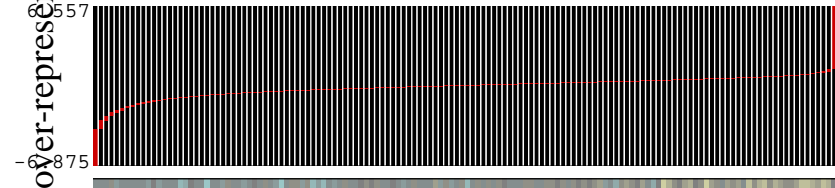


over-representation

under-representation



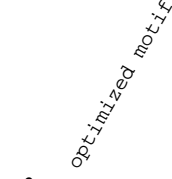
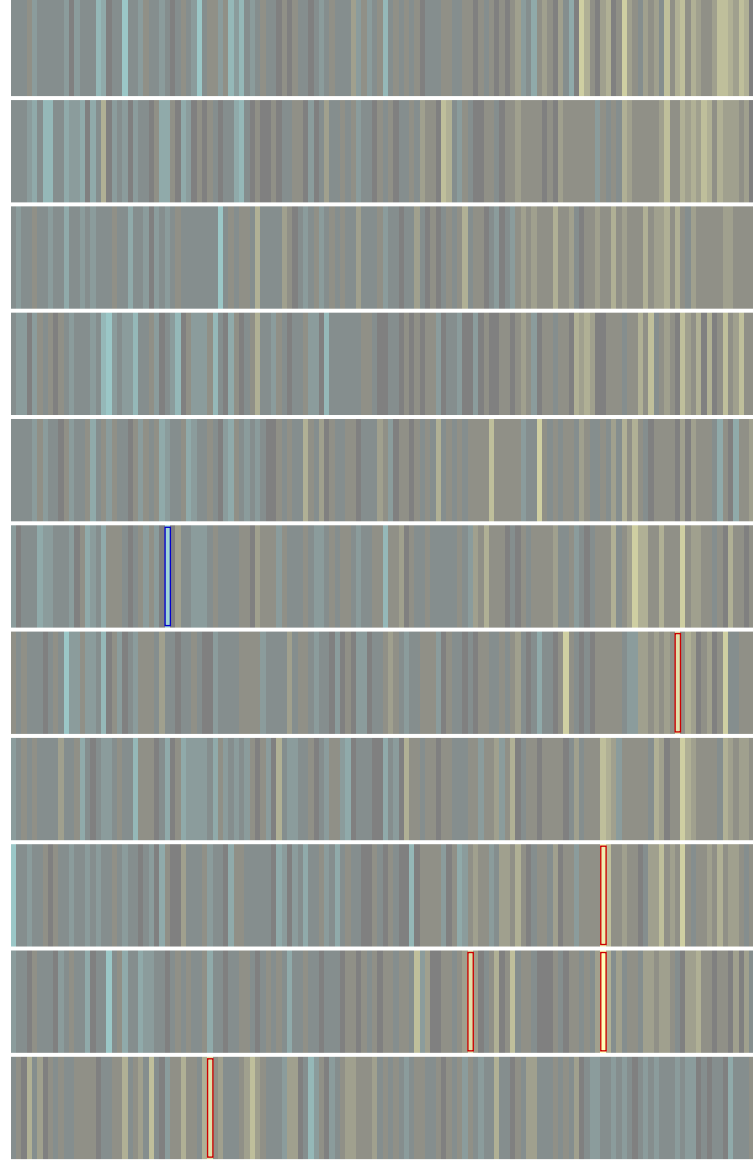
-20



structural molecule activity, $p < 0.01$

gametogenesis, $p < 0.001$

ribonucleic acid binding, $p < 0.001$



5'

0.021

15.2

10/10

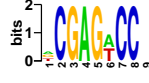
Y

-

0.99

TTCGCGC

-



5'

0.019

13.7

10/10

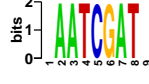
-

-

1.00

CGAGACC

-



5'

0.017

11.0

10/10

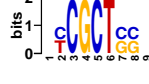
-

←

1.00

AATCGAT

-



5'

0.017

11.1

10/10

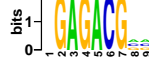
-

→

0.95

TCGCTGC

-



5'

0.015

9.1

7/10

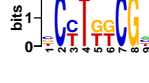
-

←

1.00

GAGACGC

-



5'

0.014

8.2

8/10

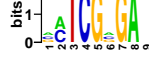
-

→

0.93

CTTTTCG

-



5'

0.014

8.1

9/10

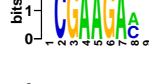
-

←

0.64

ATCGCGA

-



5'

0.014

7.7

8/10

-

-

0.69

CGAAGAA

-



3' UTR

0.013

7.3

8/10

-

→

0.99

AUUUAUU

-



5'

0.013

6.9

7/10

-

-

0.91

CGCTGTC

-



5'

0.013

6.6

6/10

-

-

0.93

ATGTATA

-

Optimized motif

Location

MI (bits)

z-score

robustness

Position bias

orientation bias

conservation index

seed

motif name