Report

	UCT30H
# contigs (>= 0 bp)	89
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1471861
Total length (>= 1000 bp)	1451933
Total length (>= 5000 bp)	1446321
Total length (>= 10000 bp)	1424175
Total length (>= 25000 bp)	1360365
Total length (>= 50000 bp)	1122656
# contigs	38
Largest contig	905470
Total length	1461527
Reference length	1521208
GC (%)	28.17
Reference GC (%)	28.18
N50	905470
NG50	905470
N90	26498
NG90	21483
auN	574986.3
auNG	552428.1
L50	1
LG50	1
L90	12
LG90	14
# misassemblies	30
# misassembled contigs	12
Misassembled contigs length	308645
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	6 + 16 part
Unaligned length	230680
Genome fraction (%)	79.193
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	777.99
# indels per 100 kbp	55.55
# genomic features	1260 + 51 part
Largest alignment	904647
Total aligned length	1225854
NA50	904647
NGA50	904647
NA90	-
NGA90	-
auNA	563737.3
auNGA	541620.4
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

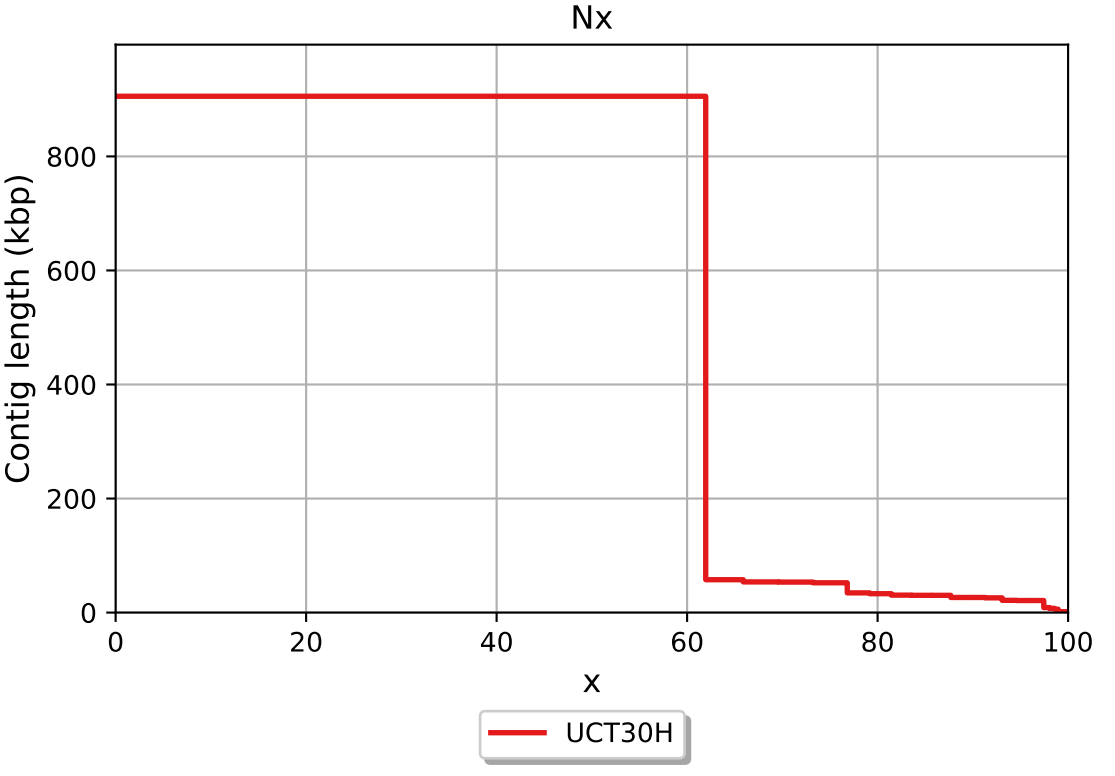
	UCT30H
# misassemblies	30
# contig misassemblies	30
# c. relocations	7
# c. translocations	20
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	308645
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9537
# indels	681
# indels (<= 5 bp)	617
# indels (> 5 bp)	64
Indels length	3422

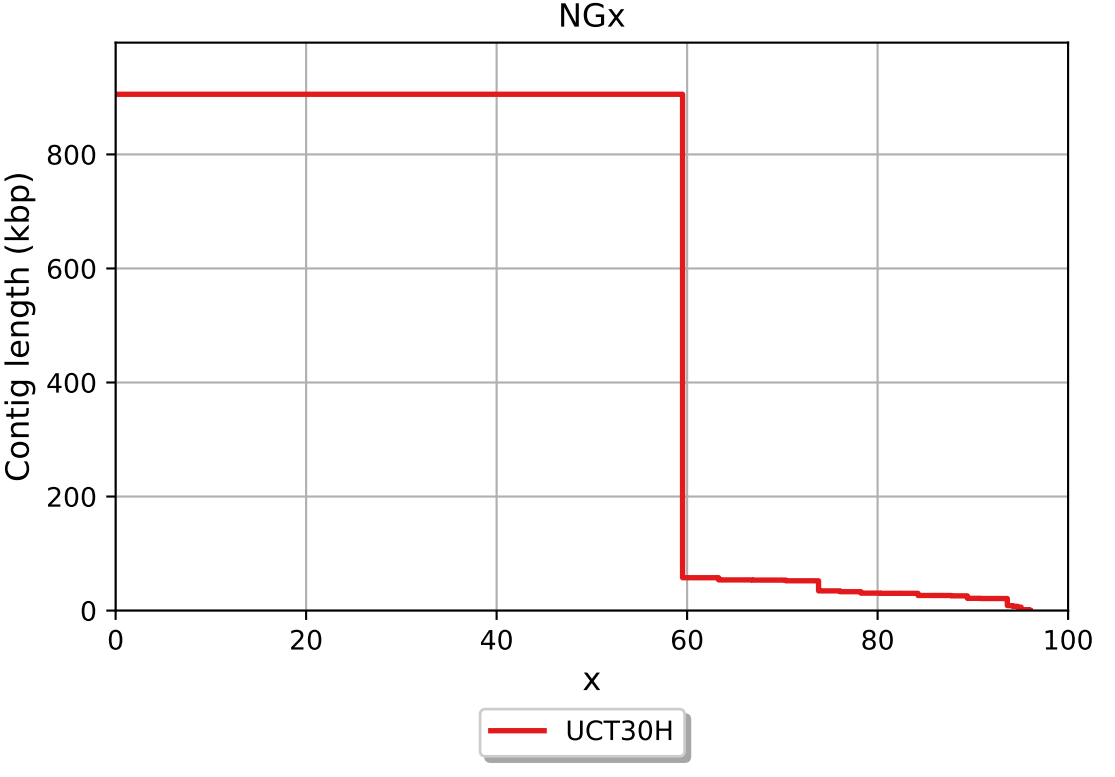
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

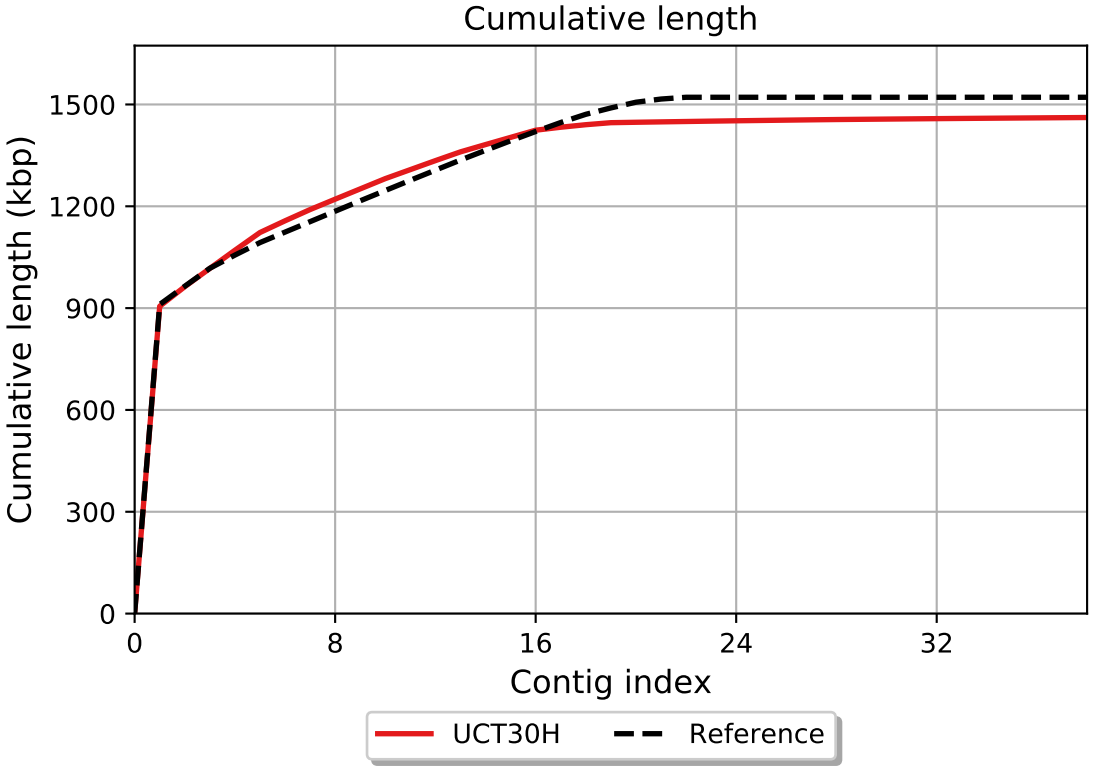
Unaligned report

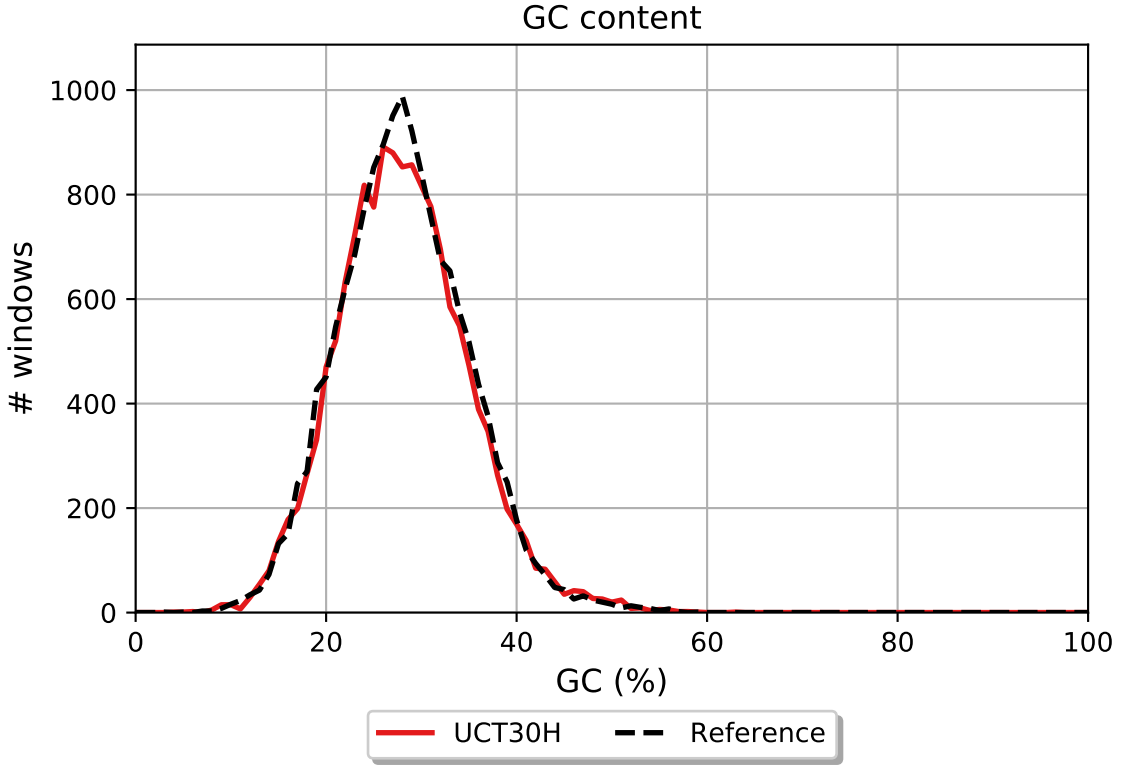
	UCT30H
# fully unaligned contigs	6
Fully unaligned length	9301
# partially unaligned contigs	16
Partially unaligned length	221379
# N's	0

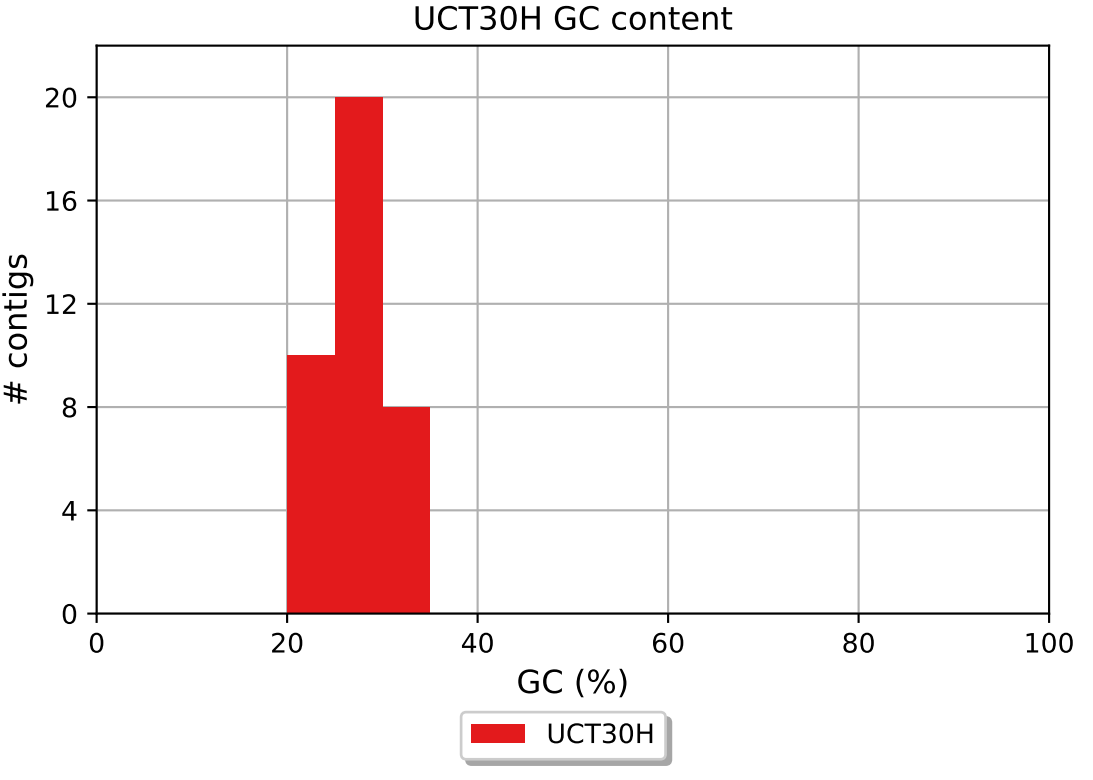
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

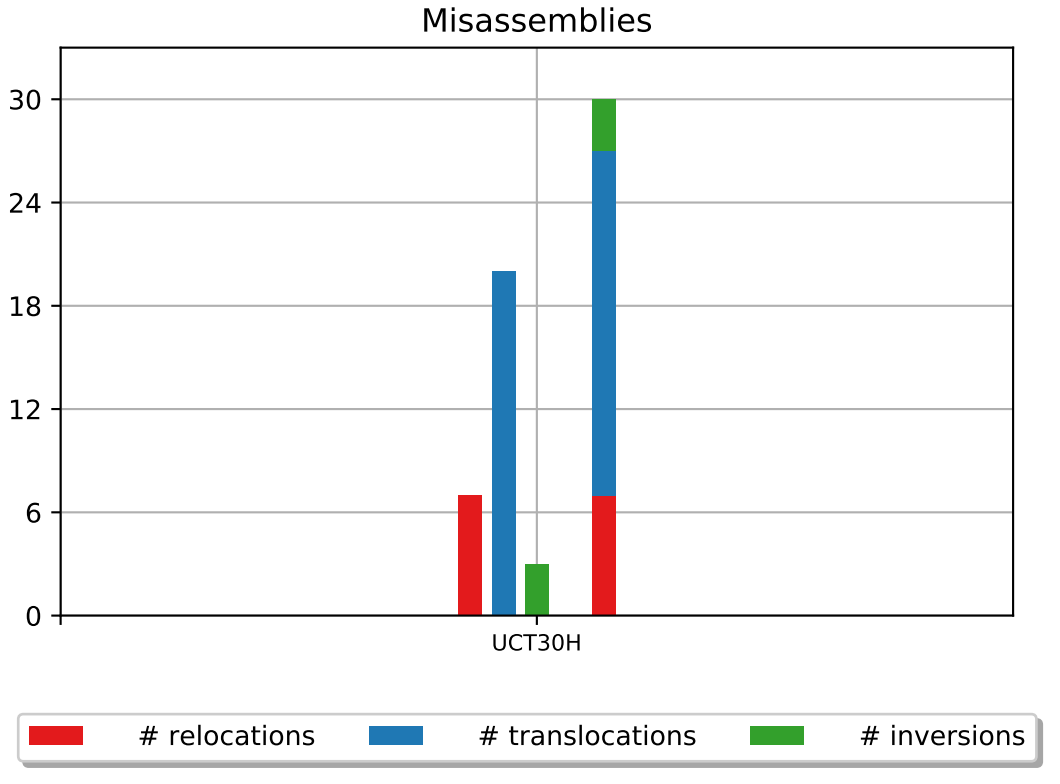

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT30H

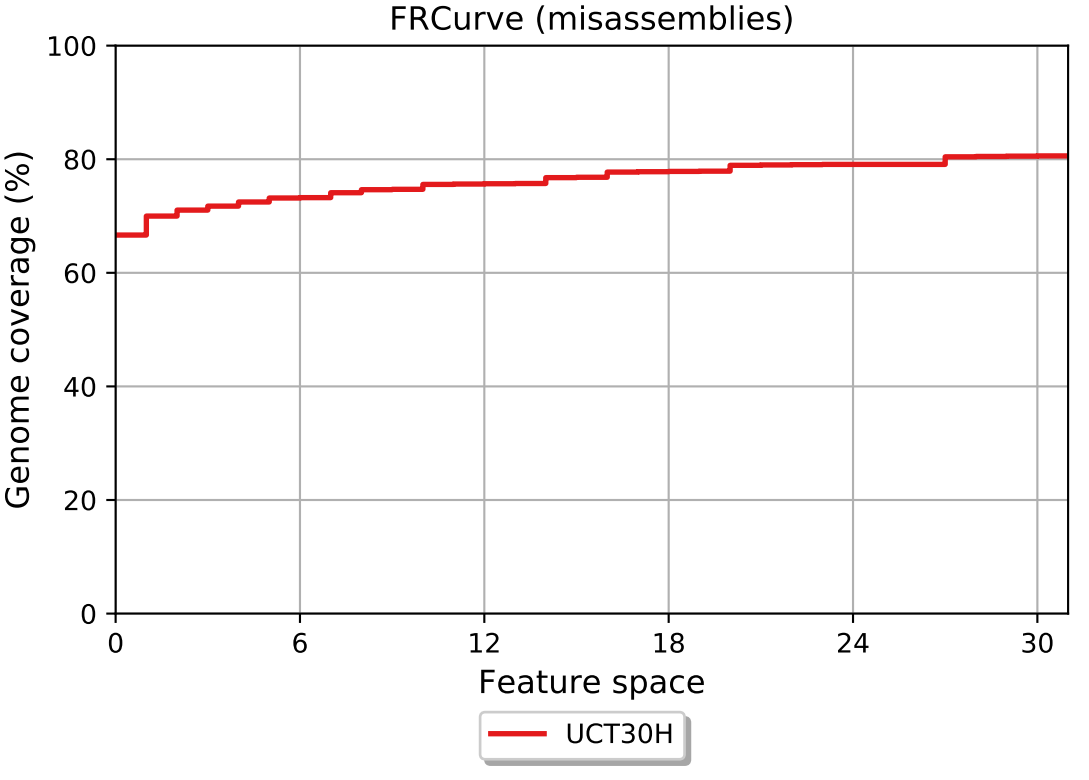

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT30H

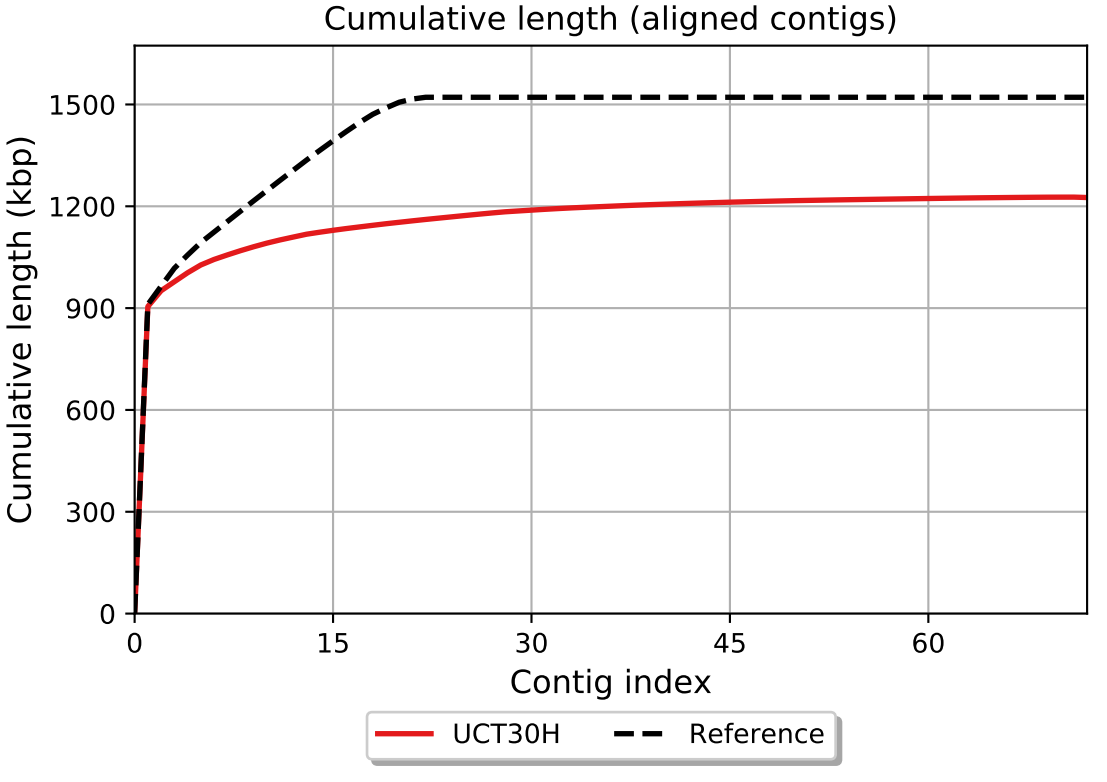

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
Contig index
UCT30H
Reference

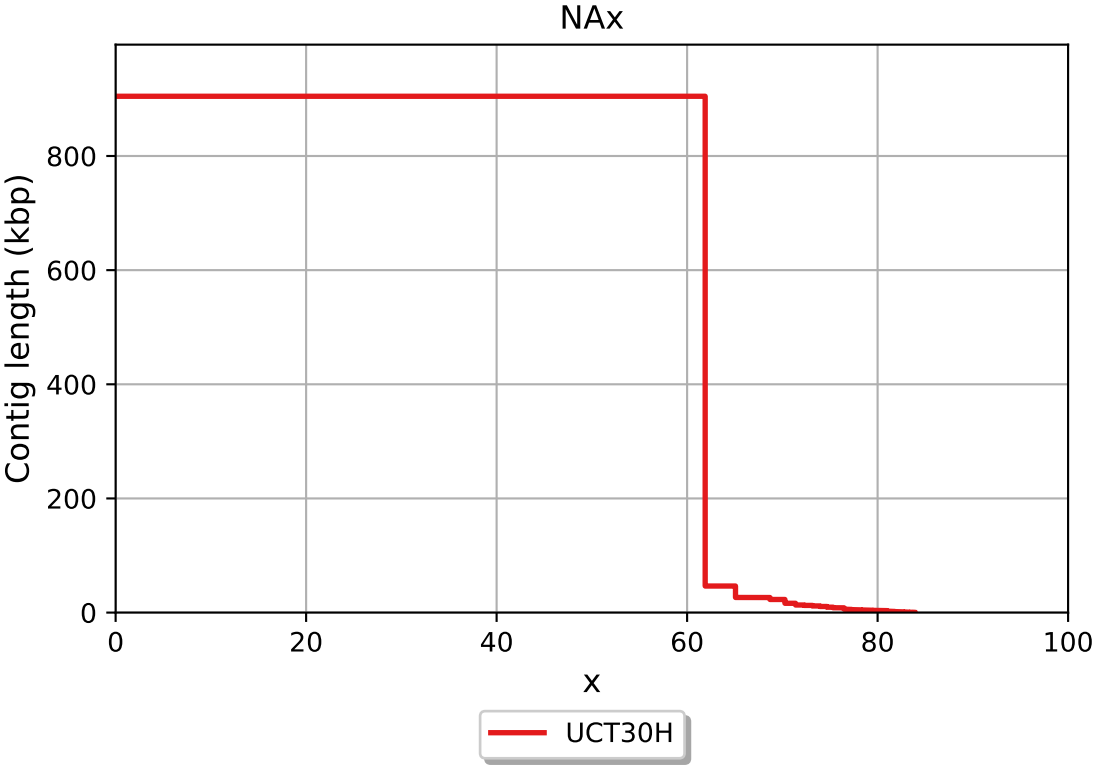

GC content
1000
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
UCT30H
Reference

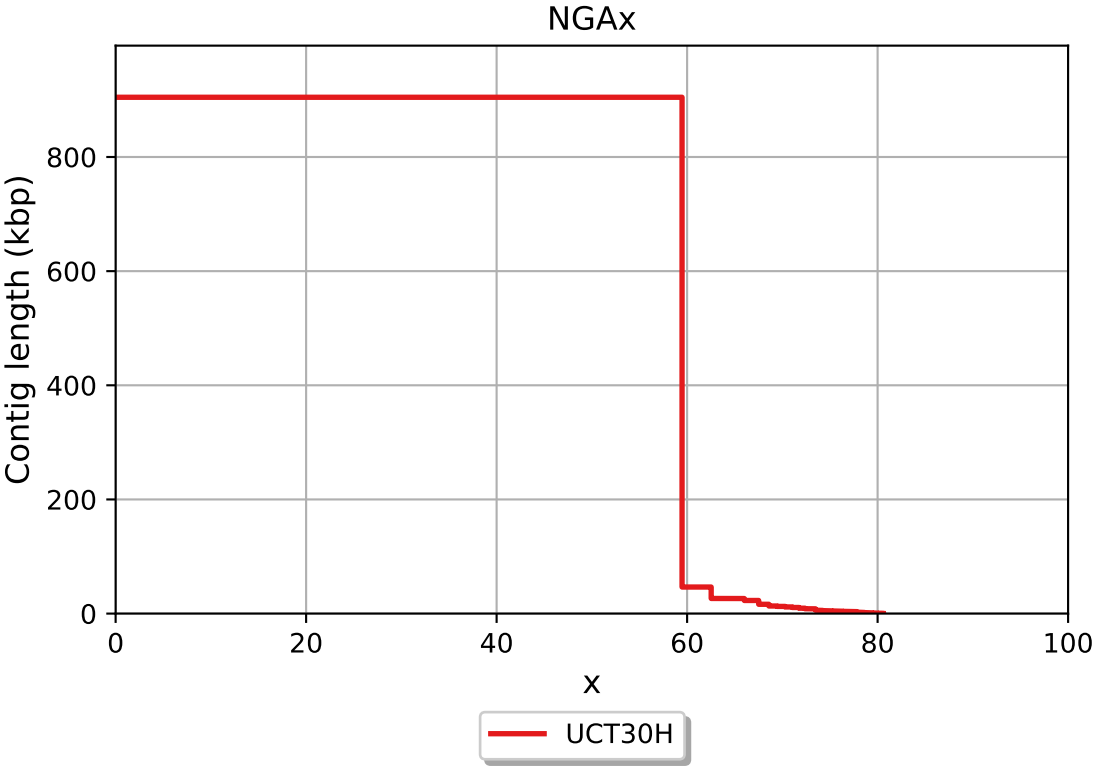

UCT30H GC content
contigs
0
4
8
12
16
20
0
20
40
60
80
100
GC (%)
UCT30H

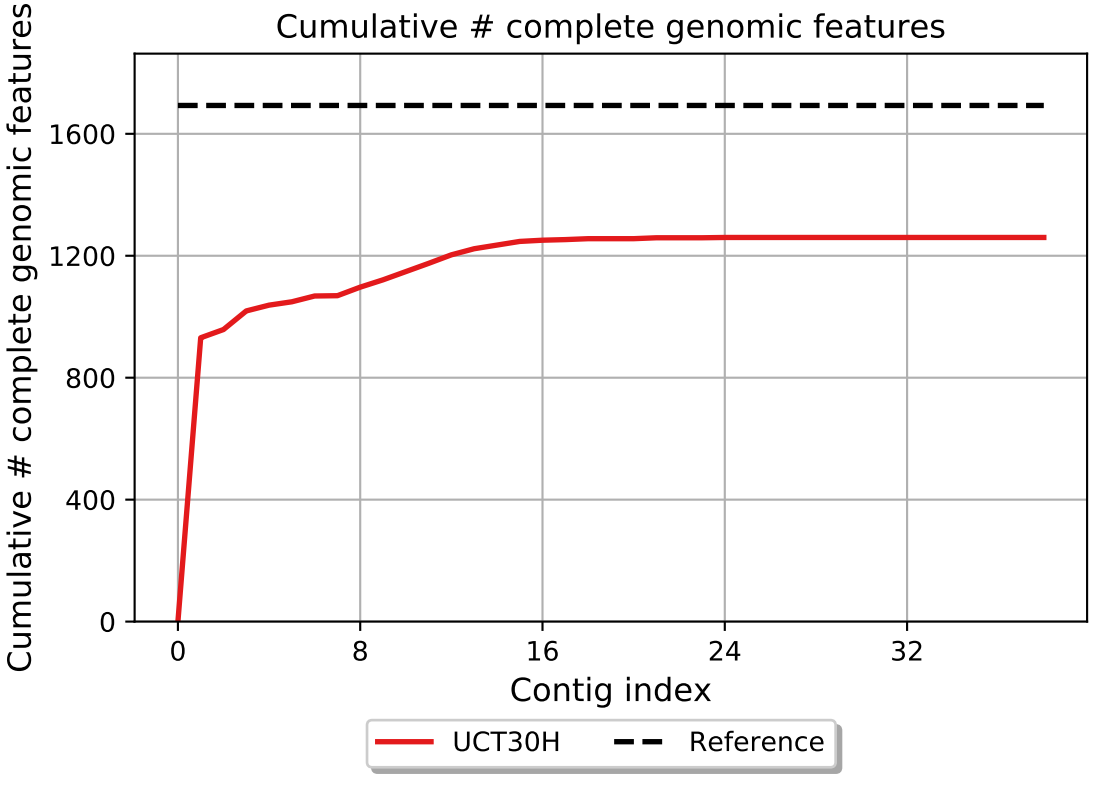

Misassemblies
30
24
18
12
6
0
UCT30H
relocations
translocations
inversions

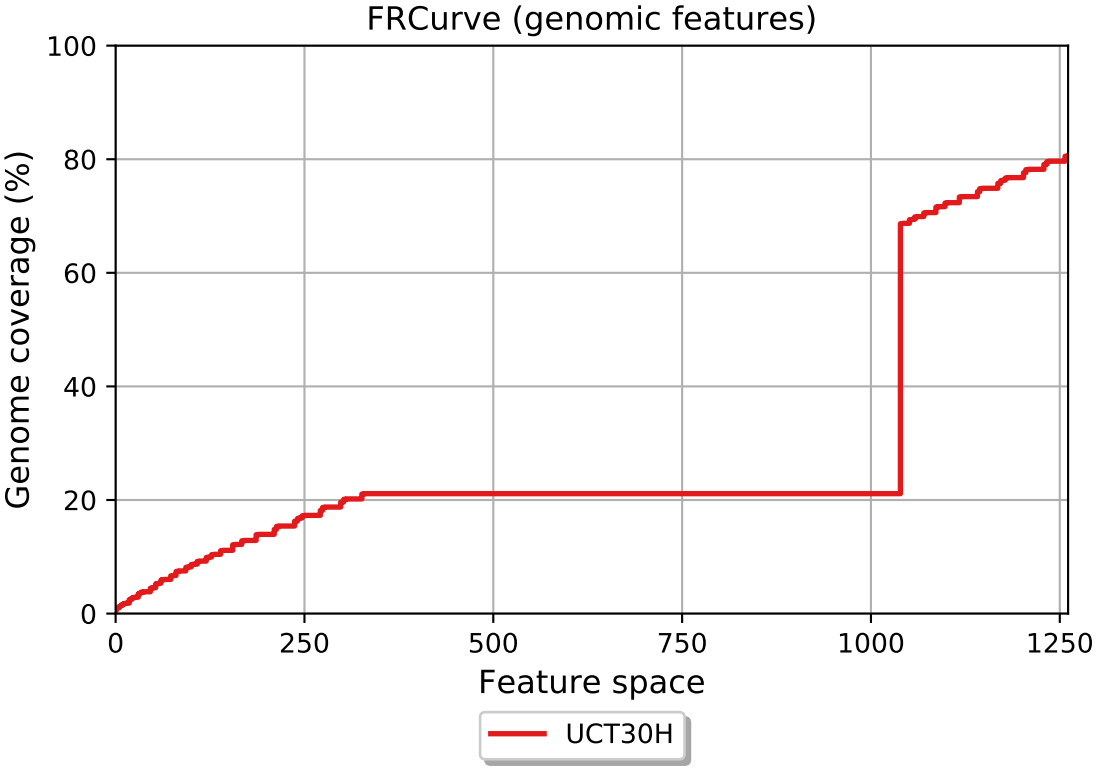

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
6
12
18
24
30
Feature space
UCT30H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
15
30
45
60
Contig index
UCT30H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT30H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UCT30H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
8
16
24
32
Contig index
UCT30H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
UCT30H