

# Report

|                                 | final.contigs |
|---------------------------------|---------------|
| # contigs ( $\geq 0$ bp)        | 2726          |
| # contigs ( $\geq 1000$ bp)     | 1769          |
| # contigs ( $\geq 5000$ bp)     | 682           |
| # contigs ( $\geq 10000$ bp)    | 187           |
| # contigs ( $\geq 25000$ bp)    | 8             |
| # contigs ( $\geq 50000$ bp)    | 0             |
| Total length ( $\geq 0$ bp)     | 9576173       |
| Total length ( $\geq 1000$ bp)  | 9146454       |
| Total length ( $\geq 5000$ bp)  | 6210374       |
| Total length ( $\geq 10000$ bp) | 2735013       |
| Total length ( $\geq 25000$ bp) | 234899        |
| Total length ( $\geq 50000$ bp) | 0             |
| # contigs                       | 2043          |
| Largest contig                  | 39629         |
| Total length                    | 9350524       |
| Reference length                | 9283304       |
| N50                             | 6852          |
| N75                             | 4016          |
| L50                             | 423           |
| L75                             | 862           |
| # misassemblies                 | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 3             |
| # unaligned contigs             | 0 + 0 part    |
| Unaligned length                | 0             |
| Genome fraction (%)             | 98.830        |
| Duplication ratio               | 1.020         |
| # N's per 100 kbp               | 0.00          |
| # mismatches per 100 kbp        | 21.79         |
| # indels per 100 kbp            | 0.02          |
| Largest alignment               | 39629         |
| NA50                            | 6852          |
| NA75                            | 4016          |
| LA50                            | 423           |
| LA75                            | 862           |

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

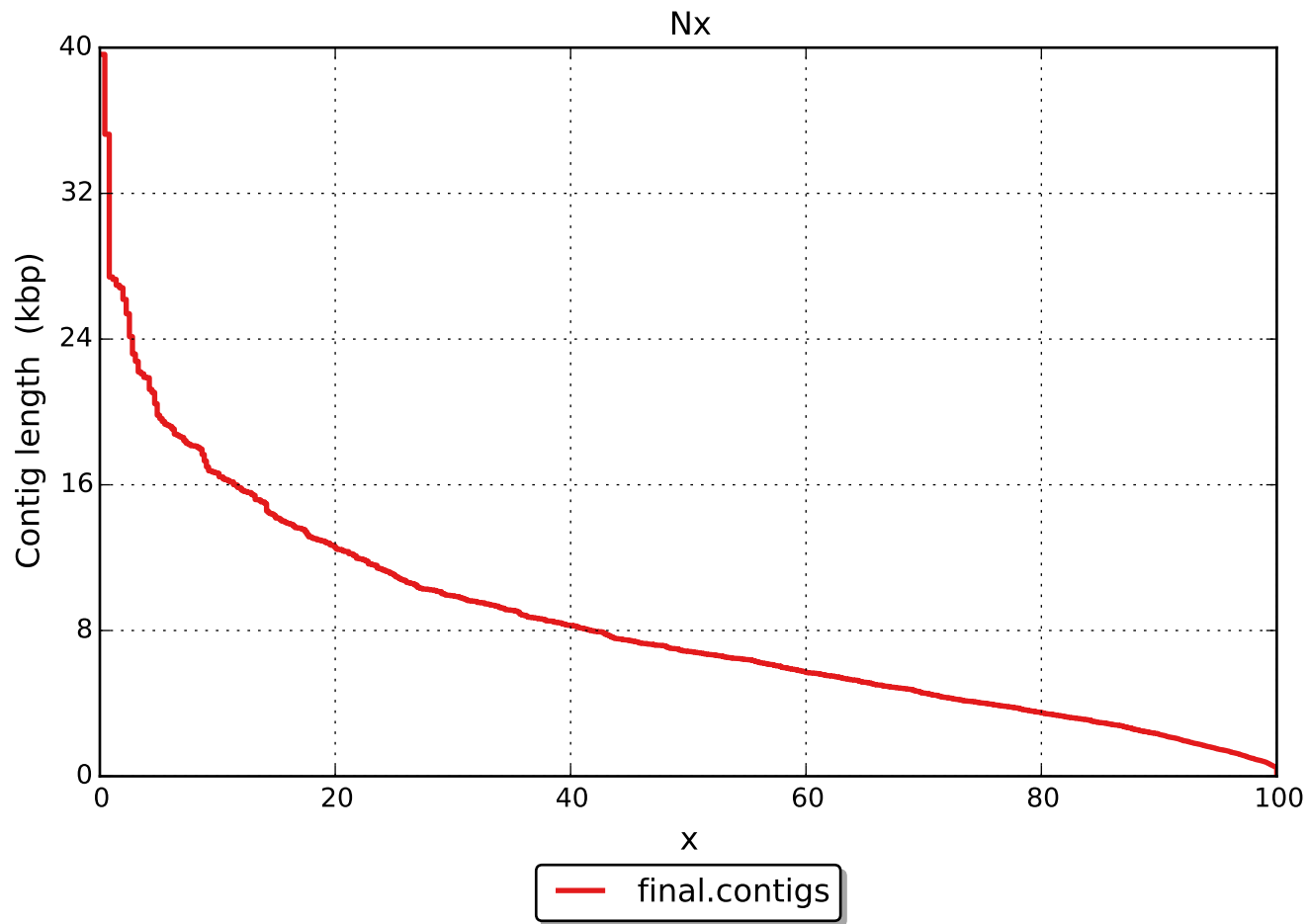
|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 0             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # interspecies translocations   | 0             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 3             |
| # mismatches                    | 1999          |
| # indels                        | 2             |
| # short indels                  | 2             |
| # long indels                   | 0             |
| Indels length                   | 2             |

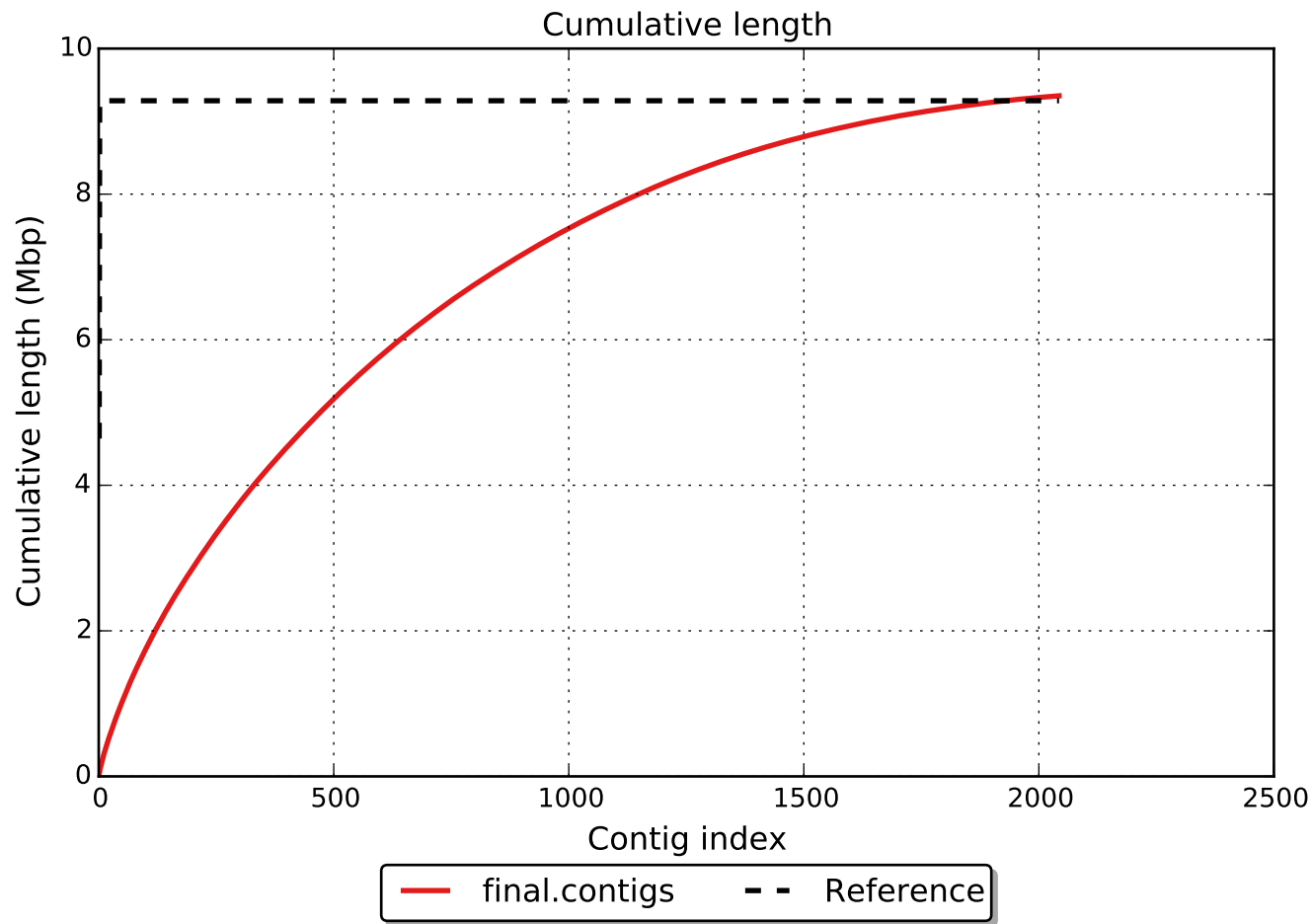
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## Unaligned report

|                               | final.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).





# Misassemblies

