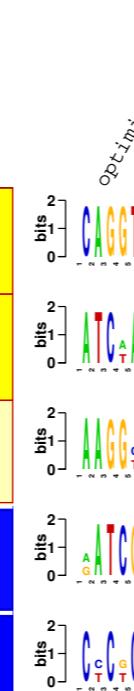
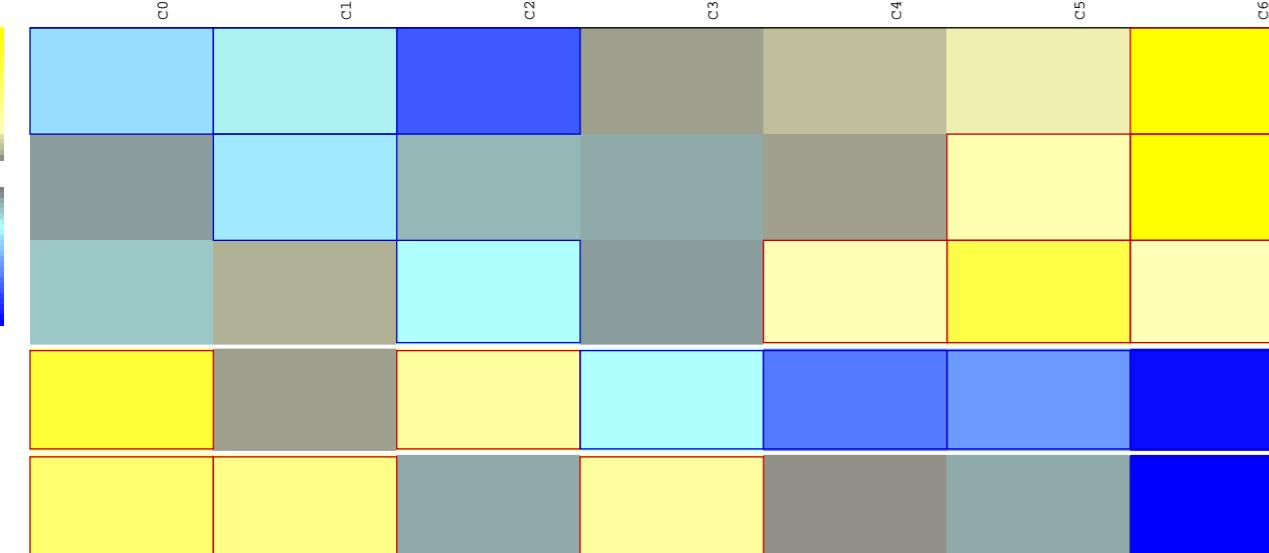


representation over-representation



location

MI (bits)

z-score

robustness

position bias

orientation bias

conservation index

seed

motif name

protein array

5'

0.014

80.6

10/10

Y

↔

1.00

CAGGTGA

SNAI_1, HLH_1.4

5'

0.004

22.4

10/10

-

↔

0.55

ATCAAAT

PIE_1

5'

0.003

14.8

8/10

-

↑

0.22

AAGGTAG

PIE_1, NSY_7

5'

0.007

37.5

10/10

-

↔

1.00

AATCGAT

PIE_1, CEH_28, CEH-28 ...

5'

0.006

32.2

10/10

Y

↔

0.98

CTCTCTC

KLU_2