Report

	GCA_002151485.1_ASM215148v1_genomic
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1301554
Total length (>= 1000 bp)	1301554
Total length (>= 5000 bp)	1301554
Total length (>= 10000 bp)	1301554
Total length (>= 25000 bp)	1284754
Total length (>= 50000 bp)	1136219
# contigs	11
Largest contig	910728
Total length	1301554
Reference length	1521208
GC (%)	28.51
Reference GC (%)	28.18
N50	910728
NG50	910728
N90	36846
NG90	-
auN	650734.9
auNG	556772.4
L50	1
LG50	1
L90	6
LG90	-
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	150115
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	13510
Genome fraction (%)	83.072
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	110.48
# indels per 100 kbp	14.05
# genomic features	1400 + 9 part
Largest alignment	910728
Total aligned length	1288038
NA50	910728
NGA50	910728
NA90	28157
NGA90	-
auNA	648292.6
auNGA	554682.8
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

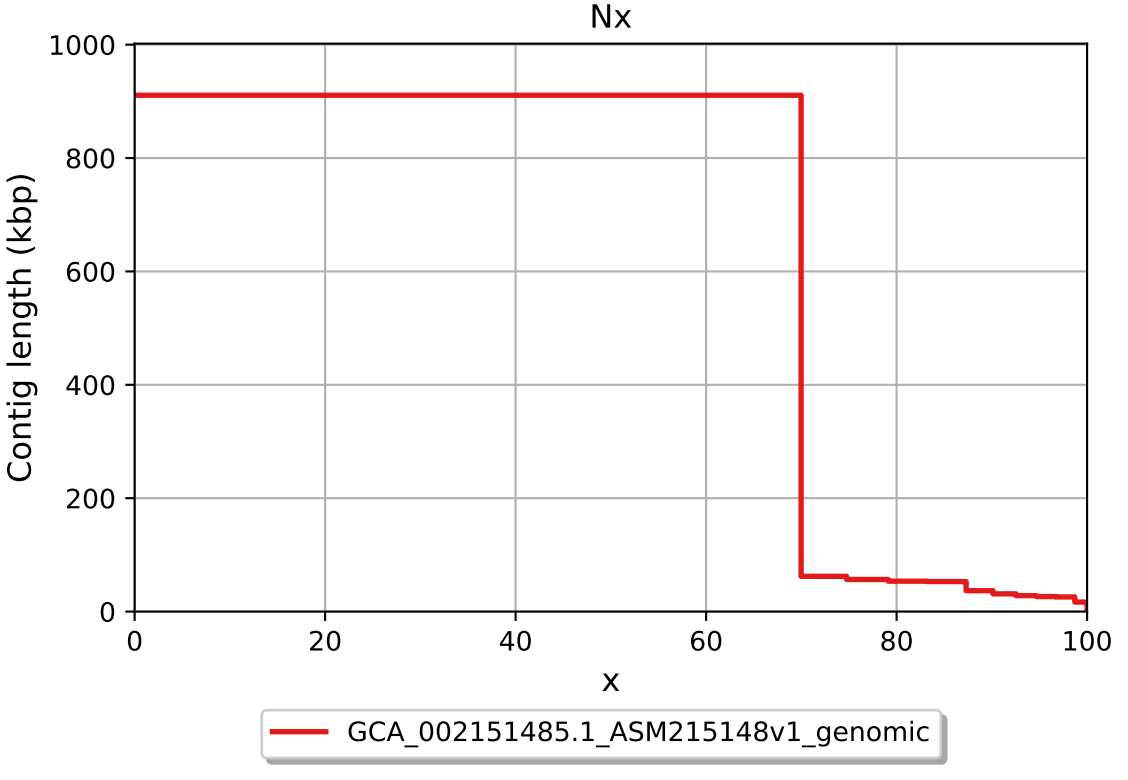
	GCA_002151485.1_ASM215148v1_genomic
# misassemblies	4
# contig misassemblies	4
# c. relocations	1
# c. translocations	3
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	150115
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1423
# indels	181
# indels (<= 5 bp)	167
# indels (> 5 bp)	14
Indels length	520

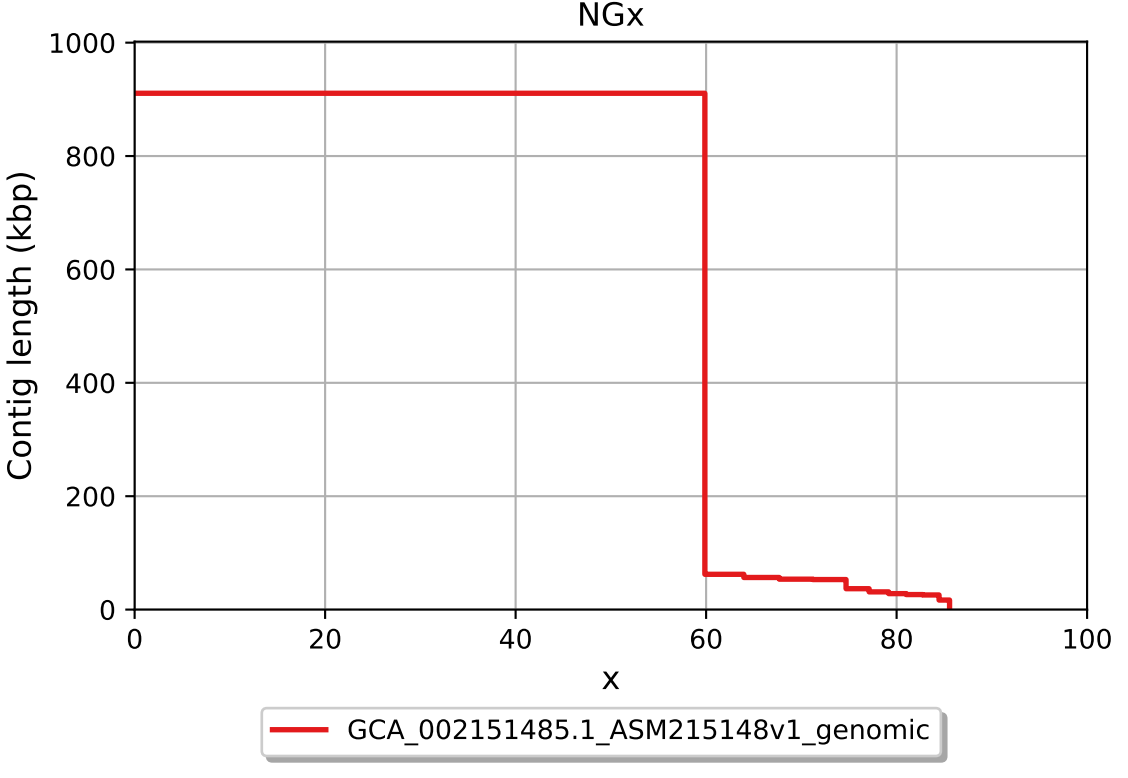
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

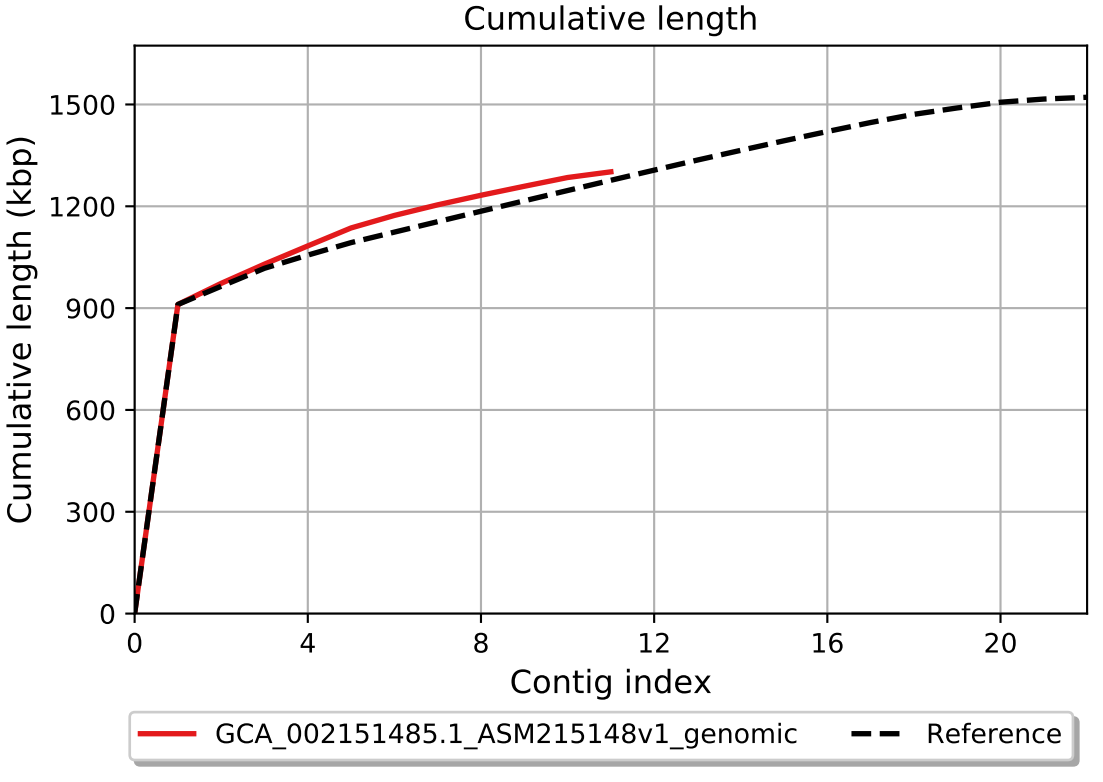
Unaligned report

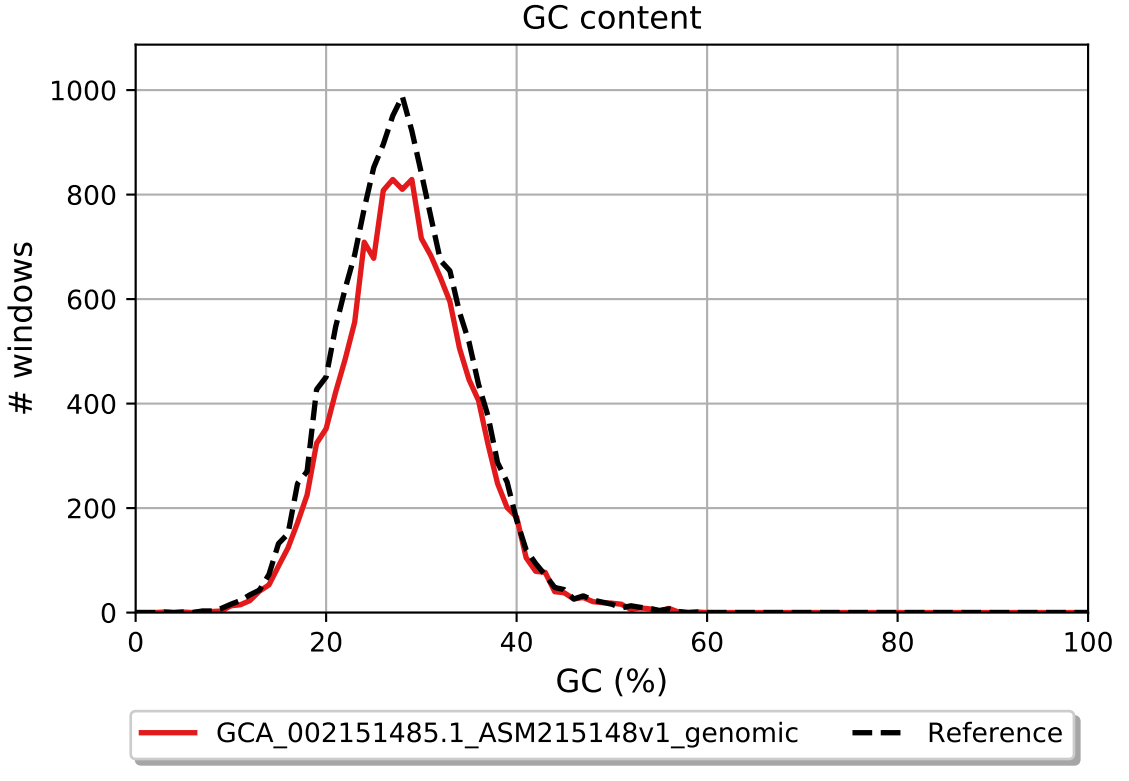
	GCA_002151485.1_ASM215148v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	13510
# N's	0

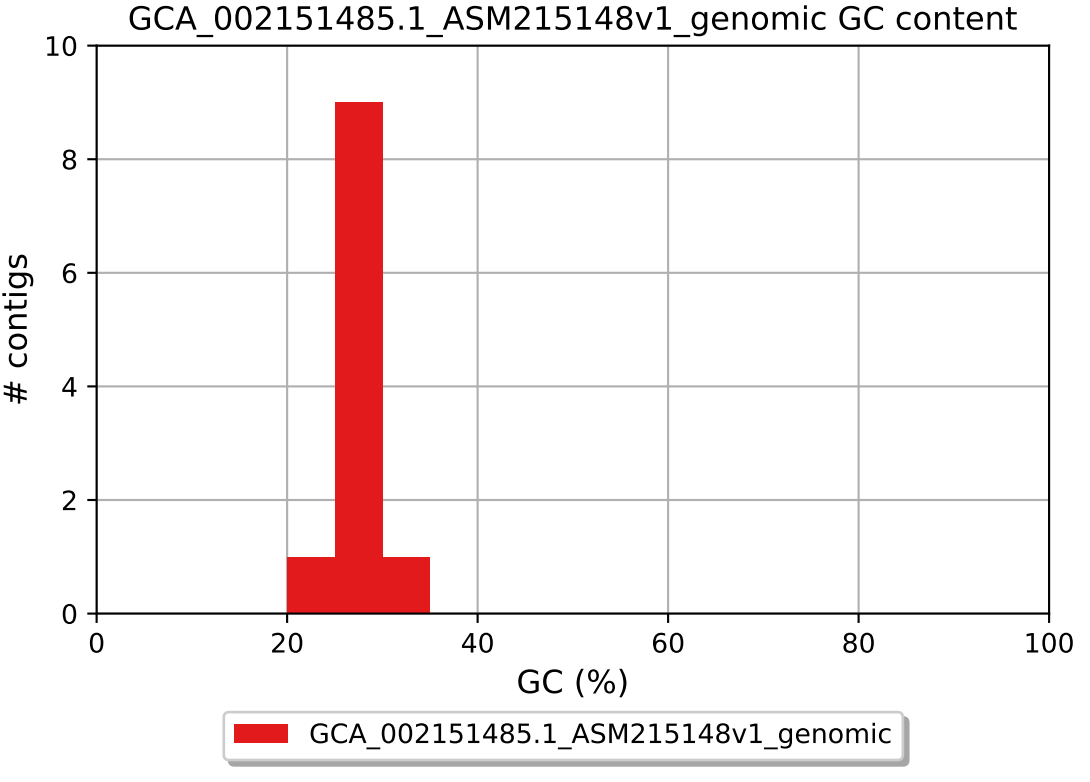
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

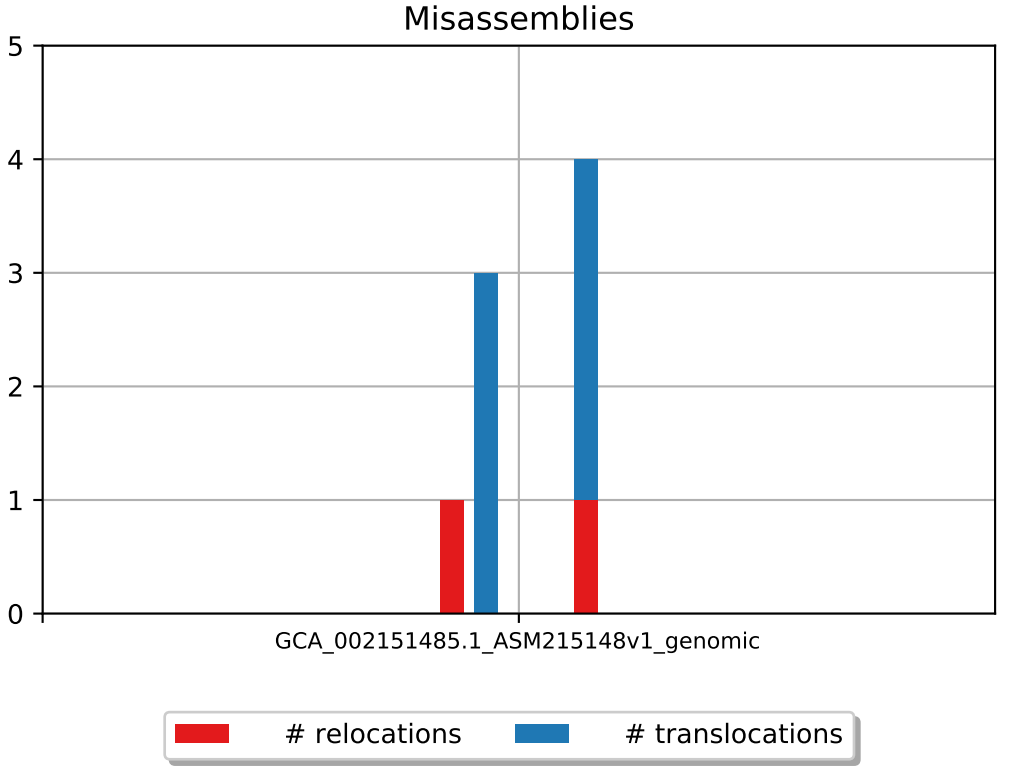

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151485.1_ASM215148v1_genomic

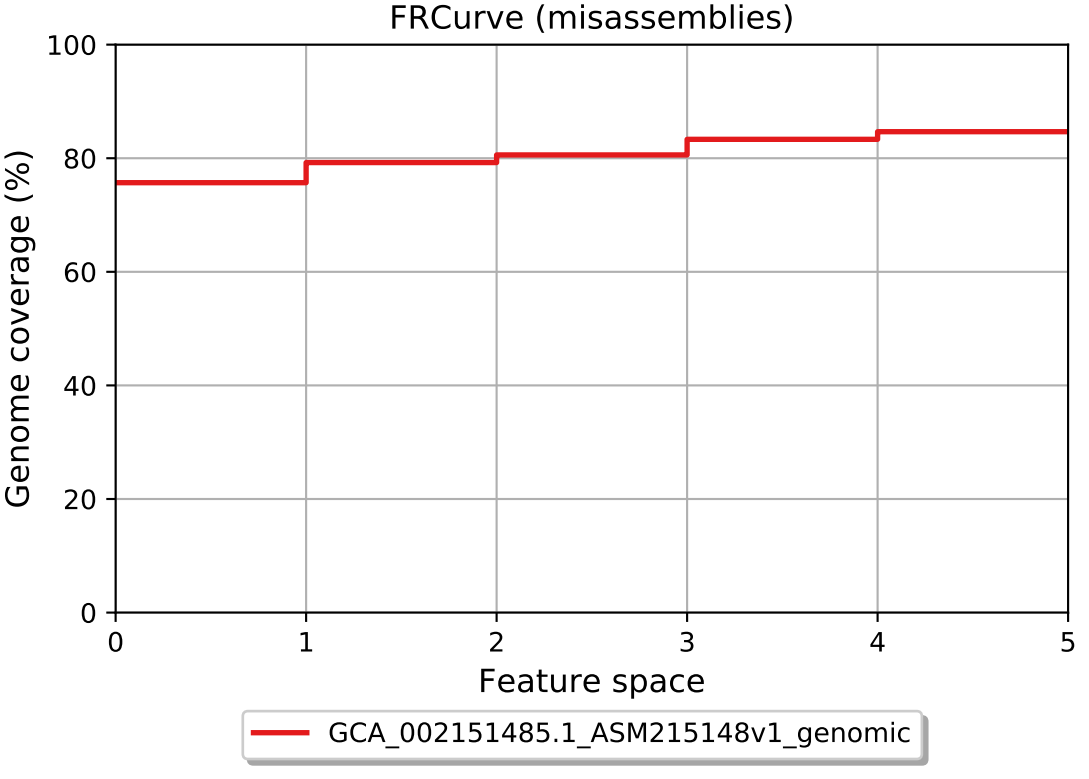

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151485.1_ASM215148v1_genomic

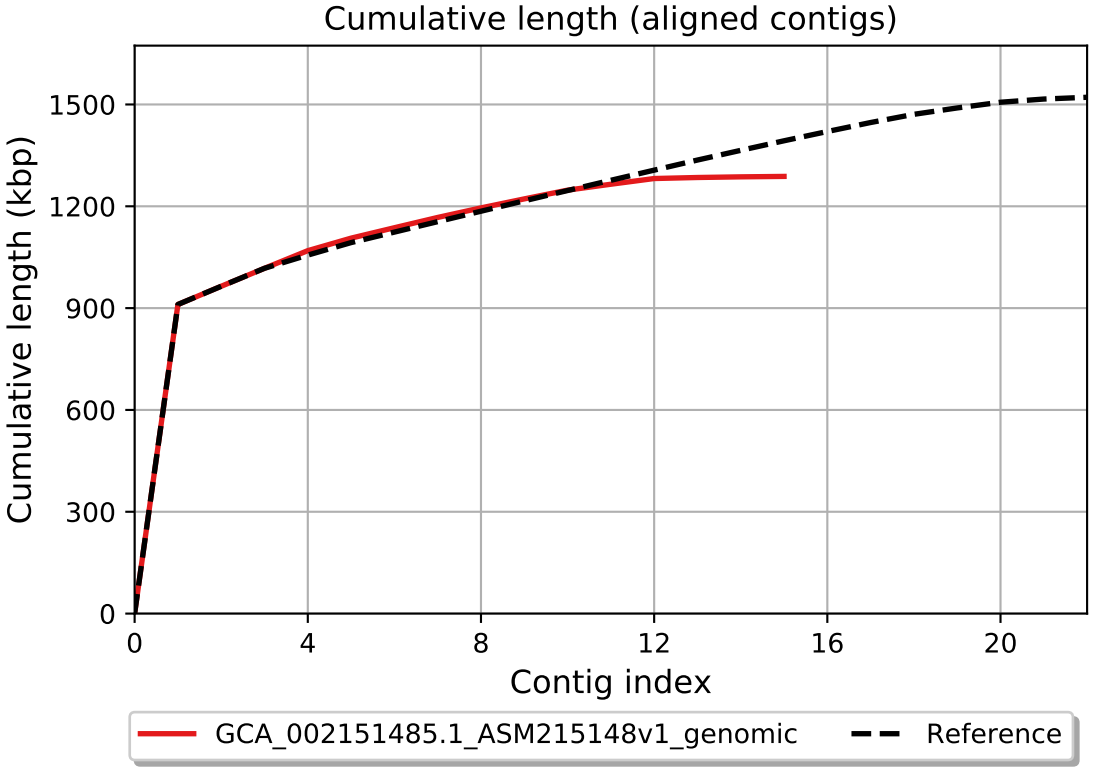

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_002151485.1_ASM215148v1_genomic
Reference

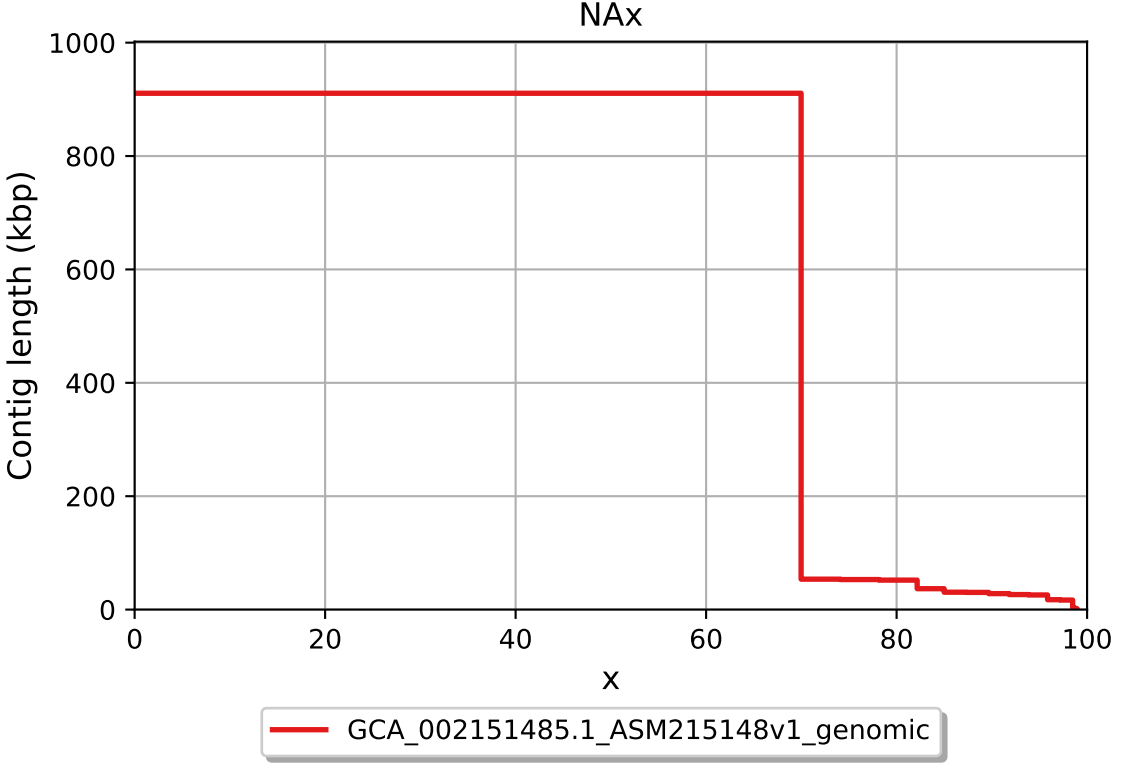

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCA_002151485.1_ASM215148v1_genomic
Reference

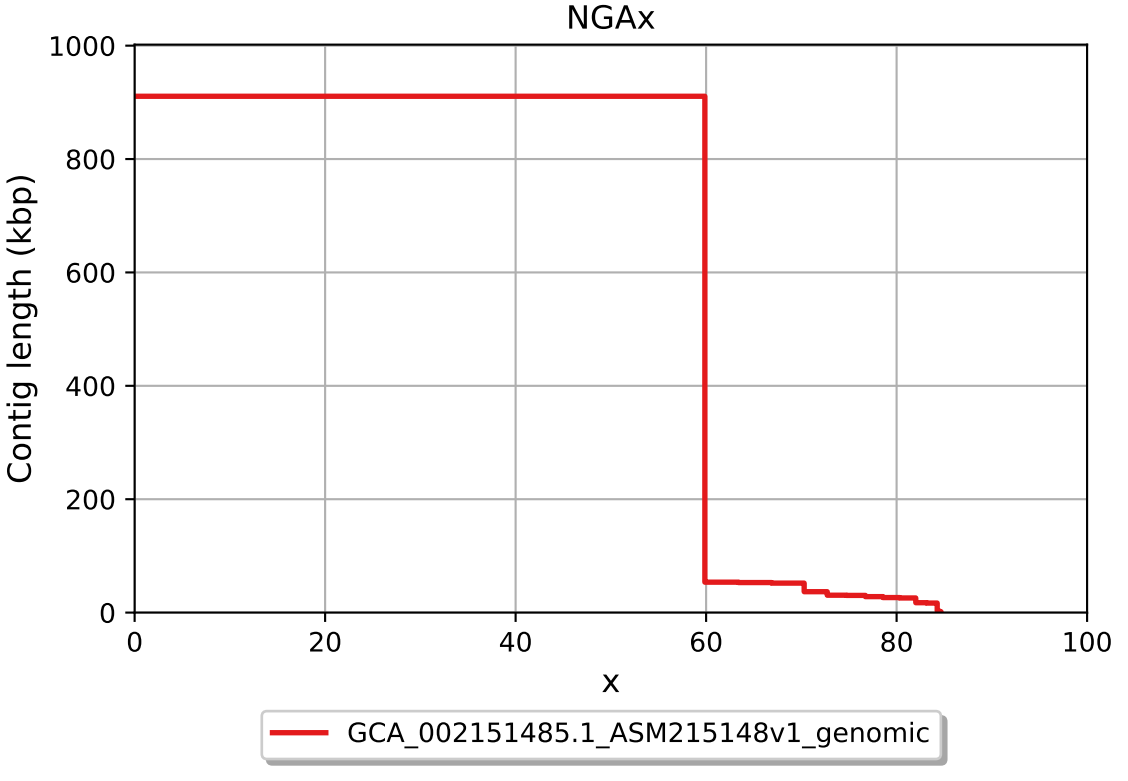

GCA_002151485.1_ASM215148v1_genomic GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
GCA_002151485.1_ASM215148v1_genomic

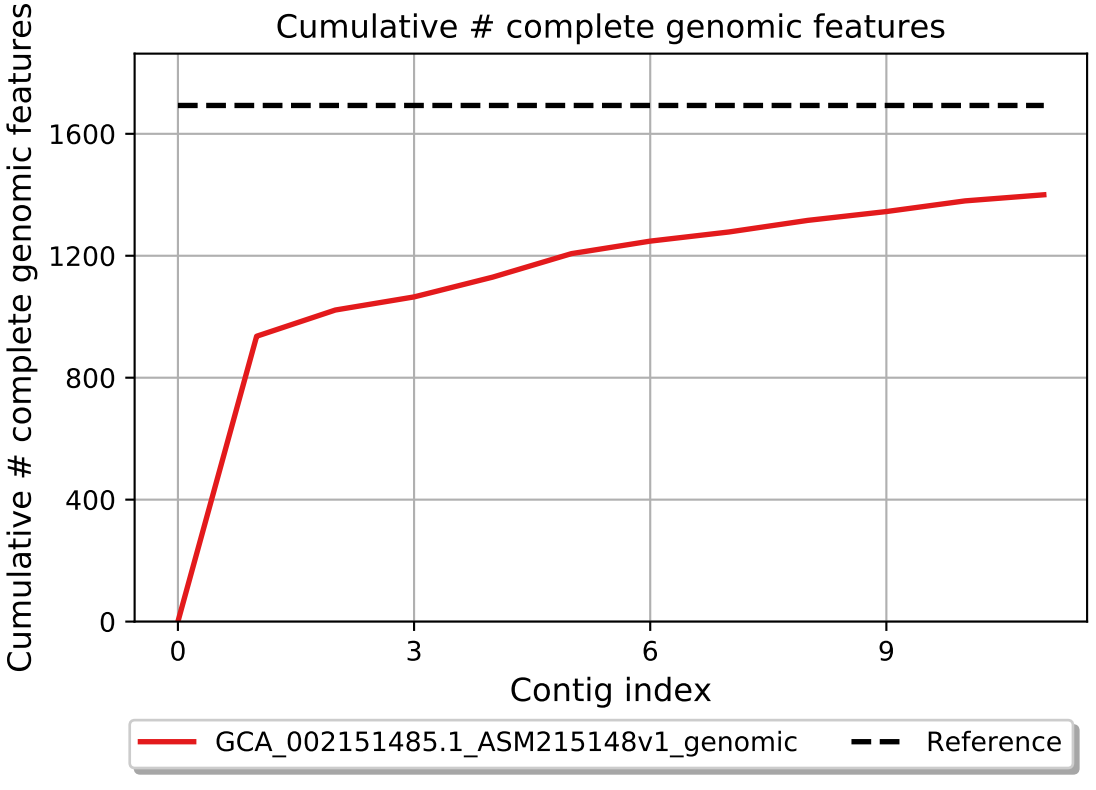

Misassemblies
5
4
3
2
1
0
GCA_002151485.1_ASM215148v1_genomic
relocations
translocations

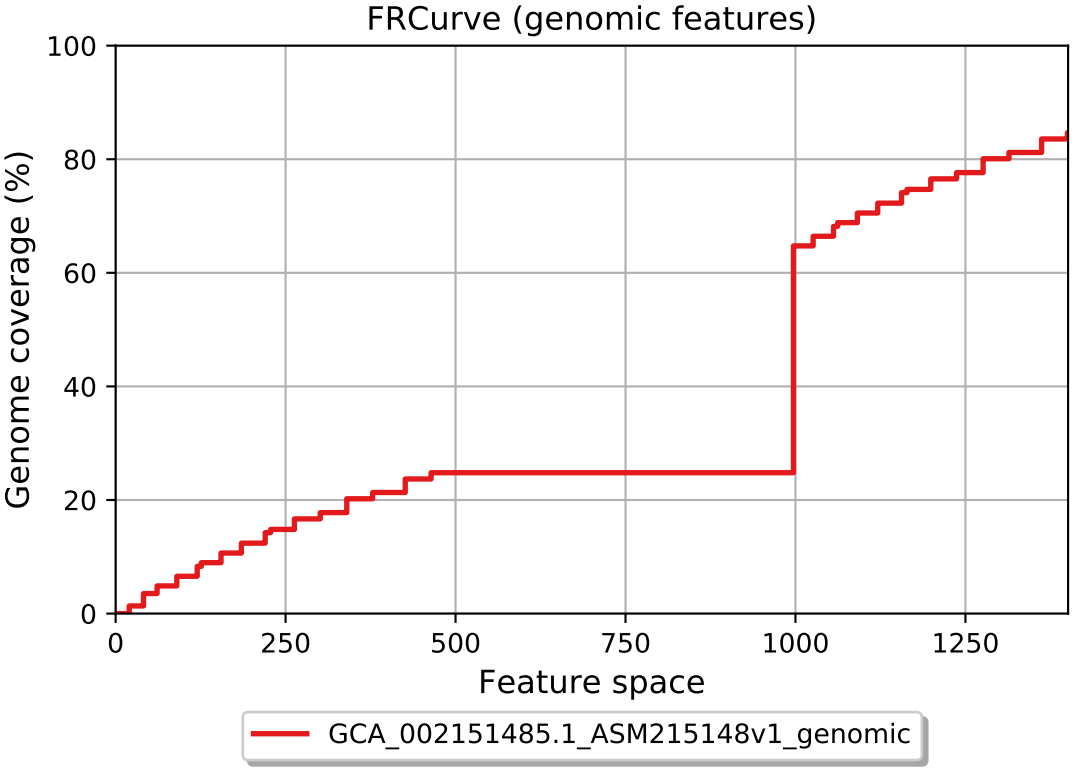

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
Feature space
GCA_002151485.1_ASM215148v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_002151485.1_ASM215148v1_genomic
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151485.1_ASM215148v1_genomic


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151485.1_ASM215148v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
3
6
9
Contig index
GCA_002151485.1_ASM215148v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCA_002151485.1_ASM215148v1_genomic