

Report

	UCT32H
# contigs (>= 0 bp)	57
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1501989
Total length (>= 1000 bp)	1490687
Total length (>= 5000 bp)	1481242
Total length (>= 10000 bp)	1473819
Total length (>= 25000 bp)	1357193
Total length (>= 50000 bp)	1027511
# contigs	34
Largest contig	921072
Total length	1495867
Reference length	1521208
GC (%)	28.20
Reference GC (%)	28.18
N50	921072
NG50	921072
N90	26514
NG90	24813
auN	579427.1
auNG	569774.7
L50	1
LG50	1
L90	14
LG90	15
# misassemblies	28
# misassembled contigs	13
Misassembled contigs length	1252893
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 18 part
Unaligned length	207098
Genome fraction (%)	80.123
Duplication ratio	1.056
# N's per 100 kbp	0.00
# mismatches per 100 kbp	932.44
# indels per 100 kbp	58.02
# genomic features	1268 + 62 part
Largest alignment	905458
Total aligned length	1287379
NA50	905458
NGA50	905458
NA90	-
NGA90	-
auNA	552389.4
auNGA	543187.4
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

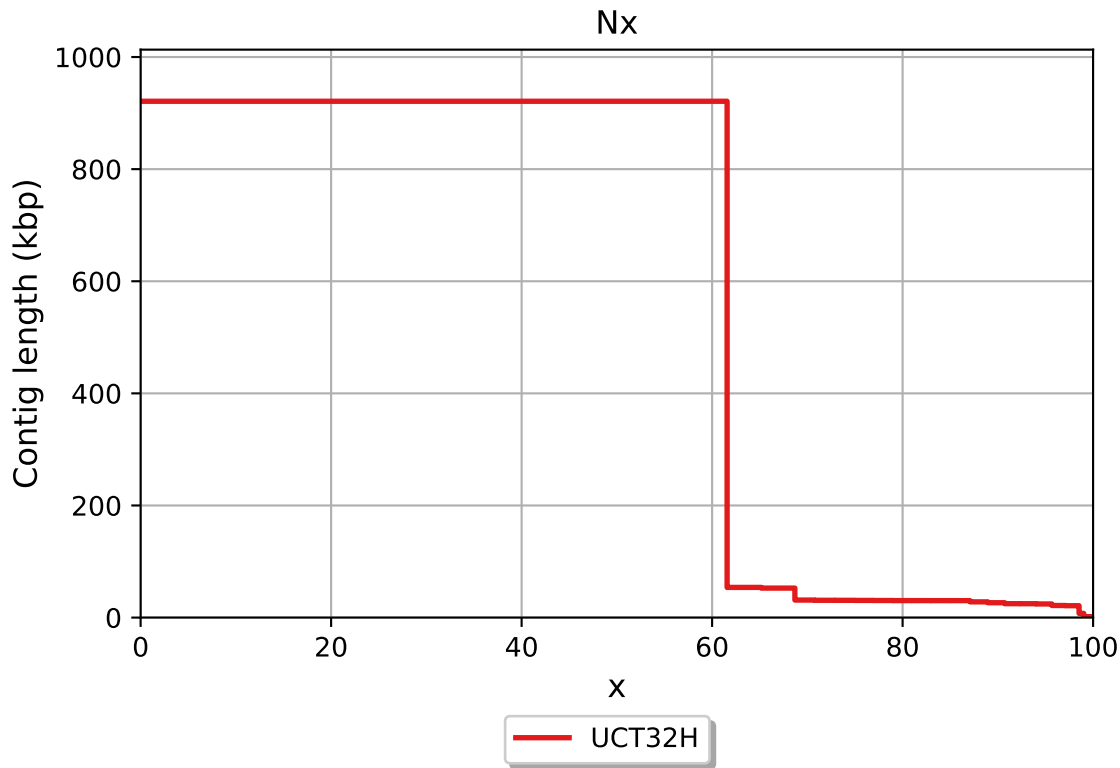
	UCT32H
# misassemblies	28
# contig misassemblies	28
# c. relocations	5
# c. translocations	22
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	1252893
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	12004
# indels	747
# indels (<= 5 bp)	681
# indels (> 5 bp)	66
Indels length	3900

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).

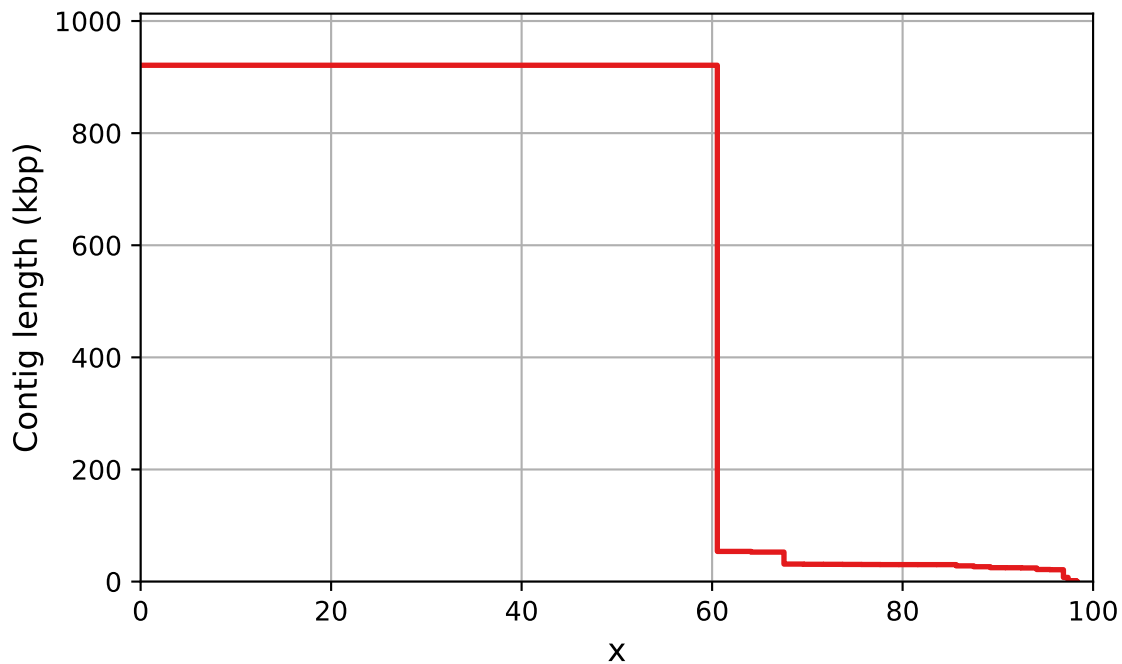
## Unaligned report

	UCT32H
# fully unaligned contigs	1
Fully unaligned length	2115
# partially unaligned contigs	18
Partially unaligned length	204983
# N's	0

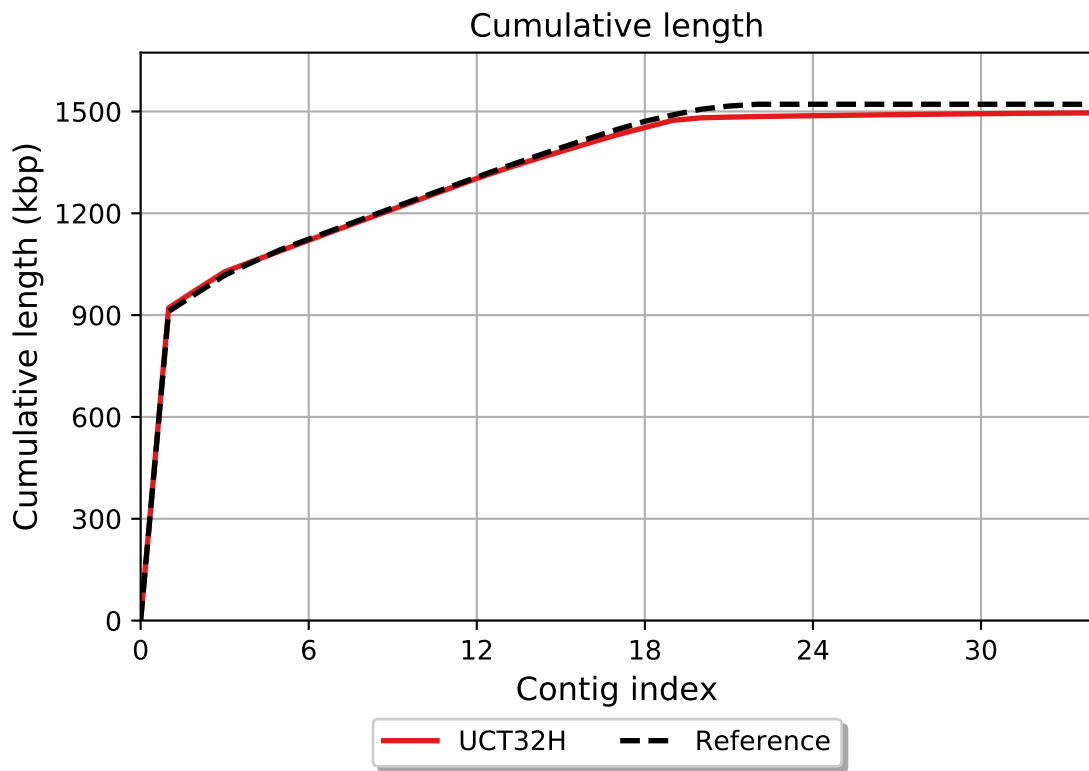
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



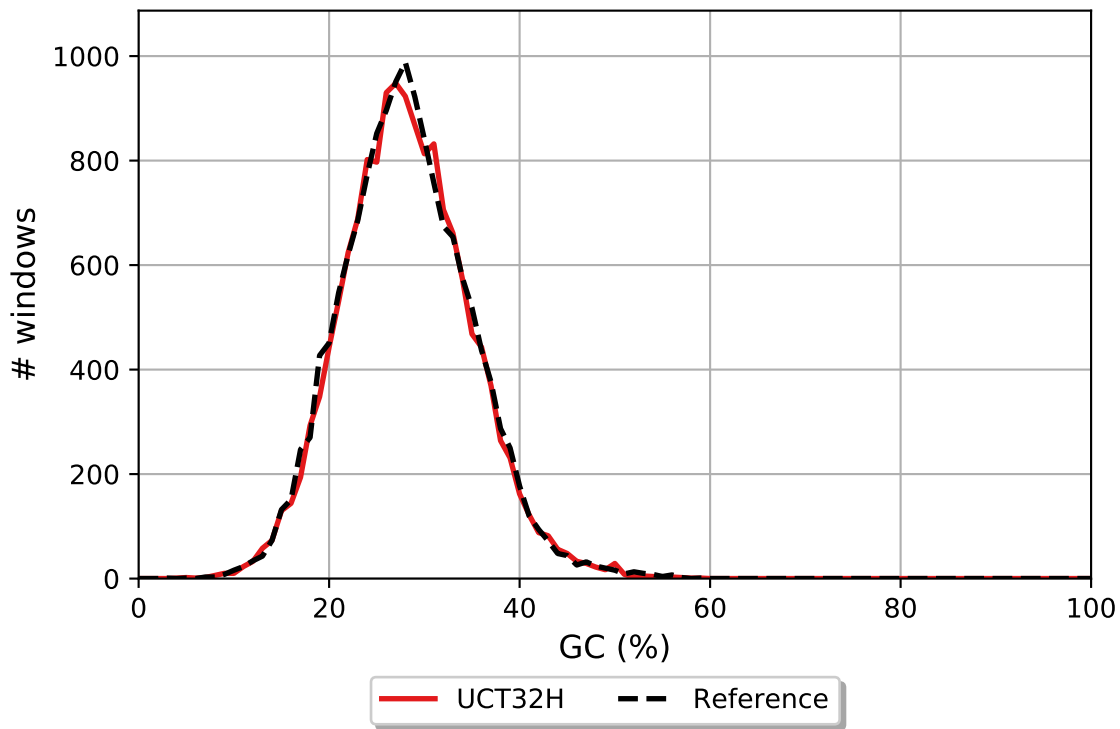
NGx



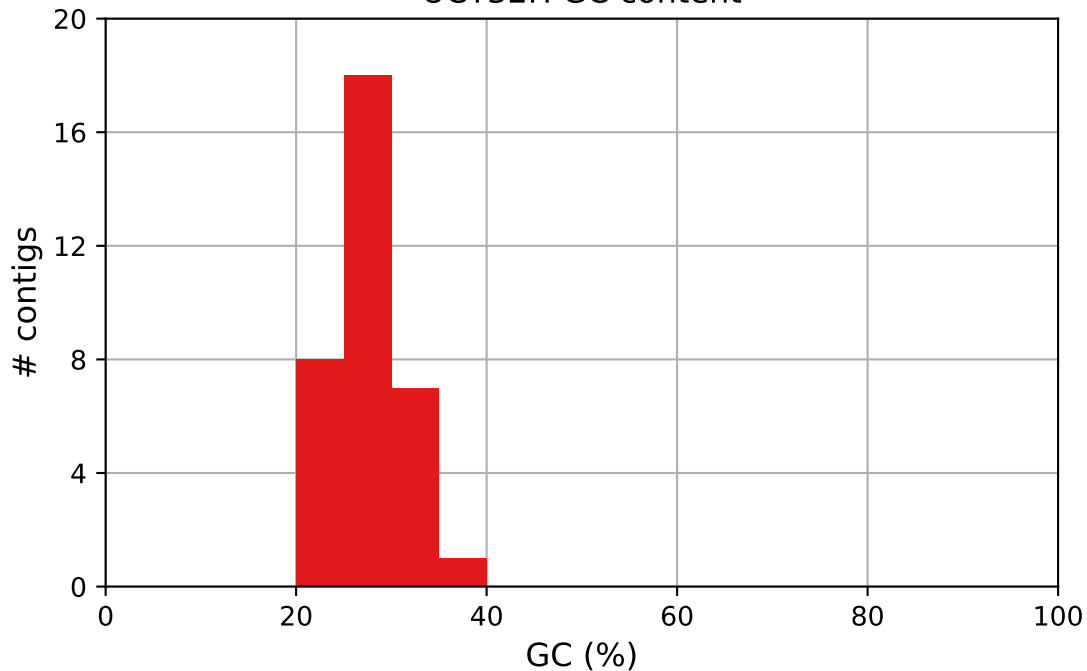
UCT32H



## GC content



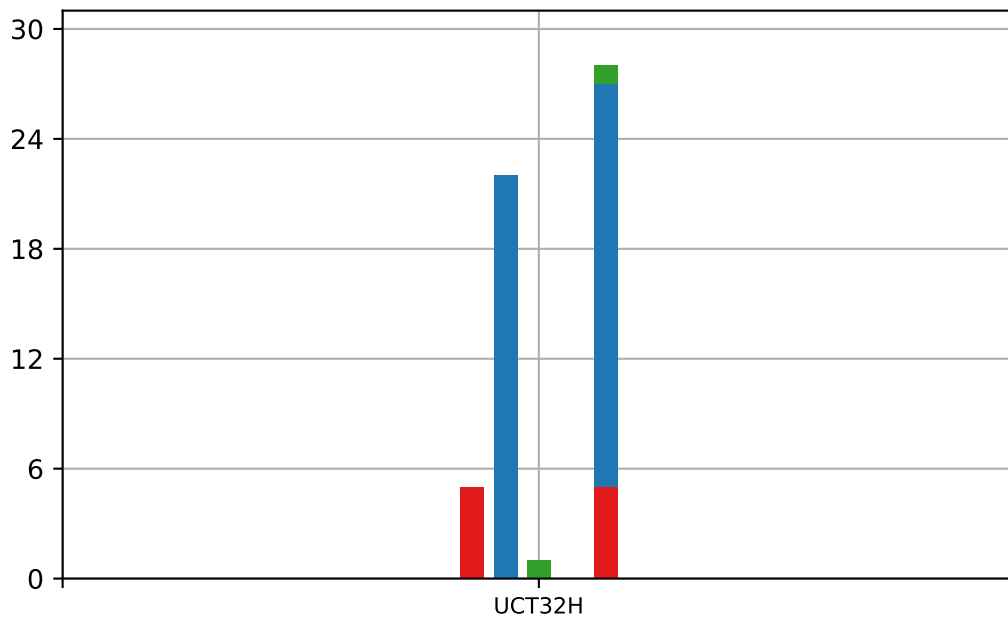
UCT32H GC content



UCT32H



## Misassemblies



# relocations

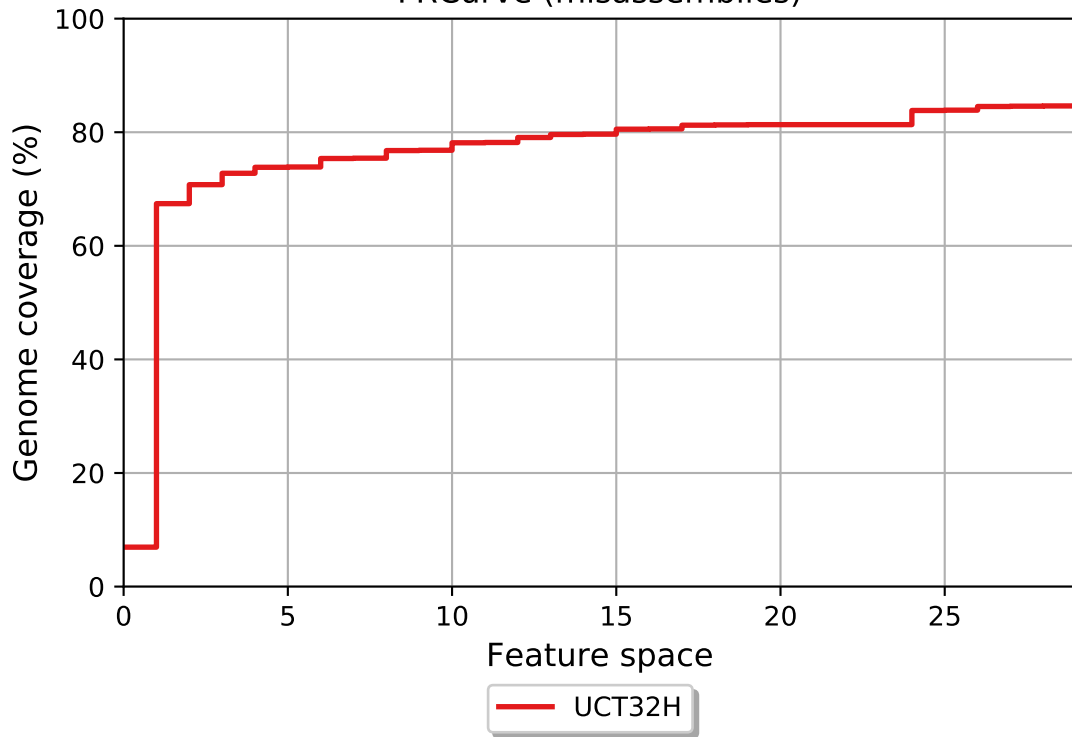


# translocations

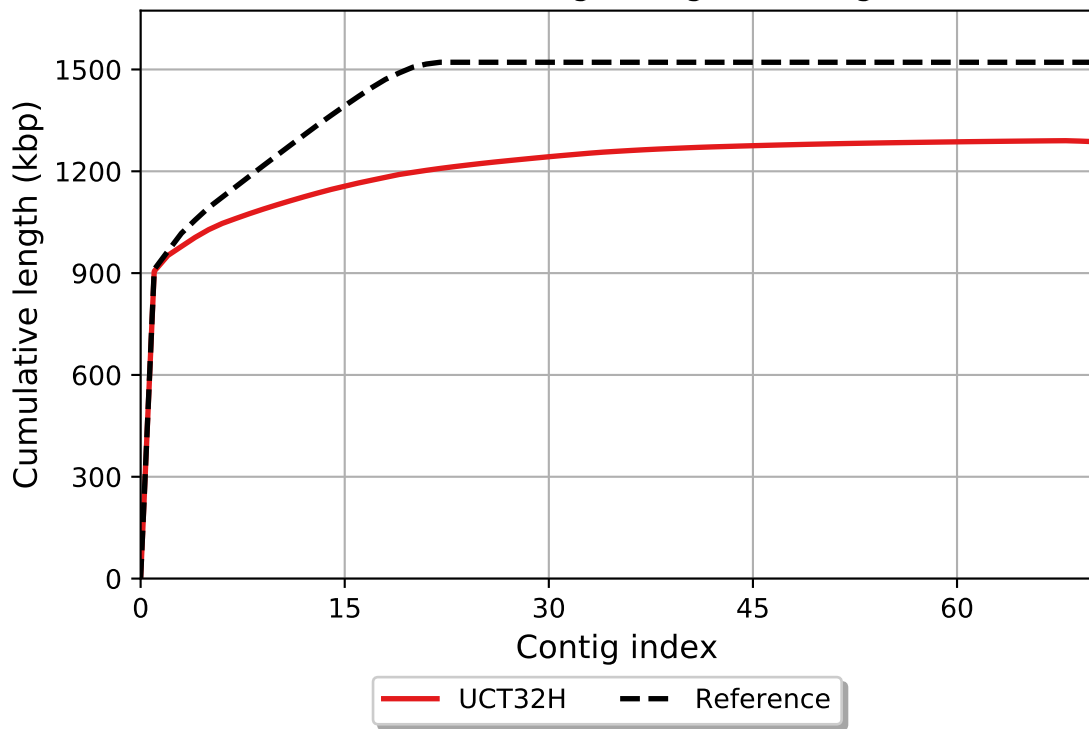


# inversions

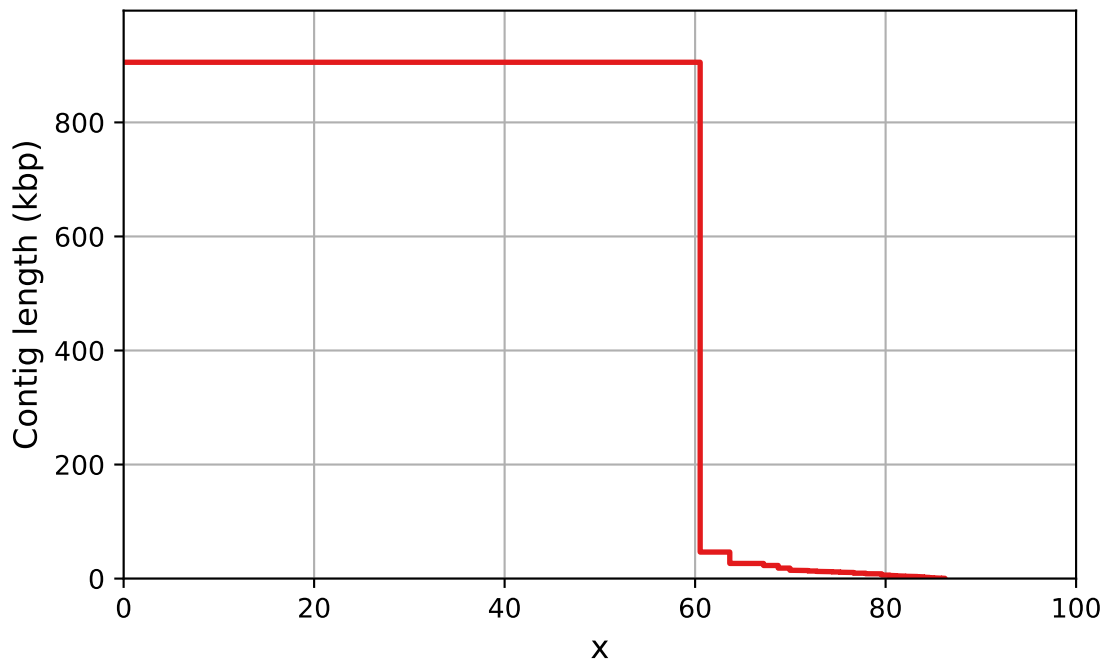
FRCurve (misassemblies)



Cumulative length (aligned contigs)

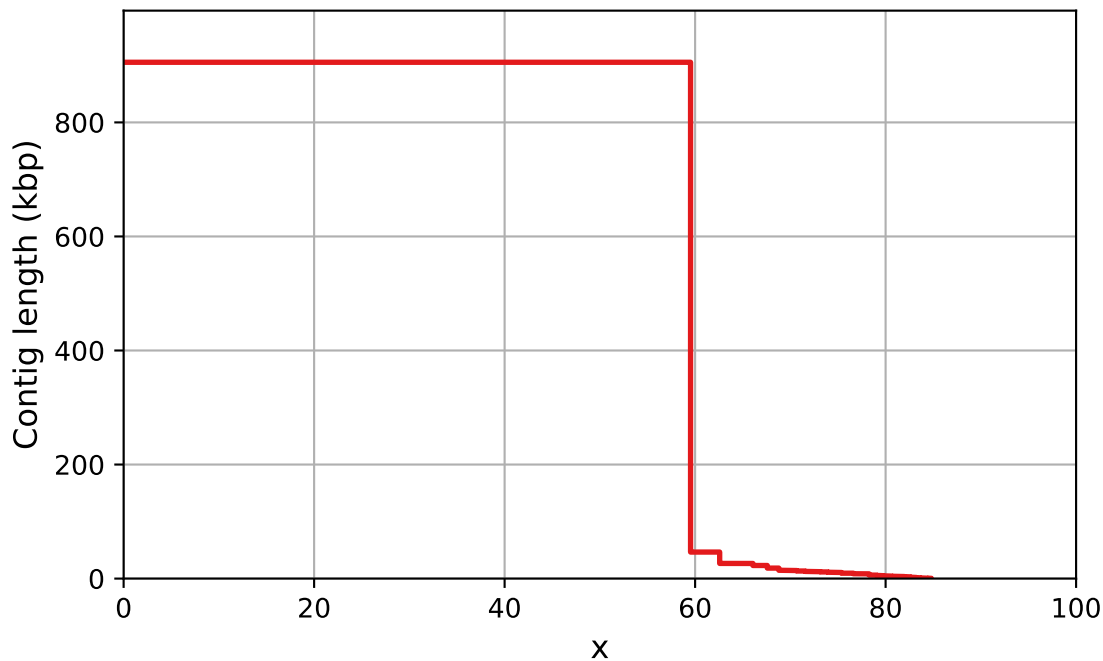


NAx



UCT32H

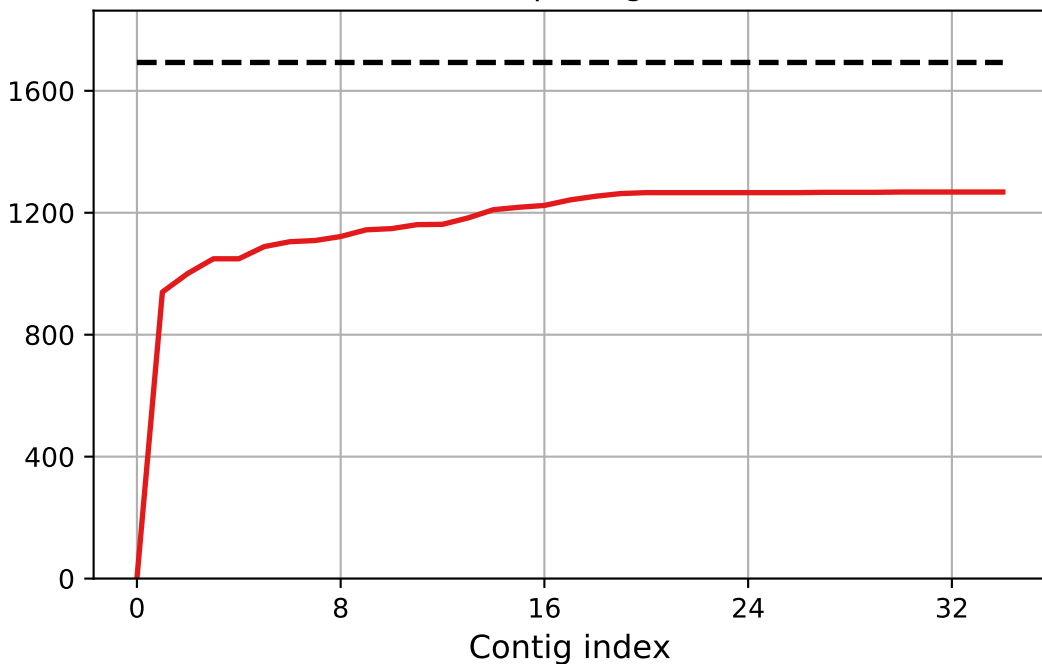
NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features



UCT32H    Reference

FRCurve (genomic features)

