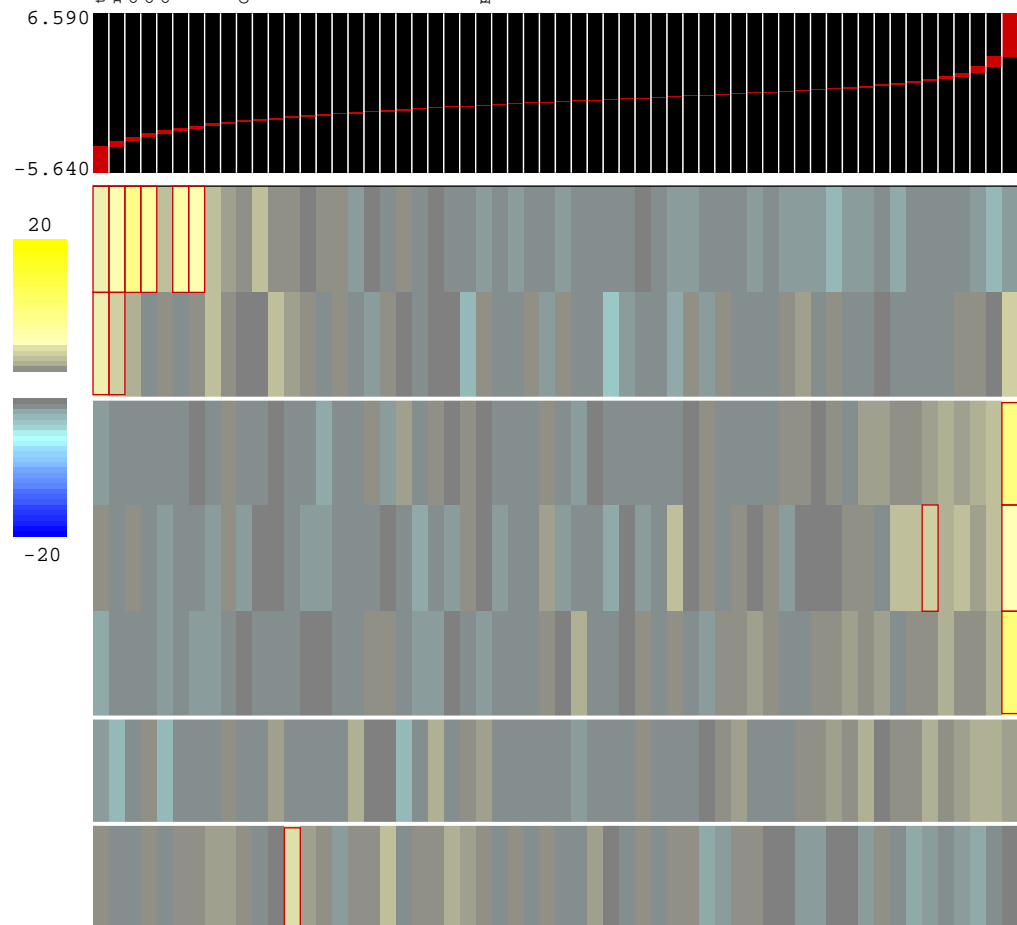


translation, p<1e-31
 ribonucleoprotein complex, p<1e-11
 cytosolic ribosome (sensu Eukaryota), p<1e-11
 cytosolic part, p<1e-07
 cytosolic part, p<1e-04

Golgi vesicle transport, p<0.01

proteasome complex (sensu Eukaryota), p<0.01



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.038	22.7	10/10	Y	-	1.00	AAAAATT	RRPE
	3'UTR	0.016	6.8	6/10	-	→	0.99	AUAAUUU	-
	5'	0.030	16.8	10/10	-	-	1.00	CCCCTTA	MSN24
	5'	0.024	12.0	10/10	-	-	1.00	ACCCCGC	PDR3
	5'	0.023	11.8	10/10	-	-	1.00	CCCTTAA	-
	3'UTR	0.018	7.3	7/10	-	→	1.00	UAUAUUC	-
	5'	0.017	7.3	6/10	-	-	0.34	CAATTC	-