Prognostic tools and candidate drugs based on plasma proteomics of patients with severe COVID-19 complications

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a Severe vs. Control **b**

Supplementary Figure 2: Functional analysis of differentially expressed proteins in plasma of patients with active SARS-CoV-2 infection. (**a-c**) Heatmaps of the expression differentially expressed proteins (DEPs) in severe (S) and mild (M) cases and control (C) are shown to the side of enrichment trees of enriched KEGG pathways using DEP.92. Upregulated and downregulated proteins and pathways are shown in red and blue respectively. The p-value for enrichment is depicted by the size of the circles in the enrichment trees. (**d**) Venn diagrams summarizing the shared and unique upregulated (top) and downregulated (bottom) DEPs. The identities of the proteins in each Venn diagram are shown in Supplementary Data 3.

Supplementary Figure 3: Functional networks of deregulated plasma proteins in severe versus mild COVID-19 disease. Differentially expressed proteins (DEPs) in patients with severe complications compared to mild-moderate disease were subjected to network analysis using the STRING database and annotation for their function as circulating proteins (**Supplementary Data 3** and **Supplementary** Notes). Of the 375 DEPs (1.25-fold change in severe vs. mild cases), 288 (77%) DEPs could be allocated to 11 functional groups considering their potential function as circulating proteins; chemotaxis, coagulopathy/fibrinolysis, immune evasion, innate immunity, T- or NK-cell immunity, T-/Th-cells dysfunction, inflammation, neutrophils/neutrophil extracellular traps (NETosis), and organ damage (lung, cardiovascular or other and multiple organs). DEPs are classified as agonists (pos.) or antagonist (neg.) for the Th1/Th17 and Th2 immune responses. The color intensities (red: upregulated, blue: downregulated; legend) depict the log2 fold-change between severe and mild-moderate cases. Interactions between the 288 DEPs are shown only for those with STRING-db confidence score ≥ 0.7 are shown (587 high-confidence interactions). Inserted table in the Figure summarizes the number of interactions across the different STRING-db confidence scores (0.4 to 0.99). The heatmaps summarize the Pearson's correlation coefficient (r) for significant correlations (p<0.05, two-tailed, GraphPad Prism) between each protein in the functional networks and the clinical blood biochemical markers and blood cell counts available in our cohort. Refer to **Supplementary Data 3** for the correlation r values of all DEPs with the clinical markers.

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Supplementary Figure 4: Protein-drug interaction network of 1.5- to 2-fold upregulated plasma proteins in severe COVID-19. Proteins with 1.5- to 2-fold upregulation in patients with severe complications versus mild-moderate disease were subjected to protein-drug interaction (PDI) using the Drug-Gene Interaction database (DGIdb, v4.2.0). Target proteins are colored red, and the intensity depicts the fold-change. Drugs which target single proteins are shown in grey boxes and blue font and those that target multiple proteins (on this Figure or in Figure 4) are depicted in black font in blue nodes. Protein-protein interactions are colored according to the STRING-db confidence scores; red: confidence score ≥ 0.7 , blue: confidence score ≥ 0.5 and < 0.7. Drugs in red bold font are notable examples discussed in the main text.

Supplementary Figure 5: The COVID-19 molecular severity score on day 0 in the SARS-CoV-2 positive and negative patients in Massachusetts General Hospital (MGH) cohort. The MGH cohort collected plasma samples on day 0 (within 24 hours of admission to the emergency department) from symptomatic patients, of whom 78 patients were found to be negative for SARS-CoV-2. The molecular severity score on day 0 was compared across the different severity levels (acuity max over 28-day period) and between SARS-CoV-2pos and SARS-CoV-2^{neg} patients. Scatter plots show the calculated scores (mean \pm SEM) and the number of patients in each group is stated under each plot. Only significant differences are depicted (two-way ANOVA with Tukey's multiple testing correction, GraphPad Prism); **** p<0.0001, exact p-values are stated otherwise.

Supplementary Figure 6: Comparison of the COVID-19 molecular severity score across the groups within the clinical parameters included in the study cohort. (**a**) Boxplots (median as center line, box marks 25th and 75th percentiles, and whiskers define minimum and maximum) for the score from the 12-protein signature across the stated groups in each of the clinical annotations in infected patients ($n = 100$). One-way ANOVA with Dunnett's multiple testing correction was used for clinical parameters with more than two groups, and unpaired two- tailed t-test was used for parameters with two groups. Significant differences are depicted as * p<0.05, ** p<0.01, *** p<0.001 and **** p<0.0001. Refer to **Supplementary Data 6** for more details of the statistical comparisons and exact p-value. (**b**) ROC curve analysis of the parameters which showed significant association with the 12-protein molecular severity score. The DeLong et al. method was used for statistical analysis. (**c**) MUVR was used for variable selection using the same parameters in panel b. Seven parameters (markers) were selected by MUVR and the boxplot summarizes the median ranking (center line), 25th and 75th percentiles (box boundaries), and minimum and maximum (whiskers) from 500 independent MUVR runs. (**d**) The model of 7 markers from MUVR was further confirmed for performance using ROC curve analysis in comparison to models which included the remaining clinical markers. There was no additional benefit from addition diabetes, SpO2 and/or eosinophil counts as judged by pairwise comparisons (DeLong et al. method) against the model of the 7 markers alone. Abbreviations; Resp. Rate: Respiratory rate, WBC: white blood cells, CRP: C-reactive protein.

Supplementary Note 1

Functional annotation and literature for Figure 2 and Supplementary Data 3. The differentially expressed proteins in patients with severe COVID-19 versus patients with mild-moderate disease were subjected to functional annotation based on information from databases and literature and concerning their role in circulation and pathogenesis.

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