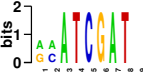
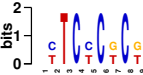
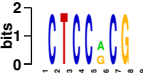
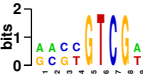




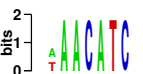


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.009	47.9	10/10	Y	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.004	18.0	10/10	-	↔	0.94	TTCTCTC	PIE_1	-
	5'	0.003	14.6	10/10	-	→	0.97	CTCCGCG	PIE_1	-
	5'	0.003	11.4	7/10	-	-	0.99	AGTGTCT	PIE_1	-
	5'	0.005	26.1	10/10	-	↔	0.84	TACCAAA	-	-
	5'	0.004	19.1	10/10	-	←	0.73	AAAGTTC	PIE_1, LIN-14, LIN-14_LIN_14	-
	5'	0.004	17.2	9/10	-	↔	0.49	ACAAATG	-	-
	5'	0.003	16.4	9/10	Y	↔	0.45	TTGTGAC	PIE_1, NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54	-
	5'	0.003	15.5	10/10	-	↔	0.88	AAACATC	FKH-9, PIE_1	-