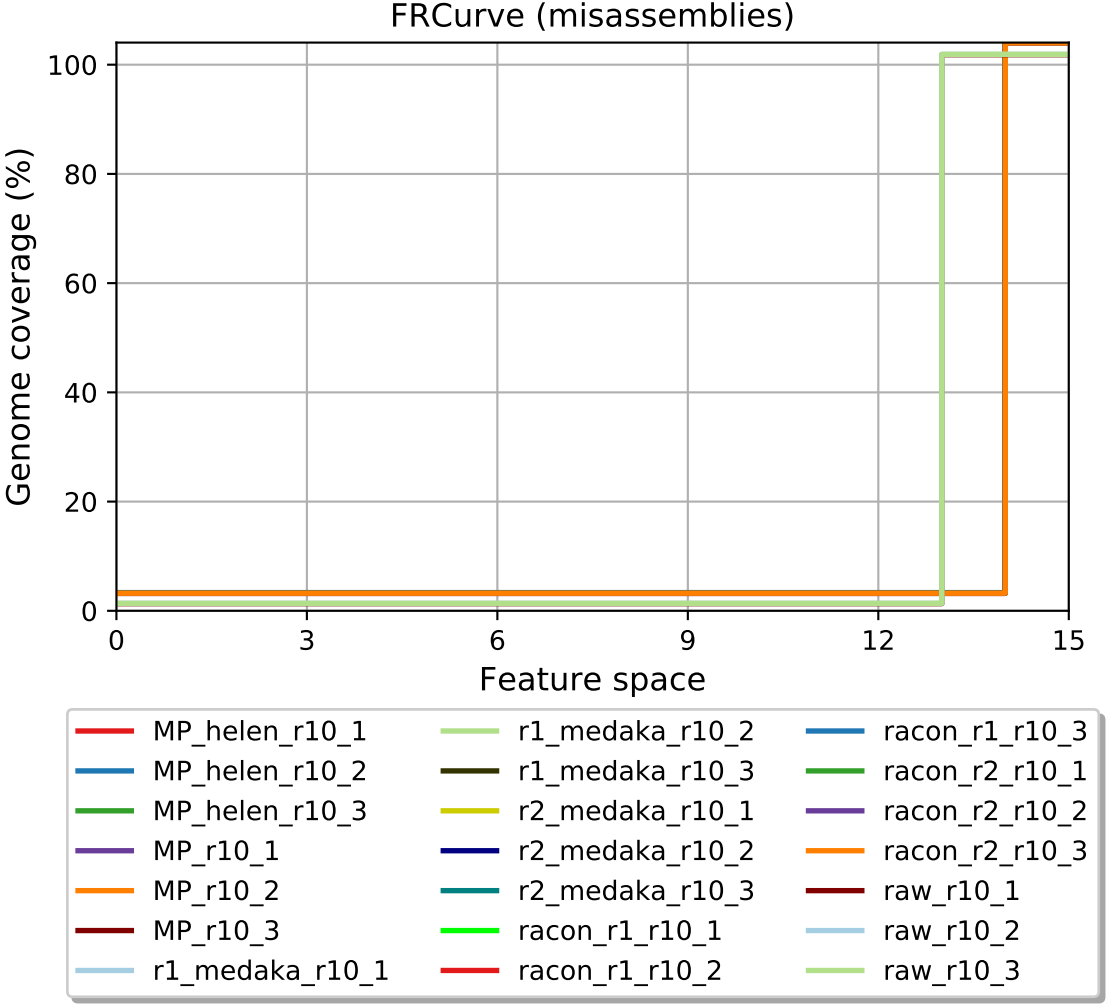
FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
MP_r10_2
MP_r10_3
r1_medaka_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r1_r10_1
racon_r1_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1
raw_r10_2
raw_r10_3