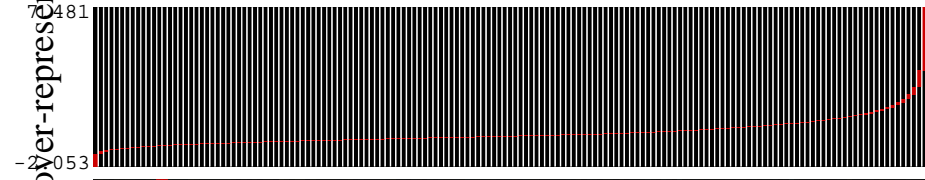


over-representation

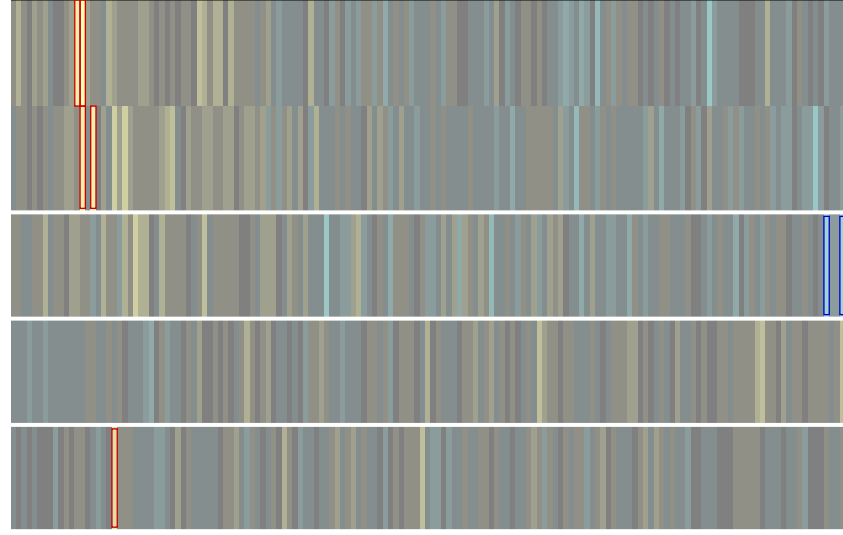
under-representation



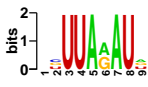




-20



ribonucleoprotein complex, p<0.01
protein biosynthesis, p<0.01



Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	3'UTR	0.014	8.0	9/10	-	→	0.99	GUUUGUA	-
	5'	0.013	8.0	8/10	-	→	1.00	CCGGAAG	NRF-2
	3'UTR	0.013	7.0	9/10	-	→	0.99	UUUAAAU	-
	3'UTR	0.013	5.7	6/10	-	→	0.48	CUGGGGC	-
	5'	0.012	5.3	6/10	-	-	0.09	ATGGCTC	-