

The structure of the mammalian bornavirus polymerase complex

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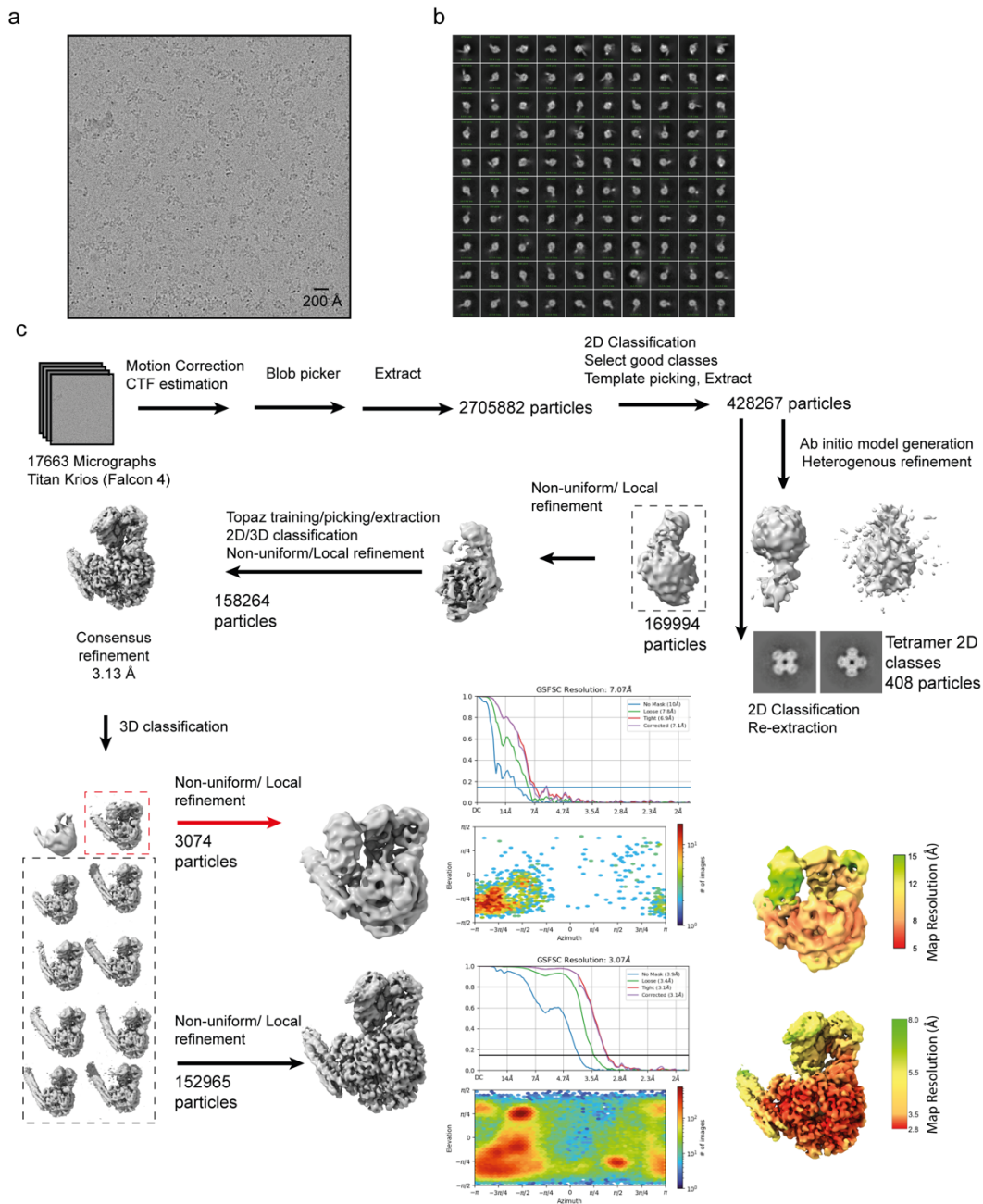
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Supplementary information. Table 1 and Figures 1-6.

	Sample 1 – RNA free Full-length EMD-51765 9H1G	Sample 2 - core EMD-51770 9H1Q	Sample 2 – Full- length EMD-51785 9H1Y
Data collection			
Microscope		Titan Krios G3i (OPIC)	
Voltage (kV)		300	
Detector		Falcon 4 - SelectrisX	
Magnification		130,000	
Movie/micrograph pixel size (Å)		0.932	
Dose rate (e-/px/sec)		6.2	
Movie exposure time (s)		7	
Total dose (e-/Å ²)		50	
Defocus range (um)		1.4 to 2.6	
EM data processing			
Number of movies/micrographs	17,665		14,249
Box size (px)		300	
Particle number (total)	428,267		588,492
Particle number (used in final map)	158,264	264,568	106,976
Symmetry		C1	
Map resolution (Å, FSC 0.143)	3.07	2.95	3.07
Local resolution range (Å)	2.8 - 30	2.8 - 30	2.8 - 30
Map sharpening B-factor (Å ²)	121	125	111
Model Building and Validation			
Initial model used	AlphaFold2	9H1G	9H1G
Model composition			
Non-hydrogen protein atoms	14581	10313	14036
Protein residues	1848	1302	1777
B factors (Å ²) - min/max/mean			
Protein	64.1/361/193	69.3/261/145	77.9/403/188
RMSD from ideal			
Bond length (Å)	0.004	0.004	0.004
Bond angles (°)	0.496	0.533	0.520
Validation			
Molprobity score	1.93	1.78	1.9
Clashscore	9.1	8.26	9.6
FSC (0.5) model- vs-map	3.6	3.3	3.7
CCmodel-vs-map (mask)	0.74	0.77	0.77
Ramachandran plot			
Favored (%)	93.1	95.3	94.3
Allowed (%)	6.9	4.7	5.7
Outliers (%)	0	0	0

23

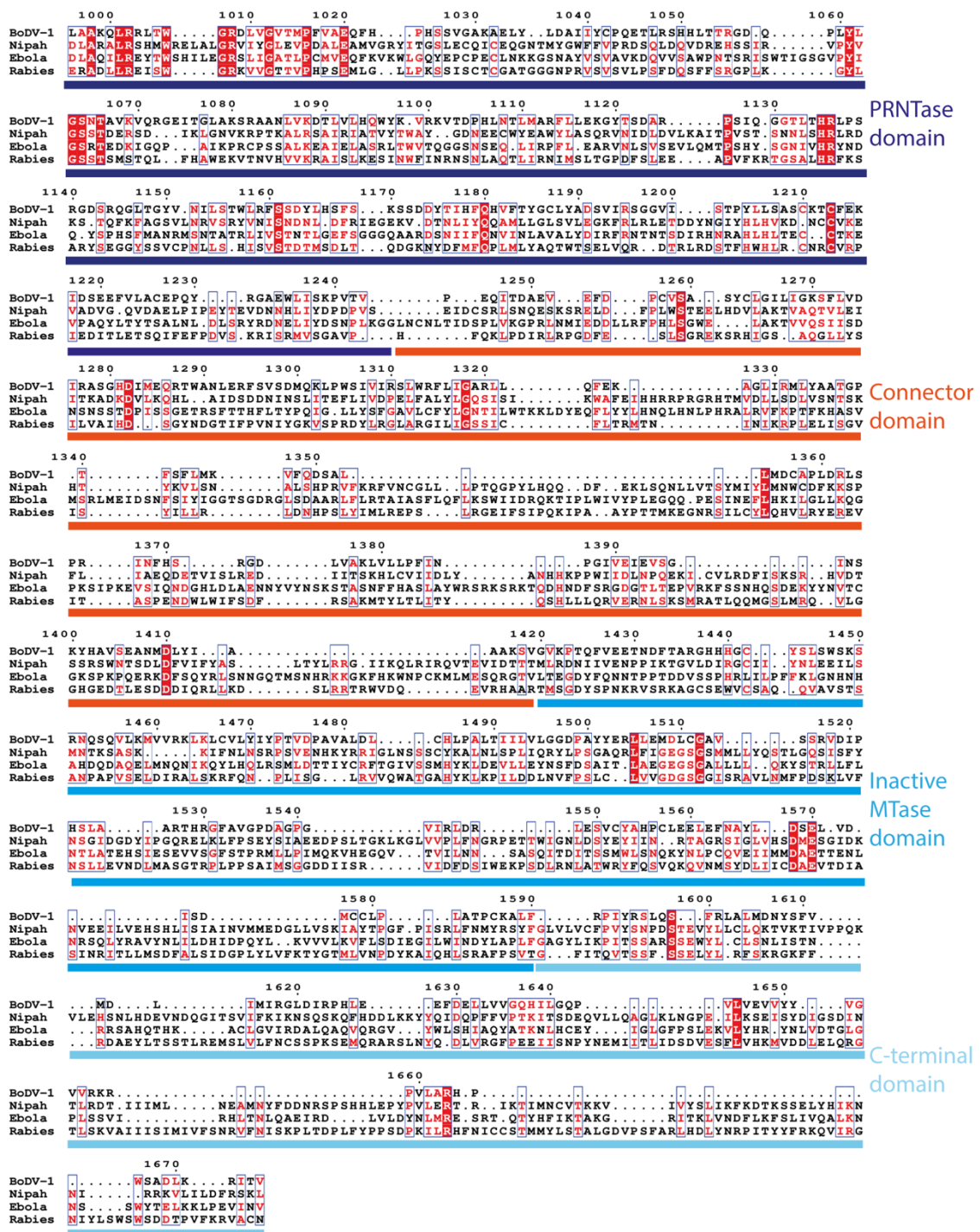
24 **Supplementary Table 1.** CryoEM collection and refinement parameters



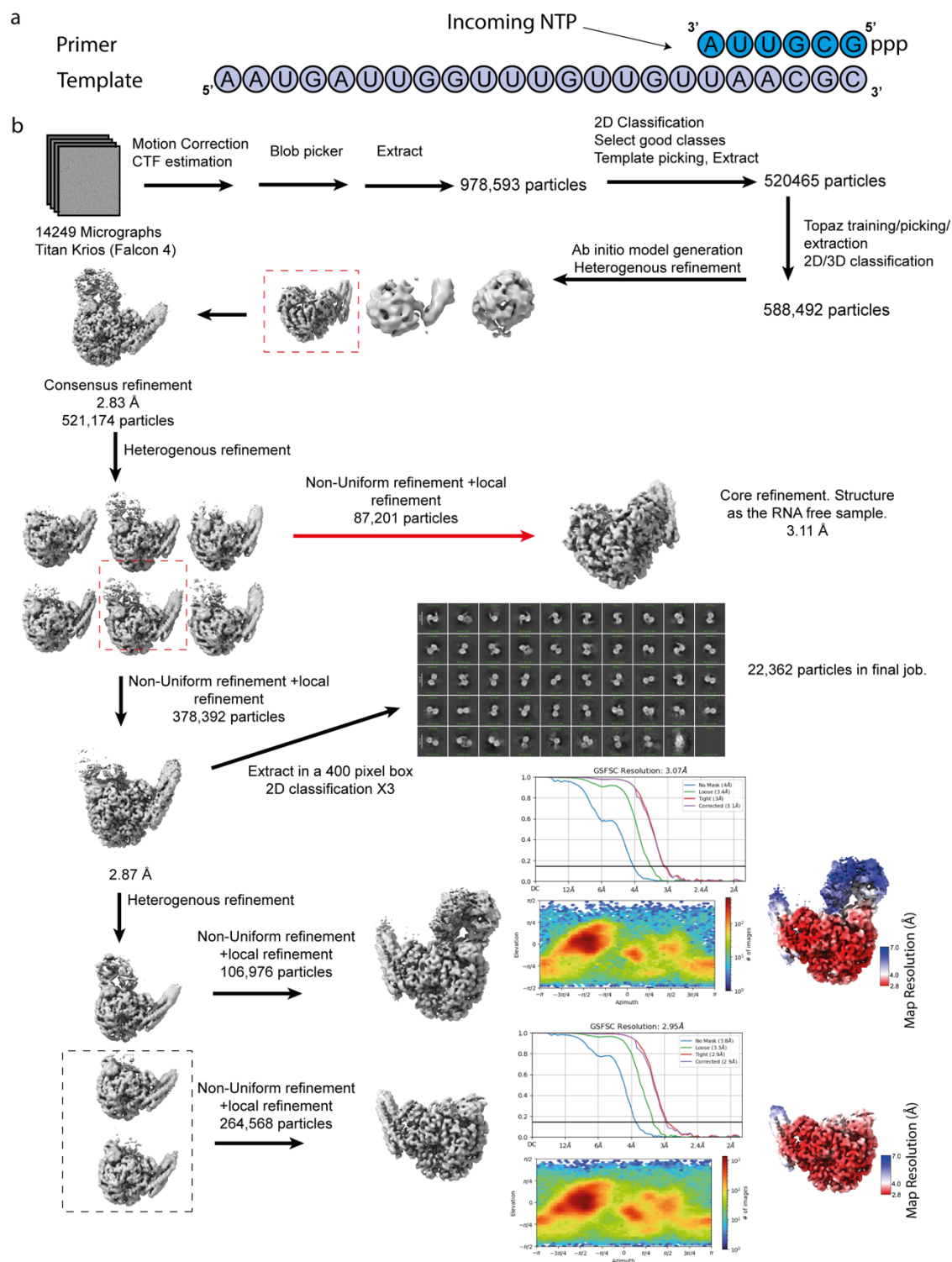
Supplementary figure 1. Sample 1 CryoEM processing workflow. a) representative electron micrograph image. b) 2D classification result showing the diversity of orientations present. c) CryoEM processing scheme.

RdRp domain

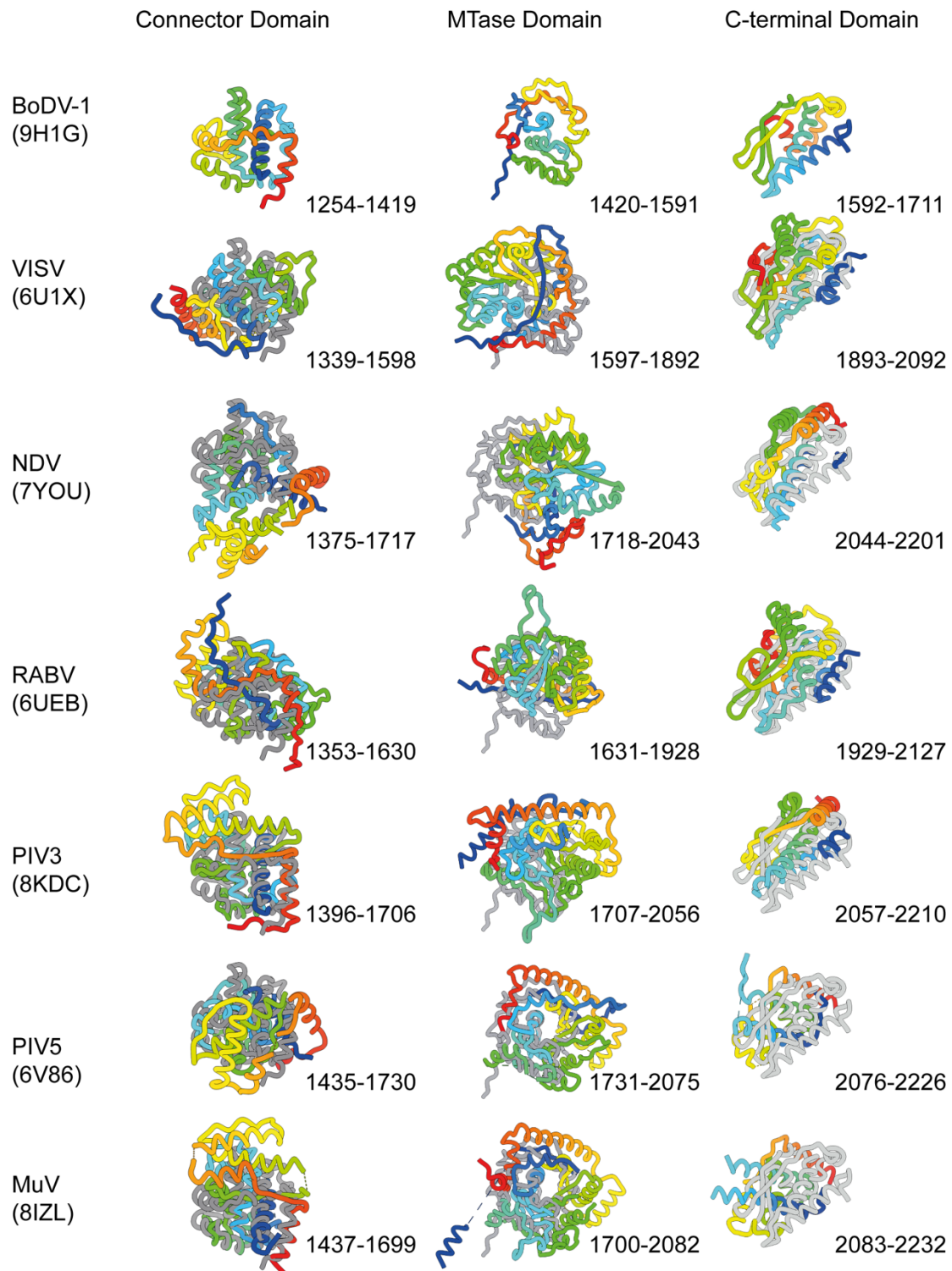
PRNTase domain



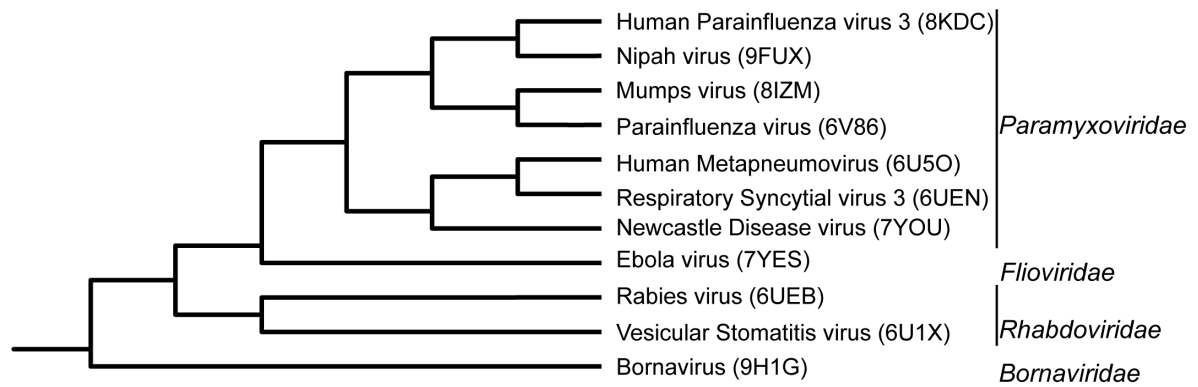
Supplementary figure 2. Sequence alignment of non-segmented negative sense RNA virus L-proteins. Sequence alignment for BoDV-1 (UniProt P0C799), Nipah virus (UniProt Q997F0), Ebola virus (UniProt Q8JPX5), and Rabies virus (UniProt Q8B6J5).



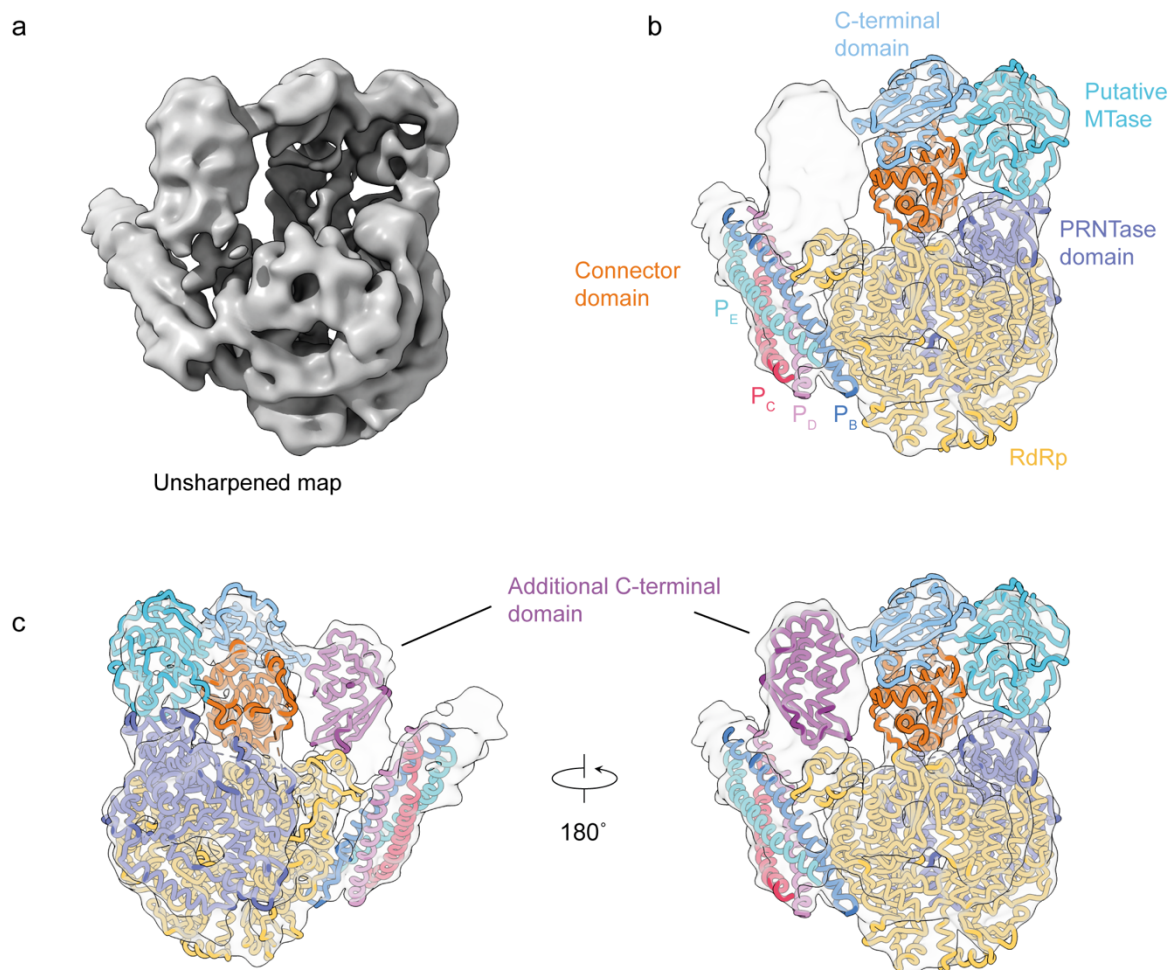
Supplementary figure 3. BoDV-1 sample 2 dataset CryoEM processing workflow. a) design and putative base pairing between the template and primer. b) cryoEM processing workflow.



Supplementary figure 4. Comparison of the C-terminal regions from a selection of nsNSV L-proteins. BoDV-1 domains are shown for comparison in grey and are conserved between all panels. Domains from other nsNSV polymerase are coloured N-to-C termini in rainbow colouring (blue to red). Values next to the images are the residue range for the nsNSV domain.



Supplementary figure 5. Structural phylogenetic analysis of experimentally determined *Mononegavirales* L protein models. PDB codes are shown in brackets.



Supplementary figure 6. Observation of an additional copy of a CTD. a) Reconstruction and b) model showing the extra map density. c) potential fit of the copy of the CTD (purple). The fit shown is for illustrative size and shape of the density, but it cannot be positioned unambiguously given the quality of electron density.