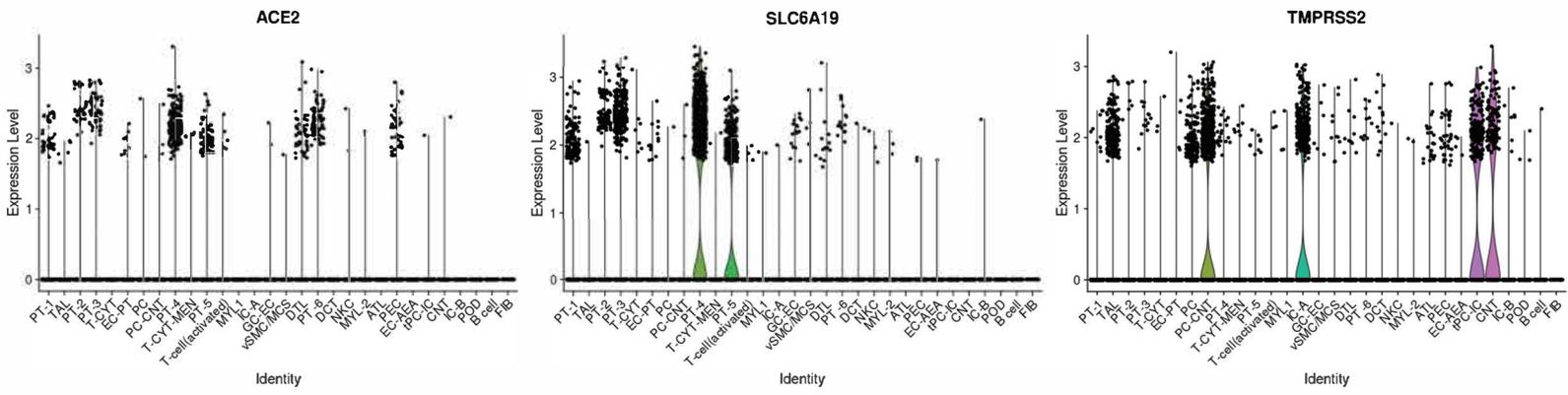
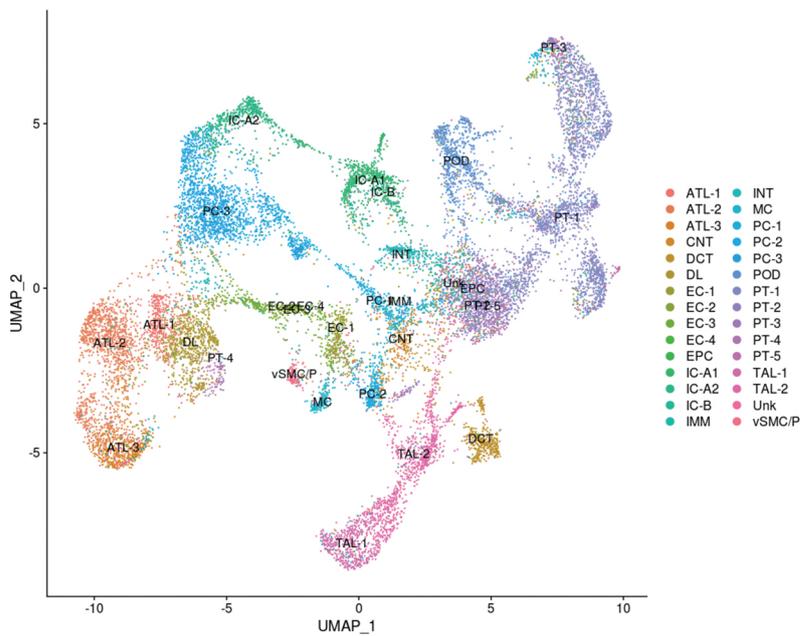
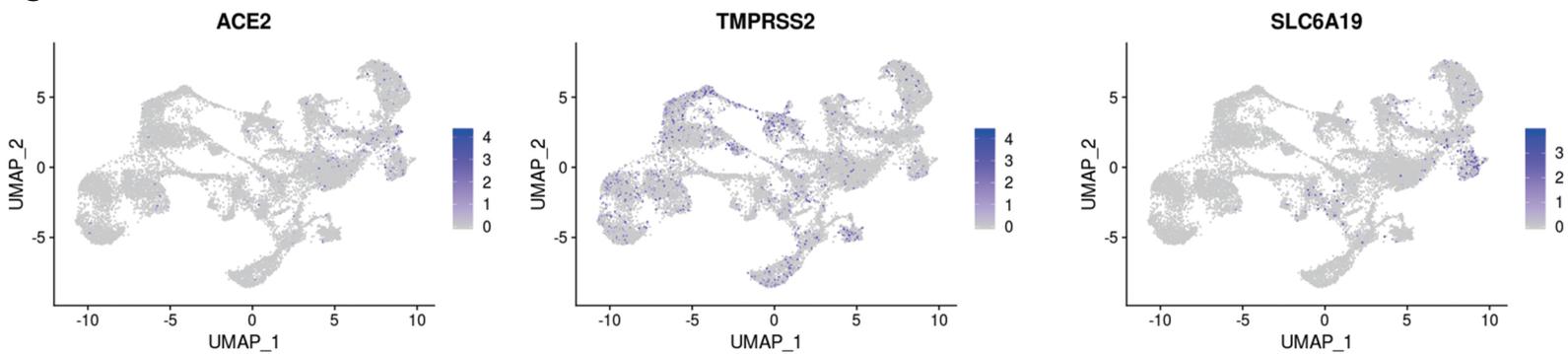
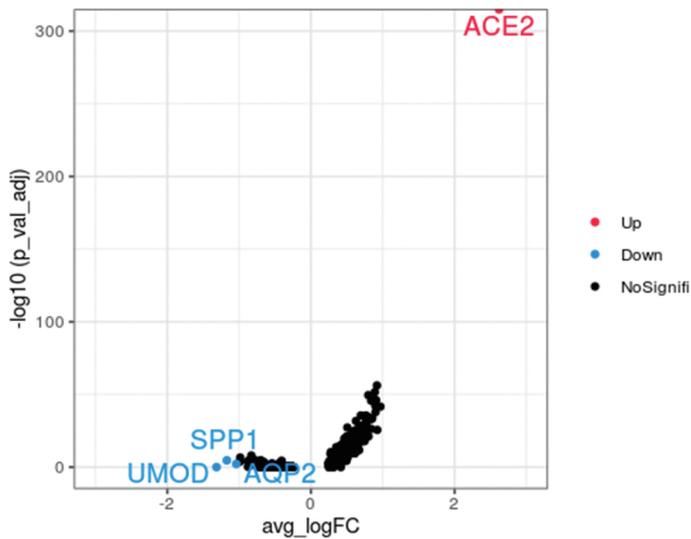


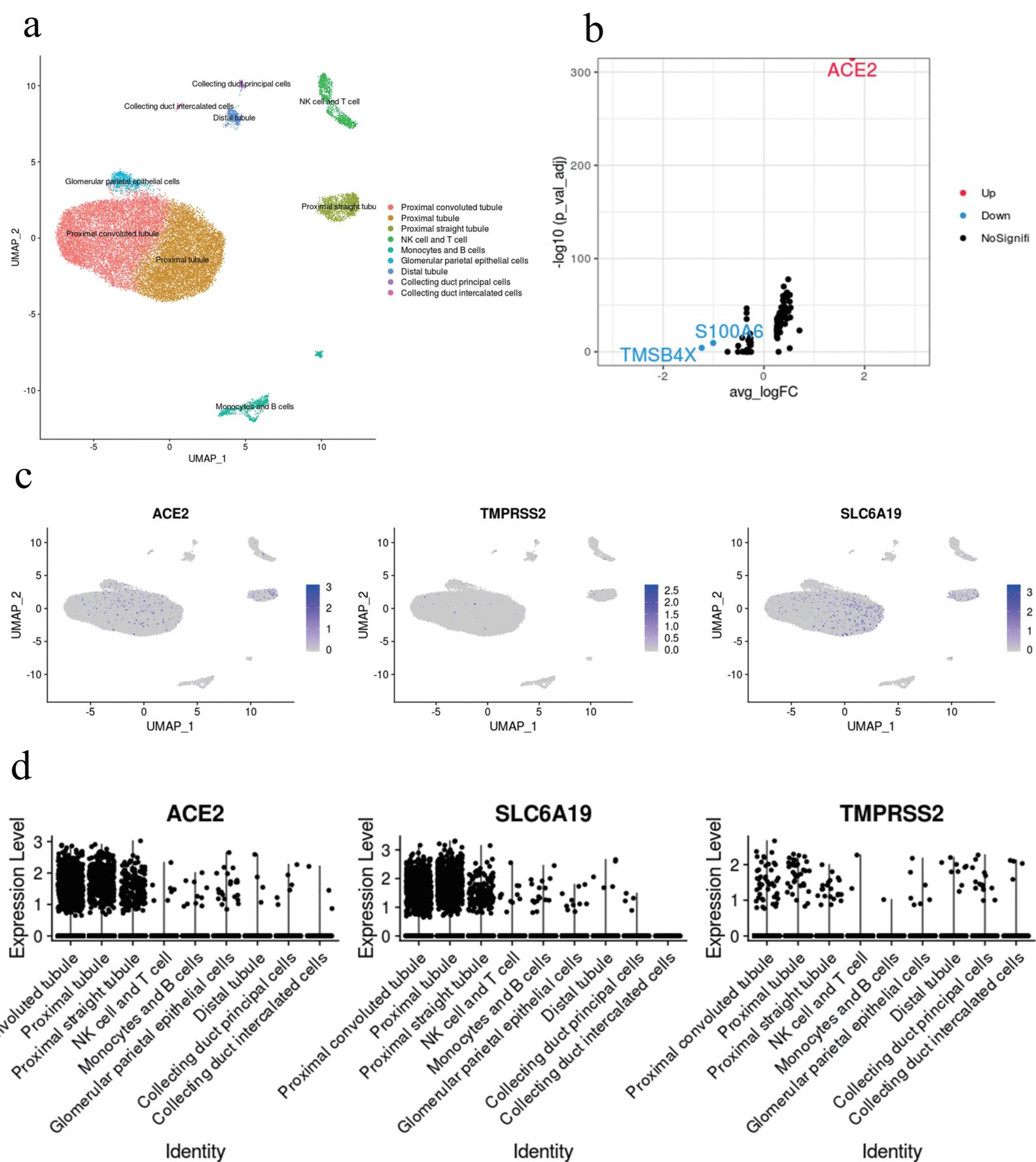
Supplementary Figure 1. Expression of ACE2 in different tissues and organs. **a:** NCBI database selected as HPA RNA-seq normal tissue; **b:** NCBI database selected as RNA sequencing of total RNA from 20 human tissues. **c:** NCBI database selected as Illumina bodyMap2 transcriptome. The data is from the website: <https://www.ncbi.nlm.nih.gov/gene/?term=59272>



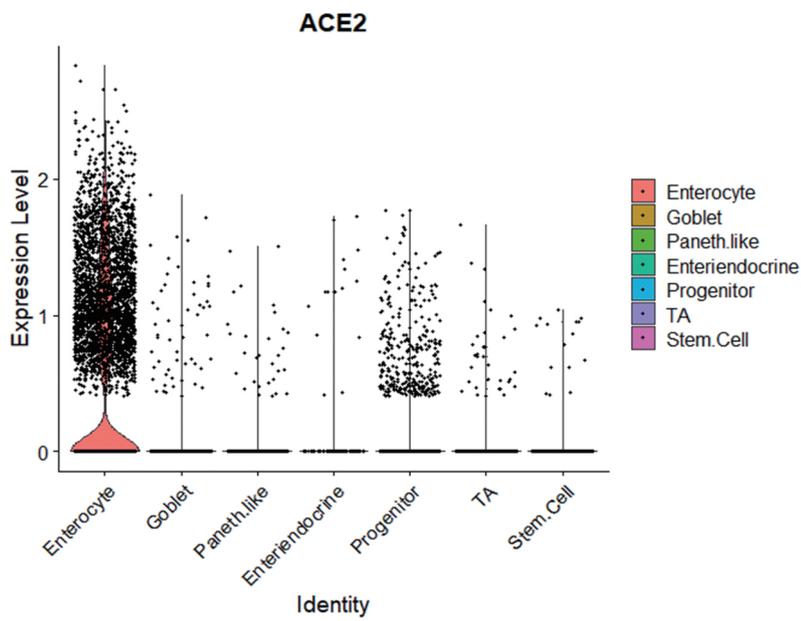
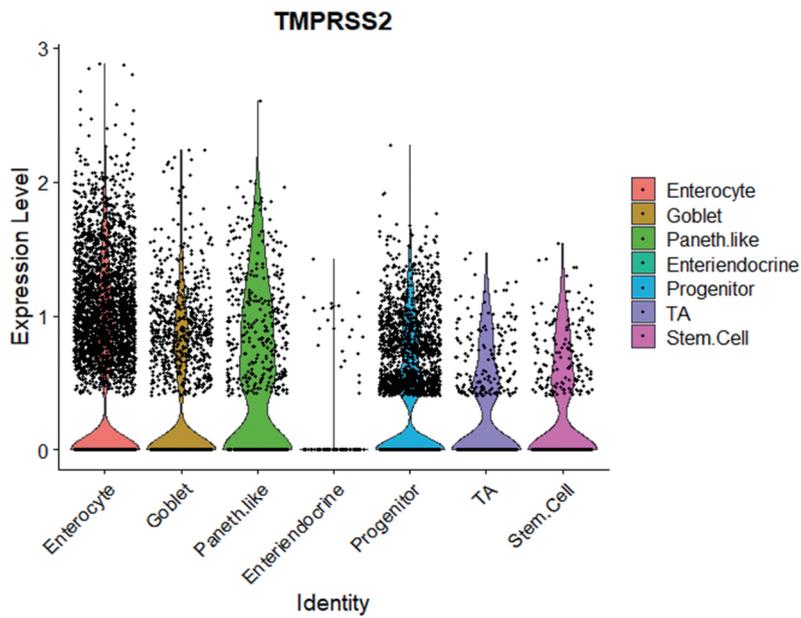
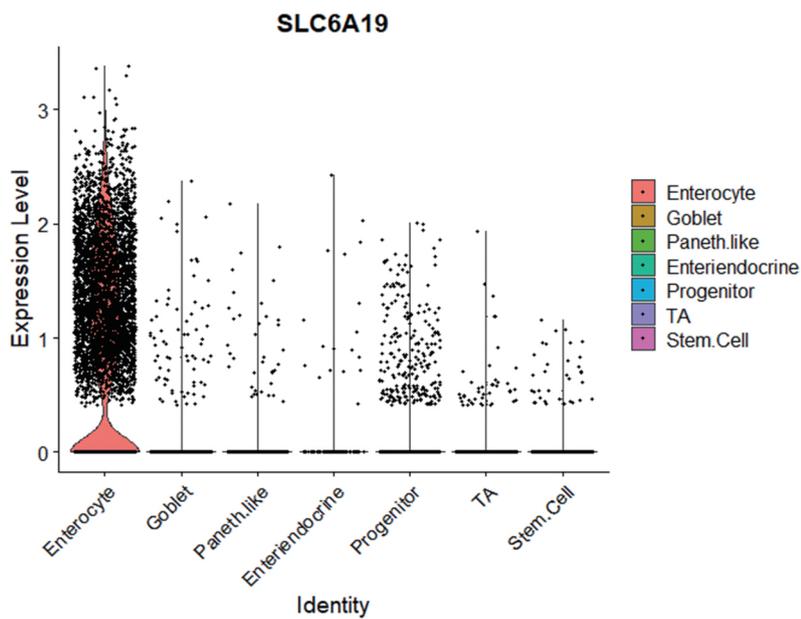
Supplementary Figure 2. Expression of genes associated with SARS-CoV-2 entry in single-cell transcriptome sequencing database. a: Violin plot showing the ACE2 (Left), SLC6A19 (Middle) and TMPRSS2 (Right) expression distribution among different cell clusters.

a**b****c**

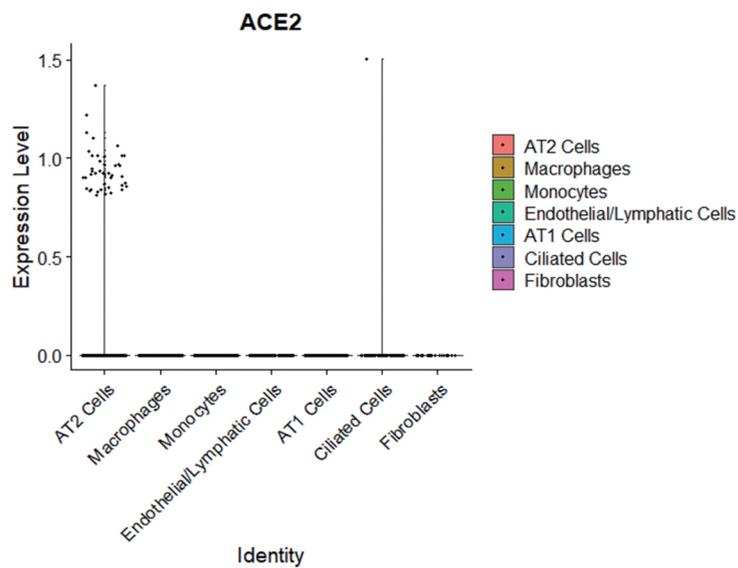
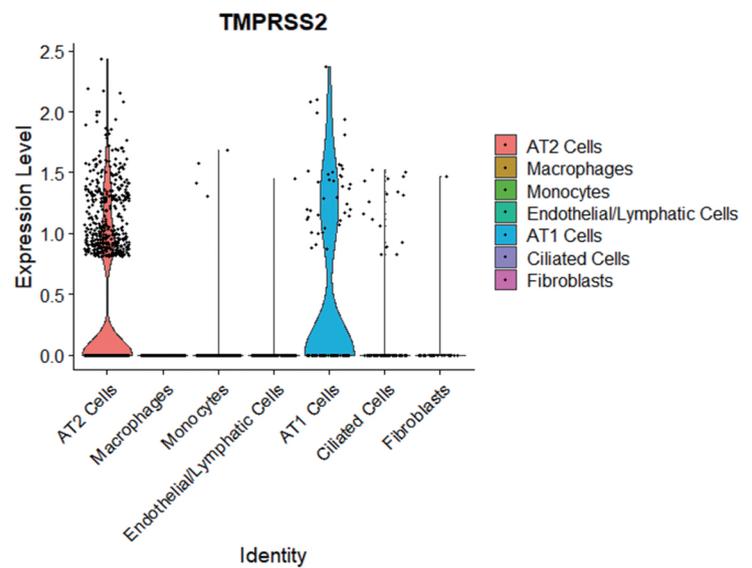
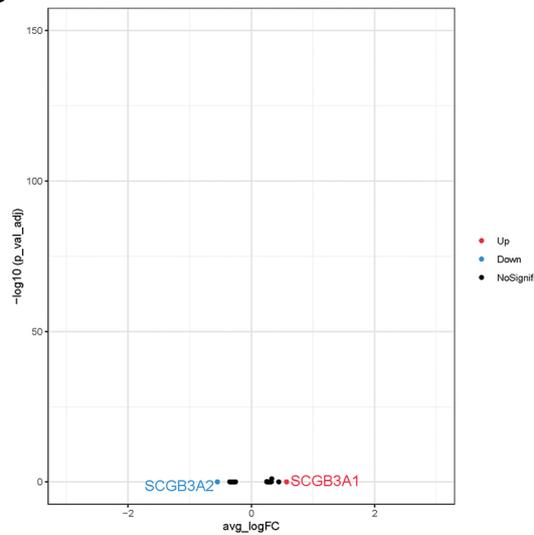
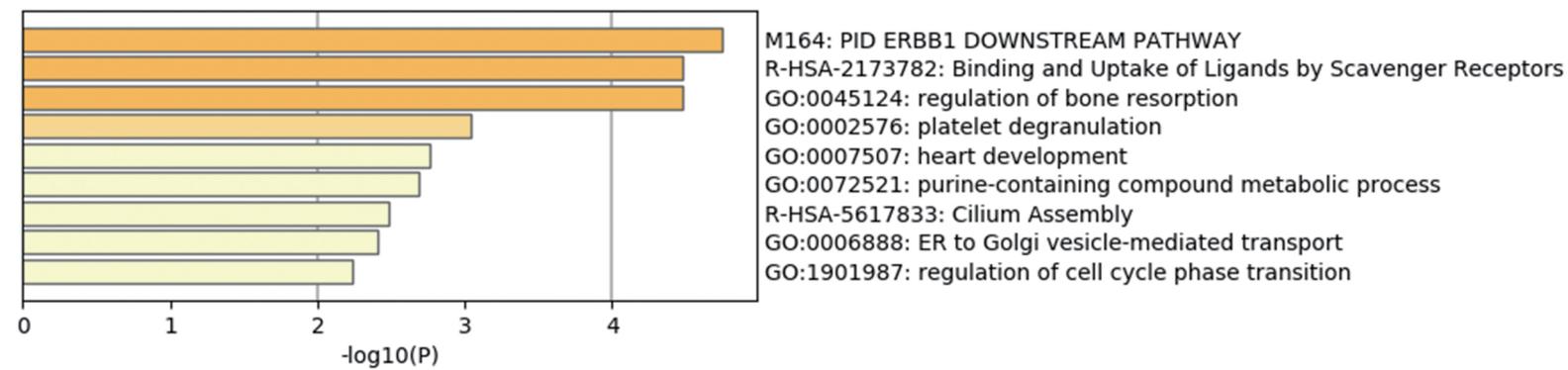
Supplementary Figure 3. Expression of genes associated with SARS-CoV-2 entry in single-nuclear transcriptome. a: UMAP visualization displaying major cell clusters (17,659 single nuclei); **b:** UMAP projection, points colored by detection of ACE2 (Left), TMPRSS2 (Middle) and SLC6A19 (Right). Blue: RNA positive, gray: RNA negative; **c:** Volcano plot displaying differential expression genes between ACE2+ PT cells and ACE2- PT cells. Red: up-regulation genes, blue: down-regulation genes.



Supplementary Figure 4. Expression of genes associated with SARS-CoV-2 entry in single-cell transcriptome sequencing database of Asians. a: UMAP visualization displaying major cell clusters (23,366 single cells); **b:** Volcano plot displaying differential expression genes between ACE2+ PT cells and ACE2- PT cells. Red: up-regulation genes, blue: down-regulation genes; **c:** UMAP projection, points colored by detection of ACE2 (Left), TMPRSS2 (Middle) and SLC6A19 (Right). Blue: RNA positive, gray: RNA negative; **d:** Violin plot showing the ACE2 (Left), SLC6A19 (Middle) and TMPRSS2 (Right) expression distribution among different cell clusters.

a**b****c**

Supplementary Figure 5. Expression of genes associated with SARS-CoV-2 entry in the small intestine. a: Violin plot showing the ACE2 expression distribution among different cell clusters; **b:** Violin plot showing the TMPRSS2 expression distribution among different cell clusters; **c:** Violin plot showing the SLC6A19 expression distribution among different cell clusters.

a**b****c****d**

Supplementary Figure 6. Expression of genes associated with SARS-CoV-2 entry in the lung. **a:** Violin plot showing the ACE2 expression distribution among different cell clusters; **b:** Violin plot showing the SLC6A19 expression distribution among different cell clusters; **c:** Volcano plot displaying differential expression genes between ACE2+ AT2 cells and ACE2- AT2 cells. Red: up-regulation genes, blue: down-regulation genes. **d:** Bar plot presenting significantly enriched GO terms obtained from GO enrichment analysis performed with differential expression genes between ACE2+ AT2 cells and ACE2- AT2 cells.