Report

	URI40H
# contigs (>= 0 bp)	82
# contigs (>= 1000 bp)	26
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1509727
Total length (>= 1000 bp)	1489695
Total length (>= 5000 bp)	1482038
Total length (>= 10000 bp)	1468459
Total length (>= 25000 bp)	1430502
Total length (>= 50000 bp)	964227
# contigs	42
Largest contig	910602
Total length	1501192
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	910602
NG50	910602
N90	28159
NG90	26498
auN	564706.4
auNG	557276.0
L50	1
LG50	1
L90	14
LG90	15
# misassemblies	15
# misassembled contigs	10
Misassembled contigs length	273034
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	3 + 7 part
Unaligned length	38594
Genome fraction (%)	93.357
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	147.59
# indels per 100 kbp	20.18
# genomic features	1538 + 39 part
Largest alignment	910602
Total aligned length	1461497
NA50	910602
NGA50	910602
NA90	15745
NGA90	11855
auNA	562201.8
auNGA	554804.4
LA50	1
LGA50	1
LA90	17
LGA90	18

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

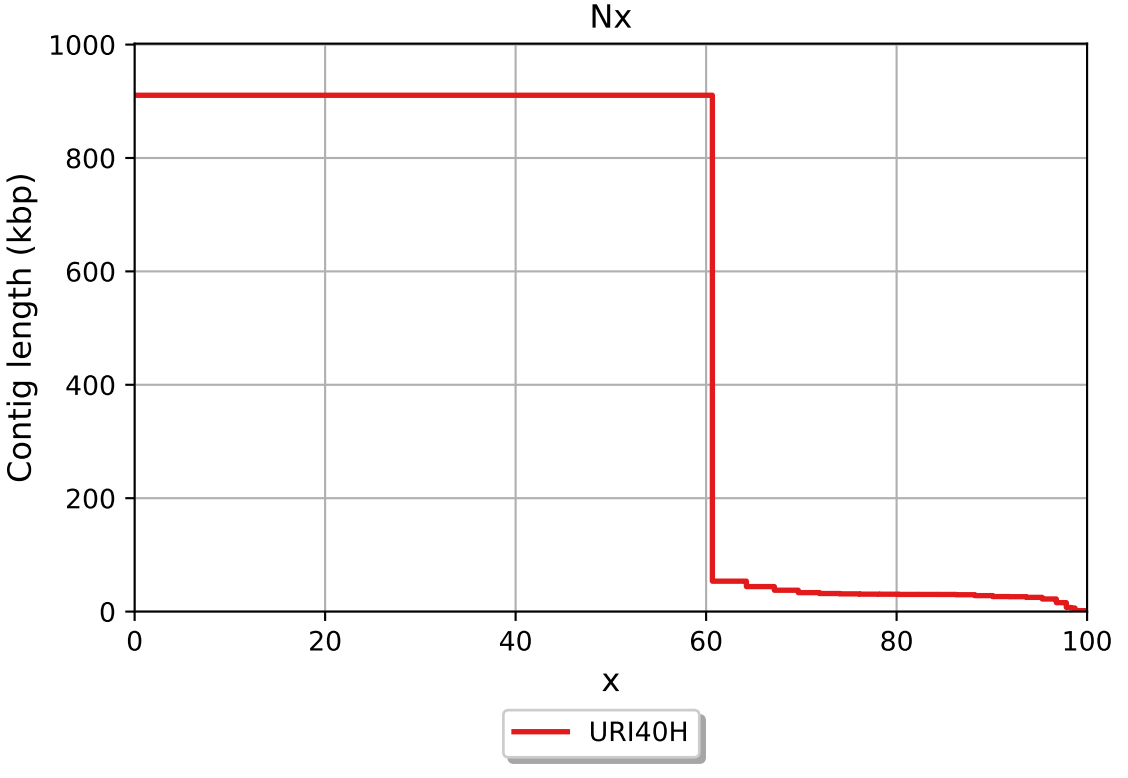
	URI40H
# misassemblies	15
# contig misassemblies	15
# c. relocations	6
# c. translocations	7
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	273034
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	2157
# indels	295
# indels (<= 5 bp)	256
# indels (> 5 bp)	39
Indels length	1362

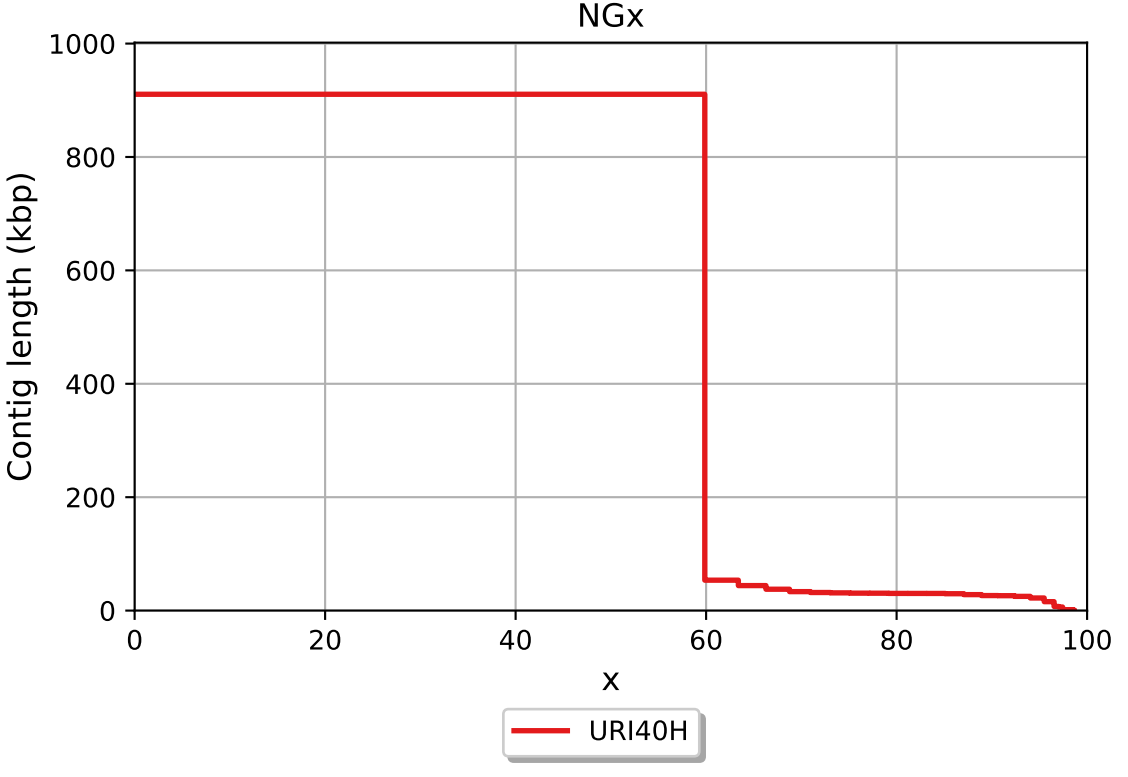
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

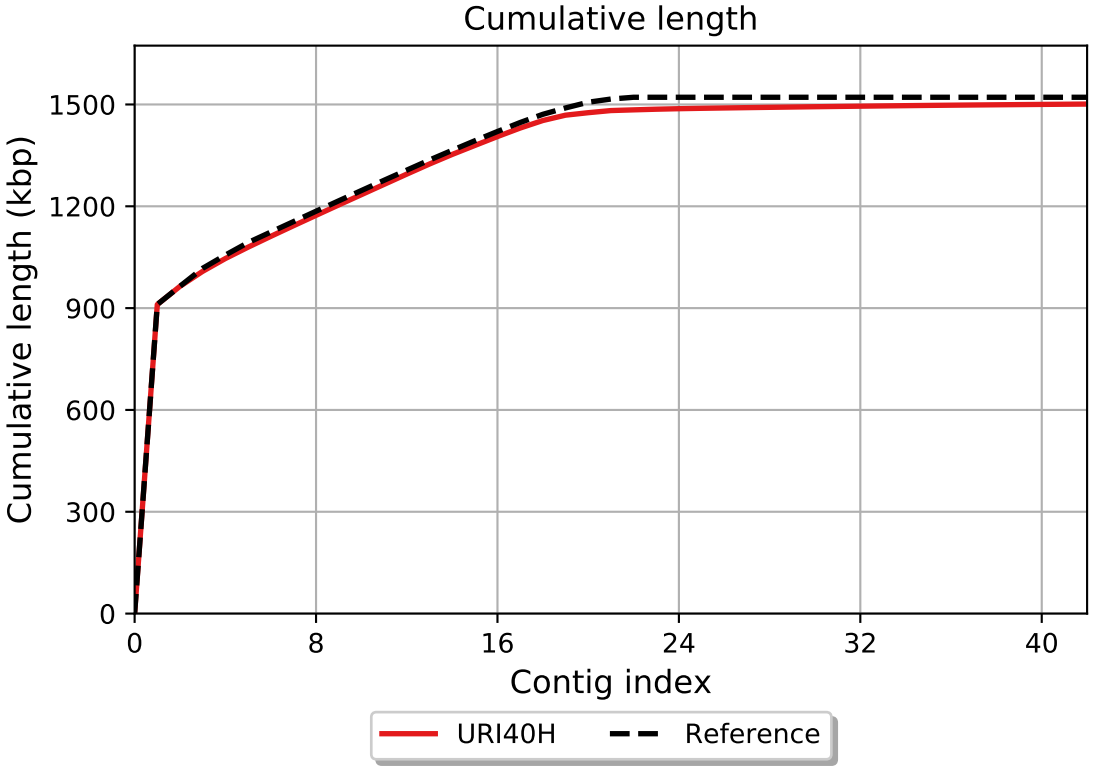
Unaligned report

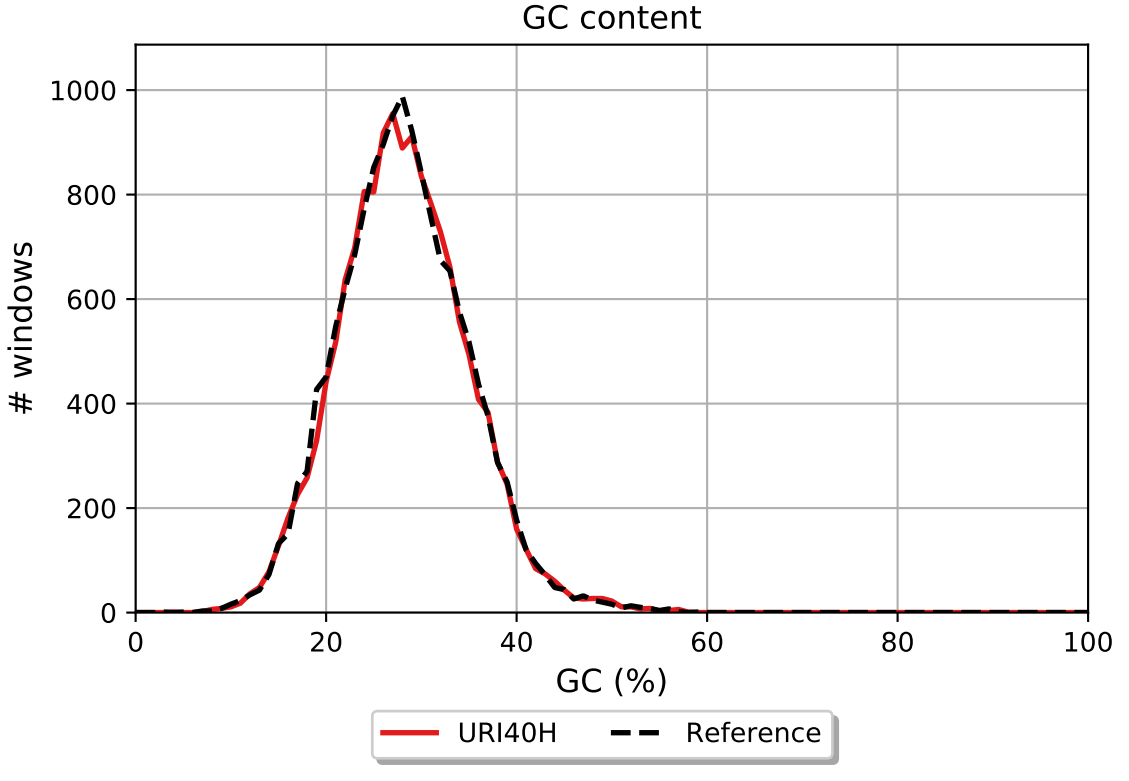
	URI40H
# fully unaligned contigs	3
Fully unaligned length	3708
# partially unaligned contigs	7
Partially unaligned length	34886
# N's	0

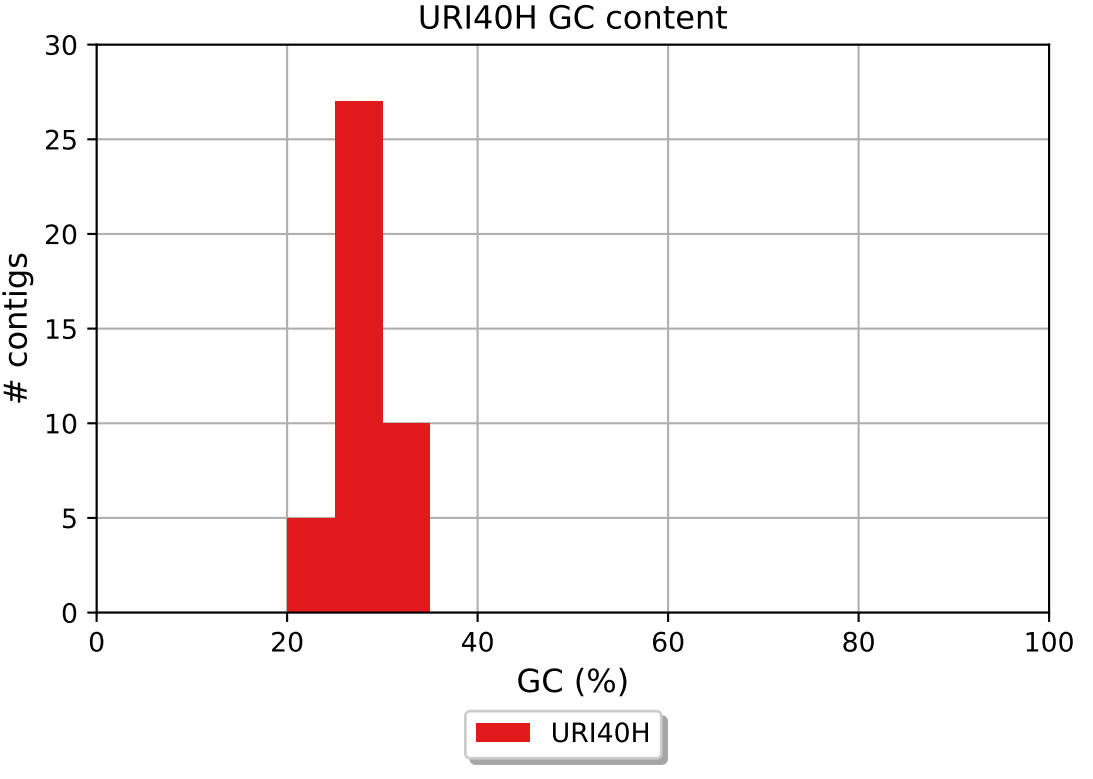
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

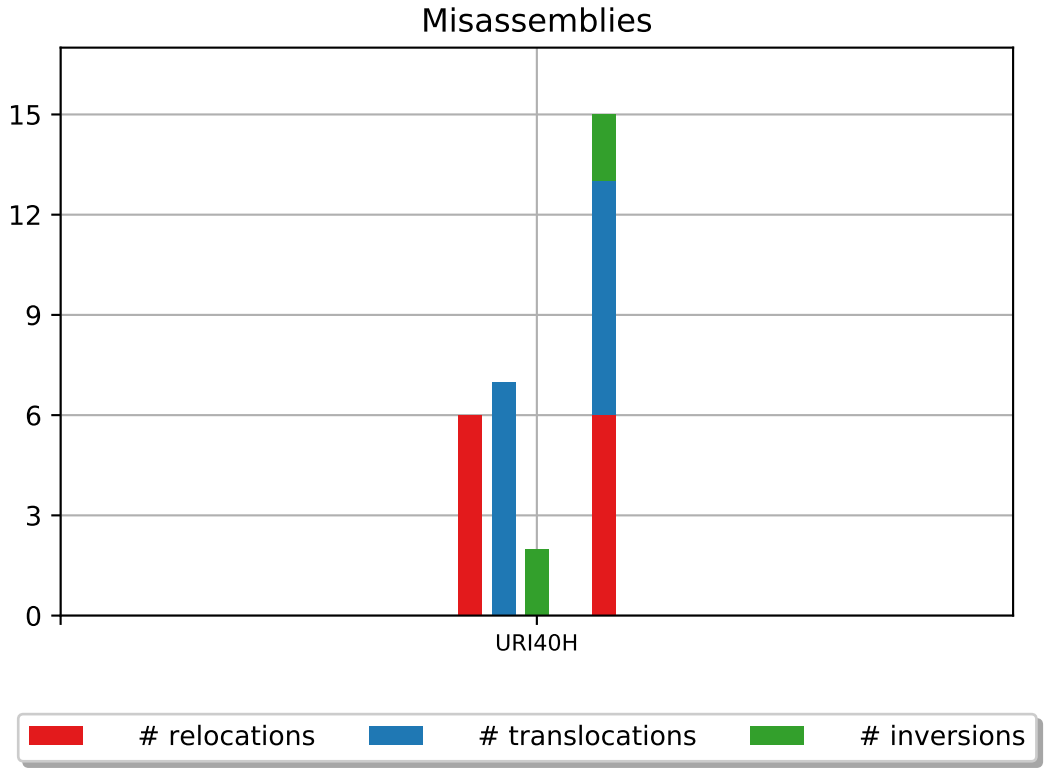

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI40H

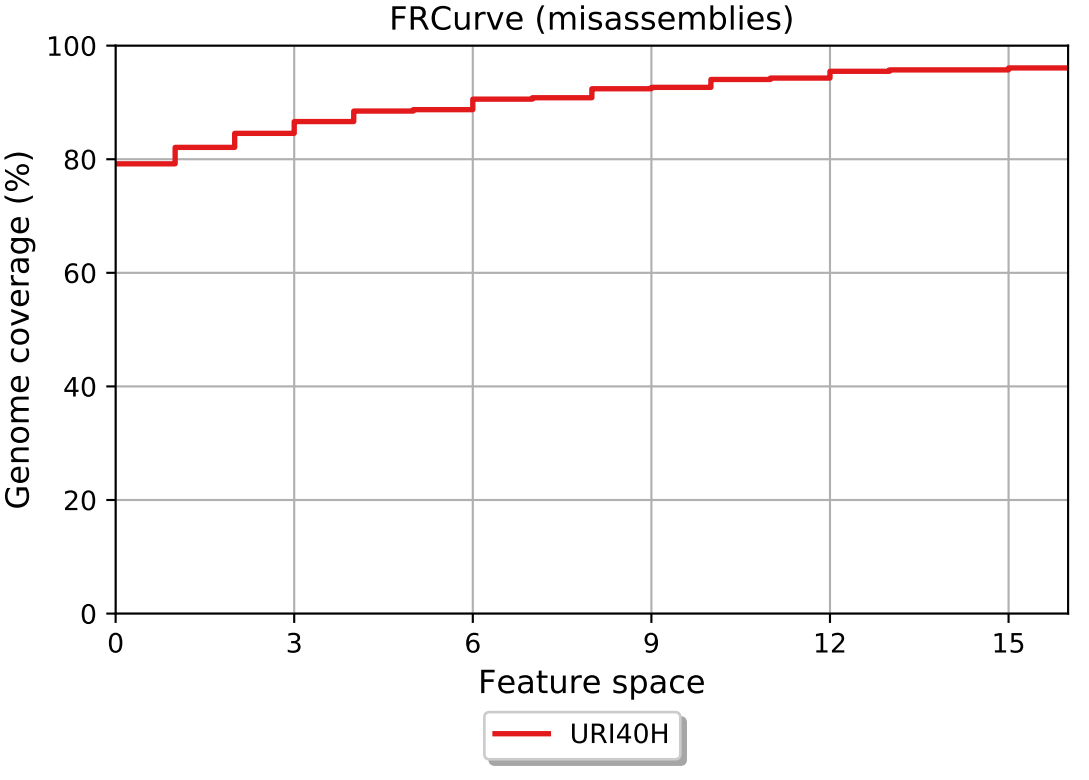

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI40H

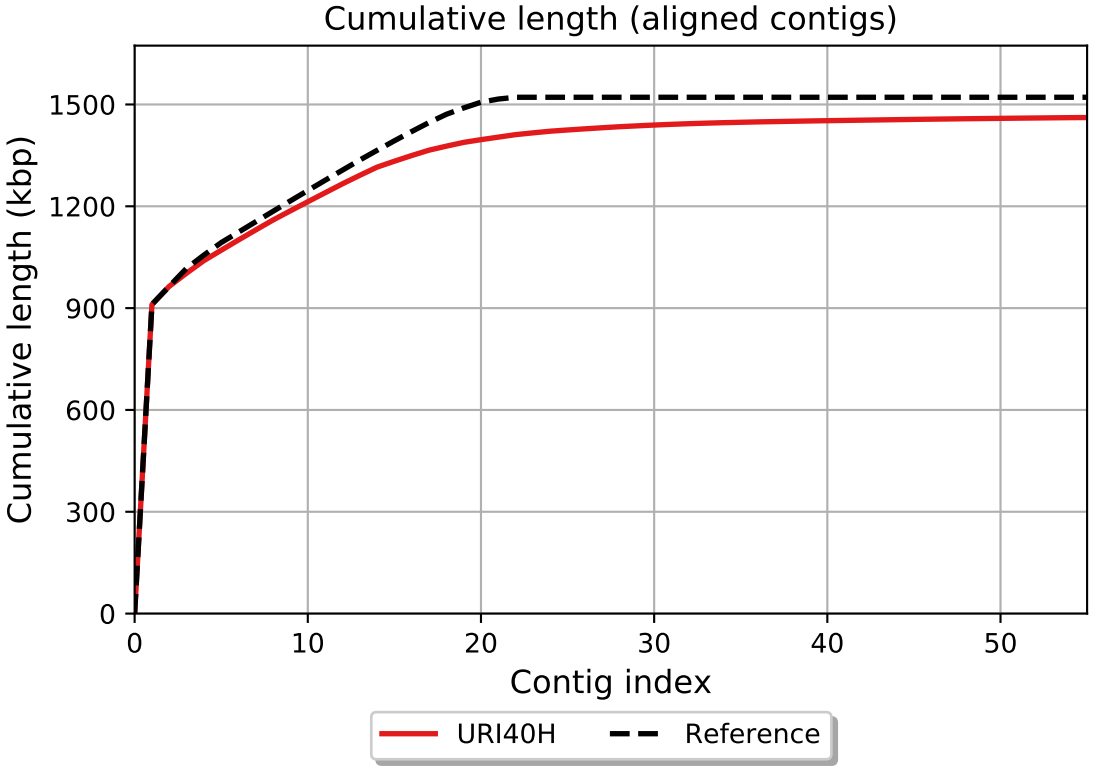

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
URI40H
Reference

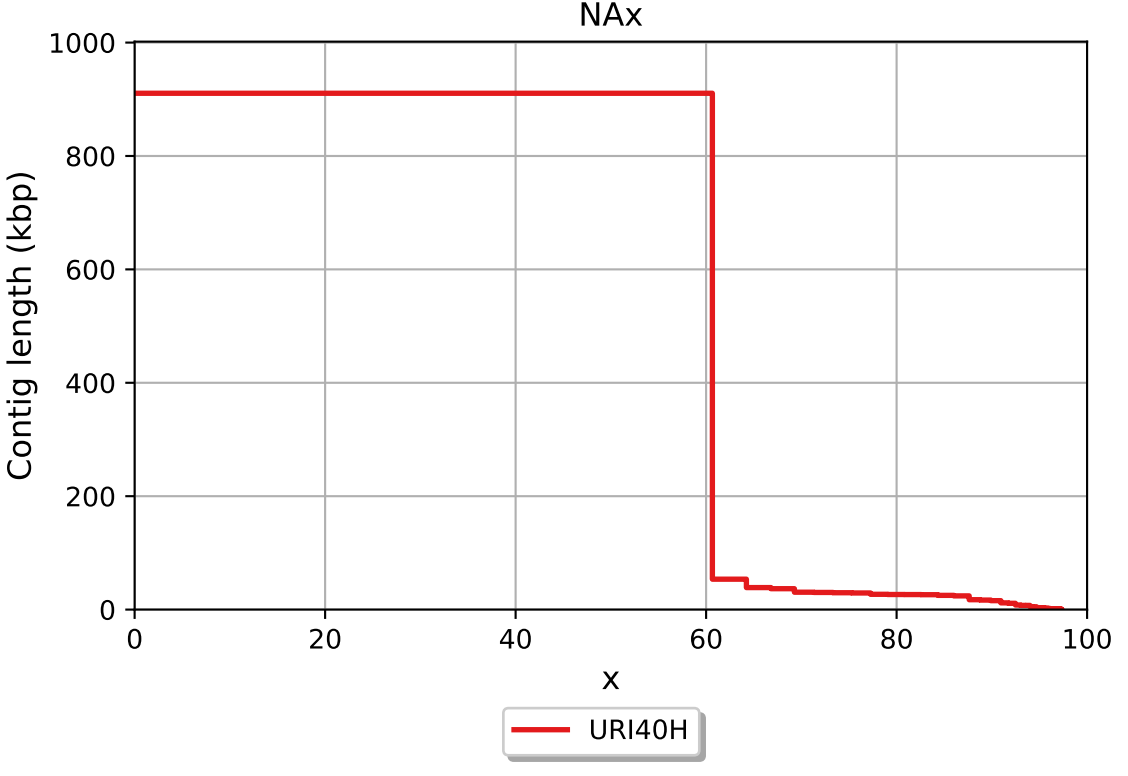

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
URI40H
Reference

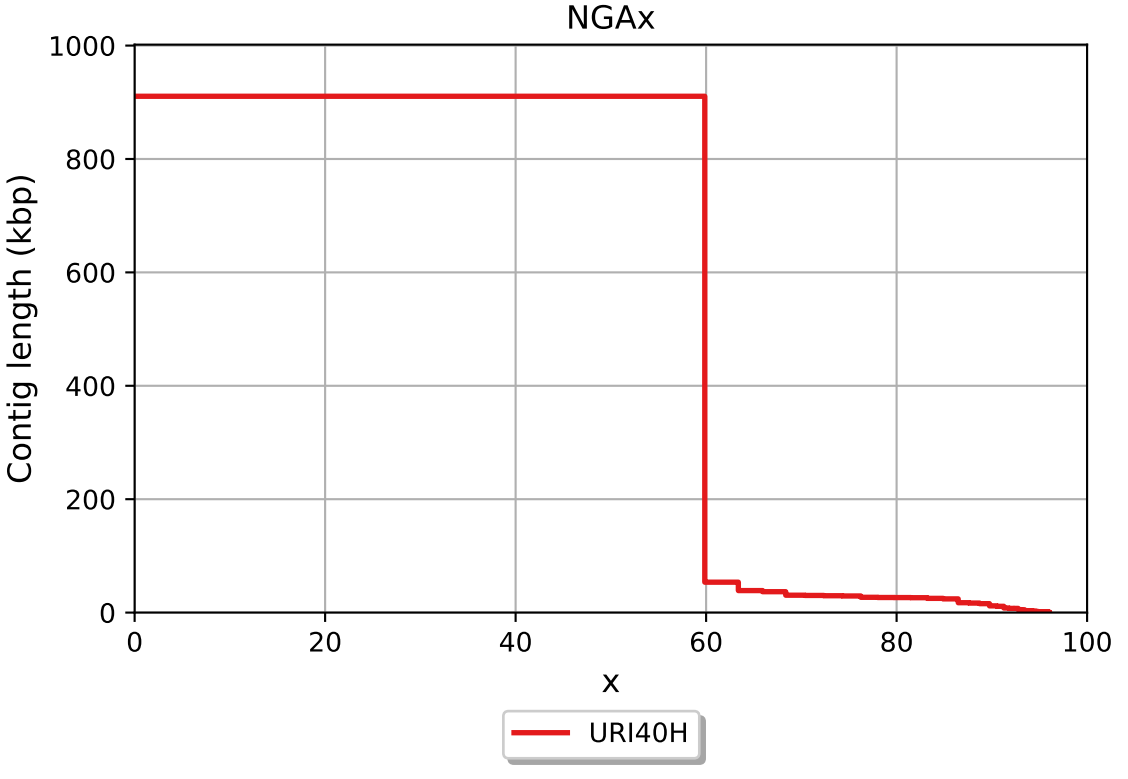

URI40H GC content
contigs
GC (%)
0
5
10
15
20
25
30
0
20
40
60
80
100
URI40H

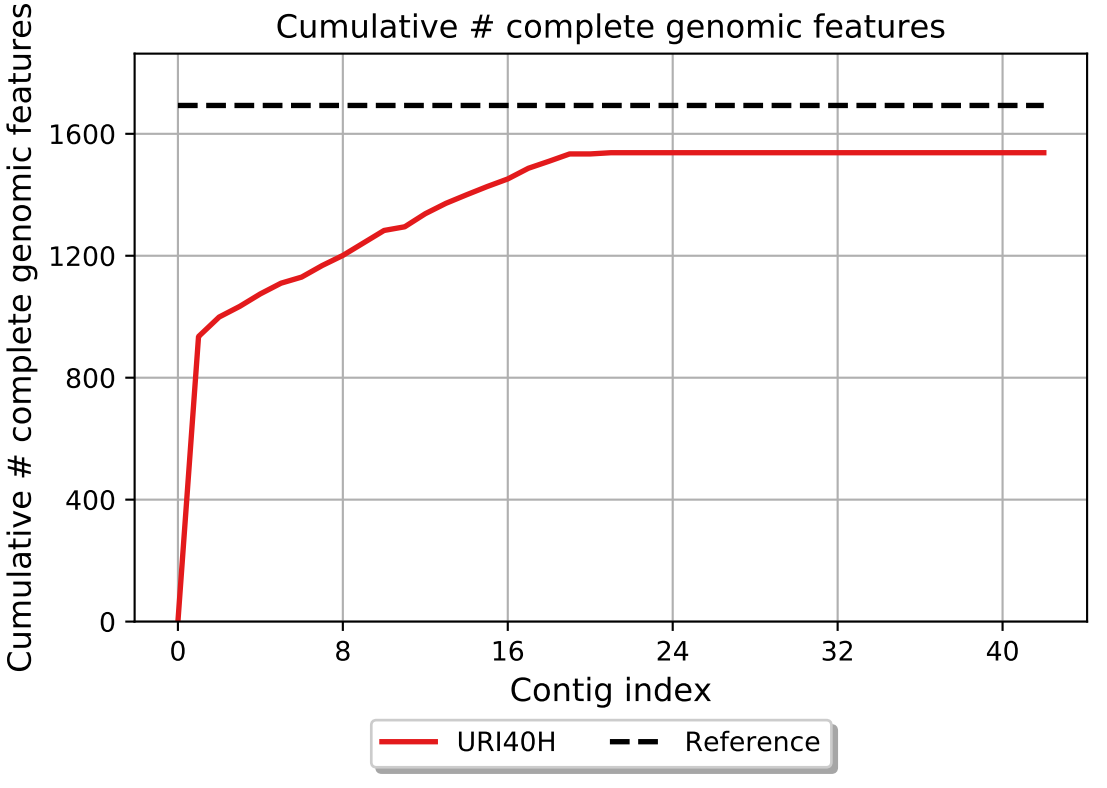

Misassemblies
15
12
9
6
3
0
URI40H
relocations
translocations
inversions

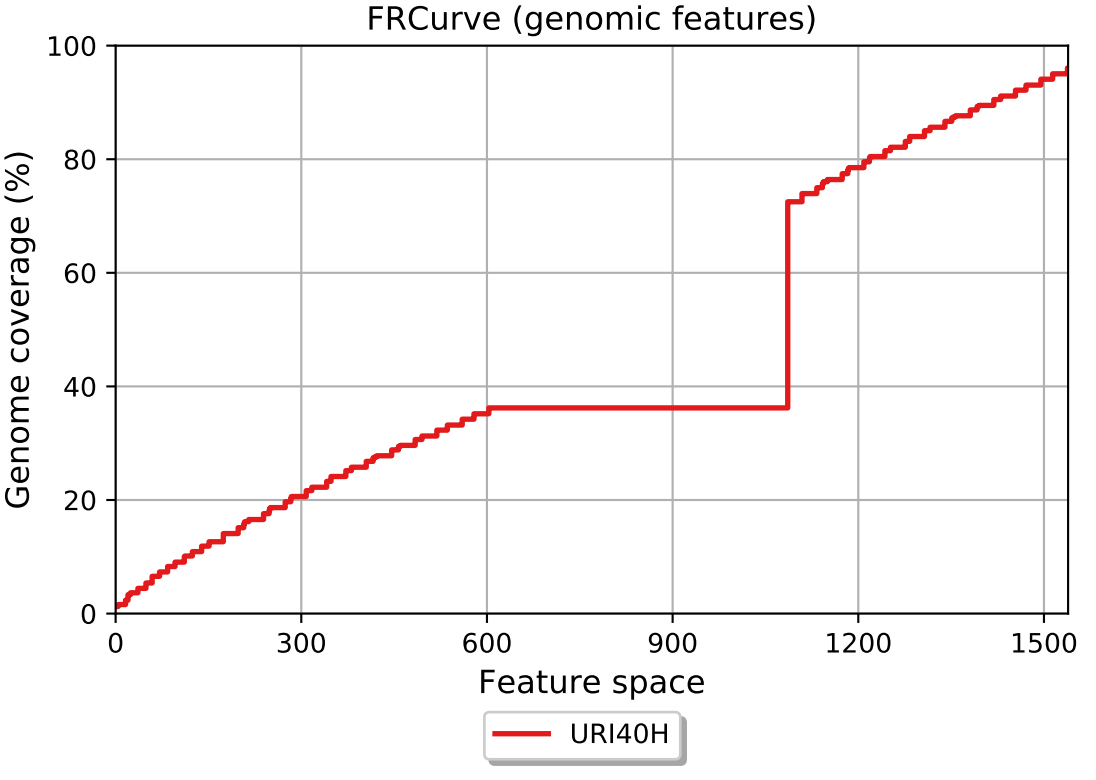

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
URI40H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
Contig index
URI40H
Reference


NAx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI40H


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI40H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
8
16
24
32
40
Contig index
URI40H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
URI40H