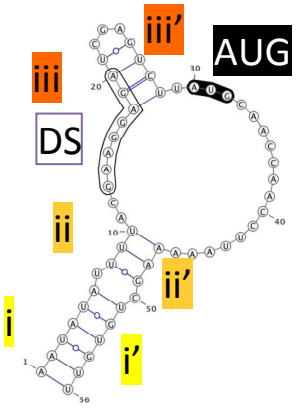
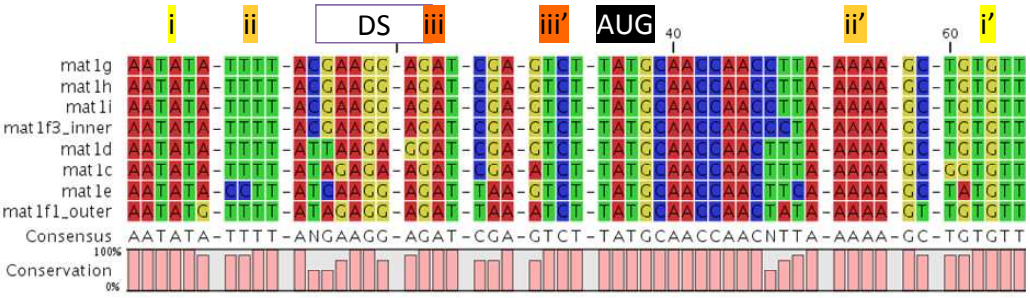

iii'
AUG
iii
DS
ii
ii'
i
i'
mat1g mat1h mat1i


i
ii
DS
iii
iii'
AUG
ii'
i'
40
60
mat1g
mat1h
mat1i
mat1f3_inner
mat1d
mat1c
mat1e
mat1f1_outer
Consensus
AATATA-TTTT-ANGAAGG-AGAT-CGA-GTCT-TATGCAACCAACNTTA-AAAA-GC-TGTGTT
100%
Conservation
0%