

Supplemental Figure 1: Cell type composition by sex, brain region, donor and classification by broad cell type markers

- (a) UMAP of 155,192 nuclei by sex (female, pink; dark blue, male)
- (b) Proportion of cell types recovered by sex
- (c) UMAP of 155,192 nuclei colored by brain region (EC, dark blue; MTG, light blue; PUT, magenta; SVZ, gold) demonstrating the region-specific origin of some cell types.
- (d) Proportion of cell types recovered by region.
- (e) UMAP projection of nuclei split by brain region and sample ID demonstrating no single cluster is derived from a single donor.
- (f) Leiden clustering at resolution 0.85 identified 23 distinct clusters after removal of low quality or poorly distinguished clusters.
- (g) Dot plot of genes used to assign broad cell type categories to Leiden clusters, where dot size indicates percentage of cells expressing a gene and color indicates level of mean expression within that cluster.
- (h) Feature plots of broad cell type markers to identify clusters as broadly as neurons, excitatory neurons, cortical inhibitory neurons, spiny projection neurons, astrocytes, endothelial cells, mural cells, ependymal cells, microglia, oligodendrocyte precursor cells, and oligodendrocytes.
- (i) Force-directed graph of developmental relationships between cell types.

Abbreviations: *ANPEP*, alanyl aminopeptidase, membrane; *AQP4*, aquaporin 4; *CSF1R*, colony stimulating factor 1 receptor; *DRD1*, dopamine receptor D1; *DRD2*, dopamine receptor D2; EC, entorhinal cortex; ExN, excitatory neuron; FLE, force-directed; *FLT1*, fms related receptor tyrosine kinase 1; *FOXJ1*, forkhead box J1; *GAD2*, glutamate decarboxylase 2; InN, inhibitory neuron; *MBP*, myelin basic protein; MTG, middle temporal gyrus; *OPALIN*, oligodendrocytic myelin paranodal and inner loop protein; OPC, oligodendrocyte precursor cell;

PDGFRA, platelet derived growth factor receptor alpha; *PLP1*, proteolipid protein 1; PUT, putamen; *RBFOX3*, RNA binding fox-1 homolog 3; *SLC17A6*, solute carrier family 17 member 6; *SLC17A7*, solute carrier family 17 member 7

Supplemental Figure 2: Unique and diverging patterns of aging across brain regions and broad cell types in absence of cell loss

- (a)** Percentage of nuclei recovered per brain region by age group (light blue, young; dark blue, old) with raw numbers expressed as 'young | old'.
- (b)** Proportion of nuclei recovered by age group and donor showed no significant differences between age groups. n.s. = not significant; $p > 0.05$, Welch's t-test.
- (c)** UpSet plot of unique vs. shared aDAGs across brain regions where rows on the x-axis correspond to [brain region] aDAG sets, columns correspond to intersection size between sets, and bar color corresponds to direction of association (blue, negative association with age; magenta, positive association with age). Lines between sets indicate shared aDAGs. Cell type sets ordered by cardinality.
- (d)** Clustermap of the top 5 aDAGs across brain regions (blue, negative association; magenta, positive association). Non-coding and pseudogenes distinguished by gray italics. Cell types ordered by hierarchical clustering.
- (e)** UpSet plot of unique and shared aDAGs across broad cell types. Only intersection sizes of ≥ 50 are displayed. Cell type sets ordered by cardinality.
- (f)** Clustermap of the top 5 positive and negative aDAGs across broad cell types. Cell types ordered by hierarchical clustering.

Abbreviations: aDAG, aging-differentially associated gene; EC, entorhinal cortex; ExN, excitatory neuron; InN, inhibitory neuron; MTG, middle temporal gyrus; OPC, oligodendrocyte precursor cell; PUT, putamen; SPN, spiny projection neuron; SVZ, subventricular zone

Supplemental Figure 3: Top aDAGs across cortical and subcortical InN subtypes and overlap with aging and disease gene sets

(a) Clustermap of the top 5 positive and negative aDAGs across cortical and subcortical InN subtypes (blue, negative association with age; magenta, positive association with age). Non-coding and pseudogenes distinguished by gray italics. Cell types ordered by hierarchical clustering.

(b) Enrichment of cortical and **(c)** subcortical InN subtype aDAGs from previous aging and disease perturbation gene sets from GEO.

Abbreviations: aDAG, aging-differentially associated gene; GEO, Gene Expression Omnibus; InN, inhibitory neuron; SPN, spiny projection neuron

Supplemental Figure 4: Top aDAGs across ExN subtypes and overlap with aging and disease gene sets

(a) Clustermap of the top 5 positive and negative aDAGs across ExN subtypes (blue, negative association with age; magenta, positive association with age). Non-coding and pseudogenes are distinguished by gray italics. Cell types ordered by hierarchical clustering.

(b) Feature scatter increased expression and association of *RHBDL3*; (c) decreased expression and association of *STAC*; and (d) increased expression and association of *STAC2* with age in ExN.

(e) Enrichment of ExN subtype aDAGS from previous aging and disease perturbation gene sets from GEO.

Abbreviations: aDAG, aging-differentially associated gene; ExN, excitatory neuron; GEO, Gene Expression Omnibus; *RHBDL3*, rhomboid like 3; *STAC*, SH3 and cysteine rich domain; *STAC2*, SH3 and cysteine rich domain 2

Supplemental Figure 5: Top aDAGs across oligodendrocyte subtypes, myelination-related genes, and overlap with aging and disease gene sets

(a) Clustermap of the top 5 positive and negative aDAGs across OPCs and oligodendrocyte subtypes (blue, negative association with age; magenta, positive association with age). Non-coding and pseudogenes are distinguished by gray italics. Cell types ordered by hierarchical clustering.

(b) Clustermap of aDAGs related to CNS myelination across cell types (blue, negative association with age; magenta, positive association with age). OPCs and oligodendrocytes are demarcated by black boxes.

(c) Enrichment of OPC and oligodendrocyte subtype aDAGS from previous aging and disease perturbation gene sets from GEO.

Abbreviations: CNS, central nervous system; ExN, excitatory neuron; GEO, Gene Expression Omnibus; OPC, oligodendrocyte precursor cell.

Supplemental Figure 6: Top aDAGs across non-neuronal, non-oligodendrocyte cells and overlap with aging and disease gene sets

(a) Clustermap of the top 5 positive and negative aDAGs across astrocytes, endothelial cells, mural cells, ependymal cells, and microglia (blue, negative association with age; magenta, positive association with age). Non-coding and pseudogenes are distinguished by gray italics. Cell types ordered by hierarchical clustering.

(b) UpSet plot of unique vs. shared aDAGs across astrocytes, endothelial cells, mural cells, ependymal cells, and microglia, where rows on the x-axis correspond to [cell type] aDAG sets, columns correspond to intersection size between sets, and bar color corresponds to the direction of association (blue, negative association with age; magenta, positive association with age)

(c) GSE of aDAGs in endothelial, ependymal, and mural cells.

Abbreviations: aDAG, aging-differentially associated gene; GSE, gene set enrichment

Supplemental Figure 7: Overlap of aDAGs across cell types with genes differentially expressed in aging human frontal cortex from GEO

(a) Astrocytes, microglia, and oligodendrocyte-3 aDAGs were significantly enriched for genes previously demonstrated to be increased in aged (28 years vs. 100 years) human frontal cortex (magenta, positive association; dark blue, negative association). Non-coding and pseudogenes are demarcated by gray italics. Cell types ordered by hierarchical clustering.

Asterisks mark cell types with significant enrichment.

(b) Feature scatter showing increased expression and association of *SERPINA3* and **(c)** *IFITM2* in with age in astrocytes

(d) Feature scatter showing increased expression and association of *CD163* and **(e)** *CD14* in with age in microglia

(f) Only neuronal subtypes were significantly enriched for genes previously demonstrated to be decreased in aged (28 years vs. 100 years) human frontal cortex (magenta, positive association; dark blue, negative association). Non-coding and pseudogenes are demarcated by gray italics. Asterisks mark cell types with significant enrichment. Cell types ordered by hierarchical clustering.

(g) Feature scatter showing decreased expression and association with age of *KCNF1* in *LHX6⁺PVALB⁺* cortical InN, **(h)** *LY6H* in cortical InN and *RORB⁺* ExN, and **(i)** *PFN1* in *LHX6⁺PVALB⁺* cortical InN

Abbreviations: aDAG, aging-differentially associated gene; EC, entorhinal cortex; ExN, excitatory neuron; *IFITM2*, interferon-induced transmembrane protein 2; InN, inhibitory neuron; *KCNF1*, potassium voltage-gated channel modifier subfamily F member 1; *LY6H*, lymphocyte antigen 6 family member H; MTG, middle temporal gyrus; OPC, oligodendrocyte precursor cell; *PFN1*, profilin 1; PUT, putamen; *SERPINA3*, serpin family A member 3; SPN, spiny projection neuron; SVZ, subventricular zone; UMAP, uniform manifold approximation and projection.

Supplemental Figure 8: Mean expression of genes nearest to AD and PD GWAS-identified risk loci across brain regions and cell types

(a) Dot plot of mean expression of genes nearest to AD GWAS-nominated risk loci across brain regions. Size of circle denotes percentage of cells in a brain region expressing a gene and color represents strength of expression (purple, high expression; light blue, low expression)

(b) Dot plot of mean expression of genes nearest to AD GWAS-nominated risk loci across cell types

(c) Dot plot of mean expression of genes nearest to PD GWAS-nominated risk loci across brain regions and **(d)** cell types

Supplemental Table 1: Donor Demographics

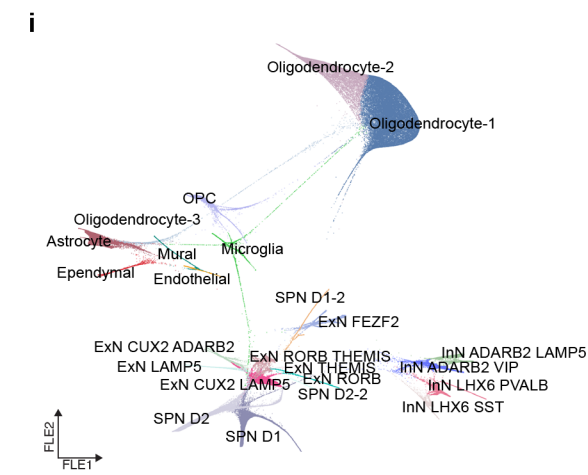
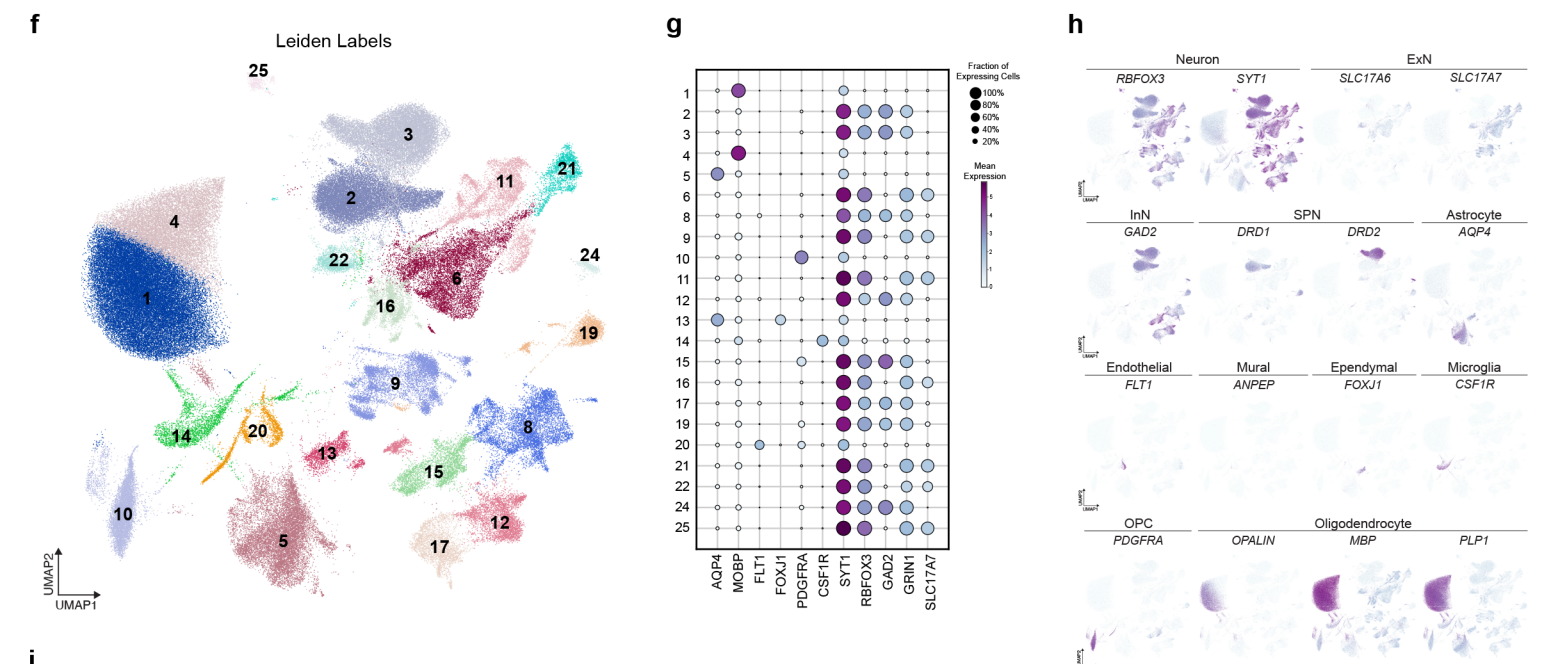
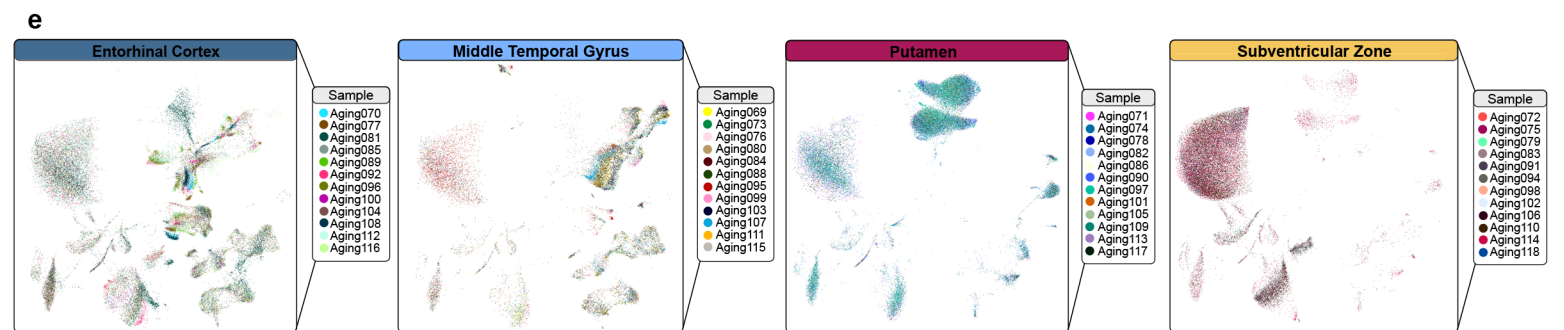
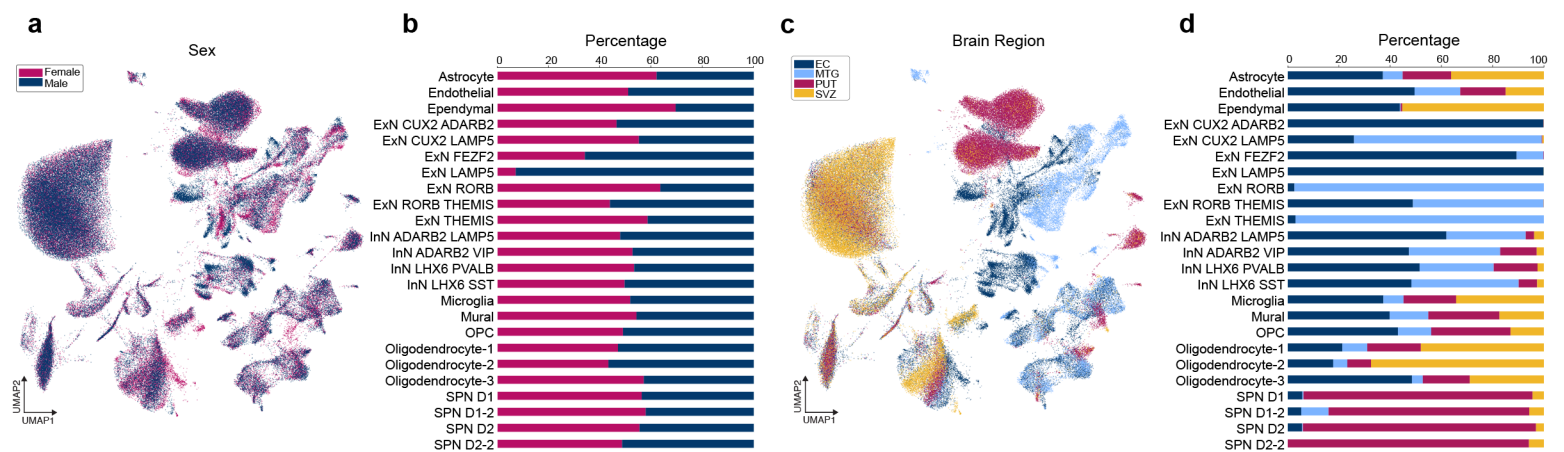
Supplemental Table 2: Number of Significant Differentially Associated Genes with Age by Brain Region, Broad Type, and Cell Subtype

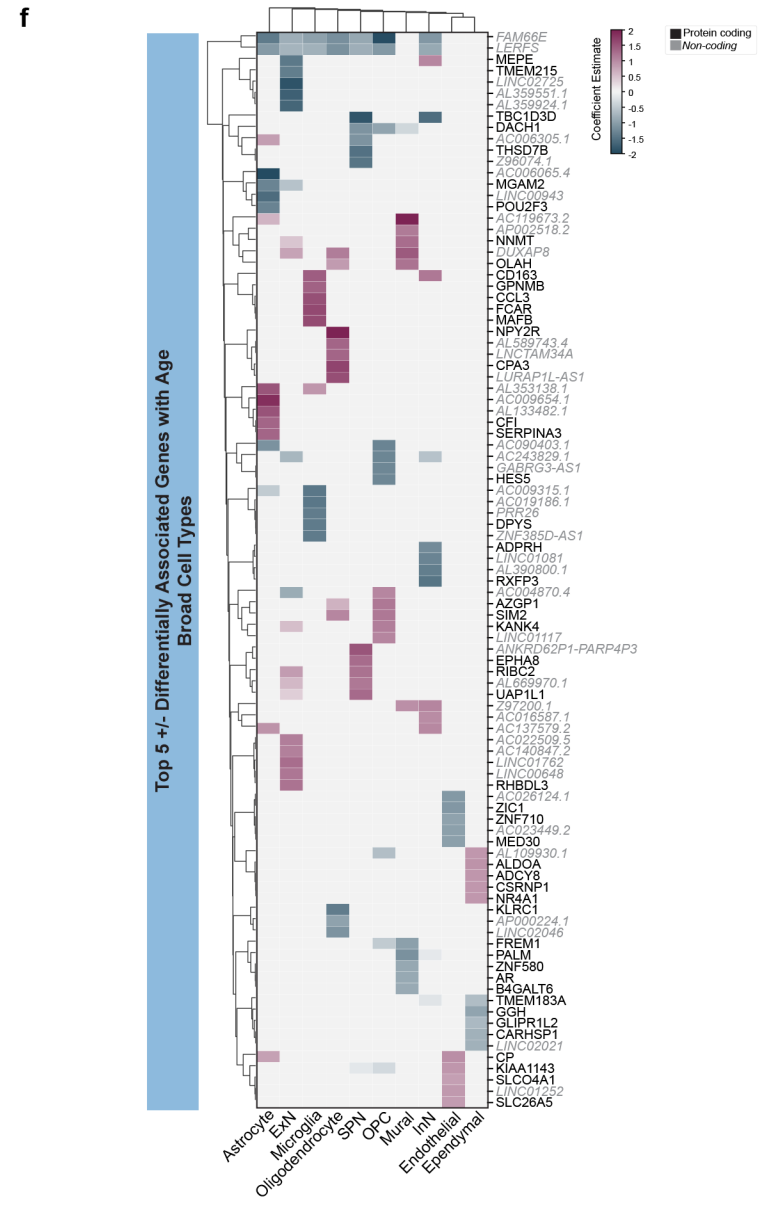
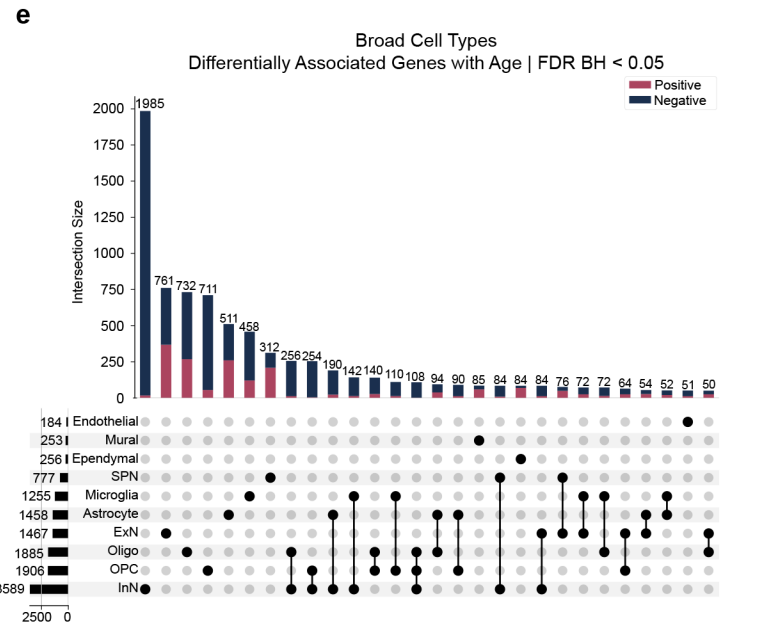
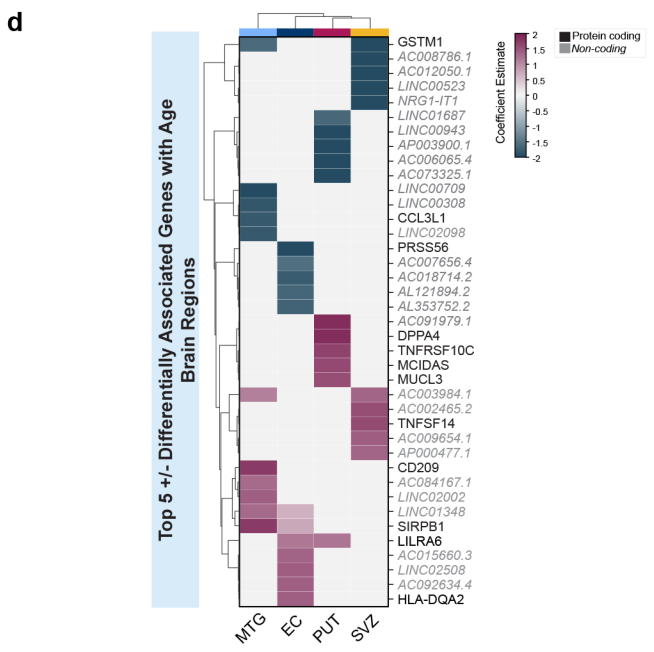
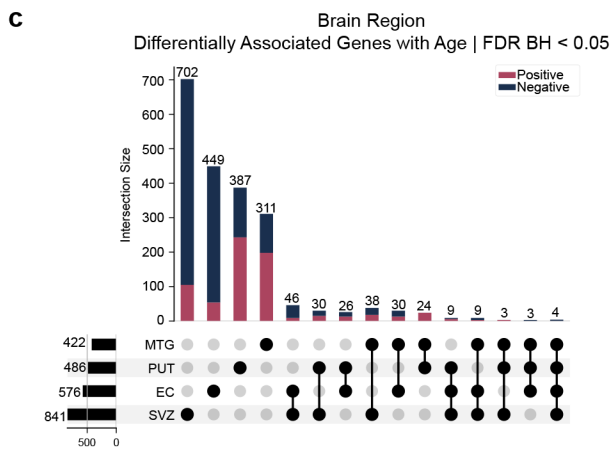
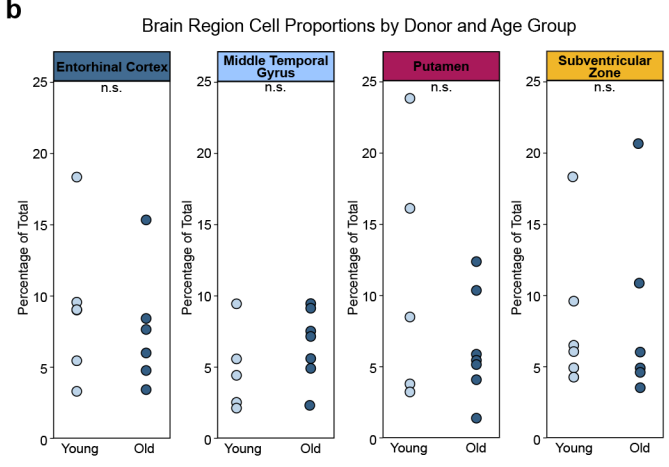
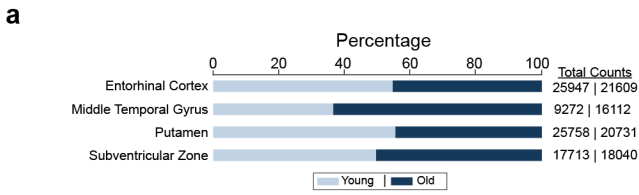
Supplemental Table 3: Coefficient estimates for significant brain region aDAGs that are also significant at the broad type level

Supplemental Table 4: glmTMB All Significant aDAGs (FDR BH < 0.05)

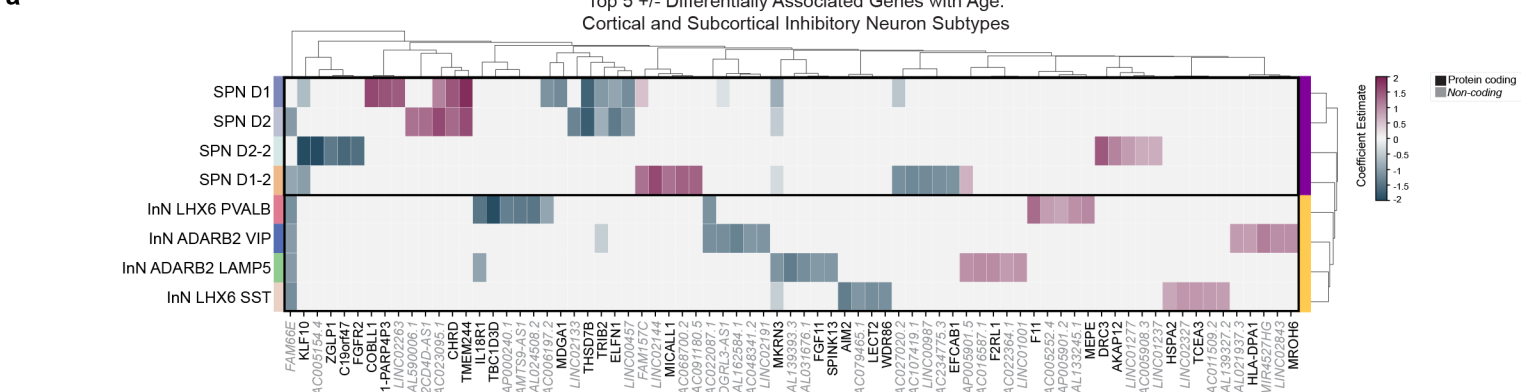
Supplemental Table 5: Oligodendrocyte Proportions by Brain Region and Age

Supplemental Information: Age-Associated Gene Set Enrichment Outputs for Brain Region, Broad Type, and Cell Type



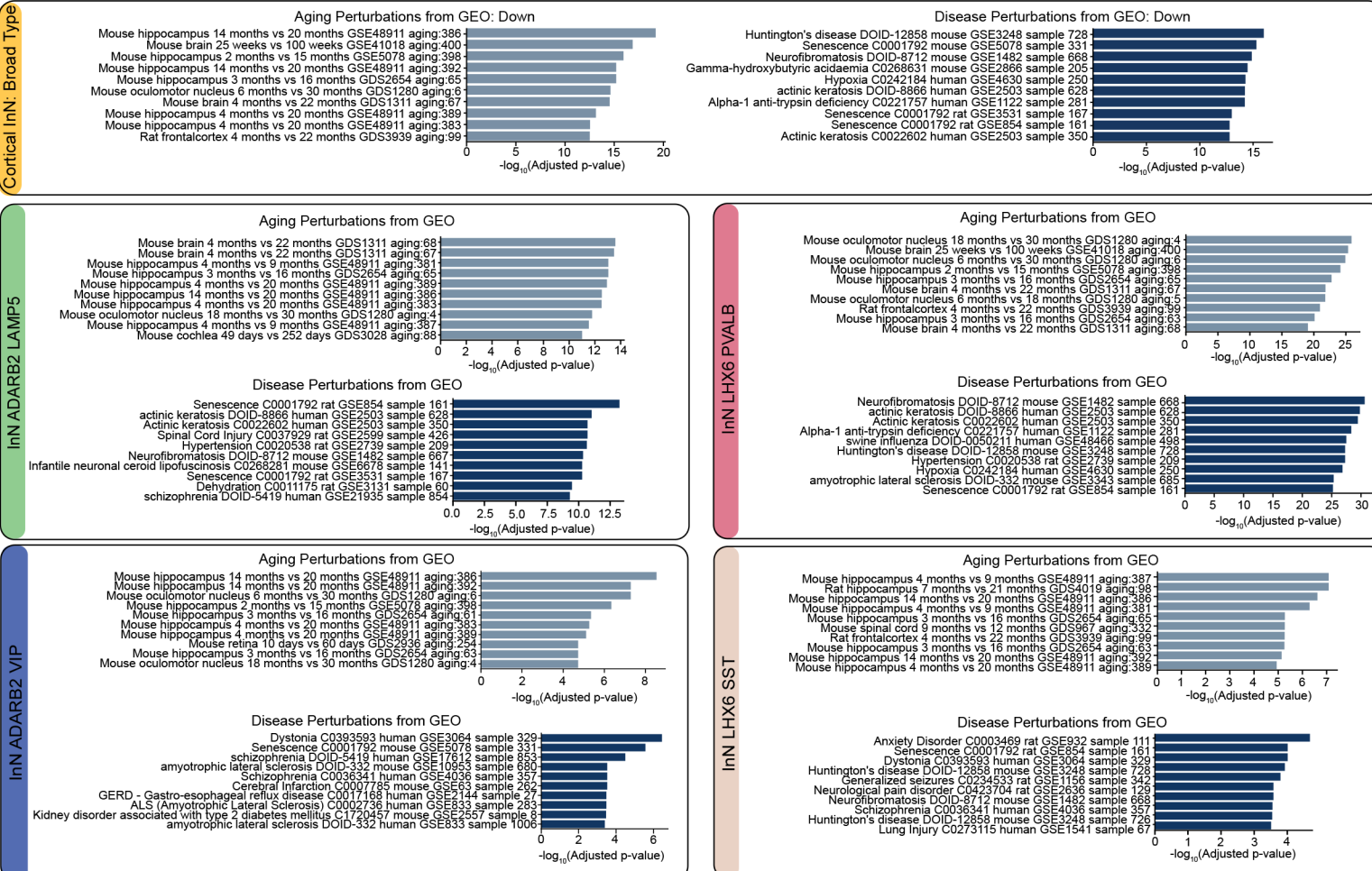


Top 5 +/- Differentially Expressed Genes with Age:
Cortical and Subcortical Inhibitory Neuron Subtypes

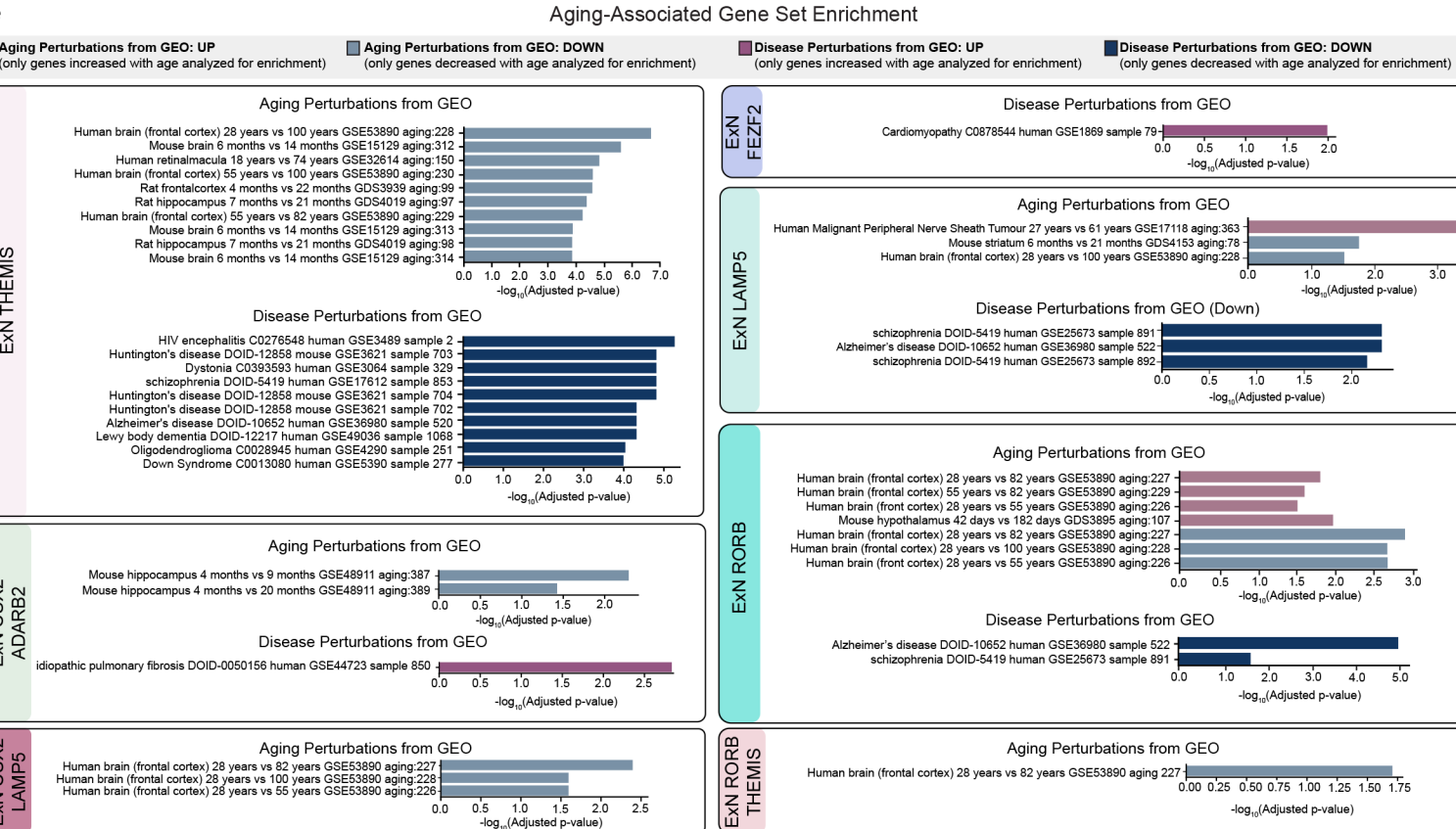
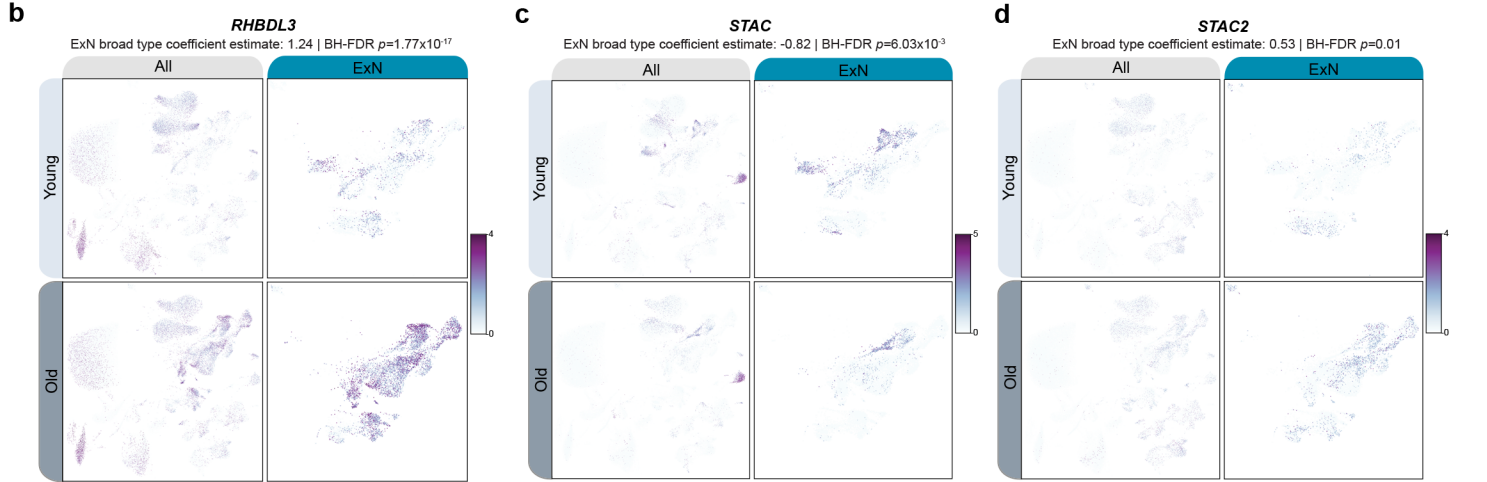
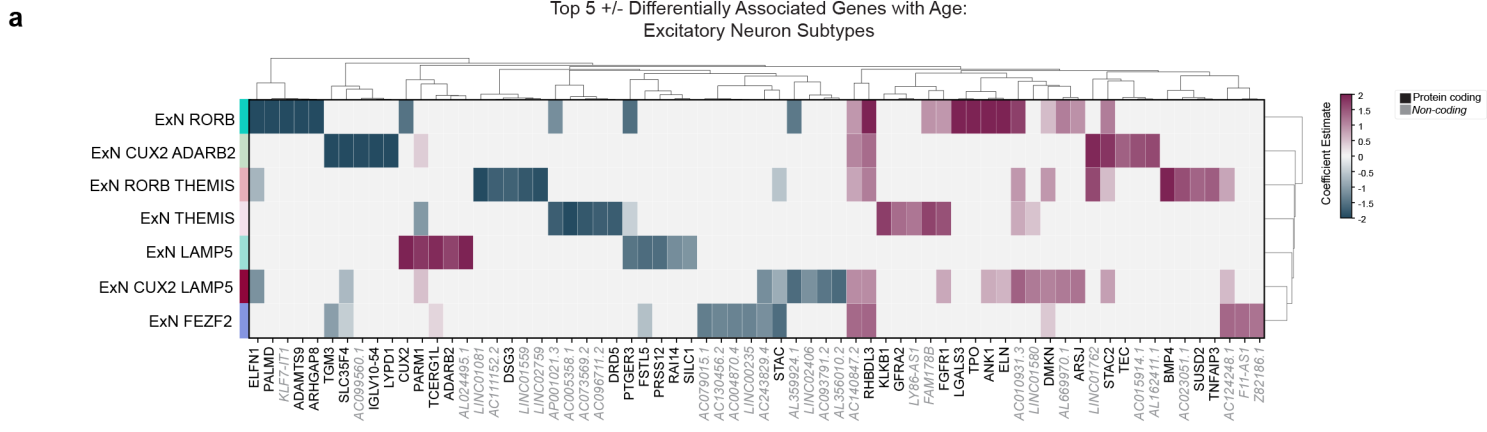


b Aging-Associated Gene Set Enrichment

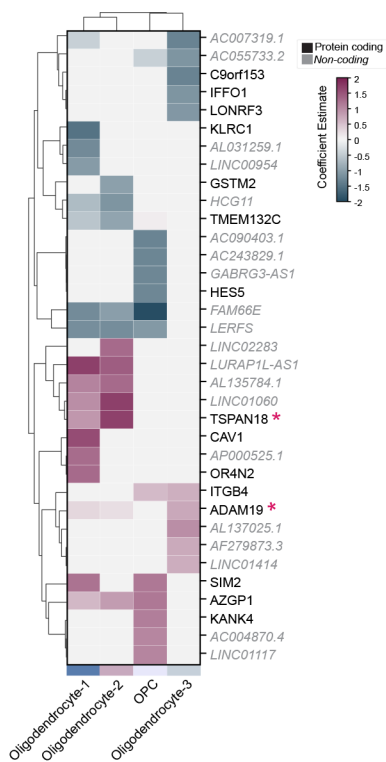
■ Aging Perturbations from GEO: UP (only genes increased with age analyzed for enrichment) ■ Aging Perturbations from GEO: DOWN (only genes decreased with age analyzed for enrichment) ■ Disease Perturbations from GEO: UP (only genes increased with age analyzed for enrichment) ■ Disease Perturbations from GEO: DOWN (only genes decreased with age analyzed for enrichment)



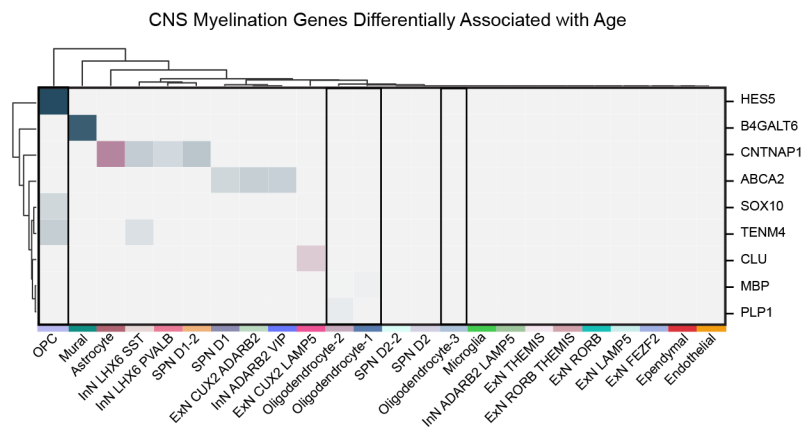
Top 5 +/- Differentially Associated Genes with Age:
Excitatory Neuron Subtypes



a Top 5 +/- aDAGs:
OPC and Oligodendrocyte

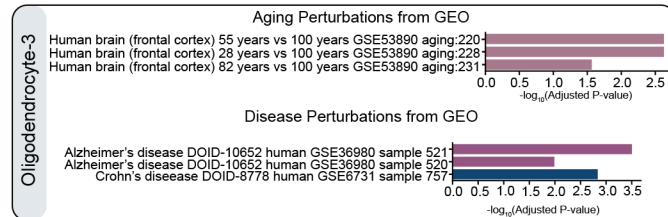
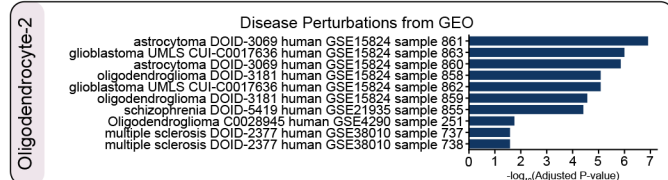
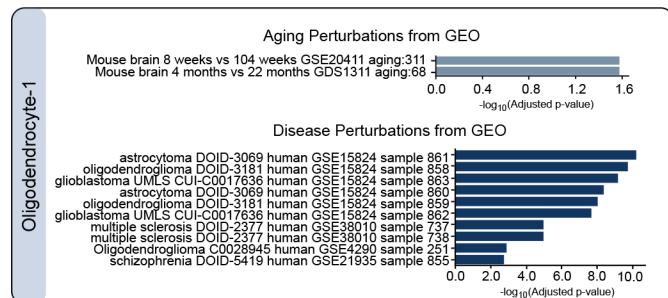
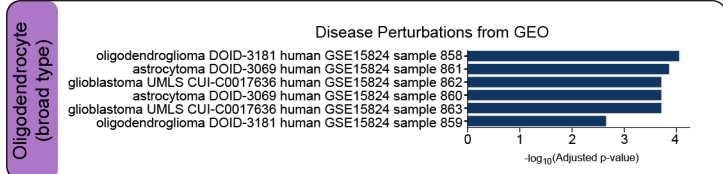
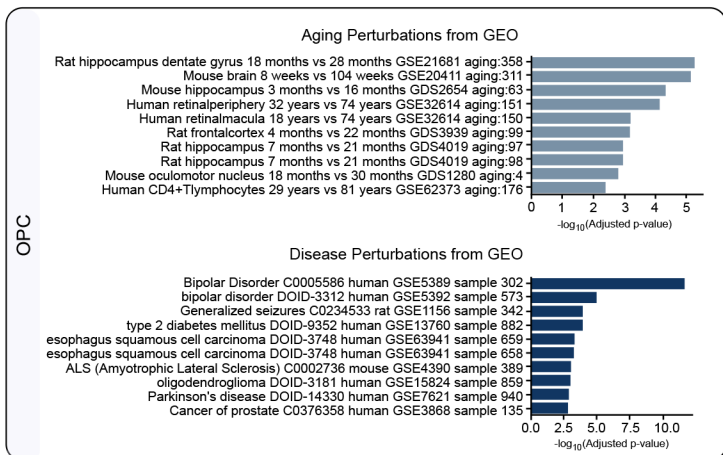
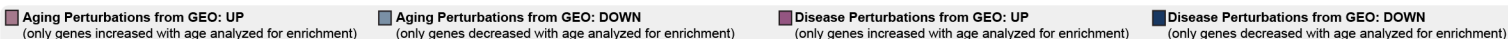


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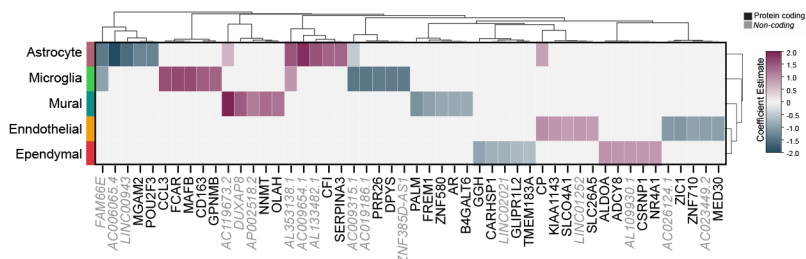


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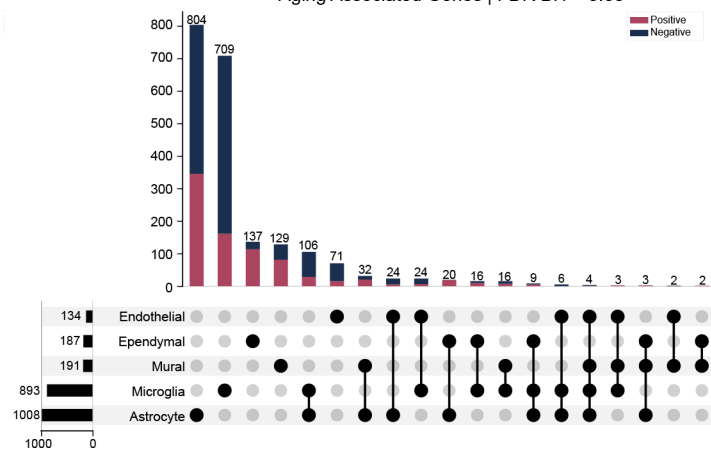
Aging-Associated Gene Set Enrichment



a Top 5 +/- Differentially Associated Genes with Age:
Non-Neuronal: Other



b Non-Neuronal: Other
Aging Associated Genes | FDR BH < 0.05



c

Ageing-Associated Gene Set Enrichment

