

# Report

|                                 | contigs    |
|---------------------------------|------------|
| # contigs ( $\geq 0$ bp)        | 144        |
| # contigs ( $\geq 1000$ bp)     | 83         |
| # contigs ( $\geq 5000$ bp)     | 65         |
| # contigs ( $\geq 10000$ bp)    | 62         |
| # contigs ( $\geq 25000$ bp)    | 55         |
| # contigs ( $\geq 50000$ bp)    | 42         |
| Total length ( $\geq 0$ bp)     | 9167402    |
| Total length ( $\geq 1000$ bp)  | 9143132    |
| Total length ( $\geq 5000$ bp)  | 9102454    |
| Total length ( $\geq 10000$ bp) | 9078759    |
| Total length ( $\geq 25000$ bp) | 8957685    |
| Total length ( $\geq 50000$ bp) | 8511042    |
| # contigs                       | 102        |
| Largest contig                  | 1053360    |
| Total length                    | 9156263    |
| Reference length                | 9283304    |
| N50                             | 224139     |
| N75                             | 132462     |
| L50                             | 11         |
| L75                             | 24         |
| # misassemblies                 | 1          |
| # misassembled contigs          | 1          |
| Misassembled contigs length     | 36005      |
| # local misassemblies           | 2          |
| # unaligned contigs             | 0 + 0 part |
| Unaligned length                | 0          |
| Genome fraction (%)             | 99.135     |
| Duplication ratio               | 1.000      |
| # N's per 100 kbp               | 0.00       |
| # mismatches per 100 kbp        | 149.81     |
| # indels per 100 kbp            | 0.72       |
| Largest alignment               | 1053360    |
| NA50                            | 224139     |
| NA75                            | 132462     |
| LA50                            | 11         |
| 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     | 36005   |
| # local misassemblies           | 2       |
| # mismatches                    | 13787   |
| # indels                        | 66      |
| # short indels                  | 65      |
| # long indels                   | 1       |
| Indels length                   | 97      |

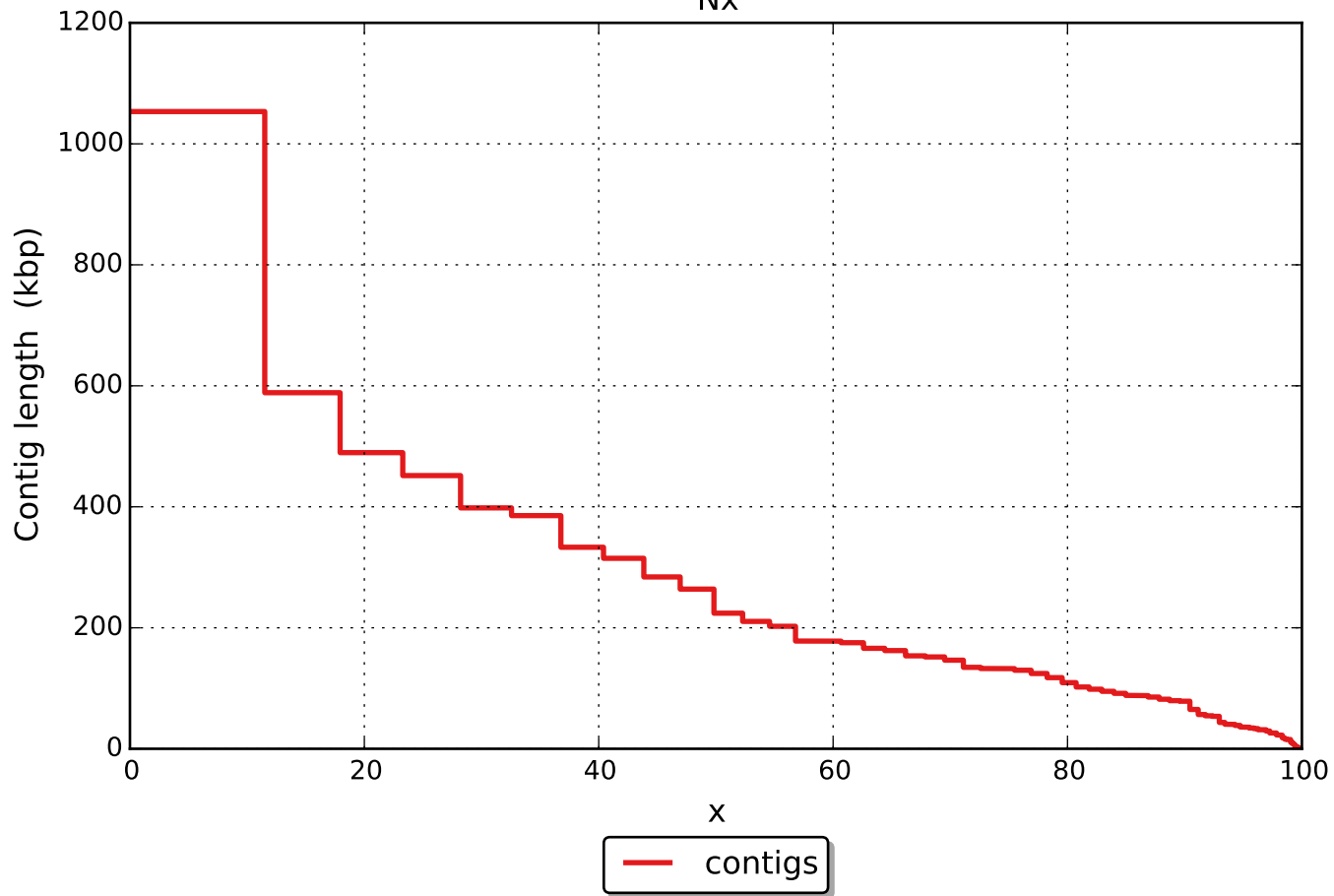
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

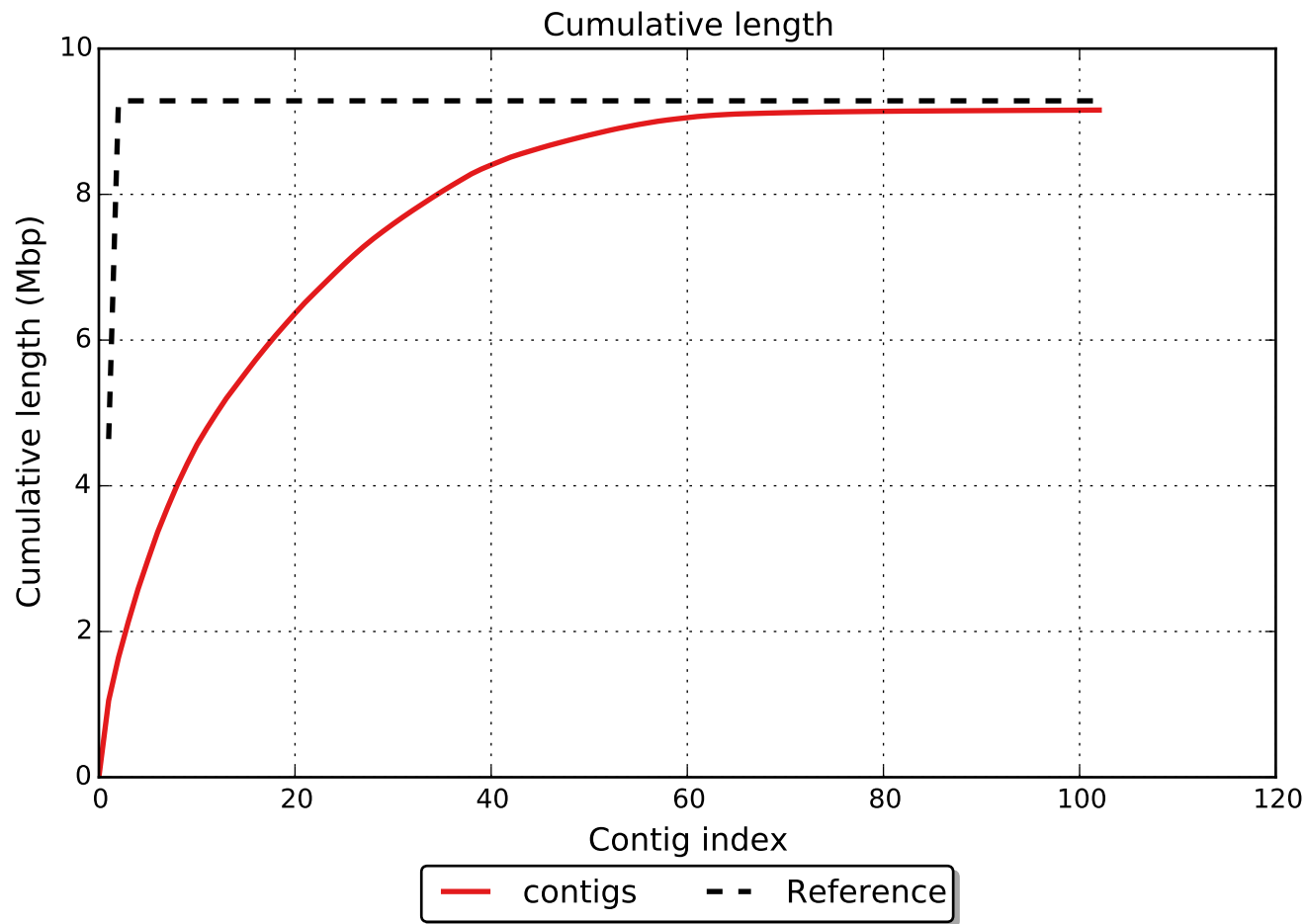
## Unaligned report

|                               | 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       |

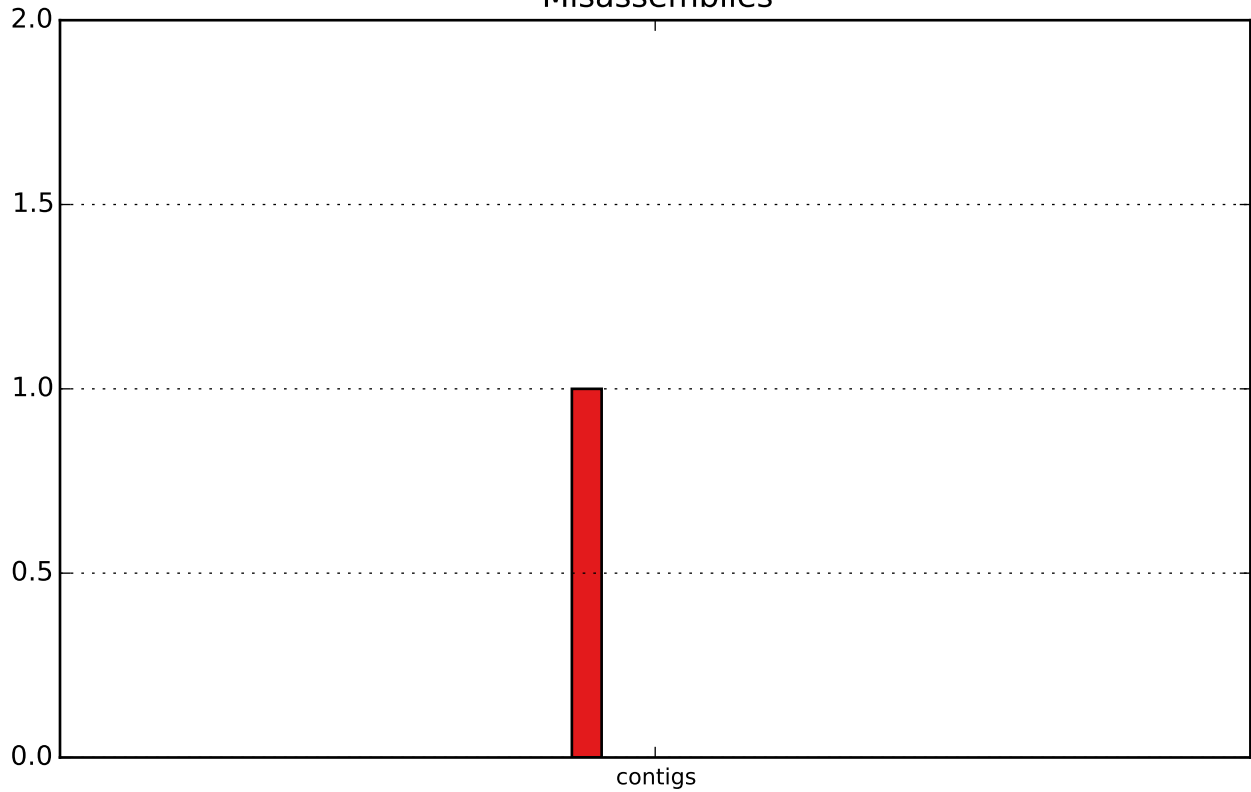
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

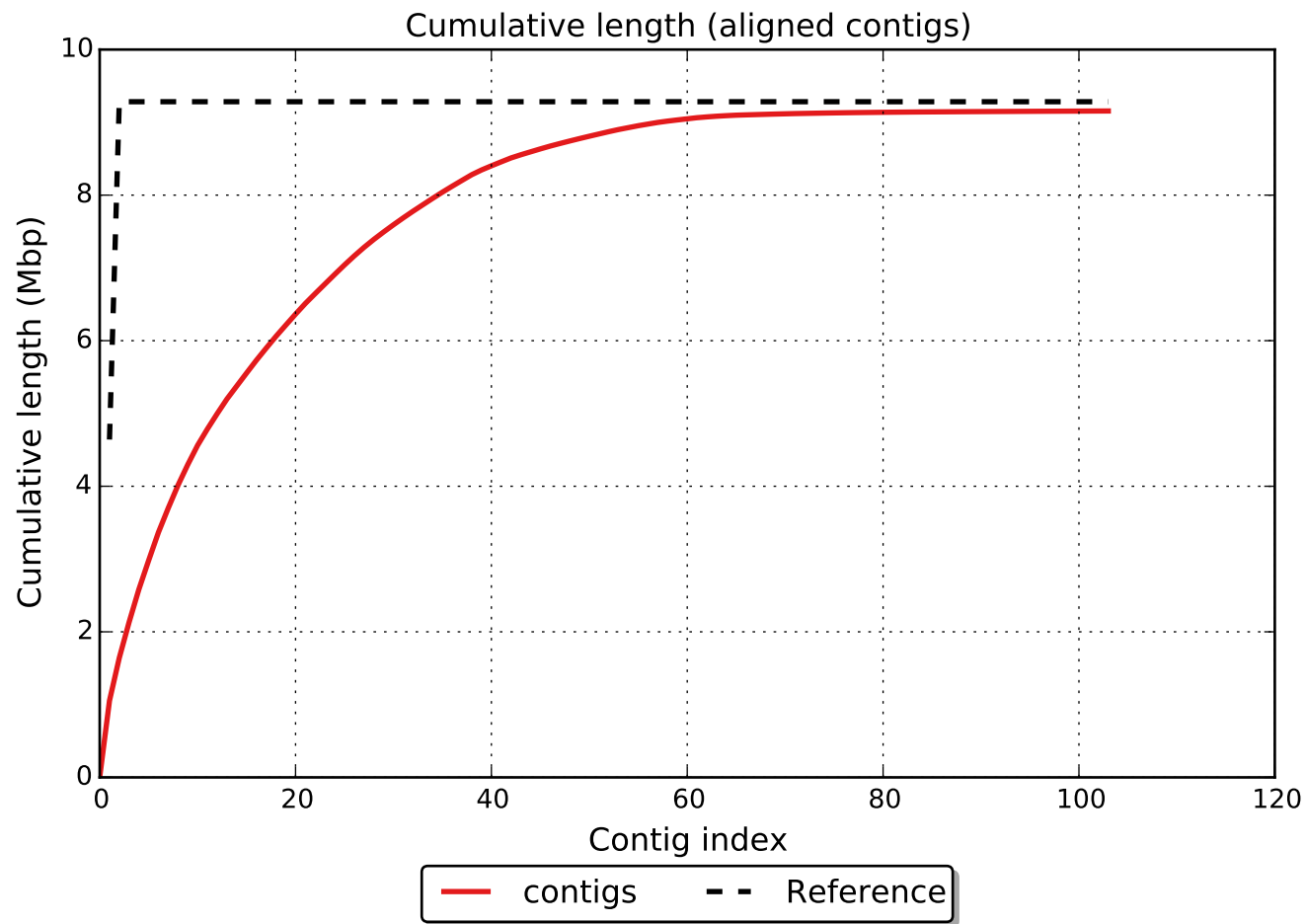
Nx





# Misassemblies





NAx

