

# Report

|                                 | contigs    |
|---------------------------------|------------|
| # contigs ( $\geq 0$ bp)        | 147        |
| # contigs ( $\geq 1000$ bp)     | 84         |
| # contigs ( $\geq 5000$ bp)     | 67         |
| # contigs ( $\geq 10000$ bp)    | 63         |
| # contigs ( $\geq 25000$ bp)    | 56         |
| # contigs ( $\geq 50000$ bp)    | 42         |
| Total length ( $\geq 0$ bp)     | 9168920    |
| Total length ( $\geq 1000$ bp)  | 9144650    |
| Total length ( $\geq 5000$ bp)  | 9108381    |
| Total length ( $\geq 10000$ bp) | 9074911    |
| Total length ( $\geq 25000$ bp) | 8958447    |
| Total length ( $\geq 50000$ bp) | 8492499    |
| # contigs                       | 99         |
| Largest contig                  | 601815     |
| Total length                    | 9155947    |
| Reference length                | 9283304    |
| N50                             | 263950     |
| N75                             | 131793     |
| L50                             | 12         |
| L75                             | 24         |
| # misassemblies                 | 1          |
| # misassembled contigs          | 1          |
| Misassembled contigs length     | 36823      |
| # local misassemblies           | 1          |
| # unaligned contigs             | 0 + 0 part |
| Unaligned length                | 0          |
| Genome fraction (%)             | 98.612     |
| Duplication ratio               | 1.000      |
| # N's per 100 kbp               | 0.00       |
| # mismatches per 100 kbp        | 192.41     |
| # indels per 100 kbp            | 0.68       |
| Largest alignment               | 601815     |
| NA50                            | 263950     |
| NA75                            | 131793     |
| LA50                            | 12         |
| LA75                            | 24         |

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

|                                 | contigs |
|---------------------------------|---------|
| # misassemblies                 | 1       |
| # relocations                   | 1       |
| # translocations                | 0       |
| # inversions                    | 0       |
| # interspecies translocations   | 0       |
| # possibly misassembled contigs | 0       |
| # misassembled contigs          | 1       |
| Misassembled contigs length     | 36823   |
| # local misassemblies           | 1       |
| # mismatches                    | 17614   |
| # indels                        | 62      |
| # short indels                  | 62      |
| # long indels                   | 0       |
| Indels length                   | 67      |

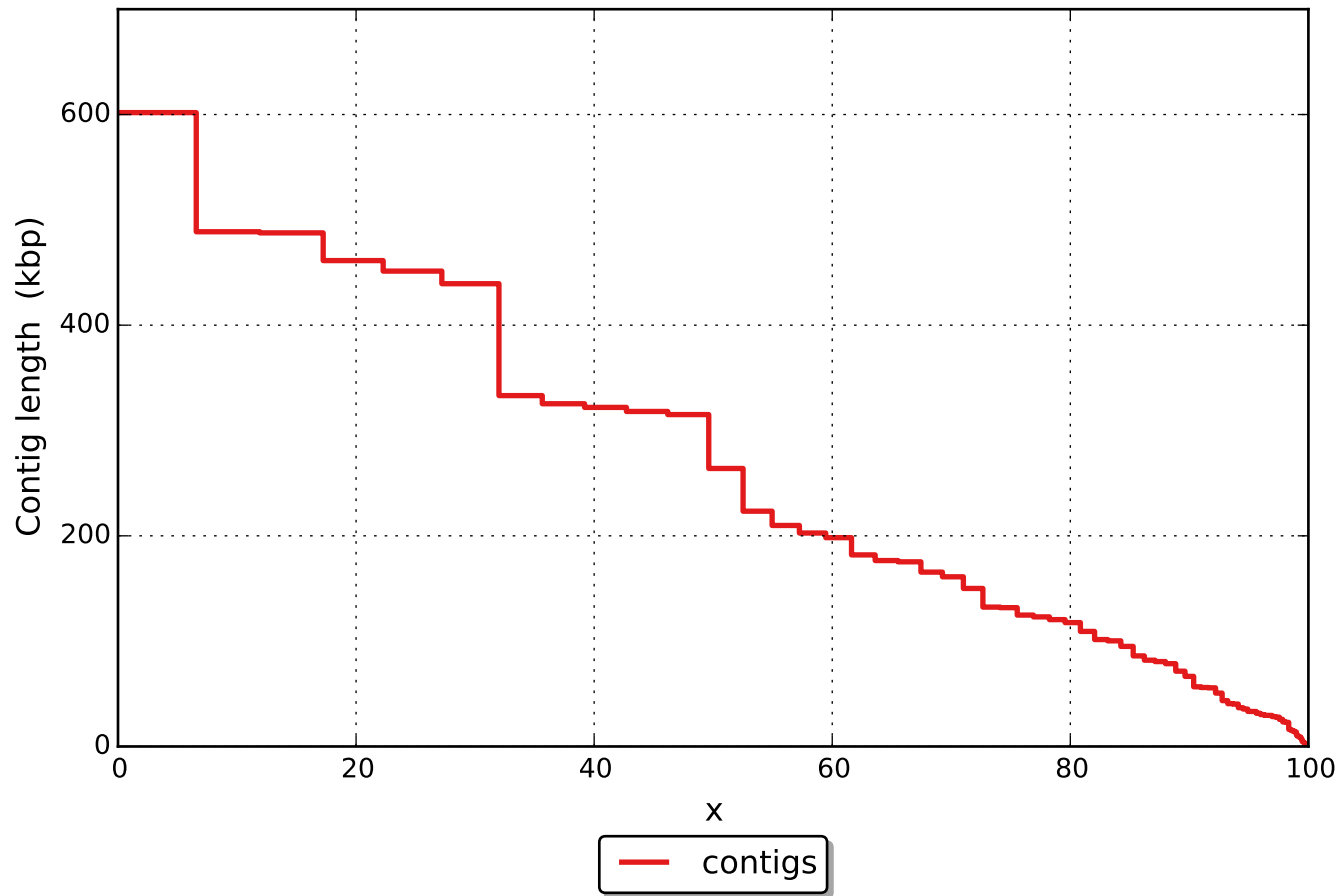
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

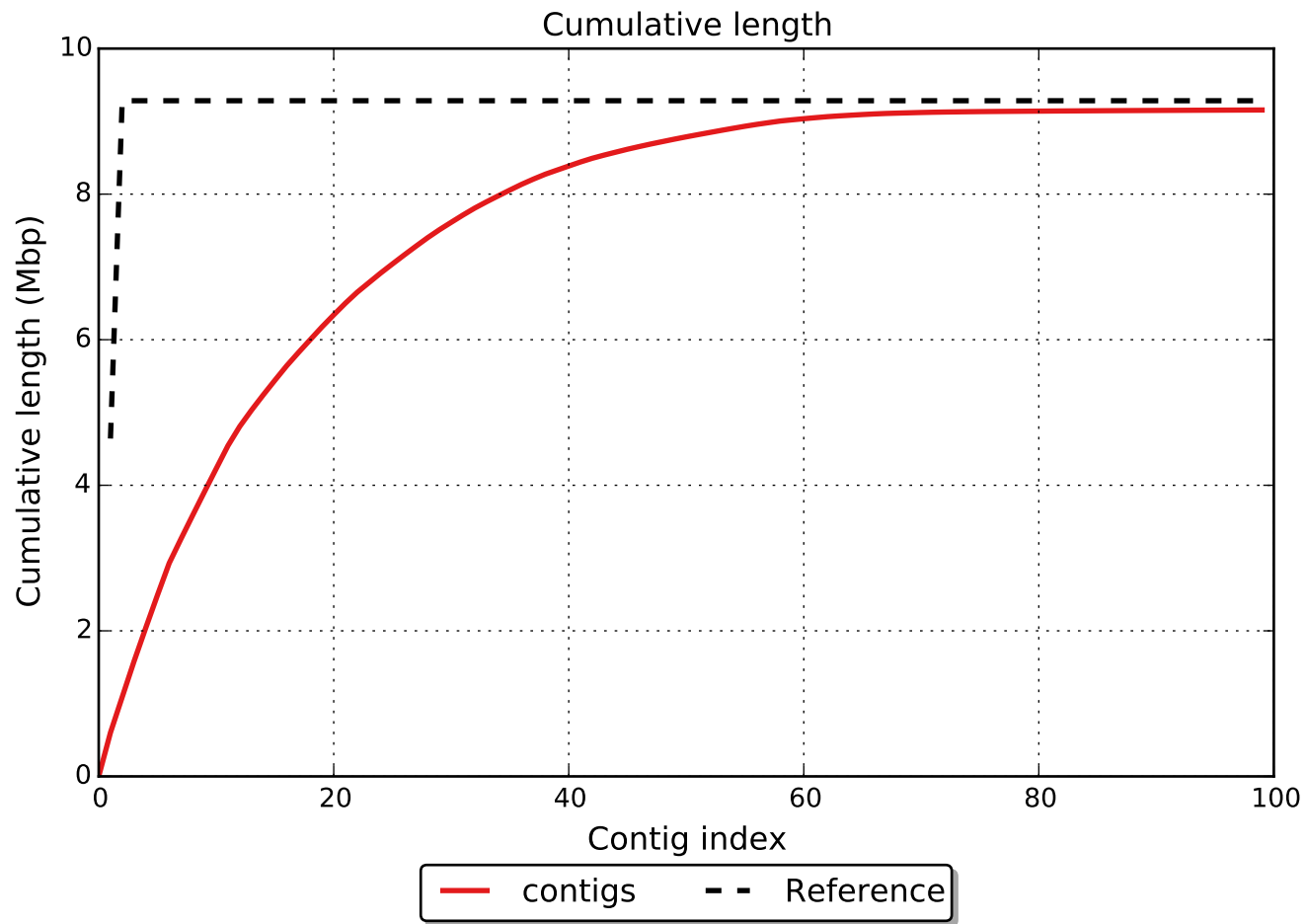
## Unaligned report

|                               | contigs |
|-------------------------------|---------|
| # 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       |

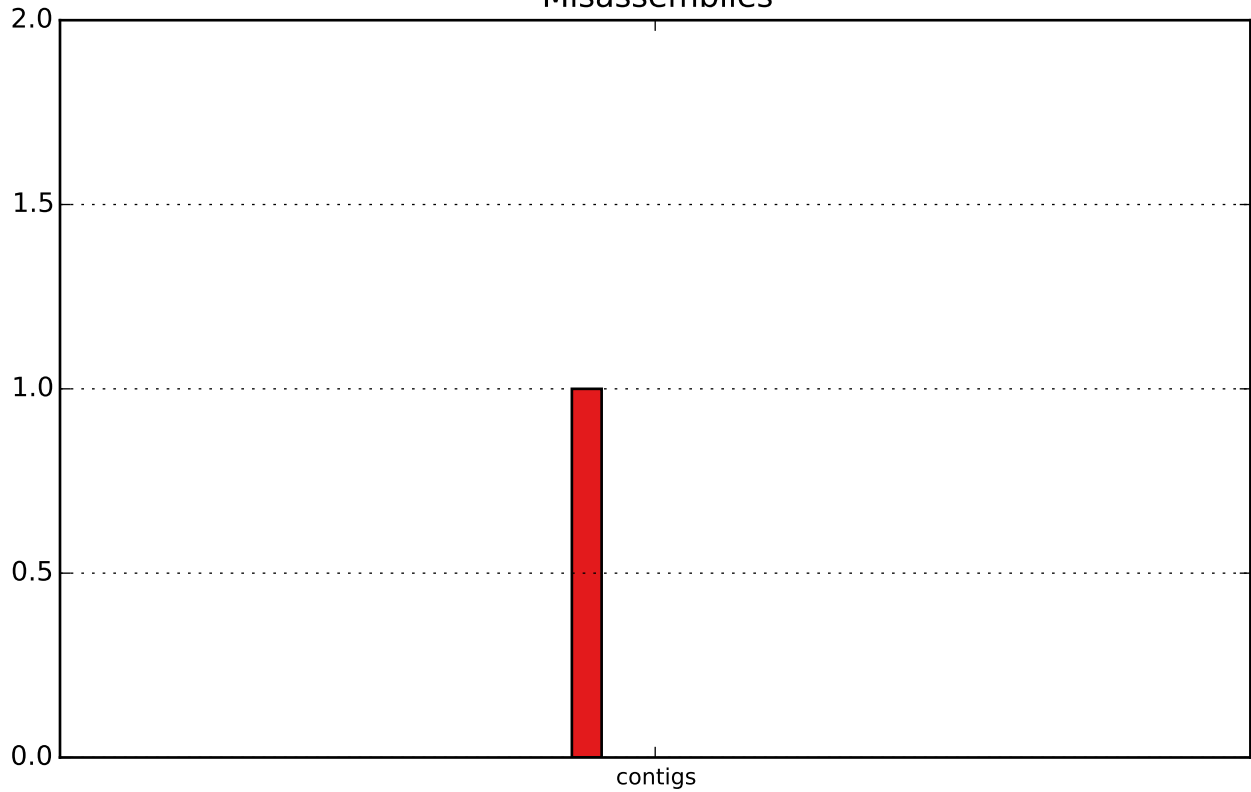
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

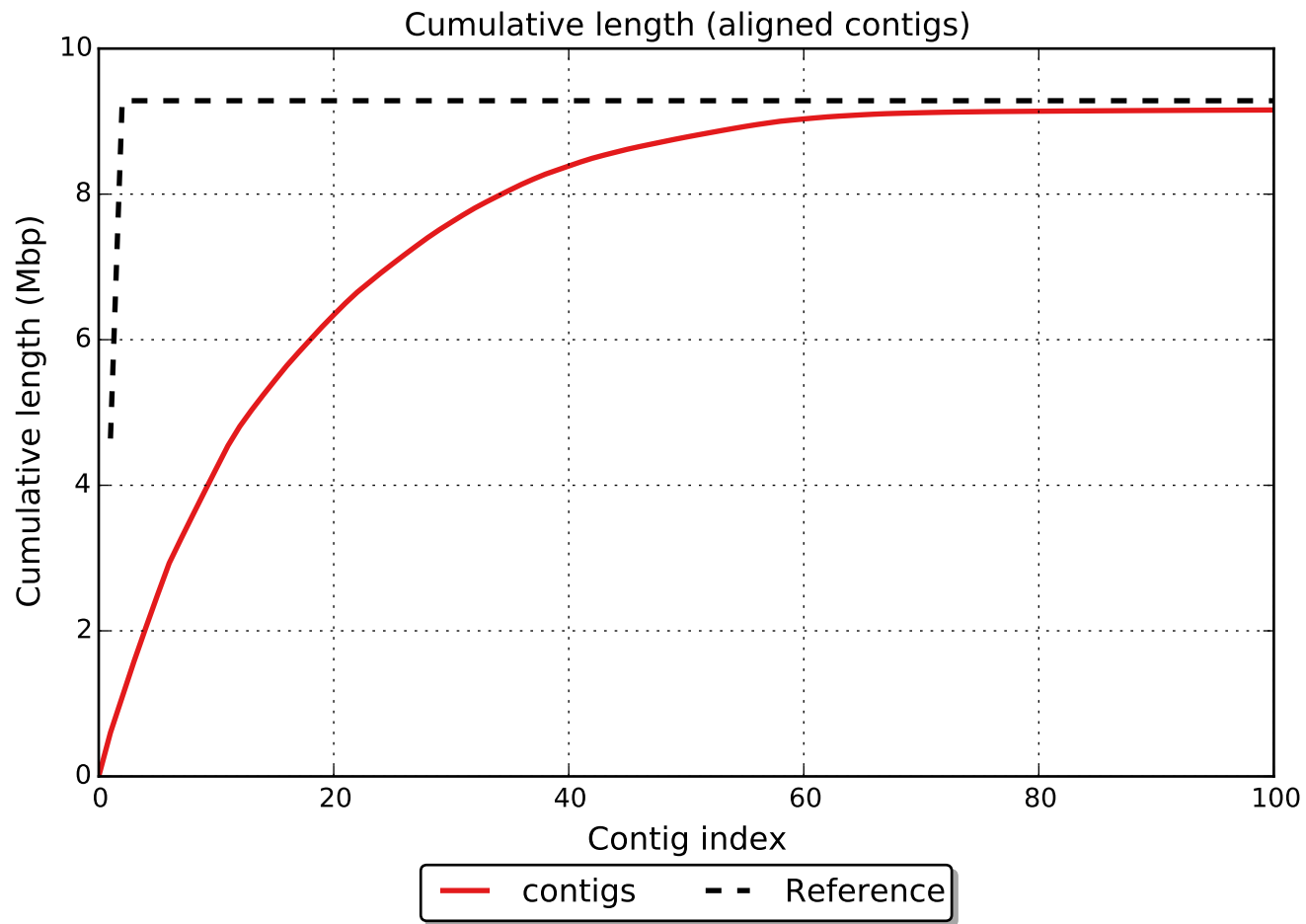
Nx





# Misassemblies





NAx

