

## Report

|                             | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp)      | 933           |
| # contigs (>= 5000 bp)      | 3             |
| # contigs (>= 10000 bp)     | 0             |
| # contigs (>= 25000 bp)     | 0             |
| # contigs (>= 50000 bp)     | 0             |
| Total length (>= 1000 bp)   | 1588298       |
| Total length (>= 5000 bp)   | 16275         |
| Total length (>= 10000 bp)  | 0             |
| Total length (>= 25000 bp)  | 0             |
| Total length (>= 50000 bp)  | 0             |
| # contigs                   | 2819          |
| Largest contig              | 5818          |
| Total length                | 2874005       |
| Reference length            | 4857432       |
| GC (%)                      | 52.23         |
| Reference GC (%)            | 52.22         |
| N50                         | 1107          |
| NG50                        | 619           |
| N75                         | 718           |
| L50                         | 789           |
| LG50                        | 2019          |
| L75                         | 1609          |
| # misassemblies             | 0             |
| # misassembled contigs      | 0             |
| Misassembled contigs length | 0             |
| # local misassemblies       | 0             |
| # unaligned contigs         | 0 + 0 part    |
| Unaligned length            | 0             |
| Genome fraction (%)         | 56.547        |
| Duplication ratio           | 1.046         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 342.62        |
| # indels per 100 kbp        | 0.11          |
| Largest alignment           | 5818          |
| NA50                        | 1107          |
| NGA50                       | 619           |
| NA75                        | 718           |
| LA50                        | 789           |
| LGA50                       | 2019          |
| LA75                        | 1609          |

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

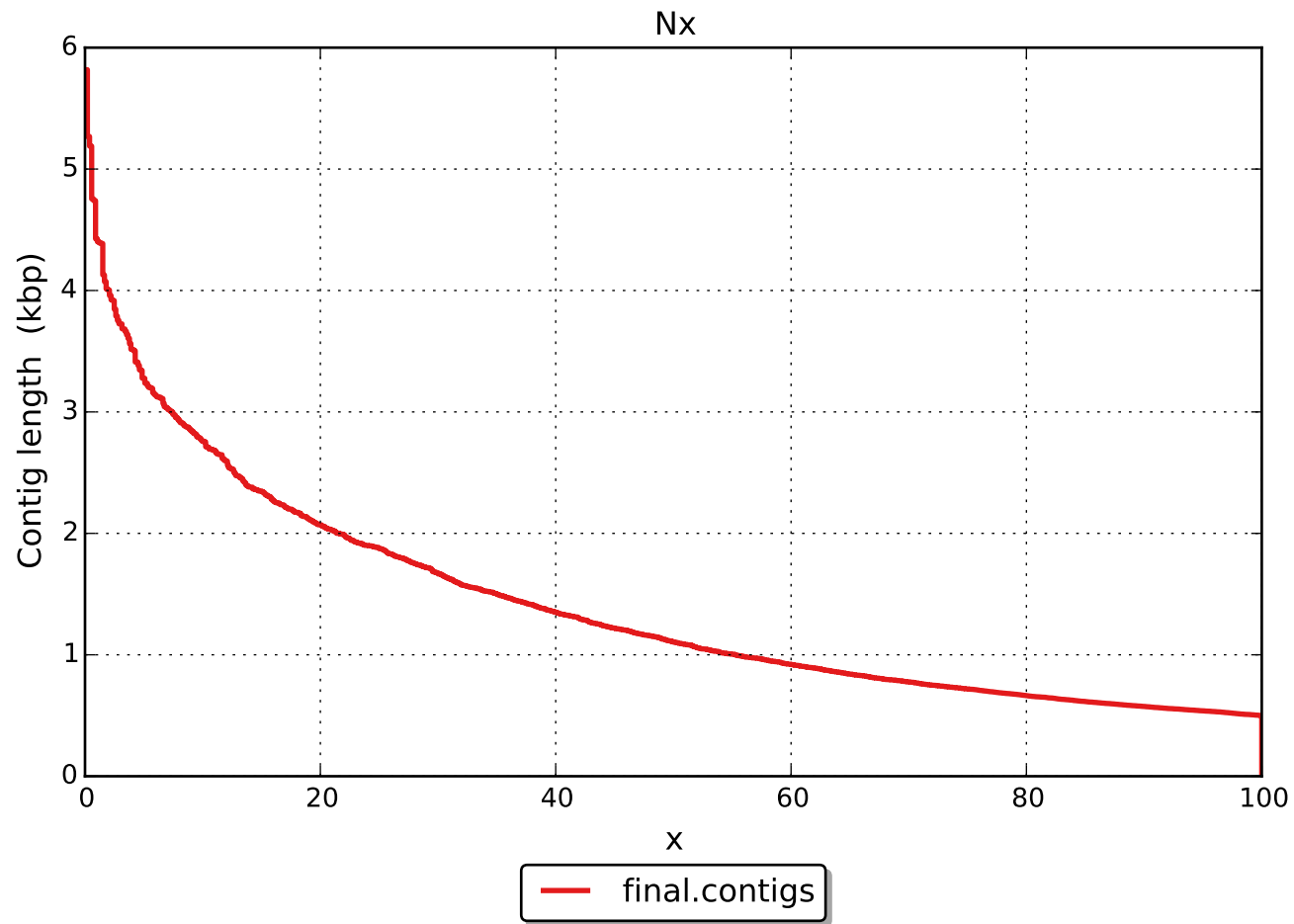
|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 0             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 0             |
| # mismatches                    | 9411          |
| # indels                        | 3             |
| # short indels                  | 2             |
| # long indels                   | 1             |
| Indels length                   | 47            |

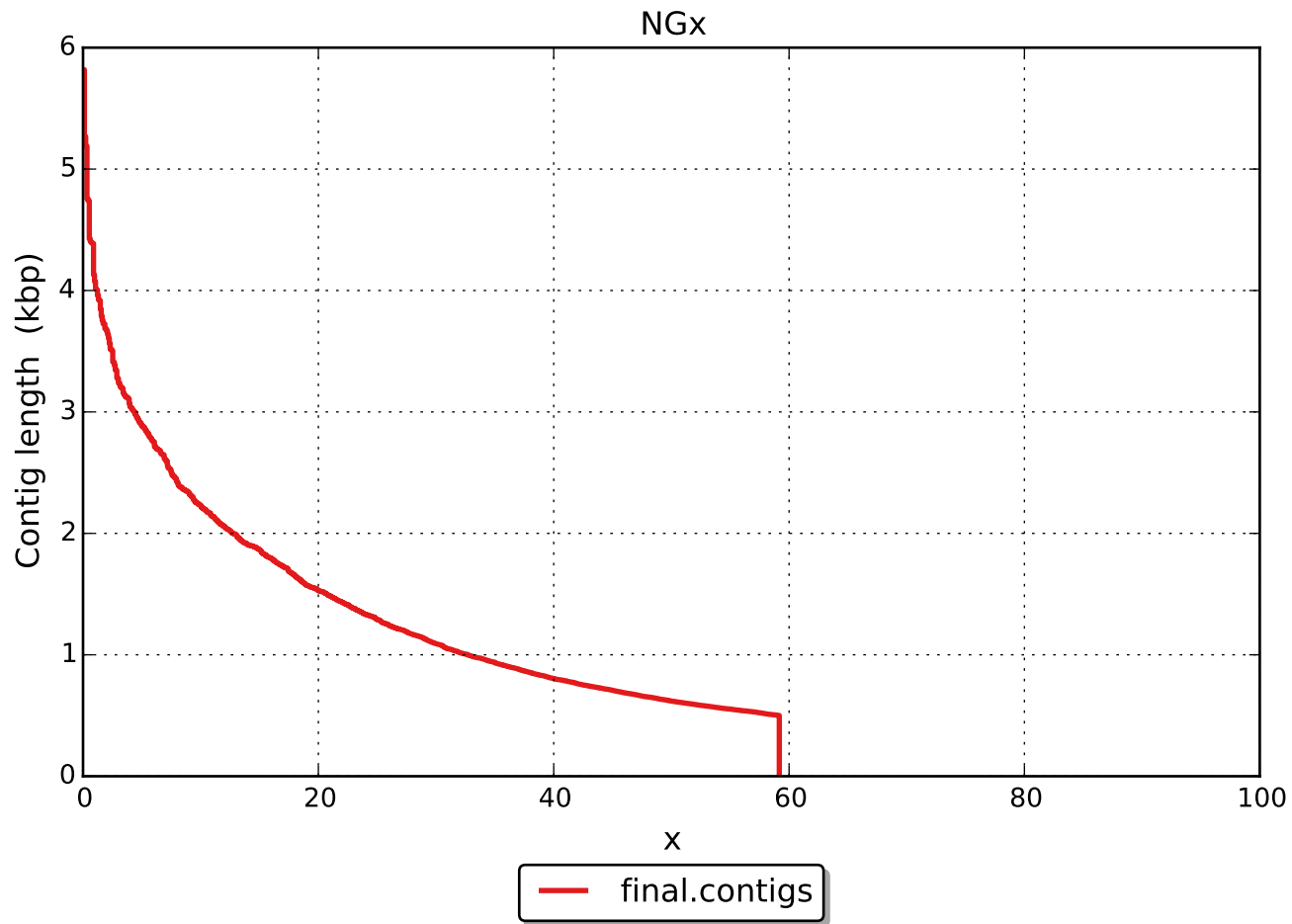
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

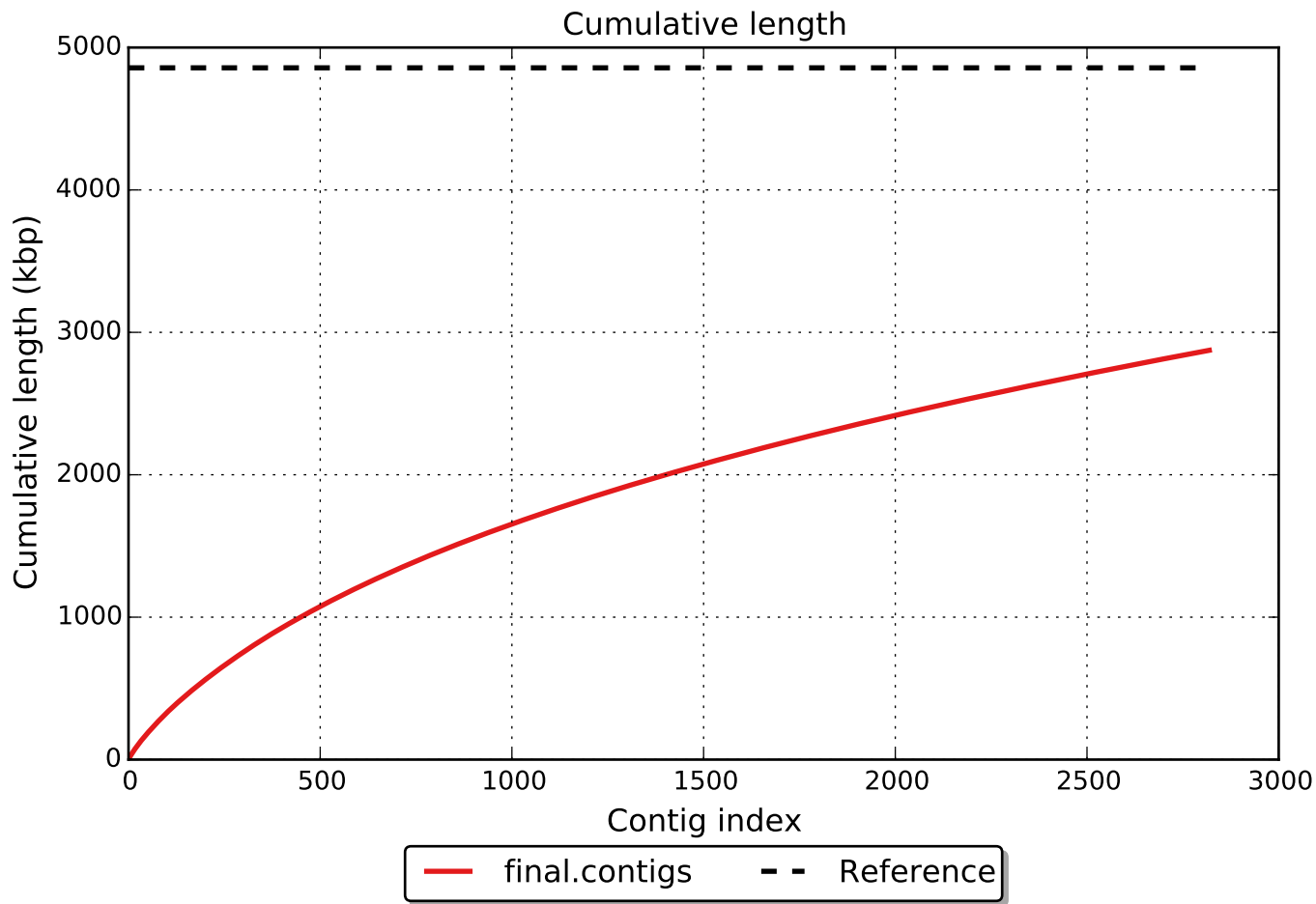
## Unaligned report

|                               | 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             |

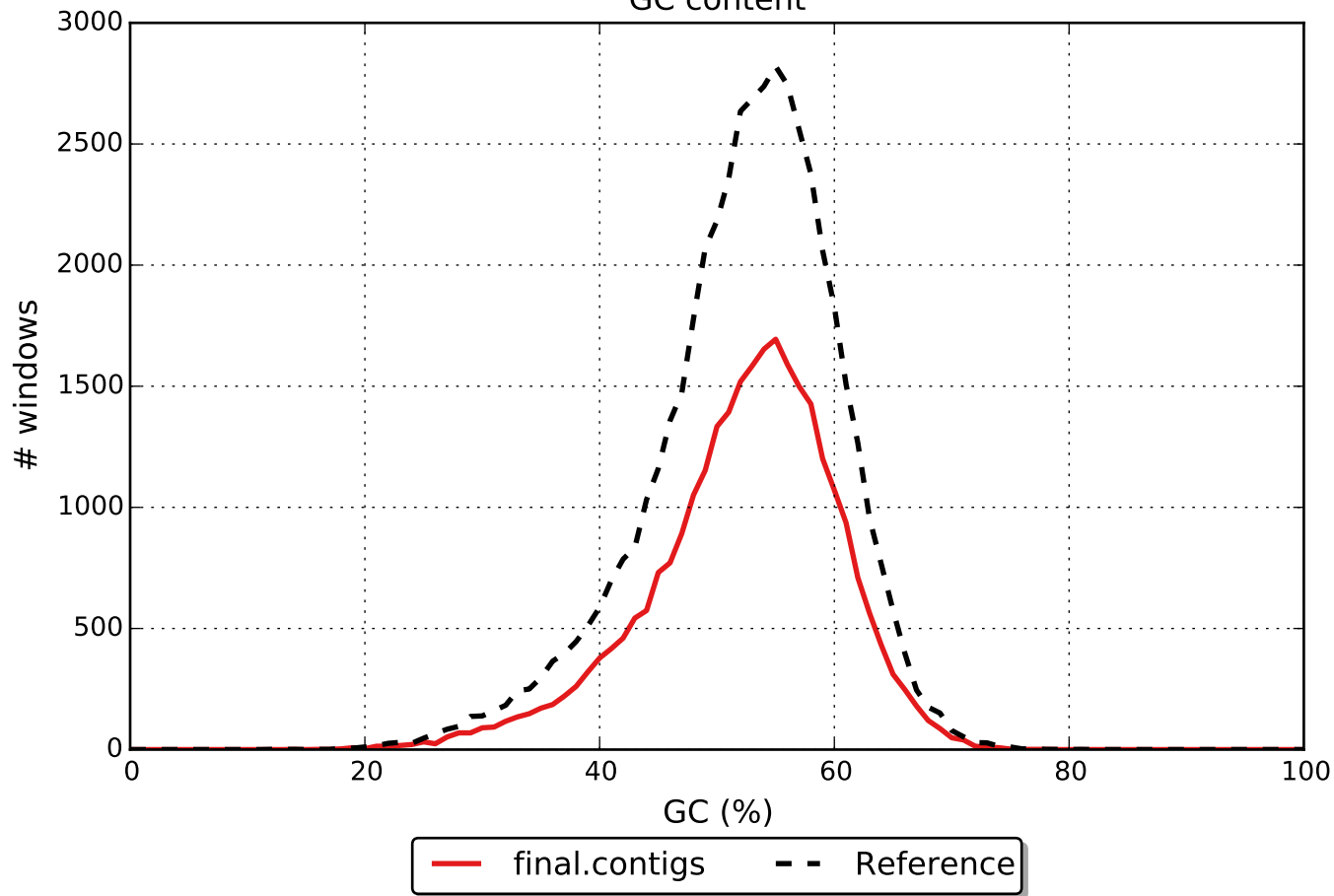
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content



# Misassemblies





Cumulative length (aligned contigs)

