



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.019	86.3	10/10	Y	↔	1.00	AAAUAAA	-	-
	5'	0.004	21.2	10/10	-	↔	0.36	AACAGTA	SNPC_4.2, ODD_2, NHR_5	-
	5'	0.003	14.9	9/10	-	→	0.65	ACTATAC	-	-
	5'	0.003	13.9	8/10	-	↔	0.37	TGCCTAC	NHR_256_NHR_79, NHR_28_NHR_53_NHR_70	-
	5'	0.003	14.3	9/10	-	↔	0.59	ACATTAG	-	-
	5'	0.008	39.2	10/10	Y	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH-38 ...	-
	5'	0.007	33.0	10/10	Y	↔	1.00	CTGCGTC	-	-
	3'UTR	0.005	21.3	10/10	Y	↔	1.00	UUUCCCC	-	-