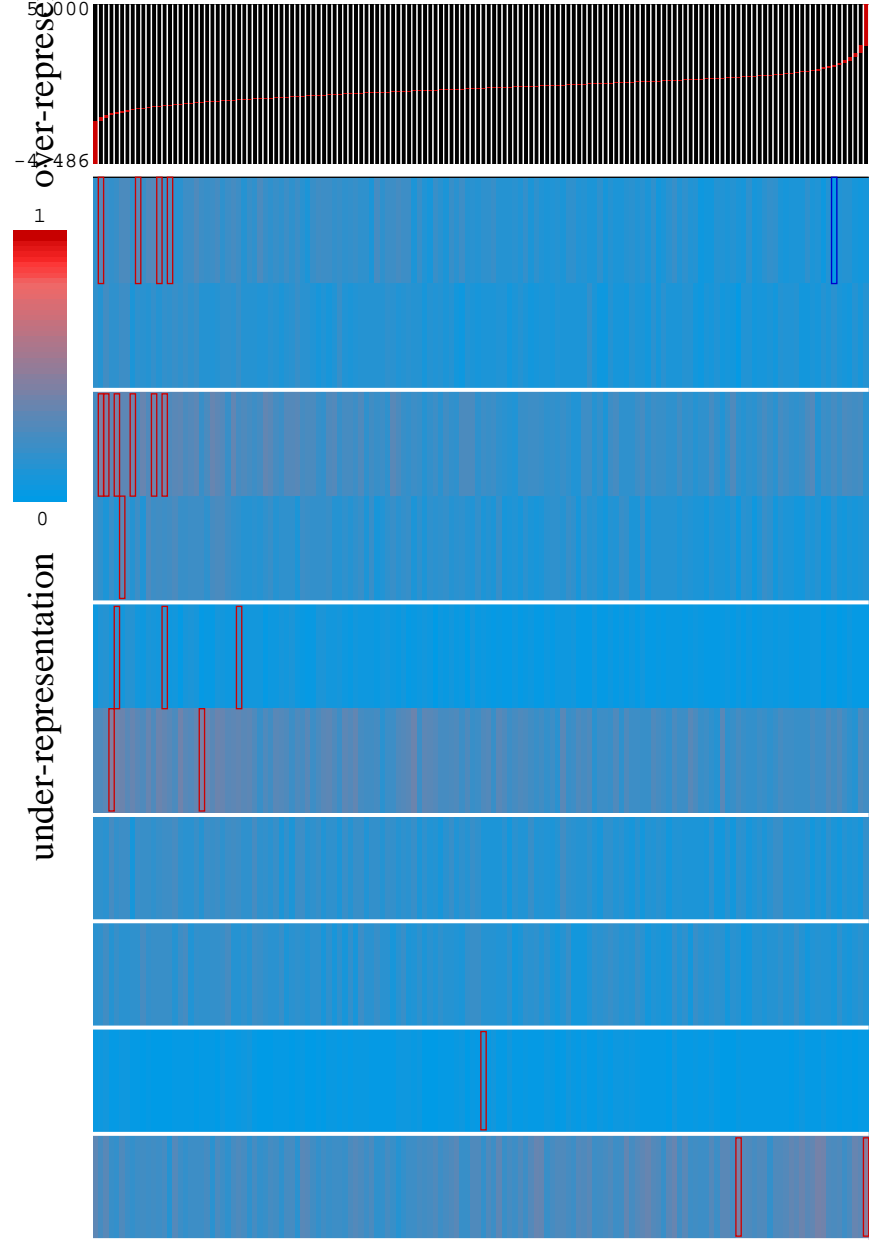


over-representation
under-representation



behavior, $p < 0.01$

phosphate transport, $p < 0.001$
structural ribosome activity, $p < 6 \times 10^{-9}$

optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.023	18.5	10/10	-	-	1.00	AACGCGC	-
	5'	0.017	11.3	10/10	-	←	0.99	TTCGCAA	-
	3' UTR	0.019	14.3	10/10	-	→	1.00	UCCCCCG	-
	5'	0.018	12.7	10/10	-	-	1.00	AATCGAT	-
	5'	0.018	12.4	10/10	-	-	1.00	CGAGACC	-
	3' UTR	0.015	9.5	10/10	-	→	0.99	UAUUUUAU	-
	5'	0.016	10.1	10/10	-	-	0.98	TGCGTAC	-
	5'	0.015	8.7	10/10	-	←	0.95	CGAAGAA	-
	3' UTR	0.014	6.3	6/10	-	→	0.26	CCACAUA	-
	3' UTR	0.013	7.1	6/10	-	→	0.99	AAAUAAA	-