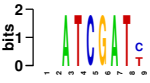

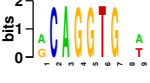
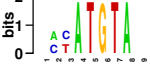
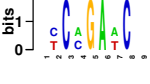
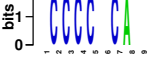
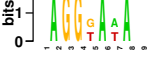
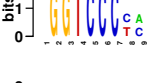
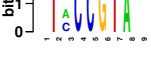


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.007	41.9	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5'	0.004	25.9	10/10	-	↔	1.00	GAGACGC	-	-
	5'	0.004	20.9	10/10	Y	↔	1.00	CAGGTGA	SNAI_1, HLH_1.4, UNC-62	-
	5'	0.003	19.8	10/10	-	↔	0.77	ATATGTA	ZTF_9	-
	5'	0.003	14.7	10/10	-	→	0.41	TCAGAAC	PIE_1	-
	5'	0.003	17.2	10/10	-	→	0.21	CCCCACA	KLU_2	-
	5'	0.003	14.3	7/10	-	→	0.09	AGGGAAA	-	-
	5'	0.002	9.7	6/10	-	-	0.49	GGTCCCC	EOR_1, PIE_1	-
	5'	0.002	11.5	6/10	-	←	0.94	TACCGTA	LSL_1, LSY_2	-