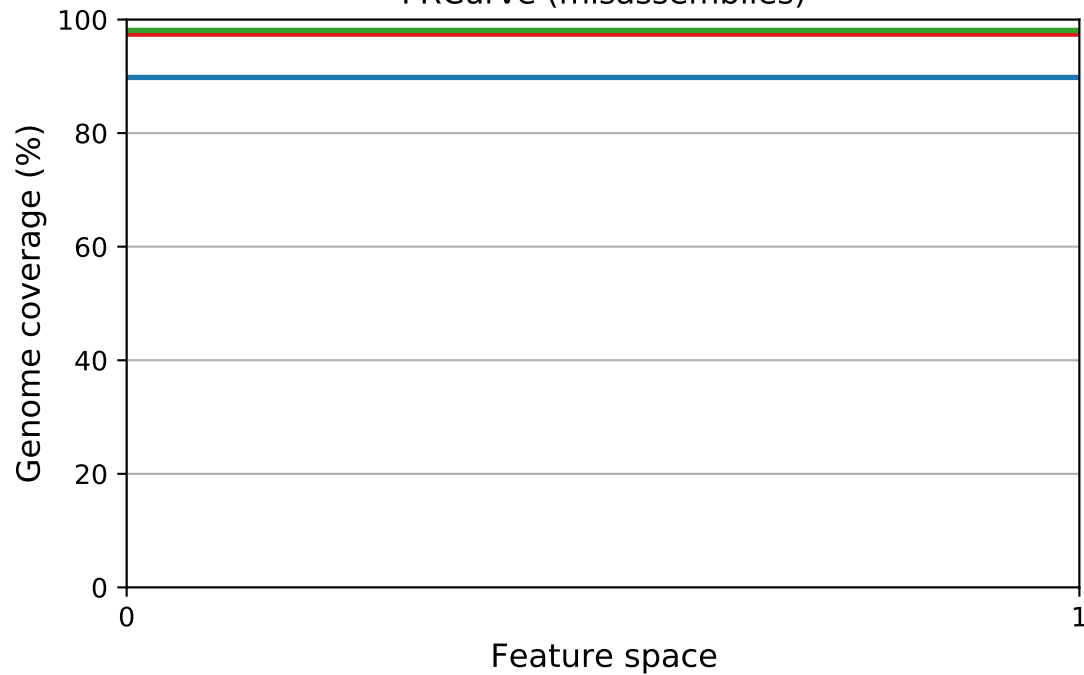FRCurve (misassemblies)

Feature space

Genome coverage (%)

SAMPLE3_SE.AF0.8.consensus.masked
SAMPLE2_PE.AF0.8.consensus.masked
SAMPLE1_PE.AF0.8.consensus.masked