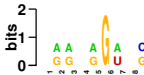
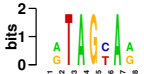
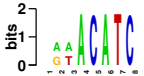
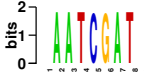
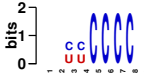
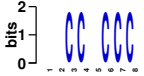
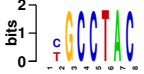
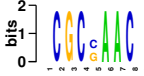


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.016	75.7	10/10	Y	↔	1.00	AAAAGUU	-	-
	5'	0.004	20.7	10/10	-	↔	0.88	ATAGTAA	MEF_2, DAF_19	-
	5'	0.004	16.9	10/10	-	↔	0.87	AAACATC	PIE_1, FKH_7_LET_381	-
	5'	0.005	24.6	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	3'UTR	0.004	16.7	10/10	-	→	1.00	AUCCCC	-	-
	5'	0.004	15.6	10/10	-	→	1.00	TCCTCCC	KLF_3, SPTF_3, KLF_1	-
	5'	0.003	12.7	8/10	-	↔	0.91	CGCCTAC	NHR_256_NHR_79	-
	5'	0.003	11.3	8/10	-	-	0.91	CGCCAAC	PIE_1	-