Report

	final.contigs
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	132532
Total length (>= 5000 bp)	100278
Total length (>= 10000 bp)	91657
Total length (>= 25000 bp)	91657
Total length (>= 50000 bp)	91657
# contigs	21
Largest contig	91657
Total length	136393
Reference length	3261541
GC (%)	57.63
Reference GC (%)	56.74
N50	91657
N75	4635
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 17 part
Unaligned length	131552
Genome fraction (%)	0.077
Duplication ratio	1.916
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2019.00
# indels per 100 kbp	118.76
Largest alignment	869
Total aligned length	3014
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

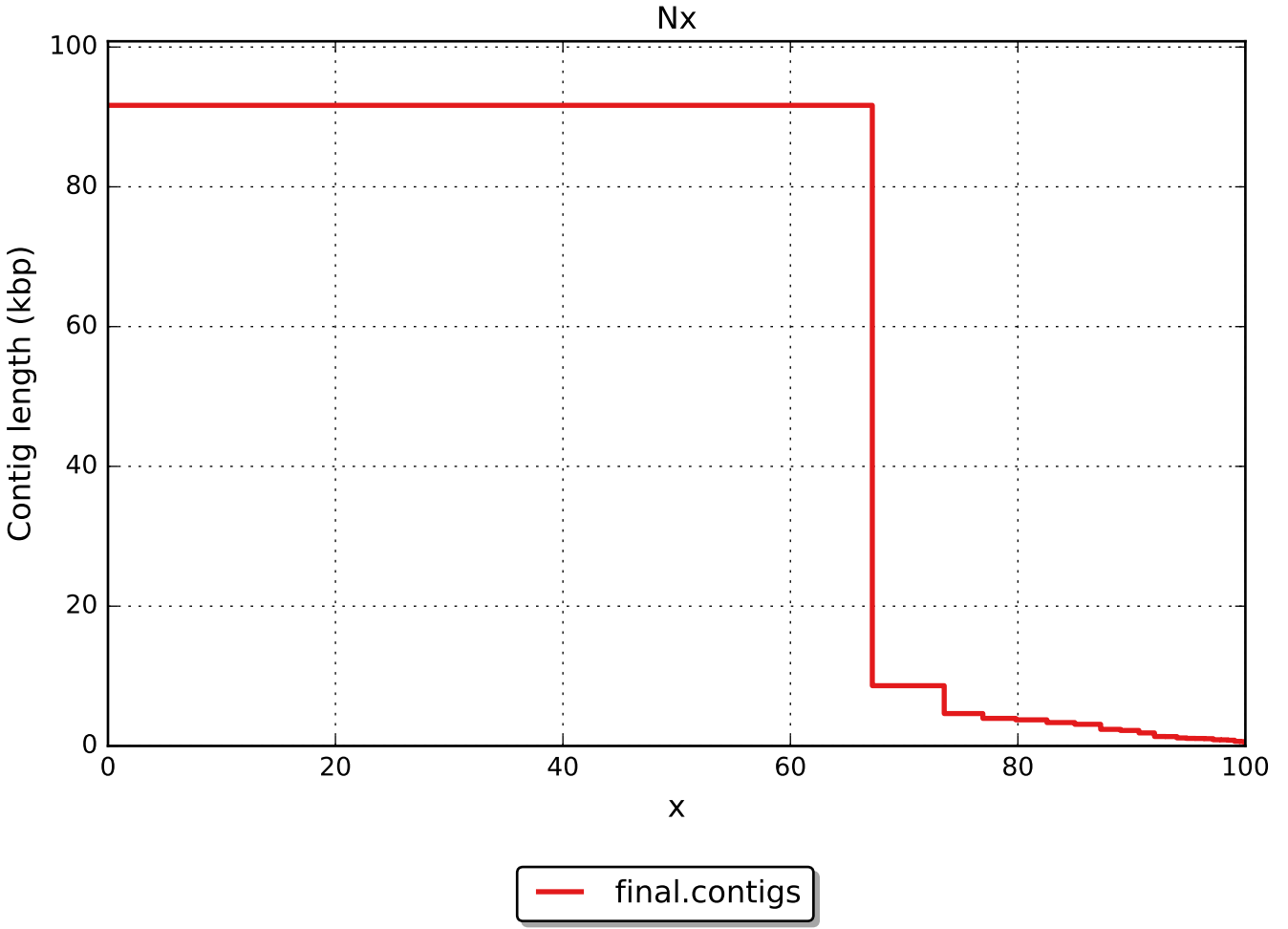
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	51
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

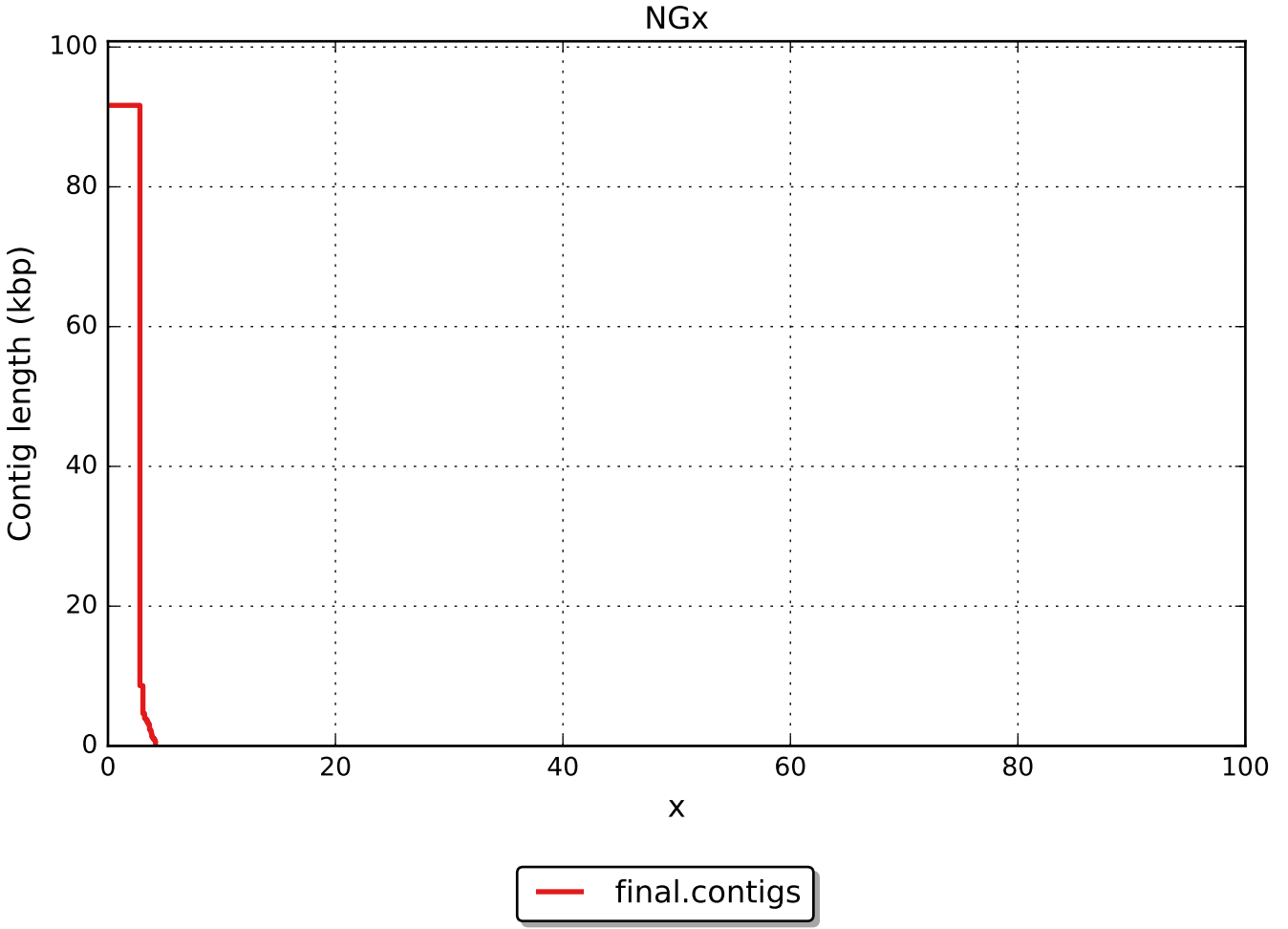
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

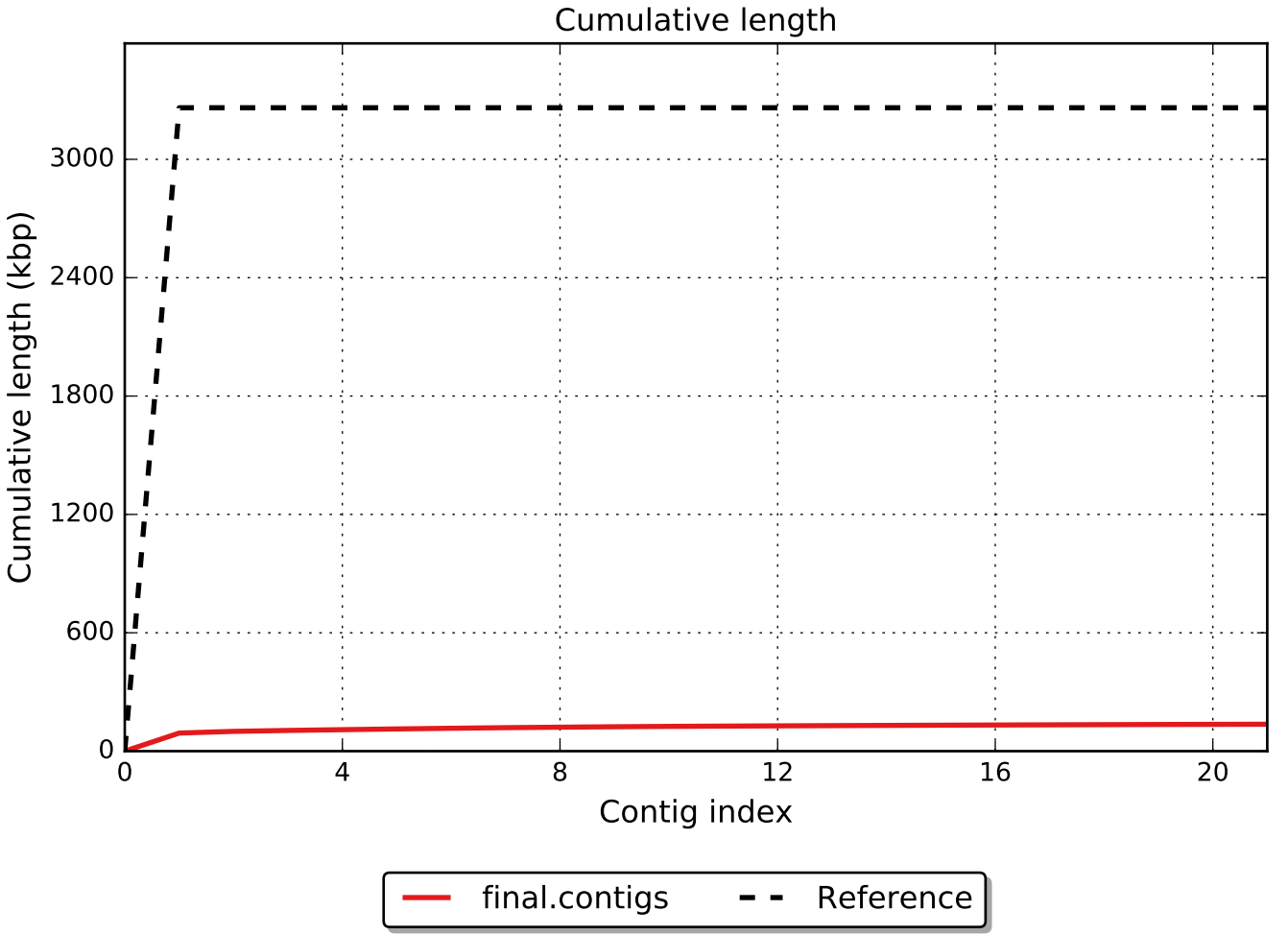
Unaligned report

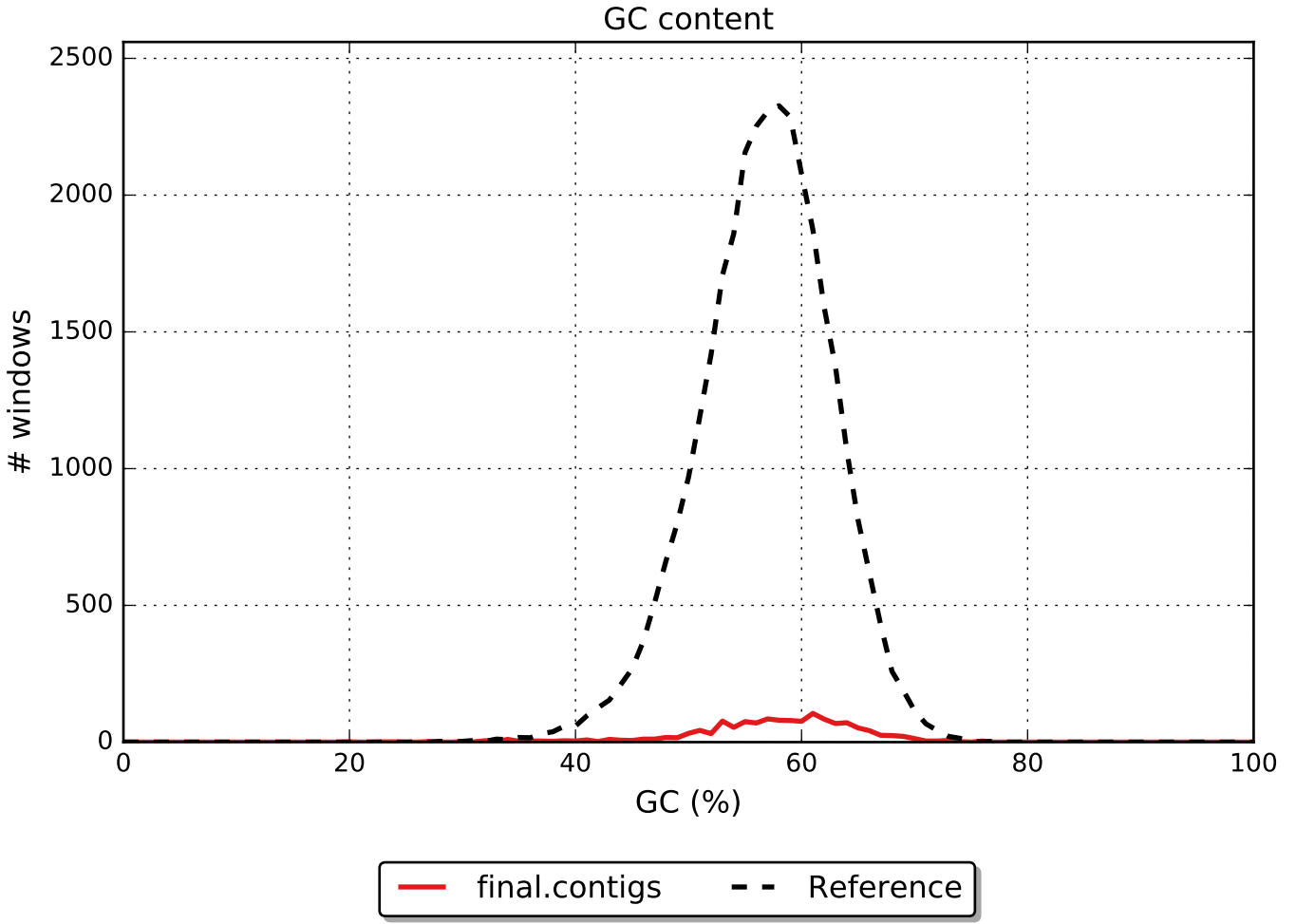
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	17
Partially unaligned length	131552
# N's	0

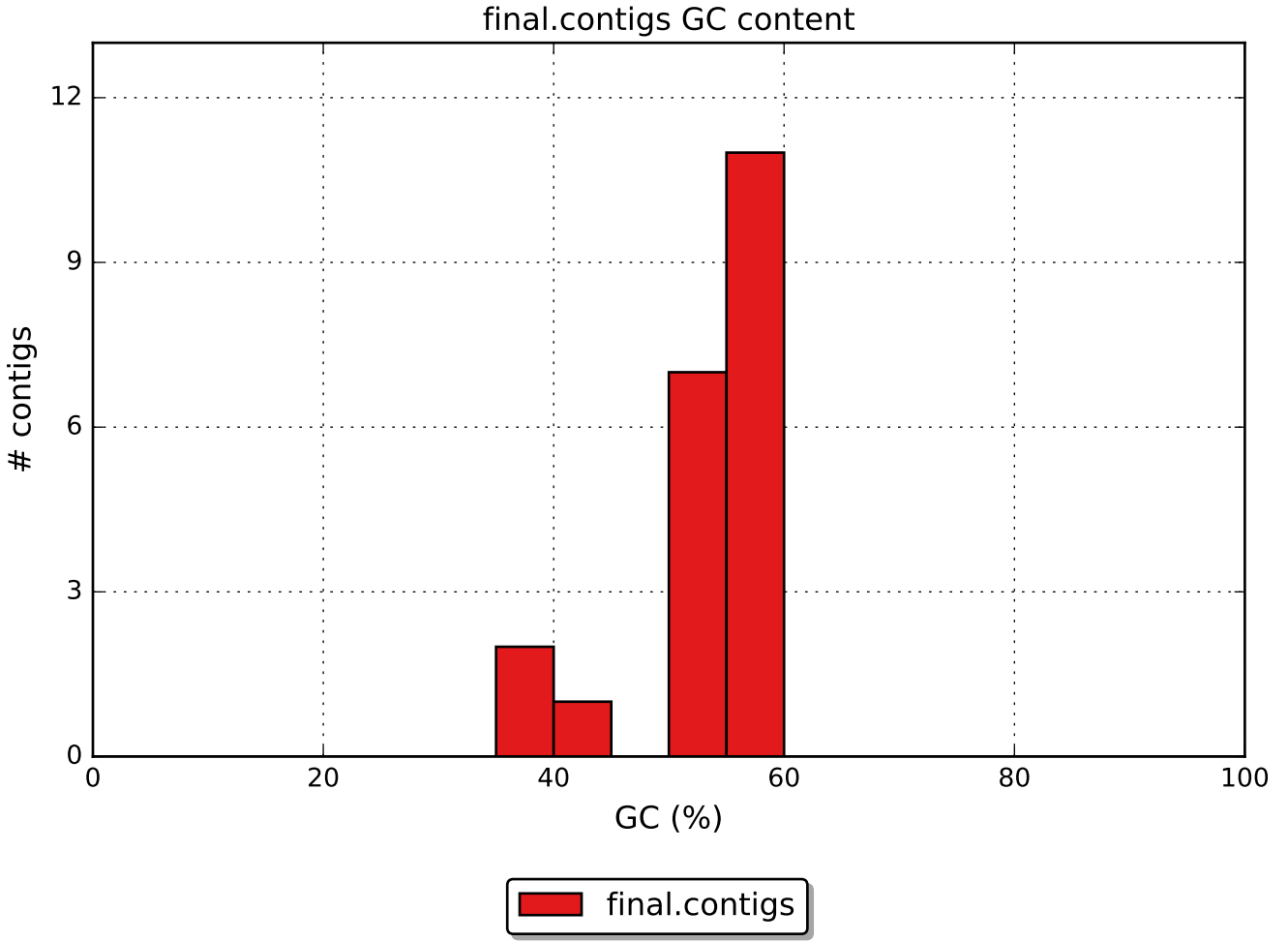
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

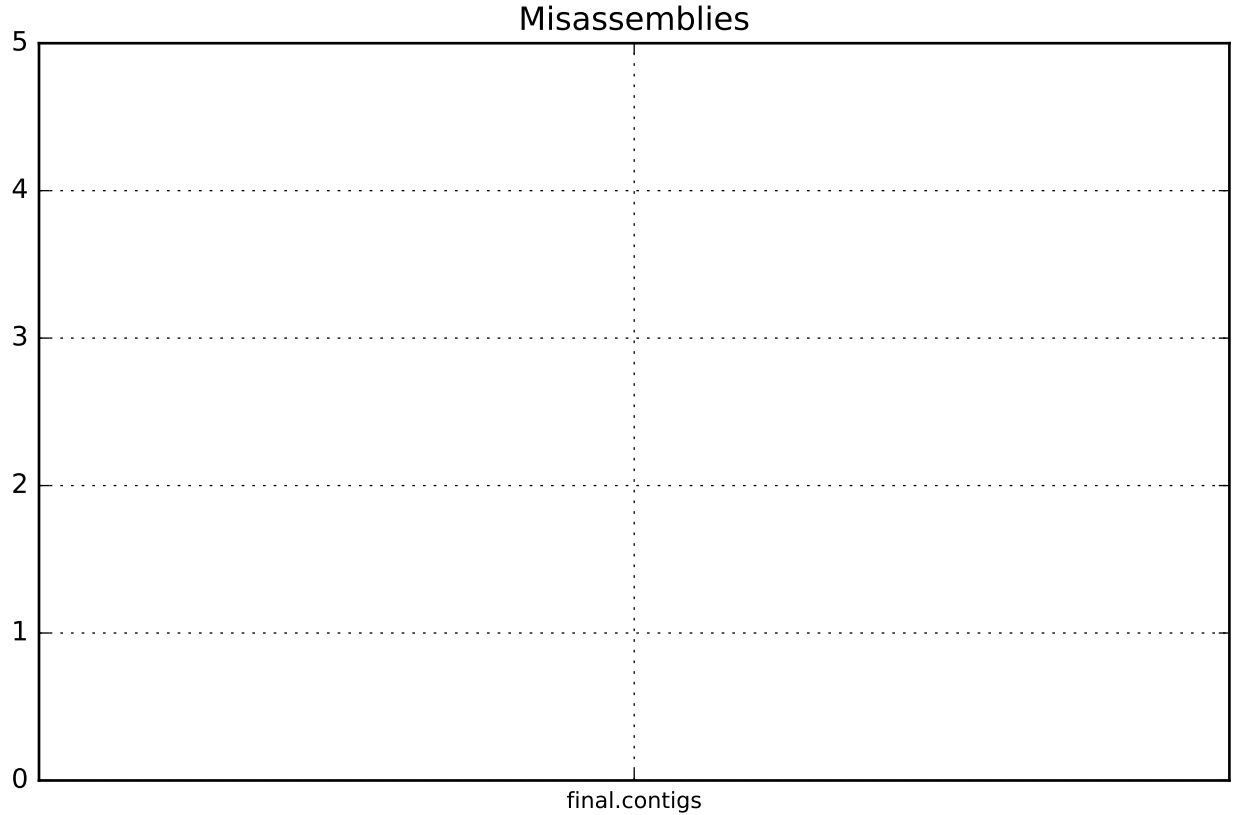

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

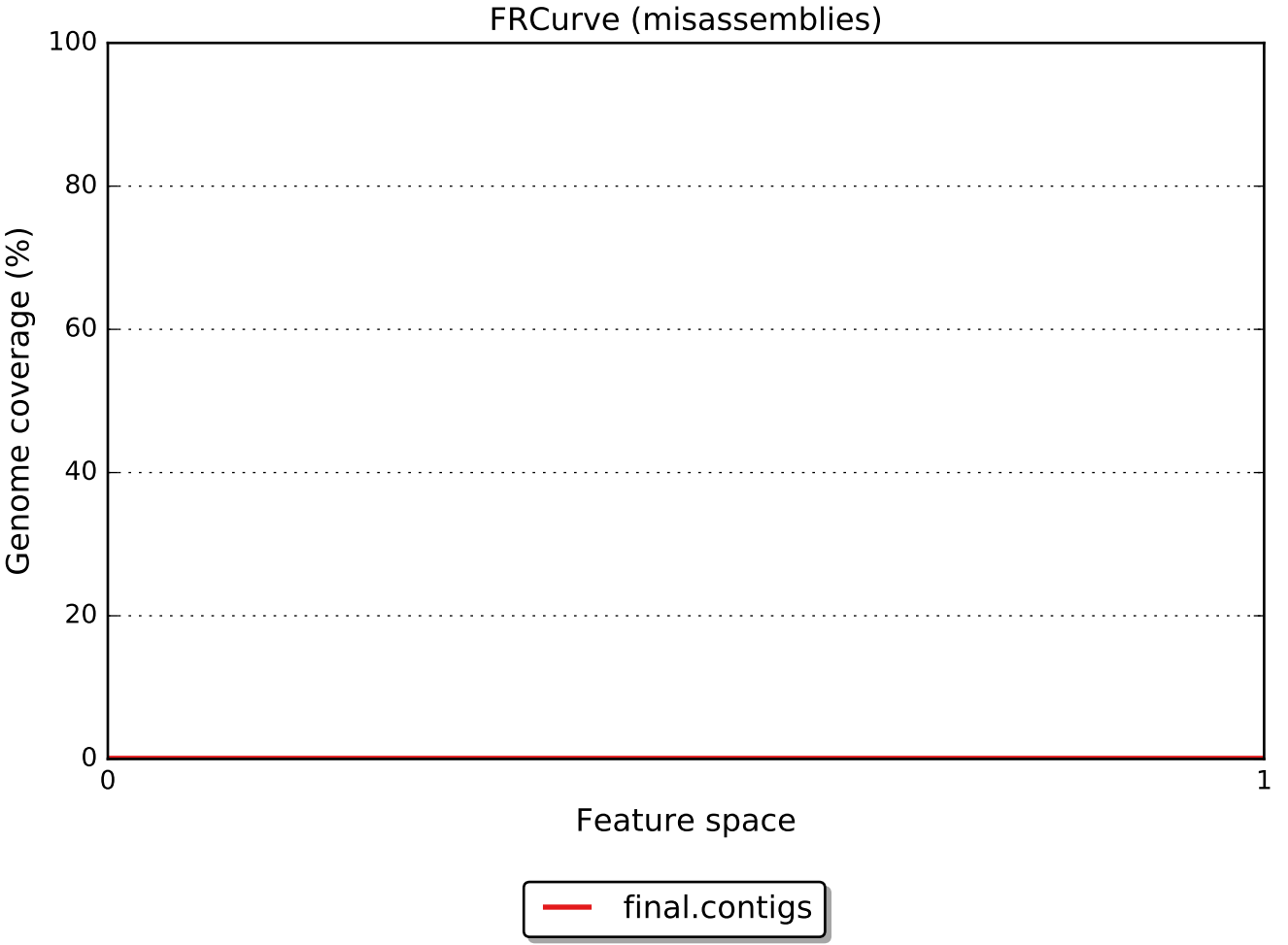

NGx
Contig length (kbp)
x
0
20
40
60
80
100
final.contigs

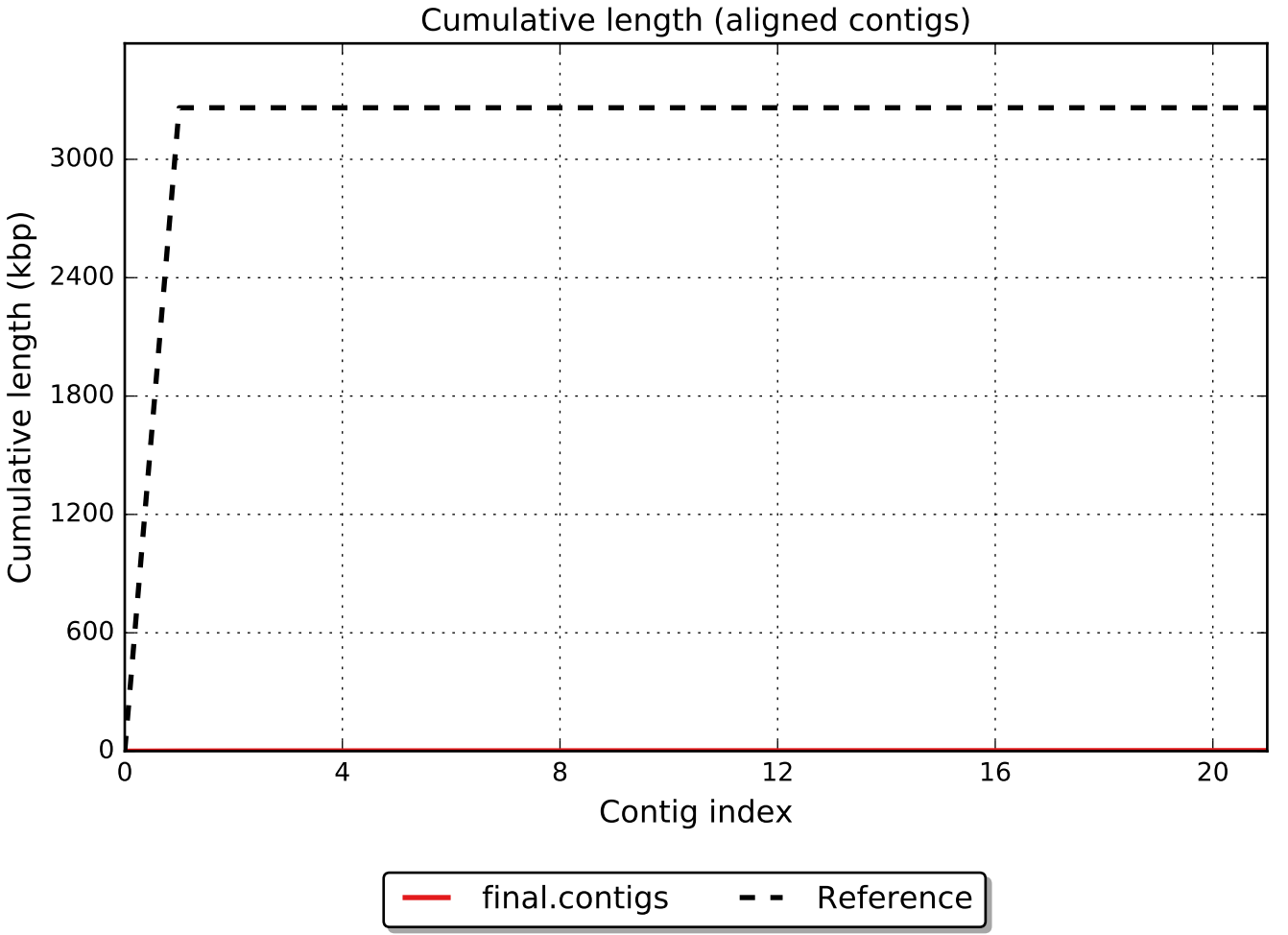

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
4
8
12
16
20
Contig index
final.contigs
Reference

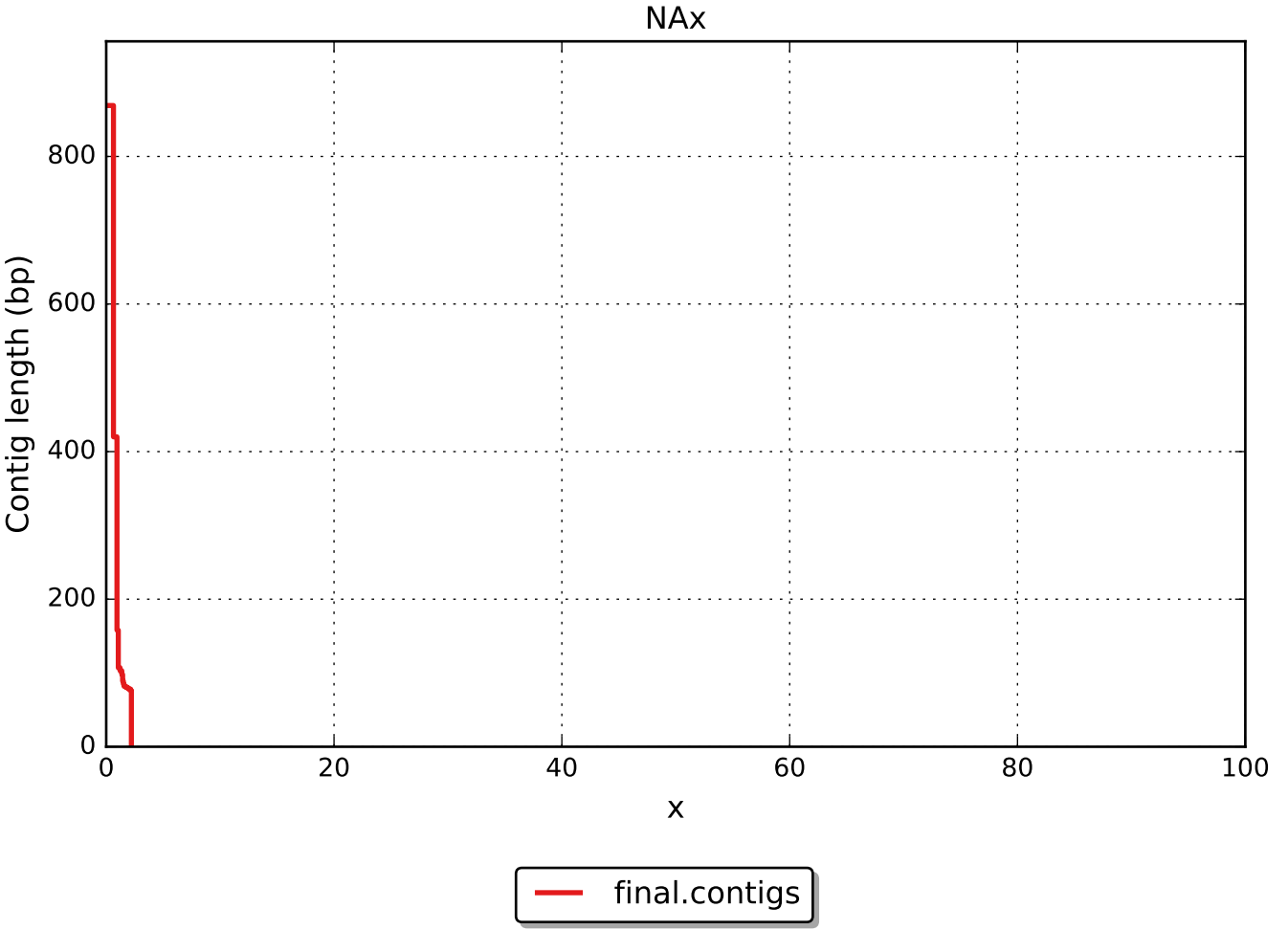

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
0
20
40
60
80
100
final.contigs
Reference

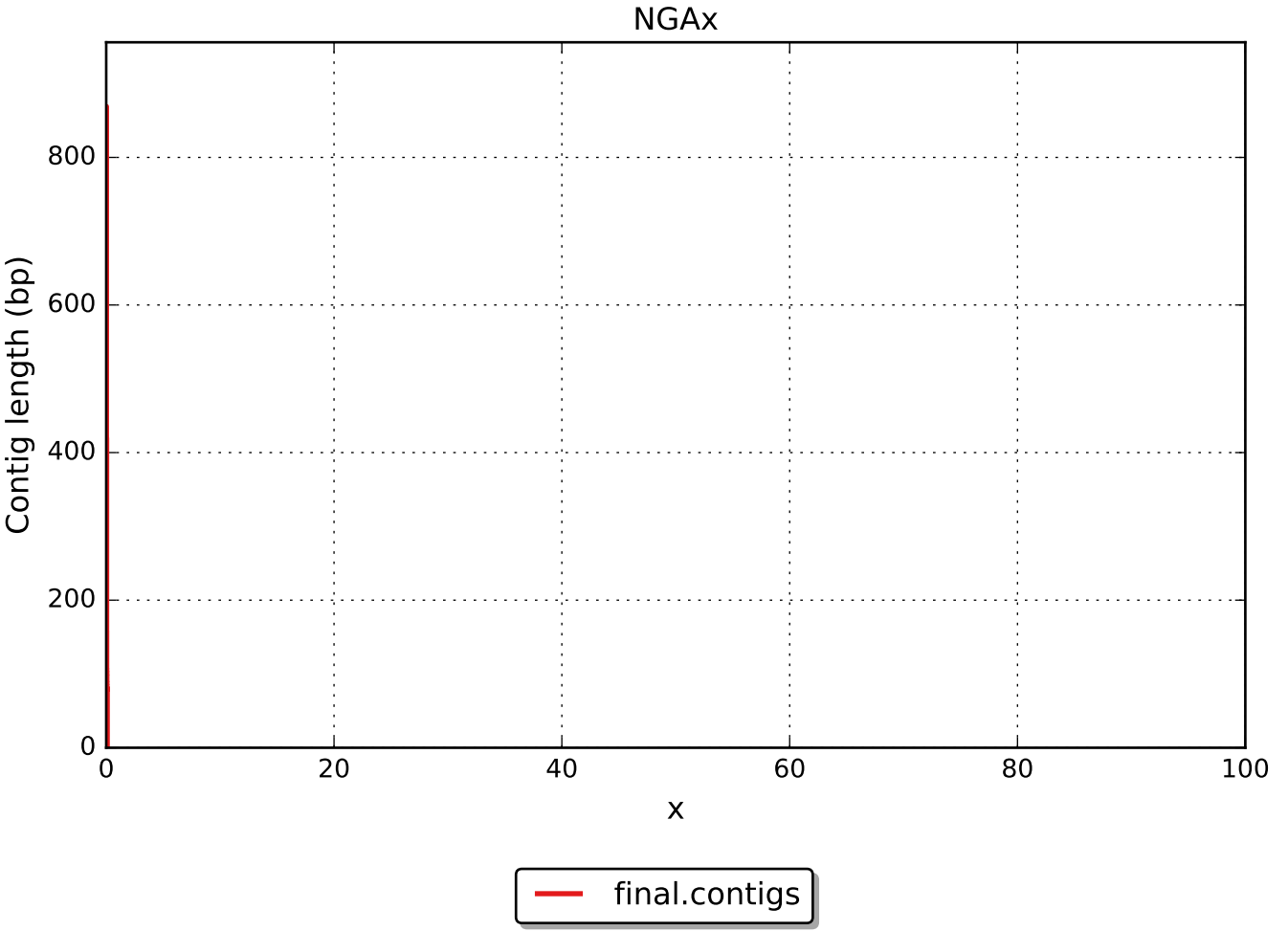

final.contigs GC content
contigs
GC (%)
0
3
6
9
12
0
20
40
60
80
100
final.contigs


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)
3000
2400
1800
1200
600
0
0
4
8
12
16
20
Contig index
final.contigs
Reference


NAx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
final.contigs