Fig. S10

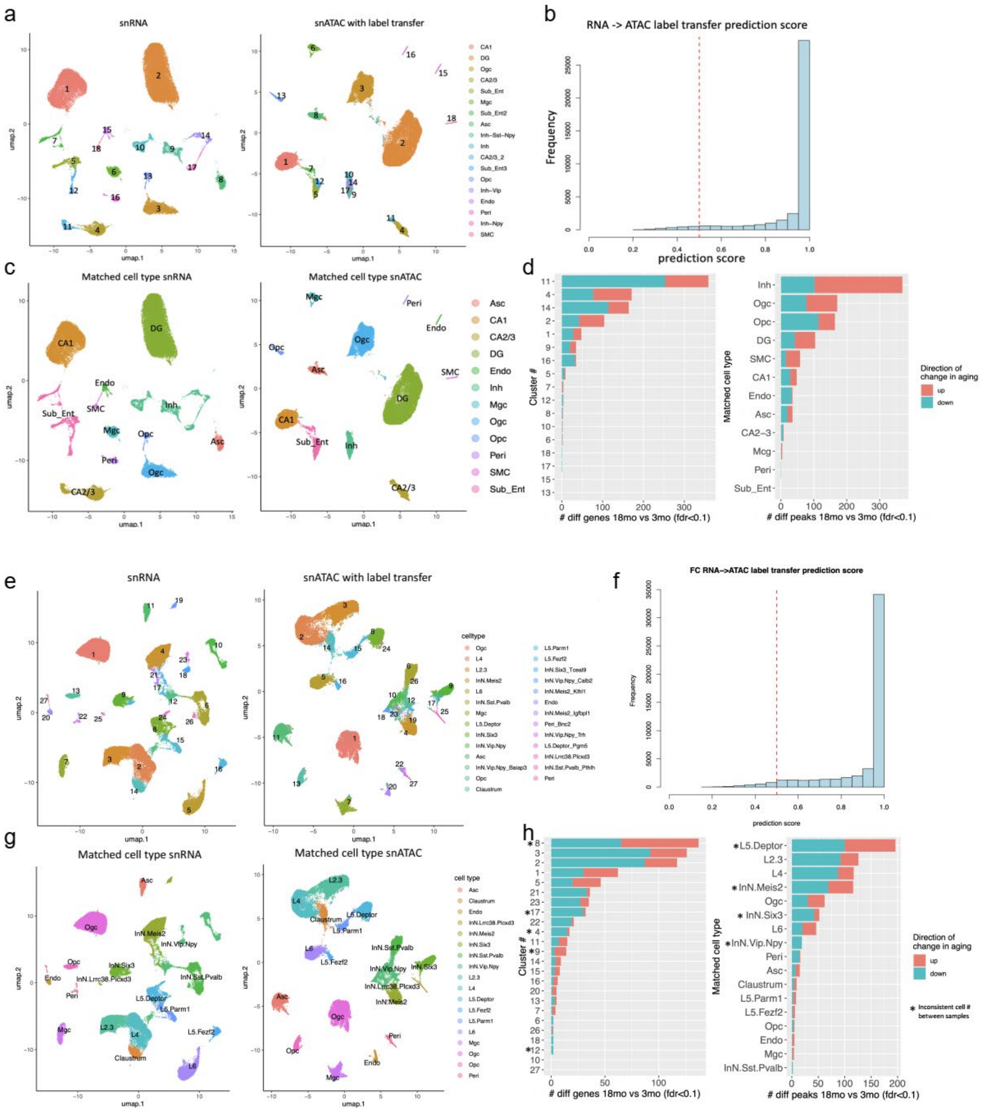

**Figure. S10. Clustering and differential expression analysis of snRNA-seq datasets and their integration of snATAC-seq datasets. a)** UMAP plot showing the projection of single cell in the transcriptomic space (left) and ATAC-seq space with the label transferred from snRNA-seq (right). **b)** Barplot showing the distribution of RNA-to-ATAC label transfer prediction score. **c)** UMAP plot showing the projection of single cell in the transcriptomic space (left) and ATAC-seq space with the label transferred from snRNA-seq (right) with consistent cell type labels that merge one-to-many matches. **d)** Boxplot showing the number of age-differential genes for each cell type. Left: cell types defined with snRNA-seq data; right: matched and consistent cell type labels from snRNA-seq and snATAC-seq data. **e-h)** Same panels as a-d) but for frontal cortex. **h)** *star denotes cell types with large variability in cell numbers between age groups.