Report

	final.contigs
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	16651
Total length (>= 5000 bp)	13479
Total length (>= 10000 bp)	13479
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6
Largest contig	13479
Total length	18683
Reference length	3714272
GC (%)	47.25
Reference GC (%)	61.03
N50	13479
N75	1678
L50	1
L75	2
# 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	0
# unaligned contigs	2 + 4 part
Unaligned length	18313
Genome fraction (%)	0.010
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2972.97
# indels per 100 kbp	0.00
Largest alignment	127
Total aligned length	370
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

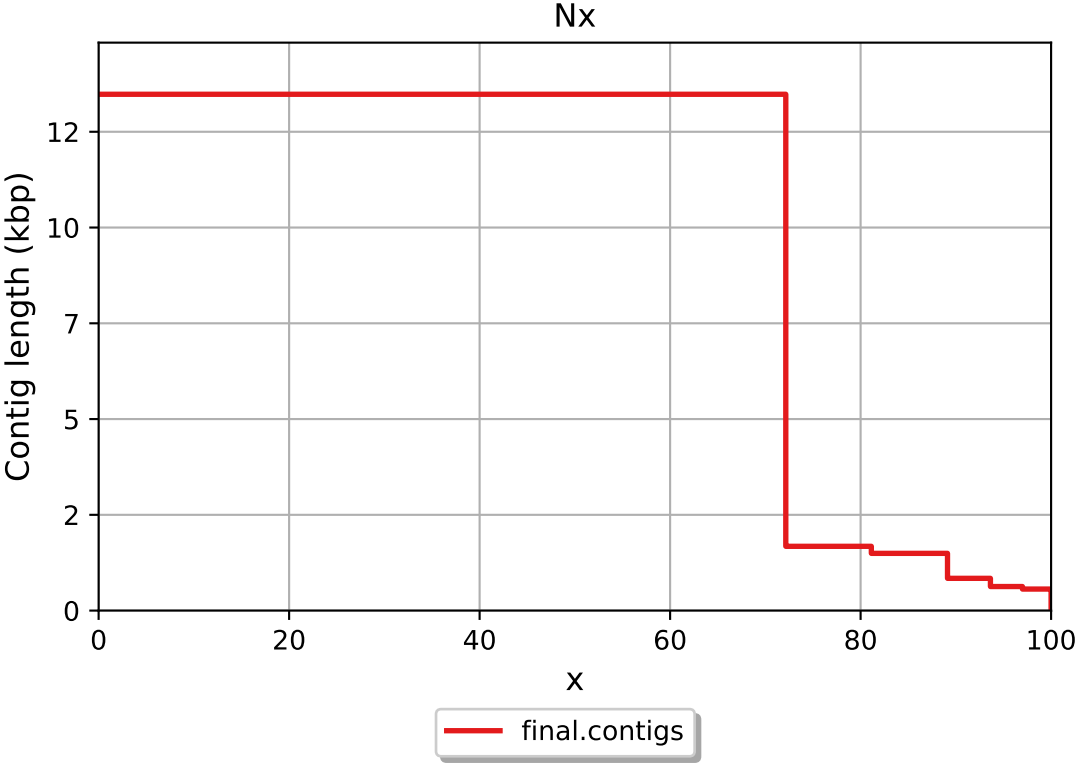
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	11
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

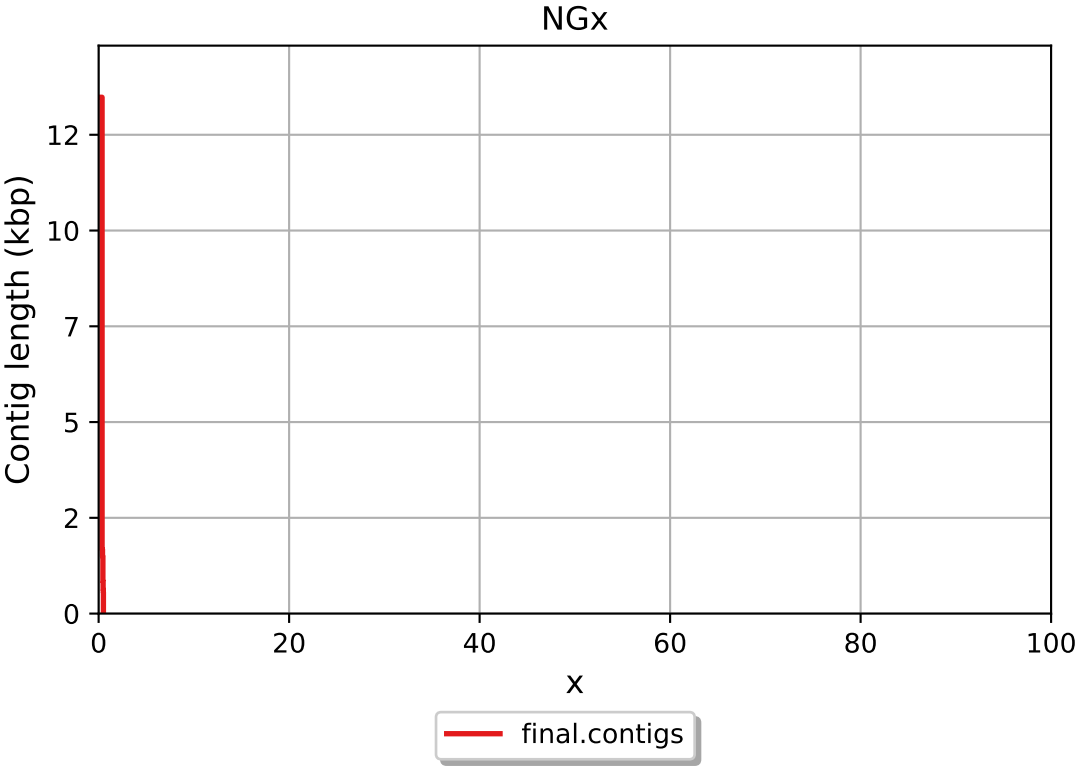
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

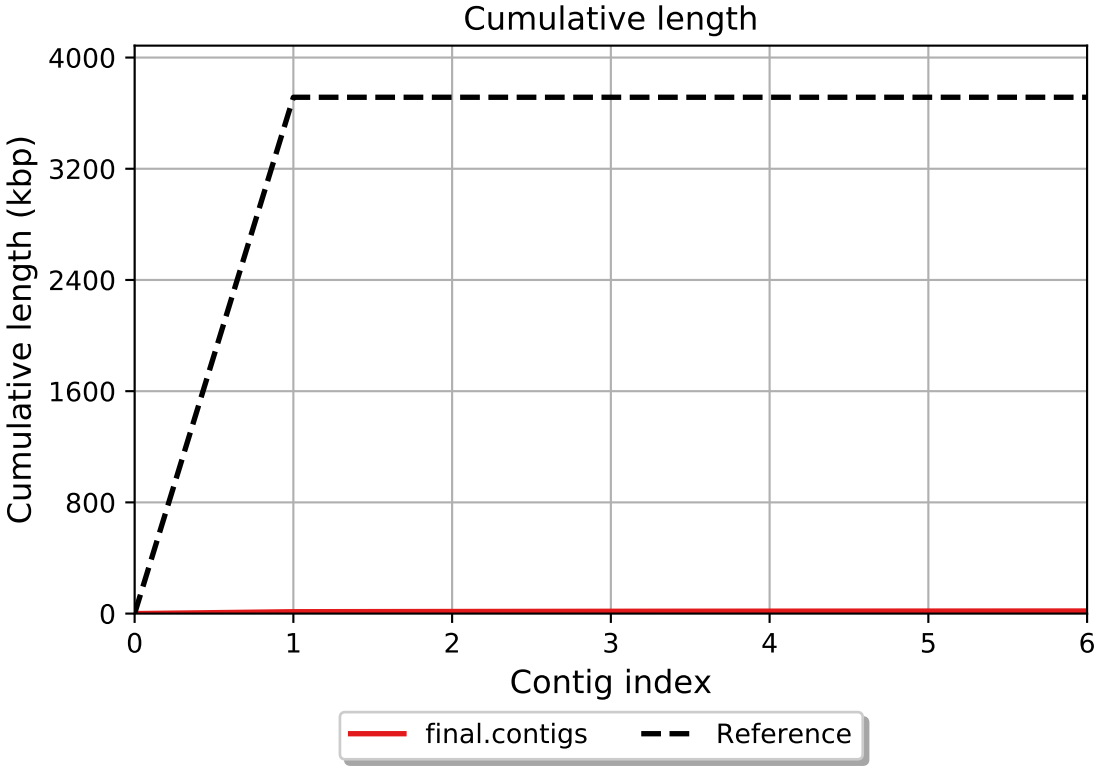
Unaligned report

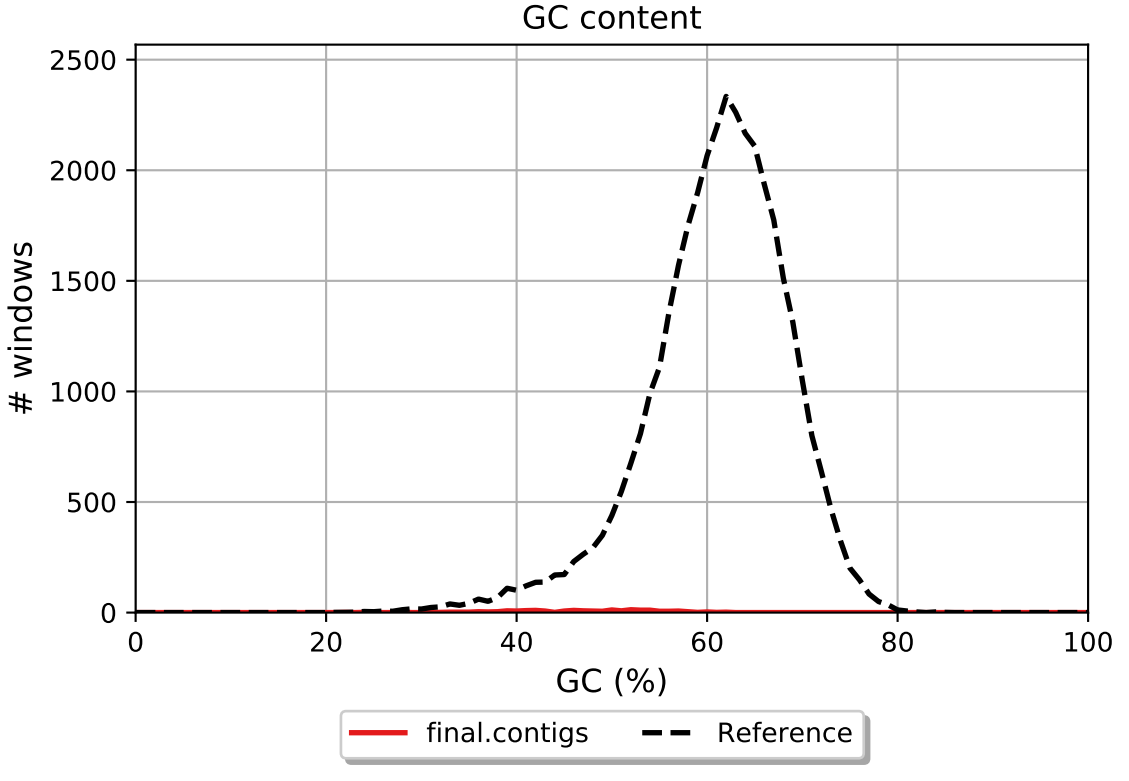
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	2056
# partially unaligned contigs	4
Partially unaligned length	16257
# N's	0

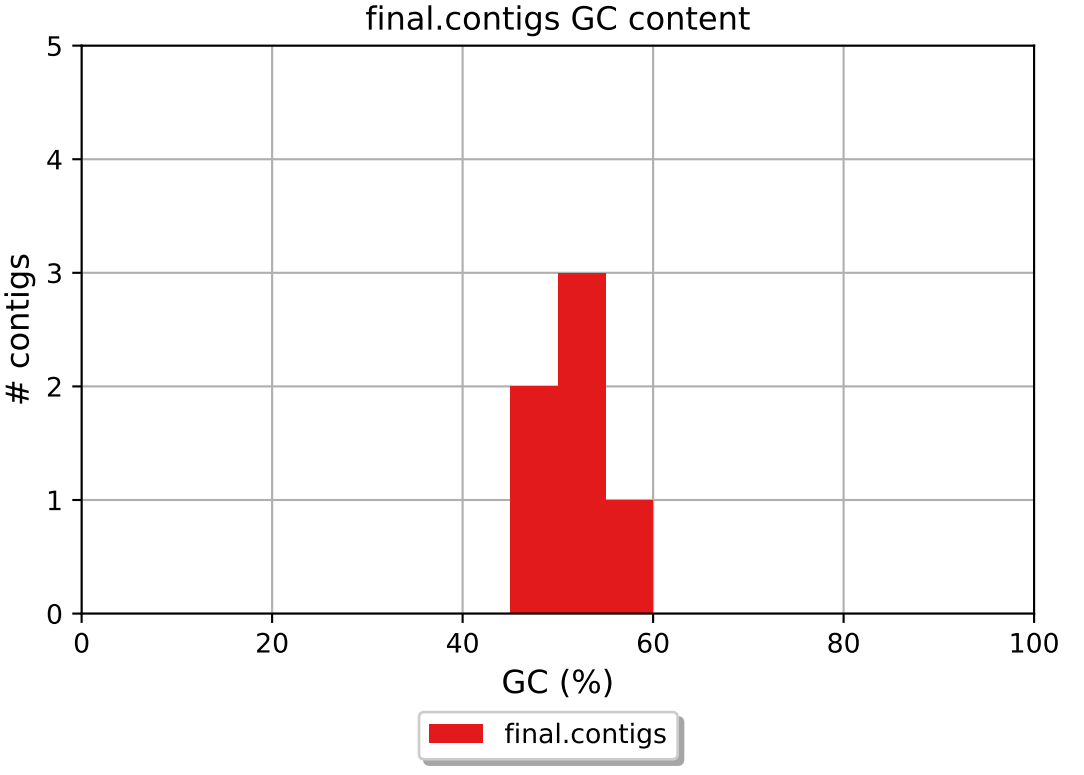
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

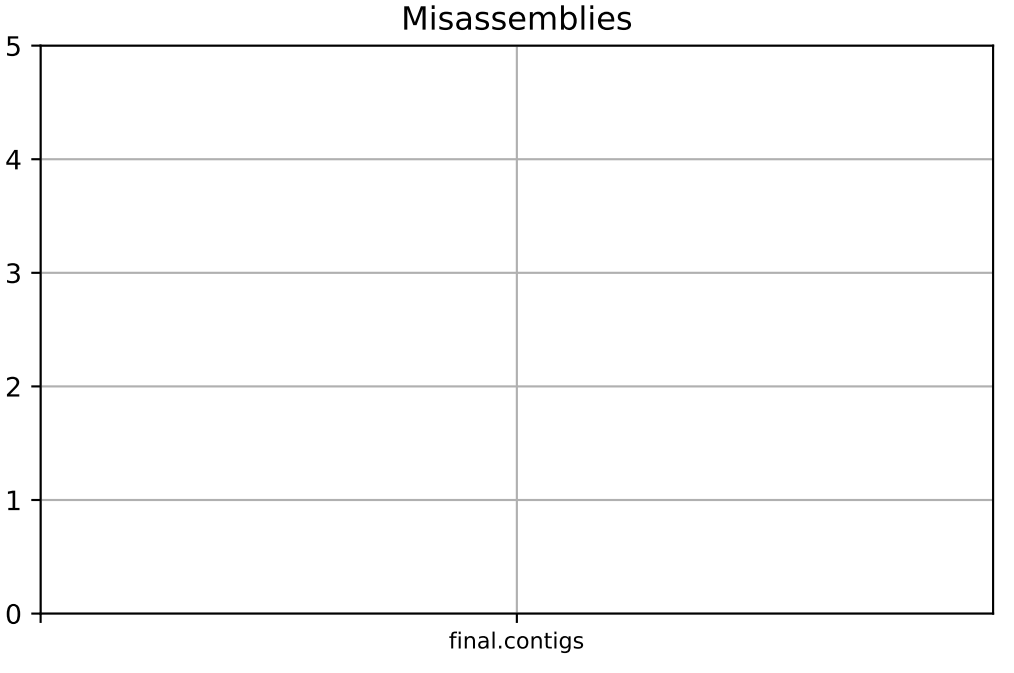

Nx
Contig length (kbp)
12
10
7
5
2
0
0
20
40
60
80
100
x
final.contigs

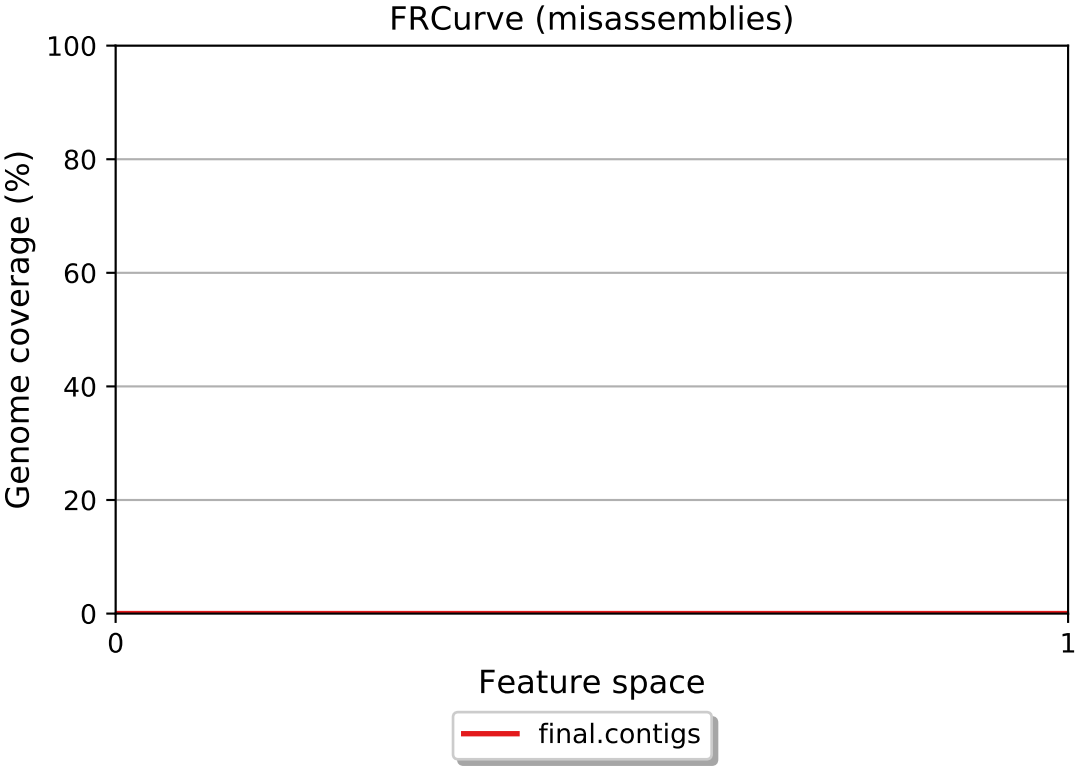

NGx
Contig length (kbp)
12
10
7
5
2
0
0
20
40
60
80
100
x
final.contigs

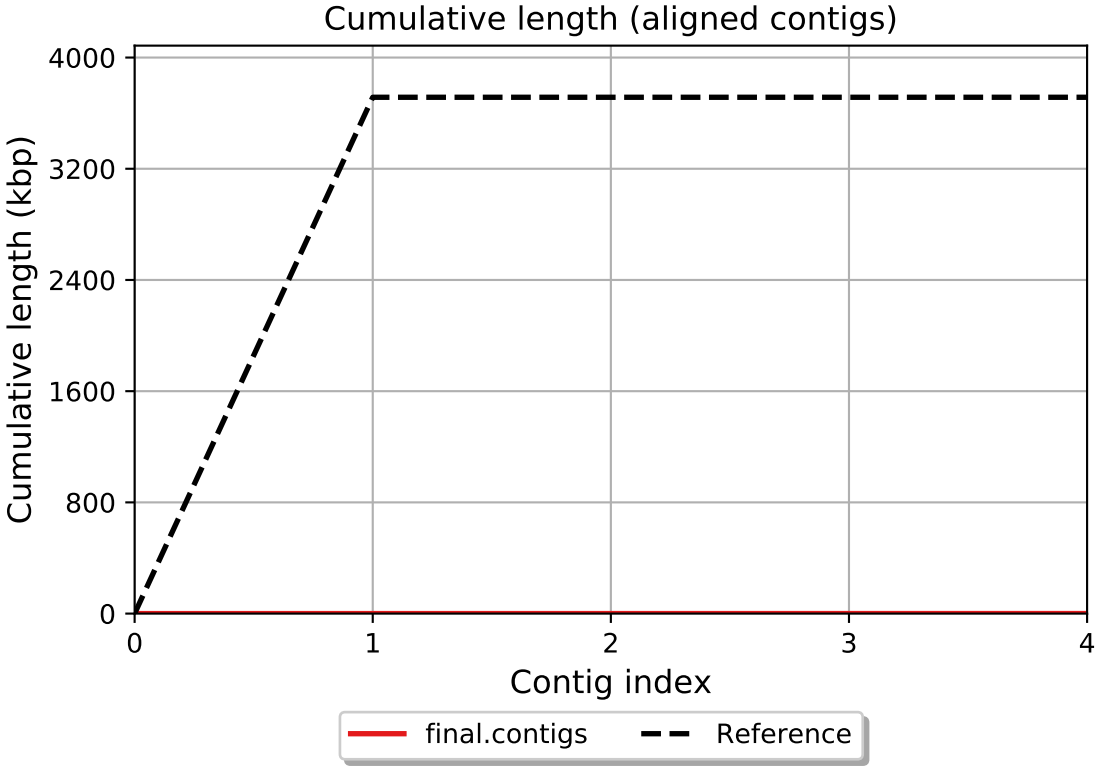

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
1
2
3
4
5
6
Contig index
final.contigs
Reference

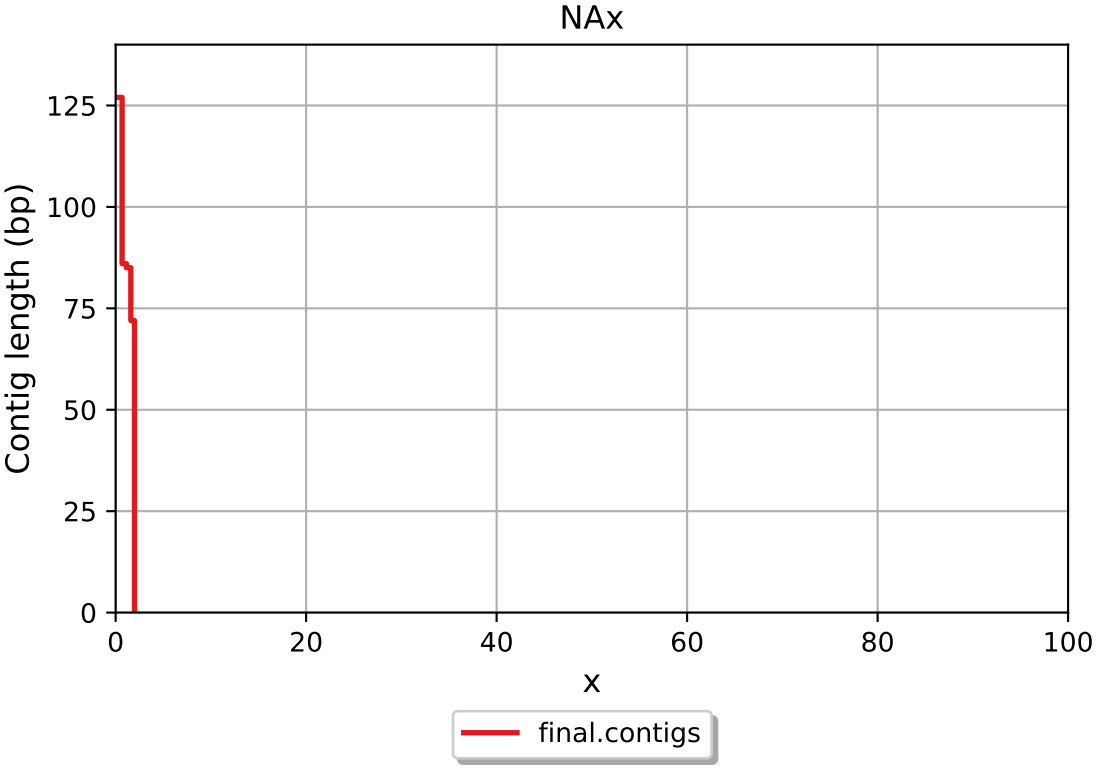

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

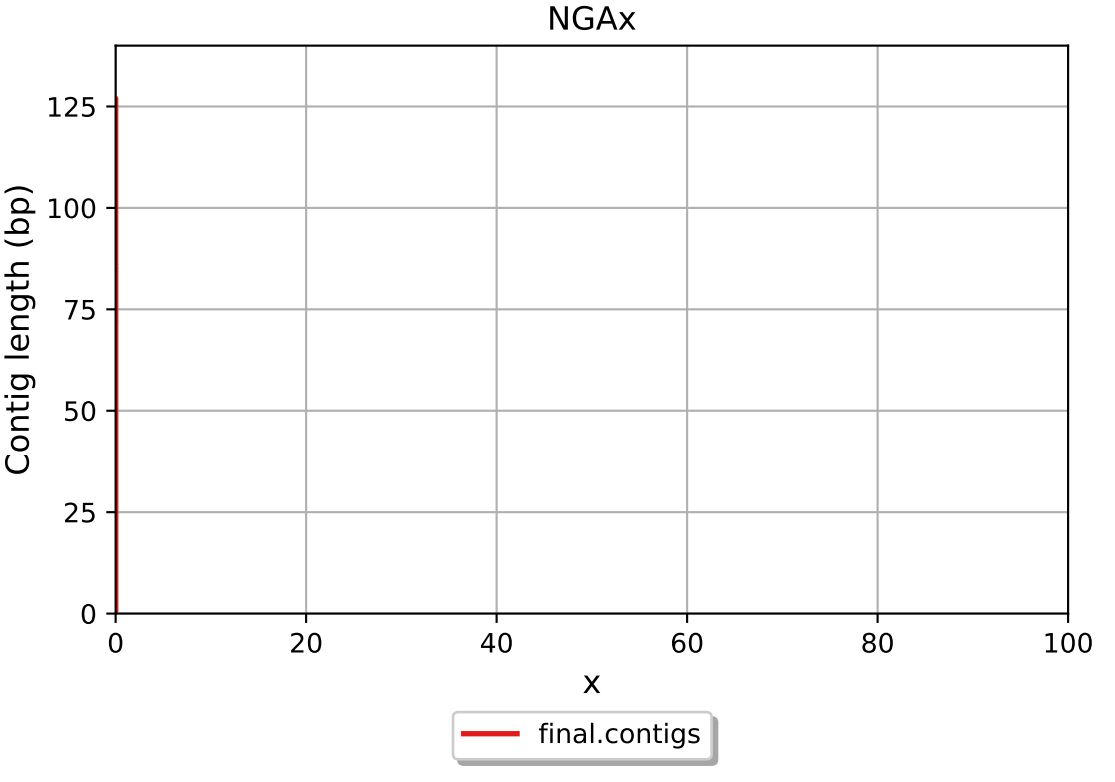

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
final.contigs


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)
4000
3200
2400
1600
800
0
0
1
2
3
4
Contig index
final.contigs
Reference


NAx
Contig length (bp)
125
100
75
50
25
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
125
100
75
50
25
0
0
20
40
60
80
100
x
final.contigs