Report

	URI44H
# contigs (>= 0 bp)	75
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1417636
Total length (>= 1000 bp)	1398063
Total length (>= 5000 bp)	1392903
Total length (>= 10000 bp)	1385077
Total length (>= 25000 bp)	1259640
Total length (>= 50000 bp)	974850
# contigs	37
Largest contig	921082
Total length	1408987
Reference length	1521208
GC (%)	28.11
Reference GC (%)	28.18
N50	921082
NG50	921082
N90	24780
NG90	21164
auN	611945.9
auNG	566802.1
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	24
# misassembled contigs	11
Misassembled contigs length	1187541
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	4 + 20 part
Unaligned length	180999
Genome fraction (%)	78.825
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	798.63
# indels per 100 kbp	51.27
# genomic features	1250 + 55 part
Largest alignment	905453
Total aligned length	1224978
NA50	905453
NGA50	905453
NA90	-
NGA90	-
auNA	585952.2
auNGA	542726.0
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

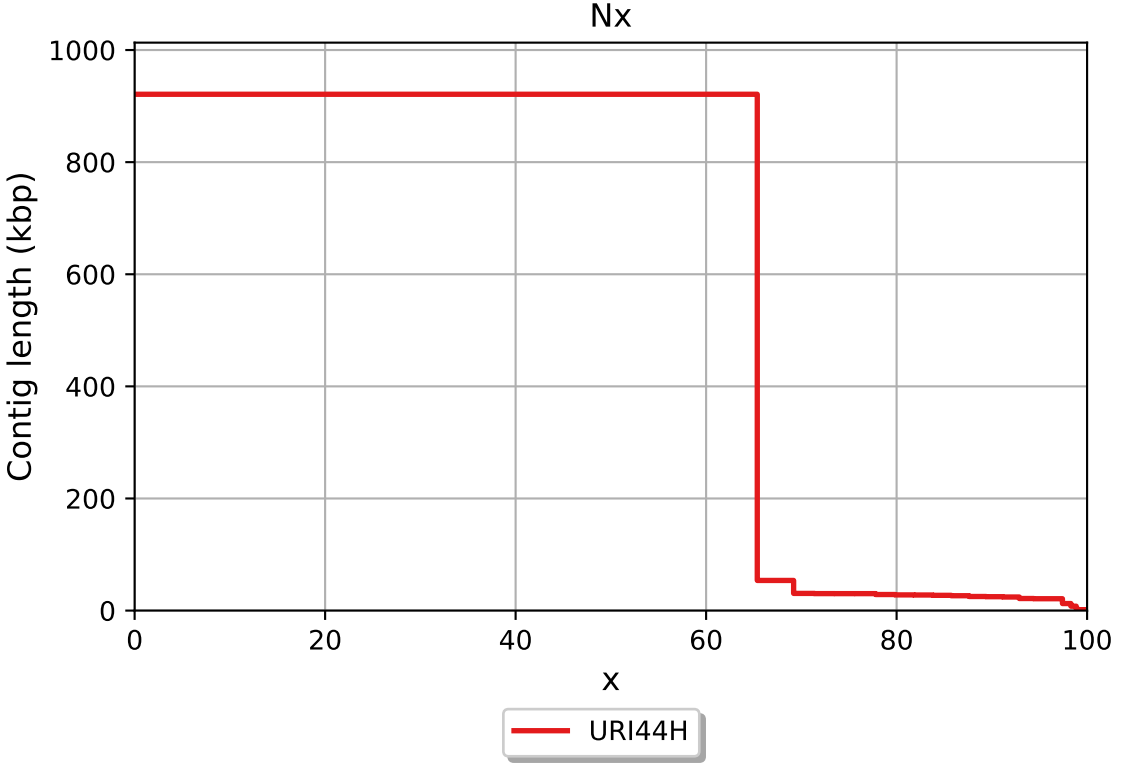
	URI44H
# misassemblies	24
# contig misassemblies	24
# c. relocations	5
# c. translocations	18
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	1187541
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	9783
# indels	628
# indels (<= 5 bp)	565
# indels (> 5 bp)	63
Indels length	3320

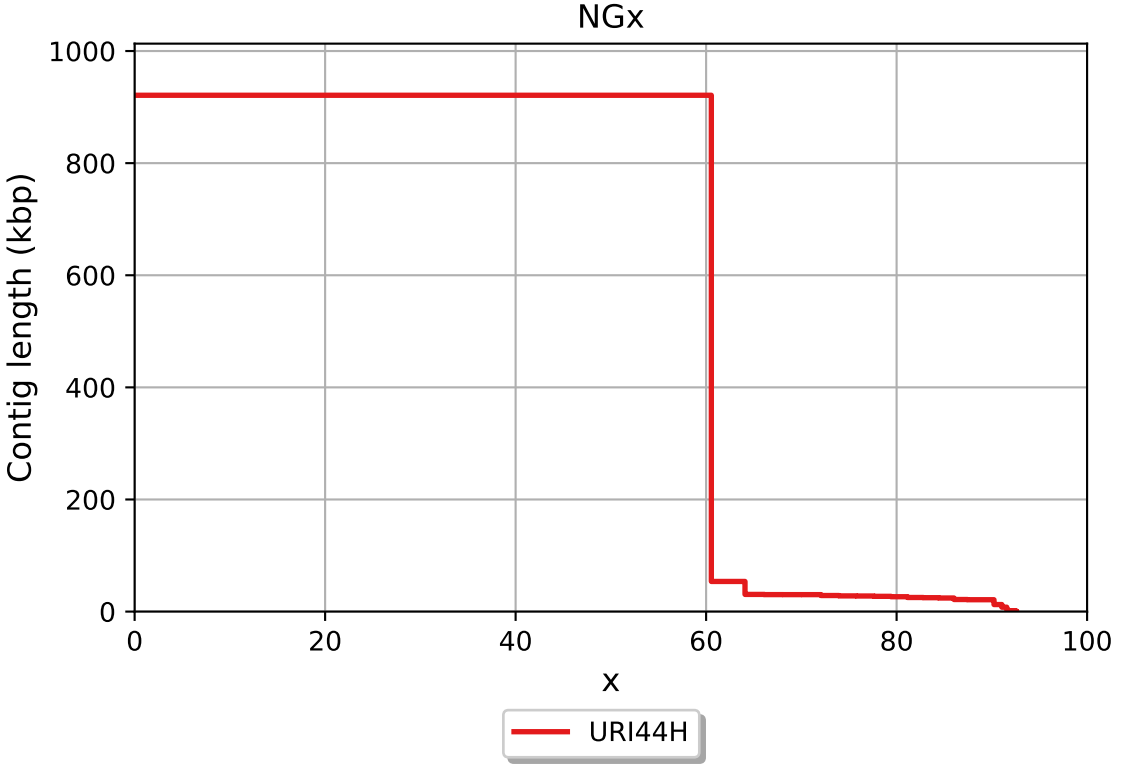
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

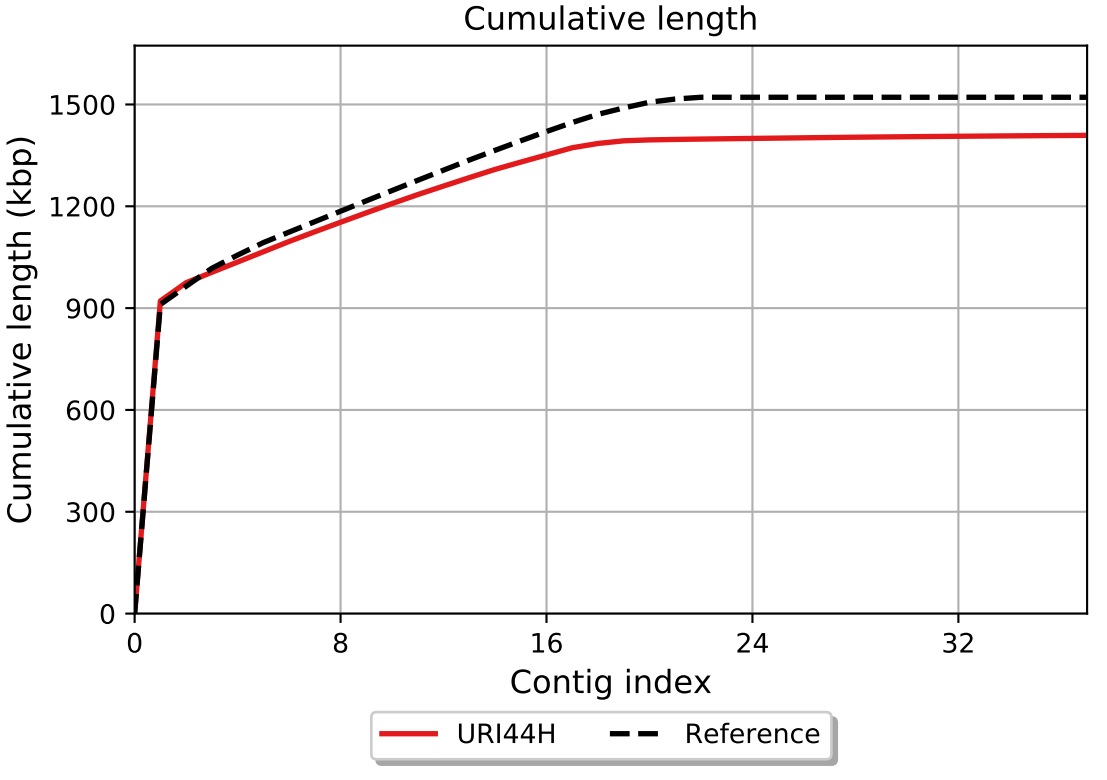
Unaligned report

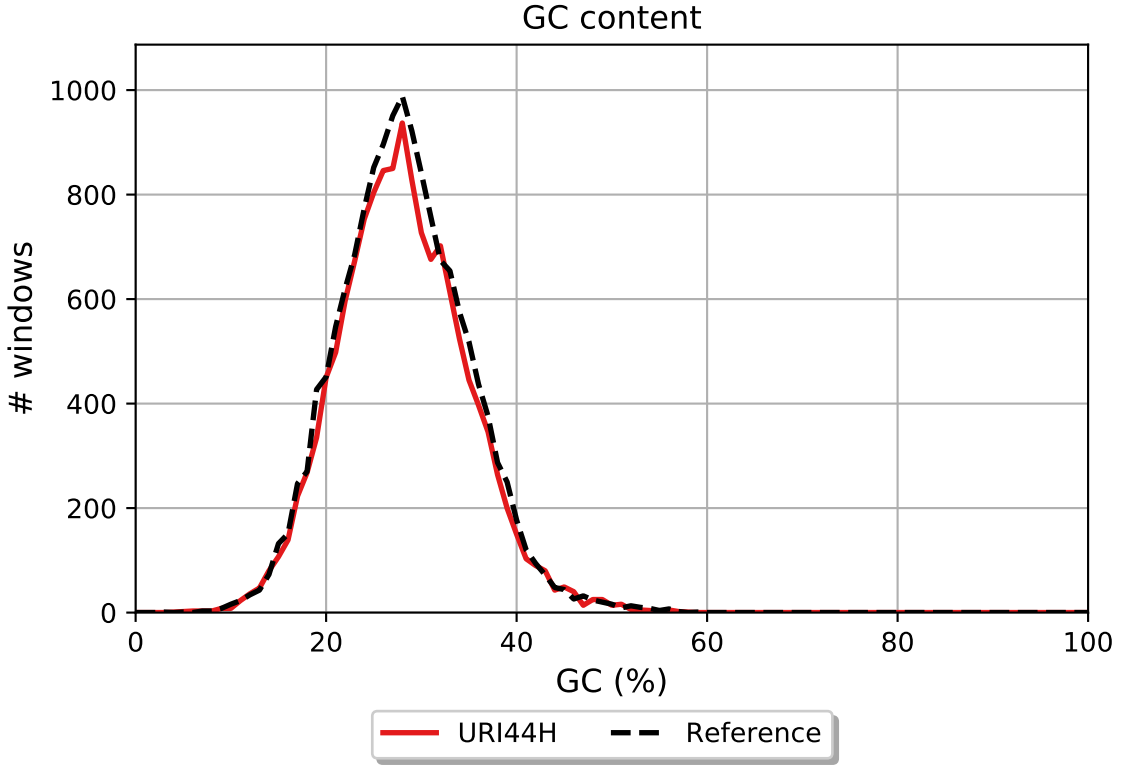
	URI44H
# fully unaligned contigs	4
Fully unaligned length	2724
# partially unaligned contigs	20
Partially unaligned length	178275
# N's	0

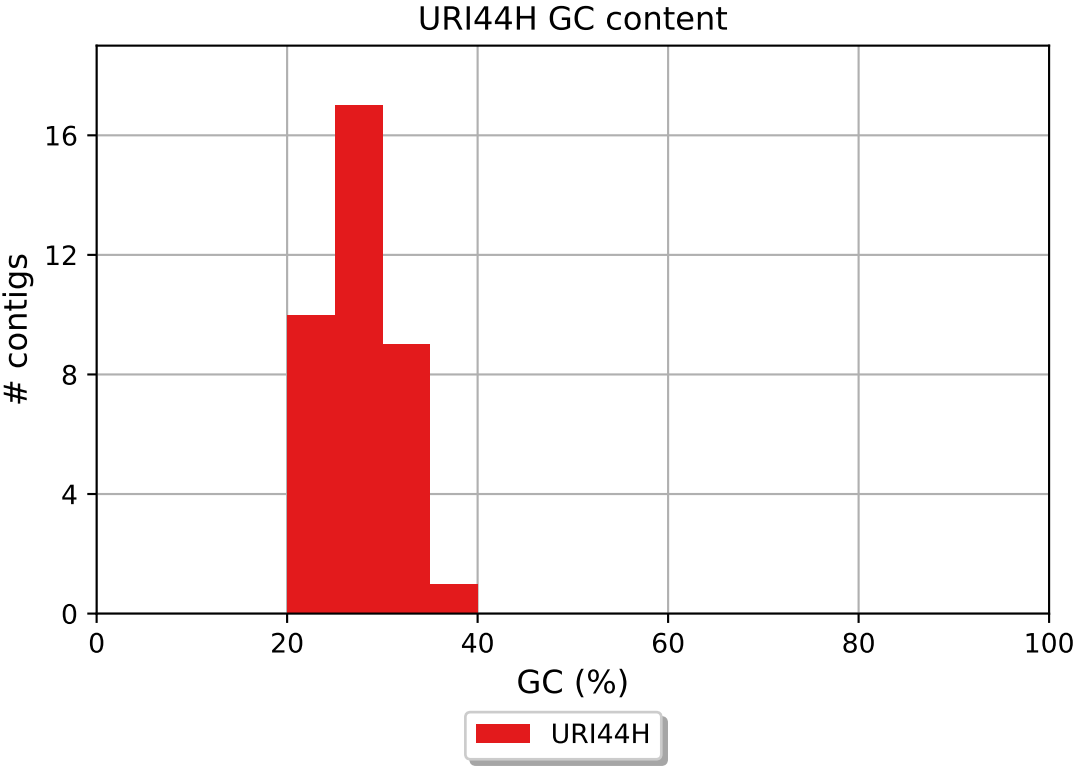
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

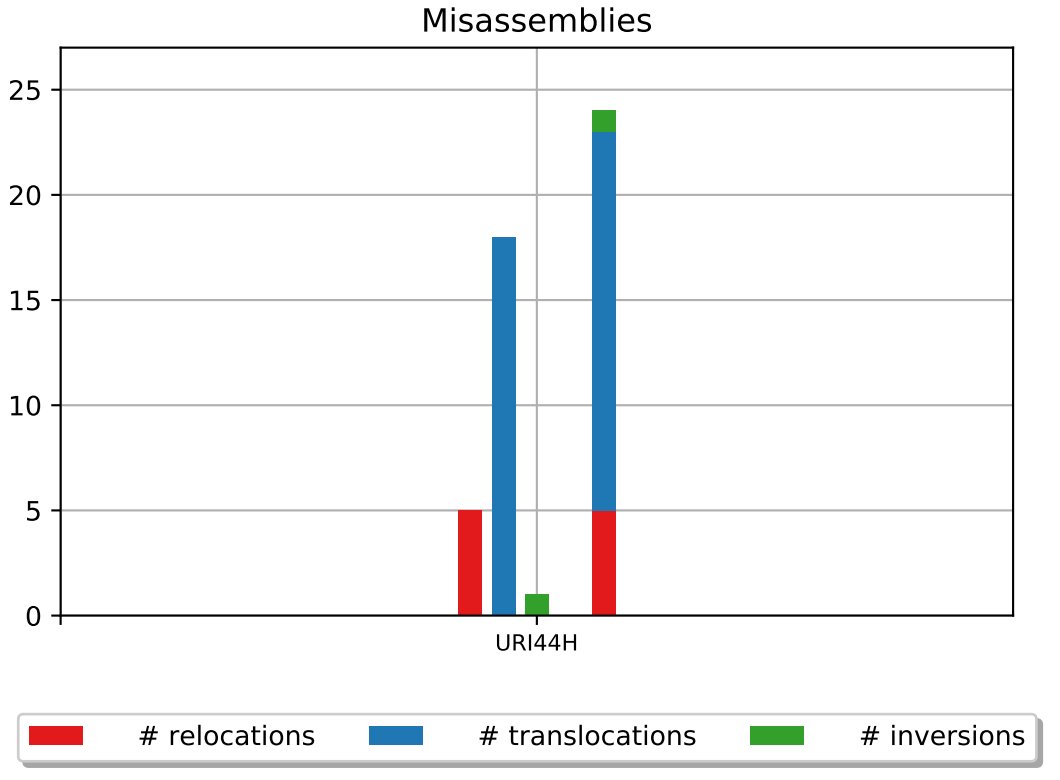

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI44H

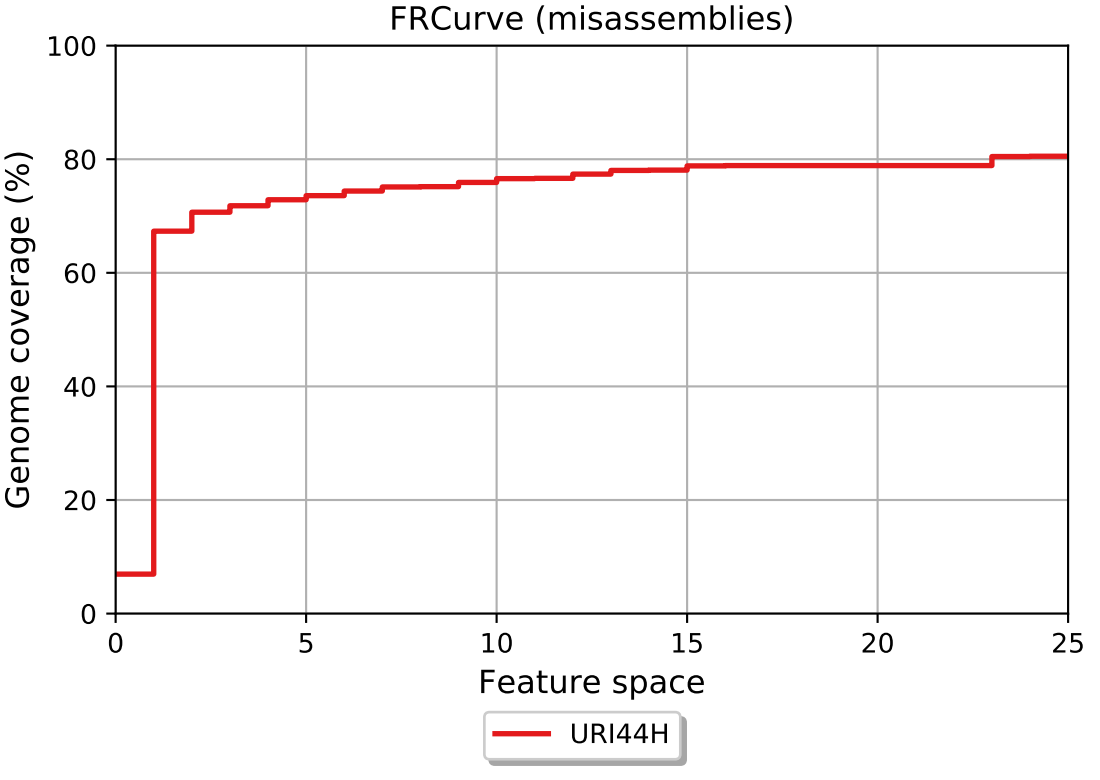

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI44H

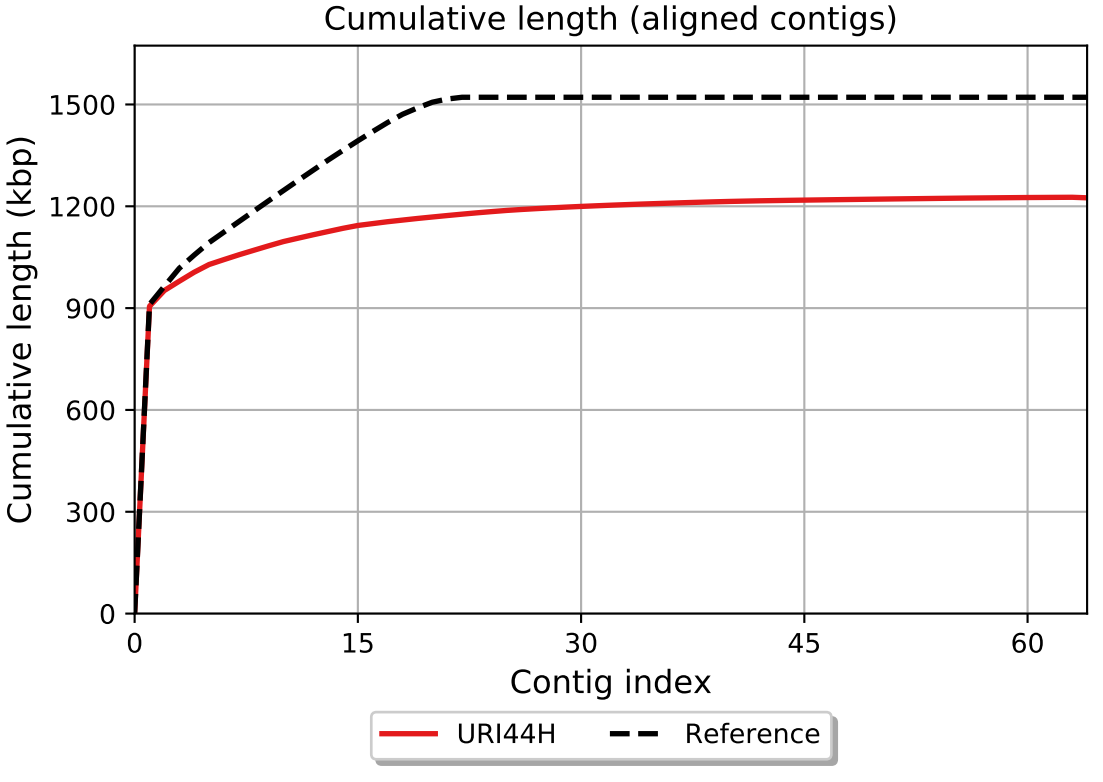

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
Contig index
URI44H
Reference

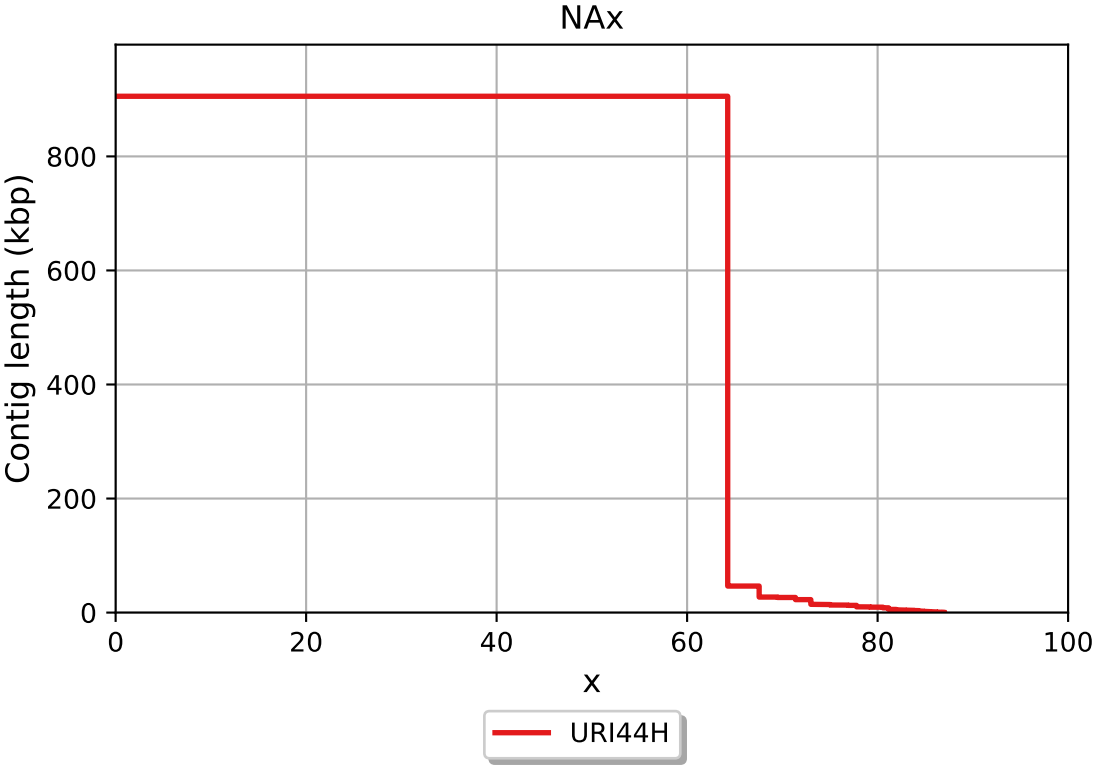

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
URI44H
Reference

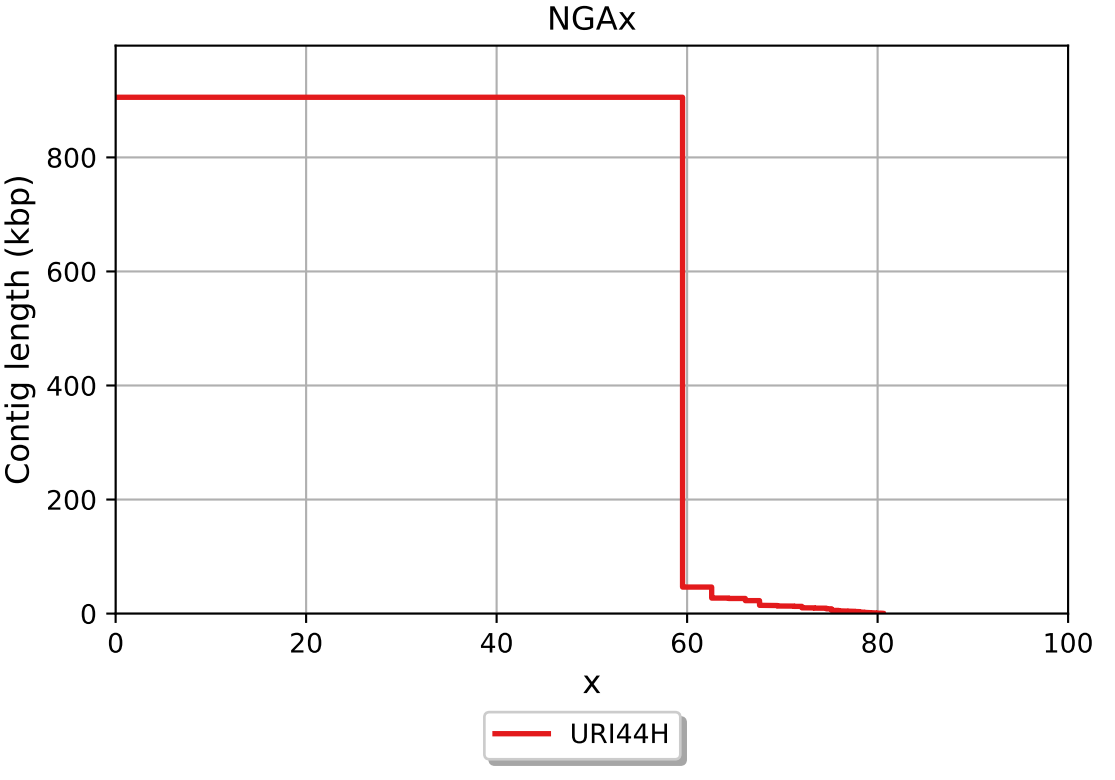

URI44H GC content
contigs
0
4
8
12
16
0
20
40
60
80
100
GC (%)
URI44H

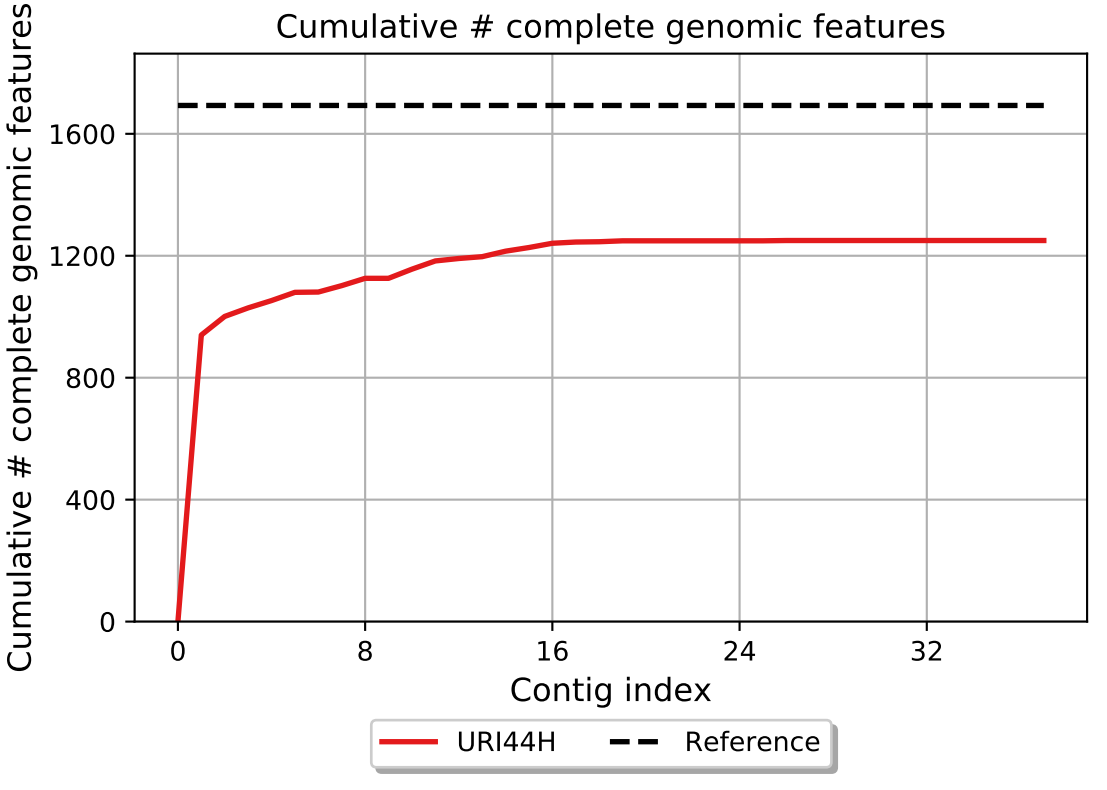

Misassemblies
25
20
15
10
5
0
URI44H
relocations
translocations
inversions

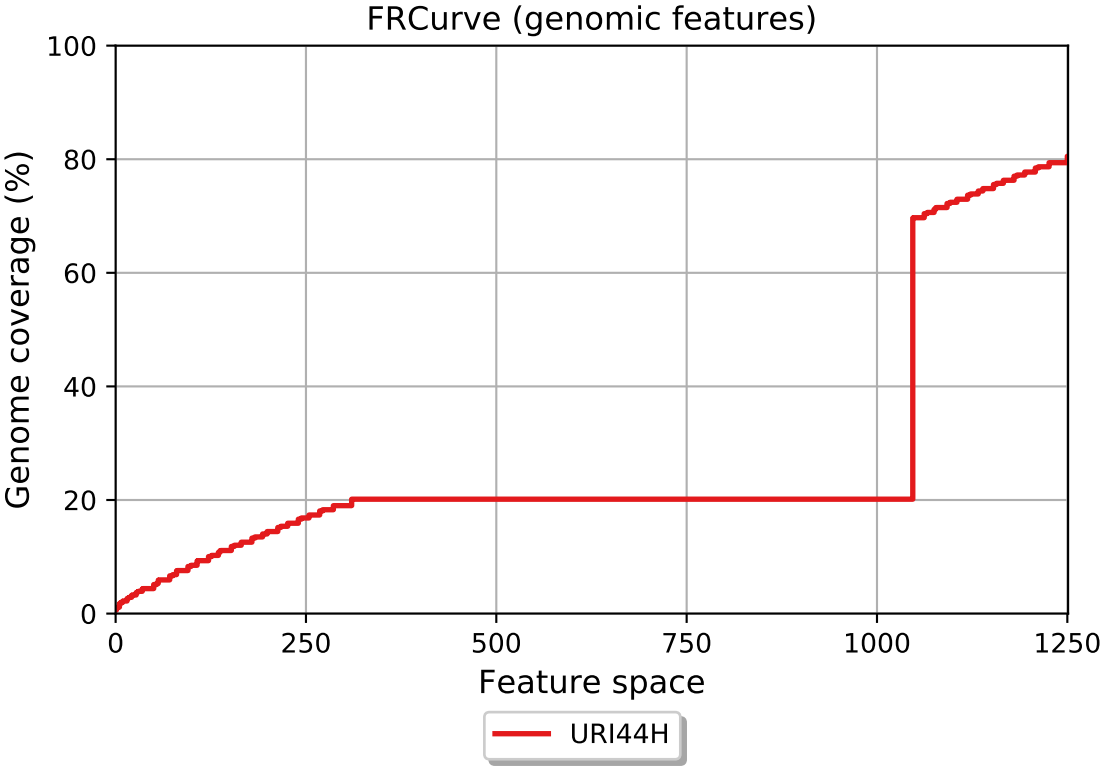

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
URI44H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
15
30
45
60
Contig index
URI44H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
URI44H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
URI44H


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
8
16
24
32
Contig index
URI44H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
URI44H