Supporting Information Methods

Data analysis for EMSA results

The intensities of each band on the gels were quantified by using Quantity One software (Bio-Rad Laboratory, Hercules, CA). The binding curves were created by plotting the fraction of RNA bound with proteins, θ (total bound RNA in all bands divided by the sum of bound and unbound RNAs) as a function of protein concentration. The binding constants K_d can be calculated by fitting the data with the Hill equation:

$$\theta = \frac{(P_0 - nR_0\theta)^n}{K_d^n + (P_0 - nR_0\theta)^n}$$

where R_0 is the total concentration of RNA added in each lane (3 nM), P_0 is

the total concentration of proteins added in each lane, and n is the Hill coefficient.