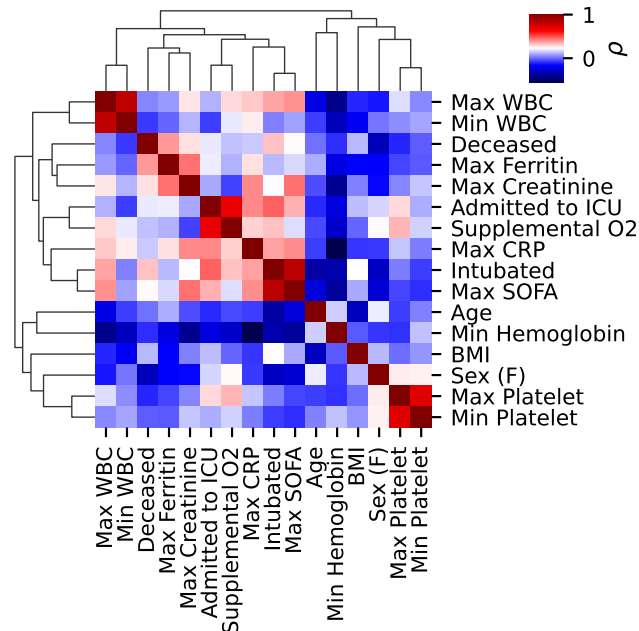# Supplementary Material

Figure S1. Correlation map showing Pearson correlation coefficients (ρ) between the clinical variables examined.
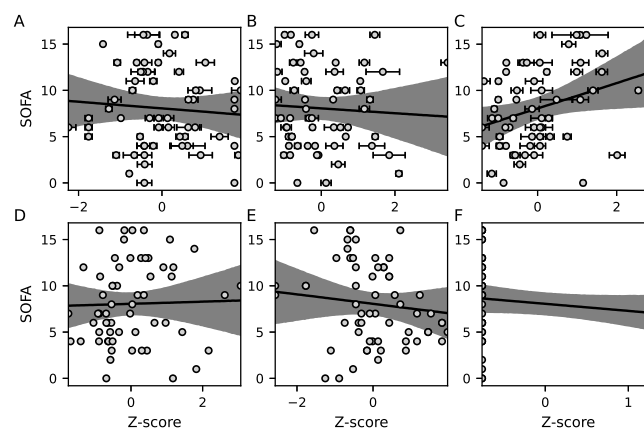

Figure S2. Scatter plots showing results of multiple linear regression predicting patient SOFA score. Regressors include total predicted (A) HLA-A, (B), HLA-B, and (C) HLA-C binding interactions for each patient toward their corresponding SARS-CoV-2 peptidome. Patient (D) age, (E) BMI, and (F) sex are also included as regressors in the analysis., Error bars represent standard deviation in the independent variable across binding probability thresholds.
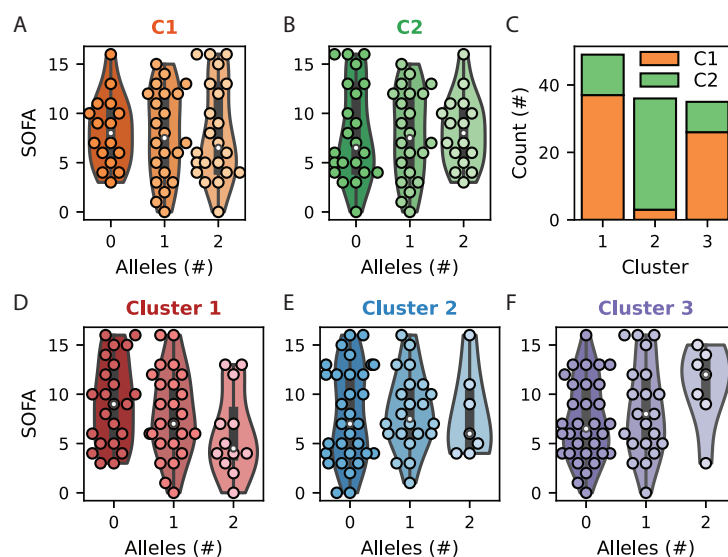
Figure S3. Dose dependence of HLA-C allele subtypes with respect to patient SOFA score. (A-B) Violin plots showing dependence of patient SOFA score on number of alleles in each of the two HLA-C KIR clusters. (C) Bar graph showing the correspondence of the sequence-based clusters identified in the present study to the previously determined KIR clusters. (D-F). Violin plots showing the dependence of patient SOFA score on number of HLA-C alleles from each of the three sequence-based clusters.