Report

	final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	6579
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	13
Largest contig	2250
Total length	12651
Reference length	5344419
GC (%)	50.99
Reference GC (%)	63.27
N50	1123
N75	714
L50	4
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	1
# unaligned contigs	0 + 6 part
Unaligned length	6025
Genome fraction (%)	0.058
Duplication ratio	2.136
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3030.30
# indels per 100 kbp	257.90
Largest alignment	1387
Total aligned length	3647
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

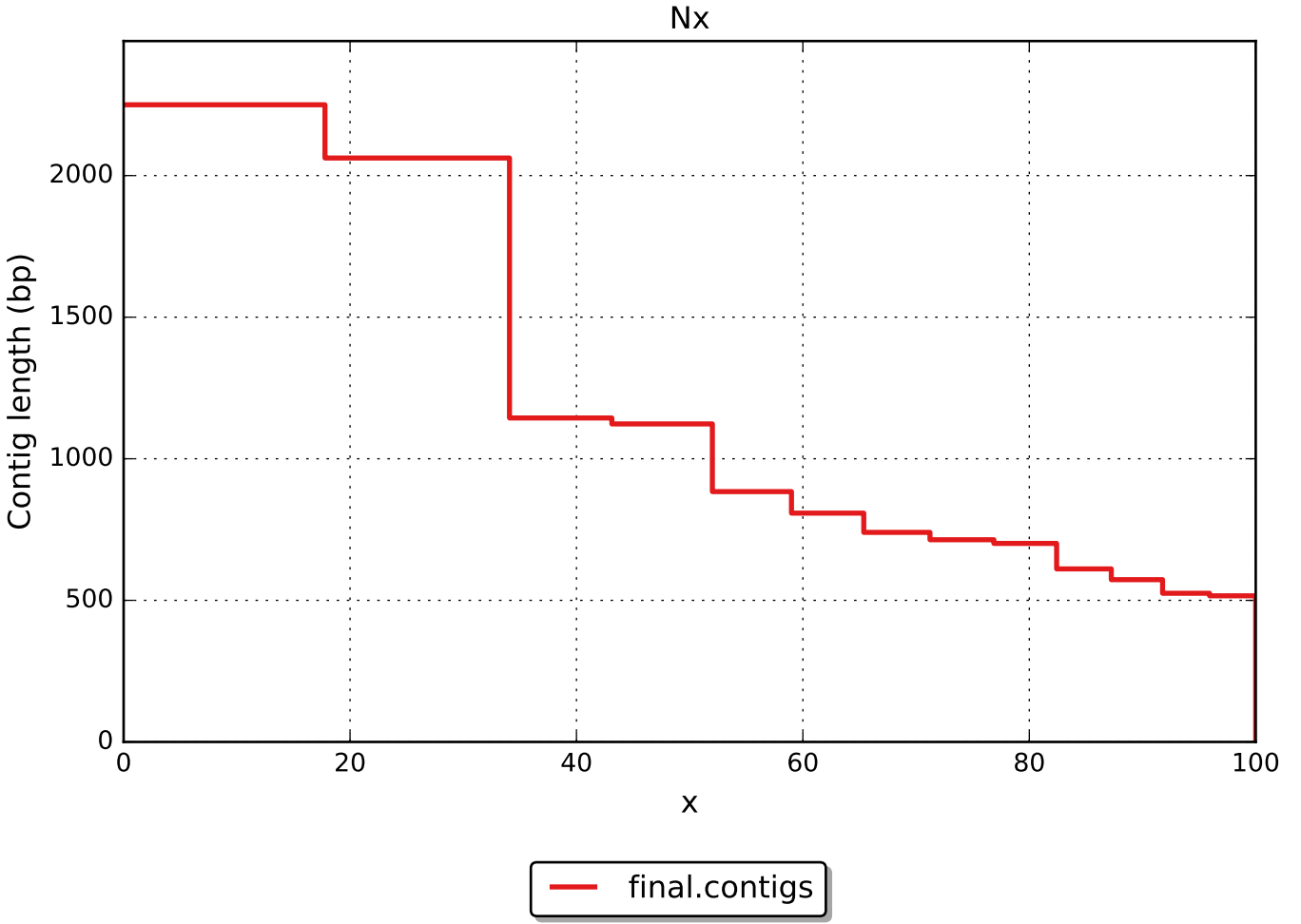
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# unaligned mis. contigs	1
# mismatches	94
# indels	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	8

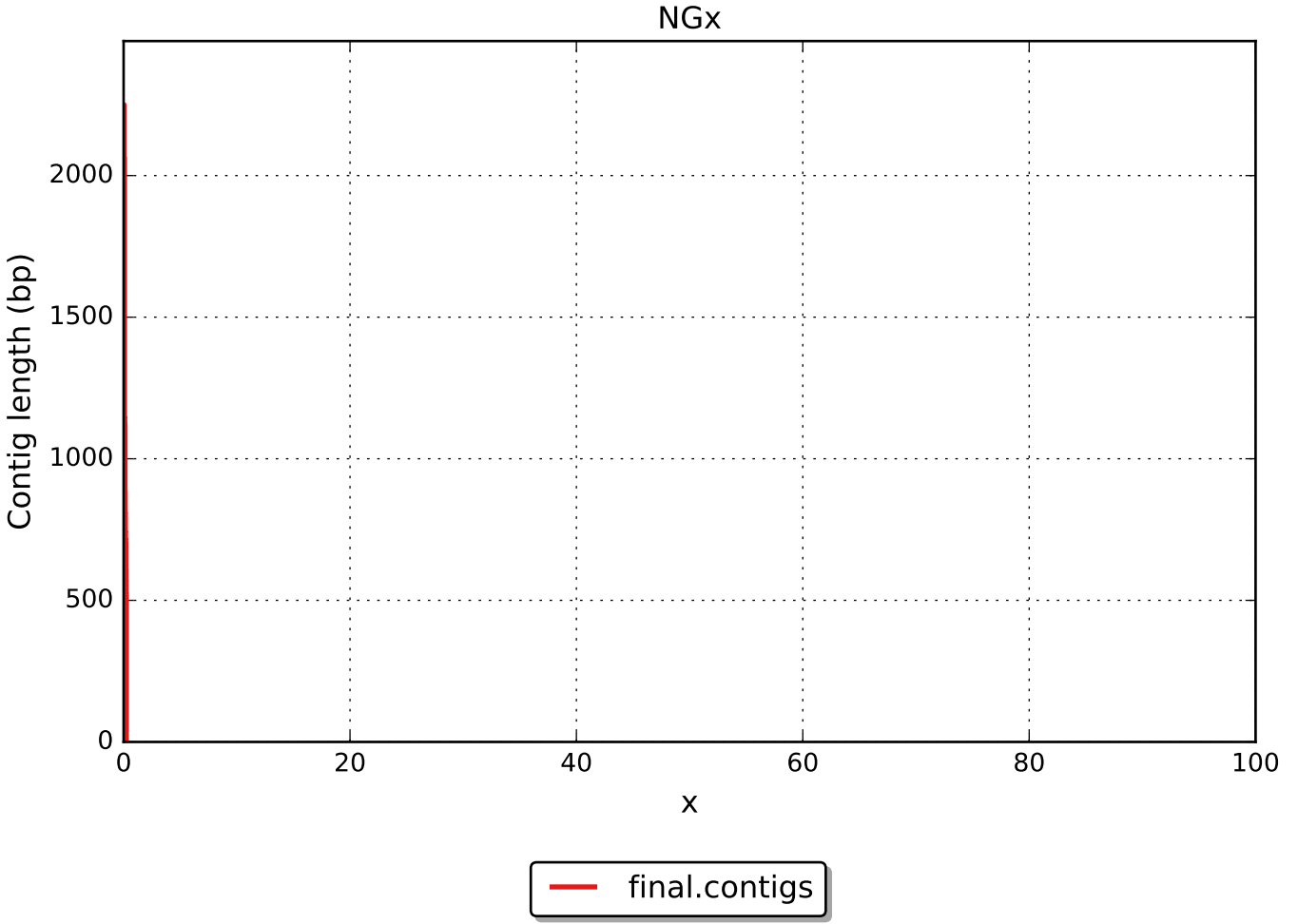
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

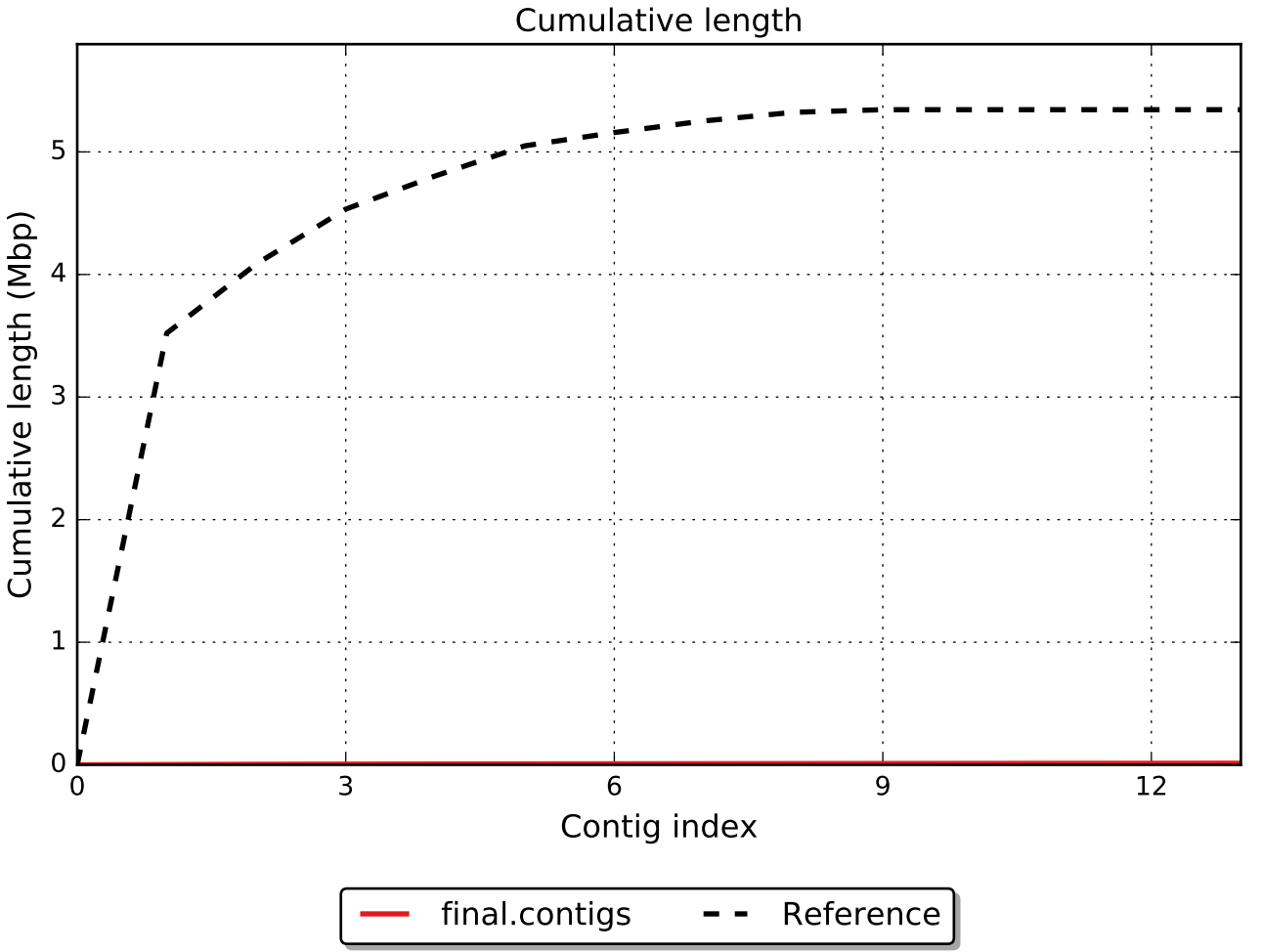
Unaligned report

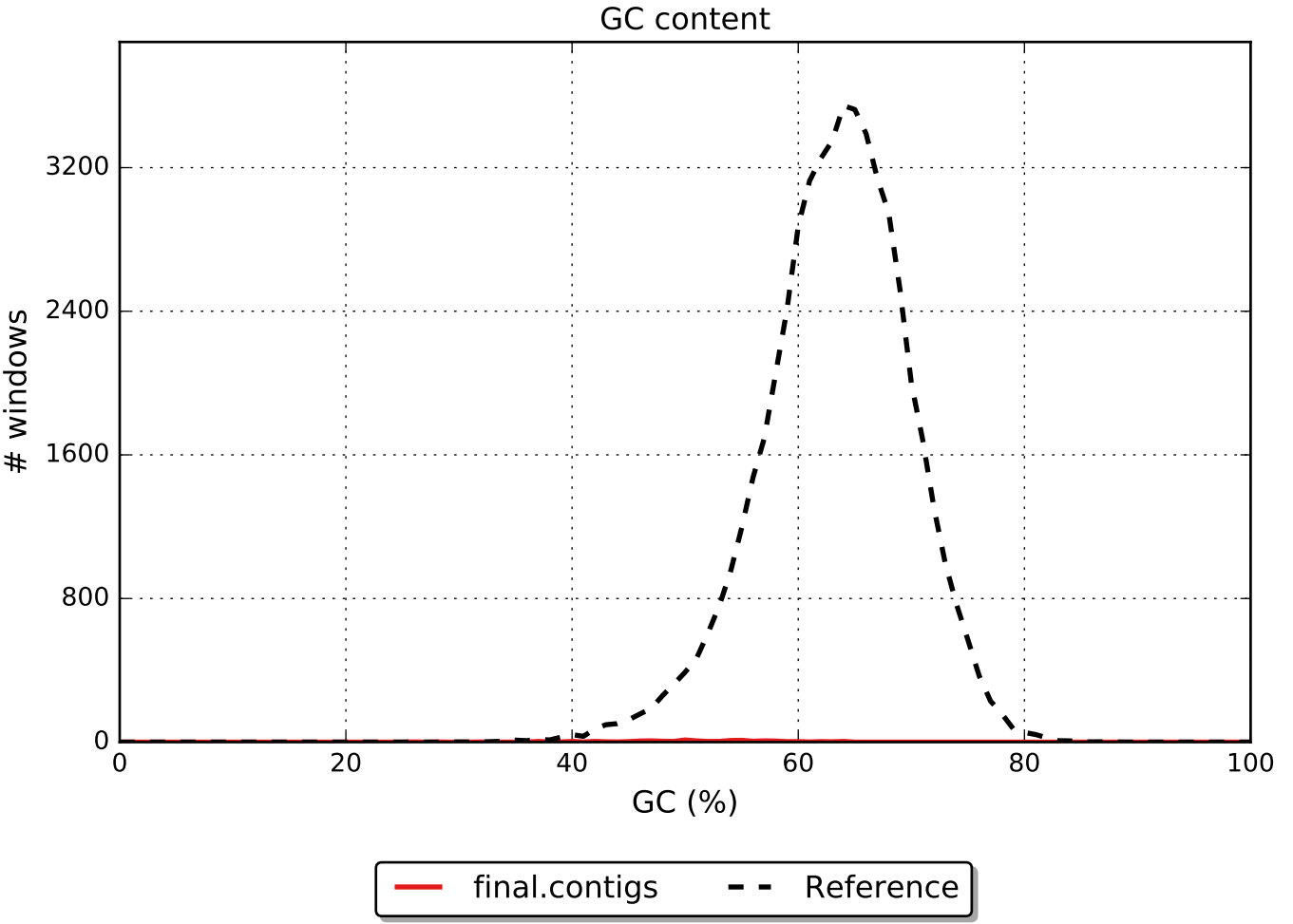
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	6025
# N's	0

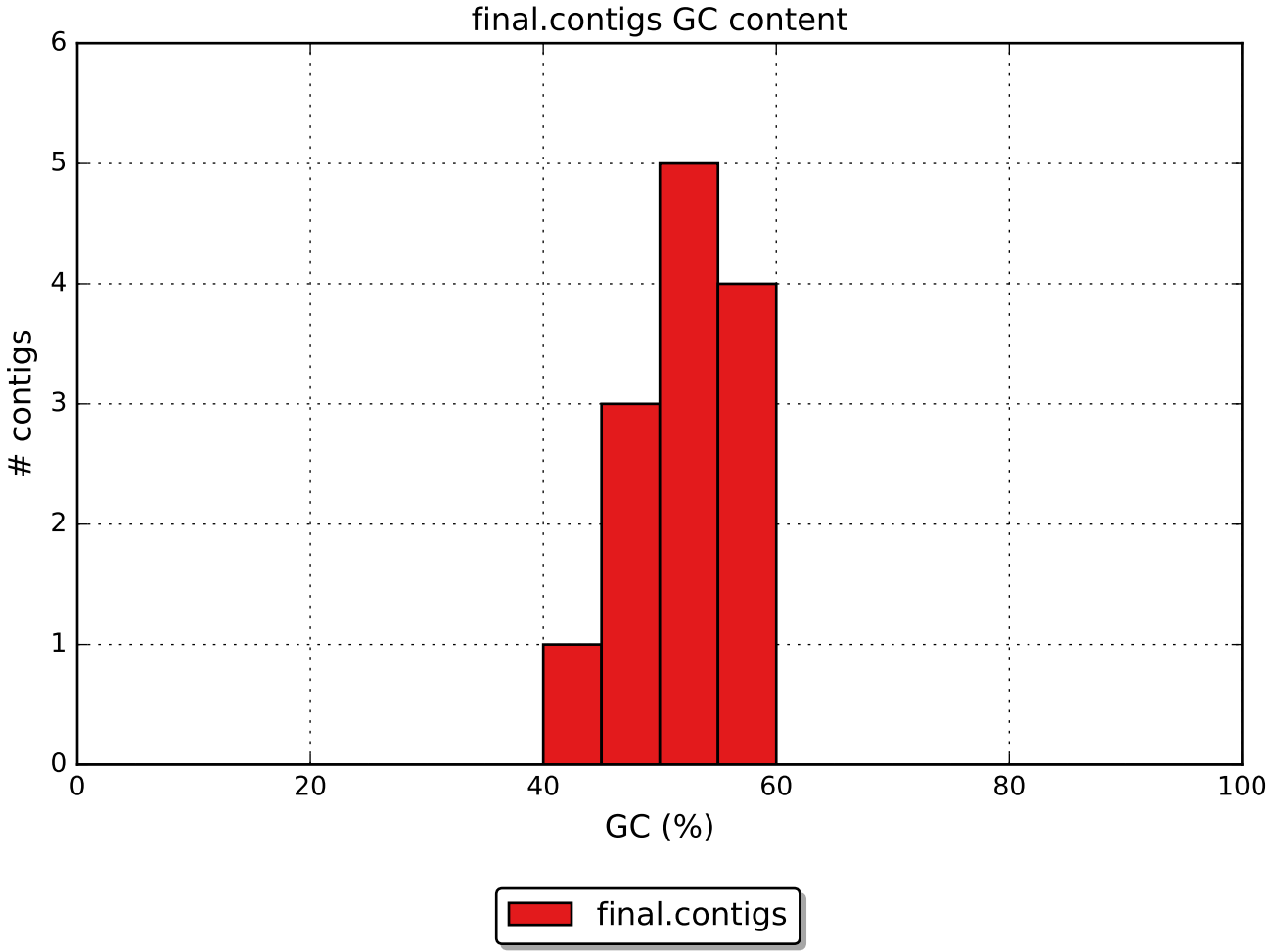
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

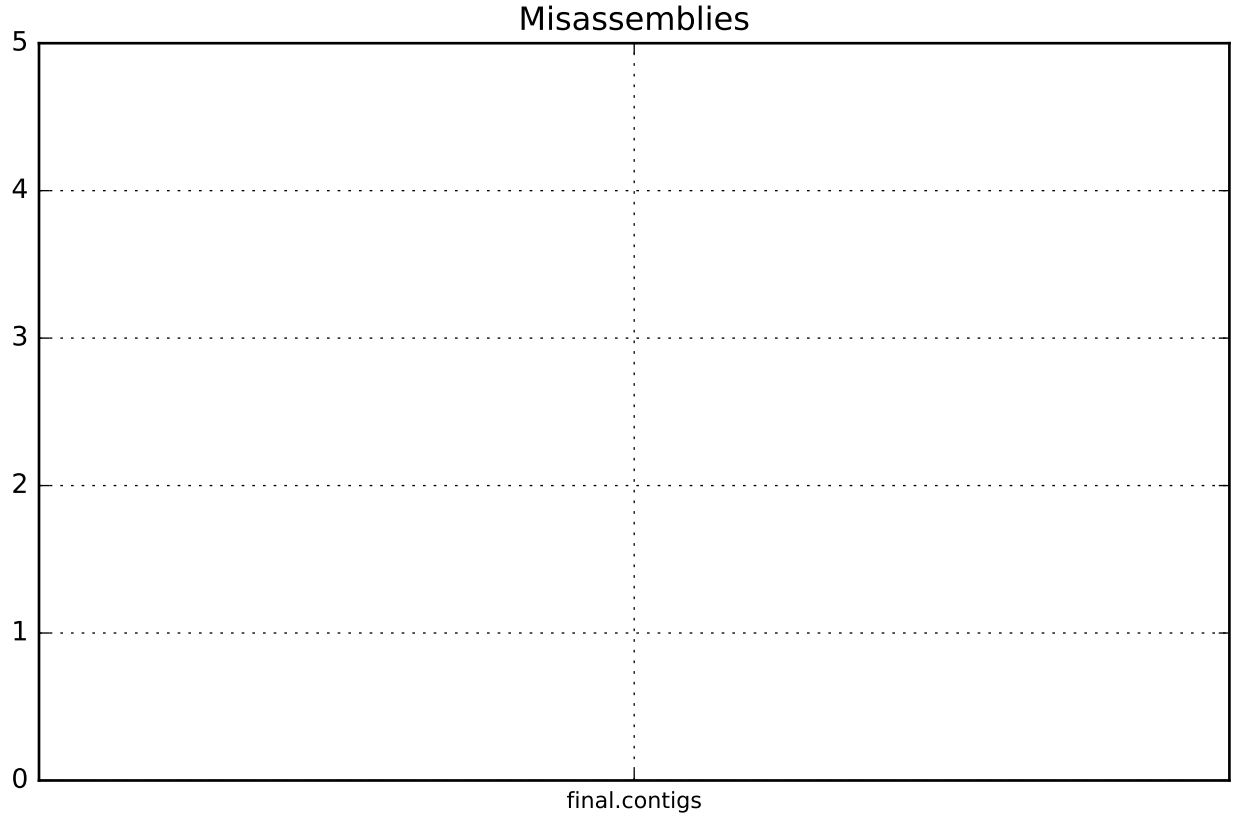

Nx
Contig length (bp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs

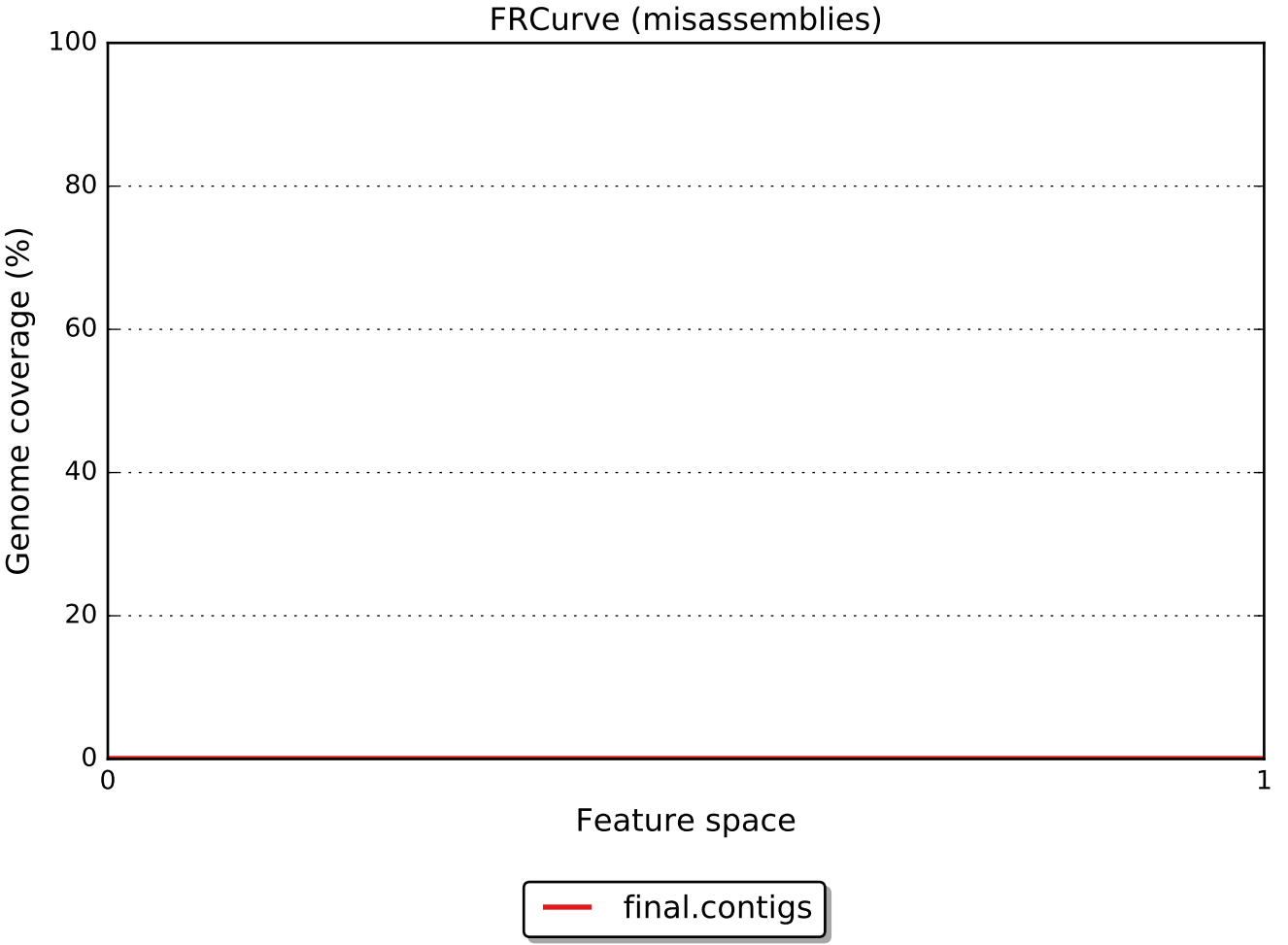

NGx
Contig length (bp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
final.contigs

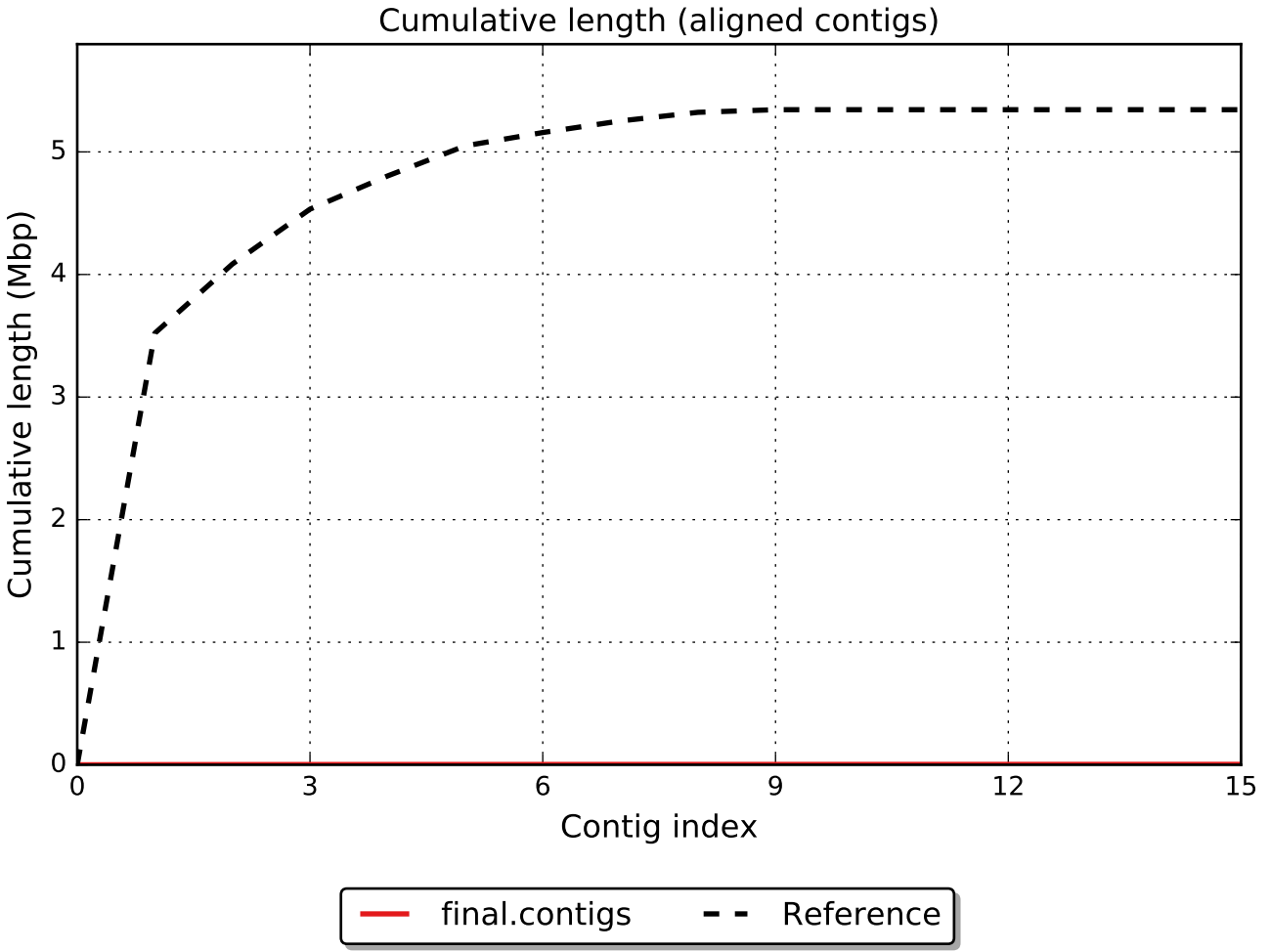

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
3
6
9
12
Contig index
final.contigs
Reference

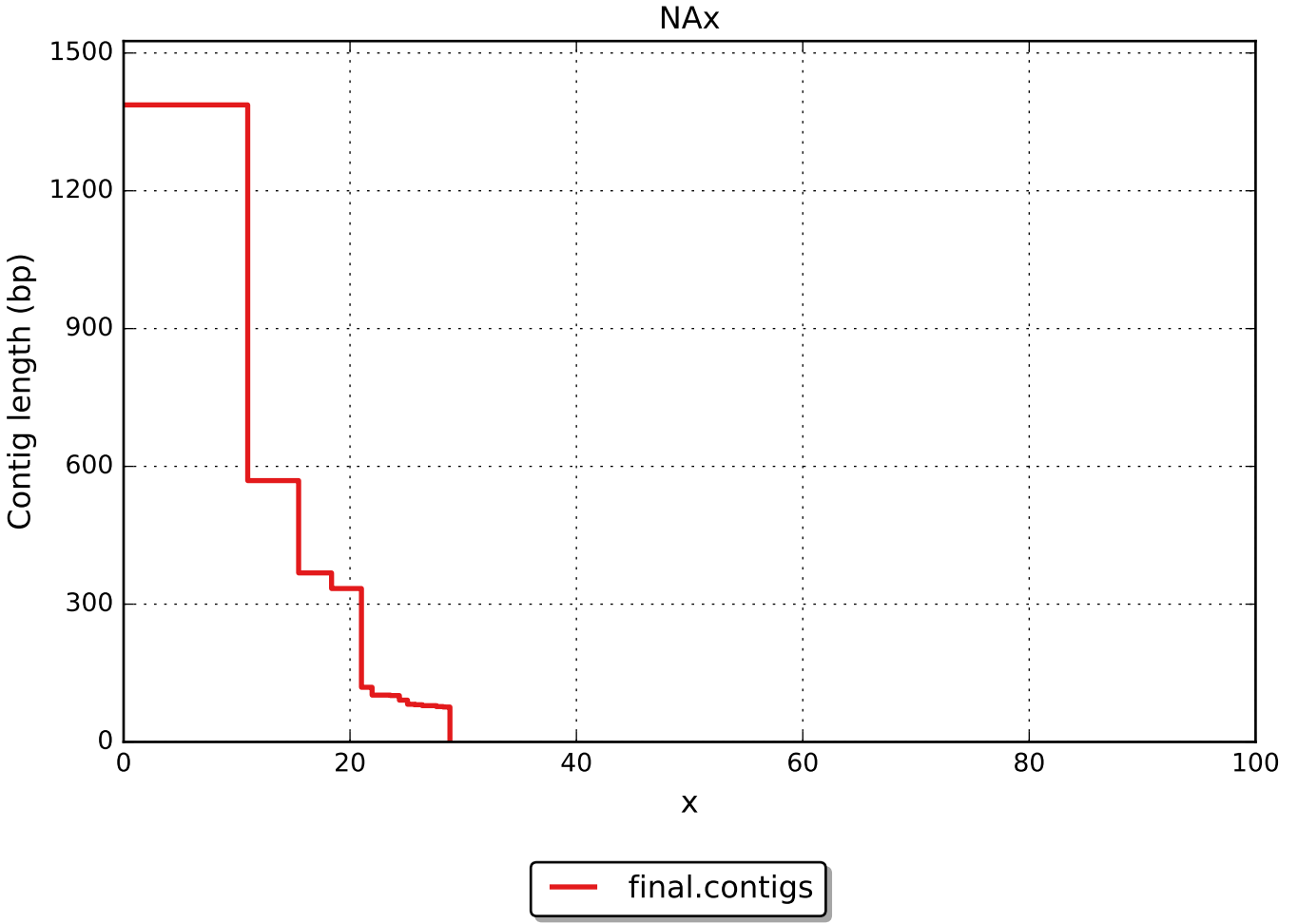

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

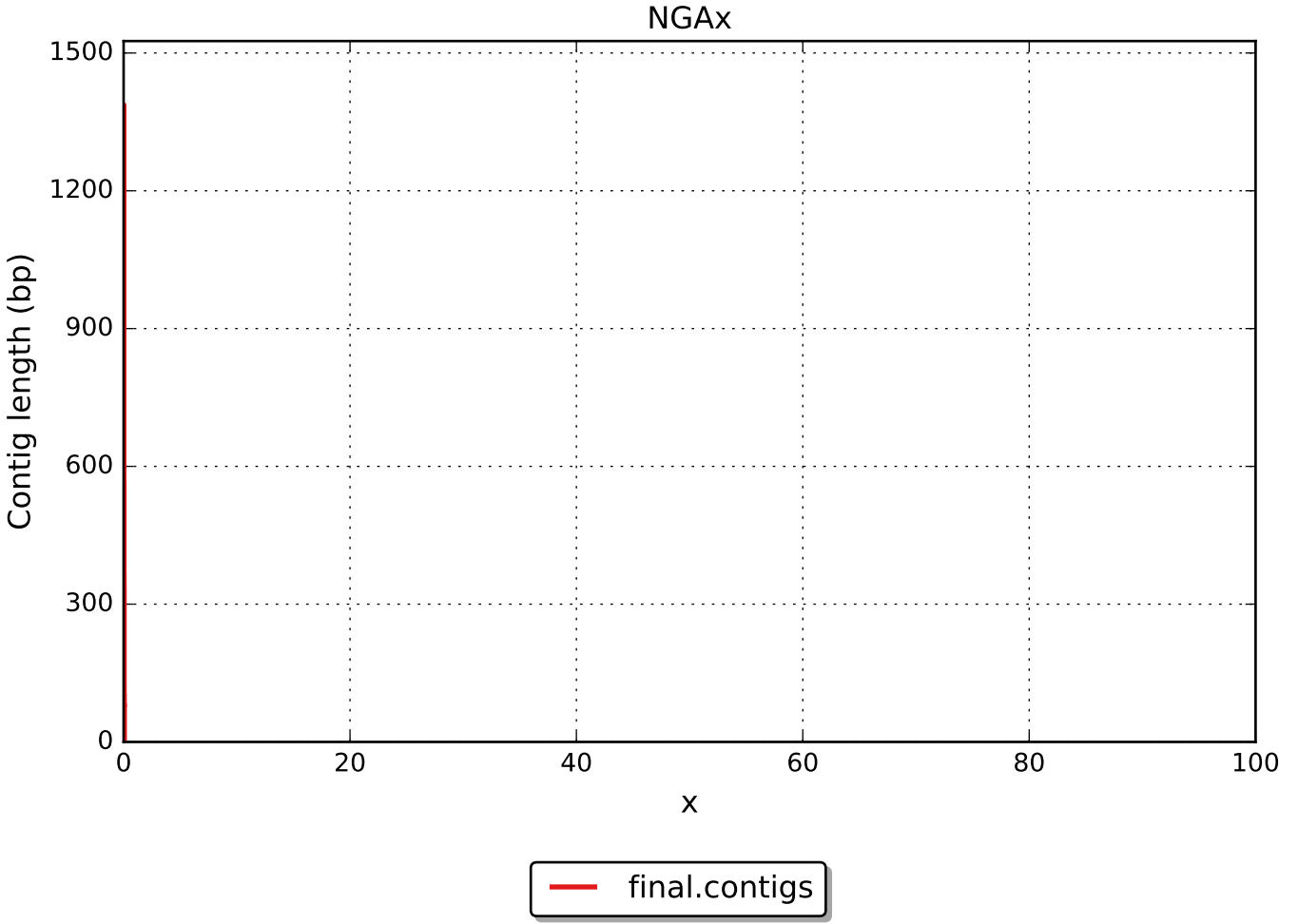

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs


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 (Mbp)
0
1
2
3
4
5
0
3
6
9
12
15
Contig index
final.contigs
Reference


NAx
1500
1200
900
600
300
0
Contig length (bp)
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