



Optimized motif	Location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	Protein array
	3'UTR	0.011	50.8	10/10	Y	↔	0.99	AAAAUAA	-	-
	5'	0.006	28.8	10/10	Y	↔	1.00	CACCTGC	SNAI_1, HLH_1.4	-
	5'	0.005	23.5	10/10	-	↔	0.33	CTAATCA	-	-
	5'	0.003	13.8	10/10	-	↔	0.24	TGGTAAC	-	-
	5'	0.003	12.4	9/10	-	-	0.52	ATAGTAA	DAF_19, MEF_2, PIE_1	-
	5'	0.003	12.6	7/10	-	-	0.29	TCTGACA	NHR_216, NHR-6_NHR_6, NHR_91 ...	-
	5'	0.003	11.4	6/10	Y	←	0.95	TTTGATC	PIE_1, NHR_216	-
	5'	0.006	28.3	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH_38 ...	-
	3'UTR	0.005	20.1	10/10	Y	→	1.00	UUUCCCC	-	-
	5'	0.004	18.1	10/10	-	↔	0.96	CTCTCTC	PIE_1	-
	5'	0.004	15.6	10/10	-	→	0.98	CTTCTTC	PIE_1	-