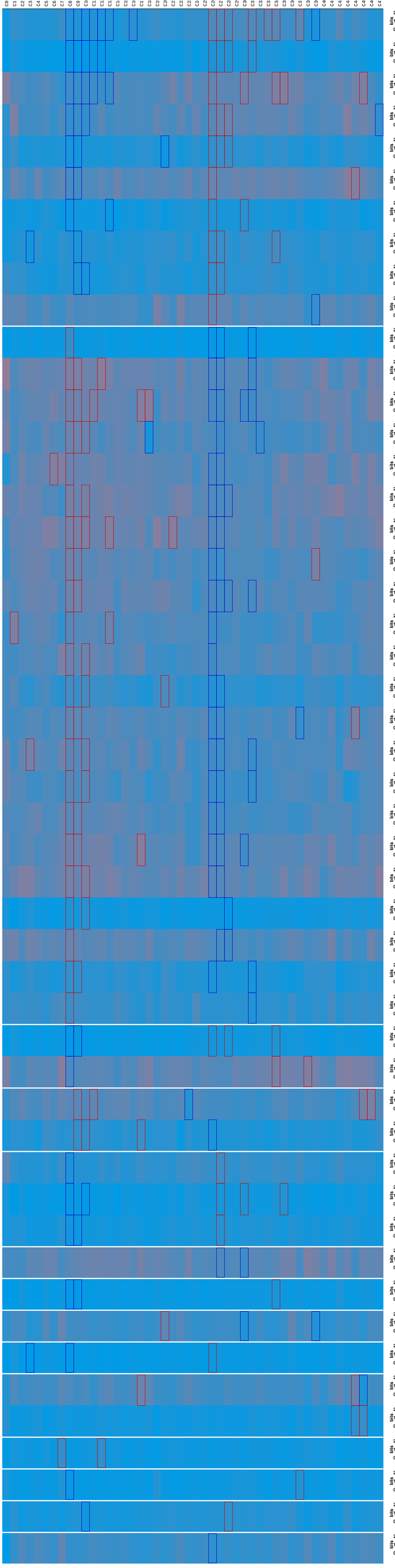

optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5′	0.024	46.1	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5′	0.016	28.3	10/10	-	↔	1.00	CGCTCTA	EFL_1, LIN_15B, PIE_1	-
	5′	0.015	27.9	10/10	-	↔	1.00	ACGCAGA	KLU_2	-
	5′	0.014	25.8	10/10	Y	↔	0.99	CGTCGTC	PIE_1	-
	5′	0.010	15.9	10/10	-	↔	0.98	TCGCGAA	PIE_1, DPY-27_DPY_27, DPY-27	-
	5′	0.008	12.7	10/10	-	→	0.55	TTTCGCC	BLMP_1.2, PIE_1	-
	5′	0.008	11.8	10/10	Y	←	1.00	CGCAAAC	PIE_1	-
	5′	0.008	12.0	10/10	-	↔	0.85	AGCGAAA	PIE_1, FKH_10	-
	5′	0.007	10.6	10/10	-	→	0.84	AATCGAC	PIE_1	-
	5′	0.006	8.7	8/10	-	→	0.94	CCTGAAA	PIE_1	-
	5′	0.021	38.7	10/10	Y	↔	0.98	CAGGTGA	SNAI_1, PIE_1, BLMP_1.2	-
	5′	0.012	20.0	10/10	-	↔	0.90	TACCAAA	TBX_40	-
	5′	0.011	19.7	10/10	-	↔	0.80	ATATGTA	-	-
	5′	0.010	16.3	10/10	Y	↔	0.61	ATGATTA	-	-
	5′	0.010	16.3	10/10	-	↔	0.54	TGCCTAC	-	-
	5′	0.010	16.4	10/10	-	↔	0.53	CAAACTA	TTX-3dmCEH-10, CEH-10dmTTX-3, PIE_1 ...	-
	5′	0.010	16.1	10/10	-	↔	0.85	AAGTTCA	PIE_1	-
	5′	0.010	15.6	10/10	-	↔	0.44	AAGTTTG	TBX_39, NSY_7, PIE_1	-
	5′	0.009	14.9	10/10	Y	←	0.35	ATACTAG	MEF_2, DMD_4, DAF_19	-
	5′	0.009	13.3	10/10	-	↔	0.41	CTAATGA	VAB_3, CEH_7, TTX_3 ...	-
	5′	0.009	13.3	10/10	-	↔	0.81	TATGTGA	CDC_5L, ZIP_7	-
	5′	0.008	12.3	10/10	-	←	0.29	CAAAGTA	PIE_1	-
	5′	0.008	12.0	10/10	-	↔	0.44	AAAGTTG	PIE_1	-
	5′	0.008	11.9	10/10	-	↔	0.34	ATGTCTA	SMA_4	-
	5′	0.008	11.5	10/10	-	←	0.09	TAAGATC	PIE_1	-
	5′	0.008	11.7	9/10	Y	↔	0.78	TTACTCA	-	-
	5′	0.008	11.6	10/10	Y	↔	0.30	TAACTCA	-	-
	5′	0.007	11.2	10/10	-	→	0.34	CAAATCA	PIE_1	-
	5′	0.007	10.4	9/10	-	↔	0.20	CATAGCA	HAM_2	-
	5′	0.007	10.7	9/10	-	→	0.23	TTTGACA	UNC-62, PIE_1, BNC_1	-
	5′	0.007	10.2	10/10	-	→	0.63	TTACTAC	DMD_4	-
	5′	0.005	6.1	7/10	-	-	0.71	ATATCAT	SKN-1_SKN_1.4, SKN-1, SKN_1 ...	-
	5′	0.009	12.7	10/10	-	↔	0.98	TCGTTGC	CES_2, ZIP_8	-
	5′	0.008	11.8	10/10	-	←	0.92	AAAAGAG	PIE_1, EOR-1, EOR_1.2	-
	5′	0.008	12.1	10/10	-	←	0.59	TATATGA	HLH_10	-
	5′	0.007	9.7	10/10	-	→	0.27	ACATGTA	UNC-62, ZTF_9	-
	5′	0.008	11.5	9/10	-	←	0.87	ACGAGAA	PIE_1	-
	5′	0.008	11.2	10/10	-	↔	0.94	ATTGCGA	PIE_1, PAL-1_PAL_1, CEBP-1 ...	-
	5′	0.005	6.4	6/10	-	-	0.83	CGAACGA	LIN-14_LIN_14, LIN-14, PIE_1	-
	5′	0.007	9.6	7/10	-	→	0.34	CTAGAAC	CEH_90	-
	5′	0.007	8.8	9/10	-	←	0.93	CGGTCGC	PIE_1	-
	5′	0.007	9.1	8/10	-	←	0.52	ACCAGCT	-	-
	5′	0.006	8.4	7/10	Y	←	0.56	ACGGCCG	-	-
	5′	0.006	8.8	9/10	Y	←	0.65	ATGAGCA	LIN_15B, PHA-4_PHA_4.2, PHA-4 ...	-
	5′	0.005	6.4	6/10	-	→	0.53	CCCGCTC	KLU_2, PIE_1	-
	5′	0.006	8.4	7/10	-	-	0.97	CACCCAC	KLF_1, KLF_3, KLU_2 ...	-
	5′	0.006	8.0	7/10	-	→	0.86	AACGCGG	PIE_1, MADF_9	-
	5′	0.006	7.8	6/10	-	→	0.71	CGCAAGC	FKH_10	-
	5′	0.006	7.8	6/10	-	←	0.50	ATAGAAG	PIE_1	-