Report

	URI101H
# contigs (>= 0 bp)	32
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1554475
Total length (>= 1000 bp)	1551460
Total length (>= 5000 bp)	1549428
Total length (>= 10000 bp)	1549428
Total length (>= 25000 bp)	1506797
Total length (>= 50000 bp)	964146
# contigs	25
Largest contig	910549
Total length	1552980
Reference length	1521208
GC (%)	28.09
Reference GC (%)	28.18
N50	910549
NG50	910549
N90	29785
NG90	29785
auN	547818.1
auNG	559259.9
L50	1
LG50	1
L90	15
LG90	15
# misassemblies	18
# misassembled contigs	12
Misassembled contigs length	337554
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 6 part
Unaligned length	53367
Genome fraction (%)	94.390
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	200.18
# indels per 100 kbp	22.77
# genomic features	1547 + 35 part
Largest alignment	910549
Total aligned length	1497642
NA50	910549
NGA50	910549
NA90	12500
NGA90	16779
auNA	544589.6
auNGA	555963.9
LA50	1
LGA50	1
LA90	18
LGA90	16

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

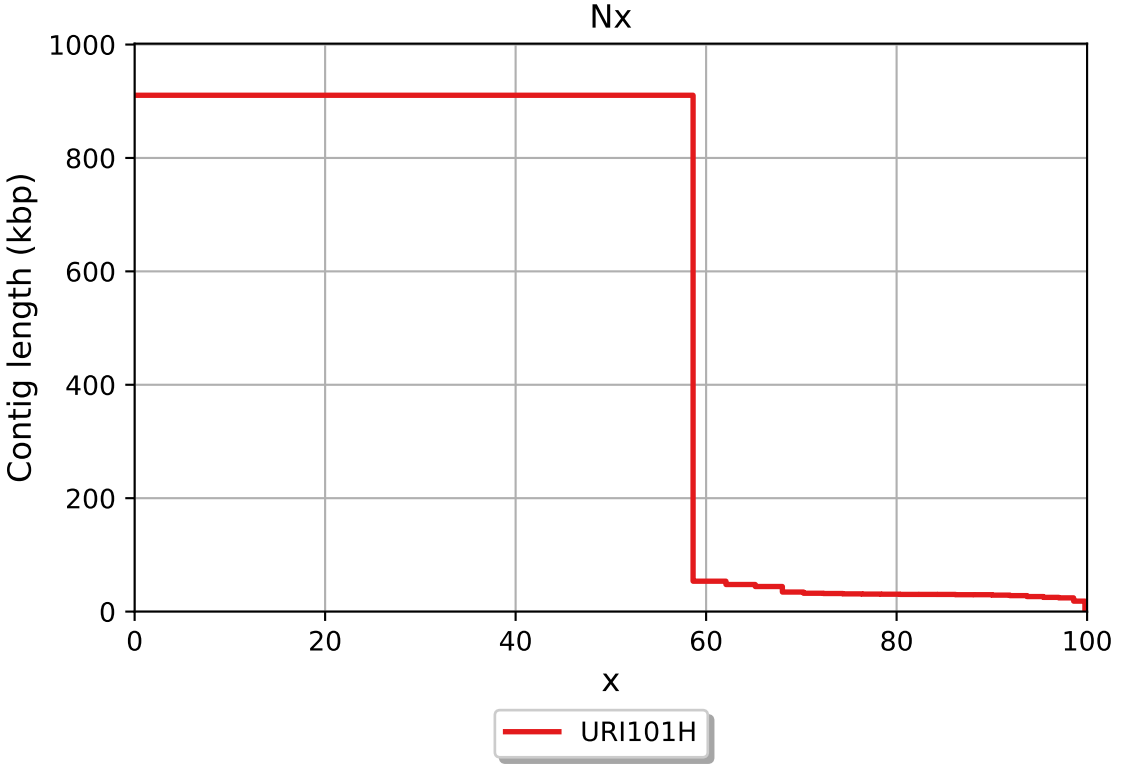
	URI101H
# misassemblies	18
# contig misassemblies	18
# c. relocations	6
# c. translocations	10
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	337554
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	2998
# indels	341
# indels (<= 5 bp)	286
# indels (> 5 bp)	55
Indels length	3822

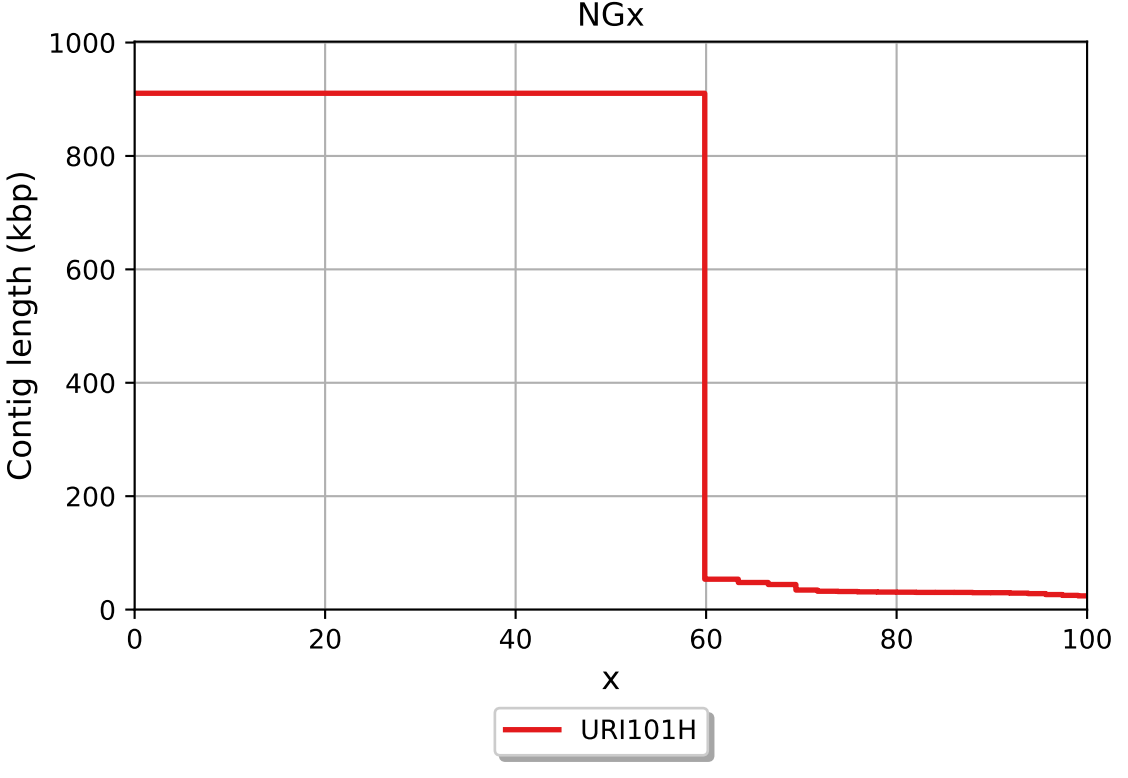
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

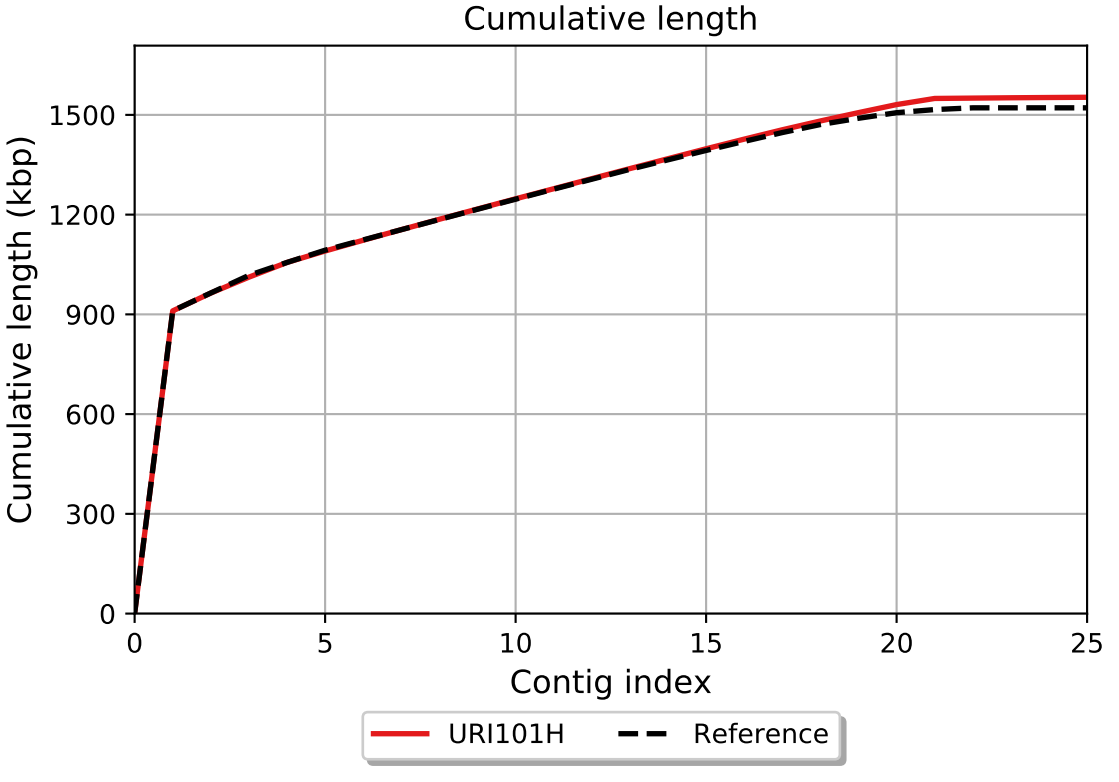
Unaligned report

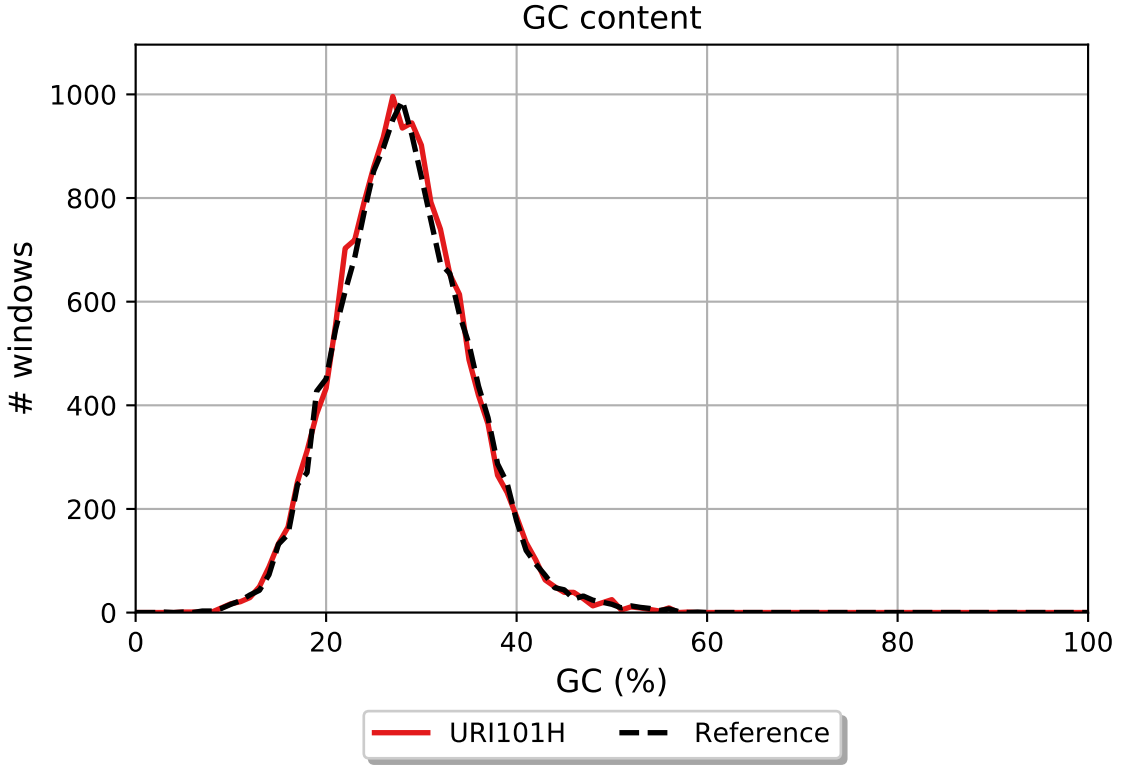
	URI101H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	53367
# N's	0

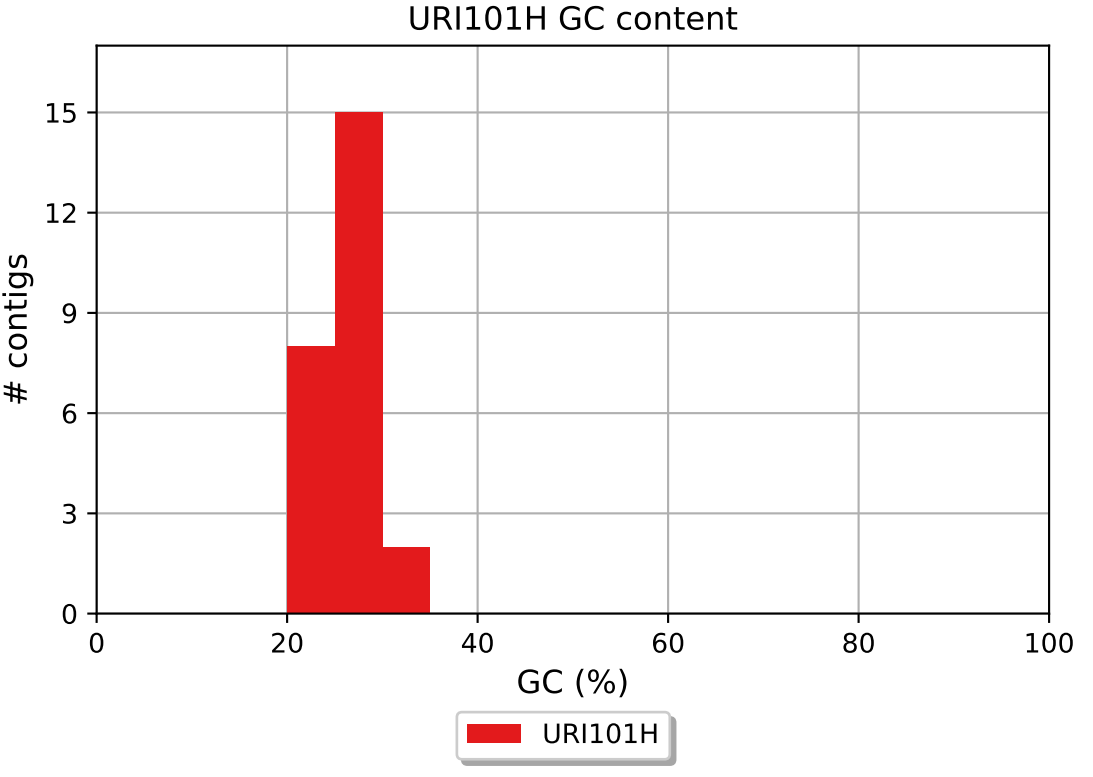
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

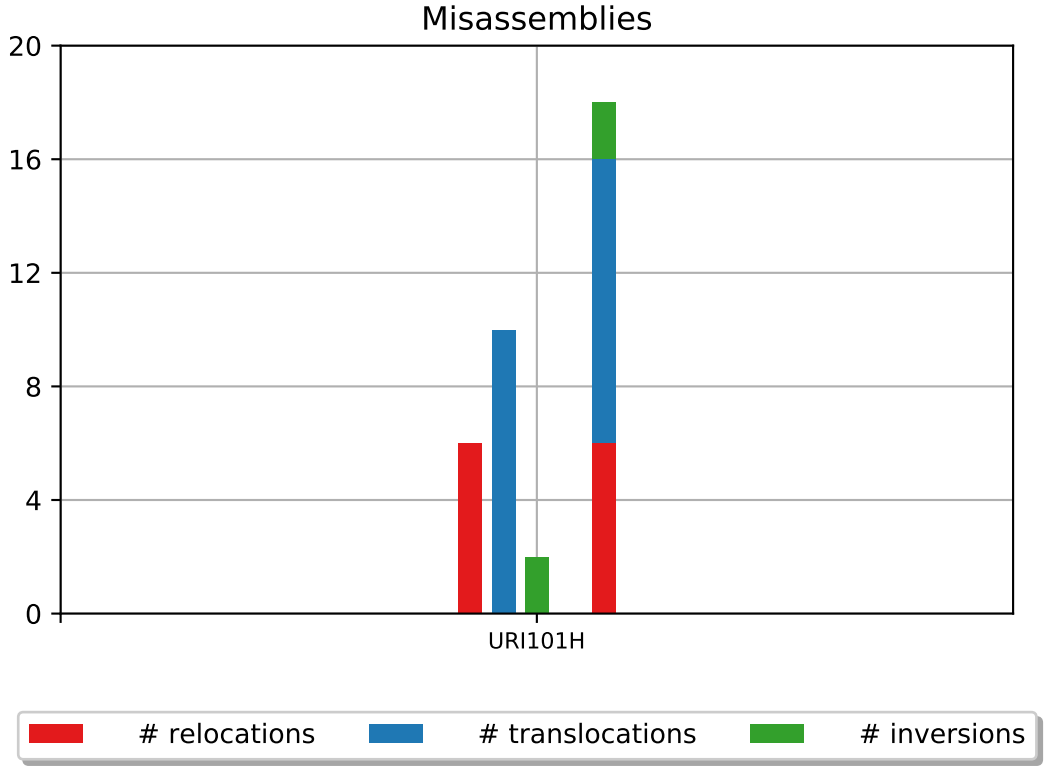

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI101H

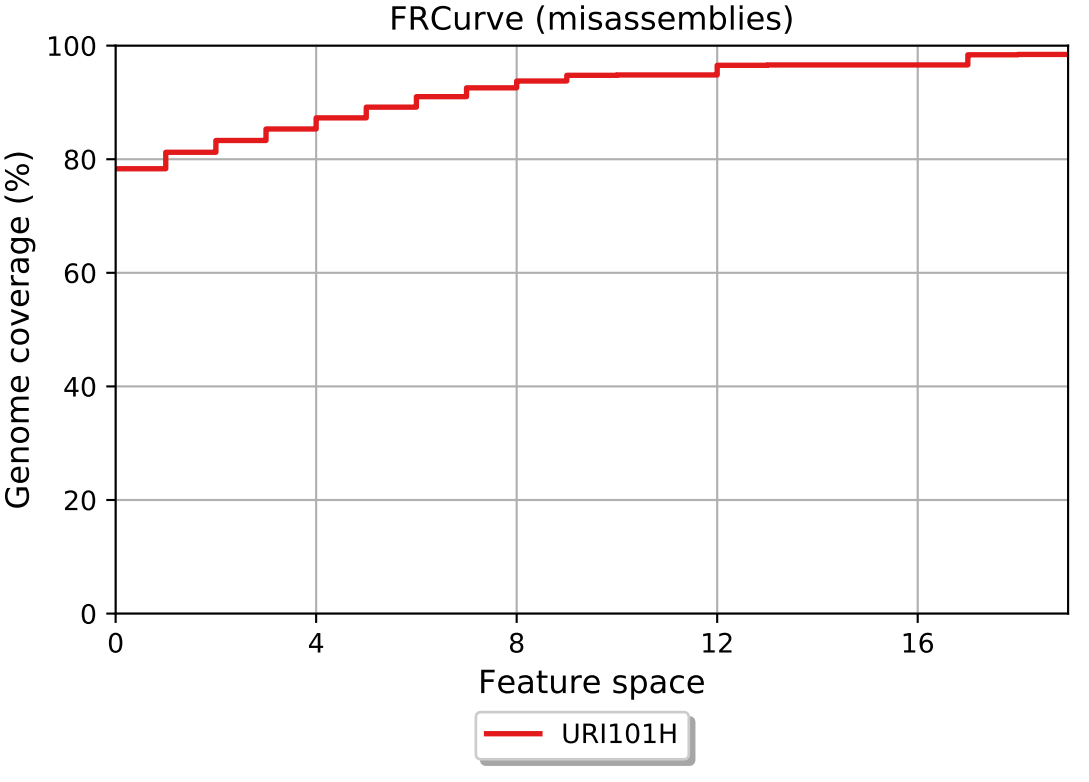

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI101H

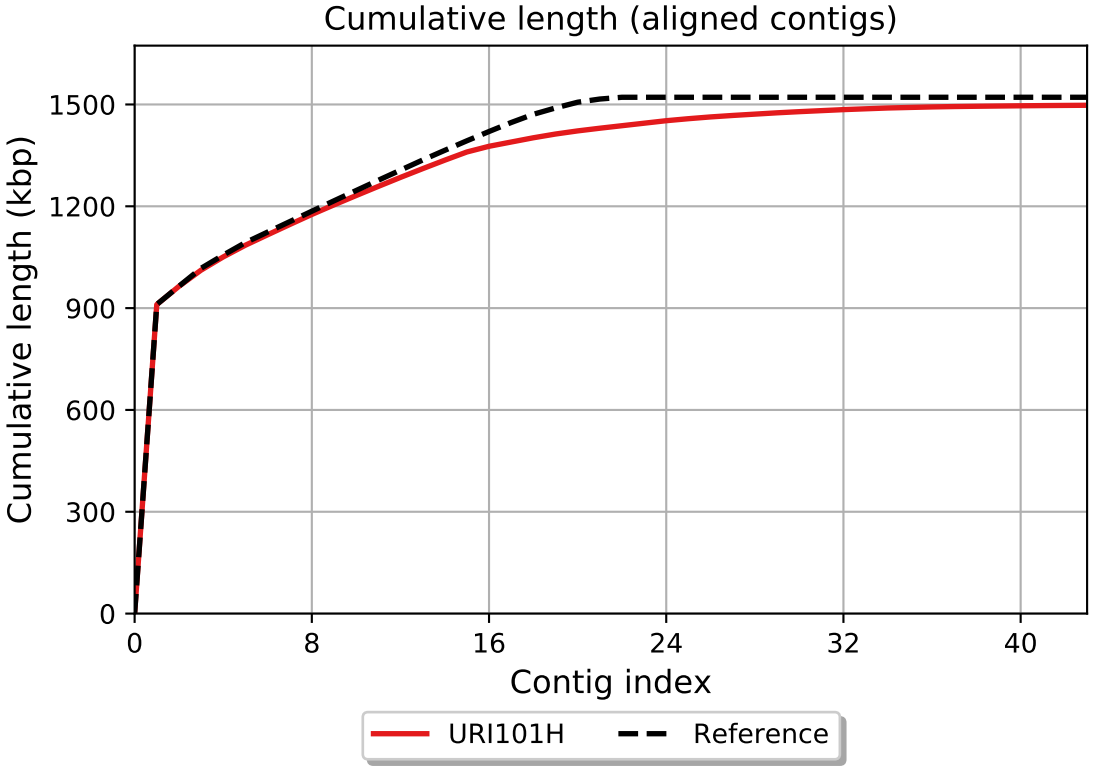

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
5
10
15
20
25
Contig index
URI101H
Reference

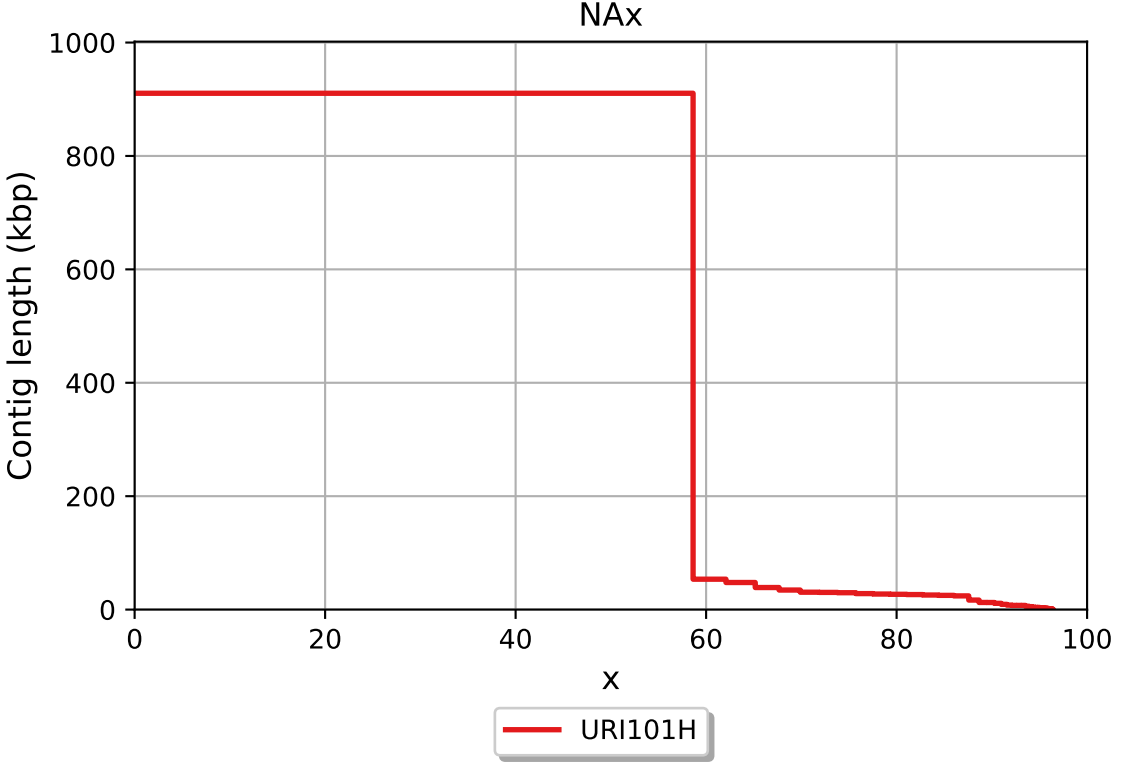

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
URI101H
Reference

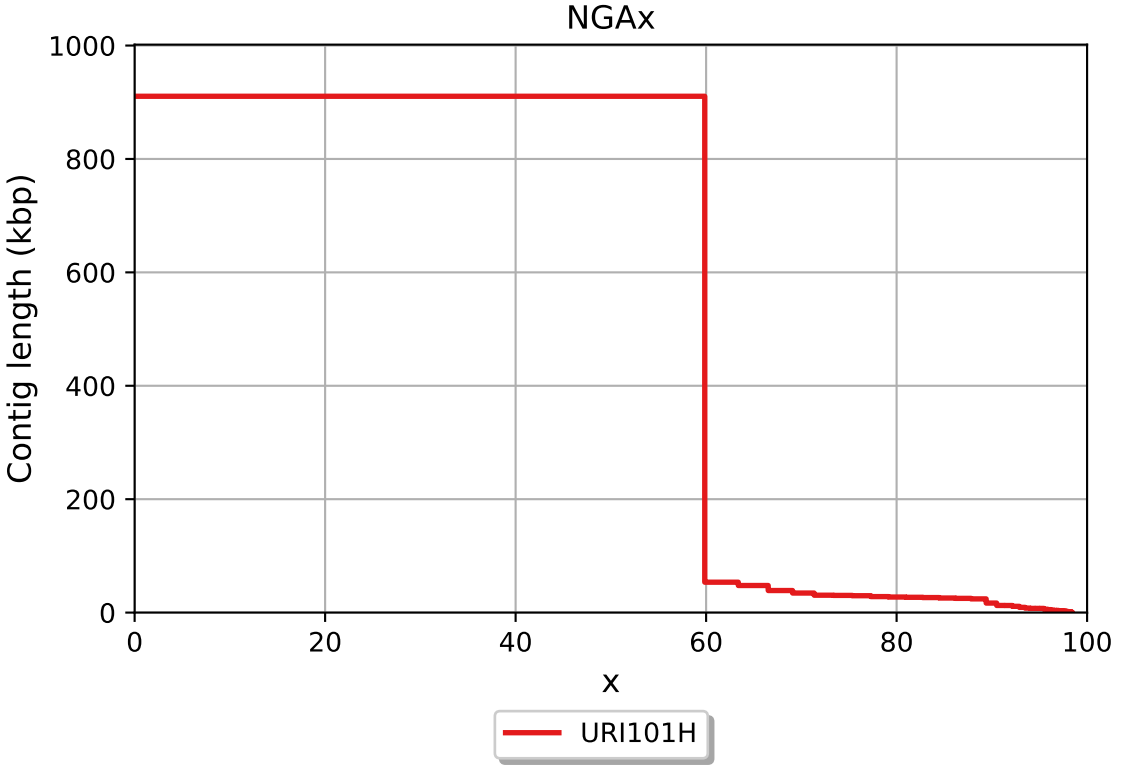

URI101H GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
URI101H

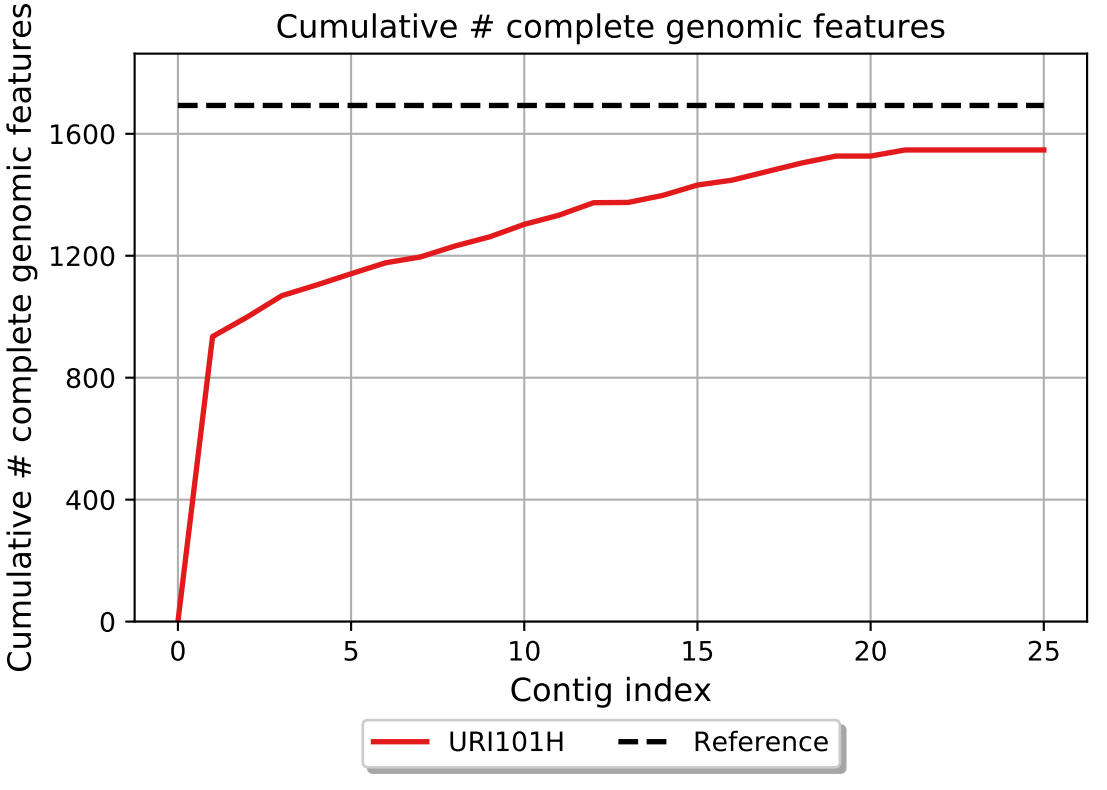

Misassemblies
20
16
12
8
4
0
URI101H
relocations
translocations
inversions

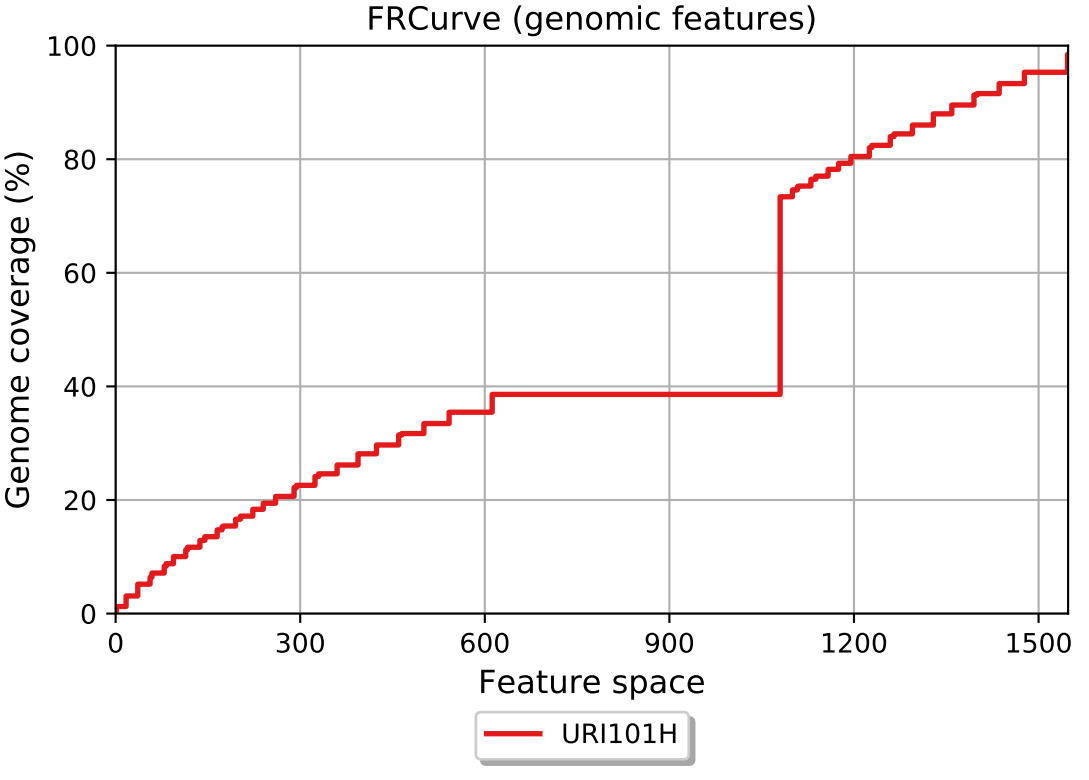

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
Feature space
URI101H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
URI101H
Reference


NAx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI101H


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI101H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
5
10
15
20
25
Contig index
URI101H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
URI101H