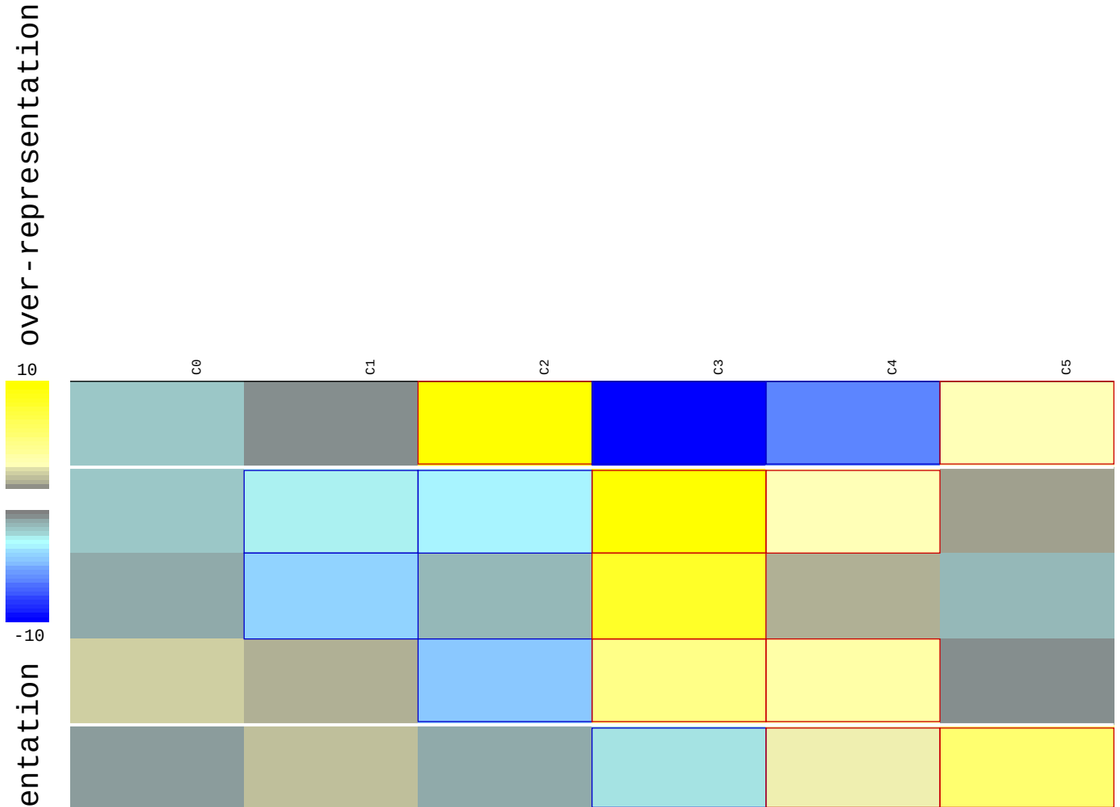
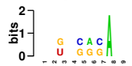
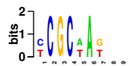
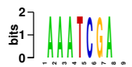
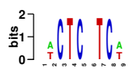
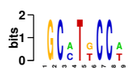


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3’UTR	0.011	64.8	10/10	Y	↔	0.98	UUUCAGA	-	-
	5’	0.003	19.8	10/10	-	↔	0.87	CGCAATA	-	-
	5’	0.003	15.8	10/10	-	↔	0.99	AAATCGA	CEH-38, CEH_28, CEH-28 ...	-
	5’	0.002	13.4	9/10	-	→	0.92	TCTCATC	PIE_1	-
	5’	0.002	10.2	6/10	-	-	0.45	GCCTGCC	-	-