Report

	GCA_040790775.1_ASM4079077v1_genomic
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1417953
Total length (>= 1000 bp)	1417953
Total length (>= 5000 bp)	1417953
Total length (>= 10000 bp)	1417953
Total length (>= 25000 bp)	1357768
Total length (>= 50000 bp)	1014483
# contigs	17
Largest contig	907632
Total length	1417953
Reference length	1521208
GC (%)	28.07
Reference GC (%)	28.18
N50	907632
NG50	907632
N90	28647
NG90	24443
auN	593516.4
auNG	553230.3
L50	1
LG50	1
L90	12
LG90	15
# misassemblies	4
# misassembled contigs	2
Misassembled contigs length	53090
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	2903
Genome fraction (%)	92.908
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.06
# indels per 100 kbp	3.96
# genomic features	1538 + 9 part
Largest alignment	907632
Total aligned length	1414283
NA50	907632
NGA50	907632
NA90	28599
NGA90	20854
auNA	593283.5
auNGA	553013.2
LA50	1
LGA50	1
LA90	12
LGA90	15

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

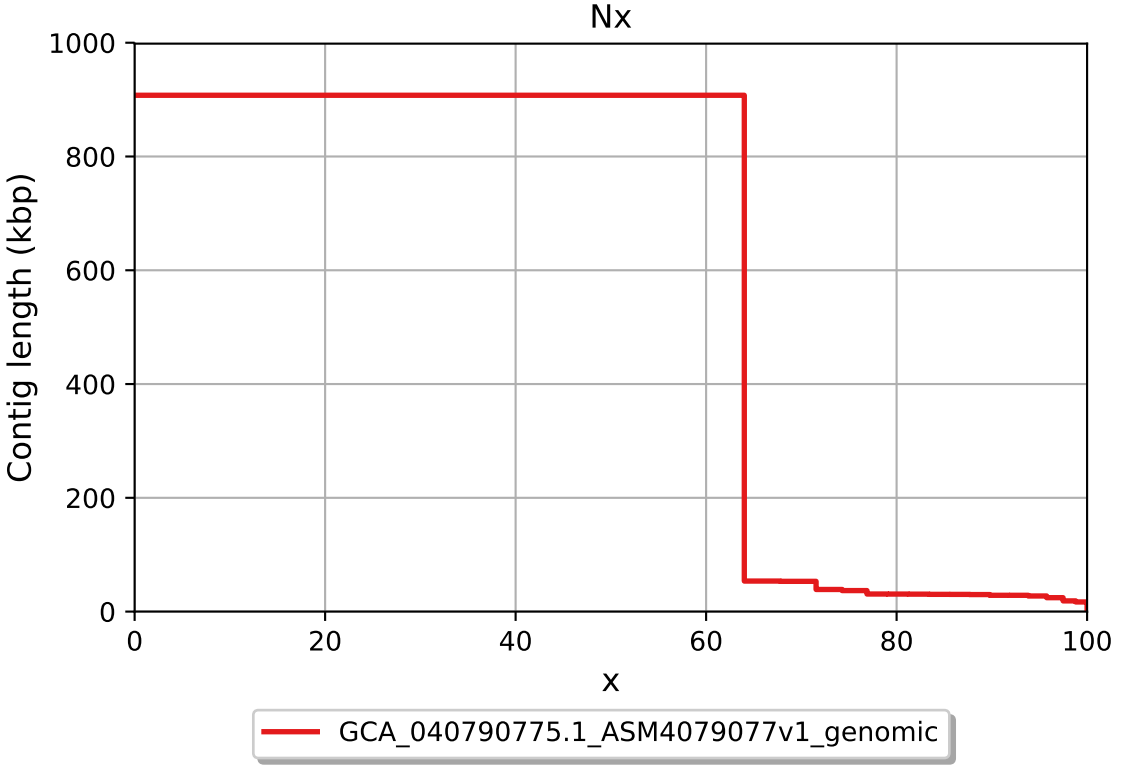
	GCA_040790775.1_ASM4079077v1_genomic
# misassemblies	4
# contig misassemblies	4
# c. relocations	2
# c. translocations	2
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	53090
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	15
# indels	56
# indels (<= 5 bp)	51
# indels (> 5 bp)	5
Indels length	249

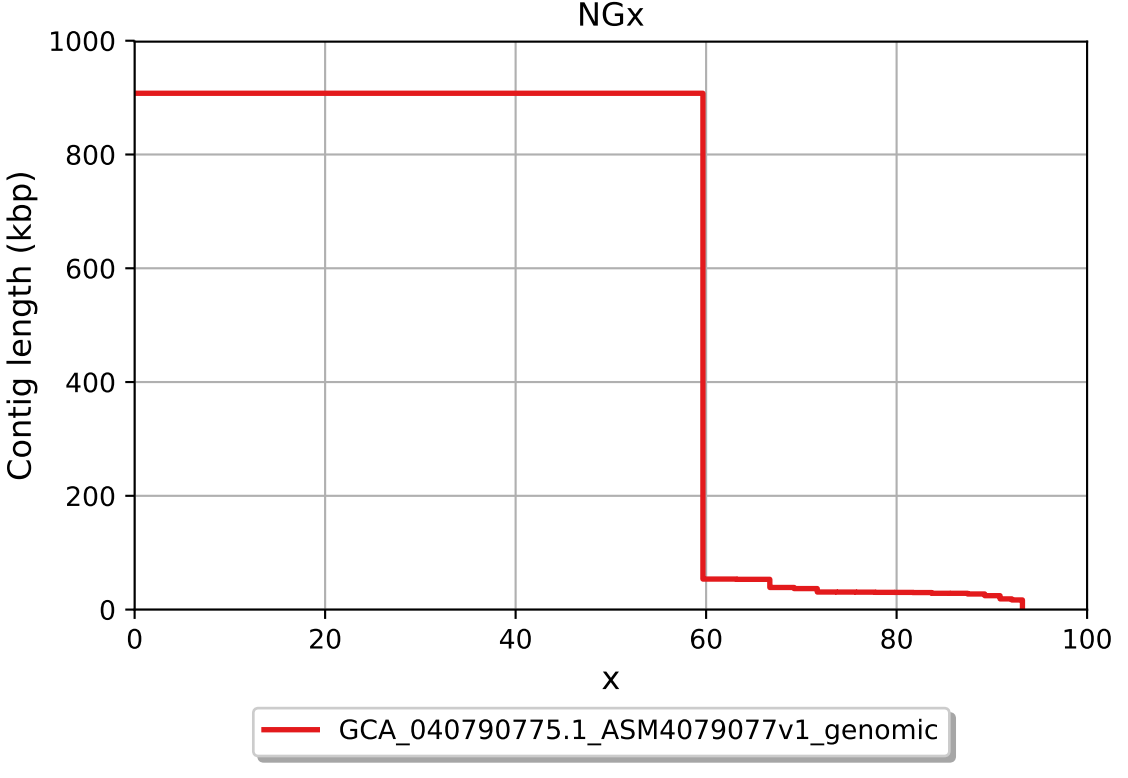
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

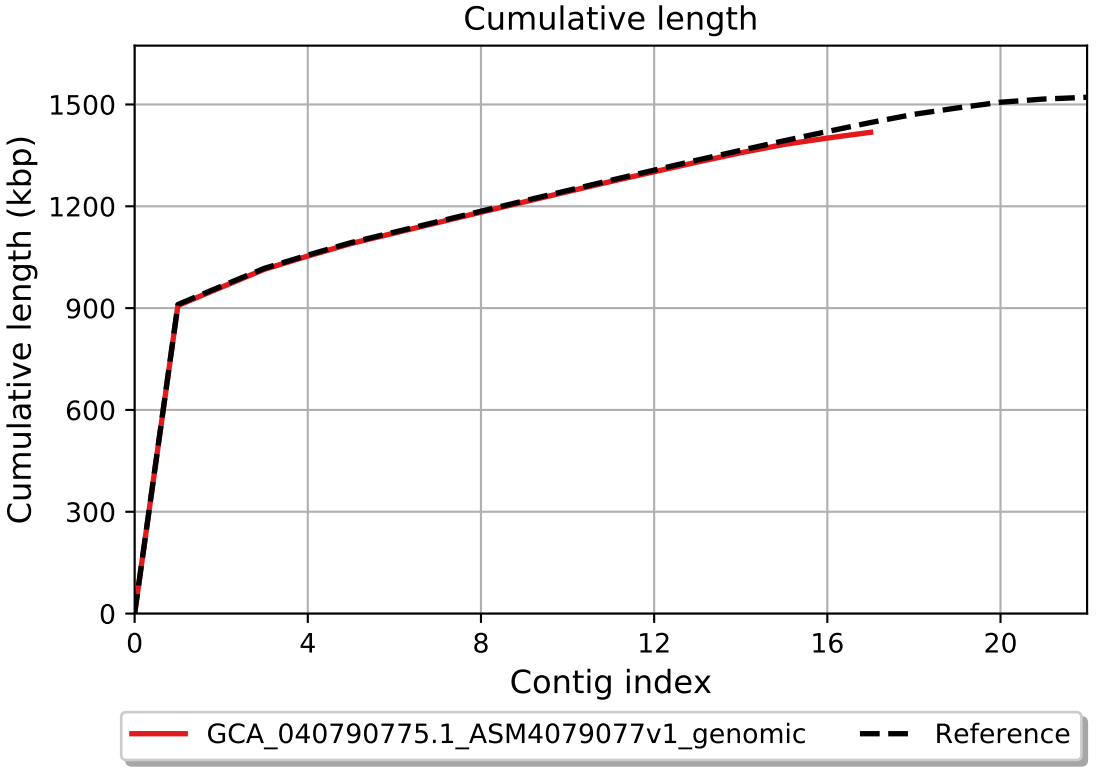
Unaligned report

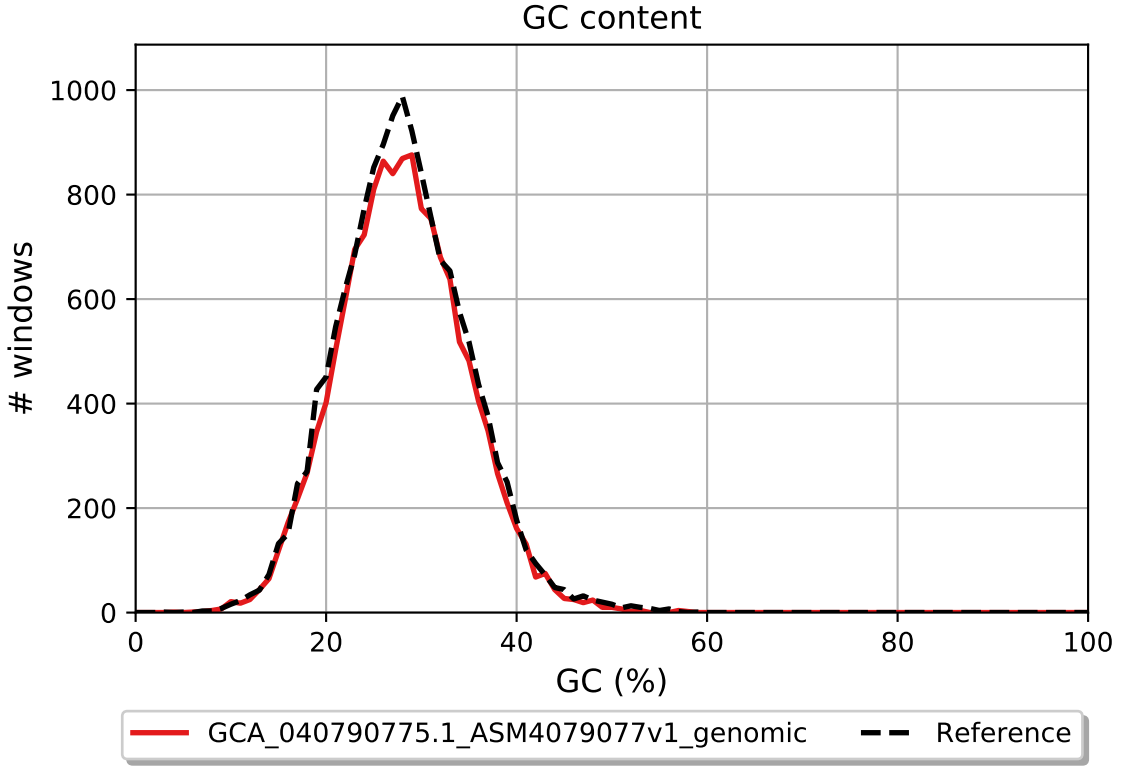
	GCA_040790775.1_ASM4079077v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2903
# N's	0

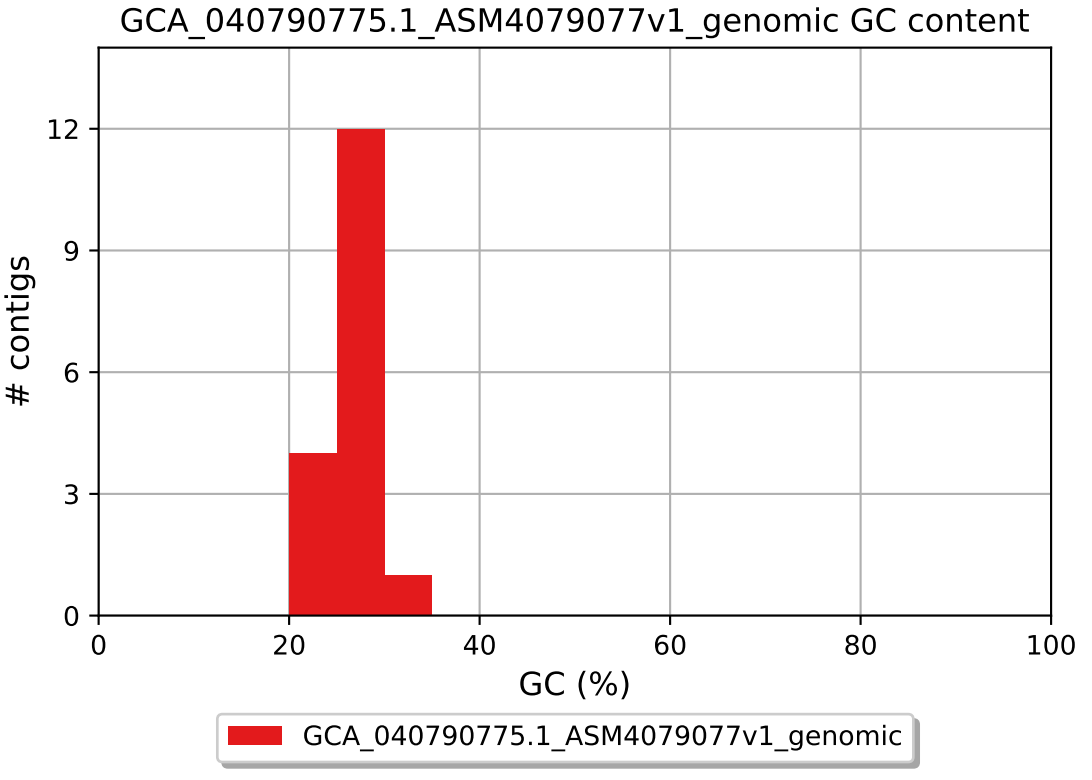
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

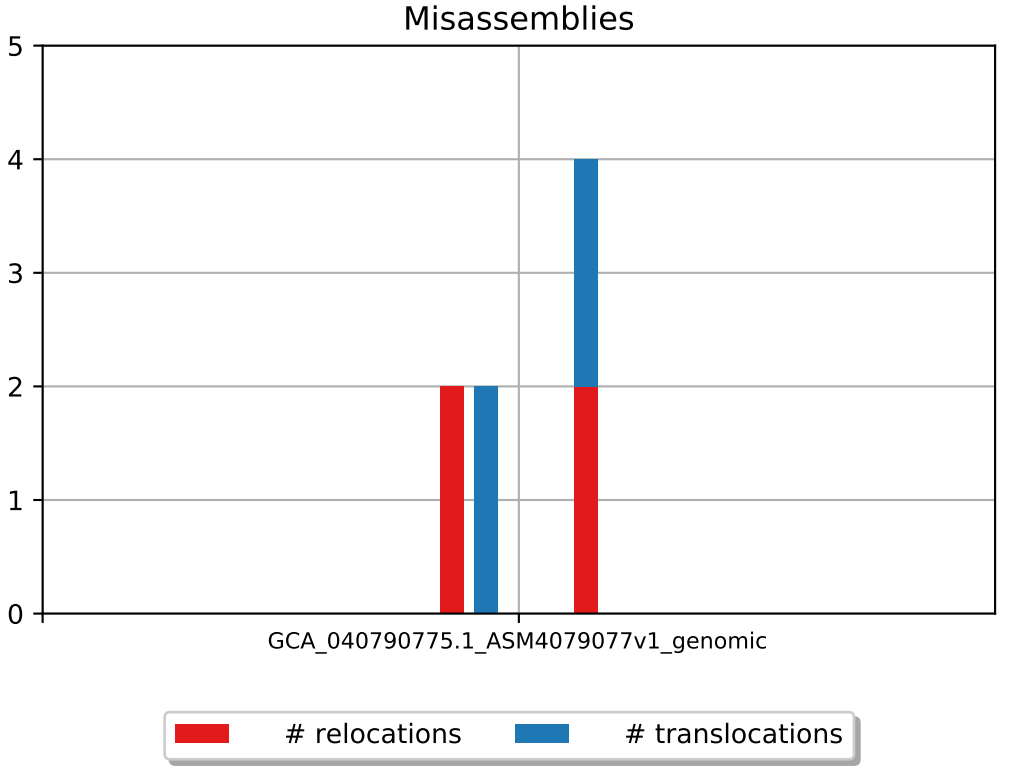

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_040790775.1_ASM4079077v1_genomic

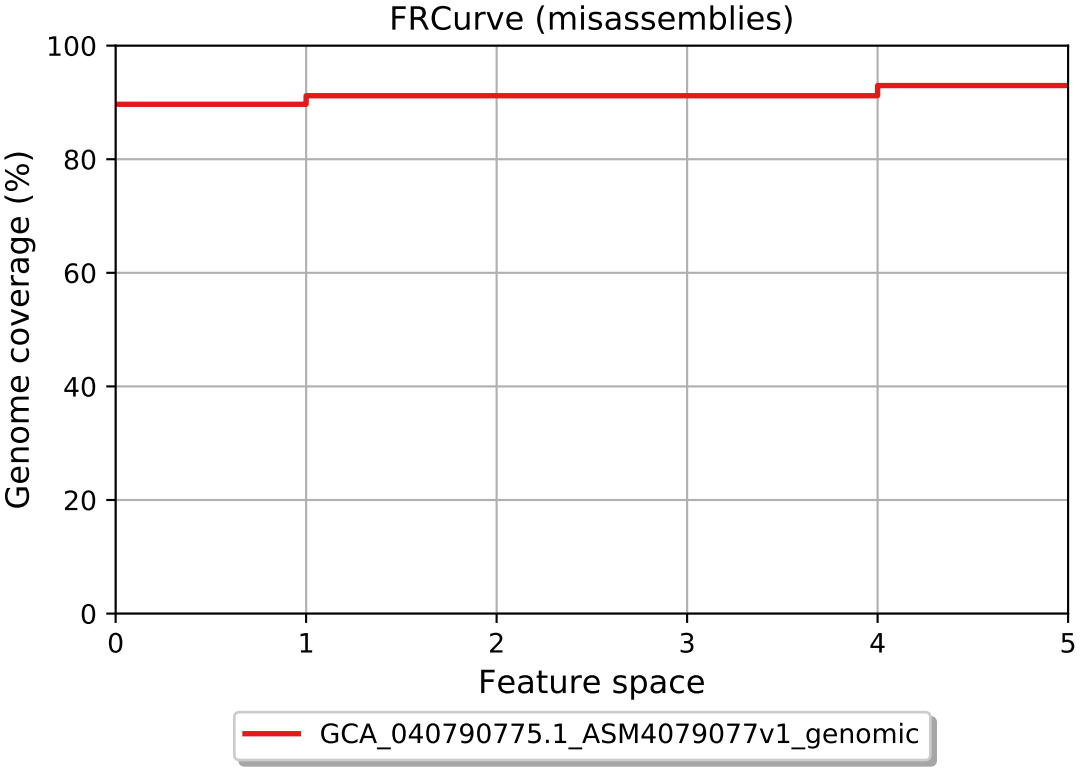

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_040790775.1_ASM4079077v1_genomic

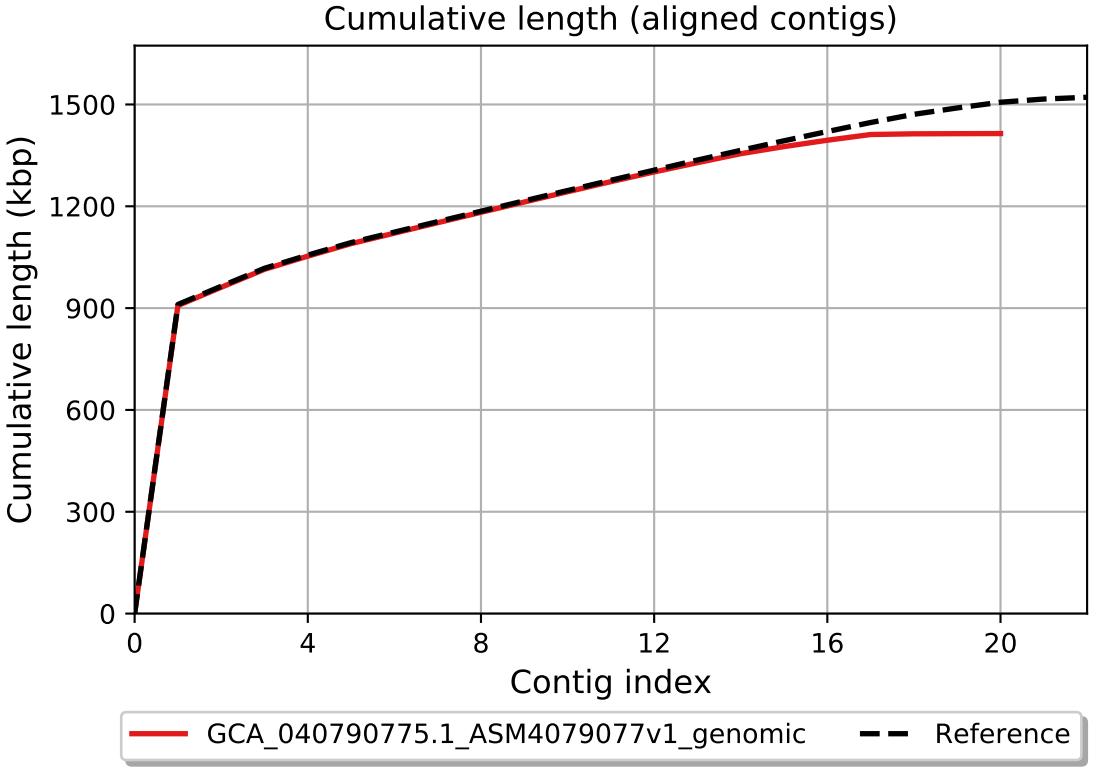

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_040790775.1_ASM4079077v1_genomic
Reference

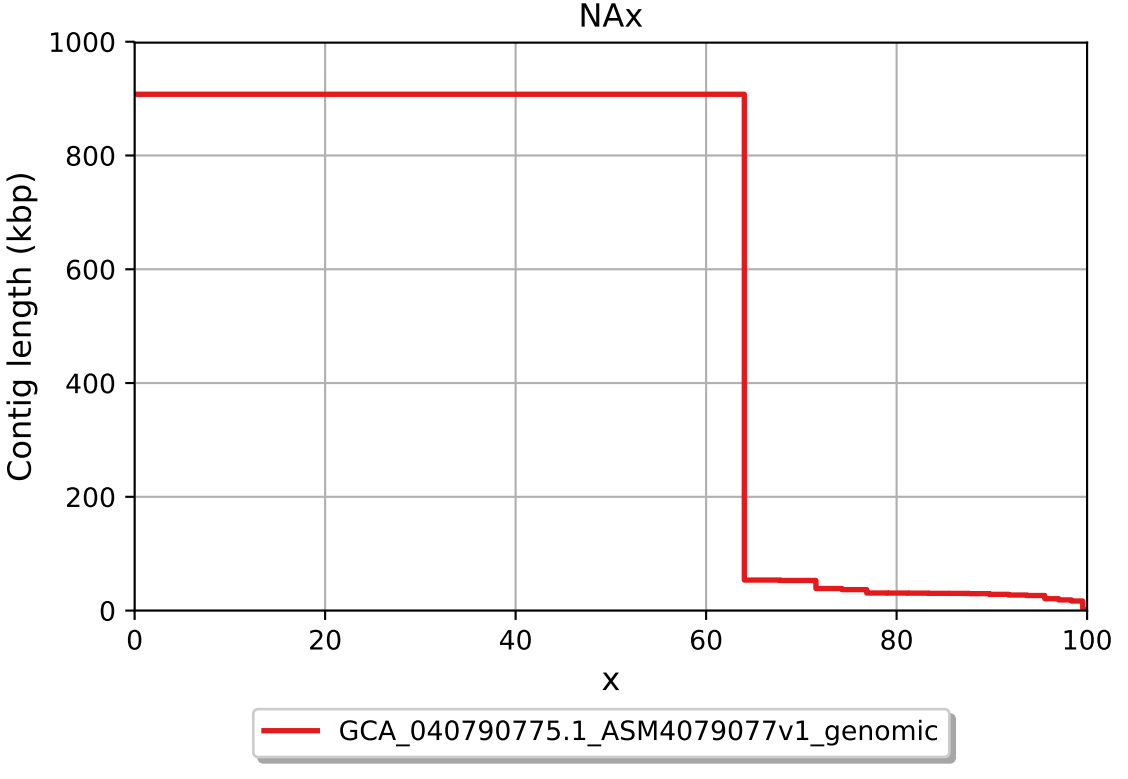

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
GCA_040790775.1_ASM4079077v1_genomic
Reference

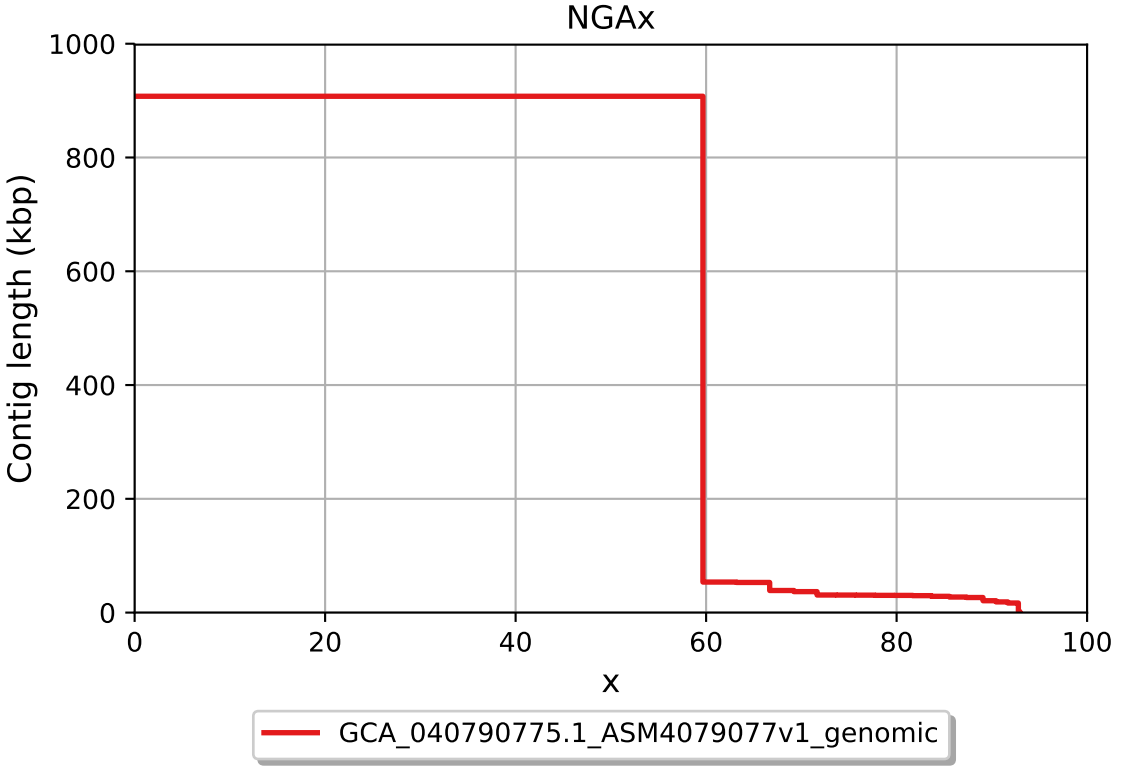

GCA_040790775.1_ASM4079077v1_genomic GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
GCA_040790775.1_ASM4079077v1_genomic

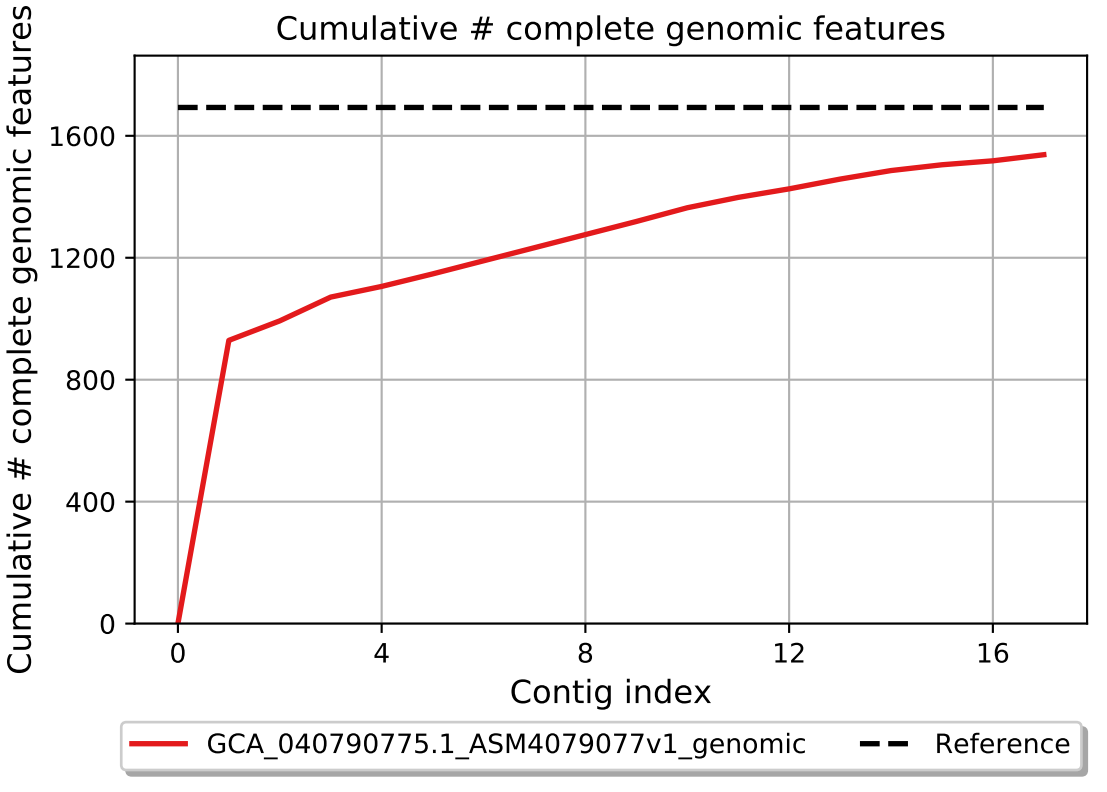

Misassemblies
5
4
3
2
1
0
GCA_040790775.1_ASM4079077v1_genomic
relocations
translocations

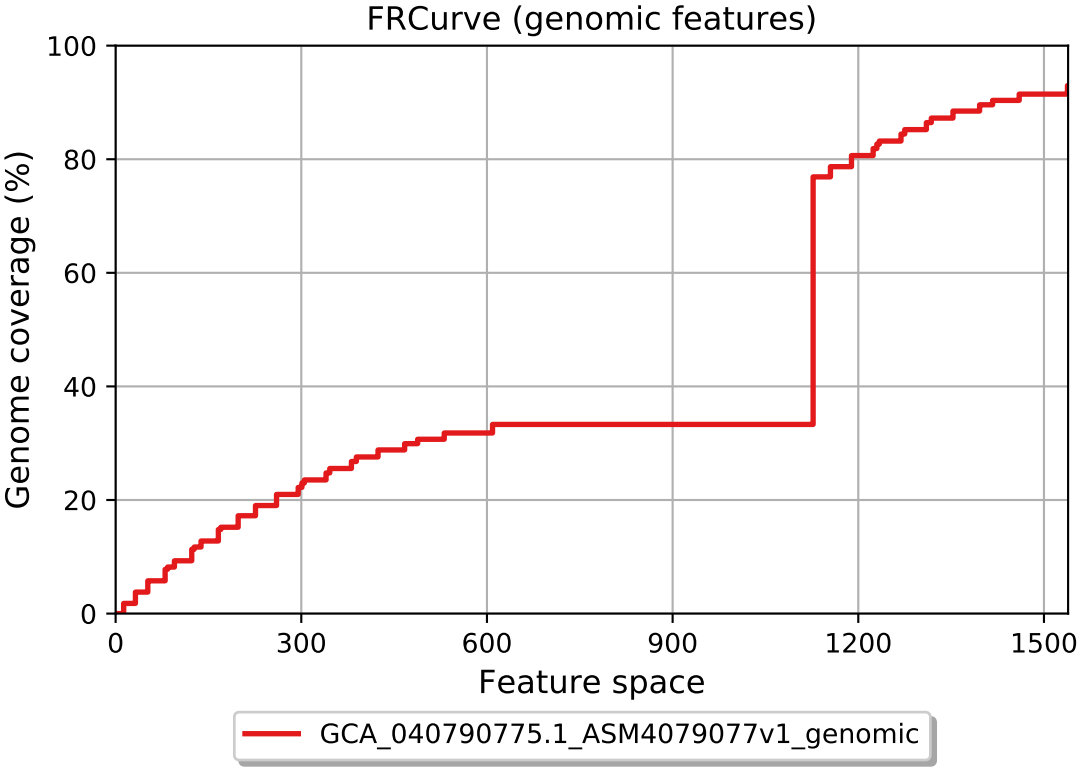

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
Feature space
GCA_040790775.1_ASM4079077v1_genomic


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
GCA_040790775.1_ASM4079077v1_genomic
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_040790775.1_ASM4079077v1_genomic


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
GCA_040790775.1_ASM4079077v1_genomic


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
GCA_040790775.1_ASM4079077v1_genomic
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
GCA_040790775.1_ASM4079077v1_genomic