

SUPPLEMENTARY MATERIAL

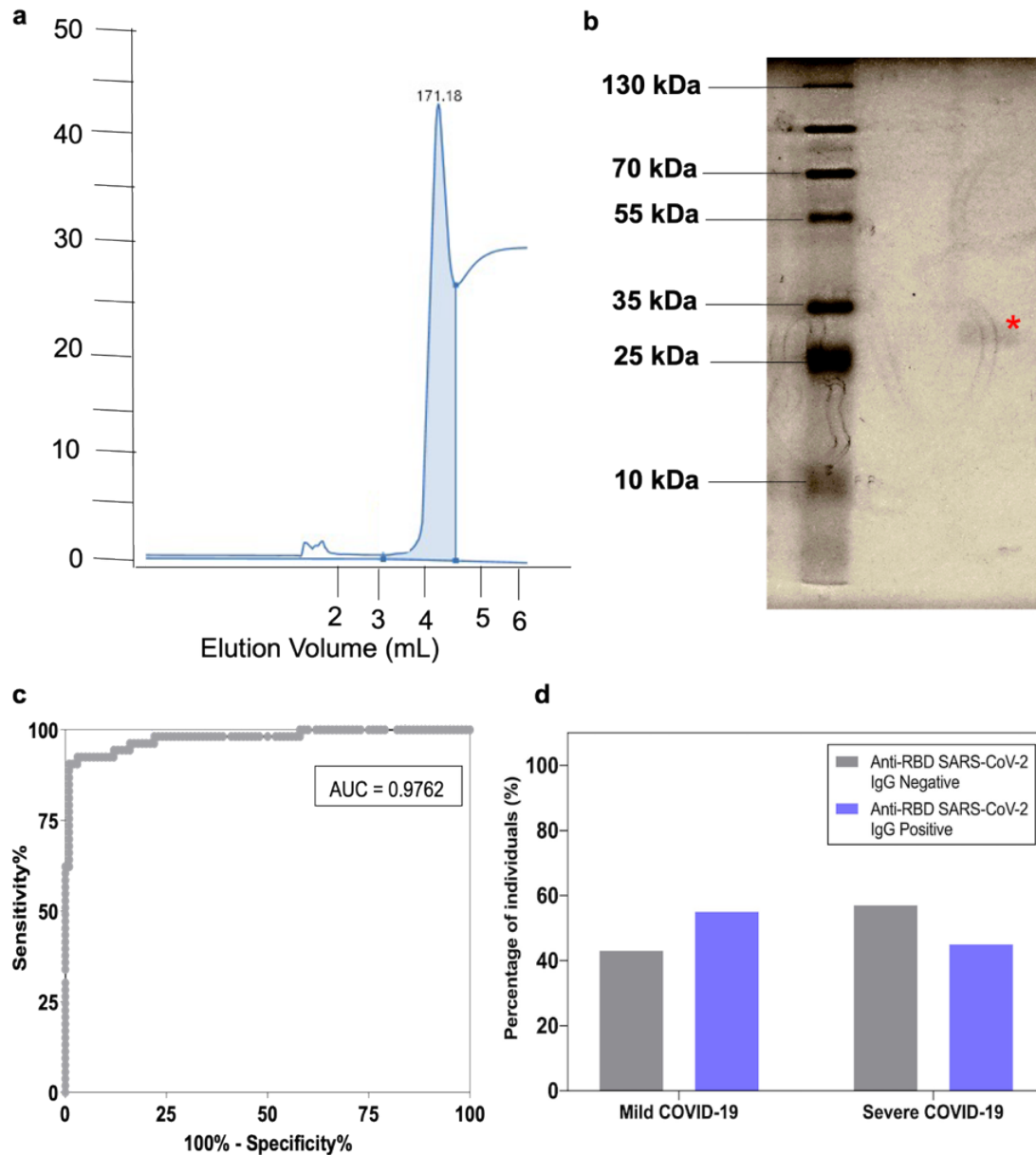


Figure S1. Production of the SARS-CoV-2 receptor binding domain protein and Anti-SARS-CoV-2 RBD IgG profiles of individuals with COVID-19 according to disease severity classification. (a) chromatogram corresponding to the purification of the RBD SARS-CoV-2 protein from lineage B (Hu-1). (b) SDS-PAGE gel performed with fractions eluted from affinity chromatography, the band with molecular weight corresponding to the protein of interest is marked with a red asterisk (*). The molecular weight marker (MPM) was Prestained Protein Marker Broad Range (Cell Signaling Technology®). The molecular weight of the B-lineage RBD proteins (Hu-1) is 30.6 kDa. mAU stands for milli absorbance units. (c) The operating characteristic curve (ROC), based on the OD test/ OD negative control (CN) ratio, was used to determine the sensitivity (92,45%), specificity (97%), and area under the ROC curve (AUC) of the in-house indirect ELISA test. (d) Frequency of IgG anti-RBD SARS-CoV-2 antibodies detection in serum samples from 72 individuals hospitalized for mild and severe COVID-19. Each individual had more than one sample collected during hospitalization, totaling 572 samples from 65 seropositive individuals and 44 samples from 7 seronegative individuals. The dotted line represents the test cut-off (4,139).

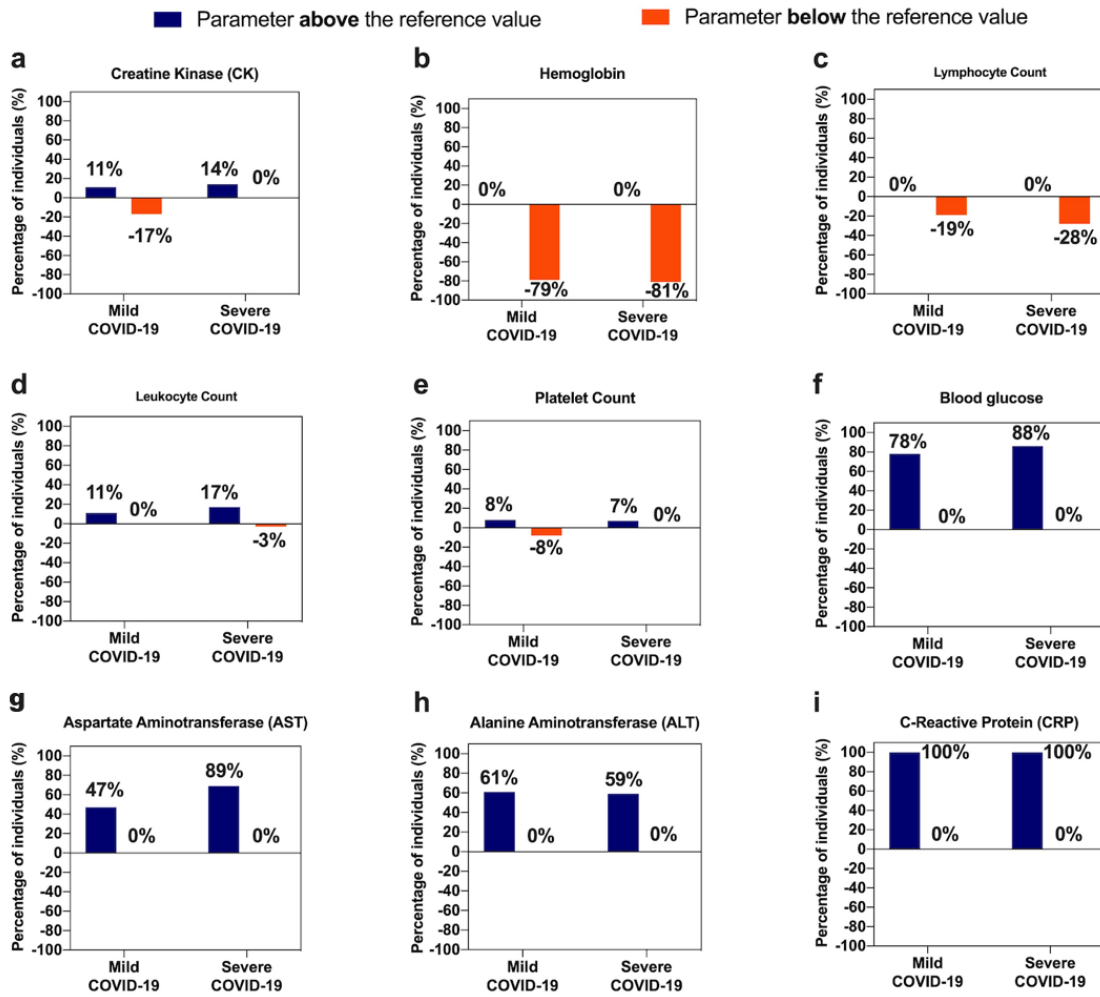


Figure S2. Variations in serological markers of individuals with COVID-19 according to disease severity classification. a) frequency of individuals with mild and severe COVID-19 and positive for the detection of anti-RBD IgG antibodies with values above (dark blue column) and below (orange column) the reference for creatine kinase, b) hemoglobin, c) lymphocyte count, d) leukocyte count, e) platelet count, f) blood glucose, g) aspartate aminotransferase, h) alanine aminotransferase, and i) c-reactive protein.

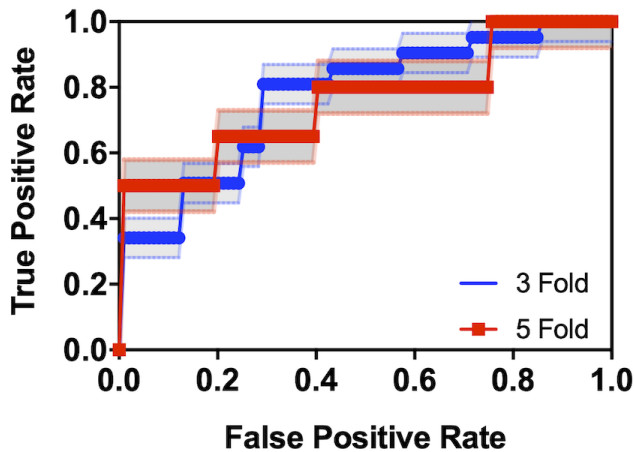


Figure S3. Evaluation of the LDA-SVC model classification through their characteristic ROC curves, considering the confidence interval for 3 fold and 5 fold cross validations.

Table SII. Collinearity statistics from the linear regression model.

| | Tolerance | VIF* |
|----------------------|------------------|-------------|
| Monocytes | 0.828 | 1.208 |
| Ferritin | 0.672 | 1.489 |
| Serum Iron | 0.572 | 1.749 |
| INR | 0.023 | 42.701 |
| ATTP | 0.07 | 1.298 |
| Prothrombin activity | 0.025 | 39.322 |

*Variance inflation factor: The ratio of the variance of a parameter estimate in a model that includes multiple terms compared to the variance of a model that includes only one term.

Table SIII. Logistic regression model’s coefficient.

| | | | | | | | 95% C.I for EXP() | |
|----------------------|---------|-----------------------|----------------|-----------|-------------|--------------|-------------------|--------------|
| | | Standard Error | Z(Wald) | df | Sig. | EXP() | Lower | Upper |
| Monocytes | 0.028 | 0.026 | 1.172 | 1 | 0.279 | 1.028 | 0.978 | 1.082 |
| Ferritin | 0.000 | 0.000 | 1.968 | 1 | 0.161 | 1.000 | 1.000 | 1.000 |
| Serum Iron | -0.71 | 0.030 | 5.585 | 1 | 0.018 | 0.931 | 0.878 | 0.988 |
| ATTP | -0.110 | 0.047 | 5.401 | 1 | 0.020 | 0.869 | 0.816 | 0.983 |
| Prothrombin activity | 0.03 | 0.001 | 6.226 | 1 | 0.013 | 1.003 | 1.001 | 1.005 |
| Constant | -11.980 | 6.998 | 2.931 | 1 | 0.087 | 0.000 | | |

β = Logistic regression coefficient; Z(Wald) = Statistical relevance of β coefficient; df = Degrees of freedom; Sig. = Z(Wald)-associated p-value; EXP(β) = Exponential value of β .

Table SIV. Classification table considering a cut value of 0.5 for the prediction of severe and mild cases using logistic regression.

| | Severe | Mild | Percentage correct |
|--------------------|---------------|-------------|---------------------------|
| Severe | 17 | 3 | 85.0 |
| Mild | 5 | 14 | 73.7 |
| Overall Percentage | | | 79.5 |