

## Report

|                                 | scaffolds  |
|---------------------------------|------------|
| # contigs ( $\geq 0$ bp)        | 88         |
| # contigs ( $\geq 1000$ bp)     | 66         |
| # contigs ( $\geq 5000$ bp)     | 49         |
| # contigs ( $\geq 10000$ bp)    | 46         |
| # contigs ( $\geq 25000$ bp)    | 40         |
| # contigs ( $\geq 50000$ bp)    | 27         |
| Total length ( $\geq 0$ bp)     | 4568666    |
| Total length ( $\geq 1000$ bp)  | 4563033    |
| Total length ( $\geq 5000$ bp)  | 4524909    |
| Total length ( $\geq 10000$ bp) | 4500958    |
| Total length ( $\geq 25000$ bp) | 4409821    |
| Total length ( $\geq 50000$ bp) | 3949295    |
| # contigs                       | 69         |
| Largest contig                  | 327064     |
| Total length                    | 4565448    |
| Reference length                | 4641652    |
| N50                             | 173982     |
| N75                             | 87064      |
| L50                             | 10         |
| L75                             | 20         |
| # misassemblies                 | 0          |
| # misassembled contigs          | 0          |
| Misassembled contigs length     | 0          |
| # local misassemblies           | 2          |
| # unaligned contigs             | 0 + 0 part |
| Unaligned length                | 0          |
| Genome fraction (▼)             | 98.303     |
| Duplication ratio               | 1.001      |
| # N's per 100 kbp               | 0.00       |
| # mismatches per 100 kbp        | 4.97       |
| # indels per 100 kbp            | 0.42       |
| Largest alignment               | 327064     |
| NA50                            | 173982     |
| NA75                            | 87064      |
| LA50                            | 10         |
| LA75                            | 20         |

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                 | 0         |
| # relocations                   | 0         |
| # translocations                | 0         |
| # inversions                    | 0         |
| # interspecies translocations   | 0         |
| # possibly misassembled contigs | 0         |
| # misassembled contigs          | 0         |
| Misassembled contigs length     | 0         |
| # local misassemblies           | 2         |
| # mismatches                    | 227       |
| # indels                        | 19        |
| # short indels                  | 19        |
| # long indels                   | 0         |
| Indels length                   | 26        |

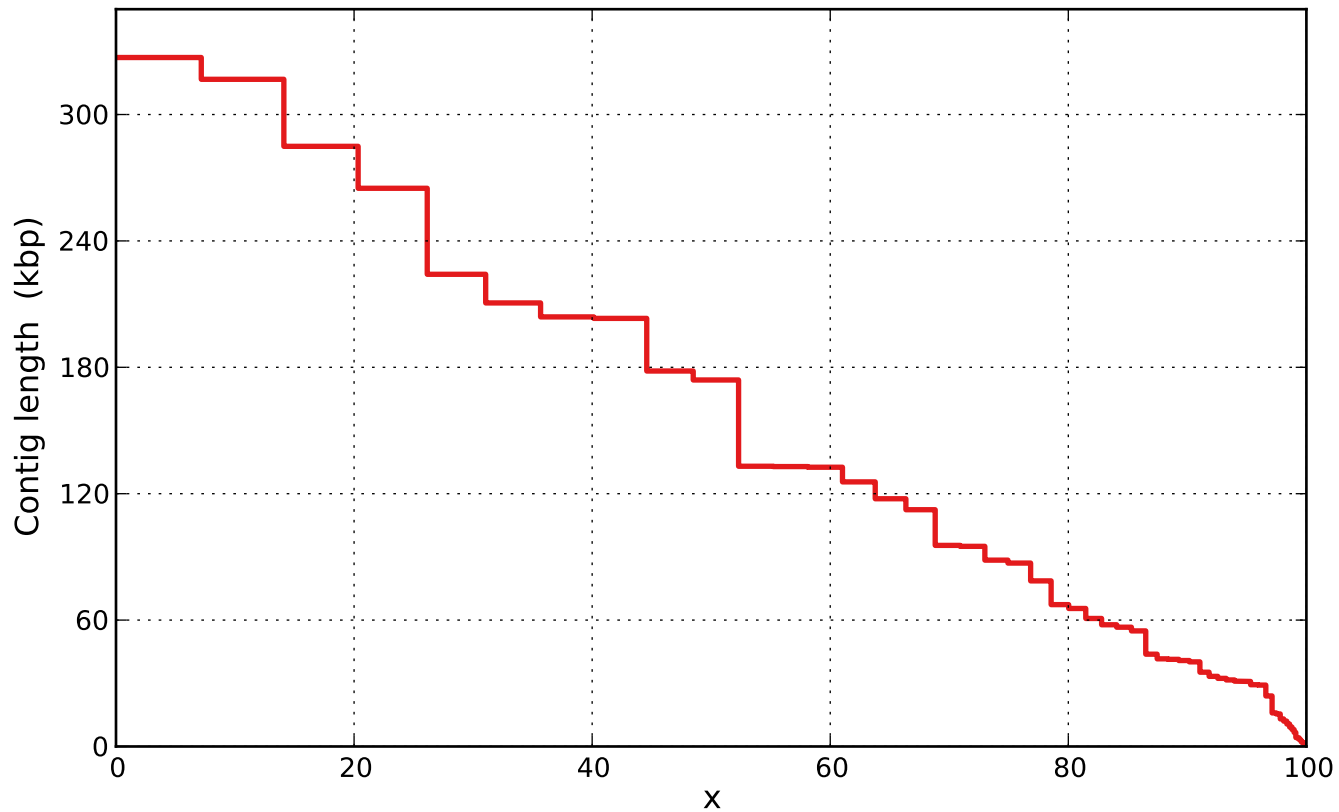
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

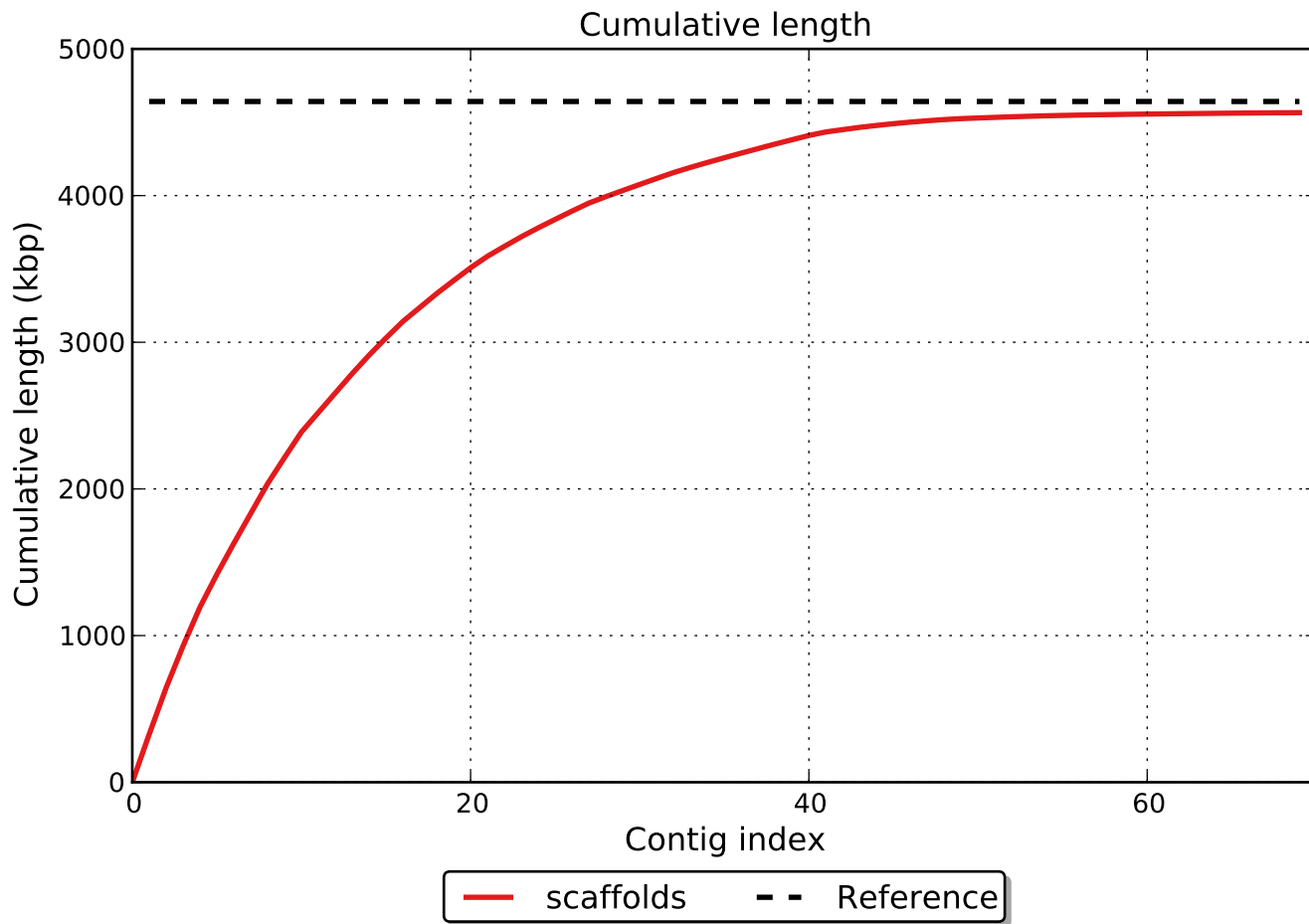
## Unaligned report

|                               | 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         |

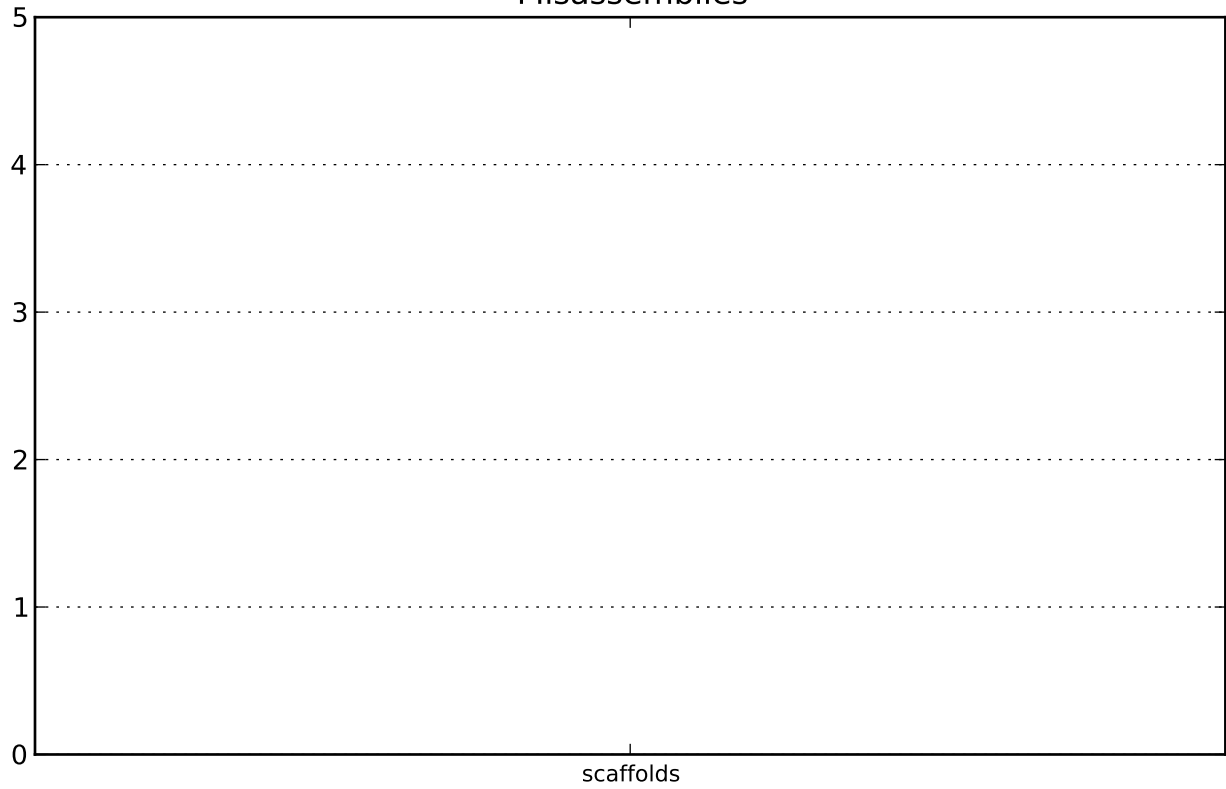
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

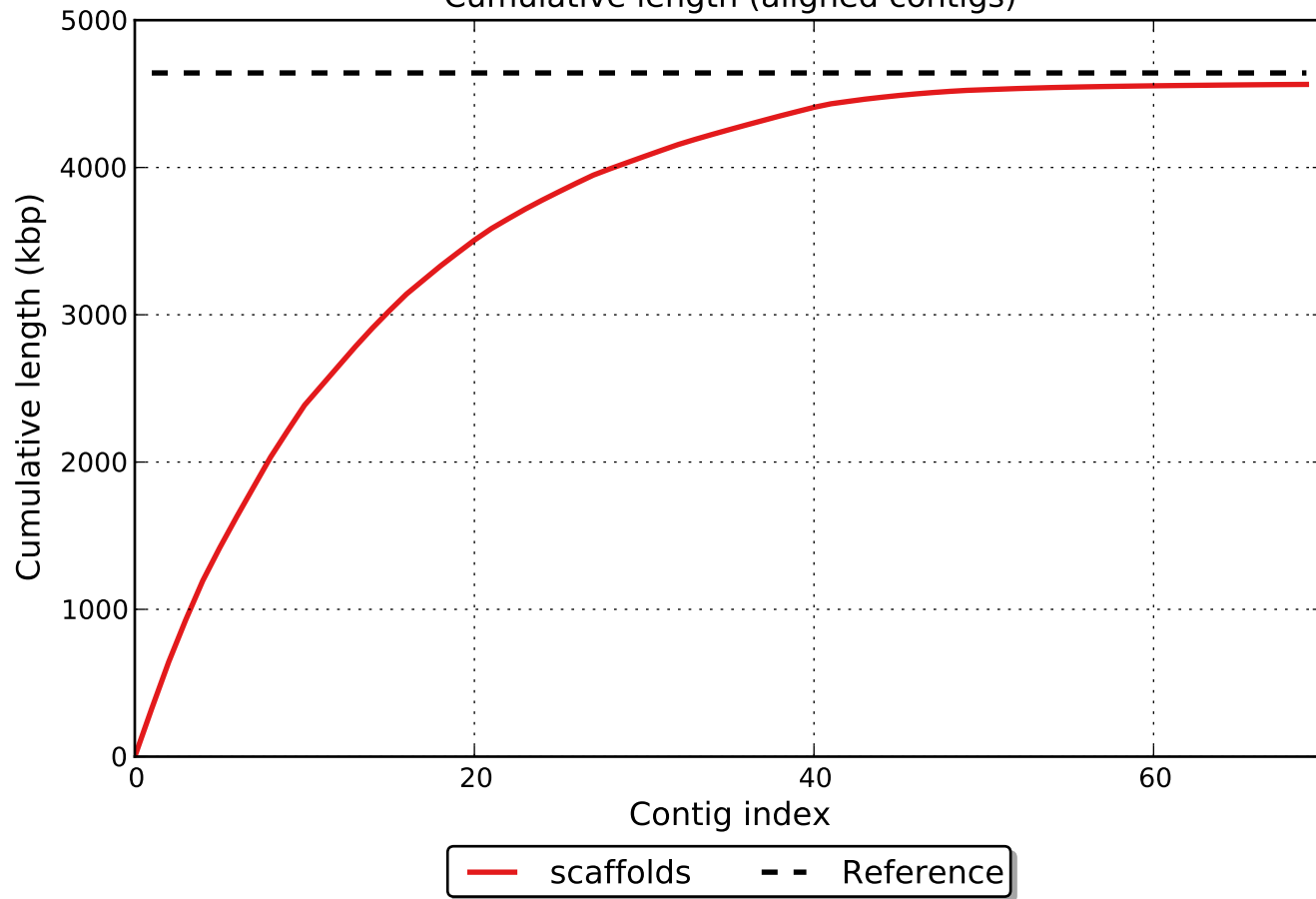




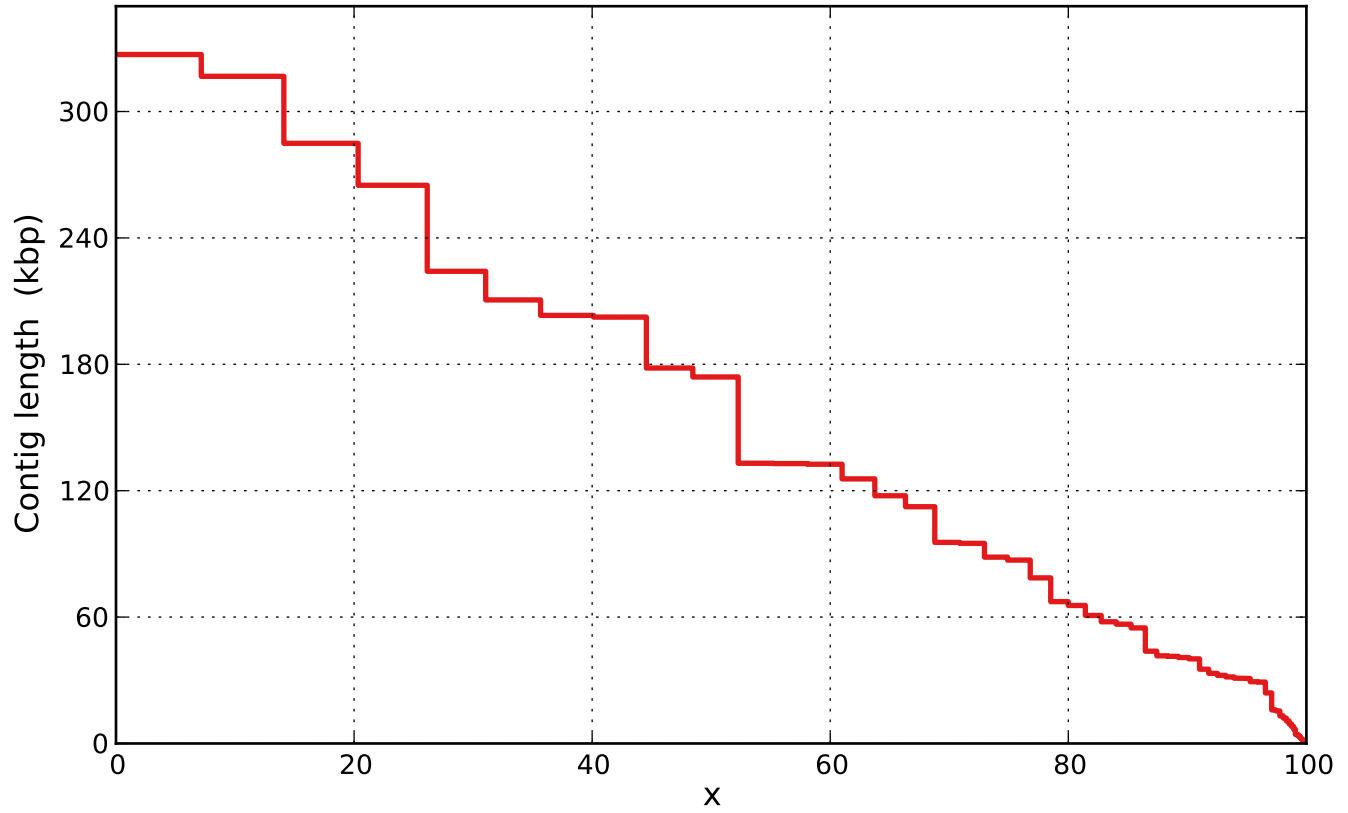
# Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds