

# Report

|                             | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp)         | 3109          |
| # contigs (>= 1000 bp)      | 48            |
| # contigs (>= 5000 bp)      | 1             |
| # contigs (>= 10000 bp)     | 0             |
| # contigs (>= 25000 bp)     | 0             |
| # contigs (>= 50000 bp)     | 0             |
| Total length (>= 0 bp)      | 1489995       |
| Total length (>= 1000 bp)   | 63684         |
| Total length (>= 5000 bp)   | 5132          |
| Total length (>= 10000 bp)  | 0             |
| Total length (>= 25000 bp)  | 0             |
| Total length (>= 50000 bp)  | 0             |
| # contigs                   | 1011          |
| Largest contig              | 5132          |
| Total length                | 677196        |
| Reference length            | 4641652       |
| GC (%)                      | 50.73         |
| Reference GC (%)            | 50.79         |
| N50                         | 648           |
| N75                         | 563           |
| L50                         | 409           |
| L75                         | 691           |
| # misassemblies             | 5             |
| # misassembled contigs      | 5             |
| Misassembled contigs length | 5903          |
| # local misassemblies       | 0             |
| # unaligned contigs         | 0 + 0 part    |
| Unaligned length            | 0             |
| Genome fraction (%)         | 14.520        |
| Duplication ratio           | 1.005         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 1395.76       |
| # indels per 100 kbp        | 0.89          |
| Largest alignment           | 5132          |
| NA50                        | 647           |
| NGA50                       | -             |
| NA75                        | 562           |
| LA50                        | 412           |
| LA75                        | 694           |

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

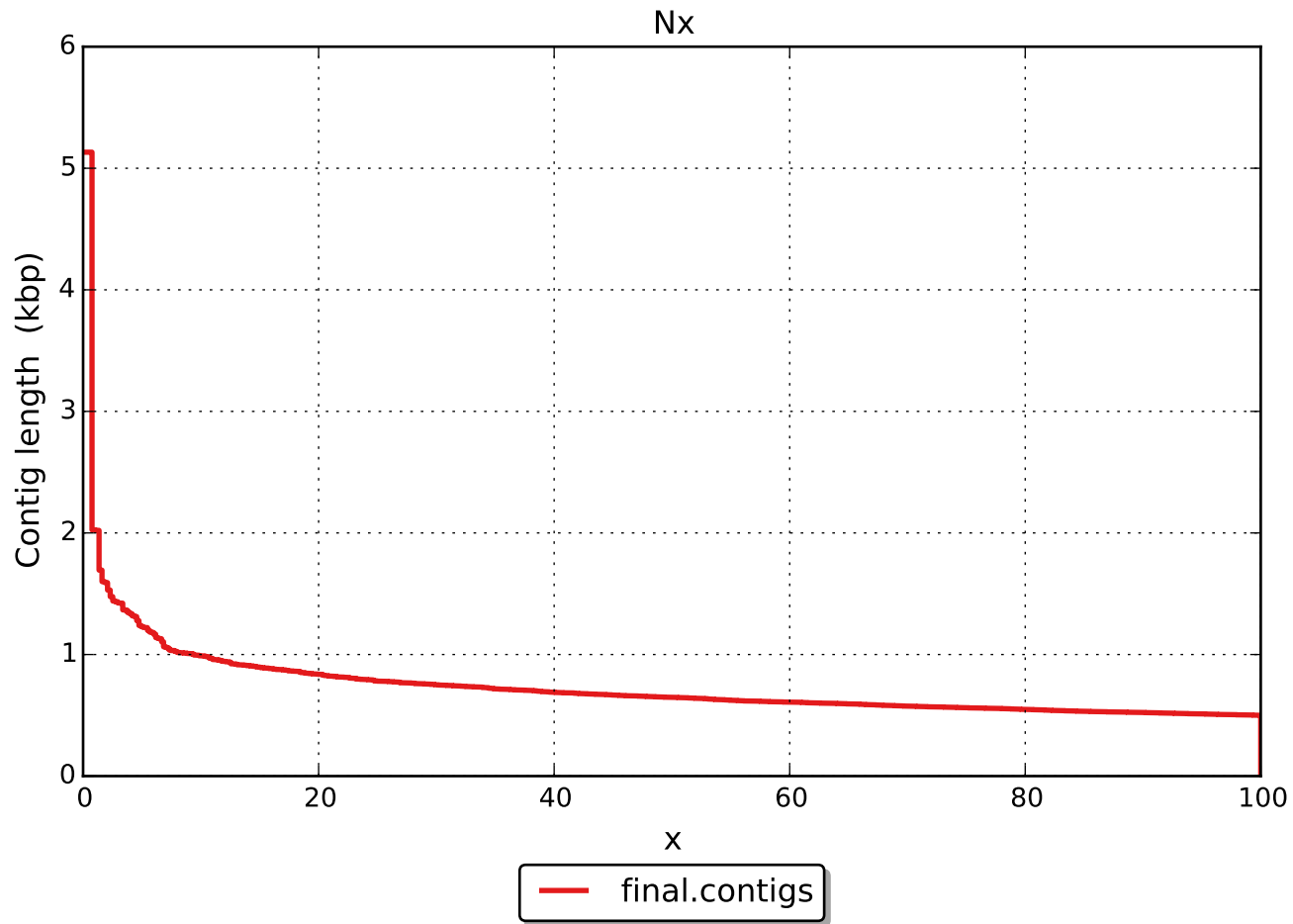
|                             | final.contigs |
|-----------------------------|---------------|
| # misassemblies             | 5             |
| # relocations               | 5             |
| # translocations            | 0             |
| # inversions                | 0             |
| # misassembled contigs      | 5             |
| Misassembled contigs length | 5903          |
| # local misassemblies       | 0             |
| # mismatches                | 9407          |
| # indels                    | 6             |
| # short indels              | 6             |
| # long indels               | 0             |
| Indels length               | 6             |

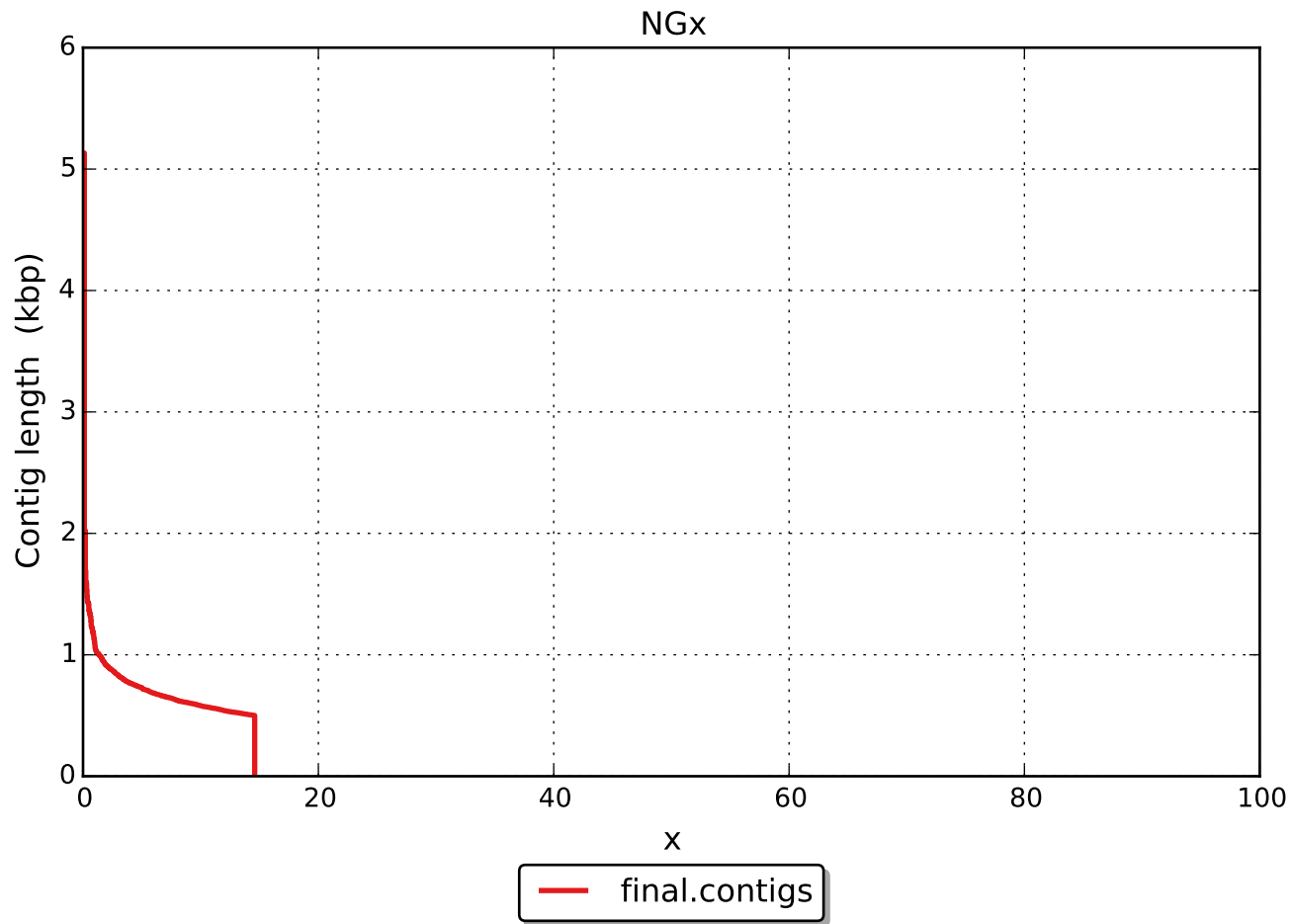
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

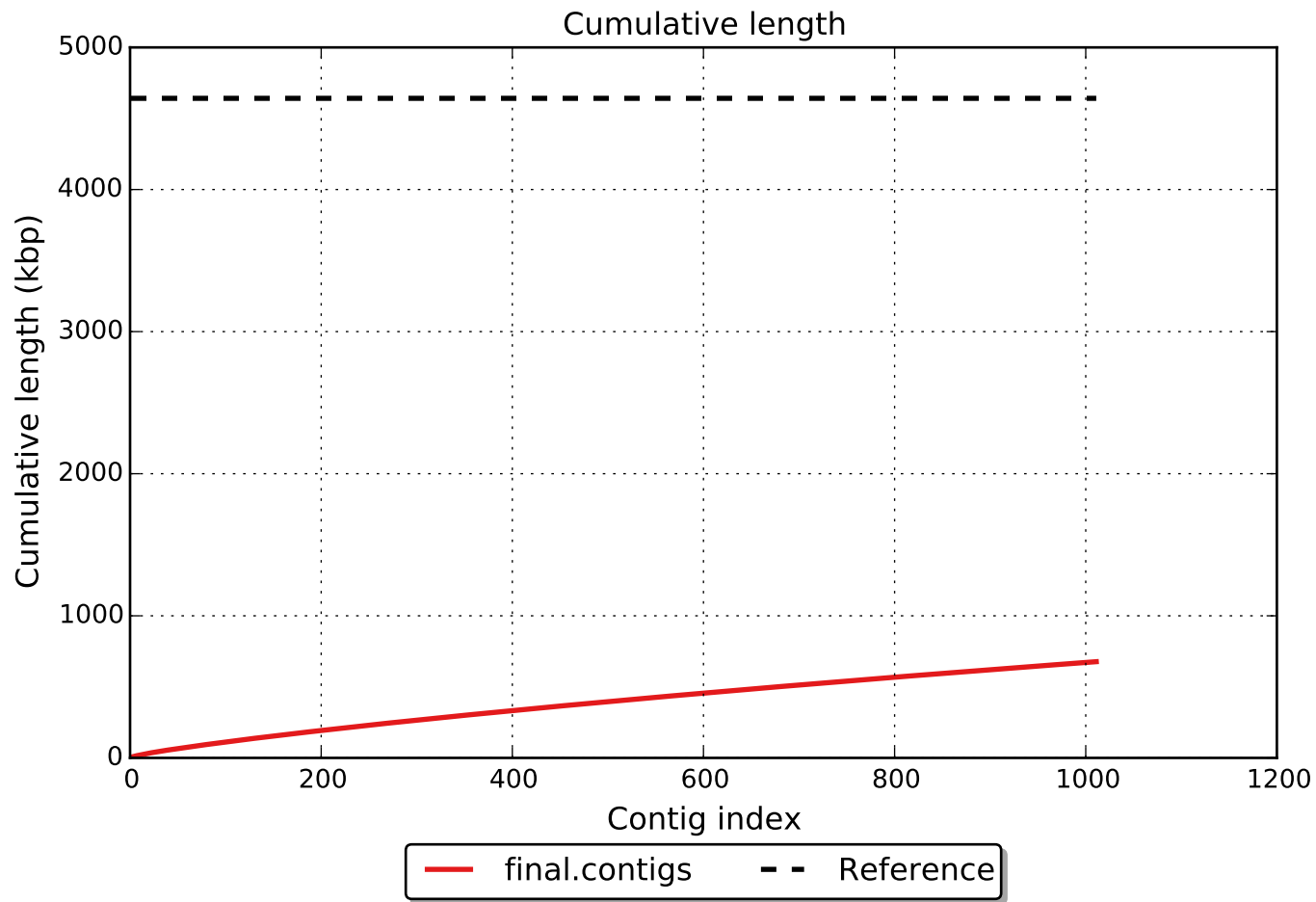
## Unaligned report

|                               | 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             |

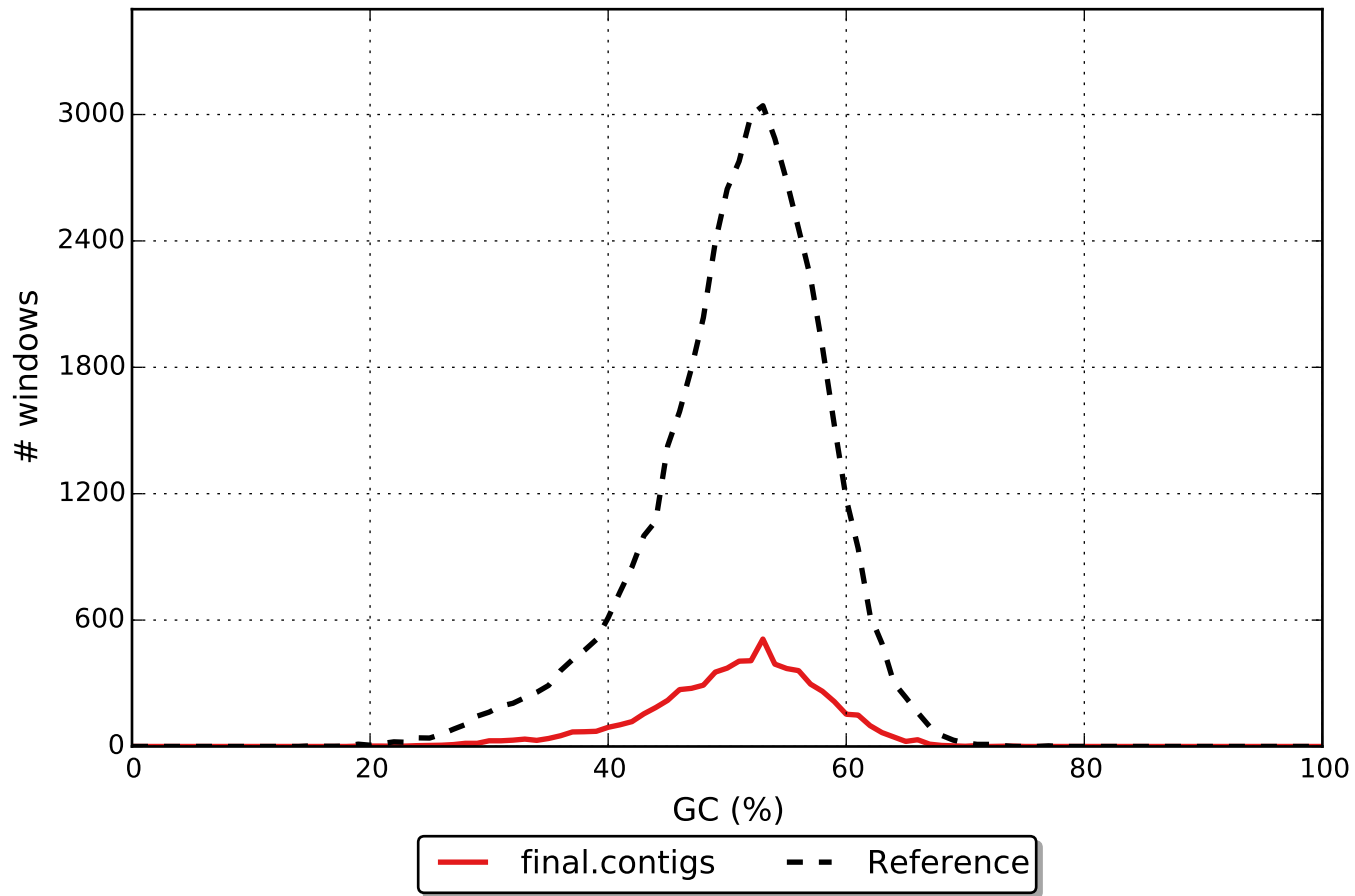
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

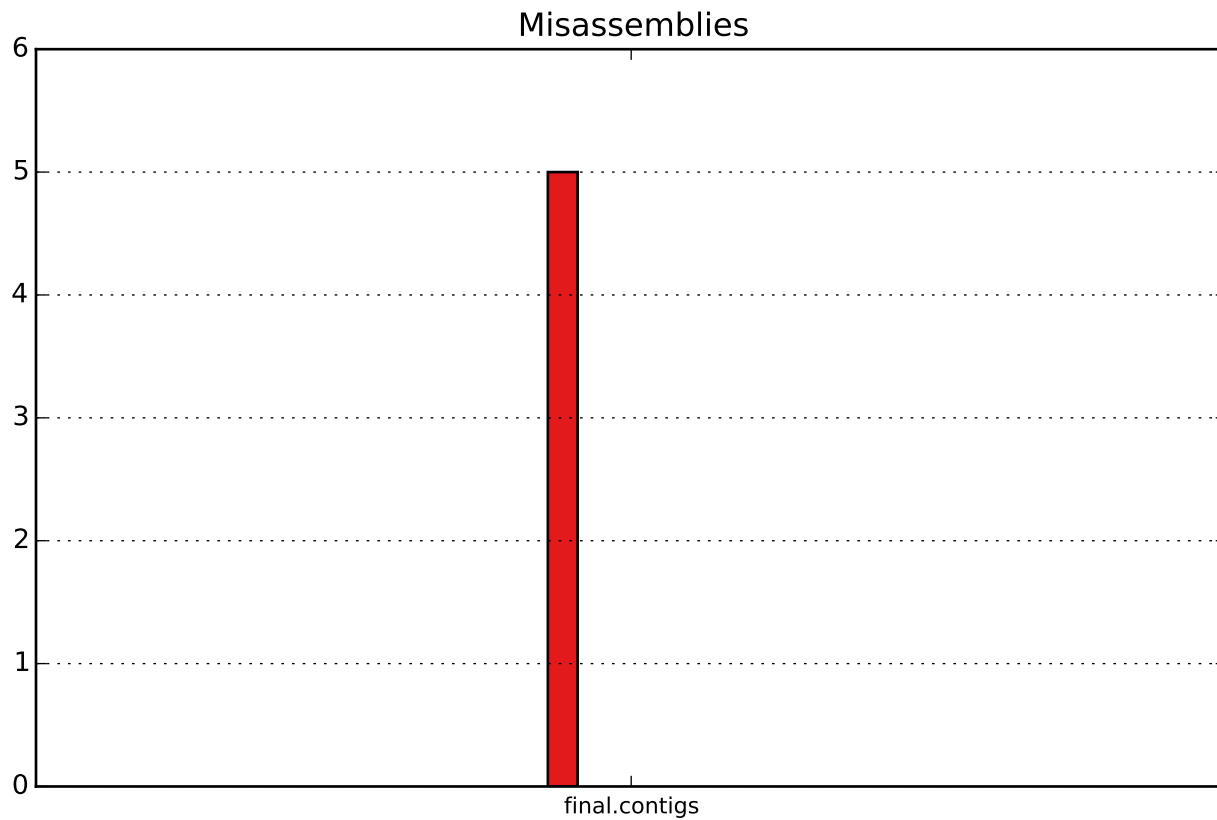






GC content







Cumulative length (aligned contigs)

