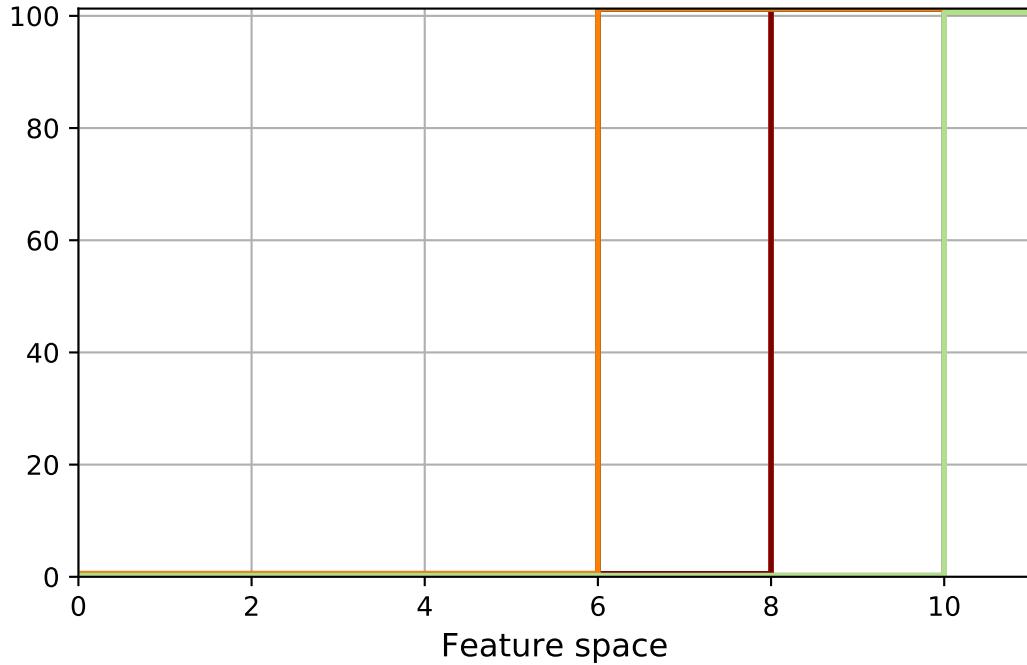


### FRCurve (misassemblies)

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