Report

	GCA_002151505.1_ASM215150v1_genomic
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	1341182
Total length (>= 1000 bp)	1341182
Total length (>= 5000 bp)	1341182
Total length (>= 10000 bp)	1341182
Total length (>= 25000 bp)	1302470
Total length (>= 50000 bp)	1077940
# contigs	13
Largest contig	909921
Total length	1341182
Reference length	1521208
GC (%)	28.45
Reference GC (%)	28.18
N50	909921
NG50	909921
N90	30651
NG90	-
auN	630401.3
auNG	555797.0
L50	1
LG50	1
L90	8
LG90	-
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	92663
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	13510
Genome fraction (%)	85.499
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	93.47
# indels per 100 kbp	15.29
# genomic features	1430 + 10 part
Largest alignment	909921
Total aligned length	1327665
NA50	909921
NGA50	909921
NA90	30222
NGA90	-
auNA	628487.5
auNGA	554109.7
LA50	1
LGA50	1
LA90	9
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

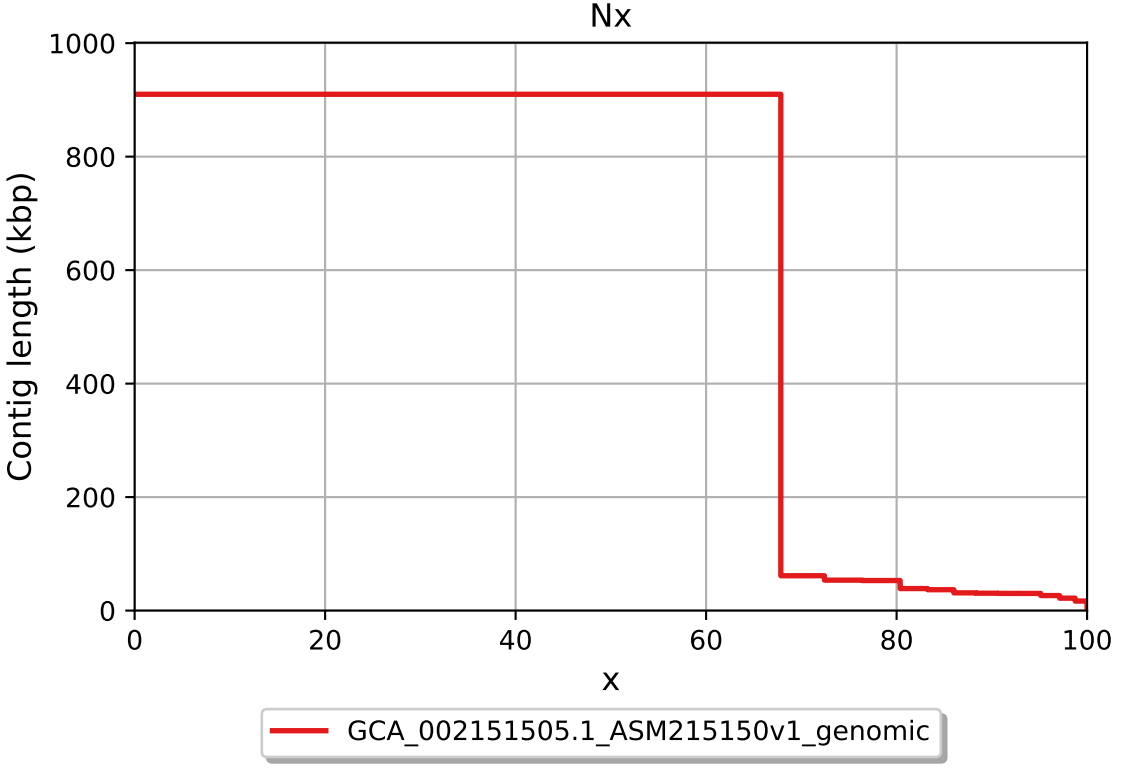
	GCA_002151505.1_ASM215150v1_genomic
# misassemblies	2
# contig misassemblies	2
# c. relocations	1
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	92663
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1241
# indels	203
# indels (<= 5 bp)	173
# indels (> 5 bp)	30
Indels length	1717

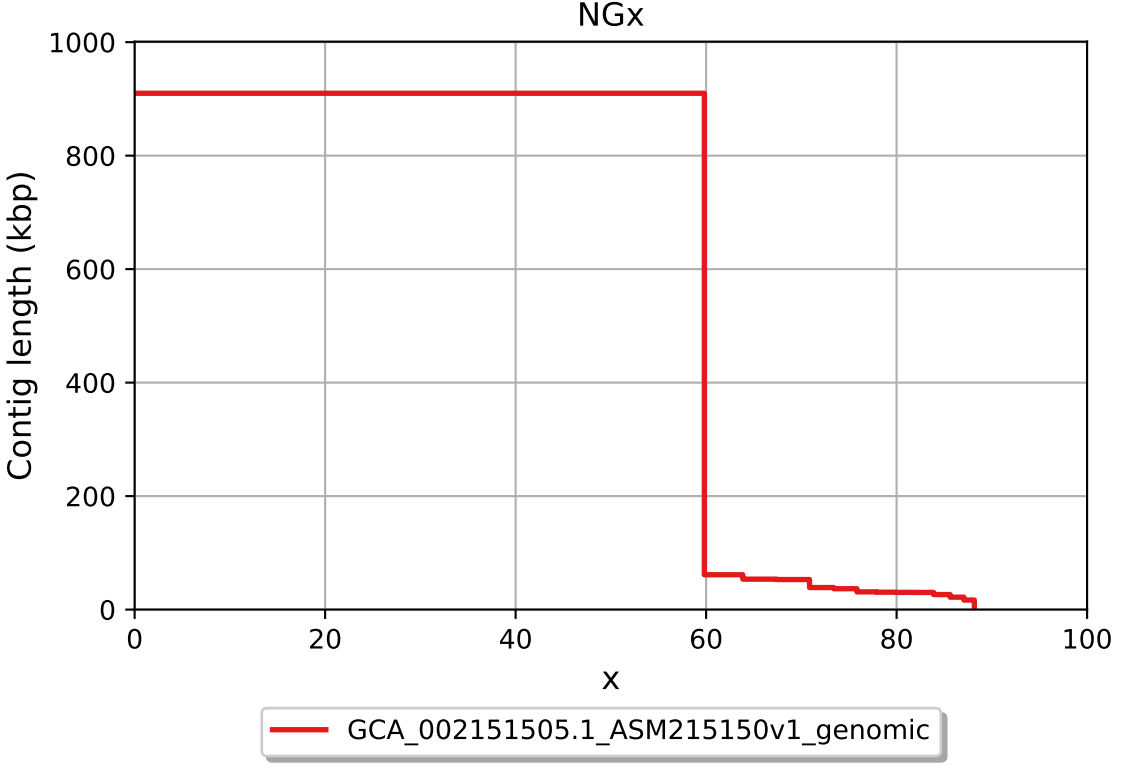
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

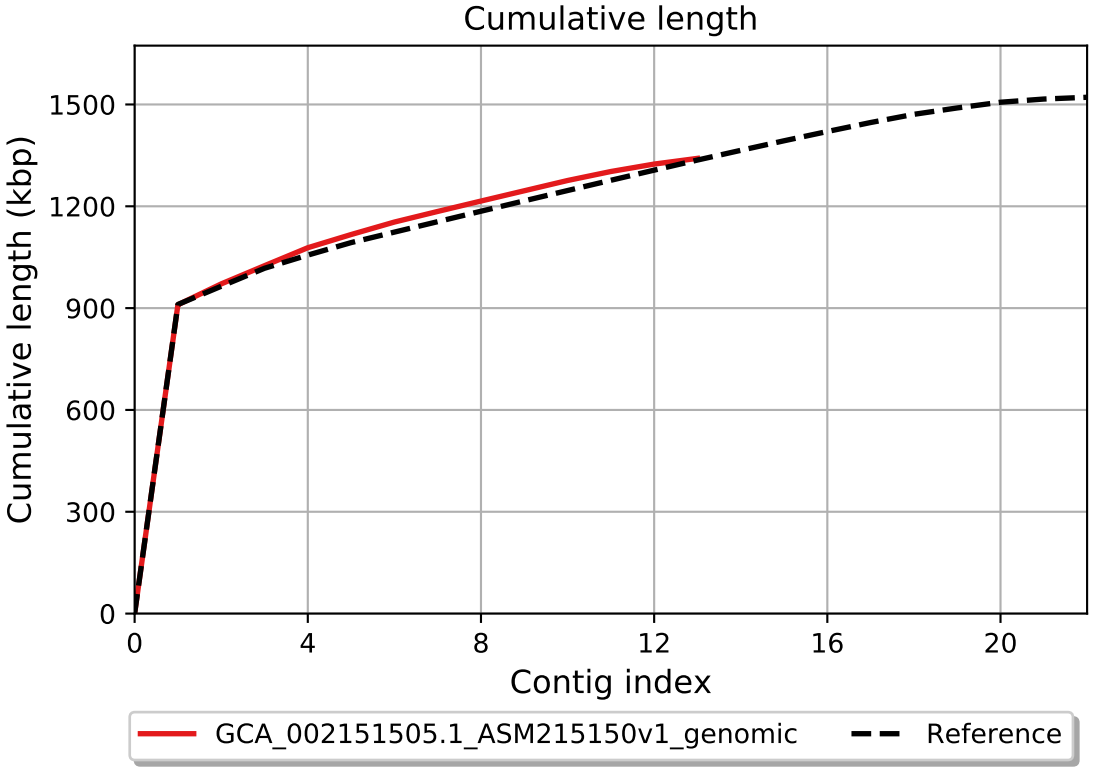
Unaligned report

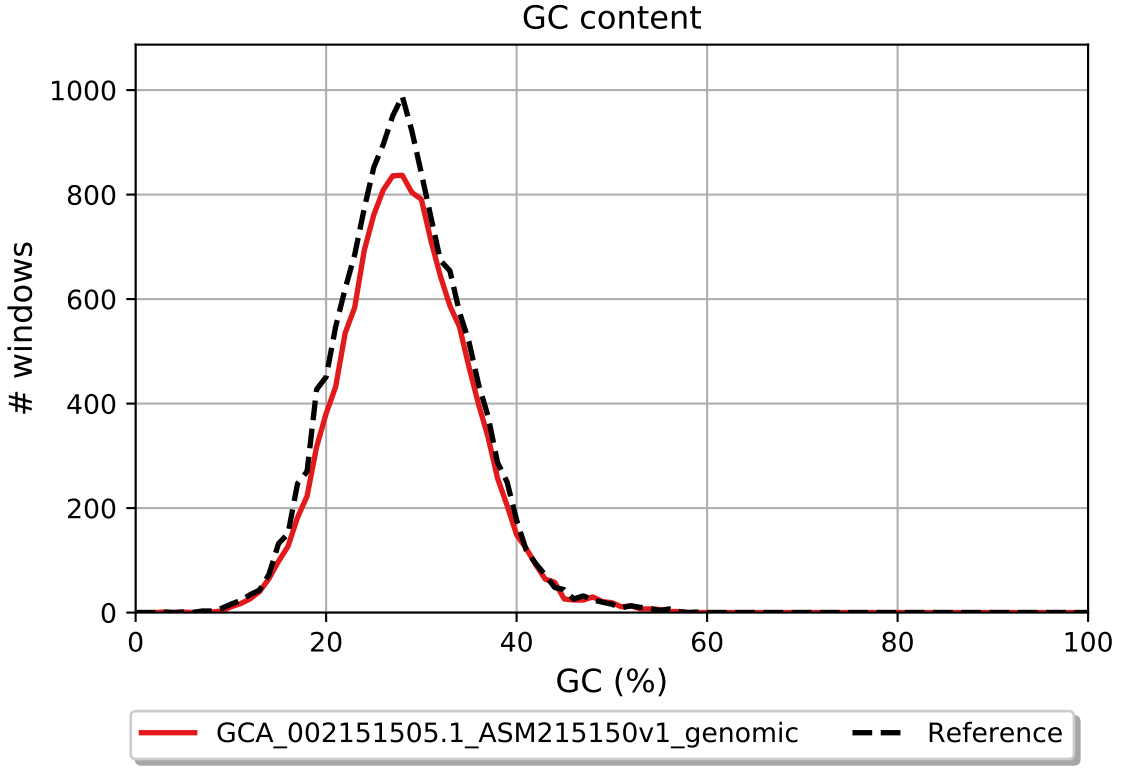
	GCA_002151505.1_ASM215150v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	13510
# N's	0

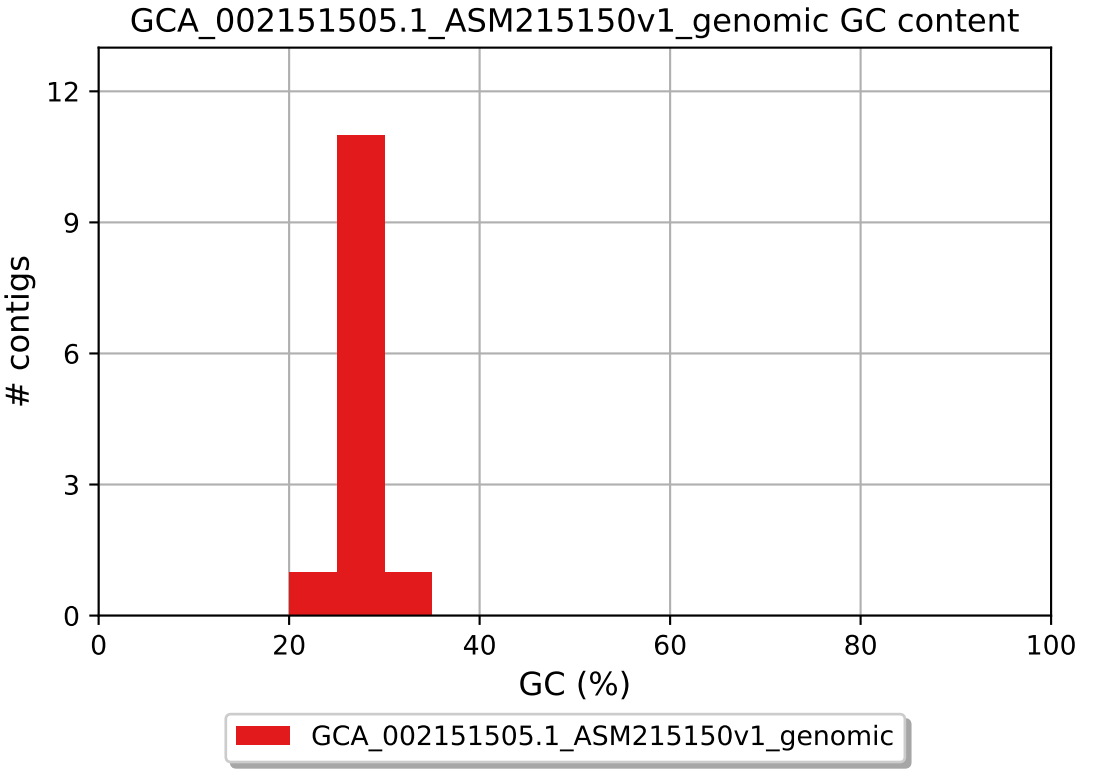
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

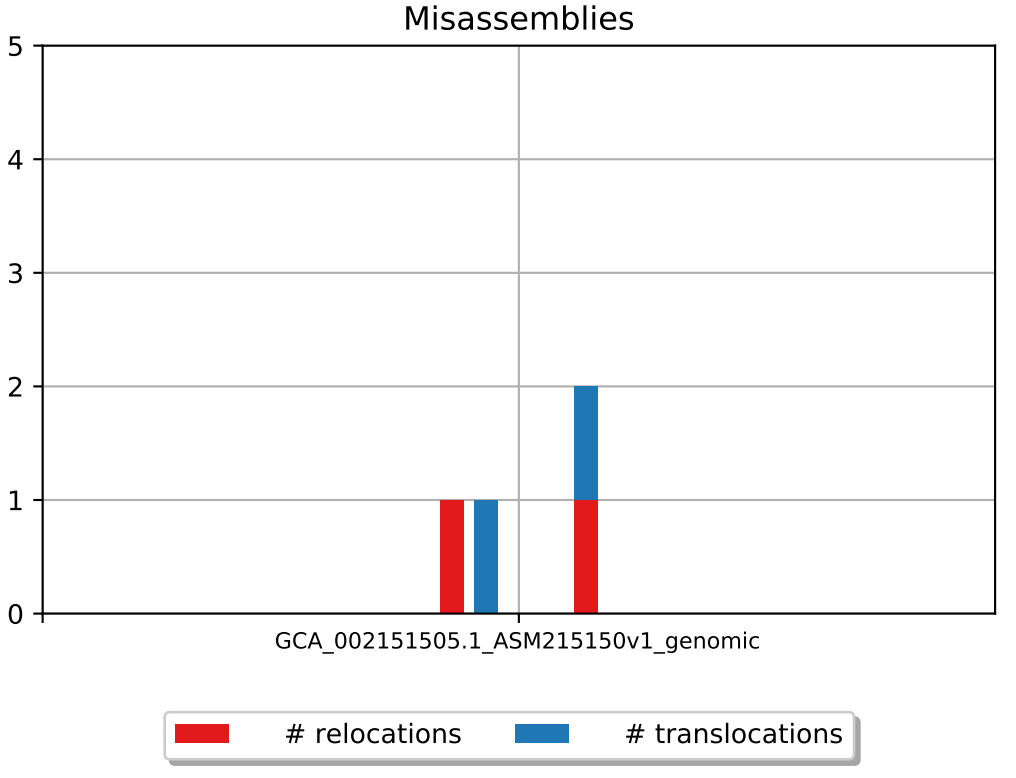

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151505.1_ASM215150v1_genomic

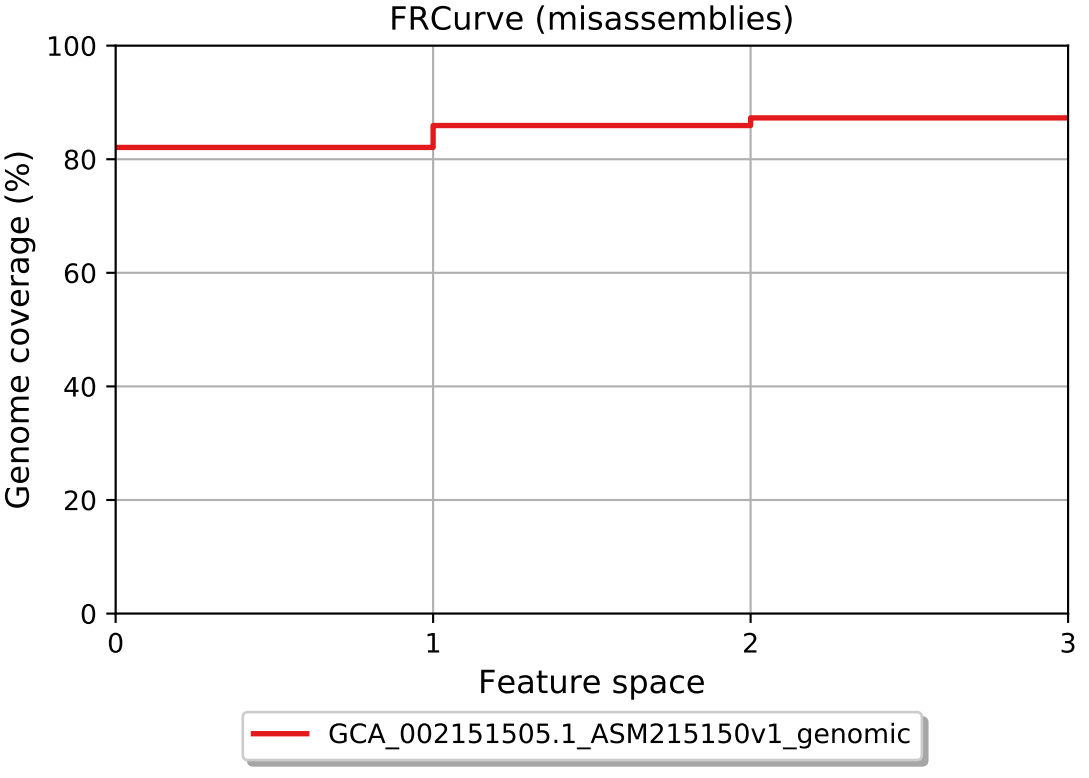

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151505.1_ASM215150v1_genomic

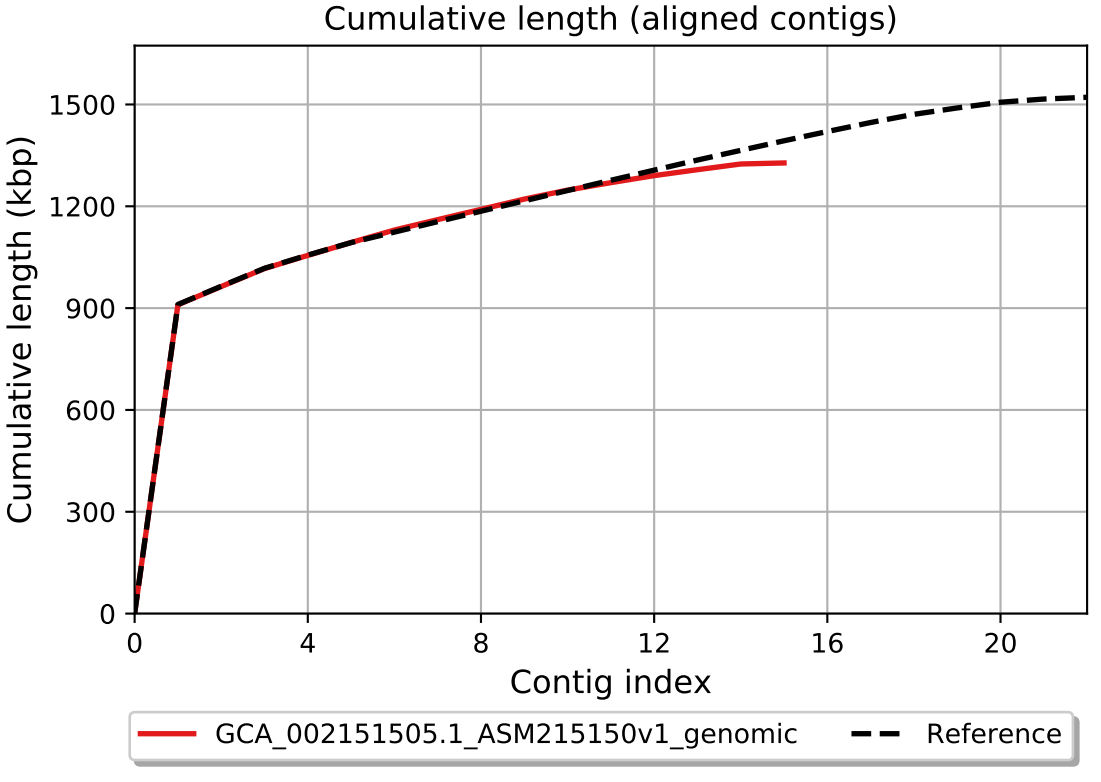

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_002151505.1_ASM215150v1_genomic
Reference

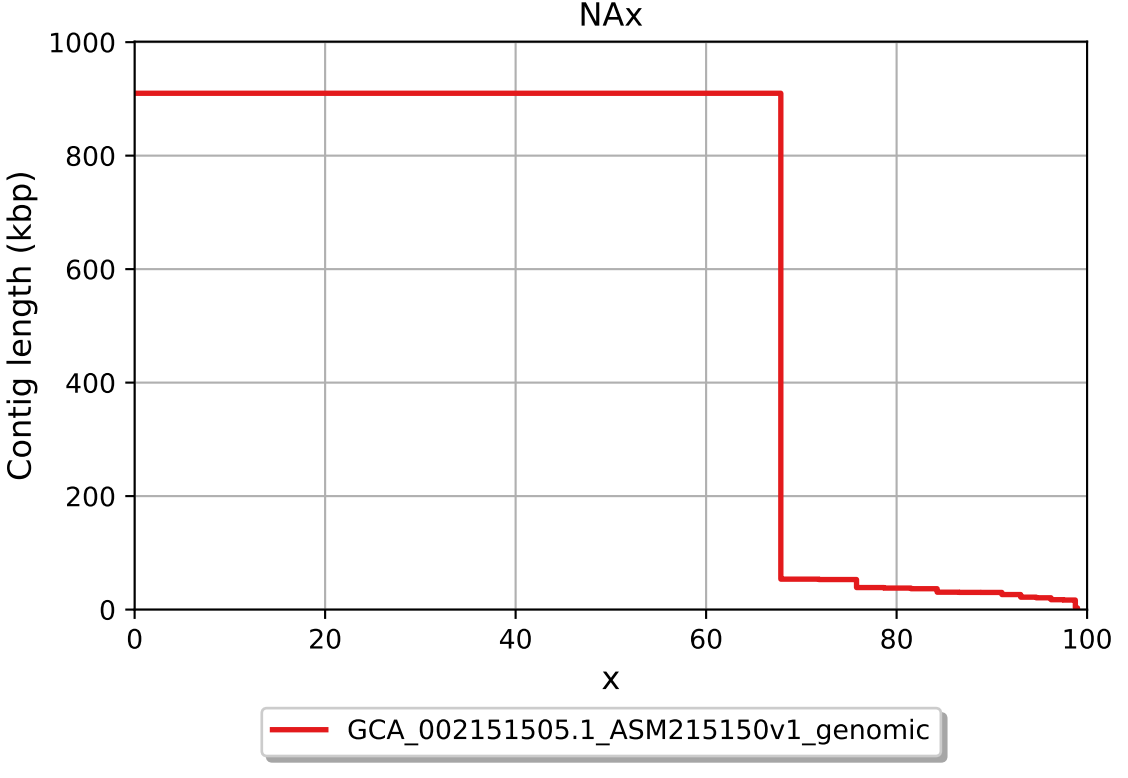

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCA_002151505.1_ASM215150v1_genomic
Reference

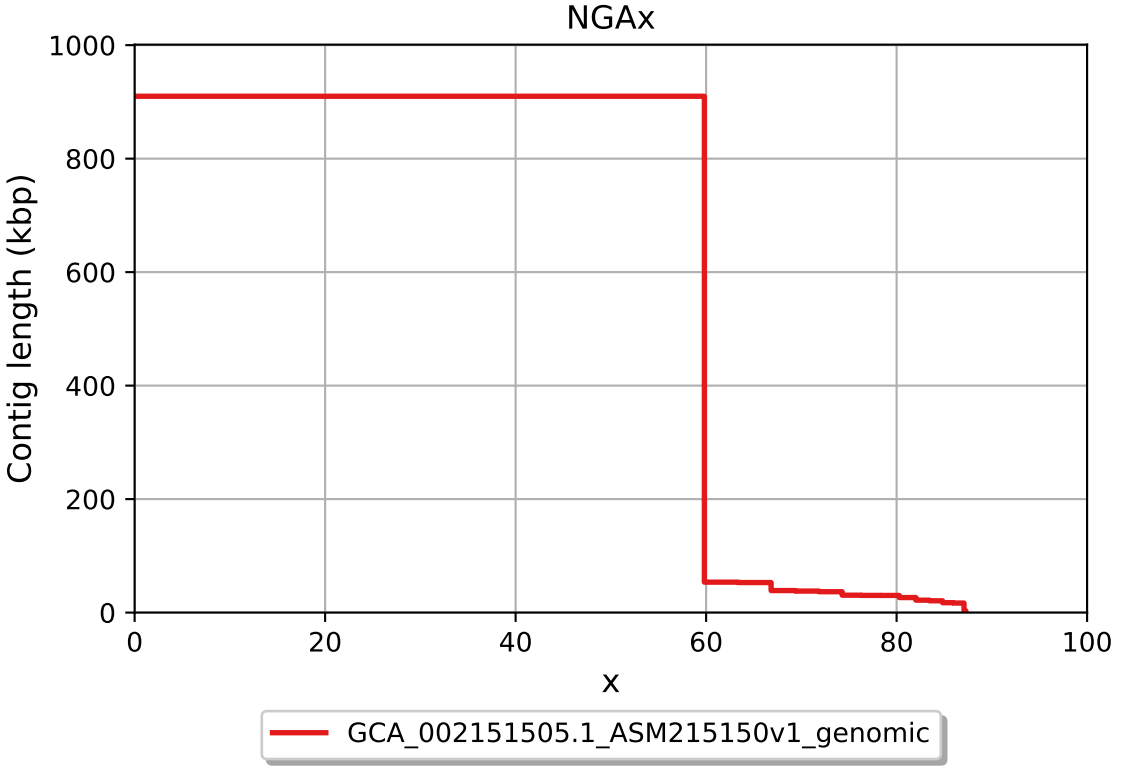

GCA_002151505.1_ASM215150v1_genomic GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
GCA_002151505.1_ASM215150v1_genomic

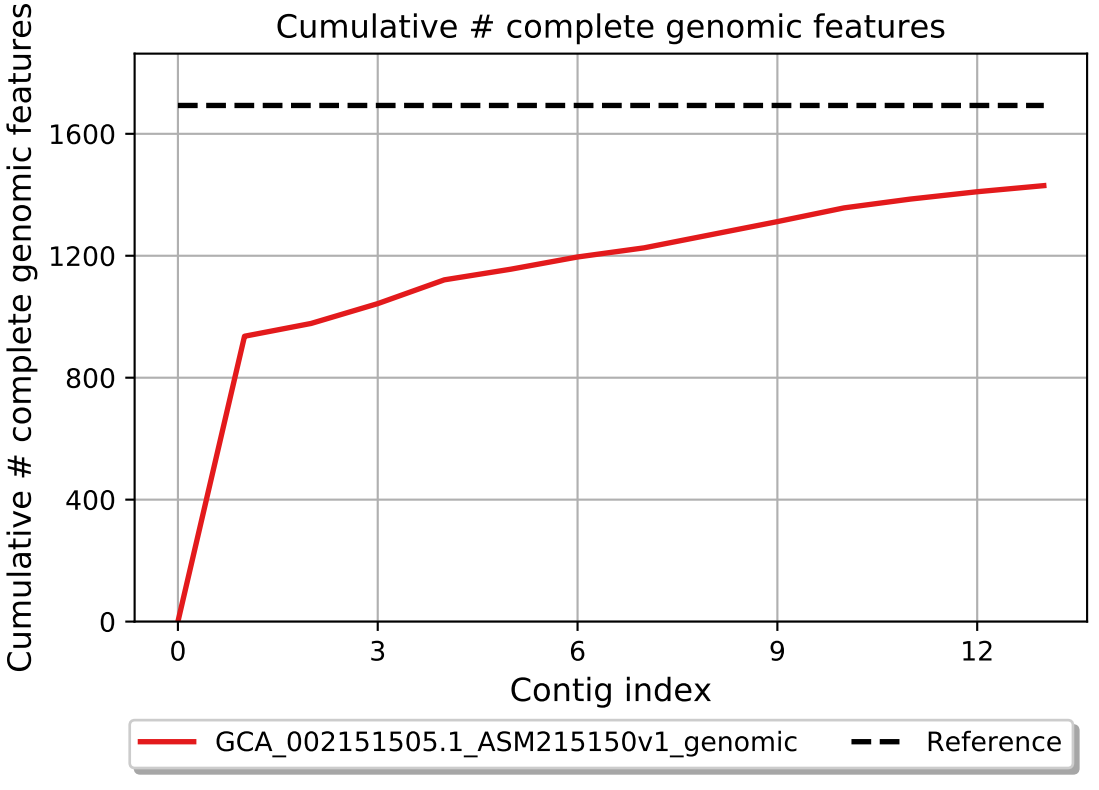

Misassemblies
5
4
3
2
1
0
GCA_002151505.1_ASM215150v1_genomic
relocations
translocations

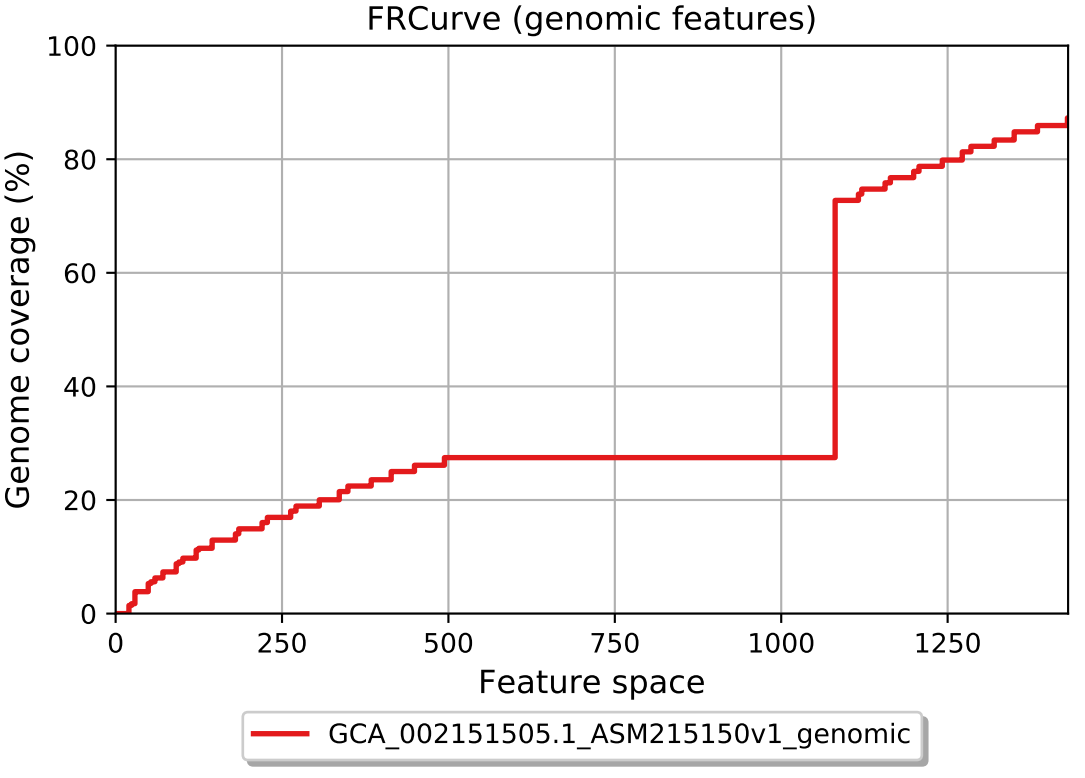

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
Feature space
GCA_002151505.1_ASM215150v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_002151505.1_ASM215150v1_genomic
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151505.1_ASM215150v1_genomic


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_002151505.1_ASM215150v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
3
6
9
12
Contig index
GCA_002151505.1_ASM215150v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCA_002151505.1_ASM215150v1_genomic