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Supplemental information

Additional mutations based on Omicron

BA.2.75 mediate its further evasion

from broadly neutralizing antibodies

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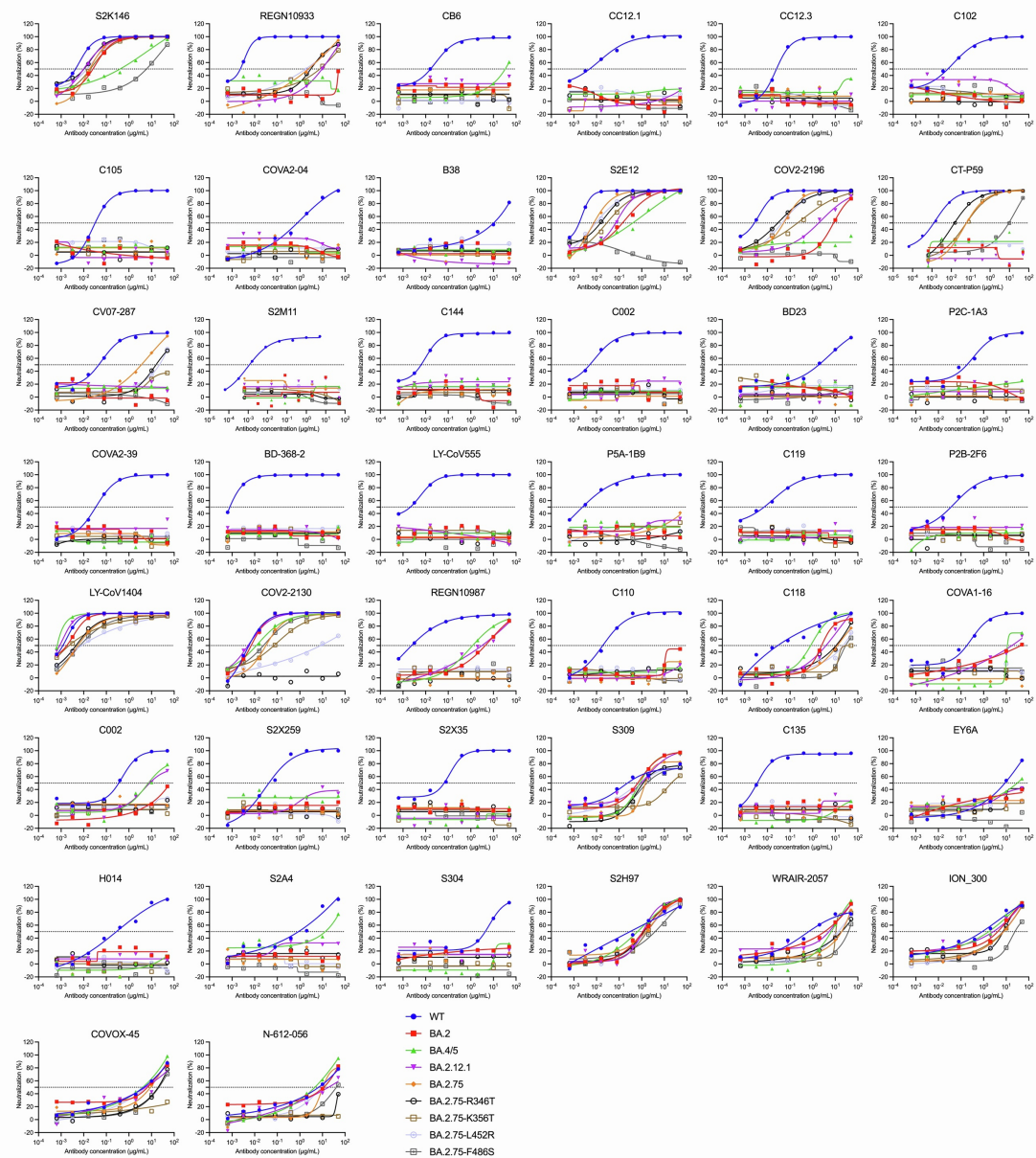


Figure S1. Neutralization curves of 44 RBD-specific mAbs against SARS-CoV-2 WT, BA.2, BA.4/5, BA.2.12.1, BA.2.75 and BA.2.75 related variants, Related to Figure 3.

All mAbs were serially diluted by 5-fold from 5 µg/mL or 50 µg/mL. A reduction of 50% in viral infectivity was indicated by a horizontal dashed line. One out of two or three independent experiments was shown.

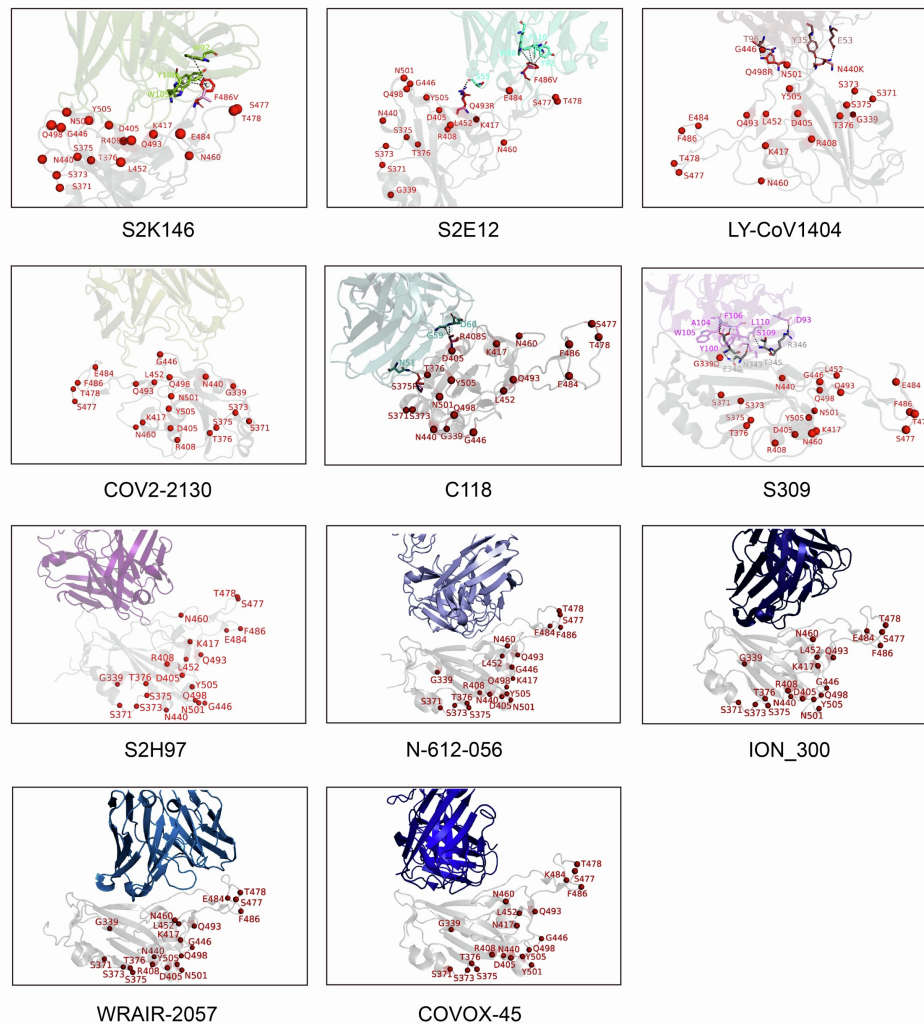


Figure S2. Structural analysis of 11 bnAbs binding to SARS-CoV-2 RBD, Related to Figure 3.

All mutations appearing on the RBD of involved Omicron subvariants including BA.2, BA.4/5, BA.2.12.1, and BA.2.75 are highlighted in brick red. The RBDs and Fabs of bnAbs are shown in gray and other colored cartoons, respectively. The binding epitopes of S2K146, S2E12, LY-CoV1404, COV2-2130, C118, and S309 are located in or near the mutated regions. The D339, F375, S408, K440, V486, R493, and R498 residues were artificially displayed on the relevant positions. The potential interactions between mAb and RBD were calculated by the PISA v1.52 (<https://www.ebi.ac.uk/pdbe/pisa/>) and shown as black dotted lines. Five S2H97-site bnAbs (S2H97, N-612-056, ION_300, WRAIR-2057, and COVOX-45) bind to the epitopes away from the mutated regions.