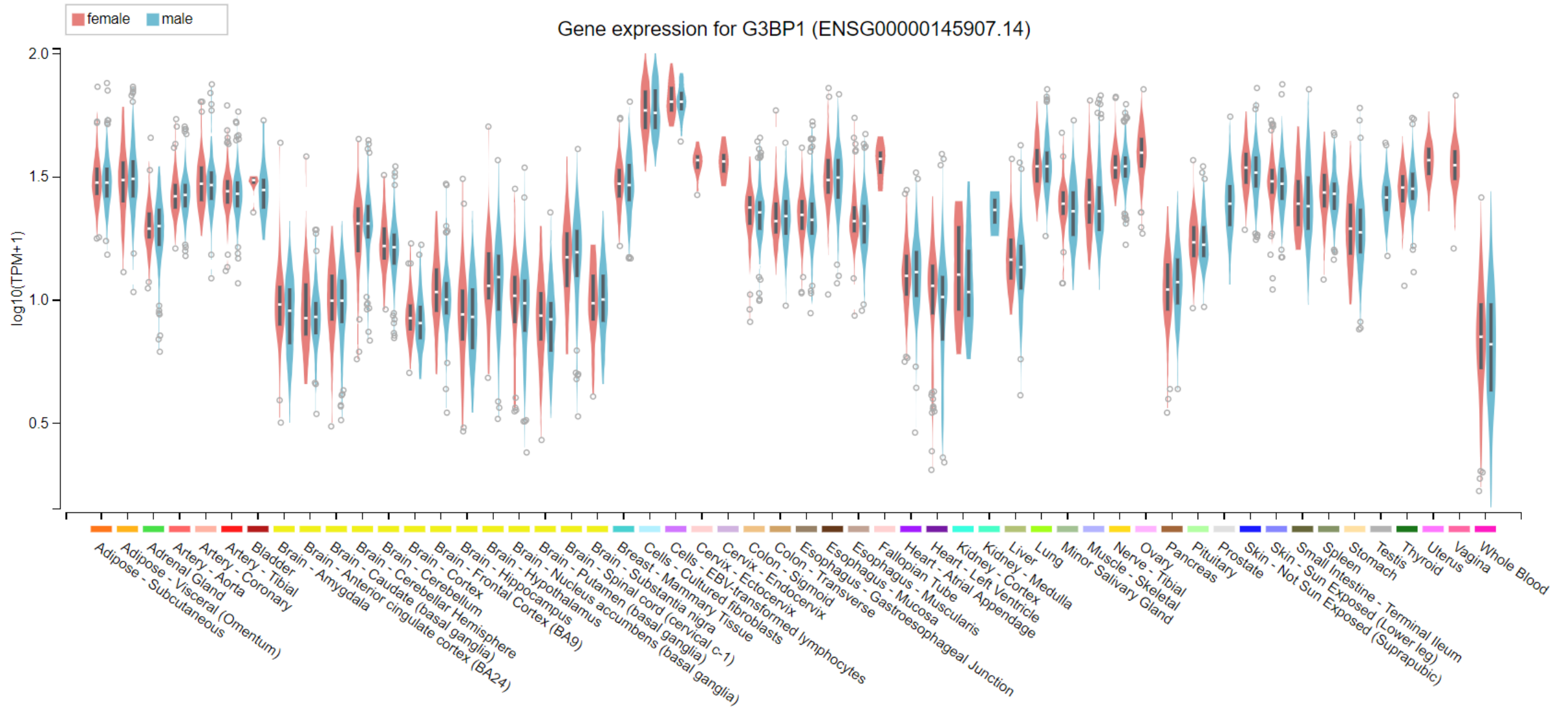
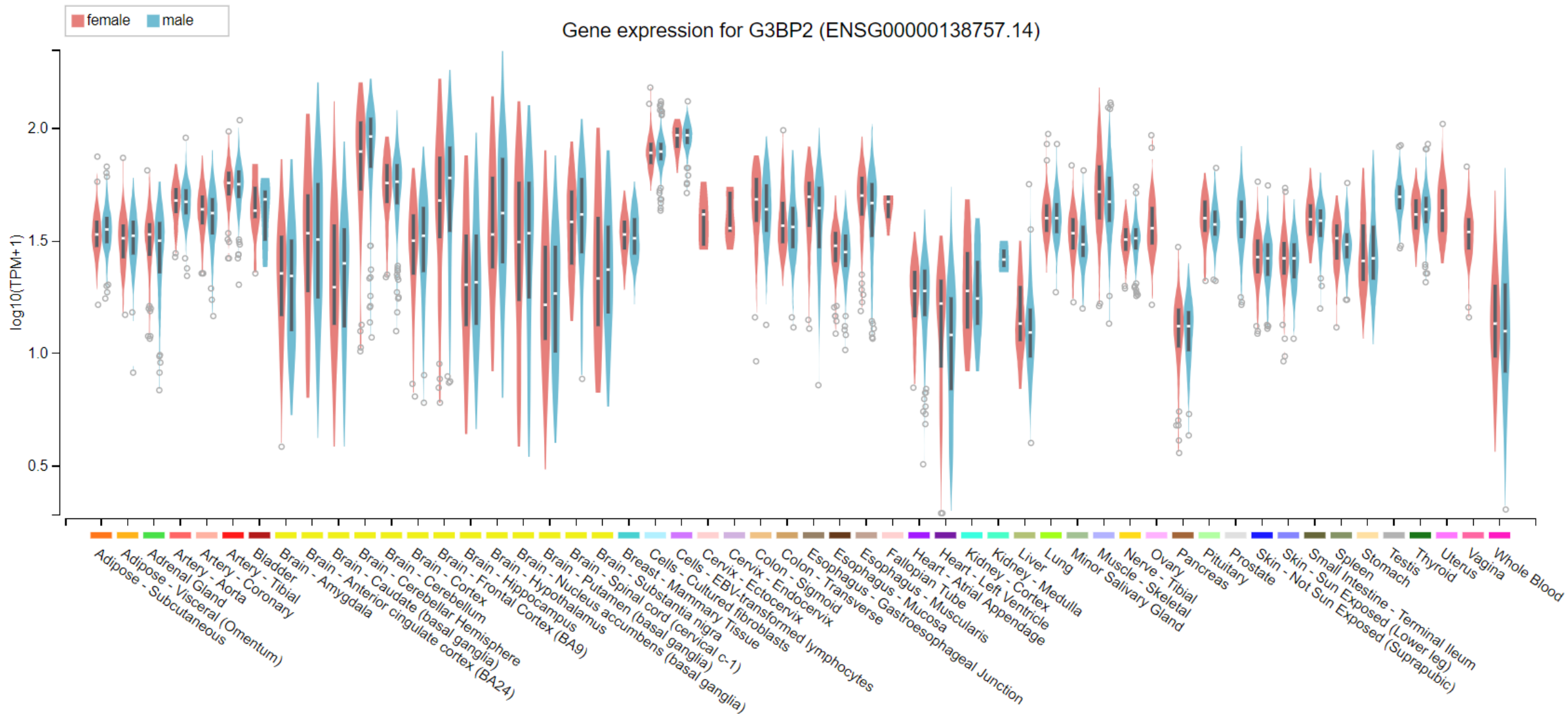
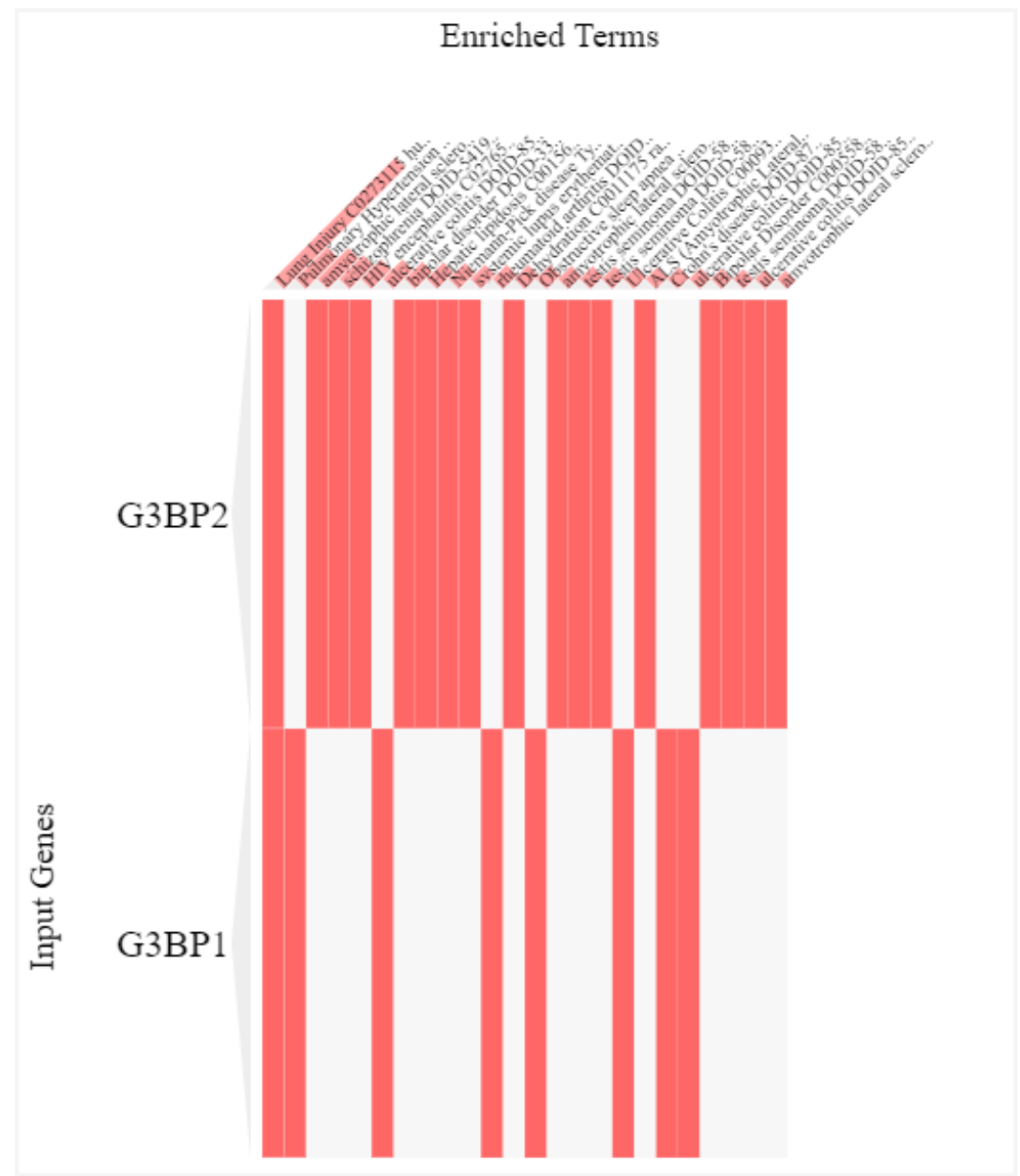
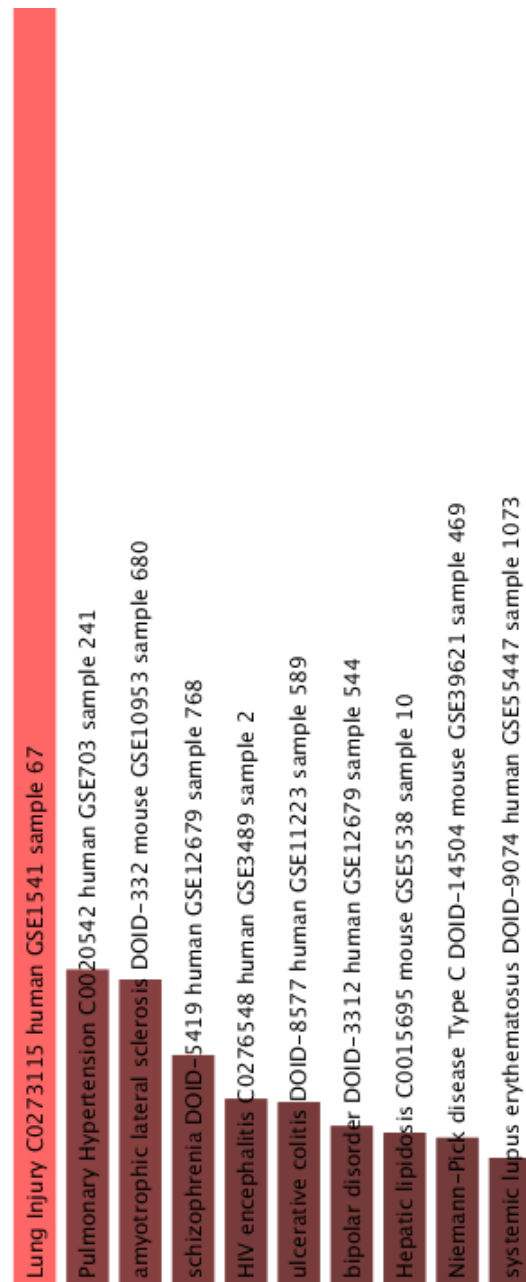


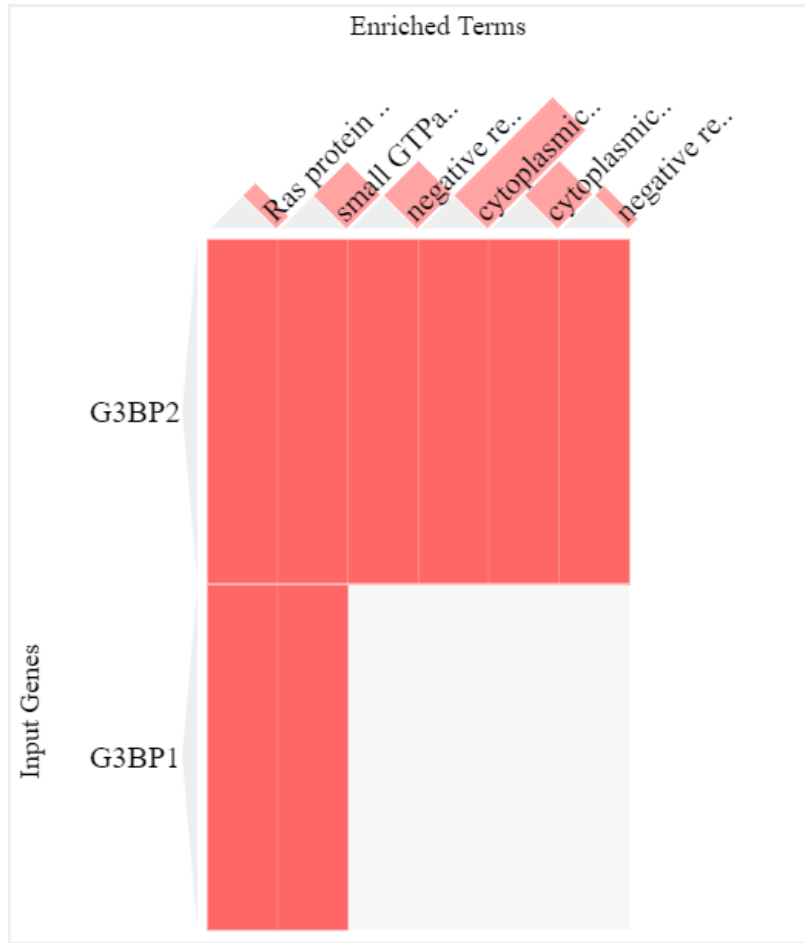
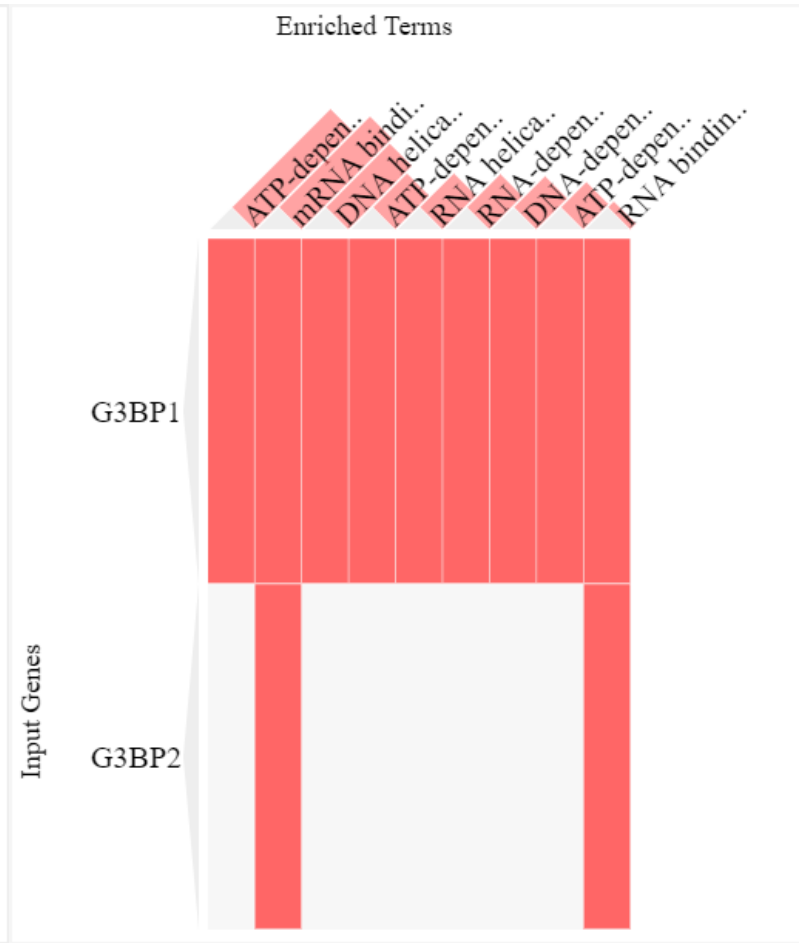
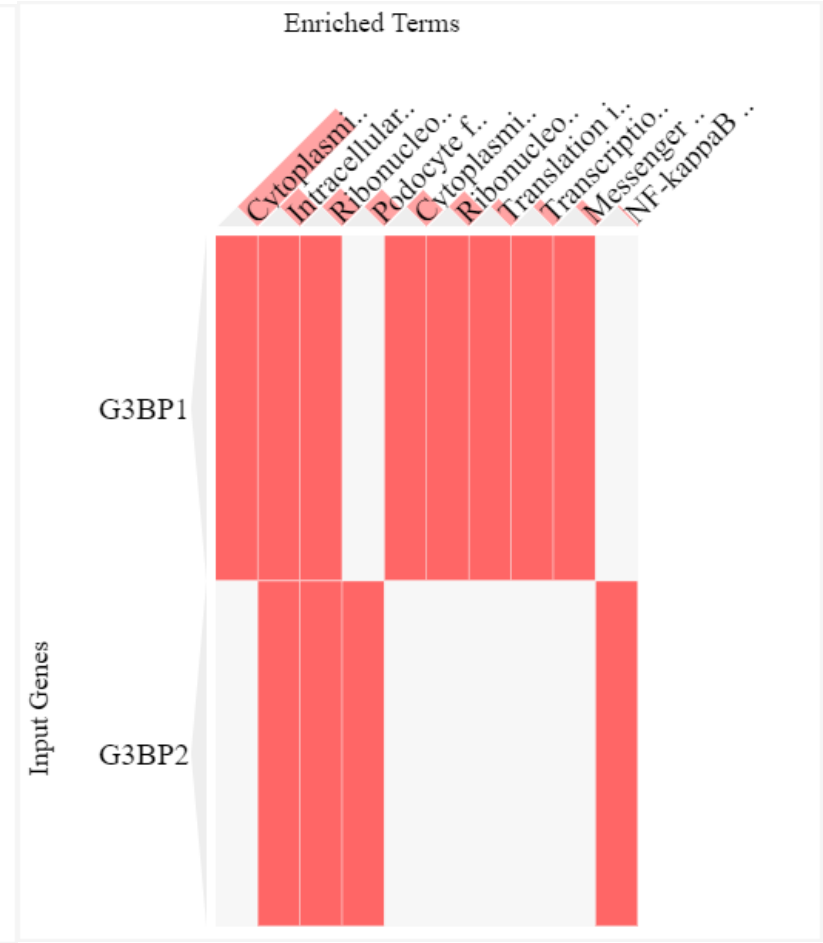
**(A)**

**(B)**

**Supplementary Figure 1.** RNA-Seq expression data of (A) G3BP1, and (B) G3BP2 genes from GTEx web portal.

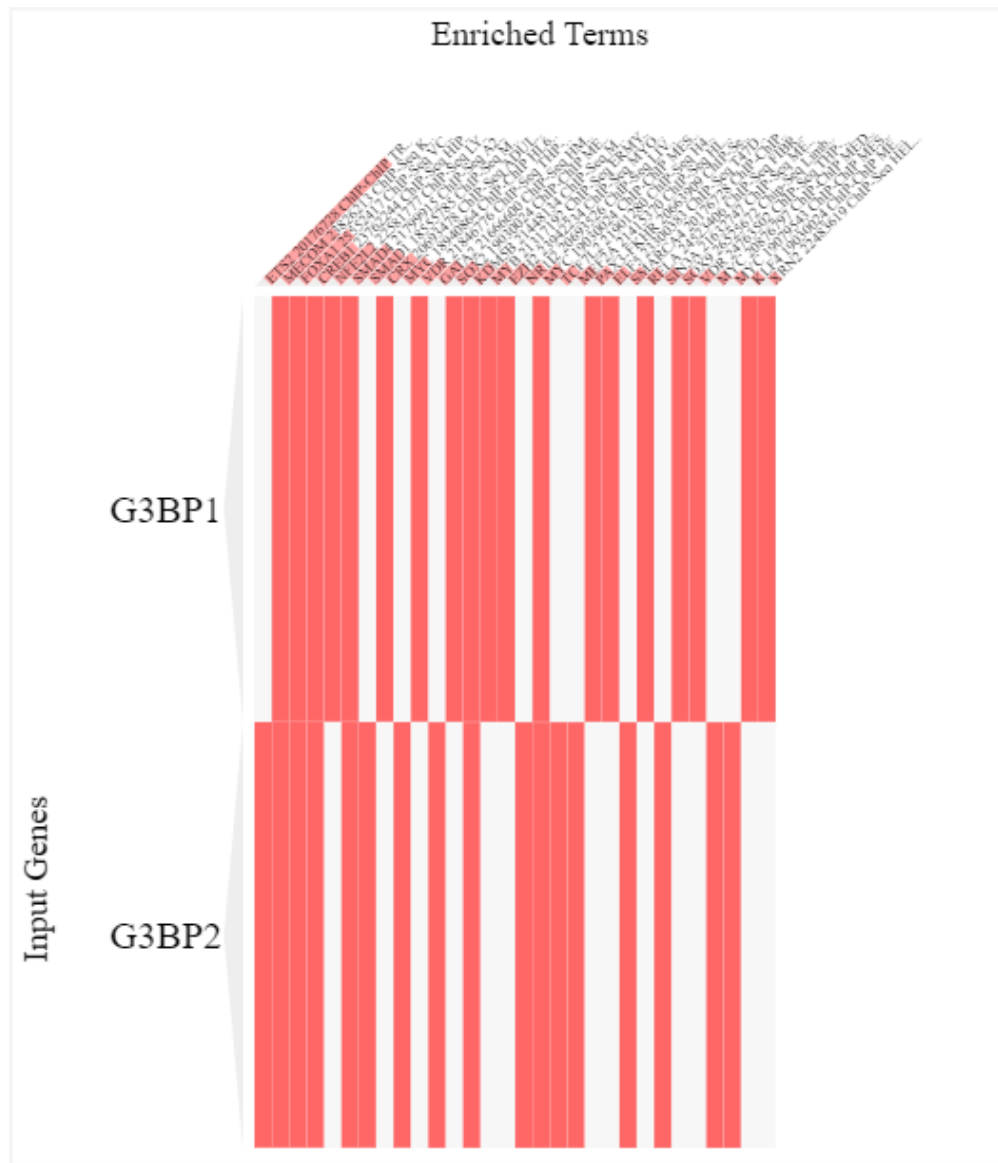


**Supplementary Figure 2.** Human disease perturbation through downregulation of G3BP1 and G3BP2 from Enrichr web server

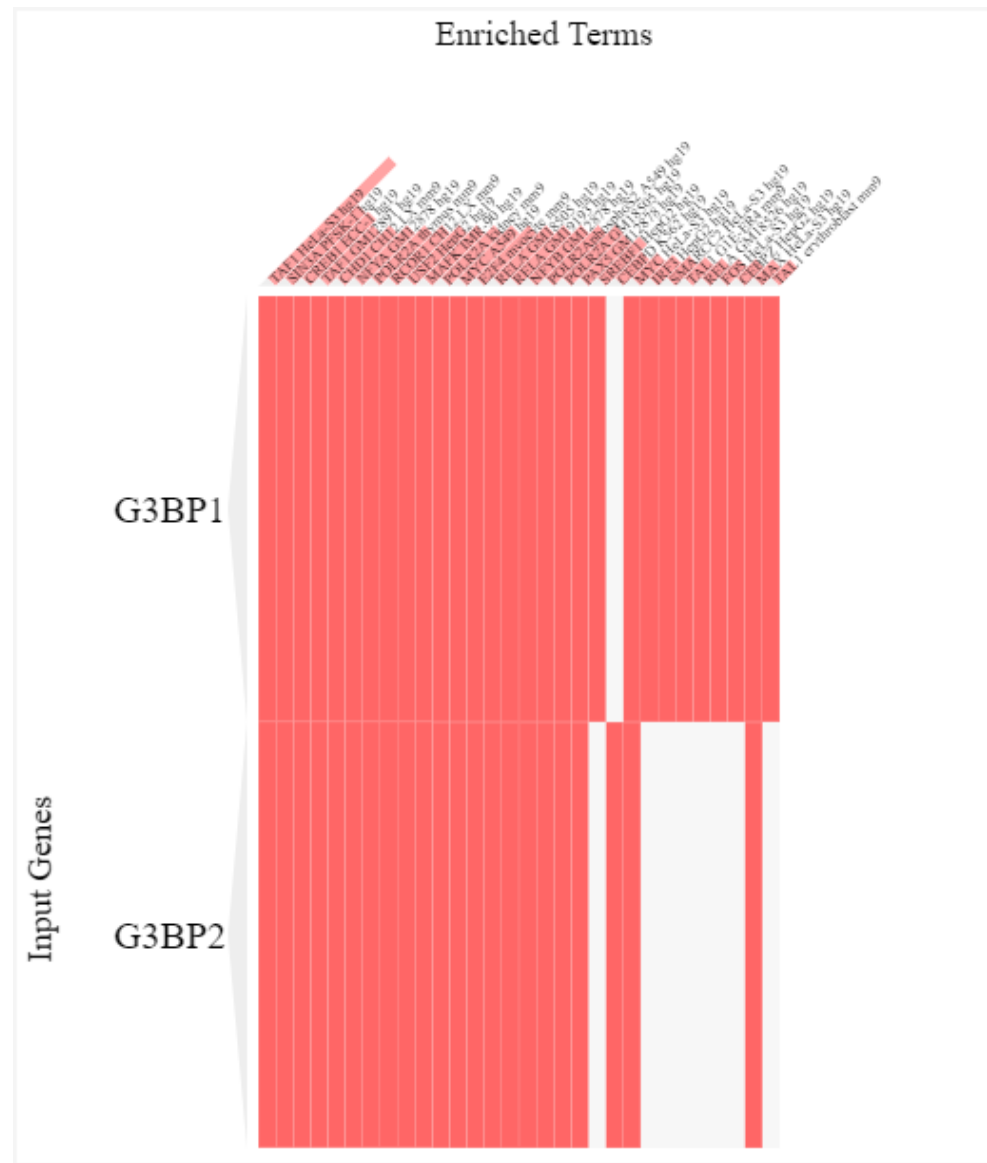
**(A)****(B)****(C)**

**Supplementary Figure 3.** Gene Ontology (GO) analysis of G3BP1 and G3BP2 genes. (A) Biological process, (B) Molecular process, and (C) Jensen compartments

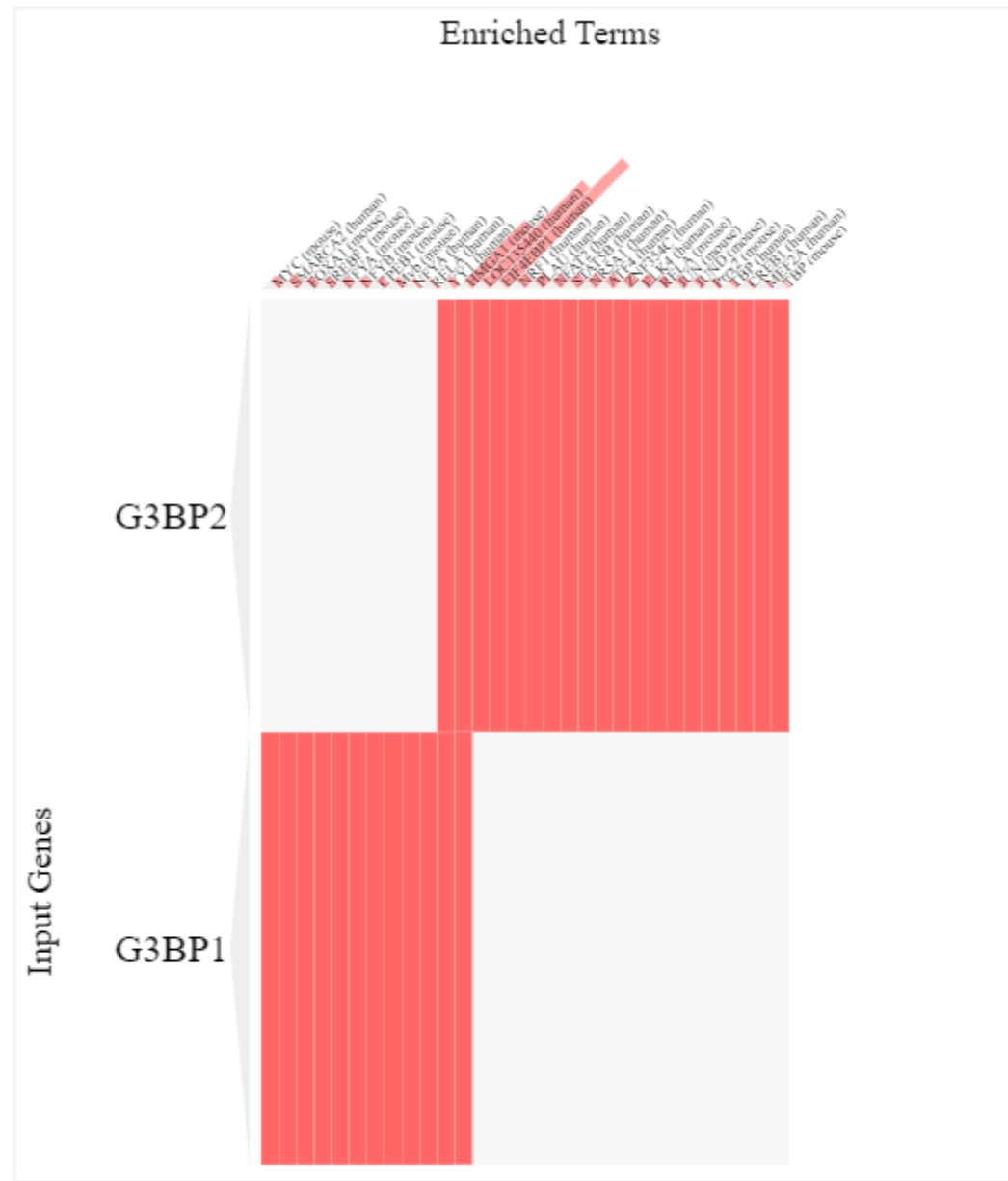
### ChEA 2016



### ENCODE TF CHIP-Seq 2015

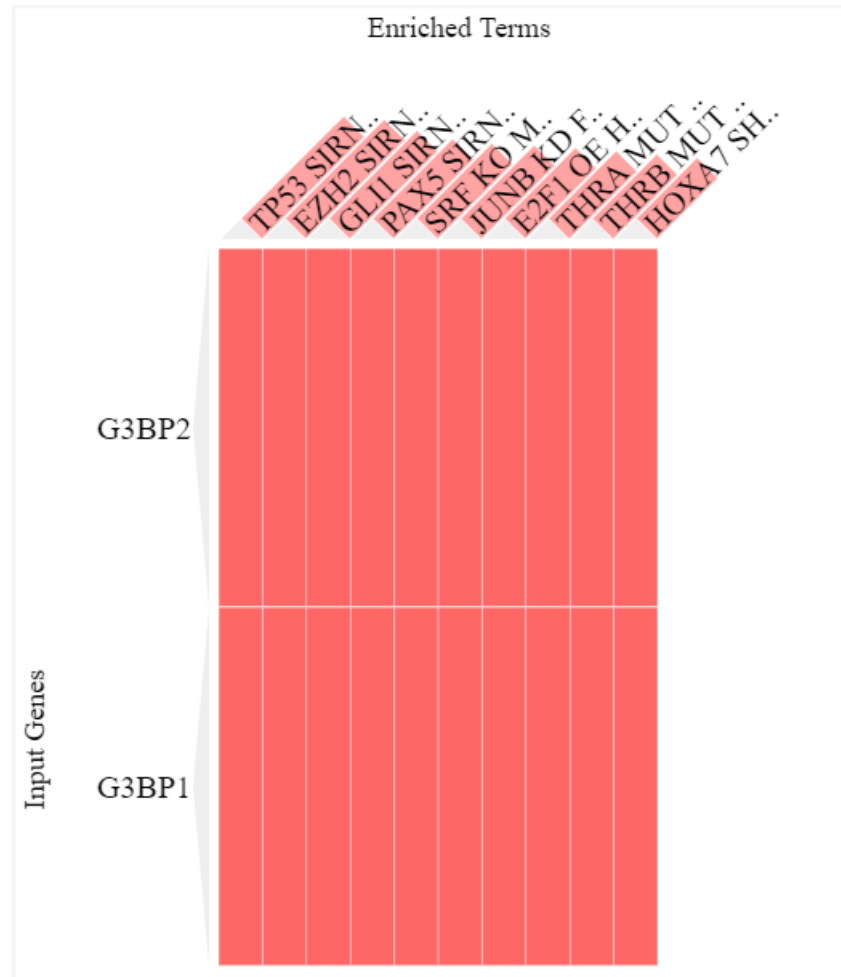


**Supplementary Figure 4.** Possible mechanisms affecting gene expression of G3BP1 and G3BP2 genes. Identifications of the enriched records of transcription factor-binding sites.

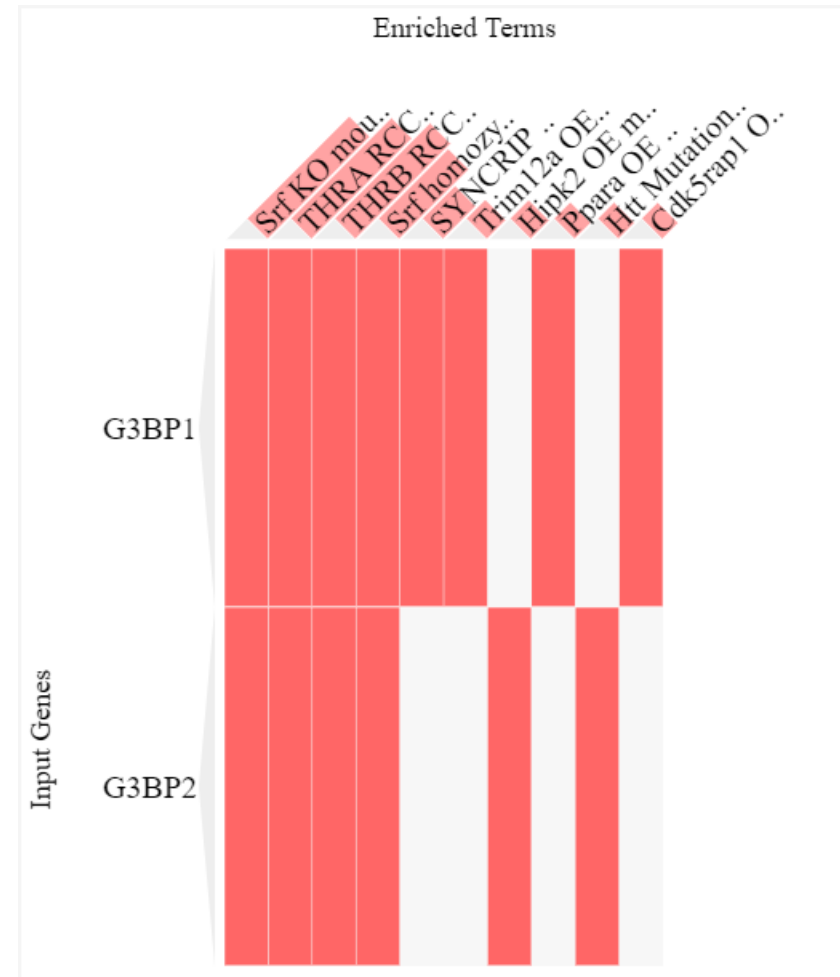


**Supplementary Figure 5.** Binding motifs were detected at the gene promoter of G3BP1 and G3BP2 using Enrichr tool through scanning the TRANSFAC and JASPAR databases.

## TF perturbations followed by expression

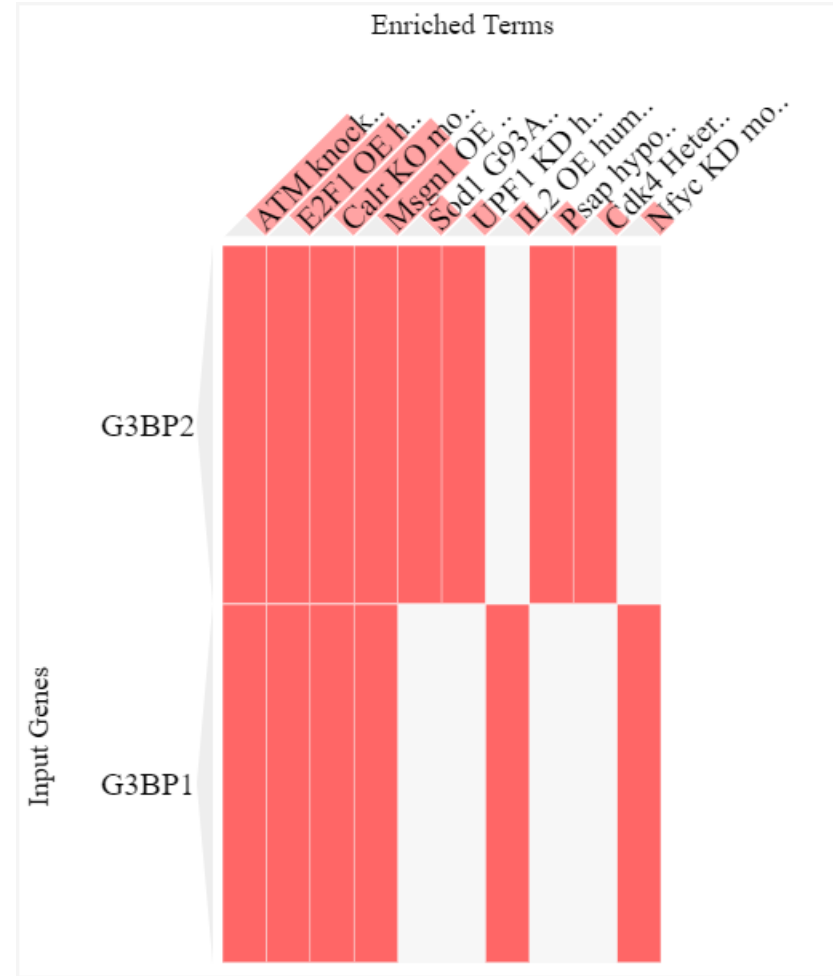
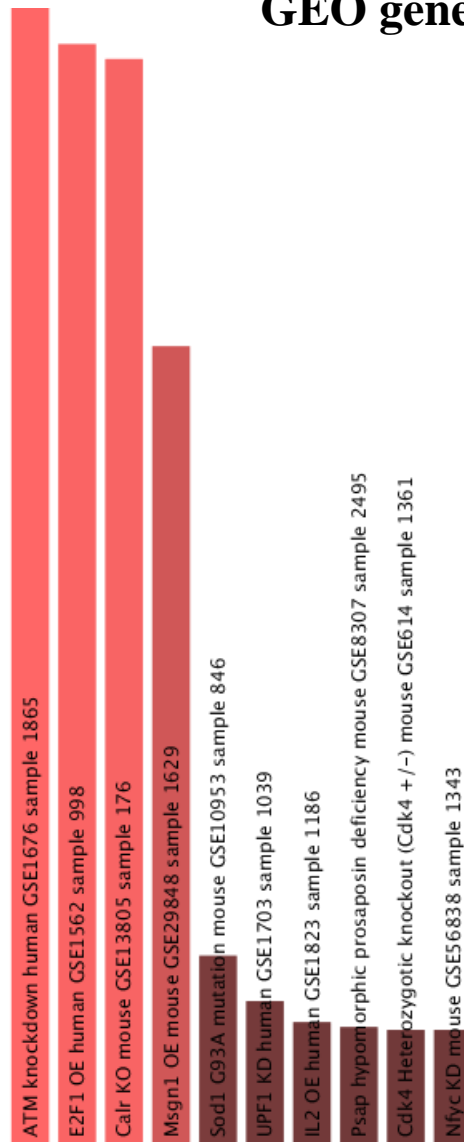


## GEO gene perturbations focused on upregulated genes



**Supplementary Figure 6.** Possible mechanisms affecting gene expression of G3BP1/2 genes. Mostly different transcription factors affect expression of the target genes. *SRF* and *THRA/B* gene product as potential repressor of the G3BP1/2 gene expression.

## GEO gene perturbations database focused on down-regulated genes

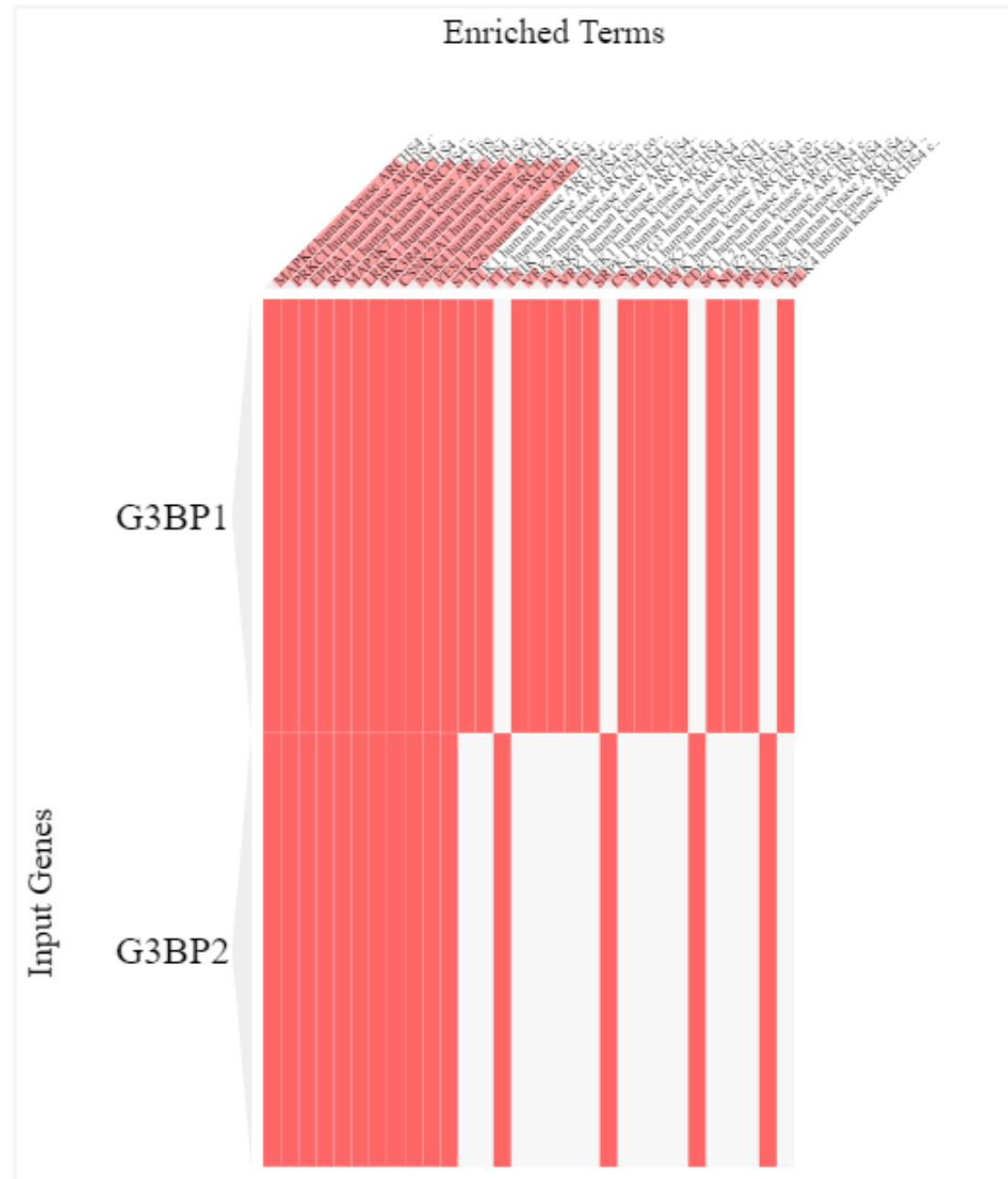


**Supplementary Figure 7.** Possible mechanisms affecting gene expression of G3BP1/2 genes. Mostly different transcription factors affect expression of the target genes. *ATM* and *E2F-1* gene product as potential activator and repressor, respectively of G3BP1/2 gene expression.



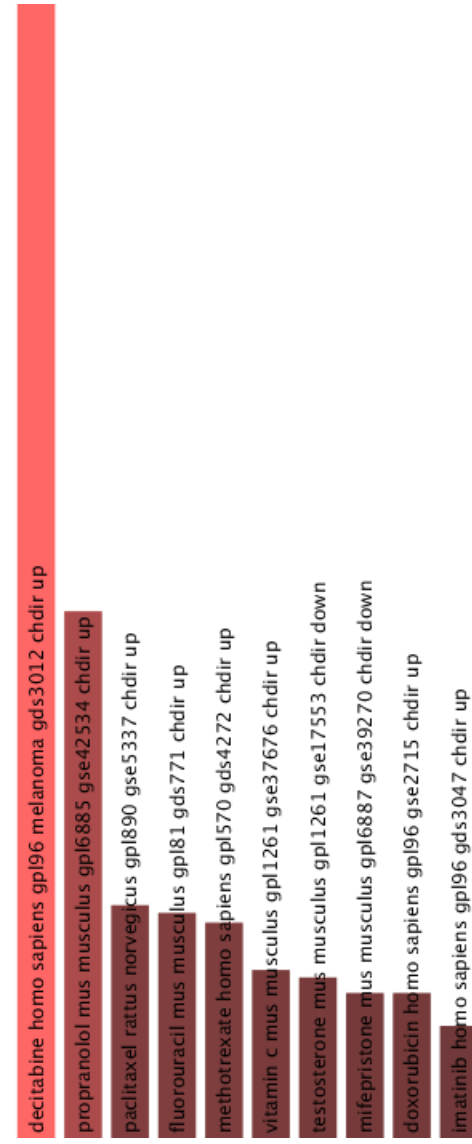
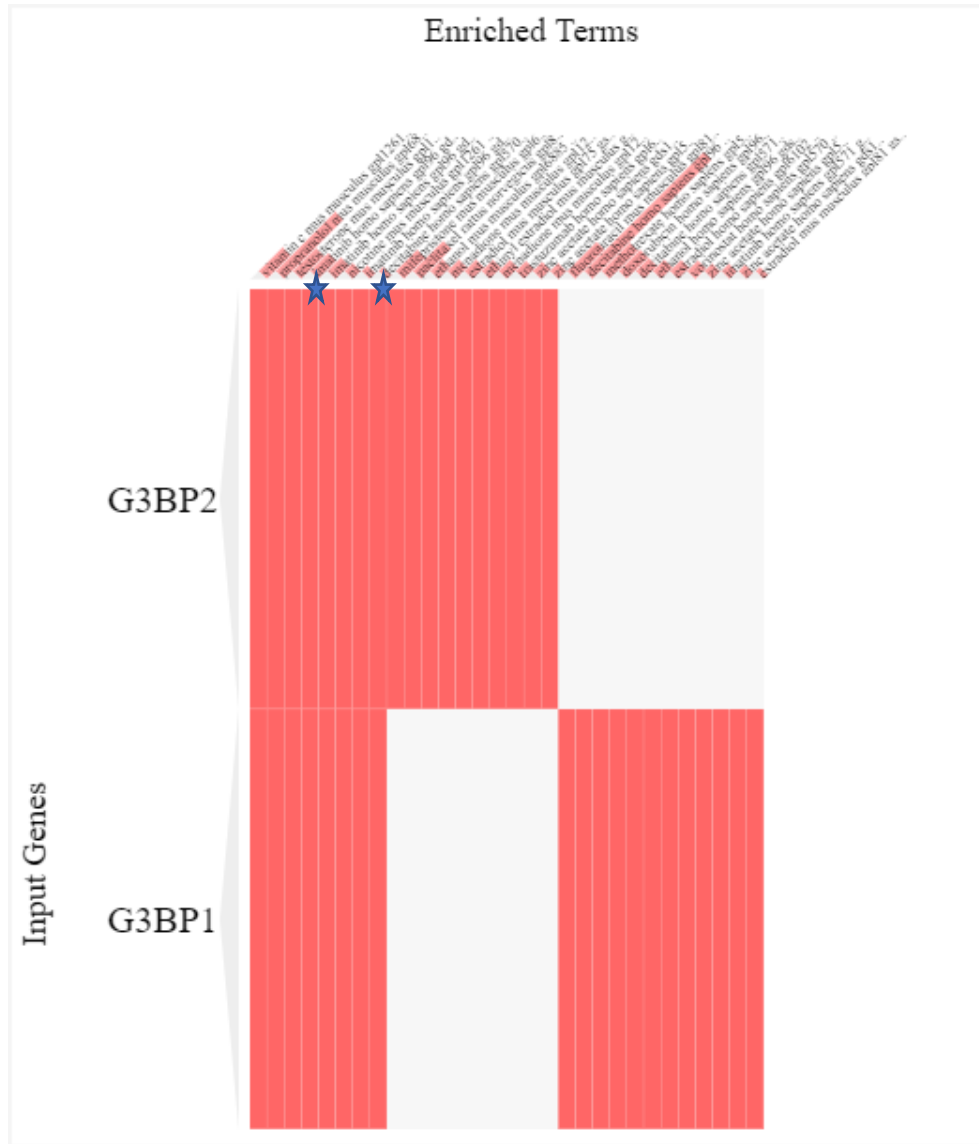
**Supplementary Figure 8.** Possible mechanisms affecting activity of G3BP1/2 genes. The kinases found to be co-expressed with the target genes.

# ARCHS4 Kinases co-expression

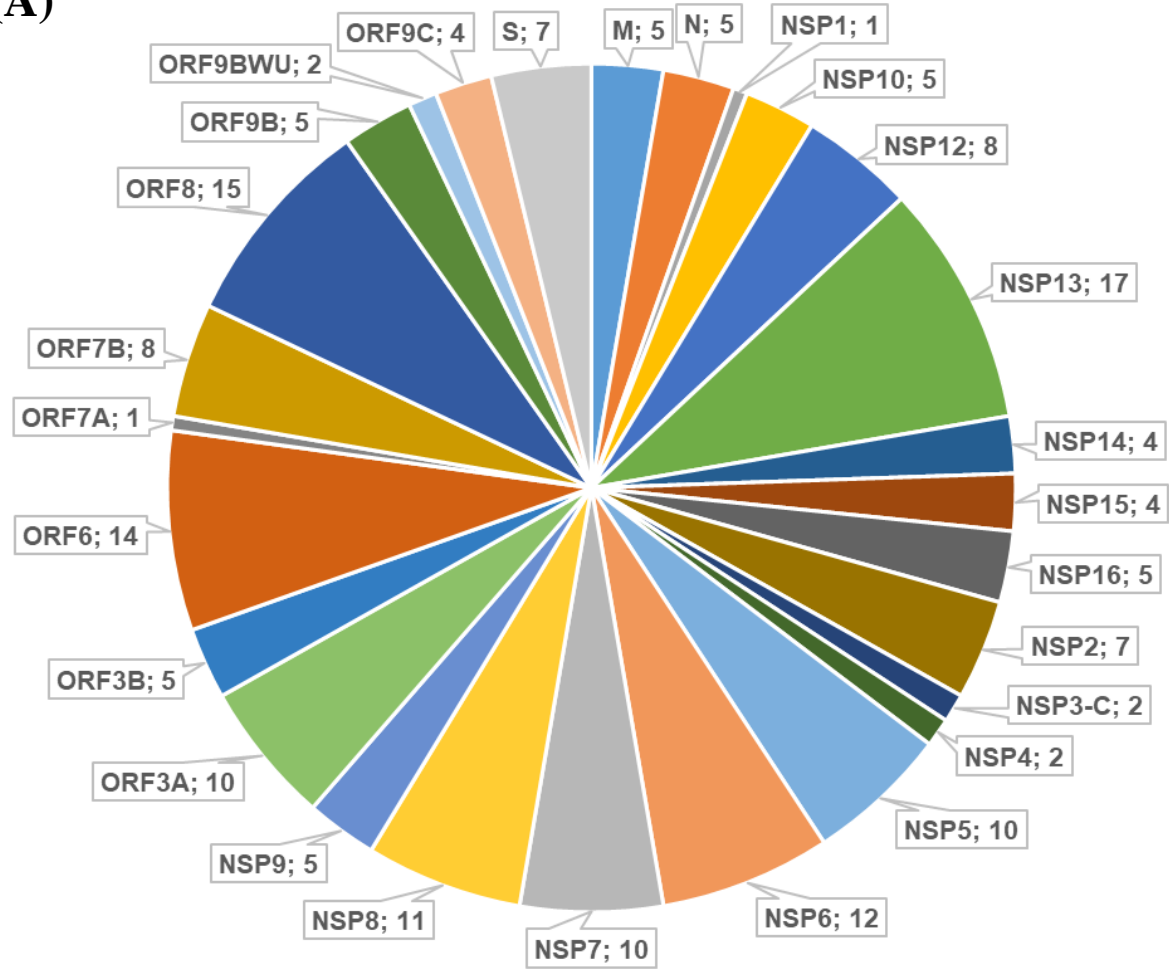
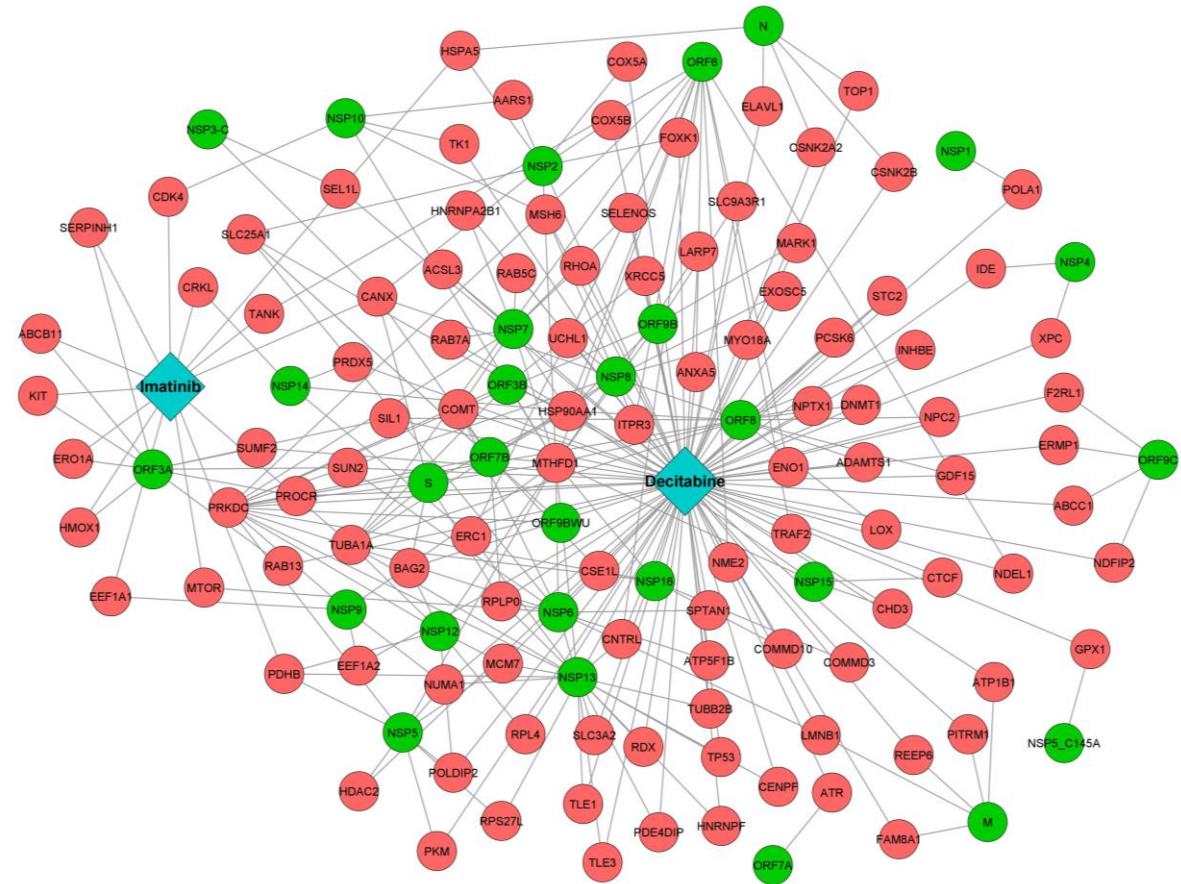




# Drug Perturbations from GEO\_2014

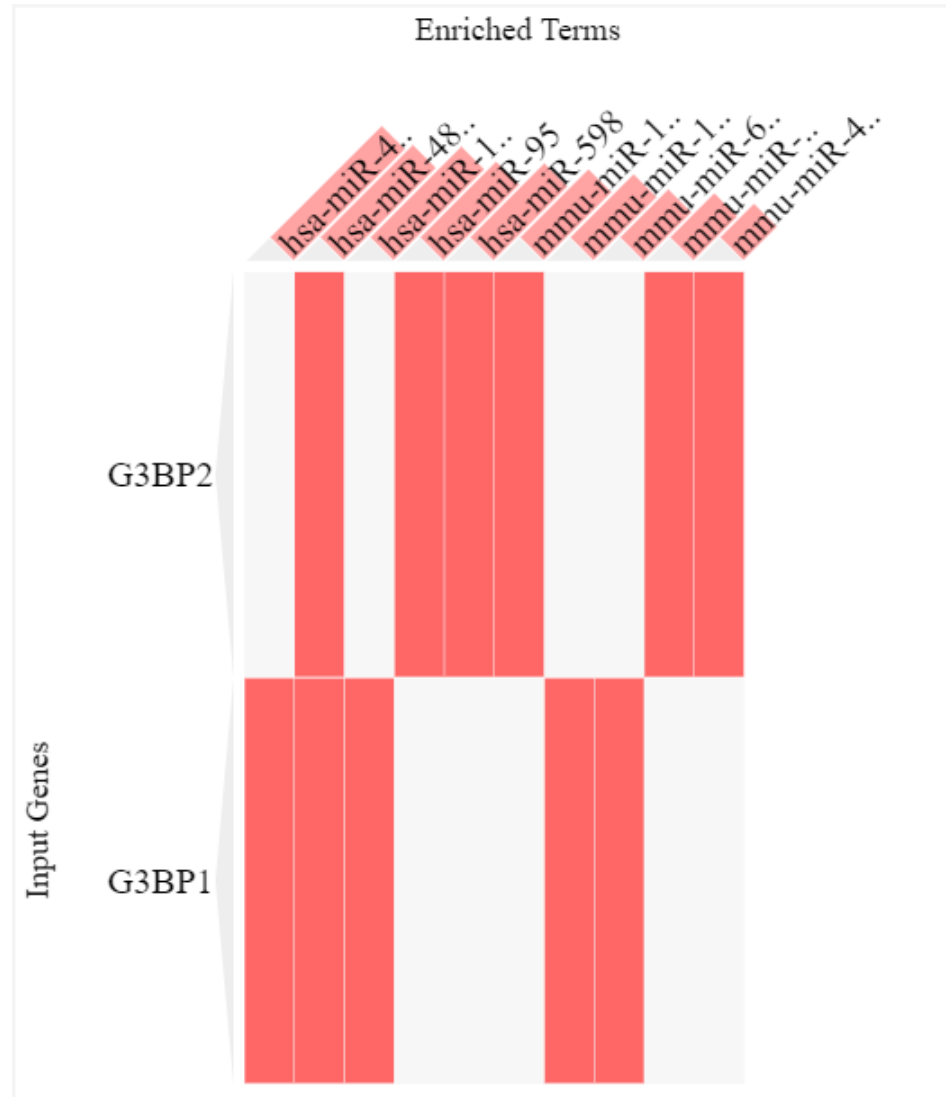


**Supplementary Figure 9.** GSEA identify Imatinib and Decitabine as potential drug candidate against SARS-CoV-2 infection.

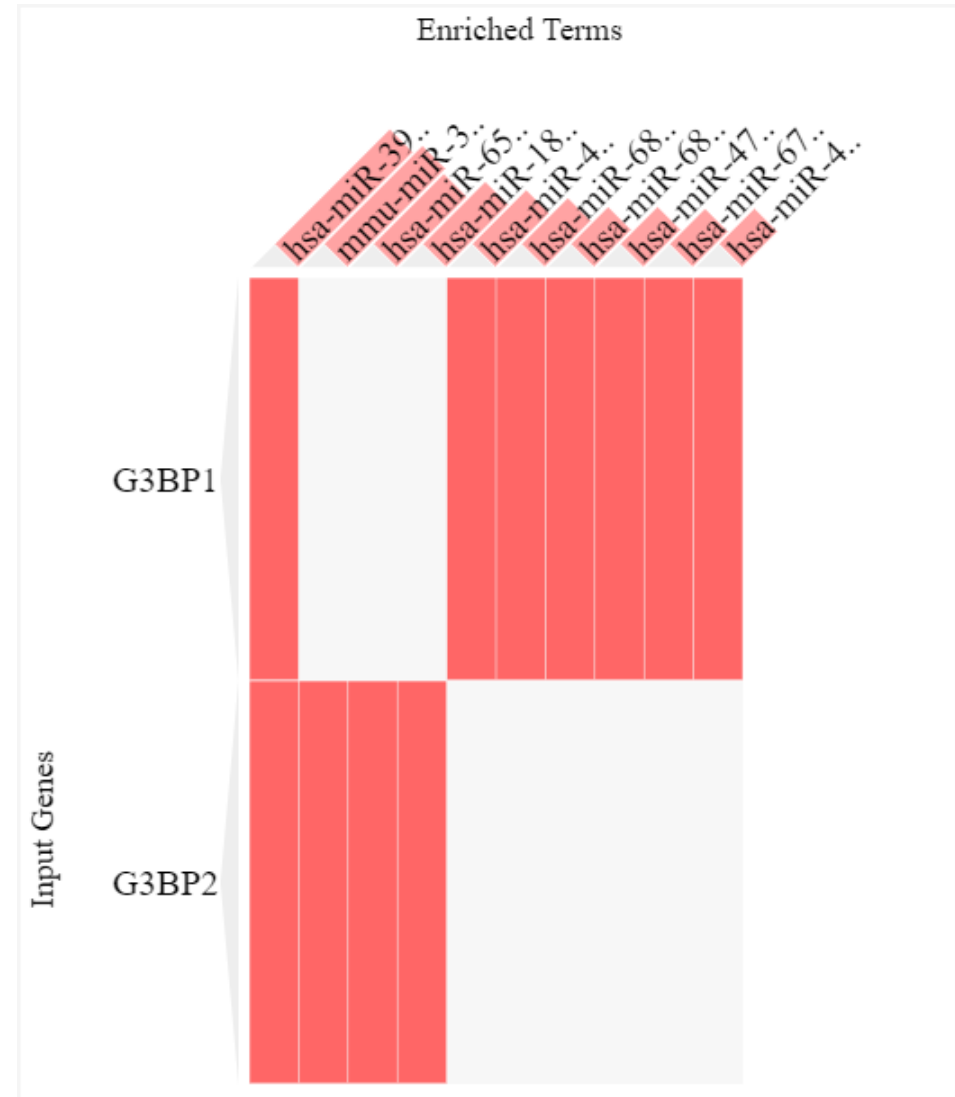
**(A)****(B)**

**Supplementary Figure 10.** Effect of bipartite combinations of imatinib and decitabine on the gene-drug network of SARS-CoV-2-human interactome. (A) Out of 809 SARS-CoV-2 human target proteins, the drug combination interacts with 106 (i.e ~13%) proteins, making 184 interactions in total, and potentially interfering all 27 SARS-CoV-2 protein. (B) Interaction network of the 106 human genes (pink) with 27 SARS-CoV-2 proteins (green).

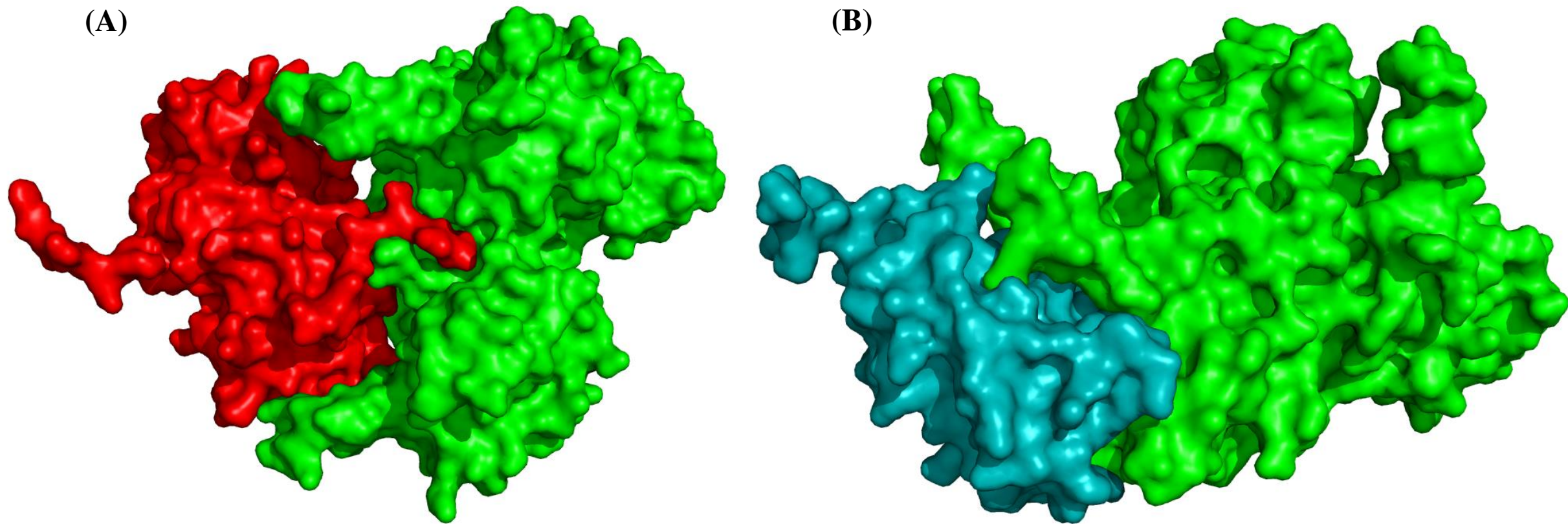
## TargetScan microRNA 2017



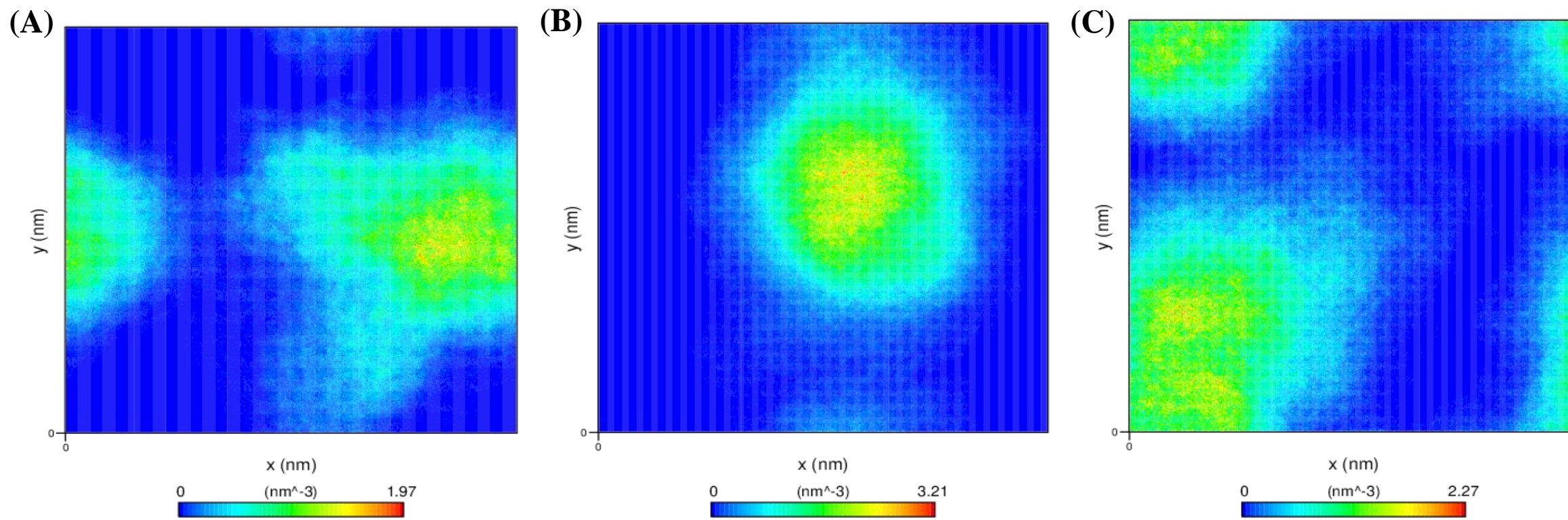
## miRTarBase 2017



**Supplementary Figure 11.** miRNAs as potential modulators of G3BP1/2 expression.



**Supplementary Figure 12.** Protein-protein docking from HDOCK server. The docking of (A) SARS-CoV-2 N (PDB ID:6M3M, green) to G3BP1 (PDB ID: 4FCJ, red) and (B) SARS-CoV-2 N (PDB ID:6M3M, green) to G3BP2 (PDB ID: 5DRV, teal). The binding pockets are similar in both the docking.



**Supplementary Figure 13.** Density distribution plot for (A) unbound G3BP1, (B) G3BP1- decitabine, and (C) G3BP1- imatinib complexes.