## Report

| | contigs |
|---|---|
| # contigs (>= 1000 bp) | 7 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 9990 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 25 |
| Largest contig | 2112 |
| Total length | 22348 |
| Reference length | 2752438 |
| GC (%) | 35.35 |
| Reference GC (%) | 36.67 |
| N50 | 853 |
| NG50 | - |
| N90 | 564 |
| NG90 | - |
| auN | 1082.1 |
| auNG | 8.8 |
| L50 | 9 |
| LG50 | - |
| L90 | 21 |
| LG90 | - |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 964 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 3 part |
| Unaligned length | 3252 |
| Genome fraction (%) | 0.690 |
| Duplication ratio | 0.997 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2958.74 |
| # indels per 100 kbp | 95.10 |
| Largest alignment | 1393 |
| Total aligned length | 18927 |
| NA50 | 764 |
| NGA50 | - |
| NA90 | - |
| NGA90 | - |
| auNA | 730.8 |
| auNGA | 5.9 |
| LA50 | 11 |
| LGA50 | - |
| LA90 | - |
| LGA90 | - |

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).
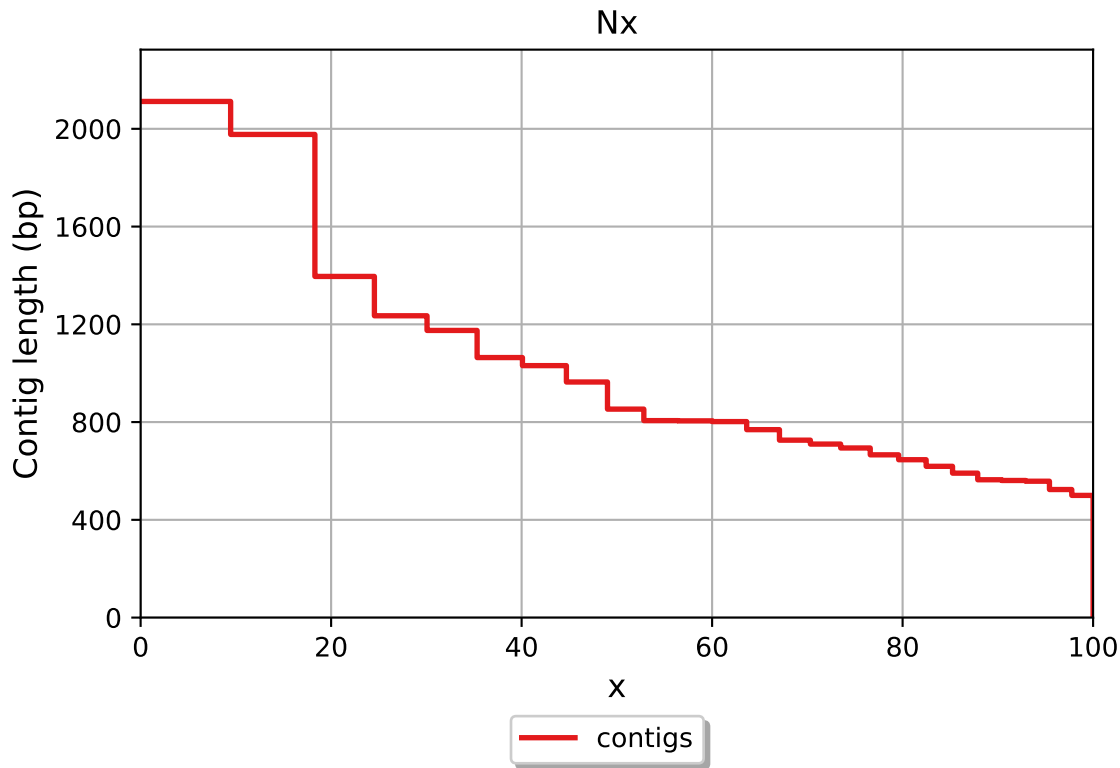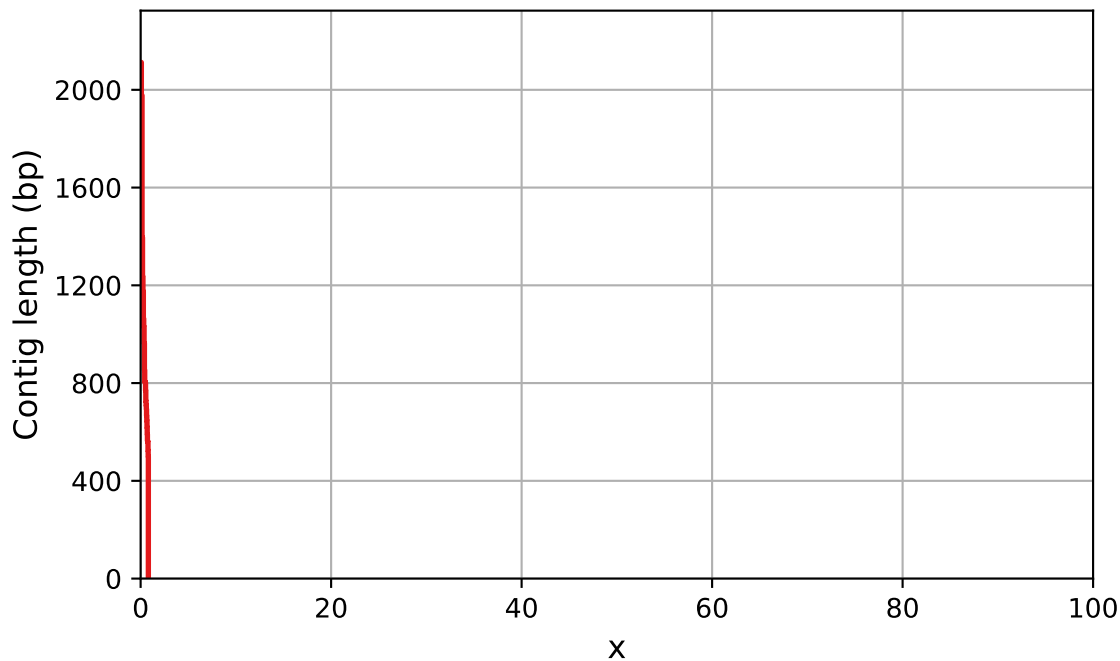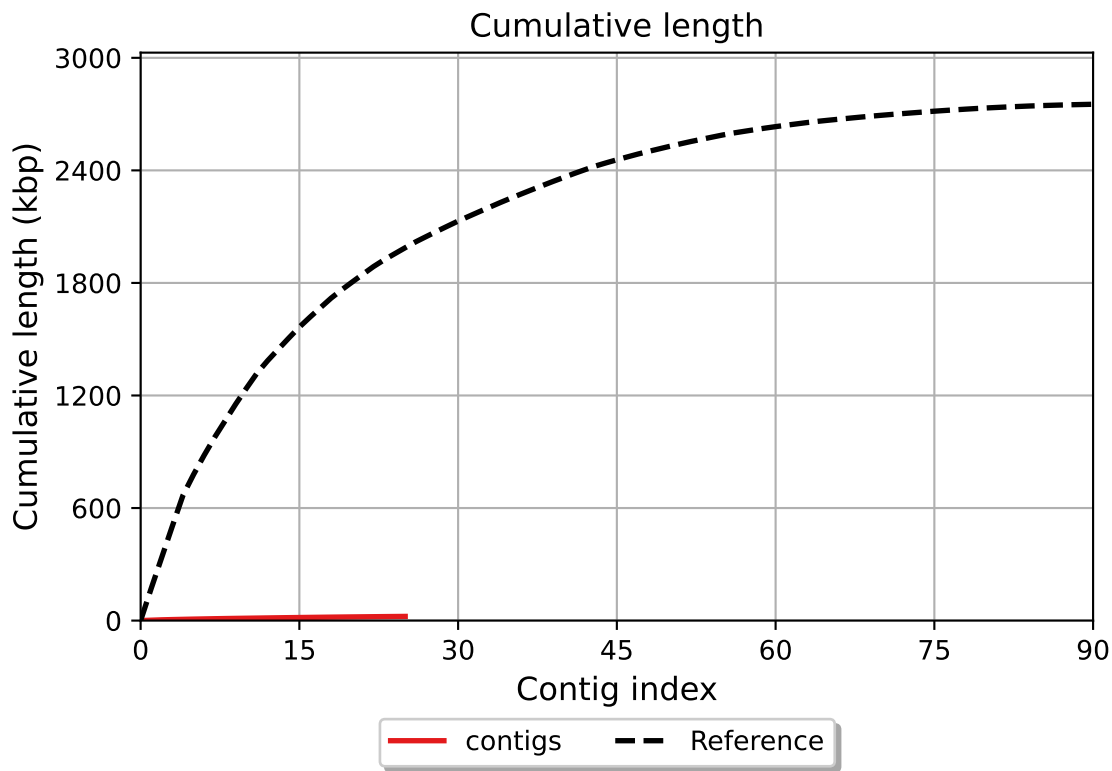
## Misassemblies report

|  | 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 | 964 |
| # possibly misassembled contigs | 2 |
| # possible misassemblies | 2 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 560 |
| # indels | 18 |
| # indels (<= 5 bp) | 15 |
| # indels (> 5 bp) | 3 |
| Indels length | 127 |

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).
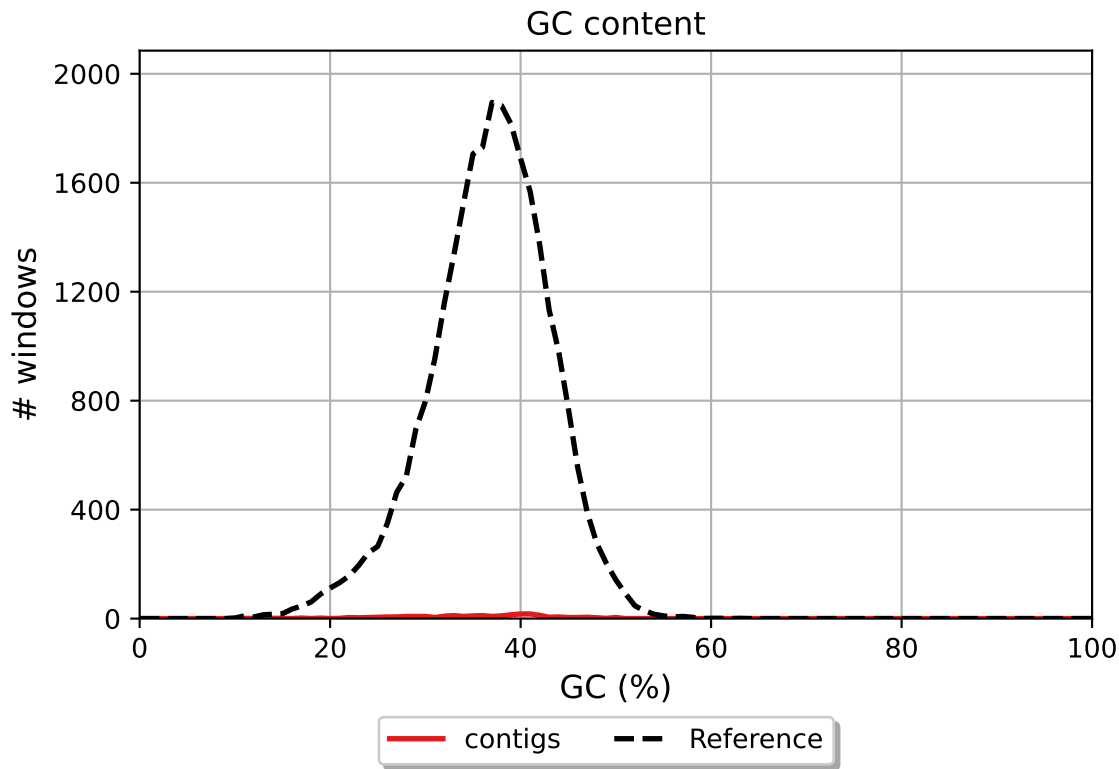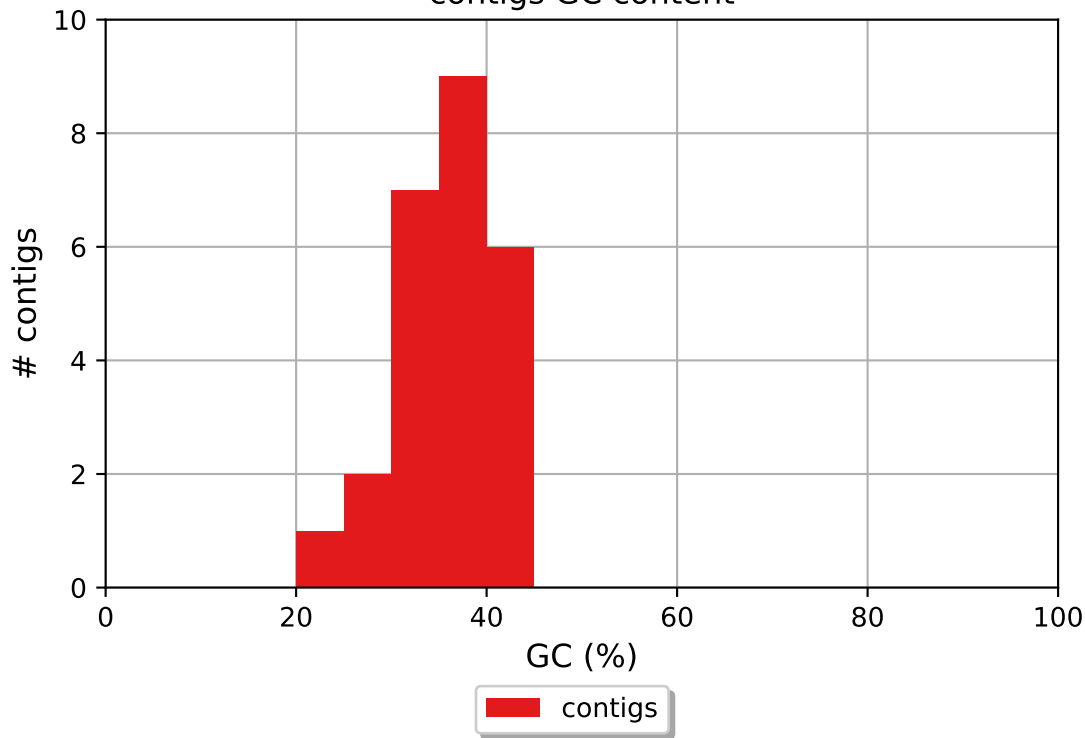
# Unaligned report

|  | contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 3 |
| Partially unaligned length | 3252 |
| # 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).

Nx

NGx

Cumulative length
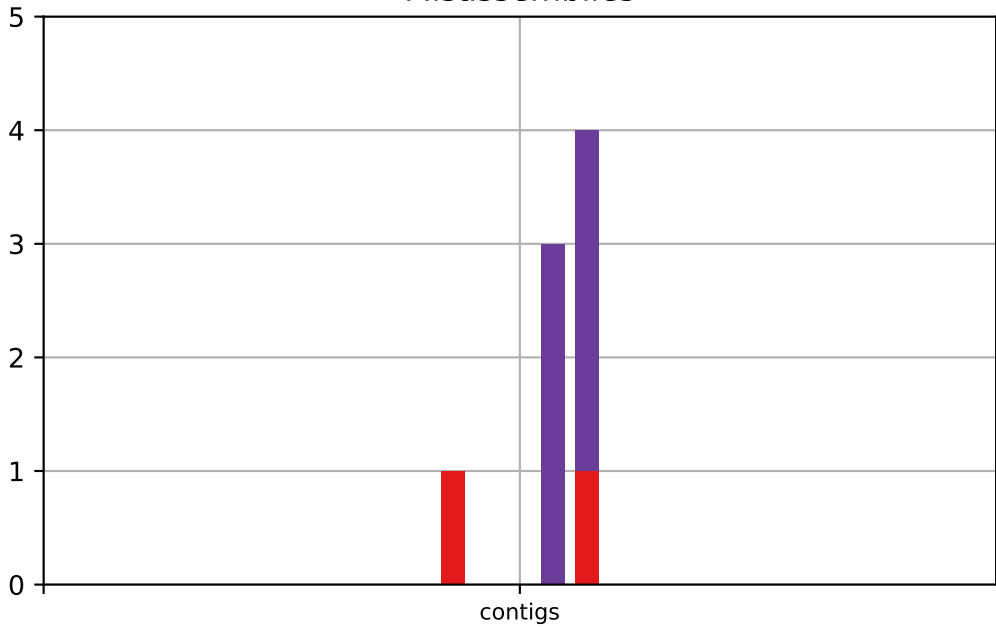
GC content

contigs GC content

Coverage histogram (bin size: 1x)
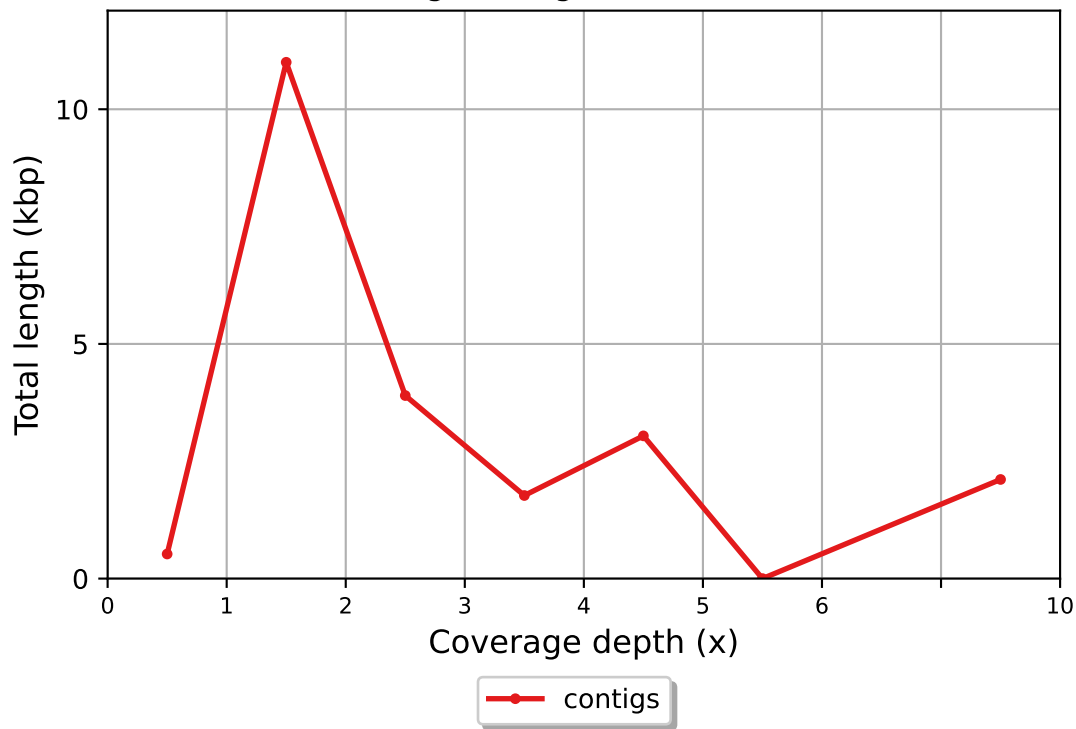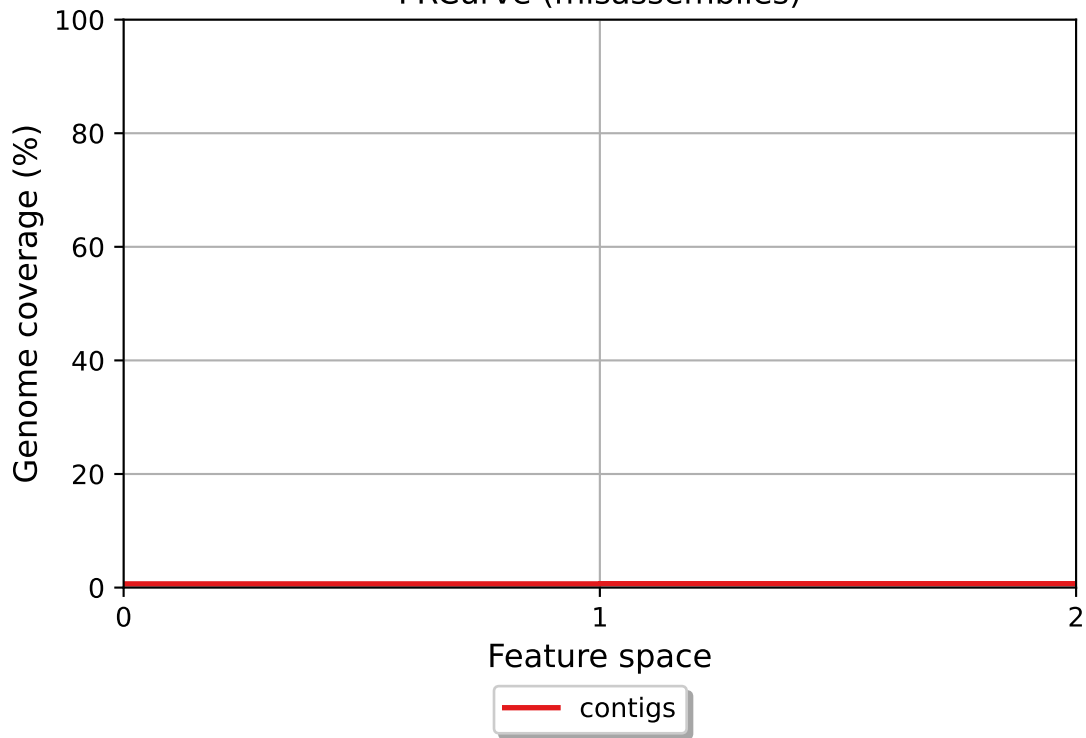
contigs coverage histogram (bin size: 1x)
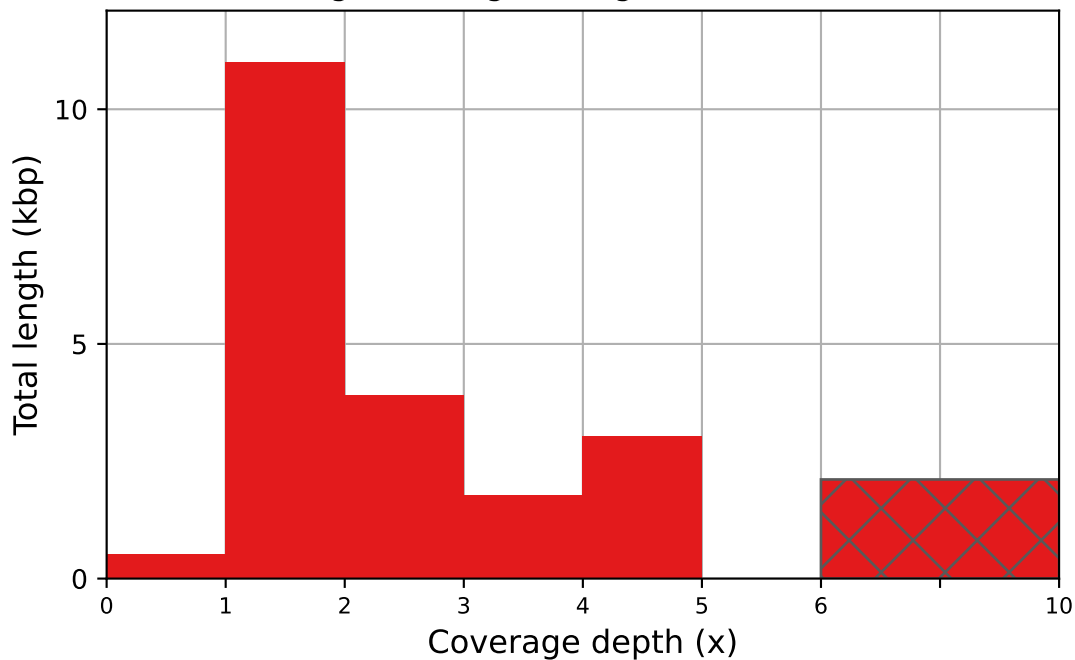
Misassemblies

- # relocations
- # interspecies translocations
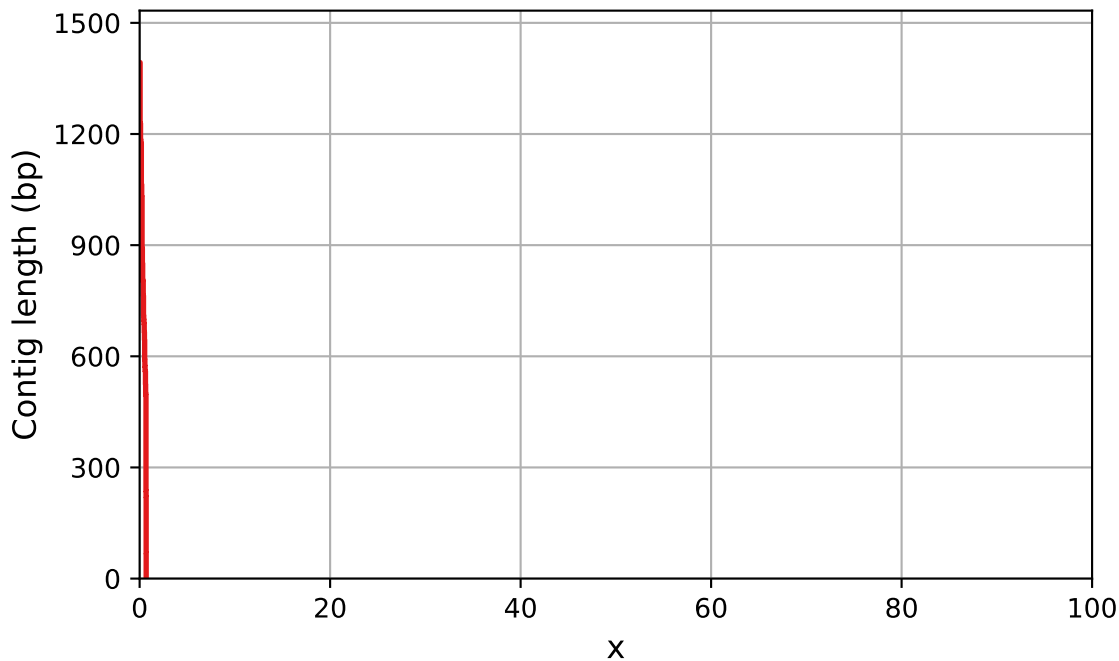
FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx

Contig length (bp) vs x

contigs