

## Report

|                                 | final.contigs |
|---------------------------------|---------------|
| # contigs ( $\geq 0$ bp)        | 49643         |
| # contigs ( $\geq 1000$ bp)     | 6             |
| # contigs ( $\geq 5000$ bp)     | 0             |
| # contigs ( $\geq 10000$ bp)    | 0             |
| # contigs ( $\geq 25000$ bp)    | 0             |
| # contigs ( $\geq 50000$ bp)    | 0             |
| Total length ( $\geq 0$ bp)     | 15338969      |
| Total length ( $\geq 1000$ bp)  | 6580          |
| Total length ( $\geq 5000$ bp)  | 0             |
| Total length ( $\geq 10000$ bp) | 0             |
| Total length ( $\geq 25000$ bp) | 0             |
| Total length ( $\geq 50000$ bp) | 0             |
| # contigs                       | 796           |
| Largest contig                  | 1226          |
| Total length                    | 449307        |
| Reference length                | 4641652       |
| N50                             | 546           |
| N75                             | 517           |
| L50                             | 364           |
| L75                             | 575           |
| # misassemblies                 | 4             |
| # misassembled contigs          | 4             |
| Misassembled contigs length     | 2168          |
| # local misassemblies           | 3             |
| # unaligned contigs             | 11 + 4 part   |
| Unaligned length                | 6860          |
| Genome fraction (▼)             | 9.147         |
| Duplication ratio               | 1.043         |
| # N's per 100 kbp               | 0.00          |
| # mismatches per 100 kbp        | 1582.01       |
| # indels per 100 kbp            | 0.24          |
| Largest alignment               | 1226          |
| NA50                            | 545           |
| NA75                            | 516           |
| LA50                            | 365           |
| LA75                            | 577           |

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

|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 4             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 4             |
| # interspecies translocations   | 0             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 4             |
| Misassembled contigs length     | 2168          |
| # local misassemblies           | 3             |
| # mismatches                    | 6717          |
| # indels                        | 1             |
| # short indels                  | 1             |
| # long indels                   | 0             |
| Indels length                   | 1             |

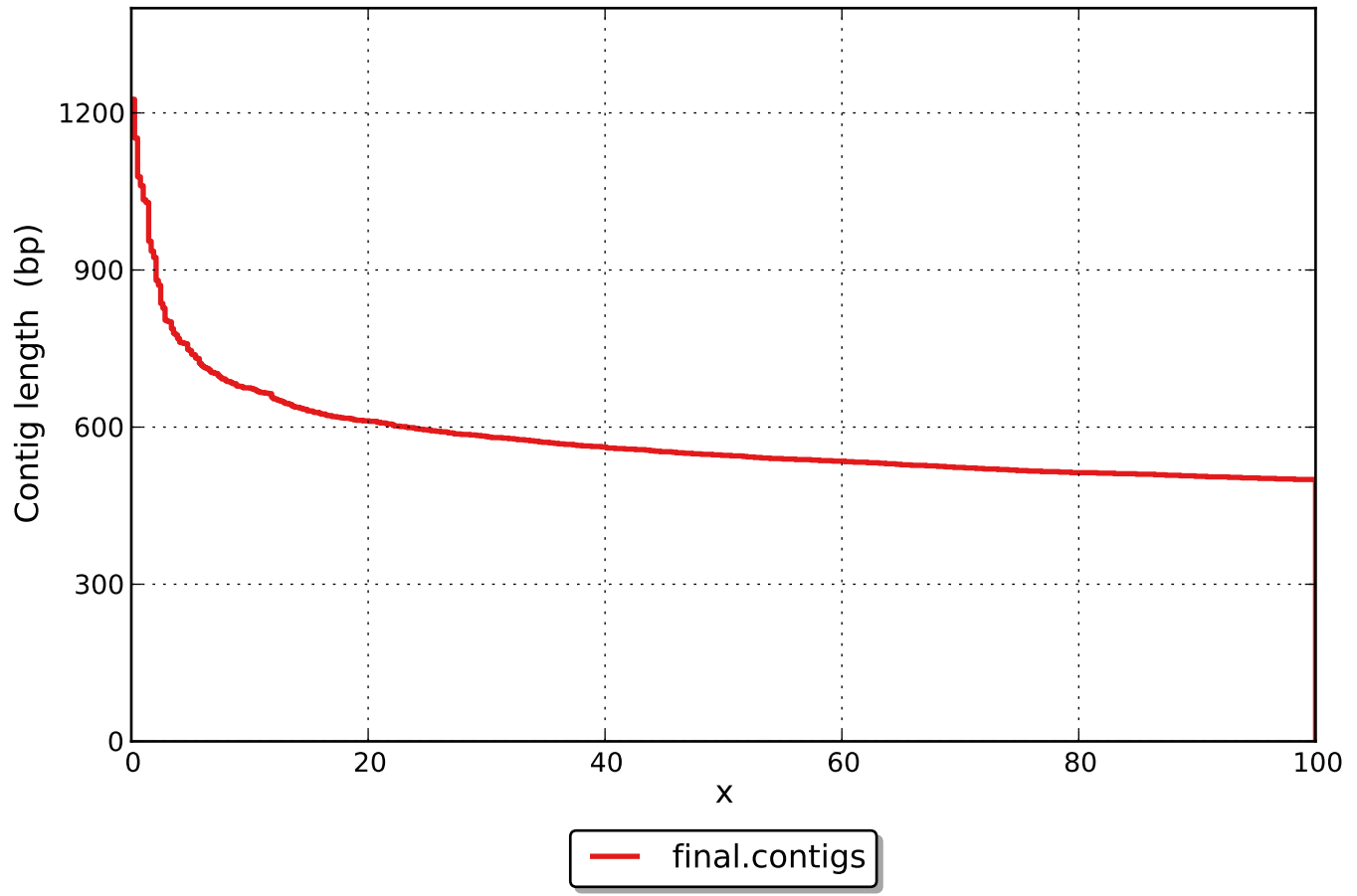
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

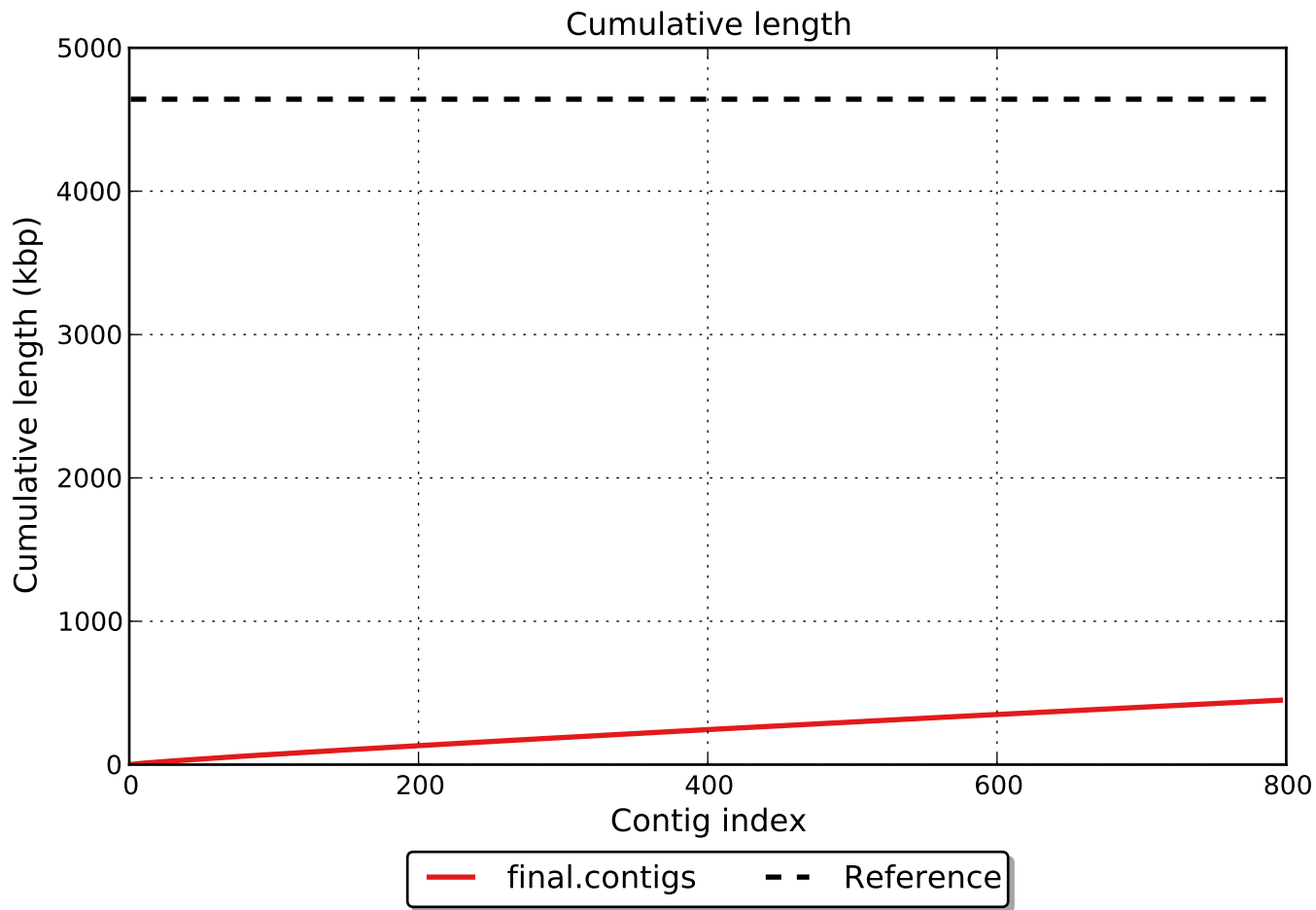
## Unaligned report

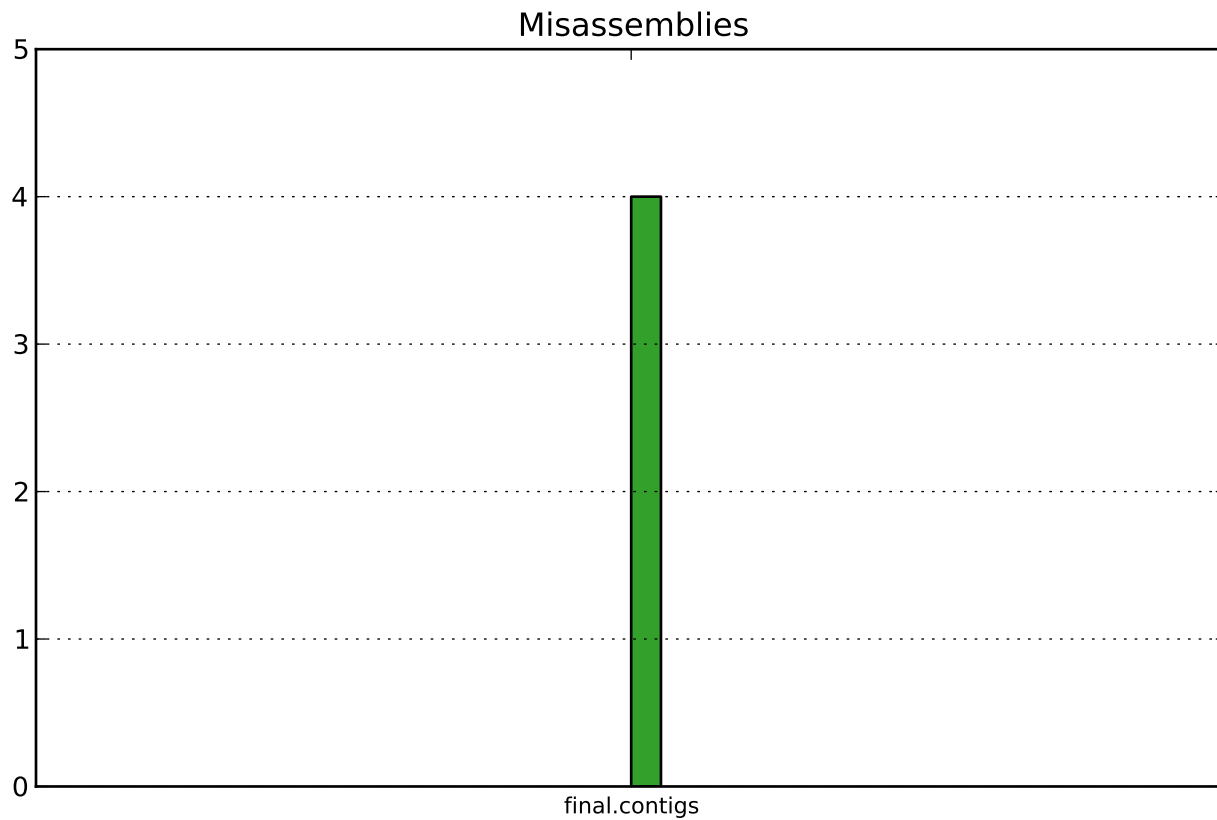
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 11            |
| Fully unaligned length        | 6038          |
| # partially unaligned contigs | 4             |
| # with misassembly            | 0             |
| # both parts are significant  | 0             |
| Partially unaligned length    | 822           |
| # N's                         | 0             |

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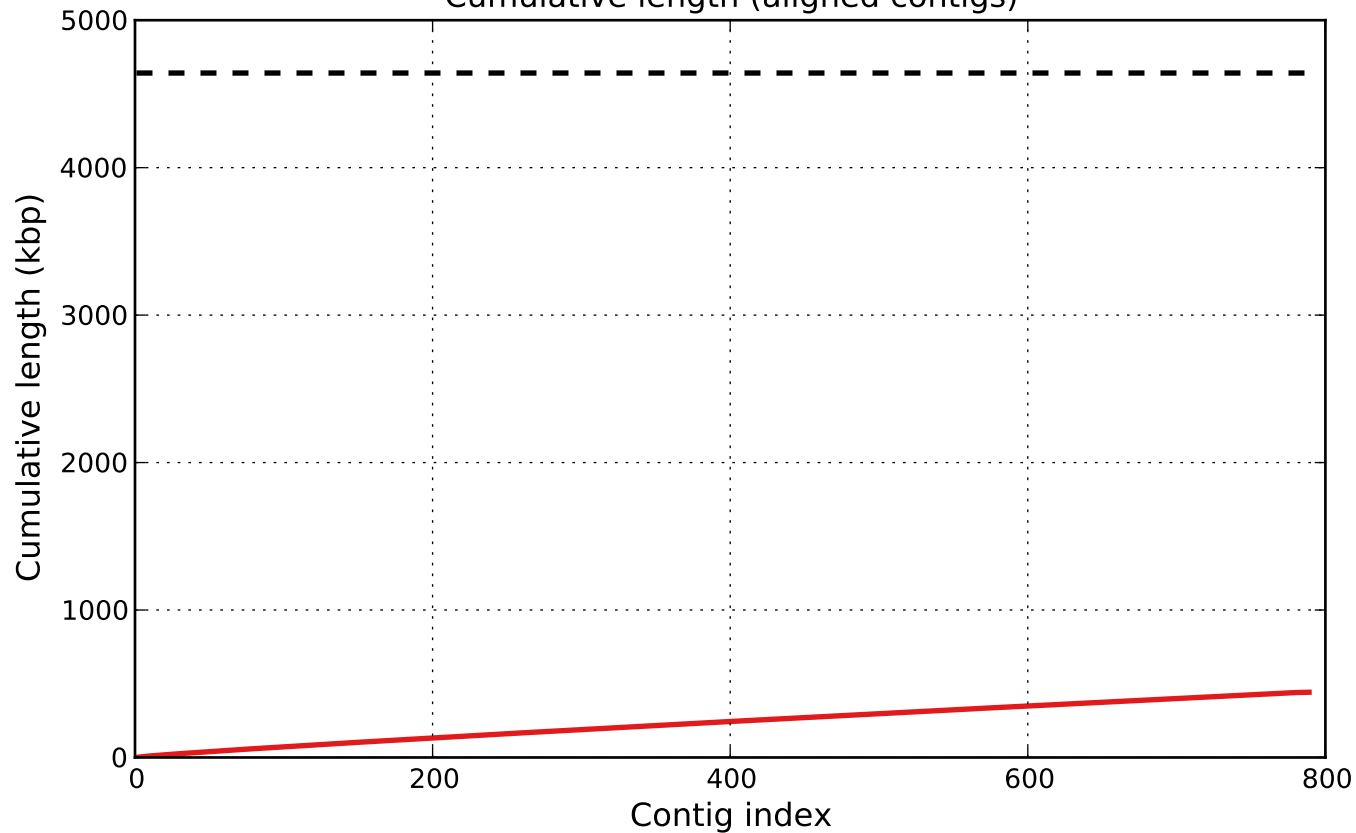
Nx





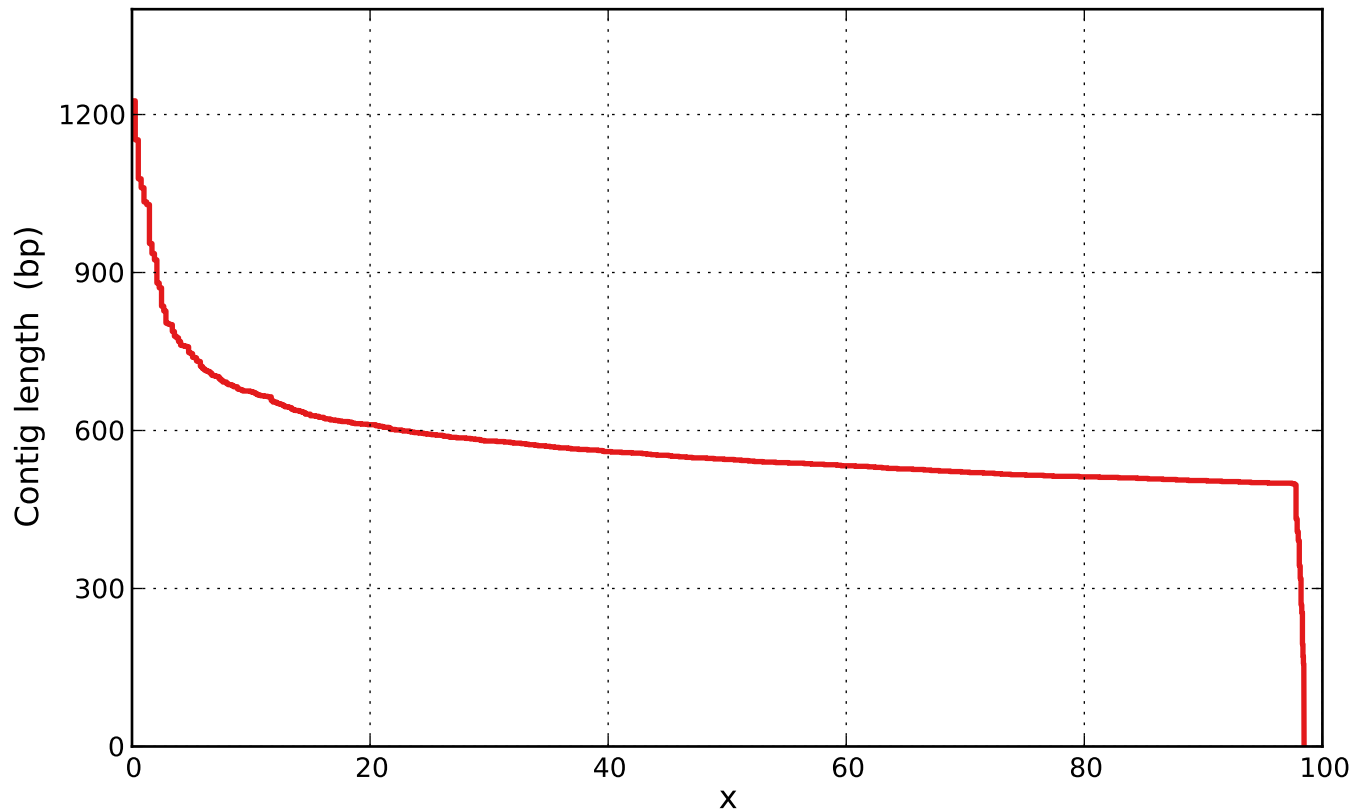


Cumulative length (aligned contigs)



— final.contigs      - - Reference

NAx



— final.contigs