Report

	lferriphilum_1contig
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2577733
Total length (>= 1000 bp)	2577733
Total length (>= 5000 bp)	2577733
Total length (>= 10000 bp)	2577733
Total length (>= 25000 bp)	2577733
Total length (>= 50000 bp)	2577733
# contigs	1
Largest contig	2577733
Total length	2577733
Reference length	2632898
GC (%)	54.22
Reference GC (%)	54.70
N50	2577733
NG50	2577733
N75	2577733
NG75	2577733
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	2235857
Genome fraction (%)	12.963
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3031.64
# indels per 100 kbp	81.16
Largest alignment	176539
Total aligned length	341904
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

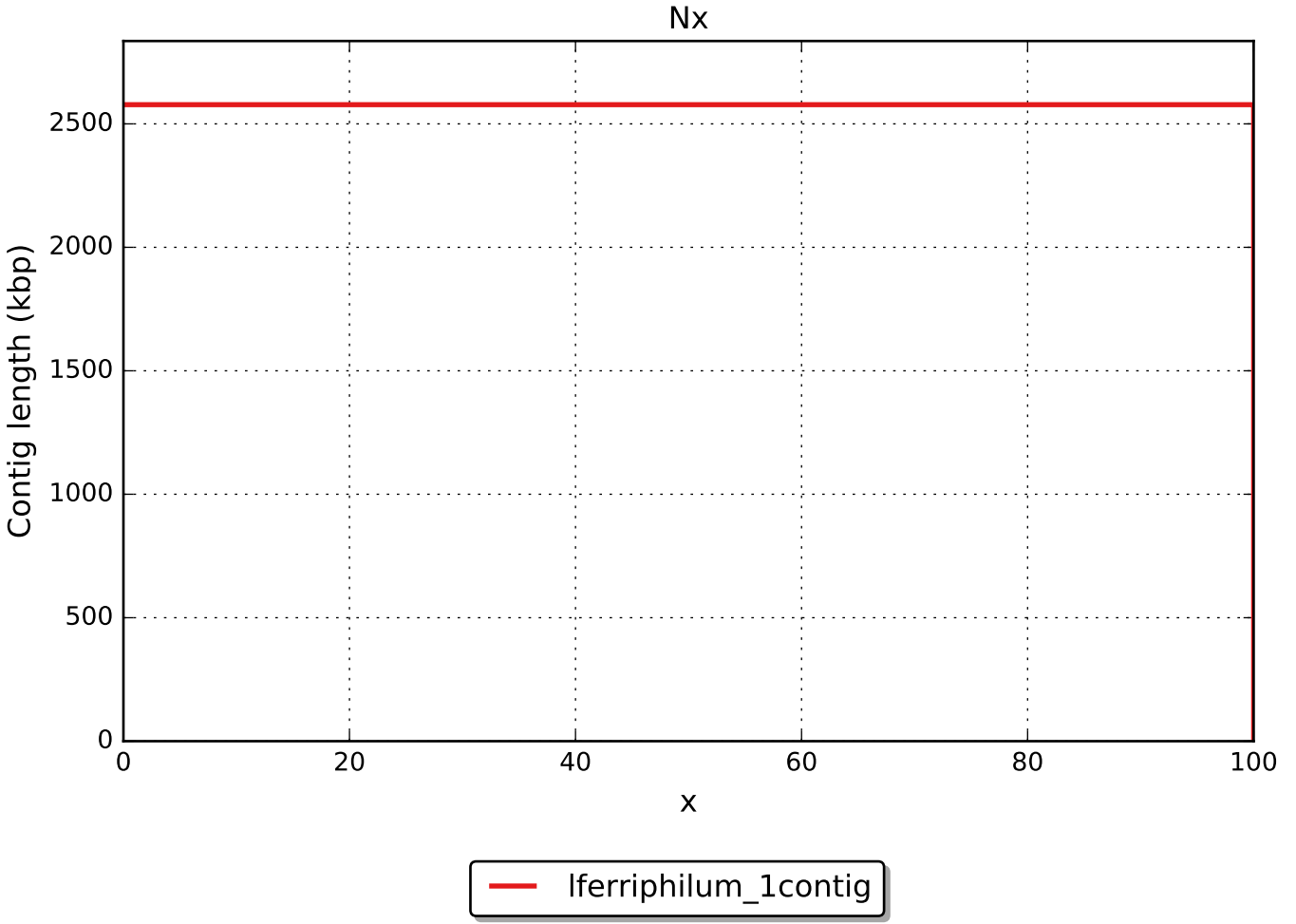
	lferriphilum_1contig
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	10347
# indels	277
# indels (<= 5 bp)	262
# indels (> 5 bp)	15
Indels length	491

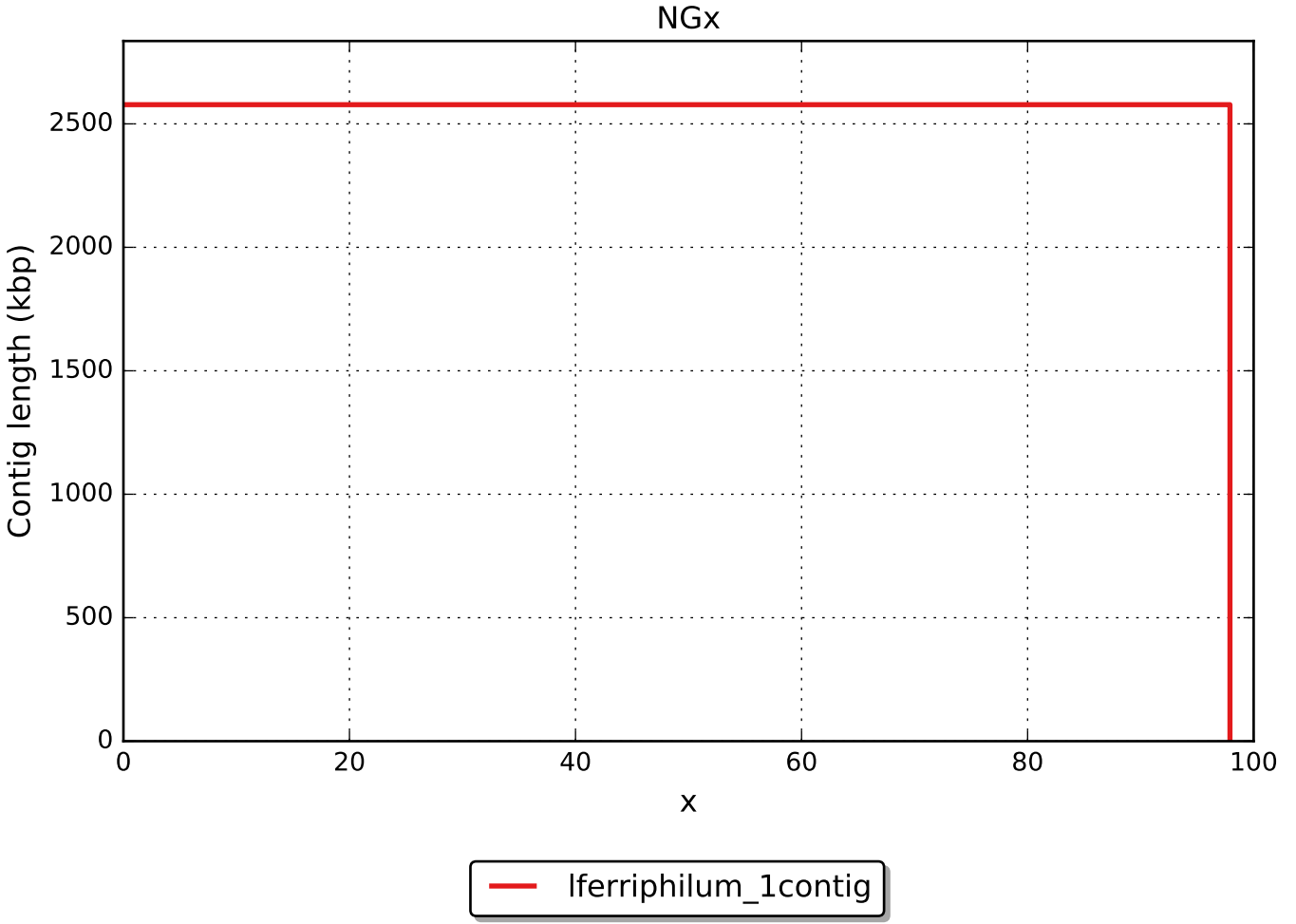
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

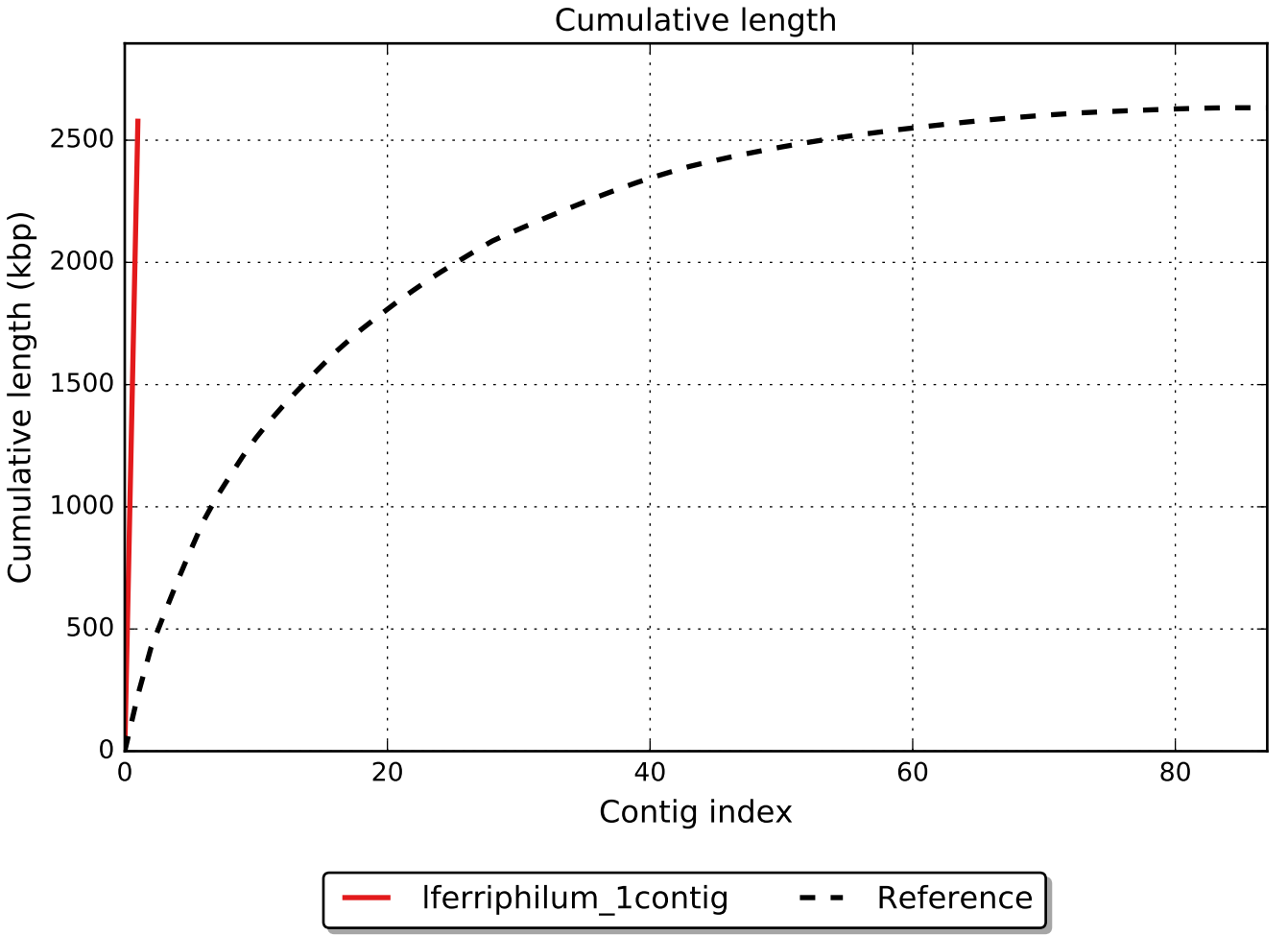
Unaligned report

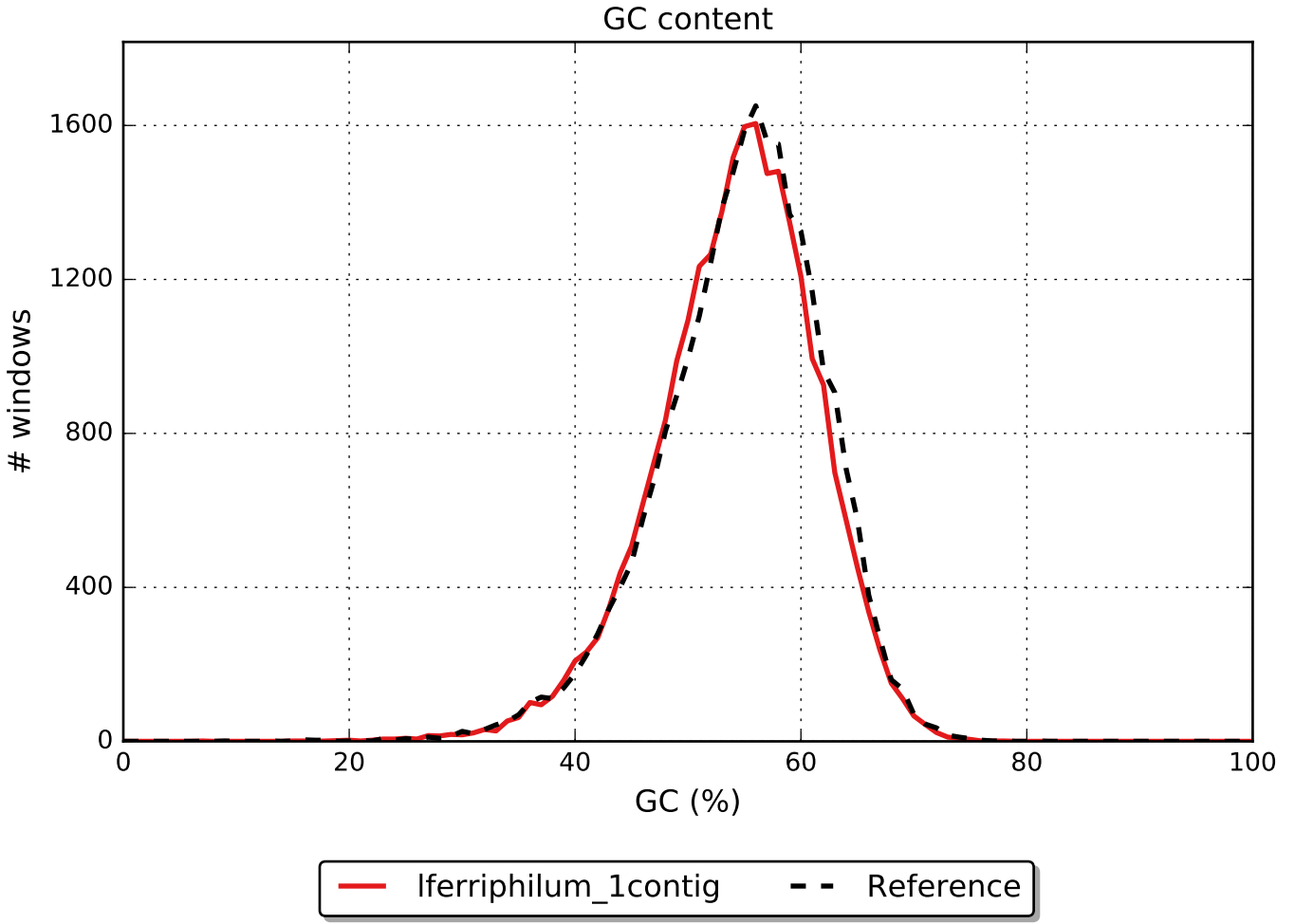
	lferriphilum_1contig
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	2235857
# N's	0

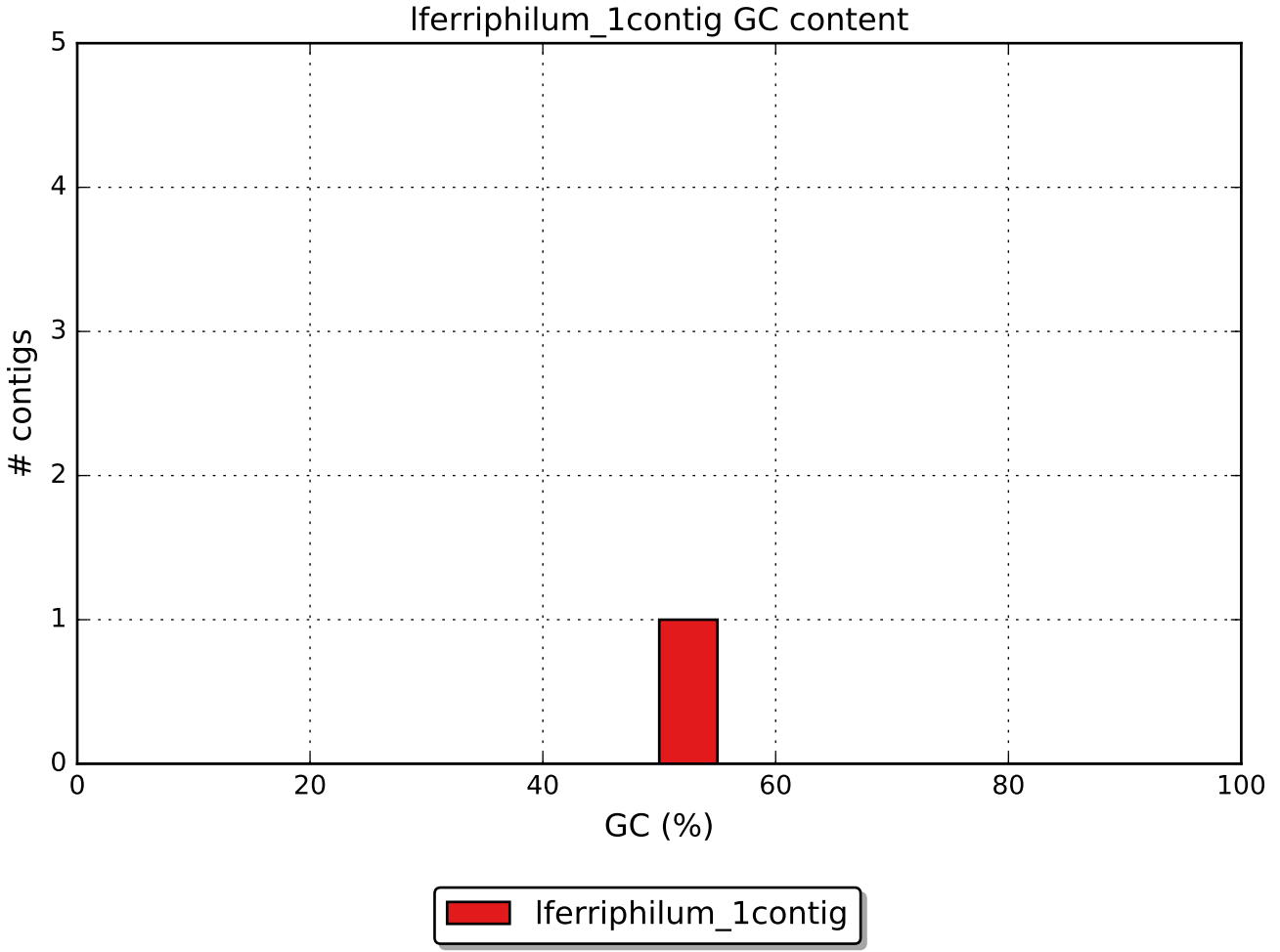
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

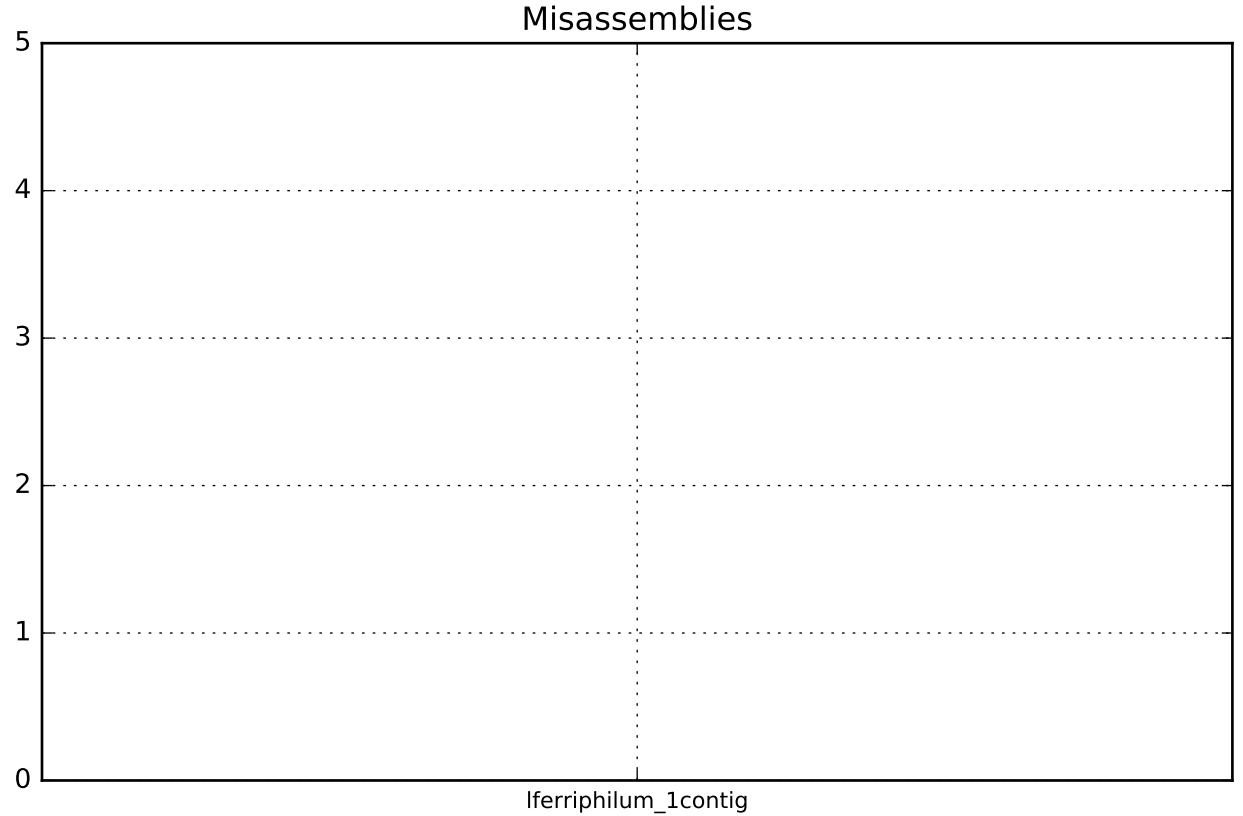

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
lferriphilum_1contig

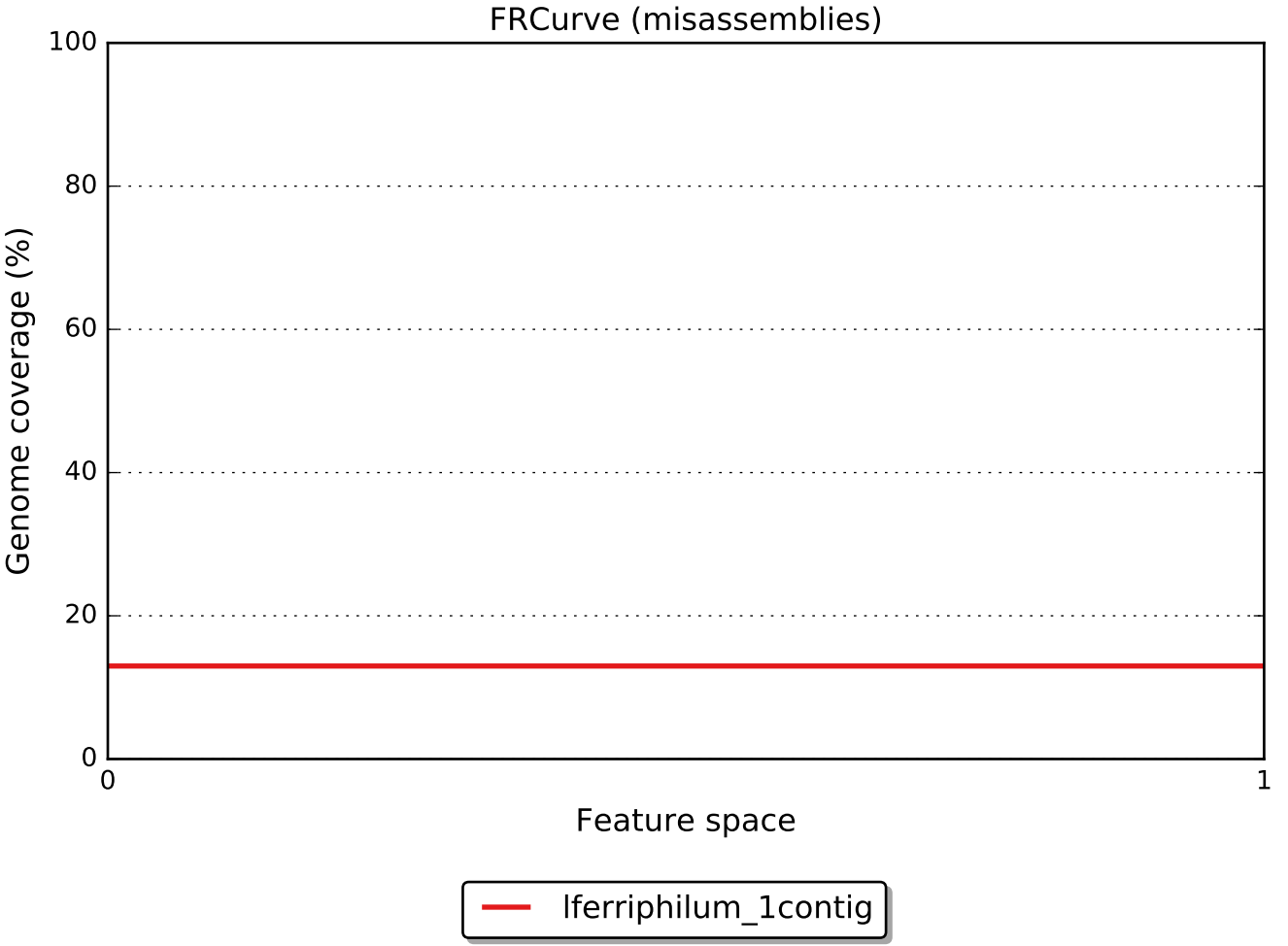

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
lferriphilum_1contig

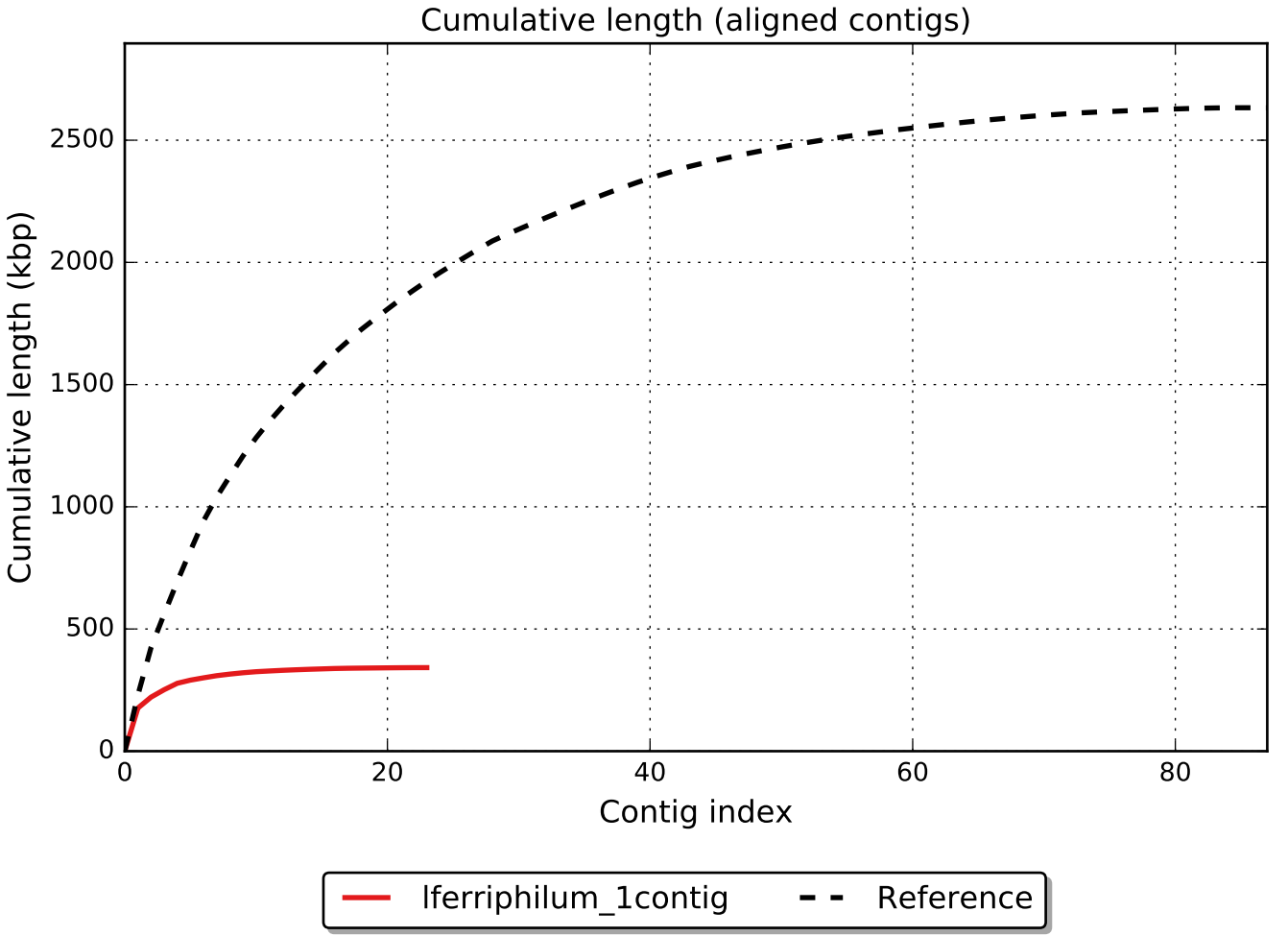

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
Contig index
lferriphilum_1contig
Reference

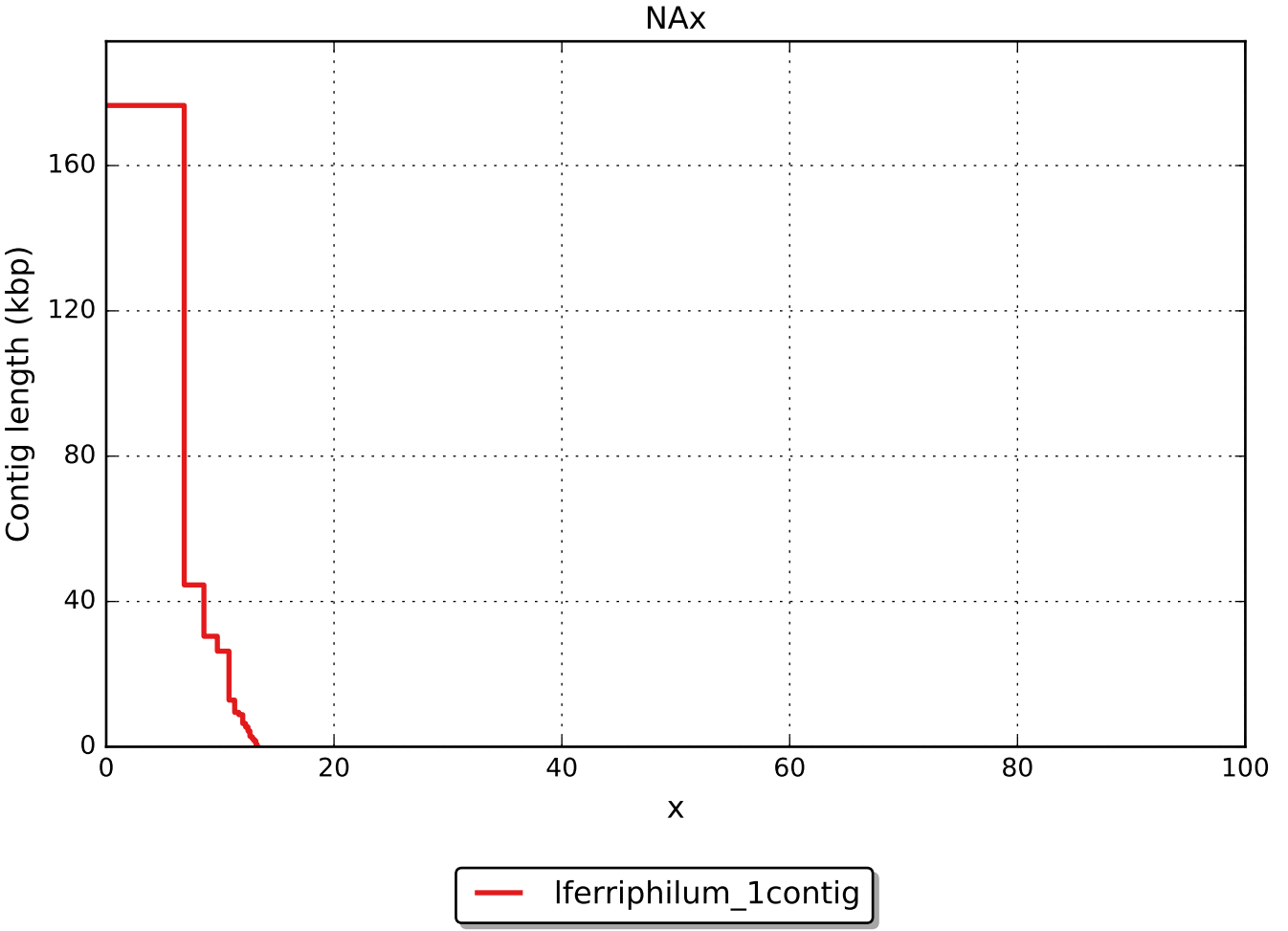

GC content
windows
GC (%)
0
400
800
1200
1600
0
20
40
60
80
100
lferriphilum_1contig
Reference

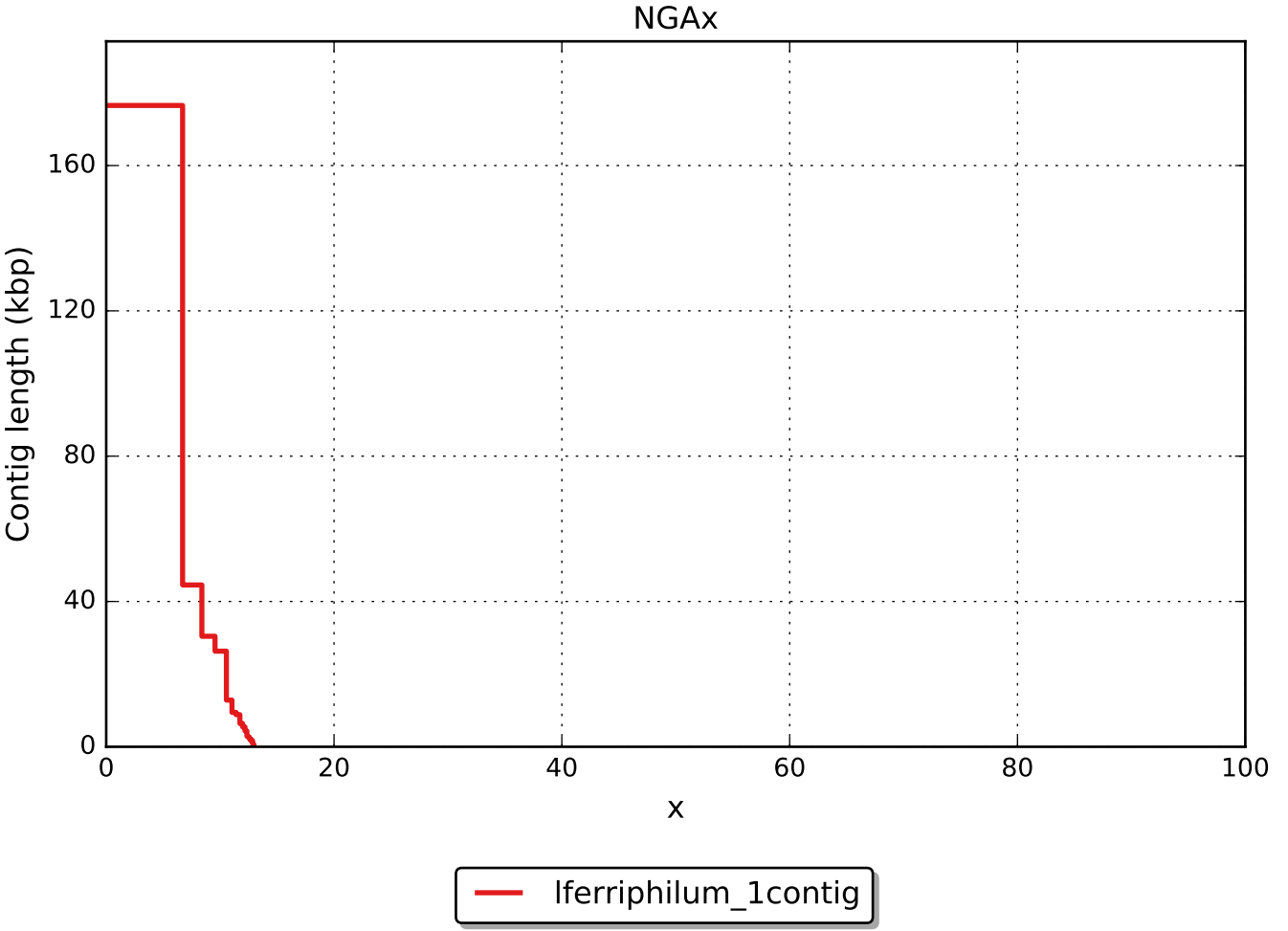

lferriphilum_1contig GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
lferriphilum_1contig


Misassemblies
5
4
3
2
1
0
lferriphilum_1contig


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
lferriphilum_1contig


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
500
1000
1500
2000
2500
0
20
40
60
80
Contig index
lferriphilum_1contig
Reference


NAx
Contig length (kbp)
0
40
80
120
160
0
20
40
60
80
100
x
lferriphilum_1contig


NGAx
Contig length (kbp)
160
120
80
40
0
0
20
40
60
80
100
x
lferriphilum_1contig