

Supplementary Information

Role of multi-omics to understand host-pathogen interaction in COVID-19 pathogenesis

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Supplementary Tables

Table S1: List of altered proteins in COVID-19 positive patients from published research articles and information for metadata analysis

Table S2: List of altered metabolites in COVID-19 positive patients from published research articles and information for metadata analysis

Supplementary Figures

Figure S1: Gene ontology analysis of the altered proteins in COVID-19 positive patients

Figure S2: Altered metabolites mapped on altered pathways in SARS-CoV2 host

Figure S3: Inter-mapped significant metabolites and proteins pathways

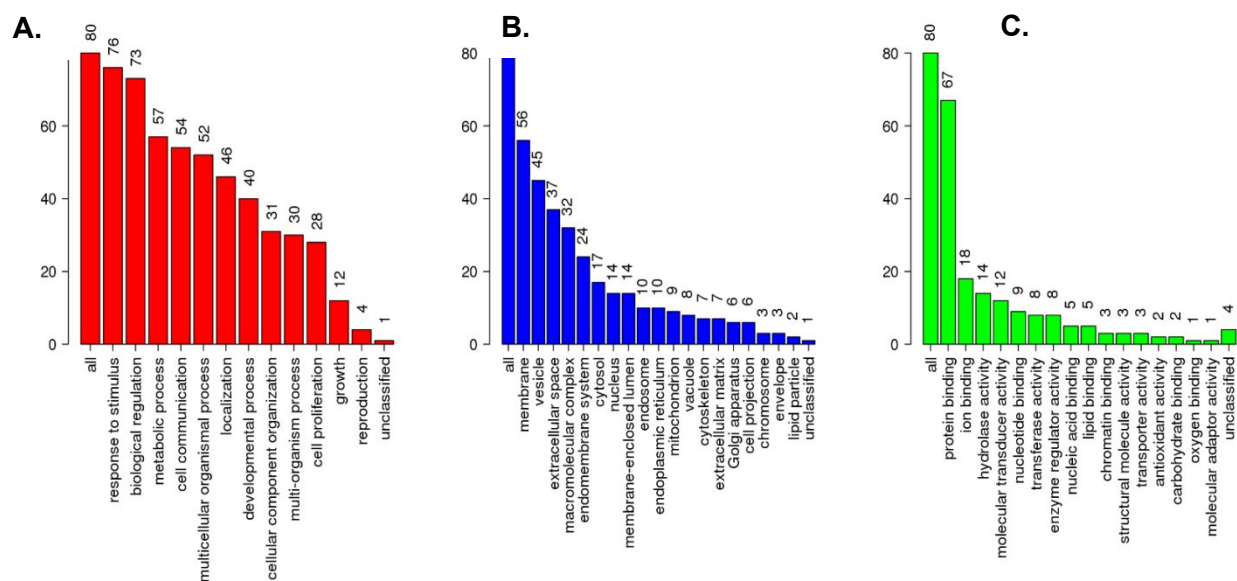
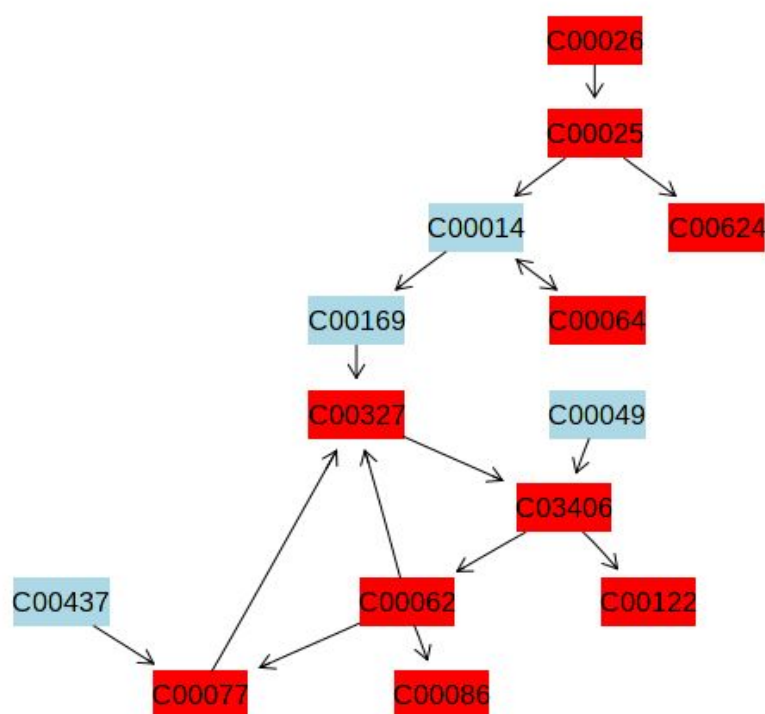
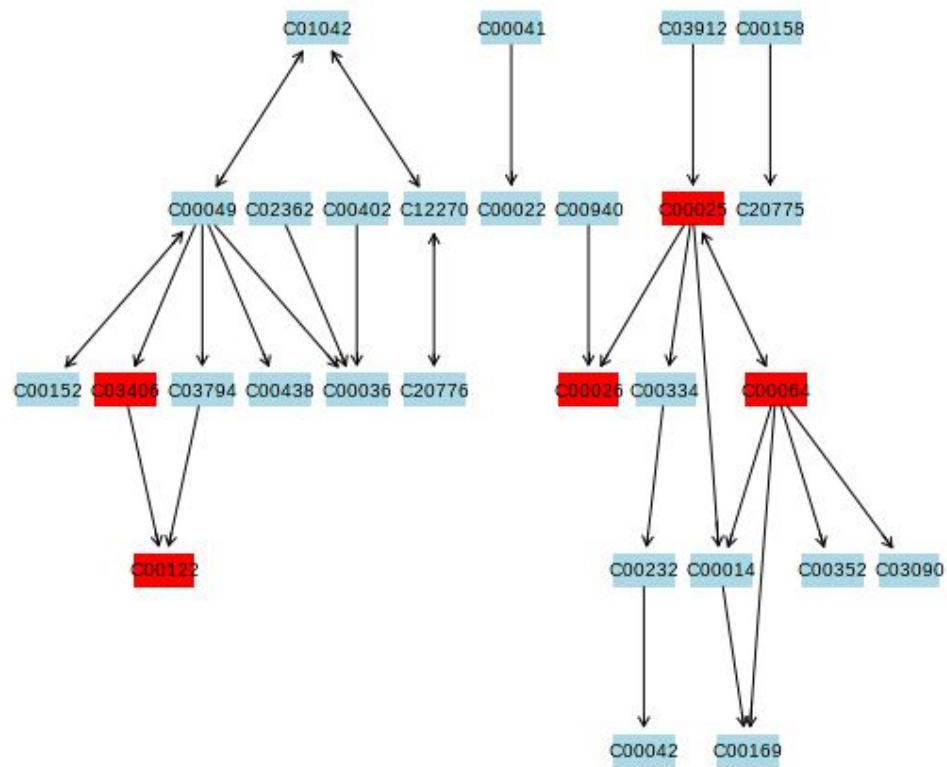


Figure S1: Gene ontology analysis of the altered proteins in COVID-19 positive patients, A. represents the bar chart of biological process categories, B. represents the bar chart of Cellular Component categories and C. represents the bar chart of Function categories

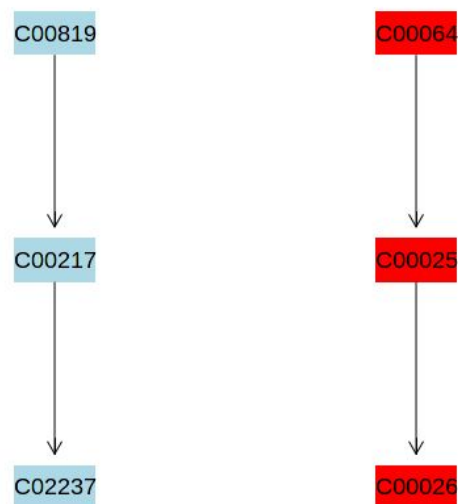
A. Arginine biosynthesis



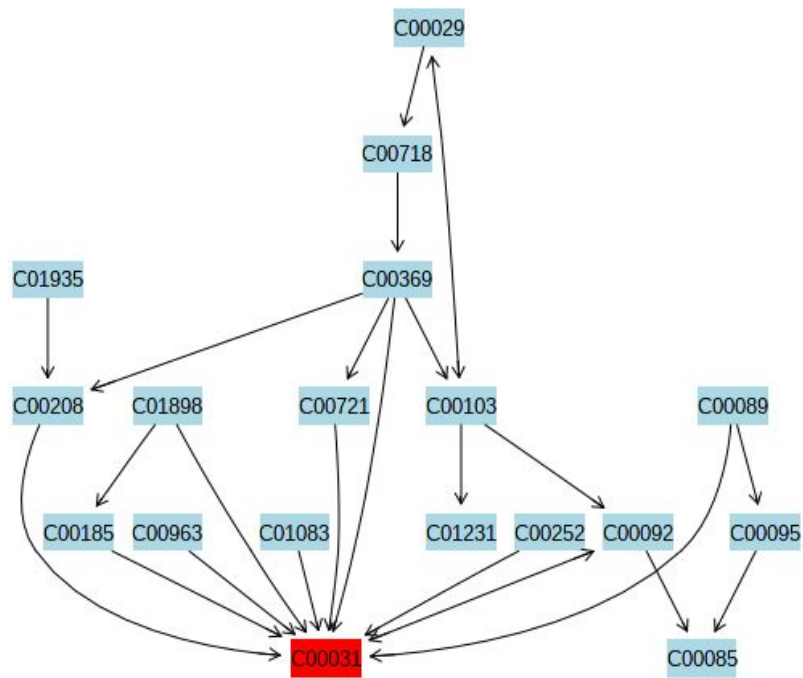
B. Alanine, aspartate and glutamate metabolism



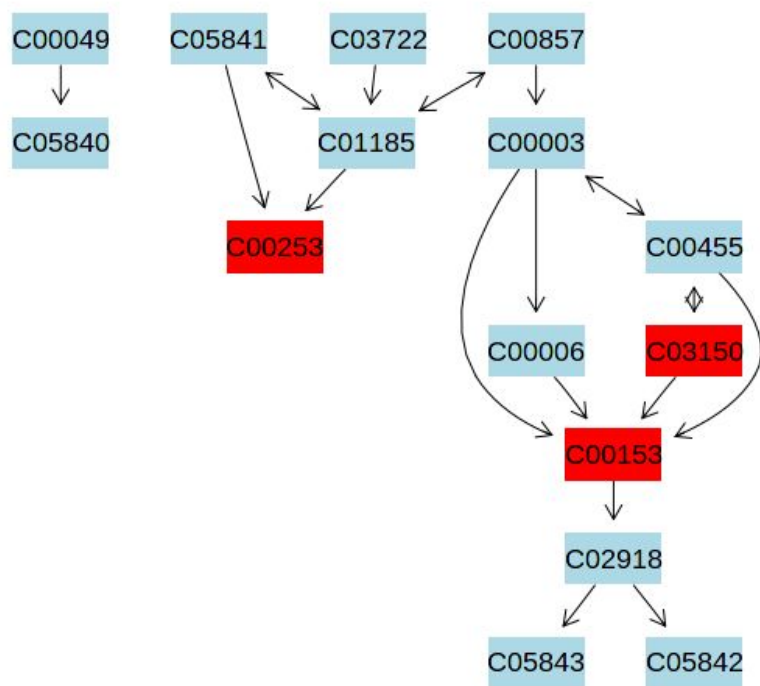
C. D-Glutamine and D-glutamate metabolism



D. Starch and sucrose metabolism



E. Nicotinate and nicotinamide metabolism



F. Aminoacyl-tRNA biosynthesis

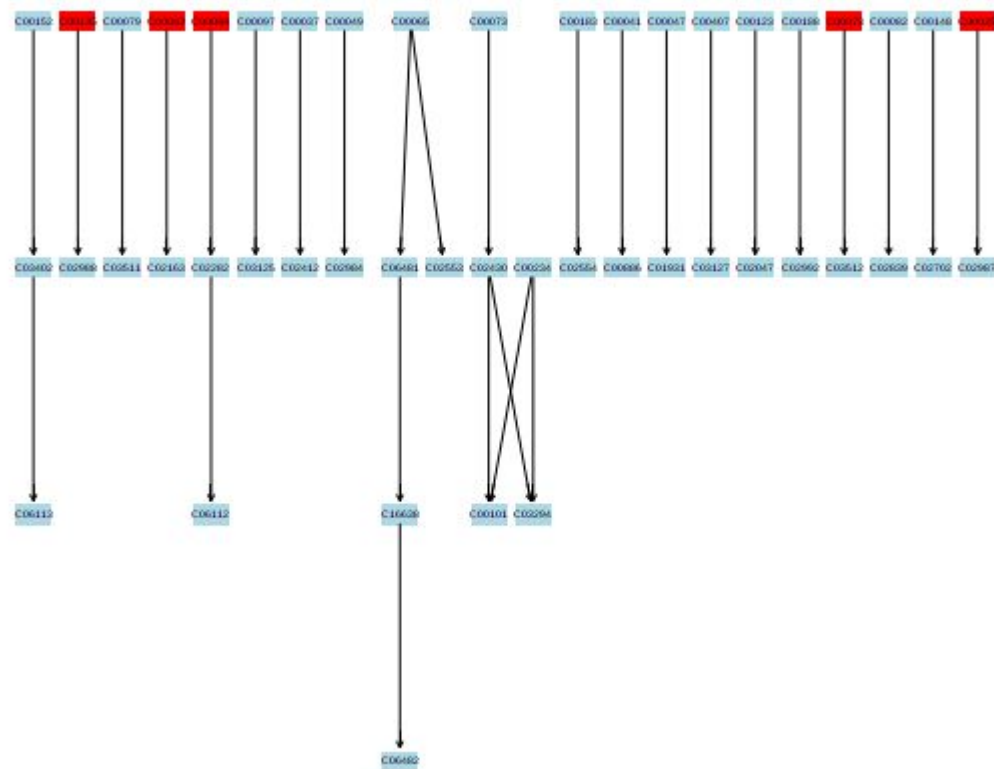
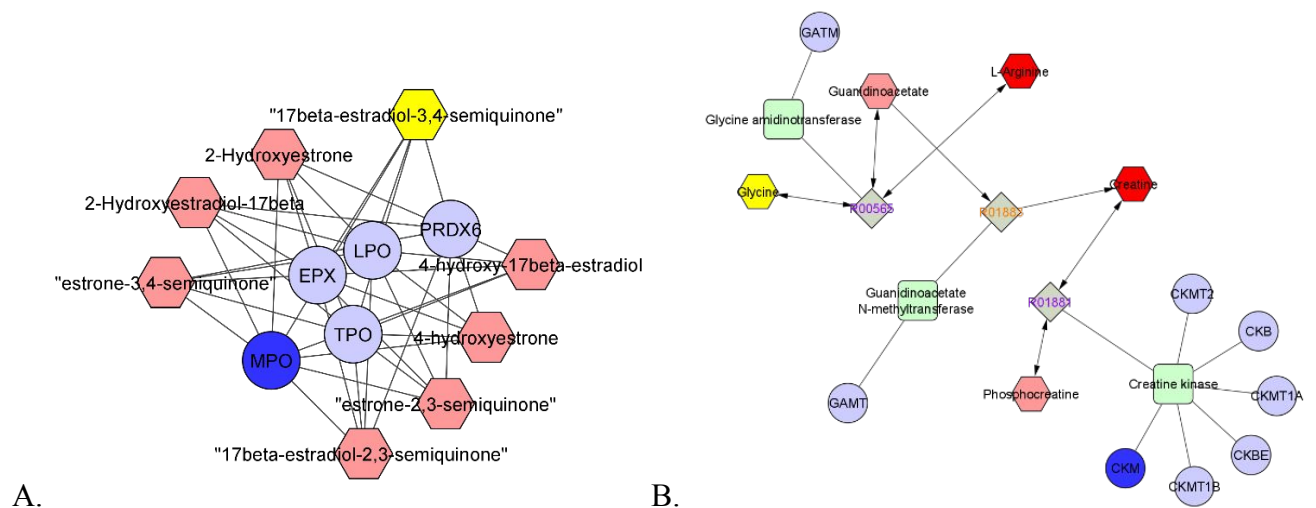


Figure S2: Altered metabolites mapped on altered pathways in SARS-CoV2 host, A. Arginine biosynthesis, B. Alanine, aspartate and glutamate metabolism, C. D-Glutamine and D-glutamate metabolism, D. Starch and sucrose metabolism, E. Nicotinate and nicotinamide metabolism and F. Aminoacyl-tRNA biosynthesis



C.

