Report

	final.contigs
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	39426
Total length (>= 5000 bp)	19447
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	25
Largest contig	6651
Total length	47591
Reference length	4487498
GC (%)	50.06
Reference GC (%)	57.67
N50	4653
N75	1349
L50	4
L75	10
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 17 part
Unaligned length	40234
Genome fraction (%)	0.054
Duplication ratio	3.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2184.67
# indels per 100 kbp	82.44
Largest alignment	516
Total aligned length	3419
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

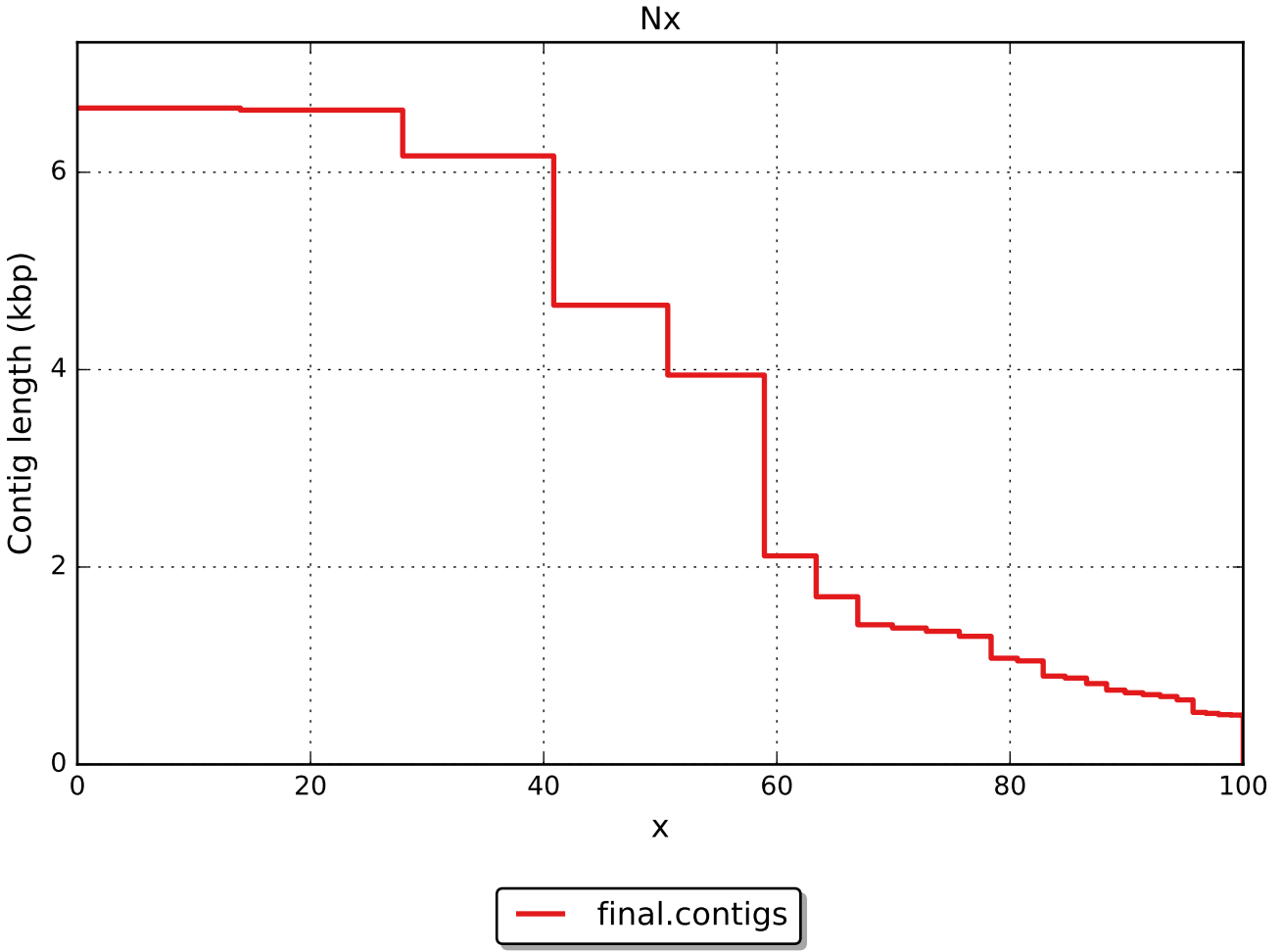
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	2
# mismatches	53
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

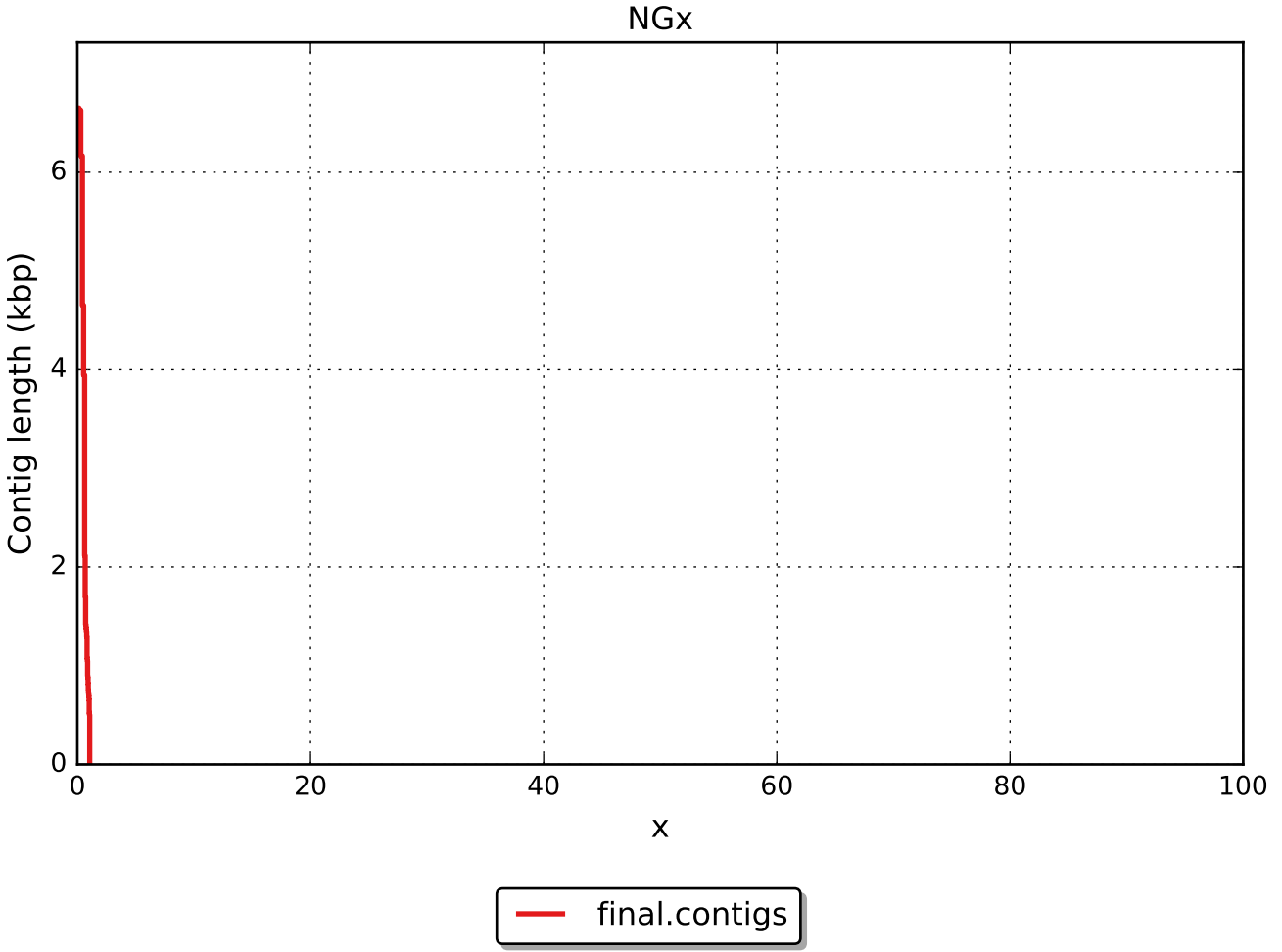
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

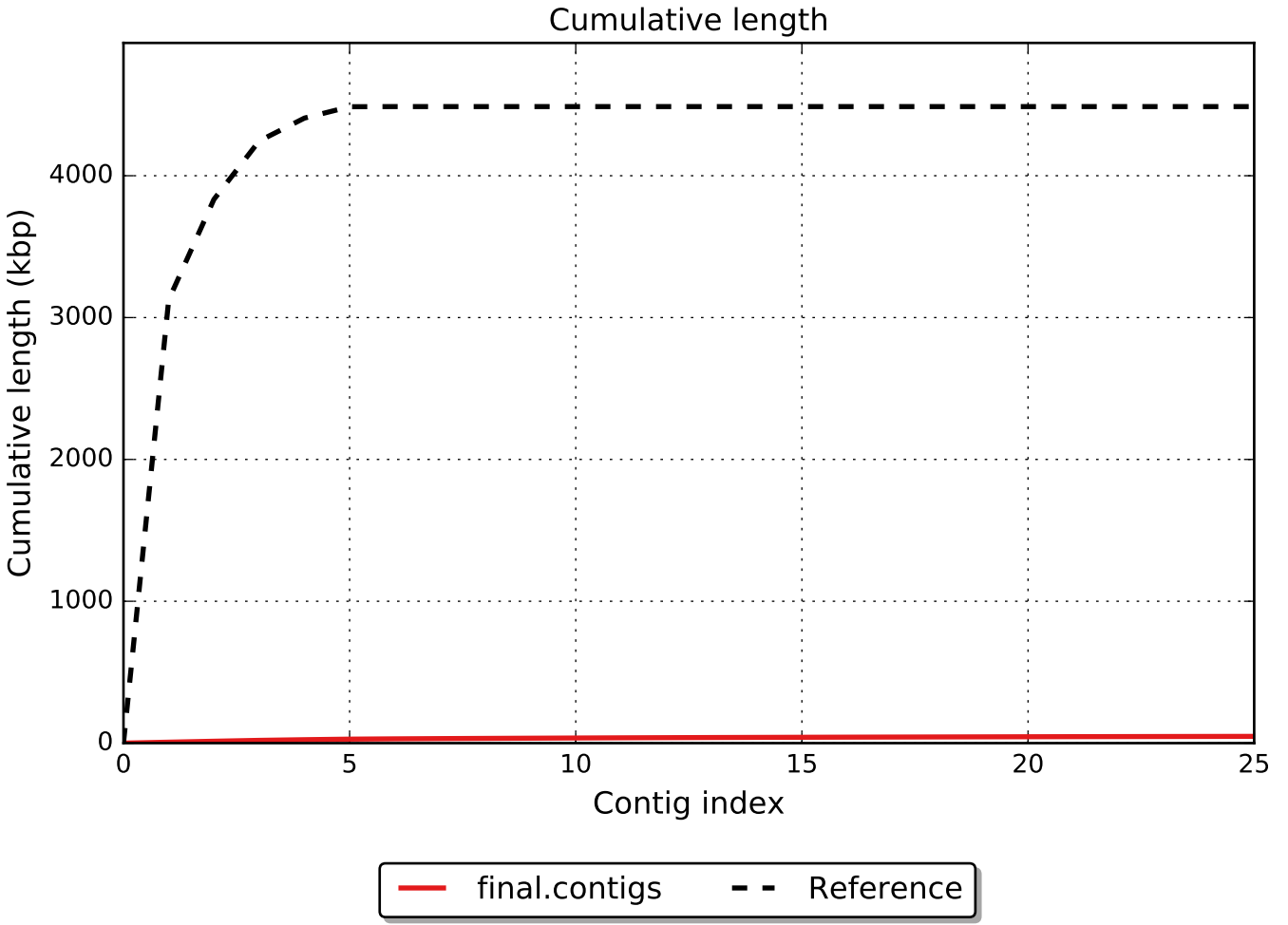
Unaligned report

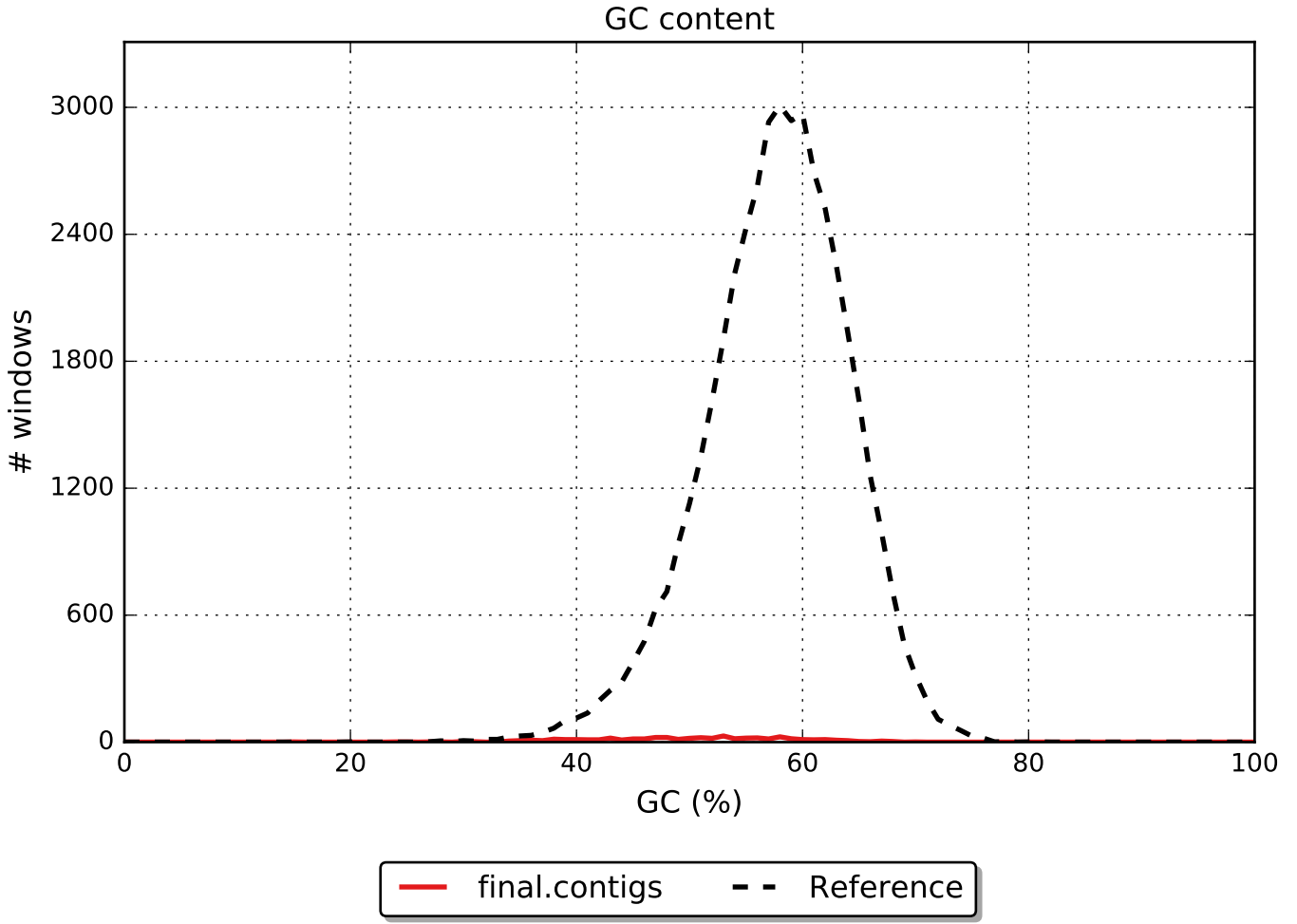
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	17
Partially unaligned length	40234
# N's	0

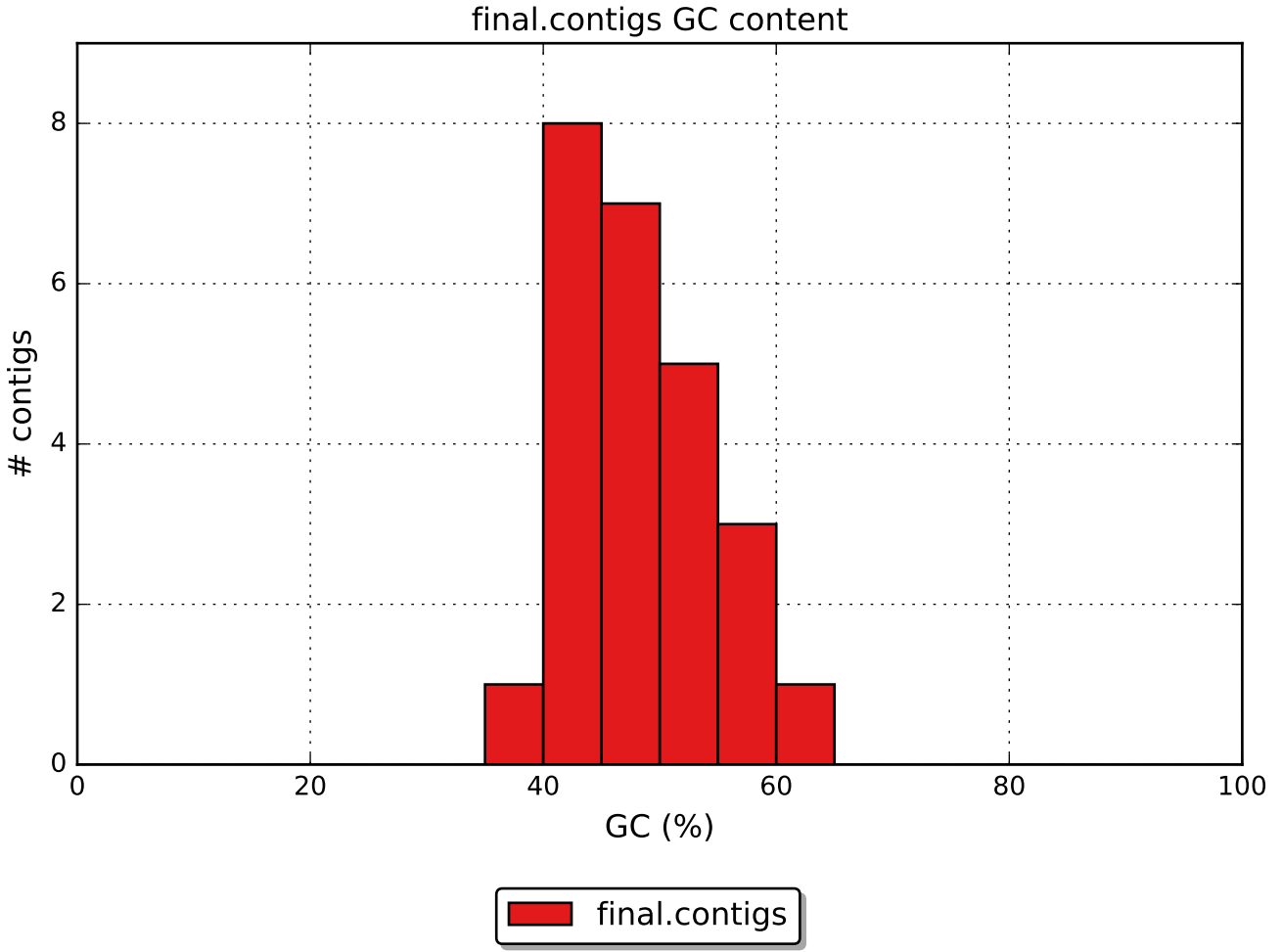
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

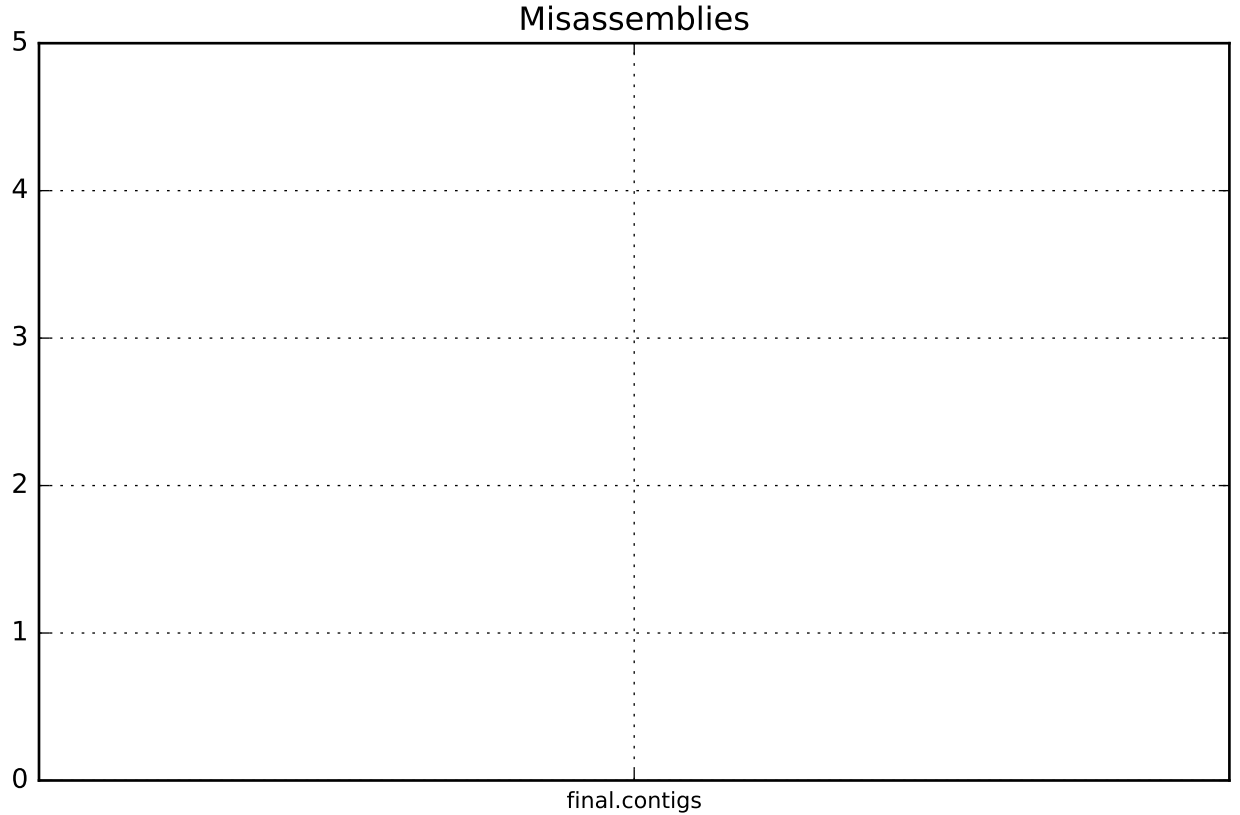

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

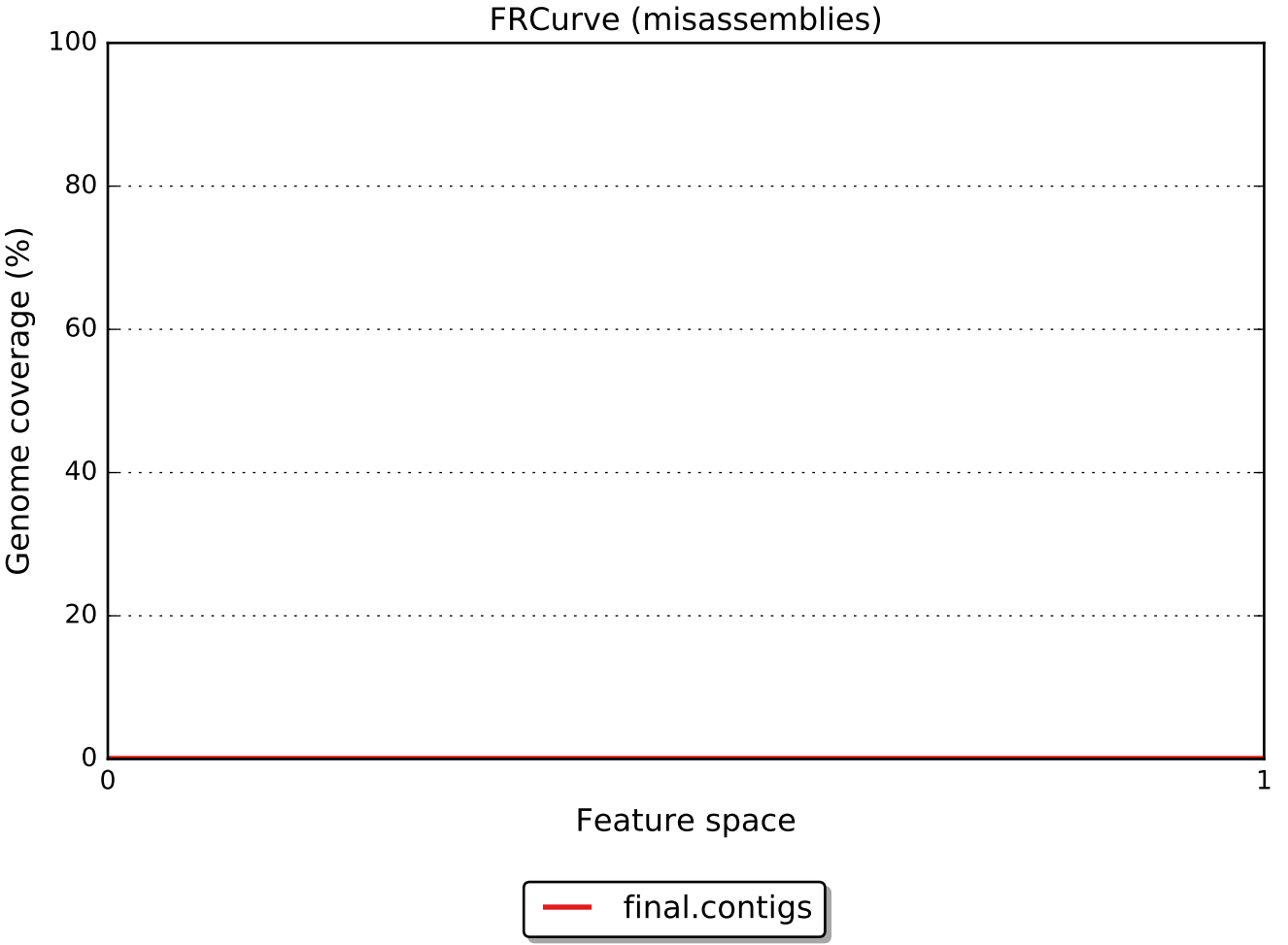

NGx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

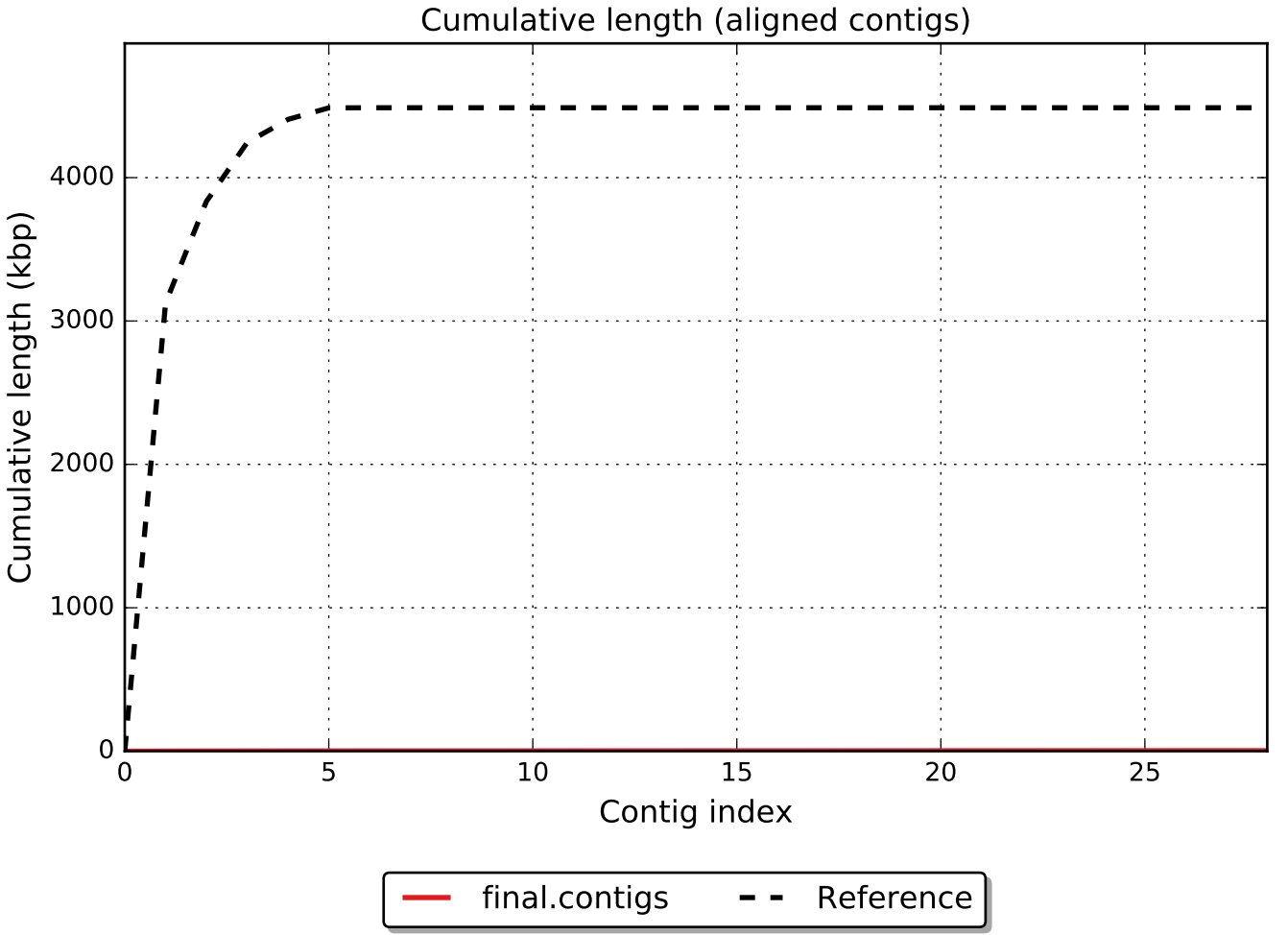

Cumulative length
Cumulative length (kbp)
0
1000
2000
3000
4000
0
5
10
15
20
25
Contig index
final.contigs
Reference

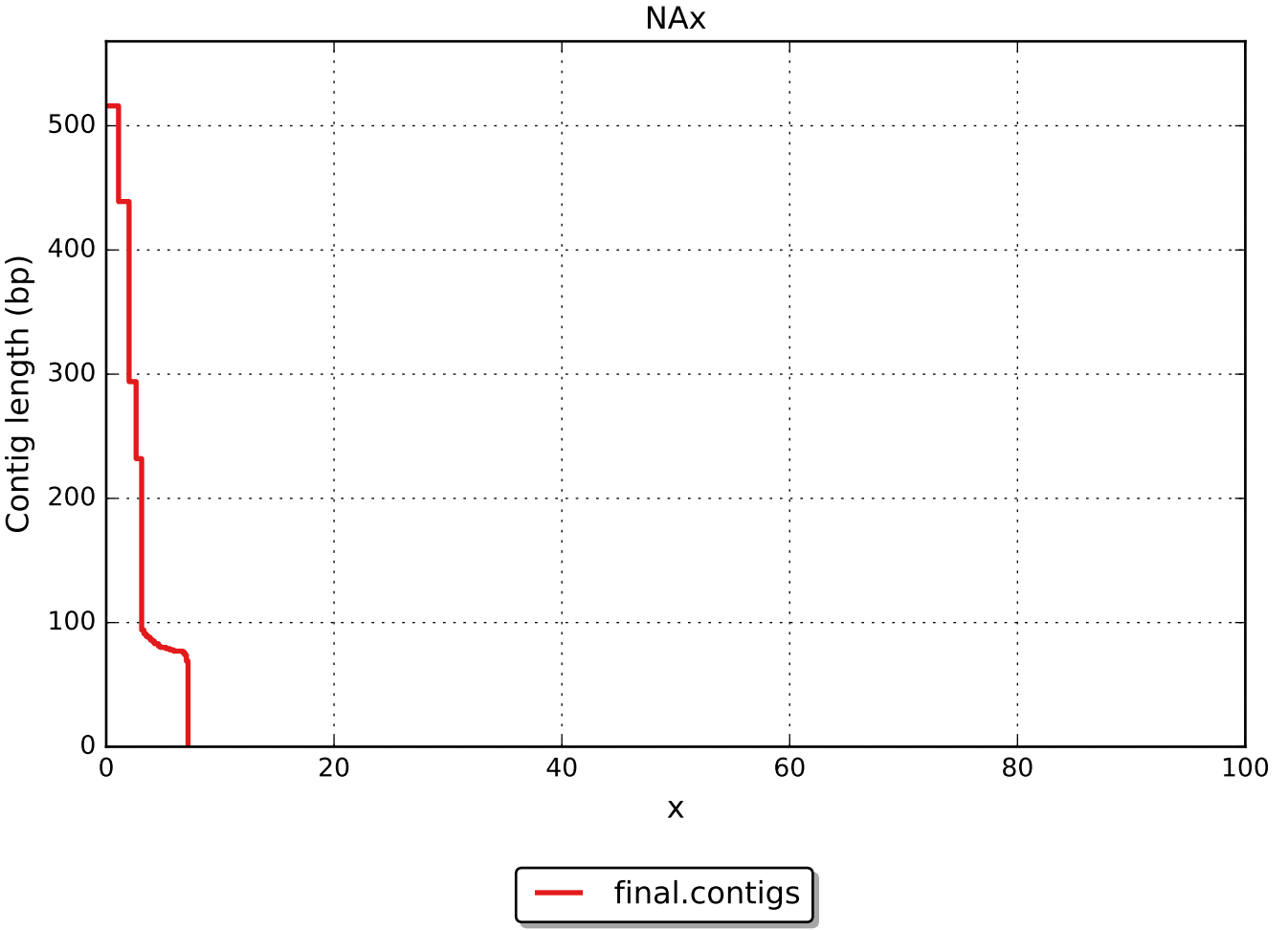

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
final.contigs
Reference

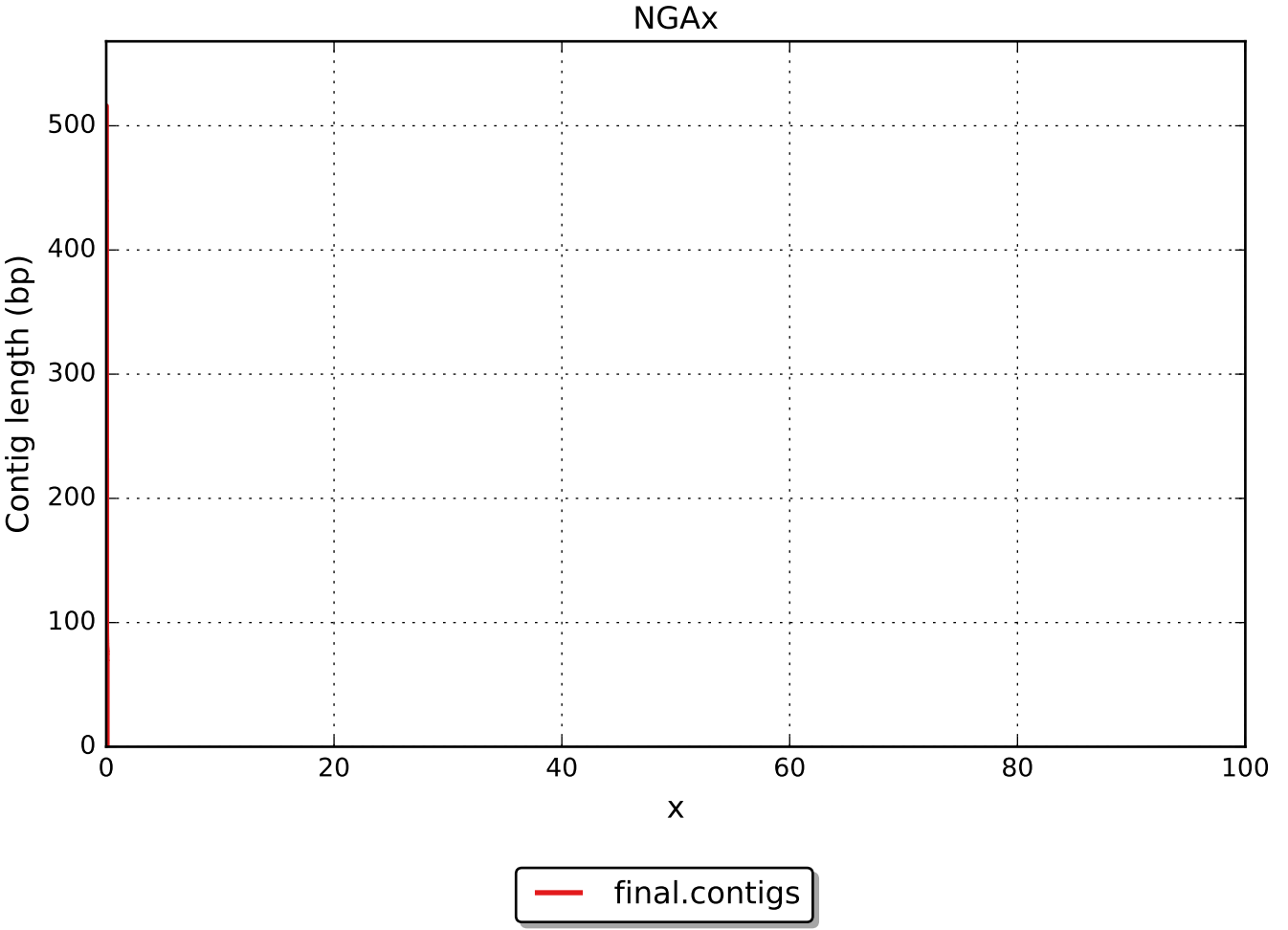

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
1000
2000
3000
4000
0
5
10
15
20
25
Contig index
final.contigs
Reference


NAx
Contig length (bp)
0
100
200
300
400
500
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
0
100
200
300
400
500
0
20
40
60
80
100
x
final.contigs