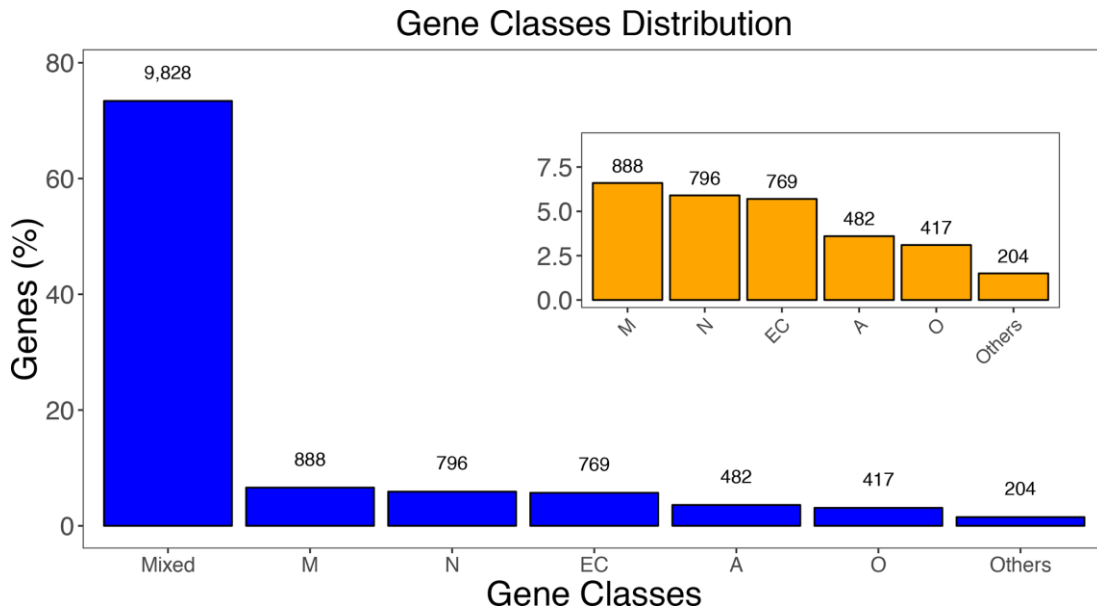
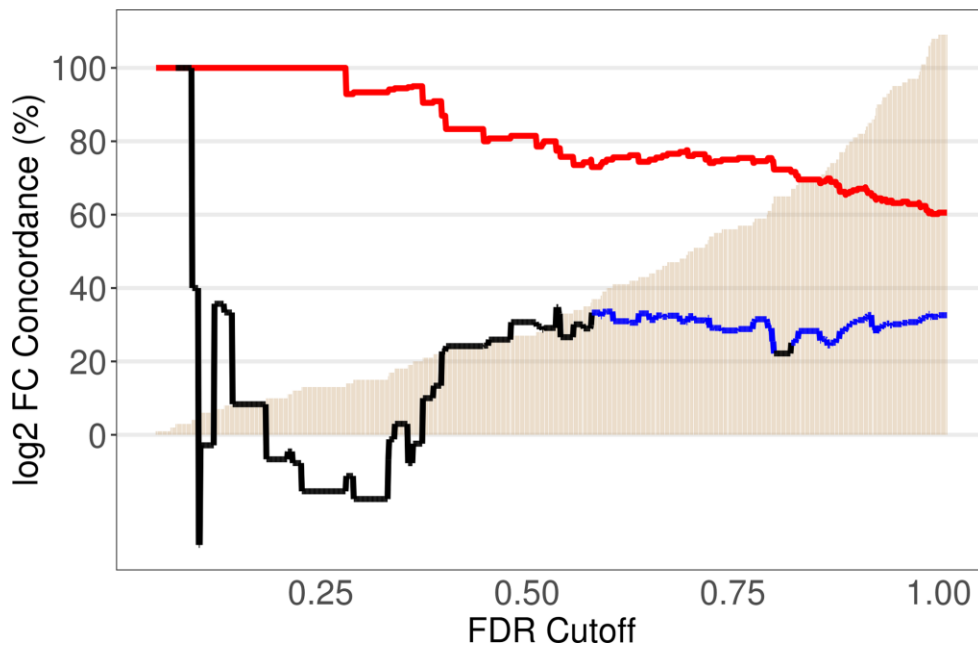


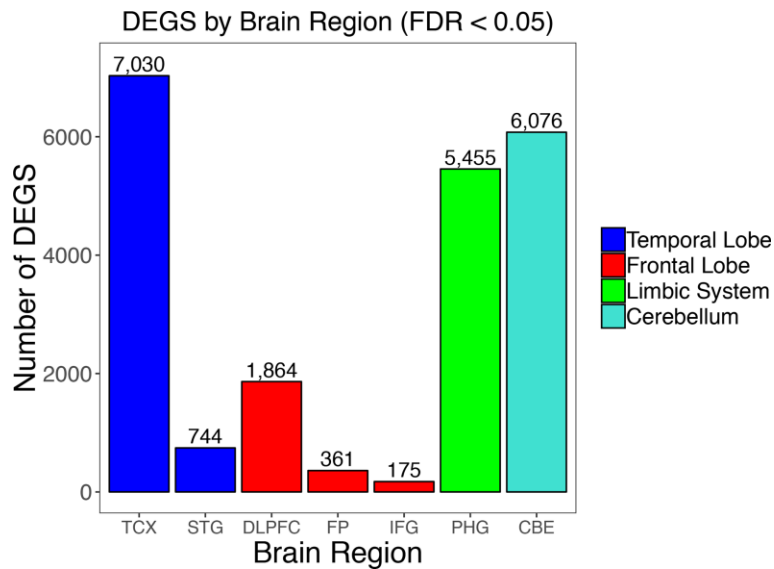
SUPPLEMENTARY FIGURES



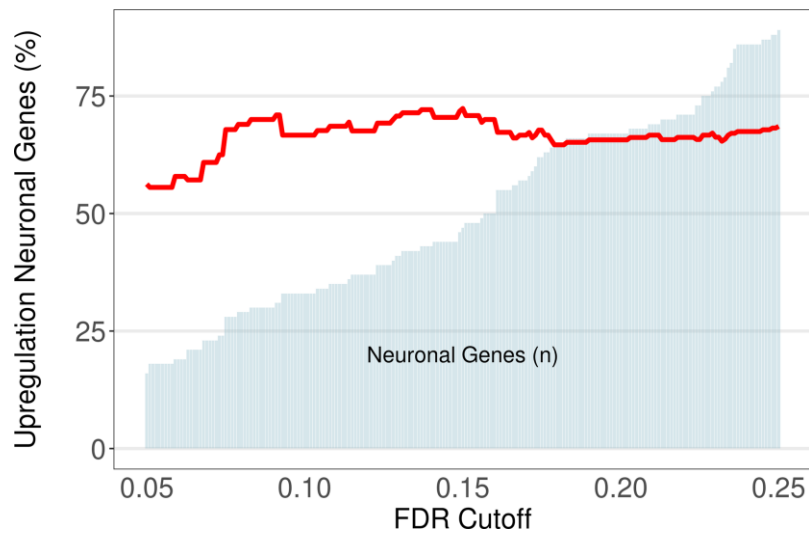
Supplementary Figure 1. Barplot representing the number of genes for each class in the Single Cell RNA sequencing database [10].



Supplementary Figure 2. Comparison of expression profiling of oligodendrocyte genes between bulk tissue and oligodendrocytes isolated by LCM in the same samples. The red line is the percent concordance of the direction of effect between bulk RNA-Seq and LCM. The Black and Blue line reflects the Spearman correlation coefficient (multiplied by 100) for the log2 fold-change between the two groups – black represents non-significant correlation coefficient results and the blue line is for significant results. The bar plot in the background reflects the number of genes included in the analysis.

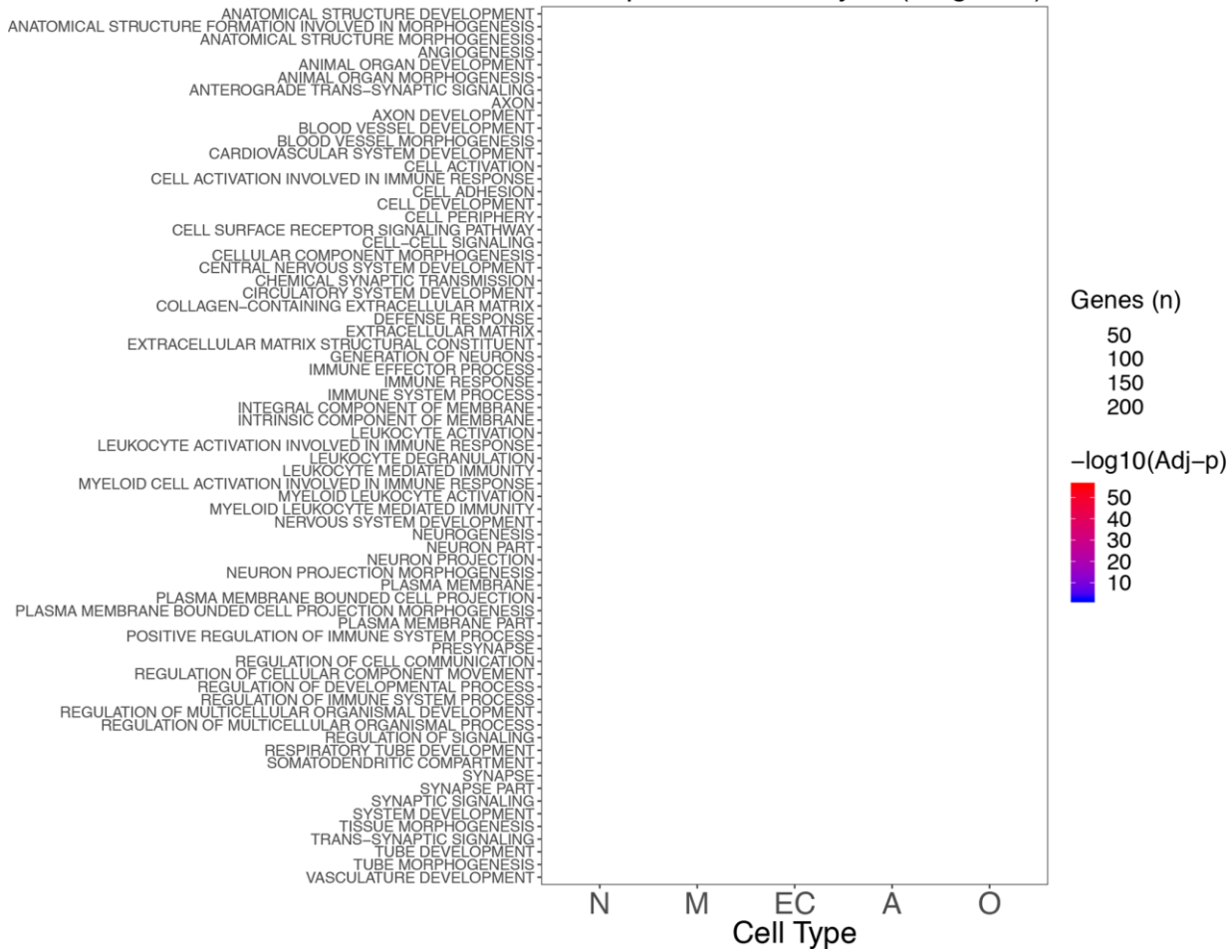


Supplementary Figure 3. Differentially expressed genes classified for the Alzheimer’s Disease dataset. TCX: temporal cortex; STG: superior temporal gyrus; DLPFC: dorso-lateral prefrontal cortex; FP: frontal pole; IFG: inferior frontal gyrus; PHG: para-hippocampal gyrus; CBE: cerebellum.

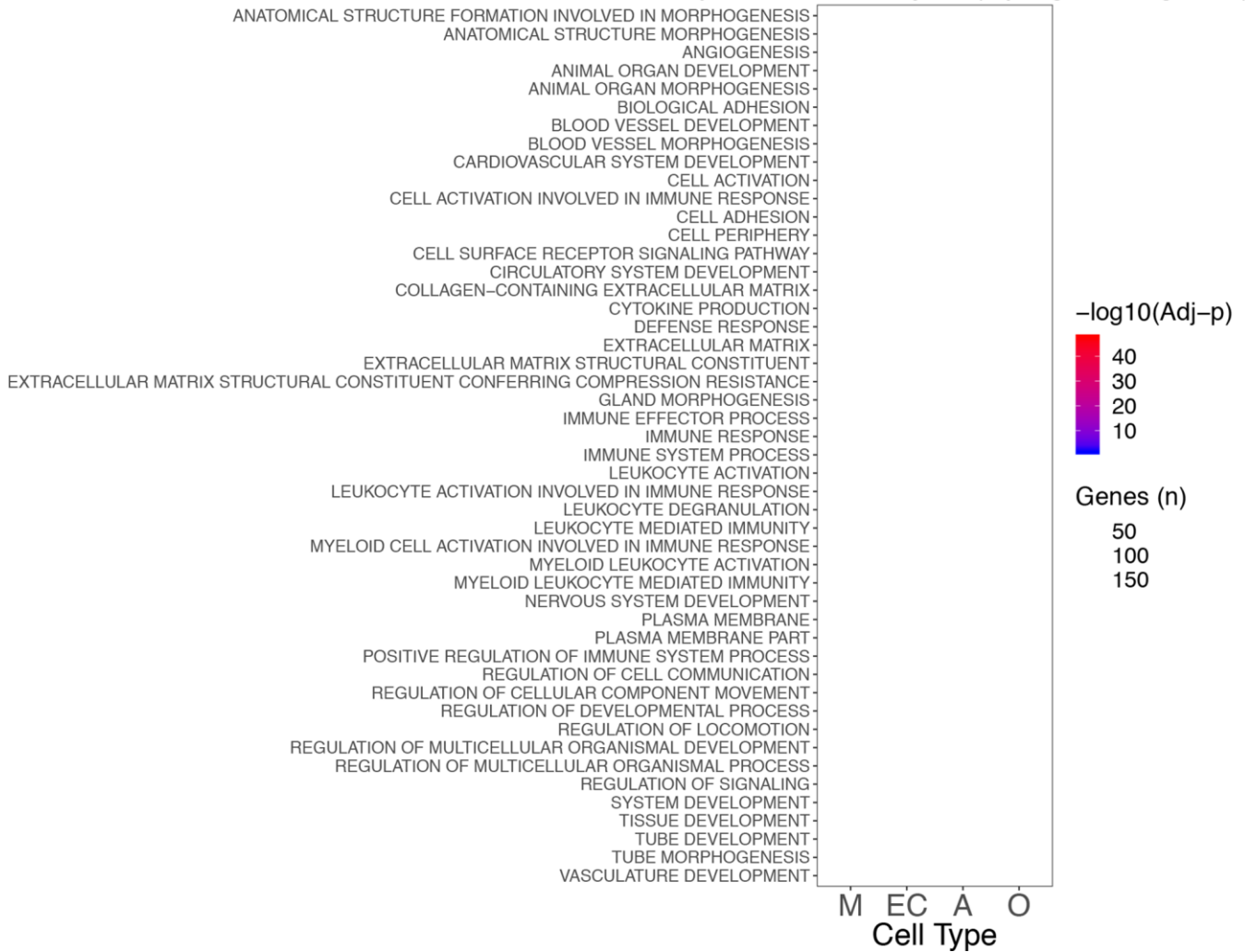


Supplementary Figure 4. Pattern of downregulation/upregulation for neuronal specific genes in FP as a function of different FDR cutoffs. The red line is the percent of upregulated neuronal genes in FP. The bar plot in the background reflects the number of genes included in the analysis depending on the FDR cutoff.

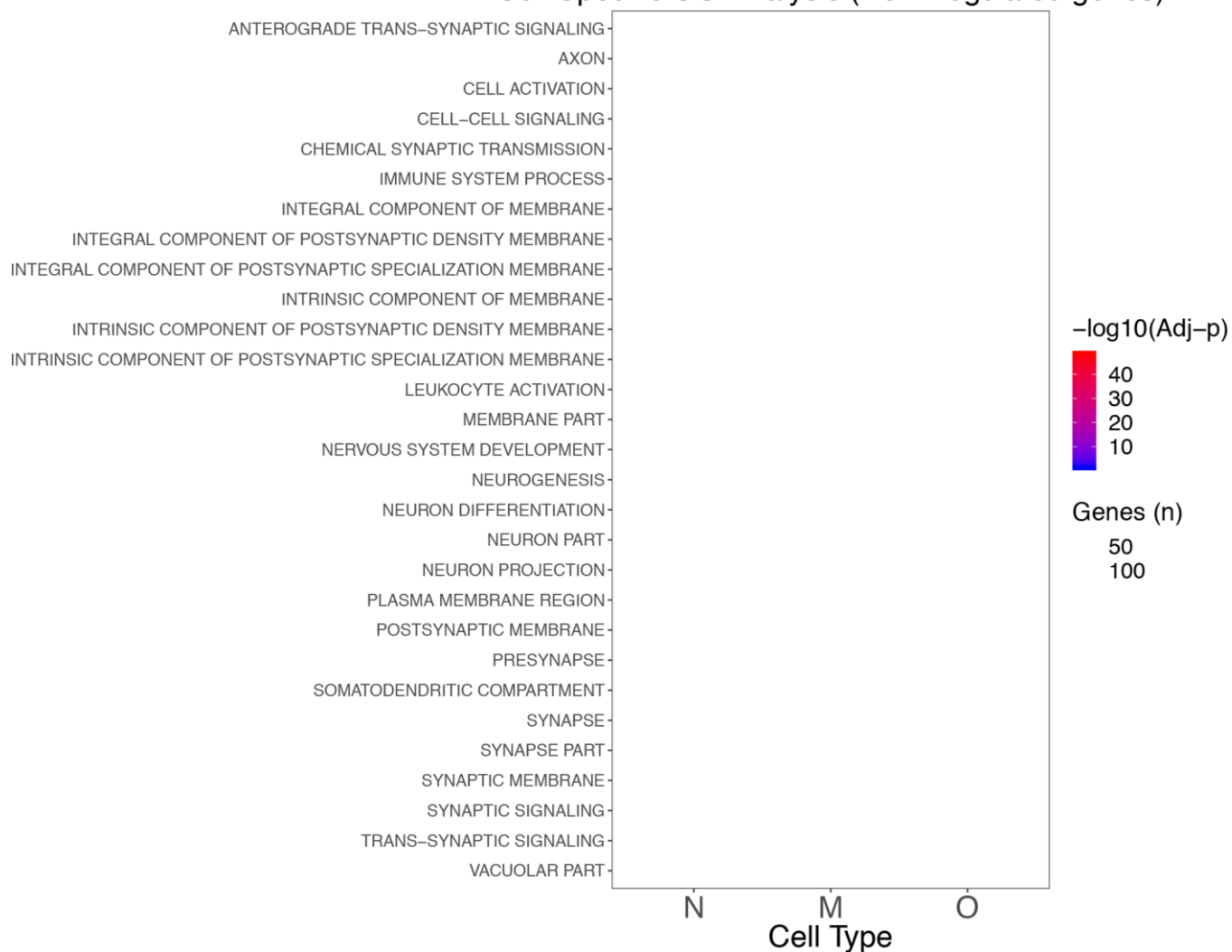
Cell Specific GO Analysis (All genes)



Cell Specific GO Analysis (Upregulated genes)

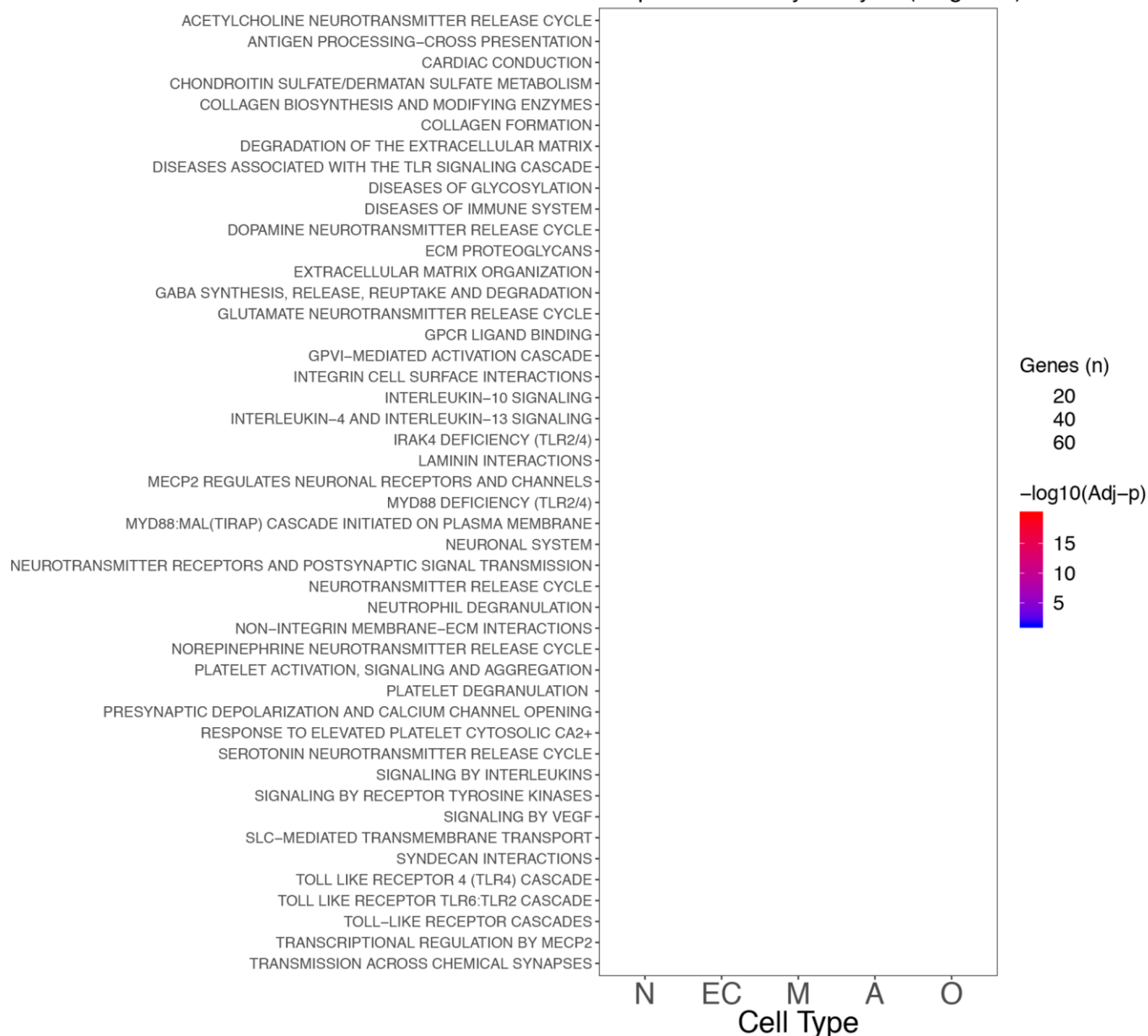


Cell Specific GO Analysis (Downregulated genes)

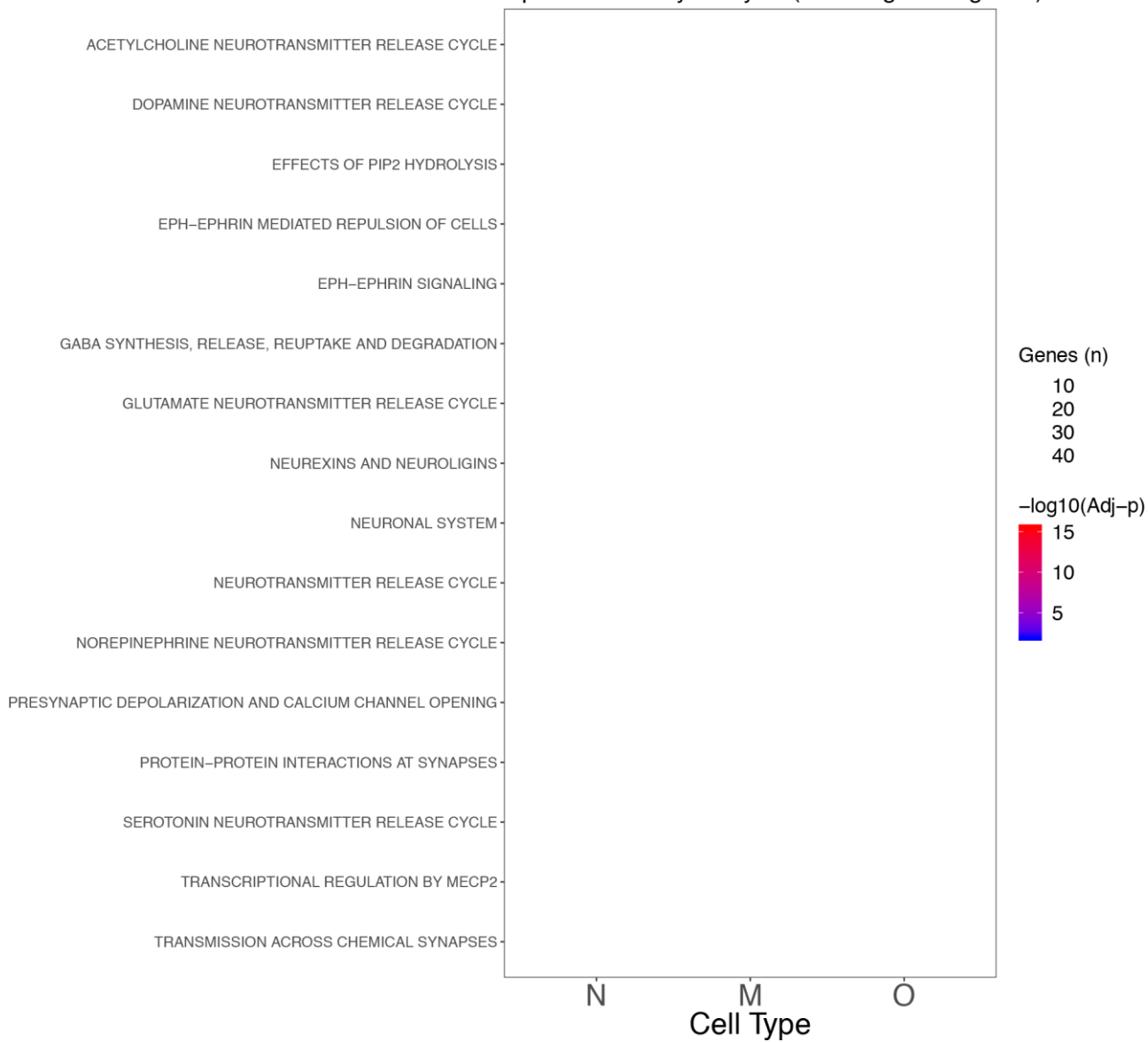


Supplementary Figure 5 (3 pages). Top 15 significant GO classes identified in the different cell types combining the results for the seven brain regions analyzed. The color scale indicates the significance (blue to red as the significance increases), whereas the size indicates the number of genes in that specific enriched class. Page 1: Upregulated and Downregulated genes. Page 2: Upregulated genes. Page 3: Downregulated genes.

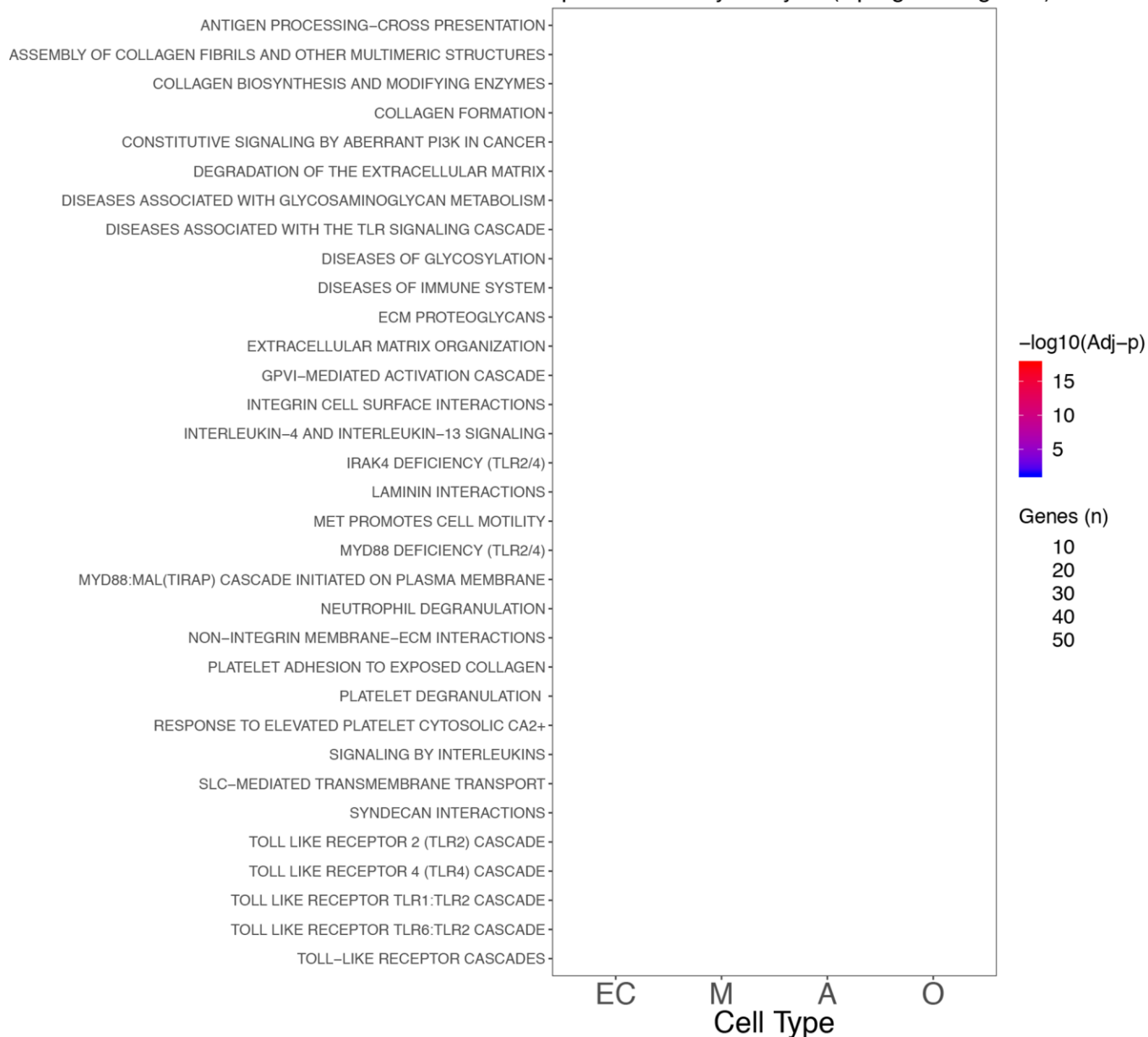
Cell Specific Pathway Analysis (All genes)



Cell Specific Pathway Analysis (Downregulated genes)

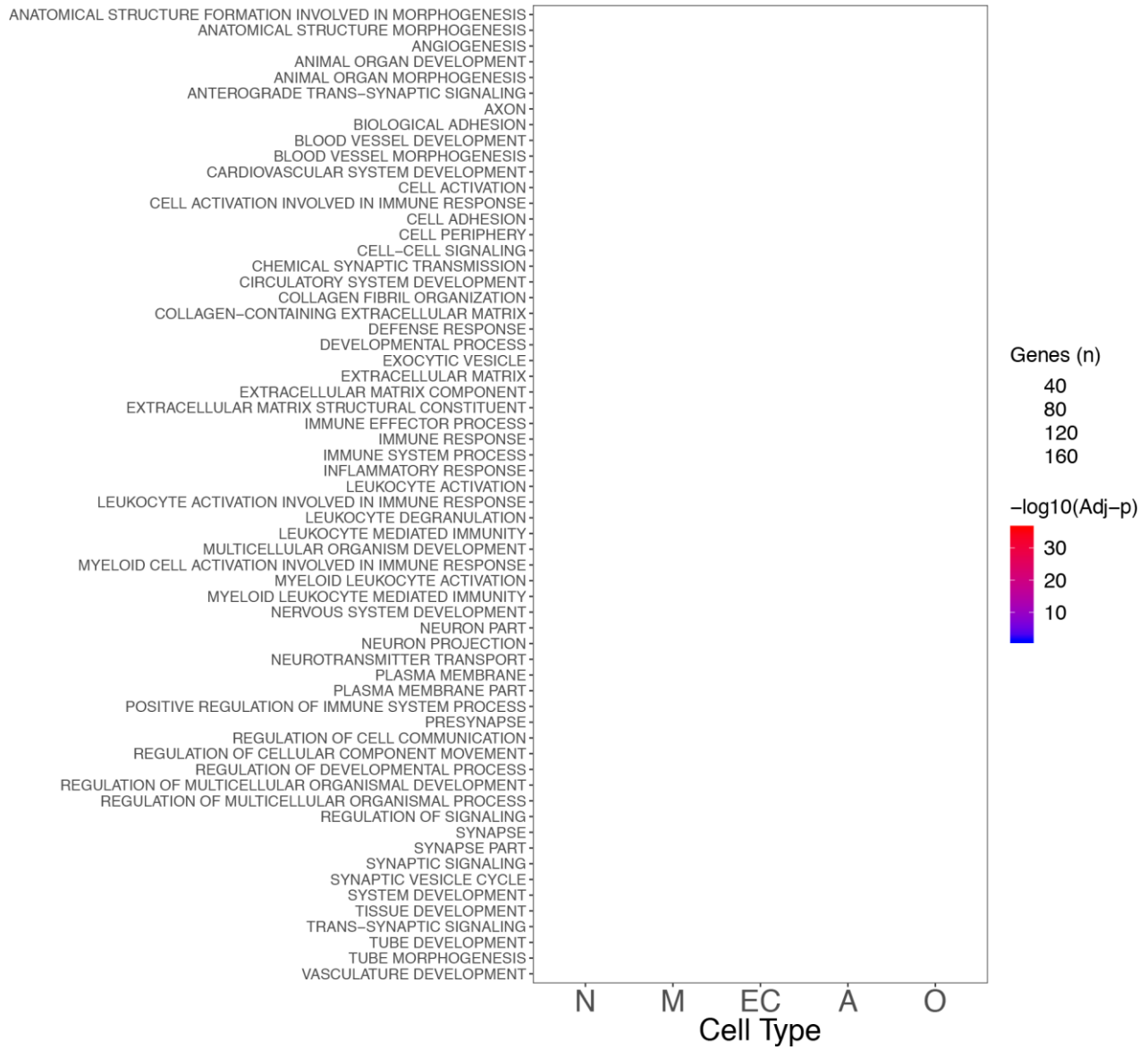


Cell Specific Pathway Analysis (Upregulated genes)

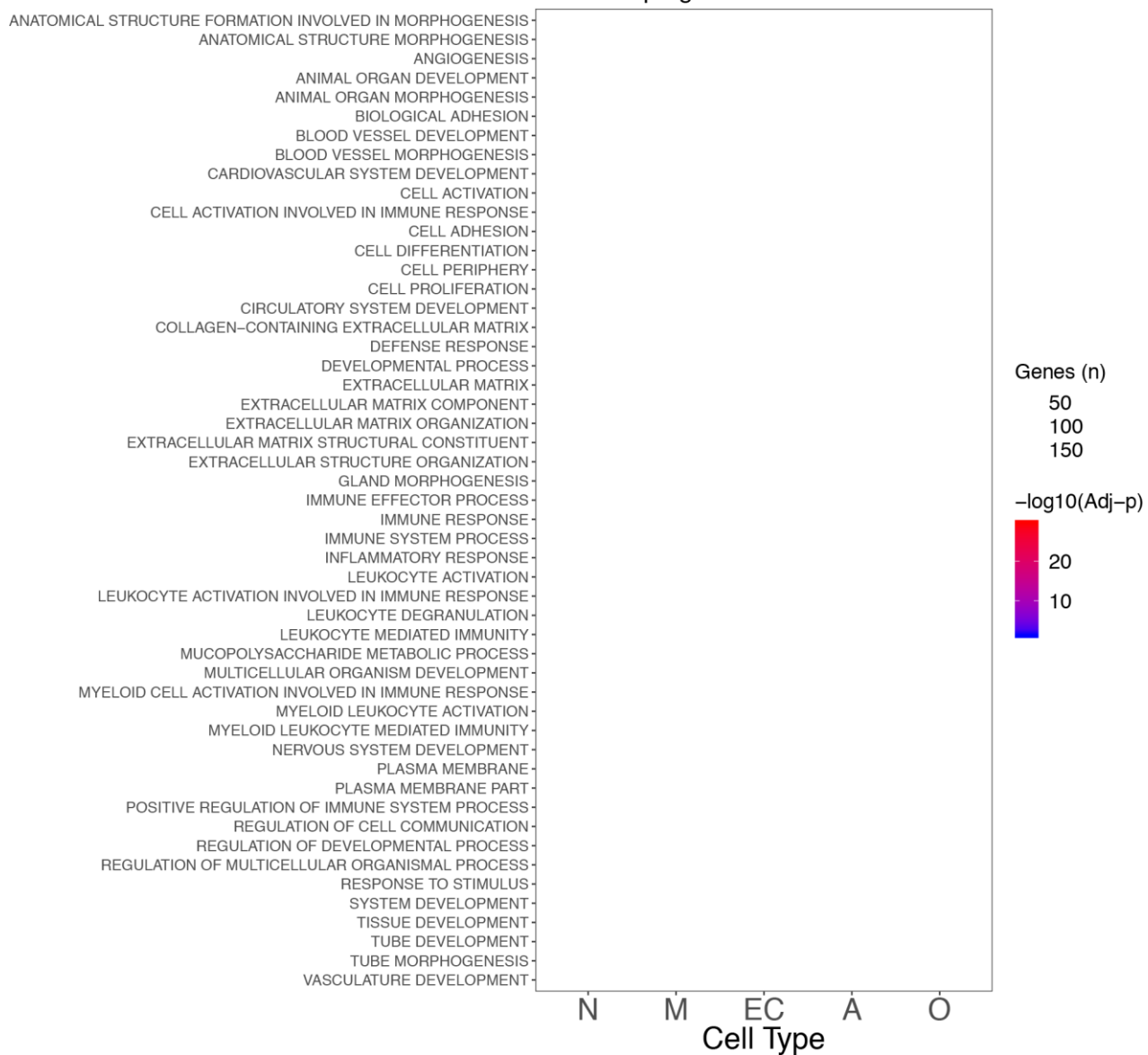


Supplementary Figure 6 (3 pages). Top 15 significant REACTOME pathways identified in the different cell types combining the results for the seven brain regions analyzed. The color scale indicates the significance (blue to red as the significance increases), whereas the size shows the number of genes in that specific enriched class. Page 1: Upregulated and Downregulated genes (same as Figure 4). Page 2: Upregulated genes. Page 3: Downregulated genes.

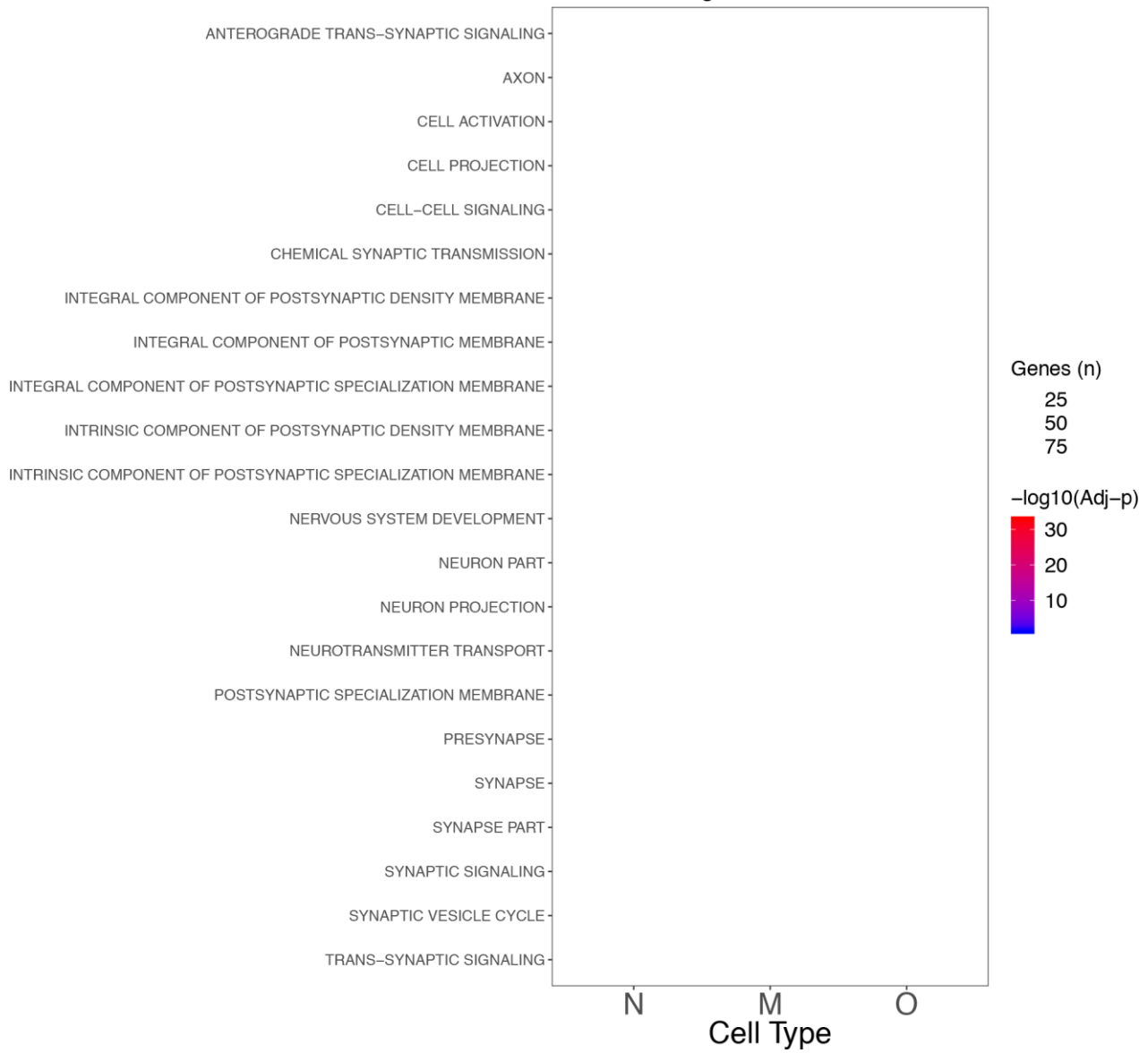
All Genes: TCX



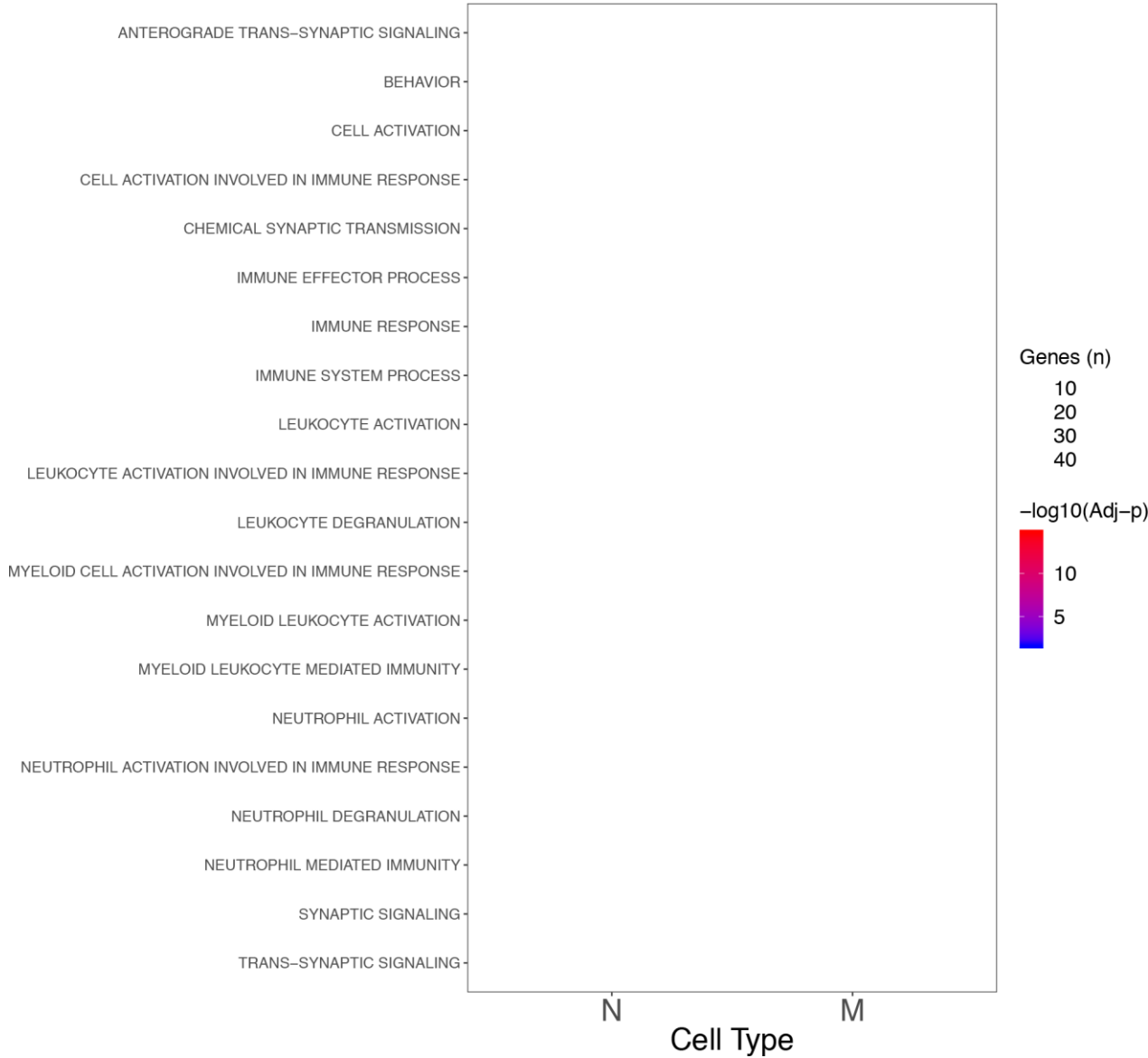
Upregulated Genes: TCX



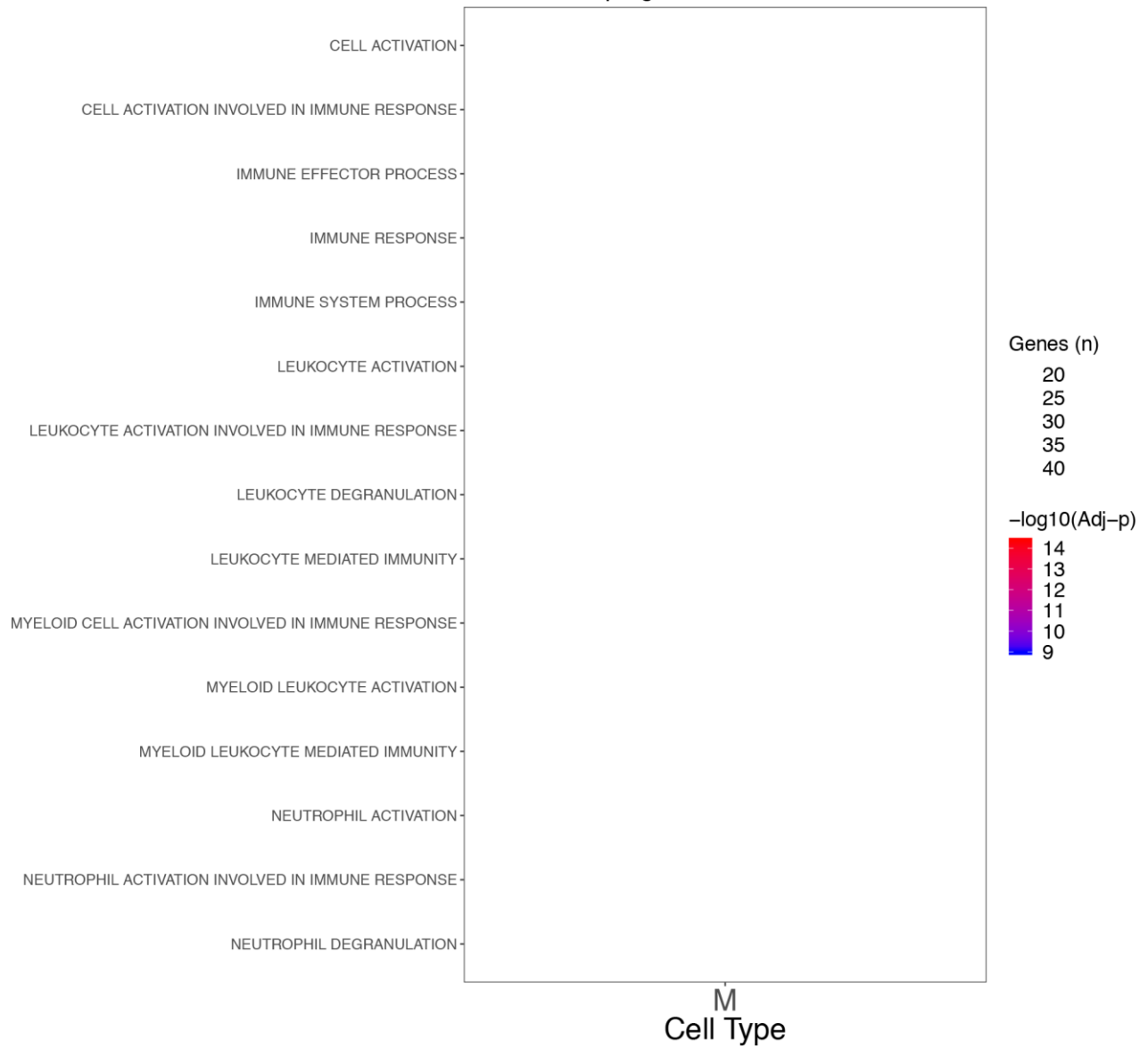
Downregulated Genes: TCX



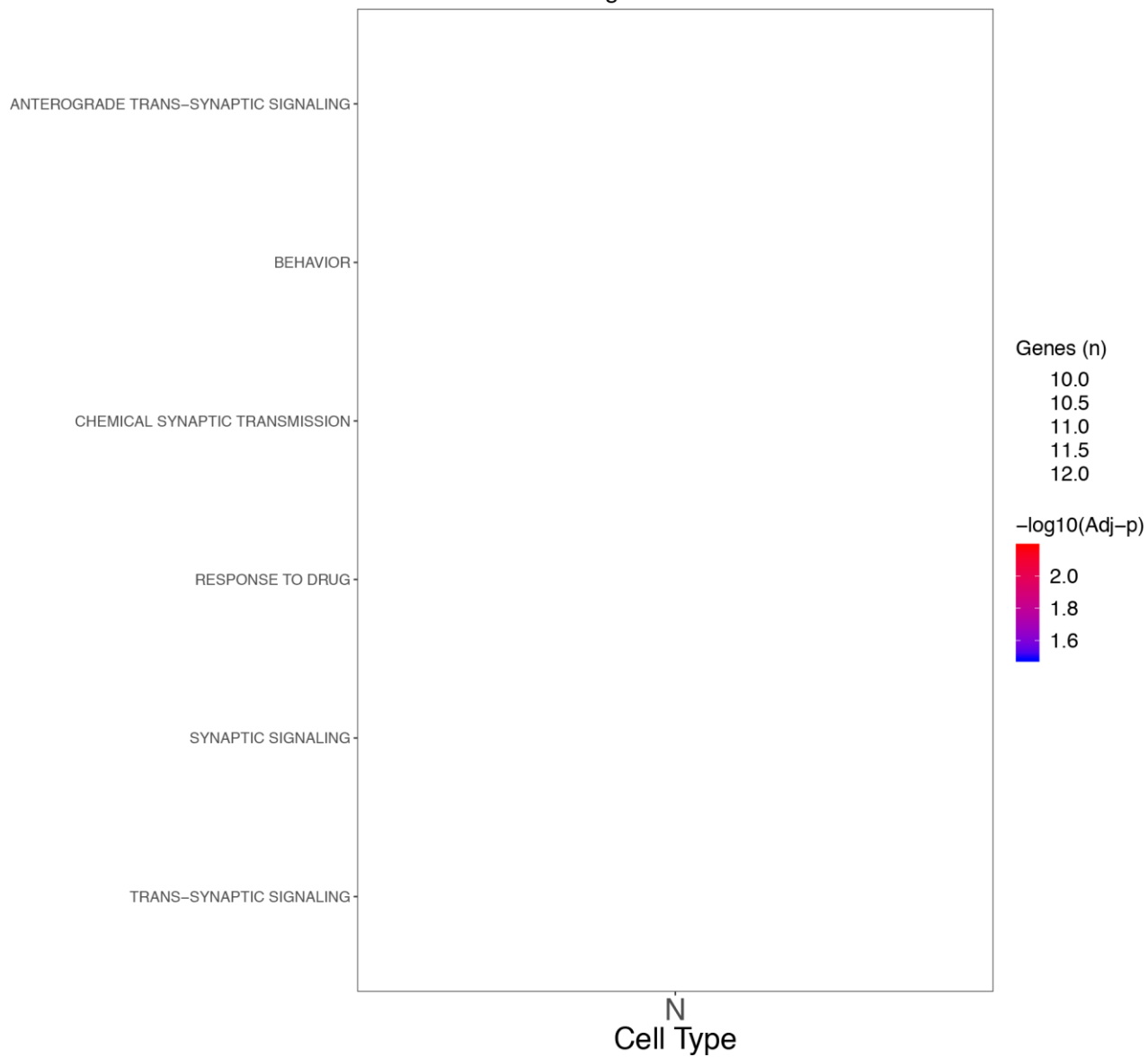
All Genes: STG



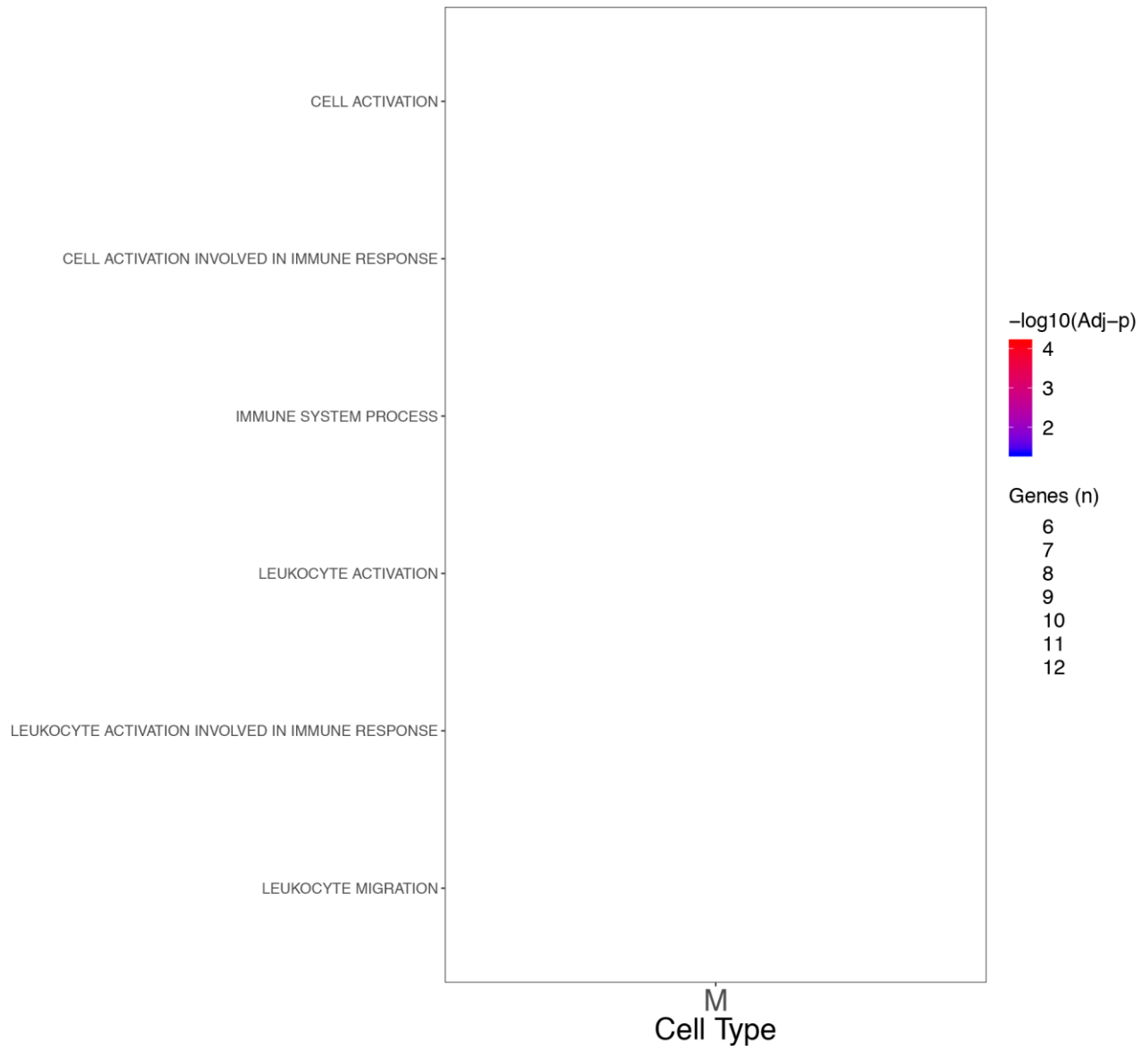
Upregulated Genes: STG



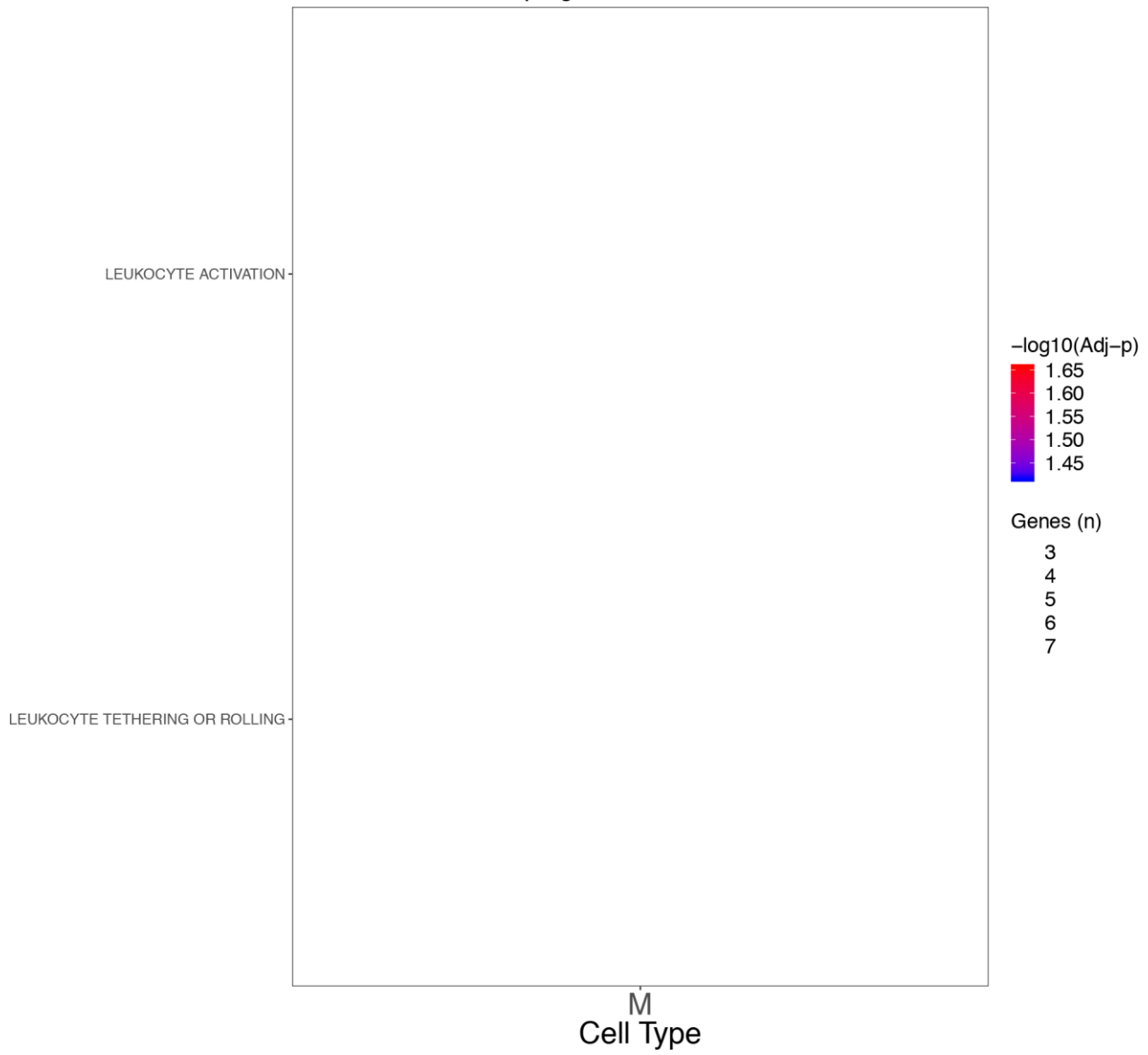
Downregulated Genes: STG



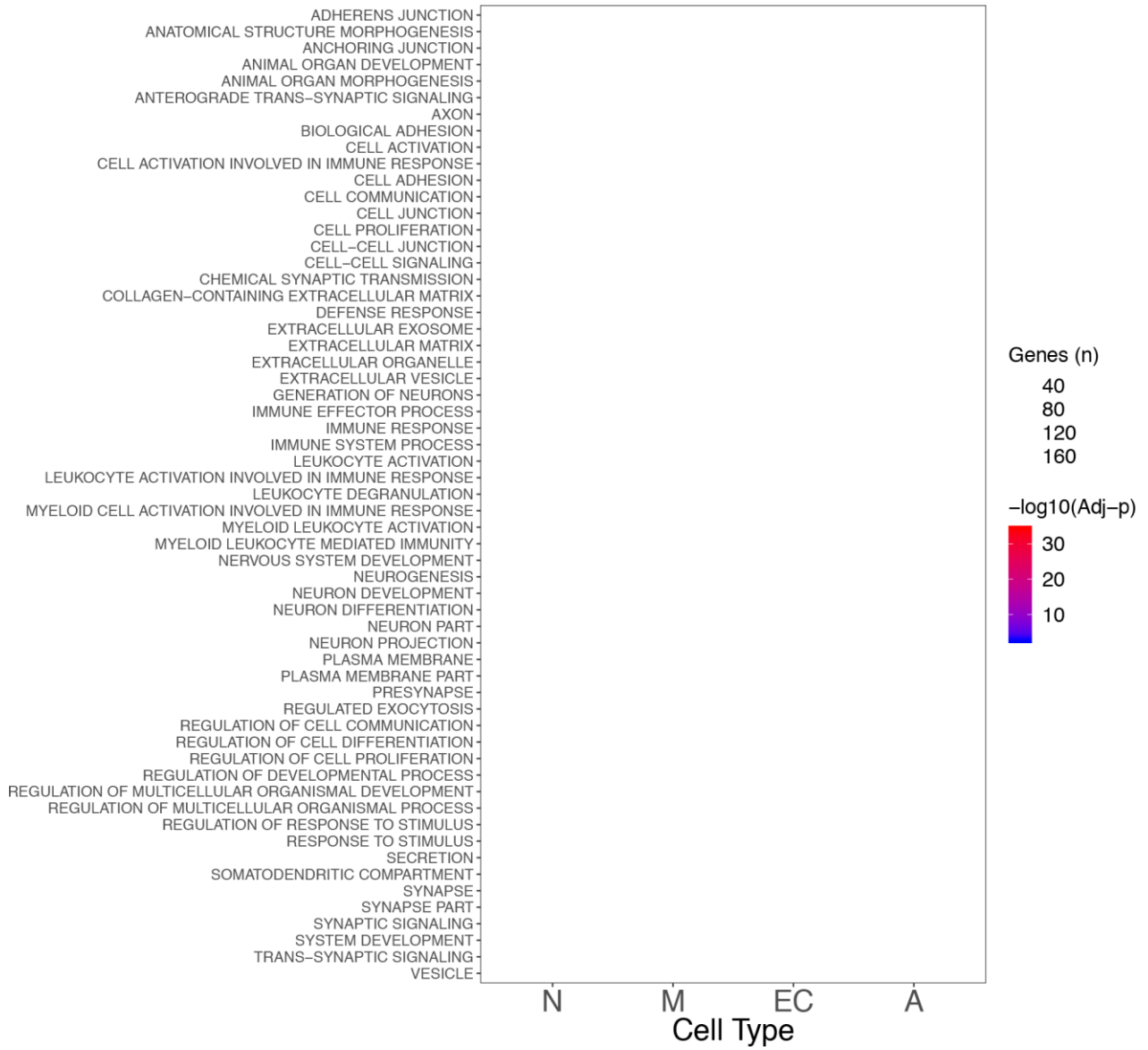
All Genes: IFG



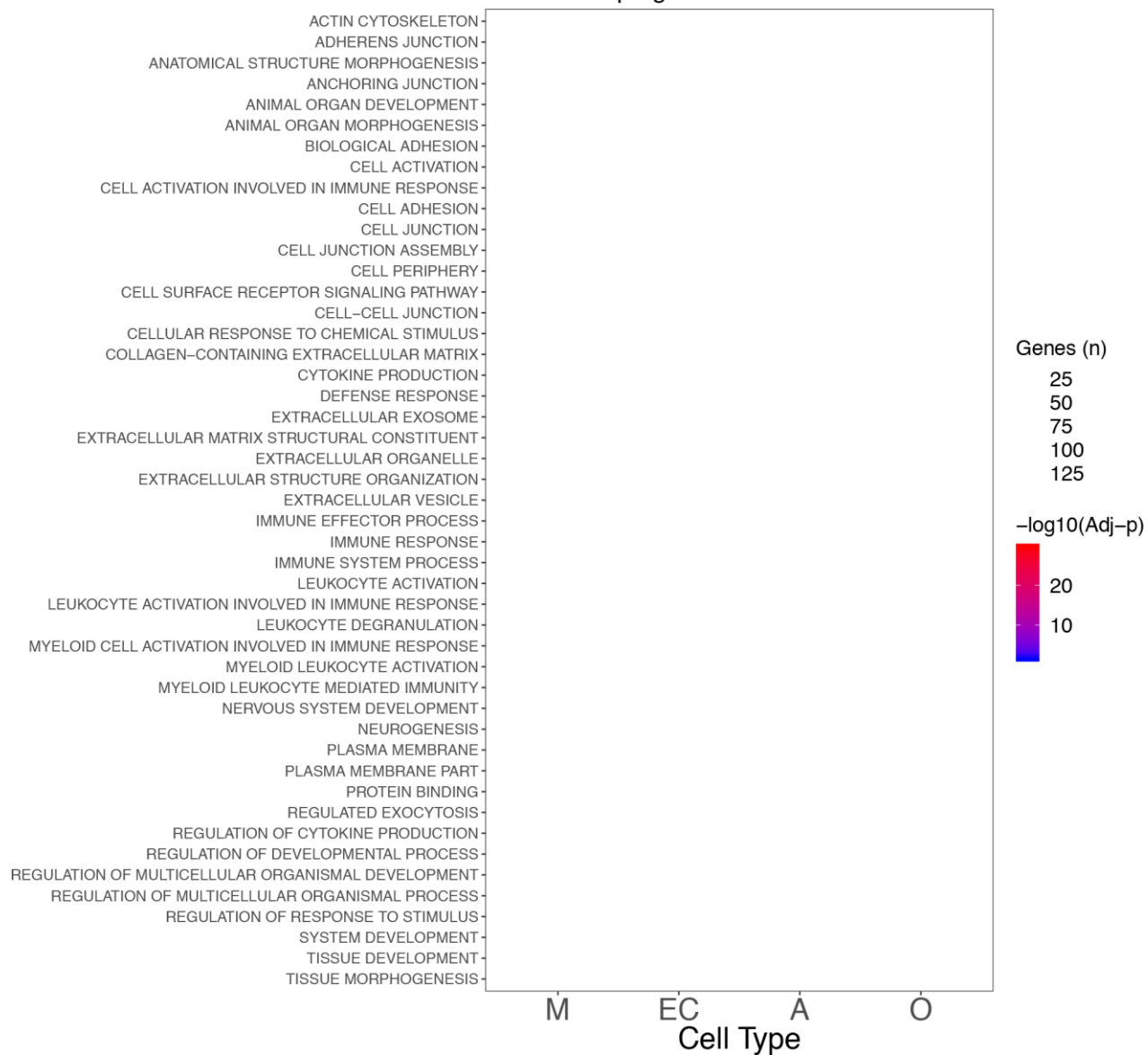
Upregulated Genes: IFG



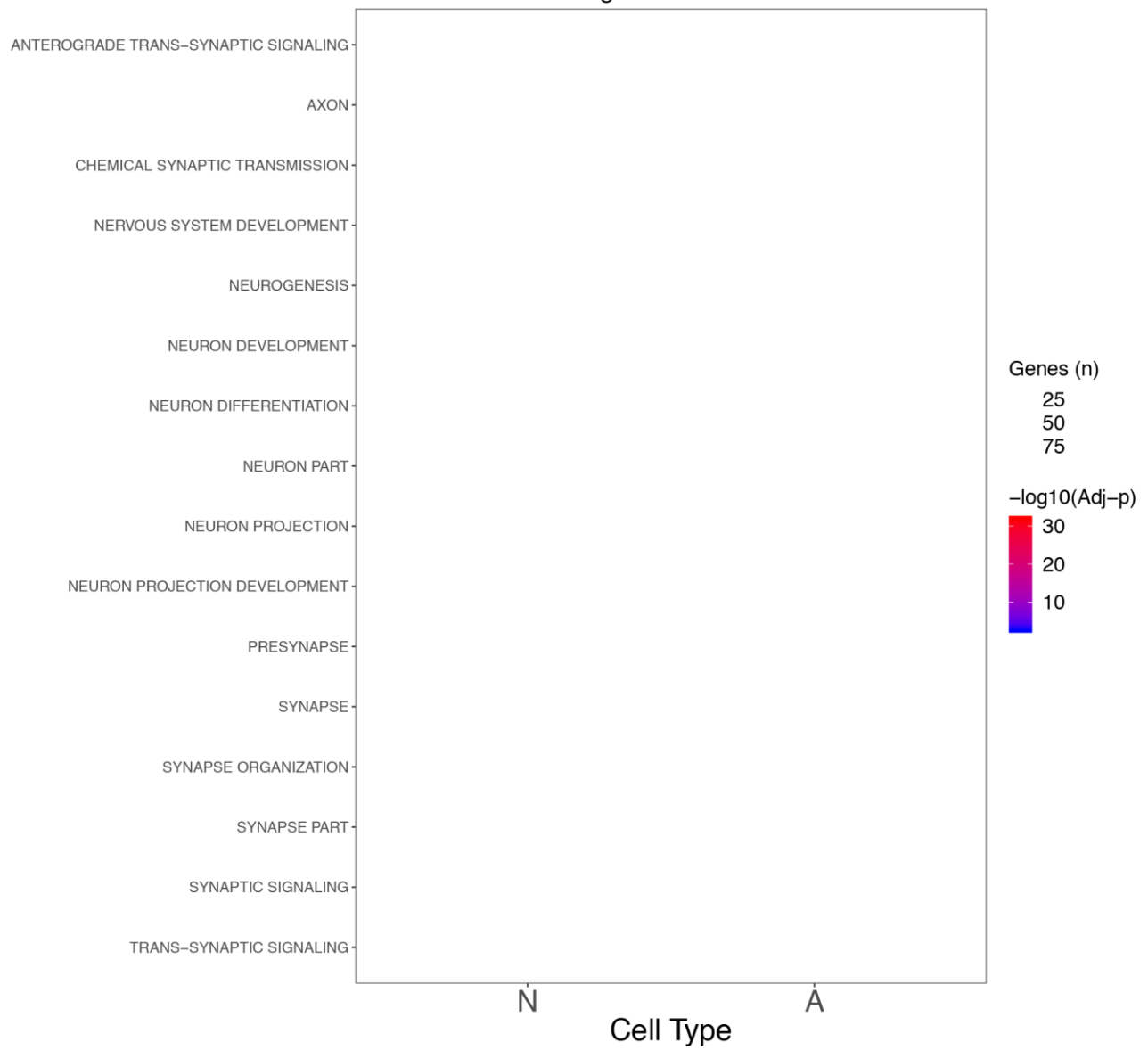
All Genes: PHG



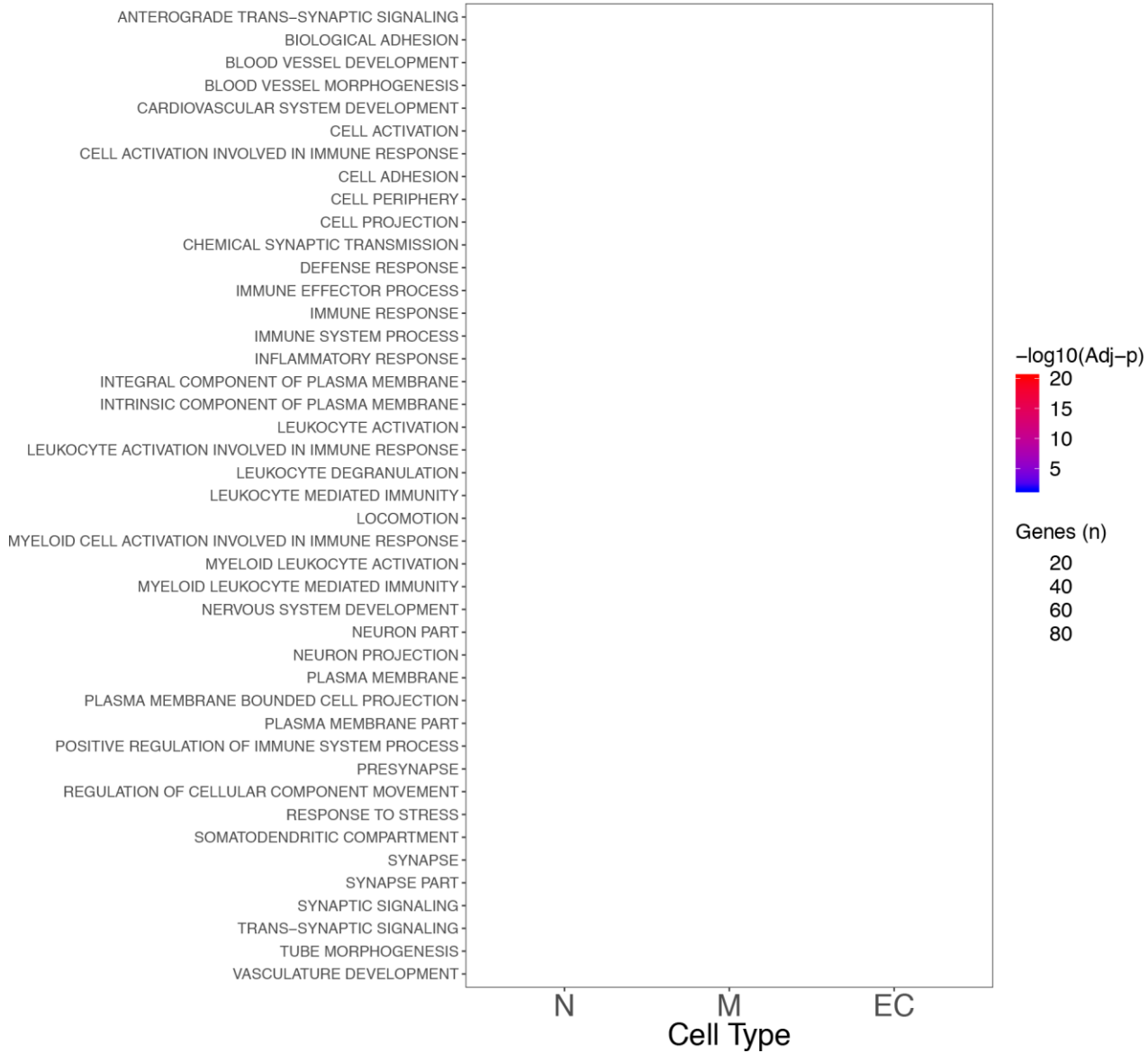
Upregulated Genes: PHG

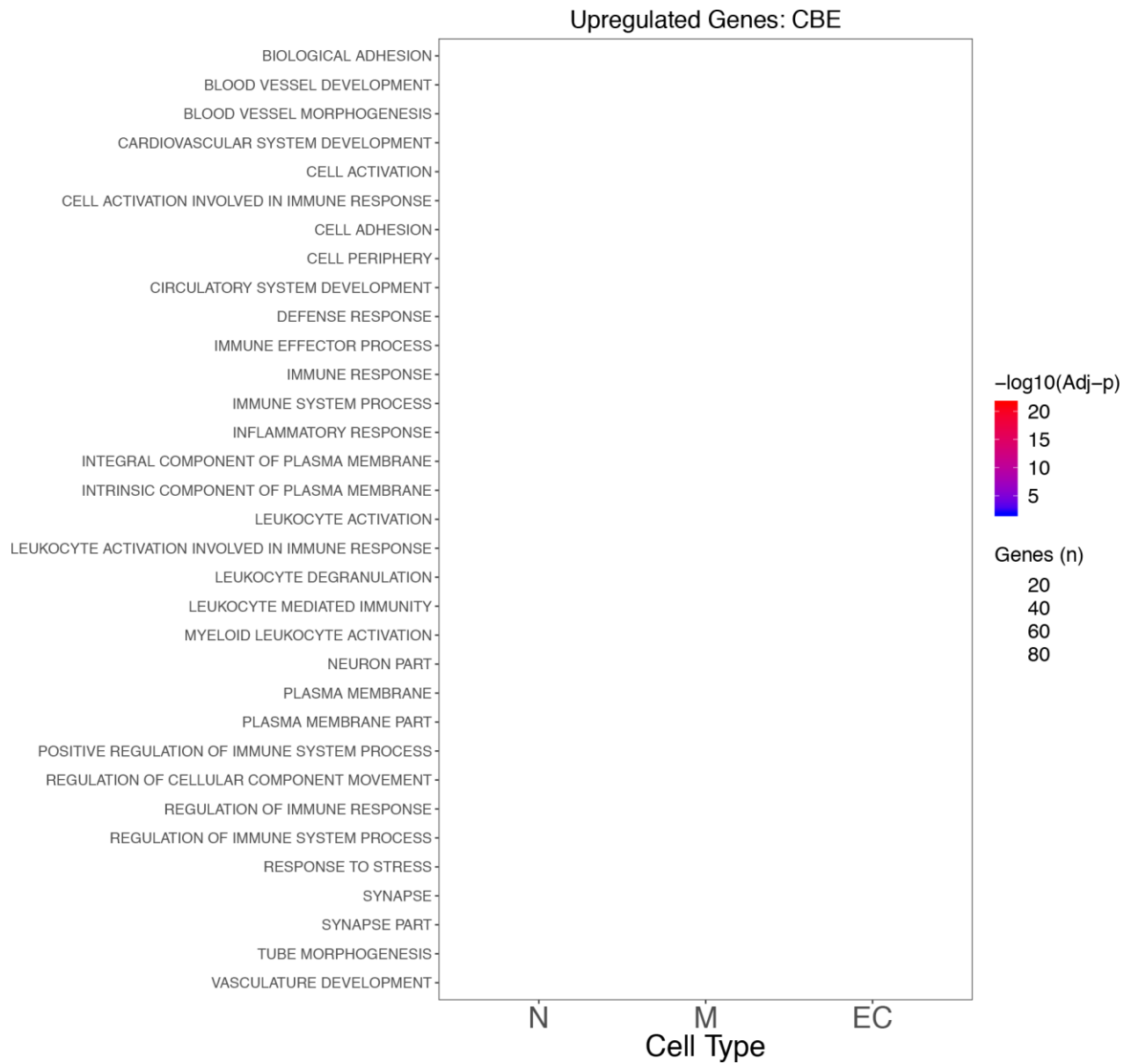


Downregulated Genes: PHG



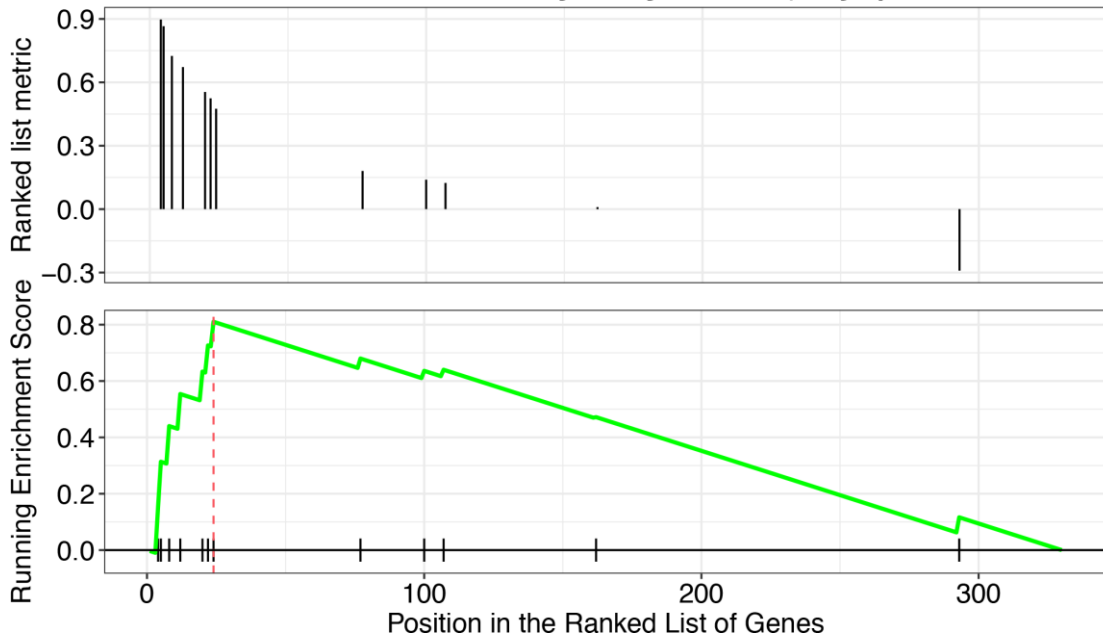
All Genes: CBE



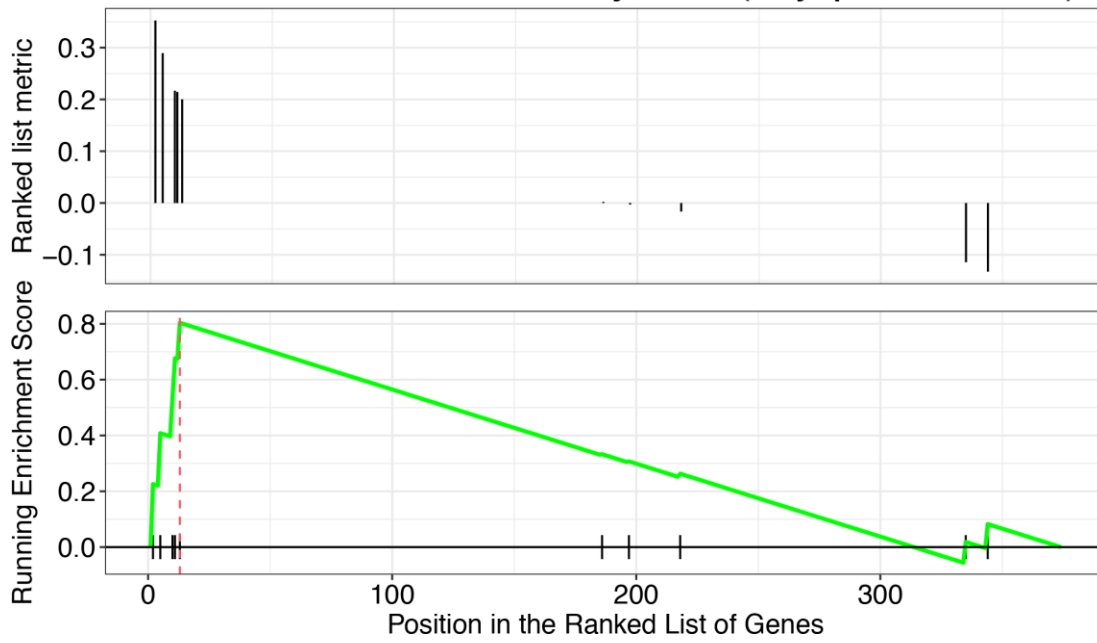


Supplementary Figure 7 (13 pages). Top 15 significant GO classes identified in the different cell types in each of the seven brain regions analyzed. The color scale indicates the significance (blue to red as the significance increases), whereas the size indicates the number of genes in that specific enriched class.

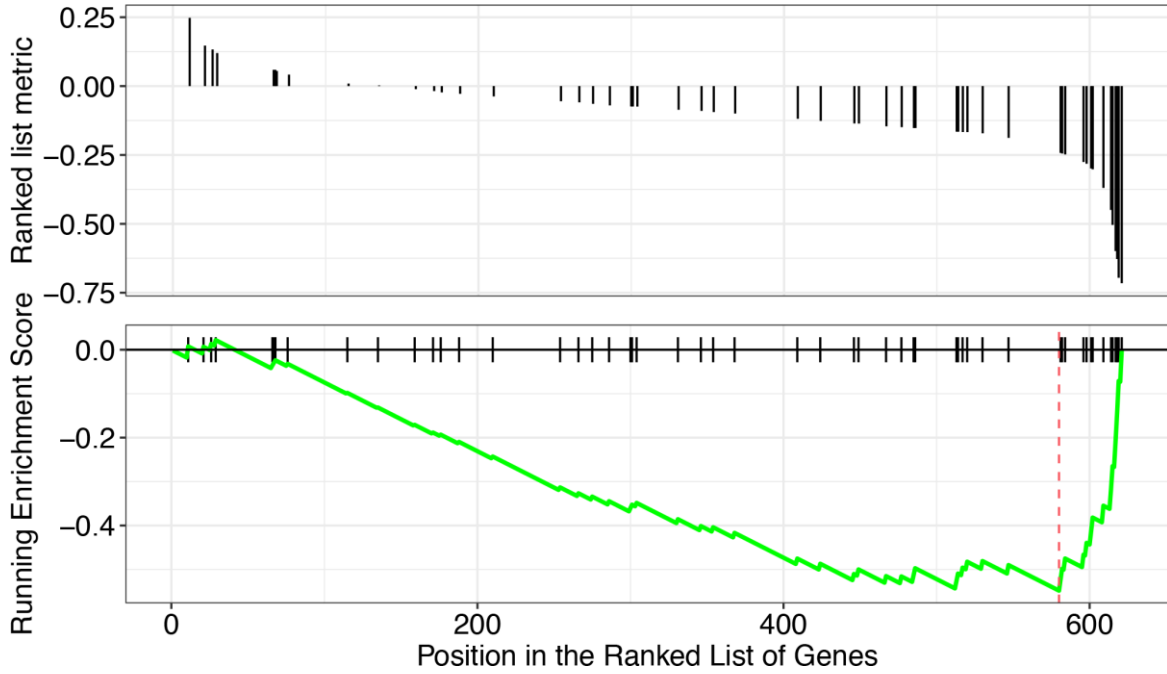
TCX – O: Diseases of Glycosylation (adj-p = 8.5E-03)



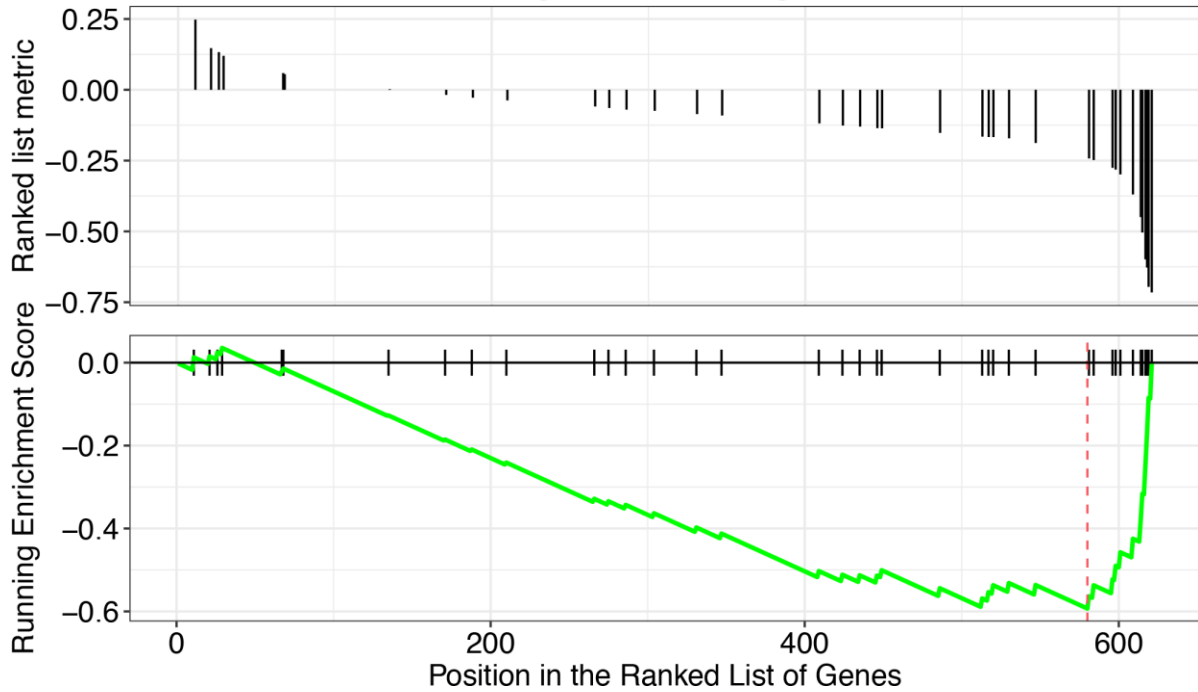
FP – A: Innate Immune System (adj-p = 5.6E-03)



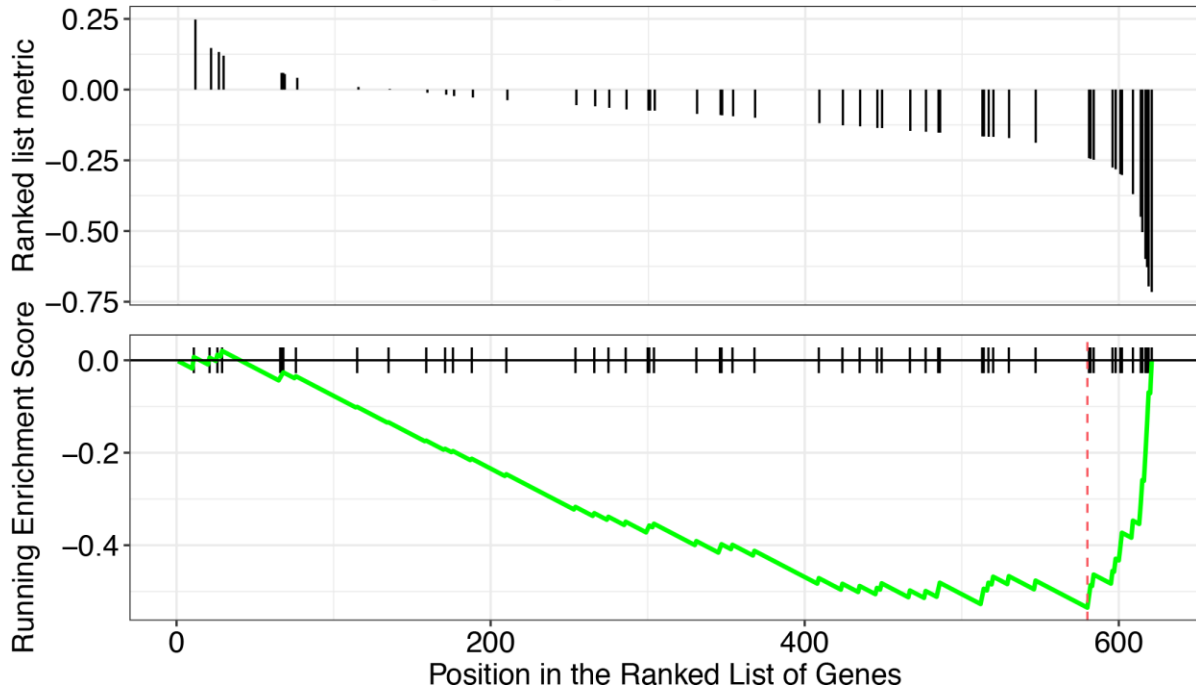
IFG – N – GPCR downstream sig. (adj-p = 1.5E-02)



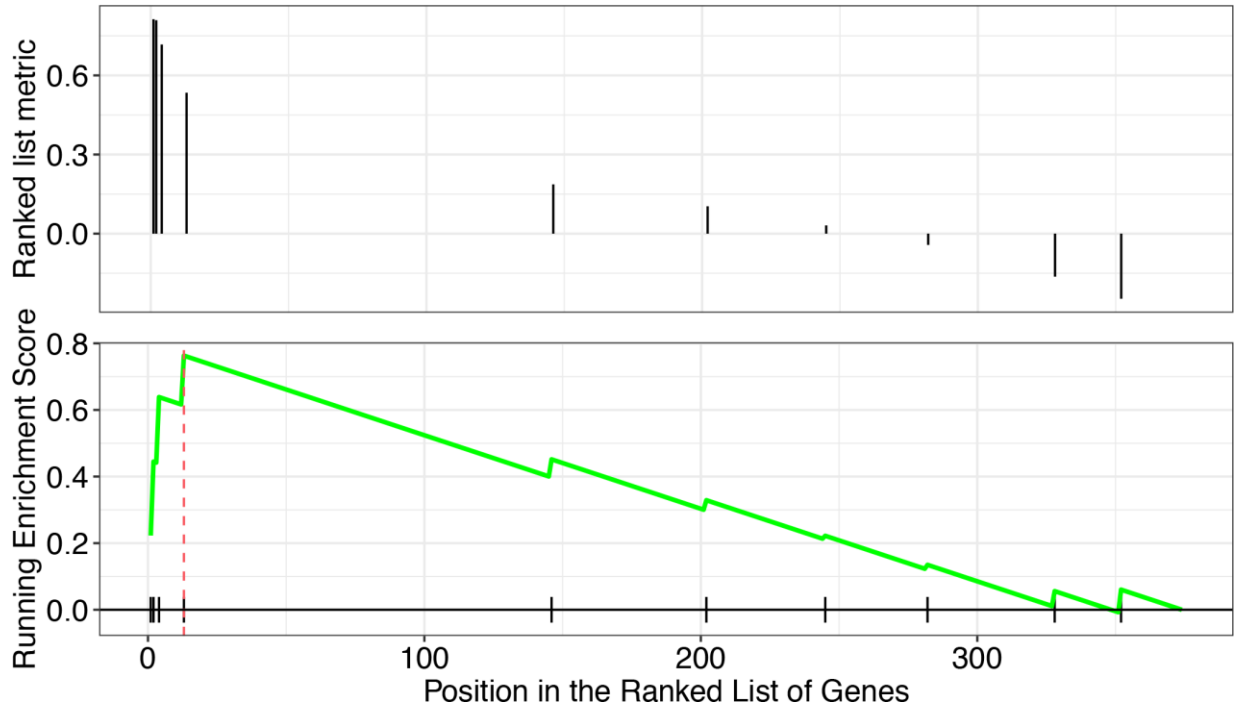
IFG – N – GPCR ligand binding (adj-p = 1.5E-02)



IFG – N – Signaling by GPCR (adj-p = 2.2E-02)



PHG – A – Innate Immune System (adj-p = 2.7E-02)



Supplementary Figure 8 (6 pages). Most relevant results from the GSEA by brain region.