

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)	5104808
Total length (>= 1000 bp)	5104808
Total length (>= 5000 bp)	5104808
Total length (>= 10000 bp)	5104808
Total length (>= 25000 bp)	5104808
Total length (>= 50000 bp)	5104808
# contigs	3
Largest contig	3318770
Total length	5104808
Reference length	4951383
GC (%)	52.19
Reference GC (%)	52.24
N50	3318770
NG50	3318770
N90	1676979
NG90	1676979
auN	2710853.5
auNG	2794852.8
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	25
# misassembled contigs	2
Misassembled contigs length	4995749
# 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	27.10
# indels per 100 kbp	3.62
Largest alignment	953688
Total aligned length	4746091
NA50	460923
NGA50	460923
NA90	72349
NGA90	101719
auNA	476077.8
auNGA	490829.7
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

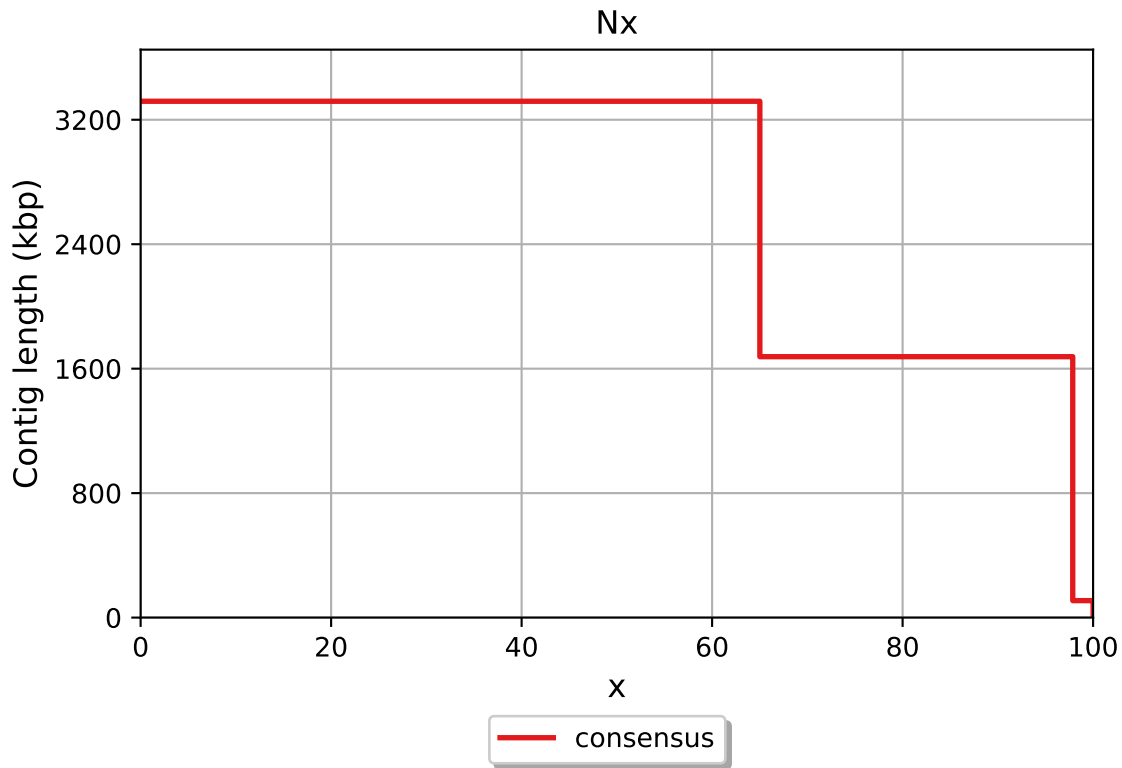
	consensus
# misassemblies	25
# contig misassemblies	25
# c. relocations	25
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	4995749
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1286
# indels	172
# indels (<= 5 bp)	142
# indels (> 5 bp)	30
Indels length	2627

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).

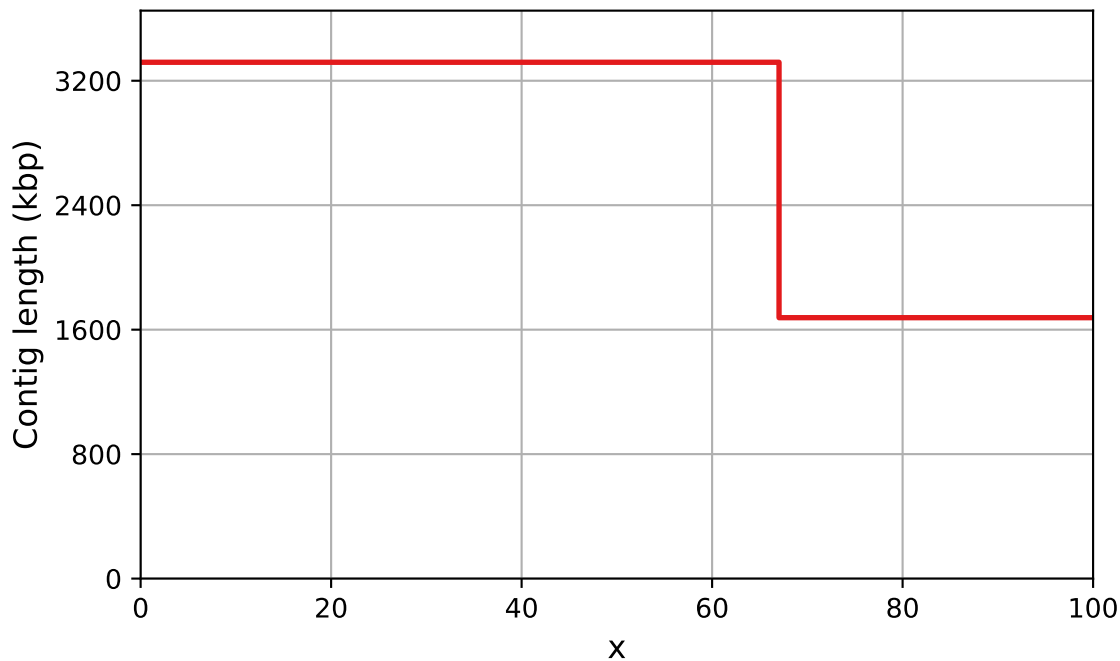
## Unaligned report

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

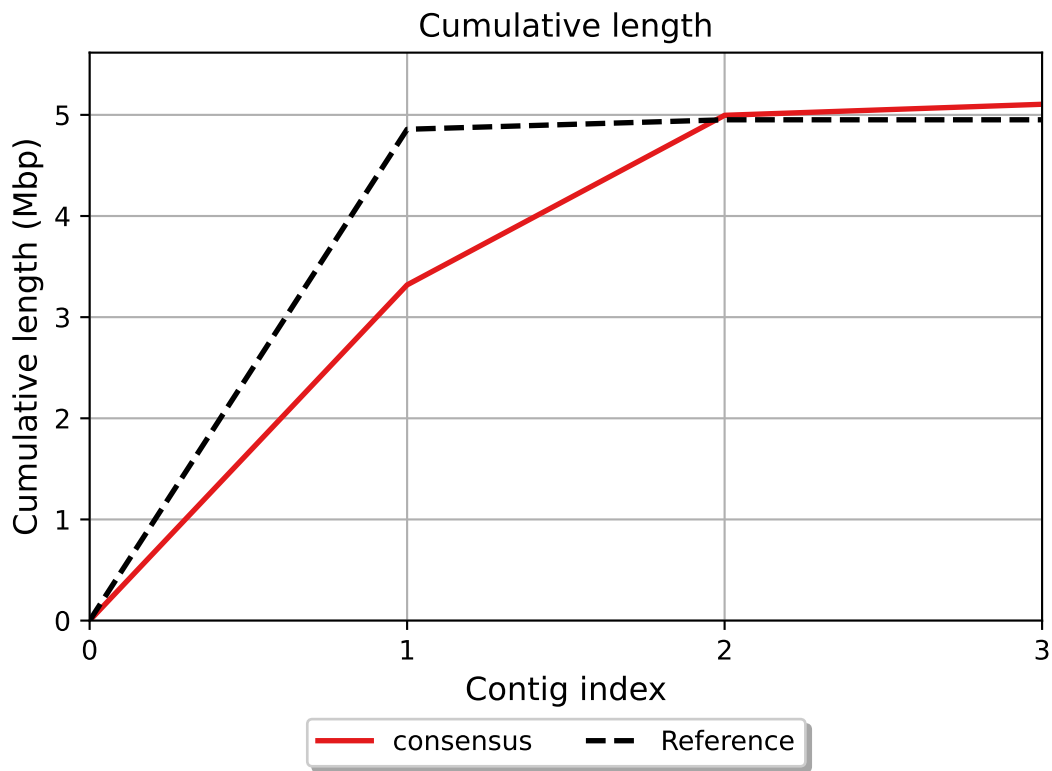
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



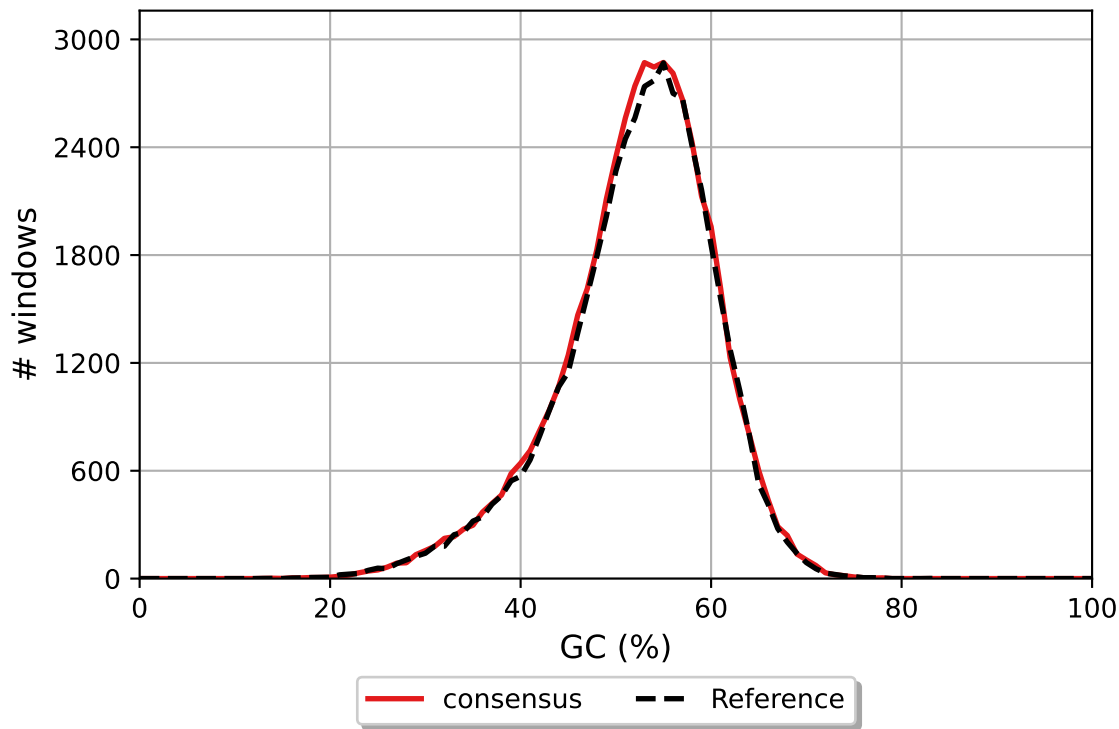
NGx



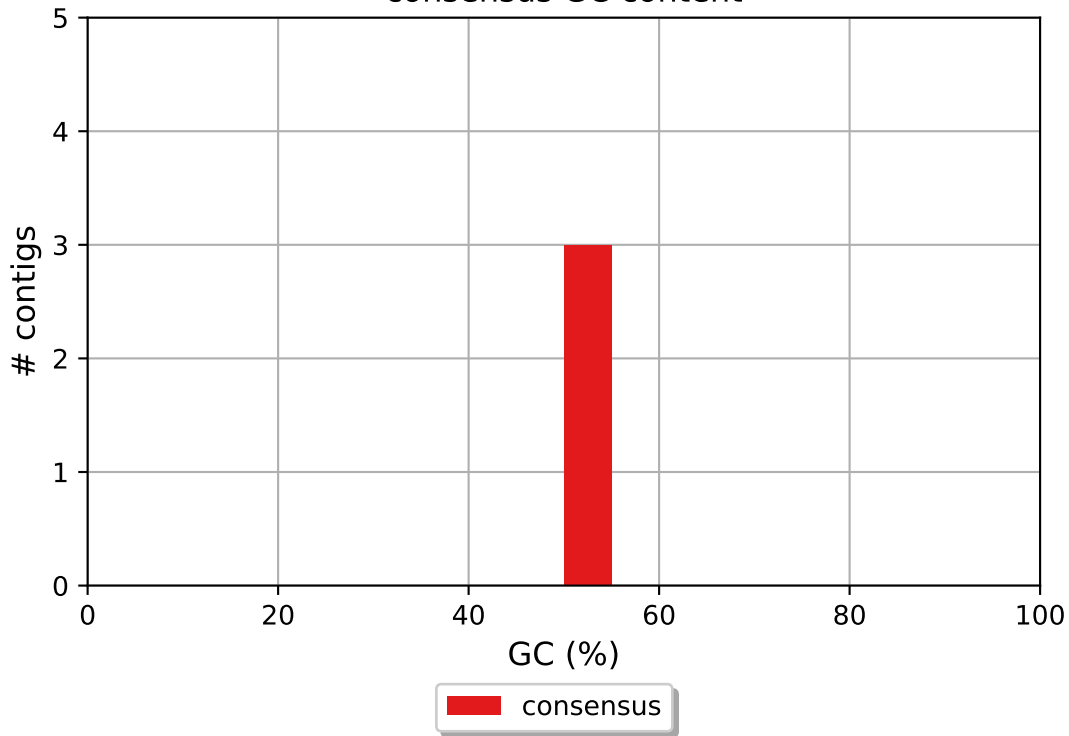
consensus



## GC content

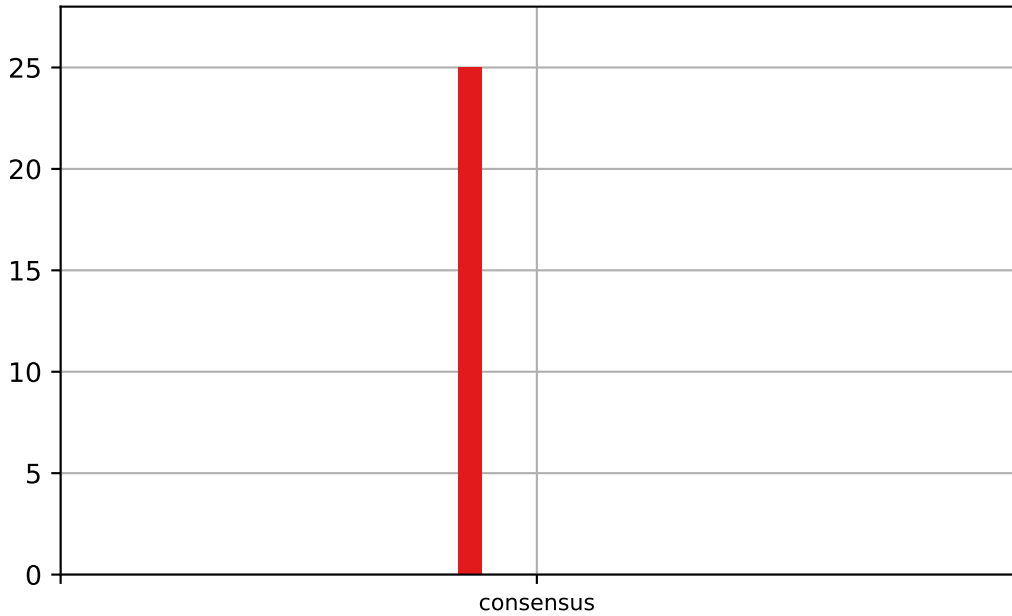


consensus GC content

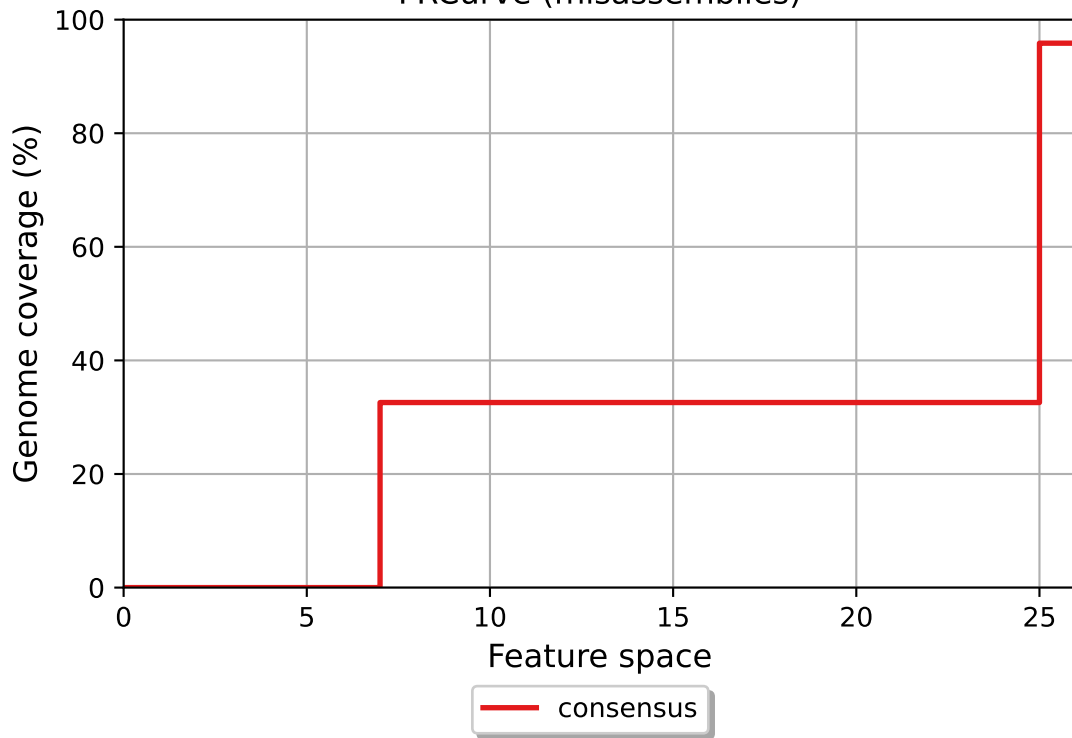




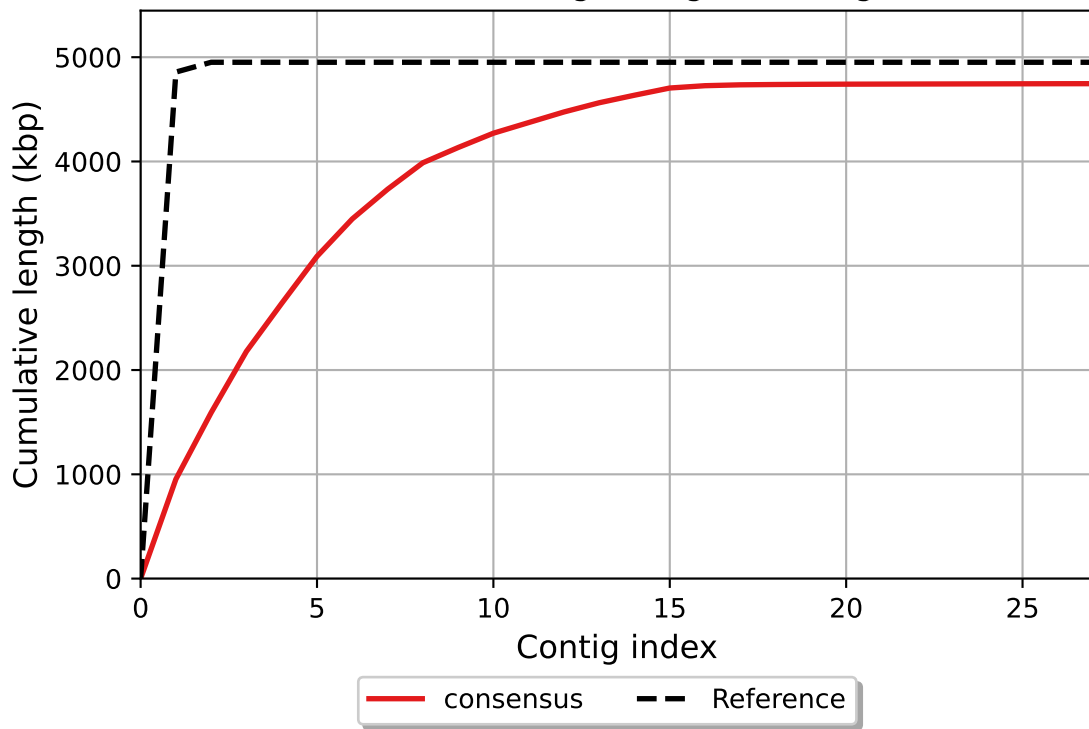
## Misassemblies



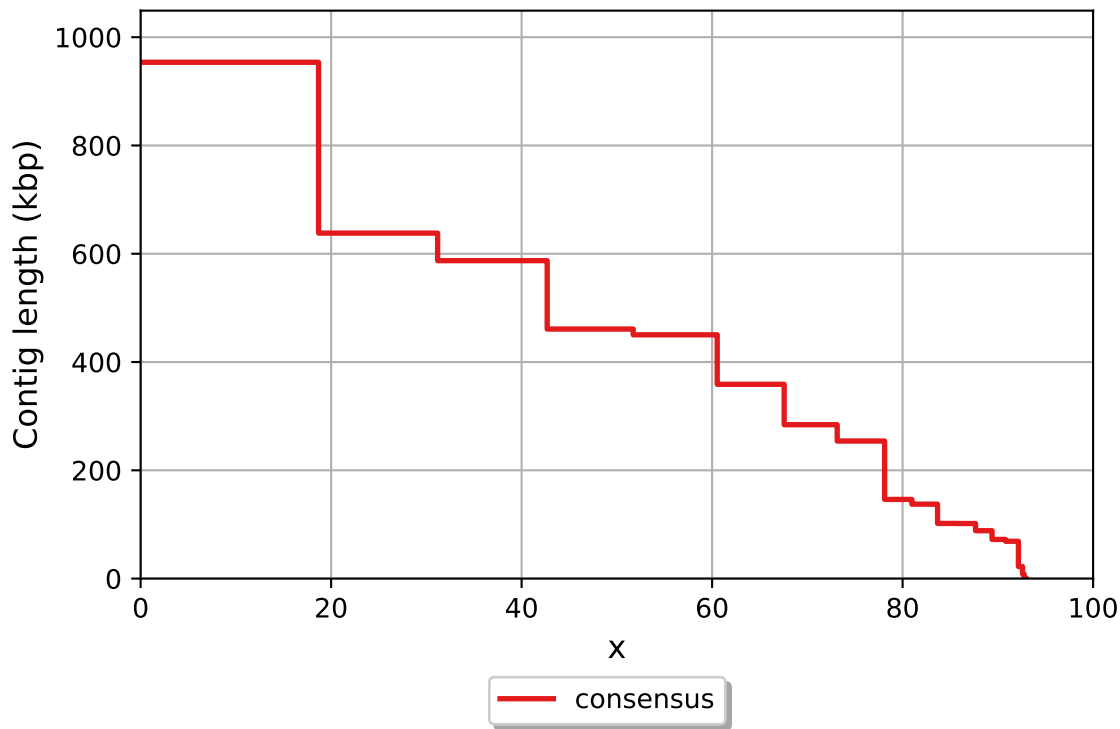
FRCurve (misassemblies)



Cumulative length (aligned contigs)



# NAx



# NGAx

