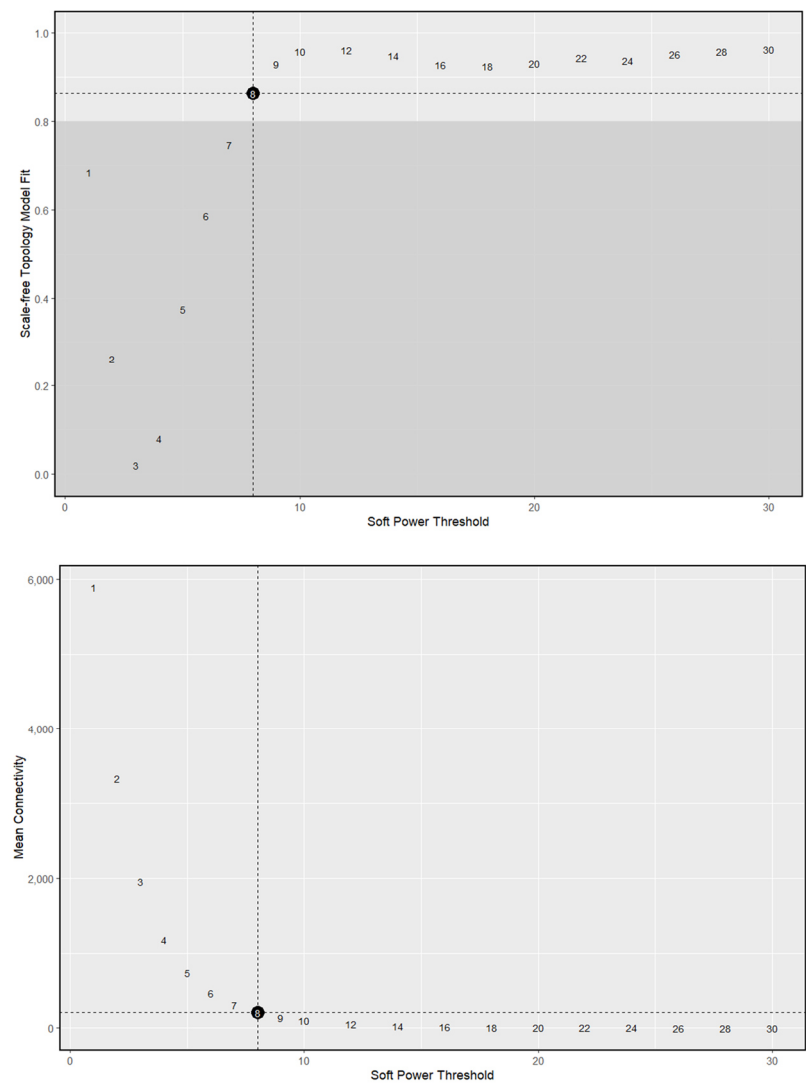


SUPPLEMENTARY FIGURES

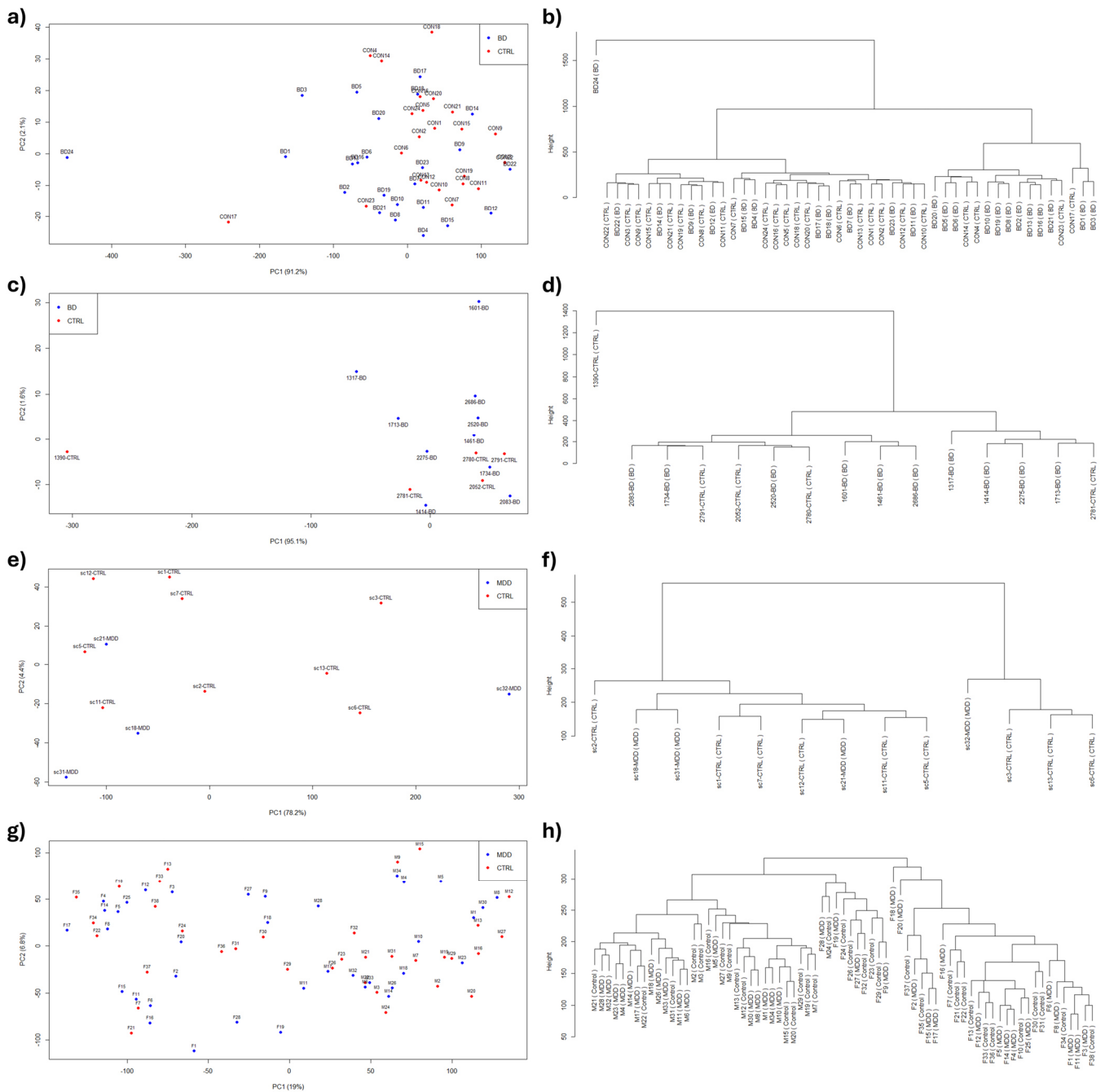
Cell-resolved cortical architecture and intercellular communication distinguish bipolar and major depressive disorders.

Giulietti et al, 2026

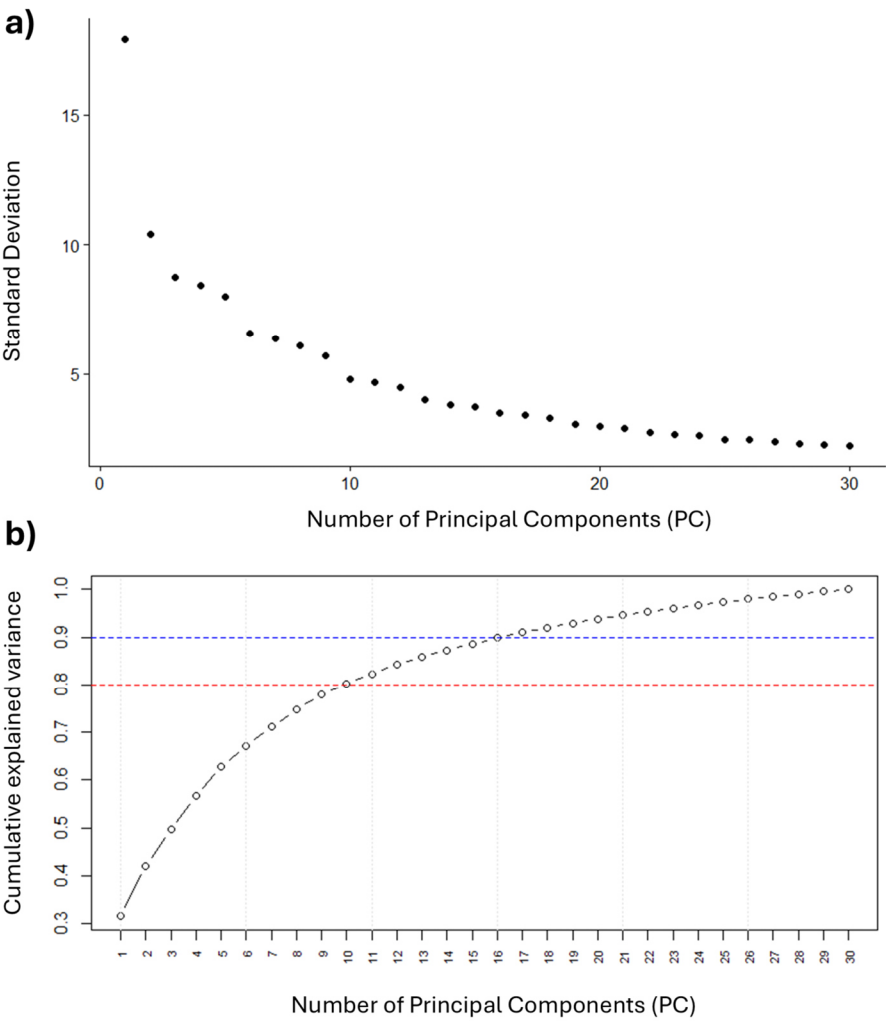
Supplementary Figure S1. Selection of the soft-thresholding power for hdWGCNA network construction. Scale-free topology analysis used to determine the optimal soft-thresholding power for network construction. The upper panel shows the relationship between soft-thresholding power and scale-free topology model fit (signed R^2), while the lower panel shows the relationship with mean connectivity. Consistent with standard WGCNA criteria, a value of $\beta = 8$ was selected as the best trade-off between achieving an approximately scale-free network topology and preserving sufficient network connectivity.



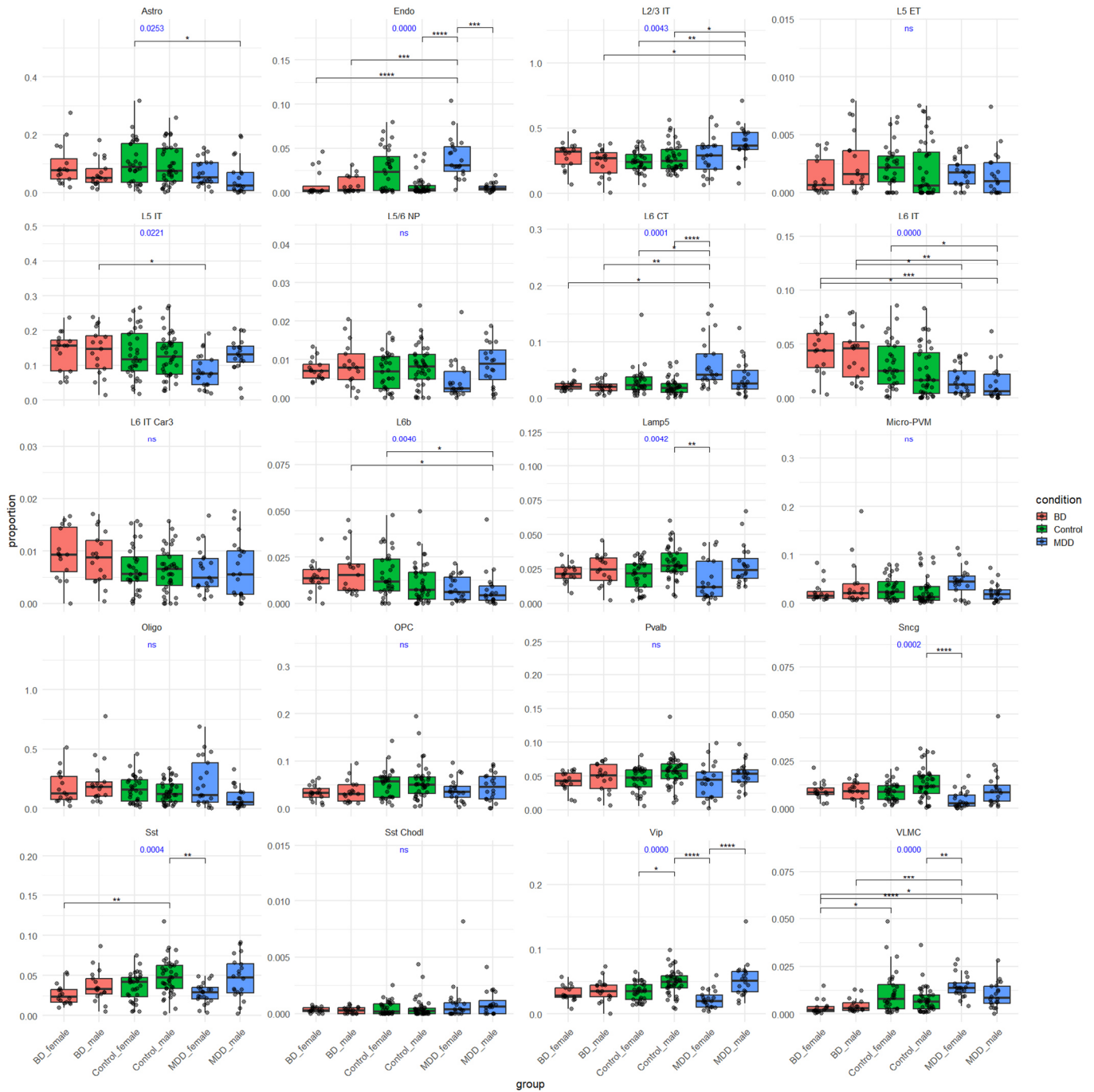
Supplementary Figure S2. Identification of outlier samples across datasets using pseudobulk PCA and hierarchical clustering. Principal component analysis (PCA; panels a, c, e, g) and hierarchical clustering (panels b, d, f, h) based on global gene expression profiles of pseudobulk data (aggregated raw counts per sample) were performed to assess sample-level variation in: (a–b) SZBDMulti-Seq, (c–d) MultiomeBrain, (e–f) PTSDBrainomics, and (g–h) GSE213982 datasets. Outlier samples BD24 in SZBDMulti-Seq (a–b) and 1390-ctrl in MultiomeBrain (c–d) were clearly distinguishable from the rest and excluded from downstream analyses. No evident outliers were detected in the PTSDBrainomics (e–f) and GSE213982 (g–h) datasets.



Supplementary Figure S3. (a) Elbow plot displaying the variance explained by each principal component (PC) across the dataset. This plot is used to identify the number of PCs to retain for downstream dimensionality reduction. (b) Cumulative variance explained by increasing numbers of PCs, providing a visual overview of how the dataset’s total variance is distributed among components. The first 16 PCs capture approximately 90% of the total variance.

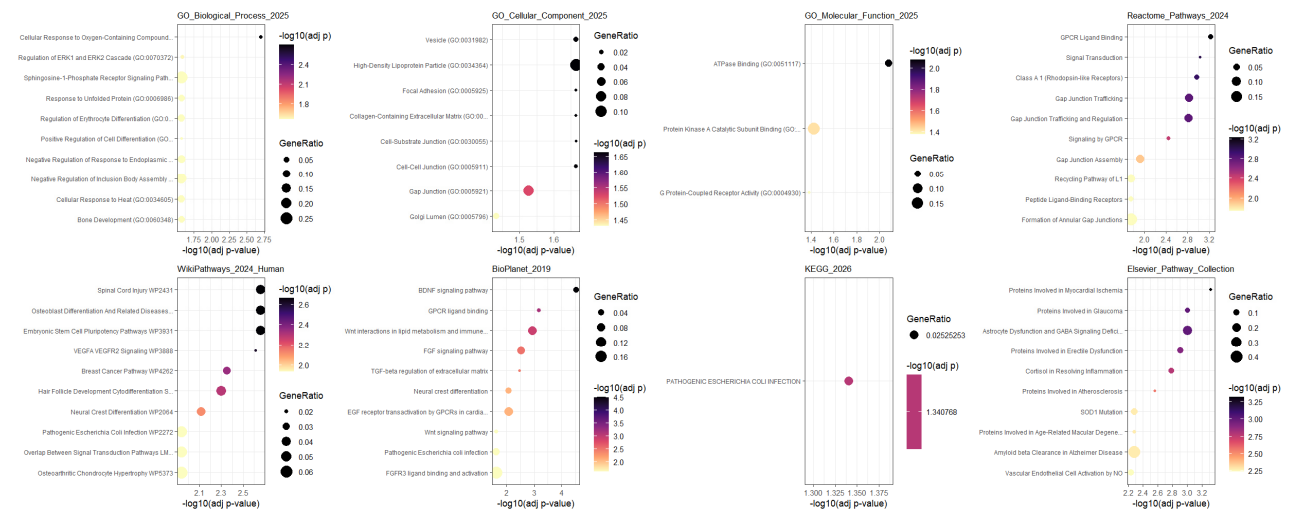


Supplementary Figure S5. Cell type proportion differences across diagnostic and sex groups (BD-female, BD-male, Control-female, Control-male, MDD-female, MDD-male). Box plots show the distribution of relative cell type proportions for each of the 20 identified cell types across the six groups defined by diagnosis and sex. Blue p-values correspond to Kruskal-Wallis tests assessing overall differences across groups. Significant pairwise comparisons from Dunn's post hoc test are indicated using the following notation: ns = not significant; * = $p < 0.05$; ** = $p < 0.01$; *** = $p < 0.001$; **** = $p < 0.0001$.

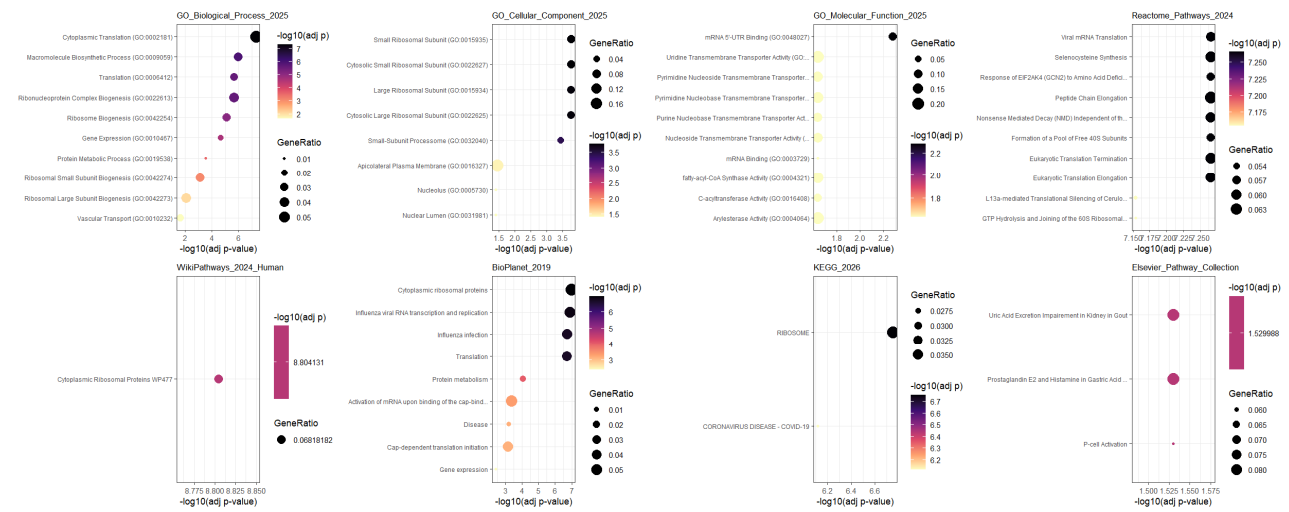


Supplementary Figure S6. Functional enrichment of (a) upregulated genes in BD vs MDD, (b) downregulated genes in BD vs MDD, and (c) downregulated genes in MDD vs CTRL. Dot plots show the top enriched terms across multiple gene set libraries for differentially expressed genes. Dot size represents the gene ratio (fraction of input genes overlapping the gene set), and color intensity corresponds to $-\log_{10}$ -transformed adjusted p-value. Only the top 10 terms per database are shown for clarity. Enrichment was performed only for DEG lists containing at least 4 genes.

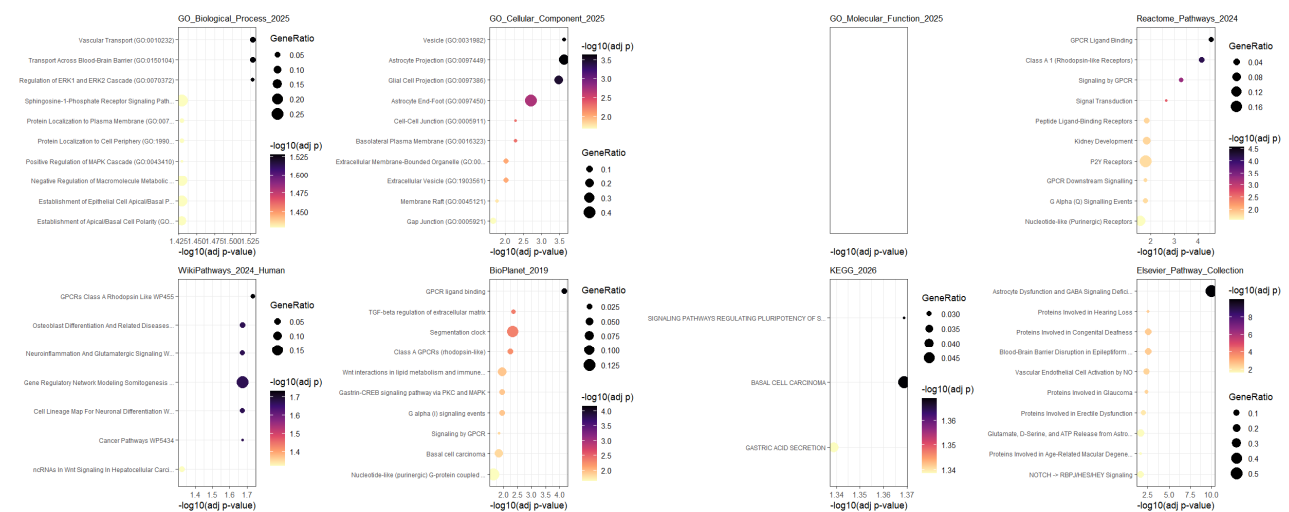
a) Functional enrichment of upregulated genes in BD vs MDD



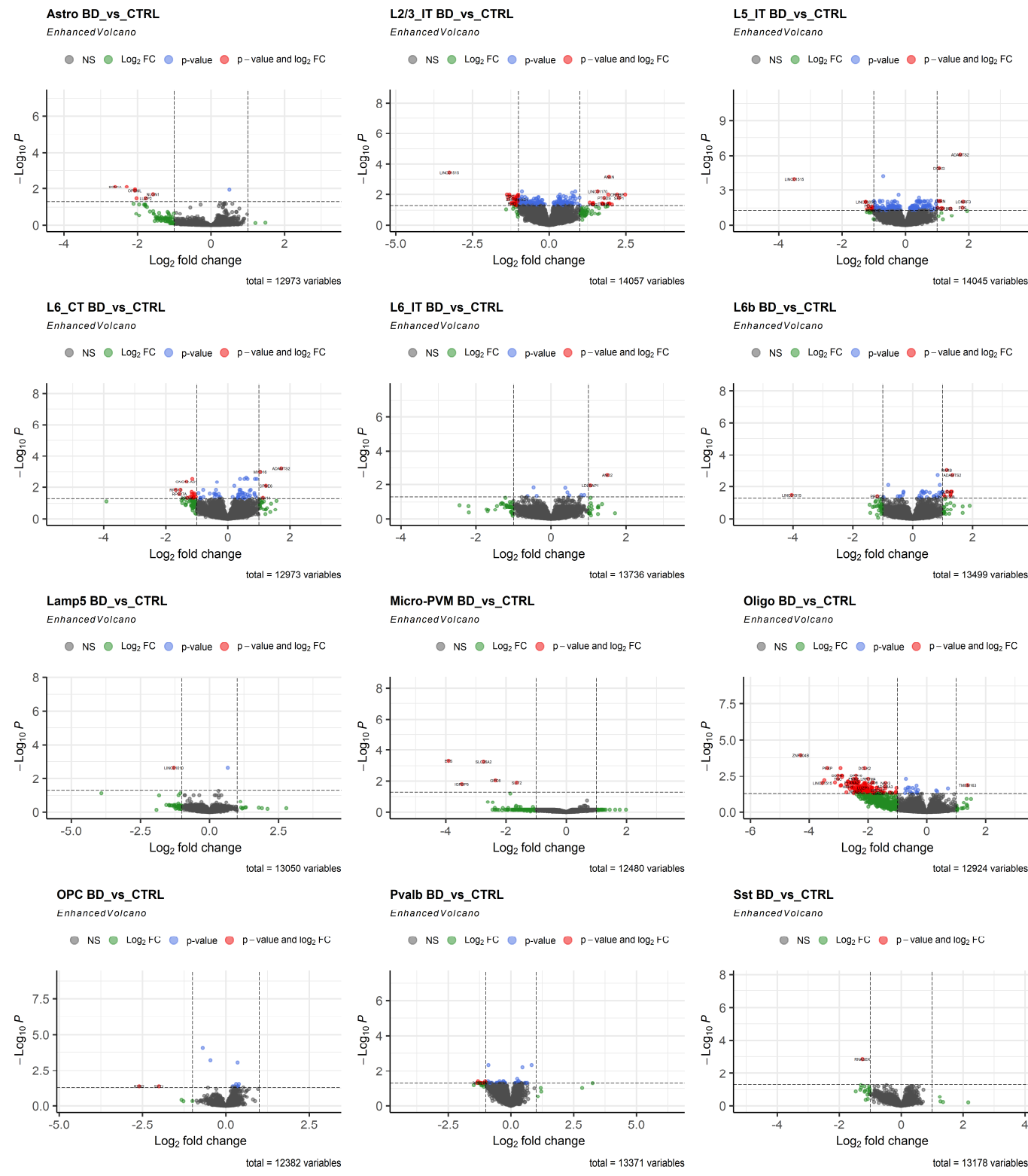
b) Functional enrichment of downregulated genes in BD vs MDD



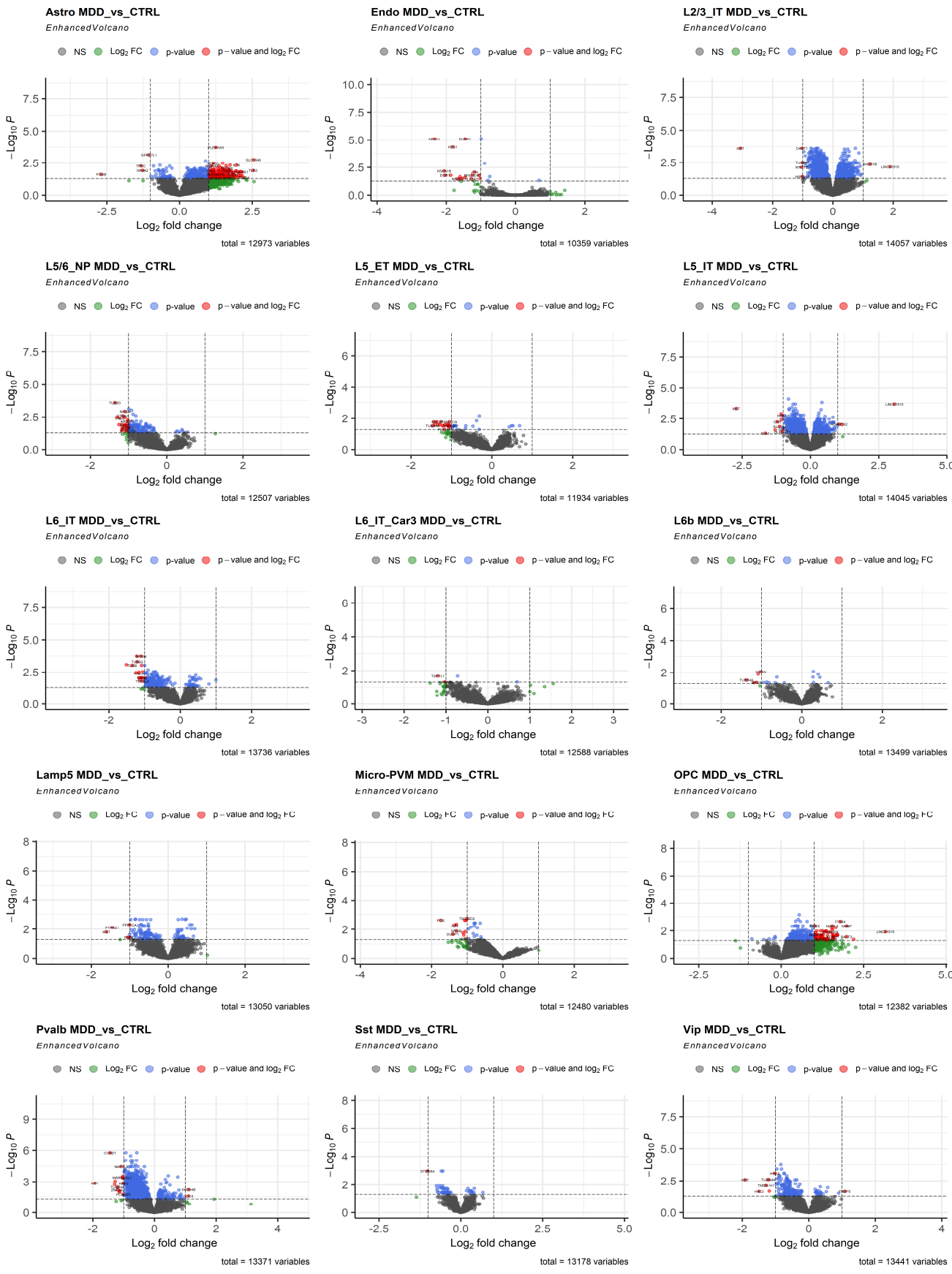
c) Functional enrichment of downregulated genes in MDD vs CTRL



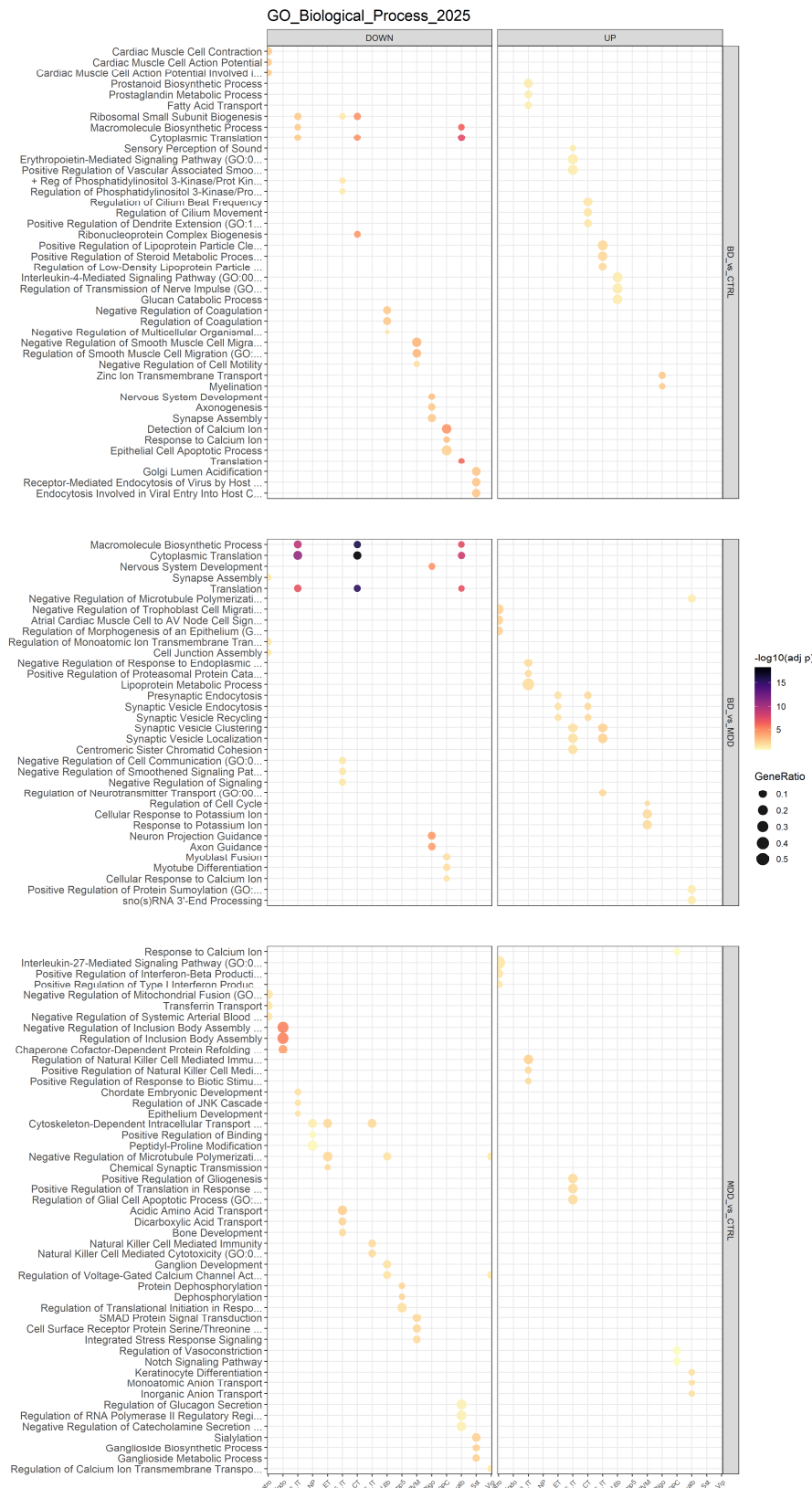
Supplementary Figure S7. Cell-type-specific volcano plots of differential gene expression in BD vs CTRL comparisons. Each point represents a gene, plotted according to its log2 fold change (x-axis) and adjusted p-value (y-axis, $-\log_{10}$ scale). Genes with FDR < 0.05 are highlighted. Volcano plots were generated independently for each cell type using pseudobulk counts and DESeq2-based differential expression analysis. Only comparisons with significant differential expression are shown.



Supplementary Figure S8. Cell-type-specific volcano plots of differential gene expression in MDD vs CTRL comparisons. Each point represents a gene, plotted according to its log2 fold change (x-axis) and adjusted p-value (y-axis, $-\log_{10}$ scale). Genes with FDR < 0.05 are highlighted. Volcano plots were generated independently for each cell type using pseudobulk counts and DESeq2-based differential expression analysis. Only comparisons with significant differential expression are shown.



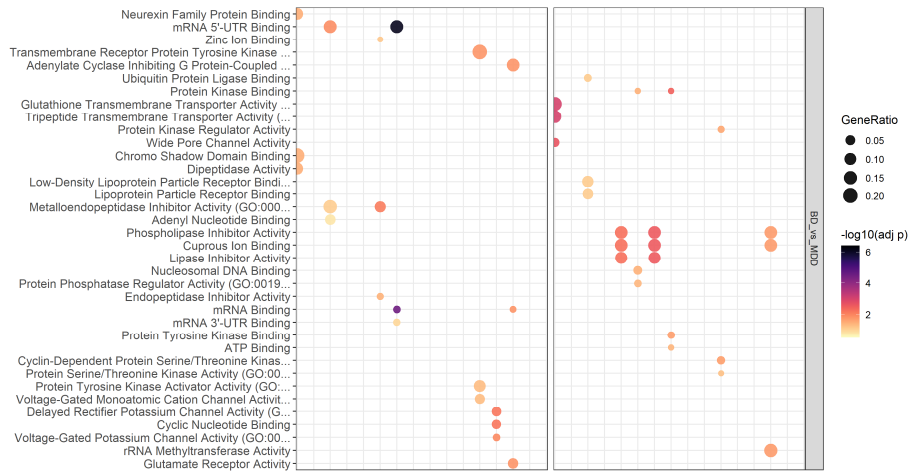
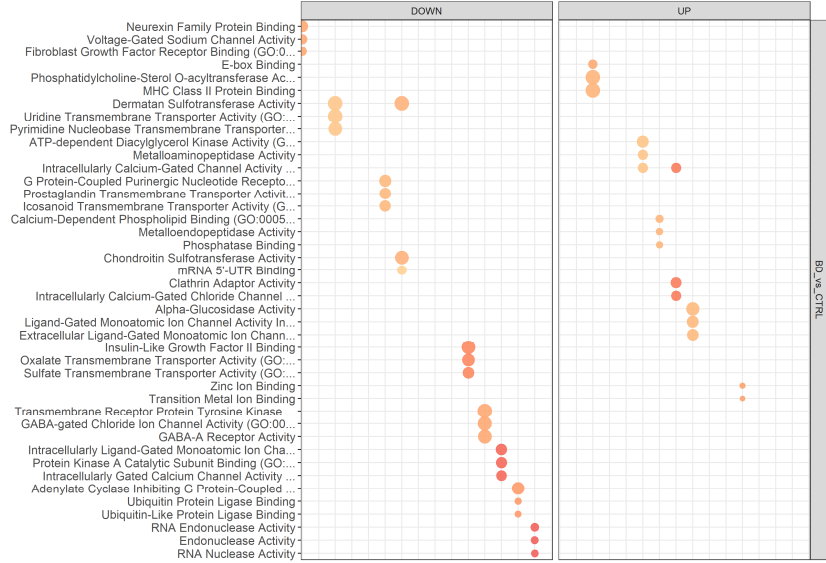
Supplementary Figure S9. Cell type-specific pathway enrichment across diagnostic contrasts in Gene Ontology Biological Process (BP), Cellular Component (GO-CC), Molecular Function (GO-MF), KEGG, Reactome, WikiPathways, BioPlanet, and the Elsevier Pathway Collection libraries. Dot plots summarizing functional enrichment results obtained from differentially expressed genes stratified by cell type, diagnostic contrast, and direction of regulation. For each comparison, only significantly enriched terms (adjusted $P < 0.05$) are shown, with up to the top 3 terms retained per library. The x-axis represents the $-\log_{10}$ adjusted P value, dot size indicates the gene ratio (overlap between input gene list and gene set), and color intensity reflects enrichment significance.



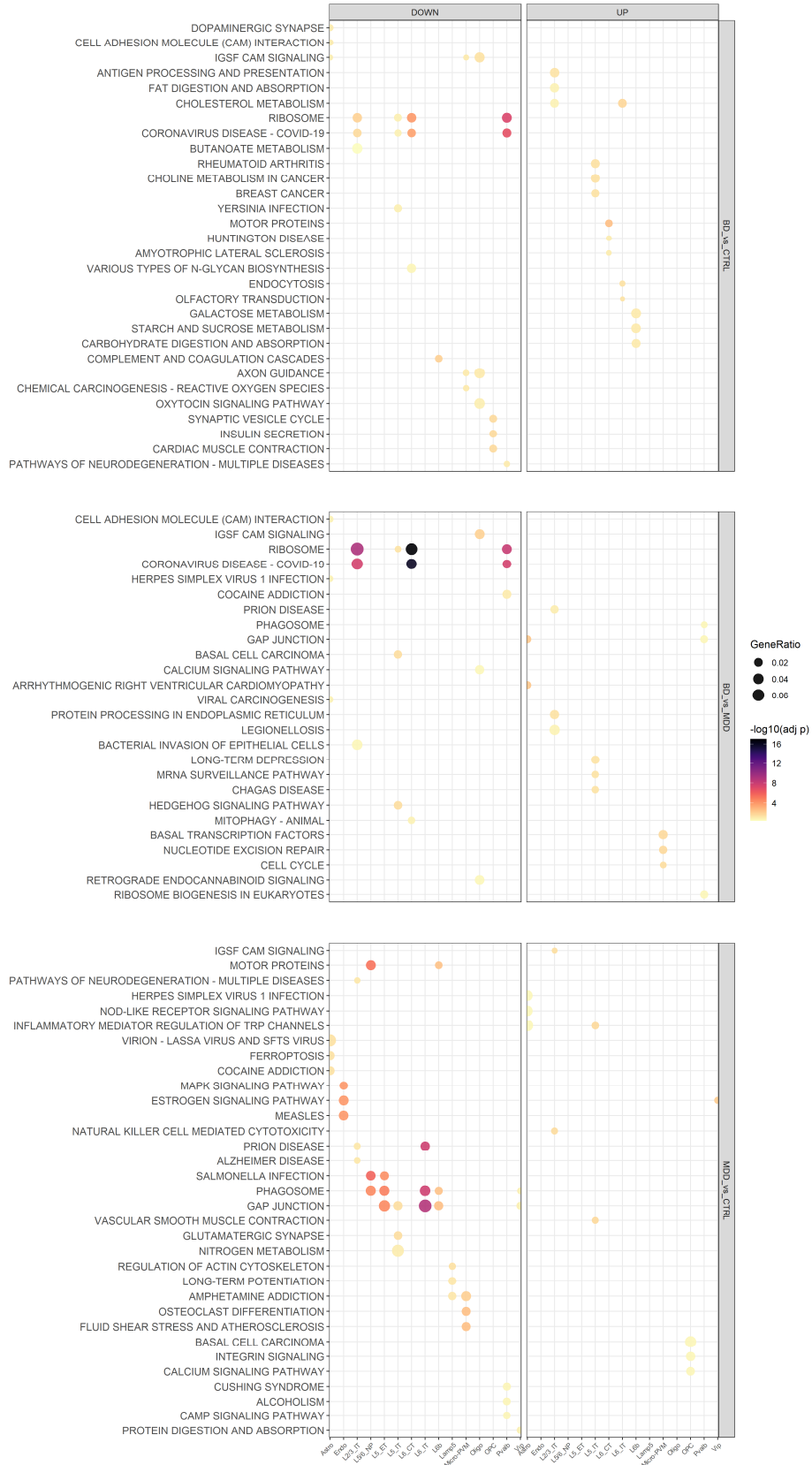
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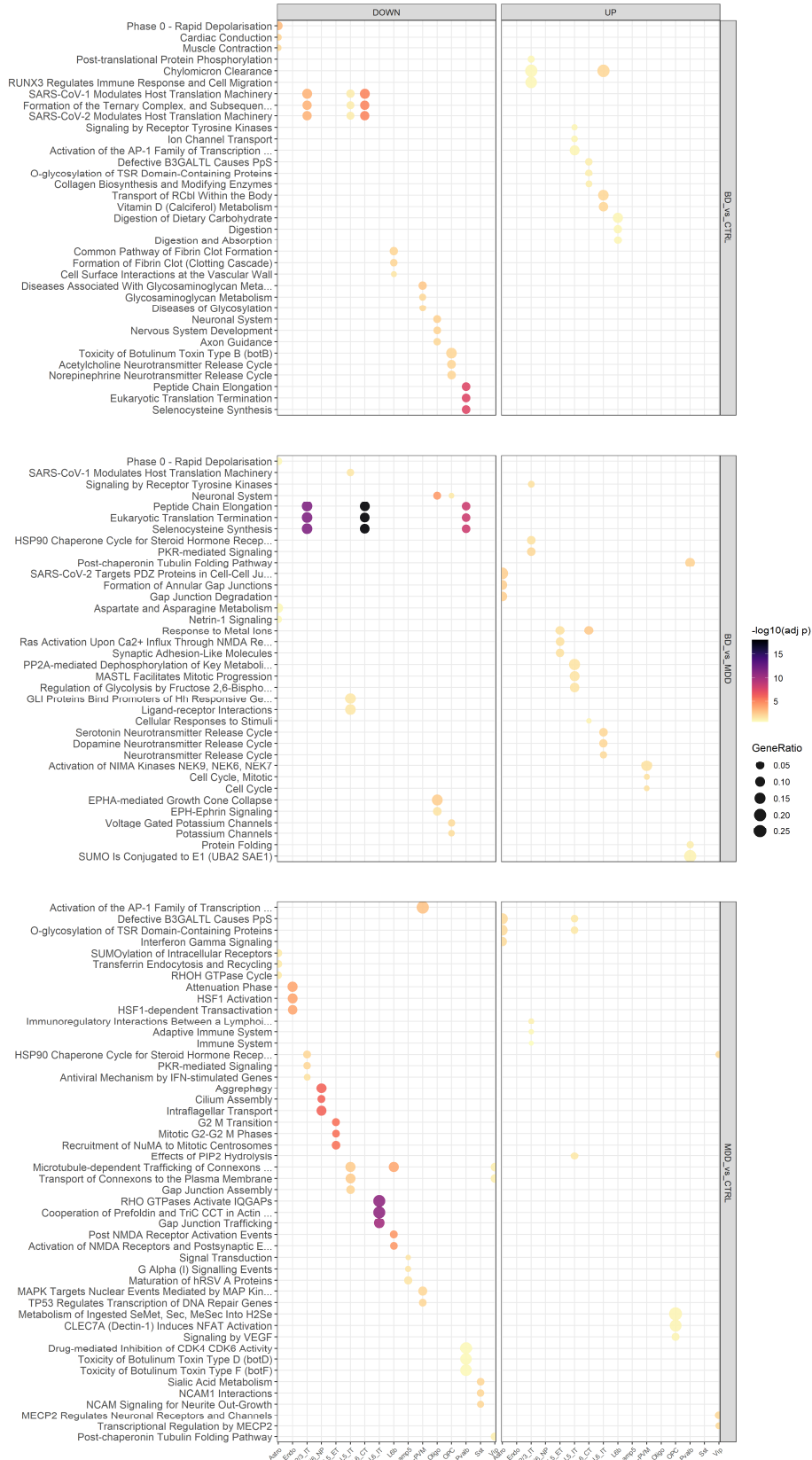
GO_Molecular_Function_2025



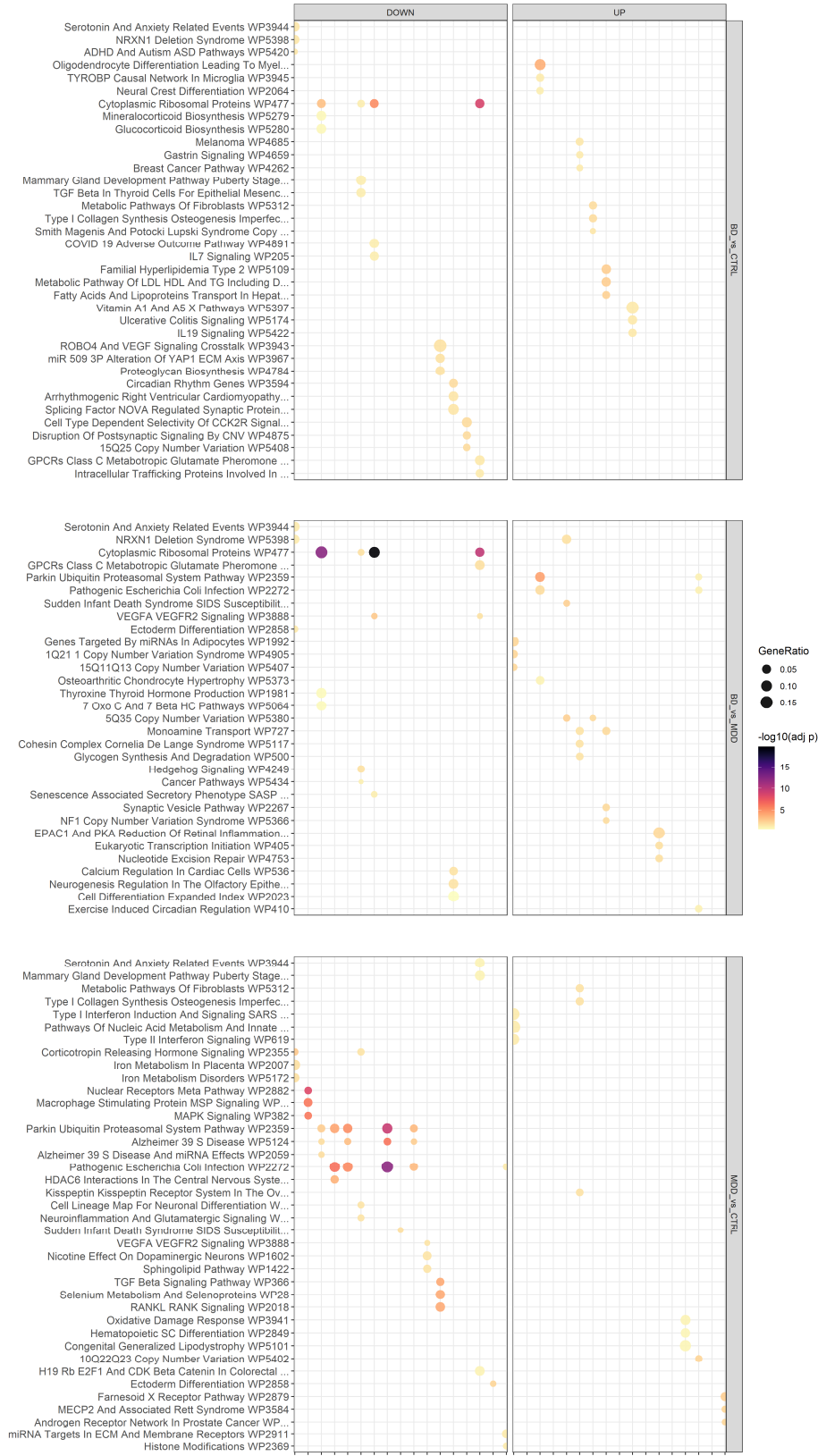
KEGG_2026



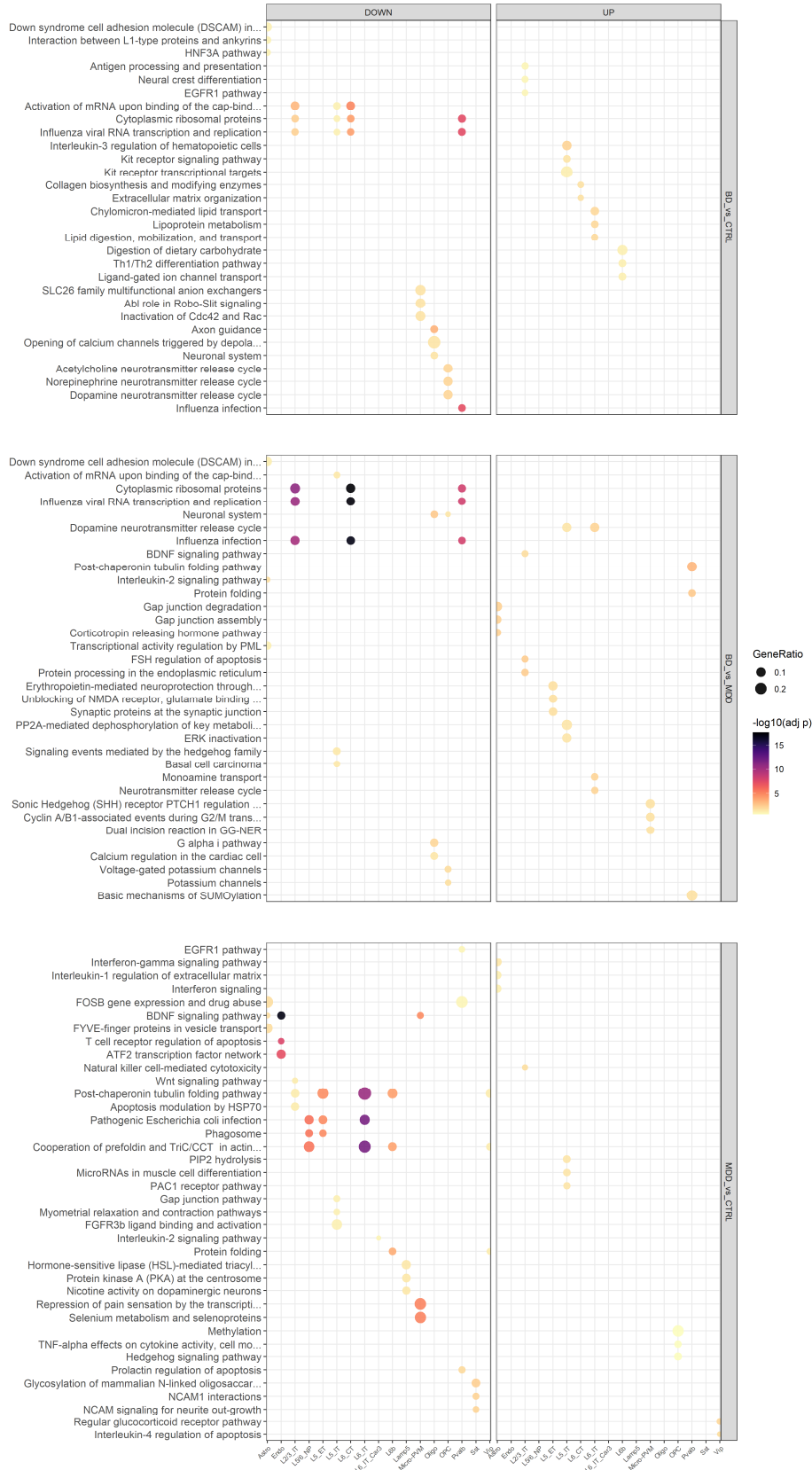
Reactome_Pathways_2024

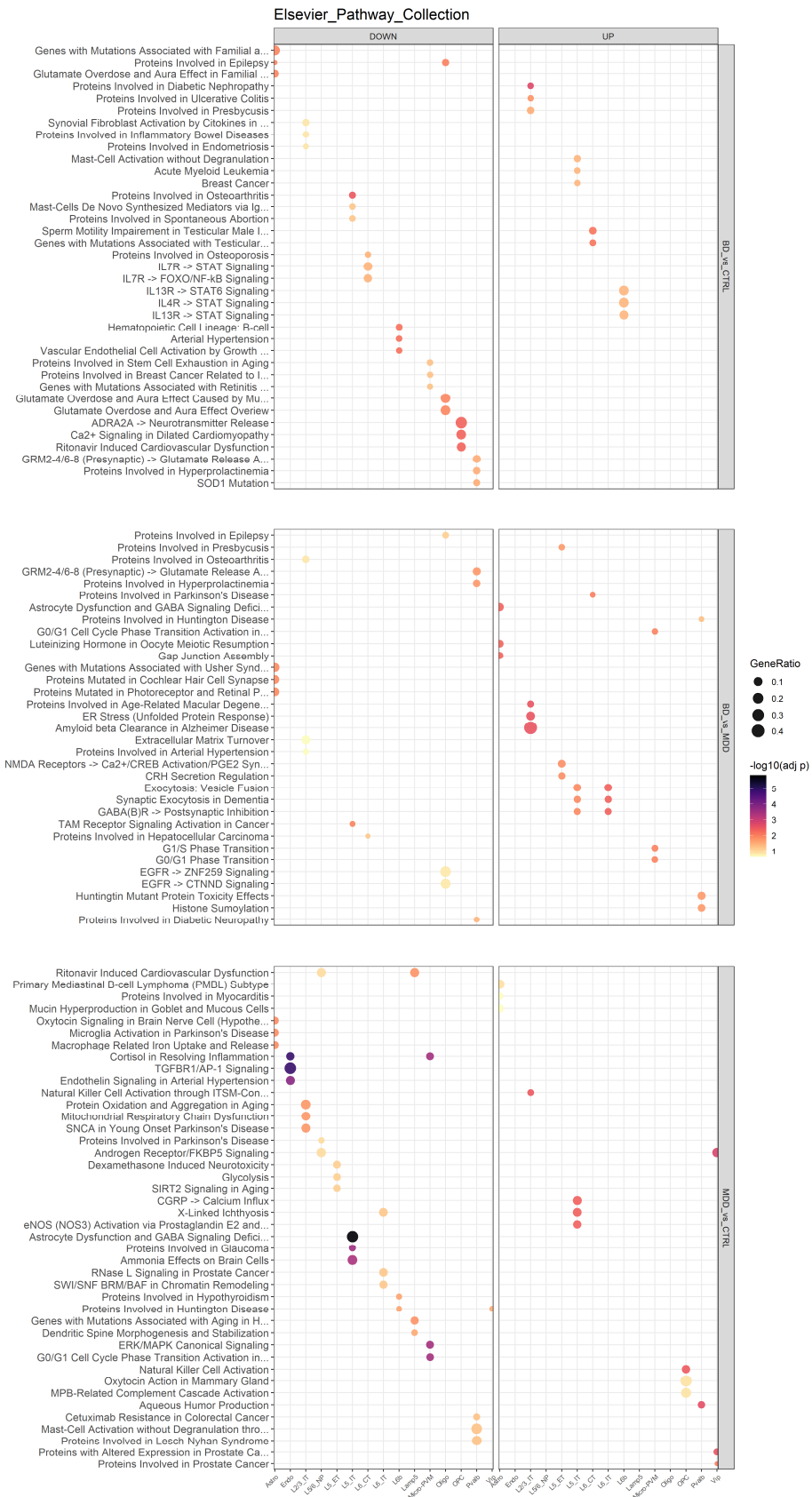


WikiPathways_2024_Human

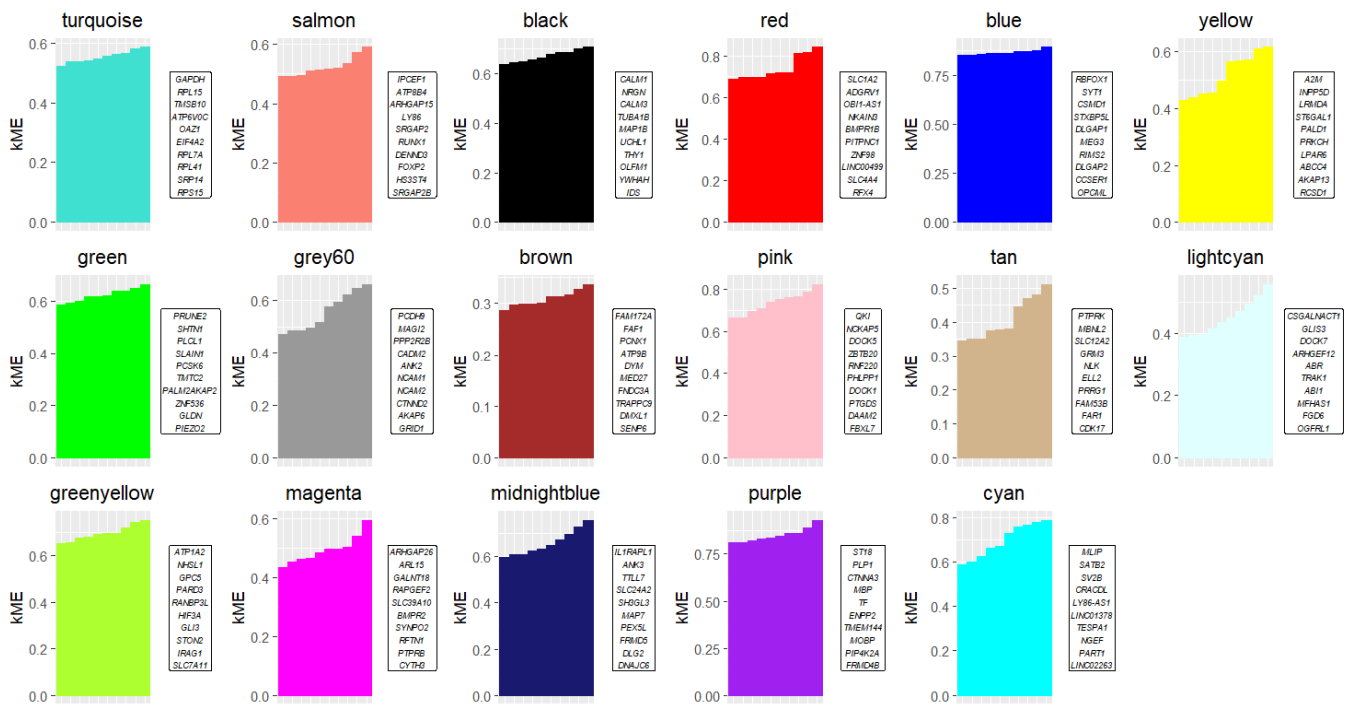


BioPlanet_2019

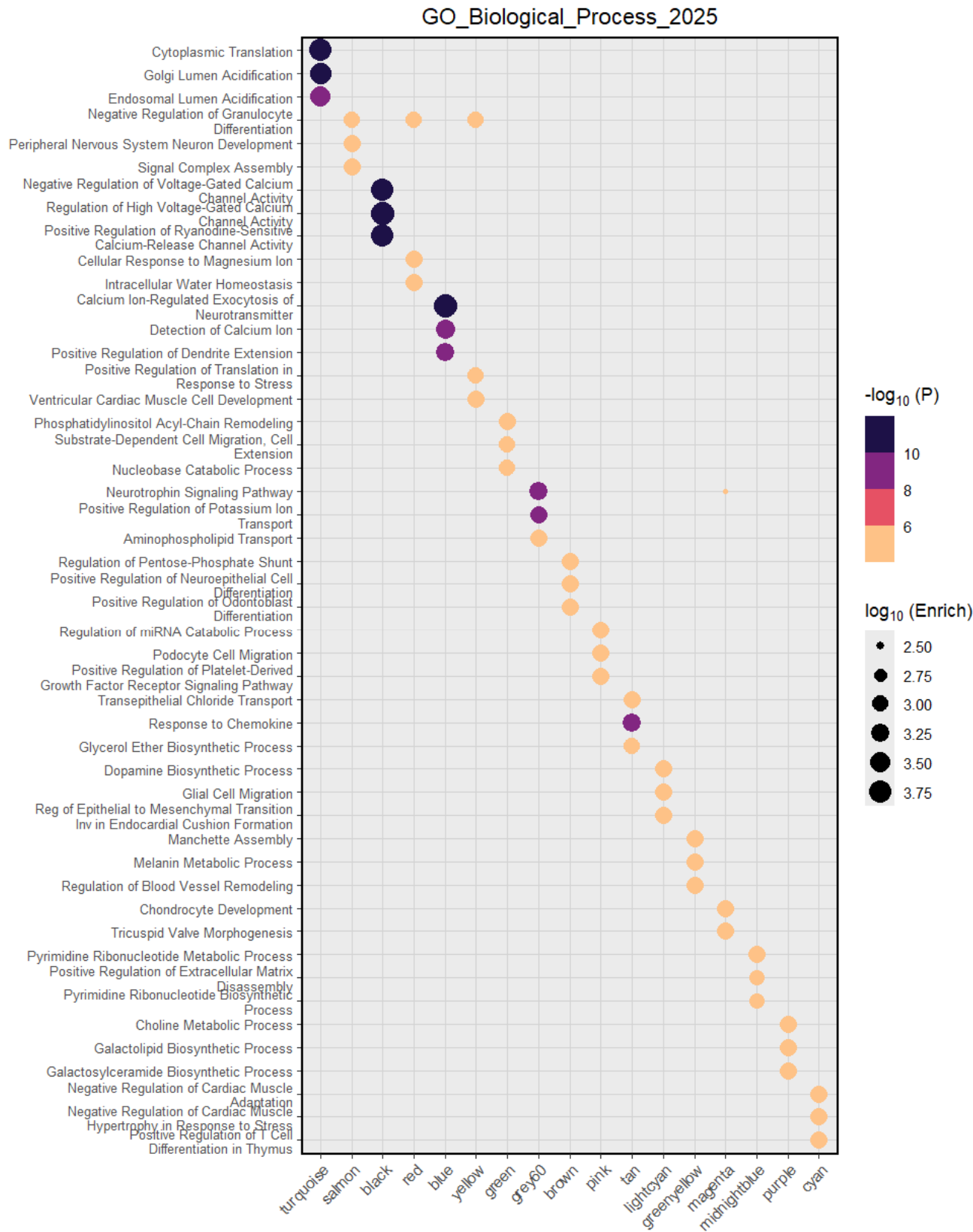




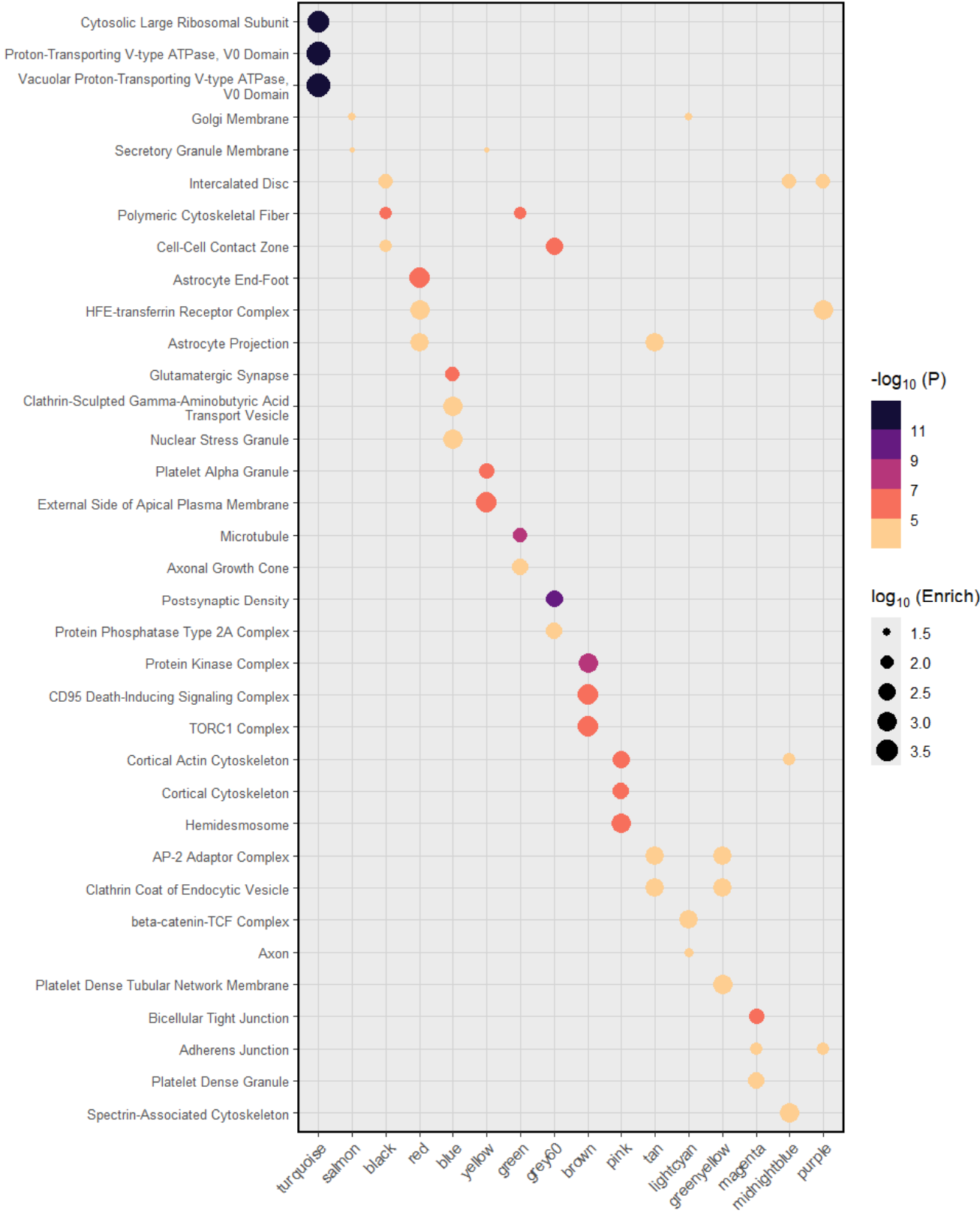
Supplementary Figure S10. hdWGCNA module architecture and top hub genes. High-dimensional weighted gene co-expression network analysis (hdWGCNA) identified 17 non-grey co-expression modules from pseudobulked single-cell RNA-seq data aggregated by patient and macro cell type. For each module, the top hub genes were ranked according to intramodular connectivity (kME). Several modules displayed clear biological identities, including purple (oligodendroglial/myelin; e.g., *PLP1*, *MBP*, *MOBP*, *MOG*), red and greenyellow (astroglial/homeostatic; e.g., *SLC1A2*, *AQP4*, *ATP1A2*, *SLC7A11*), salmon (microglial/myeloid; e.g., *ATP8B4*, *ARHGAP15*, *LY86*), yellow (vascular/perivascular immune-interface; e.g., *A2M*, *INPP5D*, *ABCB1*), and multiple neuronal modules including black, blue, midnightblue, and cyan. These hub gene profiles indicate that hdWGCNA resolved biologically coherent co-expression systems corresponding to major cortical cell lineages and functions.



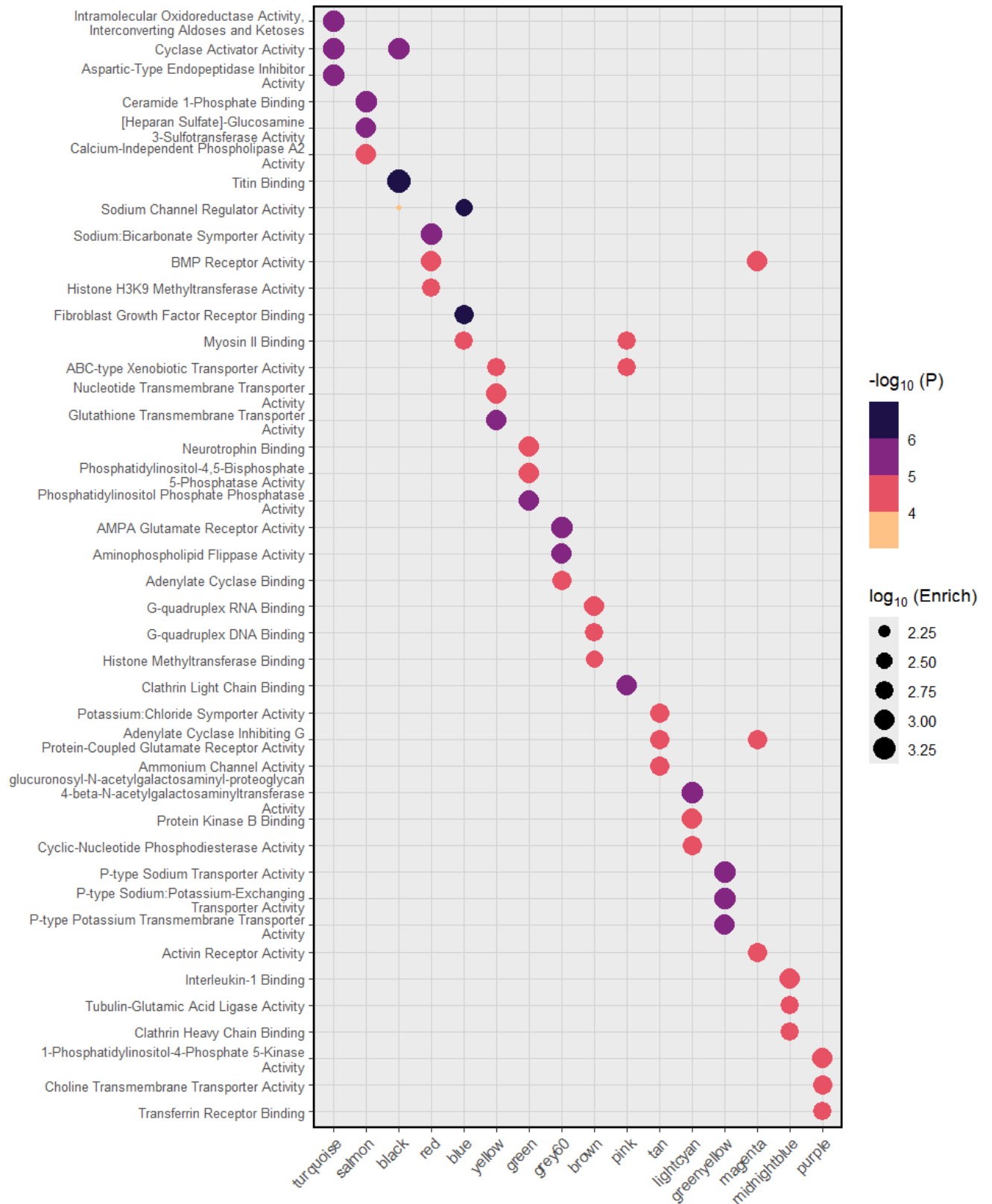
Supplementary Figure S11. Functional enrichment of hdWGCNA module hub genes across pathway libraries. Dot plots showing functional enrichment results for the top hub genes of each hdWGCNA co-expression module across eight gene set libraries: GO Biological Process, GO Cellular Component, GO Molecular Function, KEGG, Reactome, WikiPathways, BioPlanet, and the Elsevier Pathway Collection. For each module, the top three enriched terms are shown. Modules are displayed on the x-axis, and enriched terms are shown on the y-axis. Dot size represents the gene ratio, while color intensity indicates enrichment significance.



GO_Cellular_Component_2025



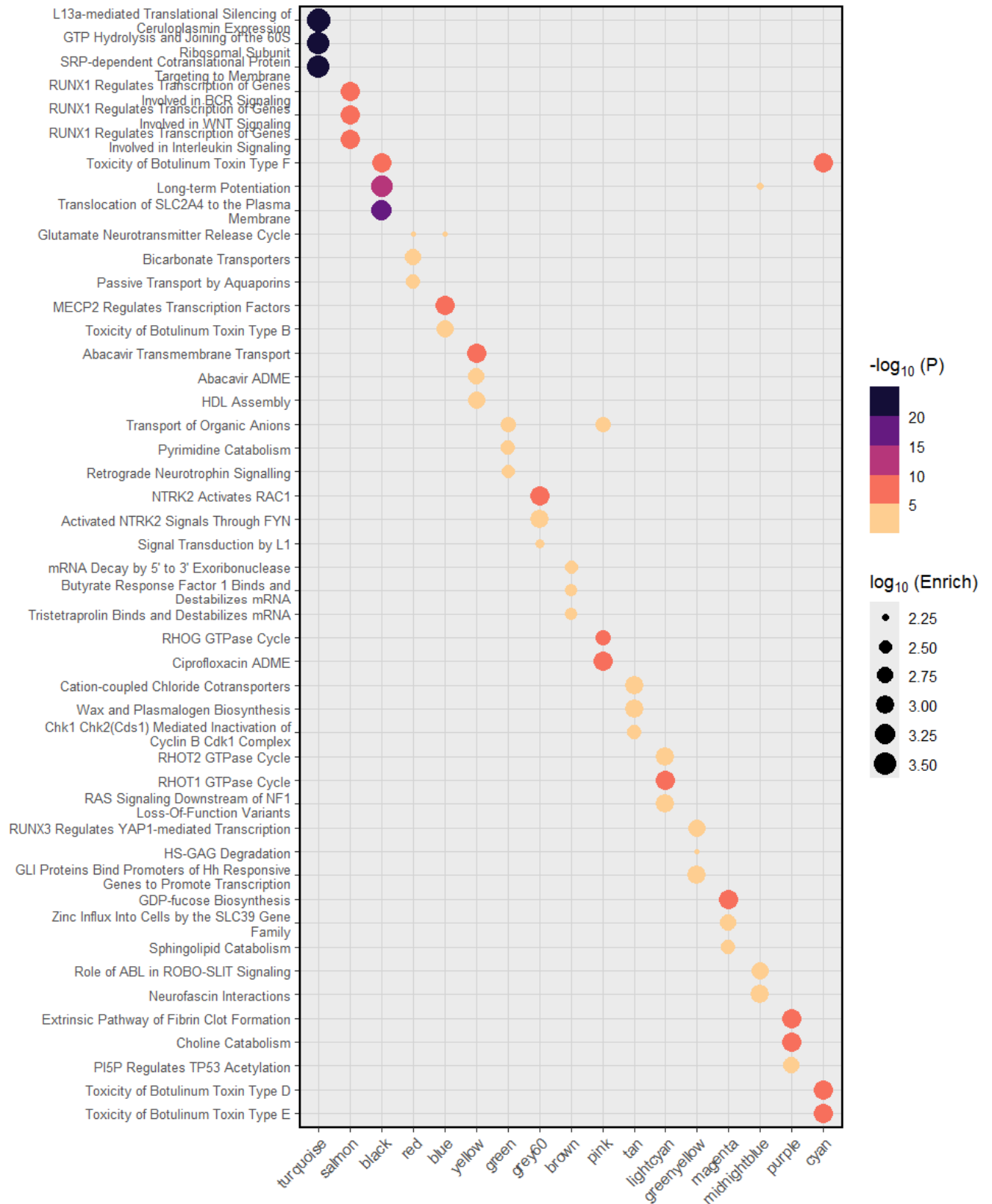
GO_Molecular_Function_2025



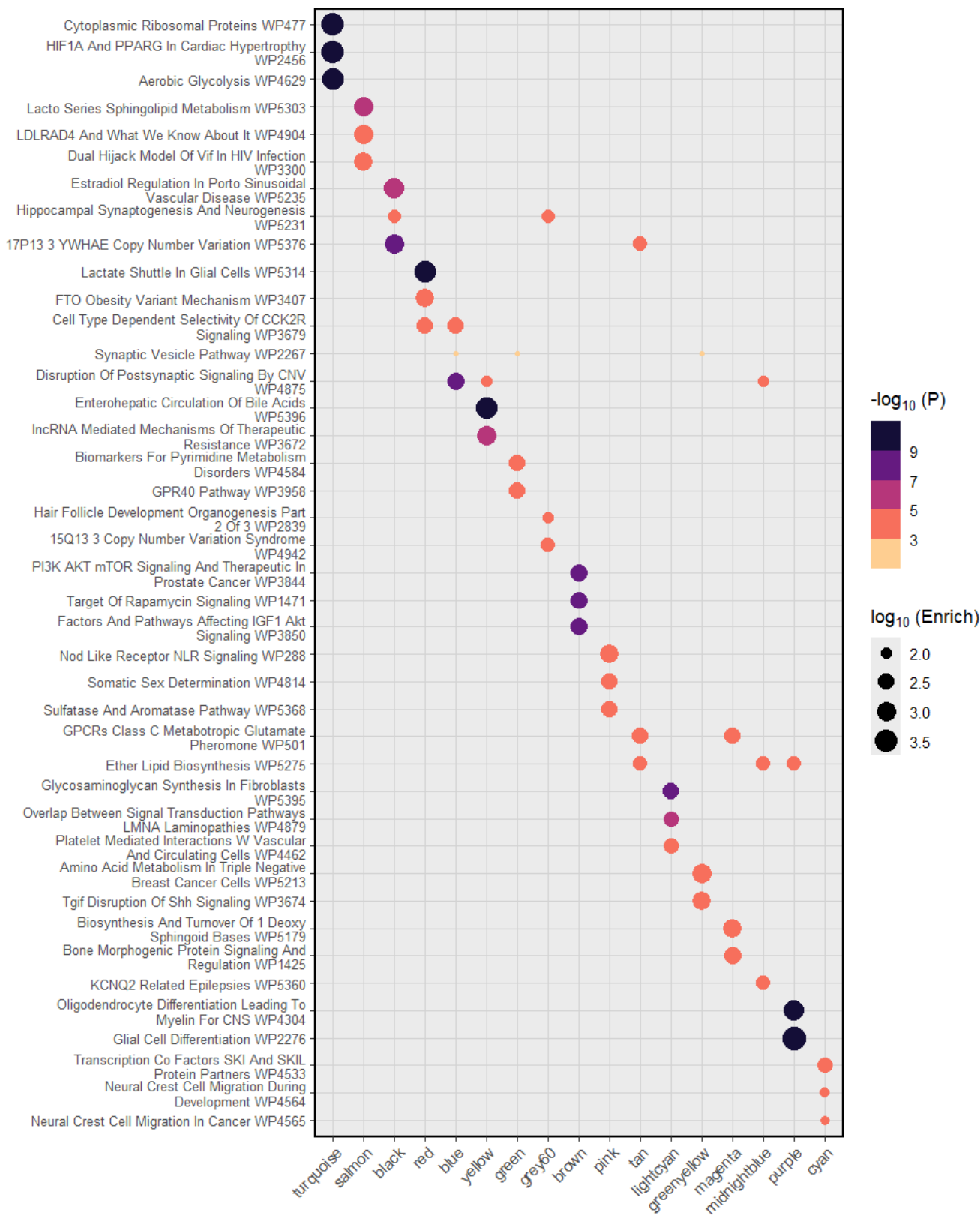
KEGG_2026



Reactome_Pathways_2024



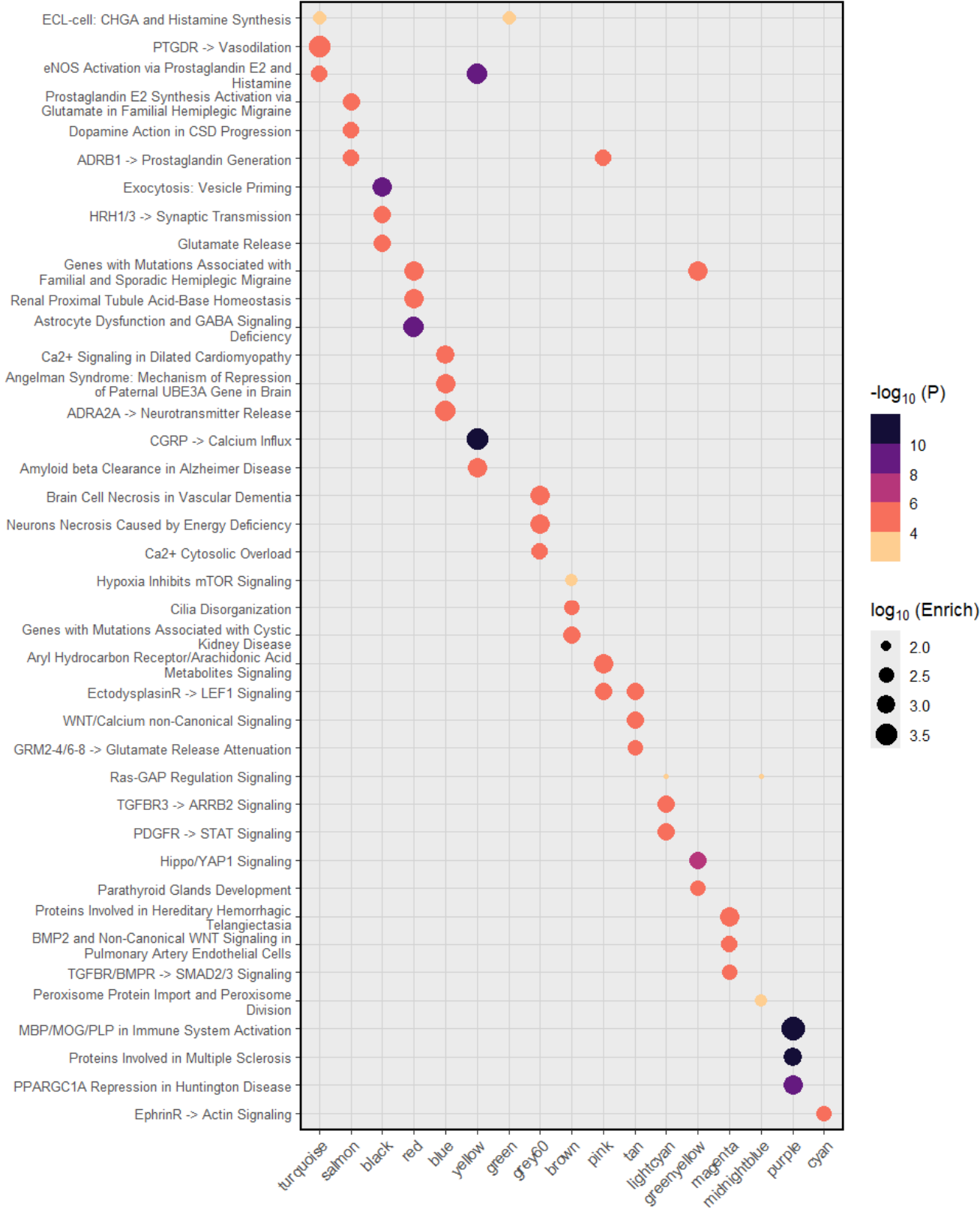
WikiPathways_2024_Human



BioPlanet_2019

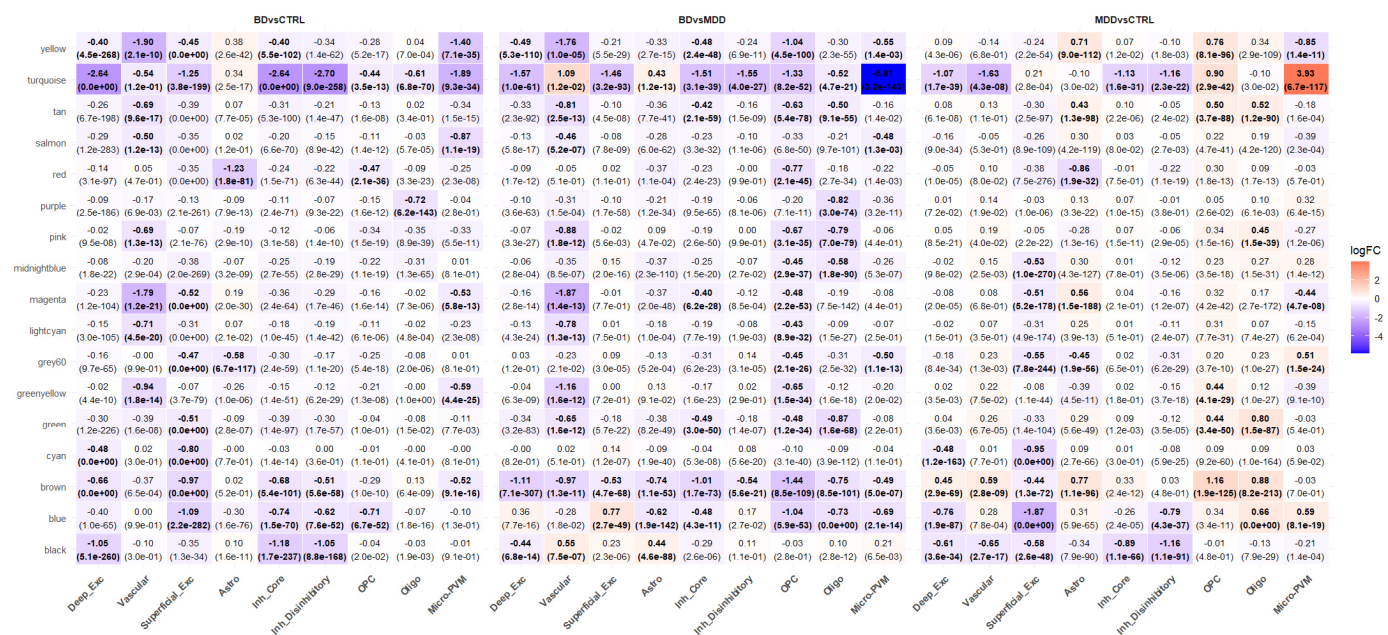


Elsevier_Pathway_Collection

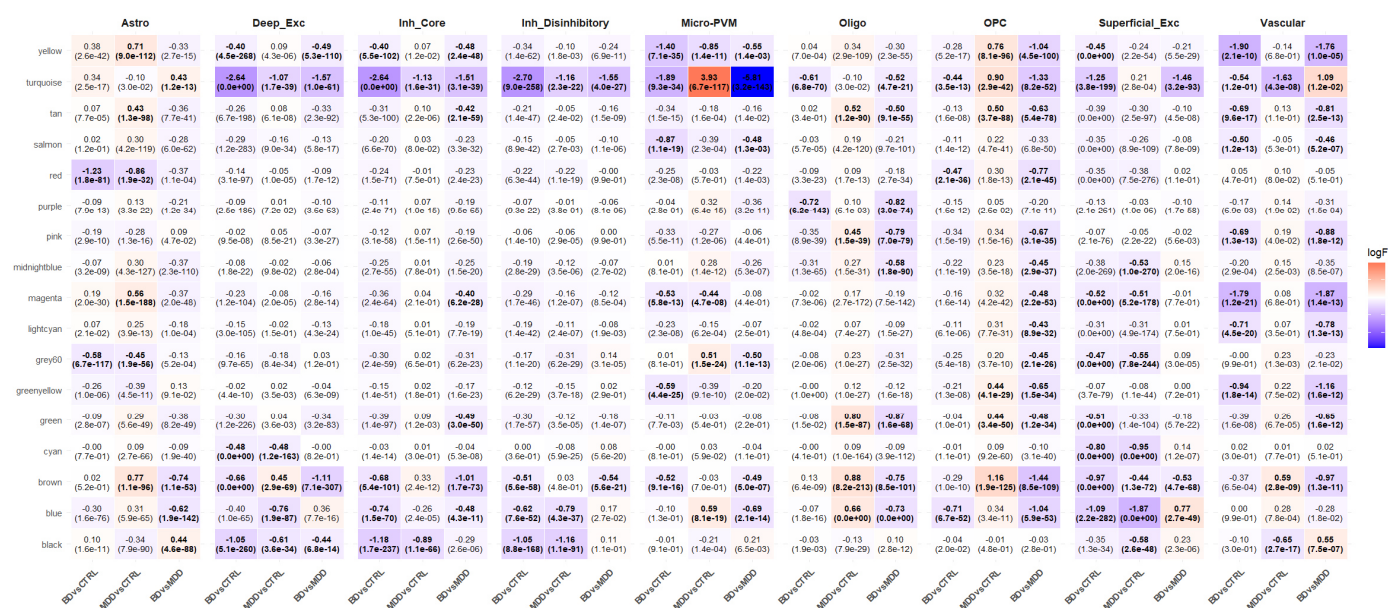


Supplementary Figure S12. Cell type-specific differential module eigengene activity across diagnostic groups. Heatmap showing differential hdWGCNA module eigengene activity within each macro cell type across the three diagnostic contrasts (BD vs CTRL, MDD vs CTRL, and BD vs MDD). Values represent model-derived log fold changes for each module within each cellular compartment, with associated adjusted *P* values shown in parentheses. For interpretive clarity, modules with |logFC| > 0.4 were highlighted in bold. Panels a) and b) show the same data organized differently: panel a) groups the data by diagnostic contrast, whereas panel b) groups them by cell type.

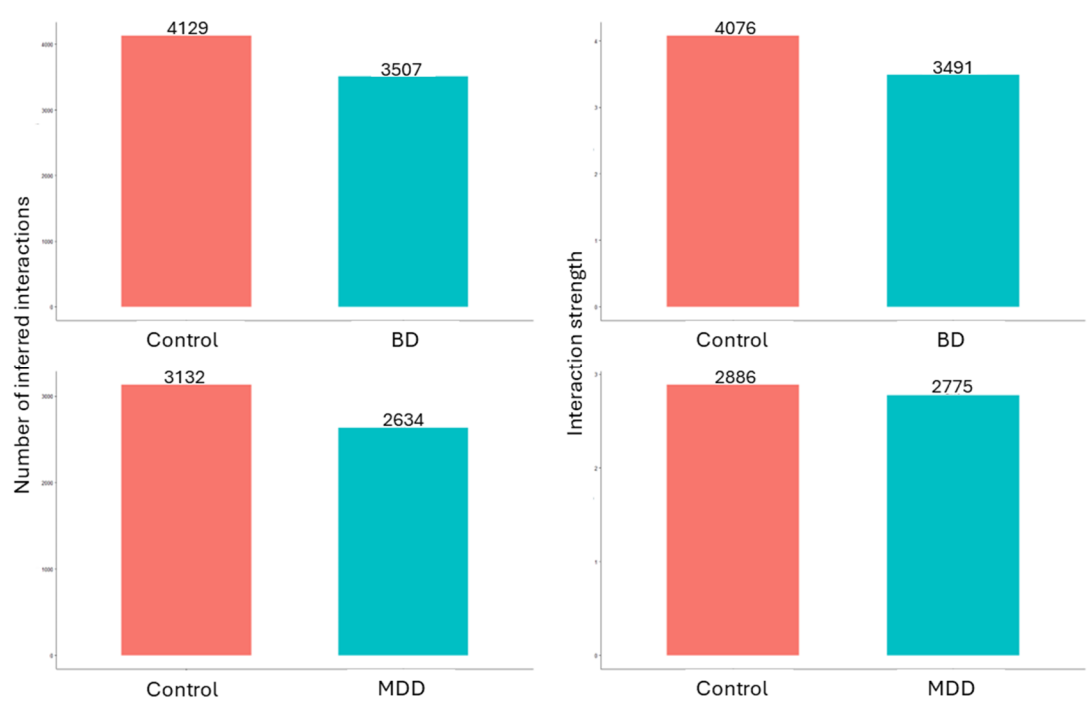
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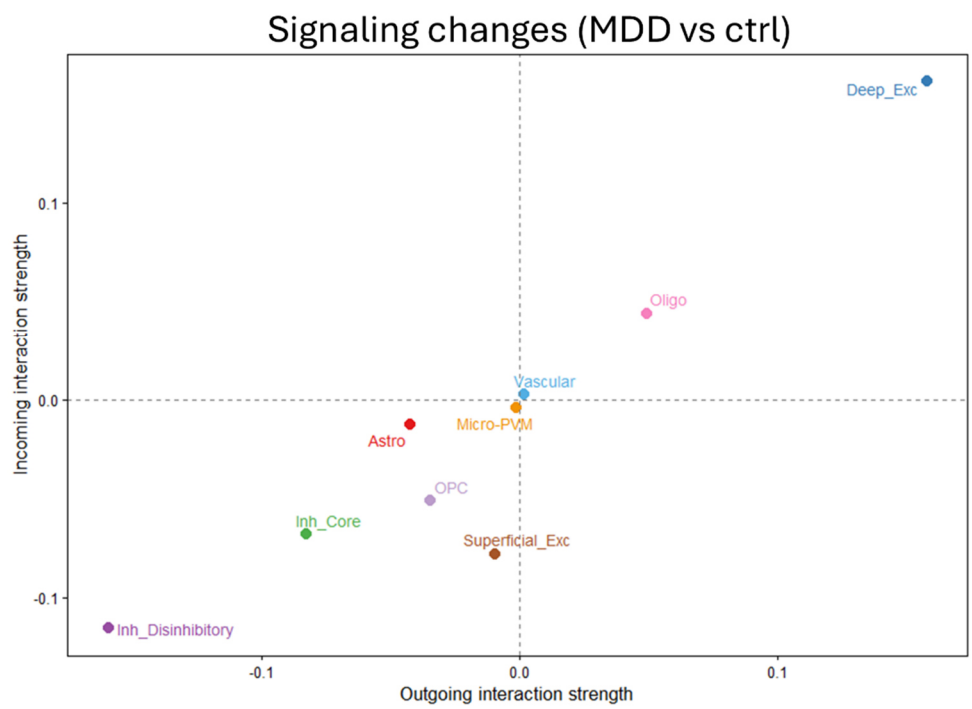
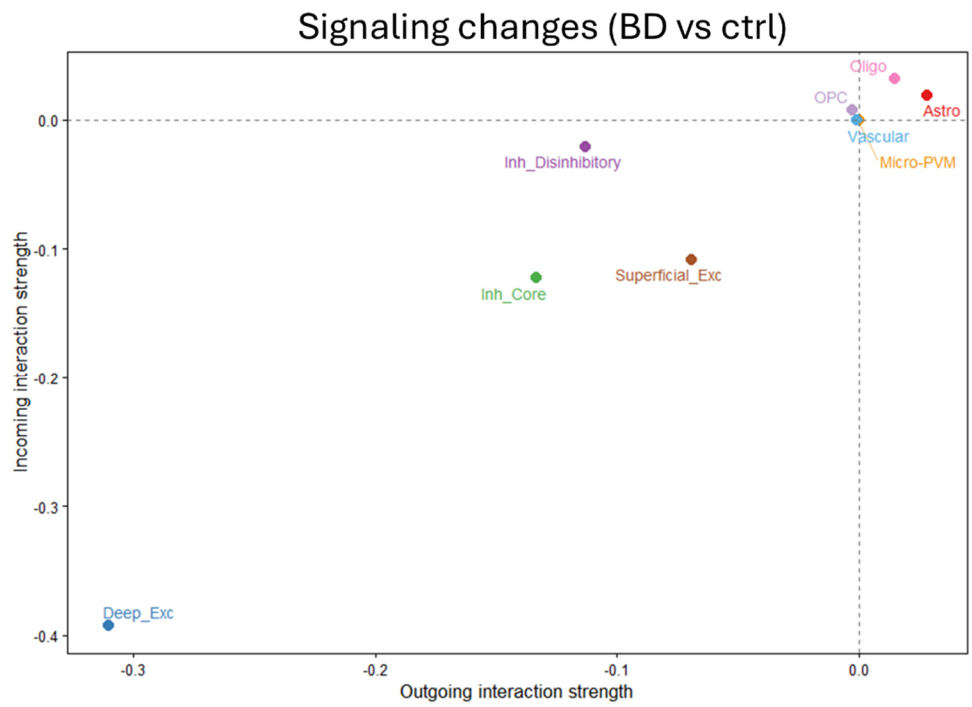
b)



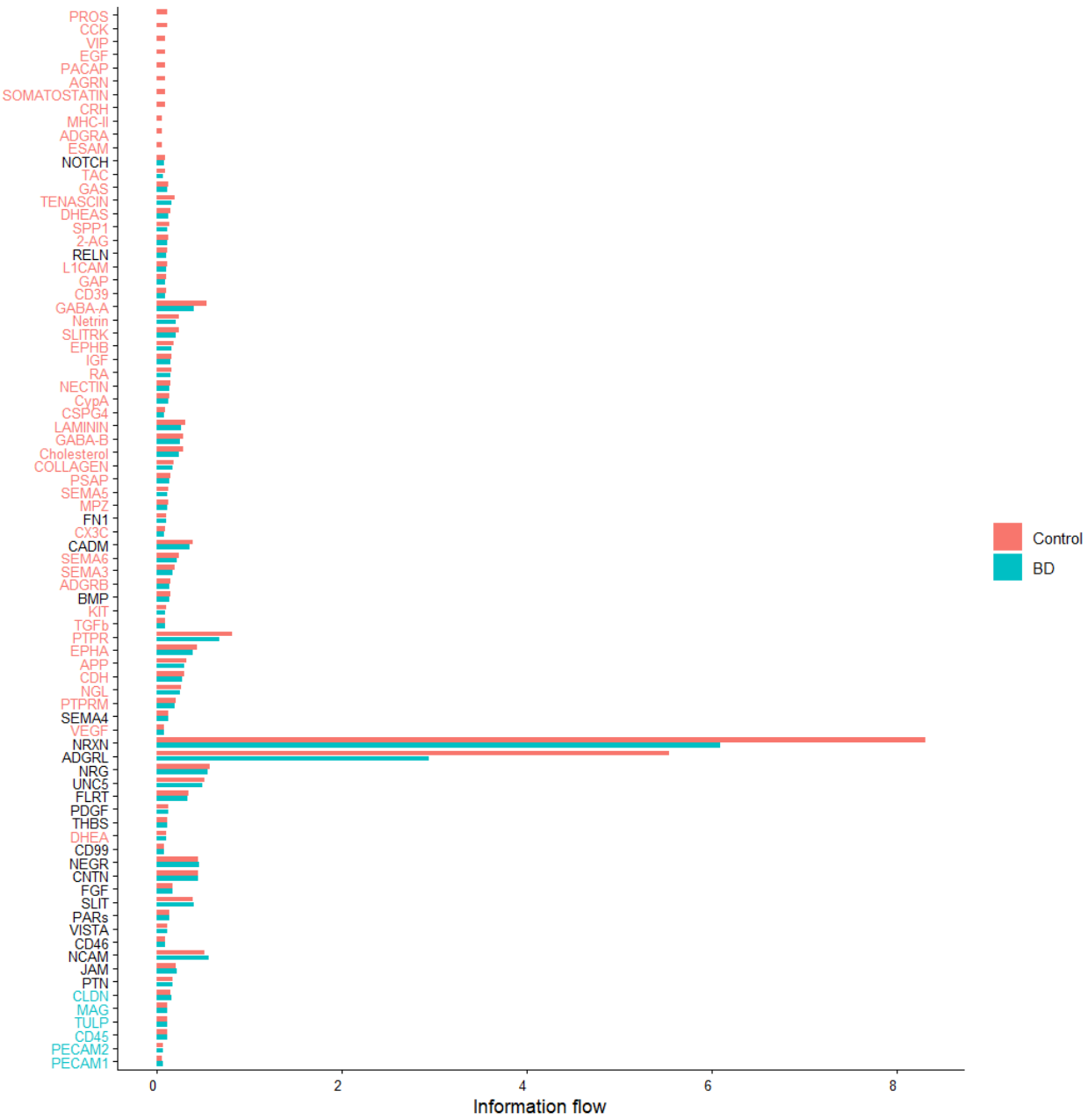
Supplementary Figure S13. Global number of inferred CellChat interactions and their strength in BD, MDD and matched controls. Bar plot showing the total number of inferred CellChat interactions and the total interaction strength in BD, MDD samples and matched controls. Interaction counts and interaction strength were calculated from the aggregated CellChat network using macro cell-type annotations.



Supplementary Figure S14. Differential sender and receiver signaling roles in BD and MDD. Scatter plot showing differential outgoing and incoming CellChat signaling roles for each macro cell type in BD and MDD relative to matched controls. The x-axis represents changes in outgoing signaling strength, and the y-axis represents changes in incoming signaling strength.



Supplementary Figure S15. Pathway-level CellChat information flow in BD and matched controls. Bar plot showing pathway-level CellChat information flow in BD samples and dataset-matched controls. Each bar represents the total inferred information flow for a CellChat signaling pathway.



Supplementary Figure S16. Pathway-level CellChat information flow in MDD and matched controls. Bar plot showing pathway-level CellChat information flow in MDD samples and dataset-matched controls. Each bar represents the total inferred information flow for a CellChat signaling pathway.

