

## Report

|                             | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp)         | 975           |
| # contigs (>= 1000 bp)      | 485           |
| Total length (>= 0 bp)      | 1337010       |
| Total length (>= 1000 bp)   | 1057848       |
| # contigs                   | 767           |
| Largest contig              | 9818          |
| Total length                | 1260254       |
| Reference length            | 1283598       |
| GC (%)                      | 26.31         |
| Reference GC (%)            | 26.29         |
| N50                         | 2043          |
| NG50                        | 2012          |
| N75                         | 1285          |
| NG75                        | 1254          |
| L50                         | 188           |
| LG50                        | 193           |
| L75                         | 386           |
| LG75                        | 400           |
| # misassemblies             | 1             |
| # misassembled contigs      | 1             |
| Misassembled contigs length | 8348          |
| # local misassemblies       | 0             |
| # unaligned contigs         | 0 + 0 part    |
| Unaligned length            | 0             |
| Genome fraction (%)         | 94.779        |
| Duplication ratio           | 1.038         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 16.03         |
| # indels per 100 kbp        | 0.08          |
| Largest alignment           | 9818          |
| NA50                        | 2043          |
| NGA50                       | 2012          |
| NA75                        | 1285          |
| NGA75                       | 1254          |
| LA50                        | 189           |
| LGA50                       | 194           |
| LA75                        | 387           |
| LGA75                       | 401           |

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

## Misassemblies report

|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 1             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # interspecies translocations   | 1             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 1             |
| Misassembled contigs length     | 8348          |
| # local misassemblies           | 0             |
| # mismatches                    | 195           |
| # indels                        | 1             |
| # short indels                  | 0             |
| # long indels                   | 1             |
| Indels length                   | 14            |

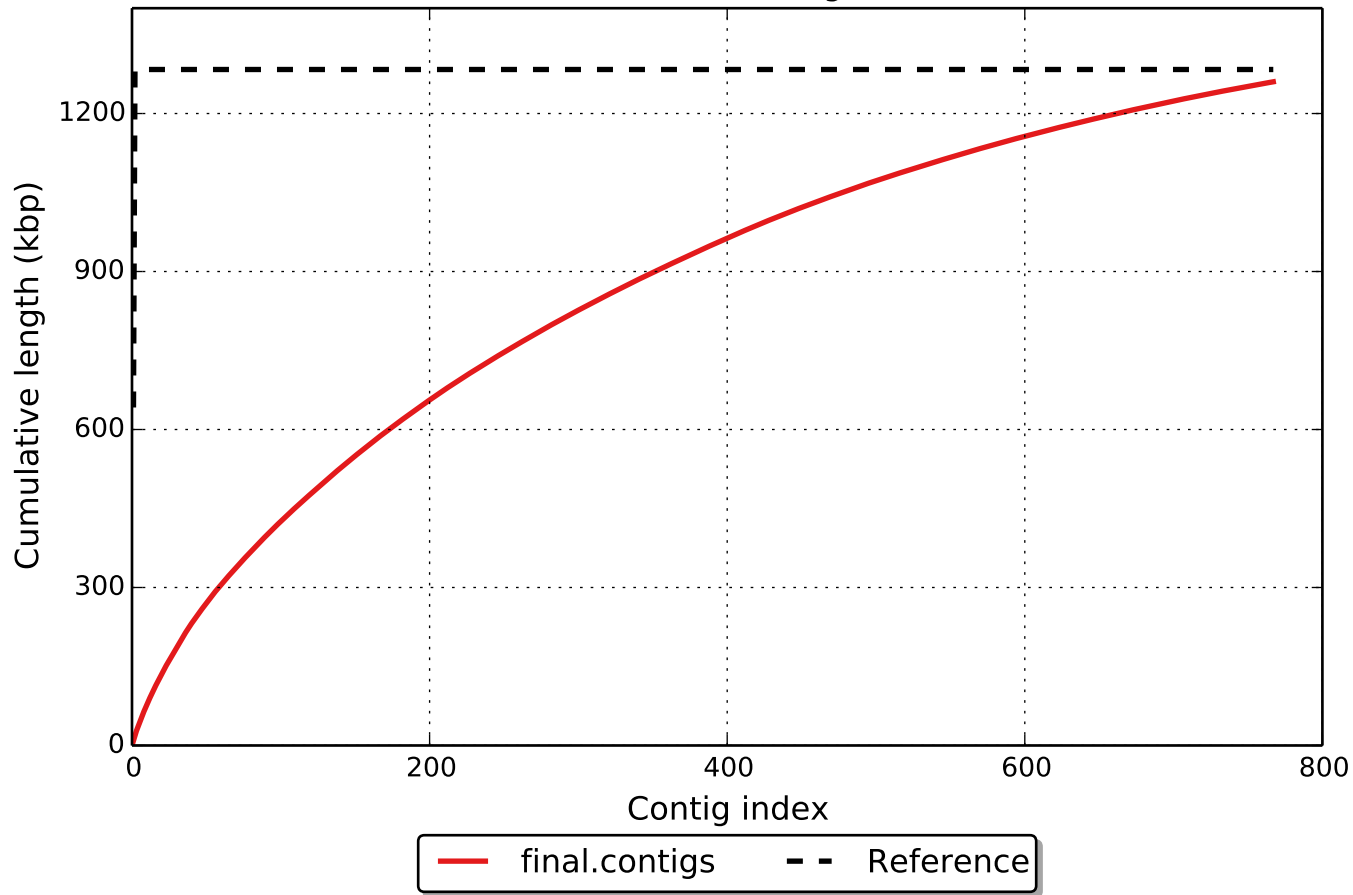
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

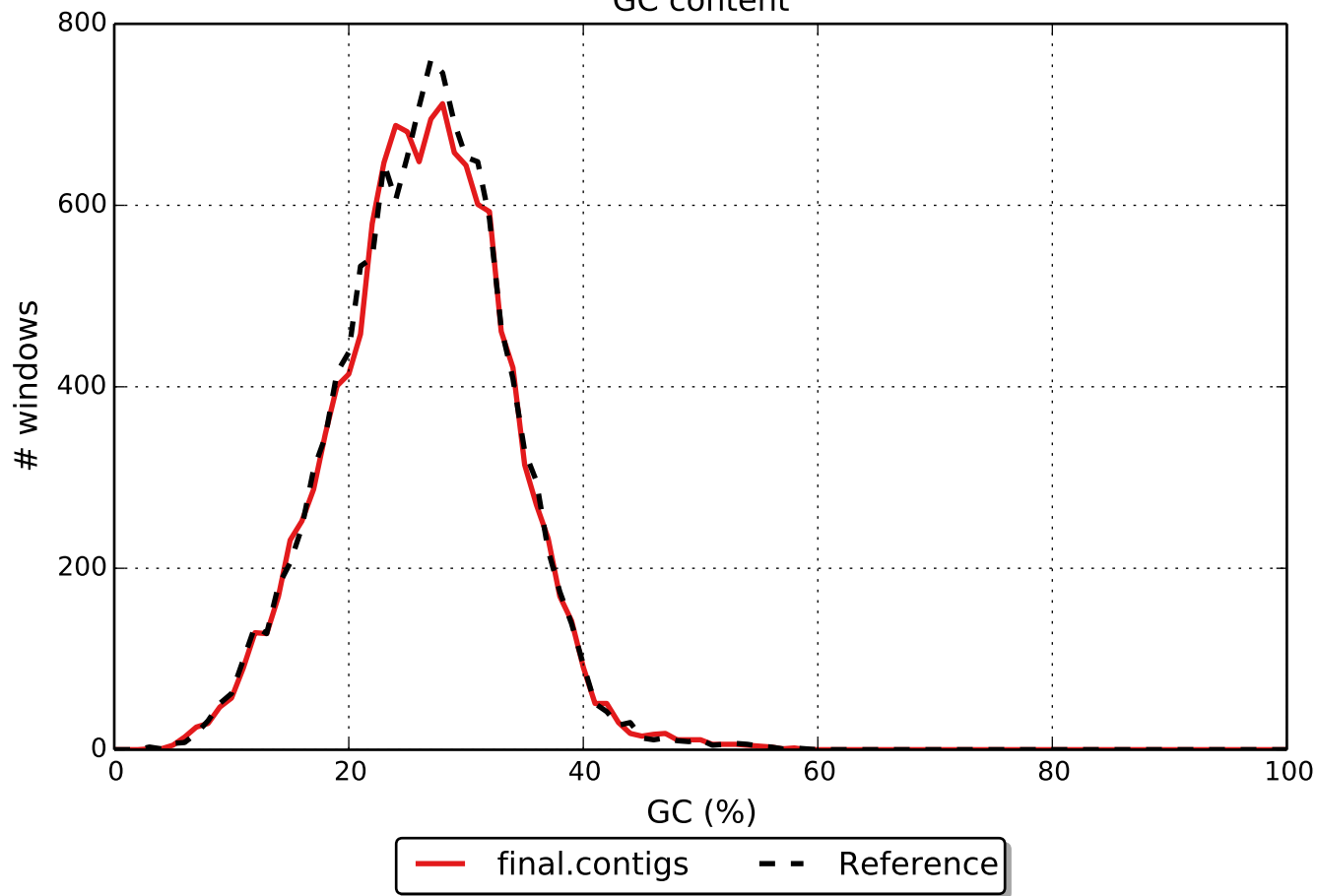
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 0             |
| # with misassembly            | 0             |
|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

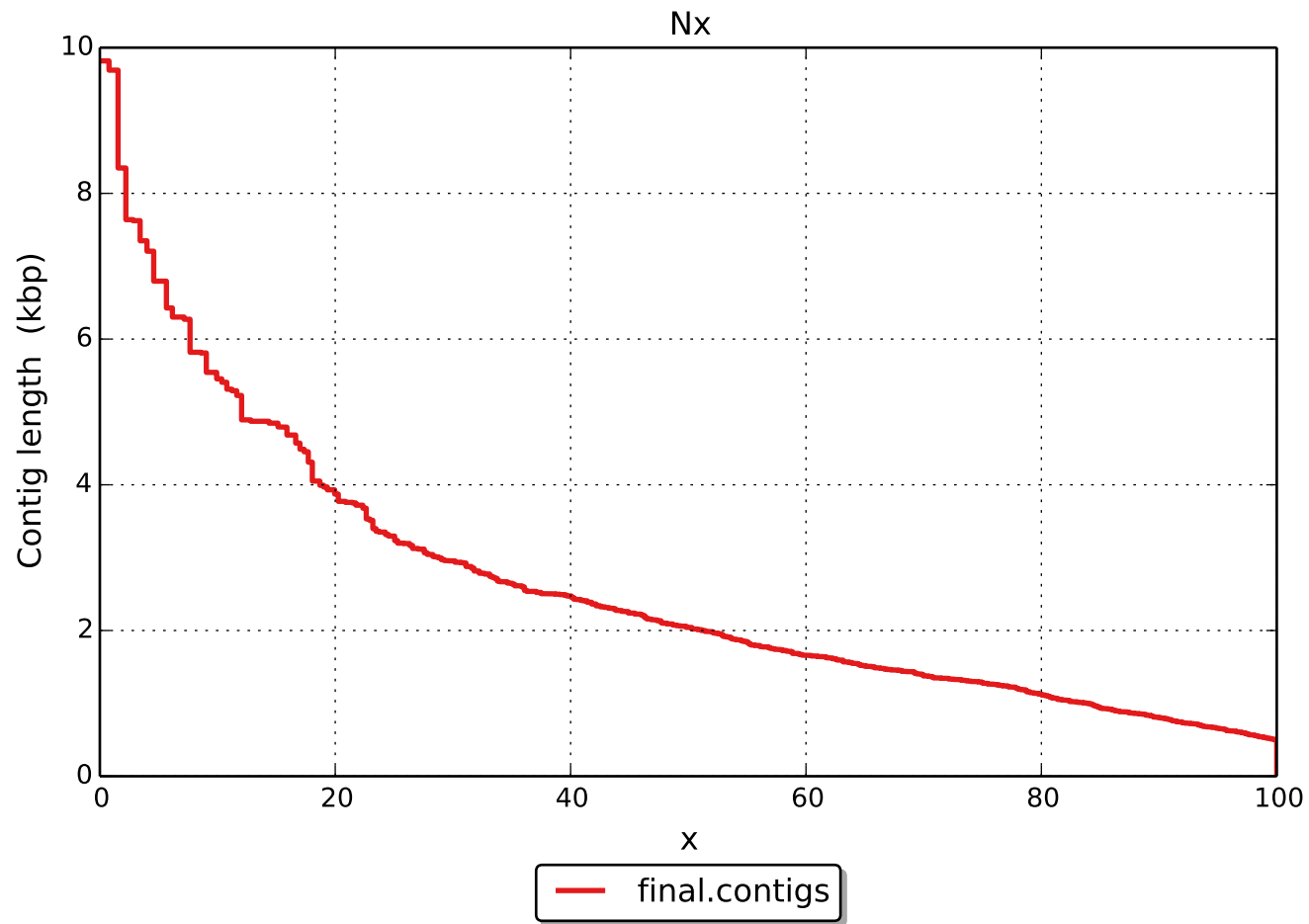
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

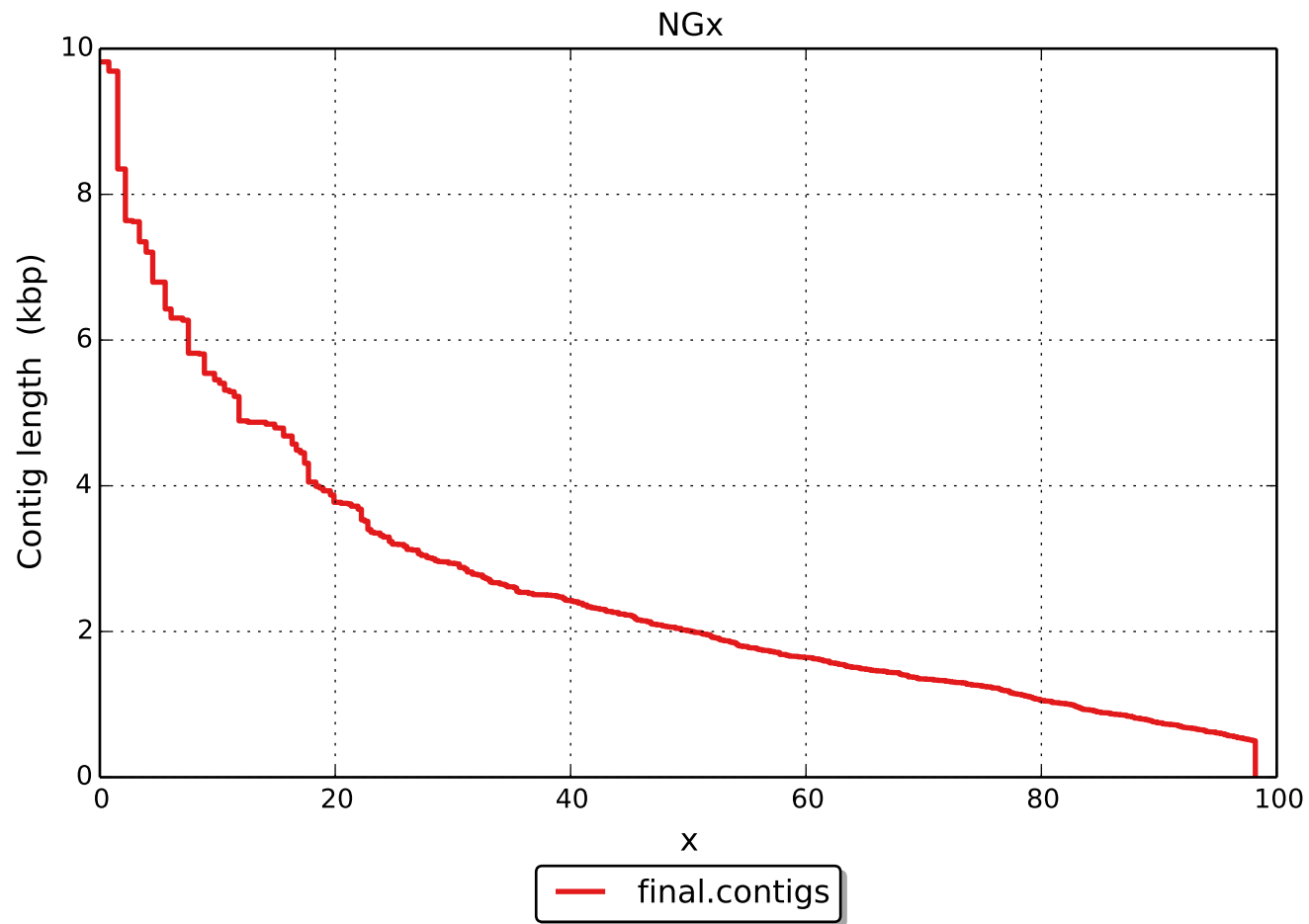
Cumulative length

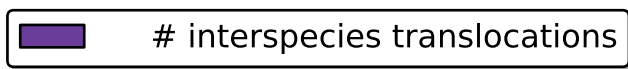
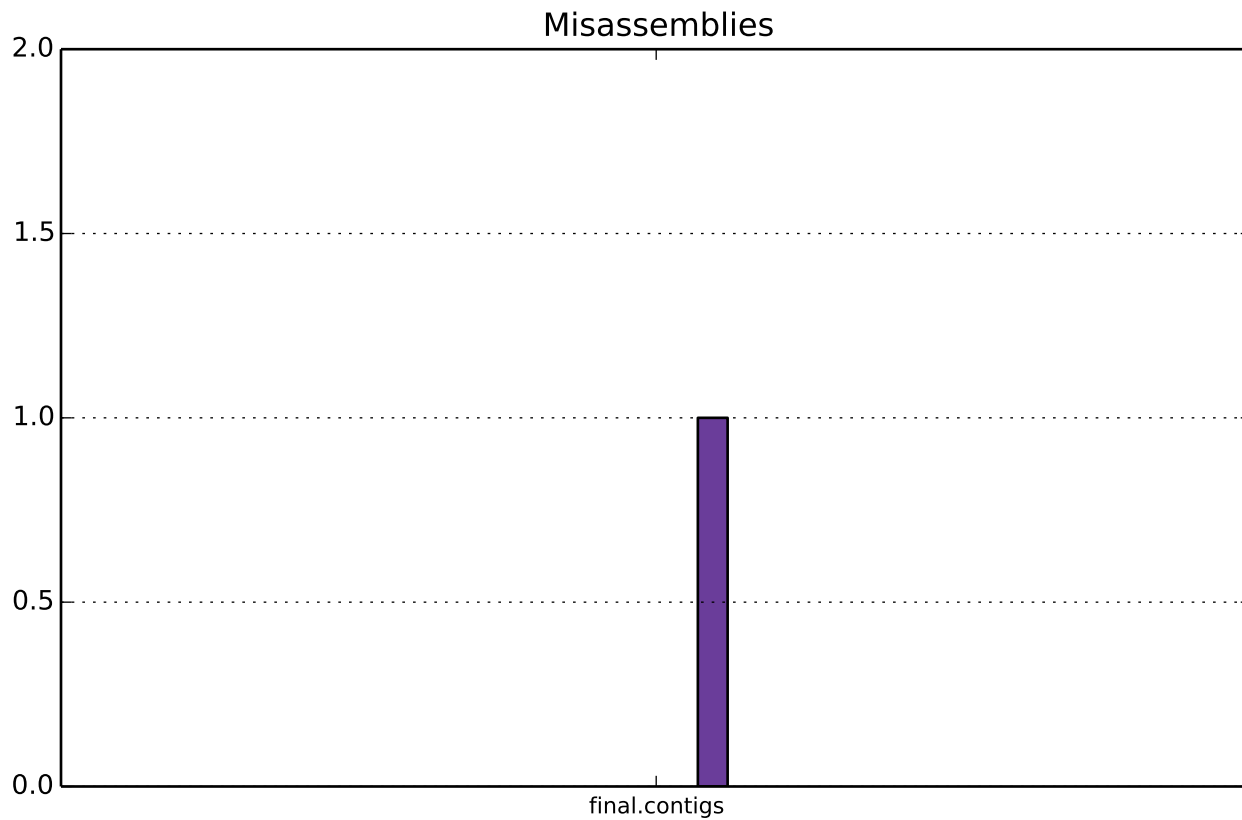


GC content











Cumulative length (aligned contigs)

