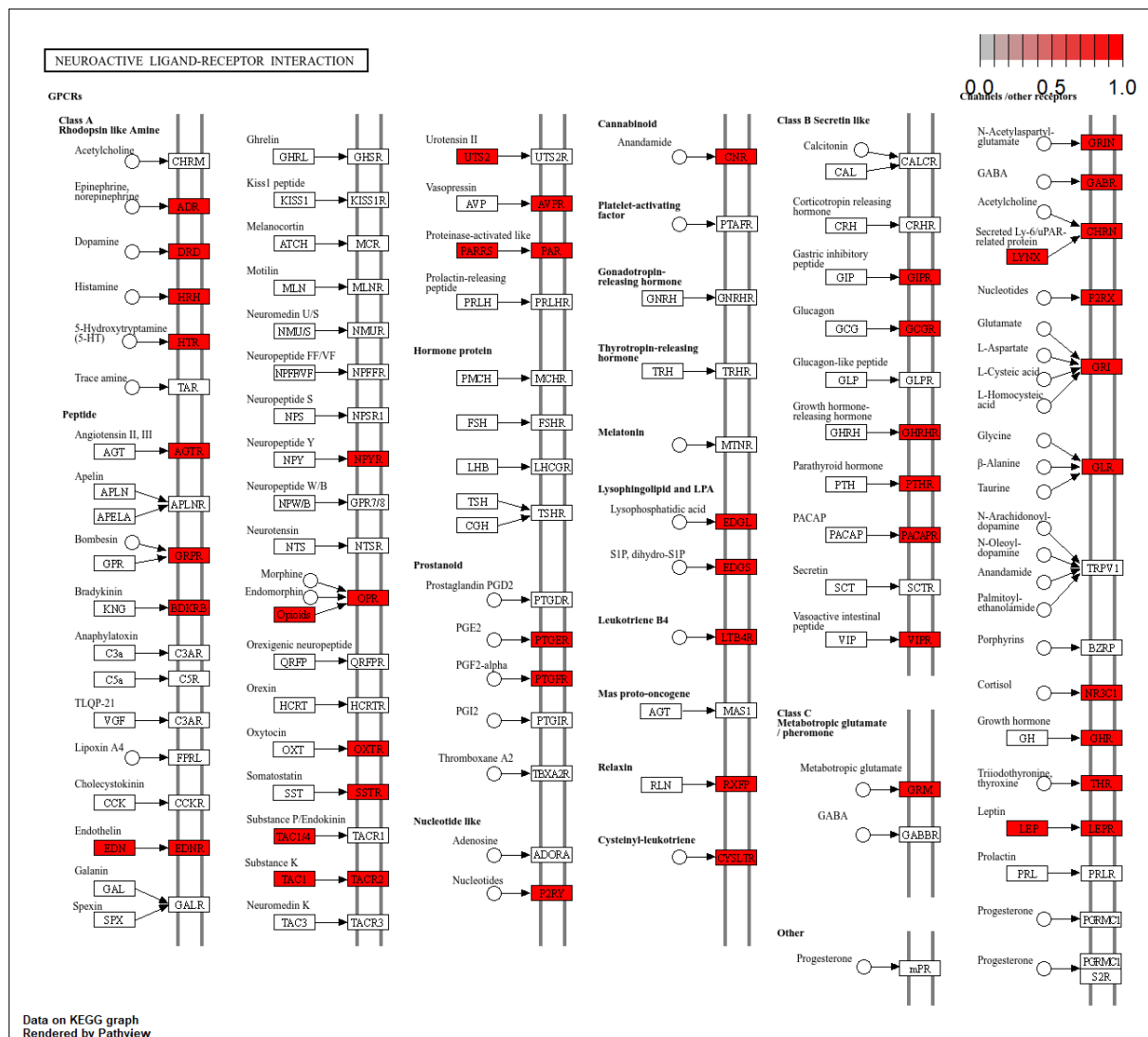
Barplot that indicates significantly enriched biological process pathways among down-regulated significant genes (pathways with lower p-values, p.adjust, and q-values are more significantly enriched).



**Figure 14**

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

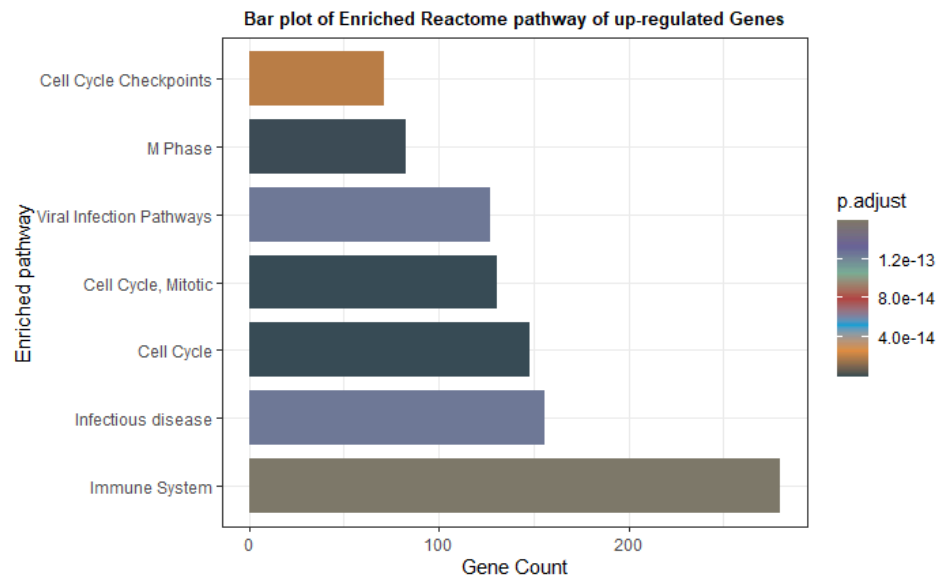




**Figure 15**

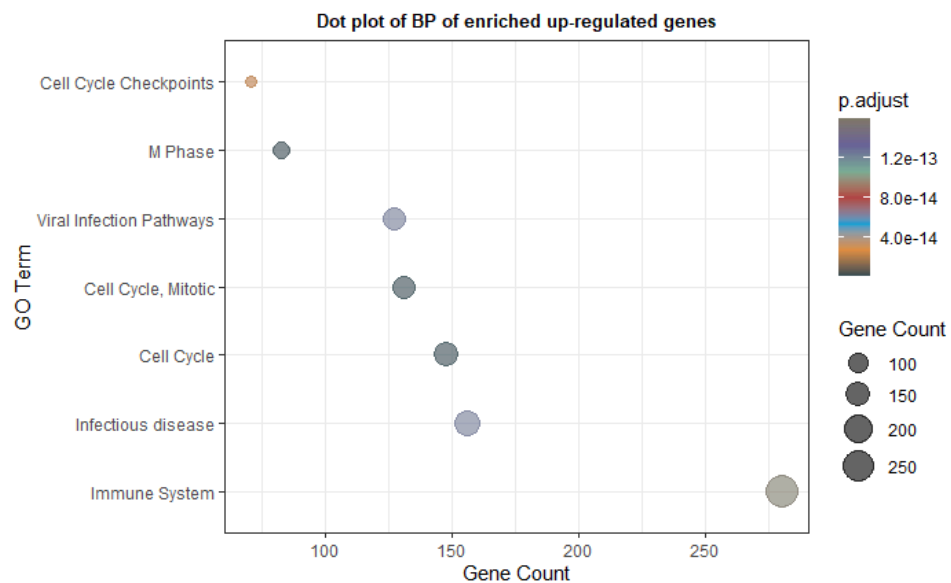
KEGG pathway map that visually represents the "Neuroactive ligand-receptor interaction" pathway (The top significant enriched pathway among down-regulated significant genes). Down-regulated genes are highlighted, indicating where they act within the pathway.

### 3) Figures of enriched Reactome pathways among up-regulated significant genes.



**Figure 16**

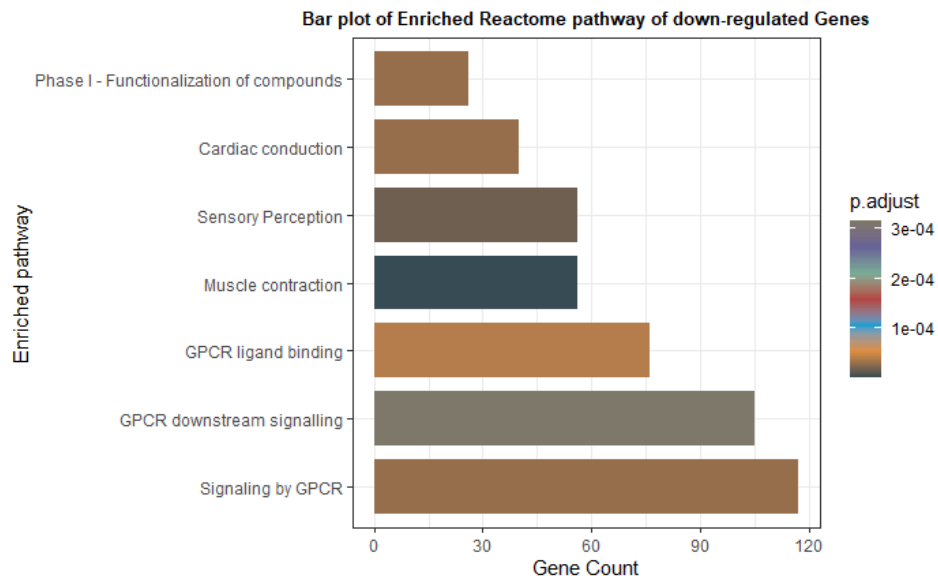
Barplot indicates significantly enriched biological process pathways among up-regulated significant genes (pathways with lower p-values, p.adjust, and q-values are more significantly enriched).



**Figure 17**

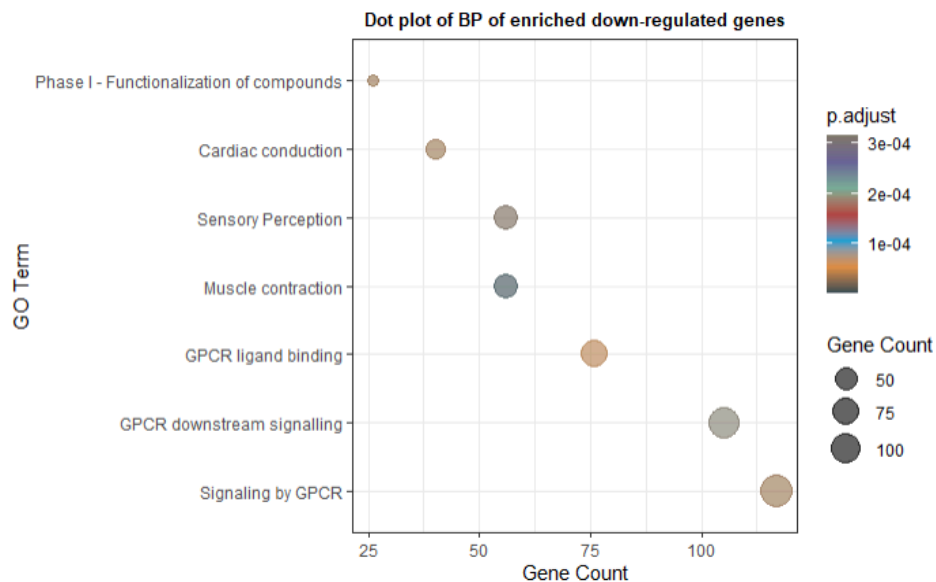
Dotplot that indicates significantly enriched biological process pathways among up-regulated significant genes. the color indicates the significance of the biological process pathways and the size indicates how many genes are contributing to the enriched pathway.

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



**Figure 18**

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



**Figure 19**

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