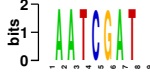
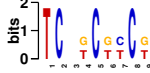
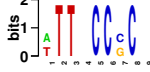
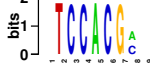
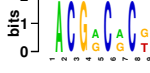
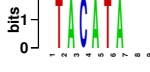
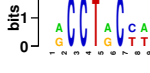

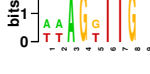


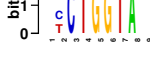
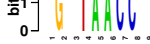


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.012	65.2	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.011	56.2	10/10	-	↔	0.99	CTGCGTC	PIE_1	-
	5'	0.005	23.8	10/10	Y	↔	0.71	TTTCCCC	EFL_1.3, EFL-1_EFL_1.2, EFL-1 ...	-
	5'	0.003	15.7	10/10	-	↔	0.98	TCCACGA	PIE_1, HLH_28_HLH_29	-
	5'	0.003	13.3	9/10	-	←	1.00	ACGACAC	-	-
	5'	0.008	42.6	10/10	-	↔	0.95	TACATAC	-	-
	5'	0.006	31.1	10/10	-	↔	0.75	GCCTACC	-	-
	5'	0.005	26.7	10/10	Y	↔	0.94	ACAGGTG	SNAI_1	-
	5'	0.004	22.3	10/10	-	↔	0.57	AAGTTTG	DMD_9, PIE_1	-
	5'	0.003	14.5	10/10	Y	→	0.99	CTGATAA	NHR_216, NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, PQM-1	-
	5'	0.003	14.1	9/10	-	←	0.98	TACGTGA	XBP_1	-
	5'	0.003	11.2	6/10	-	-	0.53	CCTGGTA	-	-
	5'	0.002	8.7	6/10	-	-	0.36	GGTAACC	PIE_1	-