Report

	GCA_024662155.1_ASM2466215v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1392060
Total length (>= 1000 bp)	1392060
Total length (>= 5000 bp)	1392060
Total length (>= 10000 bp)	1392060
Total length (>= 25000 bp)	1314493
Total length (>= 50000 bp)	956810
# contigs	18
Largest contig	903249
Total length	1392060
Reference length	1521208
GC (%)	28.26
Reference GC (%)	28.18
N50	903249
NG50	903249
N90	27525
NG90	18341
auN	596979.7
auNG	546297.1
L50	1
LG50	1
L90	12
LG90	17
# misassemblies	23
# misassembled contigs	12
Misassembled contigs length	370887
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 13 part
Unaligned length	105249
Genome fraction (%)	79.527
Duplication ratio	1.063
# N's per 100 kbp	0.00
# mismatches per 100 kbp	892.56
# indels per 100 kbp	59.71
# genomic features	1256 + 37 part
Largest alignment	903249
Total aligned length	1286194
NA50	903249
NGA50	903249
NA90	2562
NGA90	-
auNA	592135.9
auNGA	541864.6
LA50	1
LGA50	1
LA90	25
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

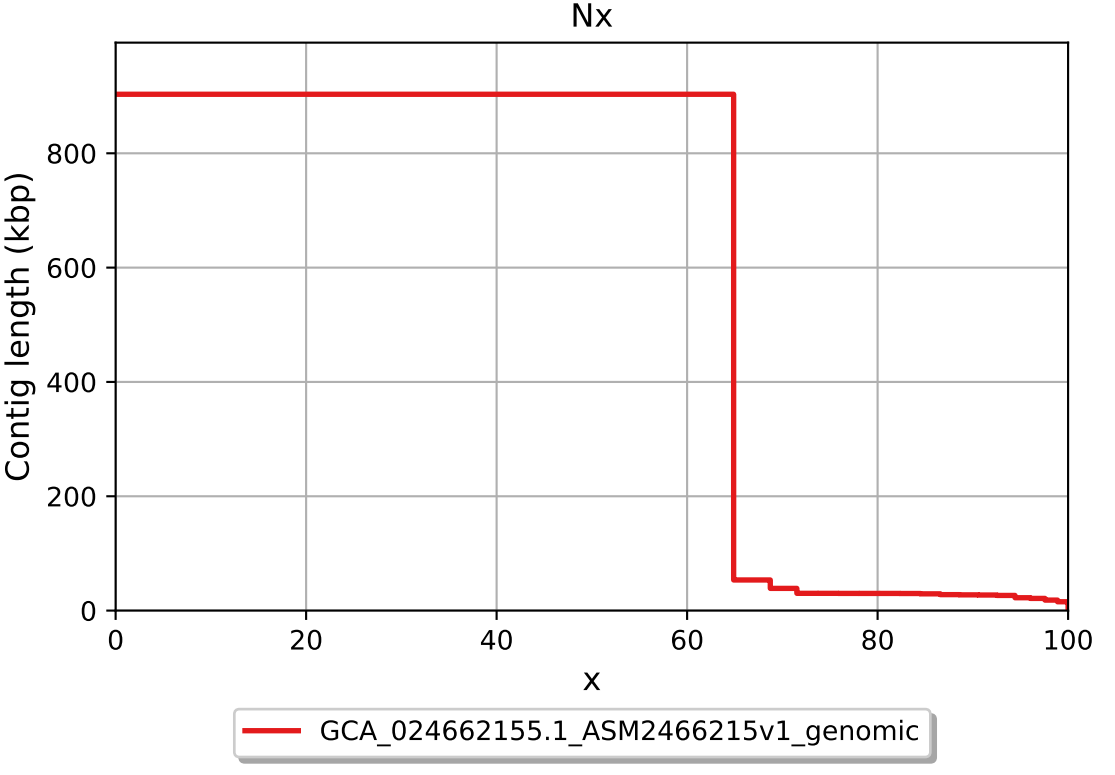
	GCA_024662155.1_ASM2466215v1_genomic
# misassemblies	23
# contig misassemblies	23
# c. relocations	3
# c. translocations	18
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	370887
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	11480
# indels	768
# indels (<= 5 bp)	685
# indels (> 5 bp)	83
Indels length	3728

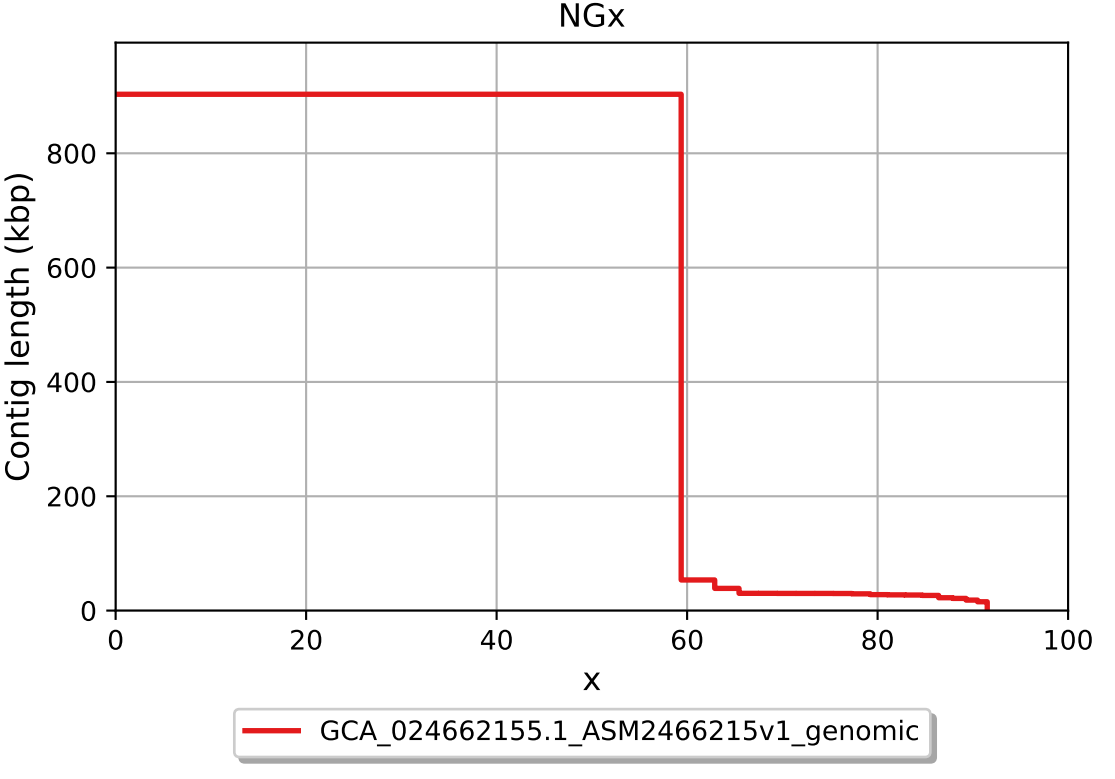
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

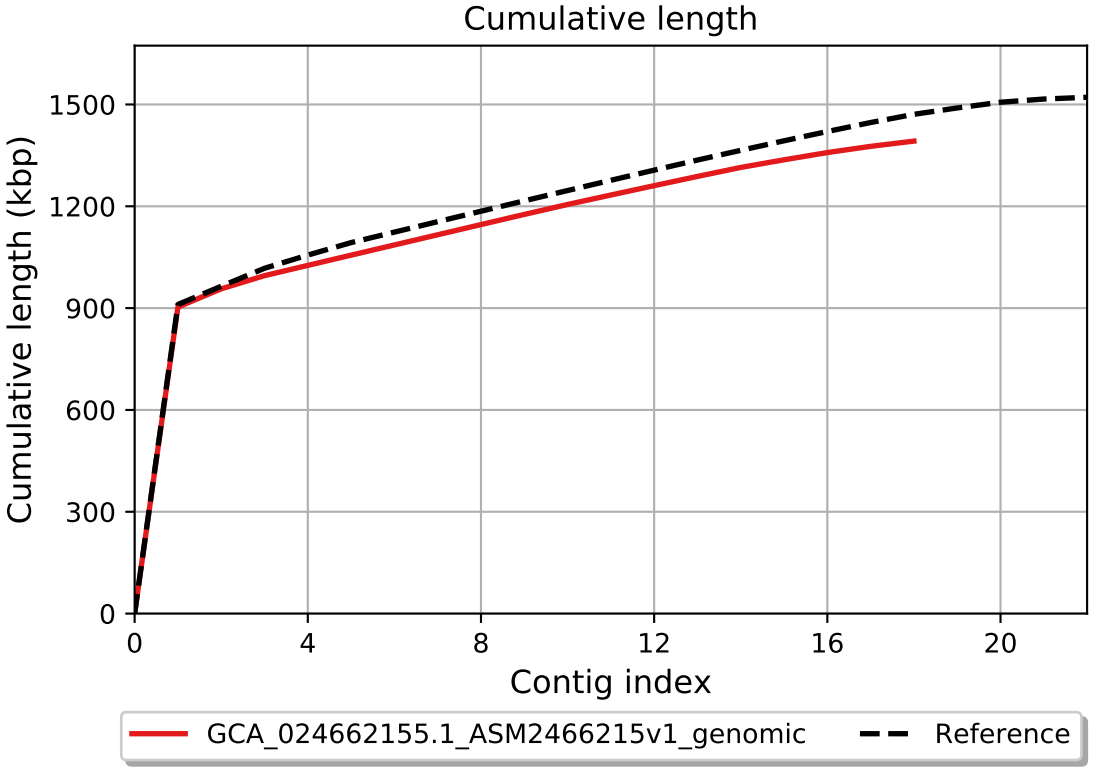
Unaligned report

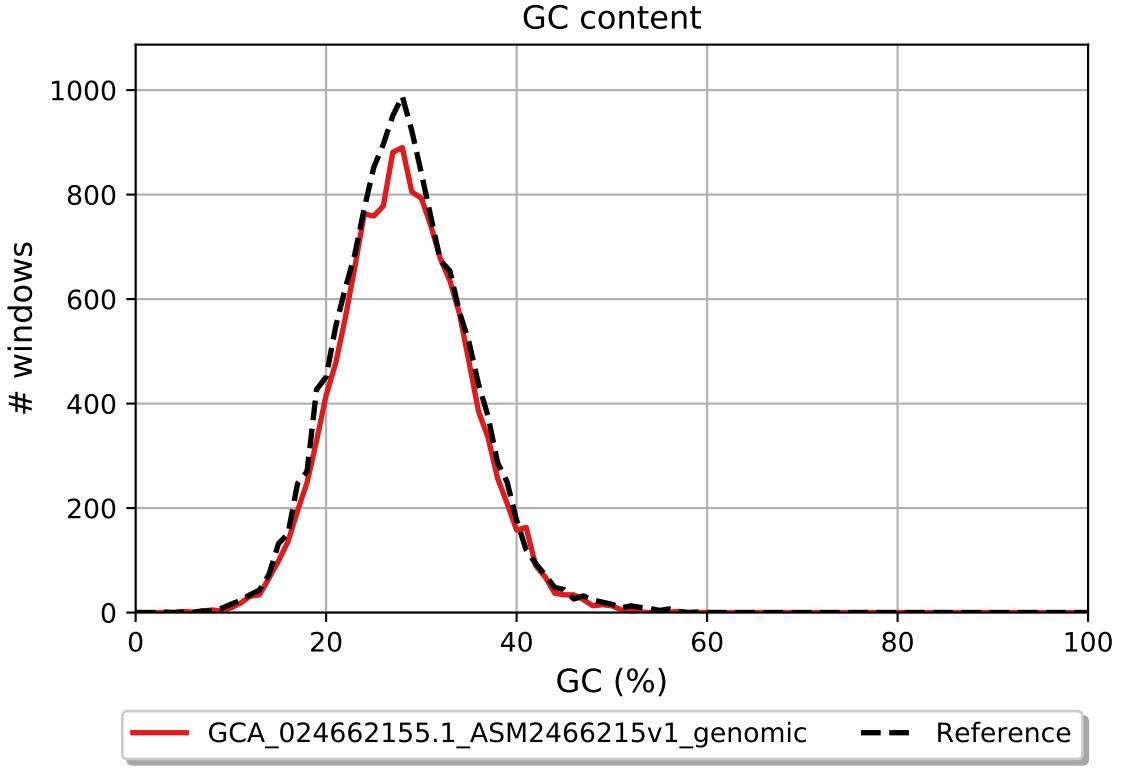
	GCA_024662155.1_ASM2466215v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	105249
# N's	0

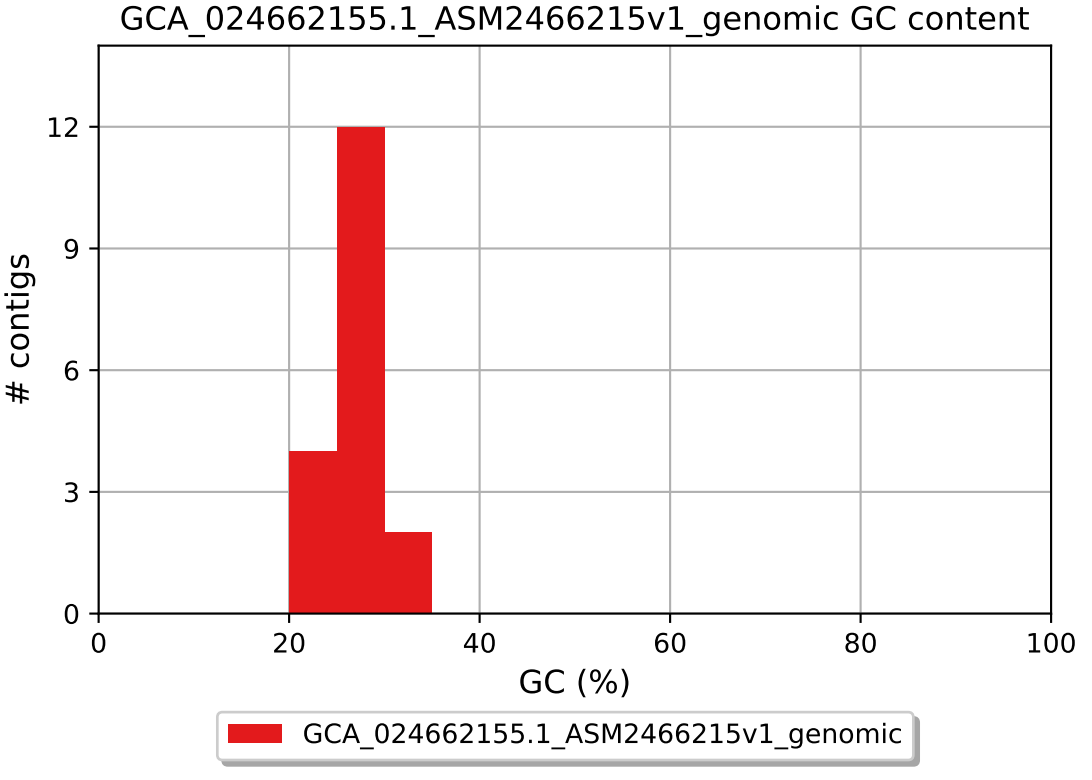
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

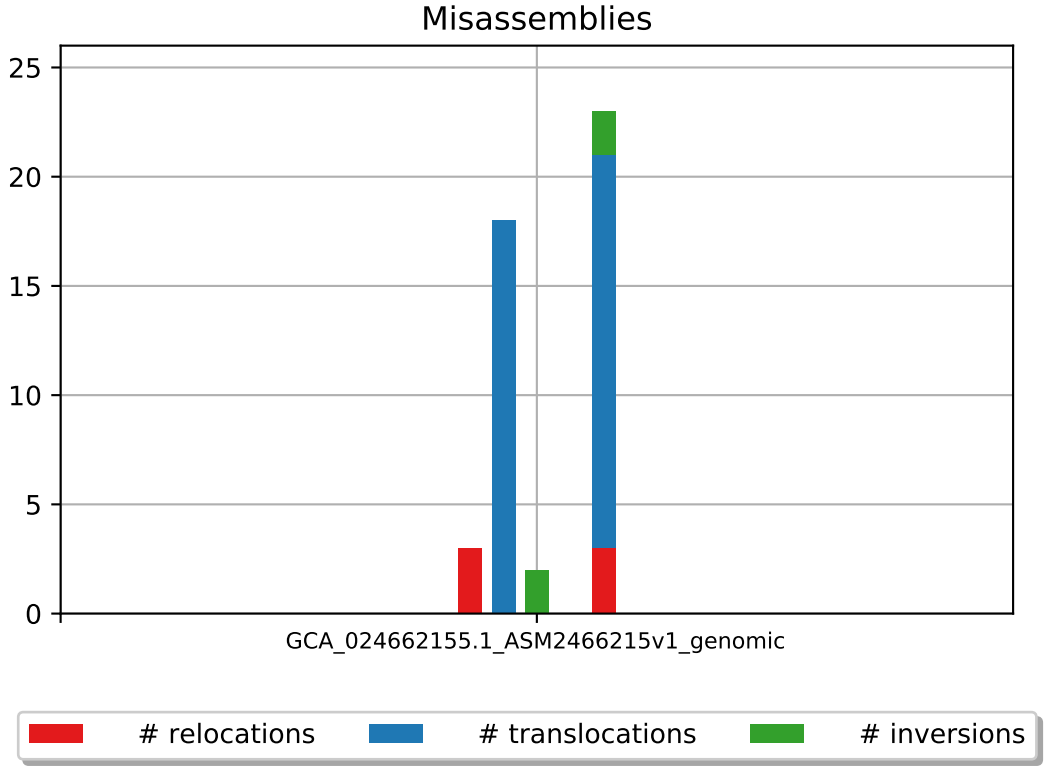

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCA_024662155.1_ASM2466215v1_genomic

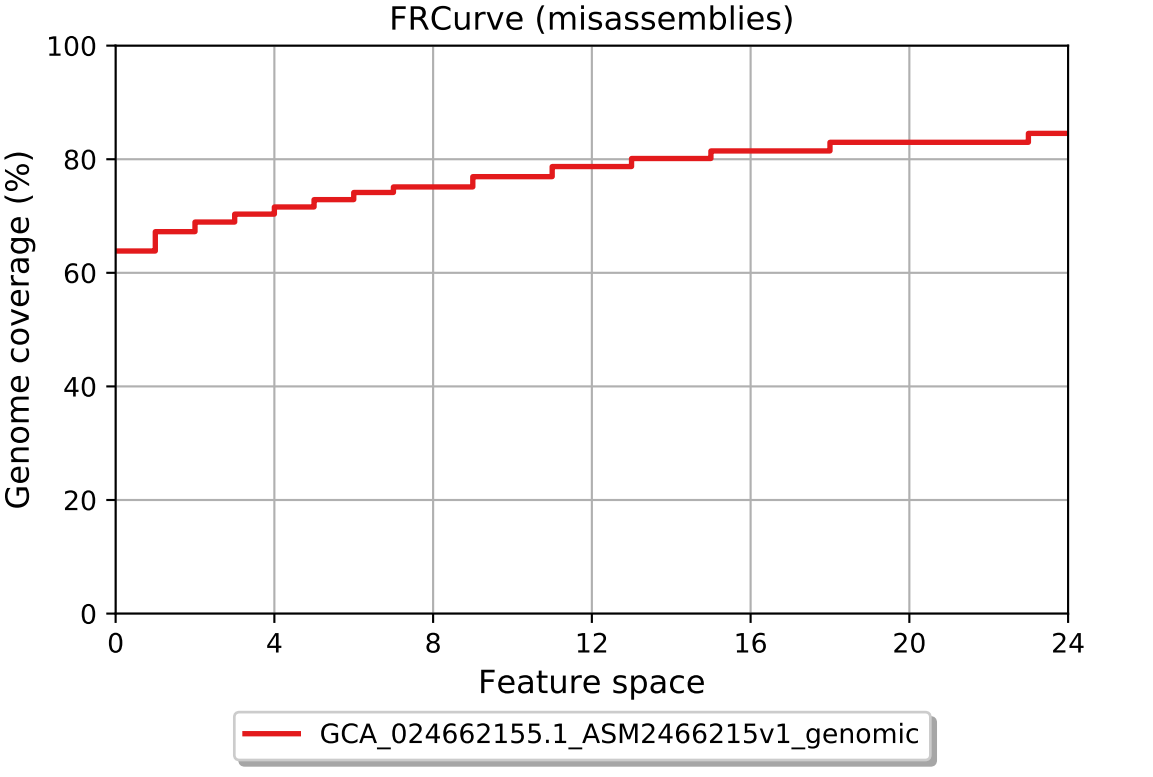

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCA_024662155.1_ASM2466215v1_genomic

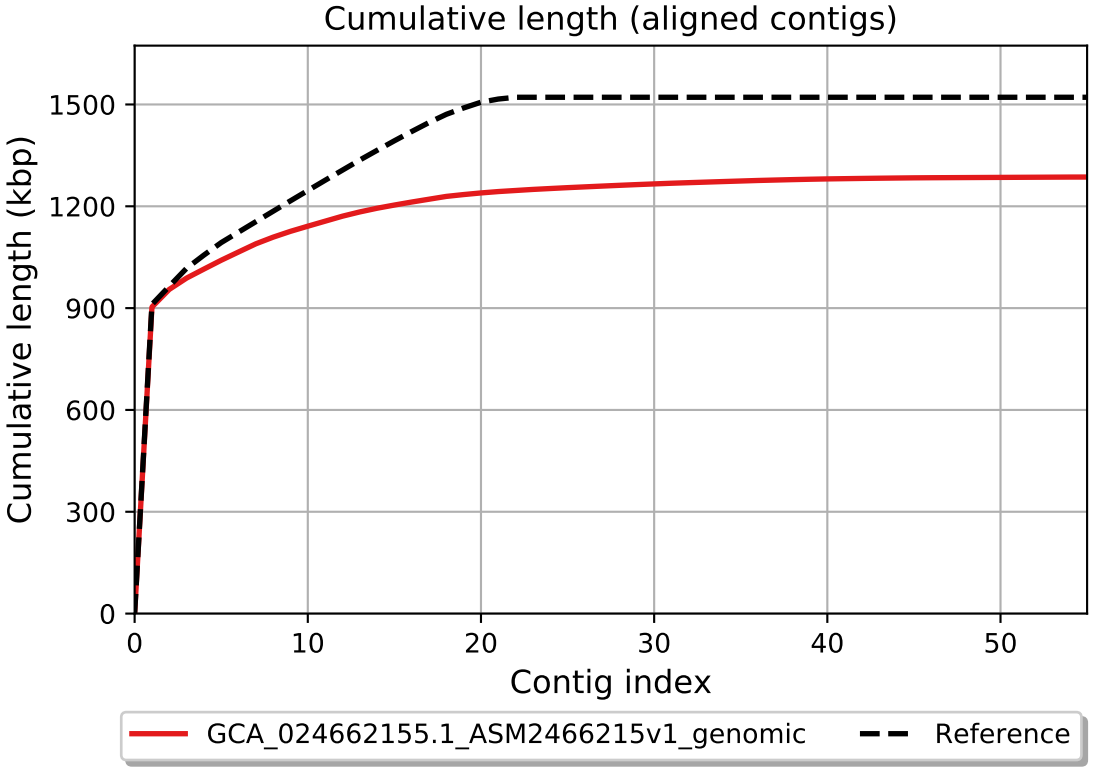

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_024662155.1_ASM2466215v1_genomic
Reference

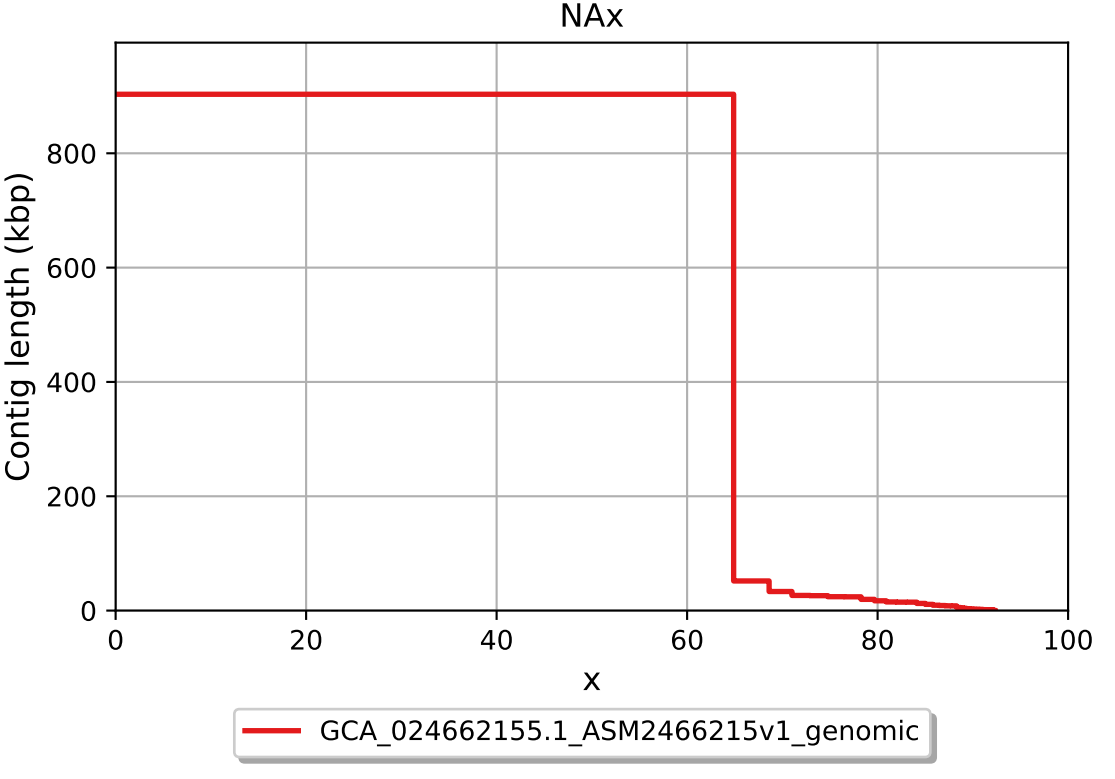

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCA_024662155.1_ASM2466215v1_genomic
Reference

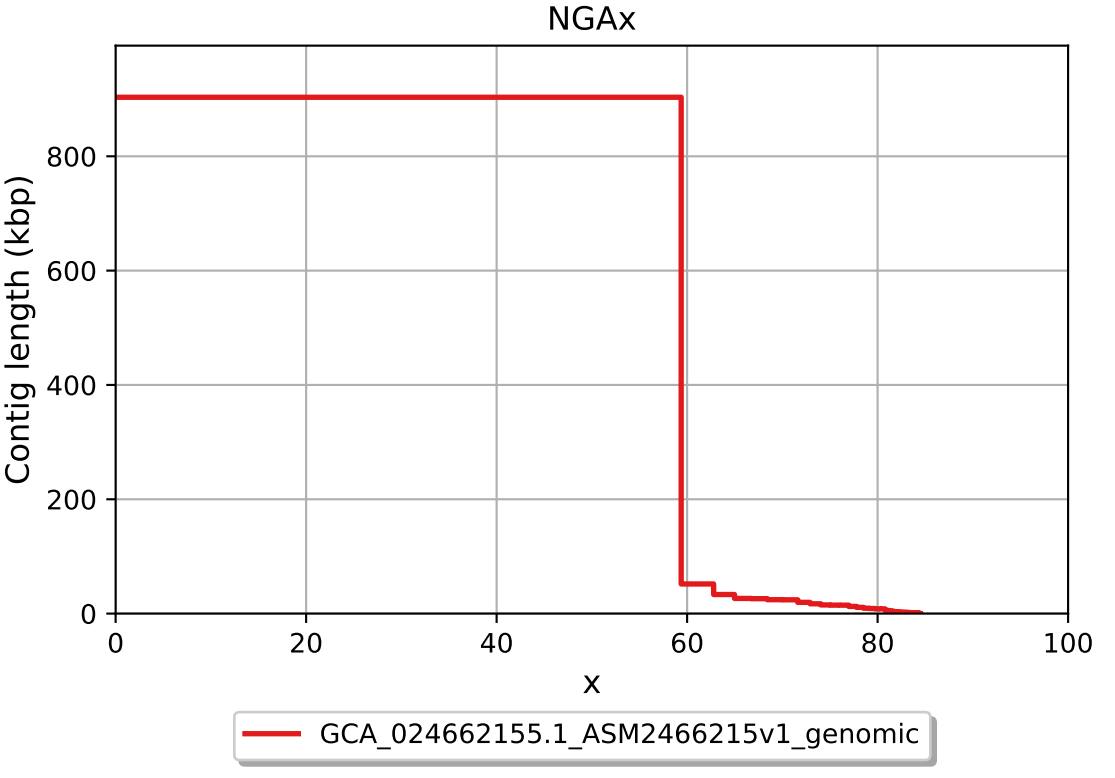

GCA_024662155.1_ASM2466215v1_genomic GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
GCA_024662155.1_ASM2466215v1_genomic

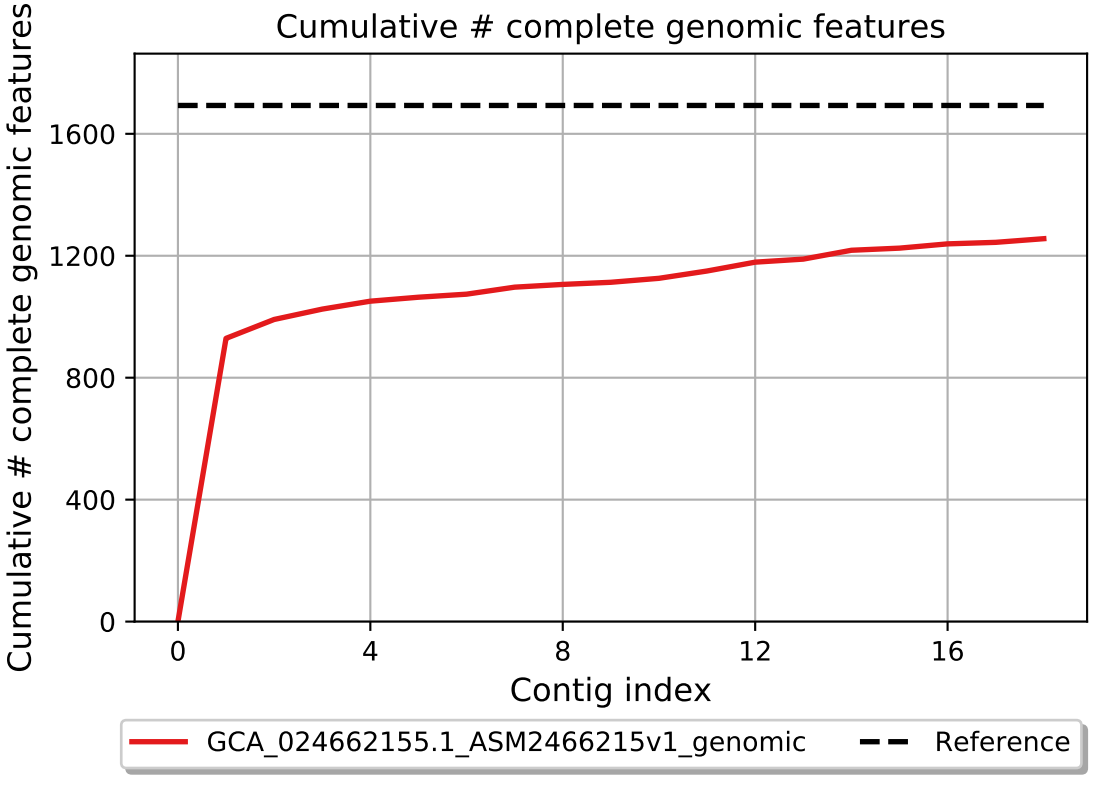

Misassemblies
25
20
15
10
5
0
GCA_024662155.1_ASM2466215v1_genomic
relocations
translocations
inversions

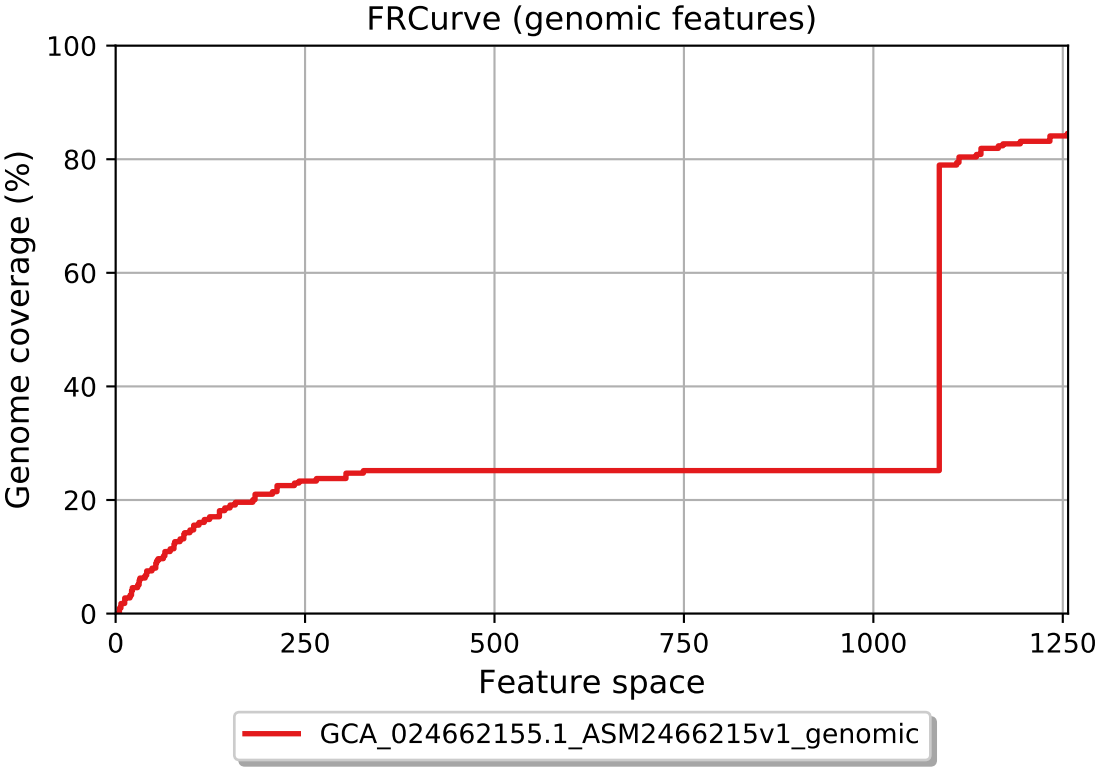

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
24
Feature space
GCA_024662155.1_ASM2466215v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
300
600
900
1200
1500
0
10
20
30
40
50
Contig index
GCA_024662155.1_ASM2466215v1_genomic
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCA_024662155.1_ASM2466215v1_genomic


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCA_024662155.1_ASM2466215v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
4
8
12
16
Contig index
GCA_024662155.1_ASM2466215v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCA_024662155.1_ASM2466215v1_genomic