Report

	GCF_040790735.1_ASM4079073v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1391486
Total length (>= 1000 bp)	1391486
Total length (>= 5000 bp)	1391486
Total length (>= 10000 bp)	1391486
Total length (>= 25000 bp)	1288594
Total length (>= 50000 bp)	963376
# contigs	18
Largest contig	909471
Total length	1391486
Reference length	1521208
GC (%)	28.27
Reference GC (%)	28.18
N50	909471
NG50	909471
N90	27192
NG90	18015
auN	605012.4
auNG	553419.5
L50	1
LG50	1
L90	12
LG90	17
# misassemblies	20
# misassembled contigs	11
Misassembled contigs length	1204252
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 16 part
Unaligned length	156722
Genome fraction (%)	78.701
Duplication ratio	1.031
# N's per 100 kbp	0.07
# mismatches per 100 kbp	833.46
# indels per 100 kbp	45.12
# genomic features	1268 + 33 part
Largest alignment	468258
Total aligned length	1234607
NA50	435179
NGA50	435179
NA90	-
NGA90	-
auNA	298641.1
auNGA	273174.2
LA50	2
LGA50	2
LA90	-
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

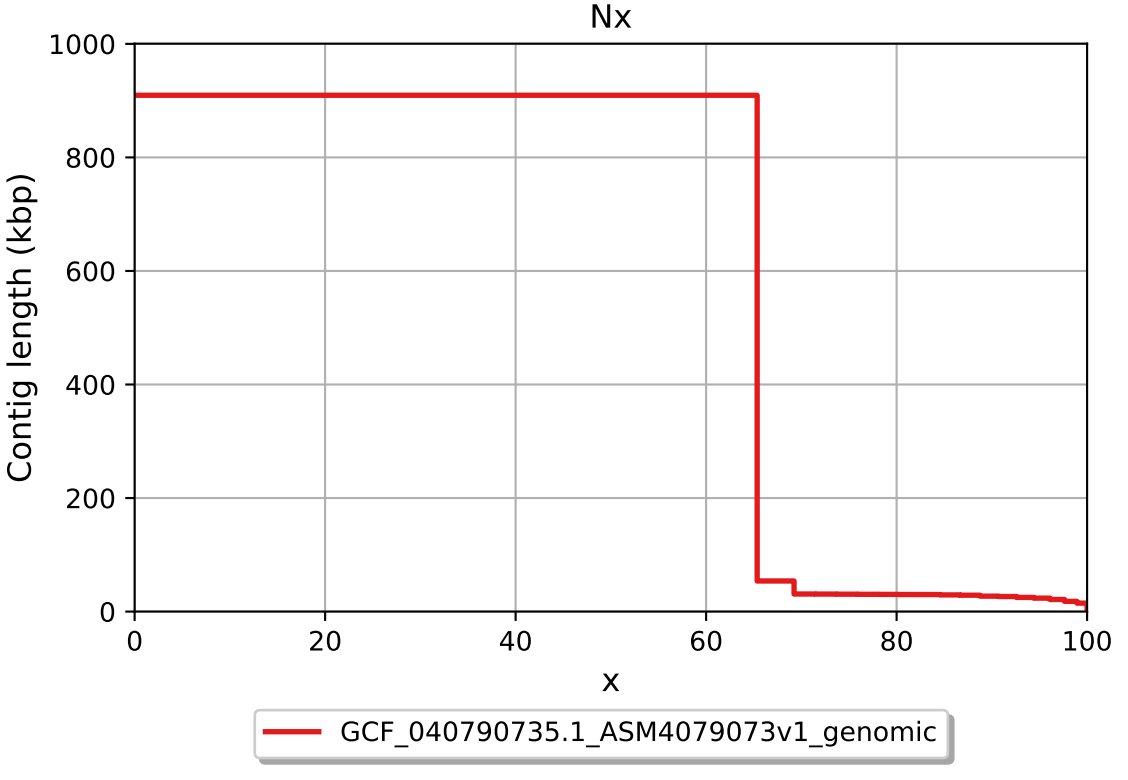
	GCF_040790735.1_ASM4079073v1_genomic
# misassemblies	20
# contig misassemblies	20
# c. relocations	6
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	1204252
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	10290
# indels	557
# indels (<= 5 bp)	496
# indels (> 5 bp)	61
Indels length	2581

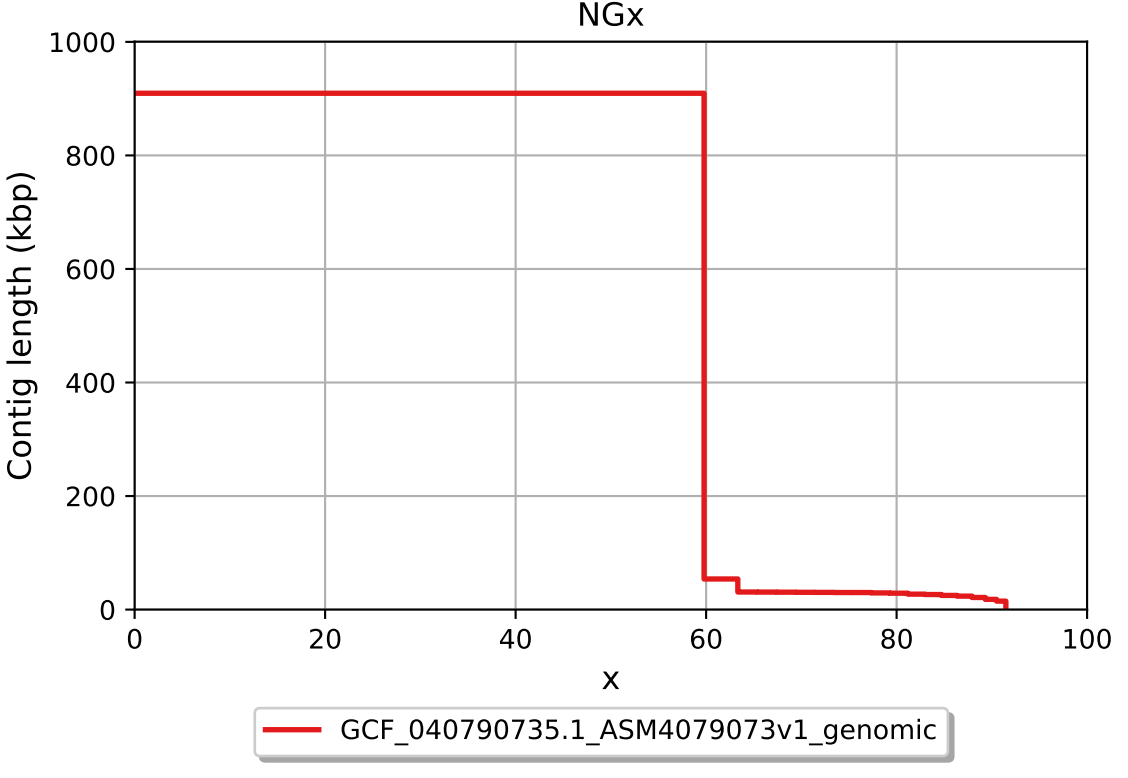
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

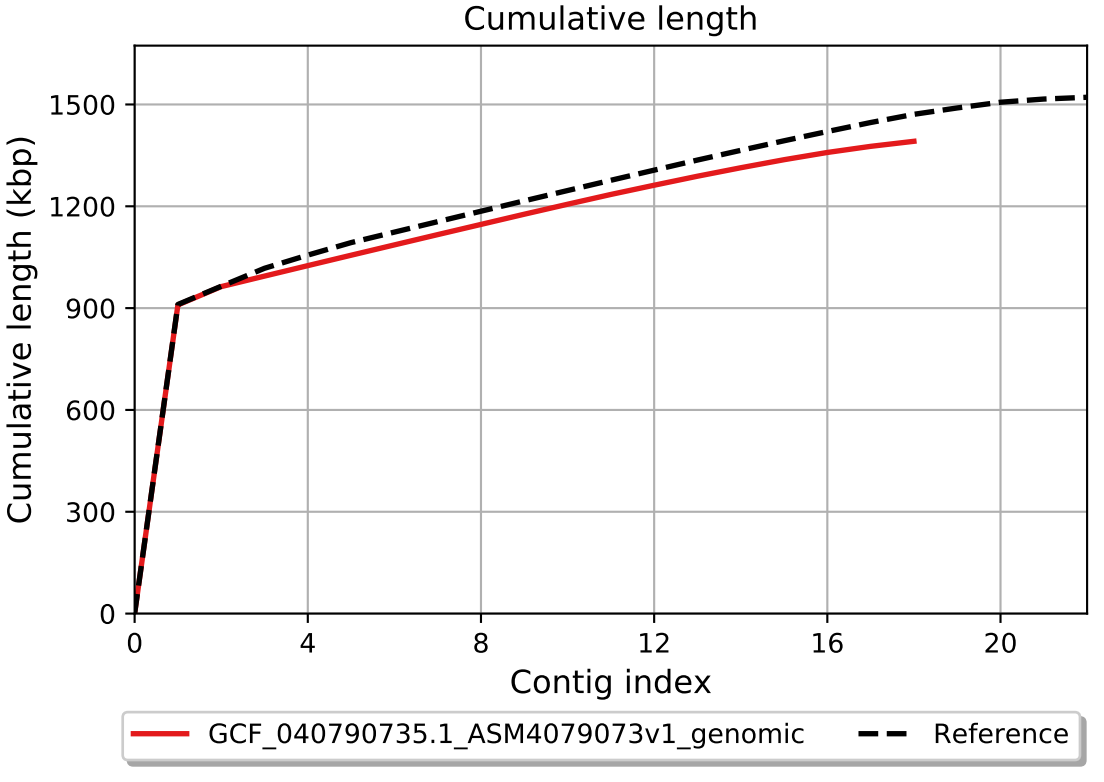
Unaligned report

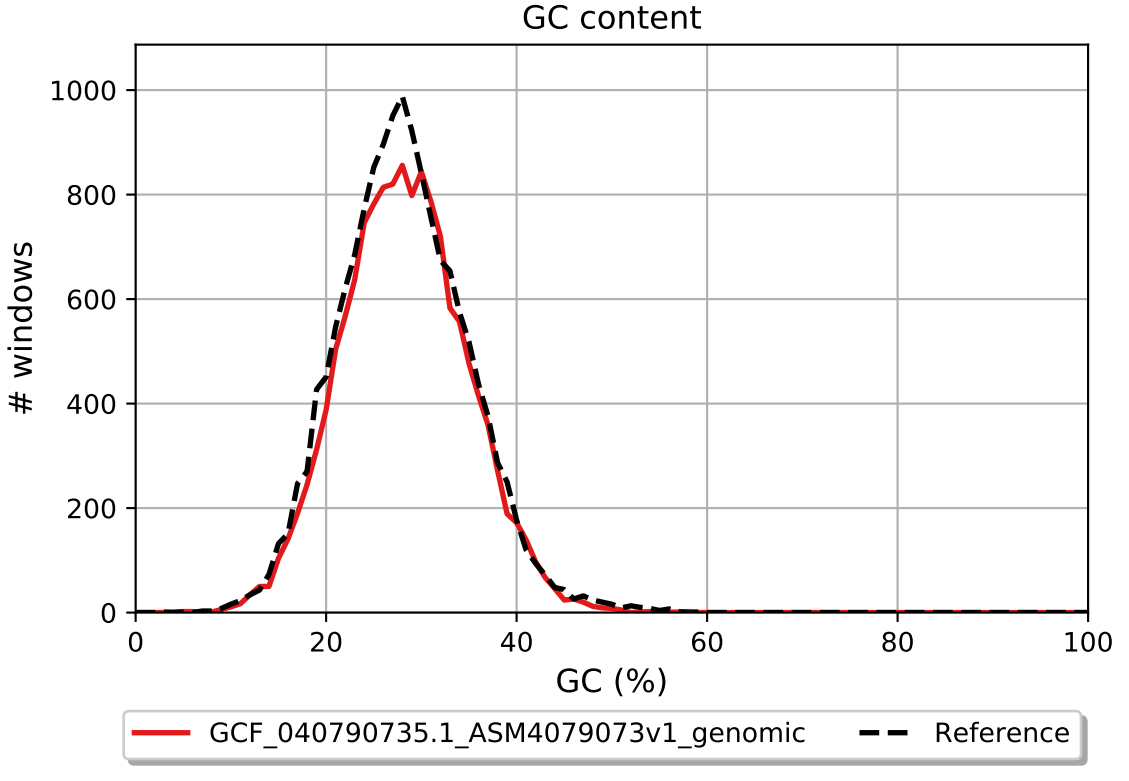
	GCF_040790735.1_ASM4079073v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
Partially unaligned length	156722
# N's	1

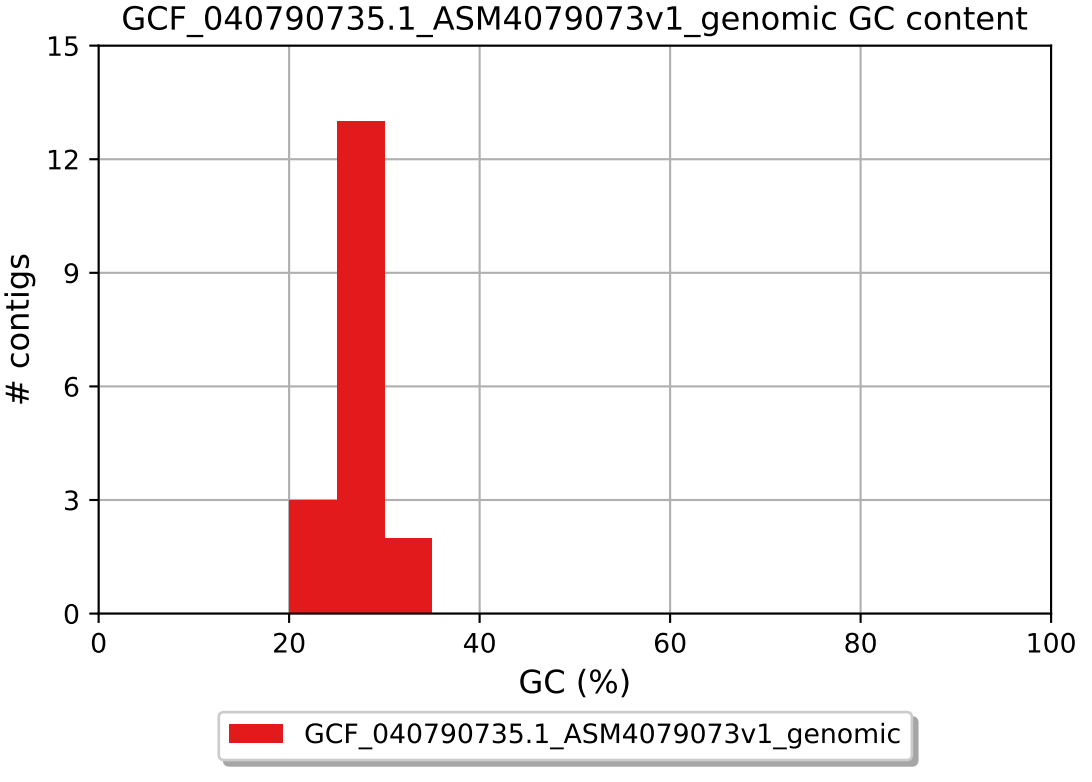
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

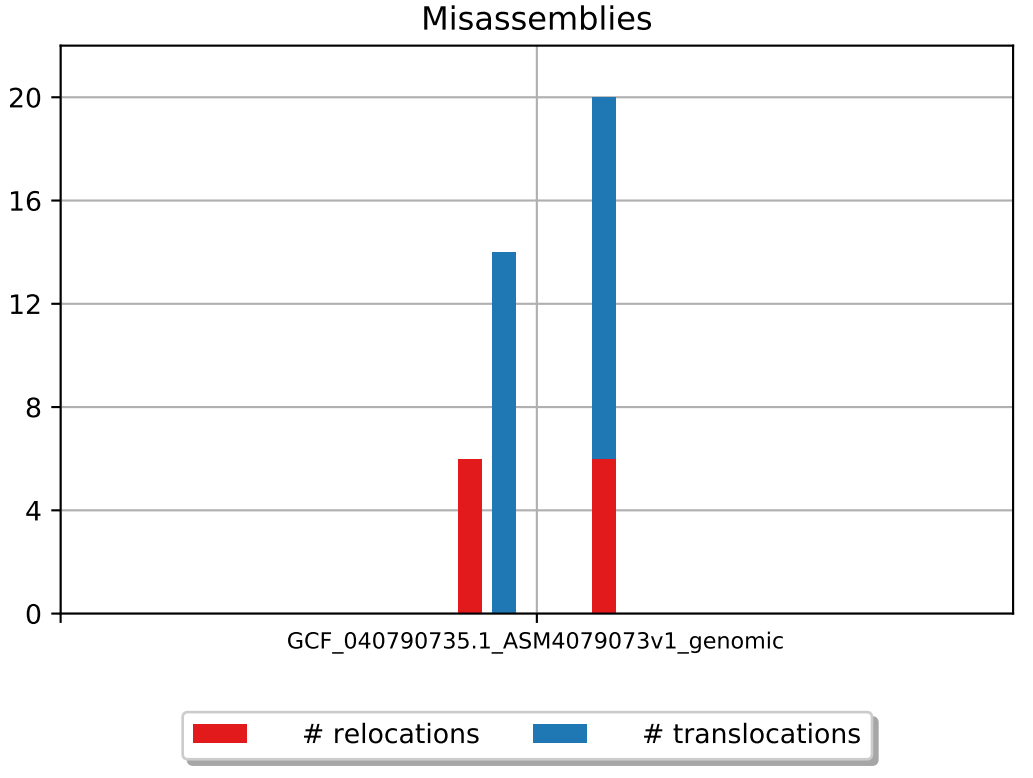

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790735.1_ASM4079073v1_genomic

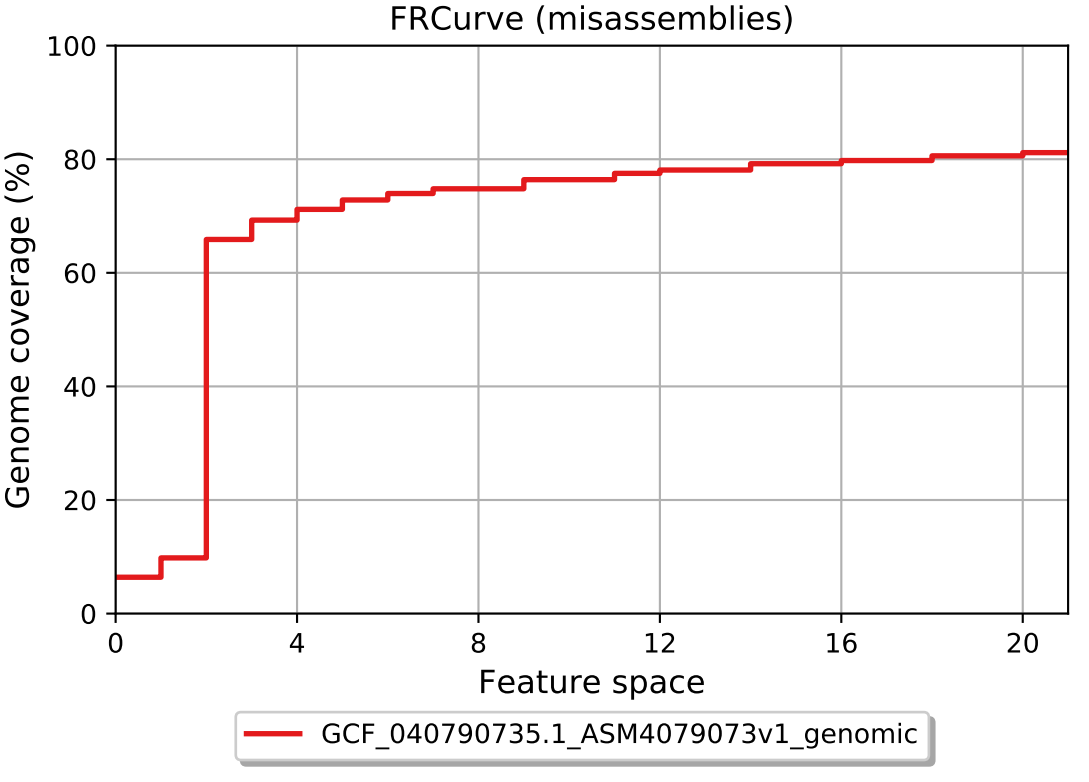

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790735.1_ASM4079073v1_genomic

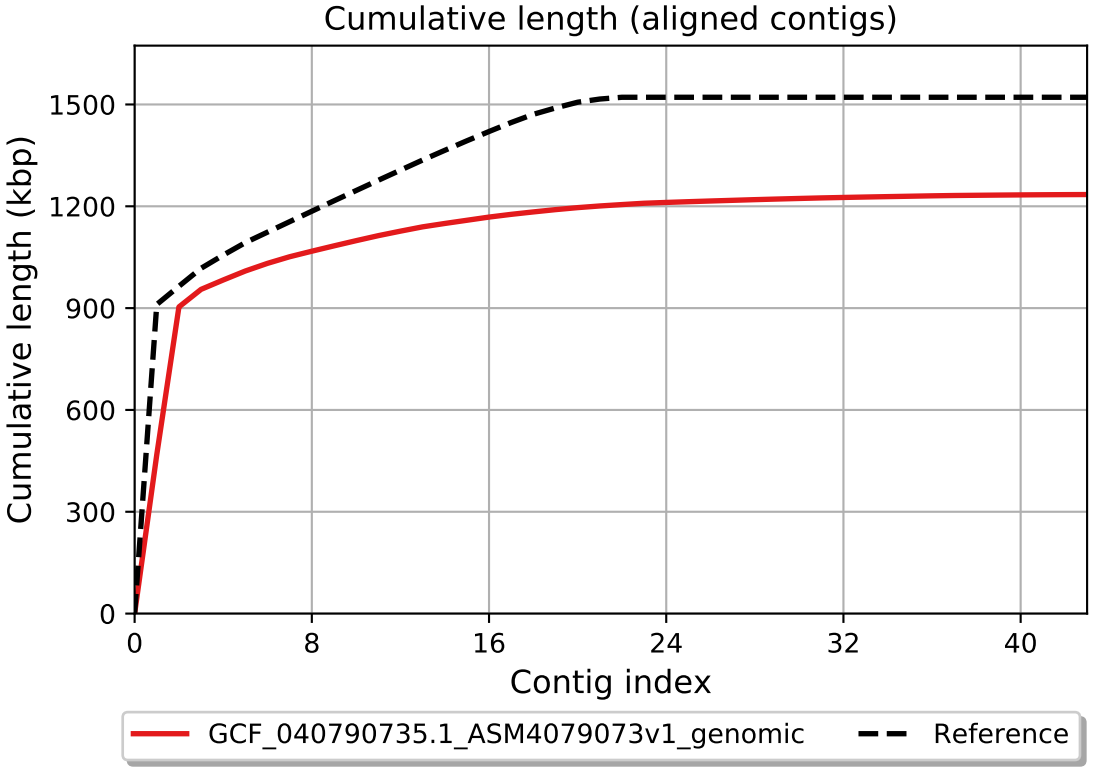

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCF_040790735.1_ASM4079073v1_genomic
Reference

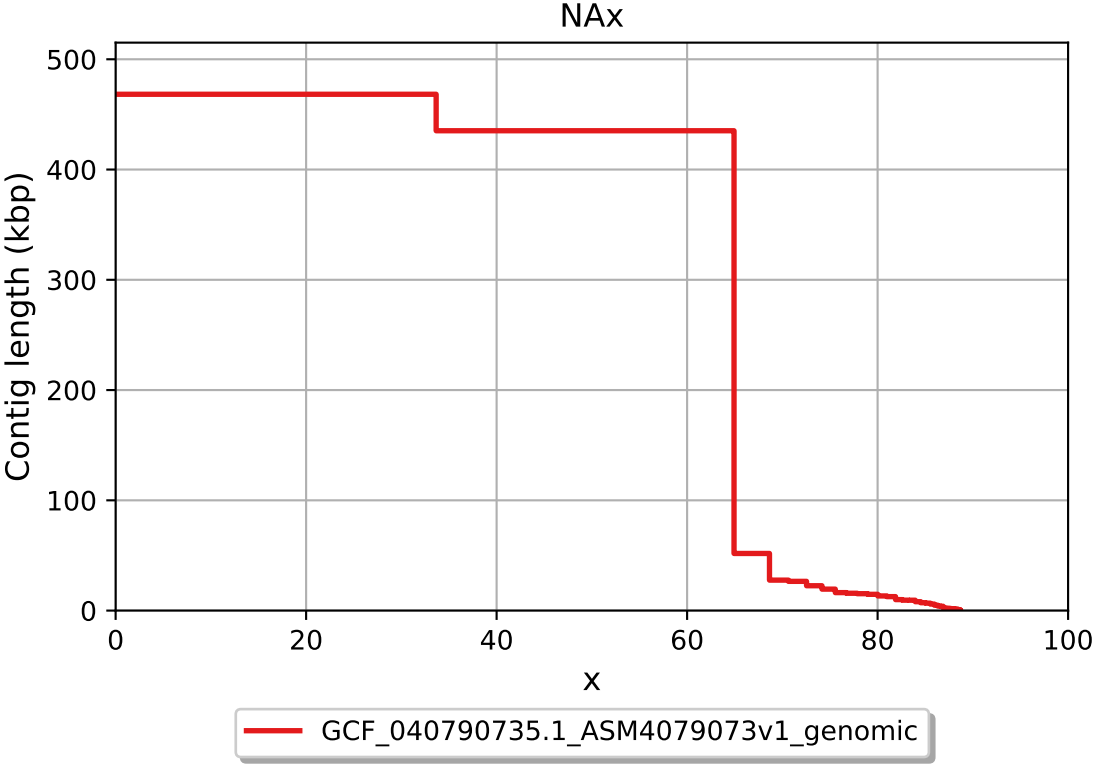

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCF_040790735.1_ASM4079073v1_genomic
Reference

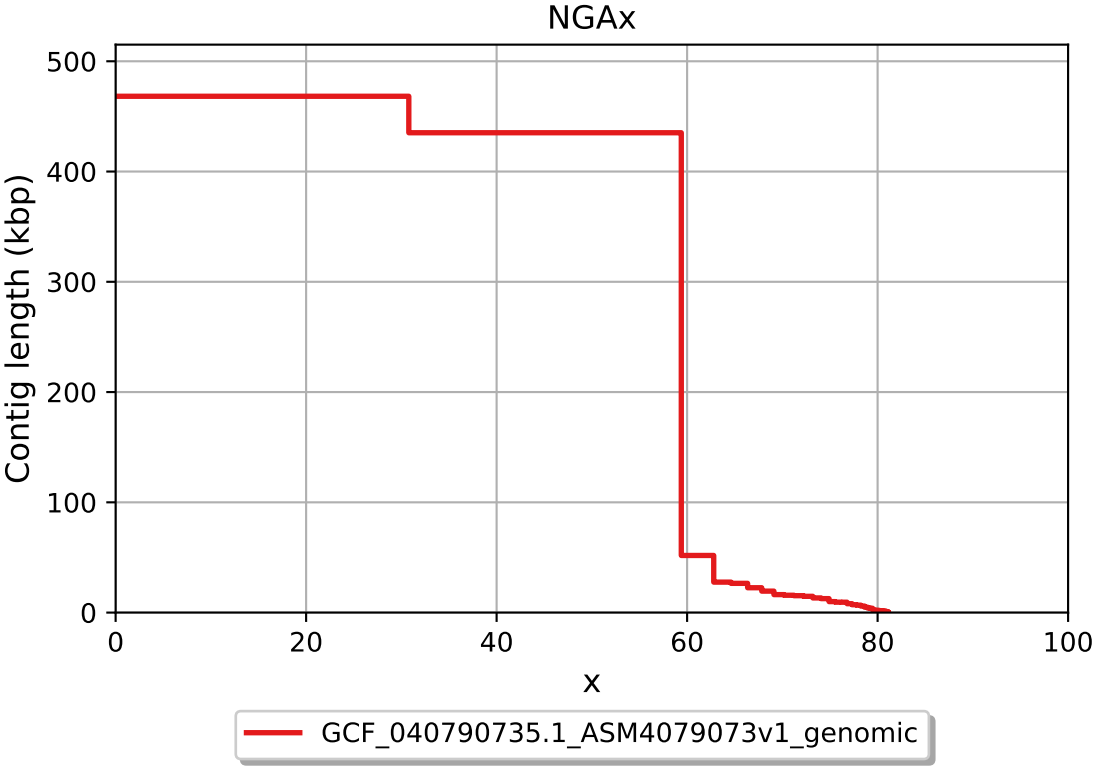

GCF_040790735.1_ASM4079073v1_genomic GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
GCF_040790735.1_ASM4079073v1_genomic

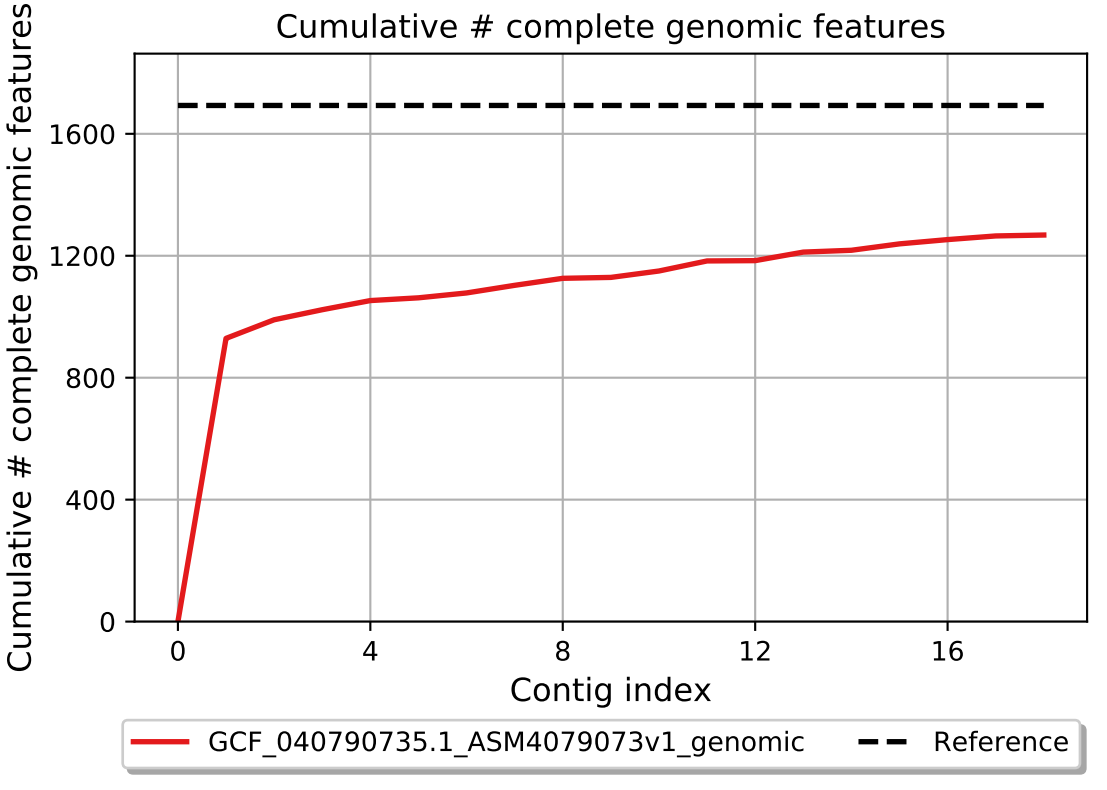

Misassemblies
20
16
12
8
4
0
GCF_040790735.1_ASM4079073v1_genomic
relocations
translocations

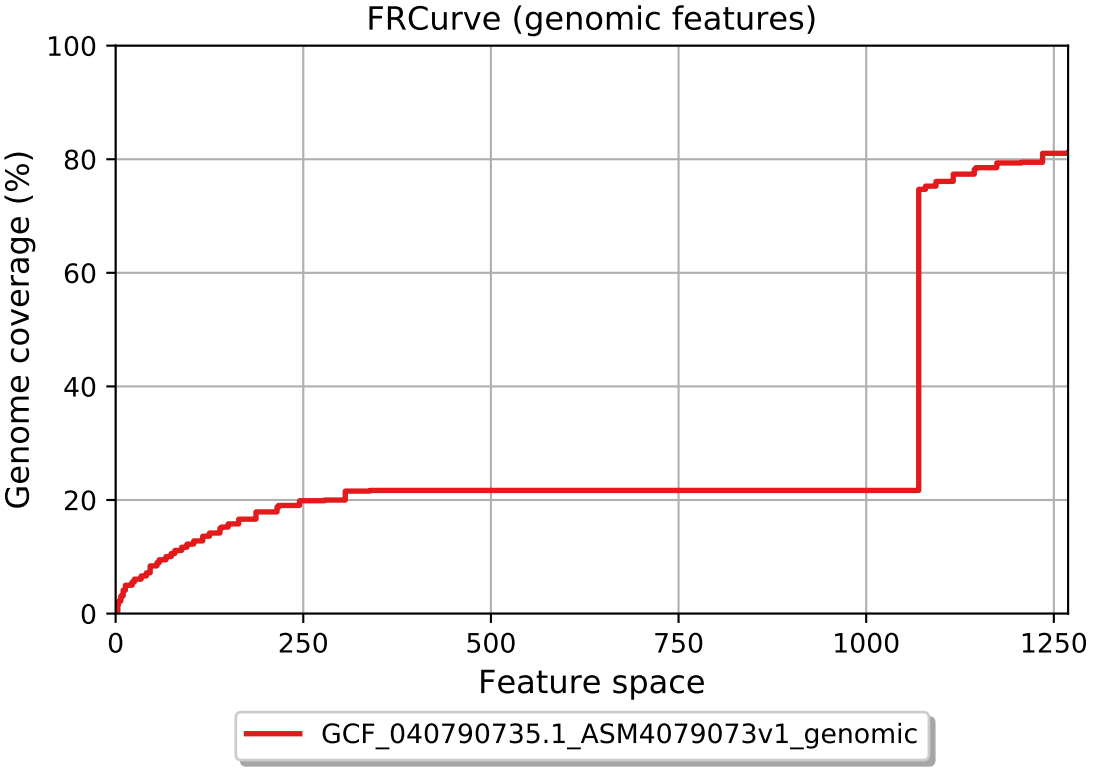

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
GCF_040790735.1_ASM4079073v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
GCF_040790735.1_ASM4079073v1_genomic
Reference


NAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
GCF_040790735.1_ASM4079073v1_genomic


NGAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
GCF_040790735.1_ASM4079073v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
4
8
12
16
Contig index
GCF_040790735.1_ASM4079073v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCF_040790735.1_ASM4079073v1_genomic