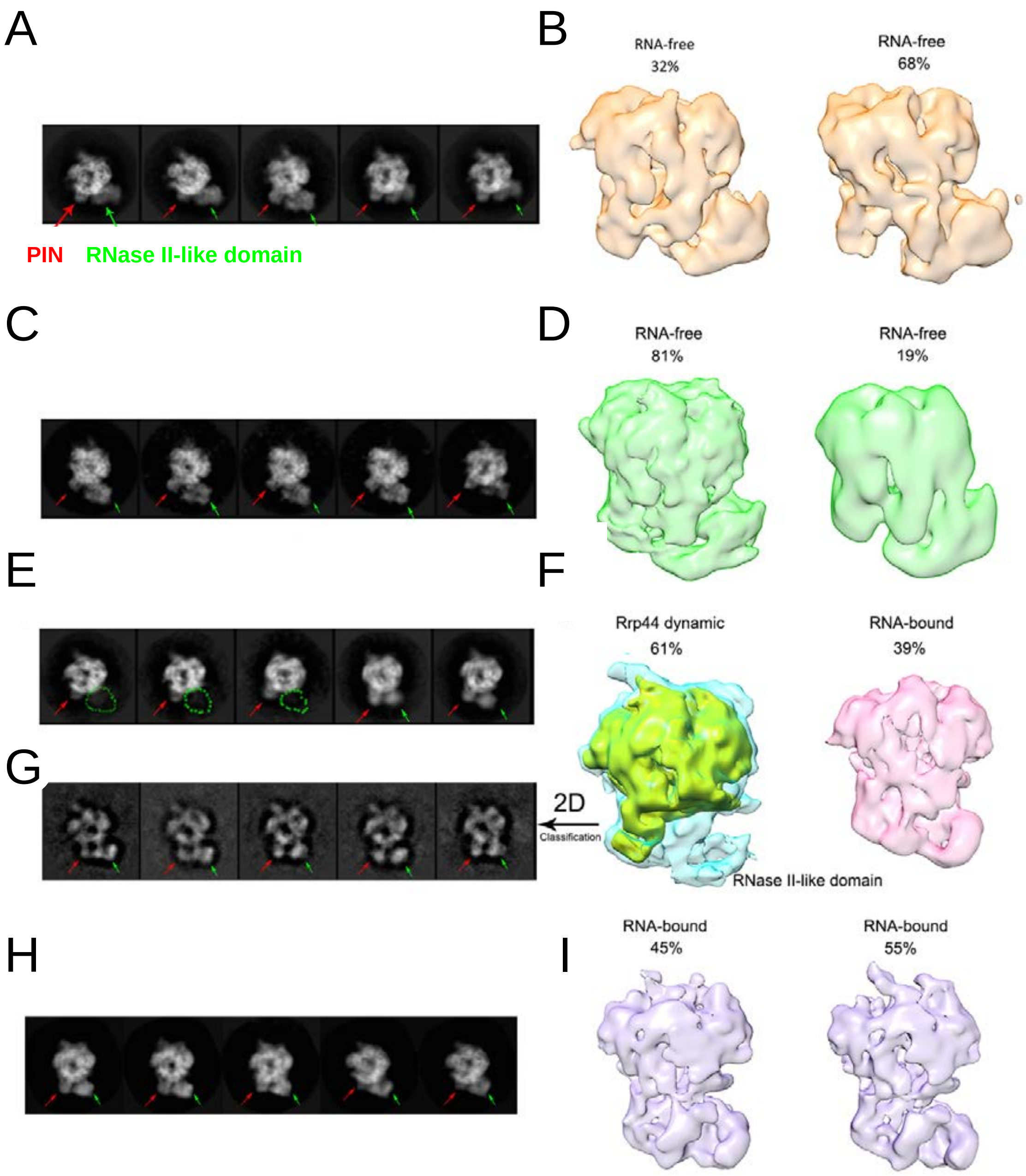

Supplementary information, Figure S6. RNA induced Rrp44 instability

(A) Representative 2D class averages of the purified Exo10 (Mg^{2+}-treated) in their side-views. (B) 3D reconstructions of the purified Exo10 (Mg^{2+}-treated) classified in two groups by RELION 1.3. (C) Representative 2D class averages of the Mg^{2+}-treated Exo10 incubated with RNA18. (D) 3D reconstructions of the Mg^{2+}-treated Exo10 incubated with RNA18 classified in two groups by RELION 1.3. (E) Representative 2D class averages of the Mg^{2+}-treated Exo10 incubated with RNA24. (F) 3D reconstructions of the Mg^{2+}-treated Exo10 incubated with RNA24 classified in two groups by RELION 1.3. In the left reconstruction state (Rrp44 dynamic), the 3D volume at a threshold of 2.18 sigma (yellow) is superimposed with the same volume at a smaller threshold of 0.61 sigma (cyan, transparent). (G) Further 2D classification of the particles belonging to the group of Rrp44 dynamic state using IMAGIC-4D software yielded 2D class averages with various conformations of the RNase-II like domain in respect to the exosome core. Five representative 2D class averages in their side views are shown. (H) 2D class averages of the Mg^{2+}-treated Exo10 incubated with RNA48. (I) 3D reconstructions of the Mg^{2+}-treated Exo10 incubated with RNA48 classified in two groups by RELION 1.3. In all the above 2D class average panels, red arrows point to the PIN domain, green arrows or contours point to the RNase II-like domains of Rrp44, respectively. In all the 3D classification panels, the conformational state of the Exo10 complex are derived from their shapes, with the particle percentages of each reconstruction labeled below.