



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.006	32.5	10/10	-	↔	0.91	ACTACAA	NHR_28_NHR_53_NHR_70, UNC_39, NHR_256_NHR_79 ...	
	5'	0.005	27.2	10/10	-	↔	0.80	TATGTAC	CES-2_CES_2.2, CES_2, ZIP_7	-
	5'	0.003	17.4	10/10	-	←	0.98	TGAATCA	PIE_1	-
	5'	0.002	11.7	7/10	Y	-	1.00	ACAGGTG	SNAI_1, HLH_1.4	-
	5'	0.006	29.9	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5'	0.005	25.8	10/10	-	→	0.94	TCTTCTC	PIE_1	-
	5'	0.004	20.1	10/10	-	↔	0.95	GGCCACC	CRH_2	-
	5'	0.002	11.1	7/10	-	→	0.46	TAATCCC	EOR_1, PIE_1	-