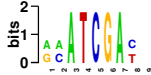
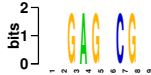

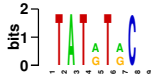
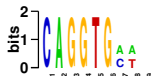

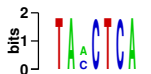
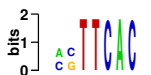



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.008	42.7	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, PIE_1	-
	5'	0.005	22.7	10/10	-	↔	1.00	AGAGACG	PIE_1	-
	5'	0.004	22.4	10/10	-	↔	0.46	TACCAAA	TBX_40, PIE_1	-
	5'	0.003	15.8	10/10	Y	↔	0.88	TATGTAC	HLH_10, PHA_4	-
	5'	0.003	14.6	9/10	Y	→	0.98	AGGTGAA	SNAI_1	-
	5'	0.003	13.6	9/10	-	←	0.94	TTGTGAC	NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, NHR_84, NHR_65 ...	-
	5'	0.003	13.4	8/10	-	←	0.24	TAACTCA	B0310.2, PIE_1, CDC_5L	-
	5'	0.002	9.4	7/10	-	-	0.84	AGTTCAC	MAB_9, PIE_1, NHR_69	-
	5'	0.002	9.7	8/10	-	←	0.37	CTTAAAG	PIE_1	-