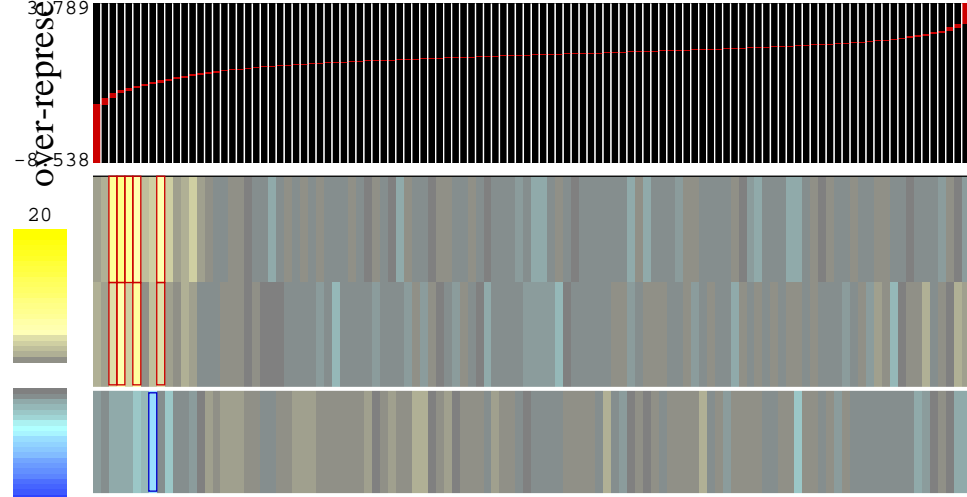


ion
-20
20
over-representation

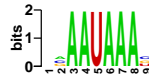
sugar binding, $p < 1e-16$
phosphate metabolism, $p < 1e-05$



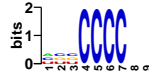
bits



optimized motif



3' UTR



3' UTR

location

MI (bits)

z-score

robustness

position bias

orientation bias

conservation index

seed

motif name

5'

0.025

18.9

10/10

Y

-

0.98

ACGTGAA

-

3' UTR

0.017

10.1

10/10

Y

→

1.00

GAAUAAA

-

3' UTR

0.016

8.7

8/10

-

→

1.00

UCCCCU

-