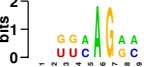

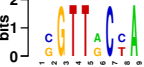
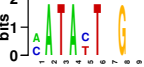
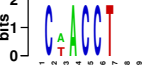
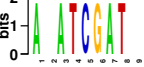
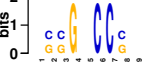
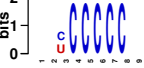


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.006	33.0	10/10	Y	→	0.94	UUUCAGA	-	-
	5'	0.005	26.1	10/10	Y	↔	0.94	CGTGGGA	-	-
	5'	0.004	20.5	10/10	Y	↔	0.96	CGTTGCC	DAF_19, PIE_1	-
	5'	0.003	14.4	10/10	-	-	0.56	ATATTTG	CEH_18, HLH_16, CEH_32	-
	5'	0.003	12.7	8/10	-	←	0.32	CAACCTA	-	-
	5'	0.005	26.5	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH-38 ...	-
	5'	0.005	25.1	10/10	Y	↔	0.94	CCGCCCC	-	-
	3'UTR	0.004	21.3	10/10	-	→	1.00	UUUUUUU	-	-