Report

	combined.final.contigs
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	133794
Total length (>= 5000 bp)	131558
Total length (>= 10000 bp)	131558
Total length (>= 25000 bp)	131558
Total length (>= 50000 bp)	89244
# contigs	5
Largest contig	89244
Total length	134965
Reference length	7777997
GC (%)	67.42
Reference GC (%)	50.45
N50	89244
N75	42314
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	133566
Genome fraction (%)	0.002
Duplication ratio	8.799
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1257.86
# indels per 100 kbp	0.00
Largest alignment	82
Total aligned length	388
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

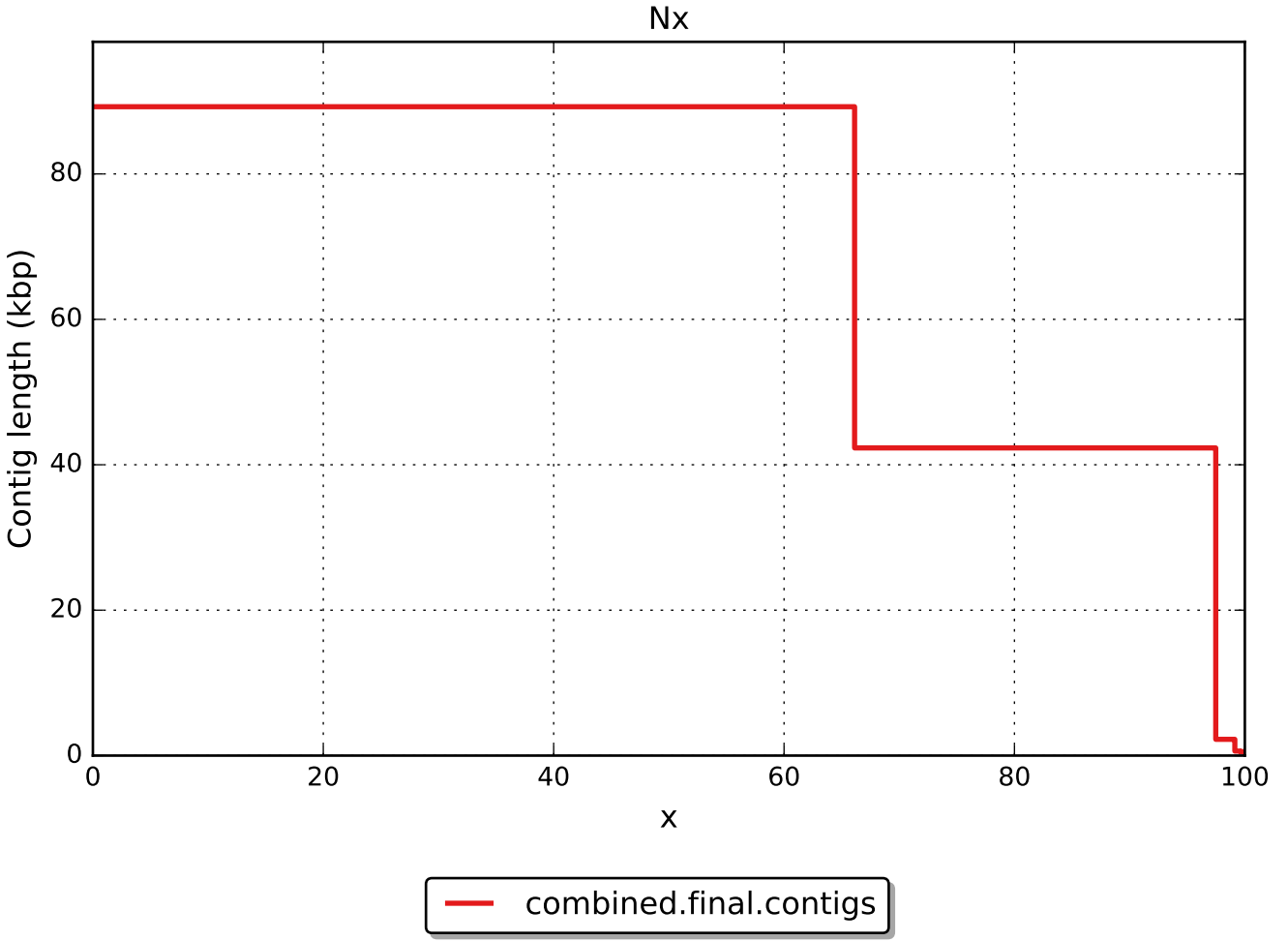
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches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

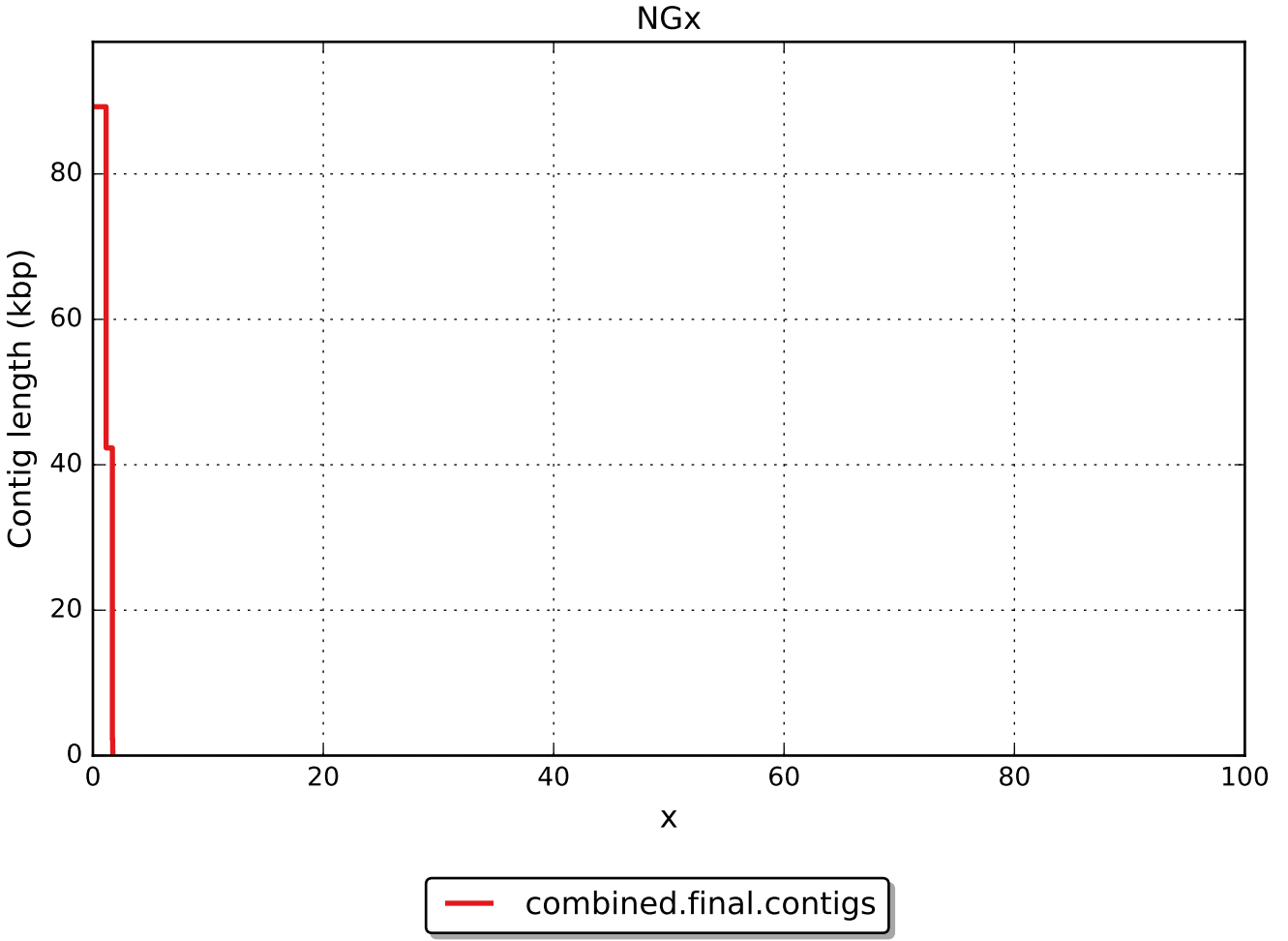
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

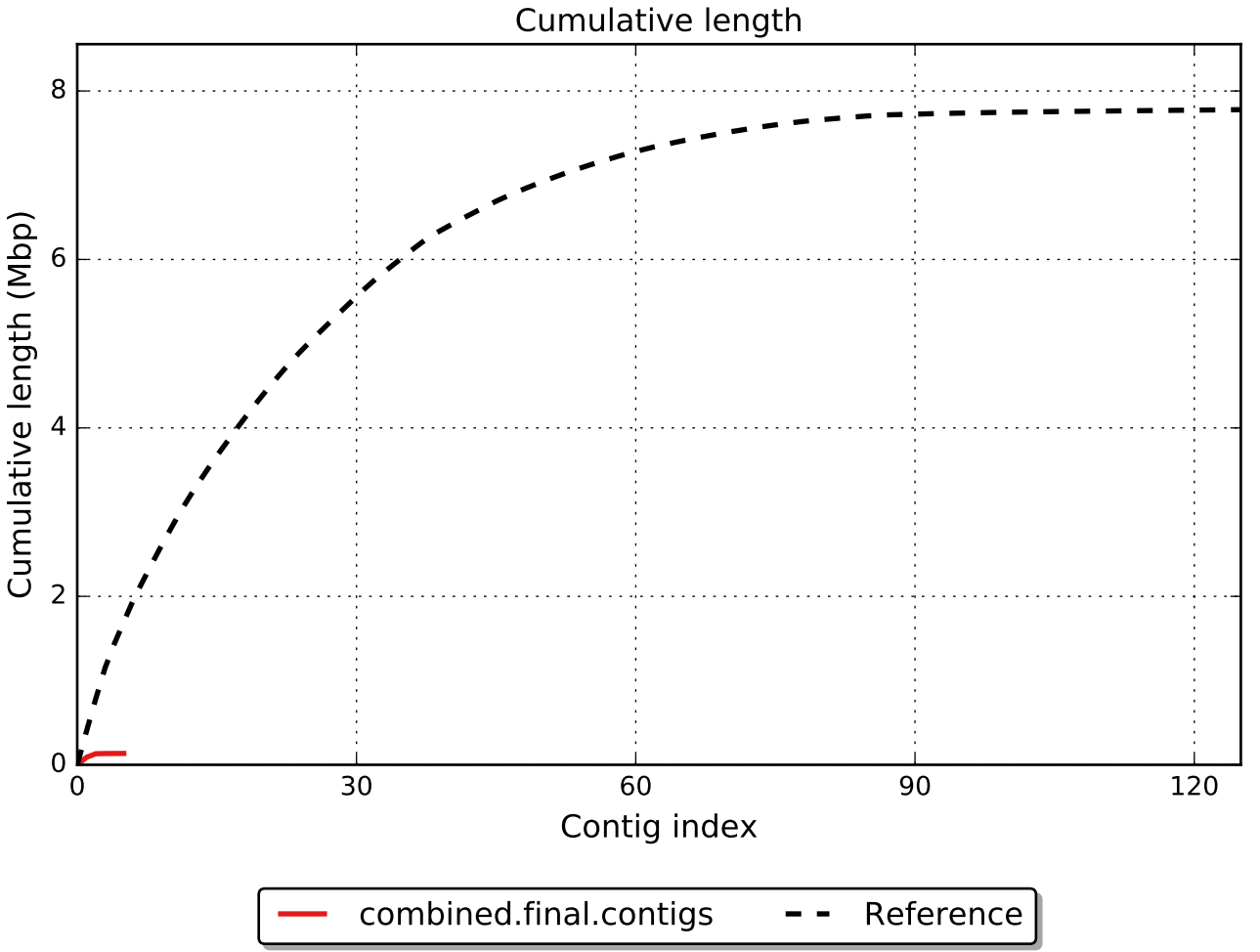
Unaligned report

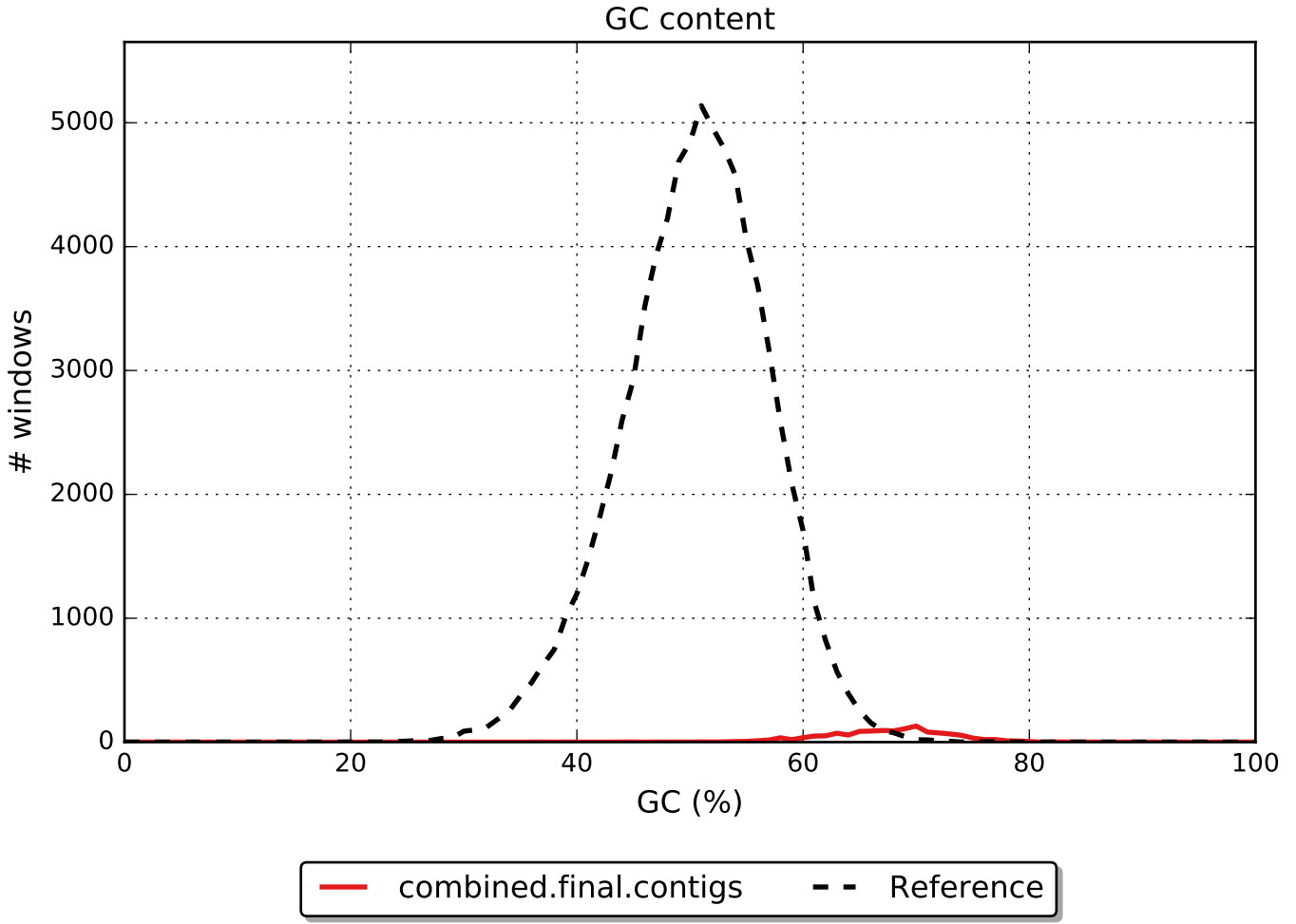
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	133566
# N's	0

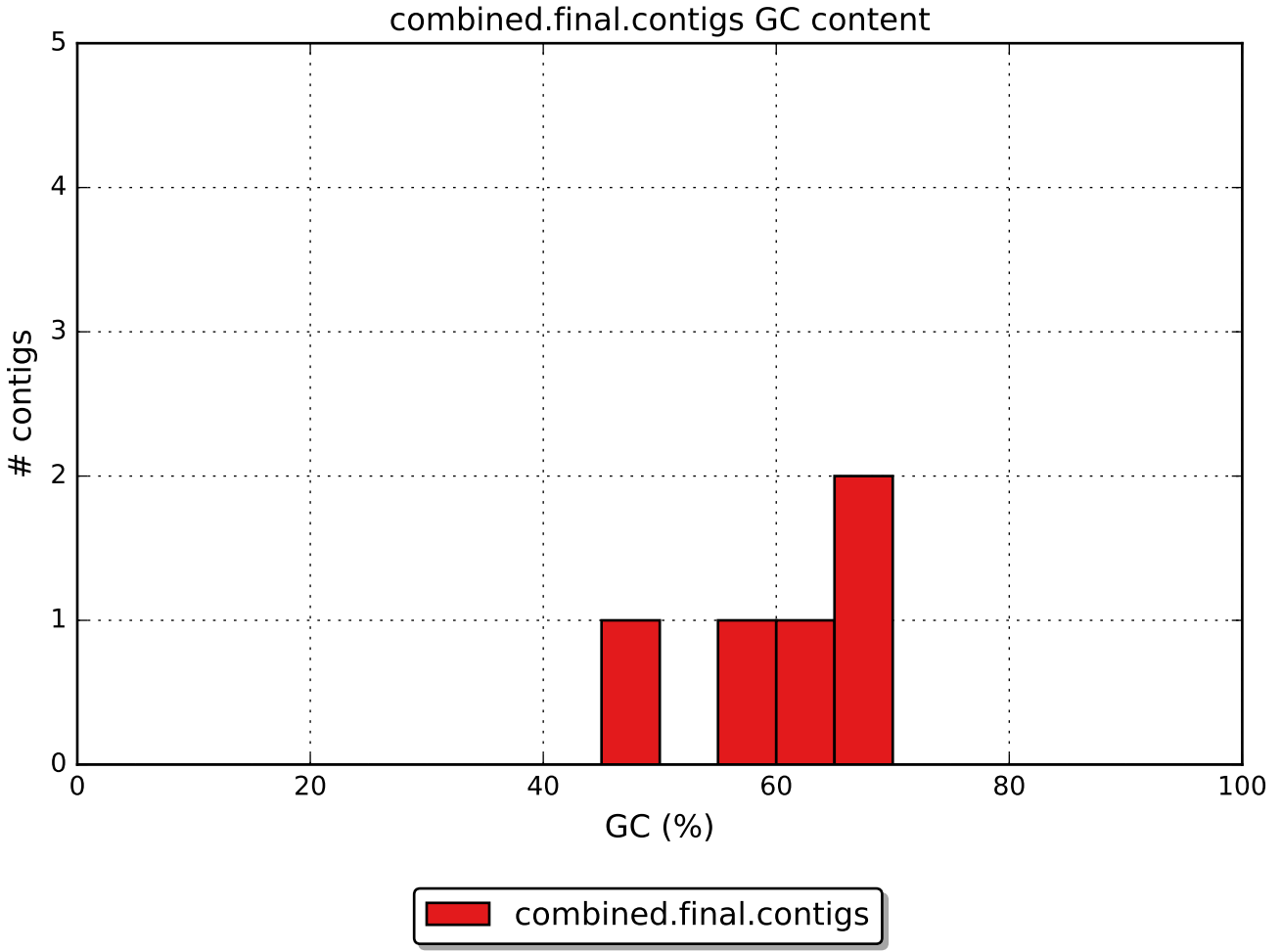
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

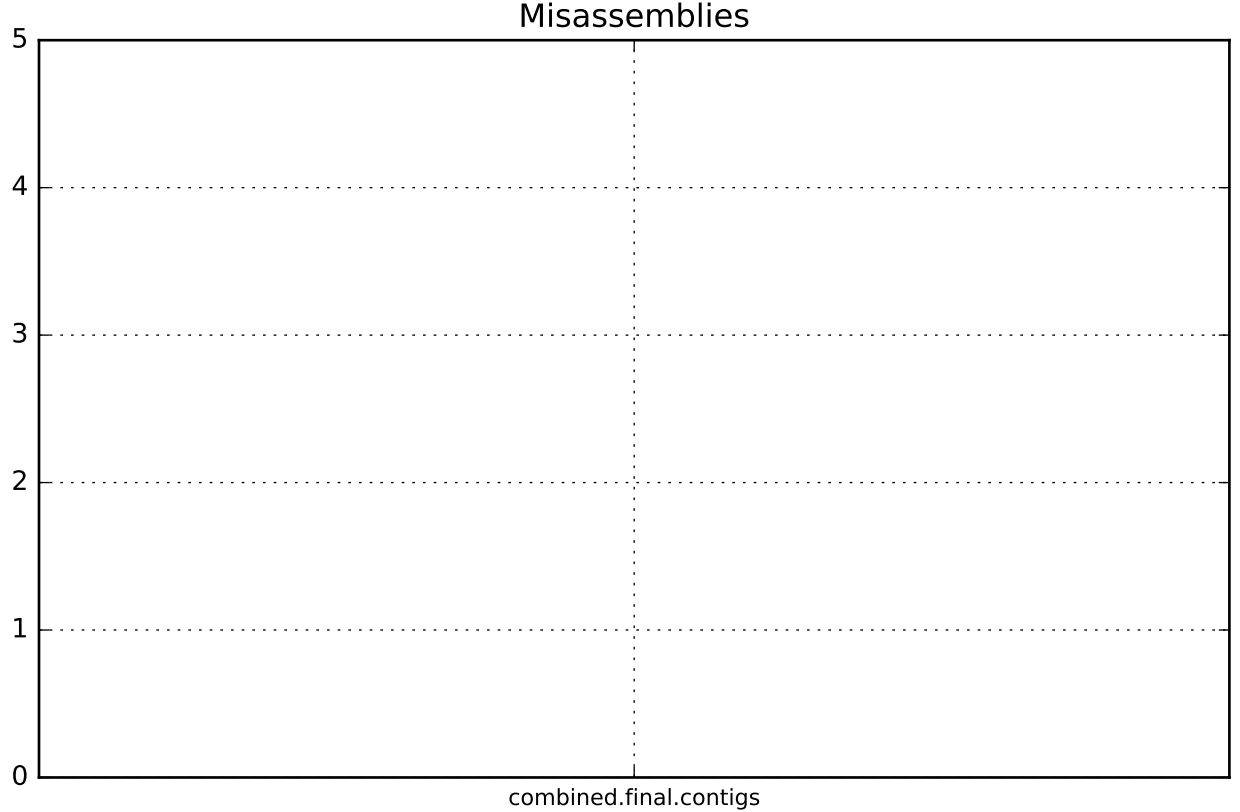

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
combined.final.contigs

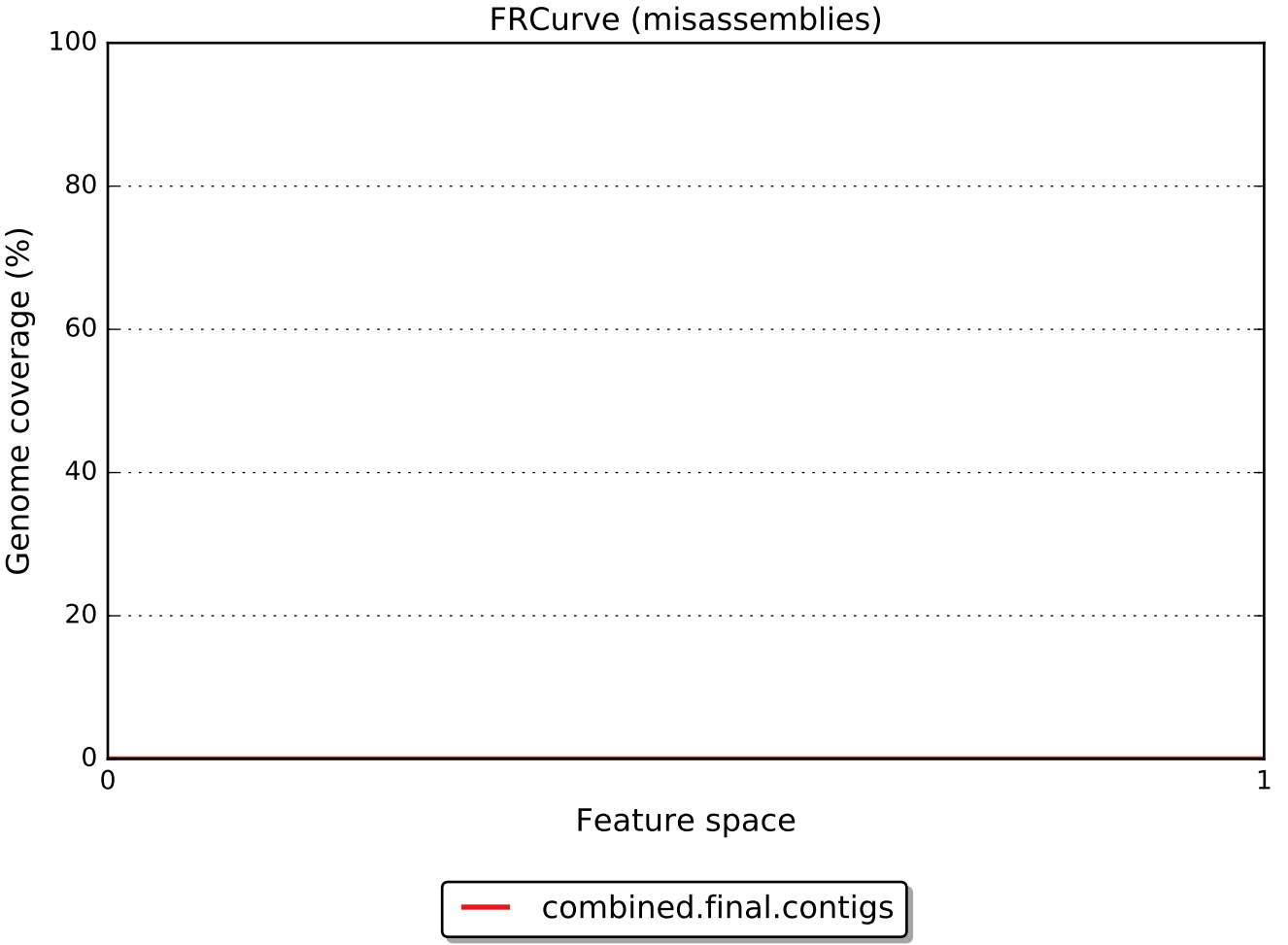

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
combined.final.contigs

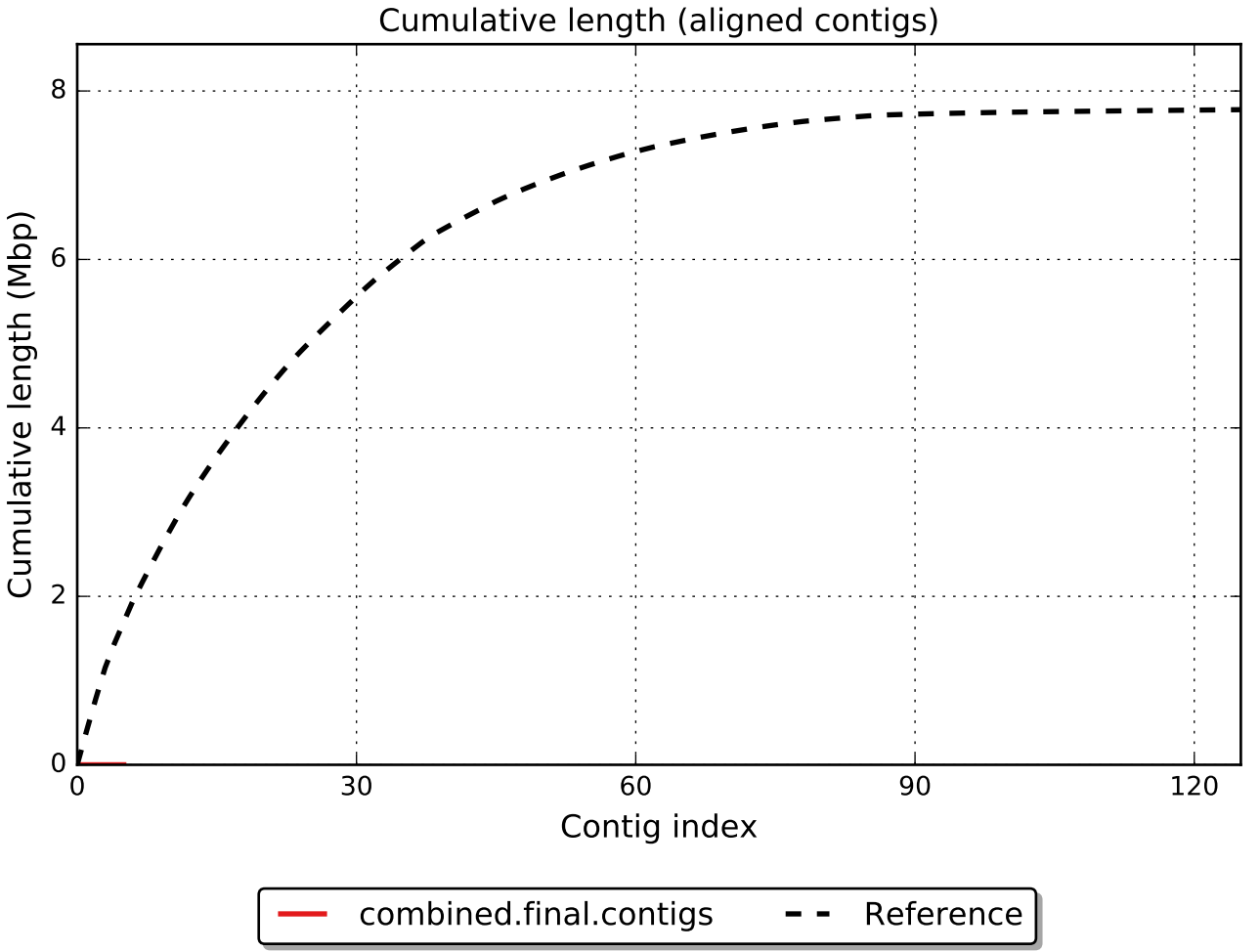

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
0
30
60
90
120
Contig index
combined.final.contigs
Reference

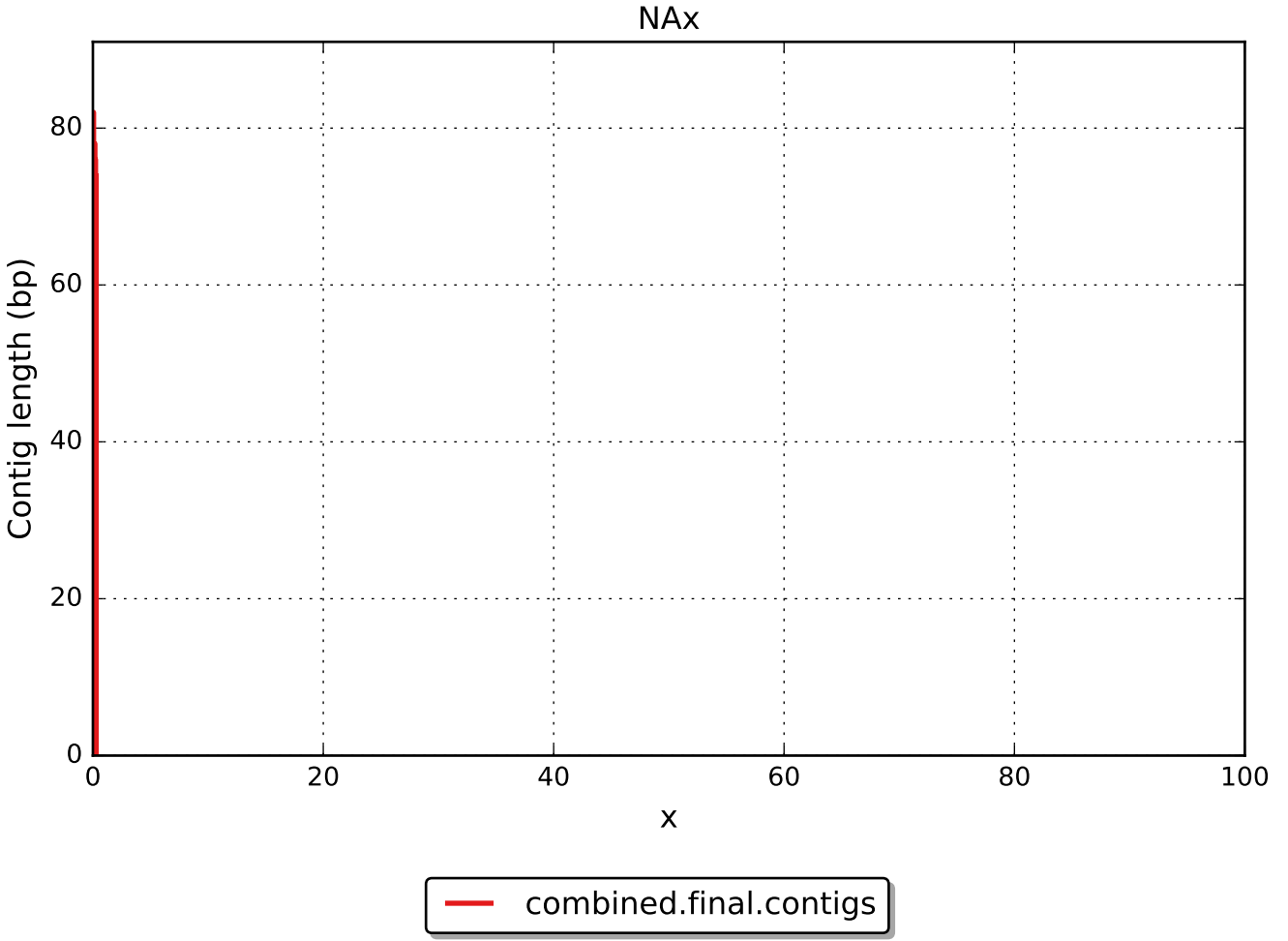

GC content
windows
GC (%)
0
1000
2000
3000
4000
5000
0
20
40
60
80
100
combined.final.contigs
Reference

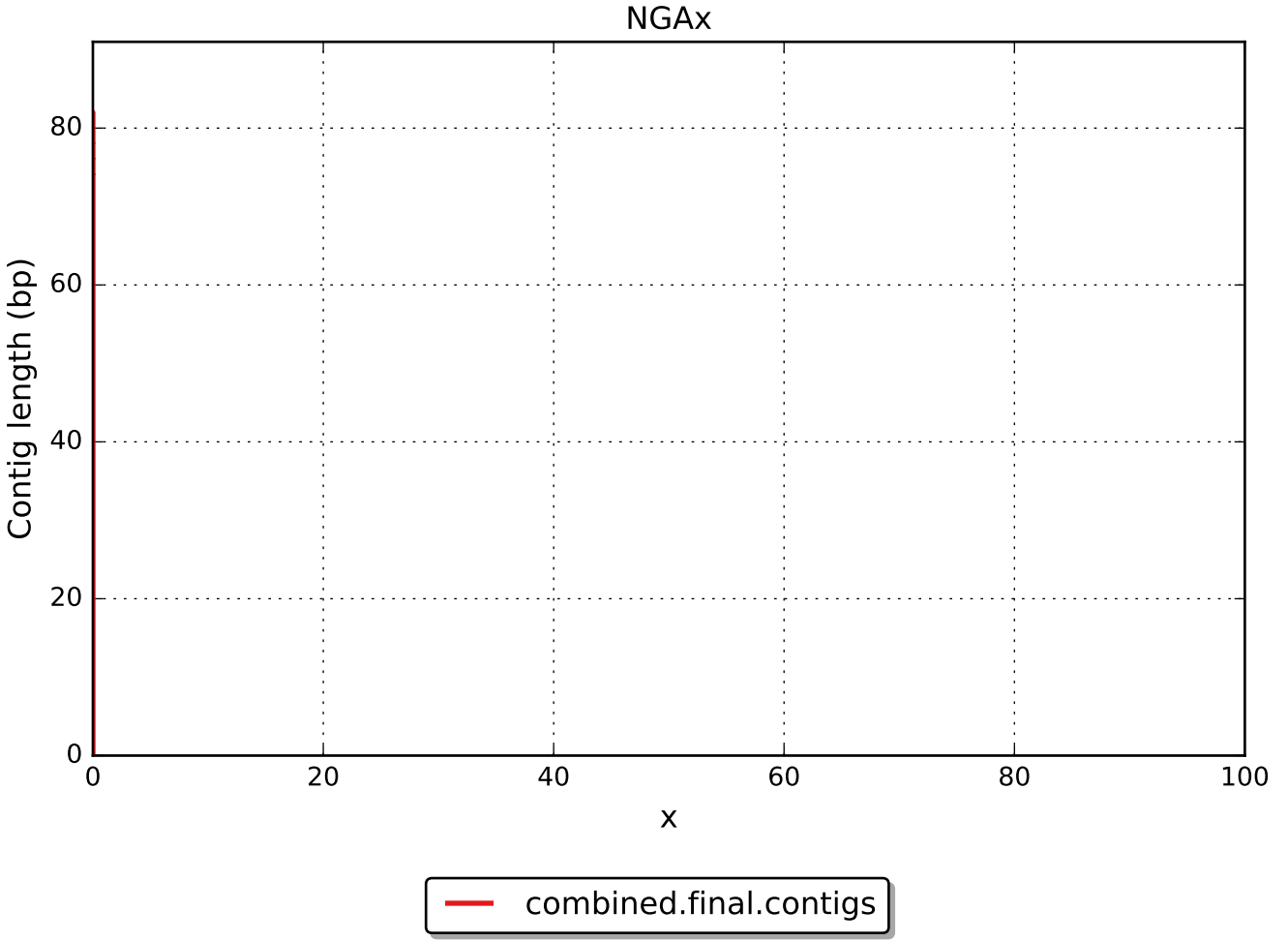

combined.final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
combined.final.contigs


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 (Mbp)
0
2
4
6
8
0
30
60
90
120
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