

Supplementary information, Fig. S4

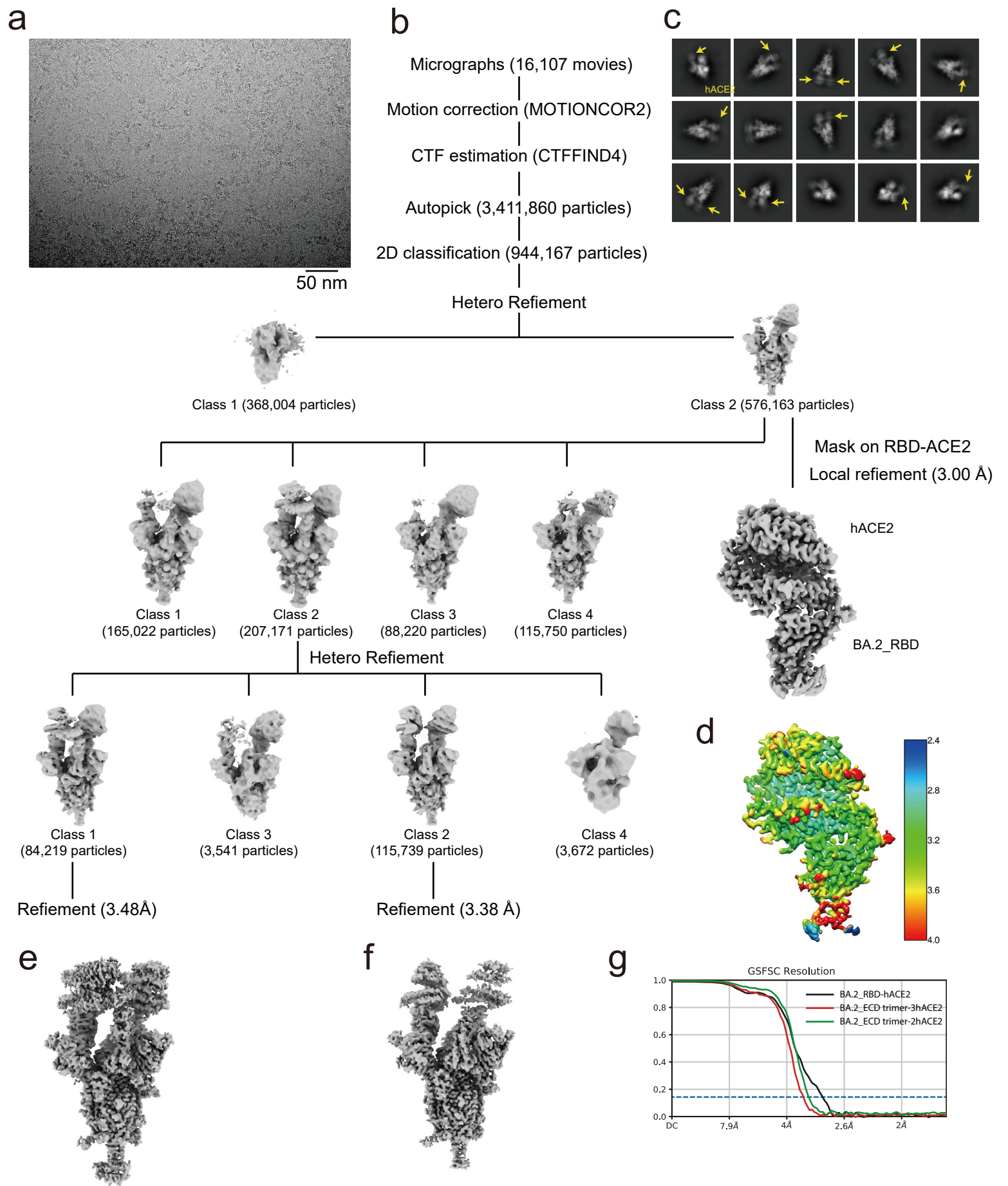


Fig. S4. Cryo-EM data processing of the Omicron BA.2 spike protein-hACE2 complex.

(a) A representative cryo-EM micrograph of Omicron BA.2 ECD-hACE2 complex with 50 nm scale bar included as a size reference. (b) Computational processing of cryo-EM data. (c) Twenty representative reference-free two-dimensional (2D) cryo-EM class averages reveal the hACE2 density (yellow arrow). (d) Local resolution of sub-reconstructions of RBD-hACE2 (left panel) and resolution bar is shown in the right panel. (e-f) The EM maps of Omicron BA.2 ECD trimer bound to 3 hACE2 (e), 2 hACE2 (f). (g) The FSC curves for the reconstructions. Color scheme: BA.2 RBD-hACE2, black; BA.2 ECD trimer-3hACE2, red; BA.2 ECD-trimer-2hACE2, green. The resolution of the reconstructions using the Fourier shell cutoff at 0.143 is shown.