Report

	final.contigs
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	54546
Total length (>= 5000 bp)	15341
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	54
Largest contig	8698
Total length	76363
Reference length	4830181
GC (%)	61.73
Reference GC (%)	67.29
N50	1501
N75	936
L50	11
L75	26
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# unaligned contigs	8 + 27 part
Unaligned length	59374
Genome fraction (%)	0.153
Duplication ratio	2.298
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4274.31
# indels per 100 kbp	135.26
Largest alignment	1497
Total aligned length	9812
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

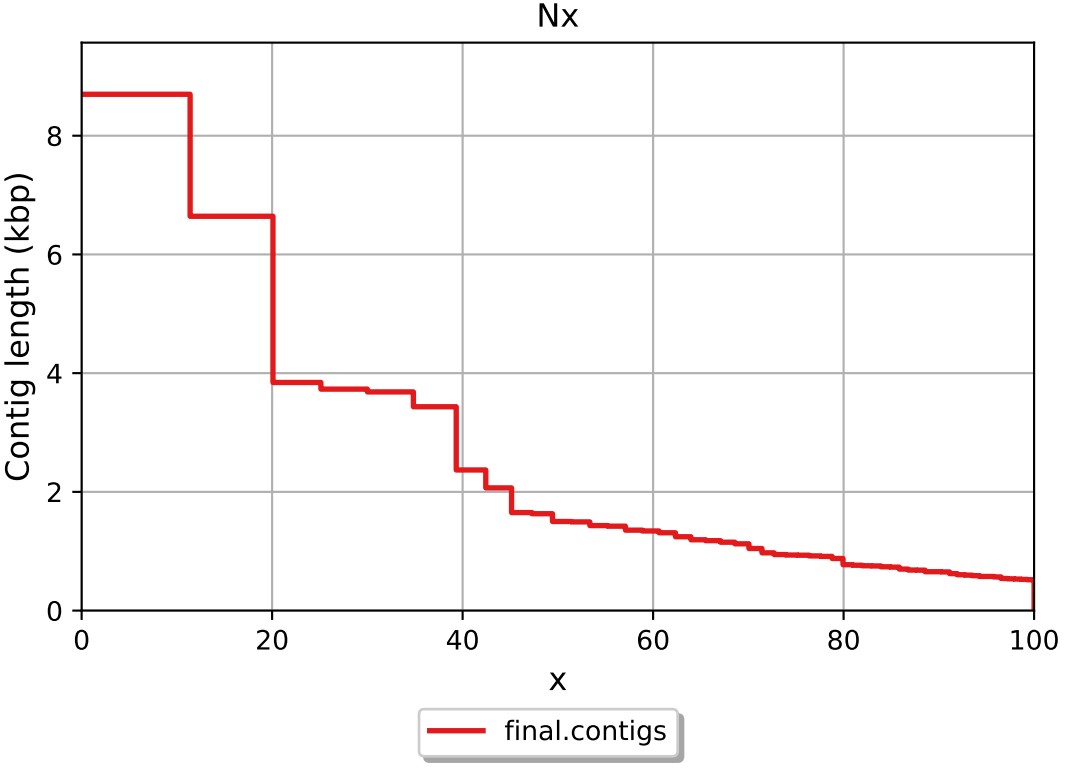
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	26
# possible misassemblies	31
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# mismatches	316
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	15

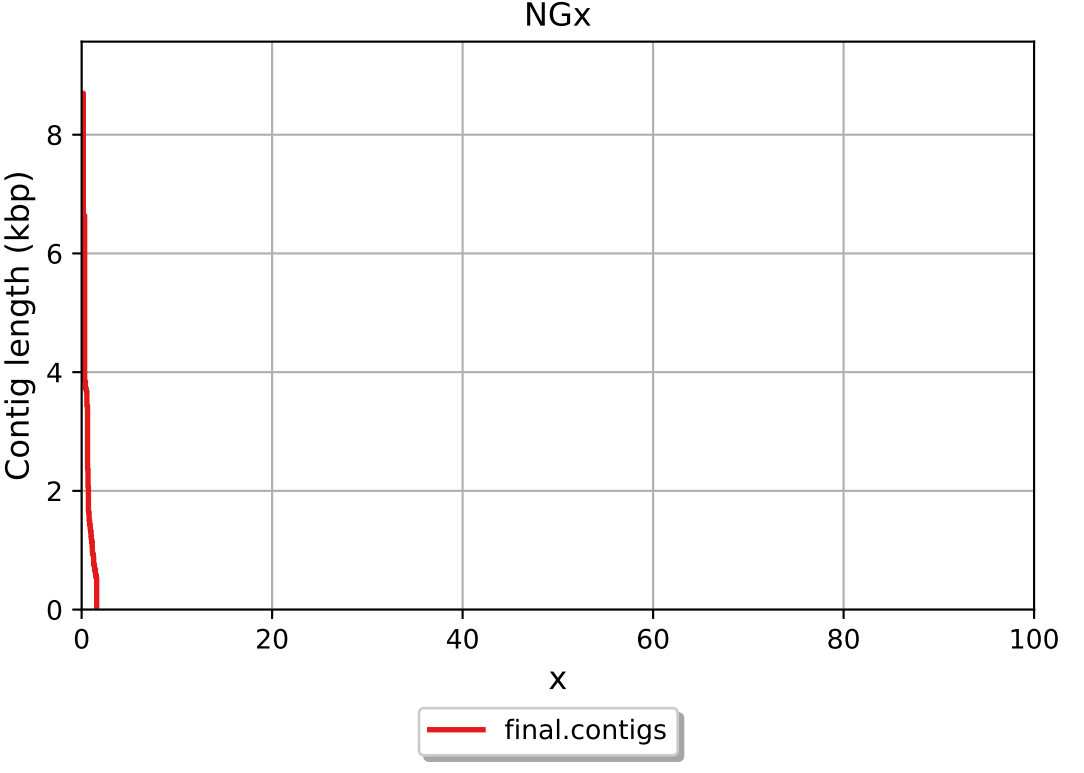
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

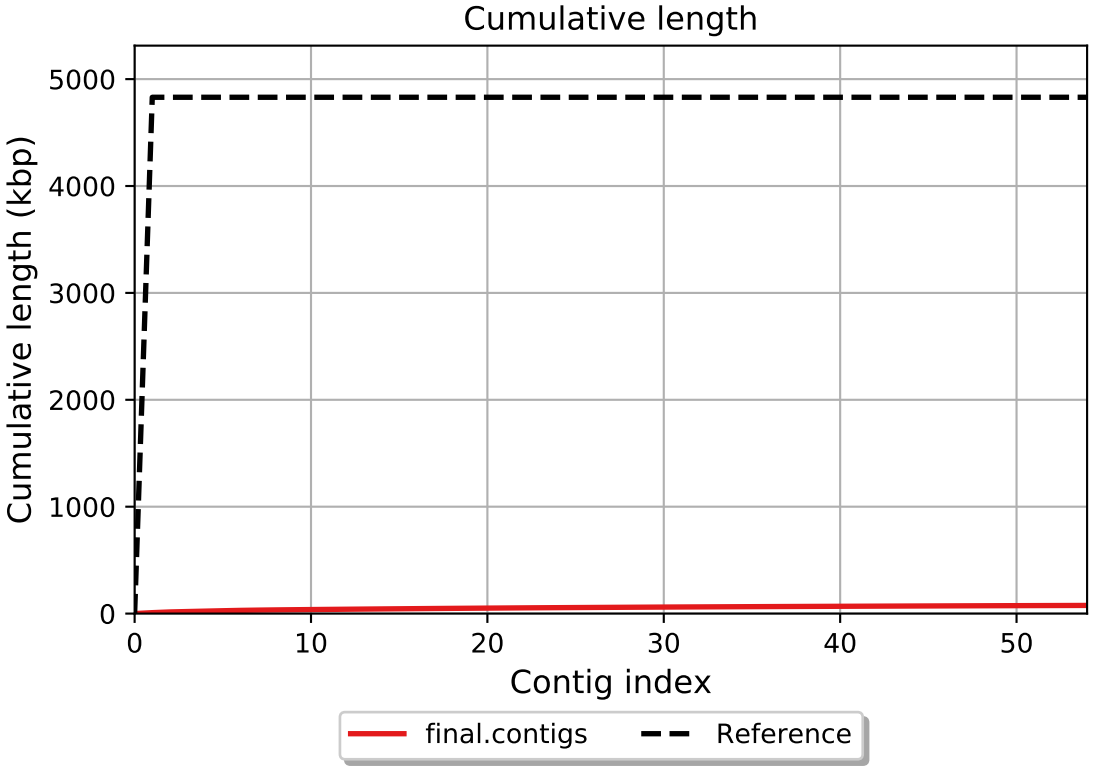
Unaligned report

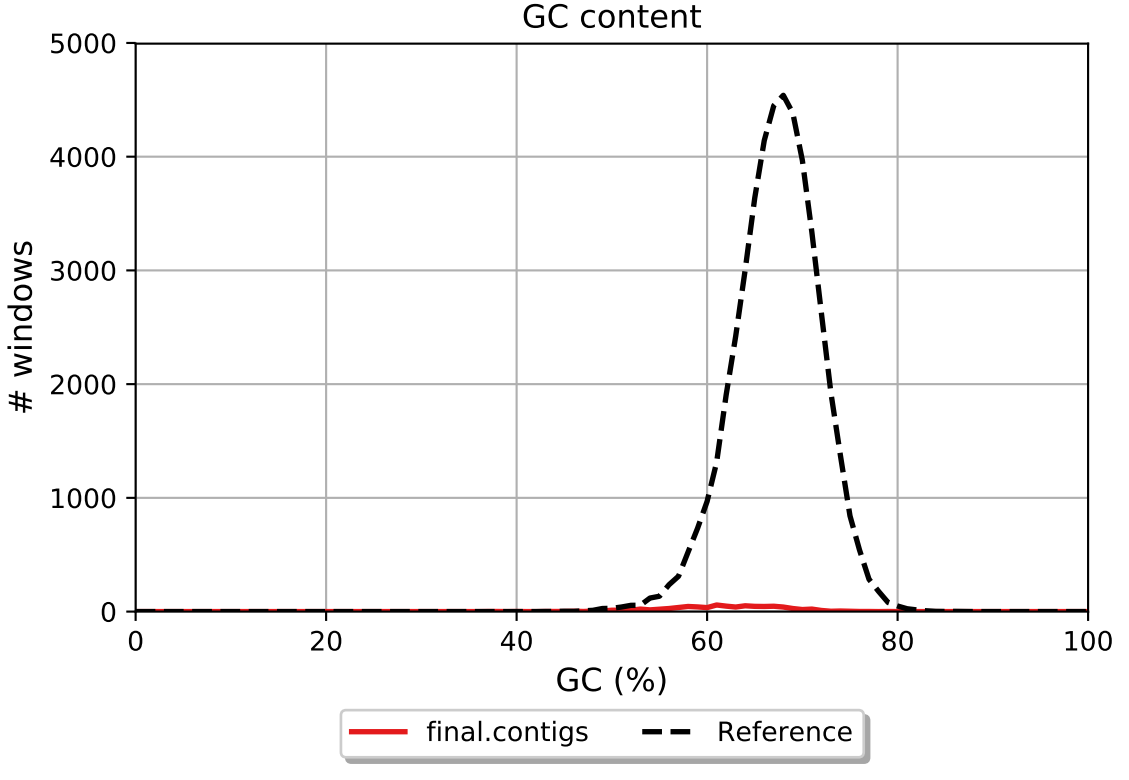
	final.contigs
# fully unaligned contigs	8
Fully unaligned length	5863
# partially unaligned contigs	27
Partially unaligned length	53511
# N's	0

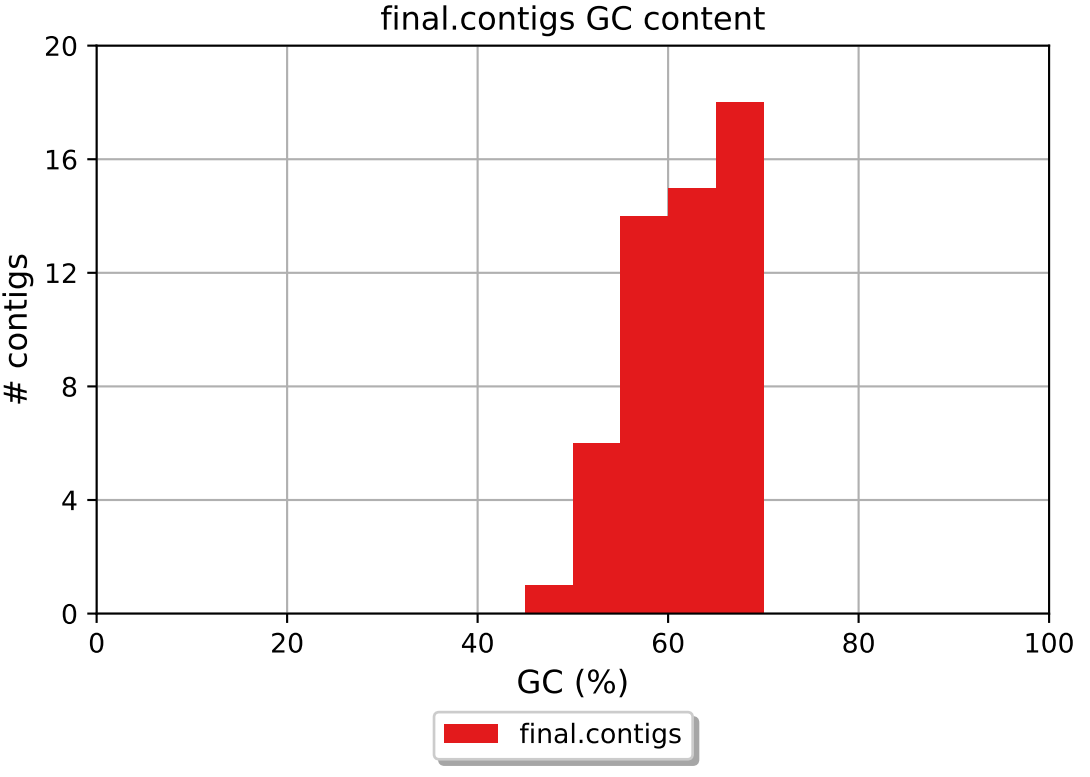
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

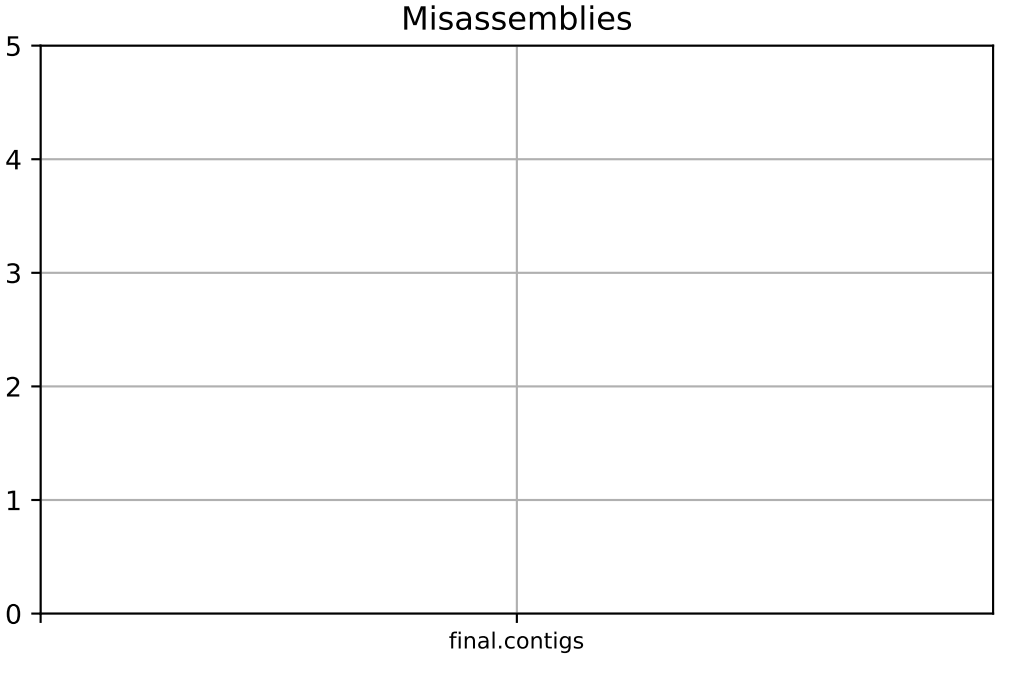

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

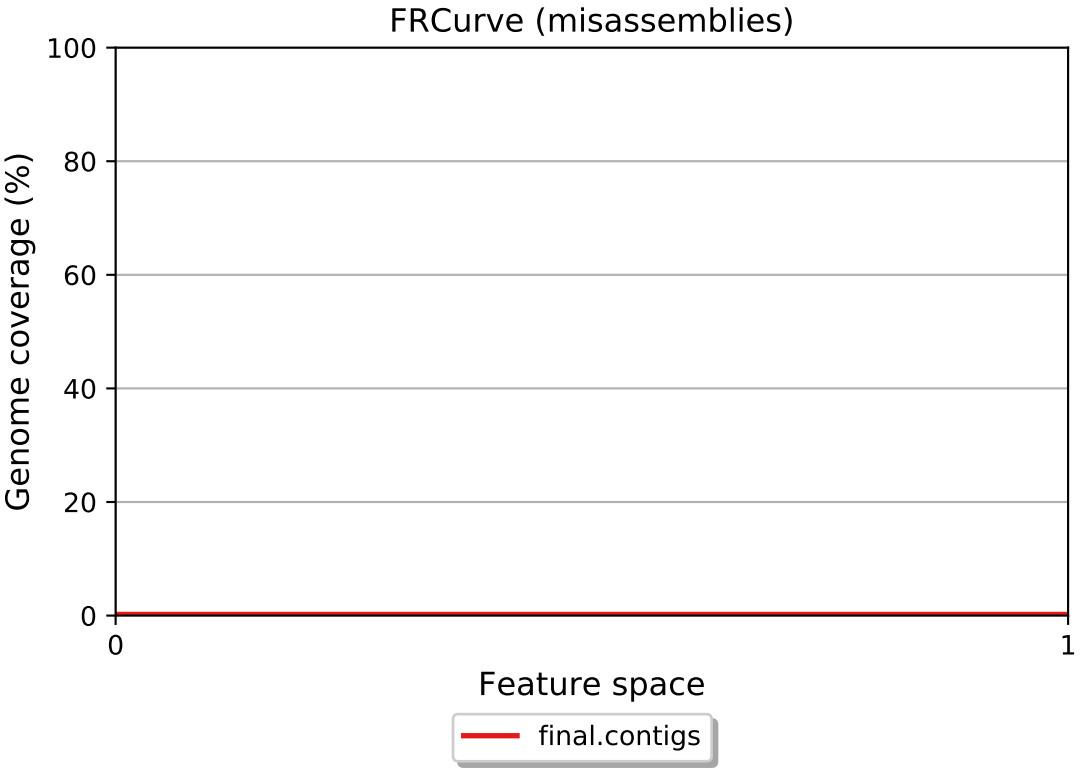

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

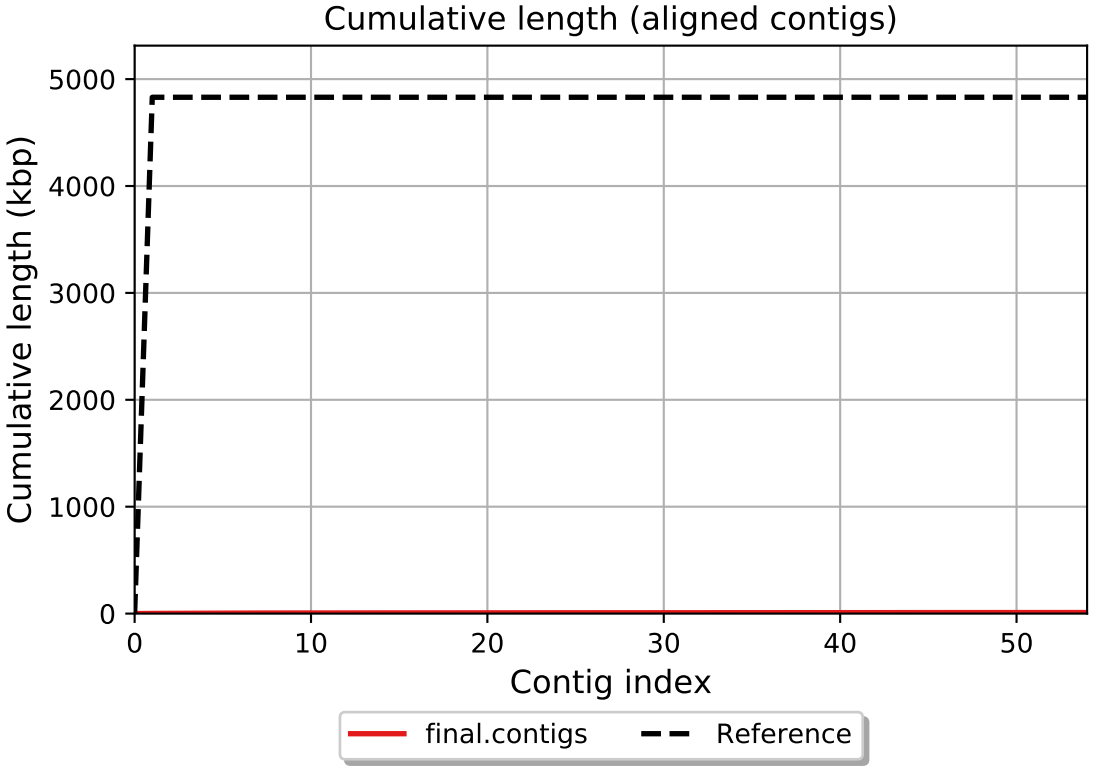

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
Contig index
final.contigs
Reference

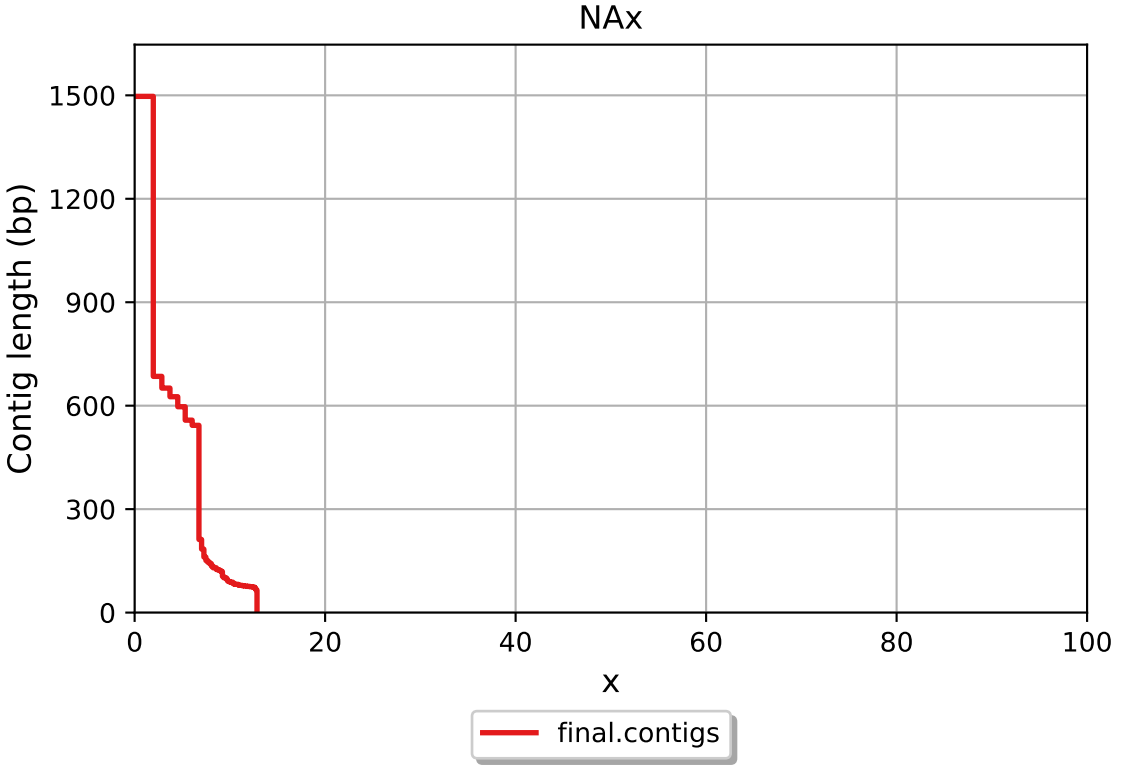

GC content
5000
4000
3000
2000
1000
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

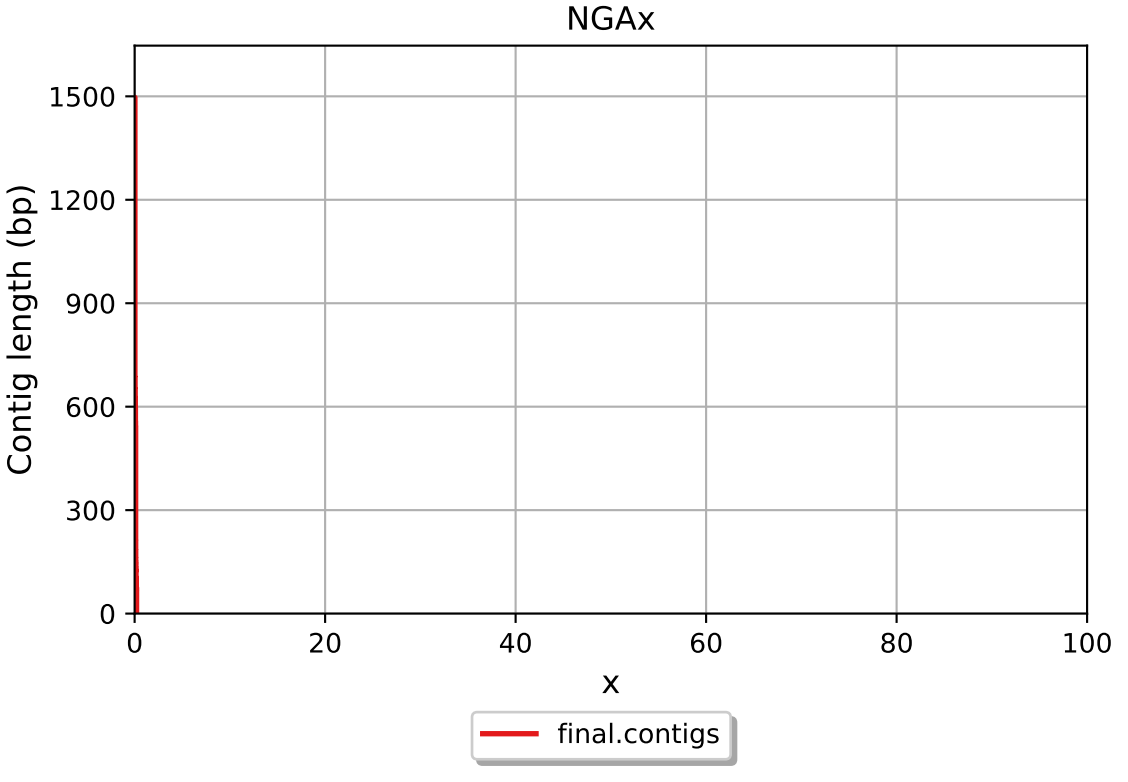

final.contigs GC content
20
16
12
8
4
0
contigs
0
20
40
60
80
100
GC (%)
final.contigs


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)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
Contig index
final.contigs
Reference


NAx
Contig length (bp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs