Report

	final.contigs
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	80285
Total length (>= 5000 bp)	53127
Total length (>= 10000 bp)	53127
Total length (>= 25000 bp)	39648
Total length (>= 50000 bp)	0
# contigs	27
Largest contig	39648
Total length	89026
Reference length	3069626
GC (%)	47.83
Reference GC (%)	57.43
N50	13479
N75	2304
L50	2
L75	6
# 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	1
# unaligned contigs	2 + 15 part
Unaligned length	80225
Genome fraction (%)	0.078
Duplication ratio	3.653
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5230.39
# indels per 100 kbp	0.00
Largest alignment	506
Total aligned length	3800
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

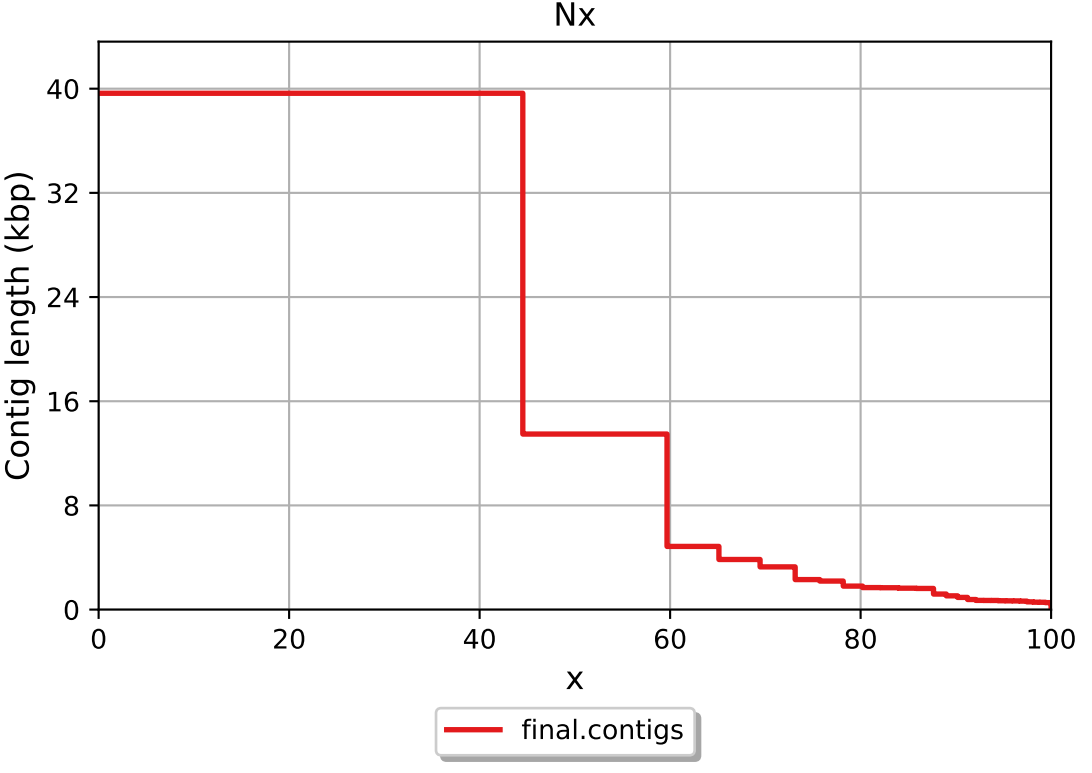
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	8
# possible misassemblies	12
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	126
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

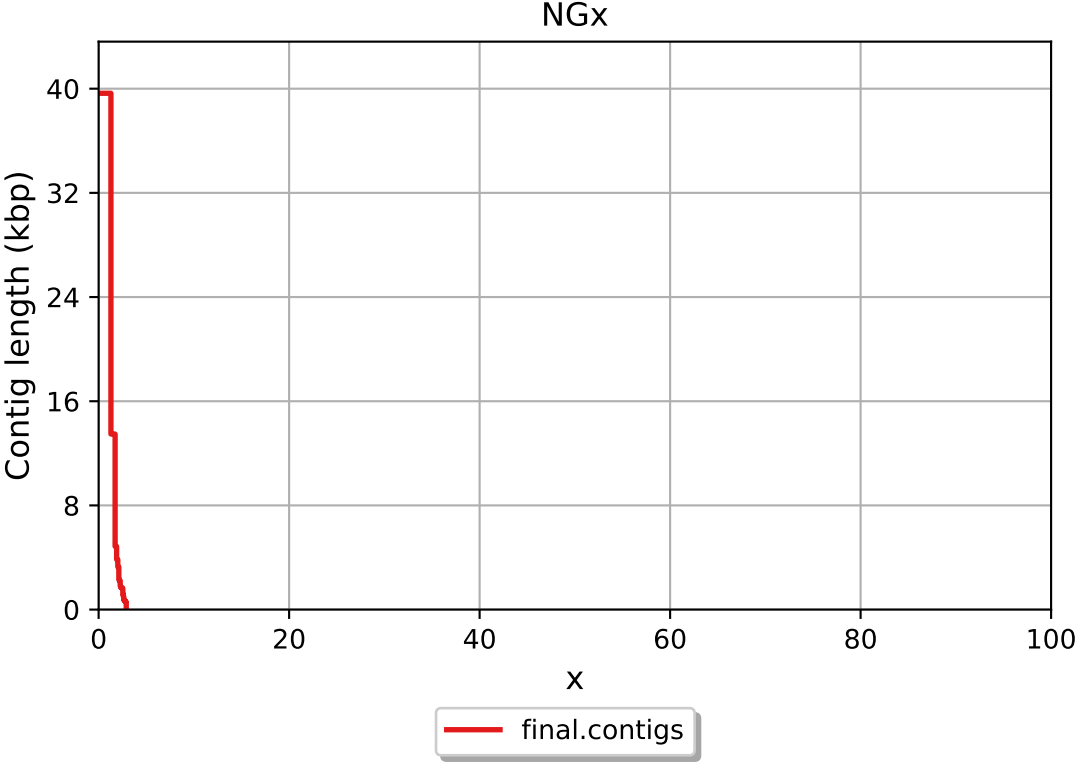
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

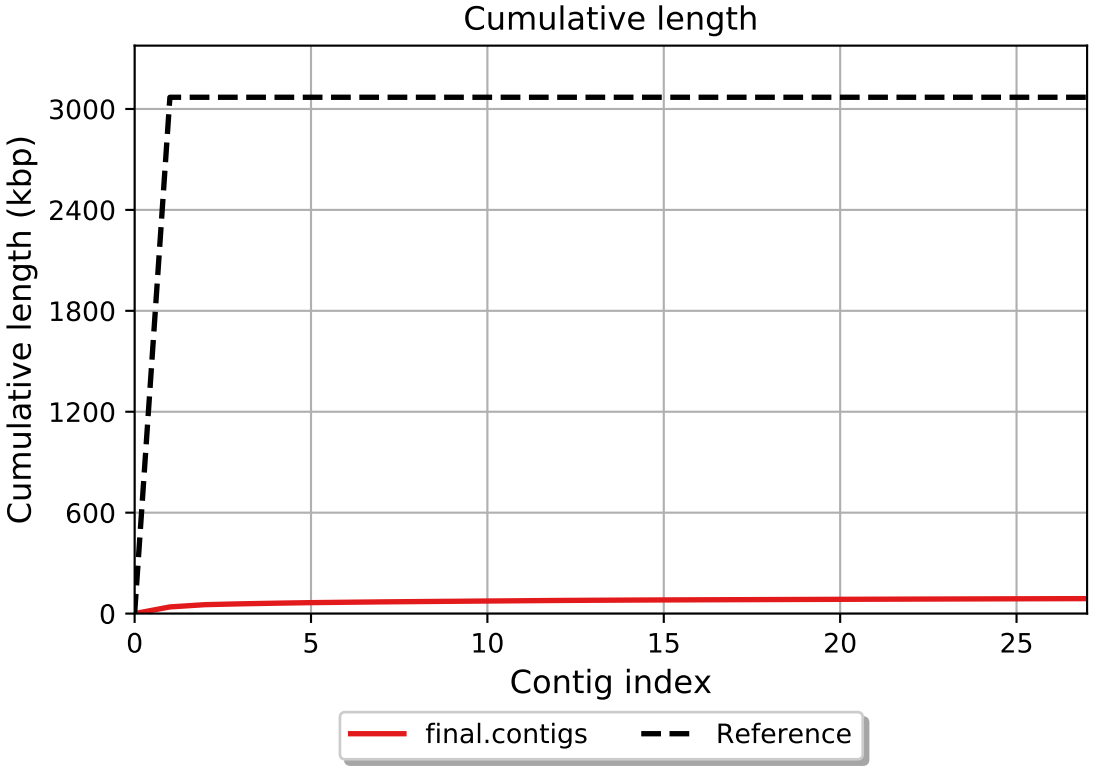
Unaligned report

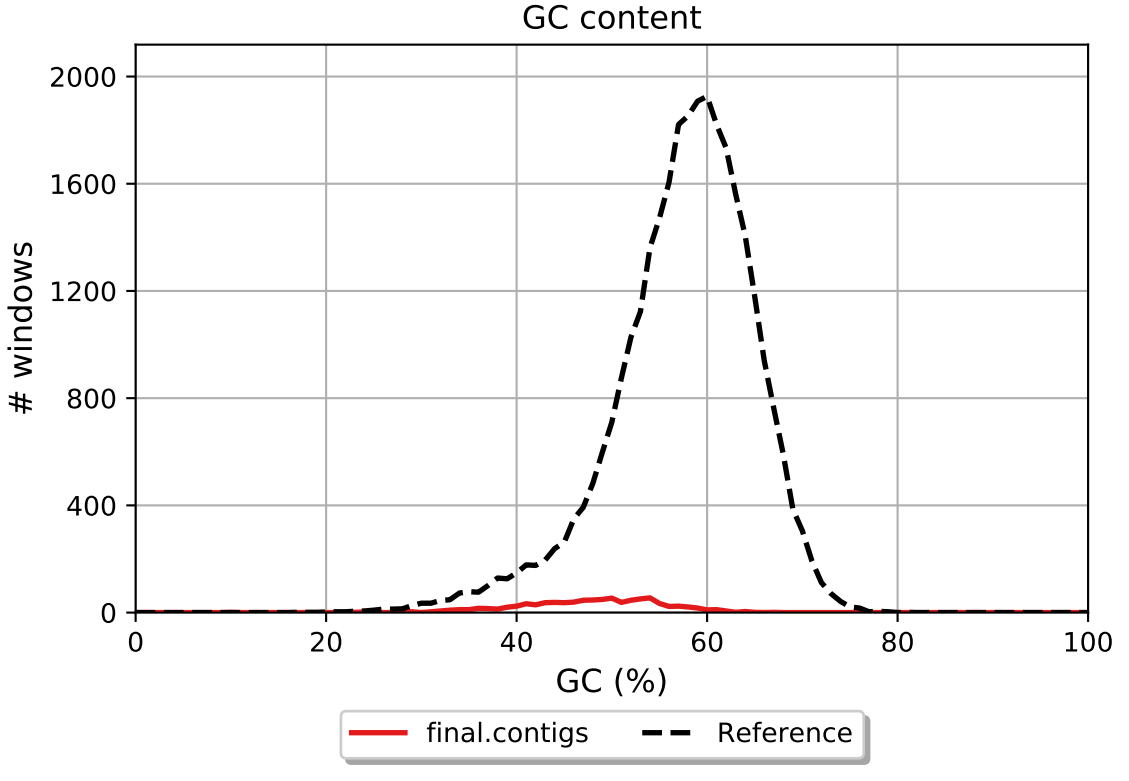
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1735
# partially unaligned contigs	15
Partially unaligned length	78490
# N's	0

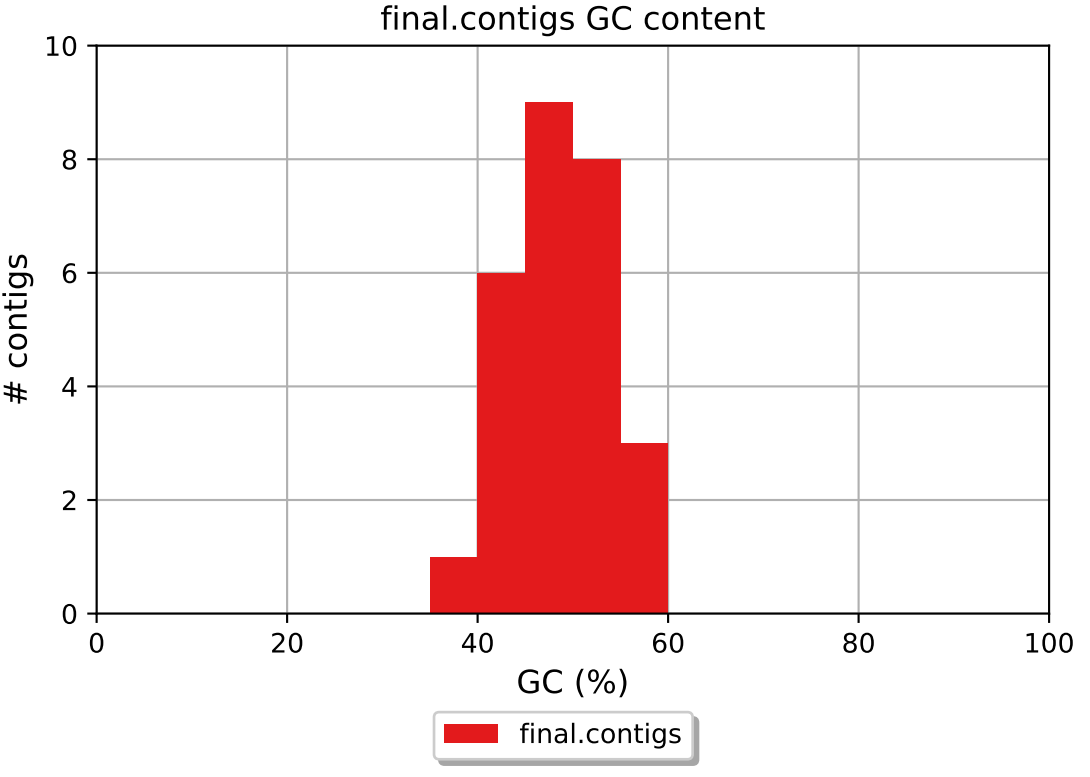
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

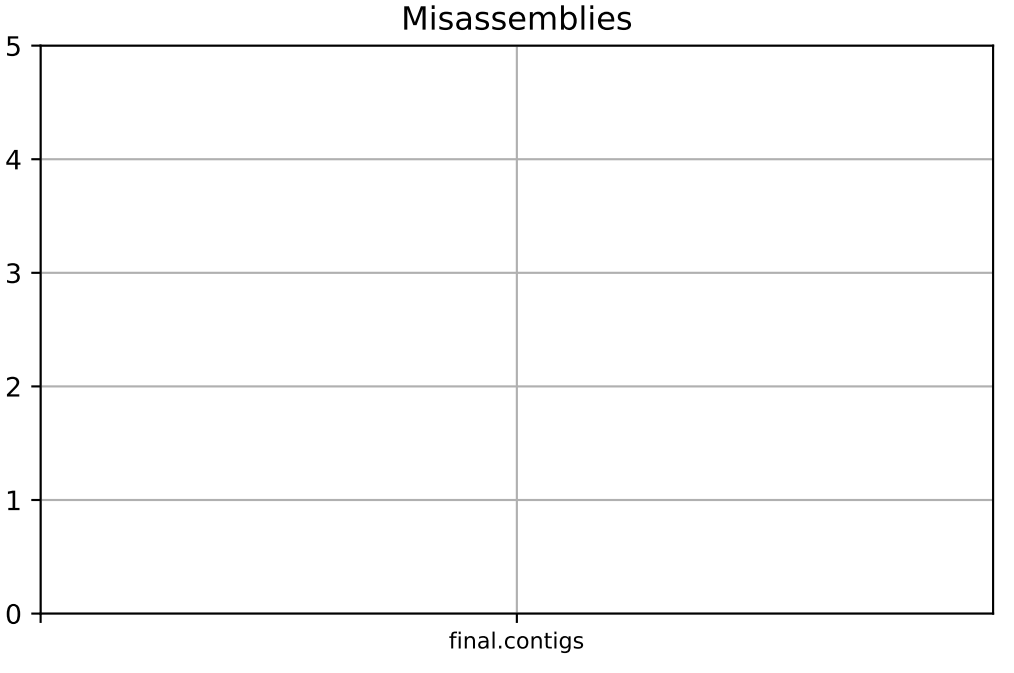

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

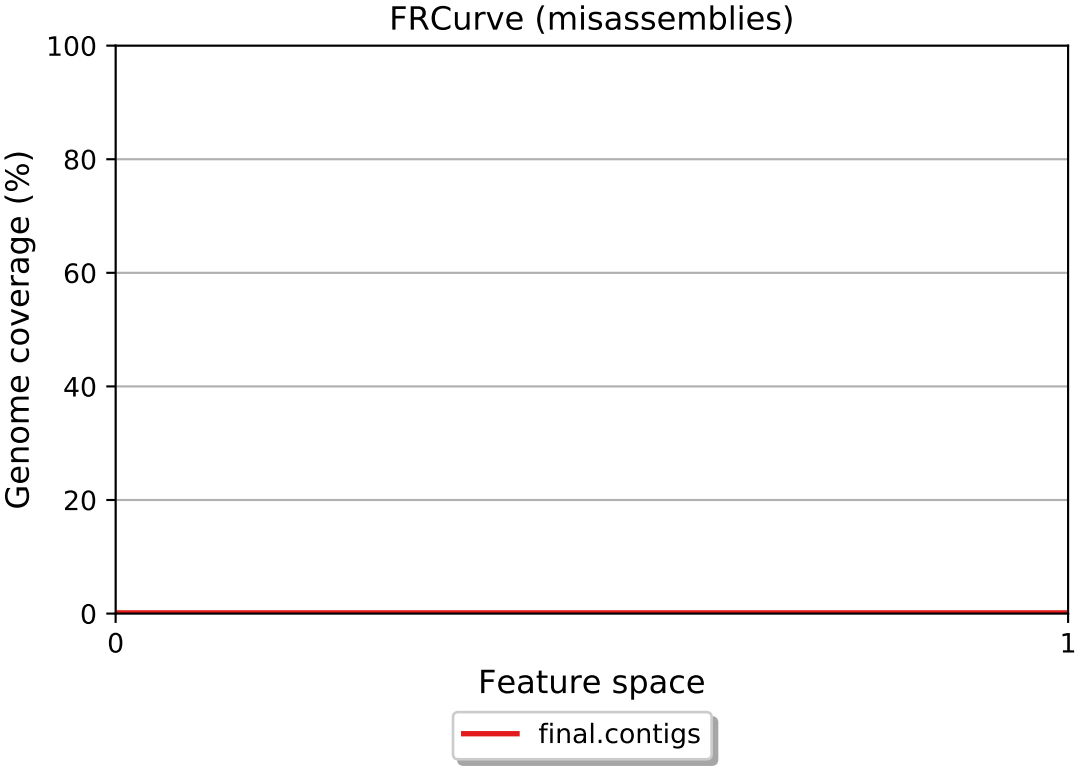

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

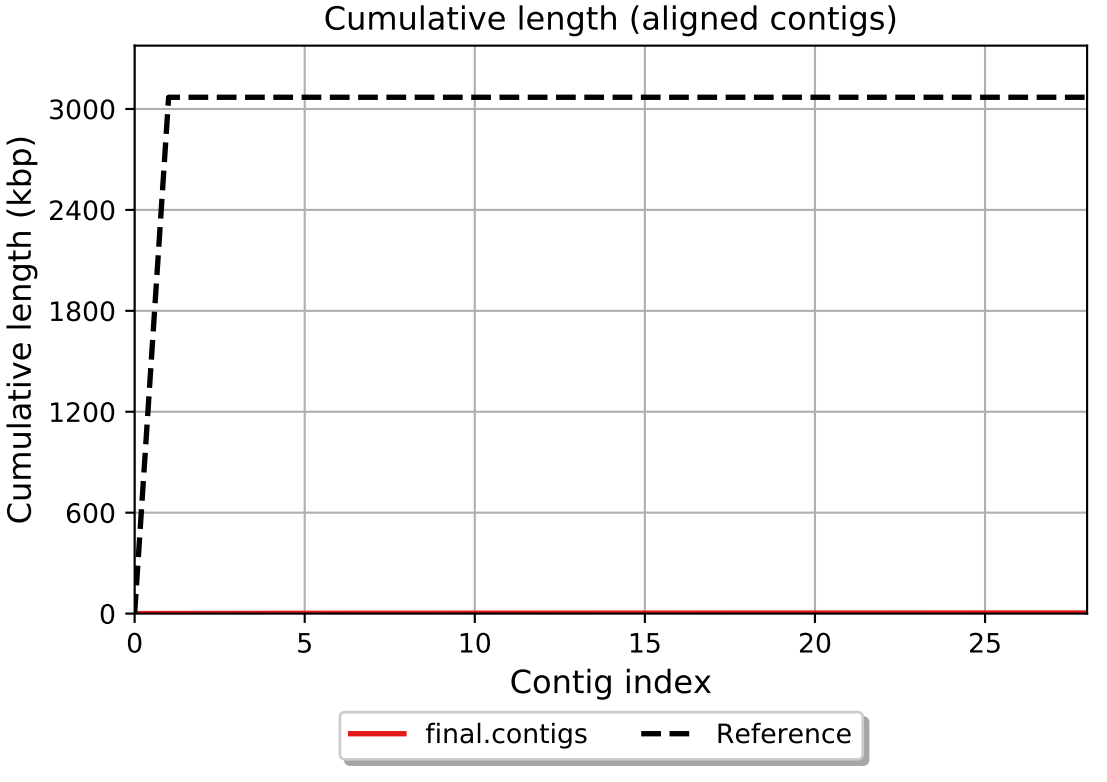

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
5
10
15
20
25
Contig index
final.contigs
Reference

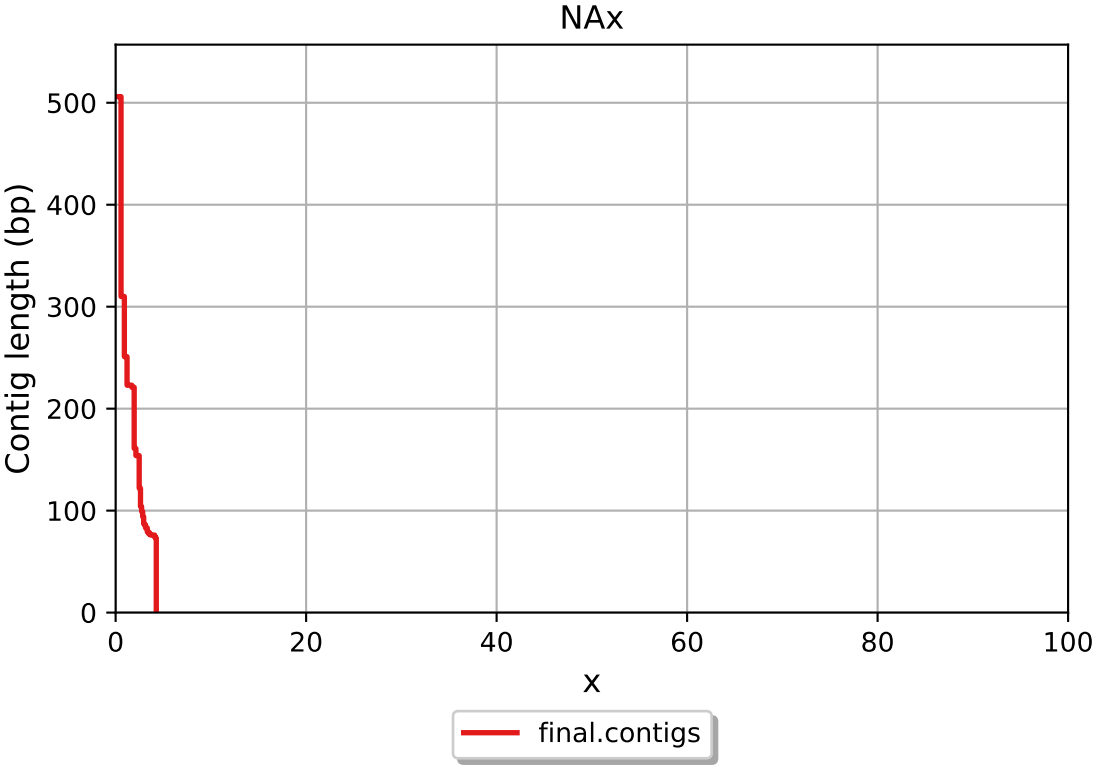

GC content
2000
1600
1200
800
400
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

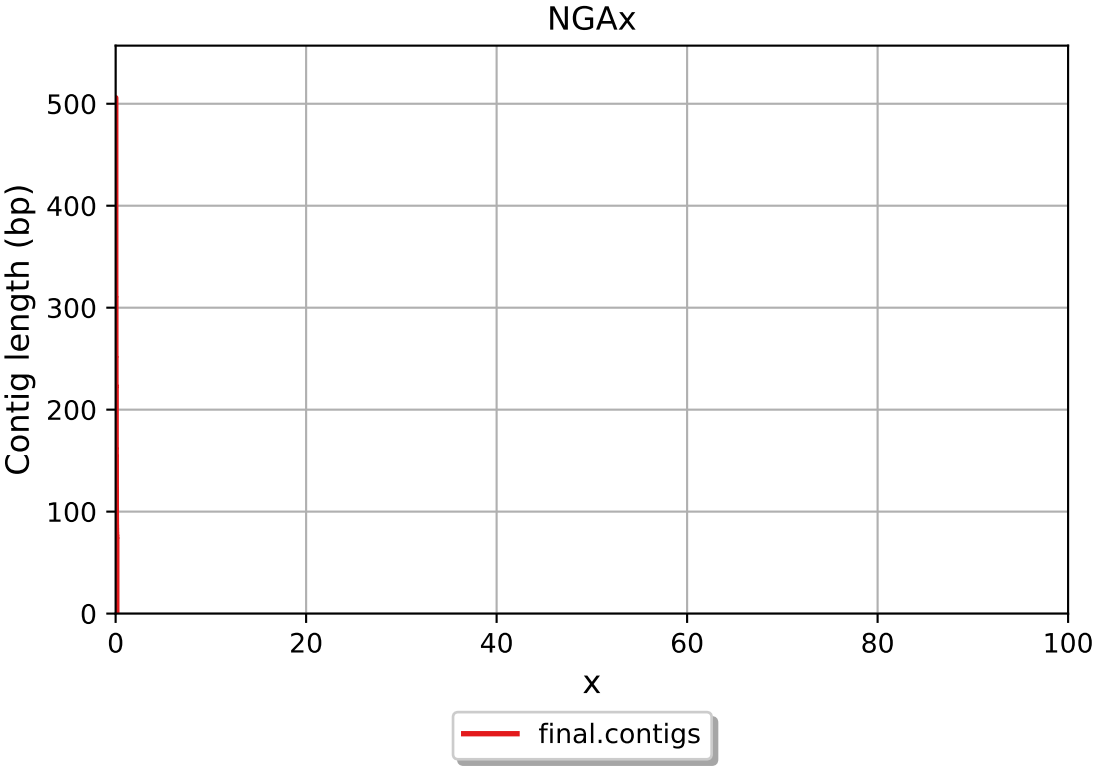

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
5
10
15
20
25
Contig index
final.contigs
Reference


NAx
Contig length (bp)
500
400
300
200
100
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
500
400
300
200
100
0
0
20
40
60
80
100
x
final.contigs