Figure. S2. Annotation of cell types and identification of cCREs from snATAC-seq data. a) Genome browser view showing the chromatin accessibility signal at the promoters of different genes for a few representative cell types. b) Barplot showing the fold enrichment of histone marks or CTCF on cCREs over random genomic segments of the same size. c) UMAP plot showing the distribution of cells by age.