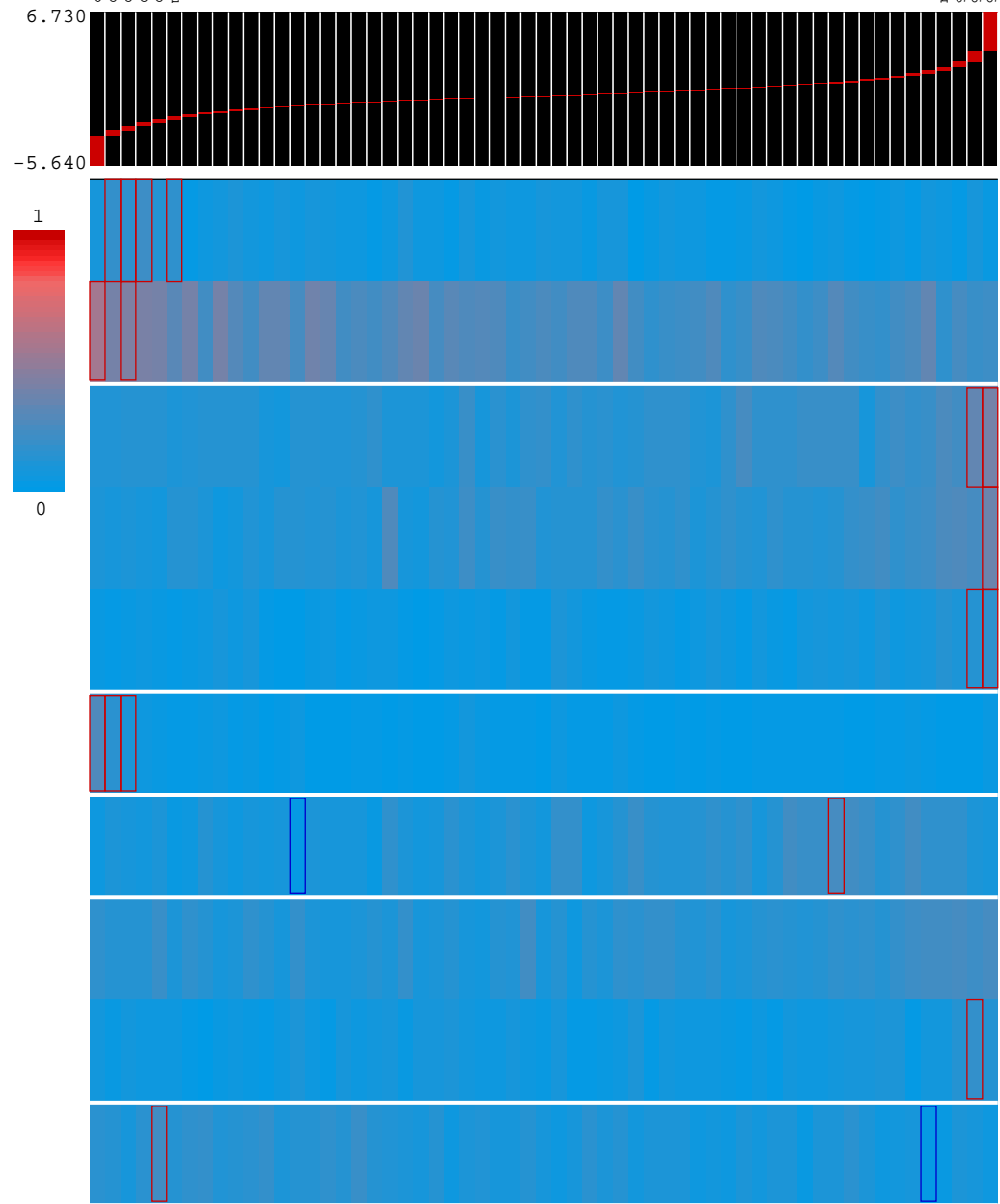


cytosolic ribosome (sensu Eukaryota), p<1e-56
 cytosolic ribosome (sensu Eukaryota), p<1e-23
 cytosolic ribosome (sensu Eukaryota), p<1e-12
 cytoplasm organization and biogenesis, p<1e-13
 cytoplasm organization and biogenesis, p<1e-04
 multi-eIF complex, p<0.001
 'de novo' IMP biosynthesis, p<0.01

nucleotide metabolism, p<0.01
 generation of precursor metabolites and energy, p<
 generation of precursor metabolites and energy, p<
 generation of precursor metabolites and energy, p<



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.039	24.0	10/10	Y	-	1.00	CTCATCG	PAC
	3'UTR	0.023	12.2	10/10	-	→	0.99	UGUAUAA	-
	5'	0.036	21.5	10/10	Y	-	1.00	CCCCTTA	MSN24
	5'	0.026	14.4	10/10	Y	-	1.00	AAAGGGG	MSN24
	3'UTR	0.020	9.0	9/10	-	→	1.00	UAUAUUC	-
	5'	0.026	13.0	10/10	Y	→	0.96	CCGTACA	RAP1
	3'UTR	0.022	11.1	10/10	-	→	1.00	GUAAAUA	PUF3
	5'	0.019	8.8	7/10	Y	-	1.00	CGCCCC	-
	5'	0.017	7.5	7/10	Y	→	0.98	CCAATCA	HAP4
	3'UTR	0.018	8.0	6/10	-	→	1.00	CAUAGAU	-