Report

	combined.final.contigs
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	66580
Total length (>= 5000 bp)	22432
Total length (>= 10000 bp)	12904
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	36
Largest contig	12904
Total length	78036
Reference length	3261541
GC (%)	52.22
Reference GC (%)	56.74
N50	2776
N75	1736
L50	7
L75	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 28 part
Unaligned length	68458
Genome fraction (%)	0.169
Duplication ratio	1.735
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2790.36
# indels per 100 kbp	181.19
Largest alignment	1456
Total aligned length	6939
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

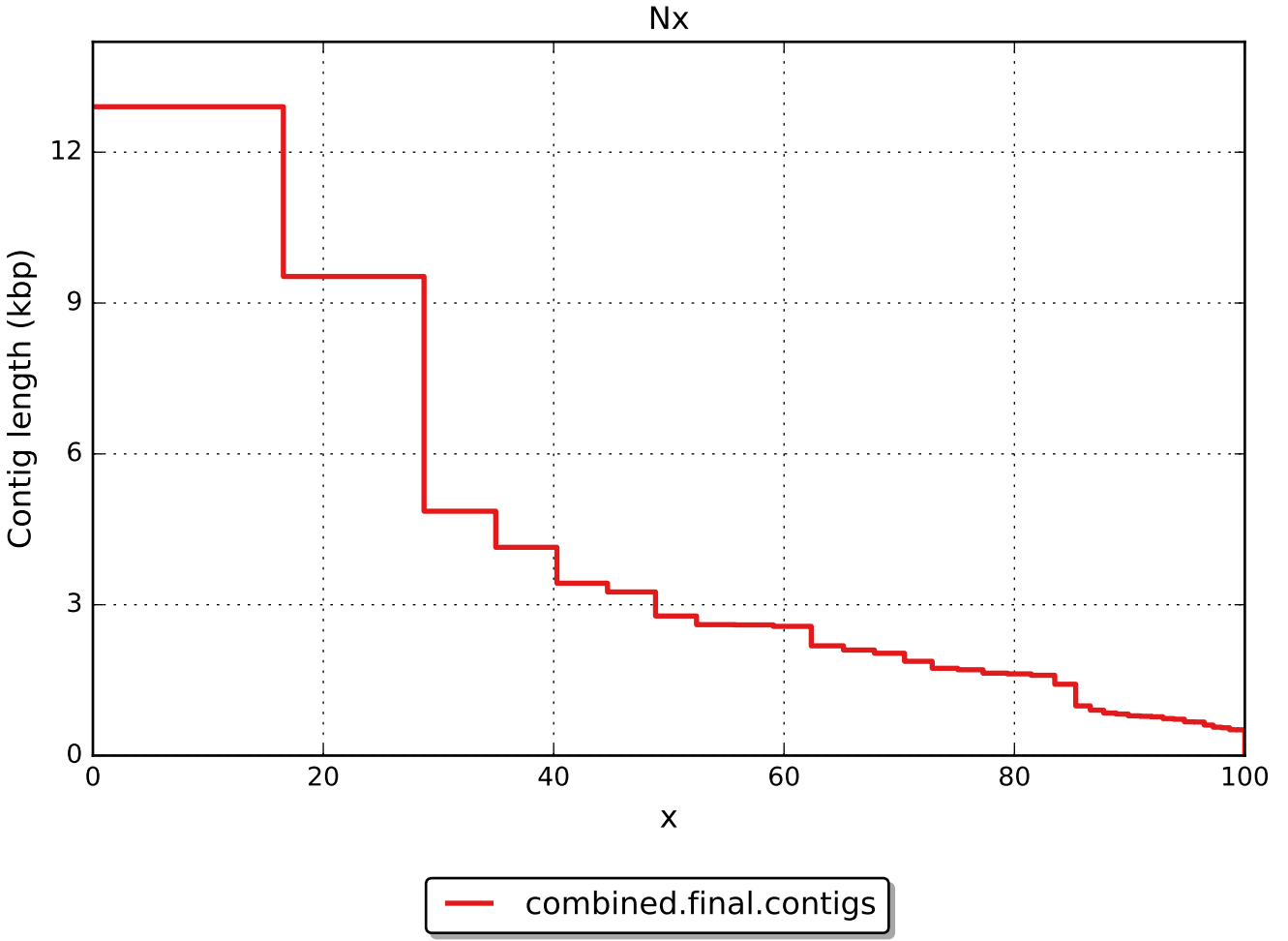
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	154
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	10

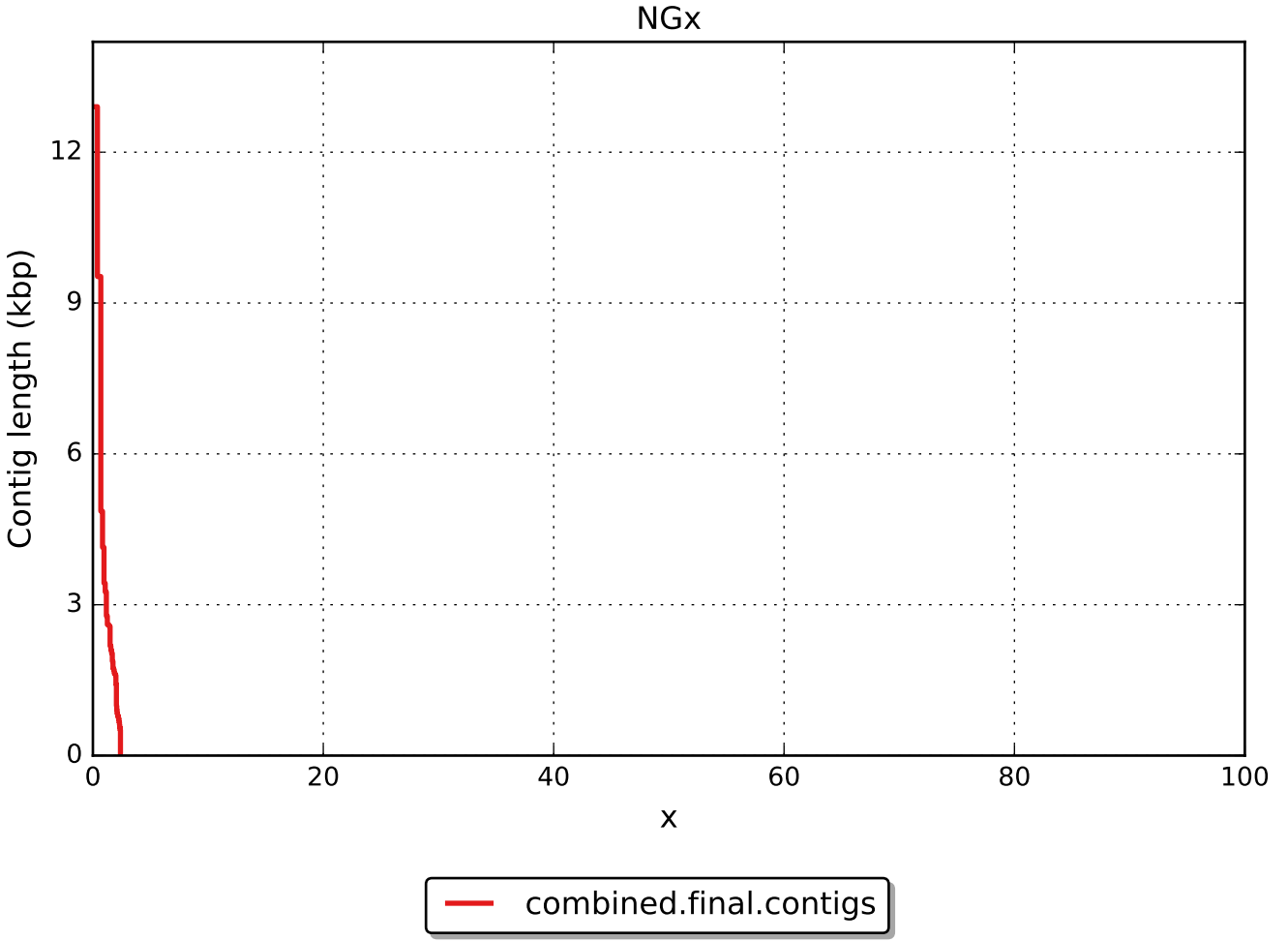
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

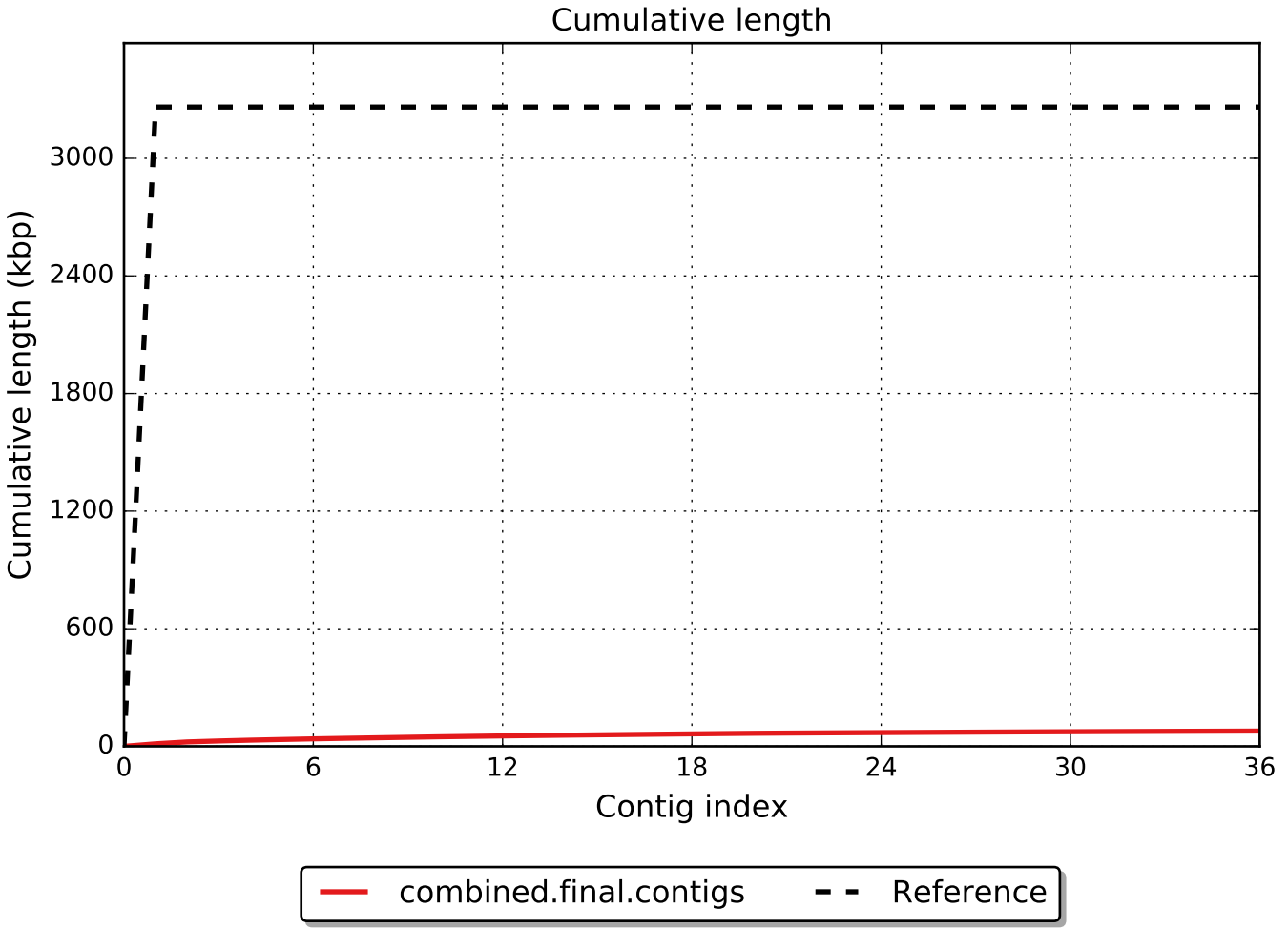
Unaligned report

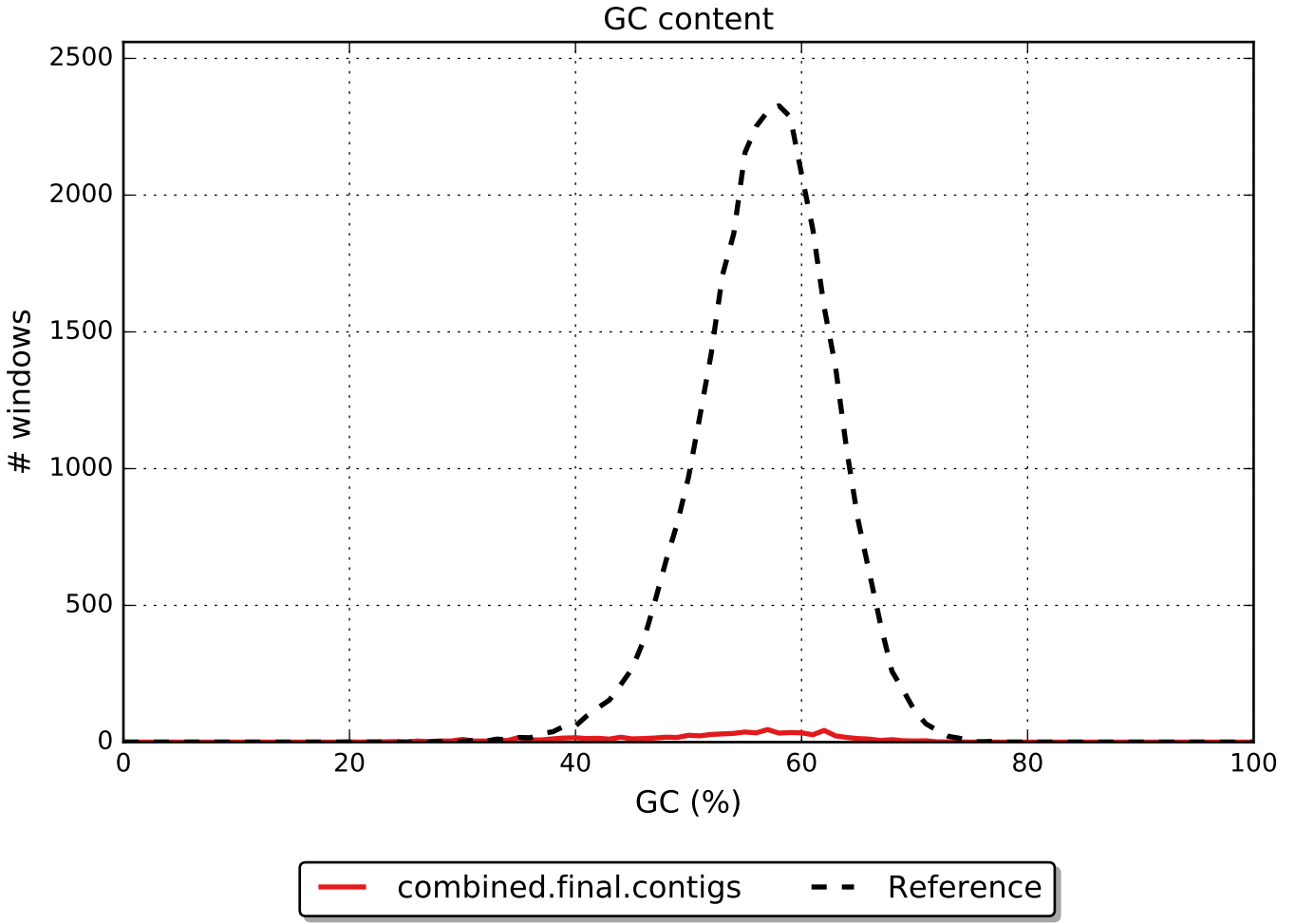
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	28
Partially unaligned length	68458
# N's	0

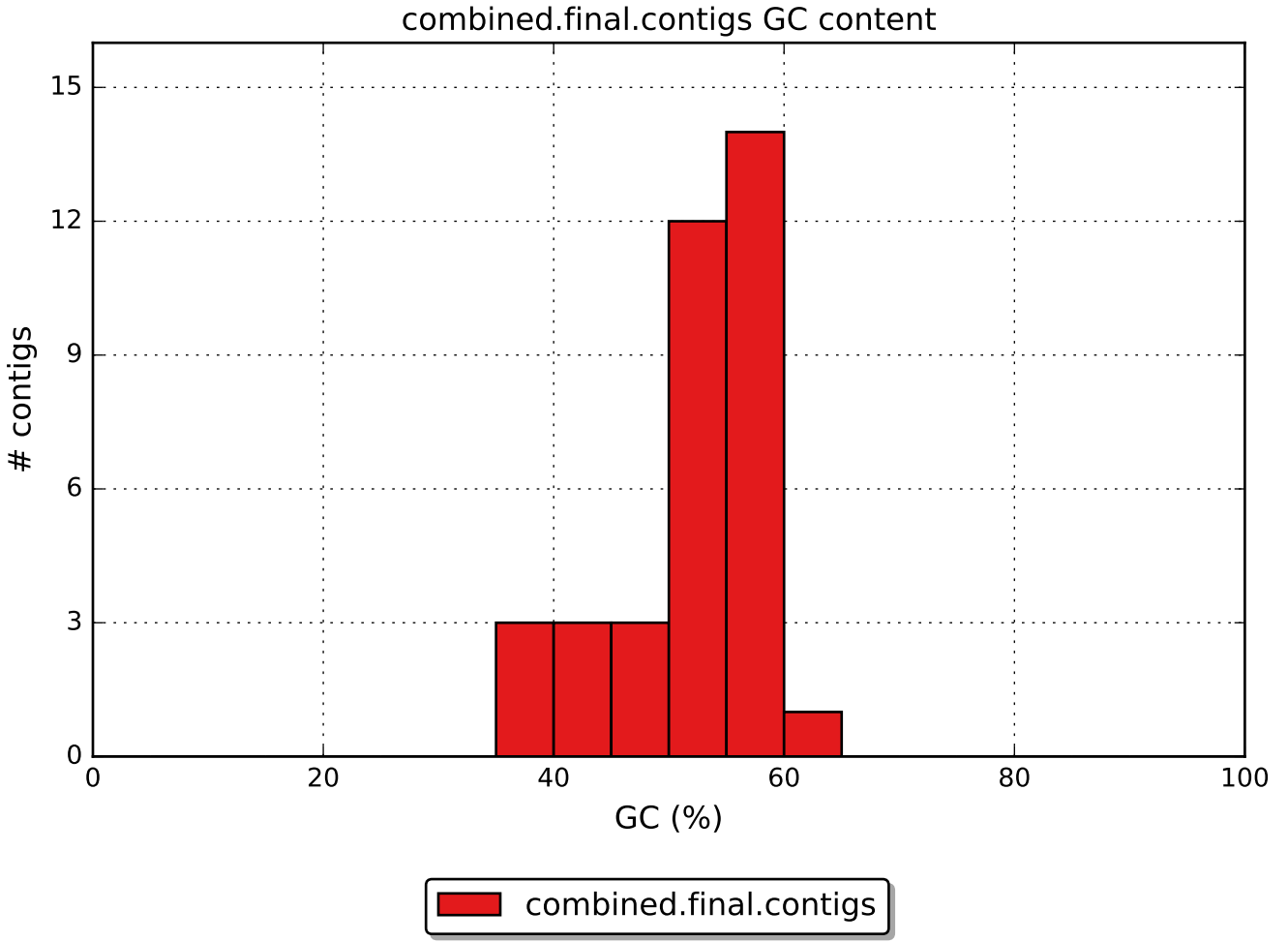
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

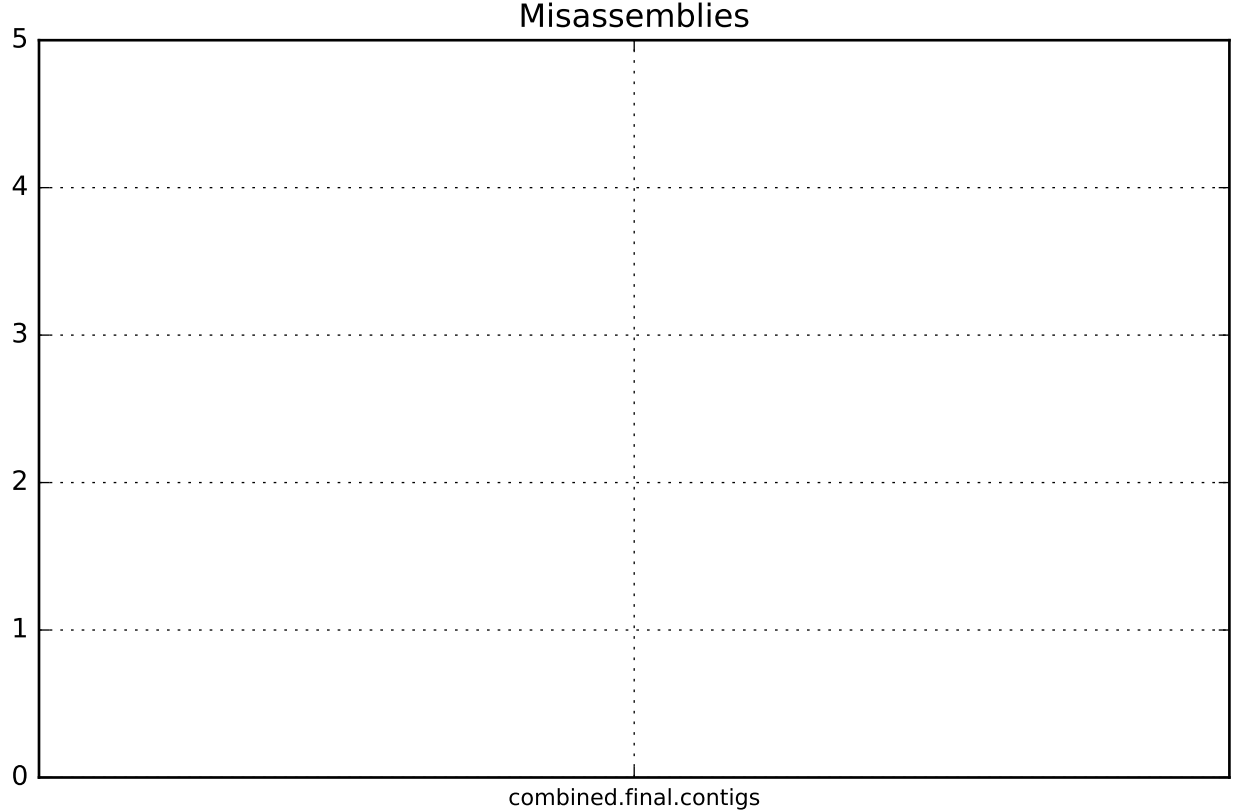

Nx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
combined.final.contigs

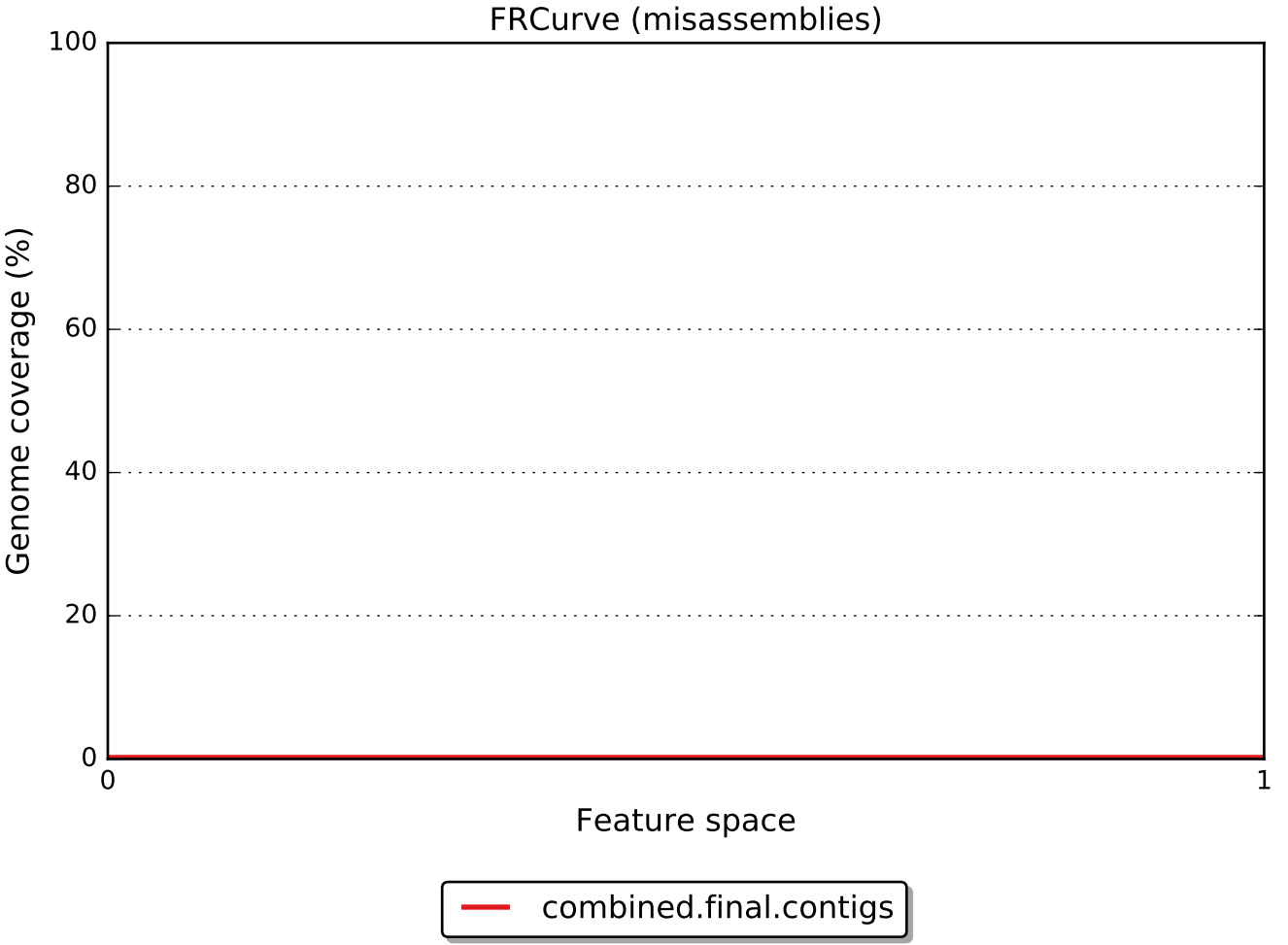

NGx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
combined.final.contigs

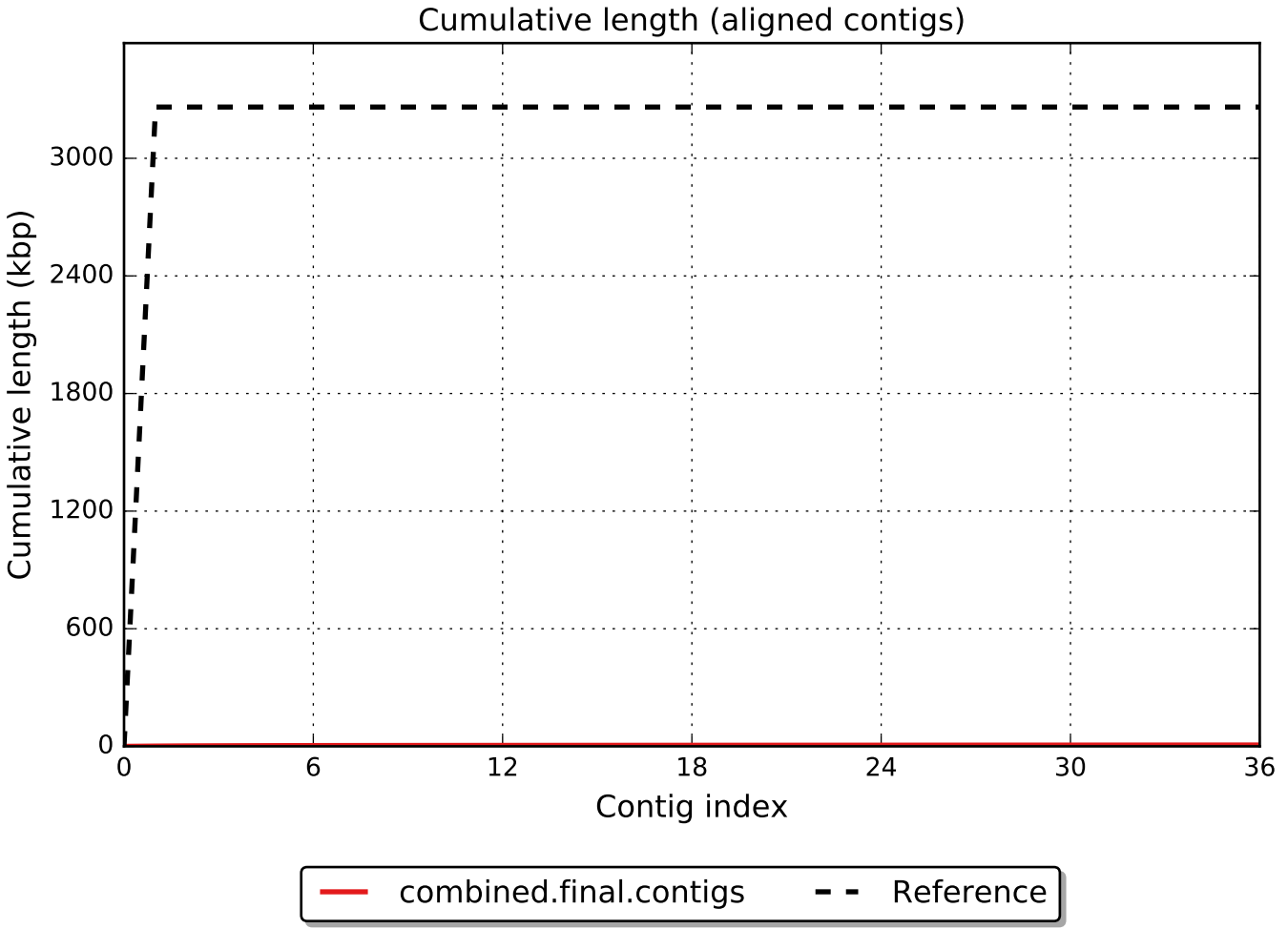

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
6
12
18
24
30
36
Contig index
combined.final.contigs
Reference

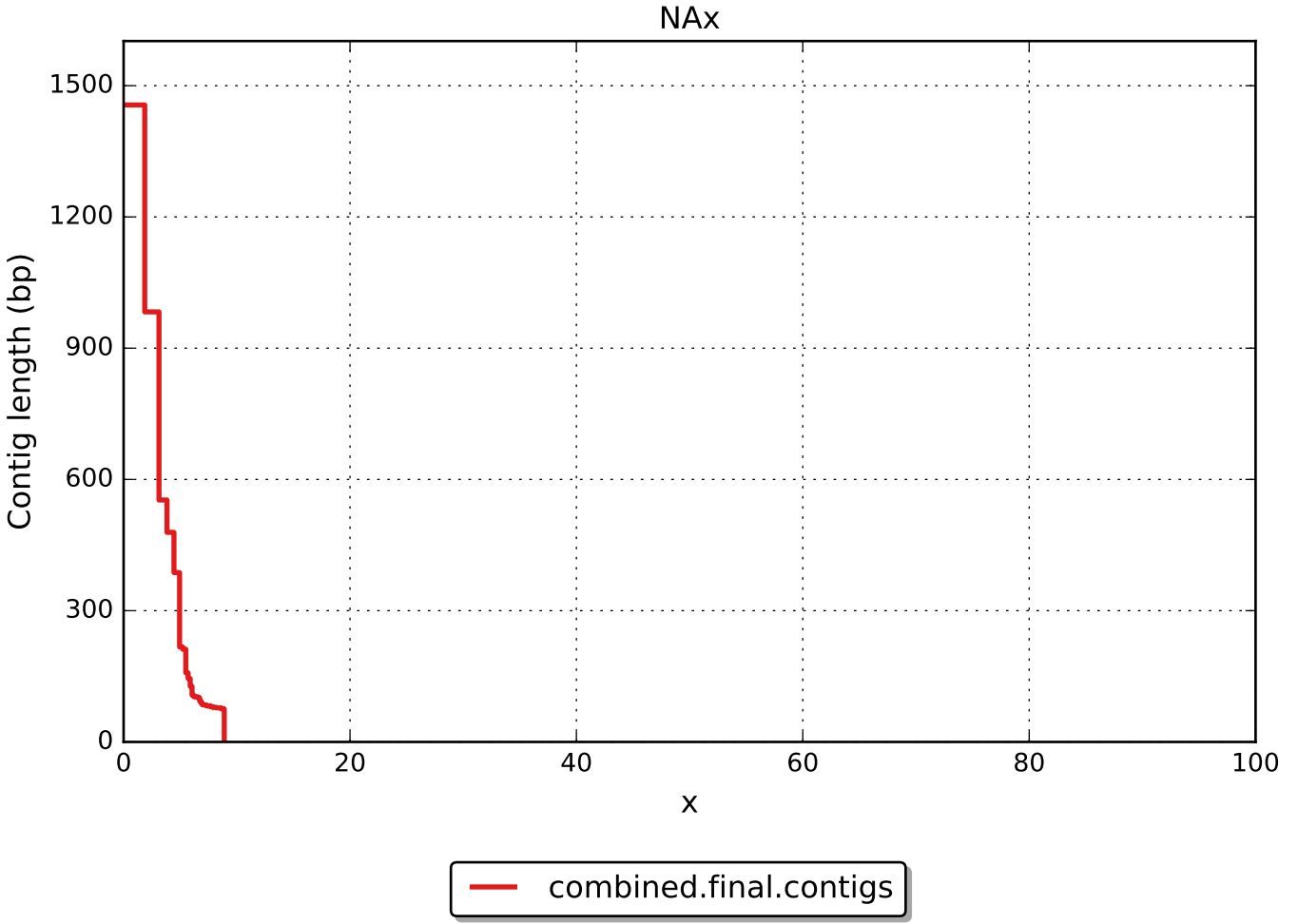

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
combined.final.contigs
Reference

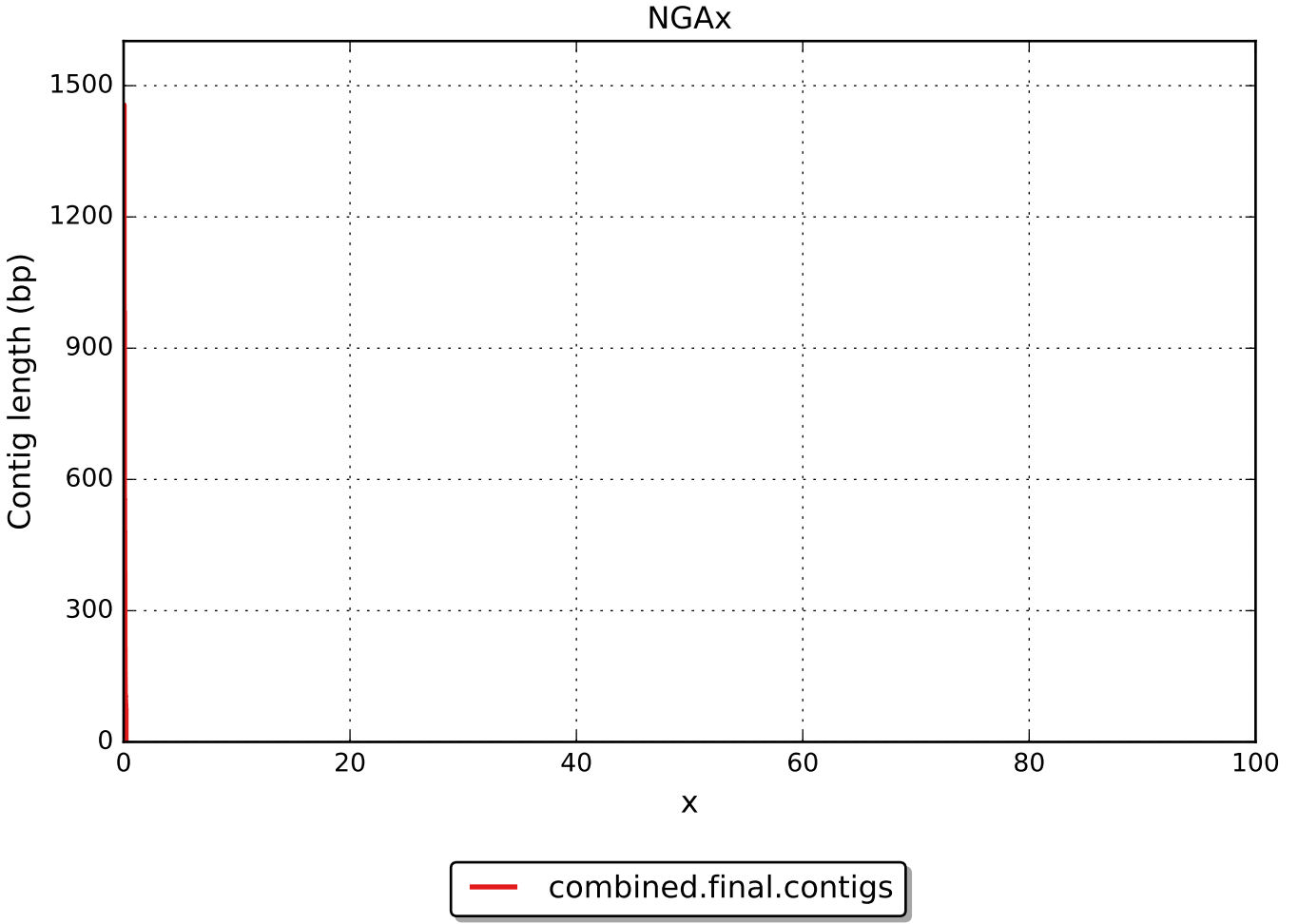

combined.final.contigs GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
combined.final.contigs


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)
3000
2400
1800
1200
600
0
0
6
12
18
24
30
36
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