

Report

|                             | output.bp.p_ctg |
|-----------------------------|-----------------|
| # contigs (>= 0 bp)         | 36              |
| # contigs (>= 1000 bp)      | 36              |
| # contigs (>= 5000 bp)      | 36              |
| # contigs (>= 10000 bp)     | 36              |
| # contigs (>= 25000 bp)     | 20              |
| # contigs (>= 50000 bp)     | 18              |
| Total length (>= 0 bp)      | 12502635        |
| Total length (>= 1000 bp)   | 12502635        |
| Total length (>= 5000 bp)   | 12502635        |
| Total length (>= 10000 bp)  | 12502635        |
| Total length (>= 25000 bp)  | 12218904        |
| Total length (>= 50000 bp)  | 12167714        |
| # contigs                   | 36              |
| Largest contig              | 1505909         |
| Total length                | 12502635        |
| Reference length            | 12157105        |
| GC (%)                      | 38.38           |
| Reference GC (%)            | 38.15           |
| N50                         | 805283          |
| NG50                        | 805283          |
| N75                         | 578501          |
| NG75                        | 609354          |
| L50                         | 6               |
| LG50                        | 6               |
| L75                         | 11              |
| LG75                        | 10              |
| # misassemblies             | 111             |
| # misassembled contigs      | 32              |
| Misassembled contigs length | 12442882        |
| # local misassemblies       | 68              |
| # scaffold gap ext. mis.    | 0               |
| # scaffold gap loc. mis.    | 0               |
| # unaligned mis. contigs    | 0               |
| # unaligned contigs         | 0 + 18 part     |
| Unaligned length            | 81395           |
| Genome fraction (%)         | 97.447          |
| Duplication ratio           | 1.048           |
| # N's per 100 kbp           | 0.00            |
| # mismatches per 100 kbp    | 225.11          |
| # indels per 100 kbp        | 24.72           |
| Largest alignment           | 843303          |
| Total aligned length        | 12408967        |
| NA50                        | 273893          |
| NGA50                       | 284119          |
| NA75                        | 154838          |
| NGA75                       | 165514          |
| LA50                        | 13              |
| LGA50                       | 12              |
| LA75                        | 28              |
| LGA75                       | 26              |

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

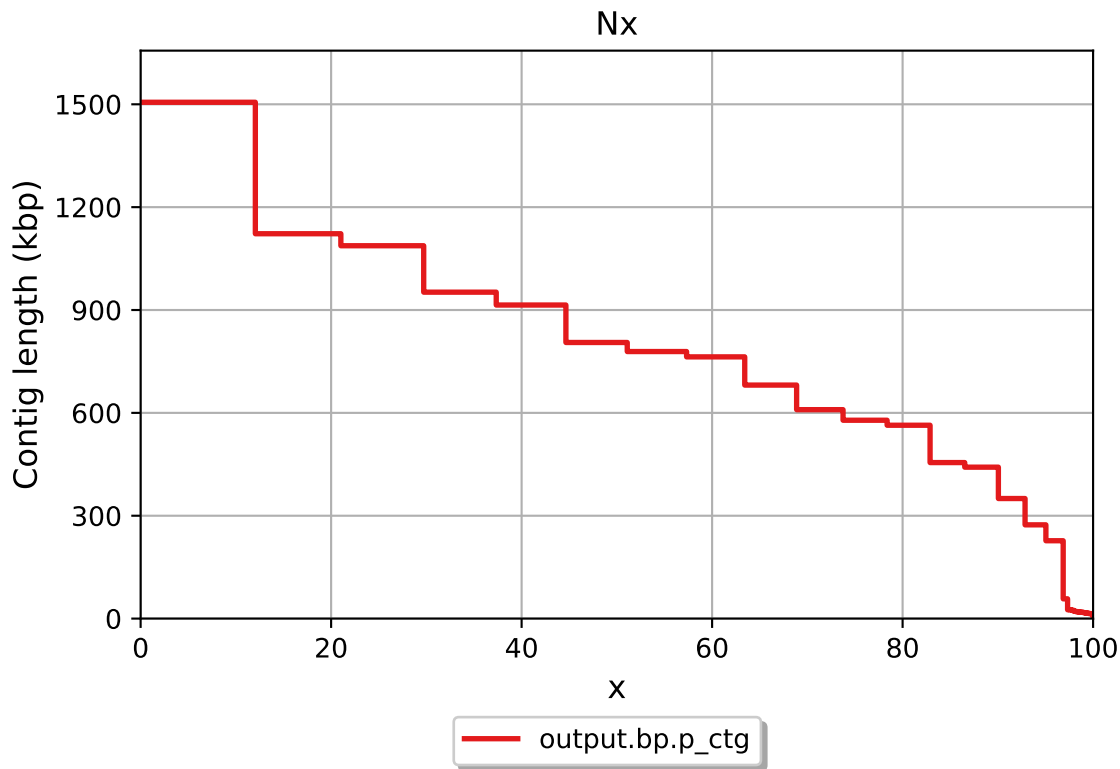
|                             | output.bp.p_ctg |
|-----------------------------|-----------------|
| # misassemblies             | 111             |
| # contig misassemblies      | 111             |
| # c. relocations            | 47              |
| # c. translocations         | 63              |
| # c. inversions             | 1               |
| # scaffold misassemblies    | 0               |
| # s. relocations            | 0               |
| # s. translocations         | 0               |
| # s. inversions             | 0               |
| # misassembled contigs      | 32              |
| Misassembled contigs length | 12442882        |
| # local misassemblies       | 68              |
| # scaffold gap ext. mis.    | 0               |
| # scaffold gap loc. mis.    | 0               |
| # unaligned mis. contigs    | 0               |
| # mismatches                | 26668           |
| # indels                    | 2928            |
| # indels (<= 5 bp)          | 2473            |
| # indels (> 5 bp)           | 455             |
| Indels length               | 14382           |

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).

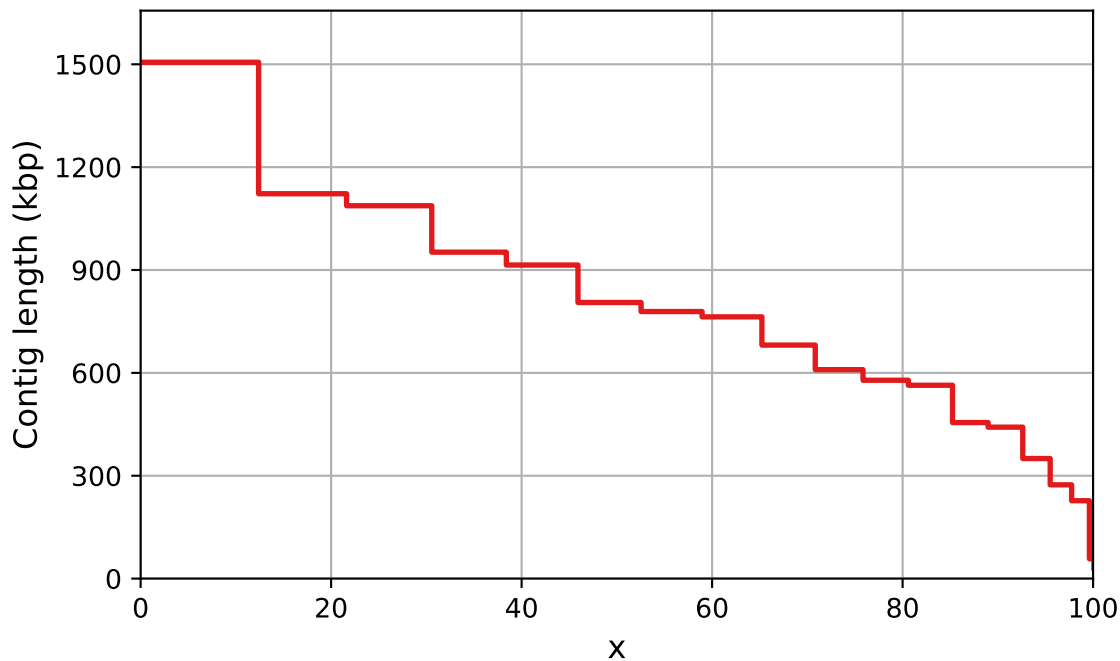
## Unaligned report

|                               | output.bp.p_ctg |
|-------------------------------|-----------------|
| # fully unaligned contigs     | 0               |
| Fully unaligned length        | 0               |
| # partially unaligned contigs | 18              |
| Partially unaligned length    | 81395           |
| # 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).

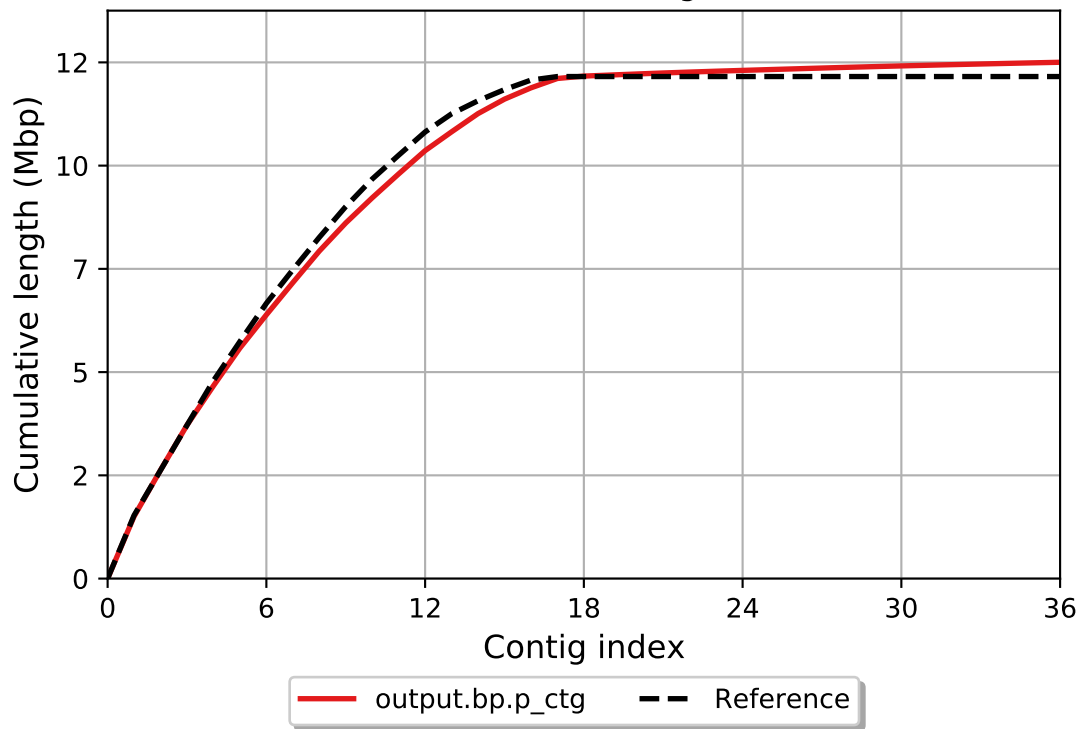


NGx

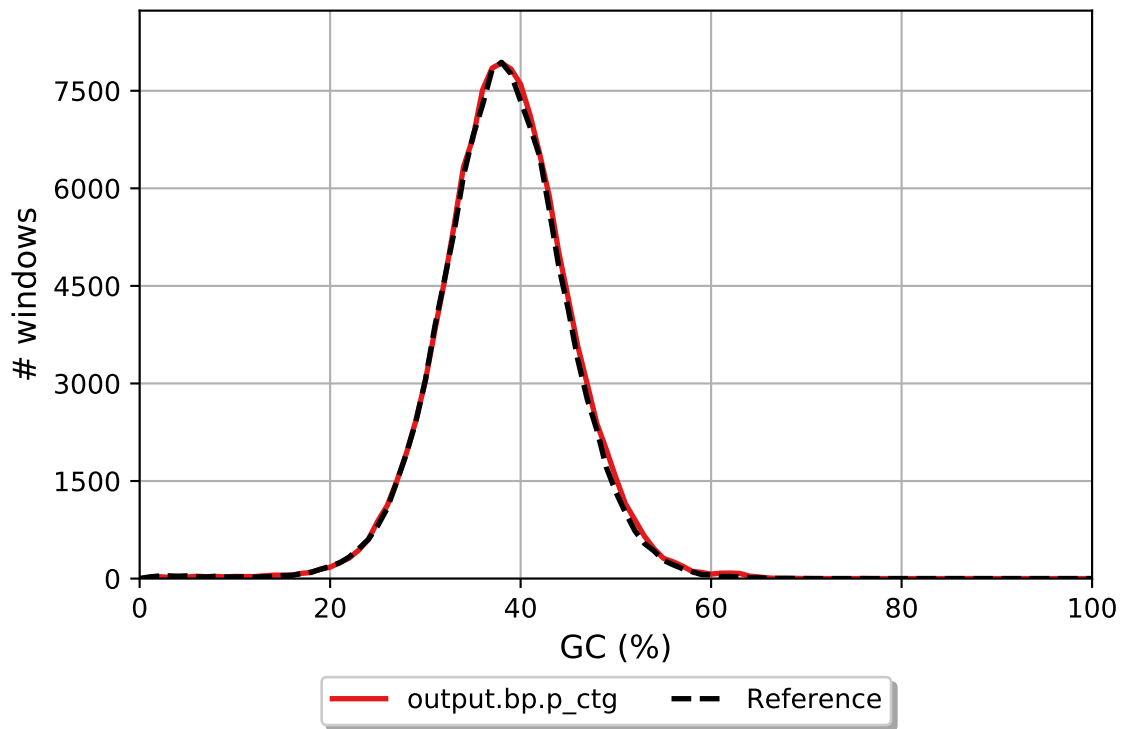


— output.bp.p\_ctg

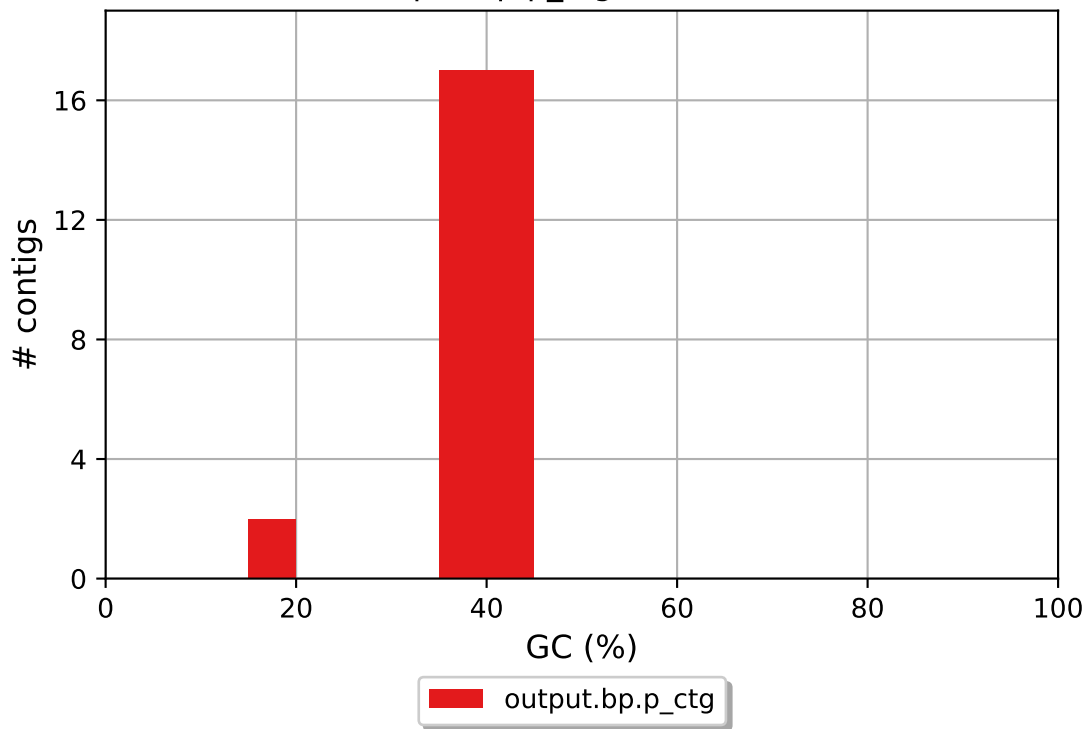
Cumulative length



## GC content

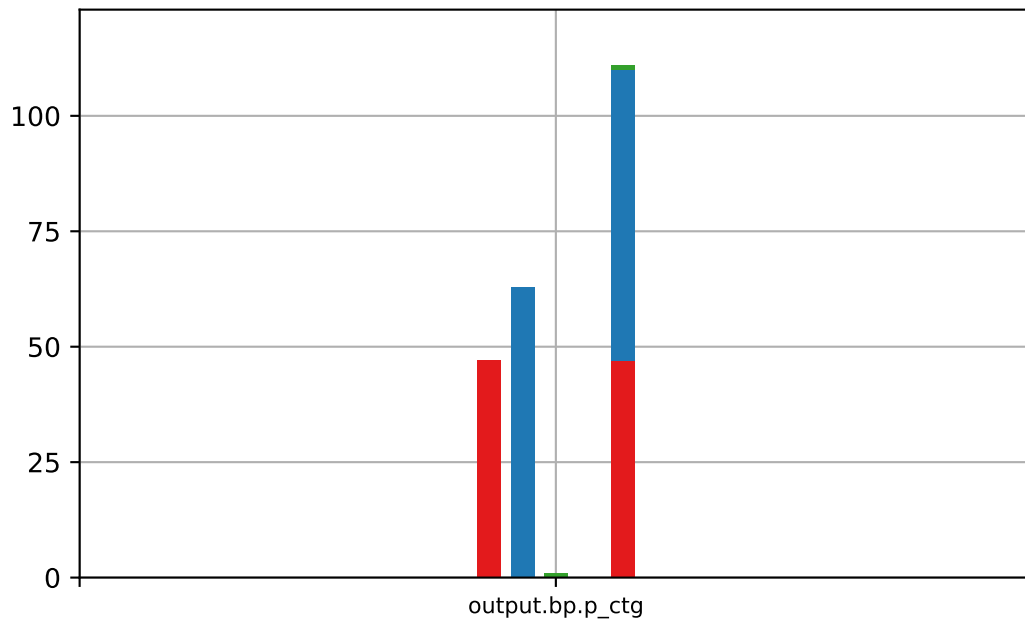


output.bp.p\_ctg GC content





## Misassemblies



# relocations

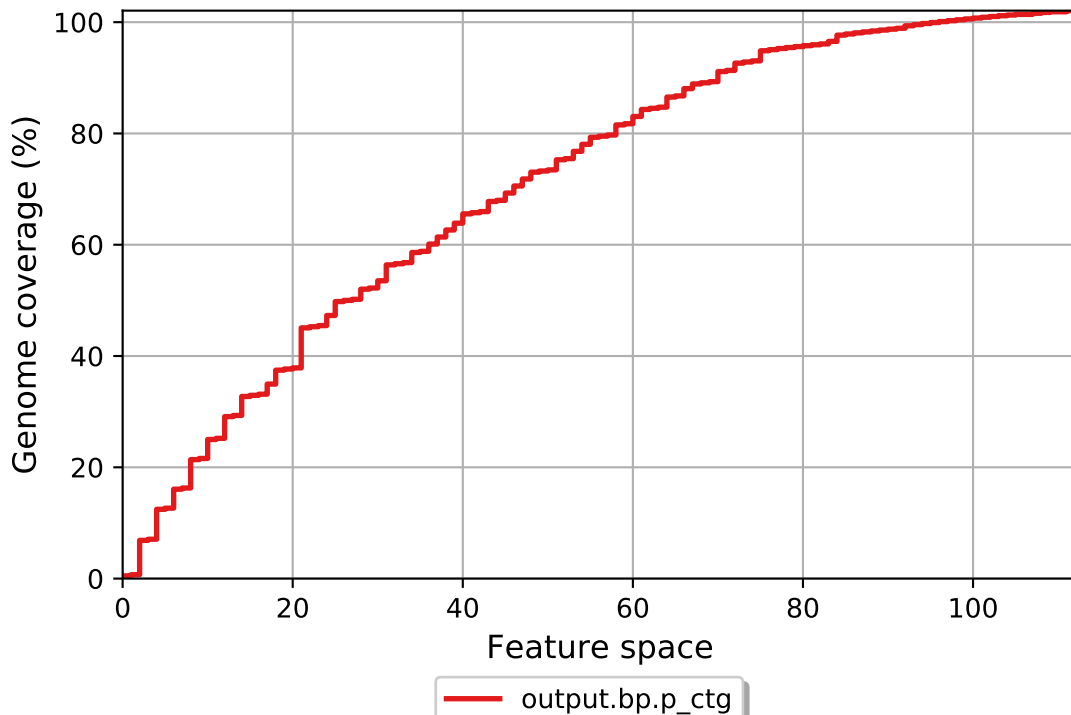


# translocations

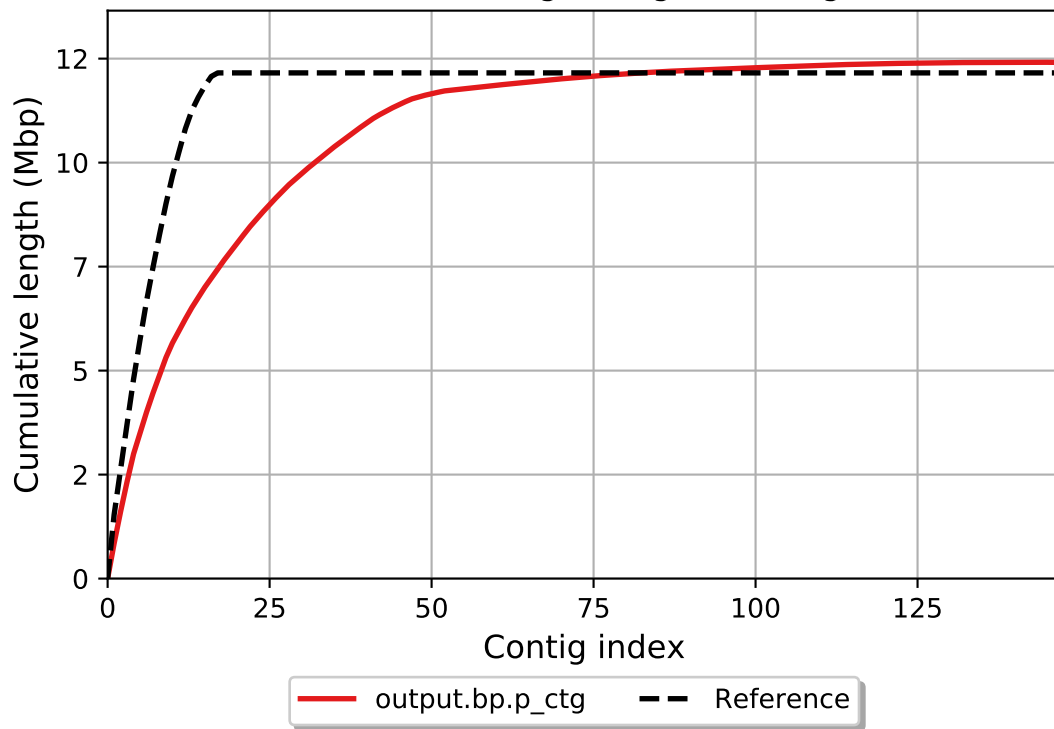


# inversions

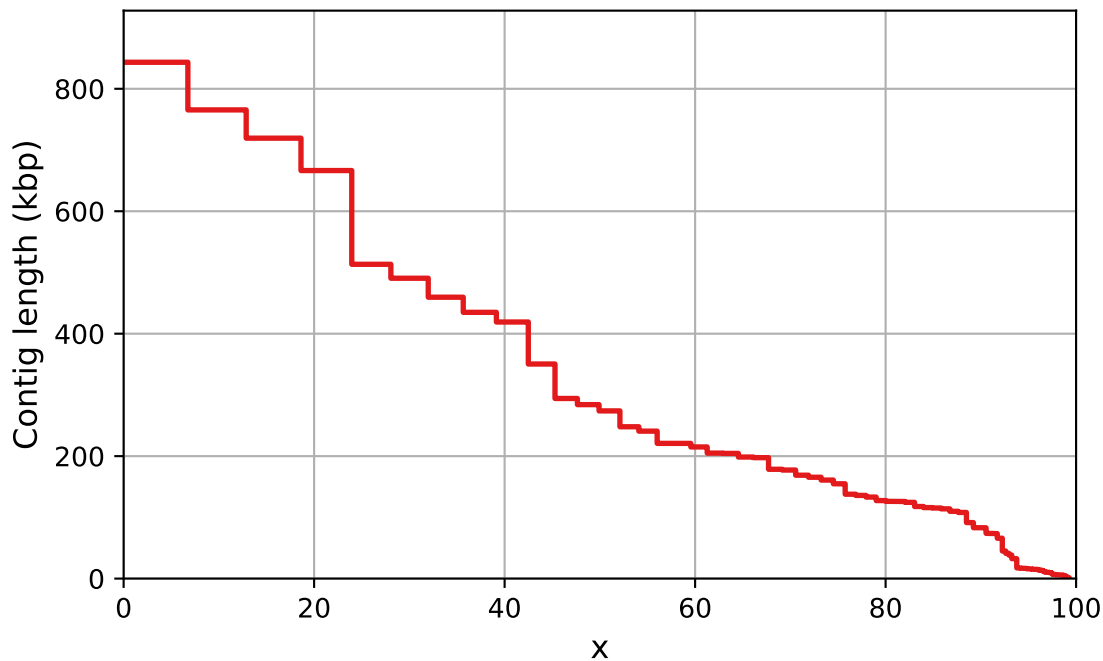
FRCurve (misassemblies)



Cumulative length (aligned contigs)

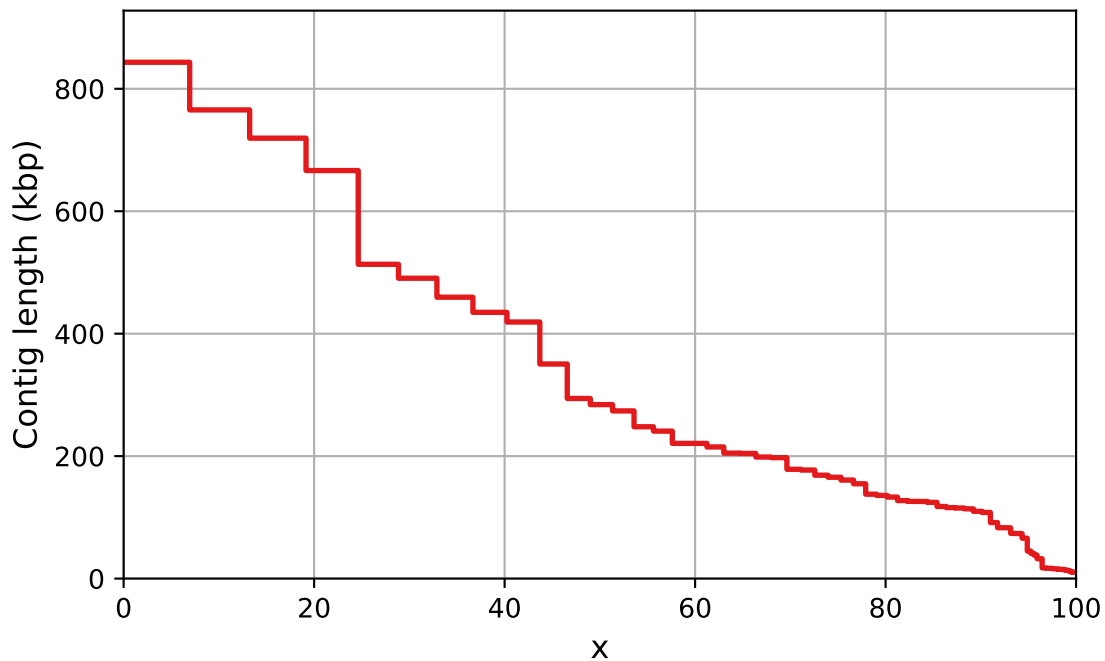


NAx



— output.bp.p\_ctg

# NGAx



— output.bp.p\_ctg