Figure S1

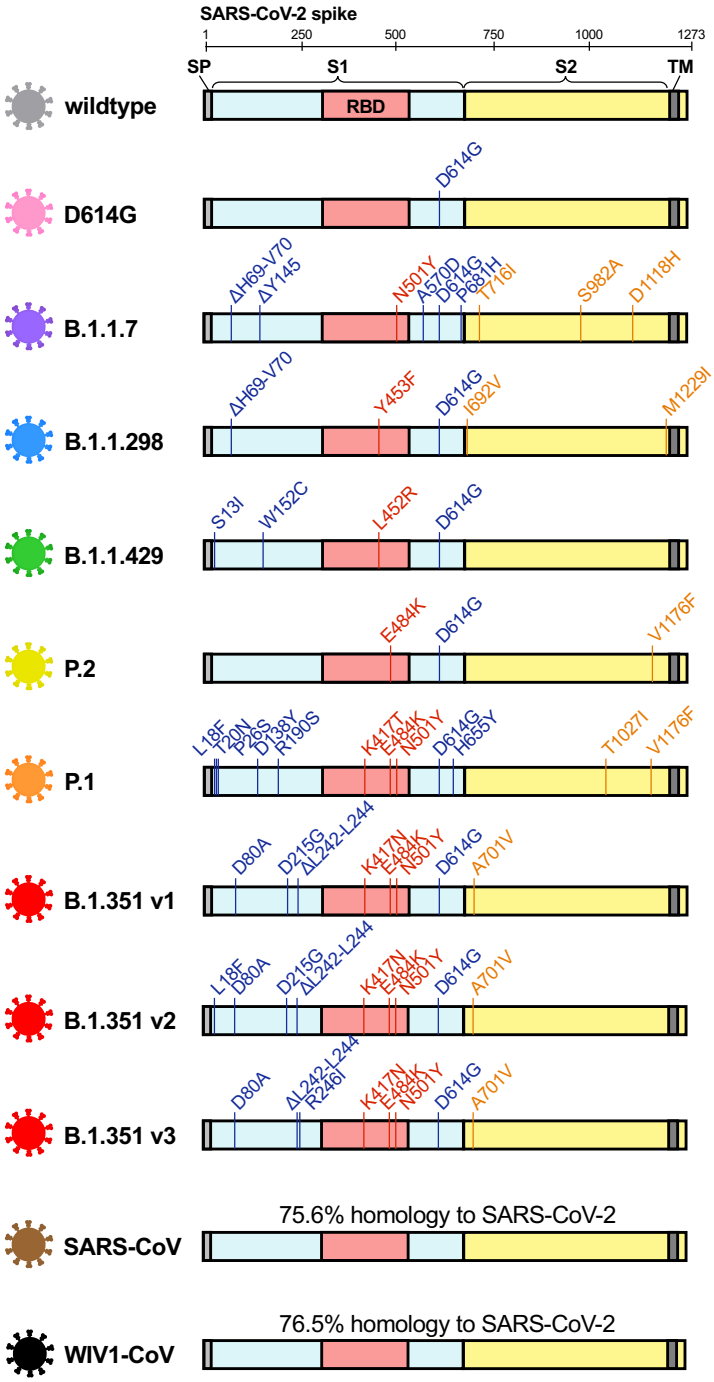

Figure S1: SARS-CoV-2 variants tested in this study.
Schematic of mutations in the spike protein sequence of the following SARS-CoV-2 variants are illustrated: wild type (grey), D614G (pink), B.1.1.7 (purple), B.1.1.298 (blue), B.1.1.429 (green), P.2 (yellow), P.1 (orange), three variants of B.1.351 (red; v1, v2, and v3), SARS-CoV (brown), and WIV1-CoV (black).

Figure S2

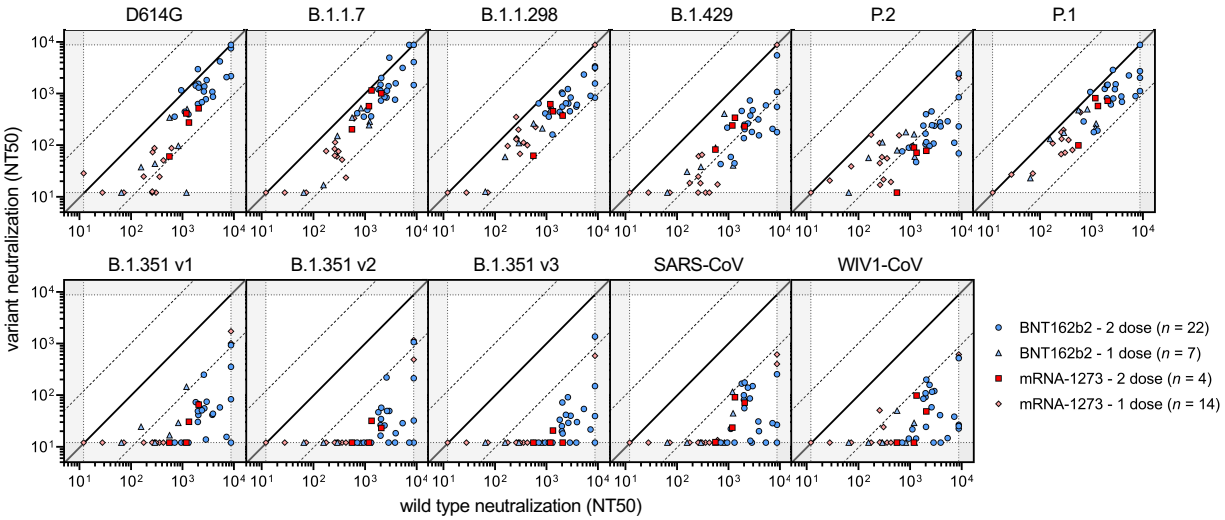

Figure S2: Correlations of SARS-CoV-2 variant neutralization titers.
Correlations between neutralization of wild-type and the indicated variant pseudoviruses are demonstrated. The solid diagonal black line indicates identical neutralization, and the dotted diagonal black lines indicate a 10-fold difference in neutralization (NT50). Four groups of vaccine recipients are indicated: (*i*) vaccine recipients >7 days out from their second dose of BNT-162b2 vaccine (*n* = 22, blue circles); (*ii*) vaccine recipients that received only one dose of the BNT-162b2 vaccine or were <7 days from their second dose (*n* = 7, light blue triangles); (*iii*) vaccine recipients >7 days out from their second dose of the mRNA-1273 vaccine (*n* = 4, red squares); and (*iv*) vaccine recipients that received only one dose of the mRNA-1273 vaccine or were <7 days from their second dose (*n* = 14, pink diamonds).

Figure S3

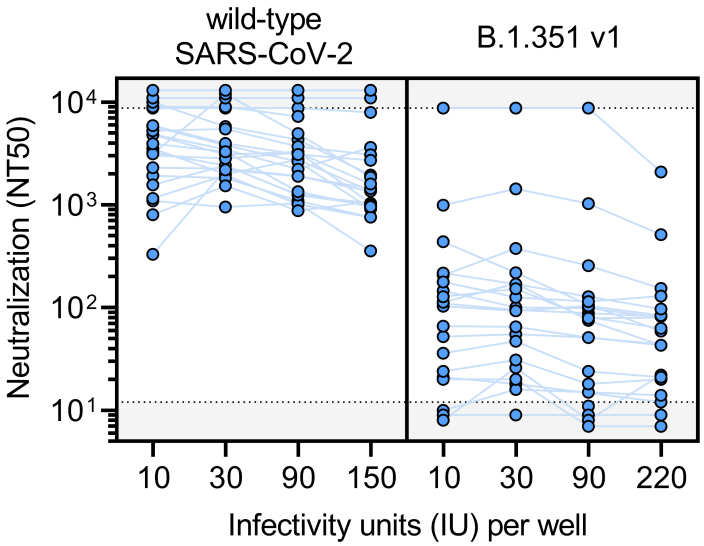

Figure S3: Determination of neutralization titers over a wide range of pseudovirus quantities
To determine the consistency of neutralization titers (NT50) measured by this assay, varying amounts of infectious units per well of wild-type SARS-CoV-2 and B.1.351 v1 pseudovirus were used to perform the neutralization assay for 22 serum samples from BNT162b2 vaccine recipients >7 days out from their second dose. These data demonstrate the robustness of calculating NT50 across a 22-fold range of infectious units of pseudovirus.