



Fig. S1 Performance of Viral-Track and PathogenTrack on simulated scRNA-seq datasets. There are 810 simulated human pbmc datasets, with which contaminated 10 virus species and 10 bacteria species reads, at various technical characteristics (UMI length, read length, PCR cycles, pathogen infection levels, and standard deviation of start position). (A) Sensitivity of Viral-Track and PathogenTrack of identifying pathogen-infected cells with a range of pathogenic read datasets. (B) Time and memory consumptions of Viral-Track and PathogenTrack on 18 simulated datasets (the number of cells: 100, 500, 1000, 2000, 3000, 4000, each with 3 replicates).