

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

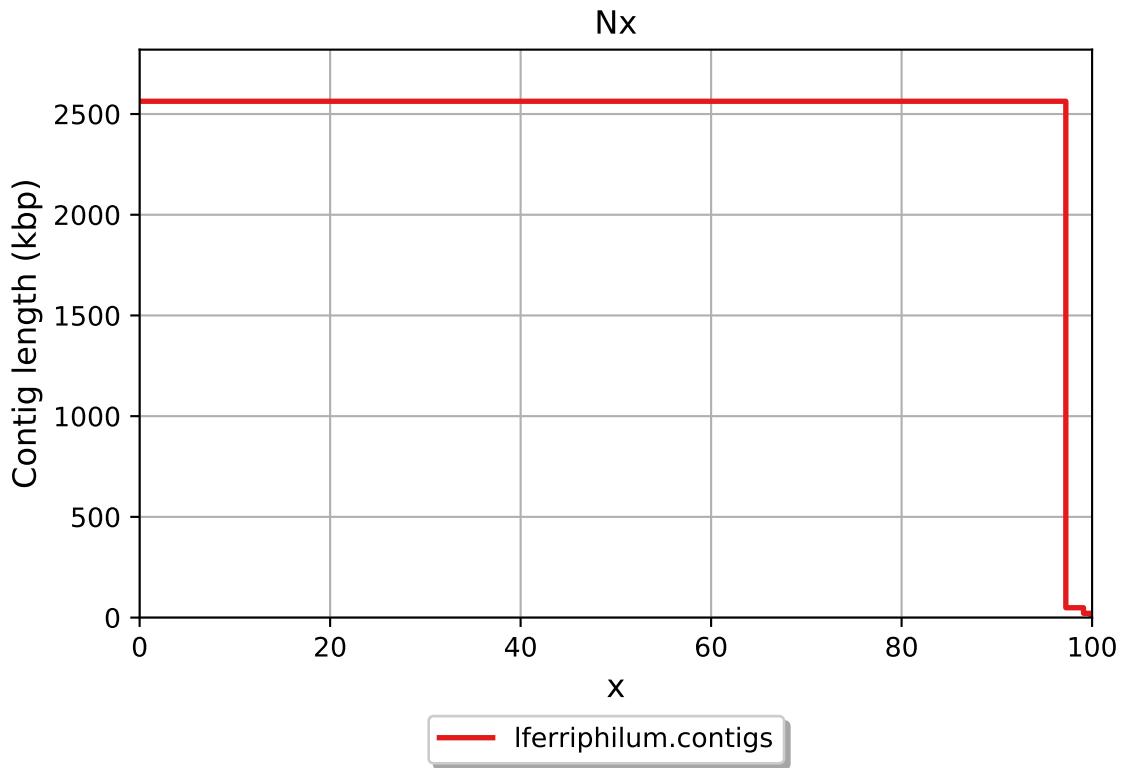
| | lferriphilum.contigs |
|-----------------------------|----------------------|
| # misassemblies | 1 |
| # contig misassemblies | 1 |
| # c. relocations | 1 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # 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 ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

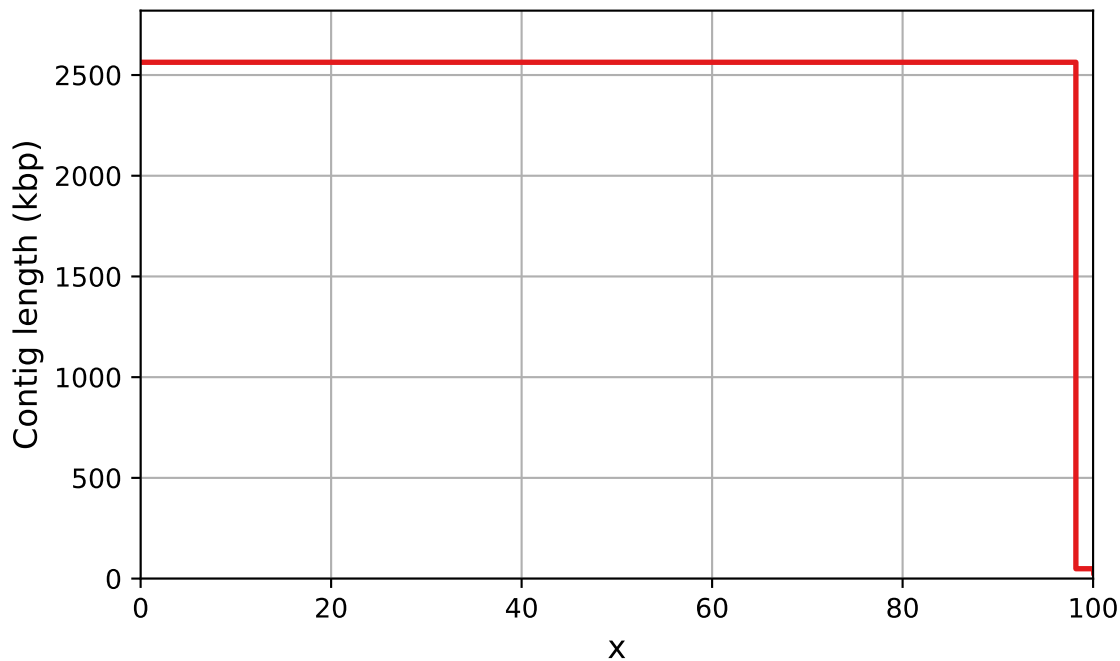
Unaligned report

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

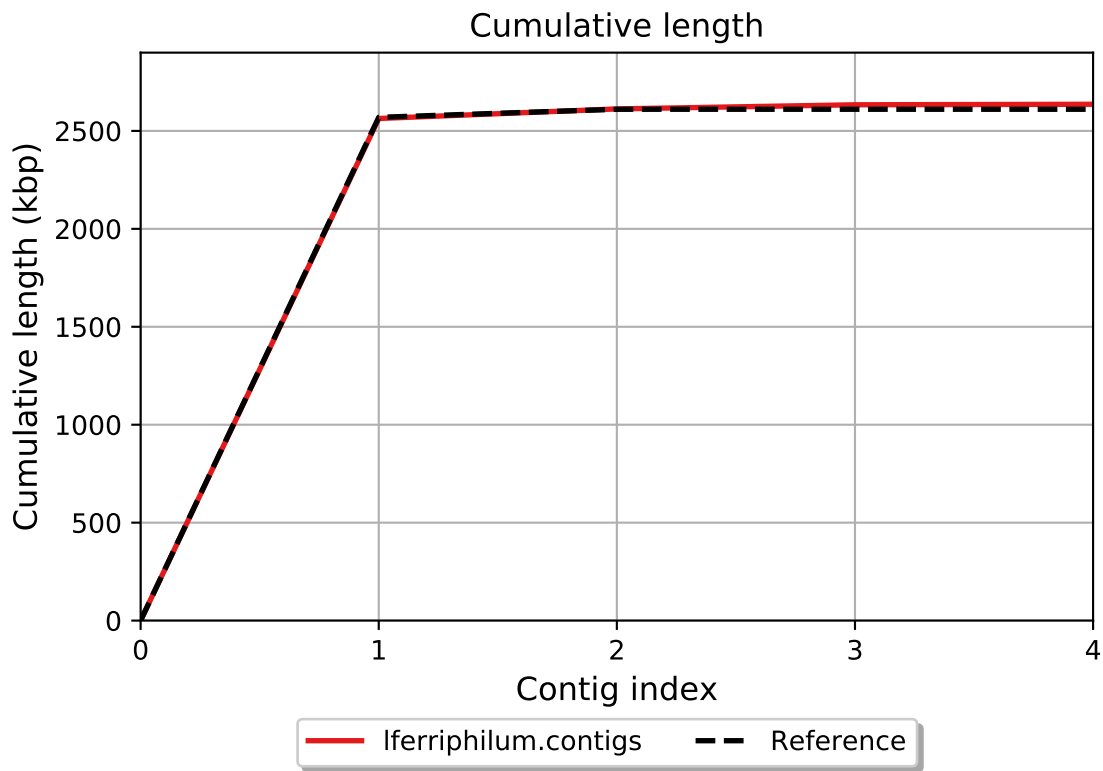
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



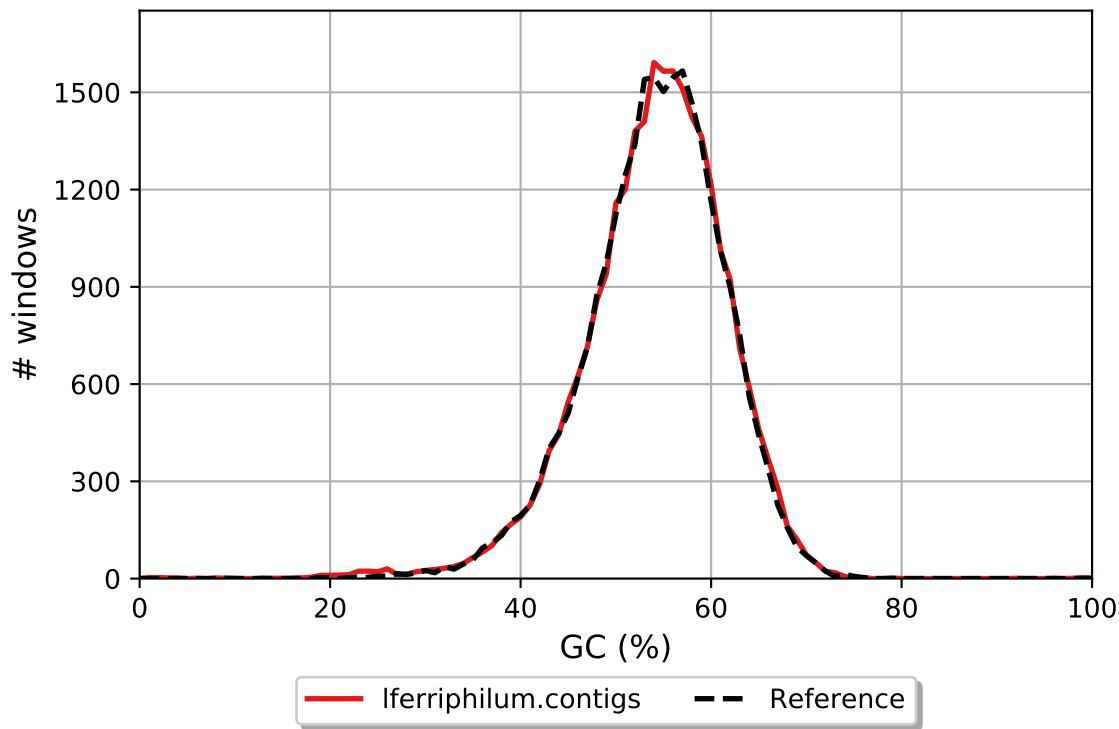
NGx



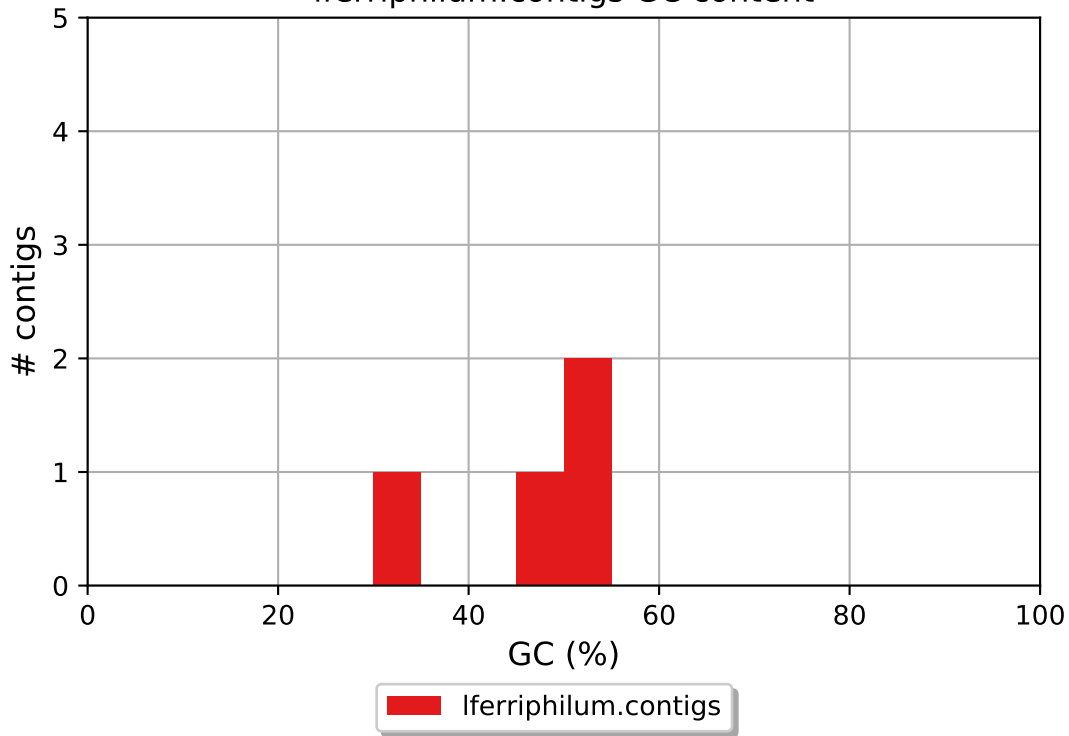
— Iferriphilum.contigs



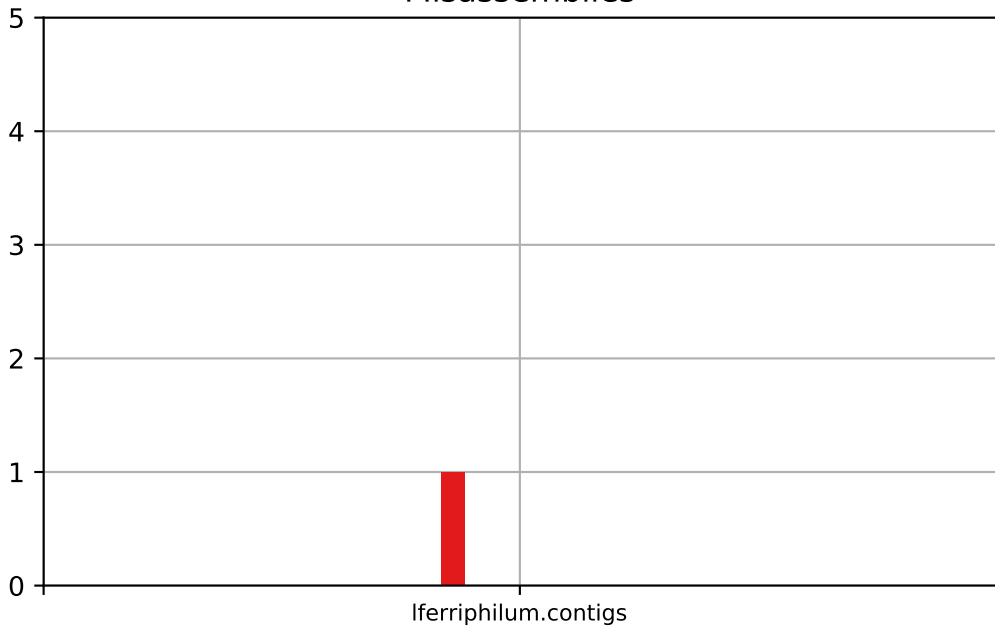
GC content



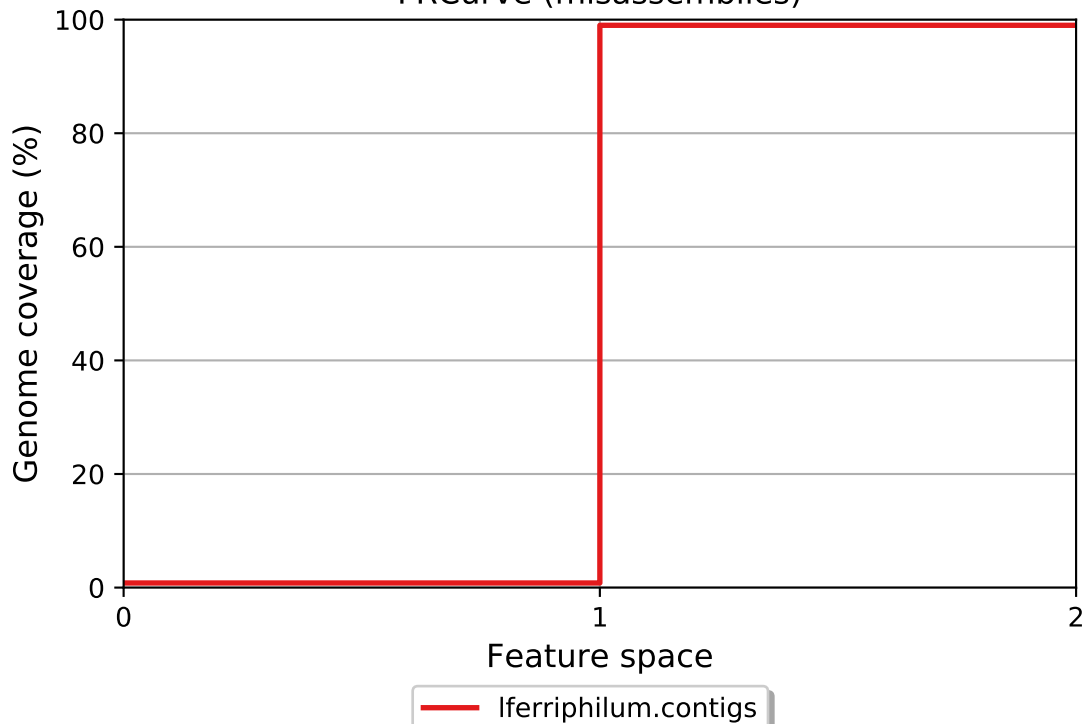
Iferriphilum.contigs GC content



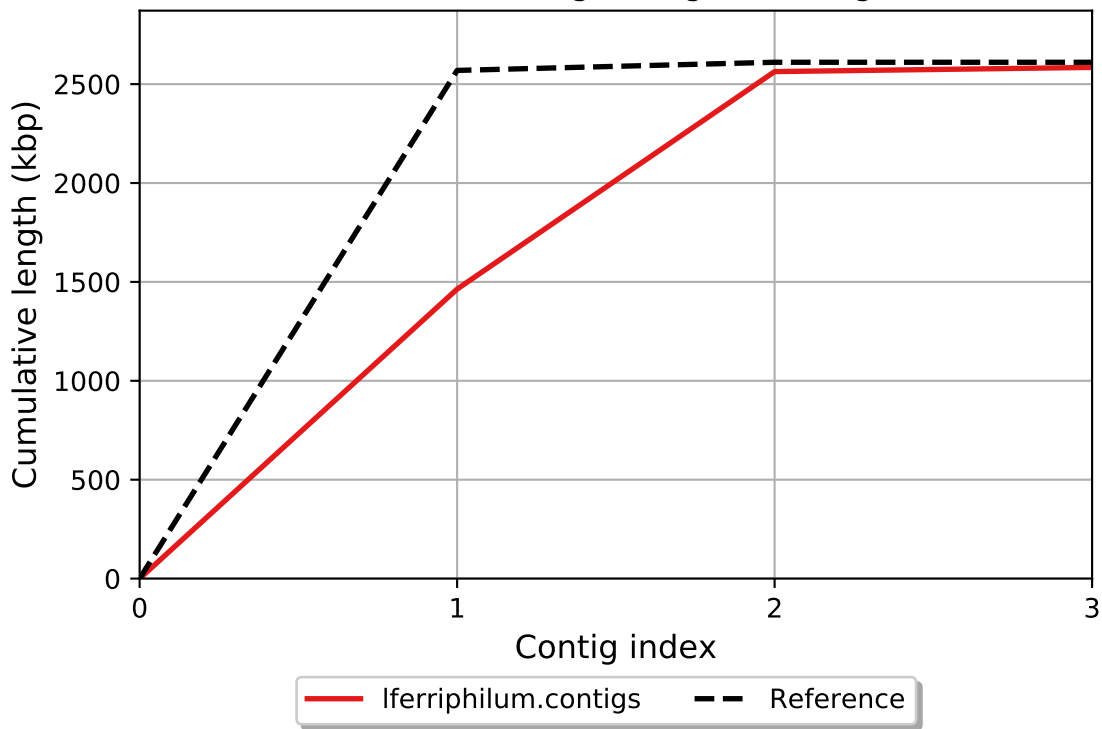
Misassemblies



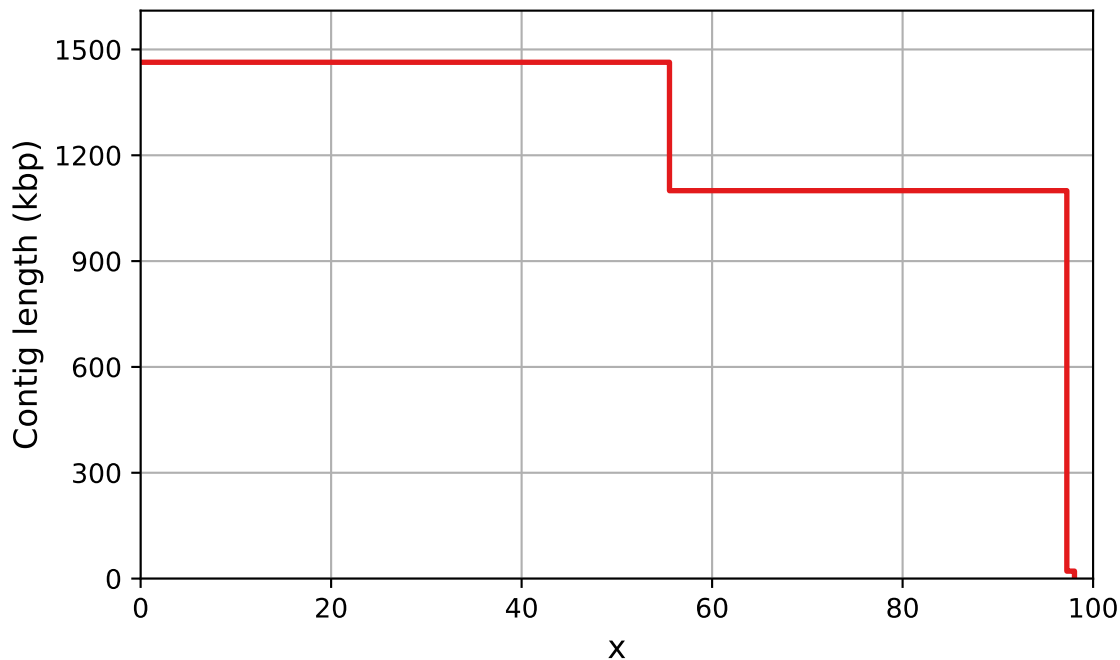
FRCurve (misassemblies)



Cumulative length (aligned contigs)

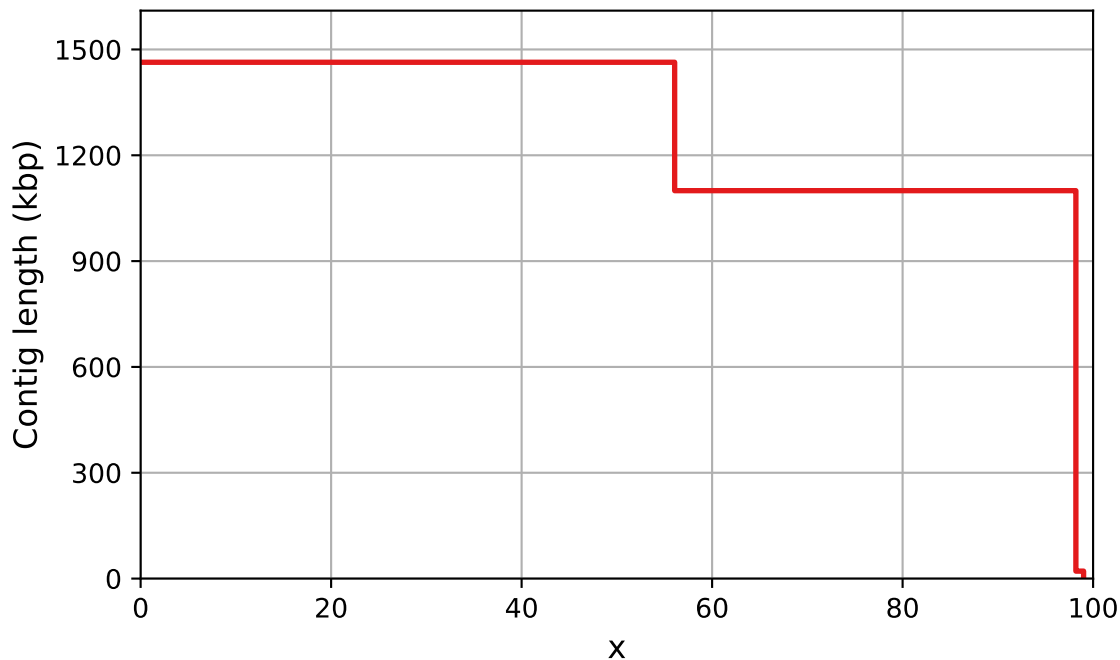


NAx



— Iferriphilum.contigs

NGAx



— Iferriphilum.contigs