An Integrated Single-cell Multi-Omics Atlas of the Human Optic Nerve

Jun Wang[1]*, Ye Zheng[2]*, Jin Li[2]*, Xuan Bao[2], Ismail Yaman[1], Tingting Yang[1], Gerda Cristal Villalba Silva[1], Jianming Shao[1,3], Jinjing Jian[1], Jean Li[2], Lei Qi[2], Leah A. Owen[4,5,6], Ivana K Kim[7,8], Emil Kriukov[7,8,9], Andrea Rivera[10], Melissa L. Cooper[11], Susannah Waxman[12], Gulab Zode[2], David H. Gutmann[13], Carl Sheridan[14], Dong Feng Chen[7,8], Zhigang He[8,15], Xian-Jie Yang[16], David Osumi-Sutherland[10], Ajith V. Pankajam[17], Richard H. Scheuermann[17], Ayellet V. Segrè[8], Pei Tan[18], Treefa Shwani[5], Han Chen[19], Petr Baranov[7,8,9], Margaret M. DeAngelis[4,5,20], John Timothy Stout[3], Yumei Li[2#], Rui Chen[2#]

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Heatmap showing chromatin accessibility of differentially accessible regions (DARs) across major cell classes. Rows represent genomic regions; columns represent cell classes.

Supplementary Figure S2. QC matrix of oligodendrocyte precursor populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by donor age. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by sample ID. **e,** Bar plot showing the distribution of cells between sexes. **f,** Bar plot showing the distribution of cell data sources. **g,** Bar plot showing the distribution of cell ancestry source. **h,** Bar plot showing the distribution of cells across ancestries. **i,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S3. Cell type annotation of oligodendrocyte precursor populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing the top 10 highly ranking genes per cell population. **c**, Dot plot showing expression of reported marker genes from previous studies. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets.

Supplementary Figure S4. QC matrix of oligodendrocyte populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by donor age. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by sample ID. **e,** Bar plot showing the distribution of cells between sexes. **f,** Bar plot showing the distribution of cell data sources. **g,** Bar plot showing the distribution of cell tissue sources. **h,** Bar plot showing the distribution of cells across ancestries. **i,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S5. Cell type annotation of oligodendrocyte populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing the top 10 highly ranking genes per cell population. **c**, Dot plot showing expression of reported marker genes from previous studies. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets. **e**, Dot plot showing the expression of mechanosensory genes across oligodendrocyte lineage populations.

Supplementary Figure S6. QC matrix of Astrocyte populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by donor age. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by sample ID. **e,** Bar plot showing the distribution of cells between sexes. **f,** Bar plot showing the distribution of cell data sources. **g,** Bar plot showing the distribution of cells across ancestries. **h,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S7. Cell type annotation of astrocyte populations

a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing the top 10 highly ranking genes per cell population. **c**, Dot plot showing expression of reported marker genes from previous studies. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets.

Supplementary Figure S8. QC matrix of fibroblast populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by donor age. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by sample ID. **e,** Bar plot showing the distribution of cells between sexes. **f,** Bar plot showing the distribution of cell data sources. **g,** Bar plot showing the distribution of cell tissue sources. **h,** Bar plot showing the distribution of cells across ancestries.

Supplementary Figure S9. Cell type annotation of fibroblast populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing the top 10 highly ranking genes per cell population. **c**, Dot plot showing expression of reported marker genes from previous studies. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets. **e**, Dot plot showing the expression of *ACTA2* and *TPM1* across fibroblast populations.

Supplementary Figure S10. QC matrix of microglia populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by donor age. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by sample ID. **e,** Bar plot showing the distribution of cells between sexes. **f,** Bar plot showing the distribution of cell data sources. **g,** Bar plot showing the distribution of cell tissue sources. **h,** Bar plot showing the distribution of cells across ancestries. **i,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S11. Cell type annotation of microglia populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing expression of reported marker genes from previous studies. **c**, Dot plot showing the top 10 highly ranking genes per cell population. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets.

Supplementary Figure S12. QC matrix of macrophage populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by donor age. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by sample ID. **e,** Bar plot showing the distribution of cells between sexes. **f,** Bar plot showing the distribution of cell data sources. **g,** Bar plot showing the distribution of cell tissue sources. **h,** Bar plot showing the distribution of cells across ancestries.

Supplementary Figure S13. Cell type annotation of macrophage populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing expression of reported marker genes

from previous studies. **c**, Dot plot showing the top 10 highly ranking genes per cell population. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets. **e,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S14. QC matrix of endothelial cell populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by cell type label. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by donor age. **e,** UMAP of cells colored by sample ID. **f,** Bar plot showing the distribution of cells between sexes. **g,** Bar plot showing the distribution of cell tissue sources. **h,** Bar plot showing the distribution of cell data sources. **i,** Bar plot showing the distribution of cells across ancestries. **j,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S15. Cell type annotation of endothelial cell populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing expression of reported marker genes from previous studies. **c**, Dot plot showing the top 10 highly ranking genes per cell population. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets.

Supplementary Figure S16. QC matrix of mural cell populations.
a, Violin plot showing distribution of mitochondrial percentages, gene counts, and UMI counts. **b,** UMAP of cells colored by cell type label. **c,** Heatmap showing sample contribution. Color scale indicates the proportion of cells contributed by each sample within each cell population. **d,** UMAP of cells colored by donor age. **e,** UMAP of cells colored by sample ID. **f,** Bar plot showing the distribution of cells between sexes. **g,** Bar plot showing the distribution of cell data sources. **h,** Bar plot showing the distribution of cell tissue sources. **i,** Bar plot showing the distribution of cells across ancestries. **j,** Dot plot showing the marker genes identified by NSForest.

Supplementary Figure S17. Cell type annotation of mural cell populations
a, Dot plot showing expression of marker genes identified from previous studies to exclude contamination from other cell types. **b**, Dot plot showing expression of reported marker genes from previous studies. **c**, Dot plot showing the top 10 highly ranking genes per cell population. **d**, Alluvial plot showing the correspondence between cell annotations from this study and from previous studies for cells derived from public datasets.

Supplementary Figure S18. Predicted transcription factor (TF) binding
a, Transcription factor binding sites and motifs predicted to be disrupted by rs7636574 with strong effects, as predicted by motifBreakR. **b,** Dot plot showing expression of TFs whose binding sites were predicted to be disrupted by rs7636574. **c,** The expression of associated TFs across astrocyte populations.