

Supplementary Table 1. Clinical metadata for all donors included in this study.

Supplementary Table 2. Relative frequencies of each cell type stratified by striatal region and condition.

Supplementary Table 3. Marker genes defining each astrocyte subpopulation identified by snRNA-seq clustering.

Supplementary Table 4. Co-expression modules identified by Hotspot analysis within the astrocyte population.

Supplementary Table 5. KEGG Parkinson's disease pathway enrichment scores for each astrocyte subpopulation, reported separately for CN and Pu.

Supplementary Table 6. Marker genes defining each microglial subpopulation identified by snRNA-seq clustering.

Supplementary Table 7. Co-expression modules identified by Hotspot analysis within the microglial population.

Supplementary Table 8. KEGG Parkinson's disease pathway enrichment scores for each microglial subpopulation, reported separately for CN and Pu