

## Report

	lferriphilum.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
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 0 part
Unaligned length	51543
Genome fraction (%)	97.567
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.86
# indels per 100 kbp	10.64
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

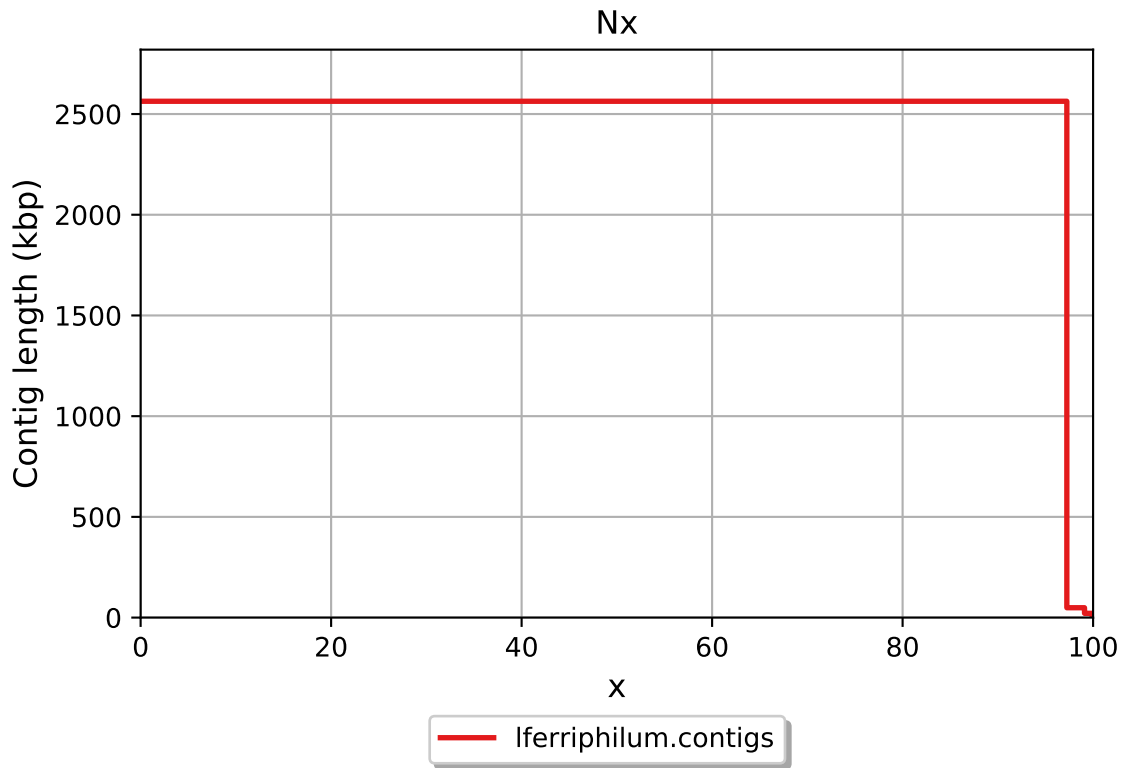
	lferriphilum.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2563357
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	22
# indels	271
# indels (<= 5 bp)	269
# indels (> 5 bp)	2
Indels length	334

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

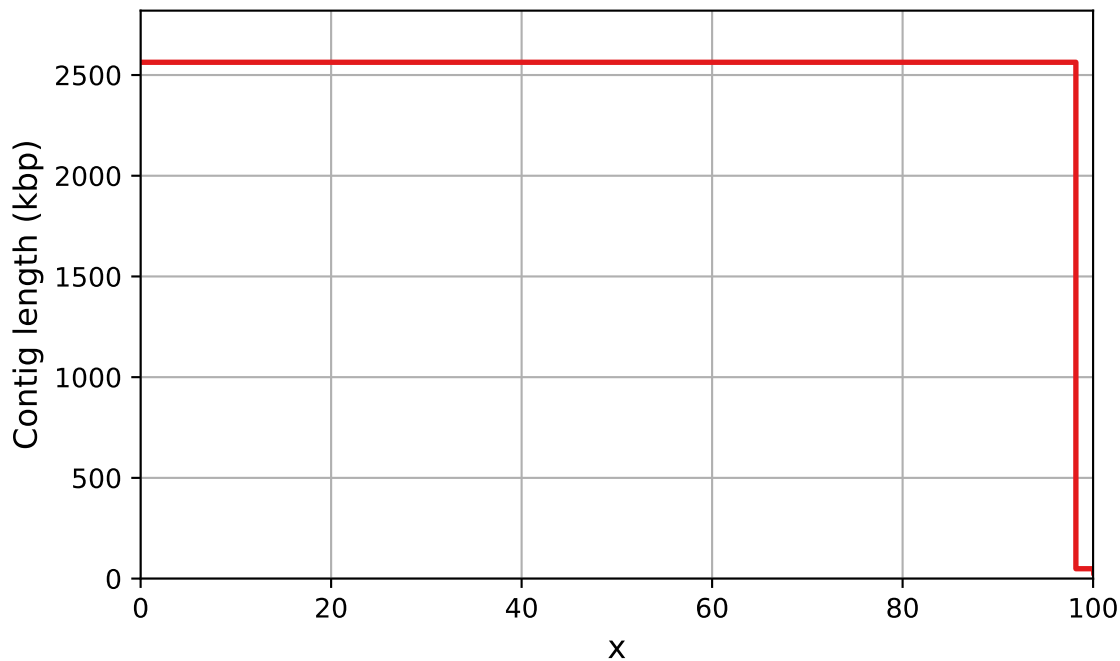
## Unaligned report

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

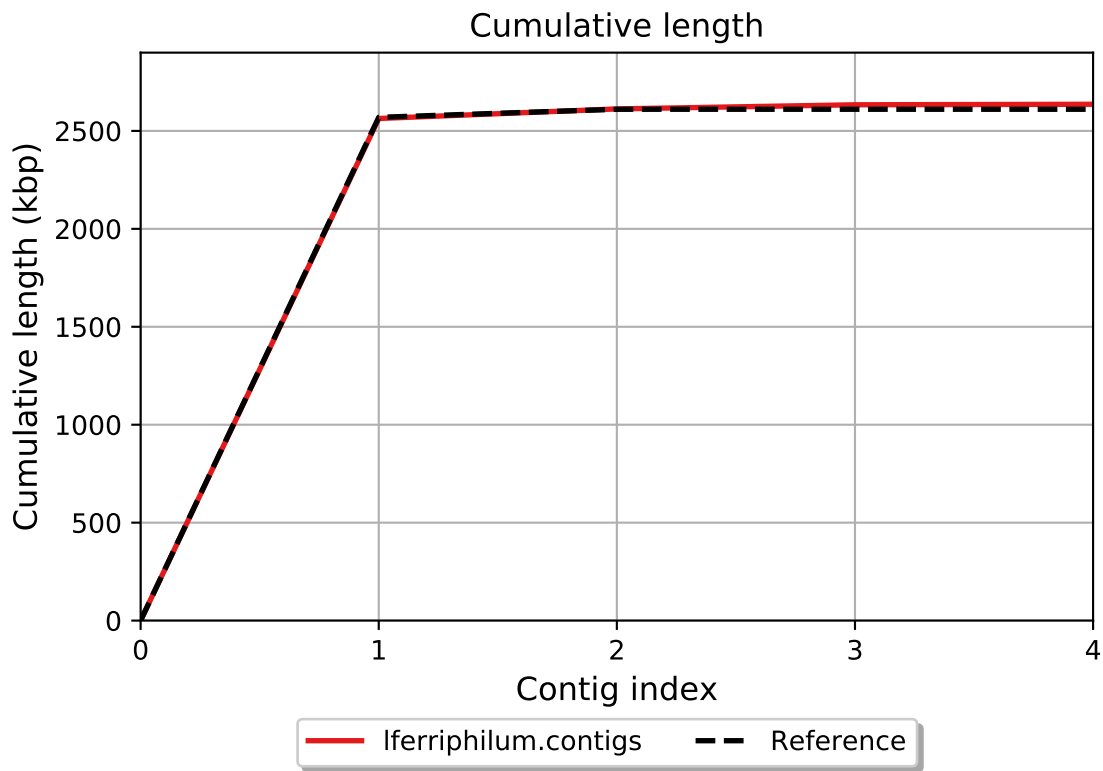
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



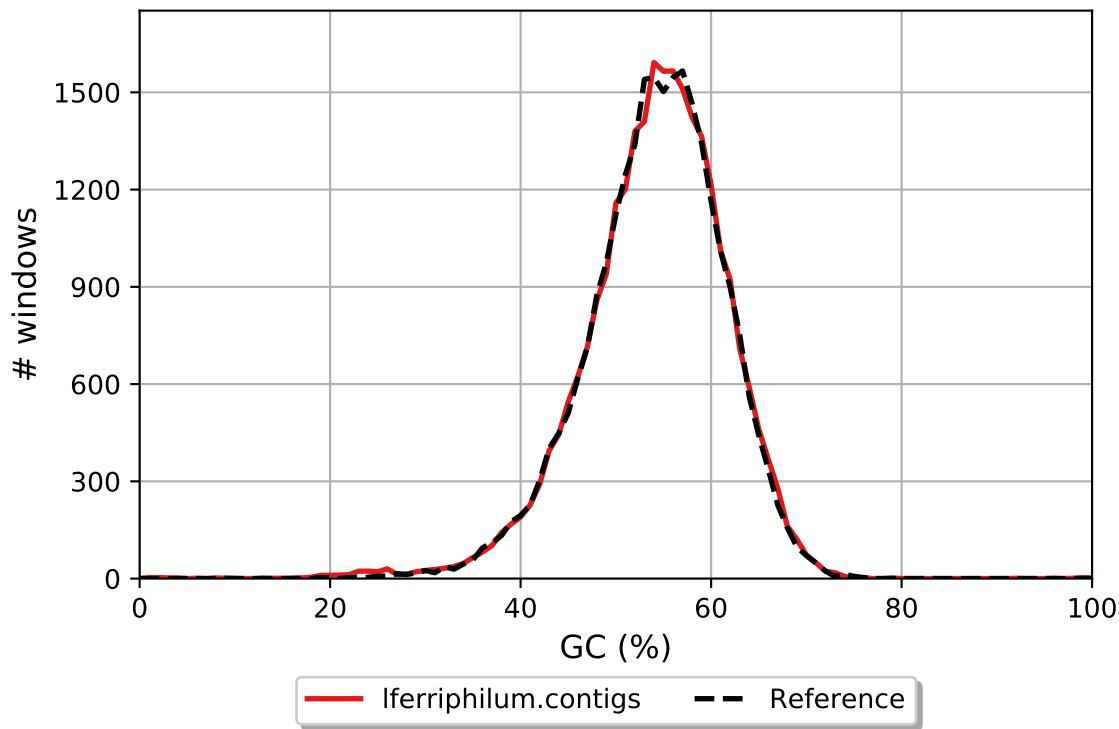
## NGx



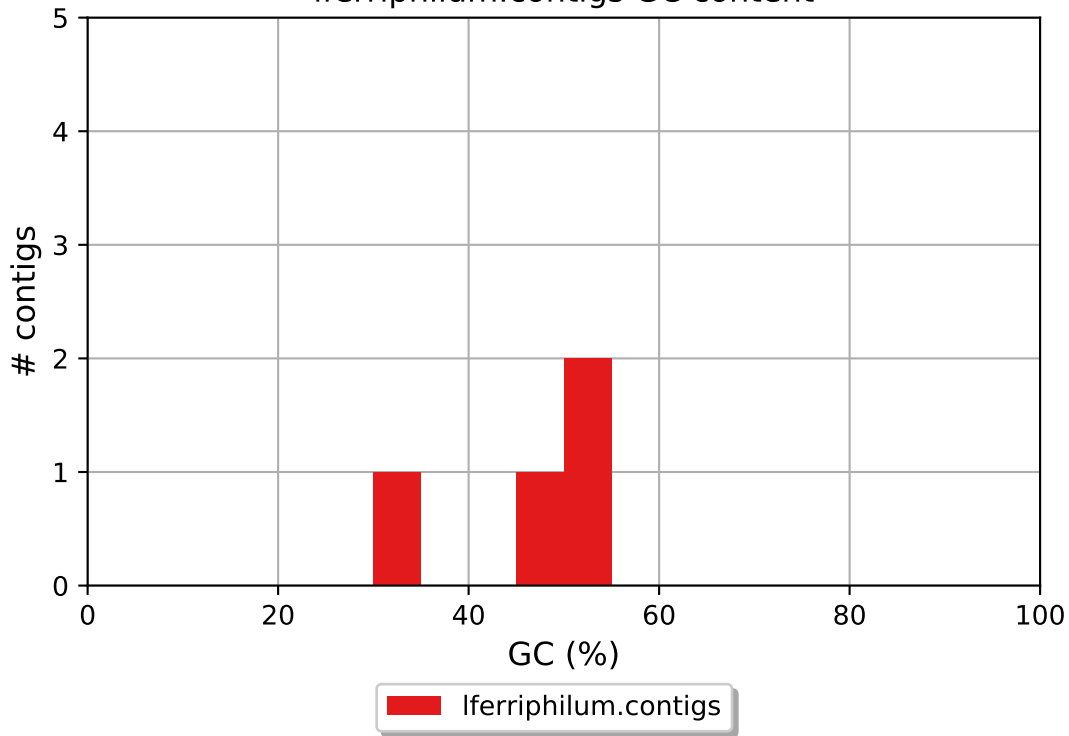
— Iferriphilum.contigs



## GC content

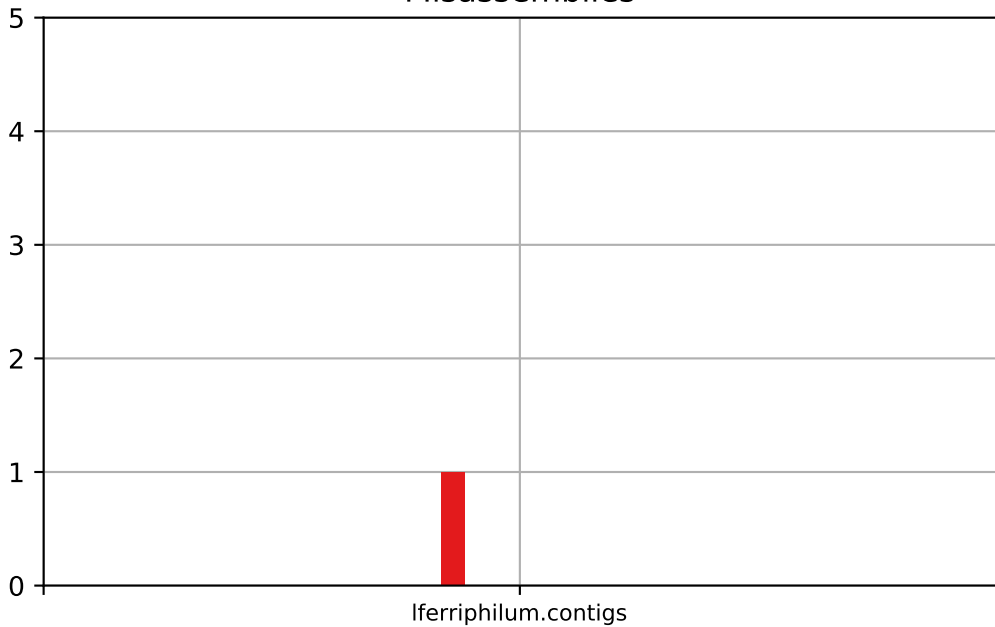


Iferriphilum.contigs GC content

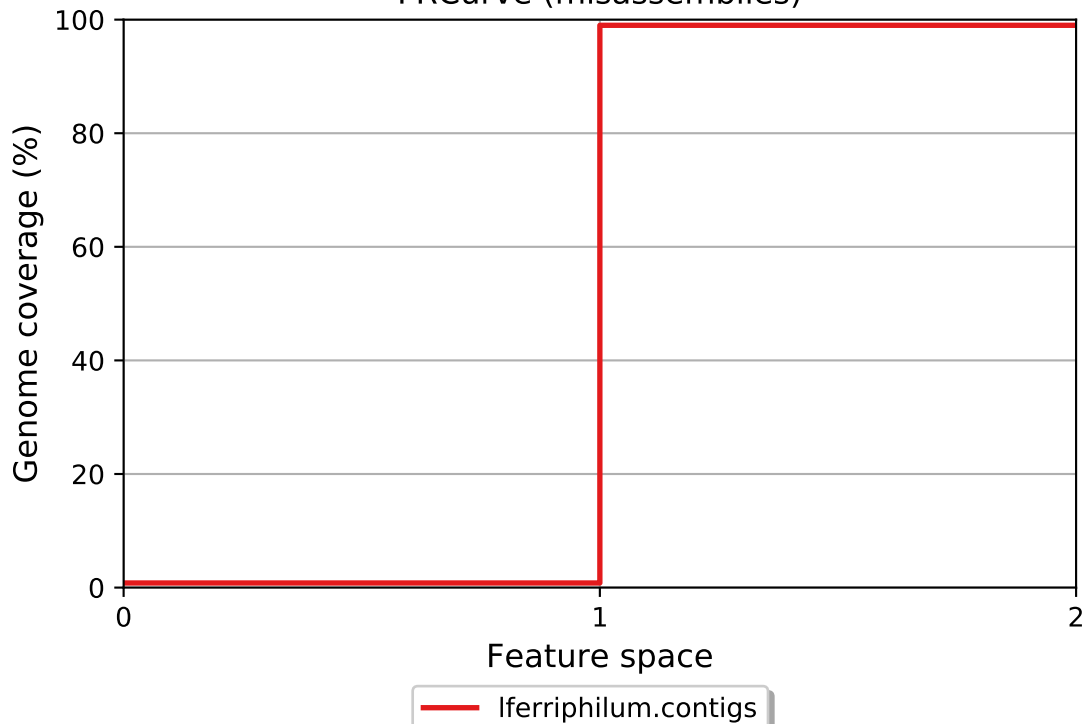




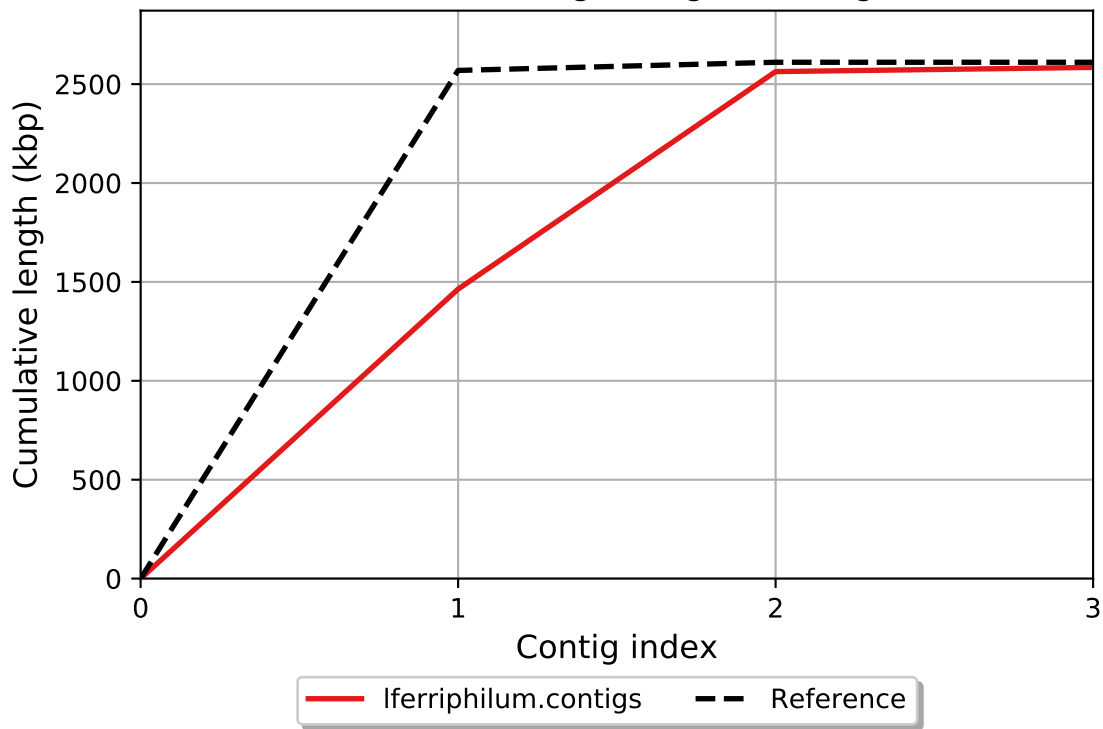
## Misassemblies



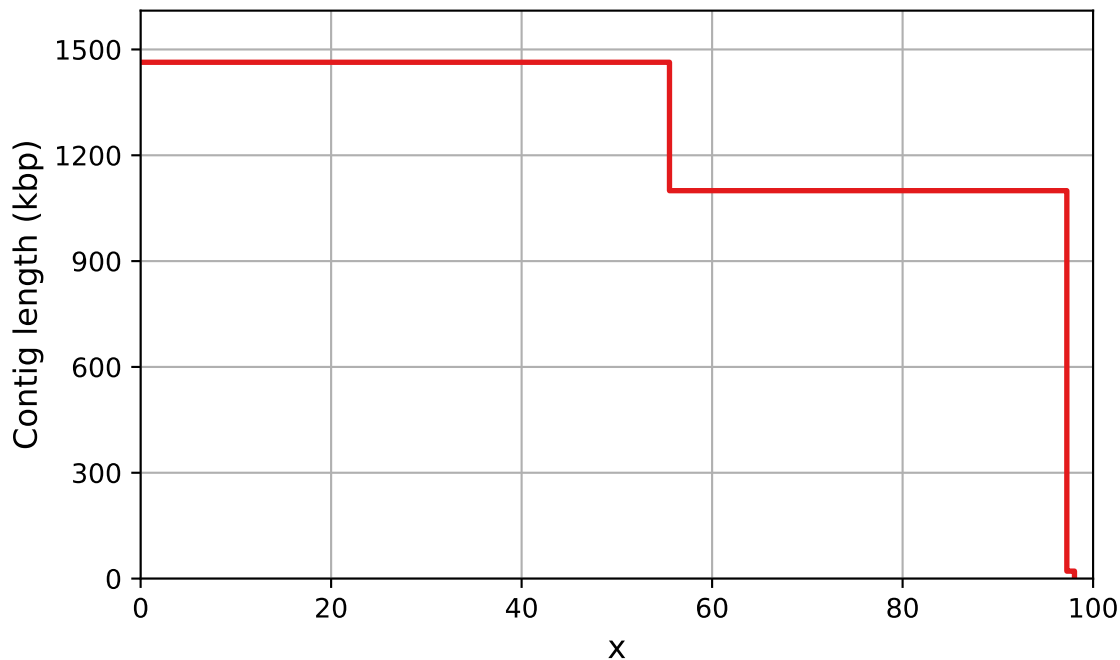
FRCurve (misassemblies)



Cumulative length (aligned contigs)

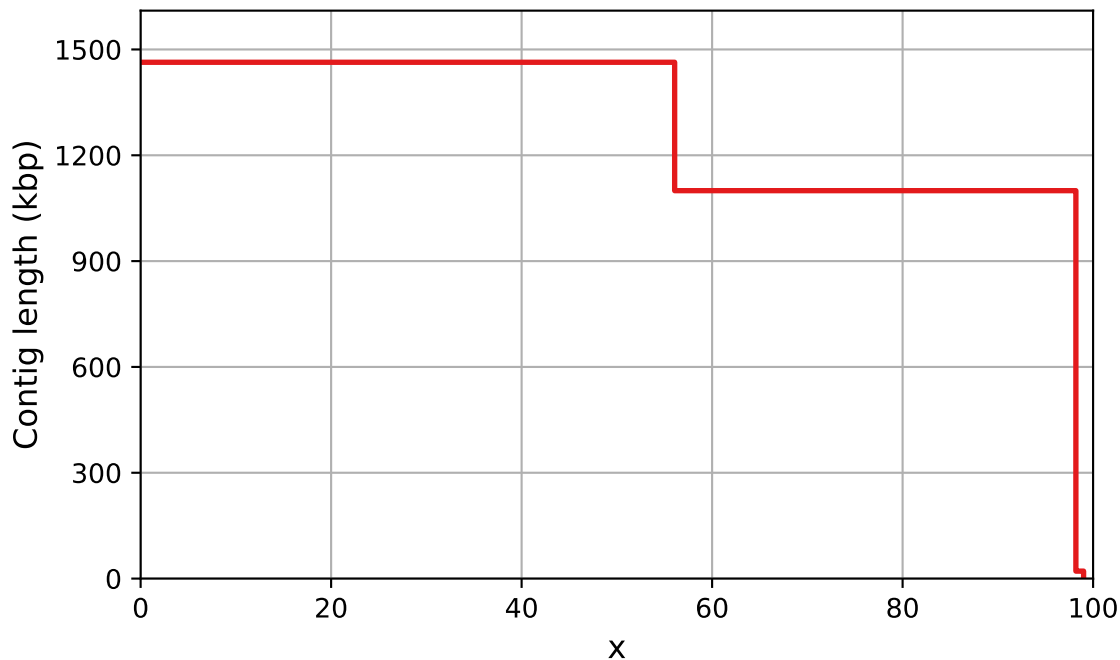


NAx



— Iferriphilum.contigs

# NGAx



— Iferriphilum.contigs