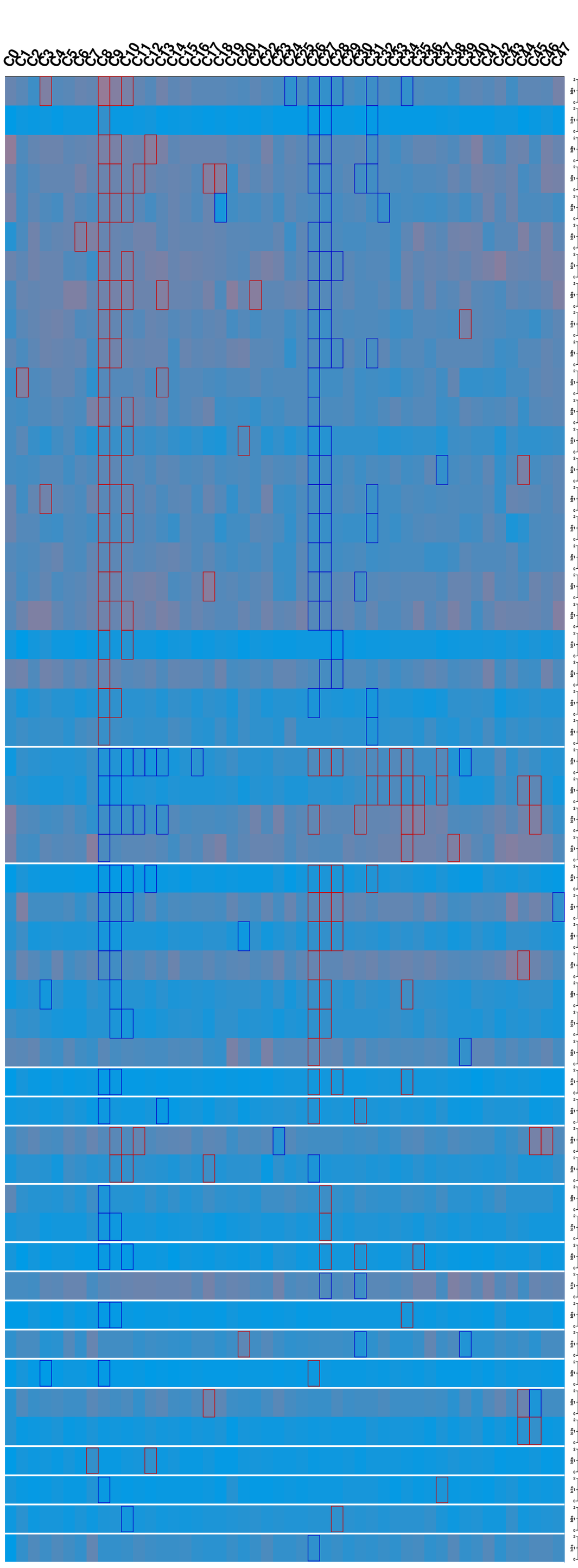

motif	location	MI (bits)	z-score	seed	motif name
	3'UTR	0.036	67.5	AAAAUAA	-
	5'	0.021	38.7	CAGGTGA	SNAI_1, PIE_1, BLMP_1.2
	5'	0.012	20.0	TACCAAA	TBX_40
	5'	0.011	19.7	ATATGTA	-
	5'	0.010	16.3	ATGATTA	-
	5'	0.010	16.3	TGCCTAC	-
	5'	0.010	16.4	CAAACTA	TTX-3dmCEH-10, CEH-10dmTTX-3, PIE_1 ...
	5'	0.010	16.1	AAGTTCA	PIE_1
	5'	0.010	15.6	AAGTTTG	TBX_39, NSY_7, PIE_1
	5'	0.009	14.9	ATACTAG	MEF_2, DMD_4, DAF_19
	5'	0.009	13.3	CTAATGA	VAB_3, CEH_7, TTX_3 ...
	5'	0.009	13.3	TATGTGA	CDC_5L, ZIP_7
	5'	0.008	12.3	CAAAGTA	PIE_1
	5'	0.008	12.0	AAAGTTG	PIE_1
	5'	0.008	11.9	ATGTCTA	SMA_4
	5'	0.008	11.5	TAAGATC	PIE_1
	5'	0.008	11.7	TTACTCA	-
	5'	0.008	11.6	TAACTCA	-
	5'	0.007	11.2	CAAATCA	PIE_1
	5'	0.007	10.4	CATAGCA	HAM_2
	5'	0.007	10.7	TTTGACA	UNC-62, PIE_1, BNC_1
	5'	0.007	10.2	TTACTAC	DMD_4
	5'	0.005	6.1	ATATCAT	SKN-1_SKN_1.4, SKN-1, SKN_1 ...
	5'	0.024	46.1	AATCGAT	PIE_1, CEH_28, CEH-28 ...
	3'UTR	0.017	29.3	UUCCCCC	-
	5'	0.015	27.9	ACGCAGA	KLU_2
	5'	0.008	11.8	AAAAGAG	PIE_1, EOR-1, EOR_1.2
	5'	0.016	28.3	CGCTCTA	EFL_1, LIN_15B, PIE_1
	5'	0.014	25.8	CGTCGTC	PIE_1
	5'	0.010	15.9	TCGCGAA	PIE_1, DPY-27_DPY_27, DPY-27
	5'	0.008	12.7	TTTCGCC	BLMP_1.2, PIE_1
	5'	0.008	12.0	AGCGAAA	PIE_1, FKH_10
	5'	0.007	10.6	AATCGAC	PIE_1
	5'	0.006	8.7	CCTGAAA	PIE_1
	5'	0.009	12.7	TCGTTGC	CES_2, ZIP_8
	5'	0.008	11.8	CGCAAAC	PIE_1
	5'	0.008	12.1	TATATGA	HLH_10
	5'	0.007	9.7	ACATGTA	UNC-62, ZTF_9
	5'	0.008	11.5	ACGAGAA	PIE_1
	5'	0.005	6.4	CGAACGA	LIN-14_LIN_14, LIN-14, PIE_1
	5'	0.008	11.2	ATTGCGA	PIE_1, PAL-1_PAL_1, CEBP-1 ...
	5'	0.007	9.6	CTAGAAC	CEH_90
	5'	0.007	8.8	CGGTCGC	PIE_1
	5'	0.007	9.1	ACCAGCT	-
	5'	0.006	8.4	ACGGCCG	-
	5'	0.006	8.8	ATGAGCA	LIN_15B, PHA-4_PHA_4.2, PHA-4 ...
	5'	0.005	6.4	CCCGCTC	KLU_2, PIE_1
	5'	0.006	8.4	CACCCAC	KLF_1, KLF_3, KLU_2 ...
	5'	0.006	8.0	AACGCGG	PIE_1, MADF_9
	5'	0.006	7.8	CGCAAGC	FKH_10
	5'	0.006	7.8	ATAGAAG	PIE_1

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