Report

	salmonella-8_fa	salmonella-8_fa_broken
# contigs (>= 0 bp)	150	-
# contigs (>= 1000 bp)	44	50
Total length (>= 0 bp)	4871073	-
Total length (>= 1000 bp)	4851265	4849928
# contigs	48	57
Largest contig	537866	537866
Total length	4853773	4853323
Reference length	4951383	4951383
GC (%)	52.19	52.19
Reference GC (%)	52.24	52.24
N50	272520	223891
NG50	272520	220071
N90	59728	54580
NG90	54580	52399
auN	301874.4	245924.9
auNG	295923.3	241054.5
L50	6	7
LG50	6	8
L90	21	26
LG90	22	27
# misassemblies	10	10
# misassembled contigs	9	9
Misassembled contigs length	2096548	1436747
# local misassemblies	6	6
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	0 + 5 part
Unaligned length	81853	81853
Genome fraction (%)	95.876	95.879
Duplication ratio	1.009	1.008
# N's per 100 kbp	9.31	0.04
# mismatches per 100 kbp	35.28	35.31
# indels per 100 kbp	3.65	3.46
# genomic features	13759 + 92 part	13748 + 94 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 4 part	2 + 4 part
Largest alignment	537775	537775
Total aligned length	4769911	4769461
NA50	232147	205673
NGA50	232147	159815
NA90	46041	41640
NGA90	37078	34129
auNA	246646.3	211989.7
auNGA	241784.0	207791.3
LA50	7	8
LGA50	7	9
LA90	26	31
LGA90	28	33

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

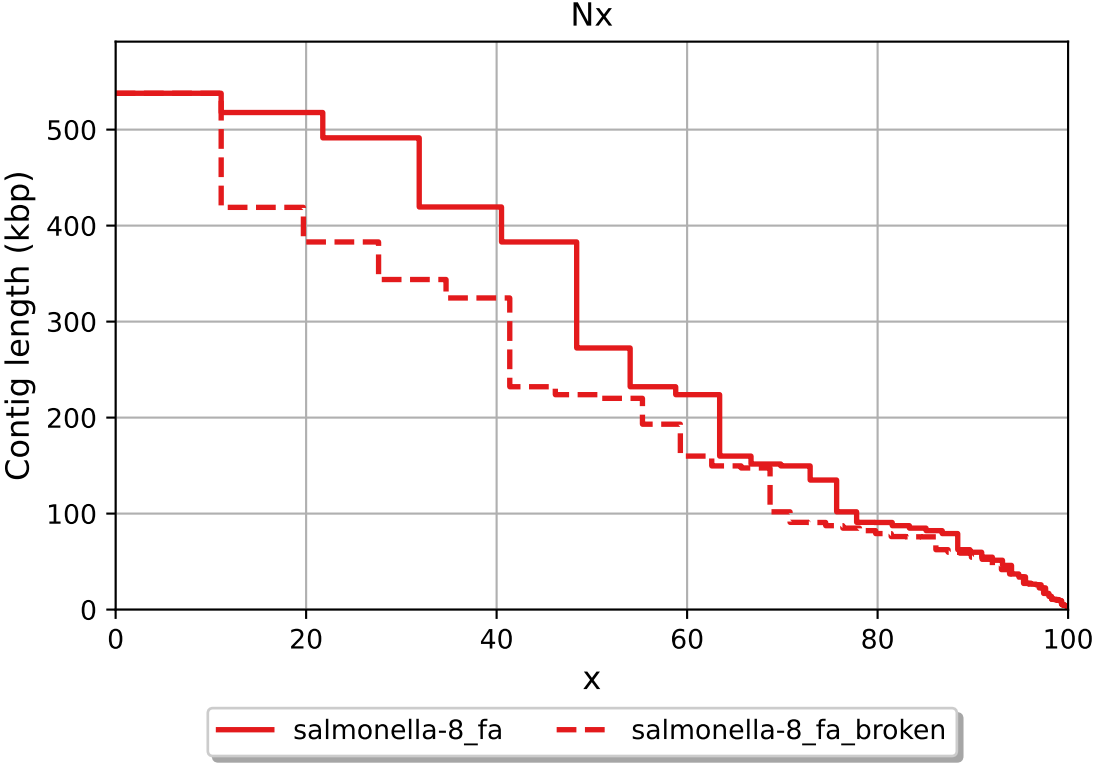
	salmonella-8_fa	salmonella-8_fa_broken
# misassemblies	10	10
# contig misassemblies	10	10
# c. relocations	10	10
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	9	9
Misassembled contigs length	2096548	1436747
# local misassemblies	6	6
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	1683	1684
# indels	174	165
# indels (<= 5 bp)	131	131
# indels (> 5 bp)	43	34
Indels length	3651	3048

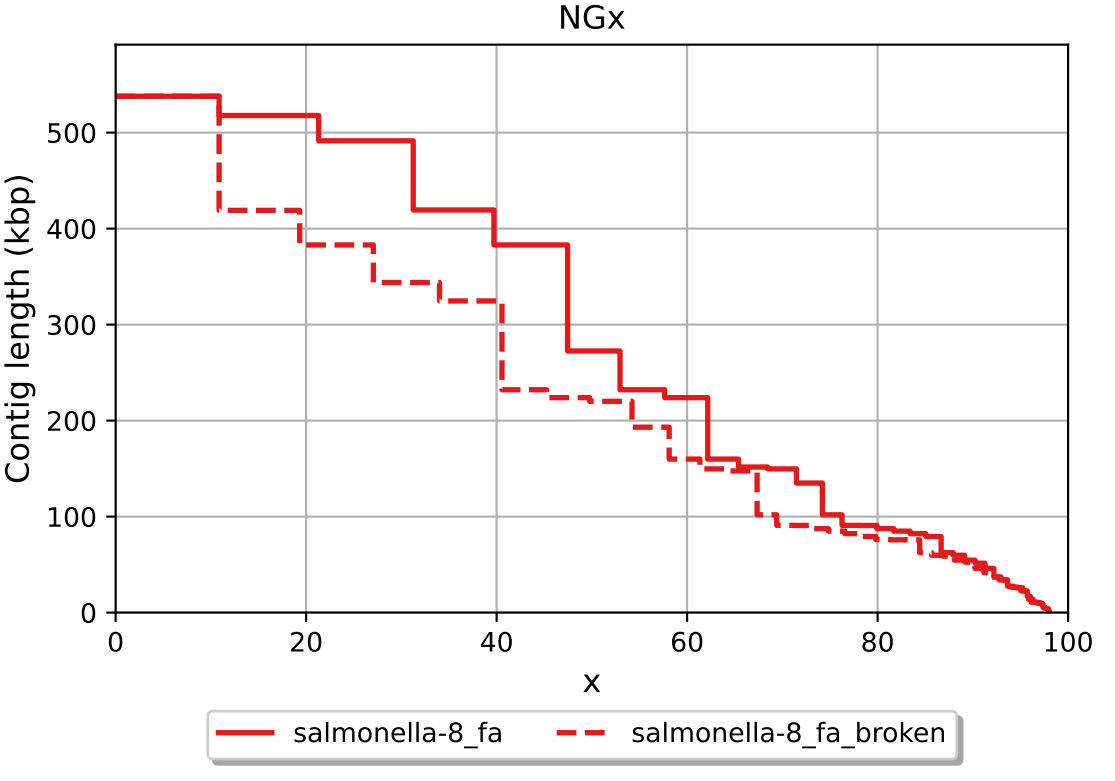
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

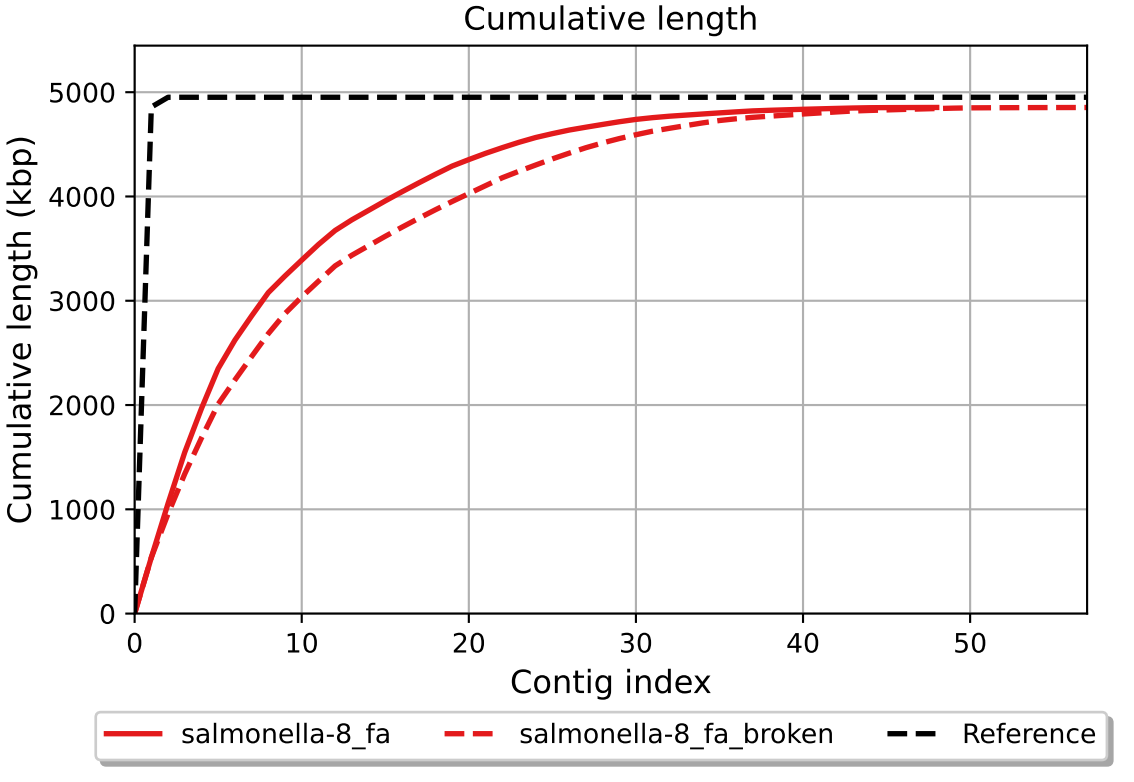
Unaligned report

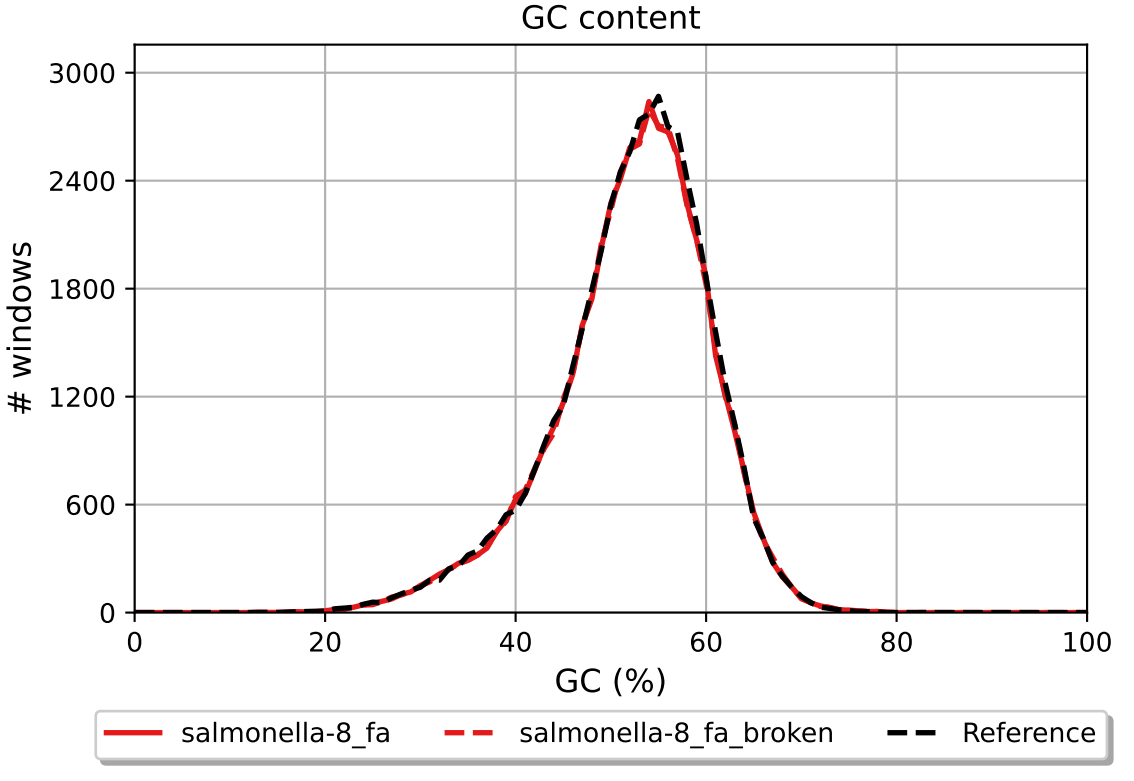
	salmonella-8_fa	salmonella-8_fa_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	5	5
Partially unaligned length	81853	81853
# N's	452	2

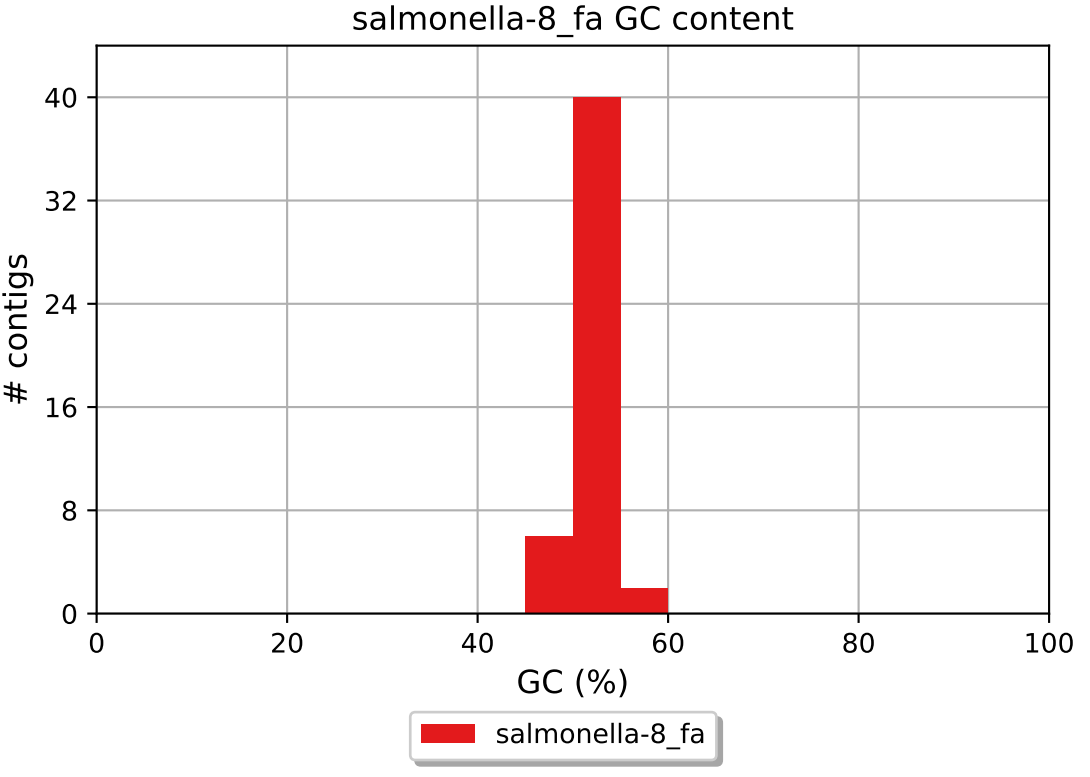
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

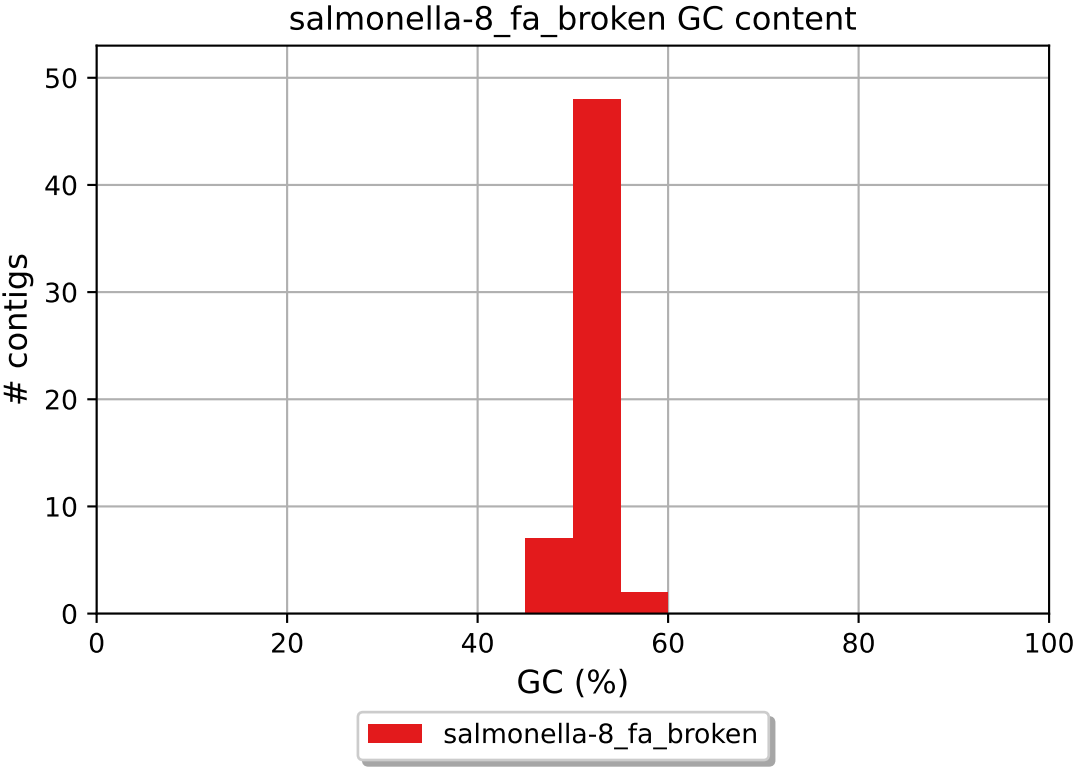

Nx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
salmonella-8_fa
salmonella-8_fa_broken


NGx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
salmonella-8_fa
salmonella-8_fa_broken

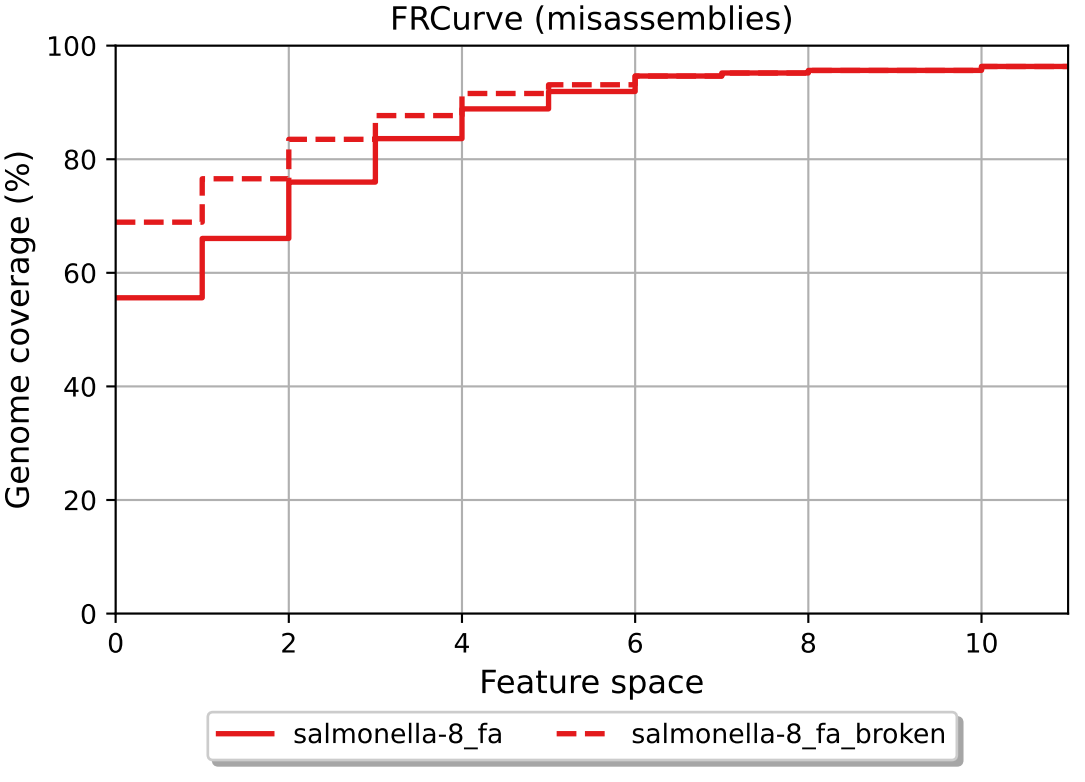

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
Contig index
salmonella-8_fa
salmonella-8_fa_broken
Reference

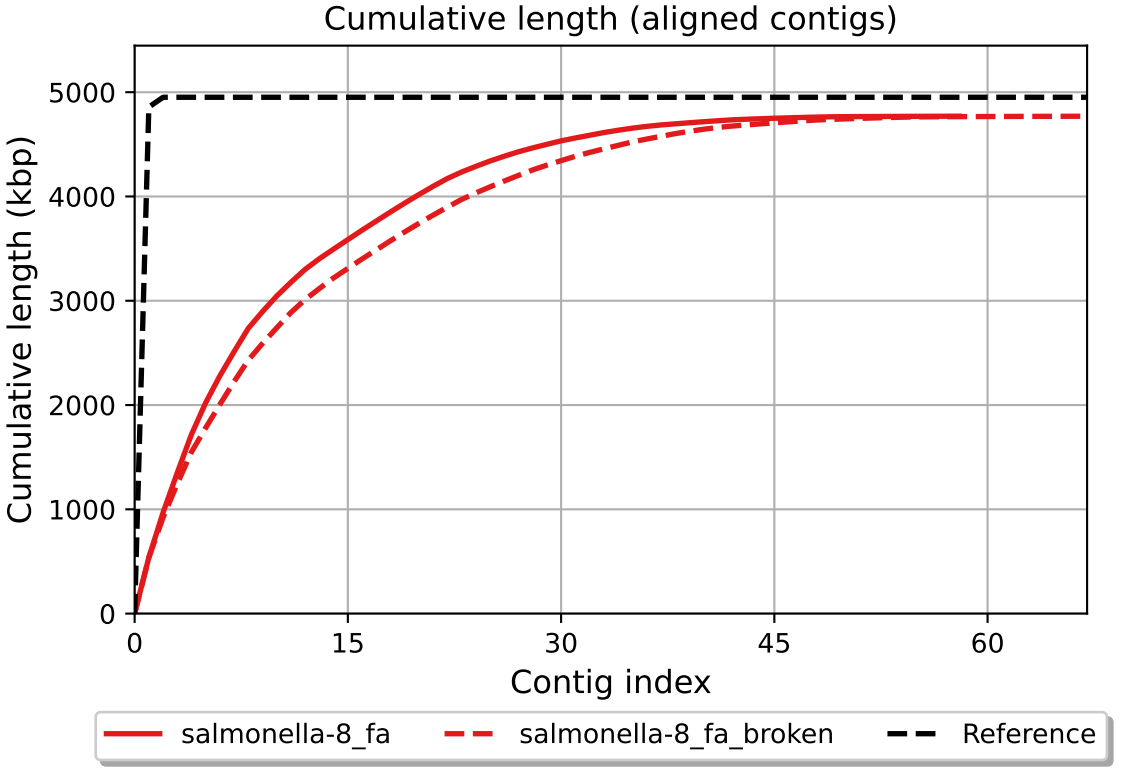

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
salmonella-8_fa
salmonella-8_fa_broken
Reference

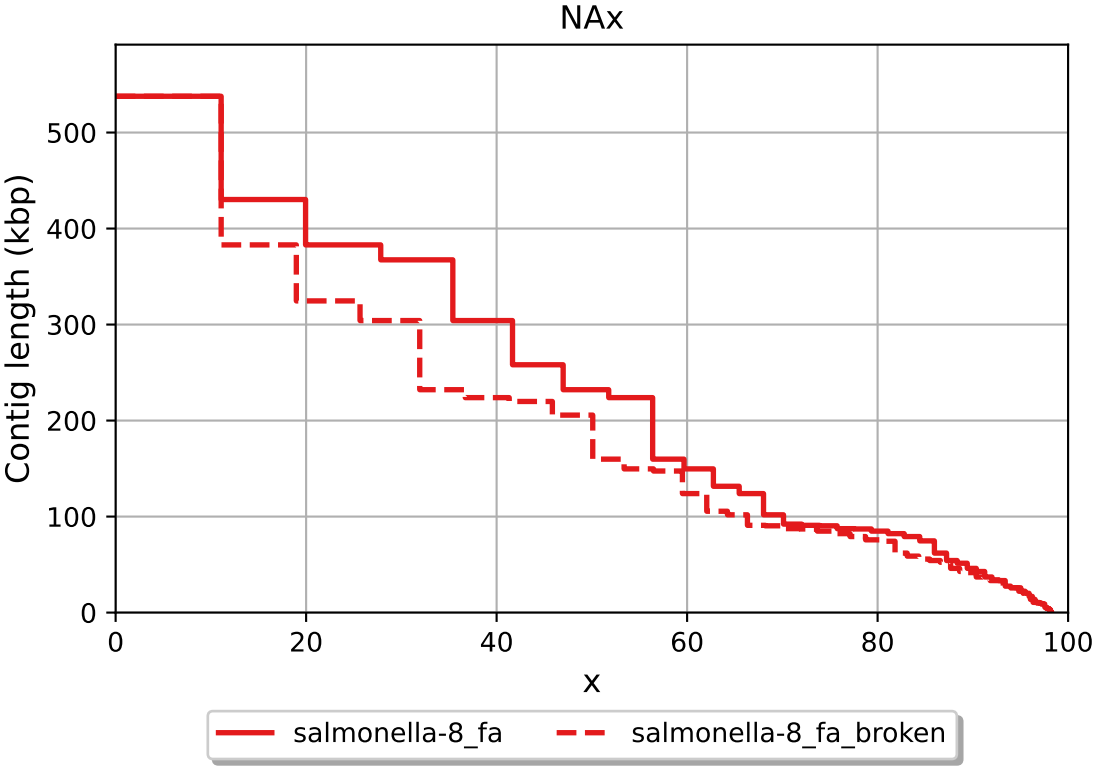

salmonella-8_fa GC content
contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
salmonella-8_fa

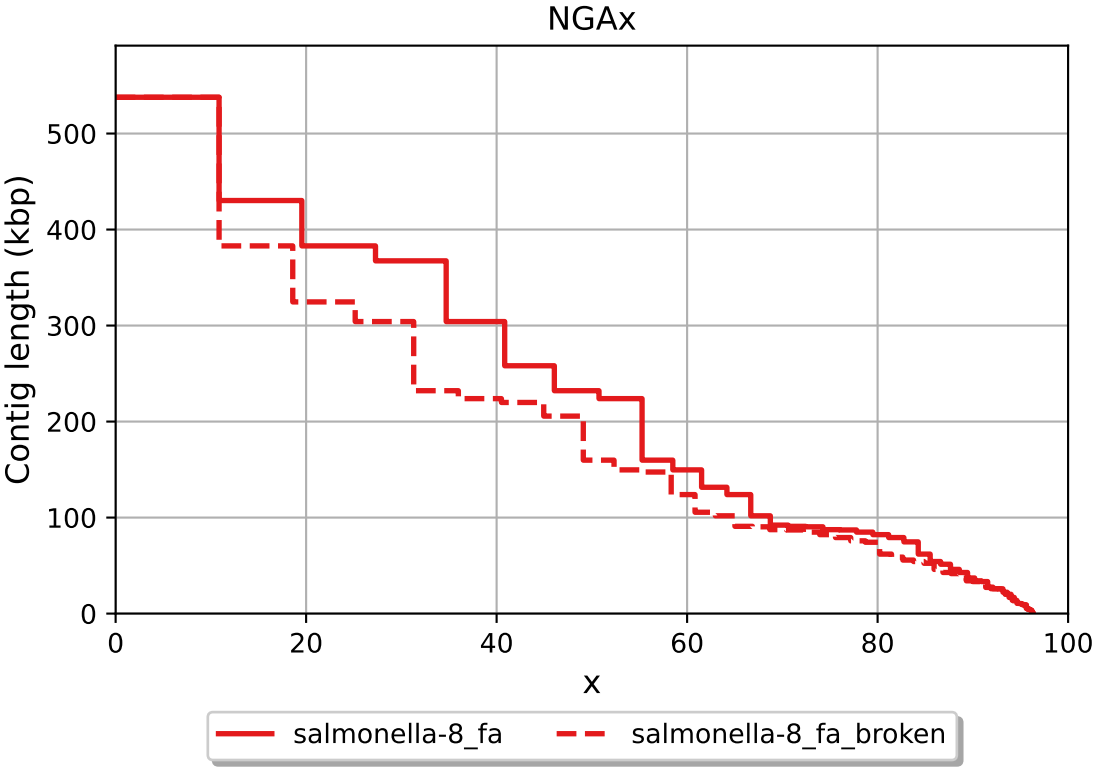

salmonella-8_fa_broken GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
salmonella-8_fa_broken

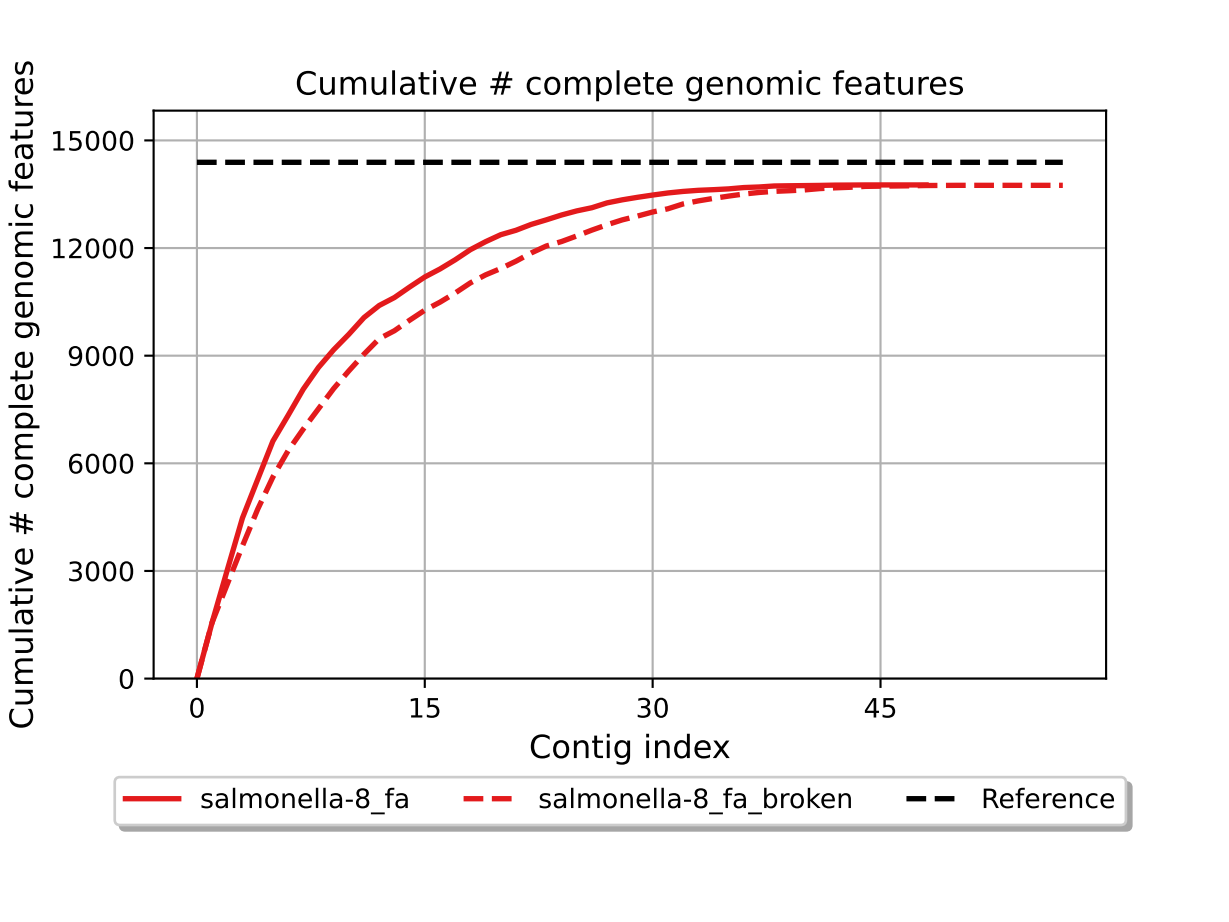
Misassemblies
10
8
6
4
2
0
salmonella-8_fa
salmonella-8_fa_broken
relocations

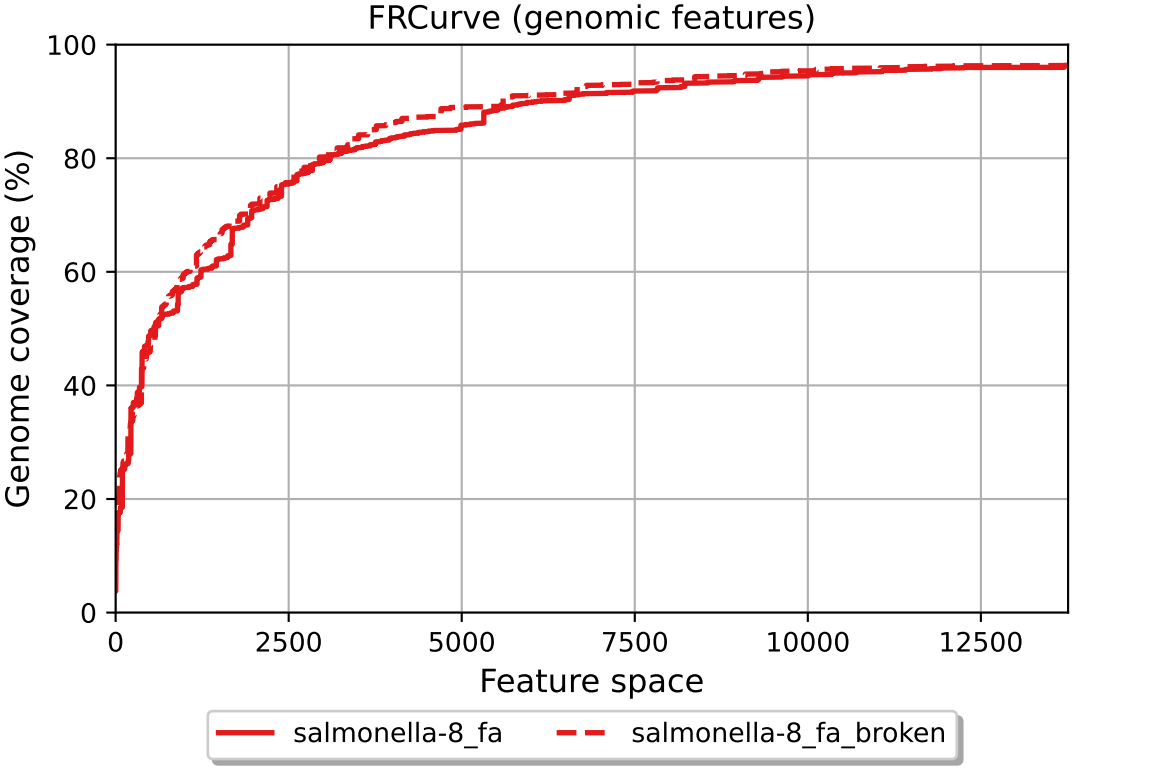

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
salmonella-8_fa
salmonella-8_fa_broken

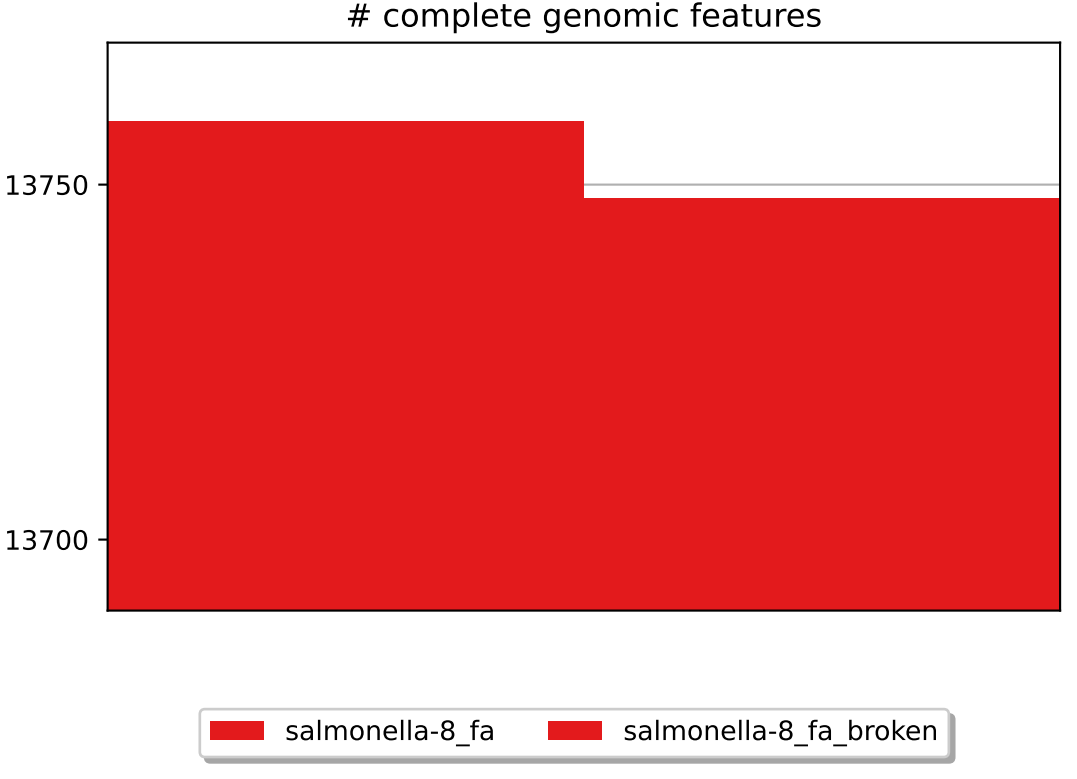

Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
15
30
45
60
Contig index
salmonella-8_fa
salmonella-8_fa_broken
Reference

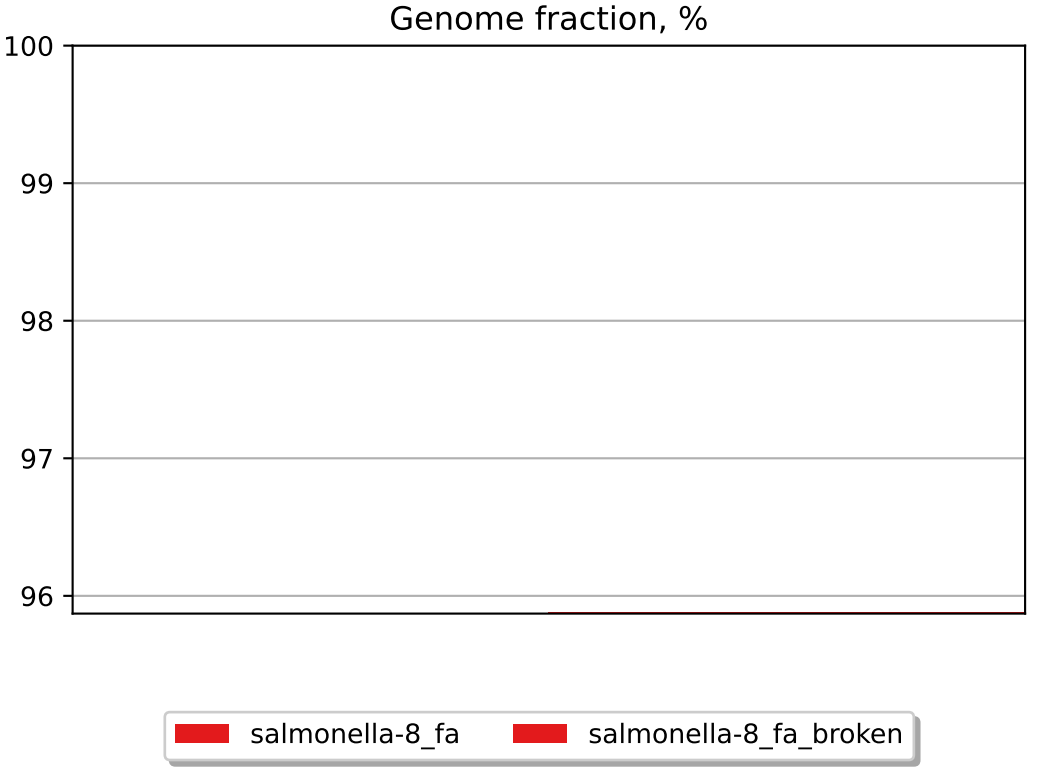

NAx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
salmonella-8_fa
salmonella-8_fa_broken


NGAx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
salmonella-8_fa
salmonella-8_fa_broken


Cumulative # complete genomic features
Cumulative # complete genomic features
15000
12000
9000
6000
3000
0
0
15
30
45
Contig index
salmonella-8_fa
salmonella-8_fa_broken
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
2500
5000
7500
10000
12500
Feature space
salmonella-8_fa
salmonella-8_fa_broken


complete genomic features
13750
13700
salmonella-8_fa
salmonella-8_fa_broken


Genome fraction, %
100
99
98
97
96
salmonella-8_fa
salmonella-8_fa_broken