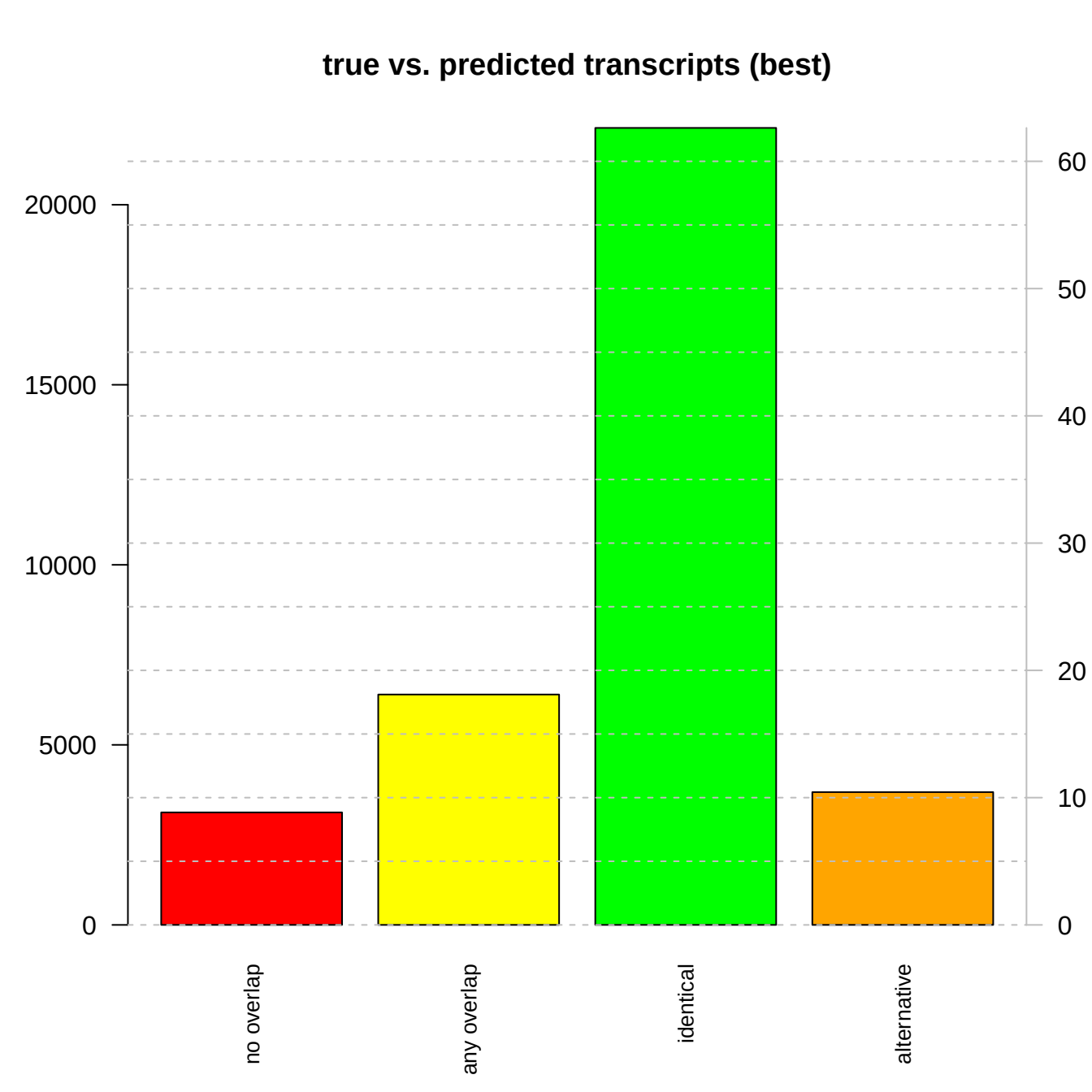
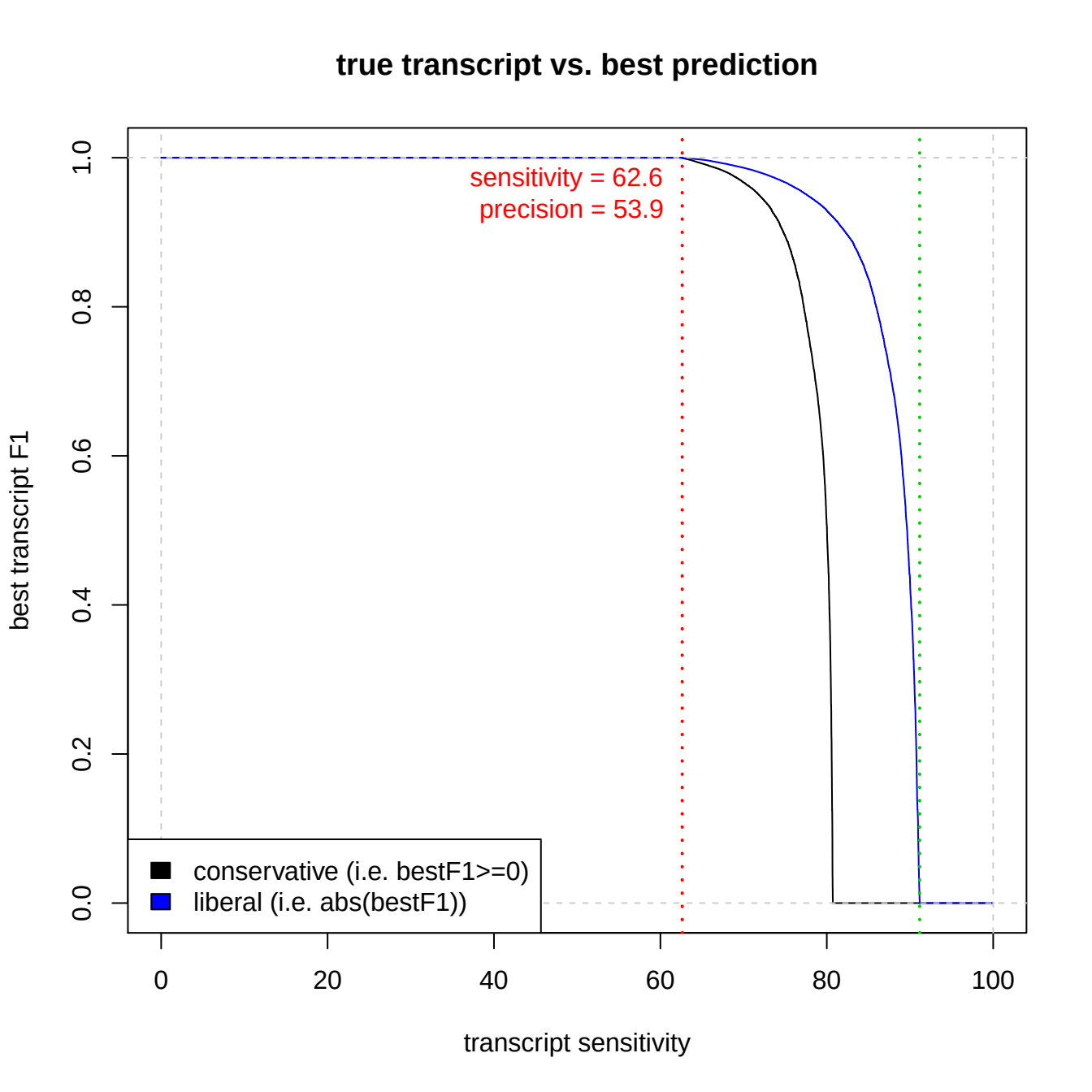
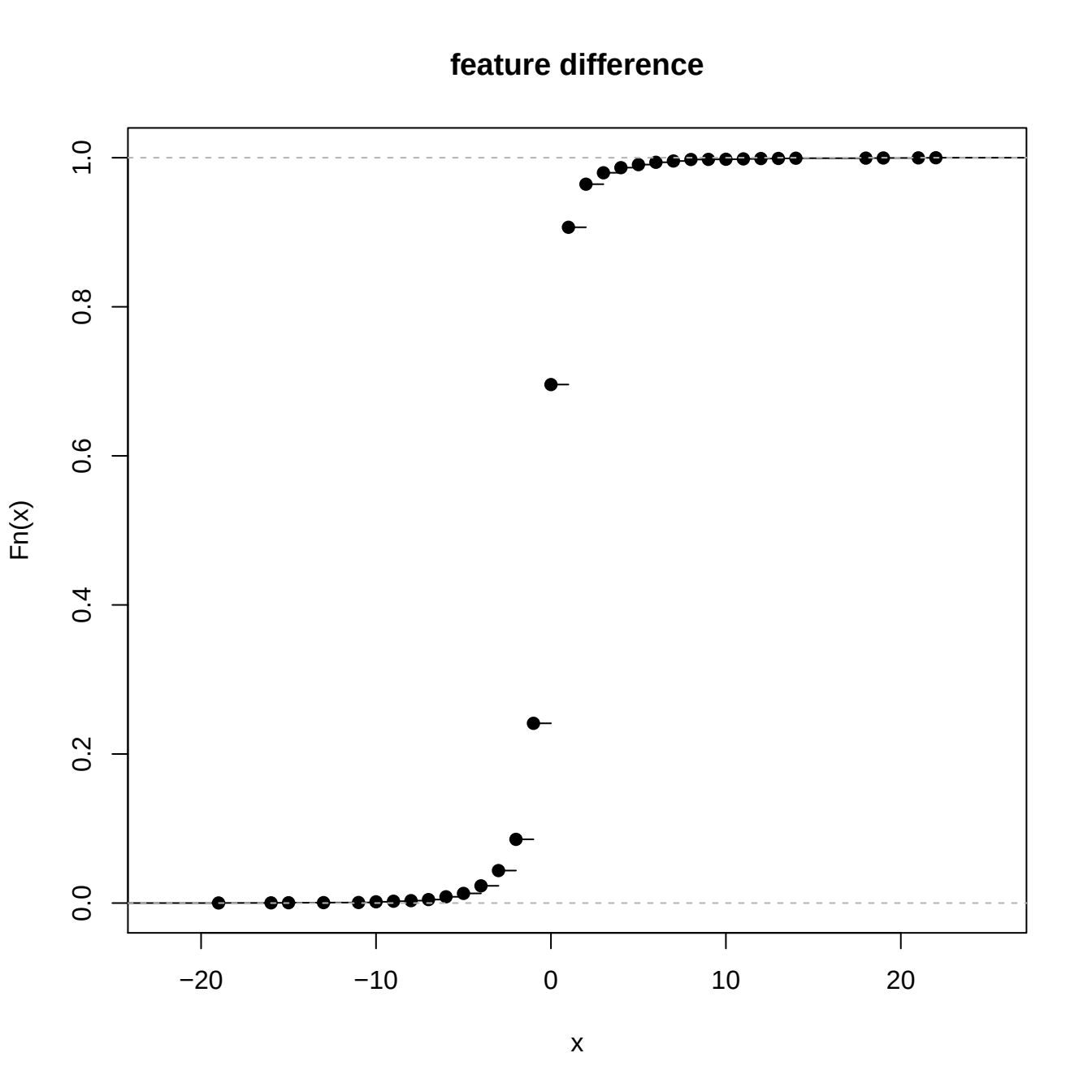
all annotations

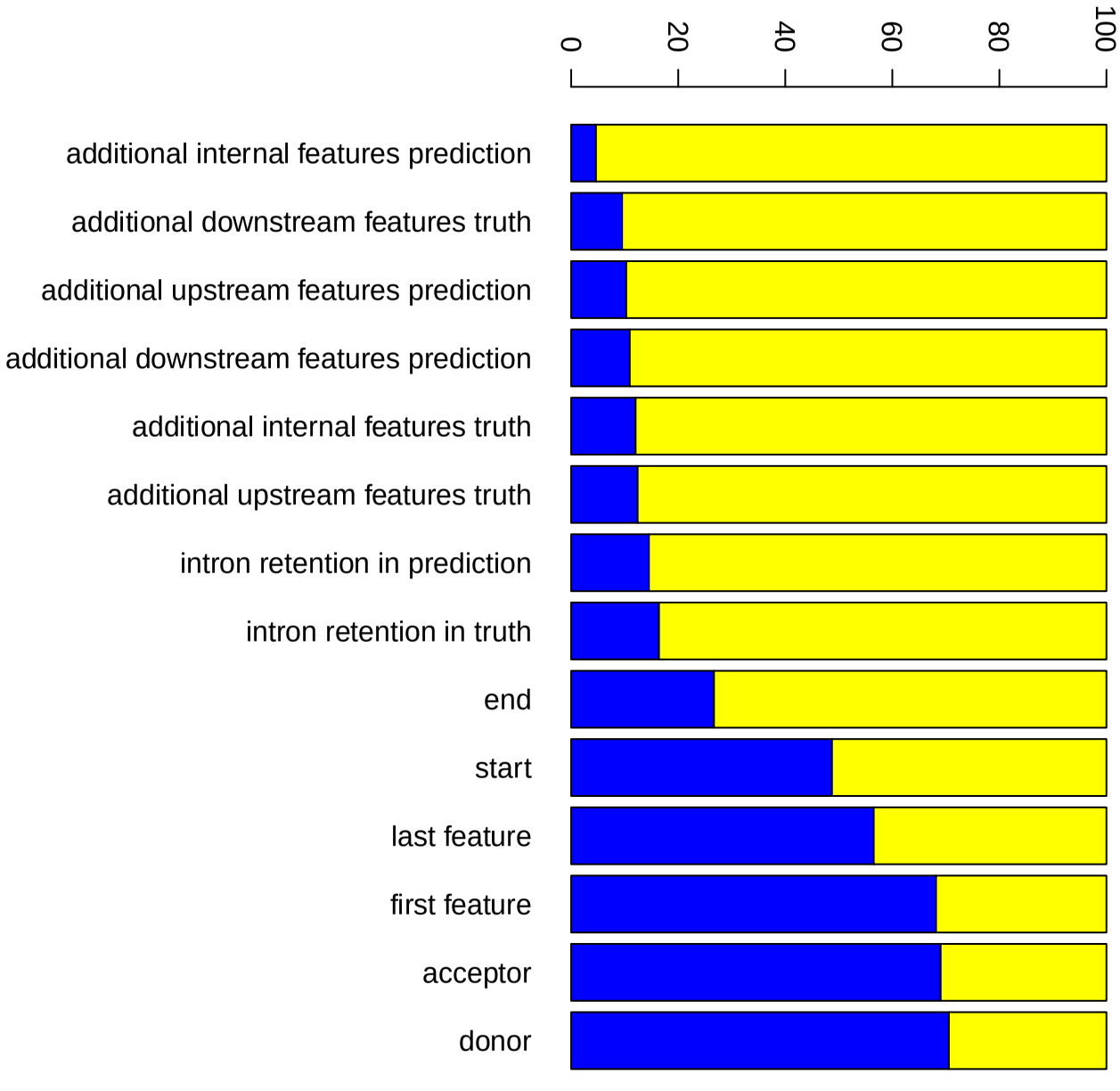

true vs. predicted transcripts (best)
20000
15000
10000
5000
0
60
50
40
30
20
10
0
no overlap
any overlap
identical
alternative


true transcript vs. best prediction
sensitivity = 62.6
precision = 53.9
conservative (i.e. bestF1>=0)
liberal (i.e. abs(bestF1))
best transcript F1
transcript sensitivity
0.0
0.2
0.4
0.6
0.8
1.0
0
20
40
60
80
100

any overlap

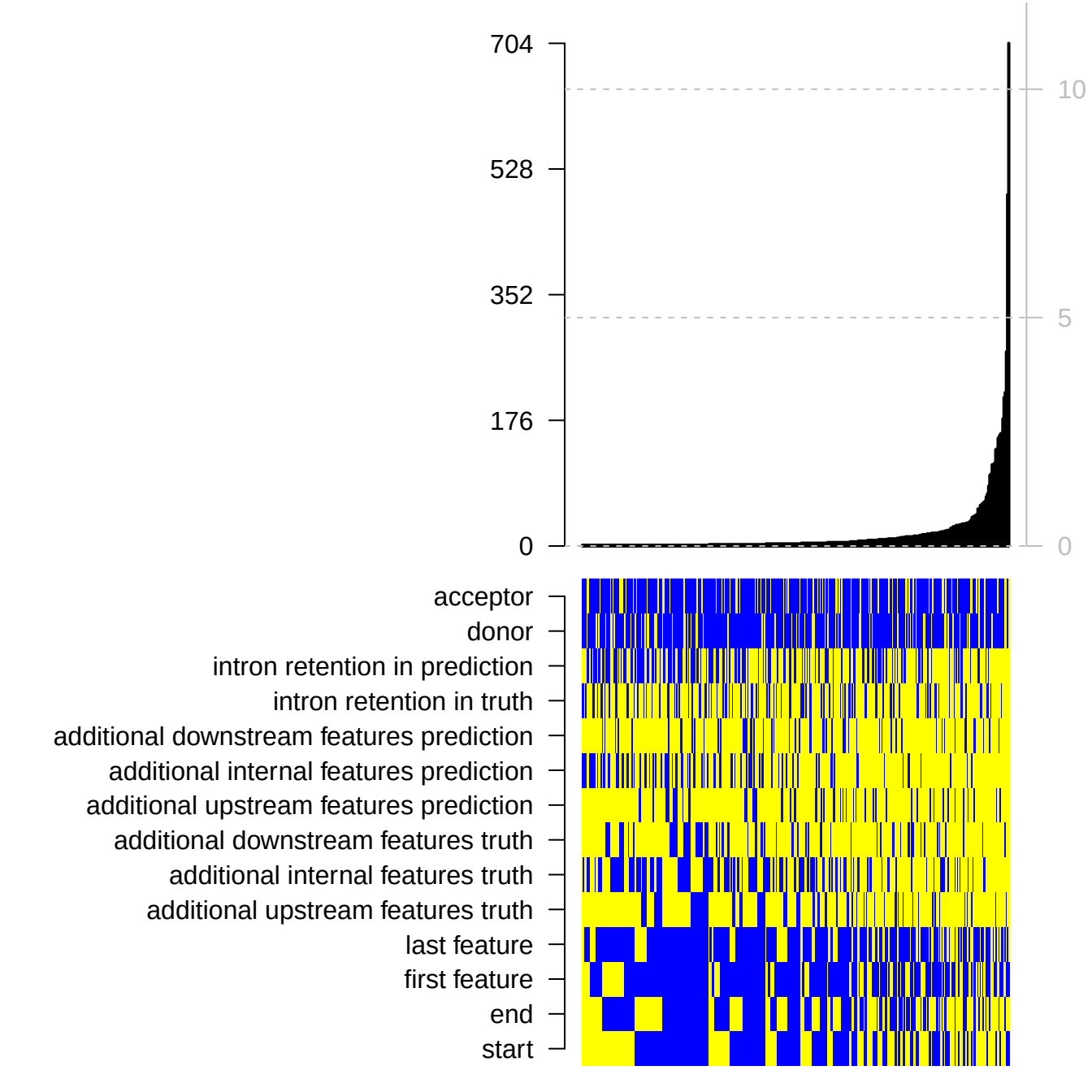
single stat

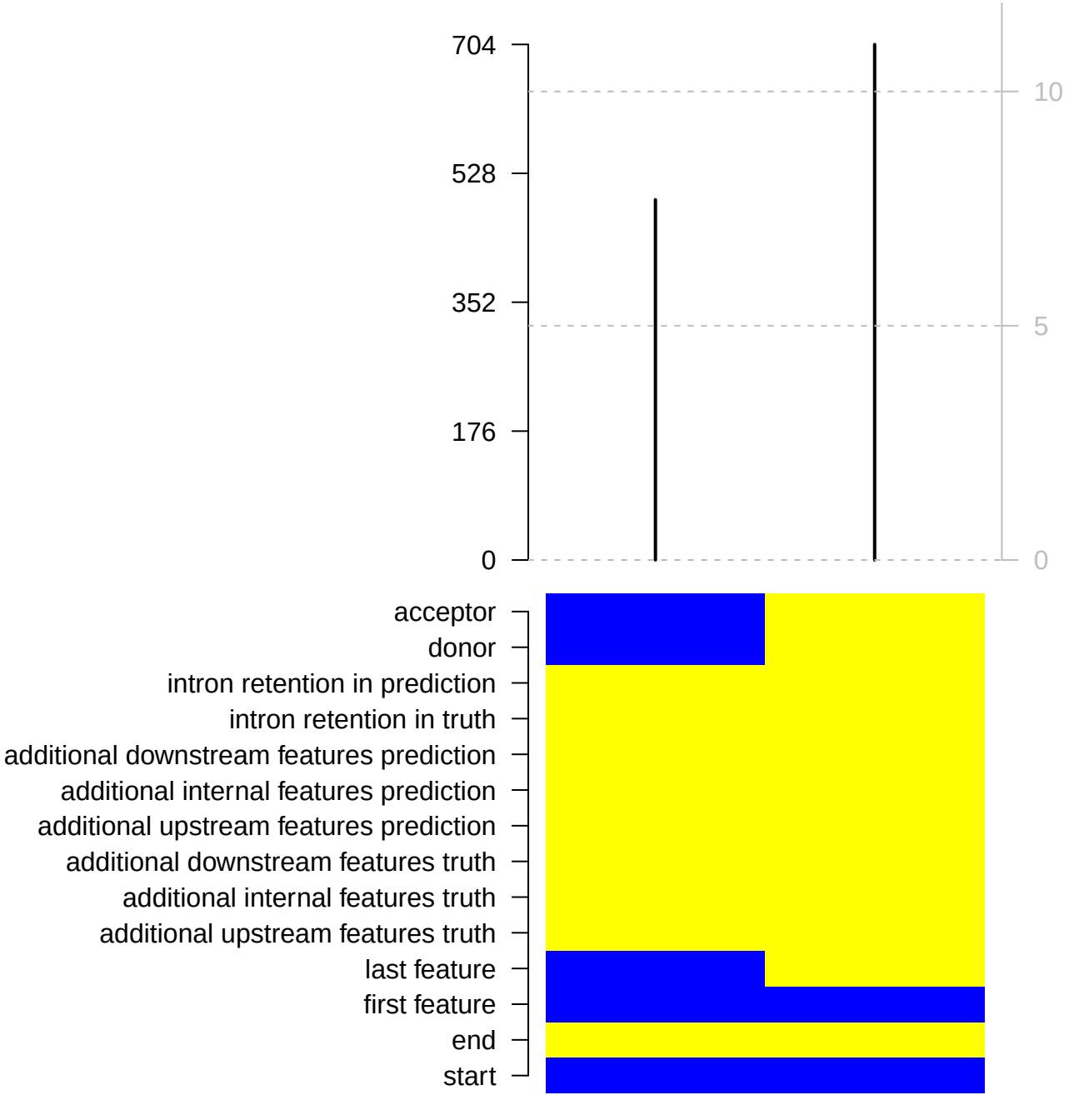

feature difference
Fn(x)
0.0
0.2
0.4
0.6
0.8
1.0
−20
−10
0
10
20
x


0
20
40
60
80
100
additional internal features prediction
additional downstream features truth
additional upstream features prediction
additional downstream features prediction
additional internal features truth
additional upstream features truth
intron retention in prediction
intron retention in truth
end
start
last feature
first feature
acceptor
donor

any overlap

combined stat


704
528
352
176
0
10
5
0
acceptor
donor
intron retention in prediction
intron retention in truth
additional downstream features prediction
additional internal features prediction
additional upstream features prediction
additional downstream features truth
additional internal features truth
additional upstream features truth
last feature
first feature
end
start


704
528
352
176
0
10
5
0
acceptor
donor
intron retention in prediction
intron retention in truth
additional downstream features prediction
additional internal features prediction
additional upstream features prediction
additional downstream features truth
additional internal features truth
additional upstream features truth
last feature
first feature
end
start