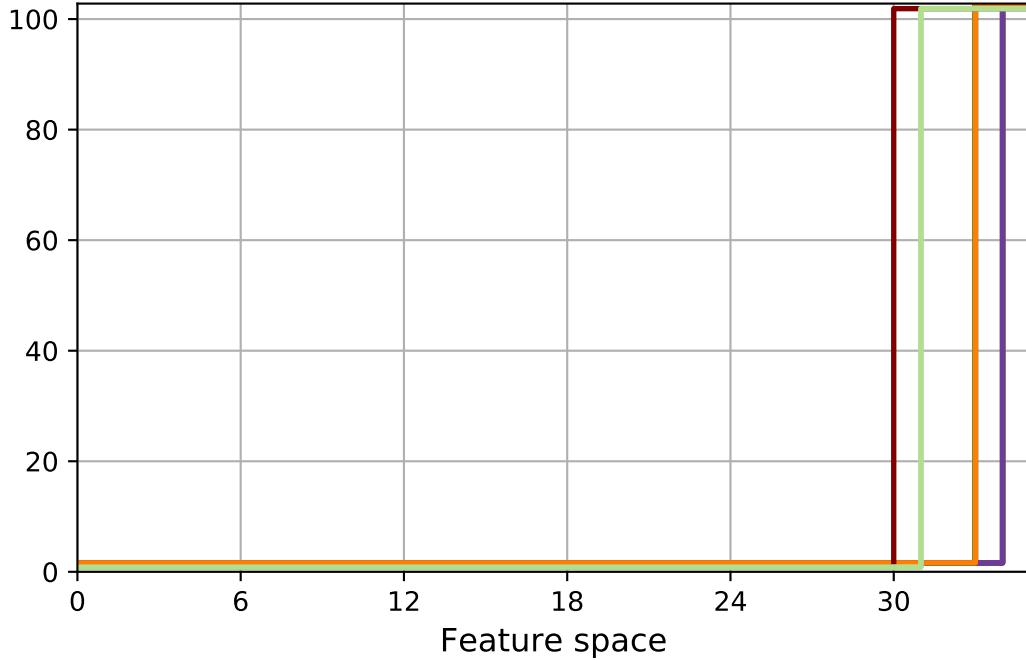


FRCurve (misassemblies)

Genome coverage (%)



Feature space

- MP_helen_r10_1 — r1_medaka_r10_2 — racon_r1_r10_3
- MP_helen_r10_2 — r1_medaka_r10_3 — racon_r2_r10_1
- MP_helen_r10_3 — r2_medaka_r10_1 — racon_r2_r10_2
- MP_r10_1 — r2_medaka_r10_2 — racon_r2_r10_3
- MP_r10_2 — r2_medaka_r10_3 — raw_r10_1
- MP_r10_3 — r1_medaka_r10_1 — raw_r10_2
- r1_medaka_r10_1 — racon_r1_r10_2 — raw_r10_3