

# Report

|                                 | contigs    |
|---------------------------------|------------|
| # contigs ( $\geq 1000$ bp)     | 497        |
| # contigs ( $\geq 5000$ bp)     | 138        |
| # contigs ( $\geq 10000$ bp)    | 29         |
| # contigs ( $\geq 25000$ bp)    | 2          |
| # contigs ( $\geq 50000$ bp)    | 0          |
| Total length ( $\geq 1000$ bp)  | 2141207    |
| Total length ( $\geq 5000$ bp)  | 1220841    |
| Total length ( $\geq 10000$ bp) | 420628     |
| Total length ( $\geq 25000$ bp) | 64579      |
| Total length ( $\geq 50000$ bp) | 0          |
| # contigs                       | 643        |
| Largest contig                  | 36999      |
| Total length                    | 2240337    |
| Reference length                | 4641652    |
| GC (%)                          | 50.77      |
| Reference GC (%)                | 50.79      |
| N50                             | 5912       |
| N75                             | 3096       |
| L50                             | 120        |
| L75                             | 254        |
| # misassemblies                 | 0          |
| # misassembled contigs          | 0          |
| Misassembled contigs length     | 0          |
| # local misassemblies           | 3          |
| # unaligned contigs             | 0 + 0 part |
| Unaligned length                | 0          |
| Genome fraction (%)             | 48.041     |
| Duplication ratio               | 1.005      |
| # N's per 100 kbp               | 0.00       |
| # mismatches per 100 kbp        | 803.10     |
| # indels per 100 kbp            | 0.63       |
| Largest alignment               | 36999      |
| NA50                            | 5912       |
| NGA50                           | -          |
| NA75                            | 3096       |
| LA50                            | 120        |
| LA75                            | 254        |

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

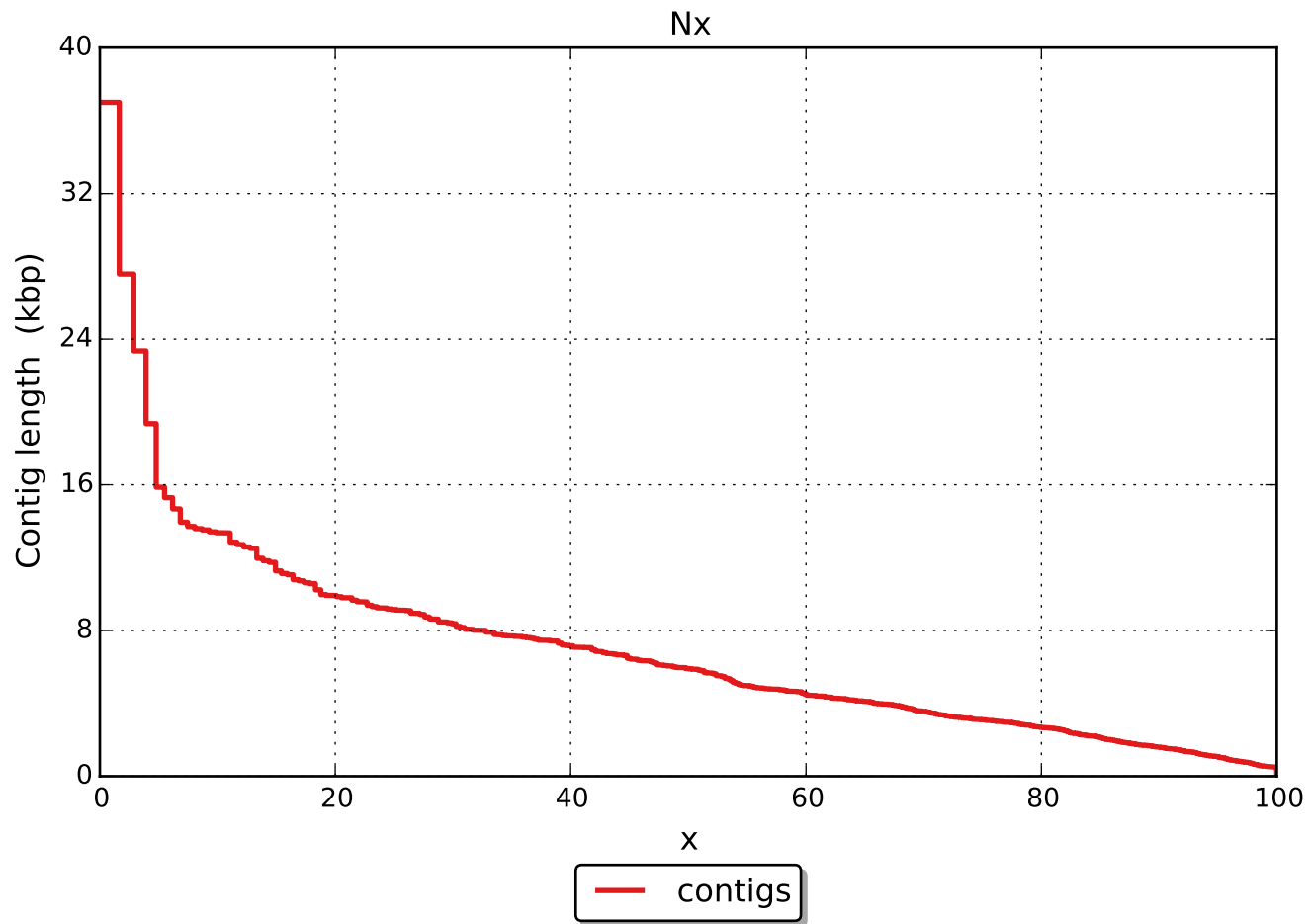
|                                 | contigs |
|---------------------------------|---------|
| # misassemblies                 | 0       |
| # relocations                   | 0       |
| # translocations                | 0       |
| # inversions                    | 0       |
| # possibly misassembled contigs | 0       |
| # misassembled contigs          | 0       |
| Misassembled contigs length     | 0       |
| # local misassemblies           | 3       |
| # mismatches                    | 17908   |
| # indels                        | 14      |
| # short indels                  | 14      |
| # long indels                   | 0       |
| Indels length                   | 16      |

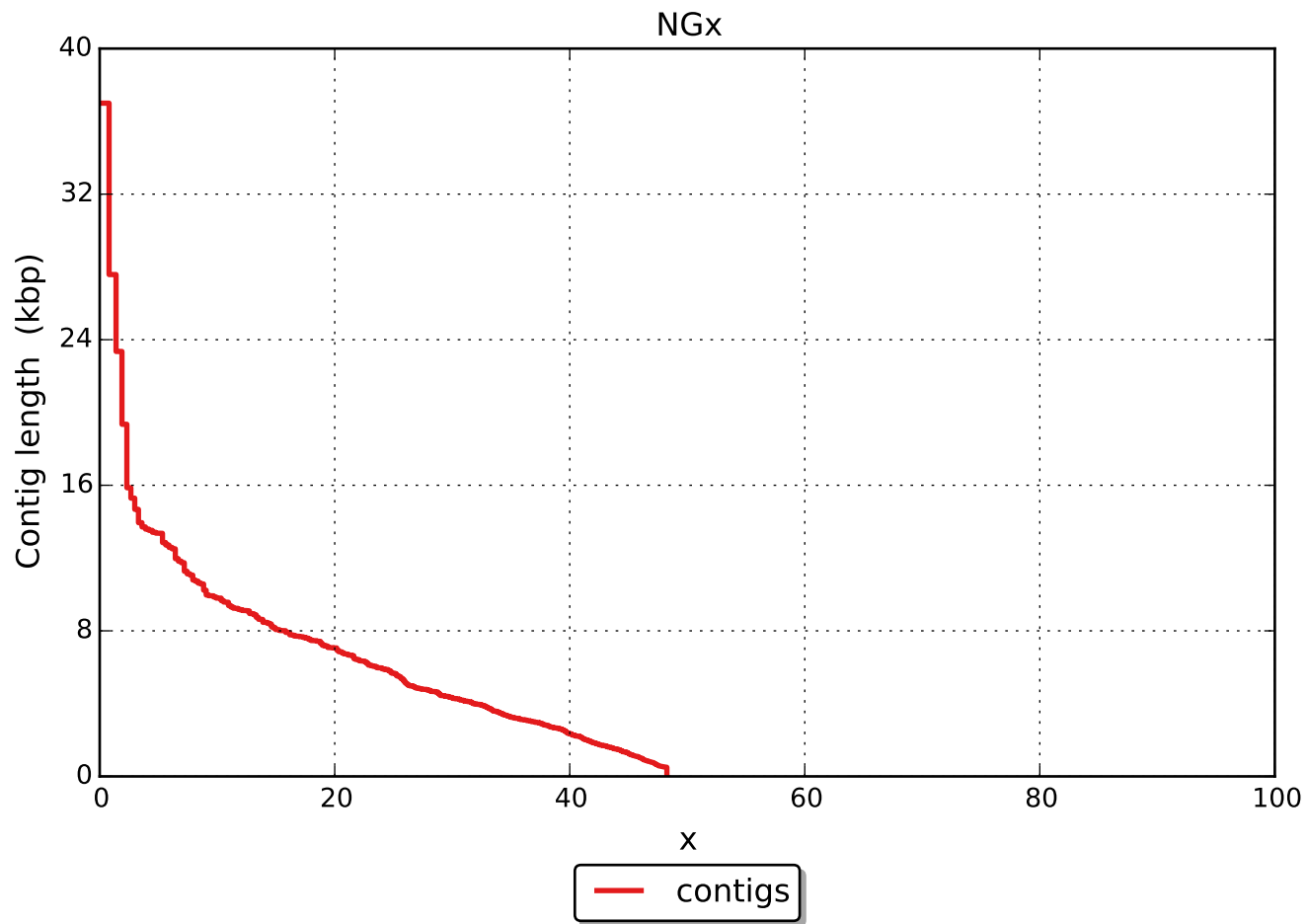
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

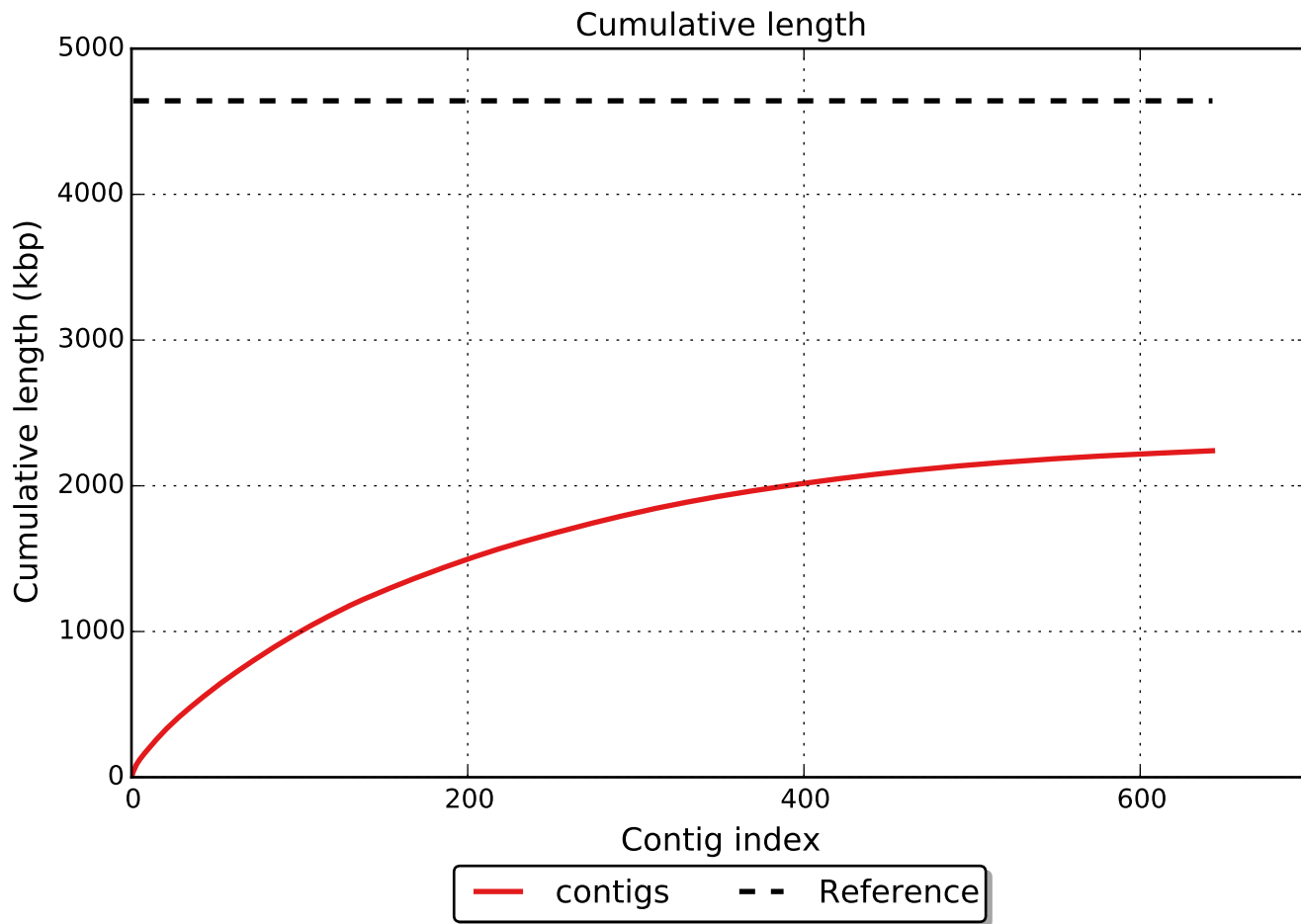
## Unaligned report

|                               | 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       |

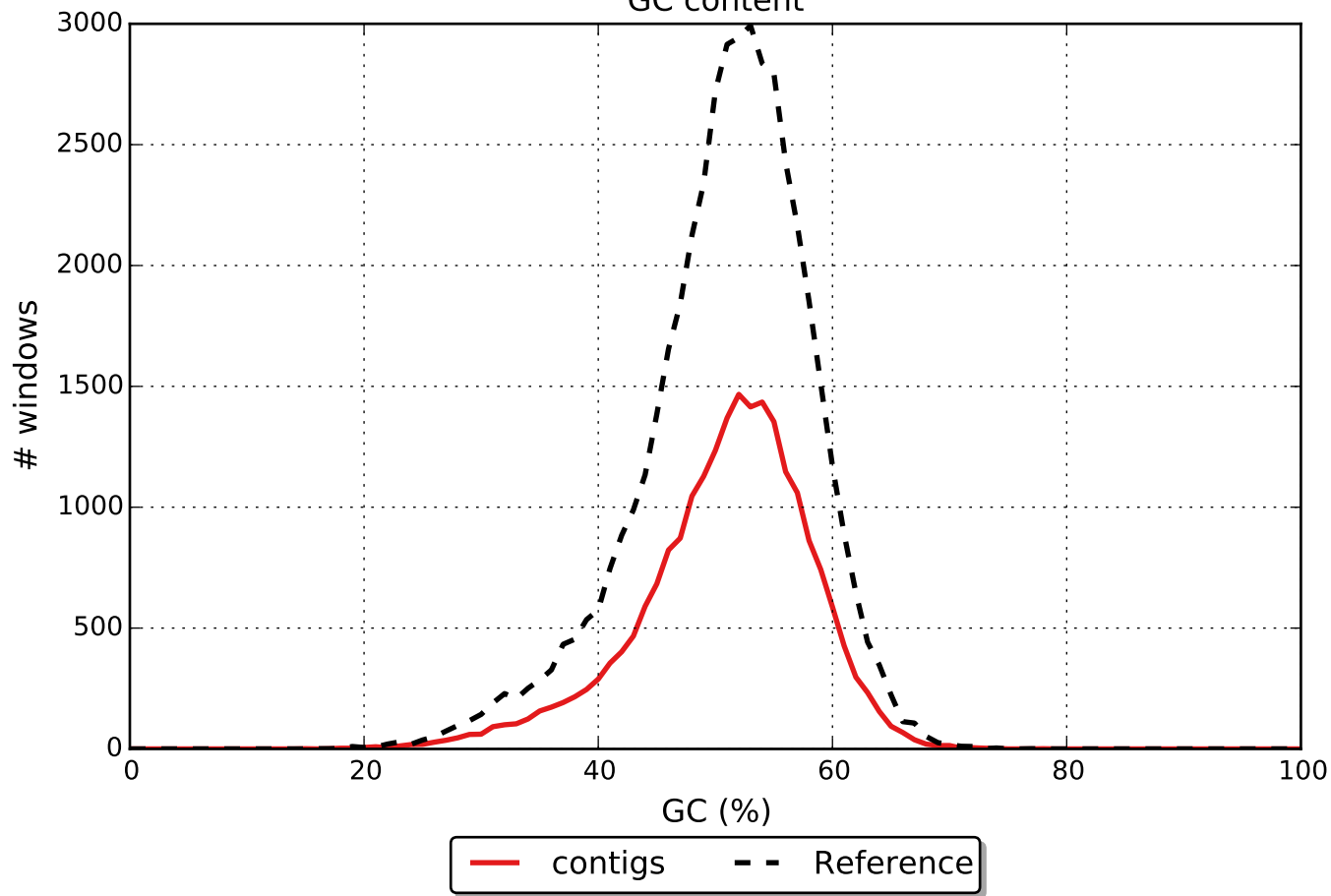
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







# GC content

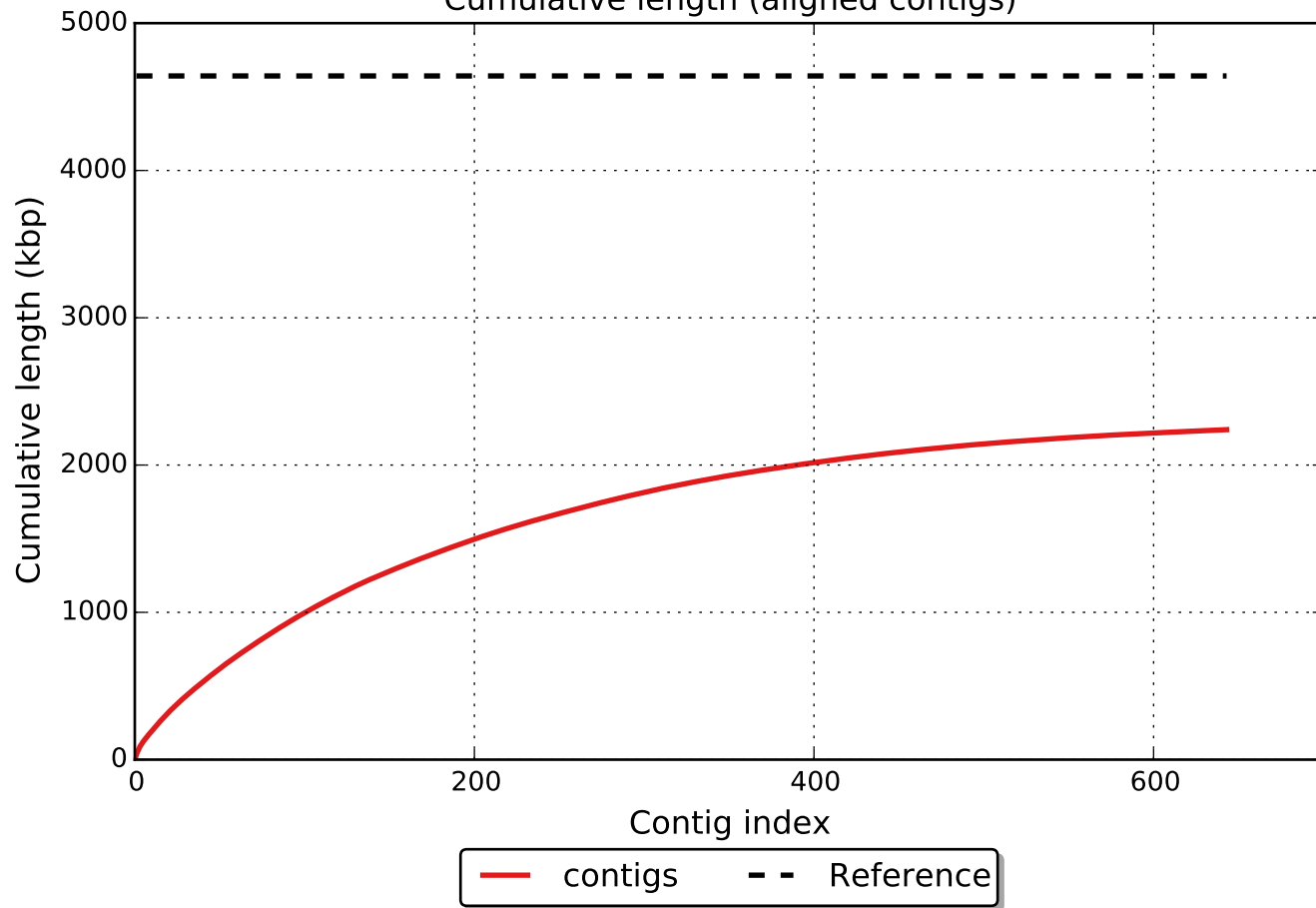


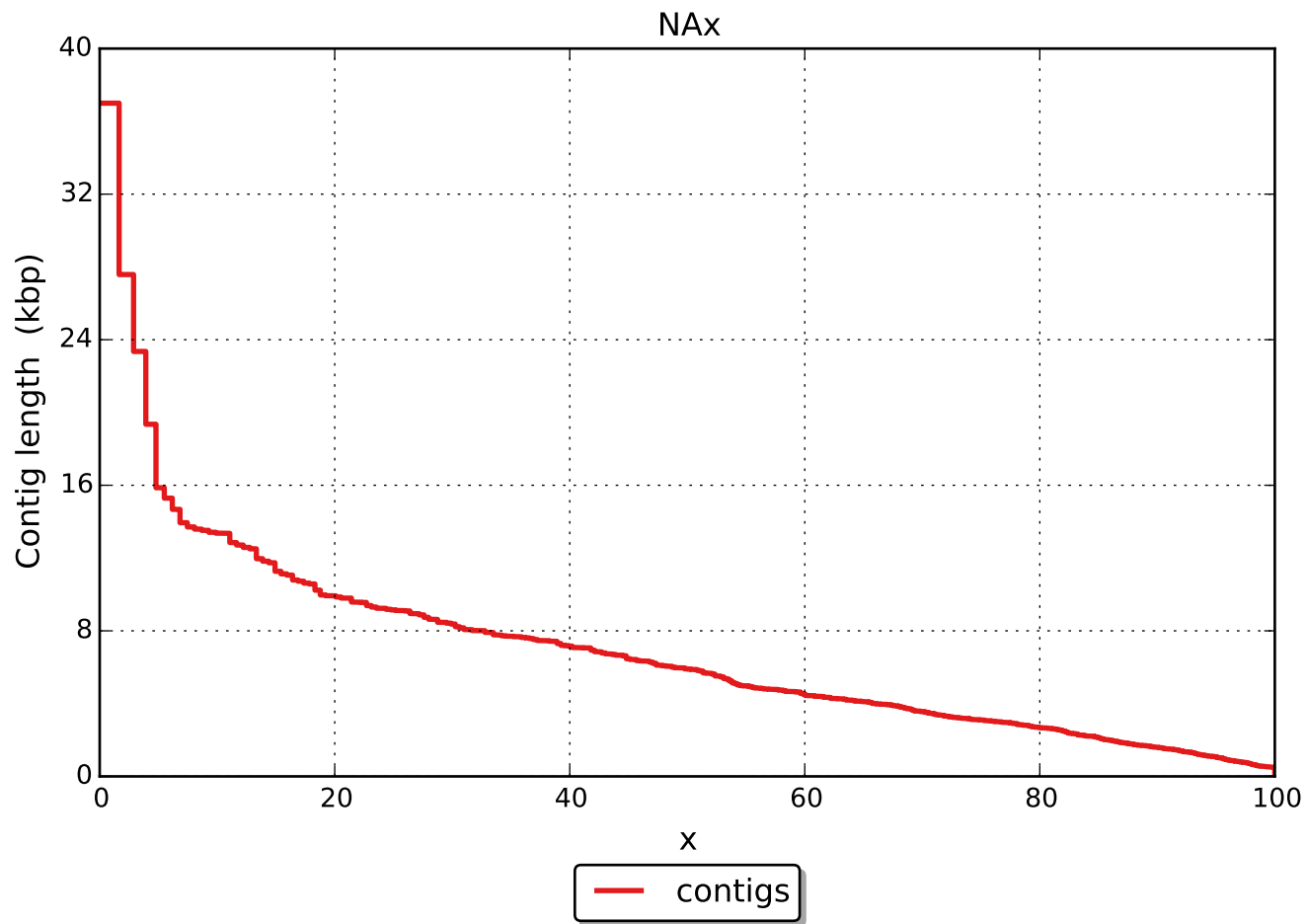
# Misassemblies





Cumulative length (aligned contigs)





NGAx

