

Report

	consensus
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	5105872
Total length (>= 1000 bp)	5105872
Total length (>= 5000 bp)	5105872
Total length (>= 10000 bp)	5105872
Total length (>= 25000 bp)	5105872
Total length (>= 50000 bp)	5105872
# contigs	3
Largest contig	3318769
Total length	5105872
Reference length	4951383
GC (%)	52.20
Reference GC (%)	52.24
N50	3318769
NG50	3318769
N90	1678044
NG90	1678044
auN	2710987.1
auNG	2795573.1
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	25
# misassembled contigs	2
Misassembled contigs length	4996813
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 2 part
Unaligned length	358694
Genome fraction (%)	95.669
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	27.11
# indels per 100 kbp	3.71
Largest alignment	953687
Total aligned length	4747118
NA50	460926
NGA50	460926
NA90	72349
NGA90	101719
auNA	476036.3
auNGA	490889.2
LA50	4
LGA50	4
LA90	14
LGA90	12

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

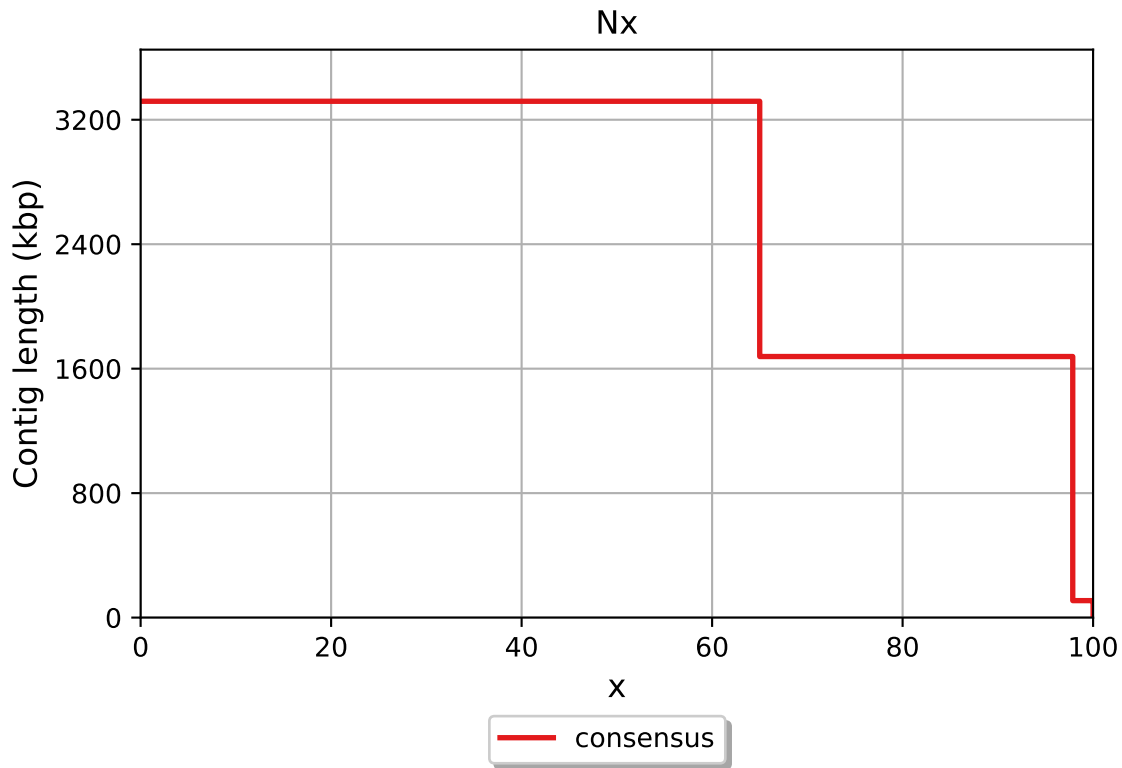
	consensus
# misassemblies	25
# contig misassemblies	25
# c. relocations	25
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	4996813
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1287
# indels	176
# indels (<= 5 bp)	146
# indels (> 5 bp)	30
Indels length	2631

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).

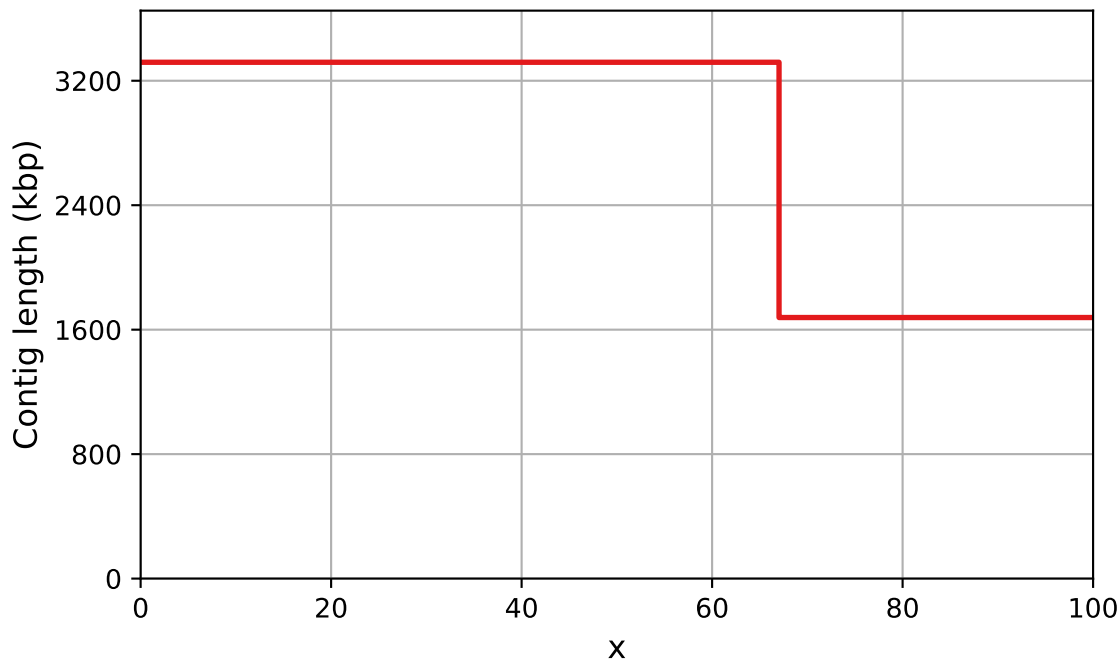
Unaligned report

	consensus
# fully unaligned contigs	1
Fully unaligned length	109059
# partially unaligned contigs	2
Partially unaligned length	249635
# N's	0

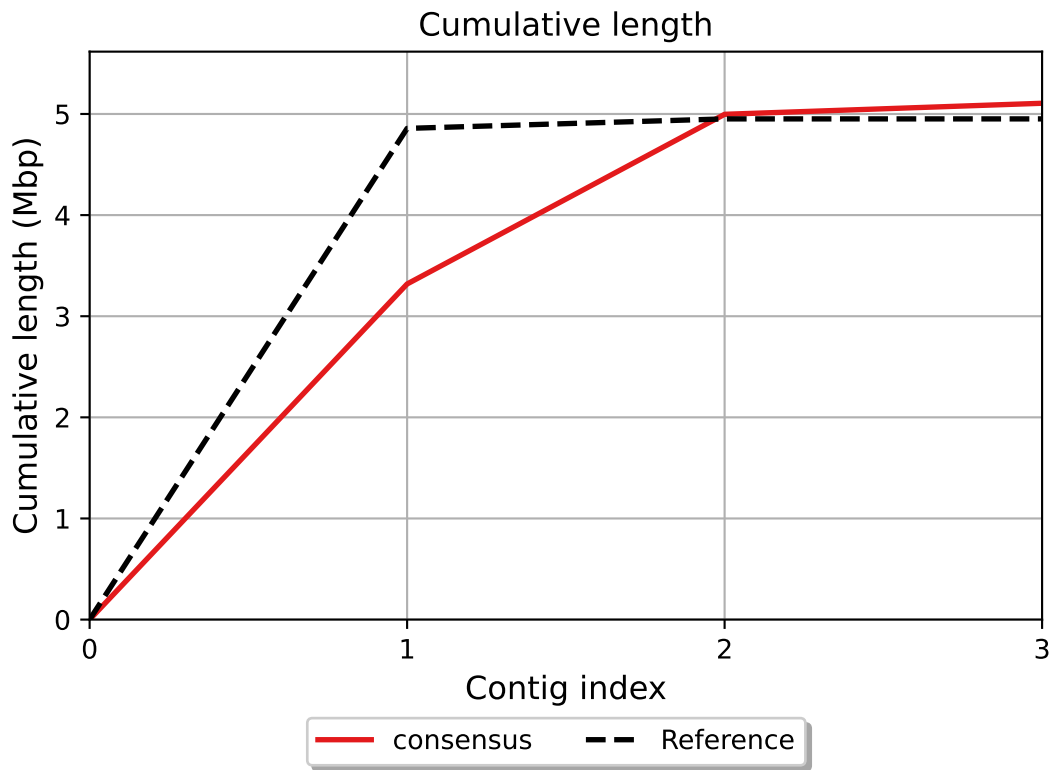
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



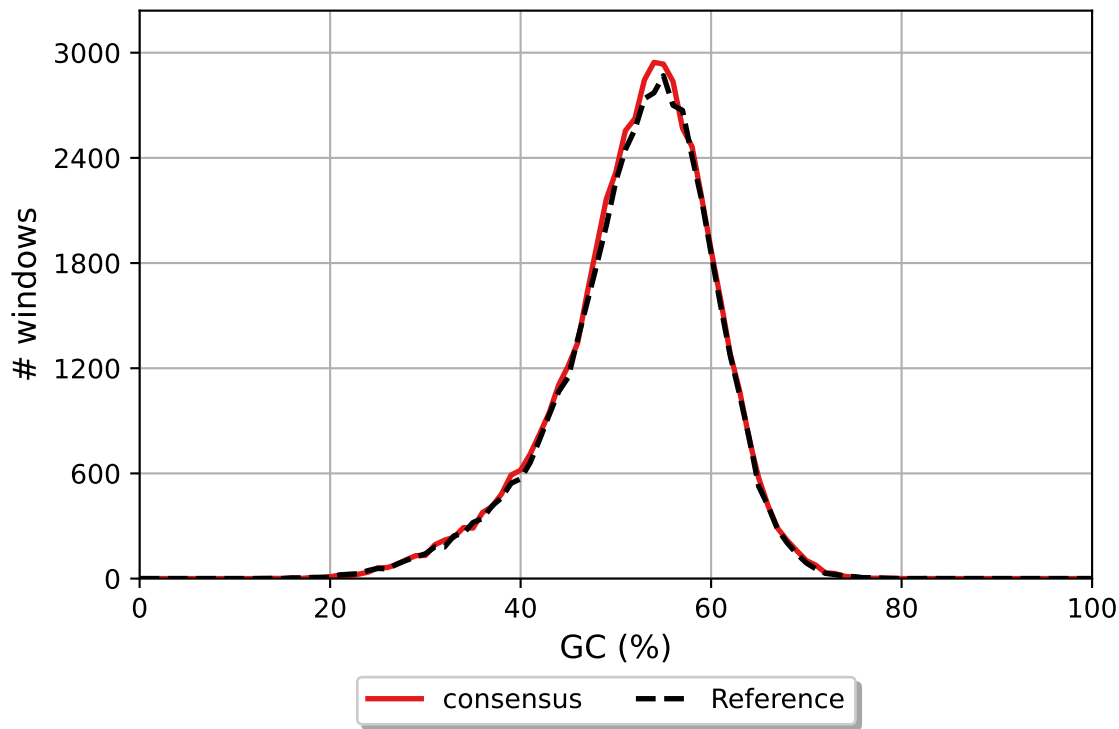
NGx



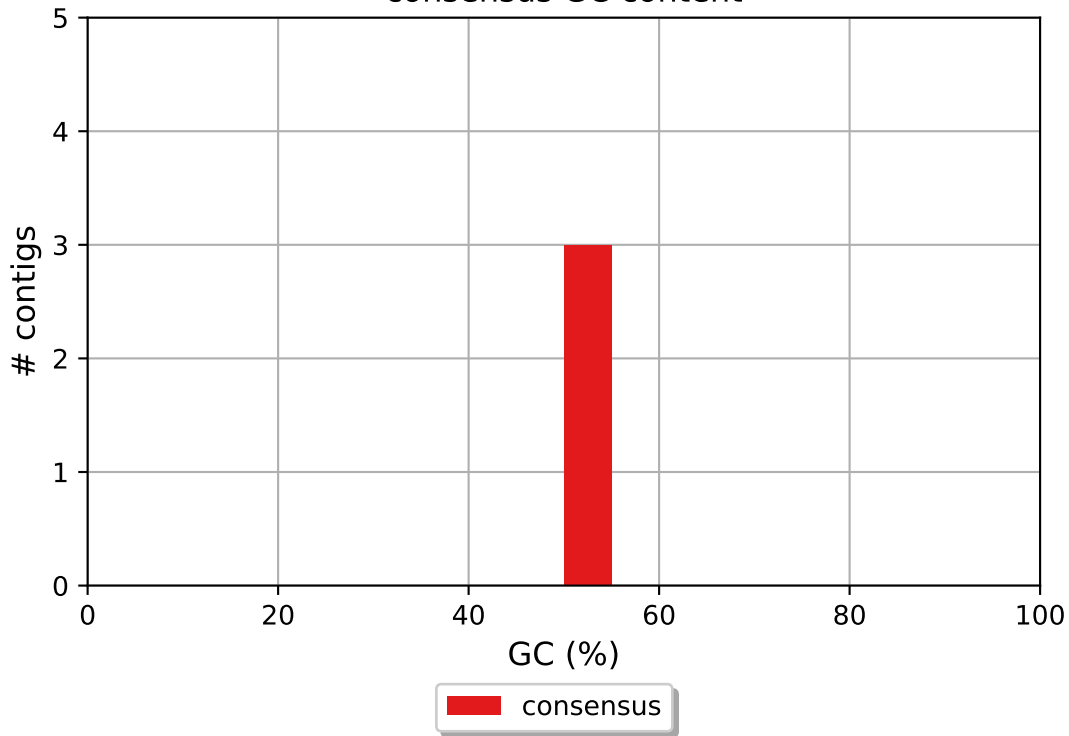
— consensus



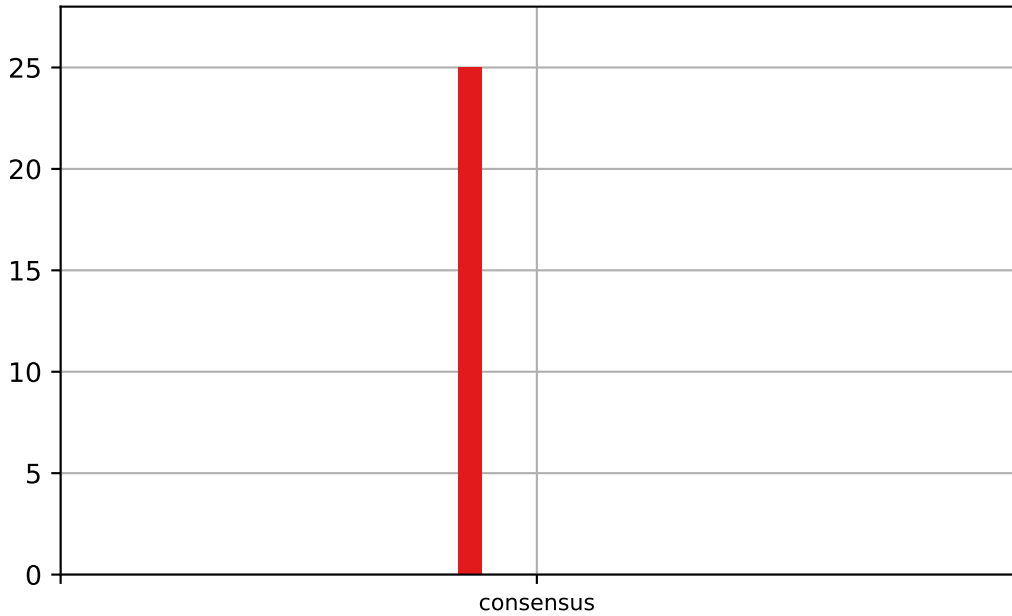
GC content



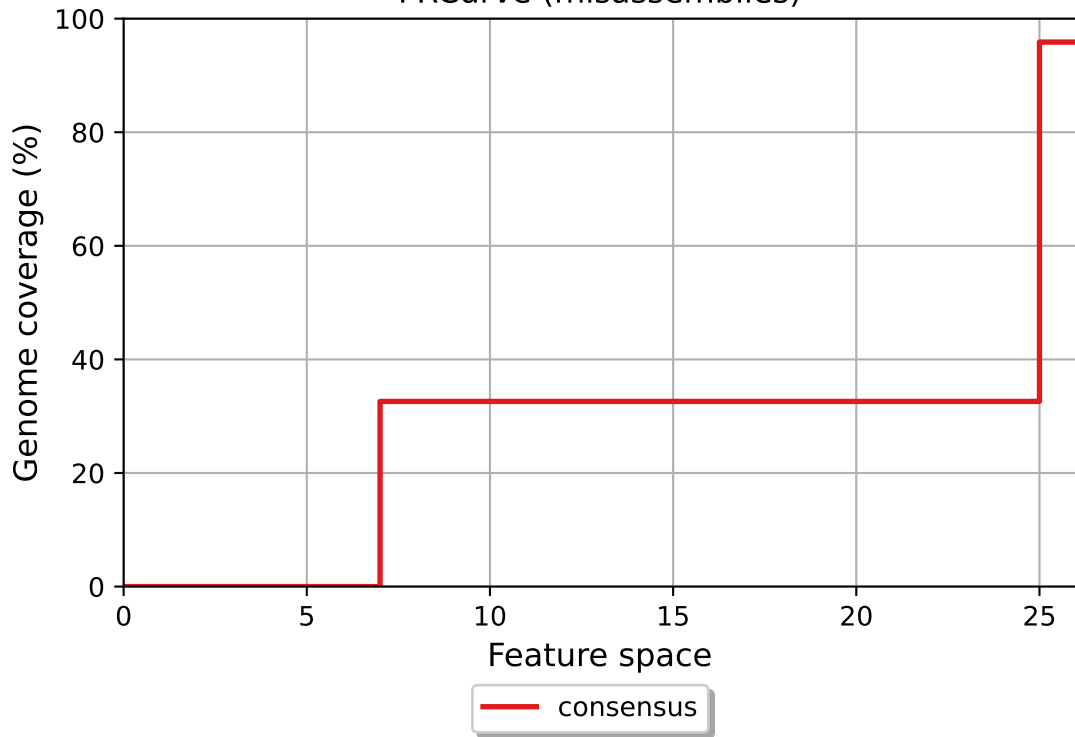
consensus GC content



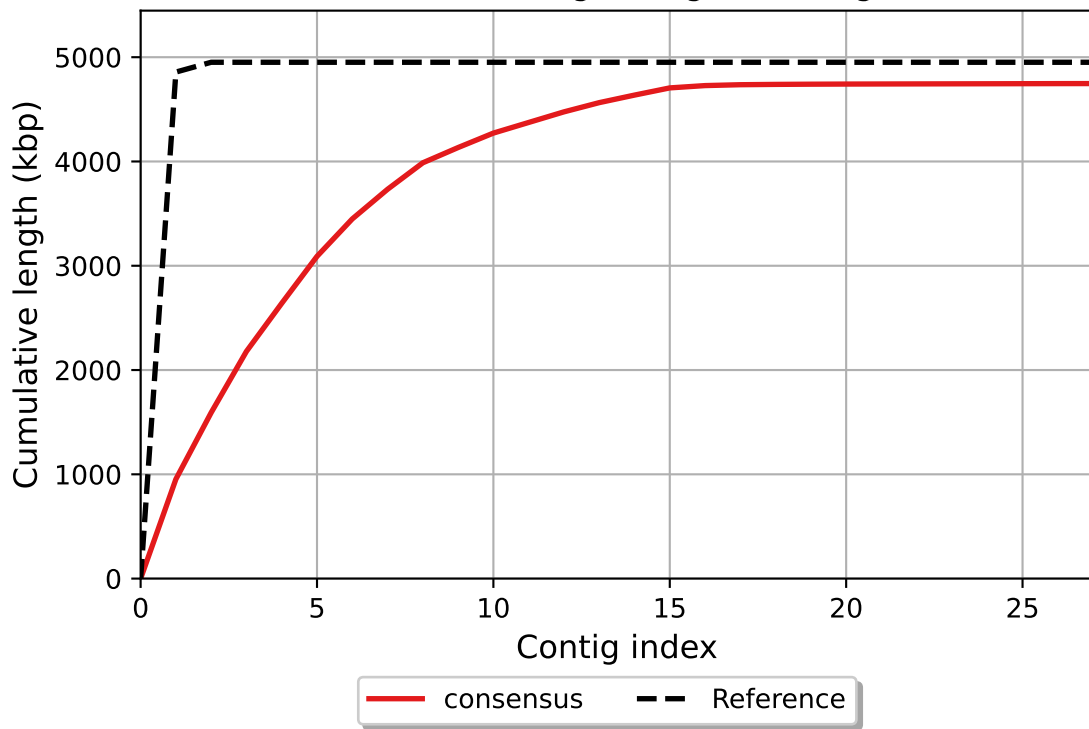
Misassemblies



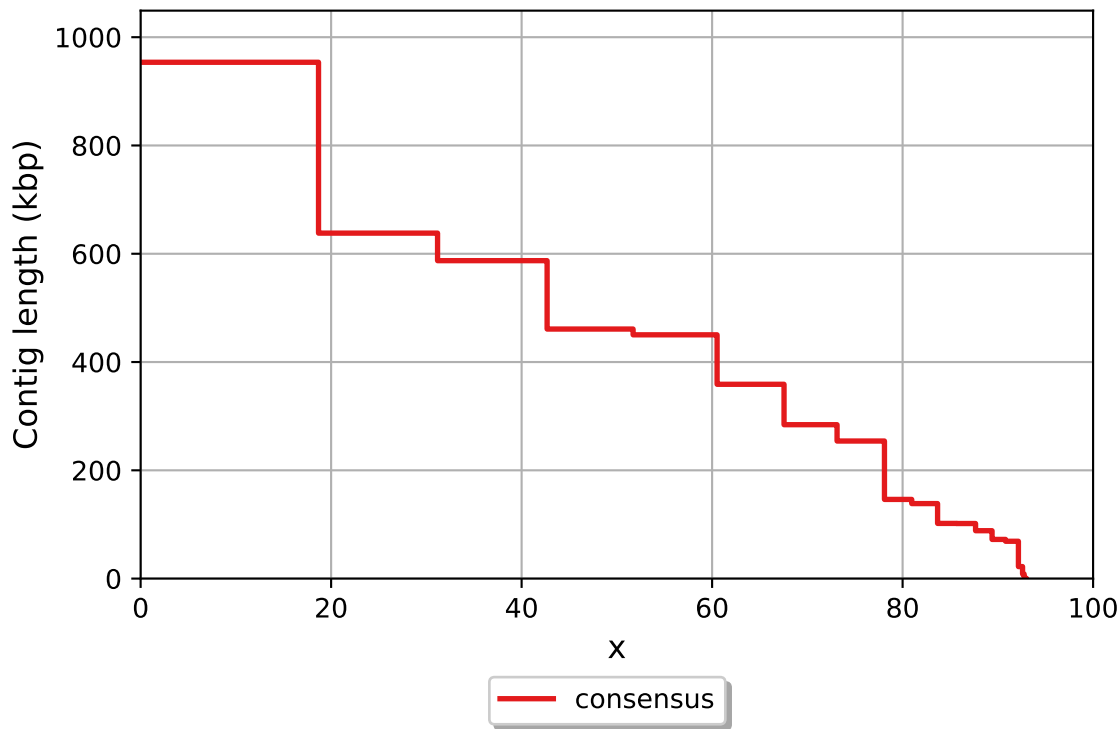
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

