

Supplementary Material for

Cryo-EM structure of the naked mole-rat ribosome reveals a stabilized split 28S rRNA

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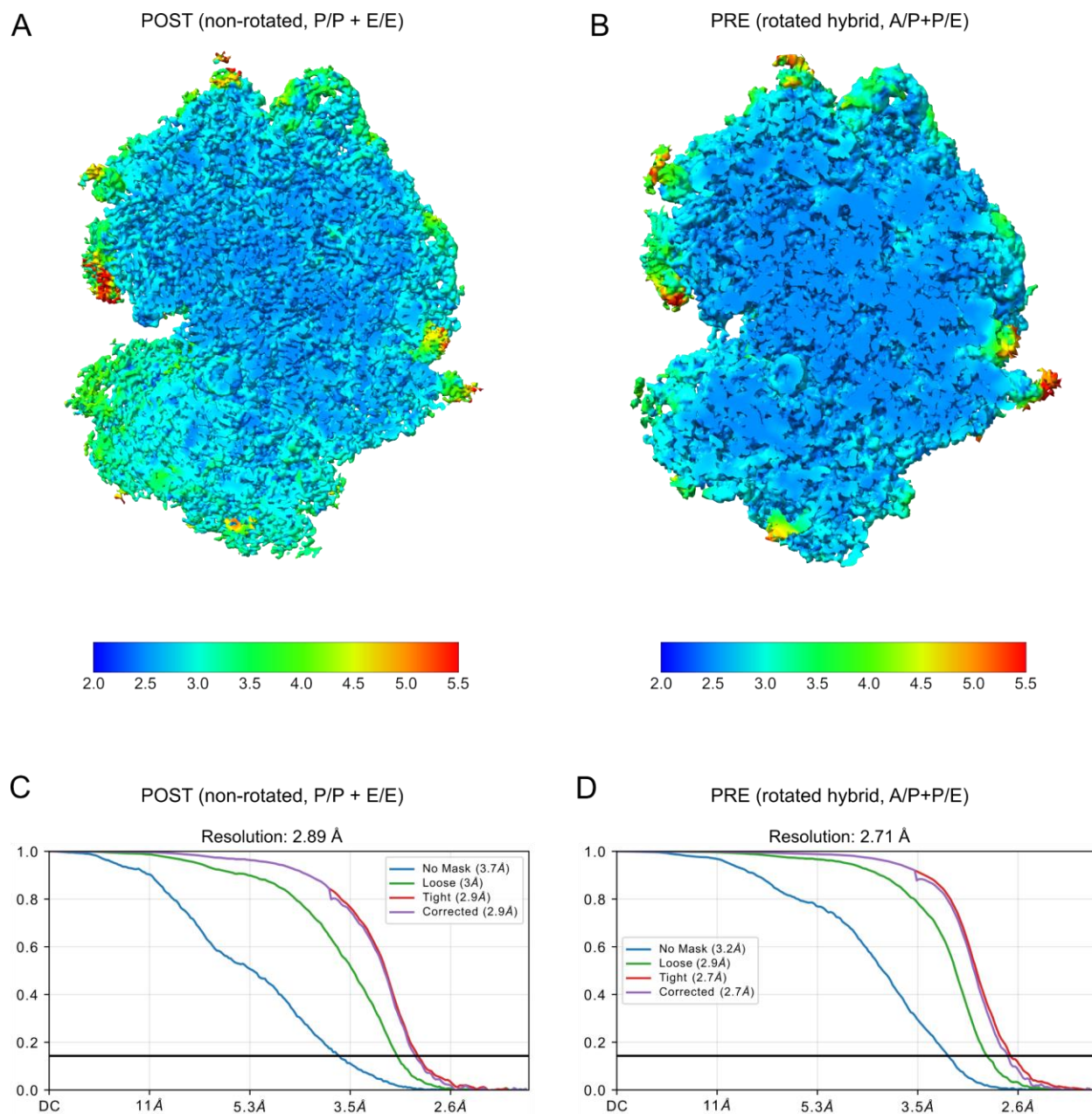
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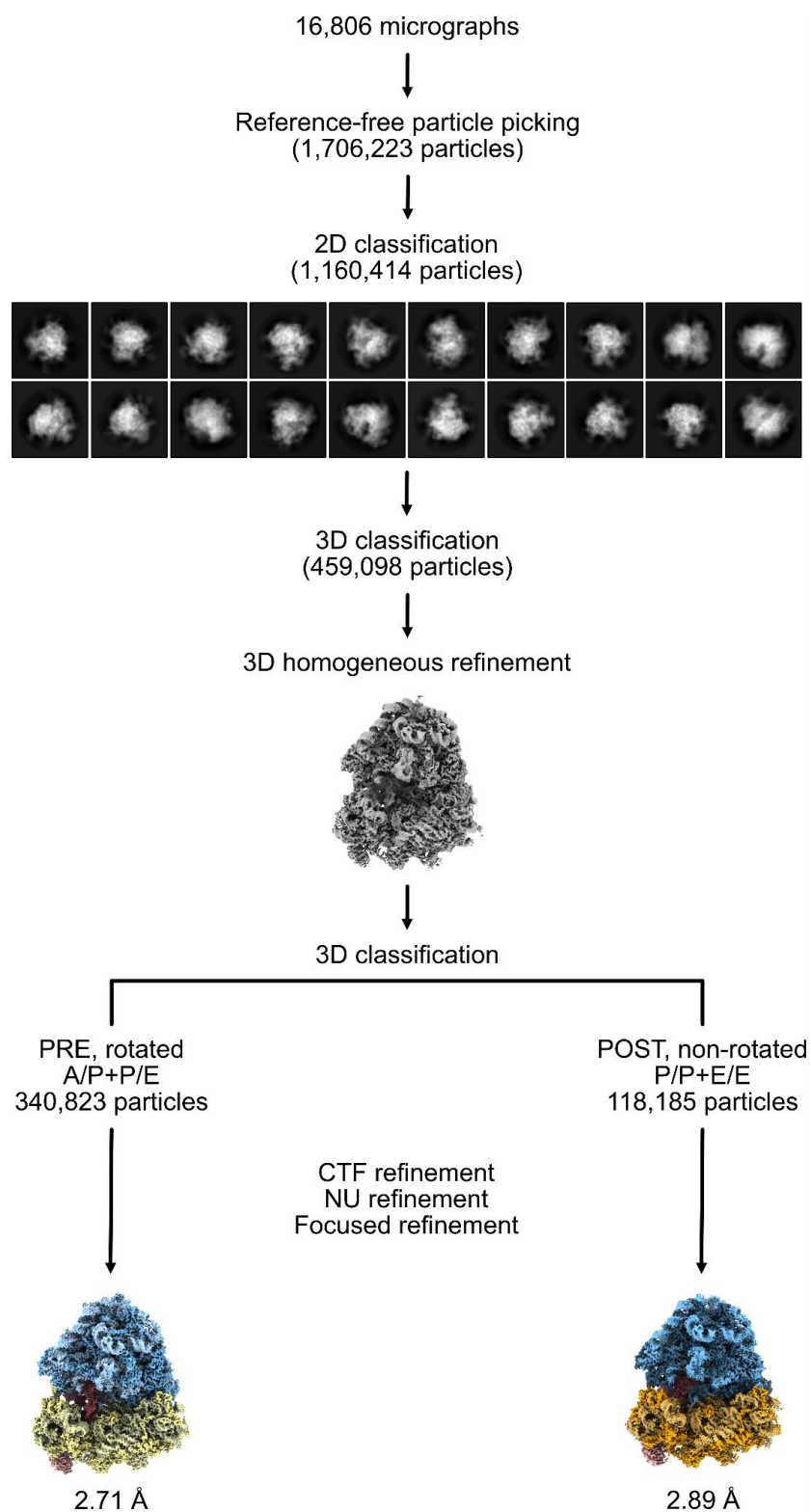
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Figures S1, S2

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Supplementary Figure S1. Cutaway view through the cryo-EM density maps of the (A) POST and (B) PRE states. The maps are colored by the local resolution as calculated in cryoSPARC. GSFSC curves for the (C) POST and (D) PRE state structures. The resolution values are shown for the cutoff value of 0.143.



Supplementary Figure S2. Cryo-EM data processing workflow.

31 **Table S1: Cryo-EM Data Collection, Refinement, and Validation Statistics**

	NMR 80S (POST)	NMR 80S (PRE)
Data Collection and Processing		
Microscope	Titan Krios G3i	Titan Krios G3i
Detector	Gatan K3 + Bioquantum GIF	Gatan K3+ Bioquantum GIF
Voltage (kV)	300	300
Electron dose (e ⁻ /Å ²)	60.04	60.04
Defocus range (μm)	-1.0 to -3.0	-1.0 to -3.0
Pixel size (Å)	0.83	0.83
Initial particles	1706223	1706223
Final particles	118185	340823
Map resolution (Å)	2.9	2.7
Map sharpening B-factor (Å ²)	-68.79	-82.94
Model Refinement		
Initial model used (PDB ID)	7CPU	7CPU
Model components	72 proteins, 4 rRNAs	72 proteins, 4 rRNAs
Map-model FSC (FSC=0.5)	3.05	2.83
Model Validation (MolProbity)		
MolProbity score	2.53	1.79
Clashscore	12.97	4.72
Ramachandran favored (%)	88.74	90.20
Ramachandran allowed (%)	8.98	8.05
Ramachandran outliers (%)	2.29	1.75
Rotamer outliers (%)	2.71	0.96
RMSD bonds (Å)	0.008	0.003
RMSD angles (°)	1.070	0.777

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