

Supporting Information

Cryo-EM of the nucleosome core particle bound to Ran-RCC1 reveals a dynamic complex

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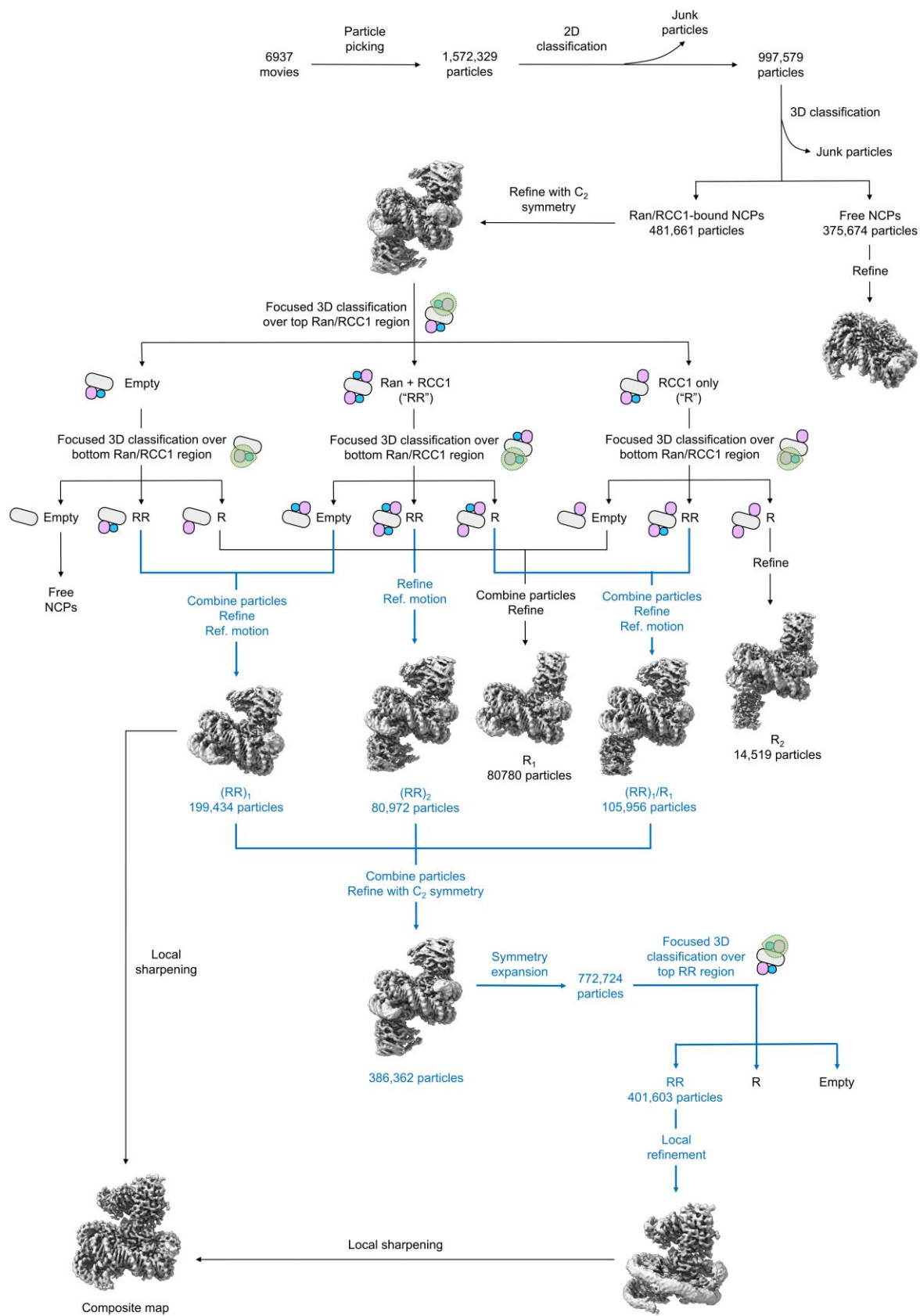


Figure S1. Cryo-EM data processing workflow. Steps in blue highlight particle classes that contributed to the final reconstruction of the RCC1-Ran region.

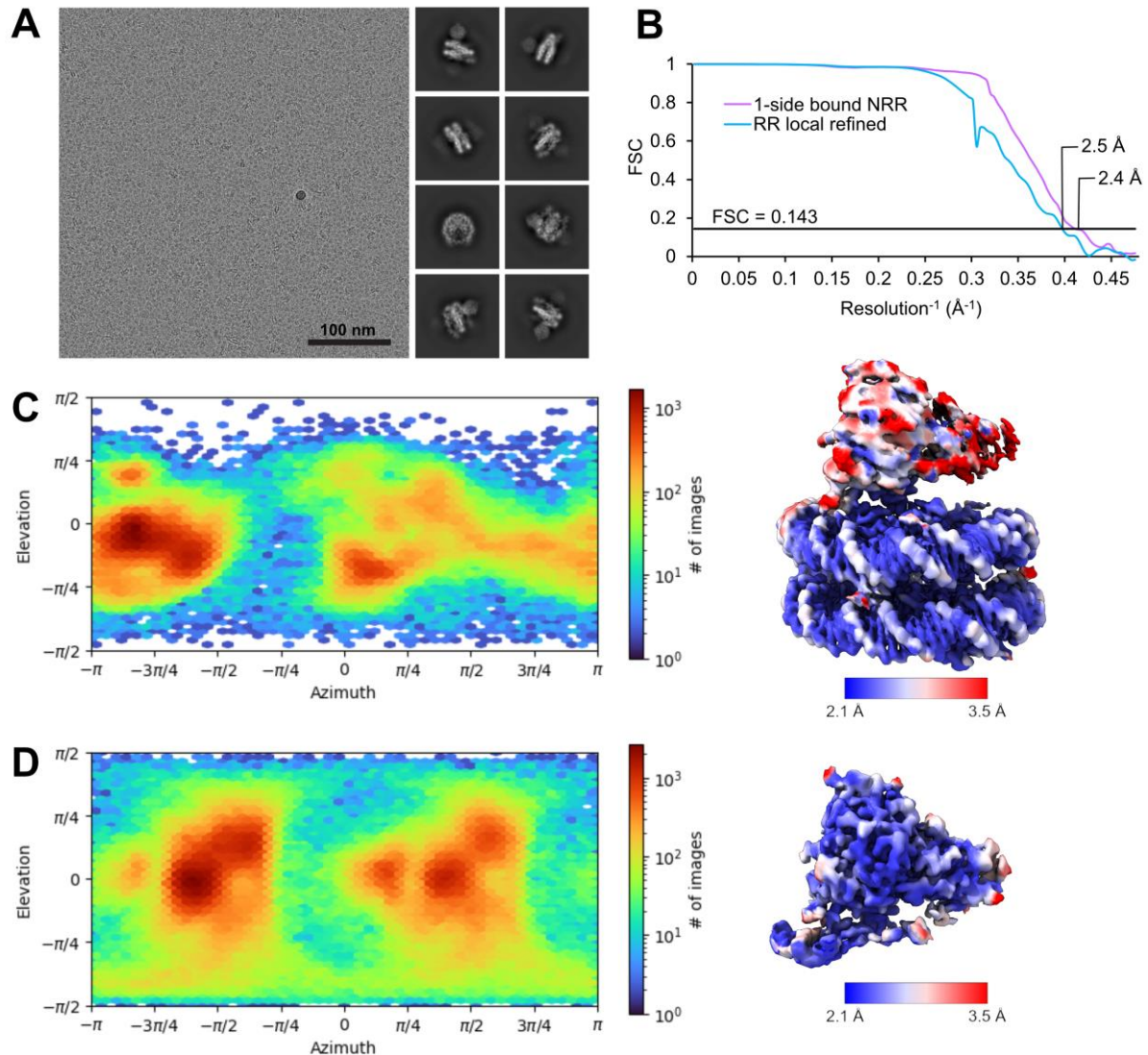


Figure S2. Cryo-EM of the NCP-RCC1-Ran complex. **A)** Representative micrograph and 2D class averages. **B)** Fourier shell correlation (FSC) curves for the 1-side bound NCP-RCC1-Ran map and the locally refined RCC1-Ran map following gold-standard refinement and corrected for the effects of masking. **C and D)** Particle orientation distribution plot (left) and local resolution estimation (right, 180°-rotated relative to Figure 2C) for the 1-side bound NCP-RCC1-Ran (NRR) map (**C**) and the locally refined RCC1-Ran (RR) map (**D**).



J259_component0.m
p4

Movie S1. 3DVA component 0 for the RCC1-Ran region of the NCP-RCC1-Ran complex.



J259_component1.m
p4

Movie S2. 3DVA component 1 for the RCC1-Ran region of the NCP-RCC1-Ran complex.



J259_component2.m
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Movie S3. 3DVA component 2 for the RCC1-Ran region of the NCP-RCC1-Ran complex.



J265_component0_to
p.mp4

Movie S4. Top view of 3DVA component 0 for the RCC1 region of the NCP-RCC1-Ran complex.



J265_component0_b
ack.mp4

Movie S5. Back view of 3DVA component 0 for the RCC1 region of the NCP-RCC1-Ran complex.



J265_component1_b
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Movie S6. 3DVA component 1 for the RCC1 region of the NCP-RCC1-Ran complex.

Table S1. Cryo-EM and atomic model building statistics

	1-side-bound NRR complex	Focus-refined RR region	Composite map
Data collection and processing			
Magnification	75,000		
Voltage (kV)	300		
Electron exposure (e ⁻ /Å ²)	42		
Defocus range (μm)	1.0-2.0		
Raw pixel size (Å)	1.03		
Symmetry imposed	C1		
Number of particle images	199,434	401,603	
Map resolution (Å)	2.4	2.5	
FSC threshold	0.143	0.143	
Map resolution range (Å)	2.4-8.5	2.5-8.5	
Map refinement			
Initial map used	Ab-initio reconstruction	Ab-initio reconstruction	
Map sharpening	LocalDeblur	LocalDeblur	
Model composition			
Nonhydrogen atoms	16395		
Protein residues	1332		
Nucleotides	291		
RMSDs			
Bond lengths (Å)	0.006		
Bond angles (°)	0.635		
Validation			
MolProbity score	1.44		
Clashscore	5.13		
Rotamer outliers (%)	1.27		
Ramachandran plot			
Favored (%)	97.55		
Allowed (%)	2.22		
Disallowed (%)	0.23		