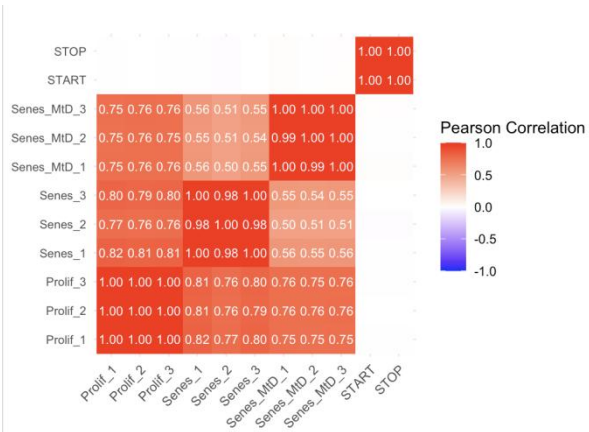
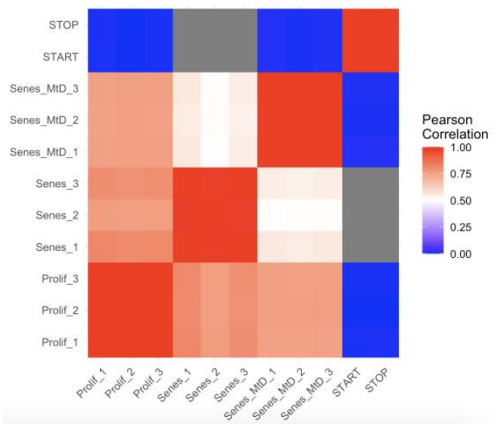
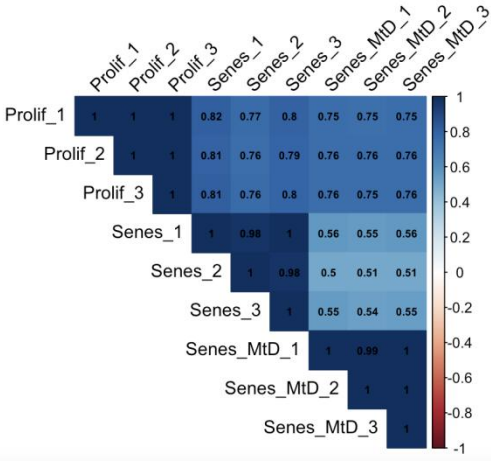
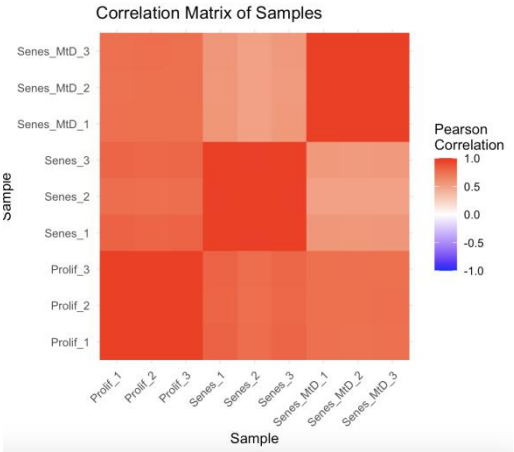


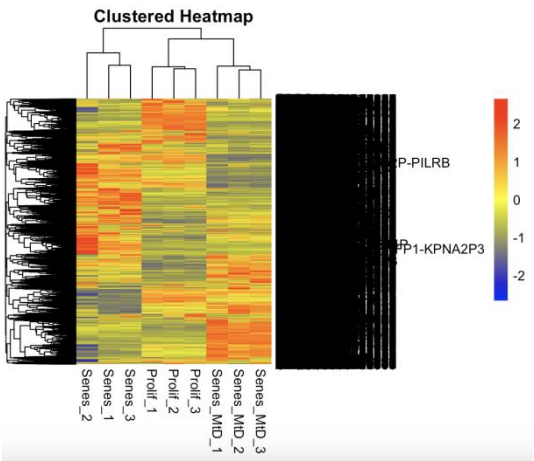
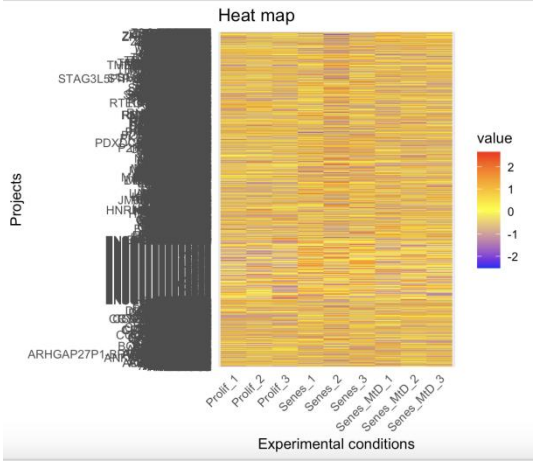
Picture  
Heat map



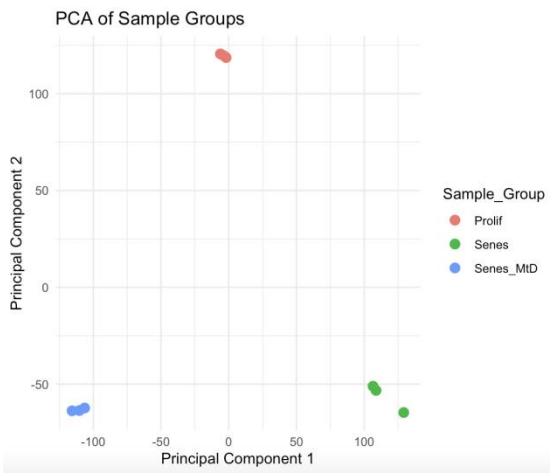
Correlation Matrix of Samples



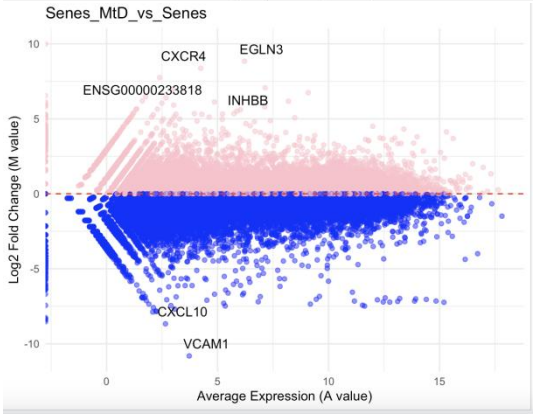
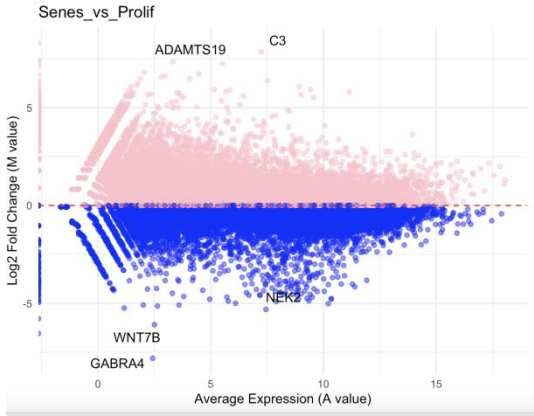
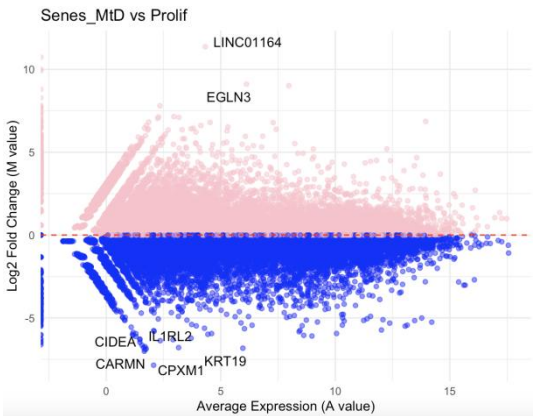
heat map and cluster



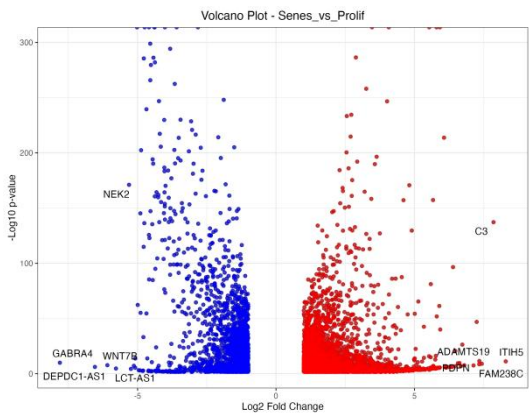
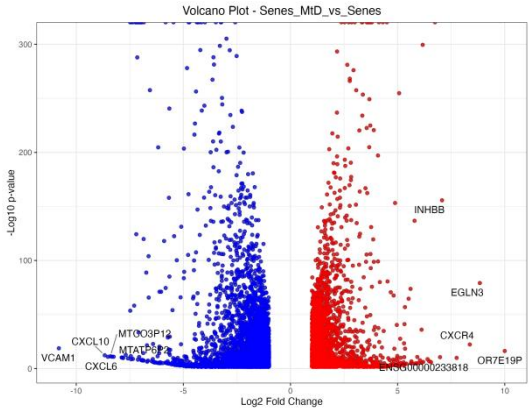
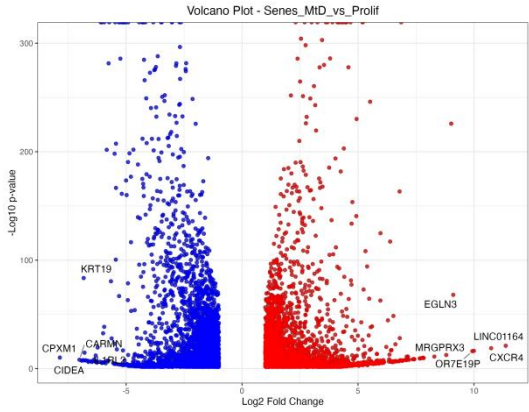
PCA



MA

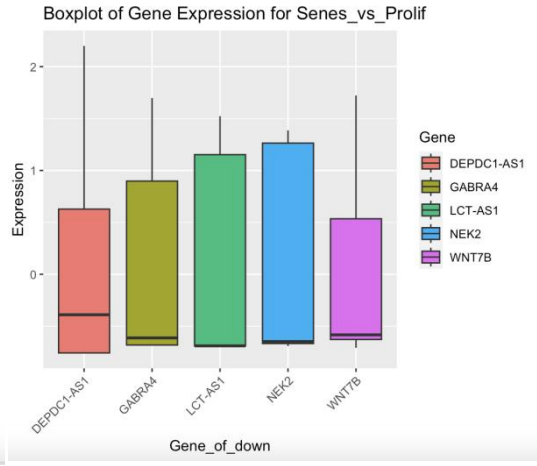
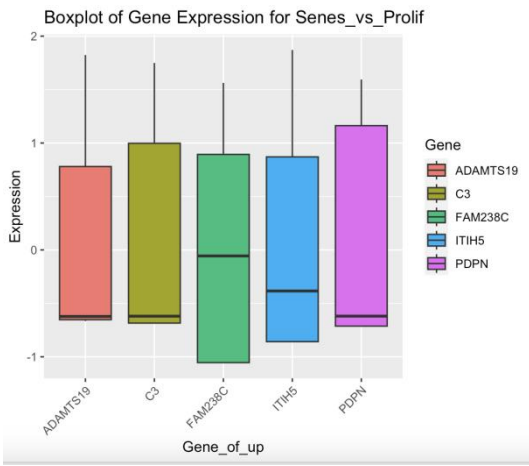


Volcano

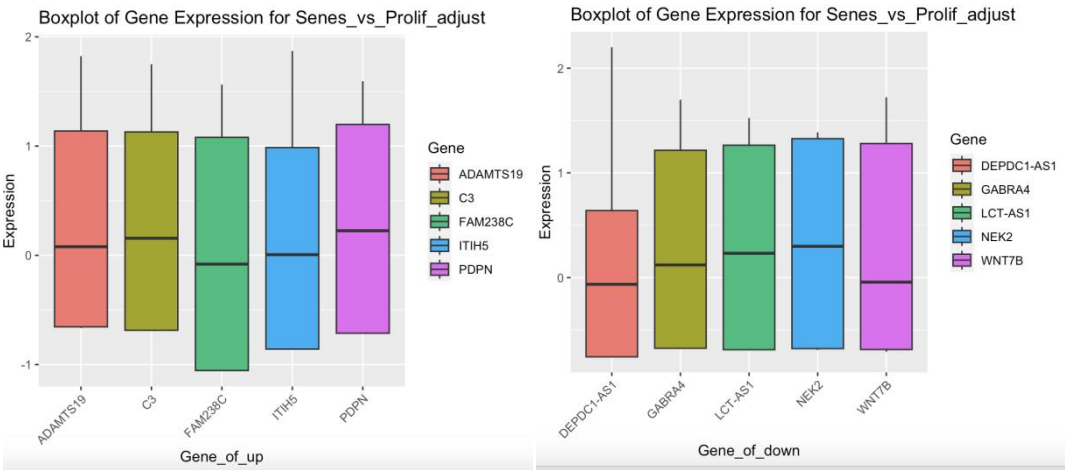


Box

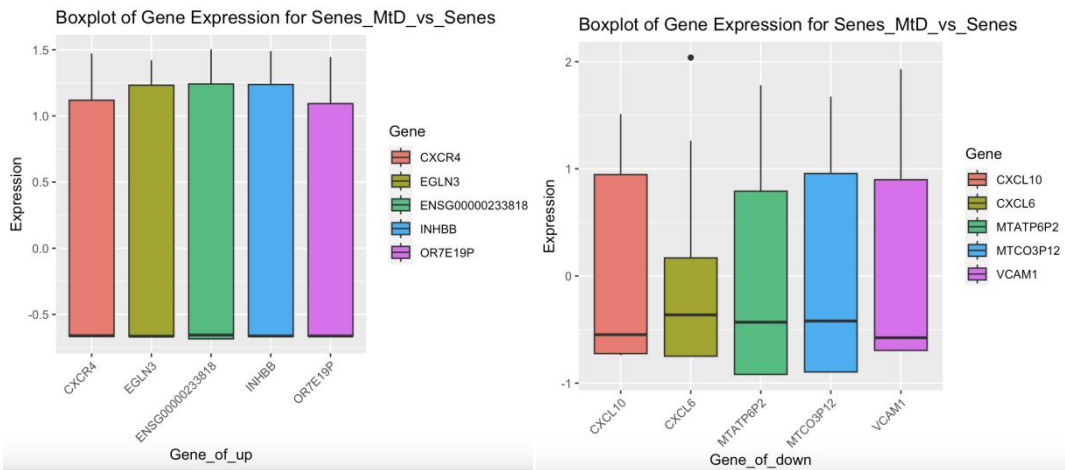
Senes\_vs\_Prolif



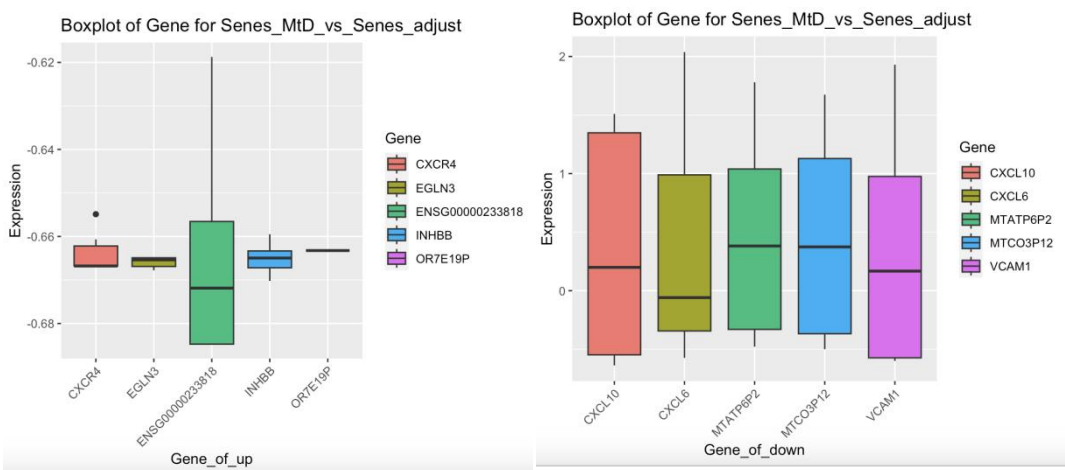
Senes\_vs\_Prolif\_adjust



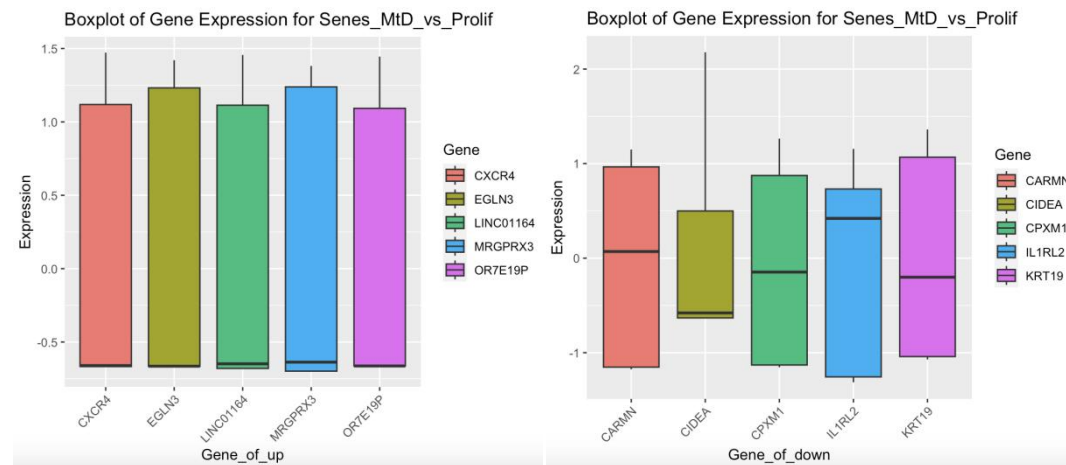
Senes\_MtD\_vs\_Senes



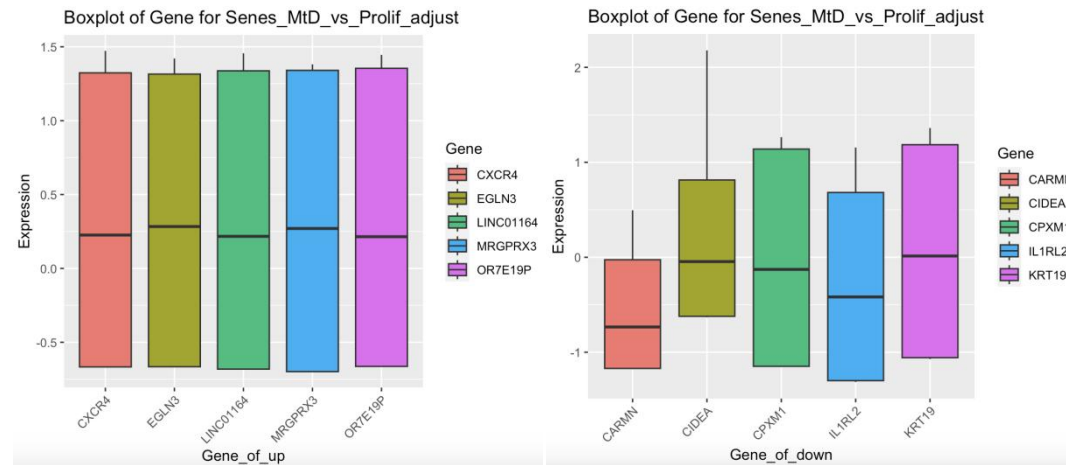
Senes\_MtD\_vs\_Senes\_adjust



Senes\_MtD\_vs\_Prolif

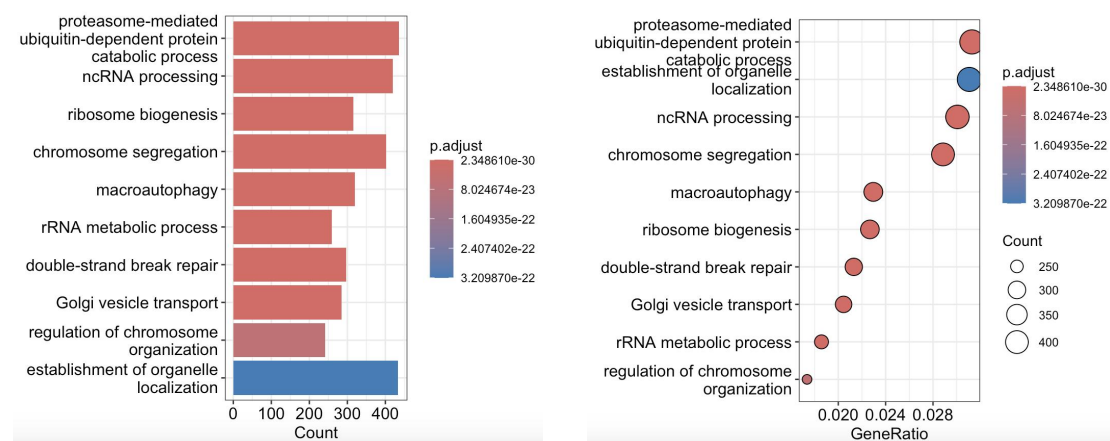


Senes\_MtD\_vs\_Prolif\_adjust

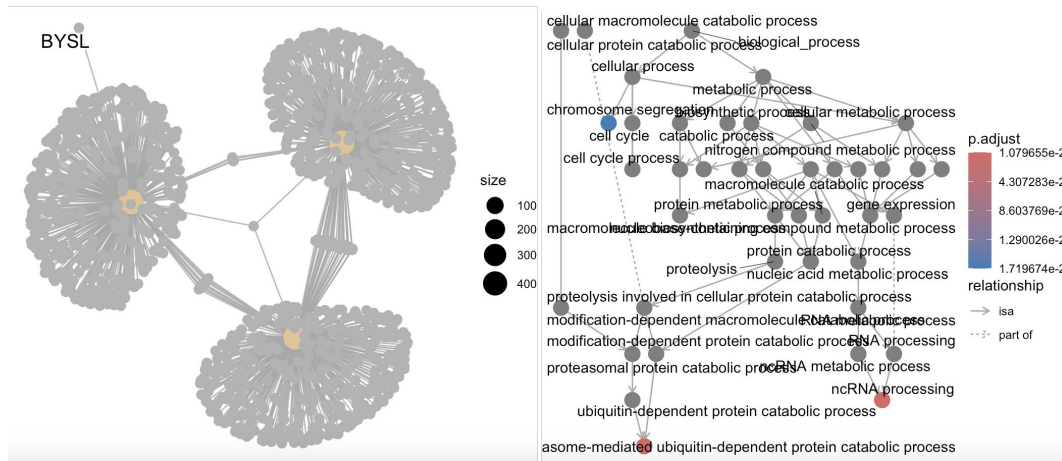


## Pathway

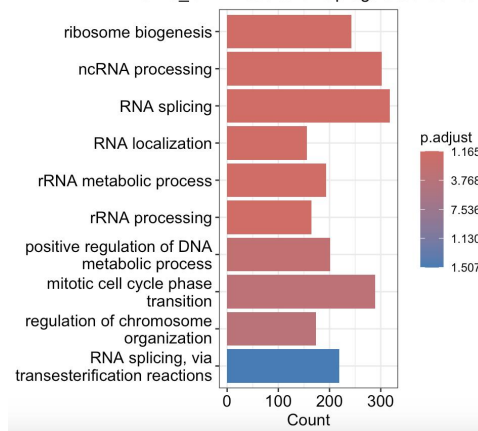
Senes\_MtD\_vs\_Prolif



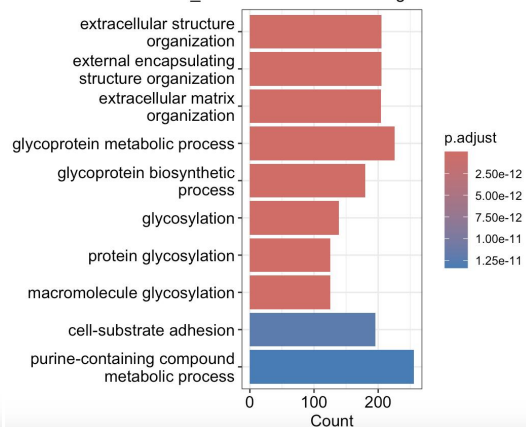




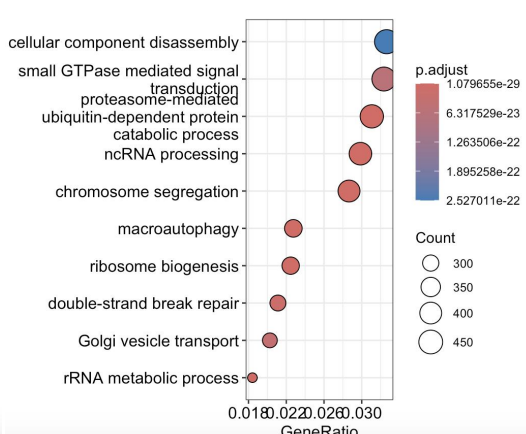
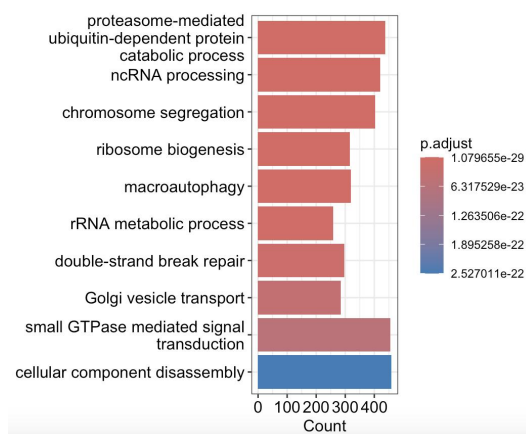
SMS\_ORA Results for Upregulated Genes

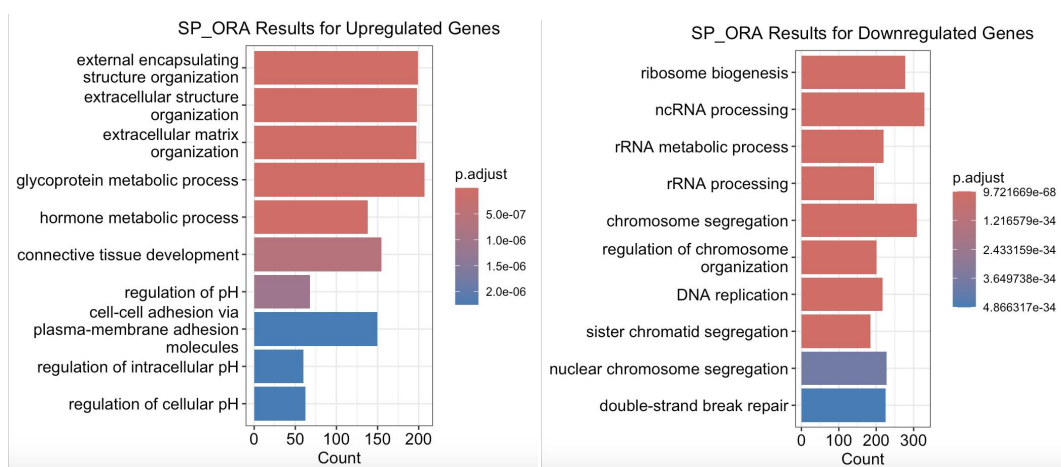
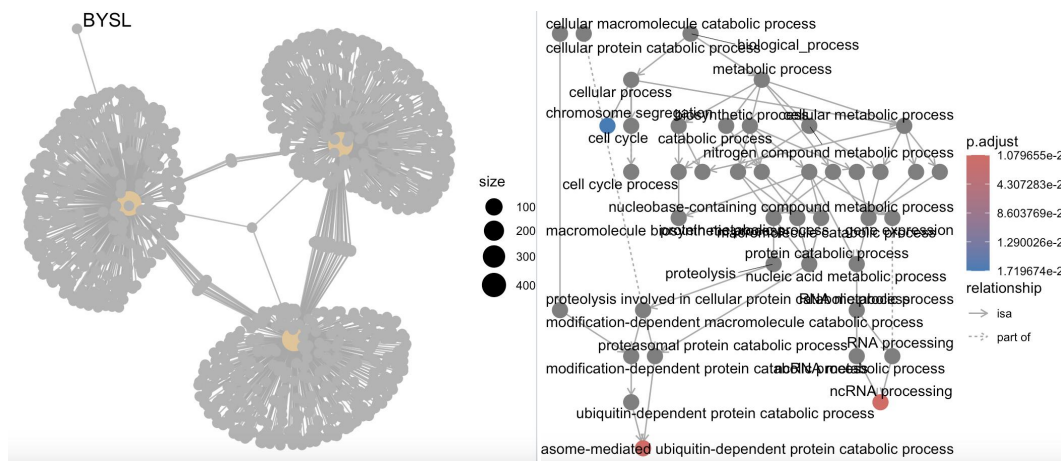


SMS\_ORA Results for Downregulated Genes



## Senes\_vs\_Prolif





In the Gene Ontology (GO) enrichment analysis experiments, the results of the Senes\_MtD\_vs\_Senes and Senes\_vs\_Prolif groups were the same, indicating similarities in their functional classifications. However, the analysis of overexpressed (upregulated) and underexpressed (downregulated) genes in these two experiments showed significant differences, suggesting that despite their functional similarities, there are notable differences at the level of gene expression regulation.