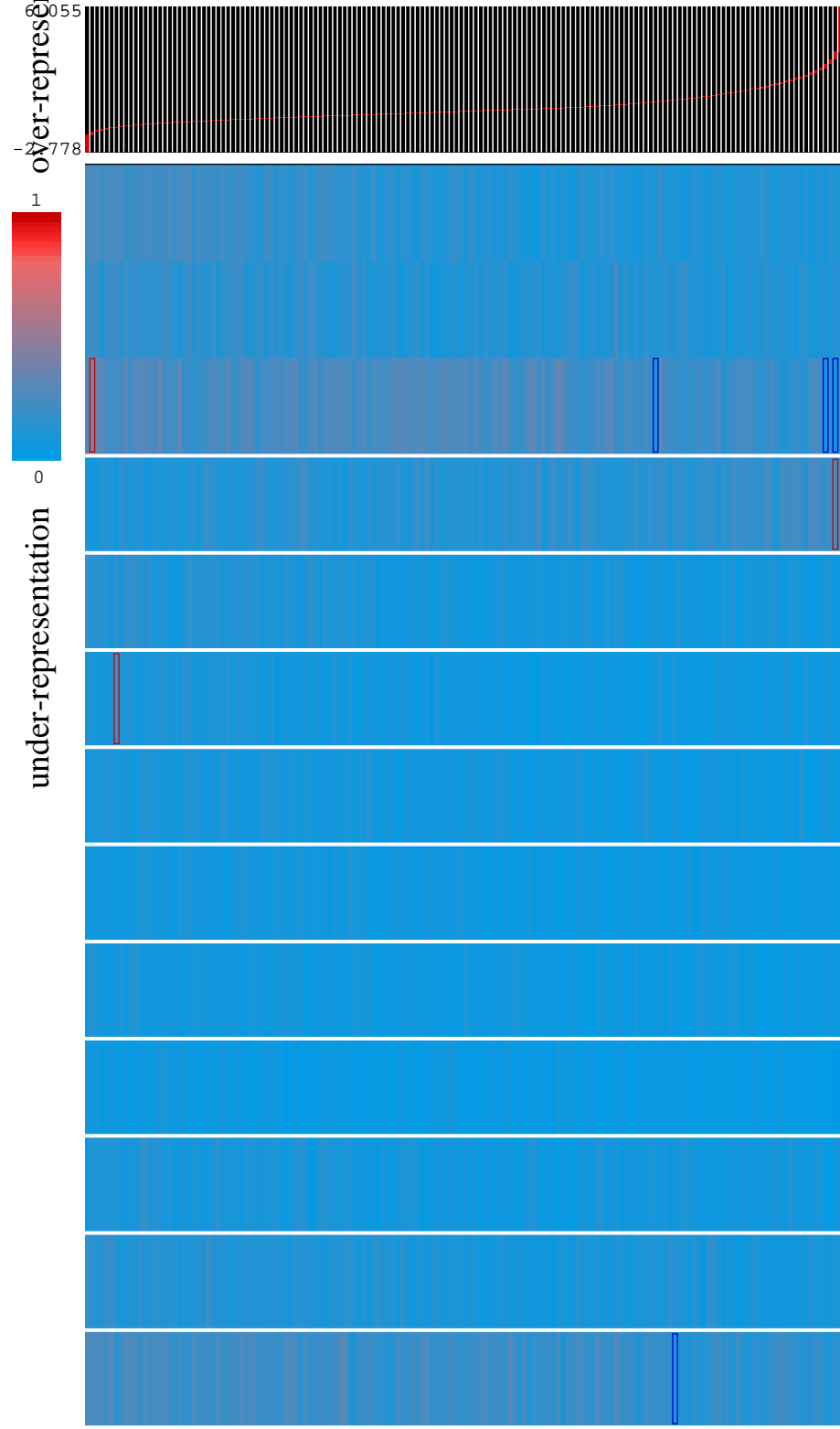


over-representation

under-representation

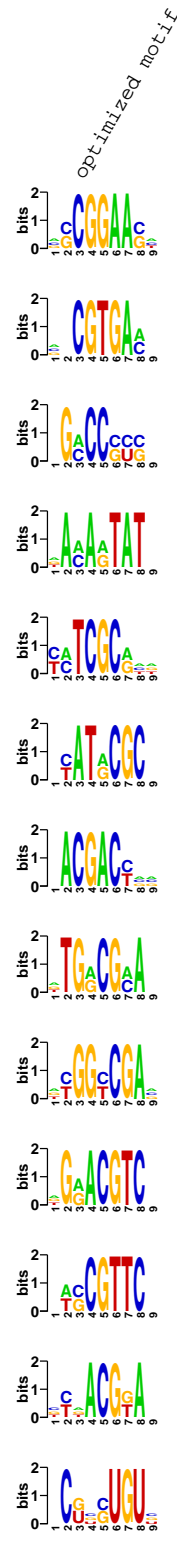
1

0

oxidoreductase activity, acting on NADH or NADPH,
protein transport, p<0.001ribonucleoprotein complex, p<0.01
protein biosynthesis, p<1e-04contractile fiber part, p<0.01
extracellular space, p<0.01

GTPase regulator activity, p<0.001

olfactory receptor activity, p<0.01



Optimized motif

location

MI (bits)

z-score

Robustness

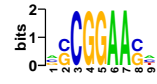
Position bias

orientation bias

conservation index

seed

motif name



5'

0.028

25.7

10/10

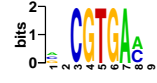
-

-

1.00

CCGGAAG

Elk-1



5'

0.014

8.9

10/10

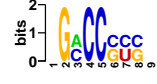
Y

←

0.96

ACGTGAC

Pax2



3' UTR

0.014

8.0

10/10

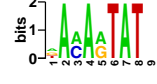
-

→

1.00

GACCCUC

-



5'

0.016

11.0

10/10

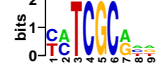
Y

-

1.00

AAAATAT

-



5'

0.015

9.9

8/10

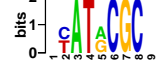
-

-

0.96

CTCGCGA

-



5'

0.015

9.6

9/10

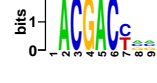
-

-

1.00

CATGCC

-



5'

0.015

9.3

10/10

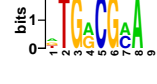
-

→

0.49

ACGACC

-



5'

0.014

8.1

8/10

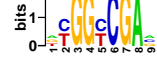
-

←

0.30

TGACGCA

CREB



5'

0.013

7.4

6/10

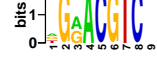
-

-

0.92

CGGCCGA

-



5'

0.013

6.9

9/10

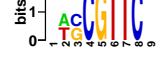
-

→

0.03

GAACGTC

bZIP910



5'

0.013

7.1

7/10

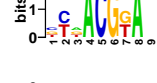
-

-

0.36

ACGTTC

-



5'

0.013

6.8

7/10

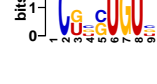
-

→

0.93

CACGGA

-



3' UTR

0.013

6.9

7/10

-

→

0.85

CUGCUGU

-