Sample Summary Report

Order: SAMPLE1234

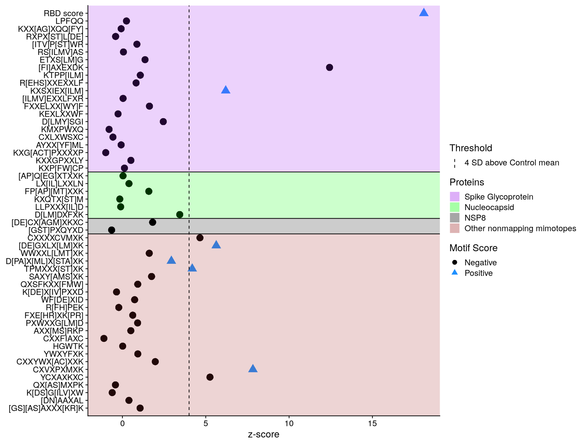
External identifier: SAMPLE1234

This report summarizes the results of the SERA SARS-CoV-2 research assay on sample SAMPLE1234.

IgG

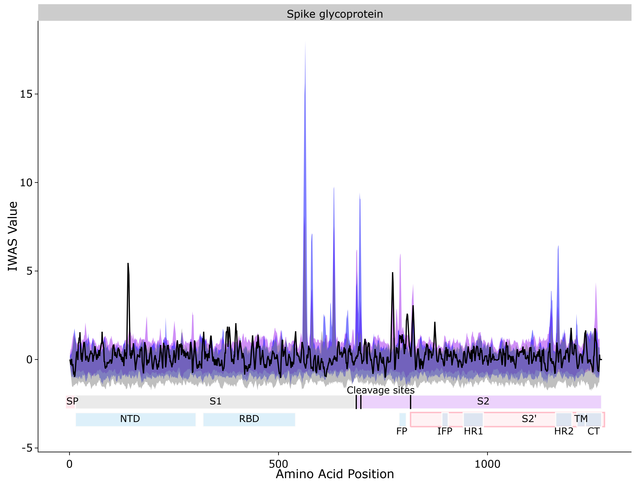
Motif data

The SERA IgG panel includes 52 motifs and features that were identified as sensitive and specific to the COVID patient poulation (n > 500) relative to a large, pre-pandemic database of controls (n > 2000). A subset of these motifs map linearly to SARS-CoV-2 antigens (i.e. nucleoprotein, spike). The non-mapping motifs likely represent mimotopes of structural epitopes to SARS-CoV-2. Individual motif enrichments for the sample (black) are shown relative to the pre-pandemic controls (grey).

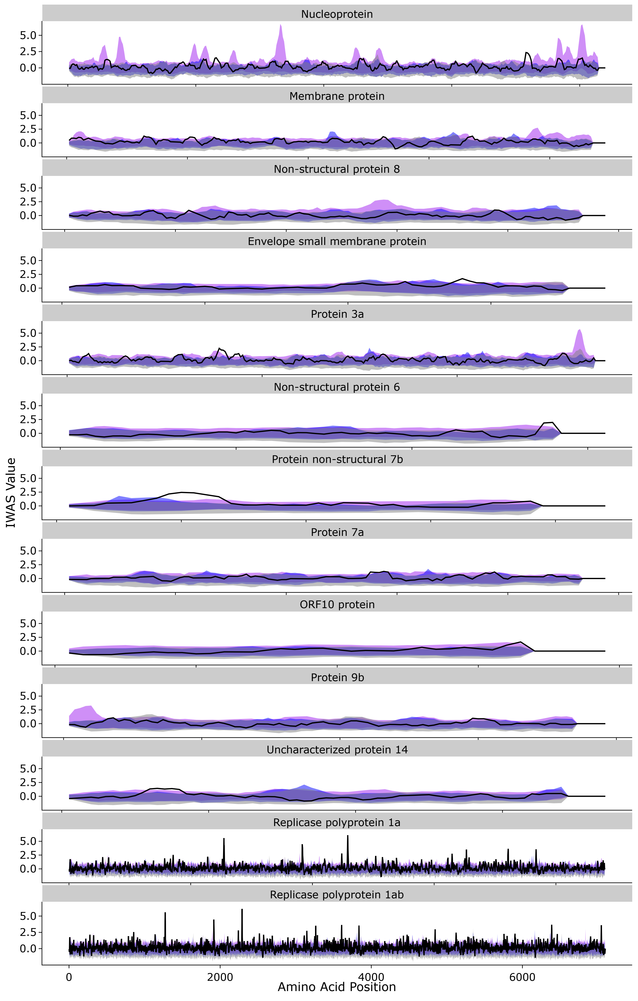


IgG SARS-CoV-2 tiling plots

The PIWAS tool was applied to provide amino acid resolution tiling data for the entirety of the SARS-CoV-2 proteome (Uniprot proteome: UP000464024). The plots below provide this tiling information for the sample (black) relative the the 5th-95th quantile bands for the COVID patients (purple) and controls (grey). The first plot show spike glycoprotein annotated with important functioning sites along its amino acid sequence. Abbreviations: Signal Peptide (SP), N-terminal domain (NTD), receptor-binding domain (RBD), fusion peptide (FP), internal fusion peptide (IFP), two heptad-repeat domains (HR1 and HR2), transmembrane protein (TM), and C-terminal domain (CT). HTML plots are interactive. You may: mouse over to see values, click and drag to zoom, and double click to un-zoom. For the legend you can select and de-select any series by clicking on the label under Sample Comparison Cohorts.



The following page shows the PIWAS tiling of the remainder of the SARS-CoV-2 Proteins.



References

Haynes WA, Kamath K, Bozekowski J, et al. High-resolution mapping and characterization of epitopes in COVID-19 patients. medRxiv 2020.11.23.20235002; doi: https://doi.org/10.1101/2020.11.23.20235002

Haynes WA, Kamath K, Daugherty PS, Shon JC. Protein-based Immunome Wide Association Studies (PIWAS) for the discovery of significant disease-associated antigens. bioRxiv 2020.03.18.997759; doi: https://doi.org/10.1101/2020.03.18.997759

Pantazes, R., Reifert, J., Bozekowski, J. et al. Identification of disease-specific motifs in the antibody specificity repertoire via next-generation sequencing. Sci Rep. 2016. https://doi.org/10.1038/srep30312

Reifert J, Kamath K, Bozekowski J, et al. Serum epitope repertoire analysis enables early detection of Lyme disease with improved sensitivity in an expandable multiplex format. Journal of Clinical Microbiology. 2020. DOI: 10.1128/JCM.01836-20

Kamath K, Reifert J, Johnston T, et al. Antibody epitope repertoire analysis enables rapid antigen discovery and multiplex serology. Sci Rep. 2020. doi:10.1038/s41598-020-62256-9