

## Report

|                             | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp)         | 666           |
| # contigs (>= 1000 bp)      | 423           |
| Total length (>= 0 bp)      | 1270220       |
| Total length (>= 1000 bp)   | 1134938       |
| # contigs                   | 558           |
| Largest contig              | 11592         |
| Total length                | 1232902       |
| Reference length            | 1231960       |
| GC (%)                      | 25.33         |
| Reference GC (%)            | 25.33         |
| N50                         | 2927          |
| NG50                        | 2927          |
| N75                         | 1757          |
| NG75                        | 1757          |
| L50                         | 137           |
| LG50                        | 137           |
| L75                         | 268           |
| LG75                        | 268           |
| # misassemblies             | 0             |
| # misassembled contigs      | 0             |
| Misassembled contigs length | 0             |
| # local misassemblies       | 0             |
| # unaligned contigs         | 0 + 0 part    |
| Unaligned length            | 0             |
| Genome fraction (%)         | 97.154        |
| Duplication ratio           | 1.031         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 27.65         |
| # indels per 100 kbp        | 0.00          |
| Largest alignment           | 11592         |
| NA50                        | 2924          |
| NGA50                       | 2924          |
| NA75                        | 1757          |
| NGA75                       | 1757          |
| LA50                        | 137           |
| LGA50                       | 137           |
| LA75                        | 268           |
| LGA75                       | 268           |

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             |
| # interspecies translocations   | 0             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 0             |
| # mismatches                    | 331           |
| # indels                        | 0             |
| # short indels                  | 0             |
| # long indels                   | 0             |
| Indels length                   | 0             |

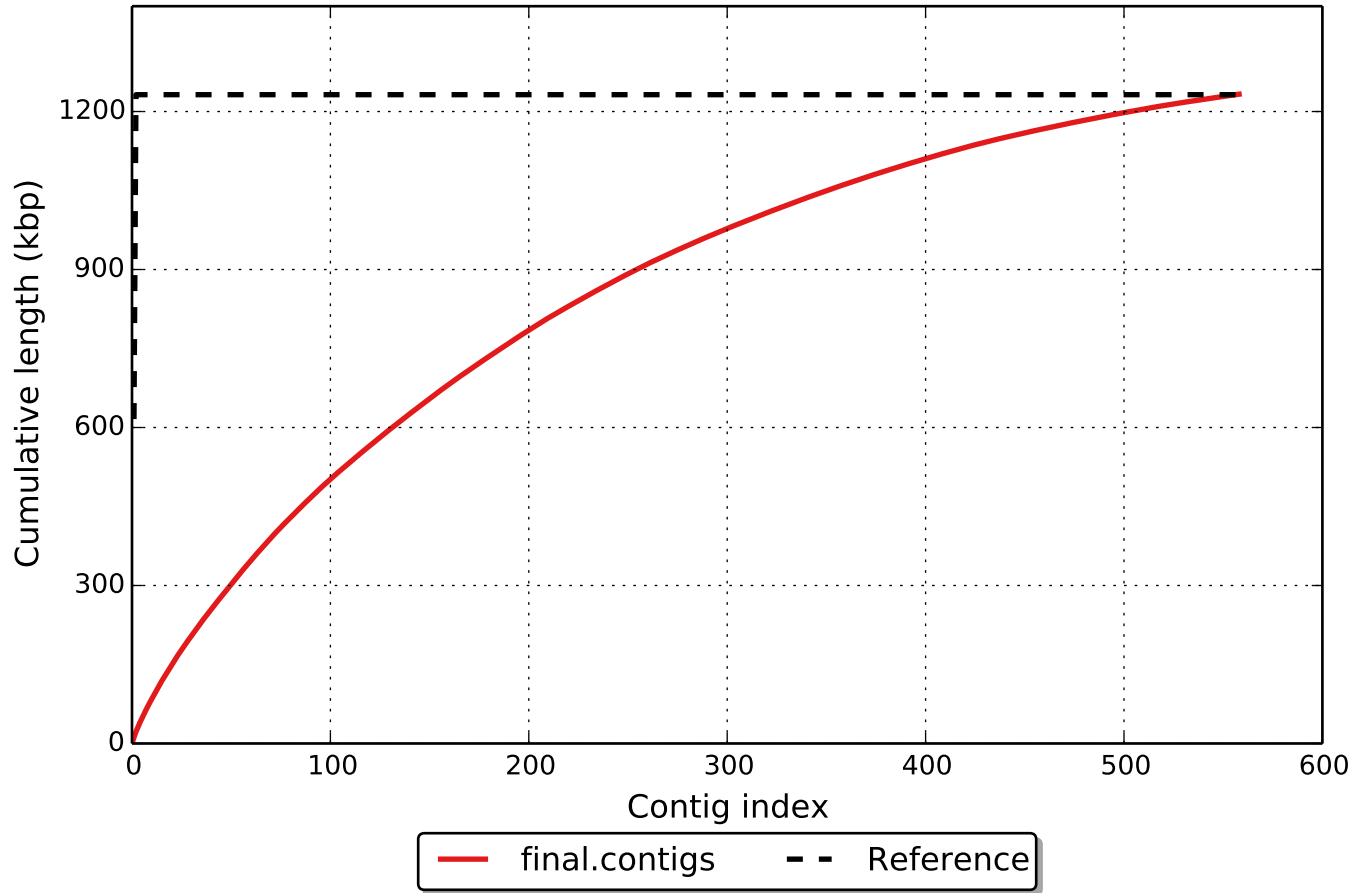
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

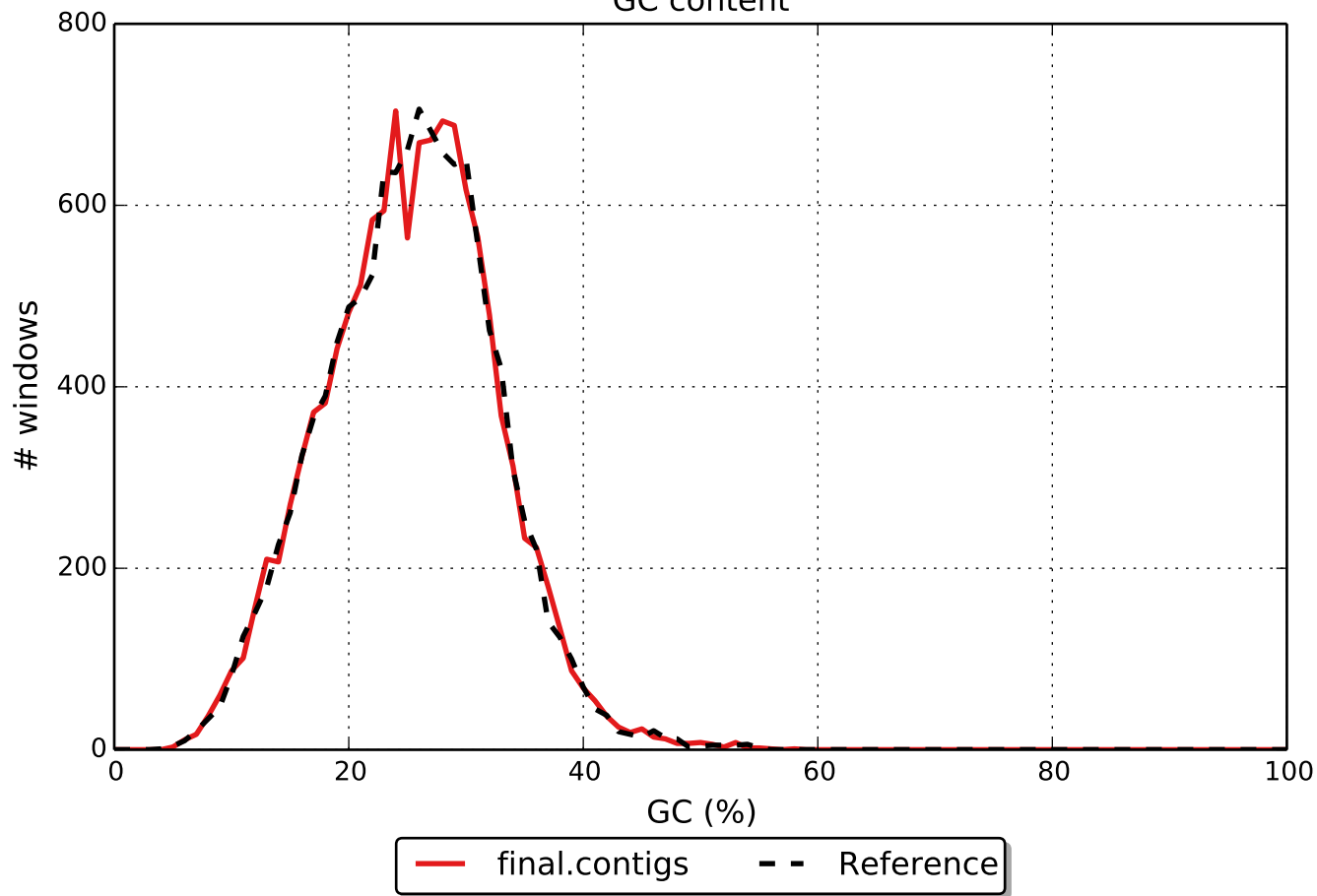
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 0             |
| # with misassembly            | 0             |
|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

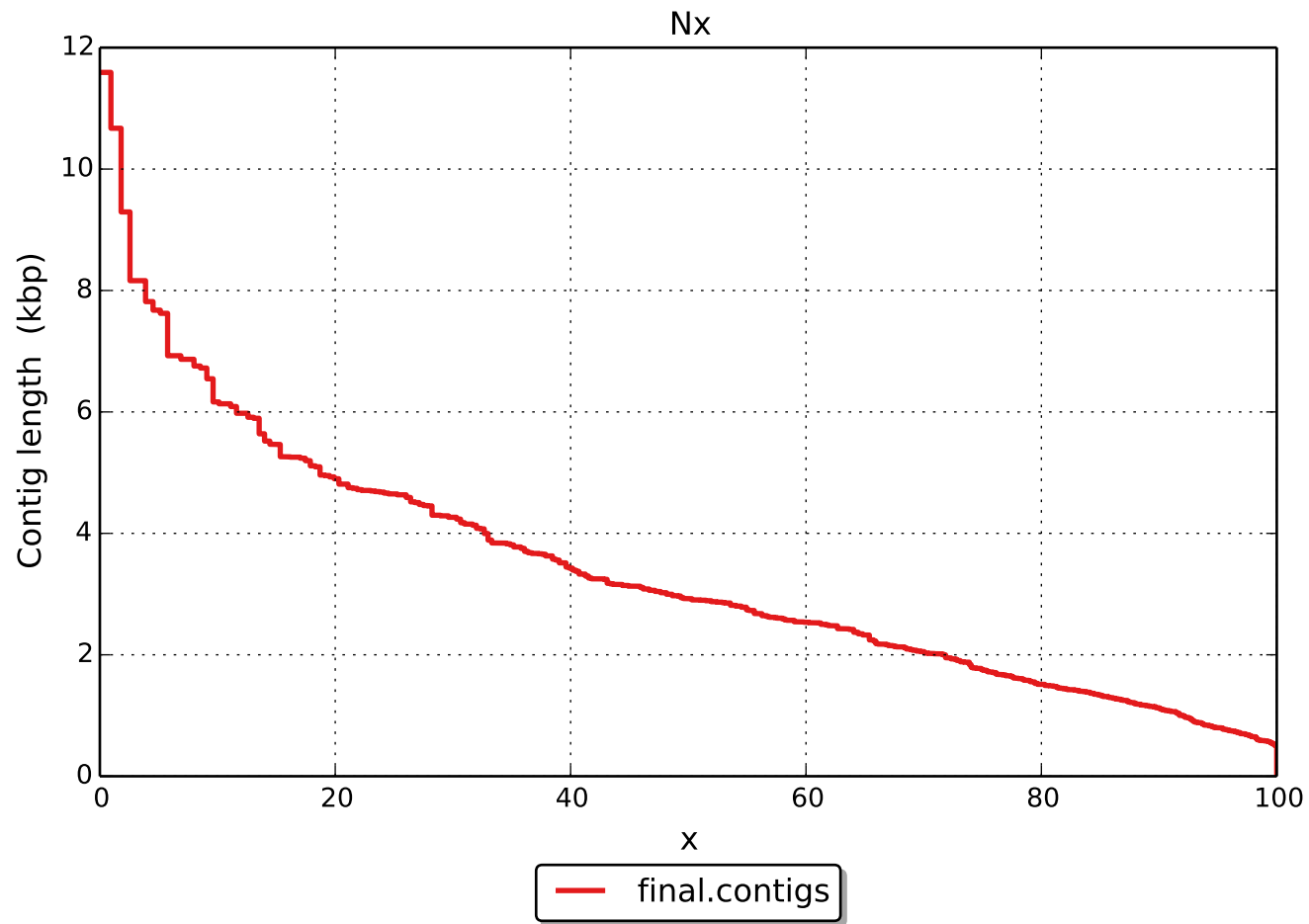
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

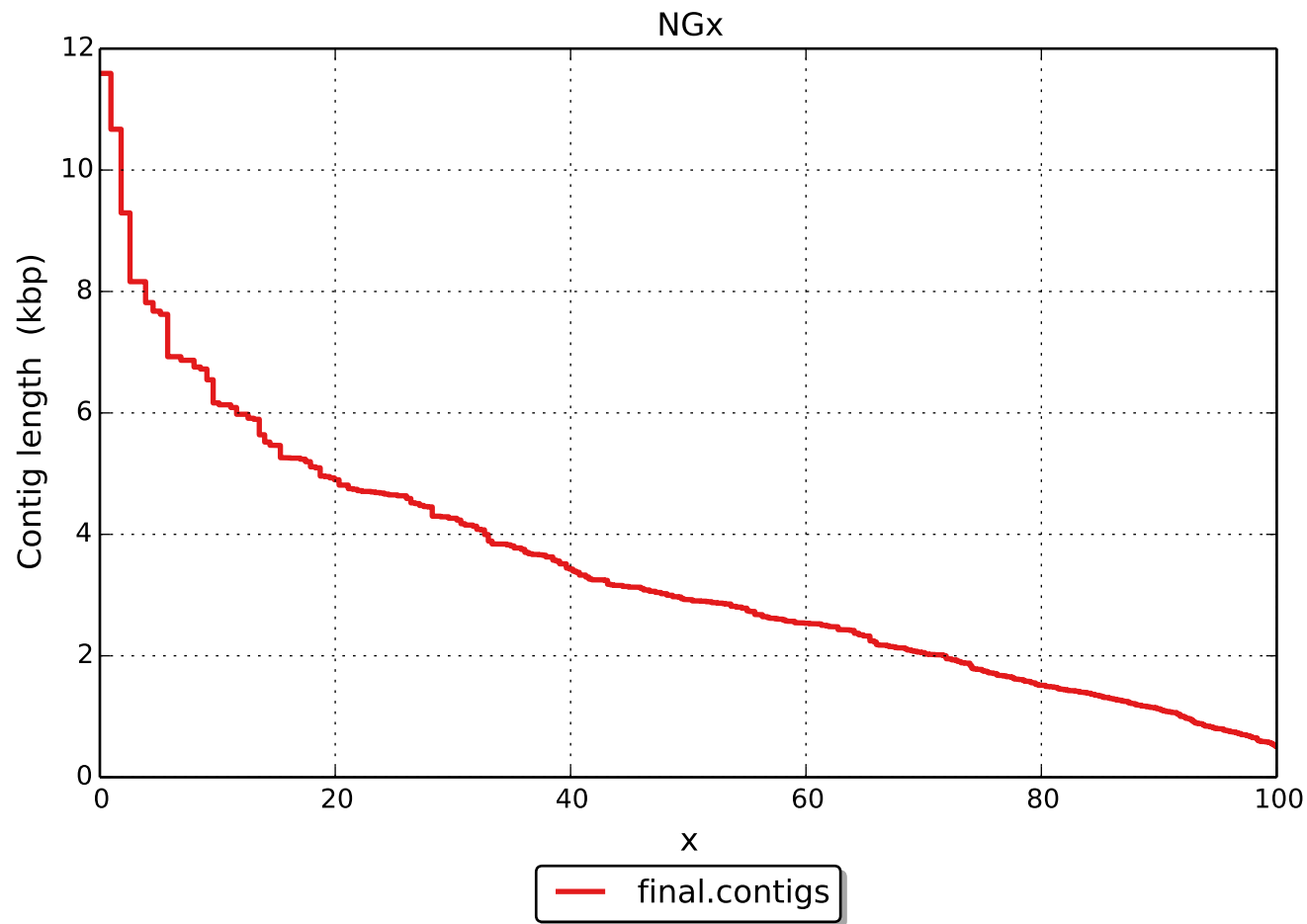
Cumulative length



GC content







# Misassemblies





Cumulative length (aligned contigs)

