Report

	GCF_002442595.2_ASM244259v2_genomic
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1409089
Total length (>= 1000 bp)	1409089
Total length (>= 5000 bp)	1409089
Total length (>= 10000 bp)	1400375
Total length (>= 25000 bp)	1318614
Total length (>= 50000 bp)	957413
# contigs	19
Largest contig	903654
Total length	1409089
Reference length	1521208
GC (%)	28.30
Reference GC (%)	28.18
N50	903654
NG50	903654
N90	27643
NG90	18340
auN	590634.8
auNG	547102.7
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	24
# misassembled contigs	12
Misassembled contigs length	374760
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 13 part
Unaligned length	113068
Genome fraction (%)	78.783
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	932.37
# indels per 100 kbp	60.88
# genomic features	1250 + 39 part
Largest alignment	903464
Total aligned length	1294341
NA50	903464
NGA50	903464
NA90	2247
NGA90	-
auNA	585142.7
auNGA	542015.4
LA50	1
LGA50	1
LA90	30
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

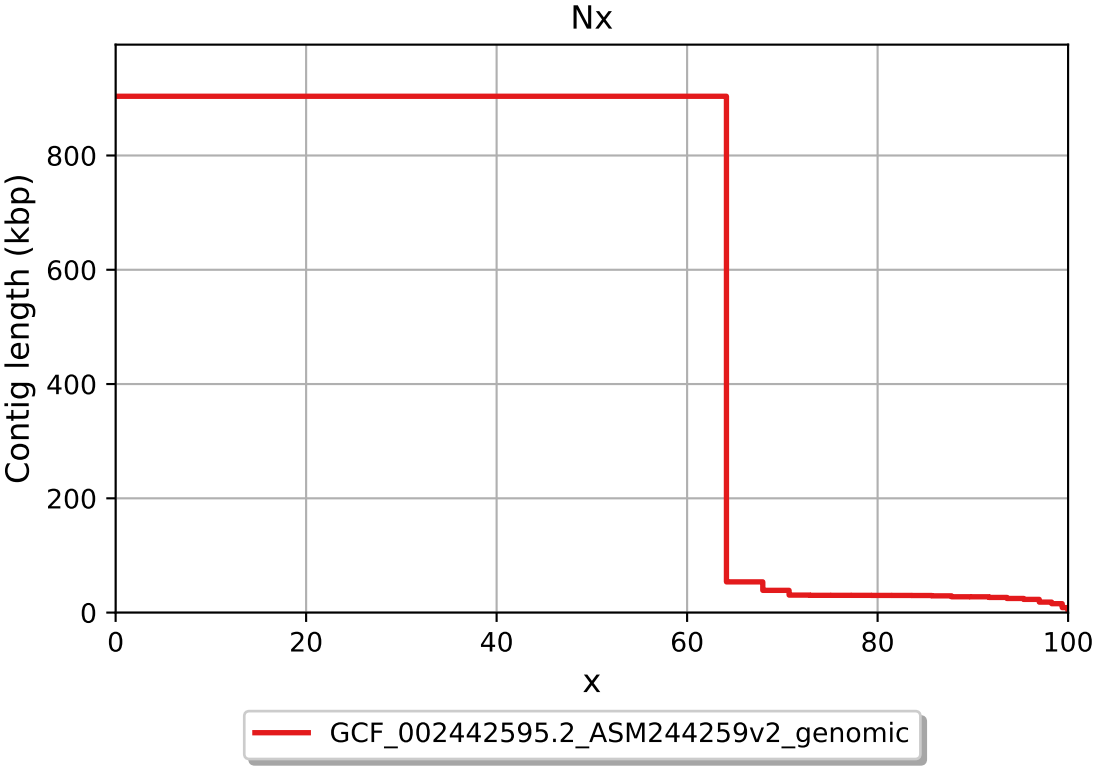
	GCF_002442595.2_ASM244259v2_genomic
# misassemblies	24
# contig misassemblies	24
# c. relocations	2
# c. translocations	20
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	374760
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	12068
# indels	788
# indels (<= 5 bp)	706
# indels (> 5 bp)	82
Indels length	3797

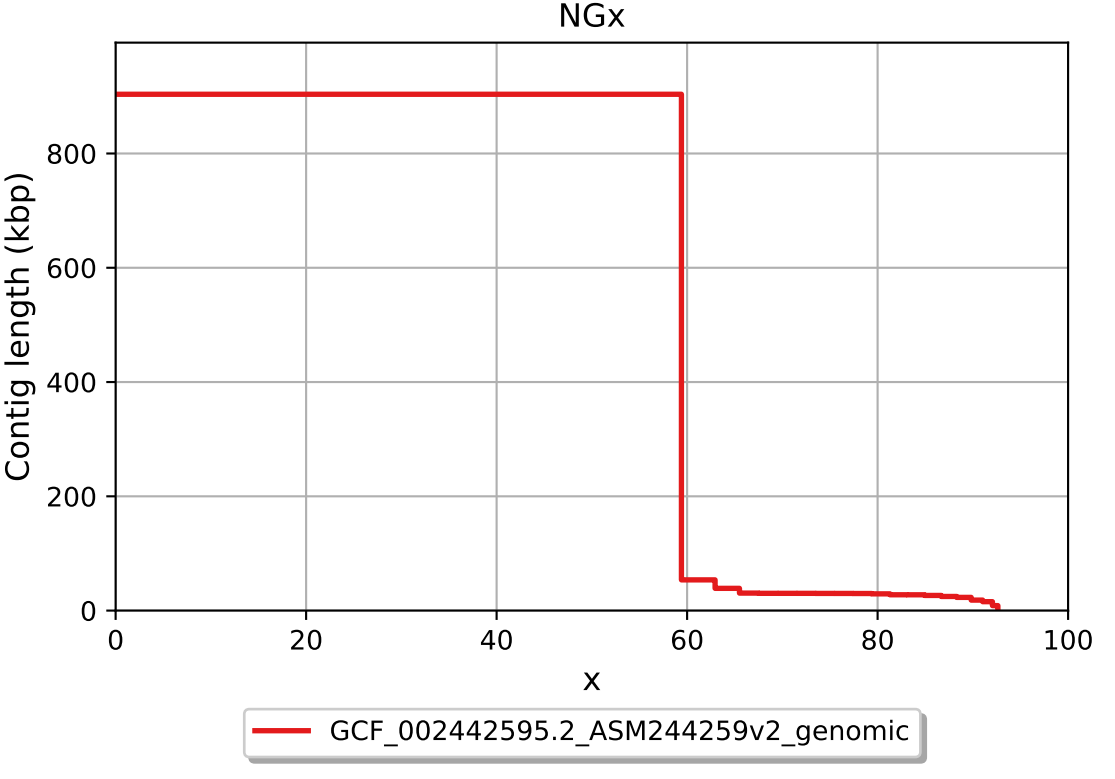
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

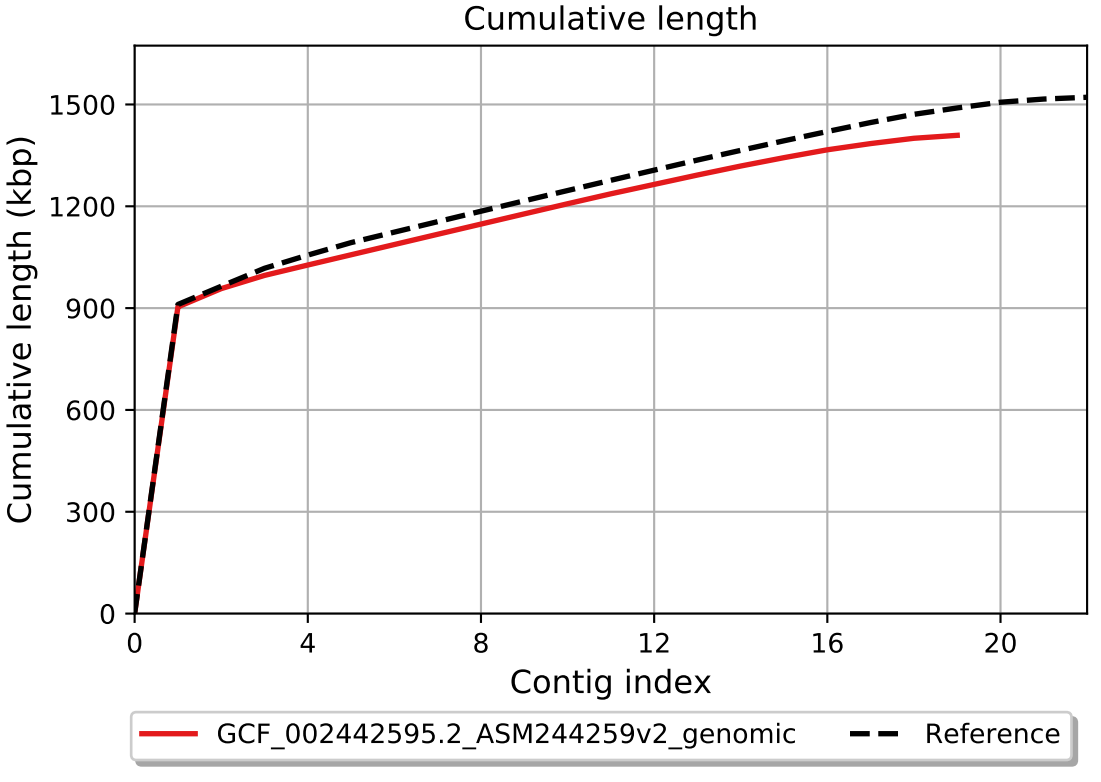
Unaligned report

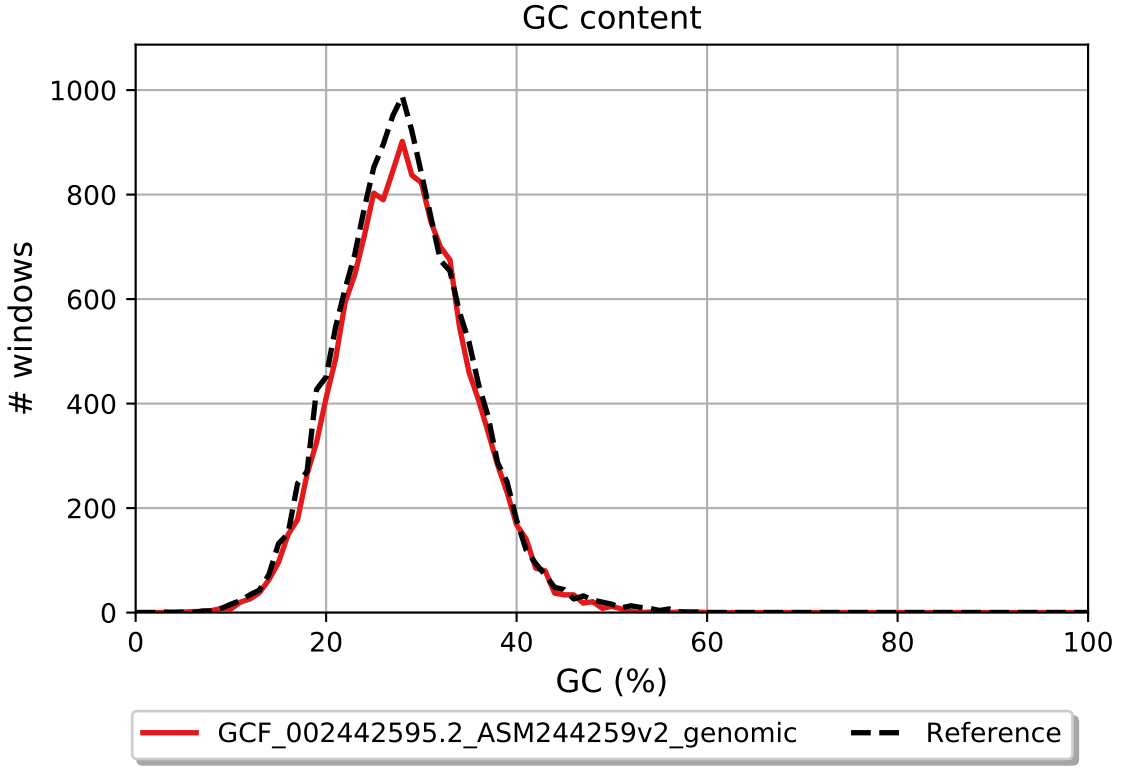
	GCF_002442595.2_ASM244259v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	113068
# N's	0

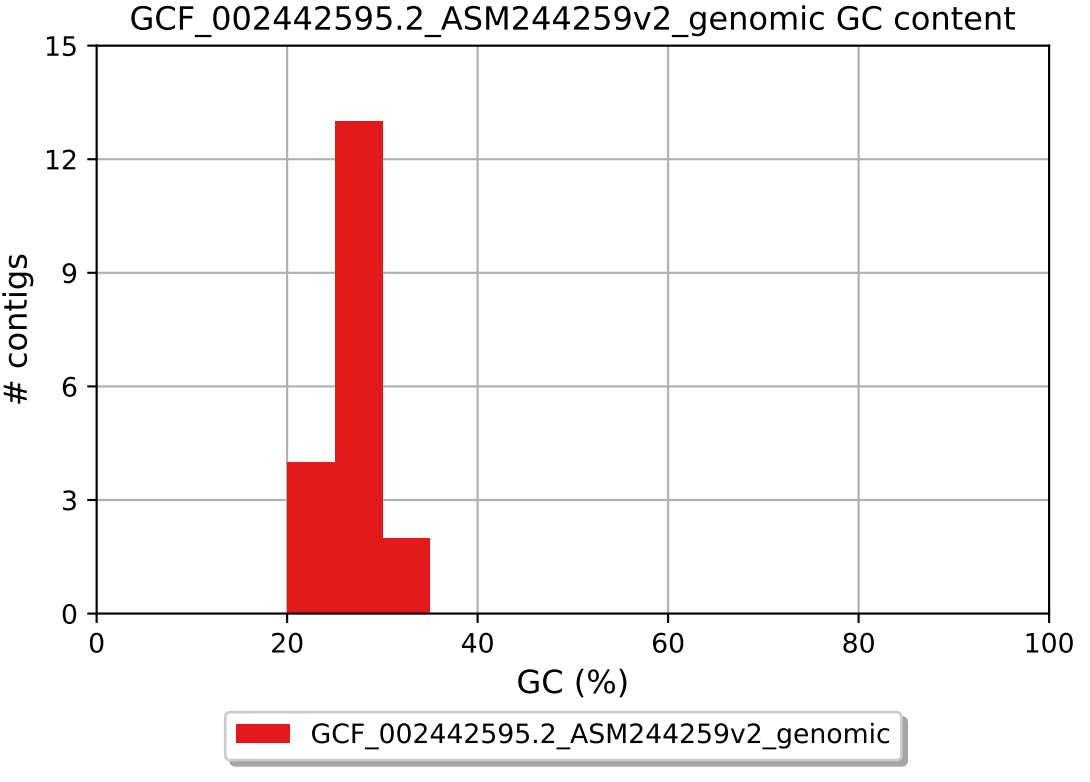
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

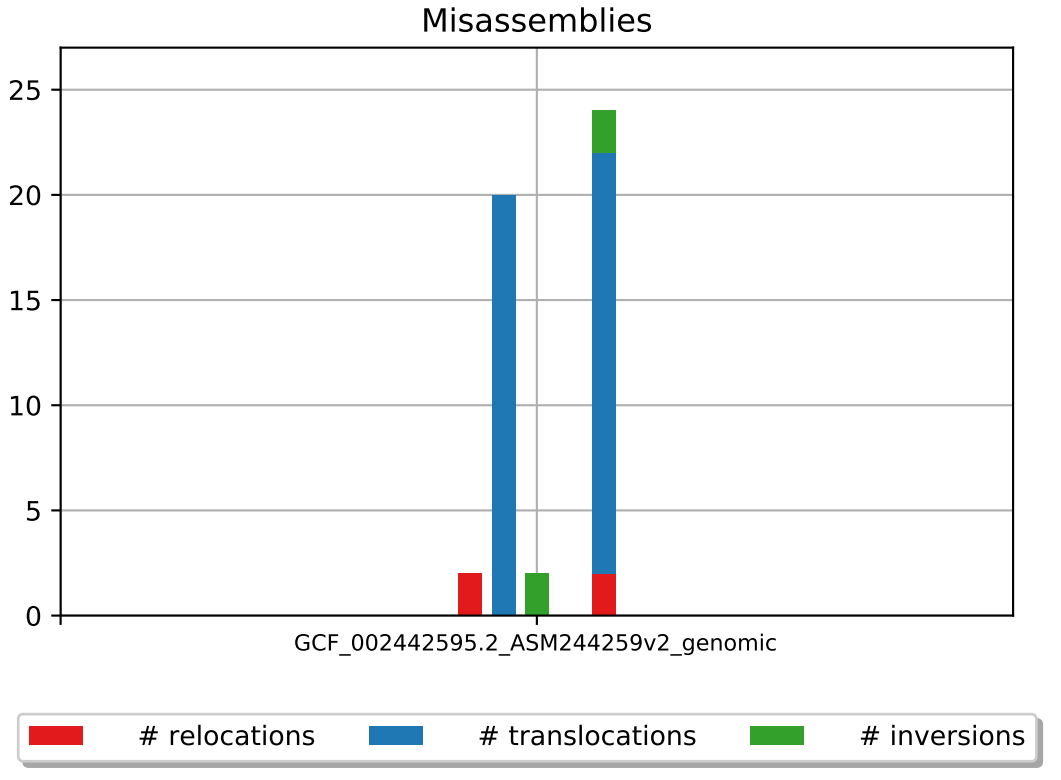

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002442595.2_ASM244259v2_genomic

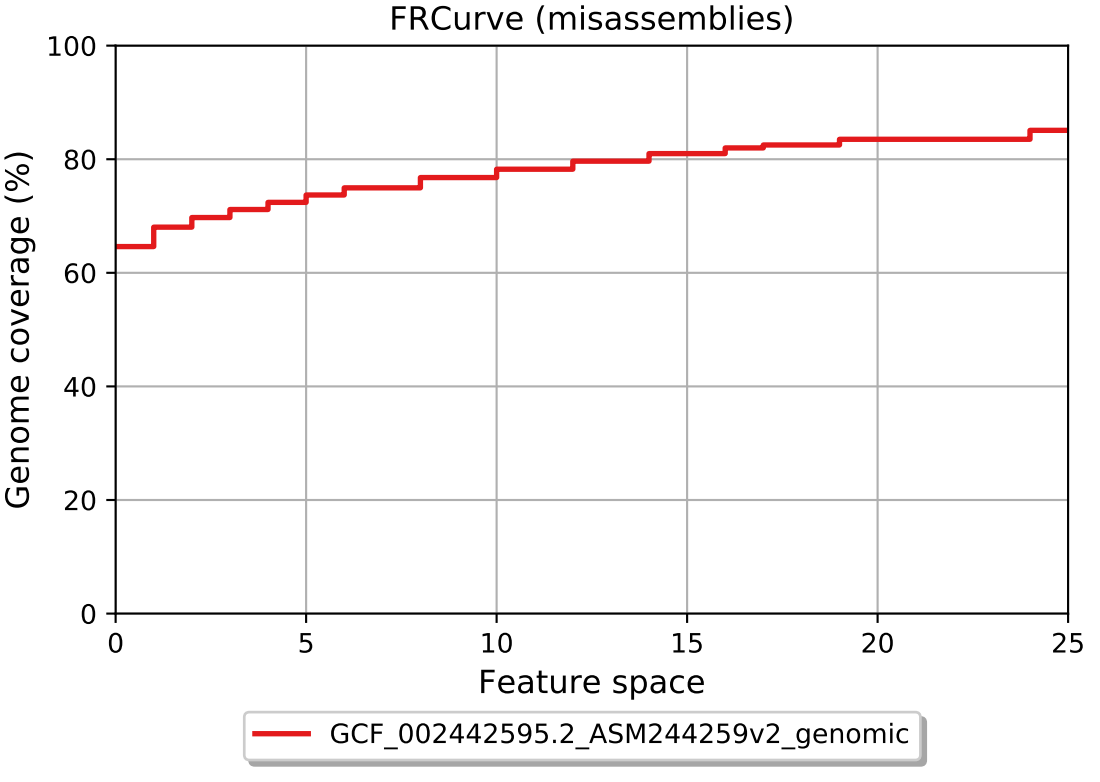

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002442595.2_ASM244259v2_genomic

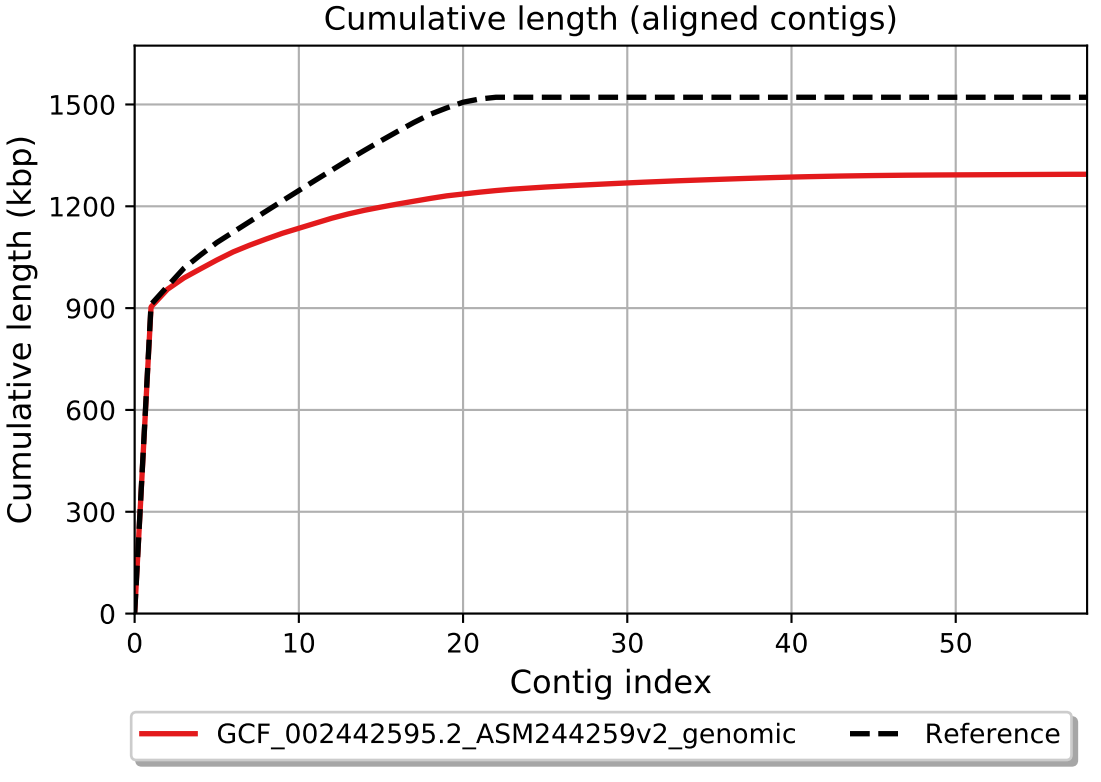

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCF_002442595.2_ASM244259v2_genomic
Reference

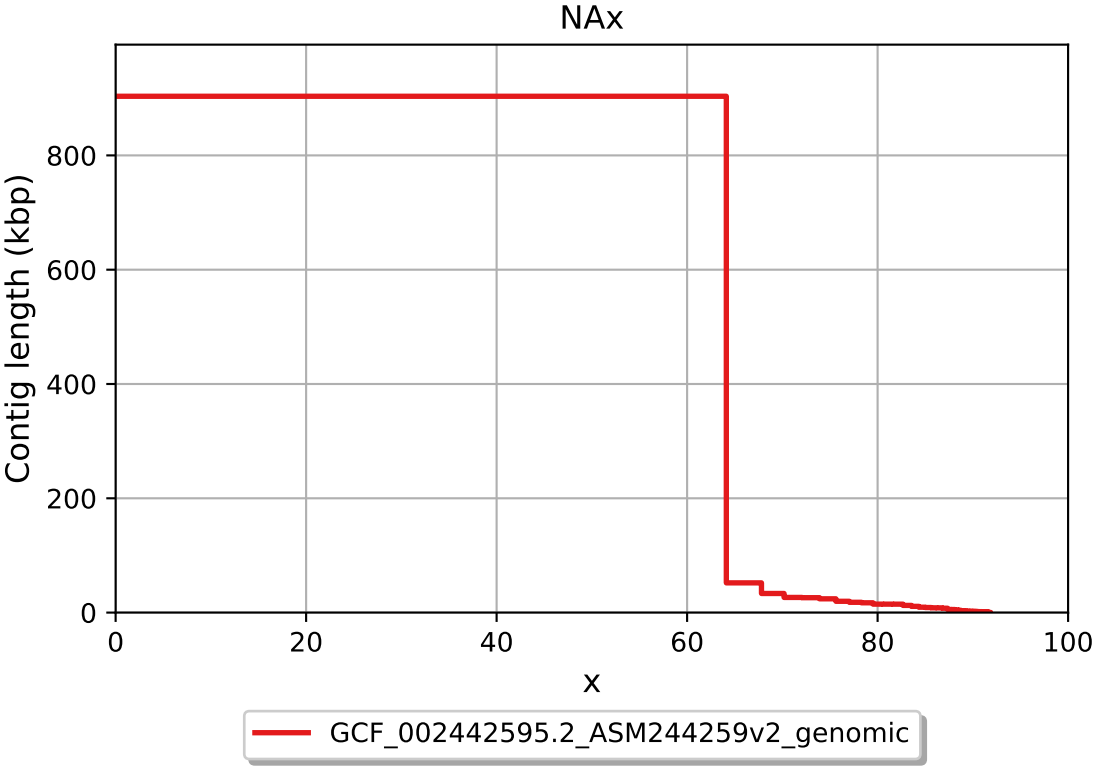

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCF_002442595.2_ASM244259v2_genomic
Reference

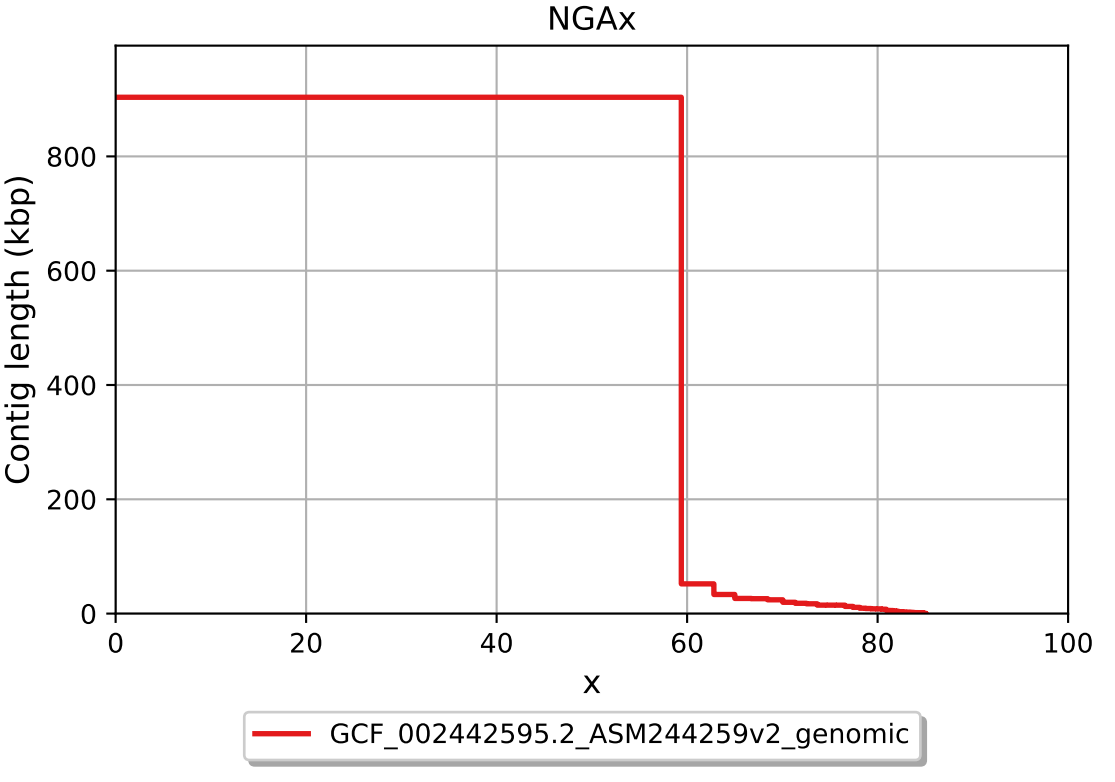

GCF_002442595.2_ASM244259v2_genomic GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
GCF_002442595.2_ASM244259v2_genomic

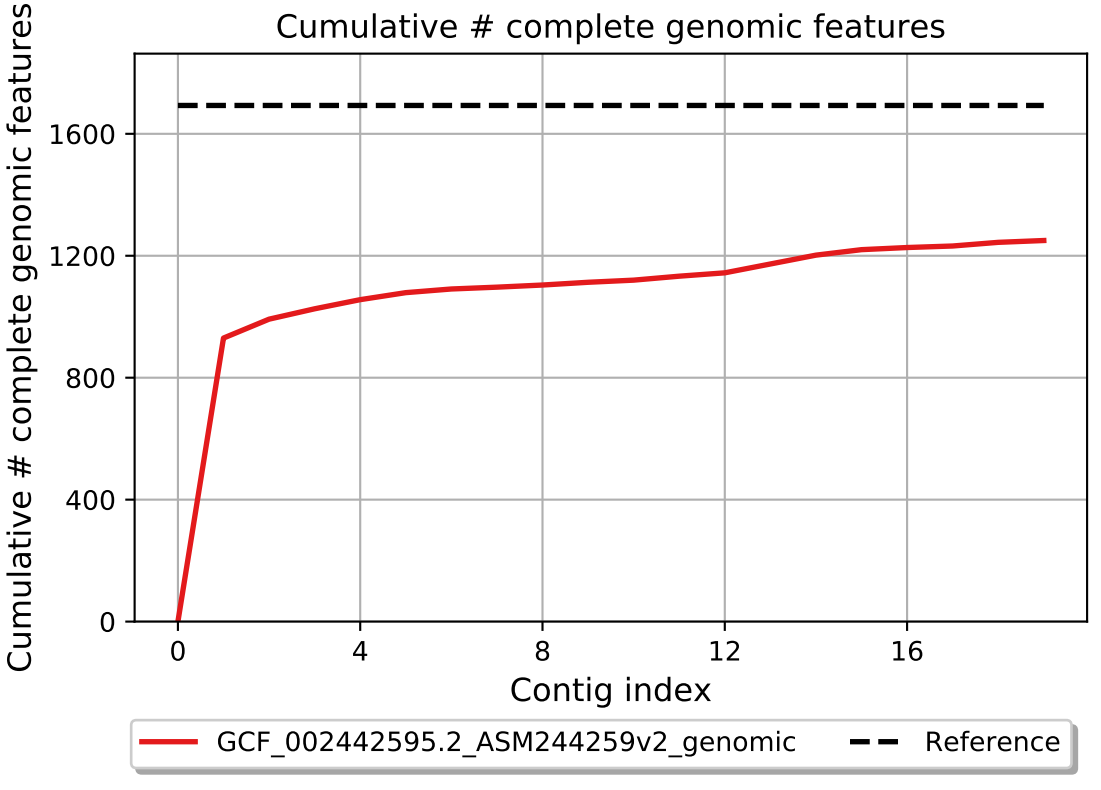

Misassemblies
25
20
15
10
5
0
GCF_002442595.2_ASM244259v2_genomic
relocations
translocations
inversions

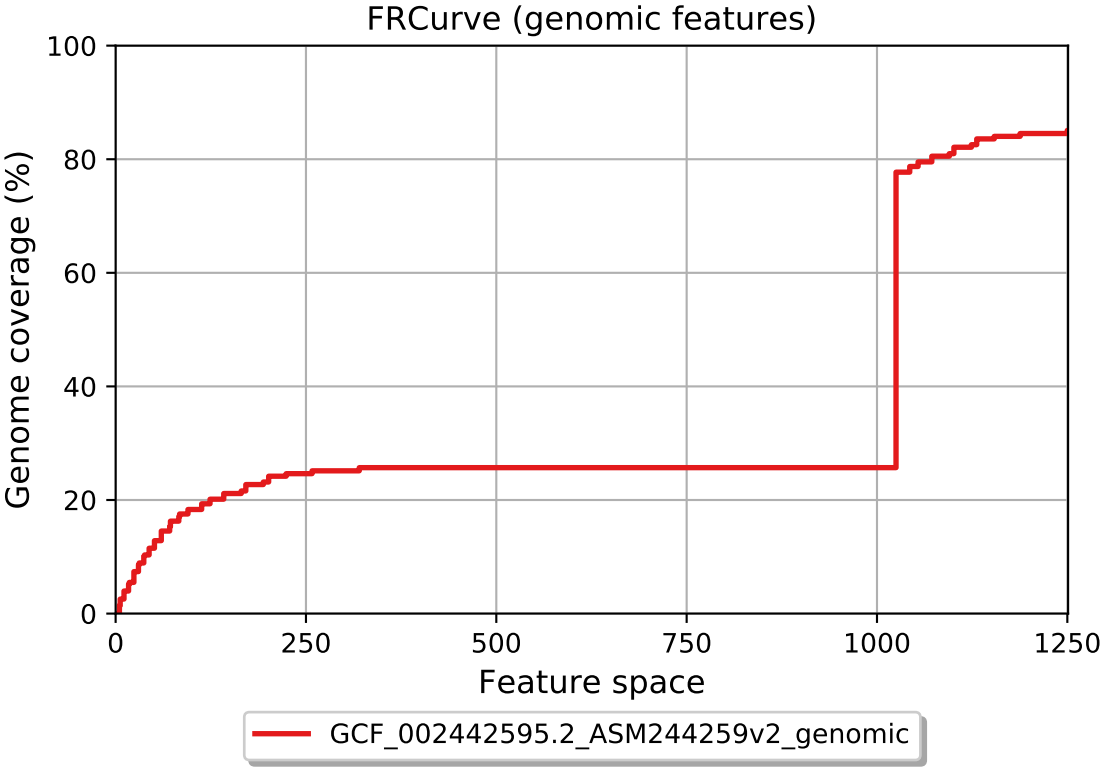

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
GCF_002442595.2_ASM244259v2_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
300
600
900
1200
1500
0
10
20
30
40
50
Contig index
GCF_002442595.2_ASM244259v2_genomic
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002442595.2_ASM244259v2_genomic


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002442595.2_ASM244259v2_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
4
8
12
16
Contig index
GCF_002442595.2_ASM244259v2_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCF_002442595.2_ASM244259v2_genomic