Supplementary Figures

Figure S1

Figure S1. Basic summary about the single cell datasets. (A) Comparison of the number of cells and genes before and after filtering. (B) Number of cells detected in each cell type. (C) Average number of UMIs sequenced in each cell type. (D) Average number of genes detected in each cell type.
Figure S2: Expression of known marker genes.
Figure S3: Expression of *supt16h*.