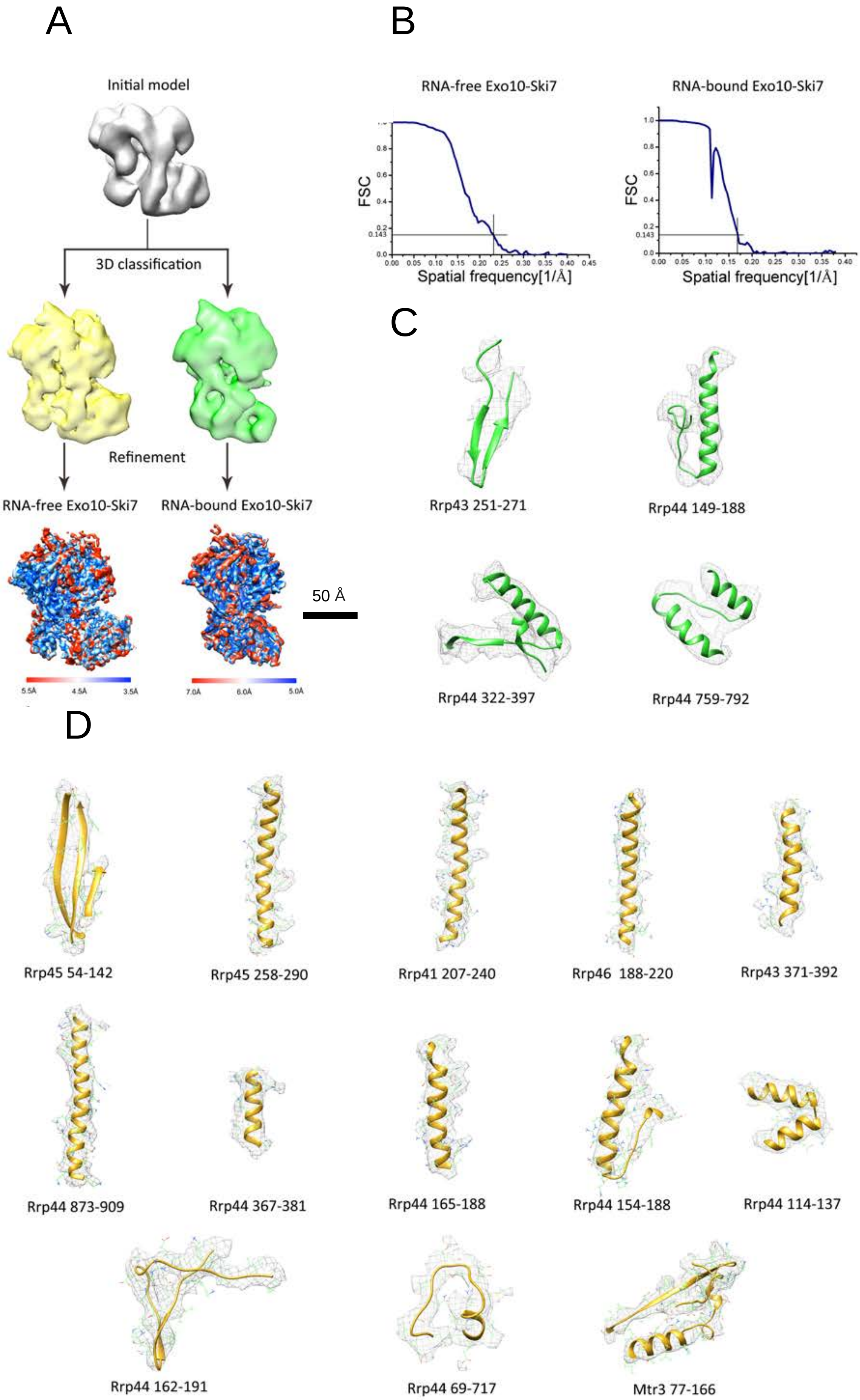
A
Initial model
3D classification
Refinement
RNA-free Exo10-Ski7
RNA-bound Exo10-Ski7
5.5Å
4.5Å
3.5Å
7.0Å
6.0Å
5.0Å
50 Å
B
RNA-free Exo10-Ski7
RNA-bound Exo10-Ski7
FSC
0.143
Spatial frequency[1/Å]
0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45
0.0 0.2 0.4 0.6 0.8 1.0
C
Rrp43 251-271
Rrp44 149-188
Rrp44 322-397
Rrp44 759-792
D
Rrp45 54-142
Rrp45 258-290
Rrp41 207-240
Rrp46 188-220
Rrp43 371-392
Rrp44 873-909
Rrp44 367-381
Rrp44 165-188
Rrp44 154-188
Rrp44 114-137
Rrp44 162-191
Rrp44 69-717
Mtr3 77-166

Supplementary information, Figure S2. 3D reconstruction and atomic model building of the Exo10-Ski7

(A) 3D reconstruction procedure of the Exo10-Ski7 complex by Cryo-EM. We used a low-pass filtered 3D reconstruction of the Exo10 complex obtained from negative staining EM as initial model to perform 3D classification of the Exo10-Ski7 complex in RELION 1.3, which generated two major classes of particles. Further refinement of the two classes led to two 3D reconstructions of the RNA-free Exo10-Ski7 and RNA-bound Exo10-Ski7 respectively. The refined models were presented with gradient color based on local resolution calculated by ResMap software. The resolution range was marked as gradient bar on the bottom of each corresponding model. (B) Gold-standard FSC curves of the two 3D reconstructions. The estimated resolution of the RNA-free Exo10-Ski7 was about 4.2 Angstrom at 0.143 criteria. The estimated resolution of the RNA-bound Exo10-Ski7 was about 5.8 Angstrom at 0.143 criteria. (C) Representative portions in the EM density map of the endogenous RNA-bound Exo10-Ski7, into which the Exo10 from atomic model 4IFD (PDB code) were docked as rigid body. The numbers of chain and sequence were marked under the corresponding portions. (D) Representative portions in the EM density map of the RNA-free Exo10-Ski7, into which the atomic model of the RNA-free Exo10 was built. Side chains were presented as green wires. The subunit and sequence number were marked under the corresponding portions.