Supplementary Figure 1: Neutralizing and binding antibody levels are not above background for participants 19C and 196C. A) Neither PID 19C nor 196C had detectable neutralizing titers at any timepoint. The limit of detection for our neutralization assay ($NT_{50} = 20$) is shown with a dashed blue line. B) Neither PID 19C nor 196C had detectable spike or RBD binding antibodies at any timepoint. The binding levels for the negative control sample (2017-2018 sera pool) are shown as dashed lines colored by assay.
Supplementary Figure 2. Titers of spike-pseudotyped lentiviral particles in 293T-ACE2 cells (BEI Resources, NR-52511) (A, B) and neutralization of these viruses with serum from an individual previously infected with SARS-CoV-2 (C). A) Titers of pseudotyped lentivirus with a ZsGreen backbone (BEI, NR-52520) pseudotyped with full-length spike (BEI, NR-52514), spike with either the last 18 (Δ18) or 21 (Δ21) amino acids truncated, VSV G, or no viral entry protein. Titers were determined as described in [1]. Positive cells were counted via flow cytometry at 60 h post-infection. The “n.d.” indicates that the titer was not detectable. Data shown are from a single representative example. B) Titers of Luciferase-IRES-ZsGreen backbone virus pseudotyped with the specified viral entry proteins. Titers were determined by measuring relative luciferase units (RLUs) per mL and then normalizing to the titers of full-length spike pseudotyped lentivirus. RLU were determined at 52 h post-infection. The RLU per mL for the spike-pseudotyped viruses are the average of seven wells of a 1:3 dilution of virus in a total volume of 150 μL. For the VSV G-pseudotyped virus, RLU per mL were averaged from six three-fold dilutions starting at a 1:48 dilution in a total volume of 150 μL. C) Neutralization assay with serum collected from an individual previously infected with SARS-CoV-2, 43 days post-symptom onset (p.s.o.). The full-length neutralization curve shows data averaged from duplicate measurements. The Δ18 and Δ21 neutralization curves display data from a single replicate. The IC50s for the full-length, Δ18, and Δ21 viruses are 1:345, 1:345, and 1:370, respectively. These values all fall within the range of IC50 values we have measured previously for this same serum sample with virus pseudotyped with full-length spike (1:320-1:375). We thank Dr. David Koelle and Dr. Anna Wald at the University of Washington for sharing this sample with us.
Supplementary Figure 3: Neutralization curve for NIBSC standard reference serum (product number 20/130). The NT$_{50}$ for this sample was calculated to be $\sim$3050.
Supplementary Figure 4: Fold change in NT50 at each timepoint colored by disease severity. There was only one asymptomatic individual with a 30-day timepoint and 90-day timepoint, so this individual was included in the Non-Hospitalized group. As in Figure 1B, only individuals with a sample at ~30 days post-symptom onset are included. P-value calculated using the Wilcoxon rank-sum test.
Supplementary Figure 5: Neutralization curves for each participant. For each participant, each sample is a different color with the legend specifying how many days post-symptom onset each sample was collected.
Supplementary File 1: Plasmid map for the spike plasmid (HDM_Spikedelta21) used in the pseudotyped lentivirus neutralization assays.

Supplementary File 2: Raw data for each sample. This csv includes the columns: sample, participant ID, Sex, Age, Severity, Days Post-Symptom Onset, IC50, NT50, RBD IgA, RBD IgG, RBD IgM, and Spike IgG. ELISA results are presented as area under the curve (AUC).
References:

1. Crawford KHD, Eguia R, Dingens AS, et al. Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. Viruses [Internet]. 2020; 12(5). Available from: http://dx.doi.org/10.3390/v12050513