Report

	GCA_030440345.1_ASM3044034v1_genomic
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1006065
Total length (>= 1000 bp)	1006065
Total length (>= 5000 bp)	1006065
Total length (>= 10000 bp)	1006065
Total length (>= 25000 bp)	988121
Total length (>= 50000 bp)	961607
# contigs	4
Largest contig	907764
Total length	1006065
Reference length	1521208
GC (%)	28.44
Reference GC (%)	28.18
N50	907764
NG50	907764
N90	907764
NG90	-
auN	822968.2
auNG	544277.7
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	53843
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	8350
Genome fraction (%)	65.394
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	529.06
# indels per 100 kbp	19.61
# genomic features	1032 + 4 part
Largest alignment	904647
Total aligned length	994593
NA50	904647
NGA50	904647
NA90	46521
NGA90	-
auNA	816478.5
auNGA	539985.6
LA50	1
LGA50	1
LA90	2
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

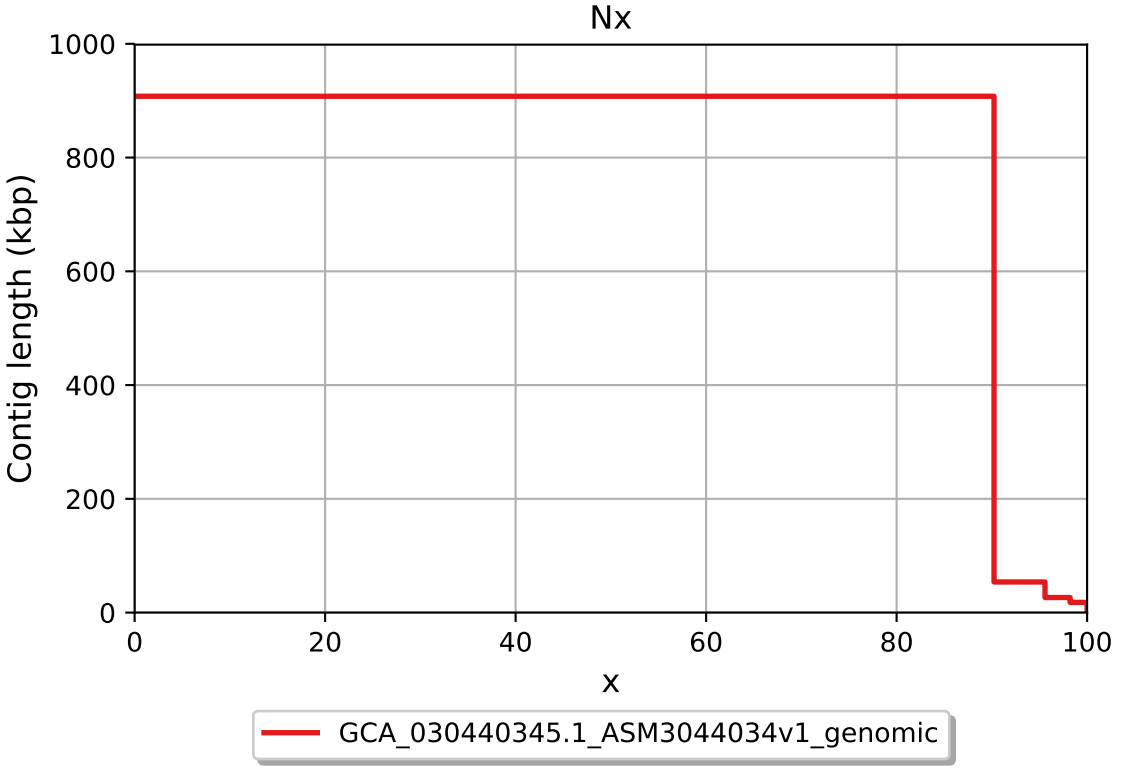
	GCA_030440345.1_ASM3044034v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	53843
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	5262
# indels	195
# indels (<= 5 bp)	169
# indels (> 5 bp)	26
Indels length	1116

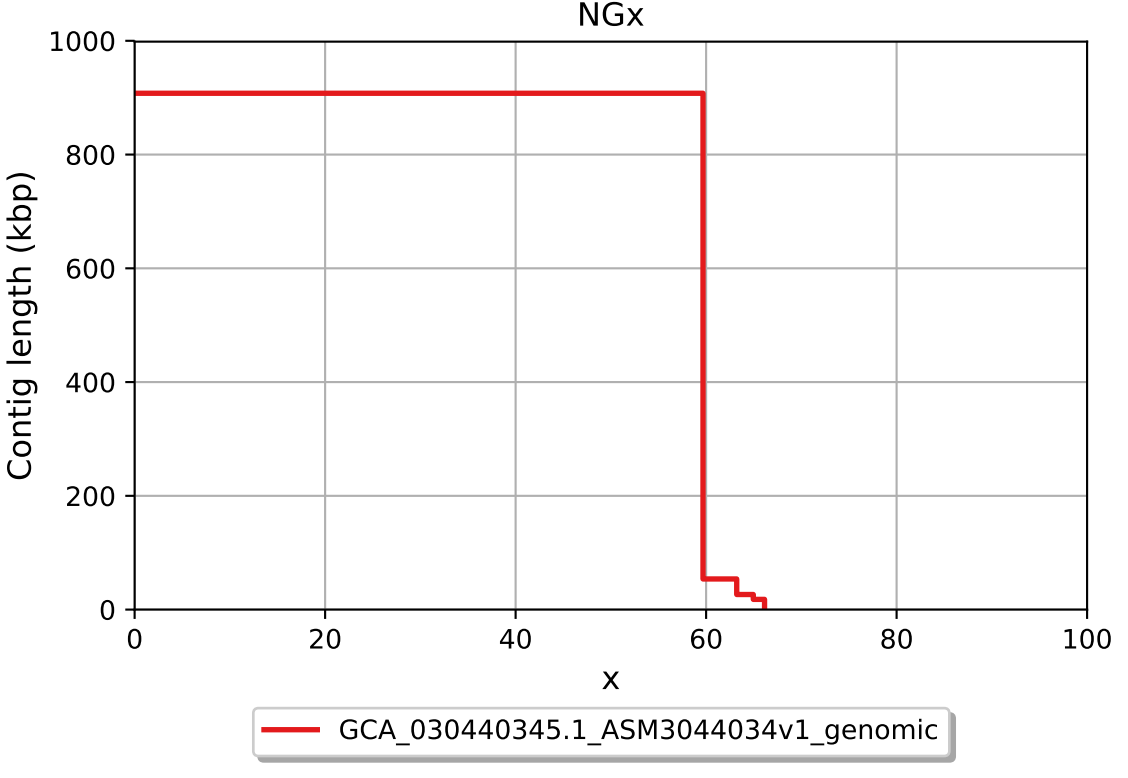
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

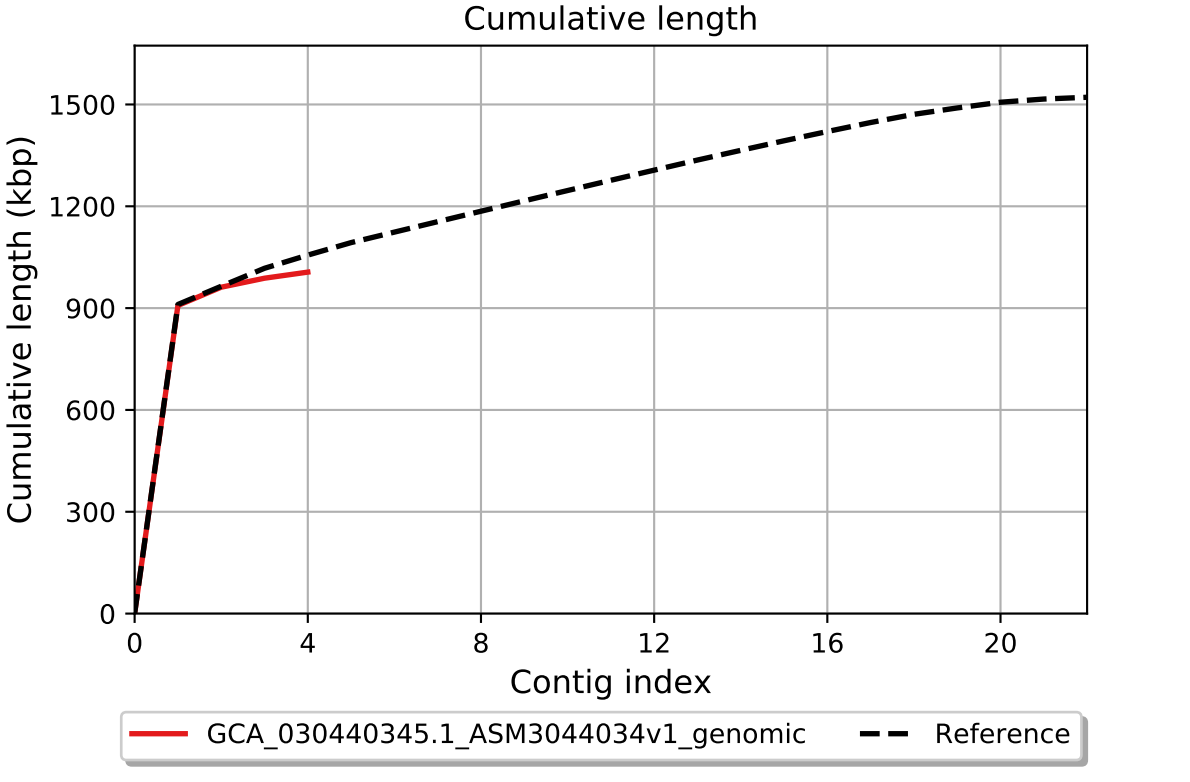
Unaligned report

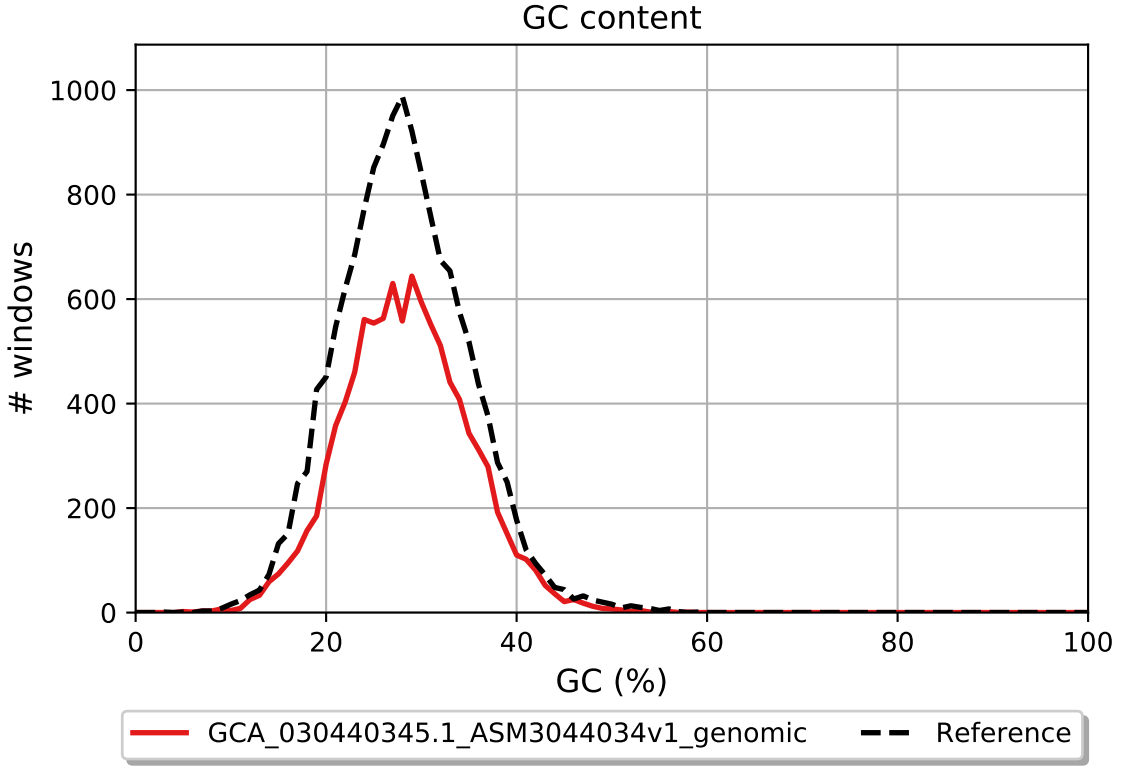
	GCA_030440345.1_ASM3044034v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	8350
# N's	0

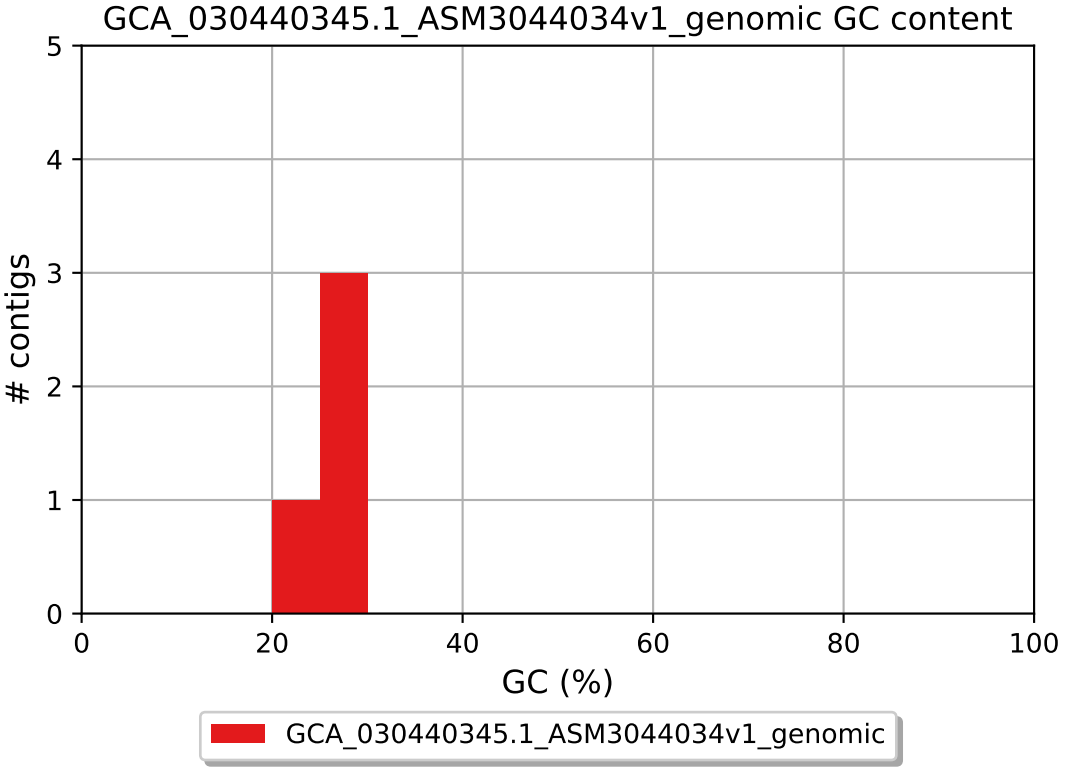
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

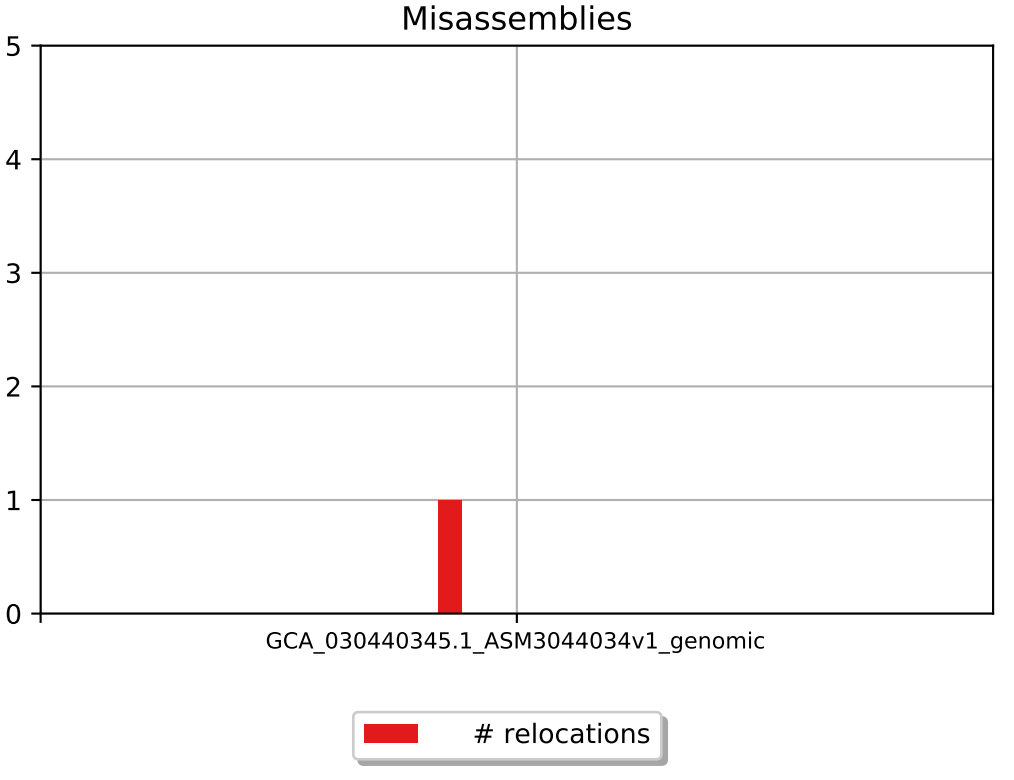

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030440345.1_ASM3044034v1_genomic

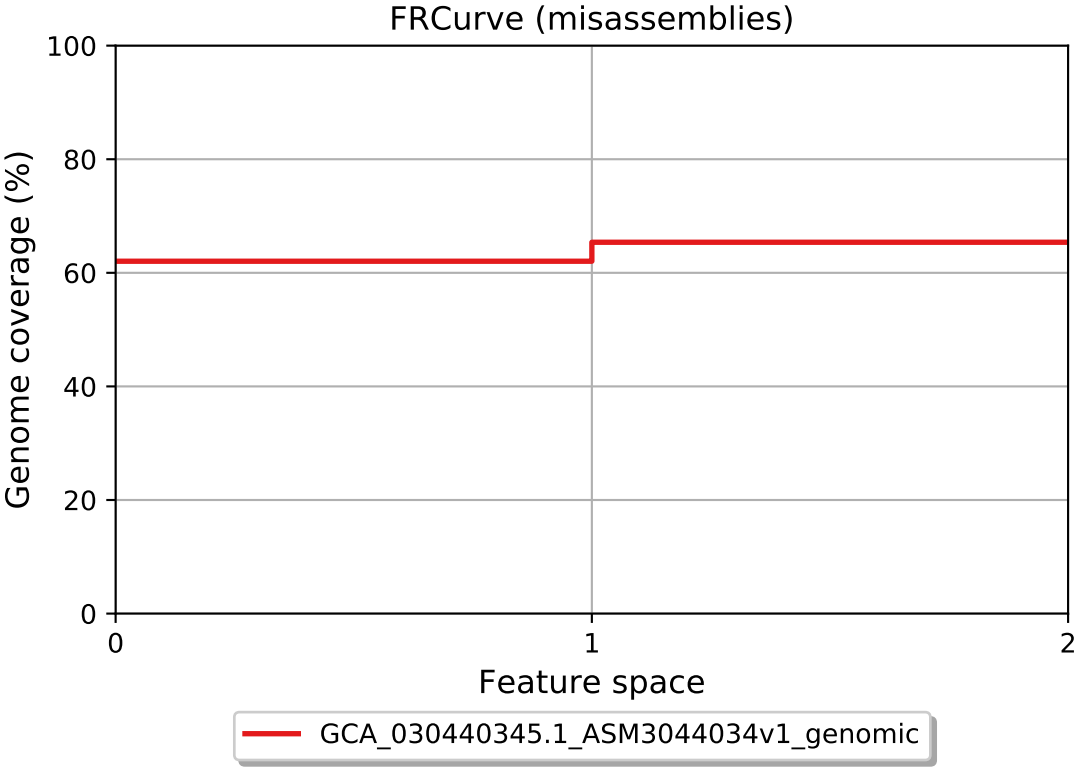

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030440345.1_ASM3044034v1_genomic

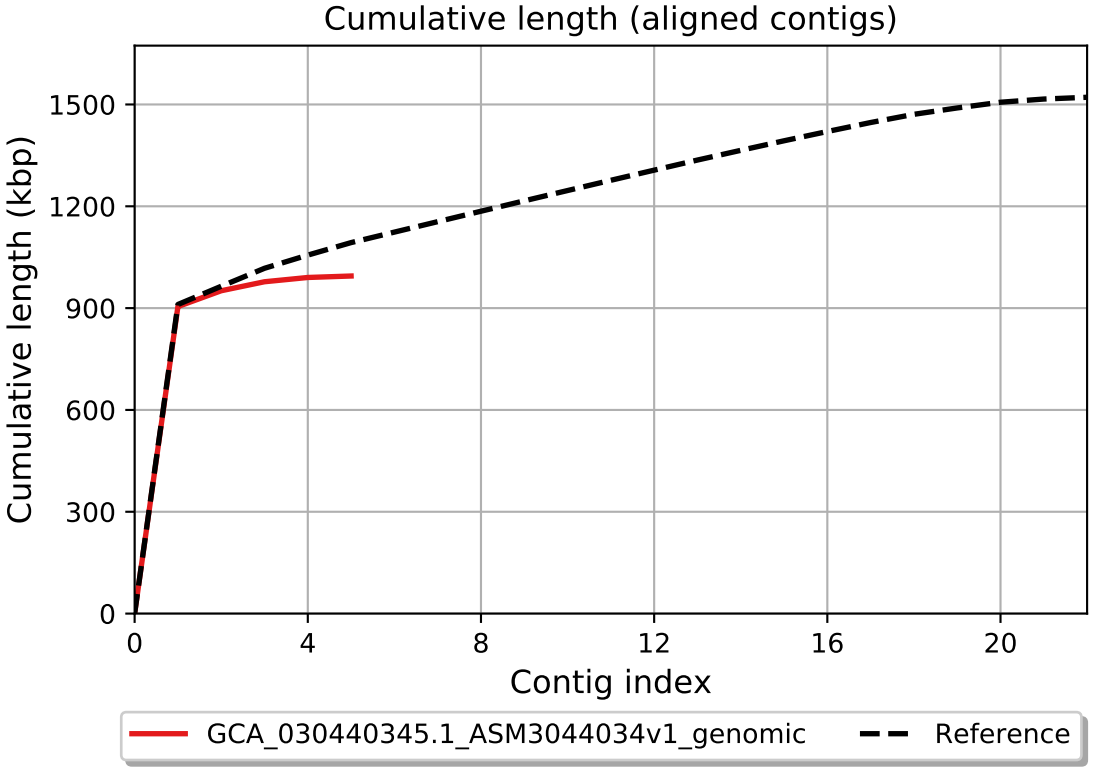

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_030440345.1_ASM3044034v1_genomic
Reference

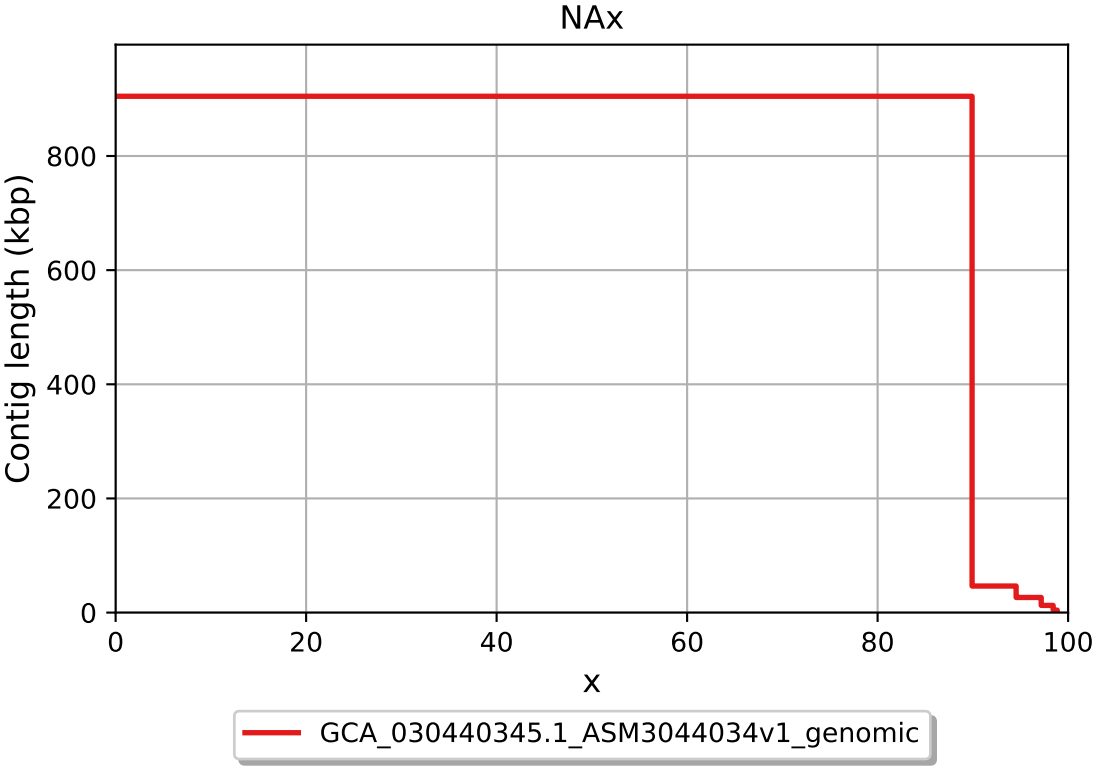

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCA_030440345.1_ASM3044034v1_genomic
Reference

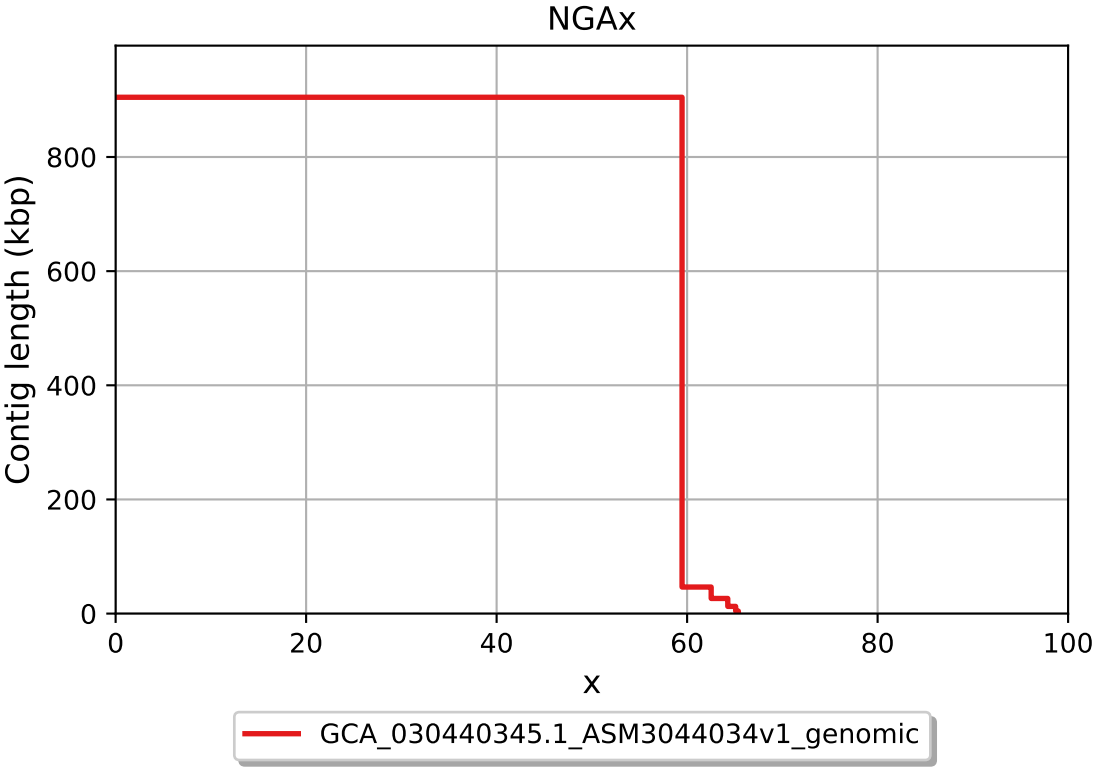

GCA_030440345.1_ASM3044034v1_genomic GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
GCA_030440345.1_ASM3044034v1_genomic

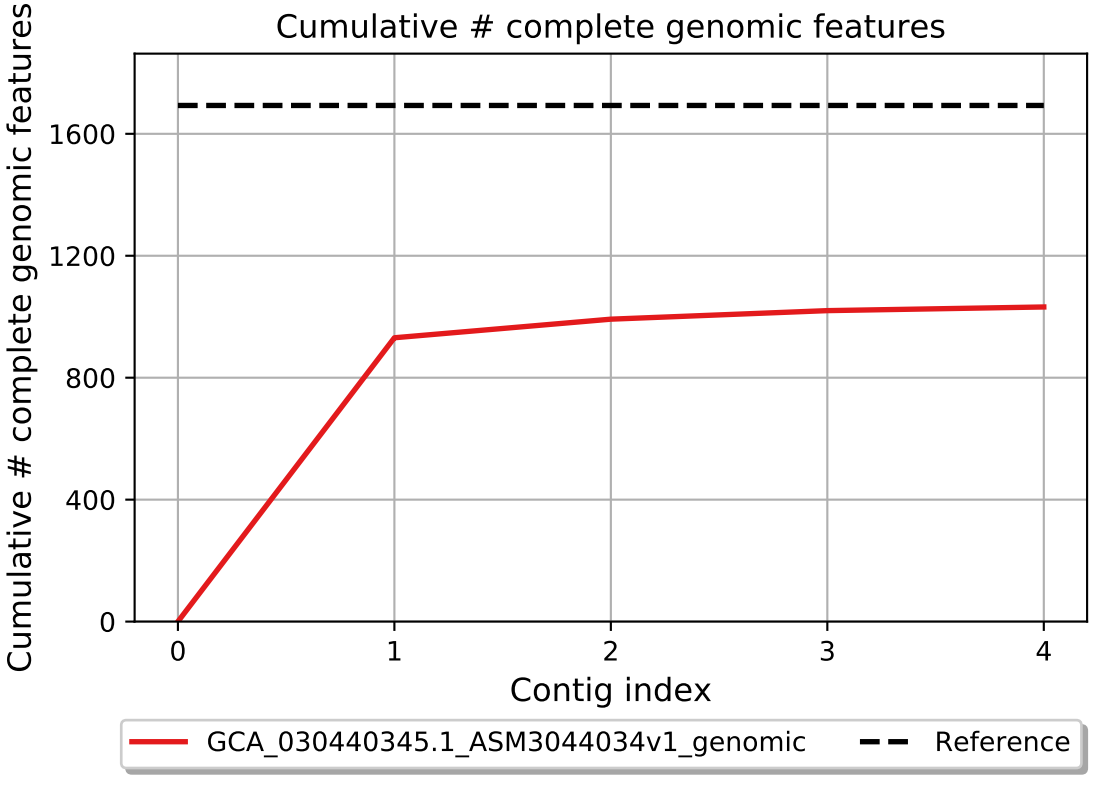

Misassemblies
5
4
3
2
1
0
GCA_030440345.1_ASM3044034v1_genomic
relocations

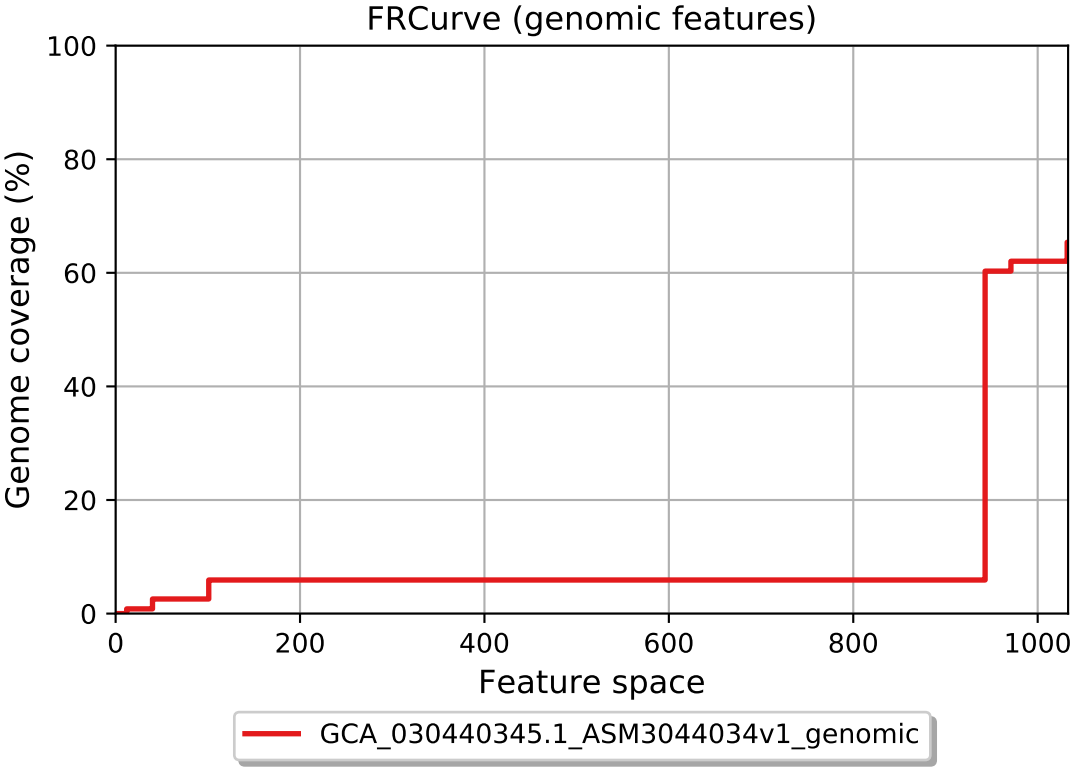

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
GCA_030440345.1_ASM3044034v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_030440345.1_ASM3044034v1_genomic
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030440345.1_ASM3044034v1_genomic


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030440345.1_ASM3044034v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
1
2
3
4
Contig index
GCA_030440345.1_ASM3044034v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Feature space
GCA_030440345.1_ASM3044034v1_genomic