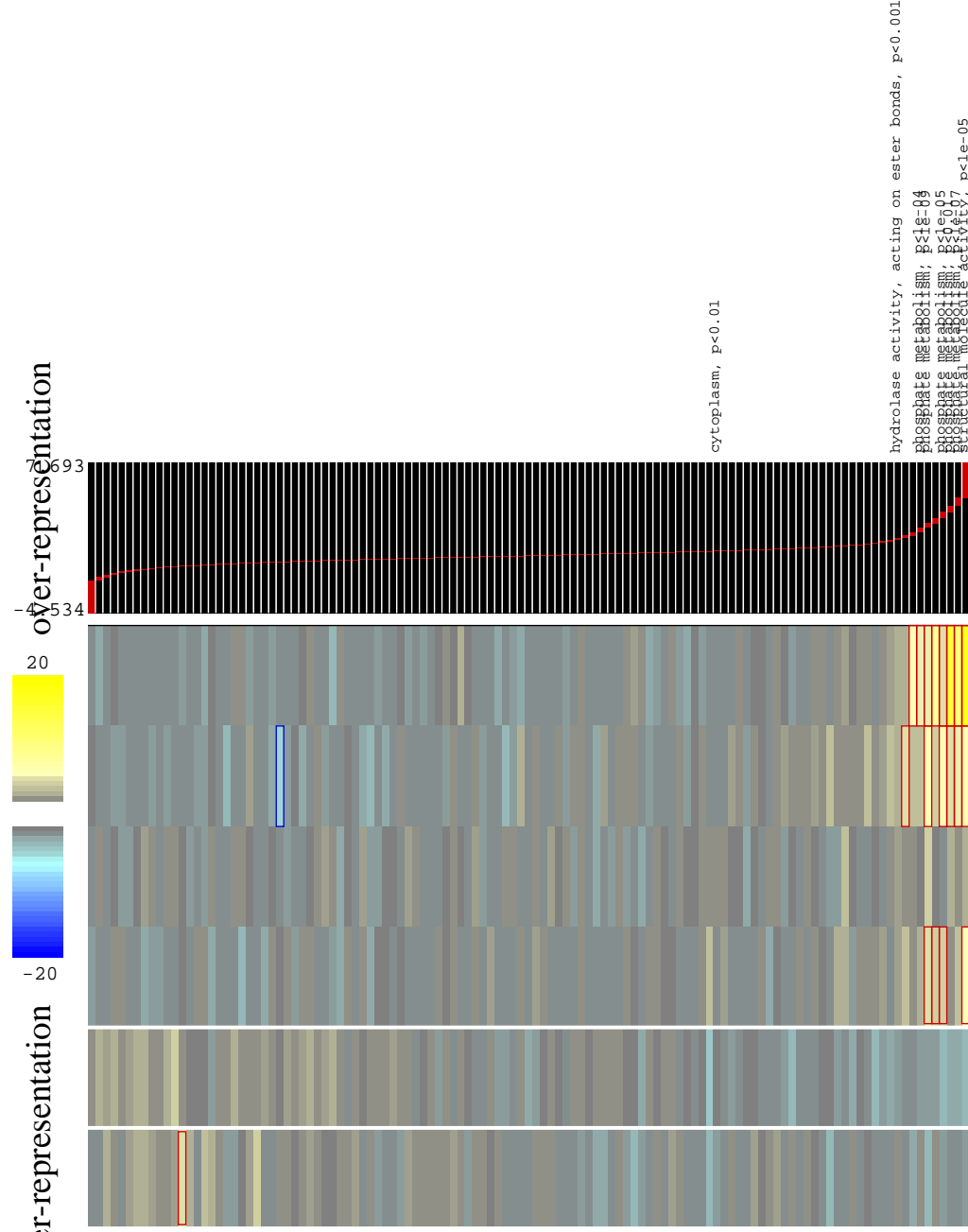


over-representation

under-representation



cytoplasm, p<0.01

hydrolase activity, acting on ester bonds, p<0.001

phosphate metabolism, p<1e-05

phosphate metabolism, p<1e-05

phosphate metabolism, p<1e-05

phosphate metabolism, p<1e-05

structural molecule activity, p<1e-05

bits	optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5'	0.030	24.5	10/10	Y	-	1.00	ACGTGAA	-	
	3' UTR	0.019	13.1	10/10	Y	→	1.00	AAUAAAG	-	
	5'	0.016	8.7	9/10	Y	←	0.79	AGTTCAC	-	
	3' UTR	0.015	7.6	7/10	-	→	0.91	GAACAGU	-	
	5'	0.016	9.1	10/10	-	-	1.00	AGCGTTC	-	
	3' UTR	0.014	7.1	6/10	-	→	1.00	AAUCUCU	-	