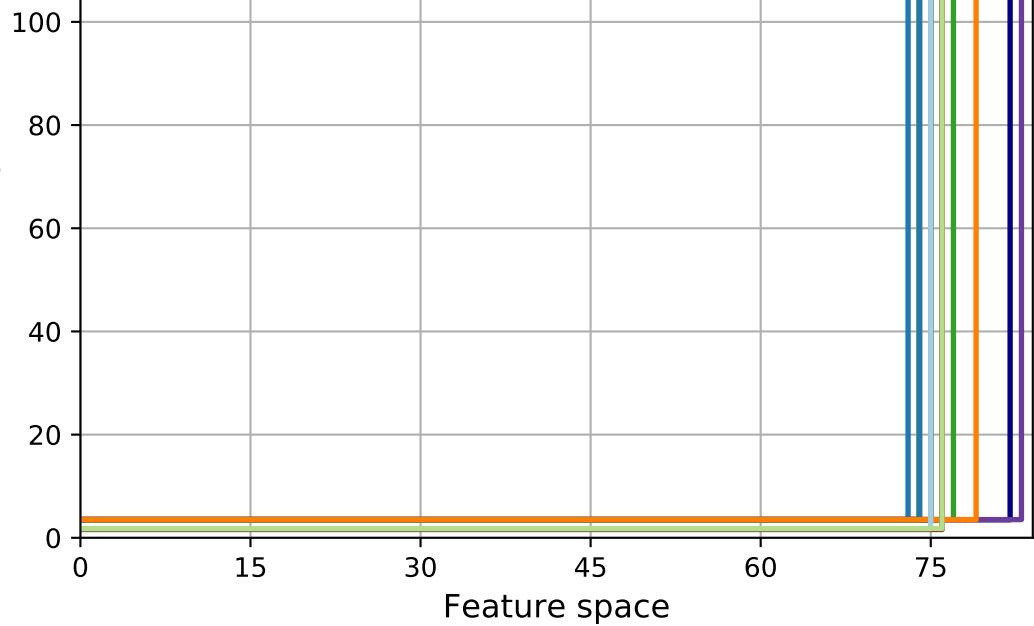


FRCurve (misassemblies)

Genome coverage (%)



- 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