Report

	combined.final.contigs
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2190
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	7
Largest contig	2190
Total length	6816
Reference length	3750771
GC (%)	51.85
Reference GC (%)	53.60
N50	866
N75	768
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 4 part
Unaligned length	4461
Genome fraction (%)	0.004
Duplication ratio	14.719
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1875.00
# indels per 100 kbp	0.00
Largest alignment	84
Total aligned length	575
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

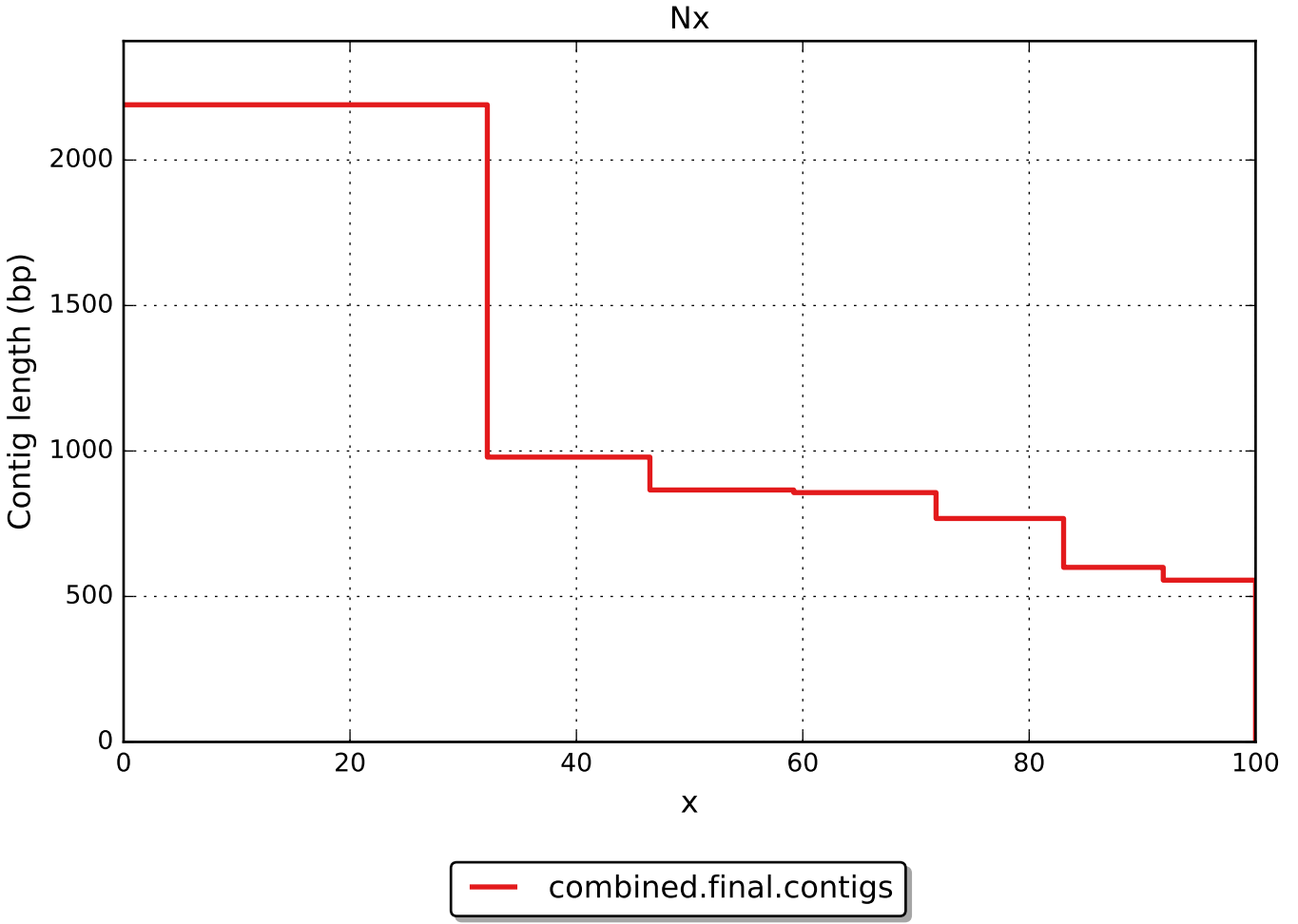
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches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

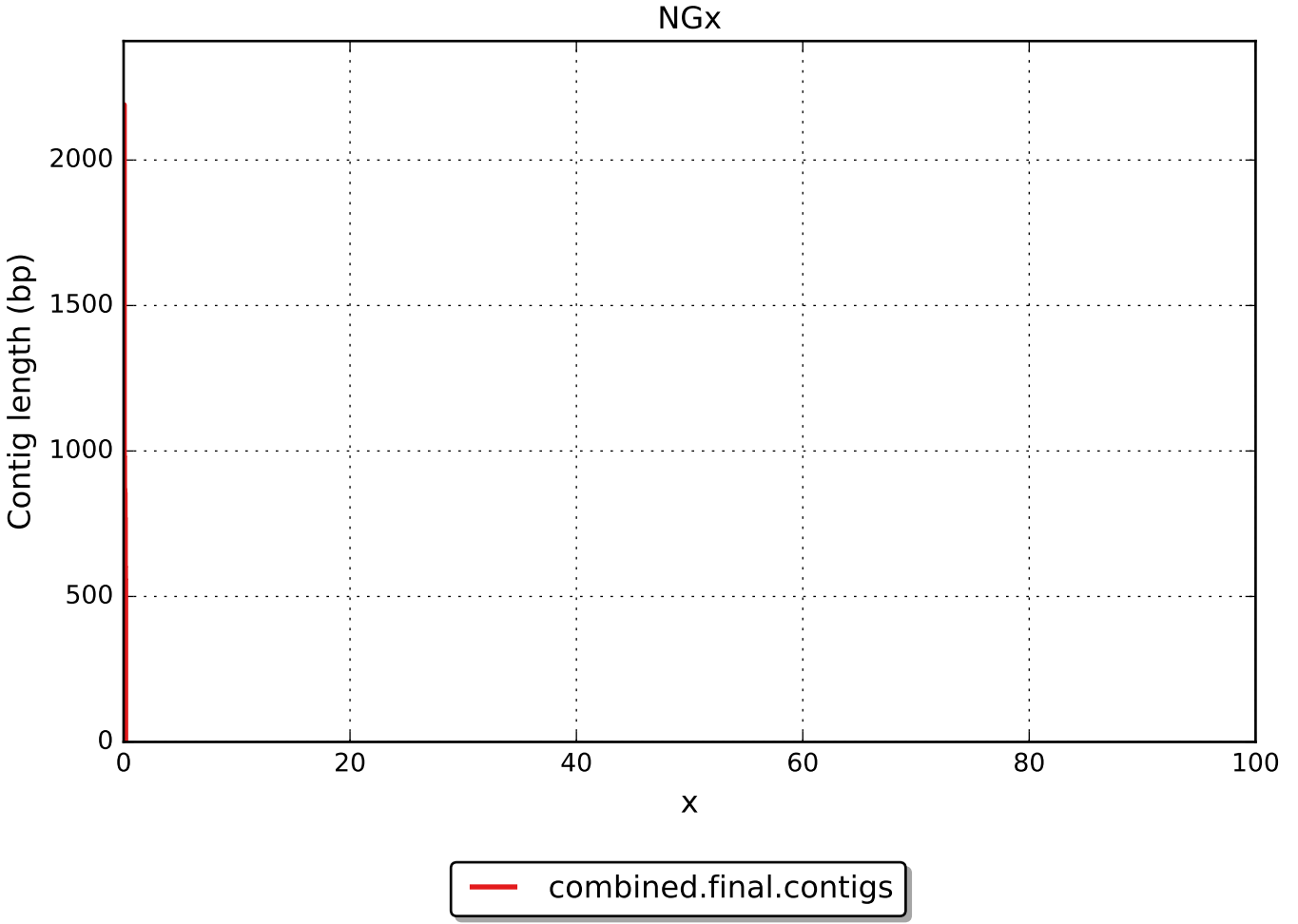
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

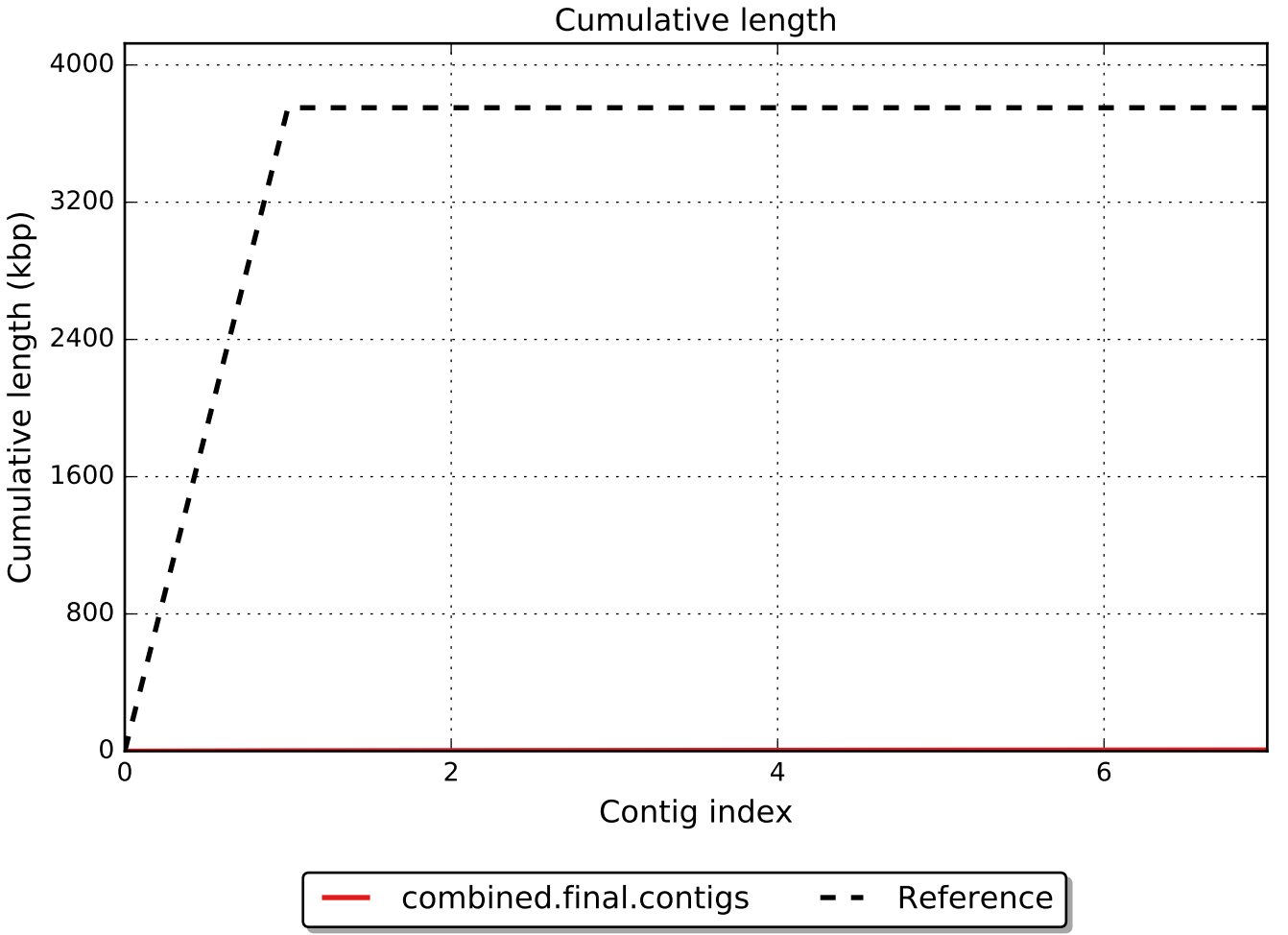
Unaligned report

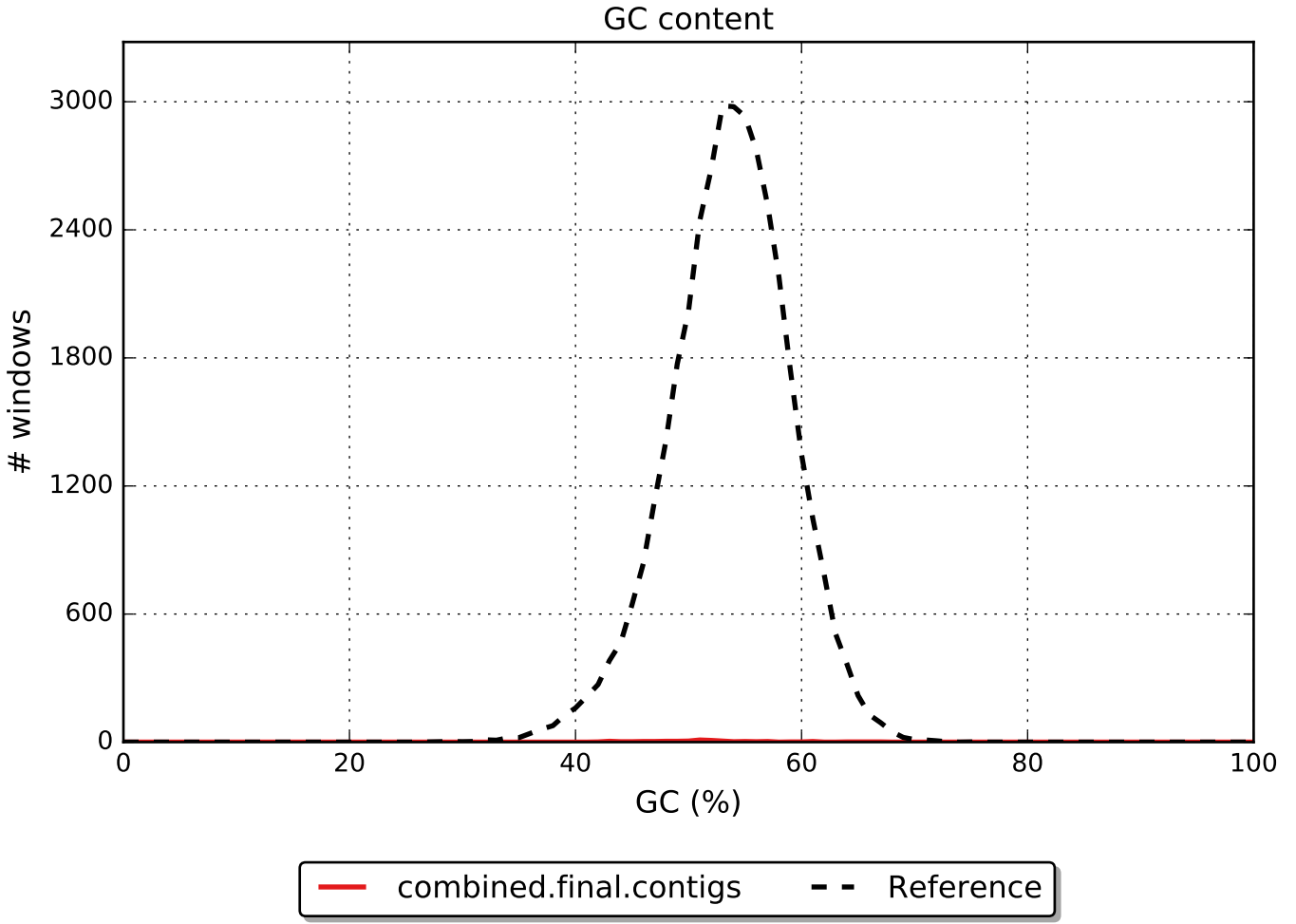
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	4461
# N's	0

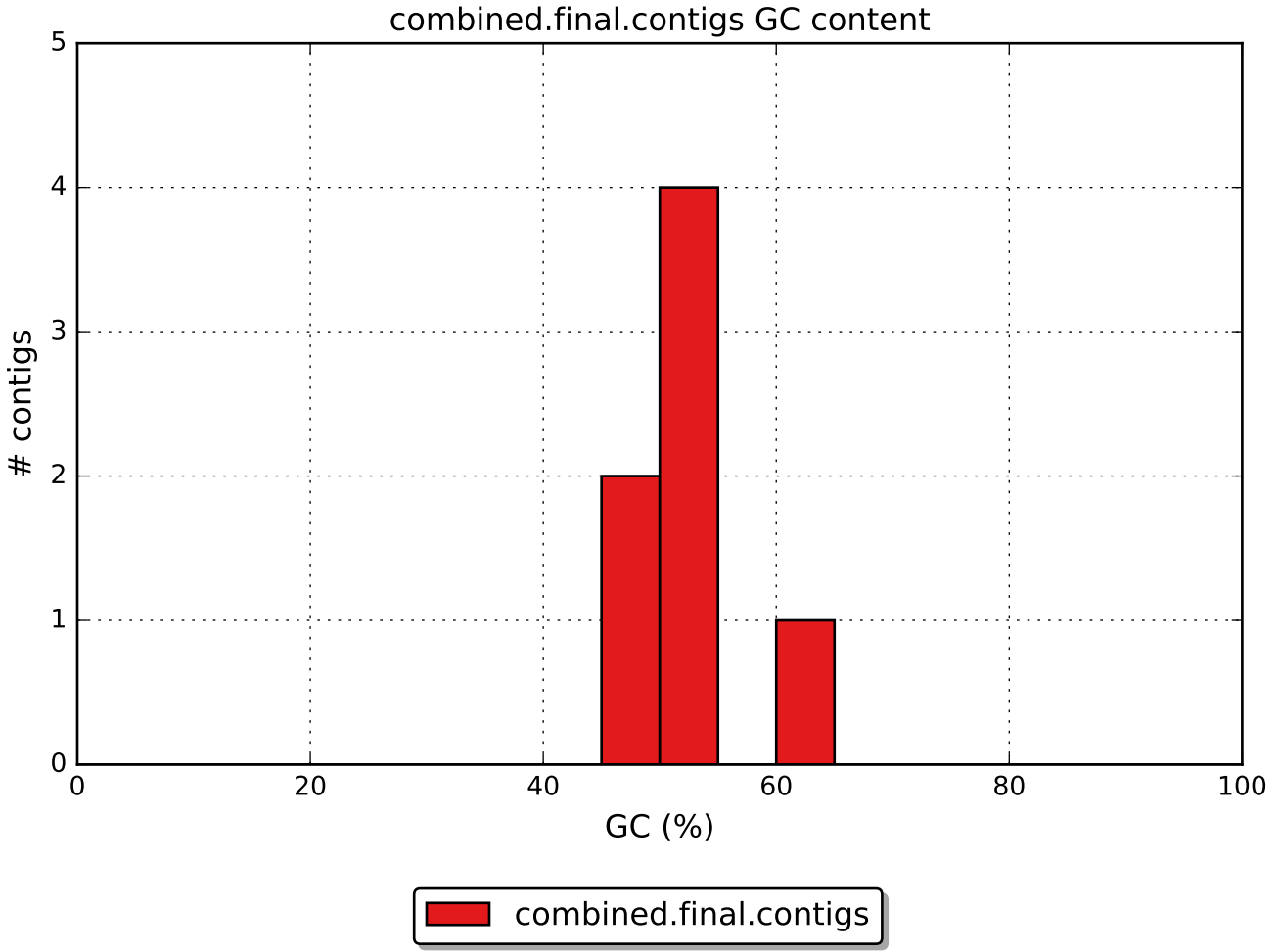
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

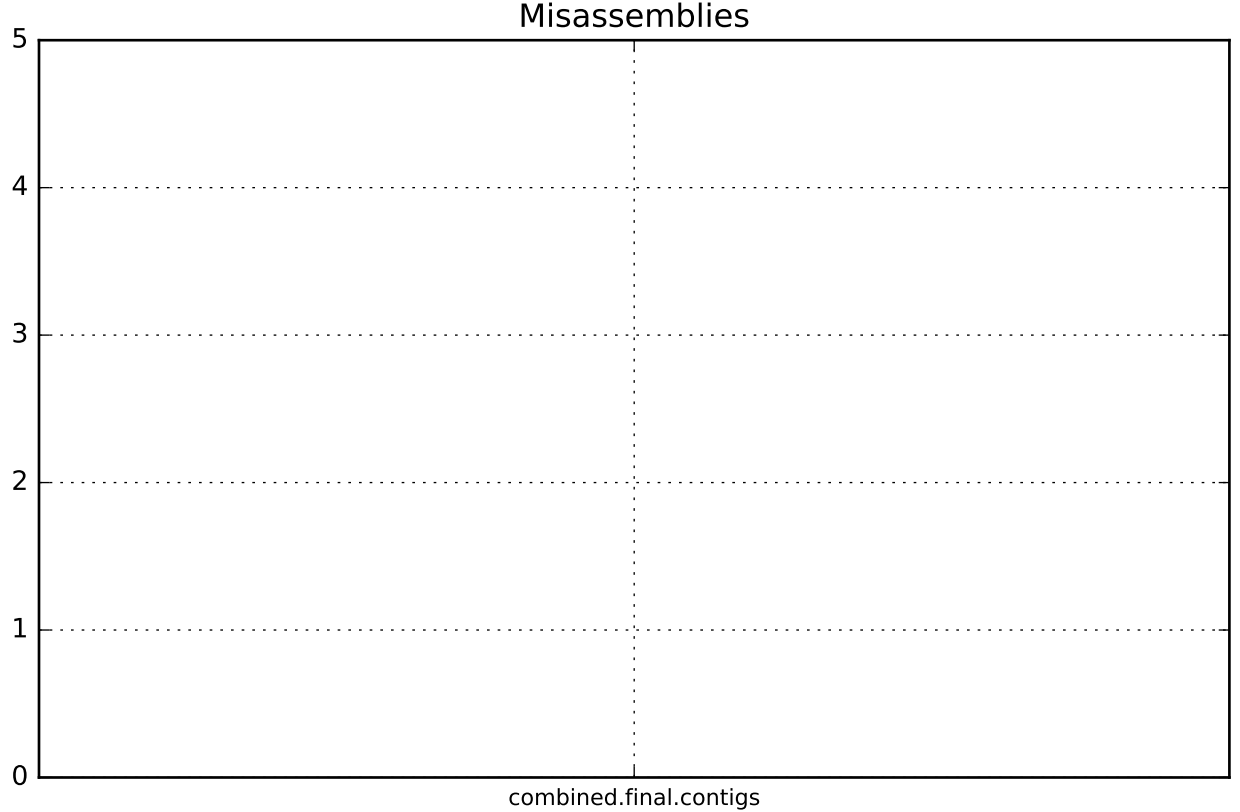

Nx
Contig length (bp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
combined.final.contigs

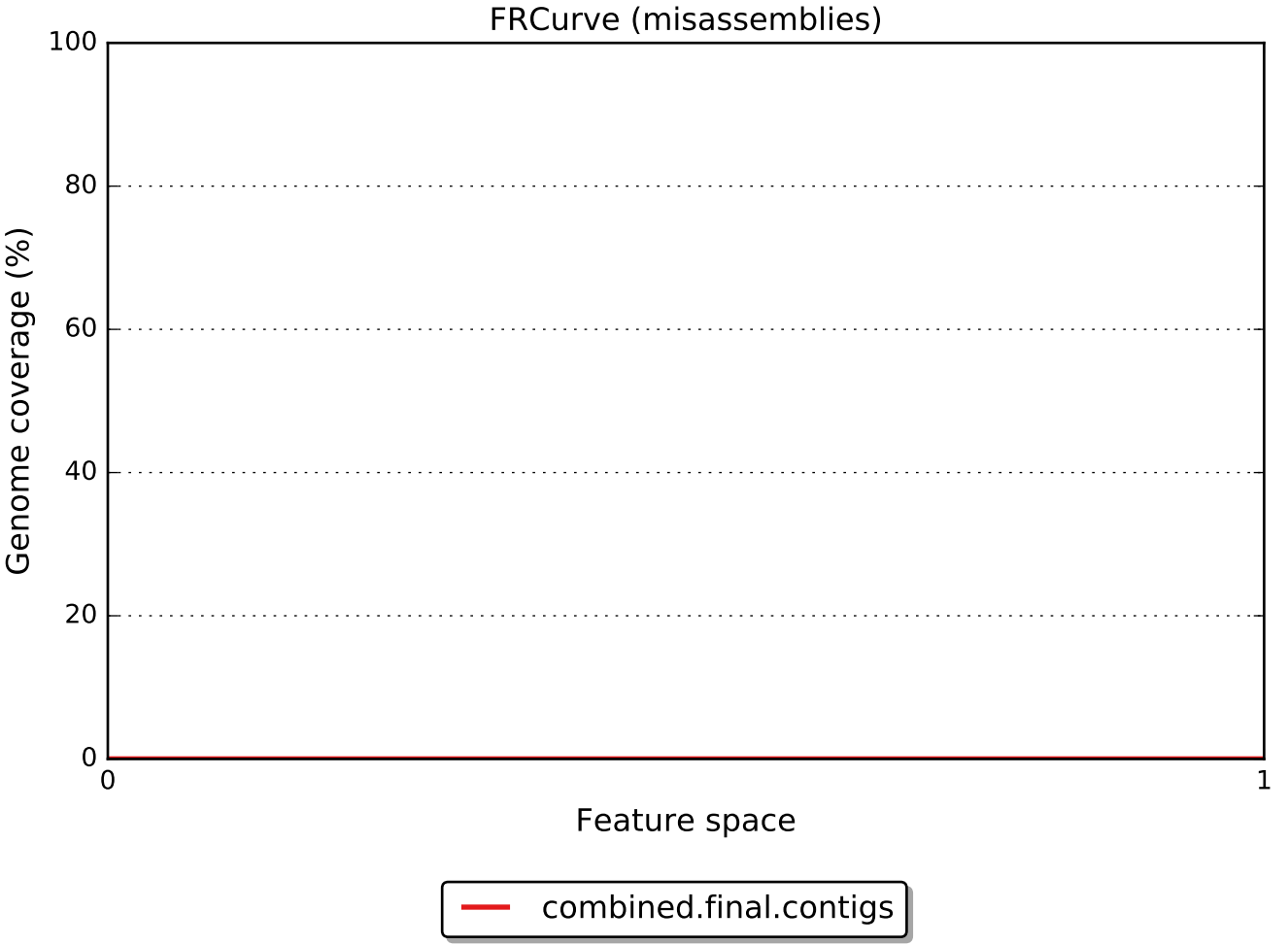

NGx
Contig length (bp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
combined.final.contigs

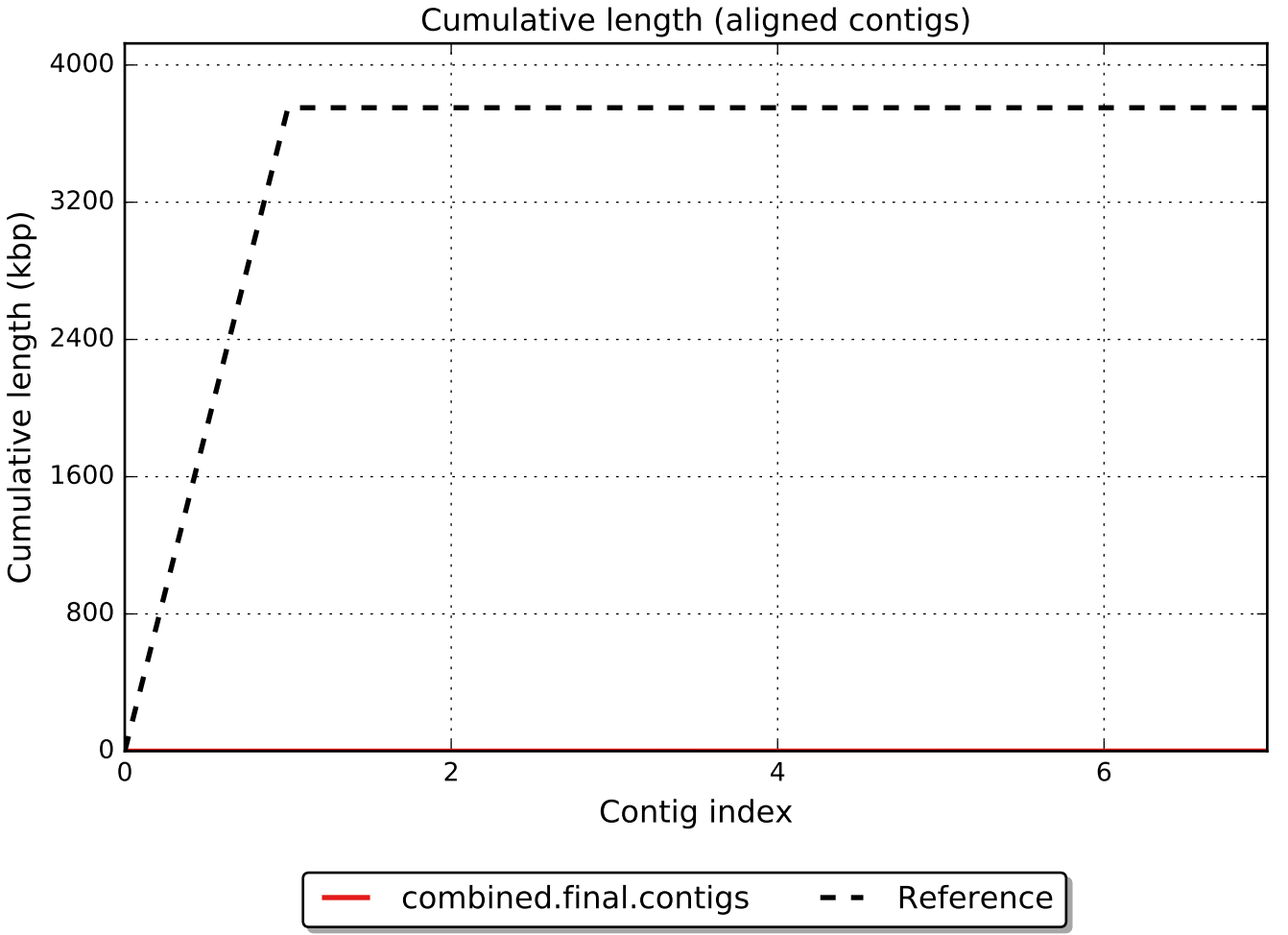

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
2
4
6
Contig index
combined.final.contigs
Reference

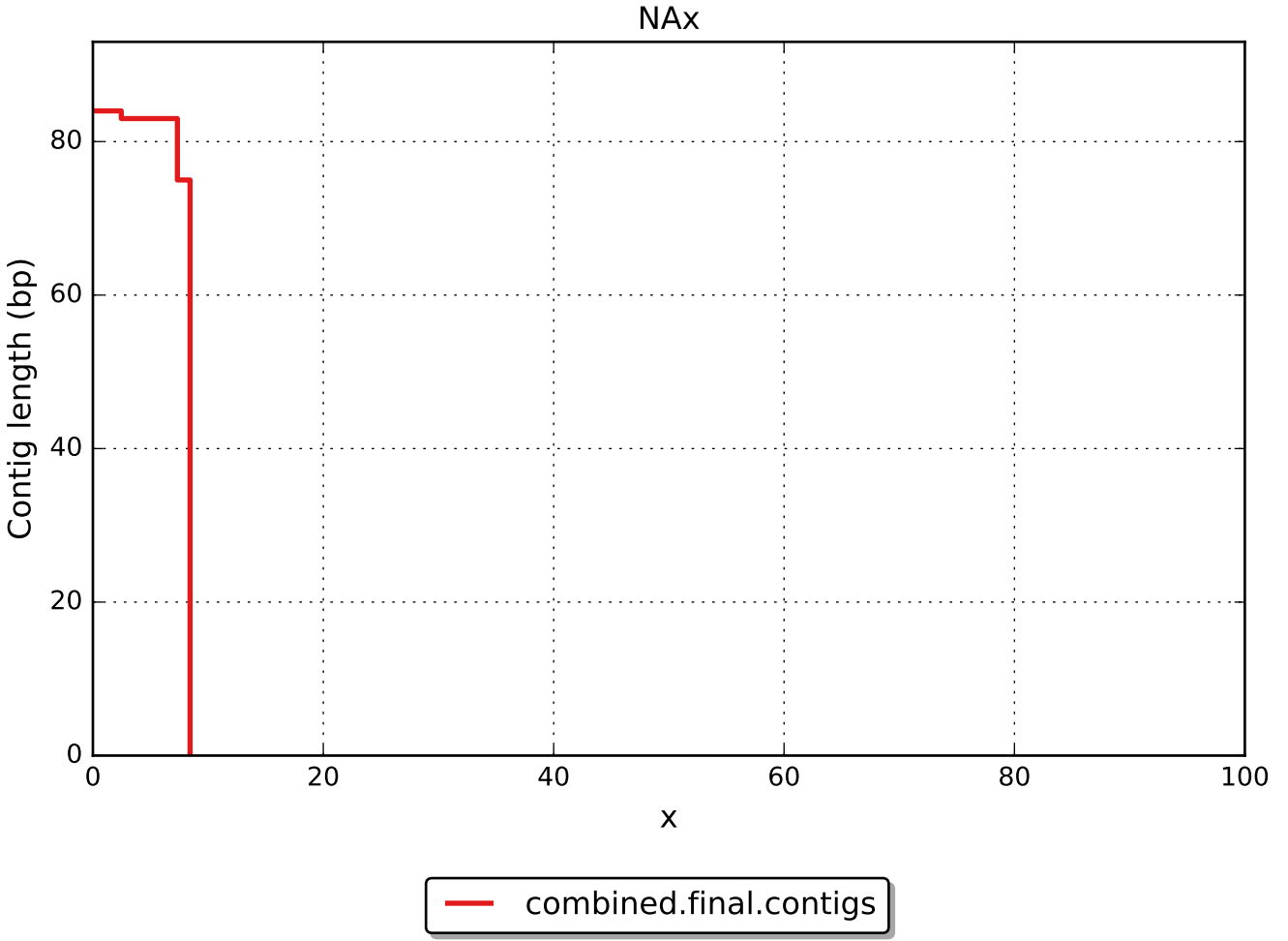

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
combined.final.contigs
Reference

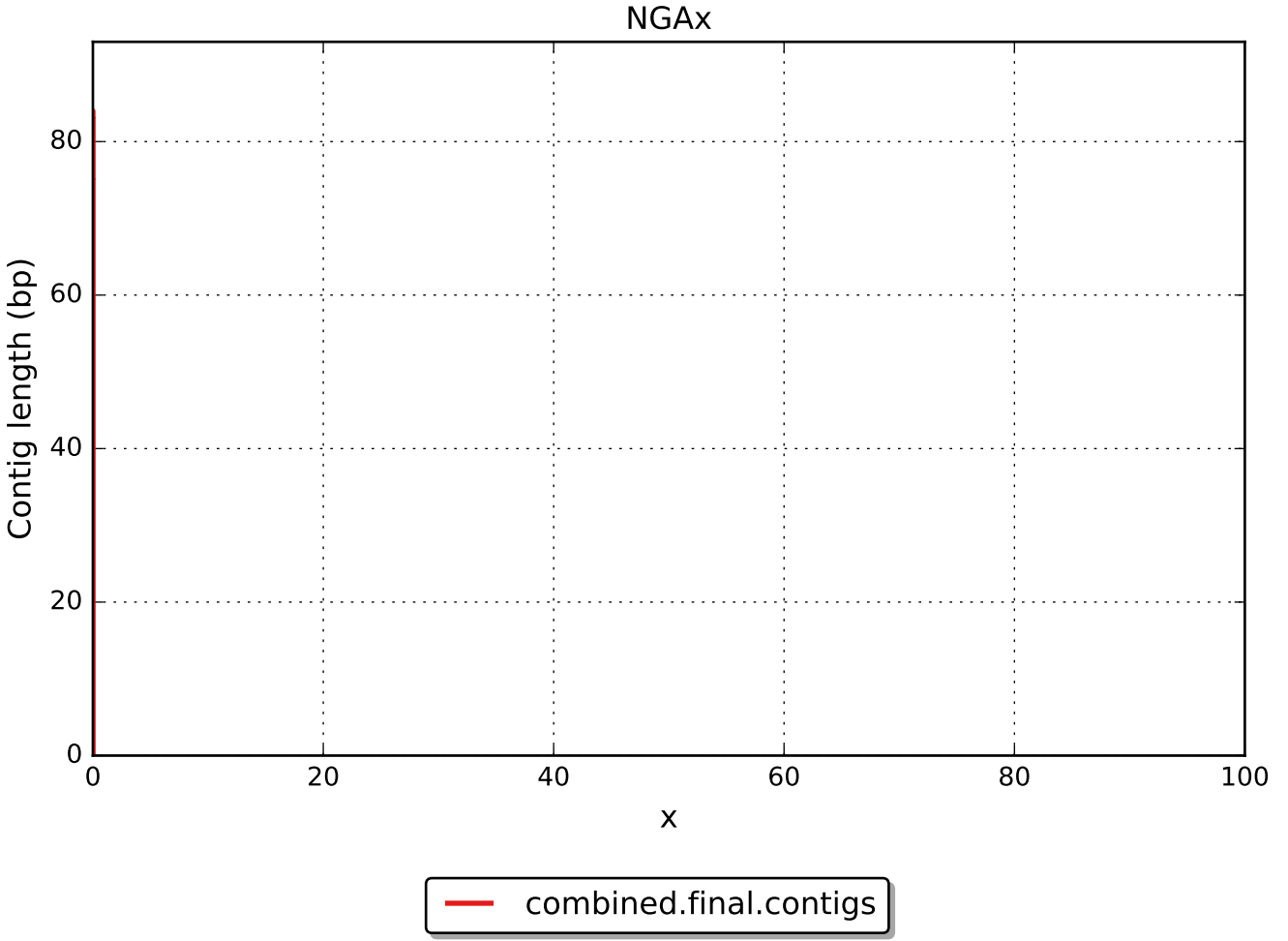

combined.final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
combined.final.contigs


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)
4000
3200
2400
1600
800
0
0
2
4
6
Contig index
combined.final.contigs
Reference


NAx
Contig length (bp)
0
20
40
60
80
0
20
40
60
80
100
x
combined.final.contigs


NGAx
Contig length (bp)
0
20
40
60
80
0
20
40
60
80
100
x
combined.final.contigs