Report

	URI103H
# contigs (>= 0 bp)	56
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1474413
Total length (>= 1000 bp)	1459331
Total length (>= 5000 bp)	1458171
Total length (>= 10000 bp)	1458171
Total length (>= 25000 bp)	1329812
Total length (>= 50000 bp)	1061719
# contigs	28
Largest contig	921058
Total length	1465528
Reference length	1521208
GC (%)	28.13
Reference GC (%)	28.18
N50	921058
NG50	921058
N90	26514
NG90	24228
auN	593368.6
auNG	571649.8
L50	1
LG50	1
L90	12
LG90	14
# misassemblies	25
# misassembled contigs	12
Misassembled contigs length	1261569
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	8 + 16 part
Unaligned length	218037
Genome fraction (%)	80.474
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	869.46
# indels per 100 kbp	52.92
# genomic features	1287 + 49 part
Largest alignment	905415
Total aligned length	1247100
NA50	905415
NGA50	905415
NA90	-
NGA90	-
auNA	563574.3
auNGA	542946.1
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

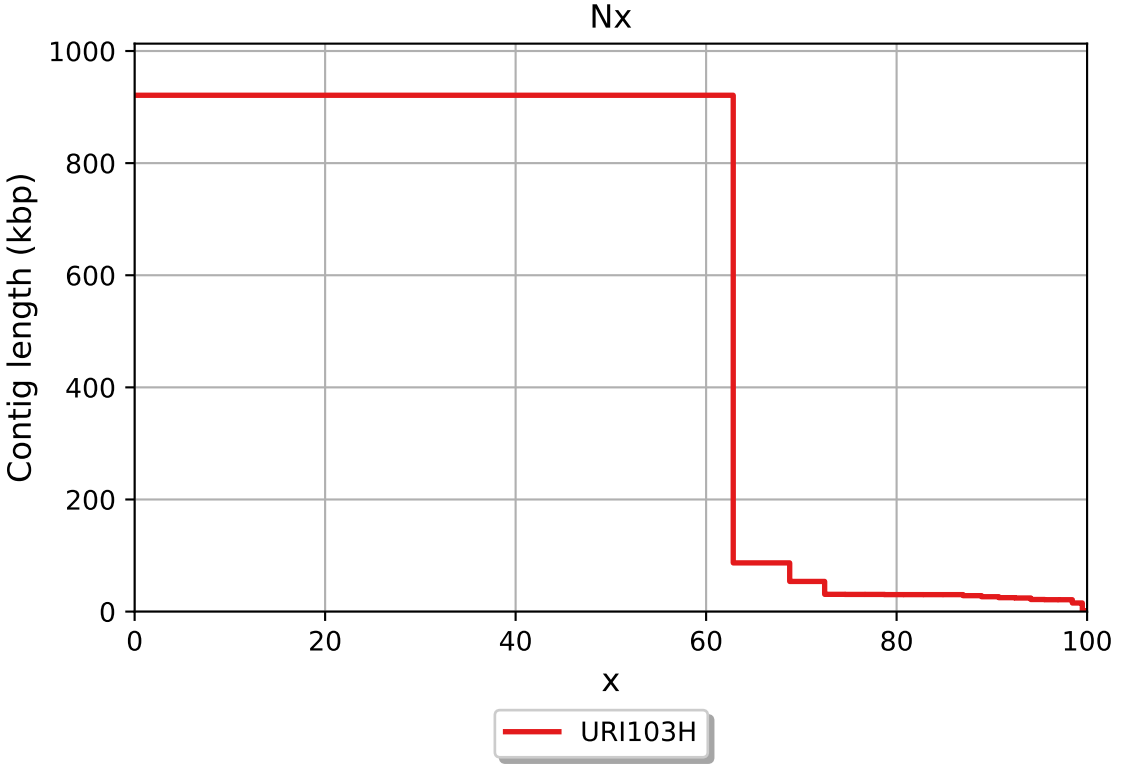
	URI103H
# misassemblies	25
# contig misassemblies	25
# c. relocations	6
# c. translocations	18
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	1261569
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	10843
# indels	660
# indels (<= 5 bp)	597
# indels (> 5 bp)	63
Indels length	3662

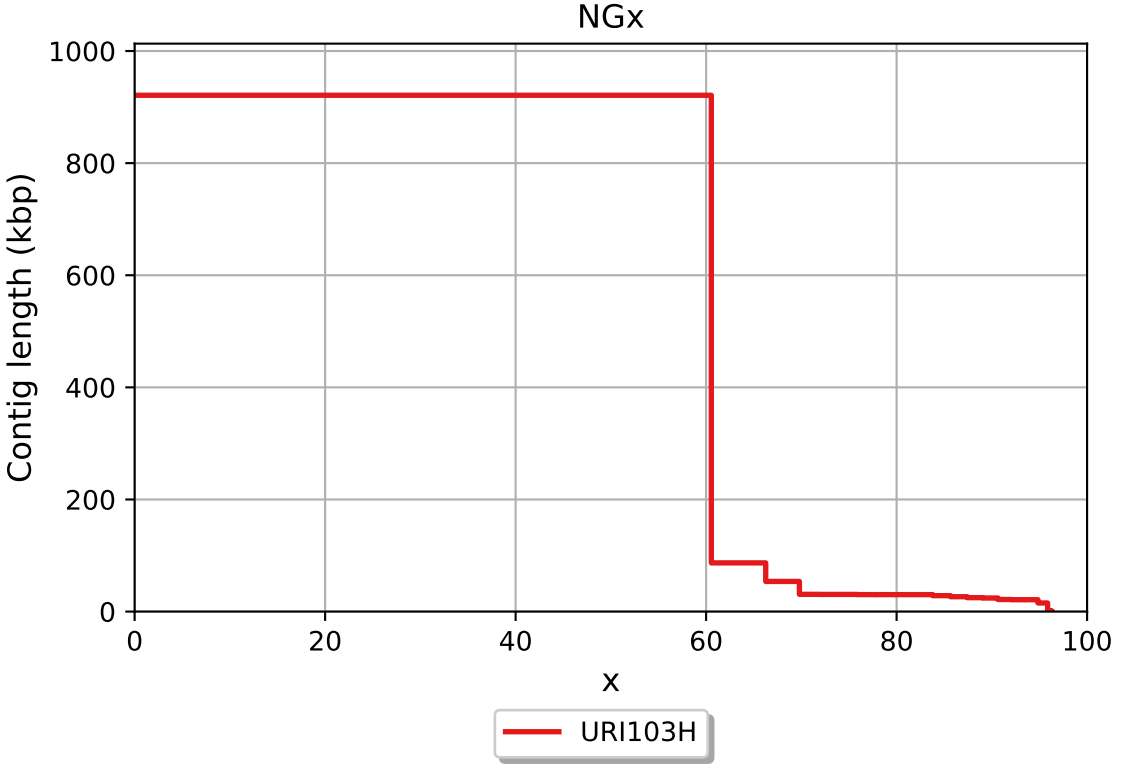
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

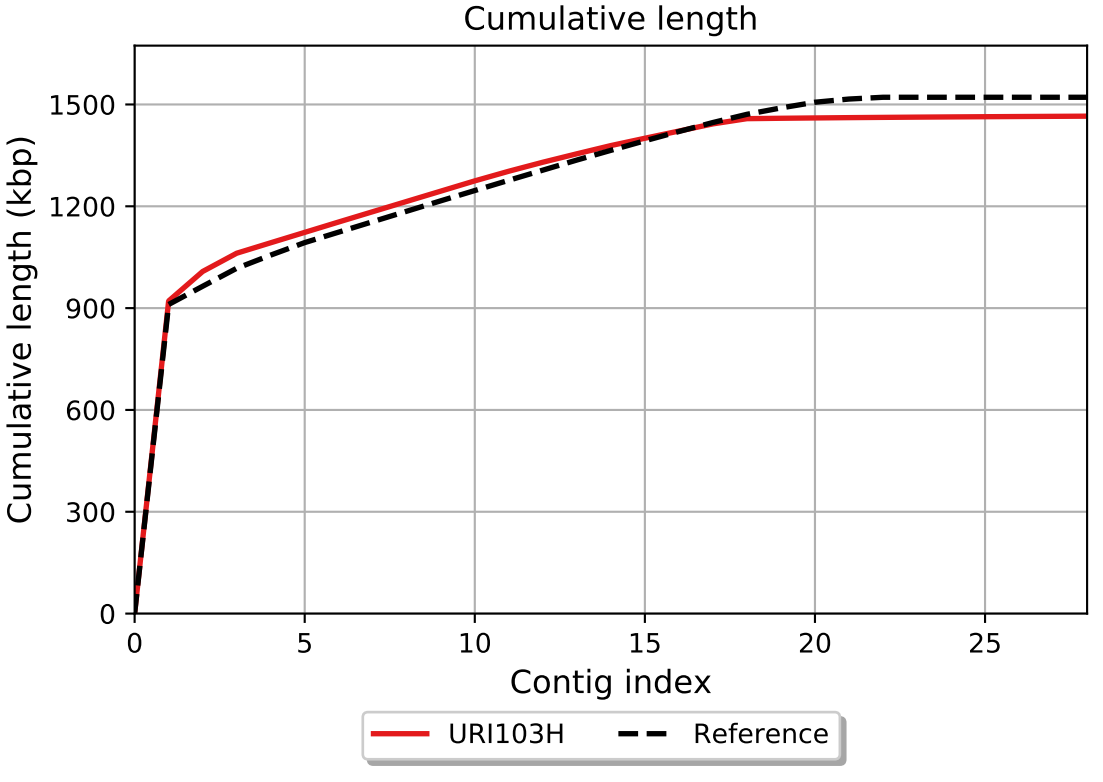
Unaligned report

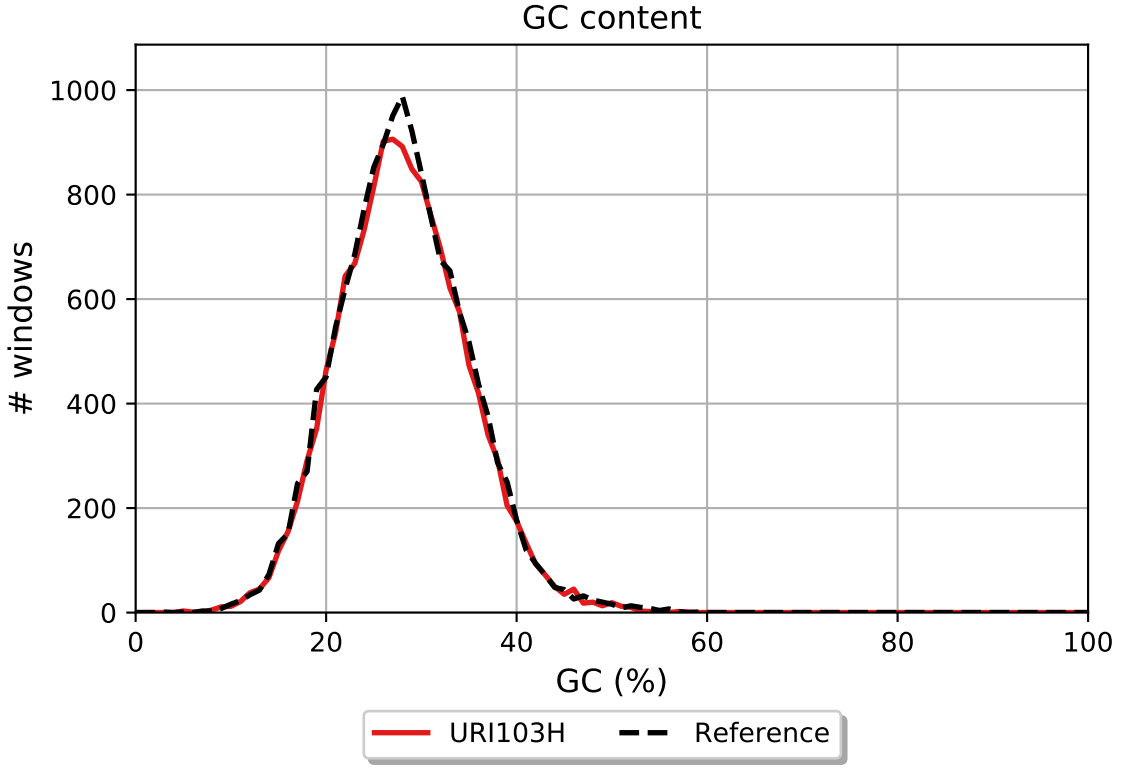
	URI103H
# fully unaligned contigs	8
Fully unaligned length	5648
# partially unaligned contigs	16
Partially unaligned length	212389
# N's	0

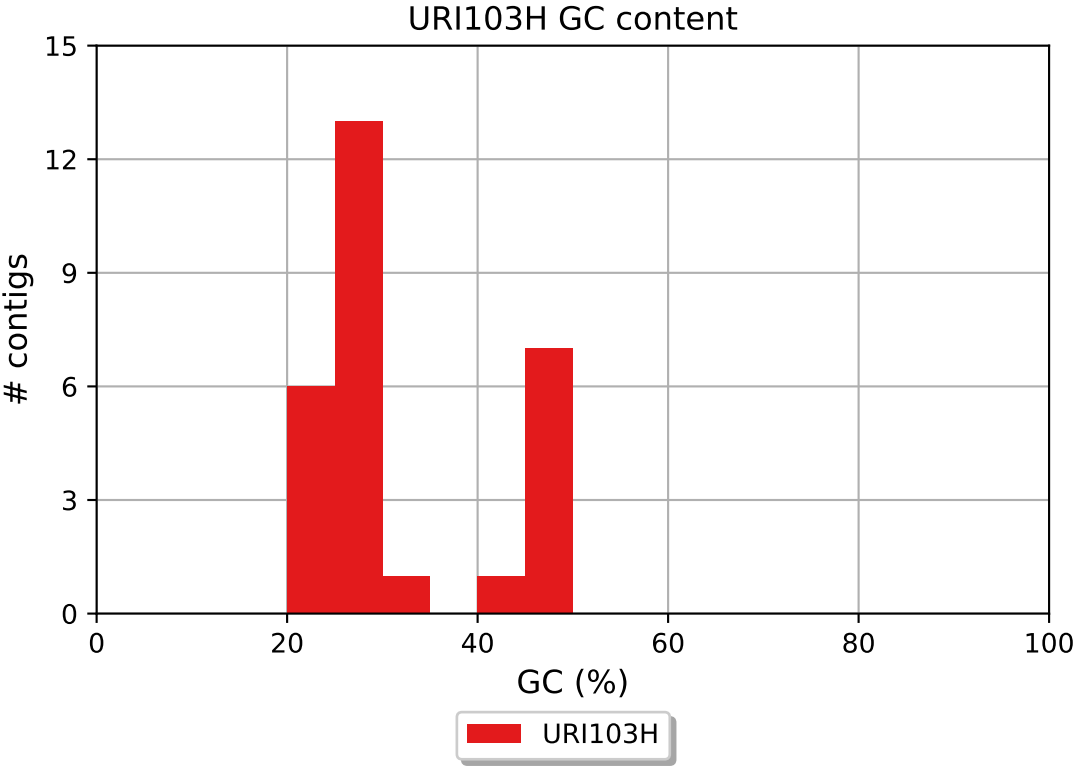
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

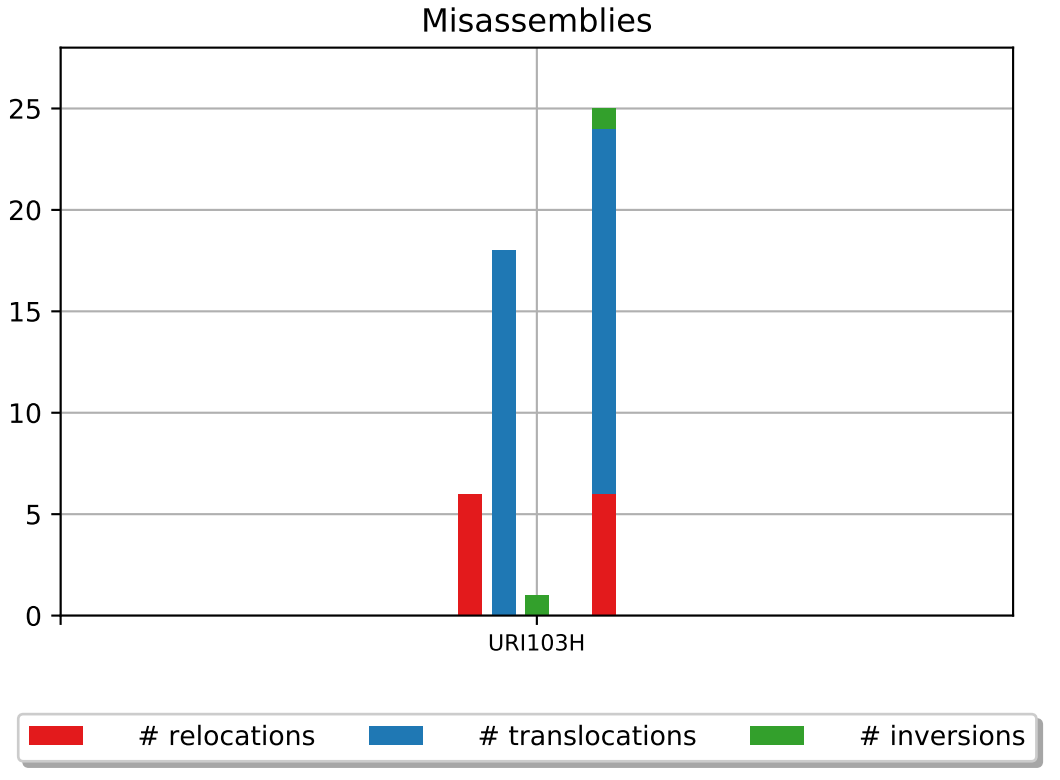

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI103H

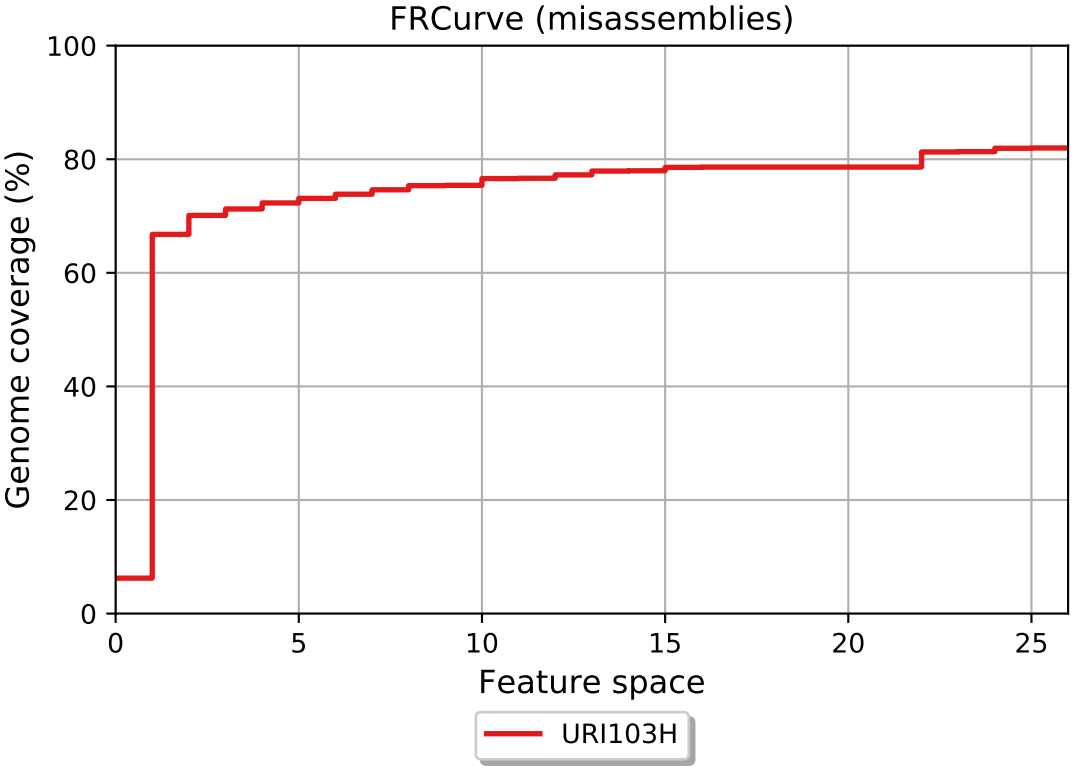

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI103H

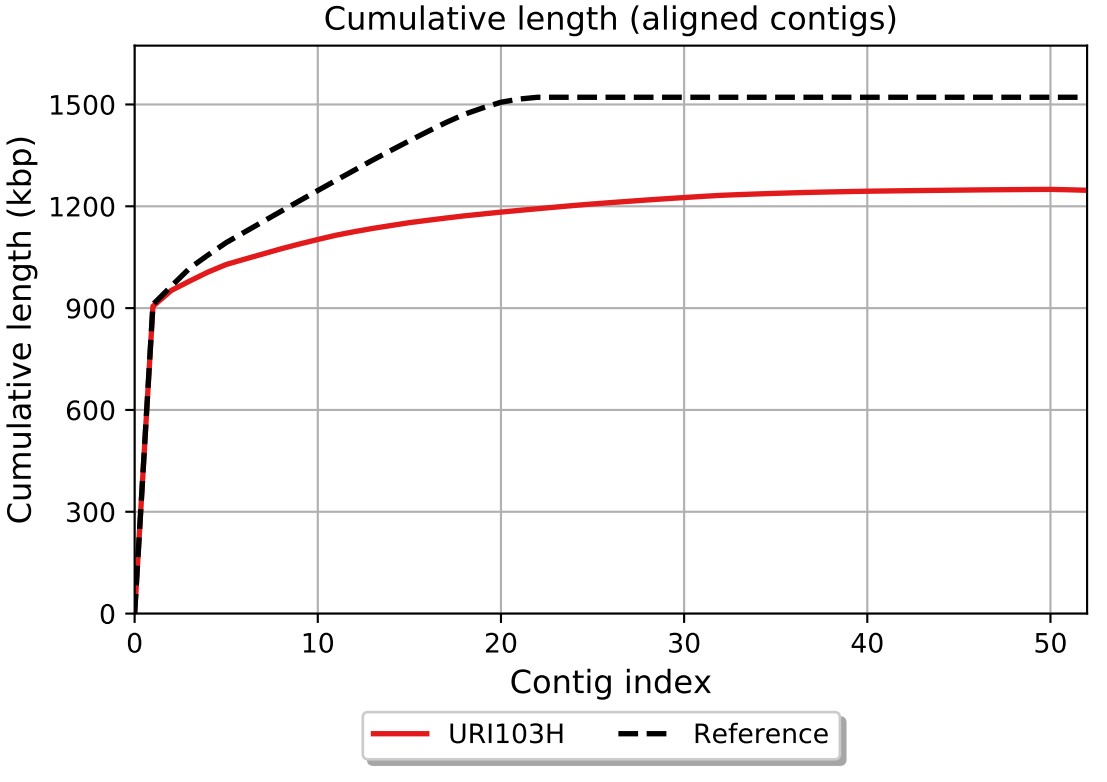

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
5
10
15
20
25
Contig index
URI103H
Reference

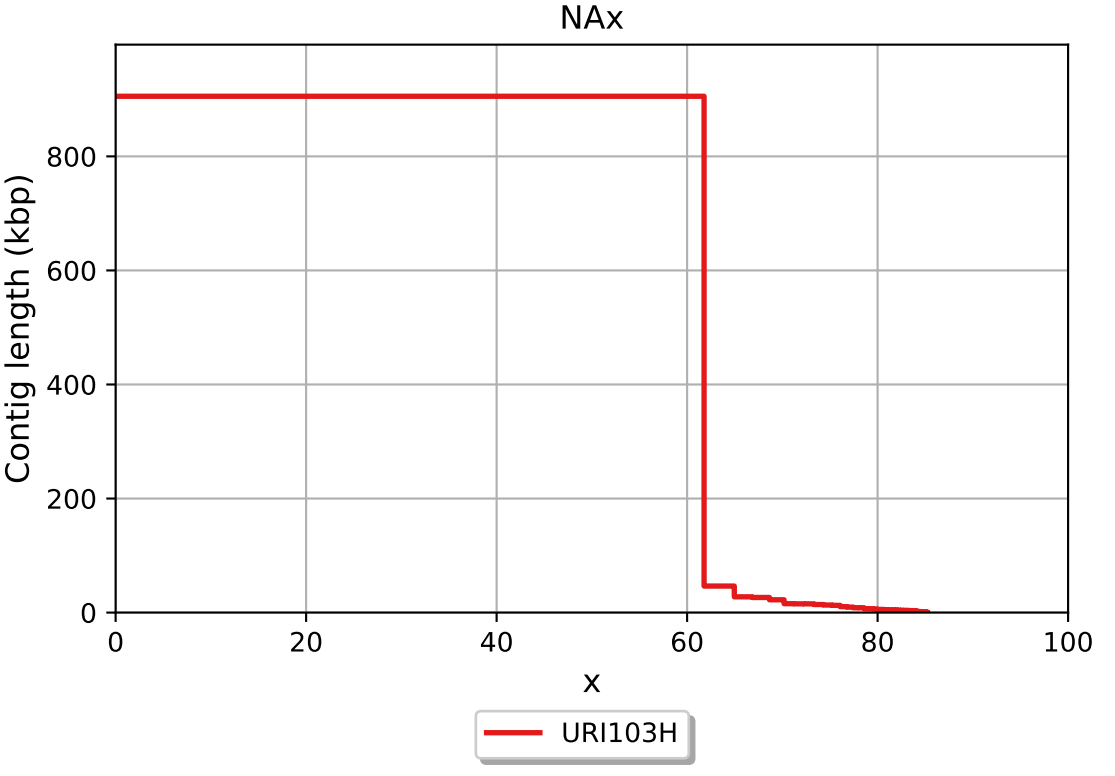

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
URI103H
Reference

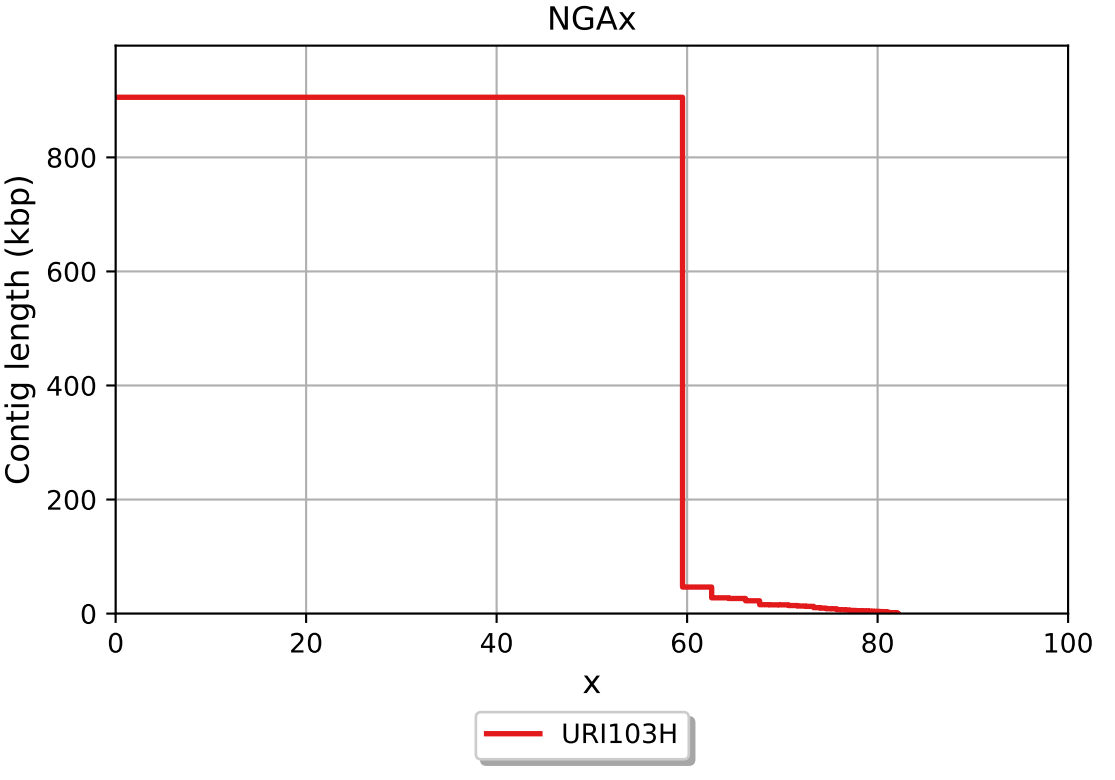

URI103H GC content
15
12
9
6
3
0
contigs
0
20
40
60
80
100
GC (%)
URI103H

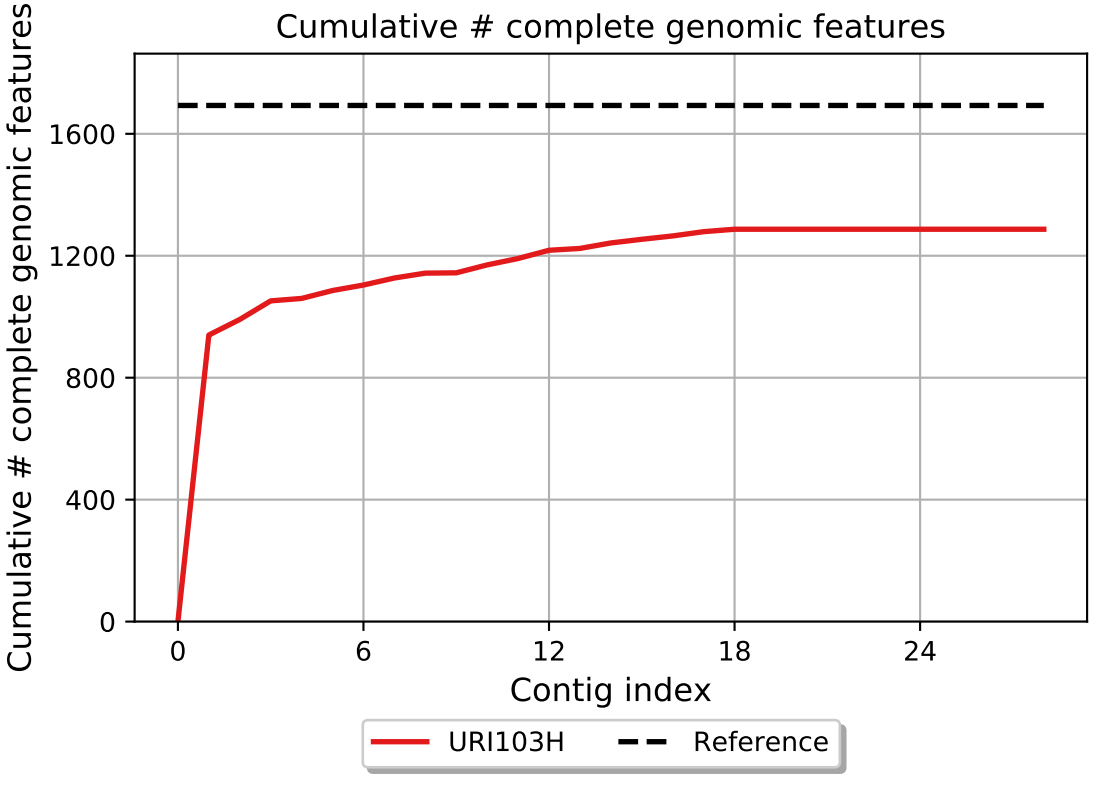

Misassemblies
25
20
15
10
5
0
URI103H
relocations
translocations
inversions

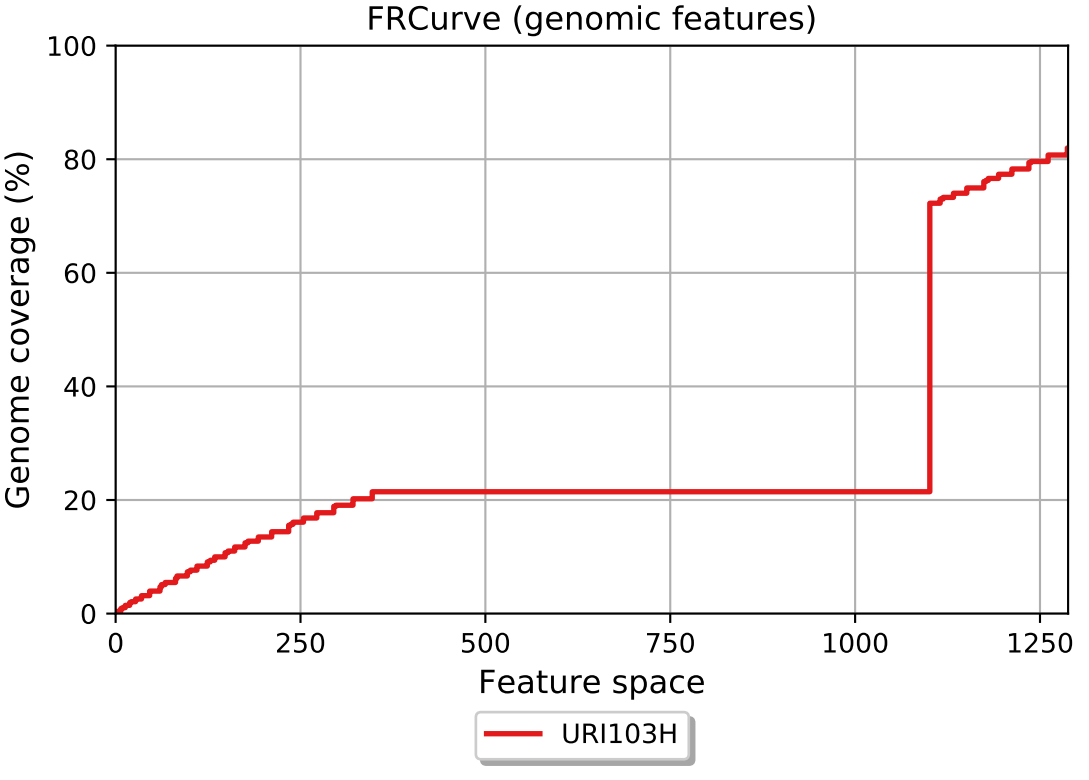

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
URI103H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
Contig index
URI103H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
URI103H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
URI103H


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
6
12
18
24
Contig index
URI103H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
URI103H