Supplementary Information

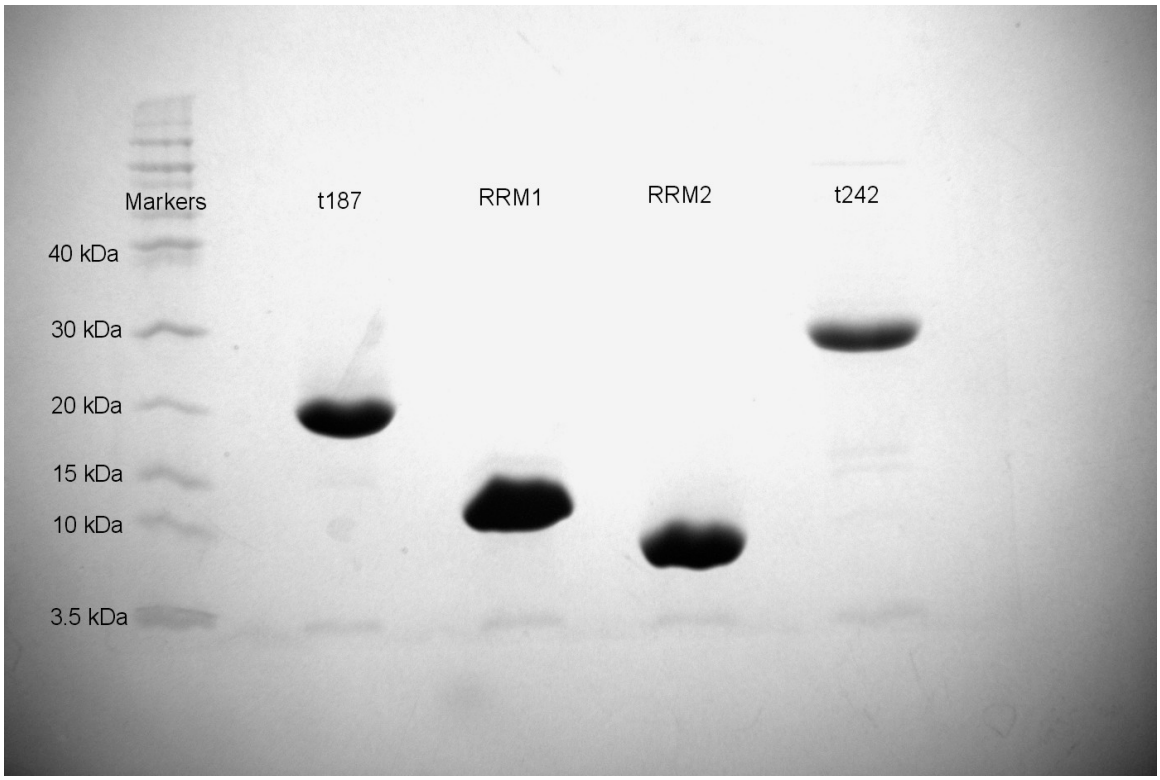

Figure S1: Gel of the four recombinant protein constructs used (T187, RRM1, RRM2 and t242).

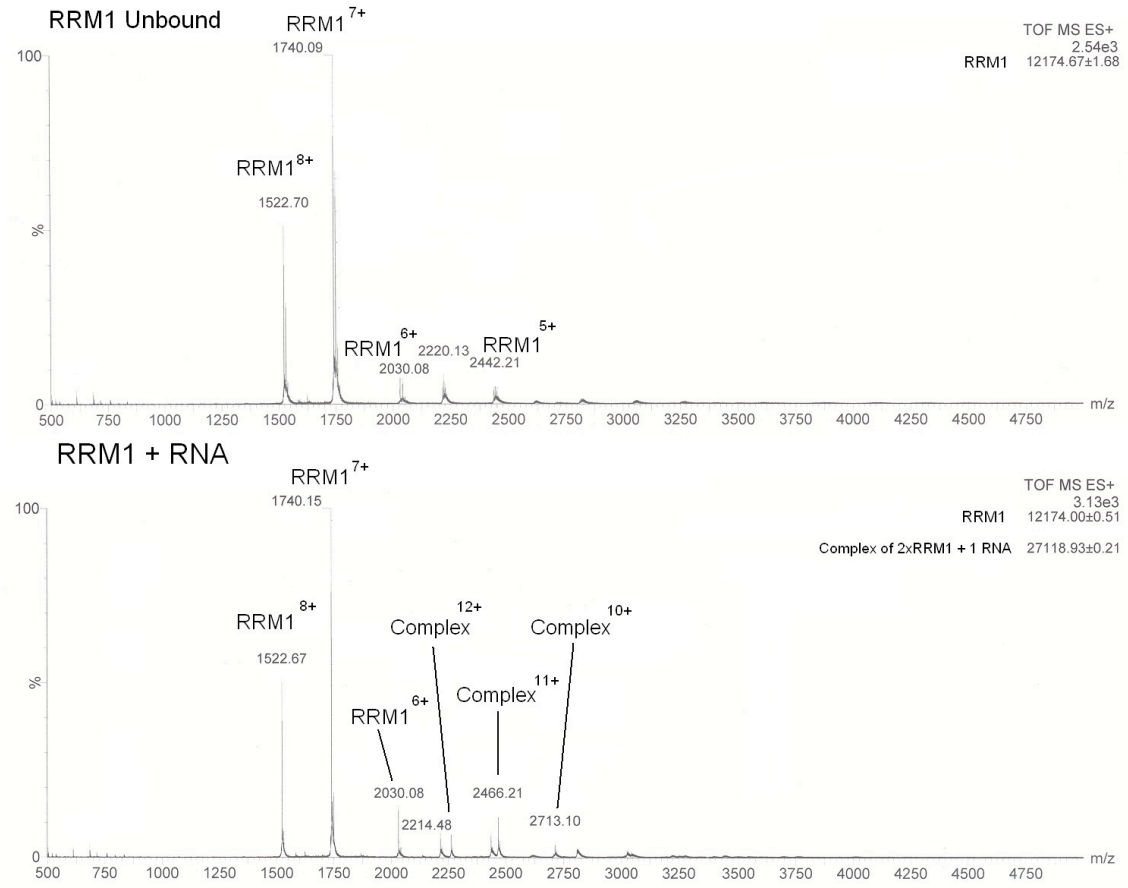

Figure S2: Mass spectra of the RRM1 construct unbound (upper) and bound to the EDEN9 RNA sequence (lower). Samples were dissolved in 50mM ammonium acetate. Protein and RNA concentrations of 10µM used. The unbound spectrum shows a single species of mass 12175, compared to a theoretical mass of 12182 for RRM1. In the presence of EDEN9 some unbound RRM1 is still present, but an additional species of mass 27119 is present. A complex with 2 molecules of RRM1 bound to one EDEN9 has a theoretical mass of 27135.6 No peak for a 1:1 complex was observed.

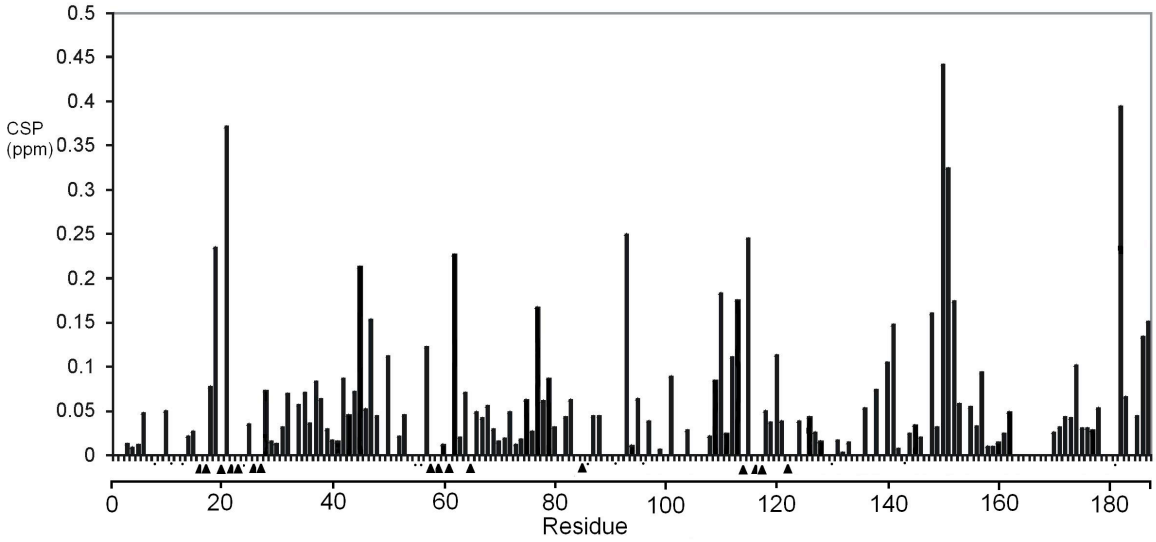

Figure S3: Chemical shift perturbation plot for the binding of EDEN11 (UGUUUGUUUGU) to t187. Proline residues are marked with a black dot. Those residues which broaden and disappear over the course of the titration are marked with black arrows.

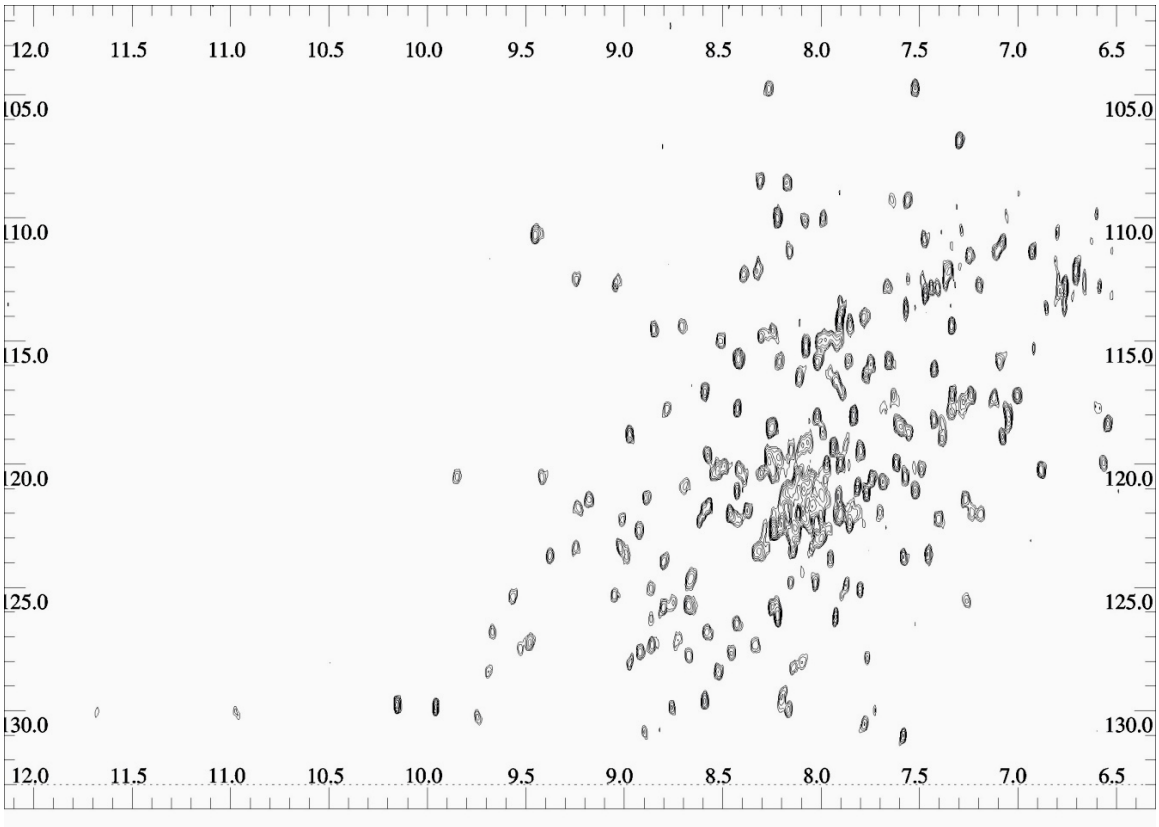

Figure S4: 2D $^{1}H/^{15}N$-TROSY NMR spectrum of T242 construct. Spectrum was collected at 298K in 25 mM phosphate buffer, 50mM NaCl, 10% D_2O (v/v), pH 7.0 with a protein concentration of approximately 250µM. Some additional peaks are seen compared to the corresponding t187 spectrum, most with chemical shifts and linewidths indicative of high flexibility.

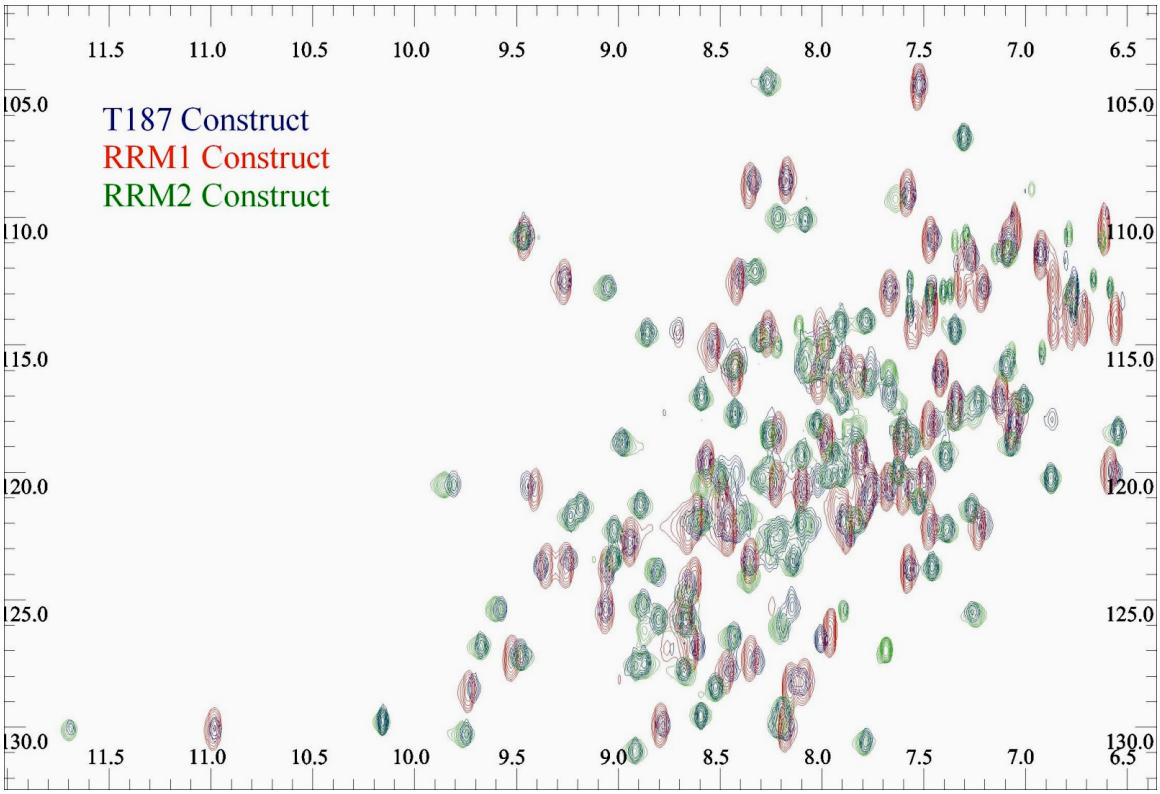

Figure S5: 2D $^{1}H/^{15}N$-TROSY NMR spectra of T187 (blue) and overlayed spectra of RRM1 (red) and RRM2 (green) showing that the longer construct is well represented by the sum of the spectra of the individual domains, except for a few perturbations at the domain boundaries. Spectra were collected at 298K in 25 mM phosphate buffer, 50mM NaCl, 10% D_2O (v/v), pH 7.0 with protein sample concentrations in the range 400-500µM.

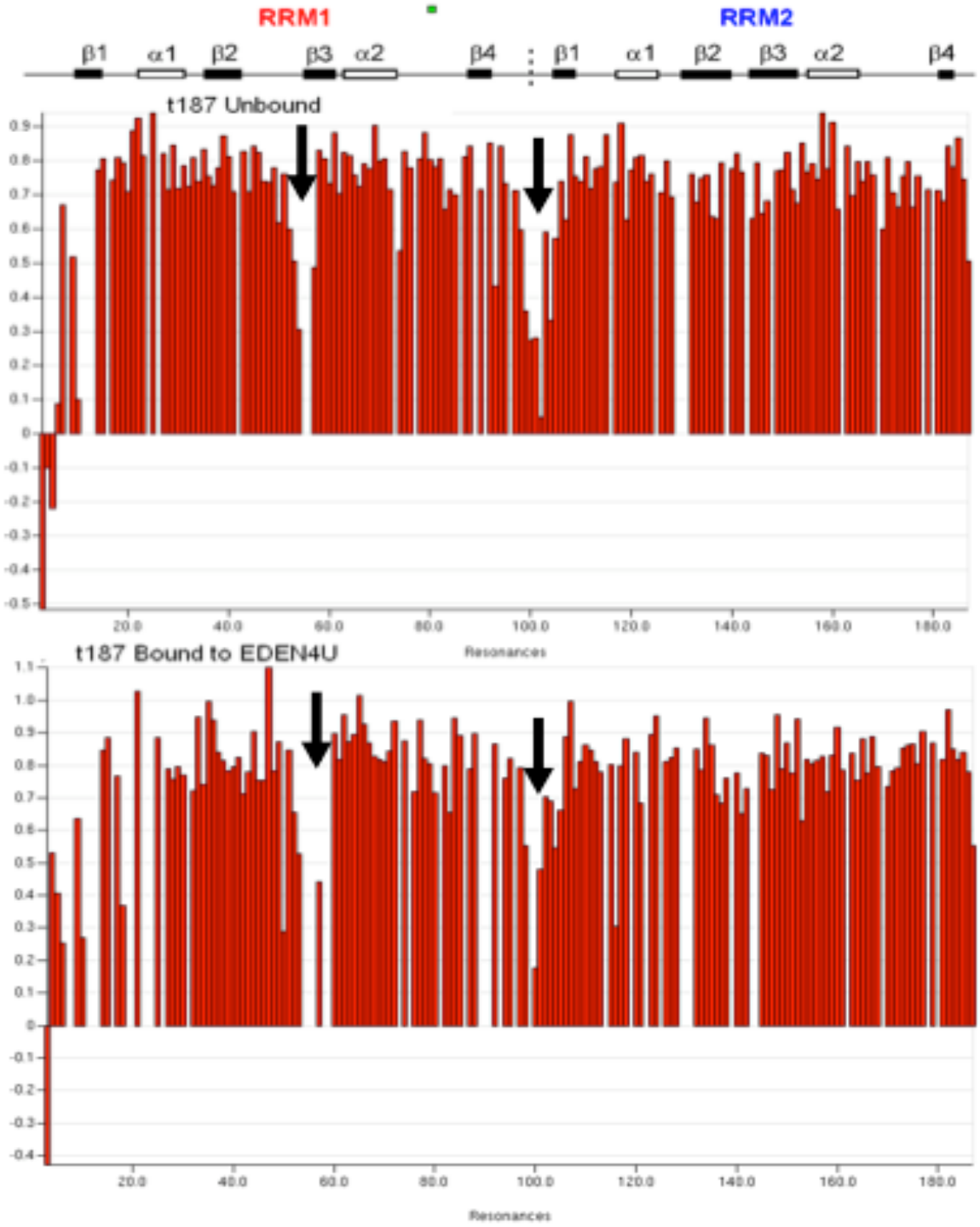

Figure S6: ^{1}H-^{15}N heteronuclear NOE data collected at 800 MHz and 298K for the unbound T187 (top) and complex with UGU$(U)_4$UGU (bottom). The flexible loop region between β-strands 2 and 3 of RRM1 is highlighted (NOEs<0.5) along with the linker sequence (residues 98-105) by arrows. The linker sequence appears to retain some flexibility in the bound state. The unbound spectrum was collected on a 500 µM protein sample in 25 mM phosphate buffer, 50mM NaCl, 10% D_2O (v/v), pH 7.0. 750 µM RNA was added to produce the bound sample.