Report

	final.contigs
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	19455
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	17
Largest contig	4182
Total length	23435
Reference length	1424092
GC (%)	46.08
Reference GC (%)	38.87
N50	1821
N75	1308
L50	5
L75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 10 part
Unaligned length	13516
Genome fraction (%)	0.445
Duplication ratio	1.565
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2351.27
# indels per 100 kbp	315.61
Largest alignment	4113
Total aligned length	7592
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

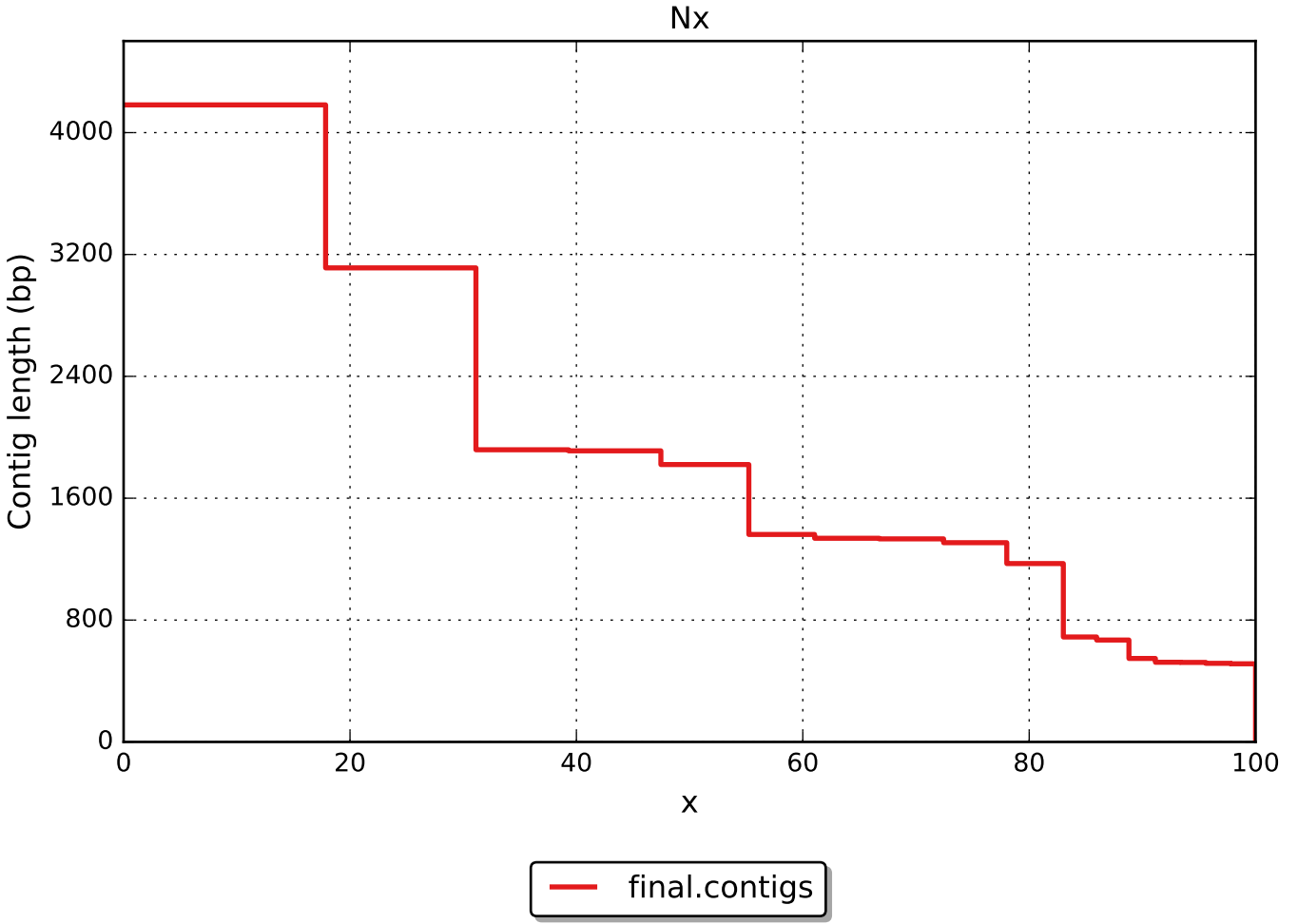
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	149
# indels	20
# indels (<= 5 bp)	19
# indels (> 5 bp)	1
Indels length	54

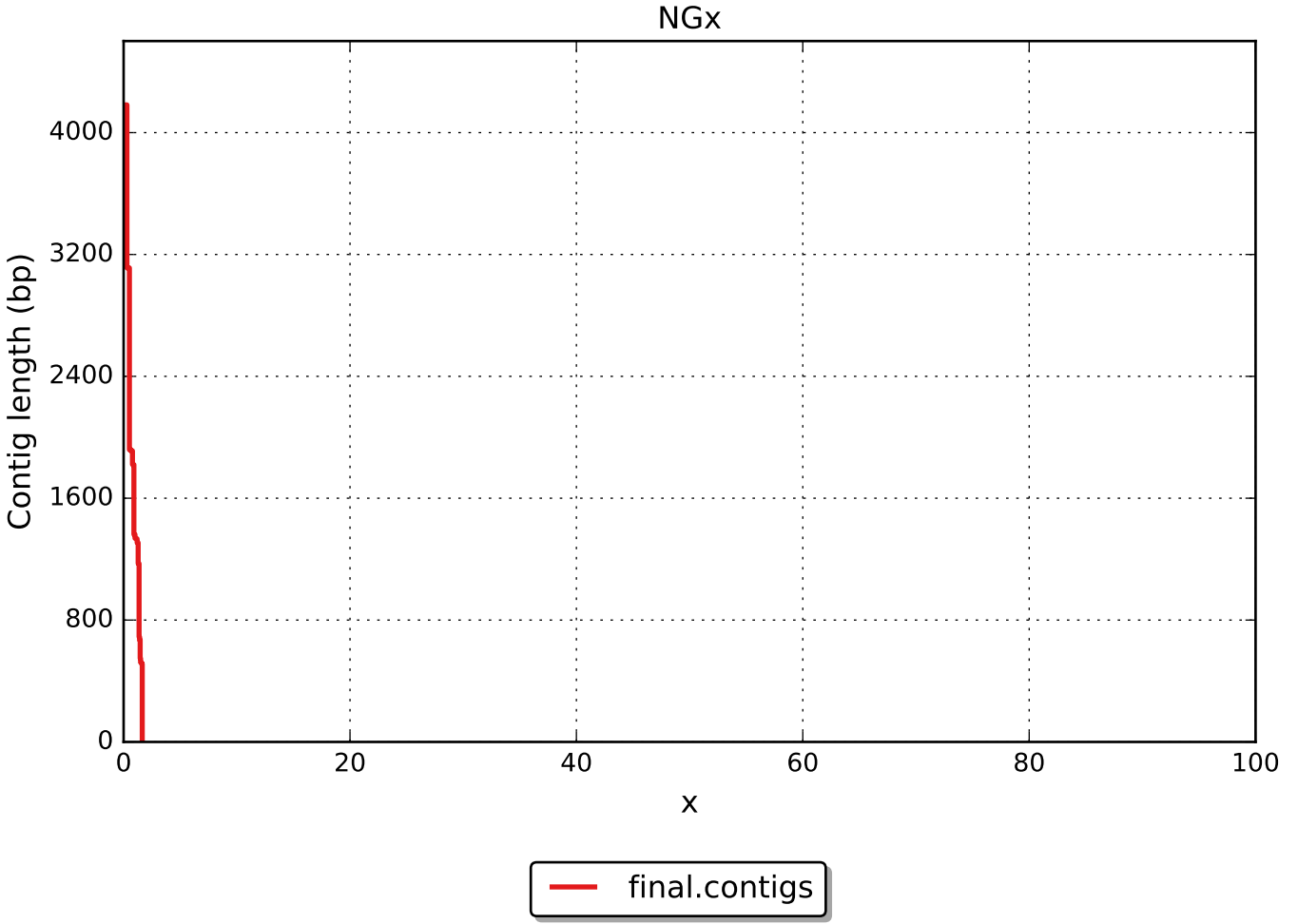
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

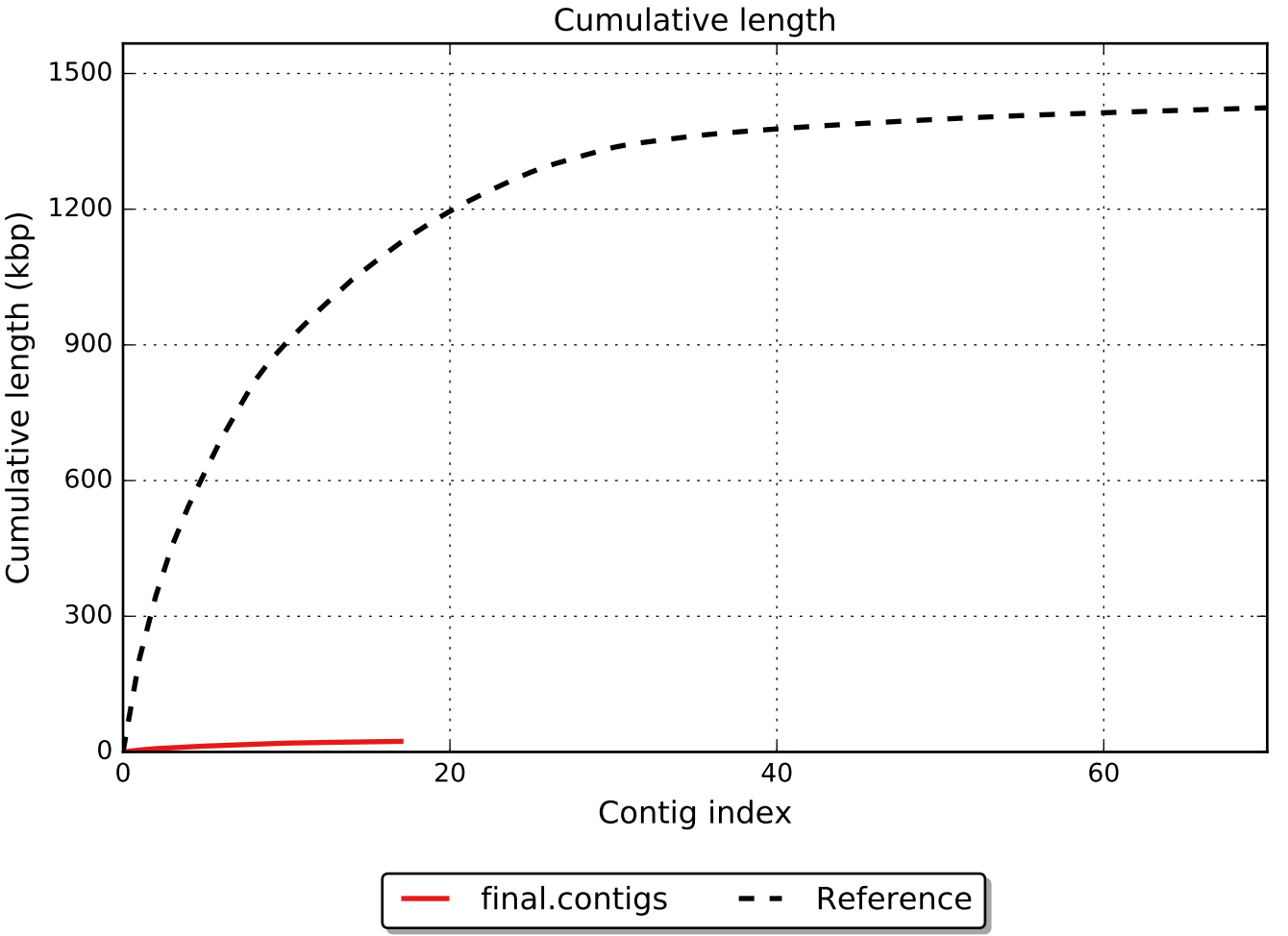
Unaligned report

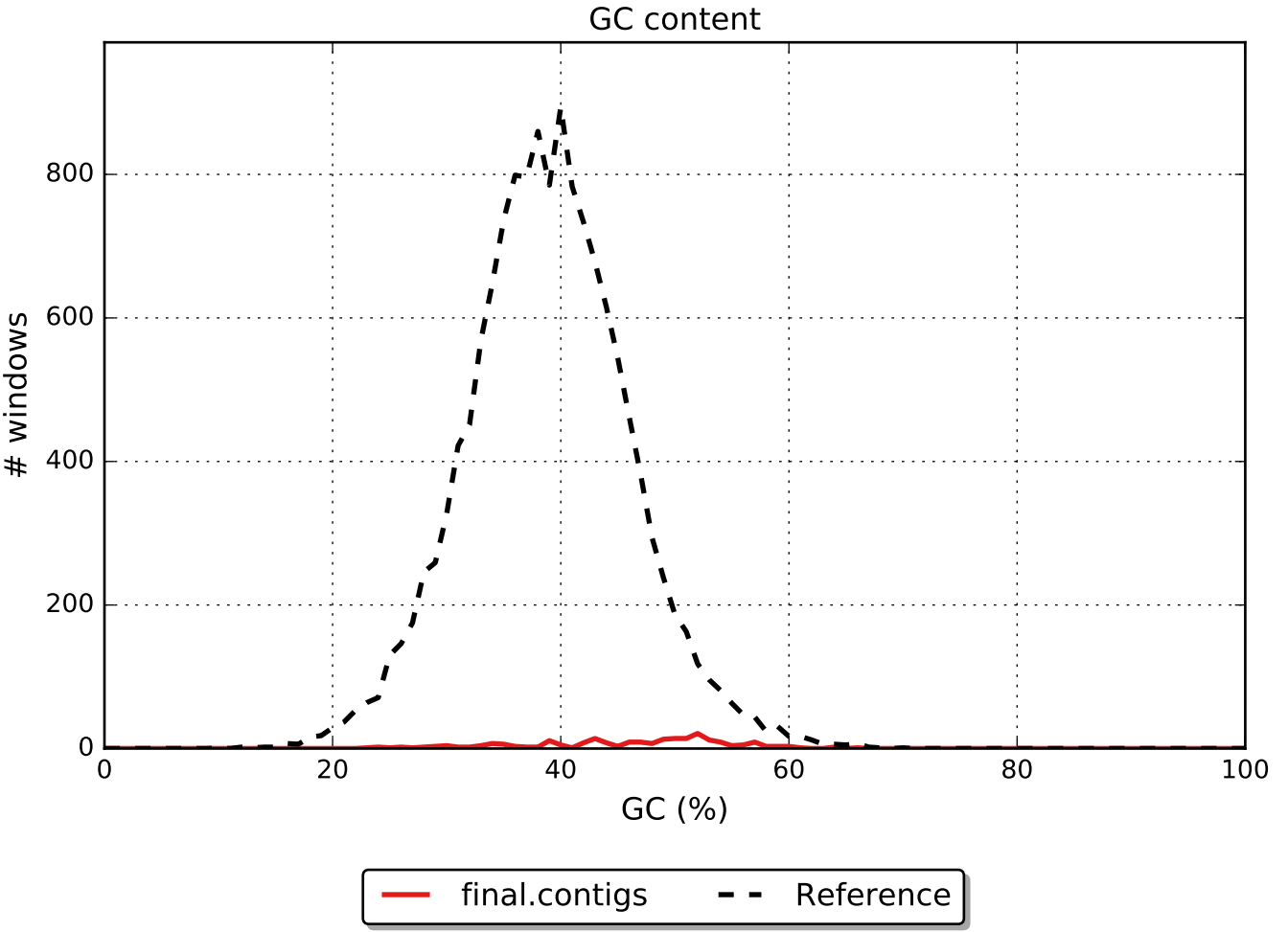
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	10
Partially unaligned length	13516
# N's	0

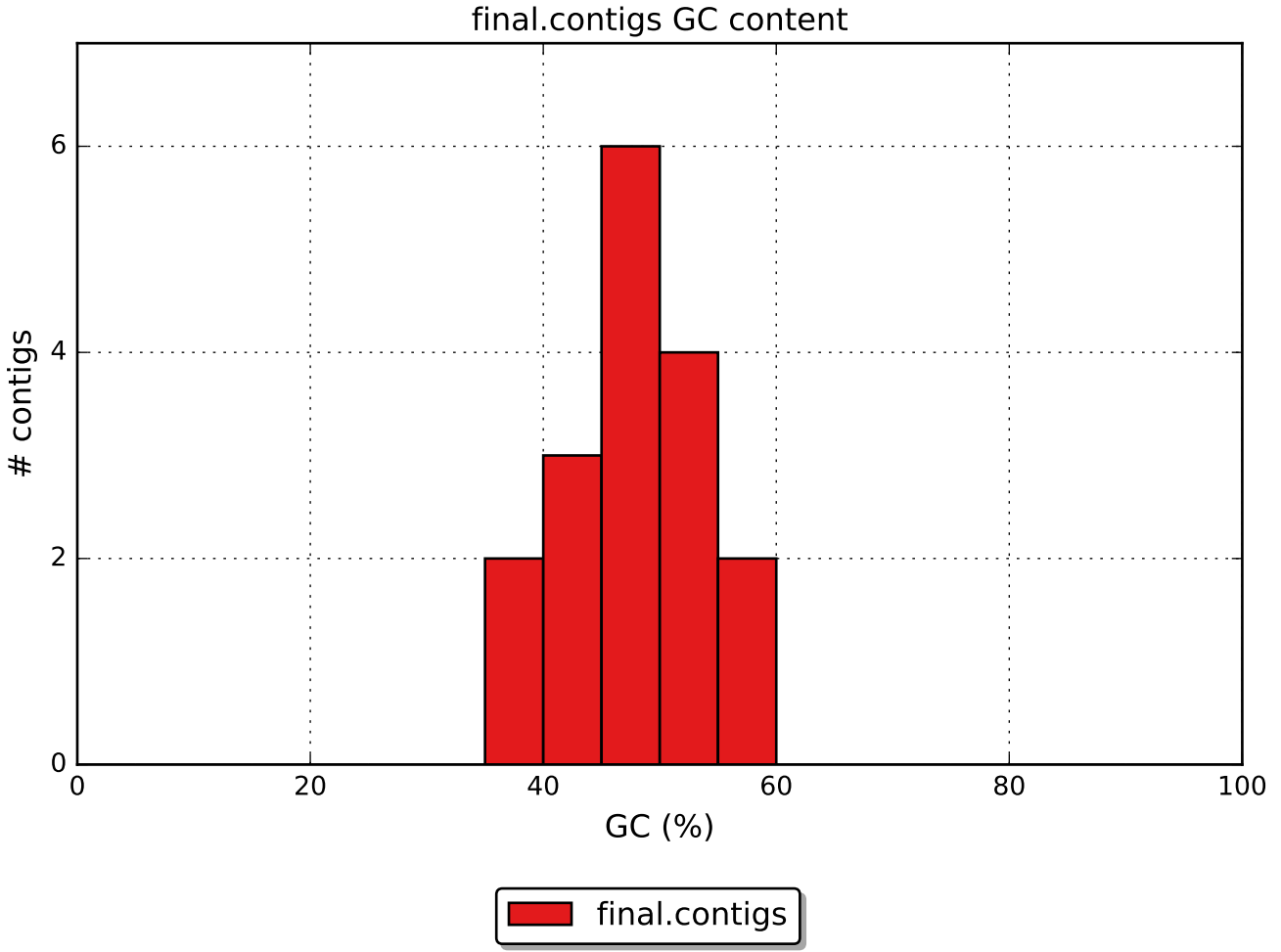
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

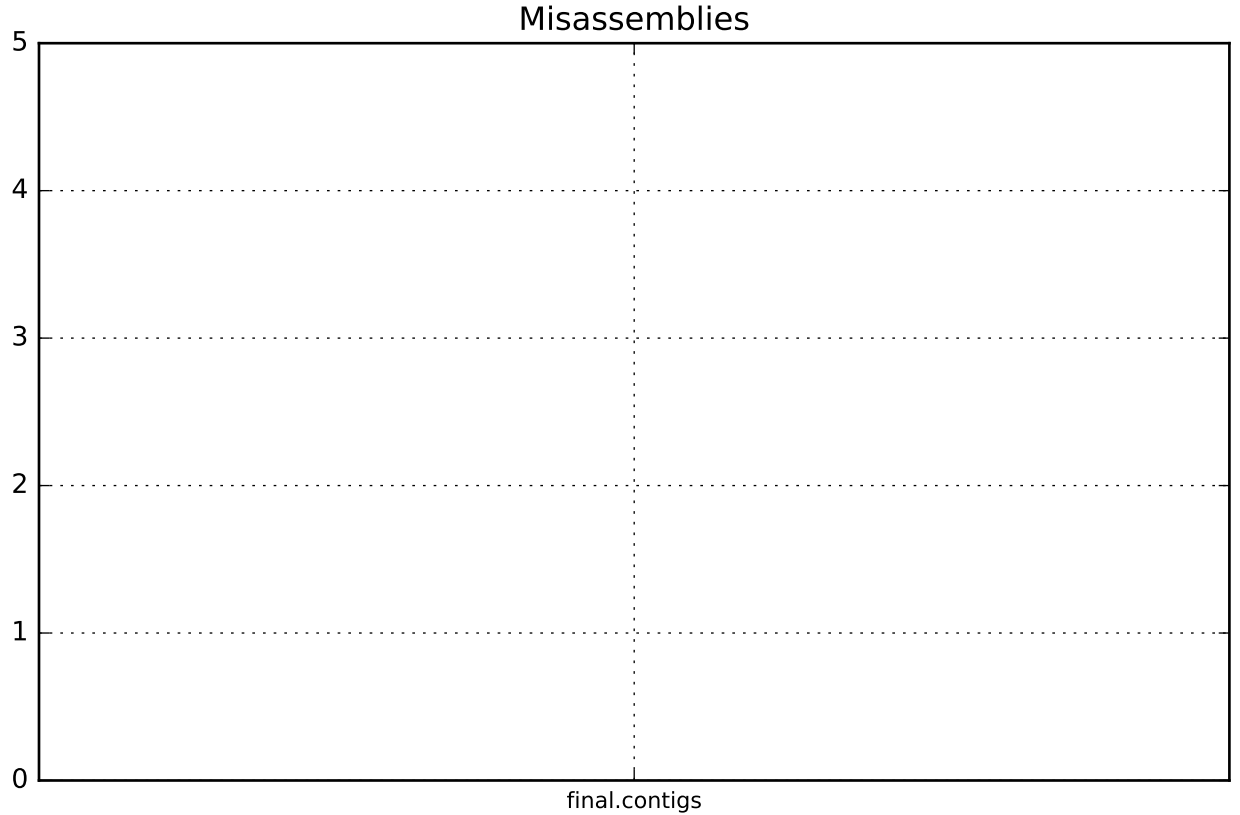

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

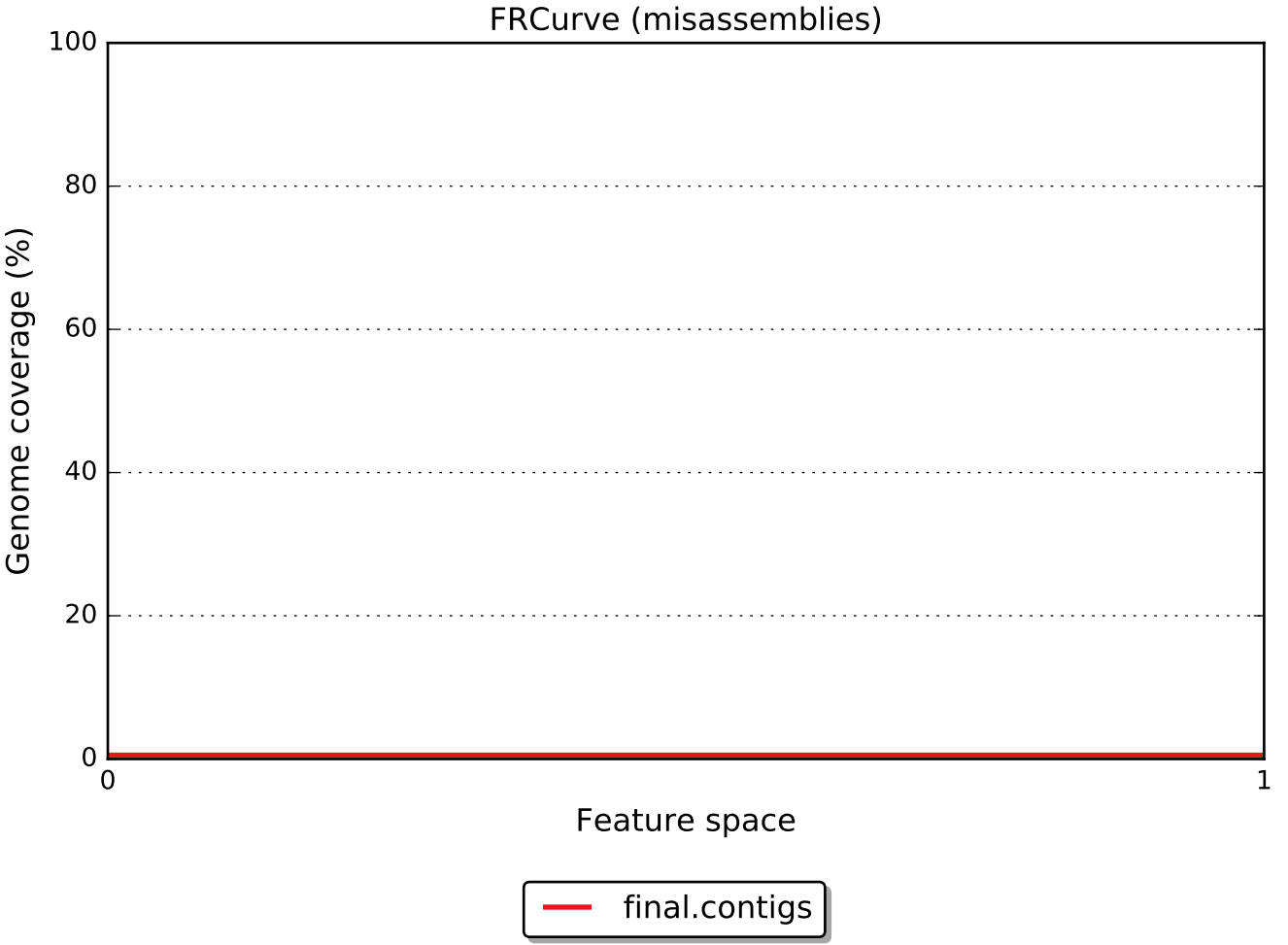

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

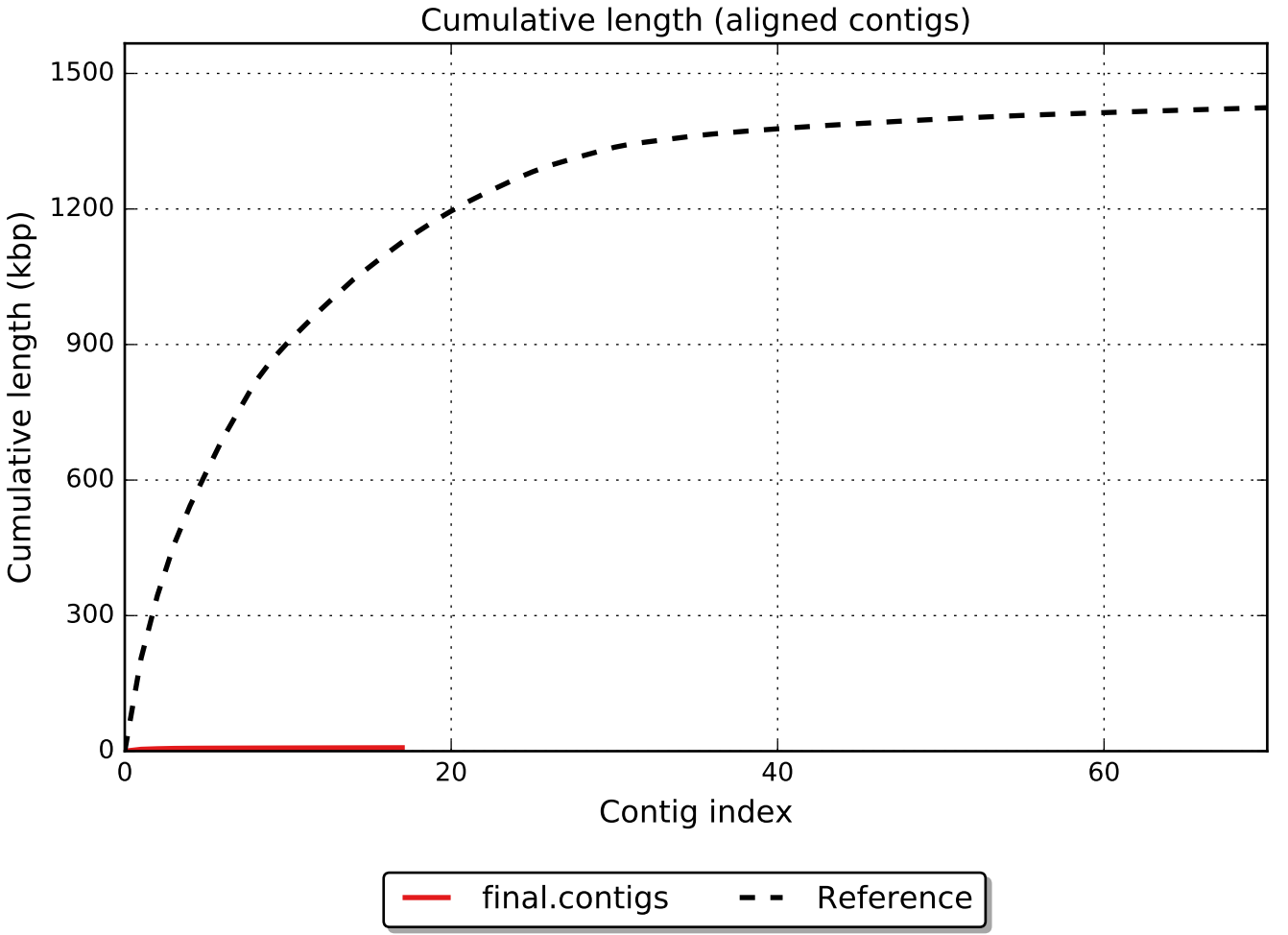

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
20
40
60
Contig index
final.contigs
Reference

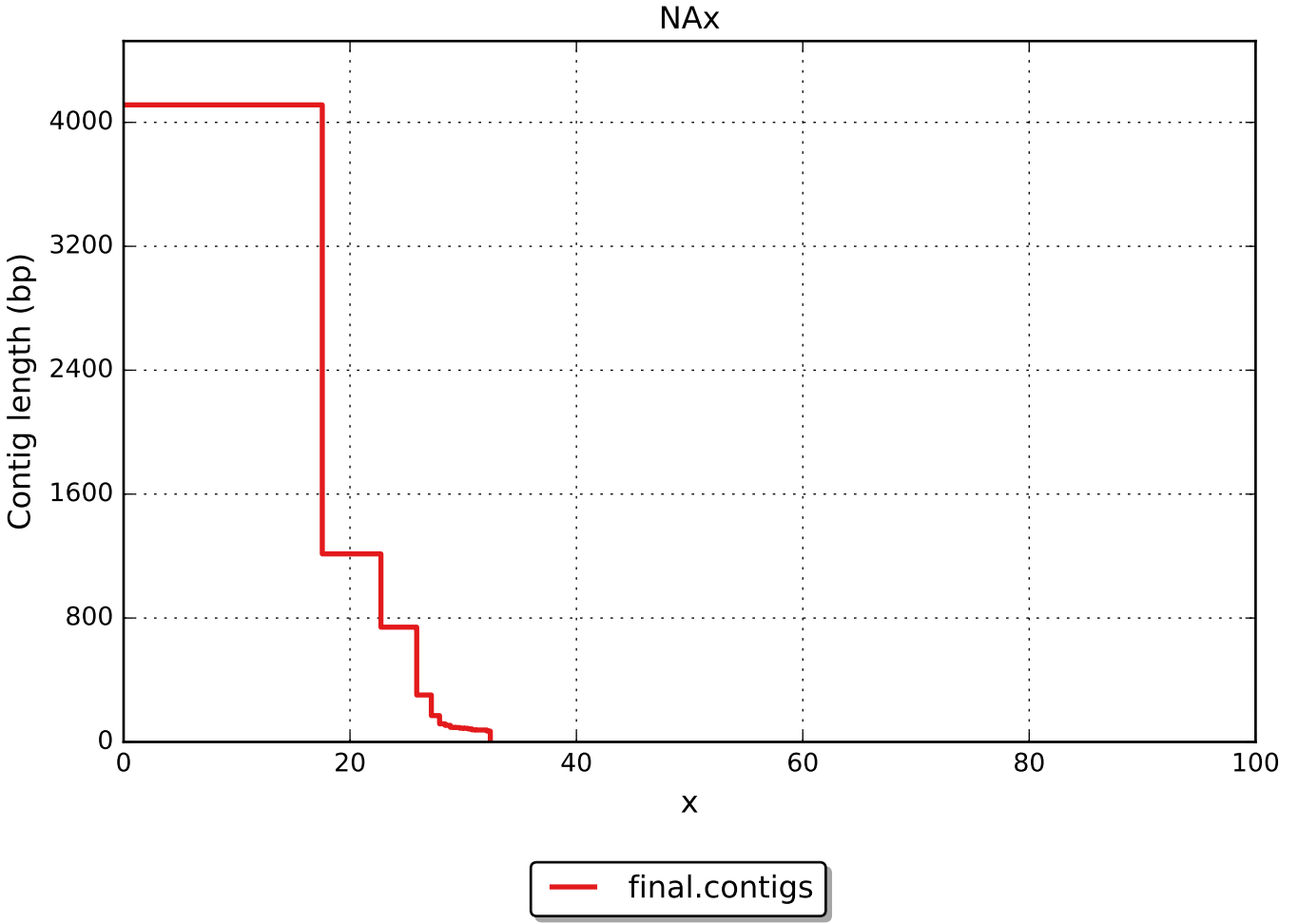

GC content
windows
GC (%)
0
200
400
600
800
0
20
40
60
80
100
final.contigs
Reference

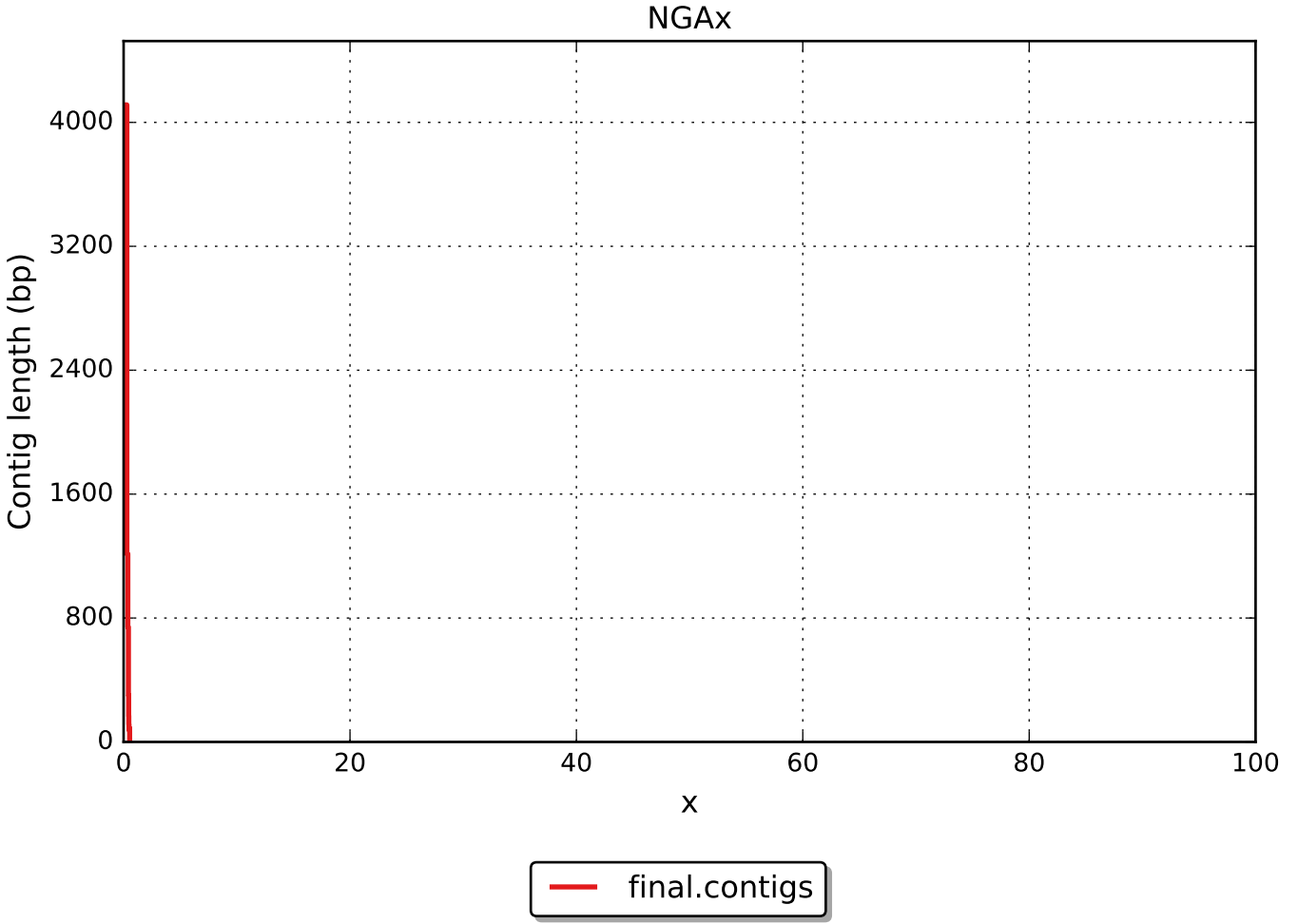

final.contigs GC content
contigs
GC (%)
0
2
4
6
0
20
40
60
80
100
final.contigs


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 (kbp)
1500
1200
900
600
300
0
0
20
40
60
Contig index
final.contigs
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs