

## Report

|                             | scaffolds  |
|-----------------------------|------------|
| # contigs (>= 1000 bp)      | 0          |
| # contigs (>= 5000 bp)      | 0          |
| # contigs (>= 10000 bp)     | 0          |
| # contigs (>= 25000 bp)     | 0          |
| # contigs (>= 50000 bp)     | 0          |
| Total length (>= 1000 bp)   | 0          |
| Total length (>= 5000 bp)   | 0          |
| Total length (>= 10000 bp)  | 0          |
| Total length (>= 25000 bp)  | 0          |
| Total length (>= 50000 bp)  | 0          |
| # contigs                   | 1          |
| Largest contig              | 879        |
| Total length                | 879        |
| Reference length            | 4641652    |
| GC (%)                      | 50.17      |
| Reference GC (%)            | 50.78      |
| N50                         | 879        |
| N75                         | 879        |
| L50                         | 1          |
| L75                         | 1          |
| # misassemblies             | 0          |
| # misassembled contigs      | 0          |
| Misassembled contigs length | 0          |
| # local misassemblies       | 0          |
| # unaligned contigs         | 0 + 0 part |
| Unaligned length            | 0          |
| Genome fraction (%)         | 0.019      |
| Duplication ratio           | 1.000      |
| # N's per 100 kbp           | 0.00       |
| # mismatches per 100 kbp    | 3526.73    |
| # indels per 100 kbp        | 0.00       |
| Largest alignment           | 879        |
| NA50                        | 879        |
| NGA50                       | -          |
| NA75                        | 879        |
| LA50                        | 1          |
| LA75                        | 1          |

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

|                                 | scaffolds |
|---------------------------------|-----------|
| # misassemblies                 | 0         |
| # relocations                   | 0         |
| # translocations                | 0         |
| # inversions                    | 0         |
| # possibly misassembled contigs | 0         |
| # misassembled contigs          | 0         |
| Misassembled contigs length     | 0         |
| # local misassemblies           | 0         |
| # mismatches                    | 31        |
| # indels                        | 0         |
| # short indels                  | 0         |
| # long indels                   | 0         |
| Indels length                   | 0         |

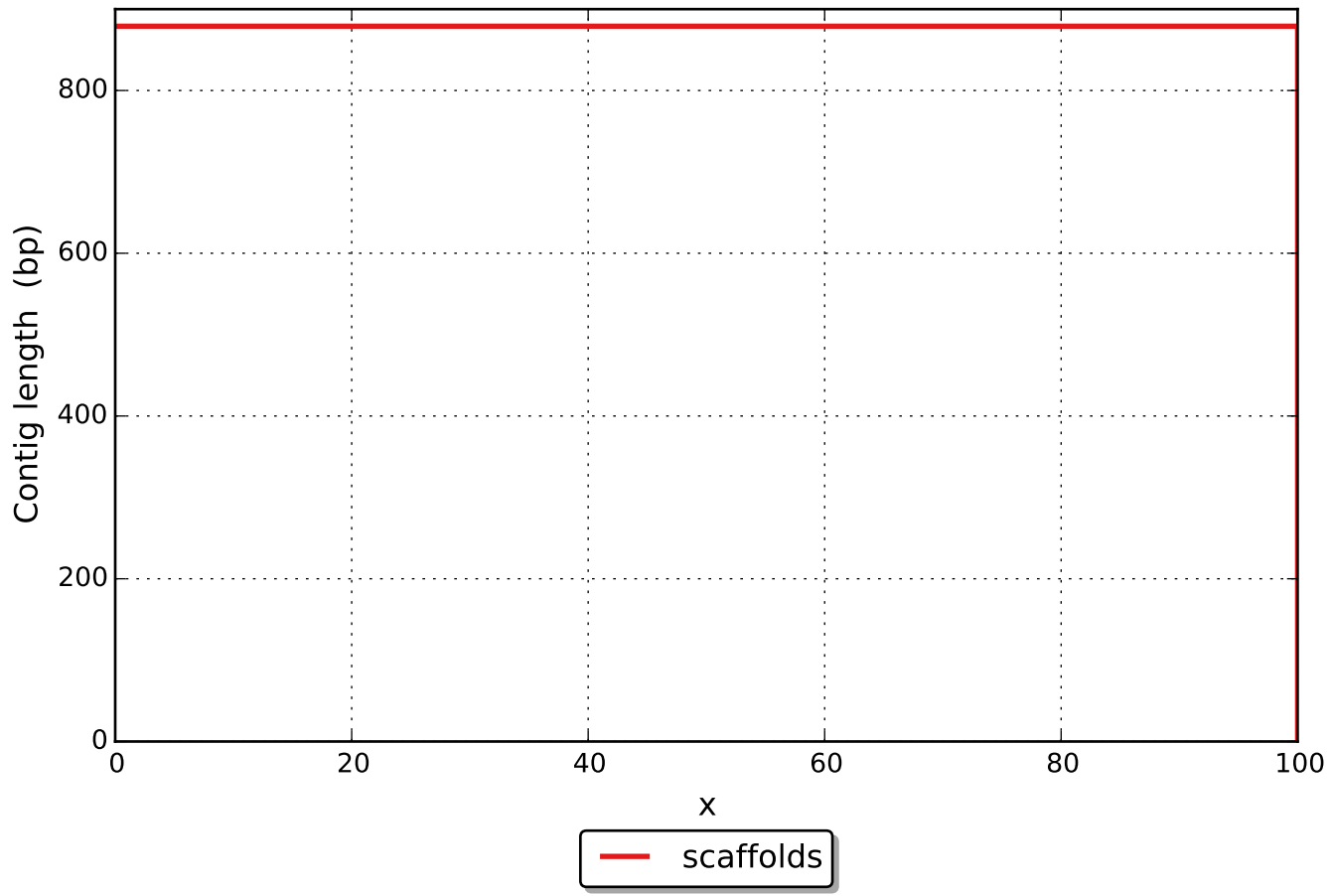
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

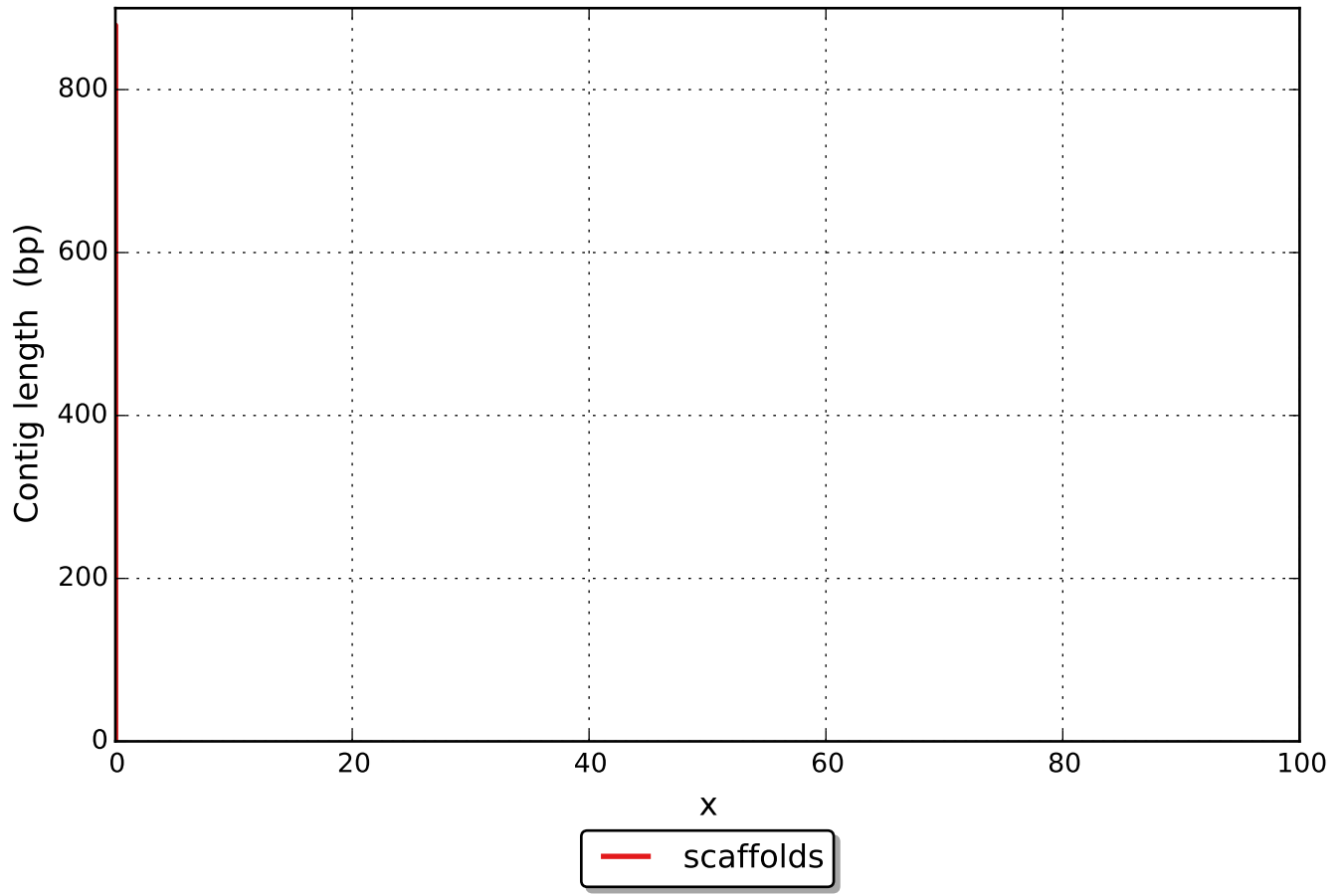
|                               | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs     | 0         |
| Fully unaligned length        | 0         |
| # partially unaligned contigs | 0         |
| # with misassembly            | 0         |
| # both parts are significant  | 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).

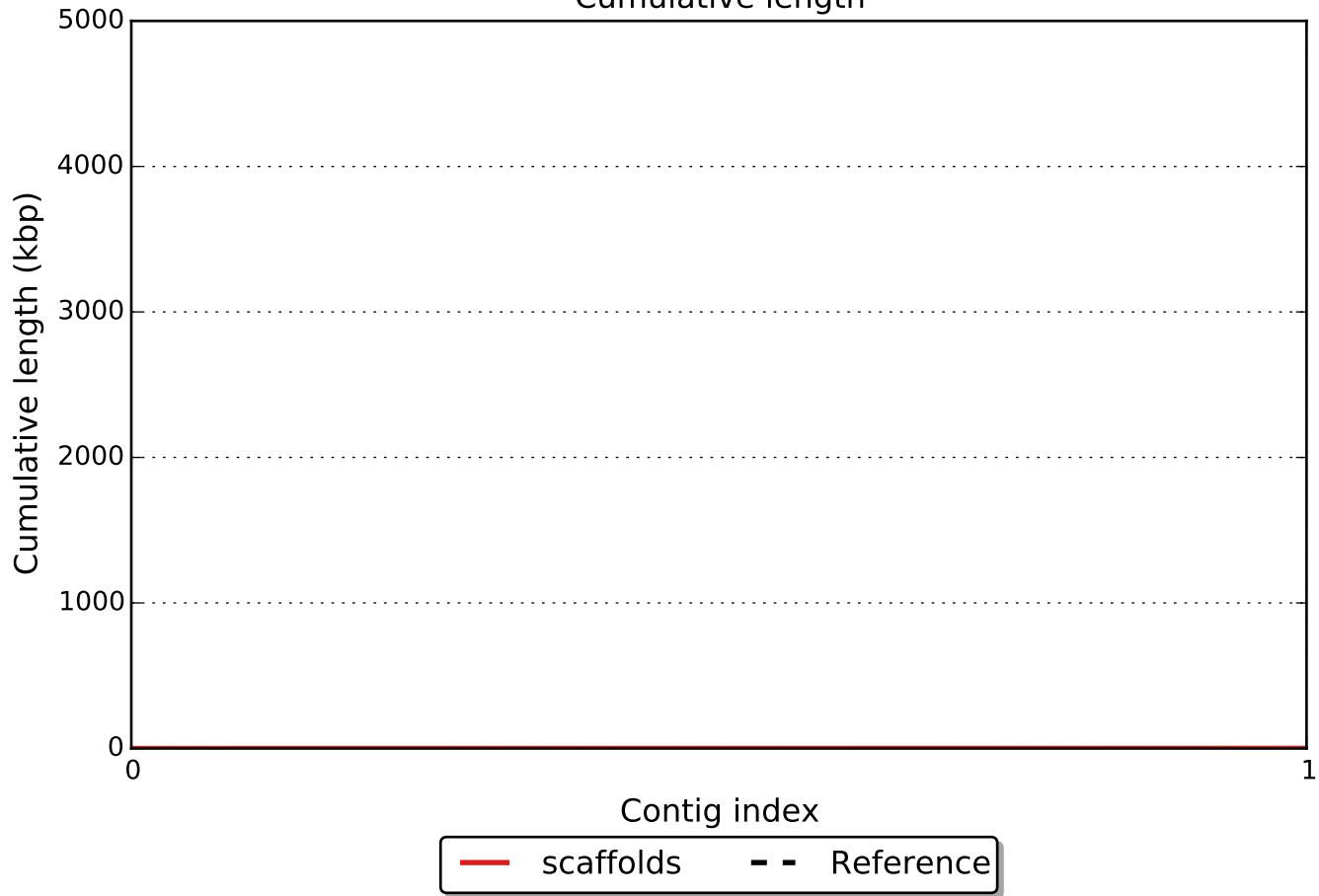
Nx



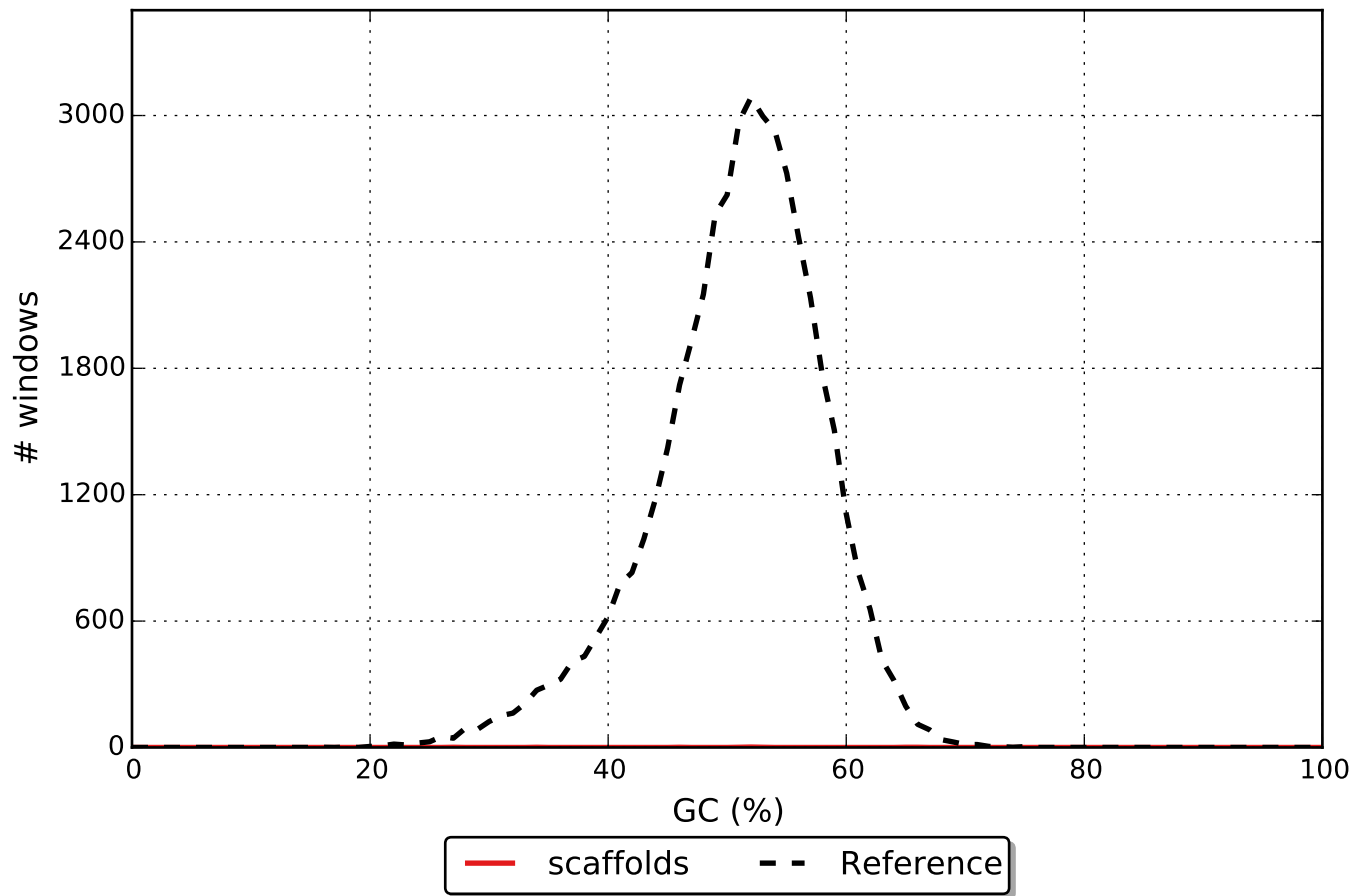
NGx



Cumulative length



# GC content

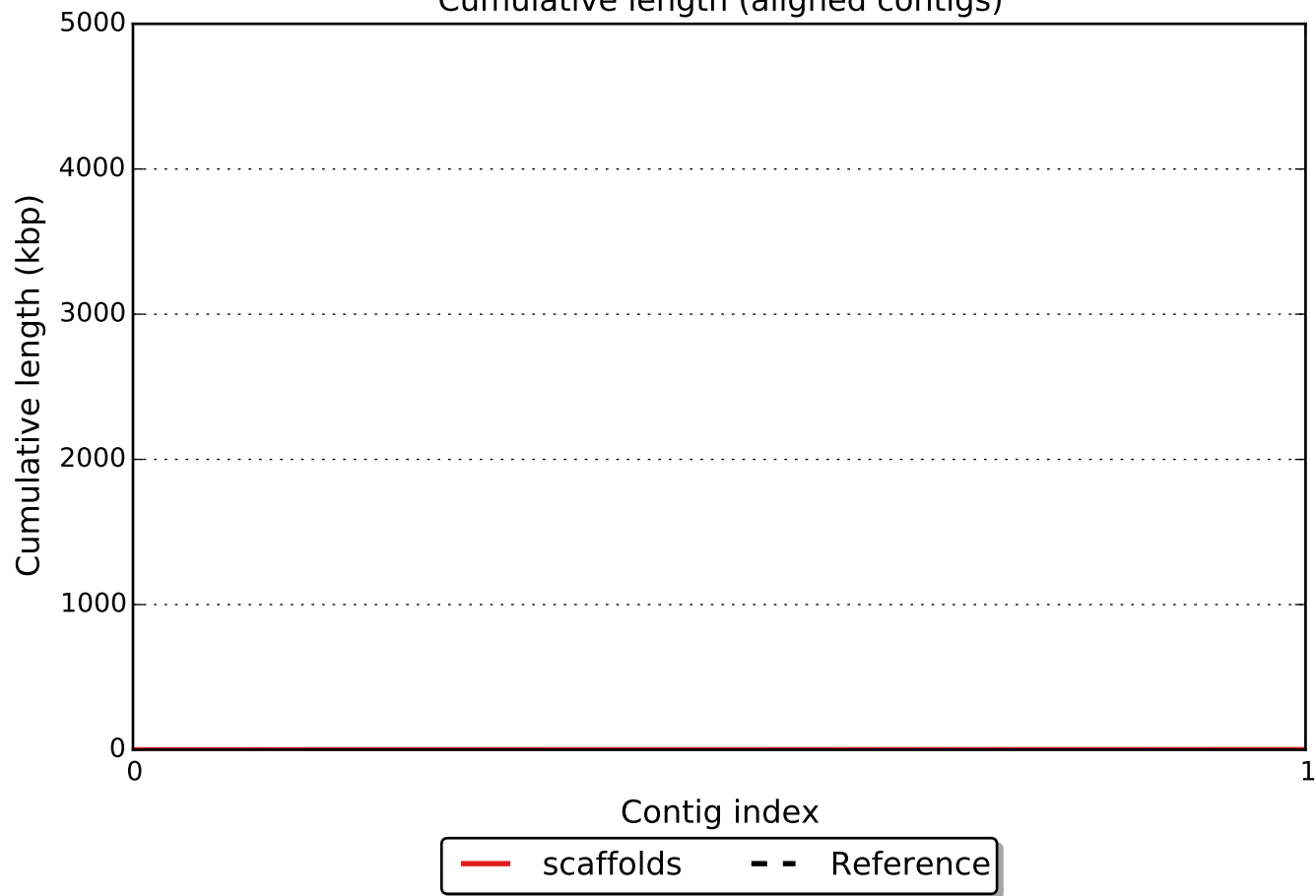


# Misassemblies

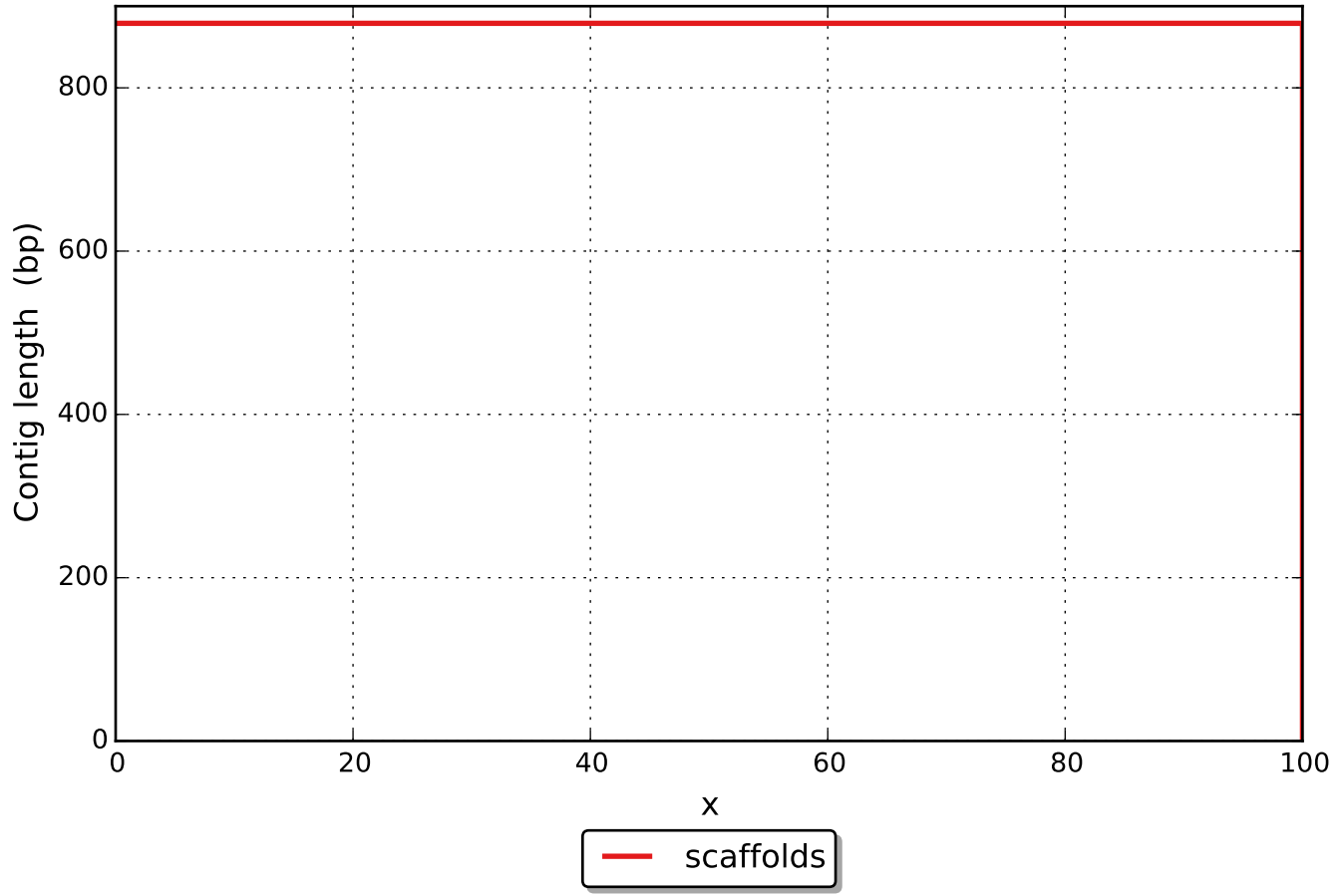




Cumulative length (aligned contigs)



NAx



NGAx

