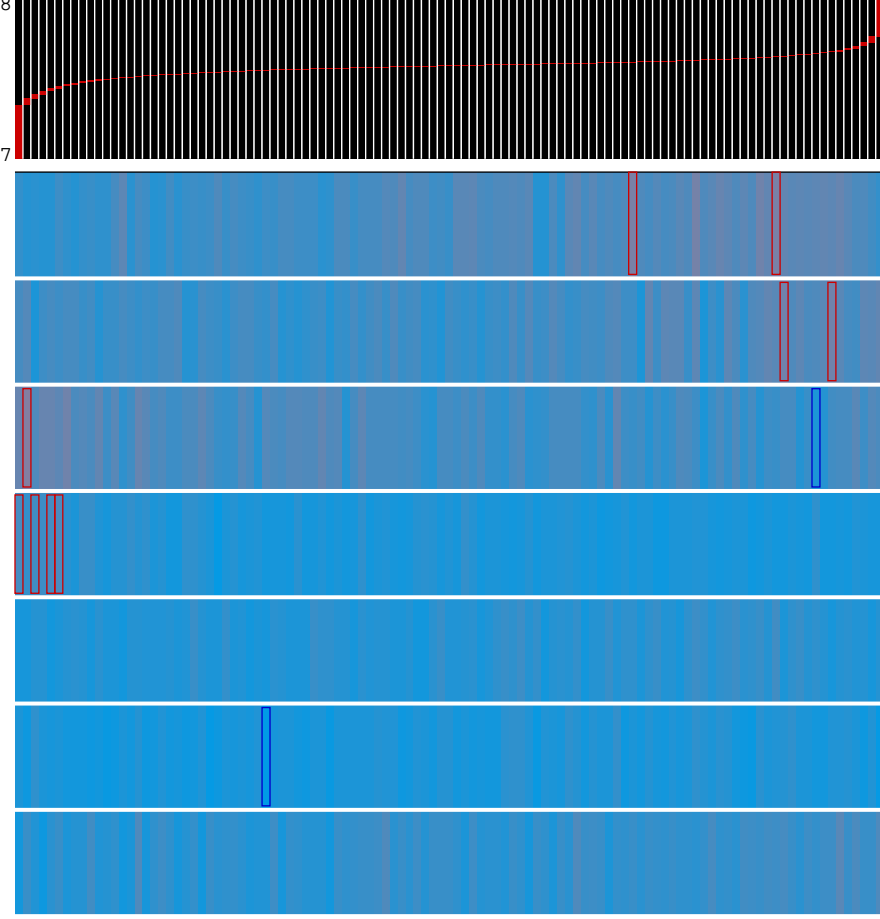


over-representation



under-representation

structural nucleic acid activity; P<0.01
cellular protein metabolic process; P<0.01
phosphate metabolism; P<0.001



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	3'UTR	0.018	11.7	10/10	-	→	1.00	UCCCAUC	-
	3'UTR	0.017	10.4	10/10	-	→	1.00	UGUAU	-
	3'UTR	0.017	9.9	10/10	Y	→	0.99	GAAUAAA	-
	5'	0.016	8.6	8/10	Y	→	0.98	ACGTGAA	-
	5'	0.015	8.6	9/10	-	←	0.99	ACGAAGA	-
	5'	0.015	7.7	7/10	-	→	1.00	AATCGAT	-
	5'	0.014	6.7	6/10	-	→	0.78	TCGTTGC	-