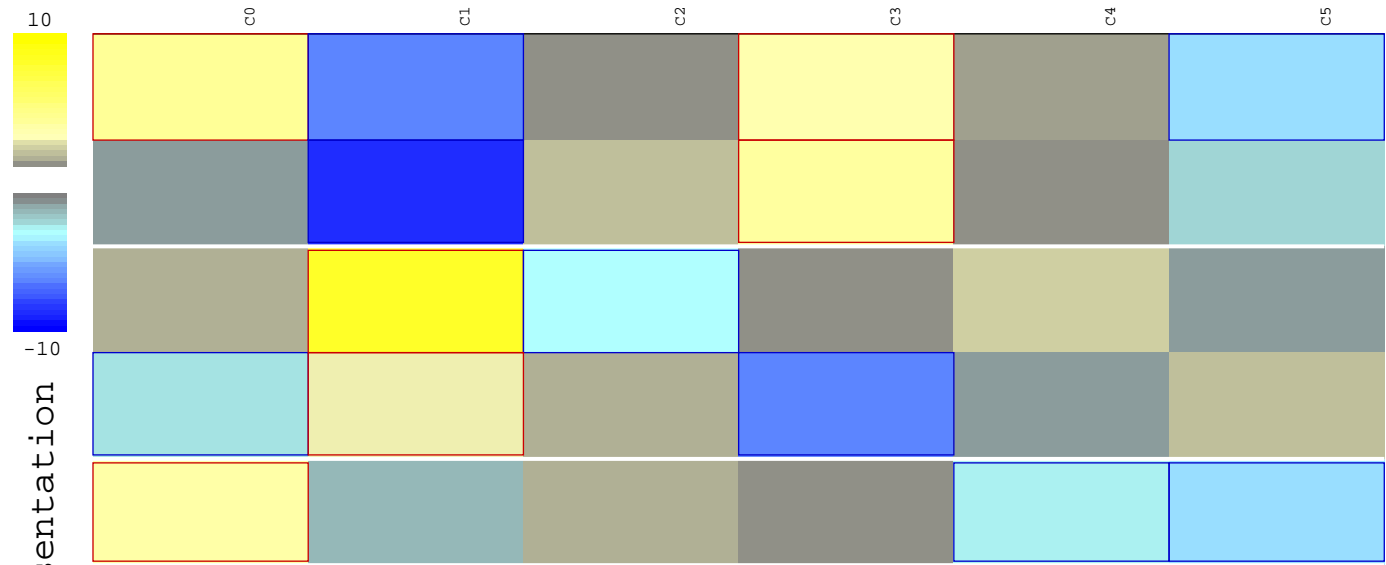


over-representation

representation



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.003	17.1	10/10	-	←	0.62	ACGATGA	PIE_1	-
	5'	0.003	15.7	10/10	-	→	0.99	AATCGAT	PIE_1	-
	5'	0.002	13.2	9/10	-	←	0.69	AAAGGTG	DMD_9, TBX_43, MAB_9	-
	5'	0.002	11.0	8/10	-	-	0.34	ACCAAAC	PIE_1	-
	5'	0.002	10.4	7/10	-	→	0.98	GACGCGC	Y44A6D.3, DPL_1, PIE_1	-