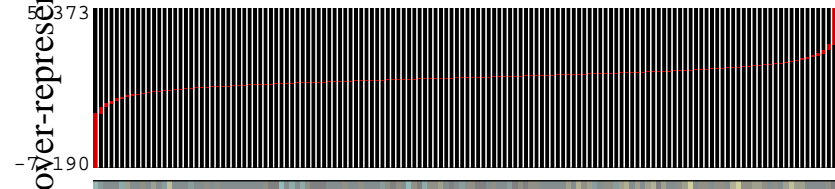
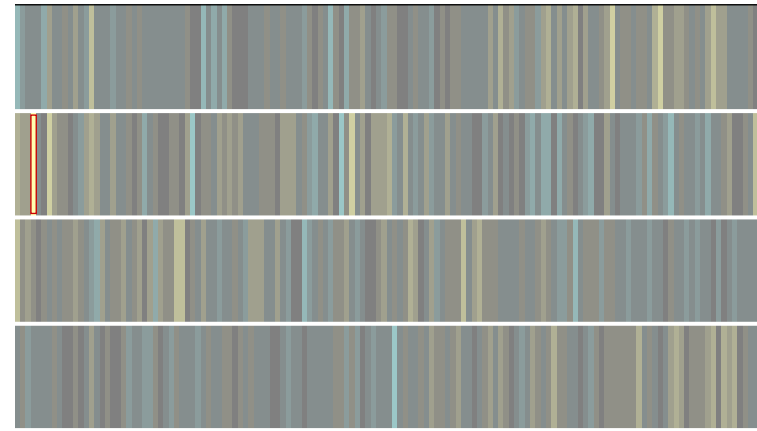


over-representation

Phosphatase-1 consensus site, p<1e-04



representation



DNA-dependent DNA replication, p<0.01
structural molecule activity, p<0.001

Optimized motif	Location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.015	8.9	10/10	-	-	1.00	AAATCGA	-
	3'UTR	0.014	7.8	7/10	Y	→	0.97	AAAUAAA	-
	5'	0.013	6.8	7/10	-	-	0.49	ATATGTA	-
	5'	0.013	6.4	8/10	-	-	1.00	AGACGCA	-