

Supplementary Table 2 Fitted molecular masses and apparent sedimentation coefficients

	Fitted molecular mass (kDa)									Sedimentation coefficient (S)							
	0 mM Mg ²⁺			1 mM Mg ²⁺			10 mM Mg ²⁺			0 mM Mg ²⁺			1 mM Mg ²⁺			10 mM Mg ²⁺	
	run 1	run 2	run 3	run 1	run 2	run 3	run 1	run 2		run 1	run 2	run 3	run 1	run 2	run 3	run 1	run 2
poly(U) ₈₅	26.80	24.71		24.48	24.59		28.92	24.91		2.60	2.51		2.63	2.60		2.98	2.95
HDV	29.96	30.12		28.69	28.06		27.63	28.27		4.20	4.23		4.27	4.22		4.34	4.32
tRNA ^{PHE}	23.70	23.01	22.18	23.21	24.22	23.59	25.32	23.98		3.57	3.60	3.61	4.03	3.91	3.94	4.06	4.04
ligase	26.90	28.82		27.05	28.87		26.16	26.50		3.77	3.76		4.01	3.99		4.26	4.23
P4P6	50.42	56.53		51.61	53.88		48.25	54.58		5.00	5.03		5.59	5.58		6.55	6.54
p1	34.75			28.15			27.54			3.82			3.88			4.05	
p2	29.39	30.25		23.73	22.58		23.26	21.77		3.88	3.95		4.94	5.07		8.46	8.24
p3	26.91			26.44			24.16			3.77			3.99			4.36	
p4	31.24			30.18			21.84			3.90			4.05			4.81	
p5	29.88	26.59		26.22	28.01		26.25	31.31		3.87	3.87		4.80	4.64		6.19	6.10
p6	29.46			28.39			28.51			3.80			3.84			4.19	
p7	29.65			26.03			26.79			3.80			4.12			3.80	
p8	29.27			29.70			23.06			3.70			4.03			5.05	
p9	29.07			24.98			28.11			3.81			4.32			5.27	
p10	28.21	29.08		27.00	28.96	26.35	38.31	35.38		3.84	3.85		4.46	4.44	4.48	5.92	6.00
i1	31.38			29.93			26.53			3.71			3.84			4.01	
i2	29.22			30.09			26.97			3.79			3.96			4.12	
i3	27.73			26.95			25.17			3.71			3.97			4.08	
i4	28.93	29.35		27.76			27.47			3.60	3.60		3.94			4.21	
i5	28.29			28.96			25.27			3.69			4.01			4.35	
i6	28.17			28.84			26.56			3.68			3.85			4.11	
i7	30.01	29.62		27.18	28.87		24.28	27.09		3.70	3.70		3.96	3.89		4.66	4.49
i8	27.22			31.57			28.07			3.71			3.94			4.10	
i9	28.92	28.91		25.22	29.67		28.66	27.83		3.53	3.53		3.96	3.88		6.53	6.32
i10	28.33			30.78			29.92	27.79		3.67			4.00			4.12	4.12

The quality of the AUC velocity sedimentation analysis is indicated by the agreement between the known anhydrous mass of the RNA (manuscript **Table 1**) and the mass values fitted to the velocity sedimentation data (listed above). Errors can be introduced by individual differences in partial specific volume, solvent density, interactions with ions, and violations of the assumptions of ideality (RNA-RNA interactions or interconverting conformers). Of 110 independent AUC runs, 57 had fitted mass estimates within 5% of the theoretical mass (values left uncolored), 34 runs had fitted masses between 5% and 10% (blue), and the remaining 19 runs had masses beyond 10% (red). No fitted mass deviated from the theoretical value by more than 38% (p10, 10 mM Mg²⁺, run 1). Italicized values for poly(U)₈₅ indicate measurements made from a separate homopolymer preparation. Fitted masses from 0 mM Mg²⁺ tend to be over-estimated, while masses from 10 mM Mg²⁺ tend to be under-estimated. The permuted cohort RNAs tend to have larger errors in their fitted molecular mass than do the isoheteropolymer RNAs.