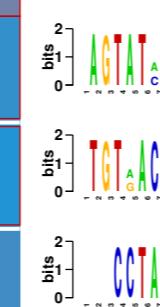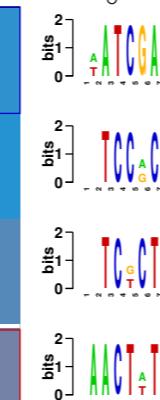| optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.005	26.5	10/10	–	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	–
	5'	0.004	18.8	10/10	–	→	0.98	CTCCACG	PIE_1	–
	5'	0.004	17.5	10/10	–	→	0.98	TTCTCTC	EOR-1, EOR_1.2, PIE_1	–
	5'	0.003	14.8	10/10	–	↔	0.84	AACTTTG	NHR_69, ZTF_11, NHR_64 ...	–
	5'	0.003	13.5	10/10	–	←	0.48	AGTATAA	–	–
	5'	0.003	13.4	10/10	–	→	0.86	TGTGACC	PIE_1, NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, NHR_84 ...	–
	5'	0.003	13.4	9/10	–	←	0.04	TGCCTAC	–	–