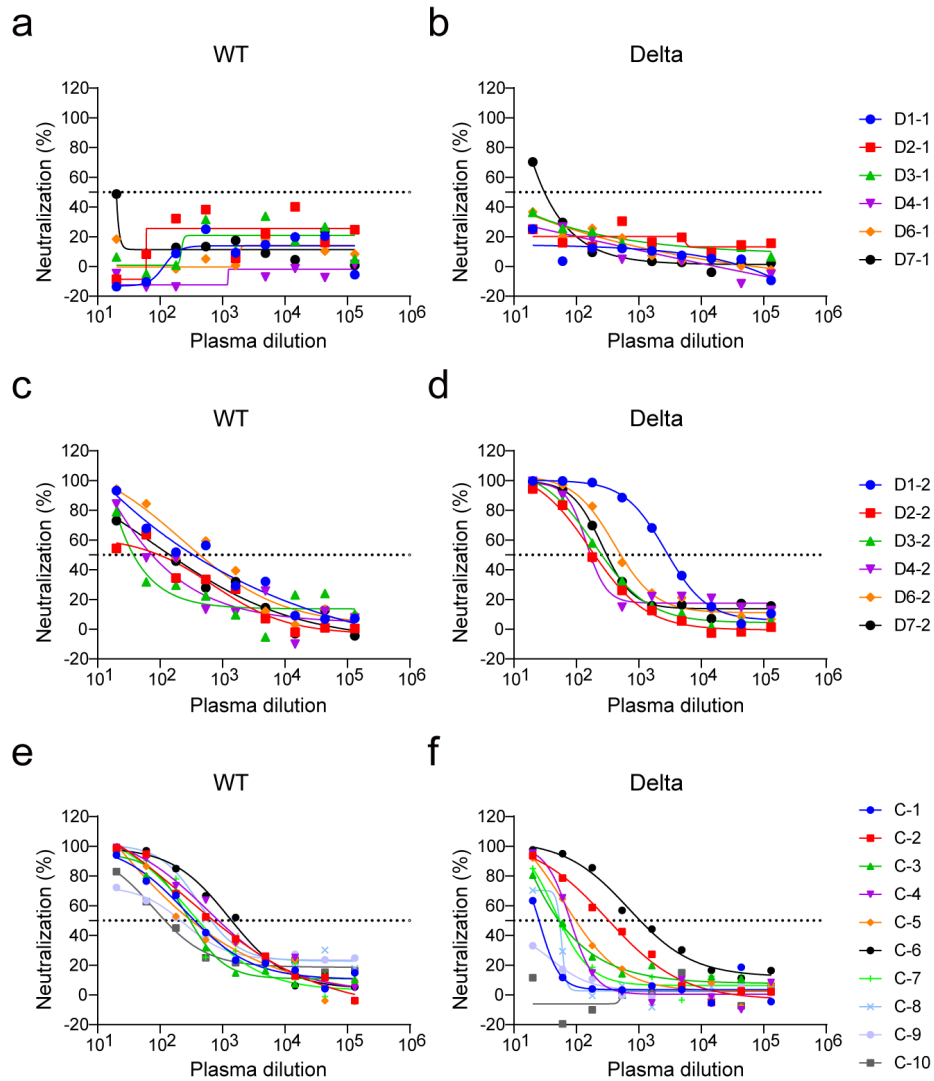


## Supplementary information

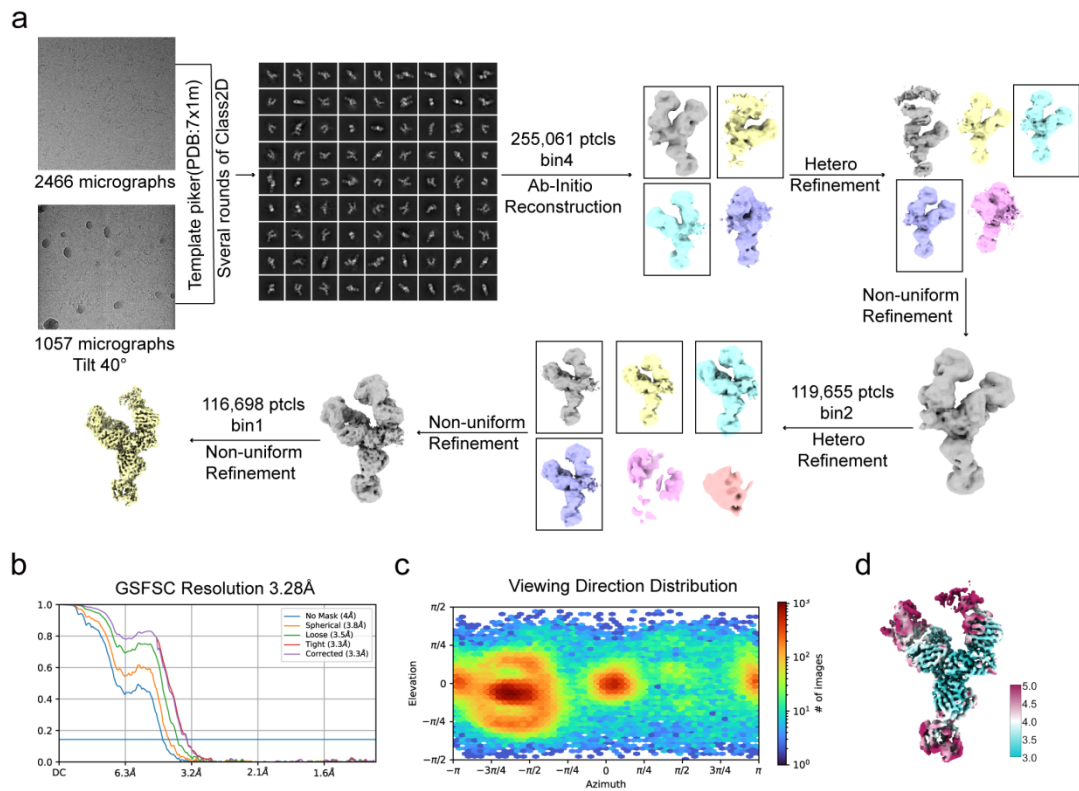


**Figure S1. Neutralization of plasma samples against SARS-CoV-2 pseudoviruses of WT and Delta.**

**(a and b)** The neutralization of WT and Delta pseudoviruses by plasma samples from 6 patients infected with Delta variant at admission.

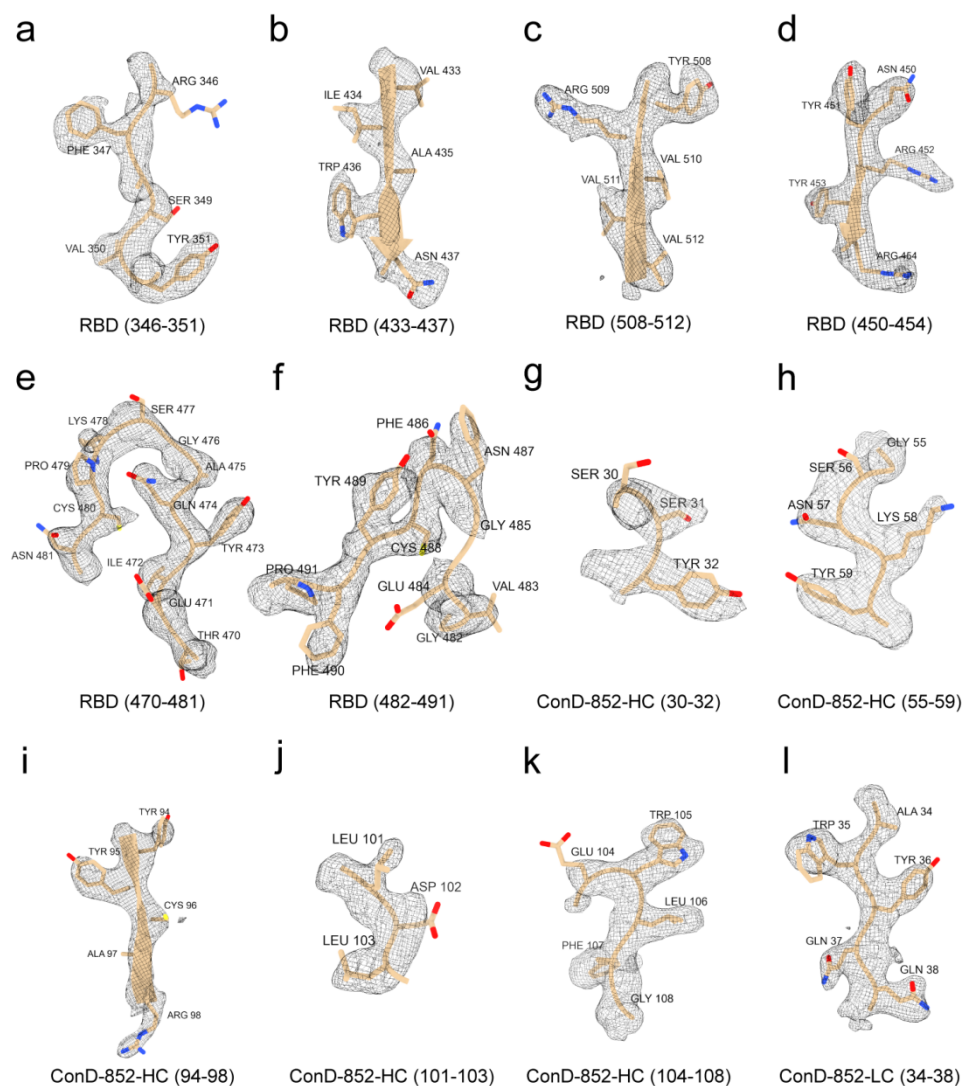
**(c and d)** The neutralization of WT and Delta pseudoviruses by plasma samples from 6 patients infected with Delta variant at convalescent.

**(e and f)** The neutralization of WT and Delta pseudoviruses by plasma samples from 10 SARS-CoV-2 WT convalescent individuals.



**Figure S2. Cryo-EM image-processing workflow for Delta-RBD, ConD-852, P2C-1F11, and S304 complex.**

**(a)** Representative cryo-EM micrographs, results of 2D classification, initial model, hetero refinement and the final density map. **(b)** FSC curve, **(c)** Viewing Direction Distribution and **(d)** local resolution for the Delta-RBD and Fabs complex.

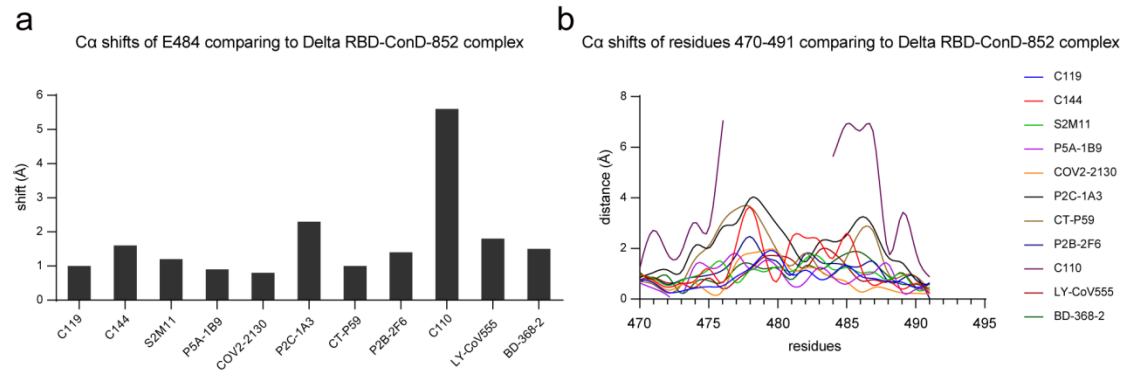


**Figure S3. Cryo-EM density maps for Delta-RBD and ConD-852 complex.** (a-f) Local density maps and models of Delta RBD. (g-k) Local density maps and models of ConD-852 heavy chain. (l) Local density maps and models of ConD-852 light chain.

WT	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	393
Alpha	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Beta	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Delta	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Epsilon	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Kappa	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Lambda	RVQPTESIVRFPNITNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
452		
WT	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	468
Alpha	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	
Beta	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	
Delta	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	
Epsilon	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	
Kappa	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	
Lambda	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDI	
452		
WT	STEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	541
Alpha	STEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	
Beta	STEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	
Delta	STEIQAGSKPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	
Epsilon	STEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	
Kappa	STEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	
Lambda	STEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	
484		

**Figure S4. Sequence alignment of RBD proteins among WT, Alpha, Beta, Delta, Epsilon, Kappa, and Lambda.**

The key interaction residues were boxed out by red boxes. Sites 452 and 484 were marked.



**Figure S5. Ca shifts of (a) E484 and (b) residues 470-491 comparing to Delta RBD-ConD-852 complex.**

**Table S1. Cryo-EM data collection and processing, model building and refinement statistics.**

Data Collection & Image Processing	
Microscope	FEI Titan Krios
Magnification	105K
Voltage(kV)	300
Automation software	SerialEM
Total dose (e <sup>-</sup> /Å <sup>2</sup> )	50
Frames	32
Defocus range (µm)	-1.5-2.5
Pixel size (Å/pixel)	0.66
Symmetry imposed	C1
Micrographs used (no.)	3523
Final particles images	116,698
Overall resolution(Å)	3.28
Model Building & Refinement	
Composition	
Nonhydrogen atoms	6766
Protein residues	874
Ligands	0
Bonds (RMSD)	
Length (Å) (# > 4s)	0.002(0)
Angles (°) (# > 4s)	0.567(1)
MolProbity score	1.77
CaBLAM outliers (%)	4.14
Clashscore	6.86
Rotamer outliers (%)	0.27
C-beta outliers (%)	0.0
Ramachandran plot	
Favored (%)	94.19
Allowed(%)	5.47
Outliers(%)	0.35