

Report

	UCT35H
# contigs (>= 0 bp)	33
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	1350407
Total length (>= 1000 bp)	1343430
Total length (>= 5000 bp)	1339686
Total length (>= 10000 bp)	1323410
Total length (>= 25000 bp)	1259344
Total length (>= 50000 bp)	1102010
# contigs	22
Largest contig	910022
Total length	1347562
Reference length	1521208
GC (%)	27.99
Reference GC (%)	28.18
N50	910022
NG50	910022
N90	27690
NG90	-
auN	629080.9
auNG	557271.2
L50	1
LG50	1
L90	8
LG90	-
# misassemblies	19
# misassembled contigs	3
Misassembled contigs length	148683
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	4 + 13 part
Unaligned length	192858
Genome fraction (%)	74.828
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	684.11
# indels per 100 kbp	34.37
# genomic features	1176 + 46 part
Largest alignment	904580
Total aligned length	1152162
NA50	904580
NGA50	904580
NA90	-
NGA90	-
auNA	611163.8
auNGA	541399.4
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

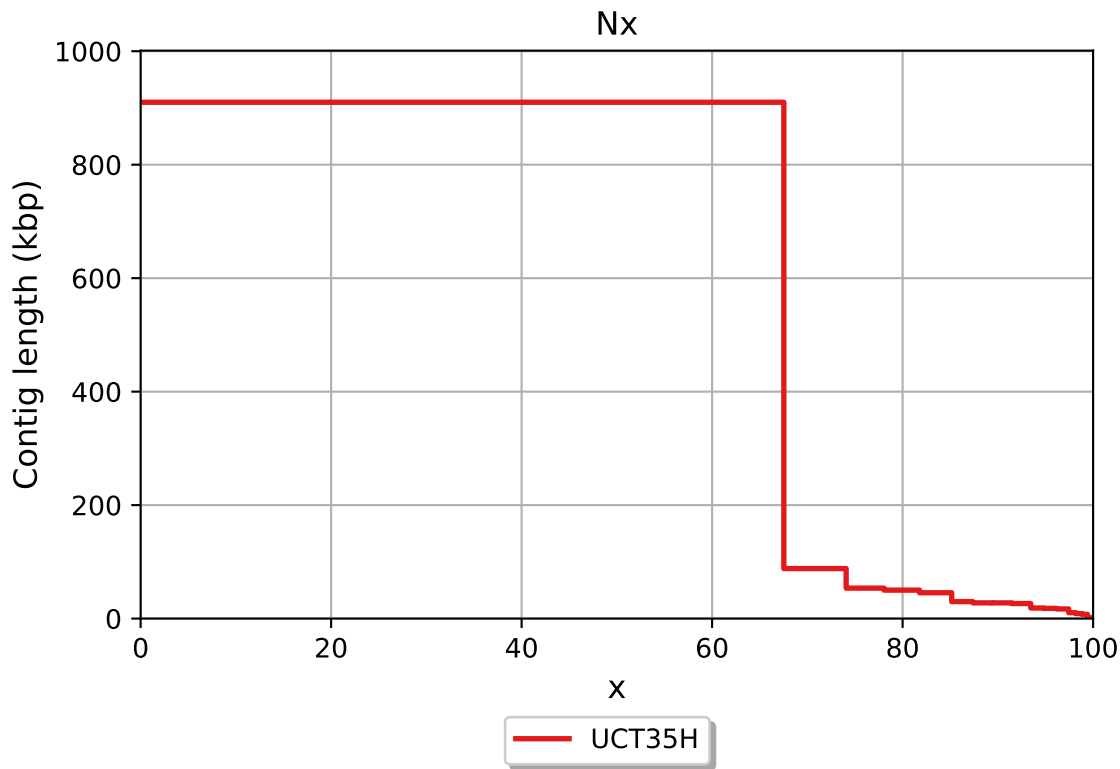
	UCT35H
# misassemblies	19
# contig misassemblies	19
# c. relocations	4
# c. translocations	13
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	148683
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	7882
# indels	396
# indels (<= 5 bp)	358
# indels (> 5 bp)	38
Indels length	1671

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).

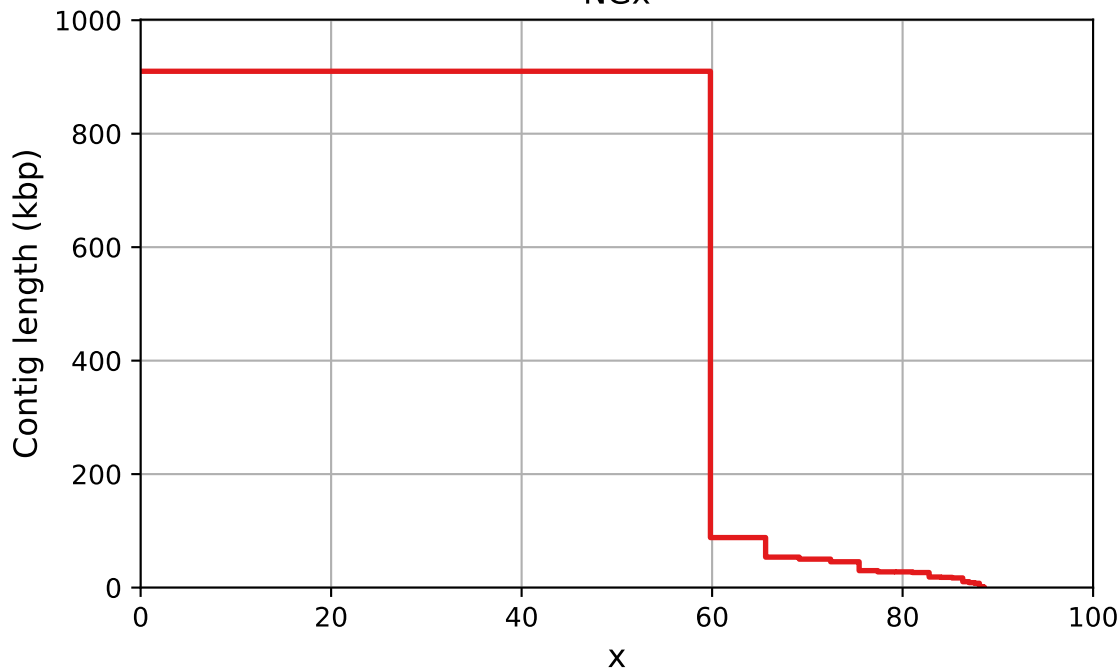
## Unaligned report

	UCT35H
# fully unaligned contigs	4
Fully unaligned length	48553
# partially unaligned contigs	13
Partially unaligned length	144305
# 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).

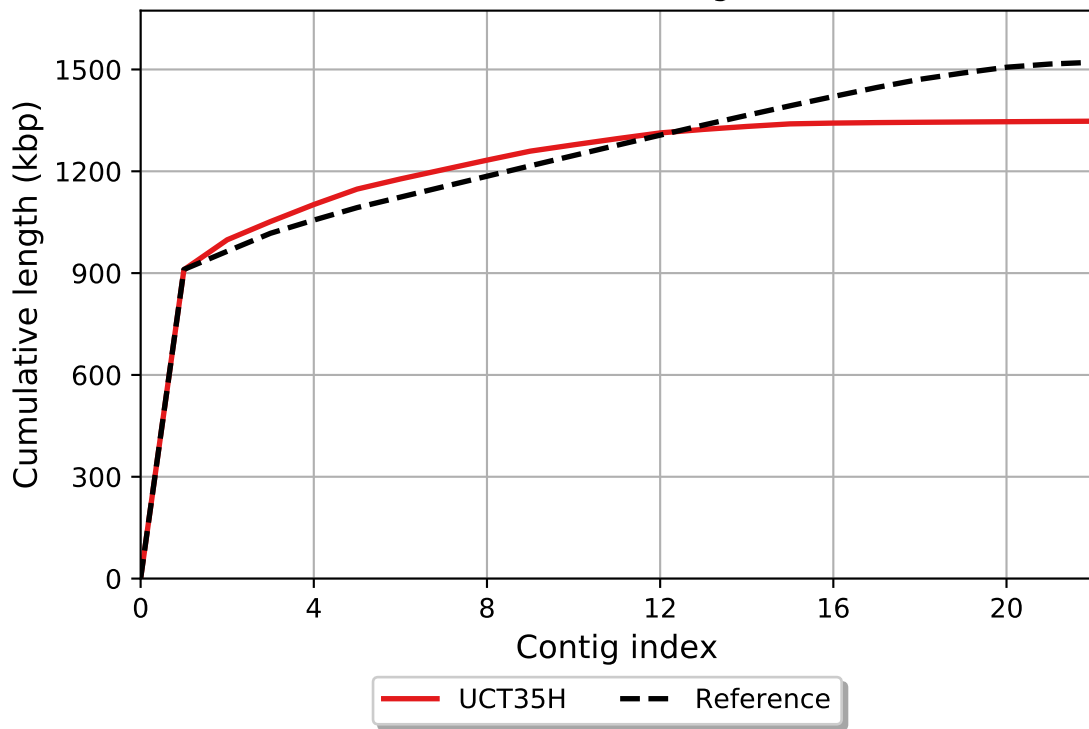


NGx

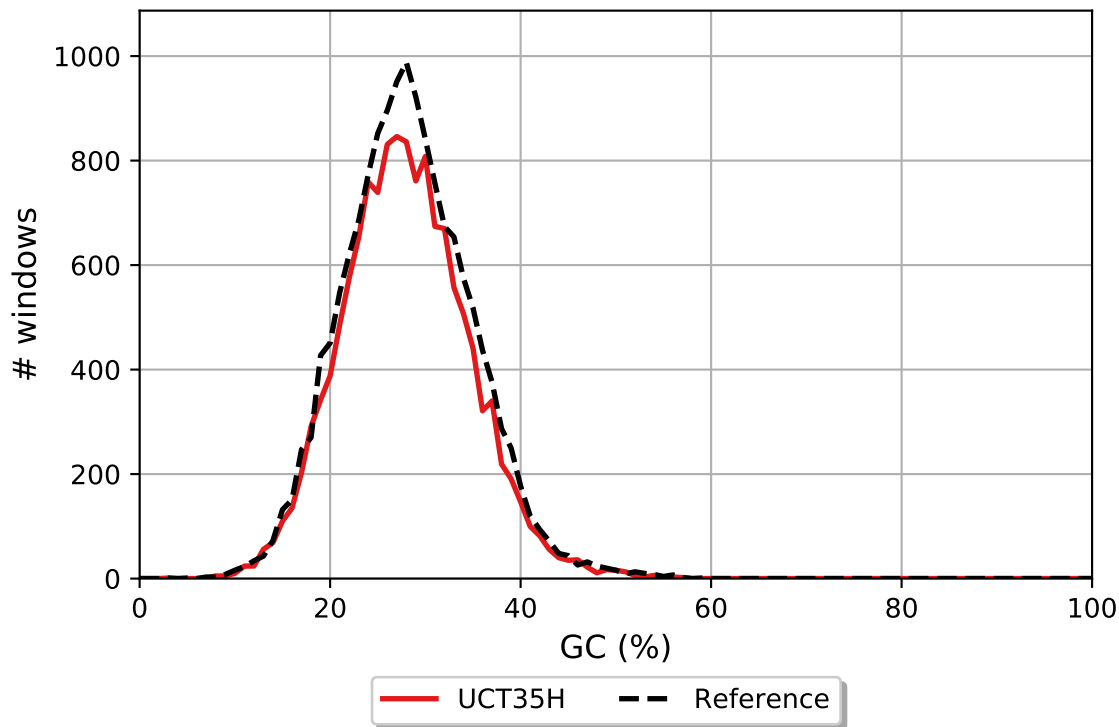


UCT35H

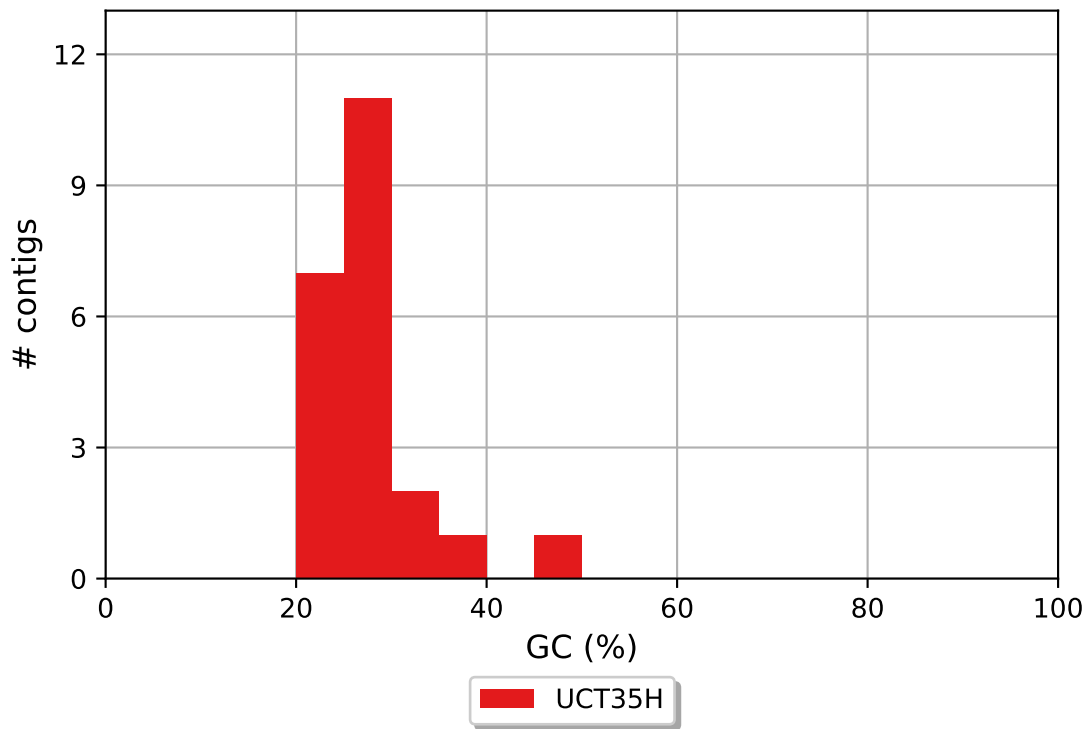
Cumulative length



GC content

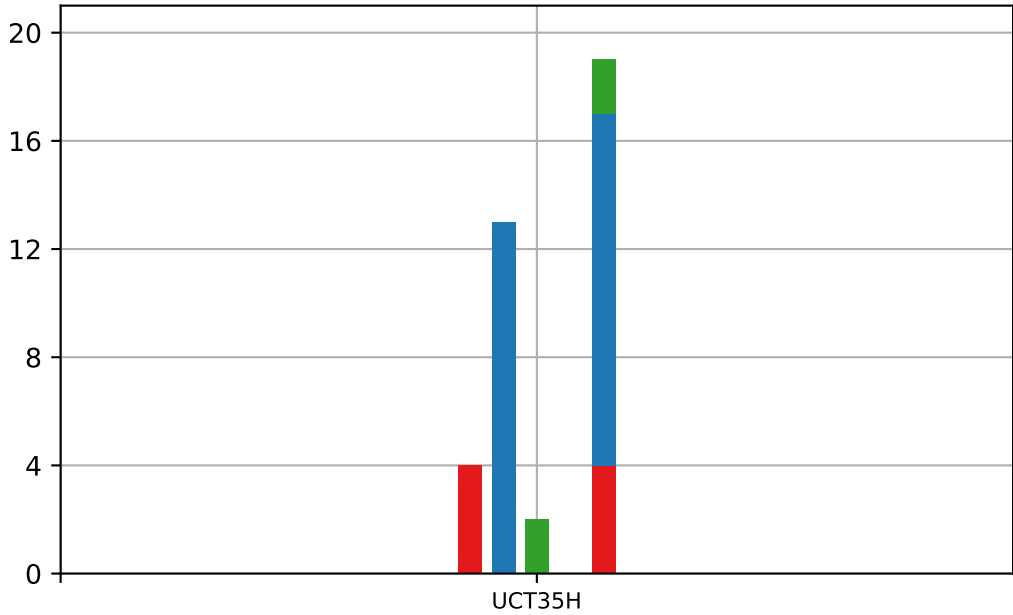


UCT35H GC content





## Misassemblies



# relocations

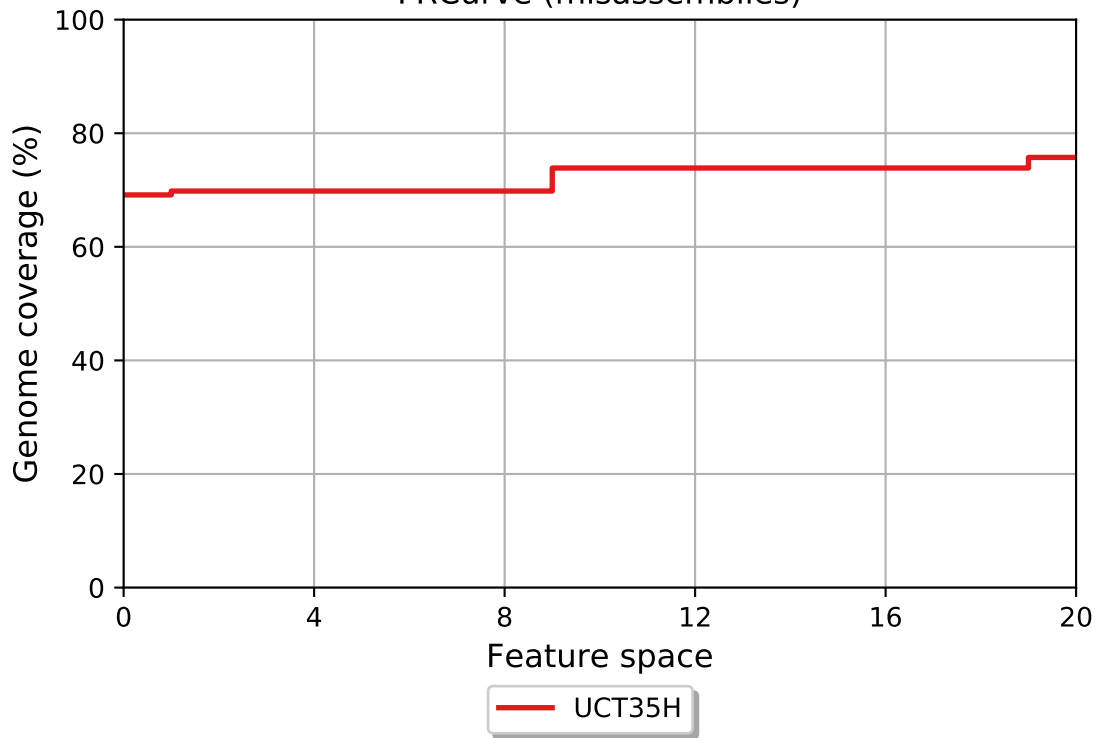


# translocations

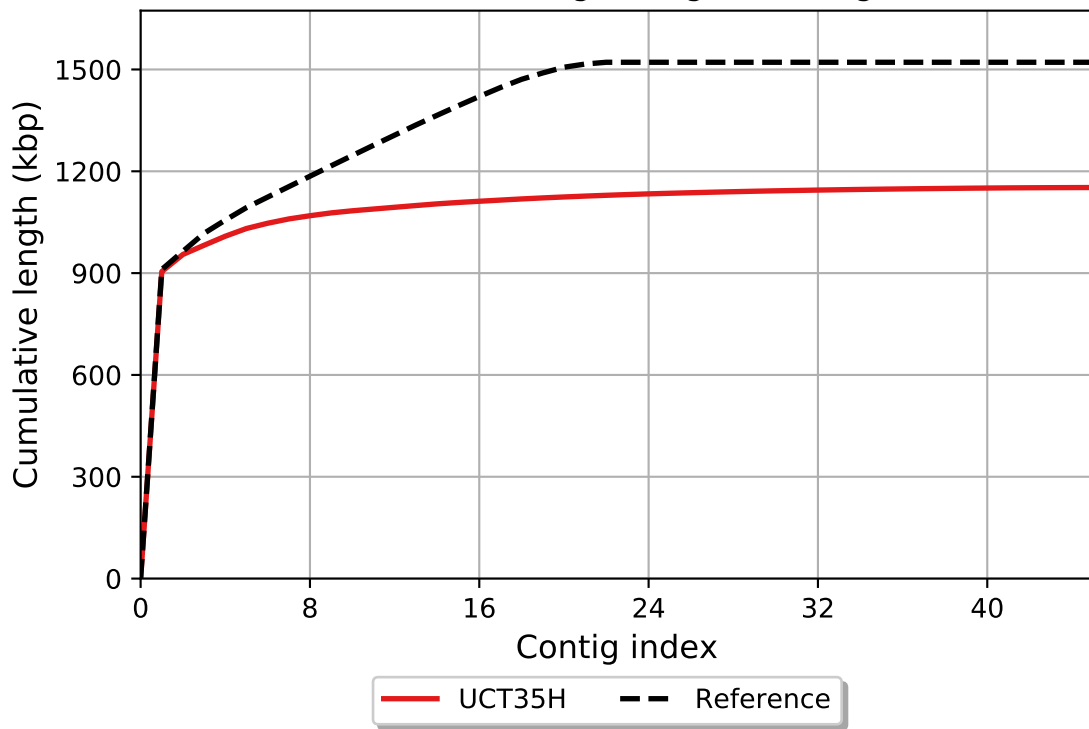


# inversions

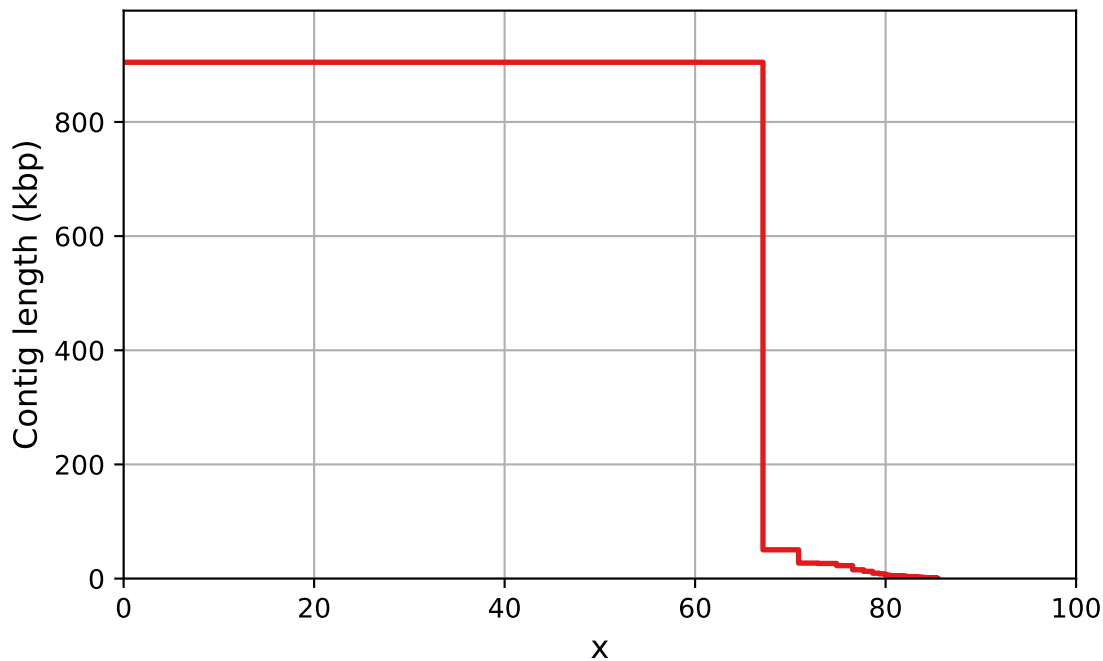
FRCurve (misassemblies)



Cumulative length (aligned contigs)

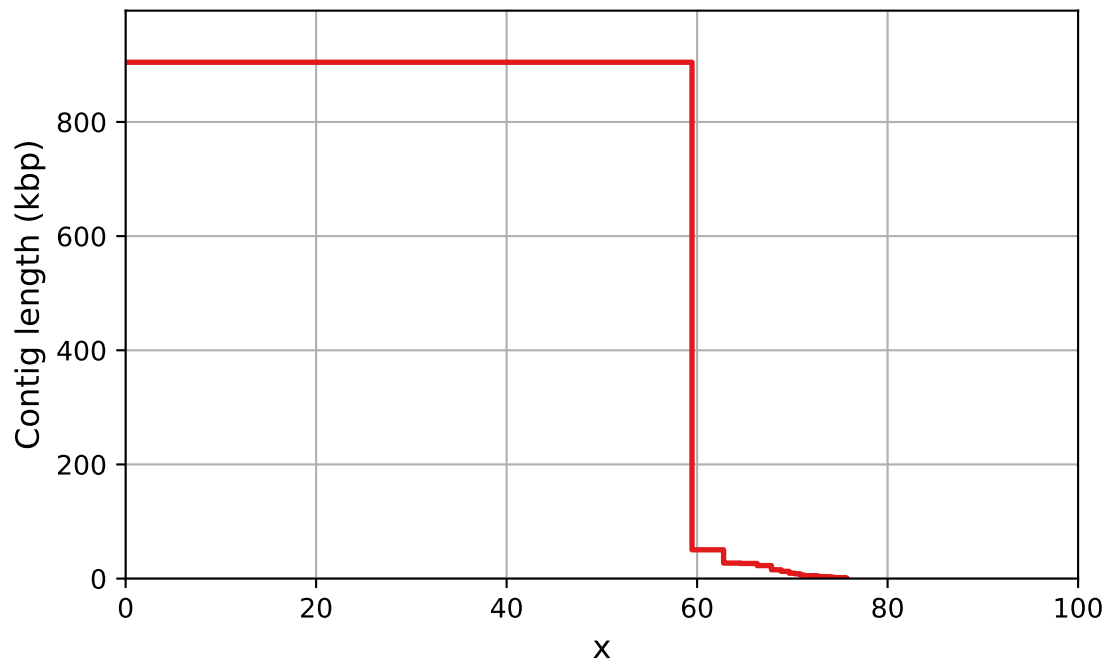


NAx

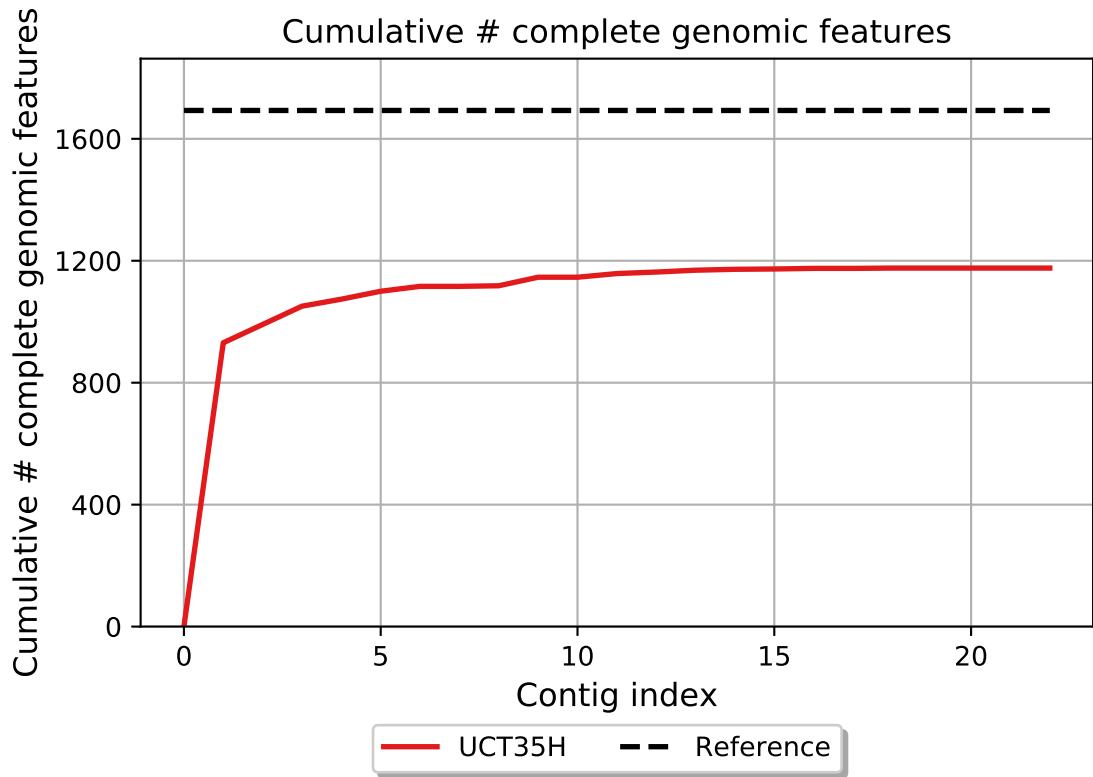


UCT35H

NGAx



UCT35H



FRCurve (genomic features)

