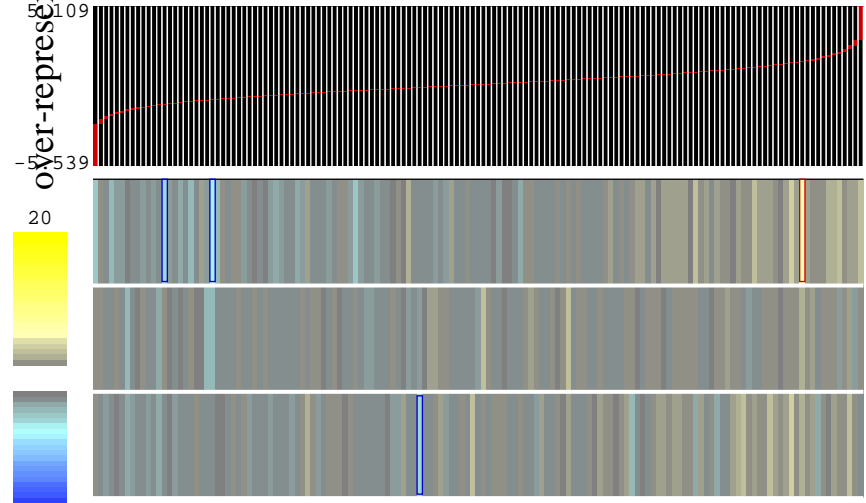





ion
over-representation

20
-20



cytoskeletal part, p<0.001
ribosomal constituent, p<0.001
cellular constituent of article, p<1e-28

Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	3'UTR	0.018	12.8	10/10	-	→	1.00	UCUCUCU	-
	5'	0.015	9.8	10/10	-	←	1.00	GAGACGC	-
	3'UTR	0.014	7.3	9/10	-	→	0.94	CUUUUCU	-