

Supplemental information

Biparatopic nanobodies targeting the receptor

binding domain efficiently neutralize SARS-CoV-2

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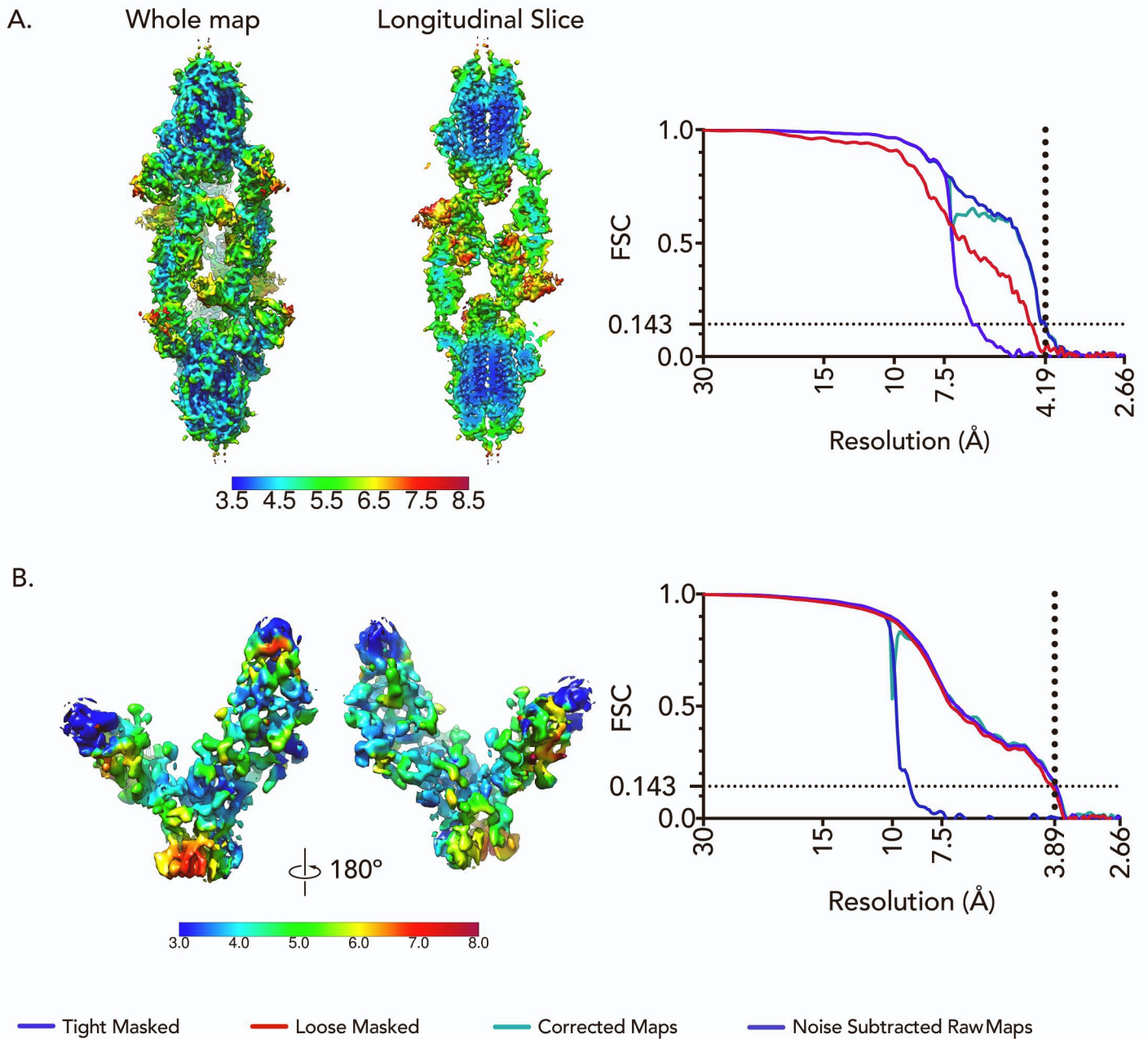


Figure S1. Cryo-EM maps coloured by local resolution of the S-BP10 complex, related to Figure 4. A. Best global refinement of the Spike-BP10 complex B. Best local refinement of a single copy of the RBD with density for two nanobodies. Highest resolution areas are coloured blue and lowest resolution areas are colored deep red. Scales and FSC curves are shown for each map. See also Figure 4.

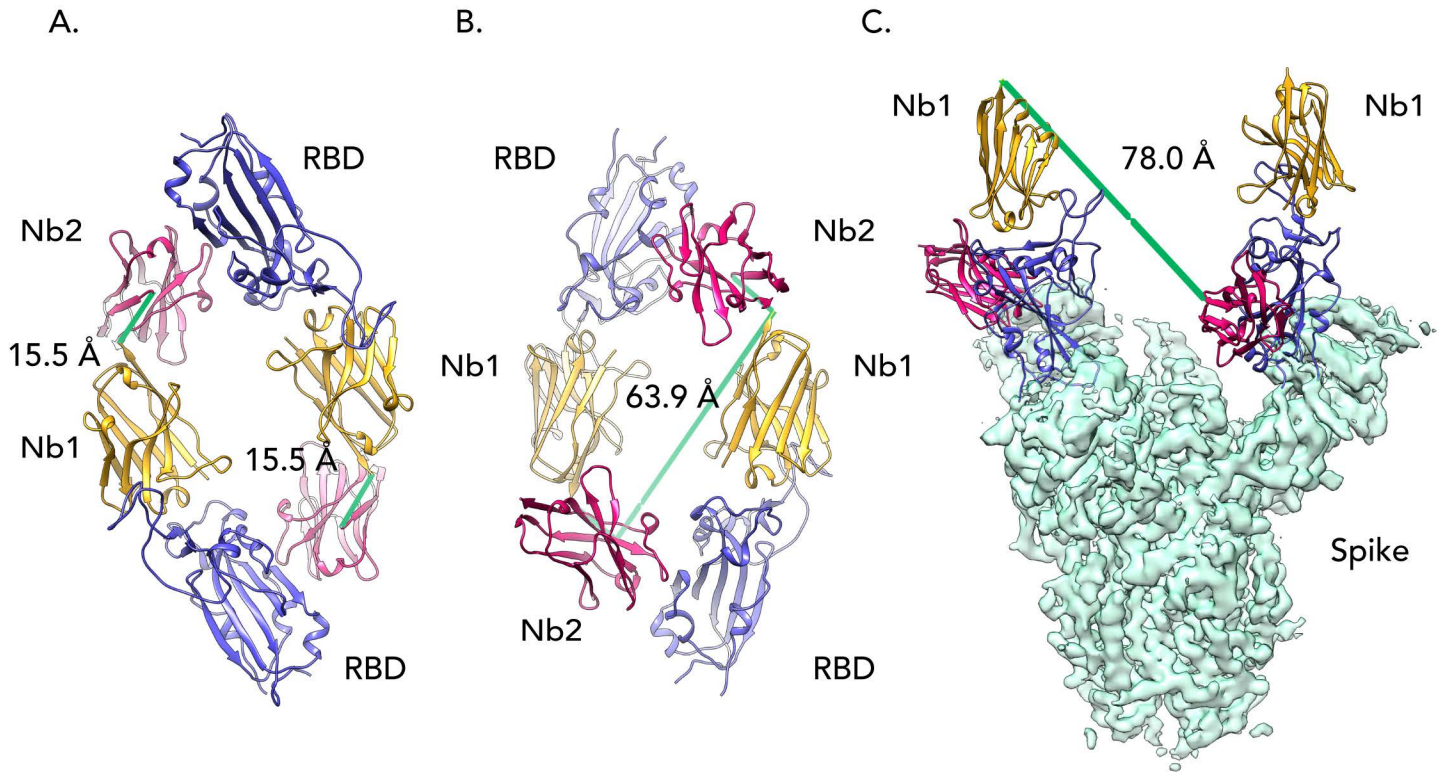


Figure S2. Linker length requirements for connecting nanobodies in the S-BP10 complex, related to figure 4. Cryo-EM maps of the BP10-spike complex showing spike (green), RBDs (purple-blue, PDB ID: 7LX5) and Nanobodies 1 (gold, PDB ID: 7KKK) and 2 (pink, PDB ID: 5IMK) distance measurements are coloured bright green. A. Distance between Nanobody 1 C-terminus and nanobody 2 N-terminus linking RBD's from different copies of Spike. B. Distance between Nanobody 1 C-terminus and nanobody 2 N-terminus on the same RBD. C. Distance between Nanobody 1 C-terminus and nanobody 2 N-terminus on adjacent RBD's on the same copy of Spike. See also Figure 4.

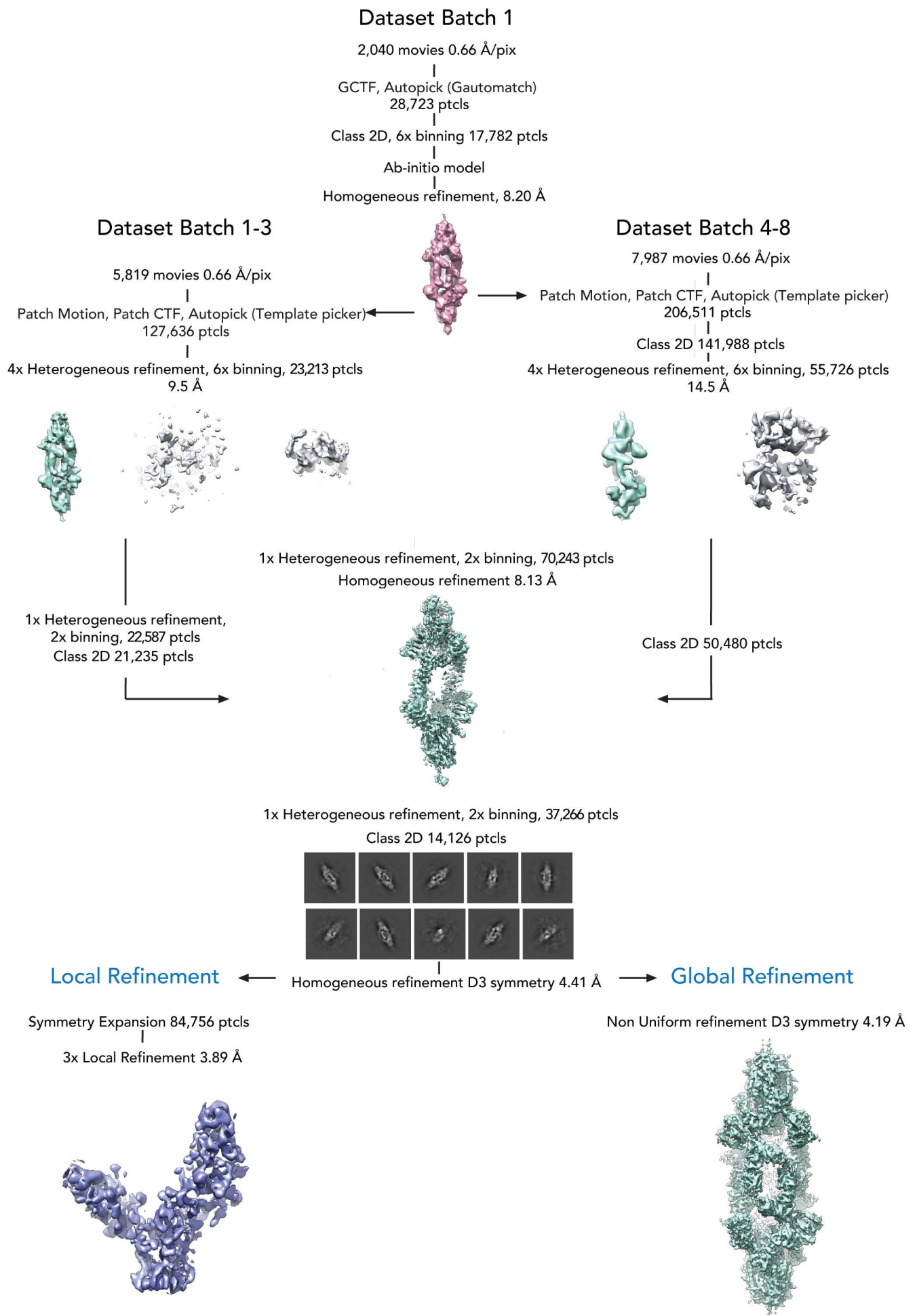


Figure S3. Cryo-EM data processing workflow for the S-BP10 complex, related to Figure 4. Details of workflow are fully described in materials and methods. See also Figure 4.

SARS-CoV-2	RVQPTEIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYAD	80
SARS-CoV-2 Alpha	80
SARS-CoV-2 Delta	80
SARS-CoV-2 Lambda	80
SARS-CoV-2 Beta	80
SARS-CoV-2 gamma	80
SARS-CoV-2 Delta plus	80
SARS-CoV-2 MuK.....	80
Bat CoV BANAL-52T.....T.....	80
Pangolin CoV GD-1T.....T.....	80
Bat CoV BANAL-236D.....T.....	80
SARS-CoV-2 Omicron BA.1D.....D.....L.P.F.....	80
SARS-CoV-2 Omicron BA.2D.....D.....F.P.FA.....	80
Bat CoV RaTG13D.....T.....T.....	80
Pangolin CoV GX-P5LI.....SK.....T.....	80
Bat CoV WIV-1	..A.SKEV.....T.P.....E.....T.....A.....S.....	80
Bat CoV RsSHC014	..A.SKEV.....T.P.....E.....I.....T.....A.....S.....	80
Bat CoV Rs2018B	..A.SKEV.....T.P.....E.....T.....A.....S.....	80
Bat CoV LYRa11	..S.SKEV.....T.P.....E.....T.....AI.....S.....	80
SARS-CoV-1	..V.SGDV.....K.P.....E..K.....TF.....A.....S.....	80
SARS-CoV-2	SFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFERDISTEIQAGST	160
SARS-CoV-2 Alpha	160
SARS-CoV-2 DeltaR.....K	160
SARS-CoV-2 LambdaR.....	160
SARS-CoV-2 BetaN.....	160
SARS-CoV-2 gammaT.....	160
SARS-CoV-2 Delta plusN.....R.....K	160
SARS-CoV-2 Mu	160
Bat CoV BANAL-52	..V.....	160
Pangolin CoV GD-1	..V.....R.....	160
Bat CoV BANAL-236	..V.....	160
SARS-CoV-2 Omicron BA.1N.....K.....S.....NK	160
SARS-CoV-2 Omicron BA.2N..S.....N.....K.....NK	160
Bat CoV RaTG13T.....KHI.A.E..F.....A.....K	160
Pangolin CoV GX-P5L	..VK.....V.....VKQ.ALT..G.....K.....	160
Bat CoV WIV-1	..VK..D.....V.....L...TR.I.ATQT...K..SL.HGK.R.....NVPFSPDGK	160
Bat CoV RsSHC014	..VK..D.....V.....L...L...T.SK..STS.....WV.R.K.N.Y..L.ND..SP.GQ	160
Bat CoV Rs2018B	..VK..D.....V.....M...L...TR.I.ATST...K..SL.HGK.R.....NVPFSPDGK	160
Bat CoV LYRa11	..VK..D.....V.....M...L...TR.I.ATSS..F..K..SL.HGK.R.....NVPFSPDGK	160
SARS-CoV-1	..VK..D.....V.....M...L...TR.I.ATST...K..YL.HGK.R.....NVPFSPDGK	160
SARS-CoV-2	PCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNF	223
SARS-CoV-2 AlphaY.....	223
SARS-CoV-2 Delta	223
SARS-CoV-2 LambdaS.....	223
SARS-CoV-2 BetaK.....Y.....	223
SARS-CoV-2 gammaK.....Y.....	223
SARS-CoV-2 Delta plus	223
SARS-CoV-2 MuK.....Y.....	223
Bat CoV BANAL-52H.....N.....I.....	223
Pangolin CoV GD-1H.....N.....Q.....	223
Bat CoV BANAL-236K...H.....N.....I.....	223
SARS-CoV-2 Omicron BA.1A.....R..S.R..Y..H.....	223
SARS-CoV-2 Omicron BA.2A.....R.....R..Y..H.....	223
Bat CoV RaTG13QT.L...Y..YR..Y..D...H.....N.....	223
Pangolin CoV GX-P5L	...QV.L...Y..ER..H..T..N..F.....NG.....L..T..D.....	223
Bat CoV WIV-1	..TP-PA...W..ND..YI..I.....N.....L..D.I..Q...	222
Bat CoV RsSHC014	S.SA-V.P...N..RP..FT.A..H.....N.....L..D.I..Q...	222
Bat CoV Rs2018B	..TP-PA...W..ND..FT..I.....N.....L..D.I..Q...	222
Bat CoV LYRa11	..TP-PA...W..ND..YT..I.....N.....L..D.IT.Q...	222
SARS-CoV-1	..TP-PAL...W..ND..YT.T.I.....N.....L..D.I..Q...	222

Figure S4. Amino acid sequence alignment of RBD variants used in sVNT assay, related to Figure 5.

Table S1. List of RBD mutants used in the alanine-scan assay, related to Figure 5.

	Mutation		Mutation
1	L335A	34	T449A
2	G339A	35	N450A
3	N354A	36	L452A
4	E324A	37	L455A
5	S359A	38	F456A
6	S366A	39	K458A
7	V367A	40	S459A
8	Y369A	41	N460A
9	A372S	42	K462A
10	S375A	43	P463A
11	S383A	44	S477A
12	P384A	45	T478A
13	T385A	46	E484A
14	K386A	47	F486A
15	N388A	48	F490A
16	D389A	49	Q493A
17	L390A	50	S494A
18	F392A	51	G496A
19	T393A	52	Q498A
20	N394A	53	T500A
21	D405A	54	N501A
22	R408A	55	G502A
23	Q414A	56	V503A
24	D427A	57	G504A
25	I434A	58	Y505A
26	A435S	59	S514A
27	N439A	60	L517A
28	N440A	61	L518A
29	L441A	62	H519A
30	S433A	63	A520S
31	K444A	64	P521A
32	V445A	65	A522A
33	G446A	66	P527A

Table S2. Cryo-EM data collection, refinement and validation statistics, related to Figure 4.

	Best Entire Spike-BP10 Complex (EMDB-28189)	RBD+BP10-Nb1+Nb2 (localized reconstruction) (EMDB-28190)
Data collection and processing		
Magnification	155K	155K
Voltage (kV)	300 keV	300 keV
Electron exposure (e-/Å ²)	1.25	1.25
Defocus range (µm)		
Pixel size (Å)	0.66	0.66
Symmetry imposed	D3	C1
Initial particle images (no.)	334,147	334,147
Final particle images (no.)	14,126	84,756 (symmetry expanded)
Map resolution (Å)	4.19	3.89
FSC threshold	0.143	0.143
Map resolution range (Å)	2.9-12.8	2.9-10.6