



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.011	55.8	10/10	Y	↔	0.99	AAAAUAA	-	-
	5'	0.003	14.7	9/10	-	←	0.95	TTGTGAC	NHR_84, NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, NHR_178_N	-
	5'	0.003	13.9	9/10	-	↔	0.61	AACTATA	UNC_39, NHR_109_NHR_12_NHR_16_NHR_273_NHR_86, NHR_28_NHR_53_NHR_7	-
	5'	0.005	27.6	10/10	Y	↔	1.00	AATCGAT	CEH_28, CEH-28, PIE_1	-
	5'	0.003	14.8	10/10	-	→	0.73	TTTCCTC	PIE_1	-
	5'	0.003	13.9	10/10	-	→	0.98	GCTCCAC	PIE_1, EFL_1, LIN_15B	-
	3'UTR	0.003	12.6	10/10	-	→	0.95	UUCCCCC	-	-
	5'	0.003	13.8	8/10	-	↔	0.49	CTACCAA	CEH_17, PIE_1	-
	5'	0.003	12.4	6/10	-	→	0.61	AACAGTA	-	-