Report

	GCF_040790765.1_ASM4079076v1_genomic
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1397896
Total length (>= 1000 bp)	1397896
Total length (>= 5000 bp)	1393143
Total length (>= 10000 bp)	1383762
Total length (>= 25000 bp)	1340585
Total length (>= 50000 bp)	963746
# contigs	19
Largest contig	910079
Total length	1397896
Reference length	1521208
GC (%)	28.28
Reference GC (%)	28.18
N50	910079
NG50	910079
N90	27762
NG90	18208
auN	603159.6
auNG	554266.3
L50	1
LG50	1
L90	12
LG90	17
# misassemblies	16
# misassembled contigs	6
Misassembled contigs length	149059
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	0 + 14 part
Unaligned length	171625
Genome fraction (%)	77.689
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	832.72
# indels per 100 kbp	44.26
# genomic features	1243 + 36 part
Largest alignment	904581
Total aligned length	1217932
NA50	904581
NGA50	904581
NA90	-
NGA90	-
auNA	589951.2
auNGA	542128.7
LA50	1
LGA50	1
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

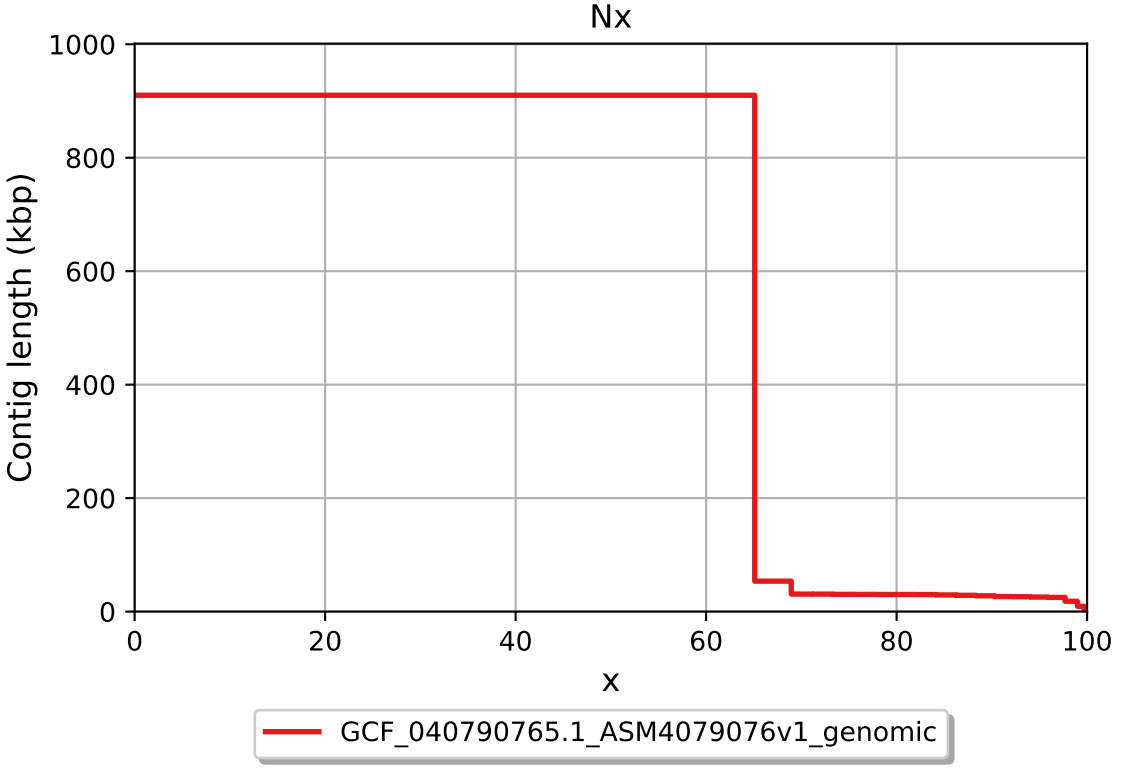
	GCF_040790765.1_ASM4079076v1_genomic
# misassemblies	16
# contig misassemblies	16
# c. relocations	1
# c. translocations	15
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	149059
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	10142
# indels	539
# indels (<= 5 bp)	484
# indels (> 5 bp)	55
Indels length	2855

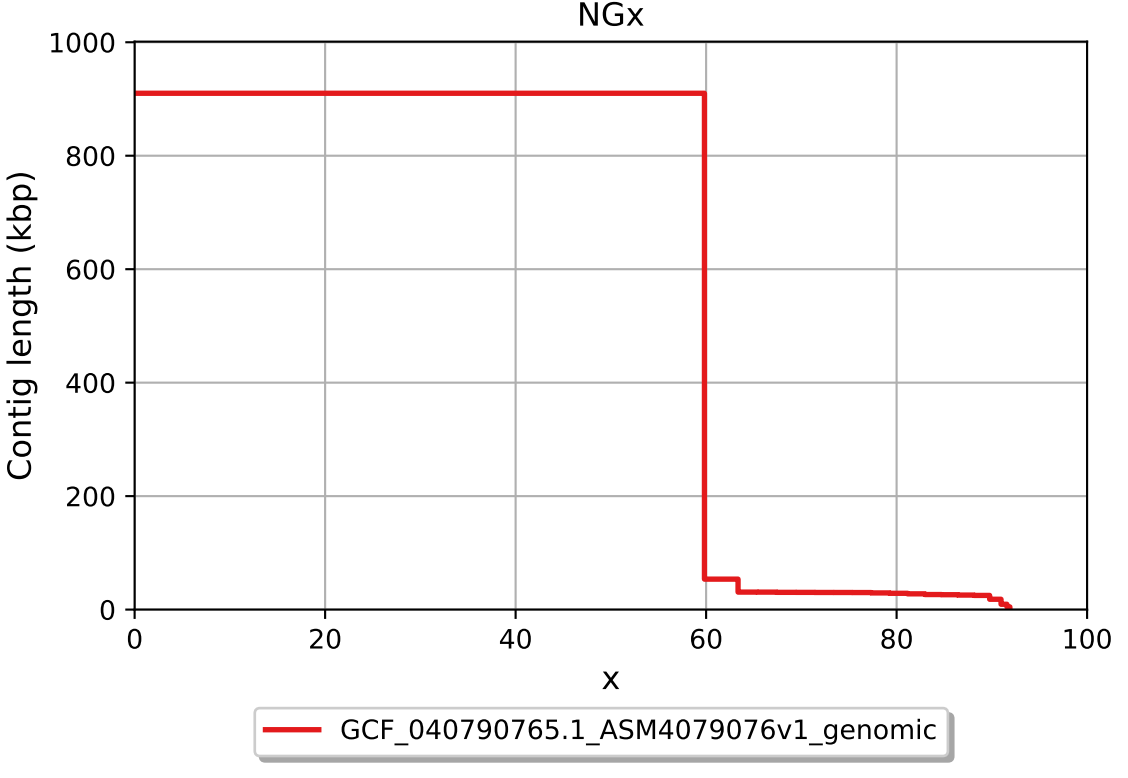
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

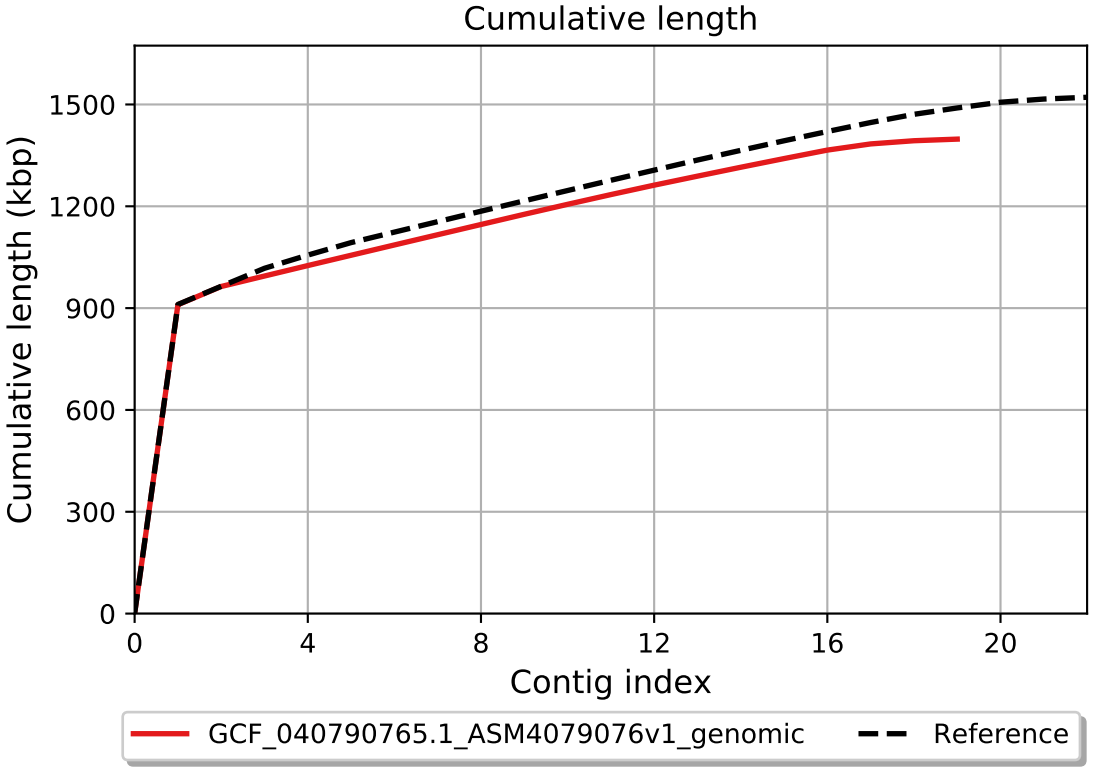
Unaligned report

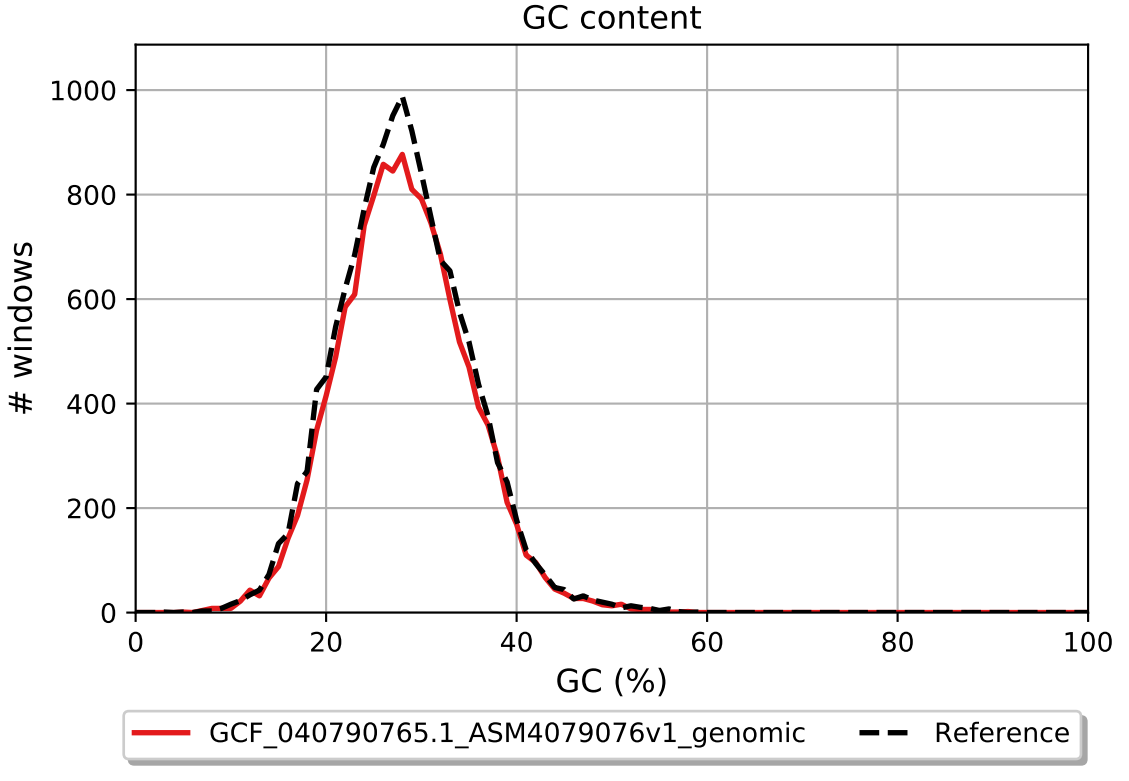
	GCF_040790765.1_ASM4079076v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
Partially unaligned length	171625
# N's	0

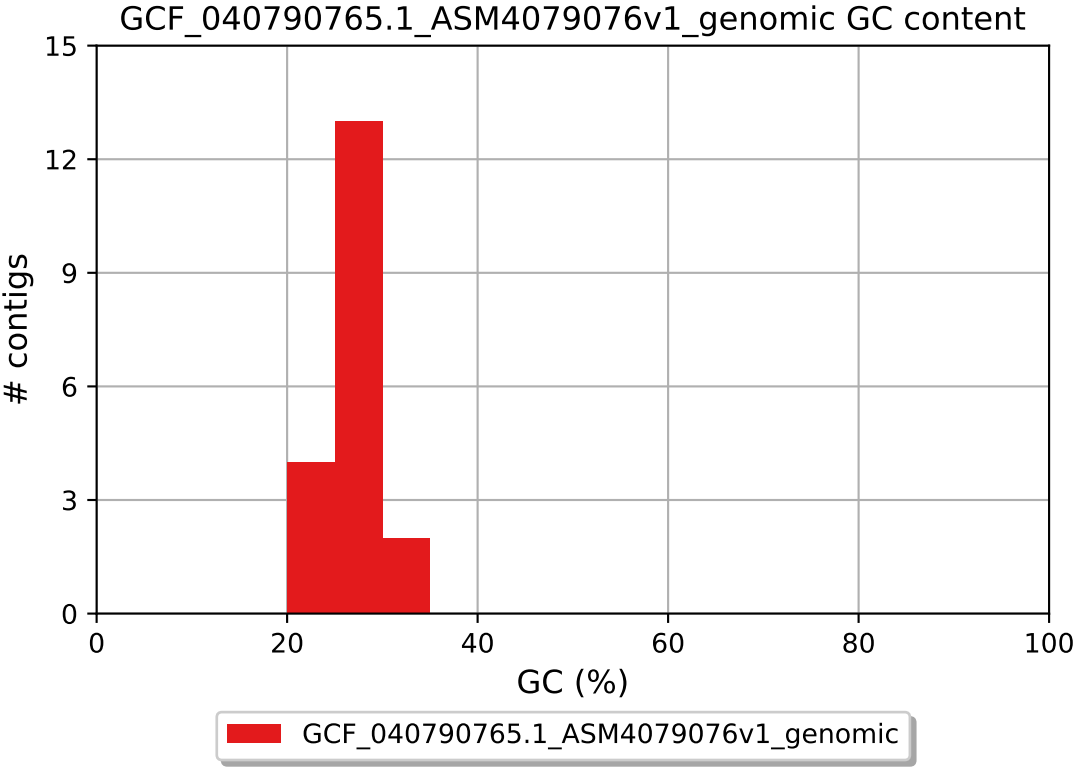
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

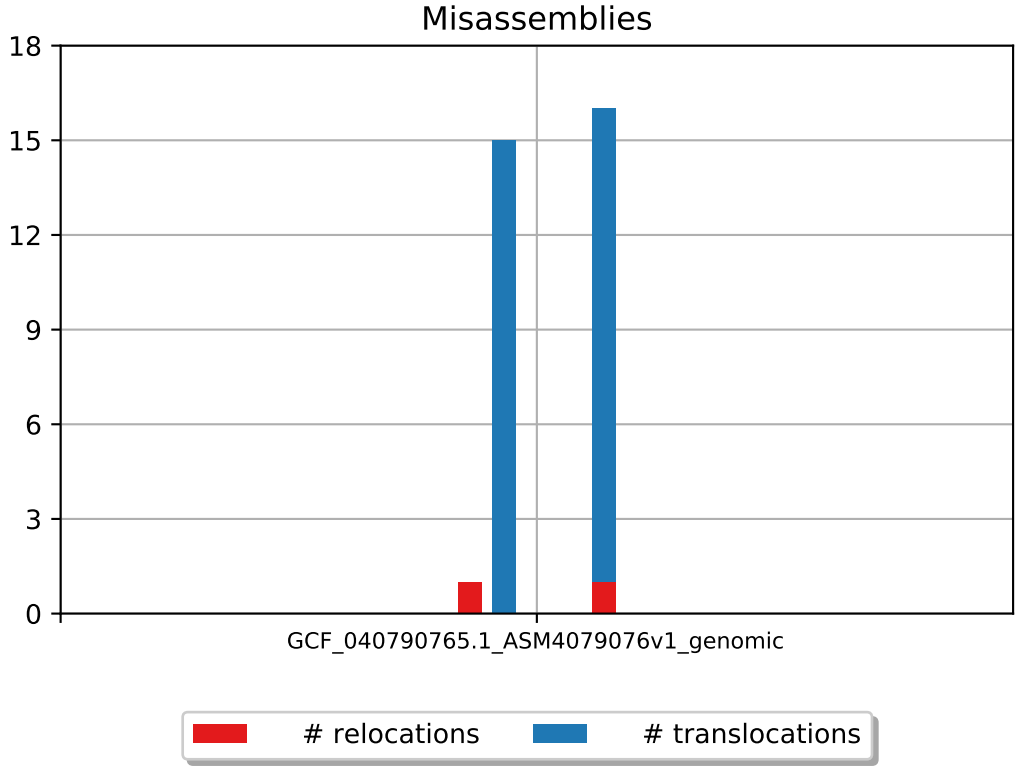

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790765.1_ASM4079076v1_genomic

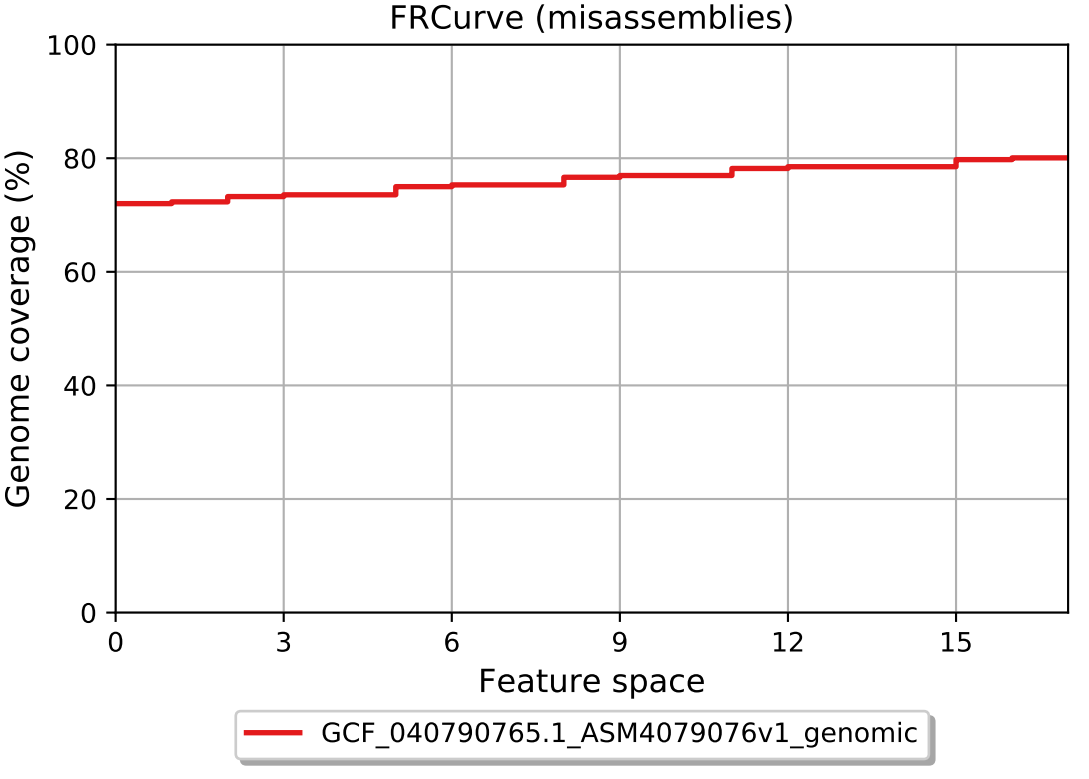

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790765.1_ASM4079076v1_genomic

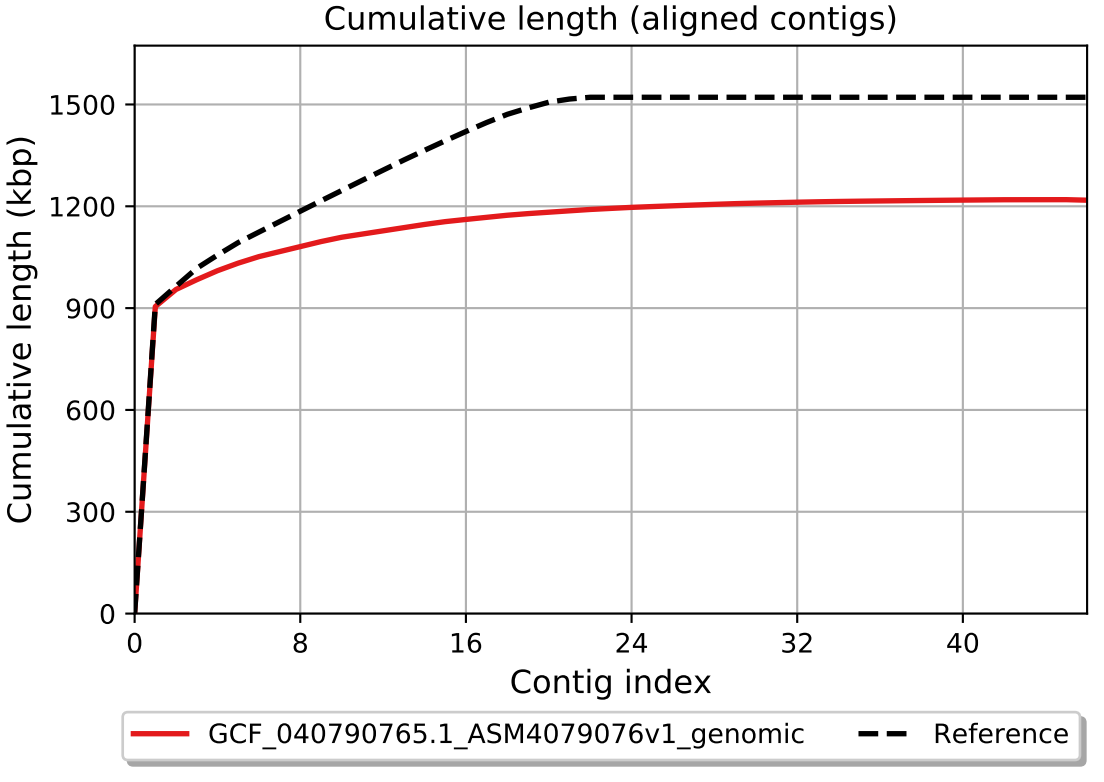

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCF_040790765.1_ASM4079076v1_genomic
Reference

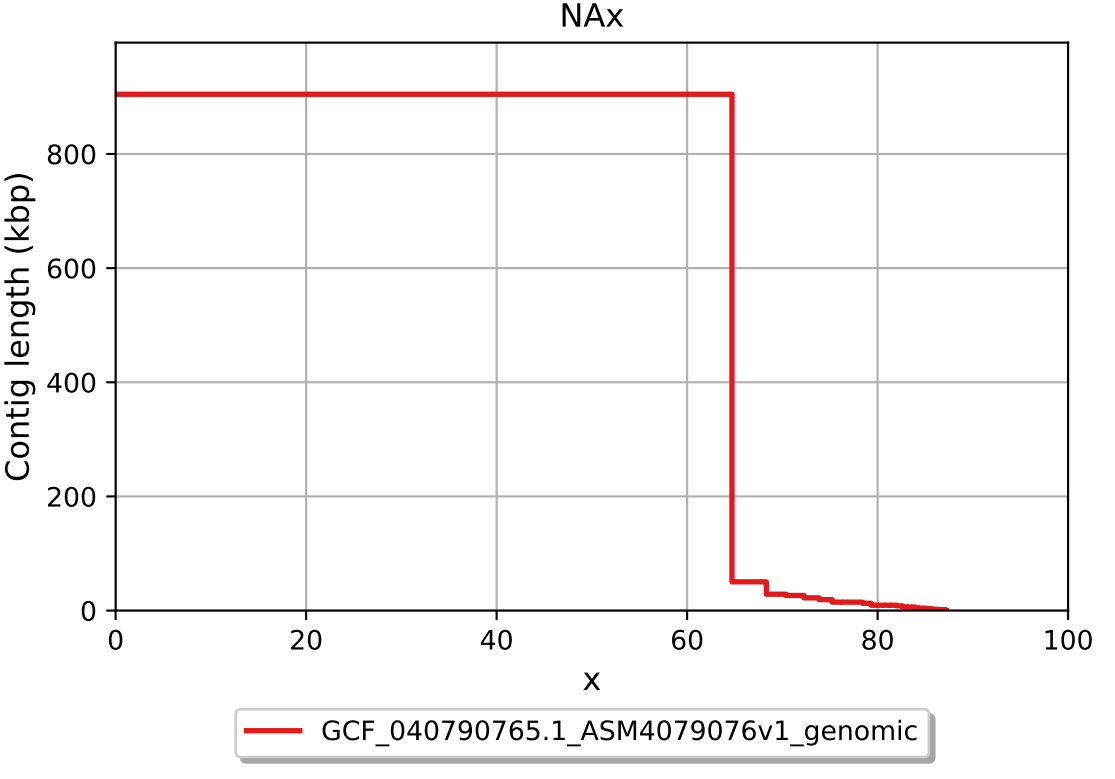

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCF_040790765.1_ASM4079076v1_genomic
Reference

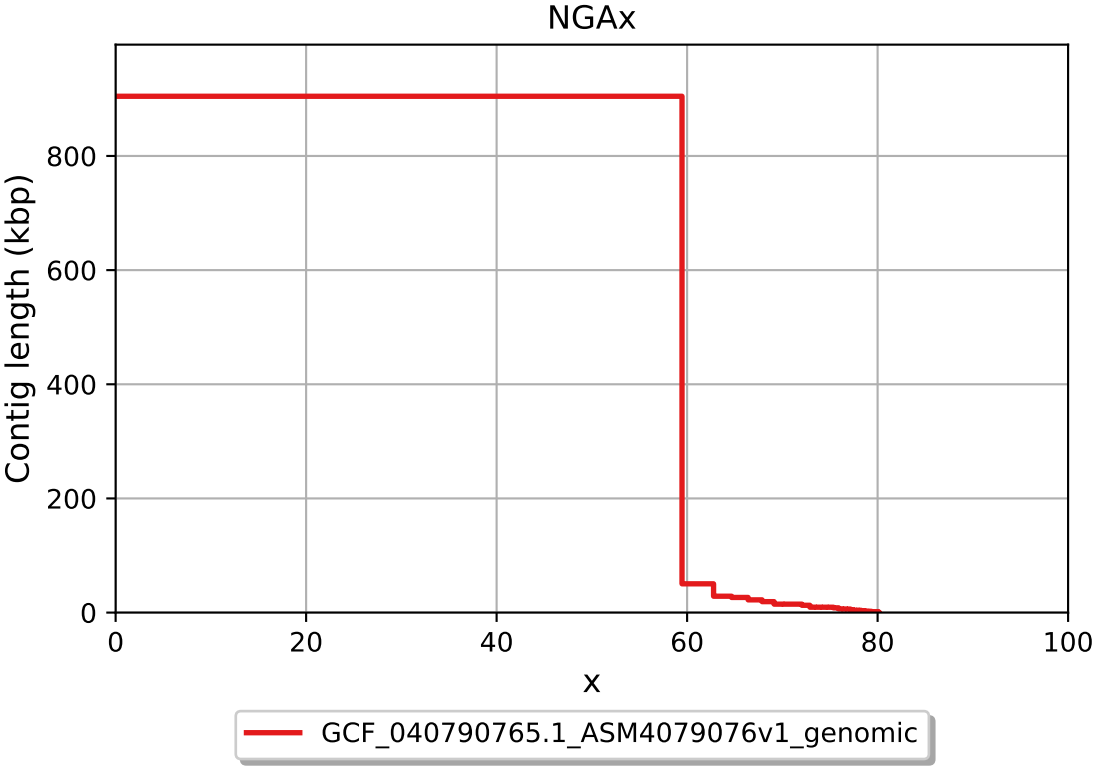

GCF_040790765.1_ASM4079076v1_genomic GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
GCF_040790765.1_ASM4079076v1_genomic

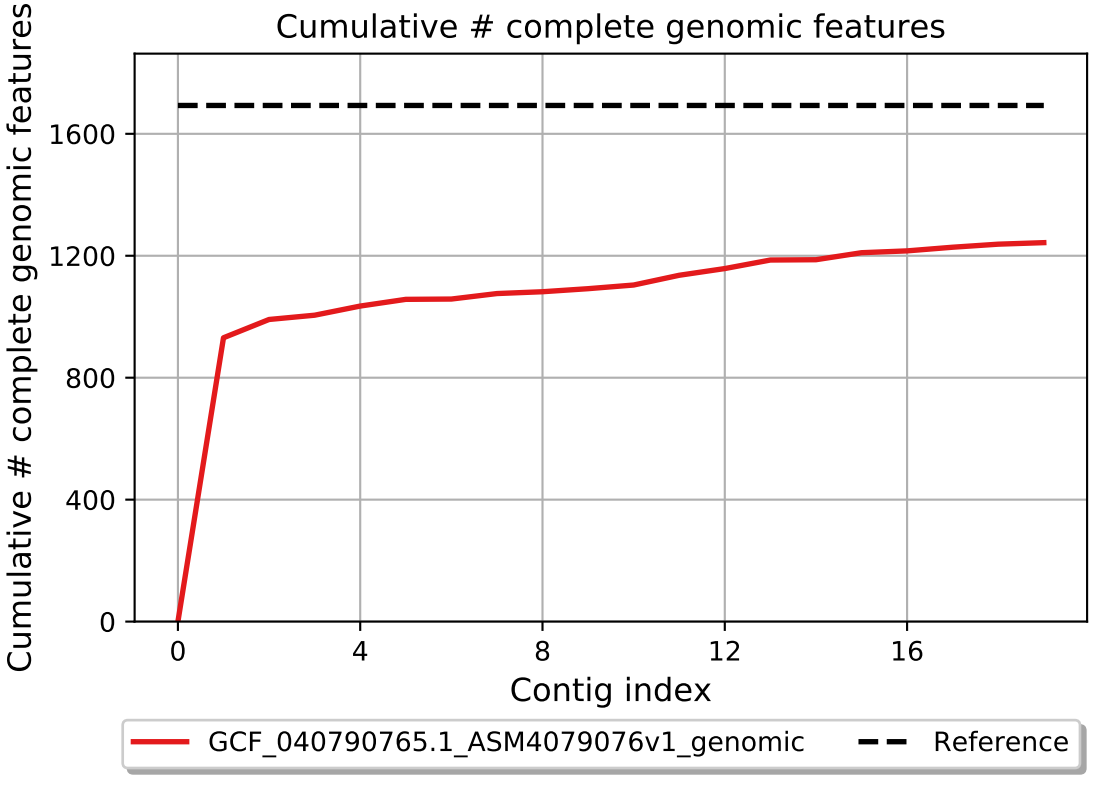

Misassemblies
18
15
12
9
6
3
0
GCF_040790765.1_ASM4079076v1_genomic
relocations
translocations

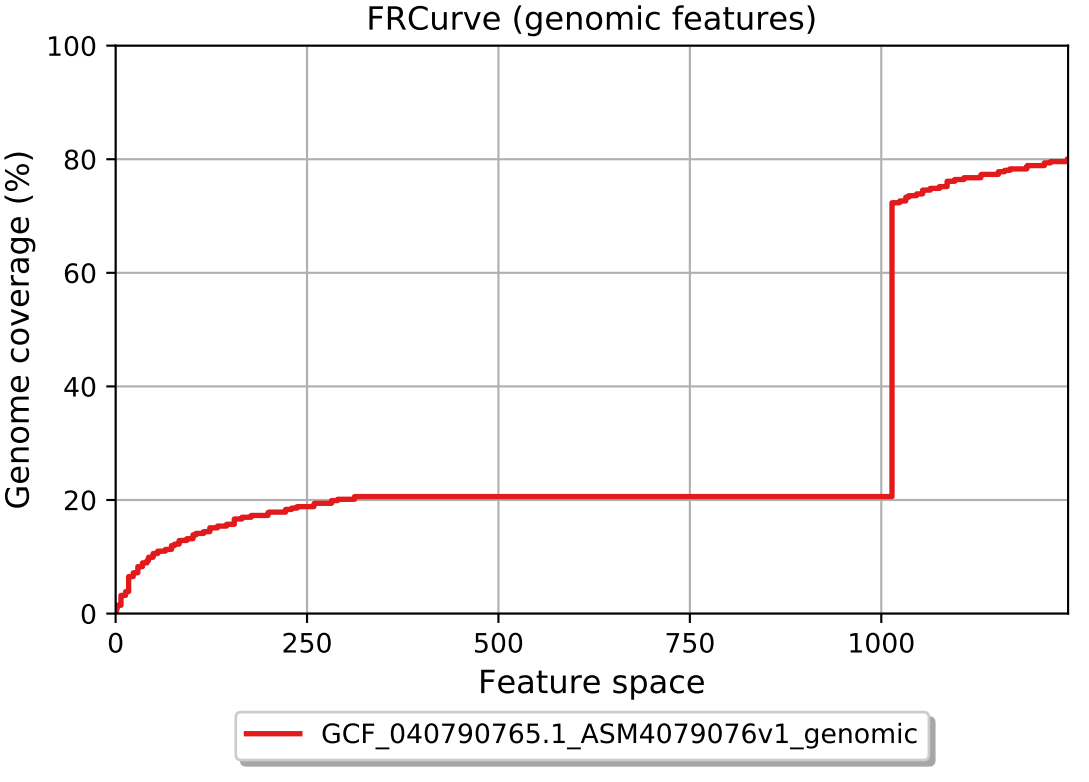

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
GCF_040790765.1_ASM4079076v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
GCF_040790765.1_ASM4079076v1_genomic
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790765.1_ASM4079076v1_genomic


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
GCF_040790765.1_ASM4079076v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
4
8
12
16
Contig index
GCF_040790765.1_ASM4079076v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
Feature space
GCF_040790765.1_ASM4079076v1_genomic