

Report

	consensus
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	5147510
Total length (>= 1000 bp)	5147510
Total length (>= 5000 bp)	5147510
Total length (>= 10000 bp)	5147510
Total length (>= 25000 bp)	5147510
Total length (>= 50000 bp)	5147510
# contigs	4
Largest contig	4708308
Total length	5147510
Reference length	4951383
GC (%)	52.19
Reference GC (%)	52.24
N50	4708308
NG50	4708308
N90	4708308
NG90	4708308
auN	4319172.3
aUNG	4490257.1
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	28
# misassembled contigs	2
Misassembled contigs length	4855832
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 1 part
Unaligned length	379398
Genome fraction (%)	95.670
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.64
# indels per 100 kbp	4.28
Largest alignment	953685
Total aligned length	4762956
NA50	460924
NGA50	460924
NA90	59287
NGA90	88434
auNA	464558.4
aUNGA	482959.8
LA50	4
LGA50	4
LA90	17
LGA90	14

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	28
# contig misassemblies	28
# c. relocations	28
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	4855832
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1364
# indels	204
# indels (<= 5 bp)	172
# indels (> 5 bp)	32
Indels length	2687

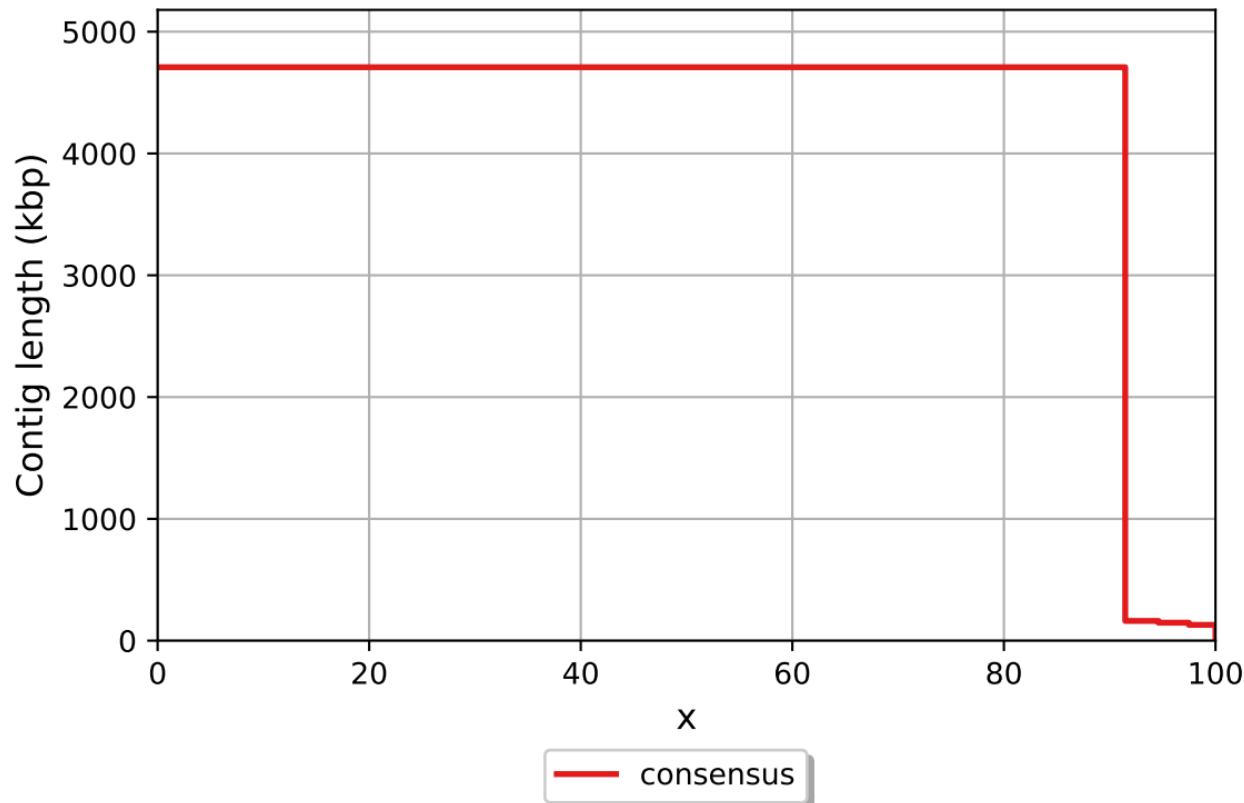
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

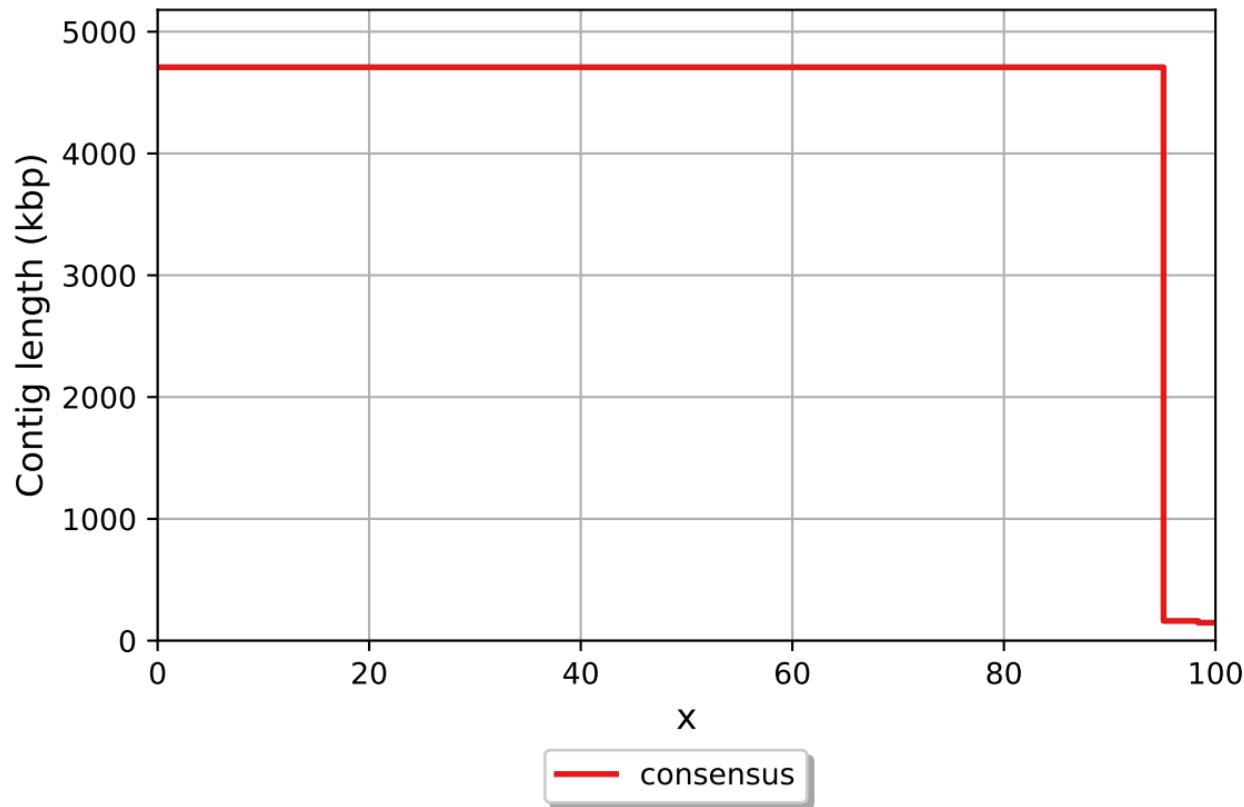
	consensus
# fully unaligned contigs	1
Fully unaligned length	129760
# partially unaligned contigs	1
Partially unaligned length	249638
# N's	0

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).

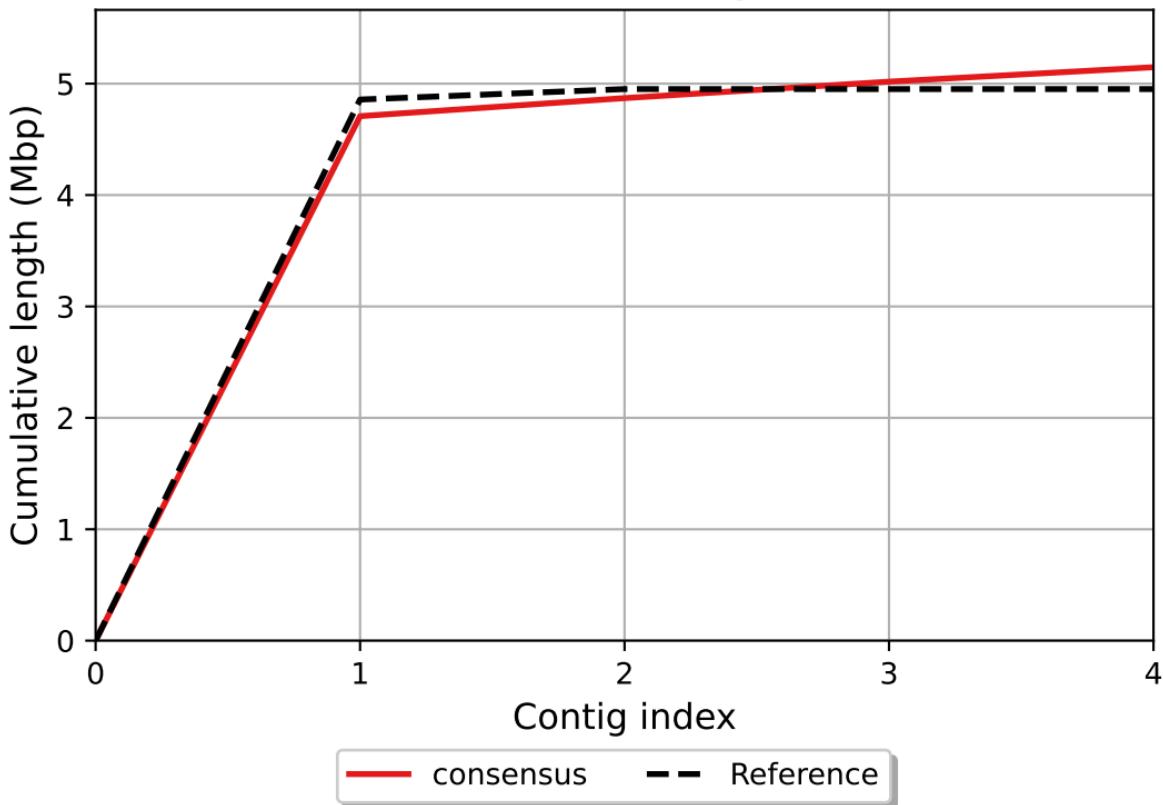
Nx



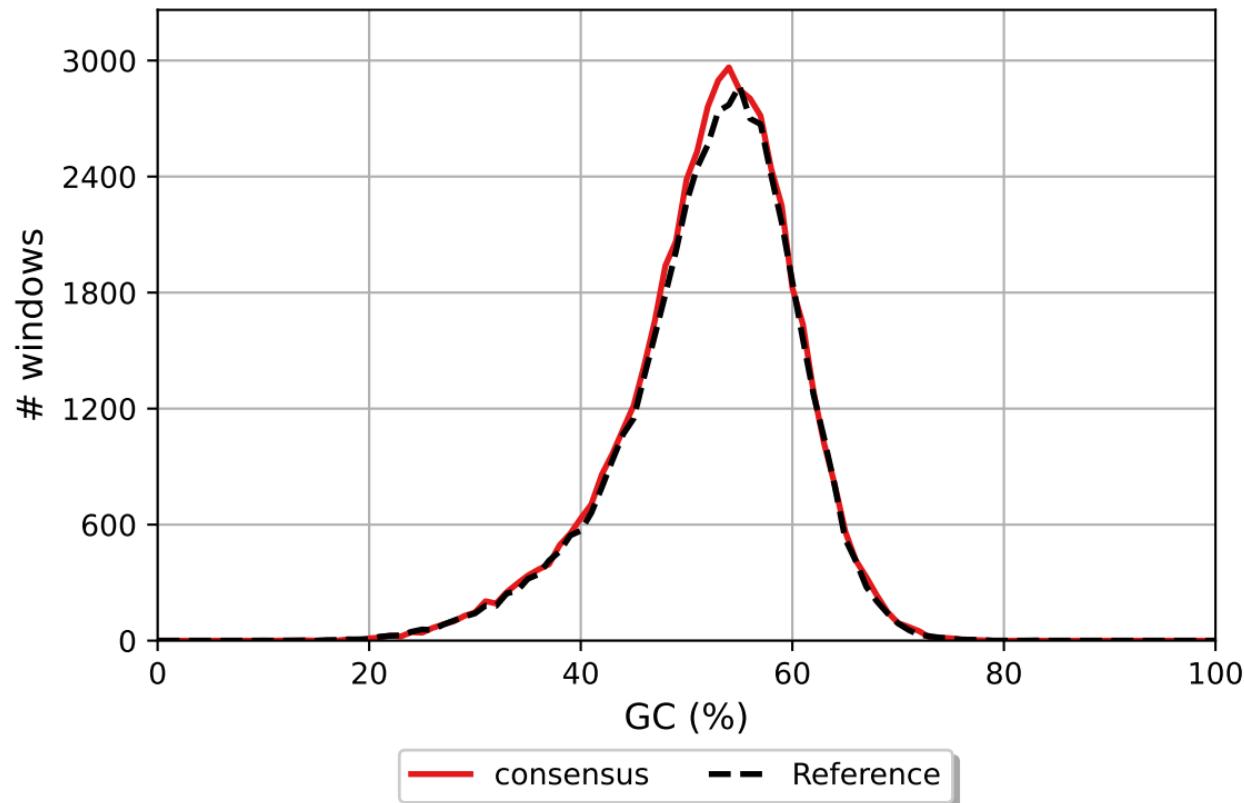
NGx



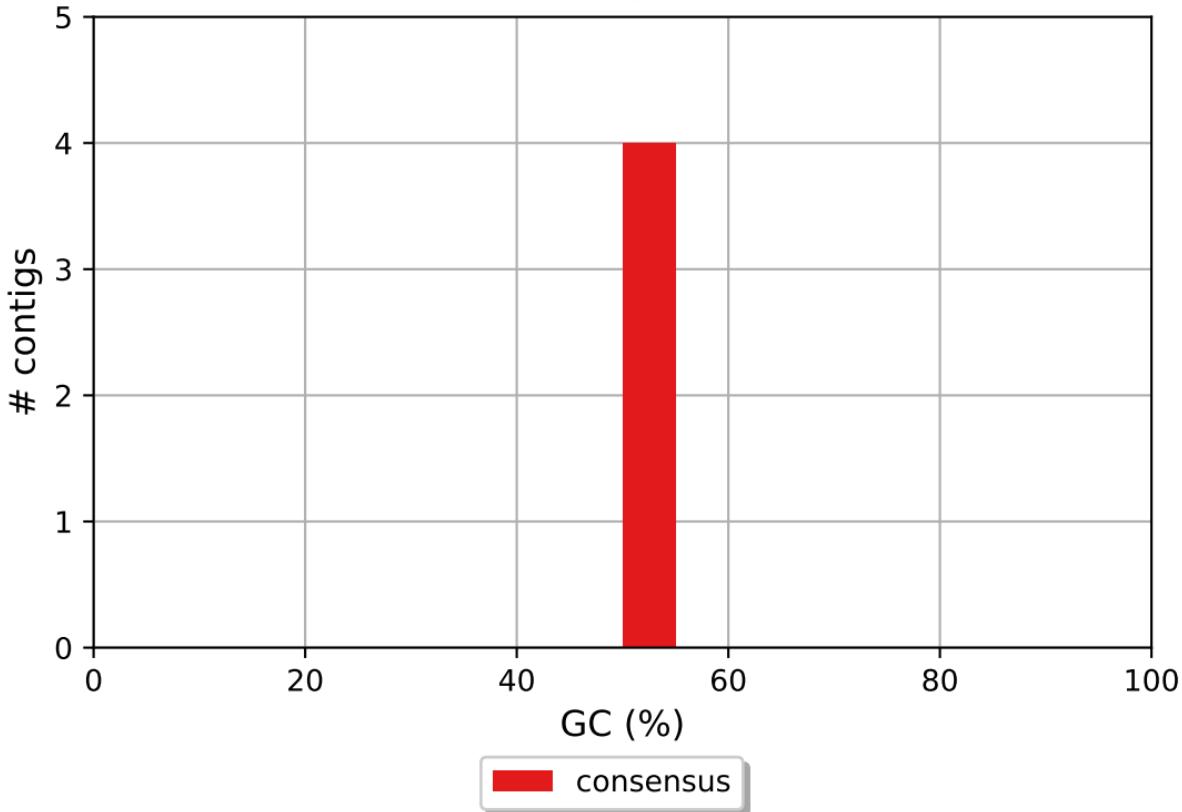
Cumulative length



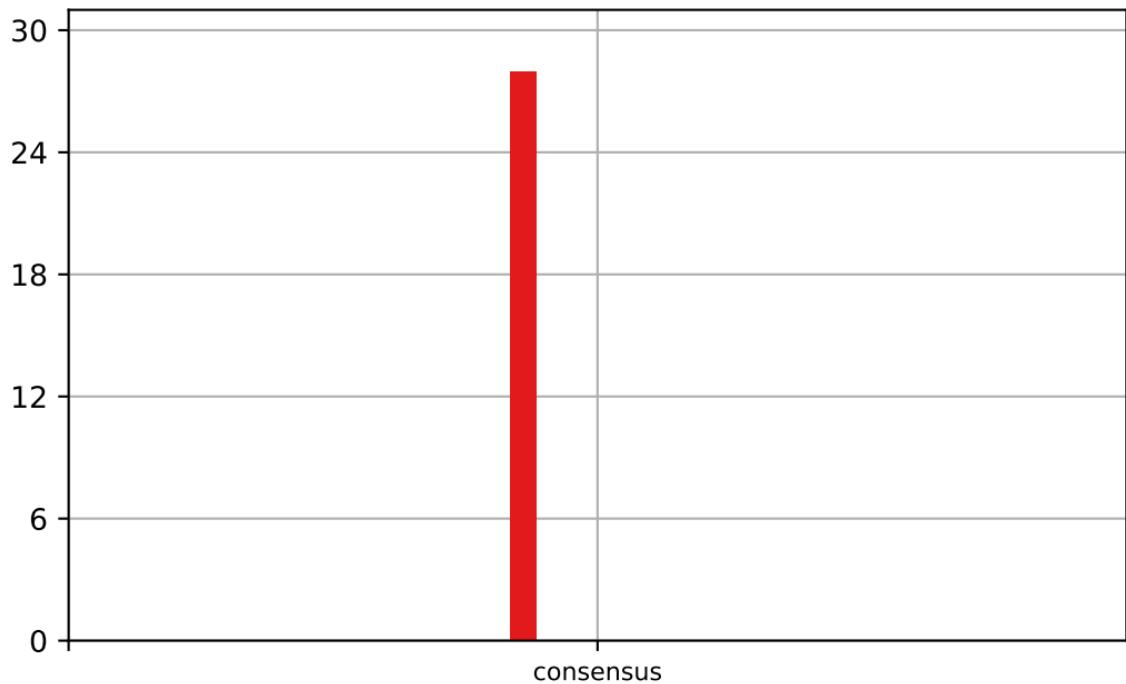
GC content



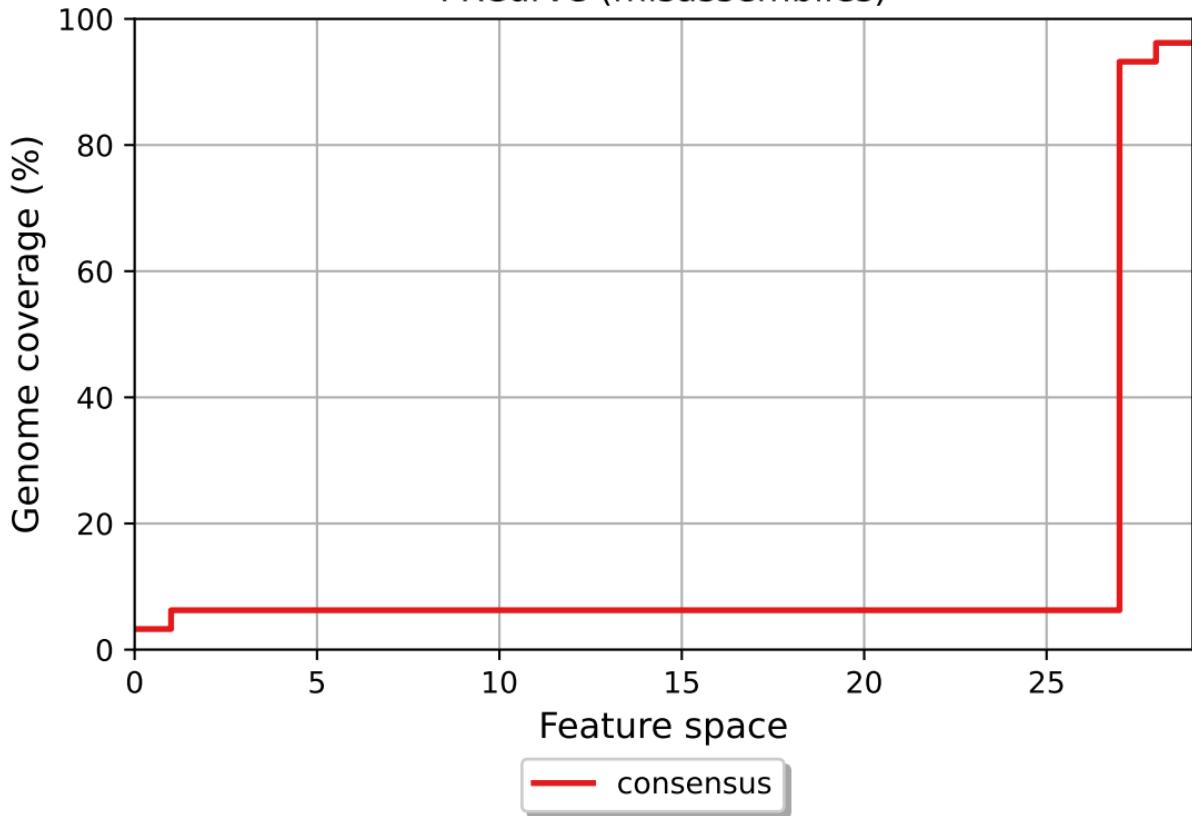
consensus GC content



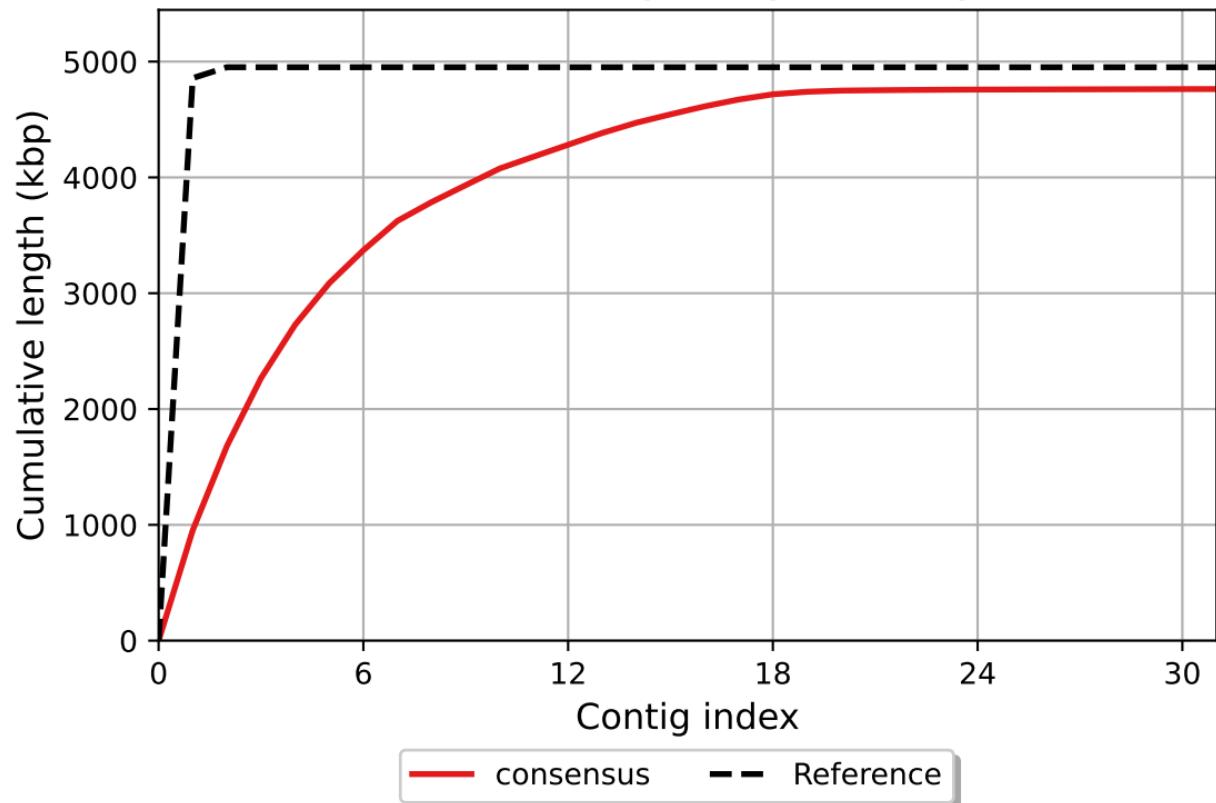
Misassemblies



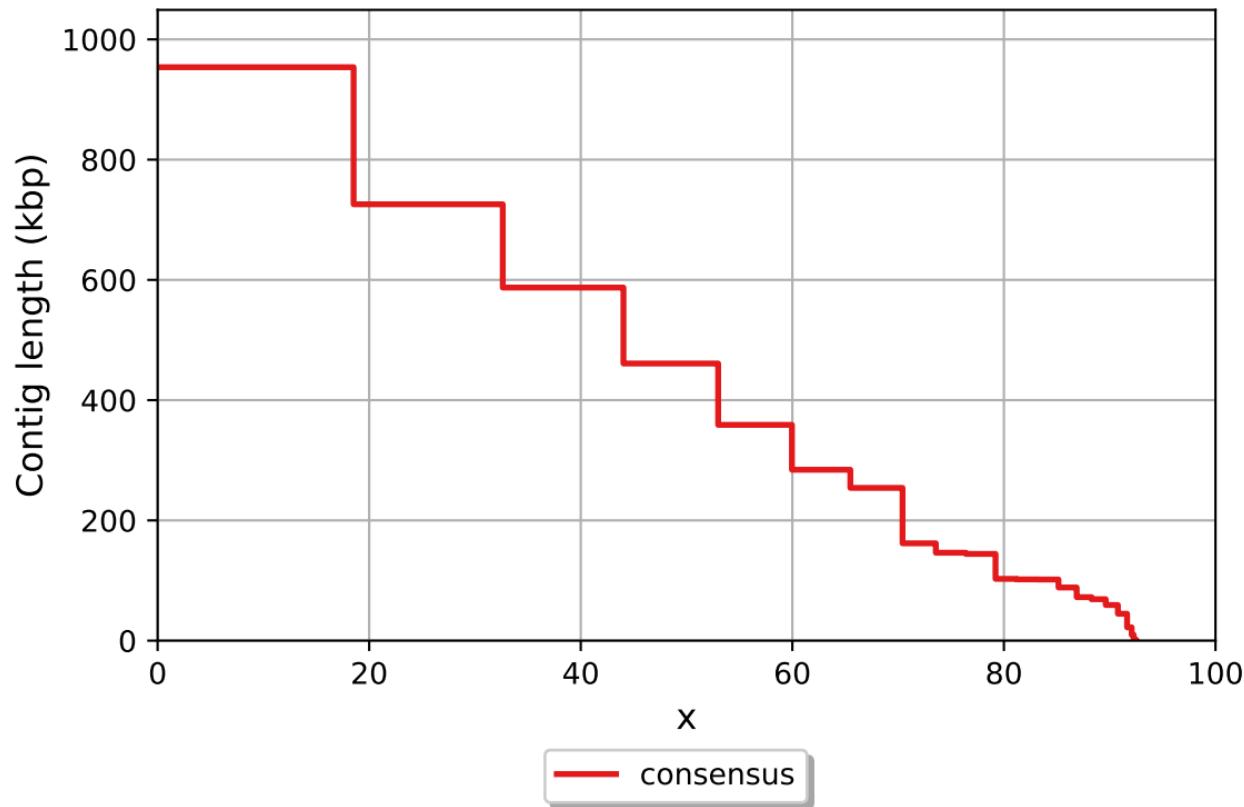
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

