

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                    |
| # unaligned mis. contigs    | 0                    |
| # unaligned contigs         | 2 + 0 part           |
| Unaligned length            | 51543                |
| Genome fraction (%)         | 97.566               |
| Duplication ratio           | 1.015                |
| # N's per 100 kbp           | 0.00                 |
| # mismatches per 100 kbp    | 0.00                 |
| # indels per 100 kbp        | 5.89                 |
| 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

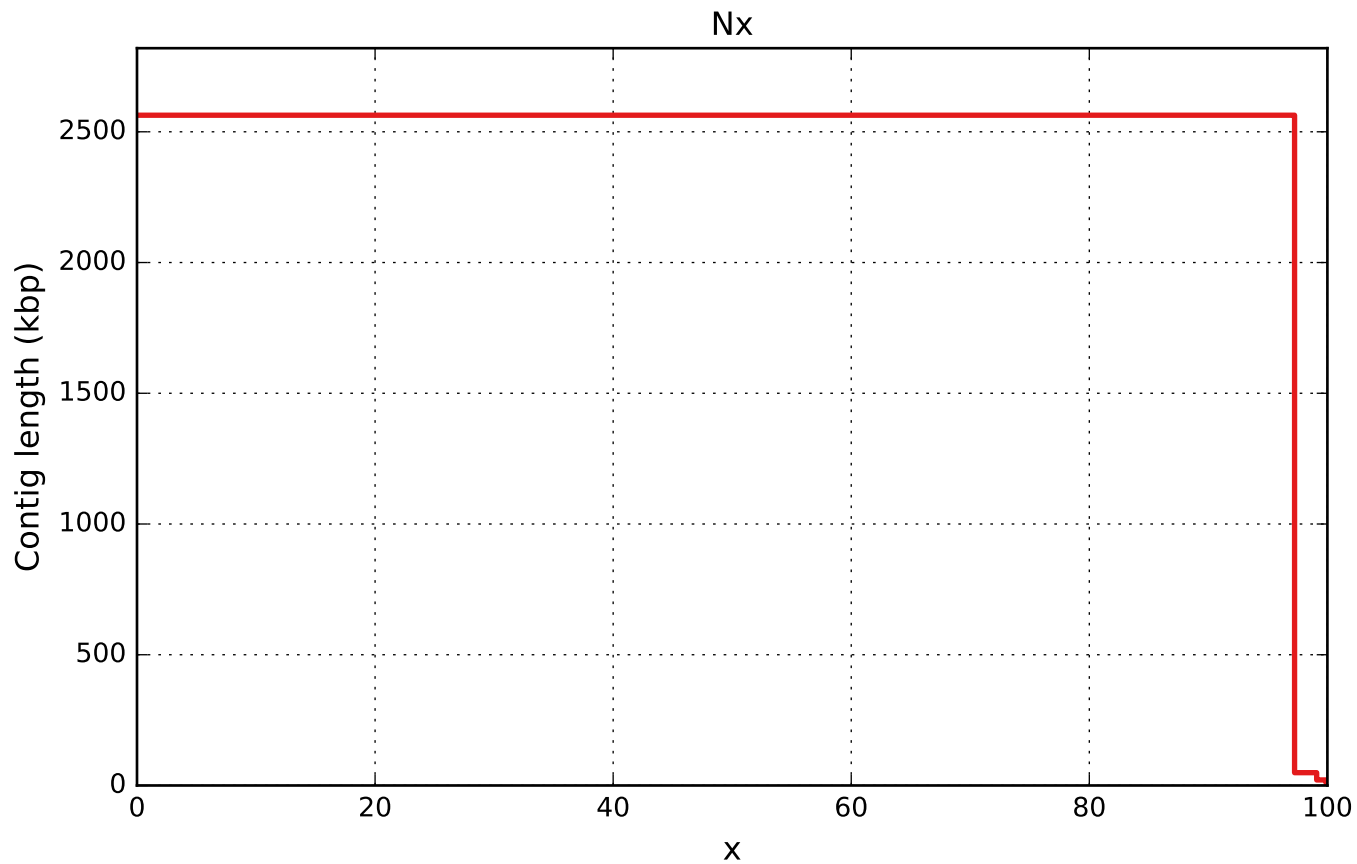
|                             | lferriphilum.contigs |
|-----------------------------|----------------------|
| # misassemblies             | 1                    |
| # relocations               | 1                    |
| # translocations            | 0                    |
| # inversions                | 0                    |
| # misassembled contigs      | 1                    |
| Misassembled contigs length | 2563357              |
| # local misassemblies       | 0                    |
| # unaligned mis. contigs    | 0                    |
| # mismatches                | 0                    |
| # indels                    | 150                  |
| # indels (<= 5 bp)          | 150                  |
| # indels (> 5 bp)           | 0                    |
| Indels length               | 153                  |

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

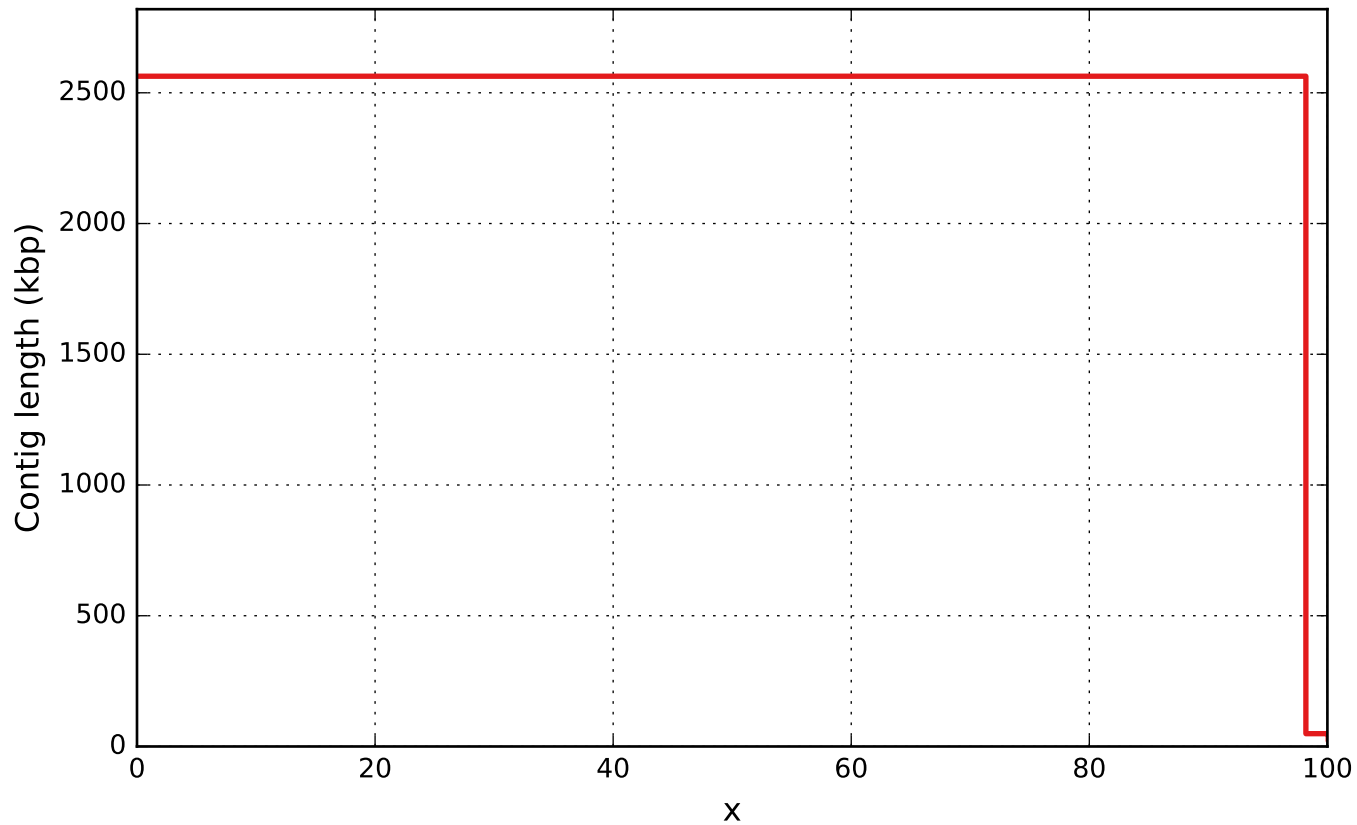
|                               | lferriphilum.contigs |
|-------------------------------|----------------------|
| # fully unaligned contigs     | 2                    |
| Fully unaligned length        | 51543                |
| # partially unaligned contigs | 0                    |
| Partially unaligned 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).

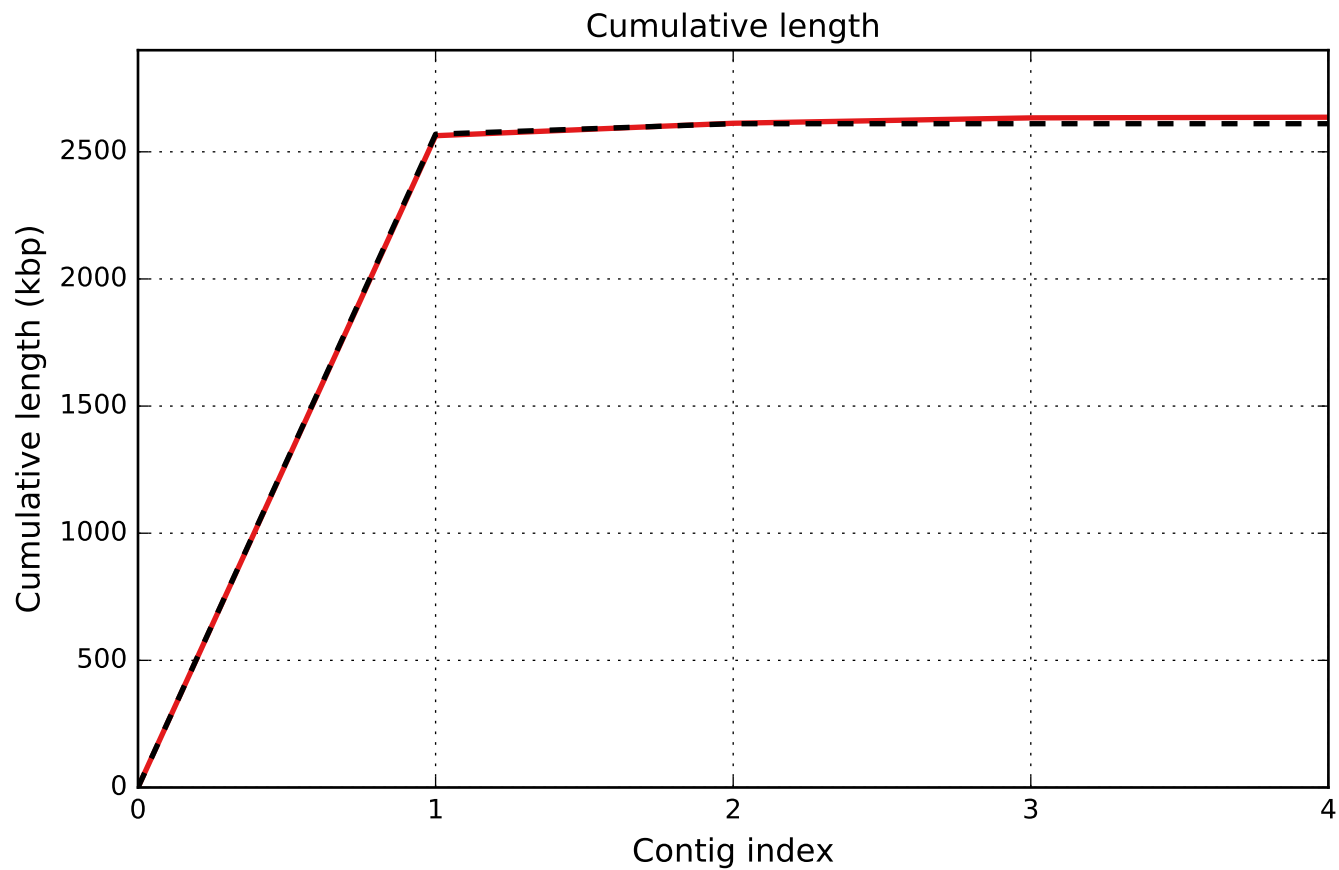


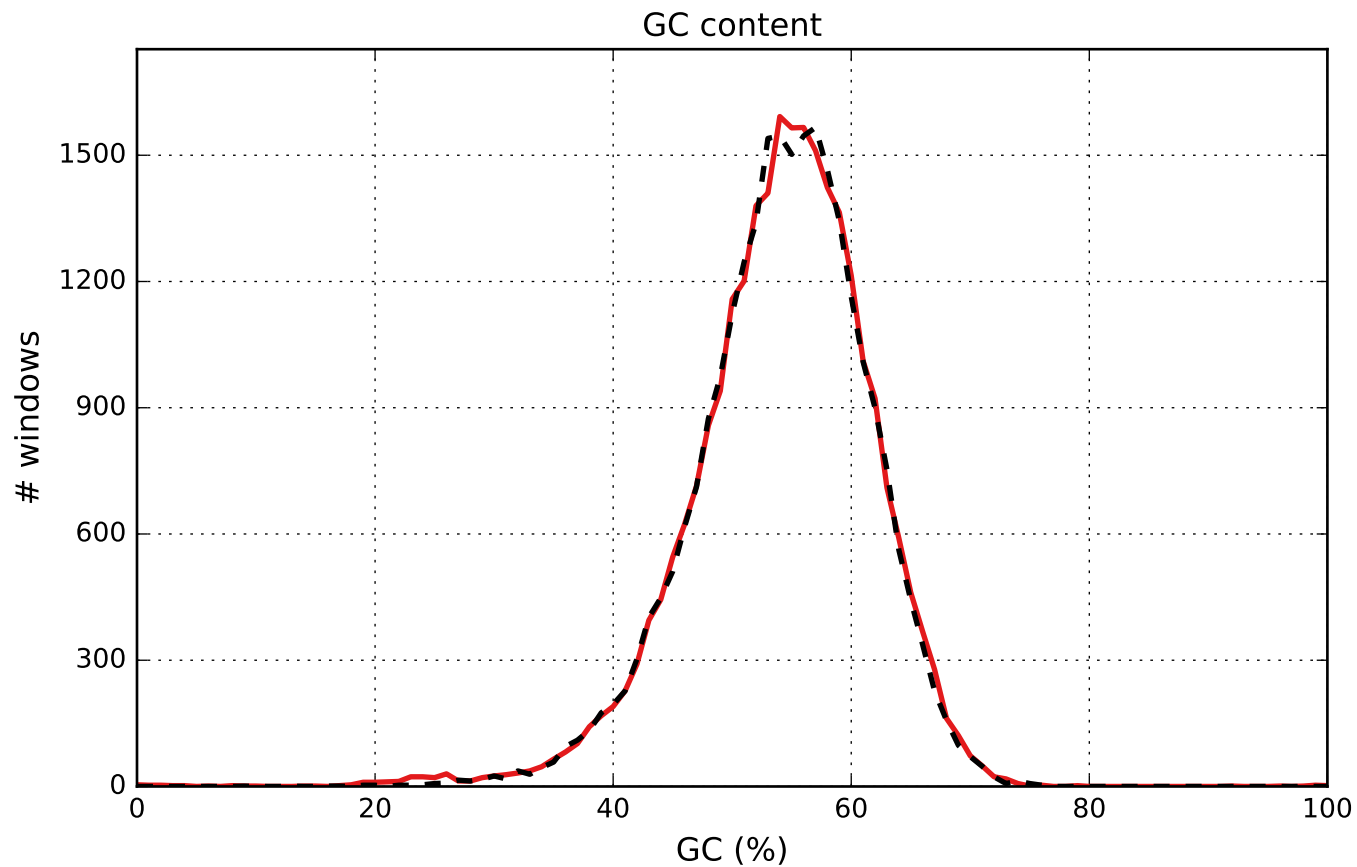
— Iferriphilum.contigs

NGx



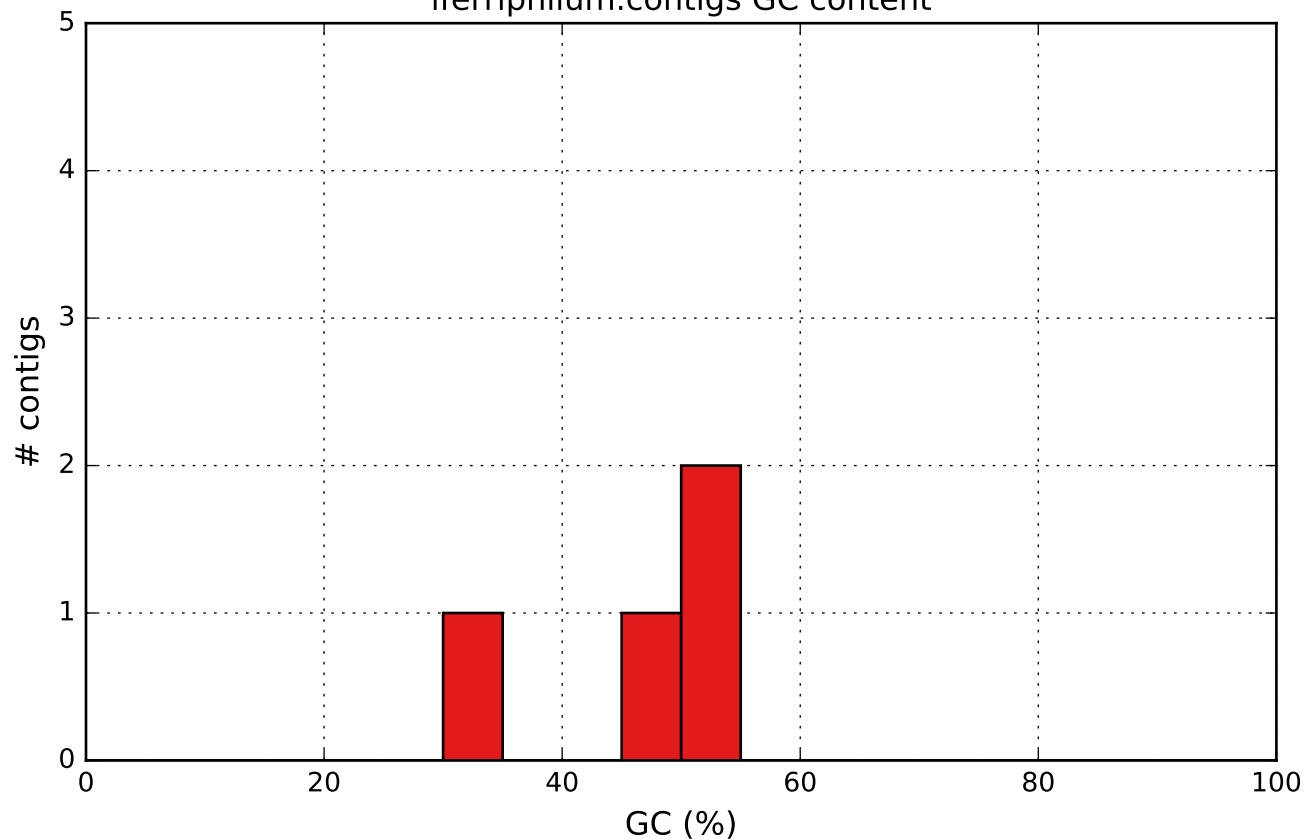
— Iferriphilum.contigs





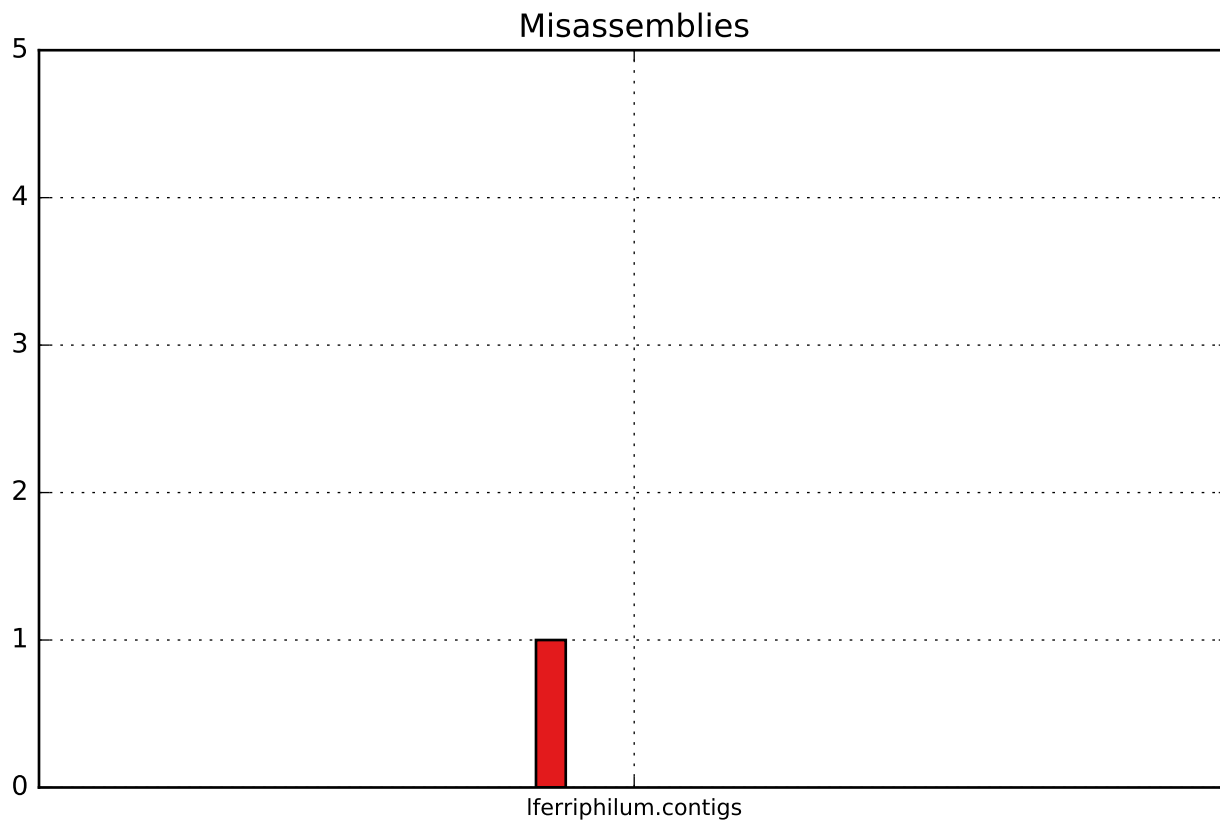
— Iferriphilum.contigs    - - Reference

Iferriphilum.contigs GC content

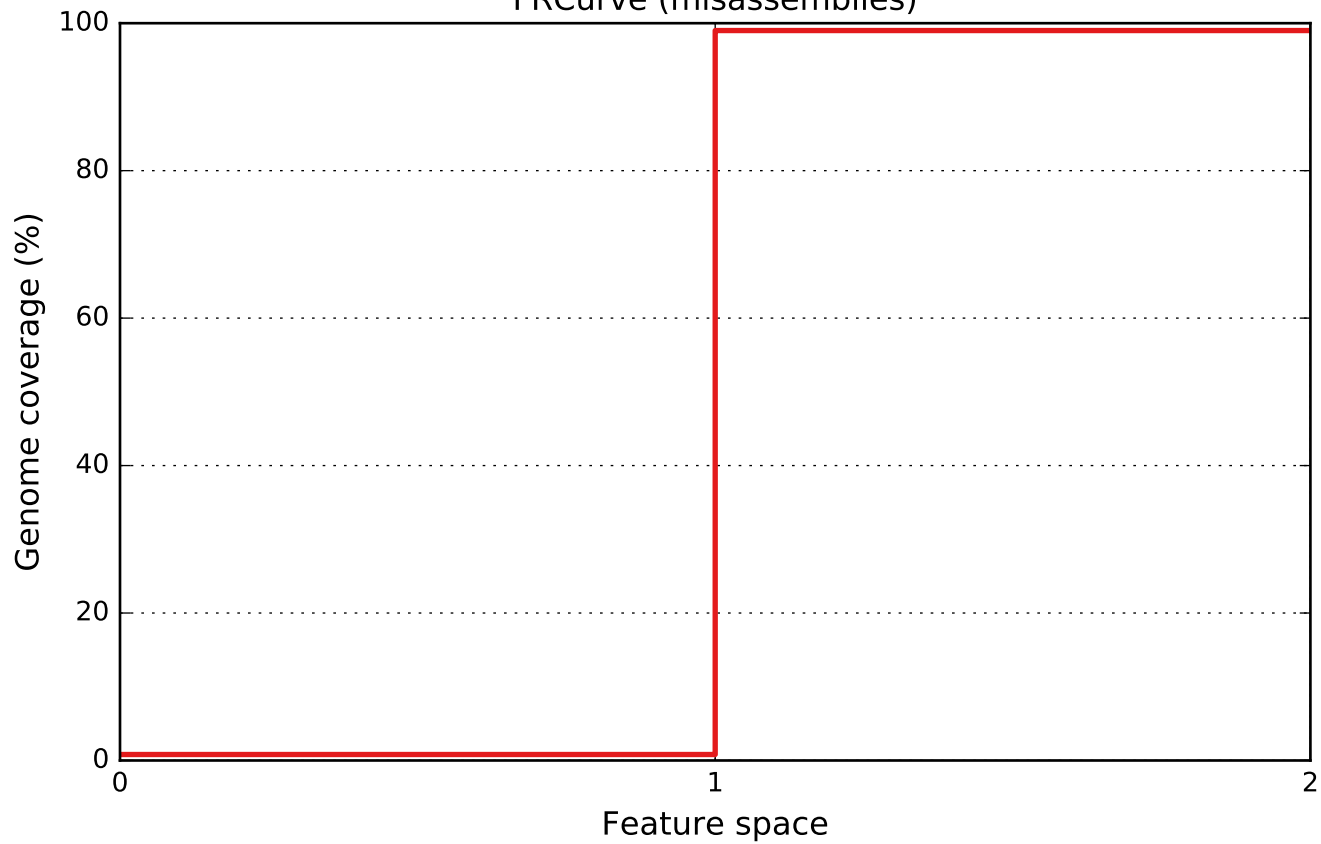


Iferriphilum.contigs



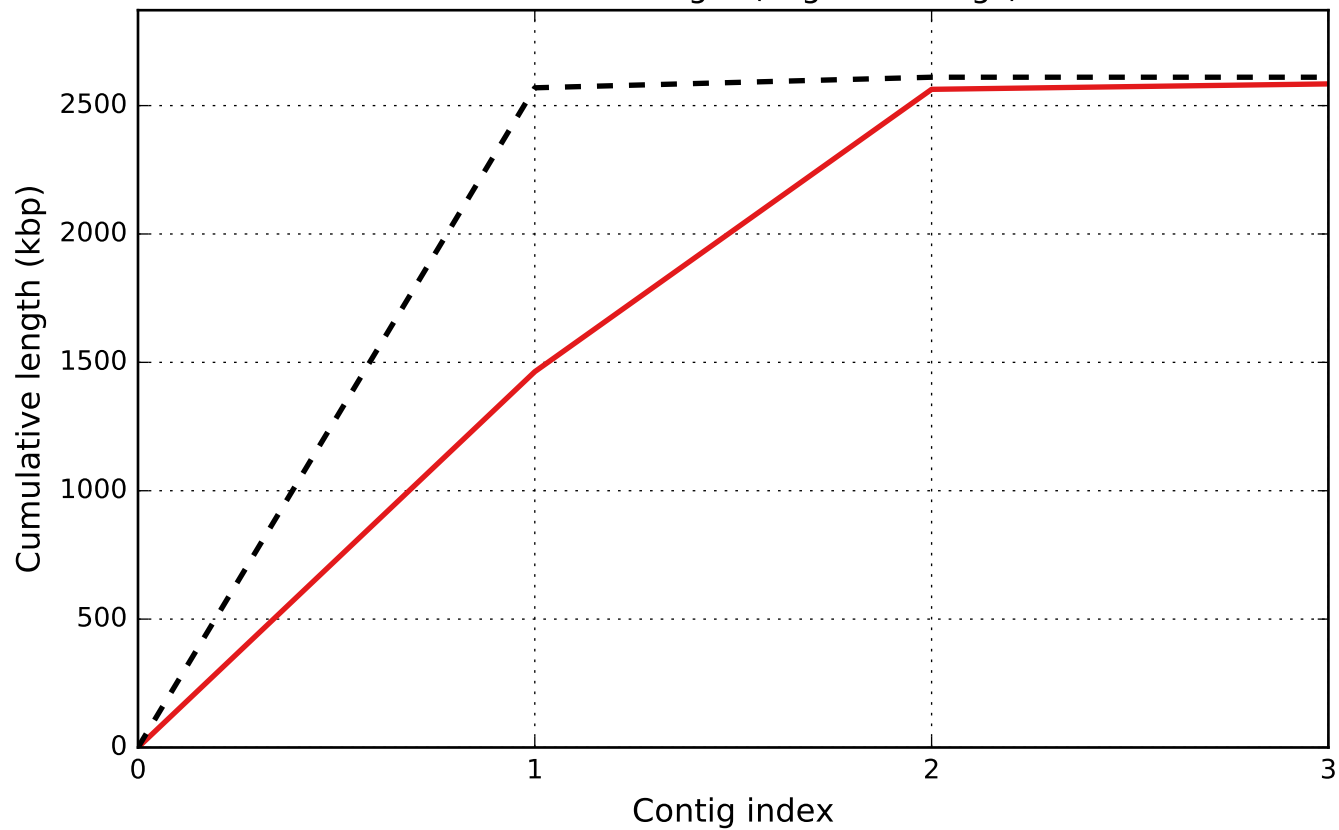


FRCurve (misassemblies)

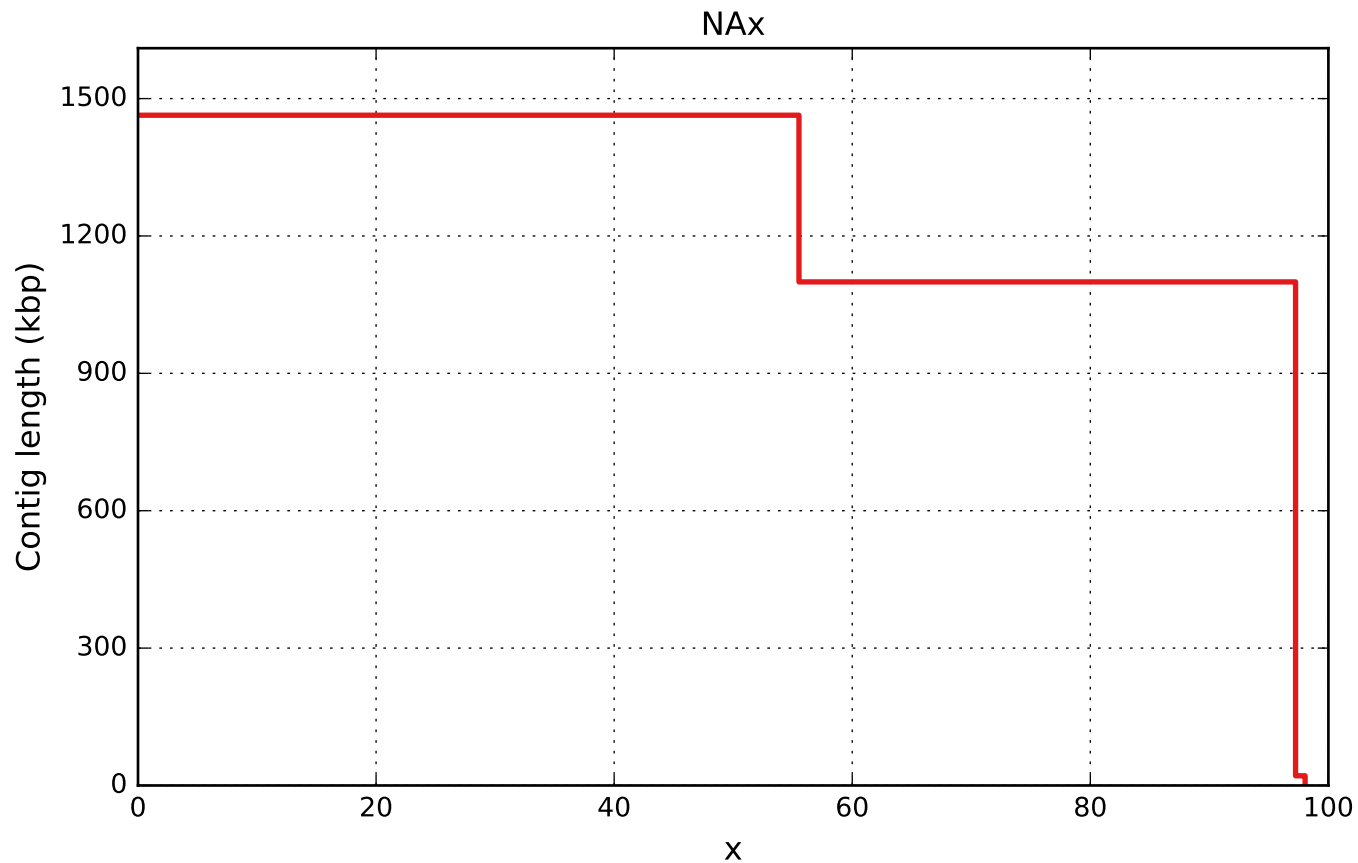


— lferriphilum.contigs

Cumulative length (aligned contigs)

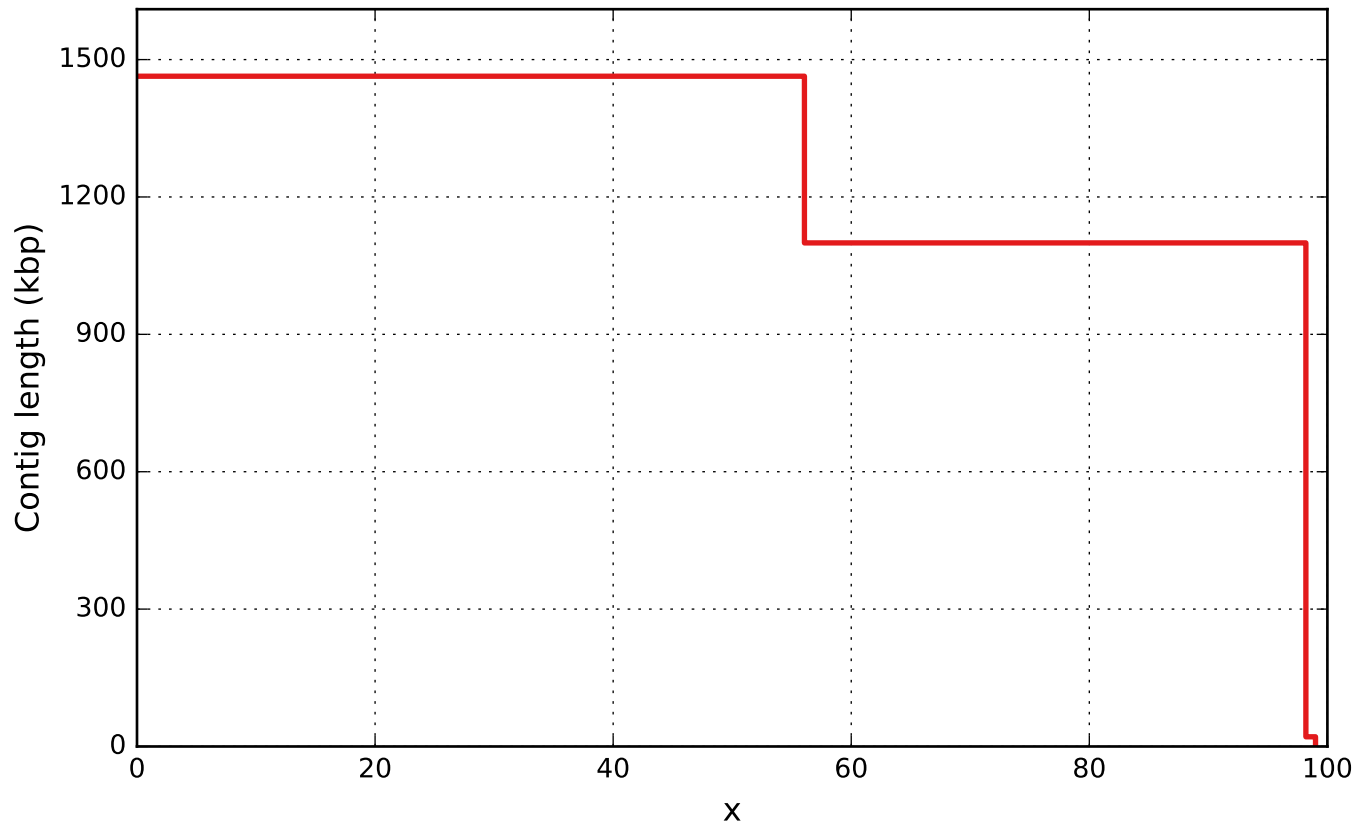


— Iferriphilum.contigs    - - Reference



— Iferriphilum.contigs

NGAx



— Iferriphilum.contigs