Supplementary Table 1. ID50 titers of thirteen INO-4800 vaccinee sera against Wuhan and SARS-CoV-2 variants pseudotyped viruses.

| Sample ID | Dose (mg)* | Wuhan | B.1.117 | B.1.351 | P.1 |
|-----------|------------|--------|---------|---------|-----|
| P1        | 1          | 71     | 46      | 41      | 66  |
| P2        | 1          | 599    | 545     | 243     | 738 |
| P3        | 1          | 407    | 180     | 26      | 382 |
| P4        | 2          | 319    | 188     | 48      | 282 |
| P5        | 2          | 978    | 887     | 310     | 1292|
| P6        | 2          | 368    | 151     | 52      | 453 |
| P7        | 1          | 372    | 185     | 33      | 406 |
| P8        | 2          | 411    | 215     | 64      | 339 |
| P9        | 2          | 251    | 167     | 60      | 297 |
| P10       | 2          | 2550   | 493     | 142     | 2079|
| P11       | 2          | 1766   | 610     | 255     | 2087|
| P12       | 2          | 84     | 84      | 37      | 25  |
| P13       | 0.5        | 187    | 89      | 53      | 190 |

|     | n   |       |        |        |     |
|-----|-----|-------|--------|-------|-----|
|     | 13  | 13    | 13     | 13    | 13  |
| Mean| 643.3 | 295.4 | 105    | 664.3 |
| SD  | 729 | 255   | 98.87  | 706.7 |
| Range min | 70.7 | 46.5  | 25.6   | 25.3 |
| Range max | 2550 | 886.7 | 309.8  | 2087 |

*The dose corresponds to the amount in mg of INO-4800 delivered per immunization period (n=1, 0.5 mg vaccine dose; n = 4, 1.0 mg; n = 8, 2.0 mg).*
Supplementary Table 2. Descriptive analysis and geometric mean titers (GMT) of neutralizing ID50 values for Wuhan, B.1.1.7, B.1.351 and P.1 variants.

|                      | Wuhan | B.1.1.7 | B.1.351 | P.1   |
|----------------------|-------|---------|---------|-------|
| Number of subjects   | 13    | 13      | 13      | 13    |
| Minimum              | 70.65 | 46.45   | 25.95   | 25.34 |
| Maximum              | 2550  | 886.7   | 309.8   | 2087  |
| Range                | 2479  | 840.3   | 283.9   | 2062  |
| Mean                 | 643.2 | 294.6   | 104.9   | 664.4 |
| Std. Deviation       | 729   | 255.5   | 98.84   | 706.7 |
| Std. Error of Mean   | 202.2 | 70.85   | 27.41   | 196   |
| Lower 95% CI of mean | 202.7 | 140.2   | 45.19   | 237.3 |
| Upper 95% CI of mean | 1084  | 449     | 164.6   | 1091  |
| Geometric mean       | 393   | 210.4   | 73.63   | 372.3 |
| Geometric SD factor  | 2.822 | 2.379   | 2.307   | 3.493 |
| Lower 95% CI of geo. mean | 209.9 | 124.6   | 44.42   | 174.8 |
| Upper 95% CI of geo. mean | 735.6 | 355.2   | 122     | 792.8 |
Supplementary Figure 1. Schematic diagram and molecular modeling of SARS-CoV-2 spike protein. A) Spike protein diagram with major features labeled: N-terminal domain (NTD, red), receptor binding domain (RBD, orange), fusion peptide (FP, green), heptad repeats 1 and 2 (HR1 and HR2, blue), transmembrane region (TM, violet), C-terminal domain (CT, dark purple). B) Molecular models of spike protein with mutations indicated for B.1.1.7, B.1.351, and P.1 variants. Trimer model is depicted with one subunit as a Ca trace and colored identically to the diagram in (A) with the two subunits outlined for clarity. Large loops not modeled are indicated by dashed lines and the stalk and membrane-spanning portion of the molecule are indicated with cylinders.