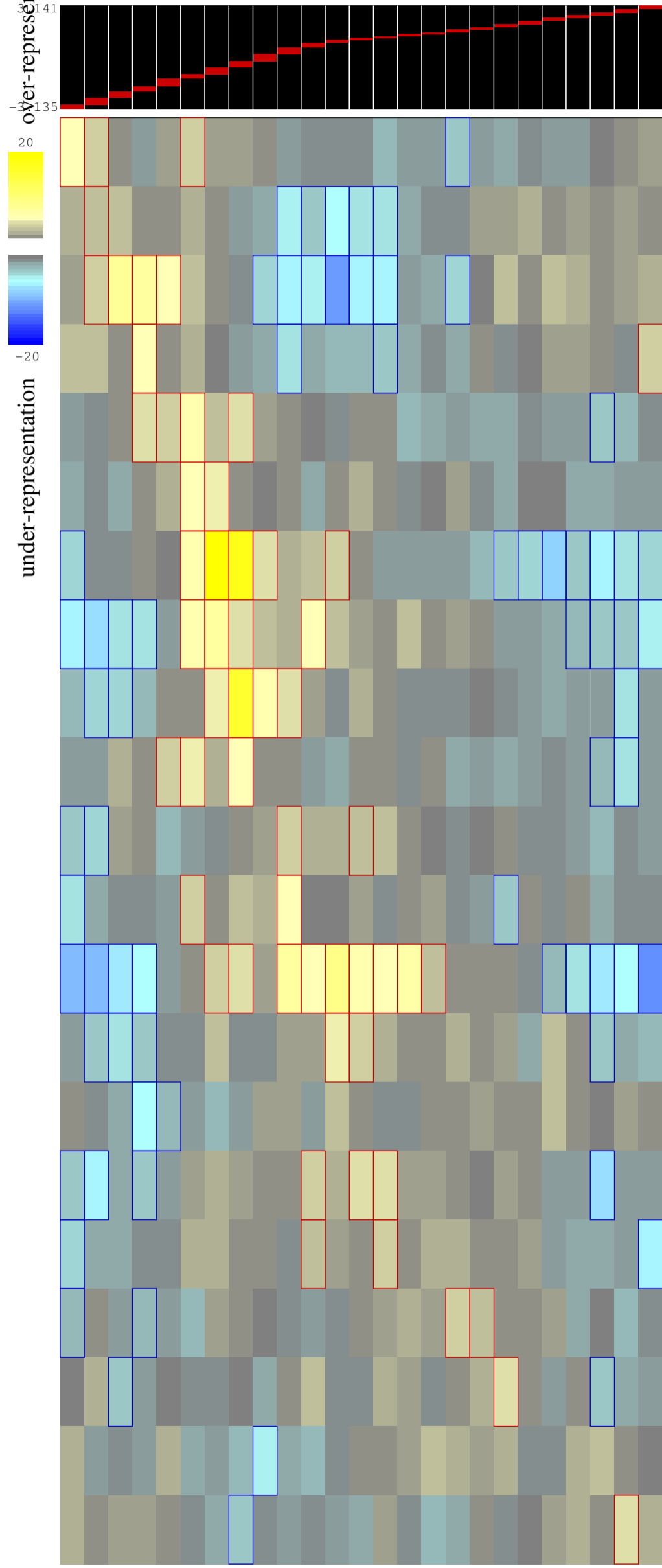


over-representation

under-representation



cytoplasmic vesicle membrane, p<0.01

DNA replication, p<0.01

protein targeting to mitochondrion, p<0.001

protein biosynthesis, p<1e-11

ribonucleoprotein complex, p<0.001

cytosolic ribosome (sensu Eukaryota), p<1e-04

Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5'	0.029	11.0	9/10	-	←	0.97	ACAACAT	-
	5'	0.045	18.9	10/10	-	-	0.99	TTCTACA	-
	5'	0.089	40.6	10/10	Y	-	0.95	ATATAGA	-
	5'	0.035	13.9	10/10	-	-	0.98	TCTATAA	-
	5'	0.038	15.5	10/10	-	-	0.96	ACATGCA	-
	5'	0.026	9.7	7/10	-	←	0.96	AGAACAA	-
	5'	0.112	52.3	10/10	-	-	1.00	AAAGACA	-
	5'	0.078	35.2	10/10	Y	-	1.00	CACACAA	-
	5'	0.059	26.6	10/10	-	-	0.99	ATGTGCA	-
	5'	0.036	14.1	10/10	-	-	0.97	TACAACC	-
	5'	0.029	10.8	9/10	-	←	0.87	TGTATTC	-
	5'	0.028	10.3	8/10	-	→	0.63	ATTTTCC	-
	5'	0.128	60.6	10/10	Y	-	1.00	ATGTGTA	-
	5'	0.038	15.6	10/10	-	-	0.79	AACACAT	-
	5'	0.025	8.8	7/10	-	→	0.97	ATTATCC	-
	5'	0.045	19.1	10/10	-	-	0.78	TACACAA	-
	5'	0.035	14.0	10/10	-	-	0.98	AGTGTA	-
	5'	0.025	9.3	7/10	-	-	0.81	TATGTCA	-
	5'	0.027	9.7	8/10	-	→	0.51	ATGATCA	-
	5'	0.031	11.9	10/10	-	→	0.96	AATGCCT	-
	5'	0.023	7.8	8/10	-	-	0.98	AATATTA	-