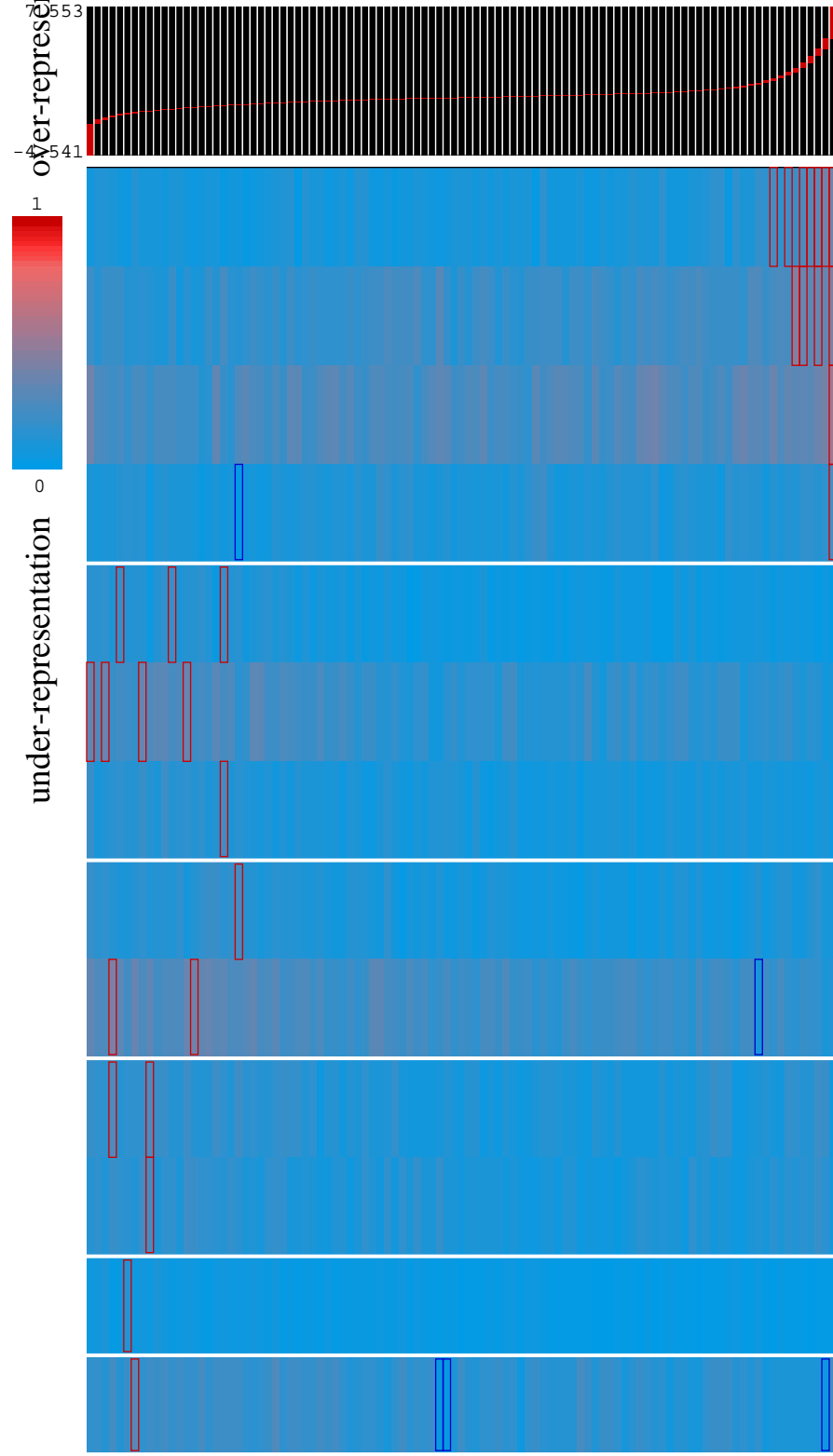


over-representation

under-representation



positive regulation of growth rate, p<0.001  
 cell organization and biogenesis, p<0.01  
 positive regulation of growth rate, p<0.01  
 structural molecule activity, p<0.001  
 protein biosynthesis, p<0.01

transferring phosphorus-cont  
 phosphate metabolism, p<1e-06  
 phosphate metabolism activity, p<1e-10

Optimized motif	Location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.028	20.1	10/10	Y	→	0.98	ACGTGAA	-
	3' UTR	0.019	11.8	10/10	Y	→	1.00	GAAUAAA	-
	3' UTR	0.016	8.6	8/10	Y	→	0.90	UGAACUU	-
	5'	0.015	7.5	8/10	Y	-	0.61	AAGTTCA	-
	5'	0.027	19.4	10/10	Y	-	1.00	AACGCGC	-
	3' UTR	0.023	15.5	10/10	-	→	1.00	CCCCAUU	-
	5'	0.018	10.4	10/10	Y	←	0.99	AGTGCGC	-
	5'	0.022	14.9	10/10	-	-	1.00	CGAGACC	-
	3' UTR	0.018	10.6	8/10	-	→	0.99	UAUUUUAU	-
	5'	0.022	14.0	10/10	-	-	1.00	AATCGAT	-
	5'	0.018	10.5	10/10	-	-	0.93	CGAAGAA	-
	5'	0.018	10.0	8/10	Y	←	1.00	TGCGTAC	-
	3' UTR	0.017	9.1	9/10	-	→	0.97	CUCGGUU	-