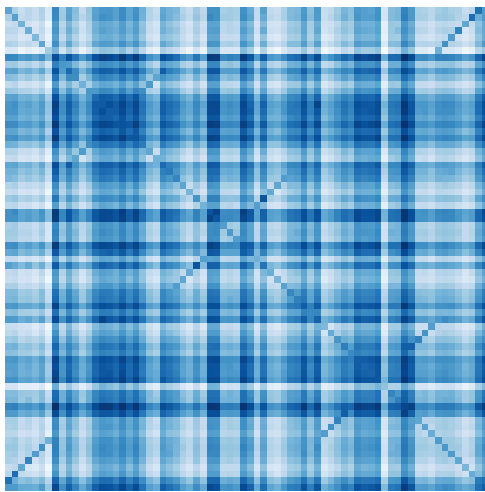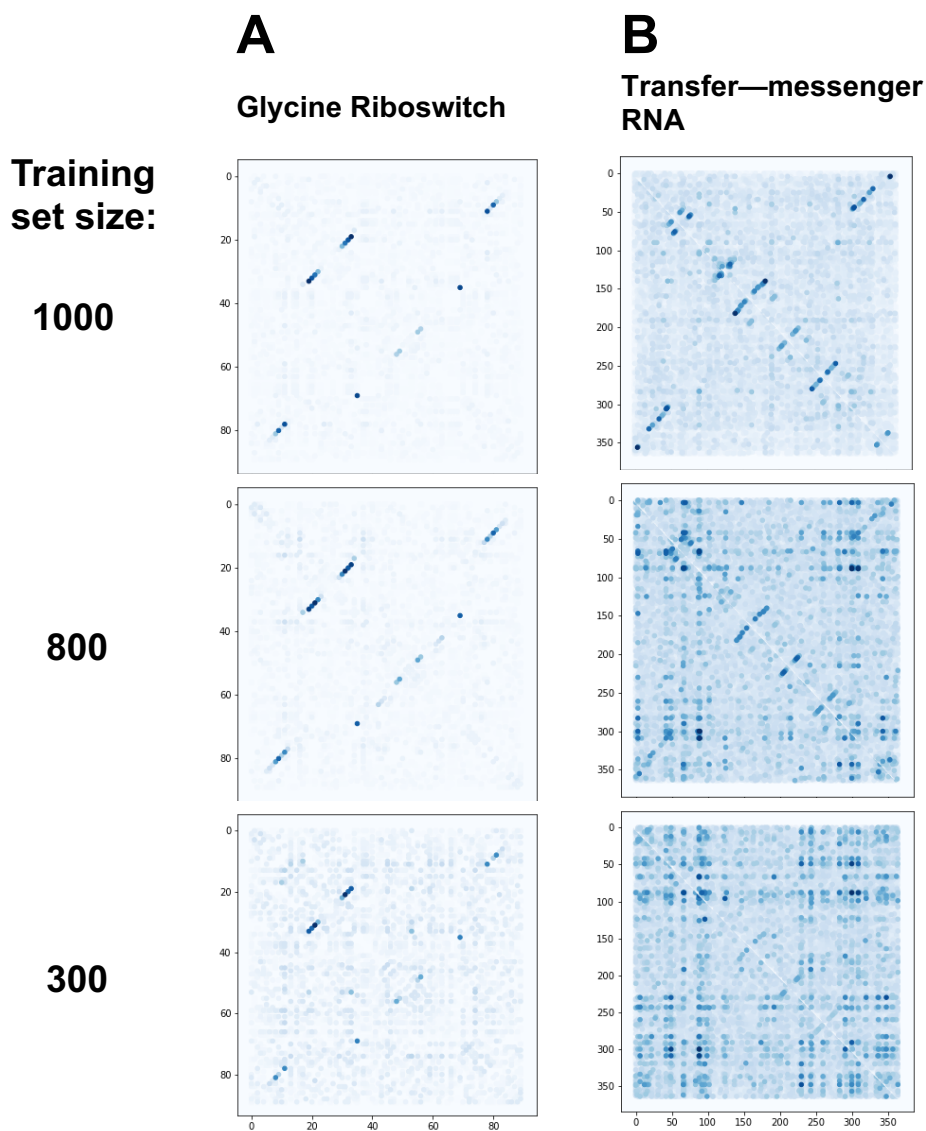# tRNA – RF00005

**Pre-APC correction**   **Post-APC correction**

Supplementary Figure 1: Example of noise reduction afforded by an APC correction on the SoM results for an MLP trained on the alignment for tRNA (RF0005). SoM scores are averaged across SoM on 500 sequences from the test set. Before the correction, there is a lot of background noise from reductions caused additive mutations in the rows and columns. An APC correction removes this noise making the scores associated with base pairs in the tRNA structure visible.

Supplementary Figure 2: Example SoM results from MLPs trained (A) Glycine Riboswitch – RF00504 (an alignment of 91 nucleotides in length) and (B) transfer-messenger RNA – RF00023 (an alignment of 366 length) at training set sizes of 1000, 800 and 300 sequences. The SoM results get less clear as the training size decreases for both families, suggesting that depth of training set is an important factor that influences an MLPs ability to learn structure. The results for MLPs trained on Glycine Riboswitch seems to be more robust to lower training sizes, suggesting that even with shallow training sets, an MLP can still learn structure if the alignment is short.

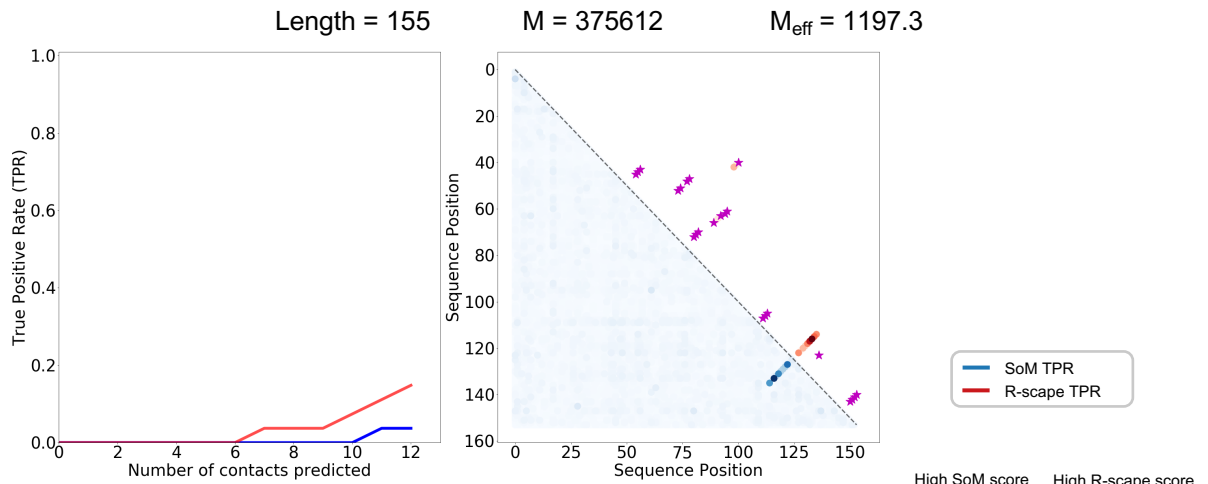# A - Metazoan signal recognition particle RNA (RF00017)

Length = 300   M = 22685 M_{eff} = 4358.5
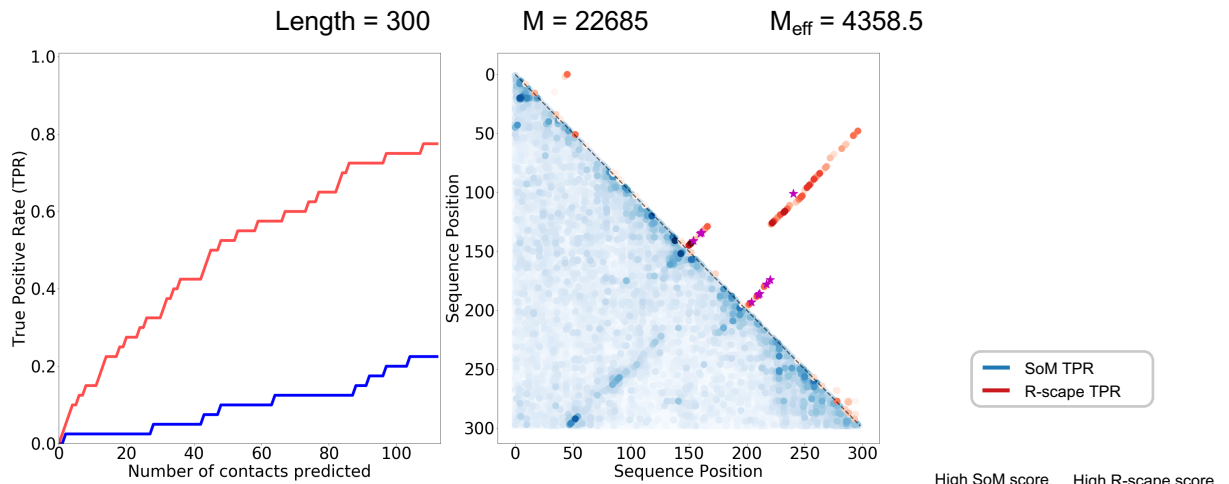
B - glmS glucosamine-6-phosphate activated ribozyme (RF00234)

Length = 161   M = 842 M_{eff} = 203.6
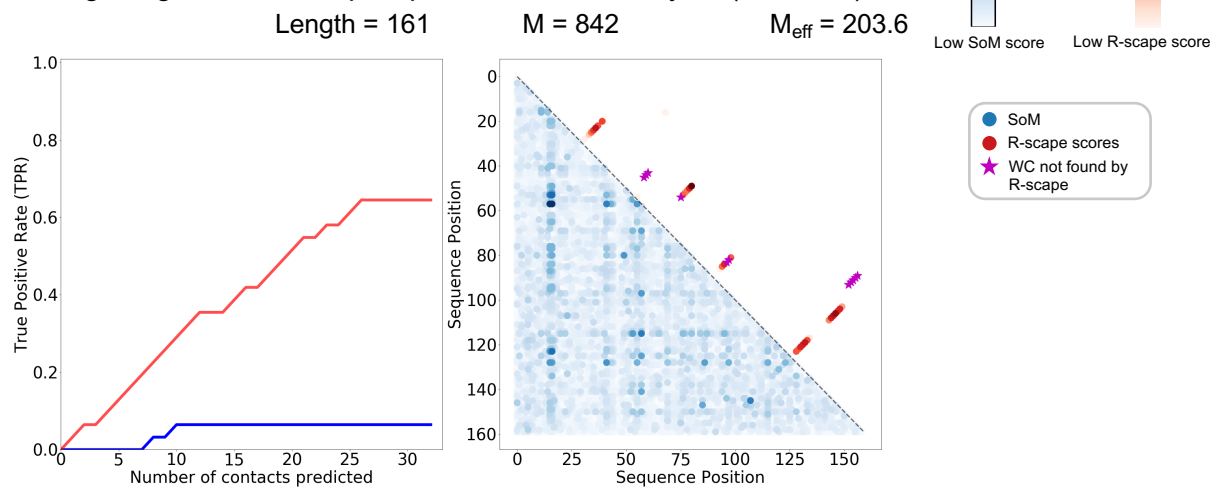
Supplementary Figure 3: continued on next page.

C - 5.8S ribosomal RNA (RF00002)

Length = 155   M = 375612 M_{eff} = 1197.3

D - SAM riboswitch (S box leader) (RF00162)

Length = 108   M = 4757 M_{eff} = 585.7
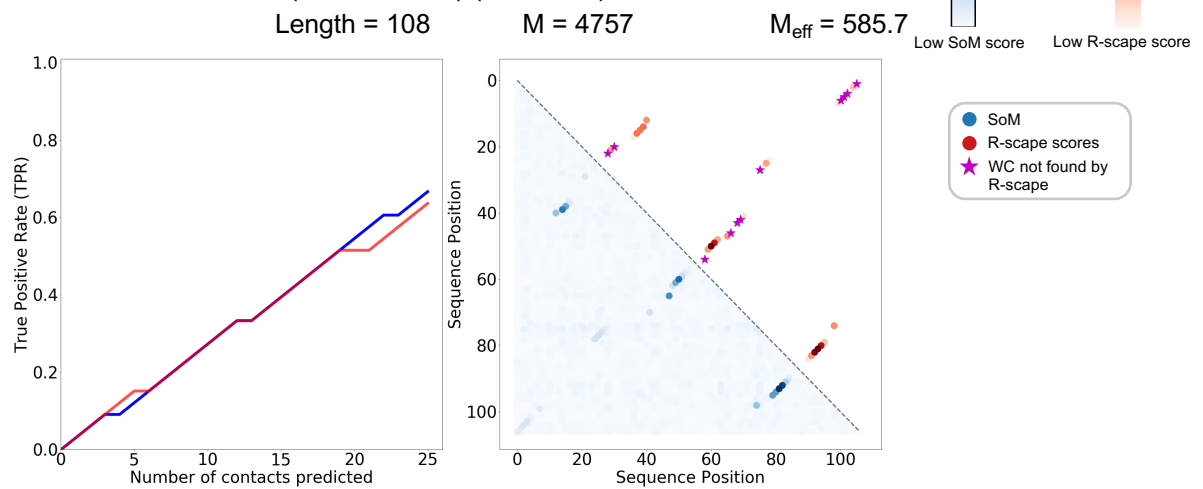
Supplementary Figure 3: ranked TPR graphs and plots of SoM scores and R-scape scores for interesting outliers of the summary TPR comparison (Figure 8), not shown in the main text: RF00017, RF00234, RF00002, RF00162.