Report

| | URI47H |
|---|---|
| # contigs (>= 0 bp) | 29 |
| # contigs (>= 1000 bp) | 21 |
| # contigs (>= 5000 bp) | 19 |
| # contigs (>= 10000 bp) | 18 |
| # contigs (>= 25000 bp) | 14 |
| # contigs (>= 50000 bp) | 4 |
| Total length (>= 0 bp) | 1512039 |
| Total length (>= 1000 bp) | 1507689 |
| Total length (>= 5000 bp) | 1505586 |
| Total length (>= 10000 bp) | 1496192 |
| Total length (>= 25000 bp) | 1407672 |
| Total length (>= 50000 bp) | 1111925 |
| # contigs | 24 |
| Largest contig | 921203 |
| Total length | 1510323 |
| Reference length | 1521208 |
| GC (%) | 28.18 |
| Reference GC (%) | 28.18 |
| N50 | 921203 |
| NG50 | 921203 |
| N90 | 26514 |
| NG90 | 26514 |
| auN | 577492.2 |
| auNG | 573360.0 |
| L50 | 1 |
| LG50 | 1 |
| L90 | 13 |
| LG90 | 13 |
| # misassemblies | 31 |
| # misassembled contigs | 16 |
| Misassembled contigs length | 1356200 |
| # local misassemblies | 16 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 3 |
| # unaligned contigs | 0 + 17 part |
| Unaligned length | 213246 |
| Genome fraction (%) | 80.907 |
| Duplication ratio | 1.050 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 924.47 |
| # indels per 100 kbp | 58.01 |
| # genomic features | 1290 + 54 part |
| Largest alignment | 905460 |
| Total aligned length | 1292852 |
| NA50 | 905460 |
| NGA50 | 905460 |
| NA90 | - |
| NGA90 | - |
| auNA | 547281.9 |
| auNGA | 543365.8 |
| 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

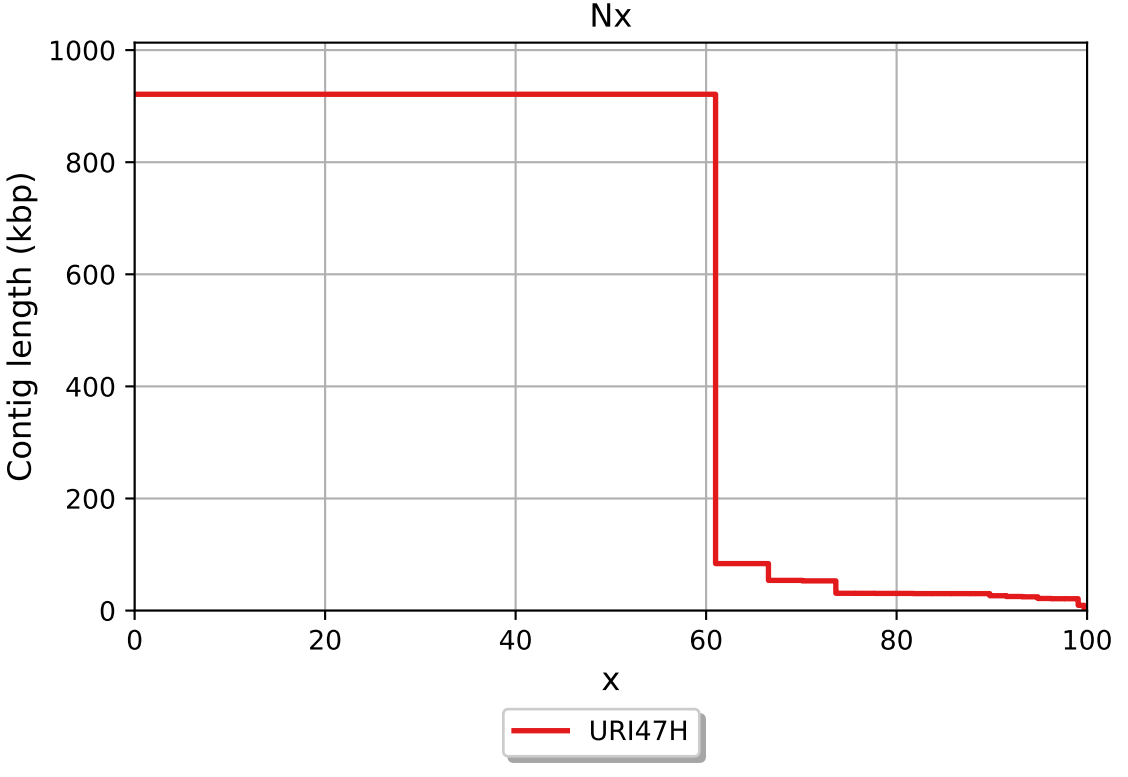
| | URI47H |
|---|---|
| # misassemblies | 31 |
| # contig misassemblies | 31 |
| # c. relocations | 4 |
| # c. translocations | 25 |
| # c. inversions | 2 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 16 |
| Misassembled contigs length | 1356200 |
| # local misassemblies | 16 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 3 |
| # mismatches | 11952 |
| # indels | 750 |
| # indels (<= 5 bp) | 682 |
| # indels (> 5 bp) | 68 |
| Indels length | 4175 |

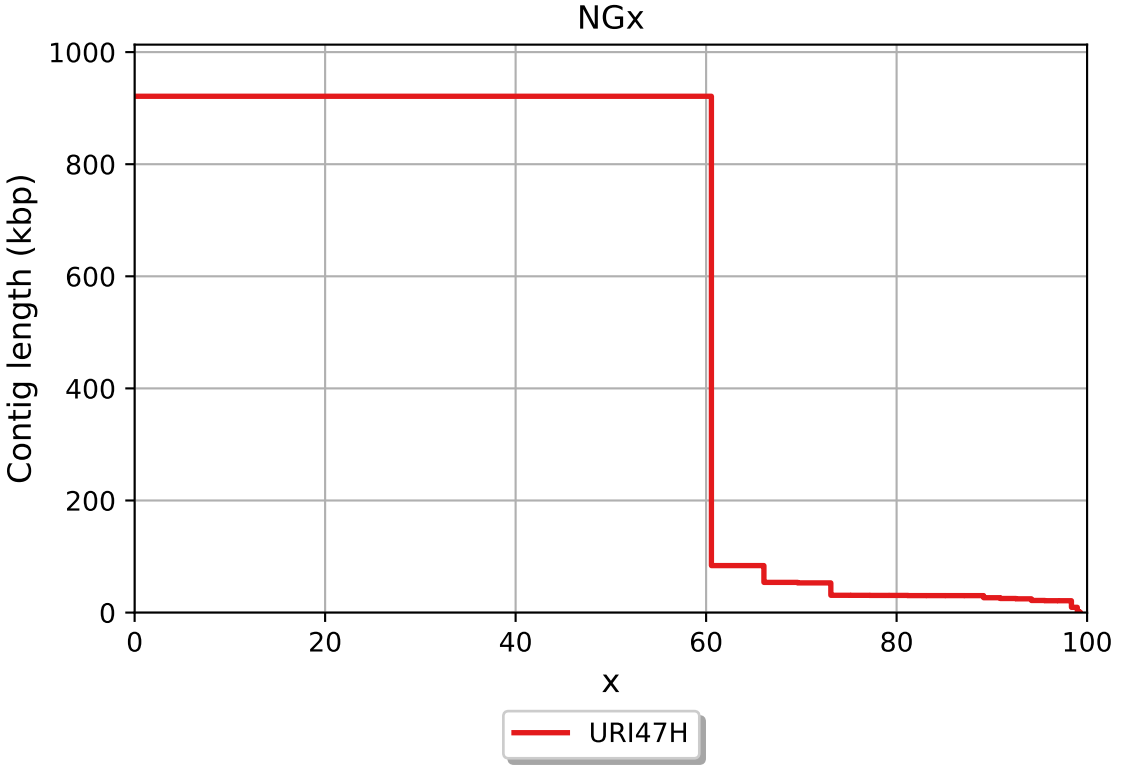
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

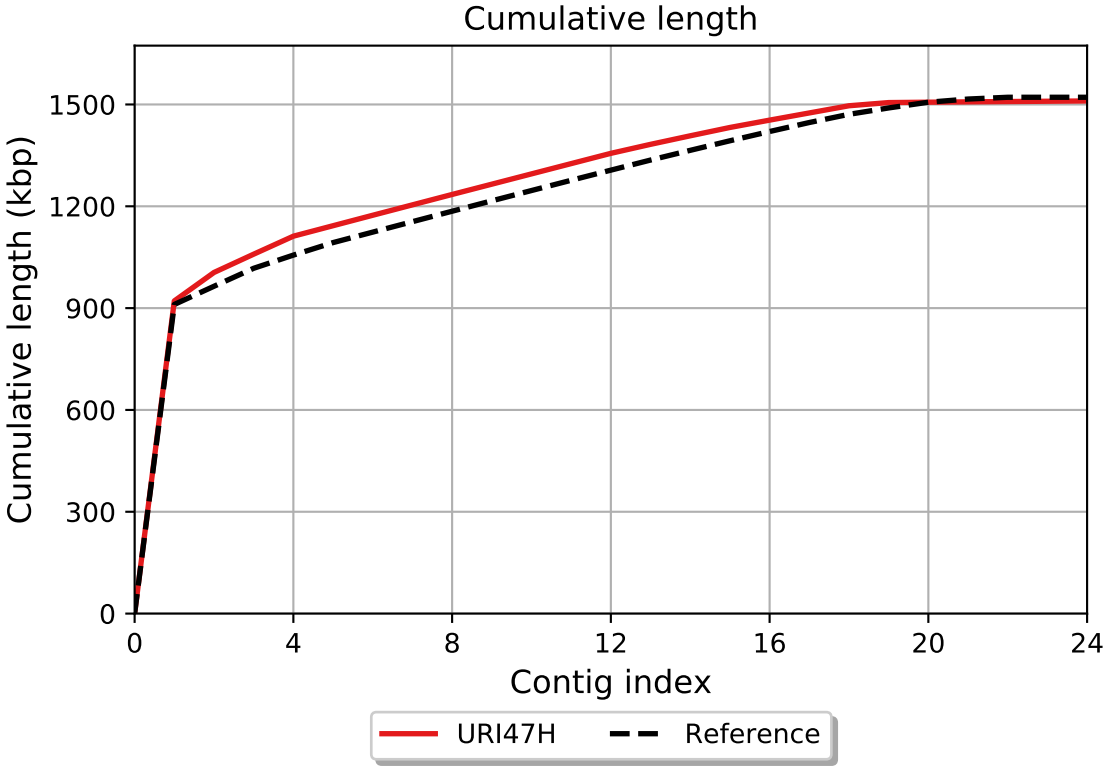
# Unaligned report

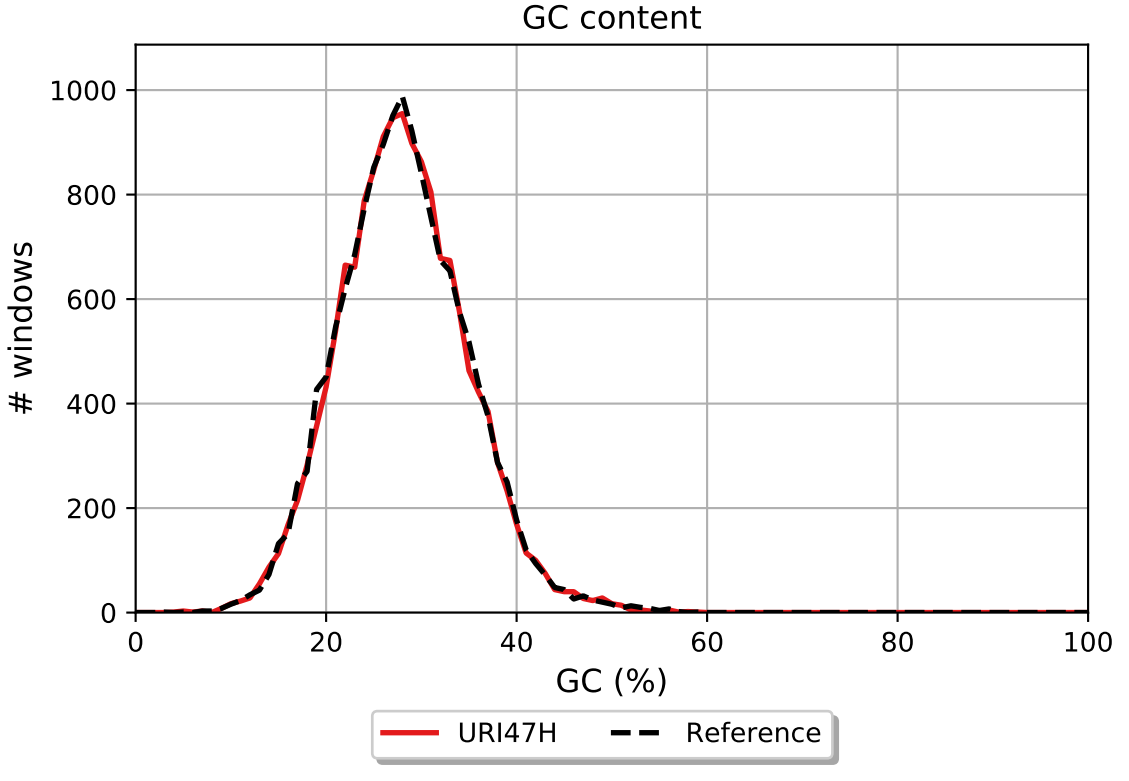
| | URI47H |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 17 |
| Partially unaligned length | 213246 |
| # N's | 0 |

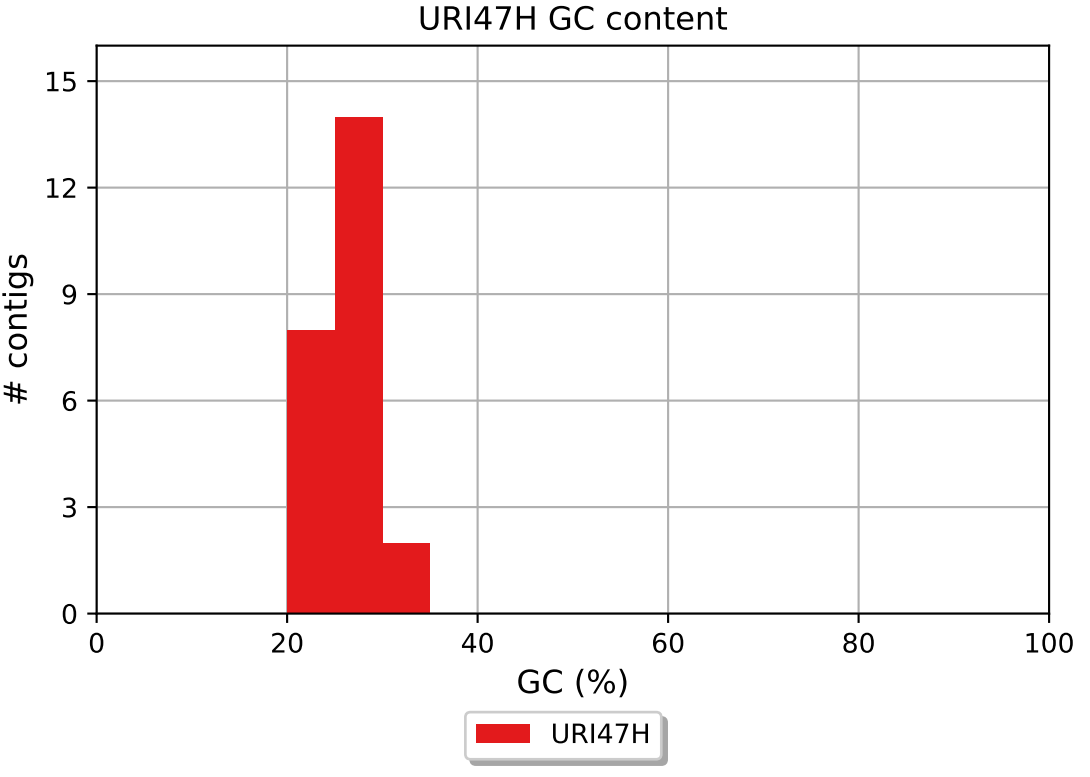
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

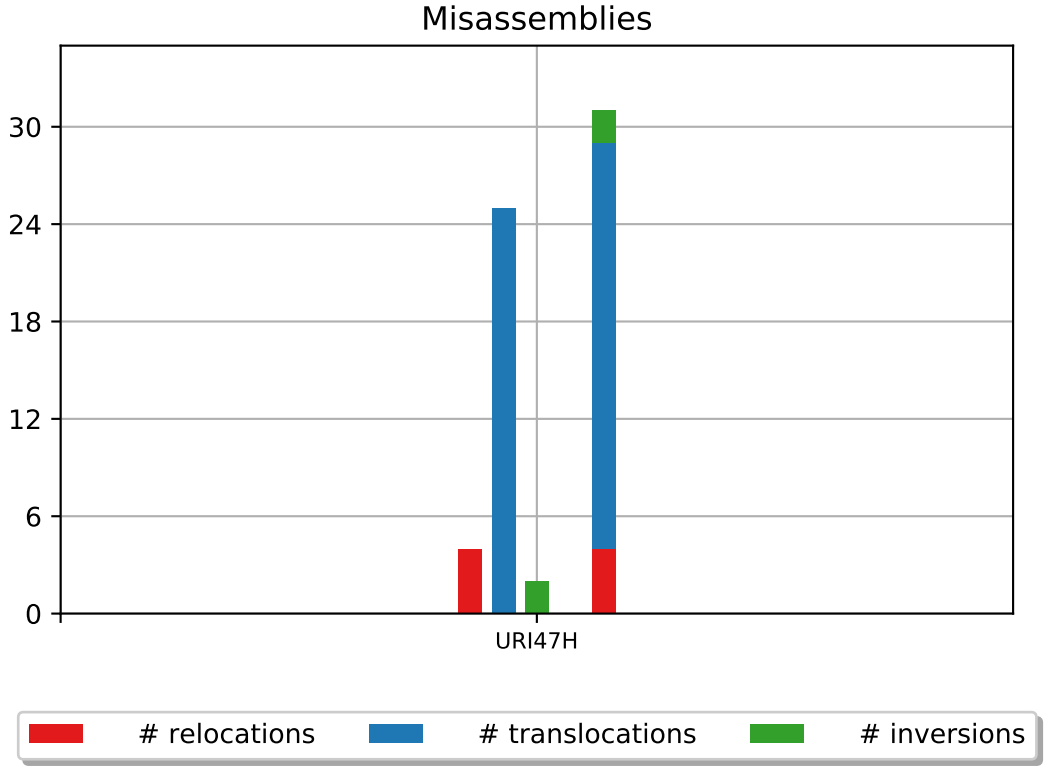

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI47H

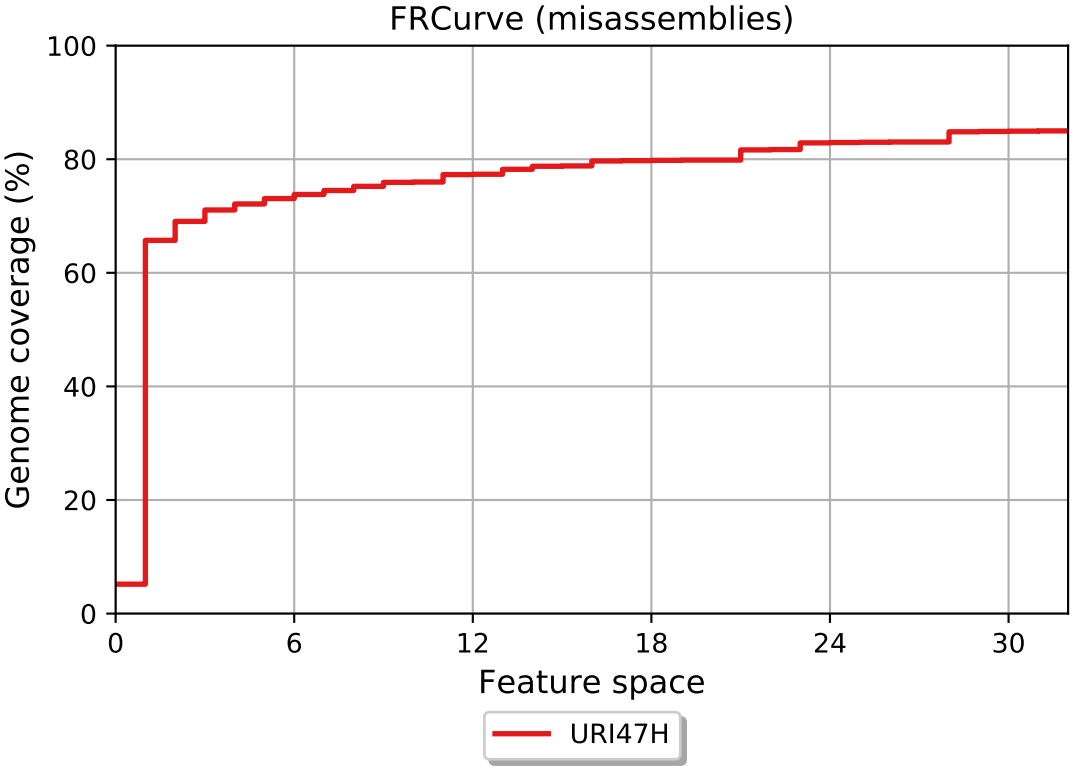

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI47H

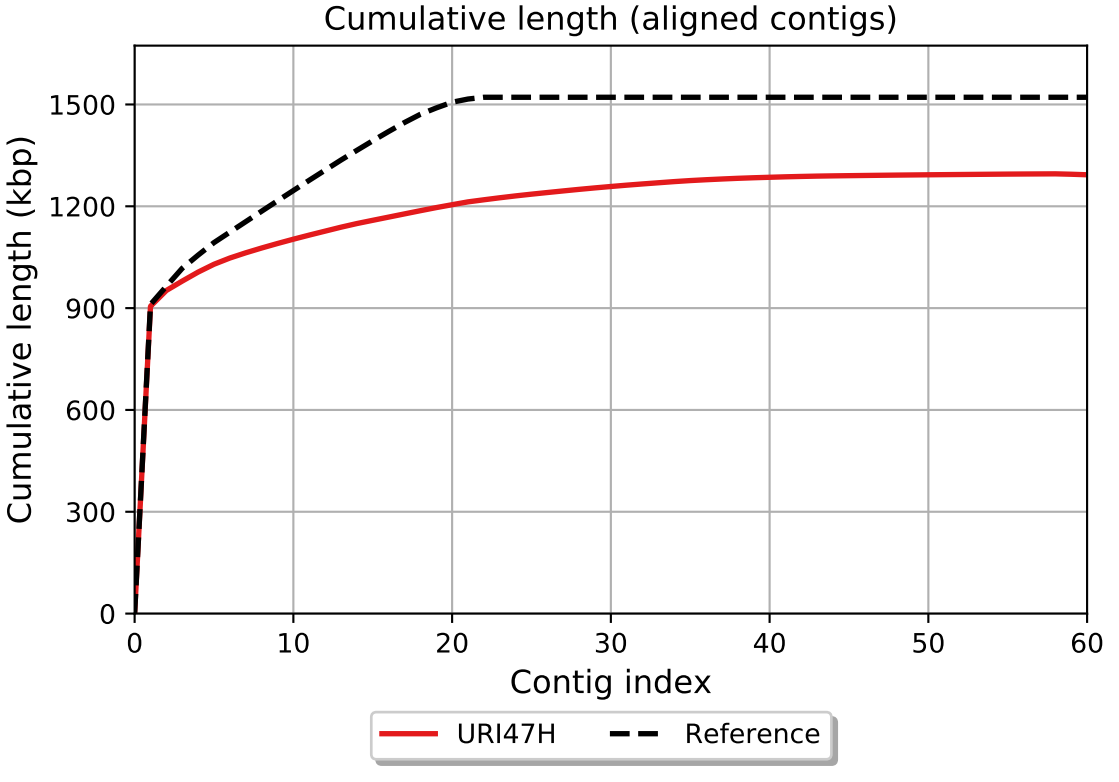

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
24
Contig index
URI47H
Reference

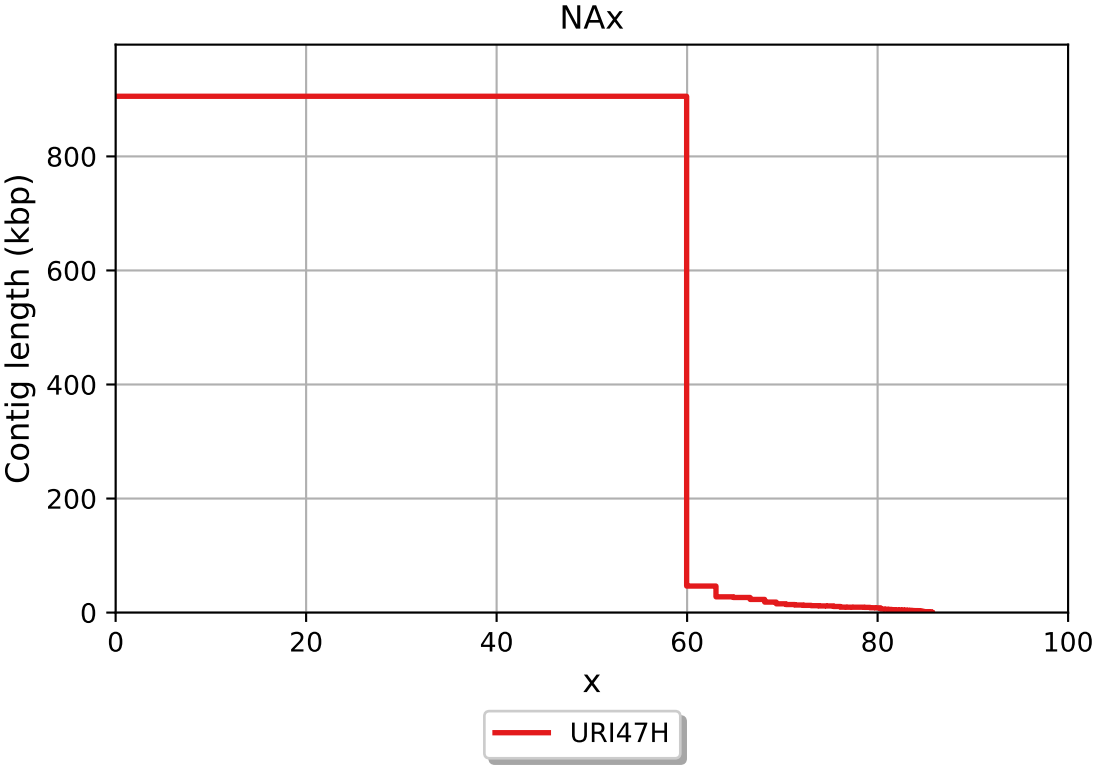

GC content
# windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
URI47H
Reference

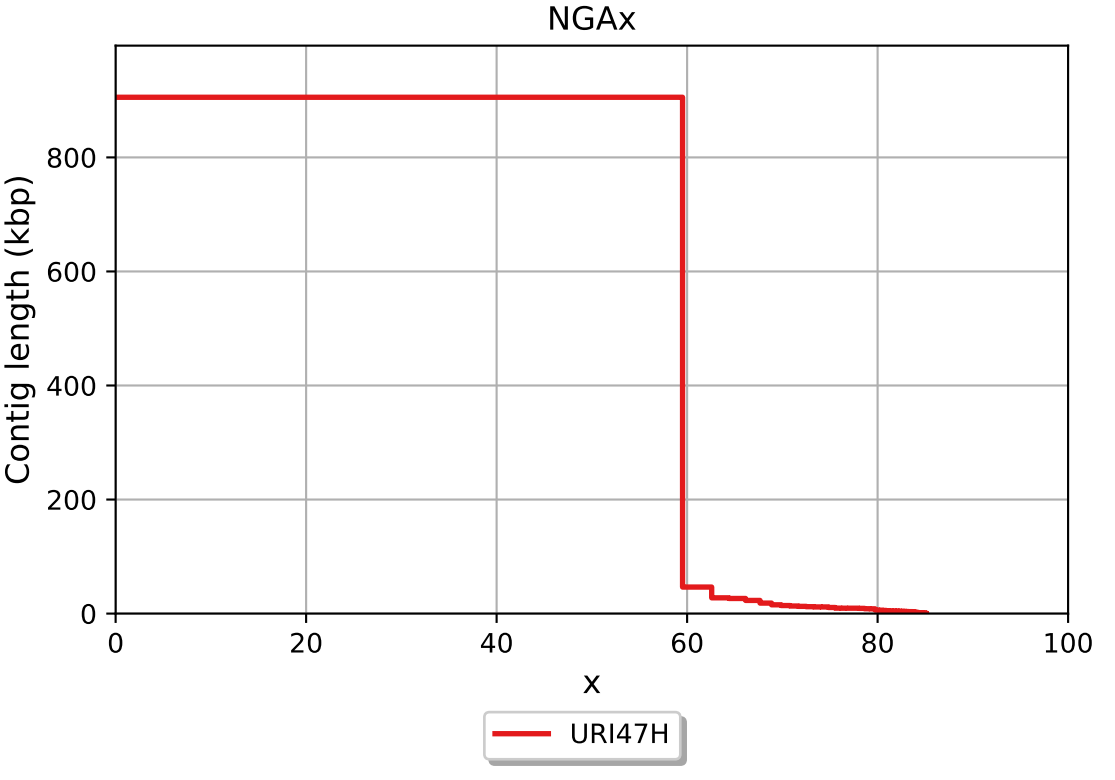

URI47H GC content
# contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
URI47H

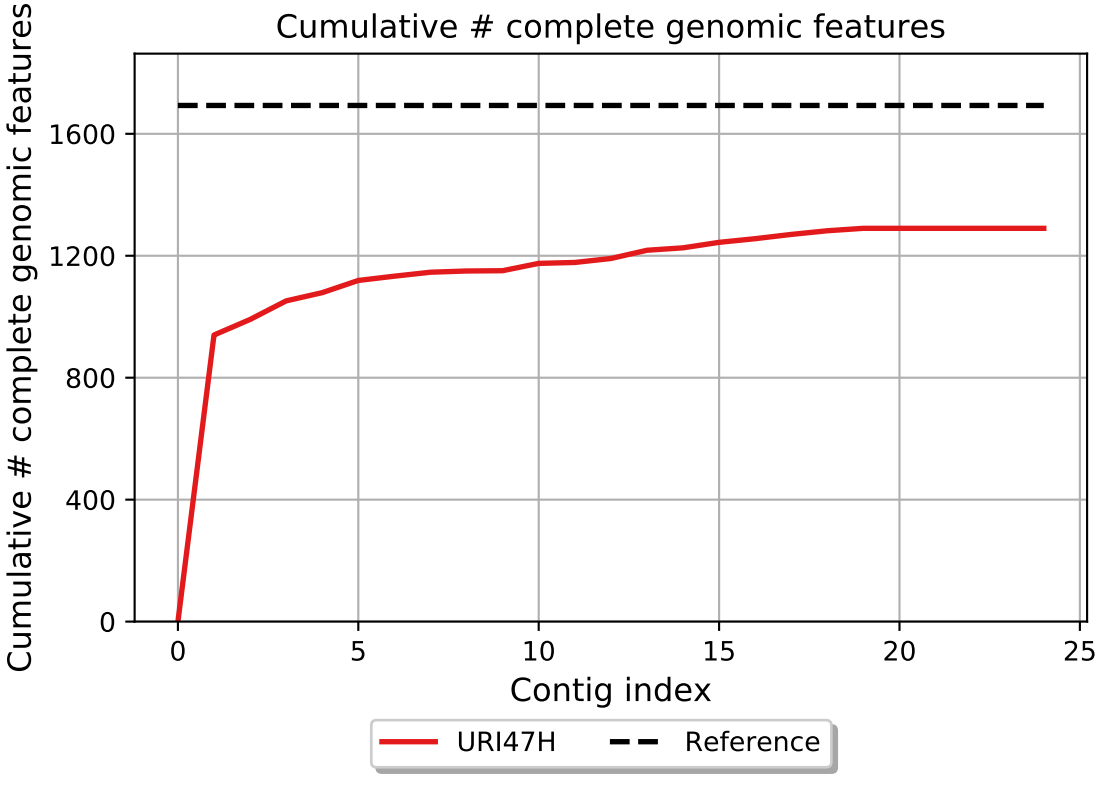

Misassemblies
30
24
18
12
6
0
URI47H
# relocations
# translocations
# inversions

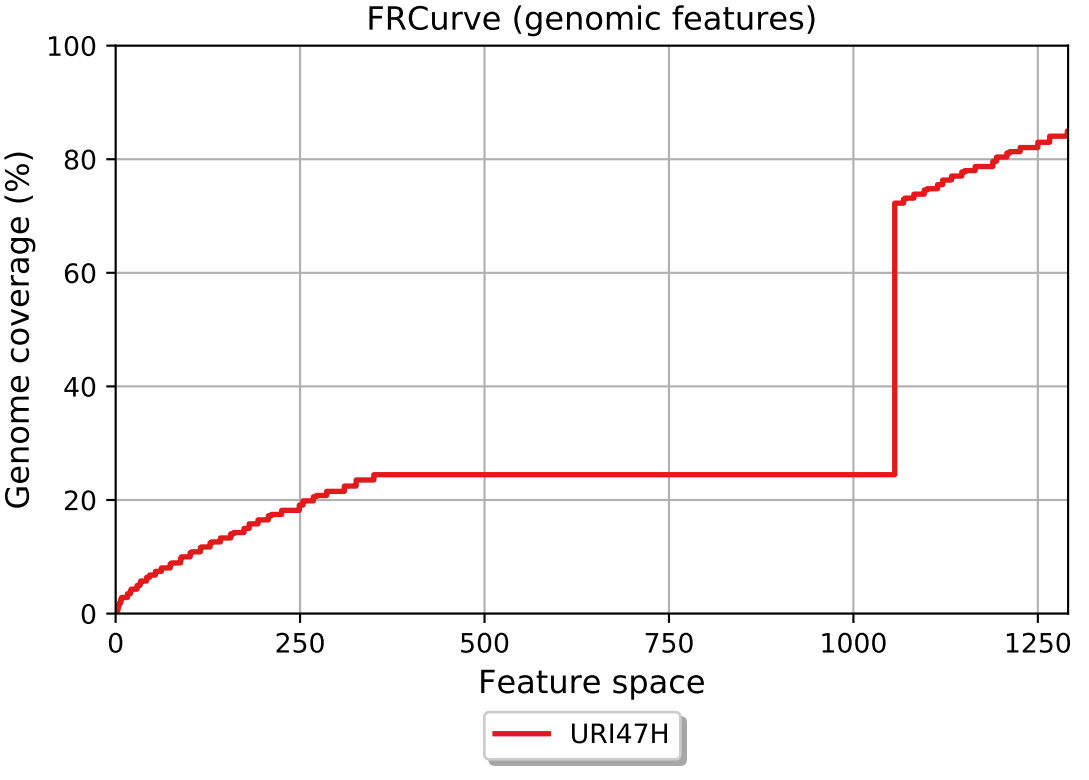

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
6
12
18
24
30
Feature space
URI47H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
60
Contig index
URI47H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
URI47H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
URI47H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
5
10
15
20
25
Contig index
URI47H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
URI47H