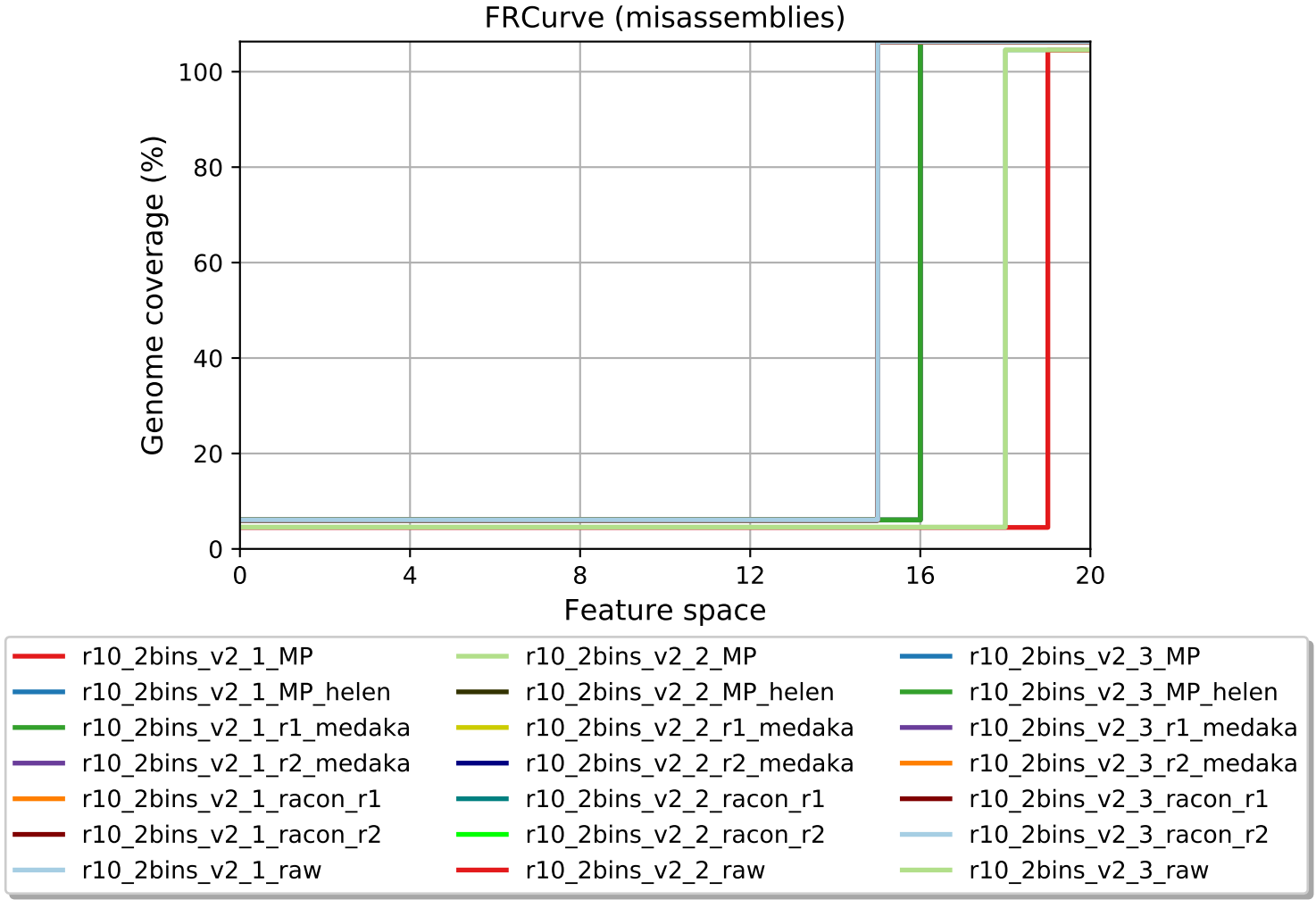
FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
4
8
12
16
20
Feature space
r10_2bins_v2_1_MP
r10_2bins_v2_1_MP_helen
r10_2bins_v2_1_r1_medaka
r10_2bins_v2_1_r2_medaka
r10_2bins_v2_1_racon_r1
r10_2bins_v2_1_racon_r2
r10_2bins_v2_1_raw
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_2_racon_r1
r10_2bins_v2_2_racon_r2
r10_2bins_v2_2_raw
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP_helen
r10_2bins_v2_3_r1_medaka
r10_2bins_v2_3_r2_medaka
r10_2bins_v2_3_racon_r1
r10_2bins_v2_3_racon_r2
r10_2bins_v2_3_raw