Report

	GCA_030439605.1_ASM3043960v1_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)	1007753
Total length (>= 1000 bp)	1007753
Total length (>= 5000 bp)	1007753
Total length (>= 10000 bp)	1007753
Total length (>= 25000 bp)	990825
Total length (>= 50000 bp)	964327
# contigs	4
Largest contig	910655
Total length	1007753
Reference length	1521208
GC (%)	28.42
Reference GC (%)	28.18
N50	910655
NG50	910655
N90	910655
NG90	-
auN	826752.1
auNG	547697.6
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	66.238
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.28
# indels per 100 kbp	3.37
# genomic features	1049 + 1 part
Largest alignment	910655
Total aligned length	1007623
NA50	910655
NGA50	910655
NA90	910655
NGA90	-
auNA	826746.2
auNGA	547693.7
LA50	1
LGA50	1
LA90	1
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

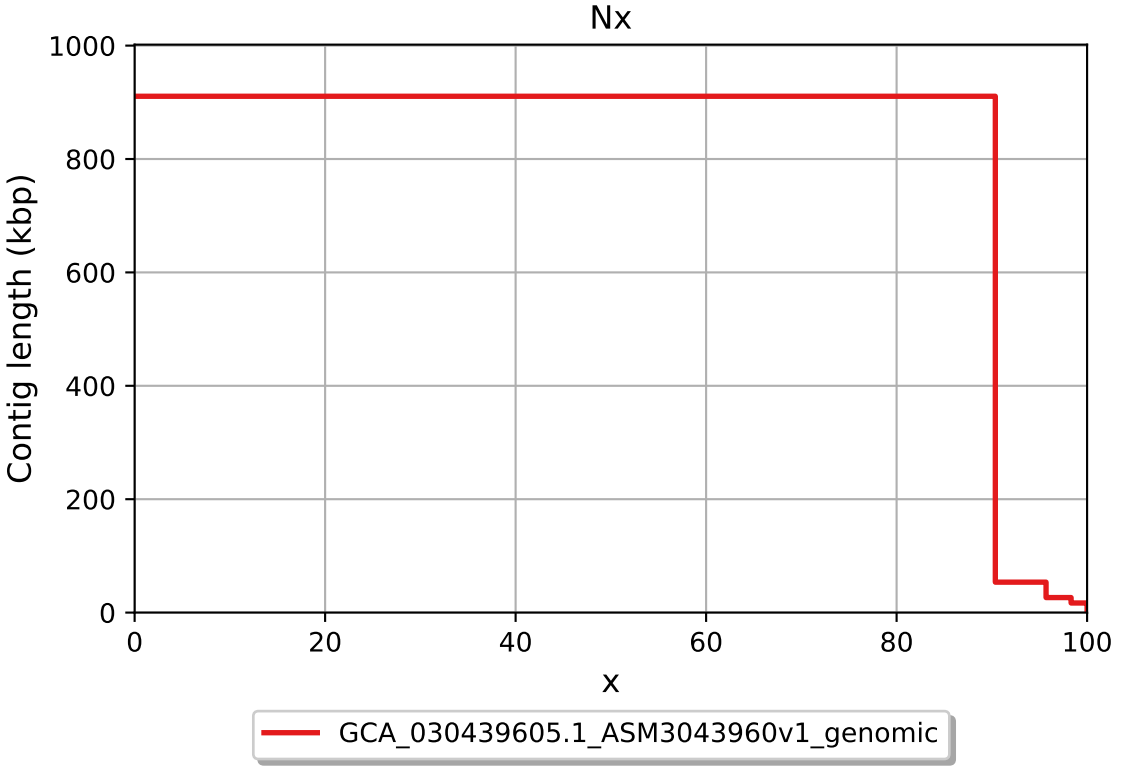
	GCA_030439605.1_ASM3043960v1_genomic
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	33
# indels	34
# indels (<= 5 bp)	32
# indels (> 5 bp)	2
Indels length	47

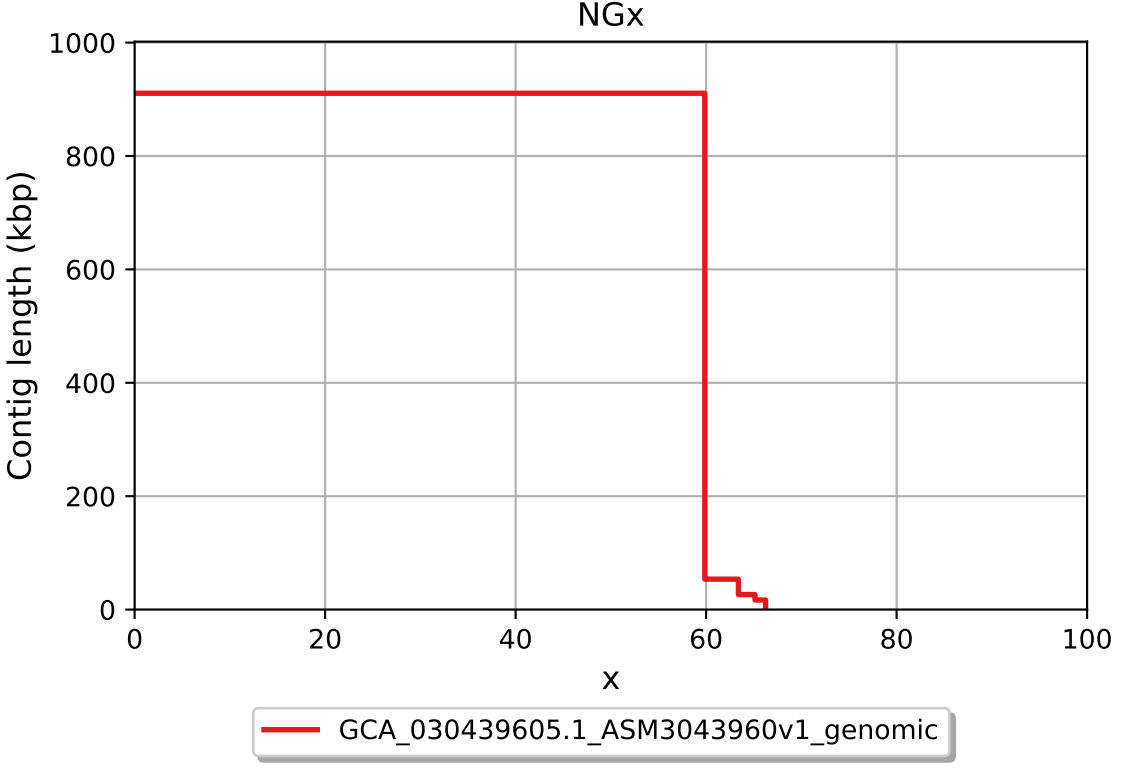
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

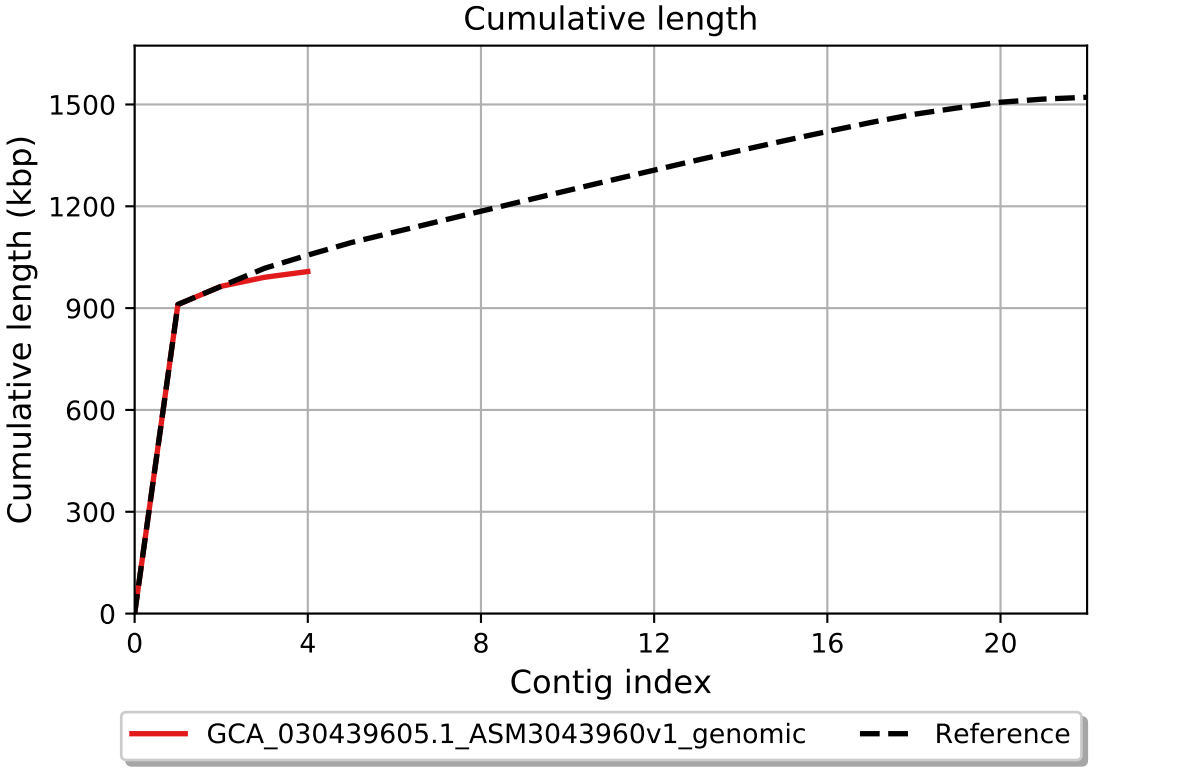
Unaligned report

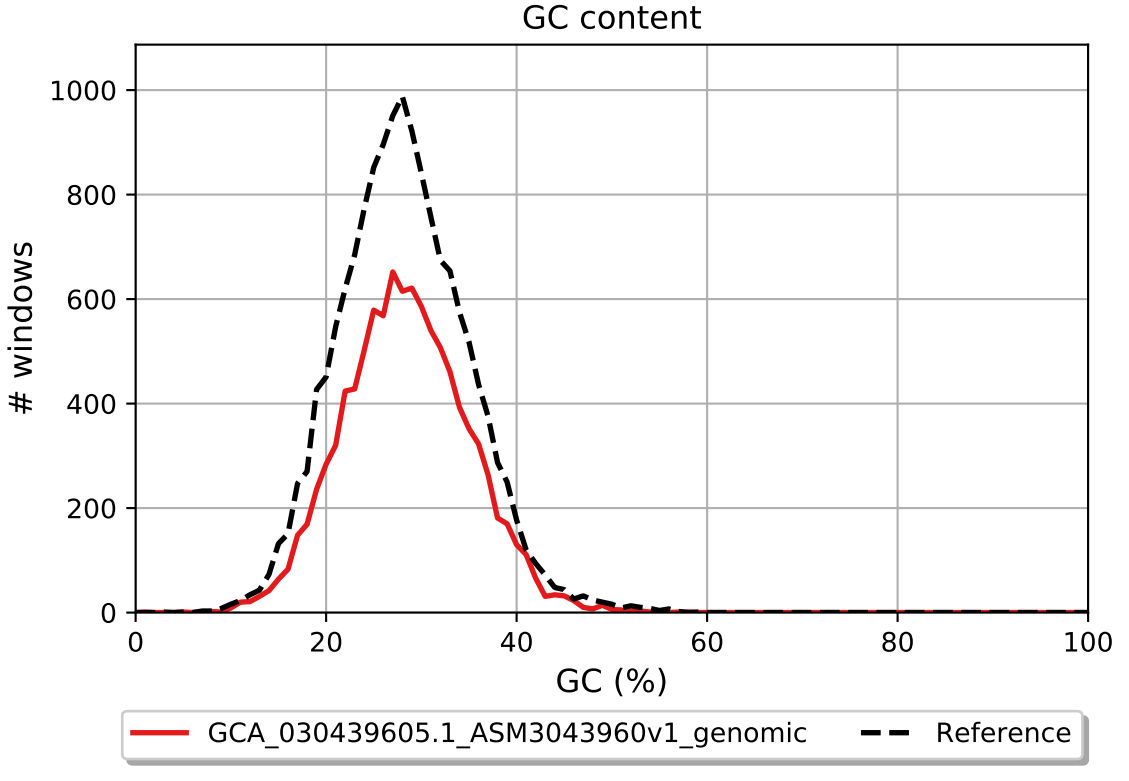
	GCA_030439605.1_ASM3043960v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

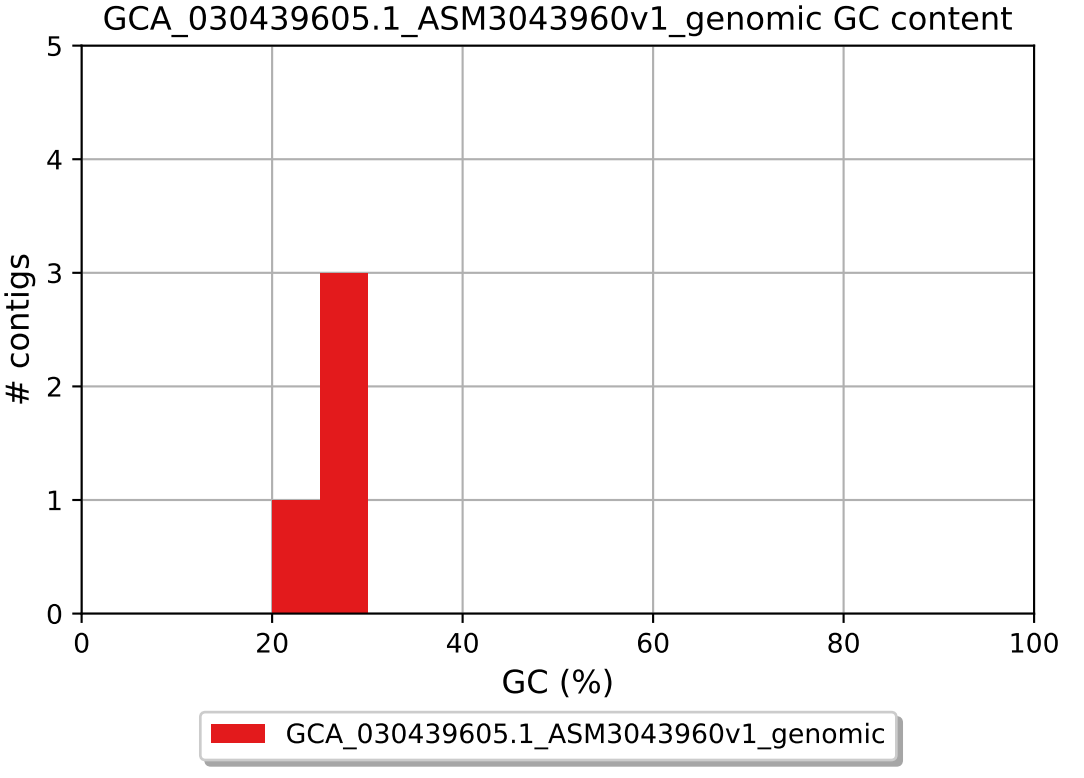
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

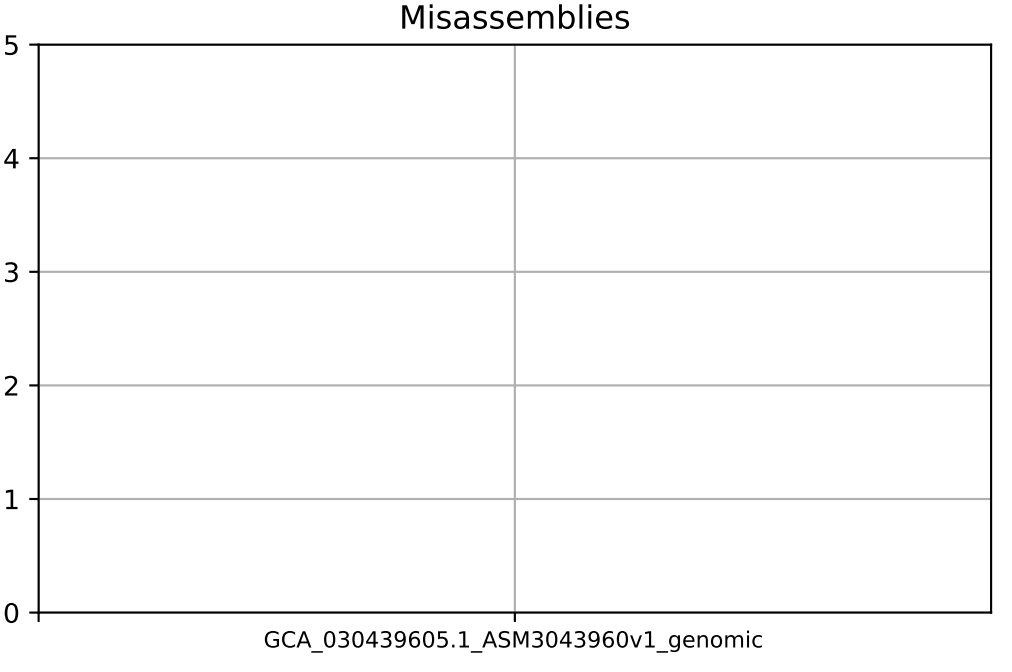

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030439605.1_ASM3043960v1_genomic

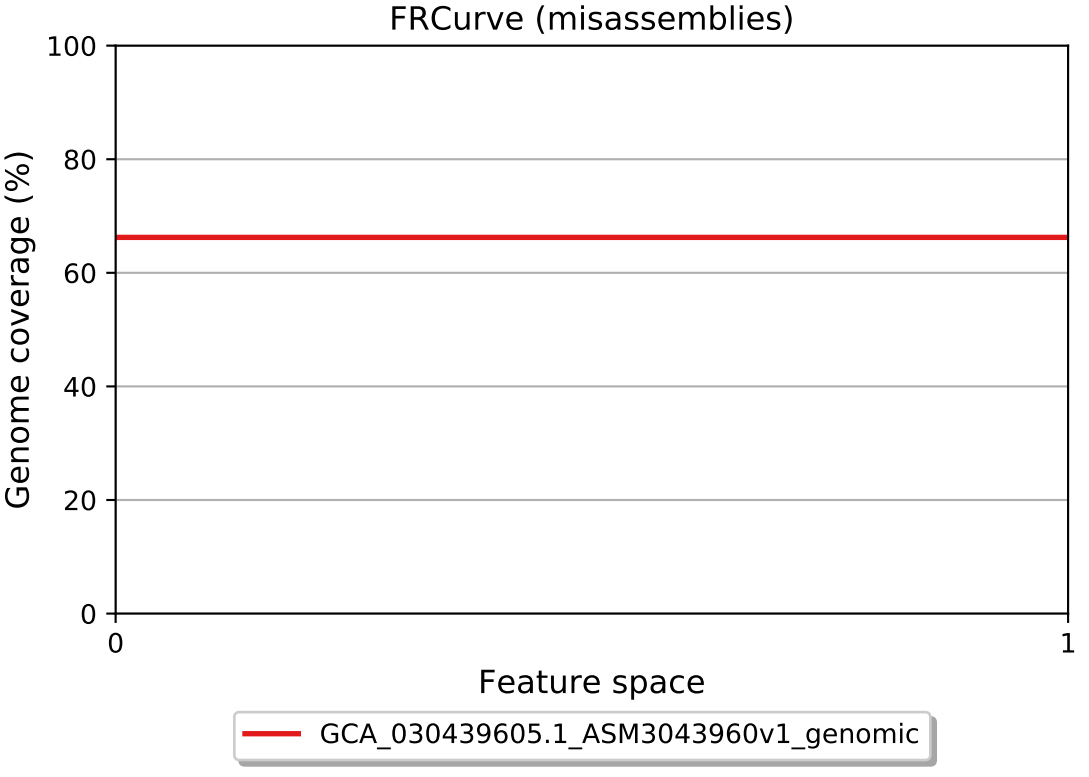

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030439605.1_ASM3043960v1_genomic

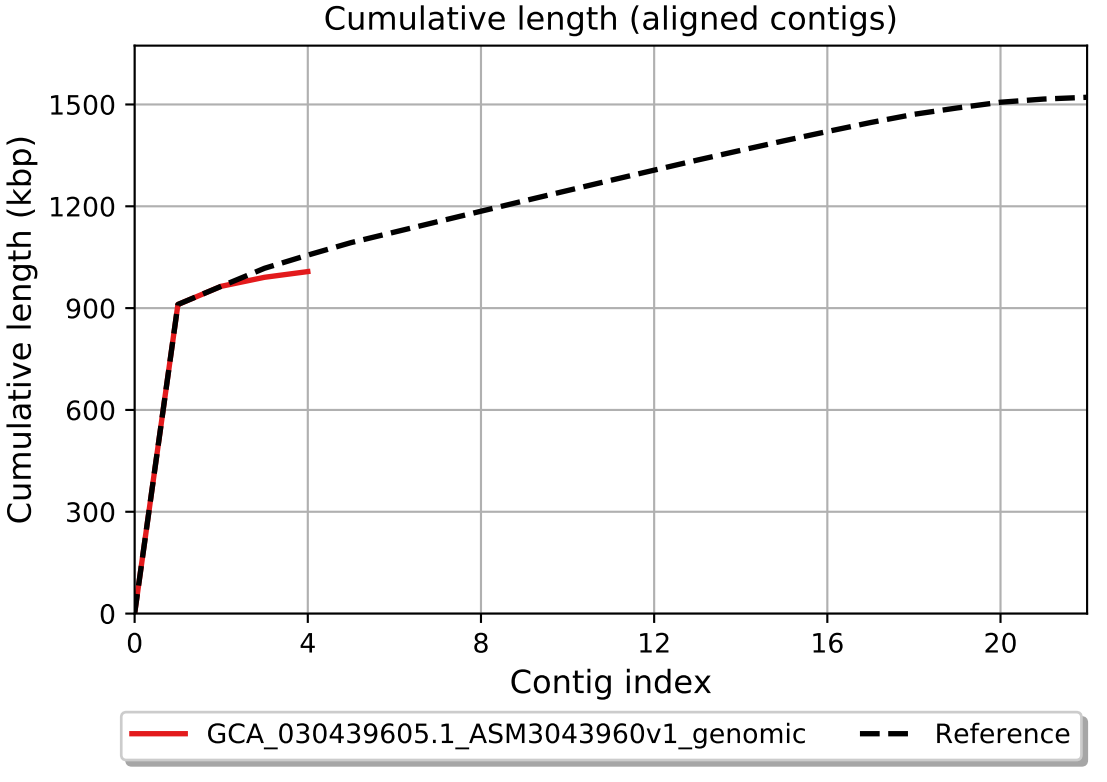

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_030439605.1_ASM3043960v1_genomic
Reference

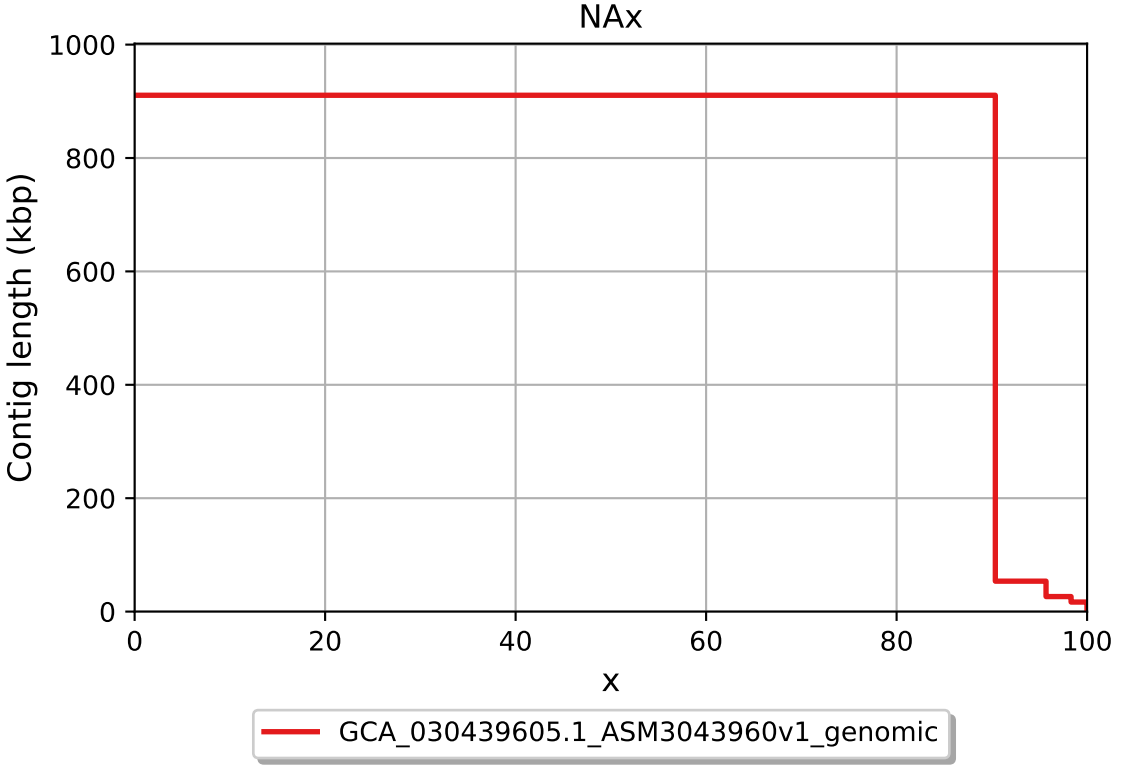

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCA_030439605.1_ASM3043960v1_genomic
Reference

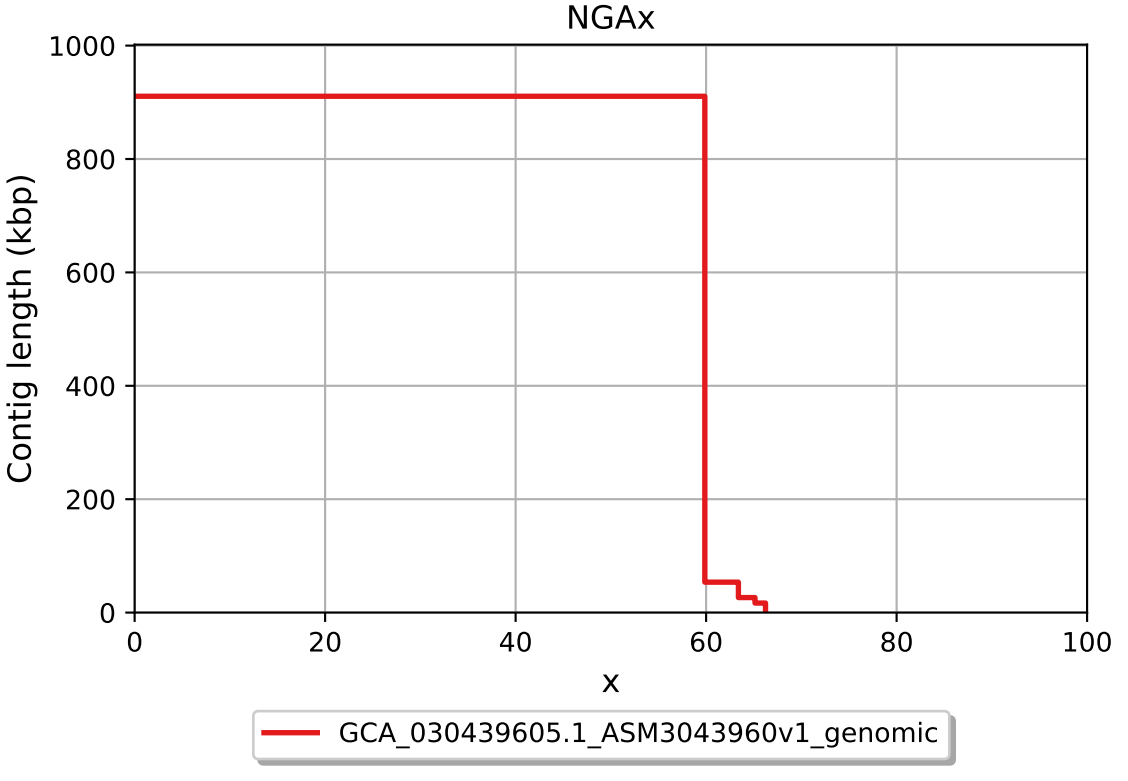

GCA_030439605.1_ASM3043960v1_genomic GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
GCA_030439605.1_ASM3043960v1_genomic

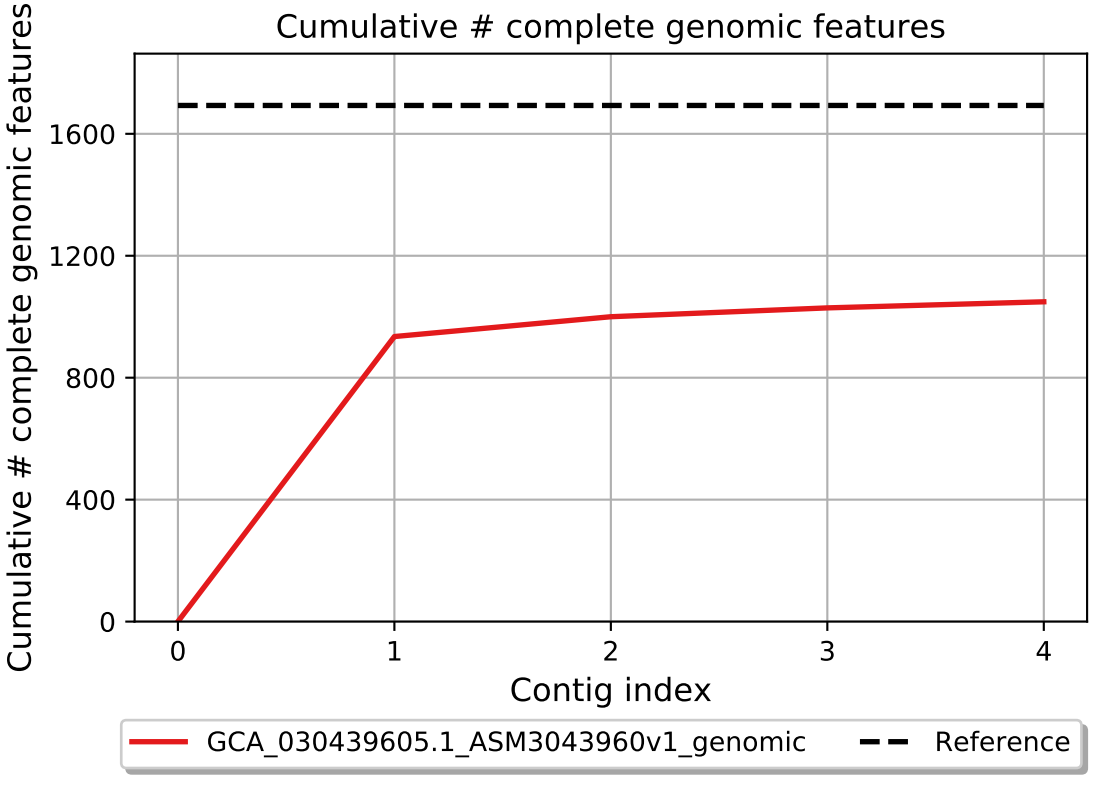

Misassemblies
5
4
3
2
1
0
GCA_030439605.1_ASM3043960v1_genomic

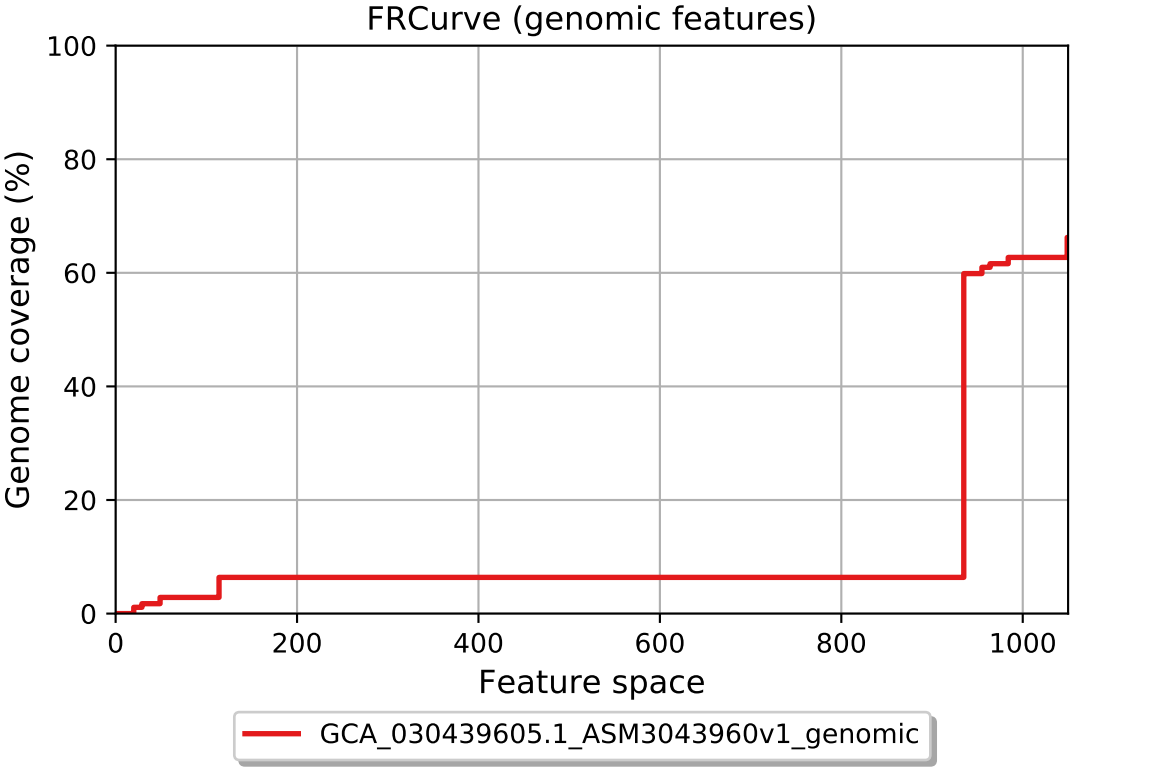

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
GCA_030439605.1_ASM3043960v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_030439605.1_ASM3043960v1_genomic
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030439605.1_ASM3043960v1_genomic


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_030439605.1_ASM3043960v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
1
2
3
4
Contig index
GCA_030439605.1_ASM3043960v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Feature space
GCA_030439605.1_ASM3043960v1_genomic