Report

	URI93H
# contigs (>= 0 bp)	29
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1474340
Total length (>= 1000 bp)	1470189
Total length (>= 5000 bp)	1469182
Total length (>= 10000 bp)	1469182
Total length (>= 25000 bp)	1444526
Total length (>= 50000 bp)	1014439
# contigs	21
Largest contig	910570
Total length	1472745
Reference length	1521208
GC (%)	28.12
Reference GC (%)	28.18
N50	910570
NG50	910570
N90	30299
NG90	29805
auN	577033.6
auNG	558650.4
L50	1
LG50	1
L90	12
LG90	14
# misassemblies	15
# misassembled contigs	8
Misassembled contigs length	251406
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	22254
Genome fraction (%)	93.435
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	137.80
# indels per 100 kbp	21.54
# genomic features	1532 + 38 part
Largest alignment	910570
Total aligned length	1448496
NA50	910570
NGA50	910570
NA90	24168
NGA90	16800
auNA	573983.1
auNGA	555697.0
LA50	1
LGA50	1
LA90	14
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

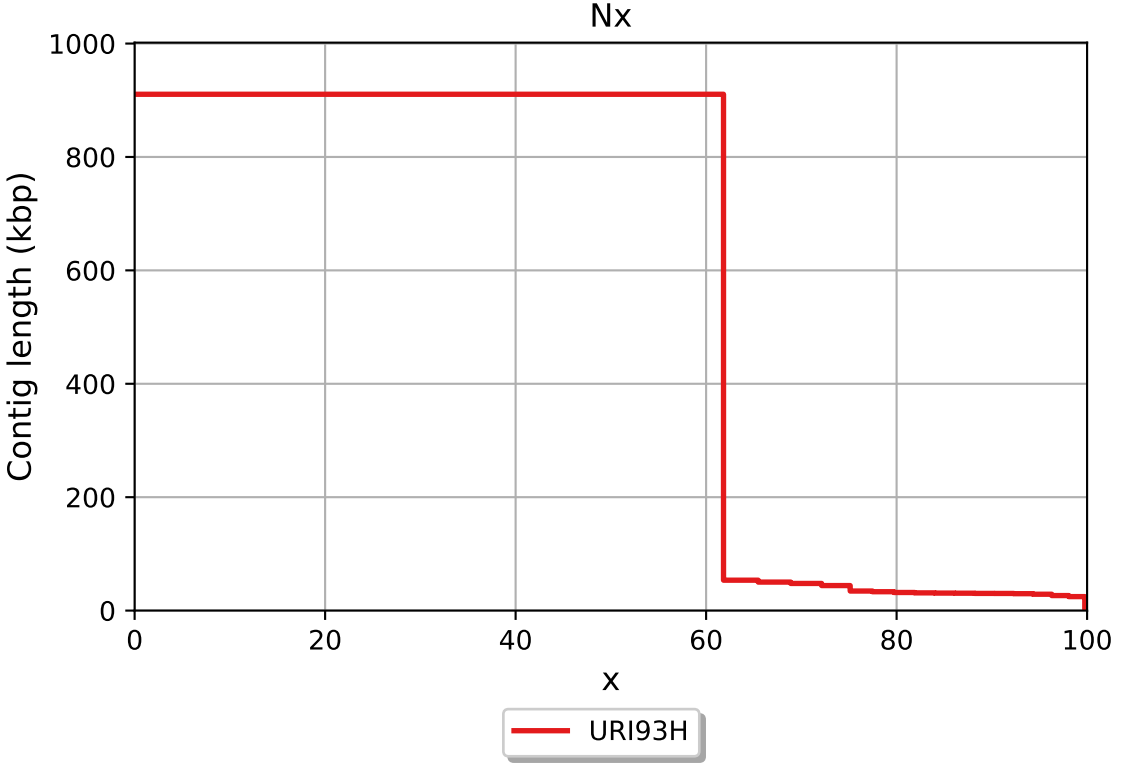
	URI93H
# misassemblies	15
# contig misassemblies	15
# c. relocations	7
# c. translocations	6
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	251406
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1996
# indels	312
# indels (<= 5 bp)	258
# indels (> 5 bp)	54
Indels length	3850

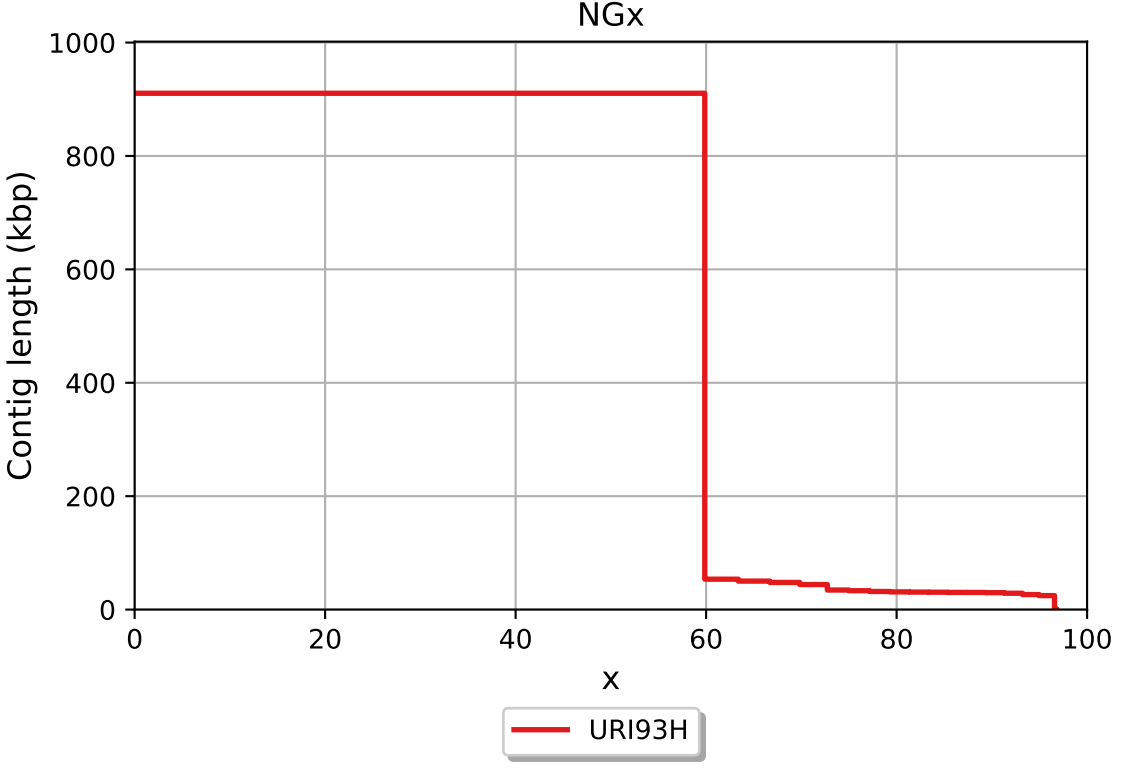
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

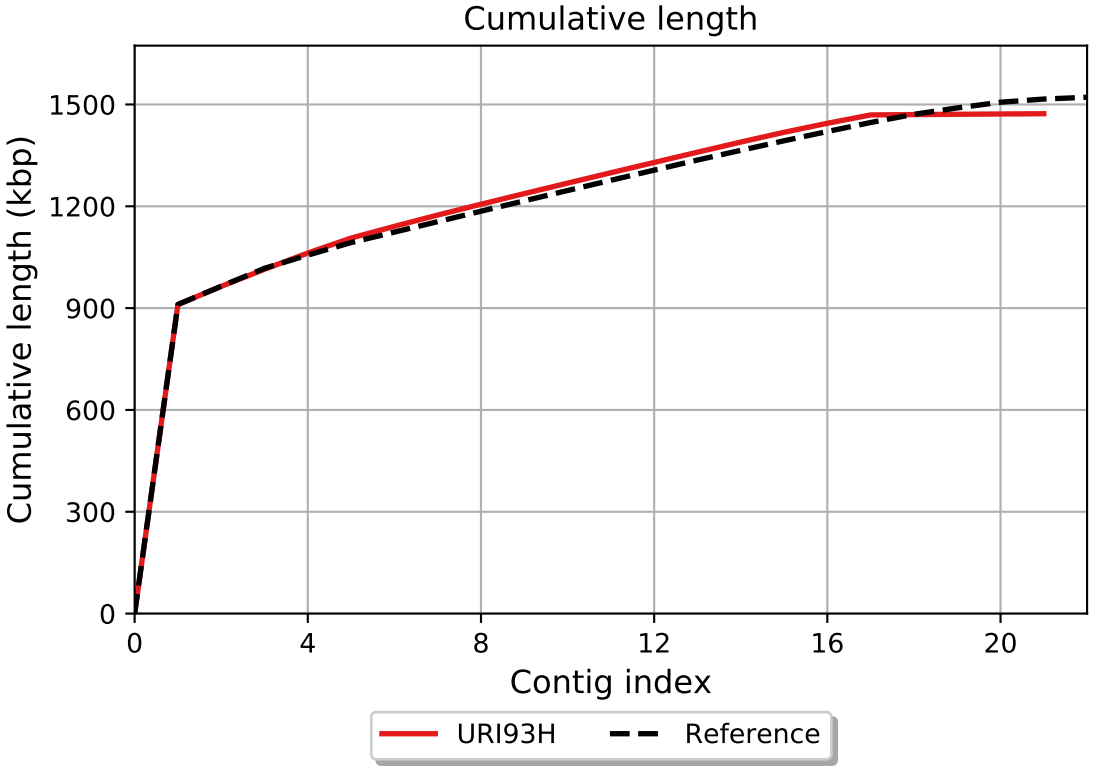
Unaligned report

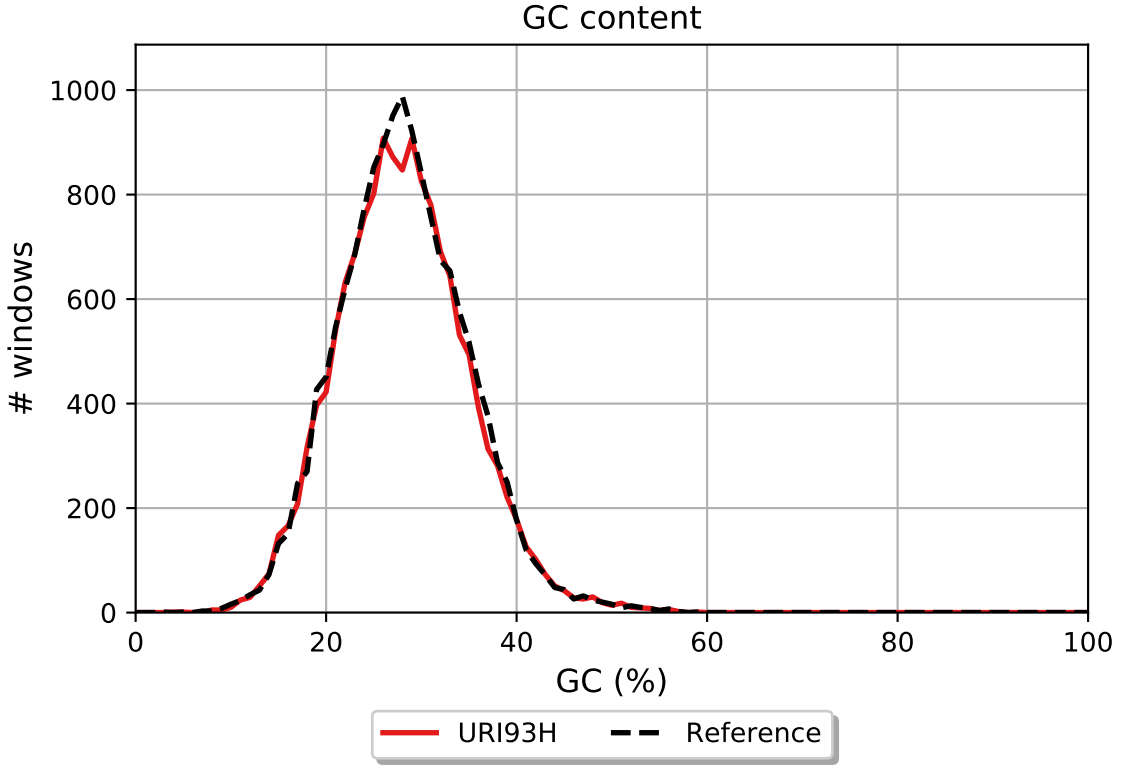
	URI93H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	22254
# N's	0

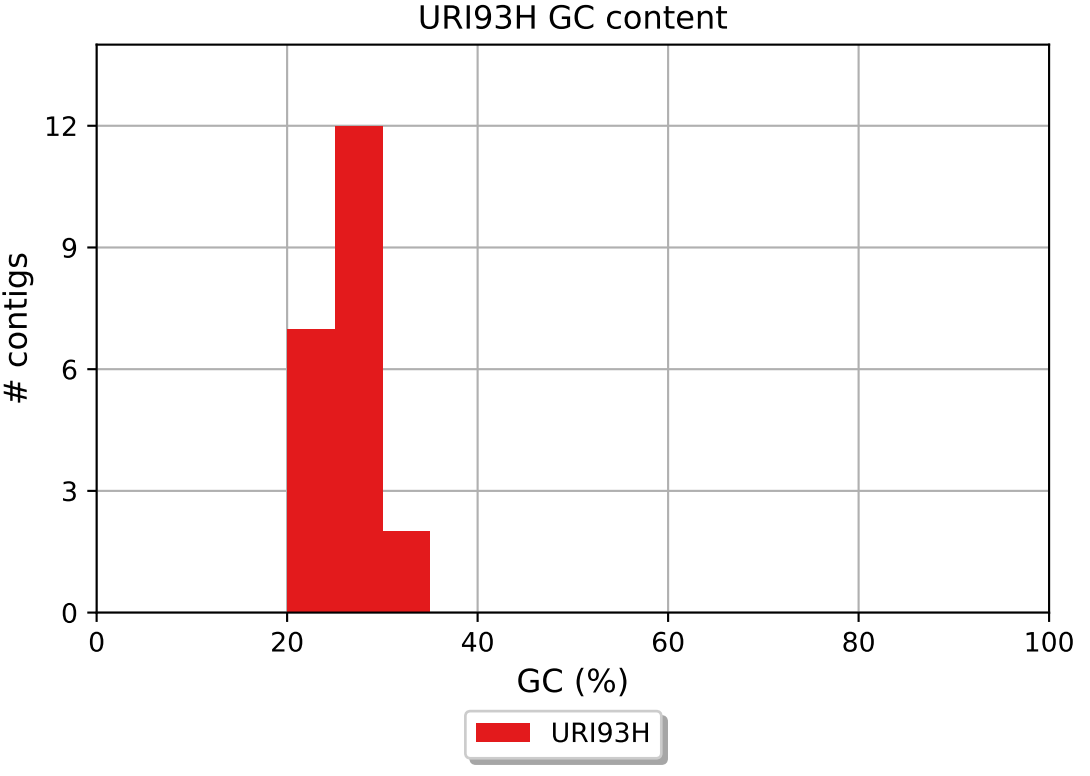
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

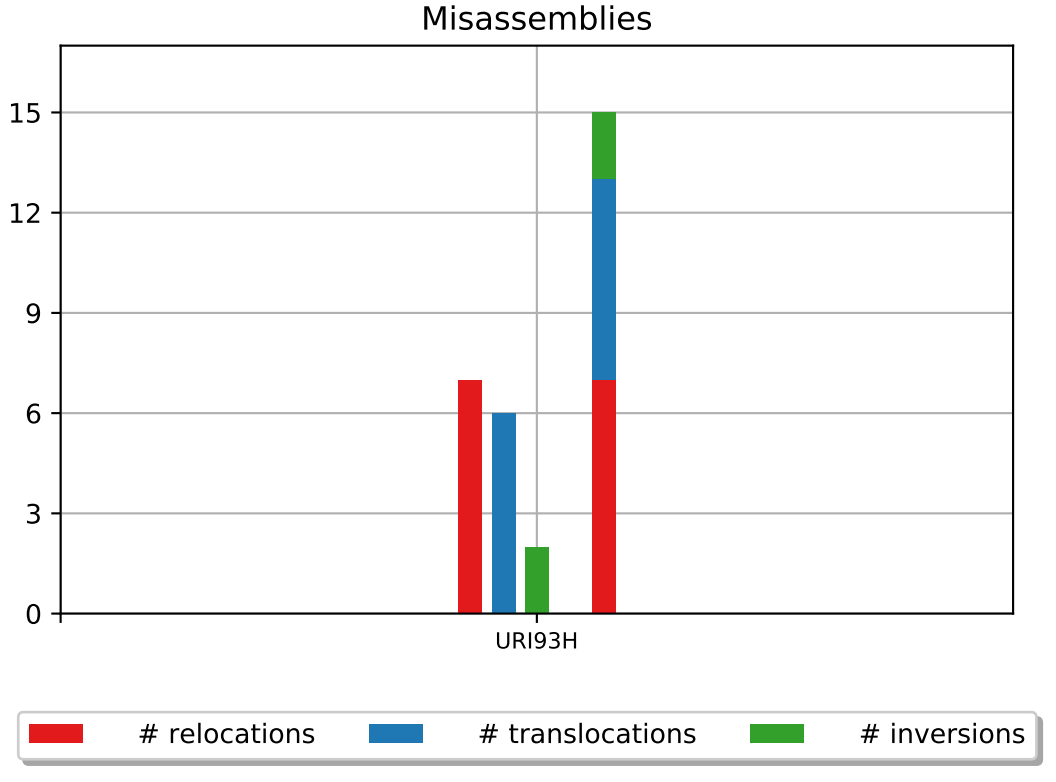

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI93H

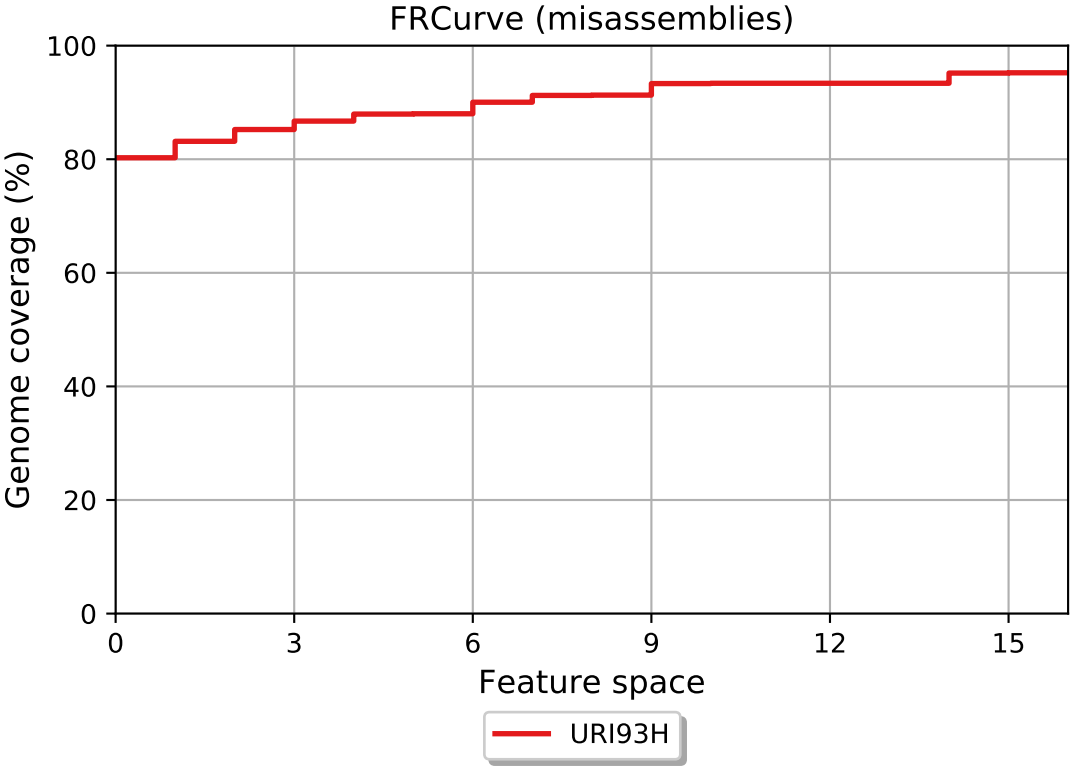

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI93H

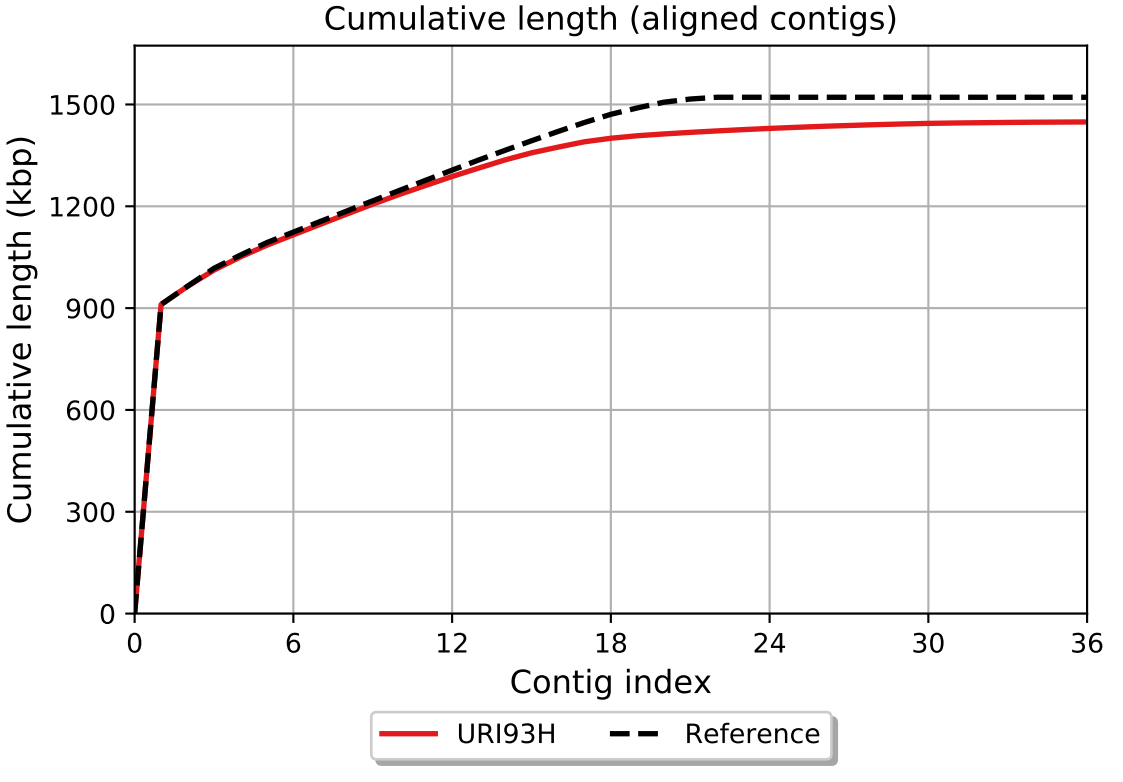

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
URI93H
Reference

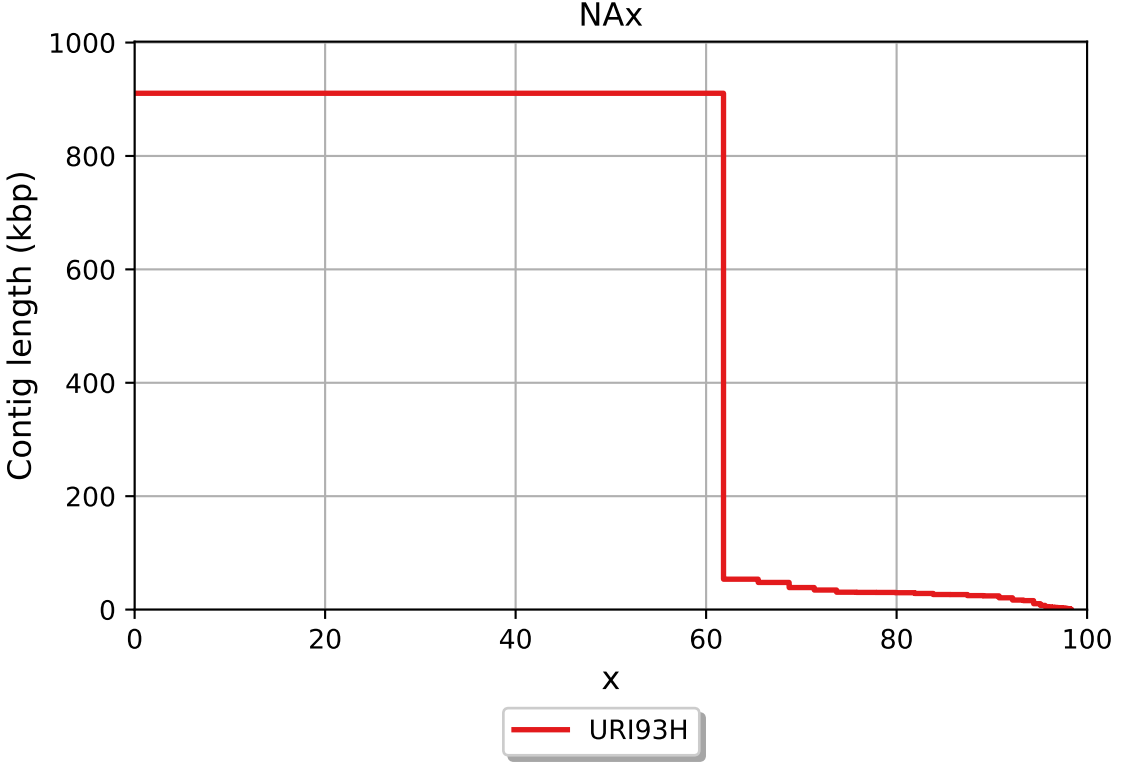

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
URI93H
Reference

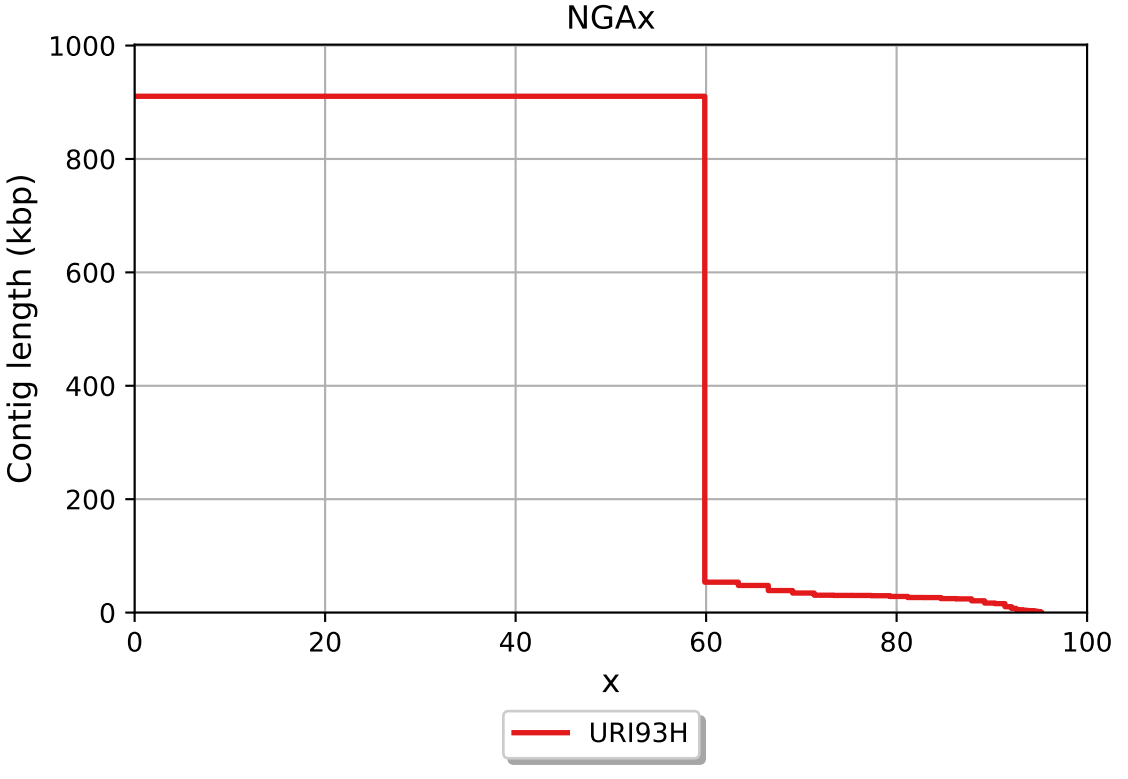

URI93H GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
URI93H

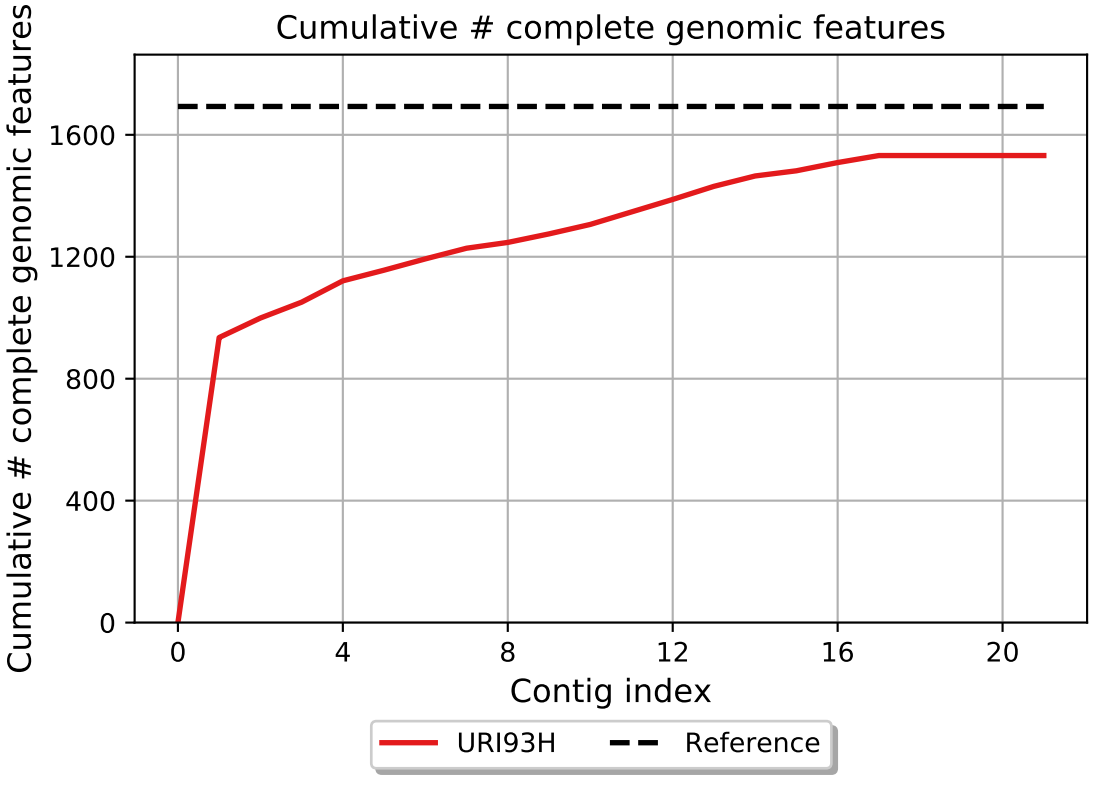

Misassemblies
15
12
9
6
3
0
URI93H
relocations
translocations
inversions

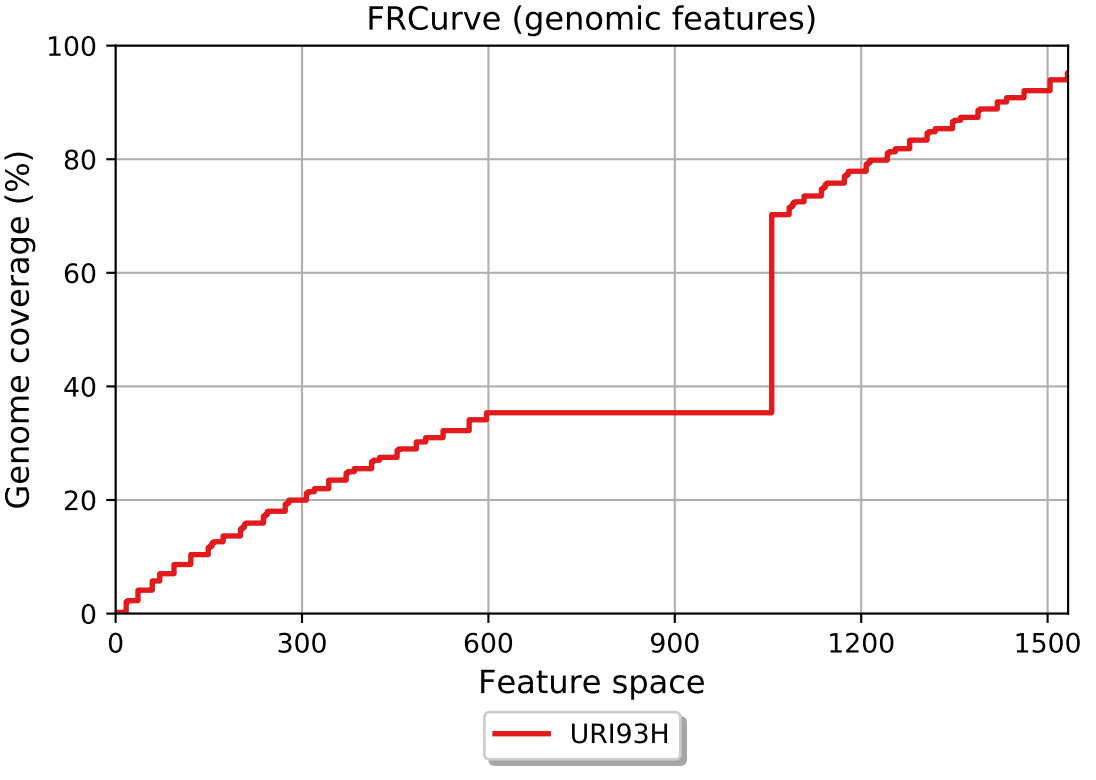

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
URI93H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
6
12
18
24
30
36
Contig index
URI93H
Reference


NAx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI93H


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI93H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
20
Contig index
URI93H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
URI93H