

# Report

	UCT29H
# contigs (>= 0 bp)	24
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1559716
Total length (>= 1000 bp)	1559264
Total length (>= 5000 bp)	1558259
Total length (>= 10000 bp)	1548879
Total length (>= 25000 bp)	1506001
Total length (>= 50000 bp)	1039953
# contigs	22
Largest contig	910485
Total length	1559264
Reference length	1521208
GC (%)	28.19
Reference GC (%)	28.18
N50	910485
NG50	910485
N90	29761
NG90	29787
auN	547345.6
auNG	561038.5
L50	1
LG50	1
L90	15
LG90	14
# misassemblies	19
# misassembled contigs	12
Misassembled contigs length	395586
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 6 part
Unaligned length	19872
Genome fraction (%)	97.068
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	224.26
# indels per 100 kbp	28.36
# genomic features	1601 + 34 part
Largest alignment	910485
Total aligned length	1537487
NA50	910485
NGA50	910485
NA90	17050
NGA90	20828
auNA	543026.4
auNGA	556611.2
LA50	1
LGA50	1
LA90	18
LGA90	16

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

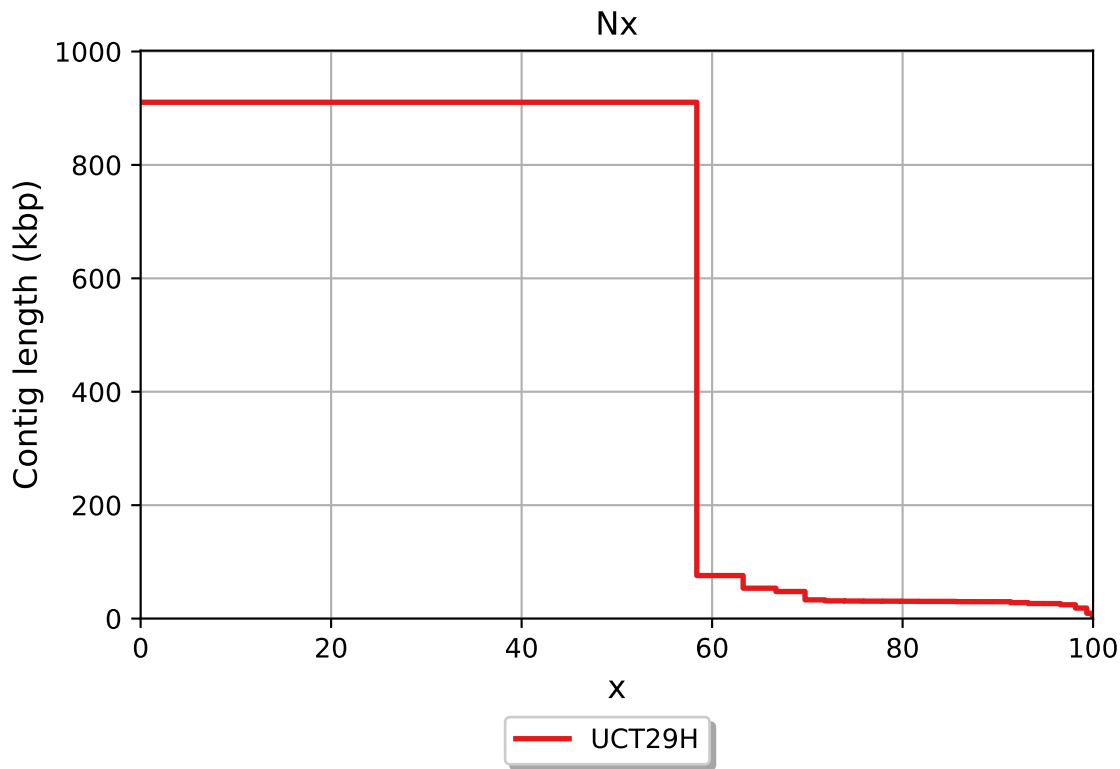
	UCT29H
# misassemblies	19
# contig misassemblies	19
# c. relocations	3
# c. translocations	14
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	395586
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3448
# indels	436
# indels (<= 5 bp)	377
# indels (> 5 bp)	59
Indels length	3463

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).

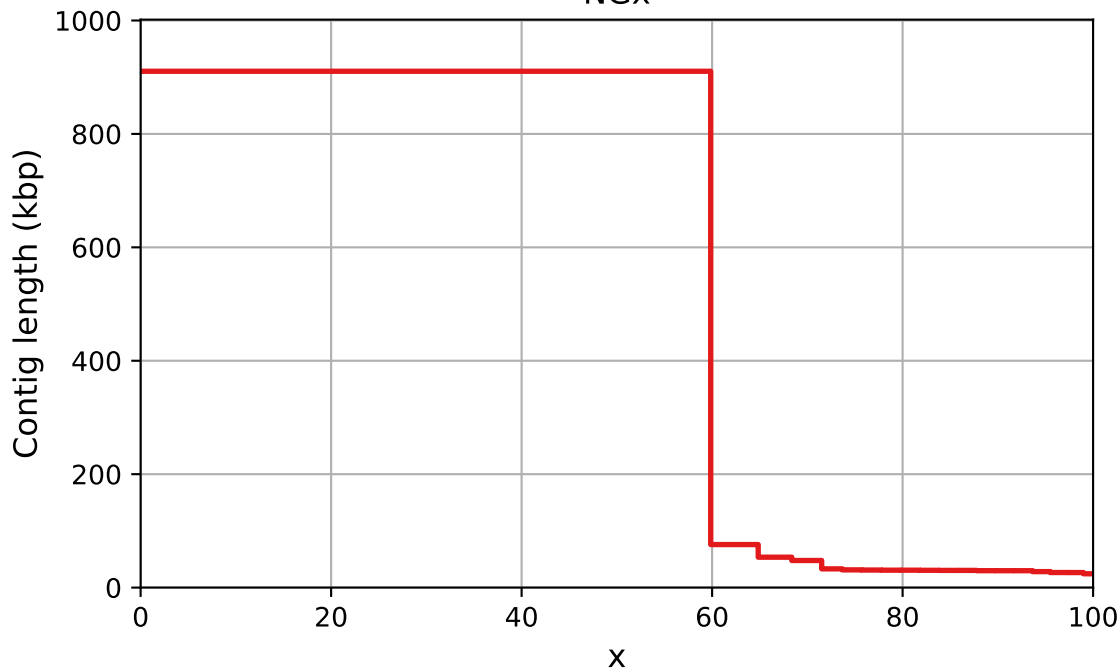
## Unaligned report

	UCT29H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	19872
# 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).

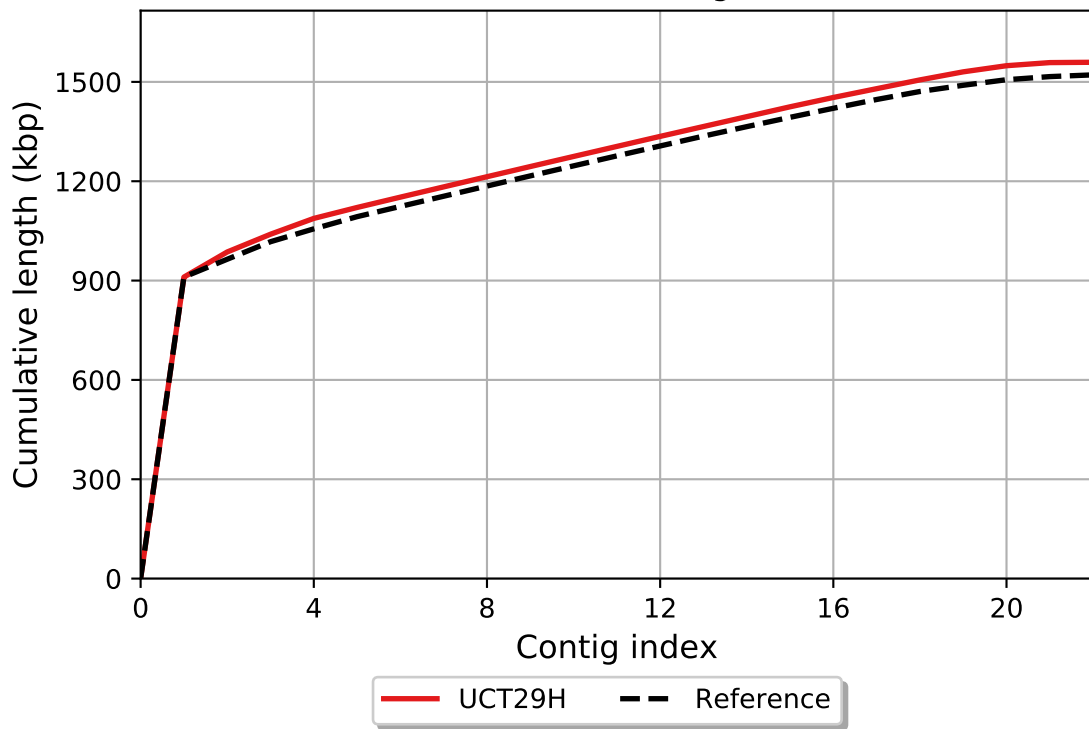


NGx

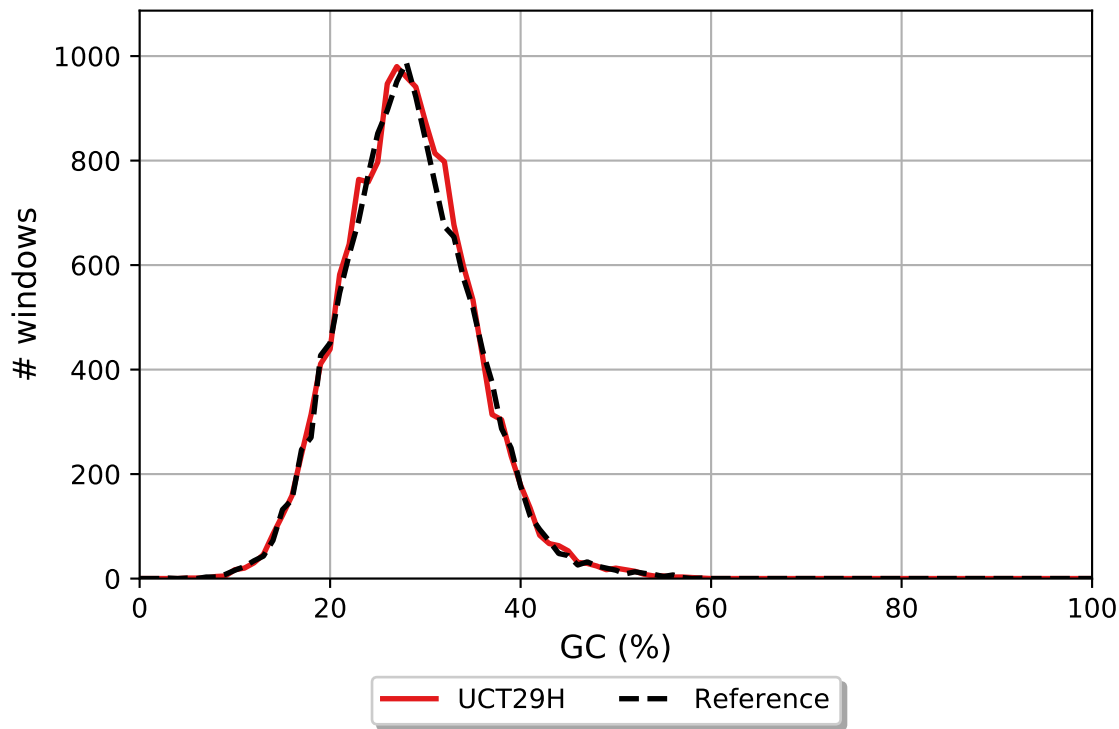


UCT29H

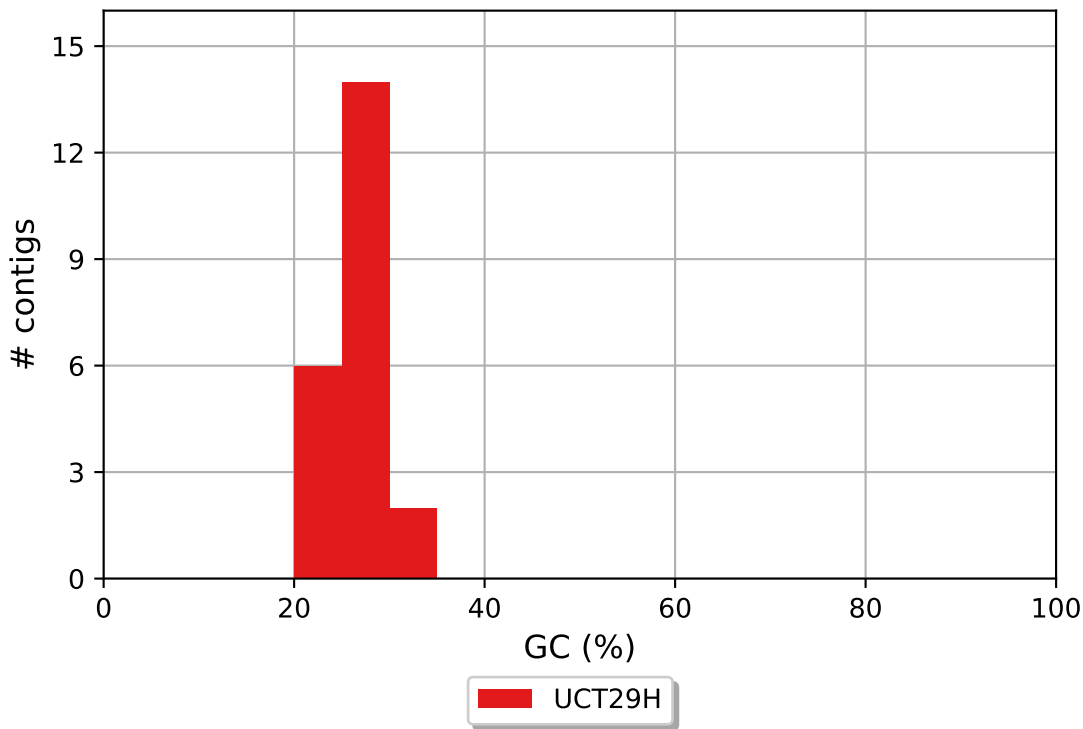
Cumulative length



GC content

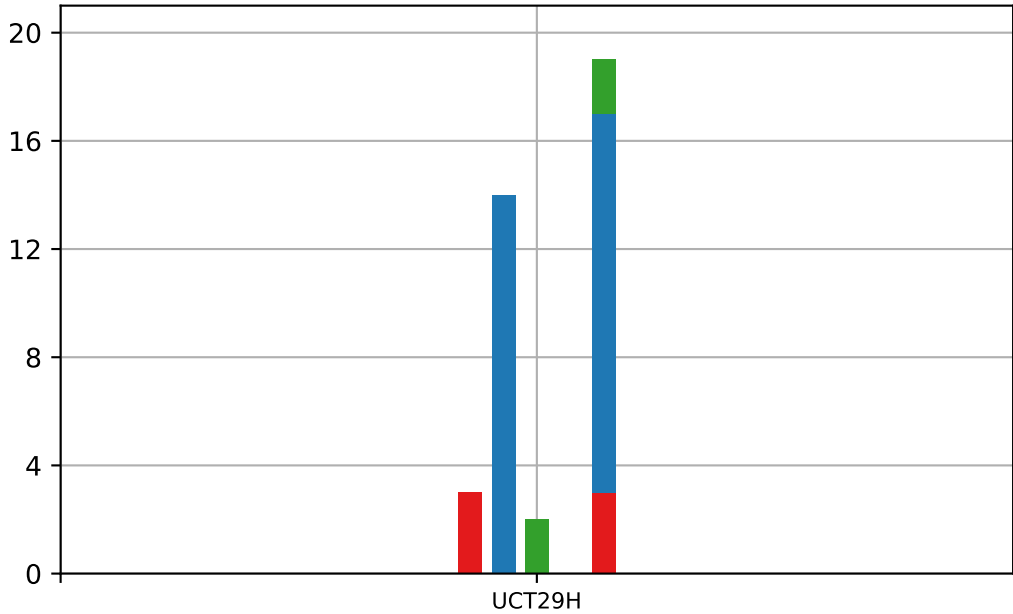


UCT29H GC content





## Misassemblies



# relocations

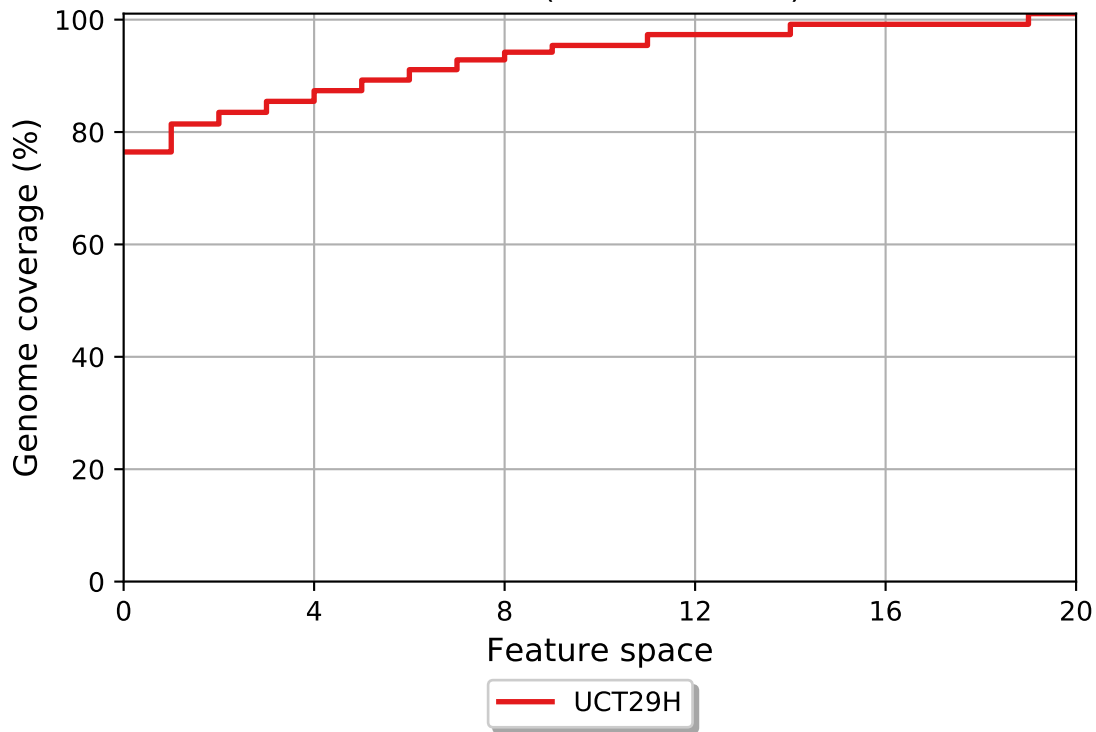


# translocations

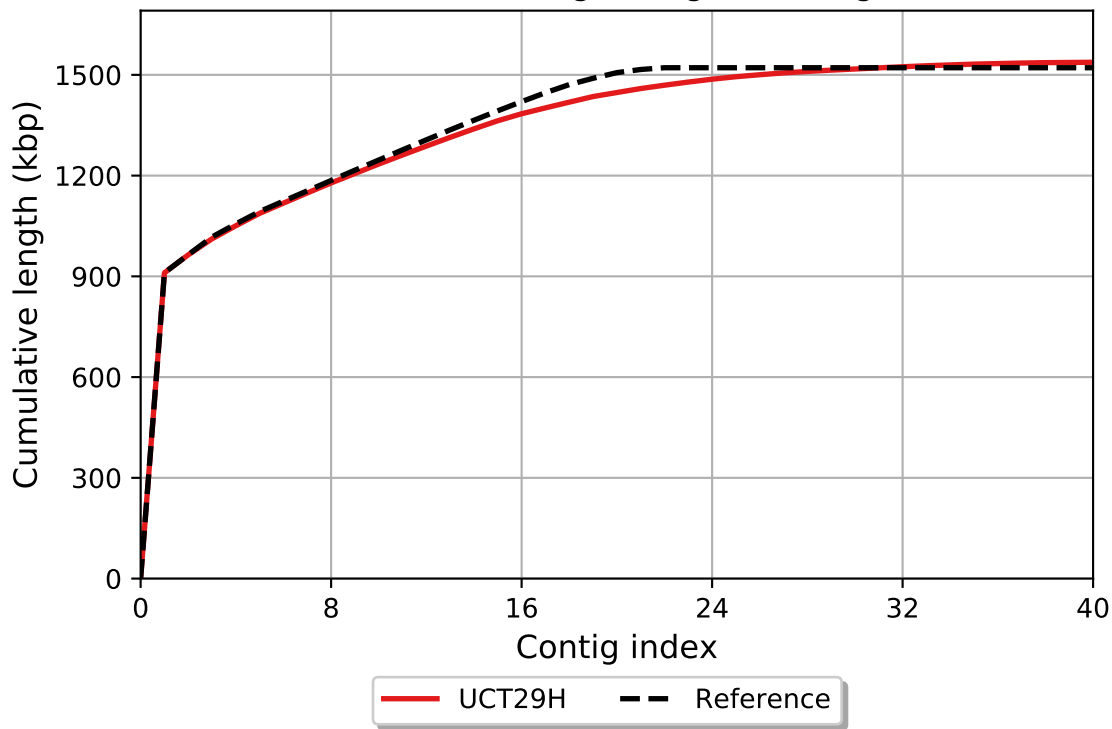


# inversions

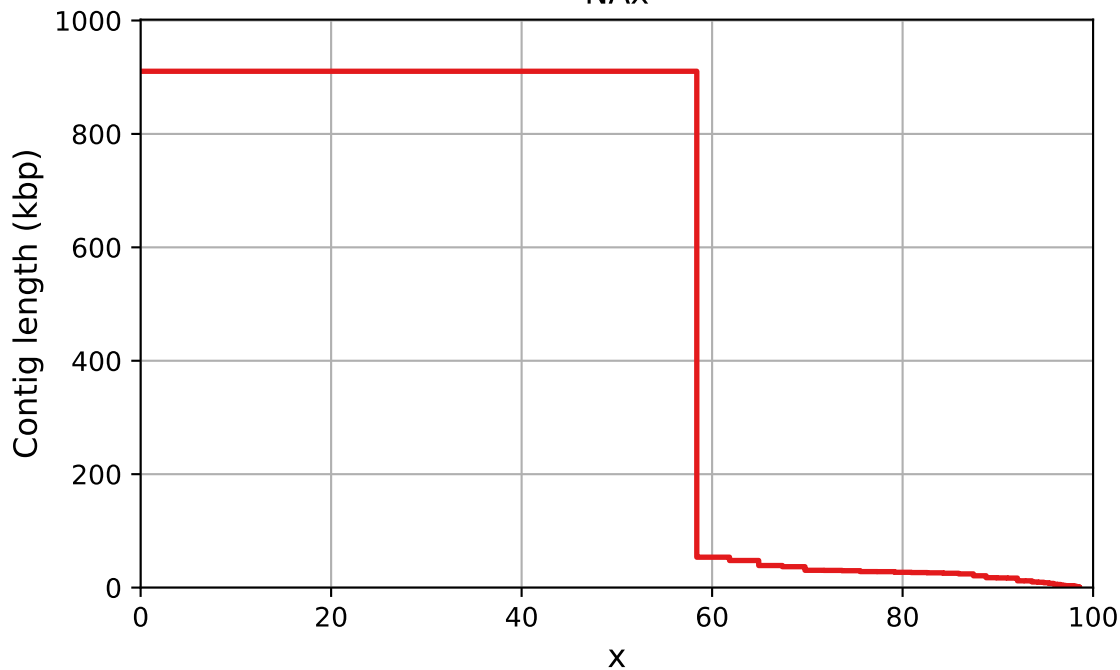
FRCurve (misassemblies)



Cumulative length (aligned contigs)

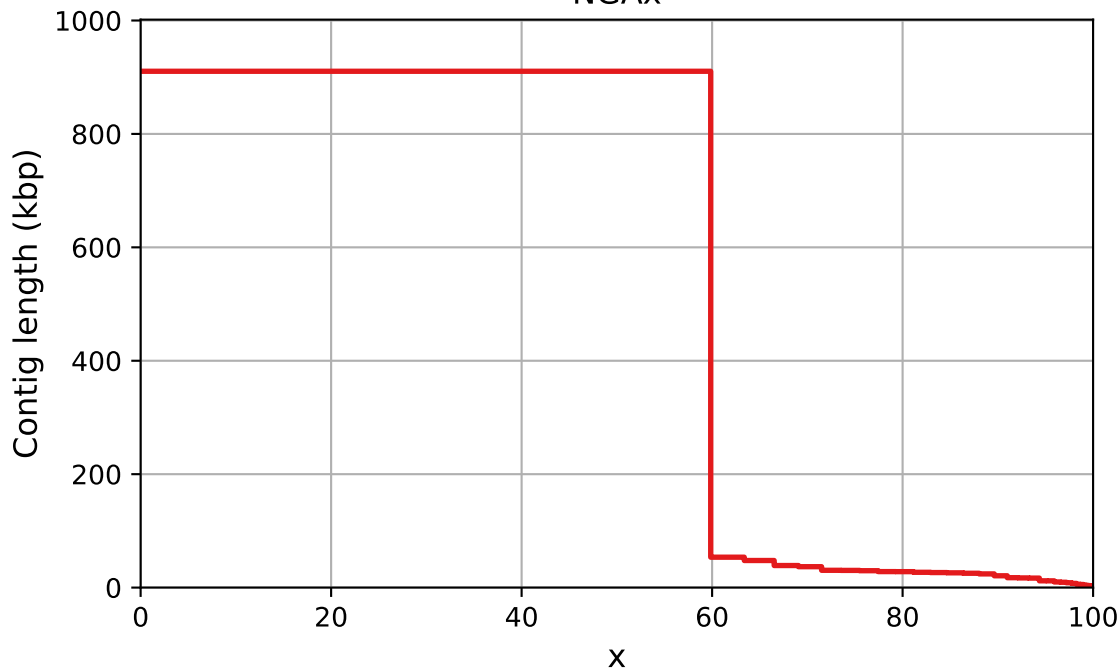


NAx

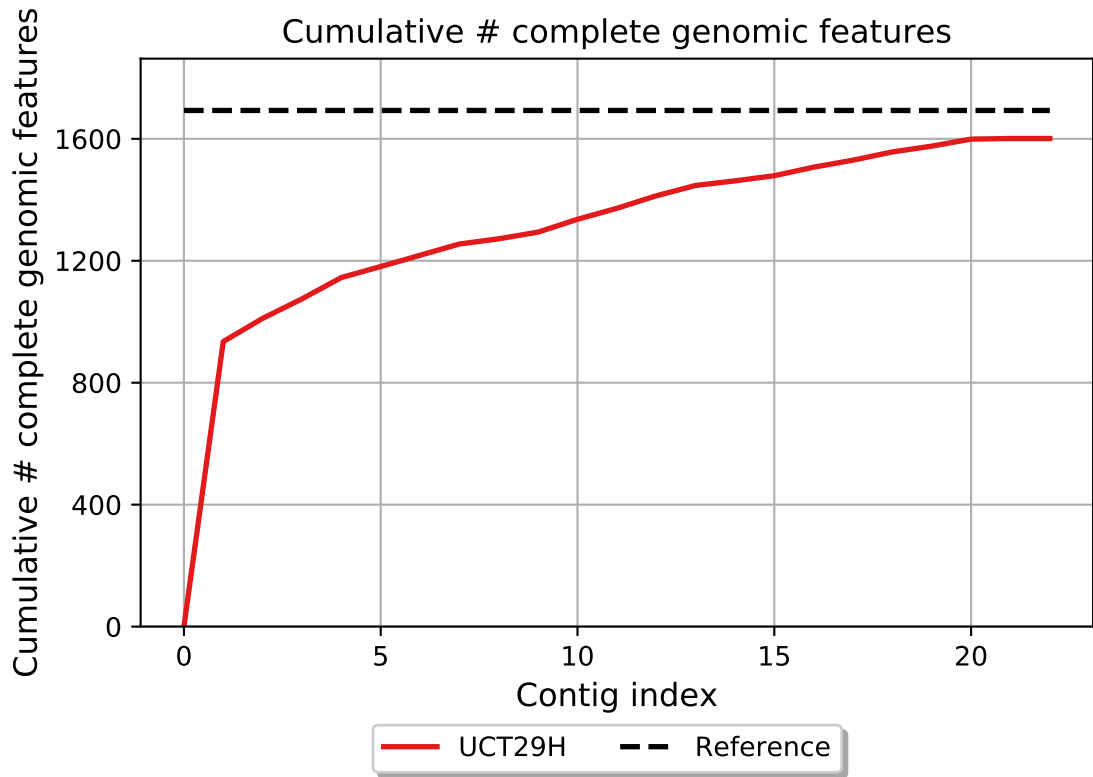


UCT29H

NGAx



UCT29H



FRCurve (genomic features)

