

## Report

	assembly_L_Ferriphilum.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)	2651532
Total length (>= 1000 bp)	2651532
Total length (>= 5000 bp)	2651532
Total length (>= 10000 bp)	2651532
Total length (>= 25000 bp)	2651532
Total length (>= 50000 bp)	2651532
# contigs	2
Largest contig	2600663
Total length	2651532
Reference length	2610531
GC (%)	54.05
Reference GC (%)	54.14
N50	2600663
NG50	2600663
N75	2600663
NG75	2600663
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	2600663
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	50869
Genome fraction (%)	97.566
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.43
# indels per 100 kbp	15.19
Largest alignment	1448830
Total aligned length	2600592
NA50	1448830
NGA50	1448830
NA75	1122402
NGA75	1122402
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

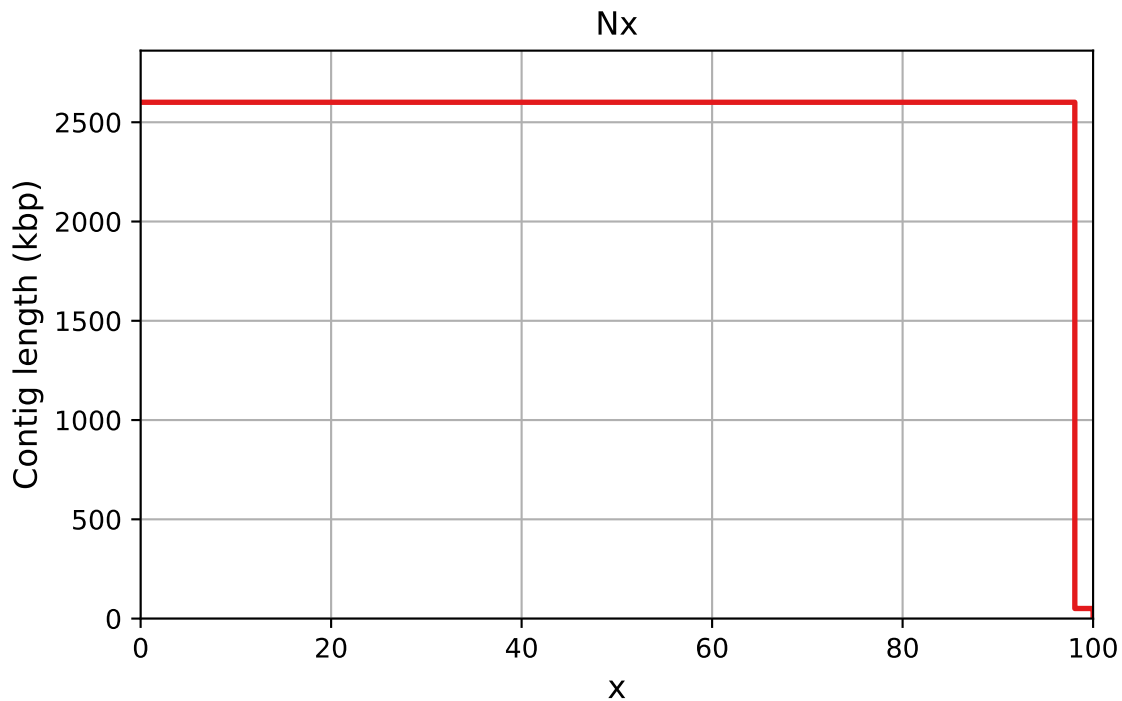
	assembly_L_Ferriphilum.contigs
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2600663
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	11
# indels	387
# indels (<= 5 bp)	386
# indels (> 5 bp)	1
Indels length	409

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

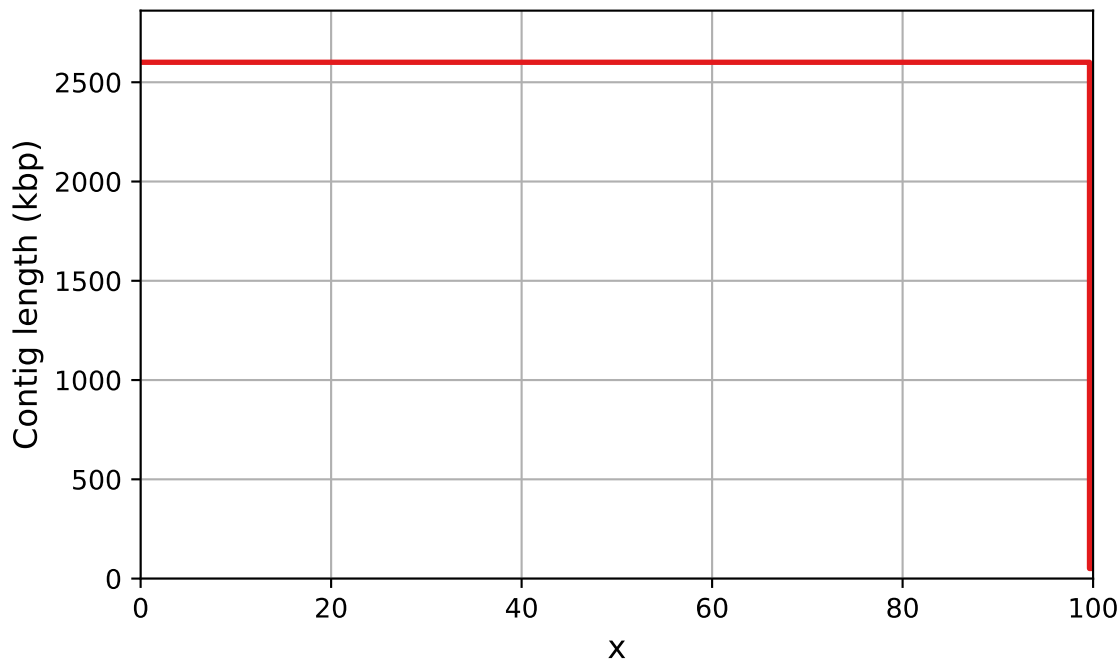
	assembly_L_Ferriphilum.contigs
# fully unaligned contigs	1
Fully unaligned length	50869
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

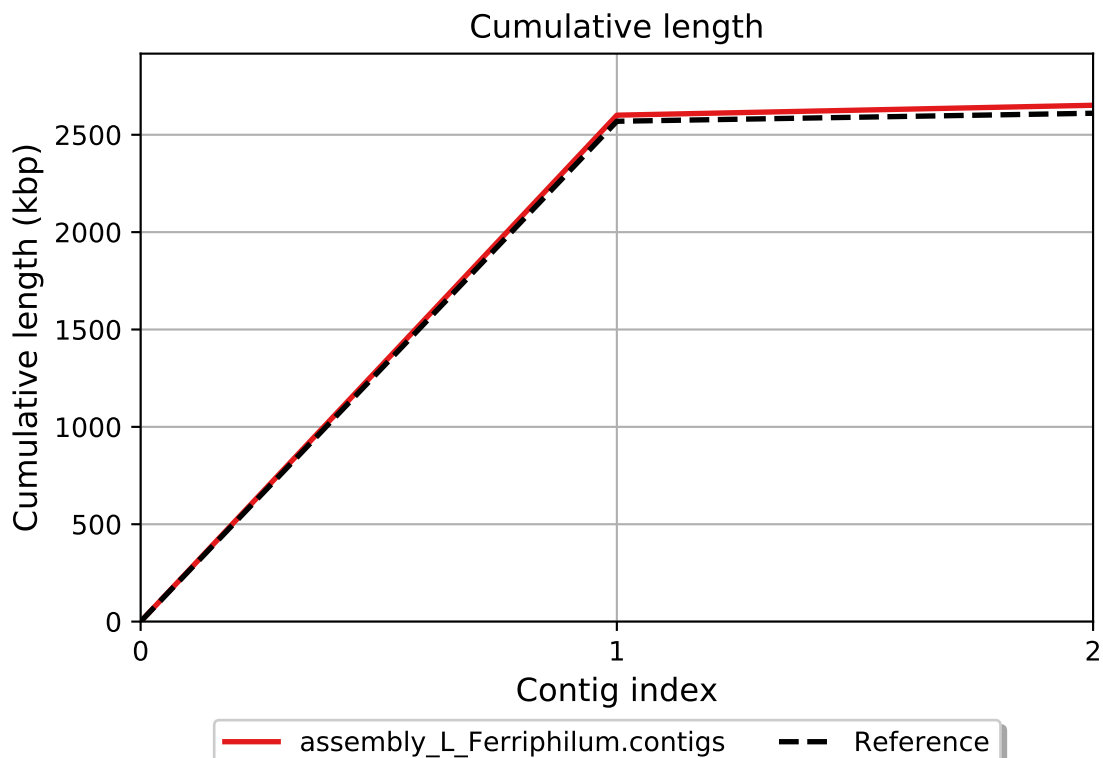


— assembly\_L\_Ferriphilum.contigs

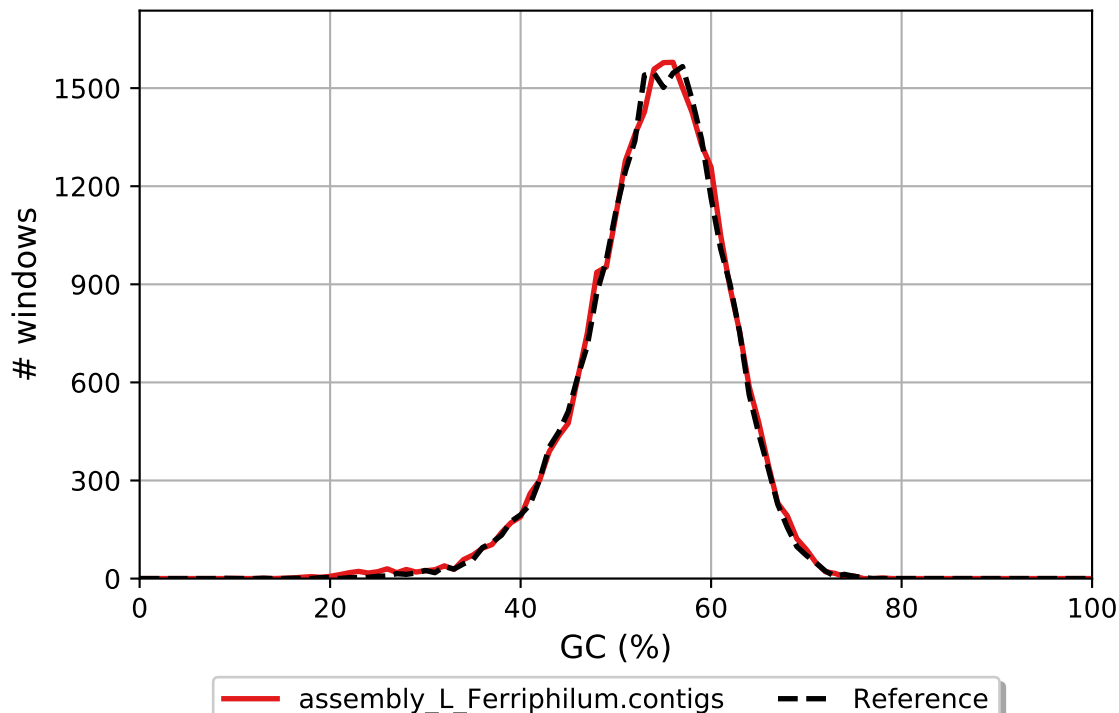
NGx



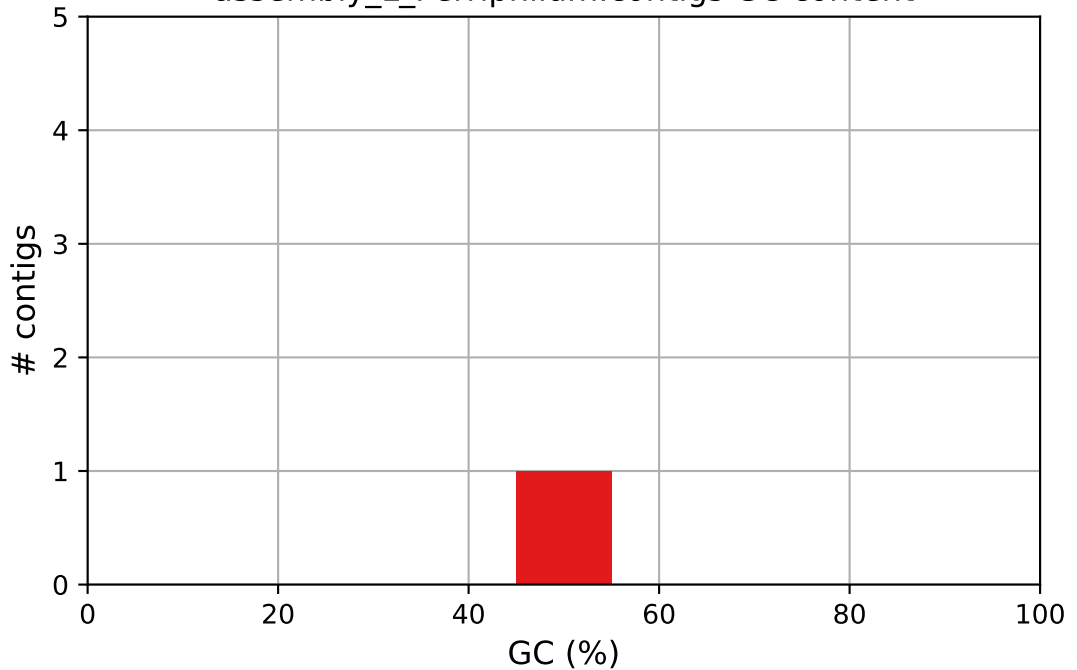
— assembly\_L\_Ferriphilum.contigs



## GC content



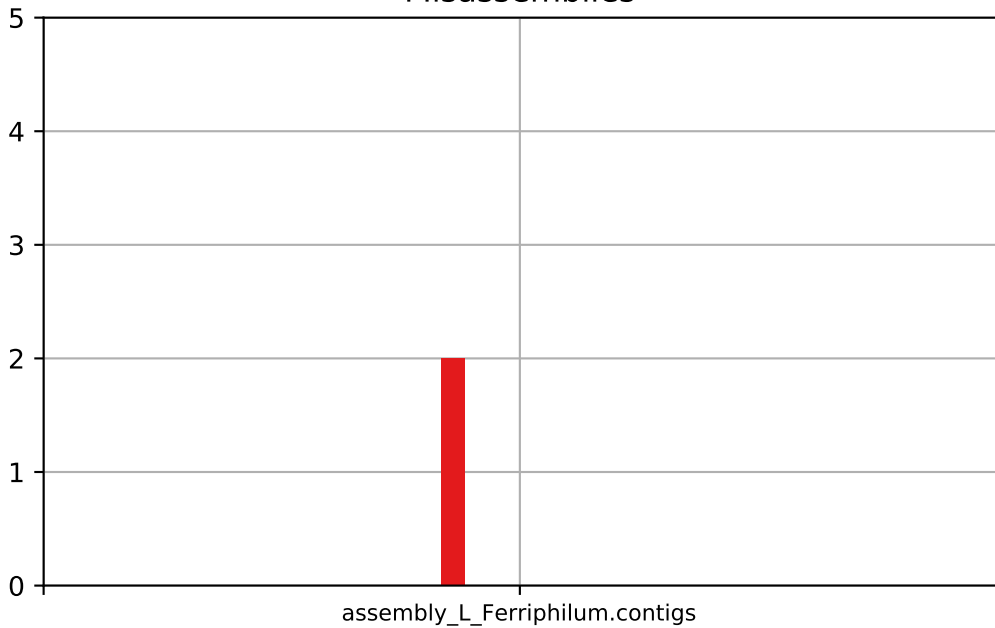
assembly\_L\_Ferriphilum.contigs GC content



assembly\_L\_Ferriphilum.contigs

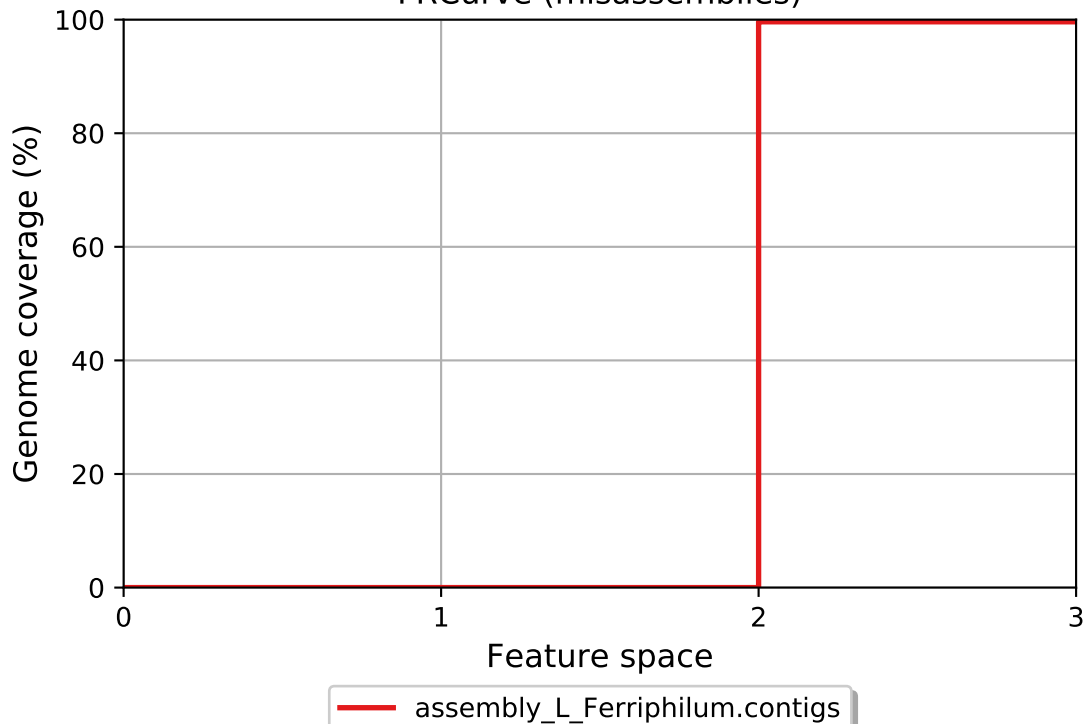


## Misassemblies

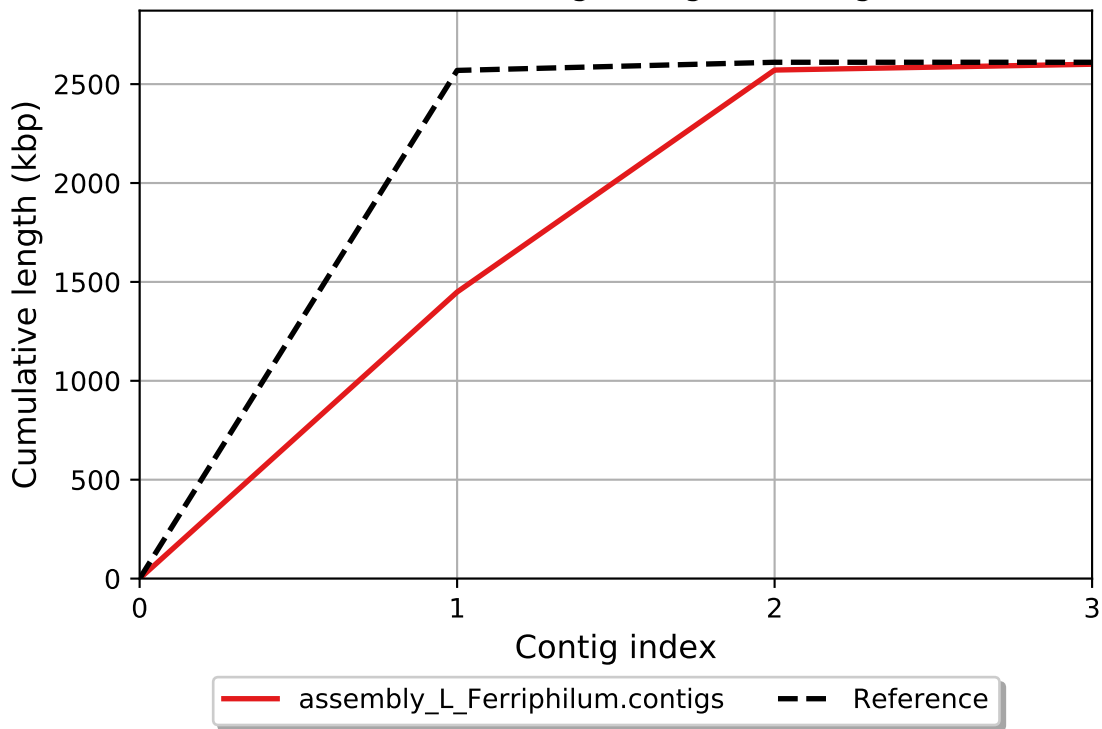


 # relocations

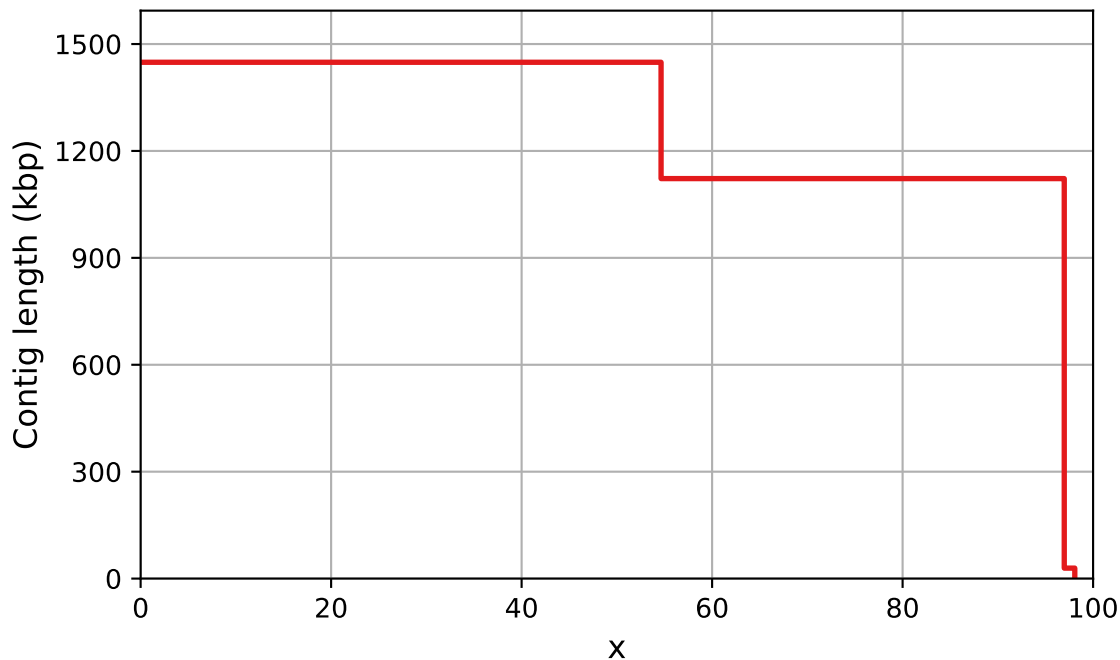
FRCurve (misassemblies)



Cumulative length (aligned contigs)

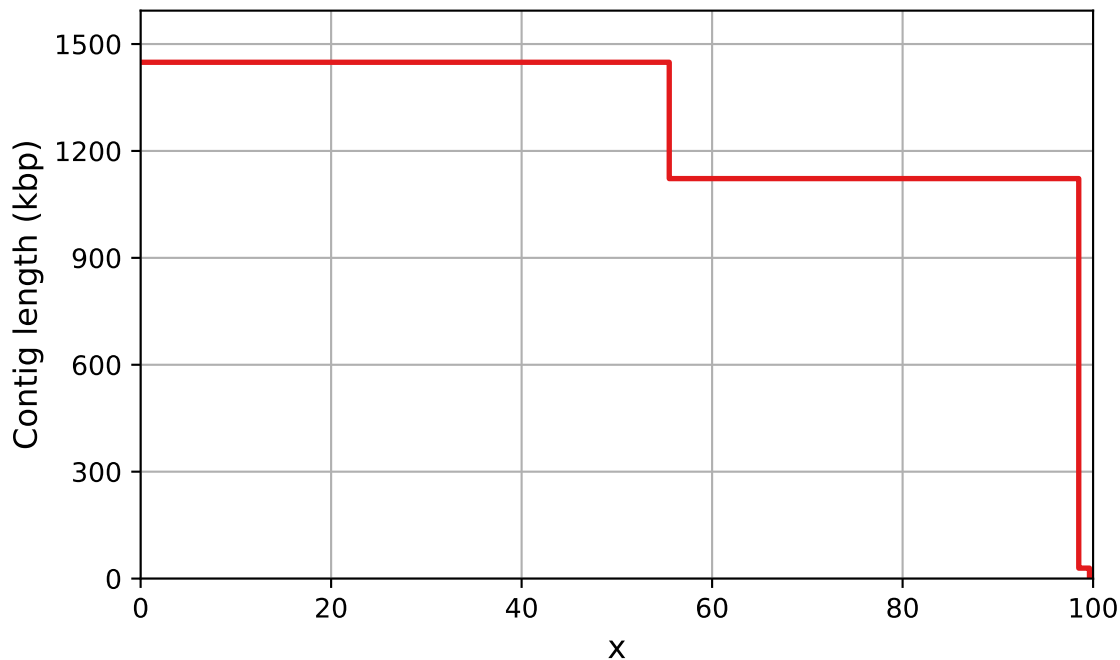


NAx



— assembly\_L\_Ferriphilum.contigs

# NGAx



— assembly\_L\_Ferriphilum.contigs