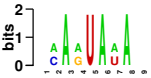


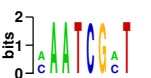
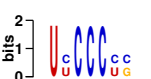
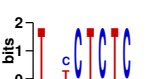
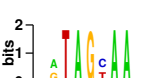



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.008	43.6	10/10	Y	→	0.99	AAAUAAA	-	-
	3'UTR	0.004	25.4	10/10	-	→	1.00	UAAUAAA	-	-
	5'	0.002	12.4	7/10	-	←	0.91	TTGTGAC	NHR_84, NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, MAB_9 ...	-
	5'	0.006	35.5	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-38, CEH-28 ...	-
	3'UTR	0.004	21.8	10/10	-	↔	1.00	UUCCCCC	-	-
	5'	0.003	16.2	10/10	-	→	0.97	TTCTCTC	EOR-1, EOR_1.2, PIE_1	-
	5'	0.003	16.8	10/10	-	→	0.73	ATAGCAA	DAF_19, MEF_2, PIE_1	-
	5'	0.002	12.4	7/10	-	←	0.30	TTGAAAC	SNPC_4.2, PIE_1	-