over-representation

under-representation

reproduction, p<0.001
translation,p<0.01

phosphate metabolism, p<1e-04
phosphate metabolism, p<1e-08
protein tyrosine phosphatase activity, p<1e-06

6679

-7920

1

0
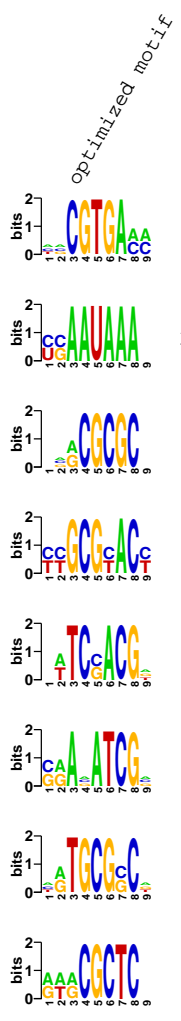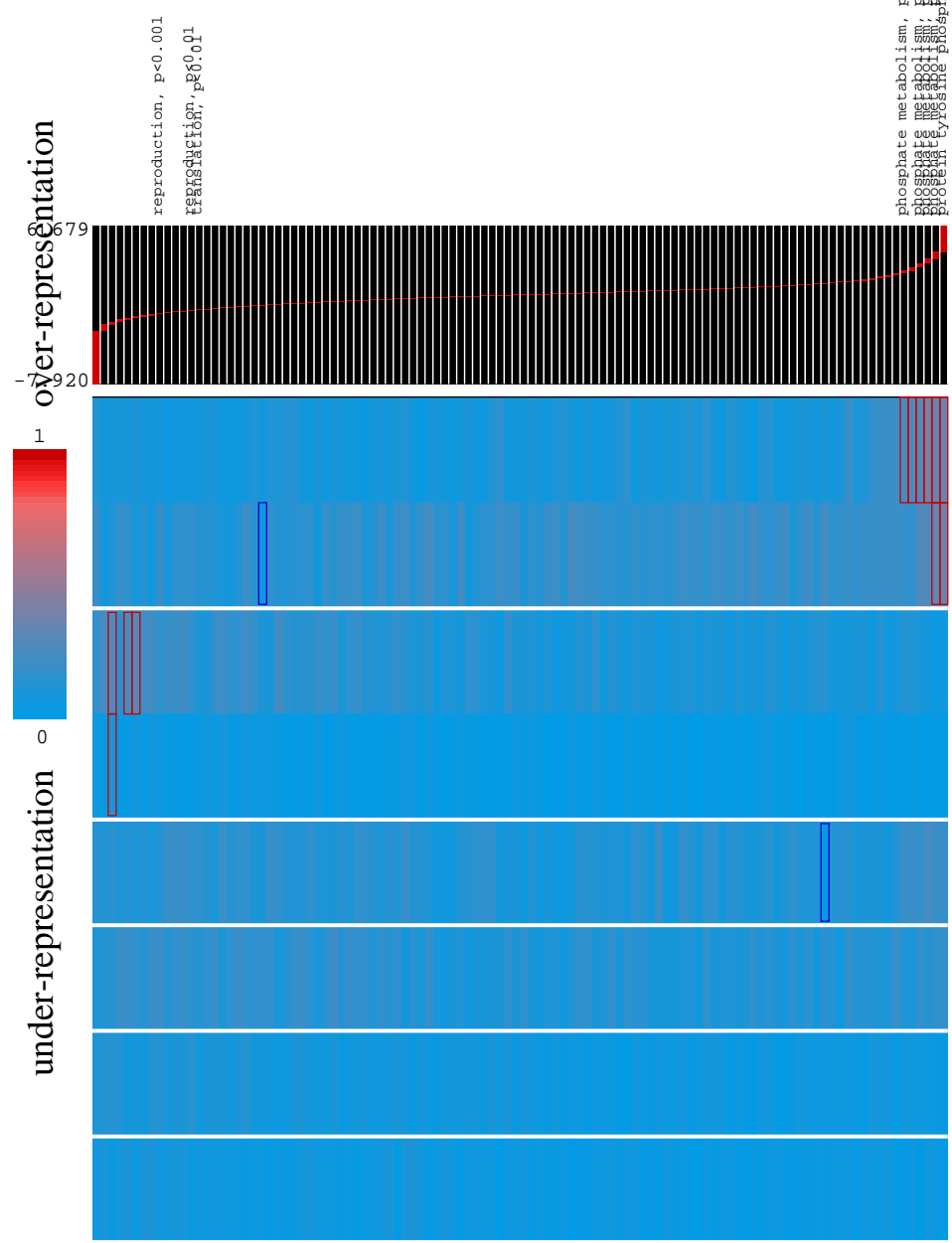
optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
CGTGA	5'	0.028	20.8	10/10	Y	→	0.98	ACGTGAA	-
AAUAAA	3'UTR	0.018	11.0	10/10	Y	→	1.00	GAAUAAA	-
CGCGC	5'	0.024	17.1	10/10	Y	-	1.00	AACGCGC	-
GCGCAC	5'	0.016	7.9	9/10	-	-	0.99	TGCGTAC	-
TCACG	5'	0.015	8.0	7/10	-	→	0.99	ATCCACG	-
CAA ATCG	5'	0.015	7.8	8/10	-	-	0.97	AAAATCG	-
TGCGC	5'	0.015	7.2	6/10	-	-	0.99	ATGCGCC	-
CGCTC	5'	0.014	6.8	6/10	Y	-	0.96	TGCGCTC	-