Report

	combined.final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	60714
Total length (>= 5000 bp)	56917
Total length (>= 10000 bp)	56917
Total length (>= 25000 bp)	56917
Total length (>= 50000 bp)	56917
# contigs	6
Largest contig	56917
Total length	62064
Reference length	4745539
GC (%)	58.55
Reference GC (%)	50.01
N50	56917
N75	56917
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	59017
Genome fraction (%)	0.061
Duplication ratio	1.056
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2495.67
# indels per 100 kbp	138.65
Largest alignment	1430
Total aligned length	2966
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

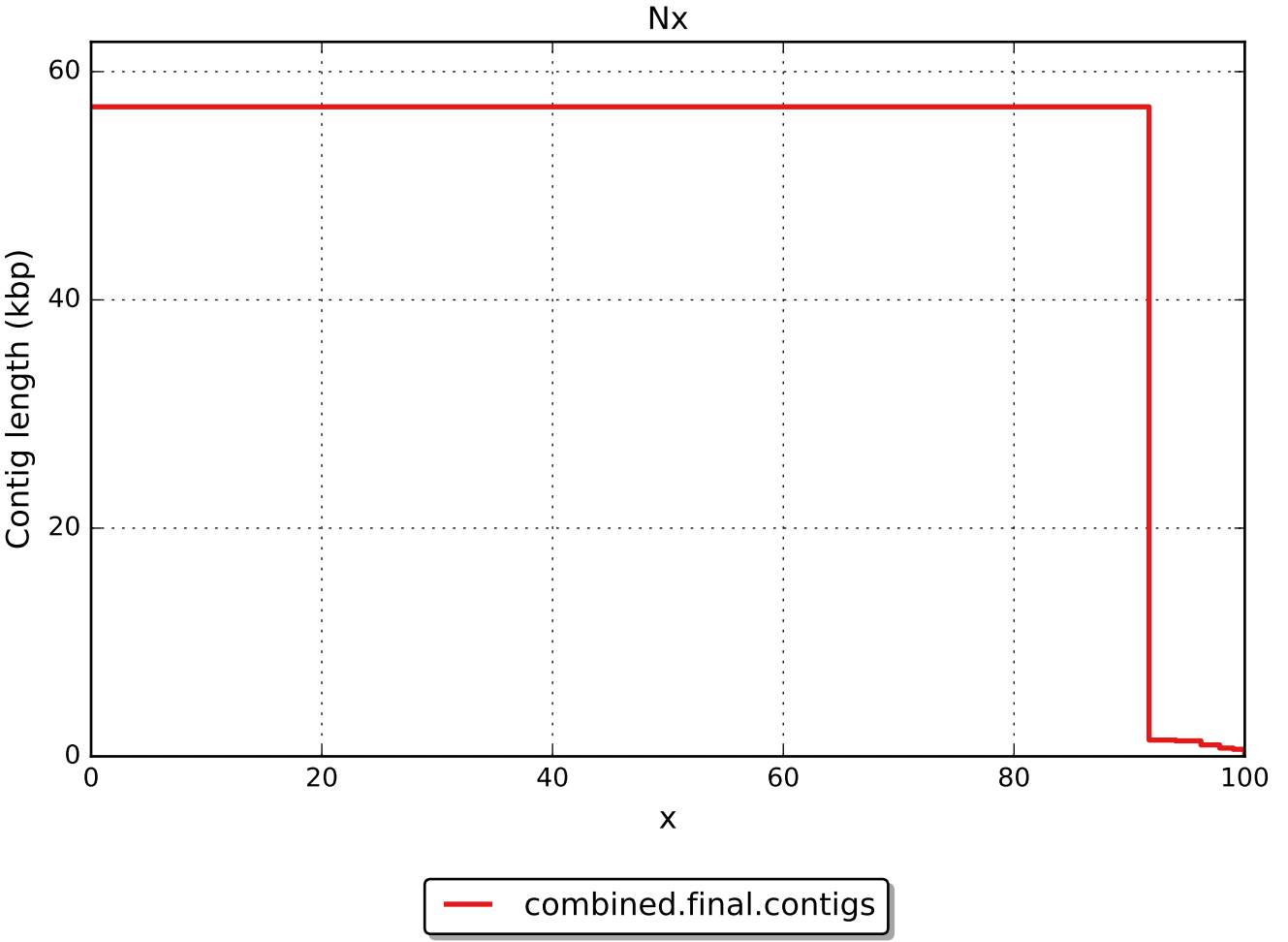
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	72
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

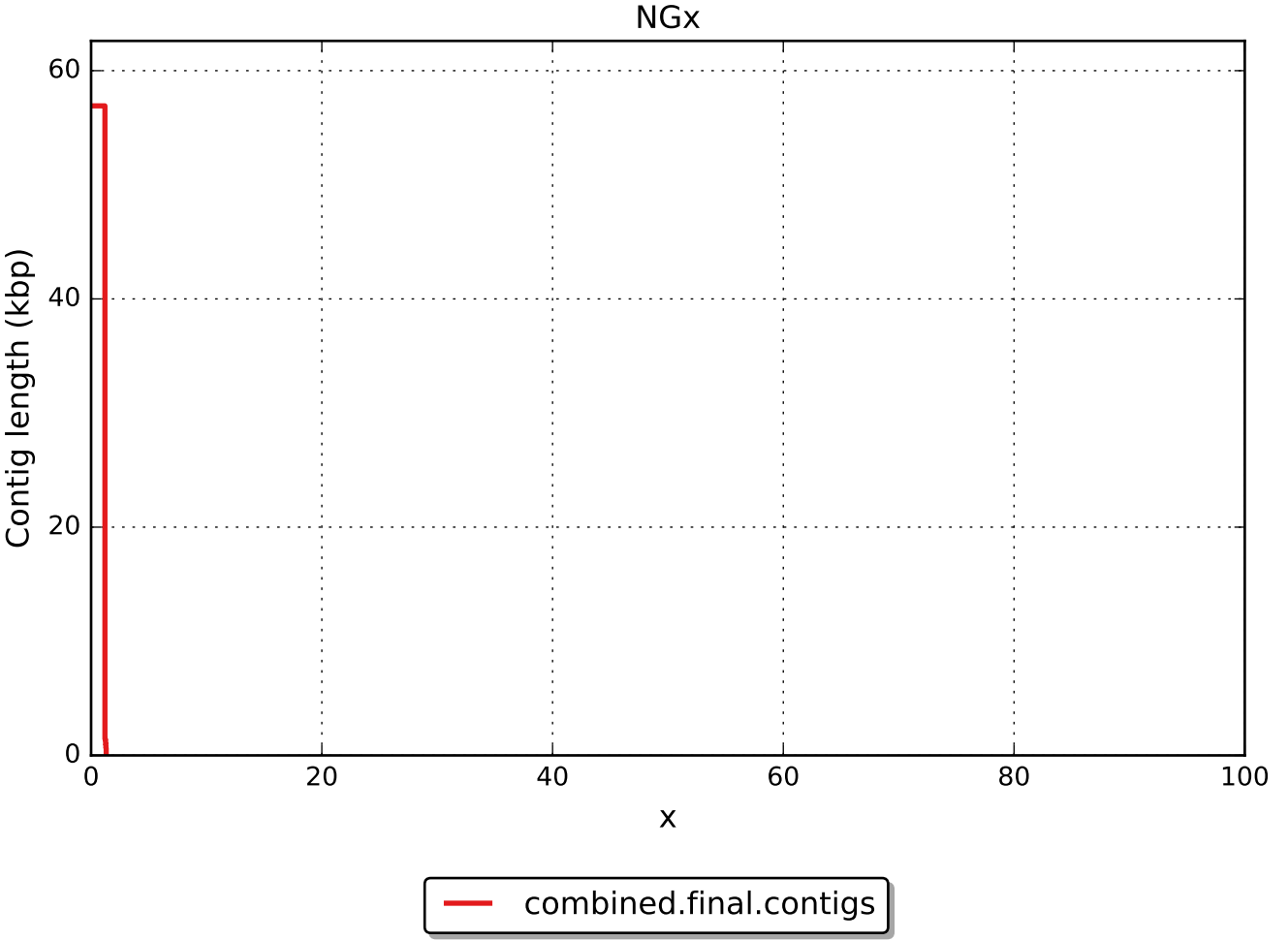
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

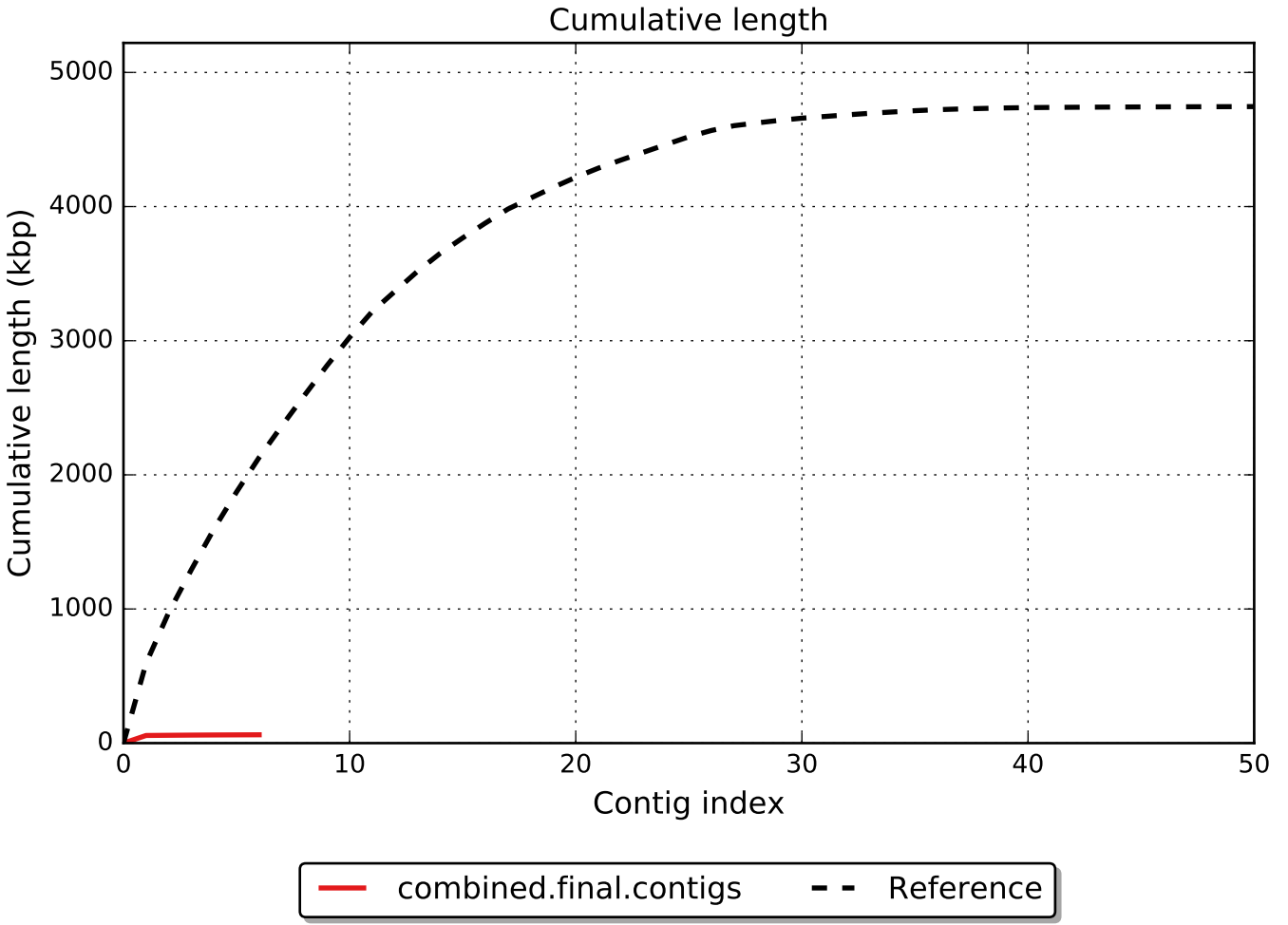
Unaligned report

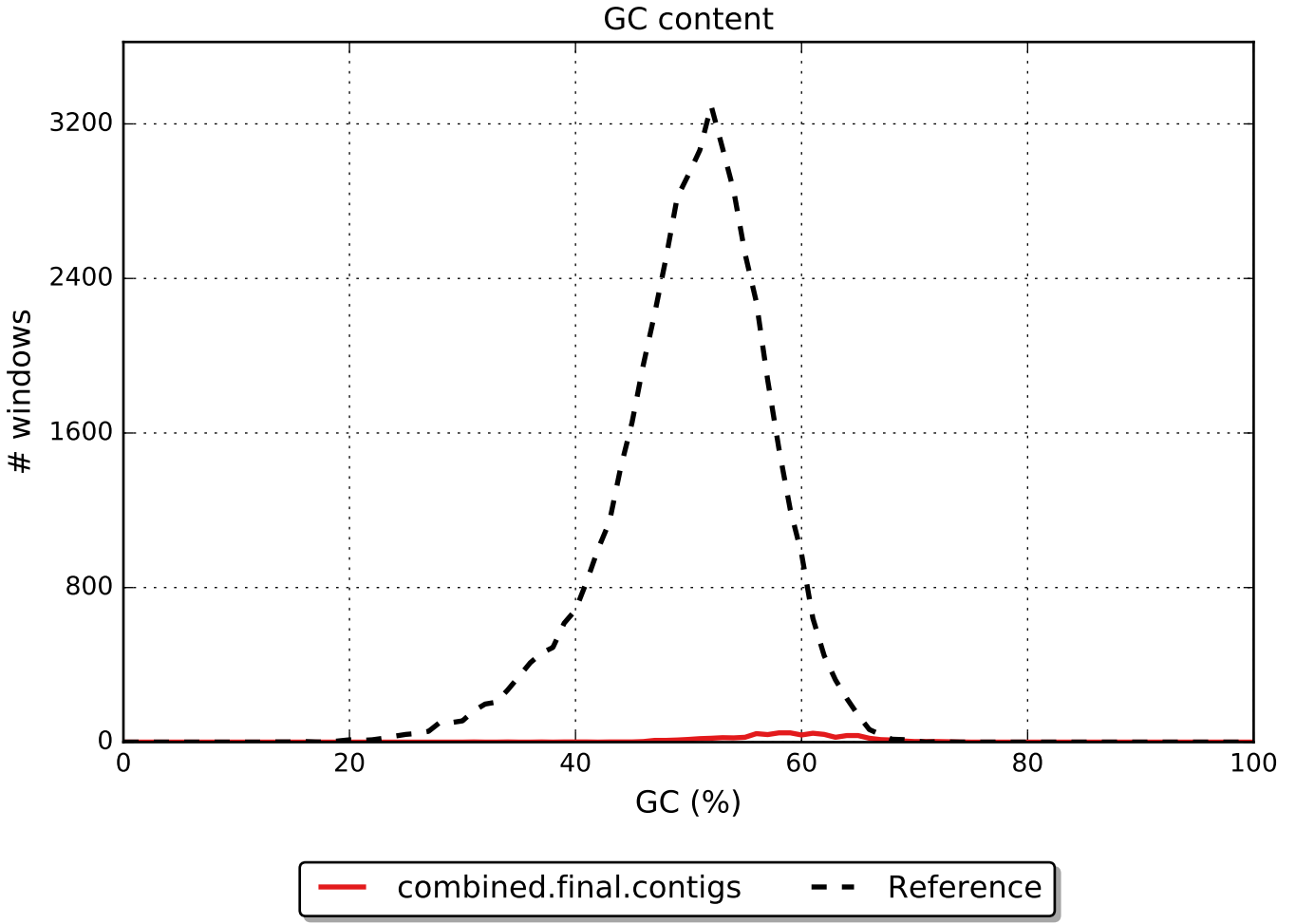
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	59017
# N's	0

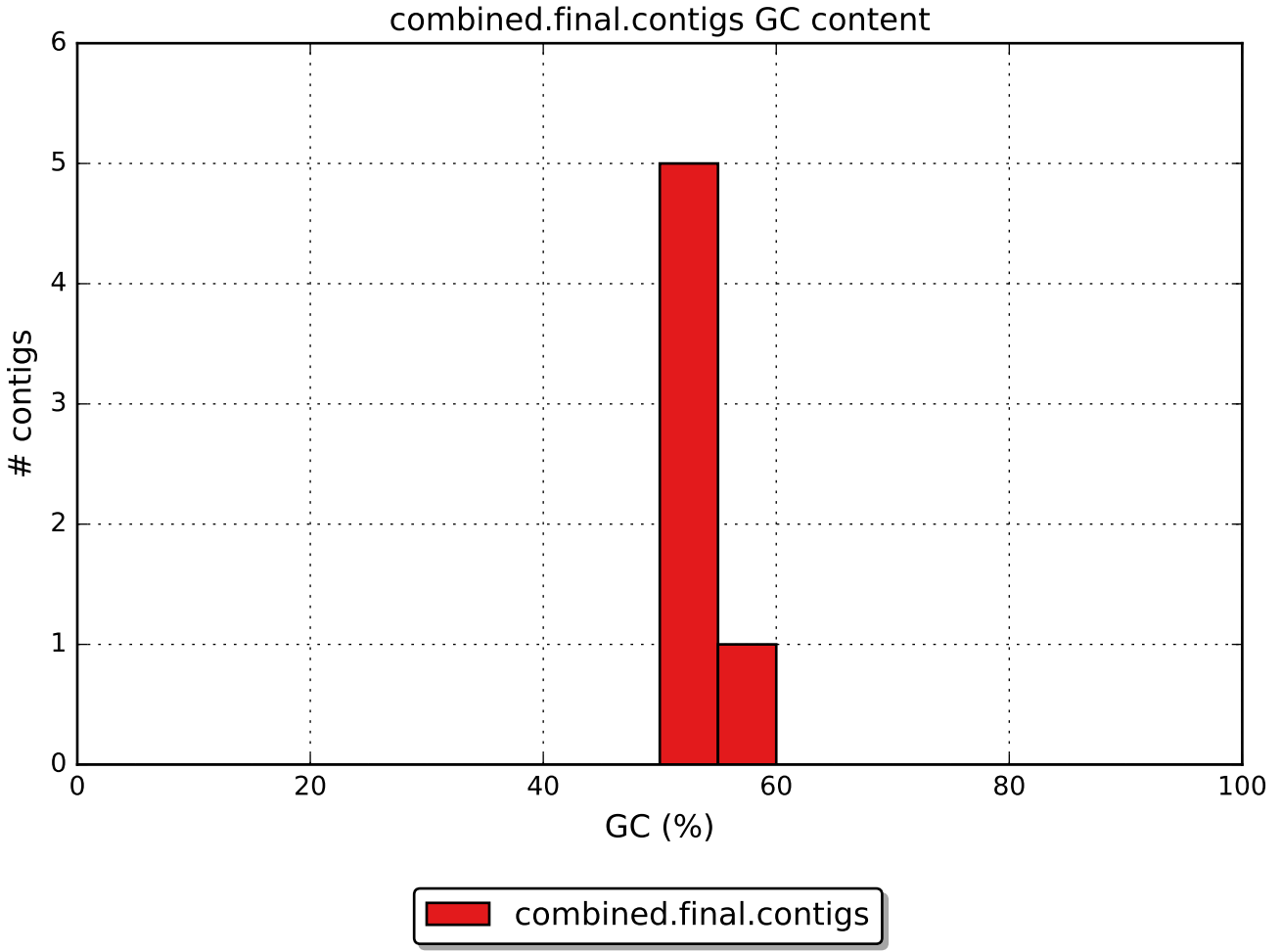
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

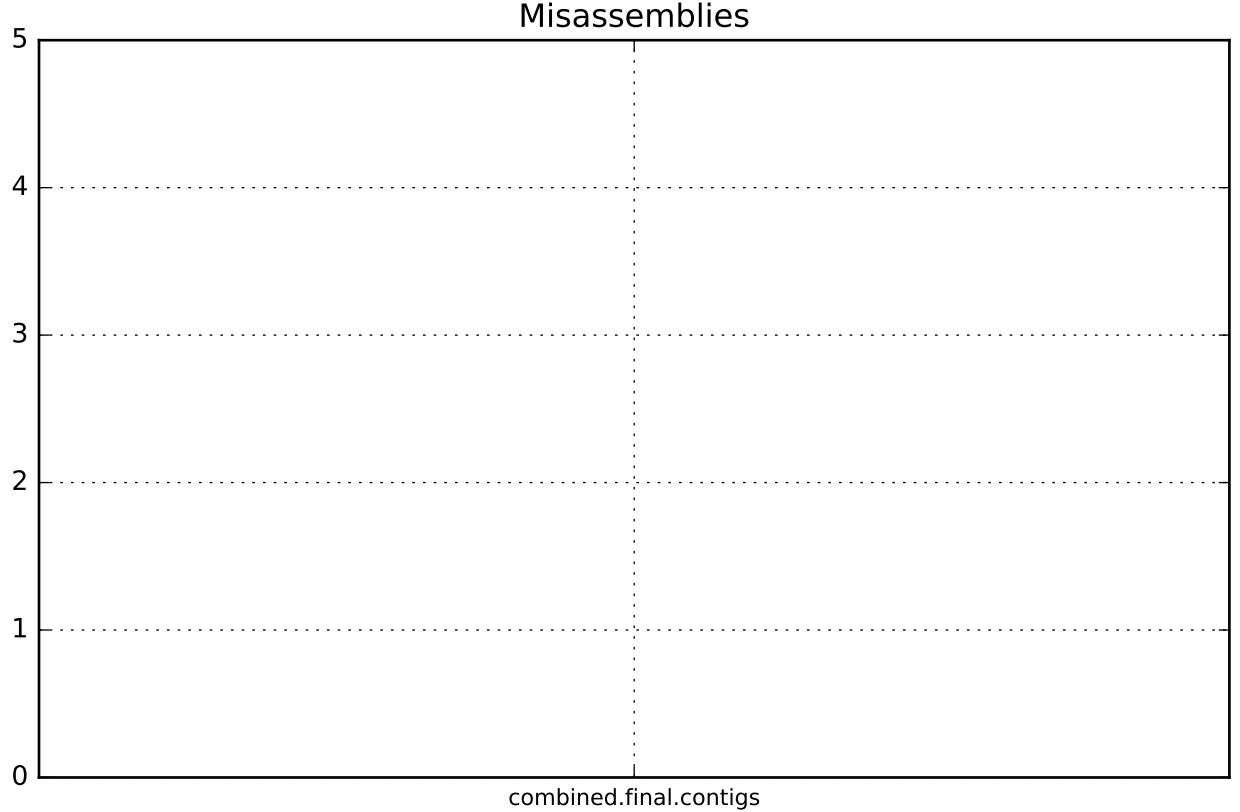

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
combined.final.contigs

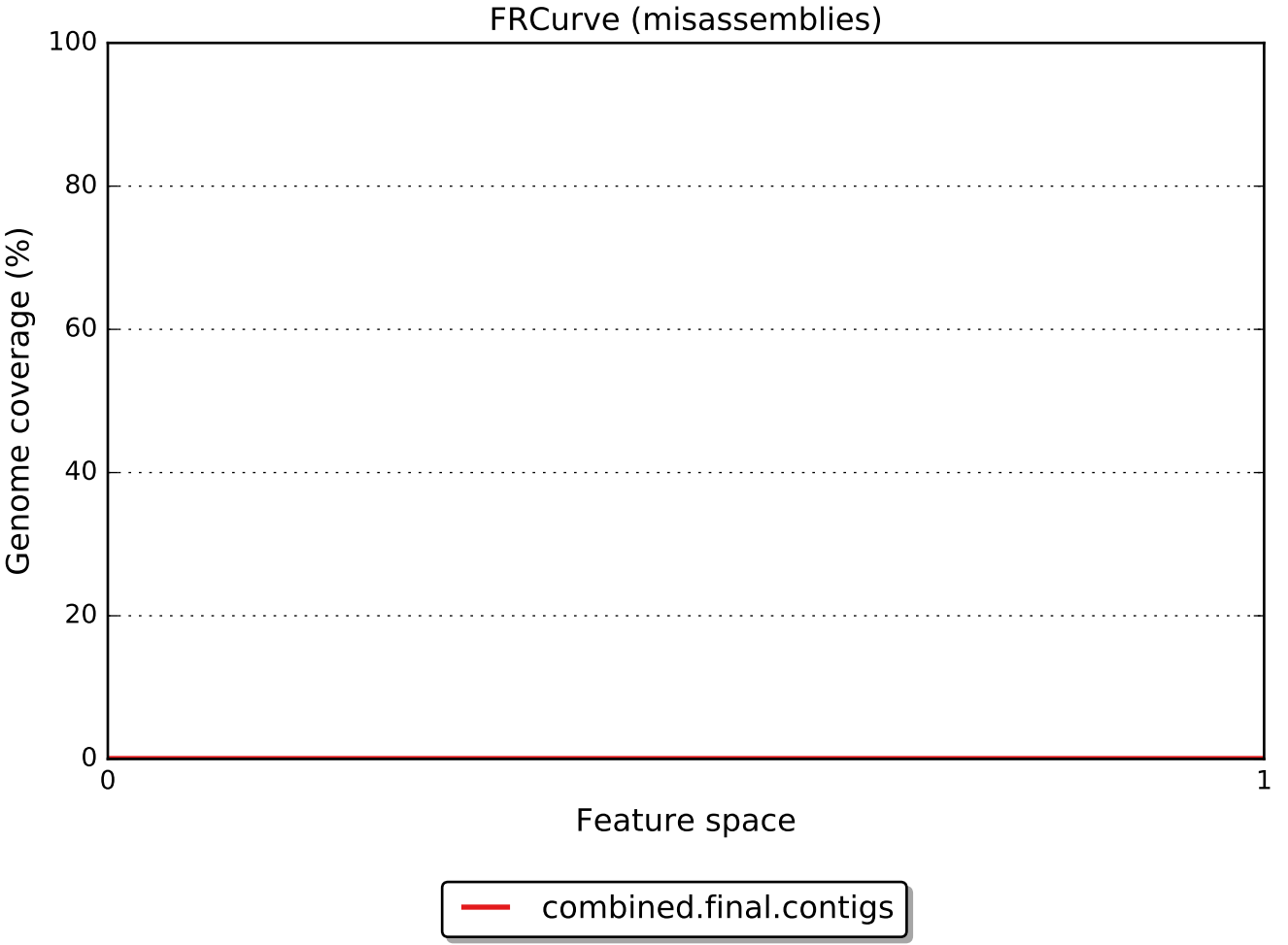

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
combined.final.contigs

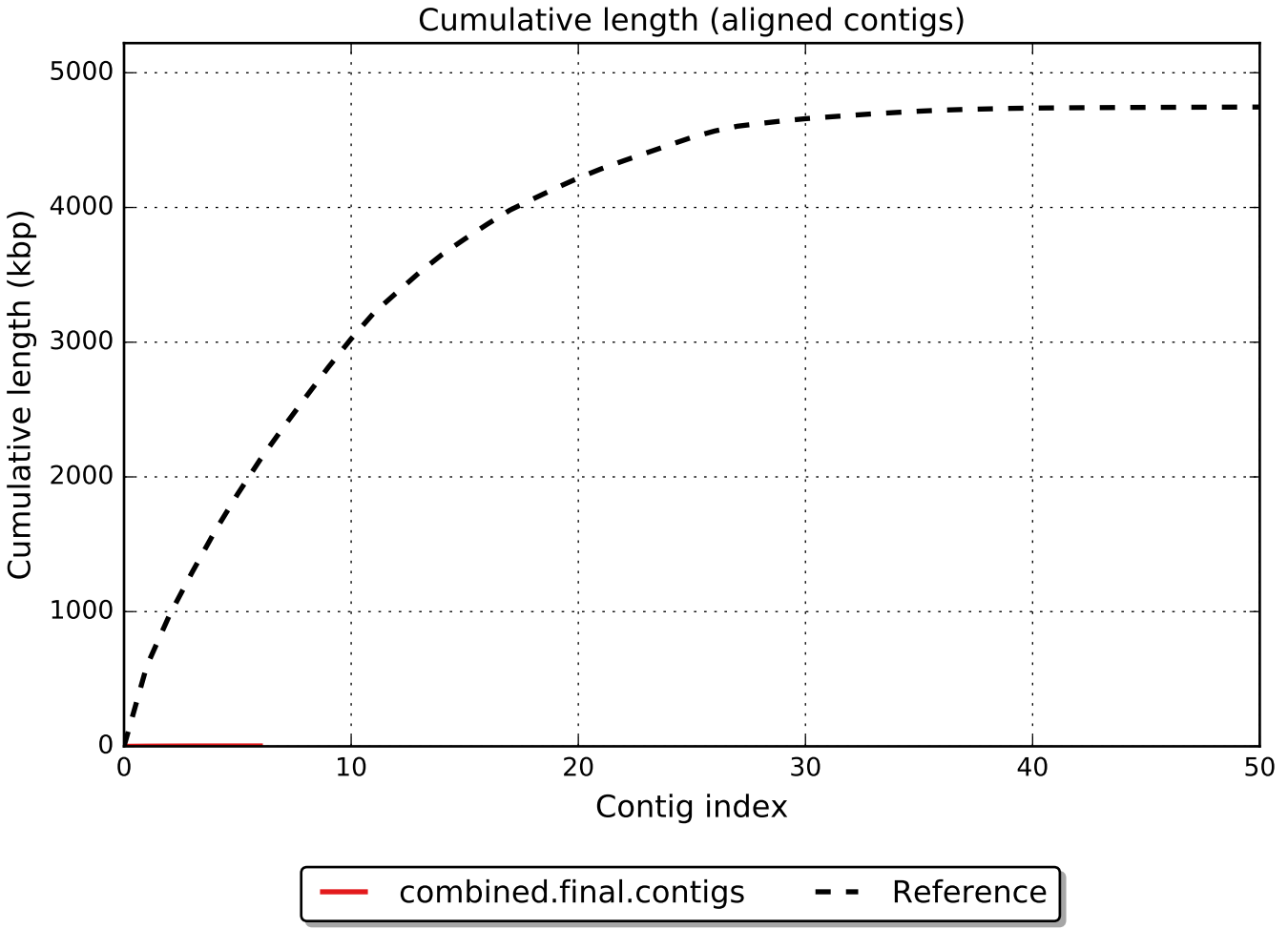

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
Contig index
combined.final.contigs
Reference

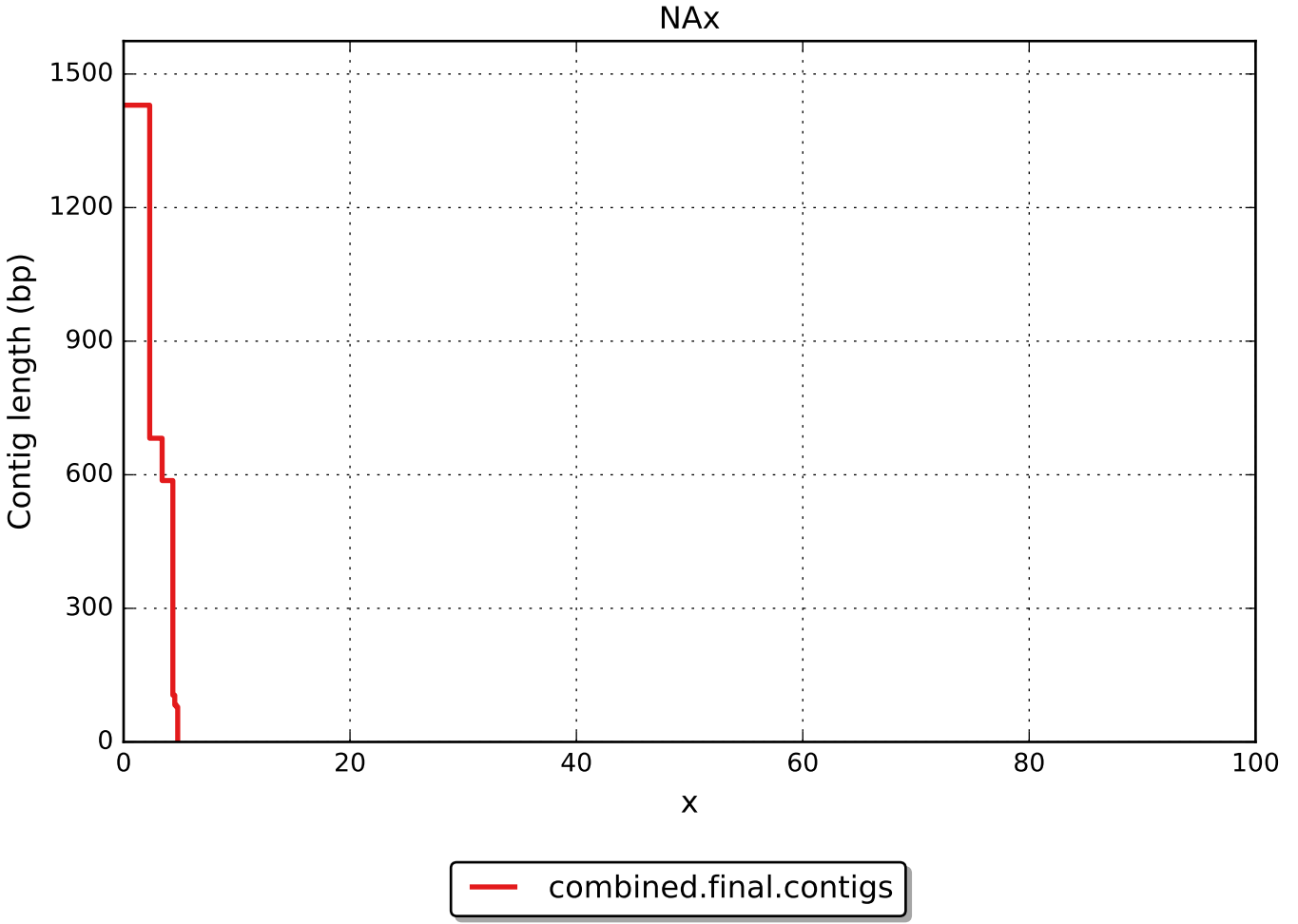

GC content
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
combined.final.contigs
Reference

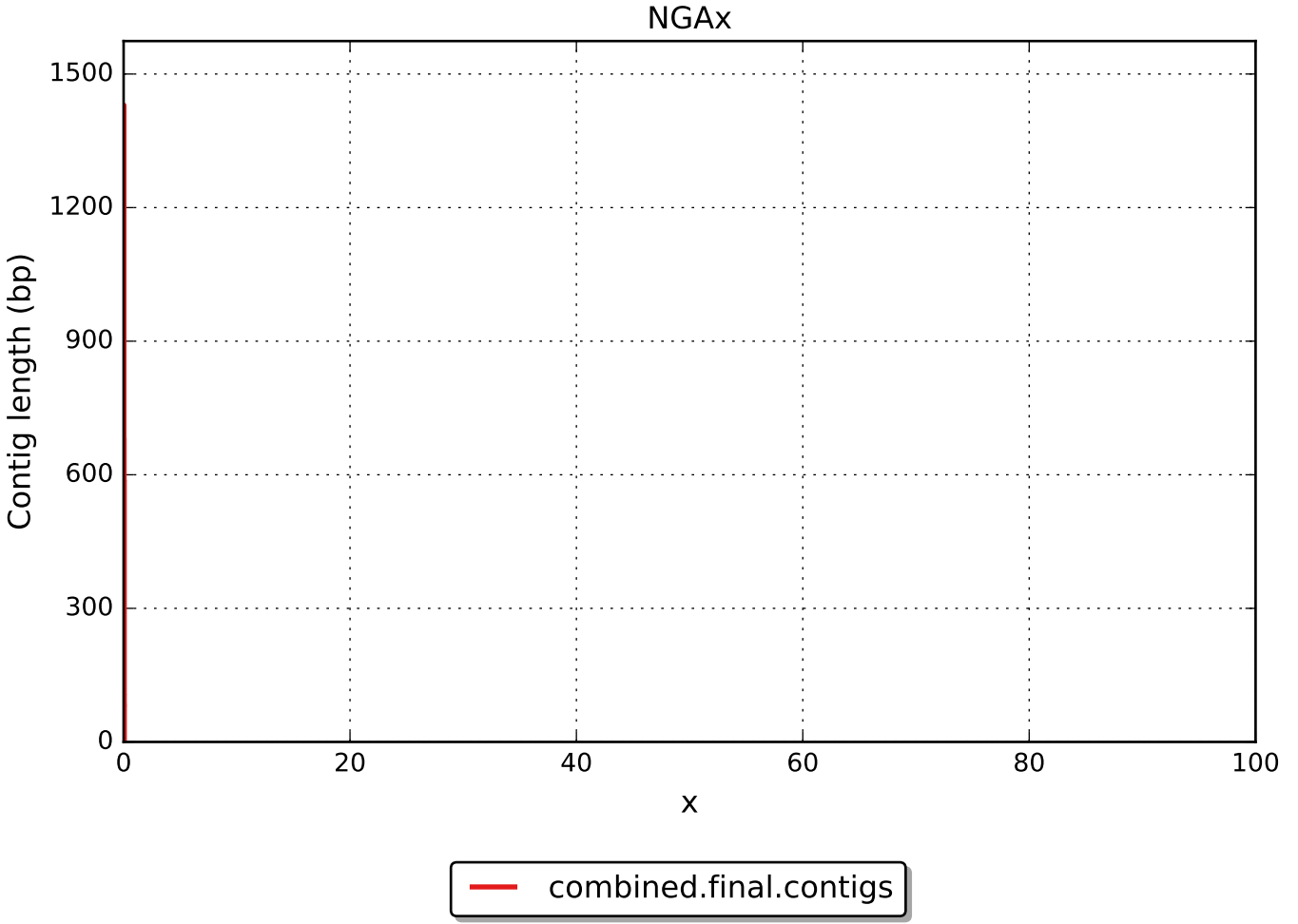

combined.final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
combined.final.contigs


Misassemblies
5
4
3
2
1
0
combined.final.contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
1000
2000
3000
4000
5000
0
10
20
30
40
50
Contig index
combined.final.contigs
Reference


NAx
Contig length (bp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
combined.final.contigs


NGAx
Contig length (bp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
combined.final.contigs