Report

	URI120H
# contigs (>= 0 bp)	105
# contigs (>= 1000 bp)	30
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1576195
Total length (>= 1000 bp)	1553420
Total length (>= 5000 bp)	1539609
Total length (>= 10000 bp)	1533955
Total length (>= 25000 bp)	1440066
Total length (>= 50000 bp)	964363
# contigs	43
Largest contig	910720
Total length	1561905
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	910720
NG50	910720
N90	26498
NG90	26958
auN	544269.8
auNG	558830.7
L50	1
LG50	1
L90	16
LG90	15
# misassemblies	15
# misassembled contigs	9
Misassembled contigs length	249035
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	2 + 6 part
Unaligned length	32234
Genome fraction (%)	94.713
Duplication ratio	1.061
# N's per 100 kbp	0.00
# mismatches per 100 kbp	241.92
# indels per 100 kbp	30.56
# genomic features	1549 + 42 part
Largest alignment	910708
Total aligned length	1528192
NA50	910708
NGA50	910708
NA90	11706
NGA90	16822
auNA	541710.3
auNGA	556202.7
LA50	1
LGA50	1
LA90	19
LGA90	17

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

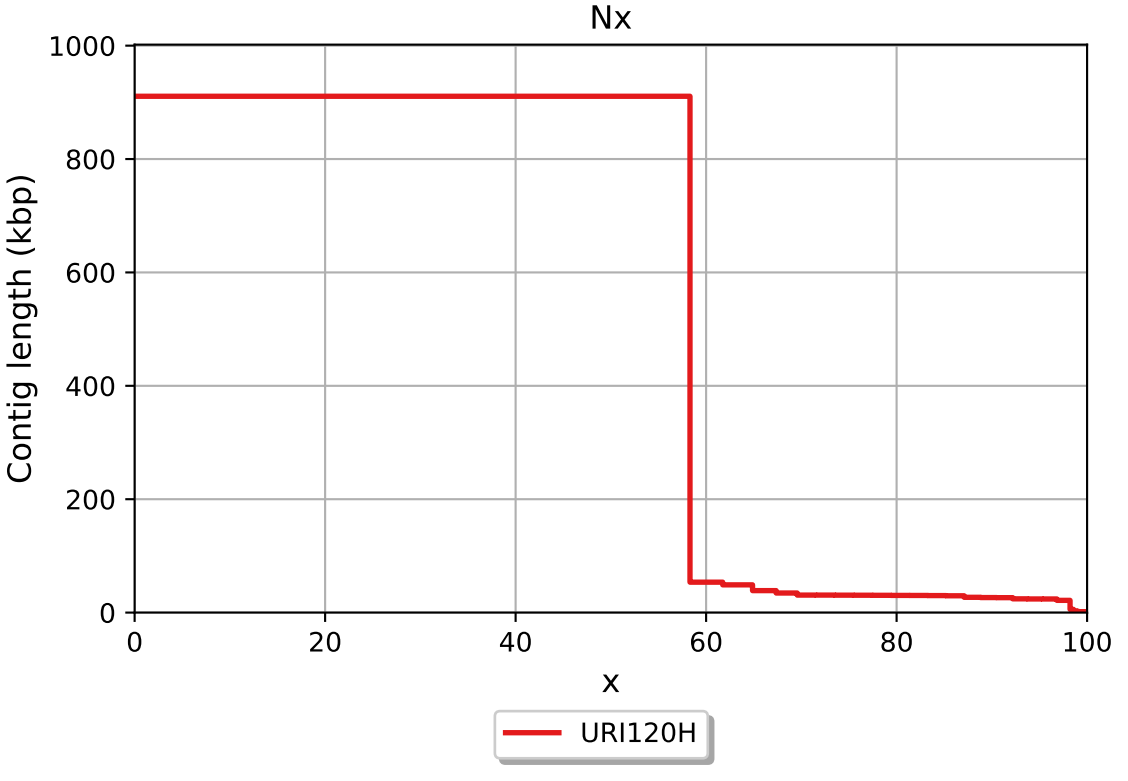
	URI120H
# misassemblies	15
# contig misassemblies	15
# c. relocations	5
# c. translocations	8
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	249035
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	3697
# indels	467
# indels (<= 5 bp)	402
# indels (> 5 bp)	65
Indels length	3624

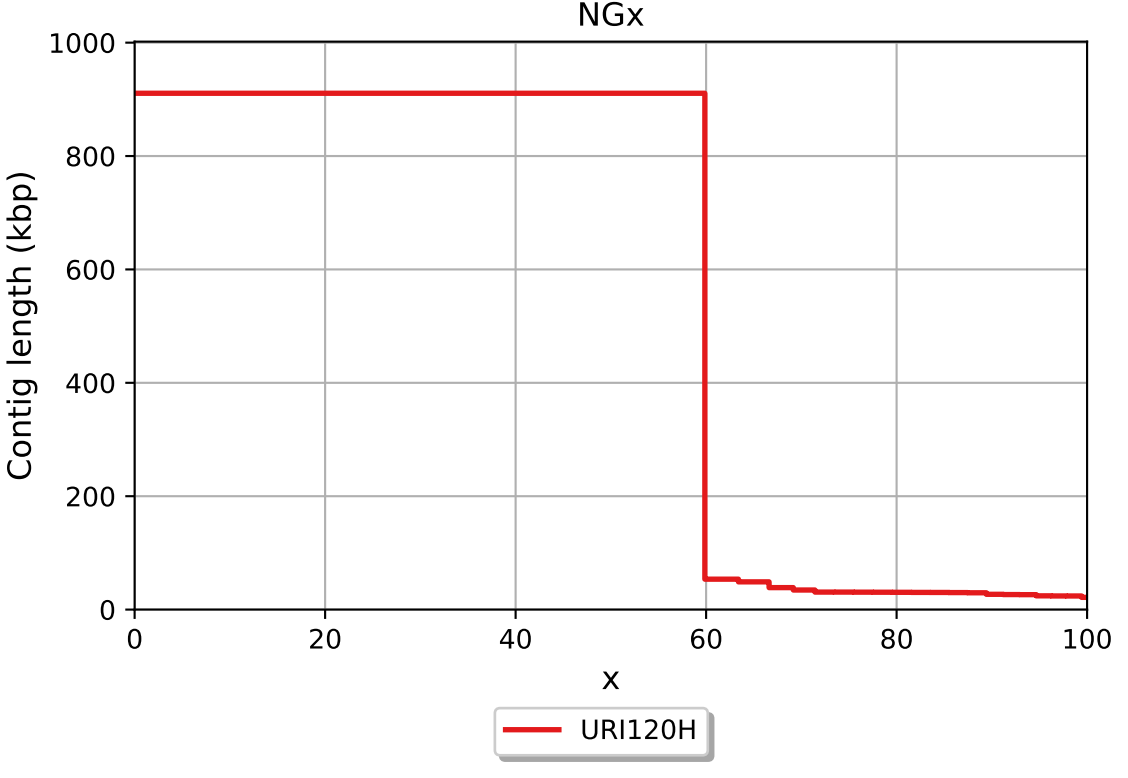
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

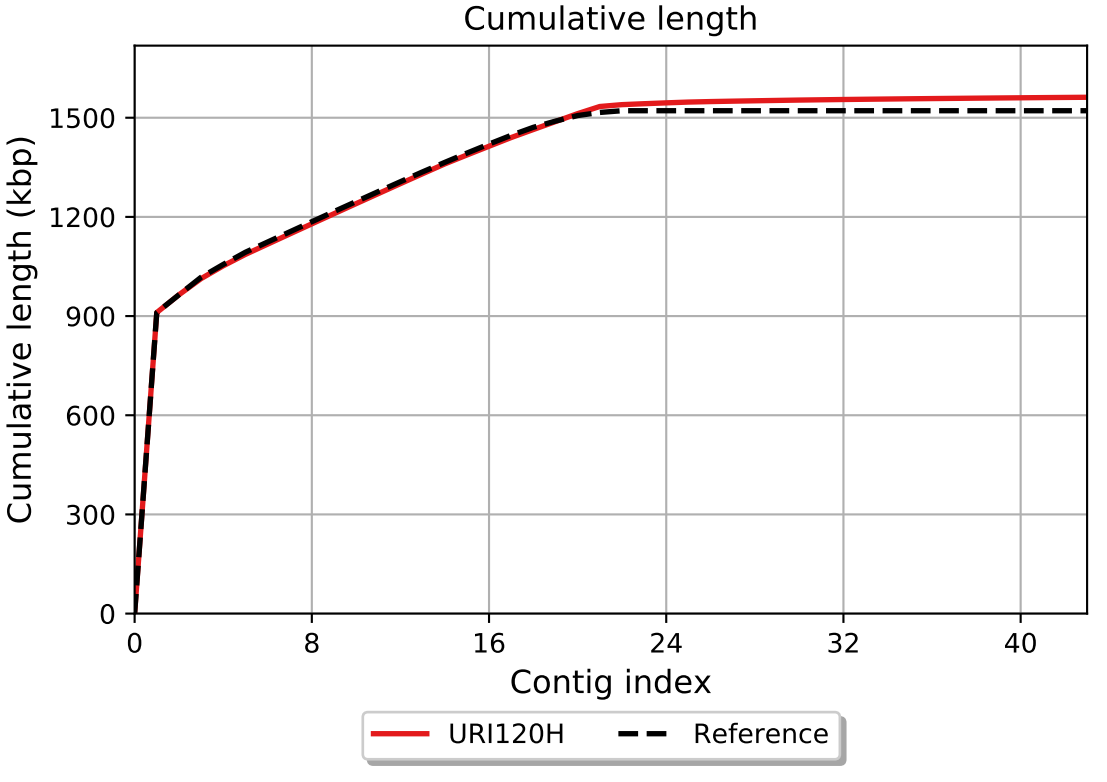
Unaligned report

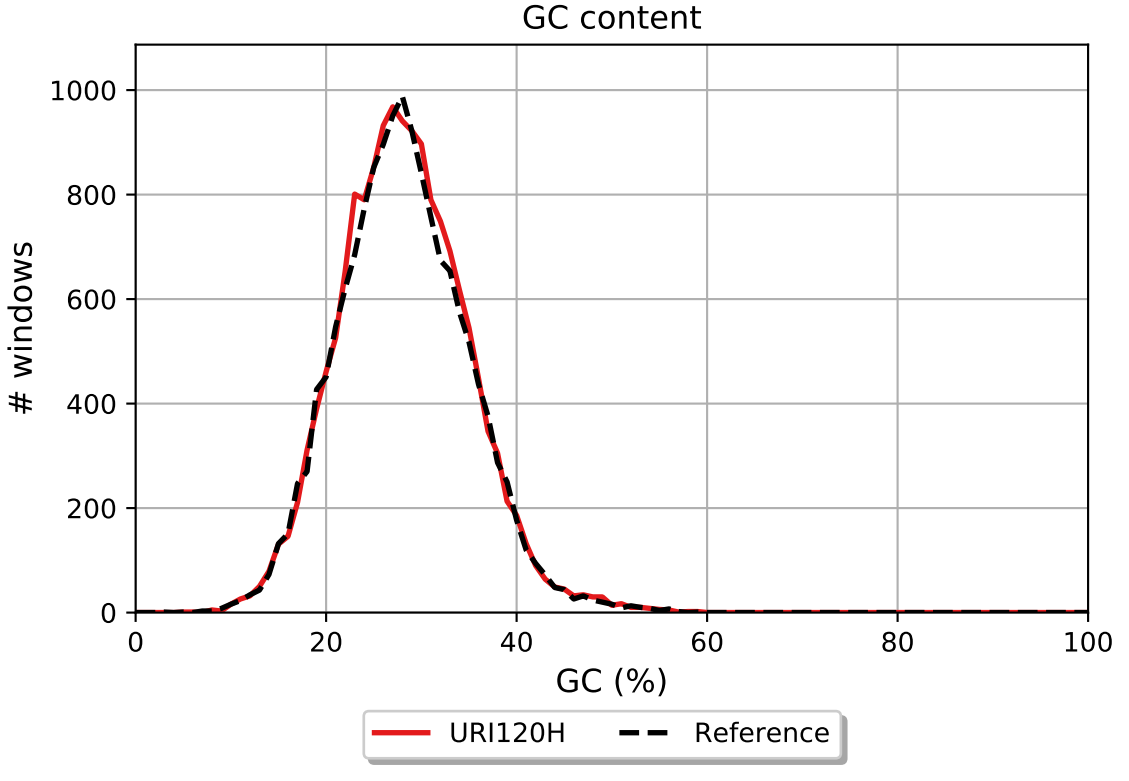
	URI120H
# fully unaligned contigs	2
Fully unaligned length	2278
# partially unaligned contigs	6
Partially unaligned length	29956
# N's	0

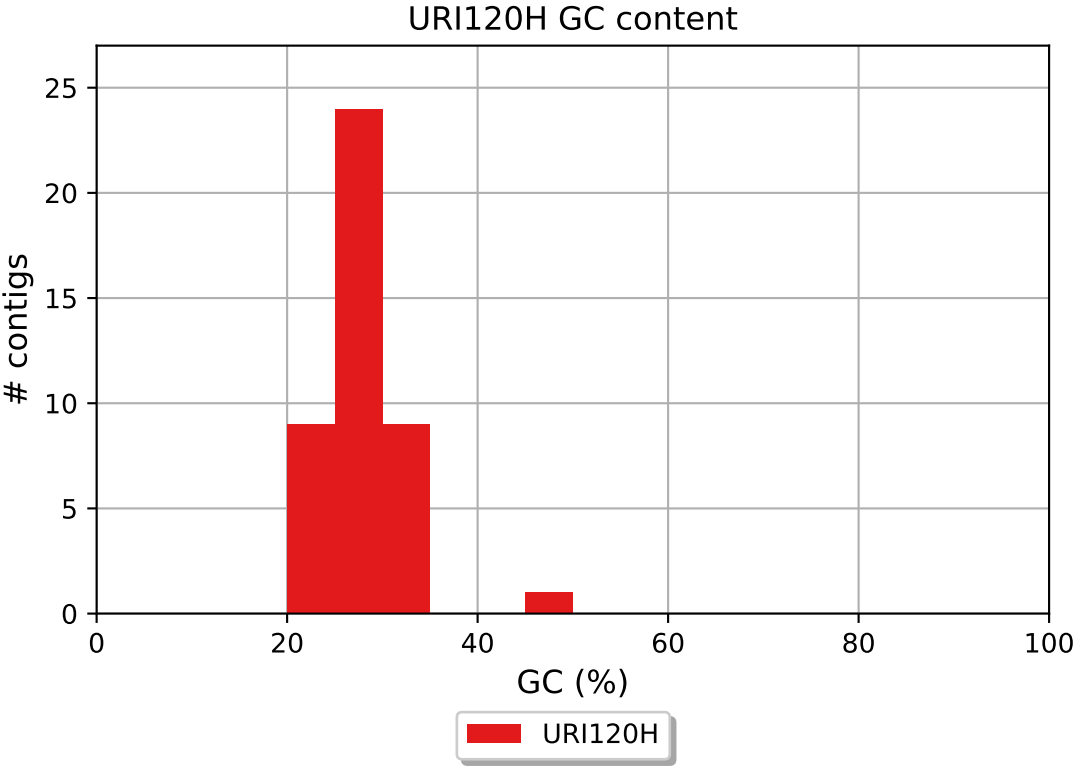
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

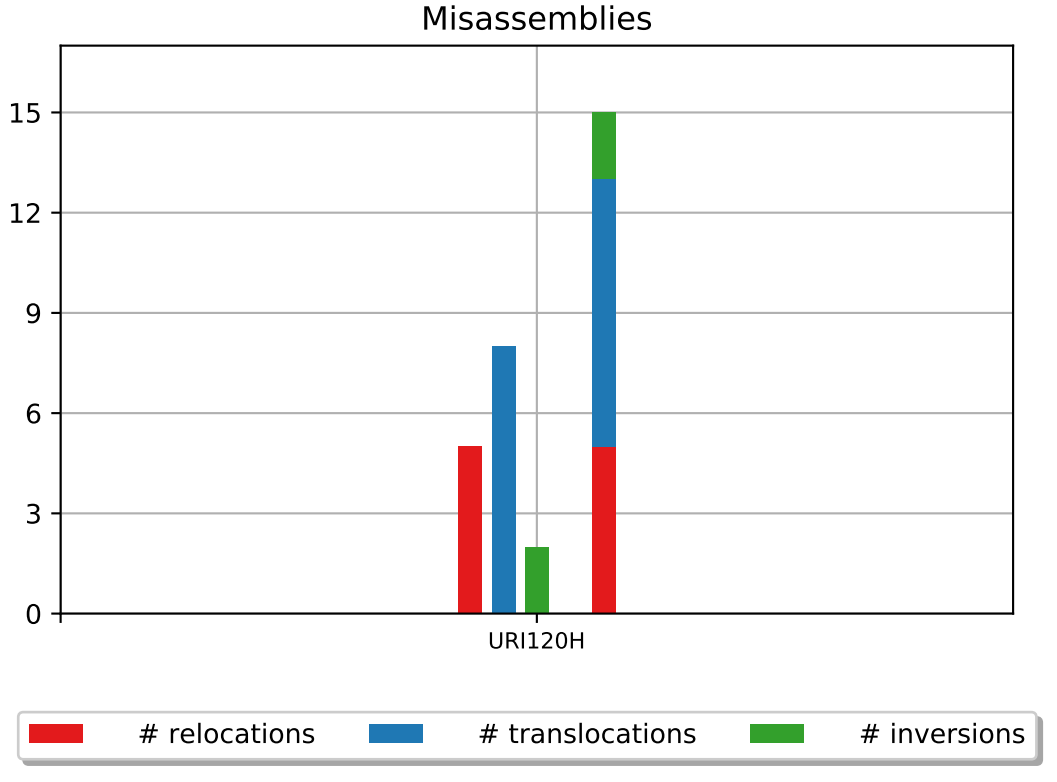

Nx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI120H

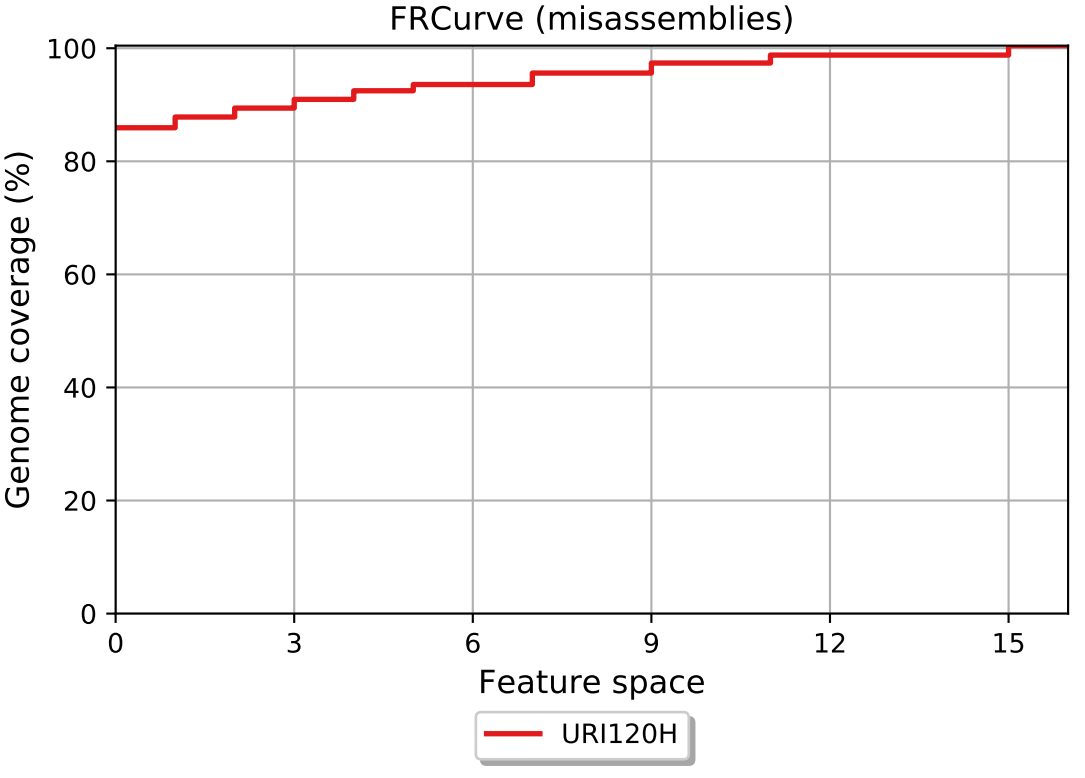

NGx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI120H

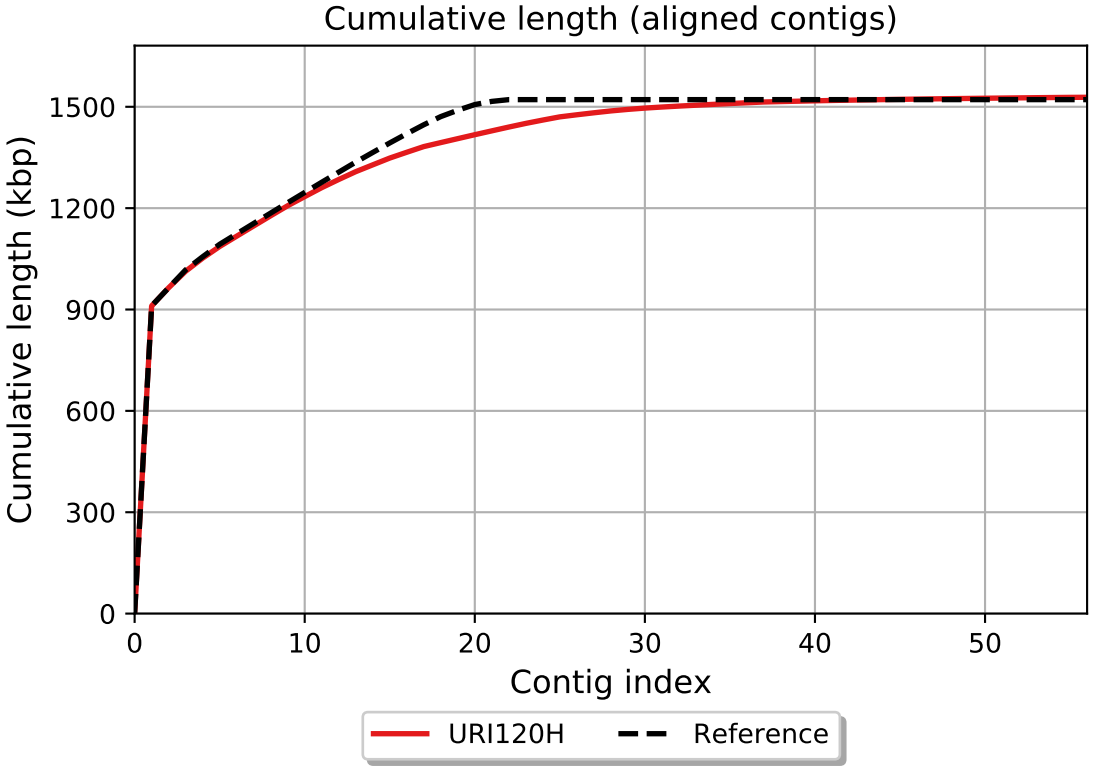

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
URI120H
Reference

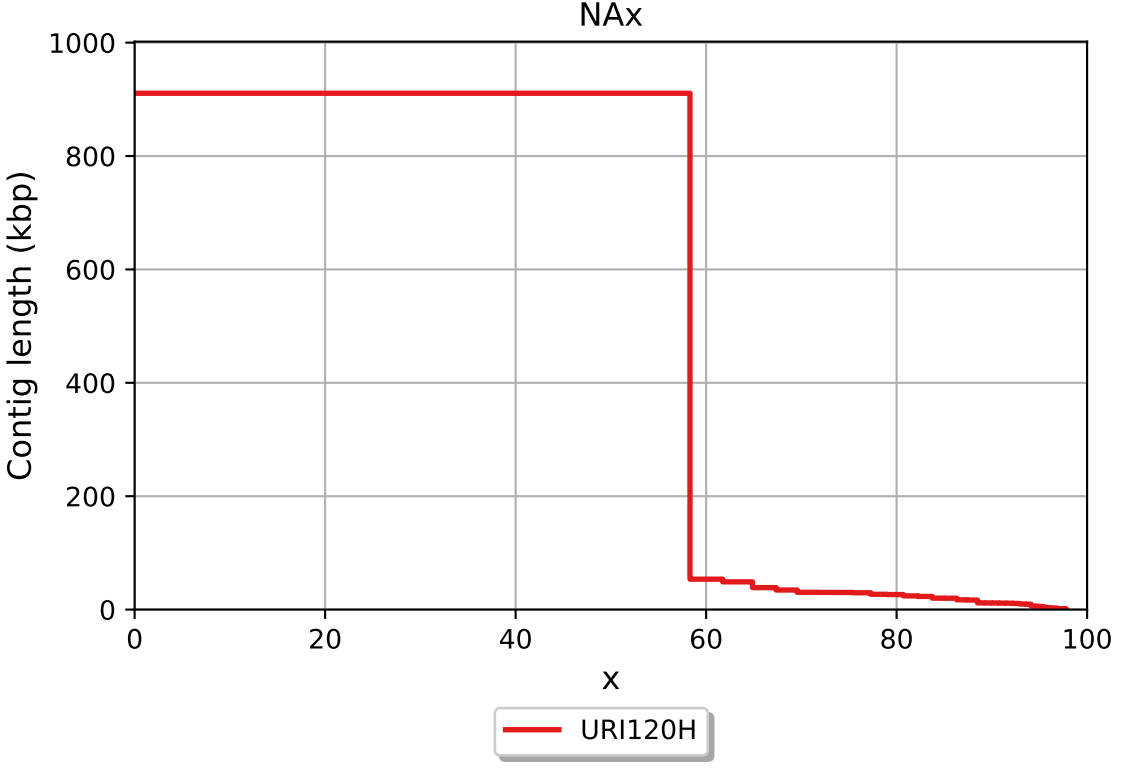

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
URI120H
Reference

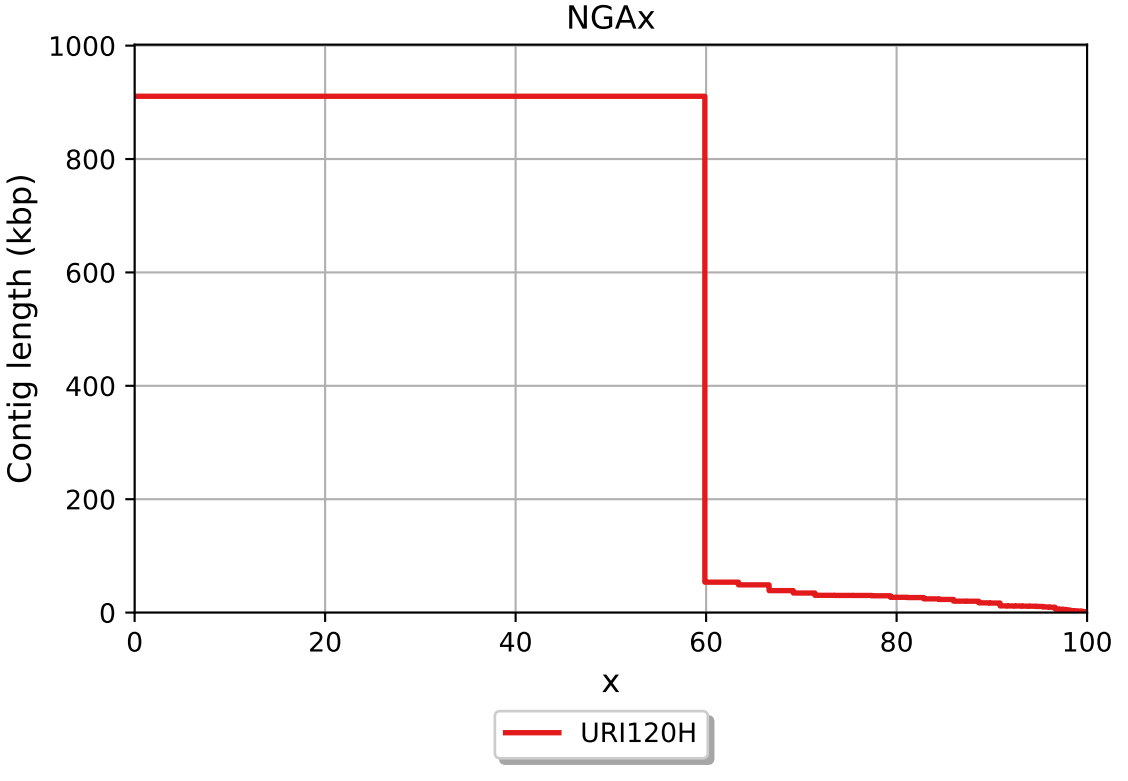

URI120H GC content
contigs
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
URI120H

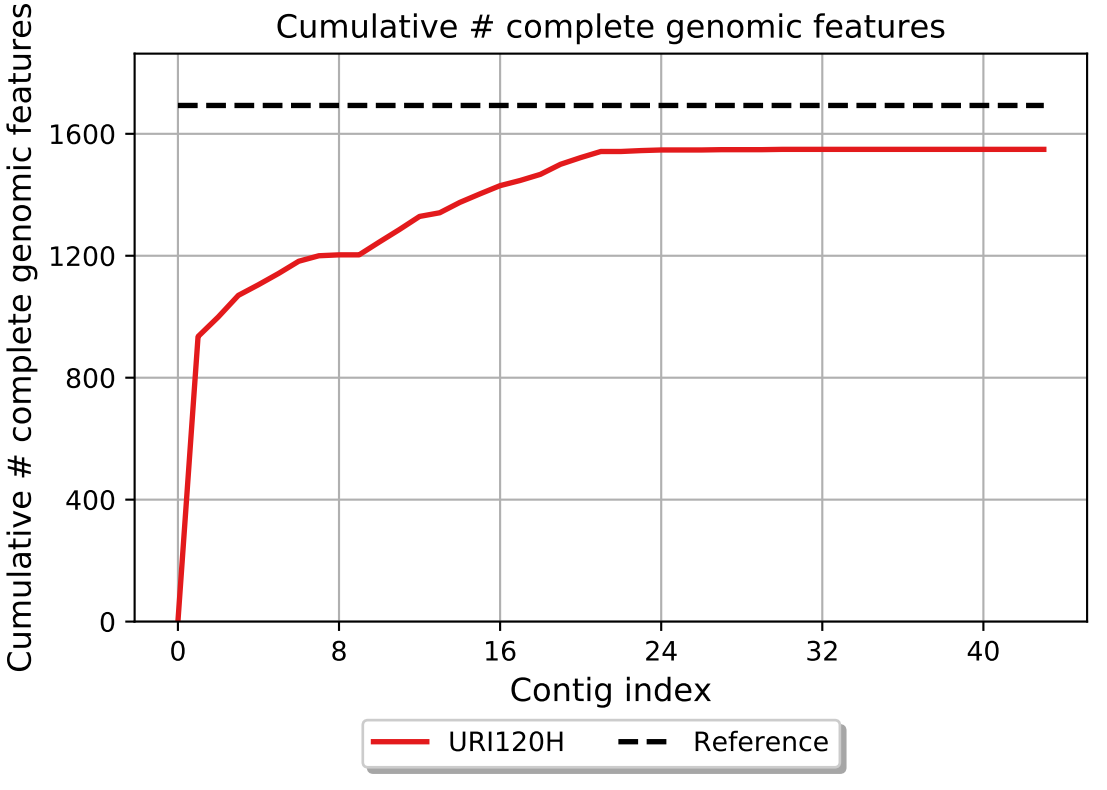

Misassemblies
15
12
9
6
3
0
URI120H
relocations
translocations
inversions

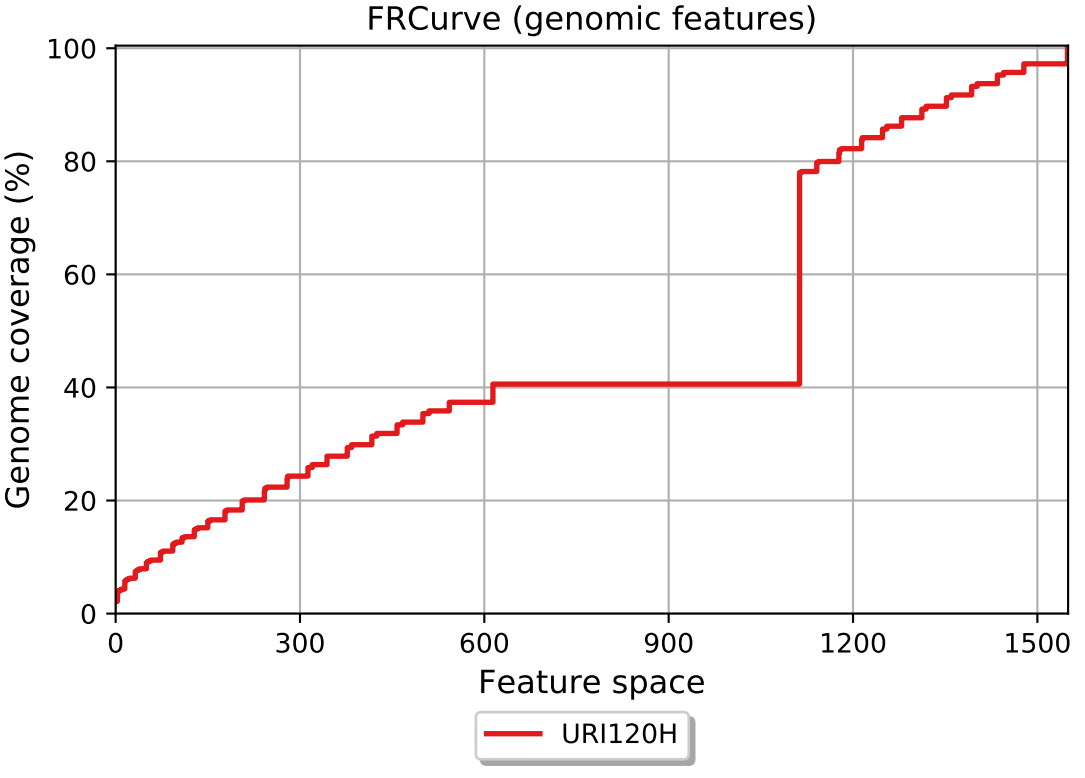

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
URI120H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
Contig index
URI120H
Reference


NAx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
URI120H


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
URI120H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
8
16
24
32
40
Contig index
URI120H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
URI120H