

## Report

|                                 | scaffolds  |
|---------------------------------|------------|
| # contigs ( $\geq 1000$ bp)     | 69         |
| # contigs ( $\geq 5000$ bp)     | 57         |
| # contigs ( $\geq 10000$ bp)    | 51         |
| # contigs ( $\geq 25000$ bp)    | 41         |
| # contigs ( $\geq 50000$ bp)    | 32         |
| Total length ( $\geq 1000$ bp)  | 4473119    |
| Total length ( $\geq 5000$ bp)  | 4451416    |
| Total length ( $\geq 10000$ bp) | 4409585    |
| Total length ( $\geq 25000$ bp) | 4236257    |
| Total length ( $\geq 50000$ bp) | 3926012    |
| # contigs                       | 91         |
| Largest contig                  | 431470     |
| Total length                    | 4486956    |
| Reference length                | 4641652    |
| GC (%)                          | 50.77      |
| Reference GC (%)                | 50.78      |
| N50                             | 105688     |
| NG50                            | 105224     |
| N75                             | 69219      |
| NG75                            | 63924      |
| L50                             | 10         |
| LG50                            | 11         |
| L75                             | 23         |
| LG75                            | 25         |
| # misassemblies                 | 7          |
| # misassembled contigs          | 2          |
| Misassembled contigs length     | 196859     |
| # local misassemblies           | 4          |
| # unaligned contigs             | 0 + 0 part |
| Unaligned length                | 0          |
| Genome fraction (%)             | 93.418     |
| Duplication ratio               | 1.035      |
| # N's per 100 kbp               | 0.00       |
| # mismatches per 100 kbp        | 949.69     |
| # indels per 100 kbp            | 1.11       |
| Largest alignment               | 431470     |
| NA50                            | 105224     |
| NGA50                           | 96103      |
| NA75                            | 63527      |
| NGA75                           | 62885      |
| LA50                            | 10         |
| LGA50                           | 11         |
| LA75                            | 24         |
| LGA75                           | 26         |

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).

## Misassemblies report

|                                 | scaffolds |
|---------------------------------|-----------|
| # misassemblies                 | 7         |
| # relocations                   | 7         |
| # translocations                | 0         |
| # inversions                    | 0         |
| # possibly misassembled contigs | 0         |
| # misassembled contigs          | 2         |
| Misassembled contigs length     | 196859    |
| # local misassemblies           | 4         |
| # mismatches                    | 41180     |
| # indels                        | 48        |
| # short indels                  | 47        |
| # long indels                   | 1         |
| Indels length                   | 57        |

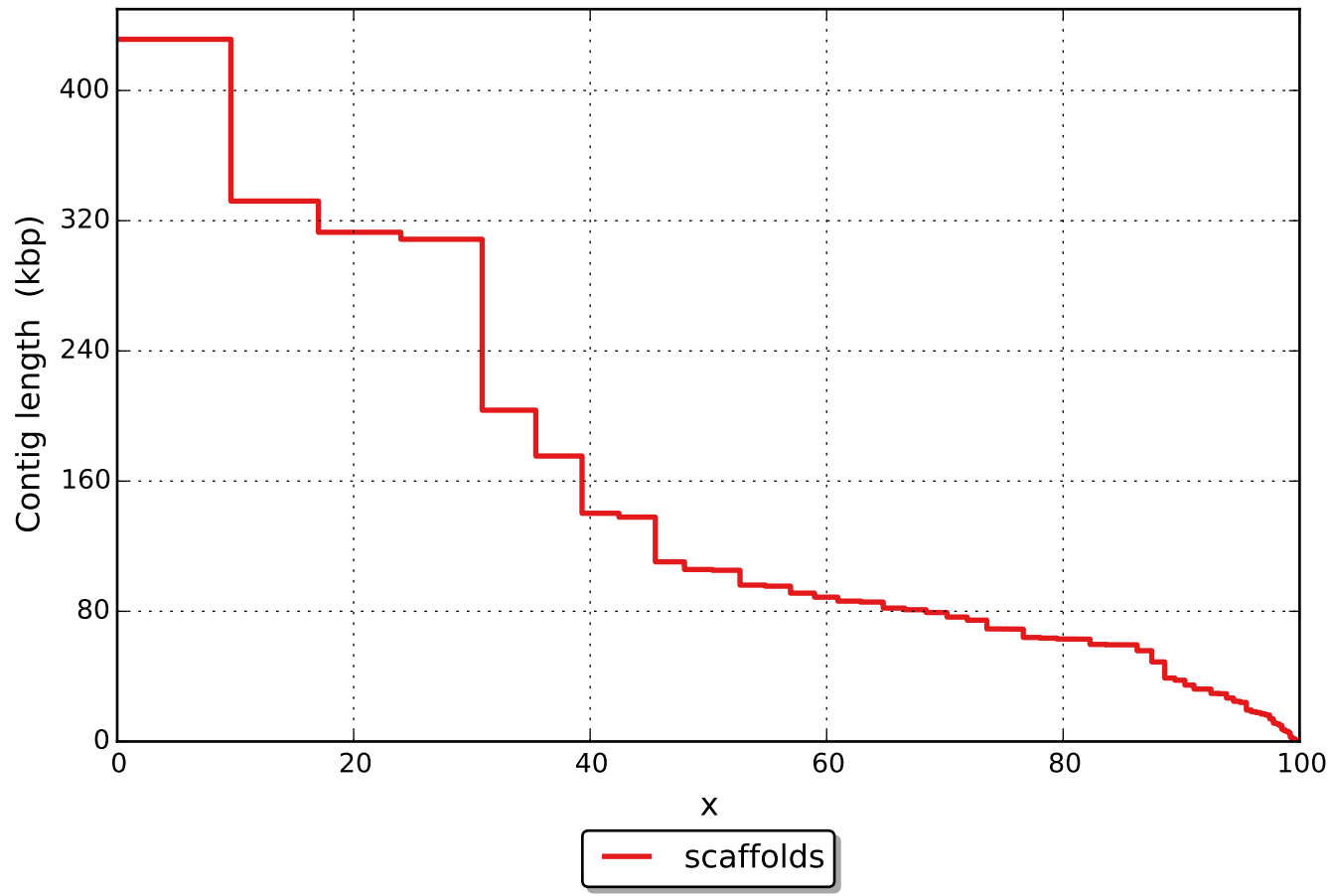
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

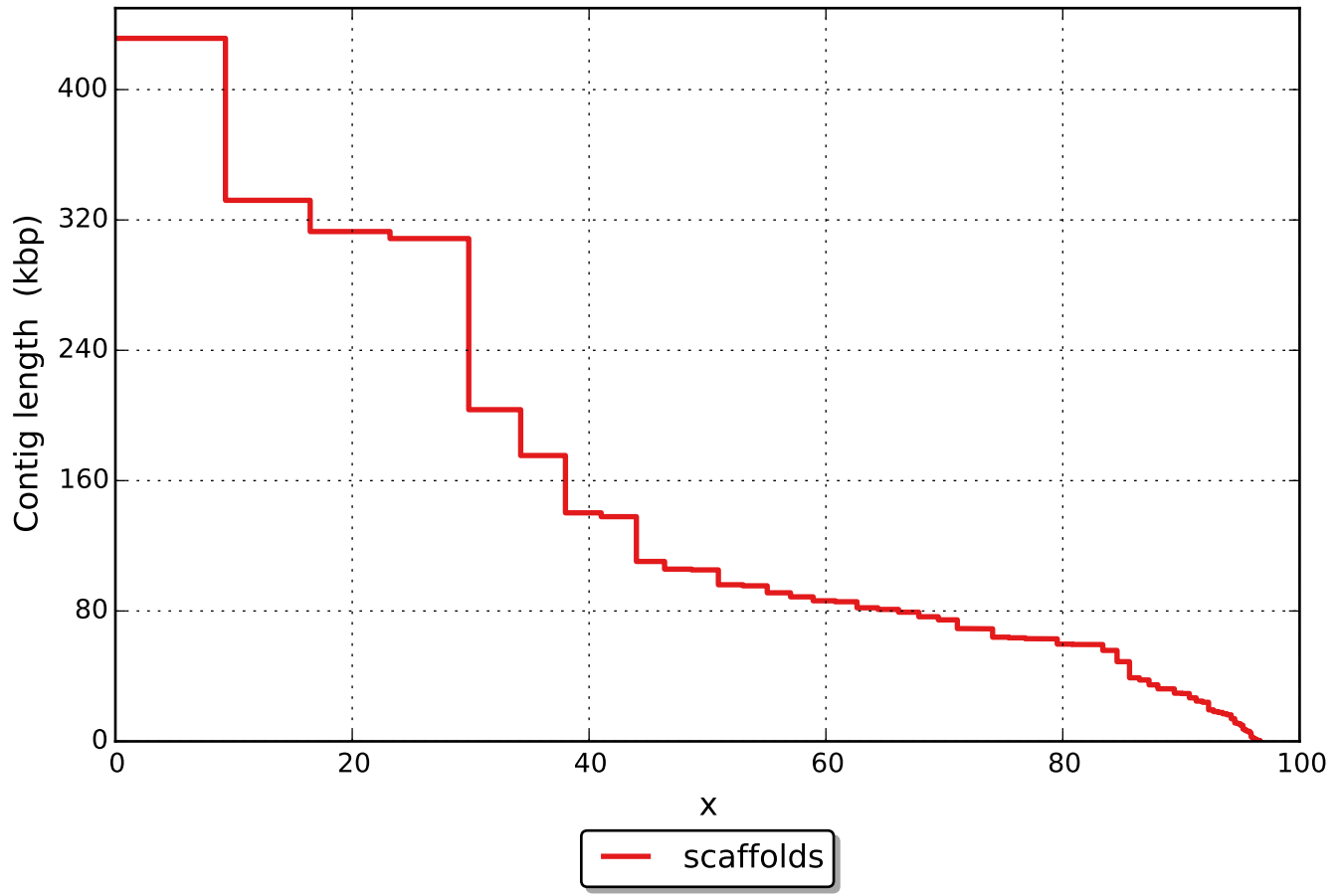
|                               | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs     | 0         |
| Fully unaligned length        | 0         |
| # partially unaligned contigs | 0         |
| # with misassembly            | 0         |
| # both parts are significant  | 0         |
| Partially unaligned length    | 0         |
| # N's                         | 0         |

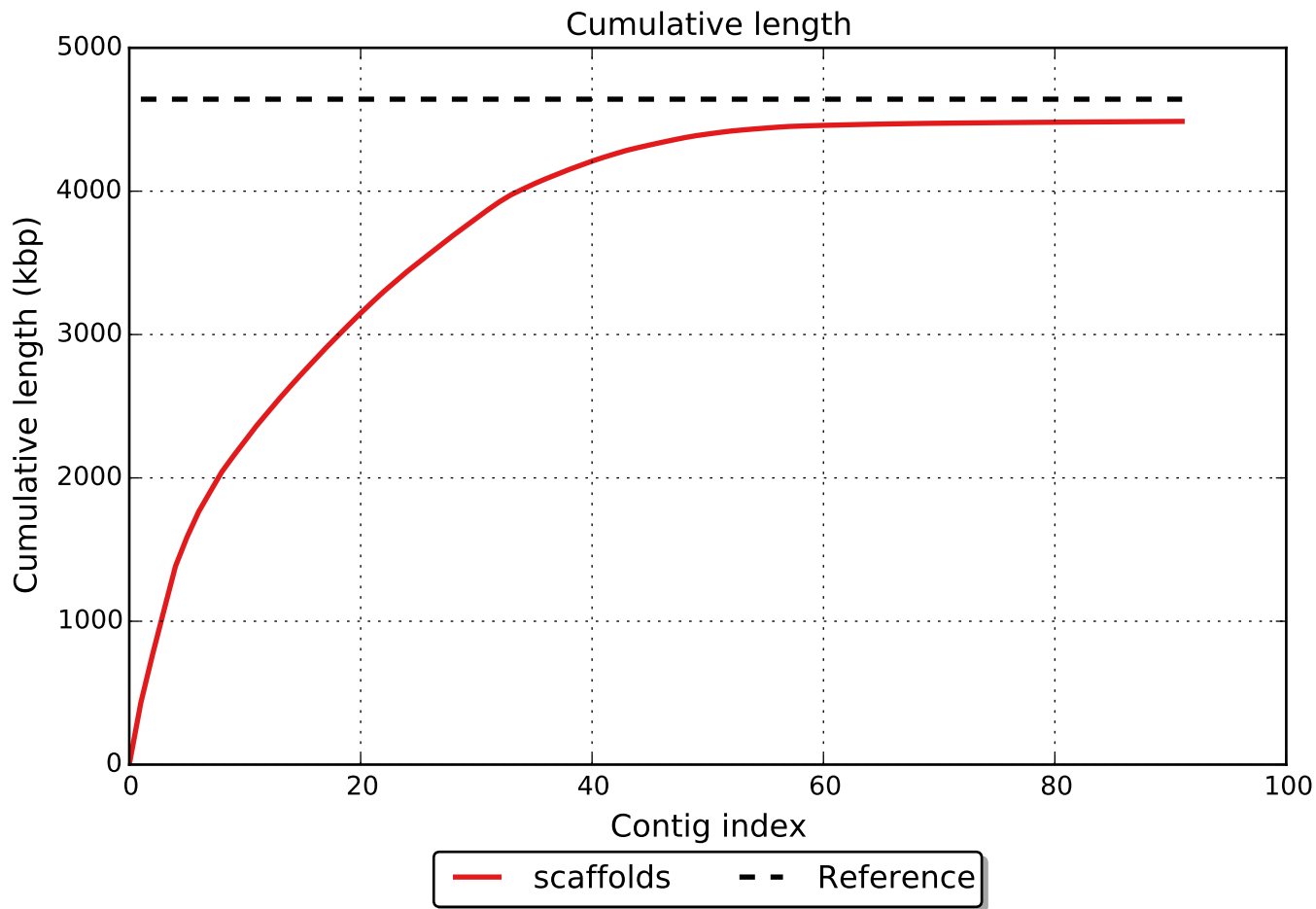
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

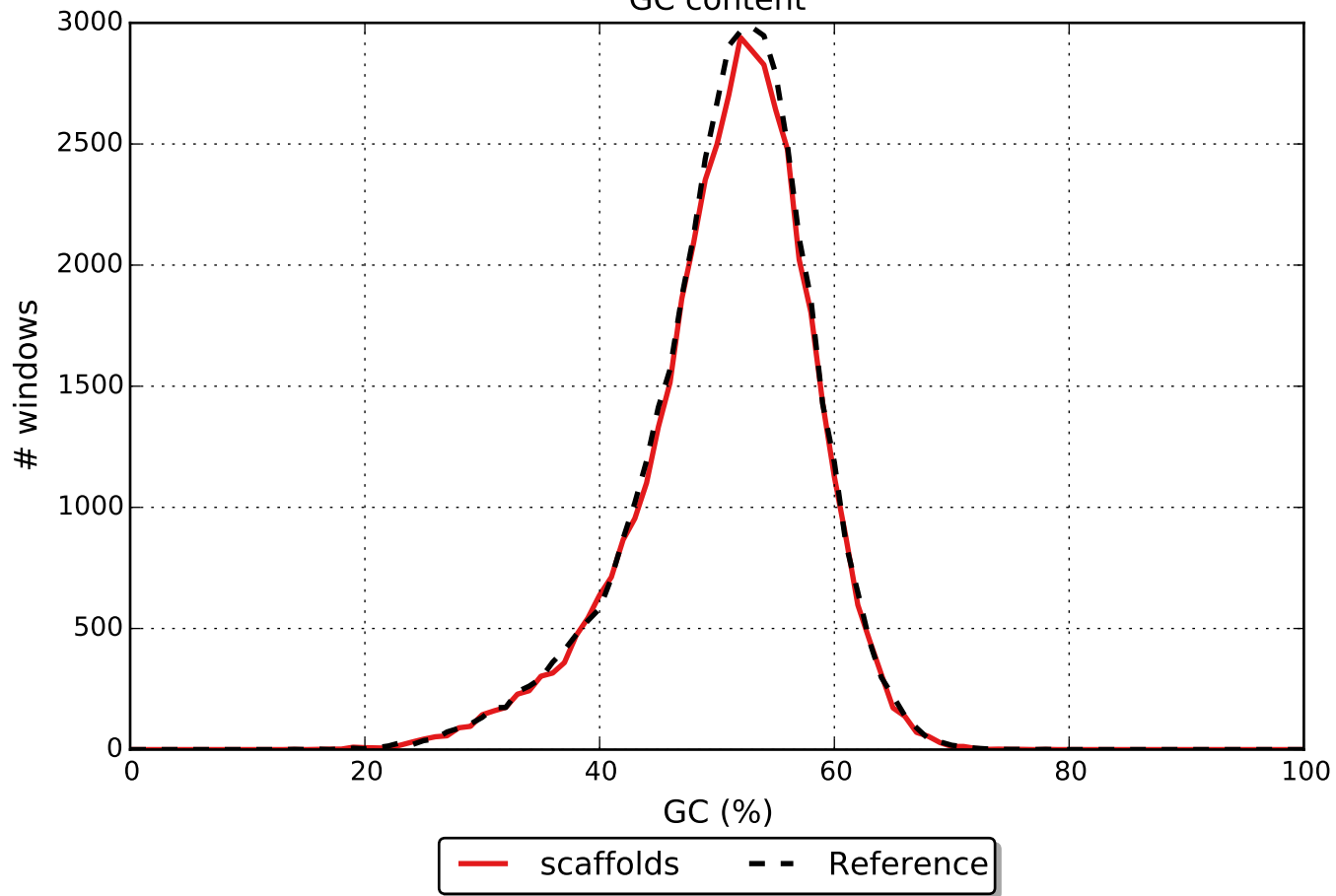


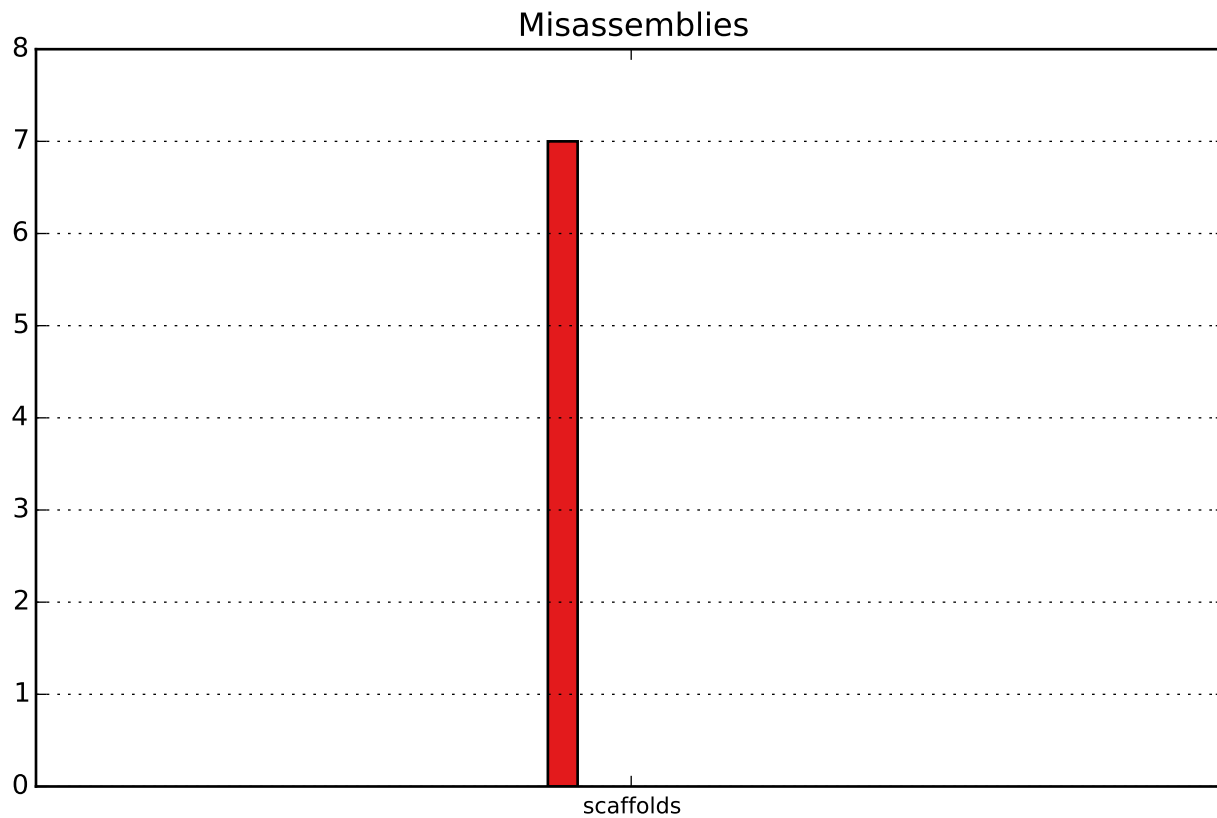
NGx





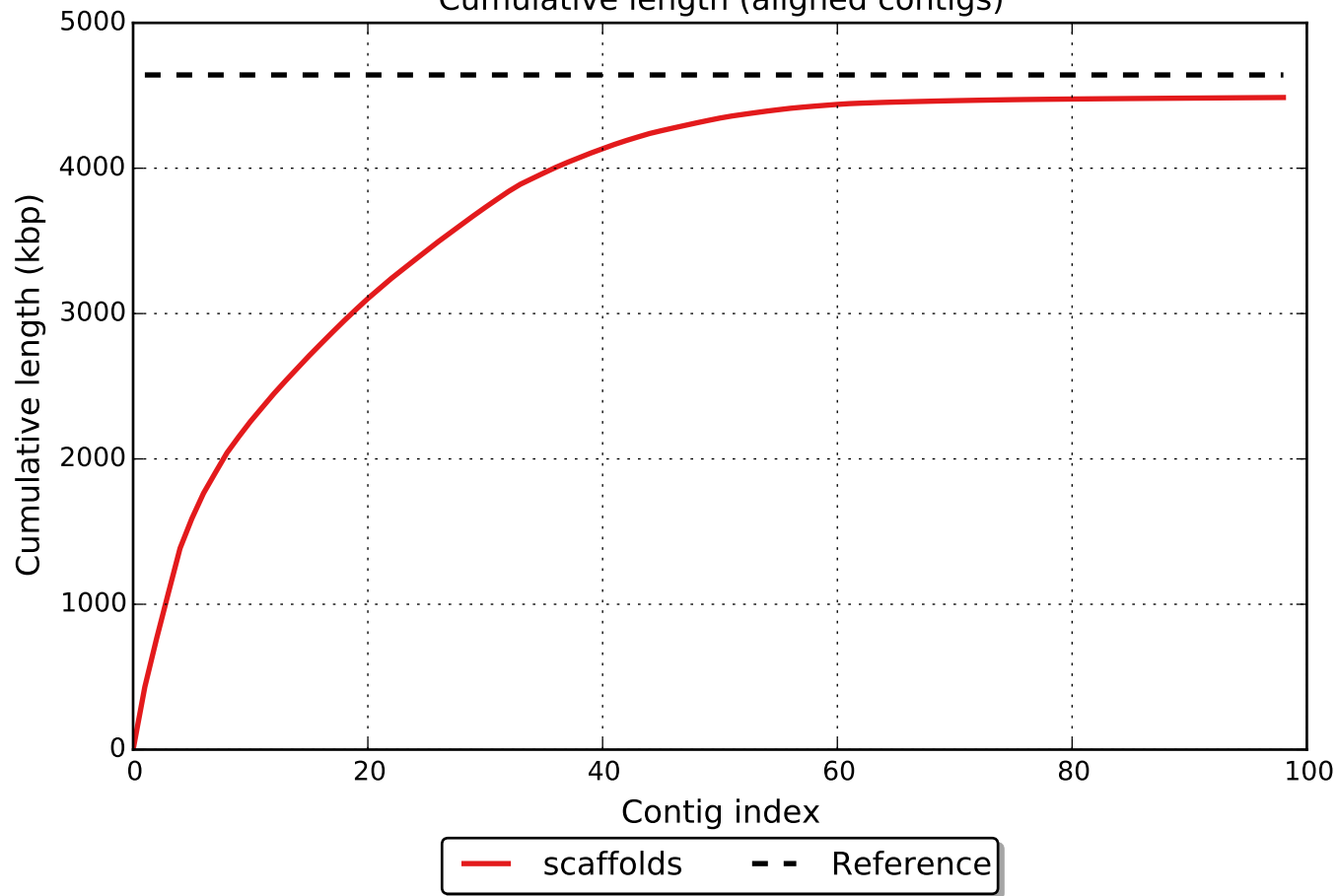
GC content



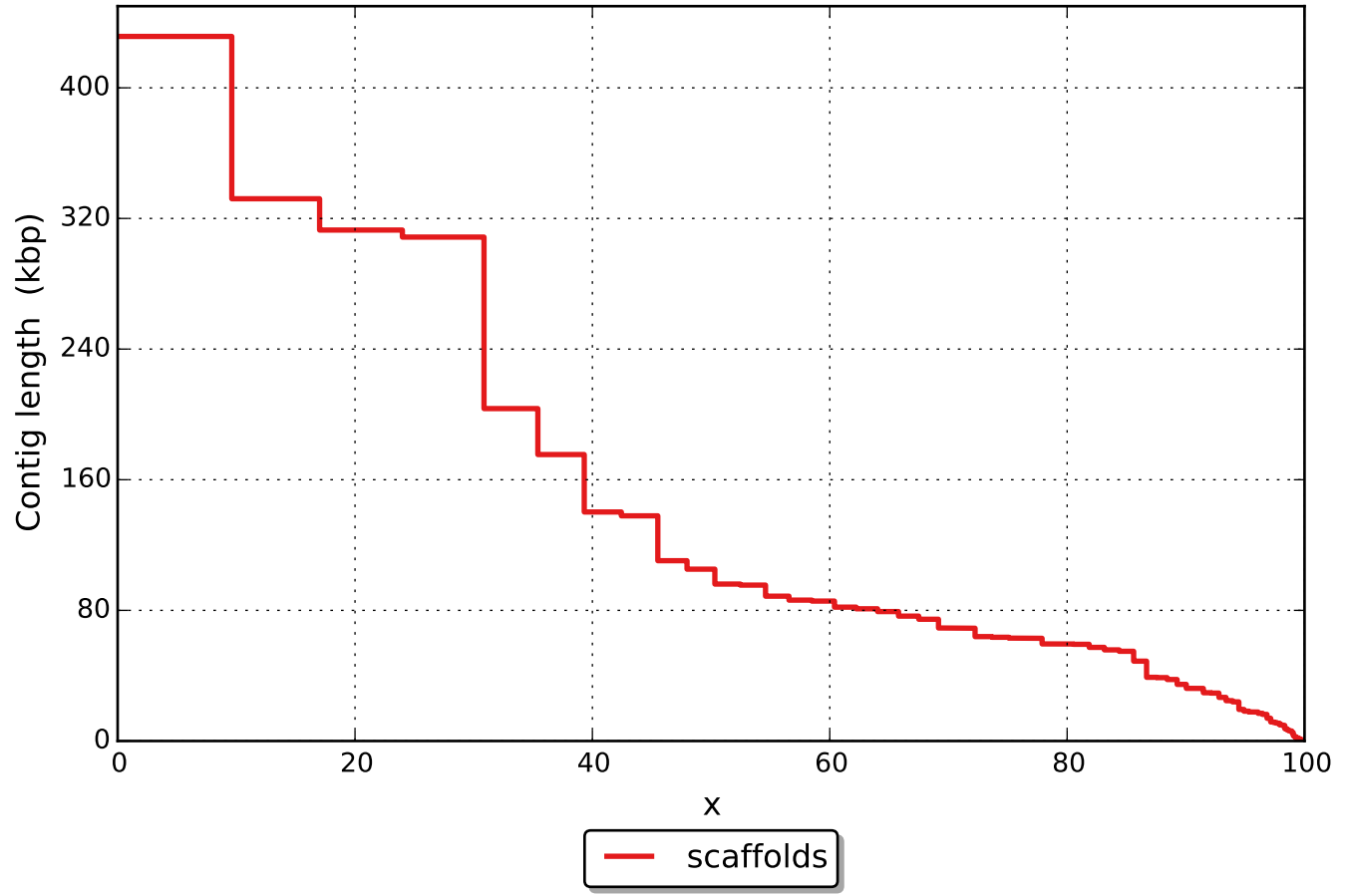




Cumulative length (aligned contigs)



NAx



# NGAx

