

Report

	UCT31H
# contigs (>= 0 bp)	32
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1531745
Total length (>= 1000 bp)	1527664
Total length (>= 5000 bp)	1527664
Total length (>= 10000 bp)	1518289
Total length (>= 25000 bp)	1496330
Total length (>= 50000 bp)	964311
# contigs	24
Largest contig	910624
Total length	1530196
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	910624
NG50	910624
N90	30001
NG90	30001
auN	555326.6
auNG	558607.8
L50	1
LG50	1
L90	15
LG90	15
# misassemblies	16
# misassembled contigs	9
Misassembled contigs length	241165
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 6 part
Unaligned length	28793
Genome fraction (%)	94.179
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	228.94
# indels per 100 kbp	28.73
# genomic features	1555 + 38 part
Largest alignment	910624
Total aligned length	1499967
NA50	910624
NGA50	910624
NA90	19402
NGA90	20834
auNA	552816.8
auNGA	556083.1
LA50	1
LGA50	1
LA90	17
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

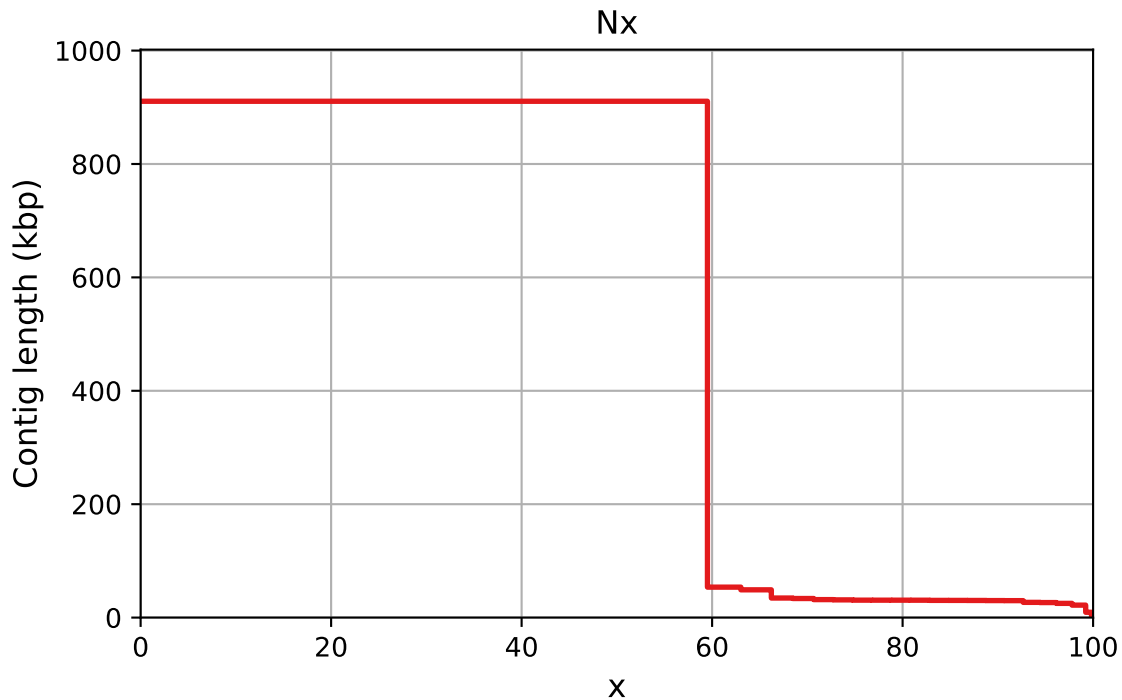
	UCT31H
# misassemblies	16
# contig misassemblies	16
# c. relocations	6
# c. translocations	7
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	241165
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3434
# indels	431
# indels (<= 5 bp)	368
# indels (> 5 bp)	63
Indels length	3878

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

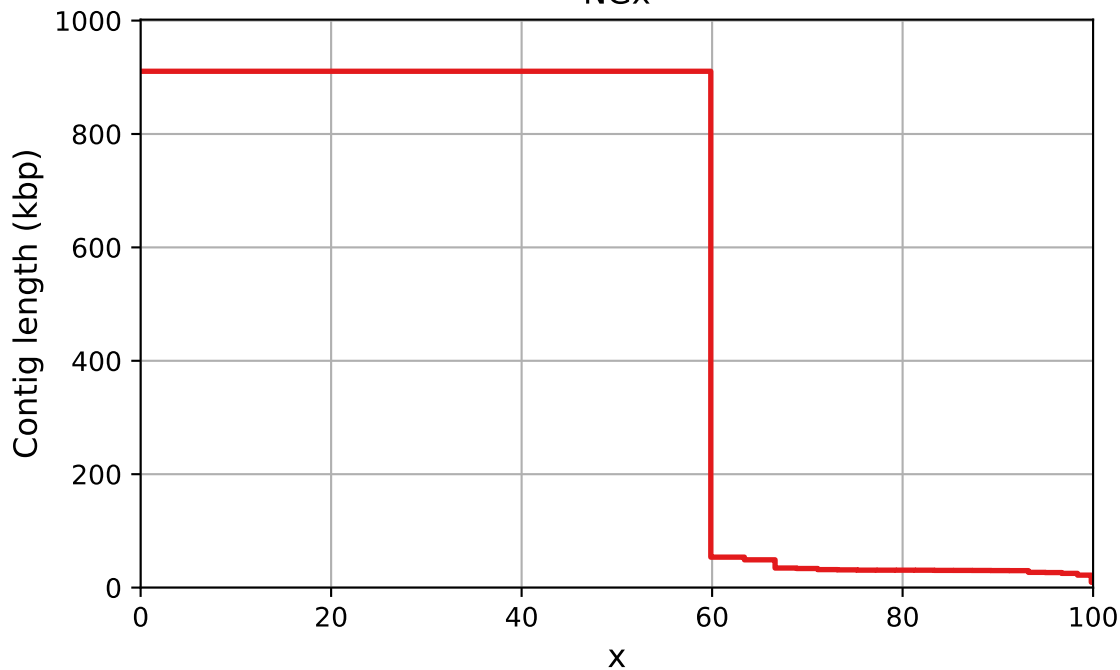
	UCT31H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	28793
# N's	0

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).

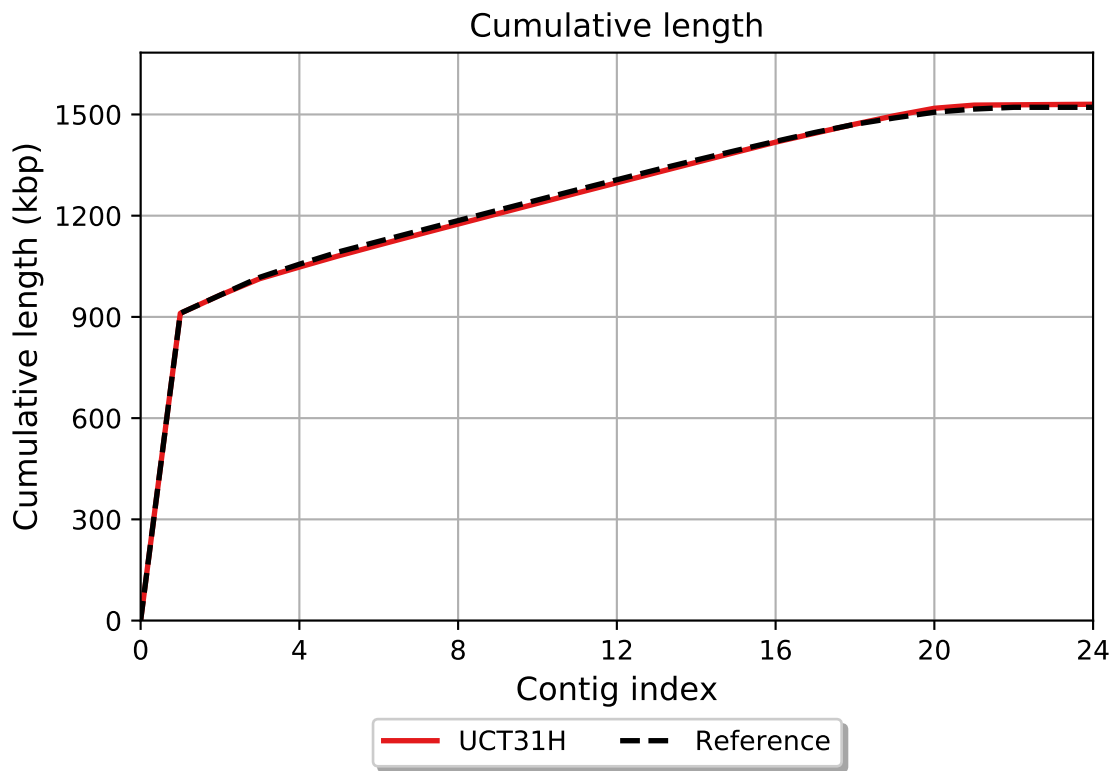


UCT31H

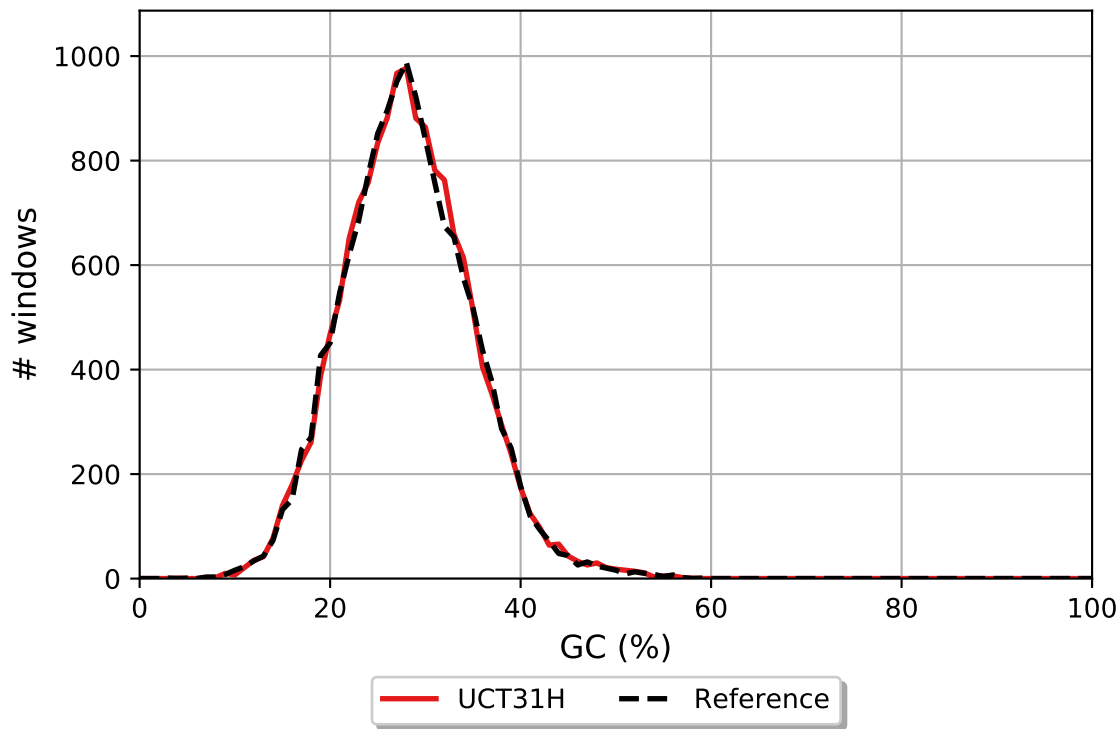
NGx



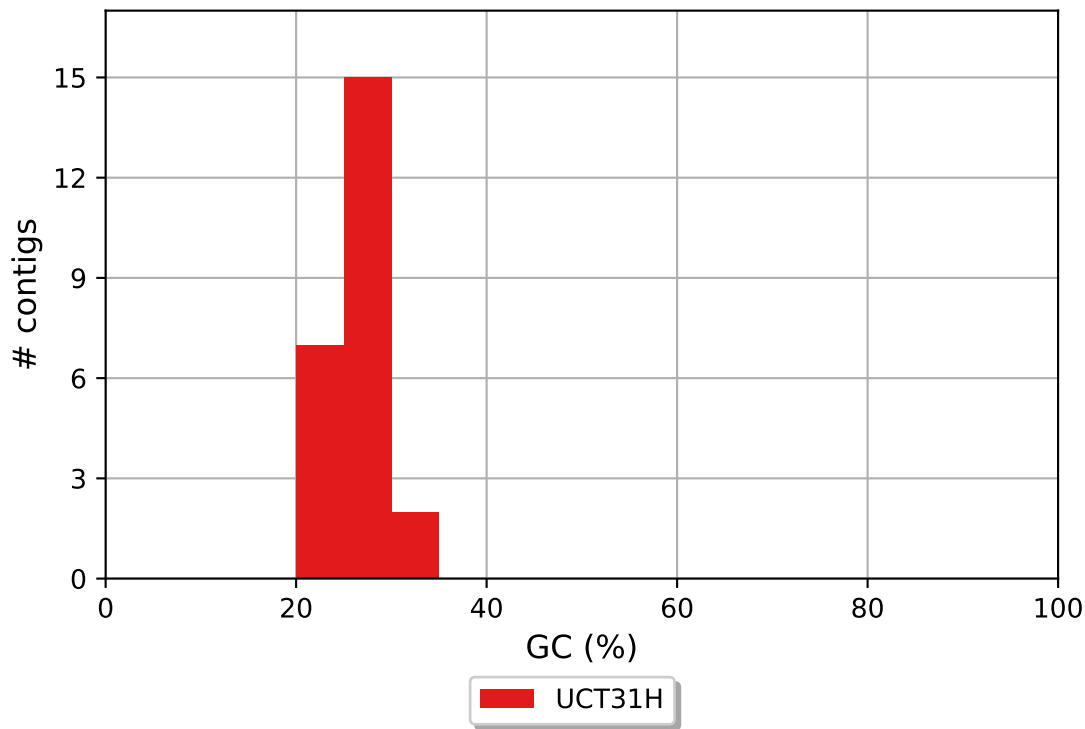
UCT31H



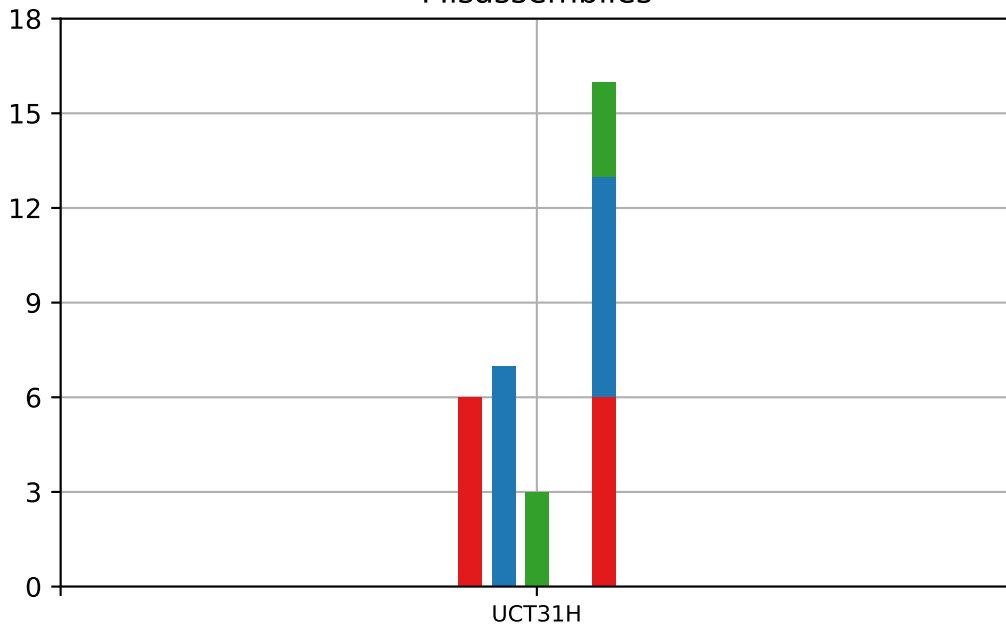
GC content



UCT31H GC content



Misassemblies



relocations

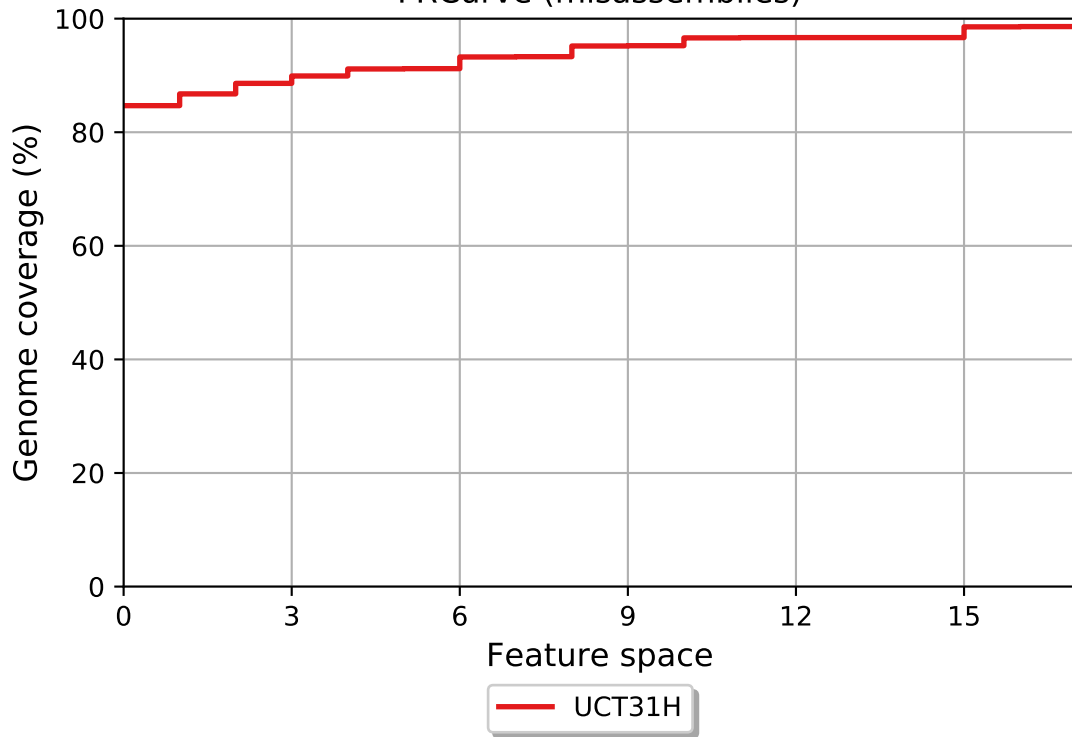


translocations

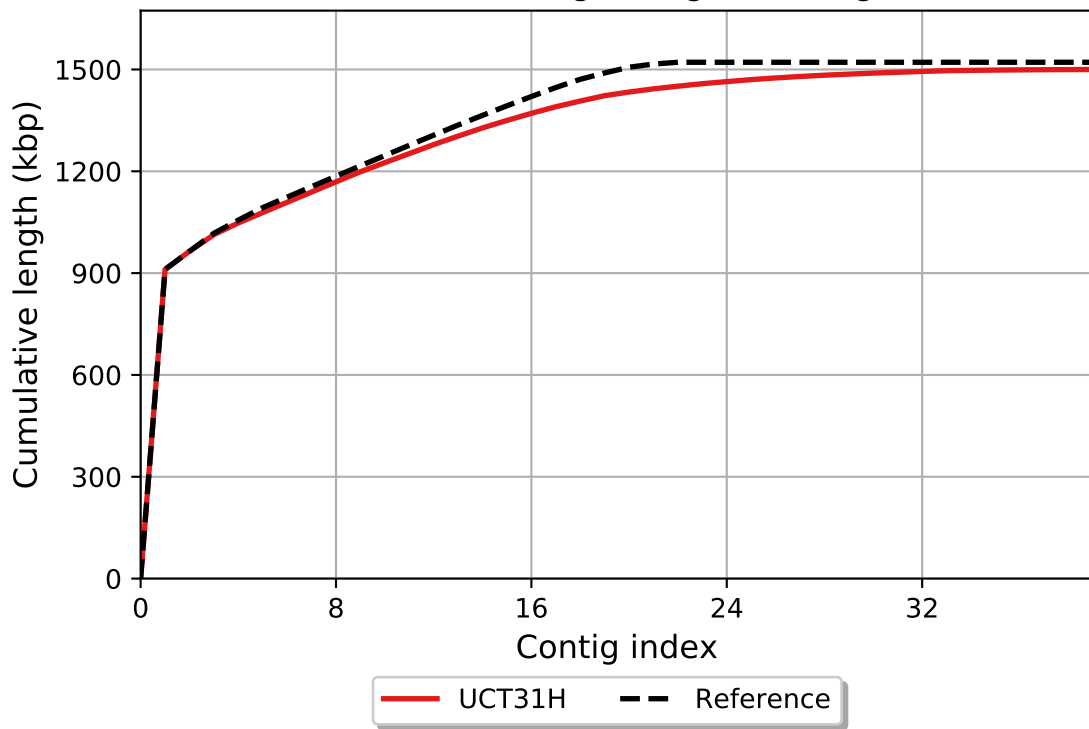


inversions

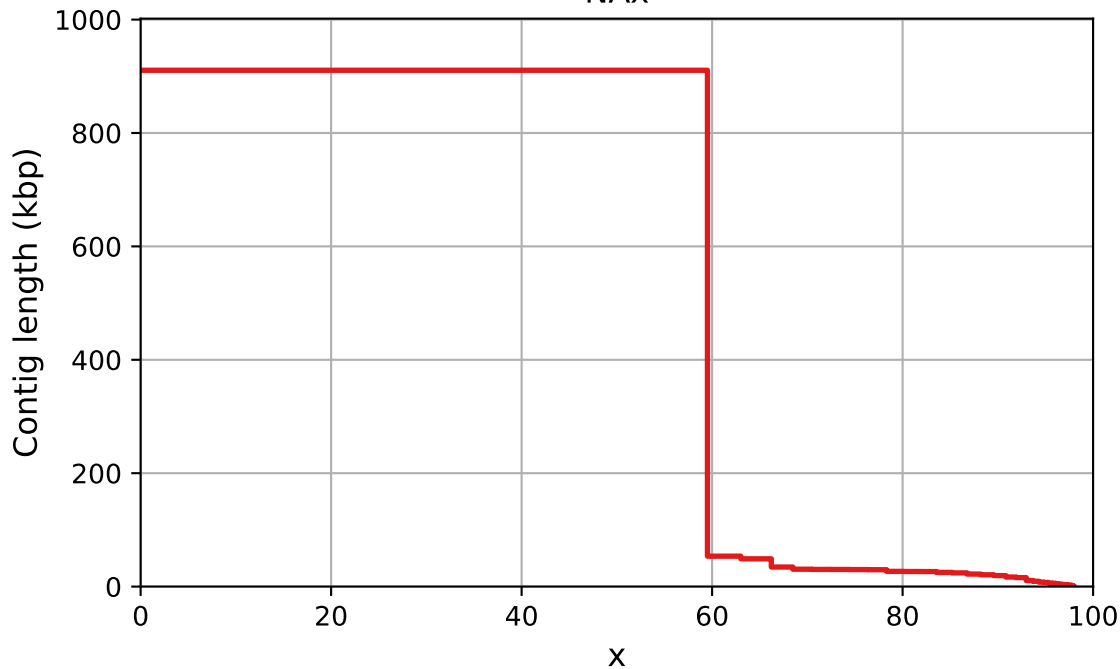
FRCurve (misassemblies)



Cumulative length (aligned contigs)

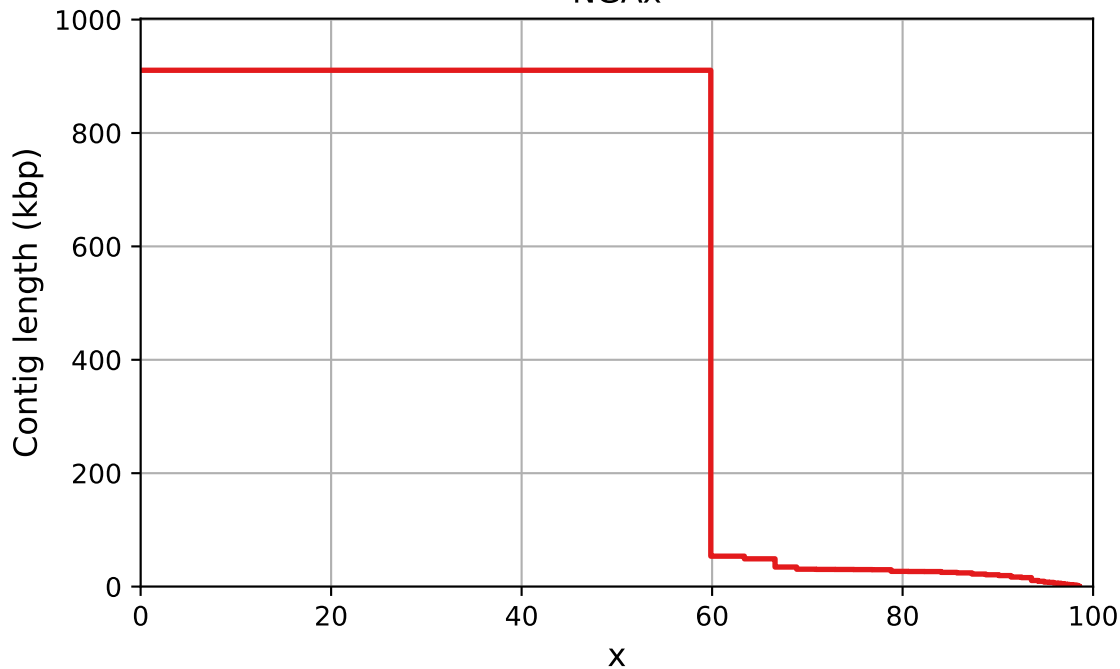


NAx

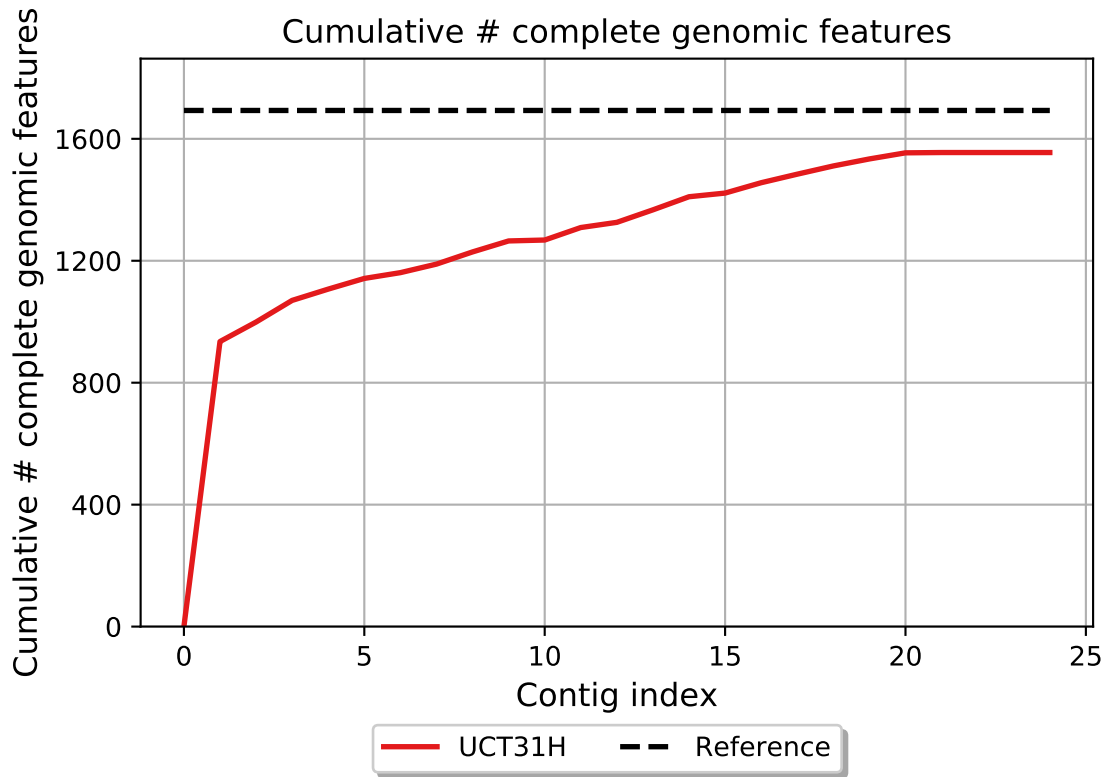


UCT31H

NGAx



UCT31H



FRCurve (genomic features)

