**Table S1:** Thermodynamics of non-specific binding of Rev-ARM to stems IA and IIB at 0.1 M KCl

| Temper-ature (K) | RNA | $K_d$ (μM) | ΔG (kcal $mol^{-1}$) | ΔH (kcal $mol^{-1}$) | TΔS (kcal $mol^{-1}$) | n (number of lattice sites occluded) |
|---|---|---|---|---|---|---|
| 283 | IA | 0.81 ± 0.19 | -7.90 ± 0.13 | -8.52 ± 1.01 | -0.62 ± 1.02 | 9.8 ± 0.55 |
| 293 | | 2.27 ± 0.27 | -7.57 ± 0.06 | -10.0 ± 0.82 | -2.48 ± 0.82 | 7.2 ± 1.01 |
| 303 | | 3.17 ± 1.67 | -7.54 ± 0.19 | -9.93 ± 0.73 | -2.40 ± 0.76 | 6.9 ± 0.17 |
| 283 | IIB | 0.51± 0.01 | -8.15 ± 0.01 | -7.40 ± 0.46 | 0.75 ± 0.46 | 9.2 ± 1.1 |
| 293 | | 0.70 ± 0.29 | -8.28 ± 0.22 | -9.18 ± 0.59 | -0.89 ± 0.63 | 9.2 ± 0.44 |
| 303 | | 0.87 ± 0.75 | -8.52 ± 0.36 | -9.18 ± 0.47 | -0.65 ± 0.59 | 10.0 ± 0.18 |

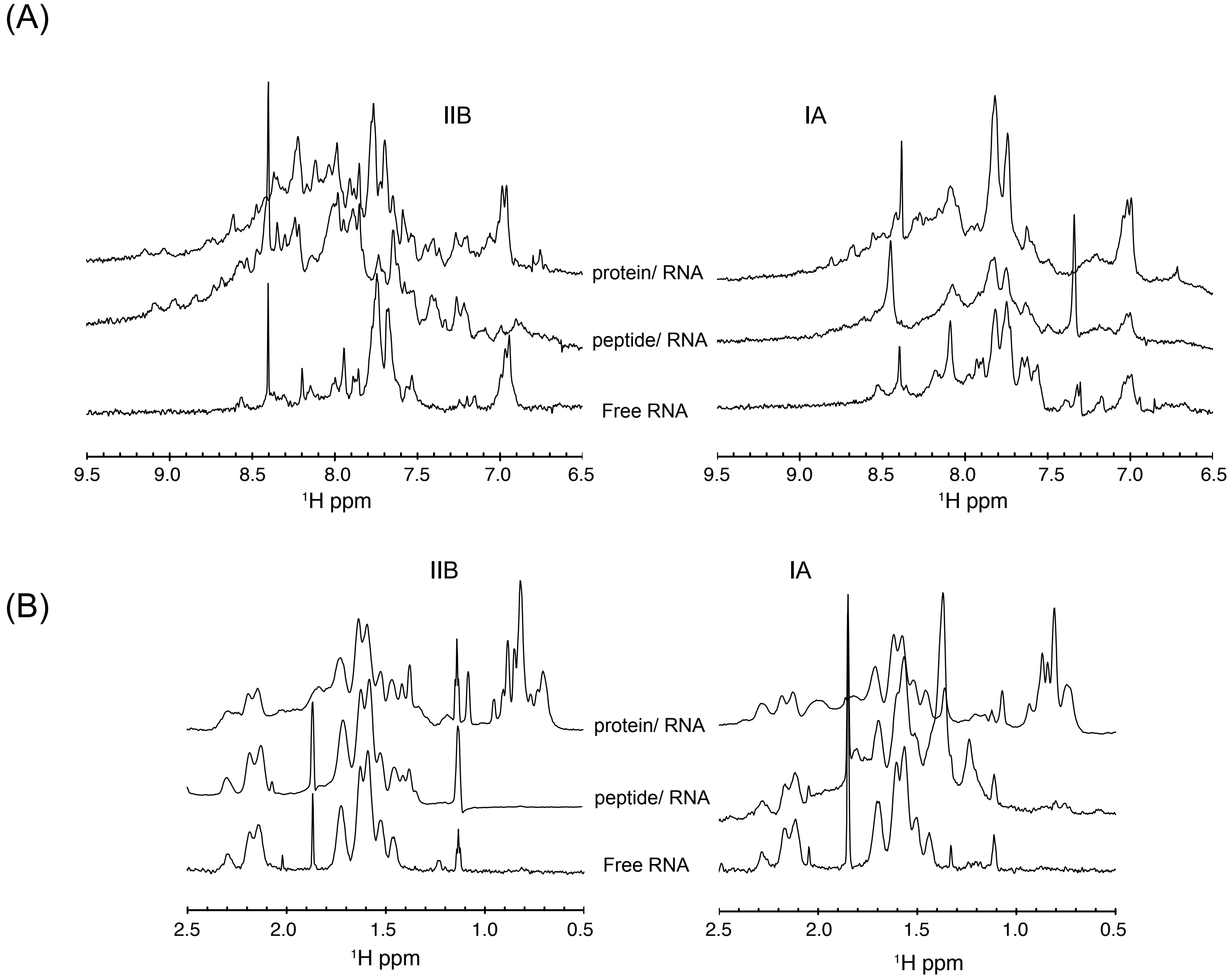
## Supporting Information Figure Legends

**Figure S1:** Selected regions from 1-1-echo $^1$H NMR spectra for free, peptide-bound and protein-bound IA and IIB RNA samples

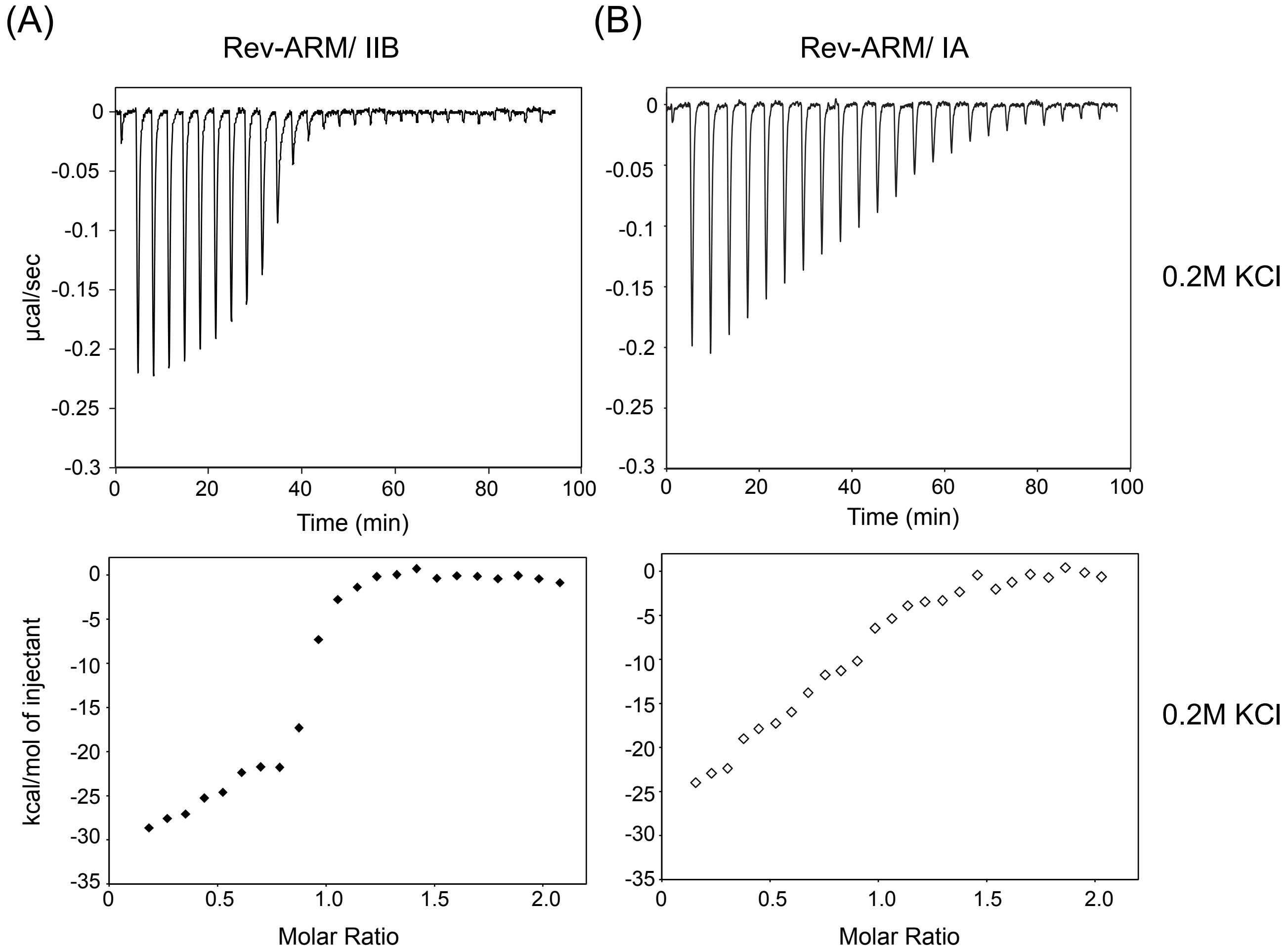
**Figure S2: Reverse titration profiles at 0.2 M KCl show weakened non-specific binding**

(A, B) ITC traces for the titration of IIB (A) or IA (B) into Rev-ARM in buffer containing 0.2 M KCl. (C, D) Integrated heats for the above traces.

Figure S1


(A)
IIB
IA
protein/ RNA
peptide/ RNA
Free RNA
9.5
9.0
8.5
8.0
7.5
7.0
6.5
$^1$H ppm
(B)
IIB
IA
protein/ RNA
peptide/ RNA
Free RNA
2.5
2.0
1.5
1.0
0.5
$^1$H ppm

# Figure S2


(A)
Rev-ARM/ IIB
(B)
Rev-ARM/ IA
0
-0.05
-0.1
-0.15
-0.2
-0.25
-0.3
µcal/sec
0
20
40
60
80
100
Time (min)
0.2M KCl
0
-5
-10
-15
-20
-25
-30
-35
kcal/mol of injectant
0
0.5
1.0
1.5
2.0
Molar Ratio
0.2M KCl