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Supplemental information

Ultrapotent and broad neutralization

of SARS-CoV-2 variants

by modular, tetravalent, bi-paratopic antibodies

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Supplementary Figures and Figure Legends

Figure S1. Binding sensorgrams for nAb:S-protein interactions, related to STAR Methods for BLI interferometry. Binding signals (red) of nAb-S-protein interactions were determined for **A)** IgG 15033-7, **B)** D-Fc 15033-7, **C)** D-Fc-F 33-7:33-7 and **D)** D-Fc-F 33-7:36 by biolayer interferometry exposing serial 2-fold nAb dilutions (from 20 nM) to immobilized sensorimmobilized S-protein. Global fits (black) were obtained using a 1:1 binding model.



Figure S2 – S-protein variant mutations used to generate pseudovirus variants, related to Fig. 5 and Table 2 A segment of the RBD of the SARS-COV-2 S-protein corresponding to residues 409-515 showing the mutations introduced in to the RBD to generate pseudovirus for infection assays



Figure S3 – SEC analysis of D-Fc-F 33-7:33-7, related to STAR Methods for Size exclusion chromatography The elution profiles of SEC-purified D-Fc-F 33-7:33-7 in HNS buffer were obtained by SEC analysis immediately following purification (T_0) or after 30- (dashed trace) and 60-days (dotted trace) incubation in HNS buffer supplemented with 0.02% sodium azide at 37°C.