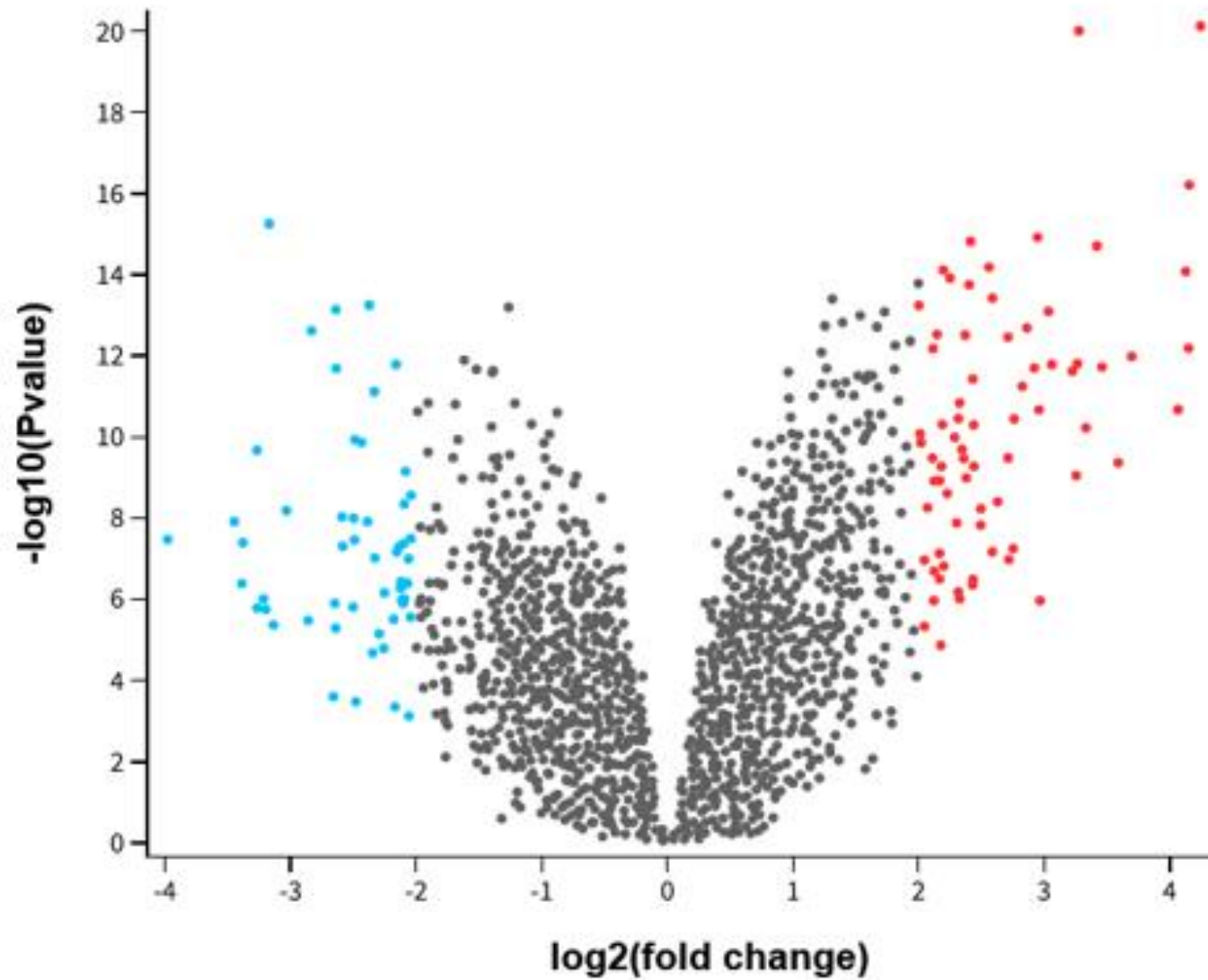
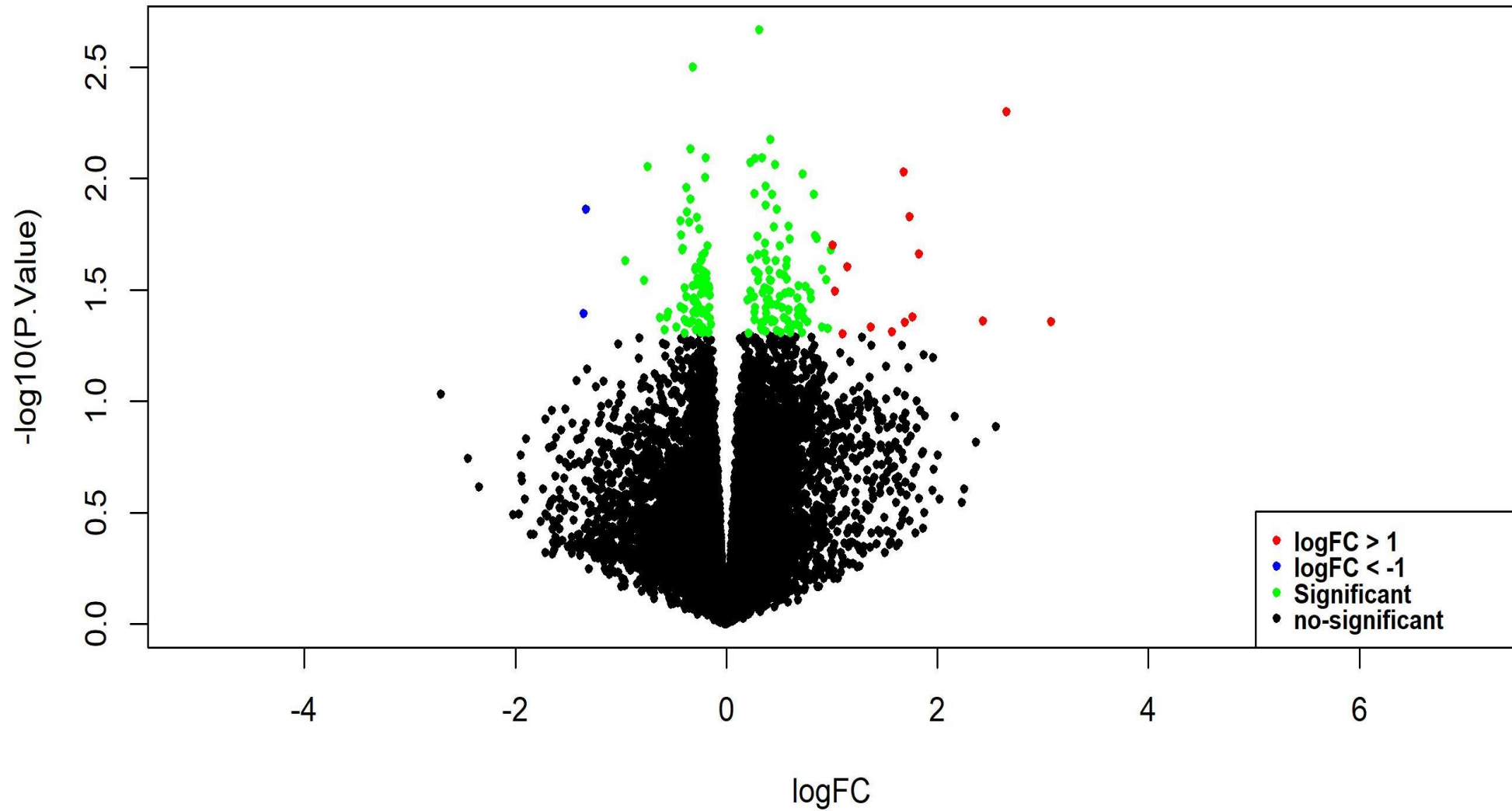


Supplementary

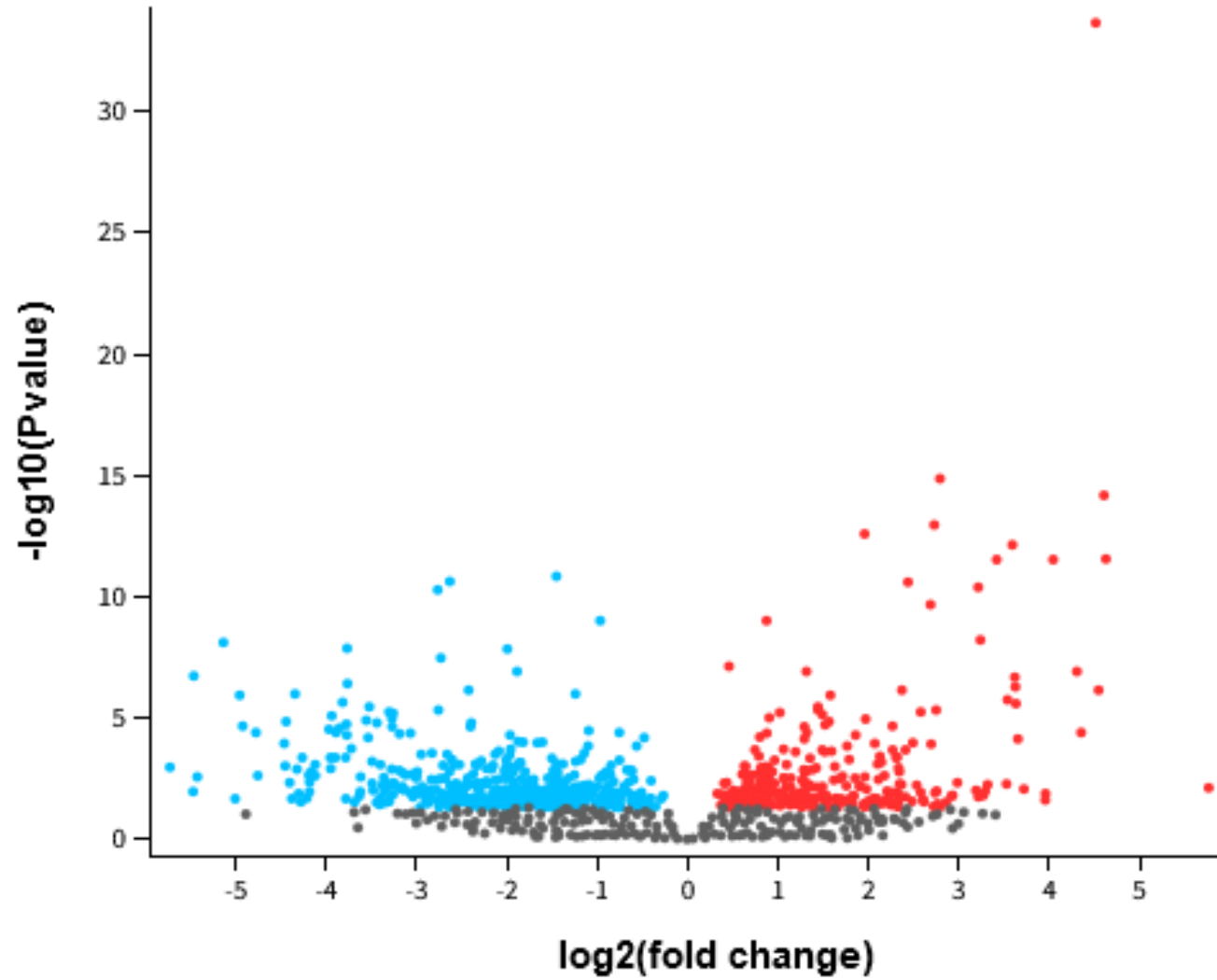
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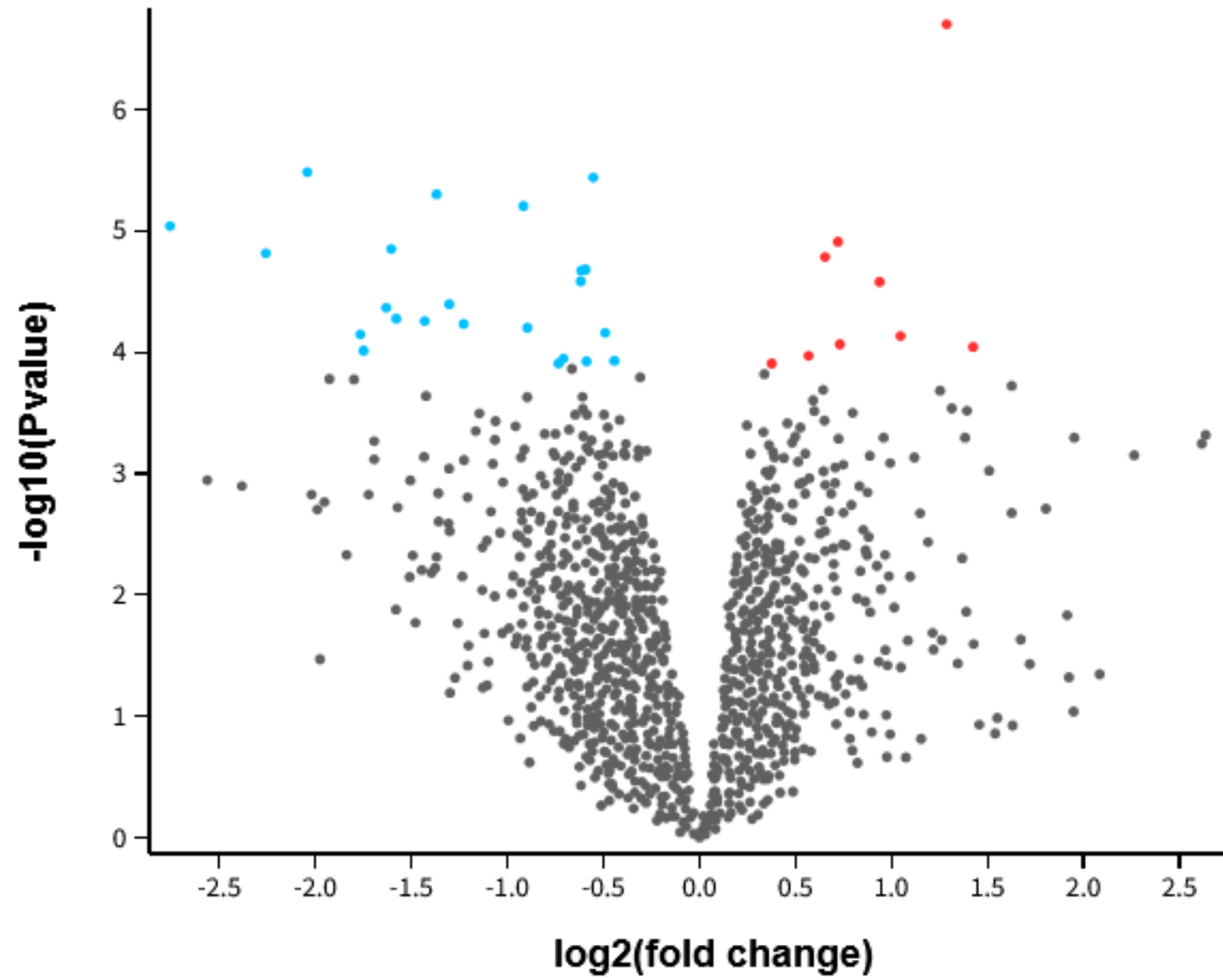
**Figure 1 .A .** The visualization of dysregulated,  $P_{adj} < 0.05$  .( Normal & Aniridia )



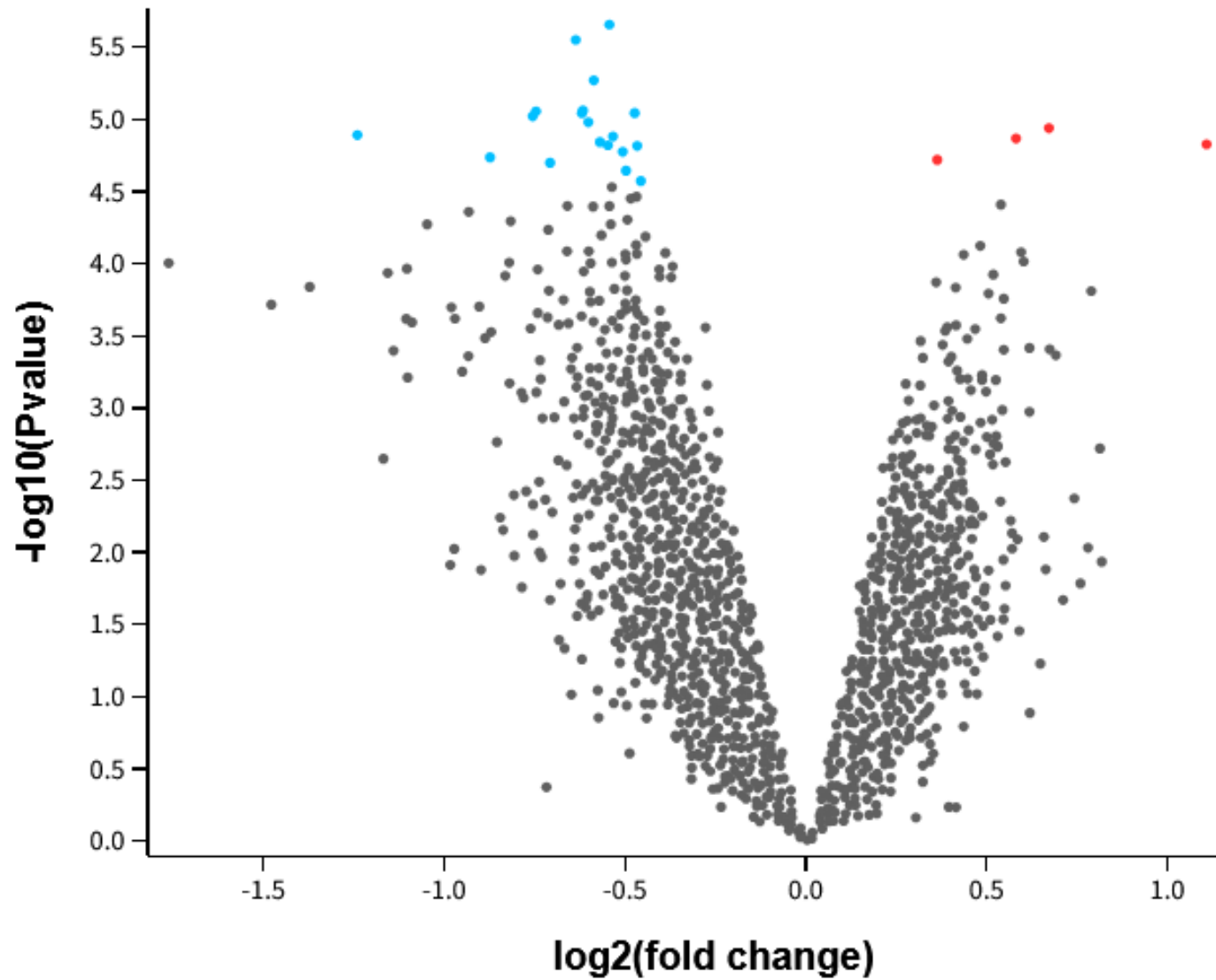
**Figure 1 .B** . The visualization of dysregulated,  $\text{P}_{\text{adj}} < 0.05$  . ( Normal & Choroideremia )



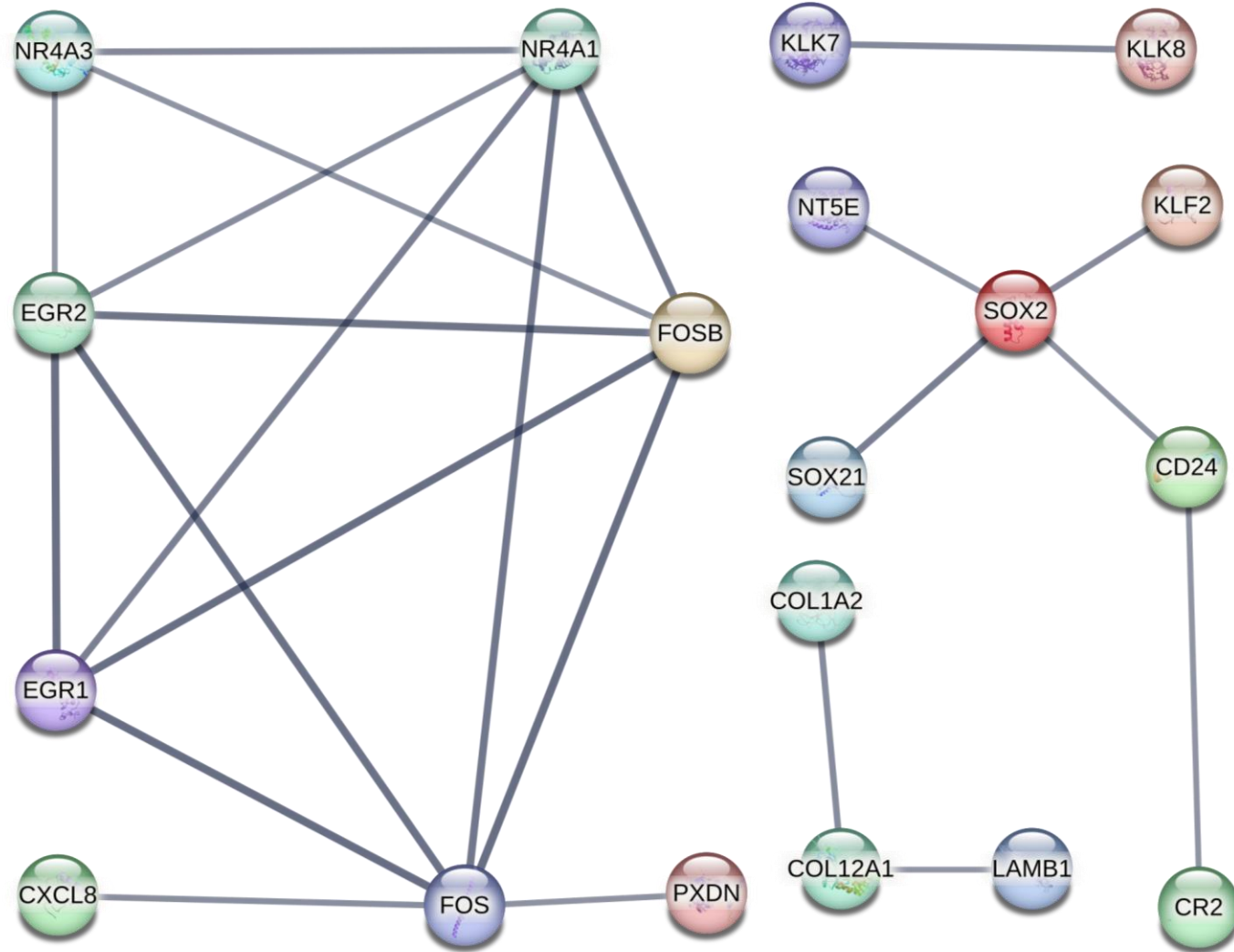
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**Figure 1 .D** . The visualization of dysregulated,  $\text{P}_{\text{adj}} < 0.05$  .( Normal & Glaucoma)

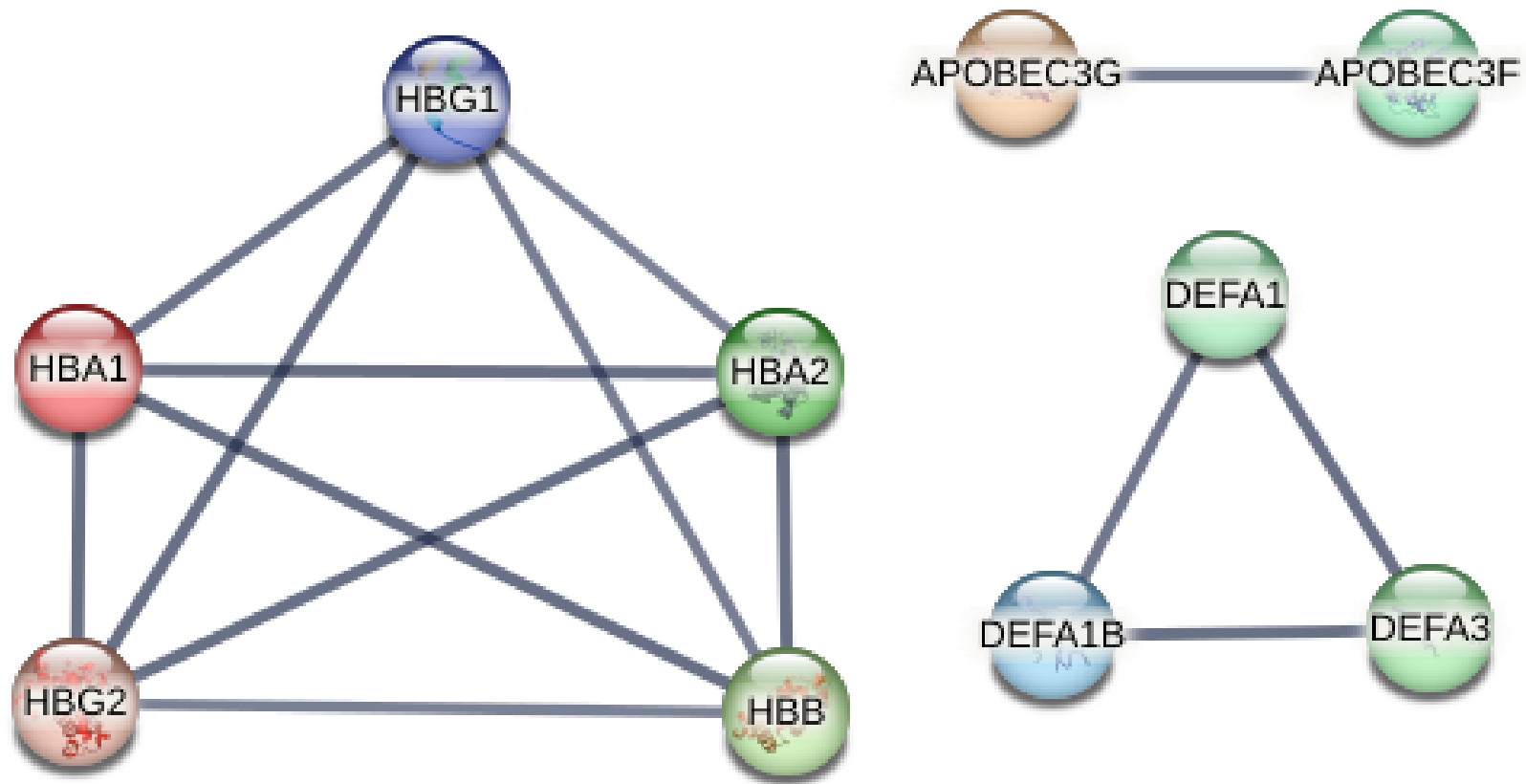


**Figure 1 .E .** The visualization of dysregulated,  $P_{adj} < 0.05$  .( Normal & AMD )



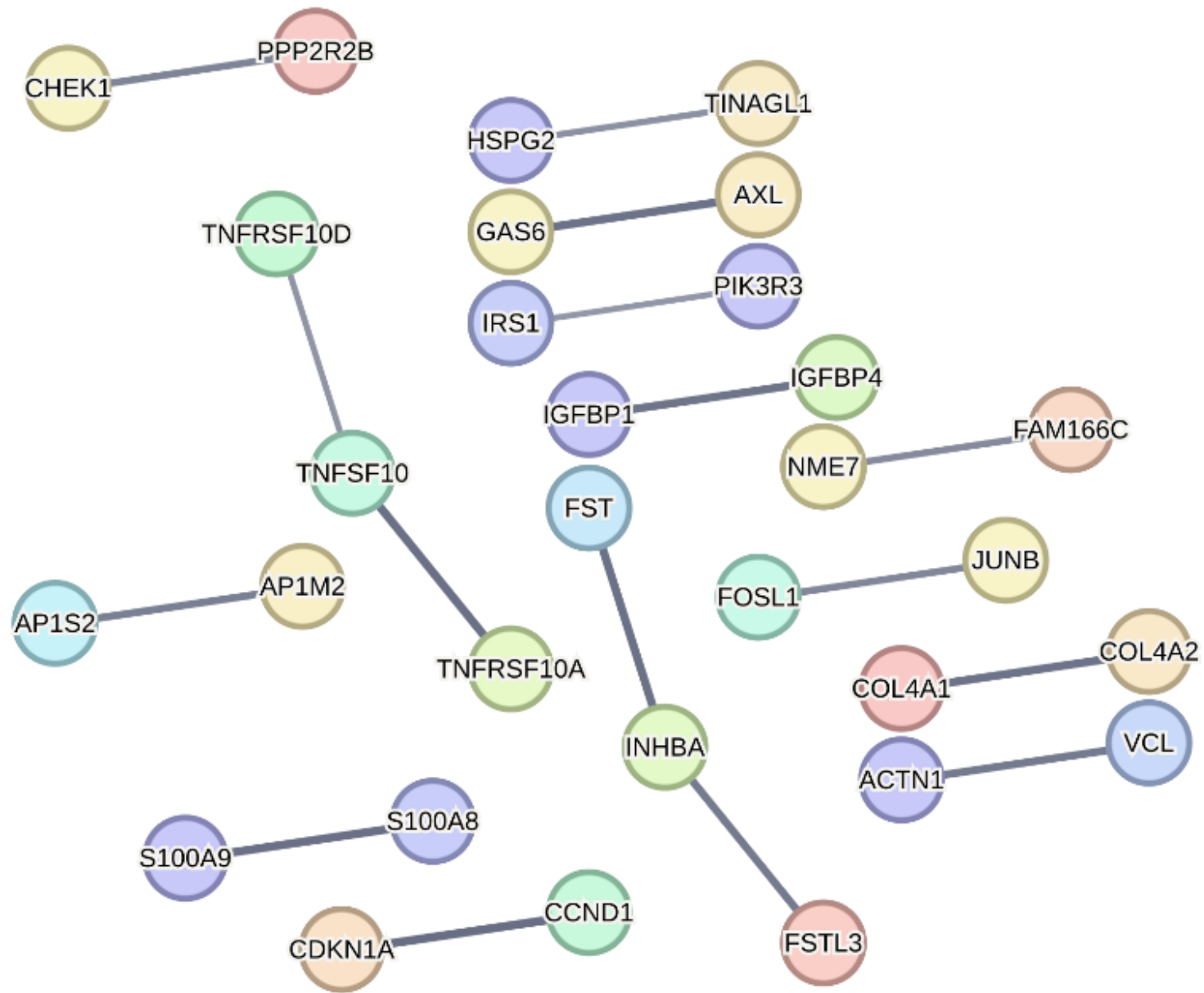
**Figure 2 .A .**

*Protein-Protein Interaction Networks of dysregulated genes for Aniridia.*



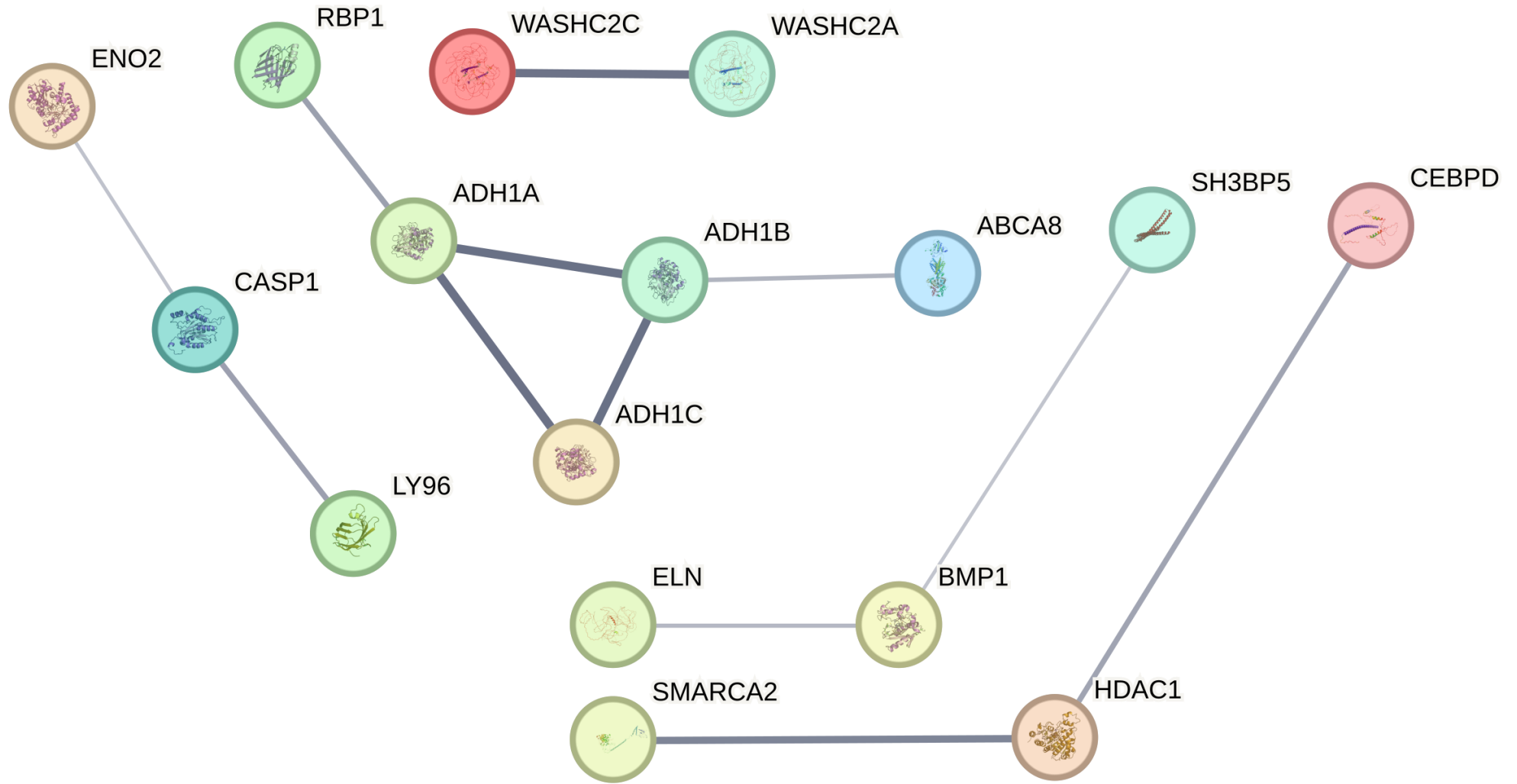
**Figure 2 .B .**

*Protein-Protein Interaction Networks of dysregulated genes for Choroideremia.*

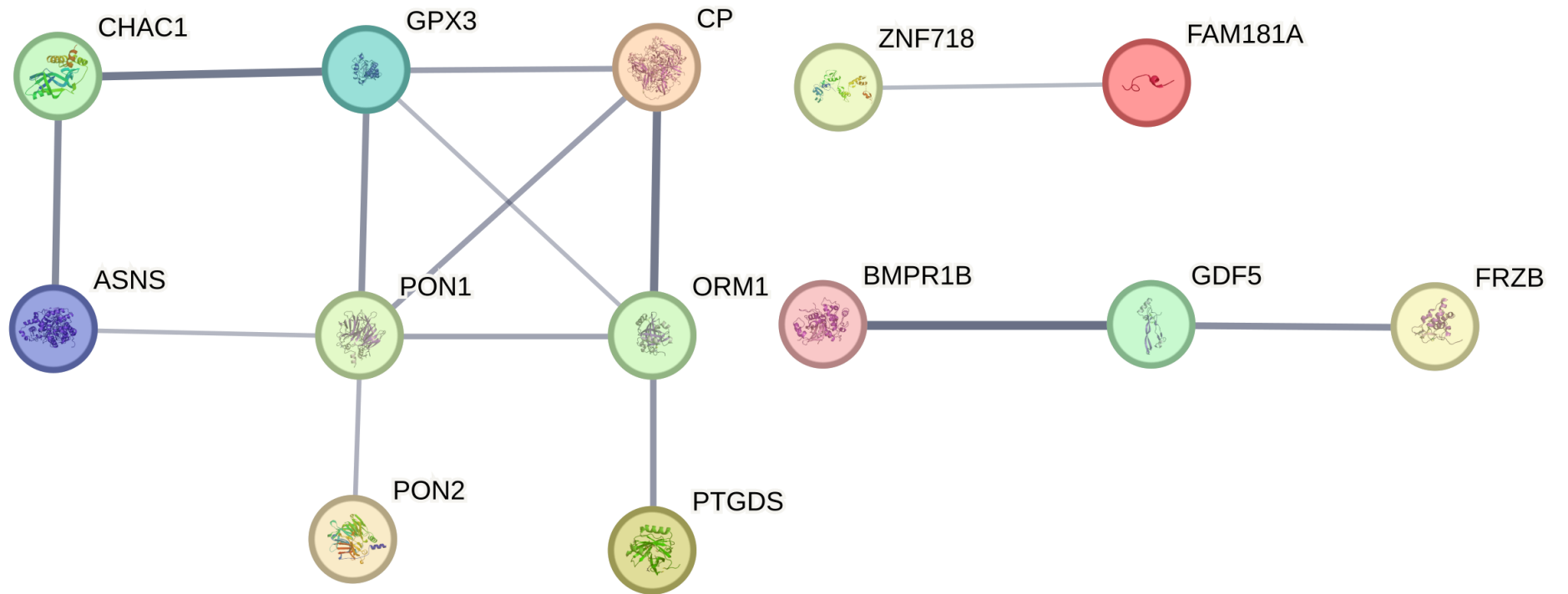


**Figure 2 .C .**

*Protein-Protein Interaction Networks of dysregulated genes for corneal dystrophy.*

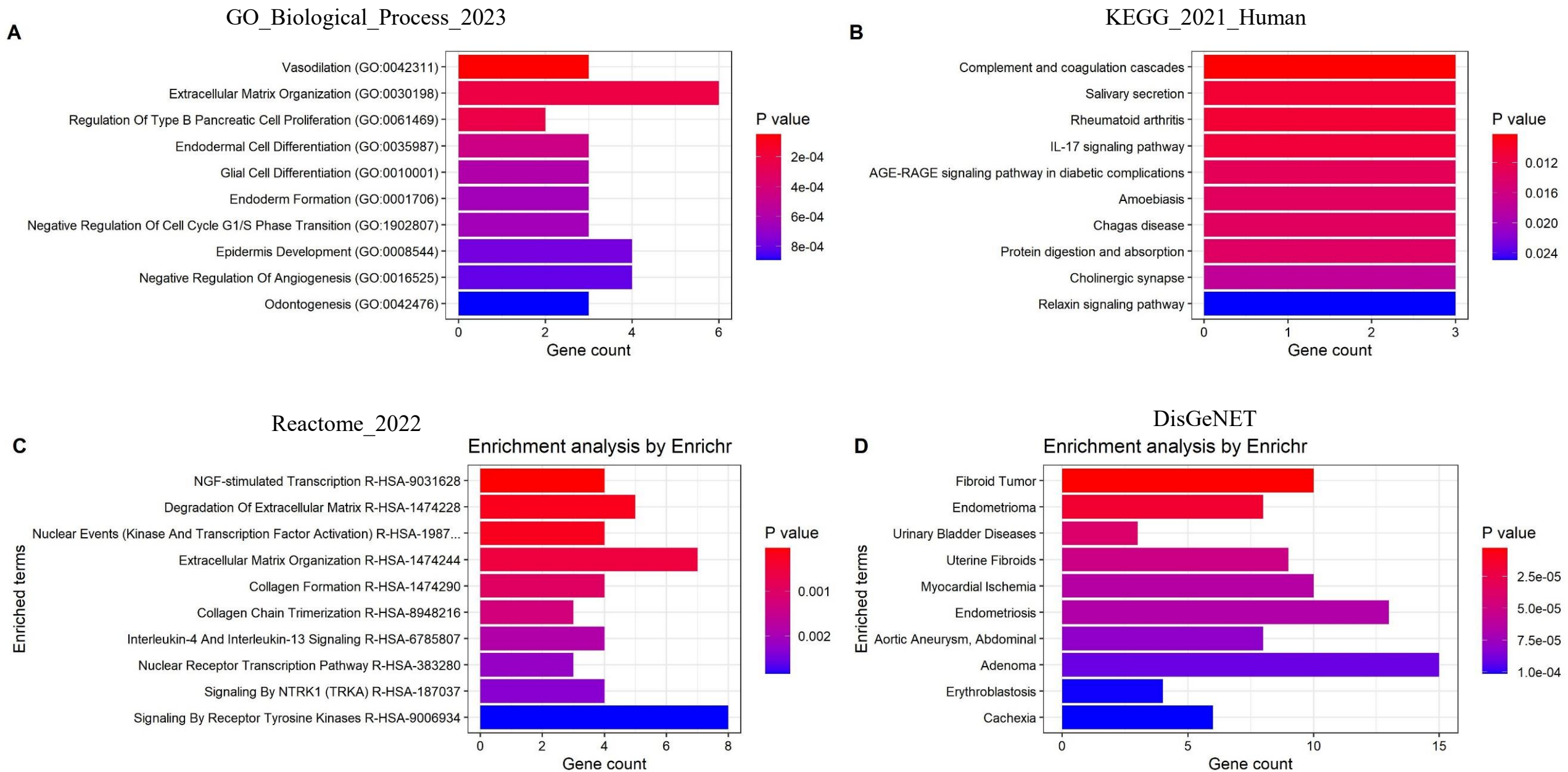


**Figure 2 .D .**  
*Protein-Protein Interaction Networks of dysregulated genes for Glaucoma .*

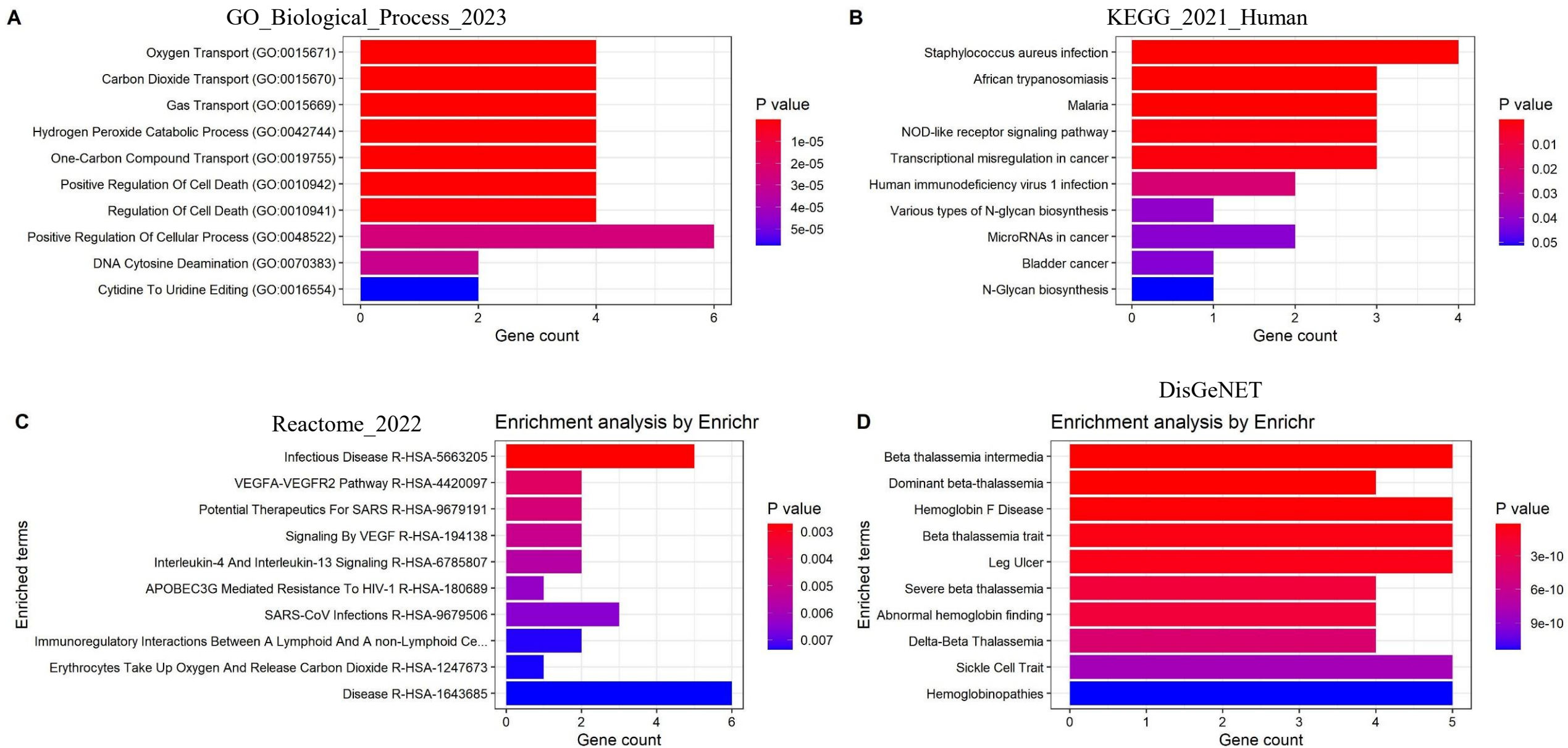


**Figure 2 .E .**

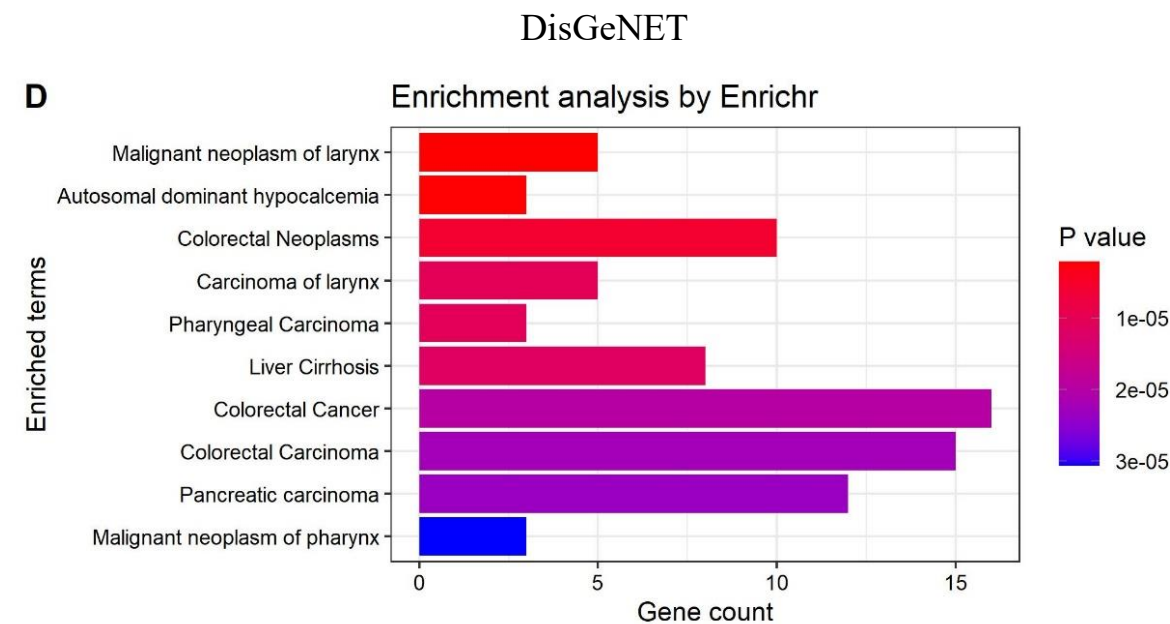
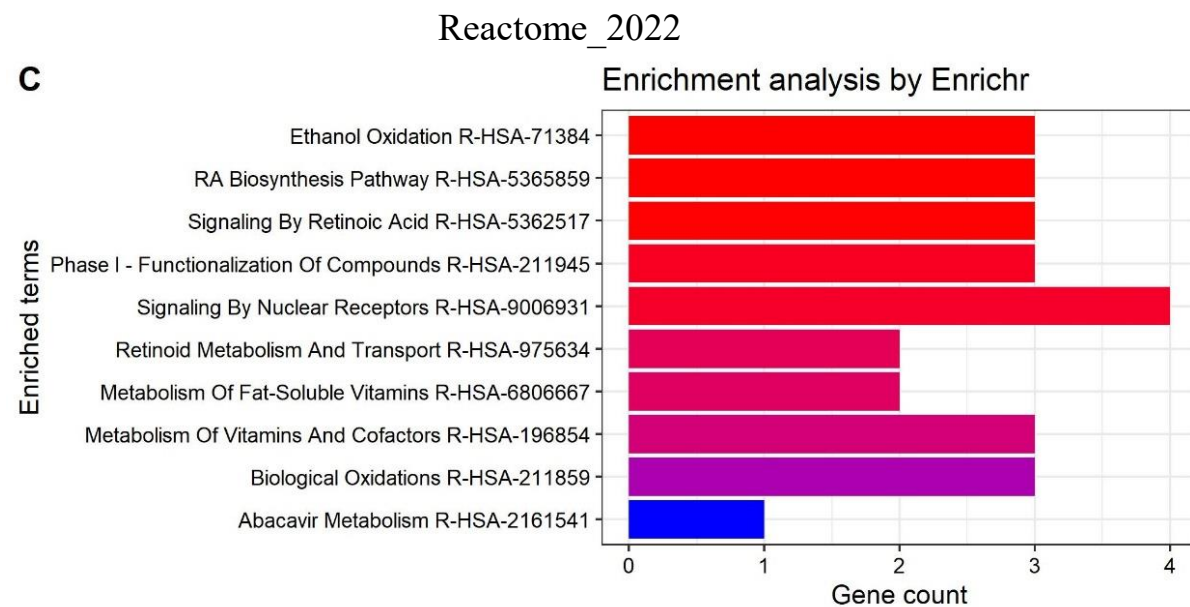
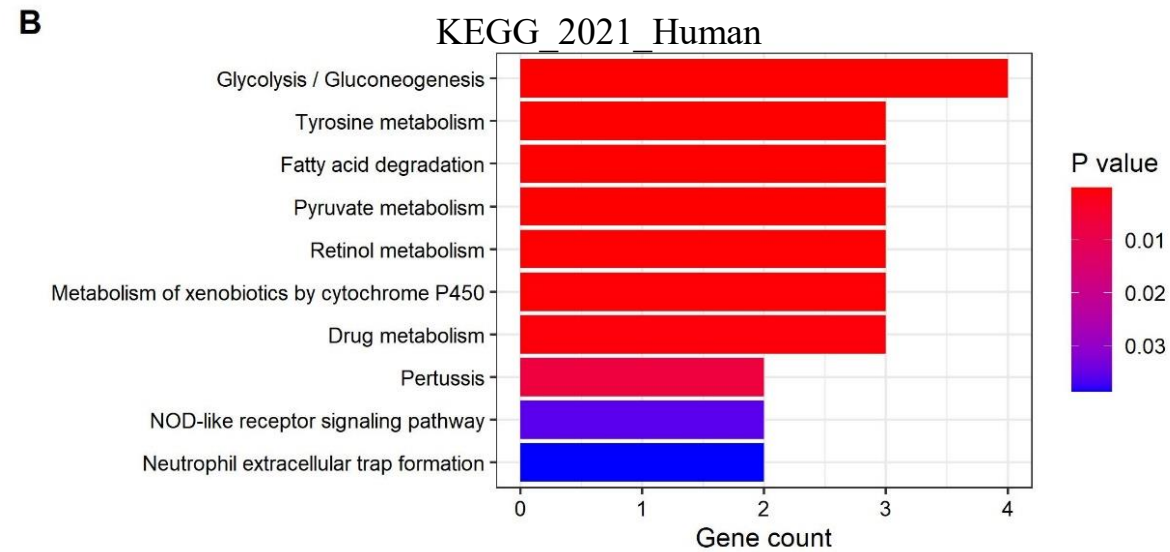
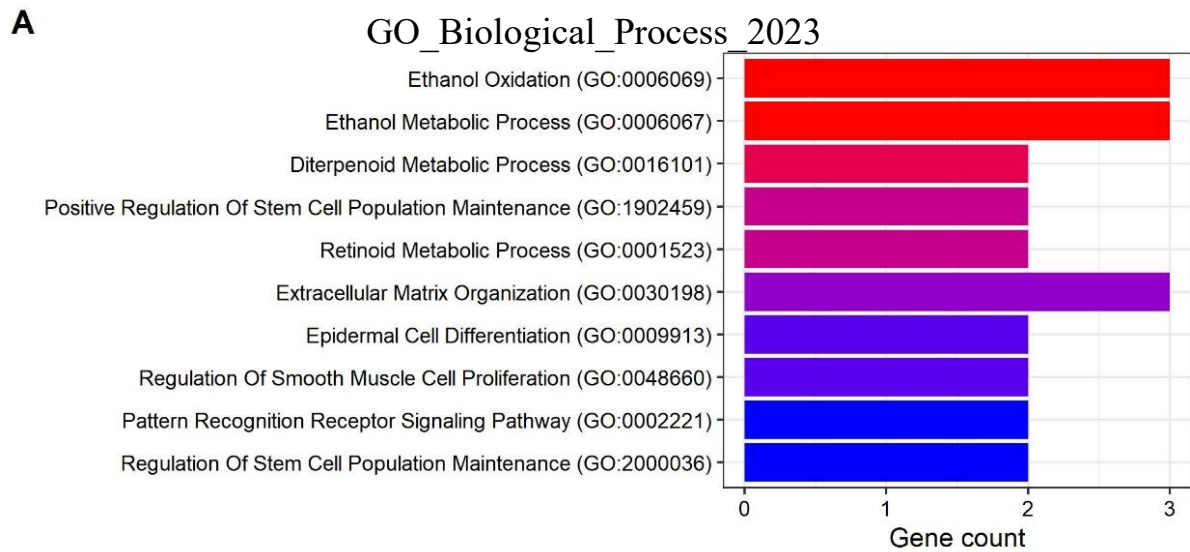
*Protein-Protein Interaction Networks of dysregulated genes for AMD.*



**Figure 3:** GO\_KEGG Biological Process (A , B) , Reactom Pathway and DisGeNET (C,D) of 125 common genes (FDR < 0.1) Aniridia .Size and color of points represent  $-\text{Log}_2$  of FDR and the number of genes associated with each term, respectively.



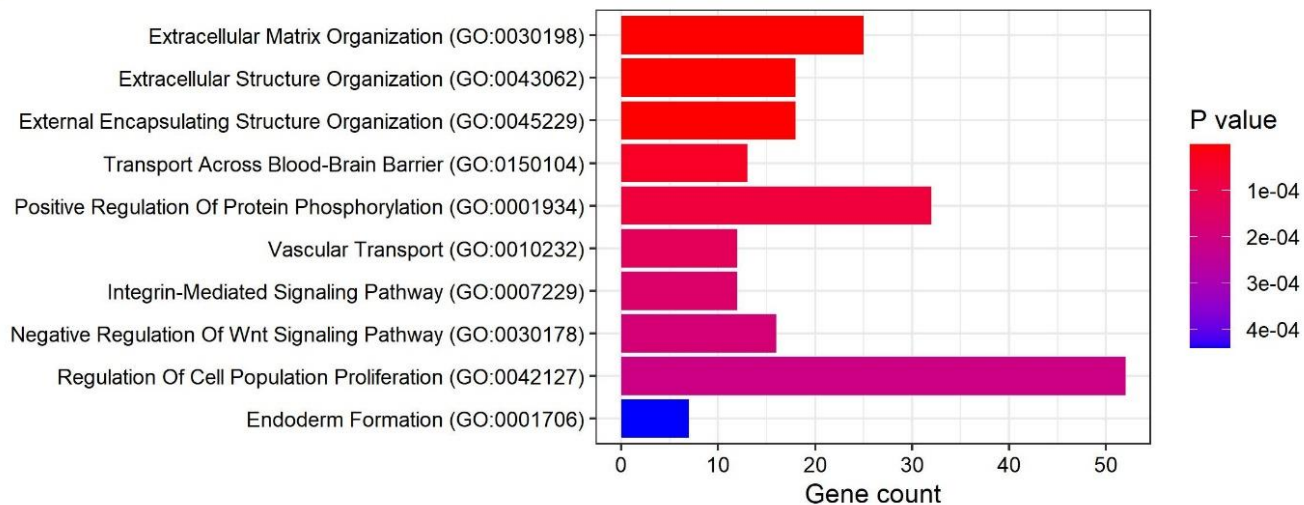
**Figure 4:** GO Biological Process (A,B) and Reactom Pathway (C,D) of 22 common genes (FDR < 0.1)CHM. Size and color of points represent  $-\log_2$  of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.



**Figure 5:** GO\_KEGG Biological Process (A , B) and Reactom Pathway (C,D) of 18 common genes (FDR < 0.1) Glaucoma. Size and color of points represent  $-\log_2$  of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.

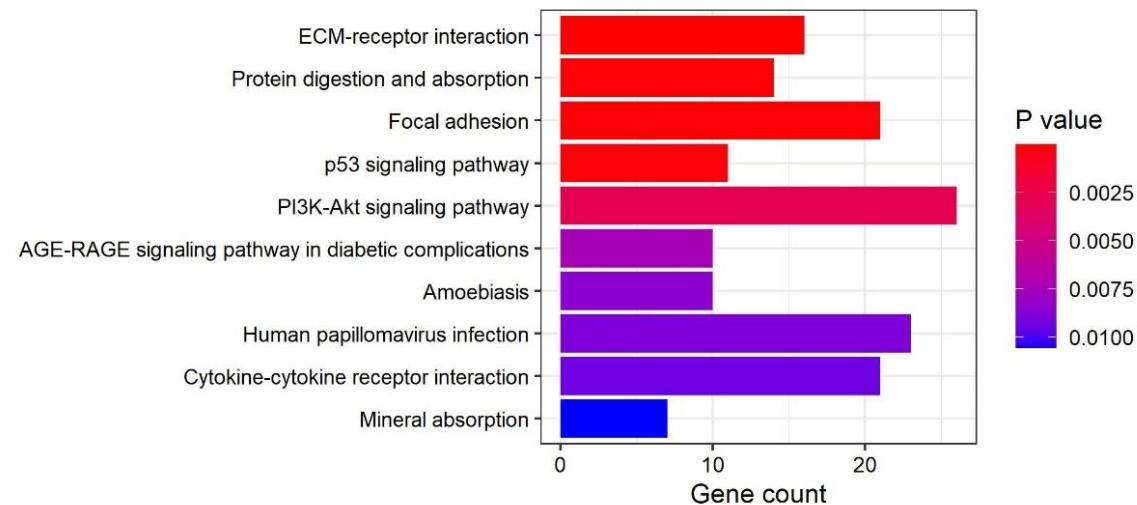
### GO\_Biological\_Process\_2023

**A**



### KEGG\_2021\_Human

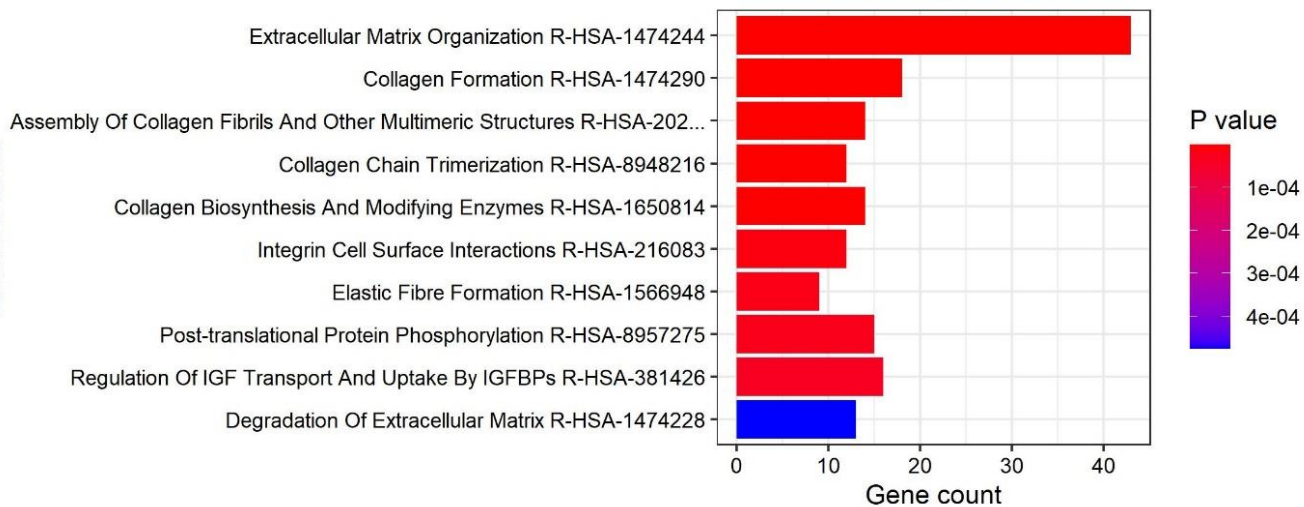
**B**



### Reactome\_2022

Enrichment analysis by Enrichr

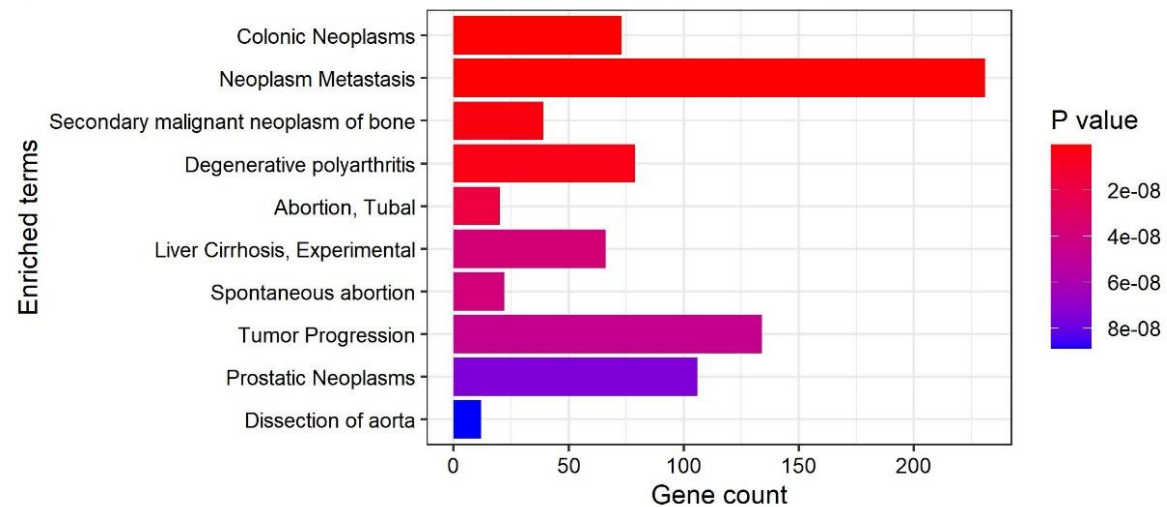
**C**



### DisGeNET

Enrichment analysis by Enrichr

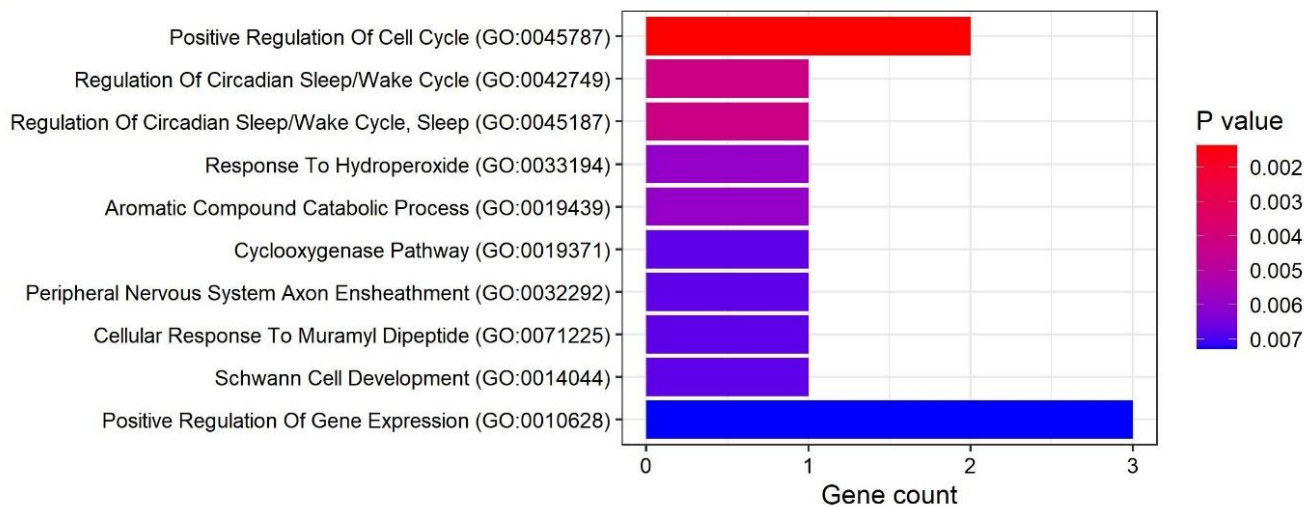
**D**



**Figure 6:** GO\_KEGG Biological Process (A, B) and Reactom Pathway (C, D) of 812 common genes (FDR < 0.1). Size and color of points represent  $-\log_2$  of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.

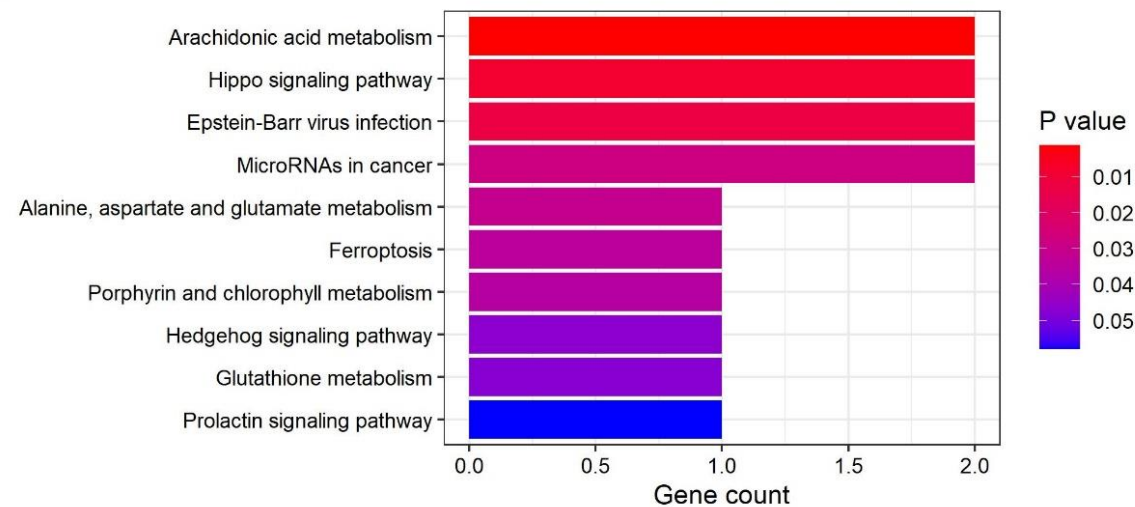
### GO\_Biological\_Process\_2023

**A**



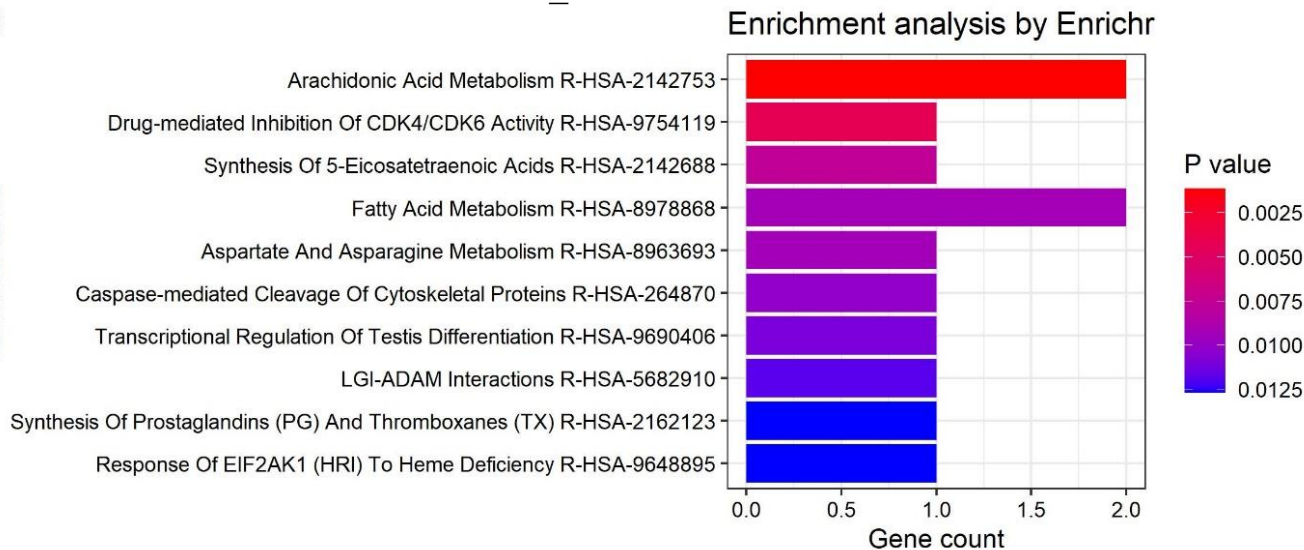
### KEGG\_2021\_Human

**B**



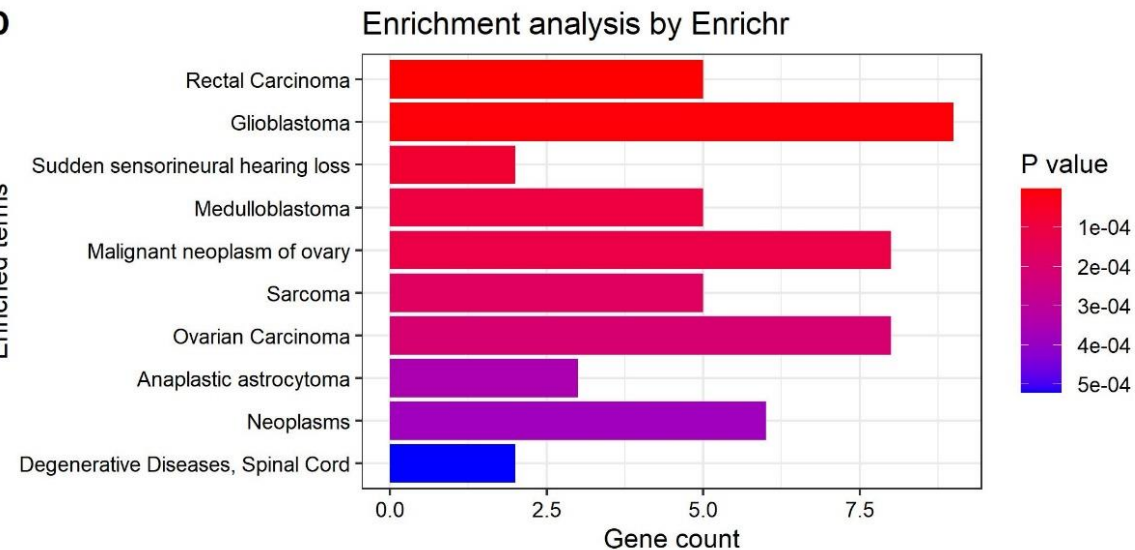
### Reactome\_2022

**C**



### DisGeNET

**D**



**Figure 7:** GO\_KEGG Biological Process (A, B) and Reactom Pathway (C,D) of 17 common genes (FDR < 0.1)MD. Size and color of points represent  $-\log_2$  of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.