

# Report

|                                 | scaffolds  |
|---------------------------------|------------|
| # contigs ( $\geq 0$ bp)        | 172        |
| # contigs ( $\geq 1000$ bp)     | 92         |
| # contigs ( $\geq 5000$ bp)     | 78         |
| # contigs ( $\geq 10000$ bp)    | 74         |
| # contigs ( $\geq 25000$ bp)    | 67         |
| # contigs ( $\geq 50000$ bp)    | 48         |
| Total length ( $\geq 0$ bp)     | 9124414    |
| Total length ( $\geq 1000$ bp)  | 9091674    |
| Total length ( $\geq 5000$ bp)  | 9067452    |
| Total length ( $\geq 10000$ bp) | 9037240    |
| Total length ( $\geq 25000$ bp) | 8933081    |
| Total length ( $\geq 50000$ bp) | 8257195    |
| # contigs                       | 115        |
| Largest contig                  | 472565     |
| Total length                    | 9108144    |
| Reference length                | 9283304    |
| N50                             | 208897     |
| N75                             | 108452     |
| L50                             | 15         |
| L75                             | 30         |
| # misassemblies                 | 3          |
| # misassembled contigs          | 3          |
| Misassembled contigs length     | 405365     |
| # local misassemblies           | 2          |
| # unaligned contigs             | 0 + 1 part |
| Unaligned length                | 46         |
| Genome fraction (%)             | 98.000     |
| Duplication ratio               | 1.001      |
| # N's per 100 kbp               | 0.11       |
| # mismatches per 100 kbp        | 484.69     |
| # indels per 100 kbp            | 0.95       |
| Largest alignment               | 472565     |
| NA50                            | 203339     |
| NA75                            | 108452     |
| LA50                            | 16         |
| LA75                            | 30         |

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                 | 3         |
| # relocations                   | 0         |
| # translocations                | 0         |
| # inversions                    | 0         |
| # interspecies translocations   | 3         |
| # possibly misassembled contigs | 0         |
| # misassembled contigs          | 3         |
| Misassembled contigs length     | 405365    |
| # local misassemblies           | 2         |
| # mismatches                    | 44095     |
| # indels                        | 86        |
| # short indels                  | 81        |
| # long indels                   | 5         |
| Indels length                   | 164       |

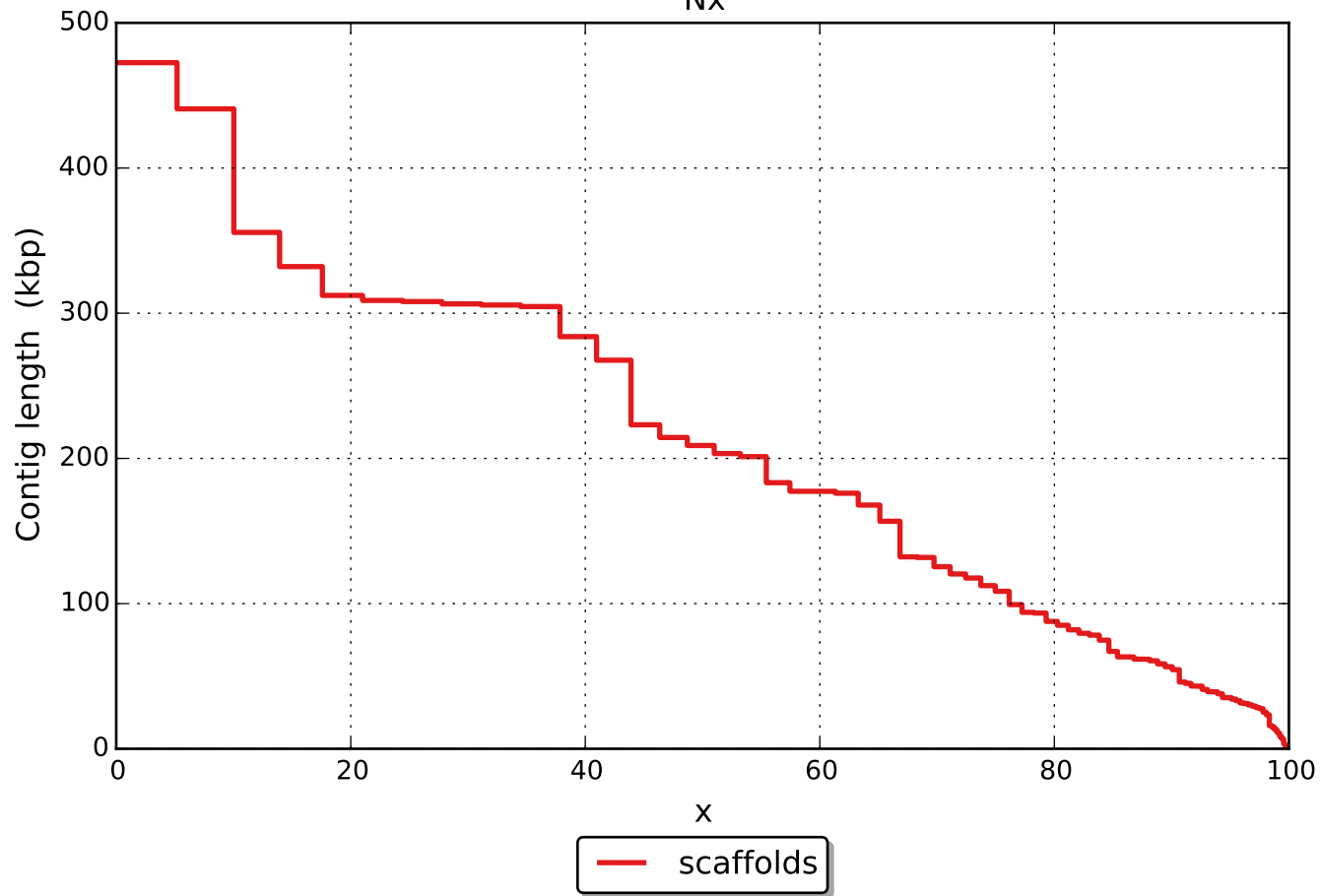
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

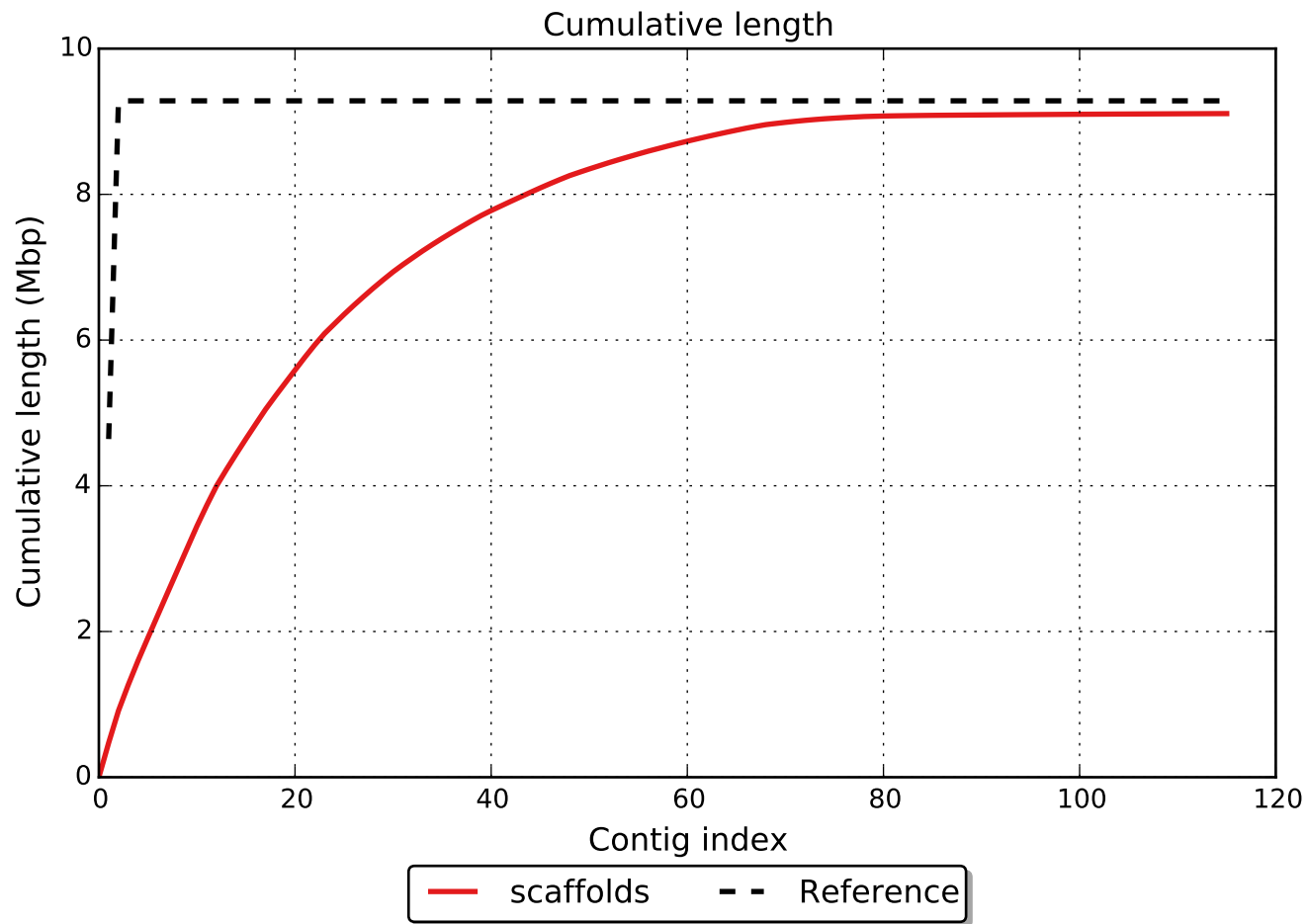
## Unaligned report

|                               | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs     | 0         |
| Fully unaligned length        | 0         |
| # partially unaligned contigs | 1         |
| # with misassembly            | 0         |
| # both parts are significant  | 0         |
| Partially unaligned length    | 46        |
| # N's                         | 10        |

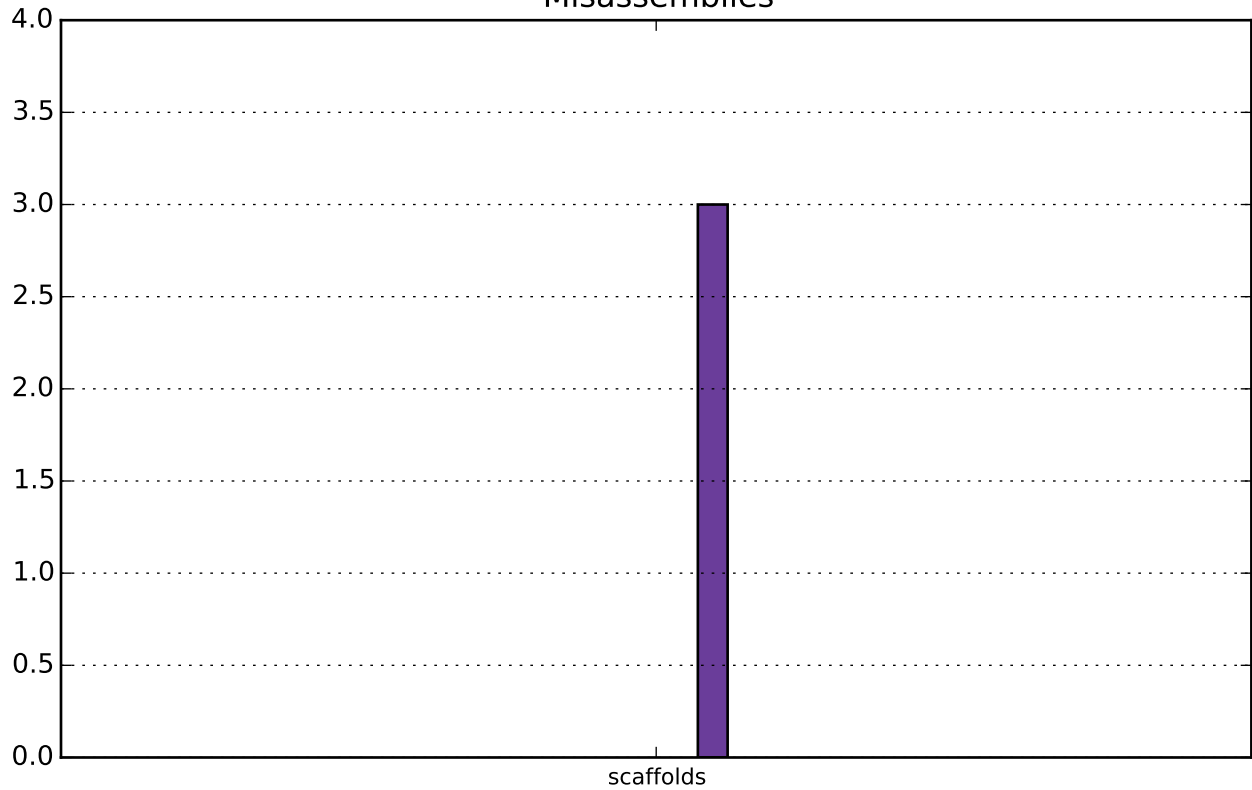
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

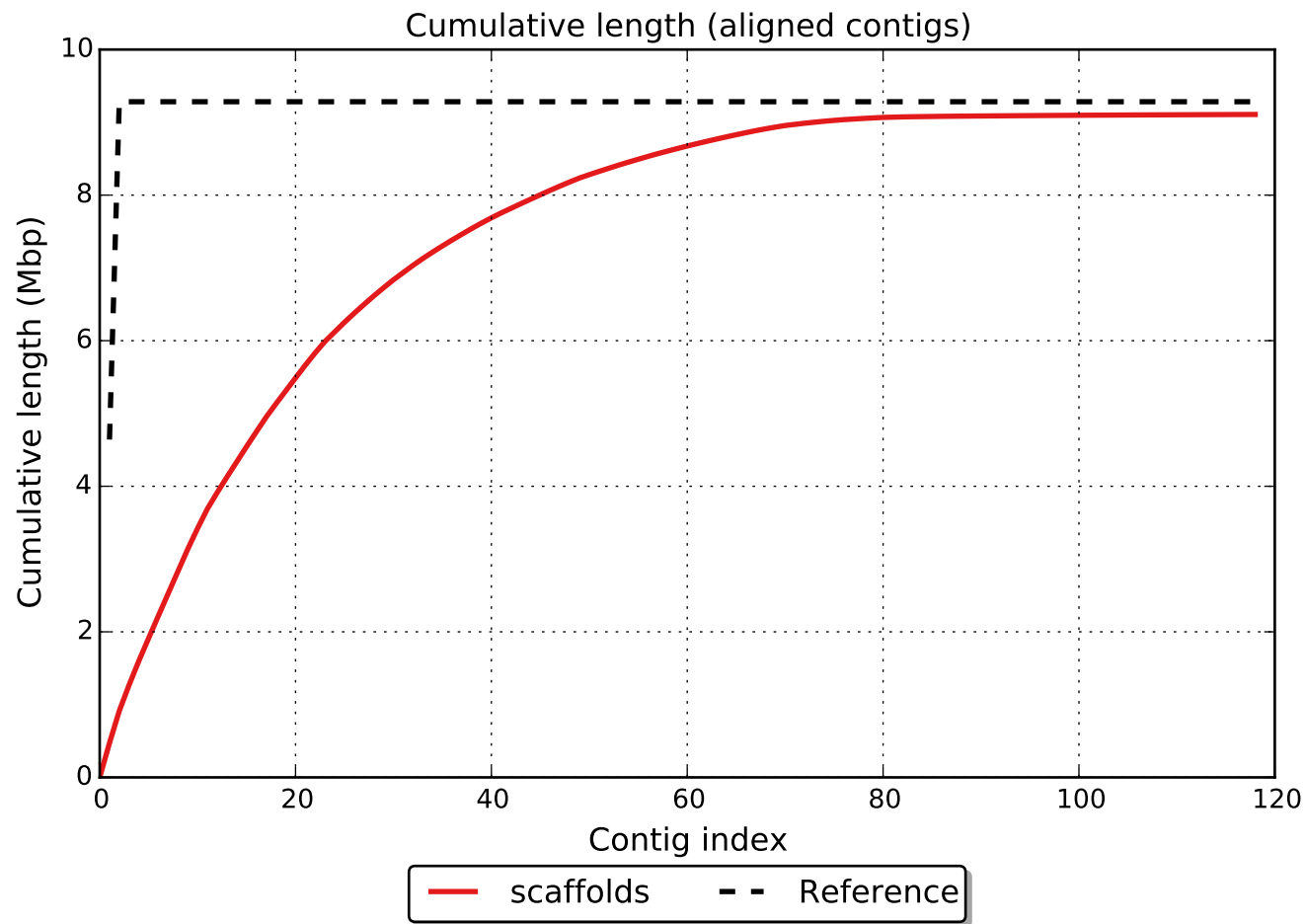




# Misassemblies



 # interspecies translocations



NAx

