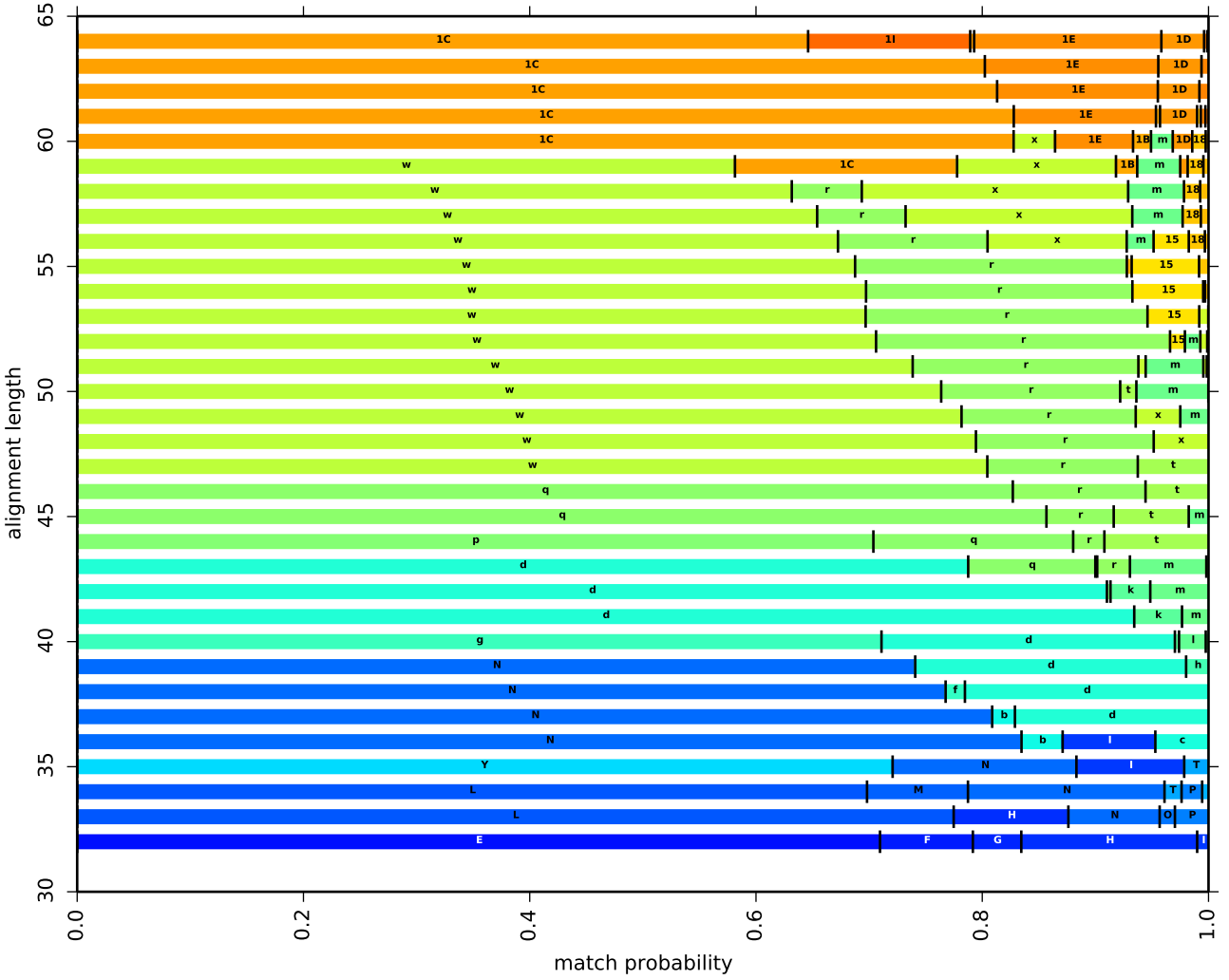
alignment length
65
60
55
50
45
40
35
30
0.0
0.2
0.4
0.6
0.8
1.0
match probability
1C 1I 1E 1D
1C 1E 1D
1C 1E 1D
1C 1E 1D
1C x 1E 1B m 1D 1B
w 1C x 1B m 1B
w r x m 1B
w r x m 1B
w r x m 15 1B
w r 15
w r 15
w r 15
w r 15 m
w r m
w r t m
w r x m
w r x
w r t
q r t
q r t m
p q r t
d q r m
d k m
d k m
g d l
N d h
N f d
N b d
N b I c
Y N I T
L M N T P
L H N O P
E F G H I