



Fig. S1. Quality control (QC) of sing-cell RNA sequencing data. (A, B) Violin plots of the total number of genes detected (nFeature\_RNA), number of transcripts (nCount\_RNA), and percentage of mitochondrial genes (percent.mt) and ribosomal genes (percent.Ribo) for each cell before (A) and after (B) QC of samples from the GSE171639 dataset. QC was performed by removing low-quality cells and doublets by the cell subset at nFeature\_RNA < 6,000 & percent.mt < 50; (C, D) Violin plots of the nFeature\_RNA, nCount\_RNA, percent.mt, and percent.Ribo for each cell before (C) and after (D) QC of samples from the GSE193649 dataset. QC was performed by the cell subset at nFeature\_RNA < 8,000 & percent.mt < 15.