Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	68695
Total length (>= 5000 bp)	55576
Total length (>= 10000 bp)	55576
Total length (>= 25000 bp)	44784
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	44784
Total length	71579
Reference length	3910325
GC (%)	58.04
Reference GC (%)	62.16
N50	44784
N75	10792
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 9 part
Unaligned length	69099
Genome fraction (%)	0.029
Duplication ratio	2.199
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1595.74
# indels per 100 kbp	354.61
Largest alignment	219
Total aligned length	1269
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

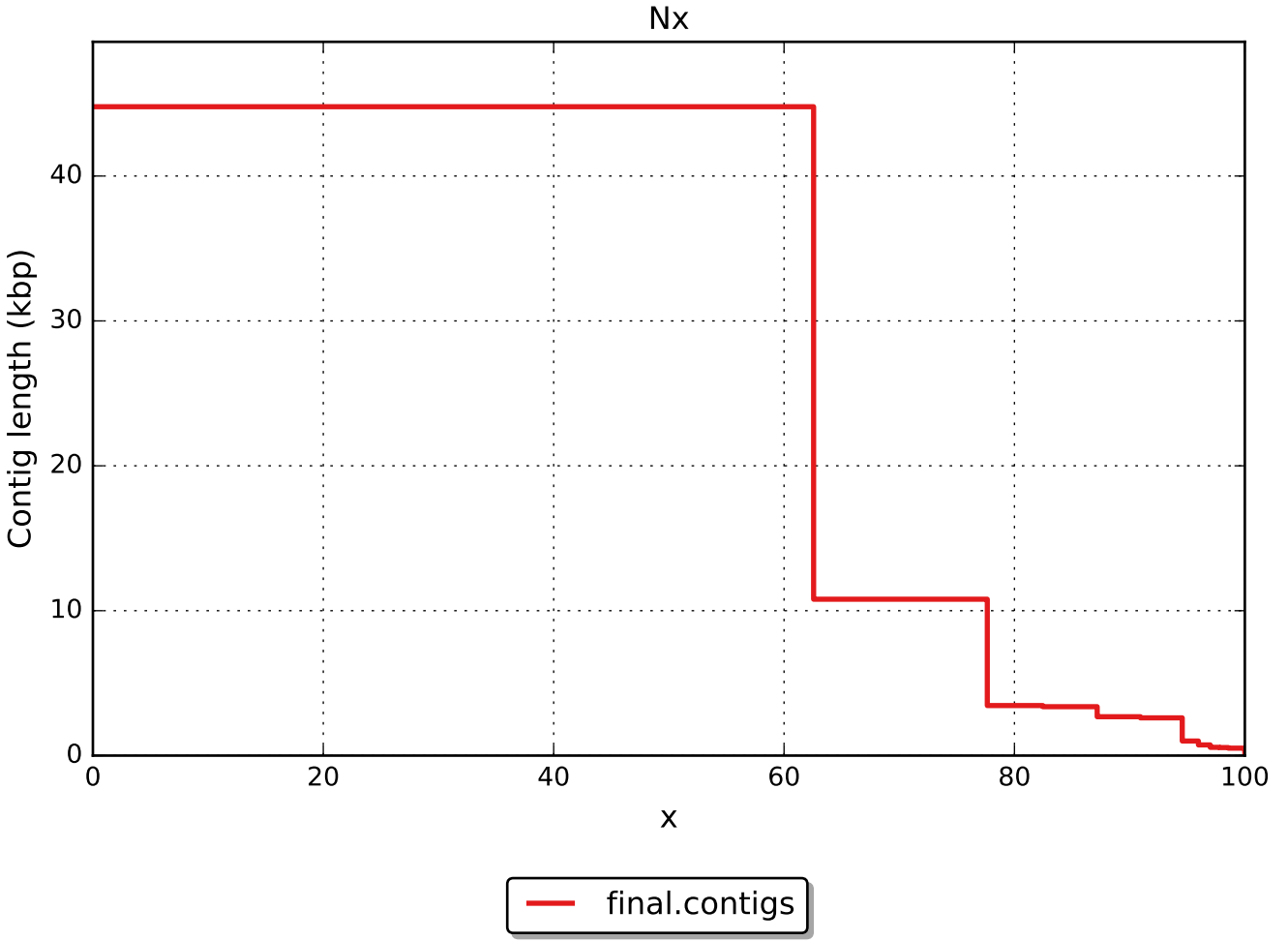
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	18
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

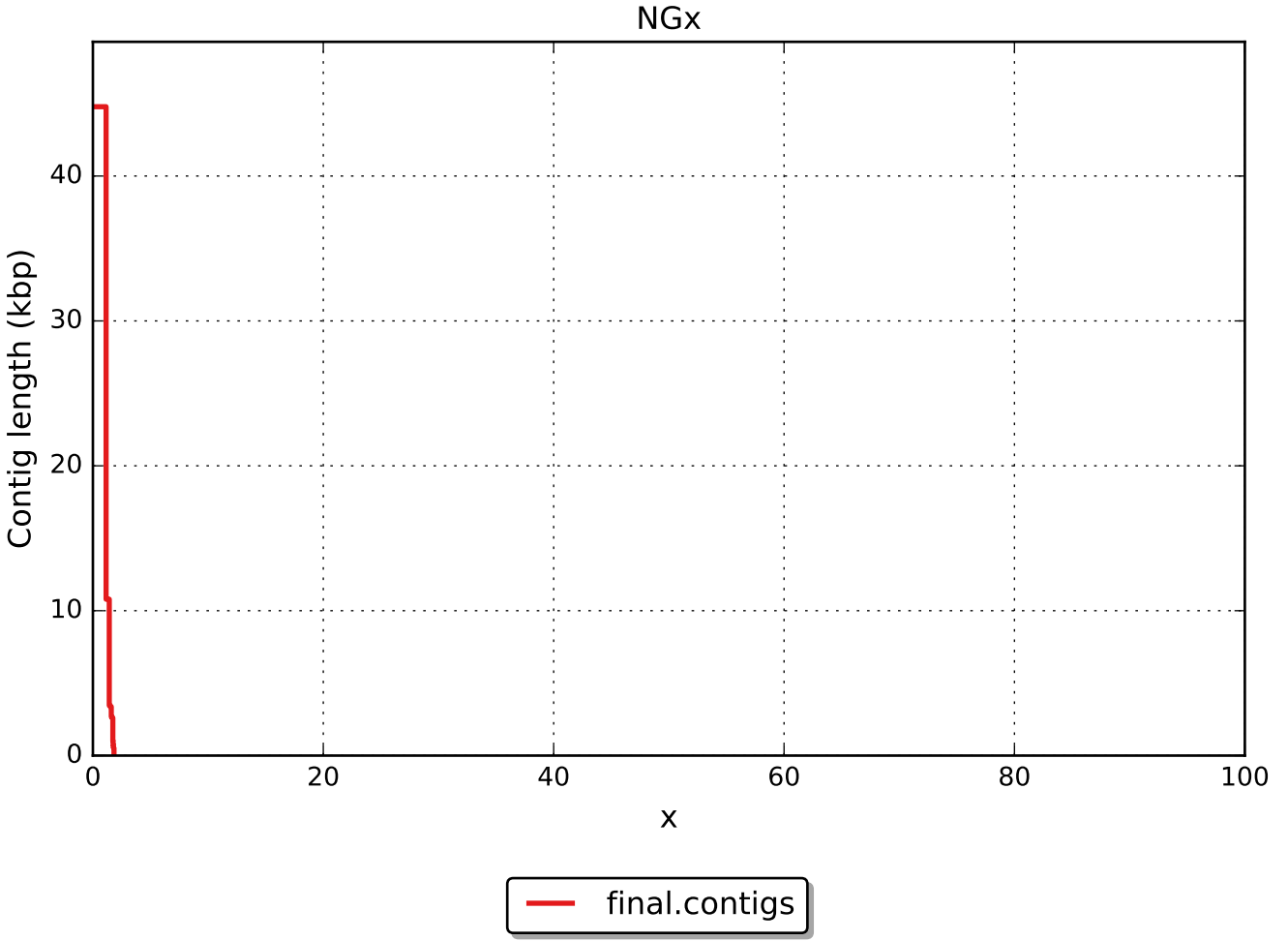
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

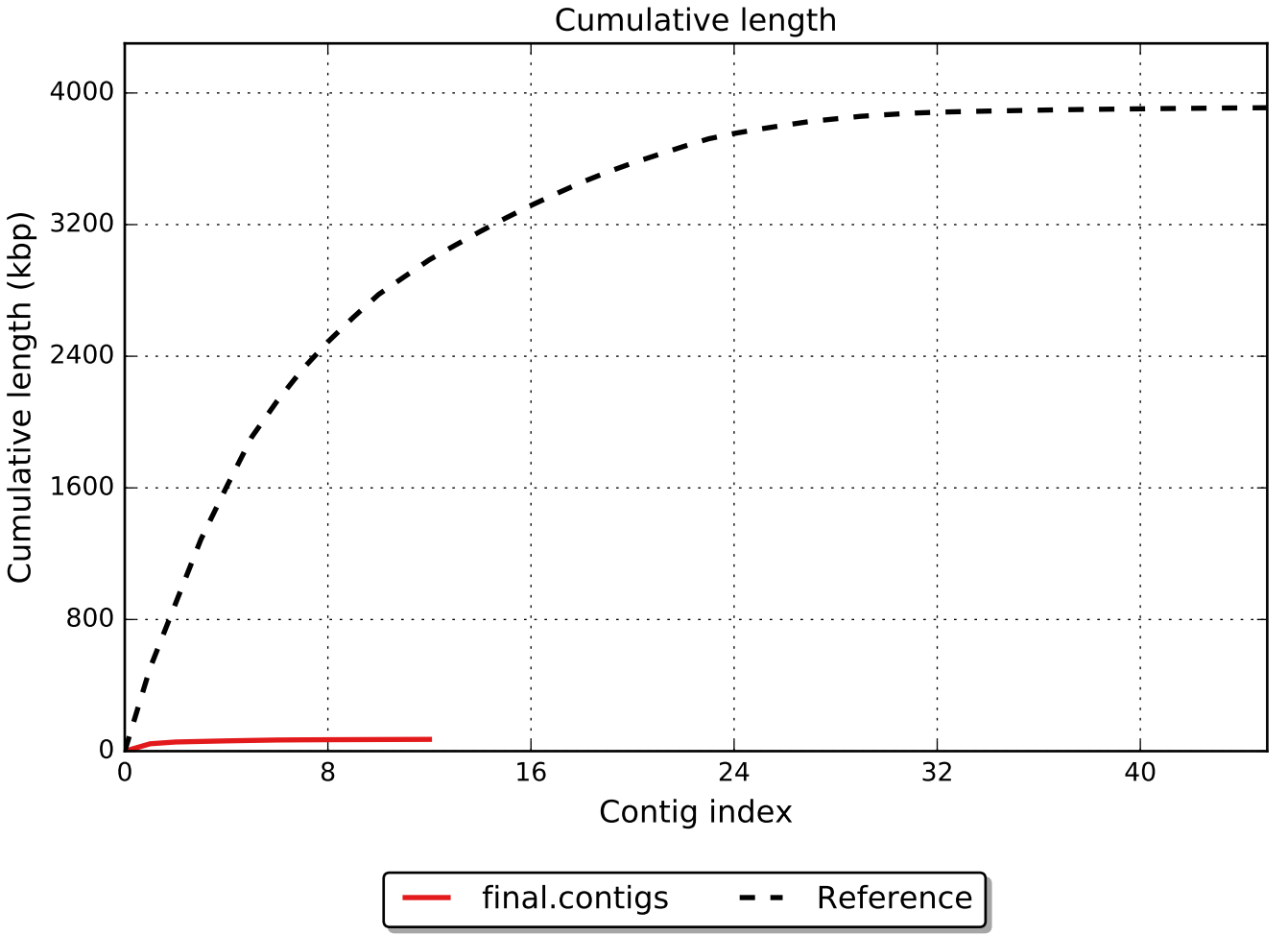
Unaligned report

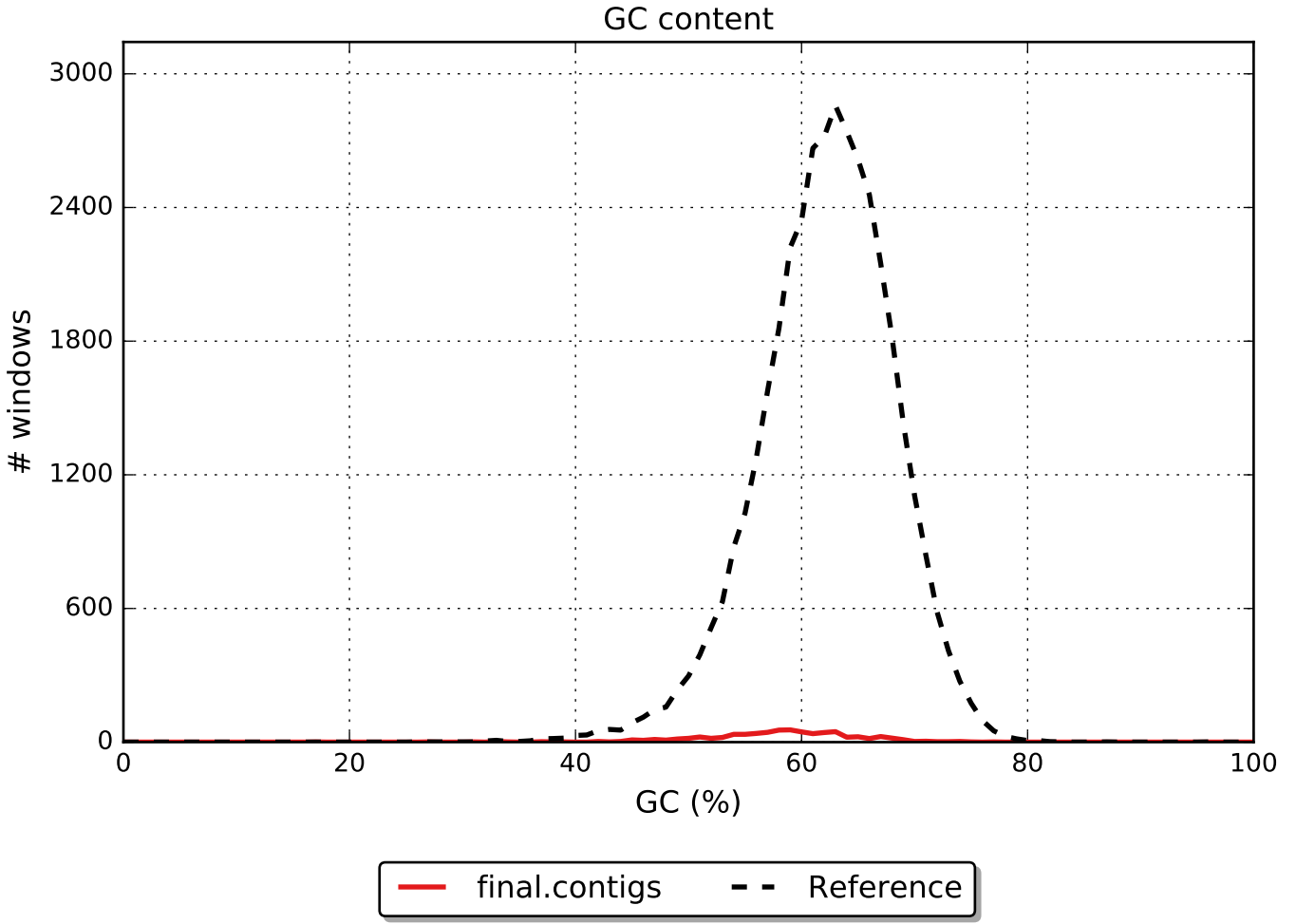
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
Partially unaligned length	69099
# N's	0

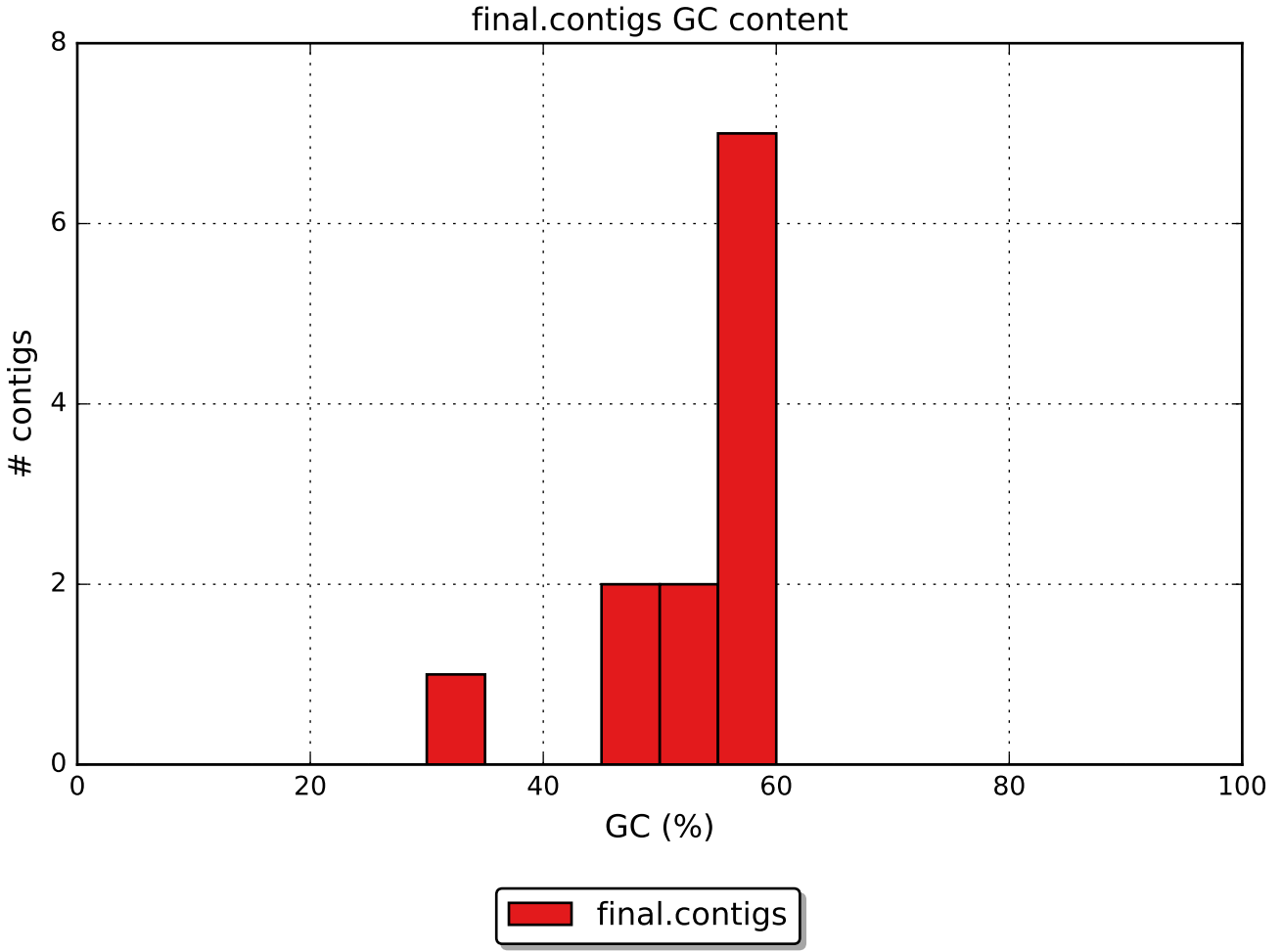
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

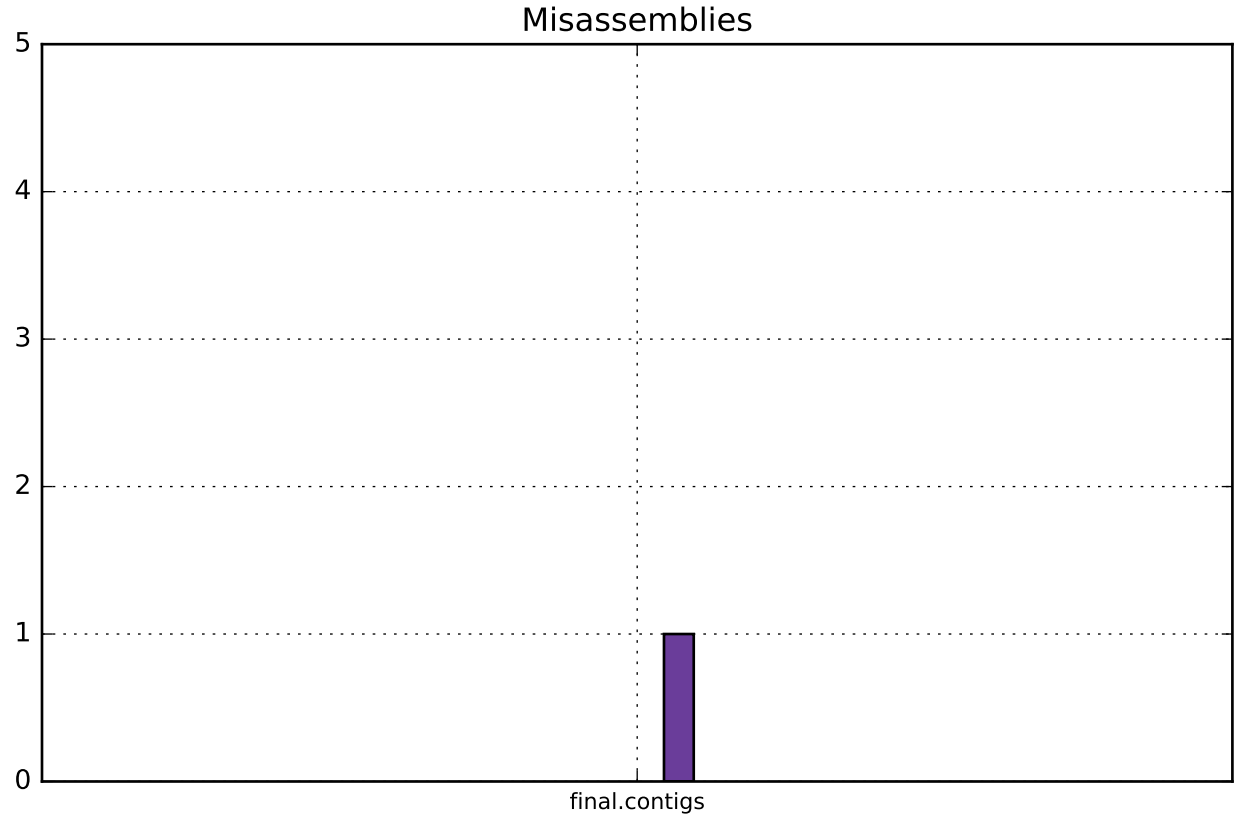

Nx
Contig length (kbp)
0
10
20
30
40
0
20
40
60
80
100
x
final.contigs

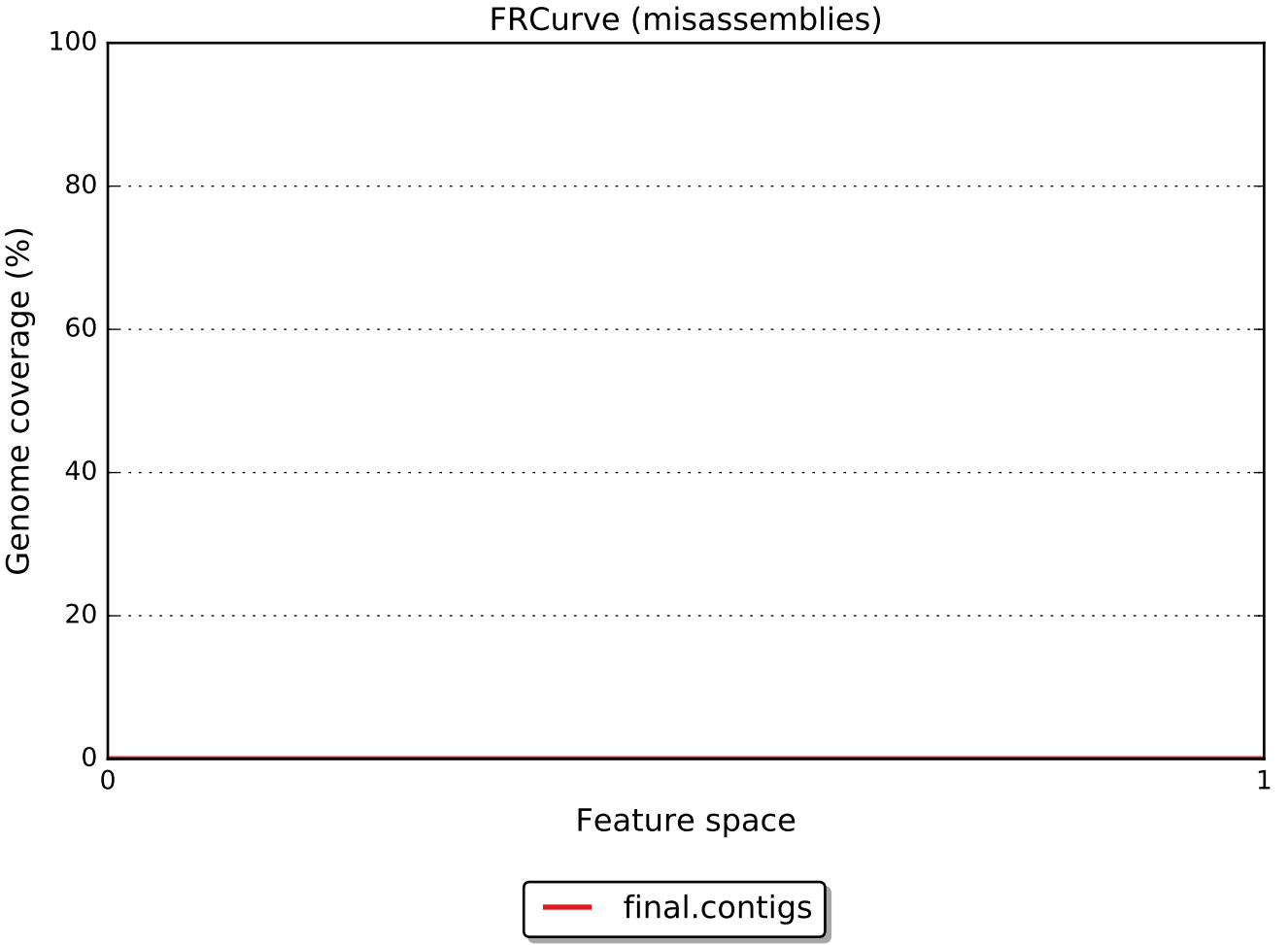

NGx
Contig length (kbp)
0
10
20
30
40
0
20
40
60
80
100
x
final.contigs

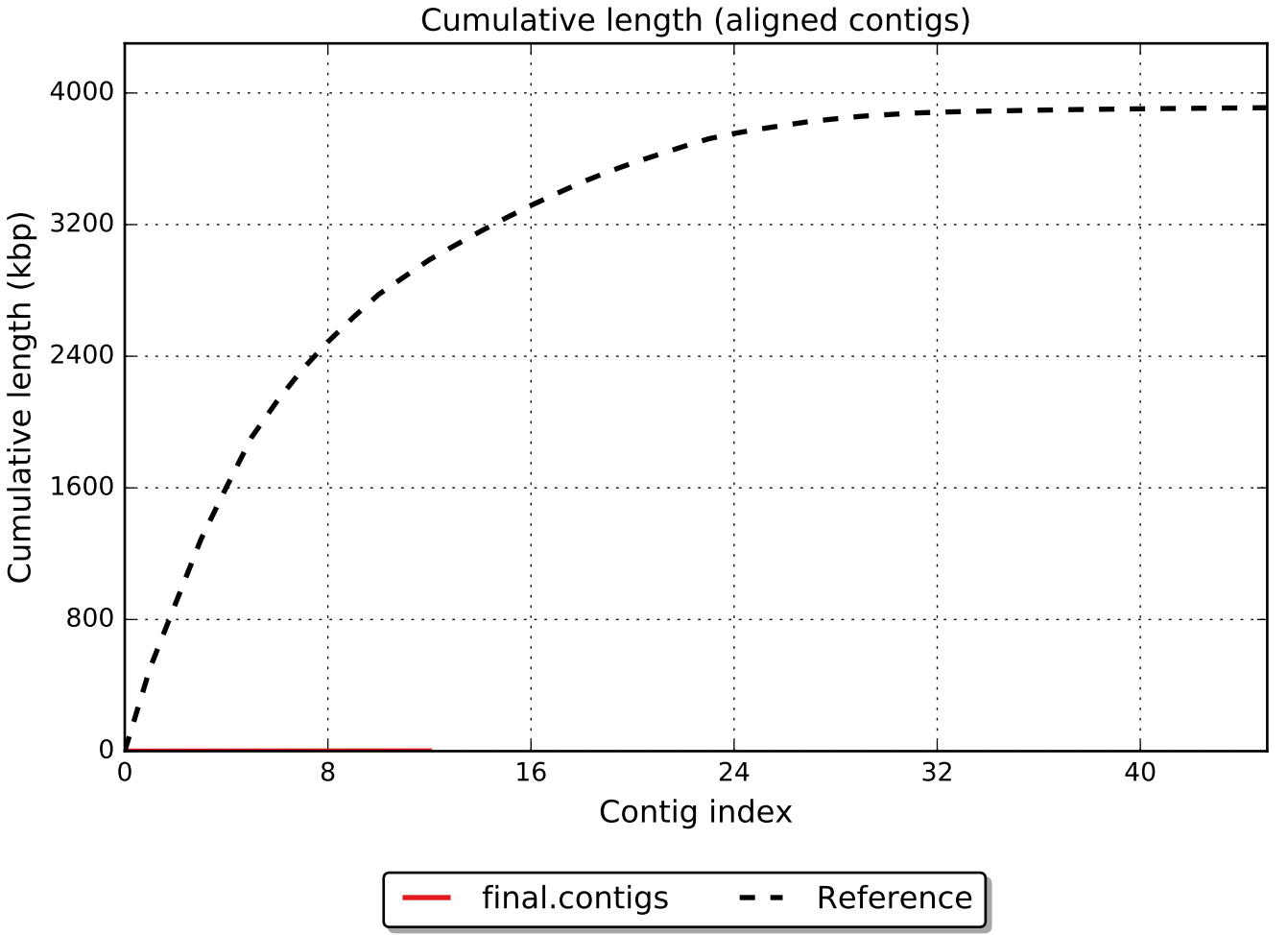

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
8
16
24
32
40
Contig index
final.contigs
Reference

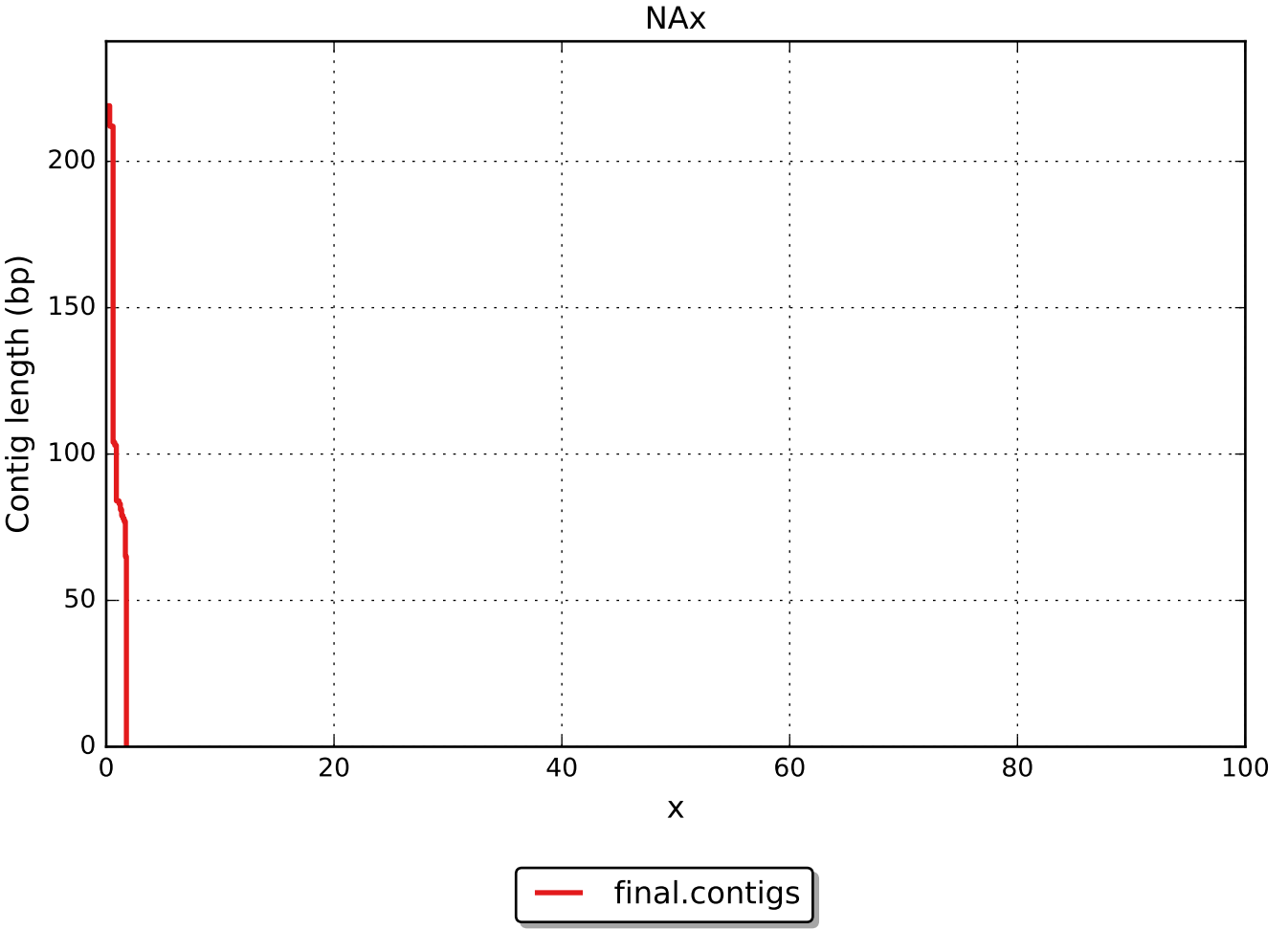

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

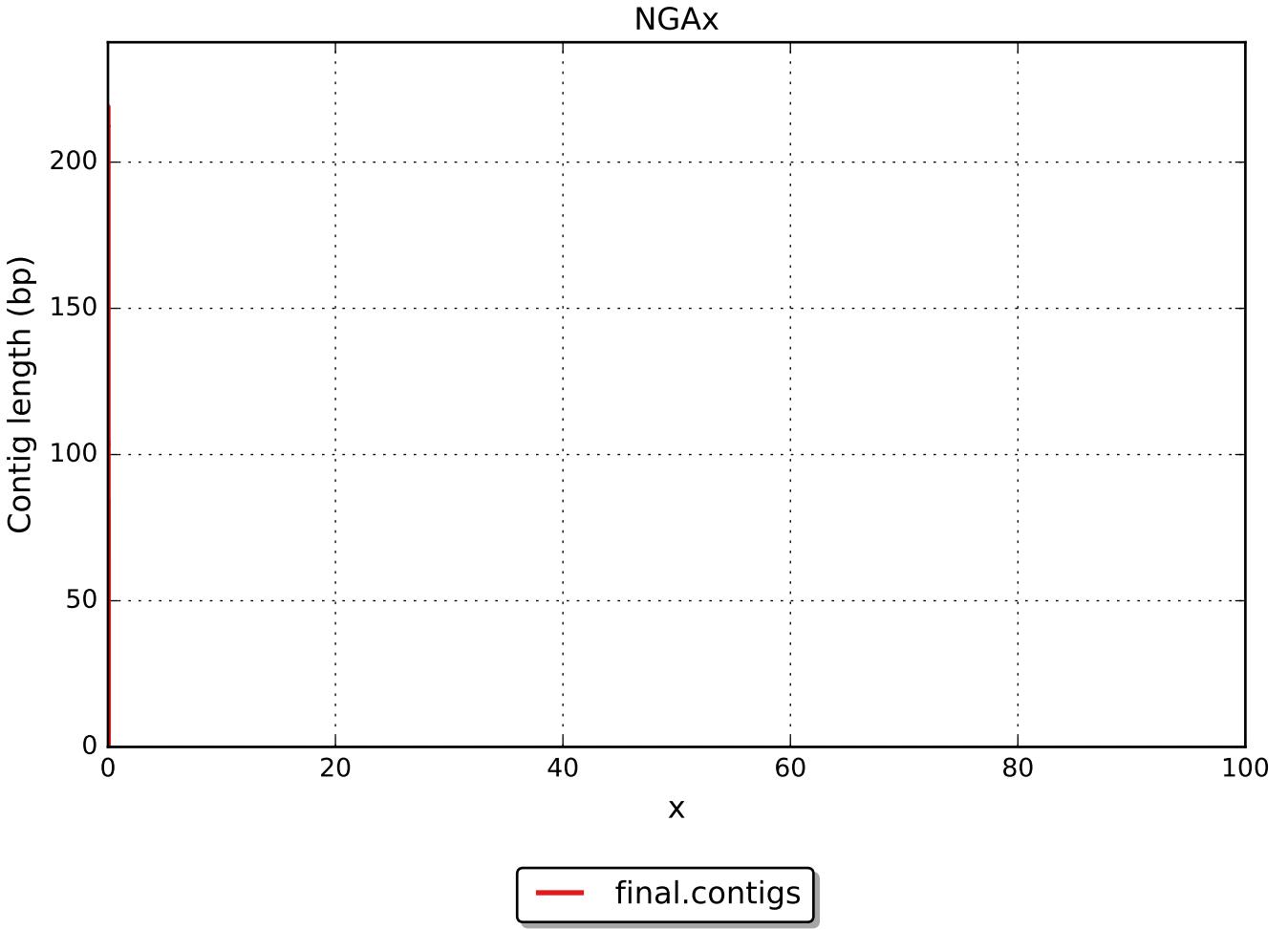

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs
interspecies translocations


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
8
16
24
32
40
Contig index
final.contigs
Reference


NAx
Contig length (bp)
0
50
100
150
200
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
0
50
100
150
200
0
20
40
60
80
100
x
final.contigs