

Fig. S1: Our icSHAPE-prediction model. The model consists of a cascade of fully connected layers. It receives as input a 41 nt-long RNA sequence and outputs a predicted icSHAPE score for the center nucleotide.

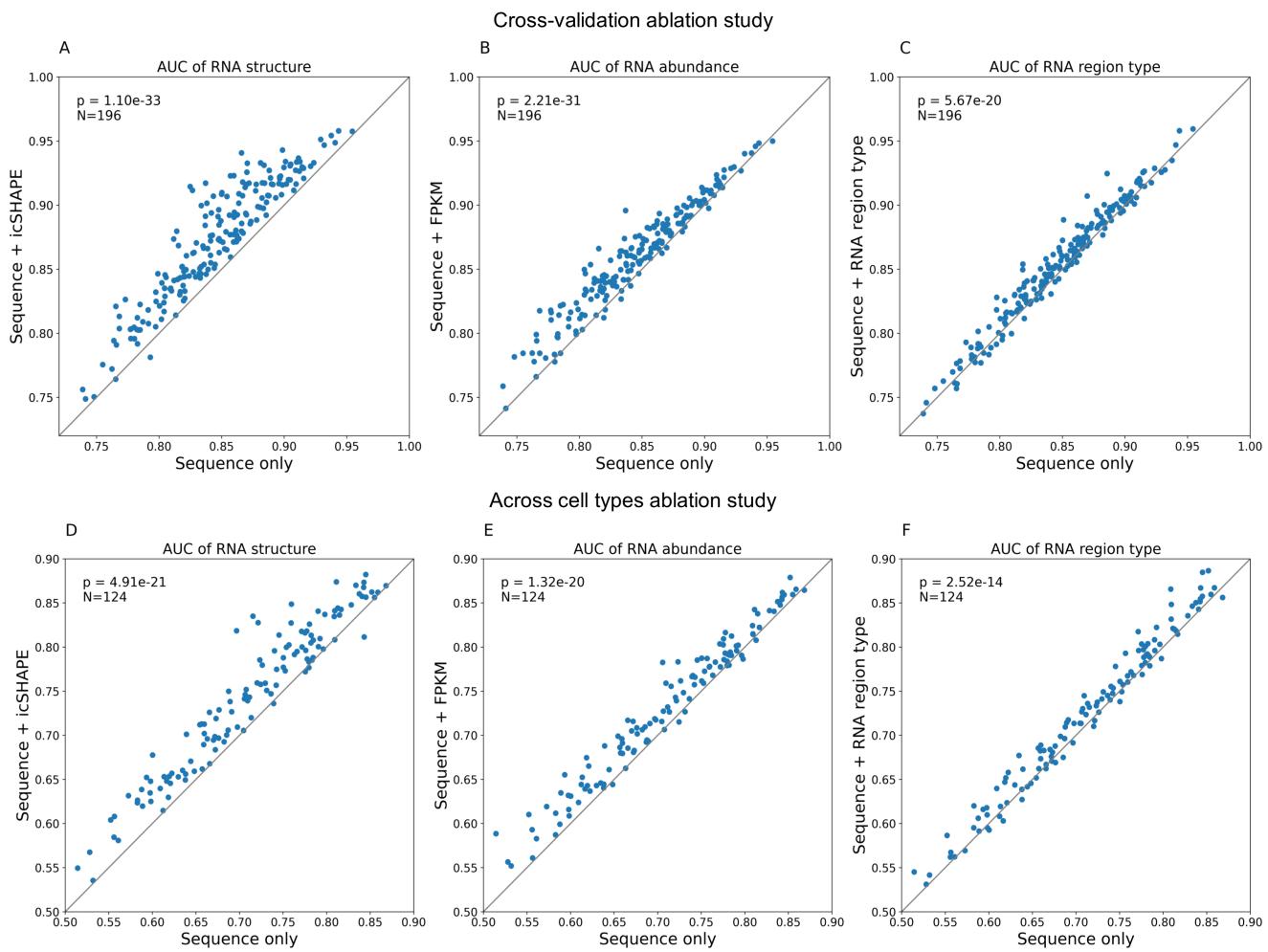


Fig. S2: Ablation analysis evaluating the contribution of each input feature. The contribution of each feature is compared to a sequence-only model in two different tests: cross-validation over 196 eCLIP experiments and across cell types over 124 experimental pairs. The input features compared are (A,D) RNA structure; (B,E) RNA abundance, and (C,F) RNA region types, respectively. Performance was evaluated on the test sets comprising 15% of the samples from each dataset.

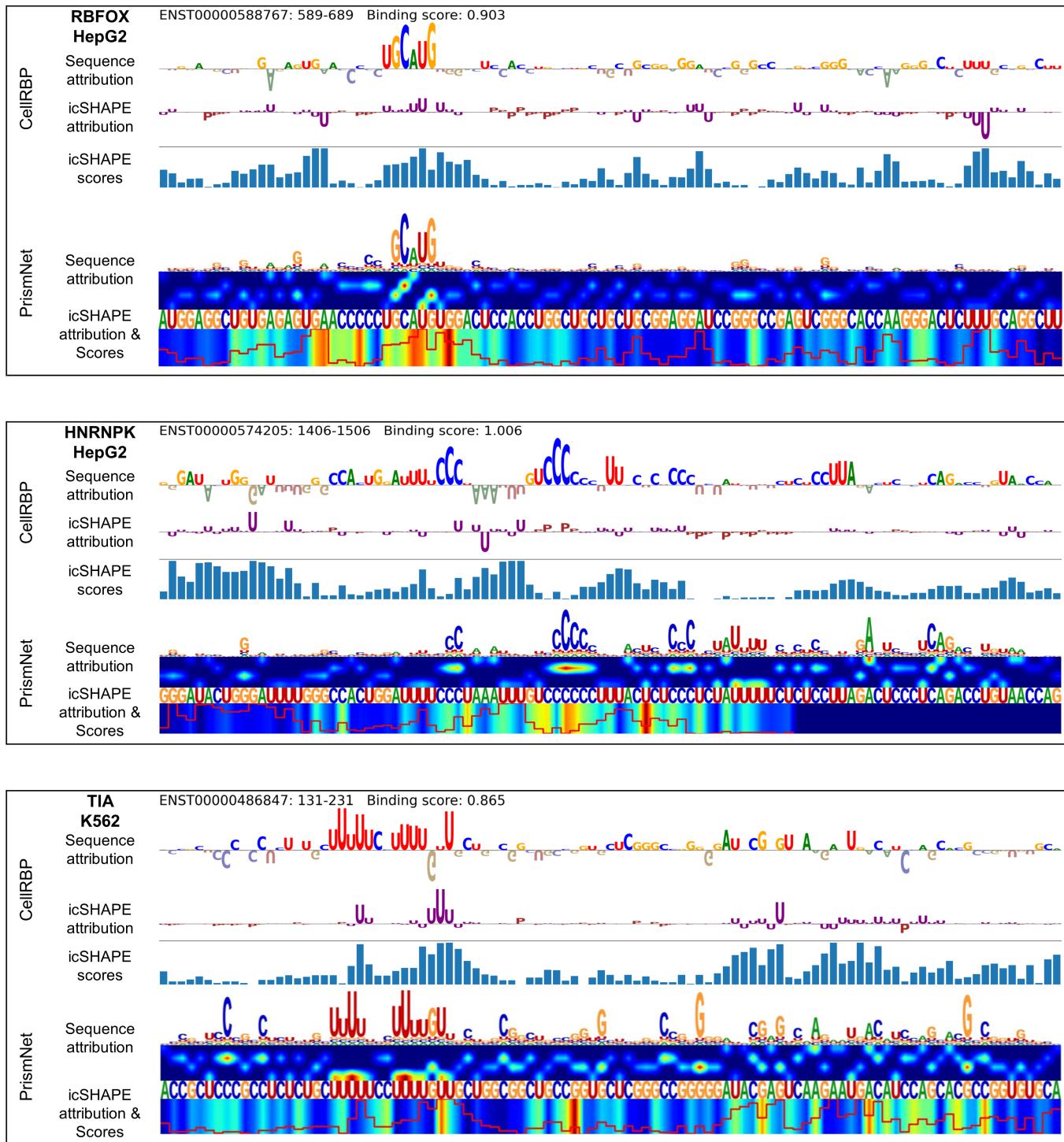


Fig. S3: Sequence and icSHAPE attribution scores accompanied by icSHAPE scores of RBFOX2 in HepG2, HNRNPK in HepG2 and TIA in K562. The title includes the RBP, cell type, transcript identifier, coordinates, and binding score predicted by CellRBP. The x-axis represents the nucleotide position, while the y-axis represents the sequence attribution scores, the icSHAPE attribution score, and the icSHAPE scores, in this order.

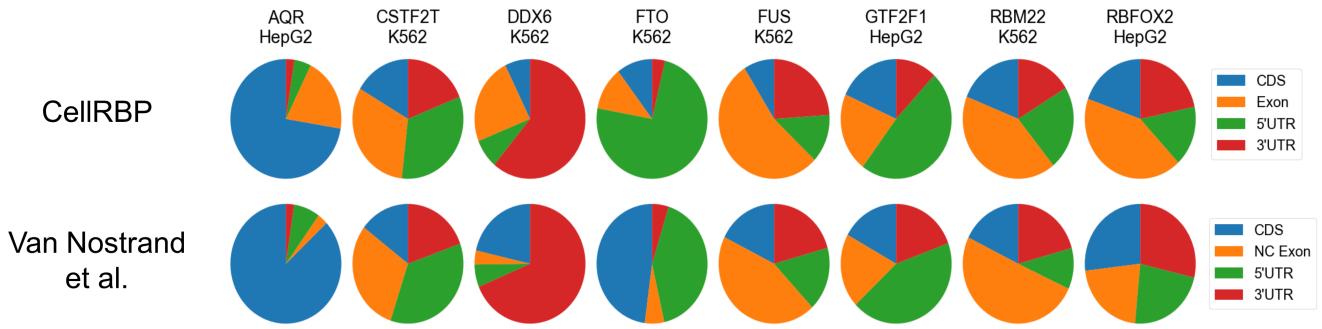


Fig. S4: Attribution scores of RNA region types are displayed as pie charts for selected RBPs. The figure of Van Nostrand et al. was adapted from (Van Nostrand et al., 2020) under a CC-BY 4.0 license.