

Description of Additional Supplementary Files

Supplementary Data 1: Differential Gene Expression (Top 50 Genes Across All Cell Types)

This table lists the top 50 differentially expressed genes across all analyzed mouse cell types after stroke from the snRNA-seq dataset. Differential gene expression was performed using Seurat v5 standard Wilcoxon rank-sum test as implemented in the FindMarkers() function. Reported values include the unadjusted P value (p_val), average log₂ fold change (avg_log2FC), and the adjusted P value (p_val_adj) using the Bonferroni correction to account for multiple comparisons. All genes listed are ranked by adjusted P value.

Supplementary Data 2: Gene Set Enrichment Analysis (Top 100 Pathways): This table lists the top 100 gene set enrichment pathways across all analyzed mouse cell types after stroke from the snRNA-seq dataset. Pathway enrichment was carried out using the clusterProfiler package. Reported metrics include normalized enrichment score (NES), raw P value, and adjusted P value (p.adjust, Benjamini-Hochberg correction). Pathways are ranked by NES. Leading-edge gene subsets and full statistics are included.

Supplementary Data 3: Top differentially expressed genes per cluster in mouse stroke host tissue. Each excel sheet represents different cell types including GABAergic neurons (GABA), Glutamatergic neurons (Glut), Astrocytes (Astro) and non-neural cells (NN).

Supplementary Data 4: Top differentially expressed genes per cluster in human graft tissue. Each excel sheet represents different cell types including GABAergic neurons, astrocytes, Stem and progenitor cells and Glutamatergic neurons.