Report

	Unknown-8_fa	Unknown-8_fa_broken
# contigs (>= 0 bp)	470	-
# contigs (>= 1000 bp)	153	171
Total length (>= 0 bp)	5586737	-
Total length (>= 1000 bp)	5526816	5523416
# contigs	165	187
Largest contig	310679	262926
Total length	5535088	5533662
Reference length	5682322	5682322
GC (%)	57.17	57.17
Reference GC (%)	57.12	57.12
N50	71324	64447
NG50	69435	63478
N90	17296	14738
NG90	13203	11176
auN	92938.0	77808.1
auNG	90529.9	75772.5
L50	25	27
LG50	26	28
L90	81	91
LG90	90	101
# misassemblies	67	63
# misassembled contigs	41	43
Misassembled contigs length	3056428	2945058
# local misassemblies	27	25
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	7	8
# unaligned contigs	14 + 65 part	17 + 65 part
Unaligned length	726427	725051
Genome fraction (%)	84.766	85.077
Duplication ratio	1.007	1.007
# N's per 100 kbp	27.50	1.73
# mismatches per 100 kbp	681.62	682.90
# indels per 100 kbp	21.22	20.85
# genomic features	9479 + 398 part	9459 + 424 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	5 + 2 part	5 + 1 part
Largest alignment	170518	170518
Total aligned length	4805769	4804975
NA50	38372	35456
NGA50	37612	32168
NA90	-	-
NGA90	-	-
auNA	47302.0	45113.7
auNGA	46076.4	43933.5
LA50	42	44
LGA50	44	47
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

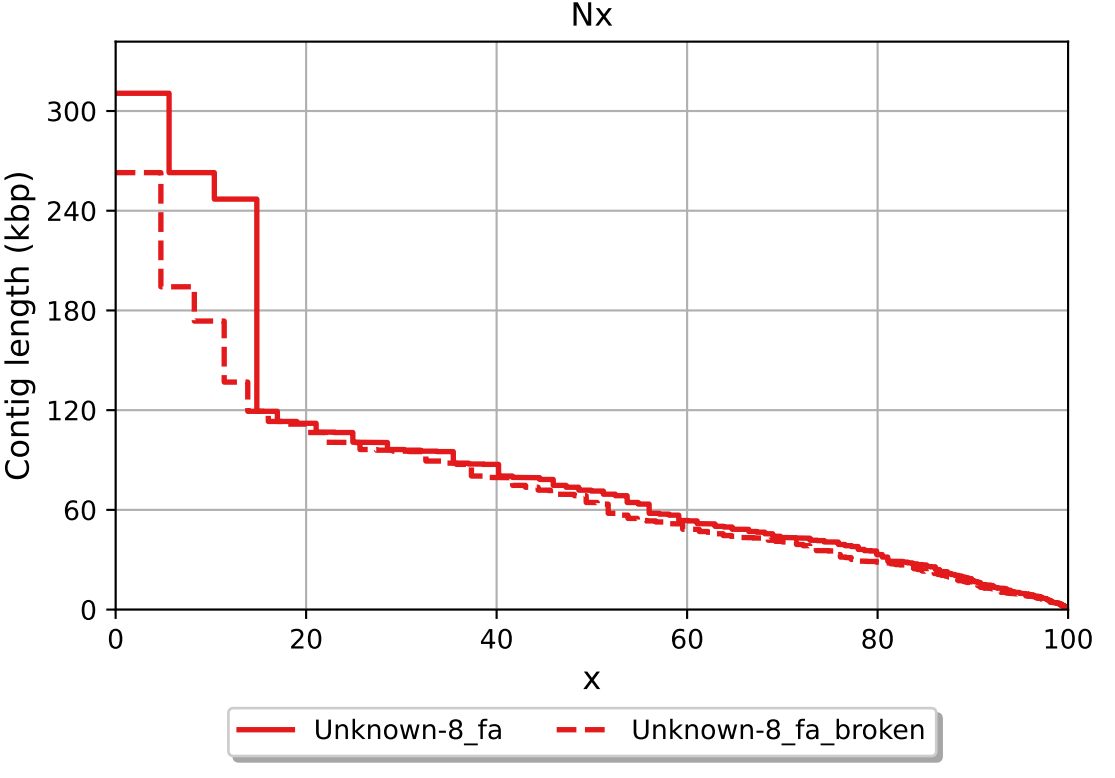
	Unknown-8_fa	Unknown-8_fa_broken
# misassemblies	67	63
# contig misassemblies	63	63
# c. relocations	59	59
# c. translocations	4	4
# c. inversions	0	0
# scaffold misassemblies	4	0
# s. relocations	4	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	41	43
Misassembled contigs length	3056428	2945058
# local misassemblies	27	25
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	7	8
# mismatches	32757	32813
# indels	1020	1002
# indels (<= 5 bp)	854	846
# indels (> 5 bp)	166	156
Indels length	11553	10649

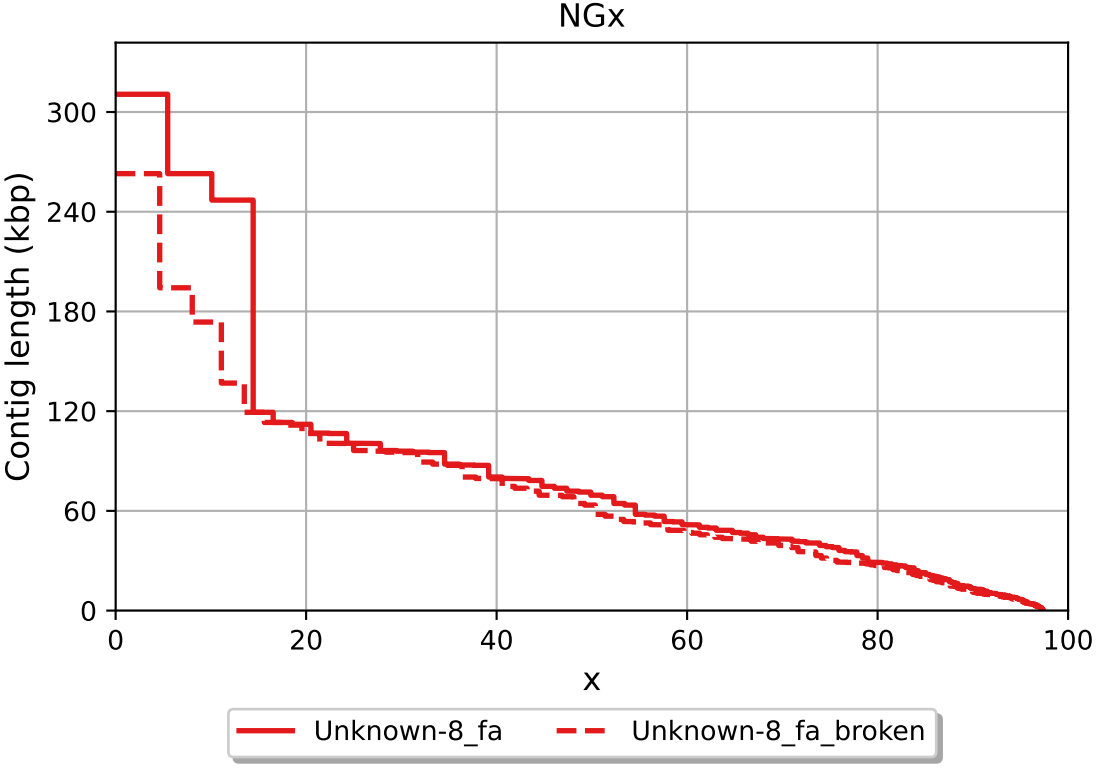
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

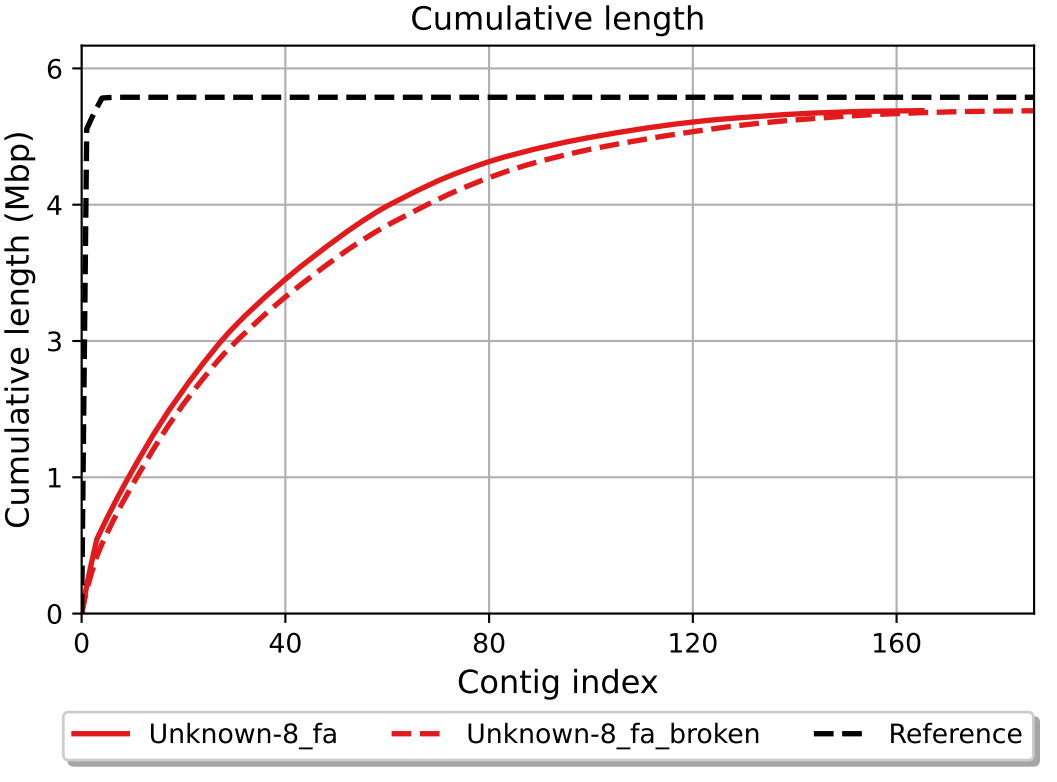
Unaligned report

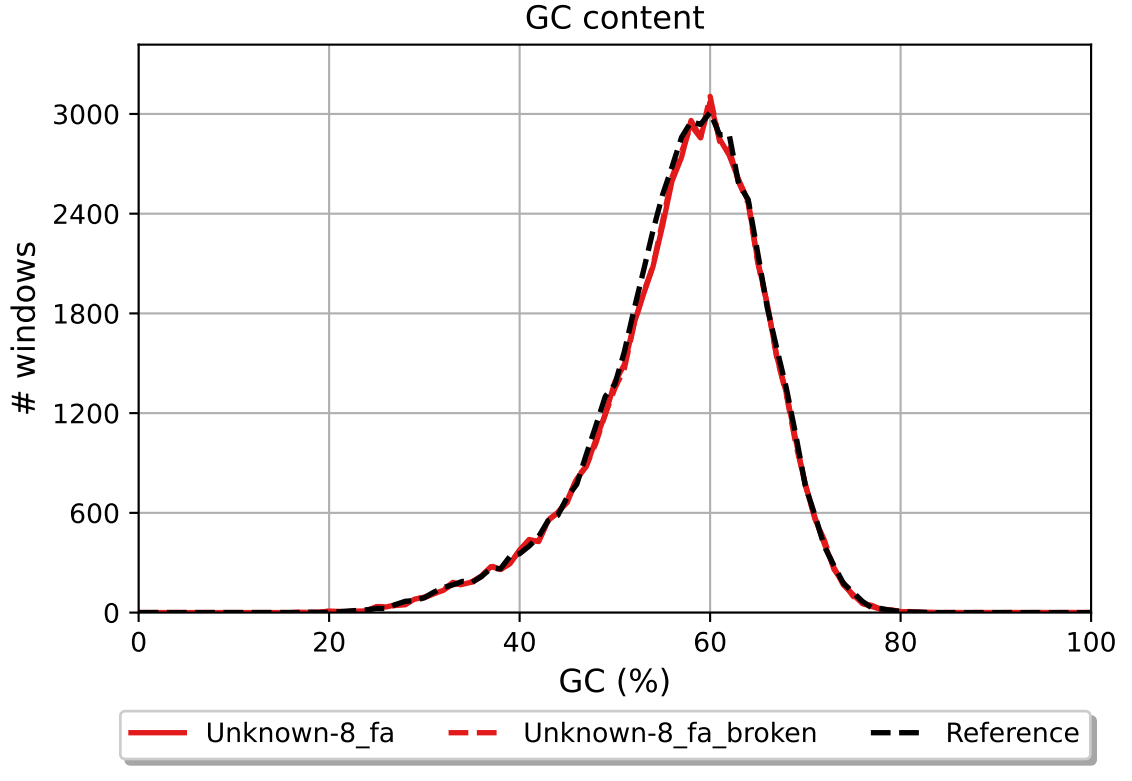
	Unknown-8_fa	Unknown-8_fa_broken
# fully unaligned contigs	14	17
Fully unaligned length	63213	71751
# partially unaligned contigs	65	65
Partially unaligned length	663214	653300
# N's	1522	96

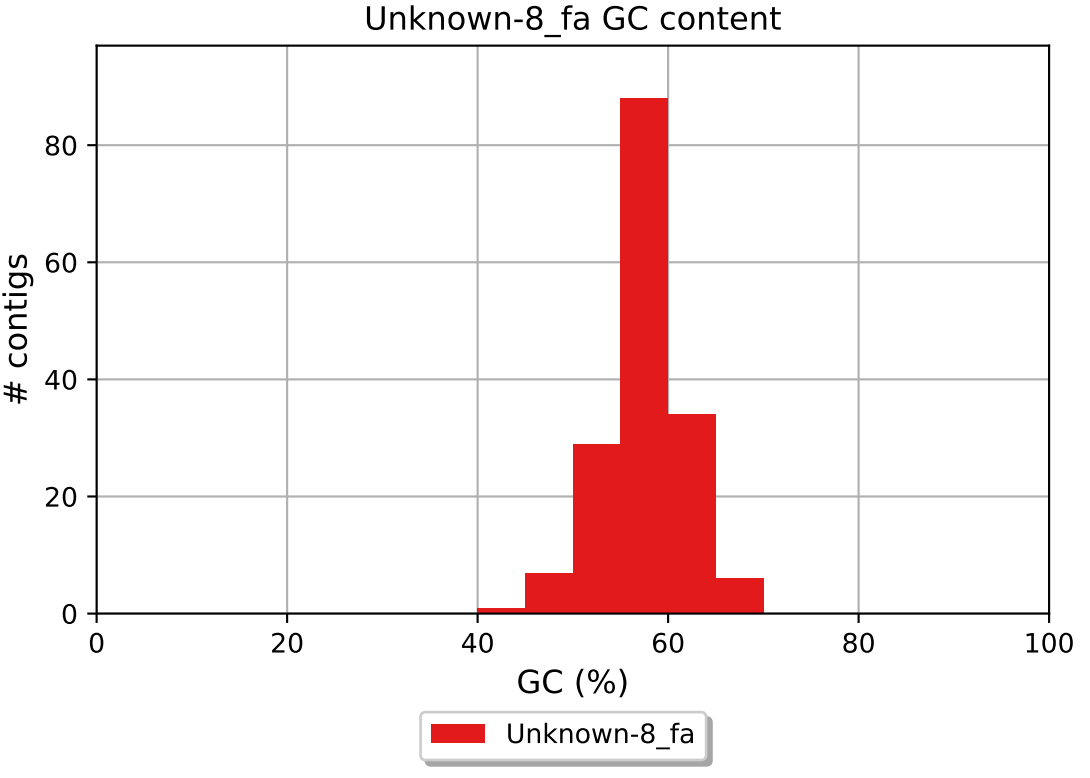
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

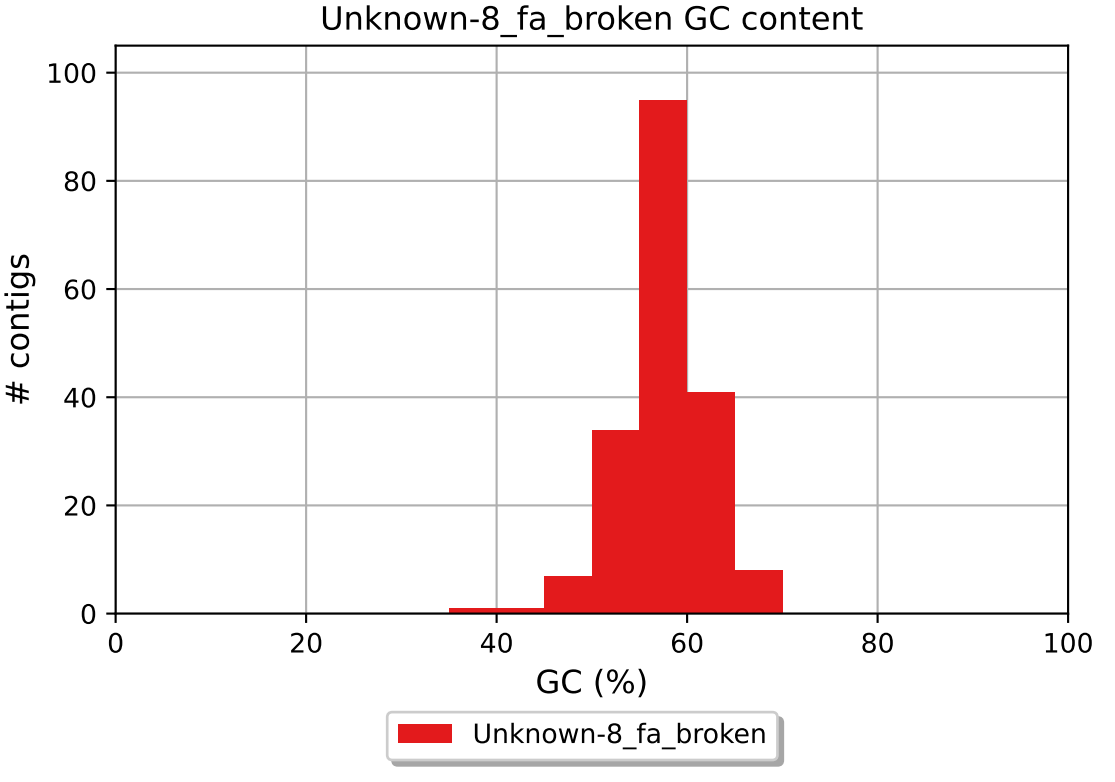

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken

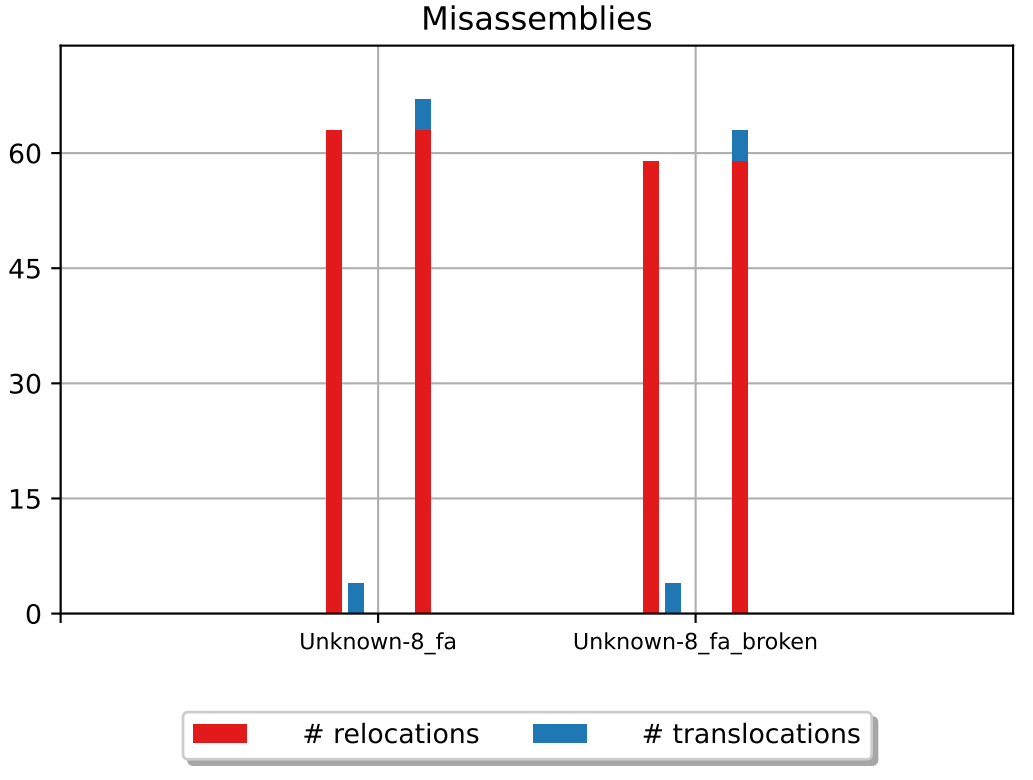

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken

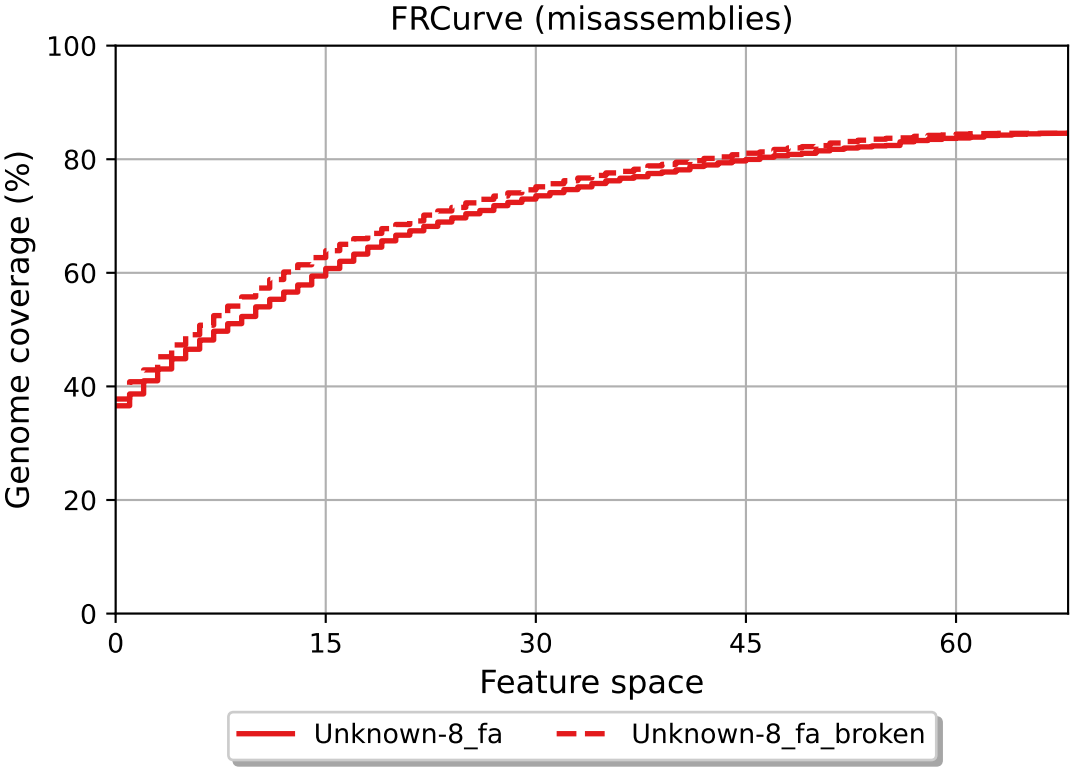

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
40
80
120
160
Contig index
Unknown-8_fa
Unknown-8_fa_broken
Reference

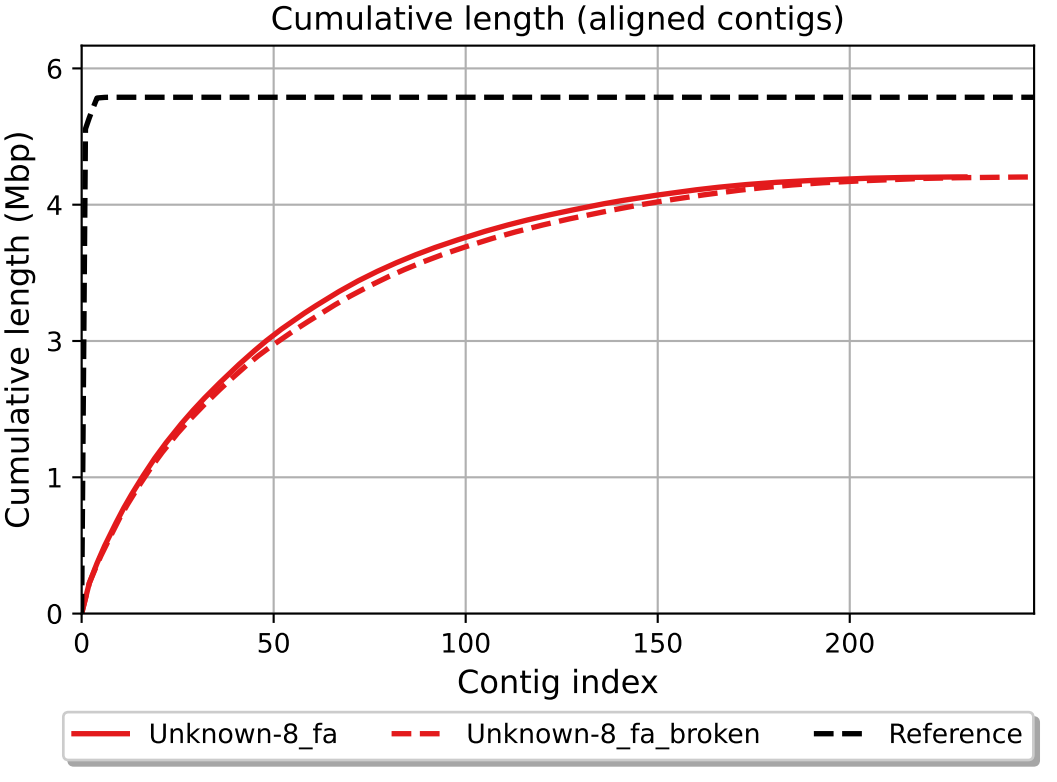

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
Unknown-8_fa
Unknown-8_fa_broken
Reference

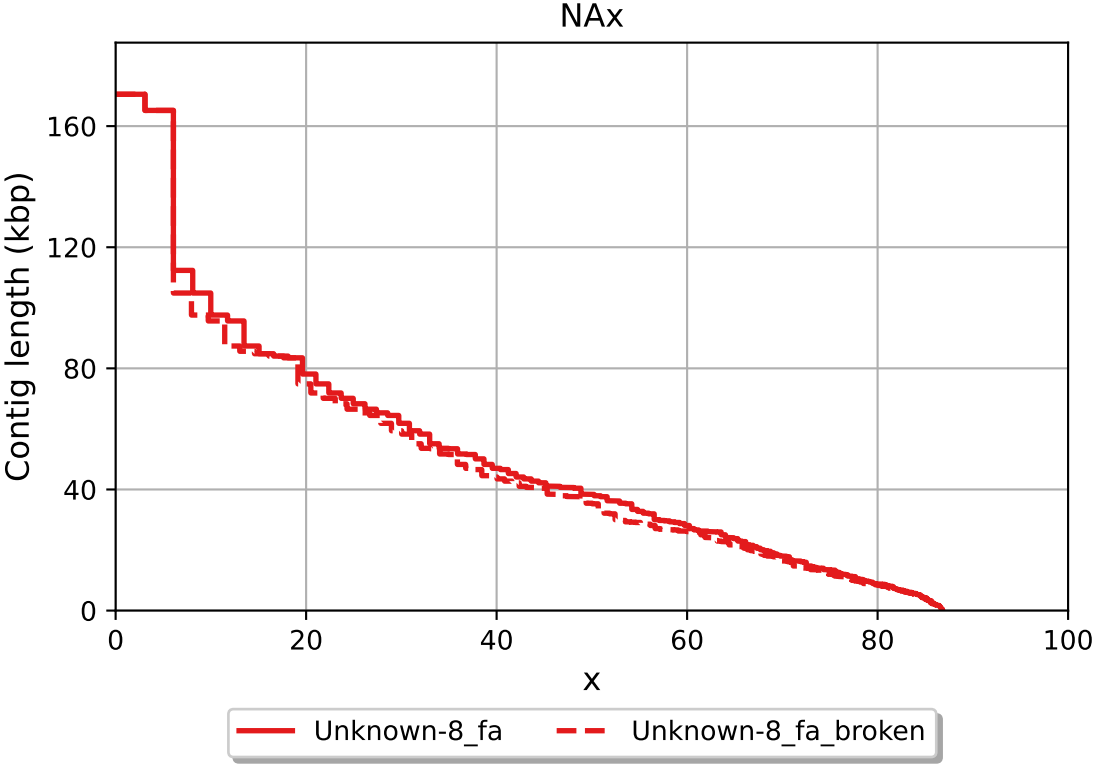

Unknown-8_fa GC content
contigs
0
20
40
60
80
0
20
40
60
80
100
GC (%)
Unknown-8_fa

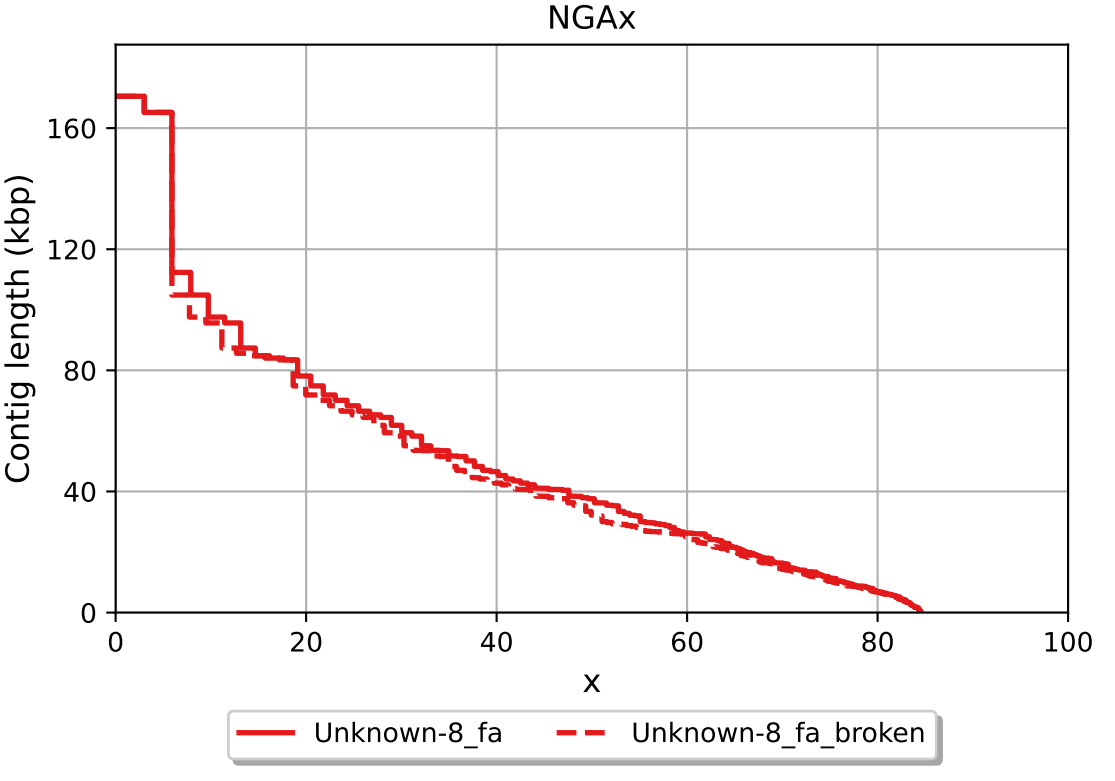

Unknown-8_fa_broken GC content
contigs
GC (%)
0
20
40
60
80
100
Unknown-8_fa_broken

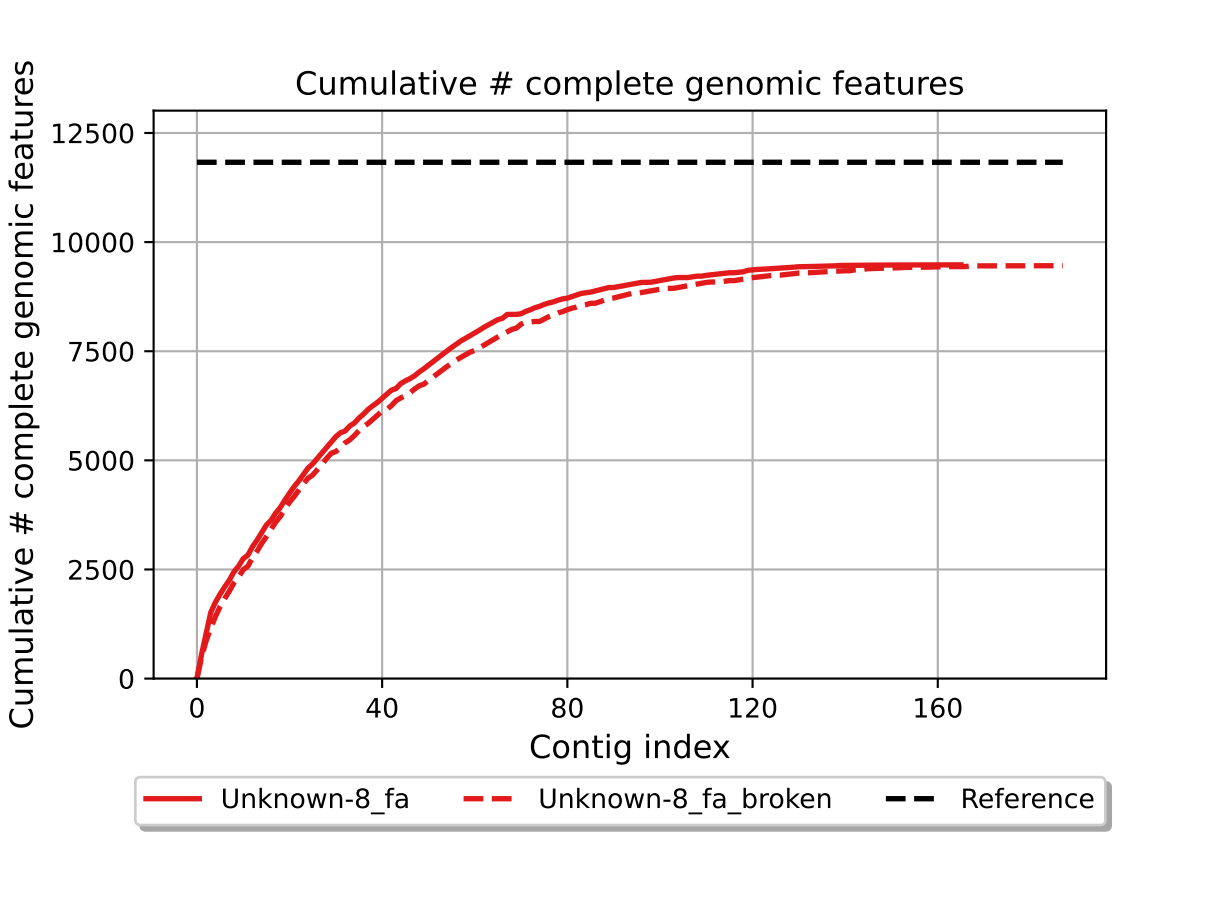

Misassemblies
60
45
30
15
0
Unknown-8_fa
Unknown-8_fa_broken
relocations
translocations

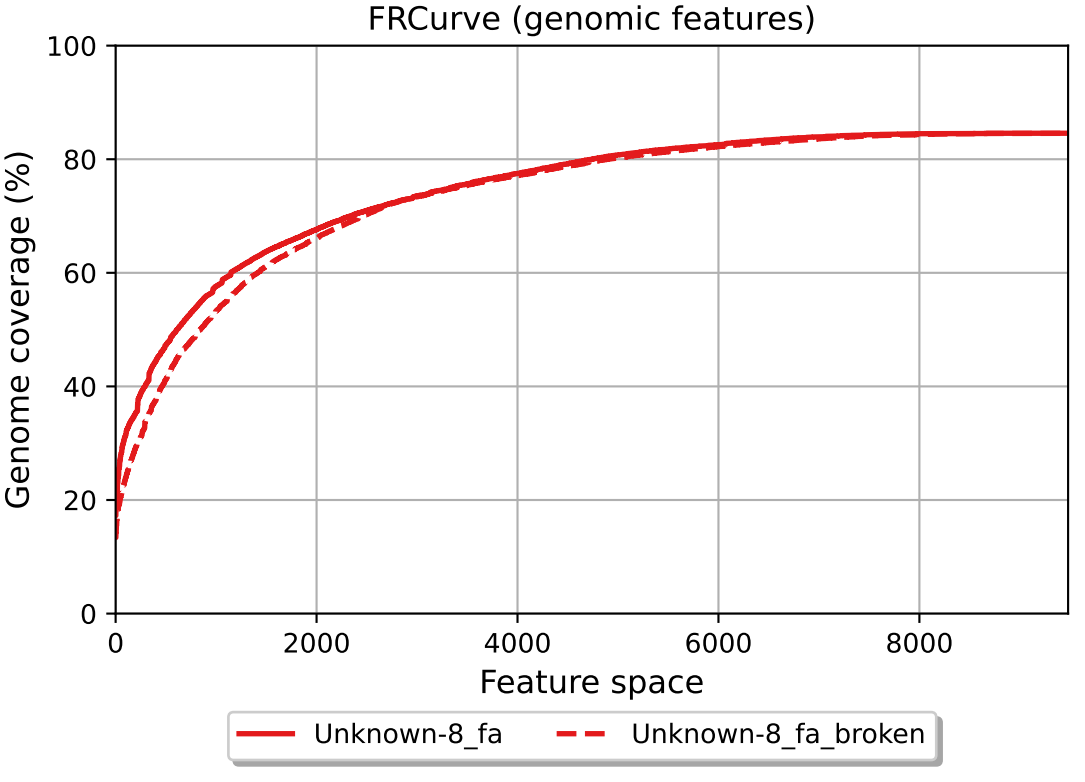

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
Feature space
Unknown-8_fa
Unknown-8_fa_broken

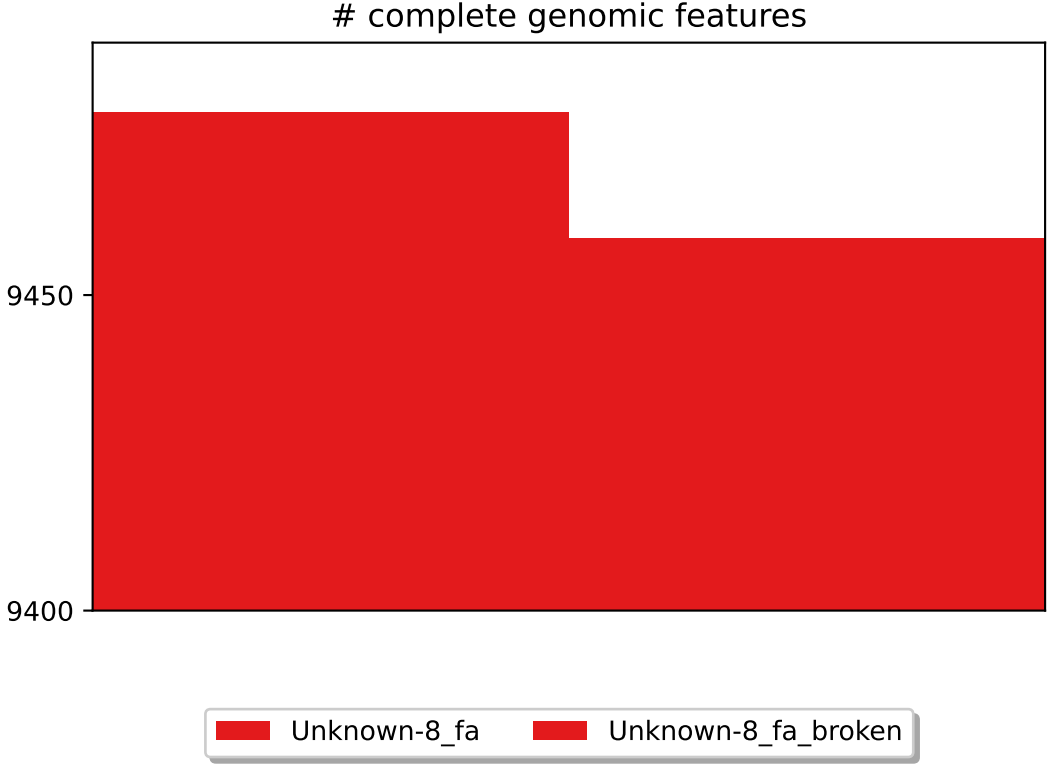

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
50
100
150
200
Contig index
Unknown-8_fa
Unknown-8_fa_broken
Reference

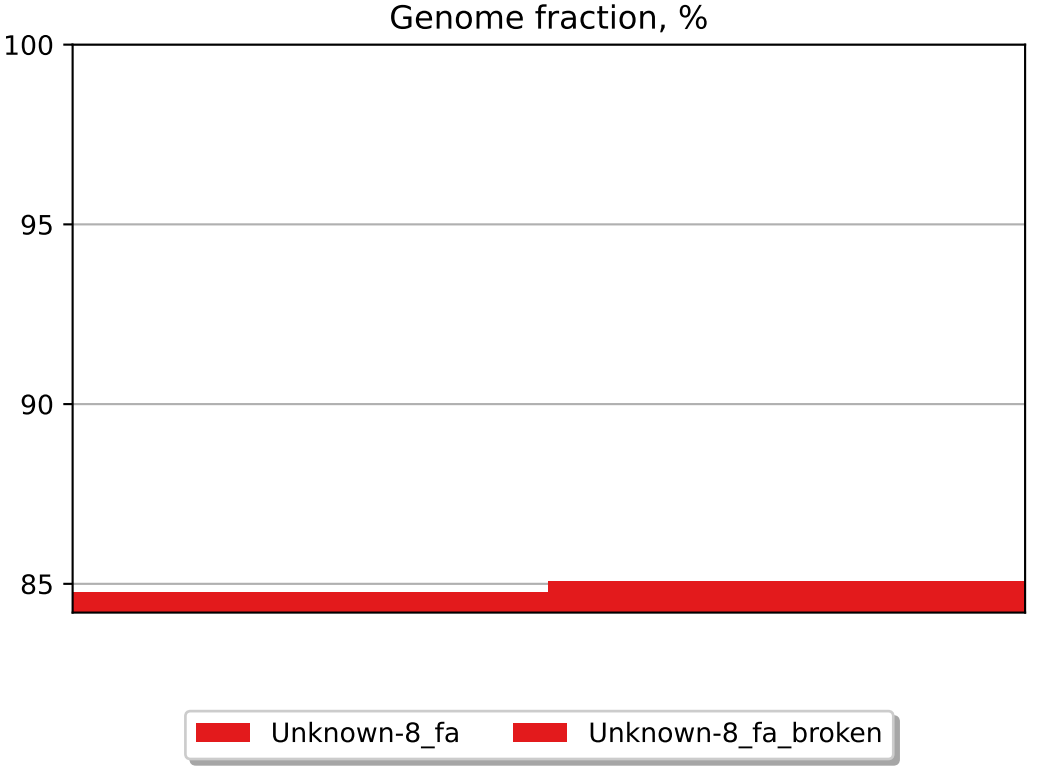

NAx
Contig length (kbp)
0
40
80
120
160
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken


NGAx
Contig length (kbp)
160
120
80
40
0
0
20
40
60
80
100
x
Unknown-8_fa
Unknown-8_fa_broken


Cumulative # complete genomic features
Cumulative # complete genomic features
12500
10000
7500
5000
2500
0
0
40
80
120
160
Contig index
Unknown-8_fa
Unknown-8_fa_broken
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
2000
4000
6000
8000
Feature space
Unknown-8_fa
Unknown-8_fa_broken


complete genomic features
9450
9400
Unknown-8_fa
Unknown-8_fa_broken


Genome fraction, %
100
95
90
85
Unknown-8_fa
Unknown-8_fa_broken