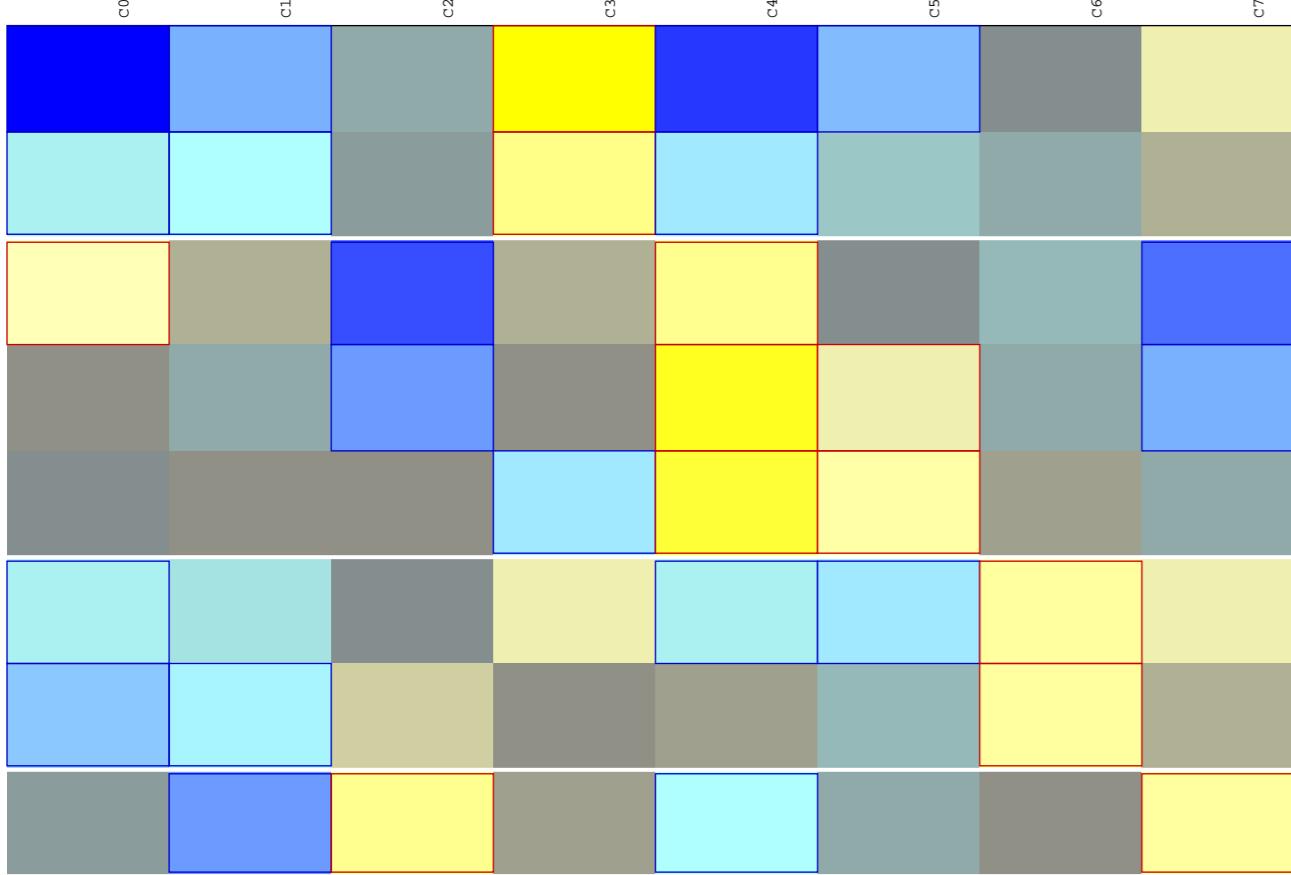


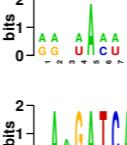
over-representation

10

-10



optimized motif



location

3' UTR

MI (bits)

0.008

41.2

10/10

Y

↔

0.97

AAAAAUU

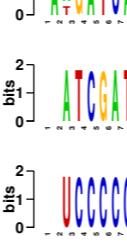
-

conservation index

seed

motif name

protein array



location

5'

MI (bits)

0.003

12.3

8/10

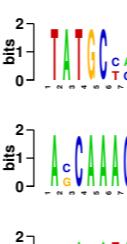
-

↔

0.94

ATGATCA

NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, NHR_119_NHR_31



location

5'

MI (bits)

0.004

21.8

10/10

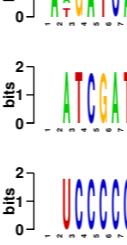
-

↔

1.00

AATCGAT

CEH_28, CEH-28, CEH_38 ...



location

3' UTR

MI (bits)

0.004

20.6

10/10

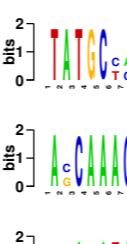
-

→

0.99

AUCCCCC

-



location

5'

MI (bits)

0.003

12.4

8/10

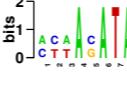
Y

→

0.90

CTCTTCC

EOR_1.2, EOR-1, PIE_1



location

5'

MI (bits)

0.003

13.7

9/10

-

↔

0.70

TATGCTA

-



location

5'

MI (bits)

0.002

10.8

8/10

-

-

0.68

ACCAAAC

PIE_1

