Report

	GCF_040790745.1_ASM4079074v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1371468
Total length (>= 1000 bp)	1371468
Total length (>= 5000 bp)	1371468
Total length (>= 10000 bp)	1362746
Total length (>= 25000 bp)	1260568
Total length (>= 50000 bp)	956638
# contigs	18
Largest contig	902797
Total length	1371468
Reference length	1521208
GC (%)	28.18
Reference GC (%)	28.18
N50	902797
NG50	902797
N90	26498
NG90	8722
auN	604810.6
auNG	545276.1
L50	1
LG50	1
L90	12
LG90	18
# misassemblies	18
# misassembled contigs	8
Misassembled contigs length	251347
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 14 part
Unaligned length	131138
Genome fraction (%)	80.962
Duplication ratio	1.006
# N's per 100 kbp	0.36
# mismatches per 100 kbp	860.85
# indels per 100 kbp	53.89
# genomic features	1284 + 53 part
Largest alignment	902617
Total aligned length	1239475
NA50	902617
NGA50	902617
NA90	912
NGA90	-
auNA	599585.0
auNGA	540564.9
LA50	1
LGA50	1
LA90	39
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

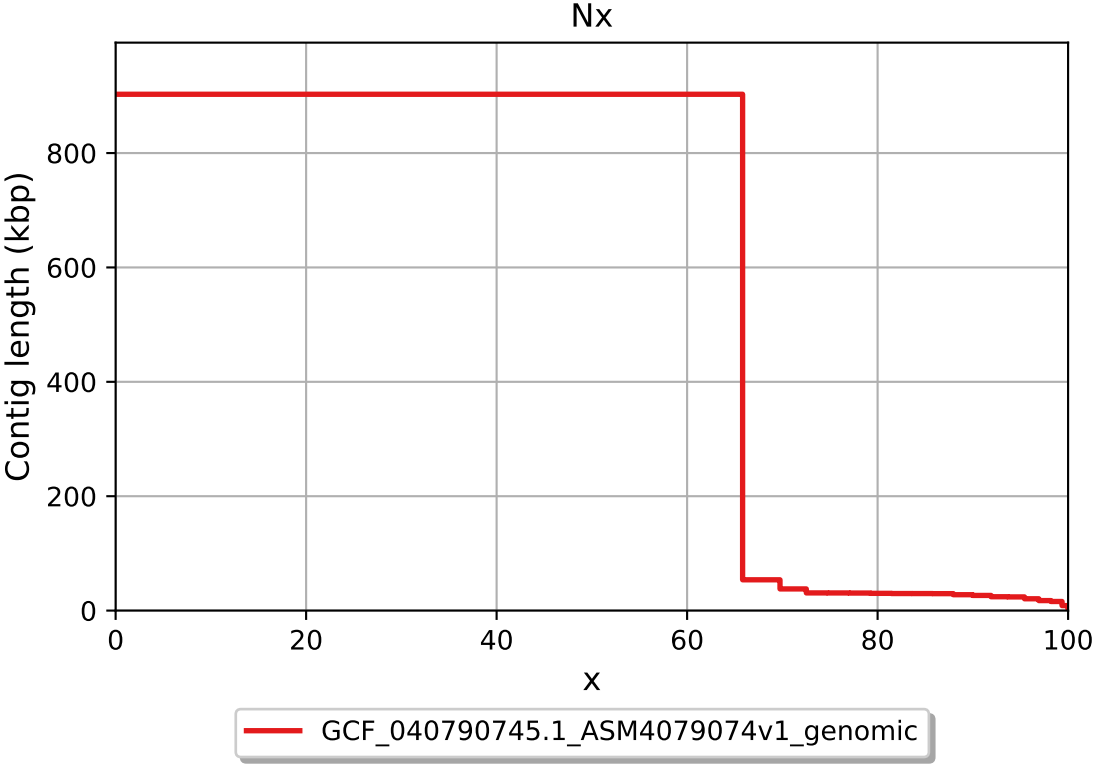
	GCF_040790745.1_ASM4079074v1_genomic
# misassemblies	18
# contig misassemblies	18
# c. relocations	4
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	251347
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	10670
# indels	668
# indels (<= 5 bp)	594
# indels (> 5 bp)	74
Indels length	3412

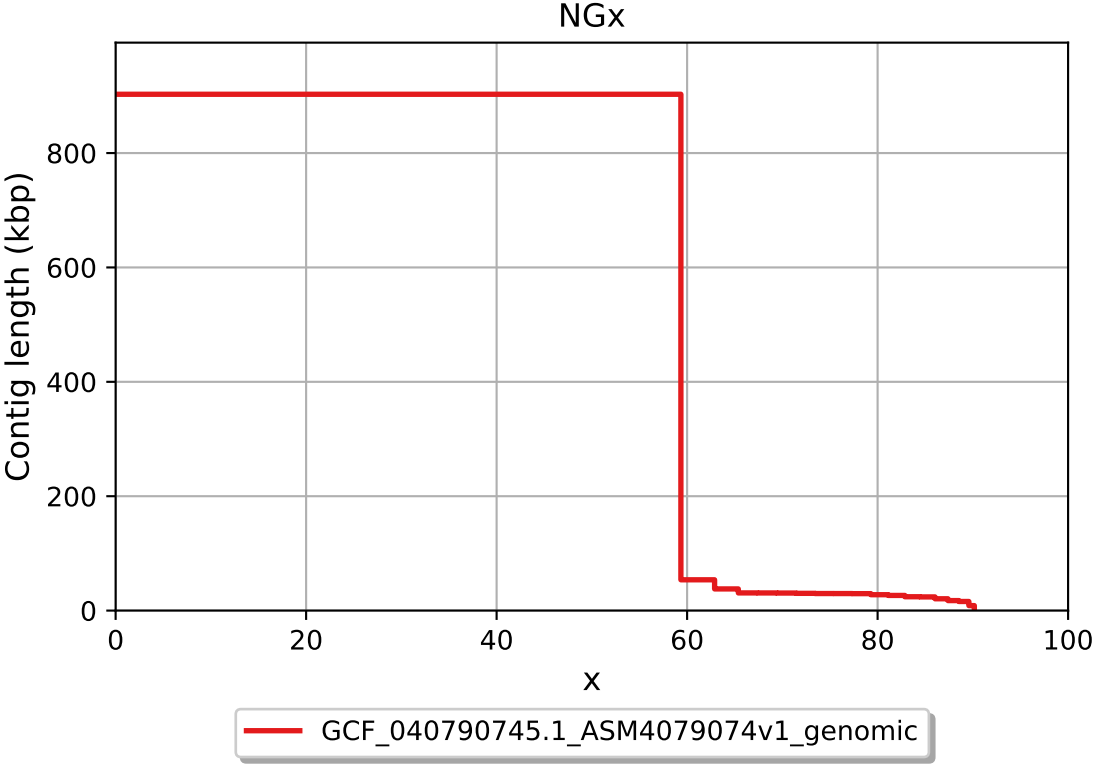
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

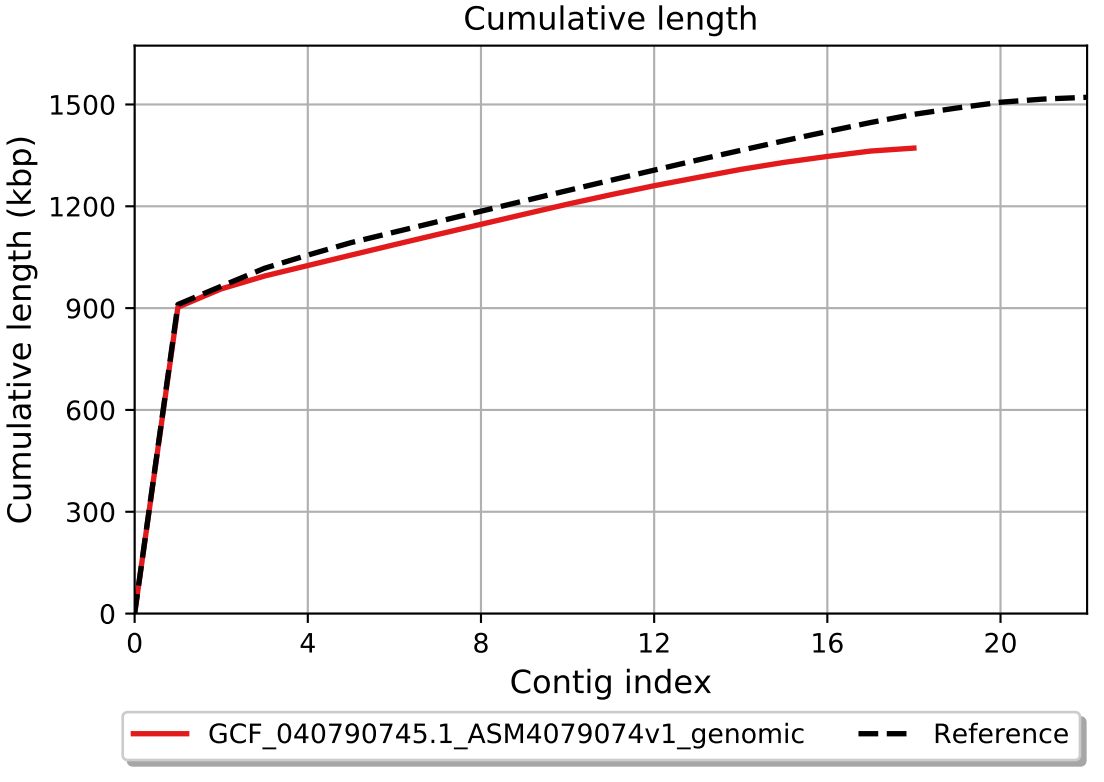
Unaligned report

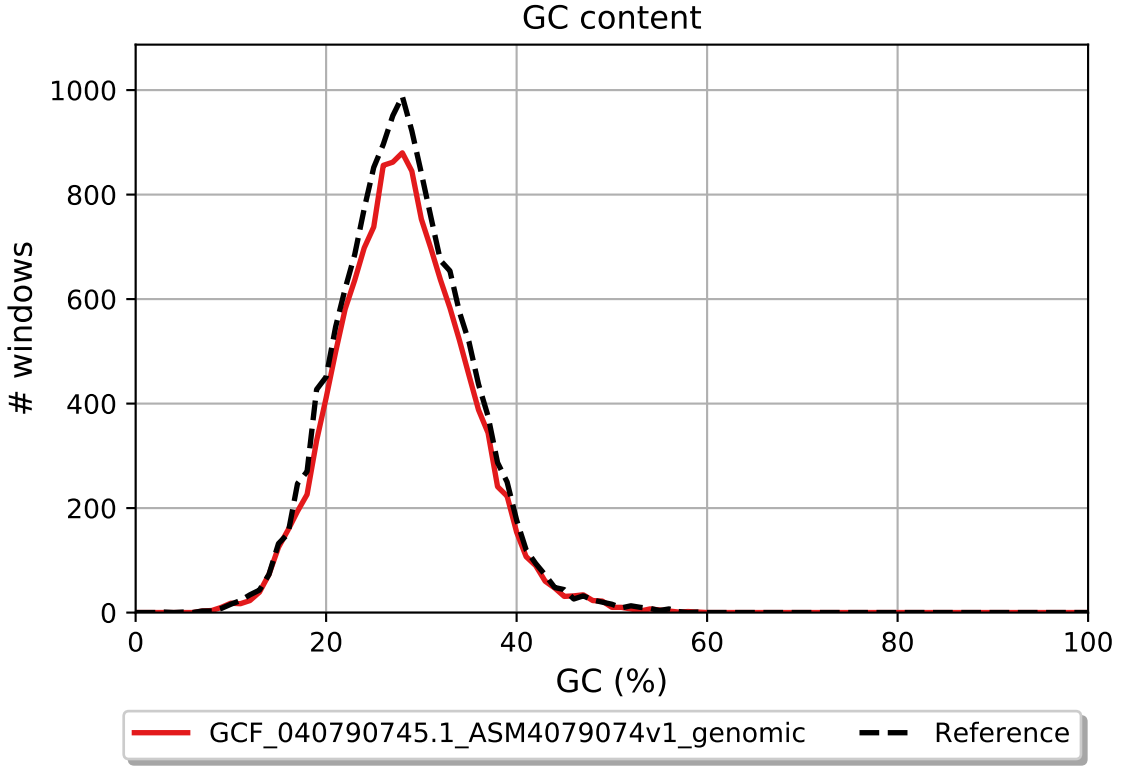
	GCF_040790745.1_ASM4079074v1_genomic
# fully unaligned contigs	1
Fully unaligned length	27767
# partially unaligned contigs	14
Partially unaligned length	103371
# N's	5

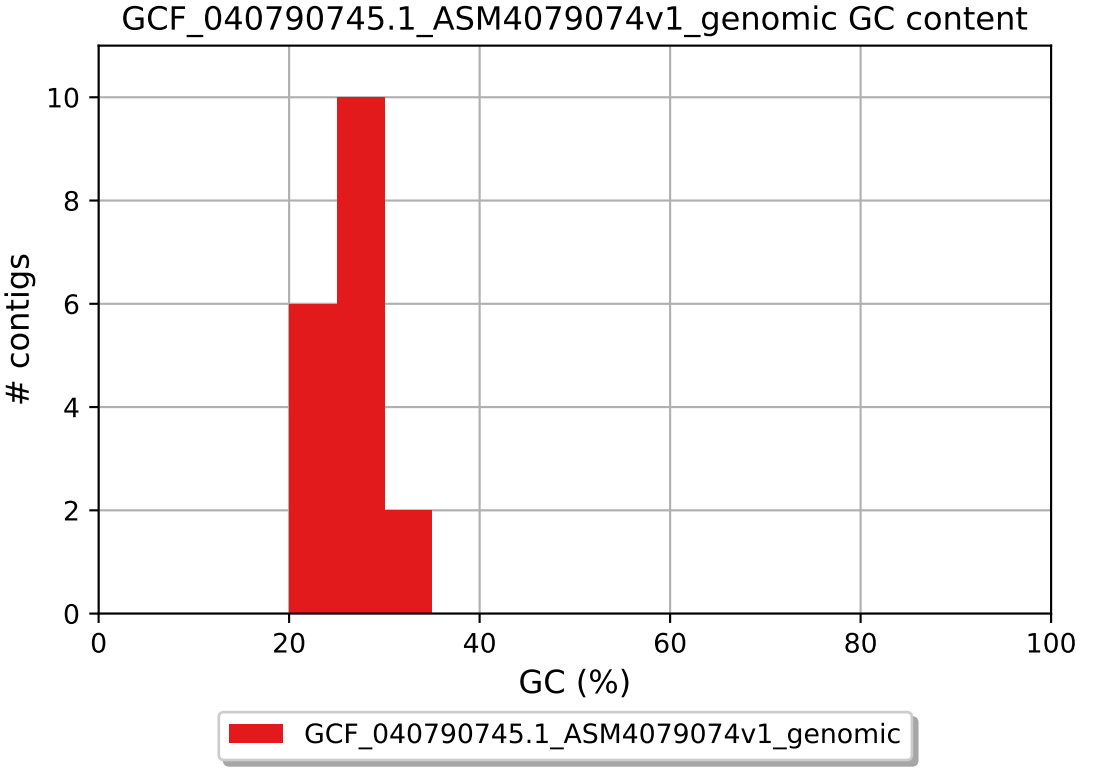
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

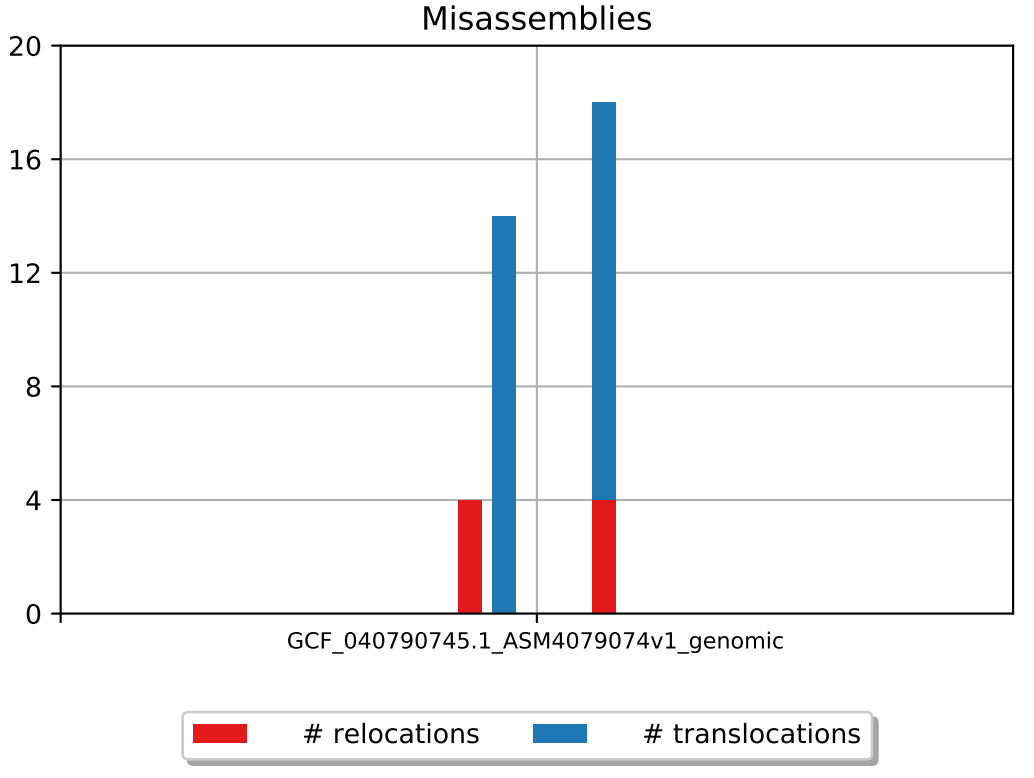

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790745.1_ASM4079074v1_genomic

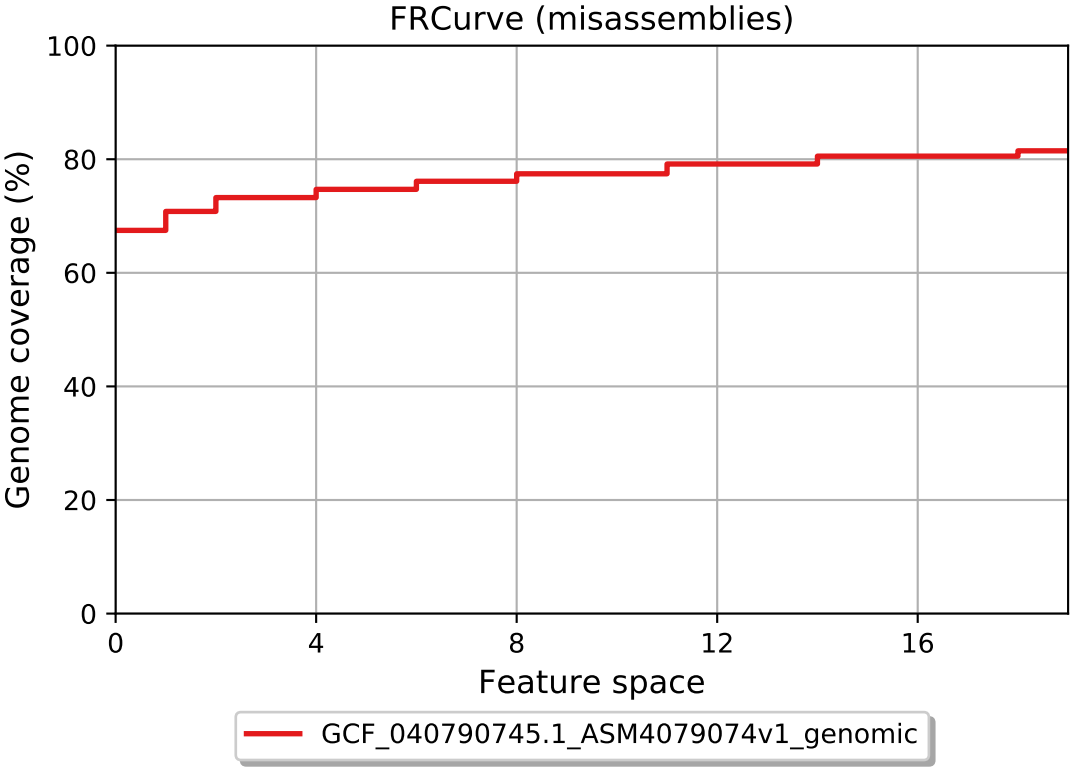

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790745.1_ASM4079074v1_genomic

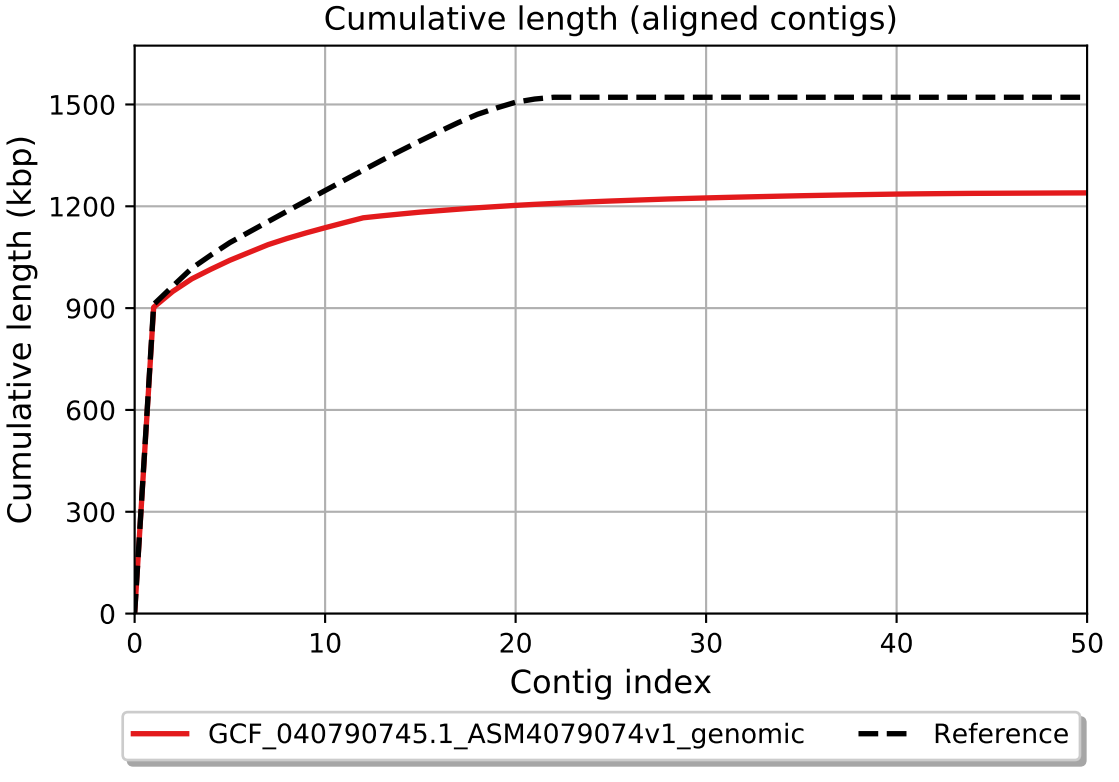

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCF_040790745.1_ASM4079074v1_genomic
Reference

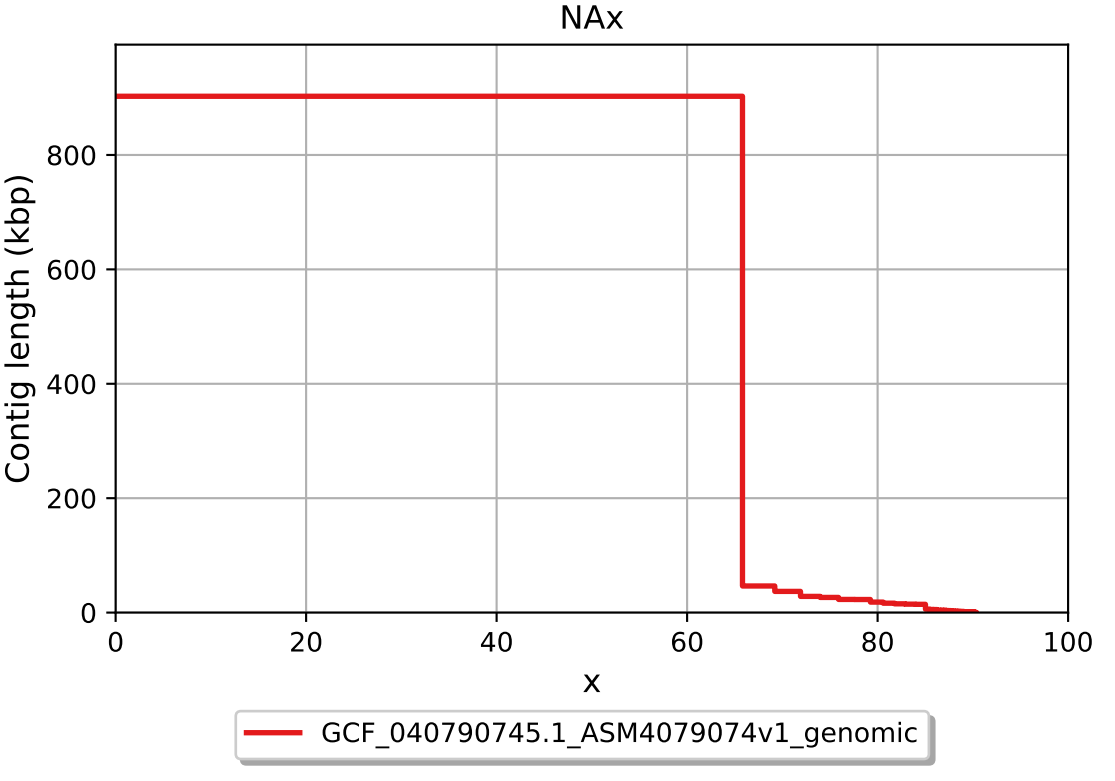

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCF_040790745.1_ASM4079074v1_genomic
Reference

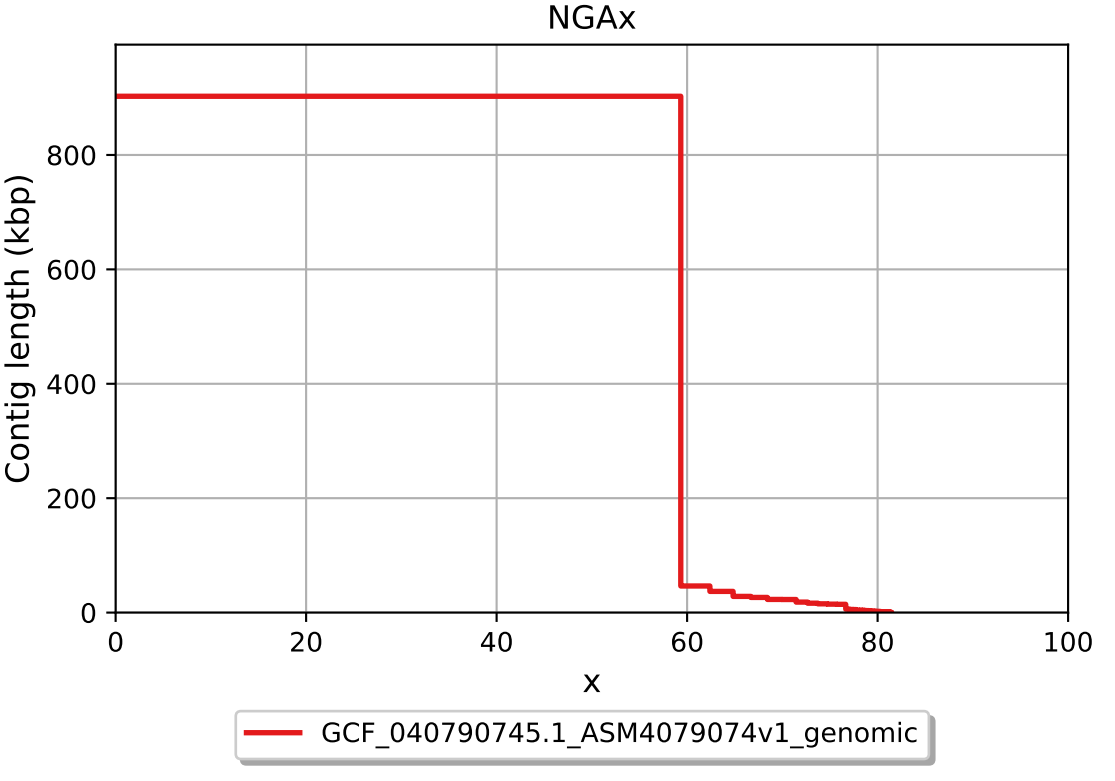

GCF_040790745.1_ASM4079074v1_genomic GC content
contigs
0
2
4
6
8
10
0
20
40
60
80
100
GC (%)
GCF_040790745.1_ASM4079074v1_genomic

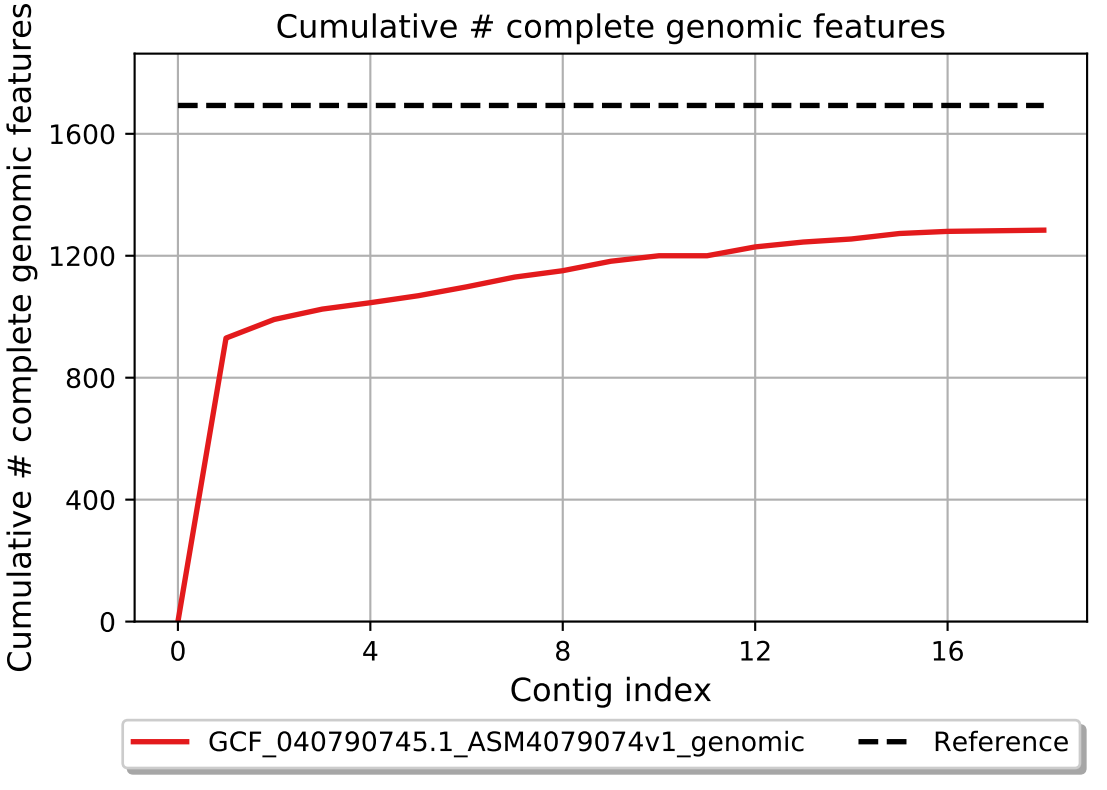

Misassemblies
20
16
12
8
4
0
GCF_040790745.1_ASM4079074v1_genomic
relocations
translocations

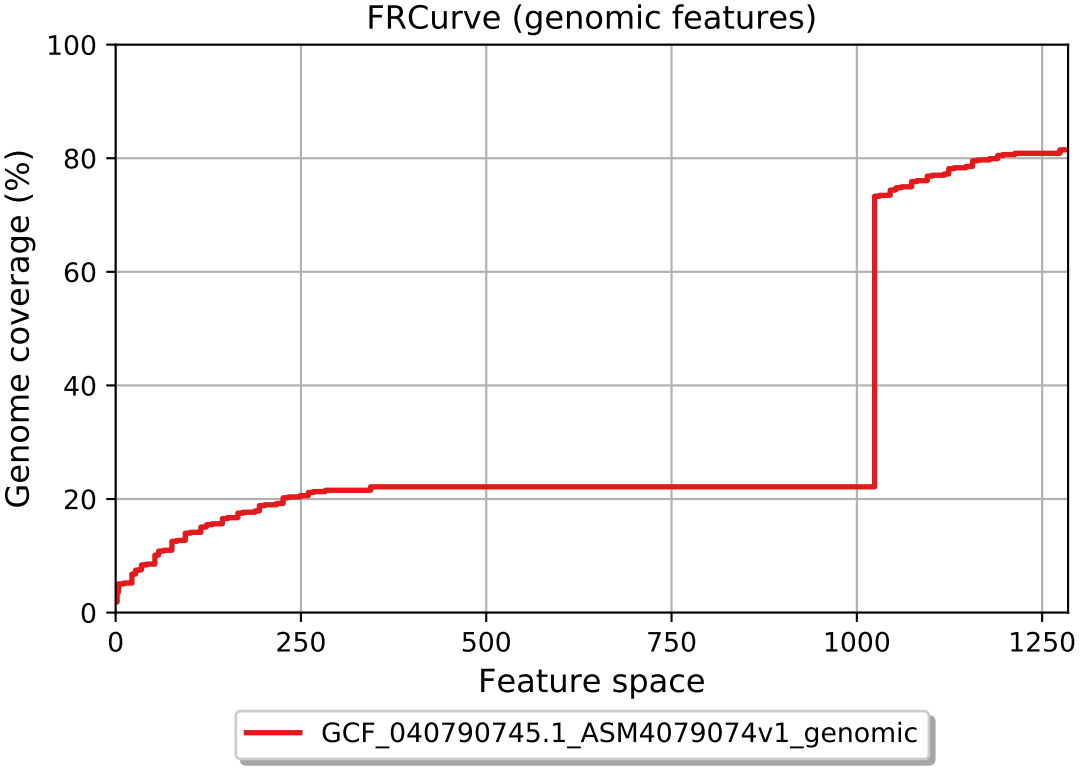

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
Feature space
GCF_040790745.1_ASM4079074v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
Contig index
GCF_040790745.1_ASM4079074v1_genomic
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790745.1_ASM4079074v1_genomic


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790745.1_ASM4079074v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
GCF_040790745.1_ASM4079074v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
GCF_040790745.1_ASM4079074v1_genomic