

Figure S1. Structure-based sequence alignment of Pat1C (**A**), Lsm2 (**B**) and Lsm3 (**C**) from *S. cerevisiae* (Sc), *S. pombe* (Sp), *D. rerio* (Dr) and *H. sapiens* (Hs). The secondary structural elements of each protein are shown above each sequence alignment. Residues involved in interactions between Pat1C and Lsm2-3 are marked as green triangles. Regions of deletion in Lsm2 (designated as Lsm2 $\Delta\alpha$ 2) and Lsm3 (designated as Lsm3 $\Delta\alpha$ 1) are labeled in orange line. Six positively charged residues (R519, R520, R591, R595, K625 and K626) of human Pat1C involved in U₃₀ RNA binding are marked as pink triangles (Braun et al. 2010).