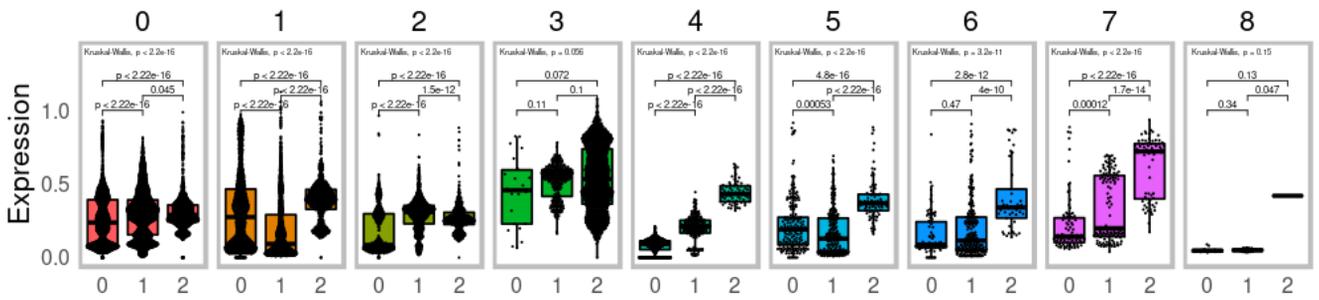
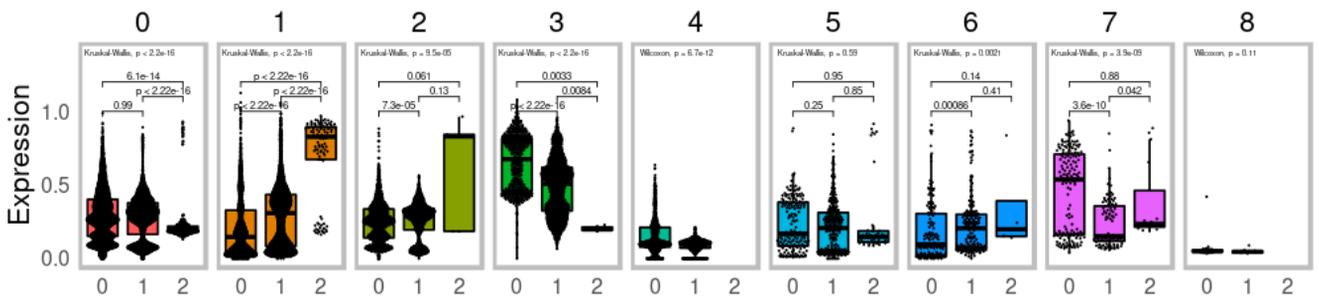


Supplemental Figure 1

A *MS4A4A* / rs1582763

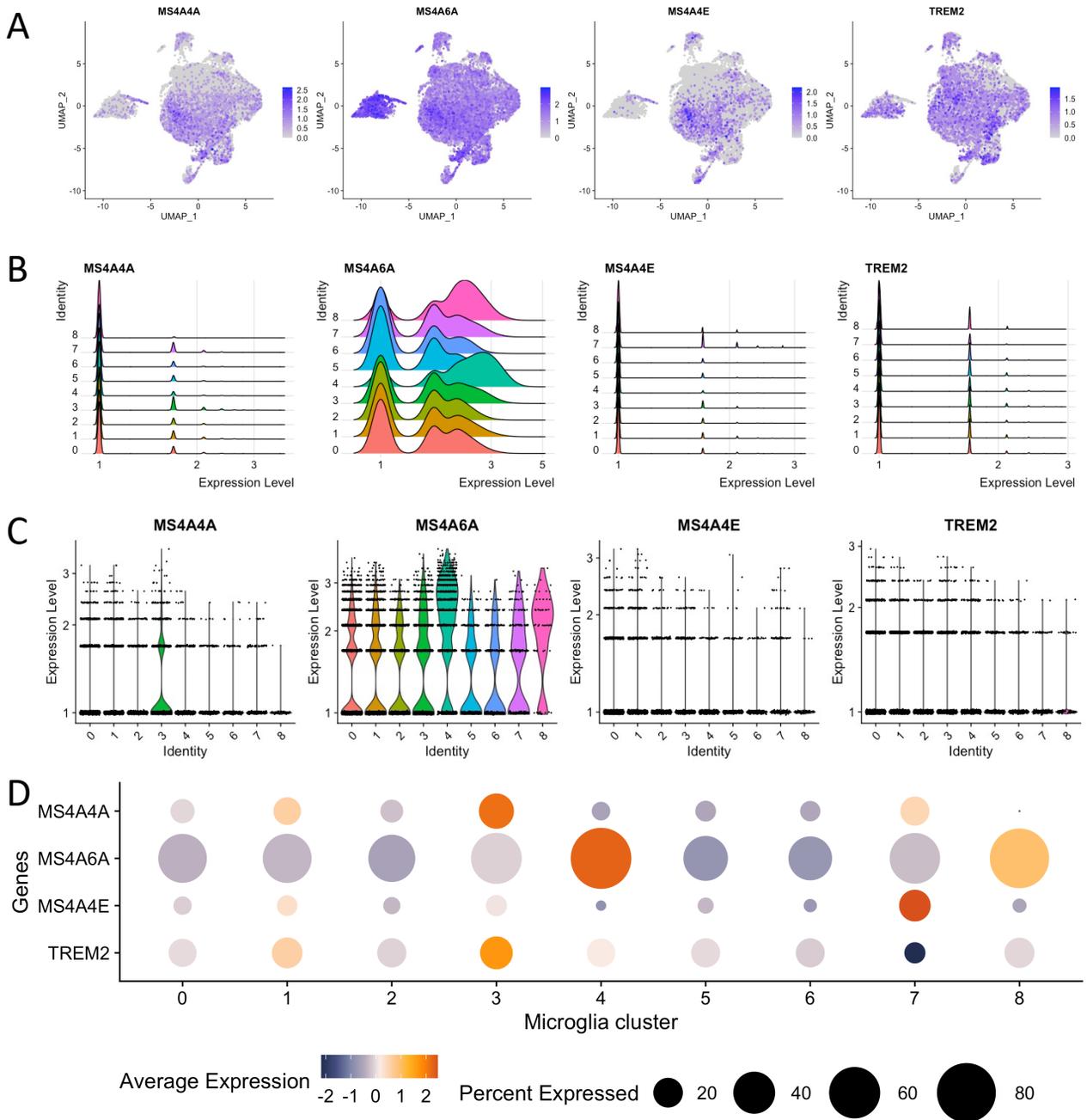


B *MS4A4A* / rs6591561



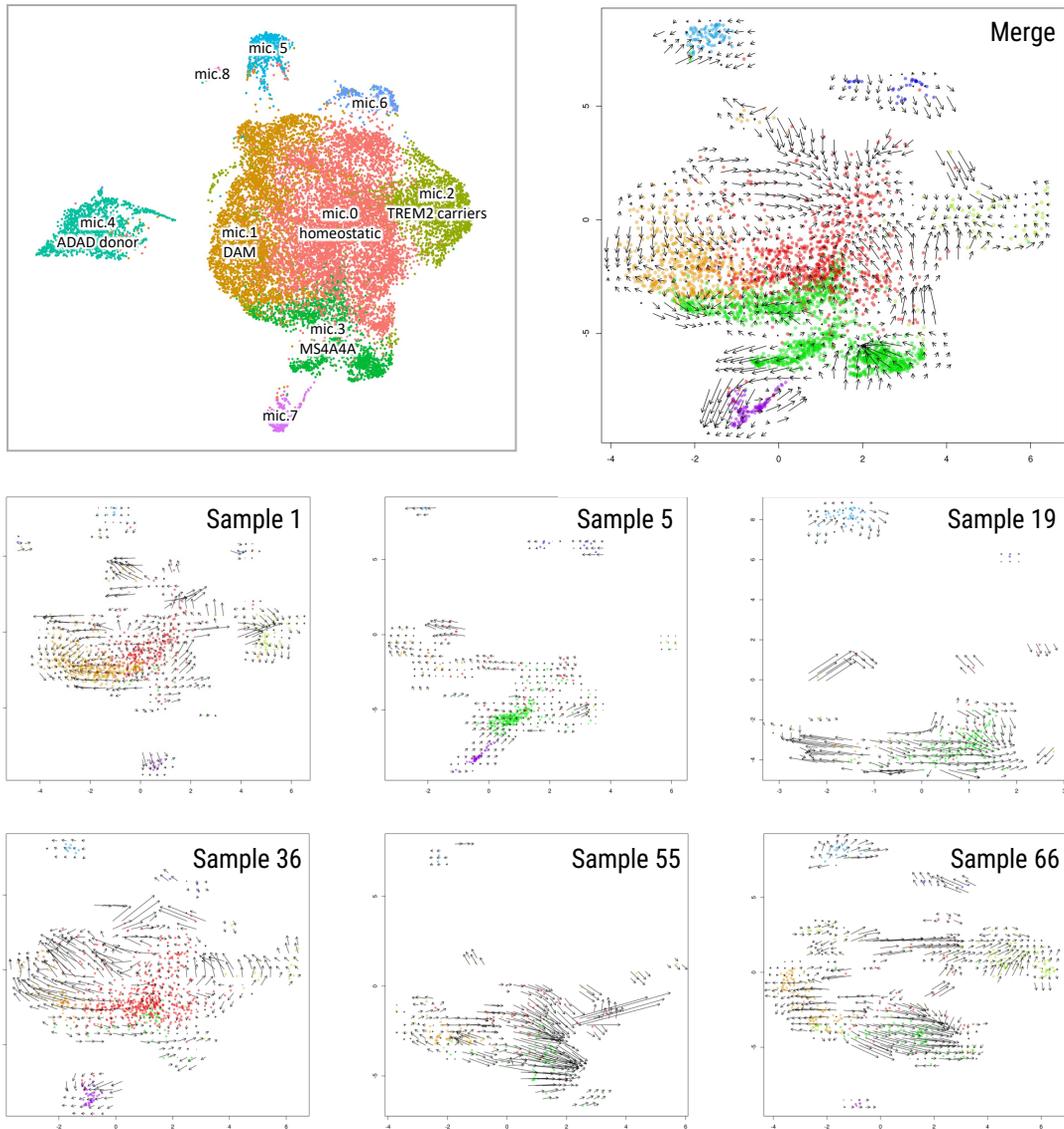
Supplemental Figure 1. *MS4A4A* expression split by (A) rs1582763 and (B) rs6591561 genotypes across microglia clusters Mic.0, Mic.1, Mic.2.

Supplemental Figure 2



Supplemental Figure 2. *MS4A4A*, *MS4A6A*, *MS4A4E* and *TREM2* expression across the microglia clusters in human brain snRNA-seq. (A) Feature plot (B) Ridge plot (C) Violin plot (D) Dot plot of *MS4A4A*, *MS4A6A*, *MS4A4E* and *TREM2* across different microglia clusters.

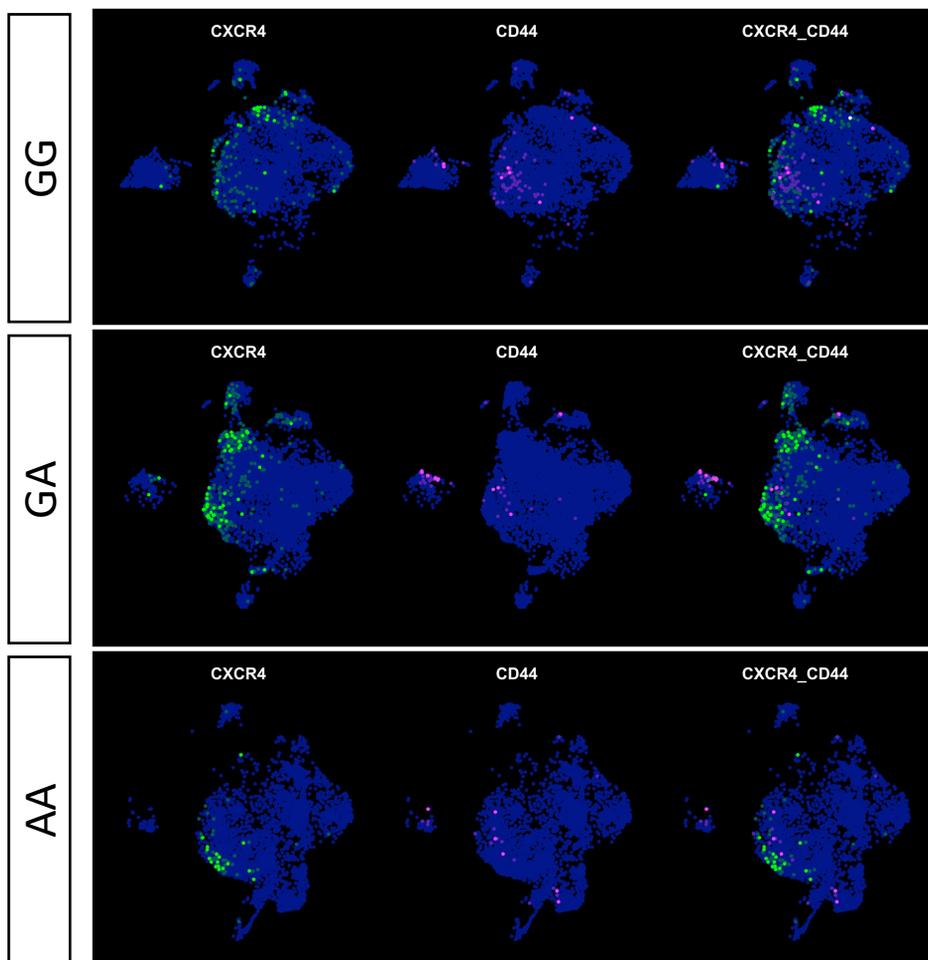
Supplemental Figure 3



Supplemental Figure 3. Examples of RNA velocity in some individual samples that contains Mic3. Top row represents merged data. Individual donors represents below.

Supplemental Figure 4

rs1582763 (G>A)



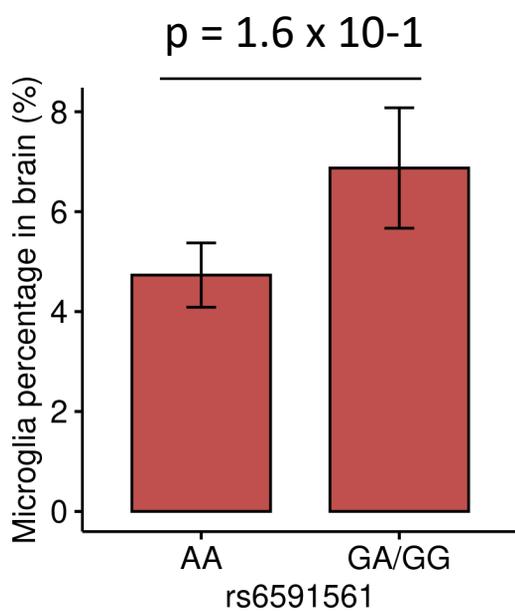
Supplemental Figure 4. Low CXCR4 and CD44 co-expression in human brain snRNAseq data. rs1582763-A minor allele carriers have less CD44+ nuclei and more CXCR4+ nuclei in microglia.

Supplemental Figure 5



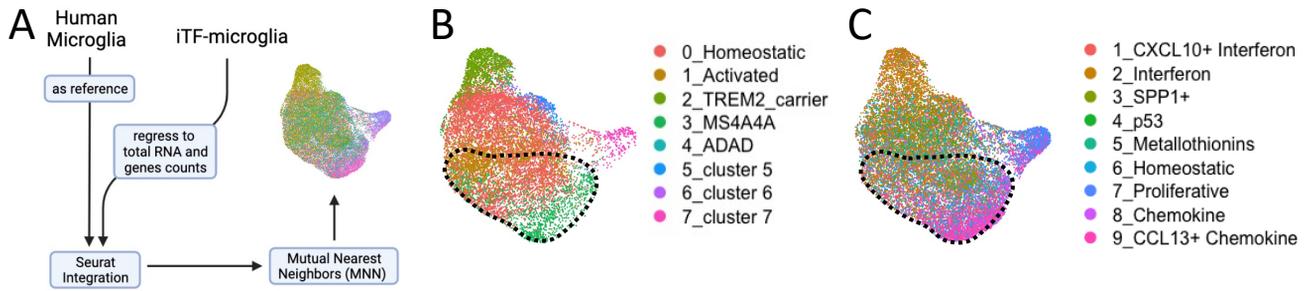
Supplemental Figure 5. CMAP predicted compounds which contradict 1582763 and mimic rs6591561 in Mic3. (Left) Compounds with effects that reverse gene expression changes associated with the protective variant rs1582763. (Right) Compounds with effects that mimic gene expression changes associated with the risk variant rs6591561.

Supplemental Figure 7



Supplemental Figure 7. Removing Mic.3 eliminated the effect of rs6591561 on overall microglia population.

Supplemental Figure 8



Supplemental Figure 8. Integration of human microglia and iTF-microglia data. A.

Schematic diagram of transcriptomic integration with human microglia and iTF-microglia using the Mutual Nearest Neighbors (MNN) method. (B) UMAP of Knight ADRC clusters. (C) iTF-microglia cluster clusters. Circle shows overlapping area between Mic.3 and iTF-microglia.8 (Chemokine) and iTF-microglia.9 (CCL13+ Chemokine).