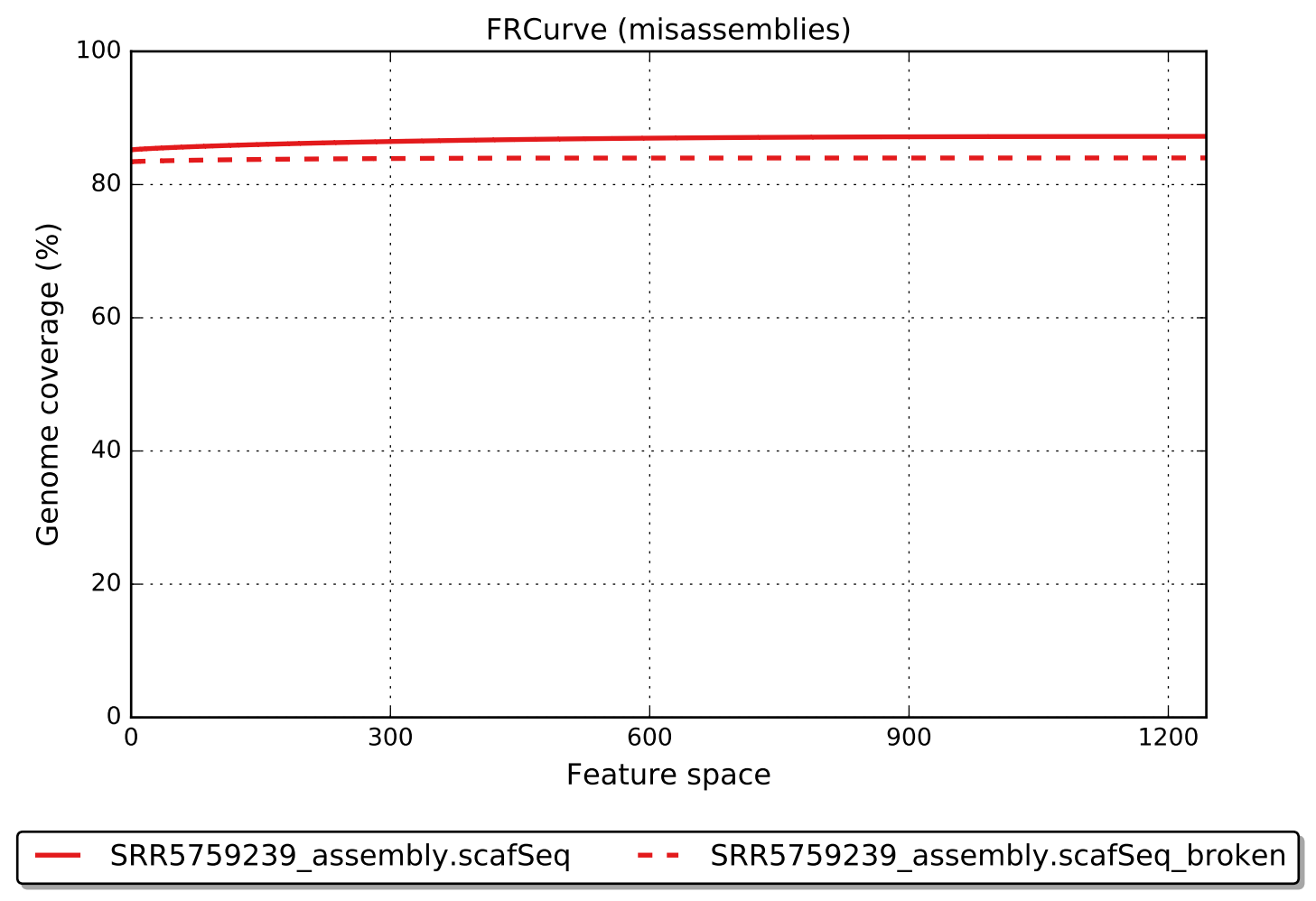
FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
Feature space
SRR5759239_assembly.scafSeq
SRR5759239_assembly.scafSeq_broken