Report

	Unknown-8_fa	Unknown-8_fa_broken
# contigs (>= 0 bp)	200	-
# contigs (>= 1000 bp)	92	102
Total length (>= 0 bp)	5525242	-
Total length (>= 1000 bp)	5493371	5488000
# contigs	103	122
Largest contig	373078	373078
Total length	5501773	5500464
Reference length	5391123	5391123
GC (%)	57.20	57.20
Reference GC (%)	57.85	57.85
N50	116072	102318
NG50	122249	106169
N90	35927	31438
NG90	43442	35275
auN	146183.8	137757.3
auNG	149184.1	140551.2
L50	15	16
LG50	14	15
L90	46	51
LG90	43	48
# misassemblies	9	8
# misassembled contigs	6	6
Misassembled contigs length	432320	402238
# local misassemblies	3	4
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	24	23
# unaligned contigs	46 + 51 part	55 + 55 part
Unaligned length	4315386	4315155
Genome fraction (%)	21.961	22.370
Duplication ratio	1.011	1.011
# N's per 100 kbp	24.57	0.78
# mismatches per 100 kbp	4133.91	4140.74
# indels per 100 kbp	88.35	88.28
# genomic features	1166 + 100 part	1165 + 119 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	5 + 2 part	5 + 1 part
Largest alignment	88406	88406
Total aligned length	1185029	1184862
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	5330.8	5254.7
auNGA	5440.2	5361.3
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

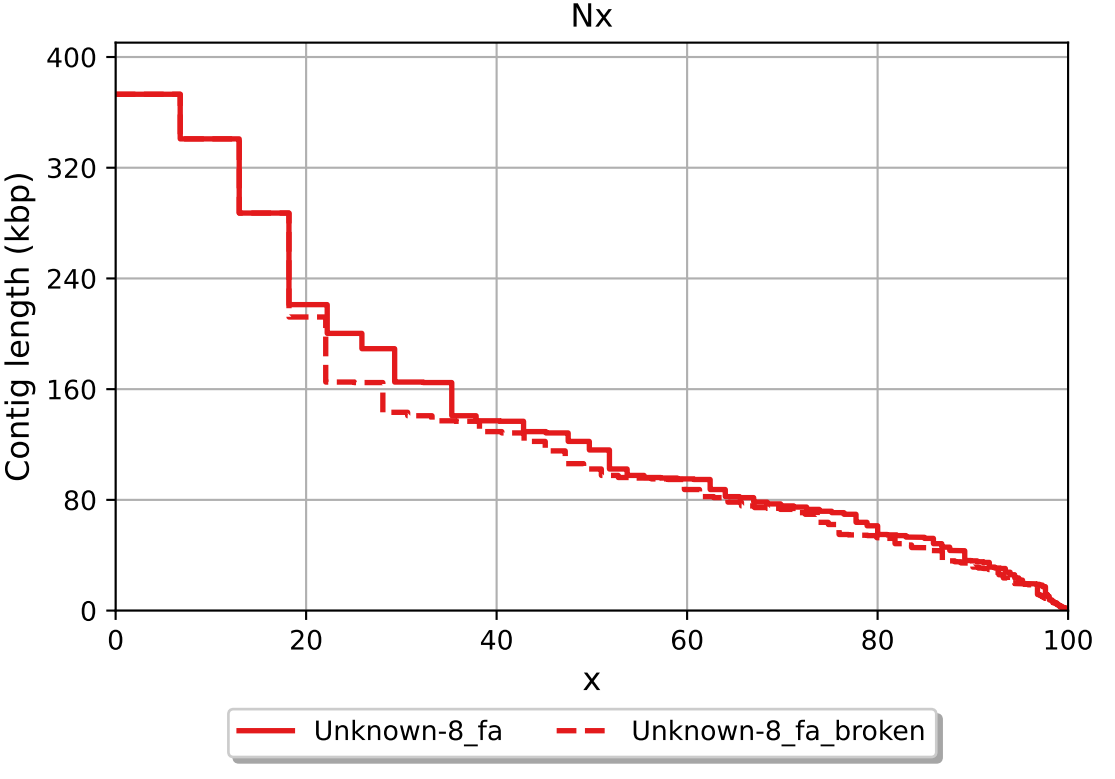
	Unknown-8_fa	Unknown-8_fa_broken
# misassemblies	9	8
# contig misassemblies	9	8
# c. relocations	9	8
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	6	6
Misassembled contigs length	432320	402238
# local misassemblies	3	4
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	24	23
# mismatches	48988	49062
# indels	1047	1046
# indels (<= 5 bp)	998	1002
# indels (> 5 bp)	49	44
Indels length	2729	2475

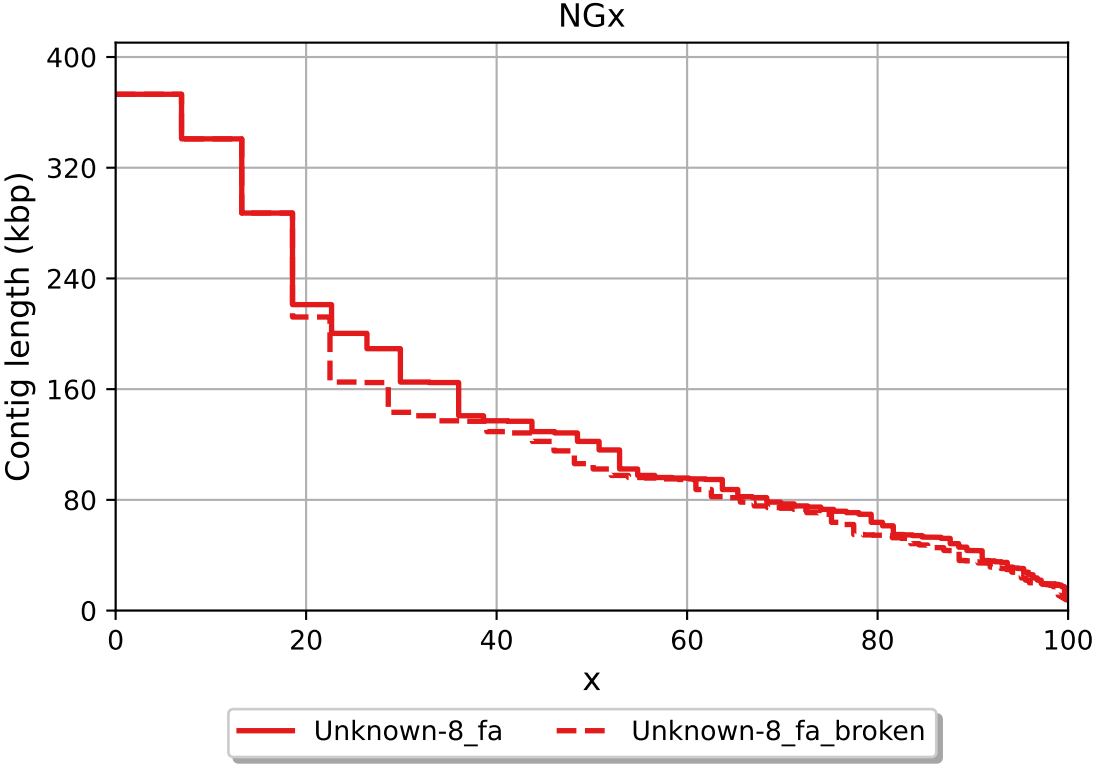
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

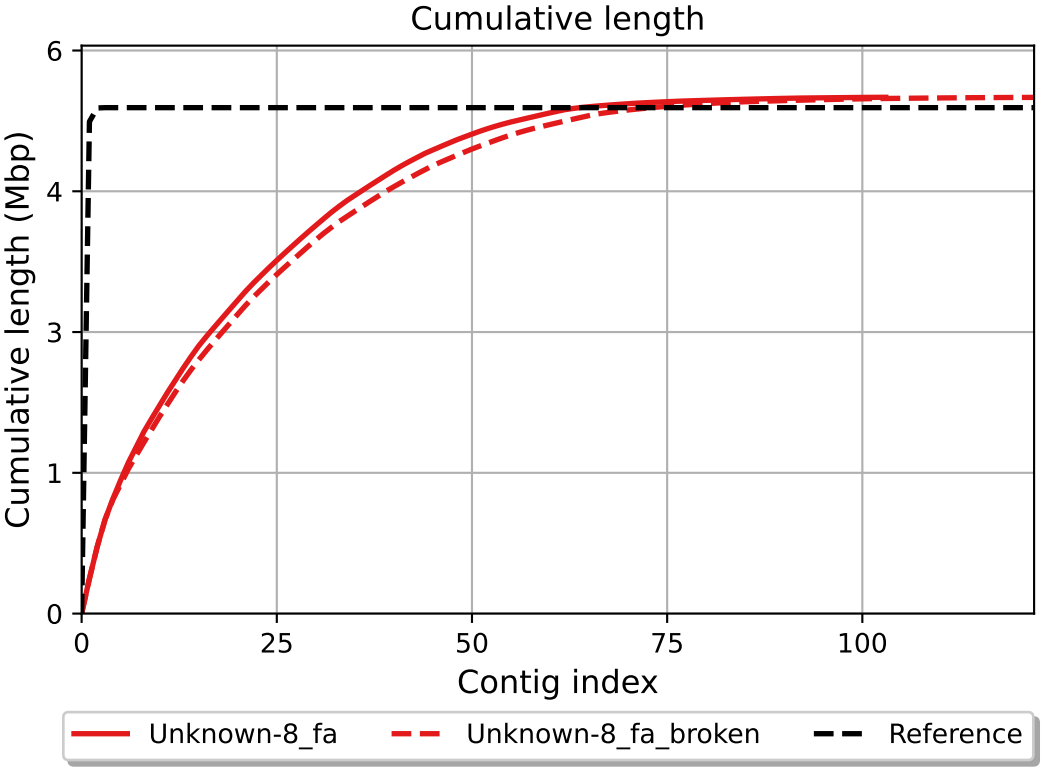
Unaligned report

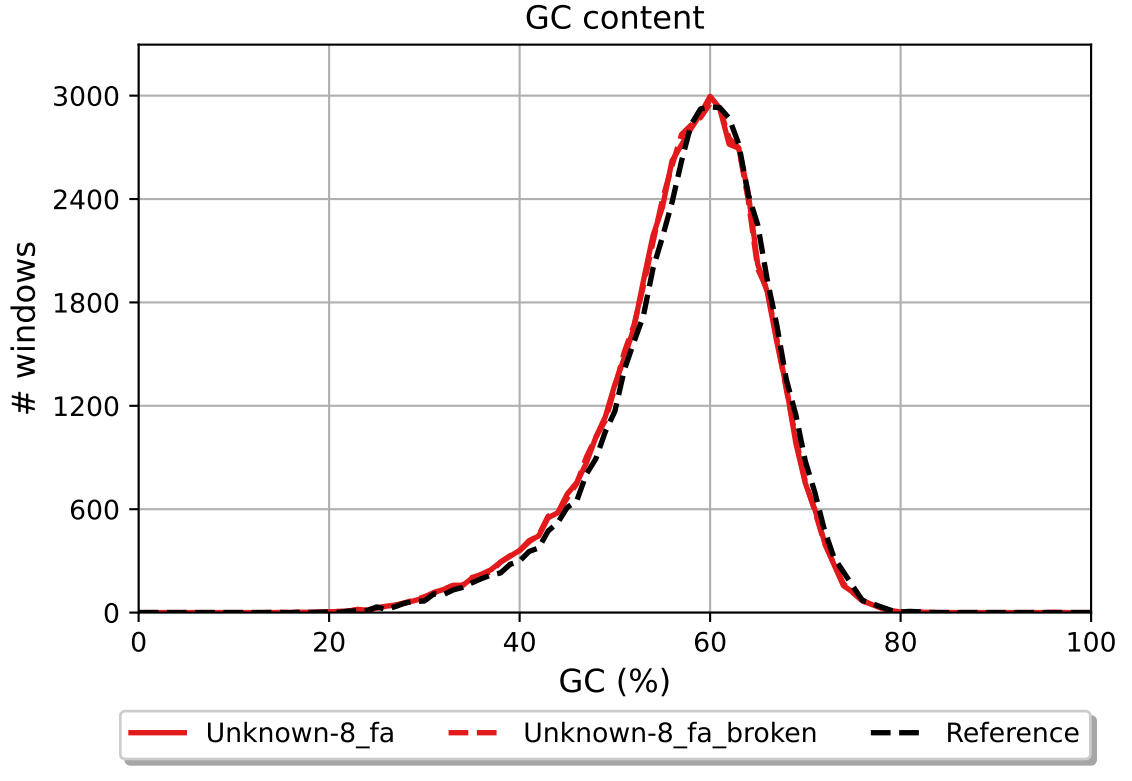
	Unknown-8_fa	Unknown-8_fa_broken
# fully unaligned contigs	46	55
Fully unaligned length	680331	790393
# partially unaligned contigs	51	55
Partially unaligned length	3635055	3524762
# N's	1352	43

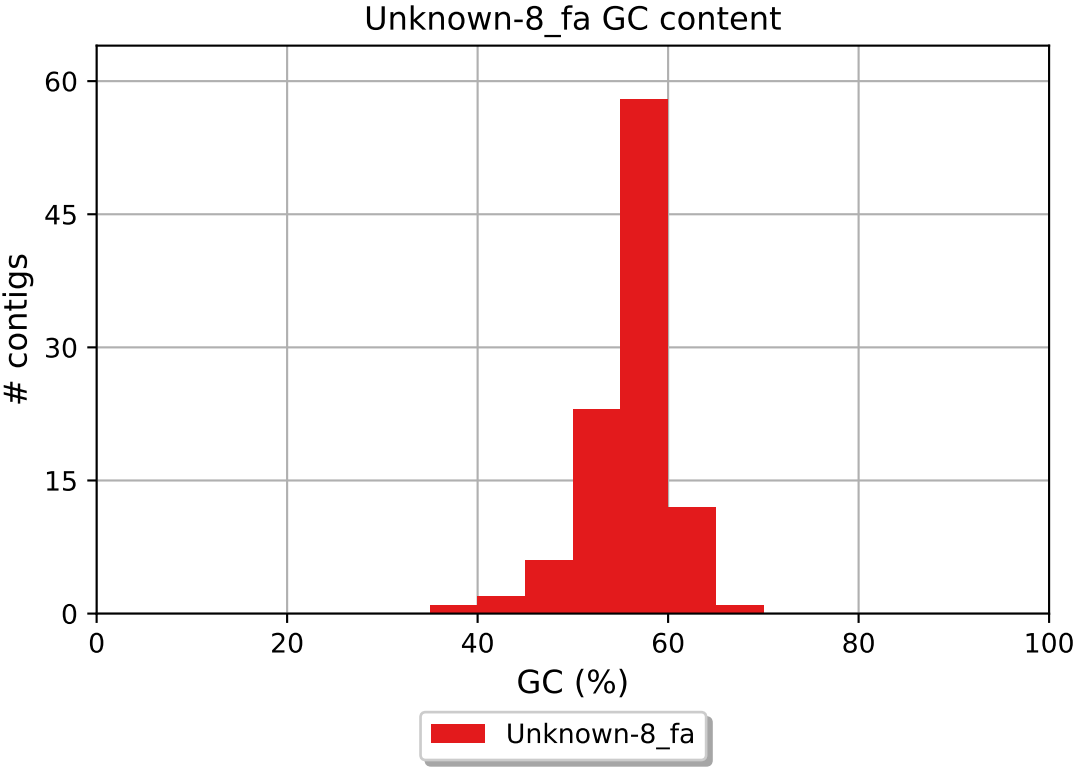
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

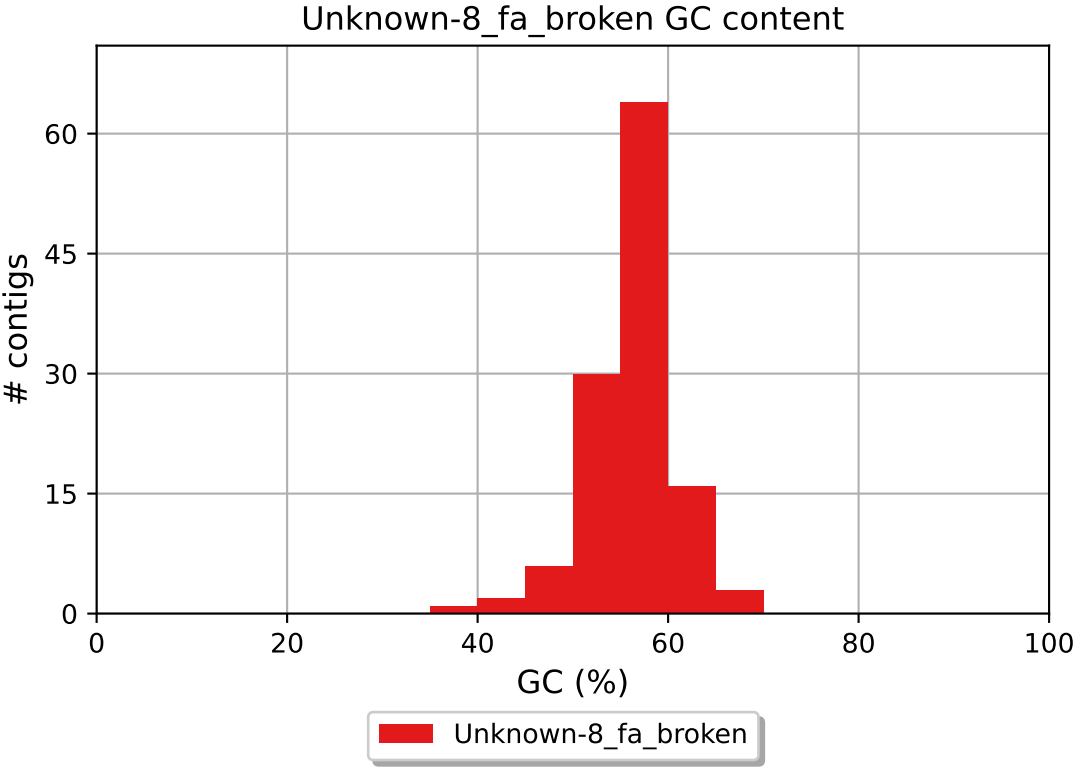

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken

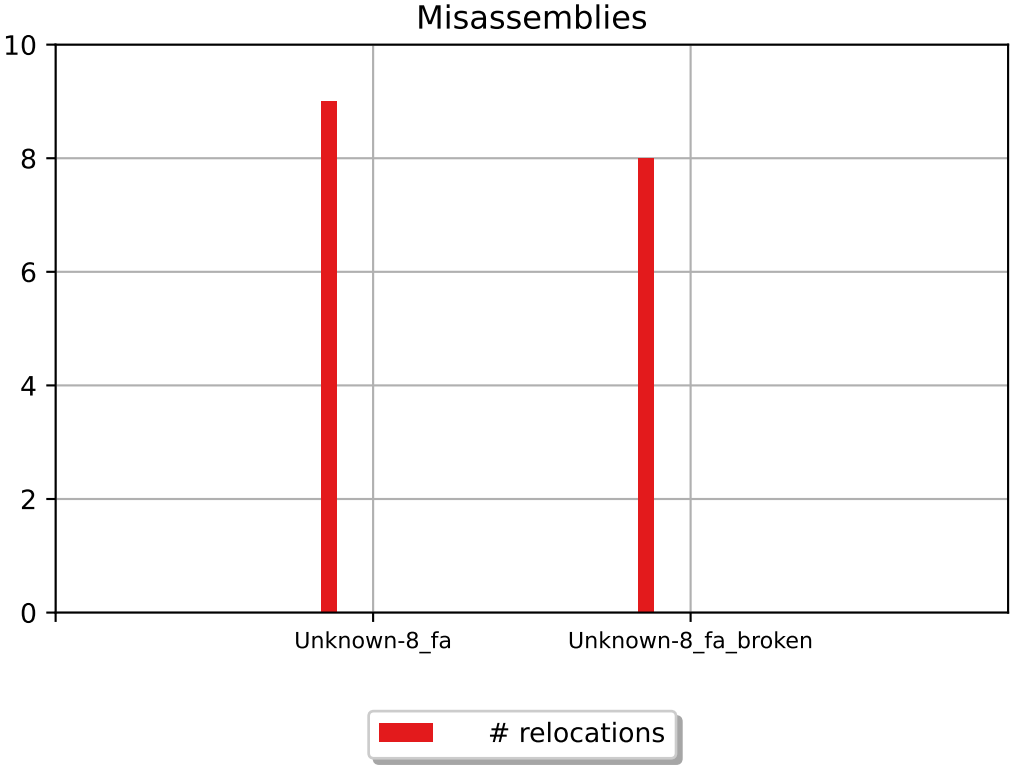

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken

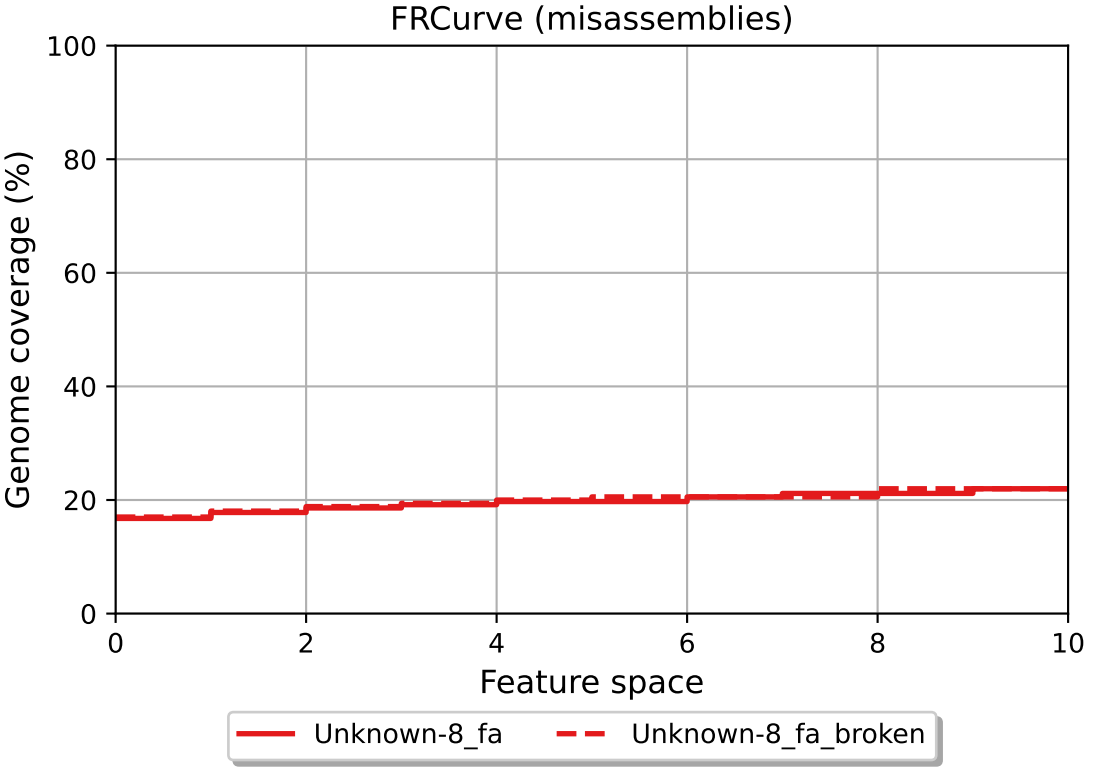

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
25
50
75
100
Contig index
Unknown-8_fa
Unknown-8_fa_broken
Reference

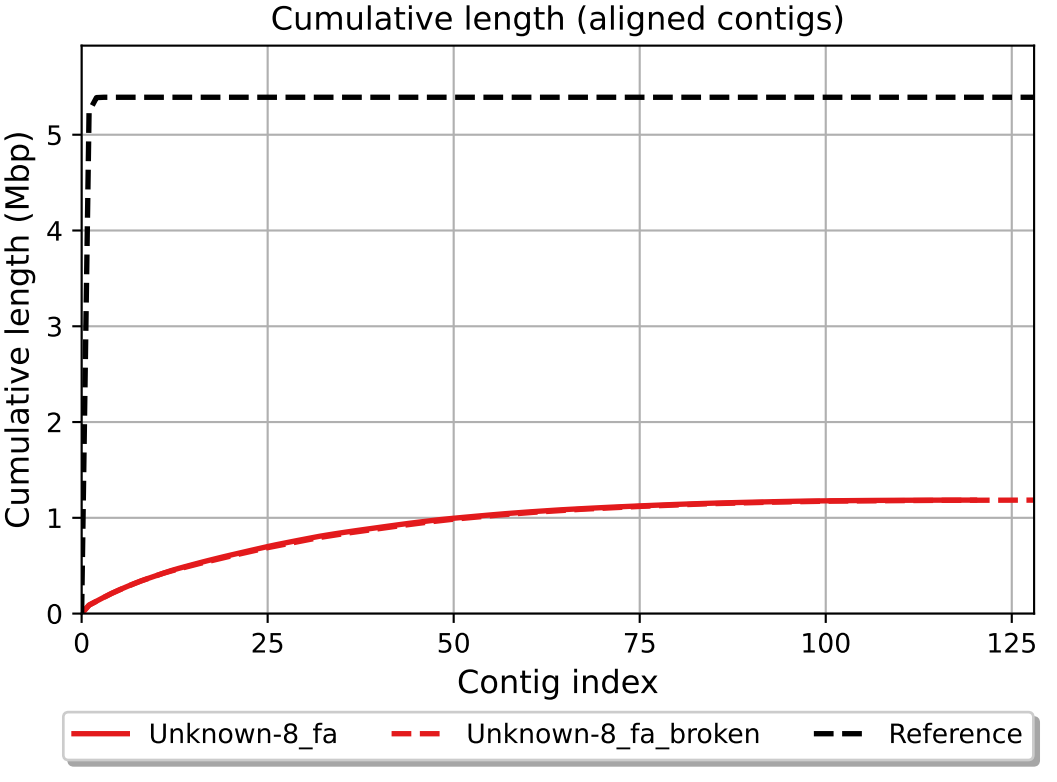

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
Unknown-8_fa
Unknown-8_fa_broken
Reference

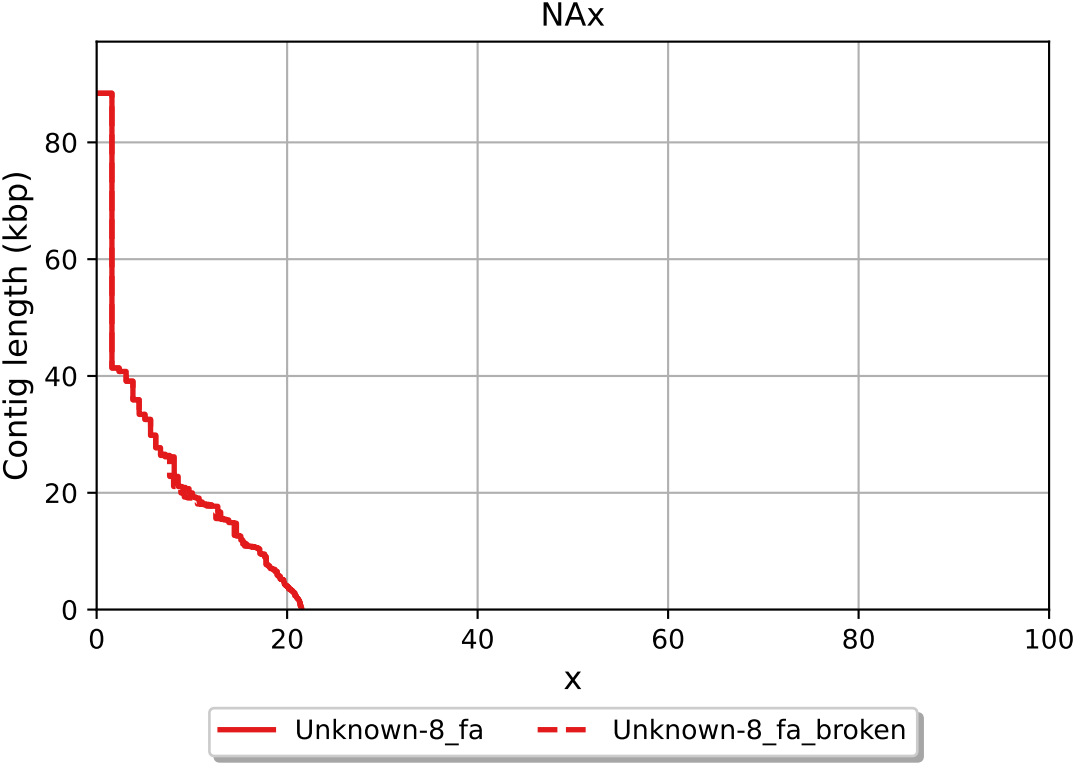

Unknown-8_fa GC content
contigs
GC (%)
0
15
30
45
60
0
20
40
60
80
100
Unknown-8_fa

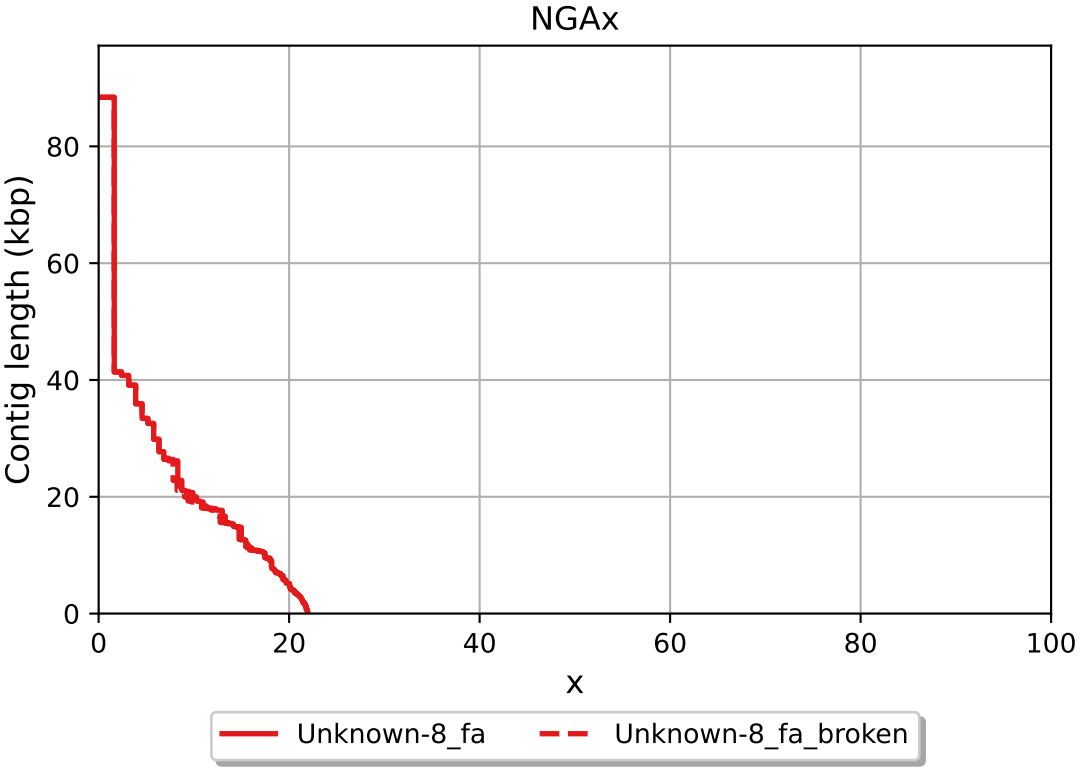

Unknown-8_fa_broken GC content
contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
Unknown-8_fa_broken

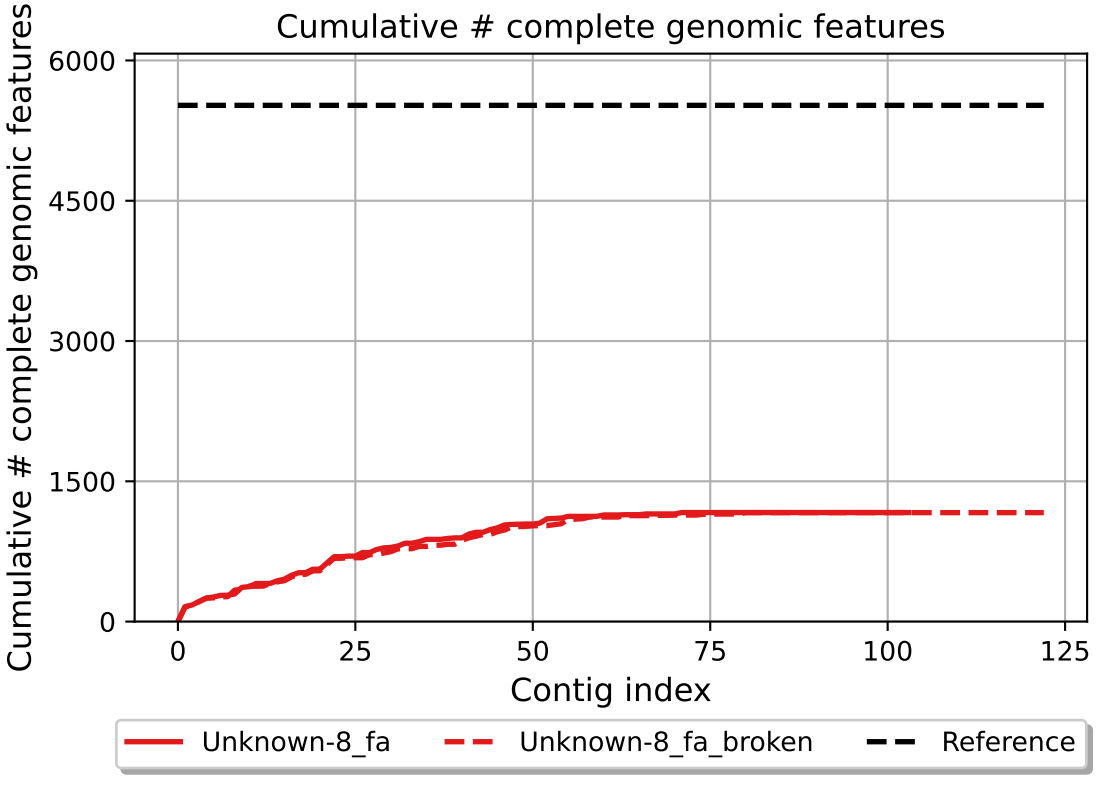

Misassemblies
10
8
6
4
2
0
Unknown-8_fa
Unknown-8_fa_broken
relocations

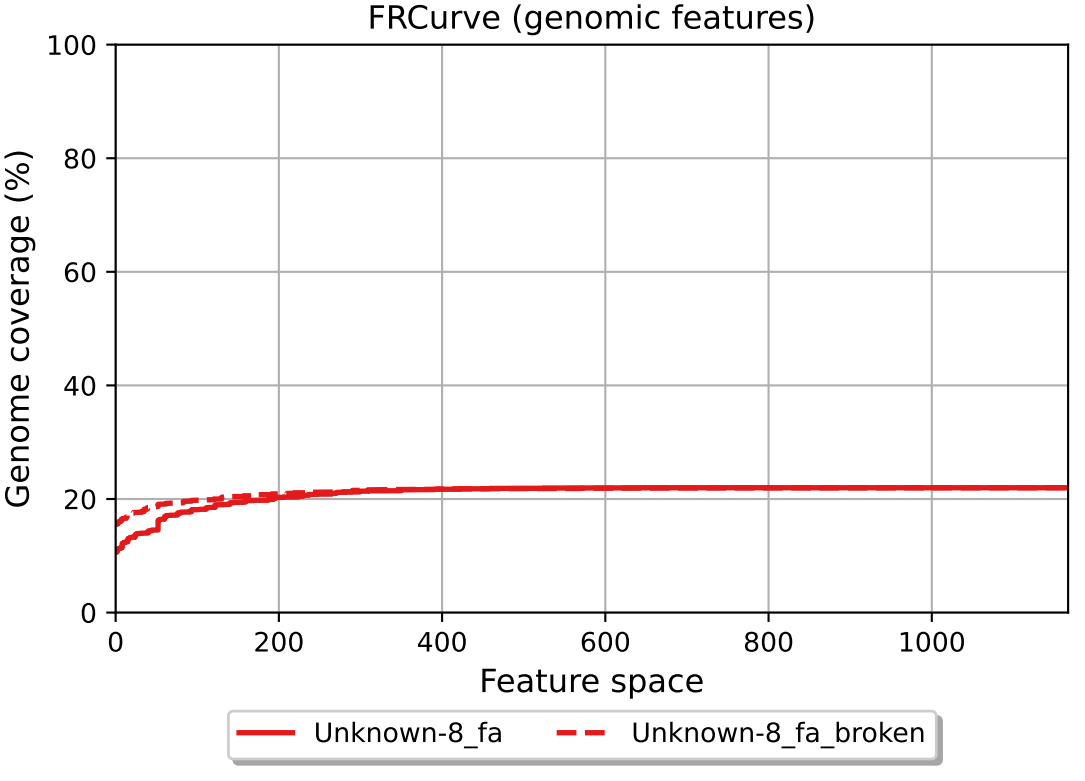

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
Unknown-8_fa
Unknown-8_fa_broken

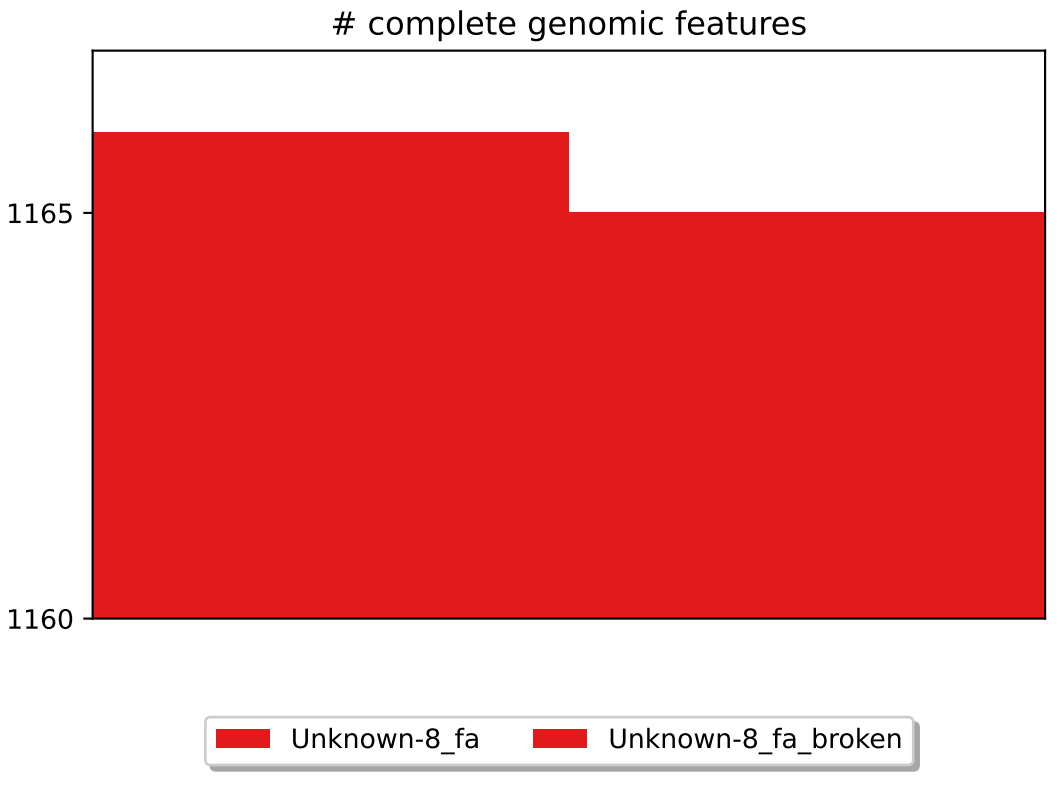

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
25
50
75
100
125
Contig index
Unknown-8_fa
Unknown-8_fa_broken
Reference

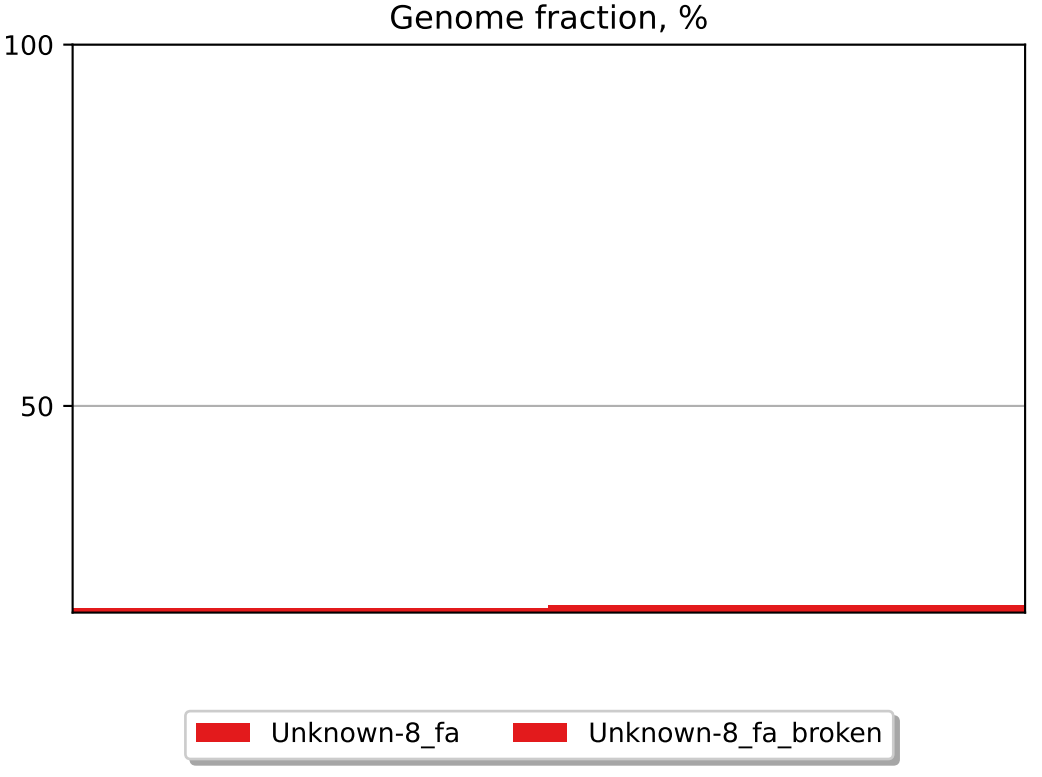

NAx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken


NGAx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken


Cumulative # complete genomic features
Cumulative # complete genomic features
6000
4500
3000
1500
0
0
25
50
75
100
125
Contig index
Unknown-8_fa
Unknown-8_fa_broken
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Feature space
Unknown-8_fa
Unknown-8_fa_broken


complete genomic features
1165
1160
Unknown-8_fa
Unknown-8_fa_broken


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