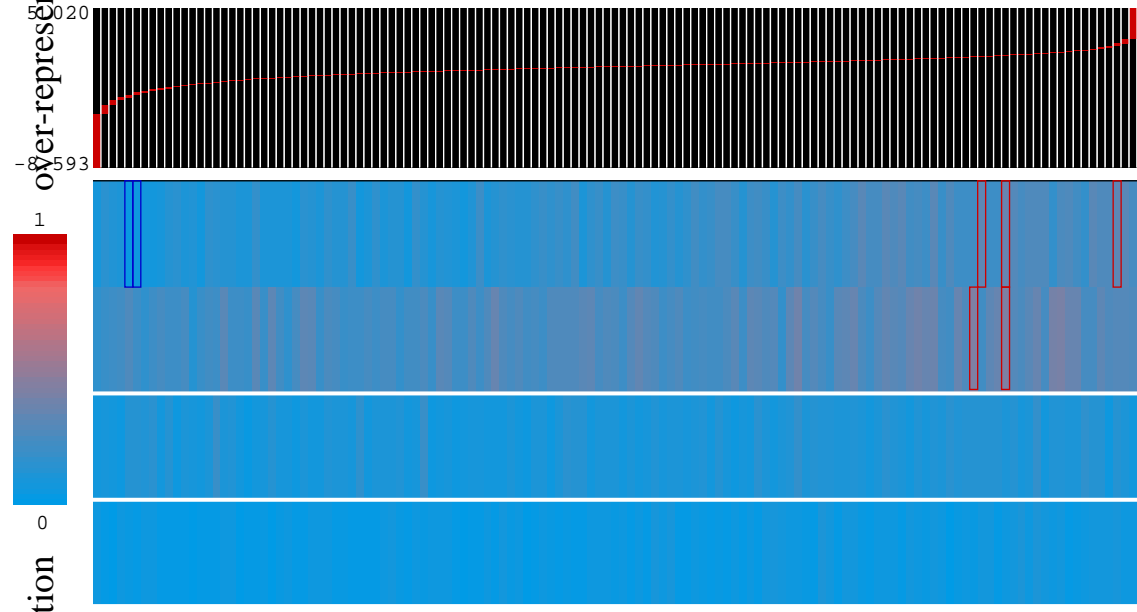


over-representation

presentation



structural molecule activity, $p < 0.001$

coenzyme binding, $p < 0.01$

cytoplasmic part, $p < 0.01$

regulation of development, $p < 0.01$

oxidoreductase activity, $p < 0.01$

bits	optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	3' UTR	0.025	19.8	10/10	-	→	1.00	UCCCCC	-	
	3' UTR	0.013	7.1	6/10	-	→	0.98	UUUCUUU	-	
	5'	0.014	8.0	8/10	-	←	0.99	AGAGAGA	-	
	3' UTR	0.014	6.5	7/10	-	→	0.81	UCCCCUC	-	