Report

	UCT95H
# contigs (>= 0 bp)	15
# contigs (>= 1000 bp)	15
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	8
Total length (>= 0 bp)	1491903
Total length (>= 1000 bp)	1491903
Total length (>= 5000 bp)	1491903
Total length (>= 10000 bp)	1483482
Total length (>= 25000 bp)	1483482
Total length (>= 50000 bp)	1275380
# contigs	15
Largest contig	893639
Total length	1491903
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	893639
NG50	893639
N90	34581
NG90	33779
auN	554359.4
auNG	543680.0
L50	1
LG50	1
L90	10
LG90	11
# misassemblies	20
# misassembled contigs	7
Misassembled contigs length	337227
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 11 part
Unaligned length	232092
Genome fraction (%)	74.381
Duplication ratio	1.110
# N's per 100 kbp	0.00
# mismatches per 100 kbp	917.34
# indels per 100 kbp	850.00
# genomic features	1195 + 46 part
Largest alignment	893337
Total aligned length	1256354
NA50	893337
NGA50	893337
NA90	-
NGA90	-
auNA	539810.7
auNGA	529411.6
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

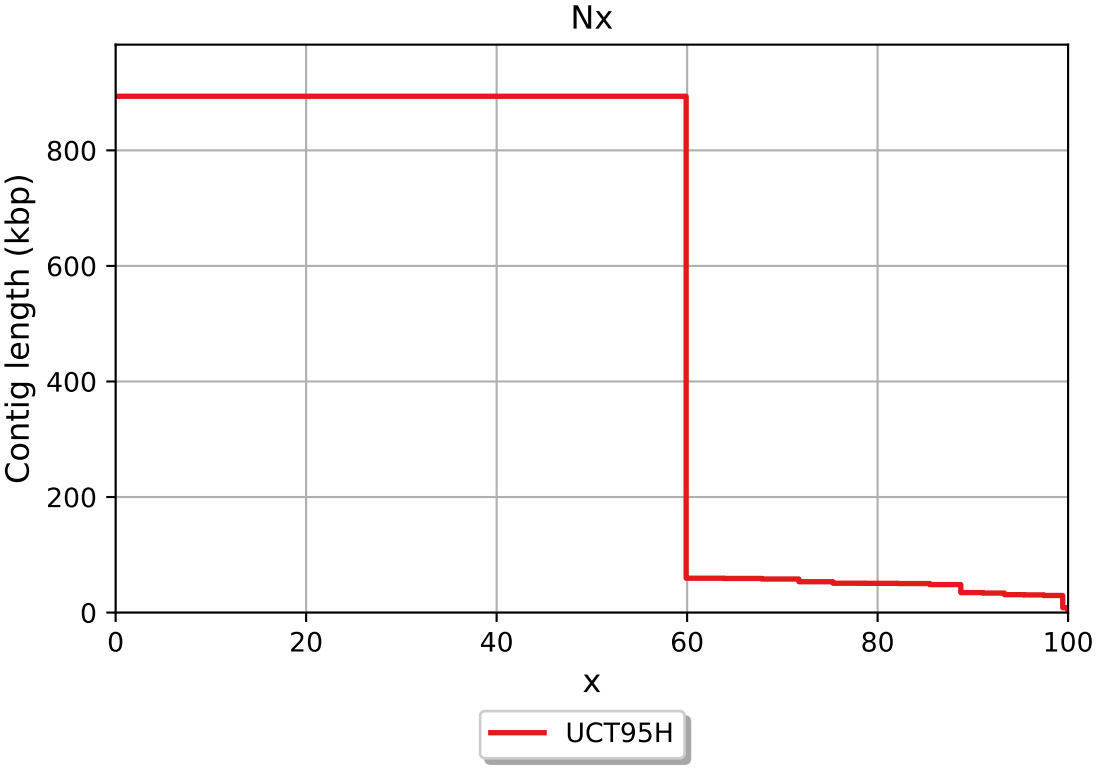
	UCT95H
# misassemblies	20
# contig misassemblies	20
# c. relocations	7
# c. translocations	13
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	337227
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	11525
# indels	10679
# indels (<= 5 bp)	10581
# indels (> 5 bp)	98
Indels length	15582

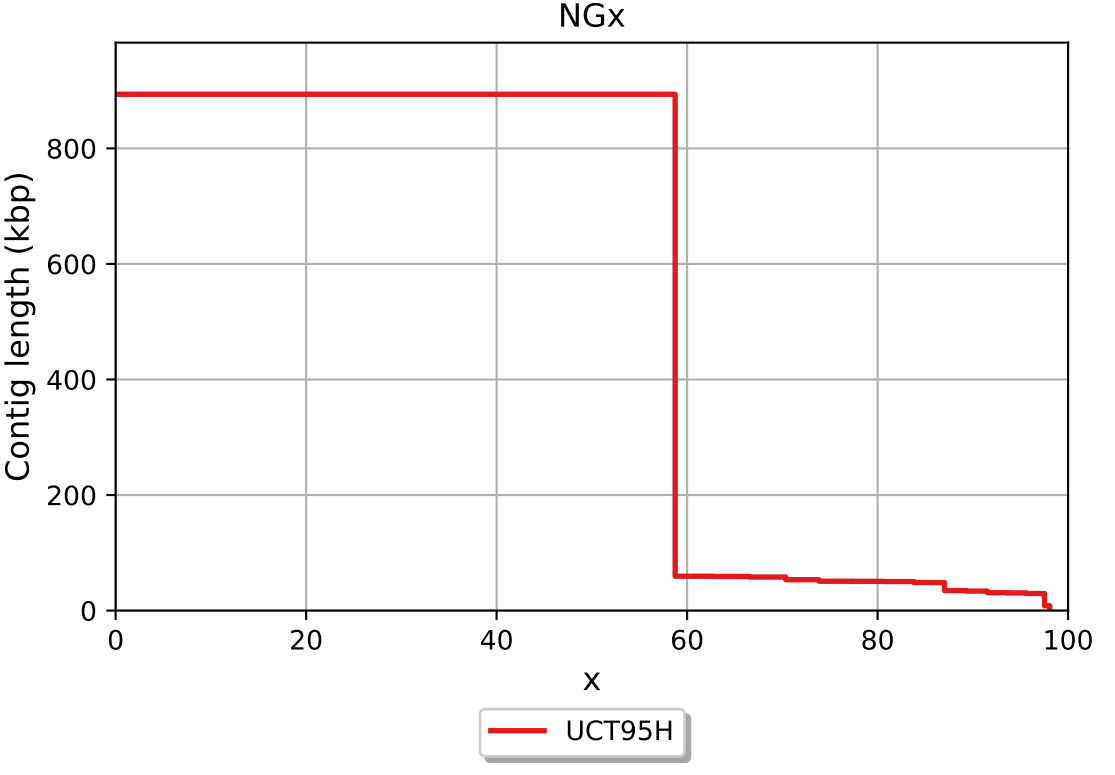
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

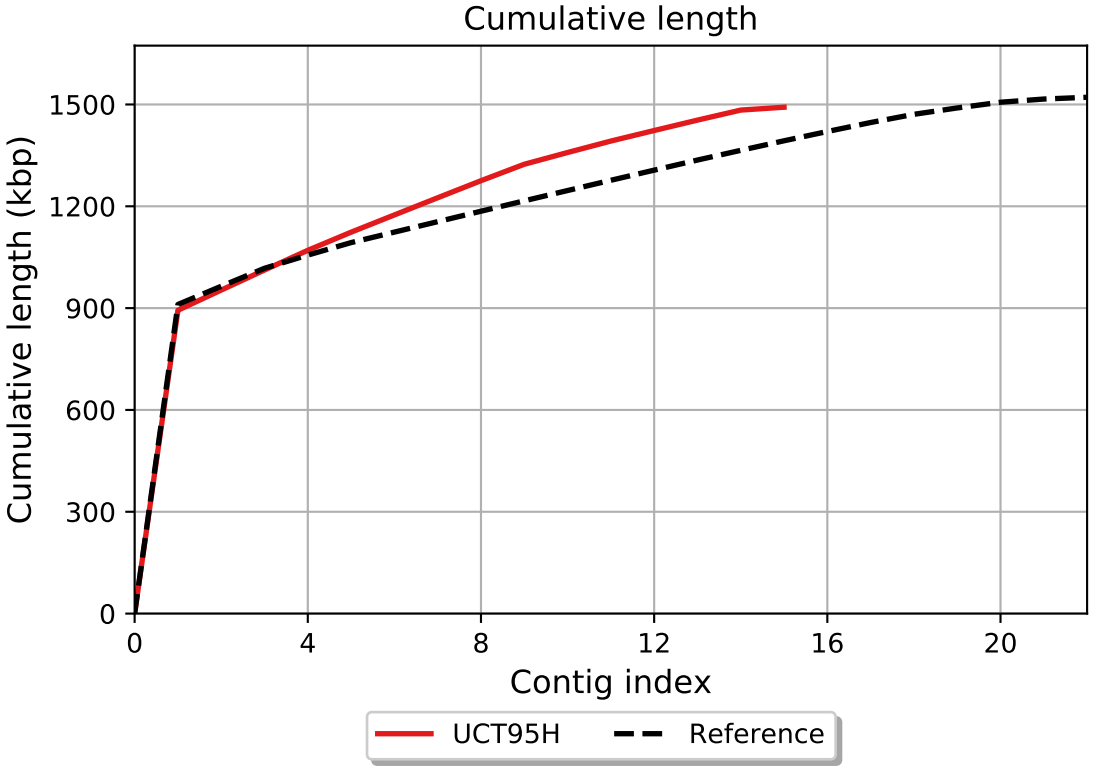
Unaligned report

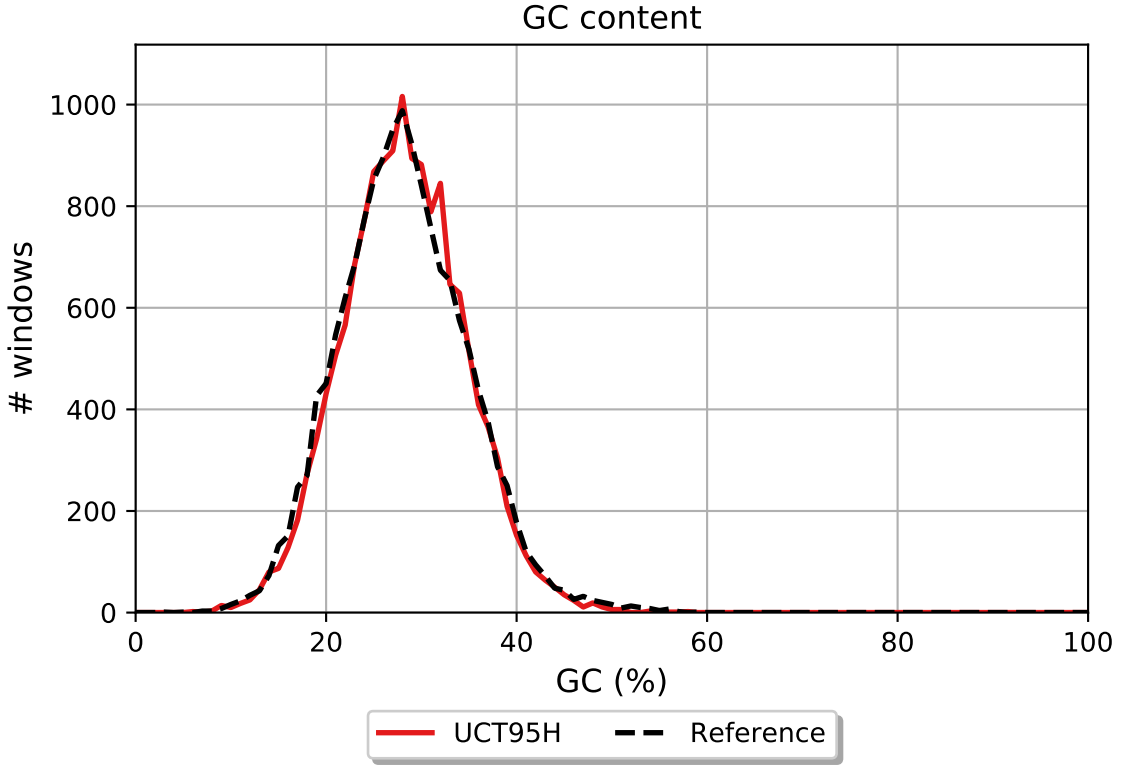
	UCT95H
# fully unaligned contigs	1
Fully unaligned length	50634
# partially unaligned contigs	11
Partially unaligned length	181458
# N's	0

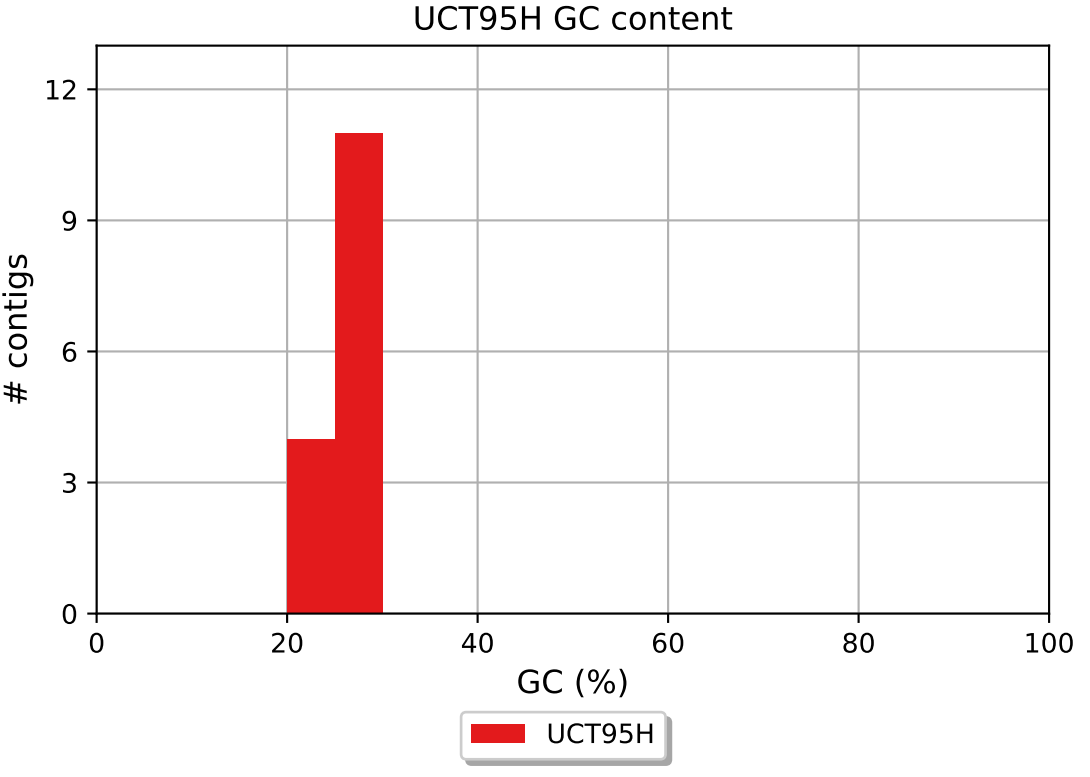
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

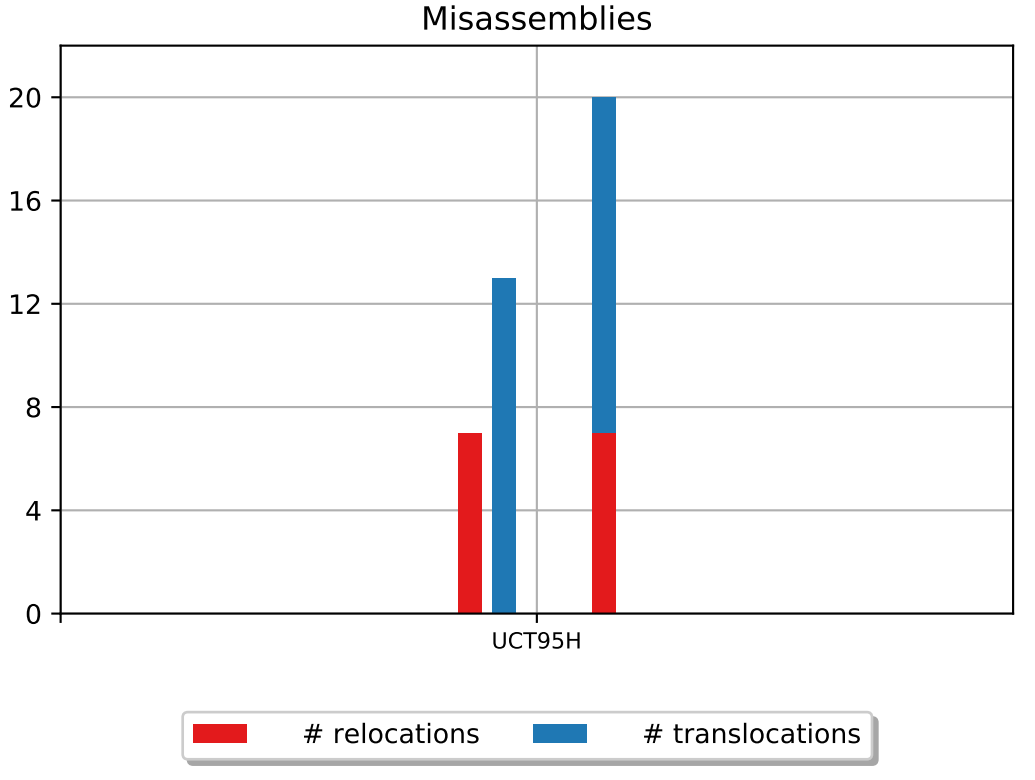

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT95H

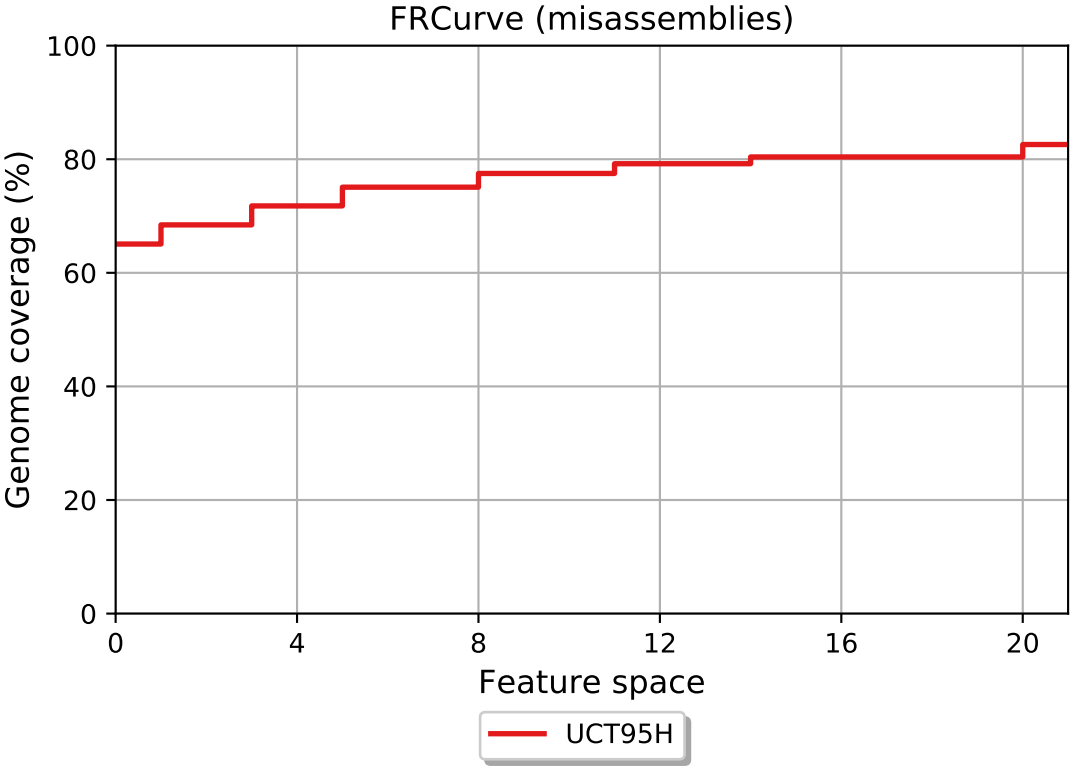

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT95H

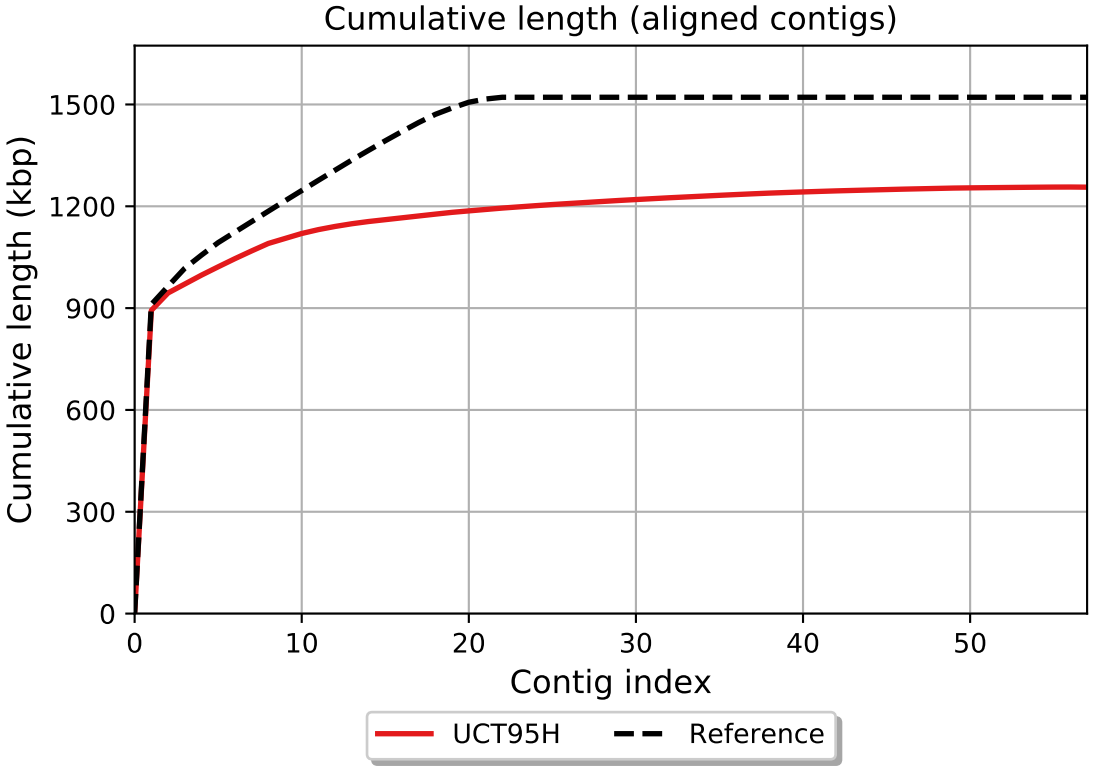

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UCT95H
Reference

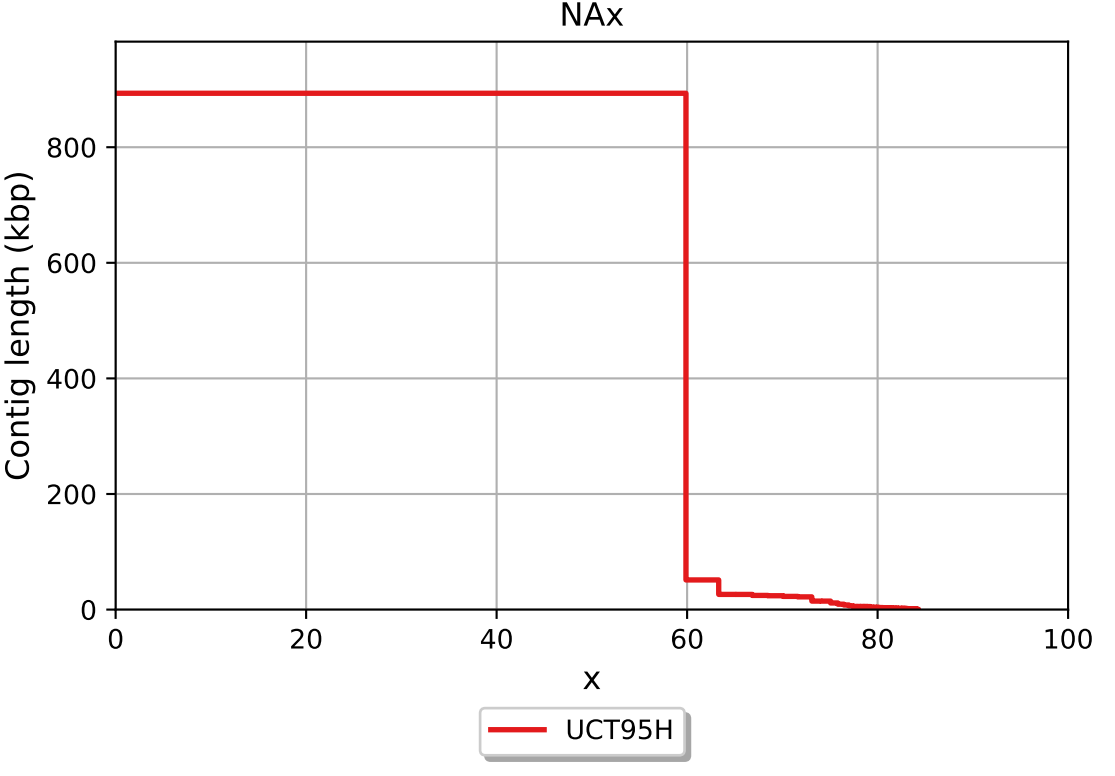

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
UCT95H
Reference

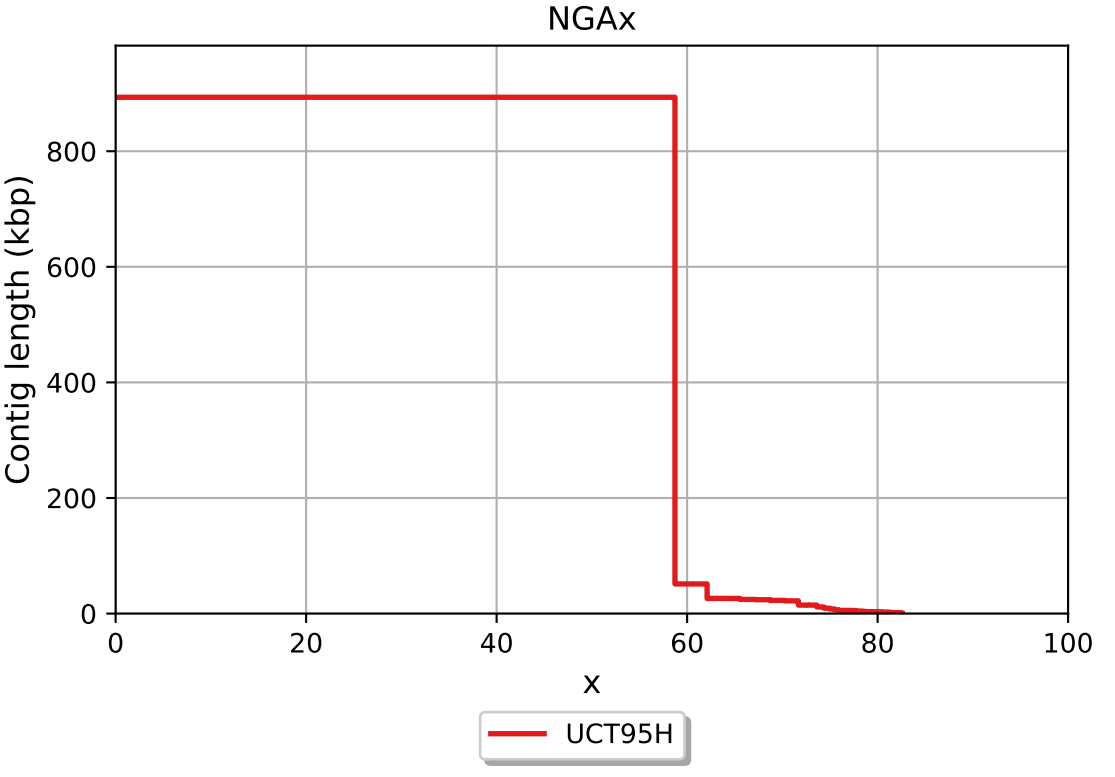

UCT95H GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
UCT95H

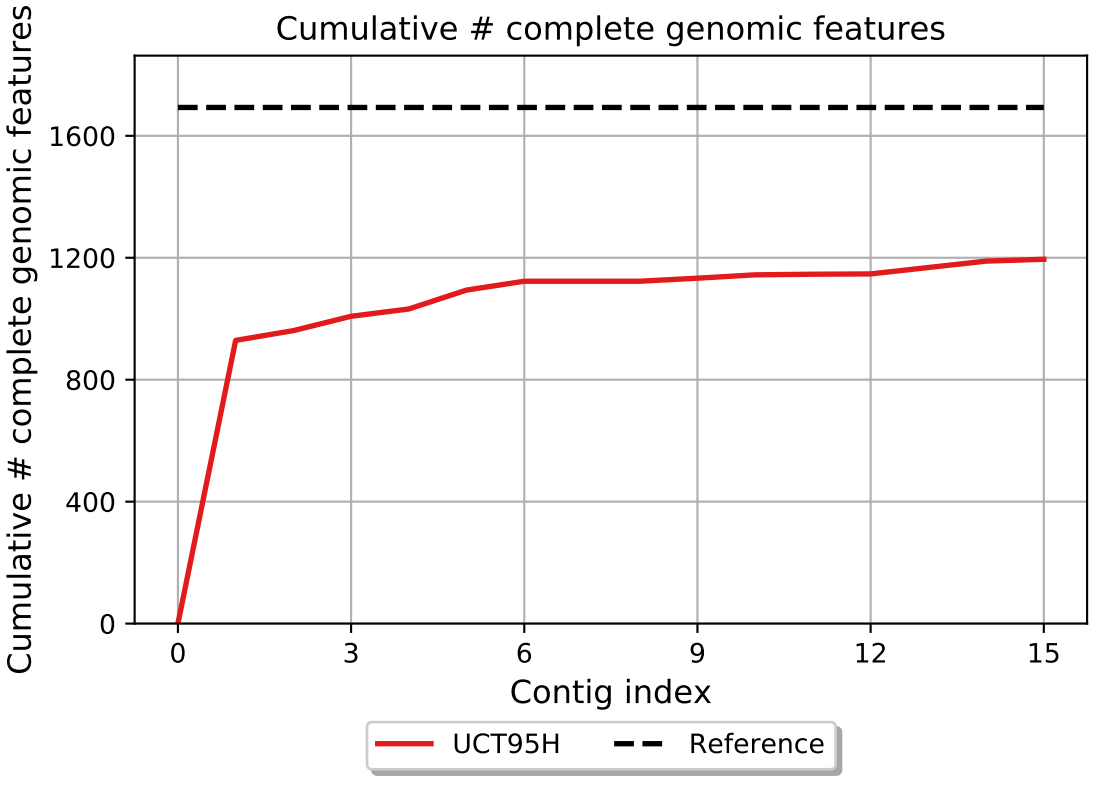

Misassemblies
20
16
12
8
4
0
UCT95H
relocations
translocations

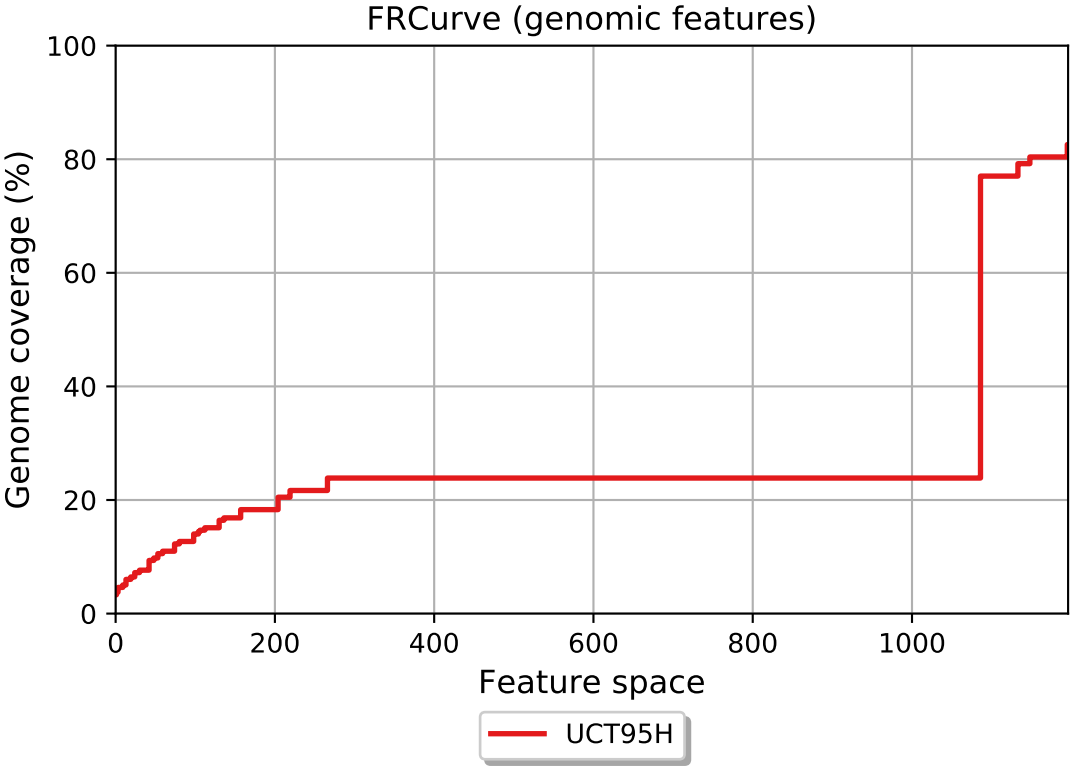

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
UCT95H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
Contig index
UCT95H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT95H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT95H


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
3
6
9
12
15
Contig index
UCT95H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Feature space
UCT95H