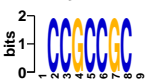

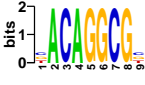

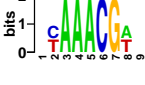
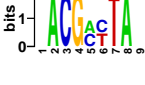
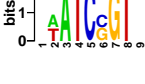
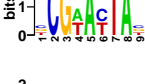
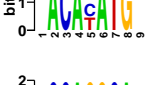



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.015	118.0	10/10	Y	-	-	CCGCCGC	-	-
	5'	0.004	31.4	10/10	-	-	-	TACGGAA	-	-
	5'	0.004	27.3	10/10	-	-	-	ACAGGCG	-	-
	5'	0.003	24.4	10/10	Y	-	-	GACTTCC	-	-
	5'	0.003	18.3	10/10	-	-	-	CAAACGA	-	-
	5'	0.002	16.4	10/10	-	-	-	ACGCCTA	-	-
	5'	0.002	15.5	10/10	-	-	-	AATCGGT	-	-
	5'	0.002	10.9	7/10	-	-	-	CGAACTA	-	-
	5'	0.004	28.9	10/10	-	-	-	ACACATG	-	-
	5'	0.002	12.1	8/10	Y	-	-	CCAGGCA	-	-