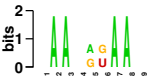
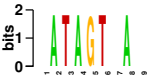
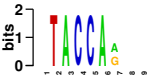





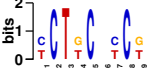
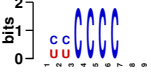
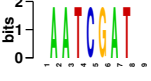
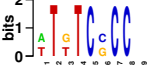

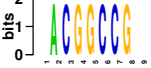


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.017	78.6	10/10	Y	↔	0.99	AAAAUAA	-	-
	5'	0.005	22.0	10/10	-	↔	0.47	ATAGTAA	-	-
	5'	0.005	21.3	10/10	-	↔	0.57	TACCAAA	TBX_40	-
	5'	0.004	19.2	10/10	-	↔	0.42	AGTATAA	MED_1_MED_2	-
	5'	0.003	14.7	10/10	-	←	0.61	AGGTAGG	NHR_2_NHR_85	-
	5'	0.003	15.0	10/10	Y	↔	0.93	ATGATCA	NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, EGL_38, PIE_1	-
	5'	0.003	12.2	9/10	Y	-	0.96	TACGTGA	ZIP_7, ATF_6	-
	5'	0.002	9.8	6/10	-	-	0.50	TGTTAGC	HAM_2, PIE_1	-
	5'	0.009	42.0	10/10	-	↔	1.00	CTGCGTC	FKH_10	-
	3'UTR	0.009	38.5	10/10	Y	↔	1.00	UUUUUUU	-	-
	5'	0.009	41.5	10/10	Y	↔	1.00	AATCGAT	CEH-38, CEH-28, CEH_28	-
	5'	0.003	13.7	9/10	Y	→	0.33	TTTCCCC	LIN-54, PIE_1	-
	5'	0.004	18.1	10/10	-	←	0.99	TCCACGA	HLH_28_HLH_29	-
	5'	0.003	11.8	8/10	-	→	0.55	ACGGCCG	-	-