Report

	GCF_000181715.2_ASM18171v2_genomic
# contigs (>= 0 bp)	25
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	6
Total length (>= 0 bp)	1295451
Total length (>= 1000 bp)	1293275
Total length (>= 5000 bp)	1286421
Total length (>= 10000 bp)	1277725
Total length (>= 25000 bp)	1217238
Total length (>= 50000 bp)	907911
# contigs	24
Largest contig	216266
Total length	1295058
Reference length	1521208
GC (%)	28.26
Reference GC (%)	28.18
N50	169491
NG50	169491
N90	26507
NG90	-
auN	131331.6
auNG	111807.2
L50	4
LG50	4
L90	15
LG90	-
# misassemblies	16
# misassembled contigs	6
Misassembled contigs length	167894
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	1 + 12 part
Unaligned length	99932
Genome fraction (%)	76.285
Duplication ratio	1.029
# N's per 100 kbp	0.08
# mismatches per 100 kbp	778.57
# indels per 100 kbp	42.03
# genomic features	1201 + 53 part
Largest alignment	216266
Total aligned length	1194492
NA50	169491
NGA50	169491
NA90	3932
NGA90	-
auNA	126815.8
auNGA	107962.7
LA50	4
LGA50	4
LA90	23
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

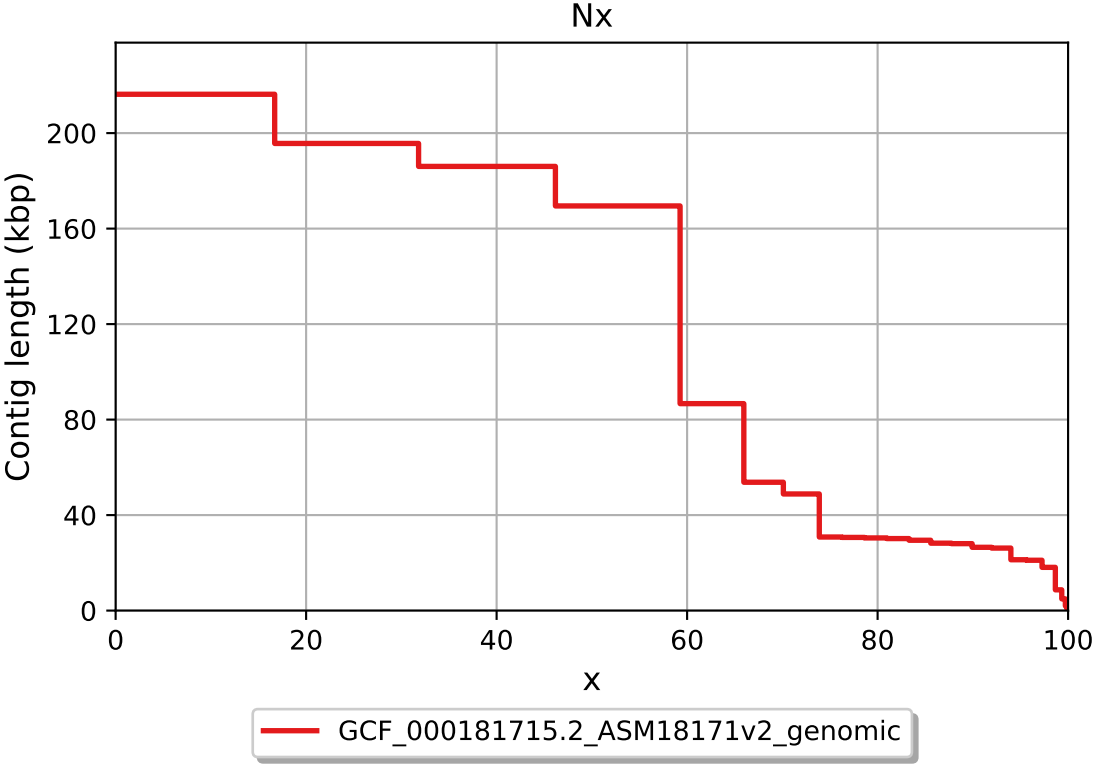
	GCF_000181715.2_ASM18171v2_genomic
# misassemblies	16
# contig misassemblies	16
# c. relocations	2
# c. translocations	13
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	167894
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	9300
# indels	502
# indels (<= 5 bp)	454
# indels (> 5 bp)	48
Indels length	1842

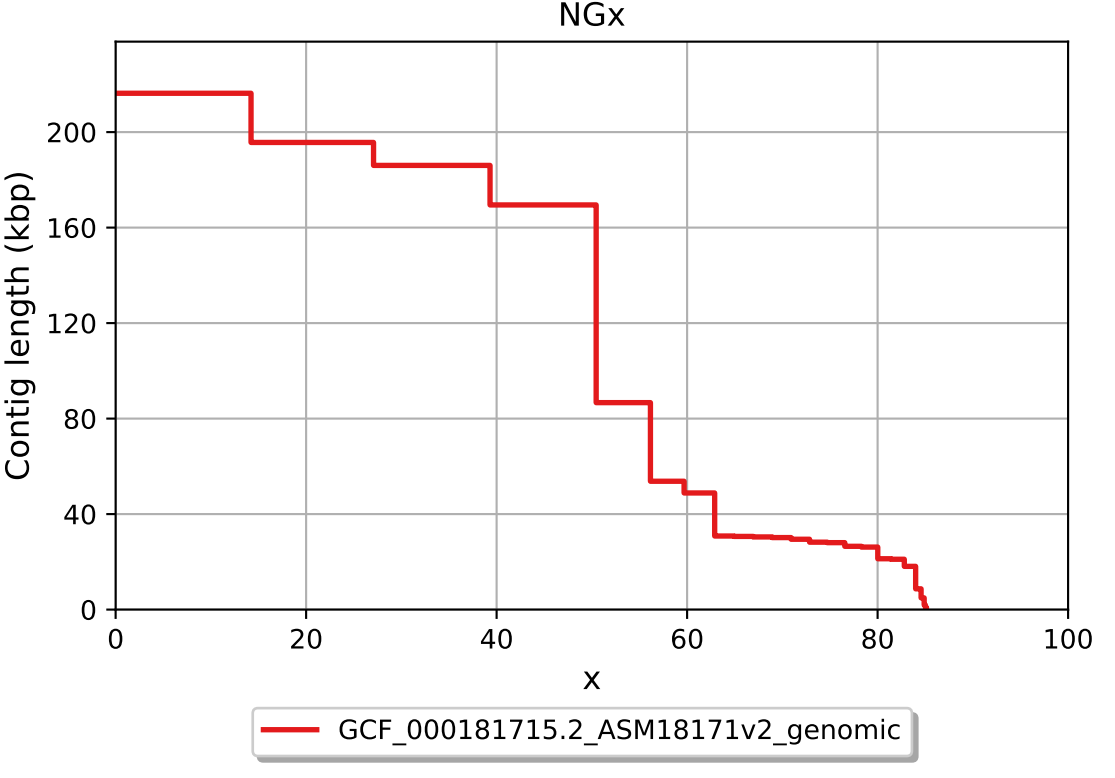
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

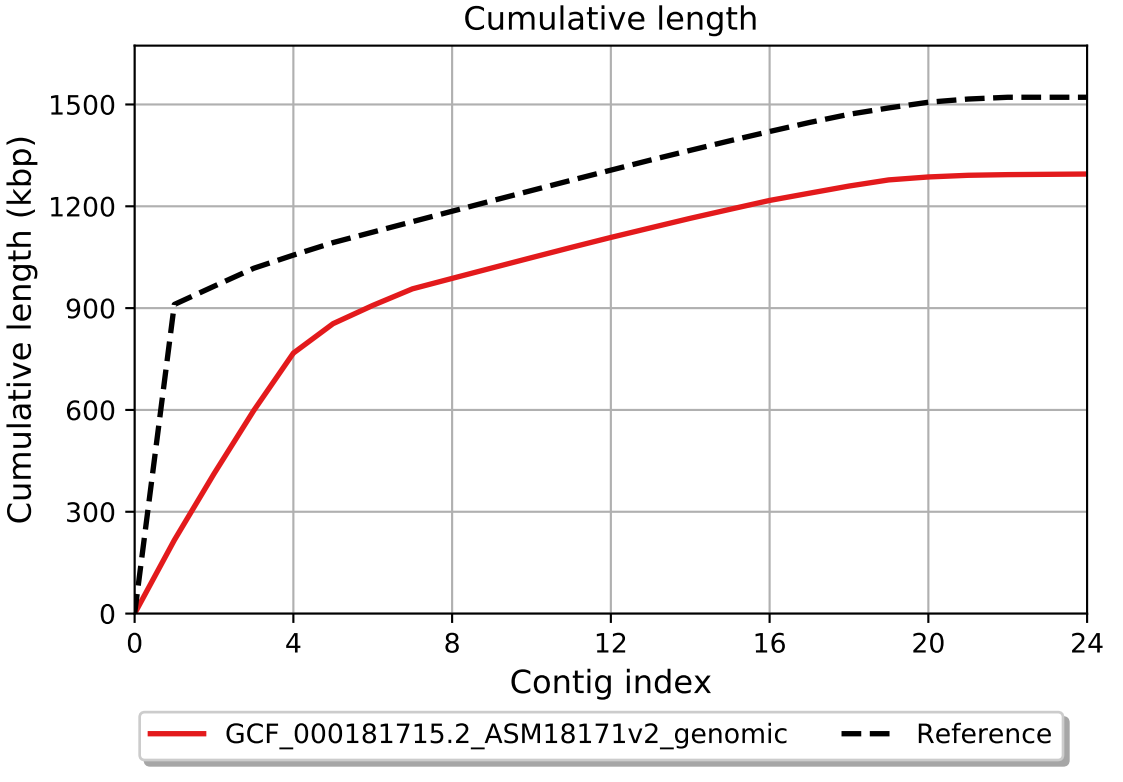
Unaligned report

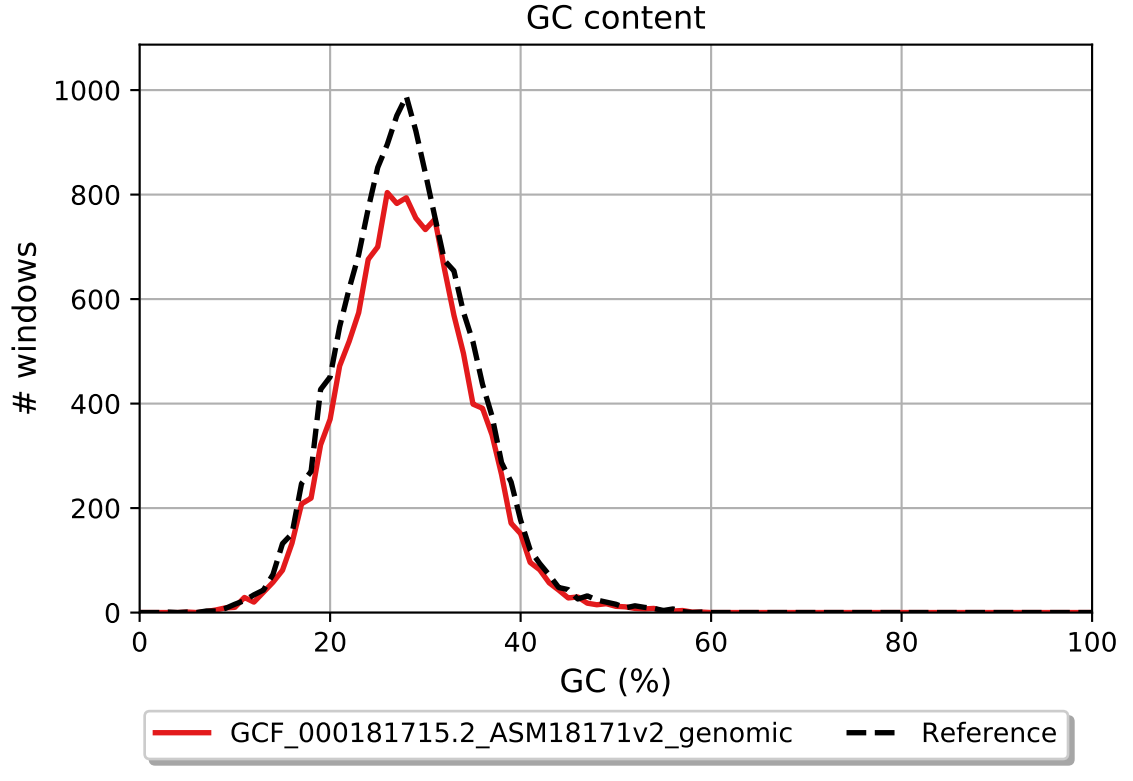
	GCF_000181715.2_ASM18171v2_genomic
# fully unaligned contigs	1
Fully unaligned length	4910
# partially unaligned contigs	12
Partially unaligned length	95022
# N's	1

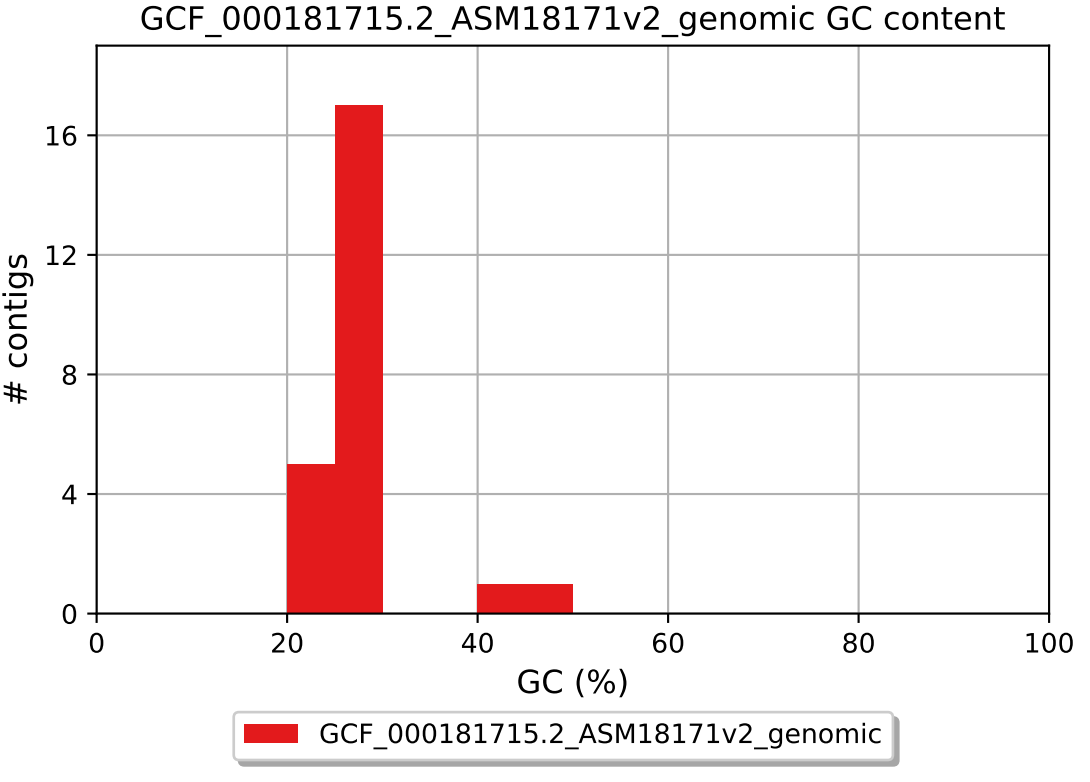
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

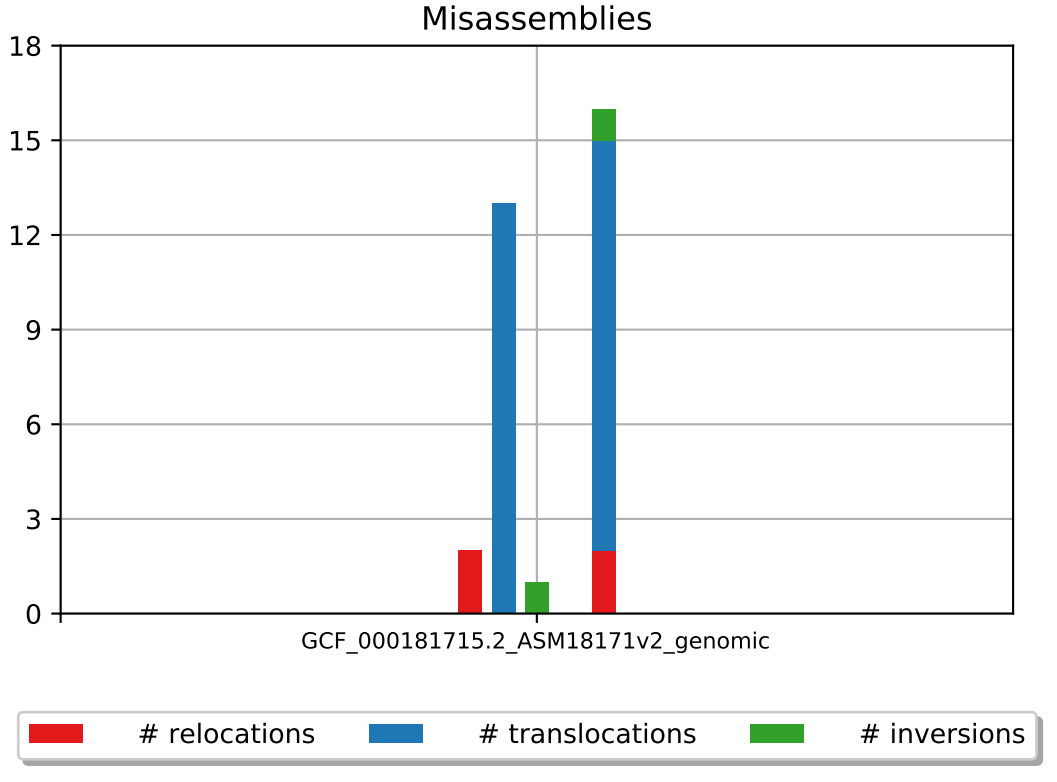

Nx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
GCF_000181715.2_ASM18171v2_genomic

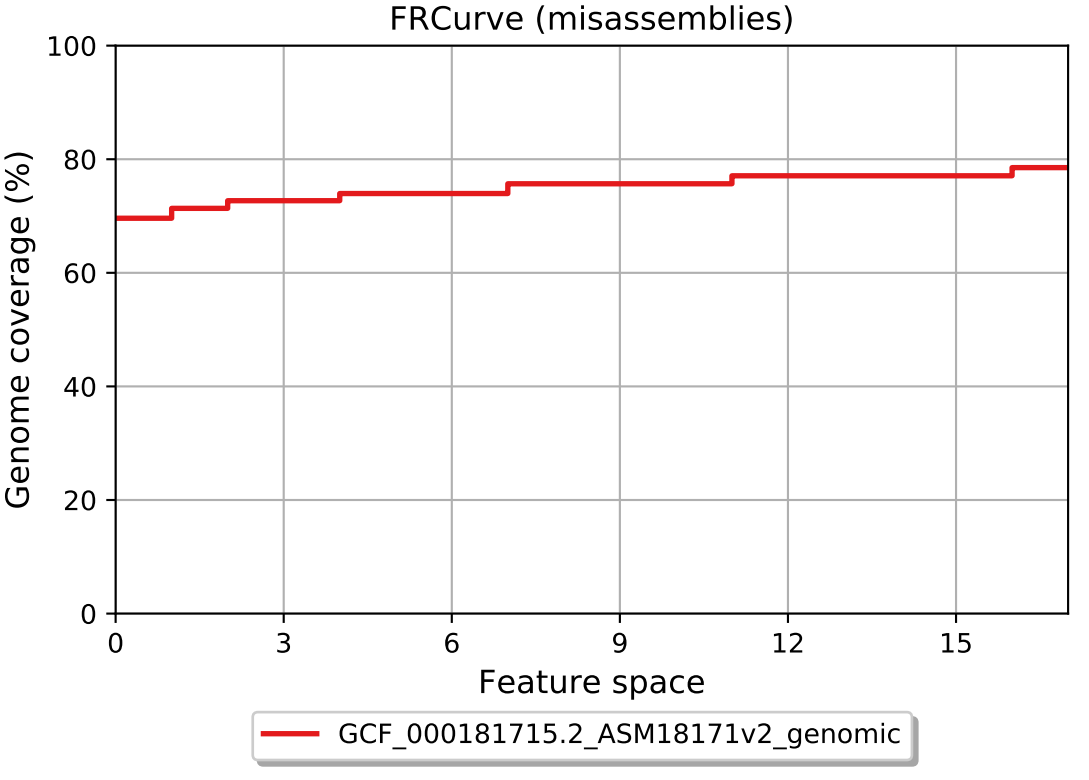

NGx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
GCF_000181715.2_ASM18171v2_genomic

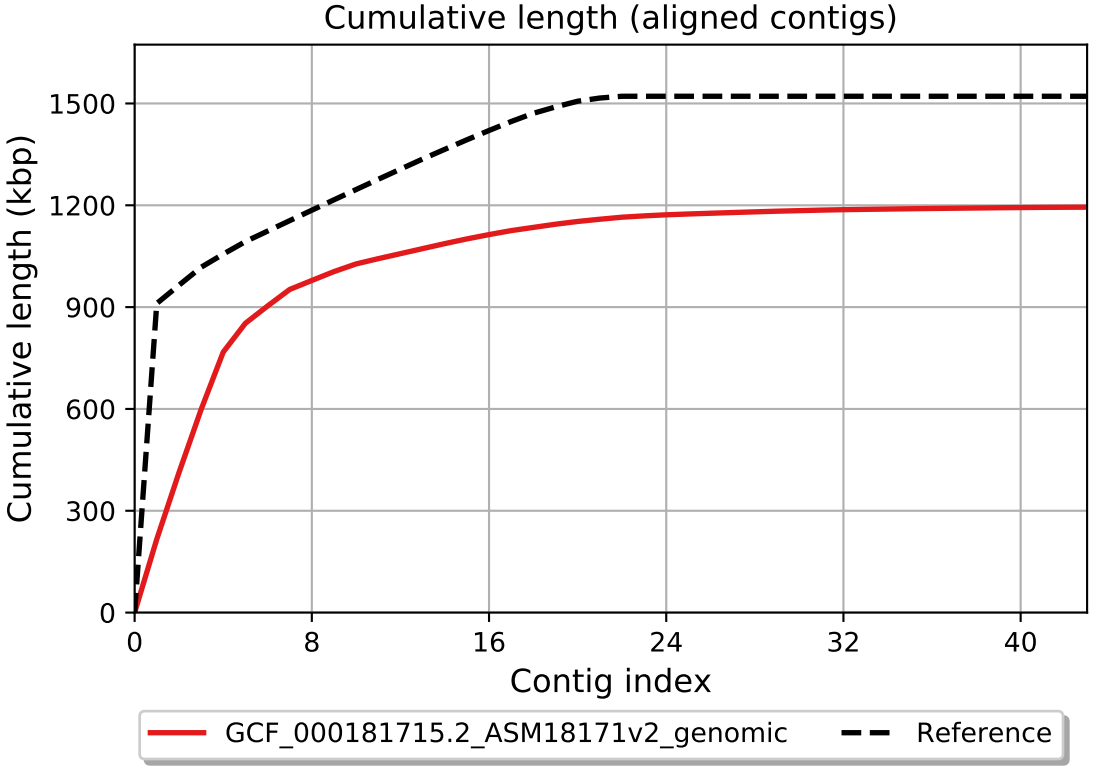

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
24
Contig index
GCF_000181715.2_ASM18171v2_genomic
Reference

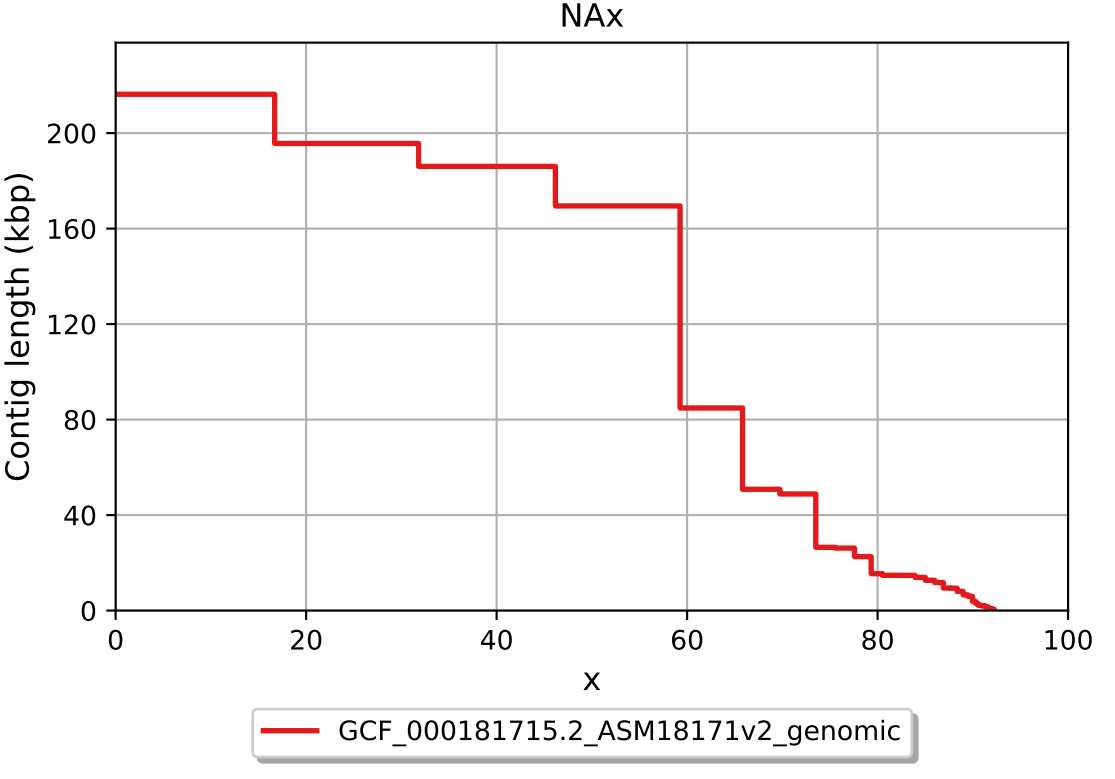

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
GCF_000181715.2_ASM18171v2_genomic
Reference

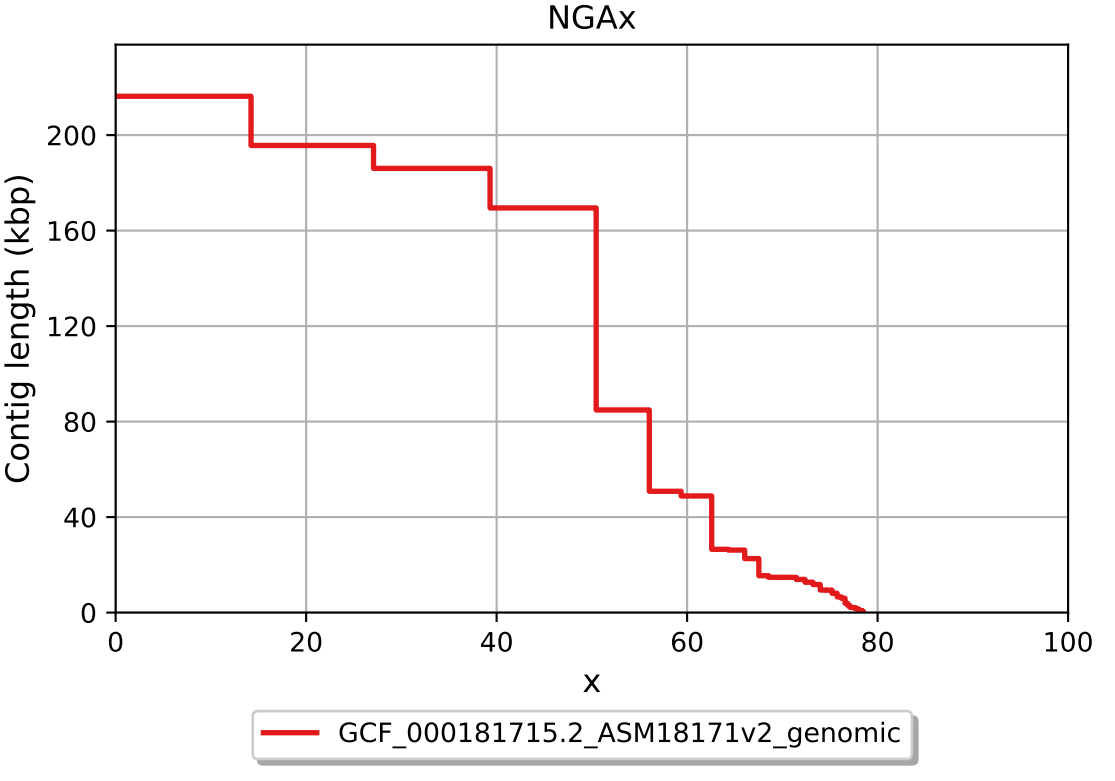

GCF_000181715.2_ASM18171v2_genomic GC content
contigs
0
4
8
12
16
0
20
40
60
80
100
GC (%)
GCF_000181715.2_ASM18171v2_genomic

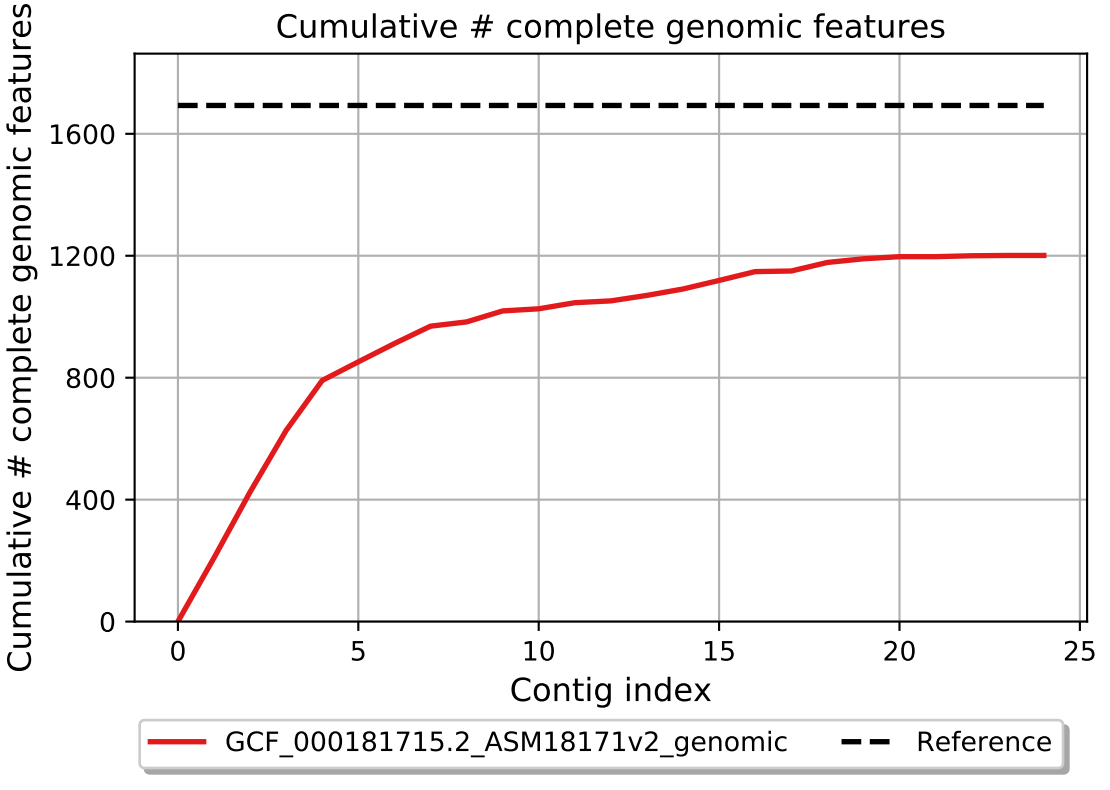

Misassemblies
18
15
12
9
6
3
0
GCF_000181715.2_ASM18171v2_genomic
relocations
translocations
inversions

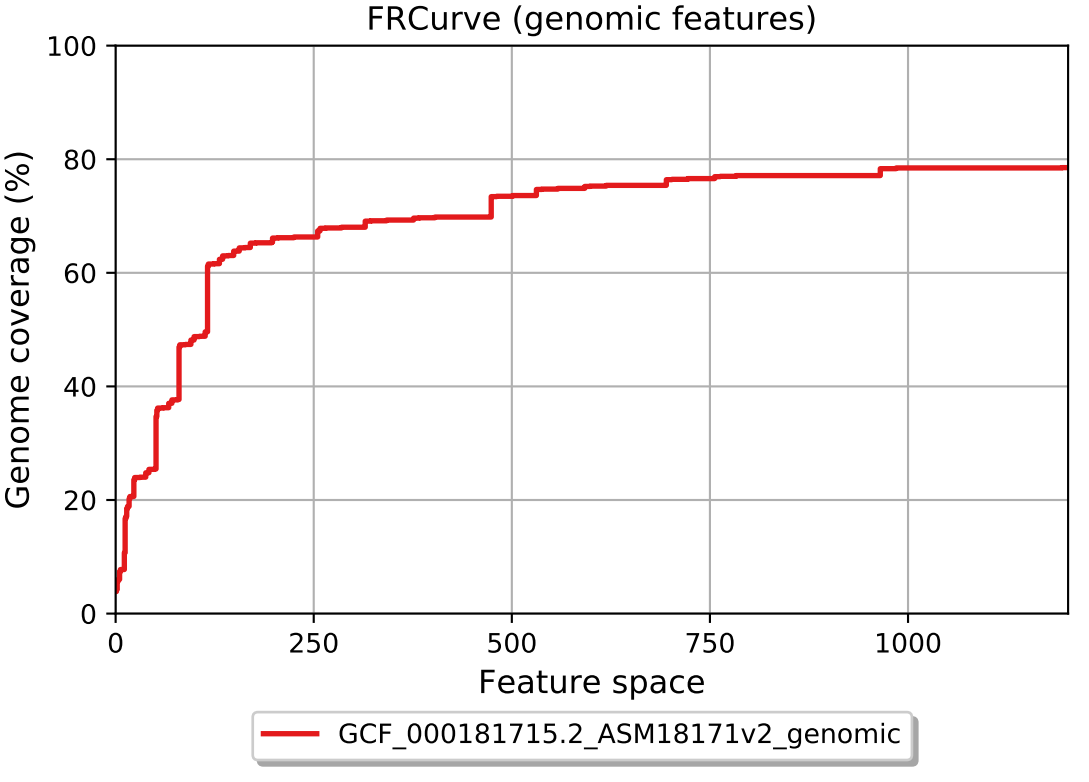

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
GCF_000181715.2_ASM18171v2_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
GCF_000181715.2_ASM18171v2_genomic
Reference


NAx
Contig length (kbp)
0
40
80
120
160
200
0
20
40
60
80
100
x
GCF_000181715.2_ASM18171v2_genomic


NGAx
Contig length (kbp)
0
40
80
120
160
200
0
20
40
60
80
100
x
GCF_000181715.2_ASM18171v2_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
5
10
15
20
25
Contig index
GCF_000181715.2_ASM18171v2_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
Feature space
GCF_000181715.2_ASM18171v2_genomic