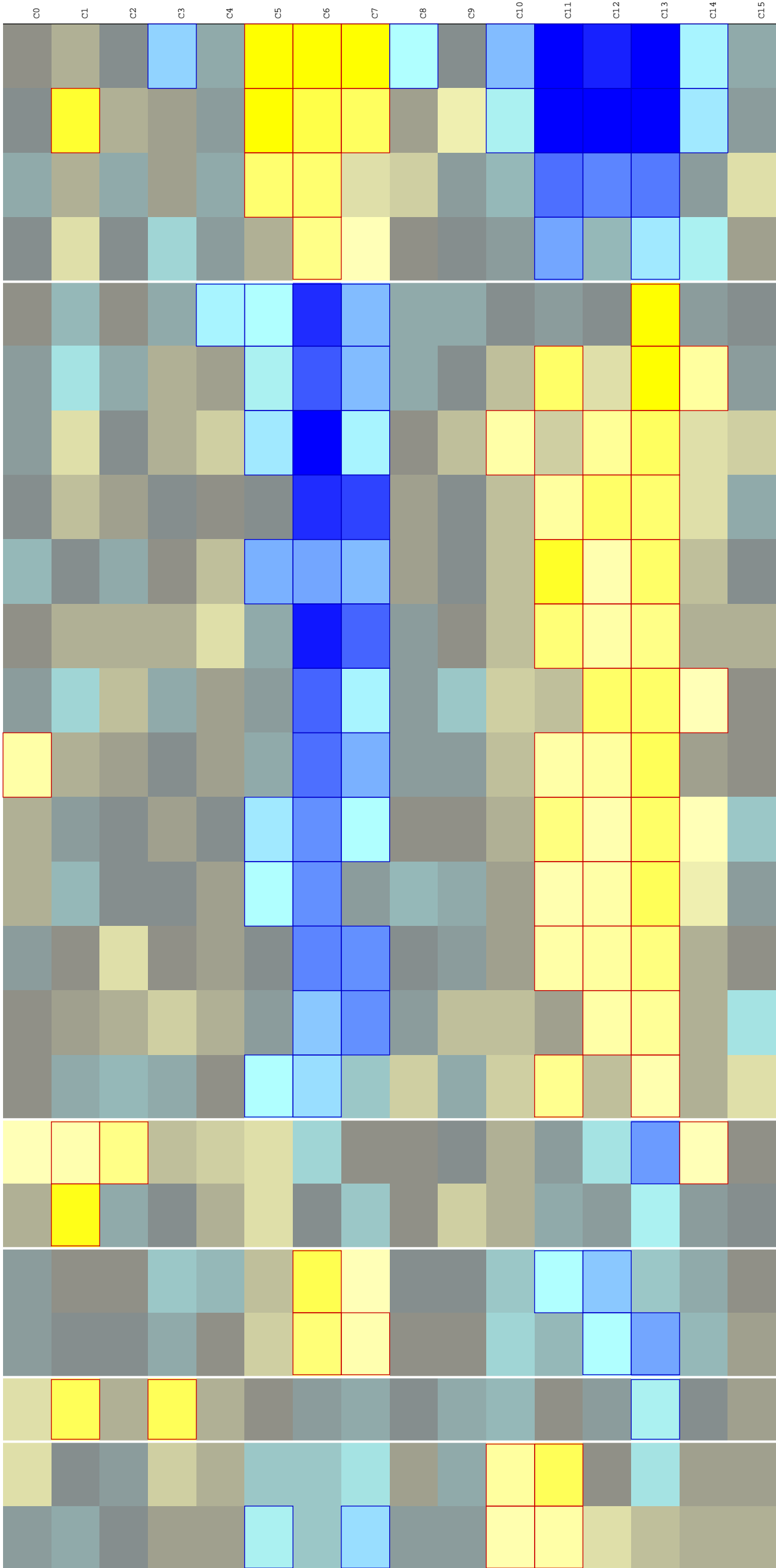


over-representation



under-representation



optimized motif	location	M _I (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.020	71.9	10/10	Y	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5'	0.016	58.1	10/10	Y	↔	1.00	CGTCGTC	-	-
	5'	0.007	23.5	10/10	-	↔	0.98	AGTGC GC	-	-
	5'	0.004	12.3	9/10	-	←	0.62	ACGGCCA	-	-
	5'	0.017	58.5	10/10	Y	↔	0.98	CAGGTGA	SNAI_1, PIE_1, BLMP_1.2	-
	5'	0.008	27.1	10/10	-	↔	0.56	AAGTTTG	PIE_1, DMD_9, TBX_39	-
	5'	0.007	24.9	10/10	Y	↔	0.79	ACATAAG	-	-
	5'	0.007	21.7	10/10	-	↔	0.45	ATACTAG	MEF_2	-
	5'	0.006	21.8	10/10	-	↔	0.79	TACCAAA	-	-
	5'	0.006	20.6	10/10	-	↔	0.58	TTACTCA	-	-
	5'	0.006	18.5	10/10	Y	↔	0.97	TTTGATC	NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, NHR_119_NHR_31_NHR_32	-
	5'	0.005	17.2	10/10	-	↔	0.70	TATATGA	-	-
	5'	0.005	16.3	10/10	-	↔	0.66	AACTACA	UNC_39	-
	5'	0.005	14.3	10/10	-	↔	0.61	AATGTTA	PIE_1, FKH-9, SOX_2_SOX_3	-
	5'	0.005	14.5	10/10	-	↔	0.27	AACCATA	CHE_1.2	-
	5'	0.004	12.8	10/10	-	↔	0.16	ATAGGCA	-	-
	5'	0.004	10.9	7/10	-	→	0.52	CCAAGTA	TBX_40	-
	5'	0.004	12.7	9/10	-	←	0.85	AAACGAA	PIE_1	-
	5'	0.003	9.1	7/10	-	→	0.53	CCCGCTC	KLU_2, PIE_1	-
	5'	0.004	11.7	9/10	-	→	0.74	AATCGCG	PIE_1	-
	5'	0.004	10.8	8/10	-	←	0.98	TCCGCAA	MAB_3, PIE_1	-
	5'	0.004	10.9	8/10	-	↔	0.91	AGGGACC	PIE_1	-
	5'	0.004	10.2	6/10	-	→	1.00	TCCGCCC	KLF_1, KLF_3, SPTF_3 ...	-
	5'	0.003	8.2	8/10	-	-	0.72	CCTATAA	-	-