

SUPPLEMENTARY DATA

Single-Cell RNA Sequencing Characterizes Microglial Phenotypic Heterogeneity Across Different Stroke Subtypes

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SUPPLEMENTARY DATA

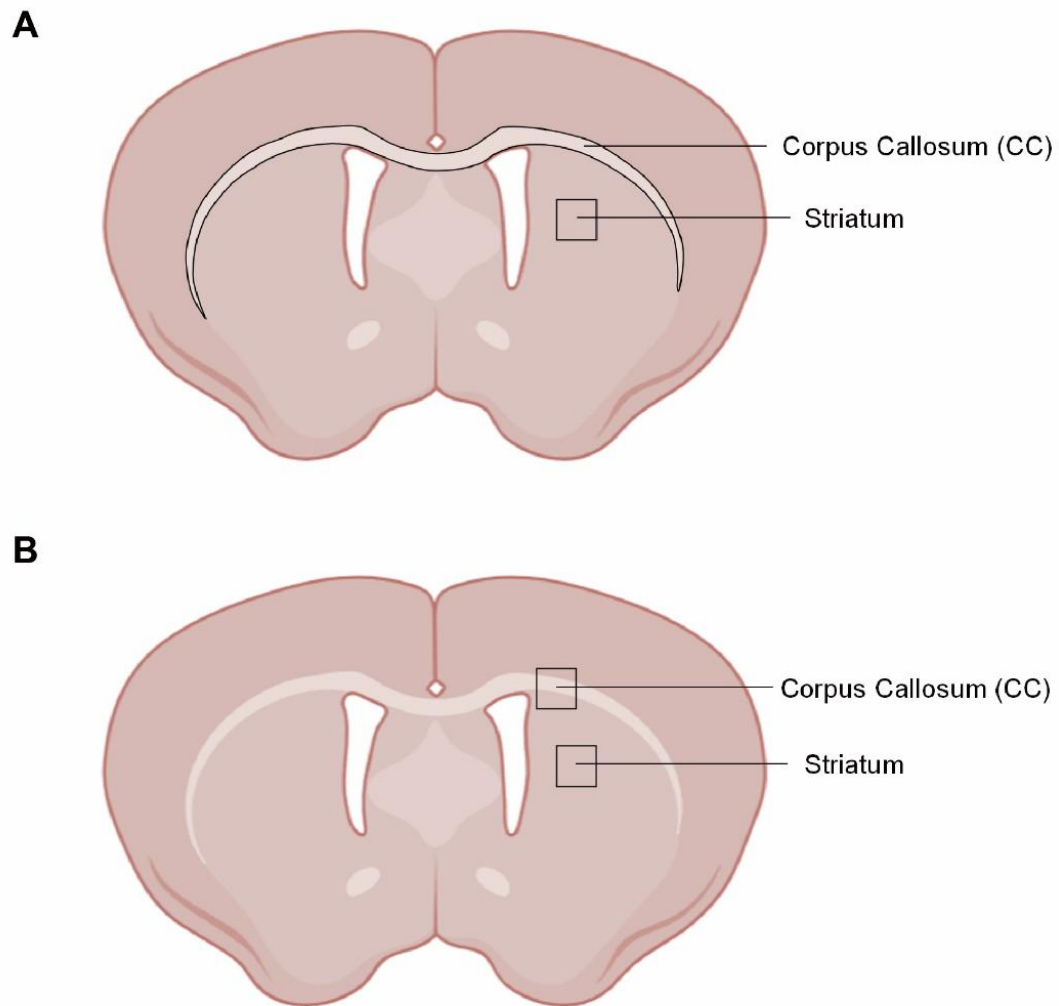


Fig S1. Schematic illustration of the sampling sites.

(A) Sampling site for single-cell sequencing in the corpus callosum (CC) and striatum.

(B) Sampling site for immunostaining; boxed regions indicate the areas selected for analysis in the CC and striatum.

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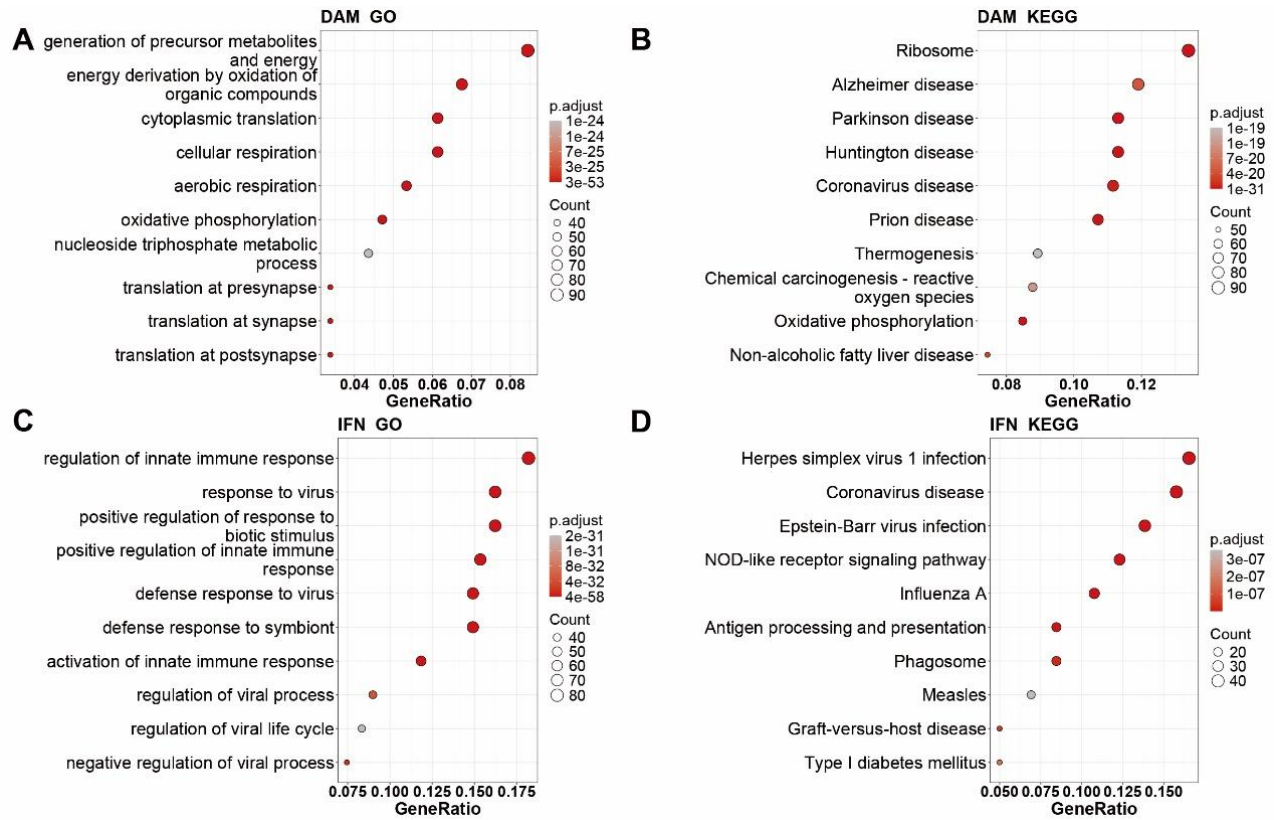


Fig S2. GO and KEGG enrichment analyses of DAM- and IFN-specific DEGs in ischemic stroke. (A) GO enrichment analysis of DAM-specific DEGs. (B) KEGG enrichment analysis of DAM-specific DEGs. (C) GO enrichment analysis of IFN-specific DEGs. (D) KEGG enrichment analysis of IFN-specific DEGs. Dot size represents gene count, dot color indicates the adjusted P value, and the x-axis represents the GeneRatio. scRNA-seq data in this figure are based on one pooled library per condition/time point and should be interpreted descriptively. DEG/pathway-related interpretations are exploratory.

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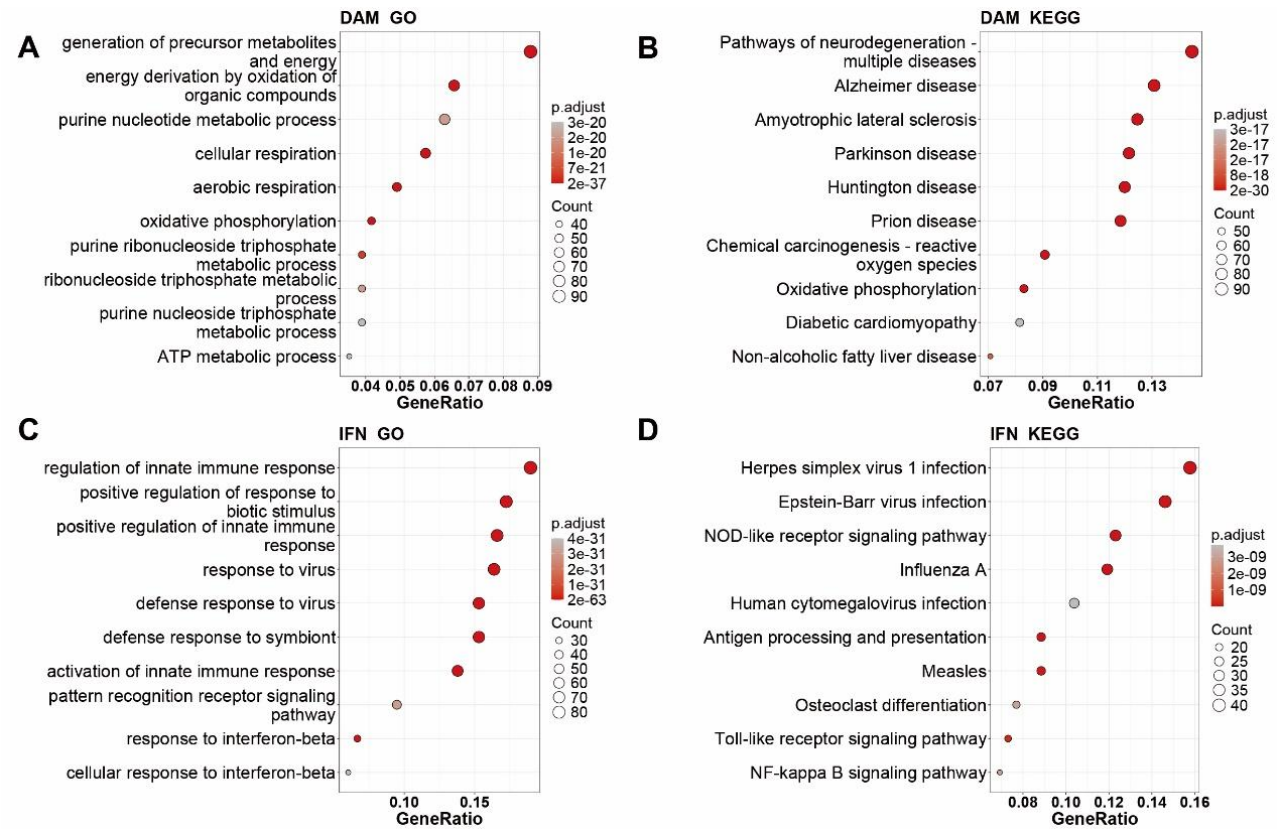


Fig S3. GO and KEGG enrichment analyses of DAM- and IFN-specific DEGs in hemorrhagic stroke.

(A) GO enrichment analysis of DAM-specific DEGs. (B) KEGG enrichment analysis of DAM-specific DEGs. (C) GO enrichment analysis of IFN-specific DEGs. (D) KEGG enrichment analysis of IFN-specific DEGs. Dot size represents gene count, dot color indicates the adjusted P value, and the x-axis represents the GeneRatio. scRNA-seq data in this figure are based on one pooled library per condition/time point and should be interpreted descriptively. DEG/pathway-related interpretations are exploratory.

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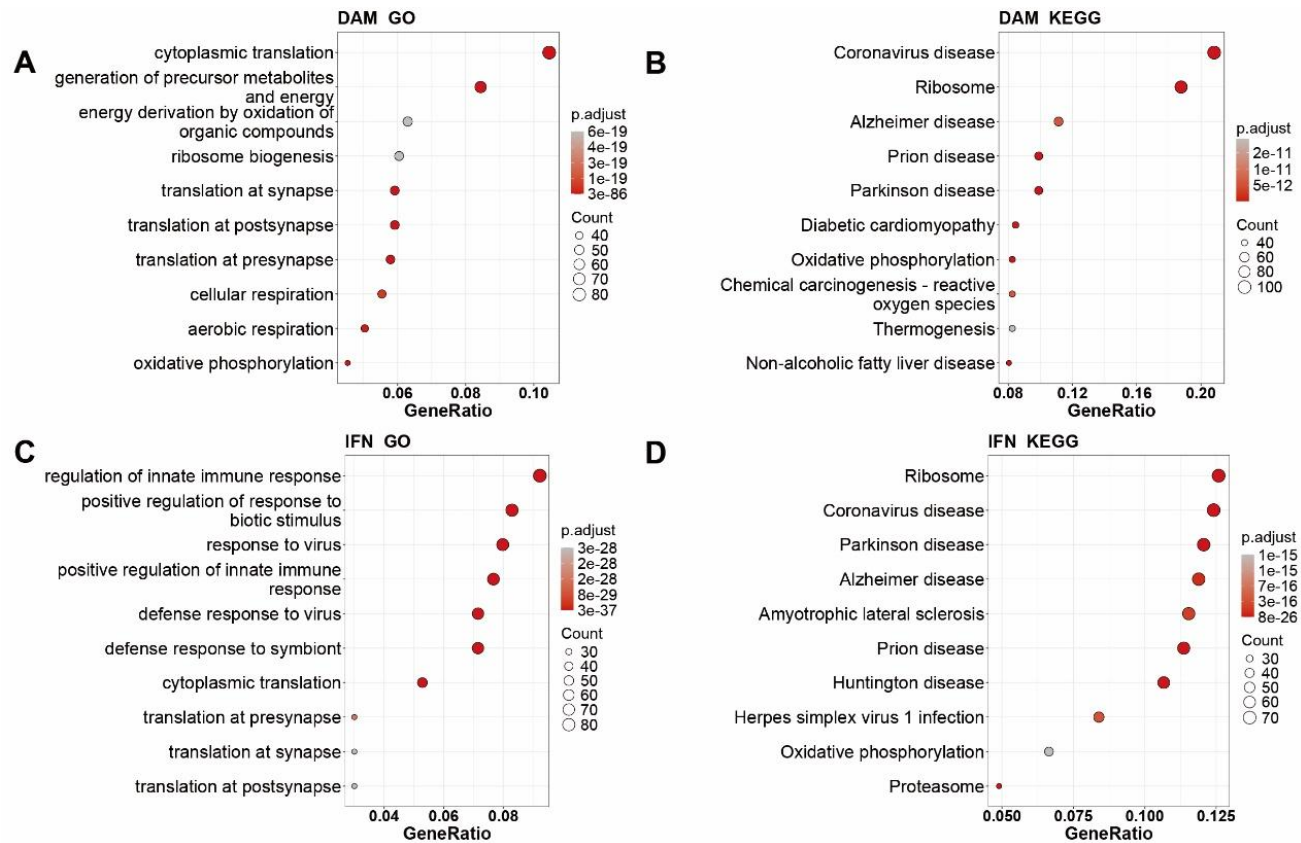


Fig S4. GO and KEGG enrichment analyses of DAM- and IFN-specific DEGs in chronic cerebral hypoperfusion.

(A) GO enrichment analysis of DAM-specific DEGs. (B) KEGG enrichment analysis of DAM-specific DEGs. (C) GO enrichment analysis of IFN-specific DEGs. (D) KEGG enrichment analysis of IFN-specific DEGs. Dot size represents gene count, dot color indicates the adjusted P value, and the x-axis represents the GeneRatio. scRNA-seq data in this figure are based on one pooled library per condition/time point and should be interpreted descriptively. DEG/pathway-related interpretations are exploratory.