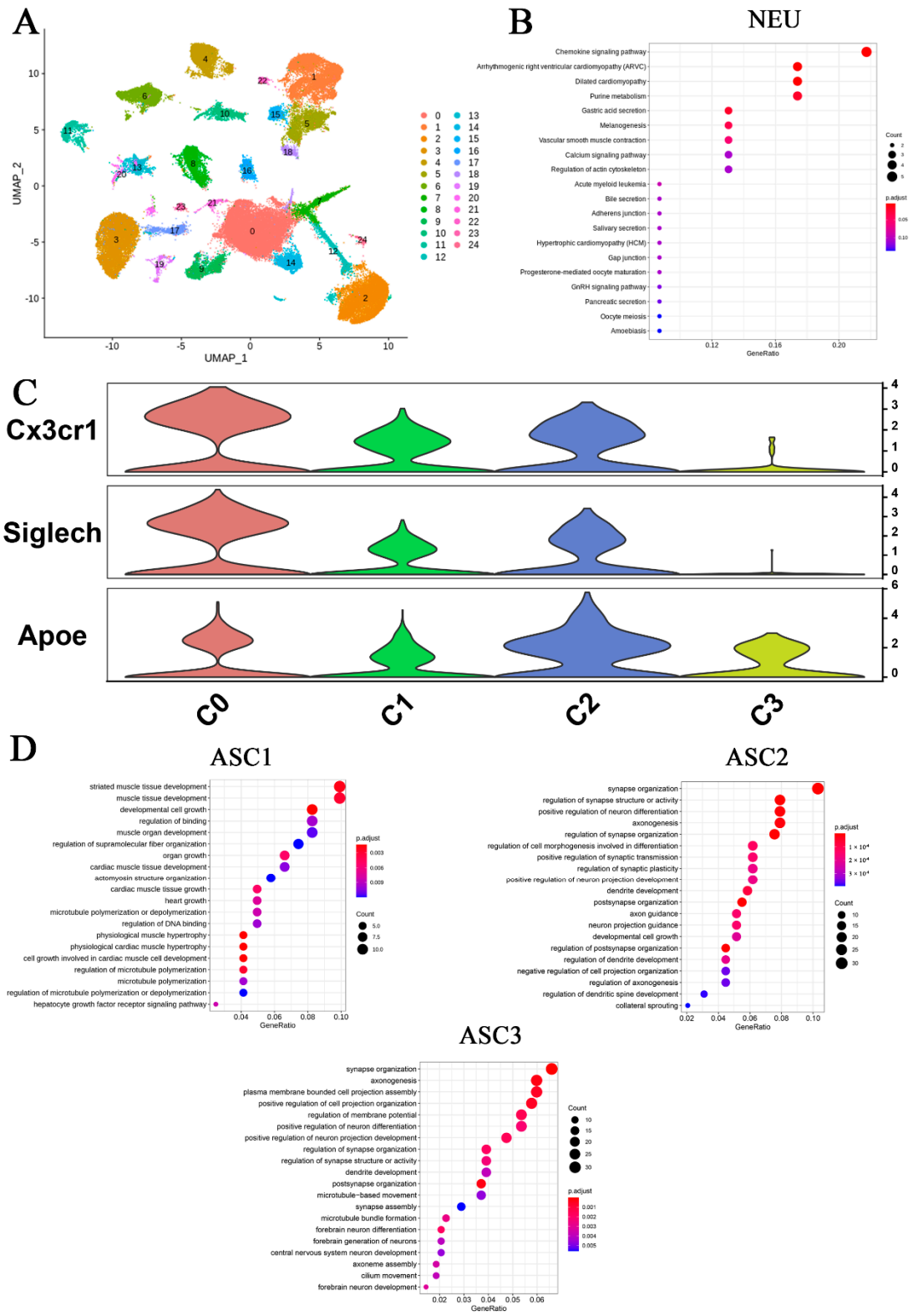


Supplementary Figure S1a: (**a**) A Uniform Manifold Approximation and Projection (UMAP) plot showing 24 clusters across the brain tissues based on data from snRNA-seq. (**b**) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways associated with the DEGs in NEUs. (**c**) A violin plot showing the expression of microglial marker genes （Cx3cr1, Siglech and Apoe）in MG subclusters. (**d**) A dot plot showing GO term enrichment based on the differentially expressed genes (DEGs) identified in the ASC subclusters.