RBPs	Sequence Motifs	RBPs	Sequence Motifs
ALKBH5	UCUCAUCCCAU AUAUCUCUCA CACCACCAUAACC	ELAVL1(A)	
C17ORF85	GUUGCAGGGGAA AAUCGCCUUUU CCCAAUUUACCG CCCAACAGC	ELAVL1(B)	
C22ORF28	CCGCACAUGUCAAUG AUAUUUUCAAUG GACACCGGUCCC UGUCGACACGAA	EWSR1	
CAPRIN1	UUUUUUUUUU AGCAAAAAAAUA GAACCCCCCCCCCCCC	FUS	
AGO2	UAUAAUAUUAUA AUAUUAUAAUAU GGCGGCGGGGGGGG	ELAVL1(C)	
ELAVL1		IGF2BP123	
SFRS1	GGGGGGGGGAAGG AAAAAAUAGGAA UUCCUACUCCC CCCUCCCCCC	MOV10	
HNRNPC		PUM2	
TDP43	AGGAAAAAAAAA AGGAAAAAAAAA GAAGGGGGGGGGG	QKI	
TIA1		TAF15	UAUUUUUUU AUAAAAAAAAAA SEEEEEEEEEE
TIAL1		PTB	
AGO1234	AAAUUUUUUAUA UUUAAAAAAUAU CCCCCCCCCCCCC	ZC3H7B	

**S4 Fig. Sequence motif calculated using max sequence response score as alignment center.** For sequence motif calculation, we followed procedures used in DeepBind with only using maximum response sequence. We calculated response values of each positive sample data, which went through first convolution layer combined with rectification (sequence response extraction point in Fig 2). In contrast to DeepBind procedure where sequence positions having response greater than zero, we only aligned maximum response value per single positive sequence. We also aligned sequence positions non-zero positive values, but improvements sequence motif extraction was not significant.

After aligning sequences, position frequency matrix (PFM) was calculated and softmax function was applied to PFM. Sequence LOGO representations were calculated using this PFM with -D transfac - F png -a AUGC -A rna -U probability --composition equiprobable -X False -Y False -S 1 -s large -- errorbars False --color green A 'A' --color orange G 'G' --color red U 'U' --color blue C 'C' option.