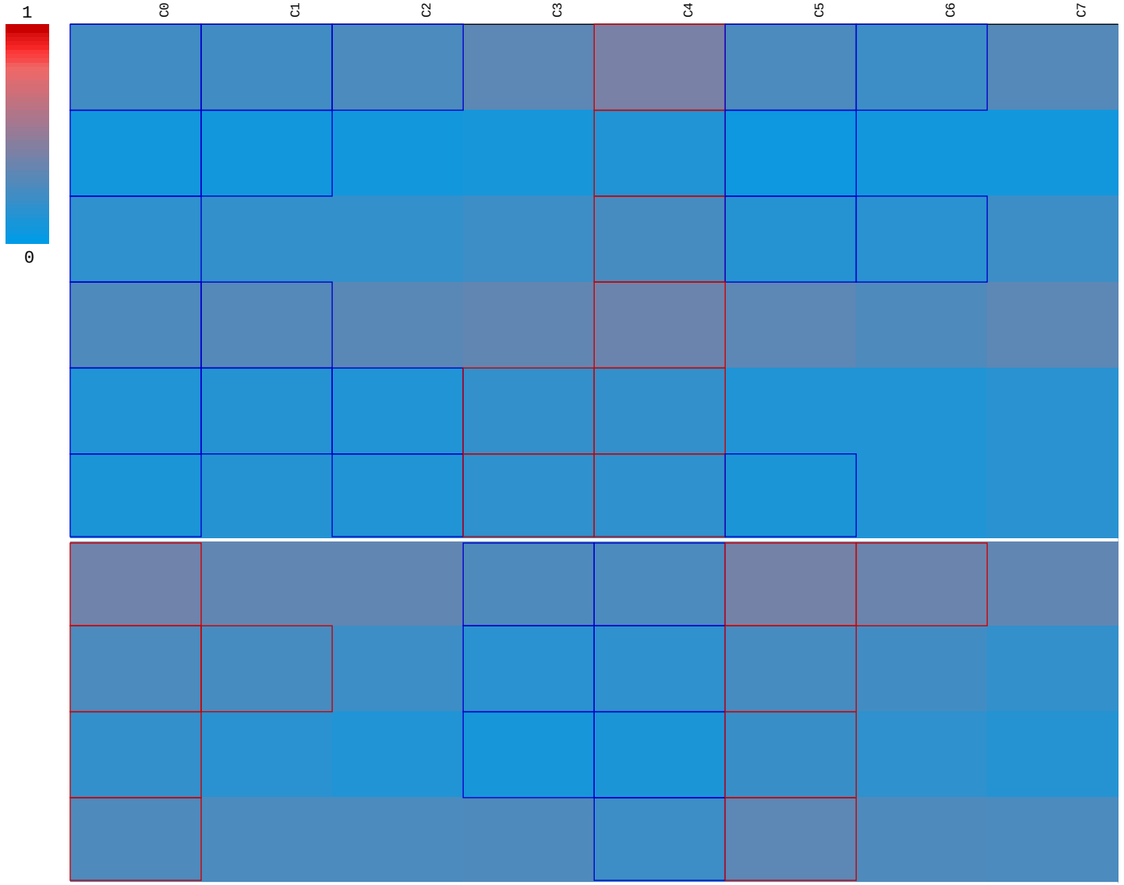
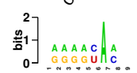
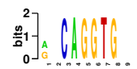
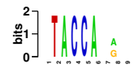
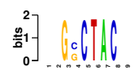
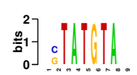
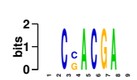
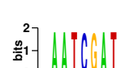
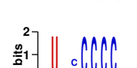
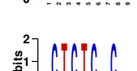


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3′UTR	0.024	119.5	10/10	Y	↔	0.99	AAAAUAA	-	-
	5′	0.005	26.8	10/10	Y	↔	1.00	ACAGGTG	SNAI_1, HLH_1.4	-
	5′	0.005	25.4	10/10	-	↔	0.74	CATATCA	HPO_39	-
	5′	0.004	22.6	10/10	-	↔	0.90	TACCAAA	TBX_40	-
	5′	0.004	22.7	10/10	-	↔	0.37	TGCCTAC	NHR_256_NHR_79, NHR_28_NHR_53_NHR_70	-
	5′	0.004	21.5	10/10	-	↔	0.37	CTATGTA	-	-
	5′	0.008	44.2	10/10	-	↔	0.99	ACGACGA	PIE_1	-
	5′	0.008	39.5	10/10	-	↔	1.00	AATCGAT	CEH-38, CEH_28, CEH-28 ...	-
	3′UTR	0.007	34.4	10/10	-	↔	0.99	UUUCCCC	-	-
	5′	0.004	17.9	10/10	Y	→	0.97	CTCTCAC	PIE_1	-