

Supplementary

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1 Additional information about public data

All data can be downloaded from public repositories, the three main sources are NCBI (1) (<https://www.ncbi.nlm.nih.gov/>) and ENA (2) (<https://www.ebi.ac.uk/ena/>) and BIG Data Center (3) (<https://bigd.big.ac.cn/>).

1.1 GSE147507 dataset (4)

From this dataset we downloaded: Biological triplicates of primary human lung epithelium (NHBE) which were mock treated or infected with SARS-CoV-2 (USA-WA1/2020) at an MOI

of 2; Biological triplicates of transformed lung alveolar (A549) cells which were mock treated or infected with SARS-CoV-2 (USA-WA1/2020) at an MOI of 0.2 or 2; Biological triplicates of transformed lung alveolar (A549) transduced with a vector expressing human ACE2, which were also mock treated or infected with SARS-CoV-2 (USA-WA1/2020) at an MOI of 0.2 or 2; Biological triplicates of transformed lung-derived Calu-3 cells which were mock treated or infected with SARS-CoV-2 (USA-WA1/2020) at an MOI of 2; COVID-19 patient samples: Uninfected human lung biopsies derived from one male (age 72) and one female (age 60) and used as control biological replicates, and lung samples derived from a single male COVID-19 deceased patient (age 74) which were processed in technical replicates. Library preparation method polyA+ selection was used to remove rRNAs before sequencing.

1.2 GSE148729 dataset (5)

From this dataset we downloaded biological replicates of Calu-3, Caco-2 and H1299 cells which were mock treated or infected with SARS-CoV-2 (patient isolate BetaCoV/Munich/BavPat1/2020/EPI_ISL_406862) or SARS-CoV (Frankfurt strain) at an MOI of 0.3. Library preparation method polyA+ selection was used to remove rRNAs before sequencing Caco-2 and H1299 cells. For Calu-3 cells, two library preparation method polyA+ selection and rRNA-depletion were used respectively to remove rRNAs before sequencing.

1.3 GSE153940 dataset

From this dataset we downloaded RNA sequencing data of Vero E6 cells which were either mock-infected or infected with SARS-CoV-2 USA-WA1/2020 (MOI = 0.3) with three replicates. However, when we downloaded the data one sample with accession number GSM4658806 was not available for downloading. Cells were harvested at 24 hours after infection, and rRNA-depletion method was used to extract RNA for sequencing.

1.4 GSE56189 dataset

From this dataset we downloaded: Biological triplicates of MRC5 and Vero E6 cells which were mock treated or infected with SARS-CoV (Urbani strain) or MERS-CoV (EMC/2012) at an MOI of 0.1 or 3. Library preparation method polyA+ selection was used to remove rRNAs before sequencing.

1.5 CRA002390 dataset (6)

This dataset is public available in <https://bigd.big.ac.cn/gsa/browse/CRA002390>. From this dataset we downloaded: The raw FASTQ data of PBMC and BALF samples of COVID-19 patients and corresponding PBMC controls.

1.6 PRJNA434133 dataset (7)

From this dataset we downloaded the raw FASTQ data for BALF healthy control samples with accession numbers SRR10571724, SRR10571730, and SRR10571732.

1.7 GSE145926 dataset (8)

From this dataset we downloaded the preprocessed single cell RNA-Seq data of BALF samples from 6 severe COVID-19 patients and 3 mild COVID-19 patients.

1.8 PRJNA526088 dataset (9)

From this dataset we downloaded the preprocessed single cell RNA-Seq data of BALF sample from a healthy control with accession number GSM3660650.

2 Supplementary figures

Fig. S1:

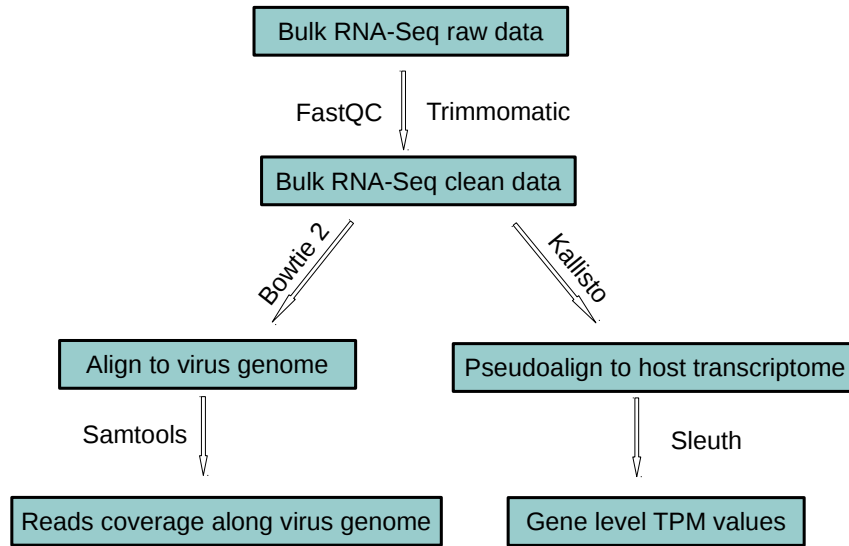


Fig. S2:

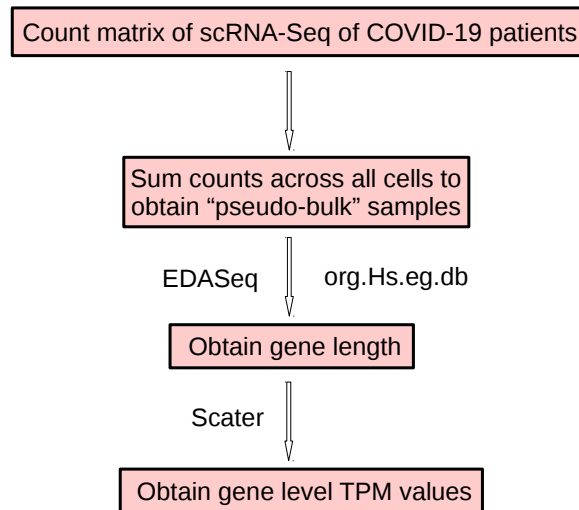


Fig. S3:

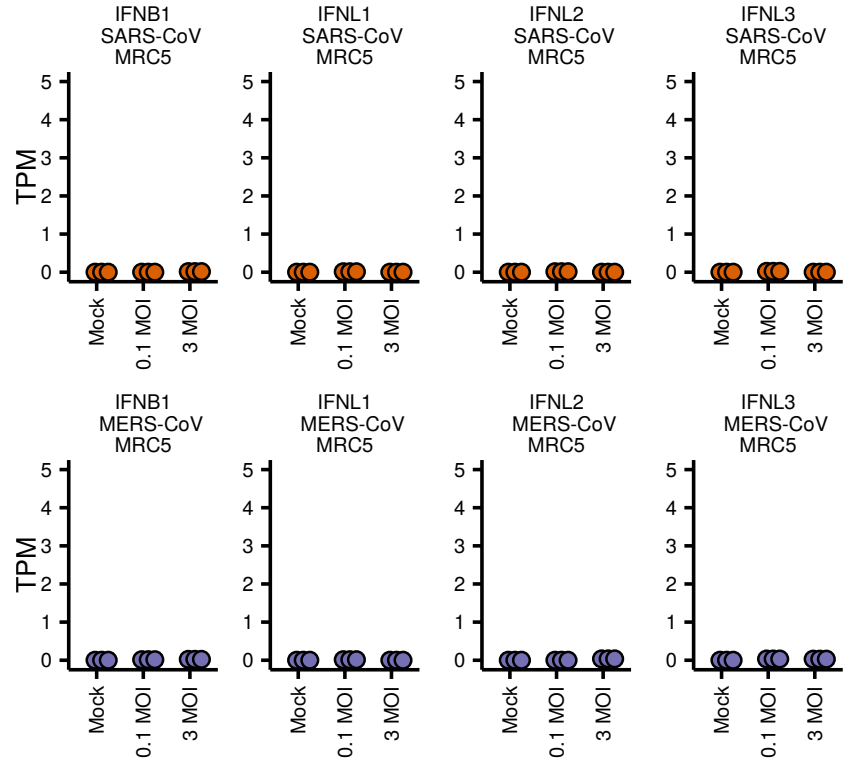


Fig. S4:

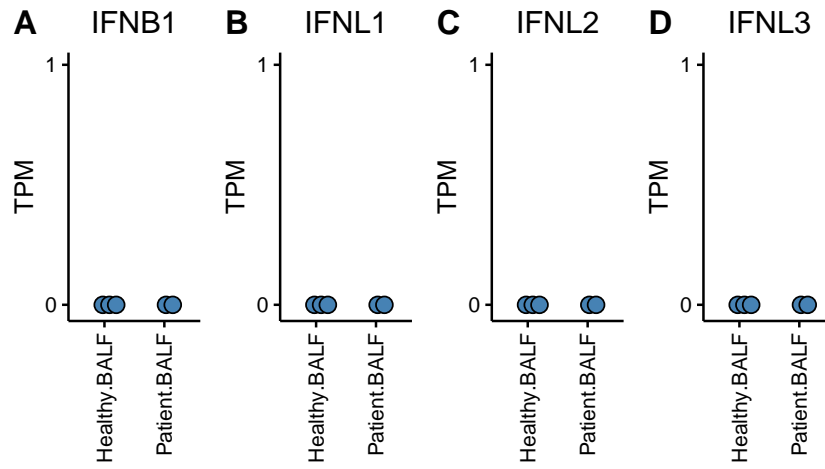


Fig. S5:

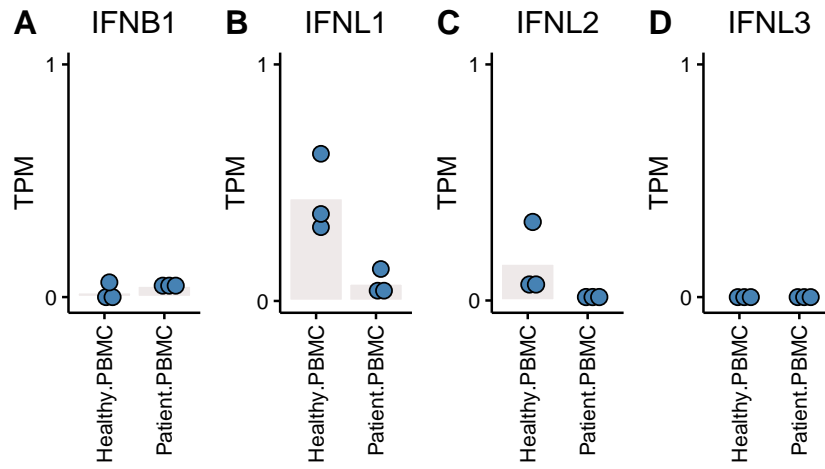


Fig. S6:

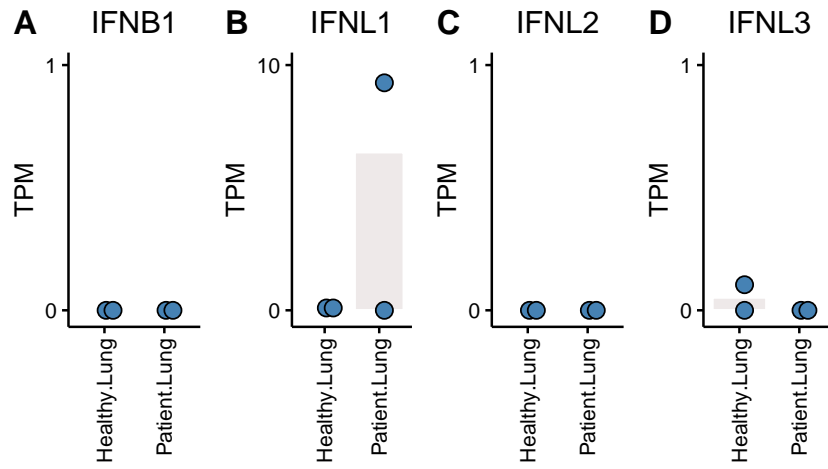


Fig. S7:

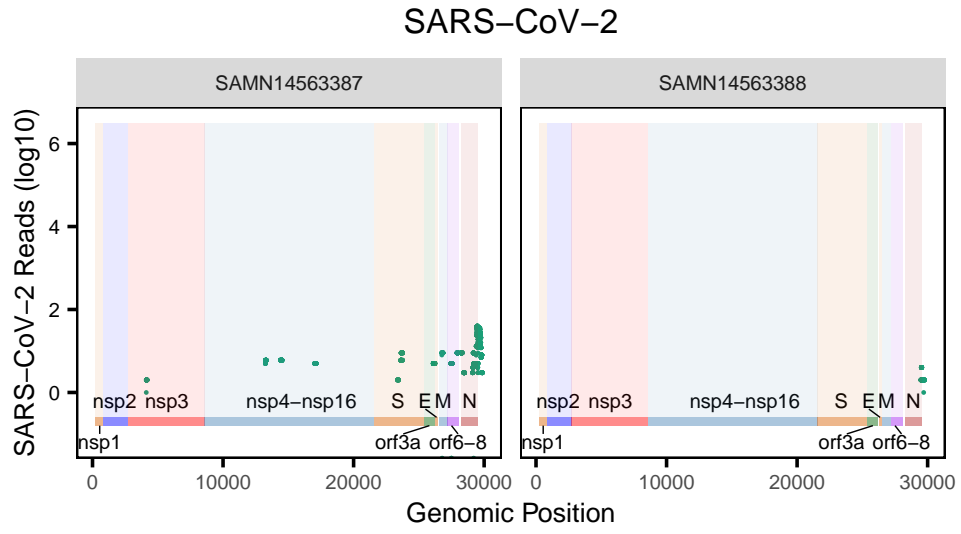
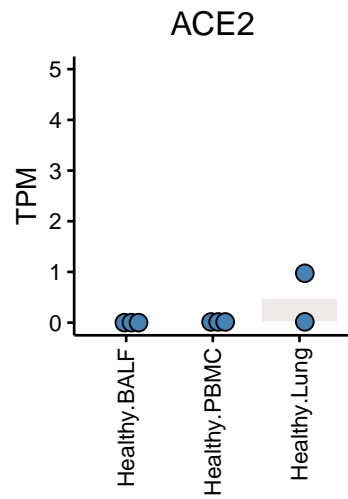


Fig. S8:



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