Report

	final.contigs
# contigs (>= 1000 bp)	29
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	102064
Total length (>= 5000 bp)	56269
Total length (>= 10000 bp)	16872
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	76
Largest contig	16872
Total length	131736
Reference length	2366980
GC (%)	60.70
Reference GC (%)	60.24
N50	3744
N75	1148
L50	10
L75	26
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 26 part
Unaligned length	89414
Genome fraction (%)	1.500
Duplication ratio	1.192
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3097.98
# indels per 100 kbp	61.96
Largest alignment	3271
Total aligned length	36339
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

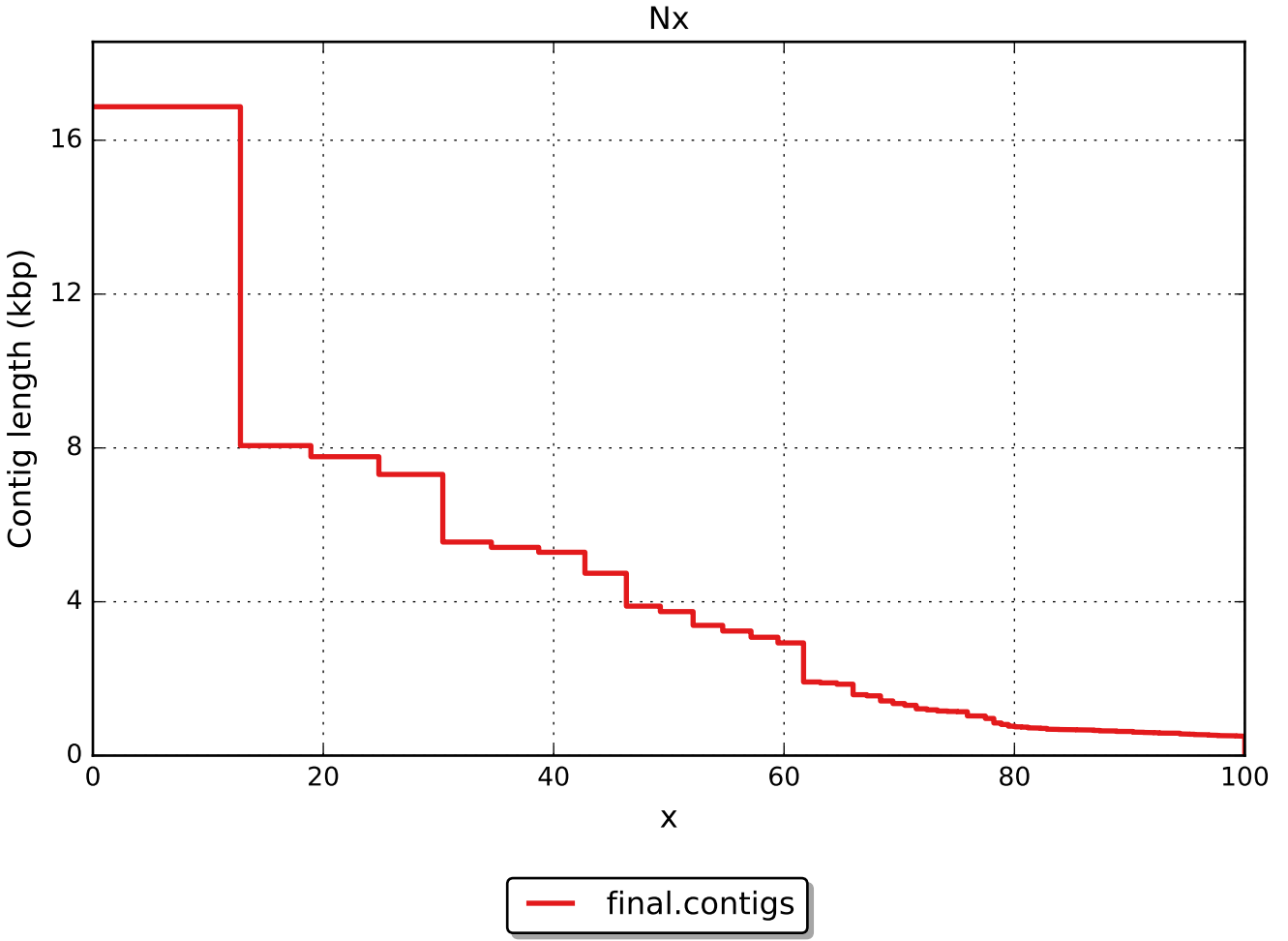
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	2
# possible misassemblies	3
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	1100
# indels	22
# indels (<= 5 bp)	22
# indels (> 5 bp)	0
Indels length	26

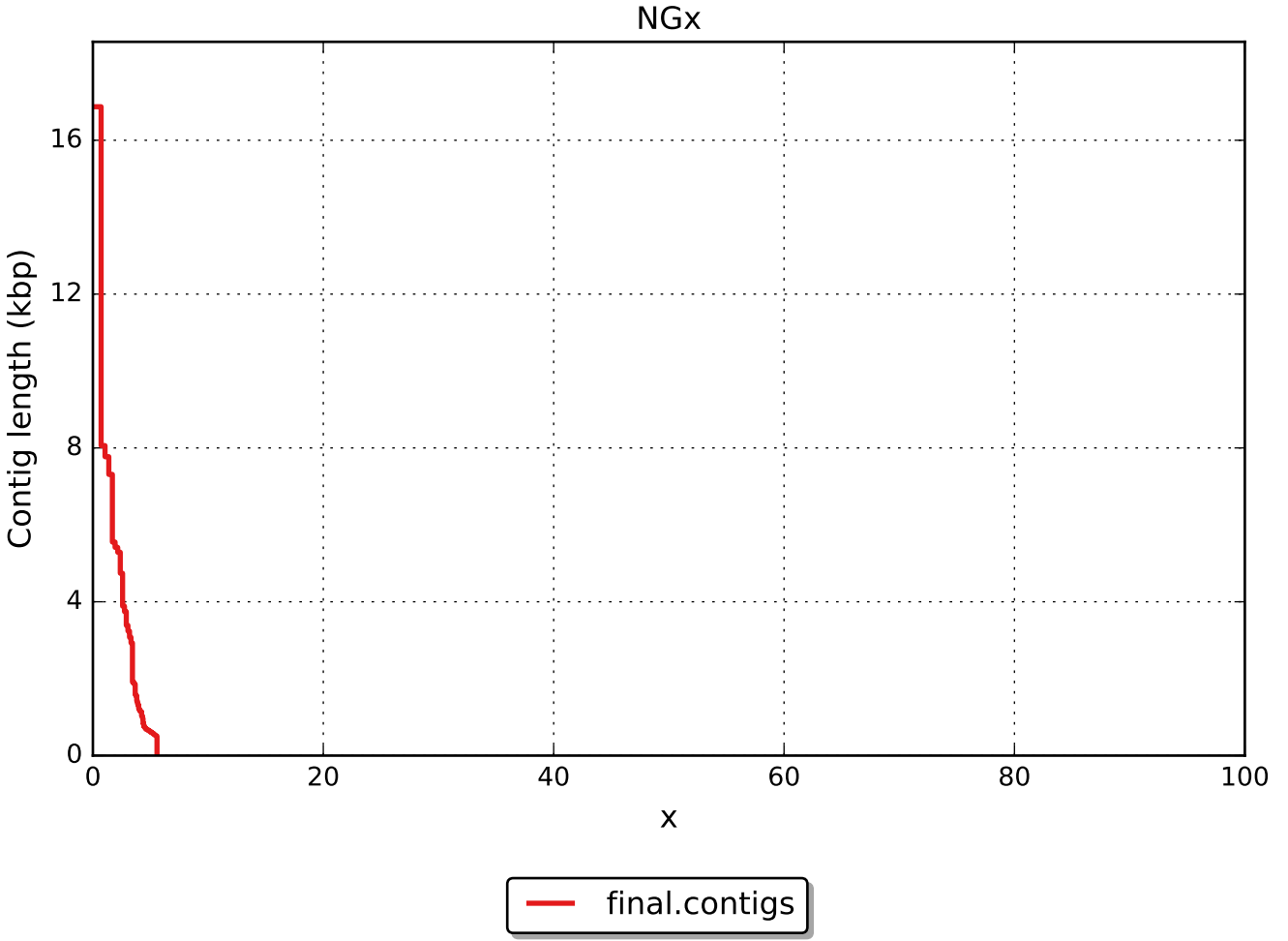
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

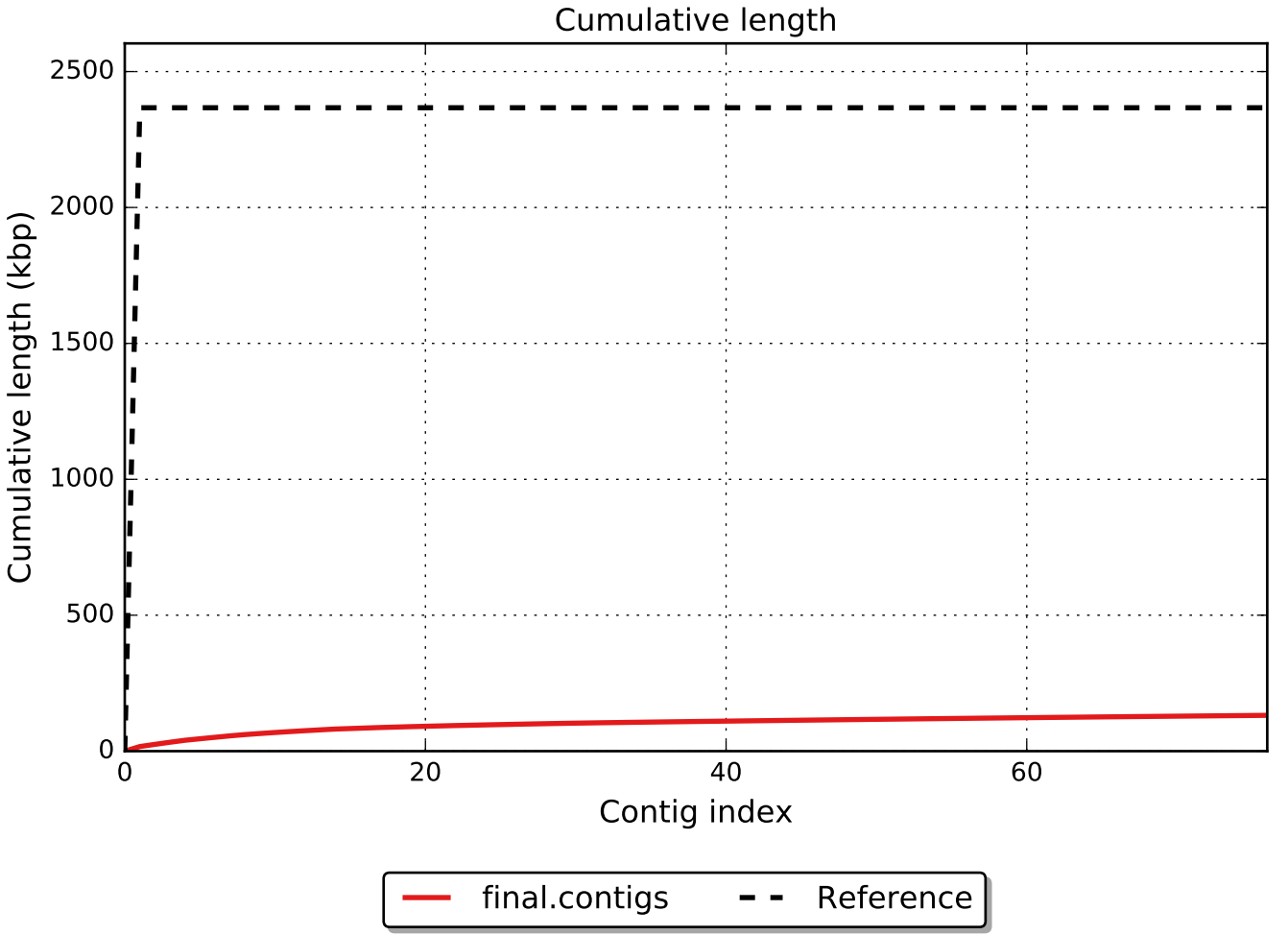
Unaligned report

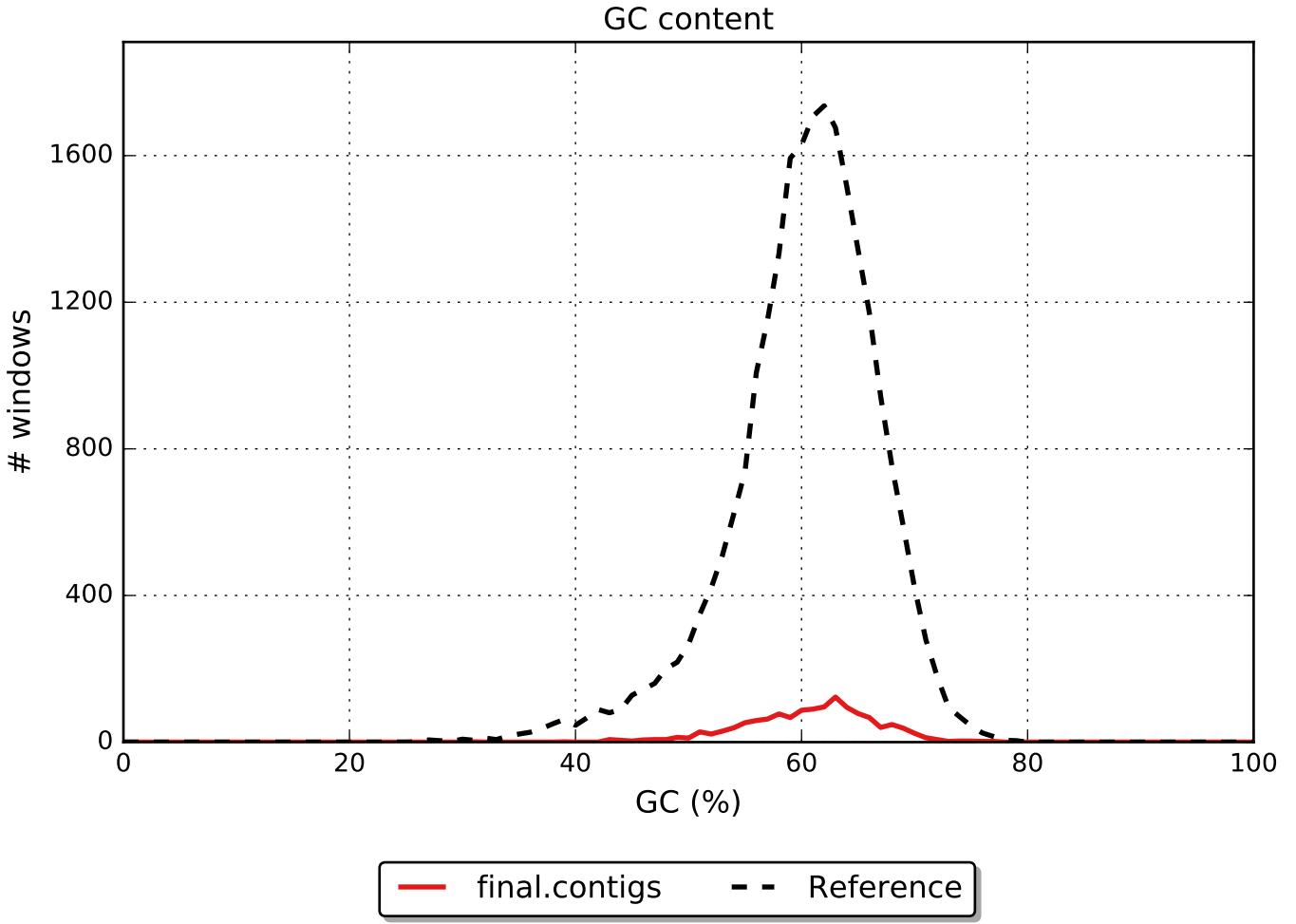
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	26
Partially unaligned length	89414
# N's	0

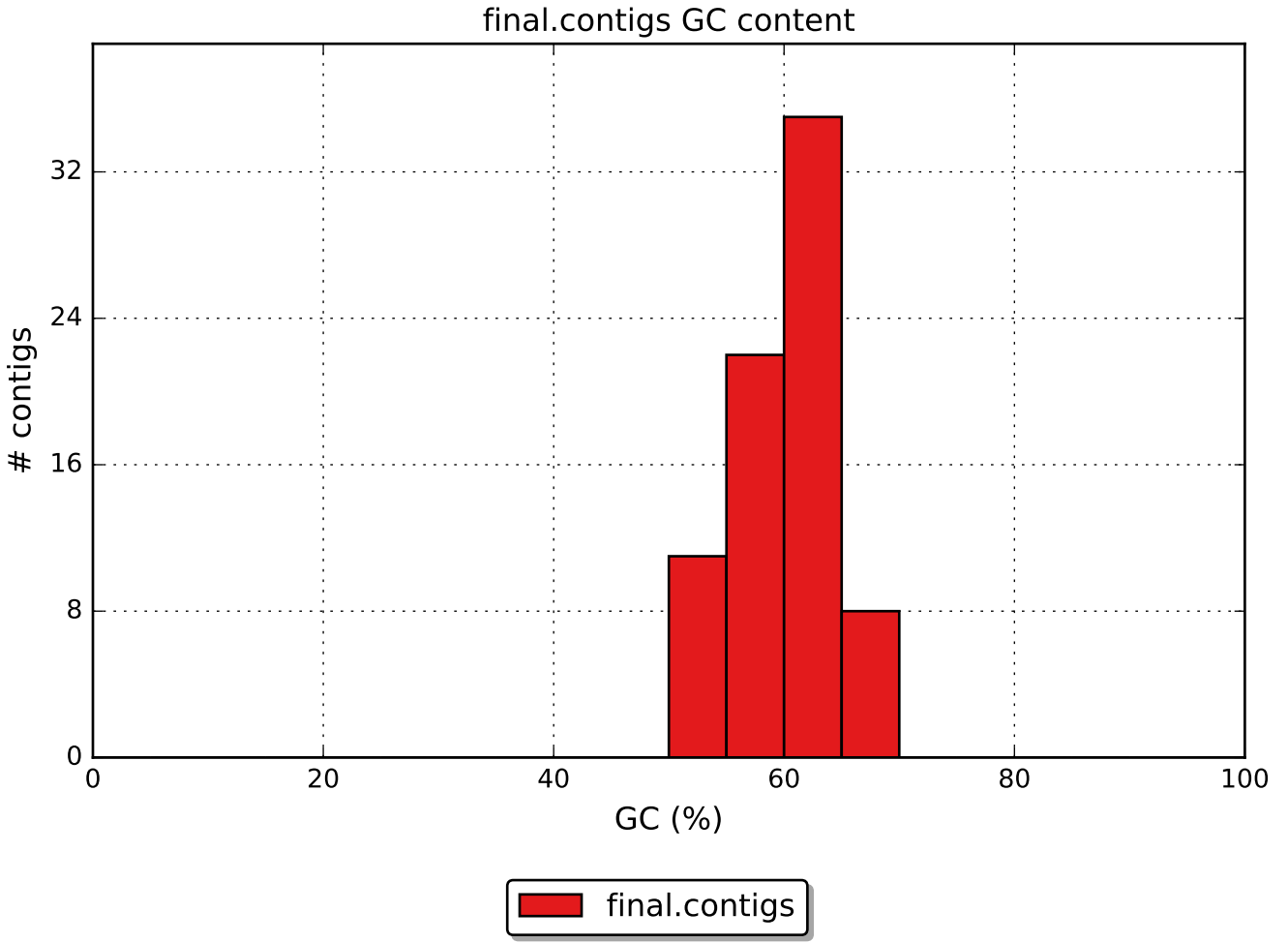
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

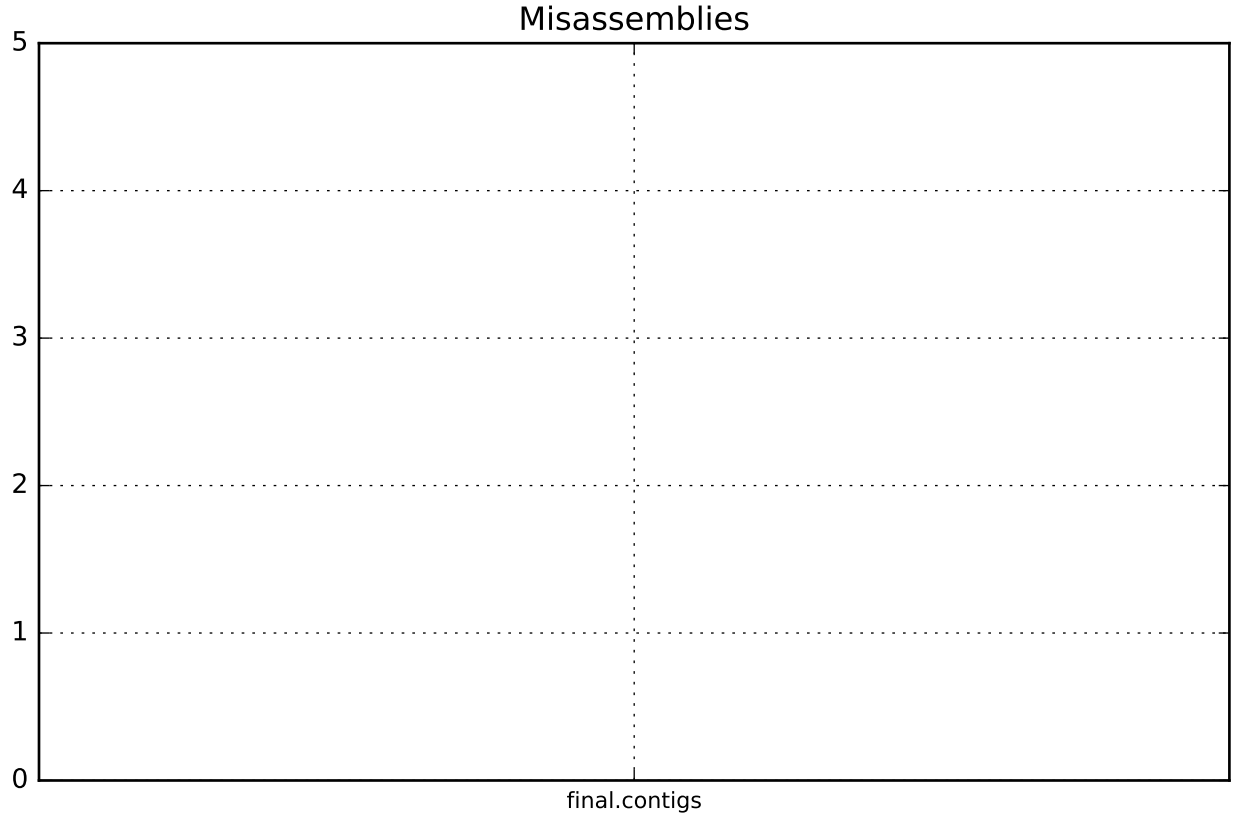

Nx
Contig length (kbp)
0
4
8
12
16
0
20
40
60
80
100
x
final.contigs

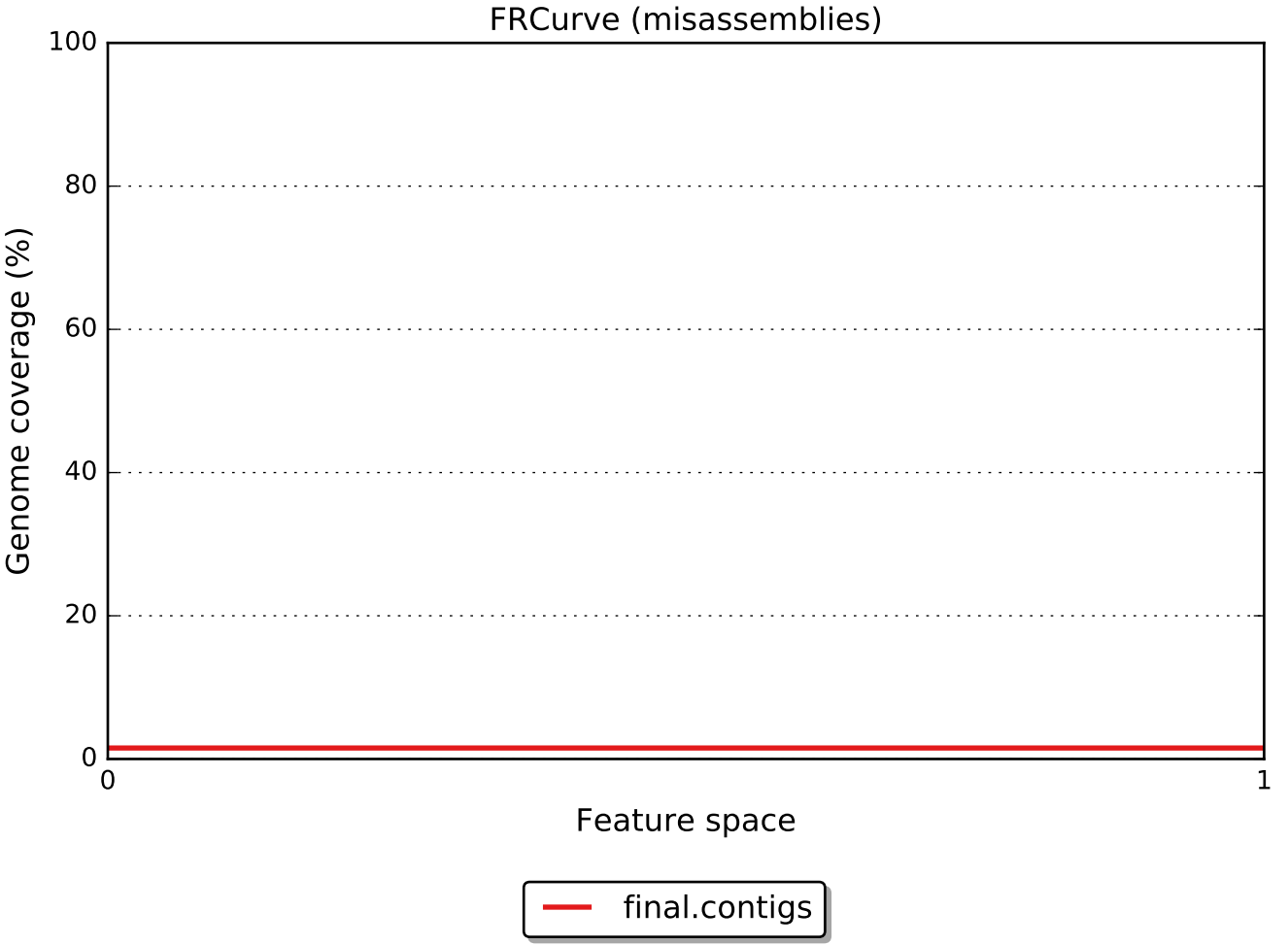

NGx
Contig length (kbp)
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

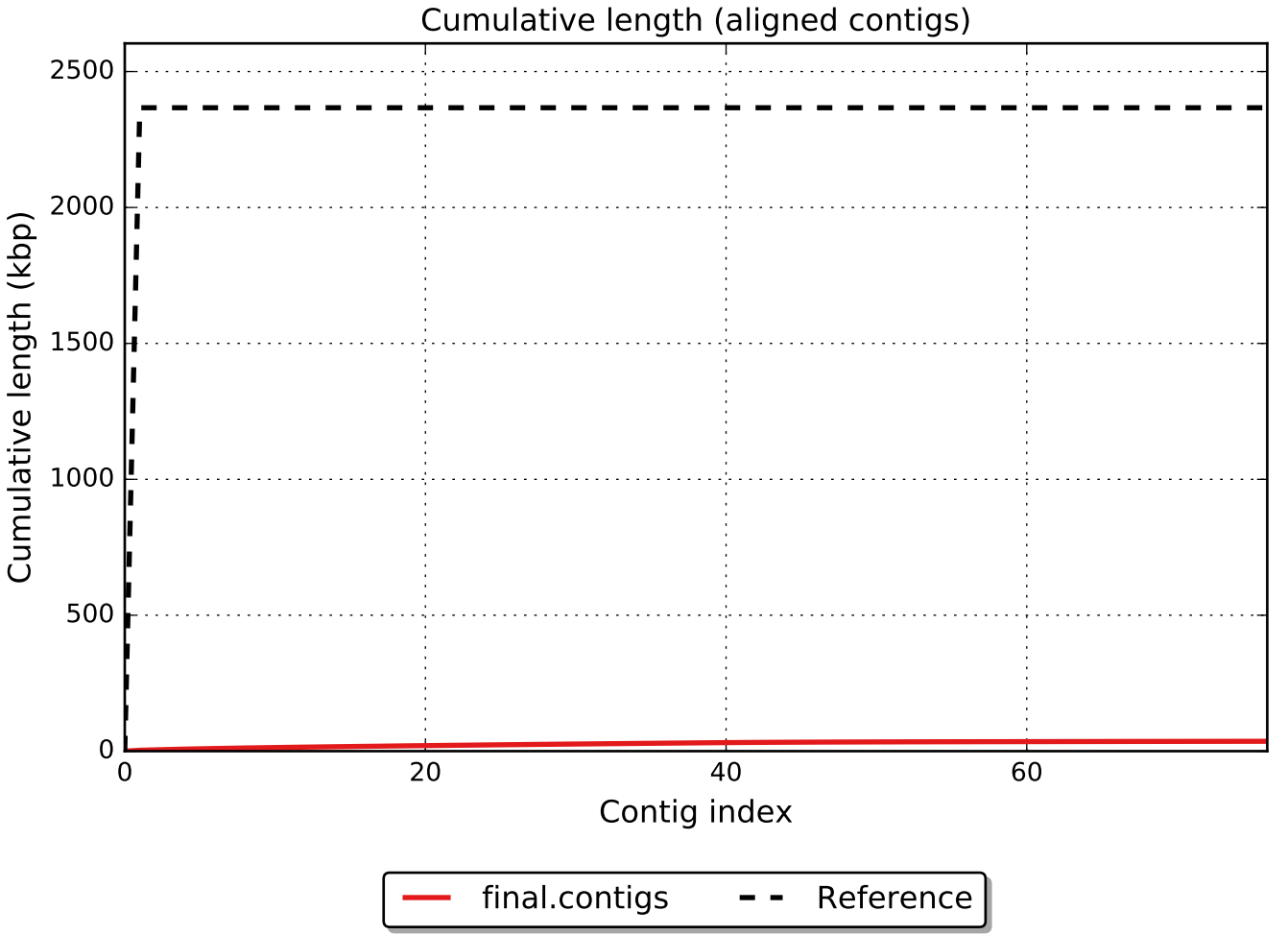

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
Contig index
final.contigs
Reference

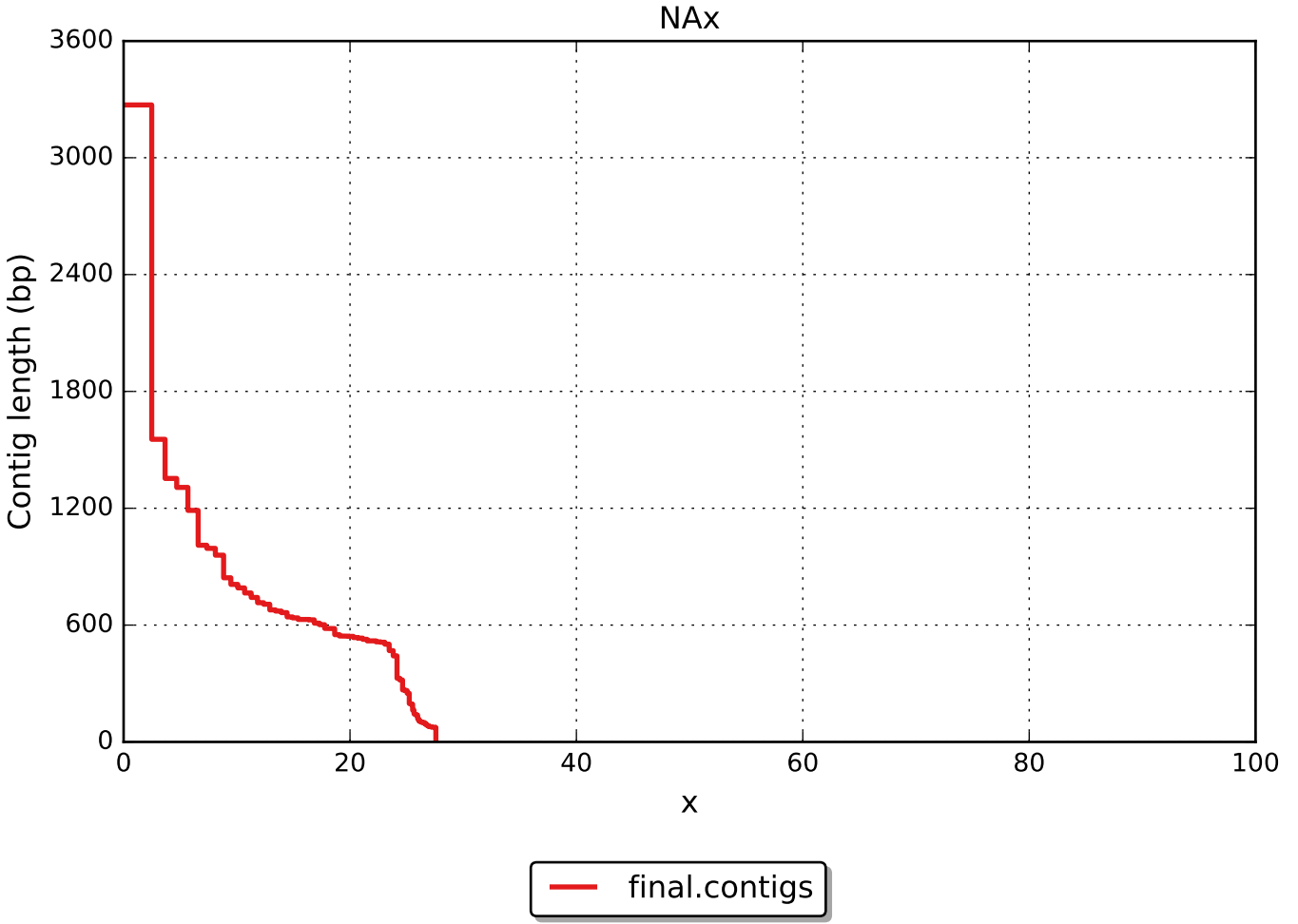

GC content
windows
GC (%)
0
400
800
1200
1600
0
20
40
60
80
100
final.contigs
Reference

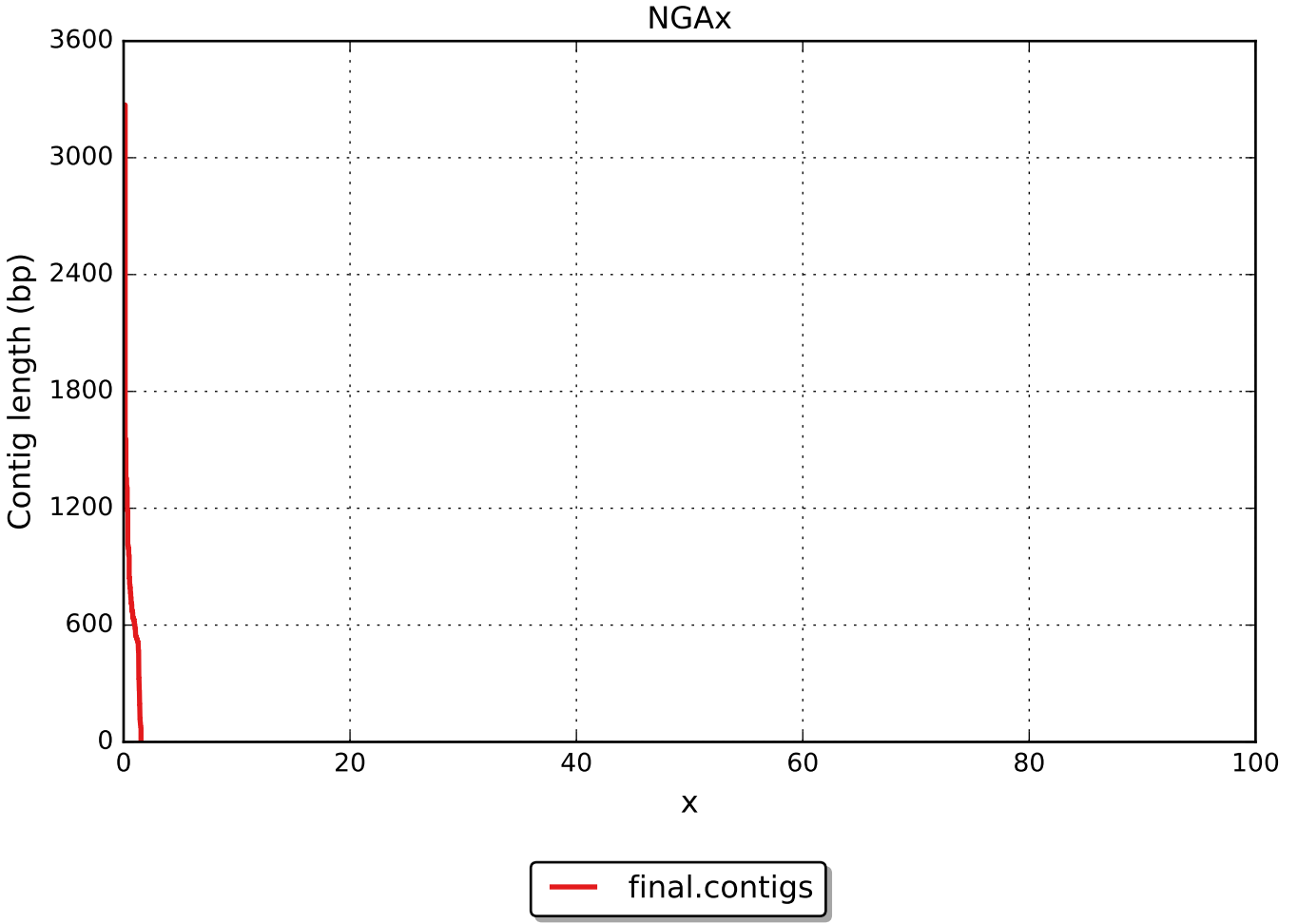

final.contigs GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
final.contigs


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)
2500
2000
1500
1000
500
0
0
20
40
60
Contig index
final.contigs
Reference


NAx
3600
3000
2400
1800
1200
600
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
3600
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs