

Introduction

Mutations and alterations of certain genes could lead to uncontrollable proliferations and tumour formation, ultimately resulting in cancer. Understanding the differential expression of specific genes helps in identifying key molecular drivers of cancer progression. The focus of this code was to analyse differential gene expression, focusing on the role of TBX2 and TBX3 in pancreatic cancer, which are transcription factors associated with cellular proliferation, differentiation, and tumorigenesis.

An enrichment analysis was performed using Enrichr, to analyse differential gene expression and to identify enriched biological pathways using multiple gene set libraries (GO Molecular Function 2023, Reactome 2022, MSigDB_Hallmark 2020, GO Biological Process 2023). This was done to provide insight into the understanding of molecular functions, signalling pathways, and biological processes relevant to pancreatic cancer. A python code was developed in a Jupyter Notebook to generate visual representations of the enrichment results, as seen in the figures below.

Explanation of results and interpretation of findings

The figures provided below assist with the interpretation of the relationship between genes TBX 2 and 3 and pancreatic cancer. The first four venn diagrams shown, show an overlap between the genes which could be an indicator of shared biological conditions and the key role both genes play in pancreatic cancer. The large number expressed in the intersecting regions indicate similarities in datasets, which could explain a possible correlation between an expression of both genes and pancreatic cancer. The non-overlapping areas indicate that the gene could be condition specific or there is a higher expression of the gene in the dataset.

The next set of data or results shown, are specific to the gene set library used. Each library contains a venn diagram, bar graph as well as a scatter plot for both genes. The graphs show biological pathways significantly associated with each gene and both the bar graph and dot plot the higher the pathway is ranked the more enriched it is. These pathways show biological relevance, and they are shown to relate to the progression of the pancreatic cancer. There are slight differences between these rankings and the gene being tested. The scatter plot also indicates statistical significance in both the height and colour of the plot (the higher and darker it is the more significant).

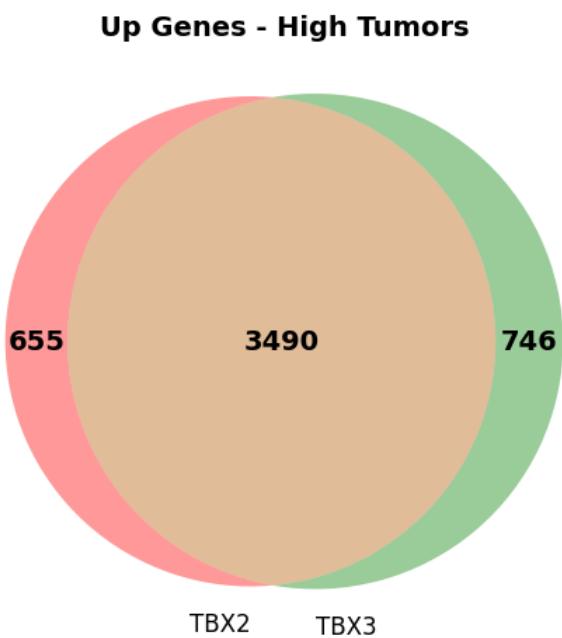


Figure 1 Venn diagram showing ug genes-High tumours between TBX2 and TBX3

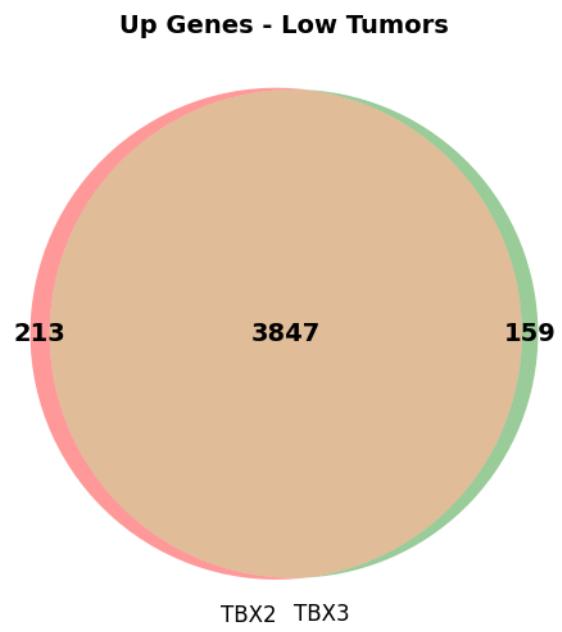


Figure 2 Venn diagram showing up genes-low tumours between TBX2 and TBX3

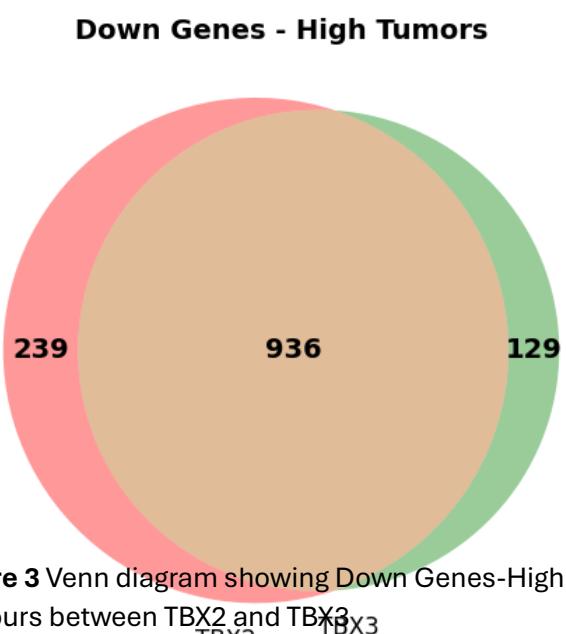


Figure 3 Venn diagram showing Down Genes-High tumours between TBX2 and TBX3

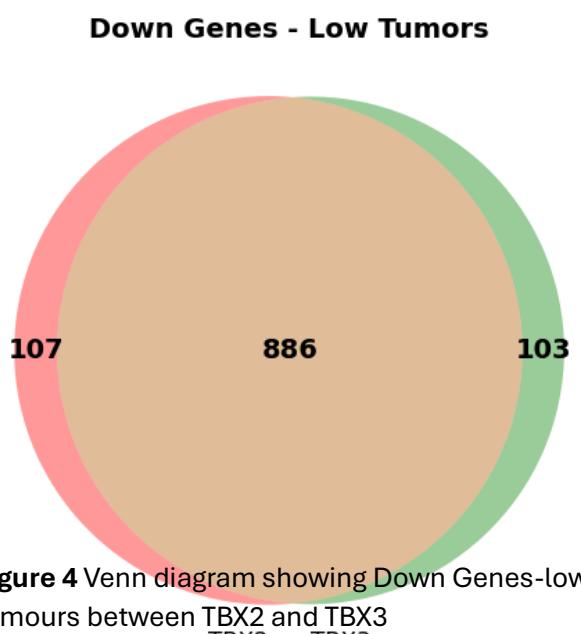


Figure 4 Venn diagram showing Down Genes-low tumours between TBX2 and TBX3

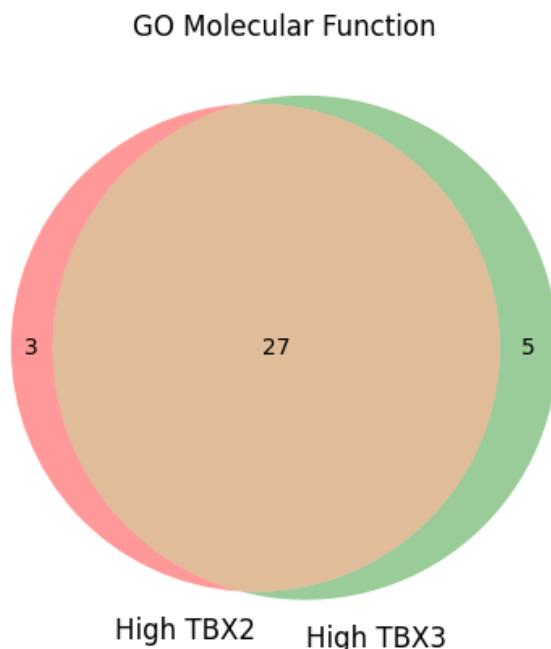


Figure 5 Venn diagram showing GO Molecular function between TBX2 and TBX3

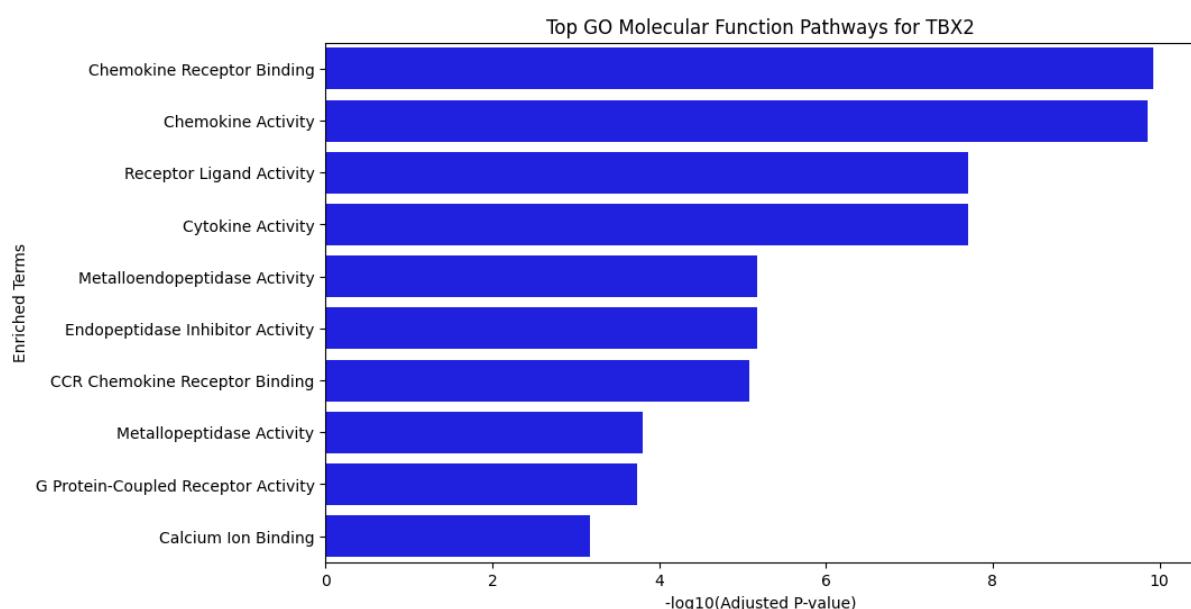


Figure 5 Bar Graph showing Top GO Molecular Function Pathways for TBX2

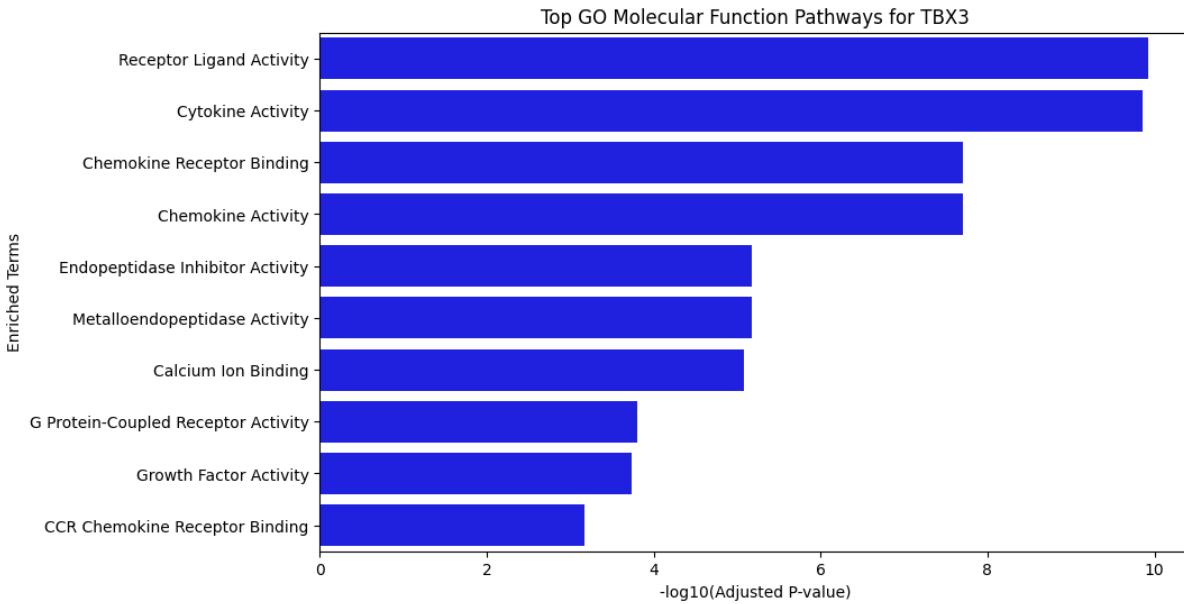


Figure 6 Bar Graph showing Top GO Molecular Function Pathways for TBX3

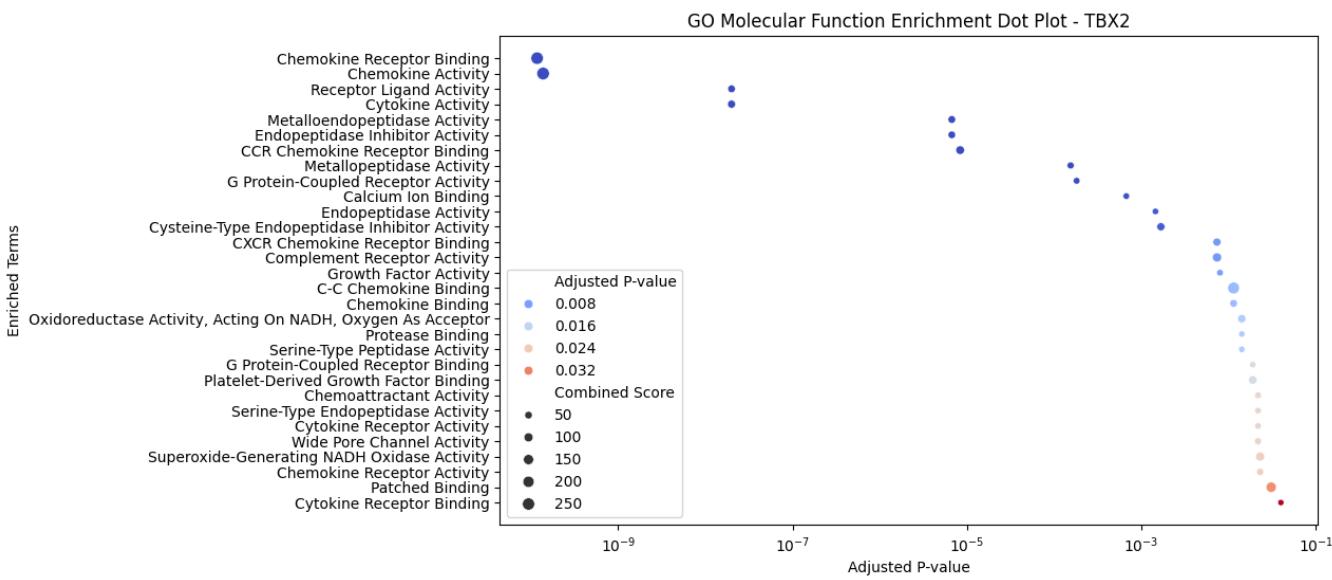


Figure 7 Dot plot showing GO Molecular Function enrichment for TBX2

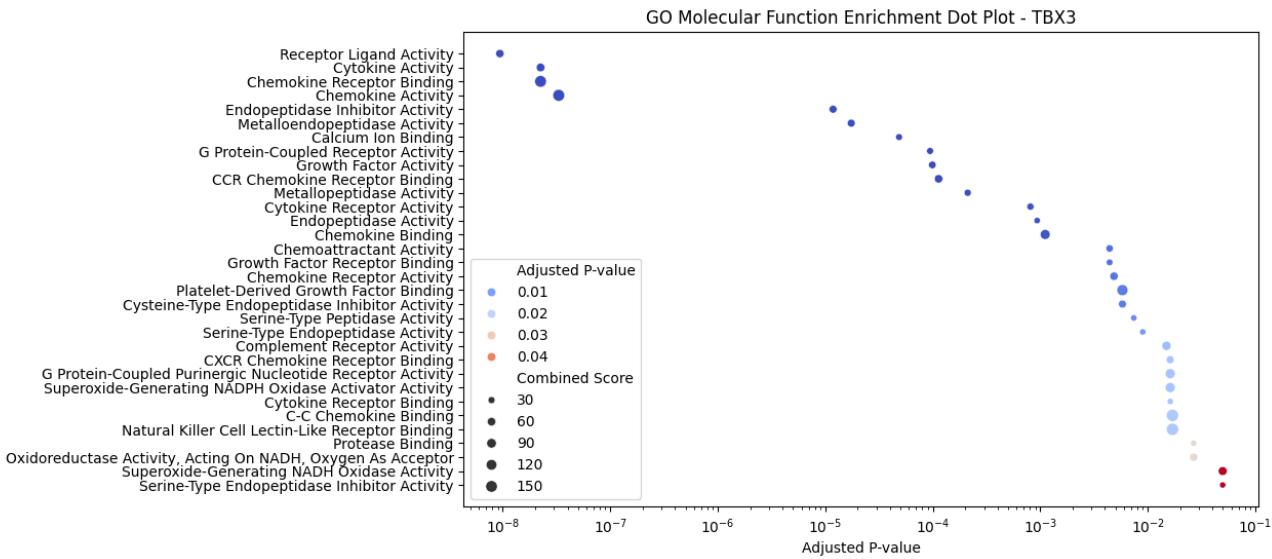


Figure 8 Dot plot showing GO Molecular Function enrichment for TBX3

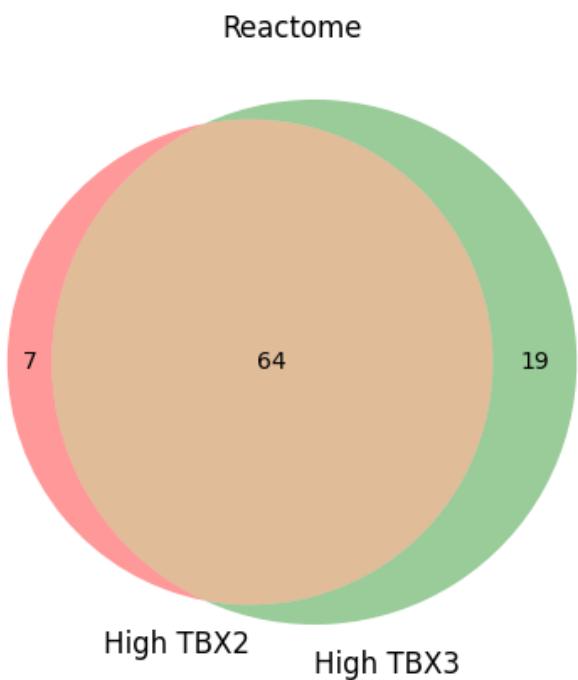


Figure 9 Venn diagram showing Reactome between TBX2 and TBX3

Enriched Terms

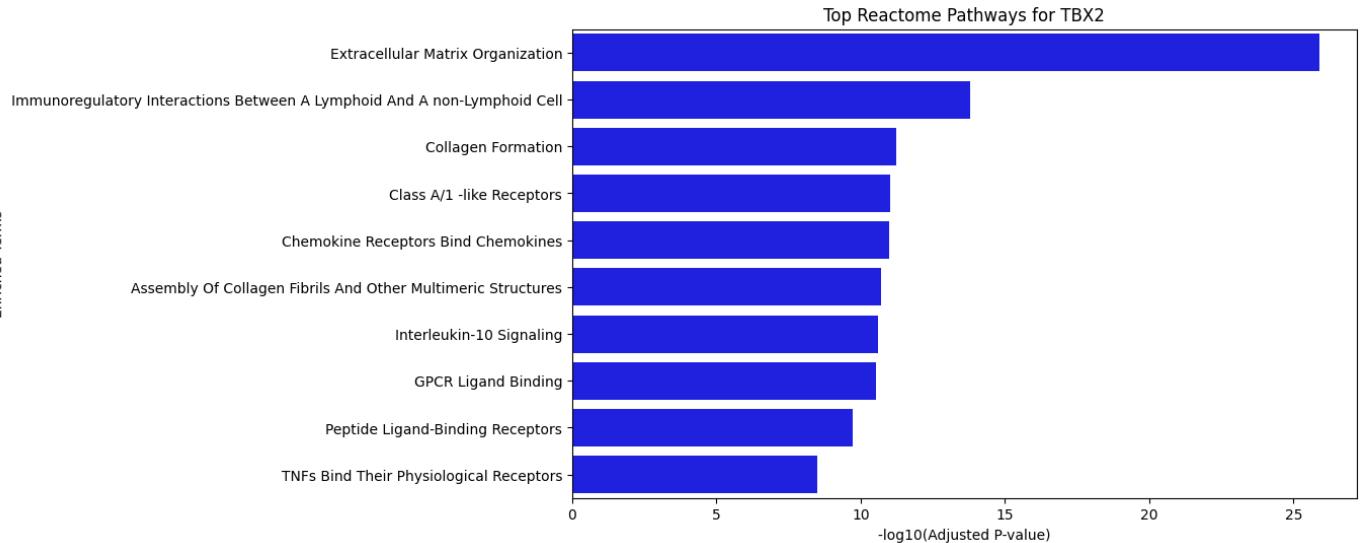


Figure 10 Bar Graph showing Top Reactome Pathways for TBX2

Enriched Terms

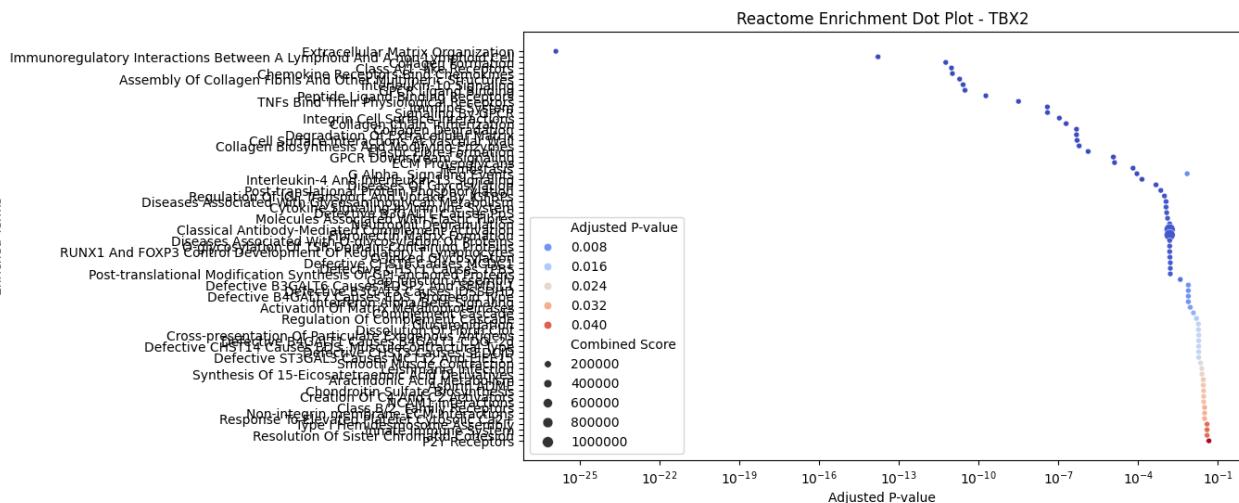


Figure 11 Dot plot showing Reactome enrichment for TBX2

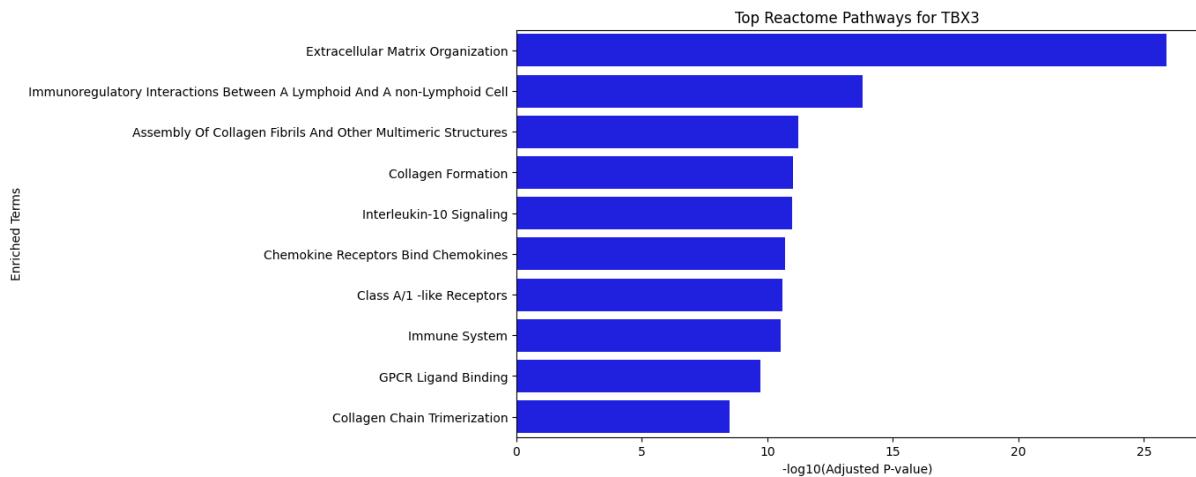


Figure 12 Bar Graph showing Top Reactome Pathways for TBX3

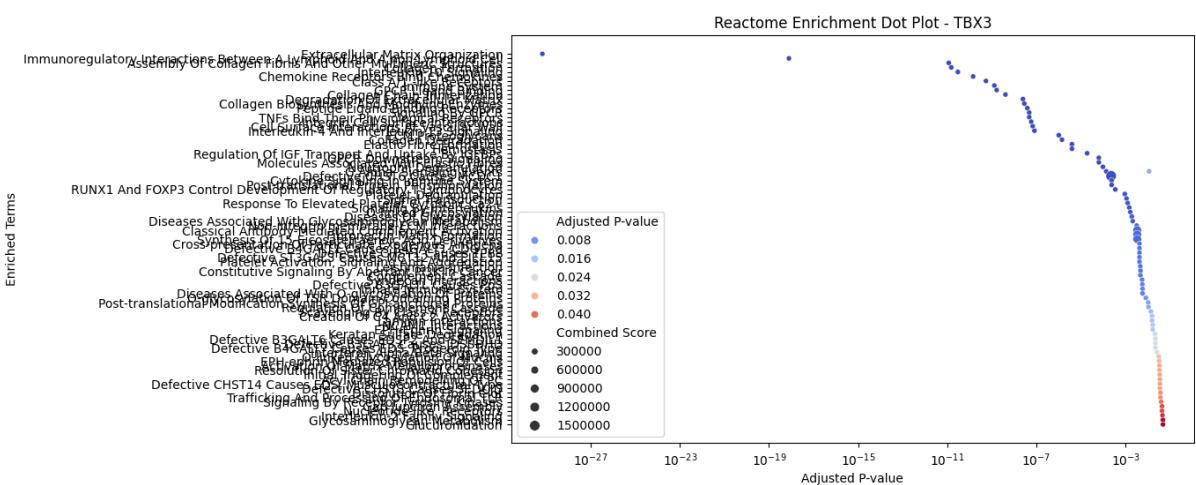


Figure 13 Dot plot showing Reactome enrichment for TBX3

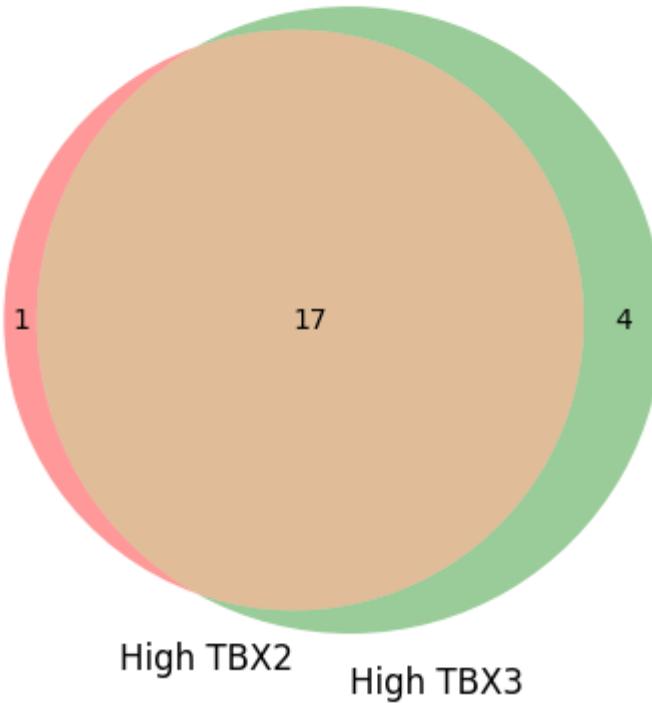


Figure 14 Venn diagram showing MSigDB Hallmark between TBX2 and TBX3

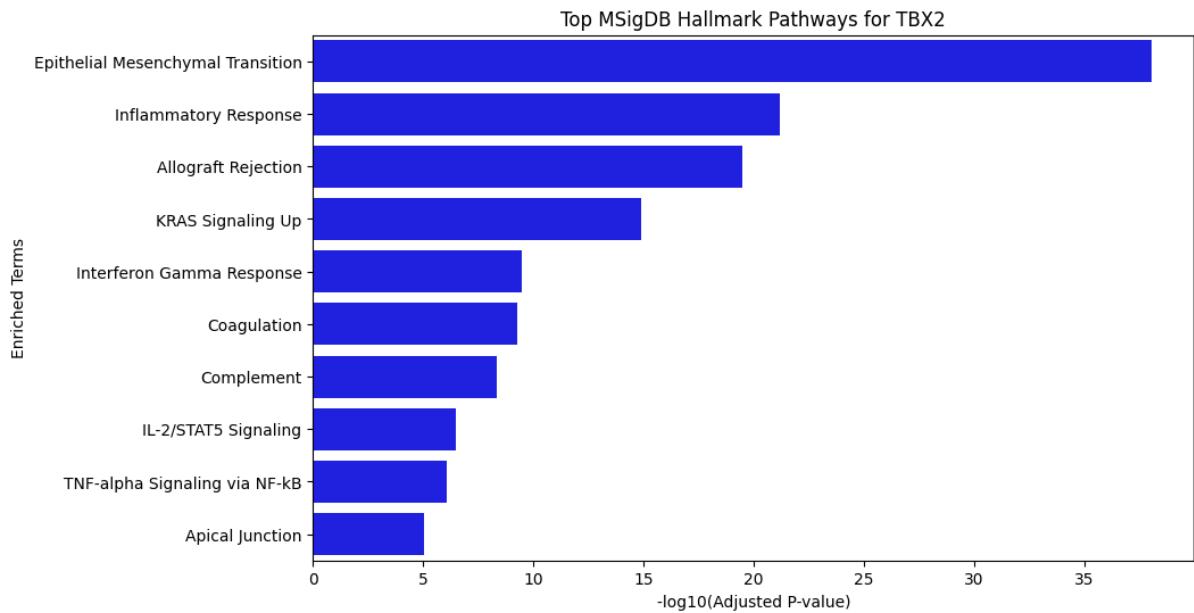


Figure 15 Bar Graph showing Top MSigDB Hallmark Pathways for TBX2

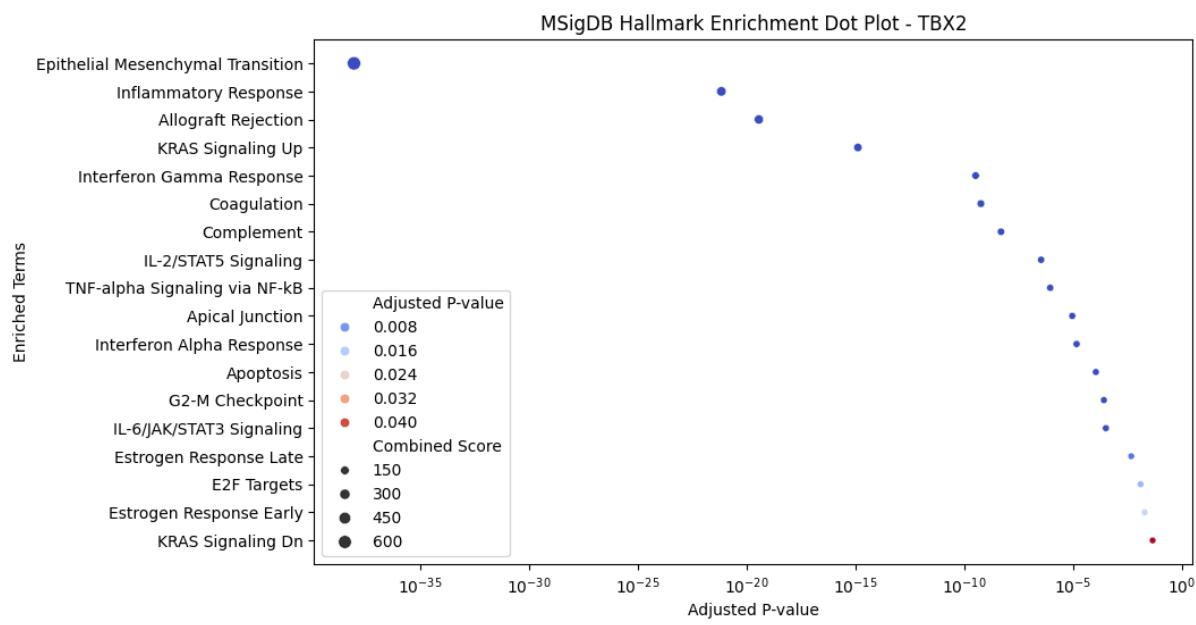


Figure 16 Dot plot showing MSigDB Hallmark enrichment for TBX2

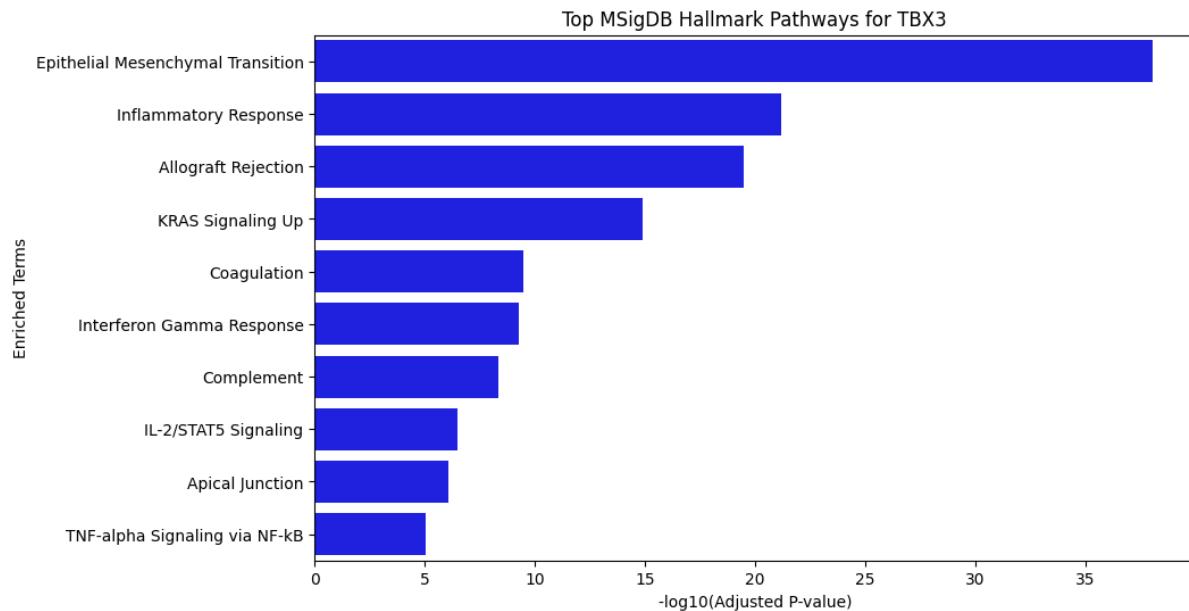


Figure 17 Bar Graph showing Top MSigDB Hallmark Pathways for TBX3

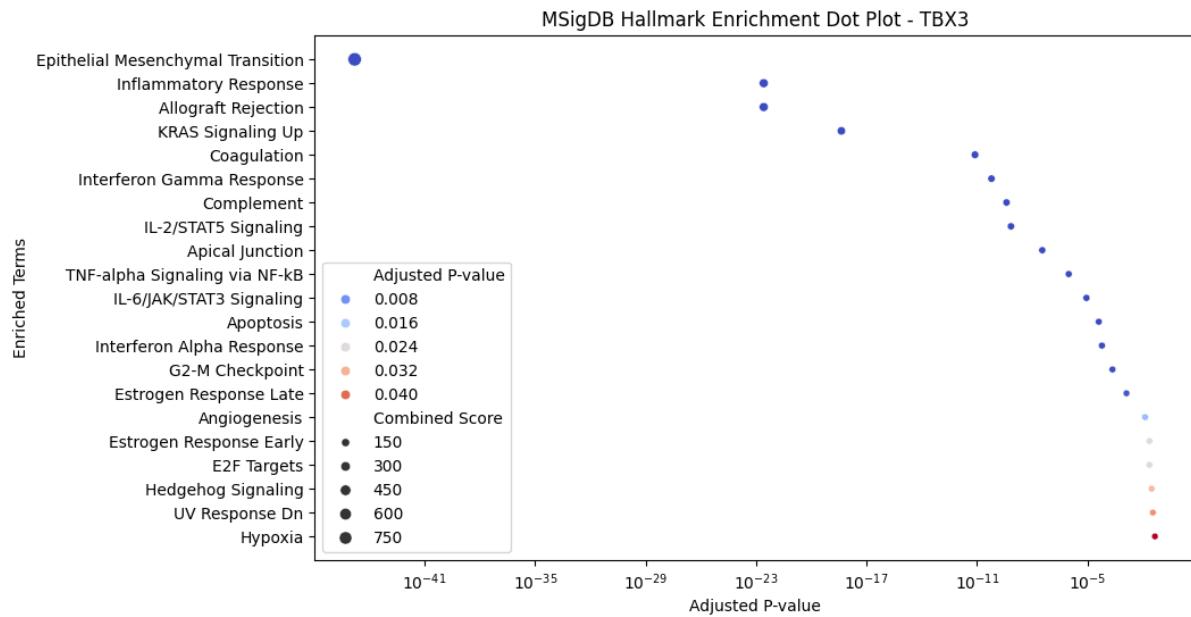


Figure 18 Dot plot showing MSigDB Hallmark enrichment for TBX3

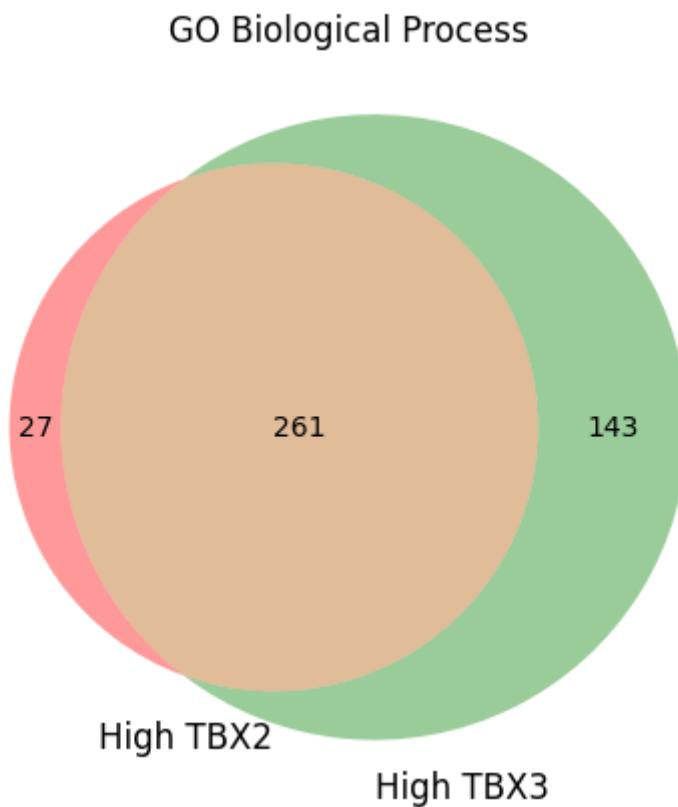


Figure 19 Venn diagram GO Biological Process between TBX2 and TBX3

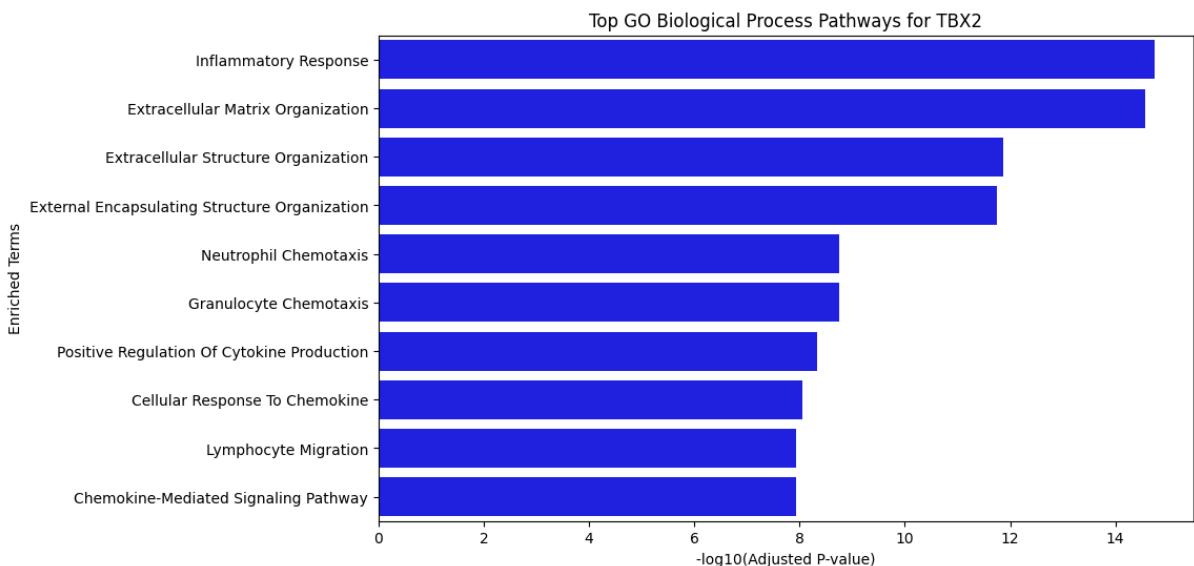


Figure 20 Bar Graph showing Top GO Biological Pathways for TBX2

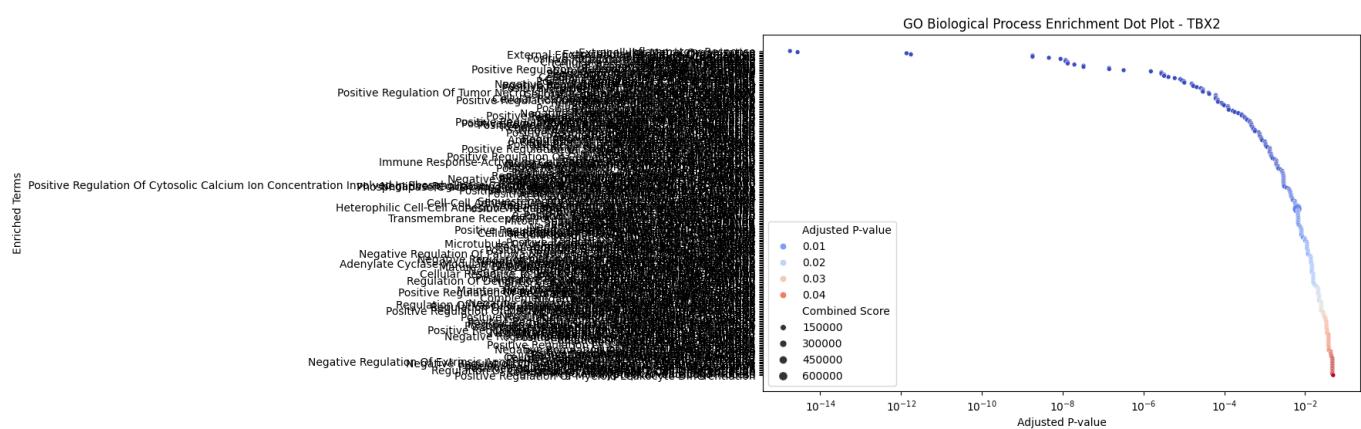


Figure 21 Dot plot showing GO Biological enrichment for TBX2

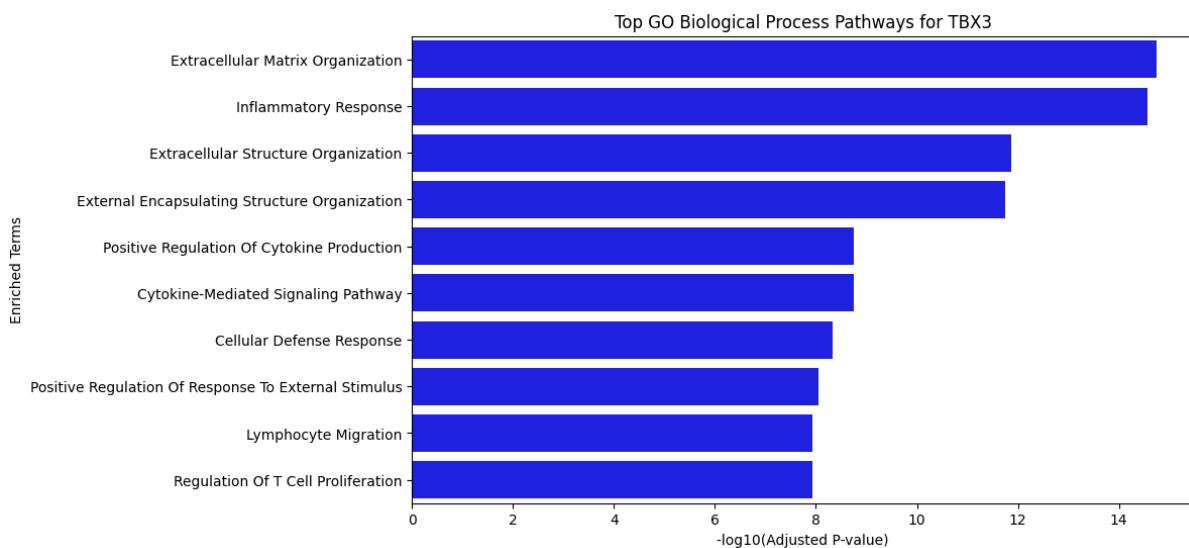


Figure 22 Bar Graph showing Top GO Biological Pathways for TBX3

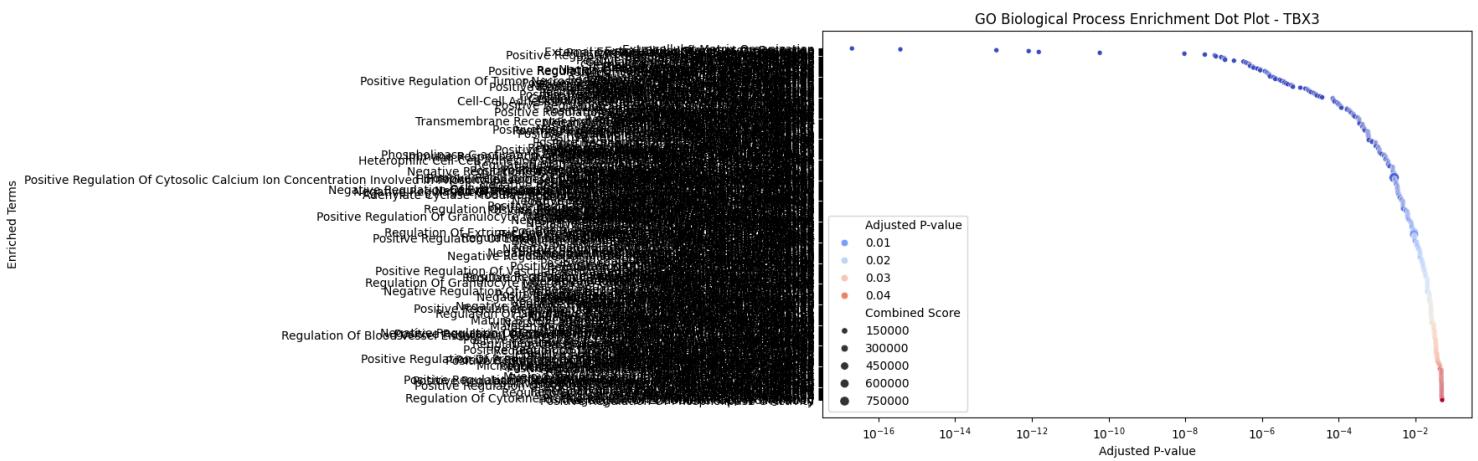


Figure 23 Dot plot showing GO Biological enrichment for TBX3

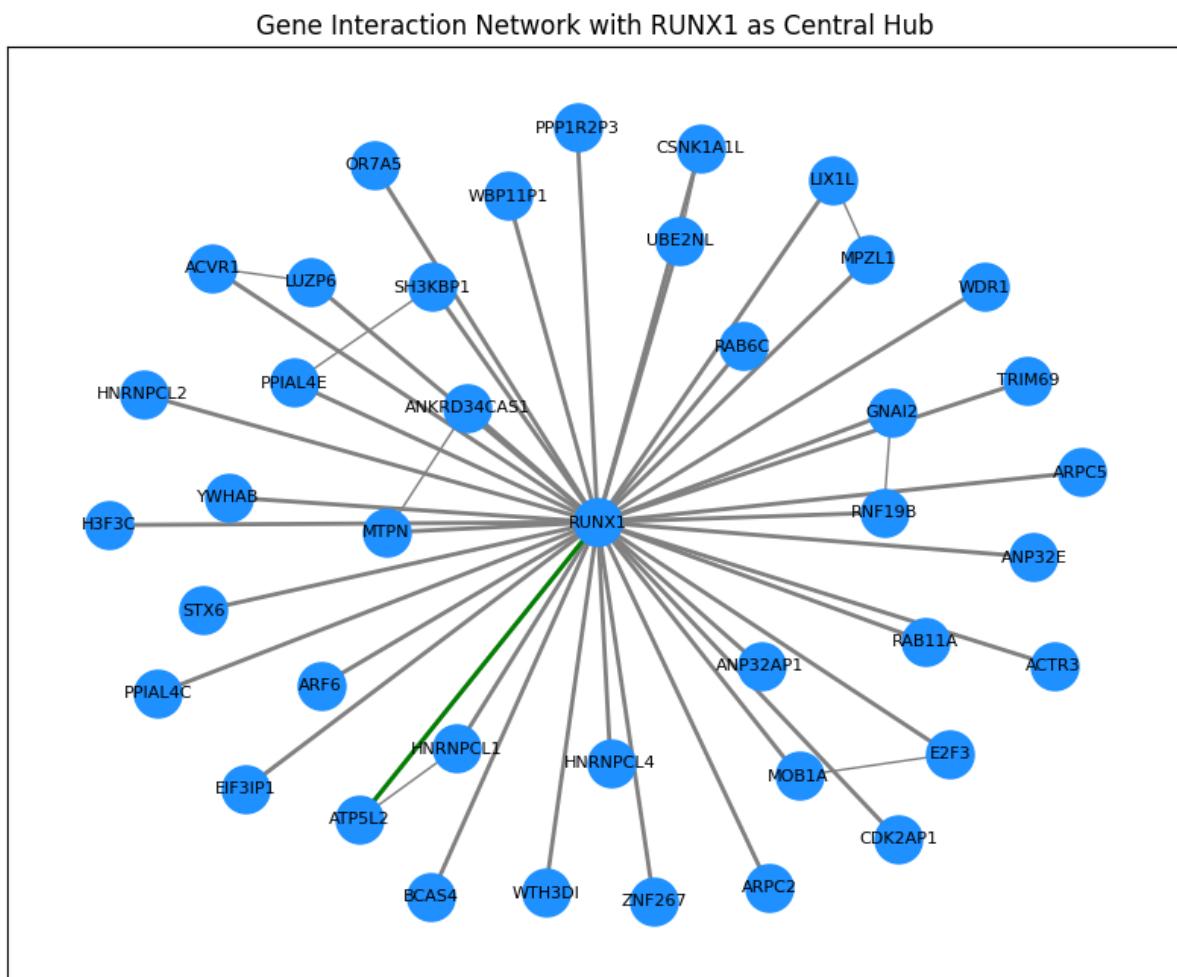


Figure 24 Gene interaction network