

## Report

|                                | final.contigs |
|--------------------------------|---------------|
| # contigs ( $\geq 0$ bp)       | 1703          |
| # contigs ( $\geq 1000$ bp)    | 1050          |
| Total length ( $\geq 0$ bp)    | 10948347      |
| Total length ( $\geq 1000$ bp) | 10687616      |
| # contigs                      | 1208          |
| Largest contig                 | 61625         |
| Total length                   | 10797999      |
| Reference length               | 11094646      |
| GC (%)                         | 50.39         |
| Reference GC (%)               | 50.49         |
| N50                            | 15437         |
| NG50                           | 14590         |
| N75                            | 9016          |
| NG75                           | 8551          |
| L50                            | 216           |
| LG50                           | 226           |
| L75                            | 448           |
| LG75                           | 473           |
| # misassemblies                | 4             |
| # misassembled contigs         | 4             |
| Misassembled contigs length    | 85153         |
| # local misassemblies          | 2             |
| # unaligned contigs            | 0 + 0 part    |
| Unaligned length               | 0             |
| Genome fraction (%)            | 97.592        |
| Duplication ratio              | 1.010         |
| # N's per 100 kbp              | 0.00          |
| # mismatches per 100 kbp       | 13.60         |
| # indels per 100 kbp           | 0.13          |
| Largest alignment              | 61625         |
| NA50                           | 15360         |
| NGA50                          | 14540         |
| NA75                           | 8988          |
| NGA75                          | 8517          |
| LA50                           | 218           |
| LGA50                          | 228           |
| LA75                           | 450           |
| LGA75                          | 475           |

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

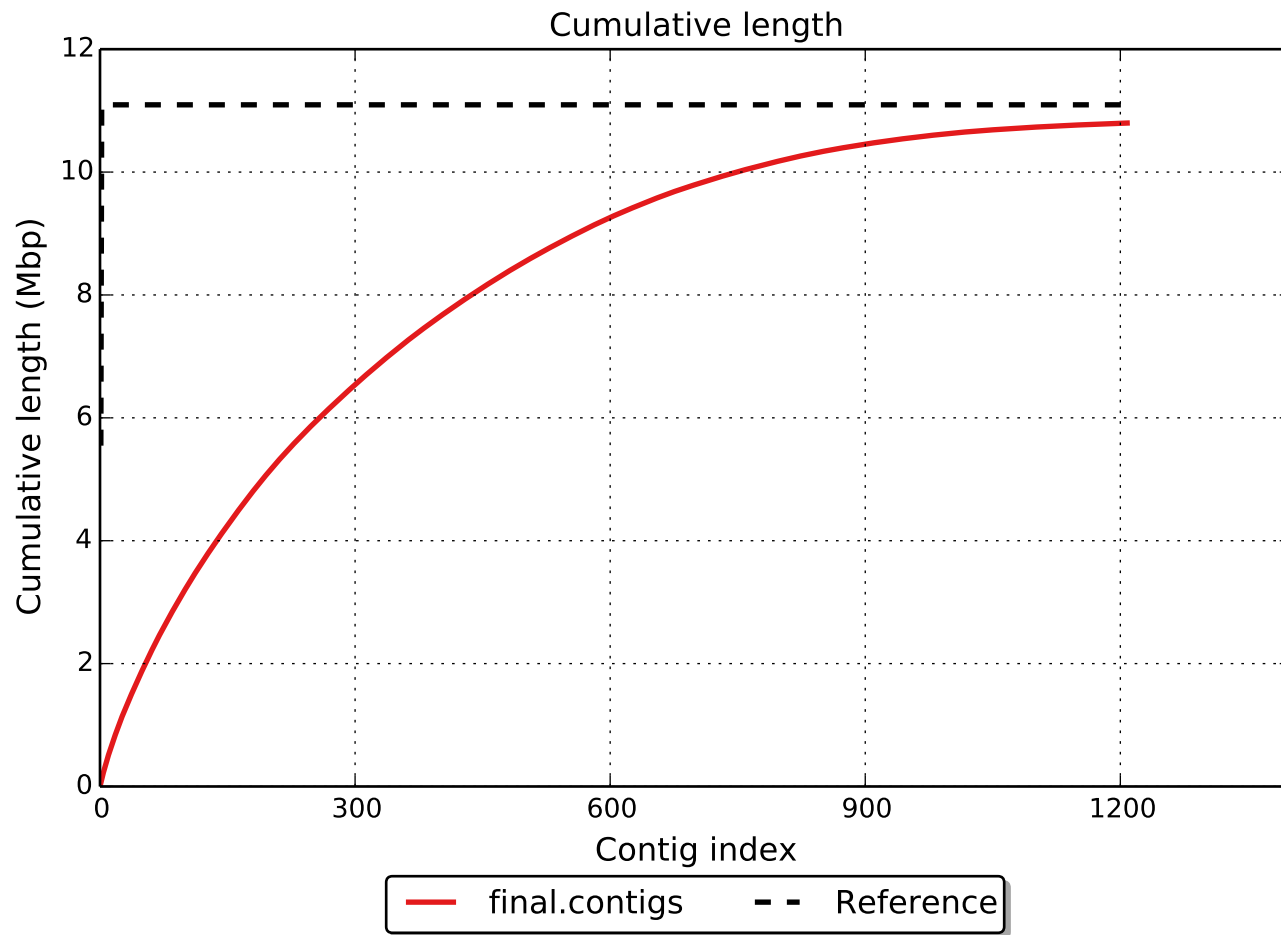
|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 4             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # interspecies translocations   | 4             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 4             |
| Misassembled contigs length     | 85153         |
| # local misassemblies           | 2             |
| # mismatches                    | 1473          |
| # indels                        | 14            |
| # short indels                  | 13            |
| # long indels                   | 1             |
| Indels length                   | 19            |

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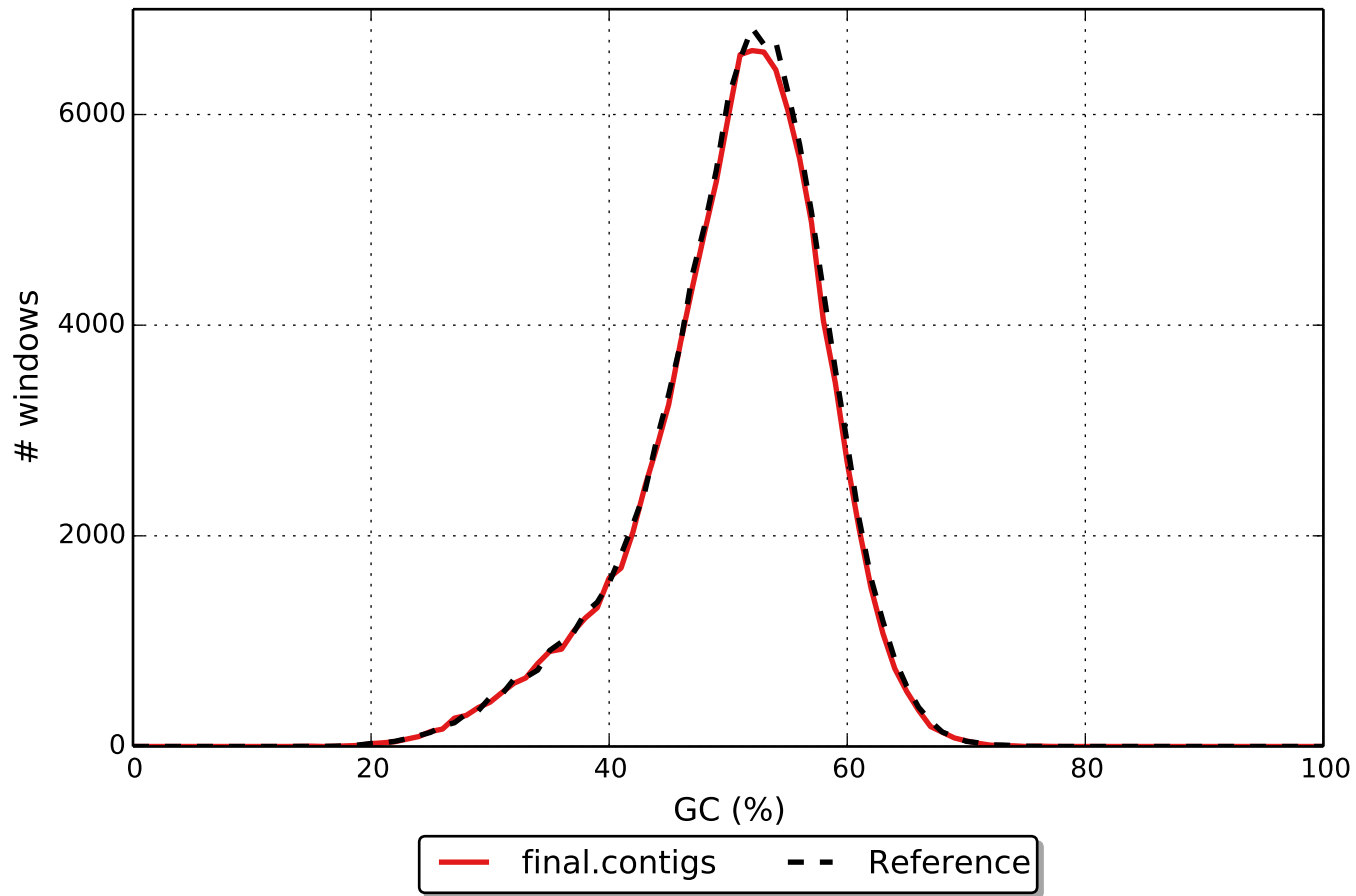
## Unaligned report

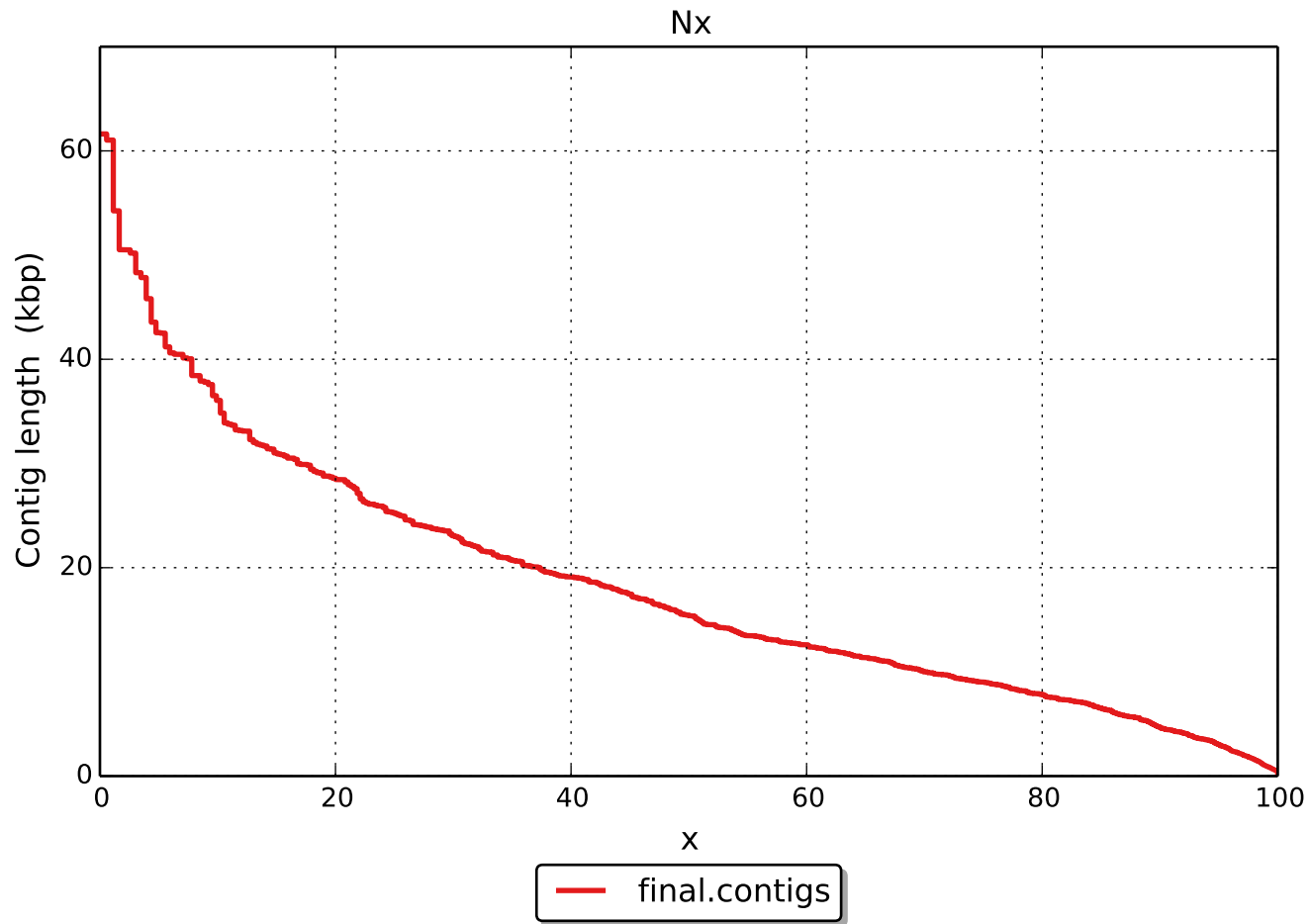
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 0             |
| # with misassembly            | 0             |
|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

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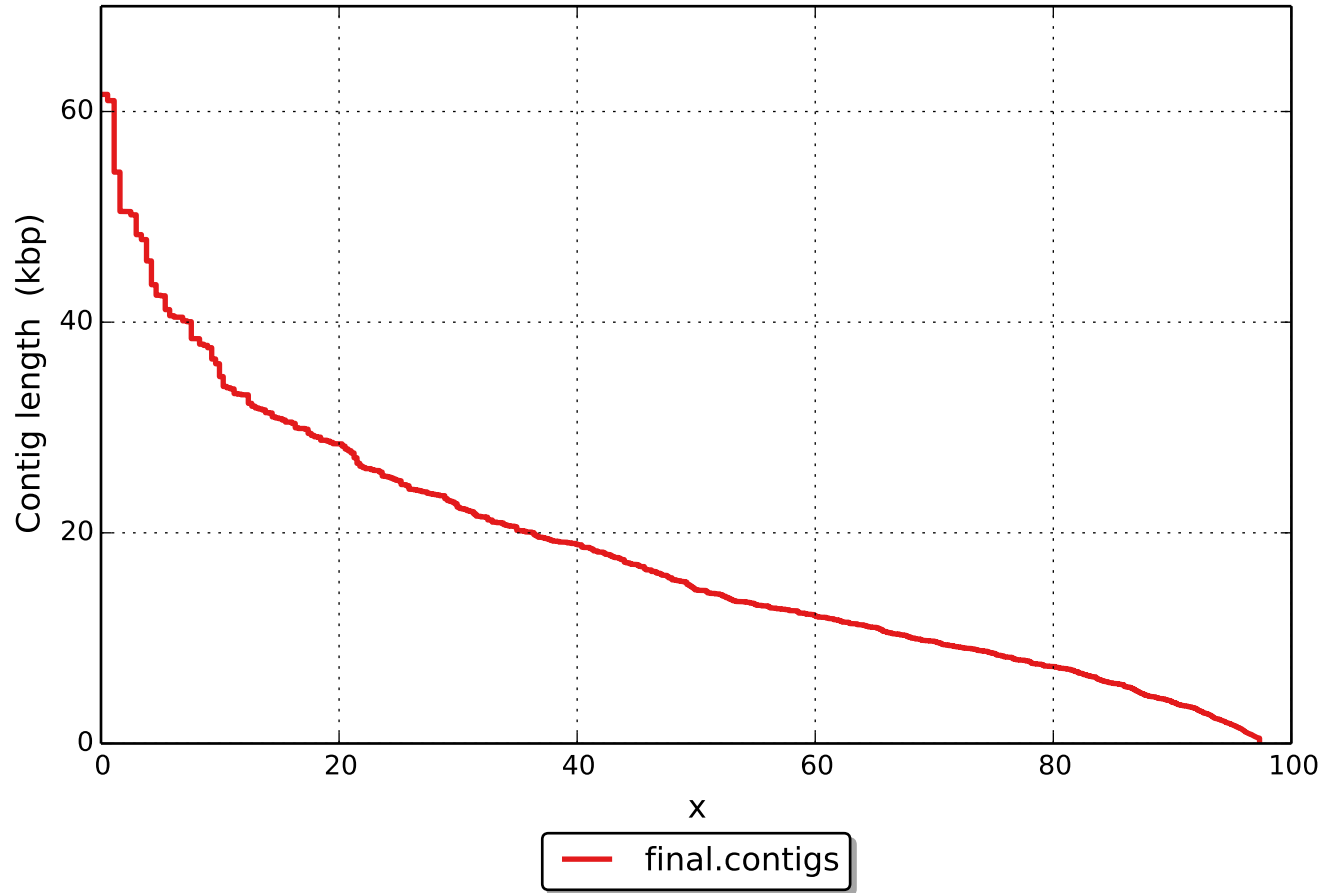


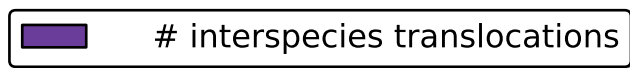
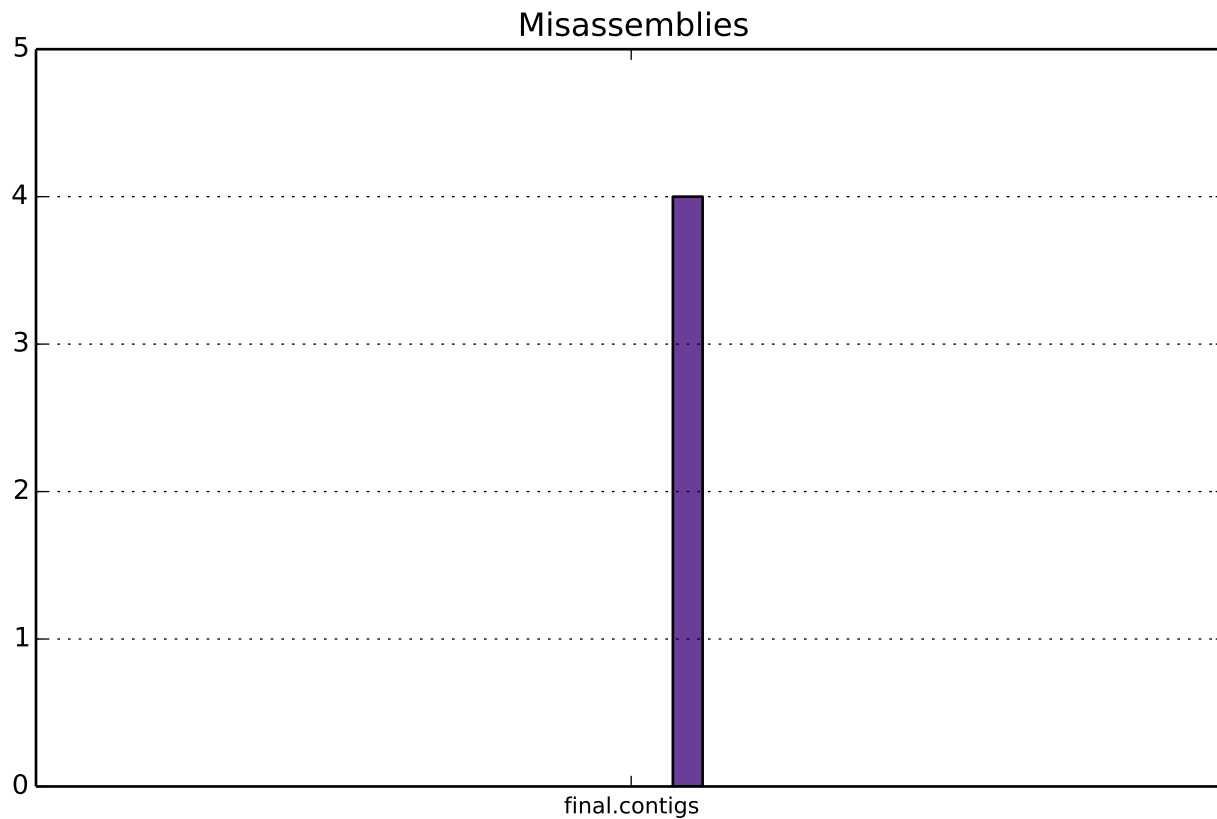
GC content



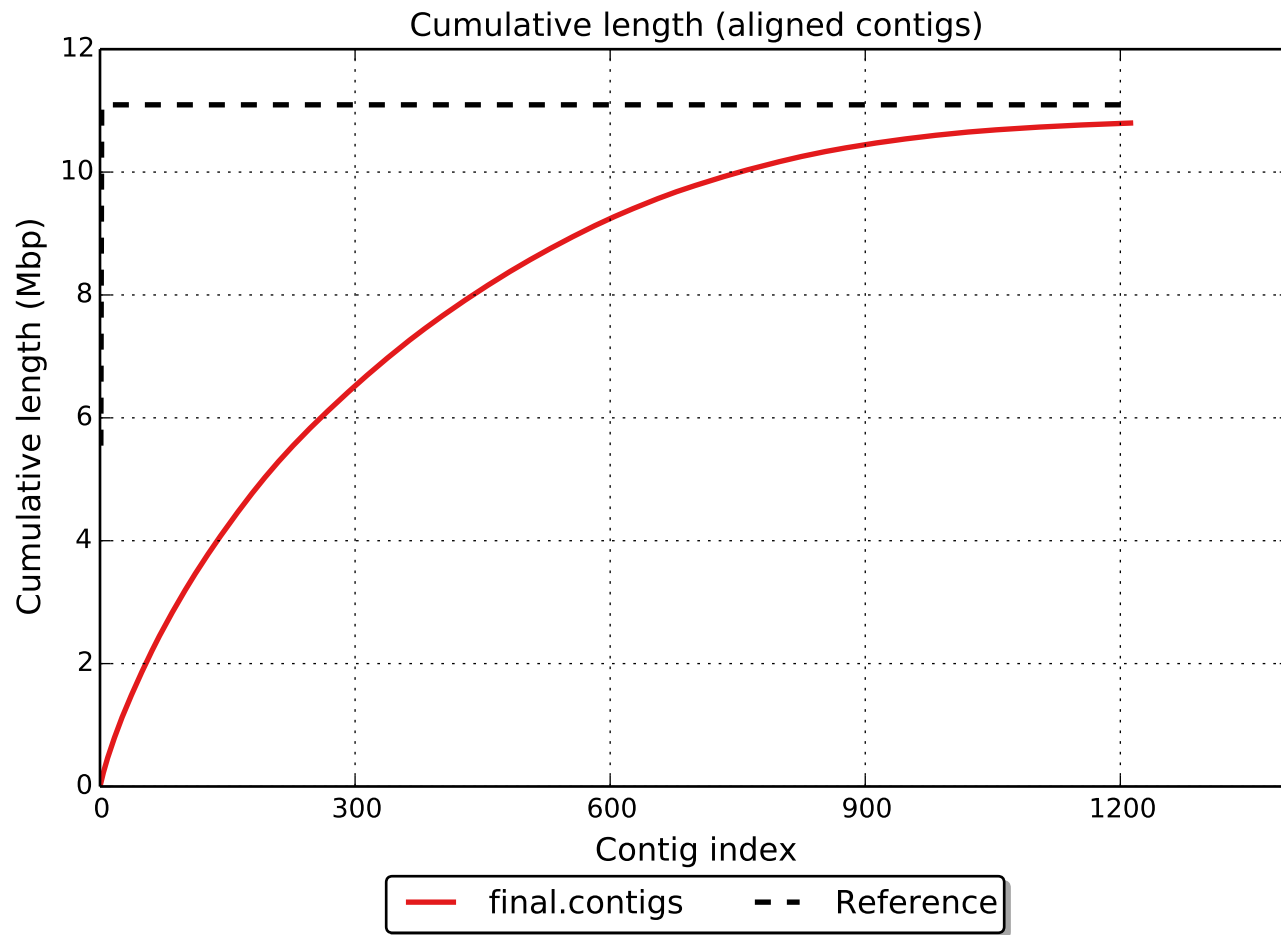


NGx

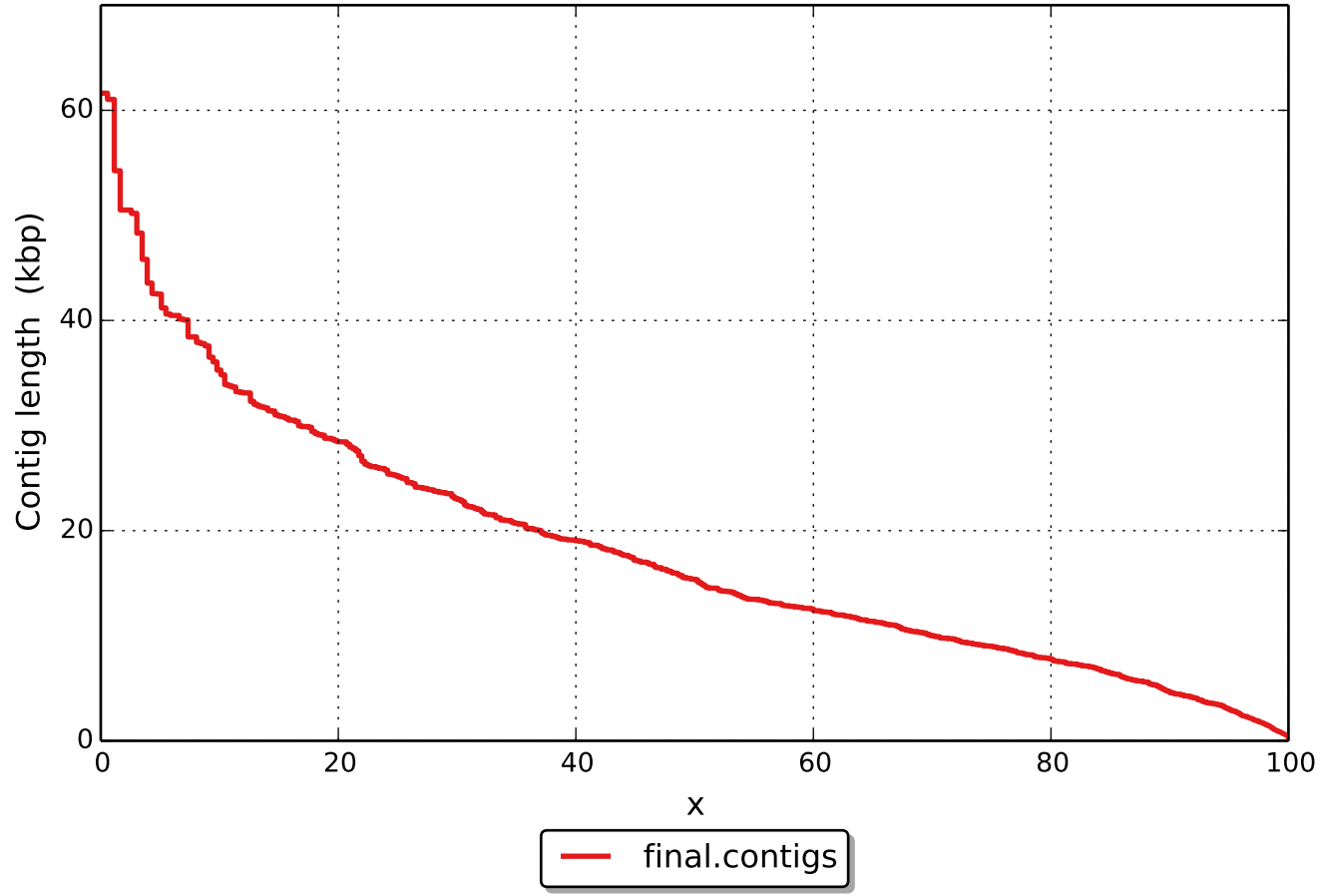








NAx



# NGAx

