# Supplemental information

Single nucleus multiomics identifies ZEB1

and MAFB as candidate regulators of Alzheimer's

disease-specific *cis*-regulatory elements

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Supplemental Figure 1

A

B

C
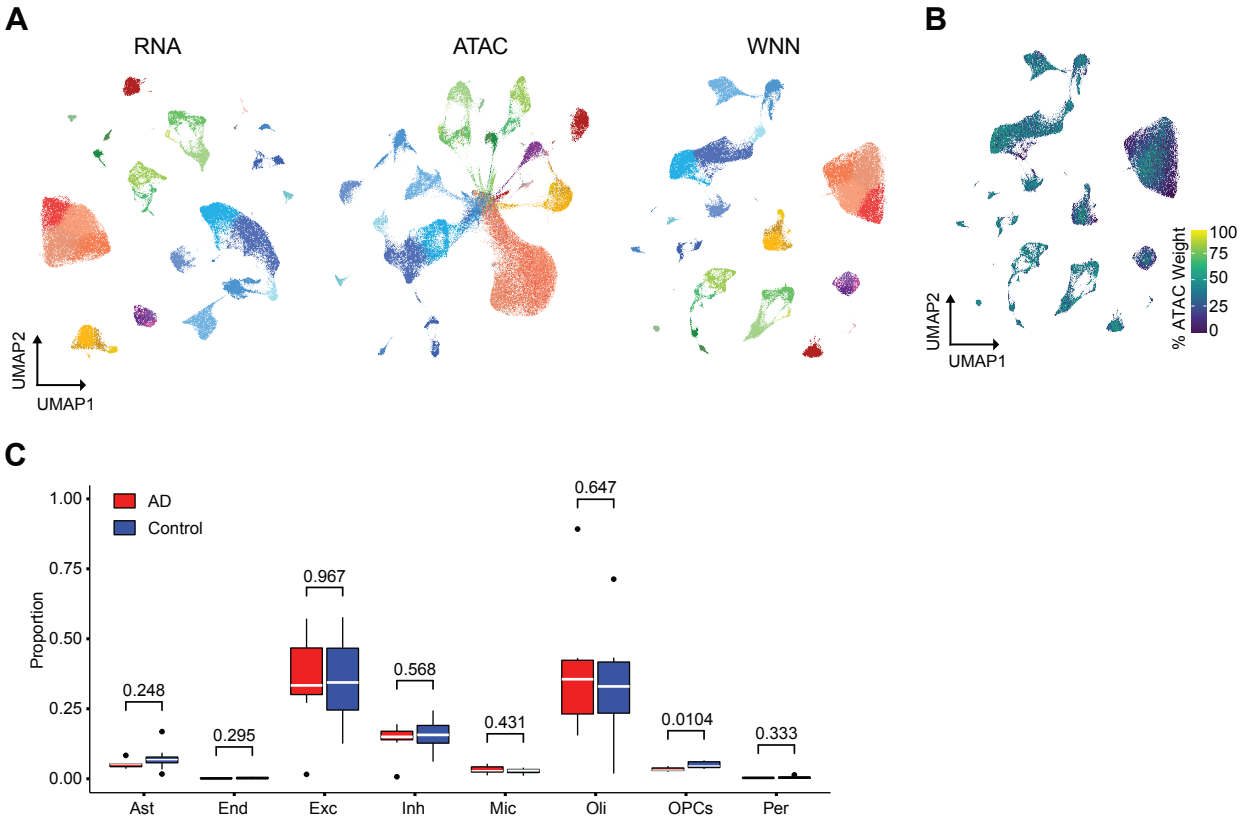
Supplemental Figure 1. Integrating snRNA-seq and snATAC-seq data, Related to Figure 1. A) UMAP visualization of cells represented by only snRNA-seq data, only snATAC-seq data, and joint WNN. Cells are colored by cell type and cluster assignment. B) WNN UMAP colored by the percent weight given to the snATAC-seq data for each cell when creating the WNN graph. C) The proportion of cells assigned to a cell type from each individual. P-values from t-test are indicated above box plots.
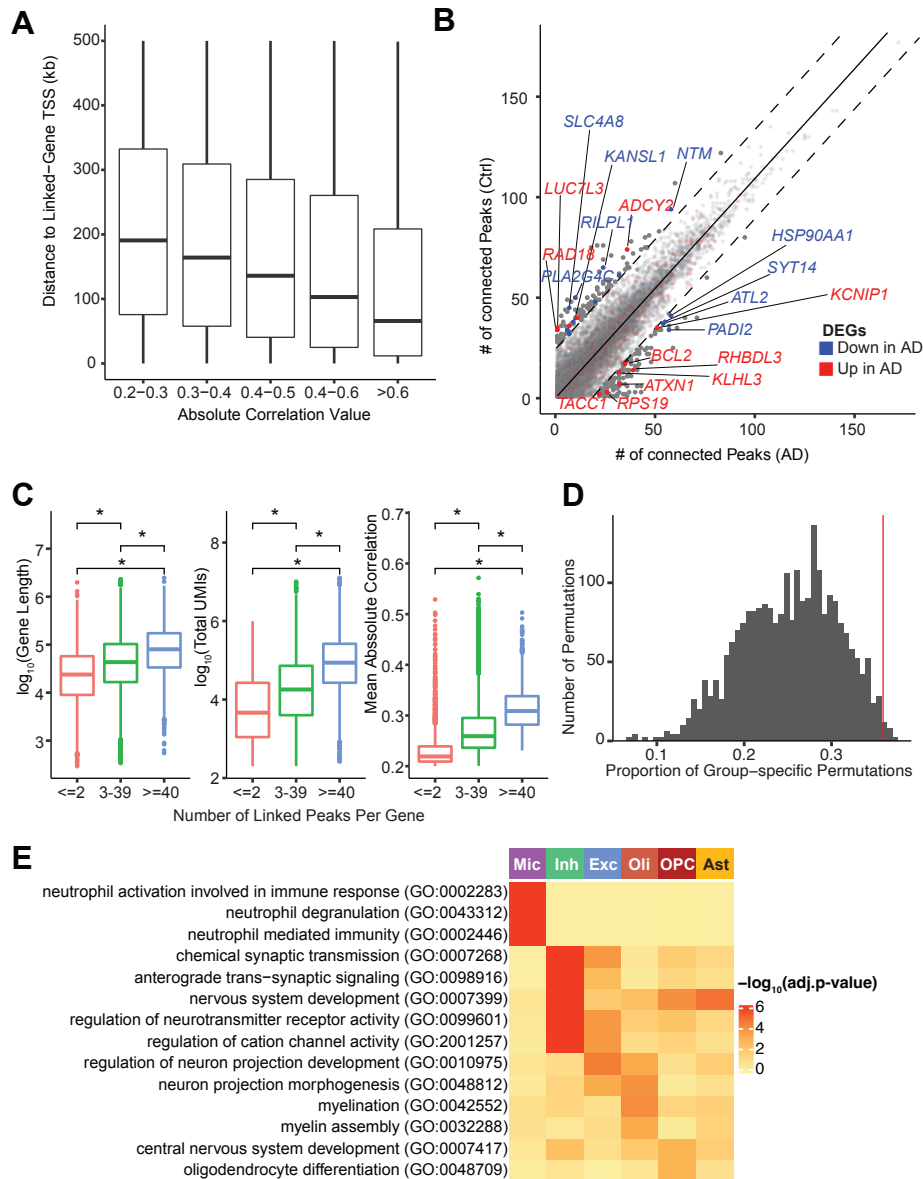
Supplemental Figure 2
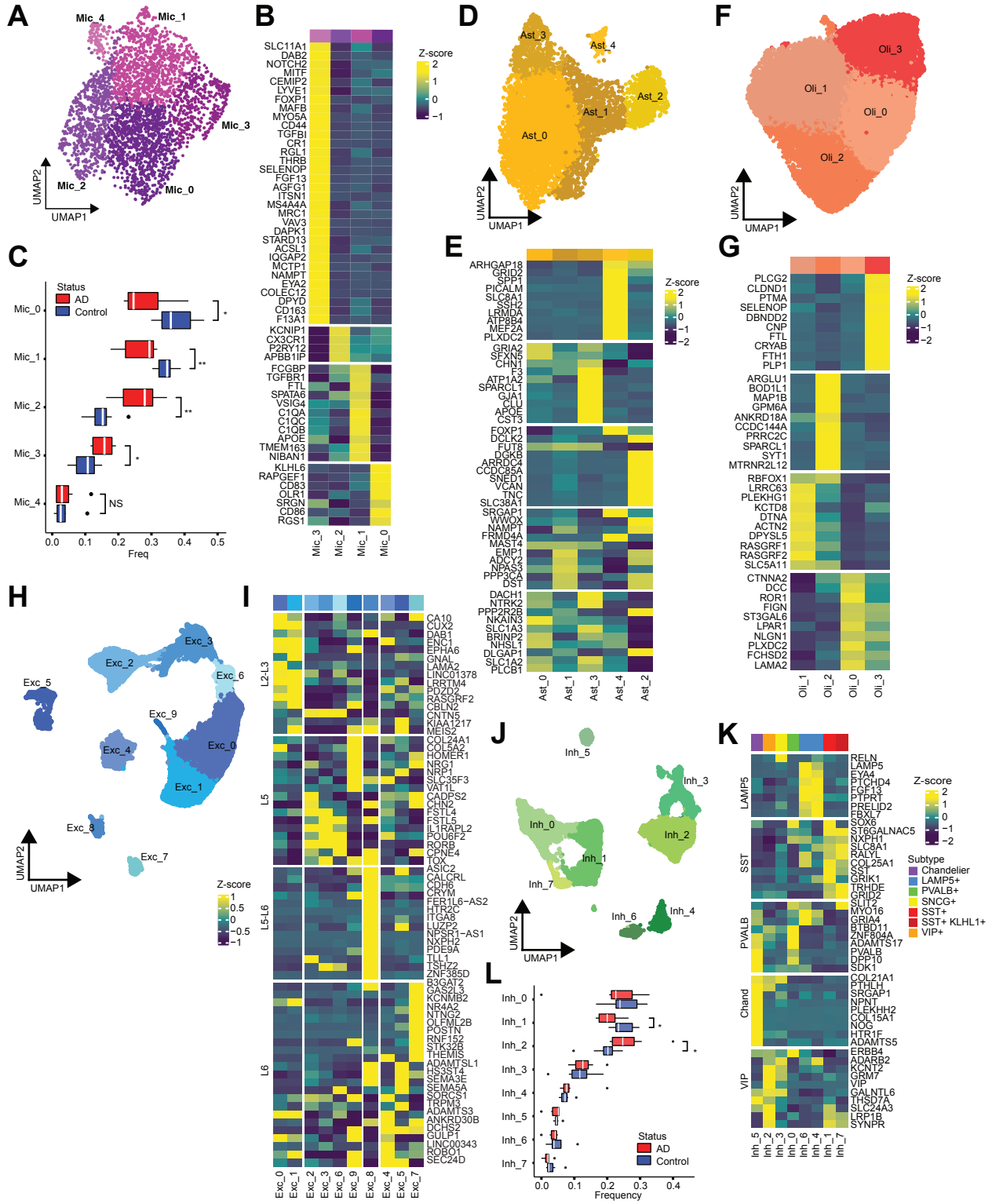
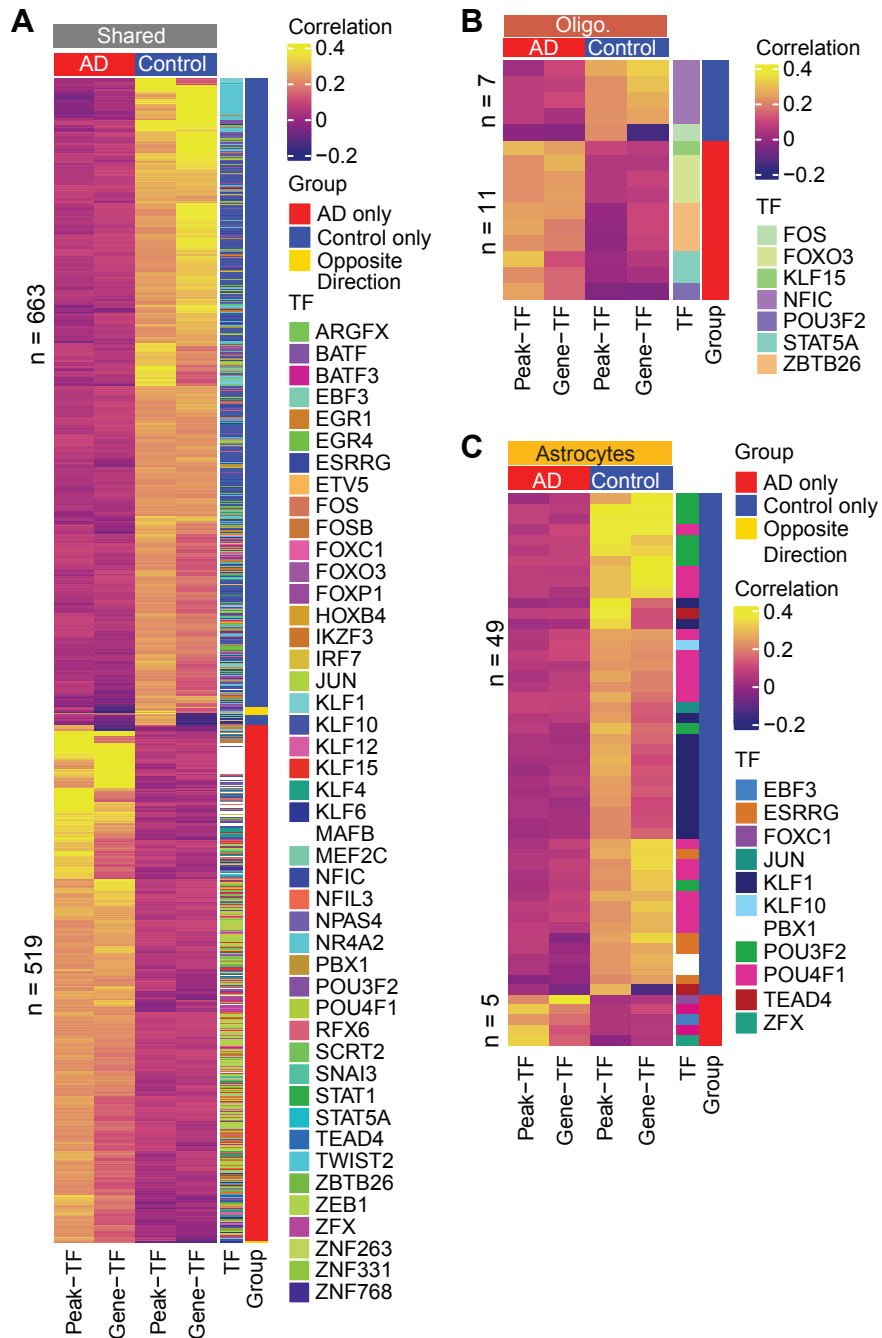**Supplemental Figure 2. Identification of cell type subclusters, Related to Figure 1.** A) UMAP visualization of 5 microglia subclusters. B) Heatmap of row-normalized expression for the top DEGs for each microglia subcluster. C) The proportion of cells assigned to each subcluster from each individual (* indicates subclusters with a t-test p-value<0.05; ** p-value< 0.01). D) UMAP visualization of 5 astrocyte subclusters. E) Heatmap of row-normalized expression for the top 10 DEGs for each astrocyte subcluster. F) UMAP visualization of the 4 oligodendrocyte subclusters. G) Heatmap of row-normalized expression for the top 10 DEGs for each oligodendrocyte subcluster. H) UMAP visualization of the 10 excitatory neuron subclusters. I) Heatmap of row-normalized expression for Azimuth Glutamatergic subtype markers. J) UMAP visualization of the 8 inhibitory subclusters. K) Heatmap of row-normalized expression for Azimuth GABAergic subtype markers. L) The proportion of cells assigned to each inhibitory subcluster from each individual (* indicated t-test p-value <0.05).
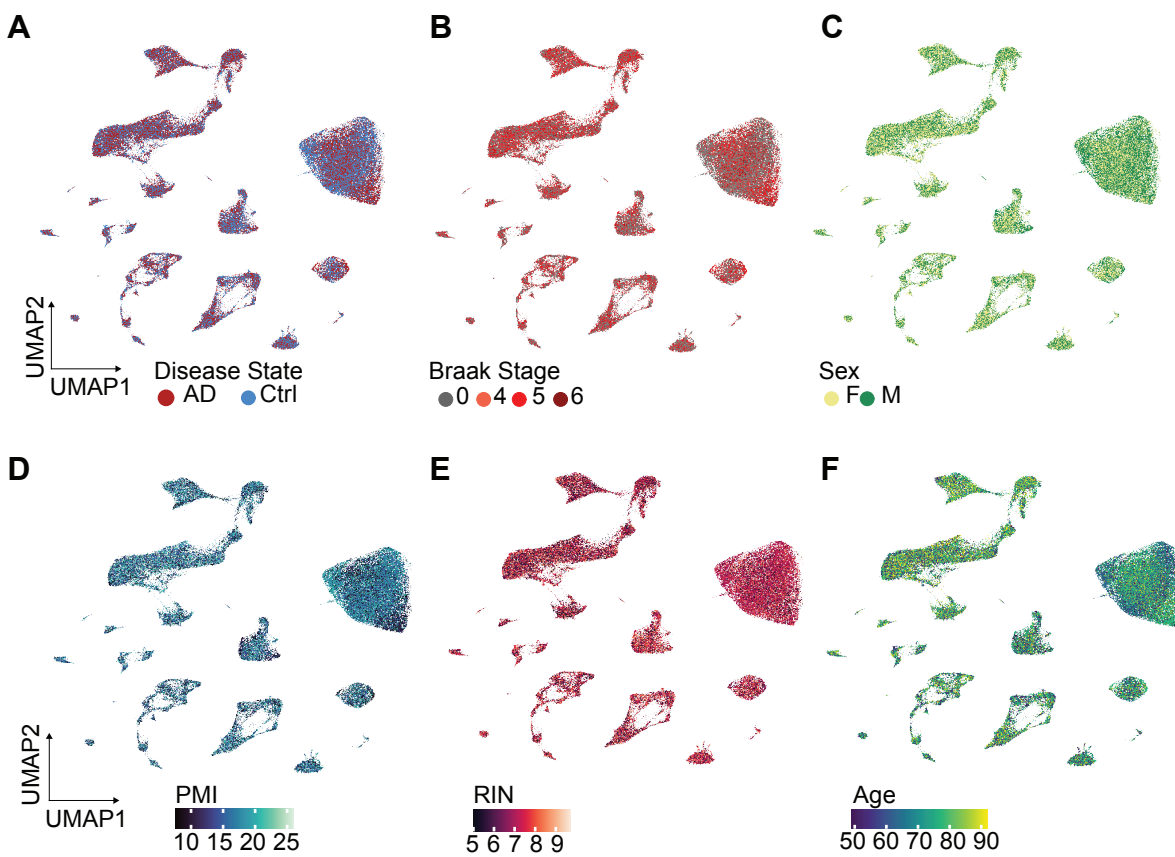
Supplemental Figure 3

Supplemental Figure 3, Related to Figure 3. Description of links identified in AD and Control samples. A) Distribution of the distance to linked gene TSS by binned absolute correlation. B) Scatter plot showing the number of links per gene for AD and control. The solid line is the best fit line and the dashed lines are the 0.01 and 0.99 residual quantiles. DEGs upregulated in AD are in red, downregulated are in blue. C) Characteristics of genes by number of links. Left panel: distribution of gene length by the number of links to the gene. Middle panel: distribution of UMIs by the number of links to the gene. Right panel: average absolute correlation score by the number of links to the gene. D) Distribution of the proportion of "group-specific" links identified in 100 permutations. Red line indicates the true proportion of AD/control-specific links identified (0.36). E) Heatmap showing the $-log_{10}$(adjusted p-value) of the significant enrichR GO terms for target genes of cell type-specific links identified in both AD and control samples.

Supplemental Figure 4

Supplemental Figure 4, Related to Figure 4. AD and control-specific peak-gene-TF trios. Heatmap of correlation values of AD and control specific trios identified in A) links shared across cell types, B) oligodendrocytes, and C) astrocytes.

Supplemental Figure 5

Supplemental Figure 5, Related to Methods. Donor characteristics across cell types. WNN UMAP colored by A) disease status, B) Braak Stage, C) sex, D) PMI, E) RIN, and F) Age.