Report

	lferriphilum.contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	2615124
Total length (>= 1000 bp)	2615124
Total length (>= 5000 bp)	2615124
Total length (>= 10000 bp)	2615124
Total length (>= 25000 bp)	2615124
Total length (>= 50000 bp)	2615124
# contigs	2
Largest contig	2562260
Total length	2615124
Reference length	2610531
GC (%)	54.12
Reference GC (%)	54.14
N50	2562260
NG50	2562260
N75	2562260
NG75	2562260
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2562260
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	52864
Genome fraction (%)	97.566
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.04
# indels per 100 kbp	13.66
Largest alignment	2282075
Total aligned length	2562260
NA50	2282075
NGA50	2282075
NA75	2282075
NGA75	2282075
LA50	1
LGA50	1
LA75	1
LGA75	1

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

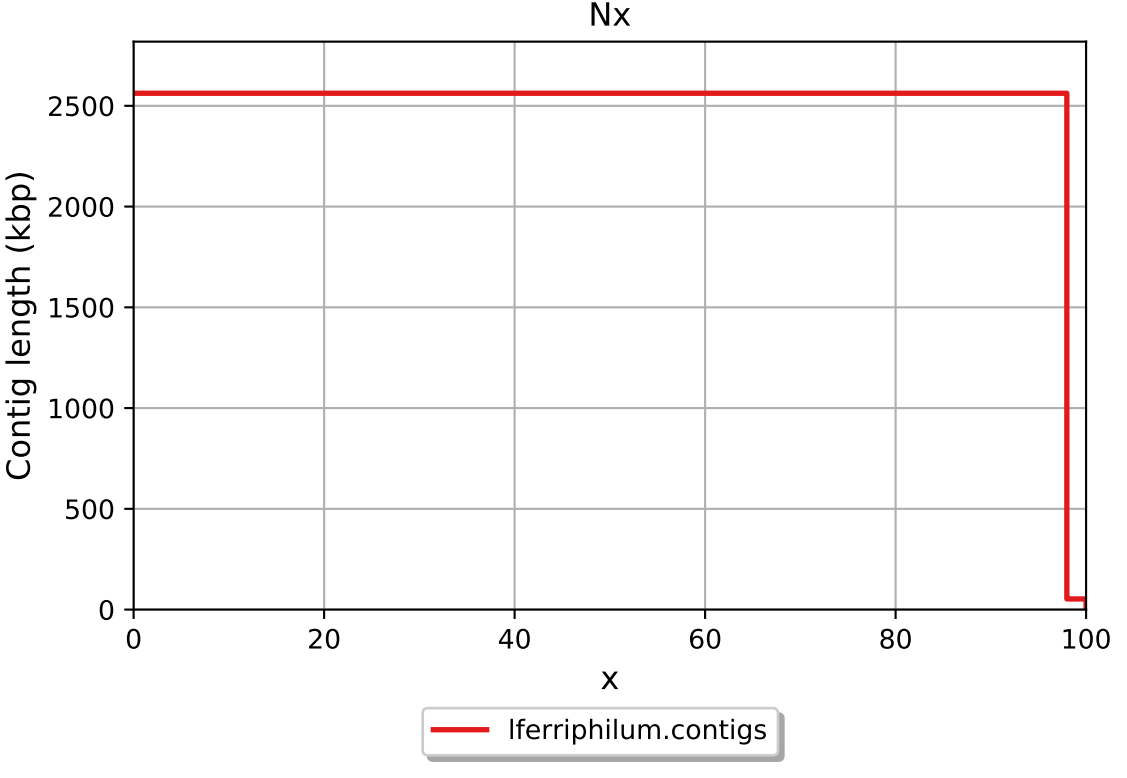
	lferriphilum.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2562260
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1
# indels	348
# indels (<= 5 bp)	348
# indels (> 5 bp)	0
Indels length	354

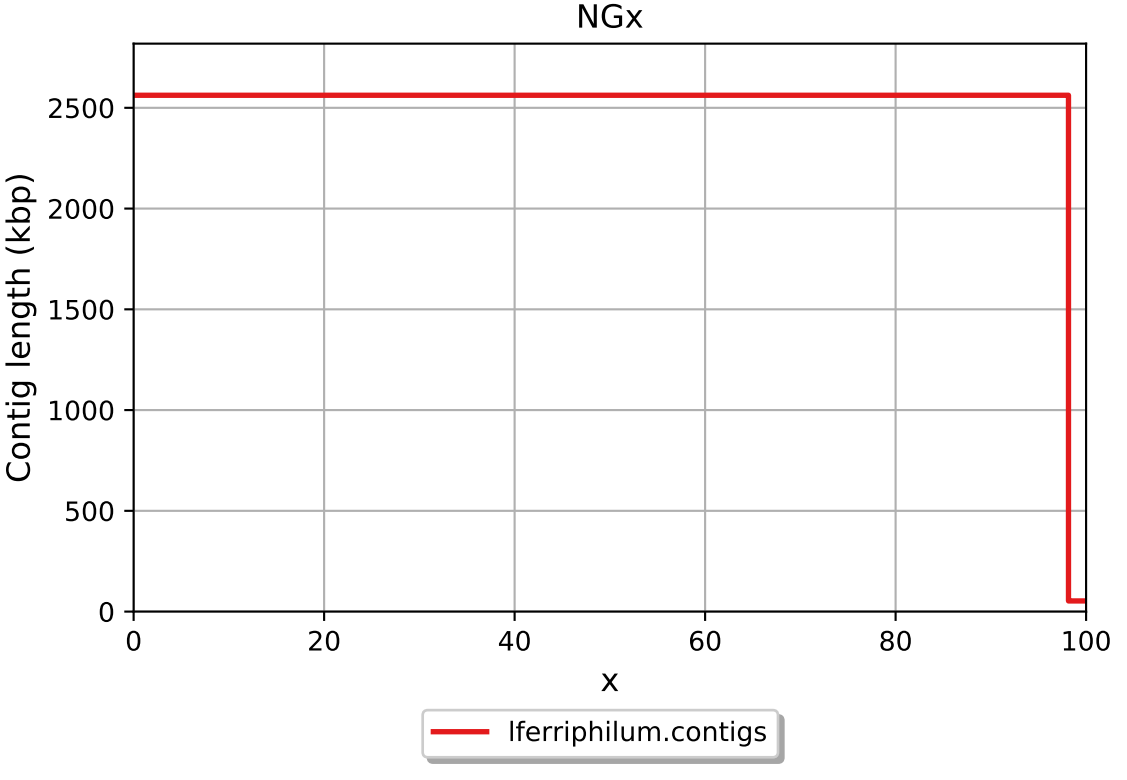
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

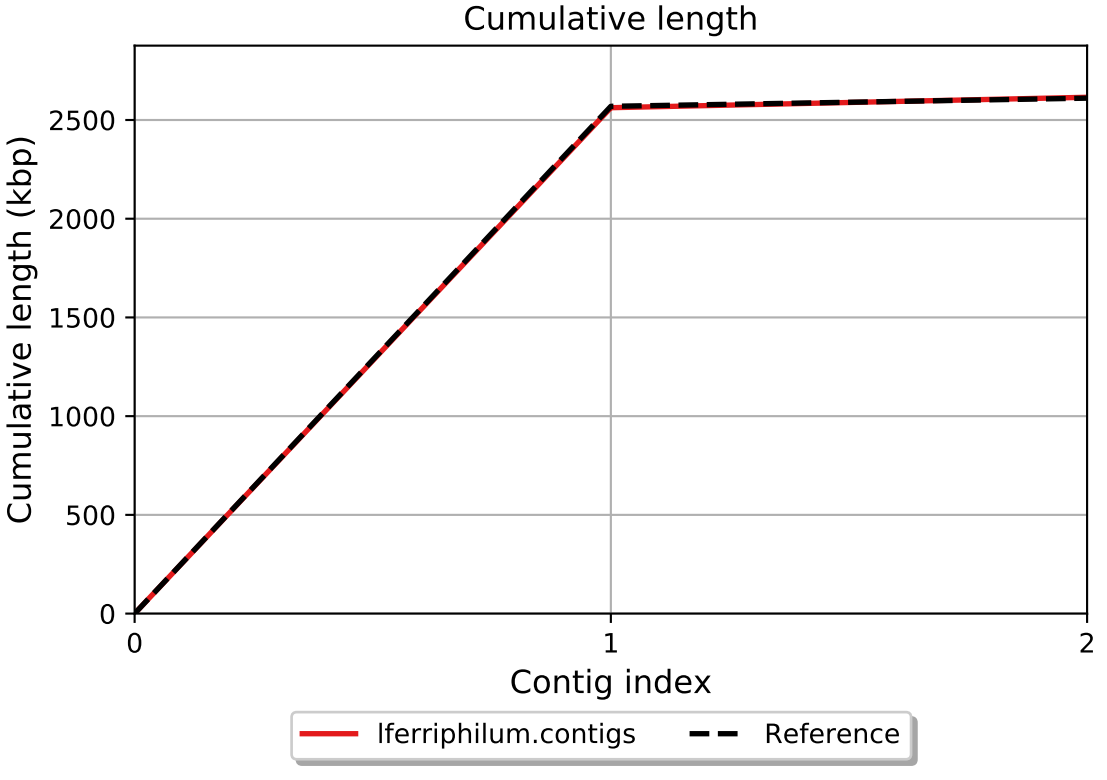
Unaligned report

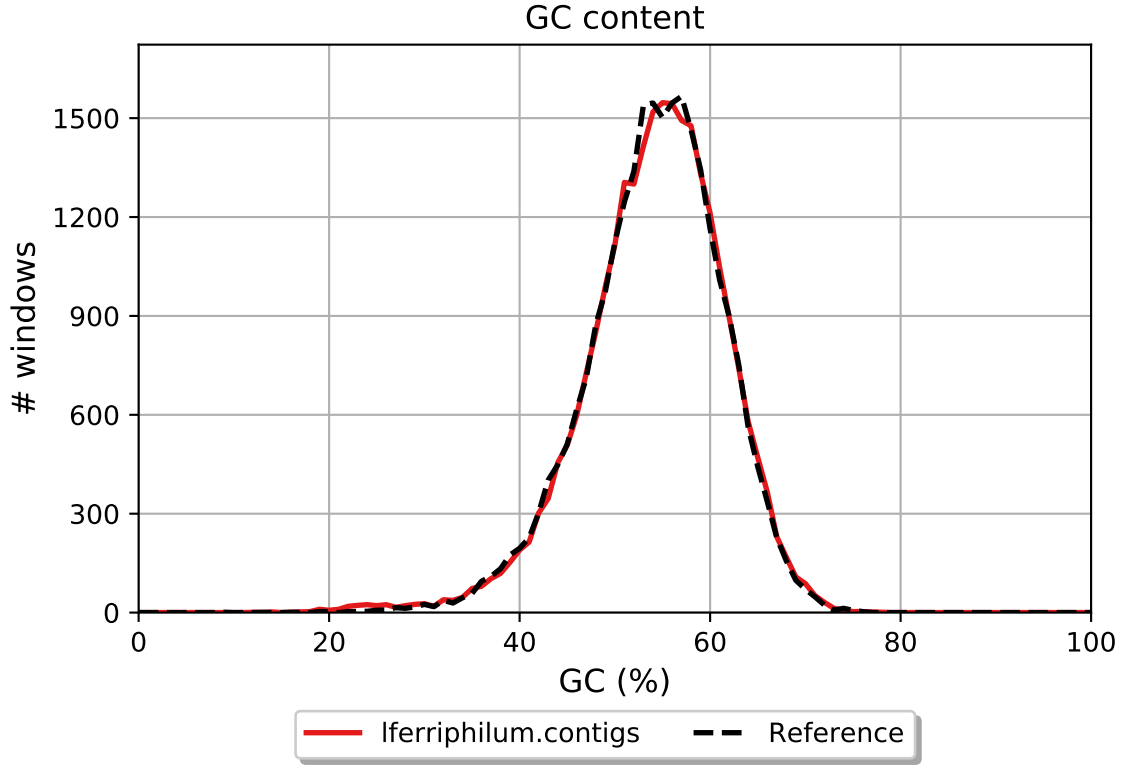
	lferriphilum.contigs
# fully unaligned contigs	1
Fully unaligned length	52864
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

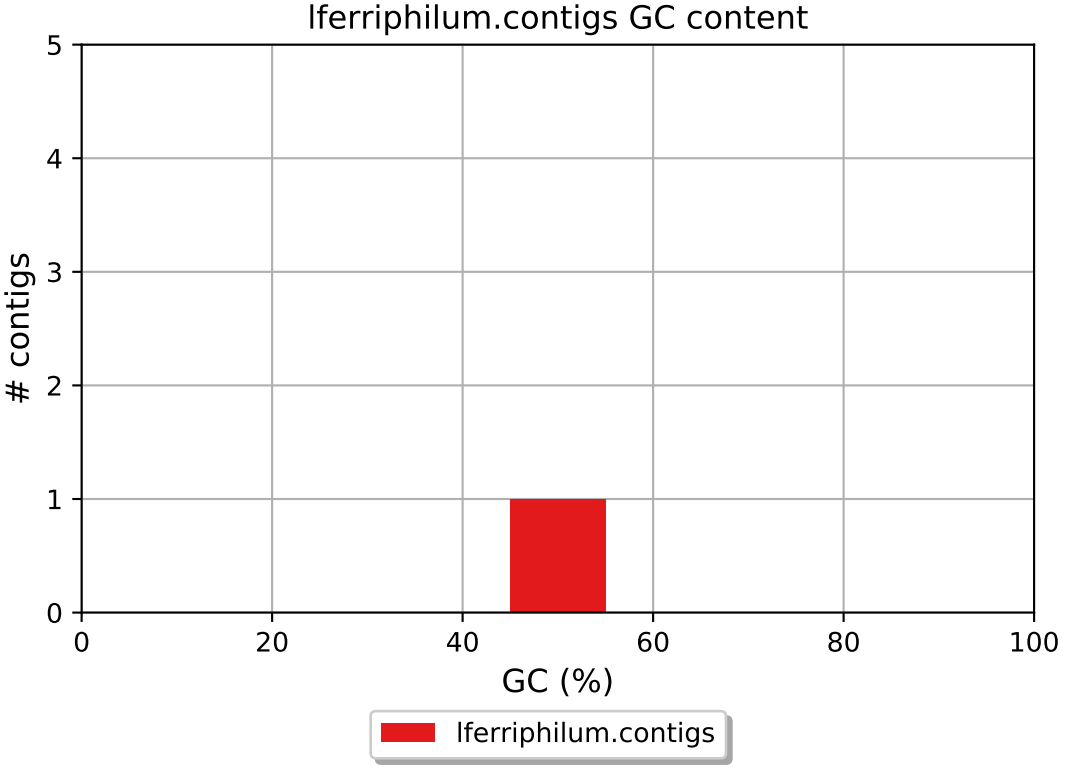
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

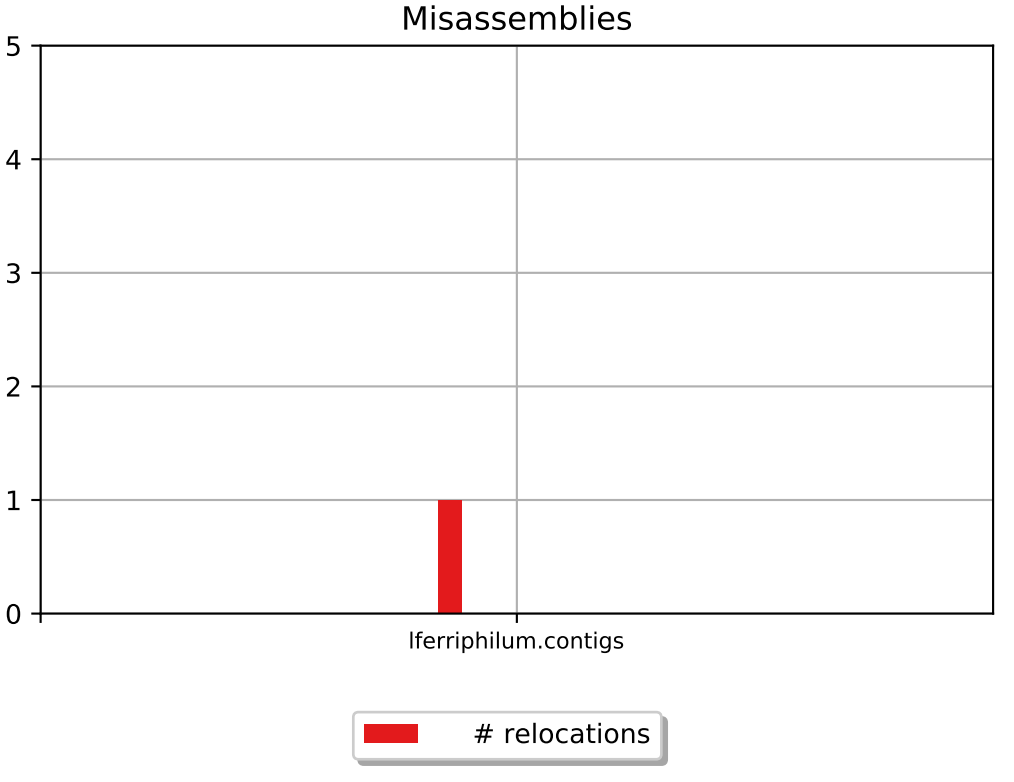

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
lferriphilum.contigs

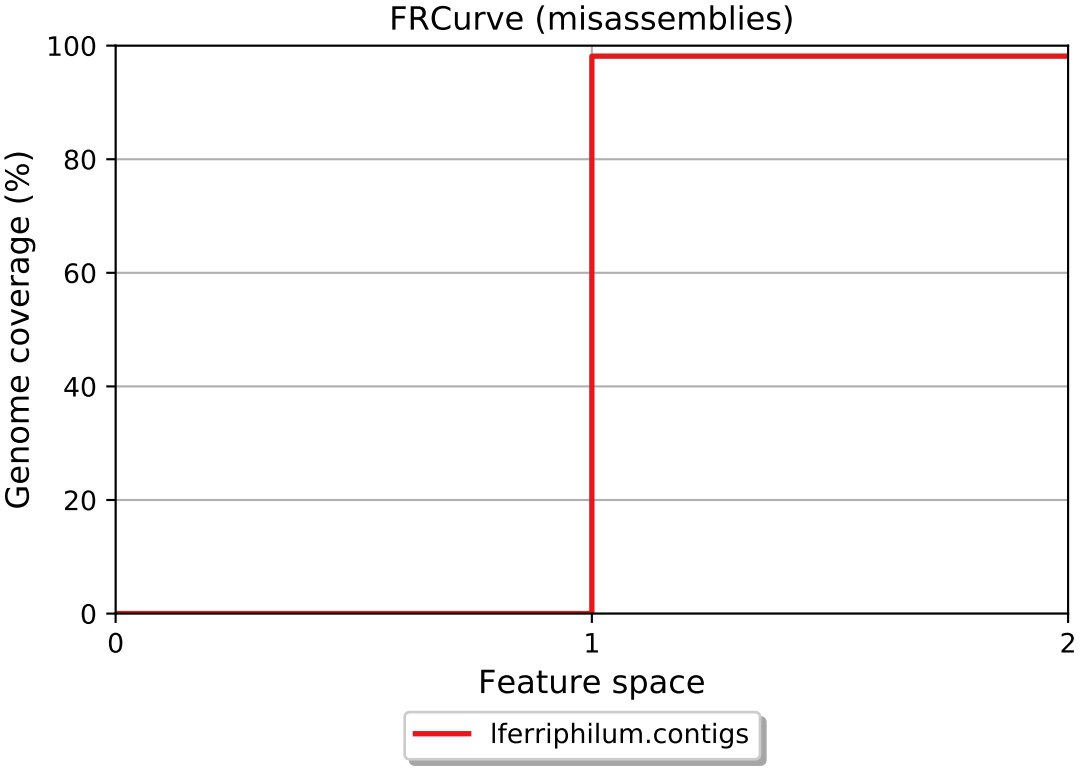

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
lferriphilum.contigs

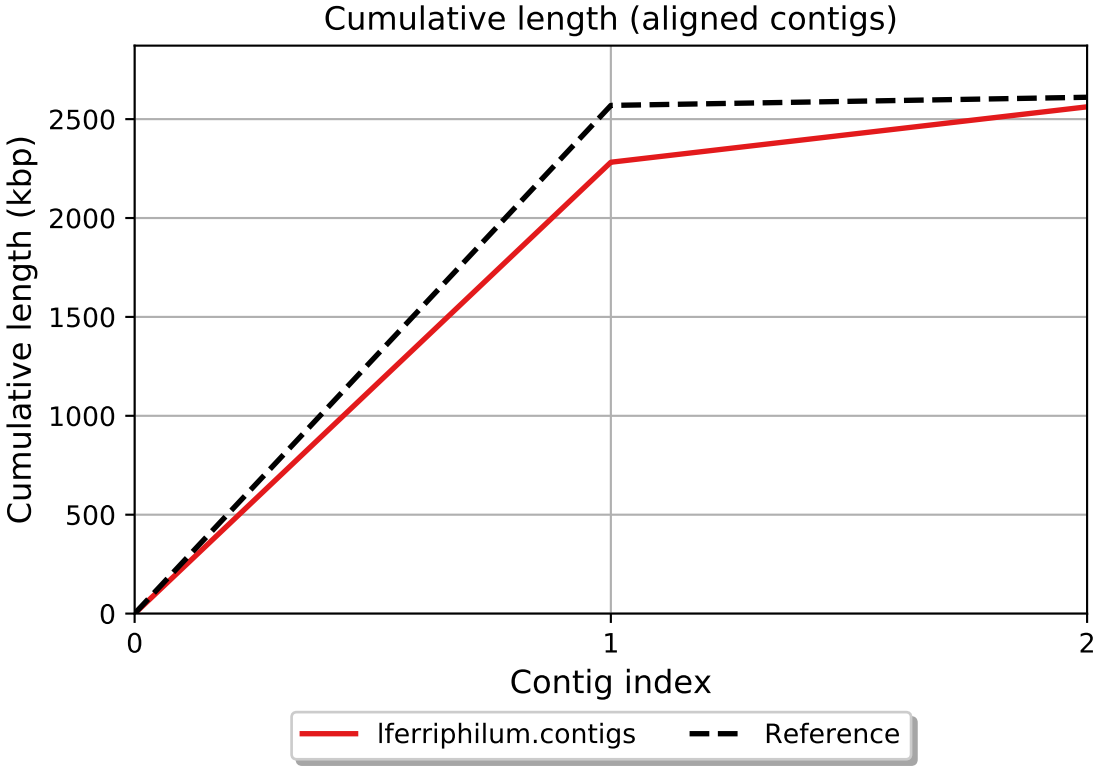

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
Contig index
lferriphilum.contigs
Reference

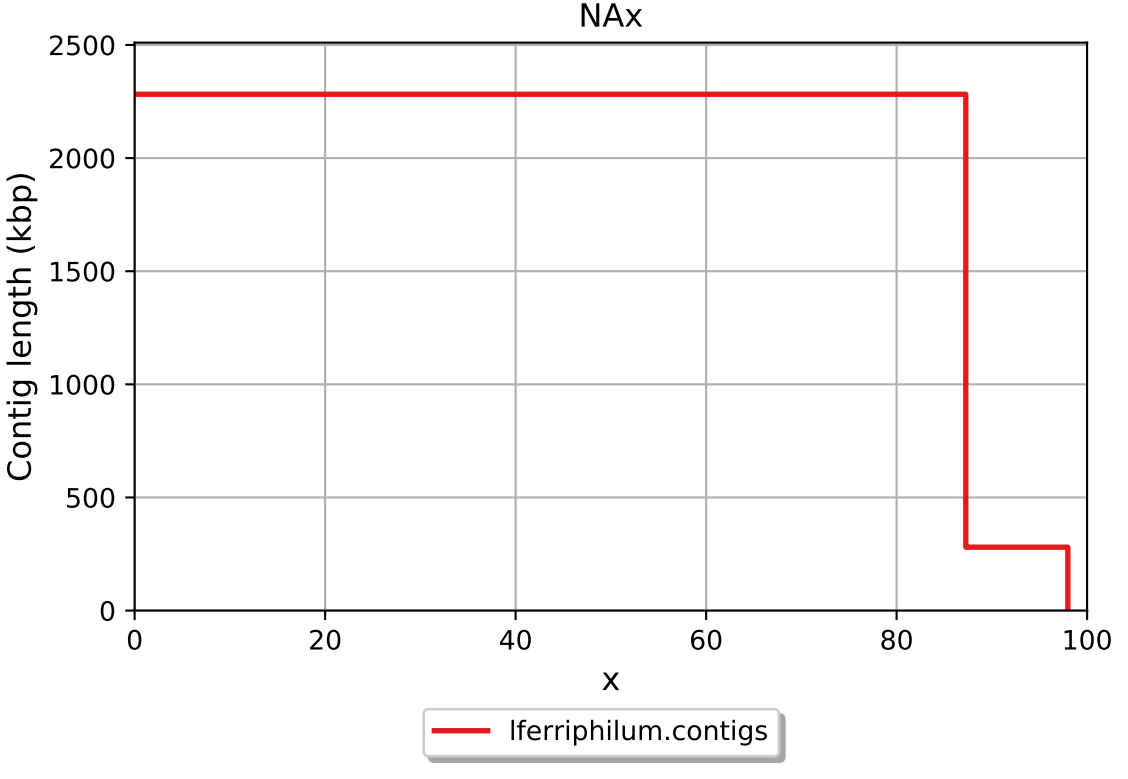

GC content
windows
1500
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
lferriphilum.contigs
Reference

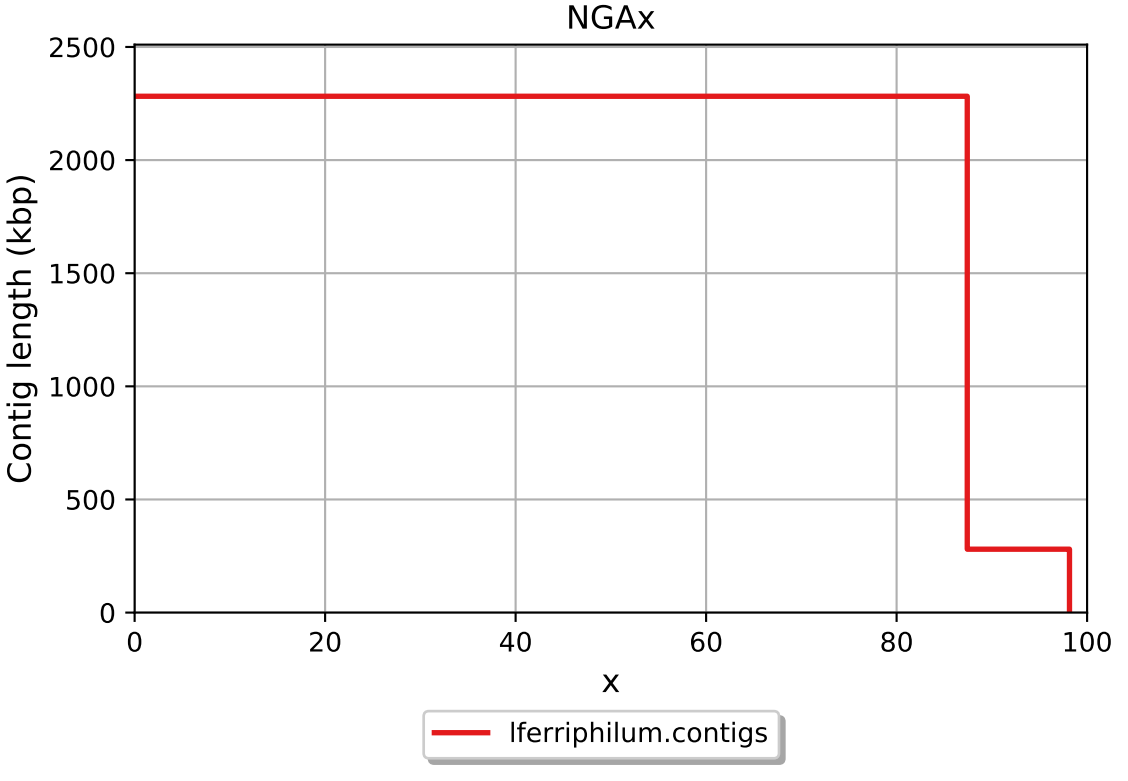

lferriphilum.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
lferriphilum.contigs


Misassemblies
5
4
3
2
1
0
lferriphilum.contigs
relocations


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


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


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


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