Report

	final.contigs
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	14441
Total length (>= 5000 bp)	5267
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6
Largest contig	5267
Total length	15119
Reference length	2077614
GC (%)	47.03
Reference GC (%)	39.47
N50	4124
N75	3047
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	14025
Genome fraction (%)	0.053
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2833.64
# indels per 100 kbp	182.82
Largest alignment	678
Total aligned length	1094
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

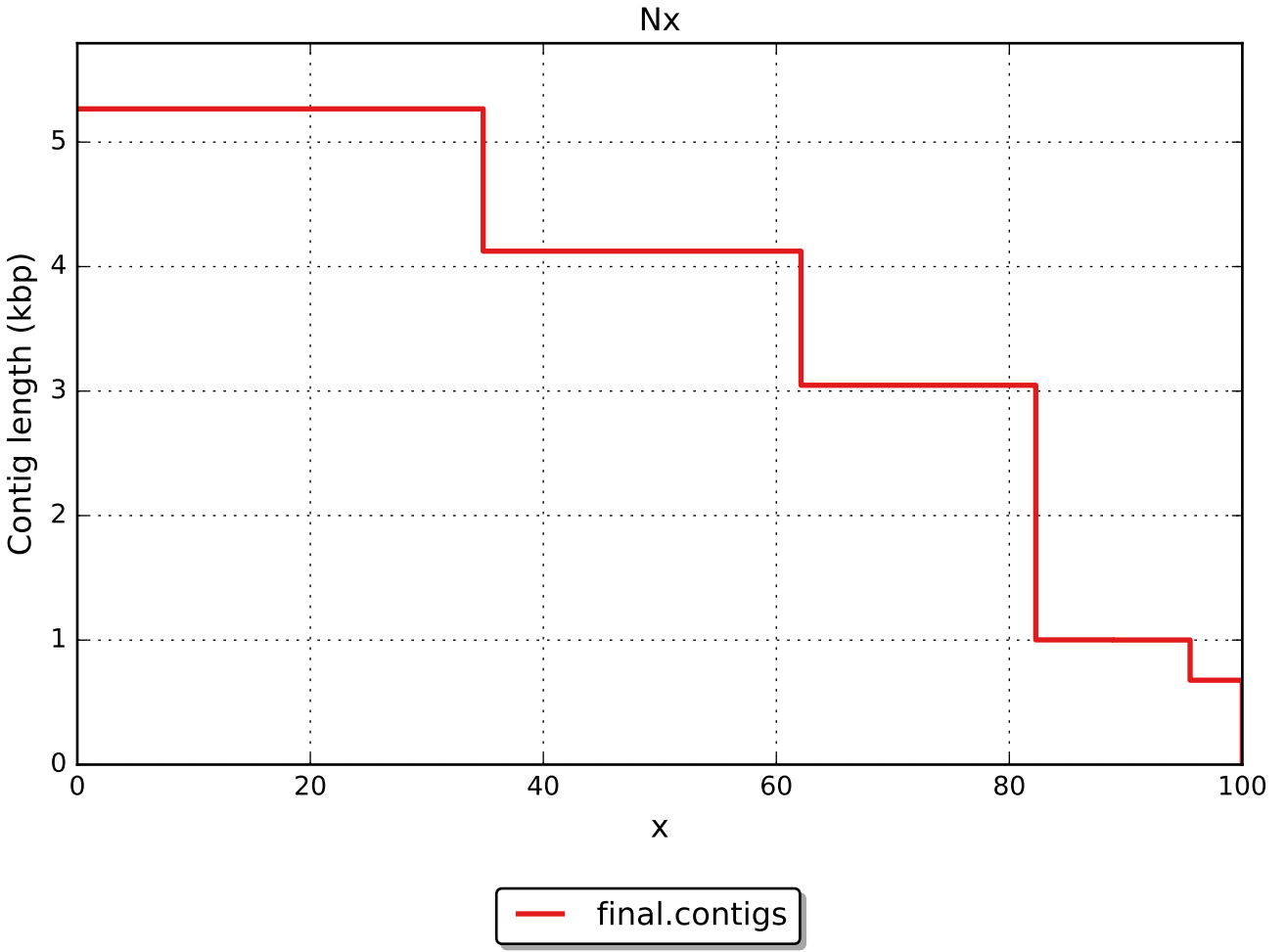
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	31
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

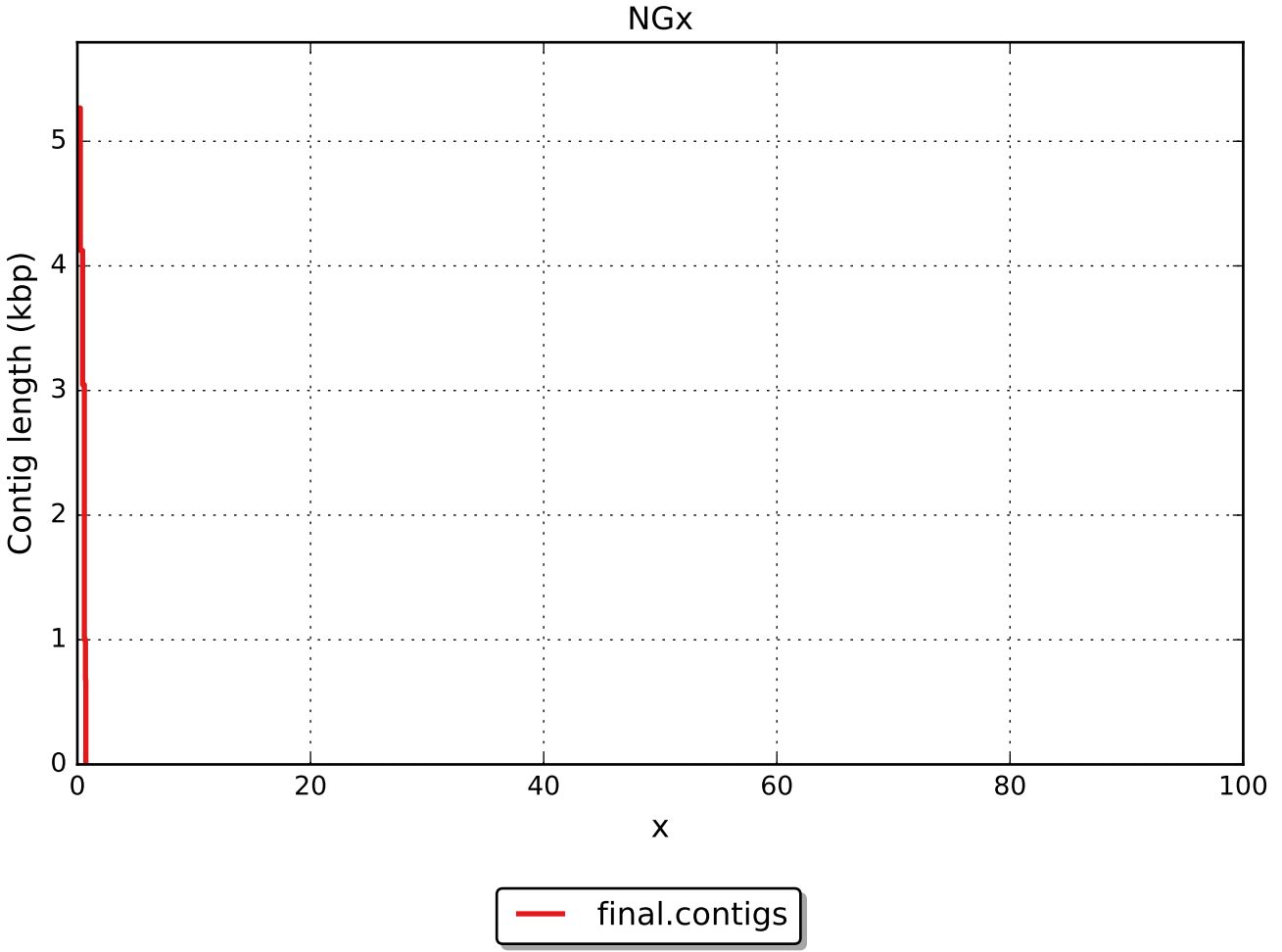
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

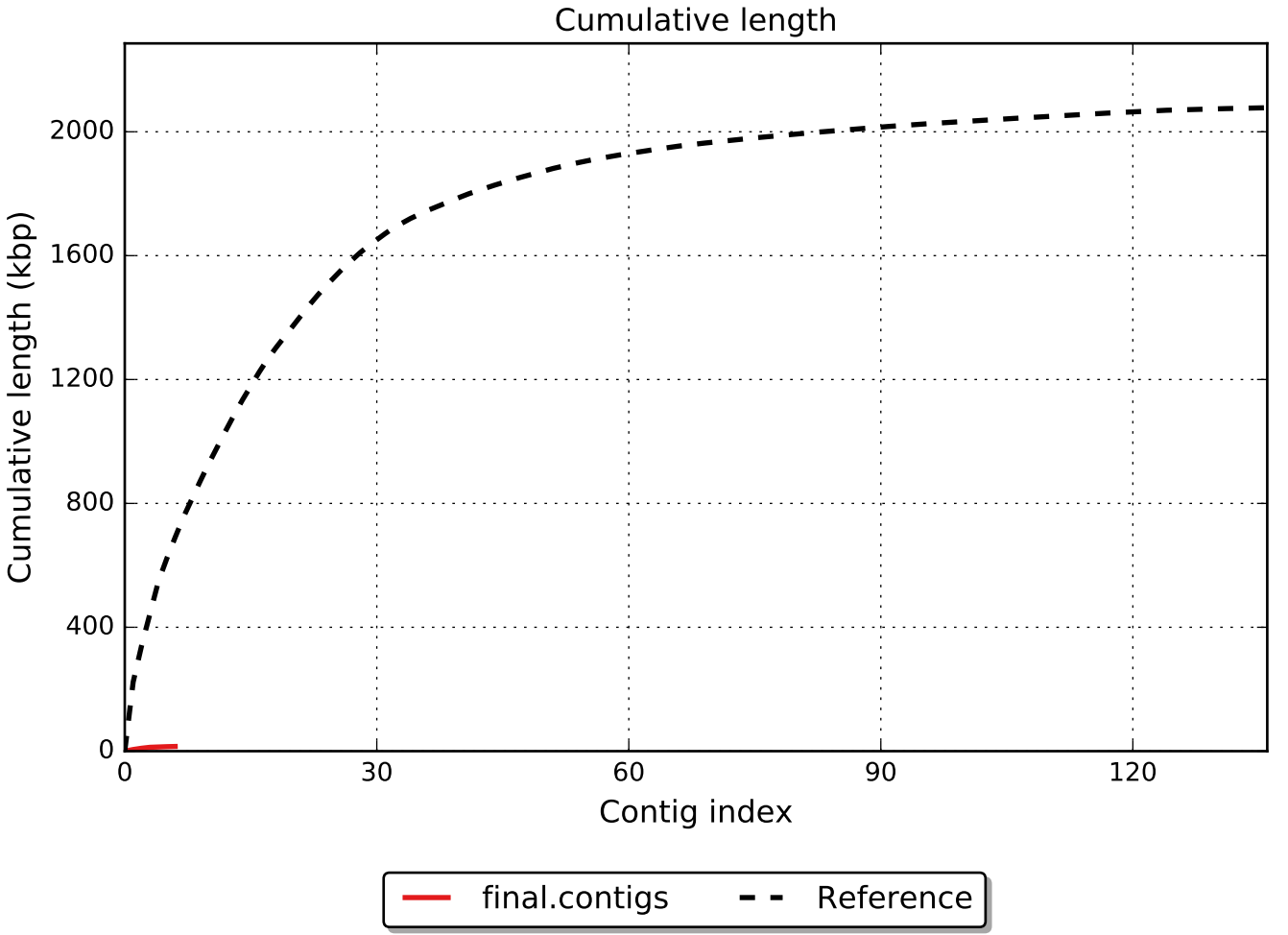
Unaligned report

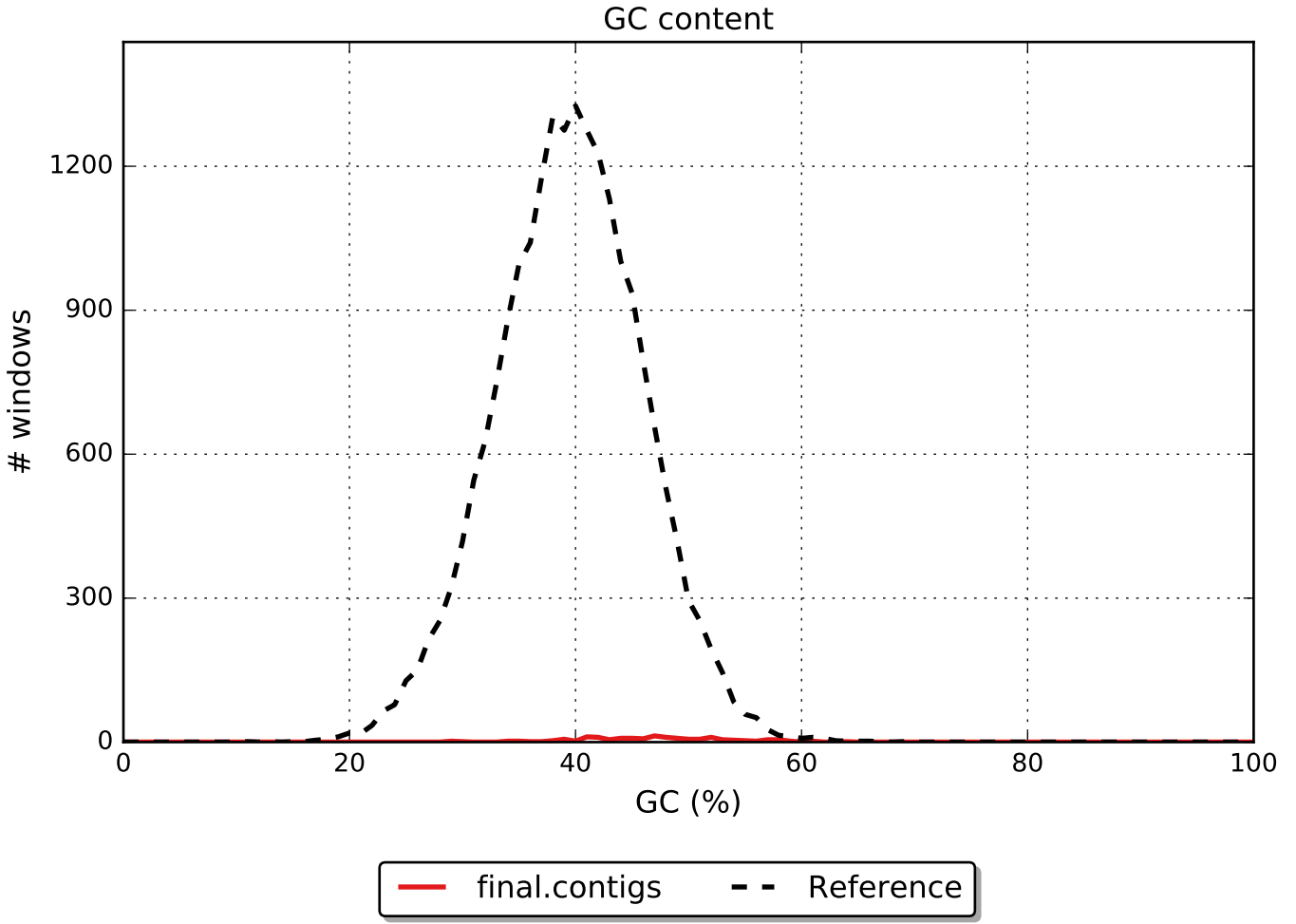
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	14025
# N's	0

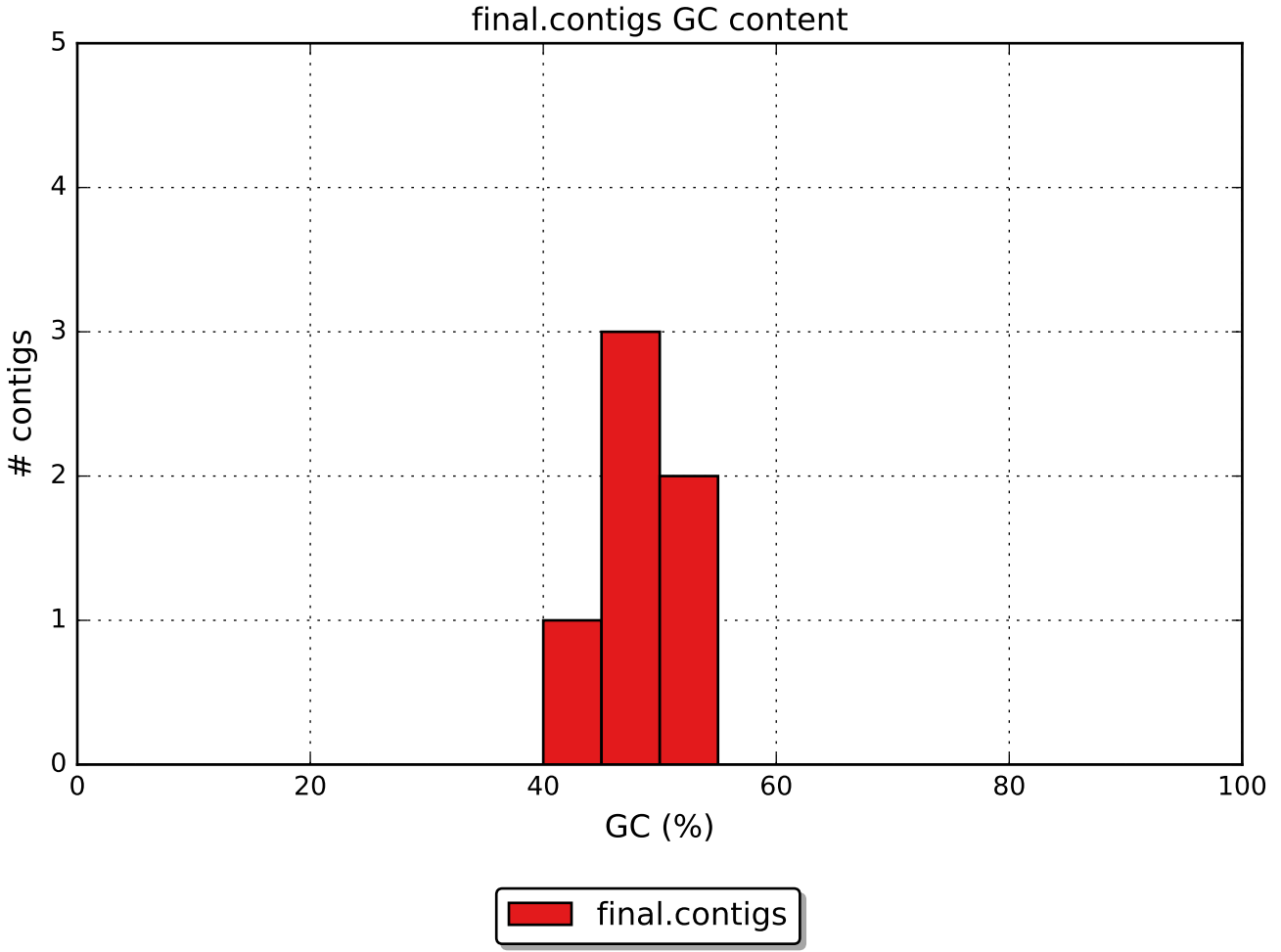
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

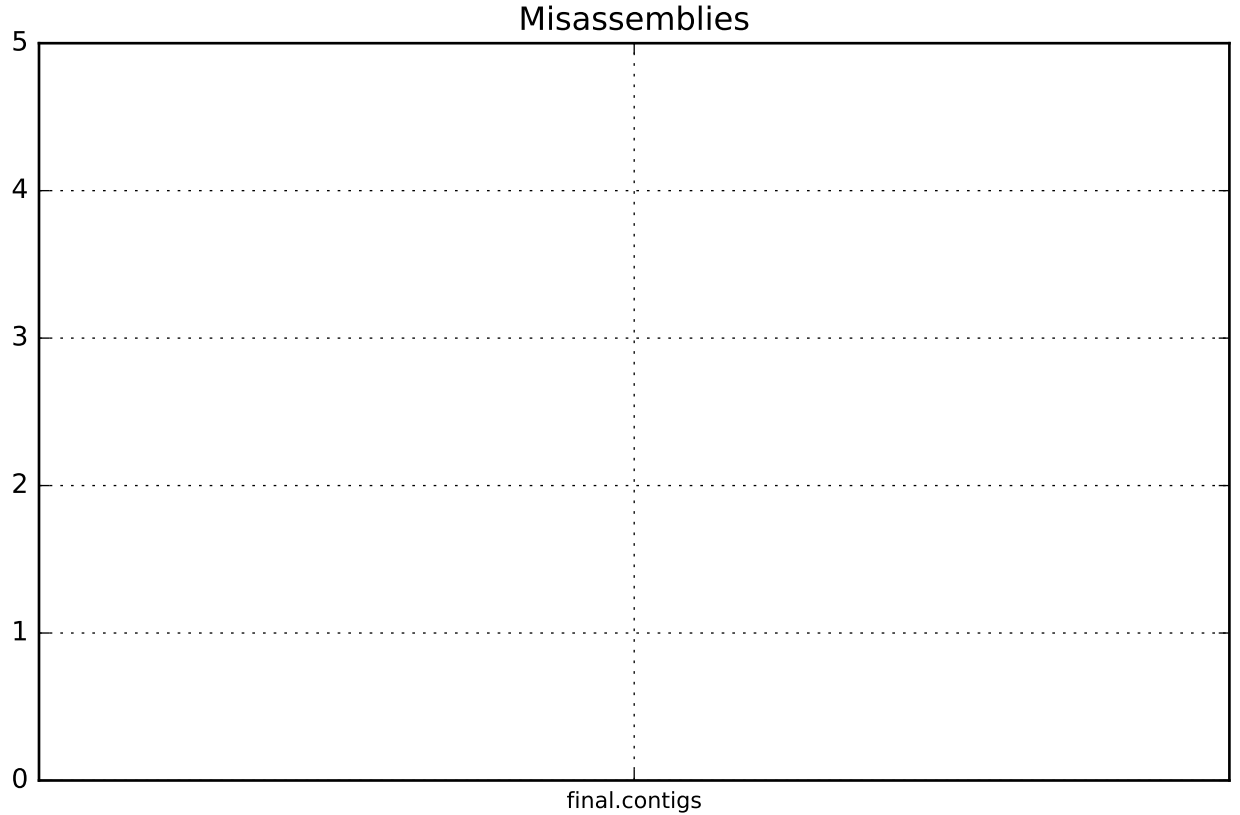

Nx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
final.contigs

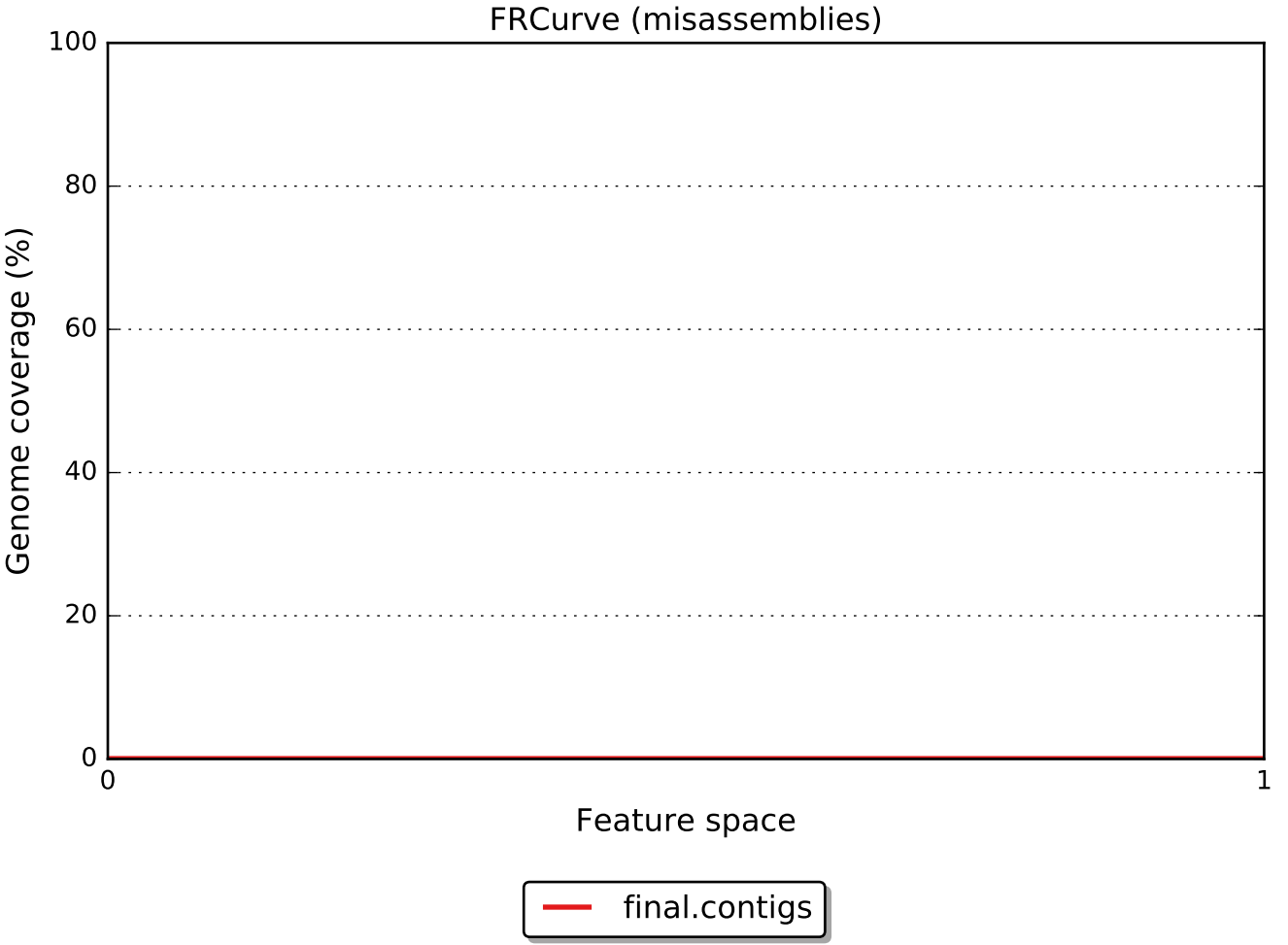

NGx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
final.contigs

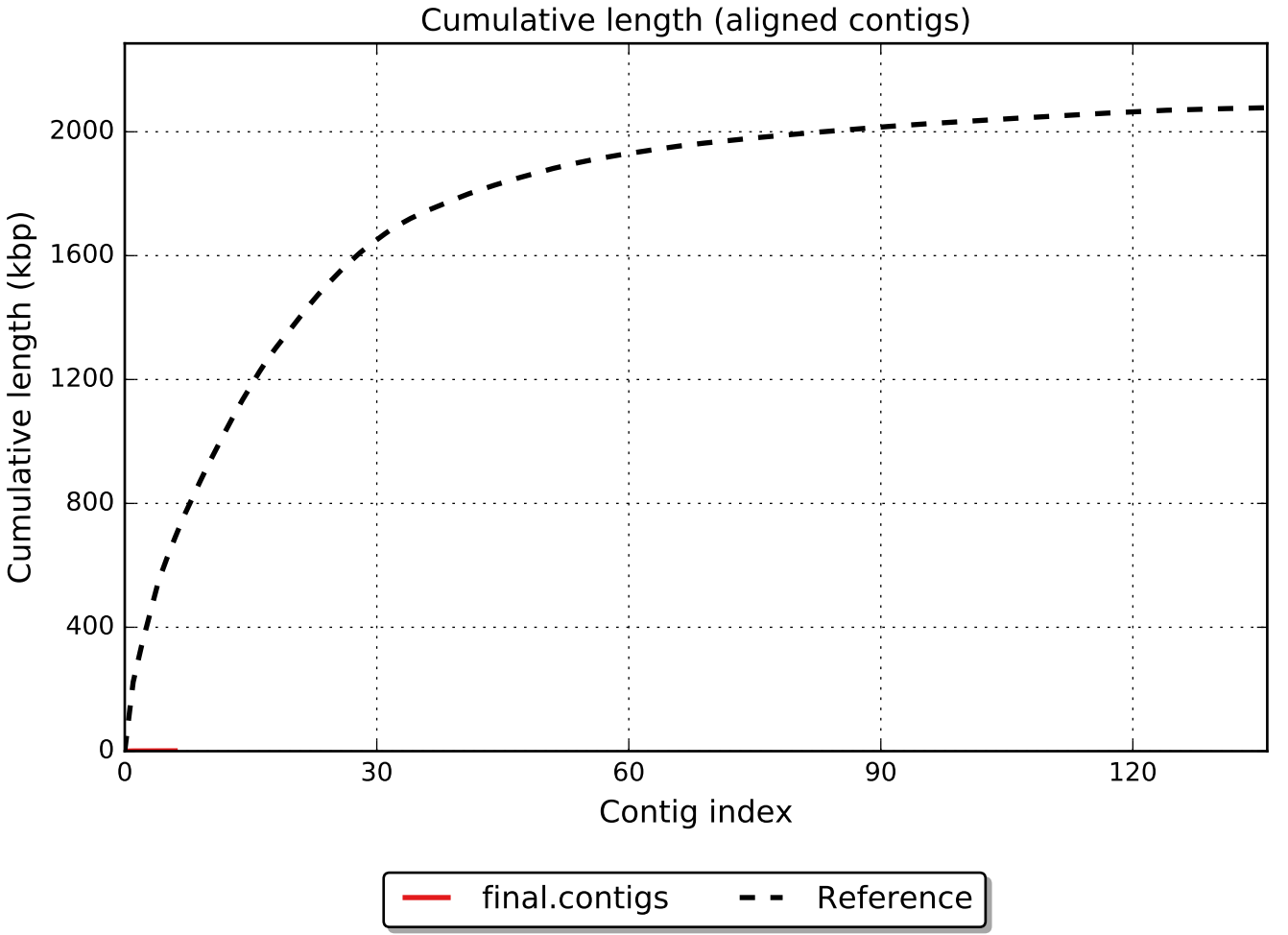

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
30
60
90
120
Contig index
final.contigs
Reference

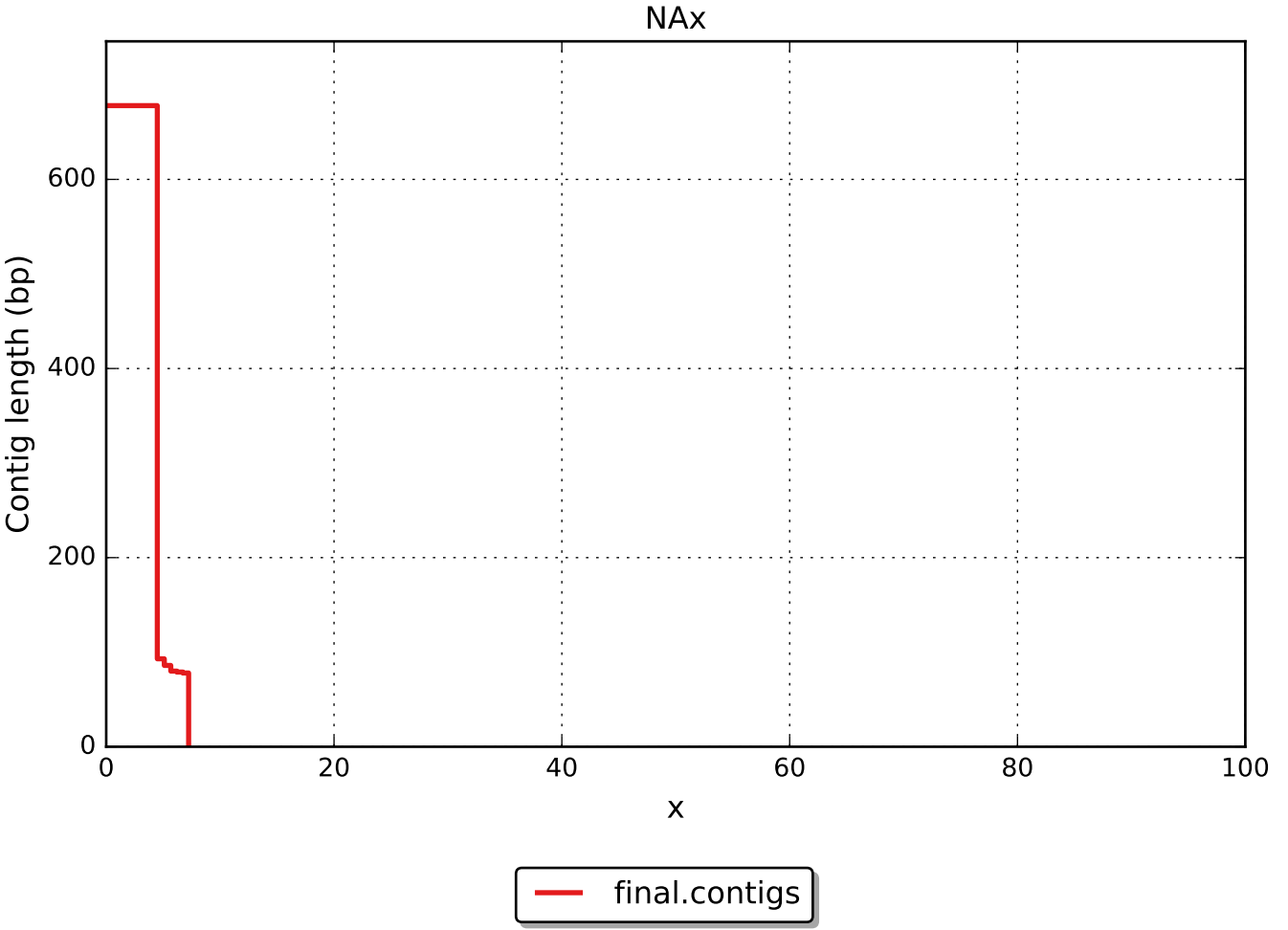

GC content
windows
GC (%)
0
300
600
900
1200
0
20
40
60
80
100
final.contigs
Reference

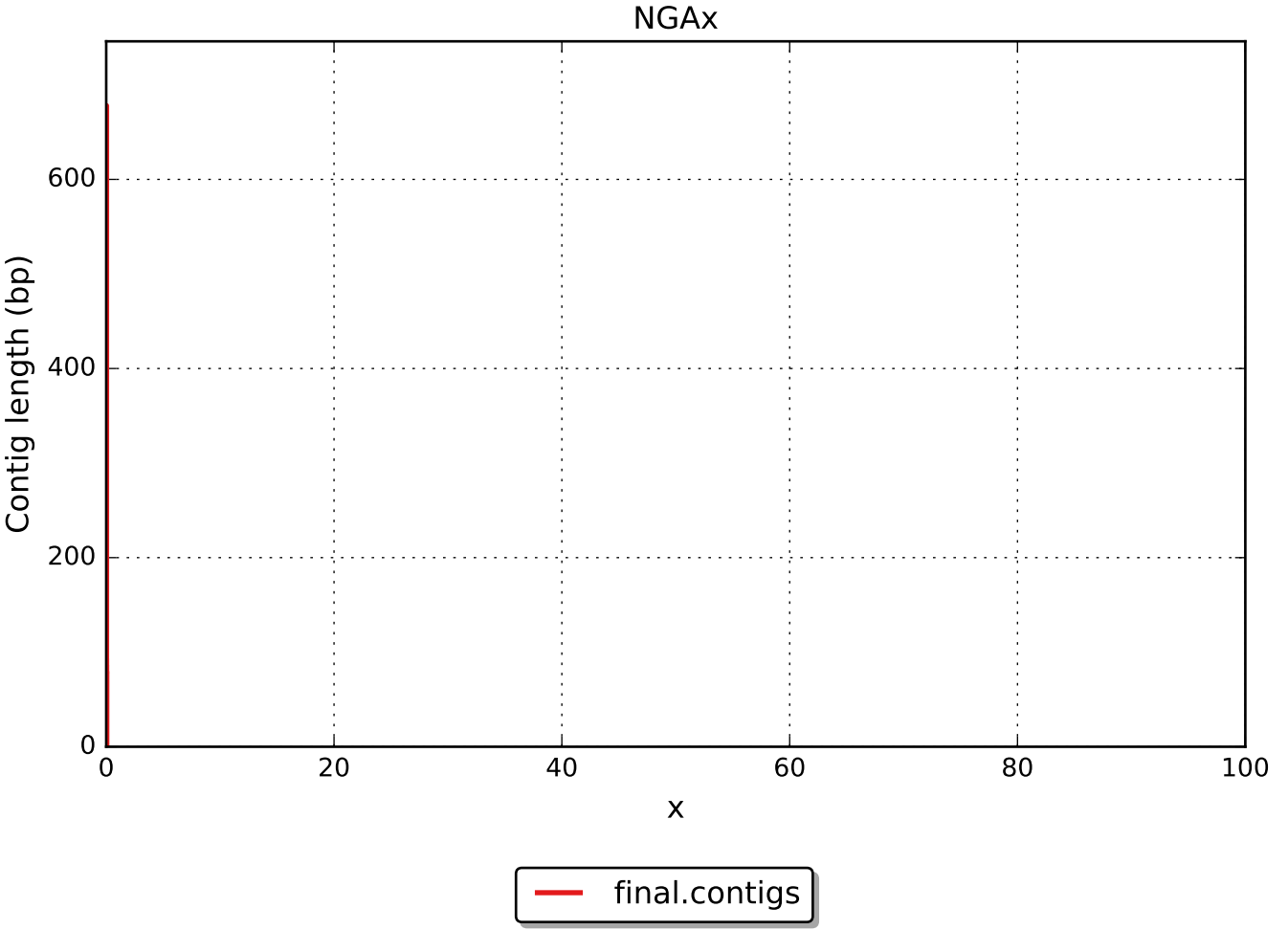

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
final.contigs


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)
2000
1600
1200
800
400
0
0
30
60
90
120
Contig index
final.contigs
Reference


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


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