

Report

	UCT110H
# contigs (>= 0 bp)	114
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1417187
Total length (>= 1000 bp)	1388643
Total length (>= 5000 bp)	1370312
Total length (>= 10000 bp)	1356626
Total length (>= 25000 bp)	1218925
Total length (>= 50000 bp)	1014186
# contigs	43
Largest contig	906810
Total length	1400171
Reference length	1521208
GC (%)	28.16
Reference GC (%)	28.18
N50	906810
NG50	906810
N90	24648
NG90	6008
auN	598070.9
auNG	550484.5
L50	1
LG50	1
L90	12
LG90	18
# misassemblies	18
# misassembled contigs	9
Misassembled contigs length	218940
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	5 + 16 part
Unaligned length	193559
Genome fraction (%)	77.967
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	747.51
# indels per 100 kbp	42.21
# genomic features	1242 + 51 part
Largest alignment	904647
Total aligned length	1203597
NA50	904647
NGA50	904647
NA90	-
NGA90	-
auNA	588375.8
auNGA	541560.8
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

	UCT110H
# misassemblies	18
# contig misassemblies	18
# c. relocations	5
# c. translocations	11
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	218940
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	8997
# indels	508
# indels (<= 5 bp)	458
# indels (> 5 bp)	50
Indels length	2620

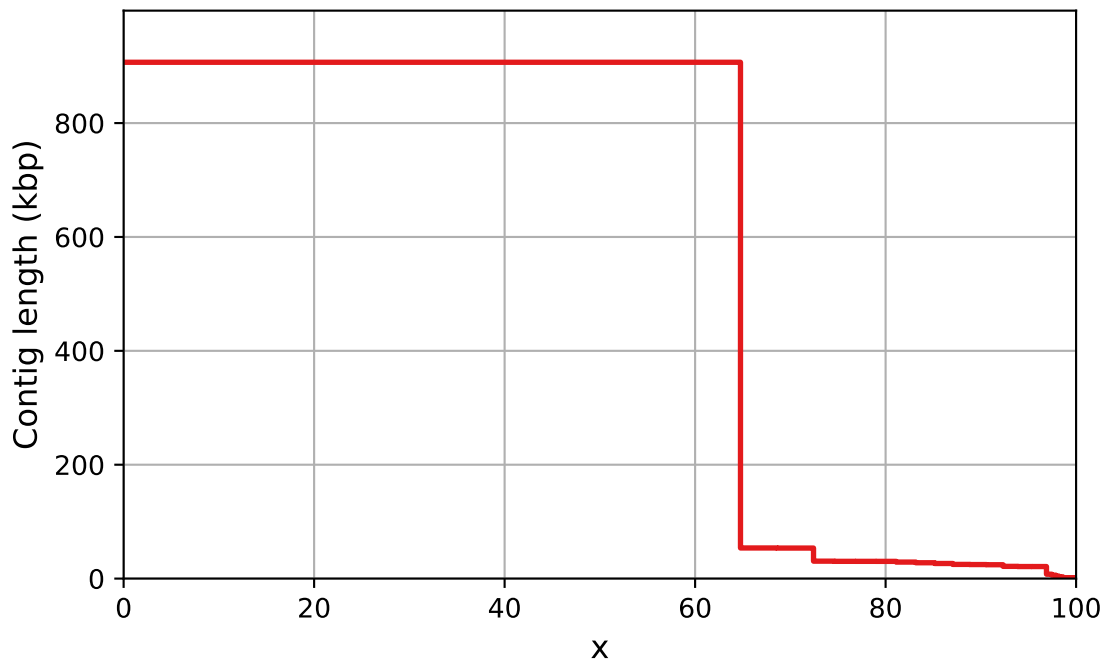
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	UCT110H
# fully unaligned contigs	5
Fully unaligned length	9348
# partially unaligned contigs	16
Partially unaligned length	184211
# N's	0

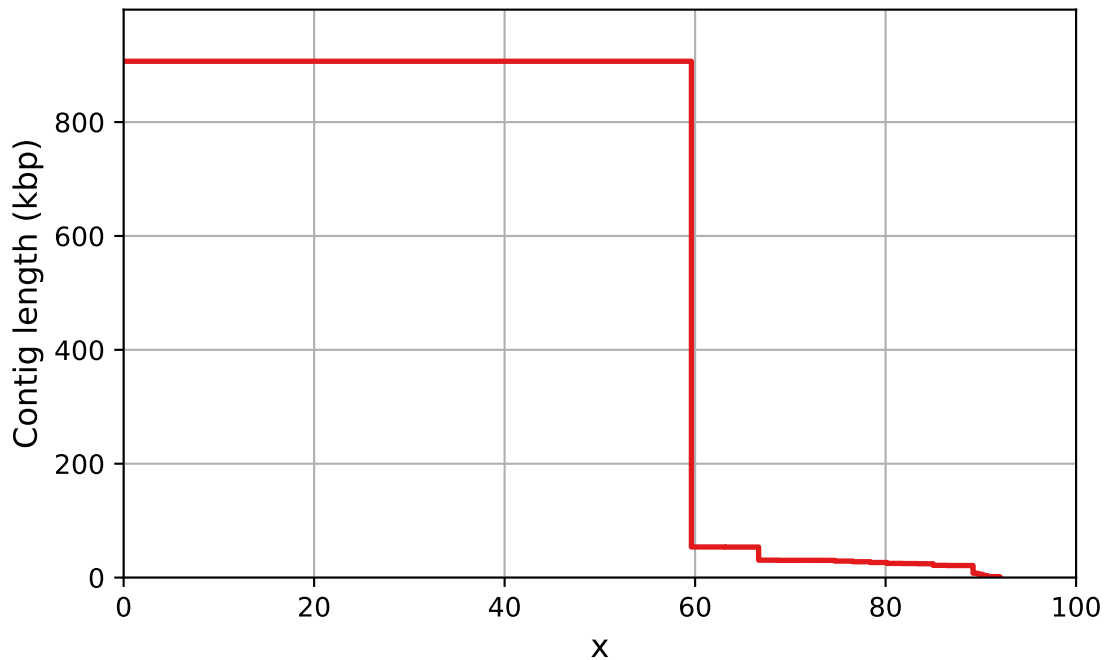
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

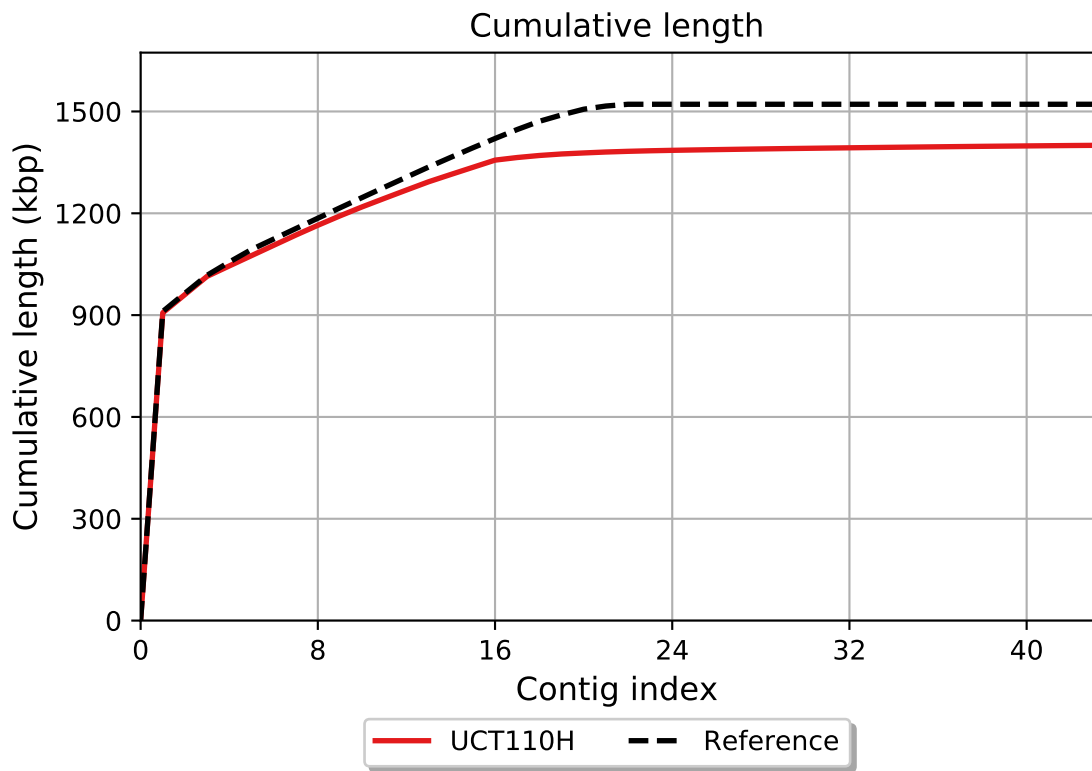


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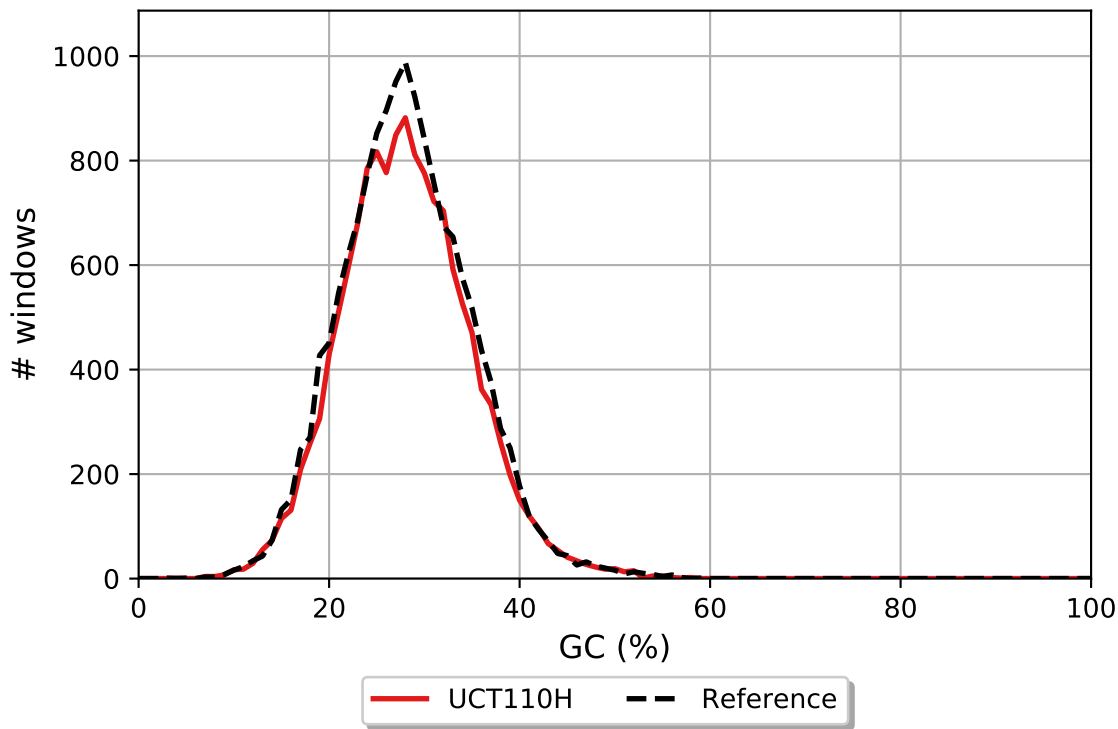
NGx



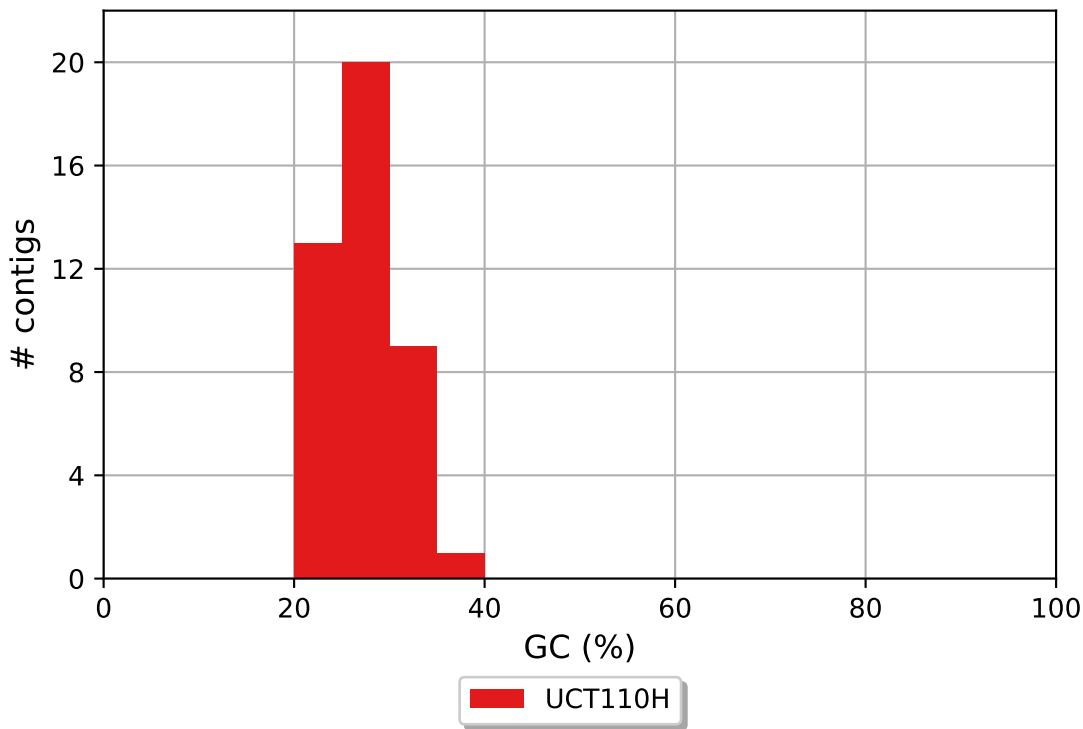
UCT110H



# GC content

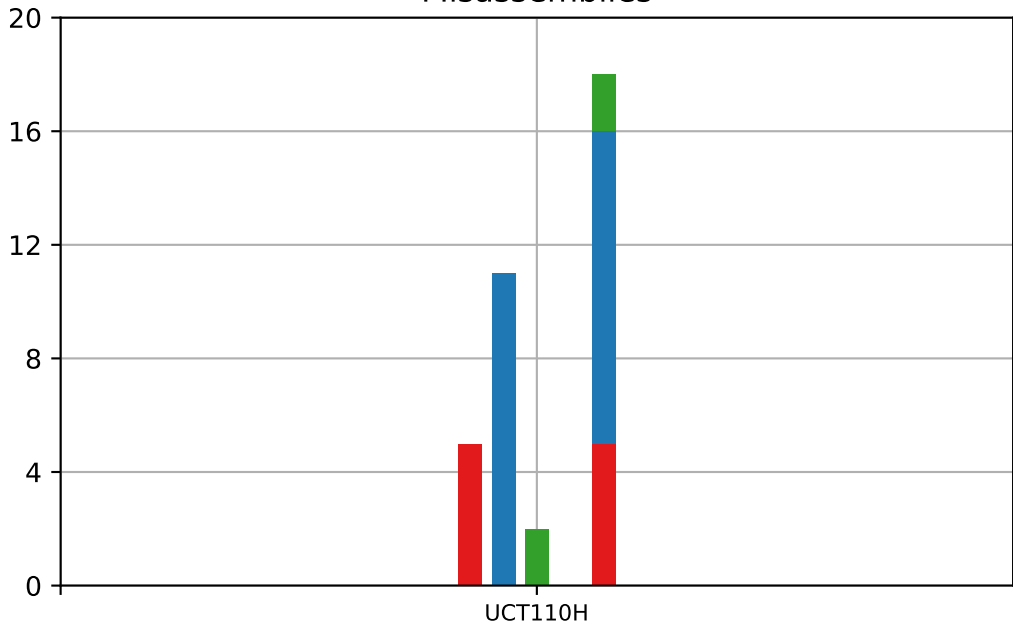


UCT110H GC content



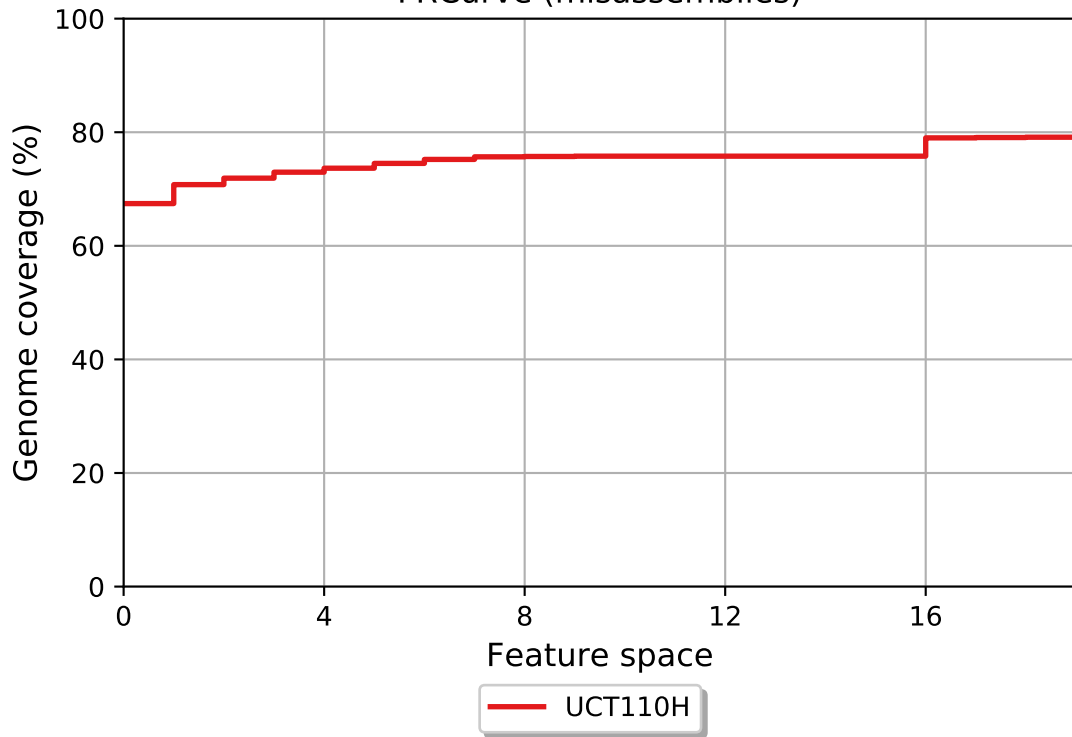


## Misassemblies

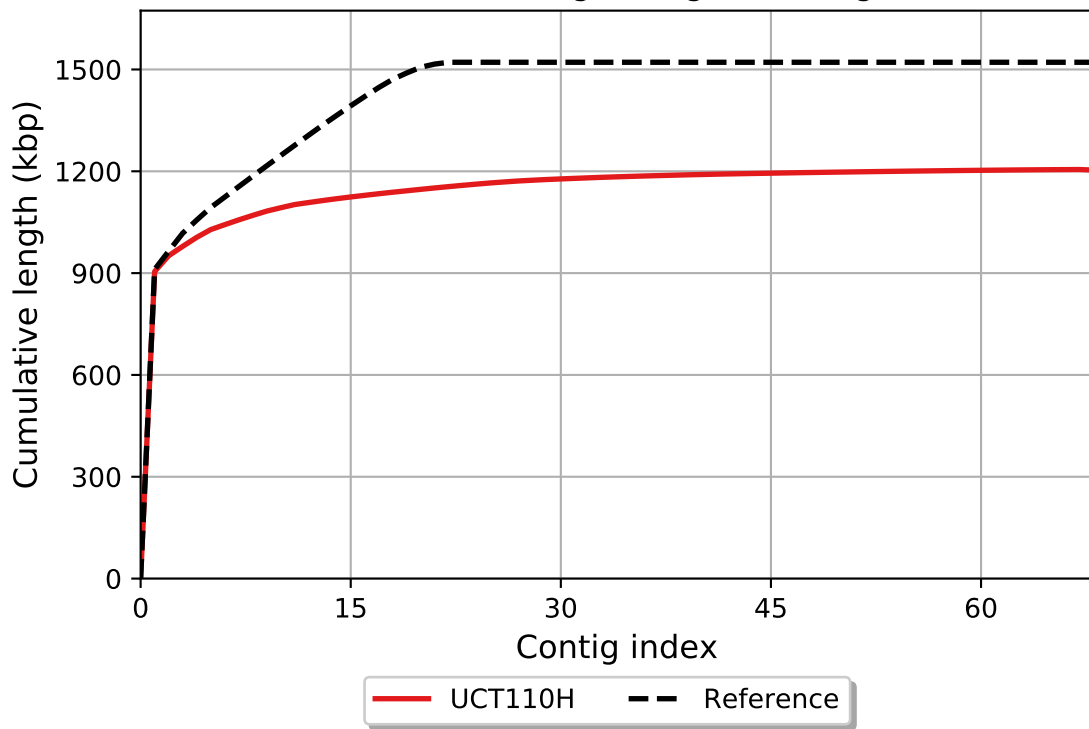


■ # relocations    ■ # translocations    ■ # inversions

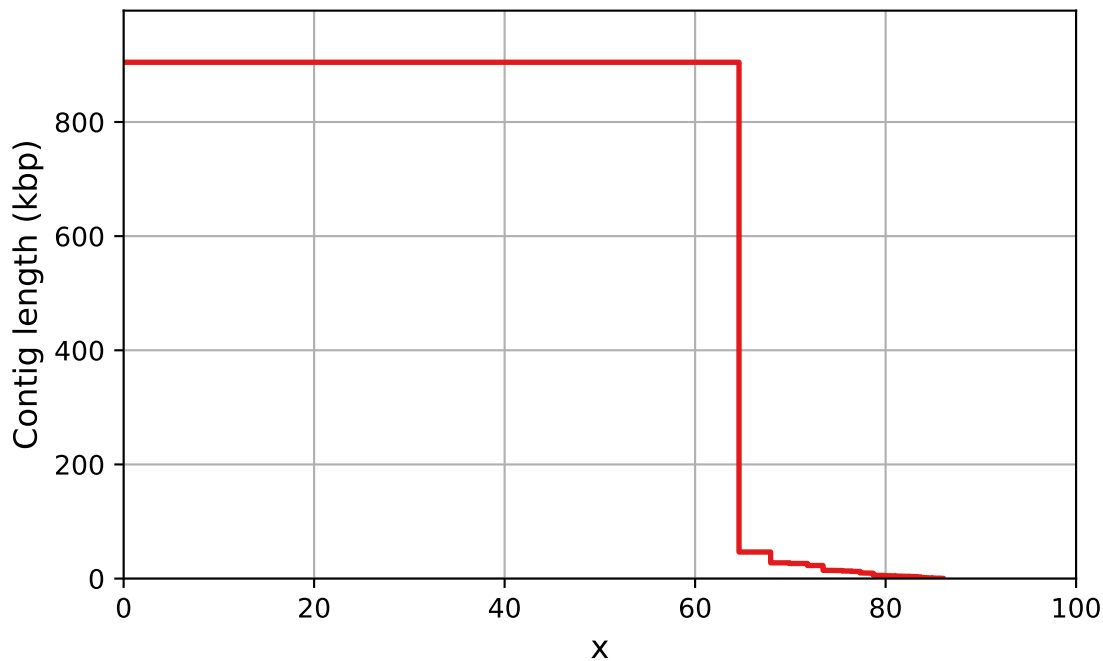
FRCurve (misassemblies)



Cumulative length (aligned contigs)

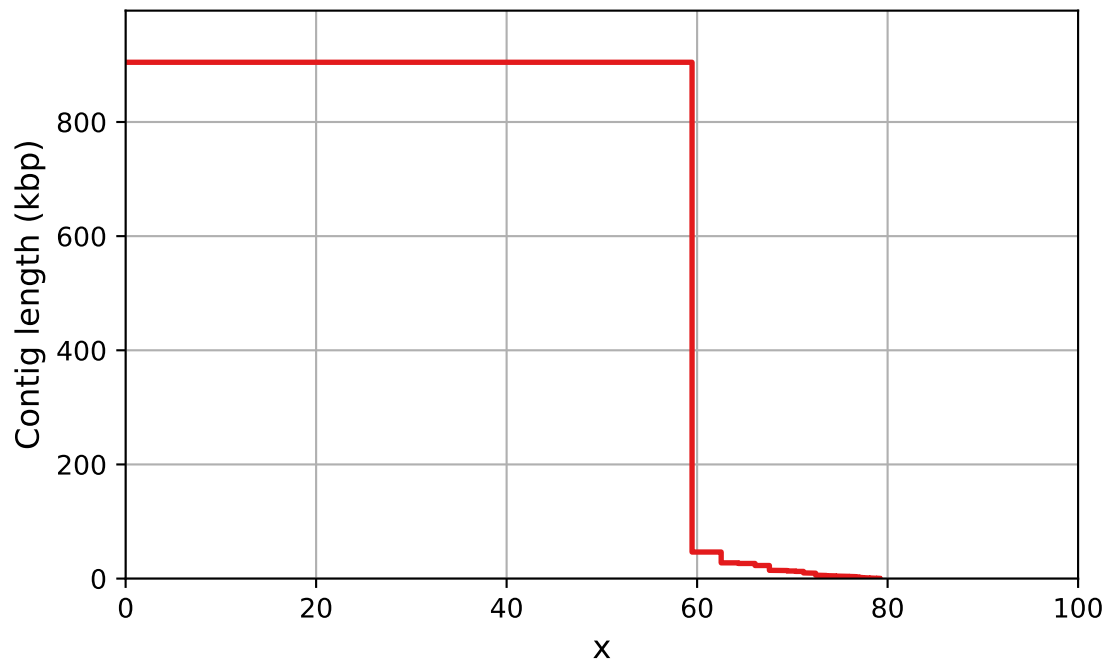


NAx



UCT110H

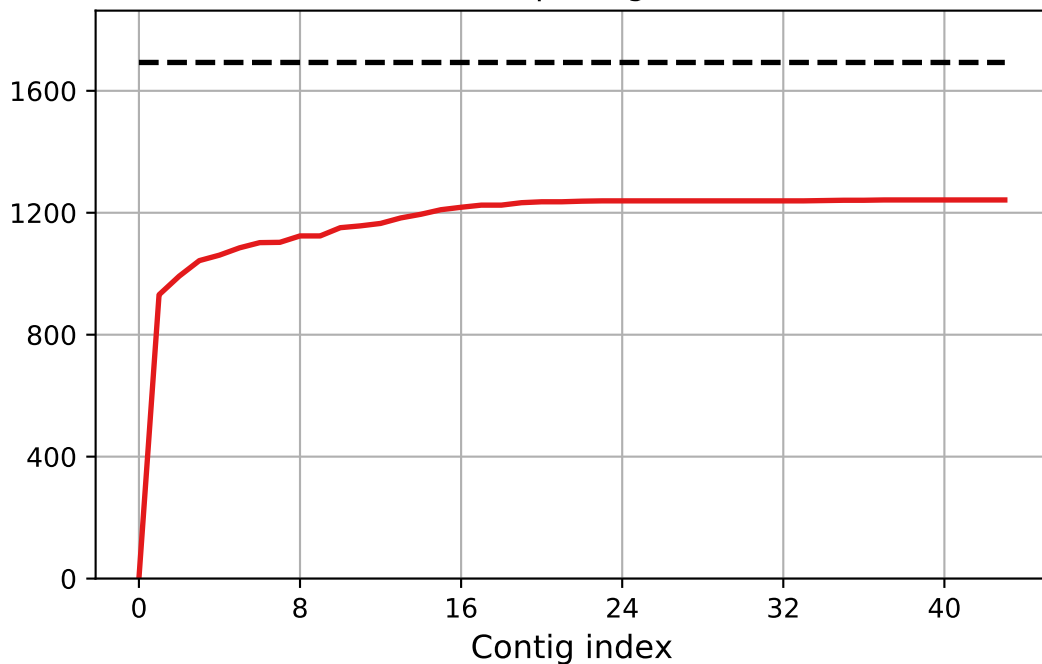
NGAx



UCT110H

Cumulative # complete genomic features

Cumulative # complete genomic features



UCT110H      Reference

FRCurve (genomic features)

