Report

	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	225882
Total length (>= 5000 bp)	216454
Total length (>= 10000 bp)	216454
Total length (>= 25000 bp)	200449
Total length (>= 50000 bp)	200449
# contigs	16
Largest contig	200449
Total length	232637
Reference length	3568533
GC (%)	59.87
Reference GC (%)	67.23
N50	200449
N75	200449
L50	1
L75	1
# 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	3 + 9 part
Unaligned length	229314
Genome fraction (%)	0.040
Duplication ratio	2.343
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3455.57
# indels per 100 kbp	0.00
Largest alignment	245
Total aligned length	1494
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

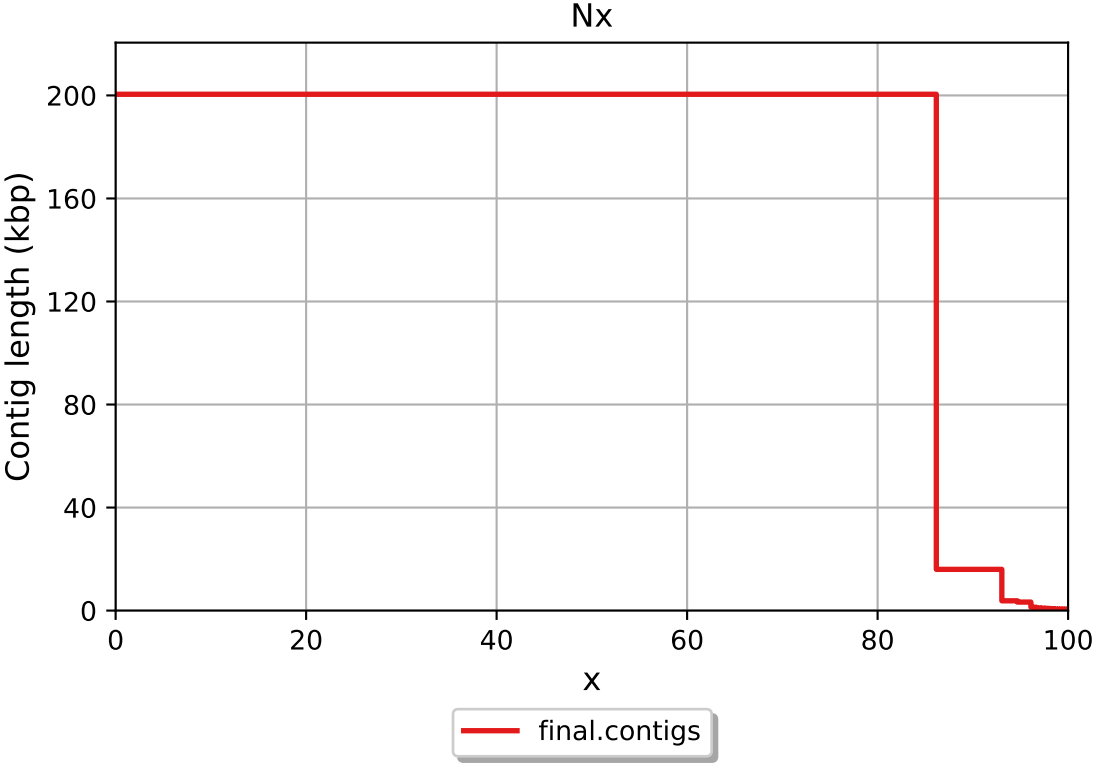
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	5
# possible misassemblies	7
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	49
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

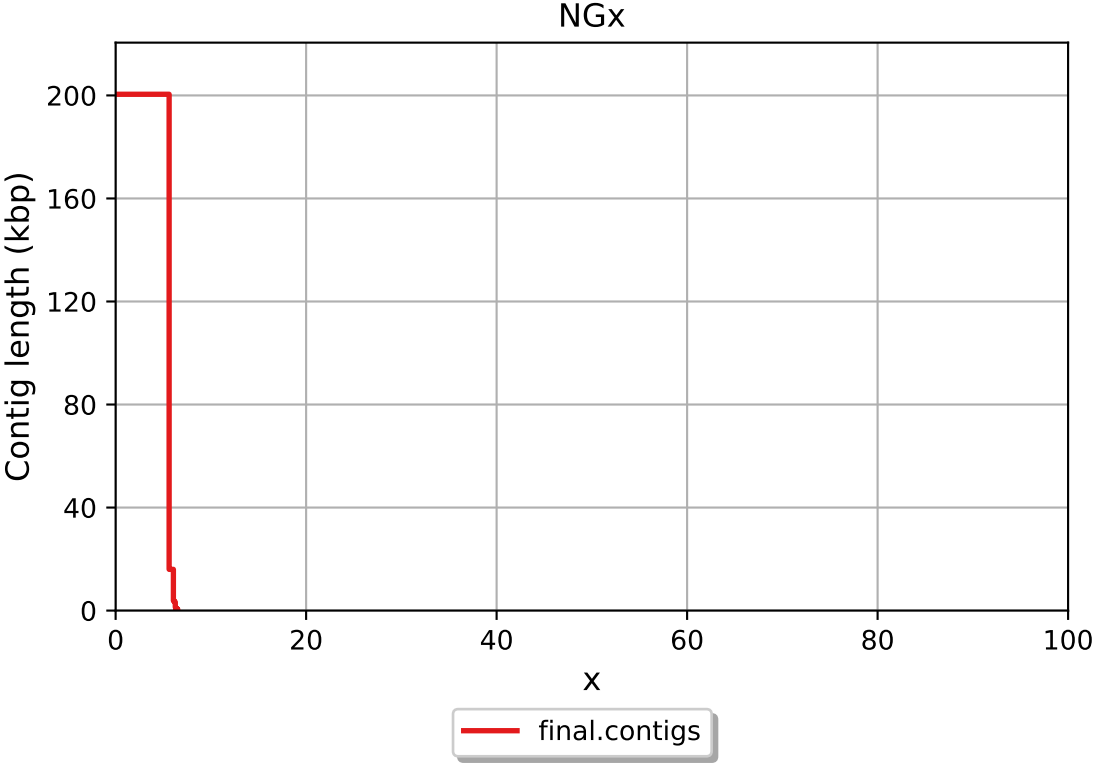
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

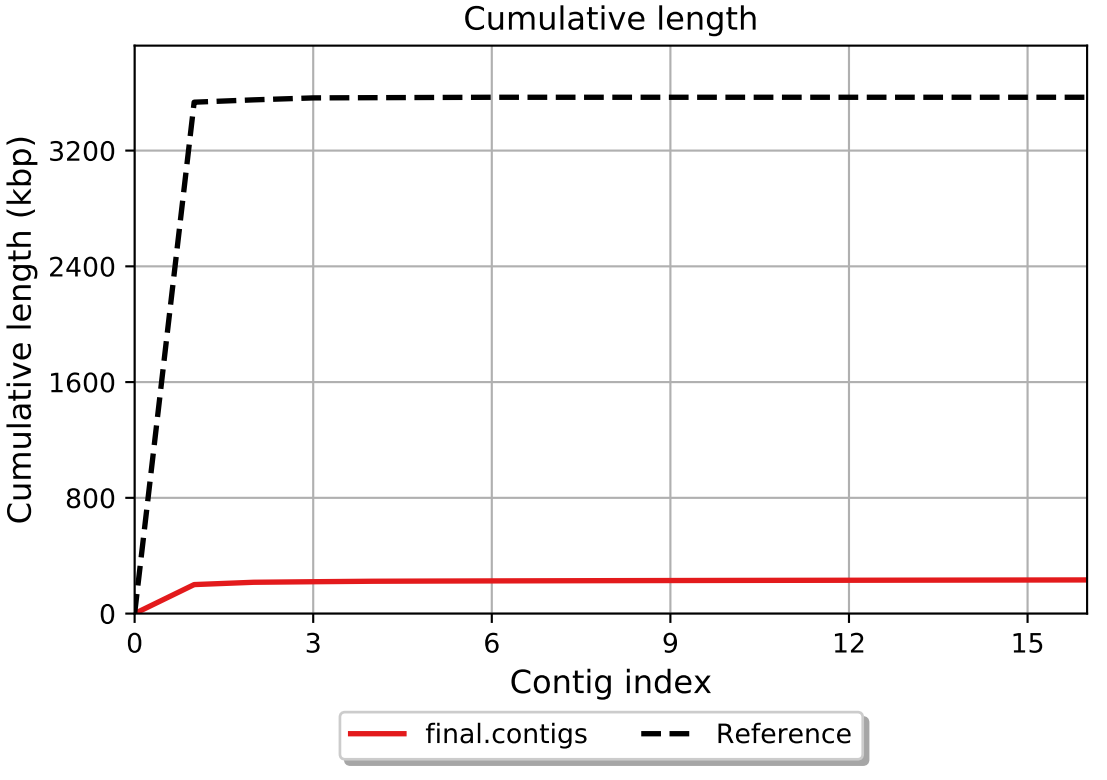
Unaligned report

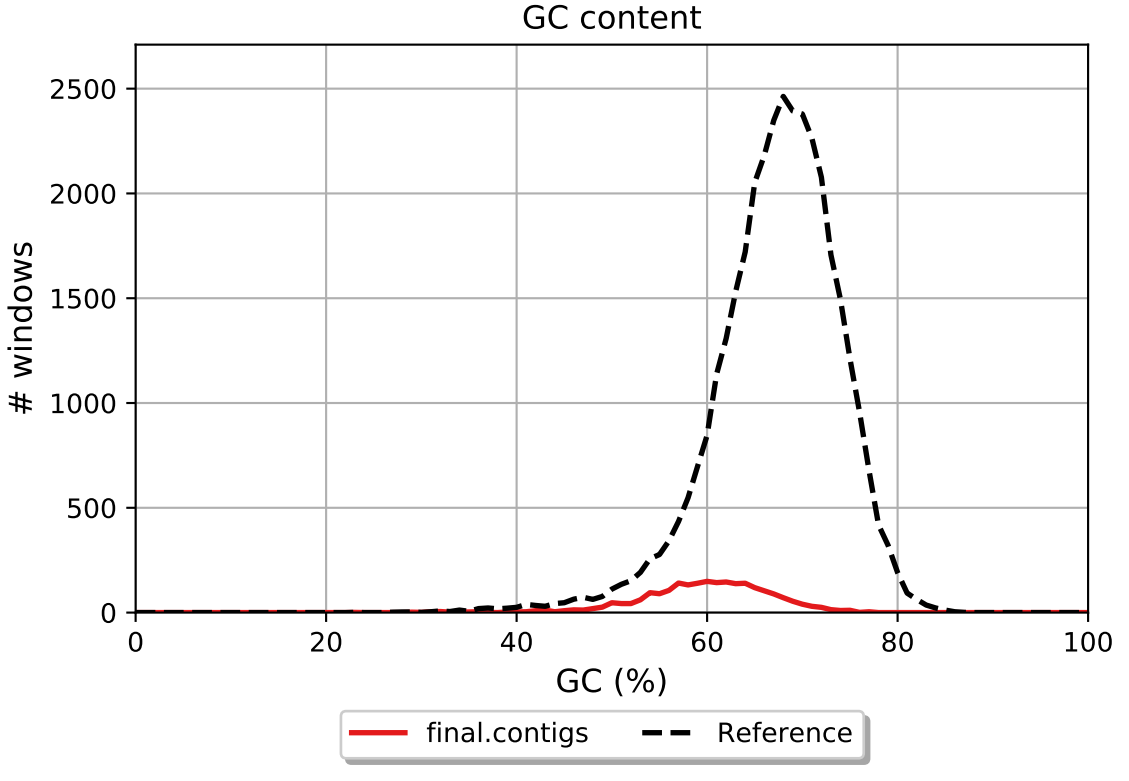
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	1739
# partially unaligned contigs	9
Partially unaligned length	227575
# N's	0

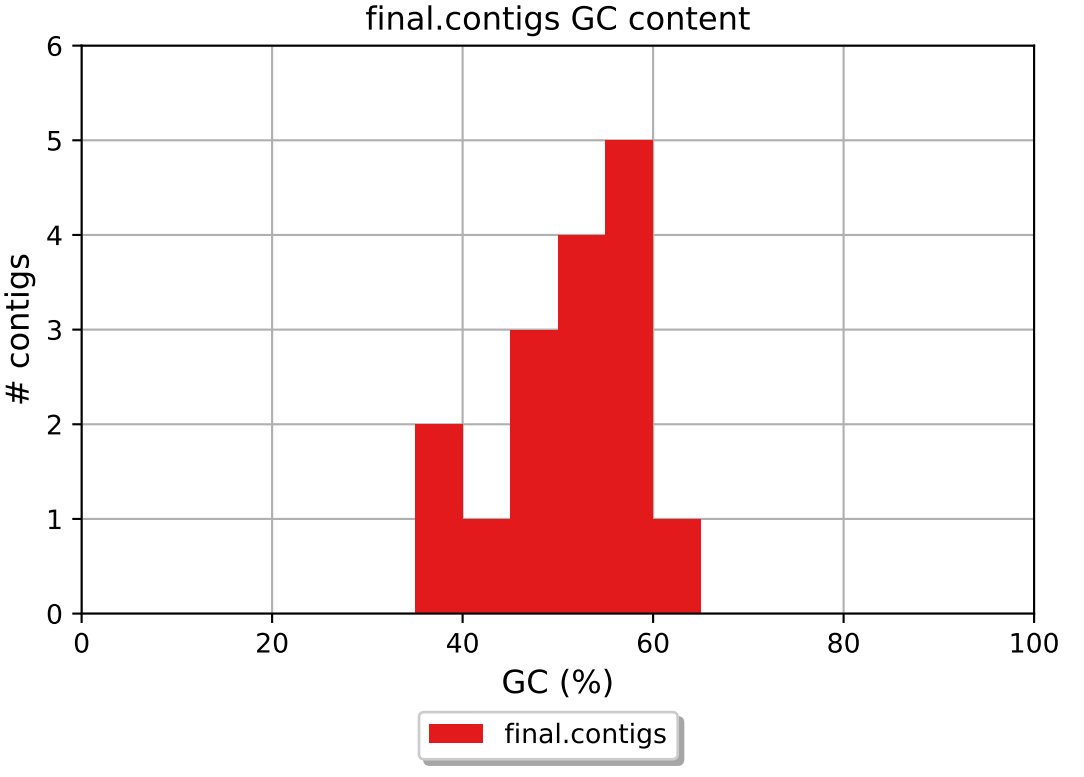
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

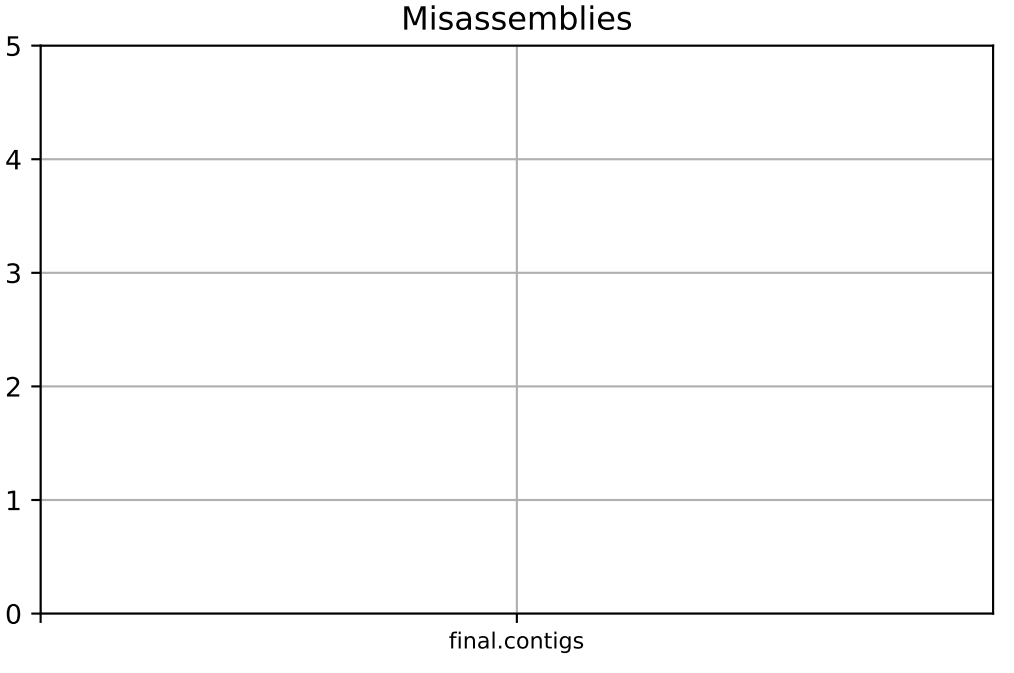

Nx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
final.contigs

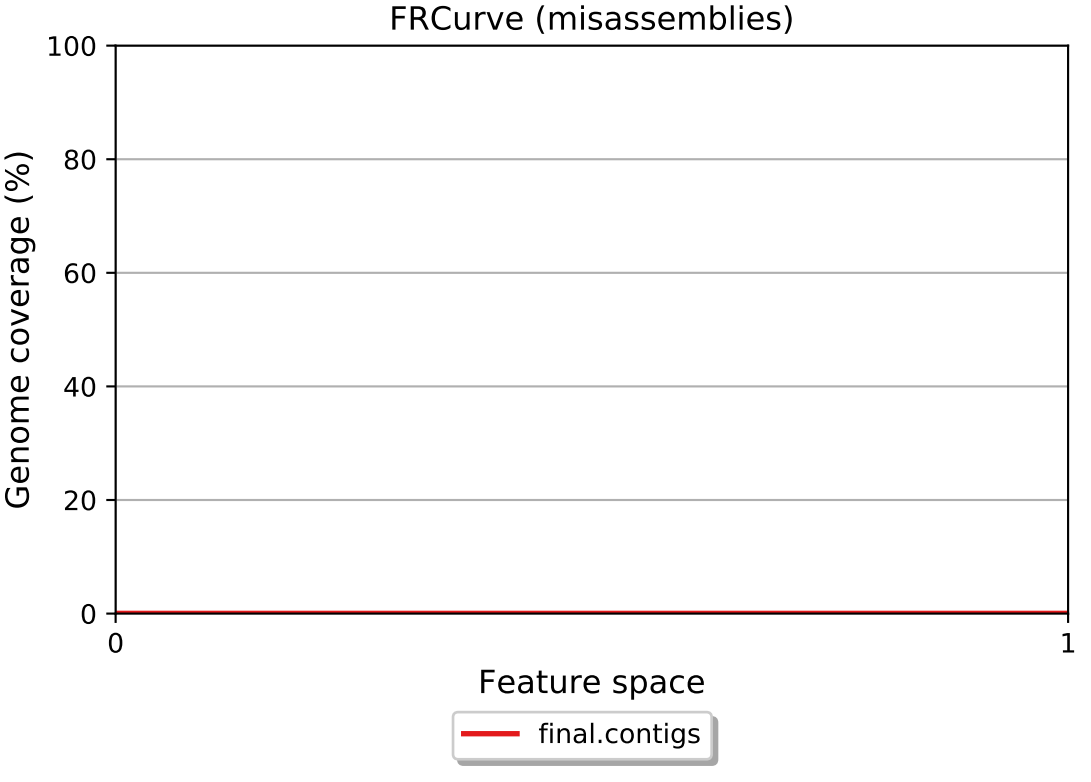

NGx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
final.contigs

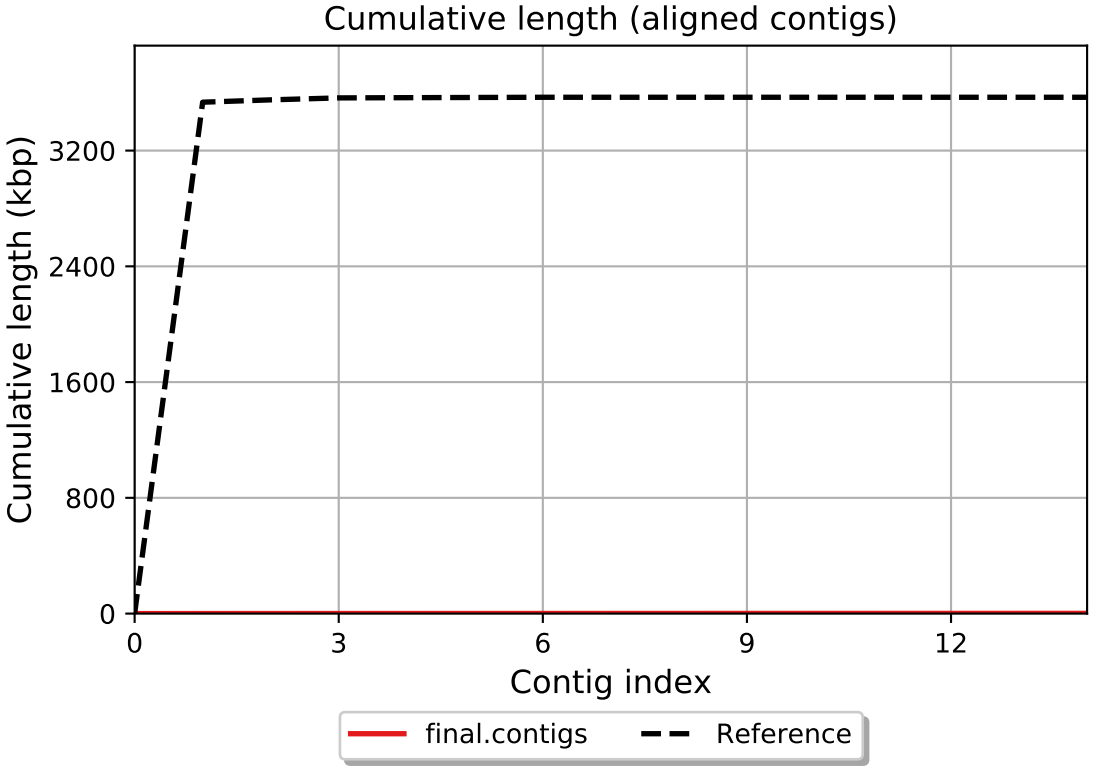

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
3
6
9
12
15
Contig index
final.contigs
Reference

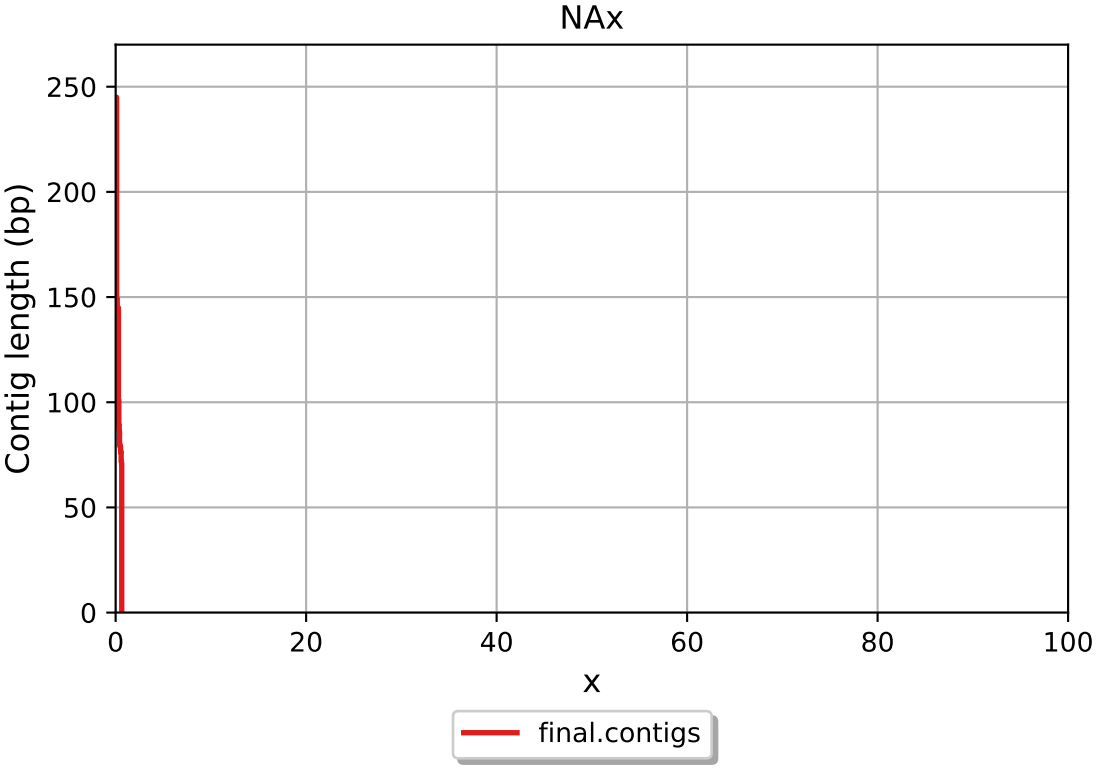

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

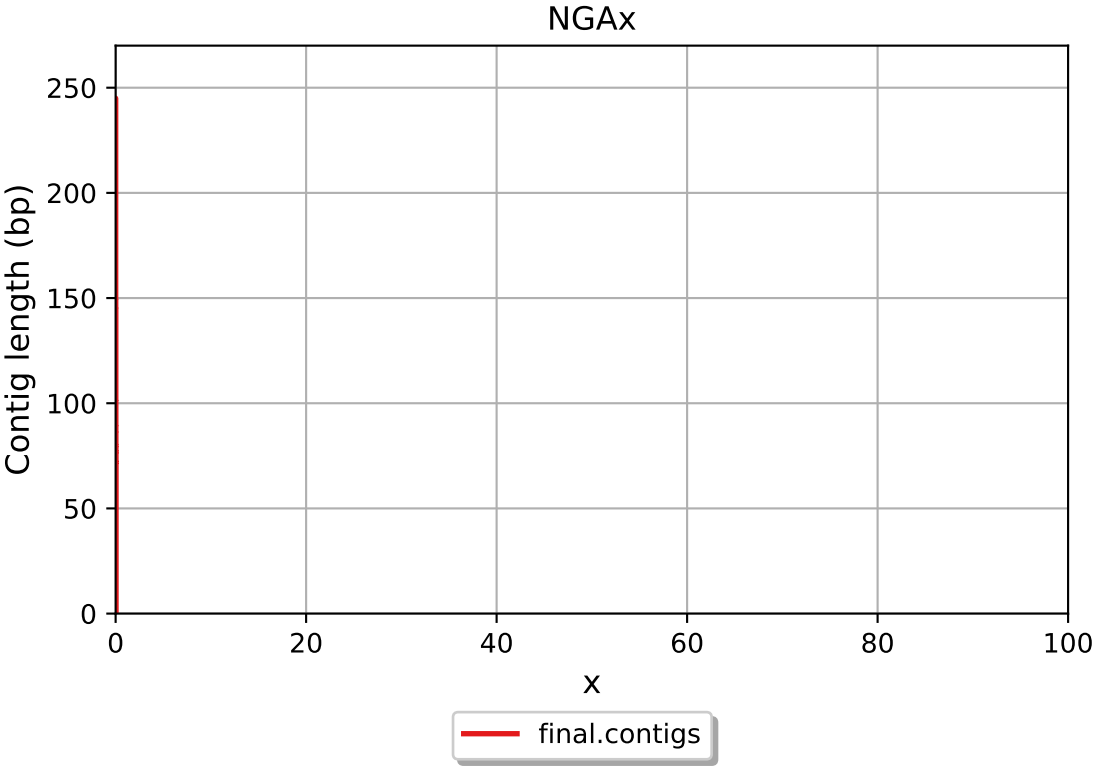

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs


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)
3200
2400
1600
800
0
0
3
6
9
12
Contig index
final.contigs
Reference


NAx
Contig length (bp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs