

Report

	LFerriphilum.contigs
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2636086
Total length (>= 1000 bp)	2636086
Total length (>= 5000 bp)	2636086
Total length (>= 10000 bp)	2636086
Total length (>= 25000 bp)	2615609
Total length (>= 50000 bp)	2565990
# contigs	3
Largest contig	2565990
Total length	2636086
Reference length	2610531
GC (%)	54.10
Reference GC (%)	54.14
N50	2565990
NG50	2565990
N75	2565990
NG75	2565990
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2565990
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	49619
Genome fraction (%)	97.567
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.16
# indels per 100 kbp	13.43
Largest alignment	1571665
Total aligned length	2586467
NA50	1571665
NGA50	1571665
NA75	994325
NGA75	994325
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

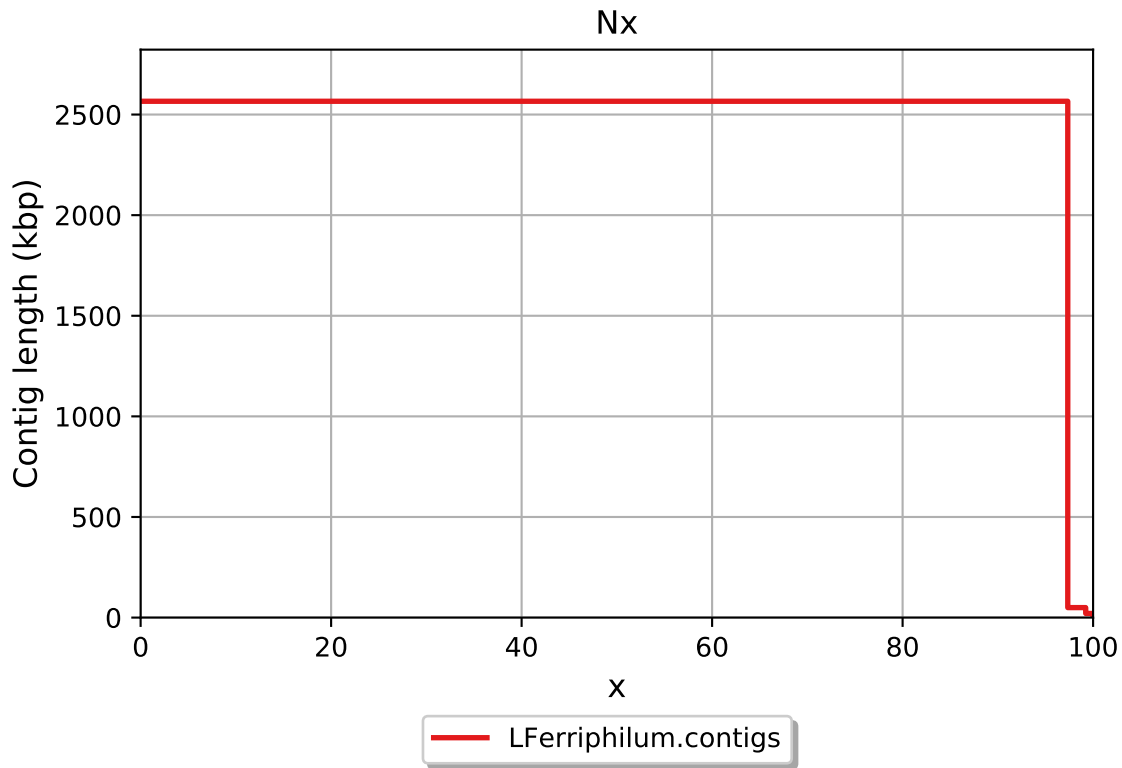
	LFerriphilum.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2565990
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	4
# indels	342
# indels (<= 5 bp)	342
# 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).

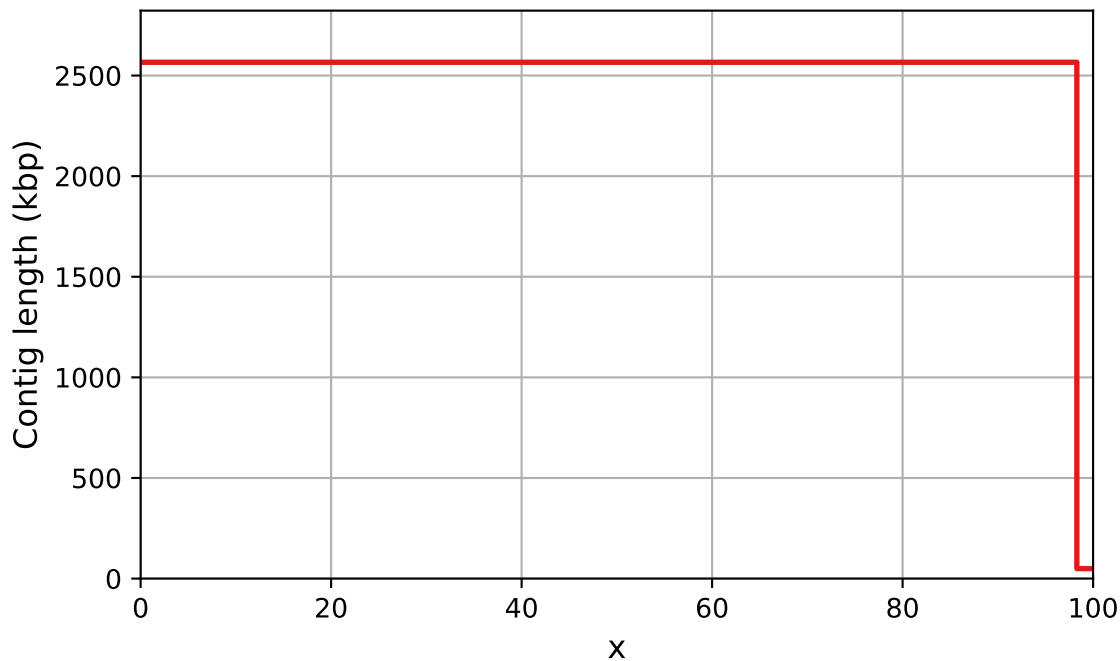
Unaligned report

	LFerriphilum.contigs
# fully unaligned contigs	1
Fully unaligned length	49619
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

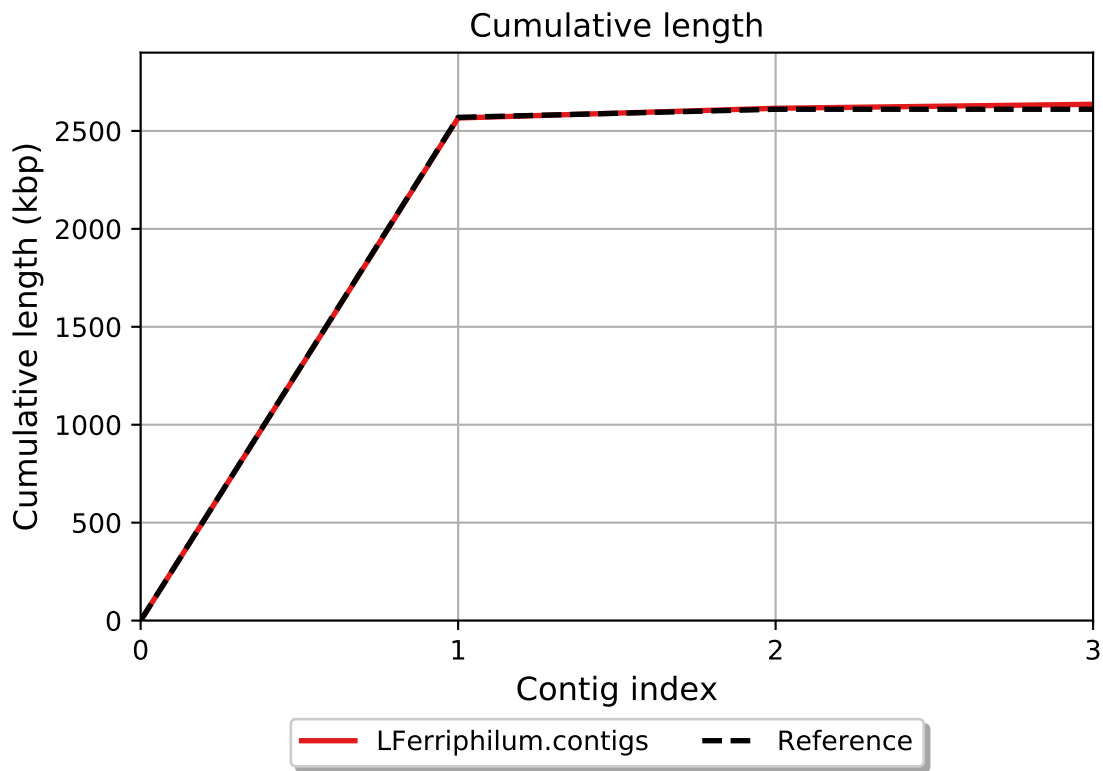
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



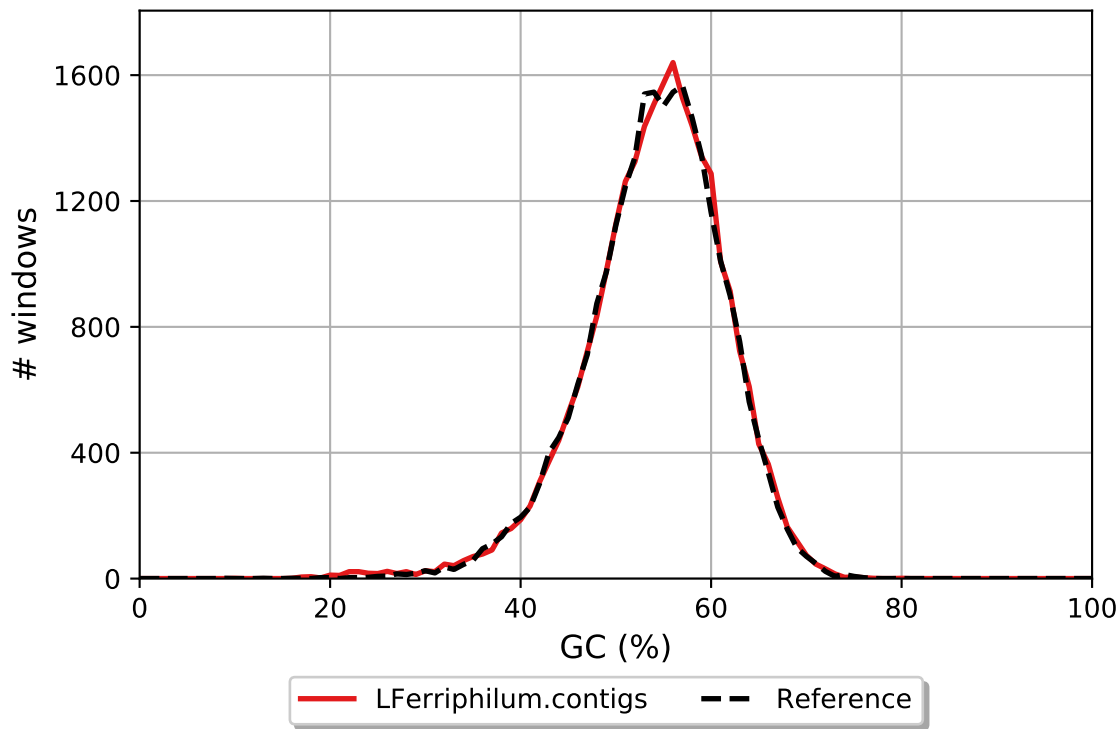
NGx



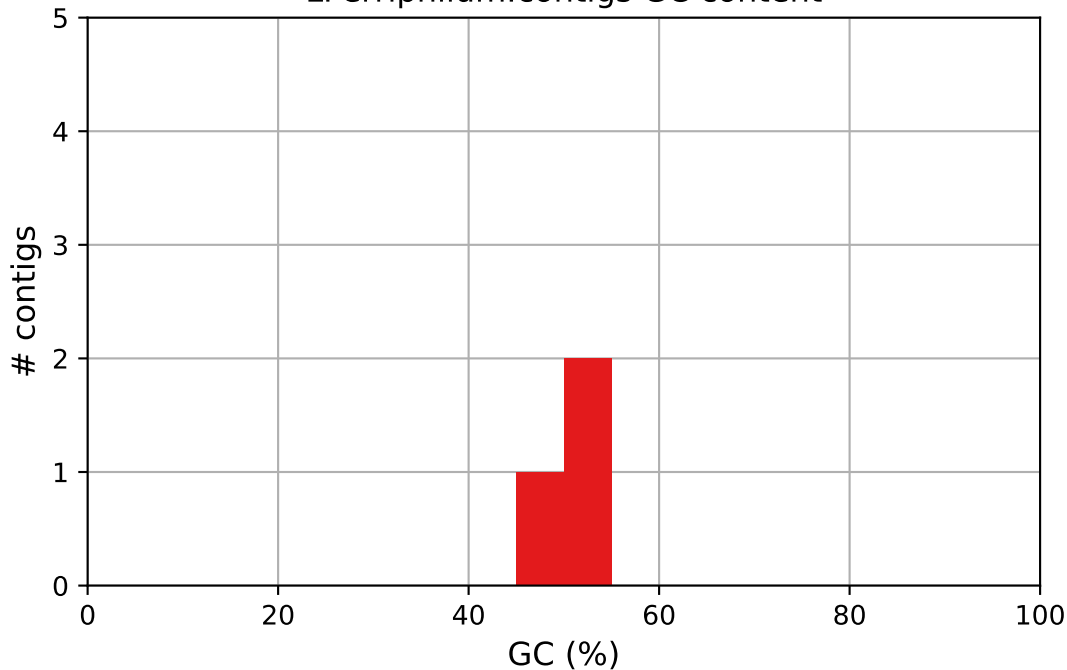
— LFerriphilum.contigs



GC content

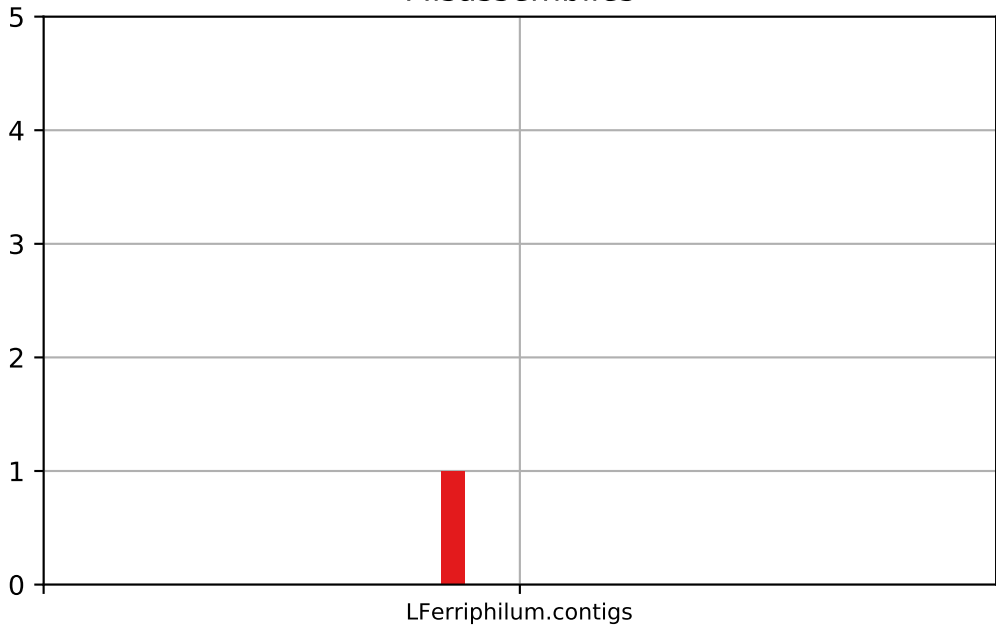


LFerriphilum.contigs GC content

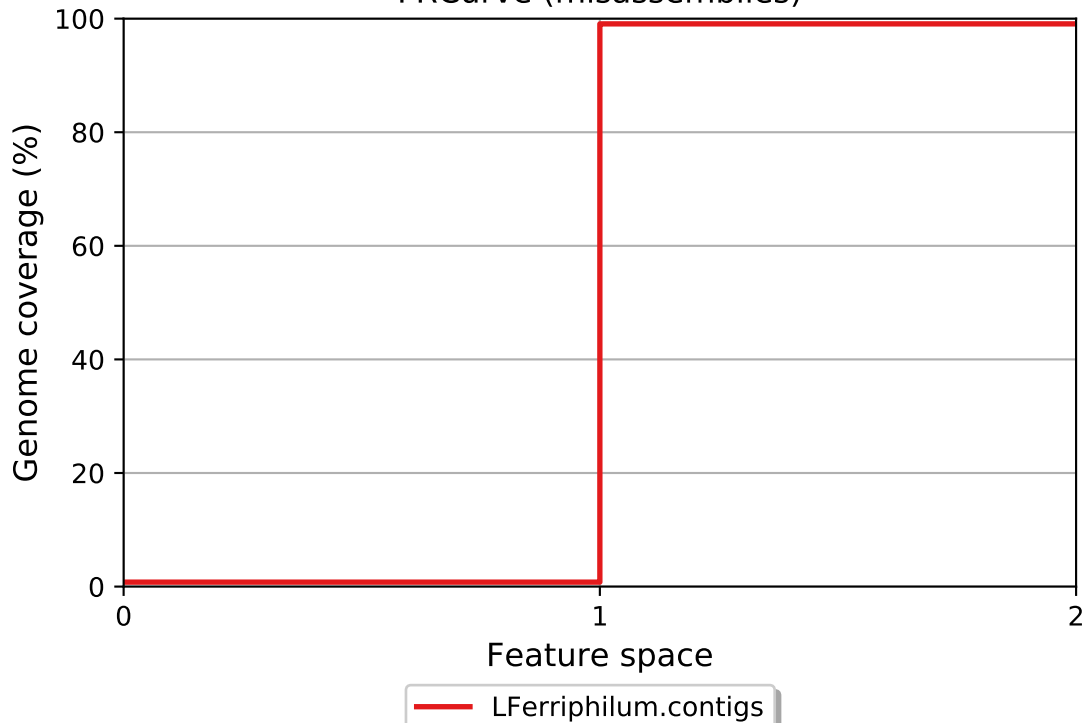


LFerriphilum.contigs

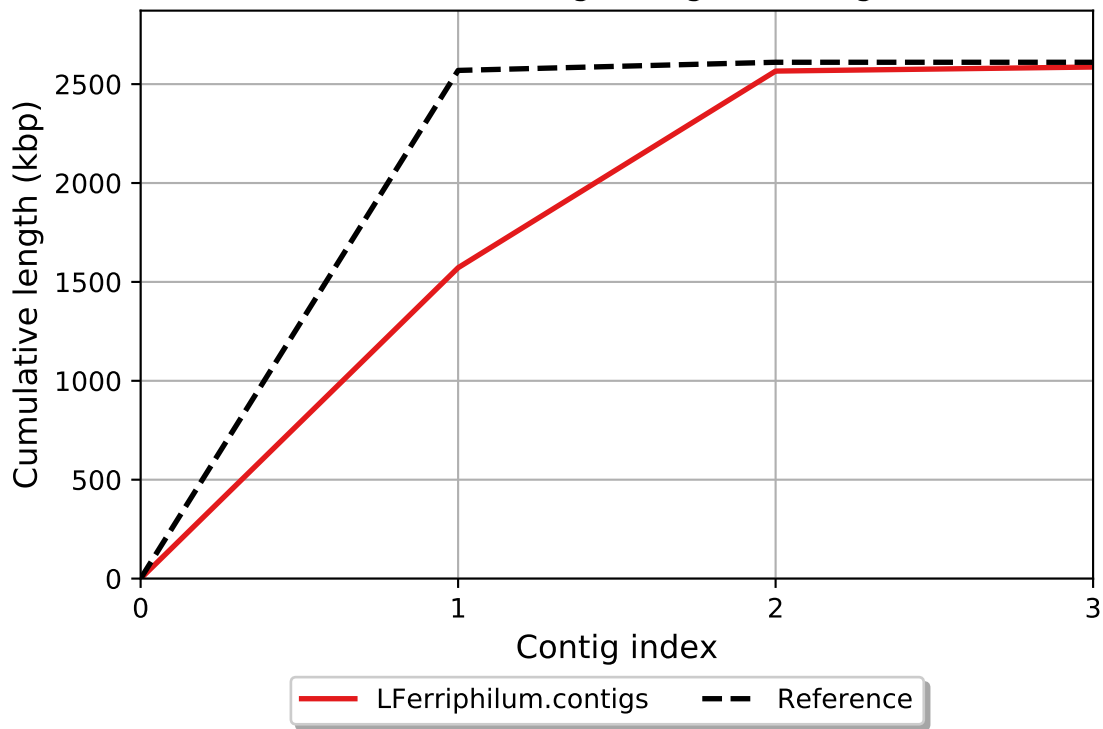
Misassemblies



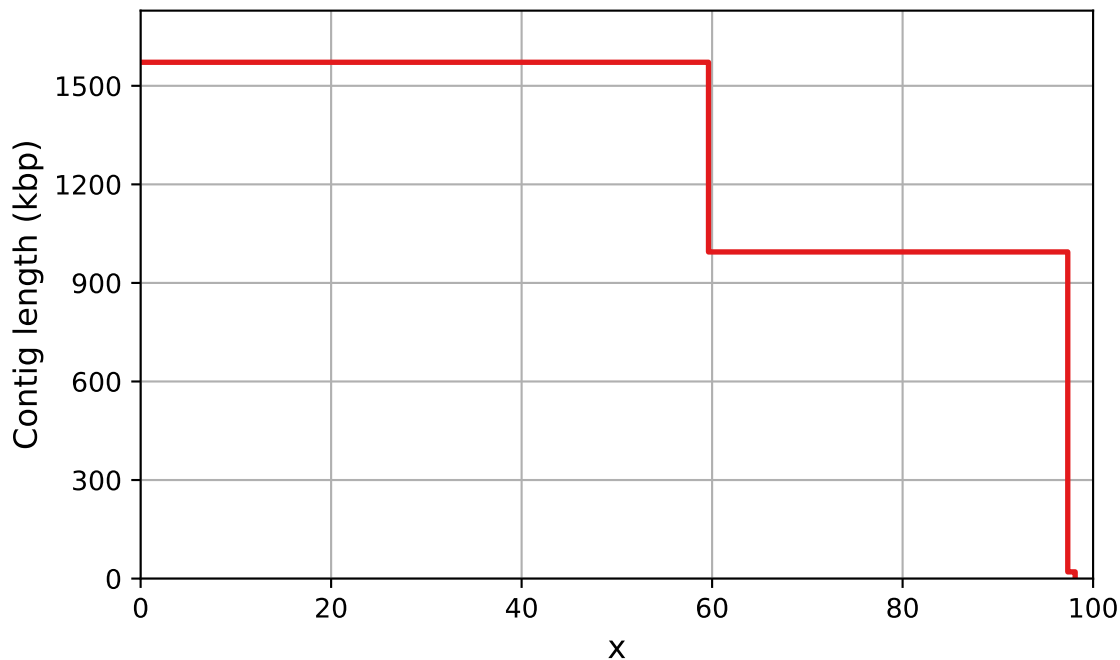
FRCurve (misassemblies)



Cumulative length (aligned contigs)

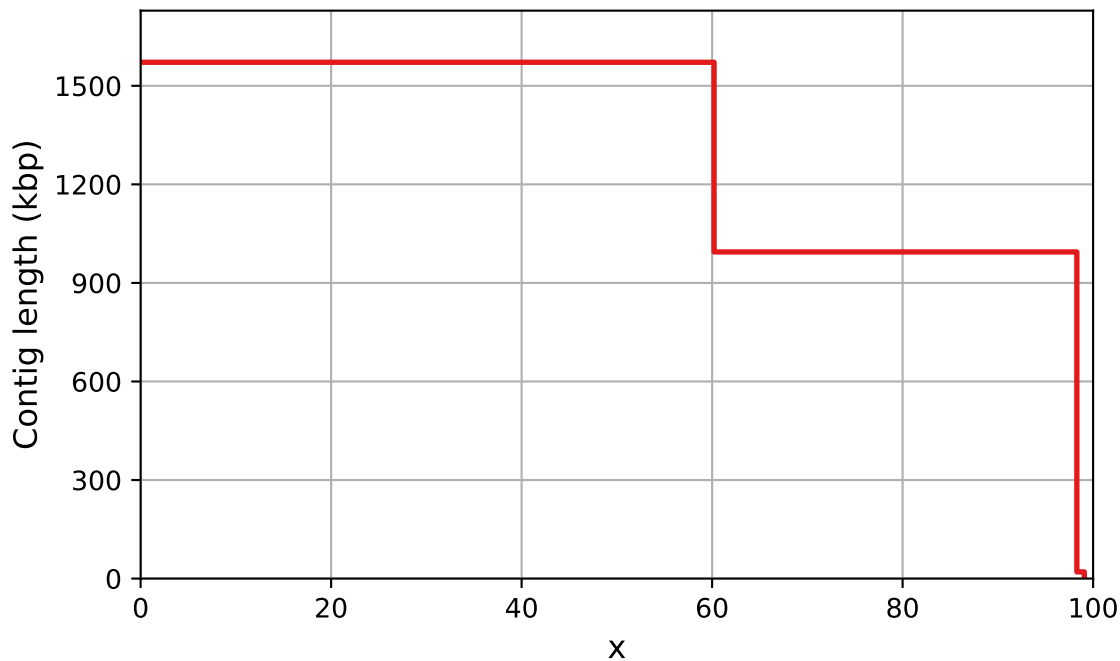


NAx



— LFerriphilum.contigs

NGAx



— LFERriphilum.contigs