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)	5147489
Total length (>= 1000 bp)	5147489
Total length (>= 5000 bp)	5147489
Total length (>= 10000 bp)	5147489
Total length (>= 25000 bp)	5147489
Total length (>= 50000 bp)	5147489
# contigs	4
Largest contig	4708310
Total length	5147489
Reference length	4951383
GC (%)	52.19
Reference GC (%)	52.24
N50	4708310
NG50	4708310
N90	4708310
NG90	4708310
auN	4319192.4
auNG	4490259.7
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	28
# misassembled contigs	2
Misassembled contigs length	4855834
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 1 part
Unaligned length	379375
Genome fraction (%)	95.670
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.04
# indels per 100 kbp	4.33
Largest alignment	953687
Total aligned length	4762958
NA50	460925
NGA50	460925
NA90	59287
NGA90	88434
auNA	464562.6
auNGA	482962.2
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

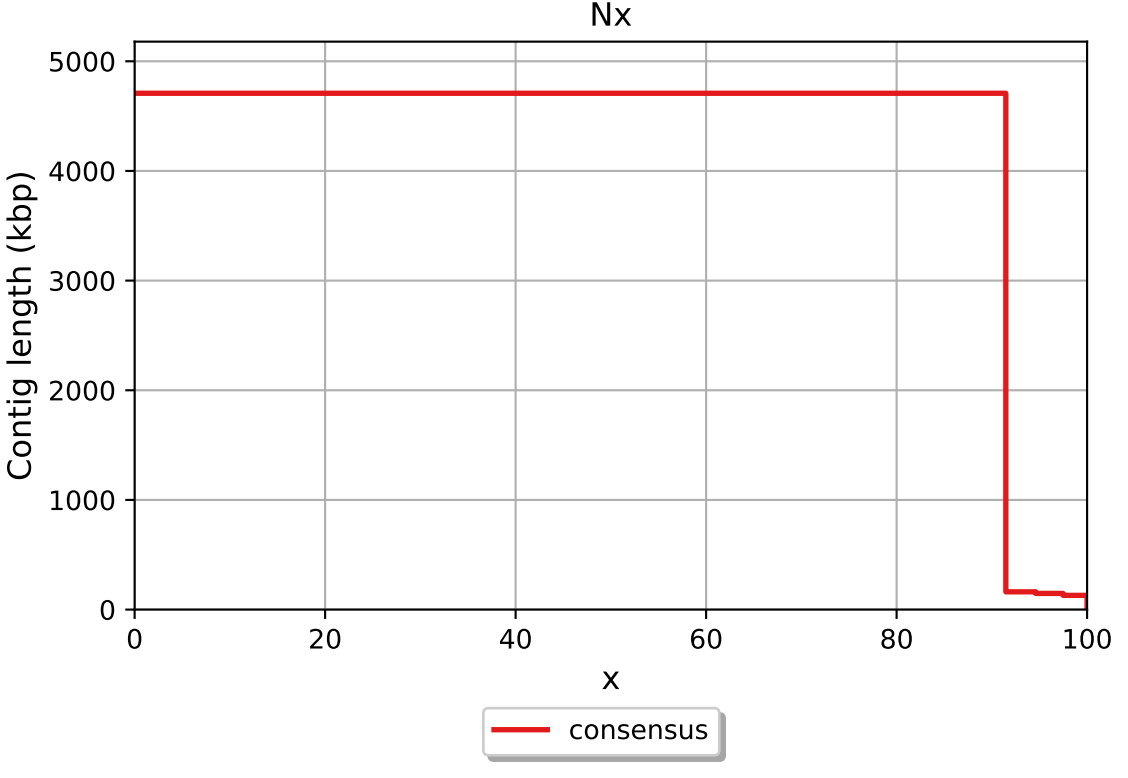
	consensus
# misassemblies	28
# contig misassemblies	28
# c. relocations	28
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	4855834
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1383
# indels	206
# indels (<= 5 bp)	174
# indels (> 5 bp)	32
Indels length	2689

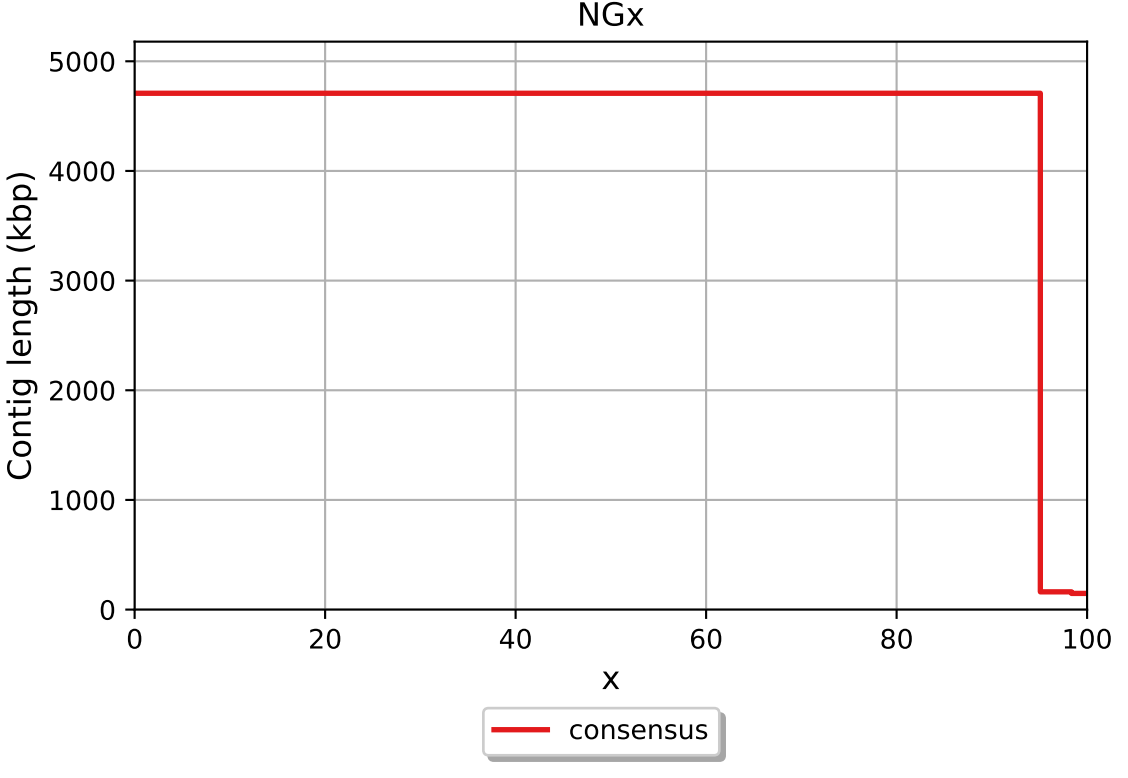
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

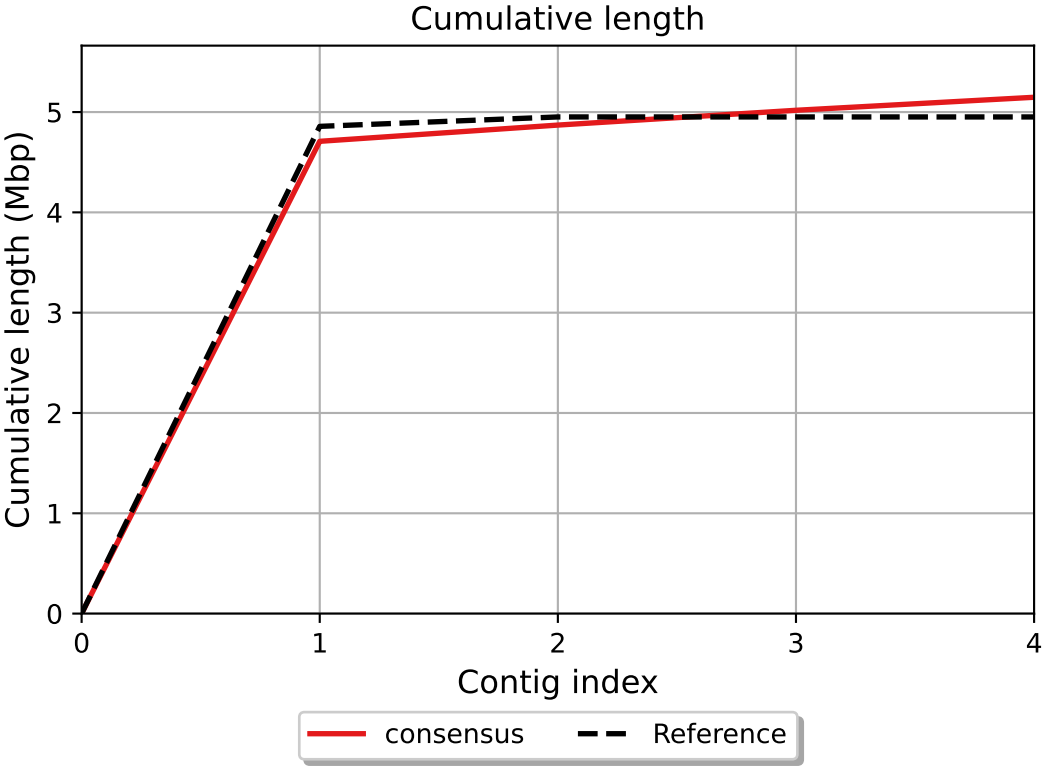
Unaligned report

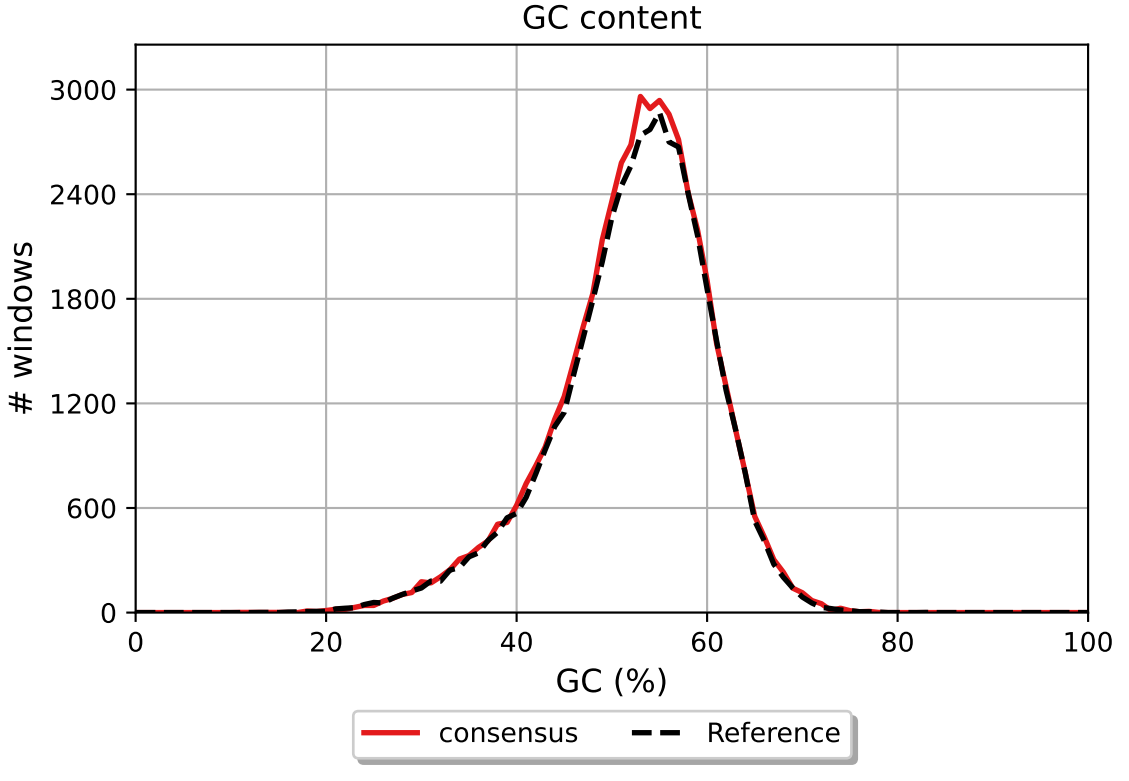
	consensus
# fully unaligned contigs	1
Fully unaligned length	129737
# partially unaligned contigs	1
Partially unaligned length	249638
# N's	0

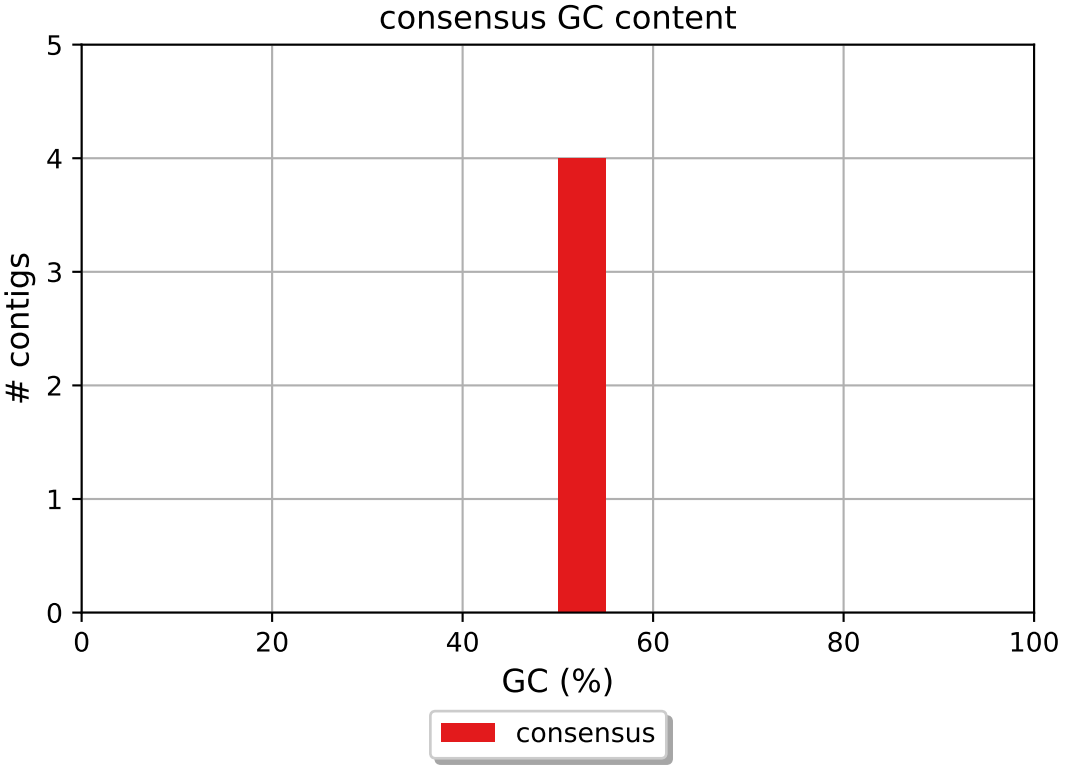
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

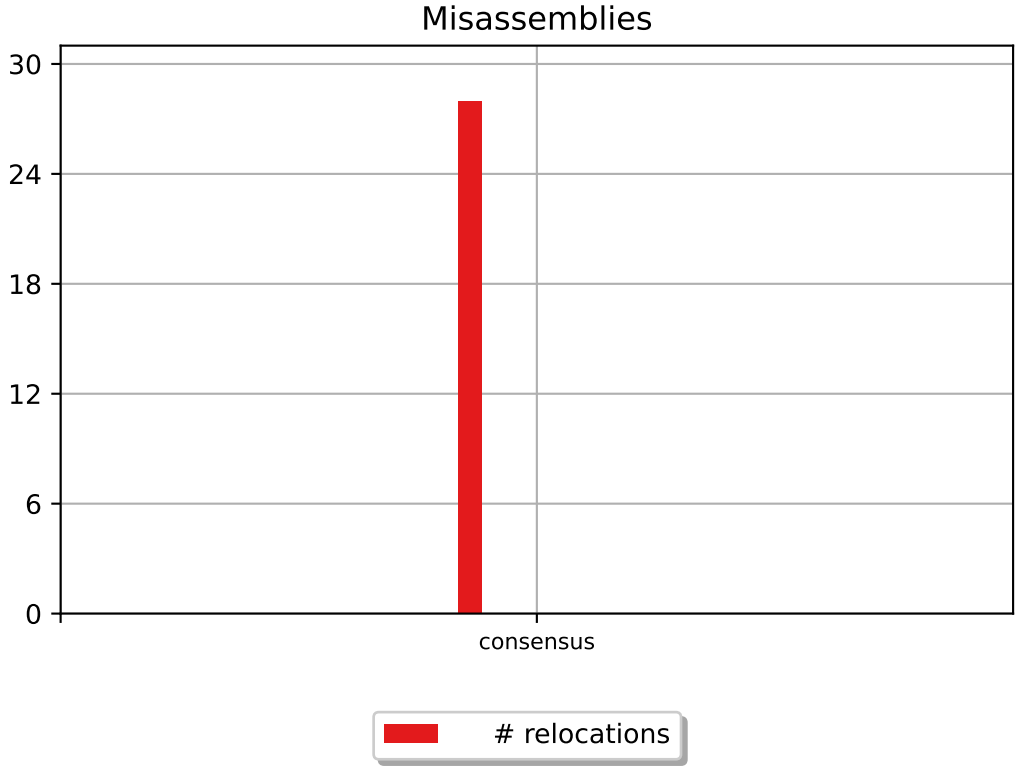

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
consensus

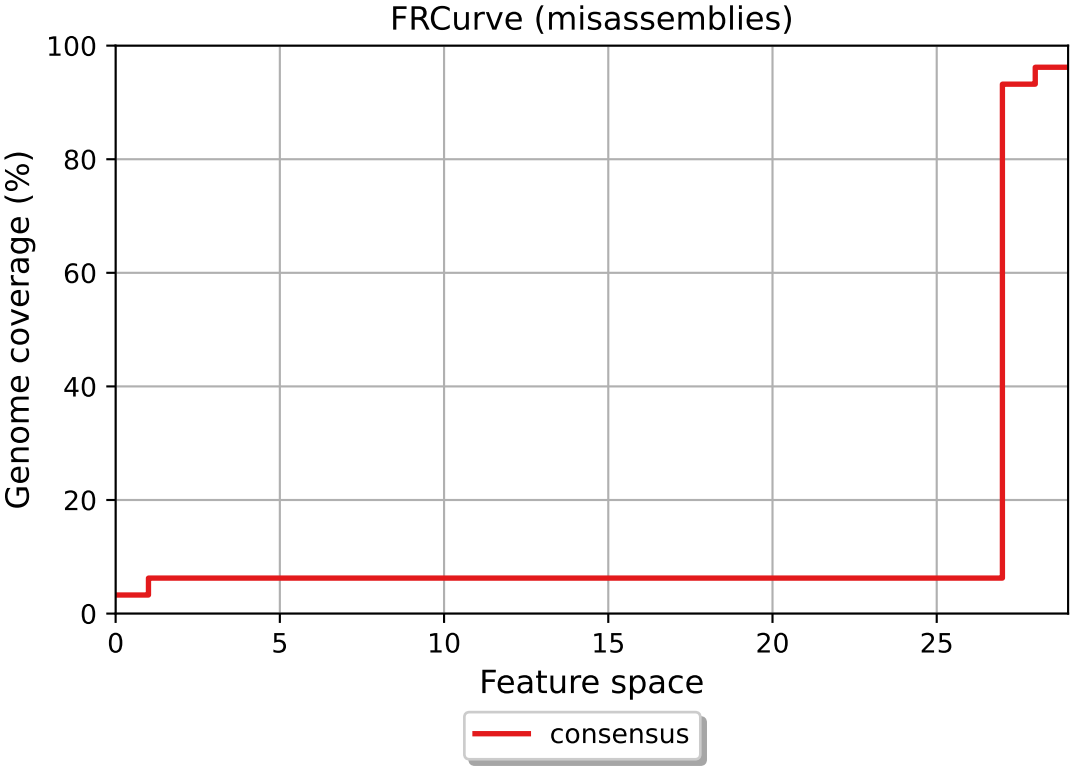

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
consensus

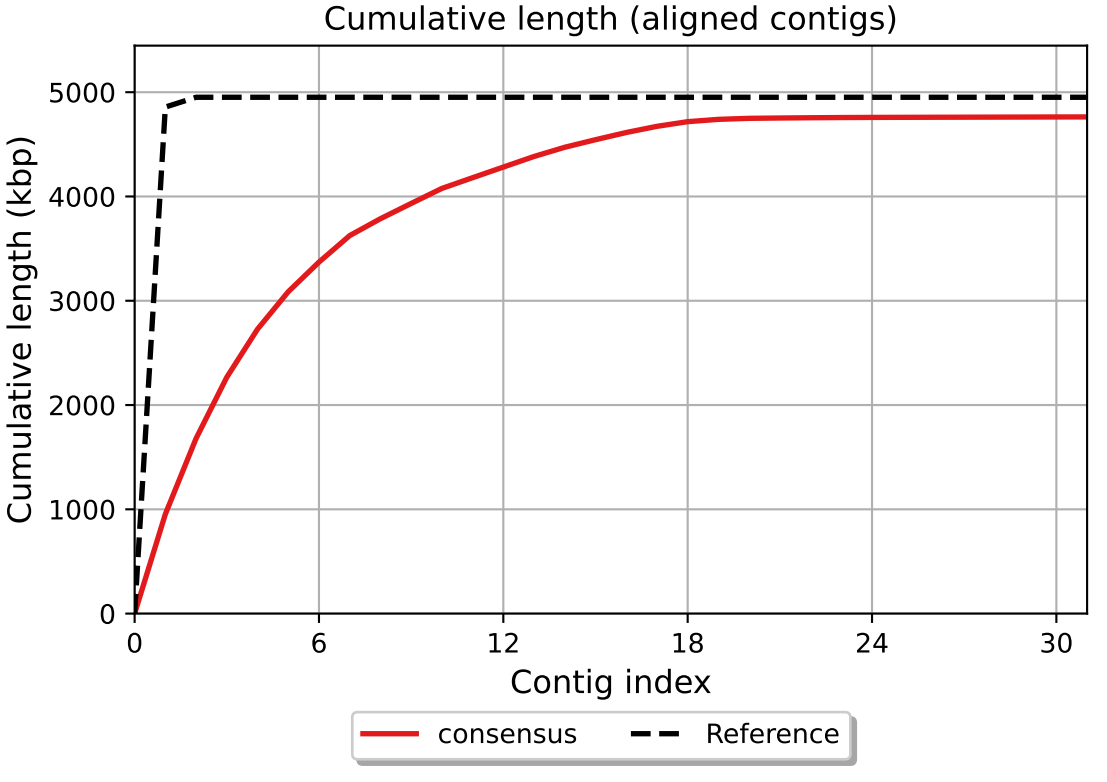

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
1
2
3
4
Contig index
consensus
Reference

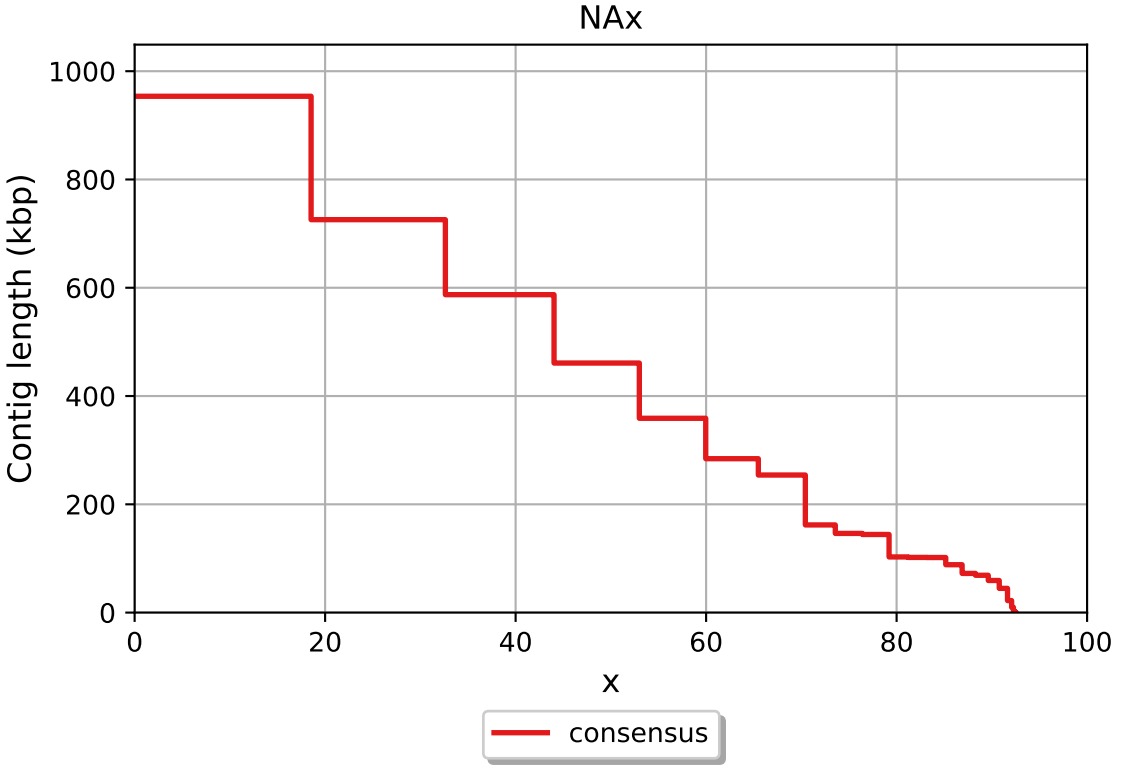

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
consensus
Reference

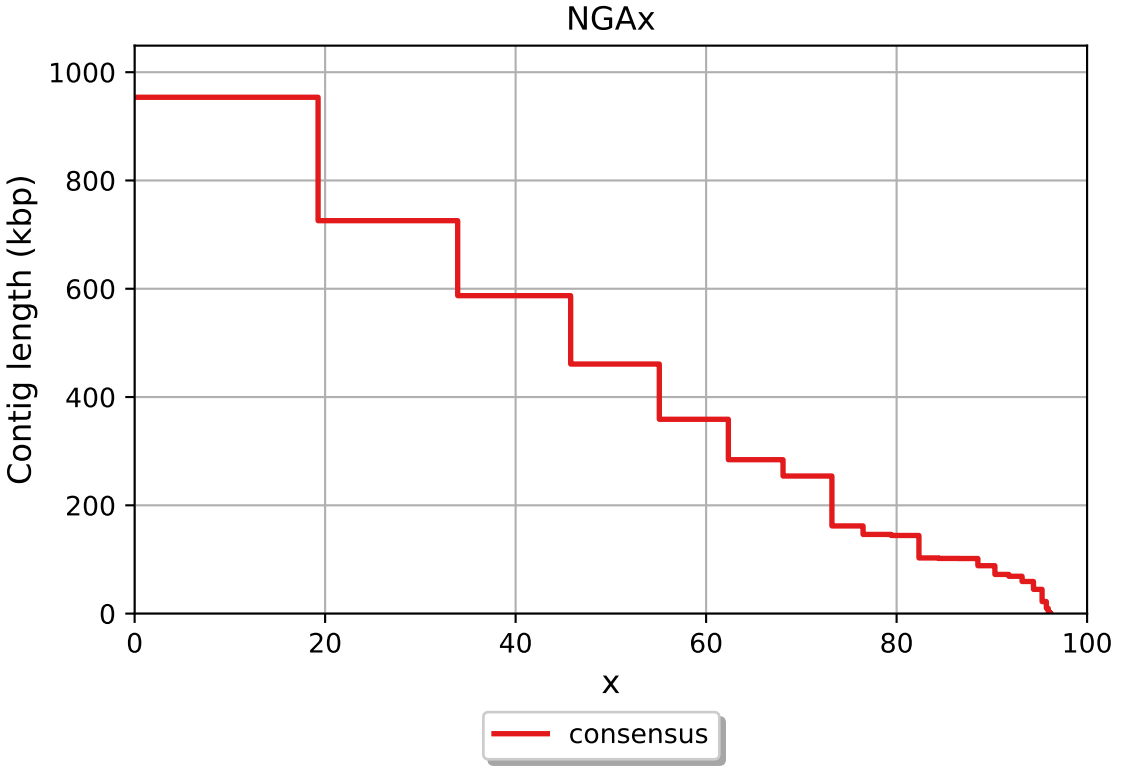

consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
consensus


Misassemblies
30
24
18
12
6
0
consensus
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
consensus


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
6
12
18
24
30
Contig index
consensus
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
consensus


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
consensus