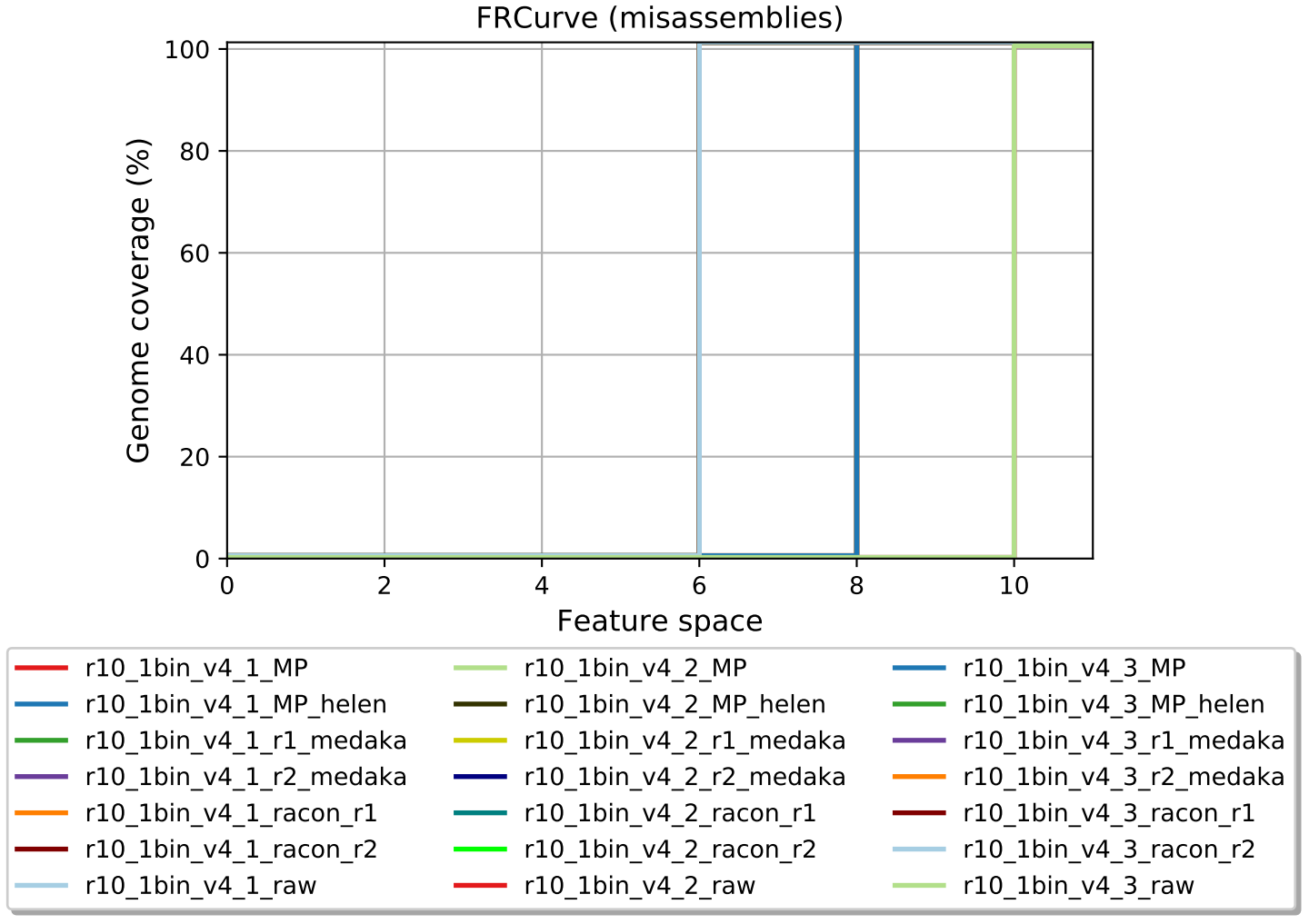
FRCurve (misassemblies)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
2
4
6
8
10
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_1_r2_medaka
r10_1bin_v4_1_racon_r1
r10_1bin_v4_1_racon_r2
r10_1bin_v4_1_raw
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_2_racon_r1
r10_1bin_v4_2_racon_r2
r10_1bin_v4_2_raw
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_helen
r10_1bin_v4_3_r1_medaka
r10_1bin_v4_3_r2_medaka
r10_1bin_v4_3_racon_r1
r10_1bin_v4_3_racon_r2
r10_1bin_v4_3_raw