Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	37438
Total length (>= 5000 bp)	19166
Total length (>= 10000 bp)	19166
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	11
Largest contig	19166
Total length	40081
Reference length	7762396
GC (%)	60.23
Reference GC (%)	72.86
N50	4306
N75	3858
L50	2
L75	4
# 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	2
# unaligned contigs	2 + 7 part
Unaligned length	37490
Genome fraction (%)	0.014
Duplication ratio	2.320
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4028.65
# indels per 100 kbp	358.10
Largest alignment	235
Total aligned length	1644
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

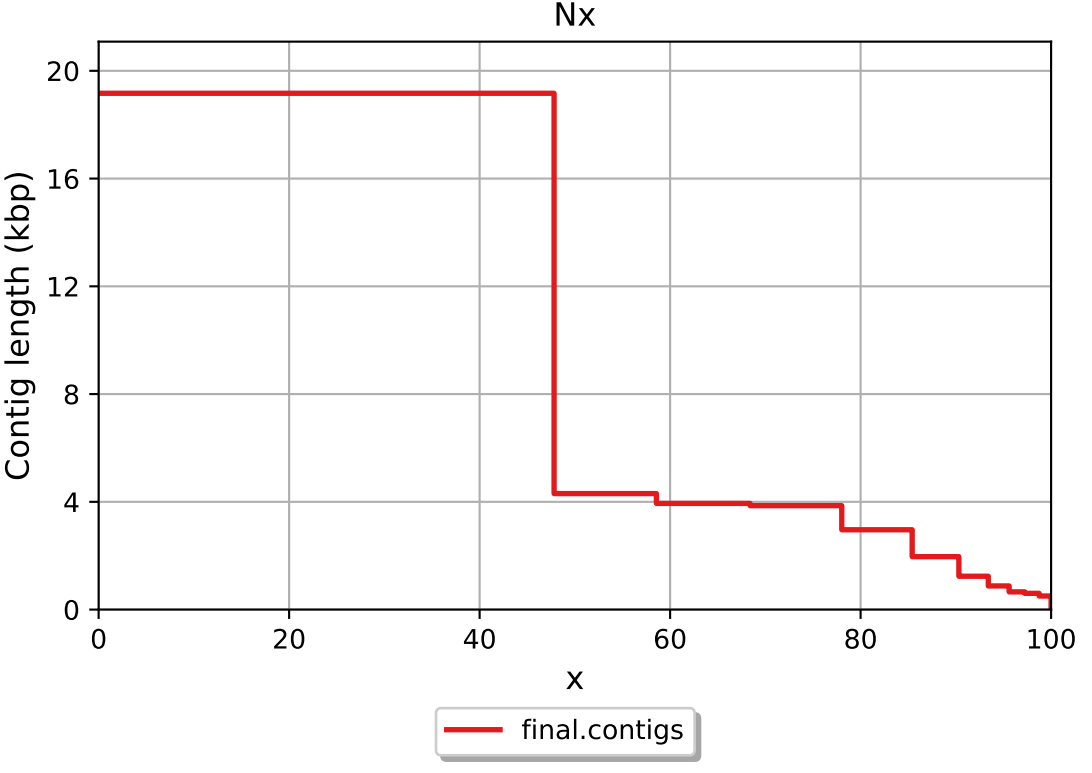
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	4
# possible misassemblies	8
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	45
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

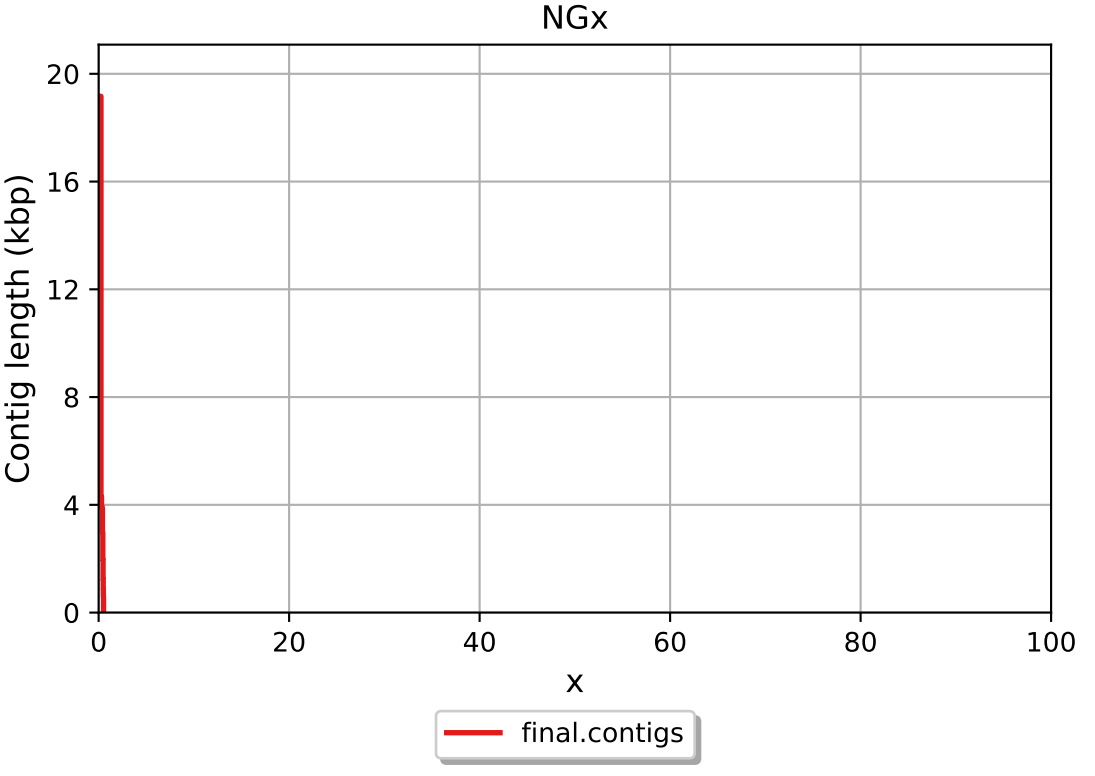
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

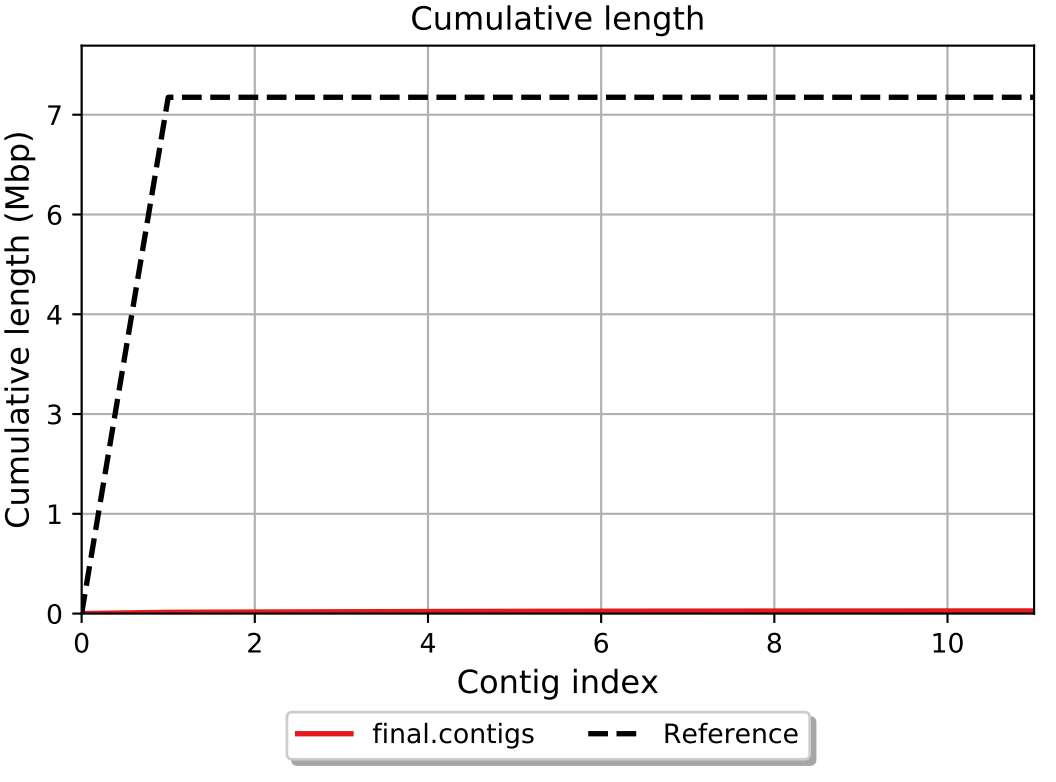
Unaligned report

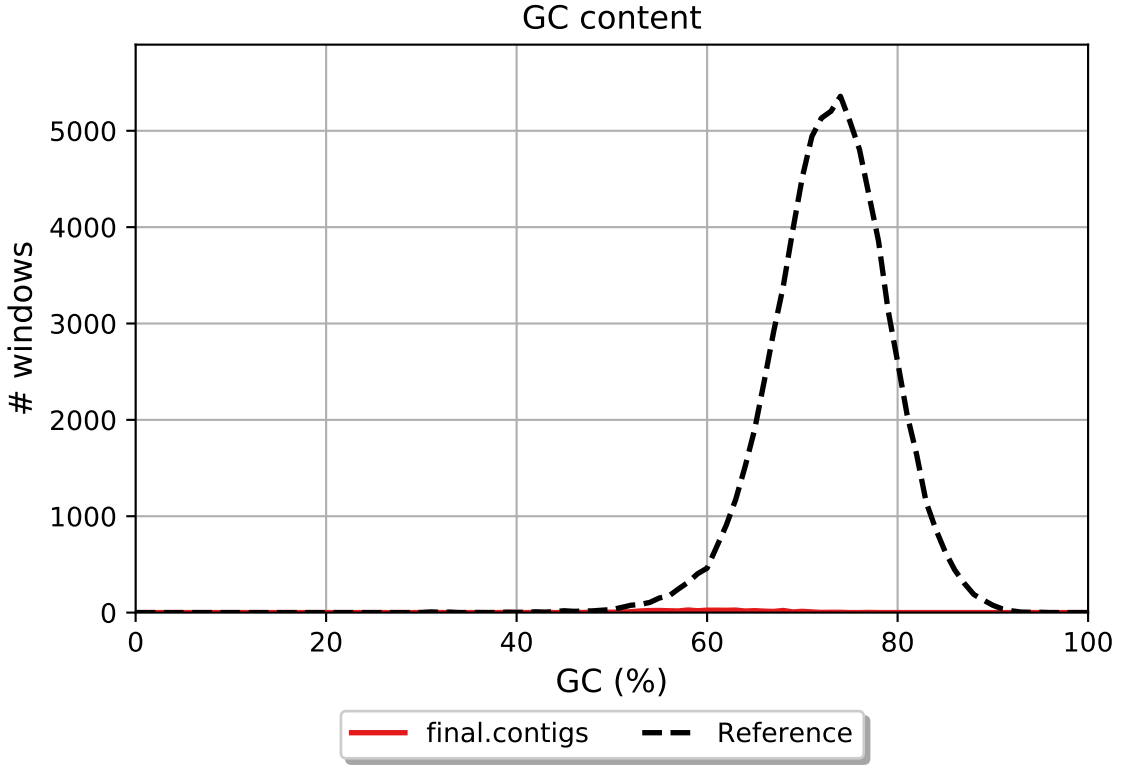
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1536
# partially unaligned contigs	7
Partially unaligned length	35954
# N's	0

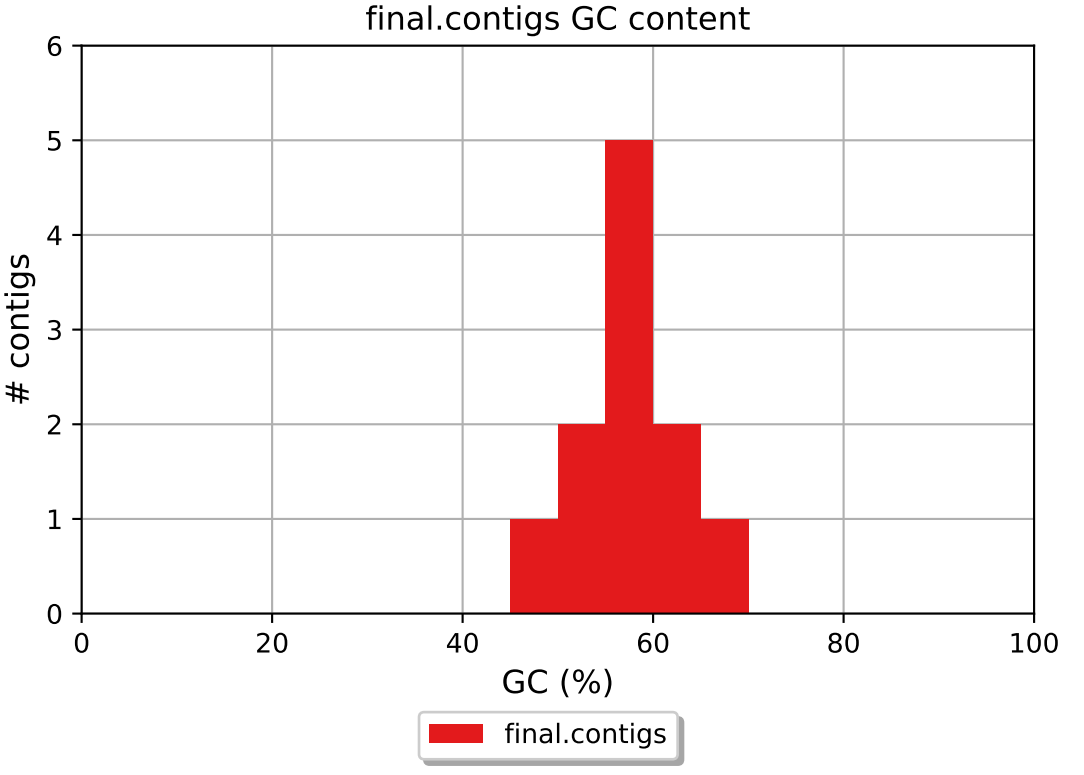
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

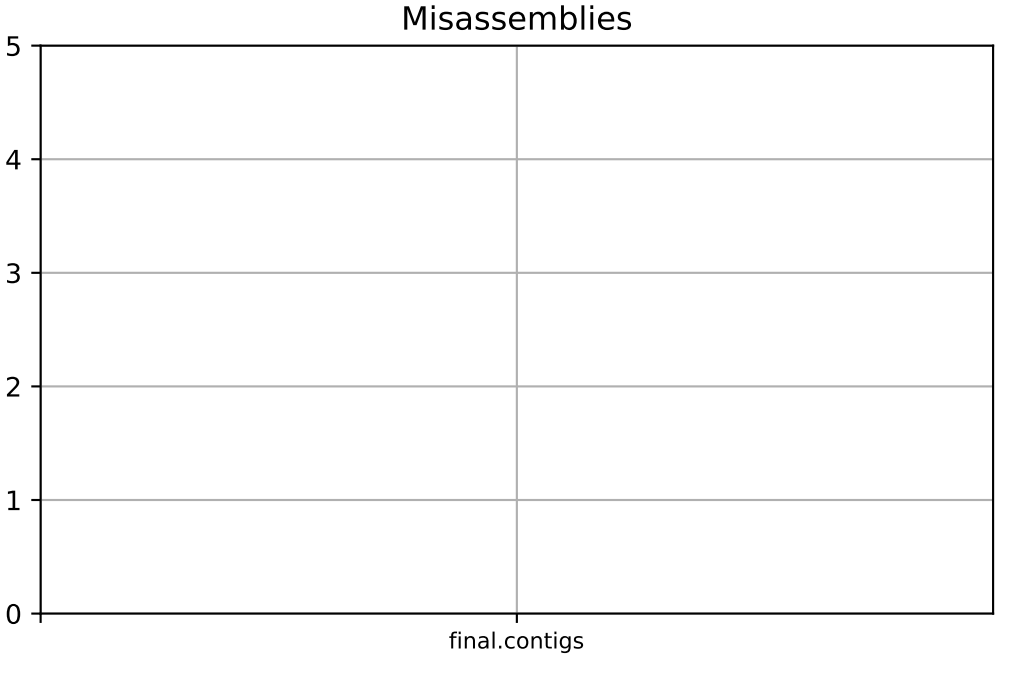

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

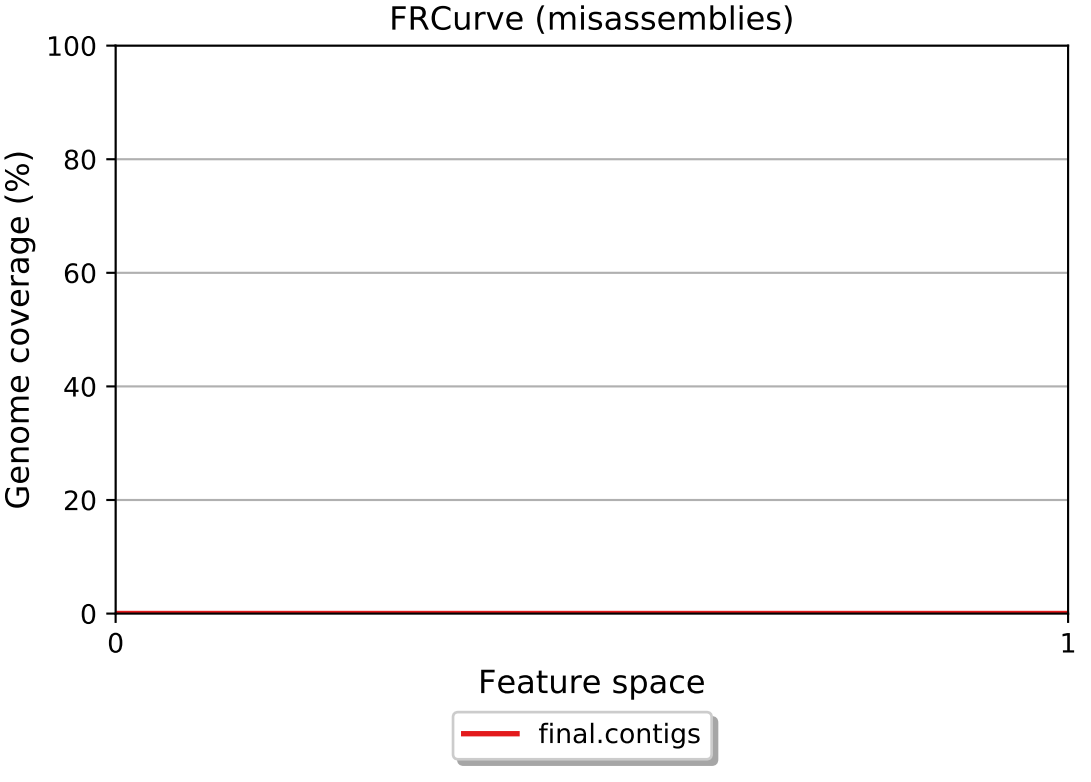

NGx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
final.contigs

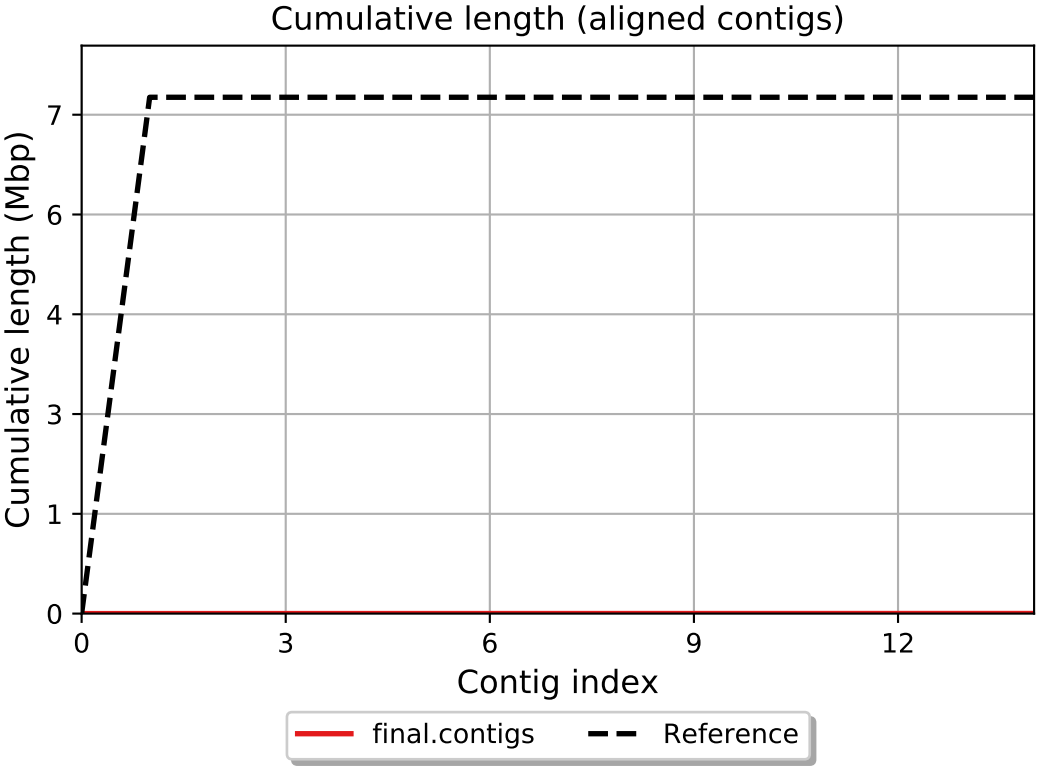

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
7
0
2
4
6
8
10
Contig index
final.contigs
Reference

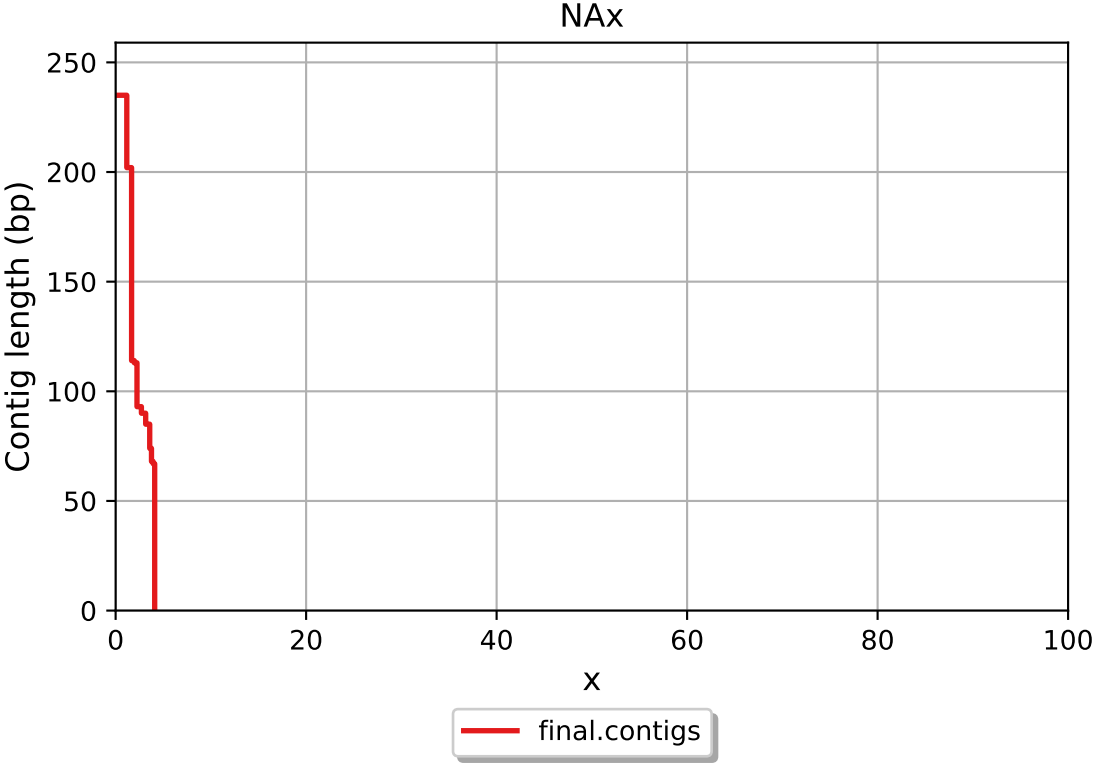

GC content
windows
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

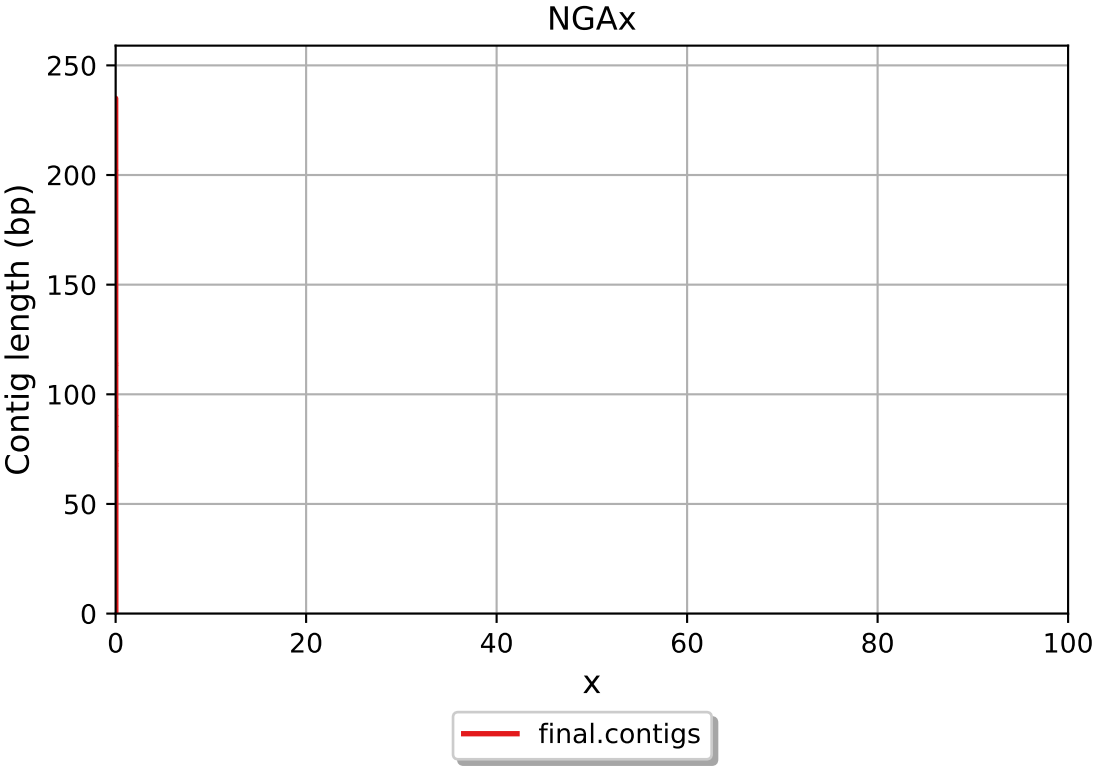

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs


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 (Mbp)
0
1
3
4
6
7
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