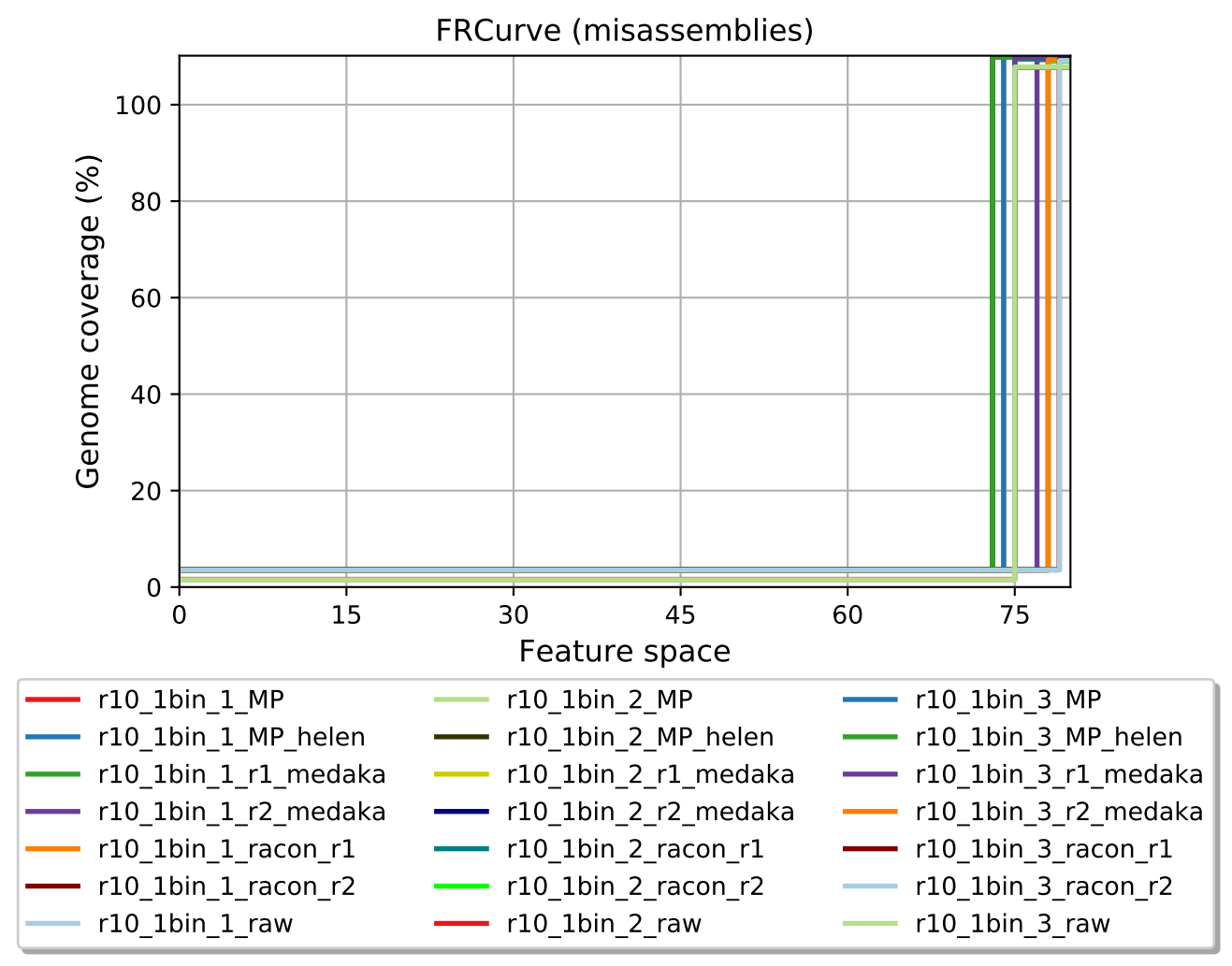
FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
15
30
45
60
75
Feature space
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_1_r2_medaka
r10_1bin_1_racon_r1
r10_1bin_1_racon_r2
r10_1bin_1_raw
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_2_r2_medaka
r10_1bin_2_racon_r1
r10_1bin_2_racon_r2
r10_1bin_2_raw
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medaka
r10_1bin_3_r2_medaka
r10_1bin_3_racon_r1
r10_1bin_3_racon_r2
r10_1bin_3_raw