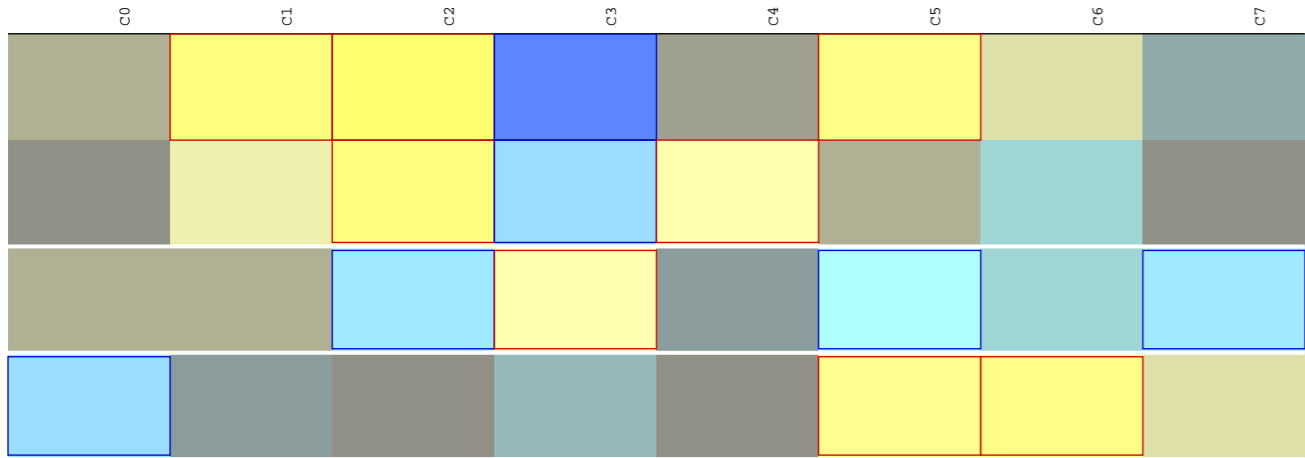


over-representation

representation



Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	Motif name	Protein array
	5'	0.004	21.8	10/10	-	↔	1.00	CTCCGCC	SPTF_3	-
	5'	0.003	12.1	7/10	-	←	0.92	AGATGAG	PIE_1	-
	5'	0.003	11.8	8/10	-	←	1.00	AATCGAT	CEH-28, CEH_28, CEH-38 ...	-
	5'	0.003	11.6	8/10	-	→	0.61	AACTTTG	NHR_69, NHR_64, PIE_1 ...	-