Report

	UCT92H
# contigs (>= 0 bp)	62
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	22
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1537760
Total length (>= 1000 bp)	1525846
Total length (>= 5000 bp)	1524653
Total length (>= 10000 bp)	1524653
Total length (>= 25000 bp)	1467020
Total length (>= 50000 bp)	960502
# contigs	29
Largest contig	906713
Total length	1530632
Reference length	1521208
GC (%)	28.17
Reference GC (%)	28.18
N50	906713
NG50	906713
N90	26061
NG90	26061
auN	549772.5
auNG	553178.4
L50	1
LG50	1
L90	16
LG90	16
# misassemblies	29
# misassembled contigs	13
Misassembled contigs length	329486
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	4 + 19 part
Unaligned length	235271
Genome fraction (%)	80.024
Duplication ratio	1.063
# N's per 100 kbp	0.00
# mismatches per 100 kbp	909.46
# indels per 100 kbp	55.27
# genomic features	1286 + 47 part
Largest alignment	904607
Total aligned length	1293626
NA50	904607
NGA50	904607
NA90	-
NGA90	-
auNA	538746.5
auNGA	542084.1
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

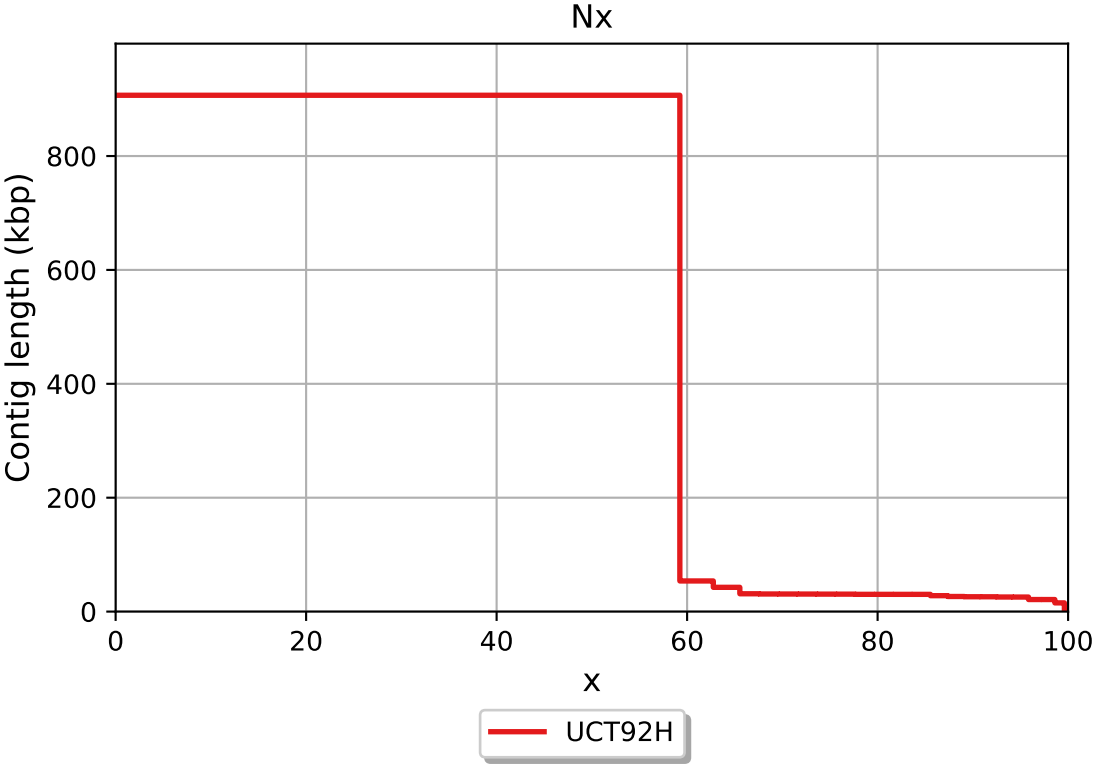
	UCT92H
# misassemblies	29
# contig misassemblies	29
# c. relocations	5
# c. translocations	23
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	329486
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	11765
# indels	715
# indels (<= 5 bp)	656
# indels (> 5 bp)	59
Indels length	2985

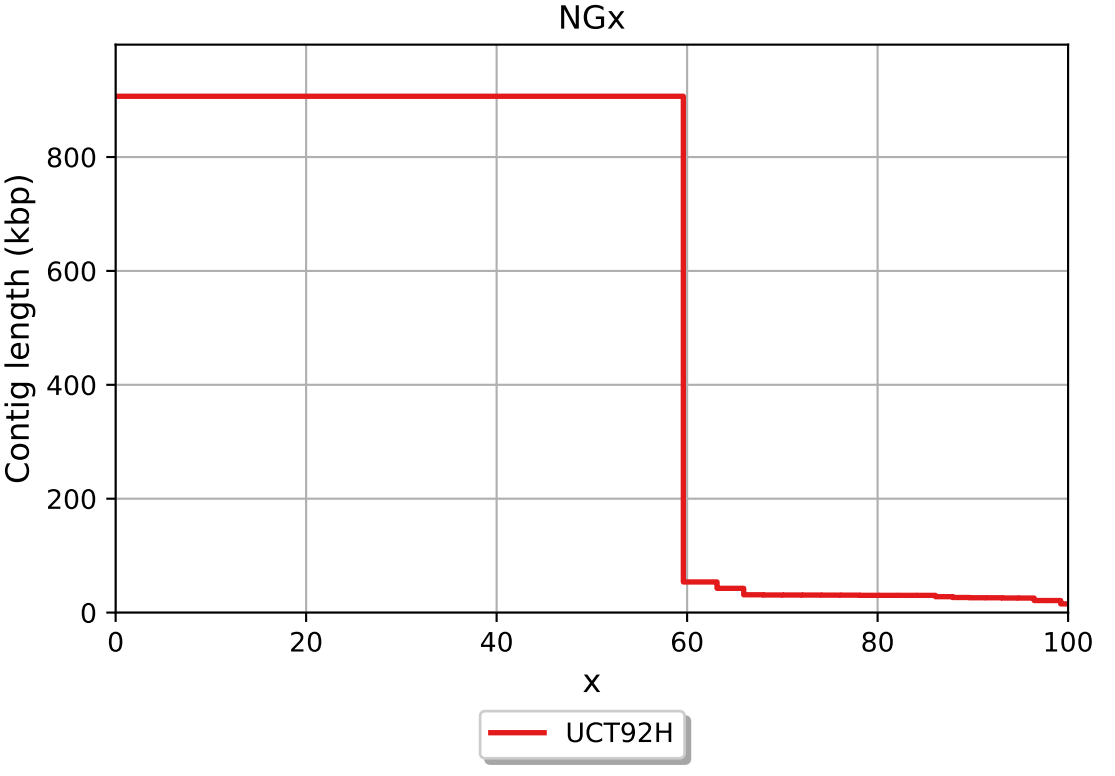
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

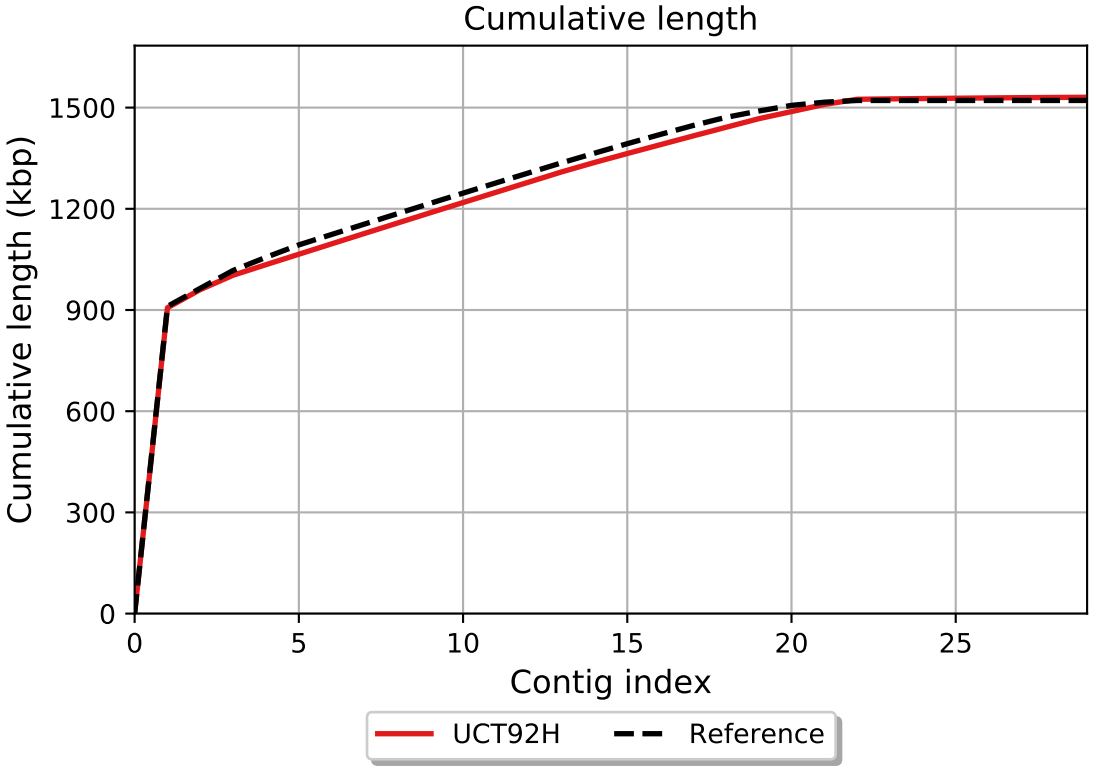
Unaligned report

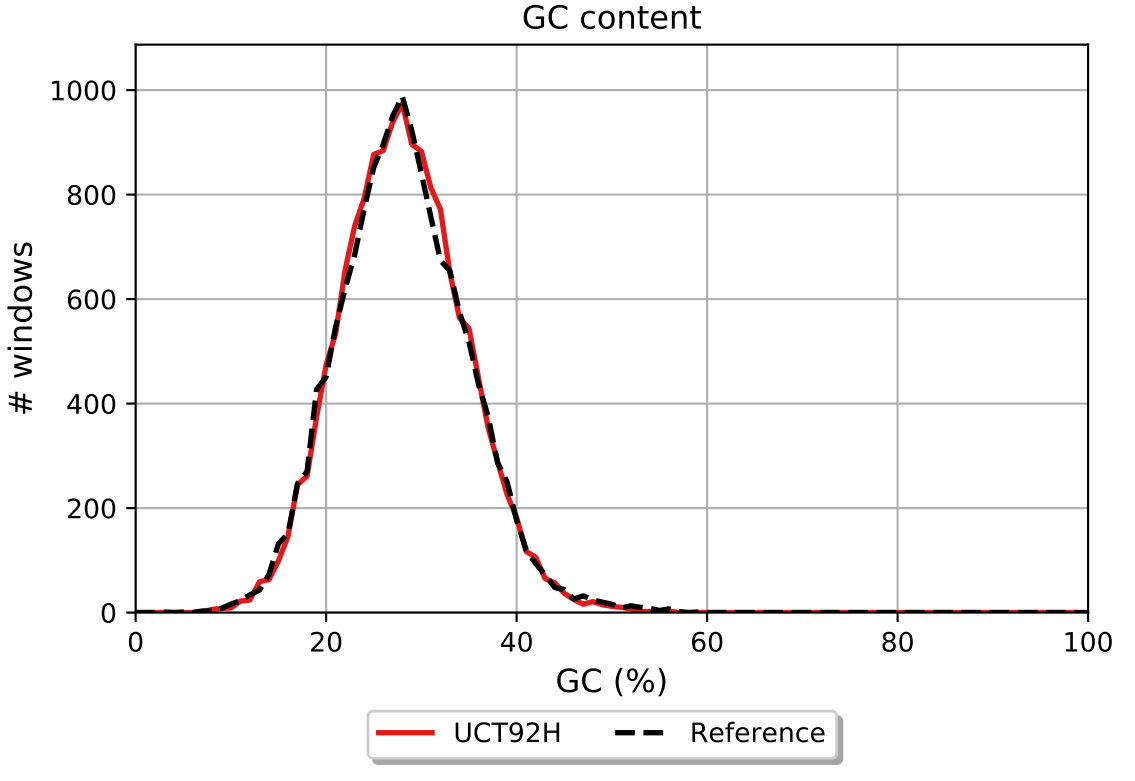
	UCT92H
# fully unaligned contigs	4
Fully unaligned length	2902
# partially unaligned contigs	19
Partially unaligned length	232369
# N's	0

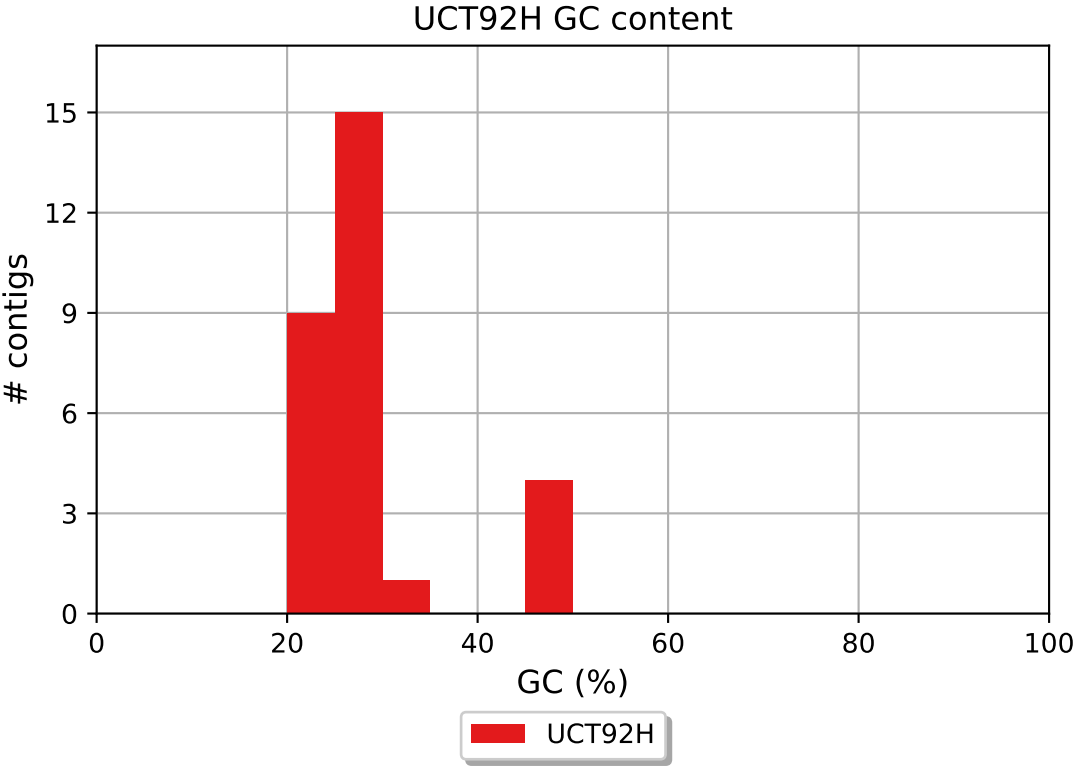
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

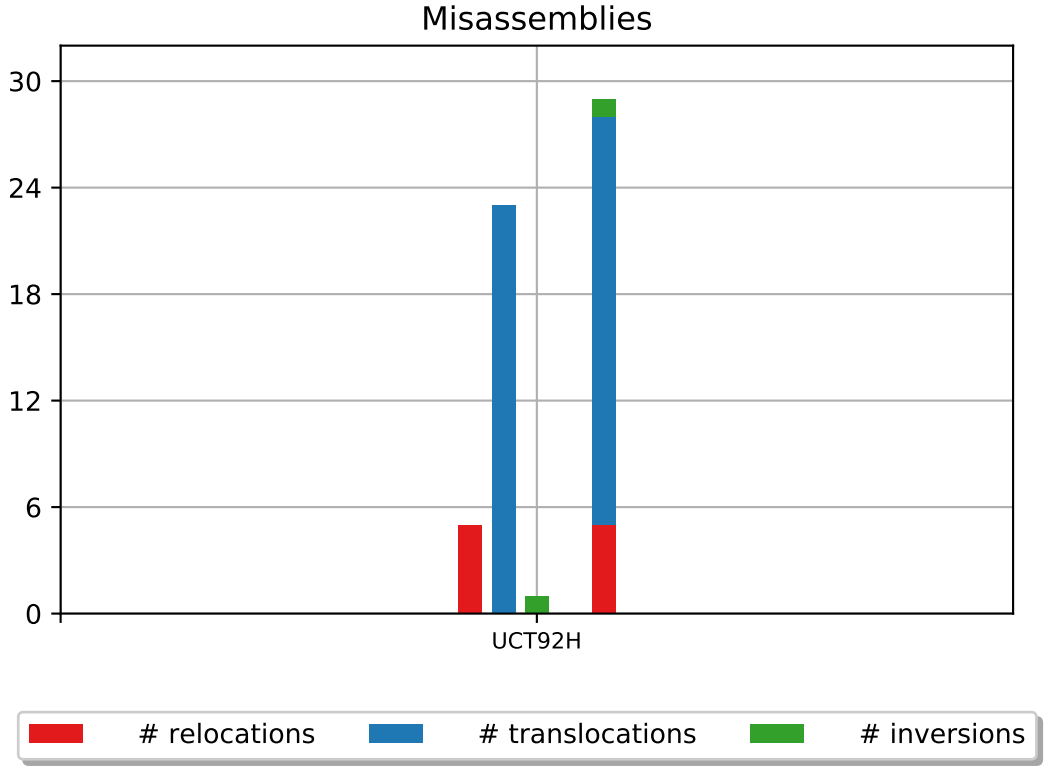

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT92H

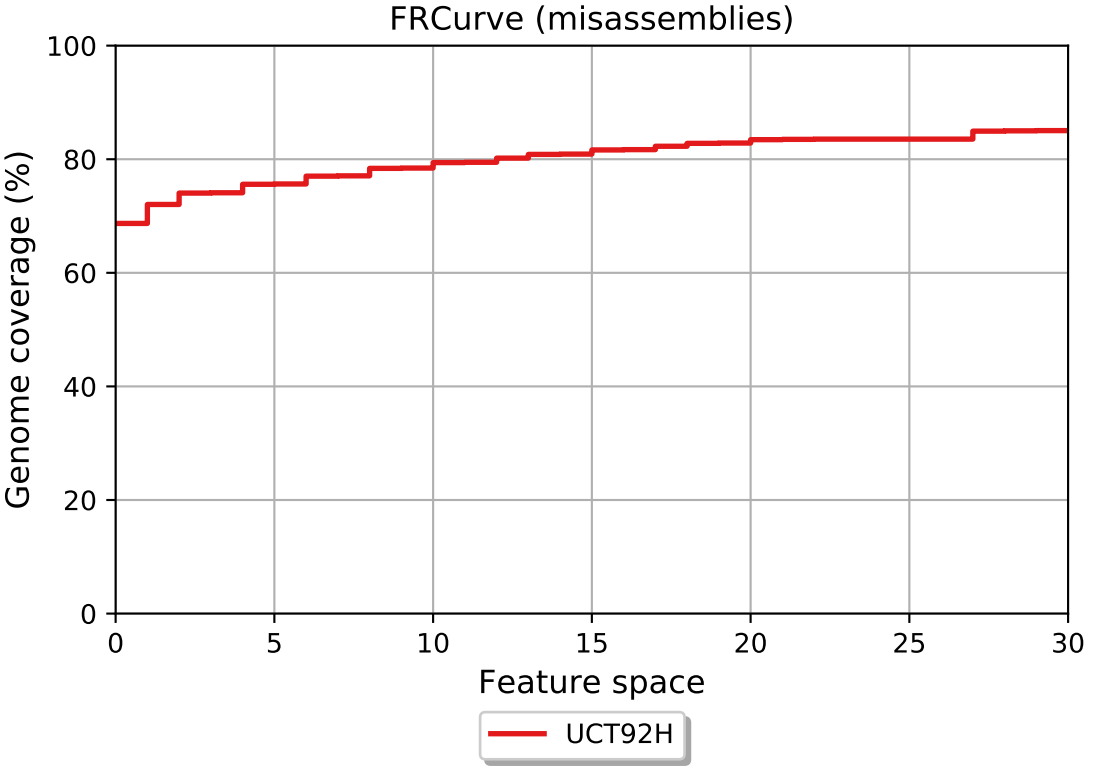

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT92H

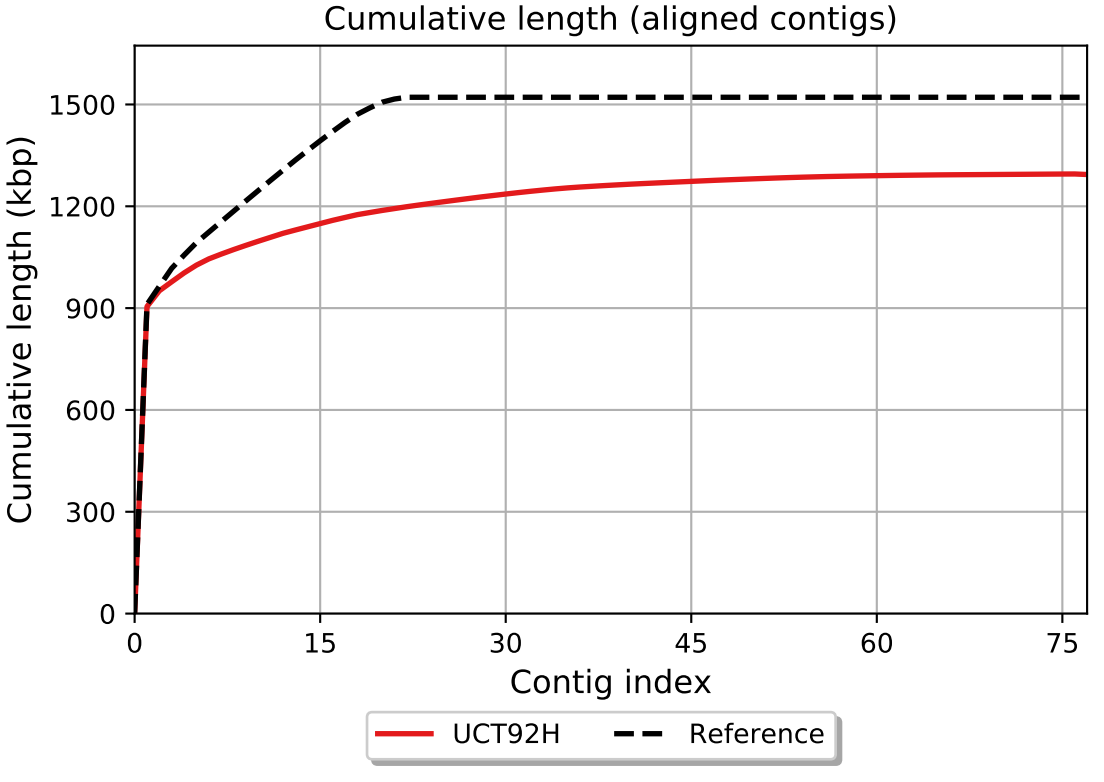

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
5
10
15
20
25
Contig index
UCT92H
Reference

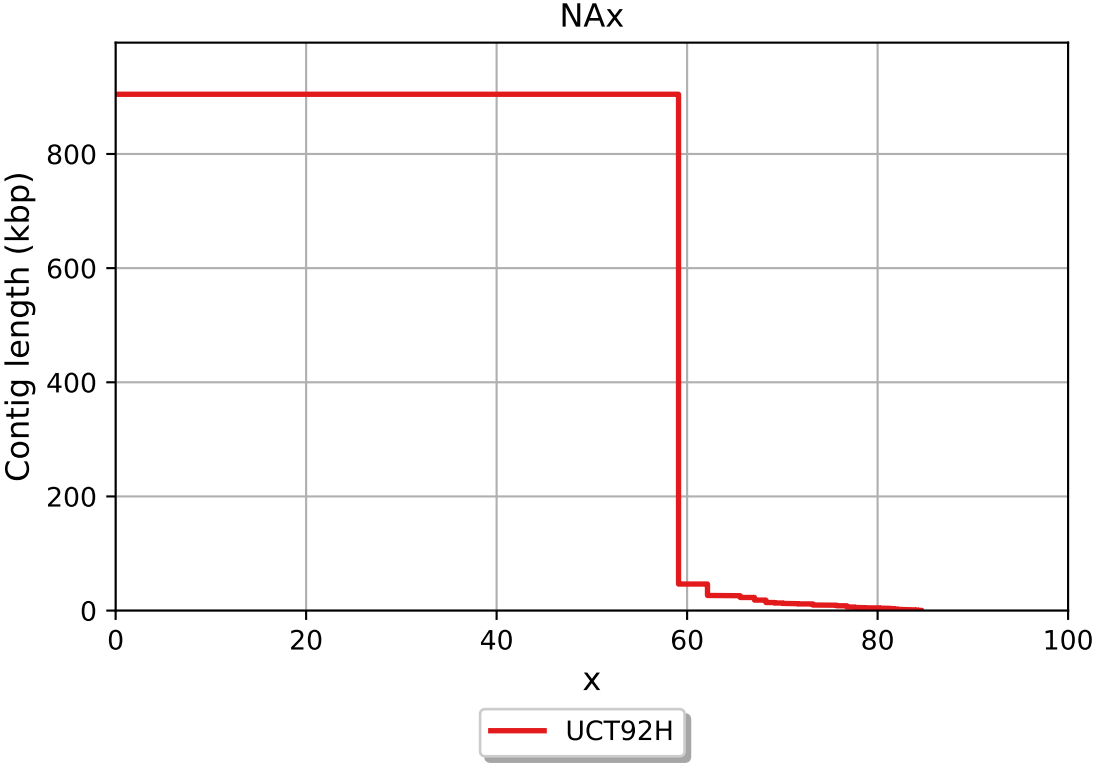

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
UCT92H
Reference

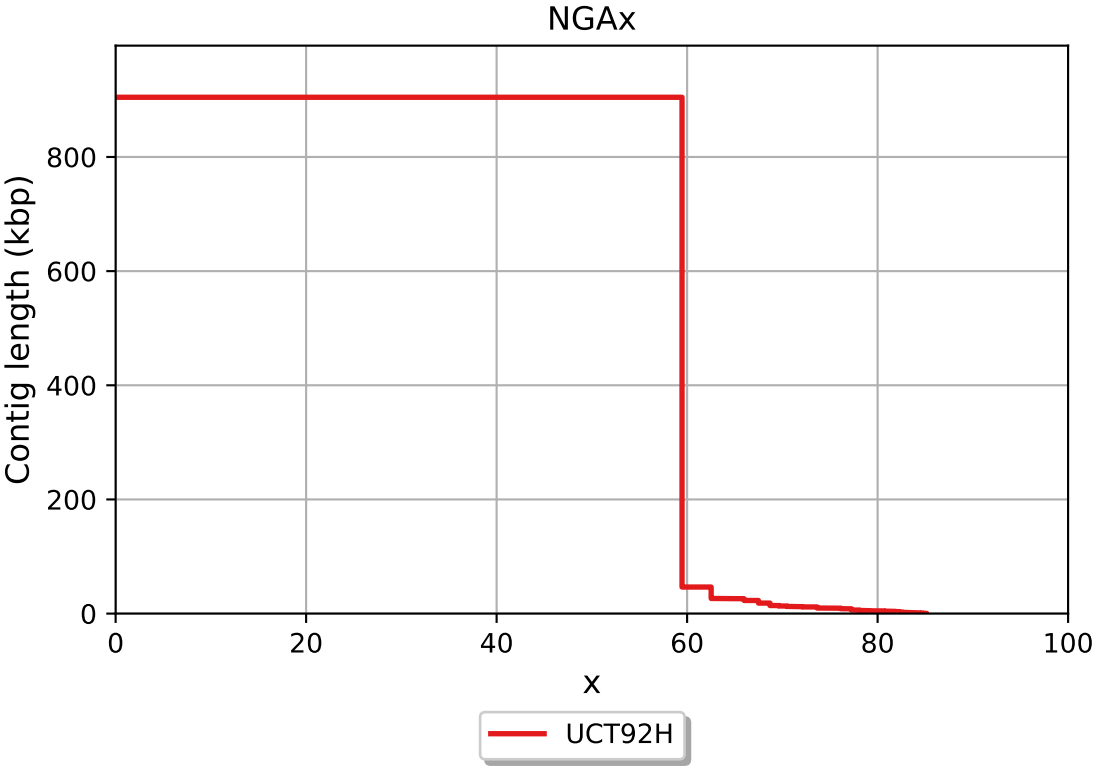

UCT92H GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
UCT92H

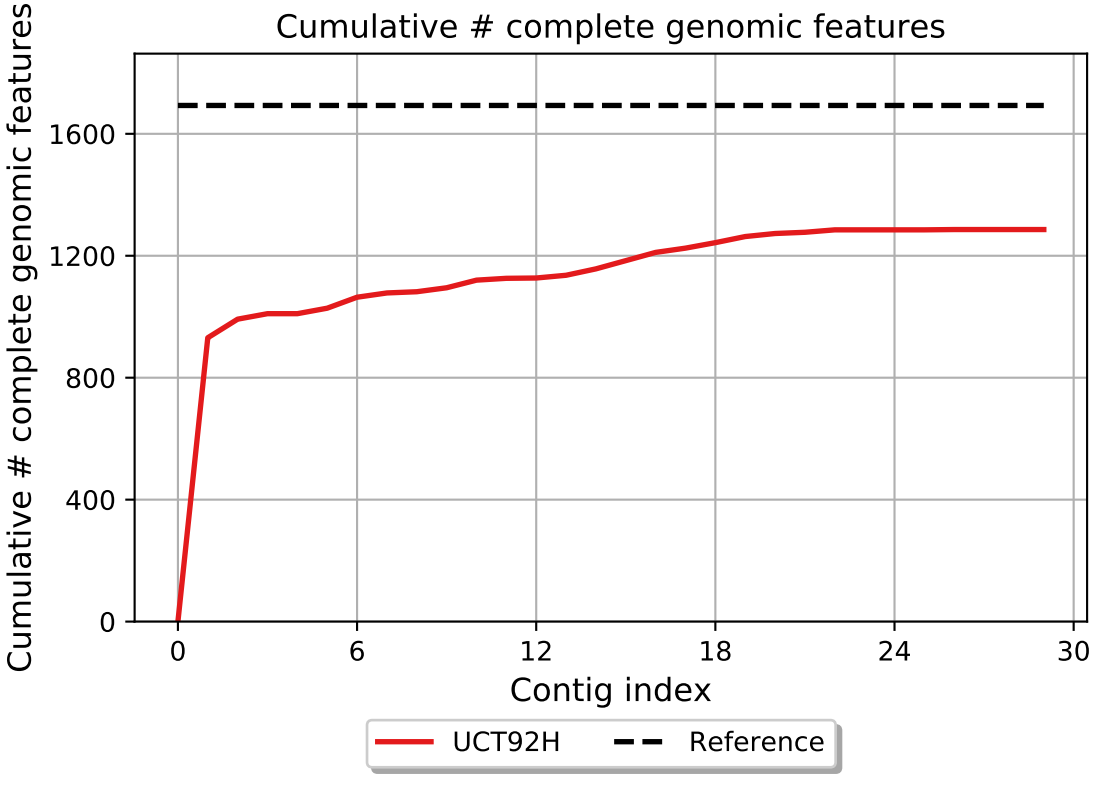

Misassemblies
30
24
18
12
6
0
UCT92H
relocations
translocations
inversions

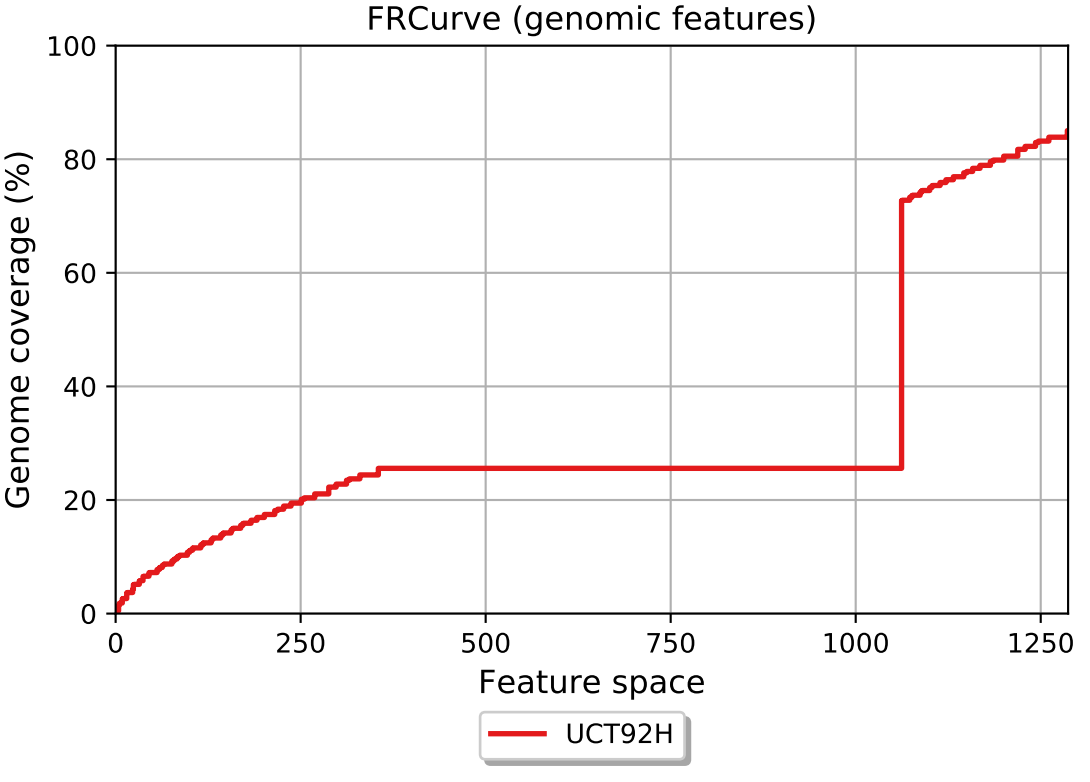

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
30
Feature space
UCT92H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
15
30
45
60
75
Contig index
UCT92H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT92H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT92H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
6
12
18
24
30
Contig index
UCT92H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
UCT92H