Report

	GCF_002151465.1_ASM215146v1_genomic
# contigs (>= 0 bp)	12
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	12
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1288112
Total length (>= 1000 bp)	1288112
Total length (>= 5000 bp)	1288112
Total length (>= 10000 bp)	1288112
Total length (>= 25000 bp)	1271292
Total length (>= 50000 bp)	1016542
# contigs	12
Largest contig	909921
Total length	1288112
Reference length	1521208
GC (%)	28.35
Reference GC (%)	28.18
N50	909921
NG50	909921
N90	30580
NG90	-
auN	653782.8
auNG	553603.1
L50	1
LG50	1
L90	8
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	30674
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	2718
Genome fraction (%)	82.706
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	44.27
# indels per 100 kbp	10.74
# genomic features	1376 + 4 part
Largest alignment	909921
Total aligned length	1285192
NA50	909921
NGA50	909921
NA90	30223
NGA90	-
auNA	653391.7
auNGA	553271.9
LA50	1
LGA50	1
LA90	8
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

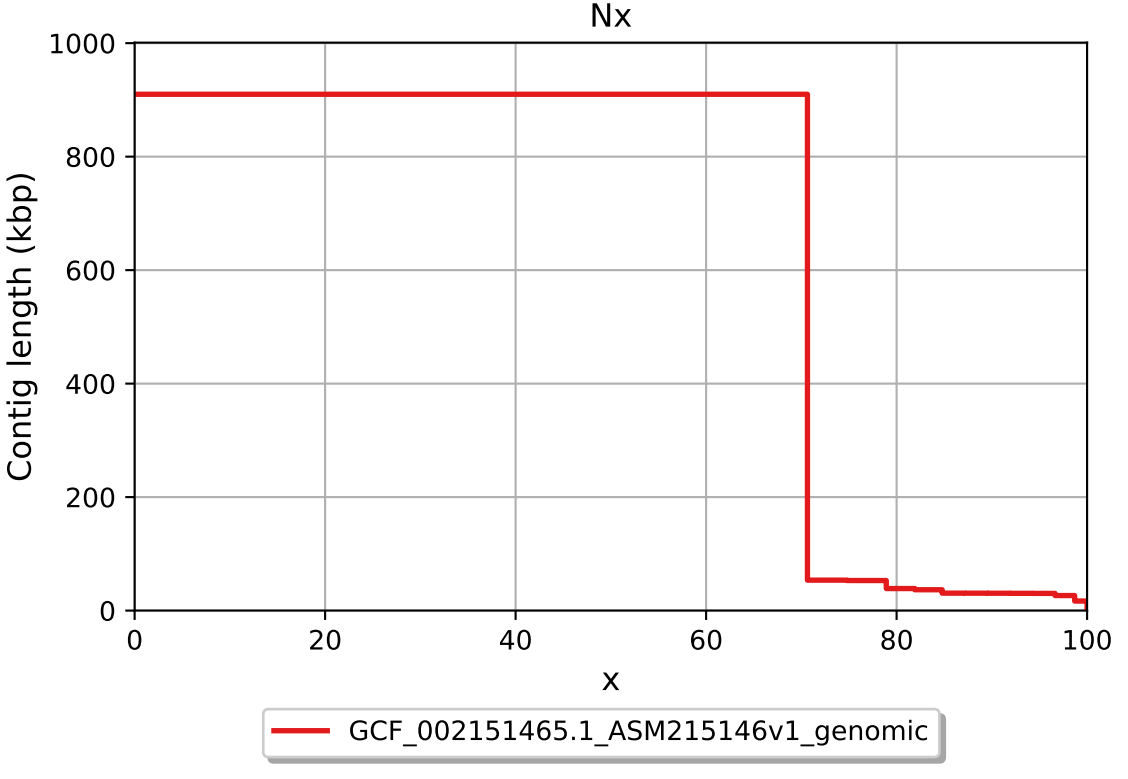
	GCF_002151465.1_ASM215146v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	30674
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	569
# indels	138
# indels (<= 5 bp)	125
# indels (> 5 bp)	13
Indels length	1191

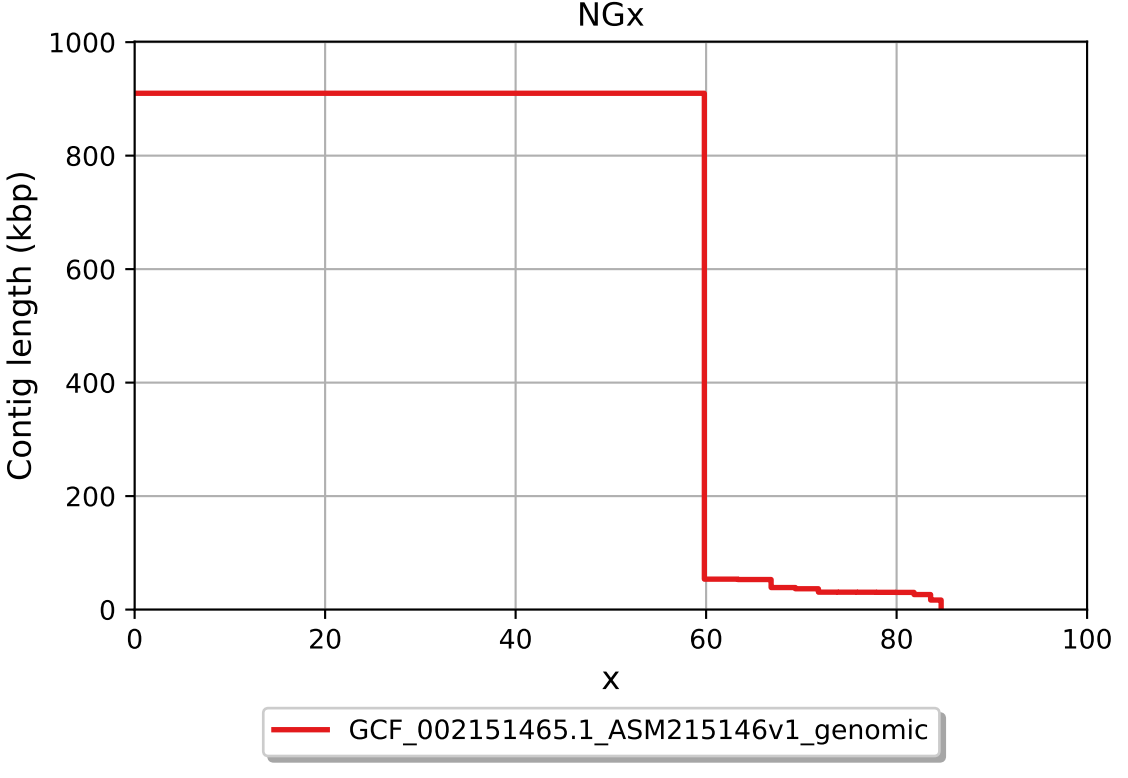
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

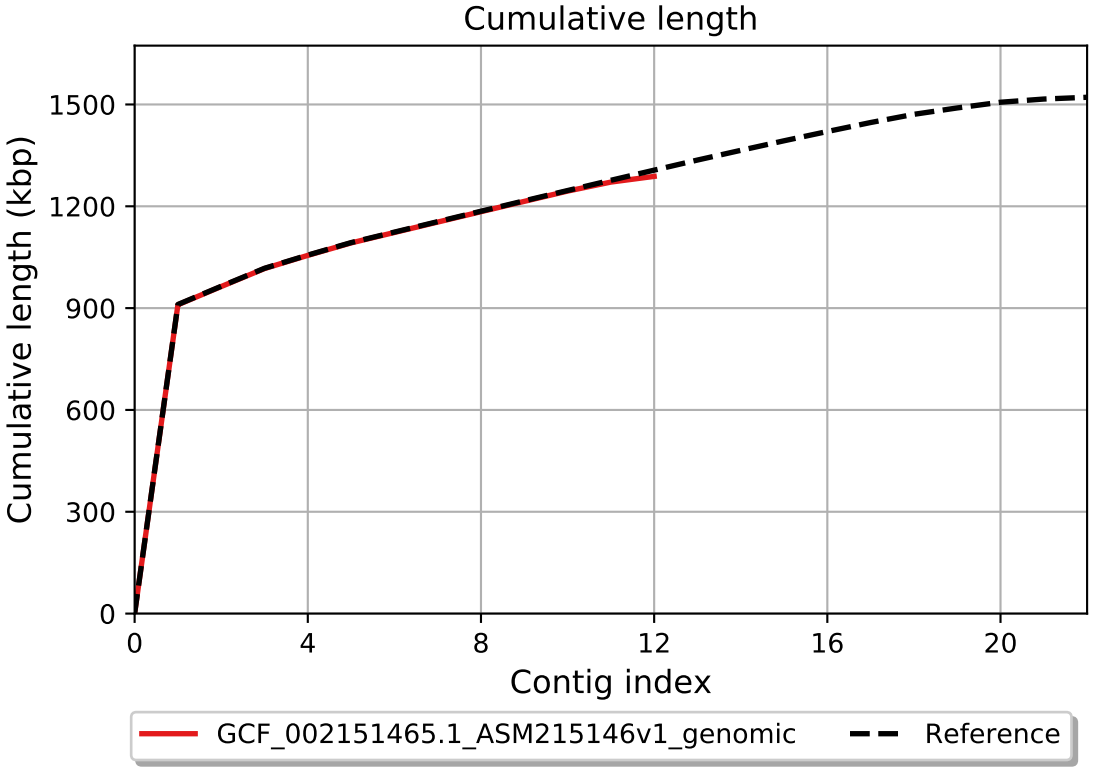
Unaligned report

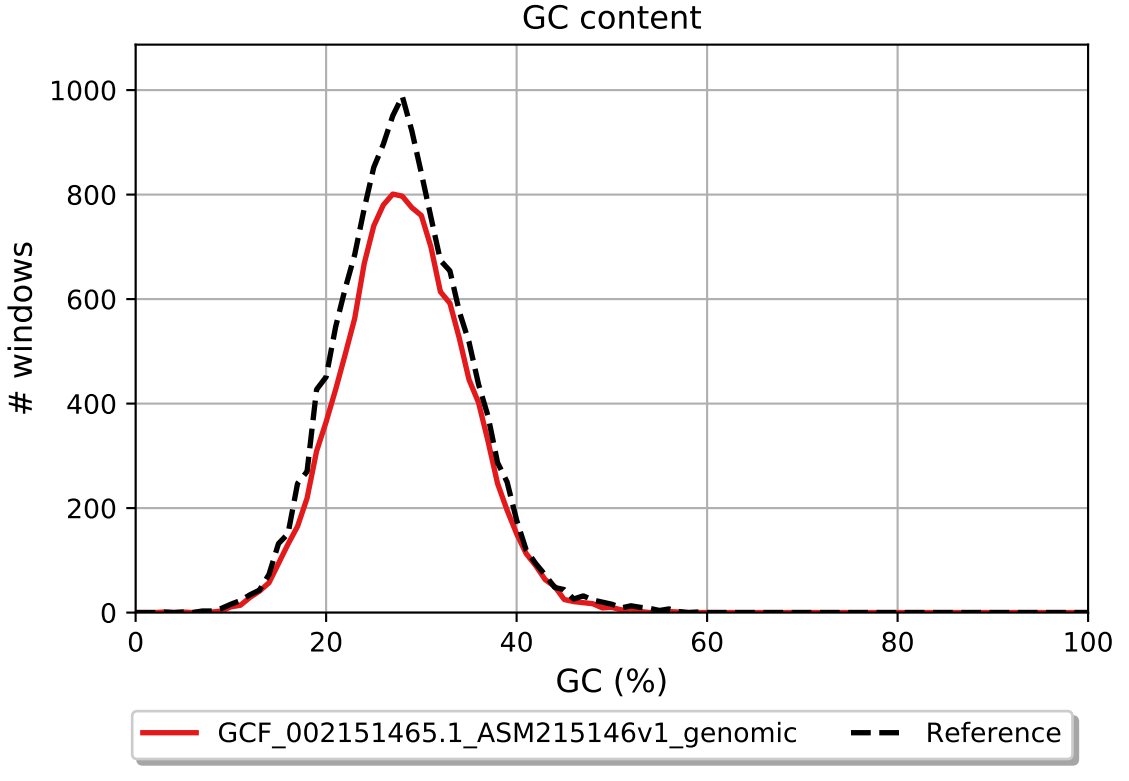
	GCF_002151465.1_ASM215146v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2718
# N's	0

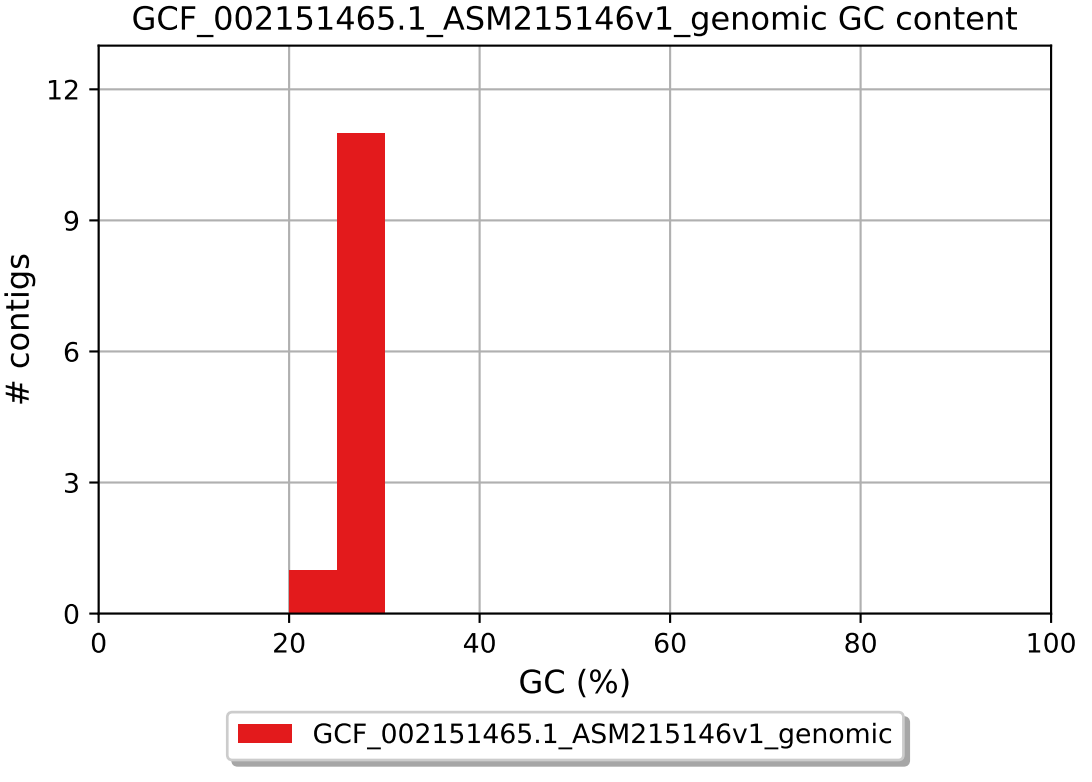
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

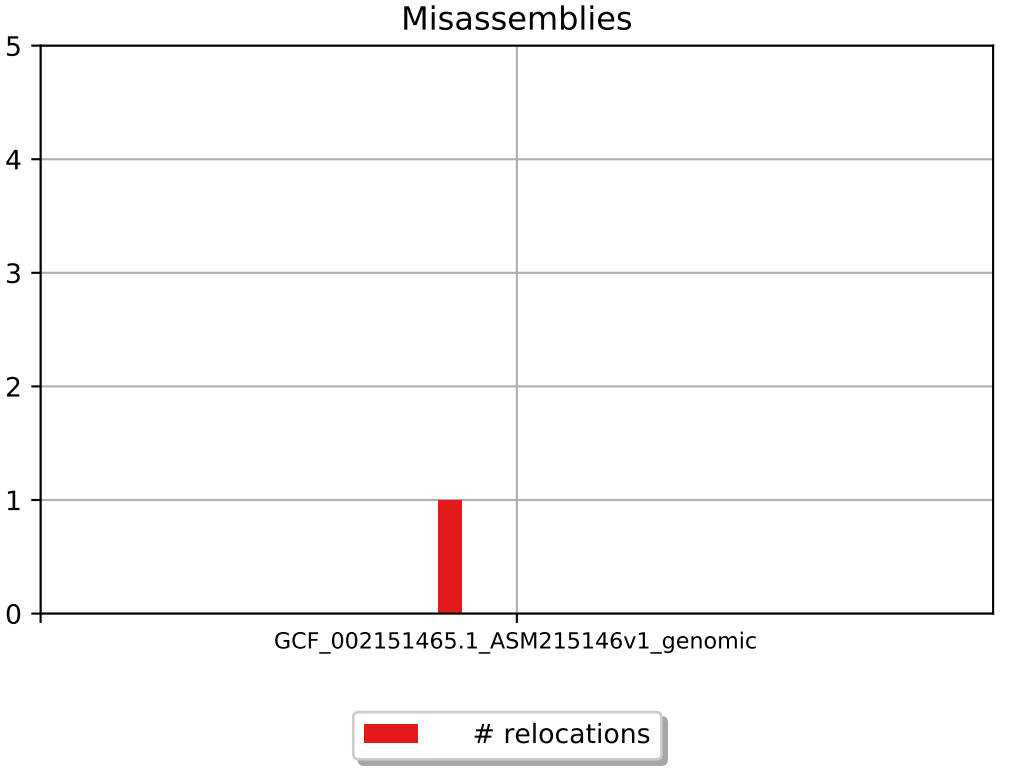

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002151465.1_ASM215146v1_genomic

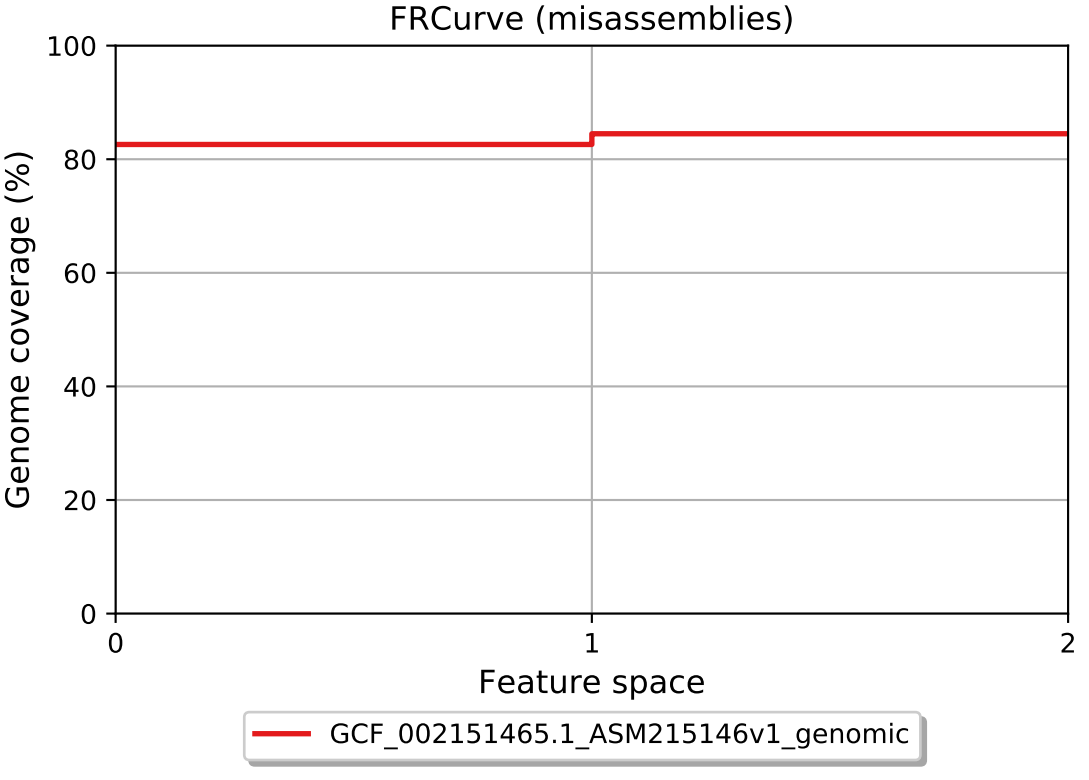

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002151465.1_ASM215146v1_genomic

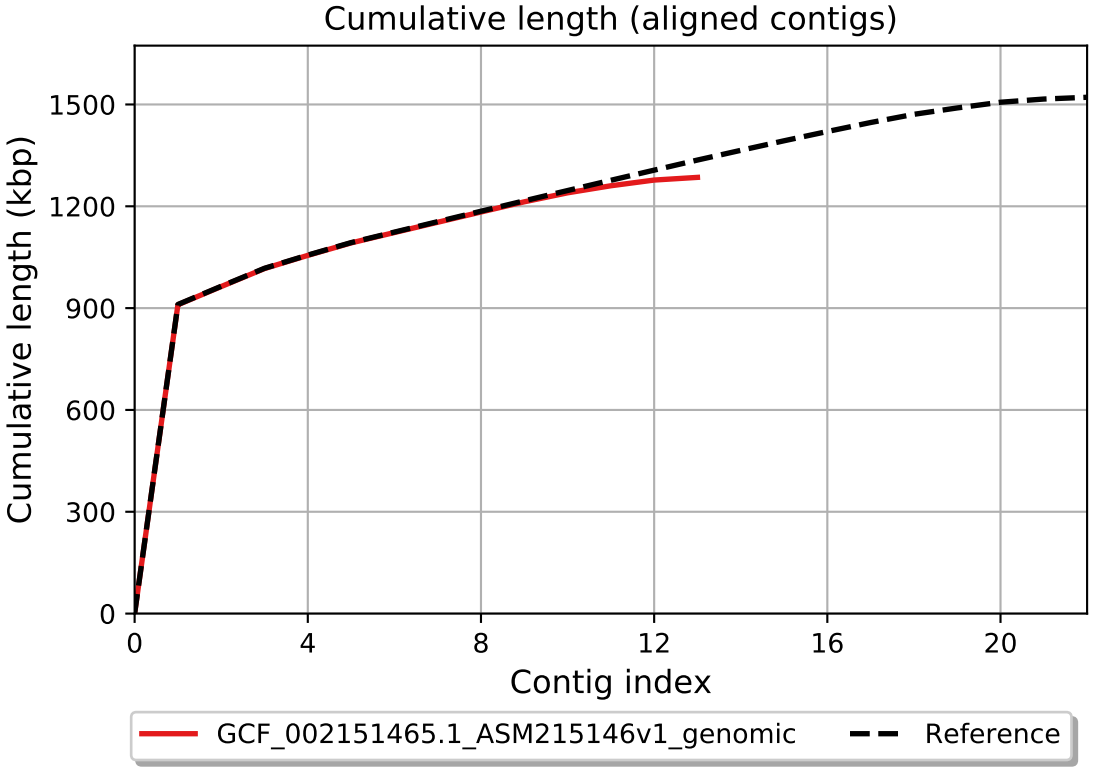

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCF_002151465.1_ASM215146v1_genomic
Reference

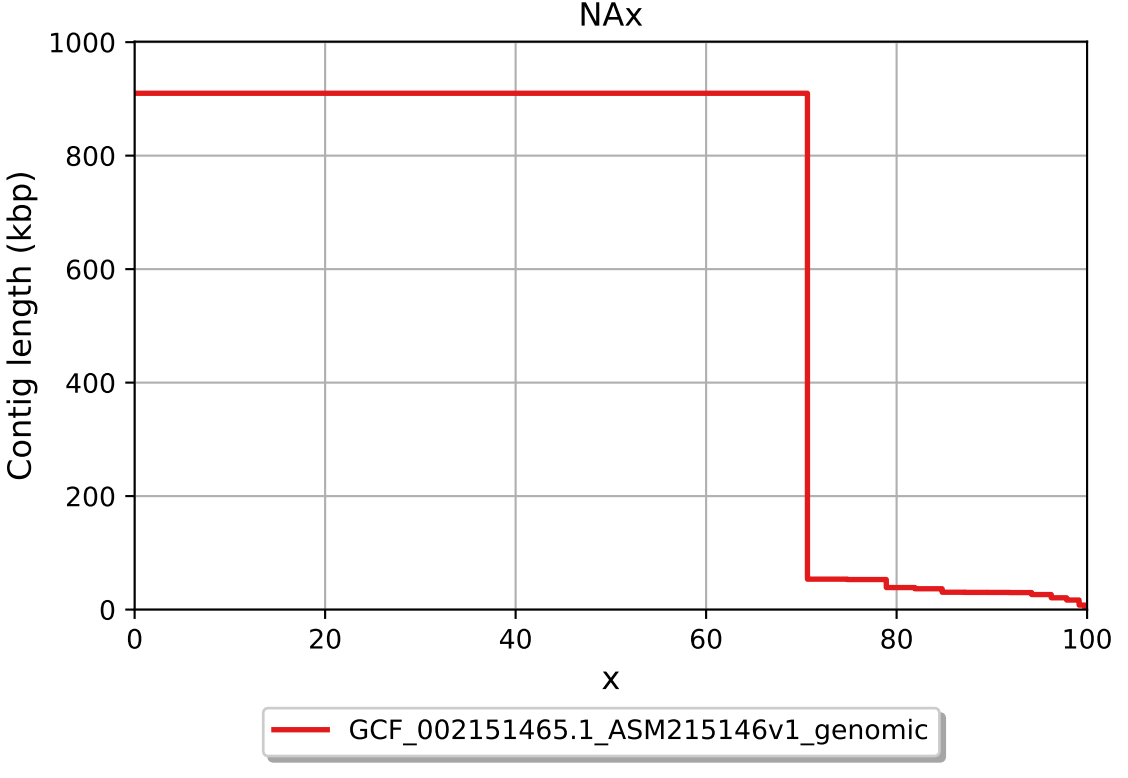

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCF_002151465.1_ASM215146v1_genomic
Reference

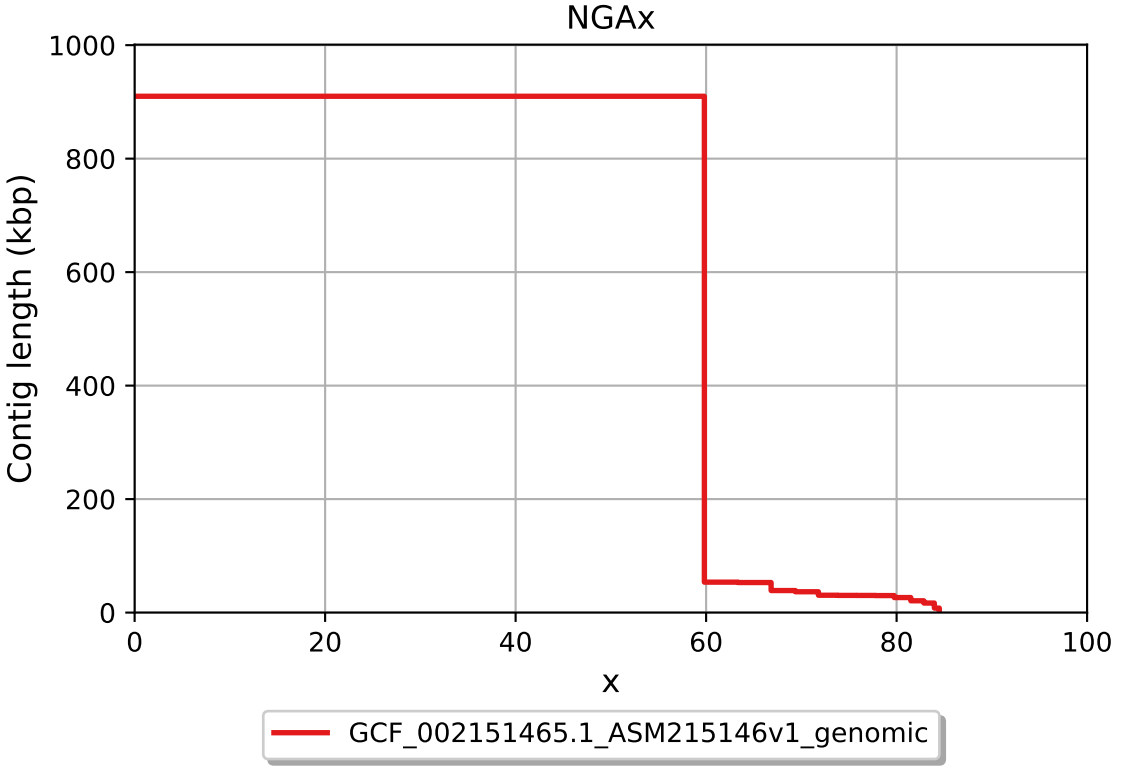

GCF_002151465.1_ASM215146v1_genomic GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
GCF_002151465.1_ASM215146v1_genomic

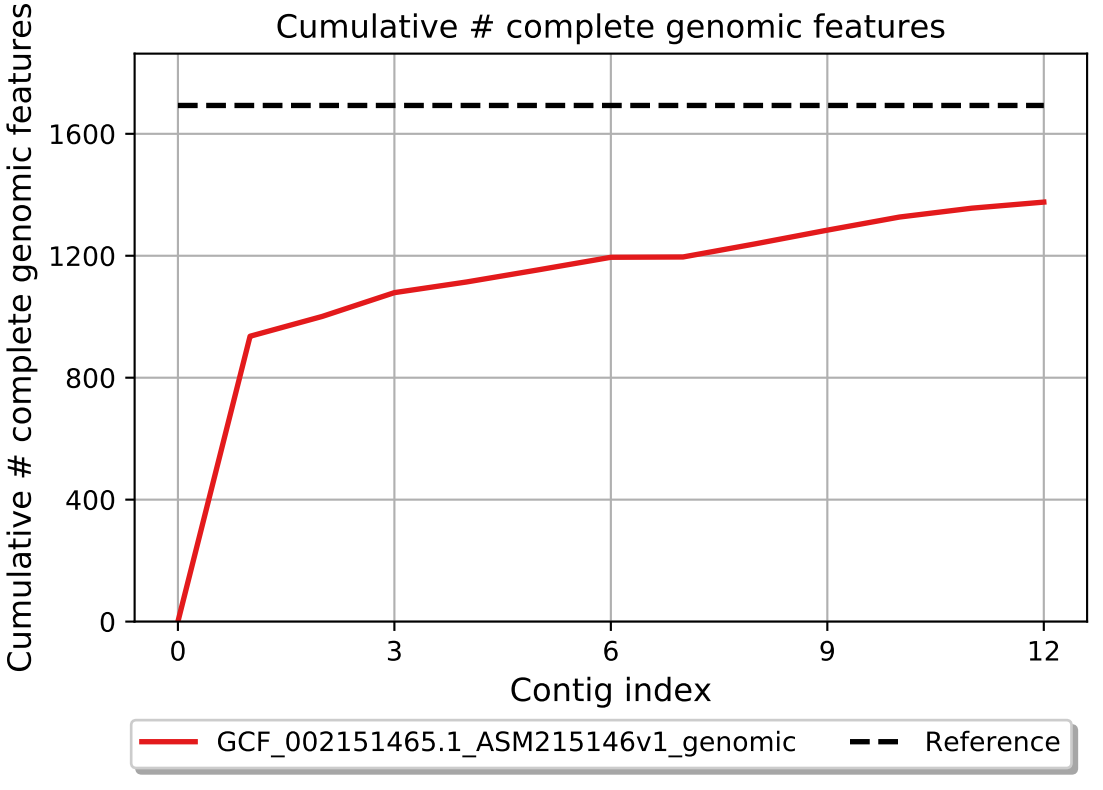

Misassemblies
5
4
3
2
1
0
GCF_002151465.1_ASM215146v1_genomic
relocations

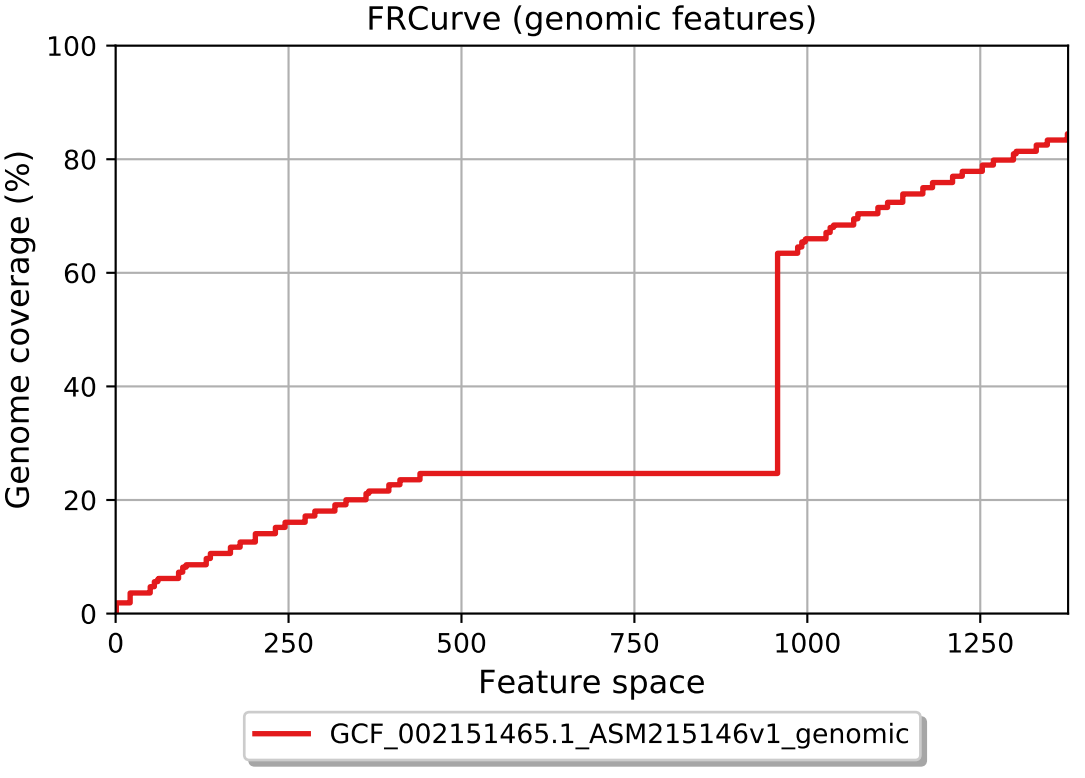

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
GCF_002151465.1_ASM215146v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCF_002151465.1_ASM215146v1_genomic
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002151465.1_ASM215146v1_genomic


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_002151465.1_ASM215146v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
3
6
9
12
Contig index
GCF_002151465.1_ASM215146v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCF_002151465.1_ASM215146v1_genomic