Report

	moraxella-8_fa	moraxella-8_fa_broken
# contigs (>= 0 bp)	55	-
# contigs (>= 1000 bp)	17	23
Total length (>= 0 bp)	1870331	-
Total length (>= 1000 bp)	1861851	1861046
# contigs	20	27
Largest contig	449683	415353
Total length	1863878	1863503
Reference length	2649137	2649137
GC (%)	41.59	41.59
Reference GC (%)	43.54	43.54
N50	270620	166697
NG50	228970	134947
N90	138522	52942
NG90	-	-
auN	301684.0	212709.1
auNG	212258.6	149627.6
L50	3	4
LG50	4	6
L90	6	10
LG90	-	-
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	13 + 5 part	18 + 7 part
Unaligned length	1860227	1860083
Genome fraction (%)	0.355	0.360
Duplication ratio	0.998	1.013
# N's per 100 kbp	20.12	0.00
# mismatches per 100 kbp	10623.71	10254.74
# indels per 100 kbp	1302.26	1241.02
# genomic features	12 + 19 part	12 + 19 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	3 + 1 part	3 + 1 part
Largest alignment	1975	1975
Total aligned length	2918	3062
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	2.3	2.3
auNGA	1.6	1.6
LA50	-	-
LGA50	-	-
LA90	-	-
LGA90	-	-

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

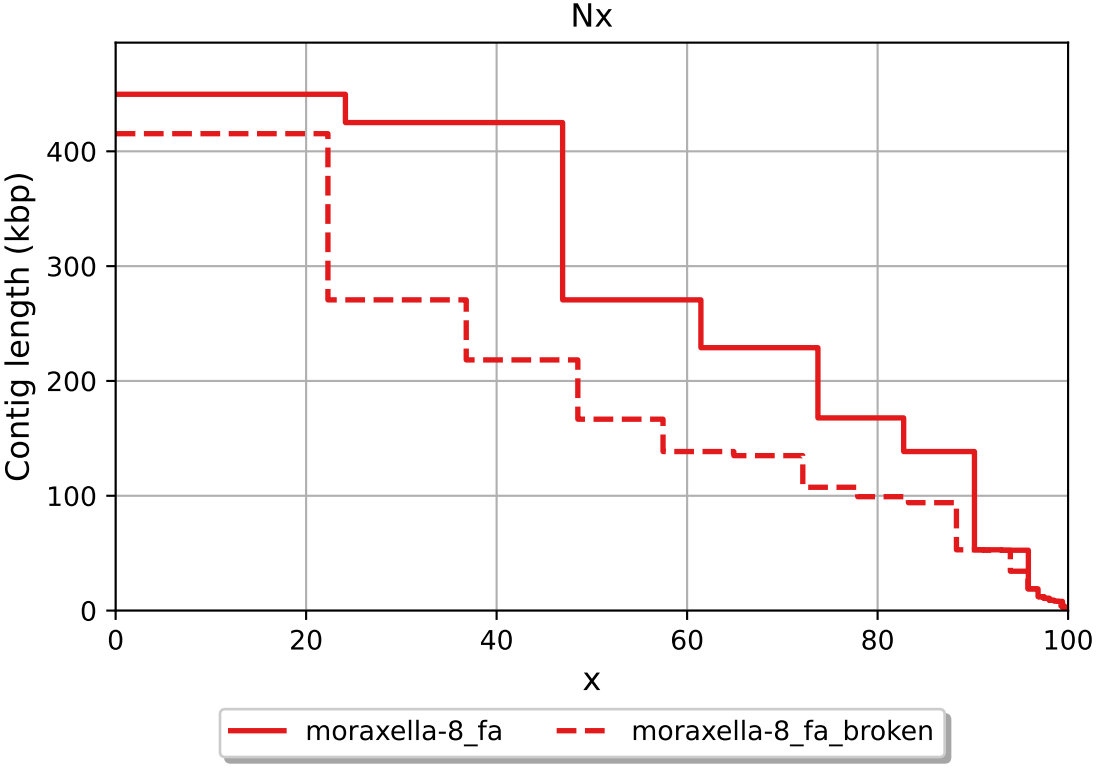
	moraxella-8_fa	moraxella-8_fa_broken
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	310	314
# indels	38	38
# indels (<= 5 bp)	38	38
# indels (> 5 bp)	0	0
Indels length	62	62

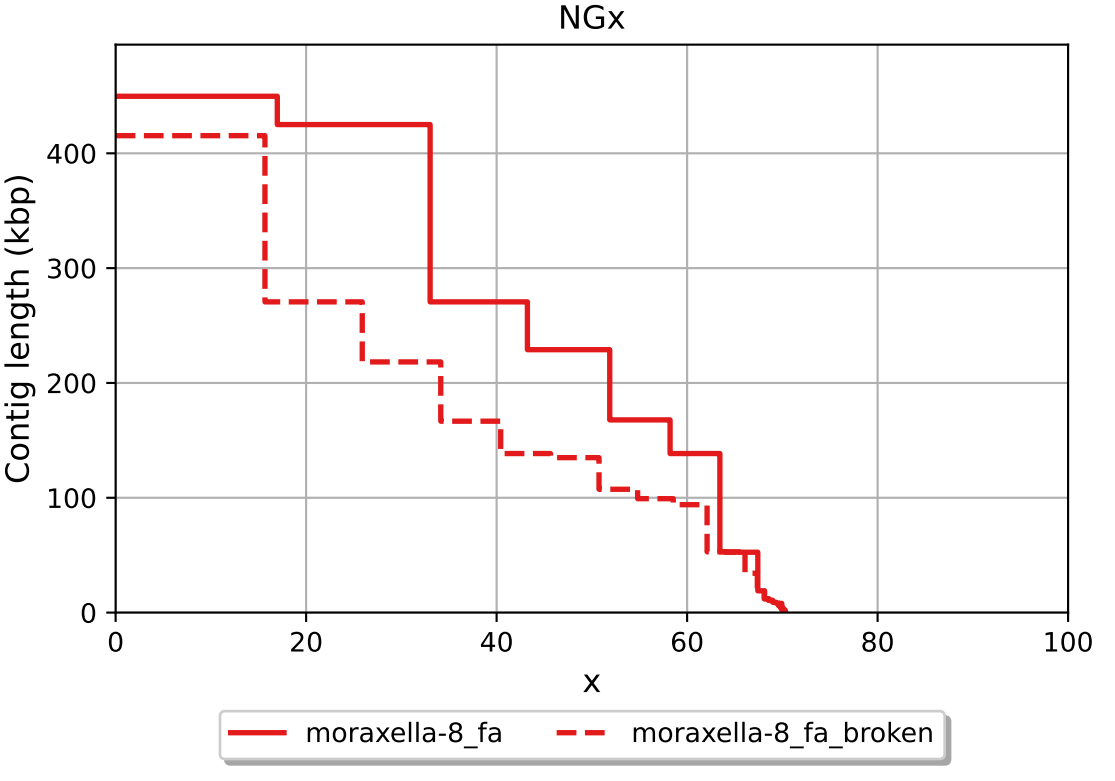
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

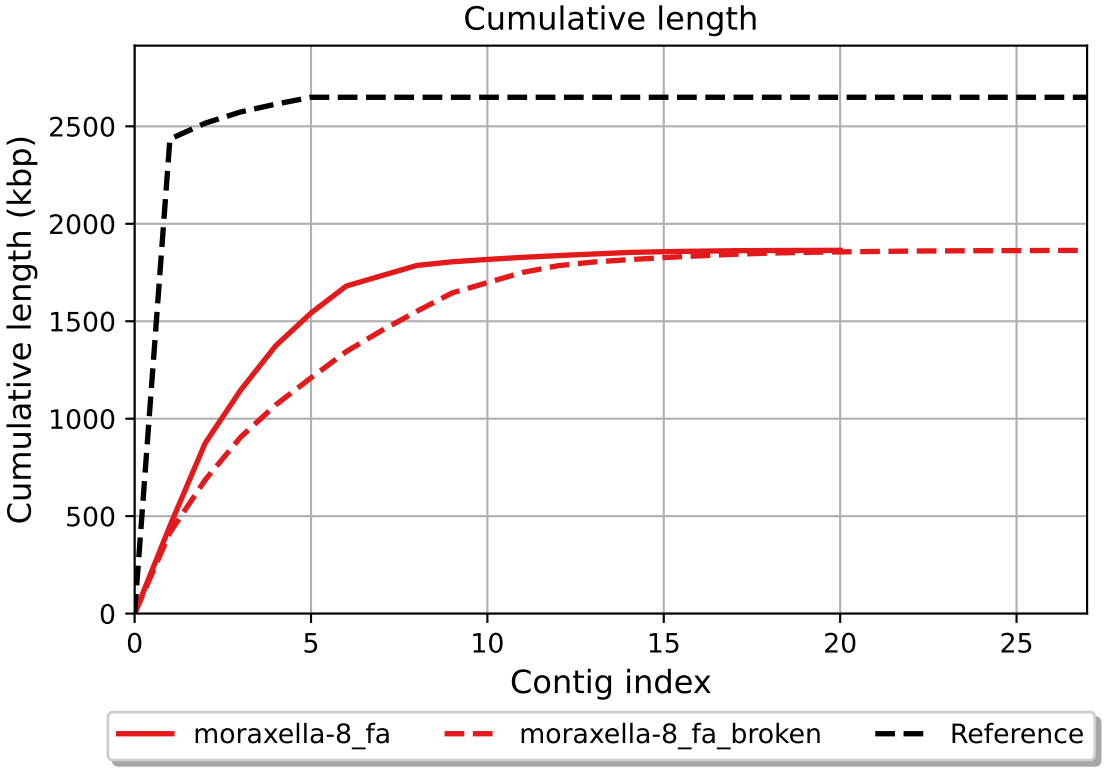
Unaligned report

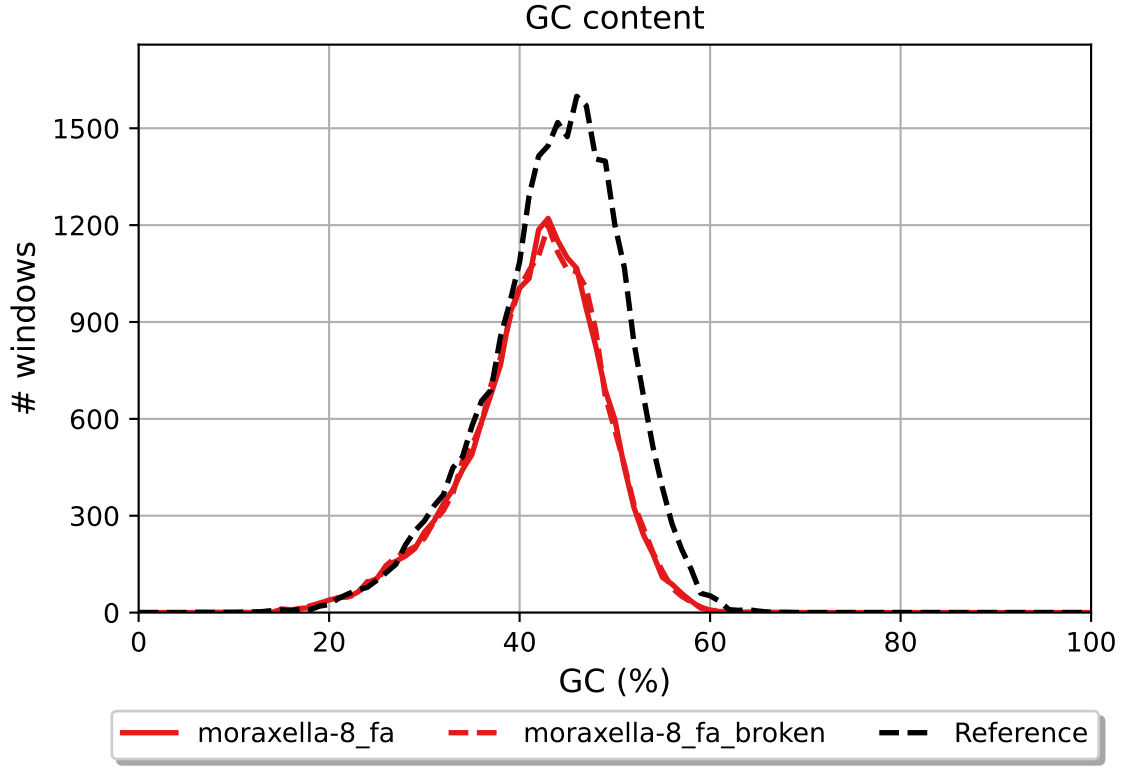
	moraxella-8_fa	moraxella-8_fa_broken
# fully unaligned contigs	13	18
Fully unaligned length	678914	779160
# partially unaligned contigs	5	7
Partially unaligned length	1181313	1080923
# N's	375	0

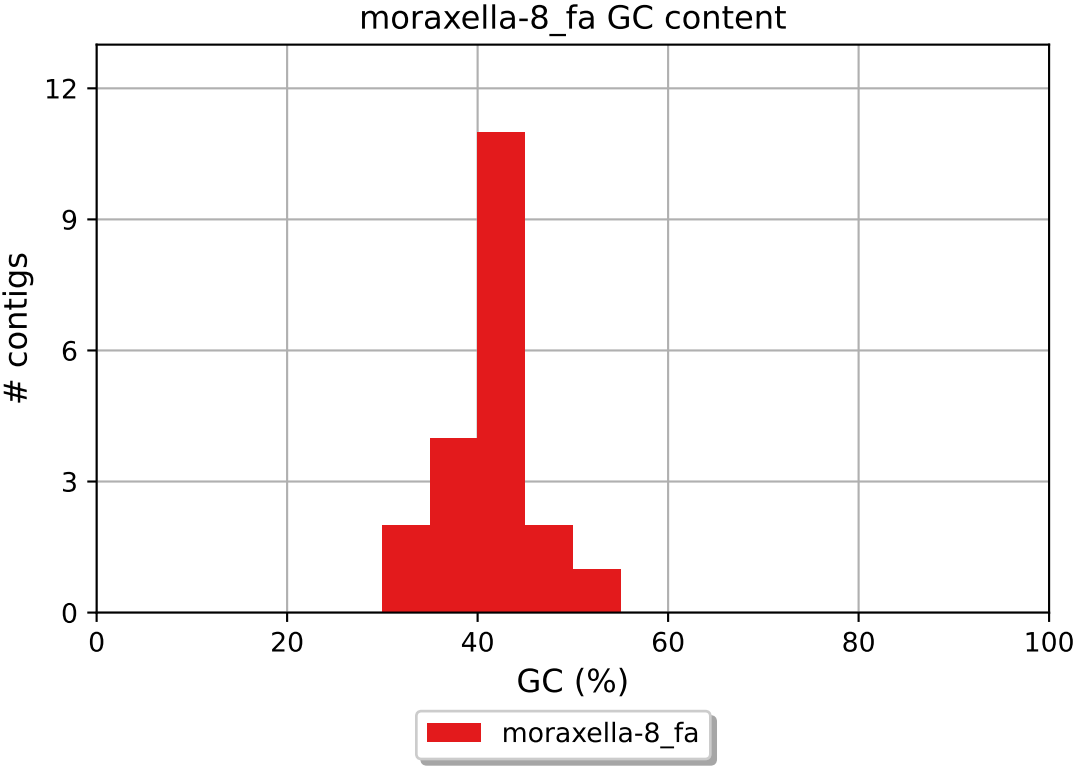
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

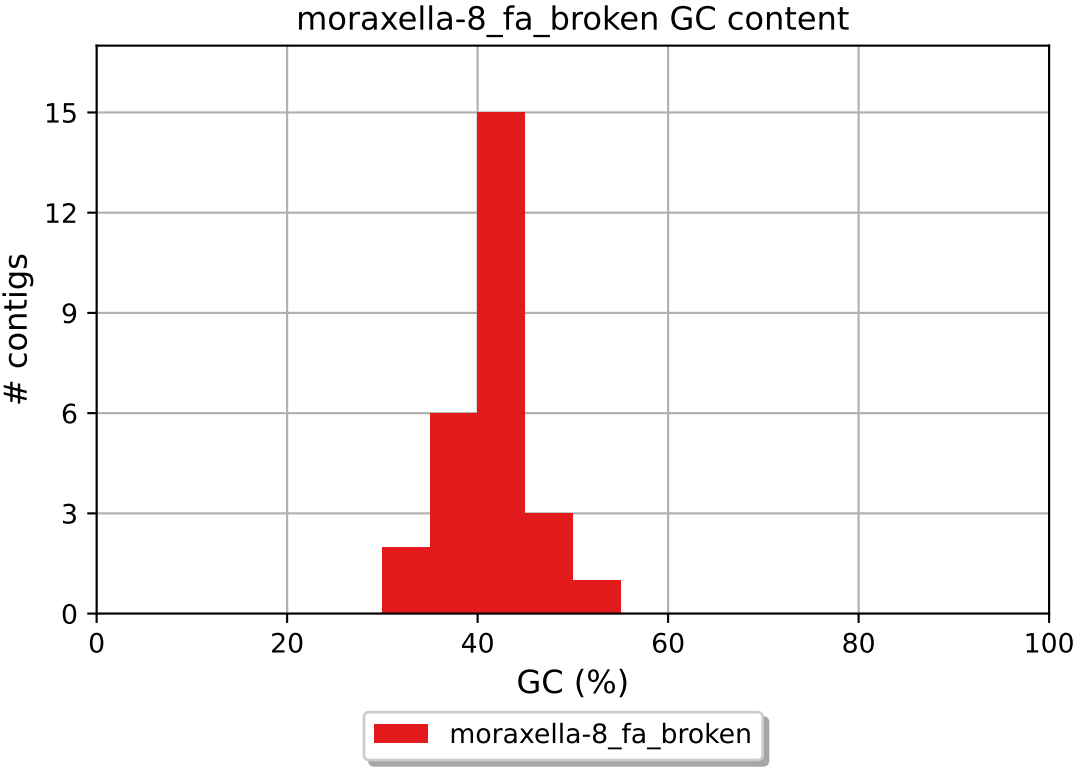

Nx
Contig length (kbp)
0
100
200
300
400
0
20
40
60
80
100
x
moraxella-8_fa
moraxella-8_fa_broken

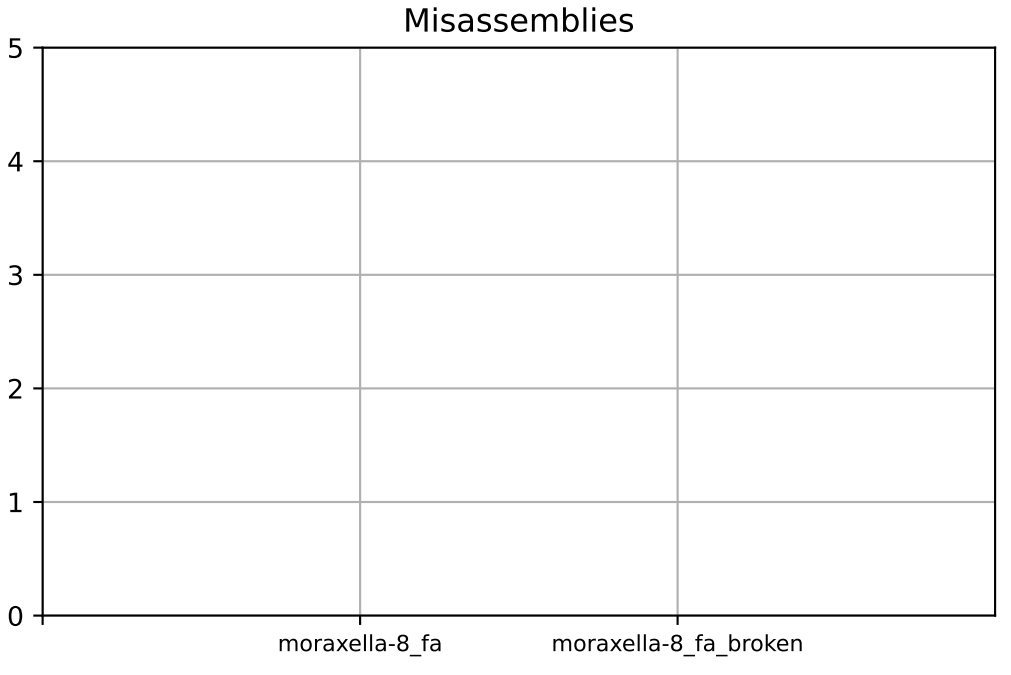

NGx
Contig length (kbp)
0
100
200
300
400
0
20
40
60
80
100
x
moraxella-8_fa
moraxella-8_fa_broken

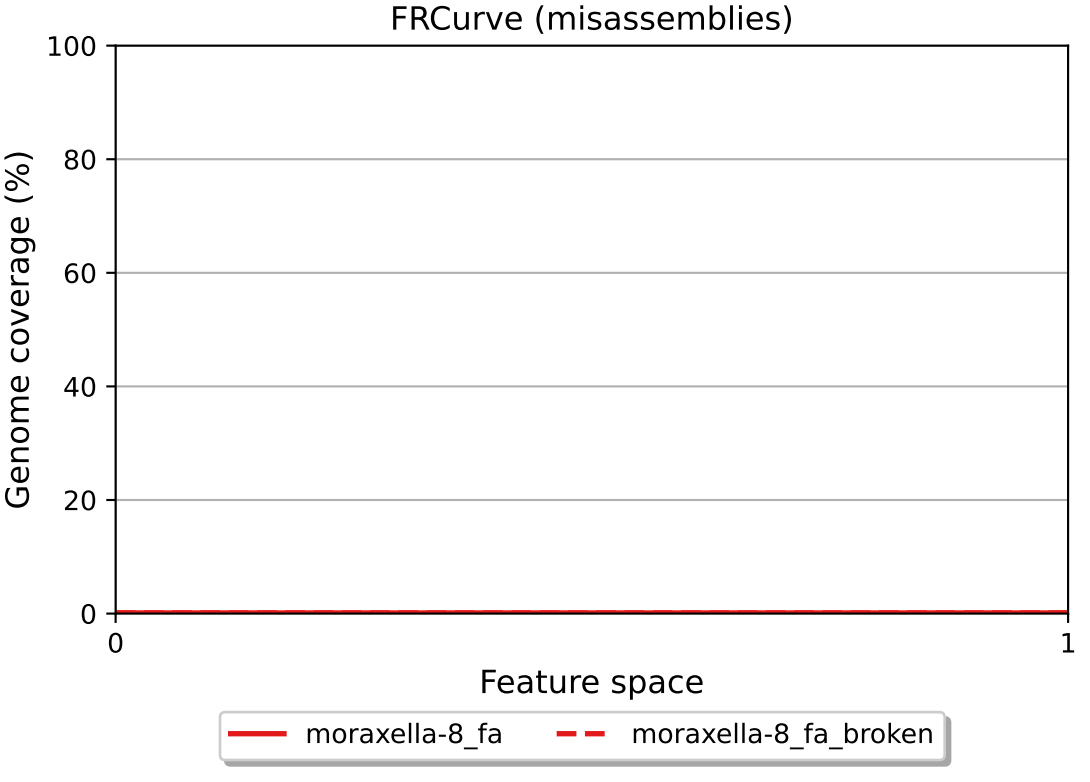

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
5
10
15
20
25
Contig index
moraxella-8_fa
moraxella-8_fa_broken
Reference

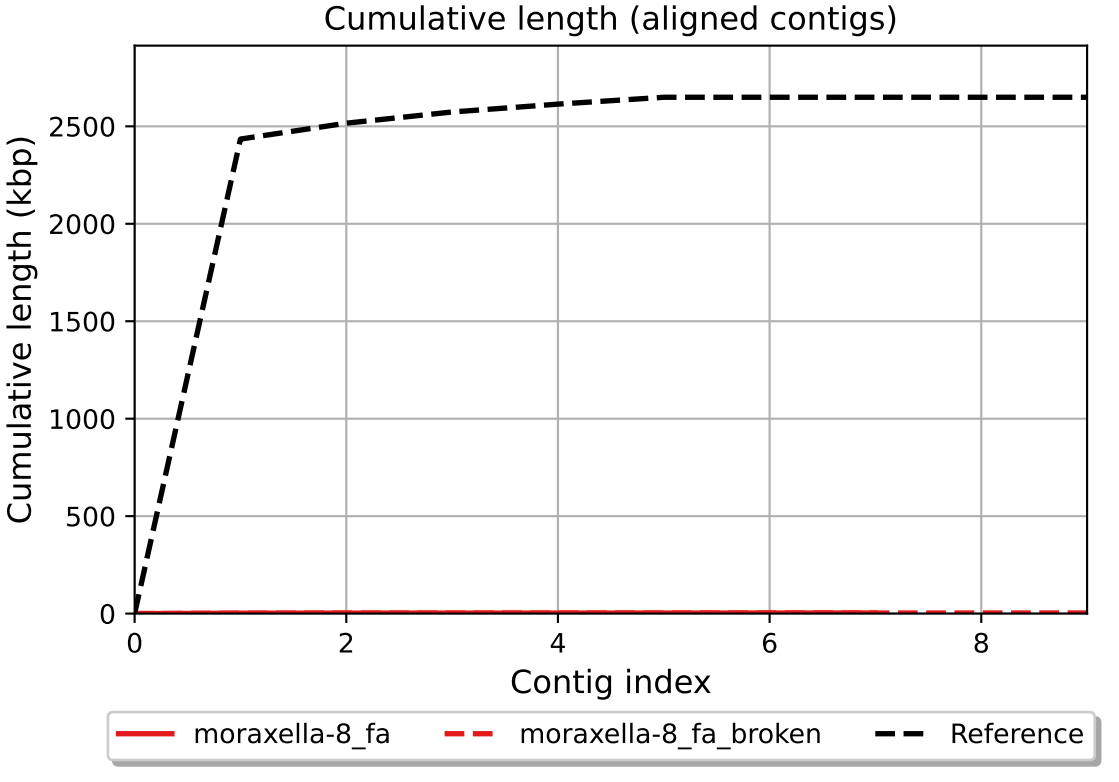

GC content
windows
1500
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
moraxella-8_fa
moraxella-8_fa_broken
Reference

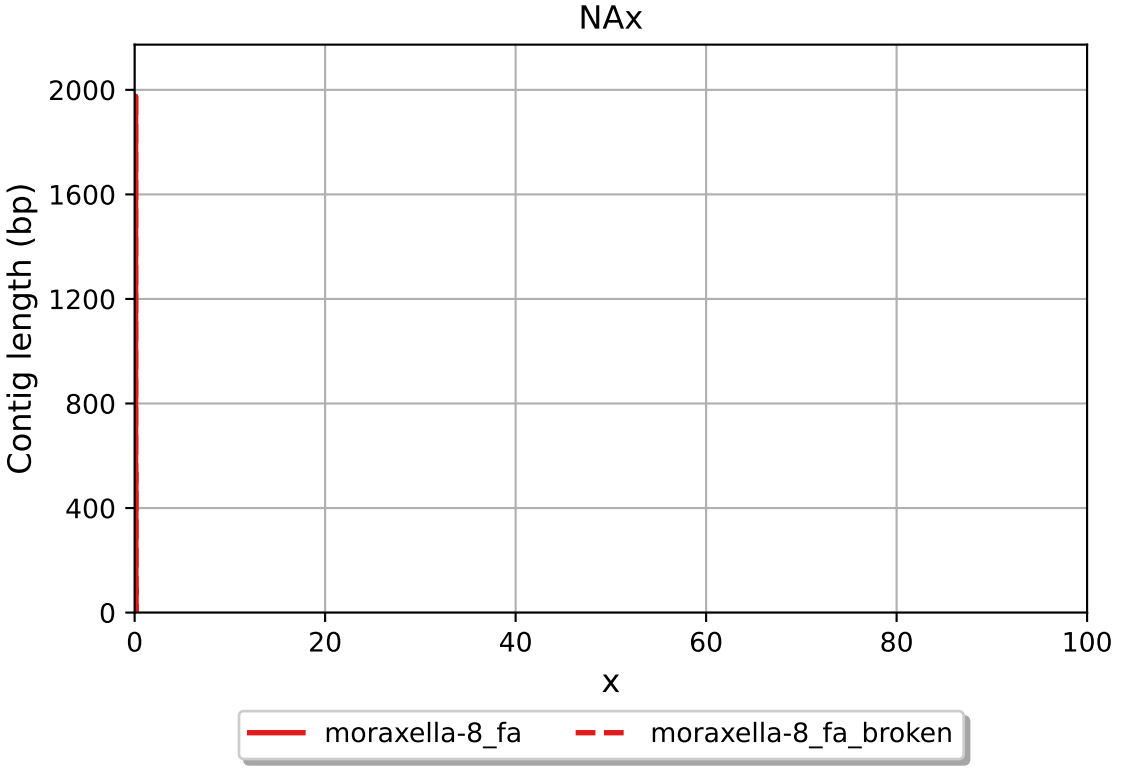

moraxella-8_fa GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
moraxella-8_fa

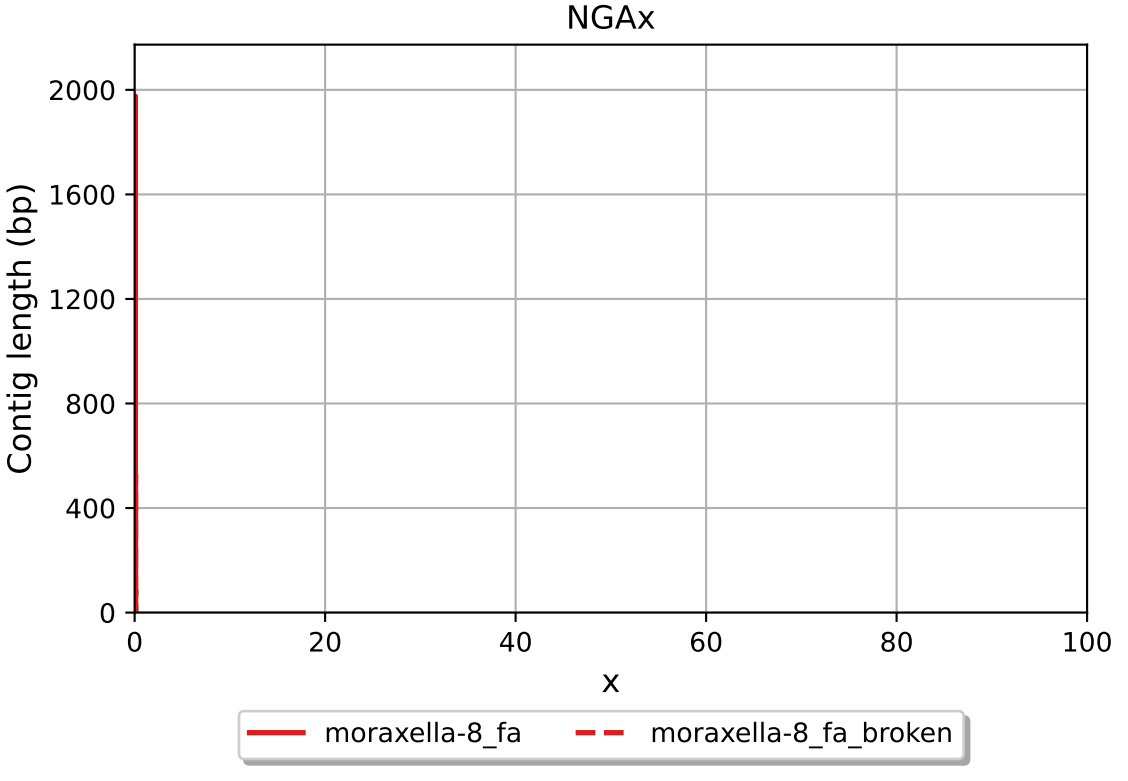

moraxella-8_fa_broken GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
moraxella-8_fa_broken

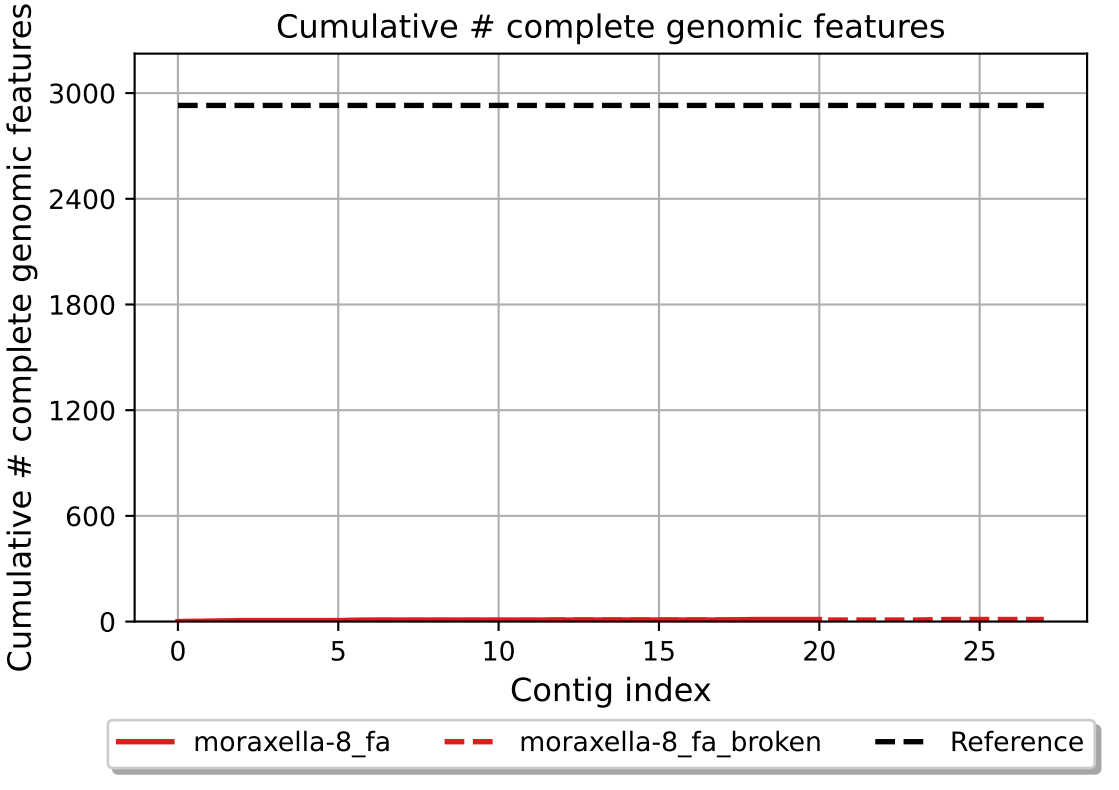

Misassemblies
5
4
3
2
1
0
moraxella-8_fa
moraxella-8_fa_broken

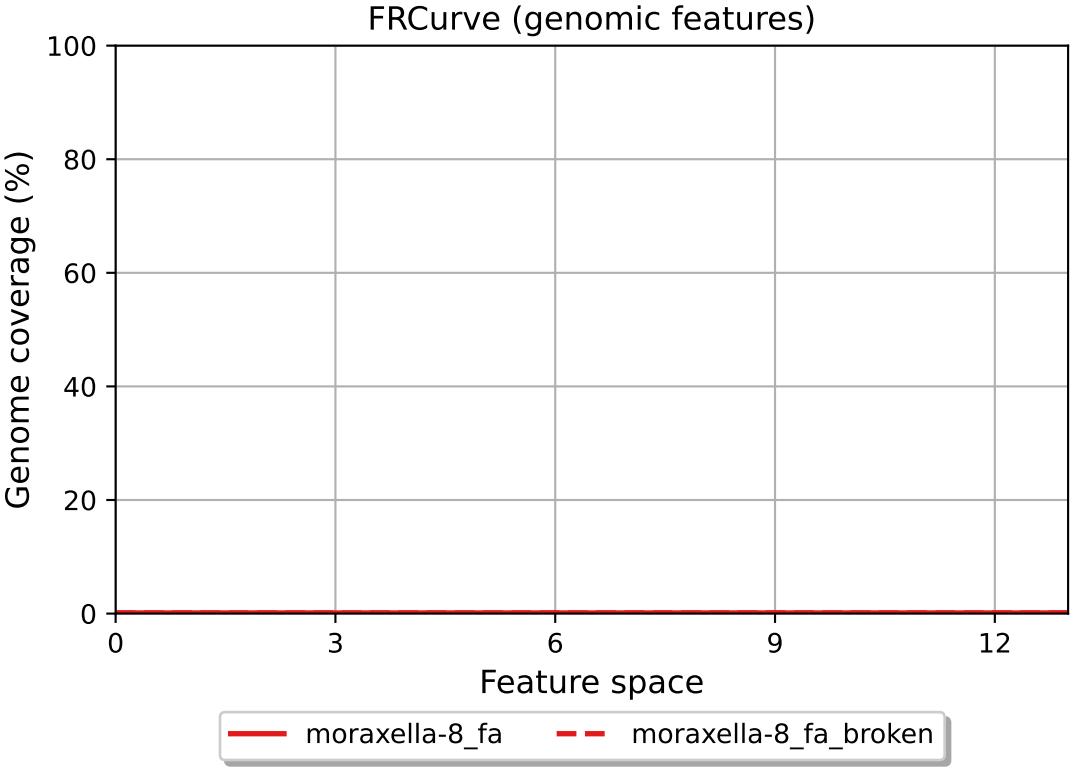

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
moraxella-8_fa
moraxella-8_fa_broken

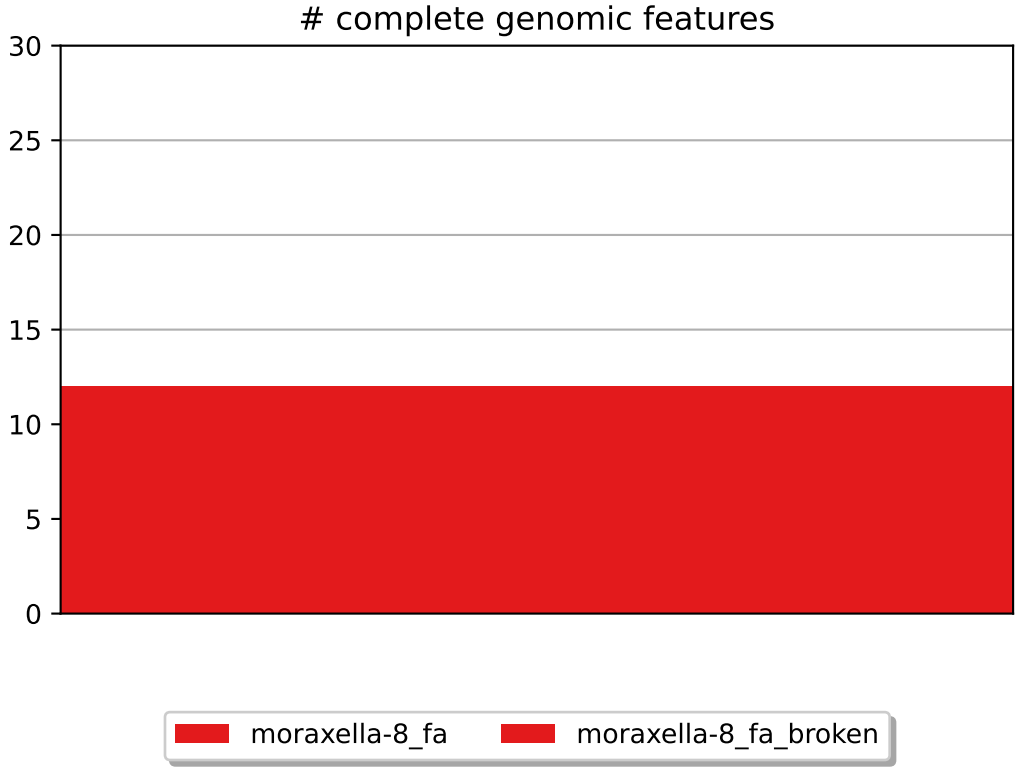

Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
2
4
6
8
Contig index
moraxella-8_fa
moraxella-8_fa_broken
Reference

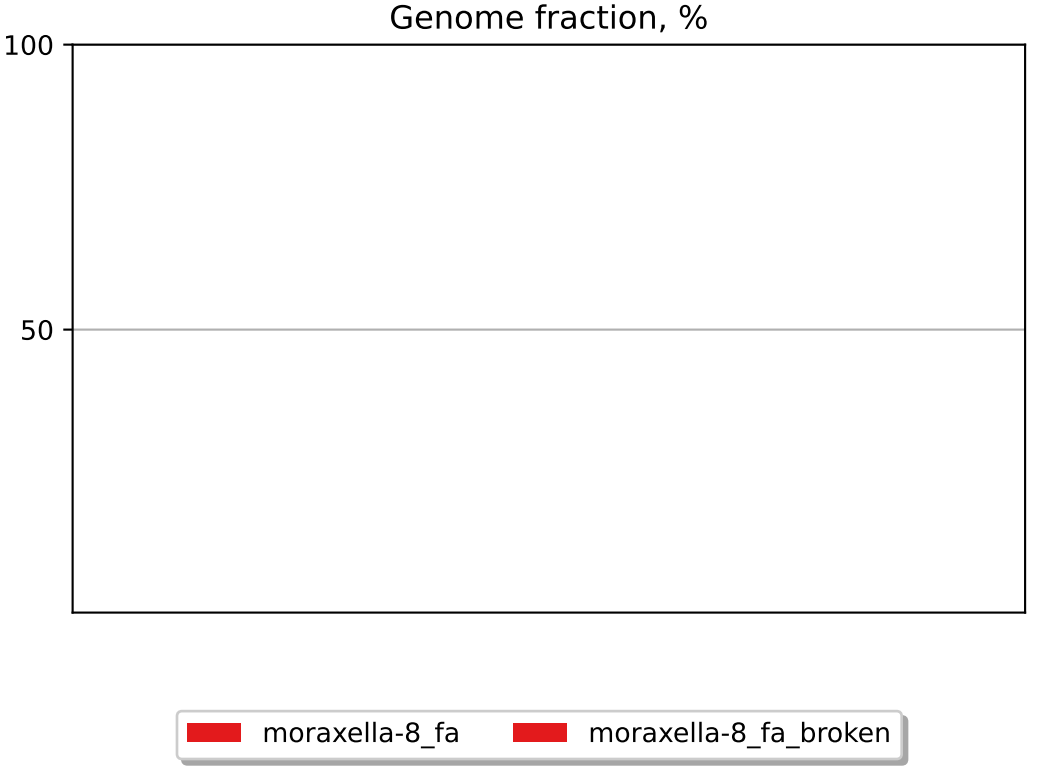

NAx
Contig length (bp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
moraxella-8_fa
moraxella-8_fa_broken


NGAx
Contig length (bp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
moraxella-8_fa
moraxella-8_fa_broken


Cumulative # complete genomic features
Cumulative # complete genomic features
3000
2400
1800
1200
600
0
0
5
10
15
20
25
Contig index
moraxella-8_fa
moraxella-8_fa_broken
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
Feature space
moraxella-8_fa
moraxella-8_fa_broken


complete genomic features
30
25
20
15
10
5
0
moraxella-8_fa
moraxella-8_fa_broken


Genome fraction, %
100
50
moraxella-8_fa
moraxella-8_fa_broken