

Report

	UCT96H
# contigs (>= 0 bp)	35
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1481271
Total length (>= 1000 bp)	1477643
Total length (>= 5000 bp)	1471437
Total length (>= 10000 bp)	1464187
Total length (>= 25000 bp)	1358955
Total length (>= 50000 bp)	954451
# contigs	26
Largest contig	900898
Total length	1479028
Reference length	1521208
GC (%)	28.17
Reference GC (%)	28.18
N50	900898
NG50	900898
N90	27034
NG90	22594
auN	560751.3
auNG	545202.8
L50	1
LG50	1
L90	14
LG90	16
# misassemblies	20
# misassembled contigs	13
Misassembled contigs length	298543
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 7 part
Unaligned length	33114
Genome fraction (%)	90.804
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	434.17
# indels per 100 kbp	32.70
# genomic features	1468 + 48 part
Largest alignment	900898
Total aligned length	1443446
NA50	900898
NGA50	900898
NA90	14517
NGA90	9670
auNA	557917.9
auNGA	542448.0
LA50	1
LGA50	1
LA90	18
LGA90	22

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

	UCT96H
# misassemblies	20
# contig misassemblies	20
# c. relocations	8
# c. translocations	11
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	298543
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	6267
# indels	472
# indels (<= 5 bp)	416
# indels (> 5 bp)	56
Indels length	2270

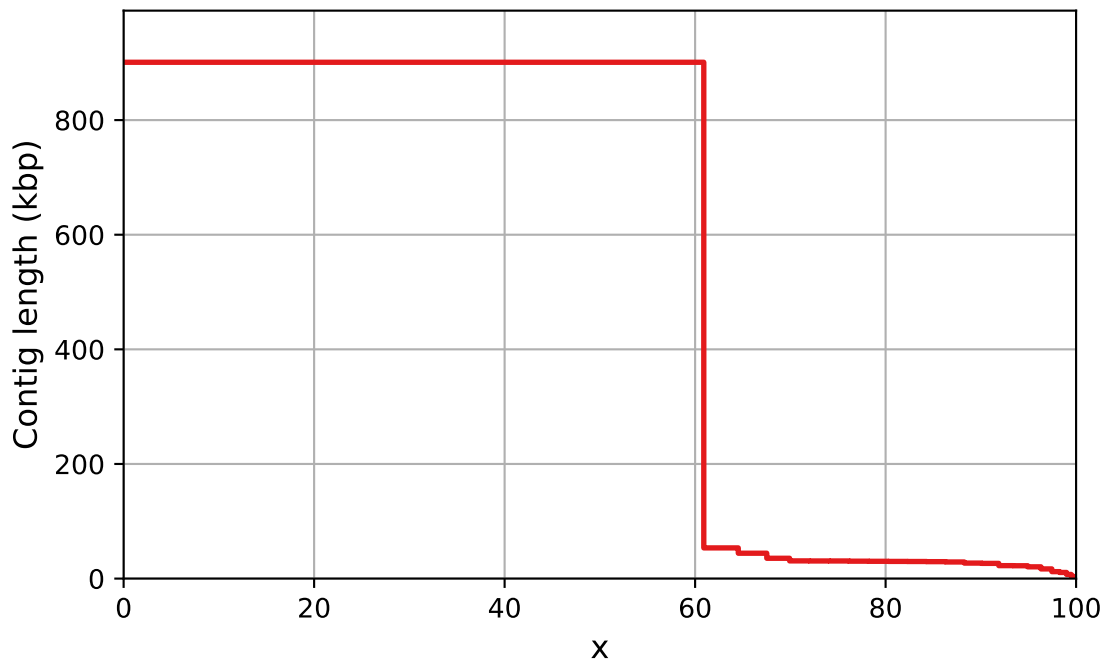
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	UCT96H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	33114
# N's	0

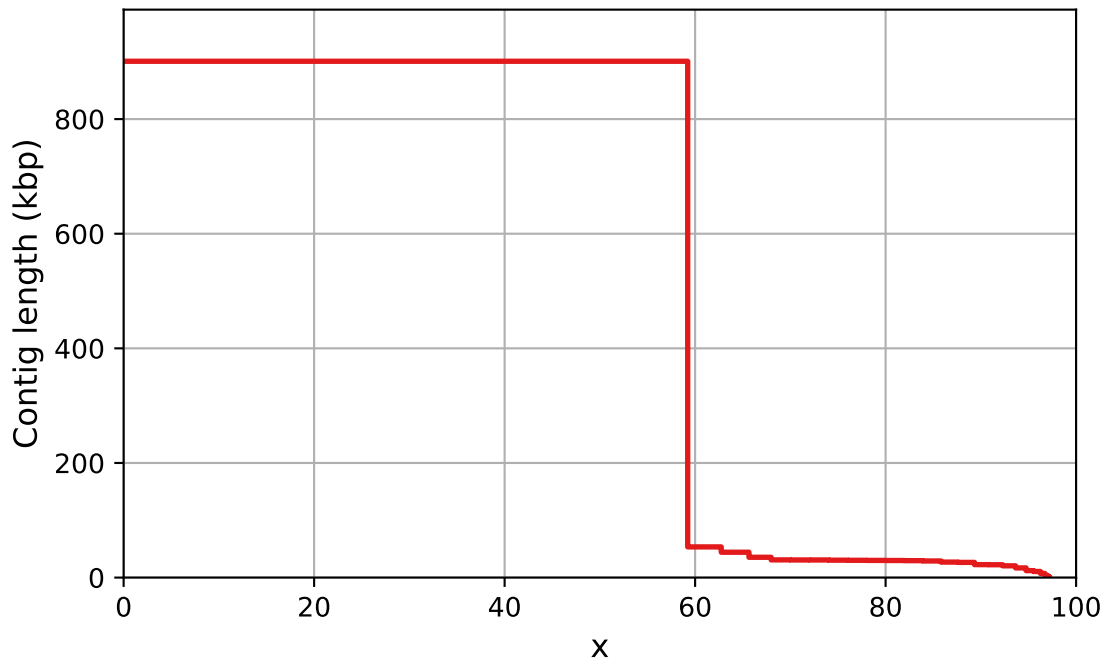
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

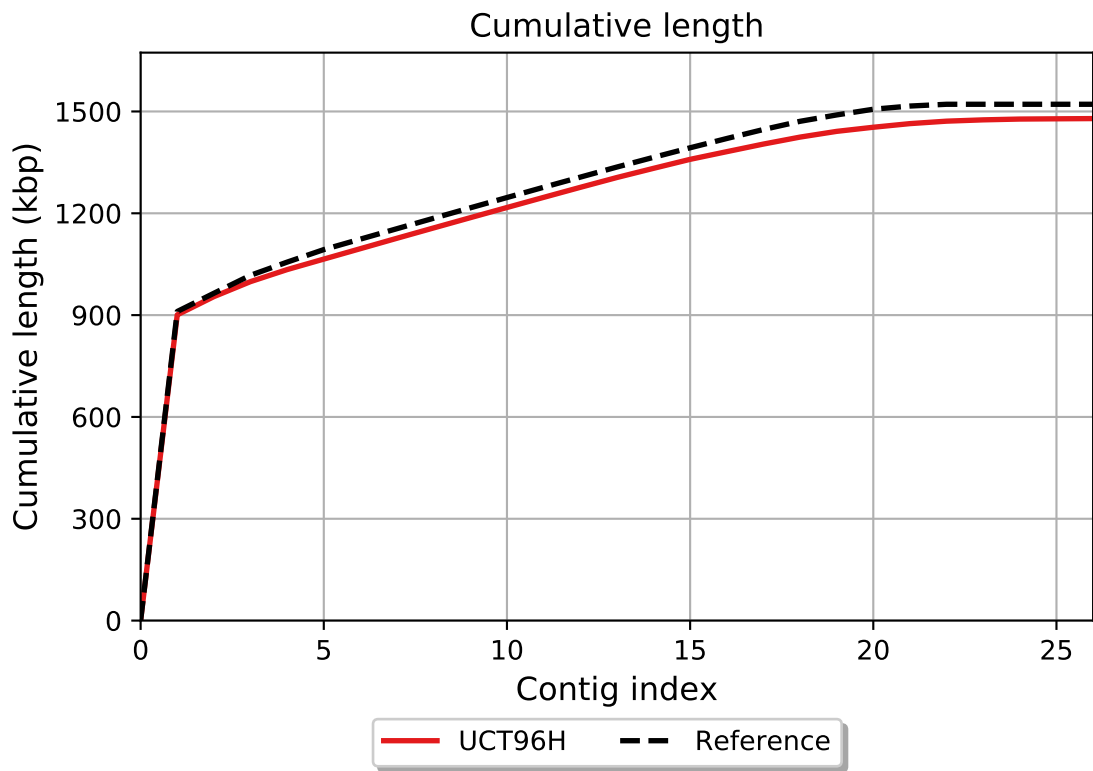


UCT96H

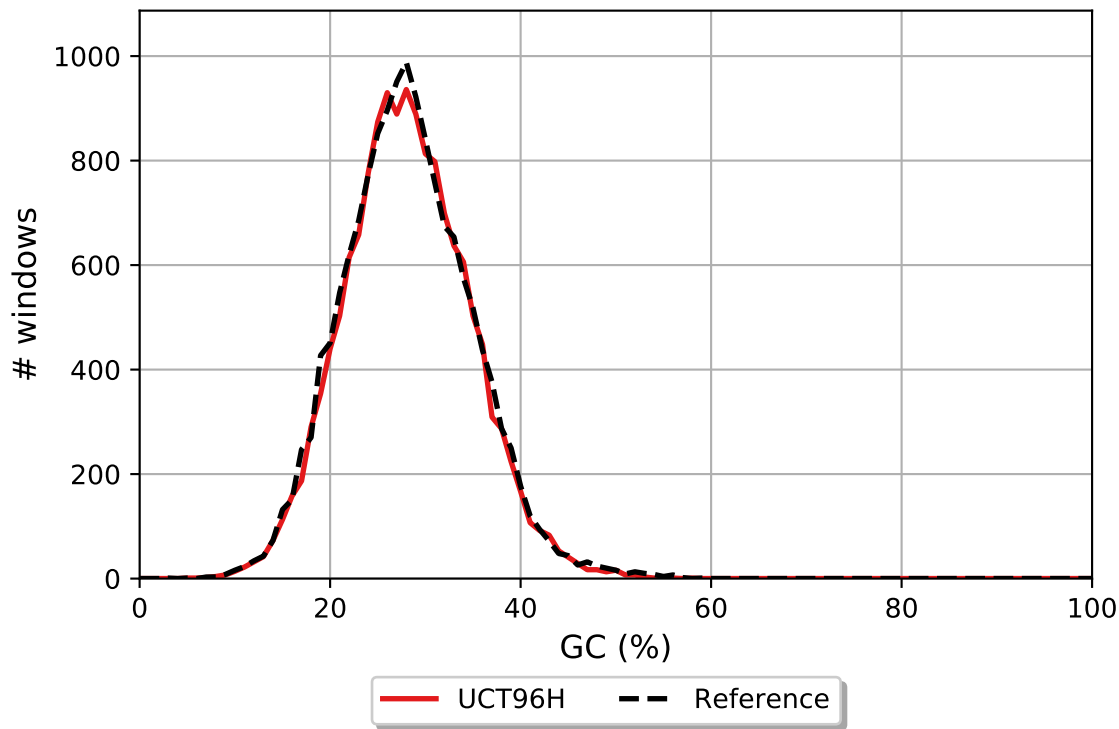
NGx



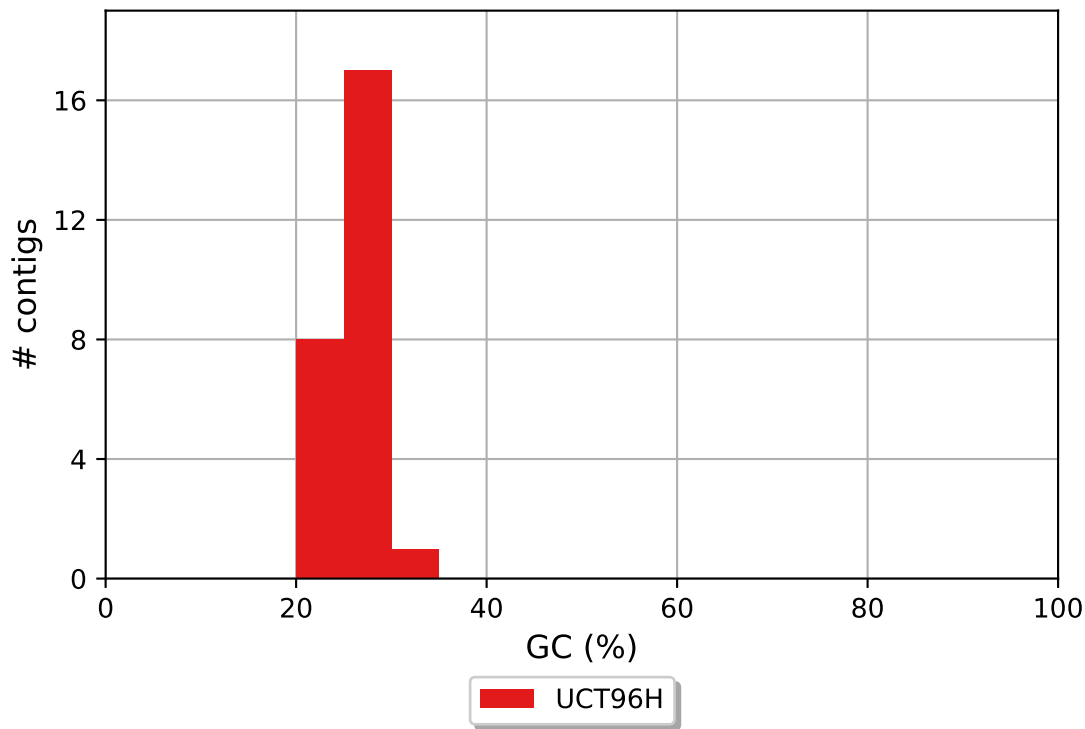
UCT96H



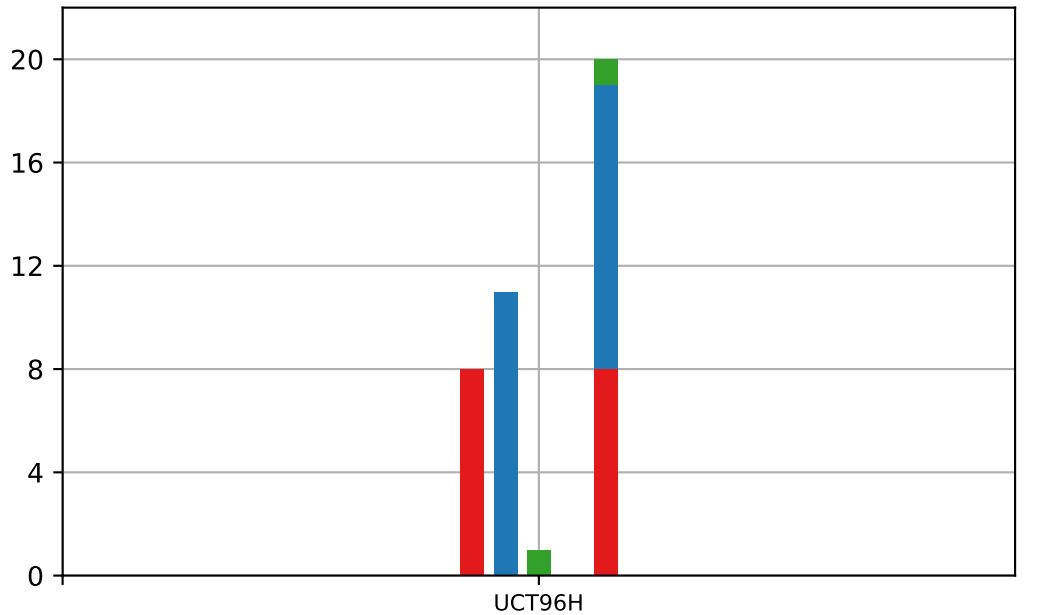
GC content



UCT96H GC content



Misassemblies



relocations

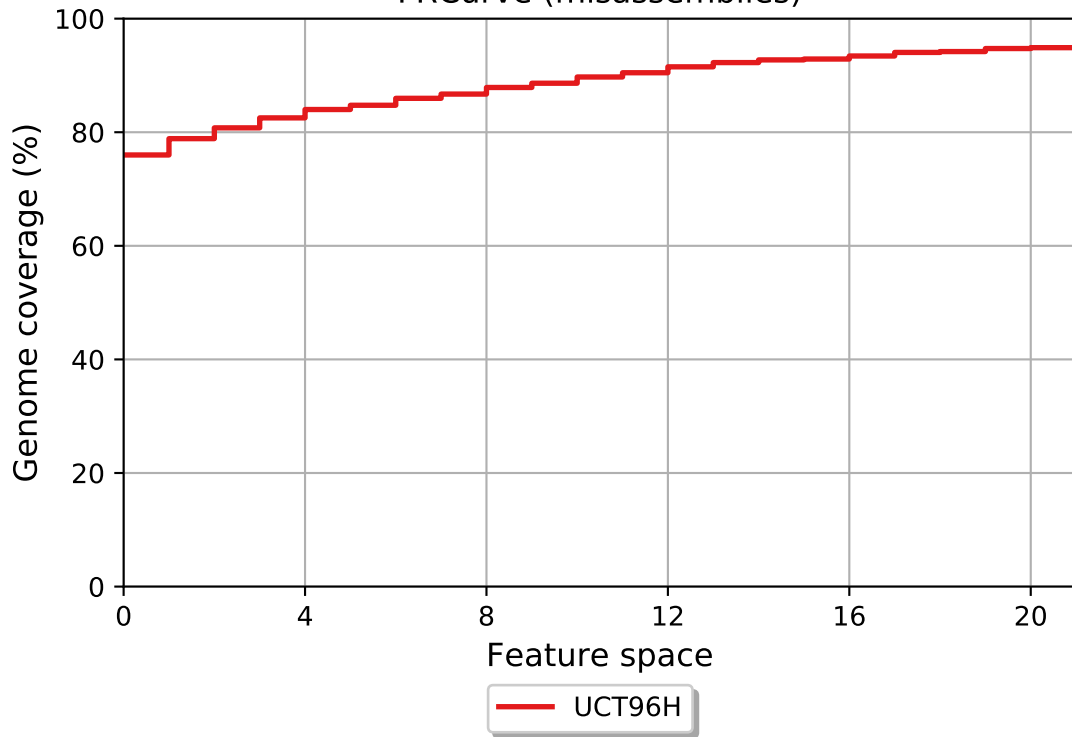


translocations

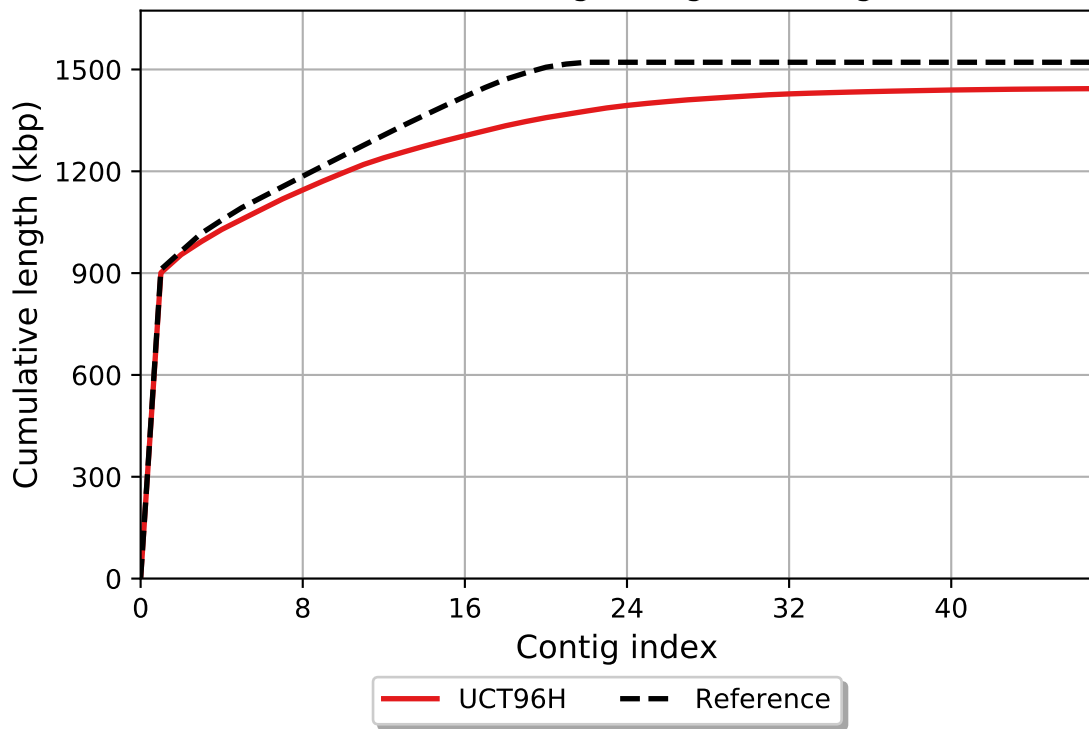


inversions

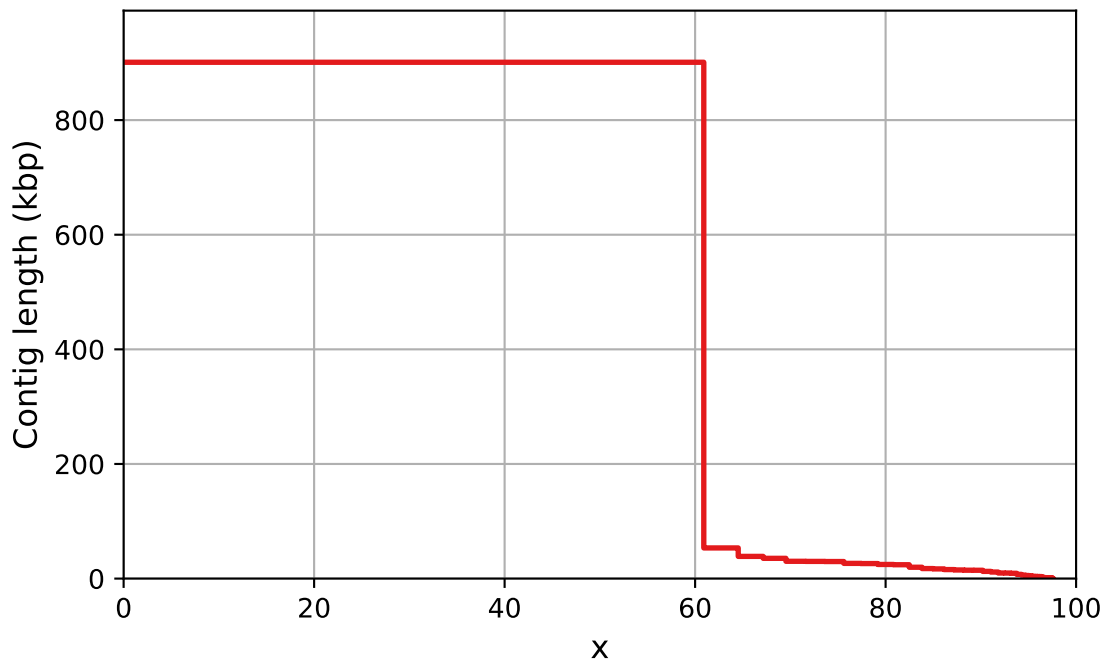
FRCurve (misassemblies)



Cumulative length (aligned contigs)

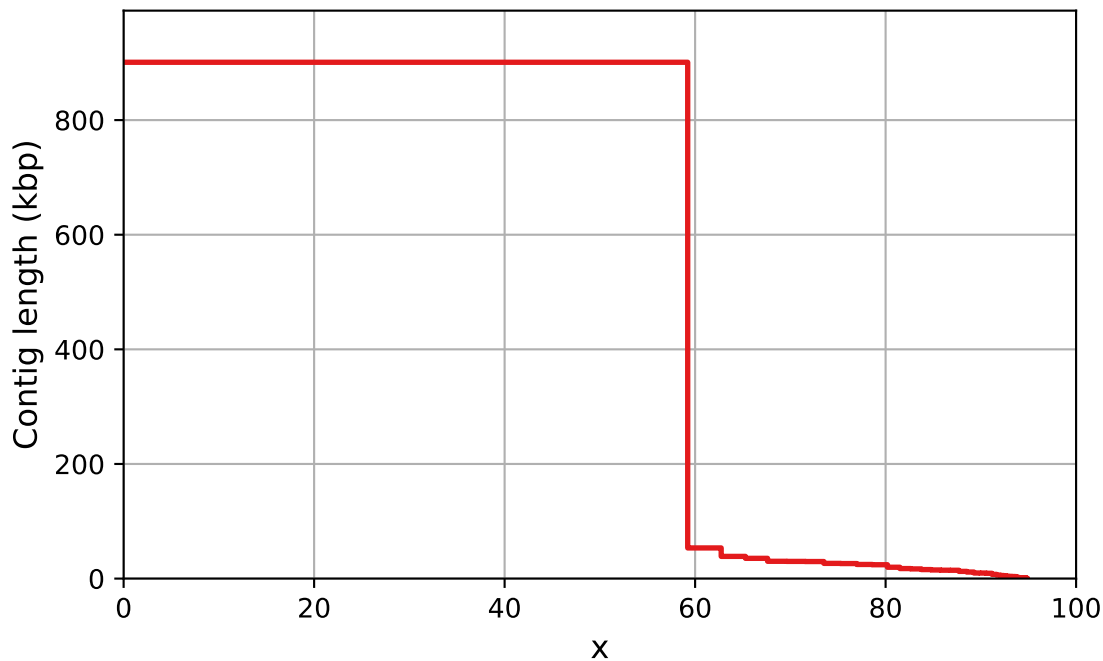


NAx



UCT96H

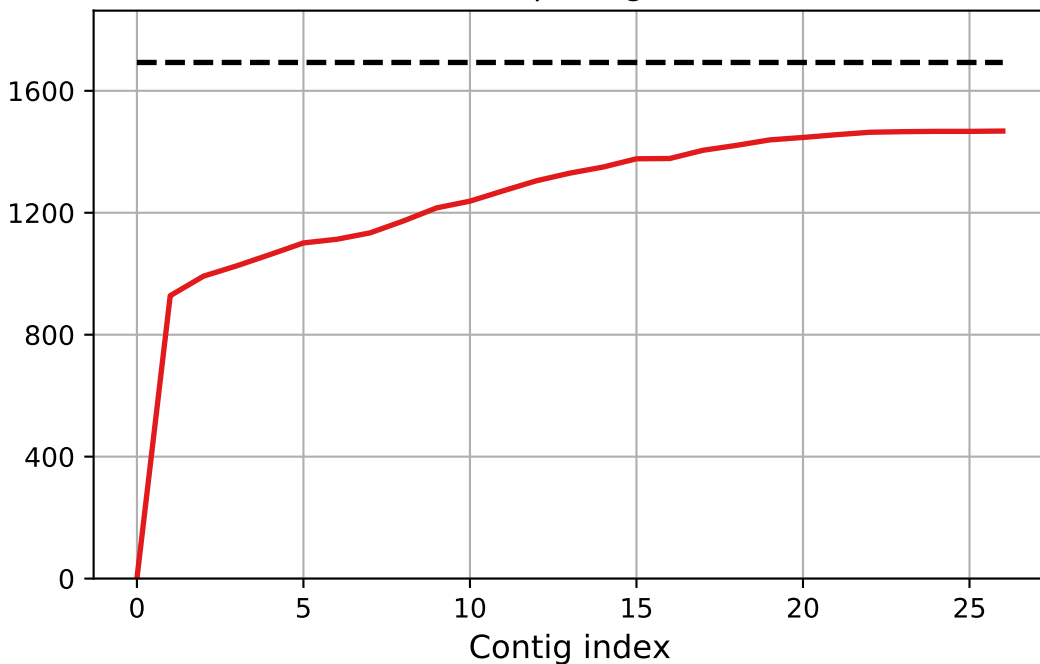
NGAx



UCT96H

Cumulative # complete genomic features

Cumulative # complete genomic features



UCT96H Reference

FRCurve (genomic features)

