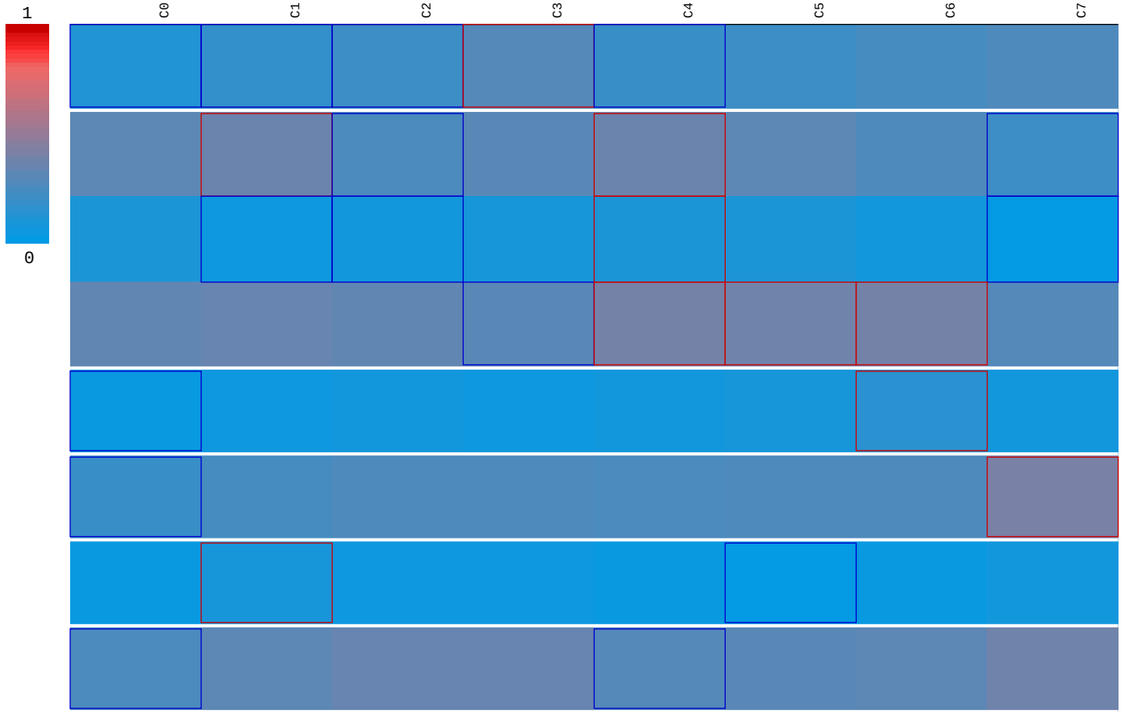
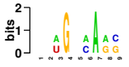
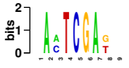
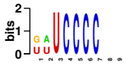
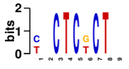
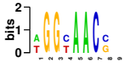
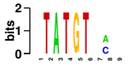
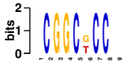
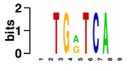


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3′UTR	0.010	49.7	10/10	Y	↔	0.99	UUGAAAA	-	-
	5′	0.004	20.9	10/10	-	↔	0.99	AATCGAT	CEH_28, CEH-28, PIE_1	-
	3′UTR	0.004	17.5	10/10	-	→	0.99	UUCCCCC	-	-
	5′	0.004	17.5	10/10	-	↔	0.98	ACTCTCT	PIE_1, EOR-1	-
	5′	0.003	14.1	10/10	Y	→	0.90	GGTAACC	PIE_1	-
	5′	0.003	14.0	9/10	-	←	0.47	TATGTAA	-	-
	5′	0.002	11.2	7/10	-	→	0.83	CGGCTCC	-	-
	5′	0.002	9.7	7/10	-	→	0.95	TTGATCA	NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, BCL_11, EGL_38	-