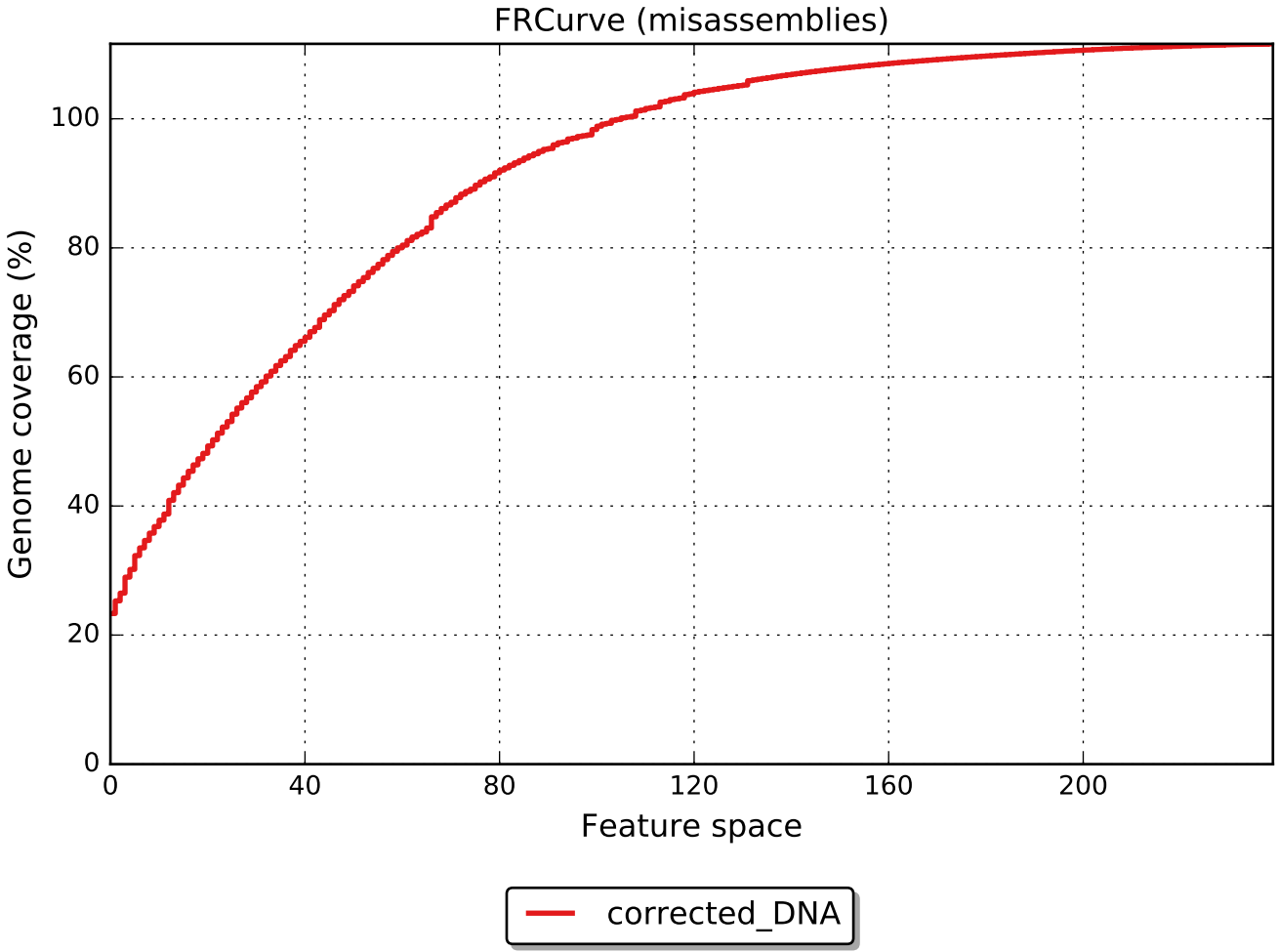
FRCurve (misassemblies)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
40
80
120
160
200
corrected_DNA