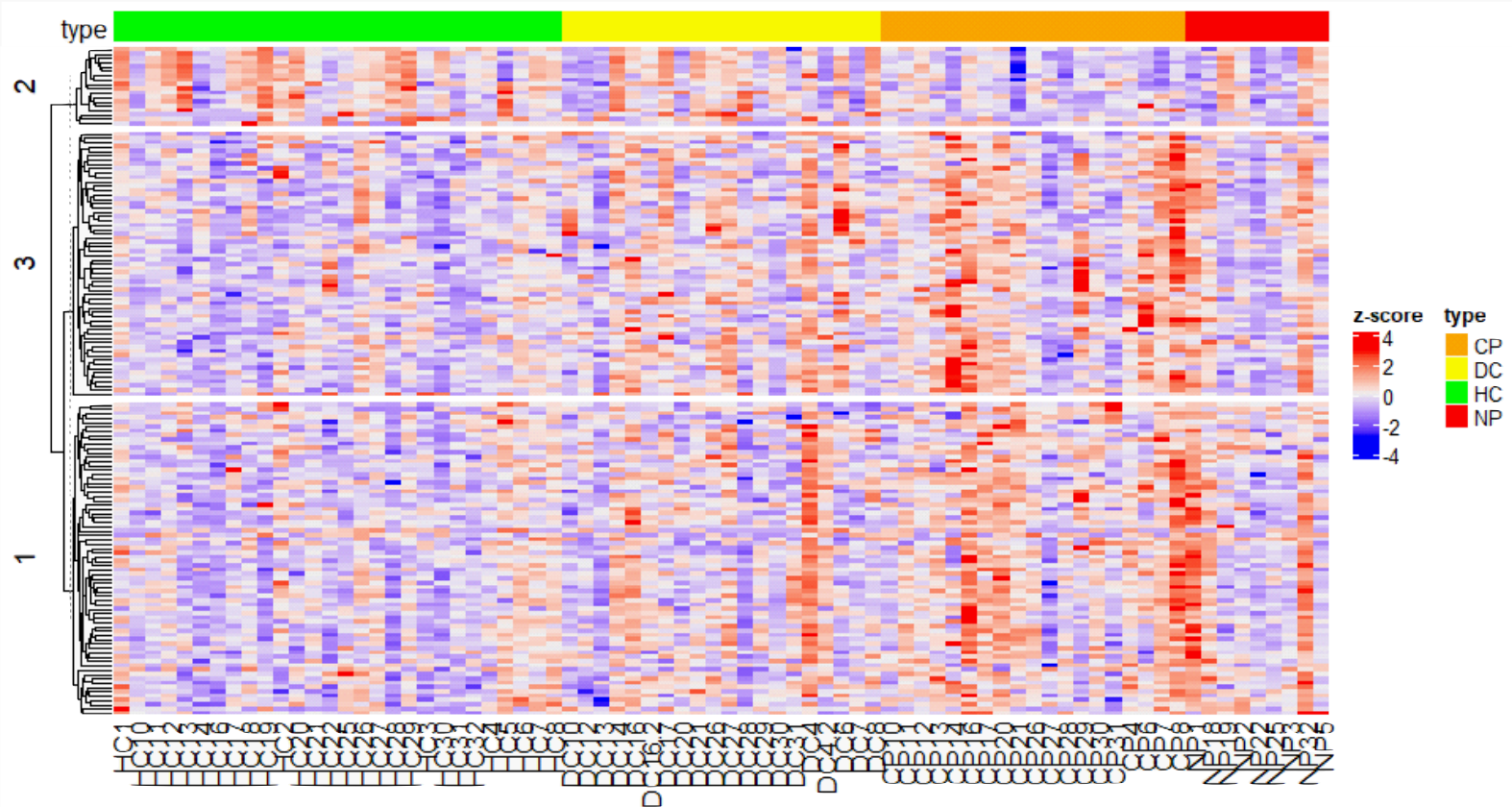


Figure S1: Protein expression in clinical groups and altered pathways in patients. **(a)** Heatmap of differentially expressed proteins (DEPs) between patients infected with SARS-CoV-2 with comorbidities and healthy controls, with z-score by row normalization and distributed by hierarchical clustering; **(b)** network of KEGG-enriched terms from DEPs between patients with comorbidities and healthy controls. Green (upregulated in patients) and red (downregulated in patients) dots indicate statistical DEPs. The node size indicates the number of genes involved in the term.

(a)



(b)

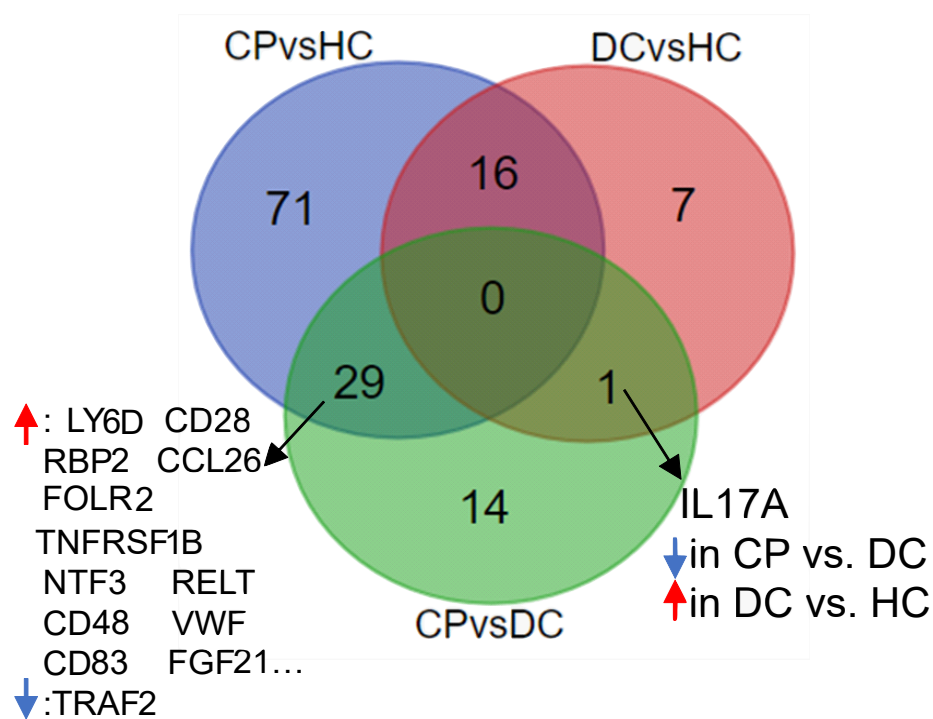


Figure S2: Protein expression in clinical groups and altered pathways in patients. **(a)** Heatmap of the DEPs among patients with comorbidities, patients without comorbidities, healthy controls, and disease controls with z-score by row normalization and distributed by hierarchical clustering. The 3 clusters were generated by K-means algorithm; **(b)** Venn diagram with DEPs of patients with comorbidities versus healthy controls, DEPs of disease controls versus healthy controls, and DEPs of patients with comorbidities versus disease controls. The red and blue arrows represent upregulation and downregulation, respectively.

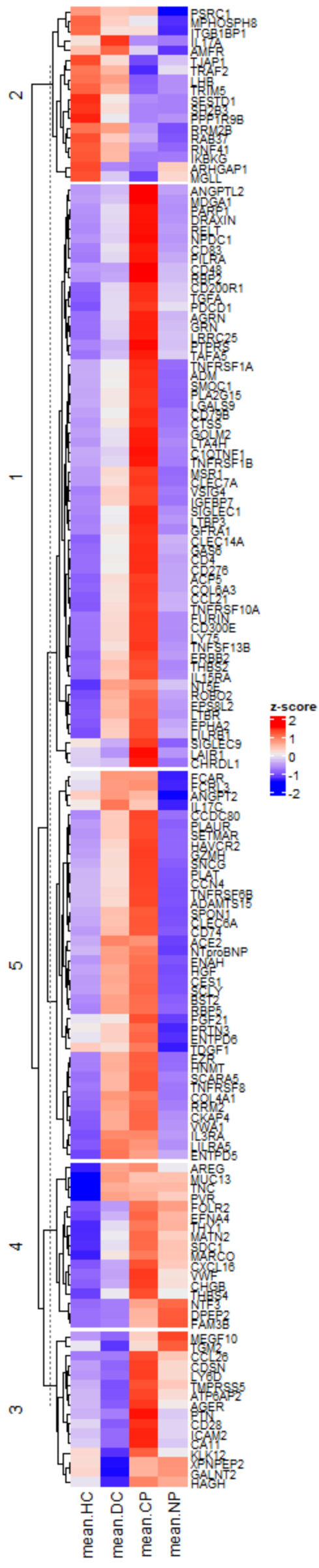
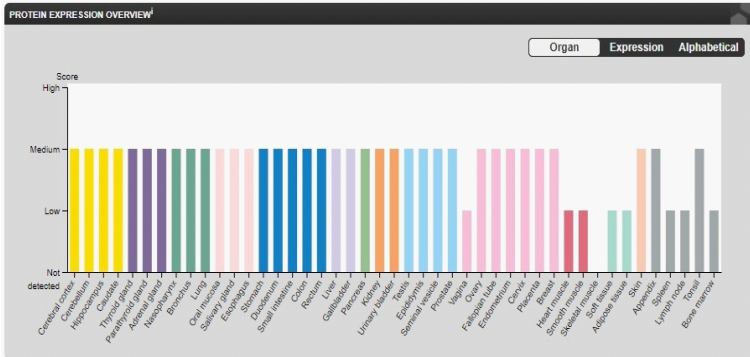
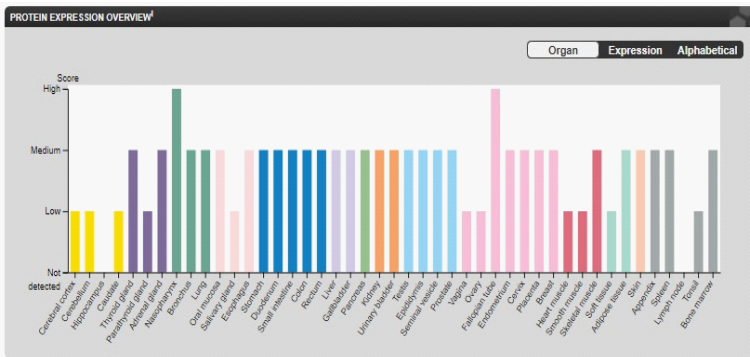


Figure S3: Clusters of protein expression in clinical groups by mean. Heatmap of the mean of DEPs for each clinical group among patients with comorbidities, patients without comorbidities, healthy controls, and diseases controls with z-score by row normalization and distributed by hierarchical clustering. The 5 clusters were generated by K-means algorithm.

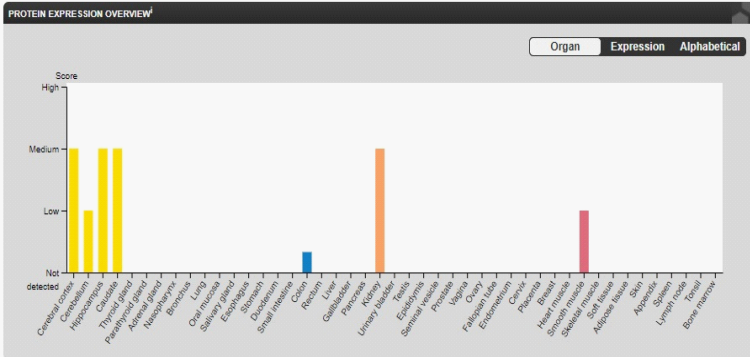
HGF



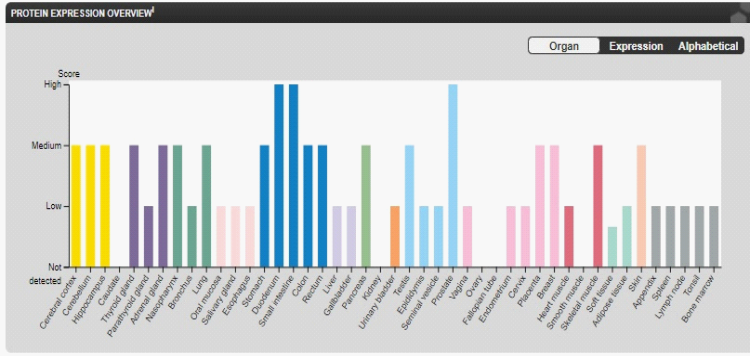
LRRC25



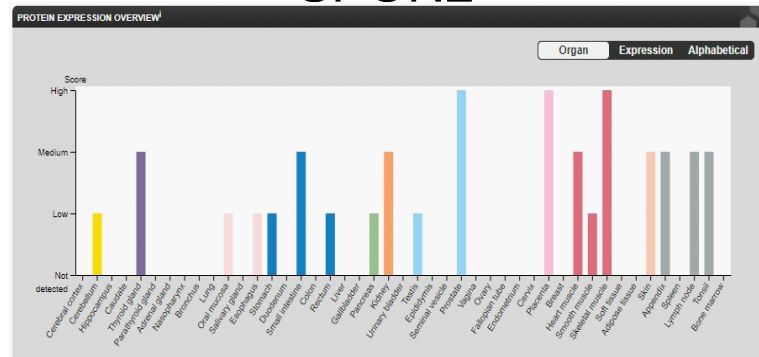
THY1



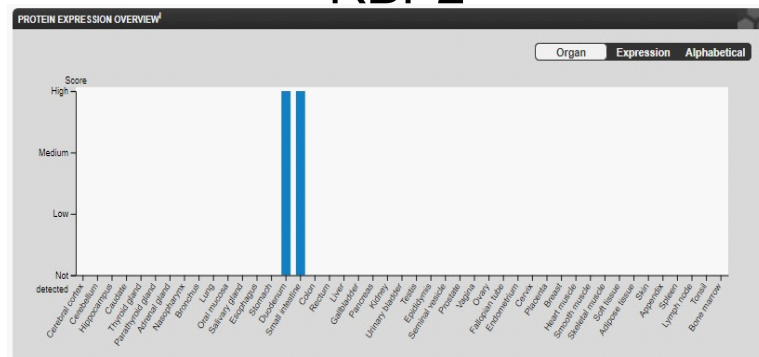
NPDC1



PTN



RBP2



SMOC1



GOLM2

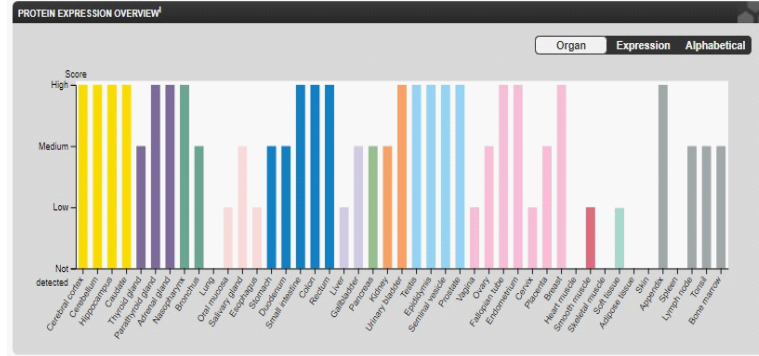


Figure S4: Cell-specific expression of selected proteins from the Human Protein Atlas. Bar plot with relative quantification (score) for each protein in different cell types.