

Supplemental Figure S2. Known structures of viral IRESes used for comparison

(A) The known structure of the HCV IRES, reconstructed from (Kieft et al. 1999). This isolate differs by 4nt from the probed structure, annotated in the figure. Cellular DMS-MaPseq data is superimposed for comparison to show local melting around the labeled translation start codon. AUROC between this structure and DMS-MaPseq data both in cells and *in vitro* is indicated. **(B)** The known structure of the EMCV IRES, reconstructed from (Pilipenko et al. 1989). The probed structure includes adjacent domains (D, E, F, and M). AUROC comparisons of the known structure to *in vitro* and cellular DMS-MaPseq data are included, and these values are computed across the shared regions of structure between the two models. In cell DMS-MaPseq data from this study is superimposed. Indexes are consistent with the probed structures.

