

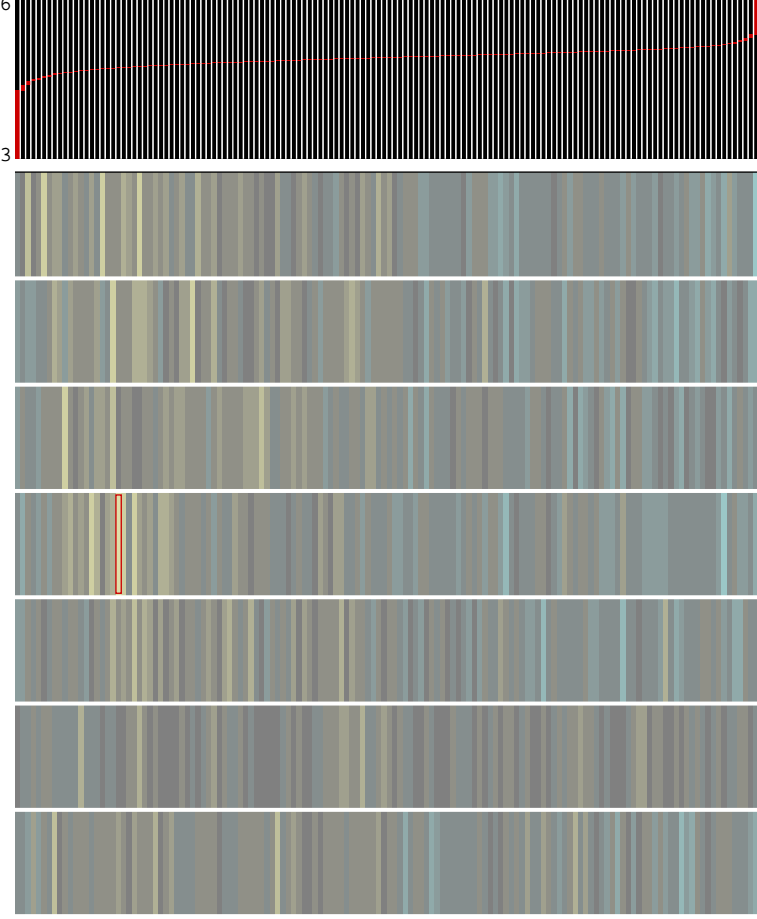
over-representation

structural molecule activity, p<0.01

20

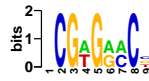
-20

under-representation



lipid metabolism, p<0.01

optimized motif



location

MI (bits)

z-score

robustness

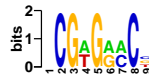
position bias

orientation bias

conservation index

seed

motif name



5'

0.018

11.8

10/10

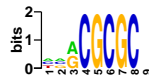
-

-

1.00

CGAGACC

-



5'

0.017

11.3

10/10

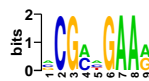
-

→

1.00

AACGCGC

-



5'

0.015

9.5

10/10

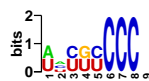
Y

-

0.96

CGAAGAA

-



3' UTR

0.015

9.3

10/10

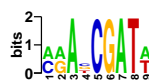
-

→

1.00

UUUCCCC

-



5'

0.014

8.2

10/10

-

←

1.00

AATCGAT

-



5'

0.014

6.1

7/10

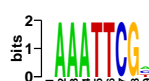
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-

0.18

CCACCCG

-



5'

0.013

7.1

6/10

-

-

0.76

AAATTCG

-