

xSUPPLEMENTARY INFORMATION

Visualizing the translation landscape in human cells at high resolution

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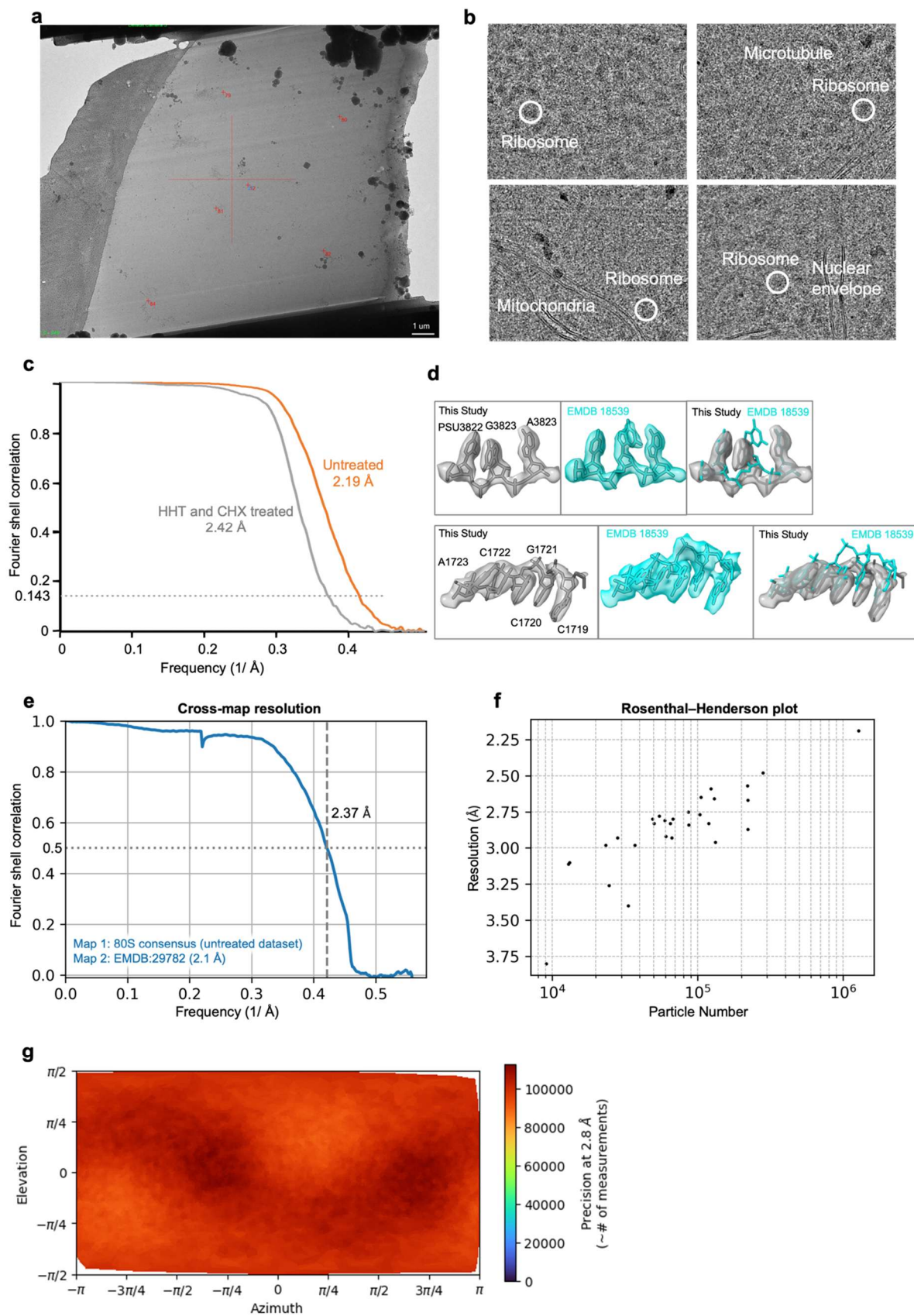
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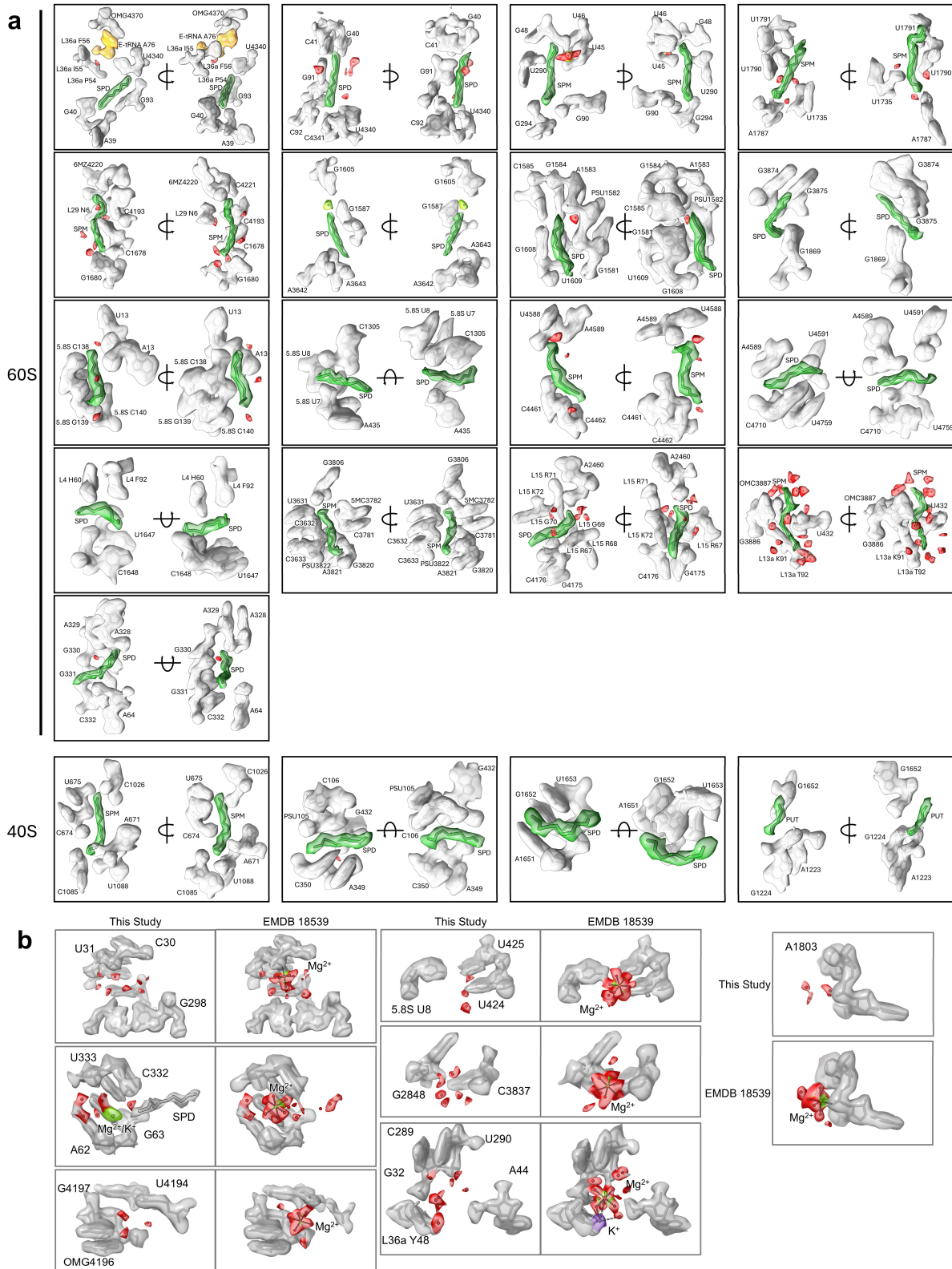
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Supplementary Fig 1: *In situ* single-particle cryo-EM results. **a** A representative transmission electron micrograph of FIB-milled lamellae. **b** Typical micrographs collected by *in situ* single-particle cryo-EM. Prominent features such as ribosomes, microtubules, mitochondria, and nuclear envelope can be visibly identified. **c** The Fourier shell correlation (FSC) curves of the consensus 80S reconstruction with data from untreated HEK293A cells and cells treated with HHT and CHX. **d** Example differences of rRNA nucleotides between *in situ* and *in vitro* structures. **e** Cross-map resolution between our consensus map and EMD-29782. **f** Rosenthal-Henderson plot of resolution vs. particle numbers. **g** Angular distribution of particles contributing to the final 3D reconstruction, displayed as a hemisphere projection.



Supplementary Fig 2. Polyamine and ion environment differences comparison with *in vitro* studies. a Native polyamines observed *in situ* in human HEK293A cells. **b** Ion environment differences between *in situ* and *in vitro* structures.

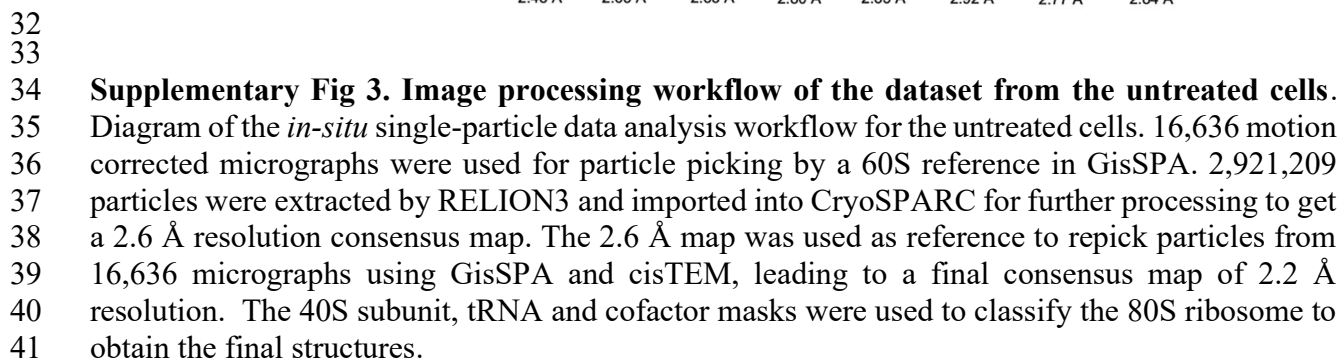
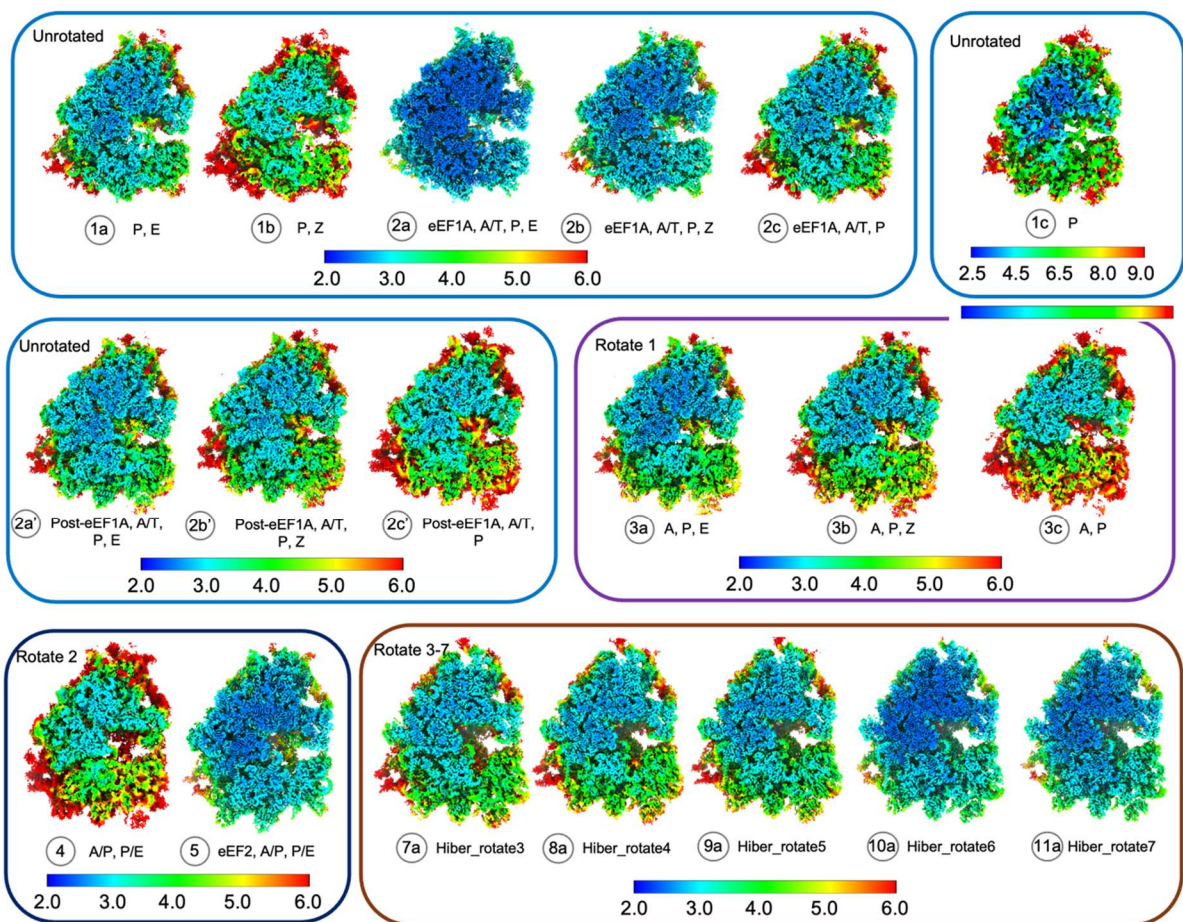
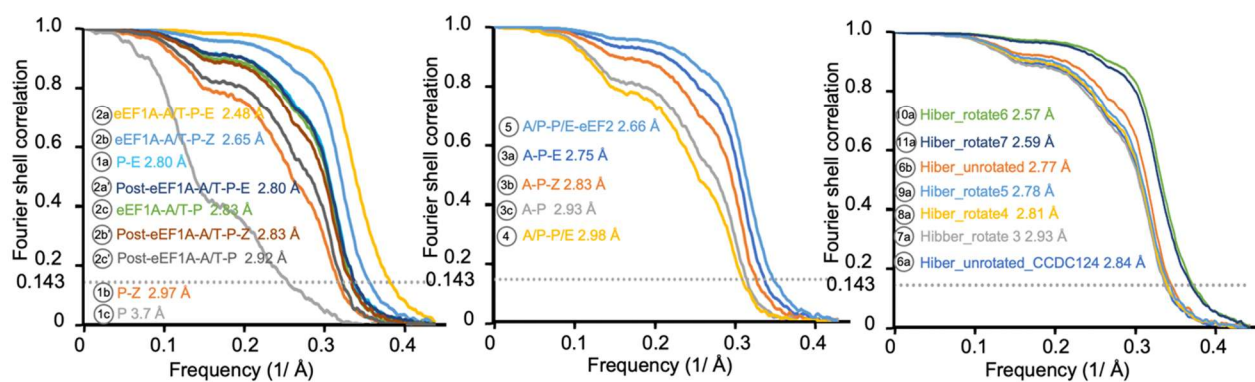


Diagram of the *in-situ* single-particle data analysis workflow for the untreated cells. 16,636 motion corrected micrographs were used for particle picking by a 60S reference in GisSPA. 2,921,209 particles were extracted by RELION3 and imported into CryoSPARC for further processing to get a 2.6 Å resolution consensus map. The 2.6 Å map was used as reference to repick particles from 16,636 micrographs using GisSPA and cisTEM, leading to a final consensus map of 2.2 Å resolution. The 40S subunit, tRNA and cofactor masks were used to classify the 80S ribosome to obtain the final structures.

A Untreated

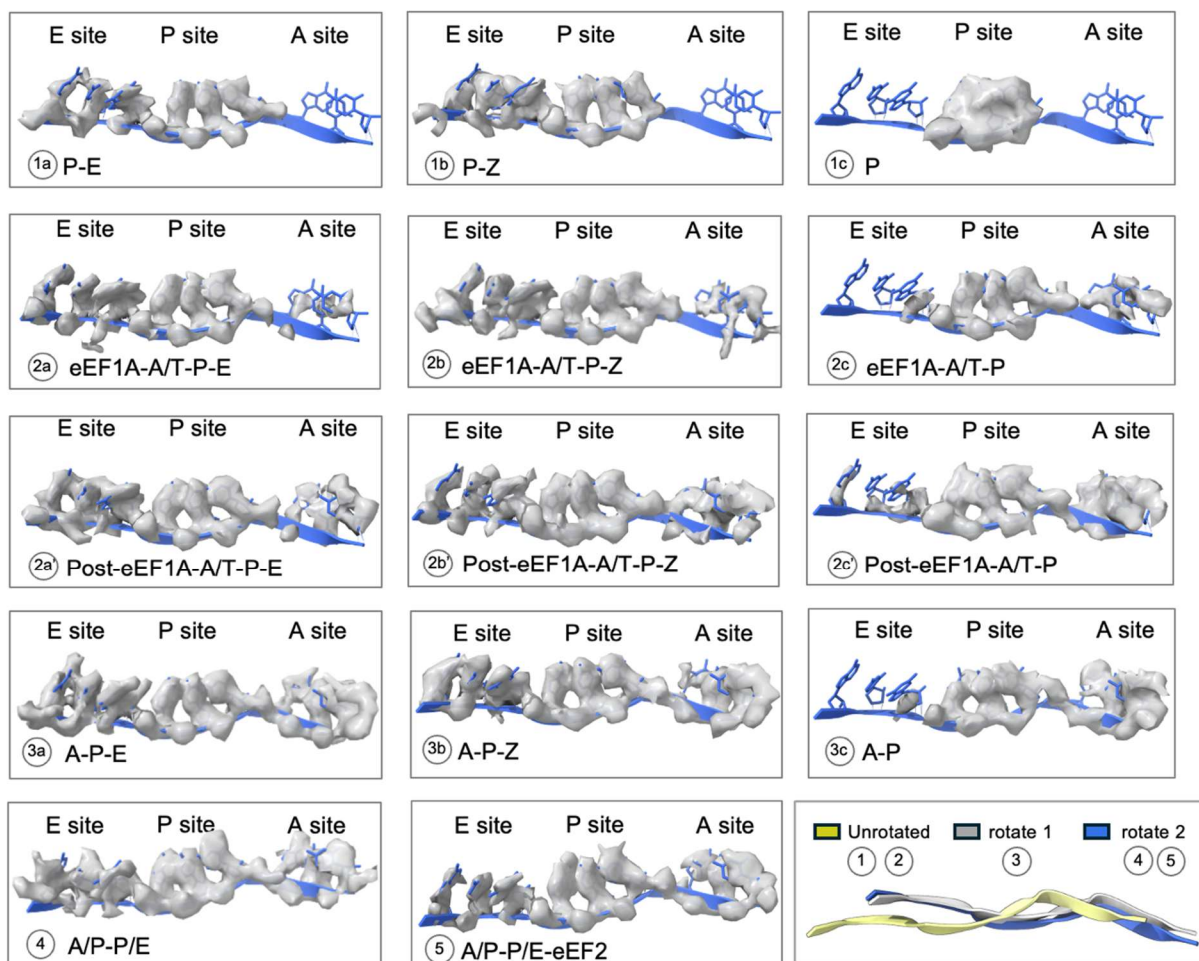


B Untreated

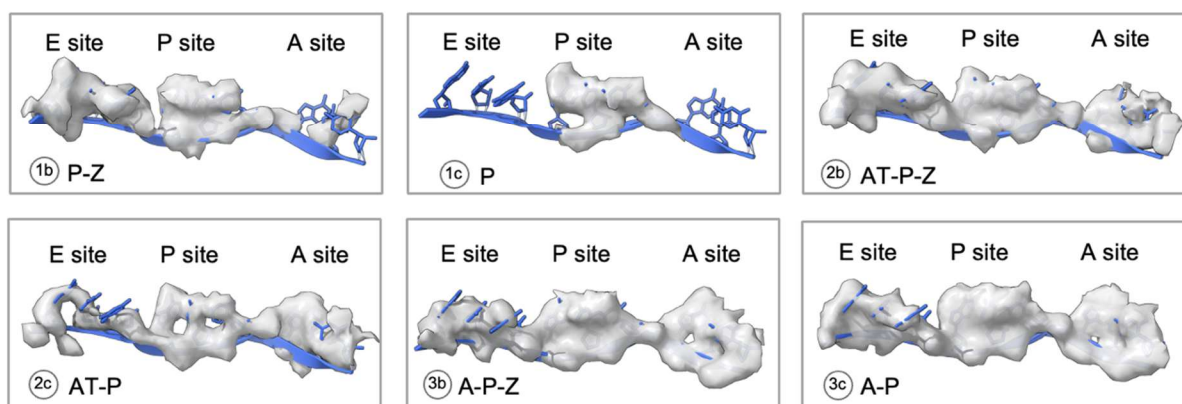


Supplementary Fig 4. Local resolution maps and FSC of ribosome states. a Local resolution maps of ribosome states in the untreated cells. **b** FSC curves of the untreated ribosome states using the 0.143 criterion.

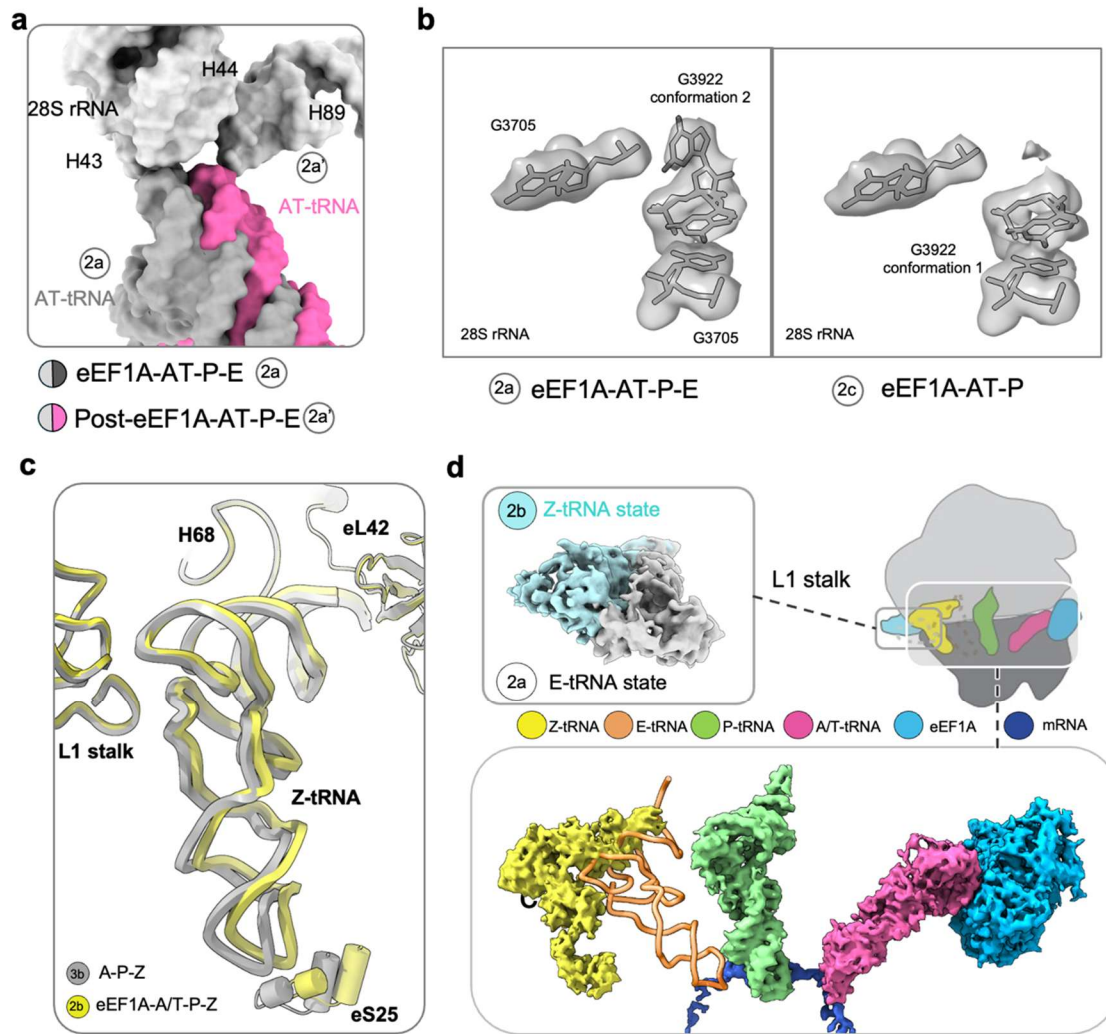
a Untreated cells



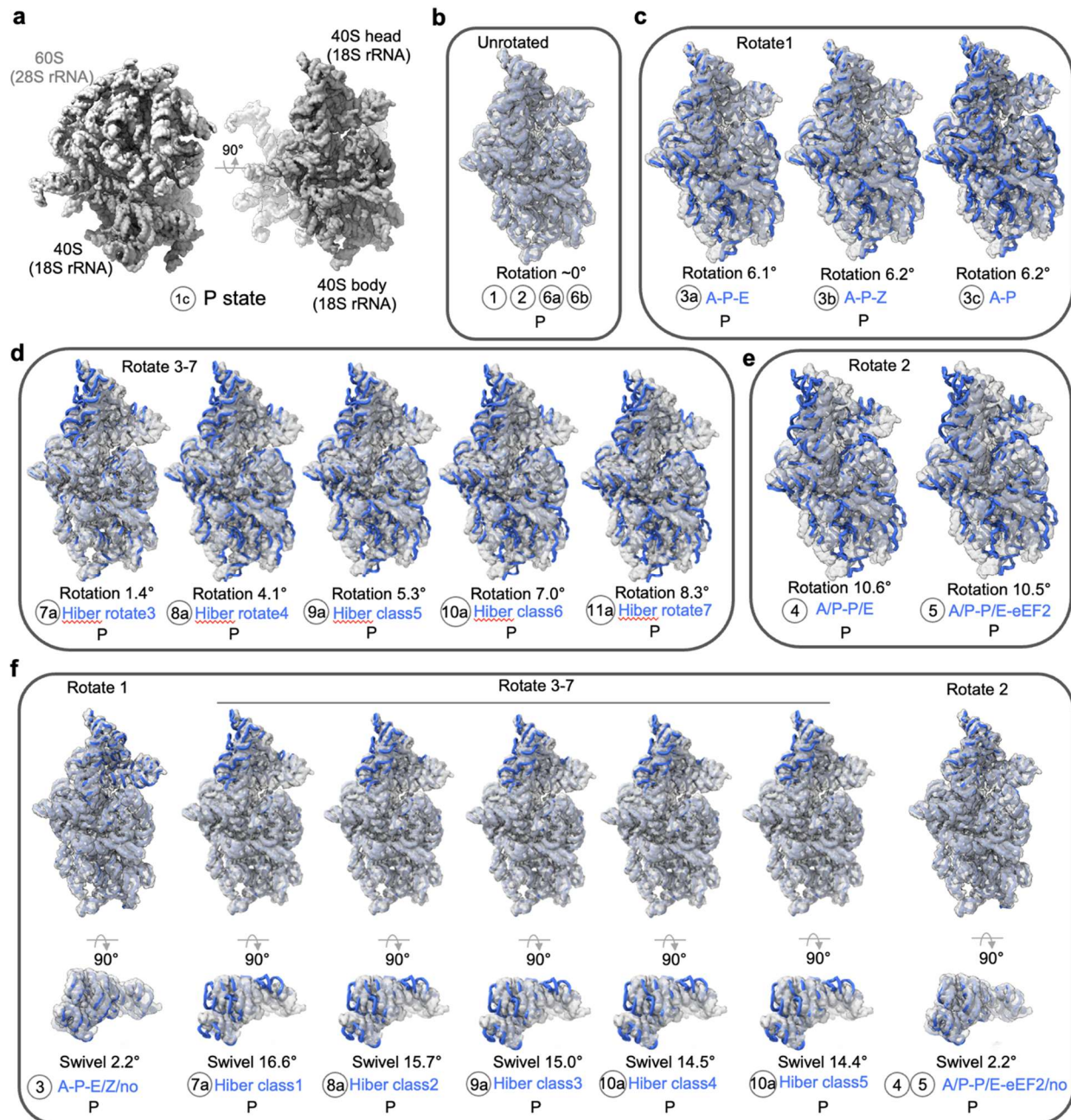
b HHT + CHX treated cells



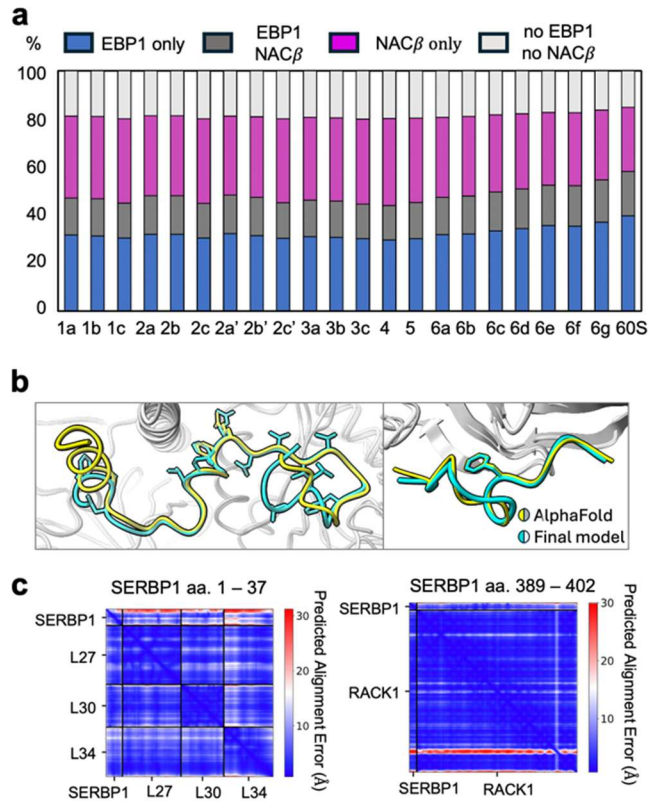
Supplementary Fig 5. mRNA densities at the A, P, and E sites in different ribosome states. a mRNA densities (white density) at A, P, E site in different ribosome states from the untreated cells. The last panel shows the relative positions of mRNA in different rotation states. Certain mRNA regions, especially those not base-paired with tRNAs, exhibit reduced resolution due to increased conformational flexibility. For example, in the P-E state, the mRNA density at the A site is notably weaker. **b** mRNA densities at A, P, and E sites in different ribosome states from the HHT+CHX-treated cells. The same contour level is used for all panels.



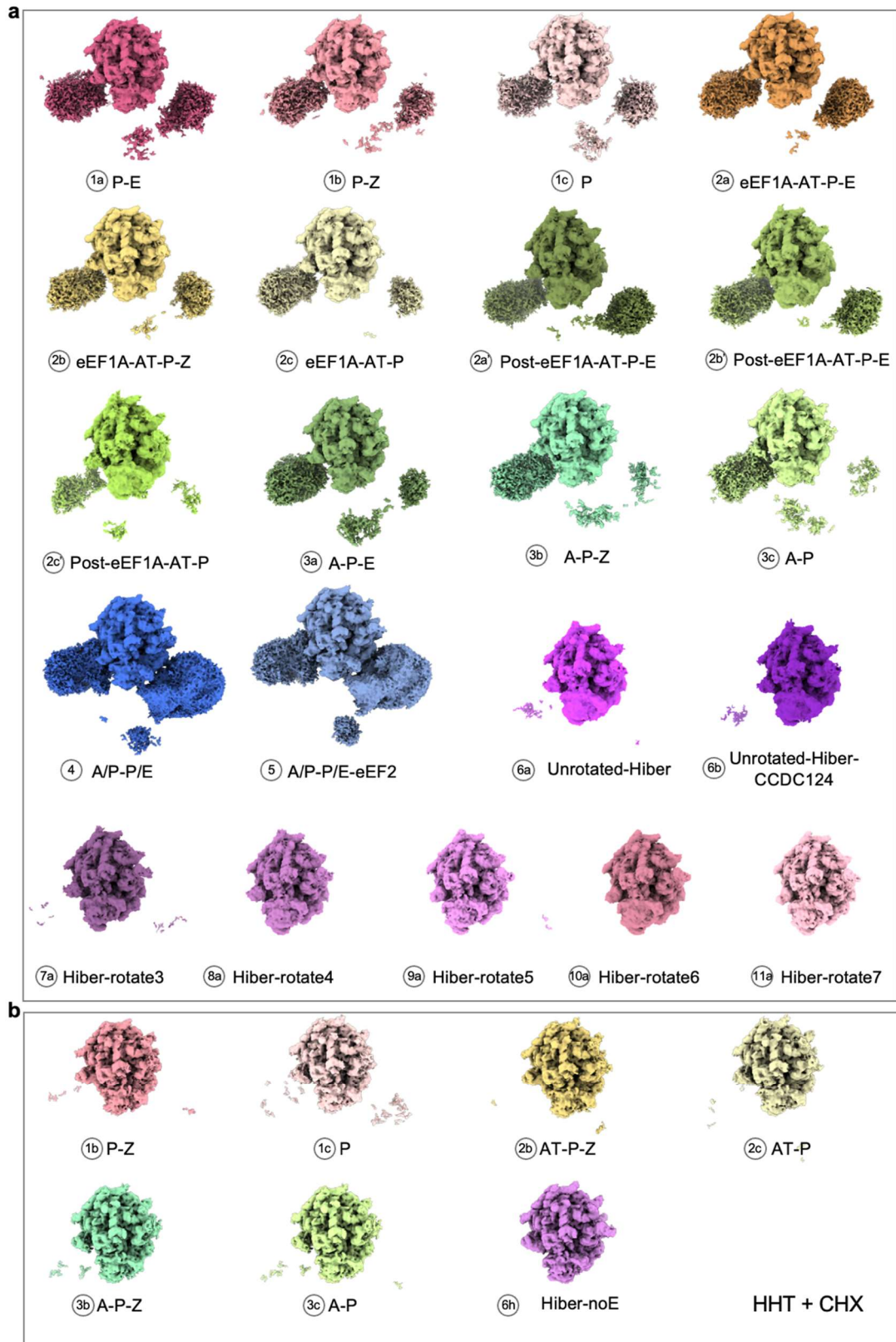
Supplementary Fig 6. The AT-tRNA and Z-tRNA in active translation ribosomes. **a** AT-tRNA movement between the codon-sampling (2a) and the post GTP hydrolysis (2a') states shows different interactions of tRNA with the 60S ribosomal subunit. **b** Alternative conformations of 28S rRNA G3922 compared with the *in vitro* study. **c** The conformational differences of 28S rRNA G3922 in different states as measure by the occupancy (integrated cryo-EM map value) ratios. **d** The Z-tRNA is held by the L1 stalk, eS25, H68, and eL42. The anticodon loop of the Z-tRNA and eS25 are displaced by ~ 3.8 Å in the A-P-Z (3b) state (grey) relative to its position in the eEF1-A/T-P-Z (2b) state (yellow). **e** A comparison between the eEF1-A/T-P-Z state (2b) and the eEF1-A/T-P-E state (2a). Top inset: cryo-EM maps of the L1 stalk (surfaces) showing it moves towards the solvent in state 2b (cyan) relative to its position in state 2a (gray). Bottom inset: Unlike the E-tRNA (orange ribbon), the Z-tRNA (yellow density) does not contact the mRNA (dark blue density). The cryo-EM map of tRNAs, eEF1A, and the mRNA in the eEF1-A/T-P-Z (2b) state is in surface representation. An E-tRNA model (orange ribbon) is shown for comparison.



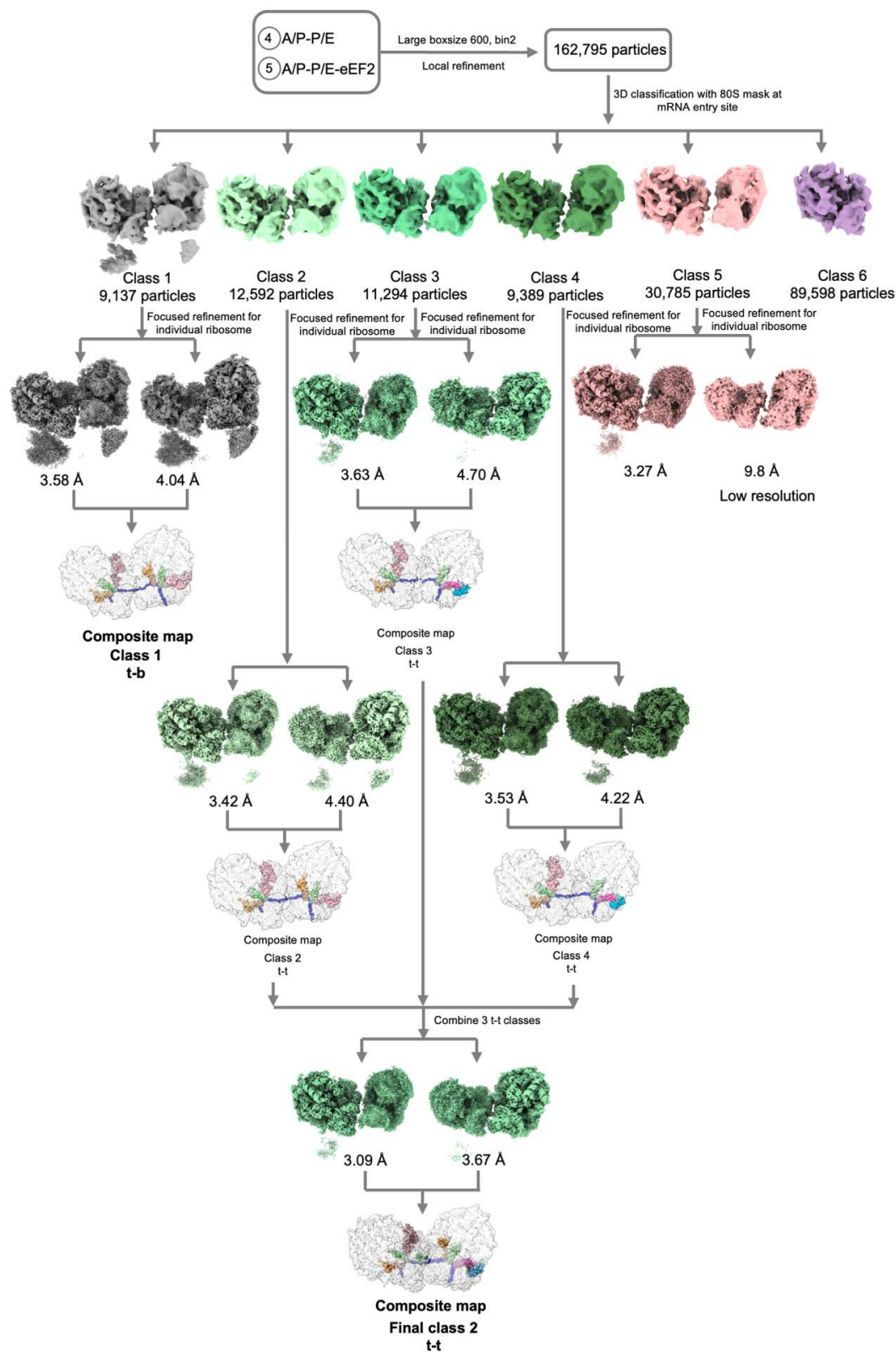
Supplementary Fig 7. The 40S subunit body domain rotation and head domain swivel for the untreated ribosome states. **a** The model (28S rRNA and 16S rRNA, surface representation) of the unrotated P state (1c) containing the 60S subunit, 40S subunit body and head domains. **b-e** Comparisons of 40S subunit body domain rotation of different states (ribbon) with unrotated P state (transparent density). **f** Comparisons of 40S subunit head domain swivel of different states (ribbon) with unrotated P state (transparent density).



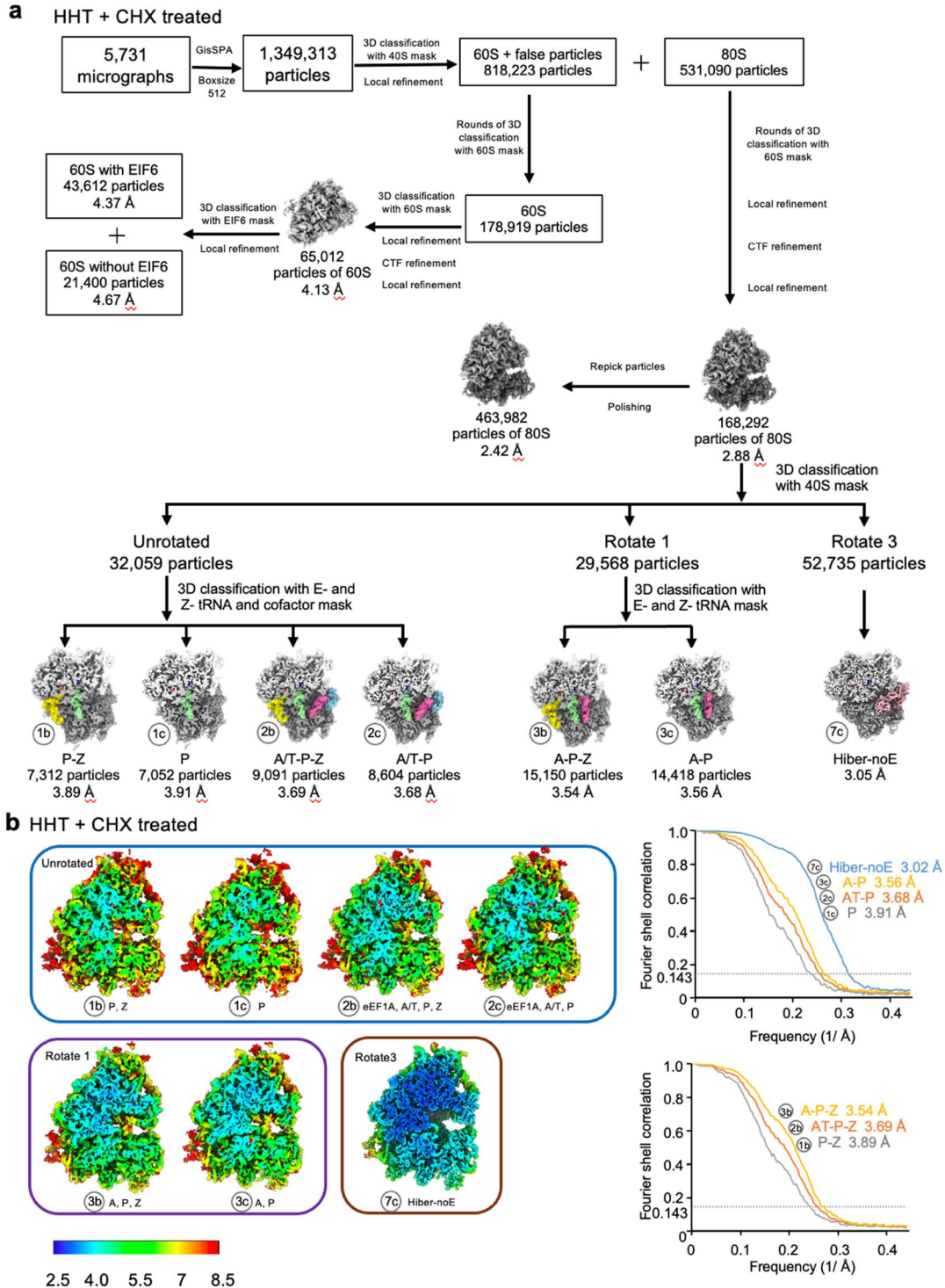
Supplementary Fig 8. Ribosome binding factors in cells. **a** The EBP1 and NAC β occupancies of different 80S conformations and free 60S subunits in the untreated cells. **b** The AlphaFold predicted model aligned to manually built model based on the experimentally determined cryo-EM map. **c** The predicted alignment error (pAE) plots of the predicted interactions of SERBP1 N- or C-terminal regions with surrounding ribosomal regions.



Supplementary Fig 9. Cryo-EM maps of *in situ* polysomes of different ribosome states. a Densities of the polysome of different states in untreated cells. The particles of different states were re-extracted using a large box size (bin4, 240 pixels) and refined. The maps are displayed using the same threshold. **b** Same as in **a**, for HHT+CHX-treated cells.

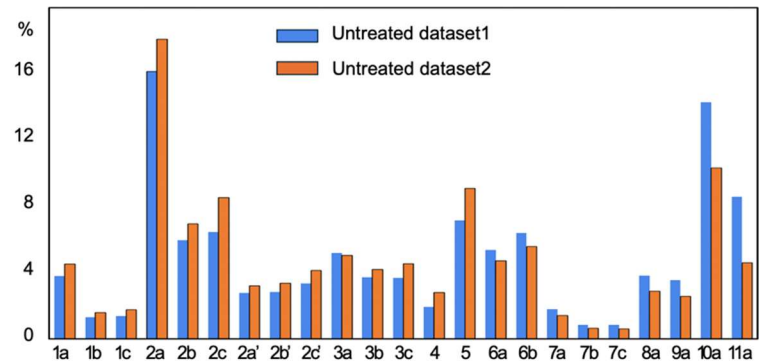


Supplementary Fig 10. Image processing workflow of the di-ribosome reconstructions.



Supplementary Fig 11. Image processing workflow of the dataset of the HHT+CHX-treated cells. **a** Diagram of the *in-situ* single-particle data analysis workflow. 5,726 motion corrected micrographs were used for particle picking by a 60S reference in GisSPA. 1,349,313 particles were extracted by RELION3 and imported into CryoSPARC for further processing. 40S, tRNA and cofactor masks were used to classify the 80S ribosome to obtain the final structures. The refined 80S density was used as reference to repick the particles and resulted in a 2.4 Å resolution consensus map with 463,982 particles after polishing. **b** Local resolution maps of ribosome states in the HHT+CHX-treated cells. FSC curves using the 0.143 criterion.

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Supplementary Fig 12. Translation state distributions of different ribosome states in the two untreated datasets. The translation state distributions were similar between the two datasets, but the first dataset contained more hibernating ribosomes, possibly because the cells were incubated with a nutrient-free live cell imaging buffer prior to freezing and were thus in a stage of starvation. Only dataset2 was used for analyzing the translation states distribution.

Supplementary Table 1 | Cryo-EM data collection, refinement and validation statistics of 80S and free 60S consensus structures for untreated and treated datasets.

	Untreated 80S composite EMD-71477 PDB-9PBE 80S consensus: EMD-71440 Focused on 60S: EMD-71441 Focused on 40S body: EMD-71442 Focused on 40D head: EMD-71443	Untreated 80S with EBP1 consensus EMD-71435 PDB-9PA7	Untreated 60S EMD-71413 PDB-9P9J	Untreated 60S with EIF6 EMD-71414 PDB-9P9K	HHT and CHX treated 80S consensus EMD-71694 PDB-9PKD
Data collection and processing					
Magnification	81,000	81,000	81,000	81,000	81,000
Voltage (kV)	300	300	300	300	300
Electron exposure (e-/Å ²)	50	50	50	50	50
Defocus range (µm)	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5
Pixel size (Å)	1.068	1.068	1.068	1.068	1.068
Symmetry	C1	C1	C1	C1	C1
Initial particle images (no.)	4,836,109	2,921,209	4,836,109	2,537,557	1,349,313
Final particle images (no.)	1,272,627	221,164	248,791	132,487	463,982
Map resolution (Å) FSC threshold 0.143	2.19	2.67	2.51	2.96	2.42
Map Sharpening B factor (Å ²)	-65	-39	-37	-34	-60
Model refinement					
Initial model (PDB code)	8QOI, 6Z6M, 6ZM7, 8A3D				
Model resolution (Å) FSC threshold 0.5	2.3	2.9	2.7	3.1	2.7
Model vs. map correlation Coefficient (cc_mask)	0.92	0.86	0.92	0.89	0.91
Model composition					
Non-hydrogen atoms	223,498	231,161	139,317	141,030	216,862
Protein residues	11,890	12,671	6,983	6,983	11,840
Nucleotide residues	5,745	5,821	3,931	3,931	5,671
Ligands	328	328	213	213	244
B factors (Å ²) (mean)					
Protein	112	160	57	108	108
RNA	107	153	68	129	129
Ligands	72	100	39	87	87
R.m.s. deviations					
Bond length (Å)	0.006	0.007	0.005	0.005	0.005
Bond angle (°)	0.7	0.7	0.7	0.7	0.6
Validation					
MolProbity score	1.49	1.55	1.34	1.43	1.50
Clash score	4.38	3.95	3.64	4.24	4.82
Poor rotamers	0	0.03	0	0.01	0
Ramachandran plot					
Favored (%)	96.02	96.03	96.91	96.58	96.28
Allowed (%)	3.97	3.95	3.09	3.41	3.71
Disallowed (%)	0.01	0.02	0	0.01	0.01

Supplementary Table 2 | Cryo-EM data collection, refinement and validation statistics of 80S states for untreated dataset (part1).

	1a	1b	1c	2a	2b	2c	2a'
	EMD-71331 PDB-9P72	EMD-71329 PDB-9P6Z	EMD-71696 PDB-9PKG	EMD-71371 PDB-9P8B	EMD-71349 PDB-9P7O	EMD-71333 PDB-9P76	EMD-71345 PDB-9P7K
Data collection and processing							
Magnification	81,000	81,000	81,000	81,000	81,000	81,000	81,000
Voltage (kV)	300	300	300	300	300	300	300
Electron exposure (e-/Å ²)	50	50	50	50	50	50	50
Defocus range (μm)	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5
Pixel size (Å)	1.068	1.068	0.89	1.068	1.068	1.068	1.068
Symmetry	C1	C1	C1	C1	C1	C1	C1
Initial particle images	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109
Final particle images	67,622	23,406	24,591	281,431	105,399	119,172	48,914
Map resolution (Å)	2.80	2.97	3.26	2.48	2.65	2.83	2.80
FSC threshold 0.143							
Map Sharpening B factor (Å ²)	-38	-23	-10	-58	-49	-36	-37
Model refinement							
Initial model (PDB code)	8QOI, 6Z6M, 6ZM7						
Model resolution (Å)							
FSC threshold 0.5	3.0	3.1	3.6	2.7	2.9	3.0	3.0
Model vs. map correlation							
Coefficient (cc_mask)	0.89	0.85	0.80	0.89	0.88	0.87	0.89
Model composition							
Non-hydrogen atoms	219,971	219,971	218,355	224,971	224,970	223,377	224,970
Protein residues	11,840	11,840	11,840	12,281	12,281	12,281	12,281
Nucleotide residues	5,820	5,820	5,745	5,896	5,896	5,821	5,896
Ligands	242	242	242	242	242	242	242
B factors (Å ²) (mean)							
Protein	98	109	167	108	117	101	113
Nucleotide	101	116	166	108	119	100	113
Ligands	59	69	118	69	77	57	60
R.m.s. deviations							
Bond length (Å)	0.003	0.006	0.006	0.005	0.005	0.006	0.003
Bond angle (°)	0.6	0.7	0.8	0.6	0.6	0.7	0.6
Validation							
MolProbity score	1.5	1.7	1.98	1.48	1.48	1.56	1.48
Clash score	4.69	5.86	12.4	4.37	4.13	4.76	4.42
Poor rotamers	0.01	0.02	0.02	0.01	0.02	0	0.01
Ramachandran plot							
Favored (%)	96.15	94.54	94.56	92.92	95.87	95.51	94.14
Allowed (%)	3.84	5.44	5.42	6.96	4.12	4.48	3.85
Disallowed (%)	0.01	0.02	0.02	0.12	0.01	0.01	0.01

Supplementary Table 3 | Cryo-EM data collection, refinement and validation statistics of 80S states for untreated dataset (part2).

	(2b)	(2c)	(3a)	(3b)	(3c)	(4)	(5)	(6a)
	EMD-71348 PDB-9P7N	EMD-71346 PDB-9P7L	EMD-71357 PDB-9P7Y	EMD-71356 PDB-9P7X	EMD-71355 PDB-9P7W	EMD-71377 PDB-9P8H	EMD-71332 PDB-9P73	EMD-71412 PDB-9P9I
Data collection and processing								
Magnification	81,000	81,000	81,000	81,000	81,000	81,000	81,000	81,000
Voltage (kV)	300	300	300	300	300	300	300	300
Electron exposure (e-/Å ²)	50	50	50	50	50	50	50	50
Defocus range (µm)	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5
Pixel size (Å)	1.068	1.068	1.068	1.068	1.068	1.068	1.068	1.068
Symmetry	C1	C1	C1	C1	C1	C1	C1	C1
Initial particle images	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109
Final particle images	50,321	60,393	86,538	64,856	66,380	36,954	130,154	103,321
Map resolution (Å)	2.83	2.92	2.75	2.83	2.93	2.98	2.66	2.77
FSC threshold 0.143								
Map Sharpening B factor (Å ²)	-34	-27	-41	-34	-27	-23	-49	-40
Model refinement								
Initial model (PDB code)	8QOI, 6Z6M, 6ZM7							
Model resolution (Å)	3.0	3.1	2.9	3.0	3.1	3.2	2.9	2.9
FSC threshold 0.5								
Model vs. map correlation	0.89	0.86	0.89	0.89	0.86	0.87	0.9	0.89
Coefficient (cc_mask)								
Model composition								
Non-hydrogen atoms	224,970	223,377	221,484	221,484	219,891	220,526	227,131	228,085
Protein residues	12,281	12,281	11,840	11,840	11,840	11,920	12,766	13,079
Nucleotide residues	5,896	5,821	5,891	5,891	1,816	5,817	5,817	5,746
Ligands	242	242	242	242	261	241	241	239
B factors (Å²) (mean)								
Protein	113	106	116	100	112	128	101	123
Nucleotide	115	104	119	107	115	132	99	110
Ligands	60	55	66	55	58	78	58	61
R.m.s. deviations								
Bond length (Å)	0.004	0.004	0.006	0.005	0.006	0.004	0.004	0.007
Bond angle (°)	0.6	0.6	0.6	0.6	0.7	0.6	0.6	0.7
Validation								
MolProbity score	1.53	1.6	1.57	1.61	1.68	1.58	1.53	1.58
Clash score	4.87	5.37	4.92	5.32	6.19	6.19	4.71	5.25
Poor rotamers	0	0.01	0.01	0.02	0.01	0	0.01	0.02
Ramachandran plot								
Favored (%)	95.94	95.45	95.56	95.41	95.15	95.94	95.8	95.67
Allowed (%)	4.06	4.54	4.42	4.58	4.84	4.02	4.17	4.32
Disallowed (%)	0	0.01	0.02	0.02	0.01	0.03	0.03	0.01

Supplementary Table 4 | Cryo-EM data collection, refinement and validation statistics of 80S states for untreated dataset (part3).

	6b	7a	7b	7c	8a	9a	10a	11a
	EMD-71411 PDB-9P9H	EMD-71334 PDB-9P78	EMD-71335 PDB-9P79	EMD-71372 PDB-9P8C	EMD-71336 PDB-9P7A	EMD-71337 PDB-9P7C	EMD-71338 PDB-9P7D	EMD-71339 PDB-9P7E
Data collection and processing								
Magnification	81,000	81,000	81,000	81,000	81,000	81,000	81,000	81,000
Voltage (kV)	300	300	300	300	300	300	300	300
Electron exposure (e-/Å ²)	50	50	50	50	50	50	50	50
Defocus range (µm)	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5
Pixel size (Å)	1.068	1.068	1.068	1.068	1.068	1.068	1.068	1.068
Symmetry	C1	C1	C1	C1	C1	C1	C1	C1
Initial particle images	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109	4,836,109
Final particle images	86,934	28,219	13,185	12,945	59,299	54,480	219,754	123,628
Map resolution (Å)	2.84	2.93	3.10	3.11	2.81	2.78	2.57	2.59
FSC threshold 0.143								
Map Sharpening B factor (Å ²)	-36	-34	-38	-39	-38	-39	-56	-52
Model refinement								
Initial model (PDB code)	8QOI, 6Z6M, 6ZM7							
Model resolution (Å)								
FSC threshold 0.5	3.0	3.1	3.5	3.6	3.0	3.0	2.8	2.8
Model vs. map correlation								
Coefficient (cc_mask)	0.88	0.87	0.83	0.84	0.89	0.89	0.88	0.81
Model composition								
Non-hydrogen atoms	228,698	228,149	228,105	226,556	228,149	228,149	228,149	228,141
Protein residues	13,152	13,087	13,082	13,087	13,087	13,087	13,087	13,086
Nucleotide residues	5,746	5,746	5,746	5,671	5,746	5,746	5,746	5,746
Ligands	239	241	241	241	241	241	241	241
B factors (Å ²) (mean)								
Protein	122	116	126	126	106	101	130	117
Nucleotide	116	112	127	127	104	102	124	112
Ligands	60	62	72	75	56	56	79	73
R.m.s. deviations								
Bond length (Å)	0.007	0.004	0.003	0.005	0.004	0.003	0.002	0.004
Bond angle (°)	0.7	0.6	0.6	0.6	0.6	0.6	0.6	0.6
Validation								
MolProbity score	1.58	1.57	1.57	1.68	1.51	1.52	1.5	1.49
Clash score	5.38	5.55	5.68	6.52	5	5.29	5.05	4.3
Poor rotamers	0	0	0	0	0.01	0.02	0.03	0.01
Ramachandran plot								
Favored (%)	95.81	96.04	96.17	95.47	96.33	96.41	96.41	96
Allowed (%)	4.18	3.95	3.81	4.53	3.66	3.59	3.58	4
Disallowed (%)	0.01	0.01	0.02	0.01	0.01	0	0.01	0

Supplementary Table 5 | Cryo-EM data collection, refinement and validation statistics of 80S states for HHT + CHX treated dataset

	(1b)	(1c)	(2b)	(2c)	(3b)	(3c)	(7c)
	EMD-71378 PDB-9P8I	EMD-71344 PDB-9P7J	EMD-71343 PDB-9P7I	EMD-71342 PDB-9P7H	EMD-71341 PDB-9P7G	EMD-71340 PDB-9P7F	EMD-71690 PDB-9PKB
Data collection and processing							
Magnification	81,000	81,000	81,000	81,000	81,000	81,000	81,000
Voltage (kV)	300	300	300	300	300	300	300
Electron exposure (e-/Å ²)	50	50	50	50	50	50	50
Defocus range (μm)	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5	-1.2 — -2.5
Pixel size (Å)	1.068	1.068	1.068	1.068	1.068	1.068	1.068
Symmetry	C1	C1	C1	C1	C1	C1	C1
Initial particle images	1,053,496	1,053,496	1,053,496	1,053,496	1,053,496	1,053,496	1,053,496
Final particle images	7,312	7,052	9,091	8,604	15,150	14,418	52,735
Map resolution (Å)	3.89	3.91	3.69	3.68	3.54	3.56	3.05
FSC threshold 0.143							
Map Sharpening B factor (Å ²)	0	0	0	0	-5	-3	-30
Model refinement							
Initial model (PDB code)	8QOI, 6Z6M, 7Q08, 8A3D						
Model resolution (Å)							
FSC threshold 0.5	4.4	4.4	4.1	4.0	4.0	4.0	3.3
Model vs. map correlation							
Coefficient (cc_mask)	0.84	0.85	0.84	0.86	0.85	0.85	0.85
Model composition							
Non-hydrogen atoms	220,030	218,437	225,029	223,436	225,029	219,950	226,615
Protein residues	11,840	11,840	12,281	12,281	12,281	11,840	13,087
Nucleotide residue	5,820	5,745	5,896	5,821	5,896	5,816	5,671
Ligands	244	244	244	244	244	244	244
B factors (Å ²) (mean)							
Protein	195	203	170	176	256	167	154
Nucleotide	194	200	173	175	215	168	154
Ligands	146	153	128	130	120	126	104
R.m.s. deviations							
Bond length (Å)	0.004	0.003	0.006	0.003	0.006	0.005	0.002
Bond angle (°)	0.6	0.6	0.7	0.6	0.8	0.6	0.6
Validation							
MolProbity score	1.93	1.71	1.85	1.69	1.85	1.82	1.54
Clash score	11.93	7.89	9.62	7.46	10.05	8.35	5.38
Poor rotamers	0	0	0.03	0.01	0.03	0.01	0
Ramachandran plot							
Favored (%)	95.78	95.97	94.97	95.9	95.28	94.72	96.23
Allowed (%)	4.02	4.02	5.01	4.1	4.71	5.28	3.76
Disallowed (%)	0.01	0.01	0.02	0.01	0.01	0	0.01

Supplementary Table 6 | Cryo-EM data collection, refinement and validation statistics of disome structures for untreated dataset.

	T-t disome Composite EMD-44052 PDB-9B0S Focused leading EMD-44057 Focused trailing EMD-44056	T-b disome composite EMD-44050 PDB-9B0Q Focused leading EMD-44054 Focused trailing EMD-44053
Data collection and processing		
Magnification	81,000	81,000
Voltage (kV)	300	300
Electron exposure (e ⁻ /Å ²)	50	50
Defocus range (μm)	-1.2 — -2.5	-1.2 — -2.5
Pixel size (Å)	1.068	1.068
Symmetry	C1	C1
Initial particle images	4,836,109	4,836,109
Final particle images	33,275	9,137
Map resolution (Å)	3.4	3.8
FSC threshold 0.143		
Map Sharpening B factor (Å ²)	-19	-4
Model refinement		
Initial model (PDB code)	6Z6M, 6ZM7	
Model resolution (Å)	3.6	4.1
FSC threshold 0.5		
Model vs. map correlation		
Coefficient (cc_mask)	0.77	0.83
Model composition		
Non-hydrogen atoms	458,132	459,641
Protein residues	25,356	25,993
Nucleotide residue	11,938	11,740
Ligands	522	522
B factors (Å ²) (mean)		
Protein	154	196
Nucleotide	161	172
Ligands	82	120
R.m.s. deviations		
Bond length (Å)	0.005	0.006
Bond angle (°)	0.8	0.8
Validation		
MolProbity score	1.98	2.12
Clash score	9.14	12.34
Poor rotamers	0.01	0.01
Ramachandran plot		
Favored (%)	91.69	91.04
Allowed (%)	8.23	8.86
Disallowed (%)	0.08	0.10

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Supplementary Table 7. Polyamines identified in the ribosome

Number	This Study	8GLP	8A3D	Interactions
L5/5313	SPM	SPD	SPM	28S A1527, 28S U1528, 28S G3918, 28S A4186, 28S G4187, L15 Y81
L5/5314	SPD	SPD	Mg	28S A39, 28S G40, 28S C41, 28S G91, 28S C92 28S G93, 28S U4340, 28S C4341, L27a H39
L5/5315	SPM	2 Mg + K	2 Mg + K	28S A44, 28S U45, 28S A47, 28S G48, 28S G90, 28S U291, 28S G293, 28S G294
L5/5316	SPM	PUT	None	28S U1735, 28S A1736, 28S A1787, 28S A1788, 28S U1790, 28S U1791, L21 Y13, L21 S16
L5/5317	SPM	PUT + Mg + K	K	28S C1678, 28S G1680, 28S G1854, 28S U4194, 28S C4204, 28S 6MZ4220, 28S C4221
L5/5318	SPD	PUT + Mg	Mg	28S G1587, 28S G1604, 28S G1605, 28S A3642, 28S A3643
L5/5319	SPD	SPD	Mg	28S A64, 28S A328, 28S A329, 28S G330, 28S G331, 28S C332, L15 R169
L5/5320	SPD	SPD	K	28S G1581, 28S PSU1582, 28S A1583, 28S G1584, 28S C1585, 28S C1607, 28S G1608, 28S U1609
L5/5321	SPD	2 Mg	Mg	28S G1869, 28S A1939, 28S G3874, 28S G3875, 28S A3877
L5/5322	SPD	SPD	None	5.8S G11, 5.8S A12, 5.8S U13, 5.8S C138, 5.8S G139, 5.8S C140
L5/5323	SPD	SPD	None	28S A435, 28S C436, 28S C1305, 28S C1306, 28C A1307, 5.8S U7
S2/1930	SPM	SPD + 2 Mg	N/A	18S A671, 18S A672, 18S G673, 18S C674, 18S U675, 18S C676, 18S G677, 18S C1026, 18S C1085, 18S U1088, 18S G1089
S2/1931	SPD	Mg	N/A	18S PSU105, 18S C106 18S A348, 18S A349, 18S C350, 18S G351, 18S G431, 18S G432
S2/1932	SPD	Mg	N/A	18S C1529, 18S A1651, 18S G1652, 18S U1653