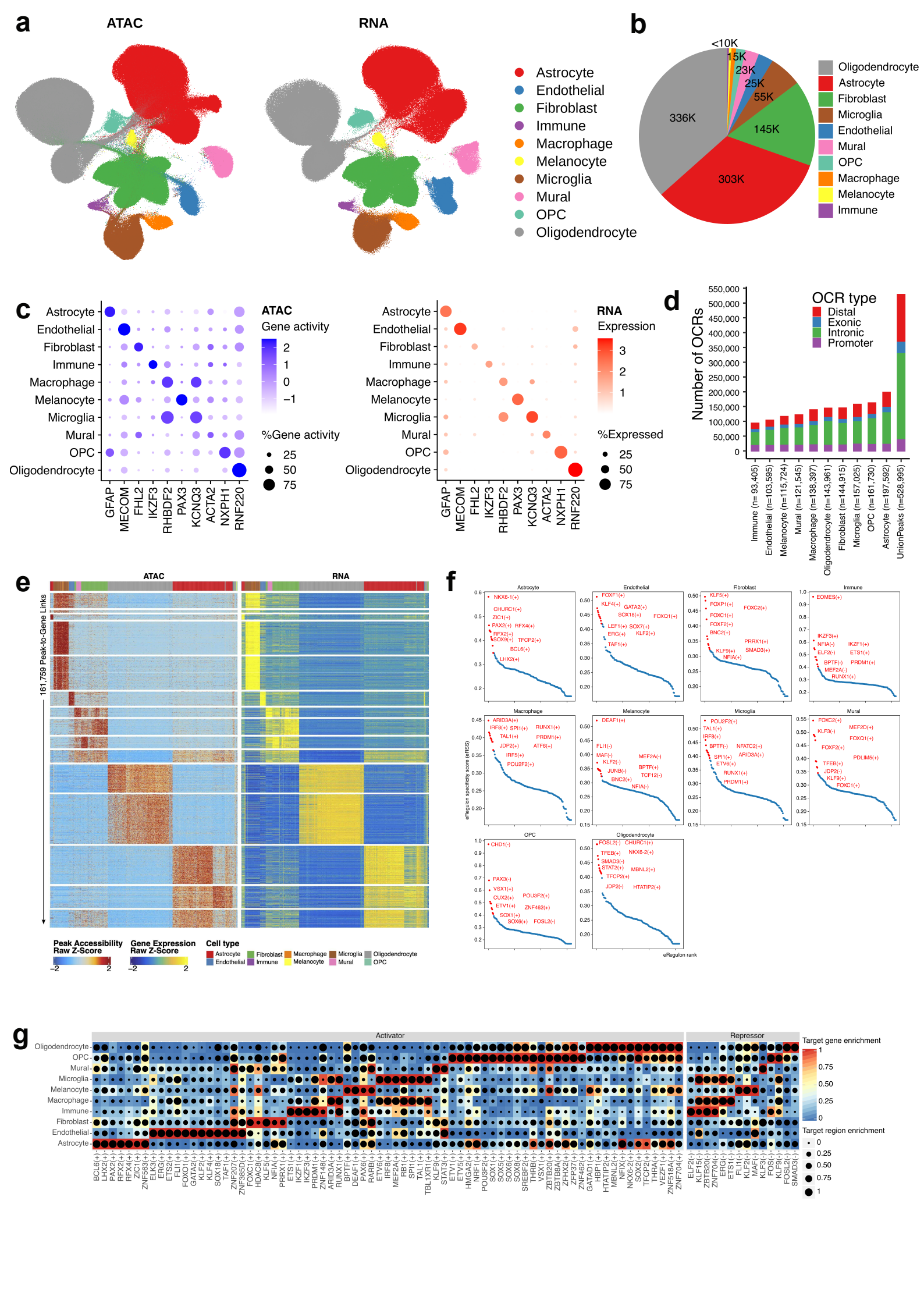
a
ATAC
RNA
Astrocyte
Endothelial
Fibroblast
Immune
Macrophage
Melanocyte
Microglia
Mural
OPC
Oligodendrocyte
b
<10K
15K
23K
25K
55K
145K
303K
336K
c
ATAC
Gene activity
%Gene activity
RNA
Expression
%Expressed
GFAP
MECOM
FHL2
IKZF3
RHBDF2
PAX3
KCNQ3
ACTA2
NXPH1
RNF220
d
OCR type
Distal
Exonic
Intronic
Promoter
Number of OCRs
Immune (n= 93,405)
Endothelial (n=103,595)
Melanocyte (n=115,724)
Mural (n=121,545)
Macrophage (n=138,397)
Oligodendrocyte (n=143,961)
Fibroblast (n=144,915)
Microglia (n=157,025)
OPC (n=161,730)
Astrocyte (n=197,592)
UnionPeaks (n=528,995)
e
ATAC
RNA
161,759 Peak-to-Gene Links
Peak Accessibility Raw Z-Score
Gene Expression Raw Z-Score
Cell type
f
eRegulon specificity score (eRSS)
eRegulon rank
g
Activator
Repressor
Target gene enrichment
Target region enrichment

**Figure 2. Chromatin accessibility of the human optic nerve cell atlas**
**a.** UMAPs showing the co-embedding of cells from snATAC-seq (left) and snRNA-seq (right) datasets, colored by major cell classes. **b.** Pie chart showing proportions of major cell classes based on chromatin accessibility profiling. Numbers within each pie chart indicate the number of ATAC-seq cells per class. **c.** Dot plots showing comparison of marker gene activity scores from snATAC-seq (left) and marker gene expression from snRNA-seq (right) across corresponding cell classes. **d.** Bar plot showing the distribution of open chromatin region (OCR) types across major cell classes, colored by genomic regions. X-axis labels indicate cell classes, with total OCR counts shown in parentheses. **e.** Heatmap of 151,001 peak-to-gene links identified across cell classes in the optic nerve. **f.** Scatter plot showing regulon specificity scores of TF regulons across cell classes. The top ten TFs are highlighted in red. **g.** Heatmap showing the 79 identified regulons, grouped as Activators and Repressors. The color key represents TF–gene enrichment scores, and dot size indicates TF–region enrichment.