

over-representation

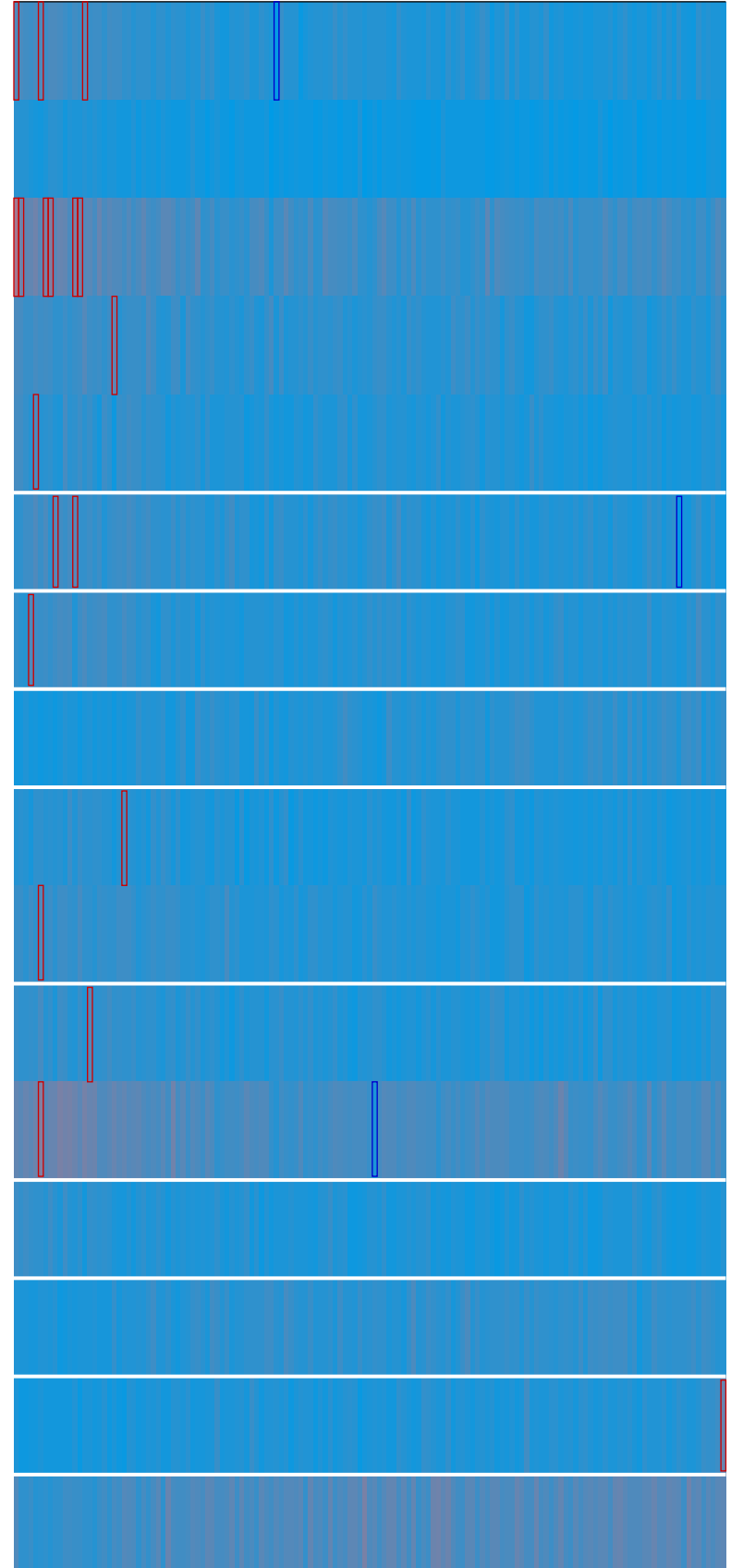
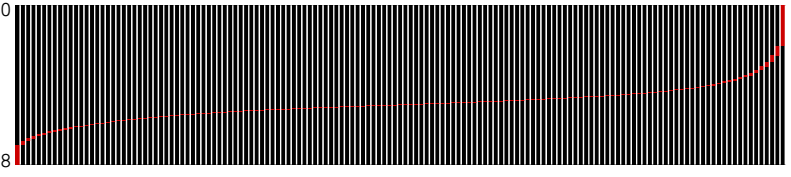
under-representation



nuclear part, p<0.01
DNA metabolism, p<0.01

transferase activity, transferring hexosyl groups,

carboxylic ester hydrolase activity, p<0.001
phosphate transport, p<1e-23
nitrite activity, p<0.001



bits	Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
bits 0 1 2 1 2 3 4 5 6 7 8 9 A C A C G C C C T T T T T T T T T	5'	0.025	20.7	10/10	Y	-	1.00	AACGCGC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 C G G A G A C C T T T T T T T T T	5'	0.022	16.9	10/10	Y	-	1.00	CGAGACC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 C C C A C C T T T T T T T T T	3'UTR	0.021	15.9	10/10	-	→	1.00	CCCAU	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A A T C C C G T T T T T T T T	5'	0.016	10.0	10/10	-	←	0.73	AAATCGC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A T T G G G C C C C C C C C C	5'	0.015	8.7	10/10	-	→	0.91	ATTGCGG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A A T C G A T G C C C C C C C C	5'	0.018	13.2	10/10	-	-	1.00	AATCGAT	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A C C T G G G G G G G G G G G	5'	0.015	9.4	9/10	-	-	0.92	AGCATCG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 C T T A T C A G G G G G G G G G	5'	0.015	8.9	8/10	-	→	1.00	CTTATCA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A G A G A A C C C C C C C C C	5'	0.015	8.7	9/10	-	←	0.72	ACGAGAA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 C G T C C G G G G G G G G G	5'	0.014	8.0	8/10	-	-	0.94	TTCGTCC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 C G A G A A G G G G G G G G G	5'	0.015	8.6	9/10	-	-	0.89	CGAAGAA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 C A U C C U G G G G G G G G G	3'UTR	0.014	8.5	8/10	-	→	0.99	AUUUAUU	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A C G G G G G G G G G G G G	5'	0.015	8.5	8/10	-	←	0.93	CACCGCG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A T A T G T A C C C C C C C C C	5'	0.014	8.5	8/10	-	←	0.79	ATATGTA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 T A T A A A G C C C C C C C C C	5'	0.014	8.3	7/10	Y	→	0.94	TATAAAA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 A A U A A A A G G G G G G G G G	3'UTR	0.014	7.8	6/10	-	→	0.99	AAUAAAA	-	