

Report

	UCT50H
# contigs (>= 0 bp)	90
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1341231
Total length (>= 1000 bp)	1316541
Total length (>= 5000 bp)	1306146
Total length (>= 10000 bp)	1290411
Total length (>= 25000 bp)	1184780
Total length (>= 50000 bp)	1022844
# contigs	41
Largest contig	902761
Total length	1329478
Reference length	1521208
GC (%)	28.33
Reference GC (%)	28.18
N50	902761
NG50	902761
N90	24152
NG90	-
auN	624359.2
auNG	545666.2
L50	1
LG50	1
L90	9
LG90	-
# misassemblies	16
# misassembled contigs	5
Misassembled contigs length	217544
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	6 + 14 part
Unaligned length	118509
Genome fraction (%)	78.509
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	796.43
# indels per 100 kbp	55.42
# genomic features	1232 + 74 part
Largest alignment	902581
Total aligned length	1210653
NA50	902581
NGA50	902581
NA90	879
NGA90	-
auNA	617489.9
auNGA	539662.7
LA50	1
LGA50	1
LA90	38
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

	UCT50H
# misassemblies	16
# contig misassemblies	16
# c. relocations	7
# c. translocations	9
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	217544
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	9642
# indels	671
# indels (<= 5 bp)	602
# indels (> 5 bp)	69
Indels length	3351

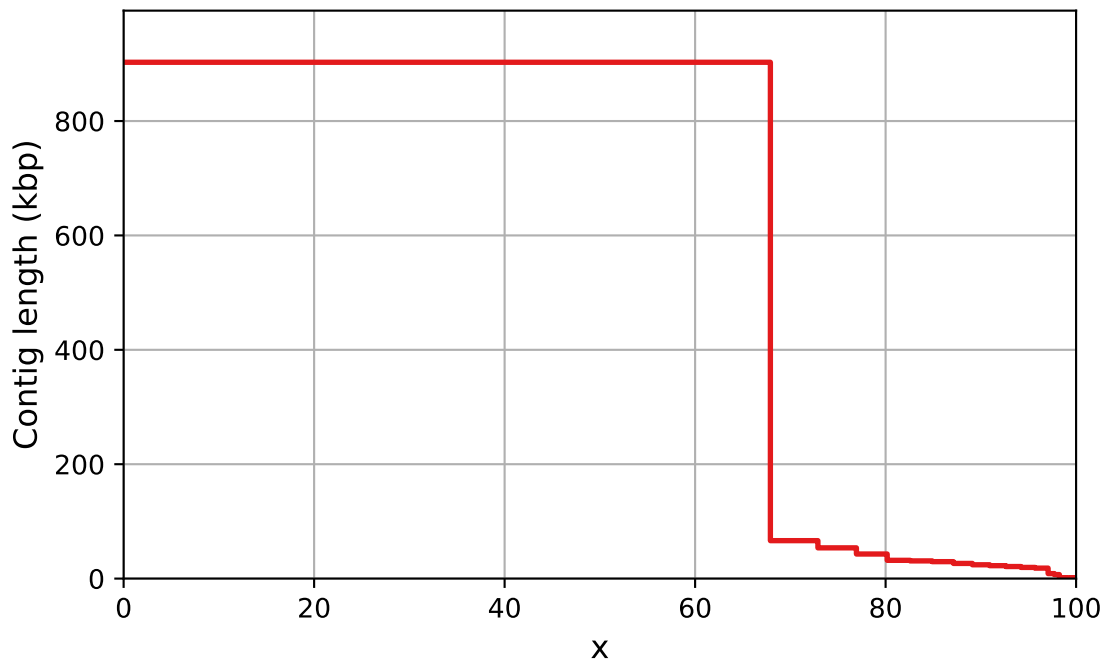
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	UCT50H
# fully unaligned contigs	6
Fully unaligned length	37268
# partially unaligned contigs	14
Partially unaligned length	81241
# N's	0

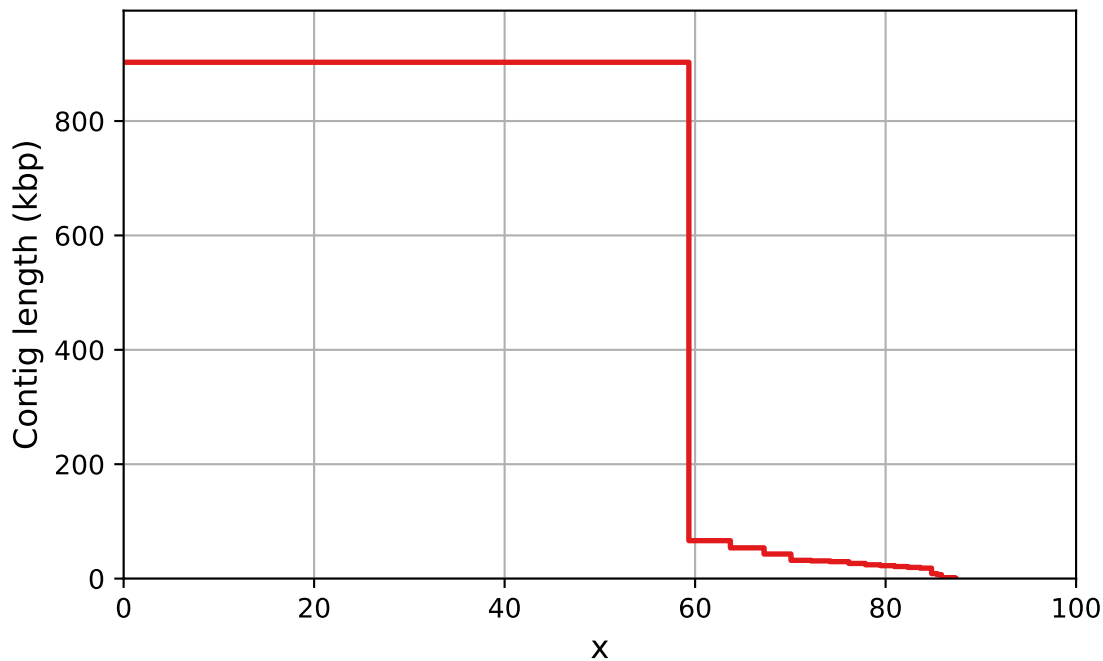
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

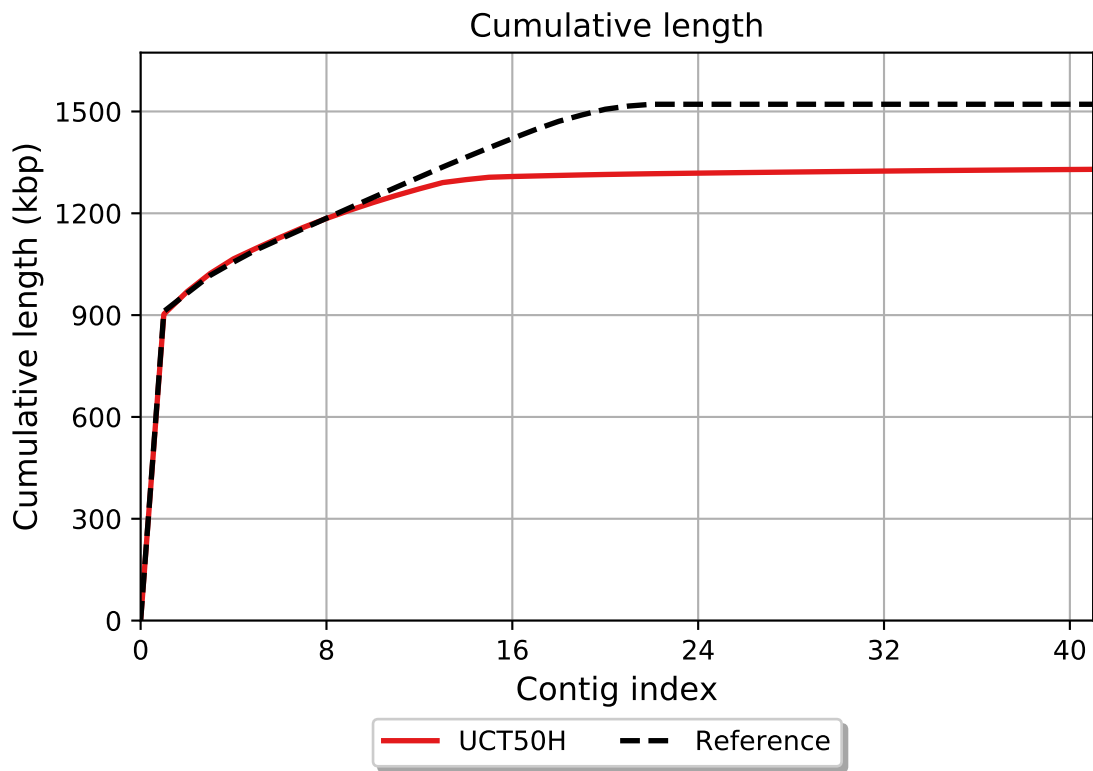


UCT50H

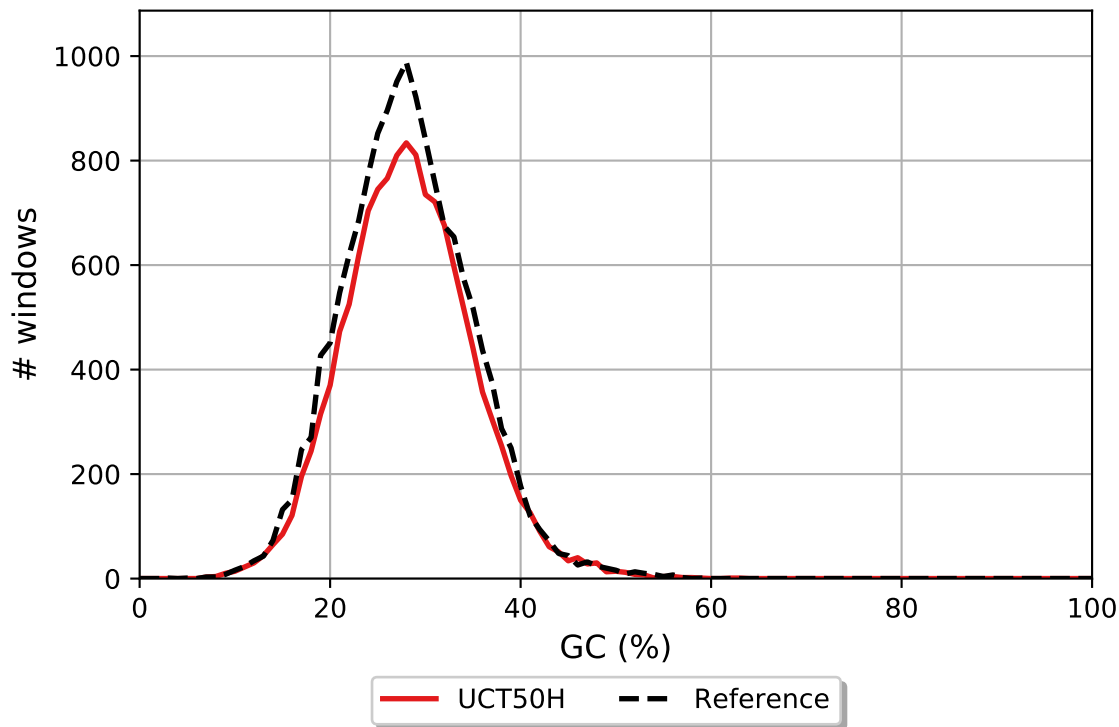
NGx



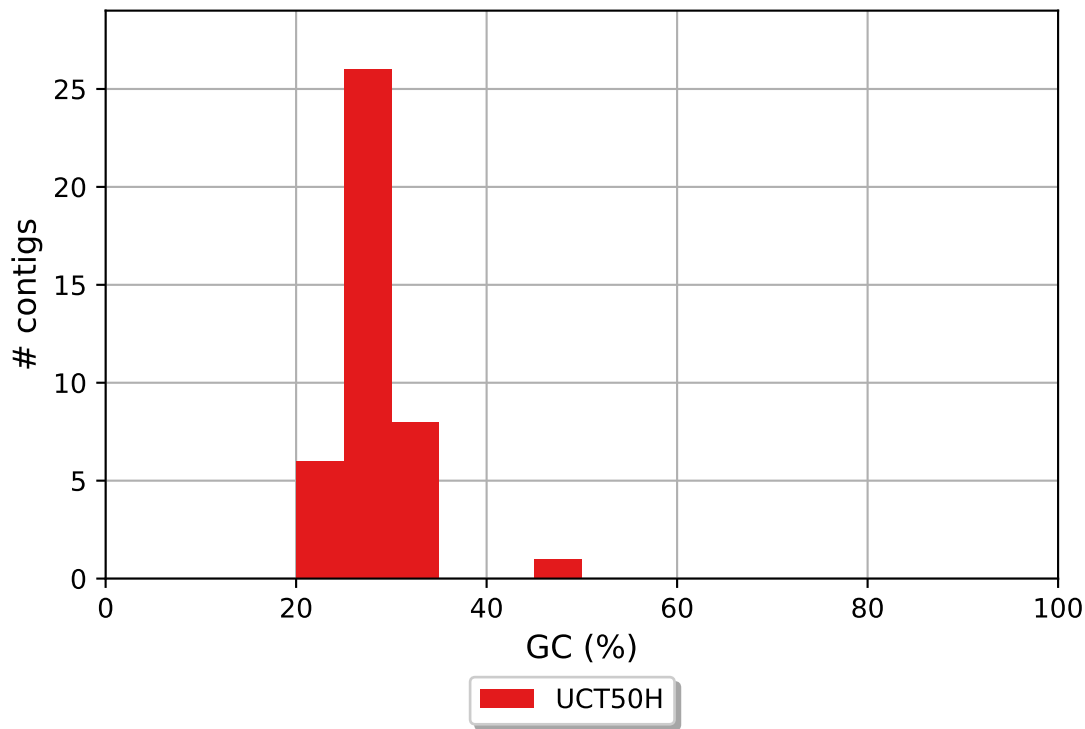
UCT50H



## GC content

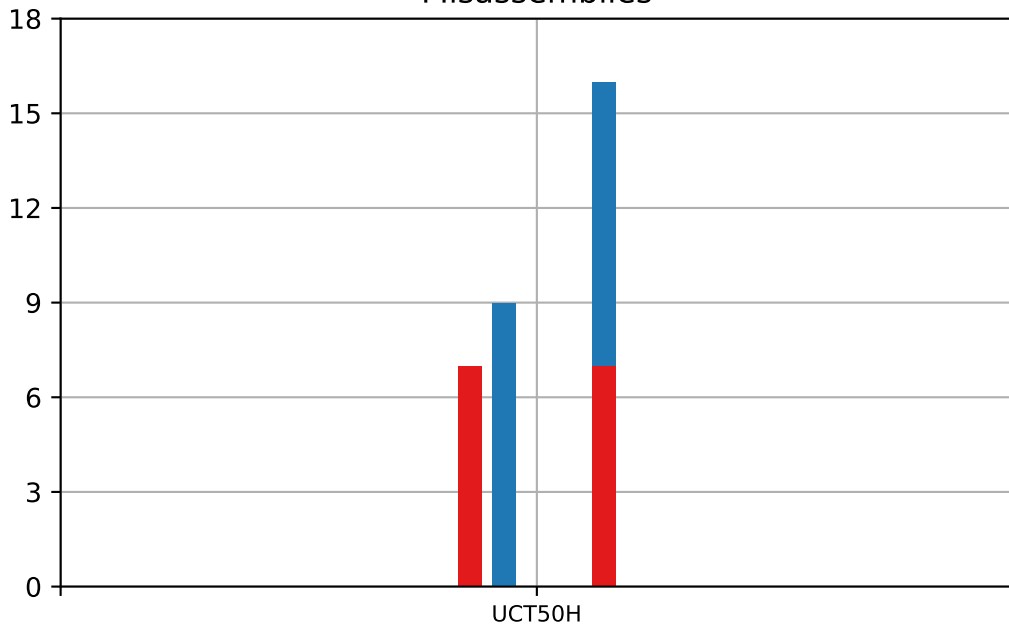


UCT50H GC content





## Misassemblies

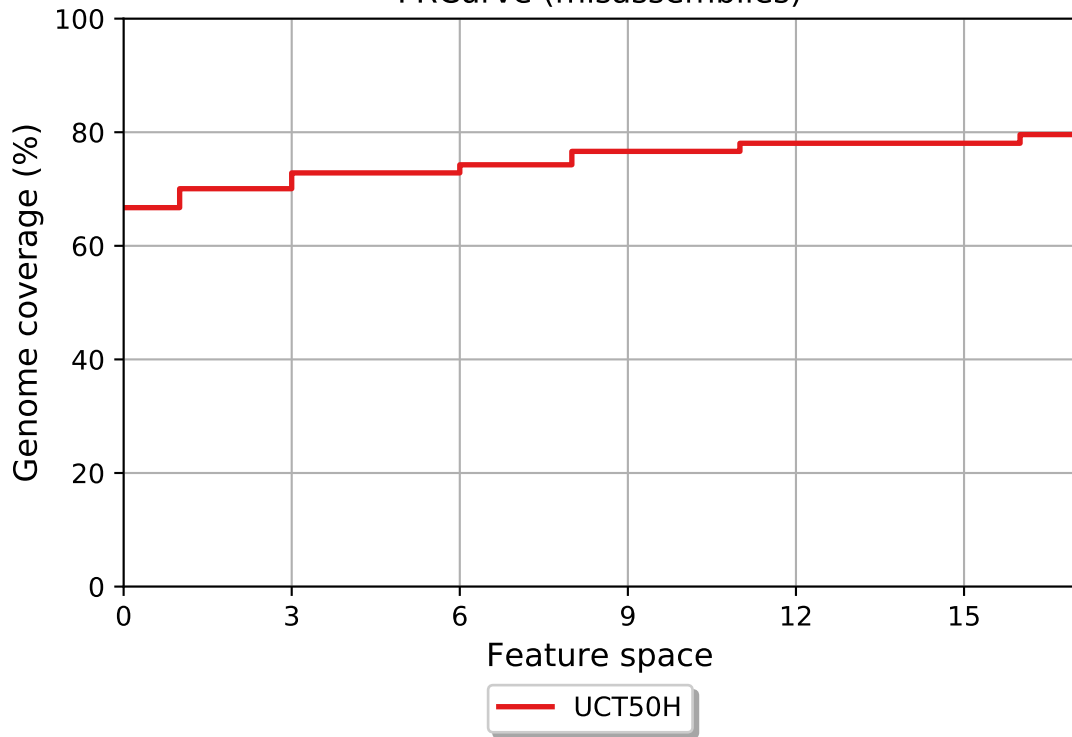


# relocations

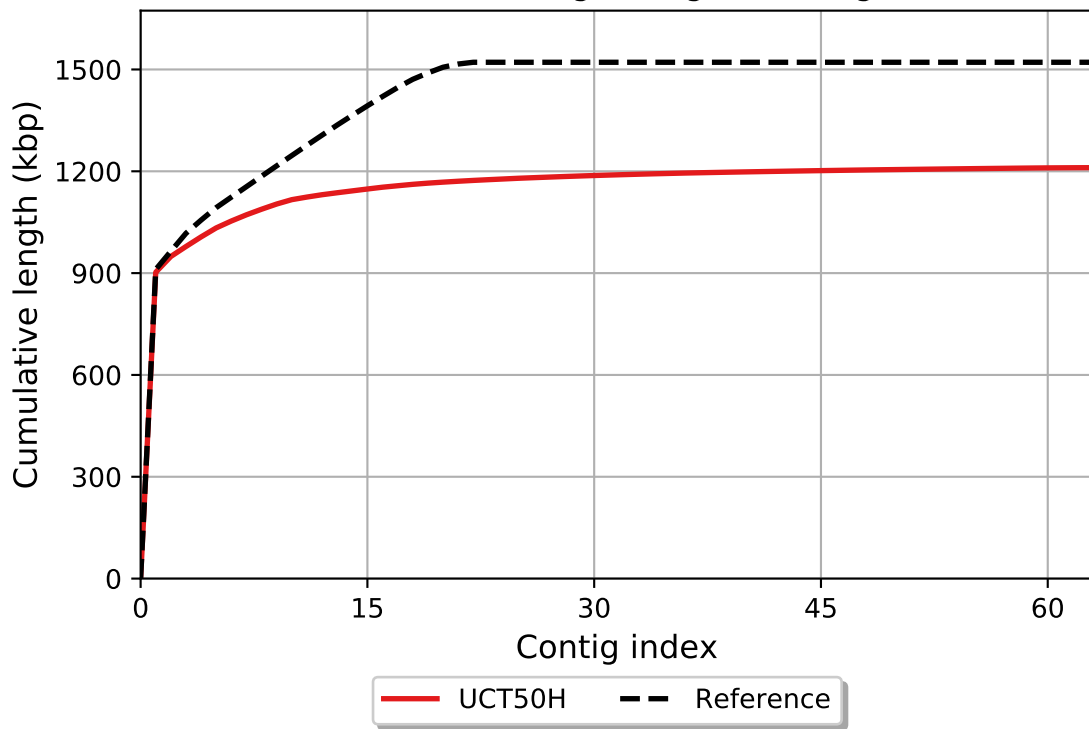


# translocations

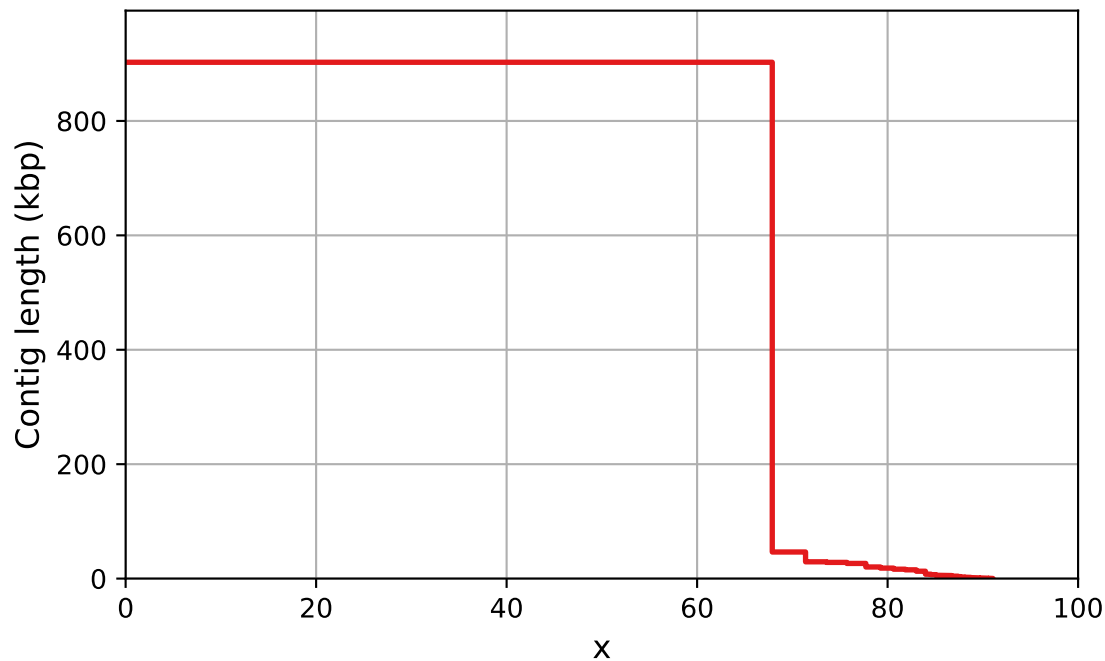
FRCurve (misassemblies)



Cumulative length (aligned contigs)

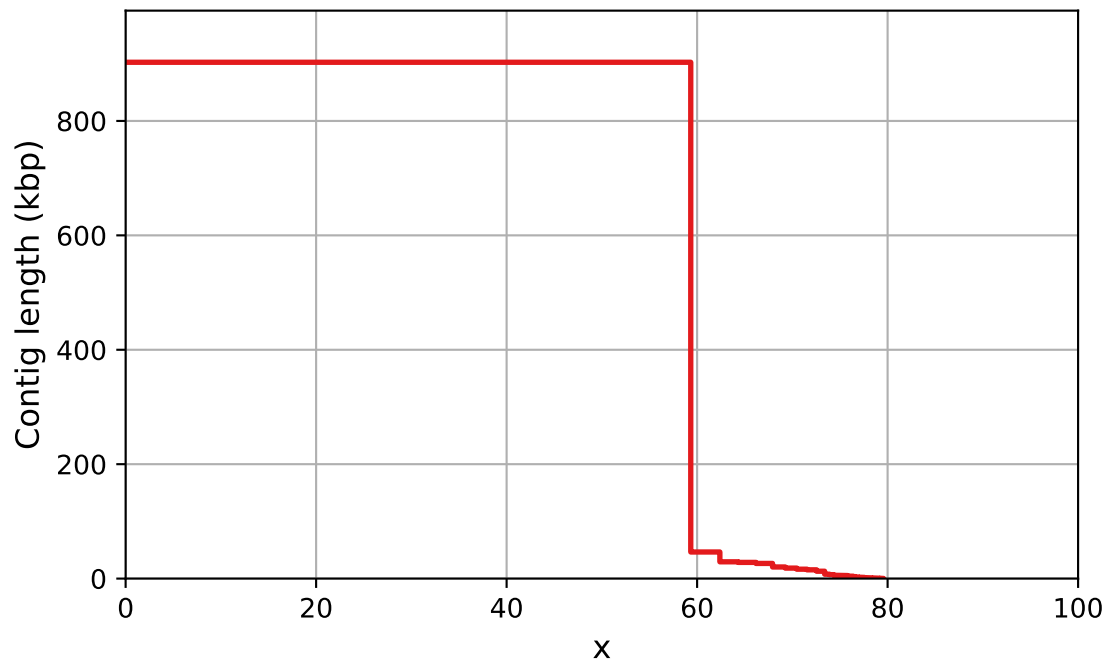


NAx

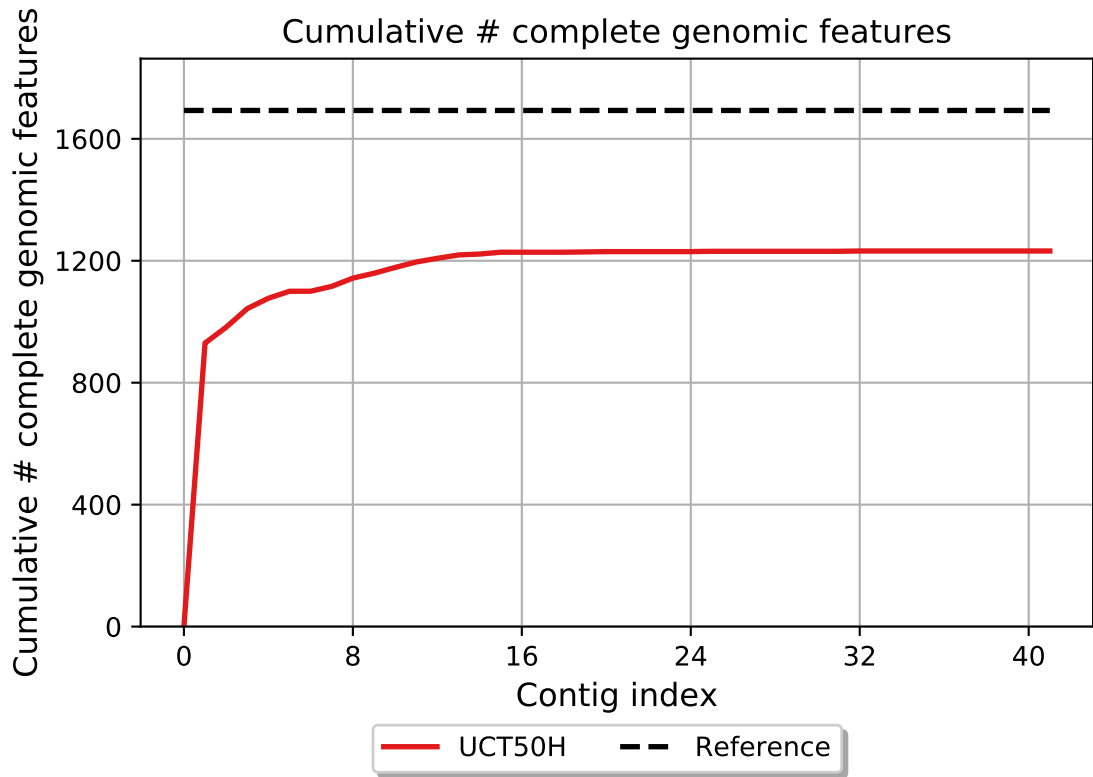


UCT50H

NGAx



UCT50H



FRCurve (genomic features)

