

Report

|                             | assembly   |
|-----------------------------|------------|
| # contigs (>= 0 bp)         | 3          |
| # contigs (>= 1000 bp)      | 3          |
| # contigs (>= 5000 bp)      | 3          |
| # contigs (>= 10000 bp)     | 3          |
| # contigs (>= 25000 bp)     | 3          |
| # contigs (>= 50000 bp)     | 3          |
| Total length (>= 0 bp)      | 5104812    |
| Total length (>= 1000 bp)   | 5104812    |
| Total length (>= 5000 bp)   | 5104812    |
| Total length (>= 10000 bp)  | 5104812    |
| Total length (>= 25000 bp)  | 5104812    |
| Total length (>= 50000 bp)  | 5104812    |
| # contigs                   | 3          |
| Largest contig              | 3318776    |
| Total length                | 5104812    |
| Reference length            | 4951383    |
| GC (%)                      | 52.19      |
| Reference GC (%)            | 52.24      |
| N50                         | 3318776    |
| NG50                        | 3318776    |
| N90                         | 1676977    |
| NG90                        | 1676977    |
| auN                         | 2710857.9  |
| auNG                        | 2794859.5  |
| L50                         | 1          |
| LG50                        | 1          |
| L90                         | 2          |
| LG90                        | 2          |
| # misassemblies             | 25         |
| # misassembled contigs      | 2          |
| Misassembled contigs length | 4995753    |
| # local misassemblies       | 10         |
| # scaffold gap ext. mis.    | 0          |
| # scaffold gap loc. mis.    | 0          |
| # unaligned mis. contigs    | 0          |
| # unaligned contigs         | 1 + 2 part |
| Unaligned length            | 358694     |
| Genome fraction (%)         | 95.669     |
| Duplication ratio           | 1.002      |
| # N's per 100 kbp           | 0.00       |
| # mismatches per 100 kbp    | 27.39      |
| # indels per 100 kbp        | 3.81       |
| Largest alignment           | 953687     |
| Total aligned length        | 4746095    |
| NA50                        | 460922     |
| NGA50                       | 460922     |
| NA90                        | 72349      |
| NGA90                       | 101719     |
| auNA                        | 476077.0   |
| auNGA                       | 490829.2   |
| LA50                        | 4          |
| LGA50                       | 4          |
| LA90                        | 14         |
| LGA90                       | 12         |

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

|                             | assembly |
|-----------------------------|----------|
| # misassemblies             | 25       |
| # contig misassemblies      | 25       |
| # c. relocations            | 25       |
| # c. translocations         | 0        |
| # c. inversions             | 0        |
| # scaffold misassemblies    | 0        |
| # s. relocations            | 0        |
| # s. translocations         | 0        |
| # s. inversions             | 0        |
| # misassembled contigs      | 2        |
| Misassembled contigs length | 4995753  |
| # local misassemblies       | 10       |
| # scaffold gap ext. mis.    | 0        |
| # scaffold gap loc. mis.    | 0        |
| # unaligned mis. contigs    | 0        |
| # mismatches                | 1300     |
| # indels                    | 181      |
| # indels (<= 5 bp)          | 151      |
| # indels (> 5 bp)           | 30       |
| Indels length               | 2637     |

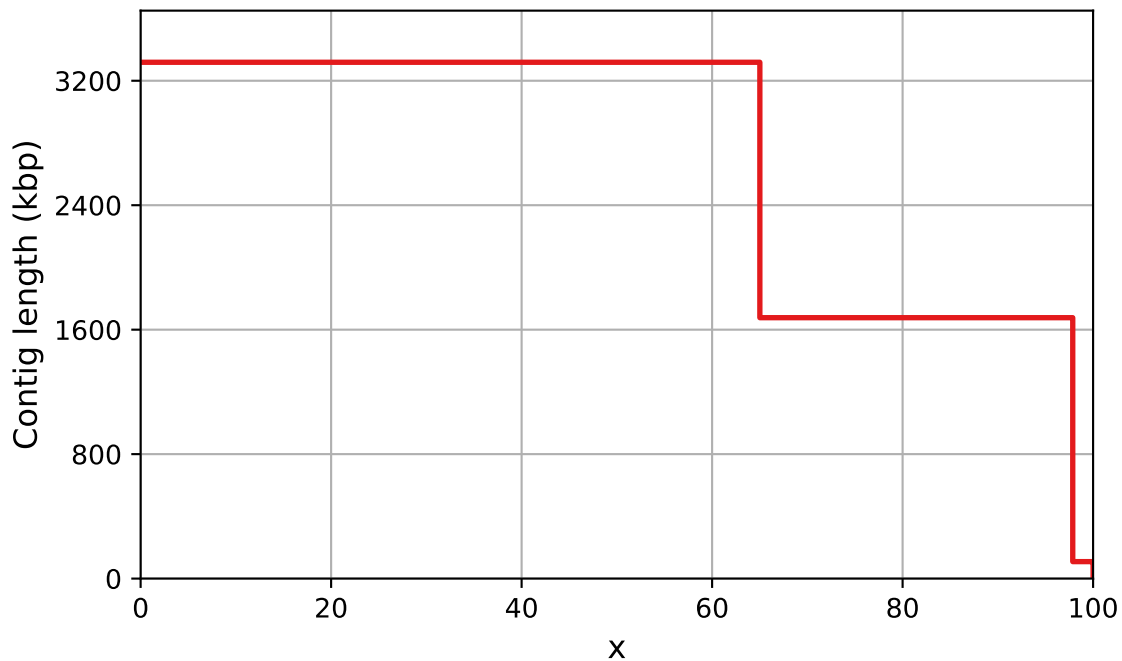
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

|                               | assembly |
|-------------------------------|----------|
| # fully unaligned contigs     | 1        |
| Fully unaligned length        | 109059   |
| # partially unaligned contigs | 2        |
| Partially unaligned length    | 249635   |
| # N's                         | 0        |

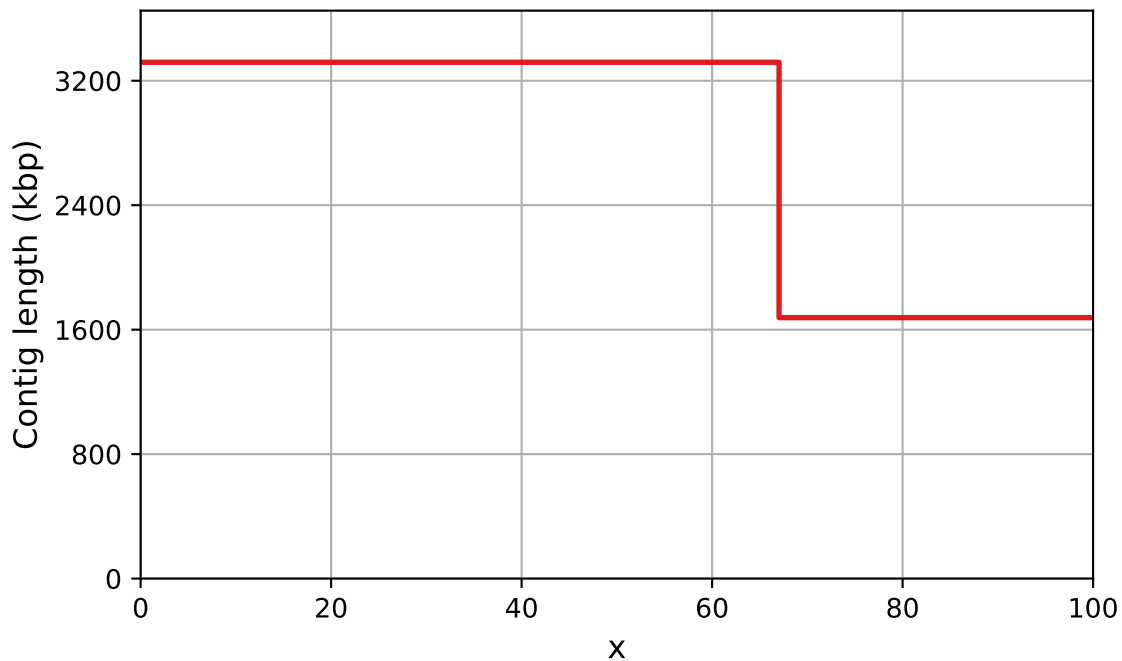
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

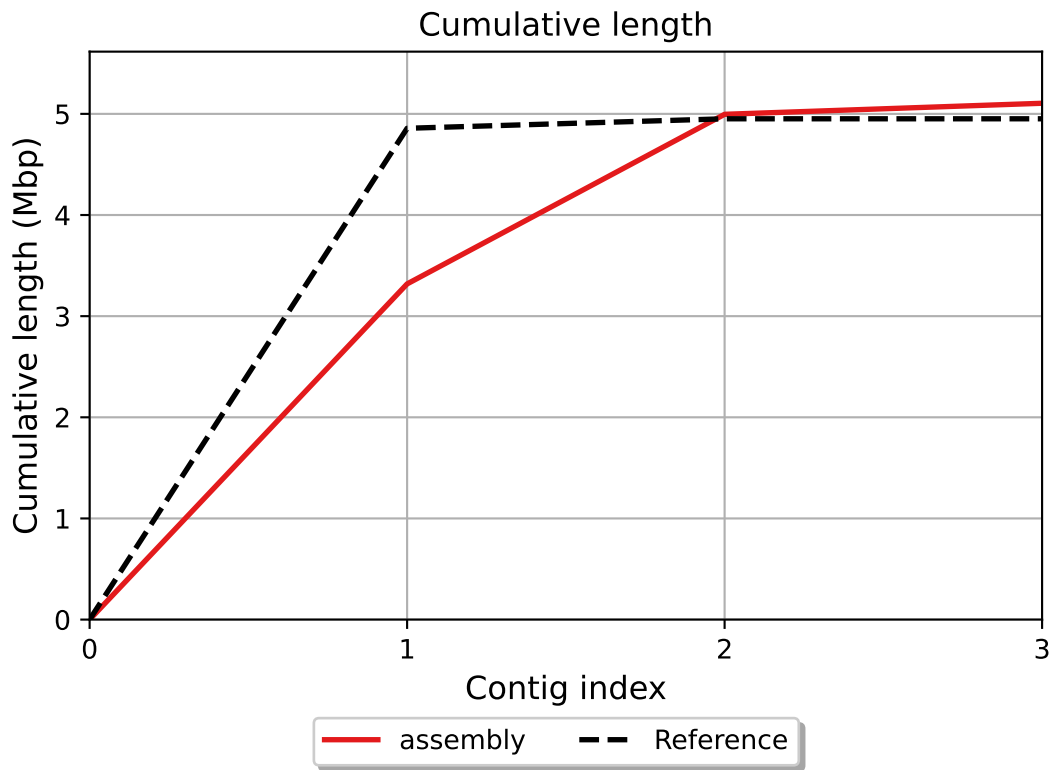


assembly

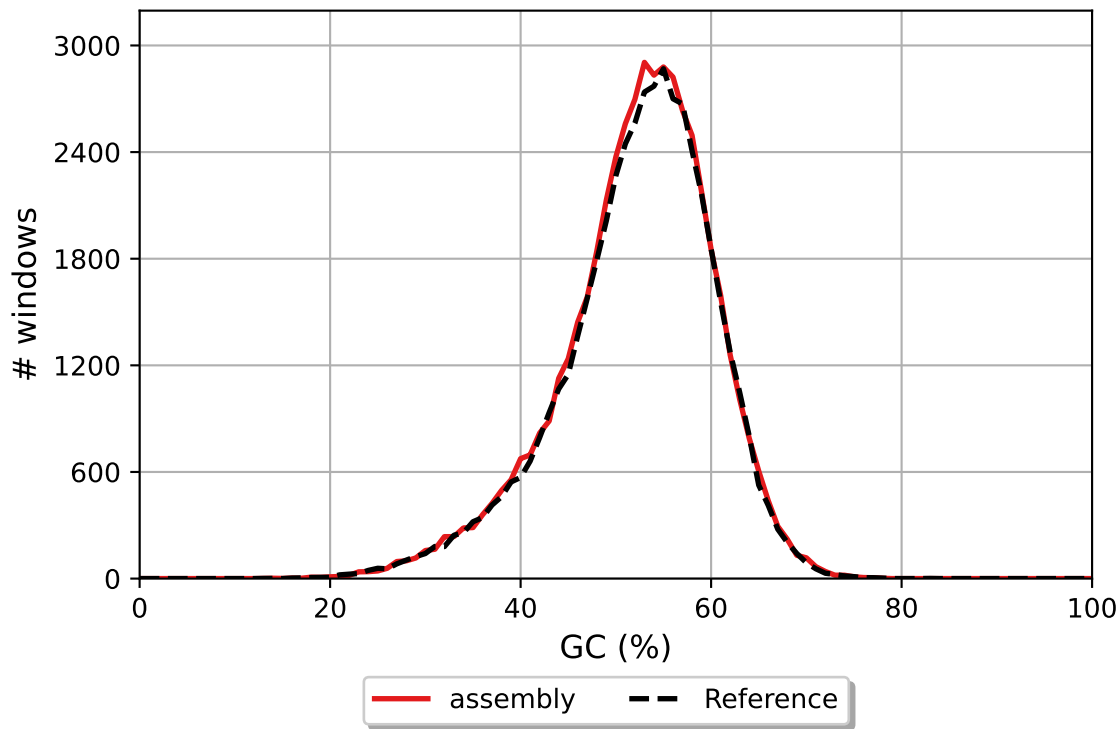
NGx



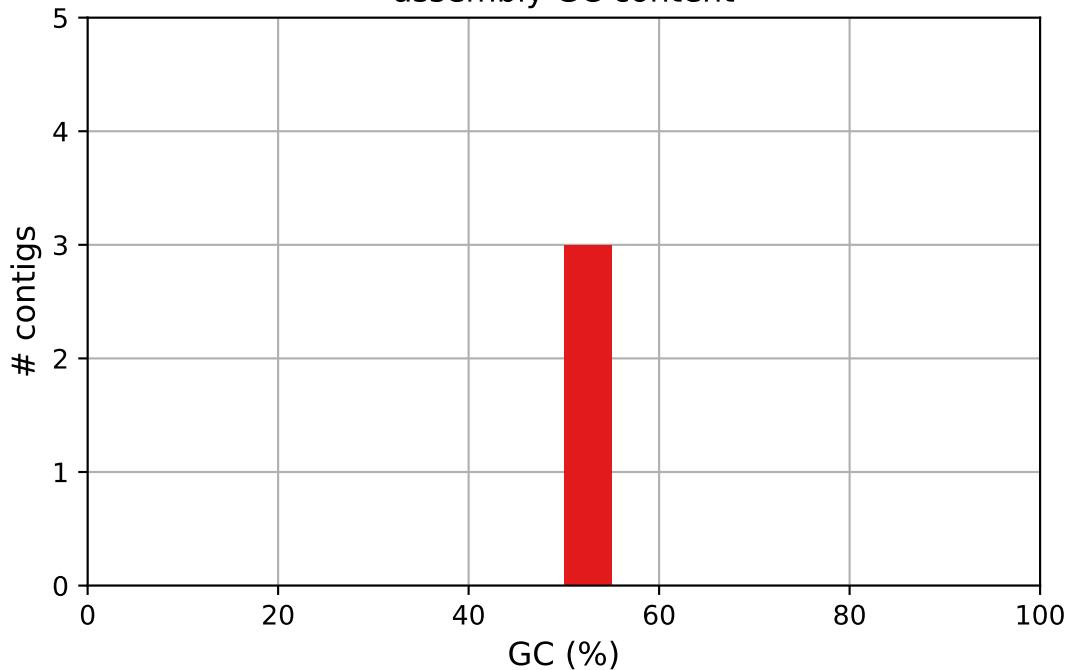
— assembly



## GC content



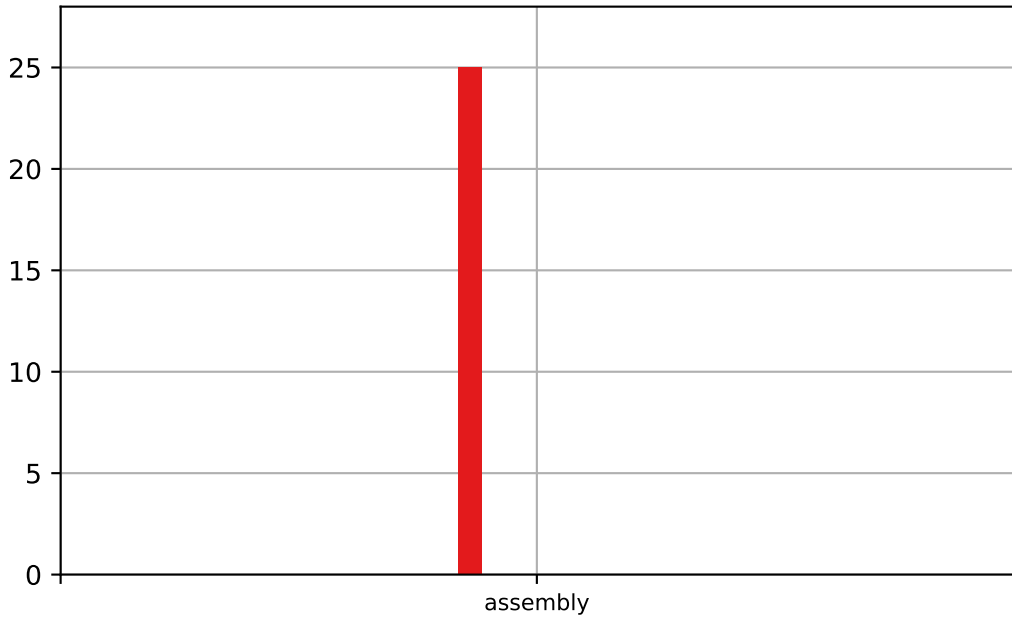
assembly GC content



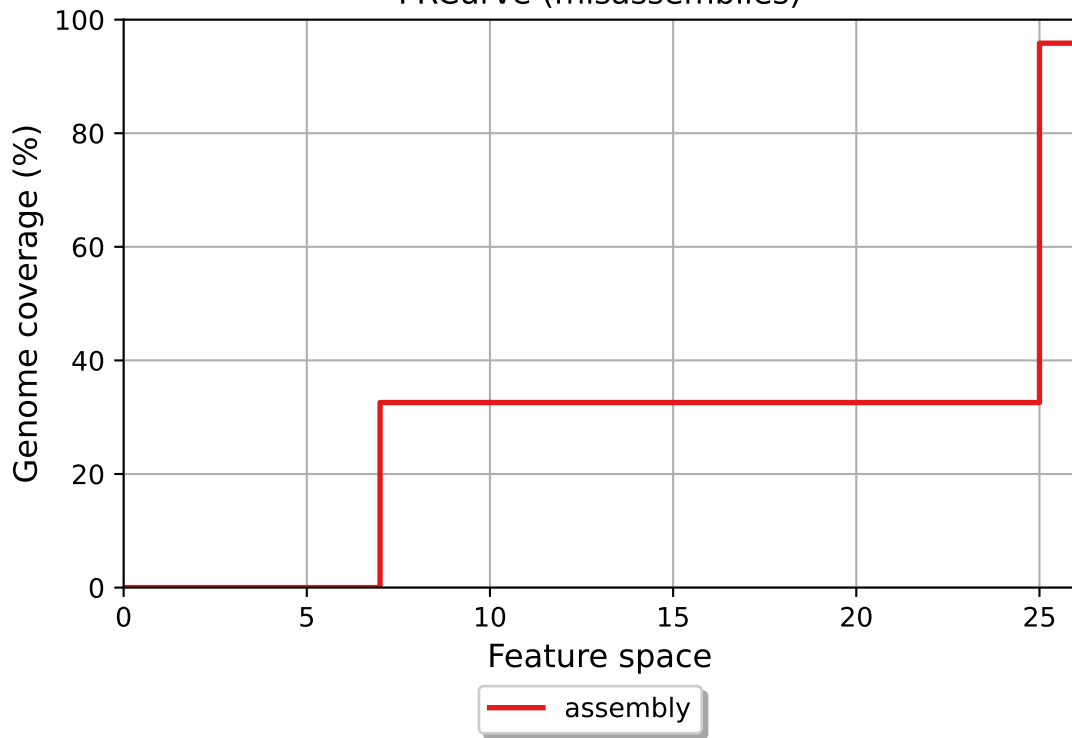
assembly



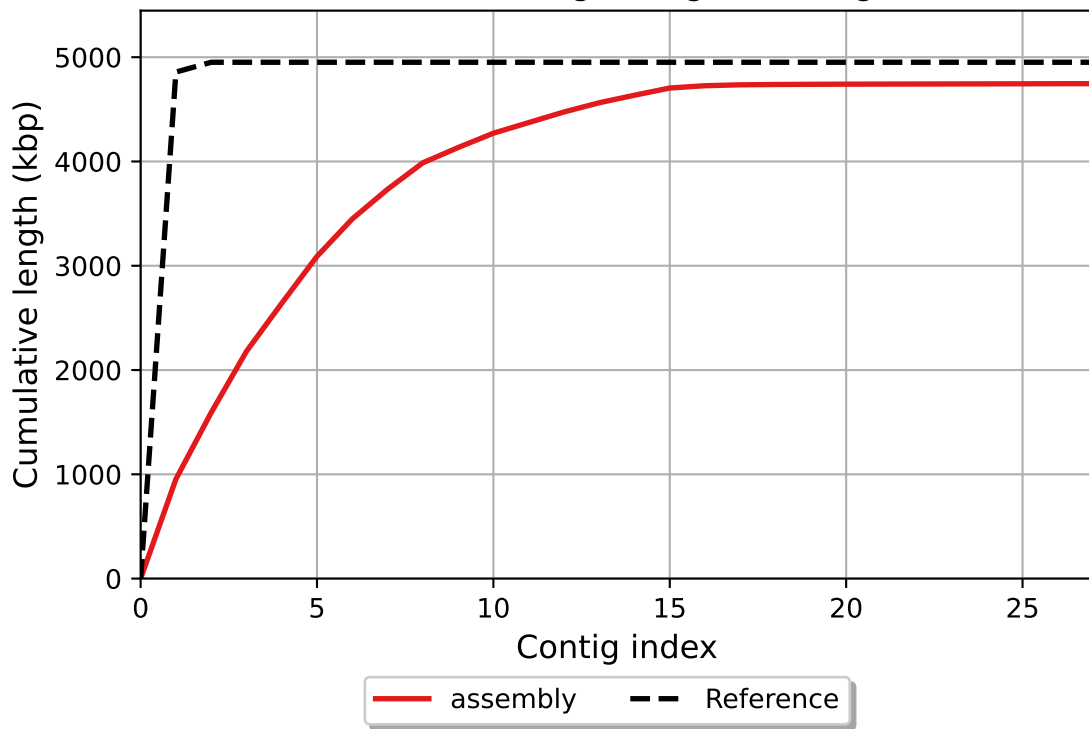
## Misassemblies



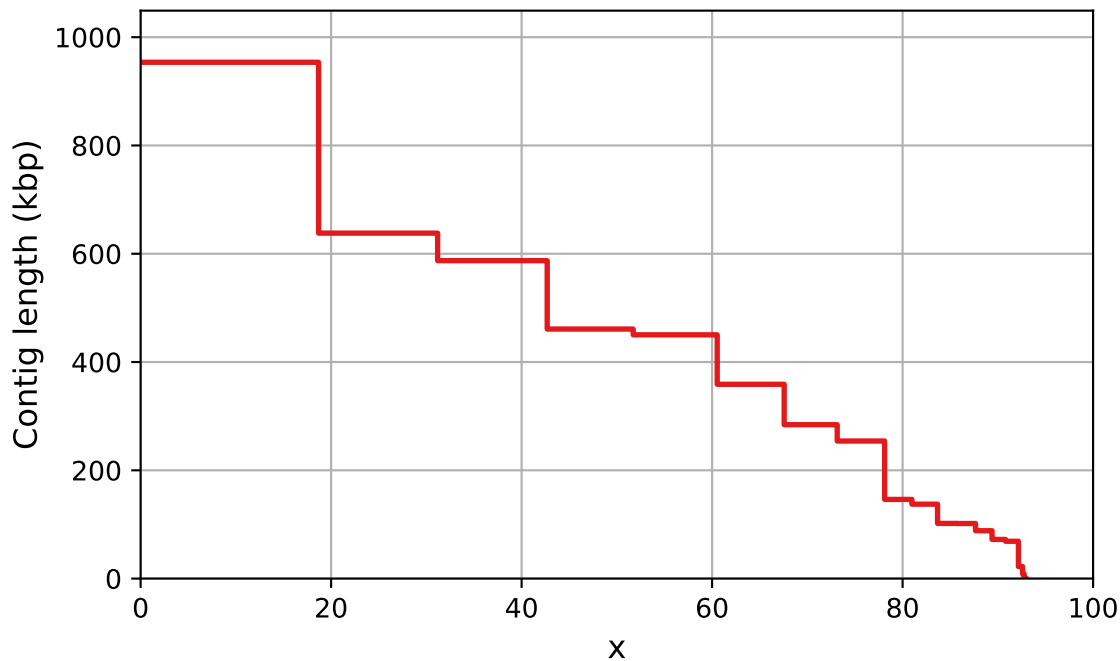
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— assembly

# NGAx

