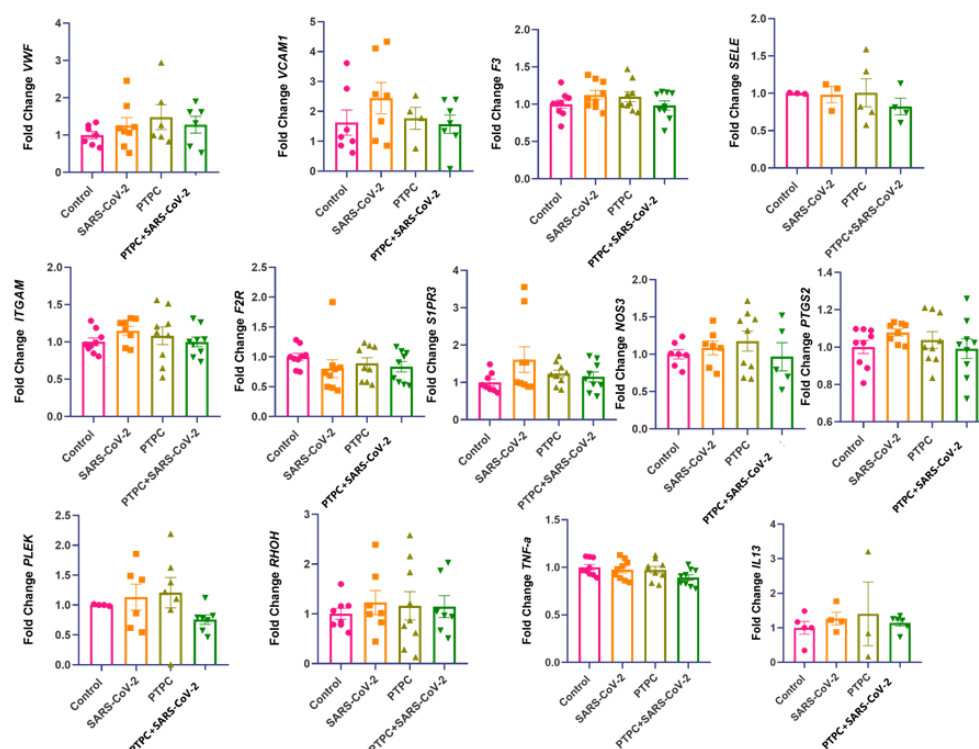
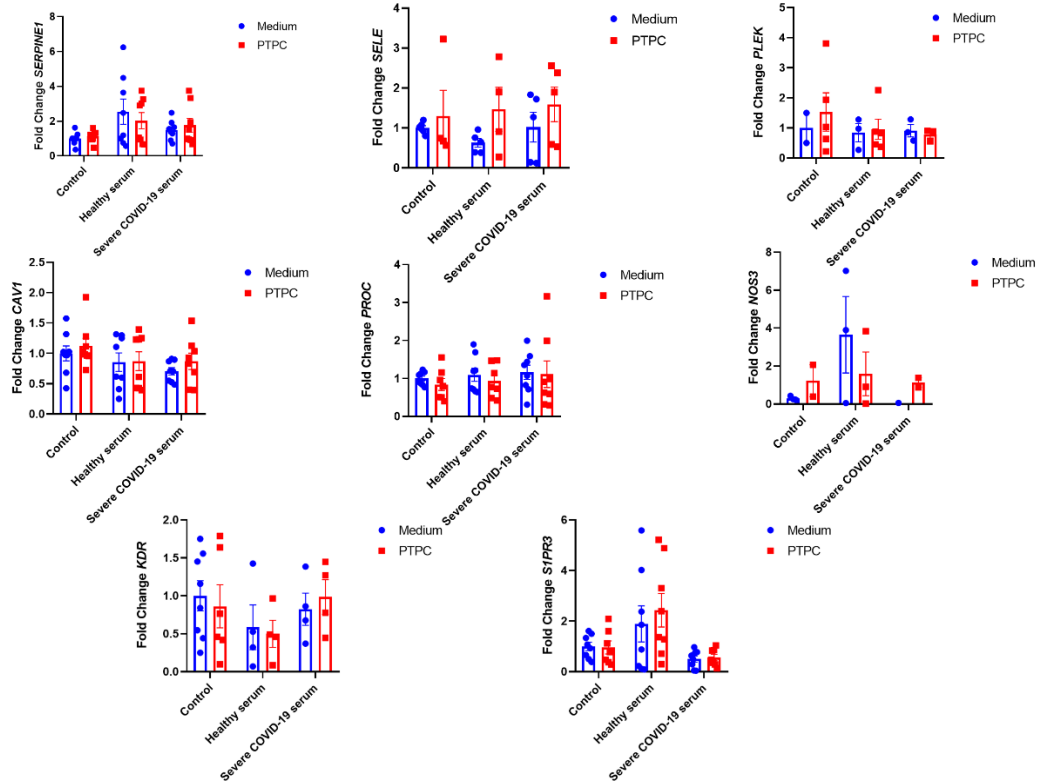


## Supplementary Materials



**Supplementary Figure S1.** HUVEC of different passages pre-treated or not with purified inactivated human protein C for four hours at a concentration of 0.8 ng/ $\mu$ l and then exposed or not to SARS-CoV-2 infection. Cells were grown in 12-well plates, with three wells per group—experimental N of 3. Cells were washed with PBS before the PC treatment, and a medium without FBS was used for the incubation. After removing the viral inoculum, the medium was replaced with DMEM or MEM without FBS. The cell lysate was collected for subsequent extraction and analysis of RNA by quantitative real-time PCR (RT-qPCR). One-way ANOVA followed by Tukey's multiple comparison test was used for statistical analyses. \*  $p \leq 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , and \*\*\*\*  $p < 0.0001$  compared to the groups indicated in the figure.



**Supplementary Figure S2.** HUVEC of different passages pre-treated or not with purified inactivated human protein C for four hours at a concentration of 0.8 ng/ $\mu$ l and then incubated with serum from patients with severe COVID-19 or healthy serum at a concentration of 5%. Cells were grown in 12-well plates, with two wells per group—experimental N of 4. Cells were washed with PBS before the PC treatment, and a medium without FBS was used for the incubation. After serum incubation for 4 h, the cell lysate was collected for subsequent RNA extraction and analysis by quantitative real-time PCR (RT-qPCR). Two-way ANOVA followed by Tukey's multiple comparison test was used for statistical analyses. \*  $p \leq 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$  and \*\*\*\*  $p < 0.0001$  compared to the groups indicated in the figure. Data are presented as mean  $\pm$  s.e.m. with individual data points indicated.