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)	36995
Total length (>= 5000 bp)	19203
Total length (>= 10000 bp)	19203
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	16
Largest contig	19203
Total length	42833
Reference length	5654316
GC (%)	60.62
Reference GC (%)	68.93
N50	4306
N75	2018
L50	2
L75	5
# 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	1 + 11 part
Unaligned length	39195
Genome fraction (%)	0.019
Duplication ratio	3.413
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5534.71
# indels per 100 kbp	187.62
Largest alignment	233
Total aligned length	1768
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

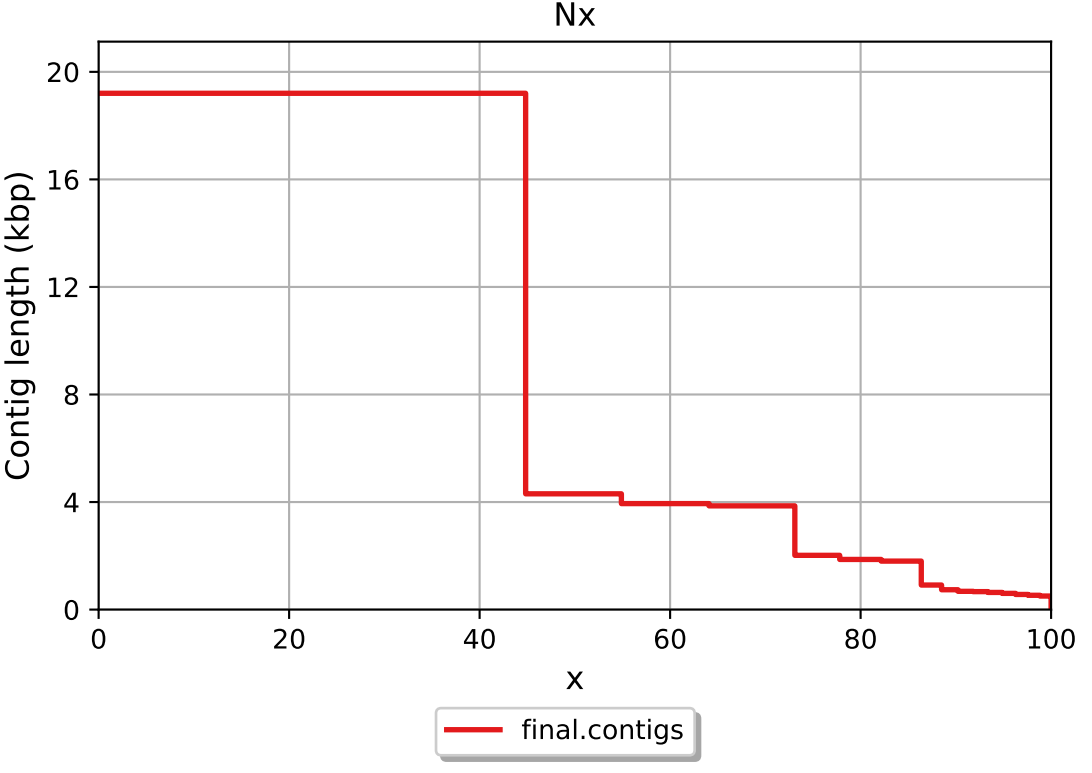
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	8
# possible misassemblies	11
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	59
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

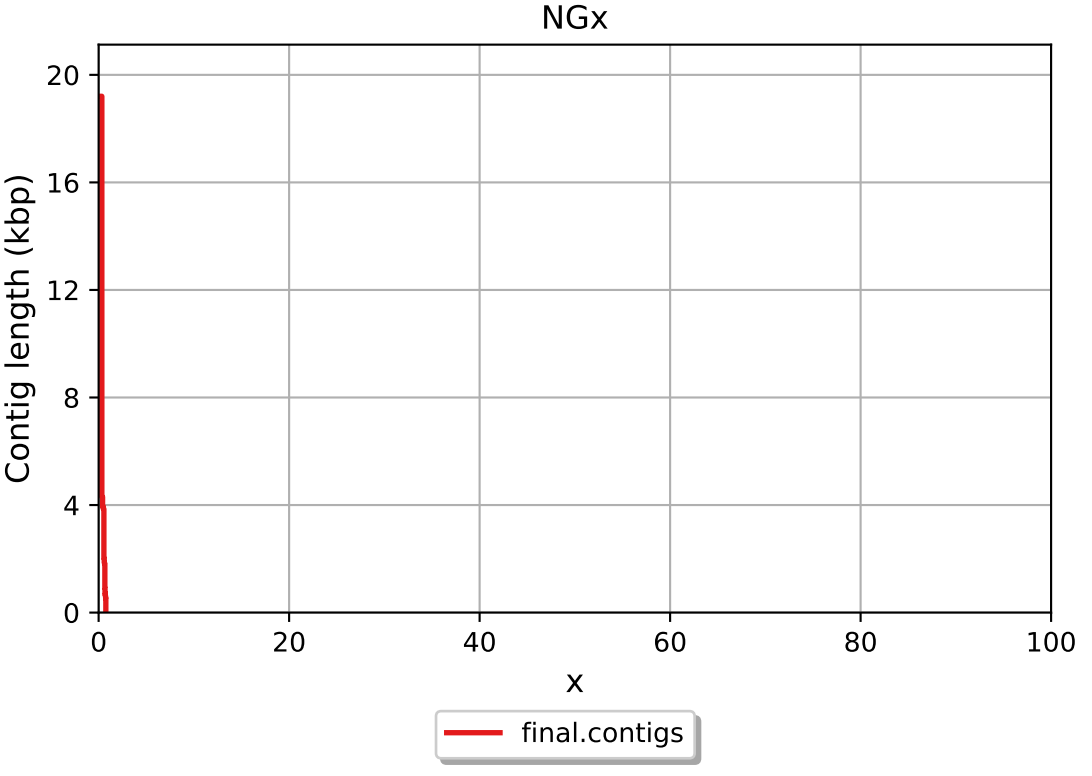
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

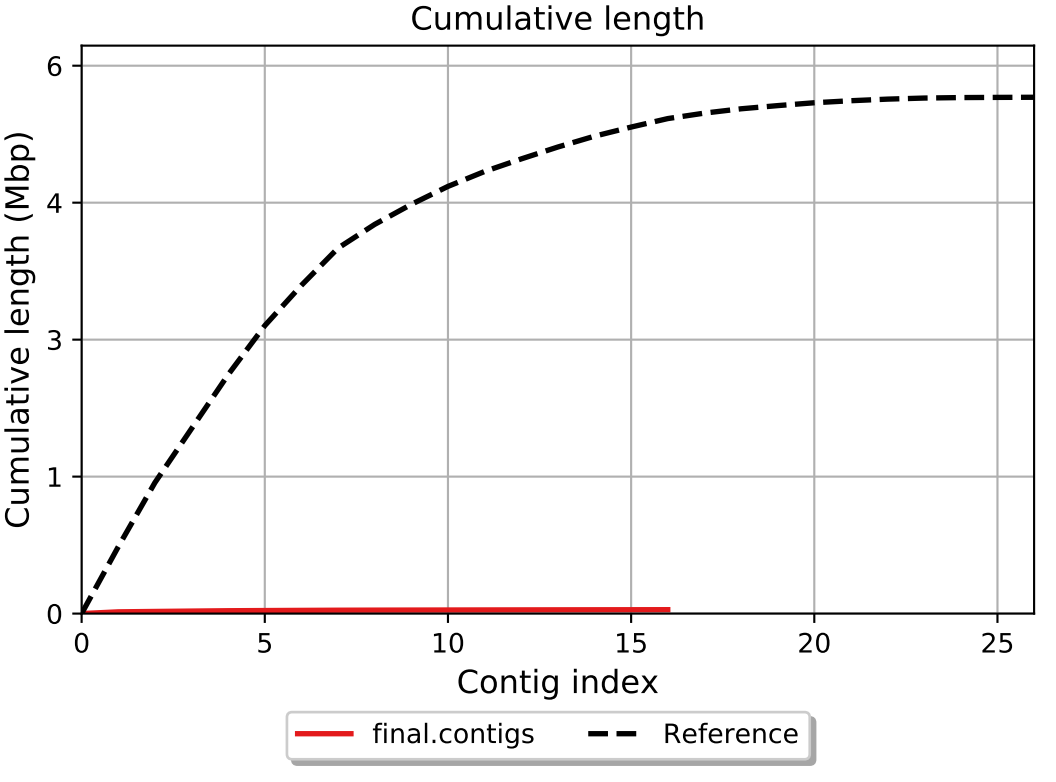
Unaligned report

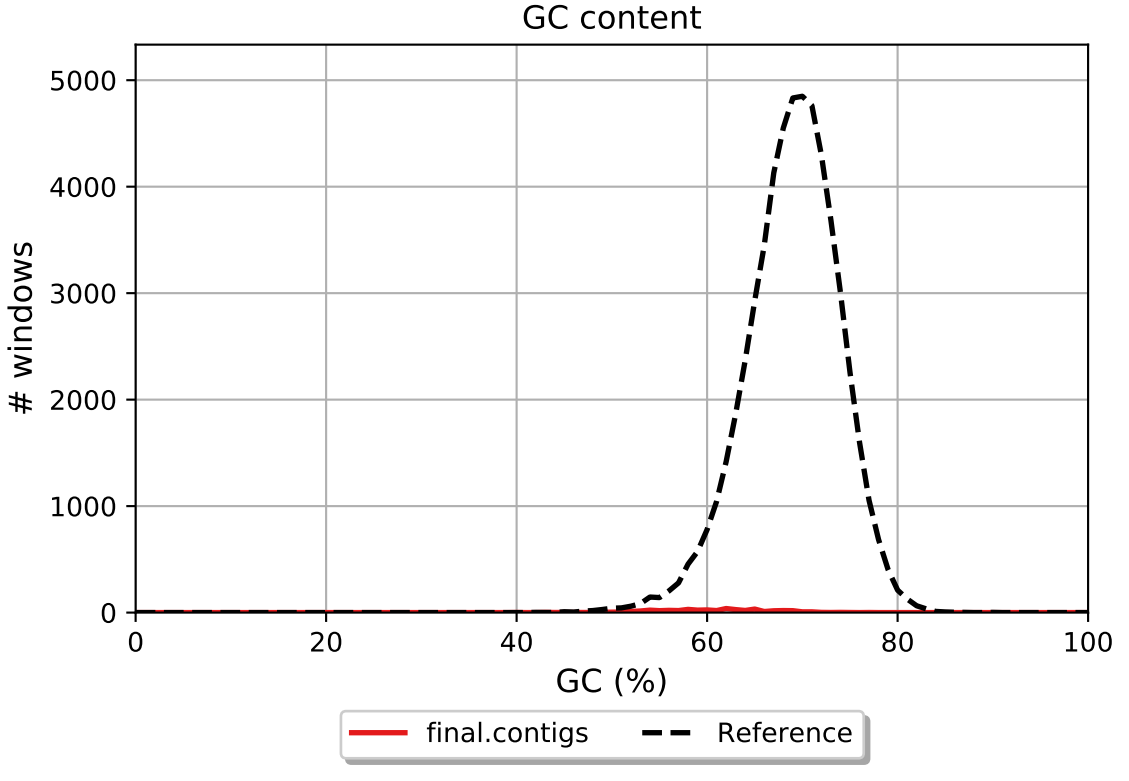
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	603
# partially unaligned contigs	11
Partially unaligned length	38592
# N's	0

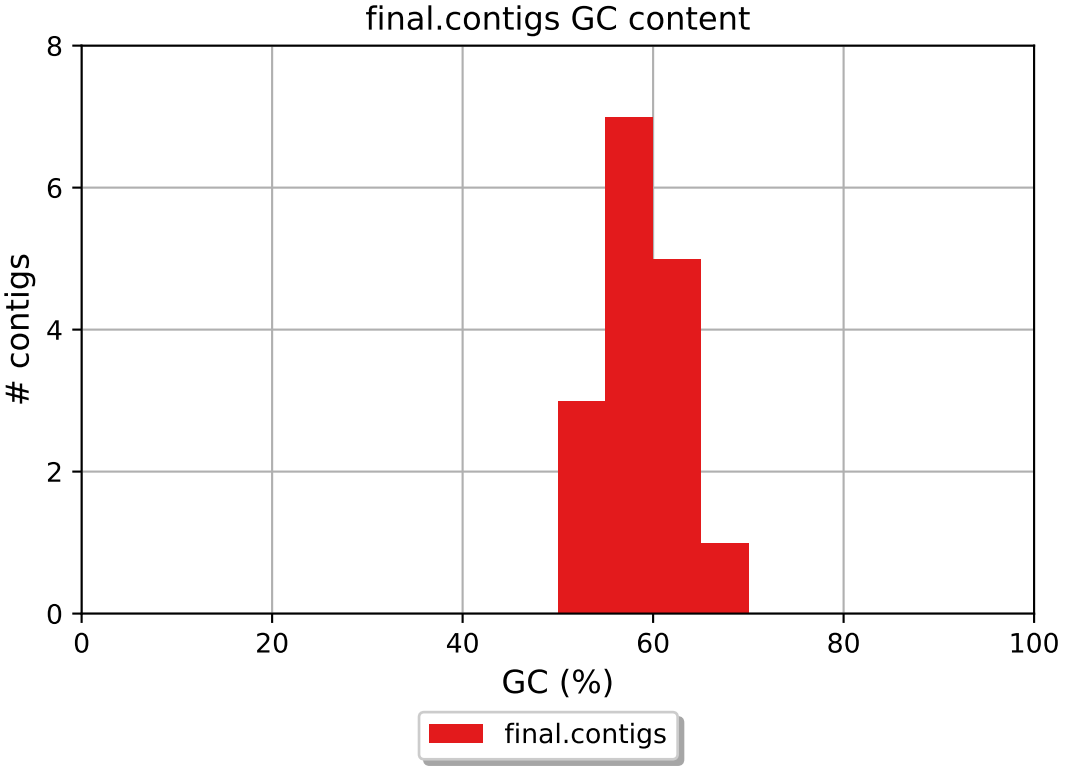
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

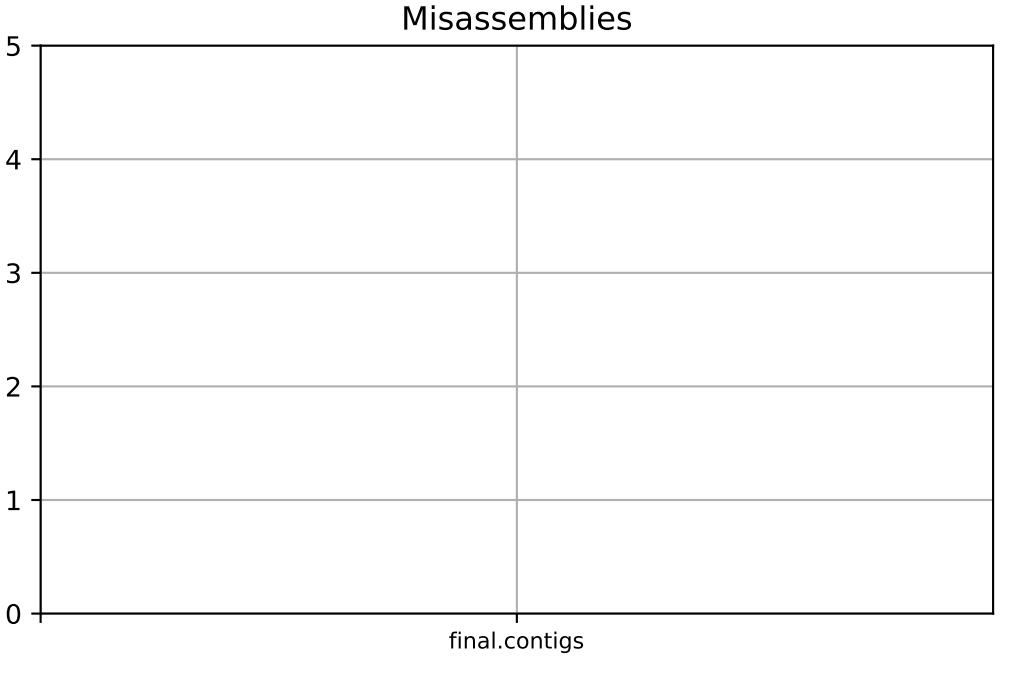

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

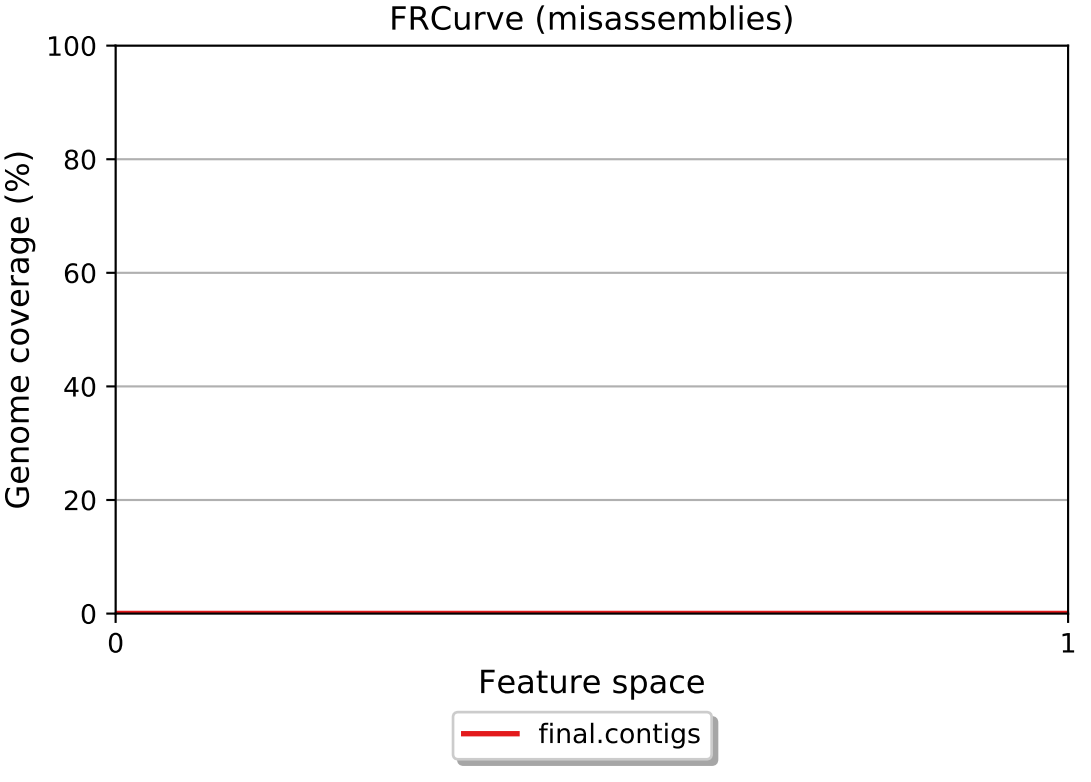

NGx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
final.contigs

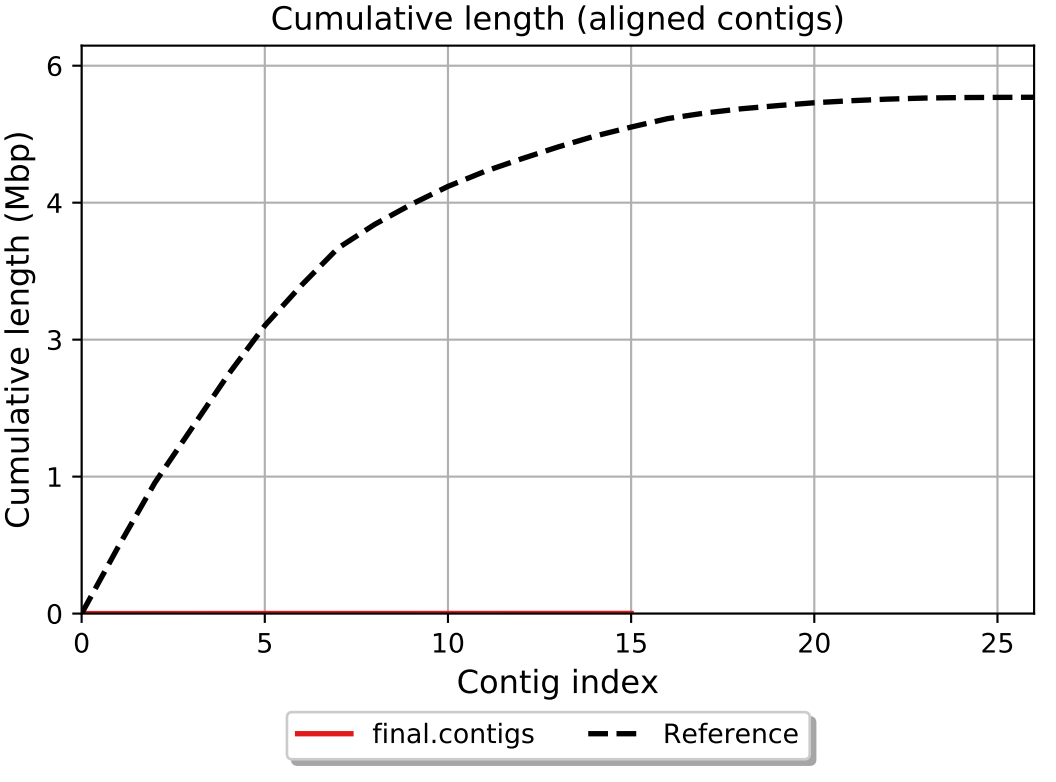

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
5
10
15
20
25
Contig index
final.contigs
Reference

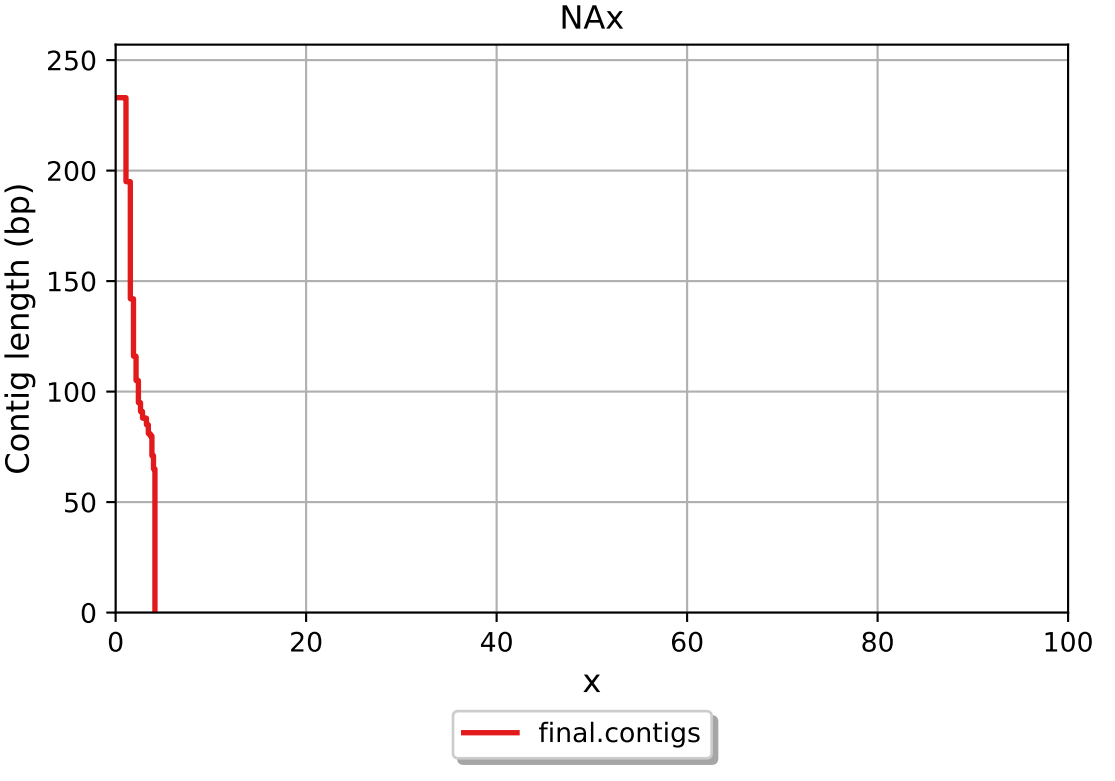

GC content
5000
4000
3000
2000
1000
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

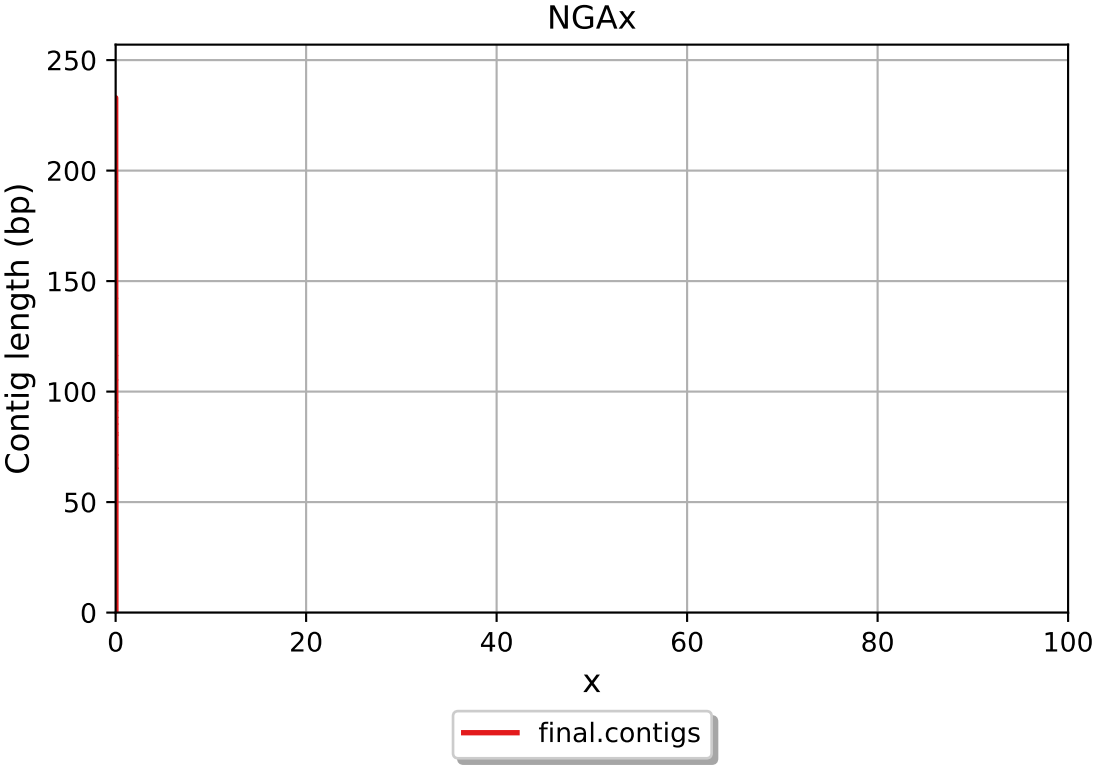

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
final.contigs


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
0
5
10
15
20
25
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