Report

	canu.contigs
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2636043
Total length (>= 1000 bp)	2636043
Total length (>= 5000 bp)	2633446
Total length (>= 10000 bp)	2633446
Total length (>= 25000 bp)	2612303
Total length (>= 50000 bp)	2563357
# contigs	4
Largest contig	2563357
Total length	2636043
Reference length	2610531
GC (%)	54.06
Reference GC (%)	54.14
N50	2563357
NG50	2563357
N75	2563357
NG75	2563357
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2563357
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 0 part
Unaligned length	51543
Genome fraction (%)	97.566
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	5.89
Largest alignment	1463673
Total aligned length	2584500
NA50	1463673
NGA50	1463673
NA75	1099684
NGA75	1099684
LA50	1
LGA50	1
LA75	2
LGA75	2

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

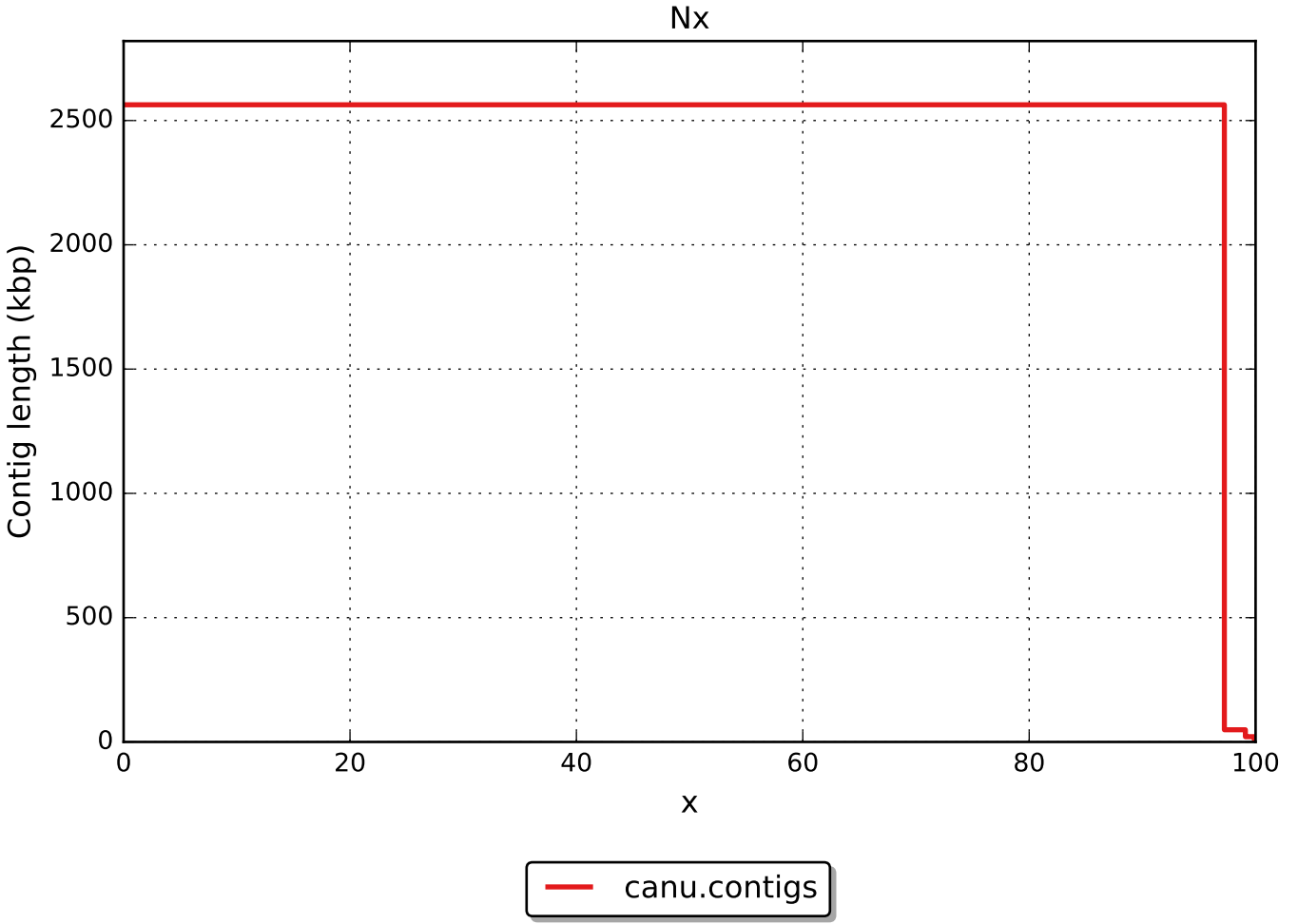
	canu.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2563357
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	150
# indels (<= 5 bp)	150
# indels (> 5 bp)	0
Indels length	153

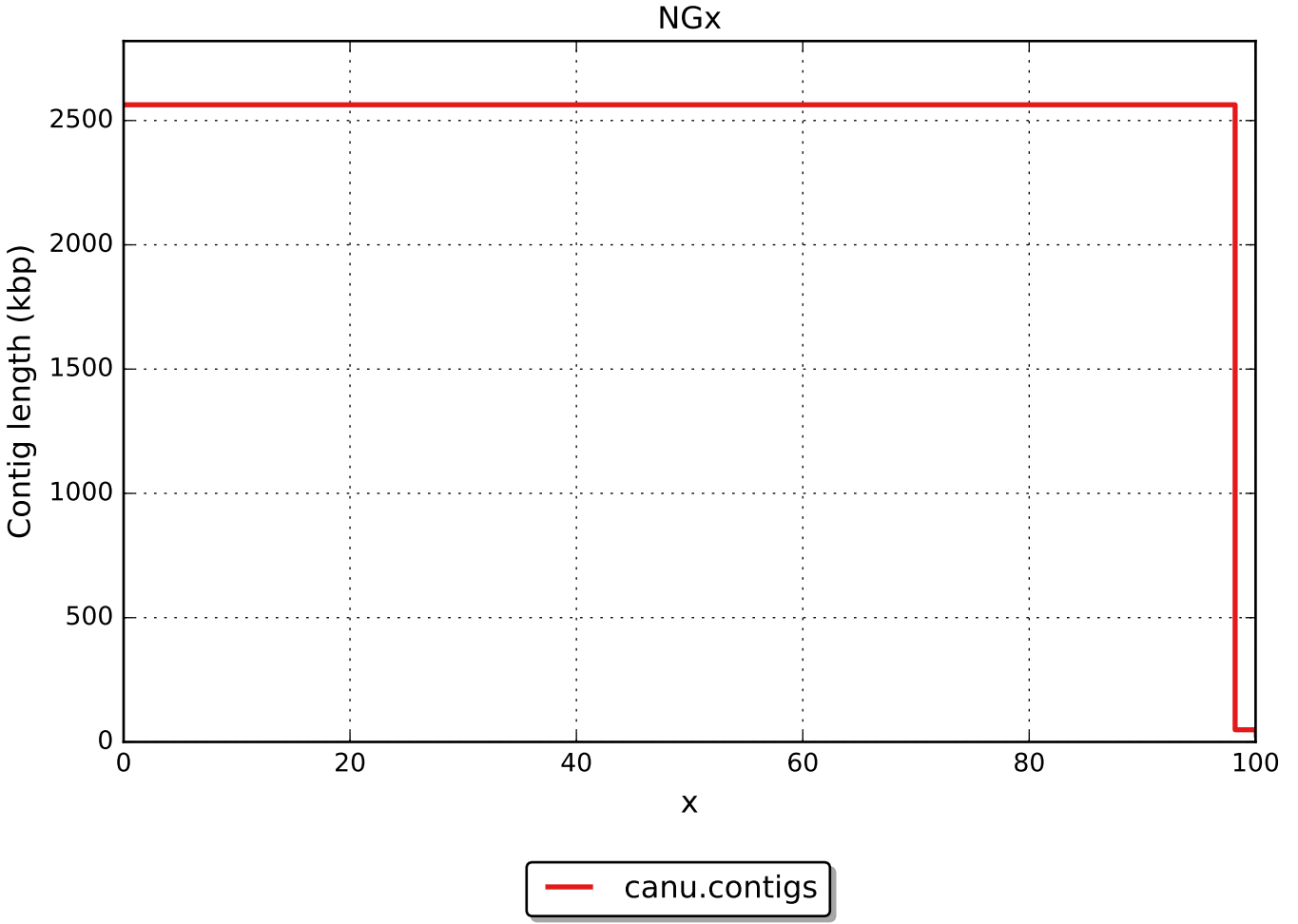
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

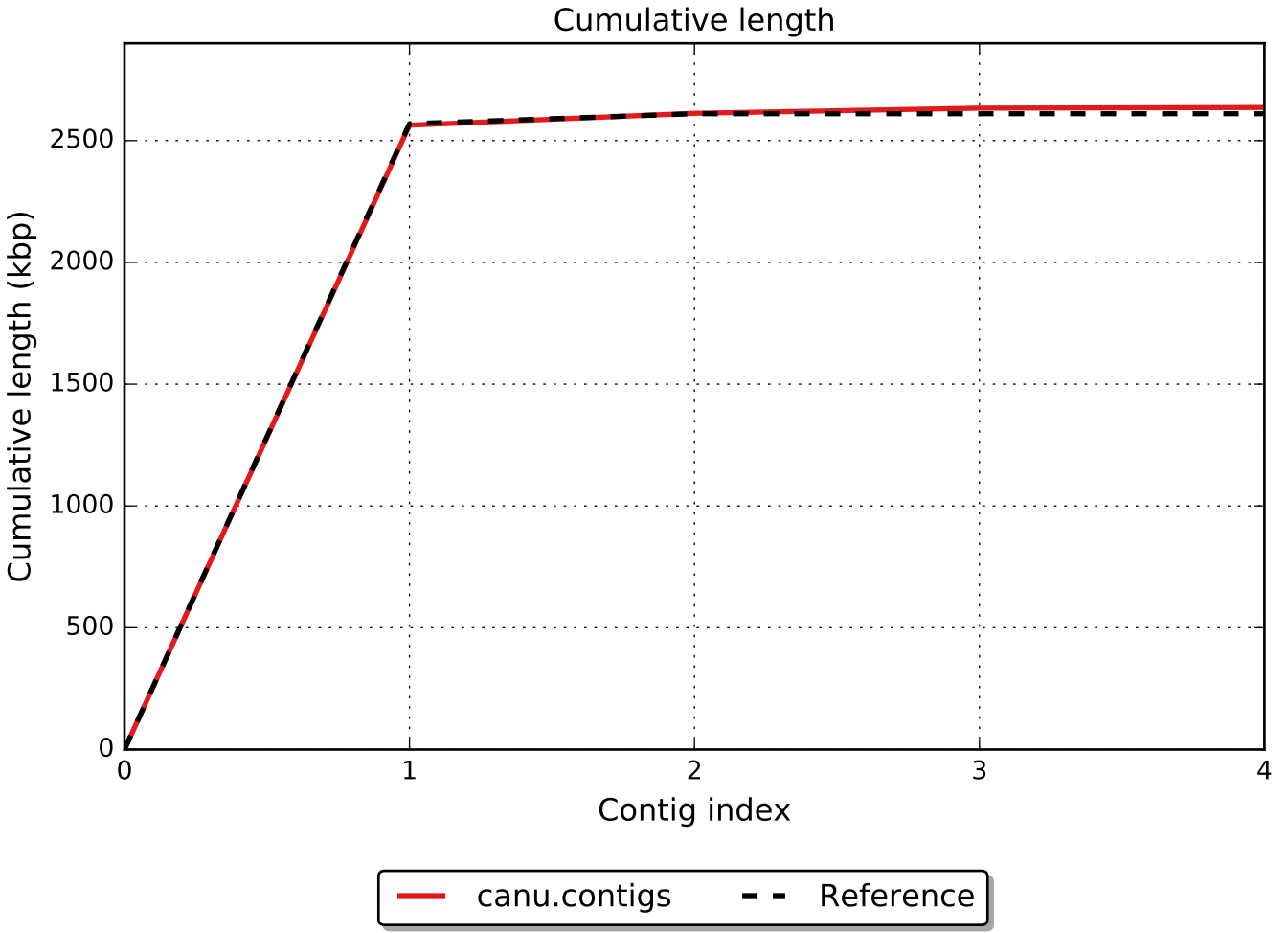
Unaligned report

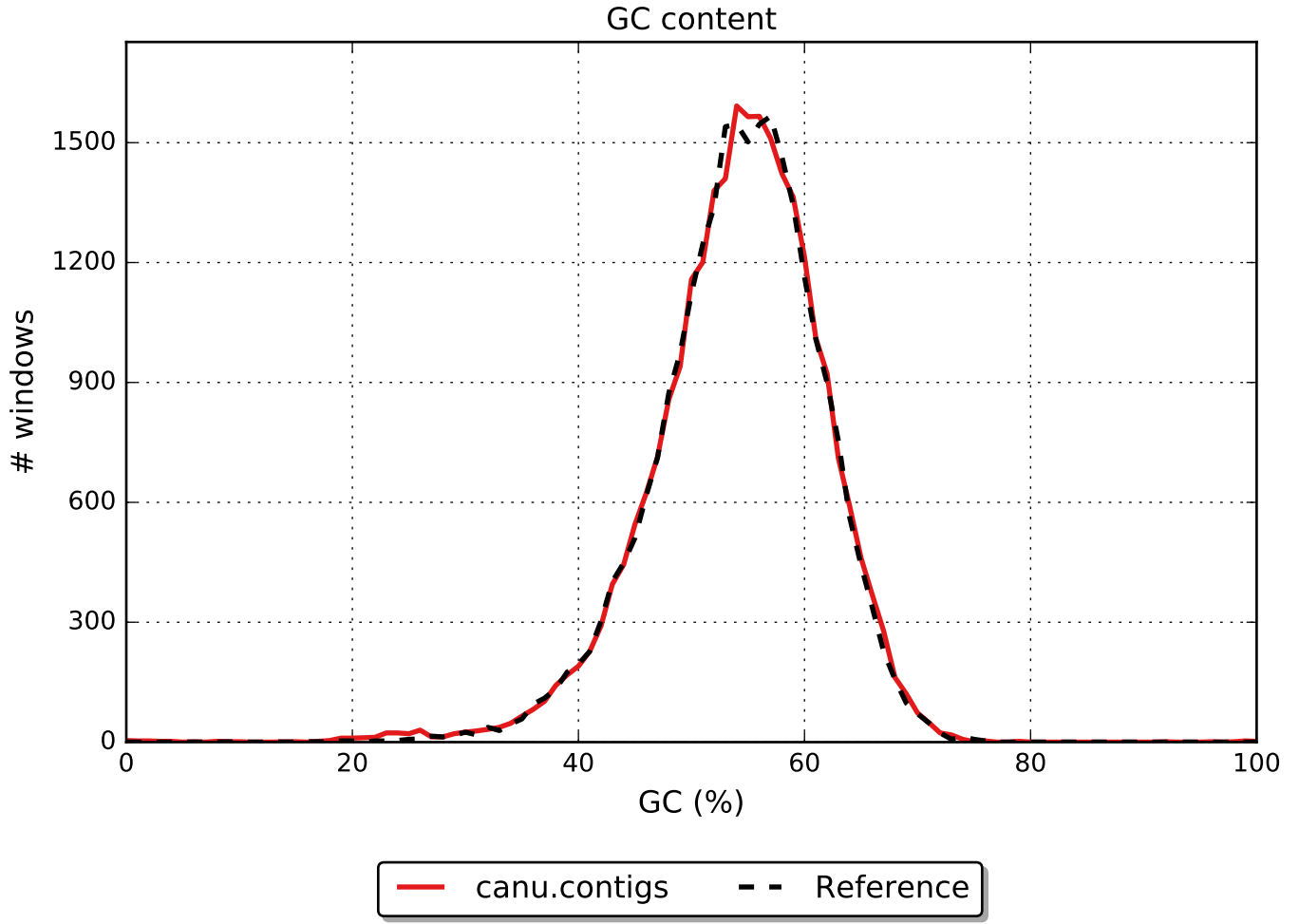
	canu.contigs
# fully unaligned contigs	2
Fully unaligned length	51543
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

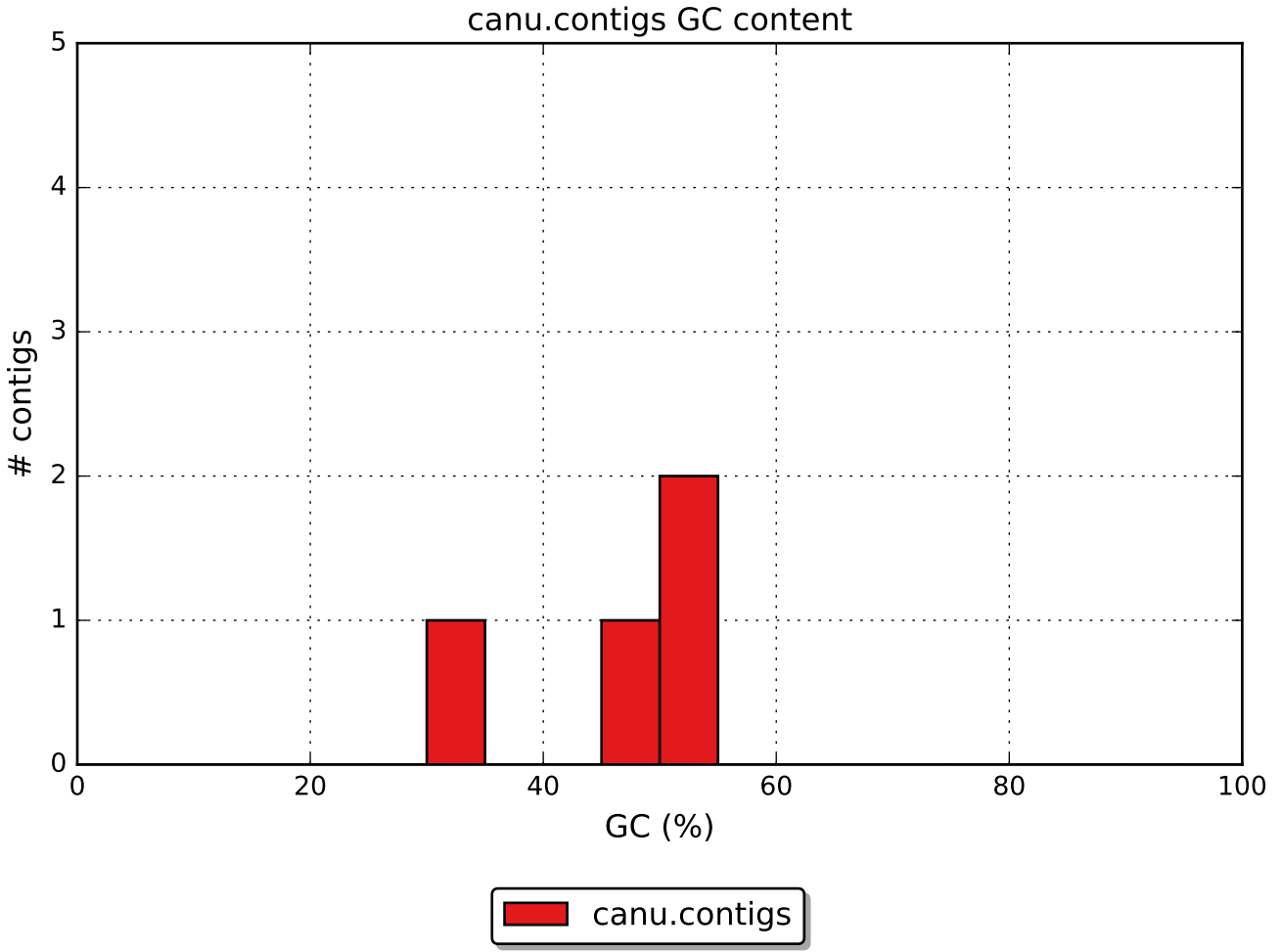
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

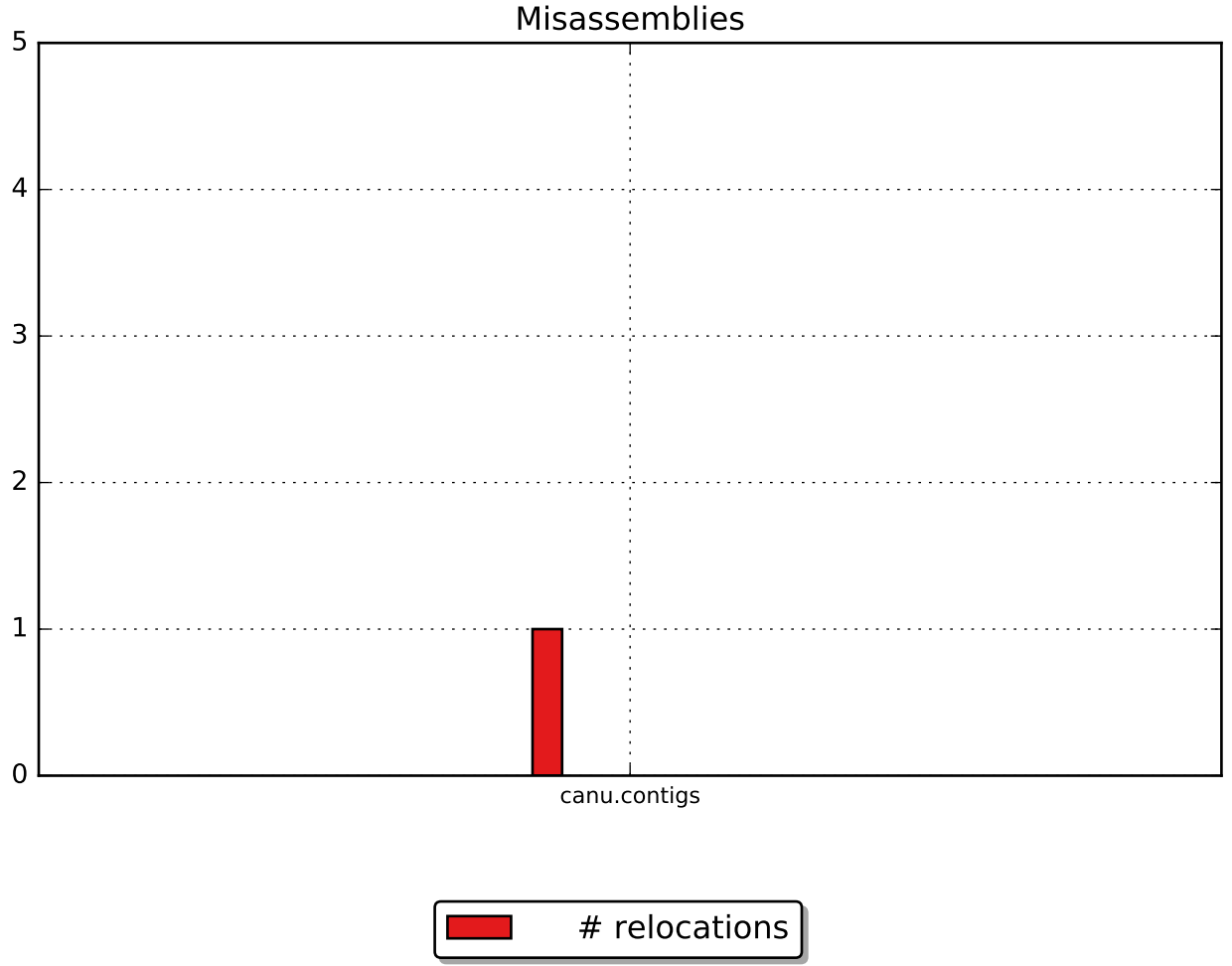

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
canu.contigs

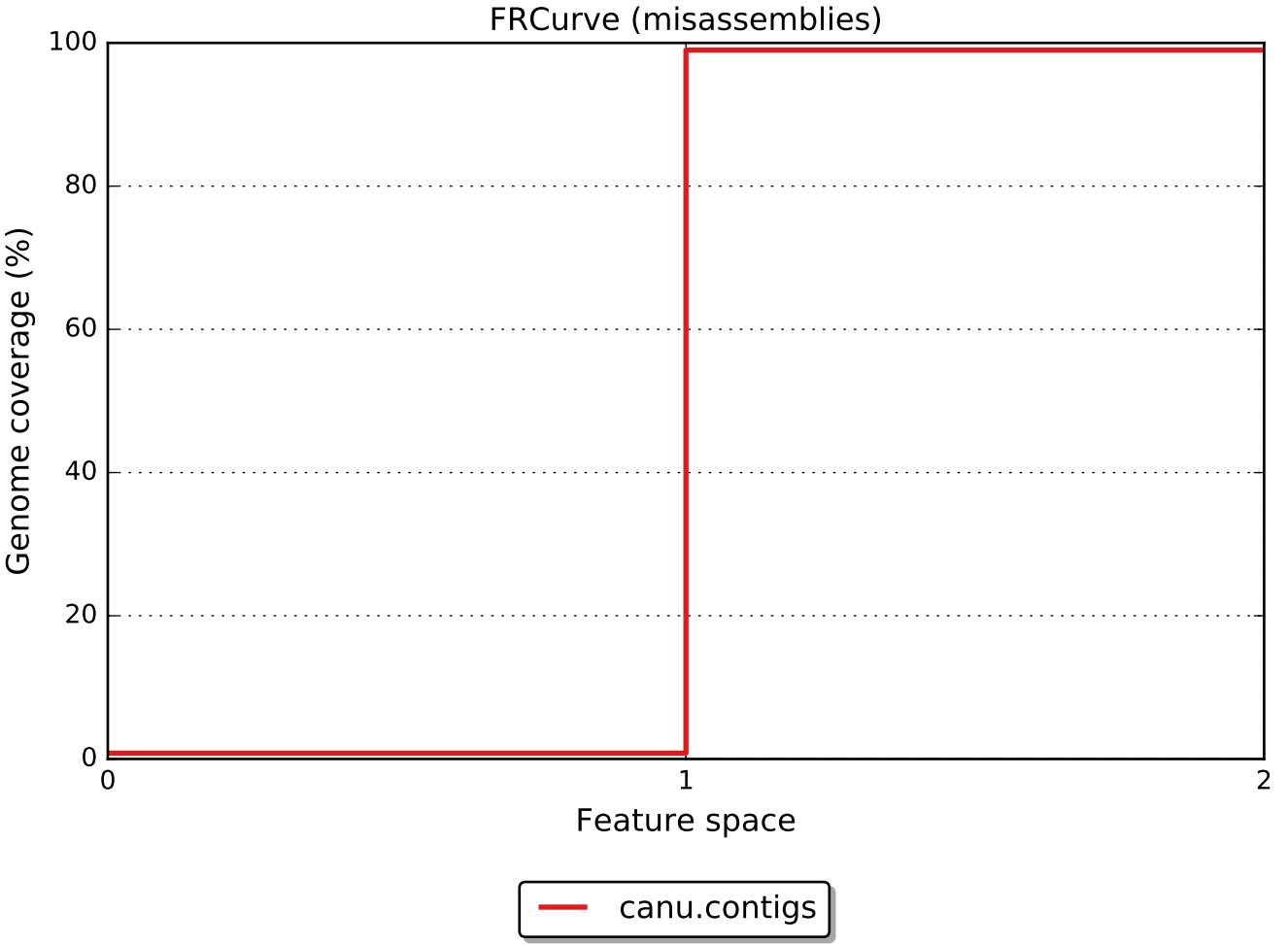

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
canu.contigs

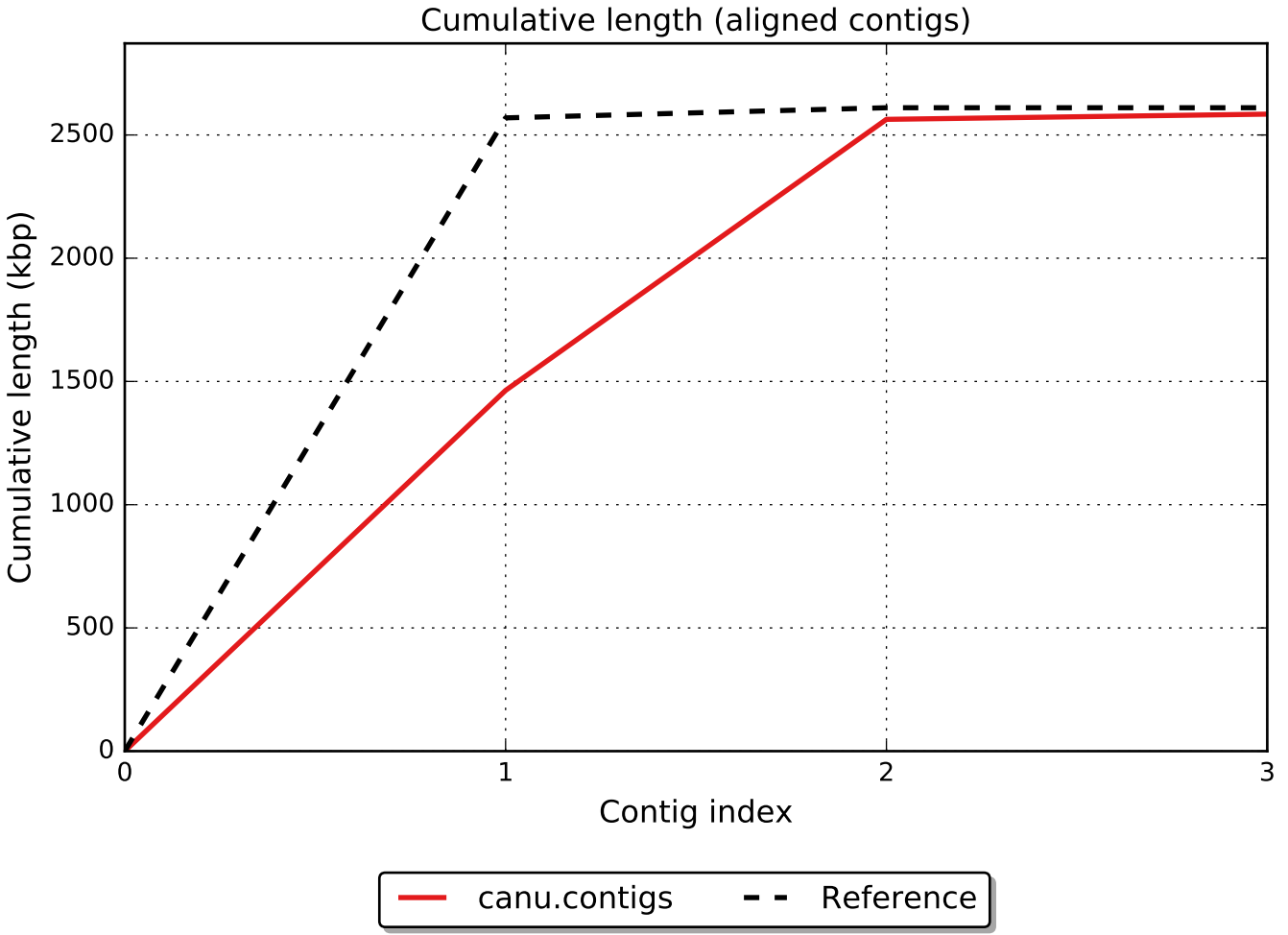

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
3
4
Contig index
canu.contigs
Reference

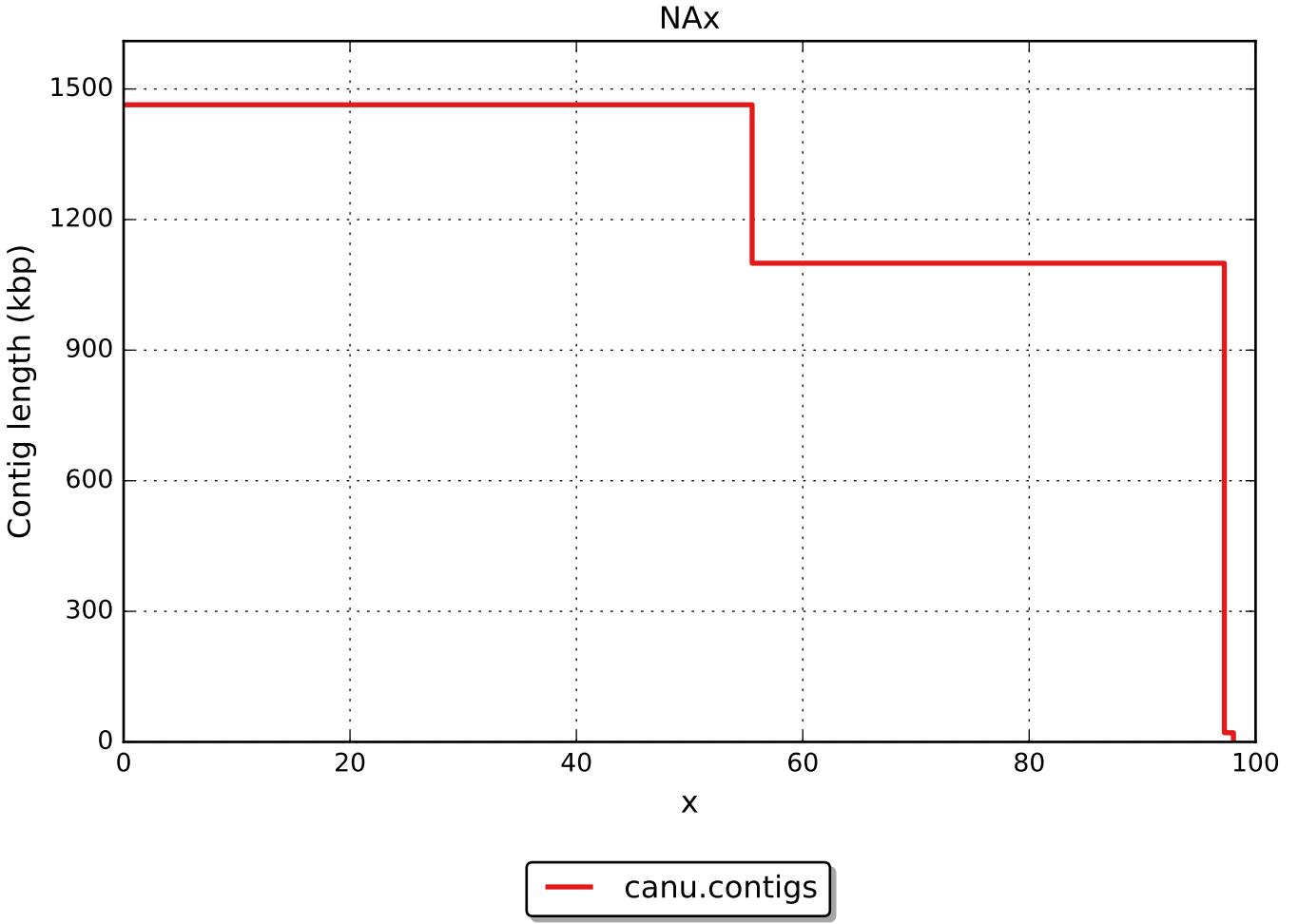

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
canu.contigs
Reference

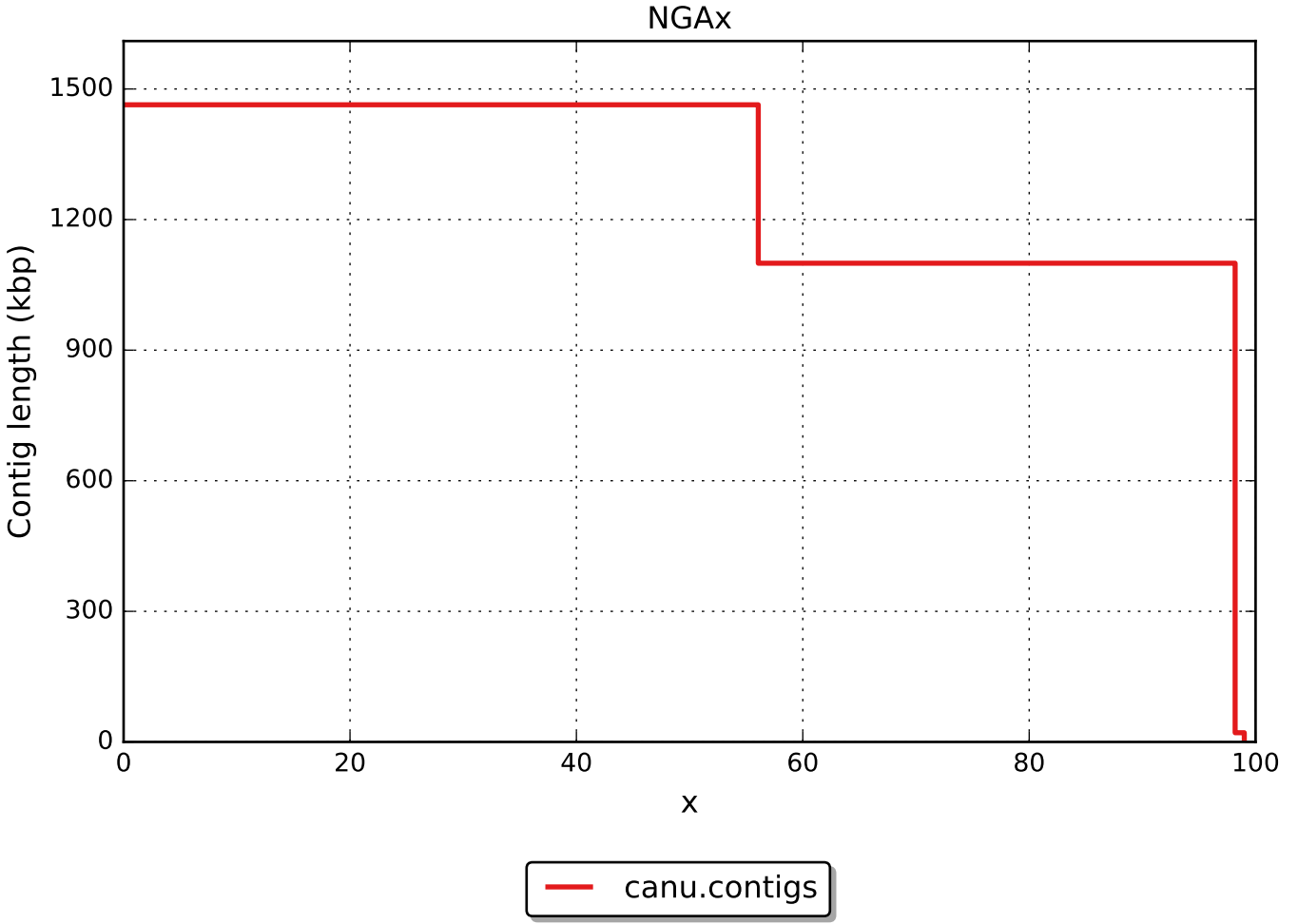

canu.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
canu.contigs


Misassemblies
5
4
3
2
1
0
canu.contigs
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
canu.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
3
Contig index
canu.contigs
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
canu.contigs


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
canu.contigs