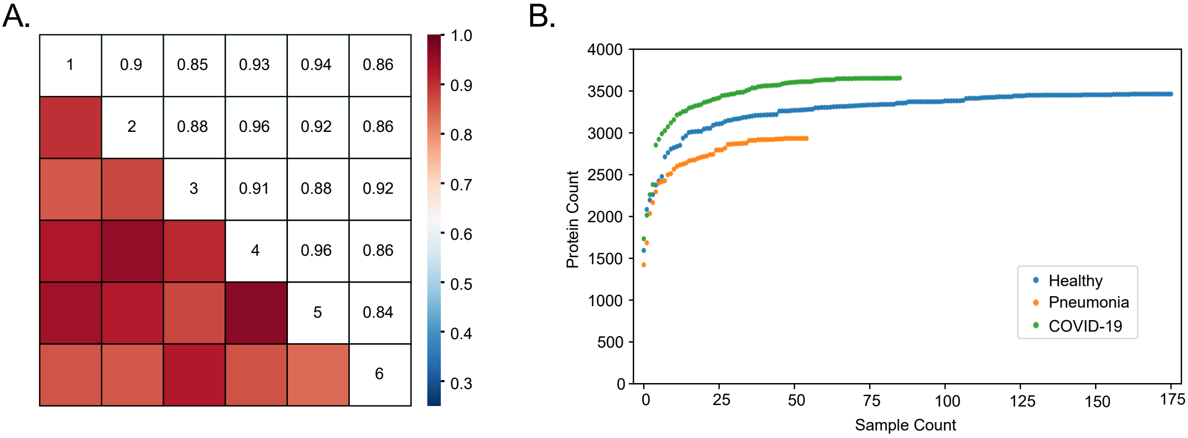

Figure S1. MS reproducibility and protein cumulative curve. Related to Figure 1.

(A) Pearson's correlation coefficients of 6 quality control samples.

(B) The cumulative number of proteins detected across healthy, pneumonia and COVID-19 samples.

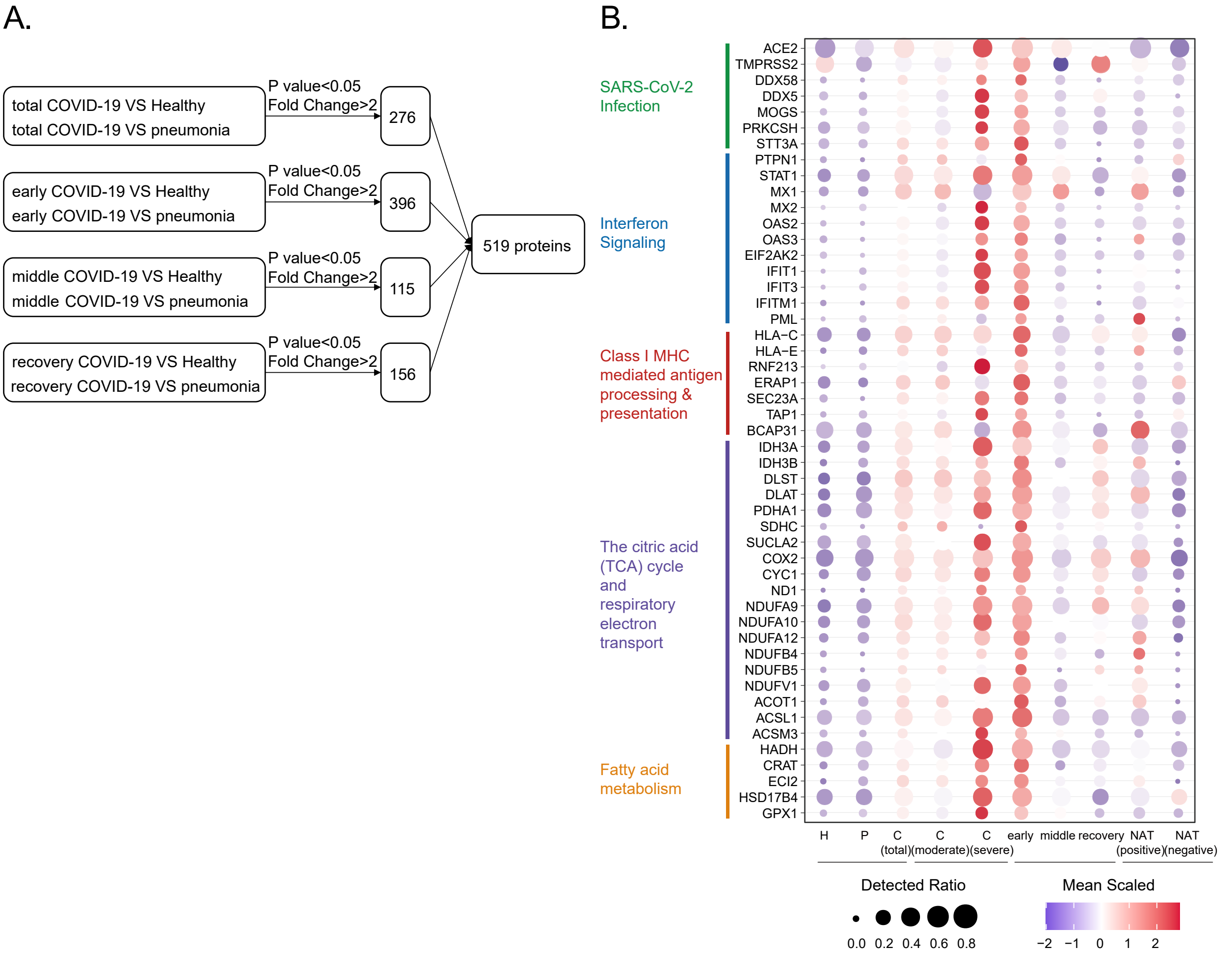

Figure S2. A urinary proteomic landscape of COVID-19 during disease progression. Related to Figure 2.
(A) COVID-19 specific DEPs were identified by comparing protein abundance as one group and at each of the three stages with those of the pneumonia and healthy controls (Mann–Whitney U test p-value<0.05, increased by >2 fold than both healthy or pneumonia controls). **(B)** Bubble plot showing all urinary proteins changed during COVID-19 progression in the 5 pathways.
H: healthy, P: pneumonia,C(total): total COVID-19, C(moderate): moderate COVID-19, C(severe): severe COVID-19, early: early stage COVID-19, middle: middle stage COVID-19, recovery: recovery stage COVID-19, NAT(postive): nucleic acid test was positive, NAT(negative): nucleic acid test was negative.

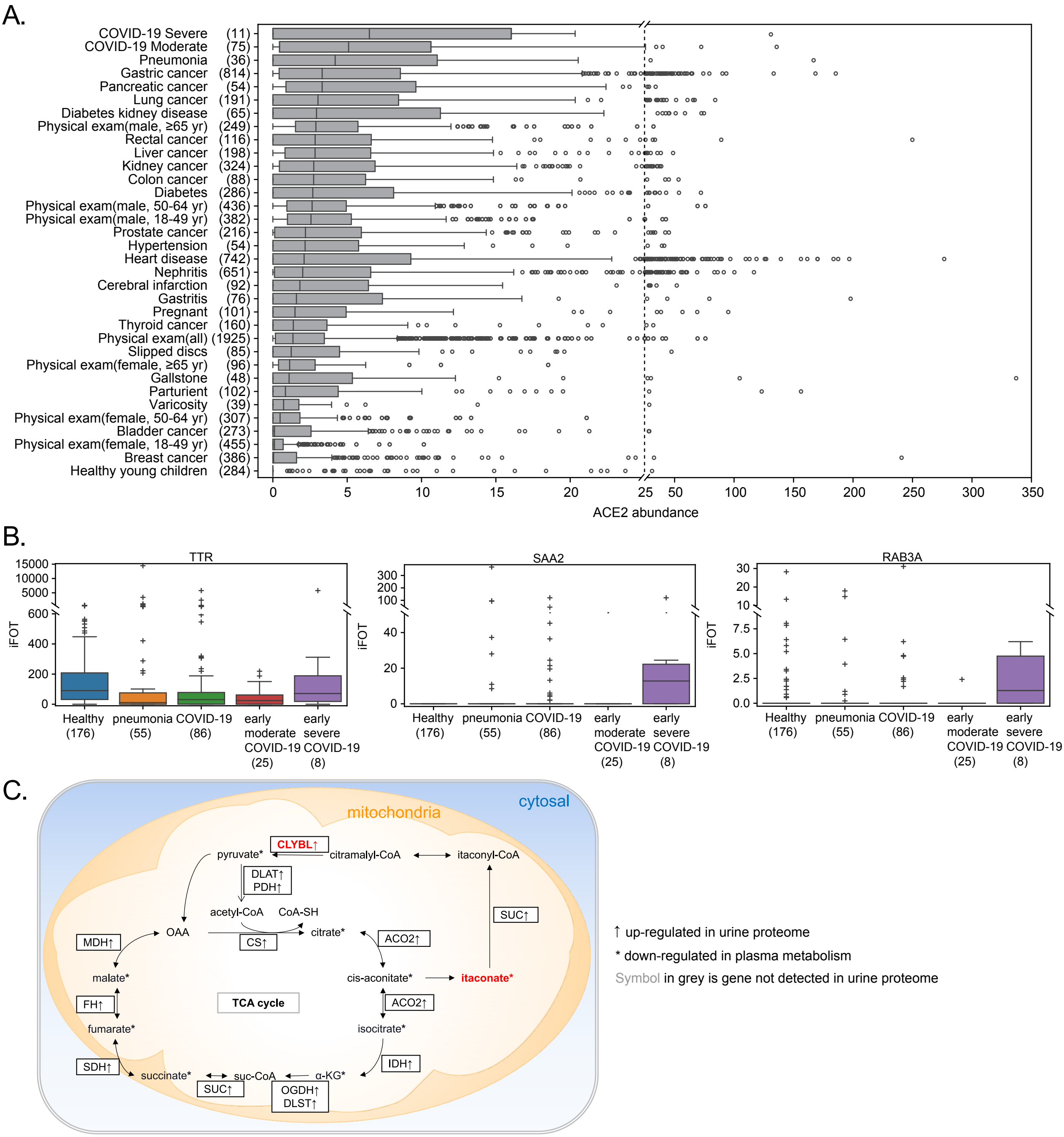

Figure S3. The abundance of ACE2, TTR, SAA2, RAB3A and activation of TCA cycle. Related to Figure 3, 4, 5. **(A)** ACE2 abundance across 34 groups. Boxplot displaying the median abundance of proteins(center line: median, bounds of box: 25th and 75th percentiles, and whiskers: from Q1 − 1.5*IQR to Q3 + 1.5*IQR). All data except COVID-19 patients were obtained from Shen et al.[23]. **(B)** Boxplot displaying the abundance of TTR, SAA2 and RAB3A across 5 group, which are candidate biomarkers to stratify high-risk patients (Healthy: n = 176, pneumonia: n = 55, COVID-19: n = 86, early moderate COVID-19: n = 25, early severe COVID-19: n = 8). Boxplot center line: median, bounds of box: 25th and 75th percentiles, and whiskers: from Q1 − 1.5*IQR to Q3 + 1.5*IQR. **(C)** Activation of TCA cycle. Itaconate is produced by activated macrophages from the TCA cycle intermediate cis-aconitate. Itaconate is converted to itaconyl-CoA, citramalyl-CoA, and, finally, pyruvate and acetyl-CoA by CLYBL. (↑ : in 519 COVID-19 specific DEPs; * : down-regulated in plasma metabolism; Symbol in grey is gene not detected in urine proteome).