Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	20486
Total length (>= 5000 bp)	8785
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	18
Largest contig	8785
Total length	27561
Reference length	4633577
GC (%)	45.14
Reference GC (%)	36.49
N50	2207
N75	850
L50	3
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	3 + 10 part
Unaligned length	23083
Genome fraction (%)	0.034
Duplication ratio	2.802
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3754.69
# indels per 100 kbp	0.00
Largest alignment	224
Total aligned length	2018
NGA50	-

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

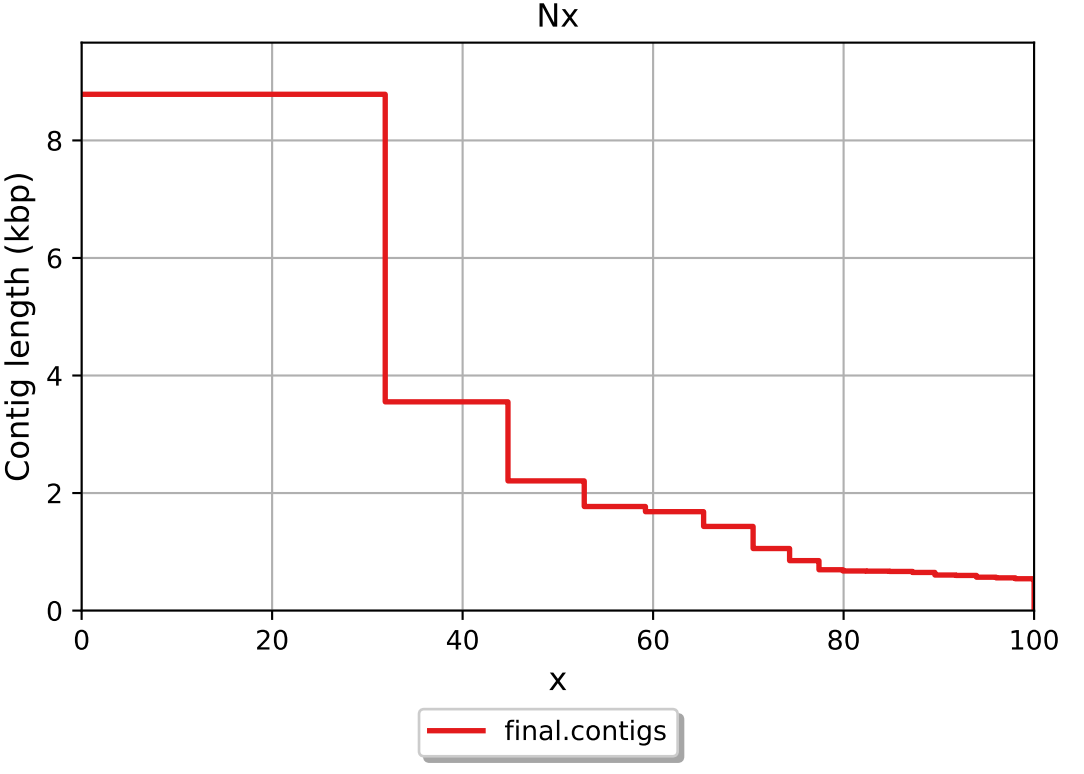
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	5
# possible misassemblies	7
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	60
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

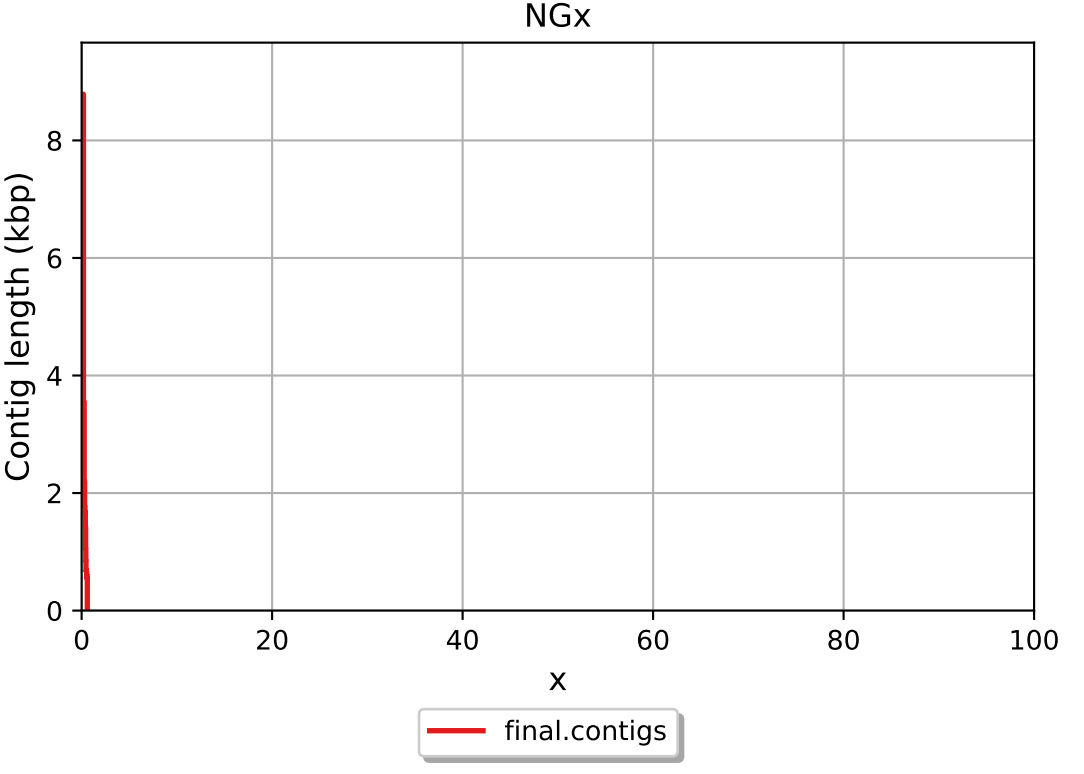
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

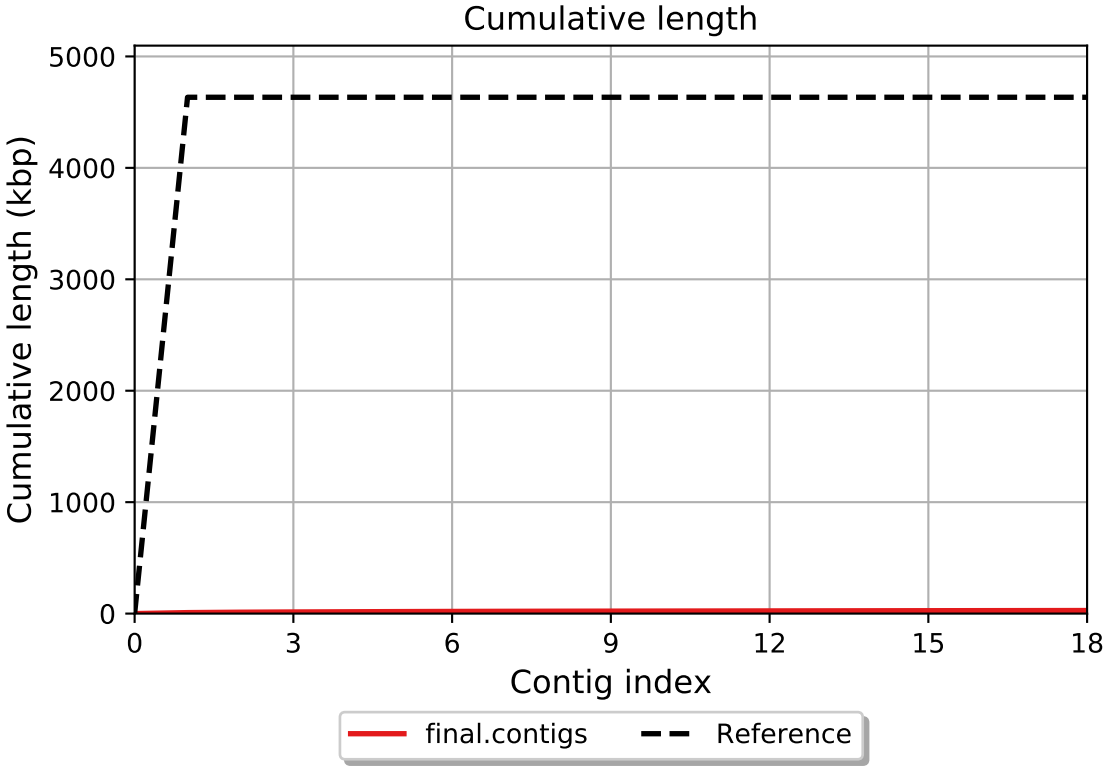
Unaligned report

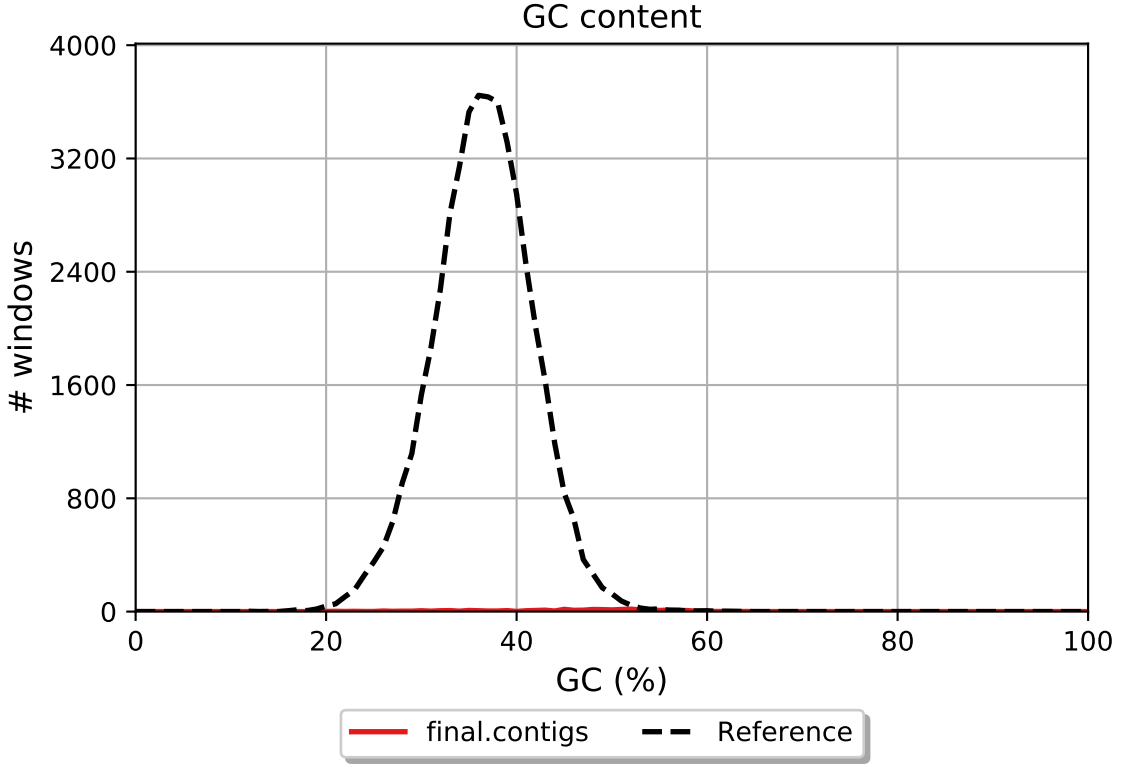
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	2018
# partially unaligned contigs	10
Partially unaligned length	21065
# N's	0

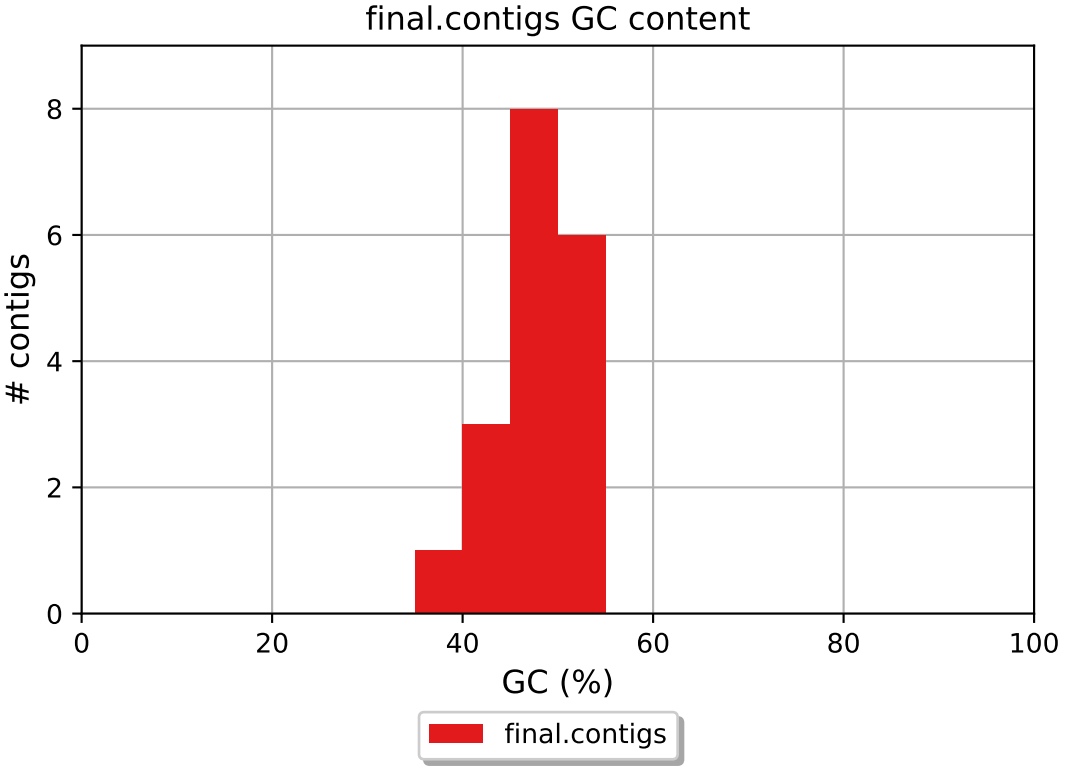
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

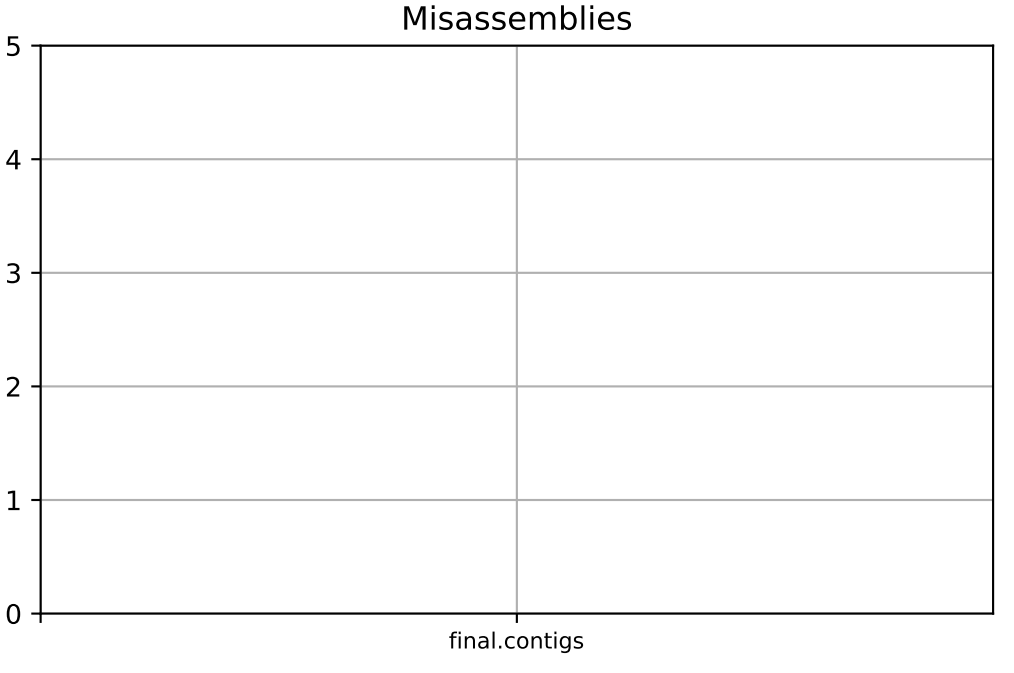

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

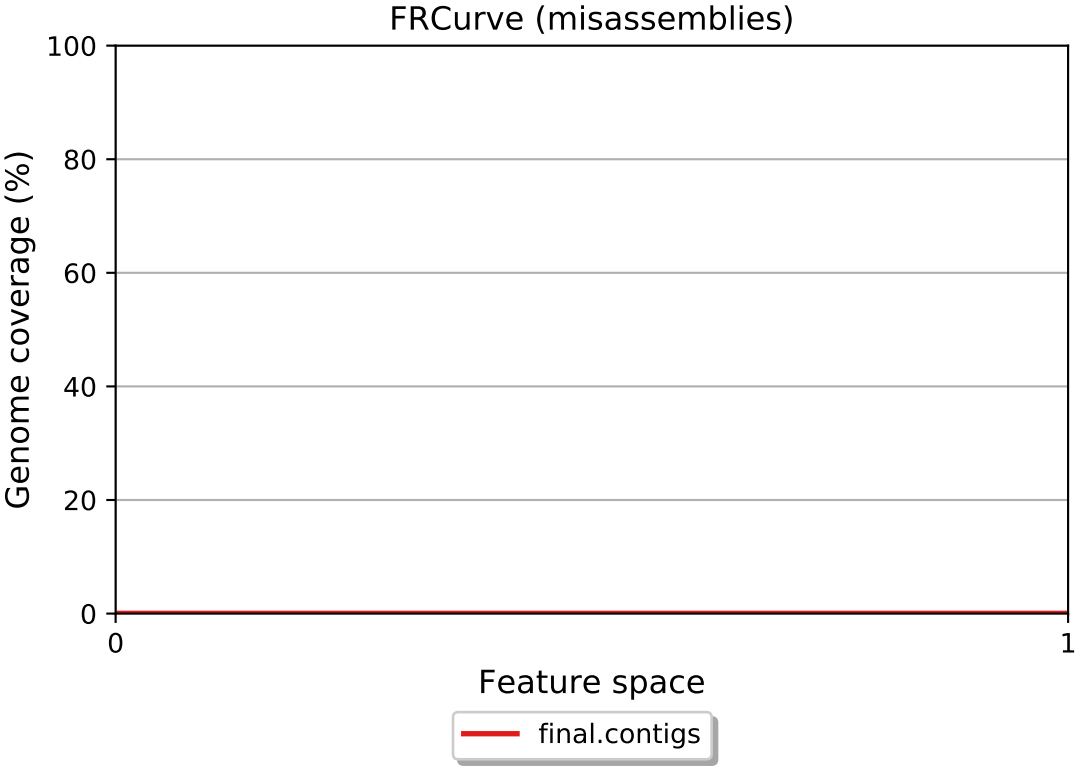

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

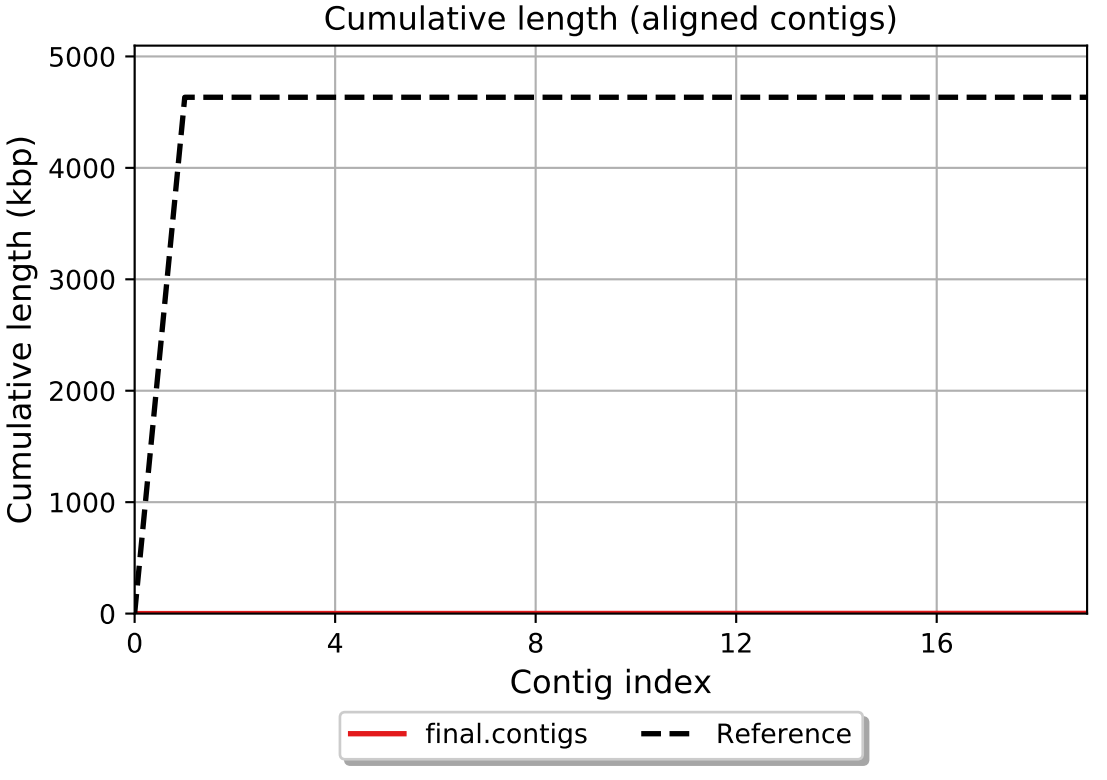

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
18
Contig index
final.contigs
Reference

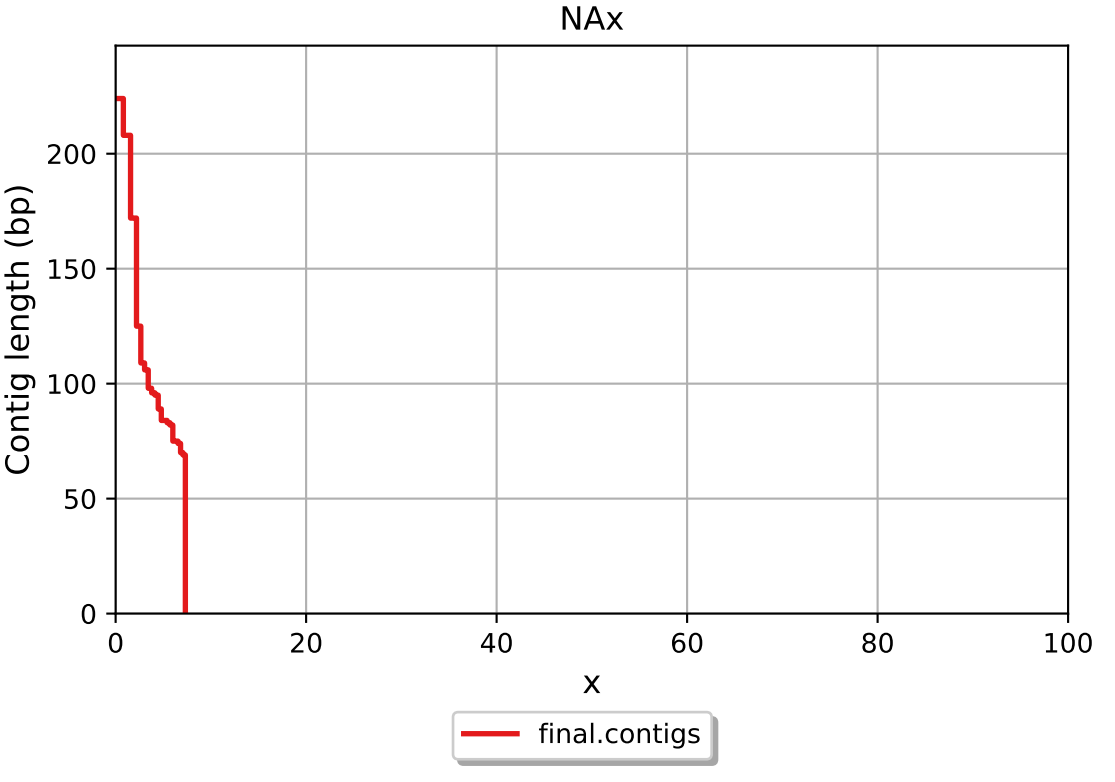

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

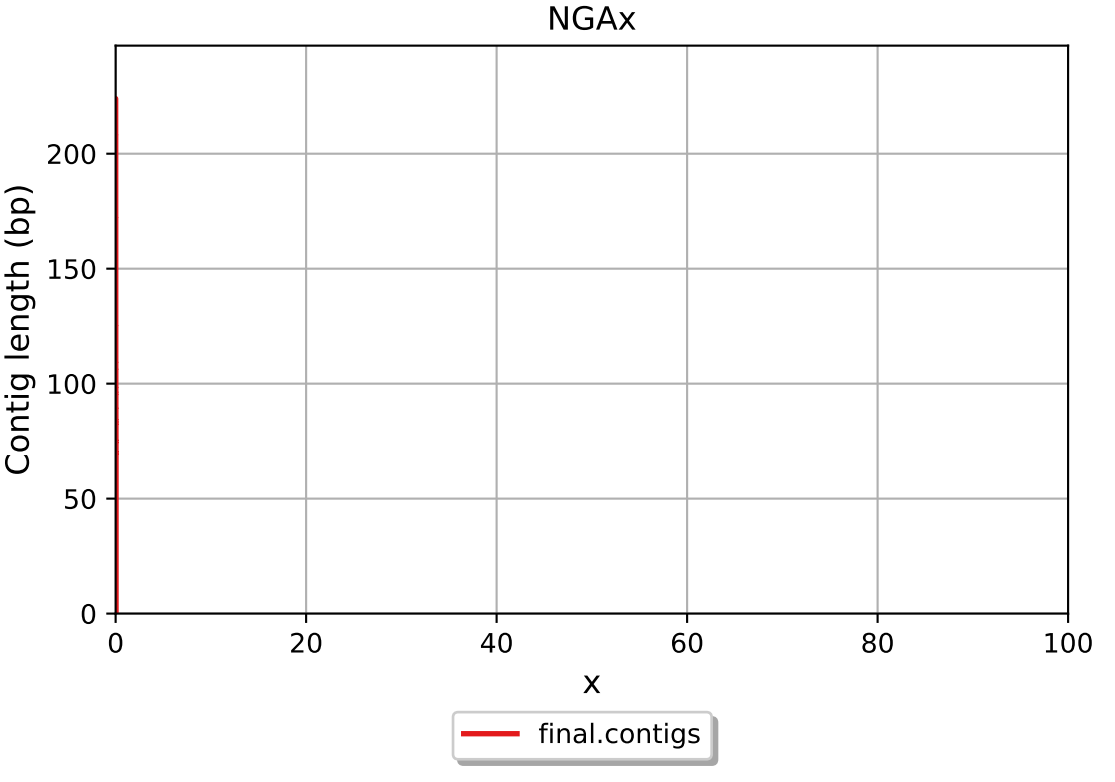

final.contigs GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
Contig index
final.contigs
Reference


NAx
Contig length (bp)
0
50
100
150
200
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
0
50
100
150
200
0
20
40
60
80
100
x
final.contigs