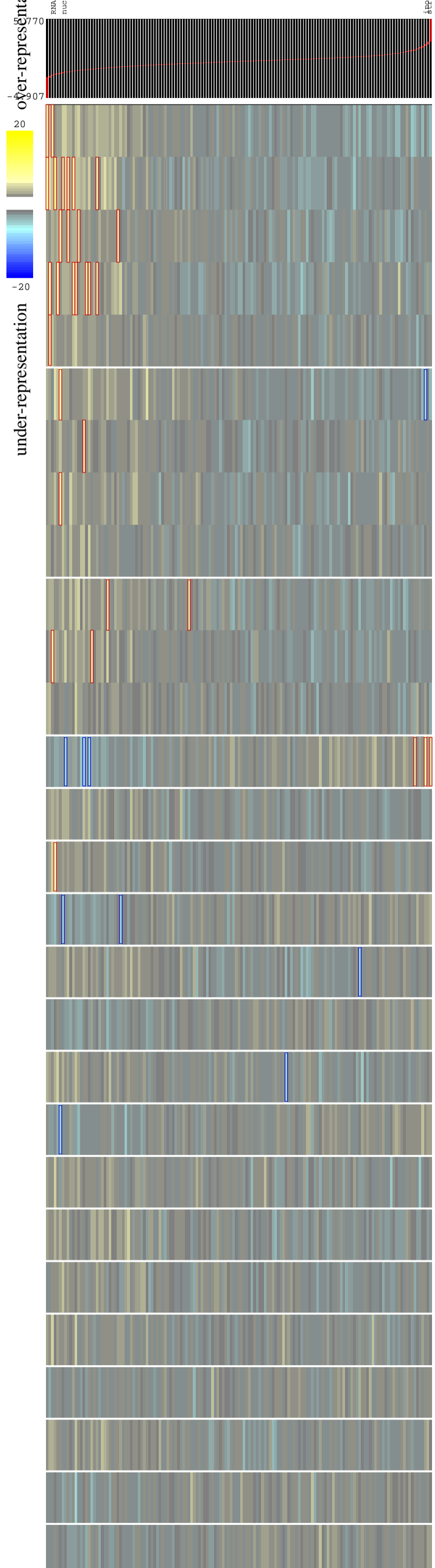


over-representation

under-representation



RNA processing, p<0.001
nucleoside-triphosphatase activity, p<0.01

atp1a1:en081:trfap08,orf1e05; p<1e-06

optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5'	0.027	23.2	10/10	Y	-	1.00	CGCGCTC	-
	3'UTR	0.023	18.7	10/10	Y	→	1.00	CUUCCCC	-
	5'	0.022	17.7	10/10	-	-	1.00	CGAGACC	-
	3'UTR	0.019	14.0	10/10	-	→	0.99	UAUUUUAU	-
	5'	0.016	10.0	10/10	-	→	0.75	AAATCGC	-
	5'	0.022	17.0	10/10	-	-	1.00	AATCGAT	-
	5'	0.017	11.5	10/10	-	←	0.93	ACGAGAA	-
	5'	0.015	9.1	9/10	-	→	0.93	CTCTTCG	-
	5'	0.015	8.8	10/10	-	←	0.97	CACGACG	-
	5'	0.018	12.2	10/10	Y	→	0.95	TTTTTCG	-
	5'	0.017	11.8	10/10	-	-	0.98	TGCGTAC	-
	5'	0.014	7.5	7/10	-	←	0.75	CGAGAGA	-
	3'UTR	0.017	11.0	10/10	-	→	1.00	AAUAAAA	-
	5'	0.015	9.5	10/10	-	-	0.82	AAATGCG	-
	3'UTR	0.015	8.4	7/10	-	→	0.84	AUUCCUC	-
	5'	0.014	8.0	8/10	-	-	0.94	CACCTAC	-
	3'UTR	0.014	8.0	10/10	-	→	0.94	UUGUUUAU	miR-44/miR-45/miR-61/miR-247
	5'	0.014	8.0	7/10	-	→	0.64	AACTTTG	-
	5'	0.014	7.9	10/10	-	←	0.97	ACCGTAG	-
	5'	0.014	7.5	6/10	-	←	1.00	CTTATCA	-
	5'	0.013	7.3	6/10	-	-	0.71	CGCCAGC	-
	5'	0.013	7.3	6/10	-	-	0.93	CCGCAG	-
	5'	0.013	7.1	7/10	-	-	0.95	ATGCGGC	-
	5'	0.013	7.1	7/10	-	←	0.94	ATTTCGC	-
	5'	0.013	6.9	6/10	-	-	0.21	AGACTTA	-
	5'	0.013	7.0	6/10	-	-	0.98	GTCCGCC	-
	5'	0.013	6.7	8/10	-	-	0.22	ATACCAA	-
	5'	0.012	5.9	6/10	-	←	0.83	AGTATGA	-