Report

	final.contigs
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	15344
Total length (>= 5000 bp)	13479
Total length (>= 10000 bp)	13479
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3
Largest contig	13479
Total length	15992
Reference length	3618700
GC (%)	45.59
Reference GC (%)	62.27
N50	13479
N75	13479
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	15757
Genome fraction (%)	0.004
Duplication ratio	1.469
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2500.00
# indels per 100 kbp	0.00
Largest alignment	86
Total aligned length	235
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

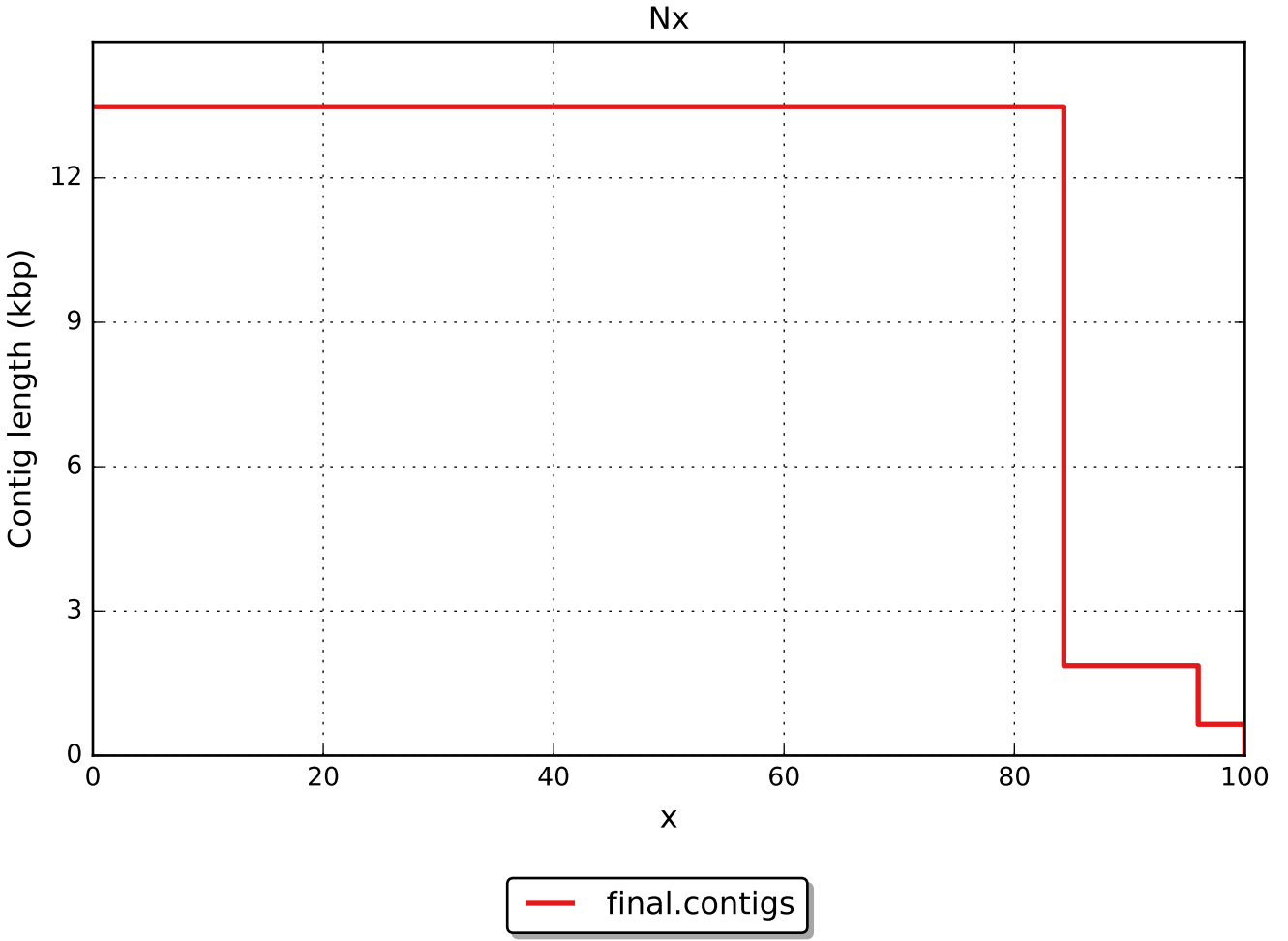
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs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

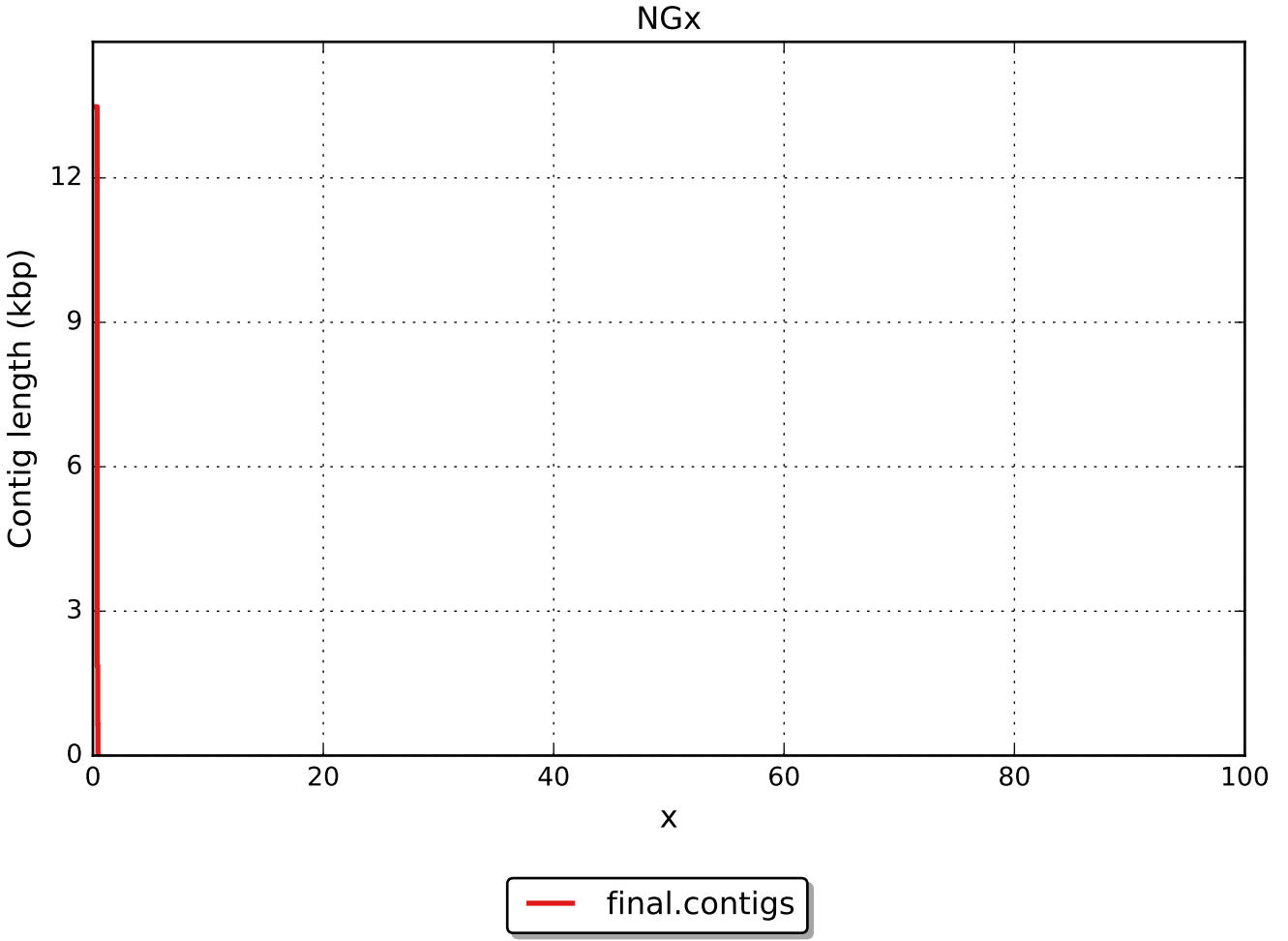
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

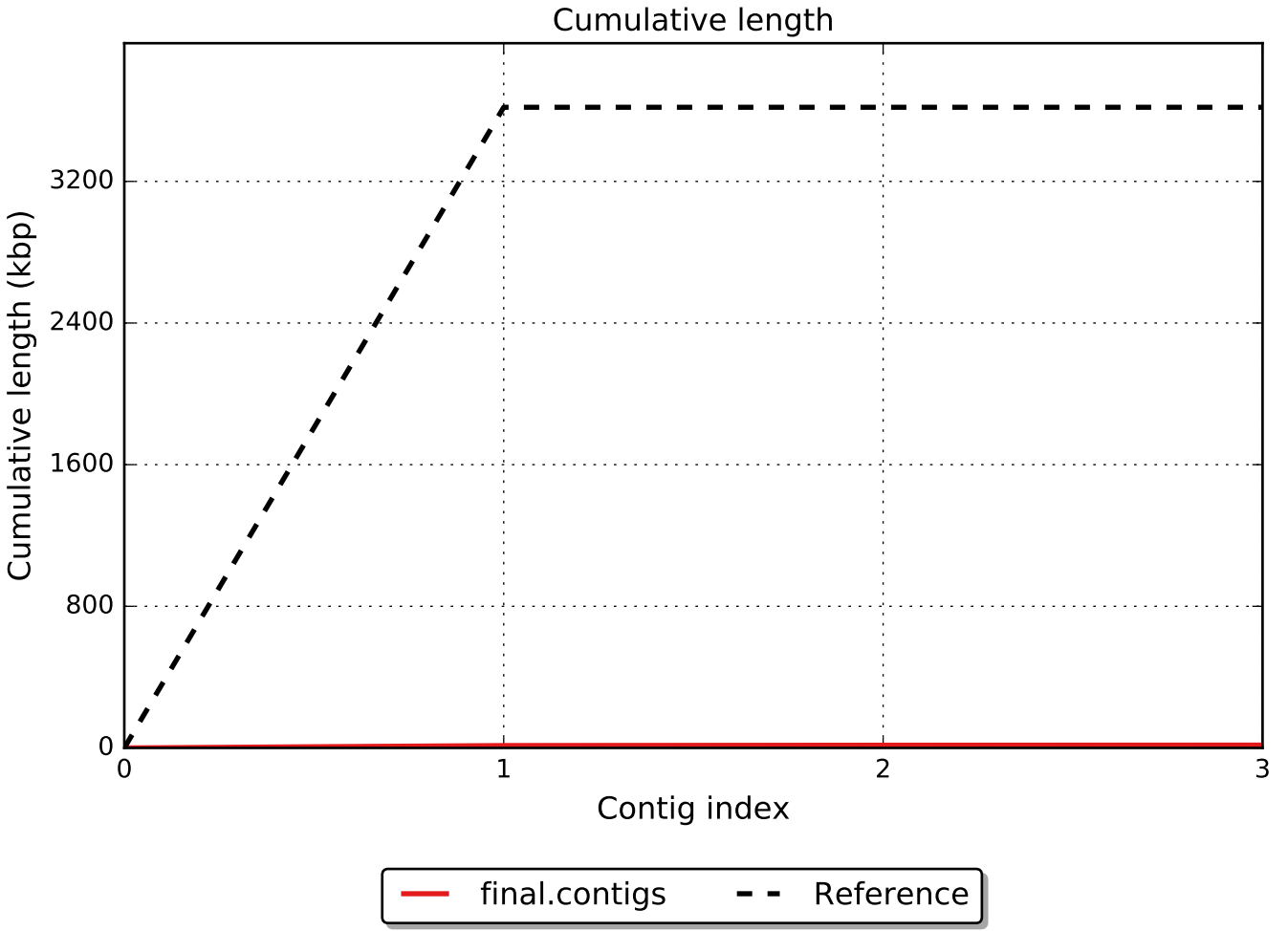
Unaligned report

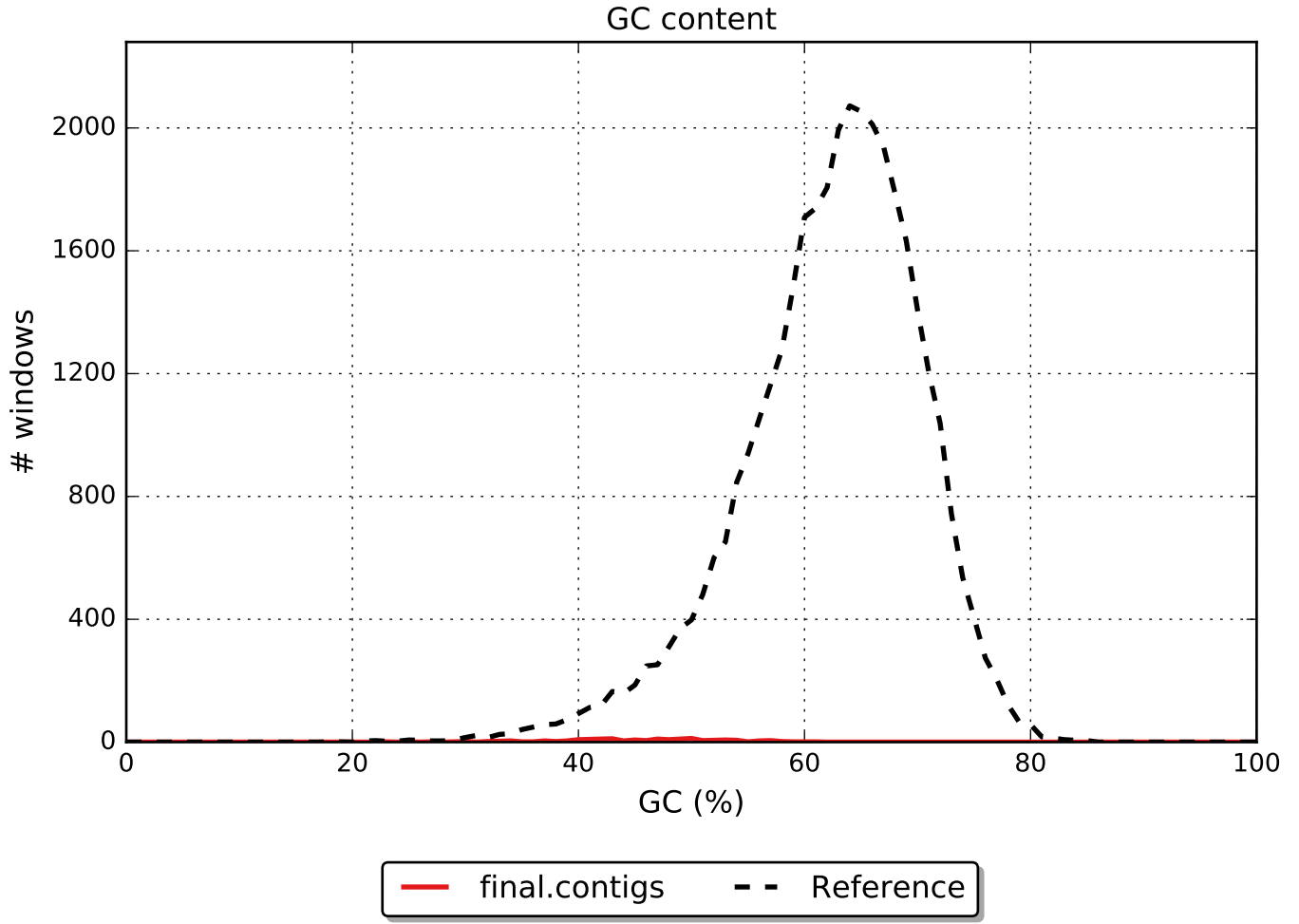
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	15757
# N's	0

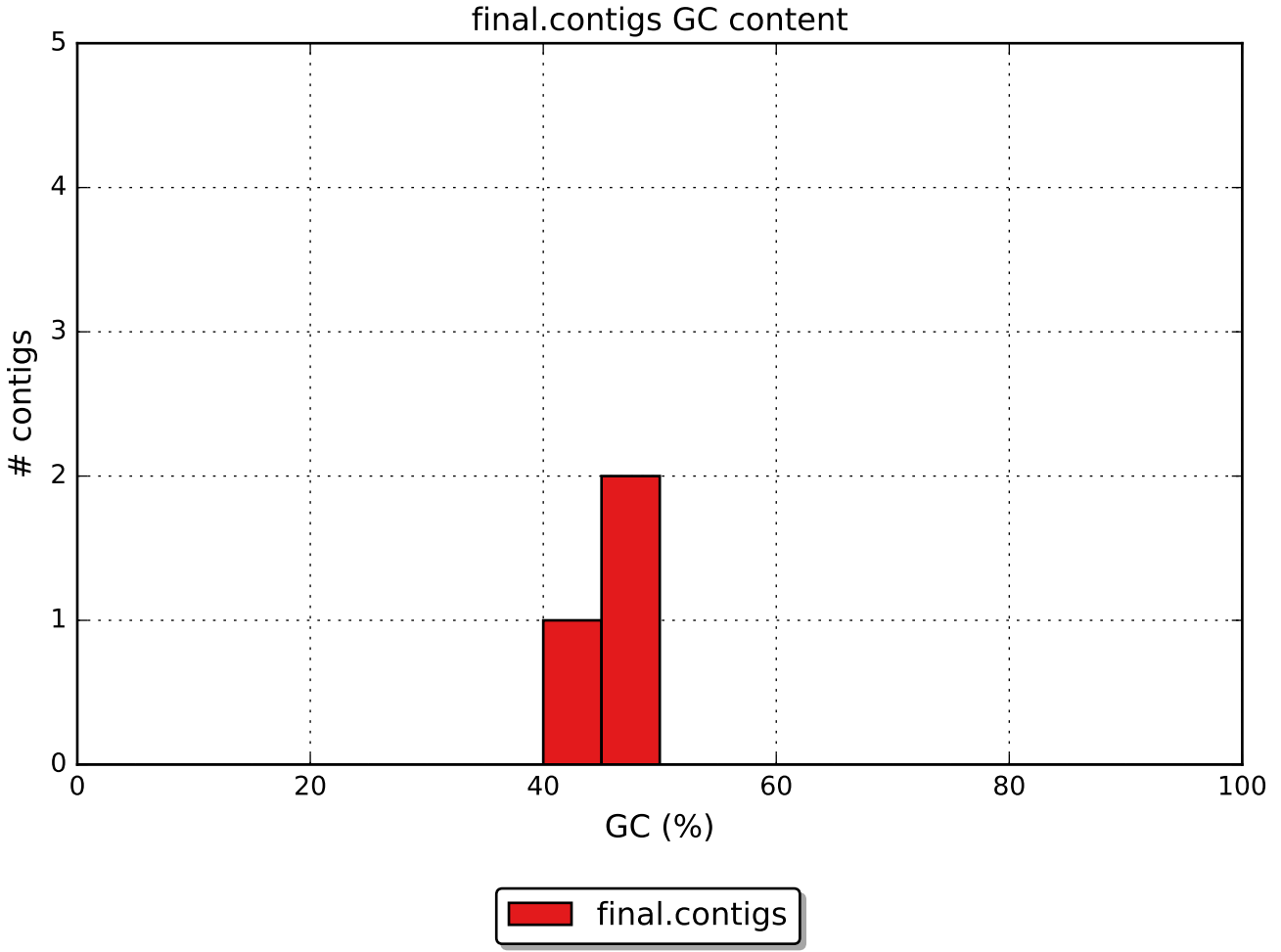
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

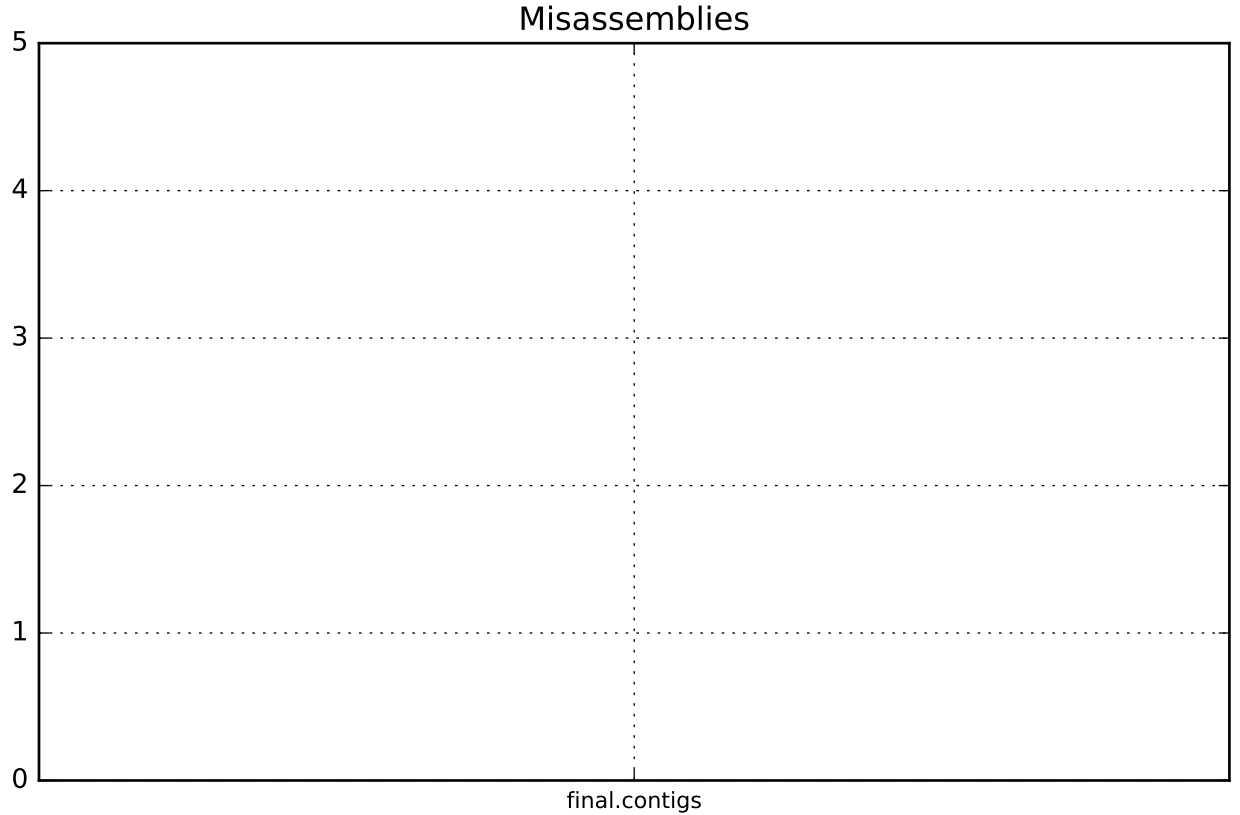

Nx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs

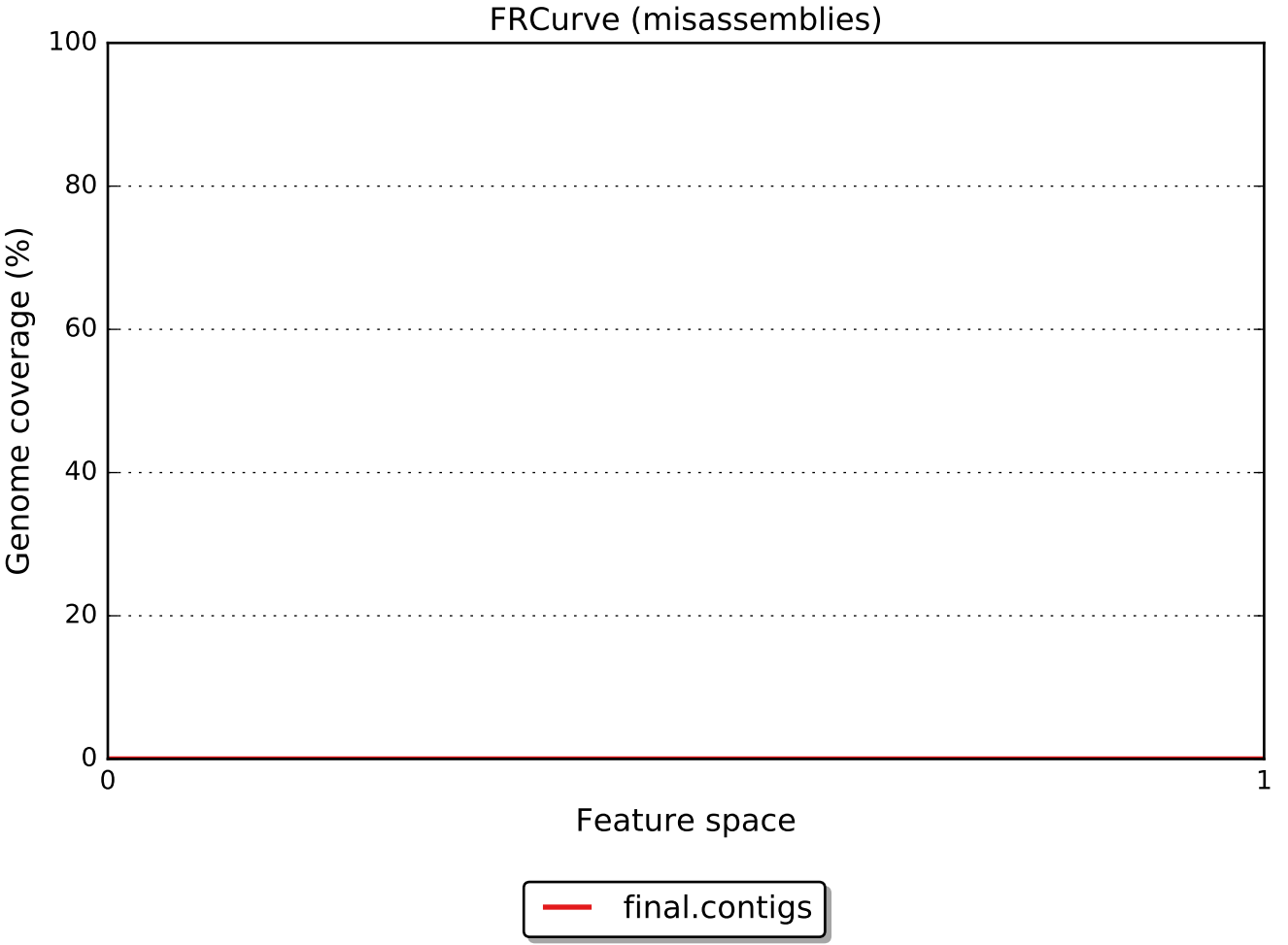

NGx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs

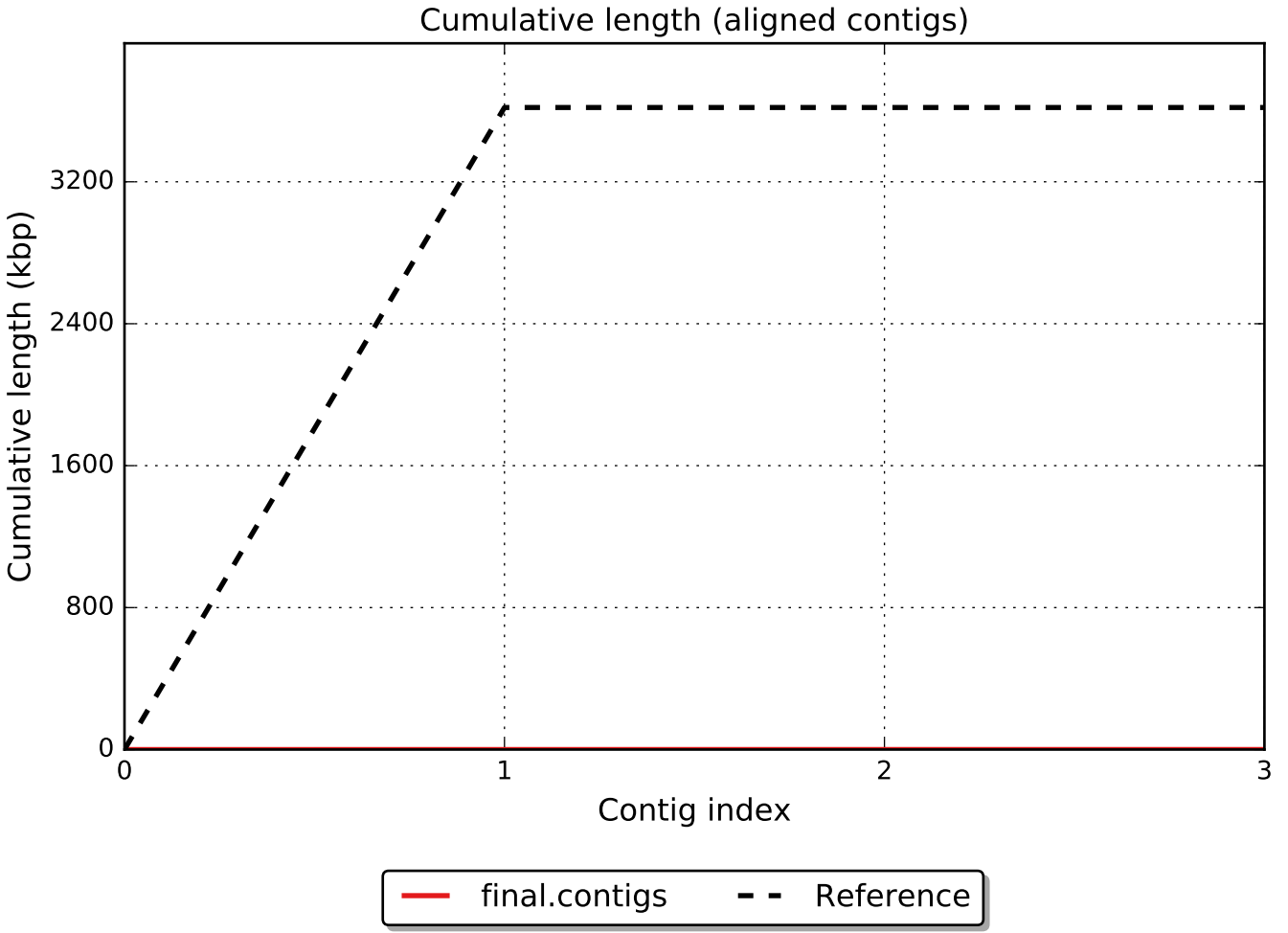

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
1
2
3
Contig index
final.contigs
Reference

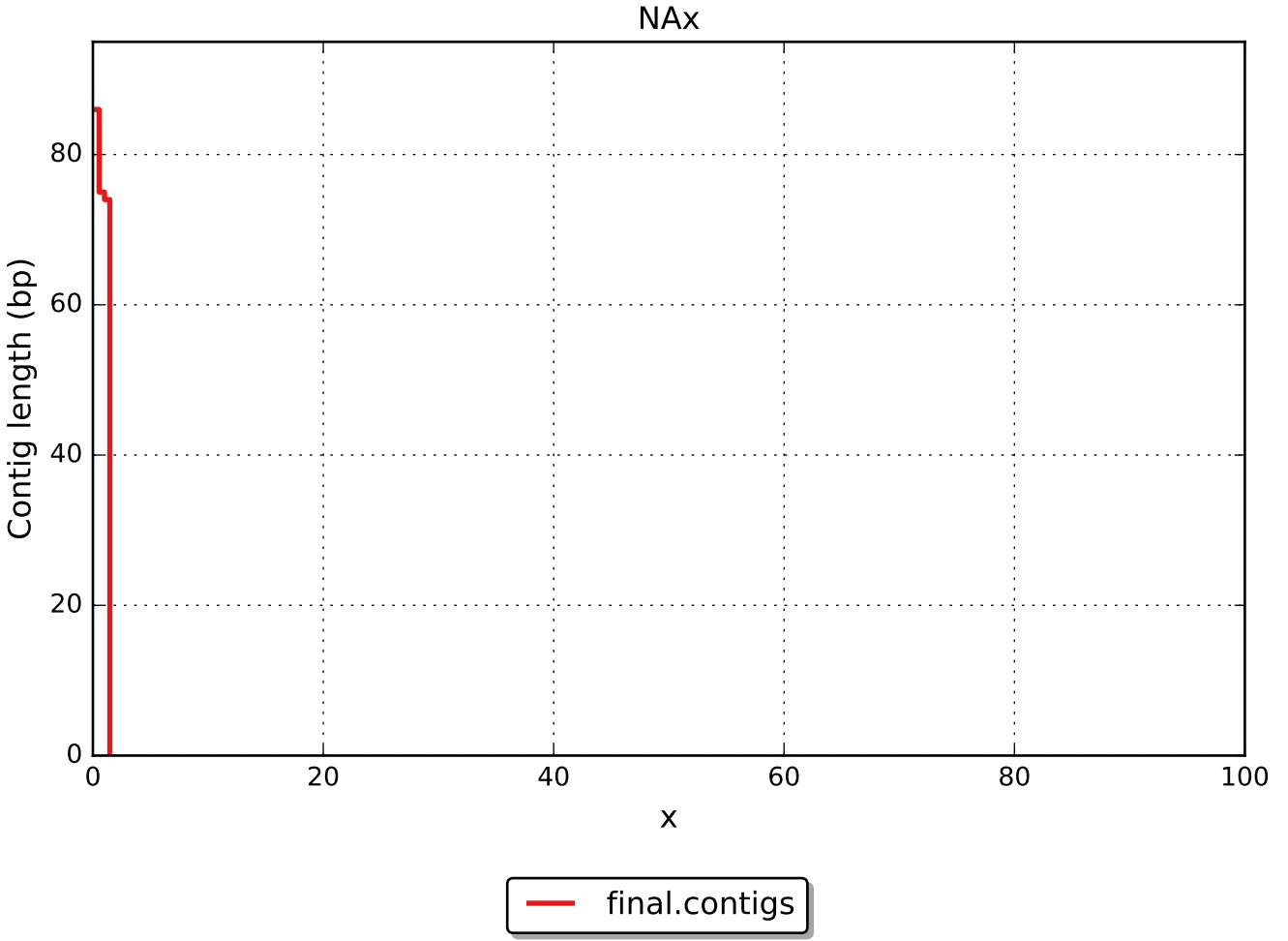

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

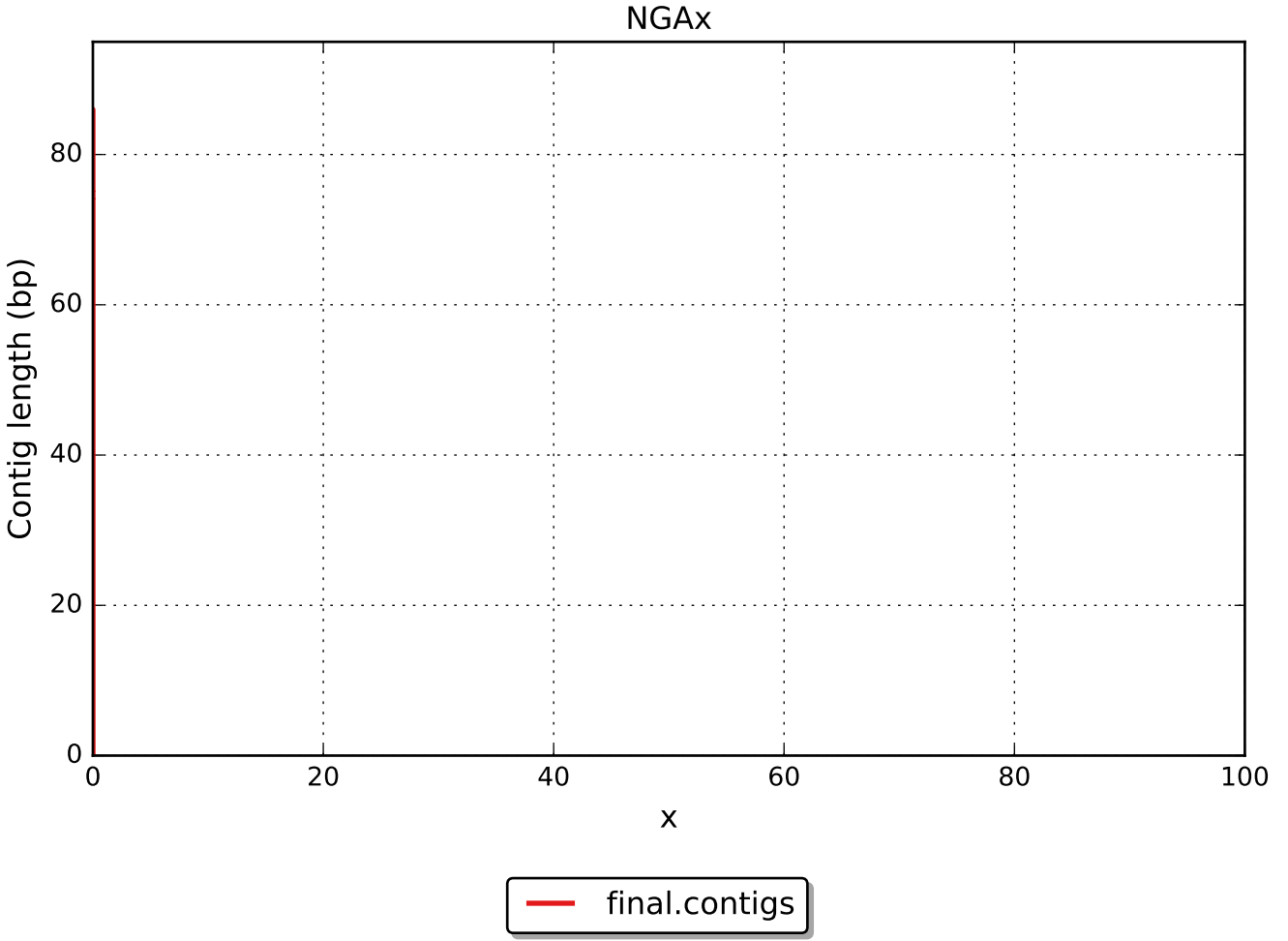

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
3200
2400
1600
800
0
0
1
2
3
Contig index
final.contigs
Reference


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


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