Expanded View Figures

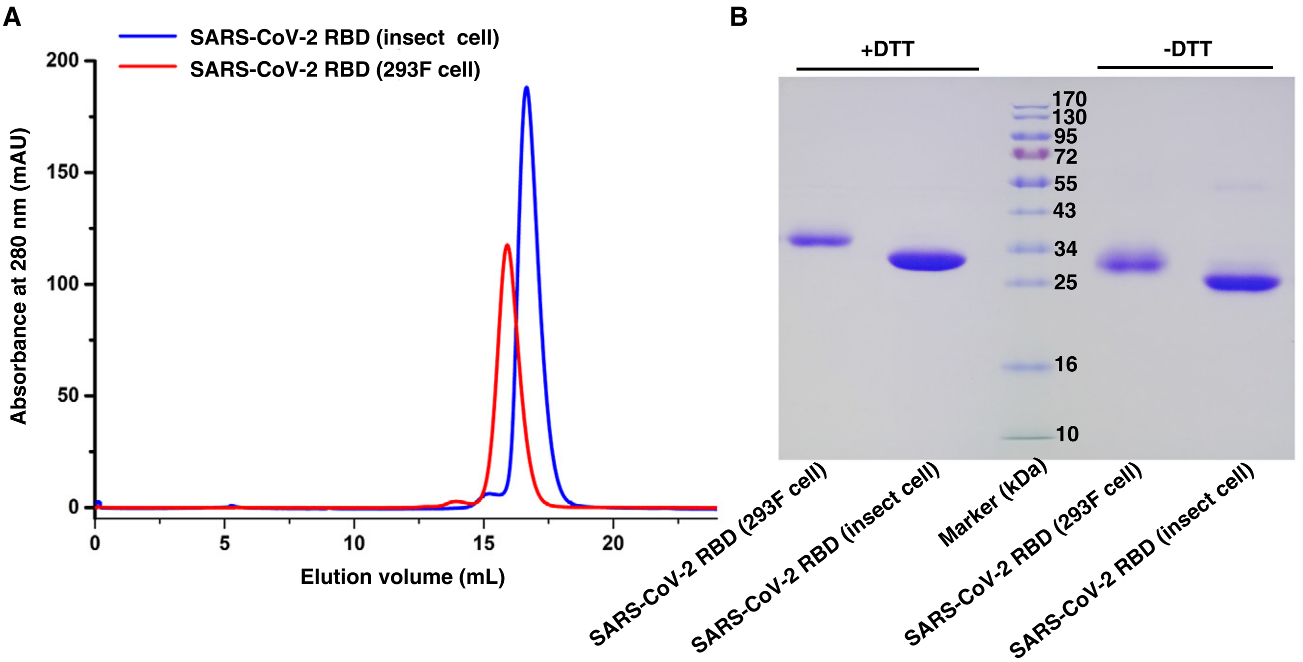

Figure EV1. Gel filtration profile of SARS-CoV-2 RBD protein.

A Gel filtration profiles of SARS-CoV-2 RBD protein obtained from insect cell (blue) and 293F cell (red).
B The separation profiles of each pooled samples on SDS–PAGE are shown in reducing (+DTT) or non-reducing (−DTT) conditions.

Source data are available online for this figure.

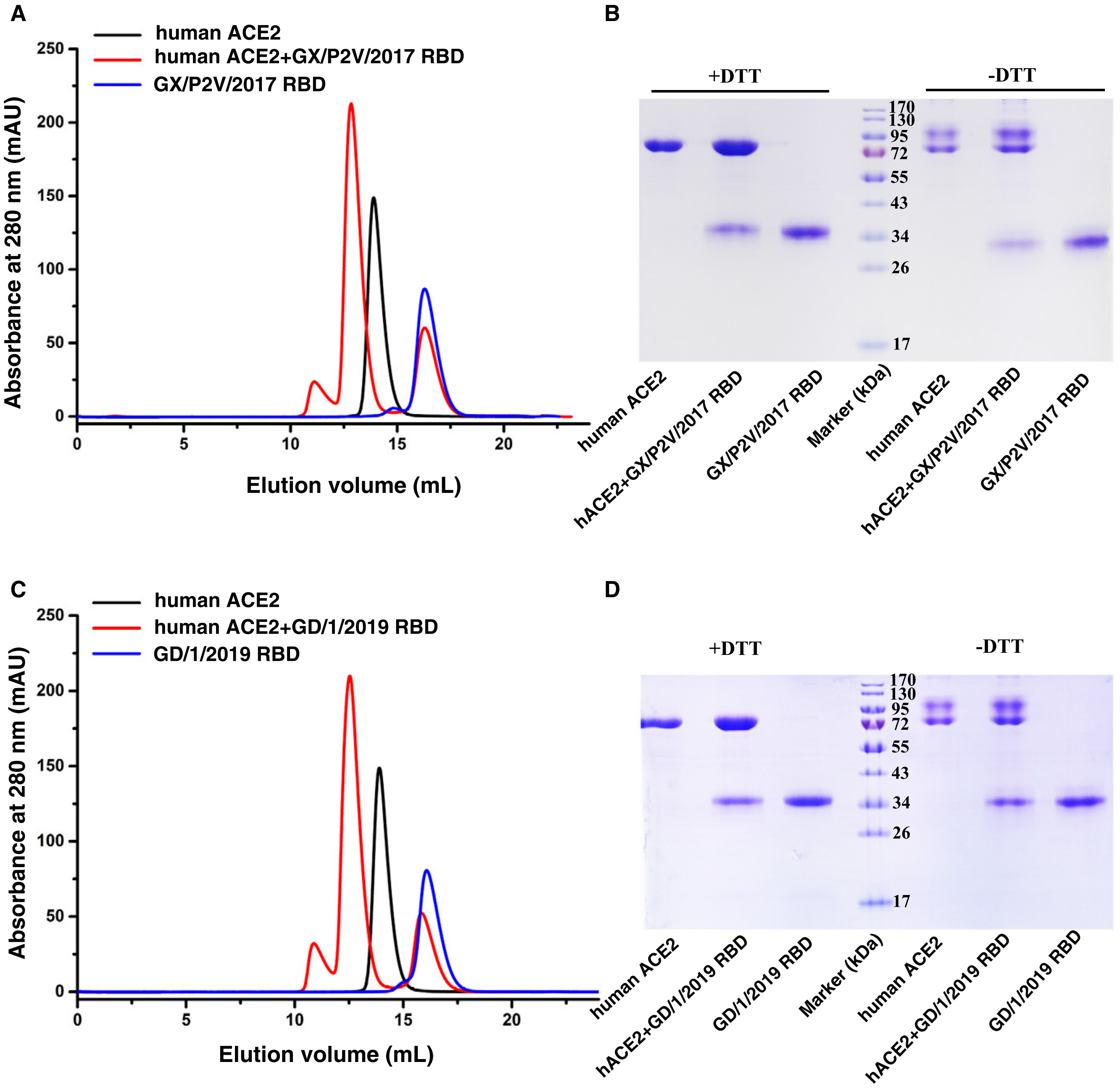

Figure EV2. Gel filtration profiles of hACE2-GX/P2V/2017 RBD and hACE2-GD/1/2019 RBD complex protein.

- A Gel filtration profiles of human ACE2 (black), GX/P2V/2017 RBD (blue), and the hACE2-GX/P2V/2017 RBD complex (red) were analyzed by size-exclusion chromatography as indicated.
- B The separation profiles of each pooled samples on SDS–PAGE are shown in reducing (+DTT) or non-reducing (—DTT) conditions.
- C Gel filtration profiles of human ACE2 (black), GD/1/2019 RBD (blue), and the hACE2-GD/1/2019 RBD complex (red) were analyzed by size-exclusion chromatography as indicated.
- D The separation profiles of each pooled samples on SDS–PAGE are shown in reducing (+DTT) or non-reducing (-DTT) conditions.

Source data are available online for this figure.

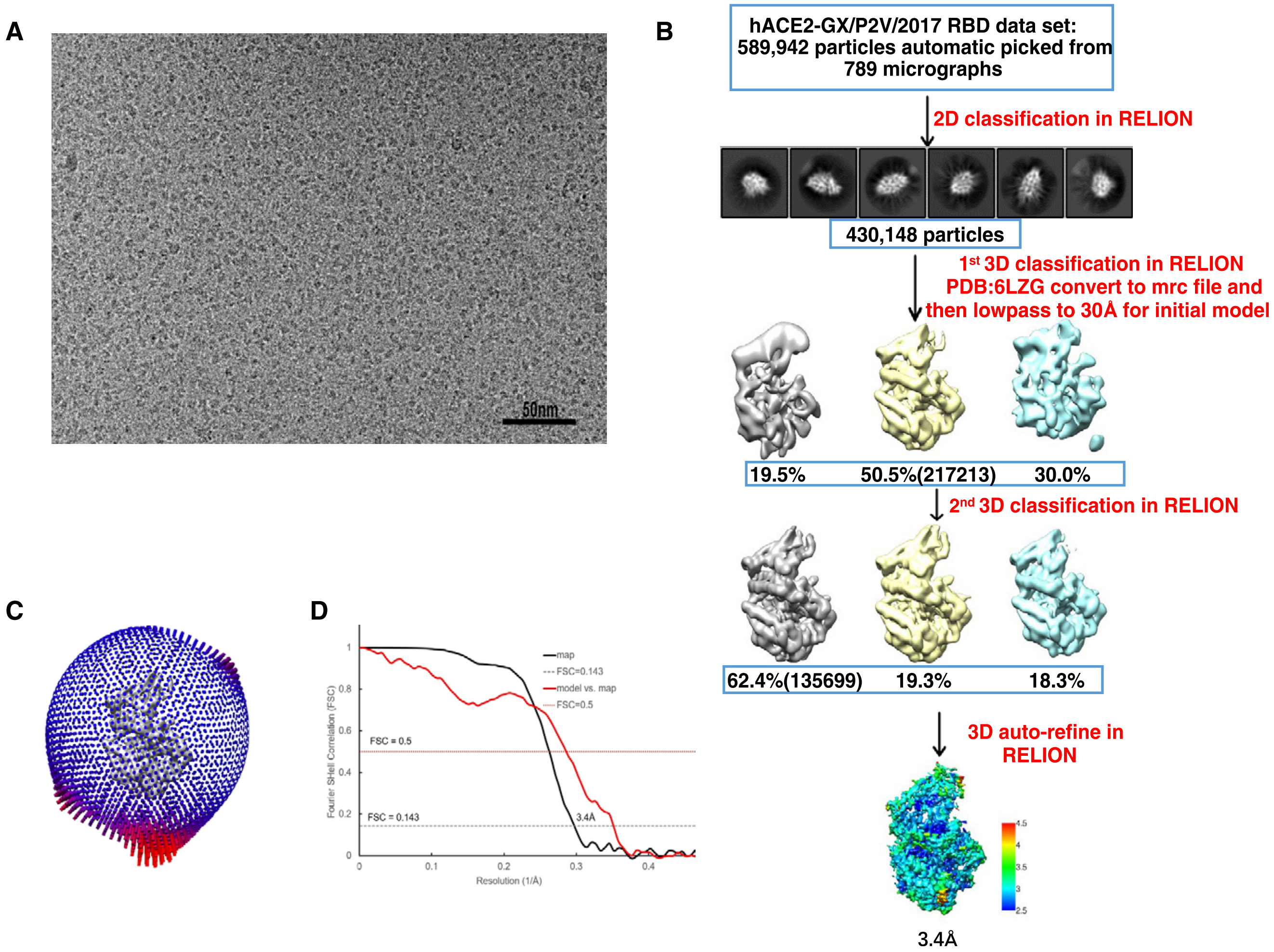

Figure EV3. EM data processing of human ACE2 and GX/P2V/2017 RBD complex.

- A One of raw summed micrographs.
- B Schematic to show steps in cryo-EM data processing.
- C Angular distribution of the particles for 3D reconstruction.
- D Fourier shell correlation (FSC) of final EM map and model vs. map.

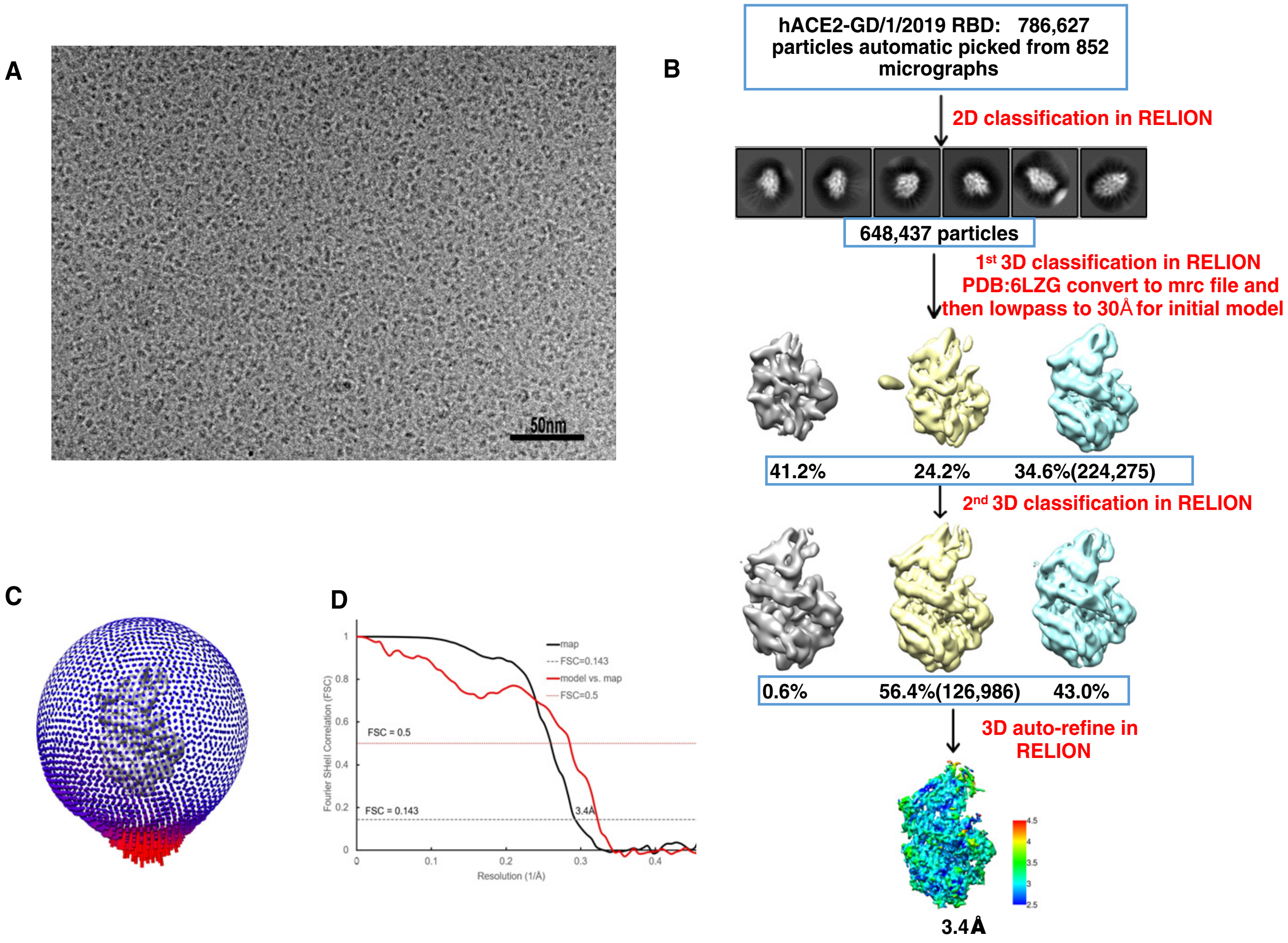

Figure EV4. EM data processing of human ACE2 and GD/1/2019 RBD complex.

A One of raw summed micrographs.

B Schematic to show steps in cryo-EM data processing.

C Angular distribution of the particles for 3D reconstruction.

D Fourier shell correlation (FSC) of final EM map and model vs. map.

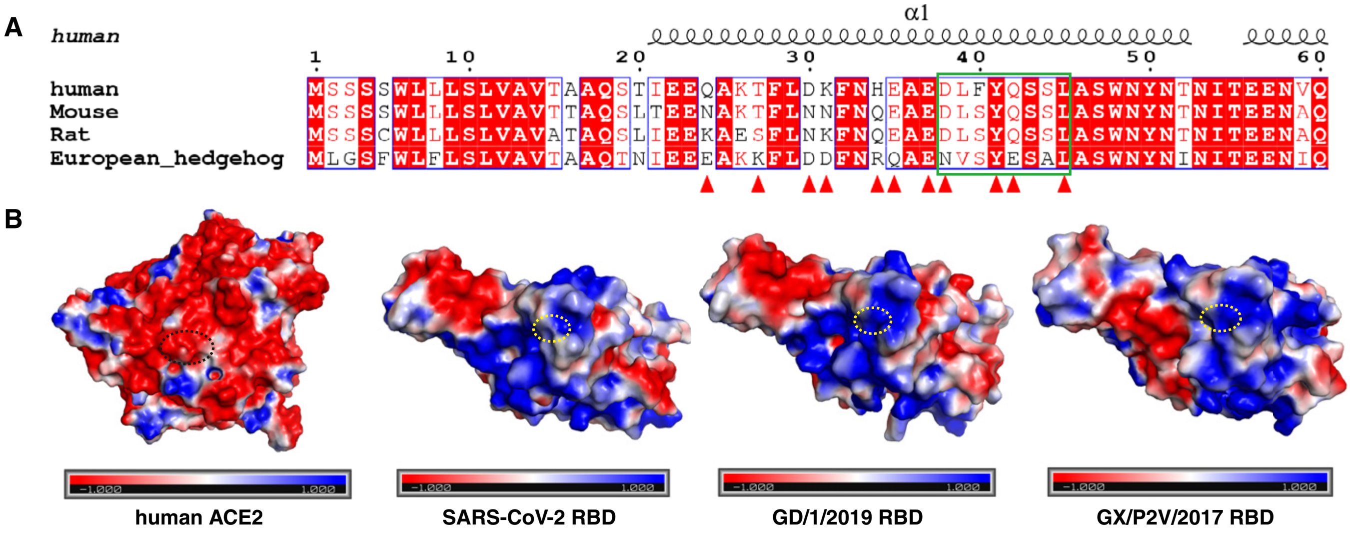

Figure EV5. Residue Q498H substitution in GD/1/2019 RBD and GX/P2V/2017 RBD strengthens the interaction with the receptor compared with the SARS-CoV-2 RBD.

A Sequence alignment of the ACE2 sequences from human, mouse, rat, and European hedgehog. The residues of hACE2 binding with GD/1/2019 RBD are indicated in red triangles, and residues from hACE2 binding with the residue 498 of RBD are indicated in green box. Identical residues are highlighted in red background, and similar residues are labeled in red and boxed in blue lines.

B The surface of hACE2, SARS-CoV-2 RBD, GD/1/2019 RBD, and GX/P2V/2017 RBD (left to right) colored for electrostatic potential: blue (basic), white (neutral), and red (acidic) at ± 1 kTe^{-1}. Residues from hACE2 binding with the residue 498 of RBDs are circled with black dotted ellipse, and residues Q498, H498, and H498 of SARS-CoV-2 RBD, GD/1/2019 RBD, and GX/P2V/2017 RBD are circled with yellow dotted ellipse.