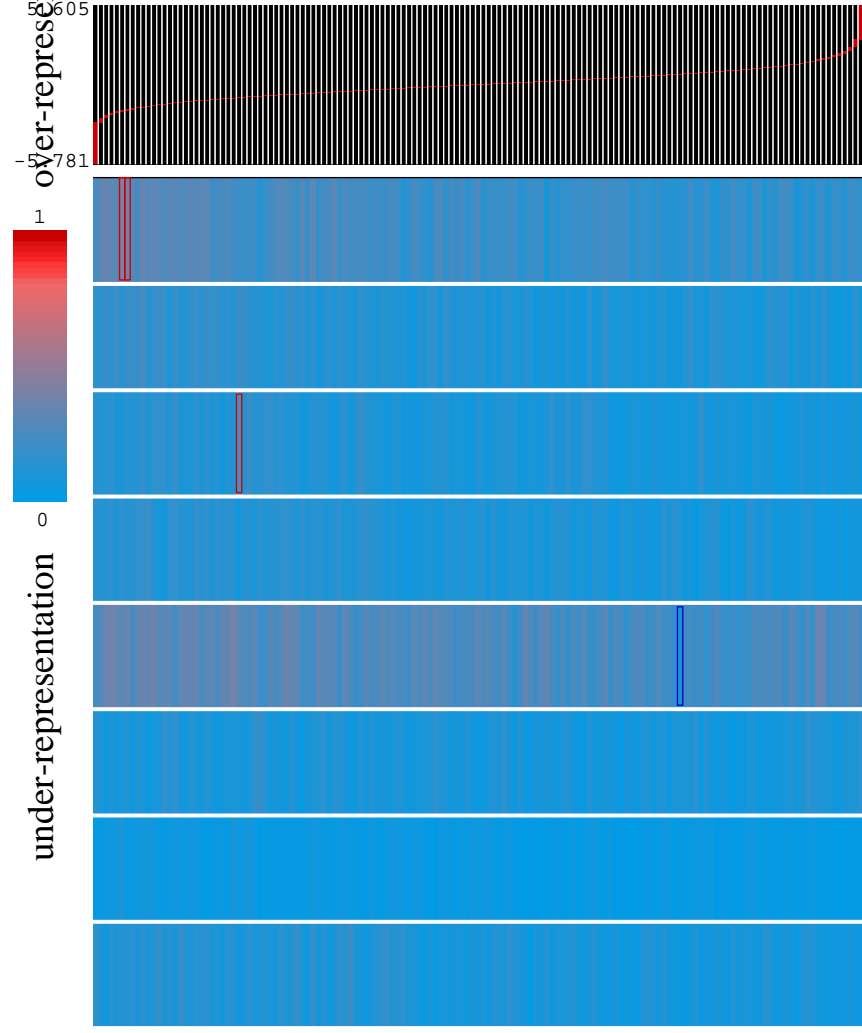


over-representation

under-representation



helicase activity, $p < 0.01$

modification-dependent macromolecule catabolism, $p < 0.01$

anion channel activity, $p < 0.01$

structural conservation of cytoskeleton, $p < 0.001$

optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	3'UTR	0.019	13.4	10/10	Y	→	1.00	UCCCCC	-
	5'	0.018	12.3	10/10	-	-	0.99	CGAGACC	-
	5'	0.016	10.2	10/10	-	-	1.00	AATCGAT	-
	5'	0.016	10.1	10/10	-	-	0.96	AACGCGC	-
	3'UTR	0.015	9.2	7/10	-	→	0.99	AUUUAUU	-
	3'UTR	0.014	7.4	7/10	-	→	0.99	CUUUAUA	-
	5'	0.013	6.7	6/10	-	-	0.82	CGCAACG	-
	5'	0.013	7.3	8/10	-	→	0.84	CACCGCG	-