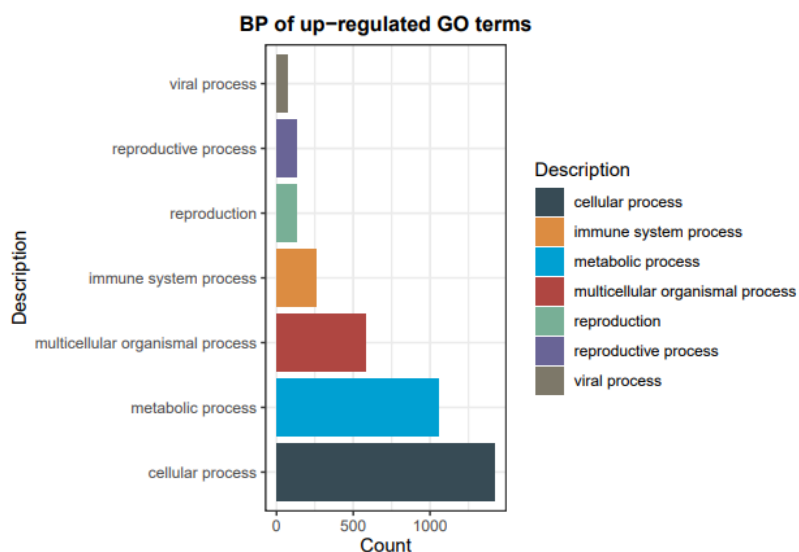
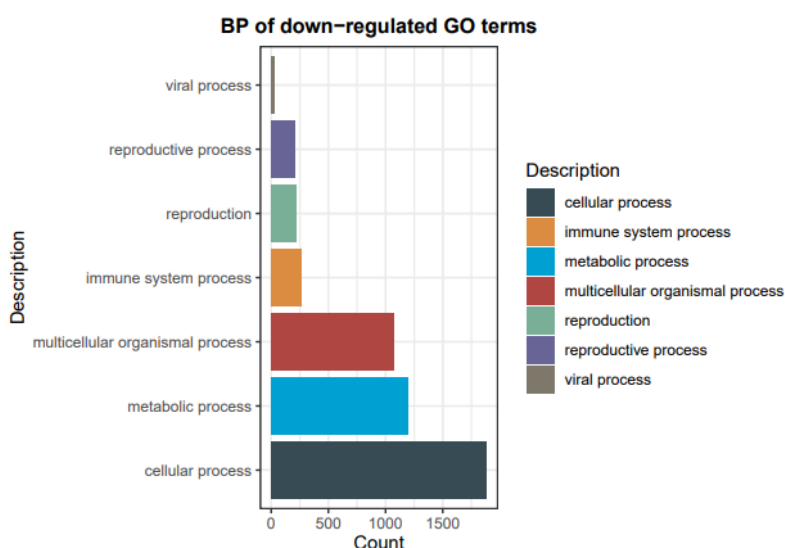


# Enrichment Analysis Figures



**Figure 1**

Barplot indicates how many up-regulated significant genes are annotated with a Biological process GO term (e.g. 72 up-regulated significant genes out of 1608 are annotated with viral process GO term).



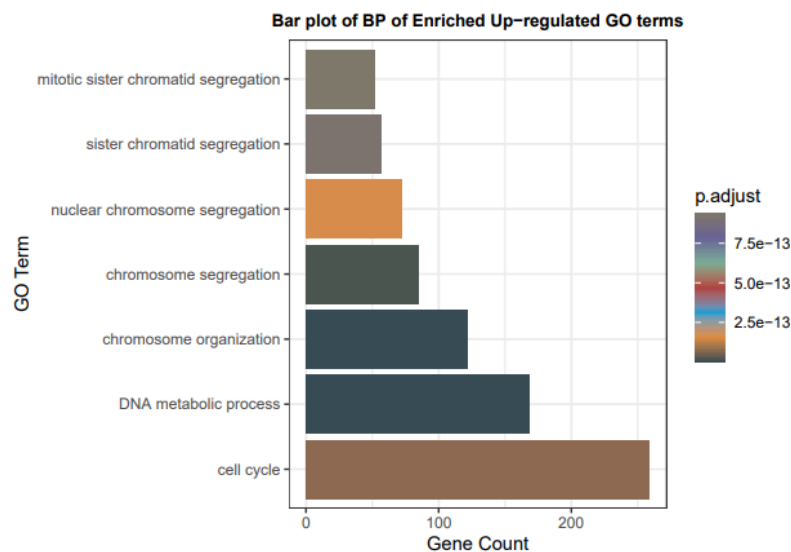
**Figure 2**

Barplot indicates how many down-regulated significant genes are annotated with a Biological process GO term (e.g. 1196 down-regulated significant genes out of 2267 are annotated with metabolic process GO term).

## Over-representation Analysis

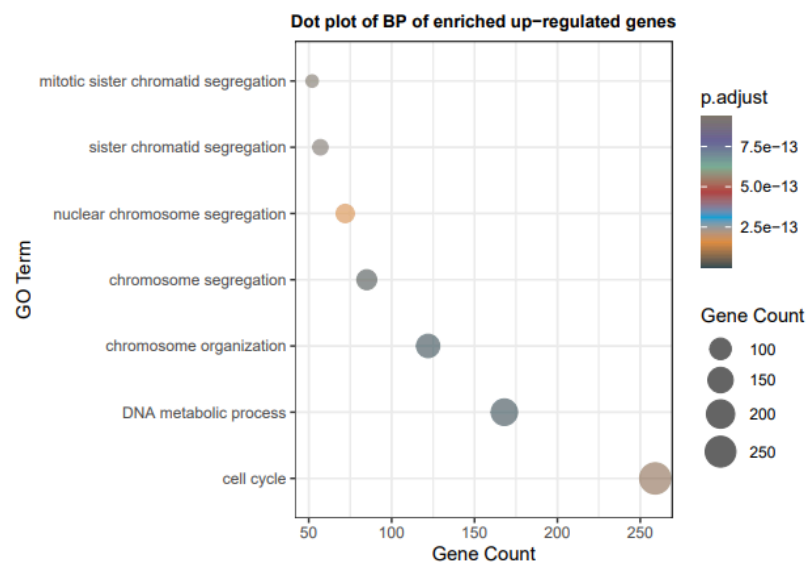
### ☐ GO Enrichment Analysis:

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



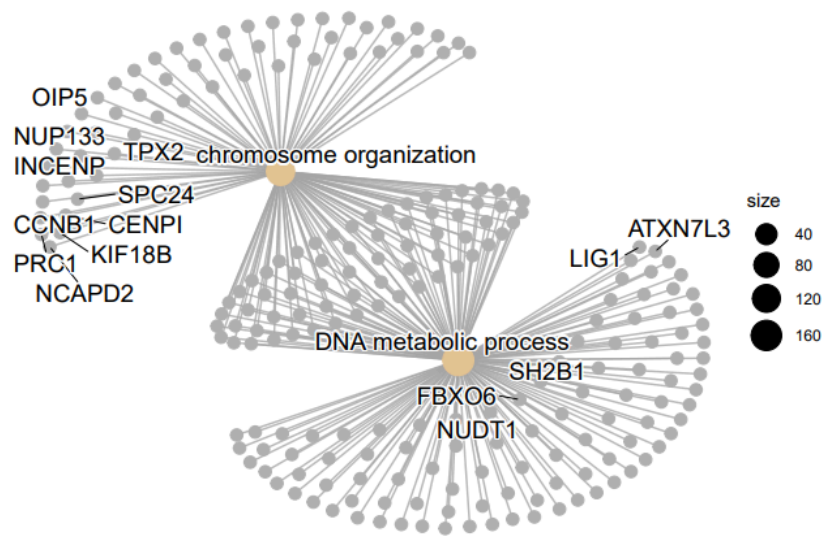
**Figure 3**

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).



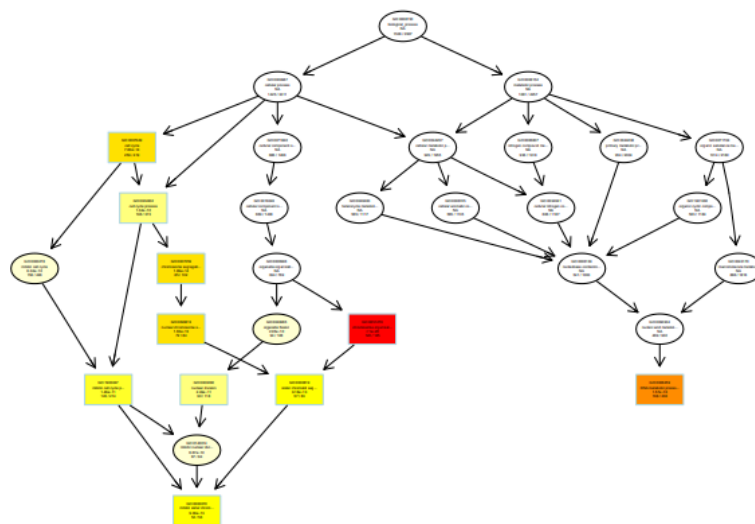
**Figure 4**

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**

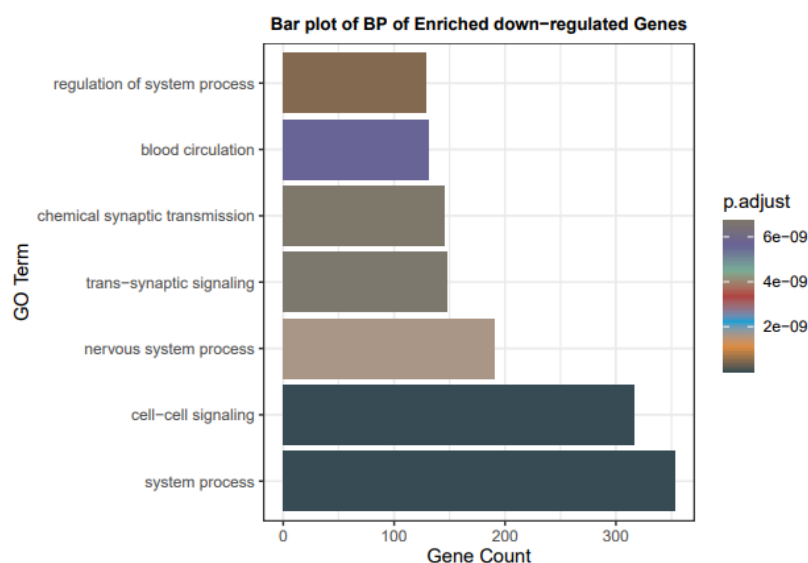
Network plot that represents two nodes of the top 2 enriched GO terms and up-regulated genes that are associated with these GO terms. The edges indicate which genes are involved in which biological processes.



**Figure 6**

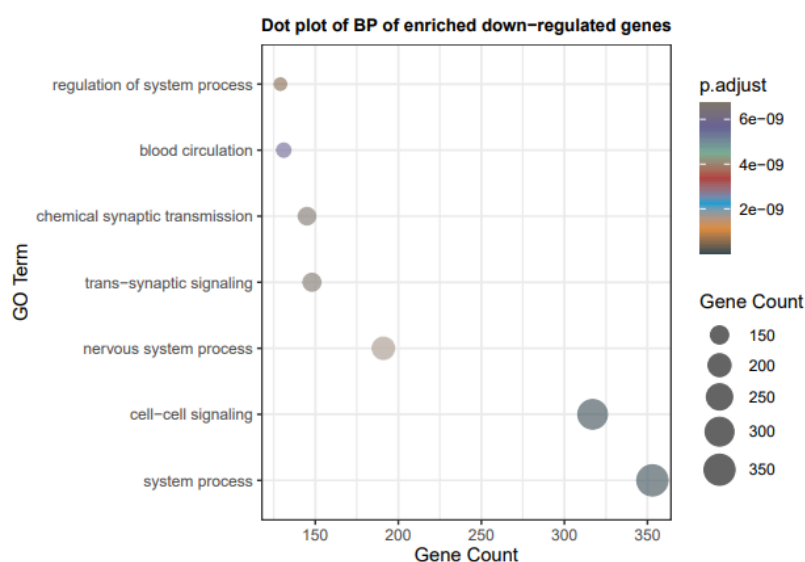
The GO graph visually represents the hierarchical relationships among enriched GO terms. Each node represents an enriched GO term. Edges represent the hierarchical relationships between GO terms, showing parent-child relationships.

## 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).



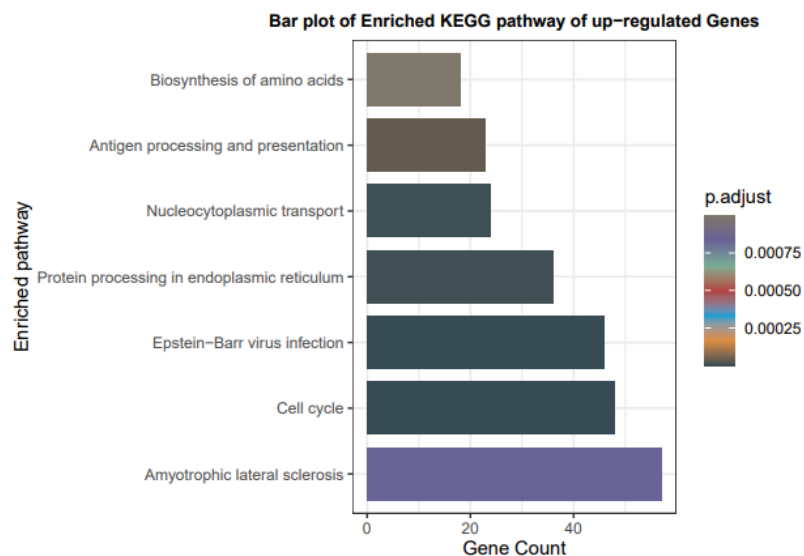
**Figure 8**

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.



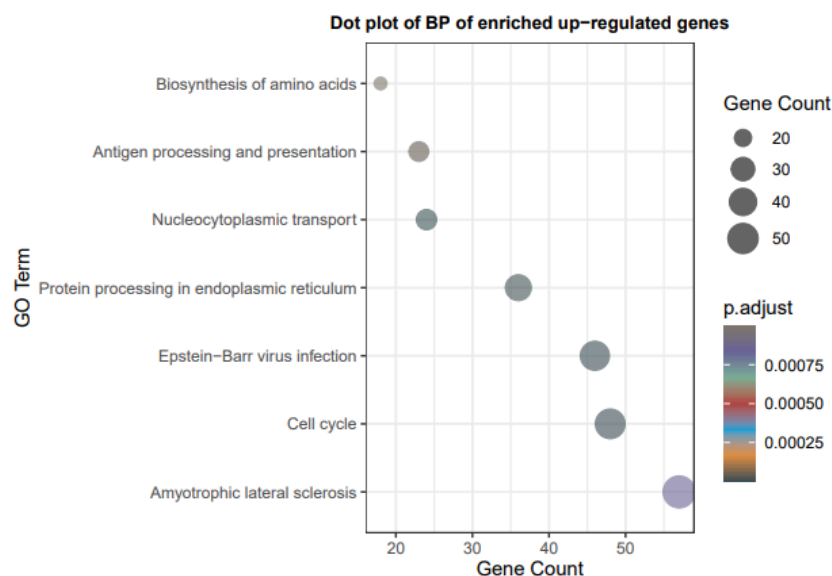
□ **Pathway Enrichment Analysis:**

**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).

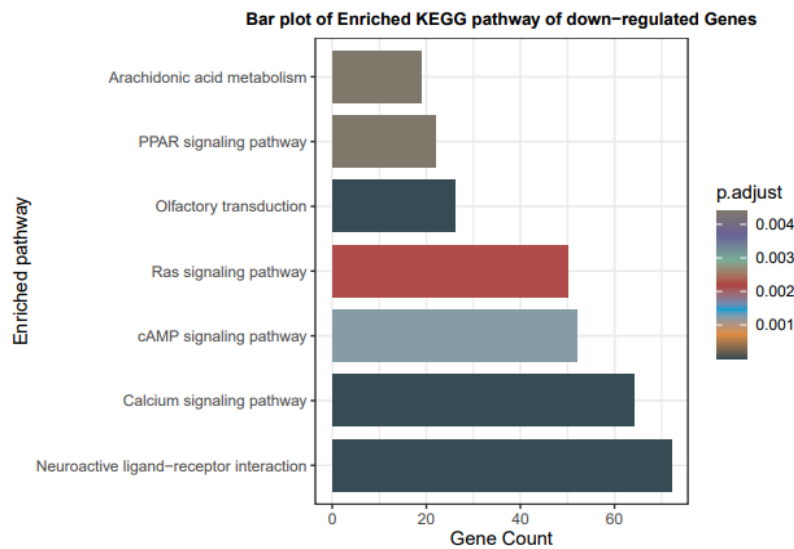


**Figure 11**

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.

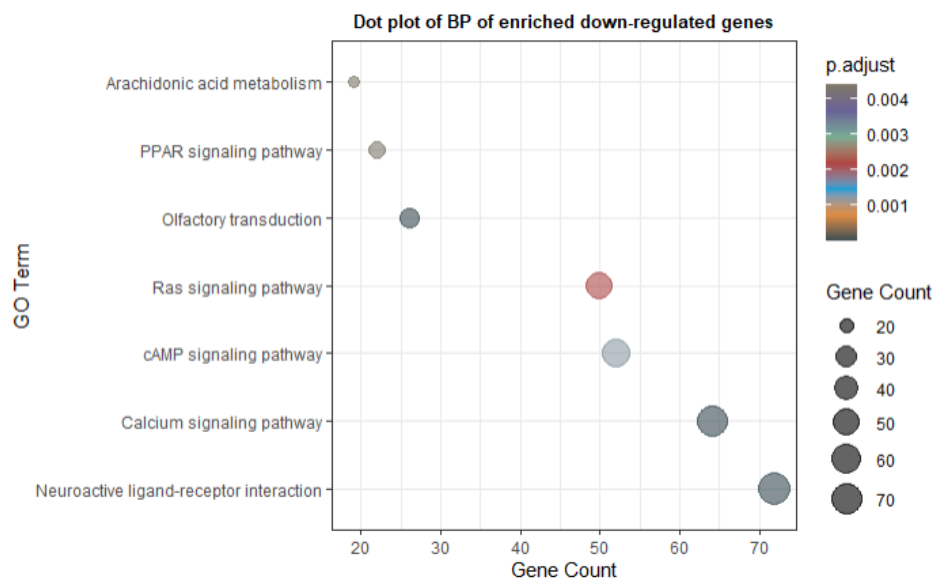


## 2) Figures of enriched KEGG pathways among down-regulated significant genes.



**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).



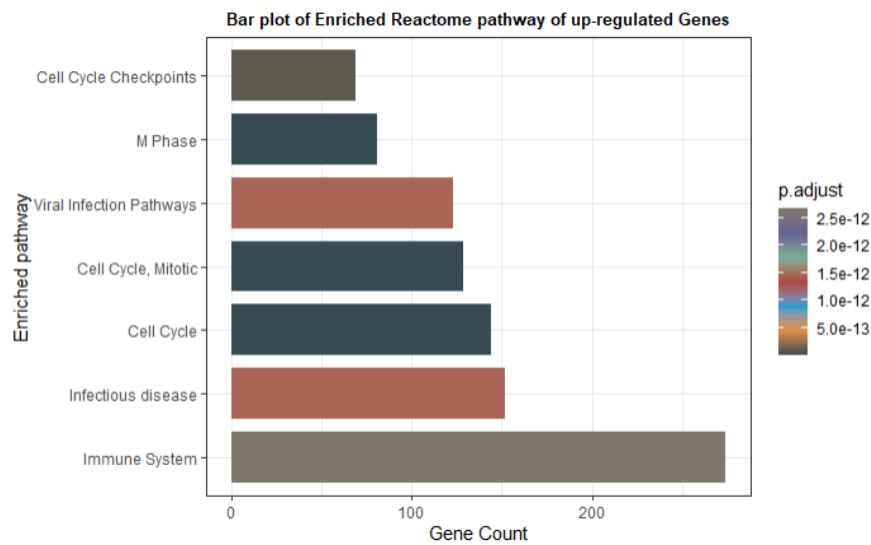
**Figure 14**

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.



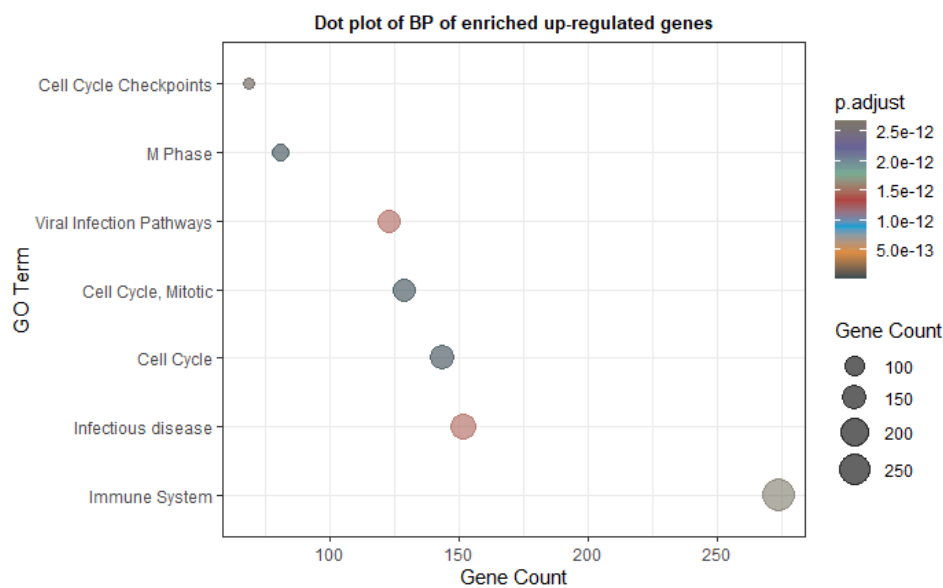


### 3) Figures of enriched Reactome pathways among up-regulated significant genes.



**Figure 16**

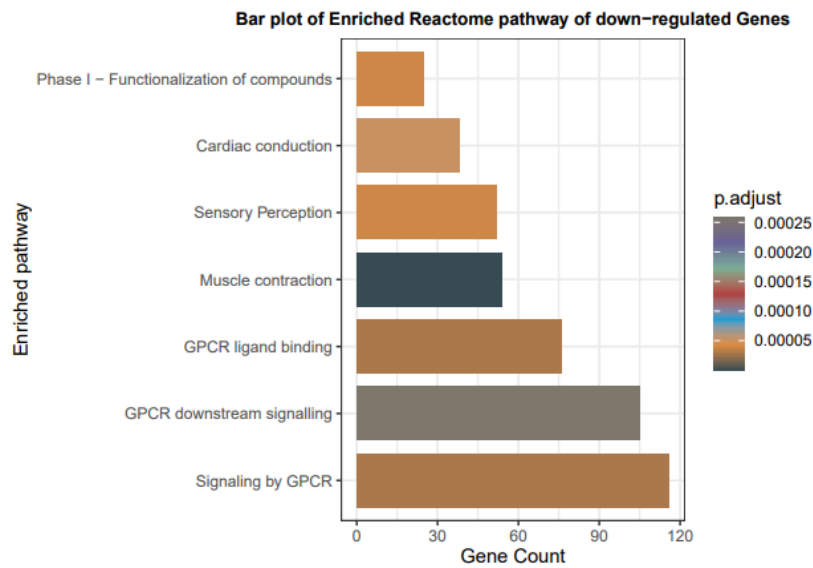
Barplot that indicates significantly enriched biological process pathways among up-regulated significant genes (pathways with lower p-values, p.adjust, and q-values are more significantly enriched).



**Figure 17**

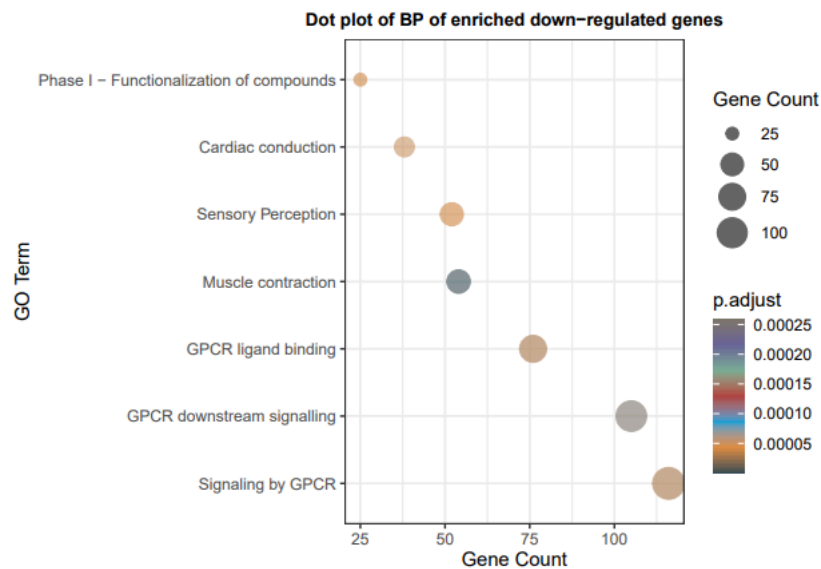
Dotplot that indicates significantly enriched biological process pathways among up-regulated significant genes. the color indicates the significance of the biological process pathways and the size indicates how many genes are contributing to the enriched pathway.

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



**Figure 18**

Barplot 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 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.