



Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.004	23.9	10/10	-	↔	0.92	ATCGATA	PIE_1, NHR_110_NHR_117_NHR_125_NHR_143_NHR_177_NHR_180_NHR_55, BE	-
	5'	0.002	12.5	8/10	-	←	0.98	CTCCACG	EGRH_1_EGRH_2	-
	5'	0.003	15.6	10/10	-	←	0.57	ATAGCAA	HAM_2, DAF_19, PIE_1	-
	5'	0.002	13.2	8/10	-	-	0.92	TCCTCCC	-	-