Report

	URI91H
# contigs (>= 0 bp)	26
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	22
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1588266
Total length (>= 1000 bp)	1587663
Total length (>= 5000 bp)	1586419
Total length (>= 10000 bp)	1586419
Total length (>= 25000 bp)	1542499
Total length (>= 50000 bp)	964288
# contigs	23
Largest contig	910690
Total length	1587663
Reference length	1521208
GC (%)	28.21
Reference GC (%)	28.18
N50	910690
NG50	910690
N90	29838
NG90	30299
auN	536832.3
auNG	560284.2
L50	1
LG50	1
L90	16
LG90	14
# misassemblies	12
# misassembled contigs	11
Misassembled contigs length	330904
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	27320
Genome fraction (%)	96.095
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	114.59
# indels per 100 kbp	13.08
# genomic features	1585 + 31 part
Largest alignment	910690
Total aligned length	1559505
NA50	910690
NGA50	910690
NA90	20069
NGA90	26498
auNA	534634.8
auNGA	557990.7
LA50	1
LGA50	1
LA90	18
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

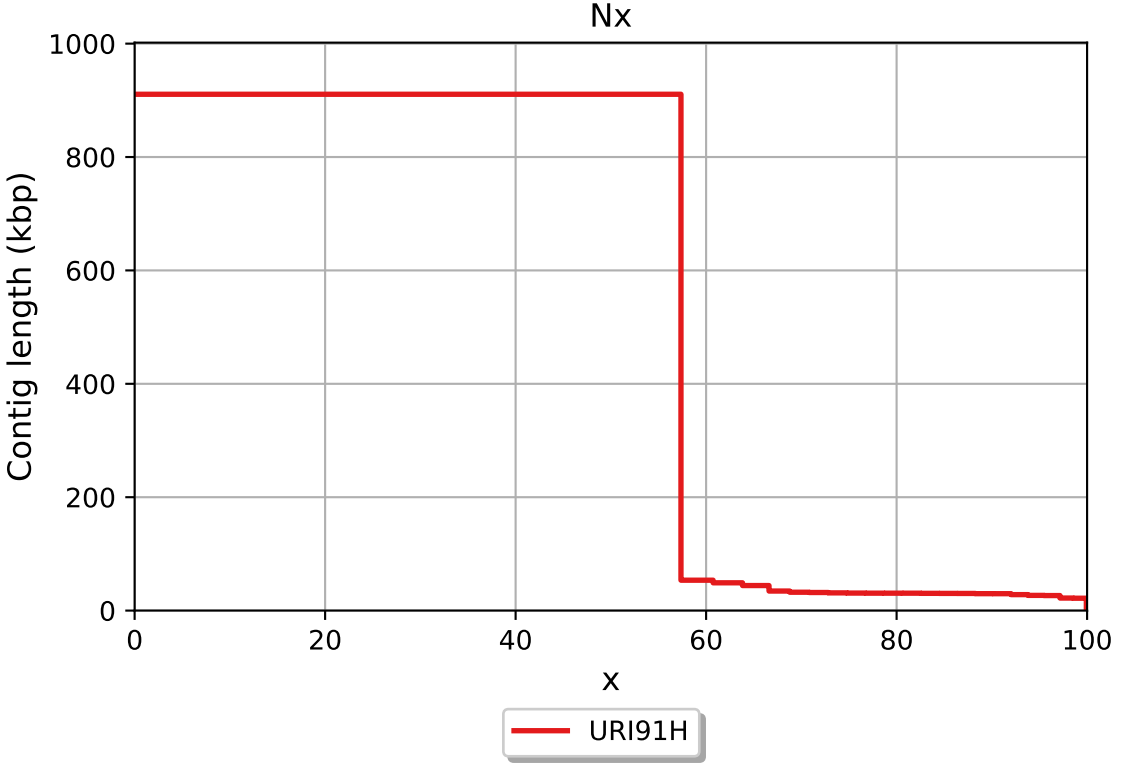
	URI91H
# misassemblies	12
# contig misassemblies	12
# c. relocations	7
# c. translocations	5
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	330904
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1787
# indels	204
# indels (<= 5 bp)	181
# indels (> 5 bp)	23
Indels length	1340

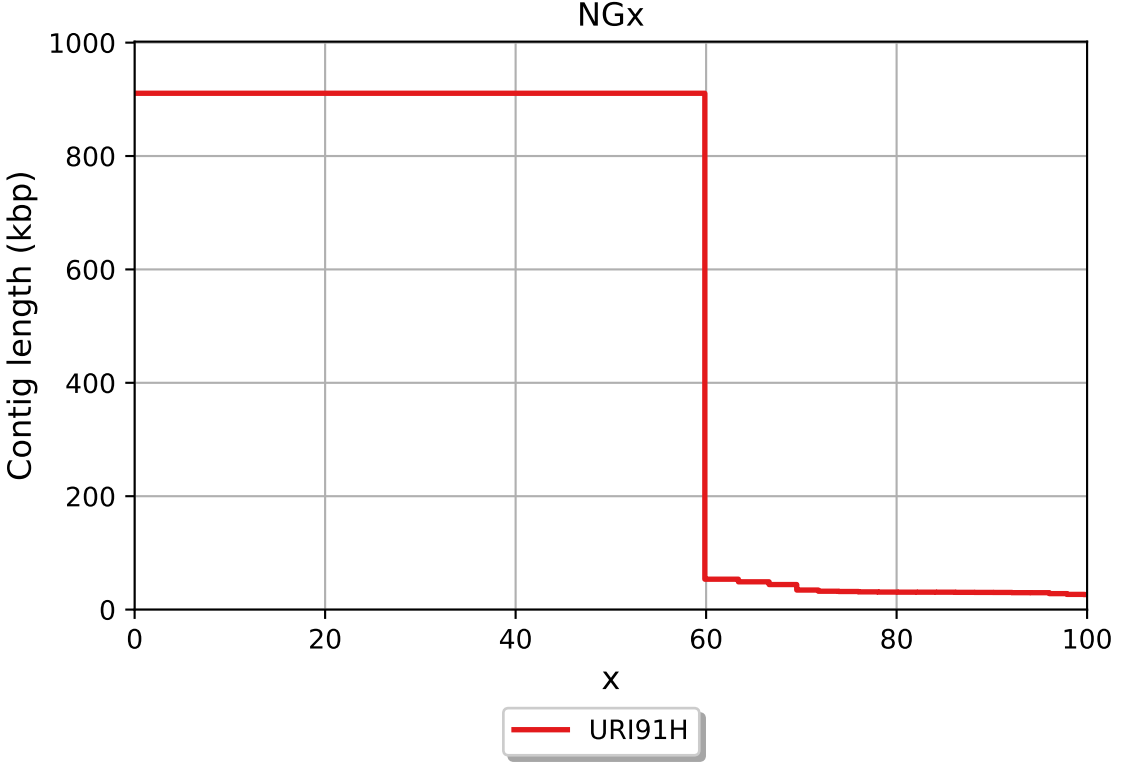
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

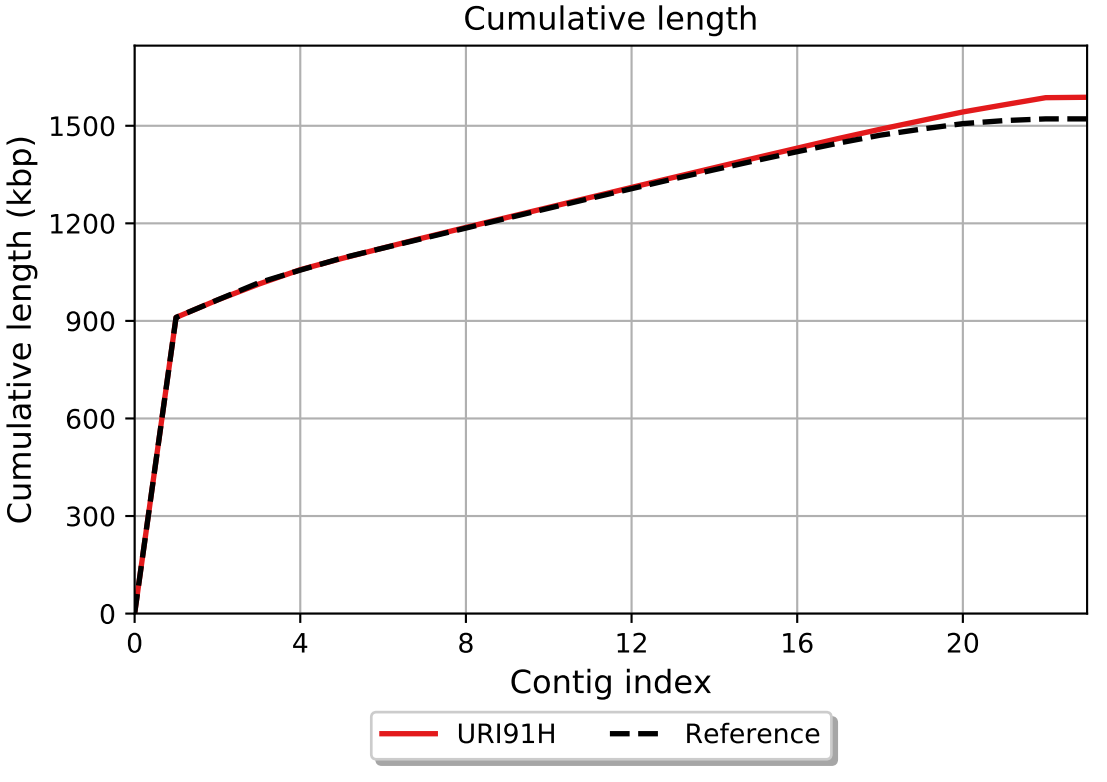
Unaligned report

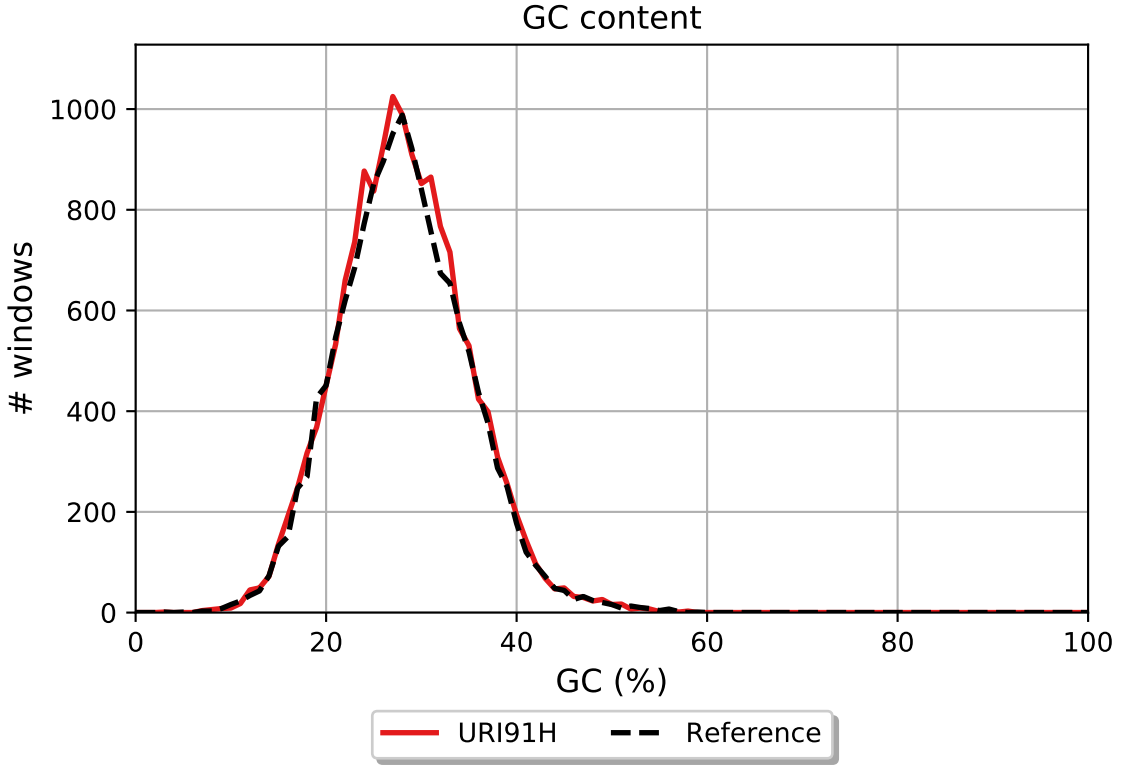
	URI91H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	27320
# N's	0

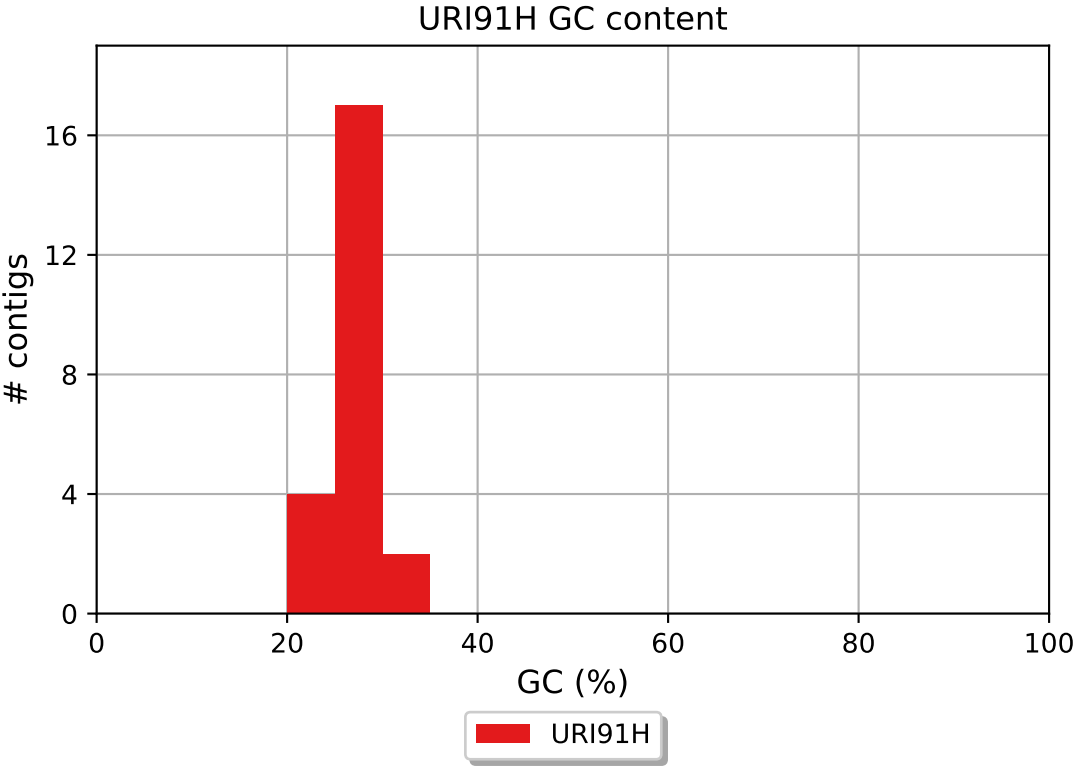
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI91H

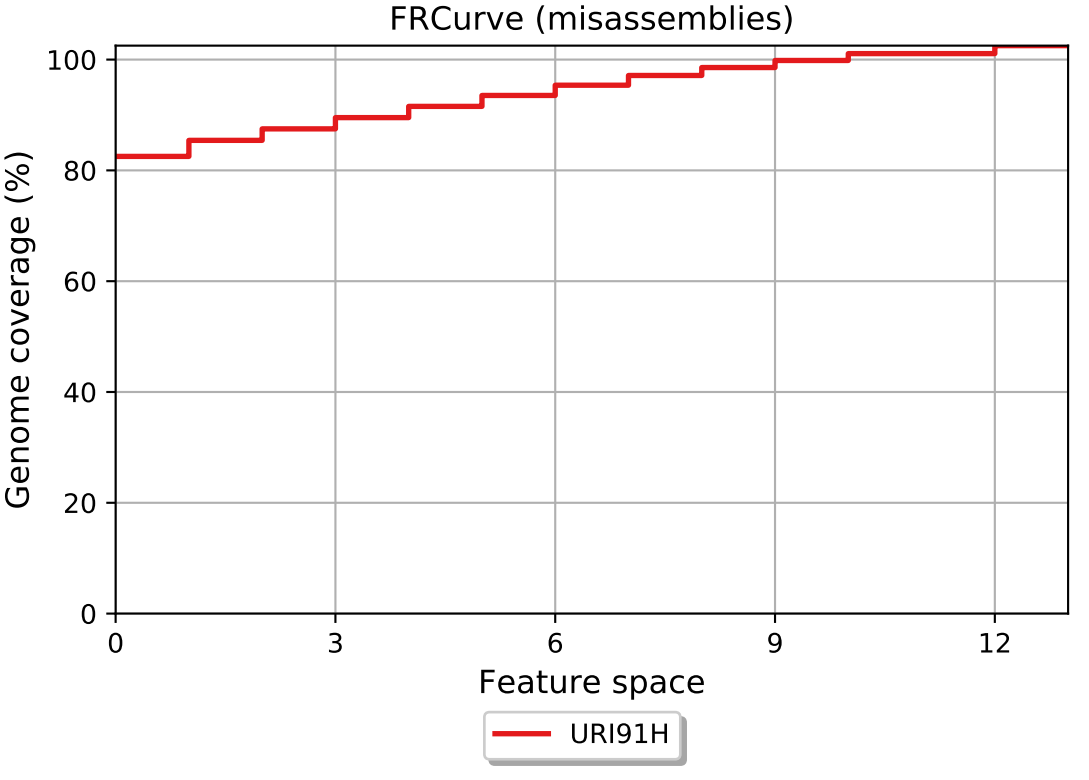

NGx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI91H

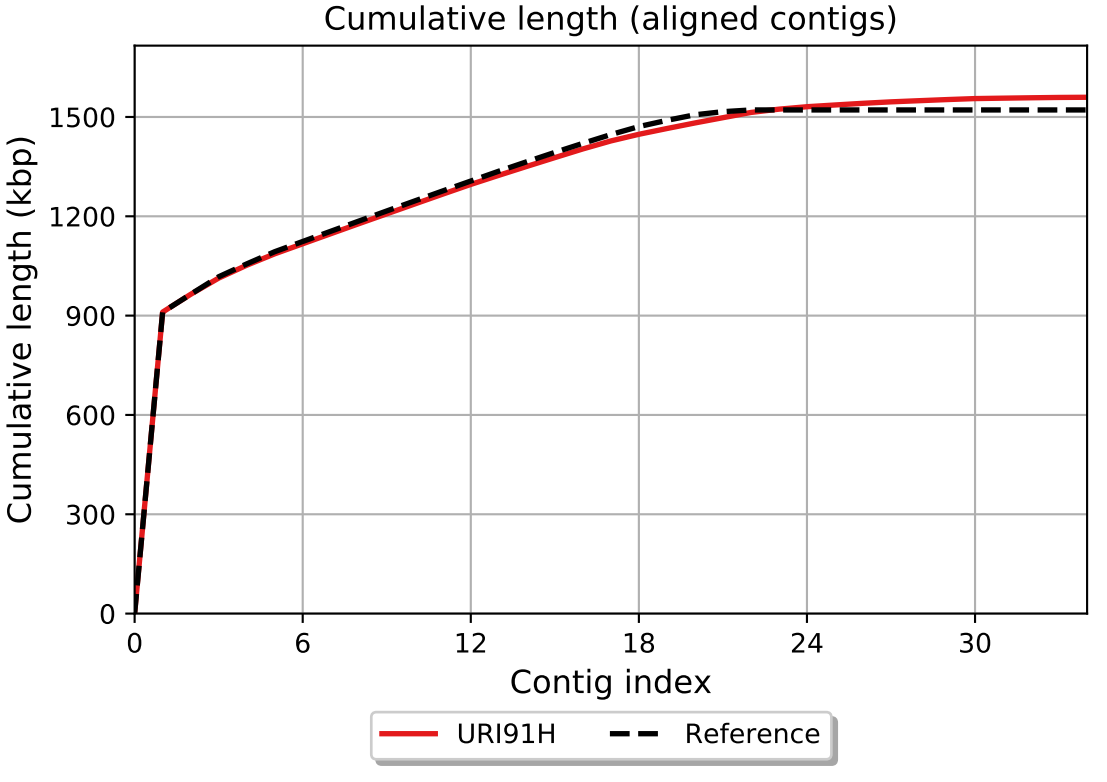

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
URI91H
Reference

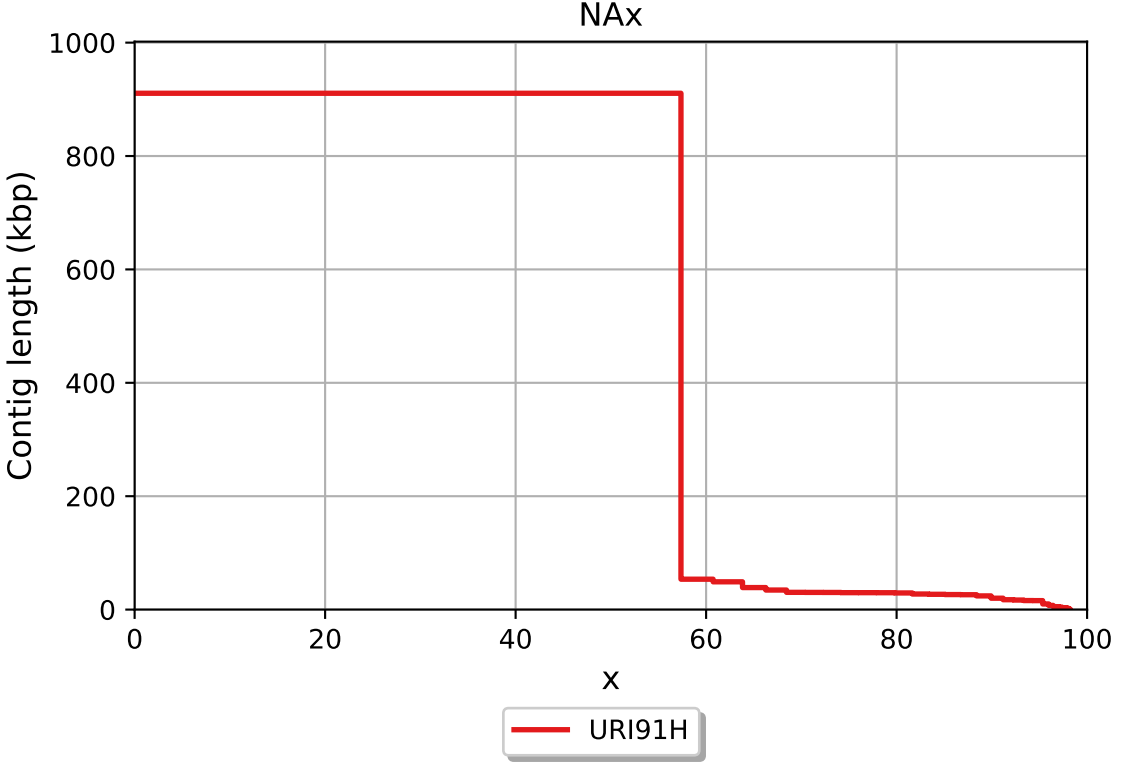

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
URI91H
Reference

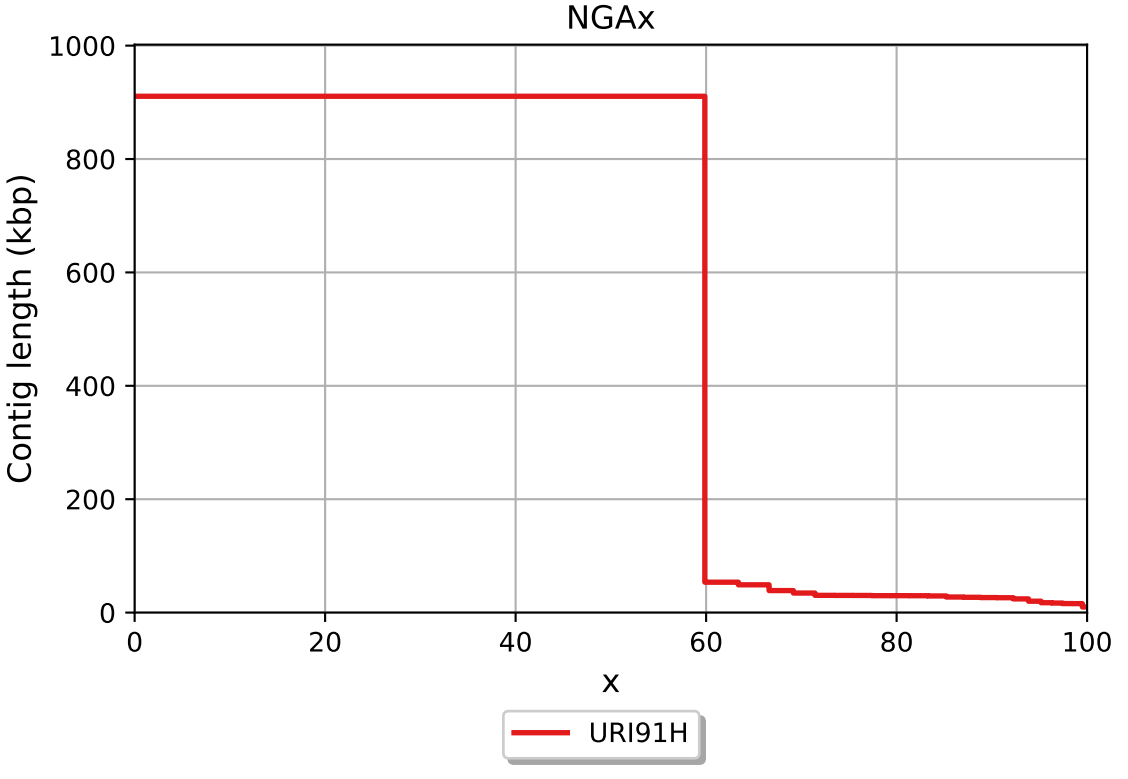

URI91H GC content
contigs
0
4
8
12
16
0
20
40
60
80
100
GC (%)
URI91H

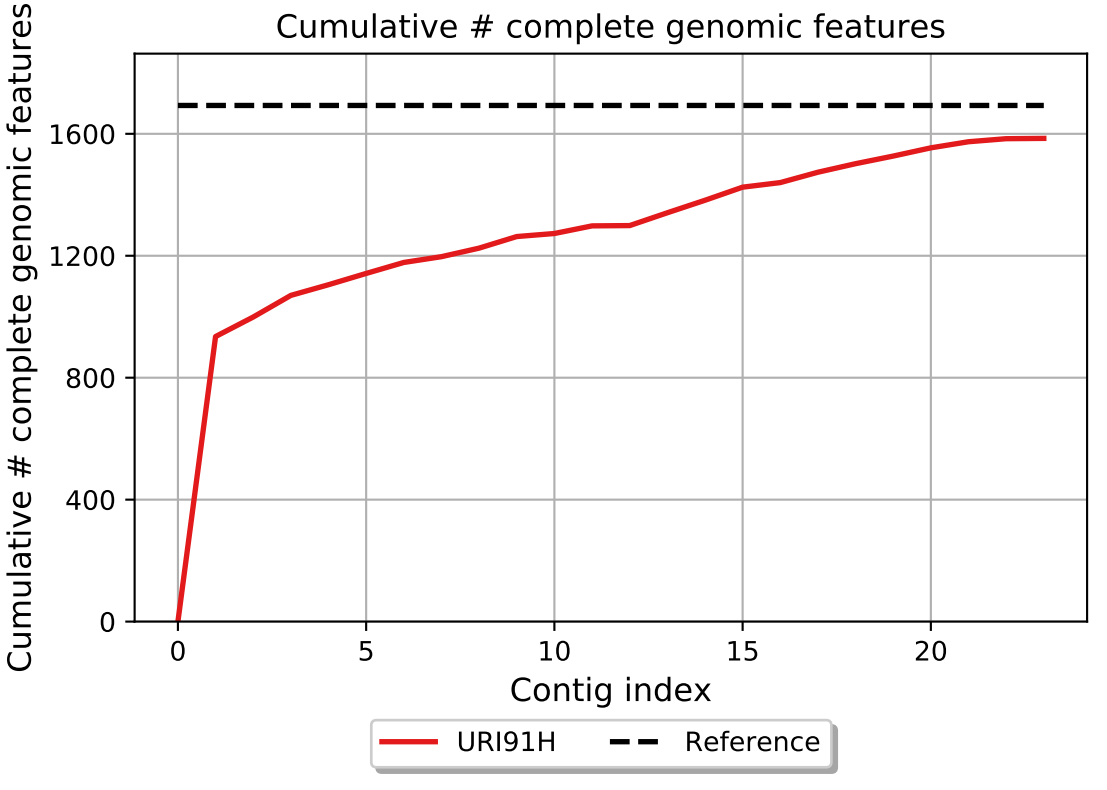
Misassemblies
12
9
6
3
0
URI91H
relocations
translocations

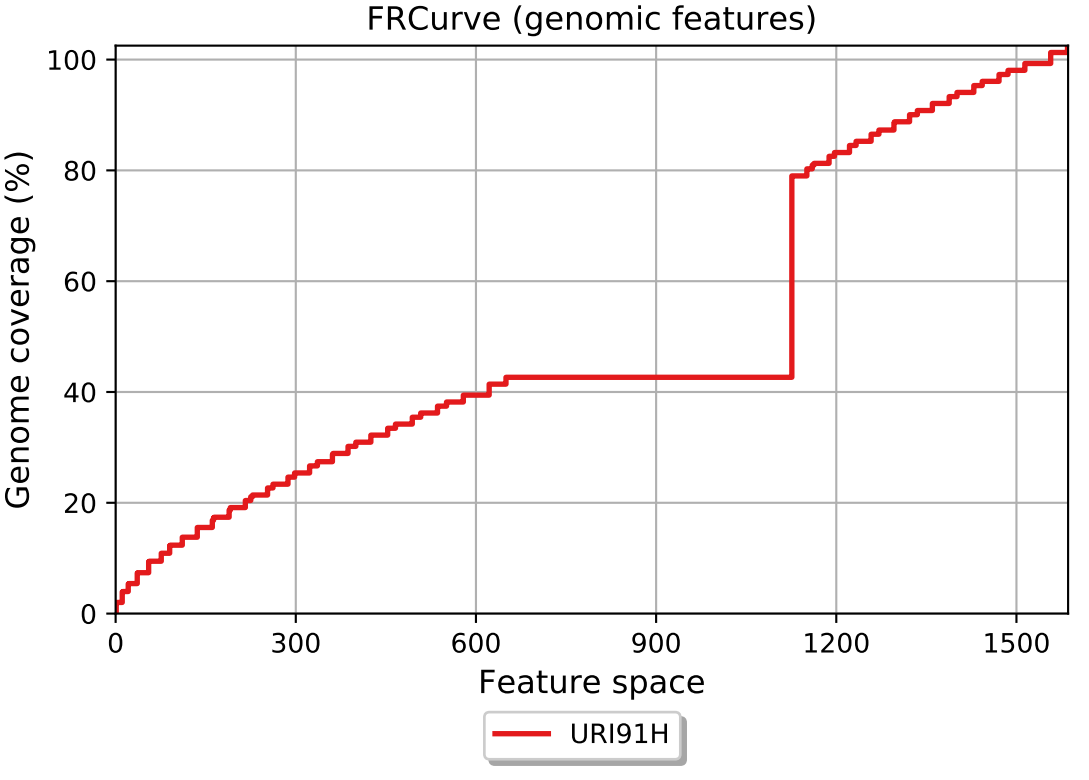

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
Feature space
URI91H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
6
12
18
24
30
Contig index
URI91H
Reference


NAx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI91H


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI91H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
5
10
15
20
Contig index
URI91H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
URI91H