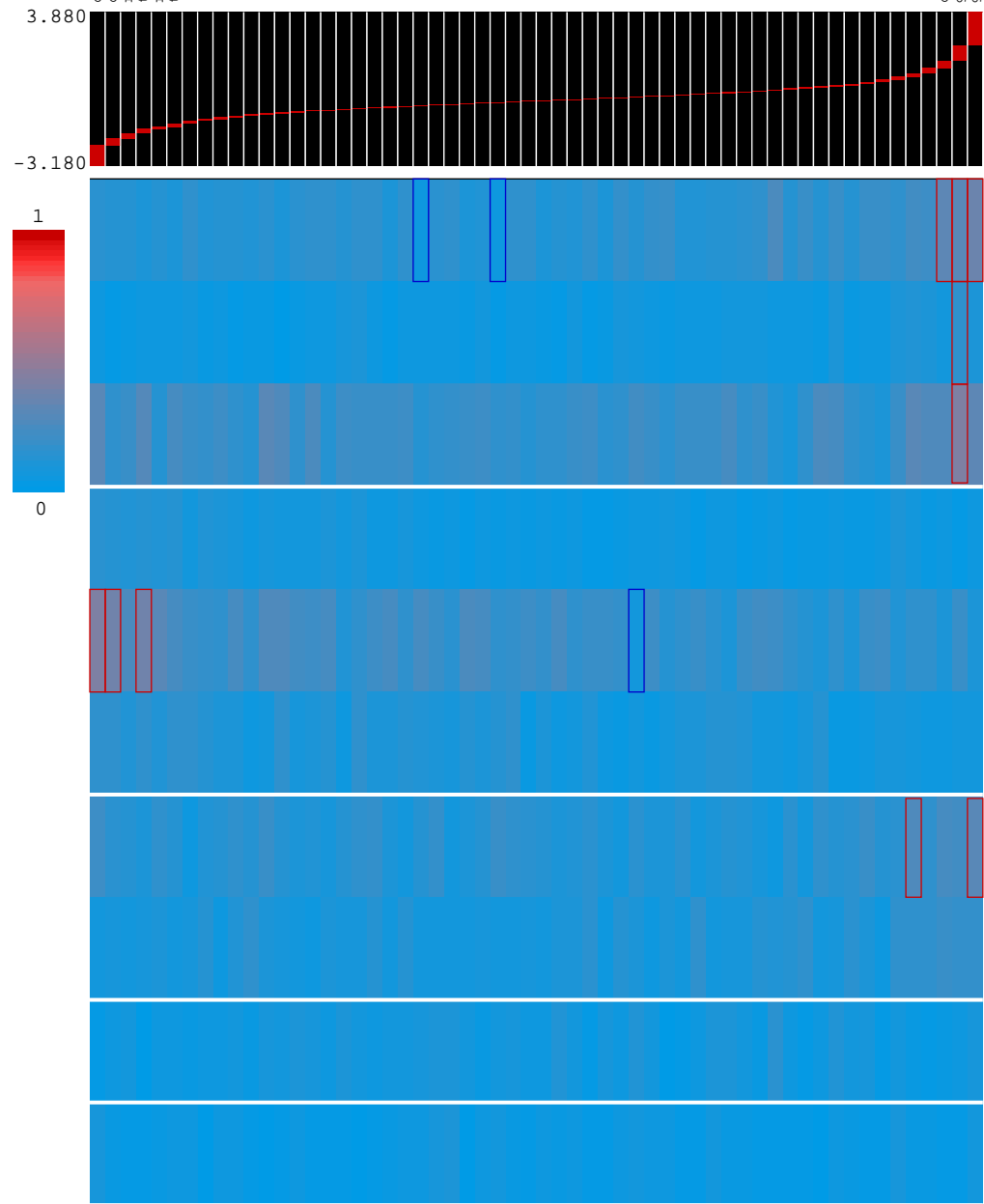
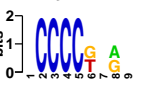




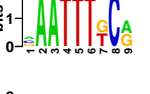



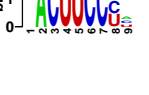


cytosolic ribosome (sensu Eukaryota), p<1e-47  
 cytosolic ribosome (sensu Eukaryota), p<1e-38  
 ribonucleoprotein complex, p<1e-09  
 translation, p<1e-05  
 ribosome biogenesis, p<0.001  
 translation initiation factor activity, p<0.001

carbohydrate metabolism, p<0.001  
 generation of precursor metabolites and energy, p<0.001  
 generation of precursor metabolites and energy, p<0.001



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.033	19.2	10/10	Y	-	1.00	CCCCTTA	MSN24
	5'	0.020	9.3	9/10	-	-	0.98	CCCTTAA	-
	3'UTR	0.018	8.3	7/10	Y	→	1.00	UUUAUUU	-
	5'	0.032	18.2	10/10	Y	-	1.00	CTCATCG	PAC
	3'UTR	0.021	10.4	9/10	-	→	1.00	UGUAUAA	PUF4
	5'	0.020	9.5	9/10	Y	→	0.98	AATTTTC	-
	5'	0.019	9.4	7/10	-	-	0.99	CCCCACC	-
	5'	0.017	7.6	6/10	-	←	0.97	CCCGGCG	-
	3'UTR	0.017	6.7	6/10	-	→	0.74	AGAACUG	-
	3'UTR	0.017	6.0	8/10	-	→	0.76	ACUUCCU	-