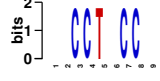
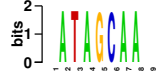
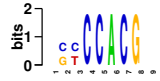
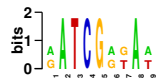
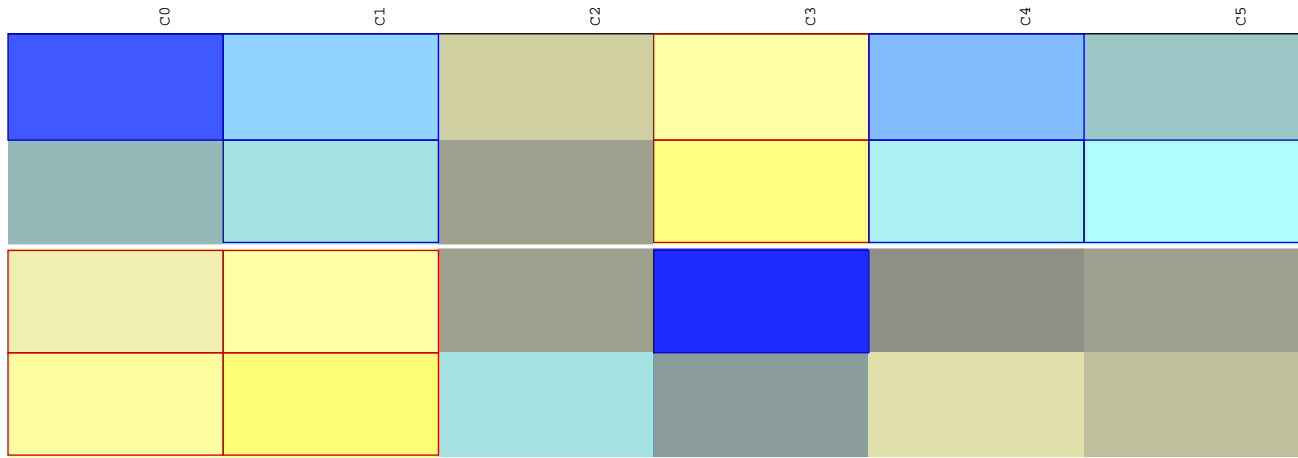


over-representation

representation



Optimized motif

location

MI (bits)

z-score

robustness

position bias

orientation bias

conservation index

seed

motif name

protein array

5'

0.004

23.9

10/10

-

↔

0.92

ATCGATA

PIE_1, NHR_110_NHR_117_NHR_125_NHR_143_NHR_177_NHR_180_NHR_55, BE

5'

0.002

12.5

8/10

-

←

0.98

CTCCACG

EGRH_1_EGRH_2

-

5'

0.003

15.6

10/10

-

←

0.57

ATAGCAA

HAM_2, DAF_19, PIE_1

-

5'

0.002

13.2

8/10

-

-

0.92

TCCTCCC

-

-