Report

	UCT109H
# contigs (>= 0 bp)	28
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1476377
Total length (>= 1000 bp)	1472225
Total length (>= 5000 bp)	1472225
Total length (>= 10000 bp)	1472225
Total length (>= 25000 bp)	1450182
Total length (>= 50000 bp)	1020649
# contigs	20
Largest contig	910570
Total length	1474783
Reference length	1521208
GC (%)	28.25
Reference GC (%)	28.18
N50	910570
NG50	910570
N90	30299
NG90	29838
auN	576600.9
auNG	559003.9
L50	1
LG50	1
L90	12
LG90	14
# misassemblies	12
# misassembled contigs	9
Misassembled contigs length	278157
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	13234
Genome fraction (%)	93.149
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	119.40
# indels per 100 kbp	16.16
# genomic features	1538 + 32 part
Largest alignment	910570
Total aligned length	1460695
NA50	910570
NGA50	910570
NA90	26498
NGA90	24180
auNA	573745.0
auNGA	556235.2
LA50	1
LGA50	1
LA90	14
LGA90	15

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

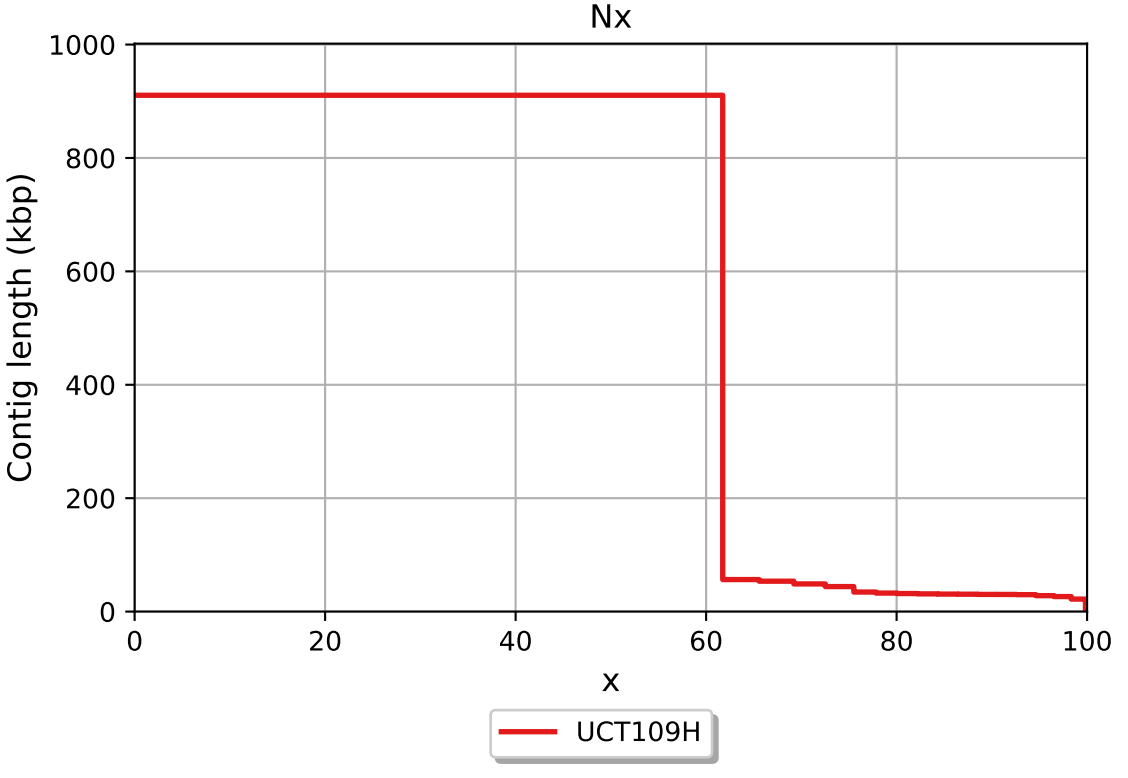
	UCT109H
# misassemblies	12
# contig misassemblies	12
# c. relocations	5
# c. translocations	7
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	278157
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1744
# indels	236
# indels (<= 5 bp)	201
# indels (> 5 bp)	35
Indels length	1845

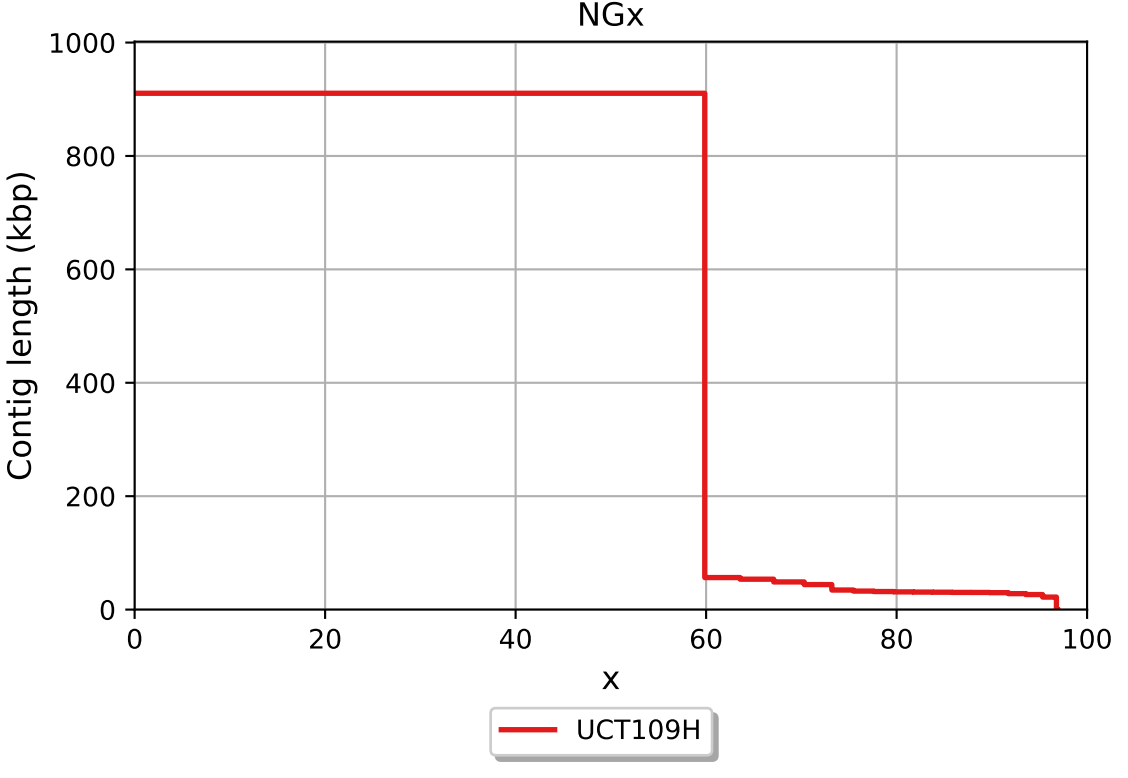
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

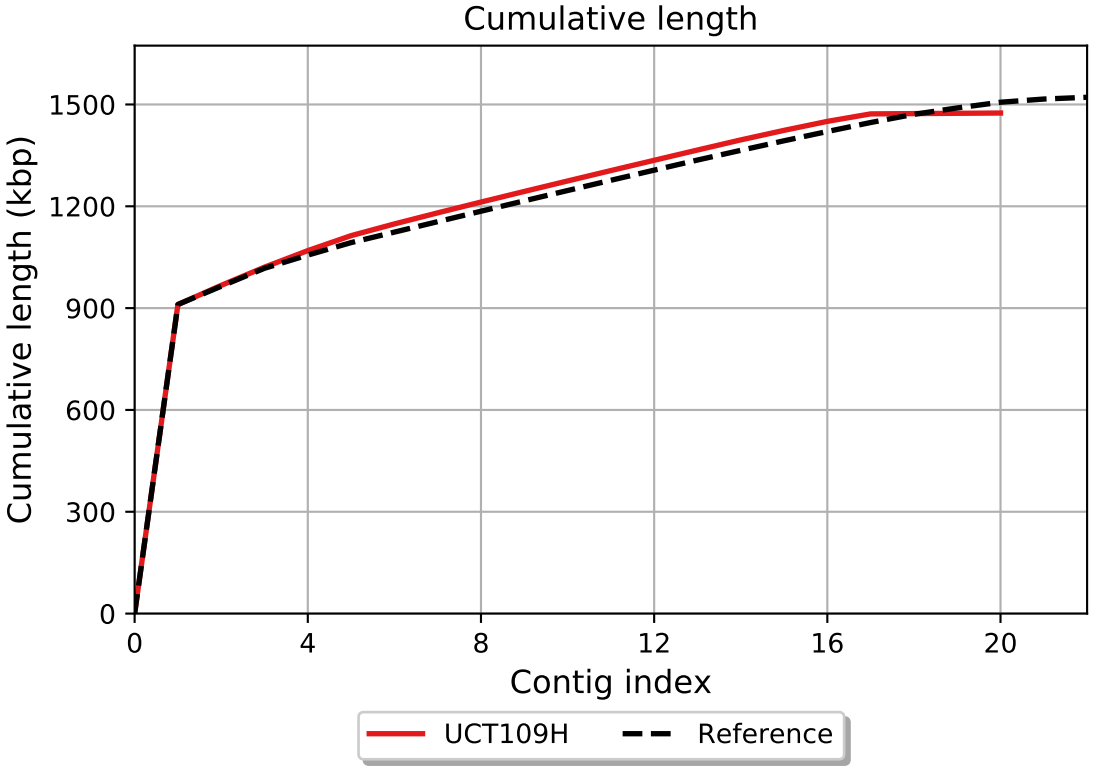
Unaligned report

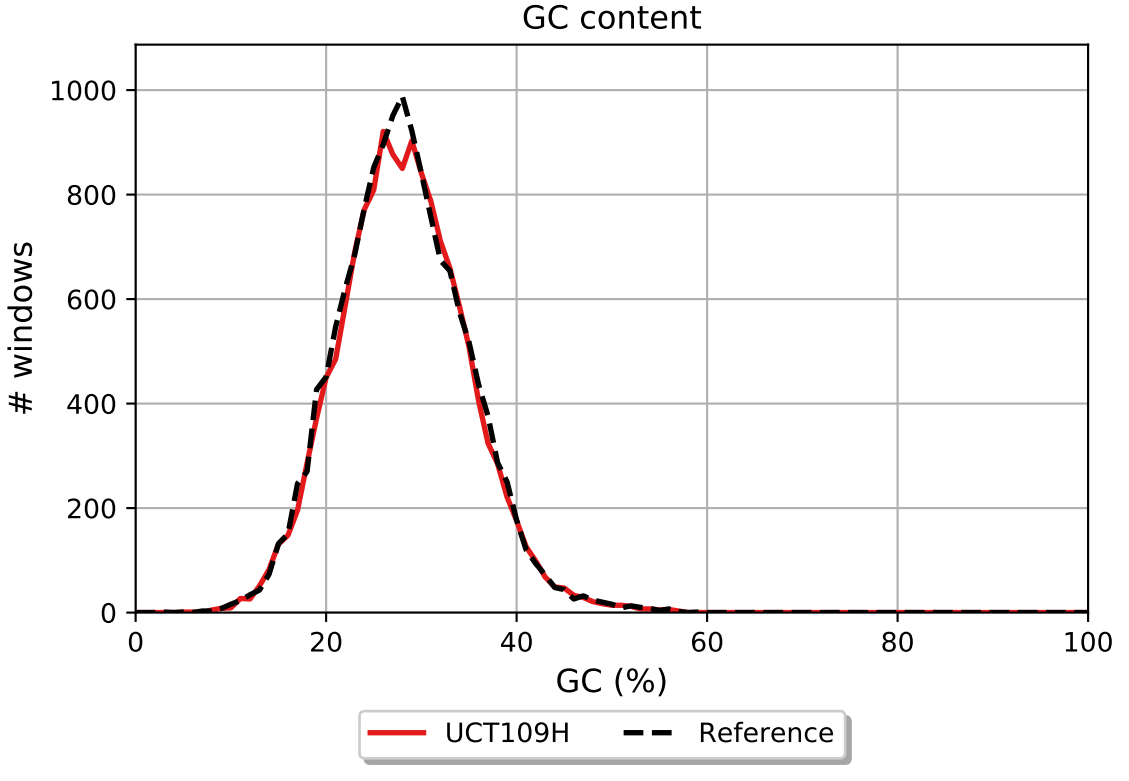
	UCT109H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	13234
# N's	0

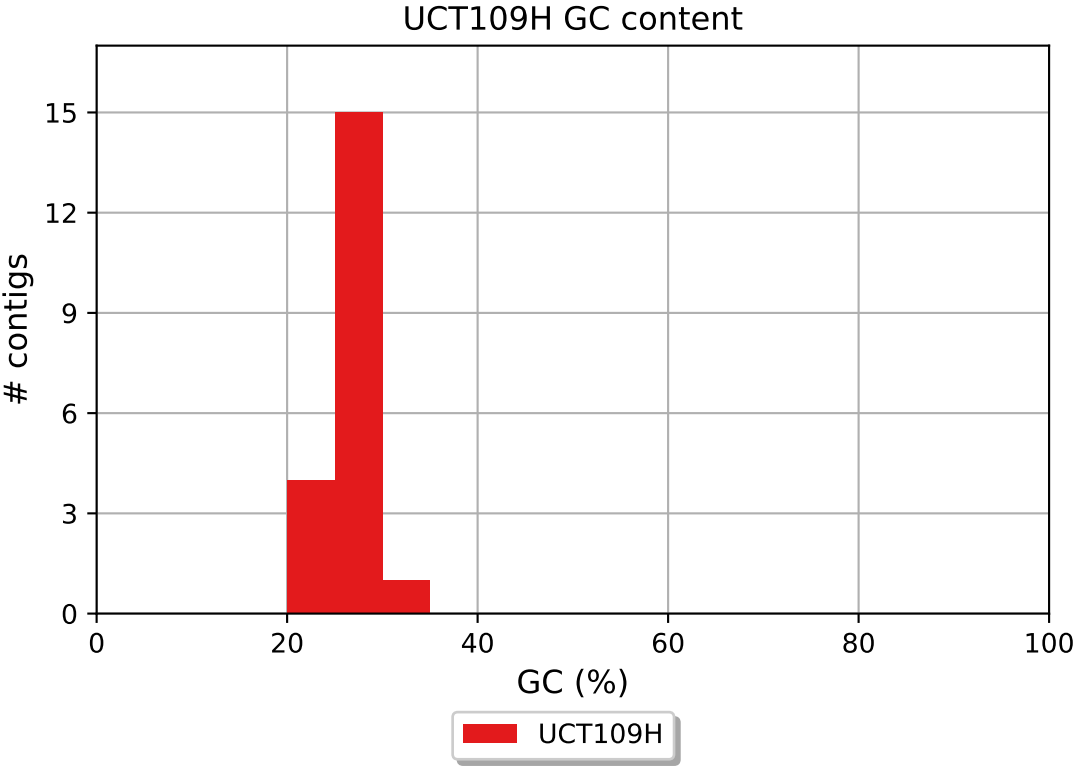
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UCT109H

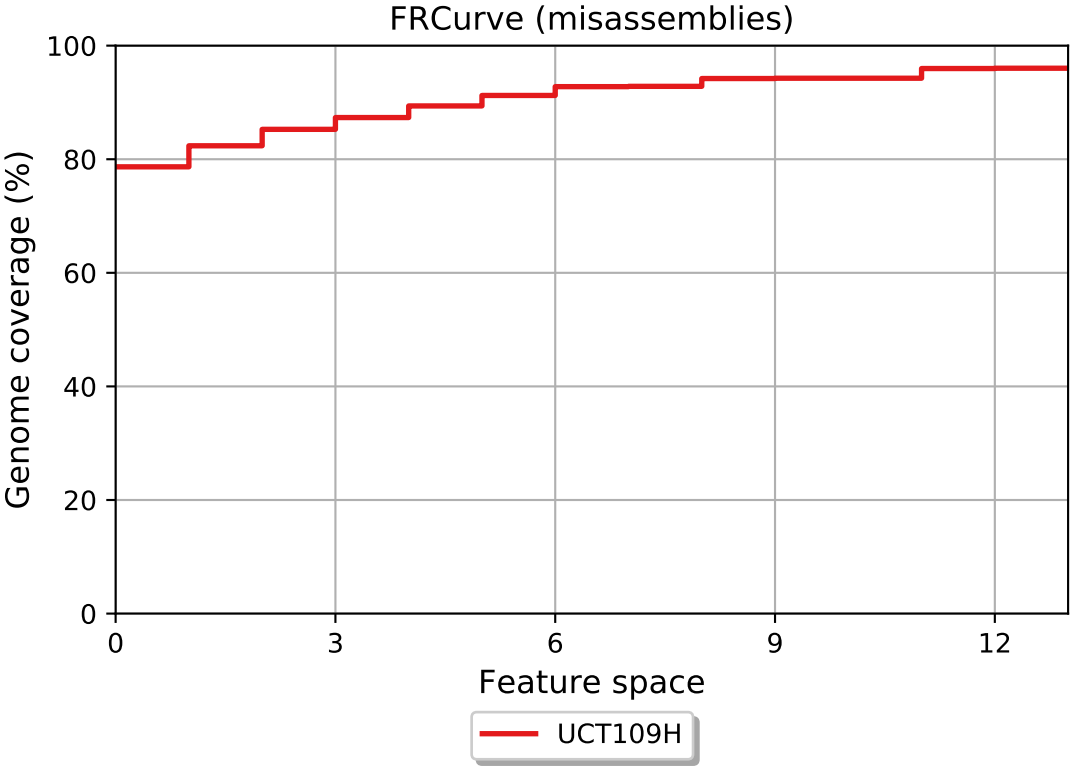

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UCT109H

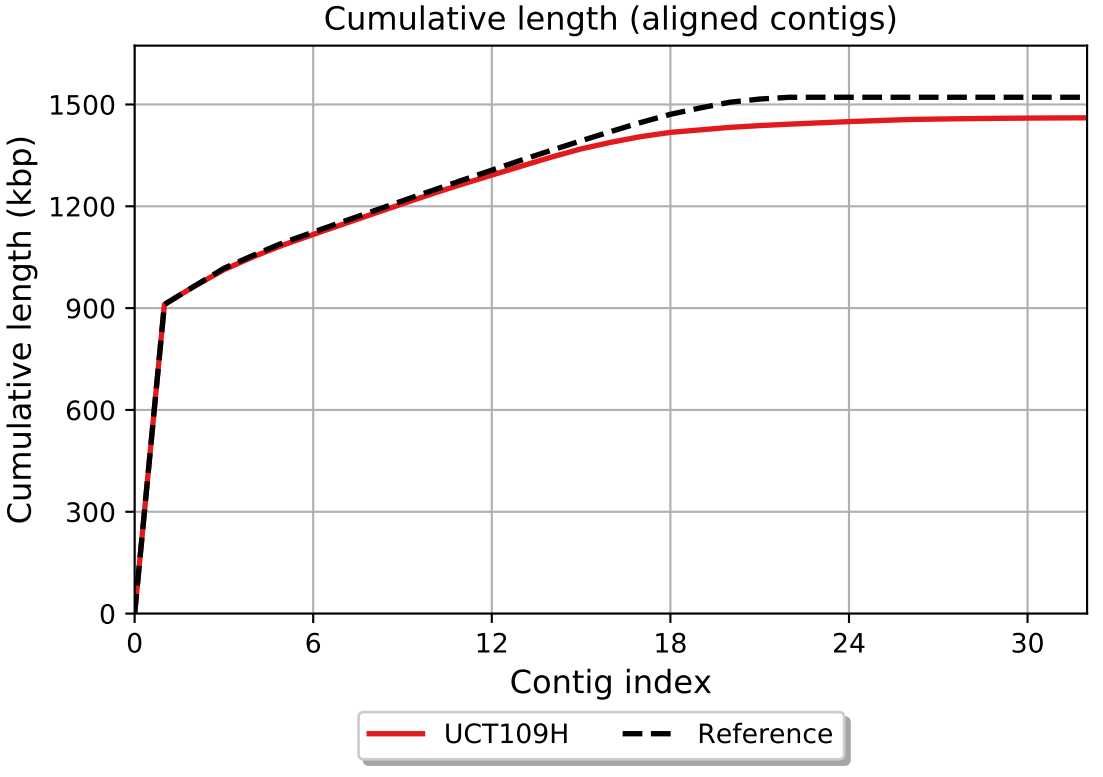

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UCT109H
Reference

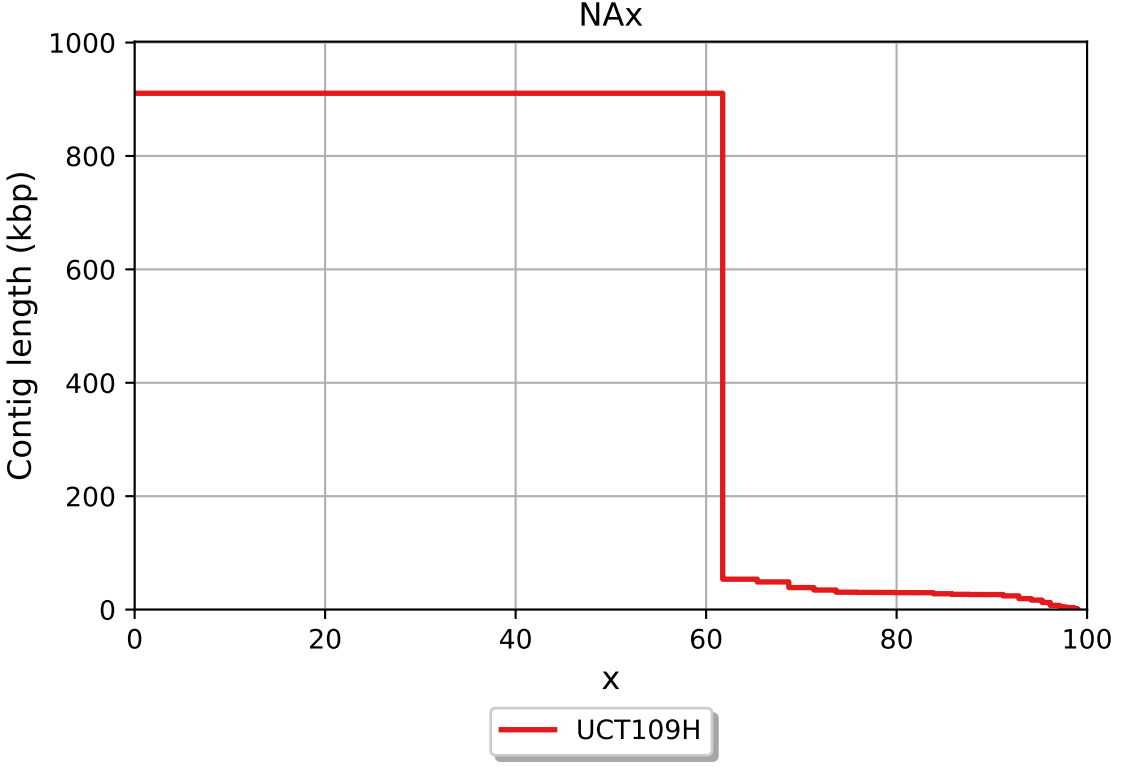

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
UCT109H
Reference

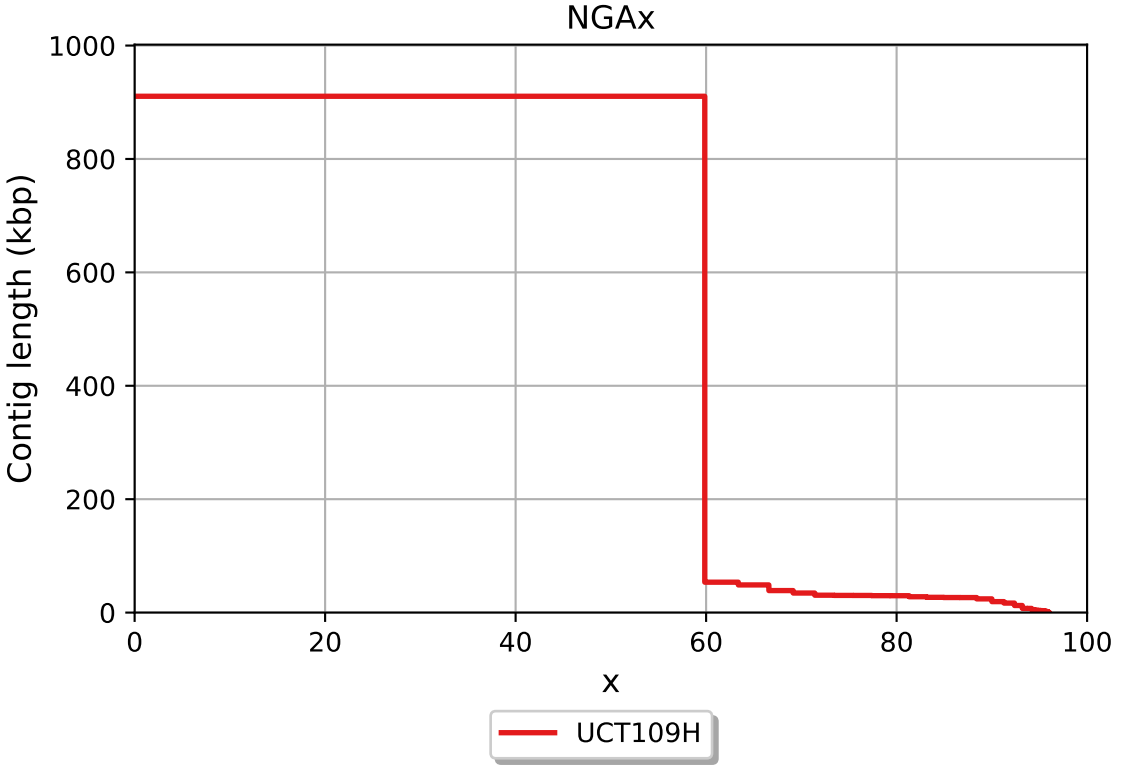

UCT109H GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
UCT109H

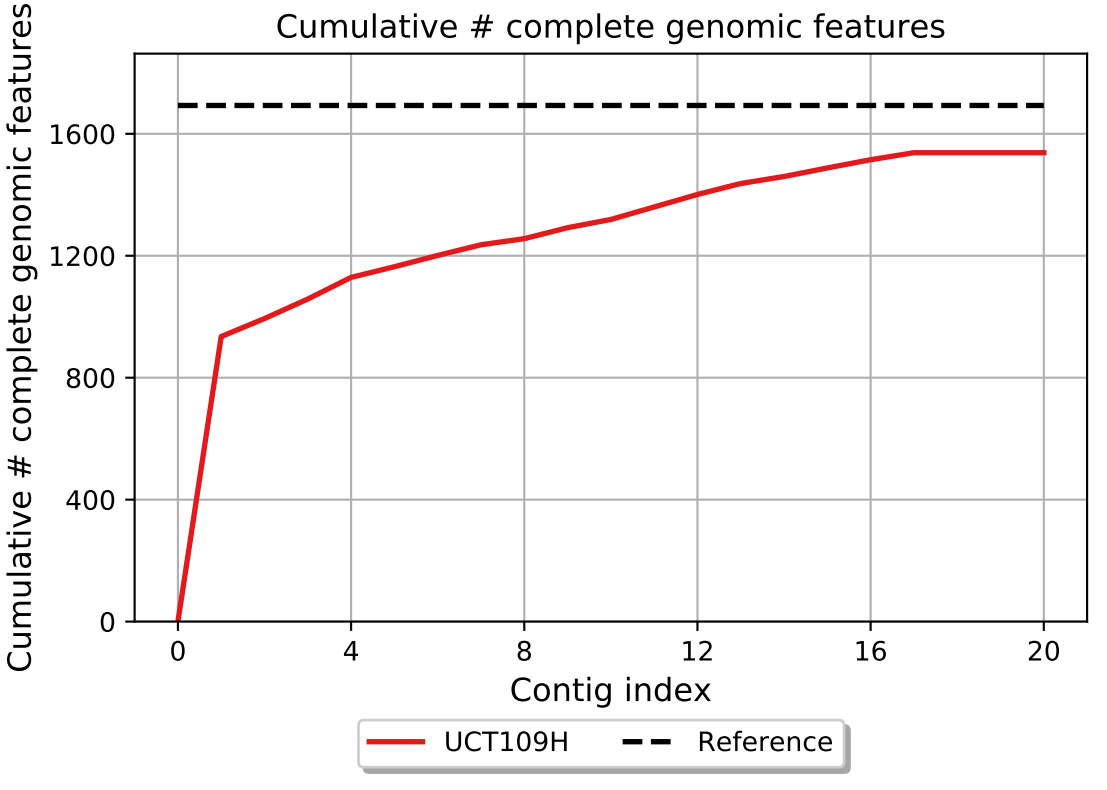
Misassemblies
12
9
6
3
0
UCT109H
relocations
translocations

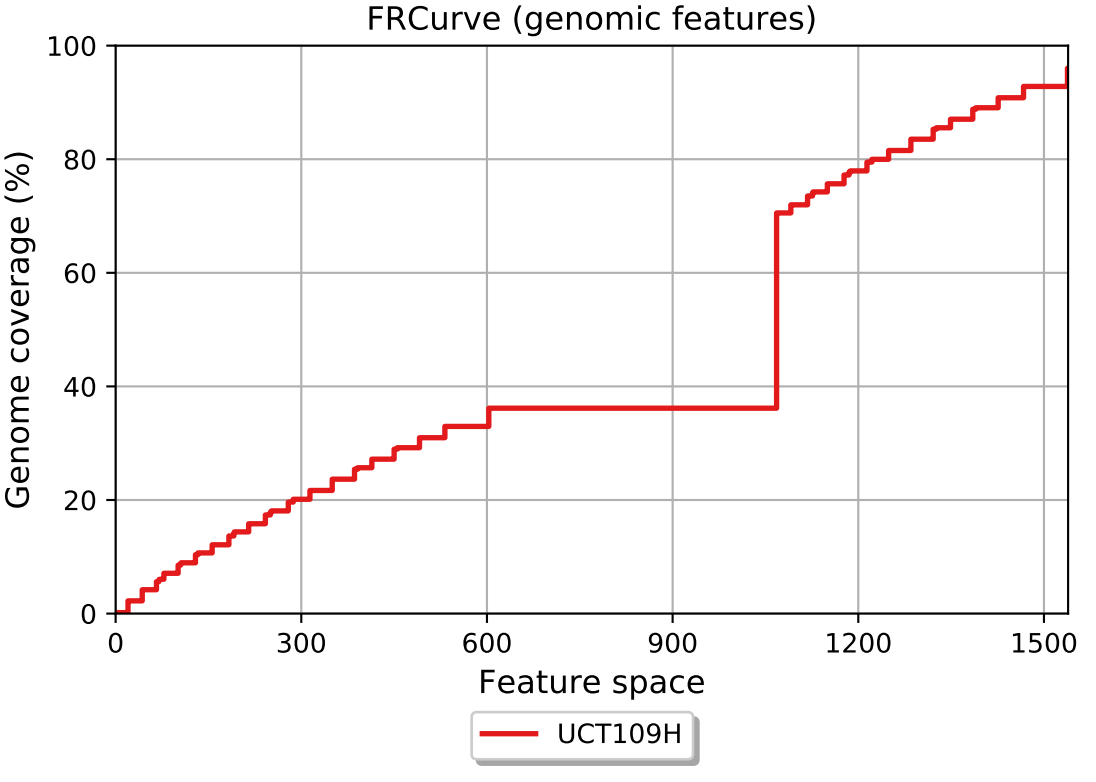

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
Feature space
UCT109H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
6
12
18
24
30
Contig index
UCT109H
Reference


NAx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
UCT109H


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UCT109H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
20
Contig index
UCT109H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
300
600
900
1200
1500
Feature space
UCT109H