Report

	final.contigs
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	235715
Total length (>= 5000 bp)	230601
Total length (>= 10000 bp)	204212
Total length (>= 25000 bp)	190885
Total length (>= 50000 bp)	79341
# contigs	14
Largest contig	79341
Total length	237483
Reference length	4830181
GC (%)	63.07
Reference GC (%)	67.29
N50	42713
N75	27989
L50	2
L75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 12 part
Unaligned length	235390
Genome fraction (%)	0.018
Duplication ratio	2.344
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1455.77
# indels per 100 kbp	447.93
Largest alignment	130
Total aligned length	1192
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

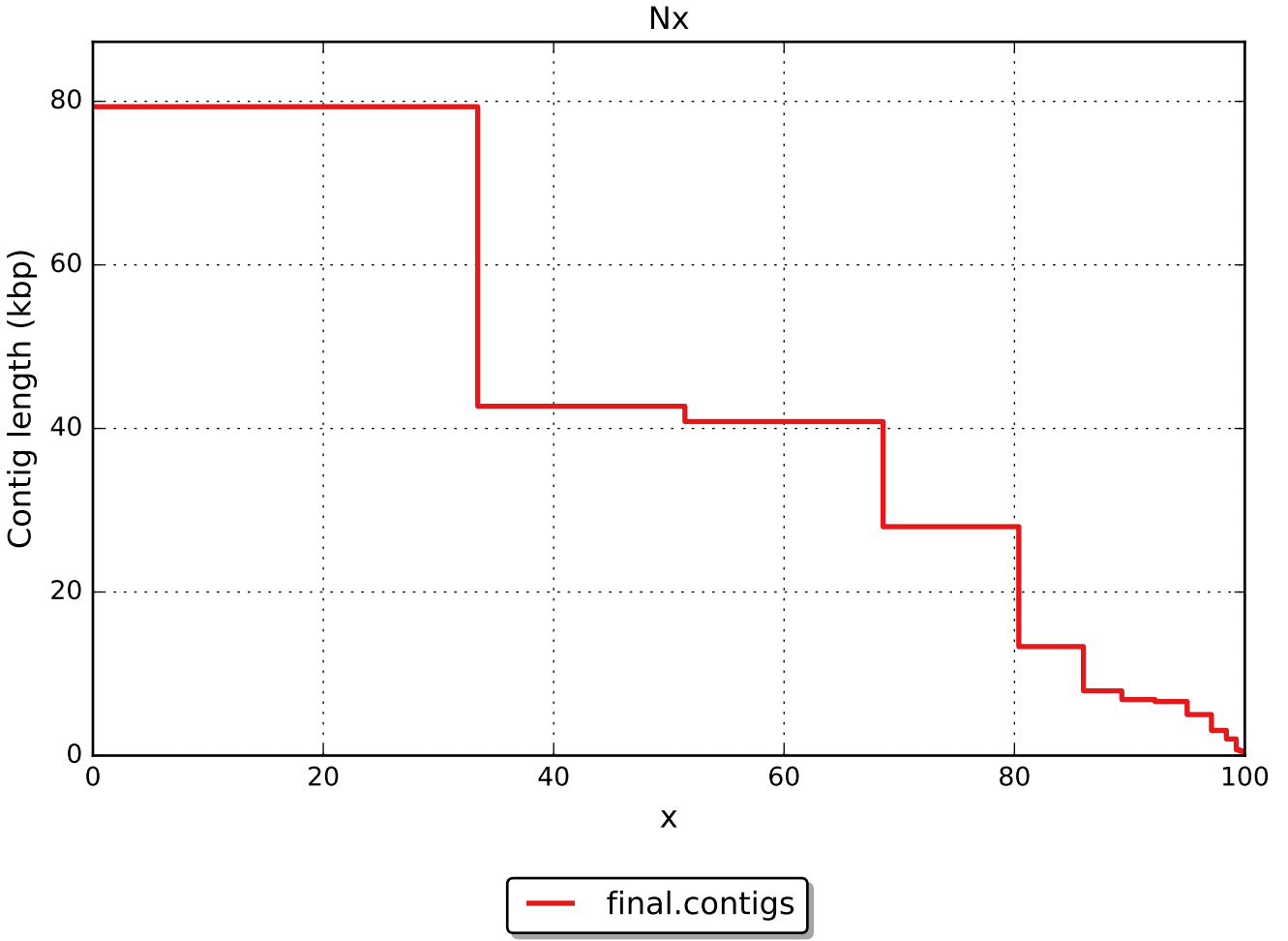
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	13
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

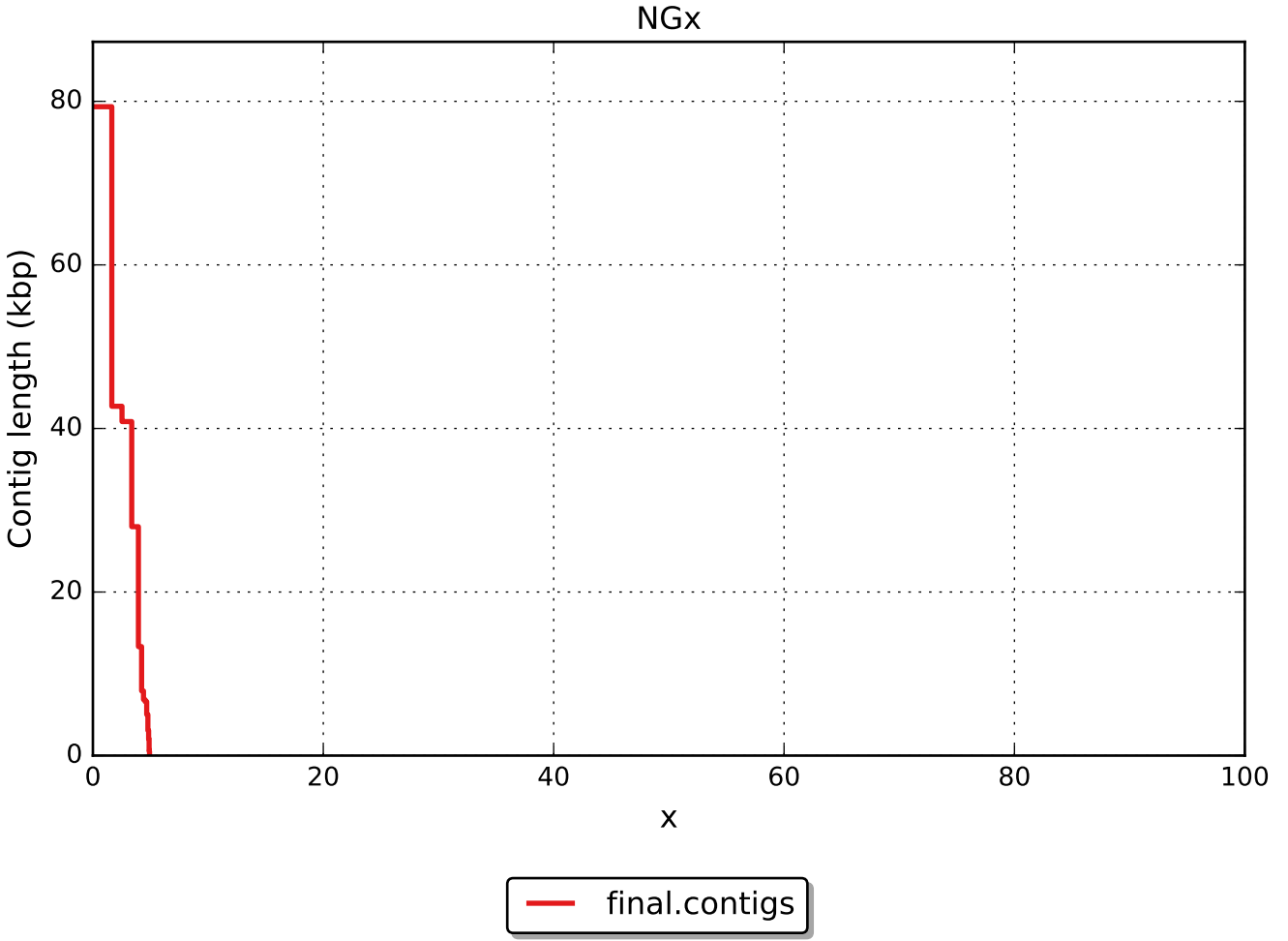
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

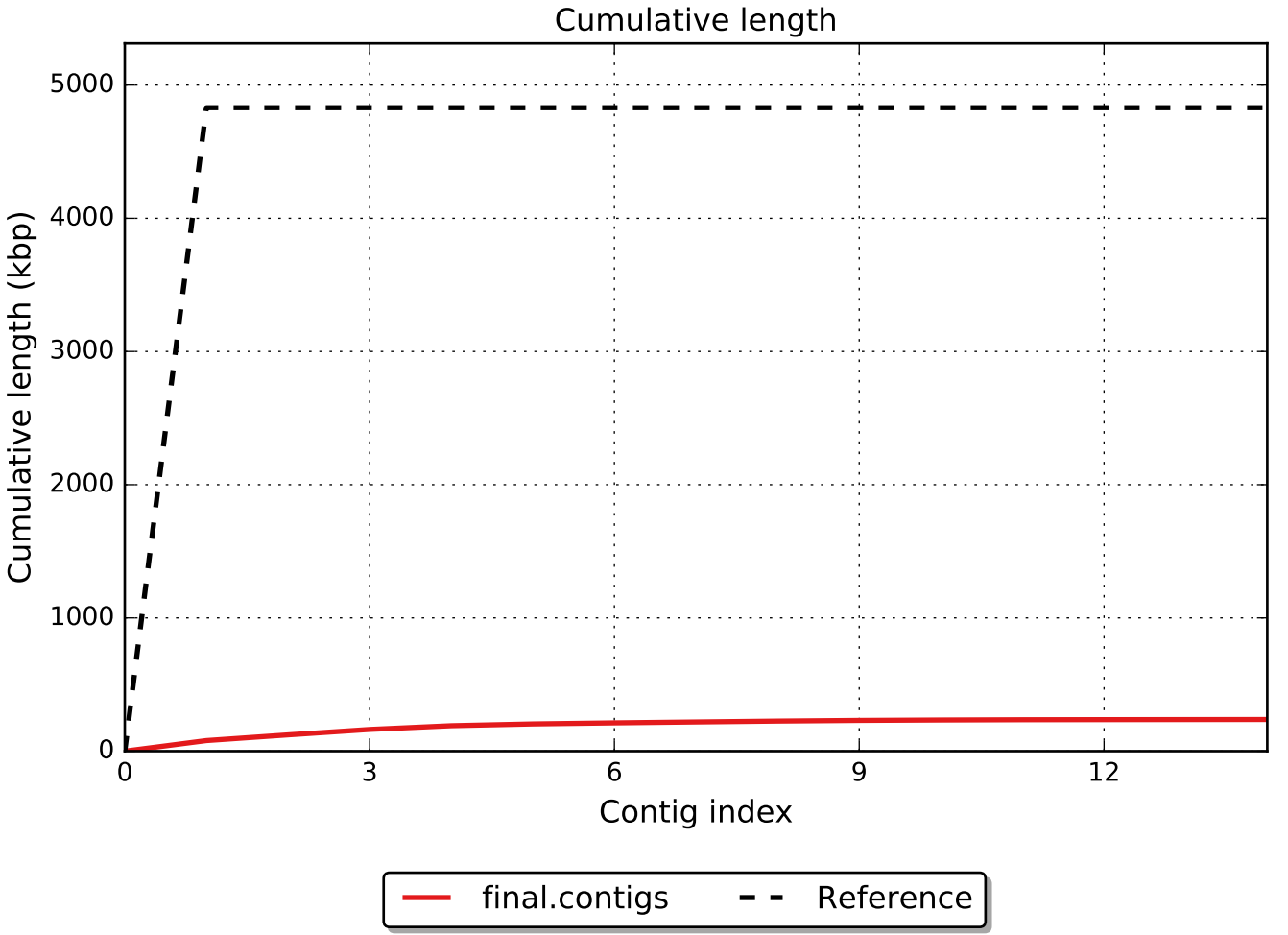
Unaligned report

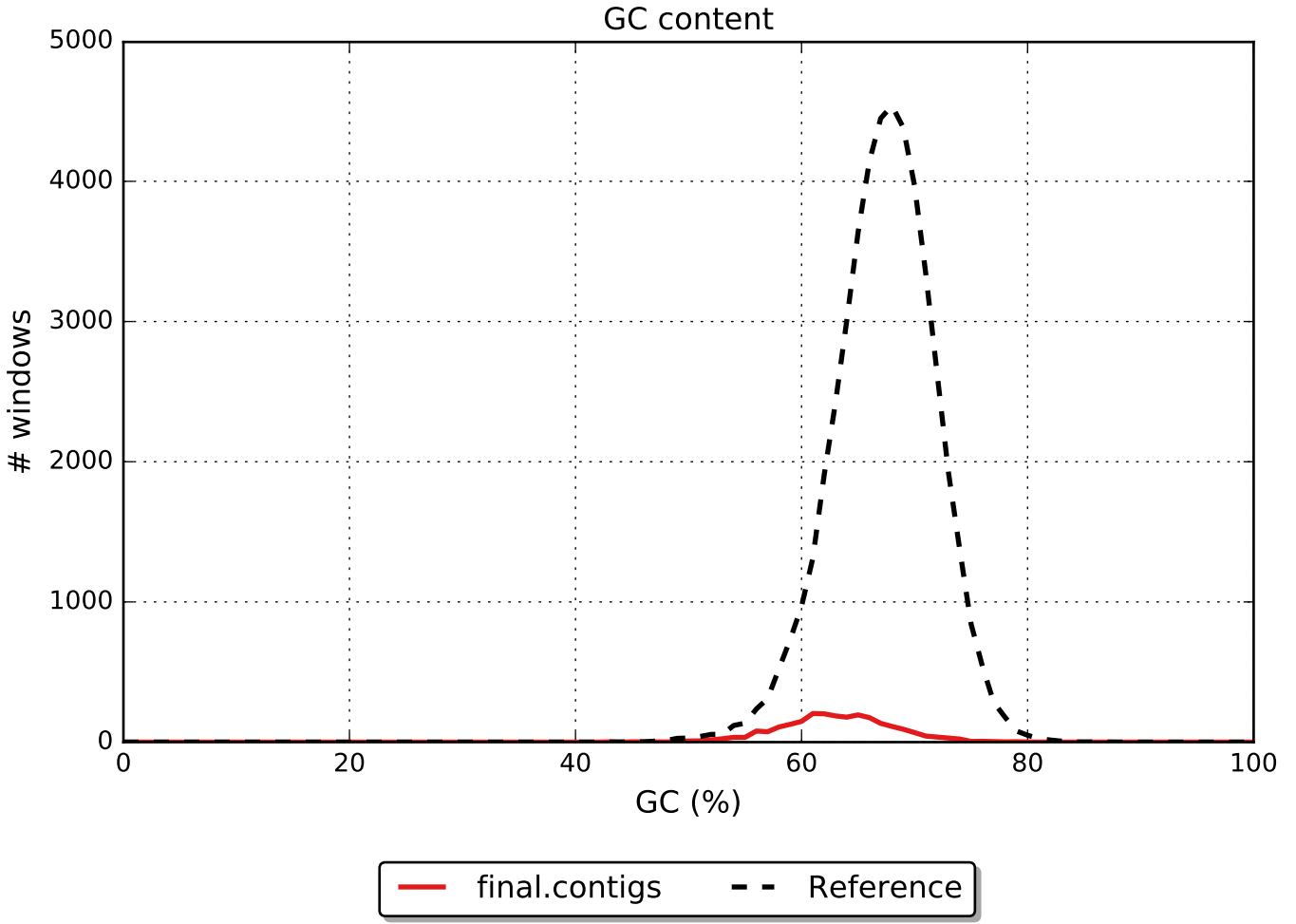
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
Partially unaligned length	235390
# N's	0

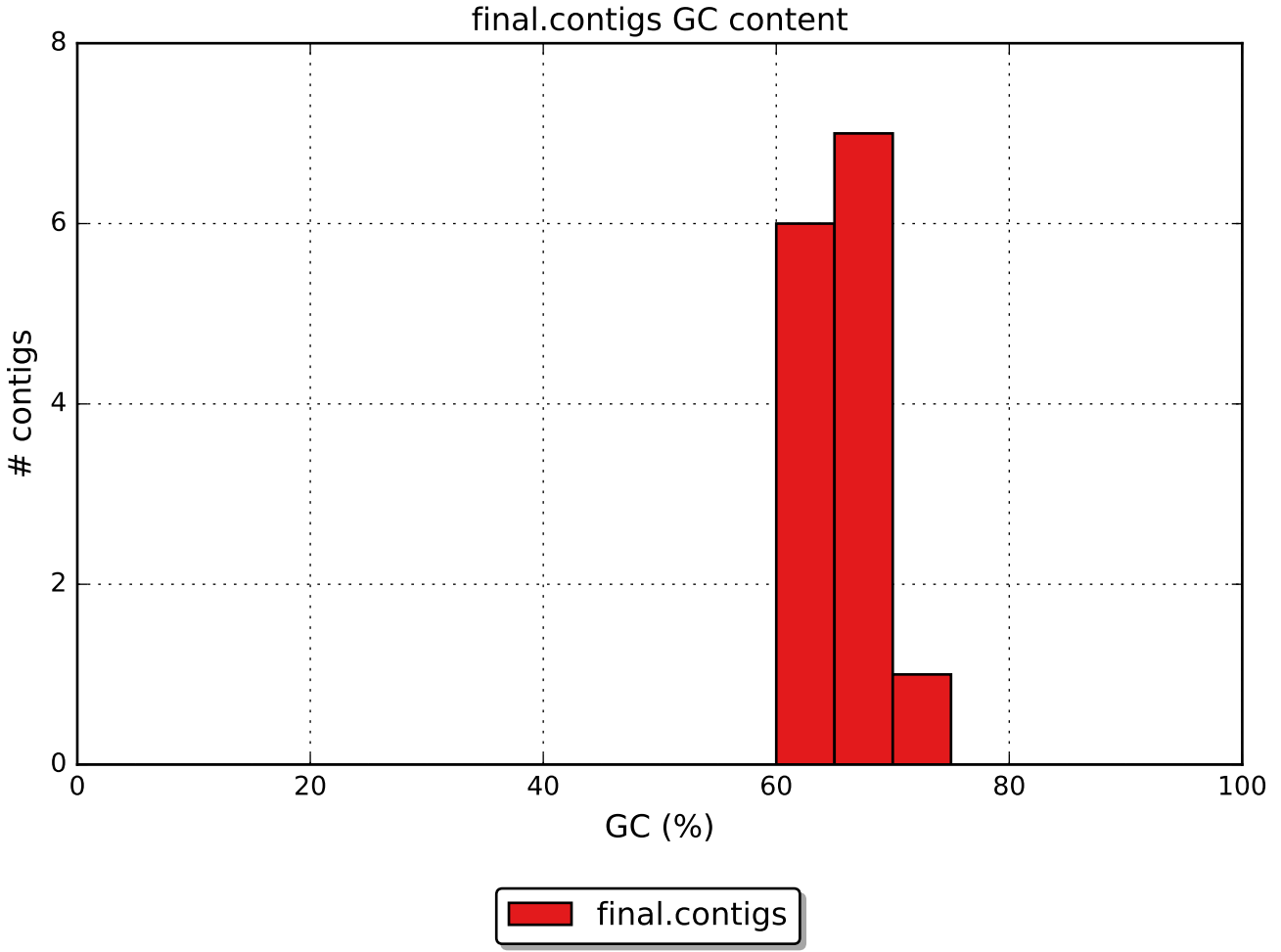
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

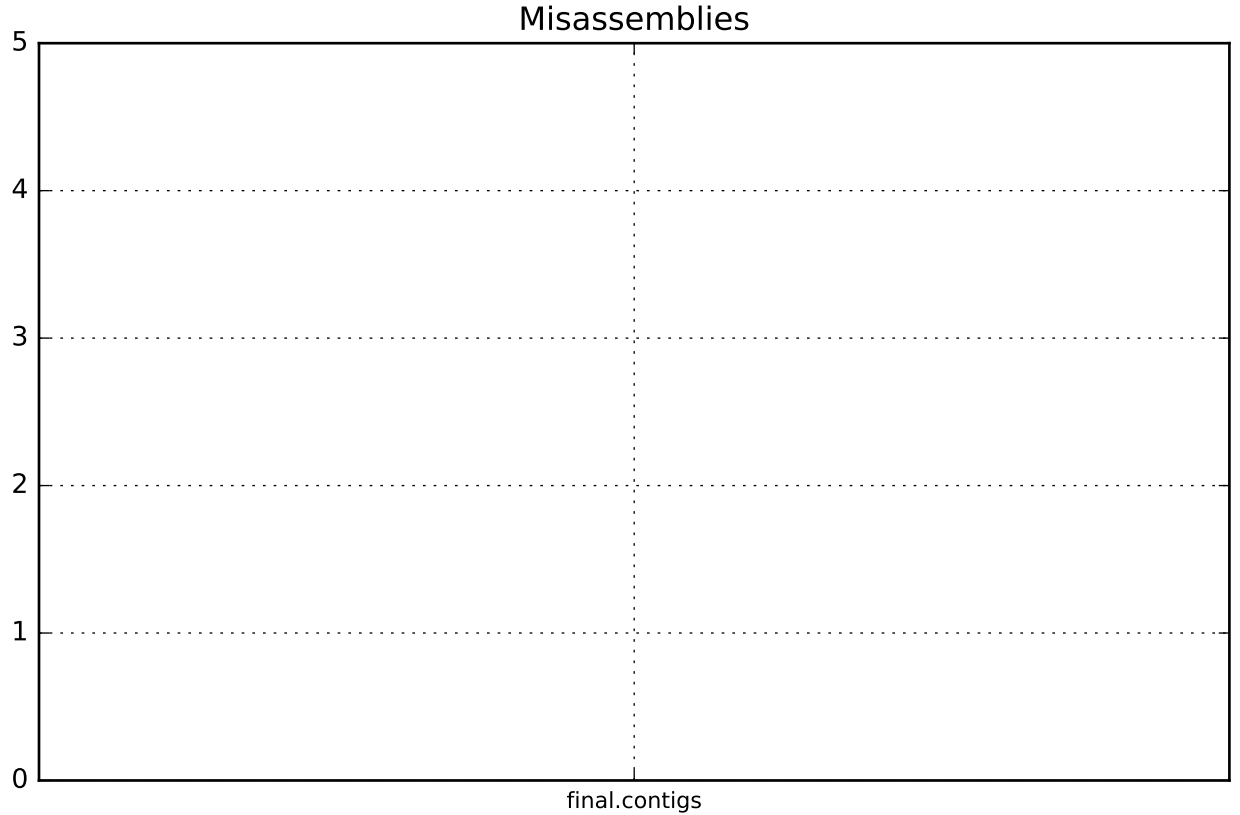

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

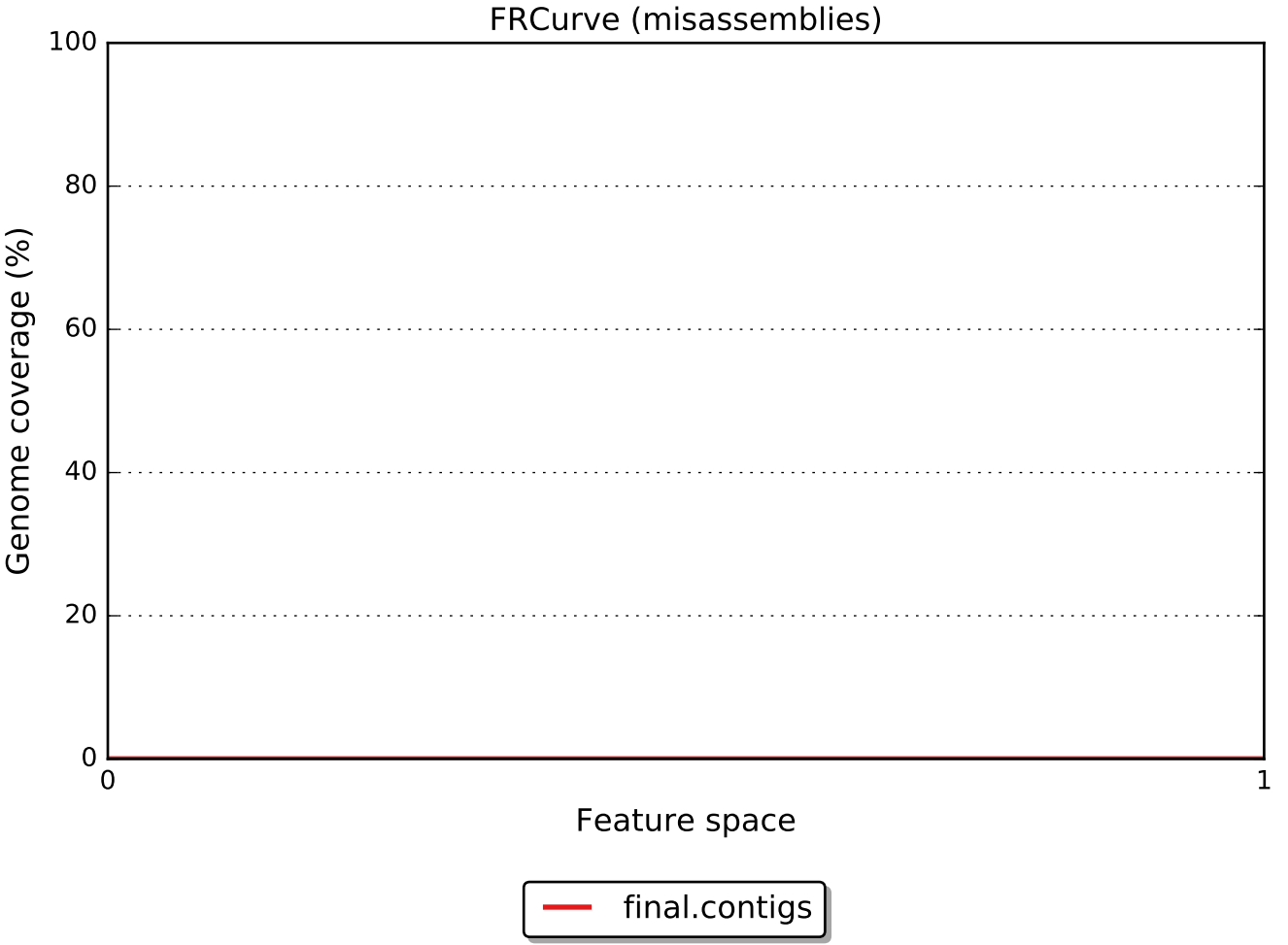

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

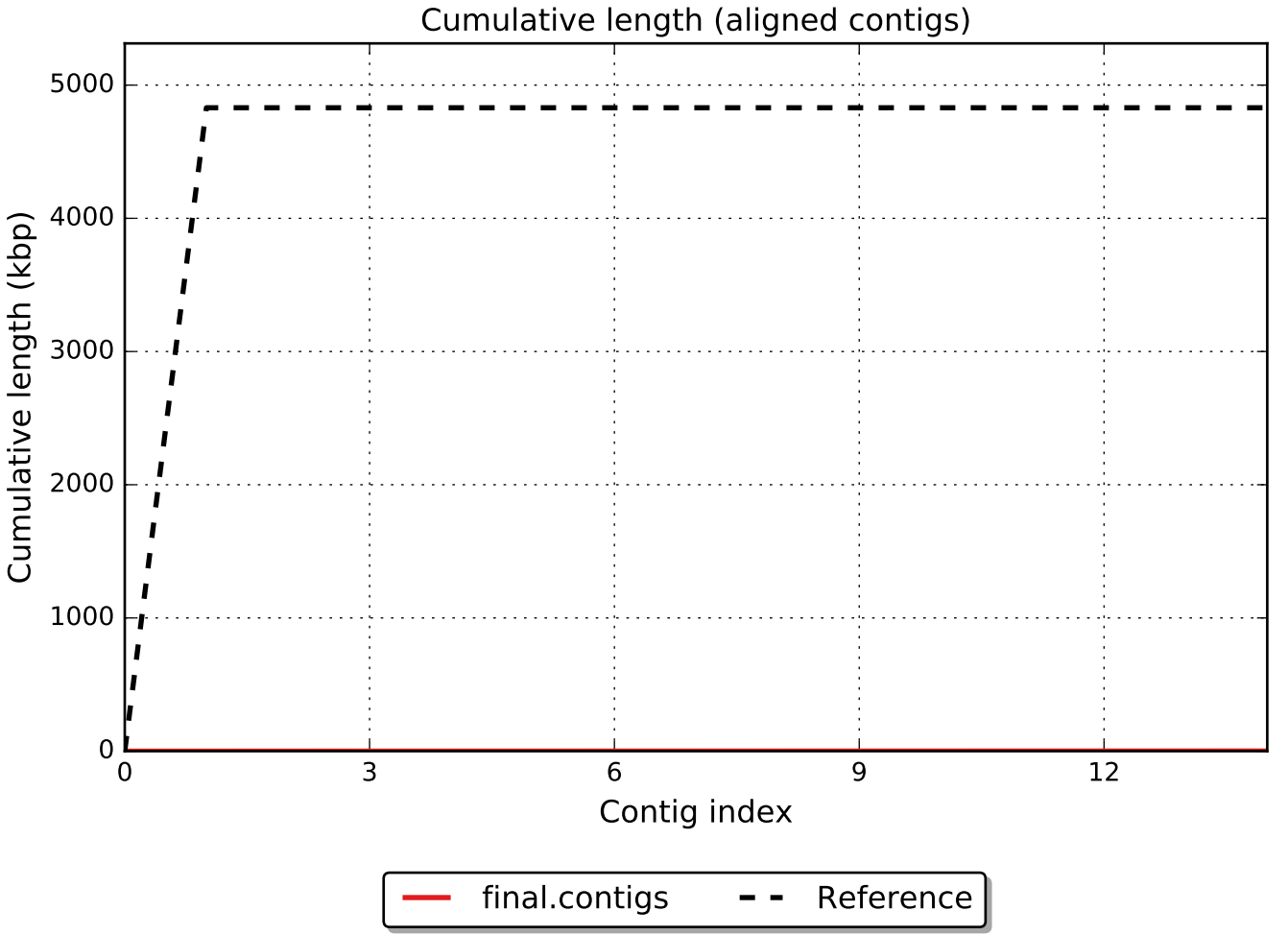

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
Contig index
final.contigs
Reference

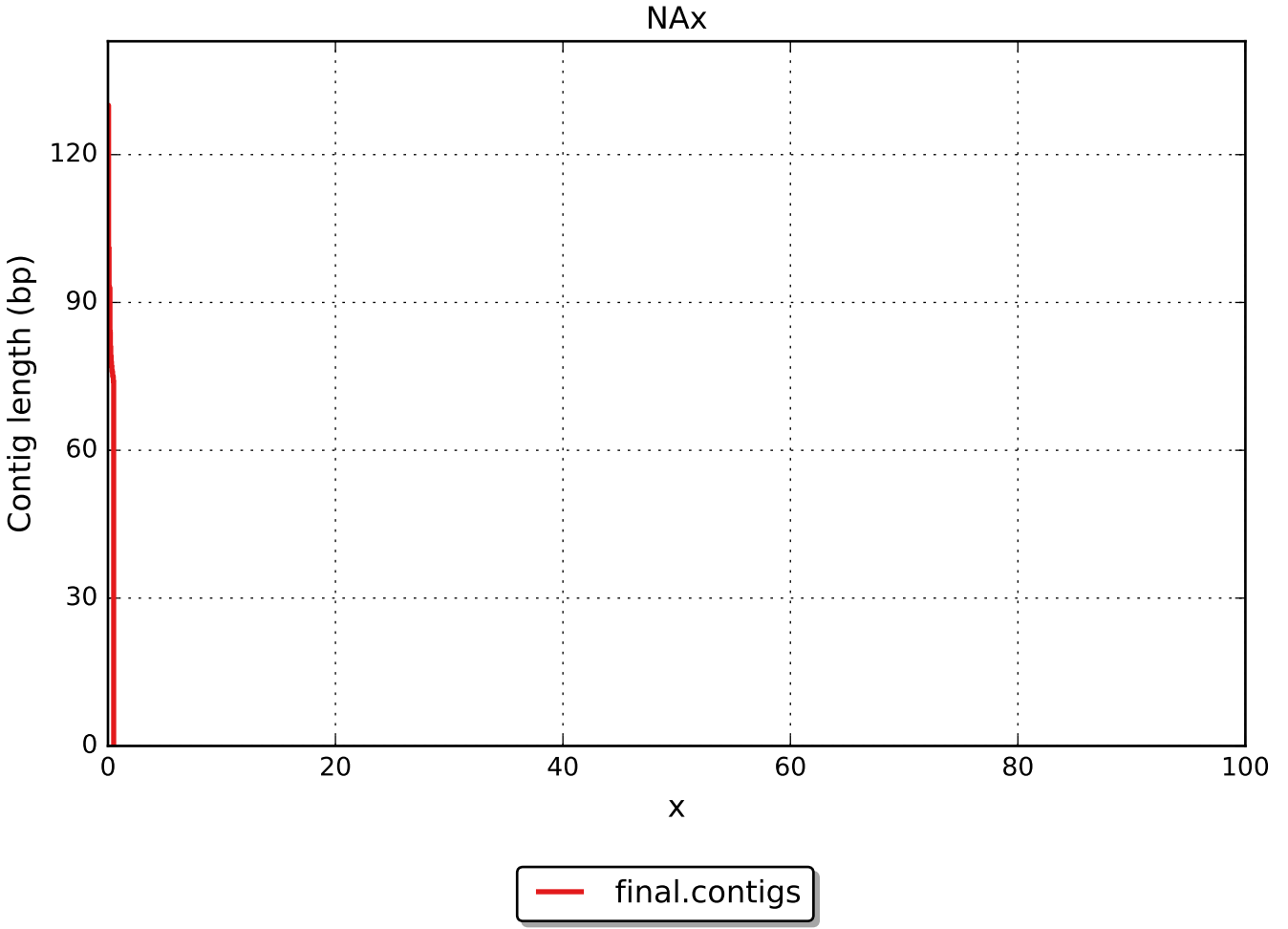

GC content
5000
4000
3000
2000
1000
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

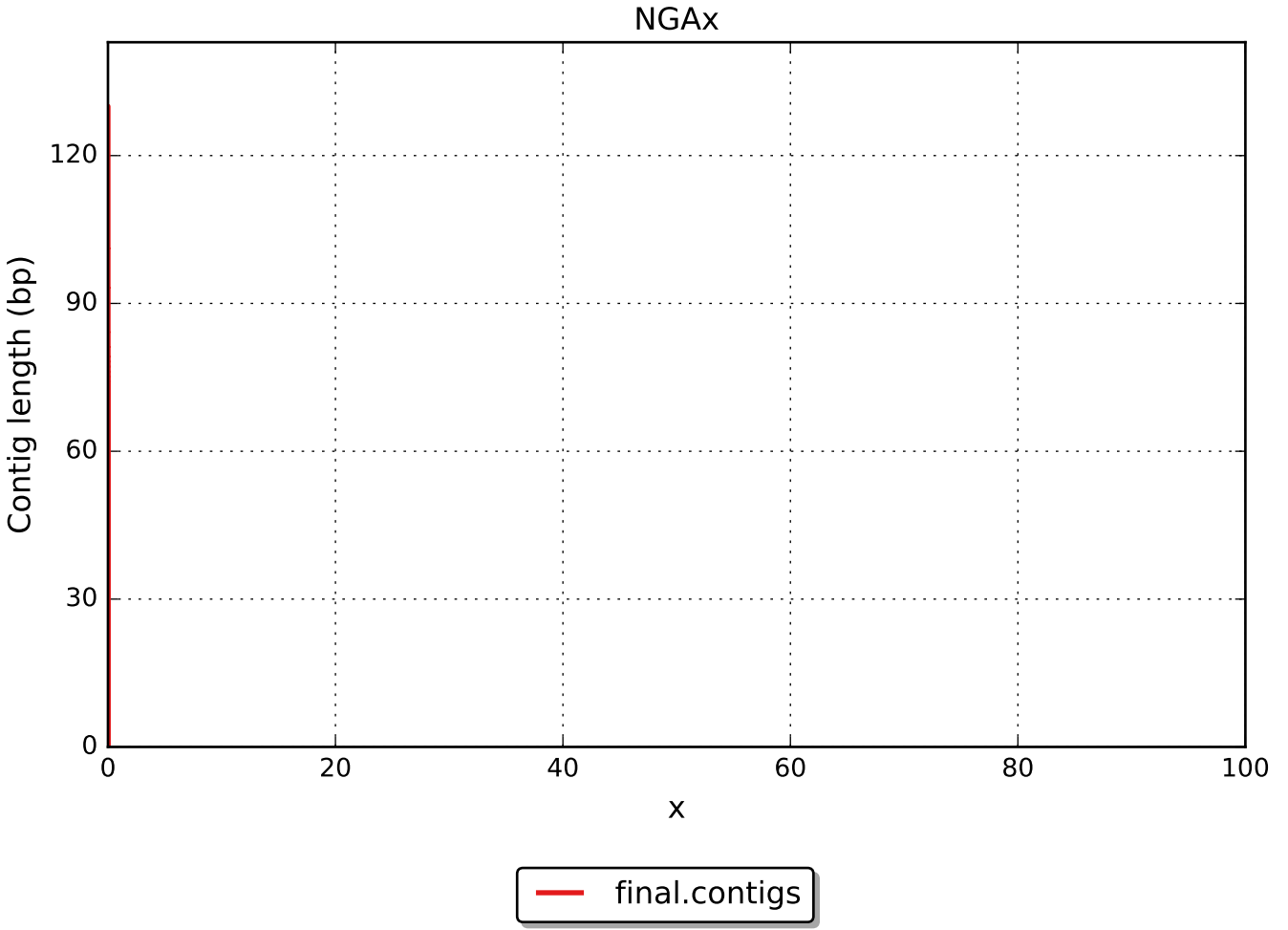

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


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


NAx
Contig length (bp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
0
30
60
90
120
0
20
40
60
80
100
x
final.contigs