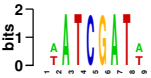
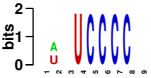
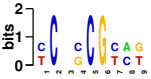
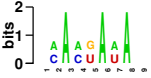
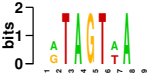
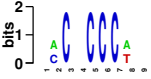

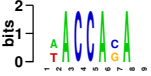


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.007	39.3	10/10	-	↔	1.00	AATCGAT	CEH-28, CEH_28, CEH-38 ...	-
	3'UTR	0.006	32.5	10/10	Y	↔	1.00	UUUCCCC	-	-
	5'	0.004	24.5	10/10	Y	→	1.00	CTGCGTC	-	-
	3'UTR	0.006	36.9	10/10	Y	→	0.99	AAAUAAA	-	-
	5'	0.003	19.9	10/10	-	←	0.44	ATAGTAA	DAF_19	-
	5'	0.003	17.3	10/10	Y	→	0.97	CCACCCA	KLF_1, KLF_3	-
	5'	0.002	11.4	7/10	-	-	0.78	ATGACTA	NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, JUN_1, NHR_84 ...	-
	5'	0.003	13.7	7/10	-	←	0.56	AACCAGA	-	-