Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	52820
Total length (>= 5000 bp)	43585
Total length (>= 10000 bp)	36014
Total length (>= 25000 bp)	36014
Total length (>= 50000 bp)	0
# contigs	16
Largest contig	36014
Total length	58286
Reference length	5695417
GC (%)	46.13
Reference GC (%)	72.40
N50	36014
N75	2806
L50	1
L75	3
# 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	4 + 9 part
Unaligned length	55272
Genome fraction (%)	0.012
Duplication ratio	4.432
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6029.41
# indels per 100 kbp	0.00
Largest alignment	105
Total aligned length	1249
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

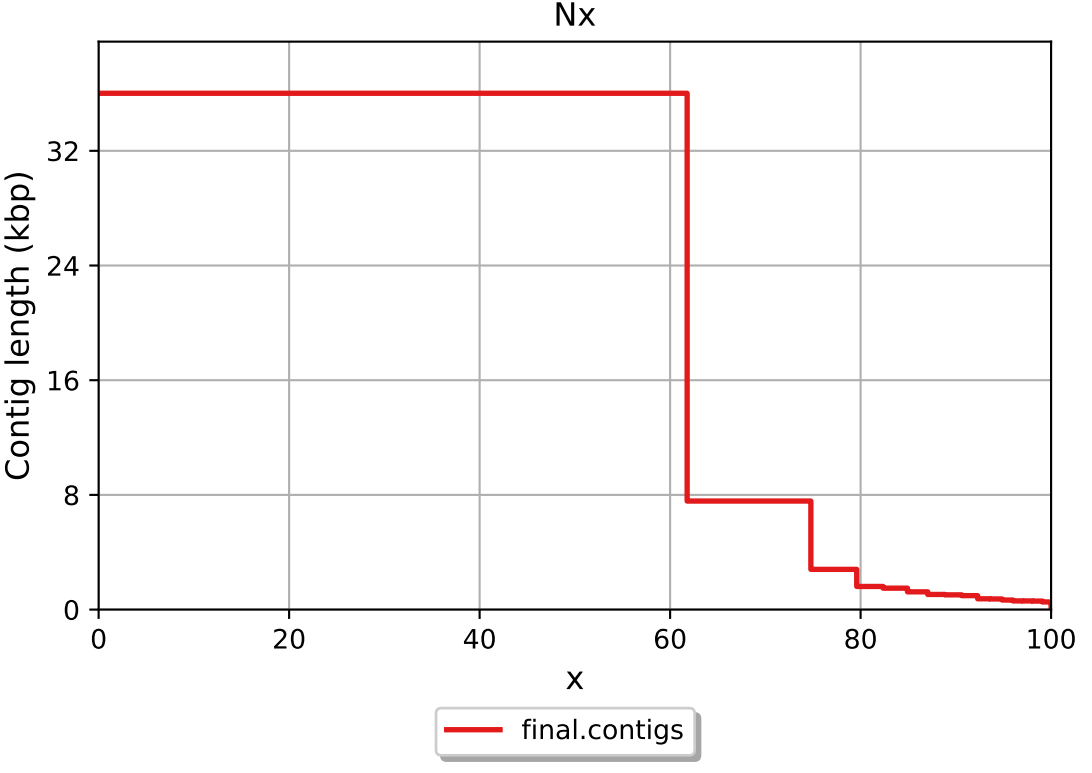
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	7
# possible misassemblies	8
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	41
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

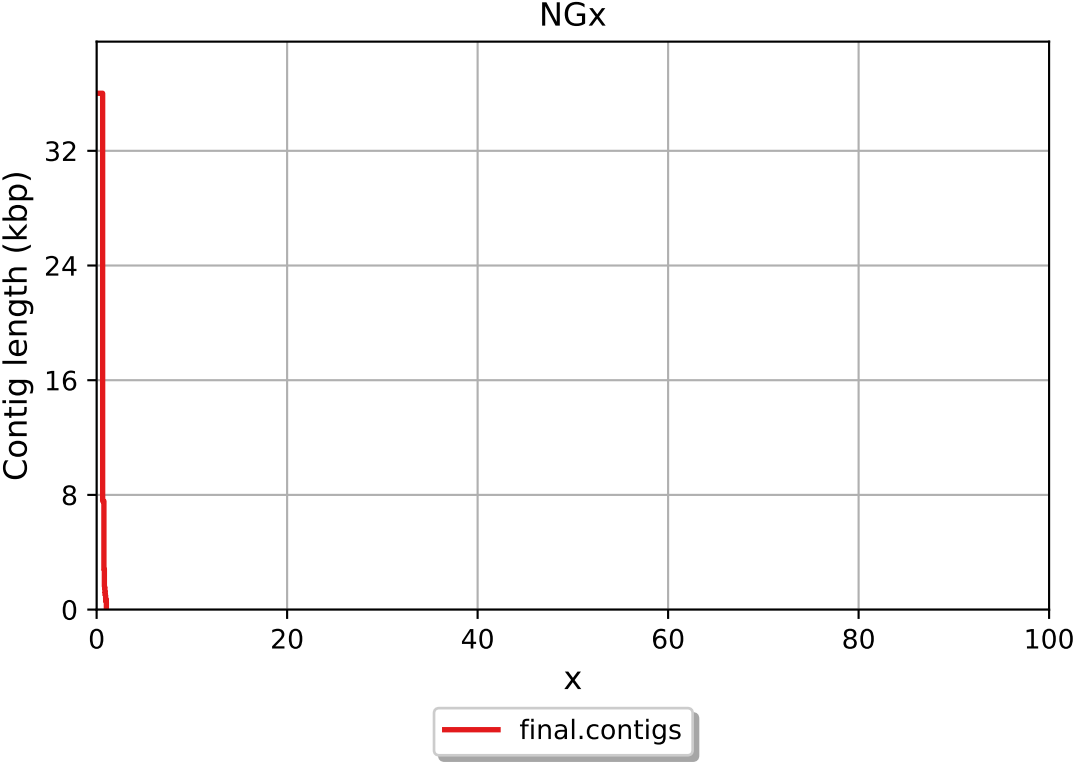
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

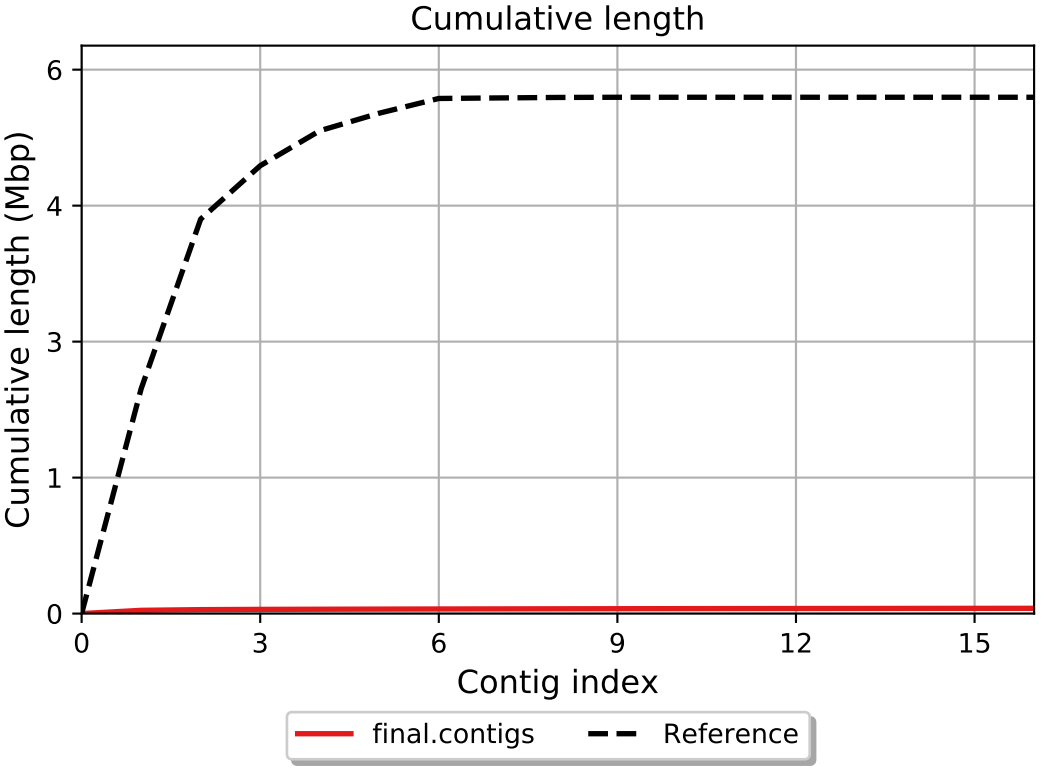
Unaligned report

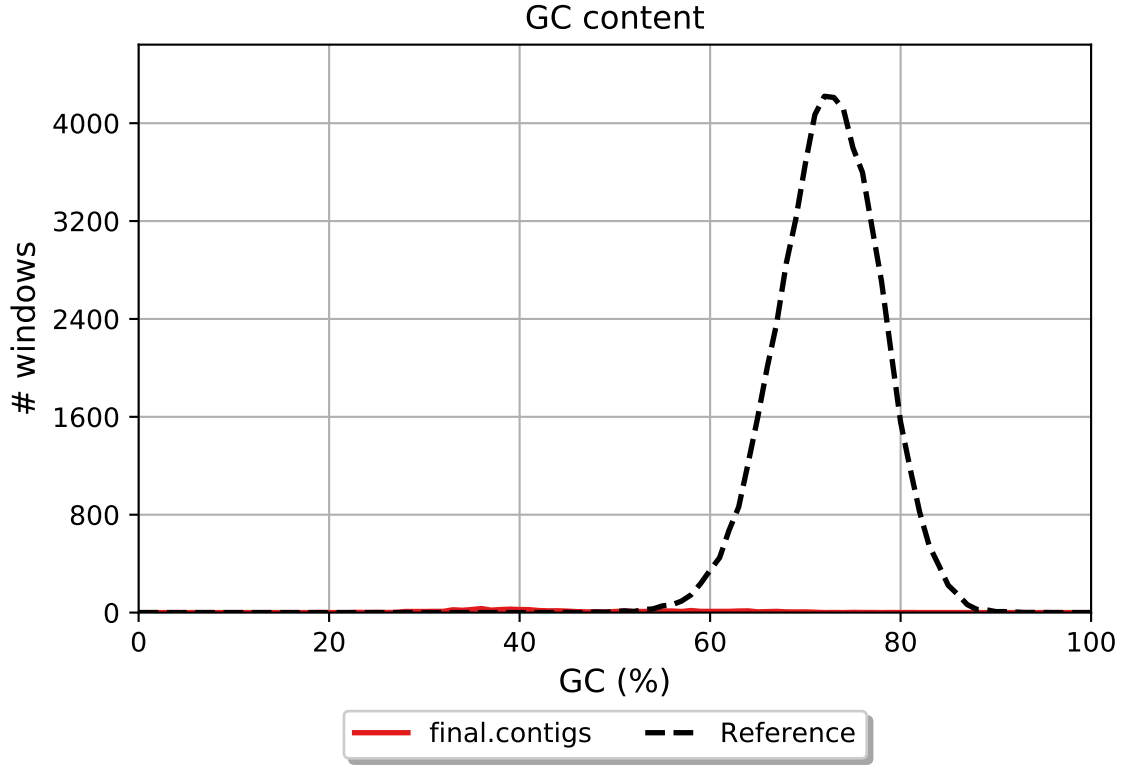
	final.contigs
# fully unaligned contigs	4
Fully unaligned length	45802
# partially unaligned contigs	9
Partially unaligned length	9470
# N's	0

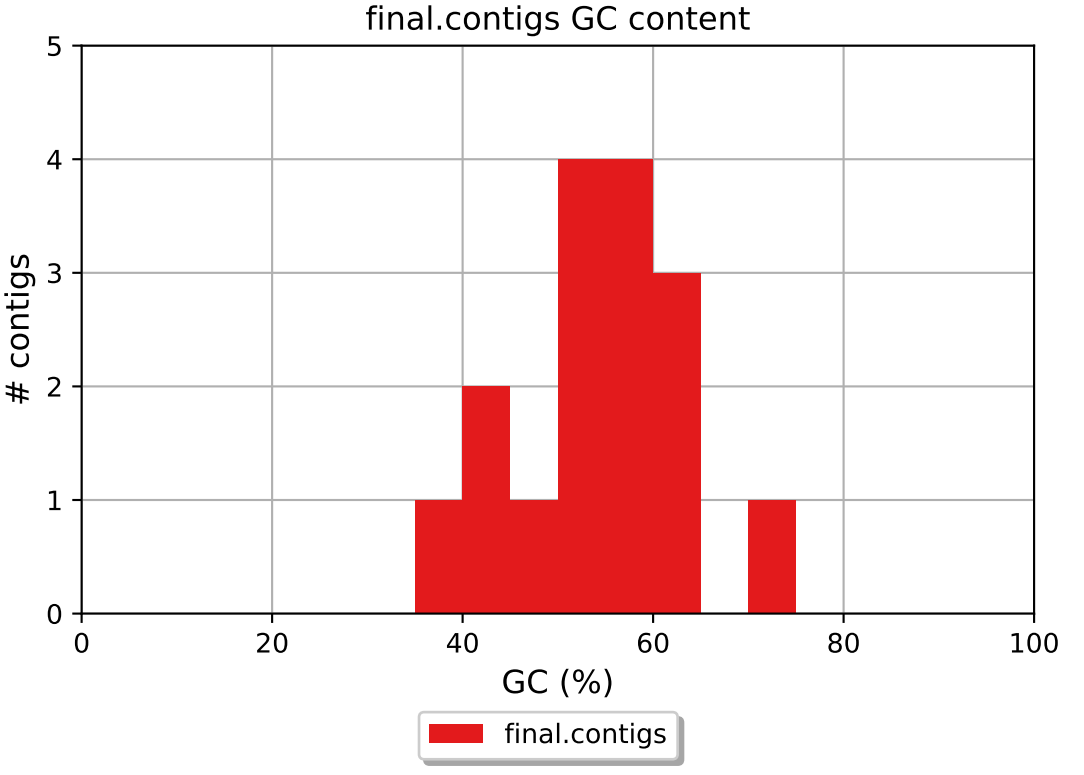
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

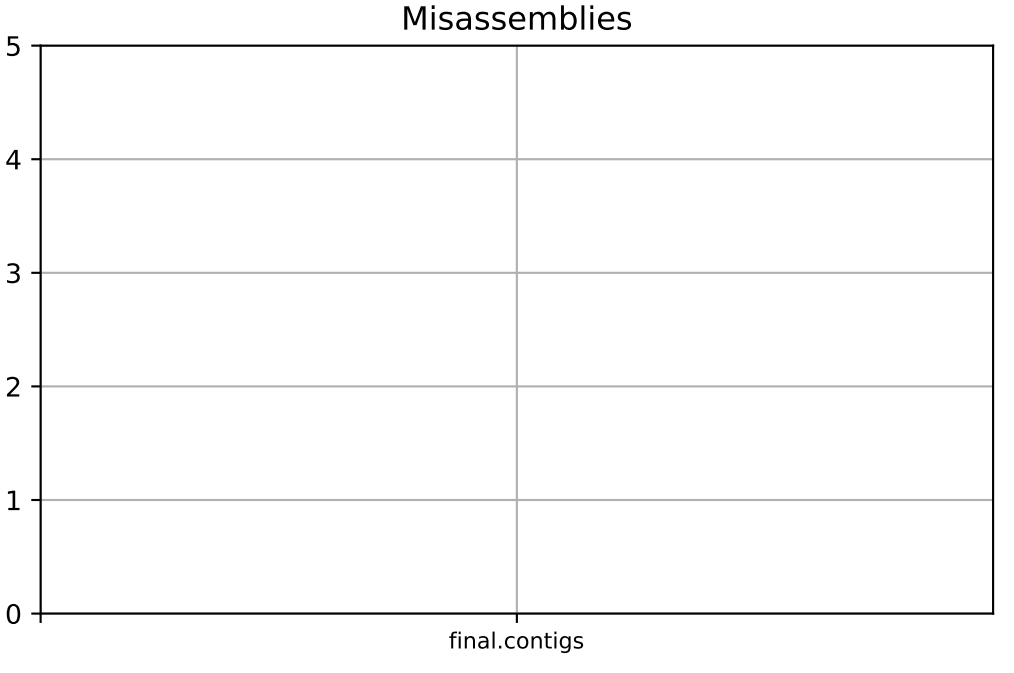

Nx
Contig length (kbp)
0
8
16
24
32
0
20
40
60
80
100
x
final.contigs

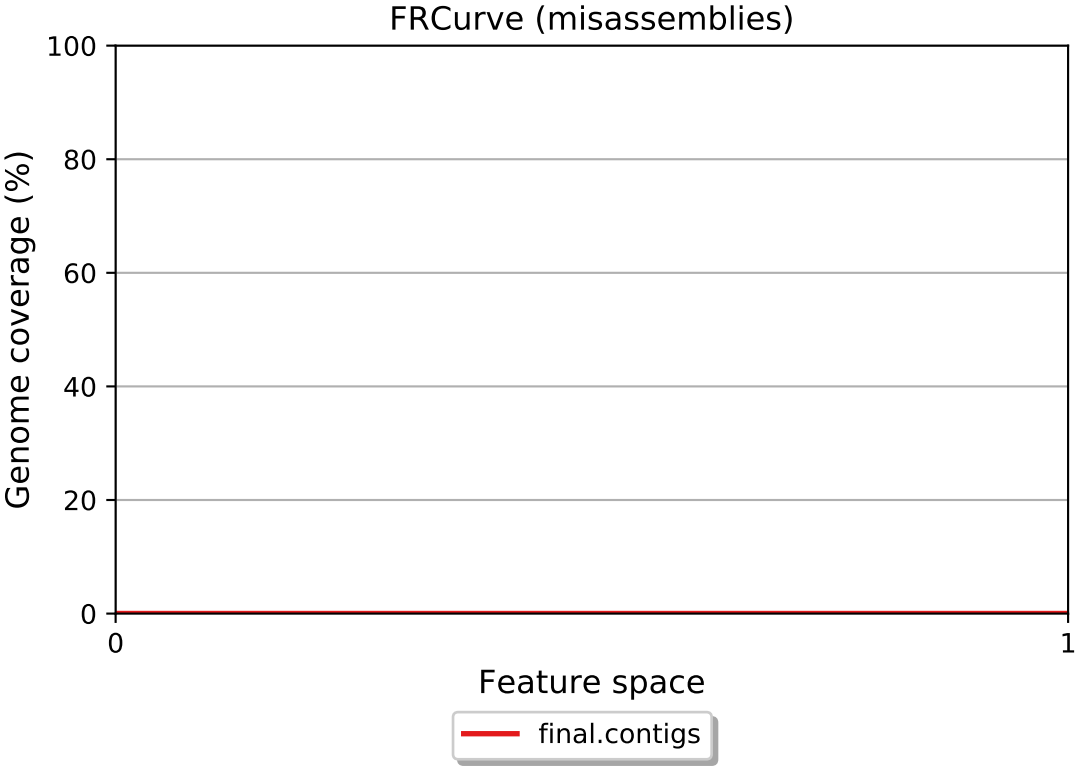

NGx
Contig length (kbp)
0
8
16
24
32
0
20
40
60
80
100
x
final.contigs

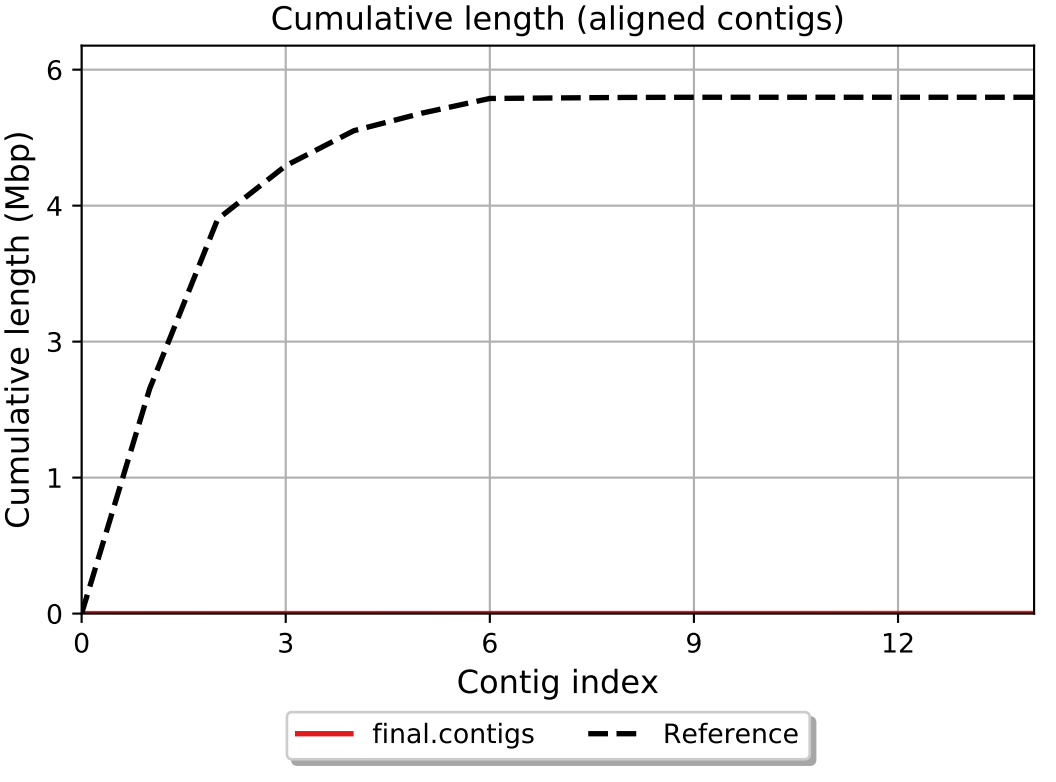

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
3
6
9
12
15
Contig index
final.contigs
Reference

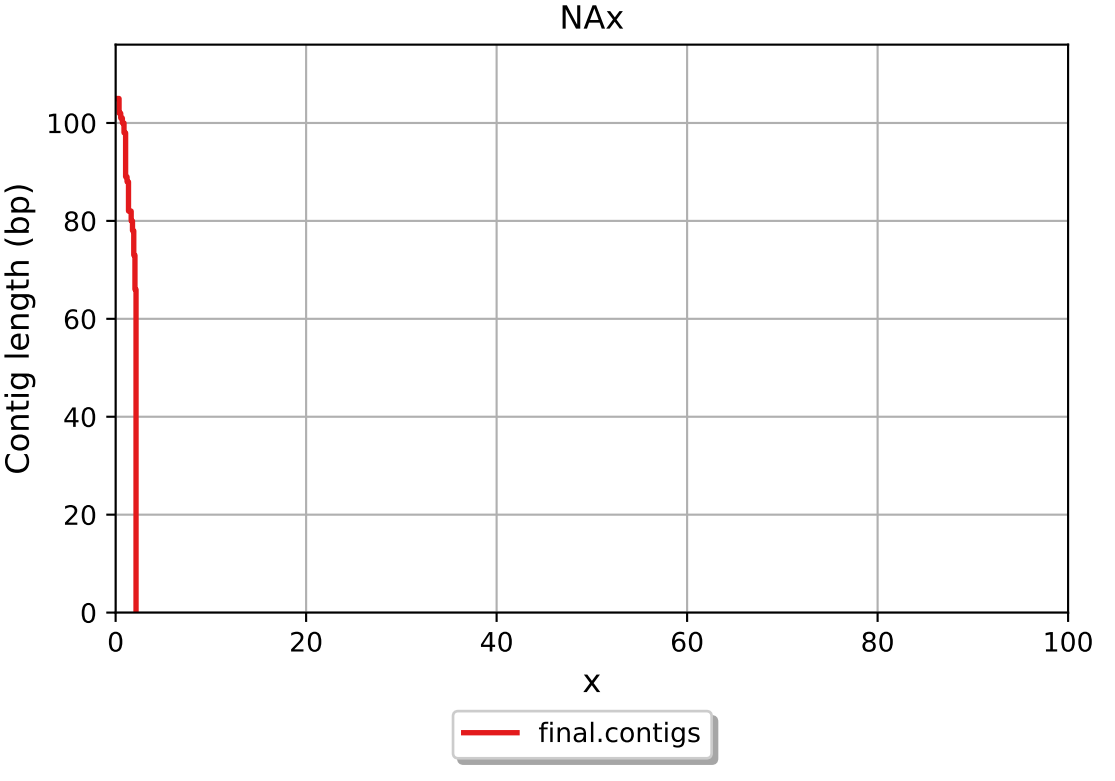

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

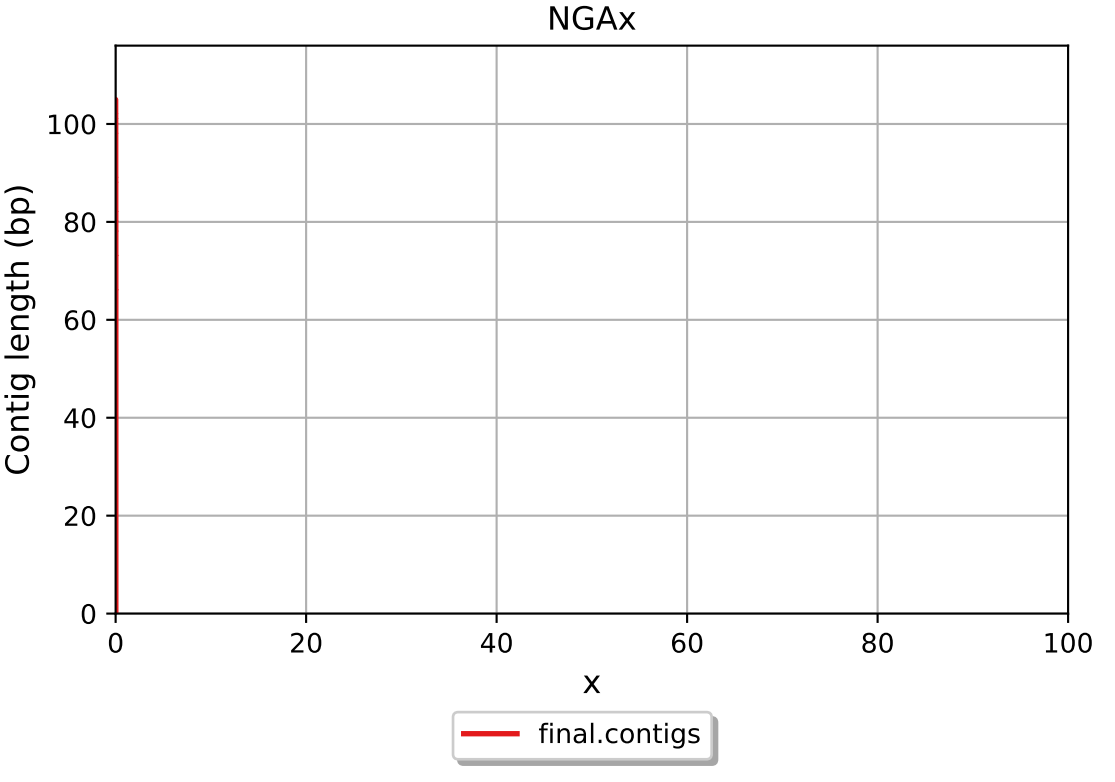

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


FRCurve (misassemblies)
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
3
6
9
12
Contig index
final.contigs
Reference


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


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