Supplementary

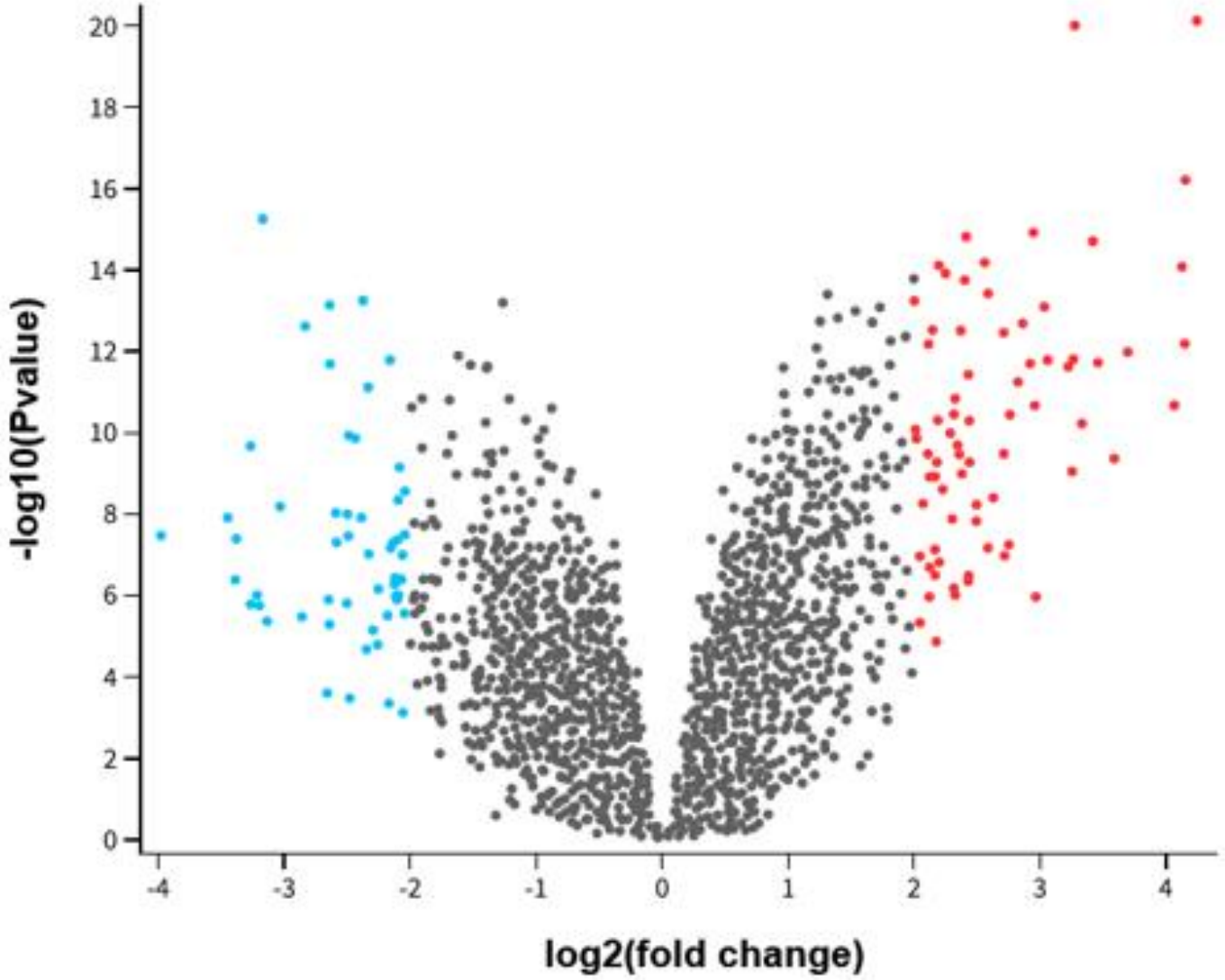

Figure 1 .A . The visualization of dysregulated, Padj<0.05 .(Normal & Aniridia)

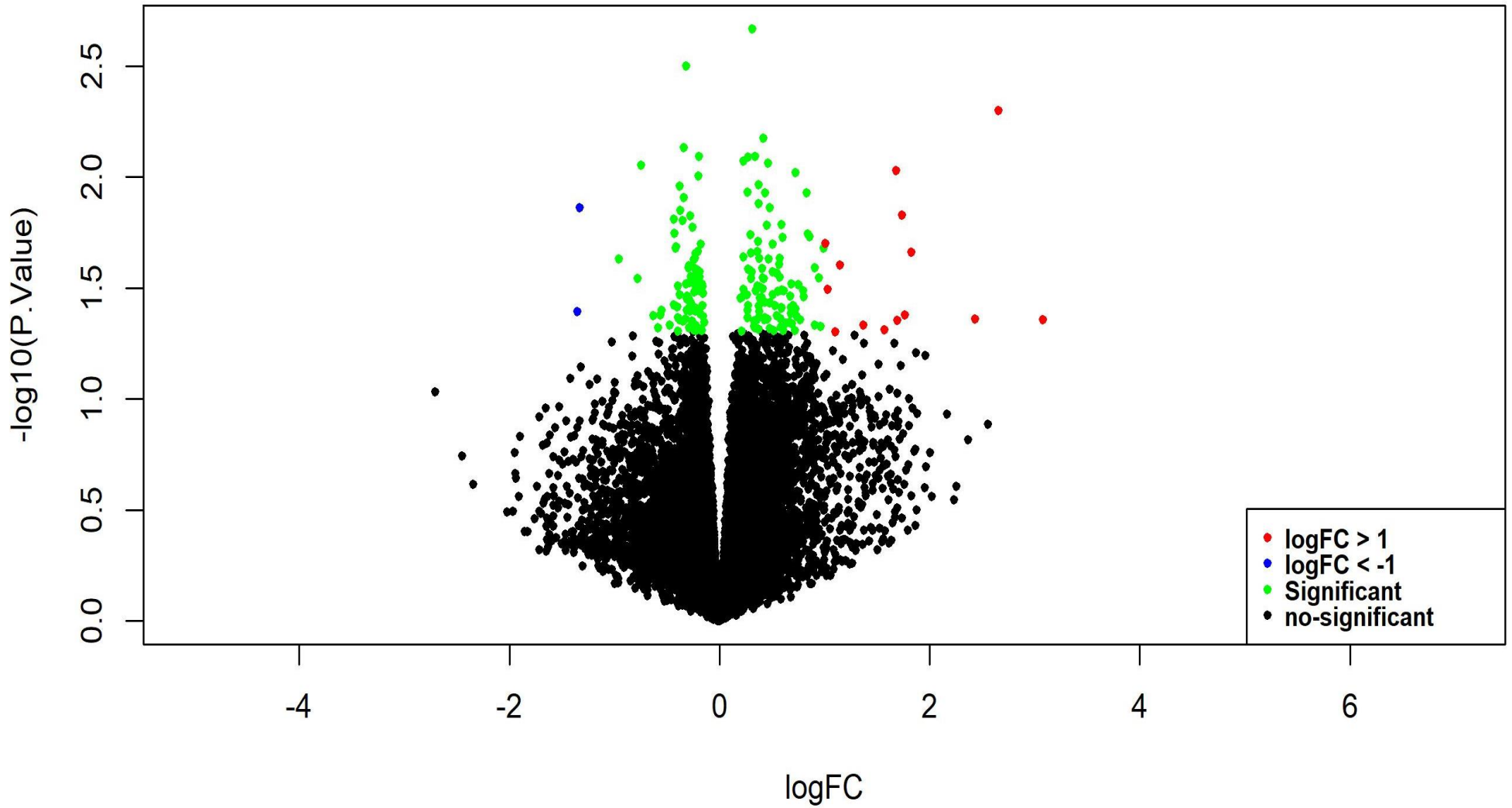

Figure 1 .B . The visualization of dysregulated, Padj<0.05 .(Normal & Choroideremia)

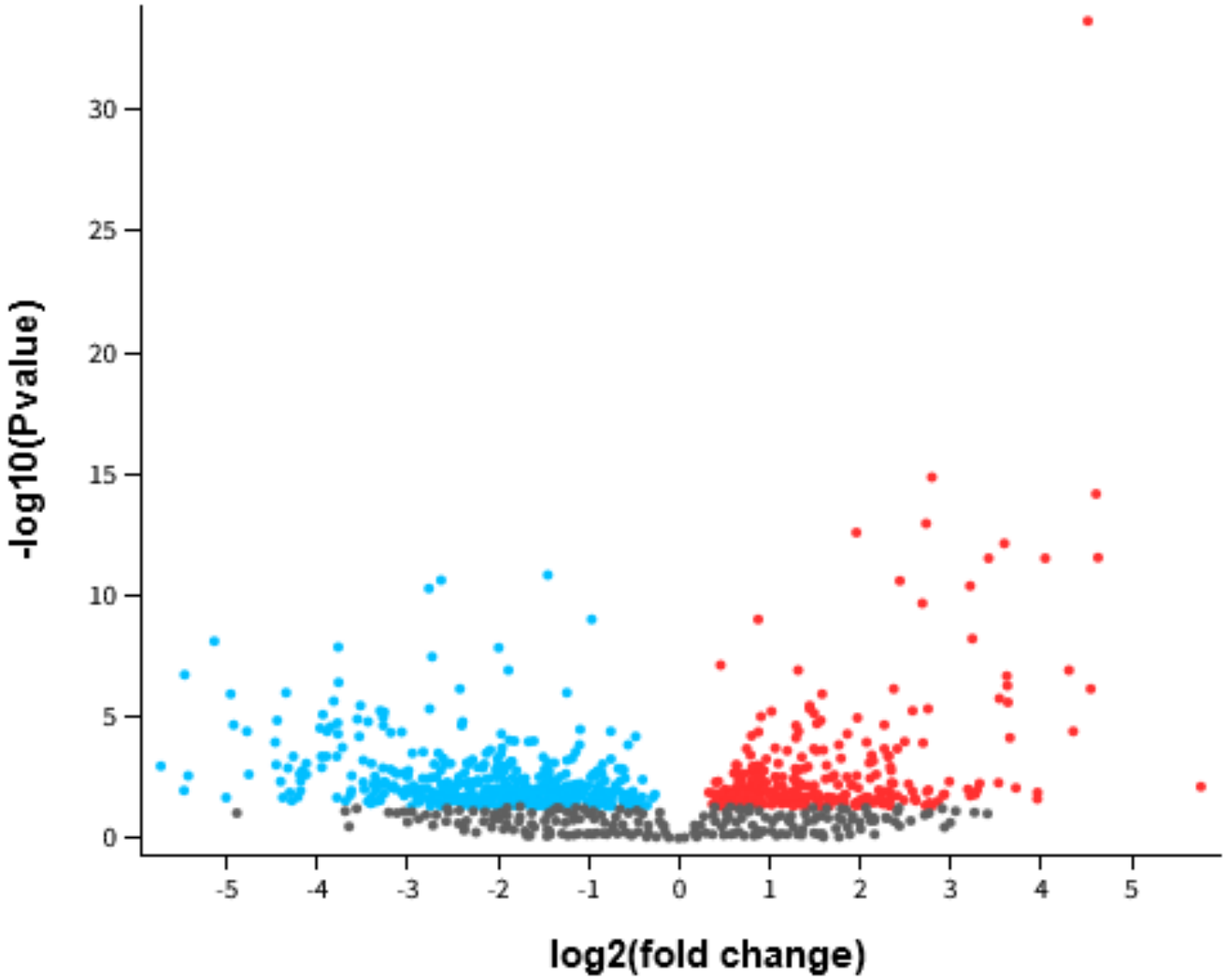

Figure 1 .C . The visualization of dysregulated, Padj<0.05 .(Normal & CD)

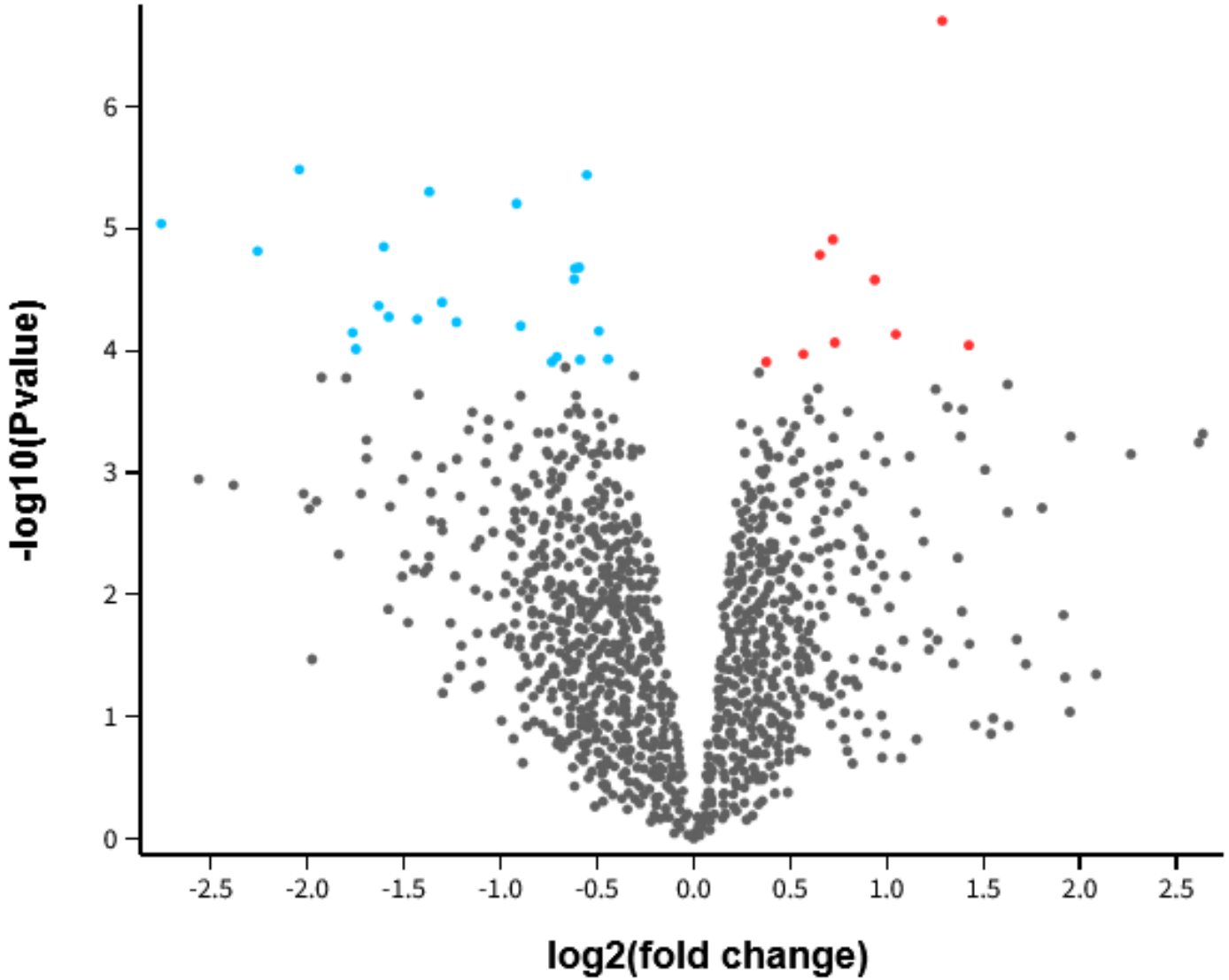

Figure 1 .D . The visualization of dysregulated, Padj<0.05 .(Normal & Glaucoma)

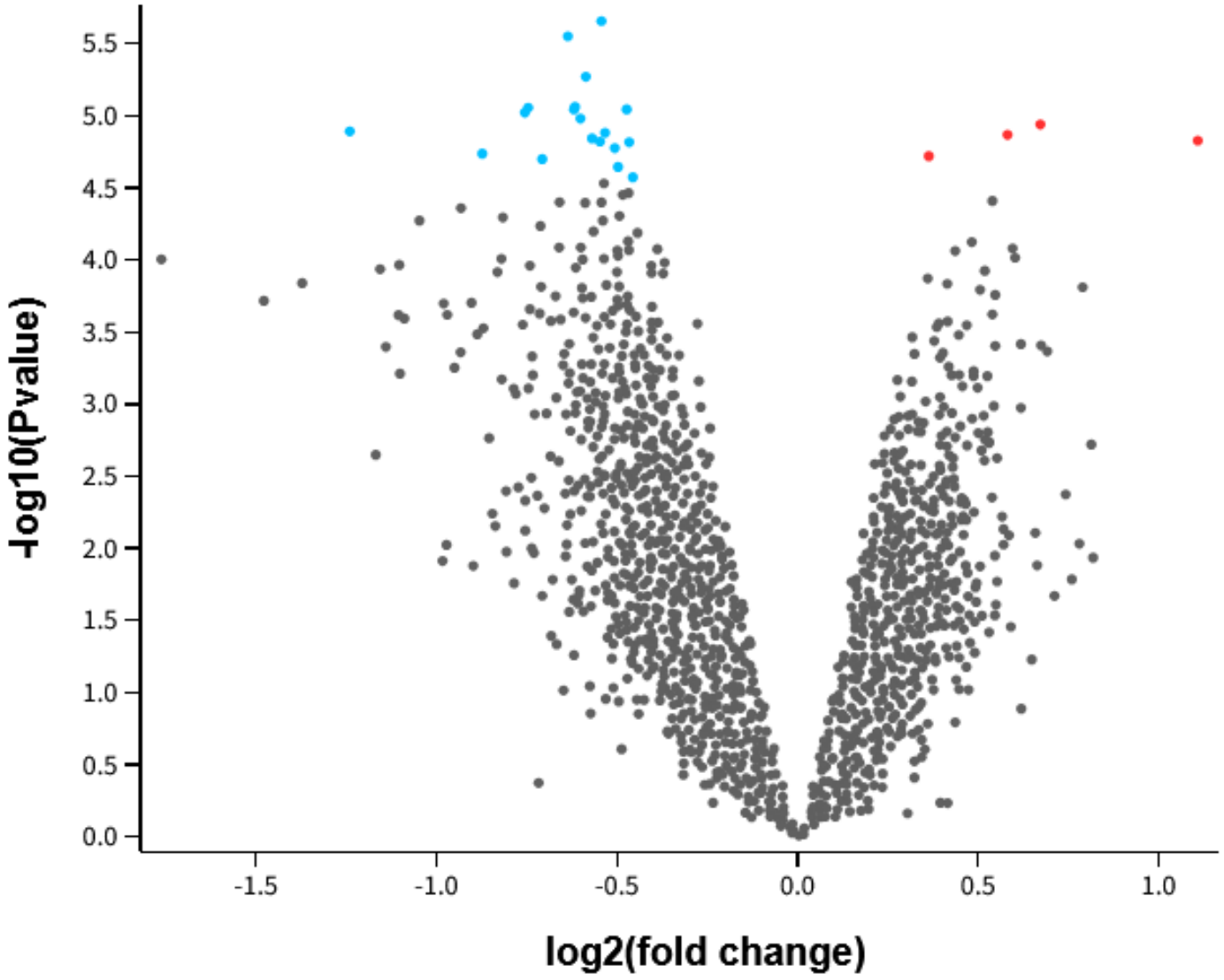

Figure 1 .E . The visualization of dysregulated, Padj<0.05 .(Normal & AMD)

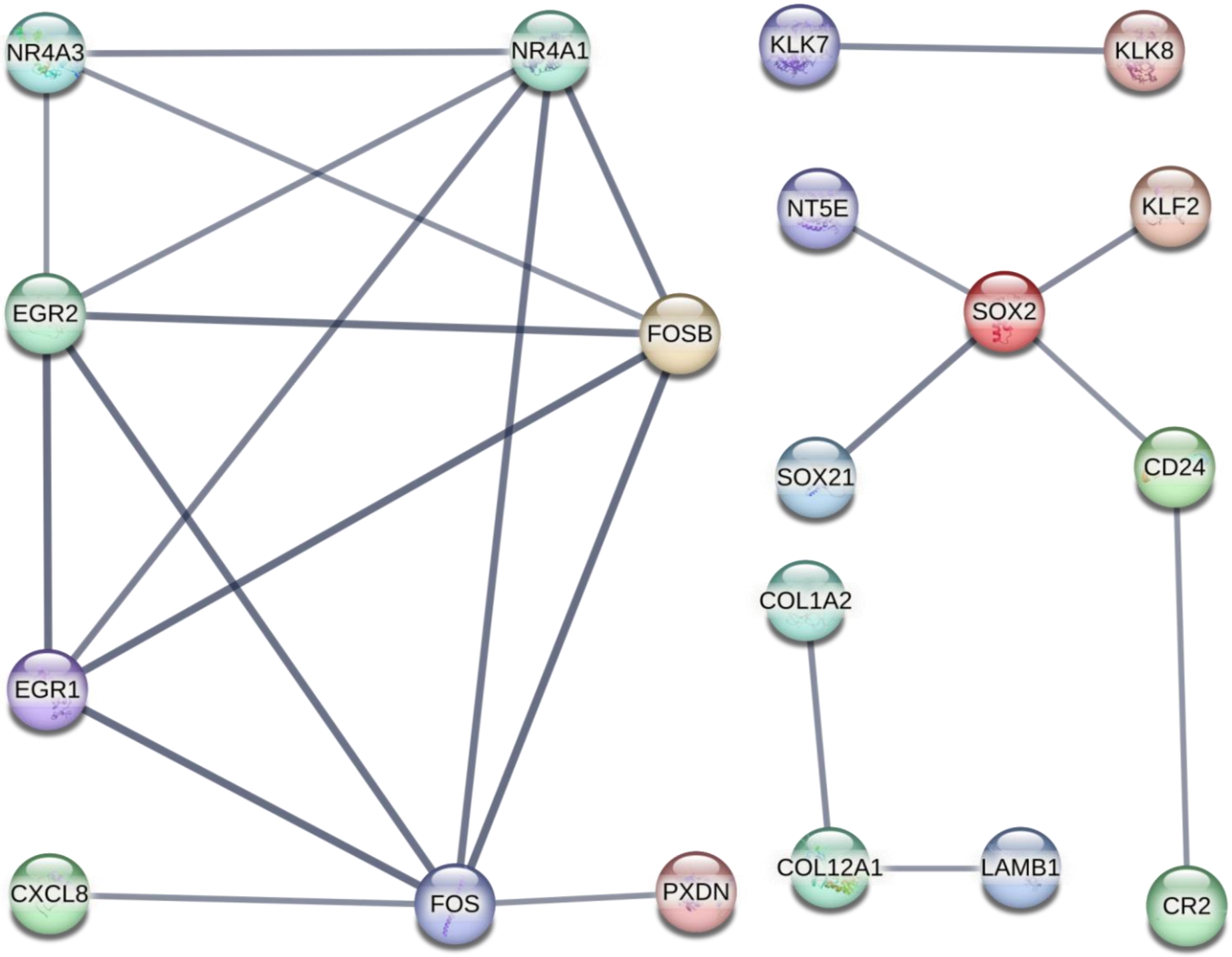

Figure 2 .A .

Protein-Protein Interaction Networks of dysregulated genes for Aniridia.

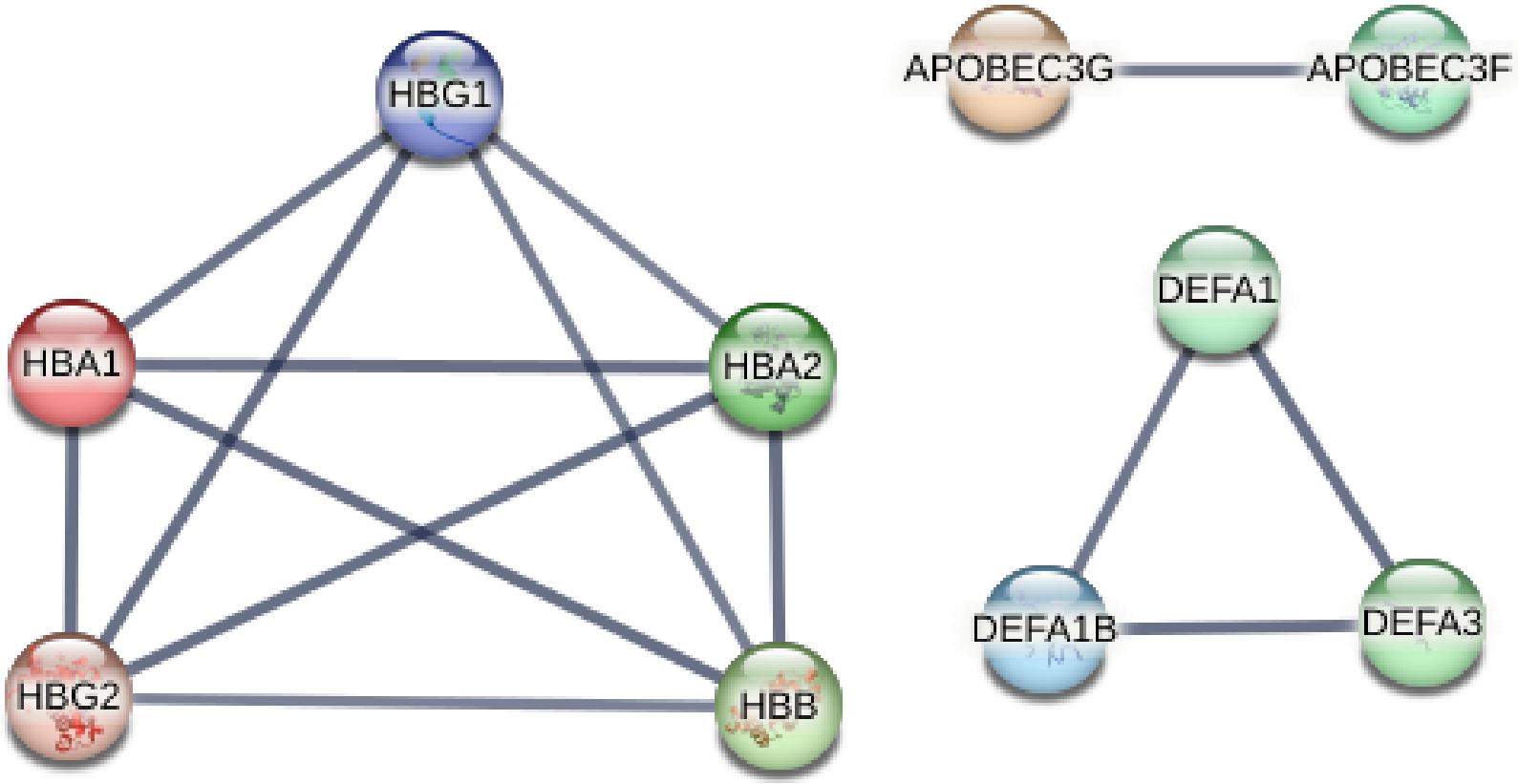

Figure 2 .B .

Protein-Protein Interaction Networks of dysregulated genes for Choroideremia.

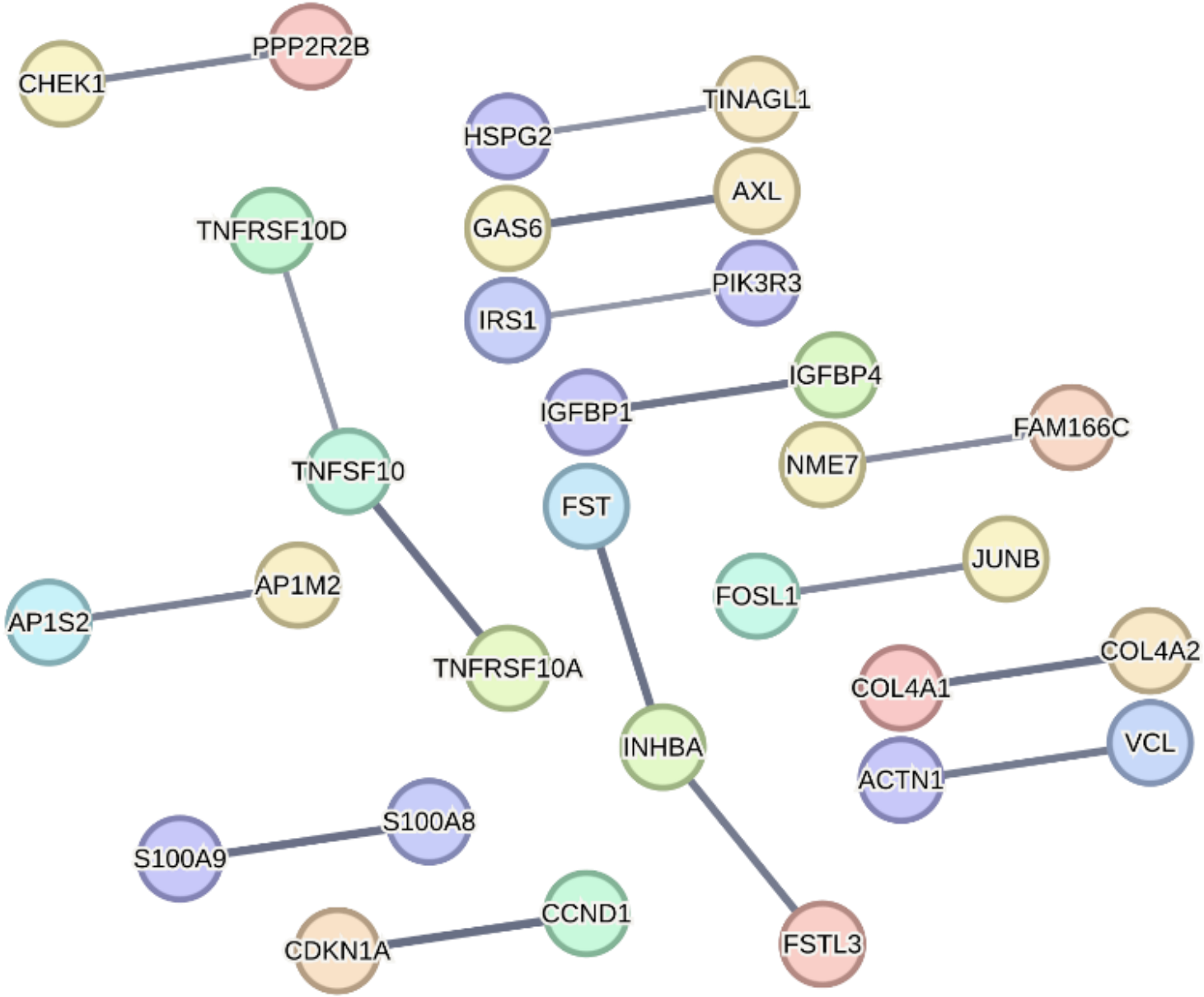

Figure 2 .C .

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

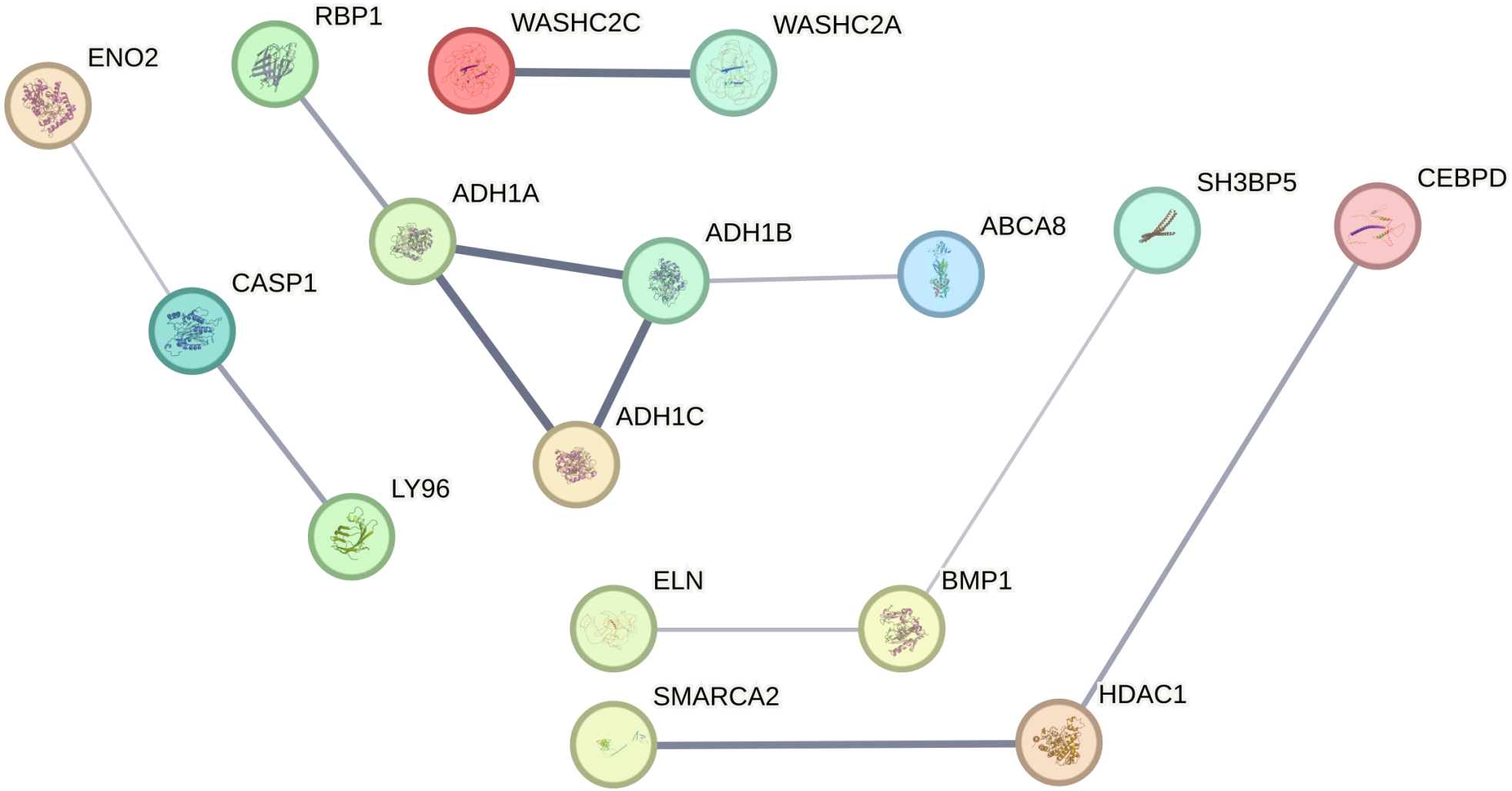

Figure 2 .D .
Protein-Protein Interaction Networks of dysregulated genes for Glaucoma .

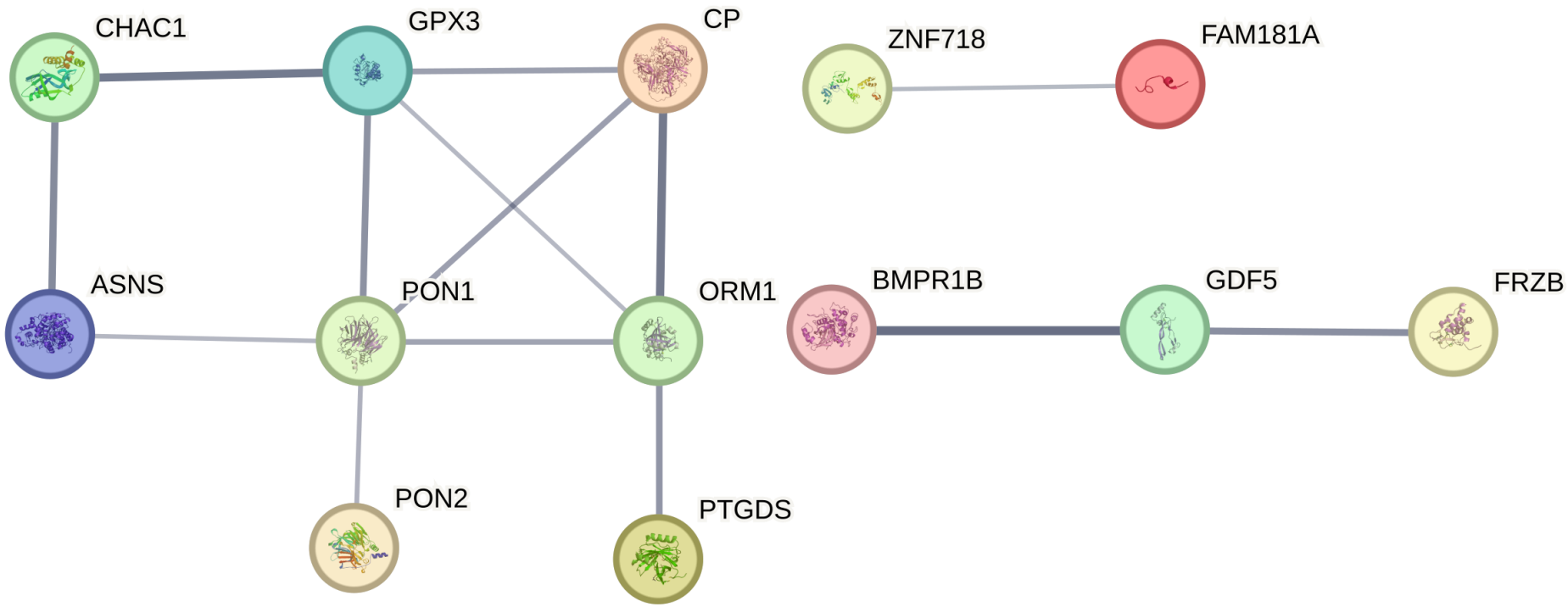

Figure 2 .E .

Protein-Protein Interaction Networks of dysregulated genes for AMD.

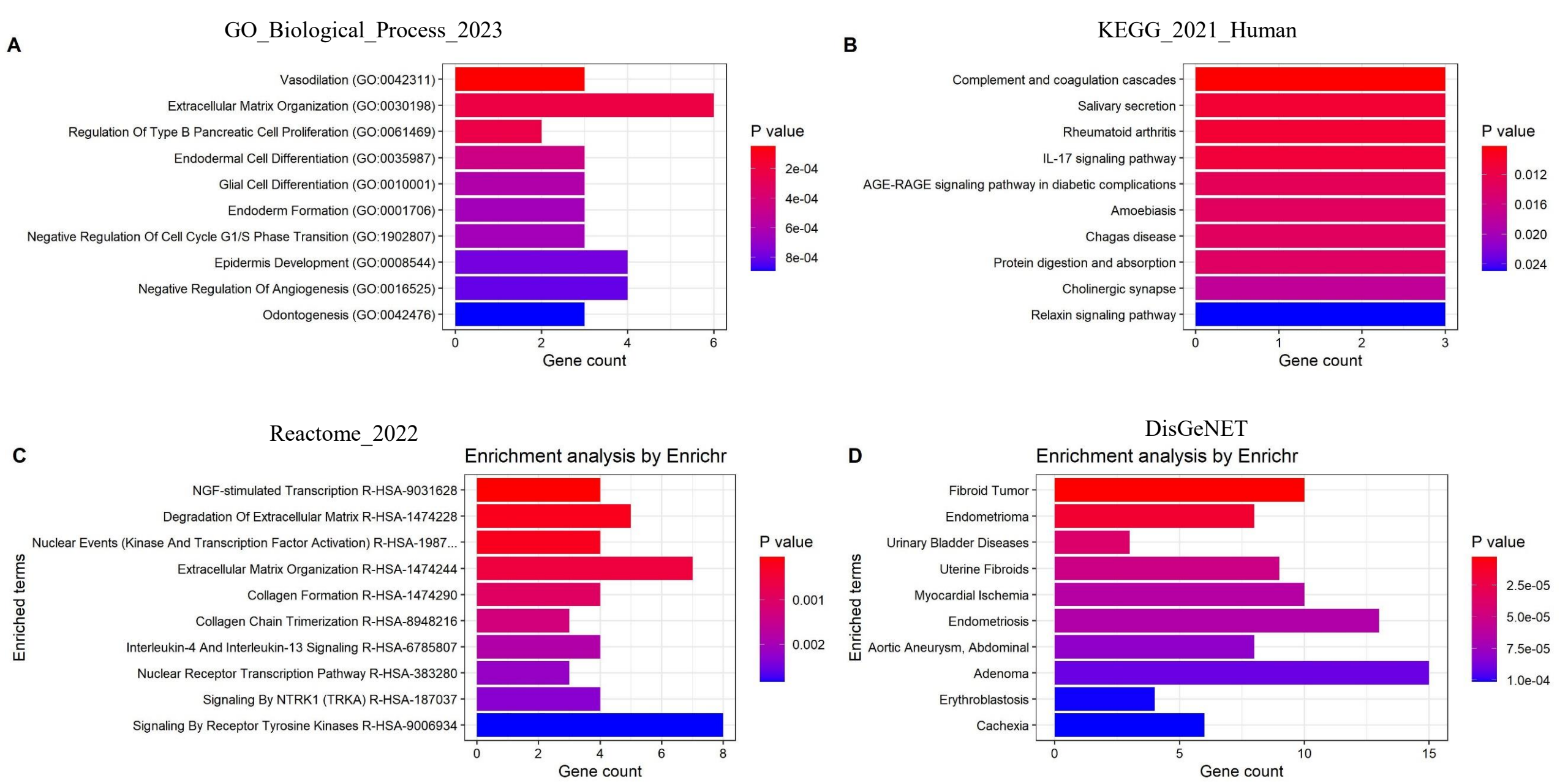

Figure 3: GO_KEGG Biological Process (A , B) , Reactom Pathway and DisGeNET (C,D) of 125 common genes (FDR < 0.1) Aniridia .Size and color of points represent -Log2 of FDR and the number of genes associated with each term, respectively.

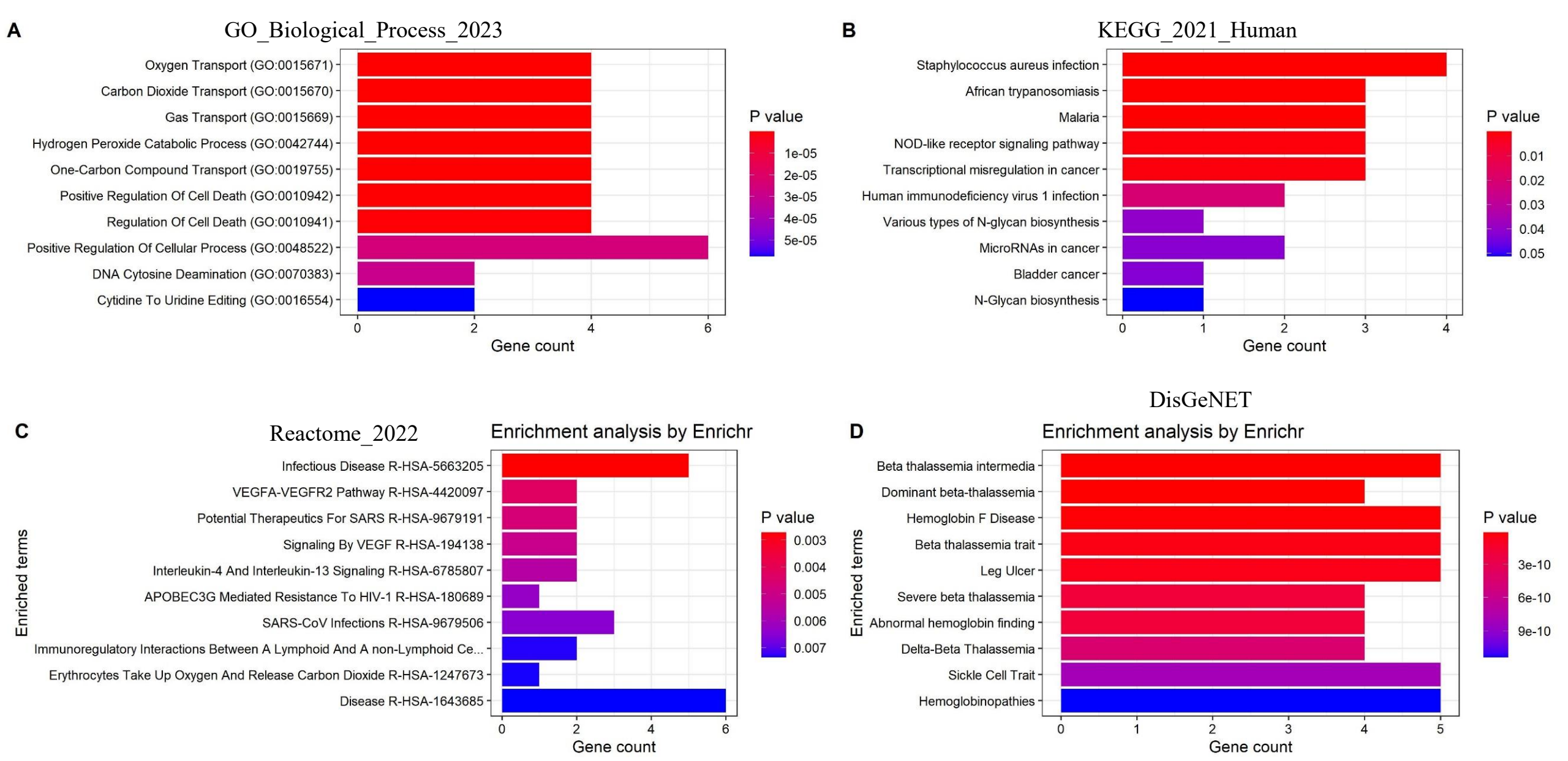

Figure 4: GO Biological Process (A,B) and Reactom Pathway (C,D) of 22 common genes (FDR < 0.1)CHM.Size and color of points represent -Log2 of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.

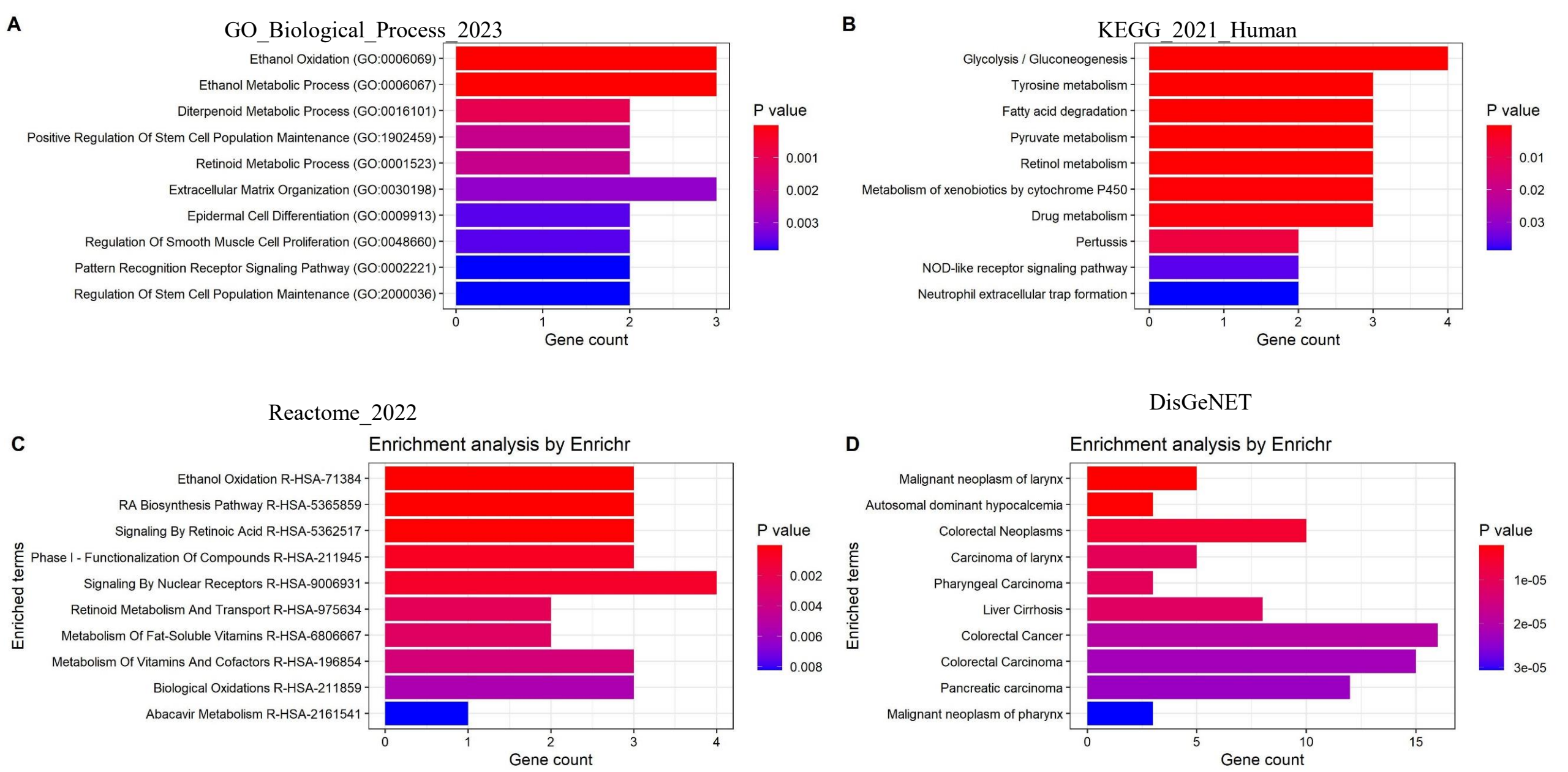

Figure 5: GO_KEGG Biological Process (A , B) and Reactom Pathway (C,D) of 18 common genes (FDR < 0.1)Glaucoma.Size and color of points represent -Log2 of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.

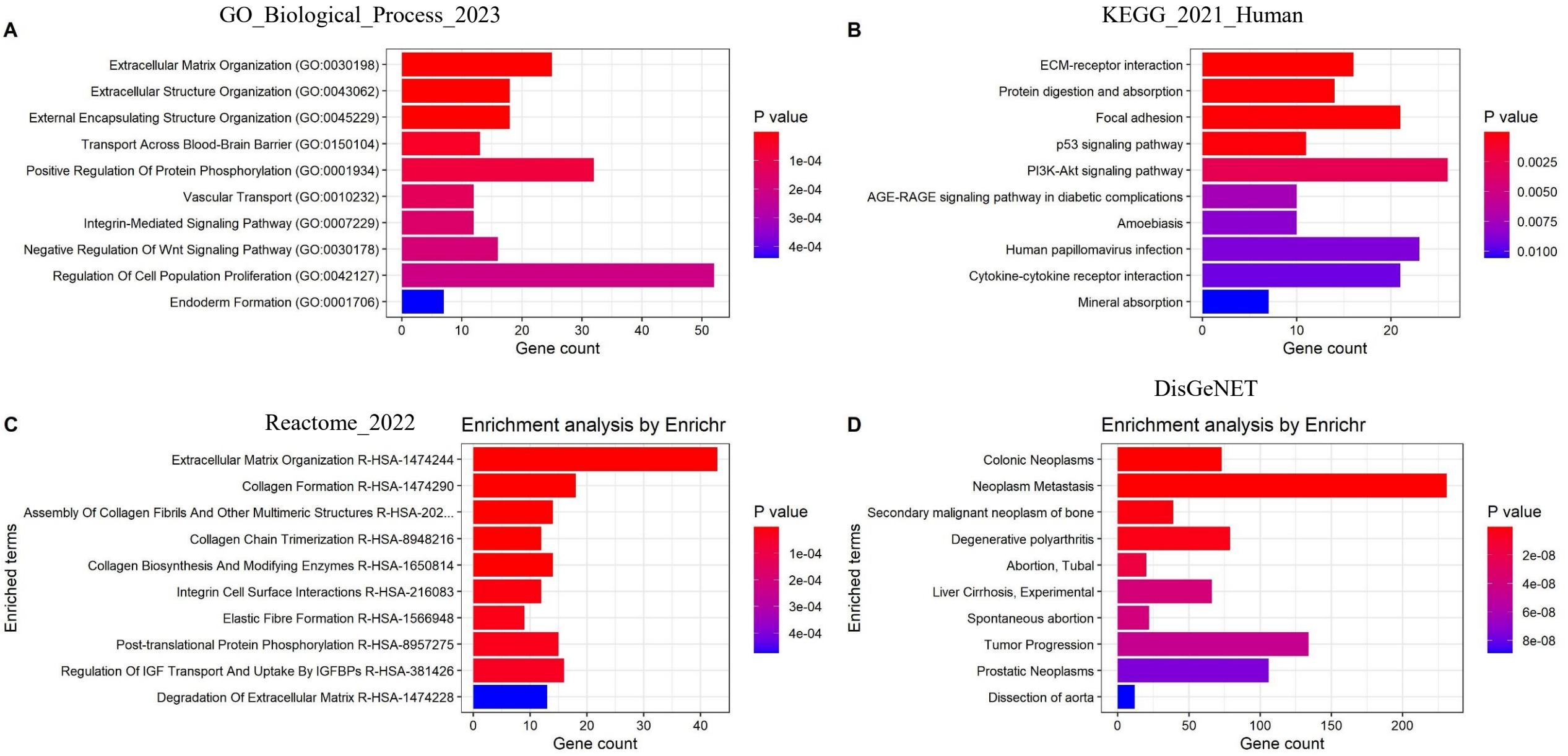

Figure 6: GO_KEGG Biological Process (A , B) and Reactom Pathway (C,D) of 812 common genes (FDR < 0.1)CD.Size and color of points represent -Log2 of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.

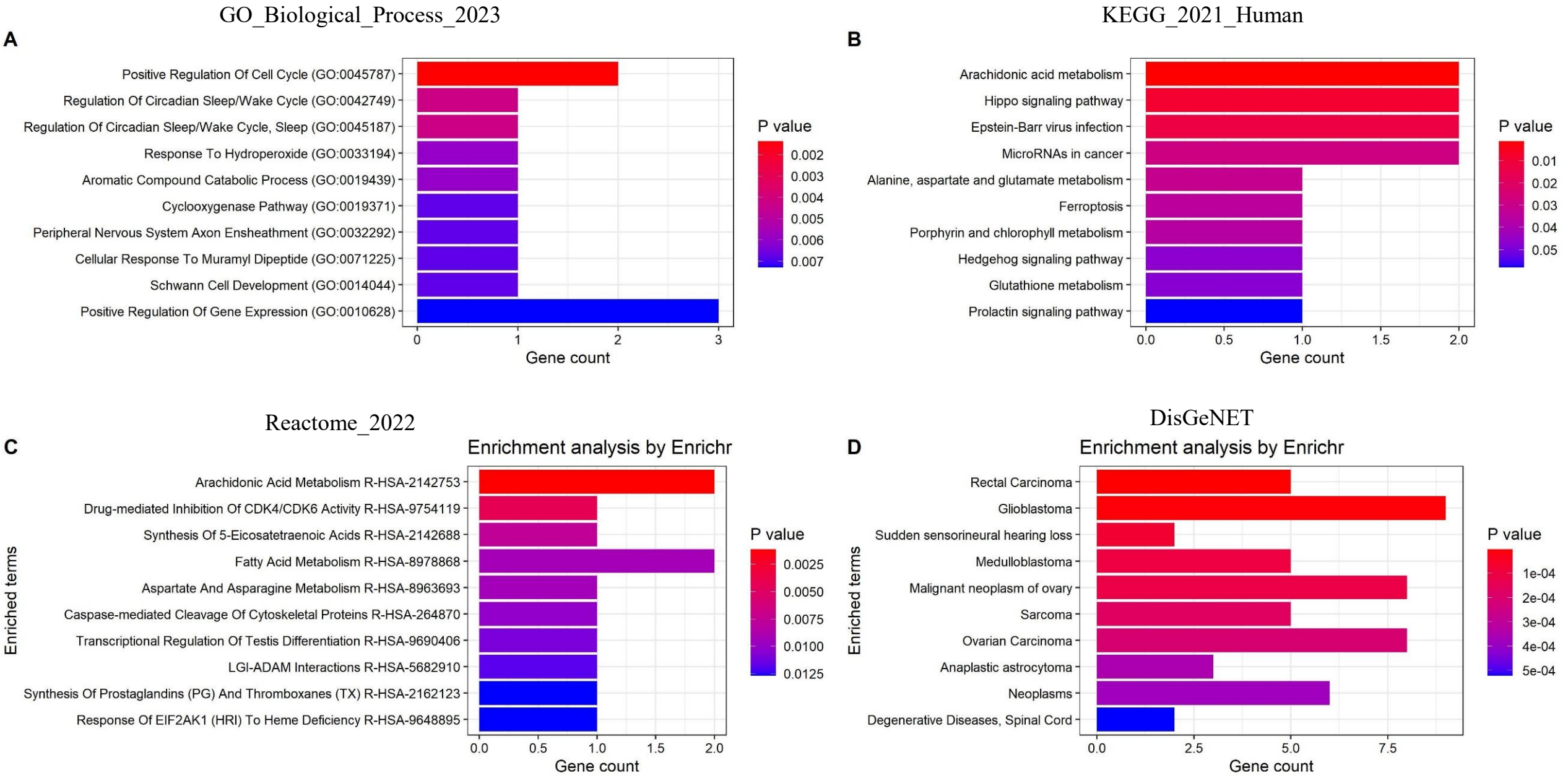

Figure 7: GO_KEGG Biological Process (A, B) and Reactom Pathway (C,D) of 17 common genes (FDR < 0.1)MD. Size and color of points represent -Log2 of FDR and the number of genes associated with each term, respectively. The fold enrichment measure is not shown for better visualization.