

## Report

|                                 | final.contigs |
|---------------------------------|---------------|
| # contigs ( $\geq 0$ bp)        | 1519          |
| # contigs ( $\geq 1000$ bp)     | 3             |
| # contigs ( $\geq 5000$ bp)     | 0             |
| # contigs ( $\geq 10000$ bp)    | 0             |
| # contigs ( $\geq 25000$ bp)    | 0             |
| # contigs ( $\geq 50000$ bp)    | 0             |
| Total length ( $\geq 0$ bp)     | 609335        |
| Total length ( $\geq 1000$ bp)  | 3352          |
| Total length ( $\geq 5000$ bp)  | 0             |
| Total length ( $\geq 10000$ bp) | 0             |
| Total length ( $\geq 25000$ bp) | 0             |
| Total length ( $\geq 50000$ bp) | 0             |
| # contigs                       | 197           |
| Largest contig                  | 1195          |
| Total length                    | 115161        |
| Reference length                | 4641652       |
| GC (%)                          | 51.00         |
| Reference GC (%)                | 50.79         |
| N50                             | 565           |
| N75                             | 523           |
| L50                             | 88            |
| L75                             | 141           |
| # misassemblies                 | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 0             |
| # unaligned contigs             | 31 + 3 part   |
| Unaligned length                | 18029         |
| Genome fraction (%)             | 2.072         |
| Duplication ratio               | 1.010         |
| # N's per 100 kbp               | 0.00          |
| # mismatches per 100 kbp        | 3502.22       |
| # indels per 100 kbp            | 9.36          |
| Largest alignment               | 1195          |
| NA50                            | 549           |
| NGA50                           | -             |
| NA75                            | 509           |
| LA50                            | 90            |
| LA75                            | 145           |

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

|                             | final.contigs |
|-----------------------------|---------------|
| # misassemblies             | 0             |
| # relocations               | 0             |
| # translocations            | 0             |
| # inversions                | 0             |
| # misassembled contigs      | 0             |
| Misassembled contigs length | 0             |
| # local misassemblies       | 0             |
| # mismatches                | 3369          |
| # indels                    | 9             |
| # short indels              | 9             |
| # long indels               | 0             |
| Indels length               | 9             |

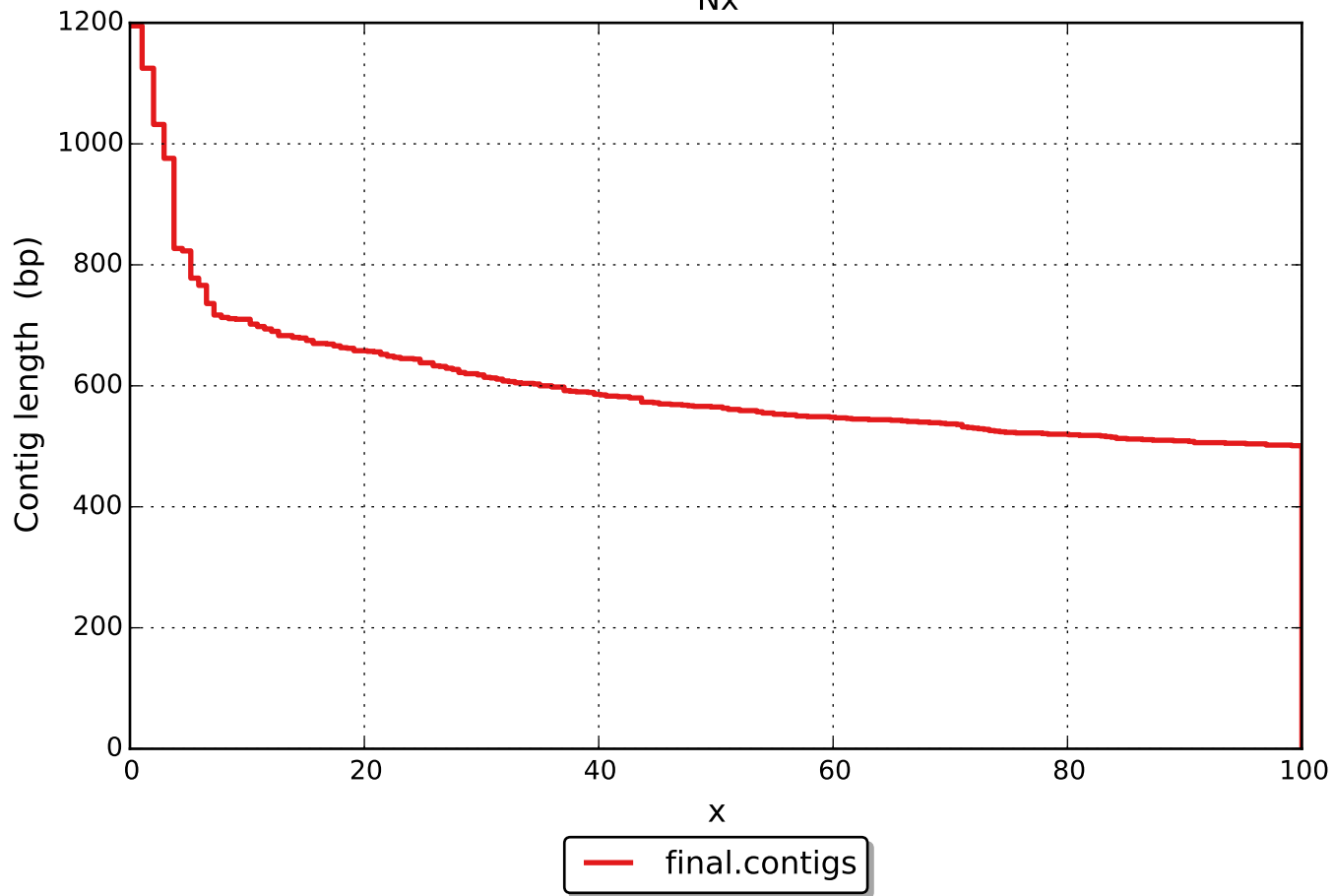
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

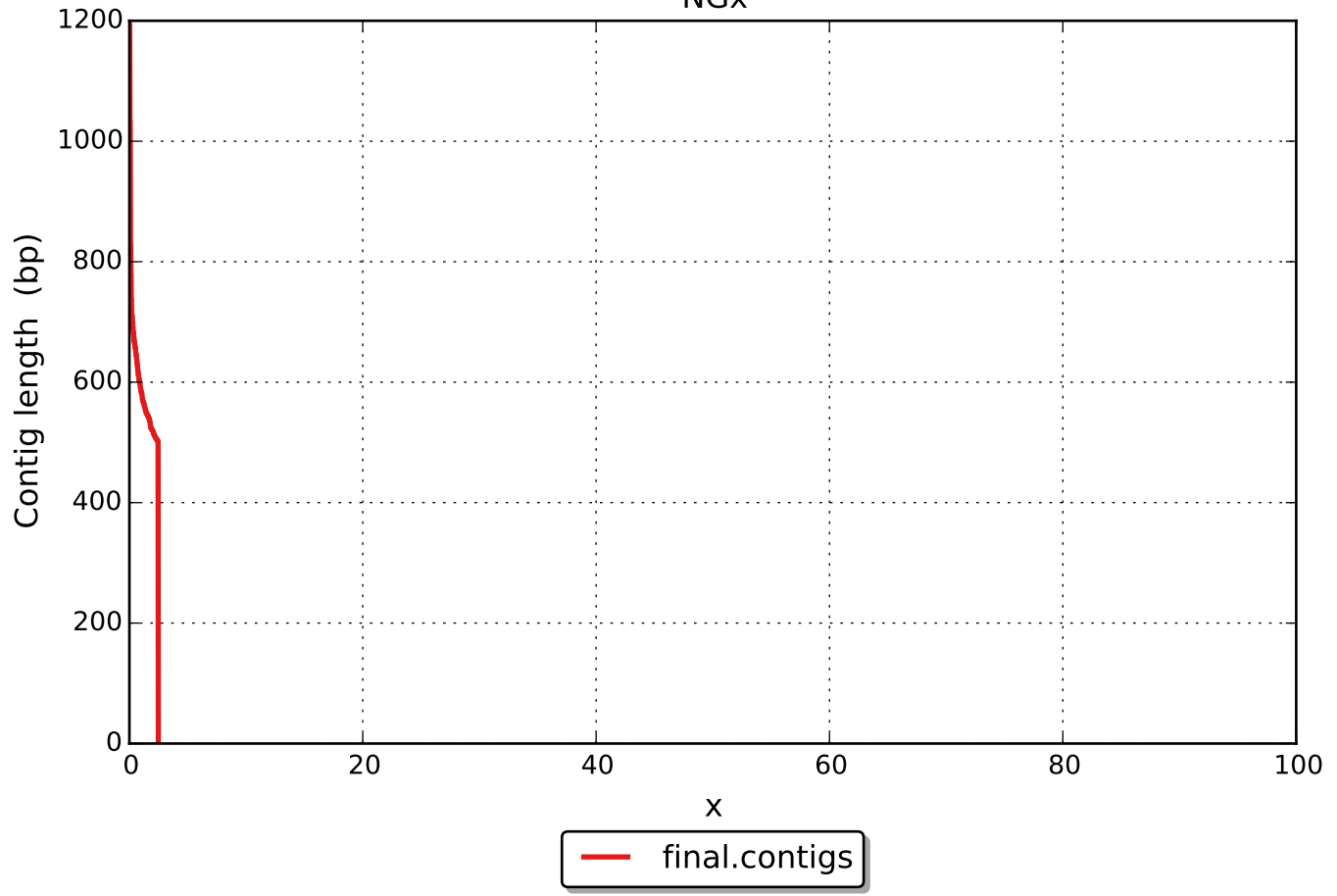
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 31            |
| Fully unaligned length        | 17576         |
| # partially unaligned contigs | 3             |
| # with misassembly            | 0             |
| # both parts are significant  | 0             |
| Partially unaligned length    | 453           |
| # N's                         | 0             |

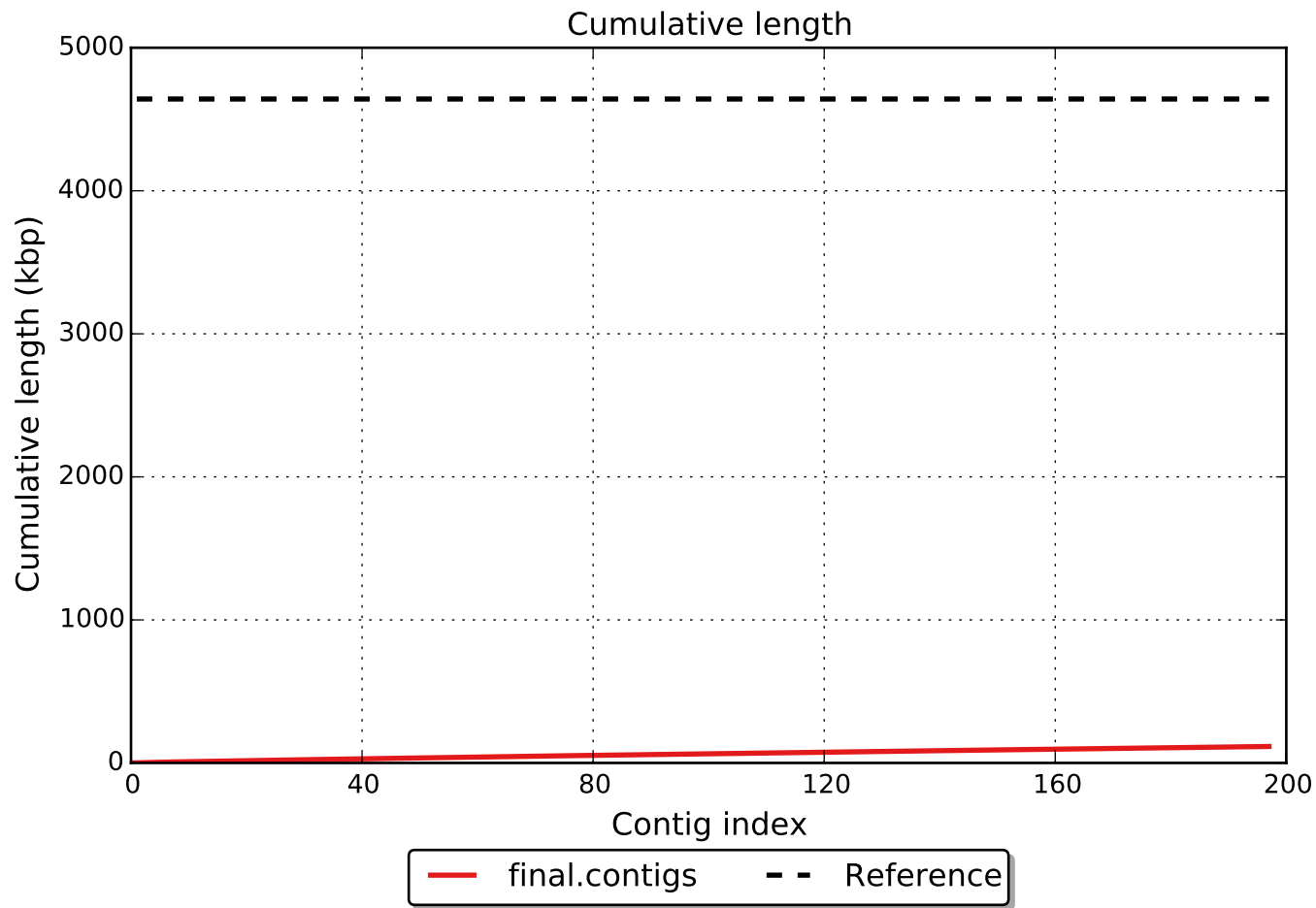
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

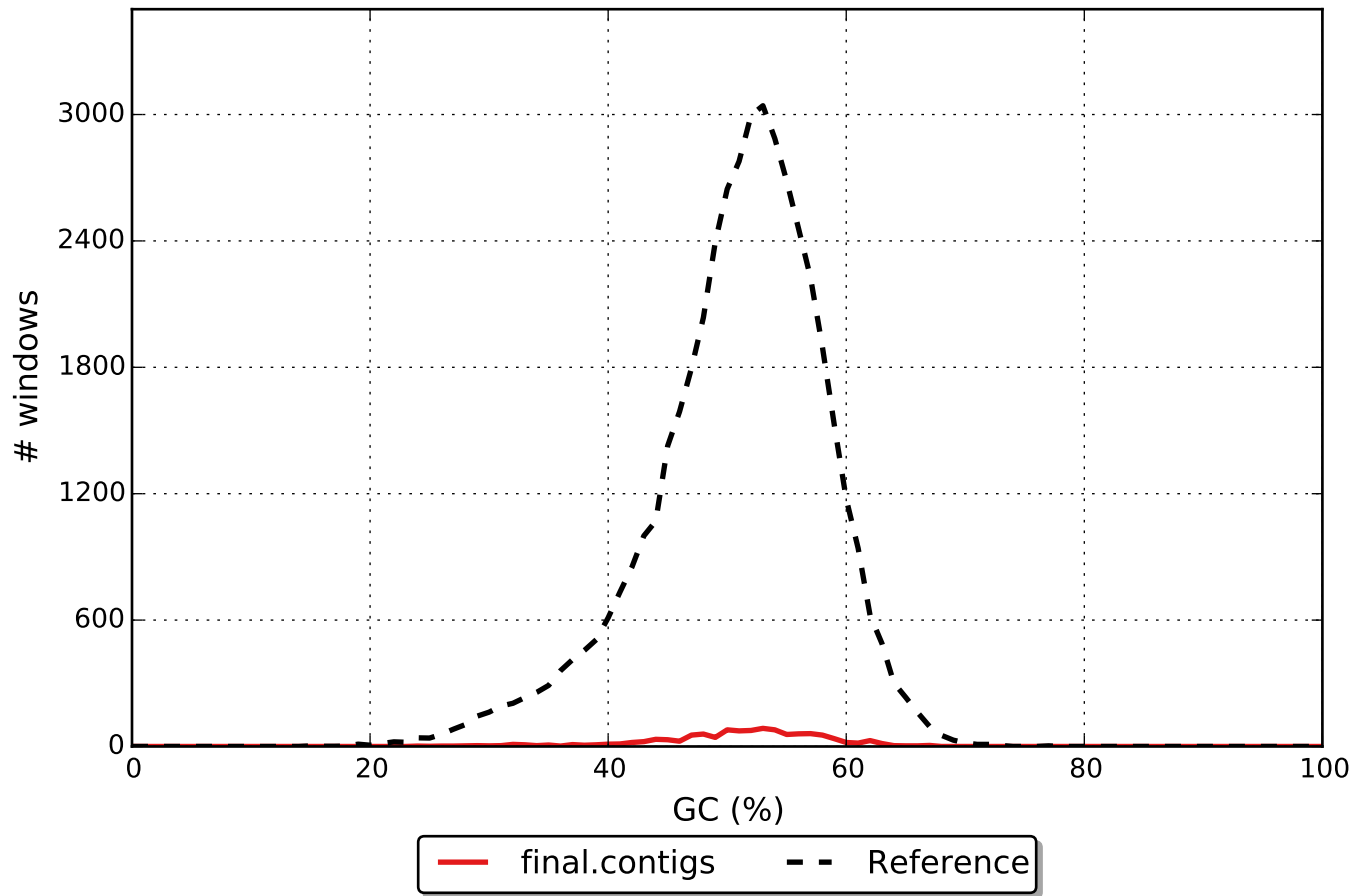


NGx





# GC content

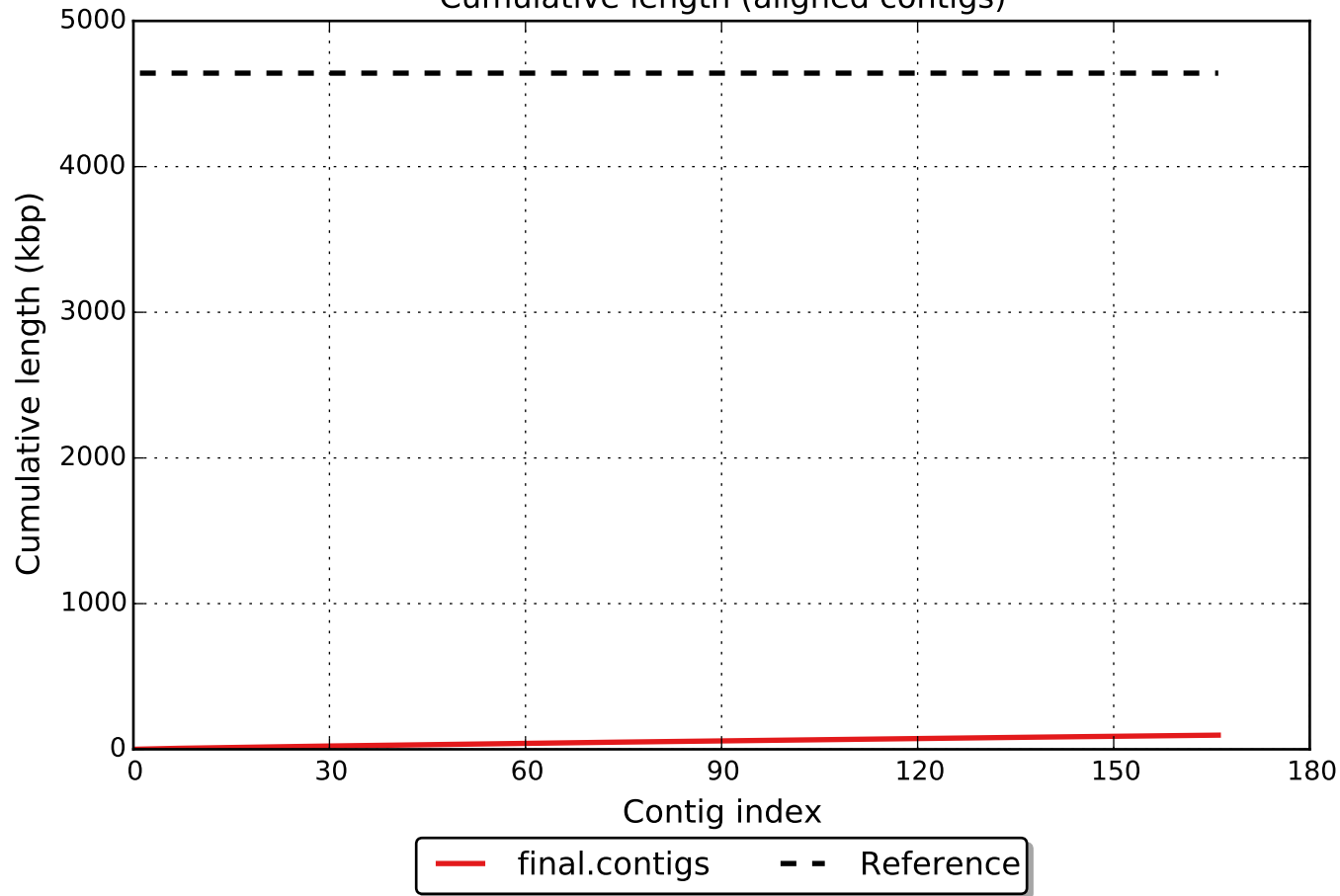


# Misassemblies

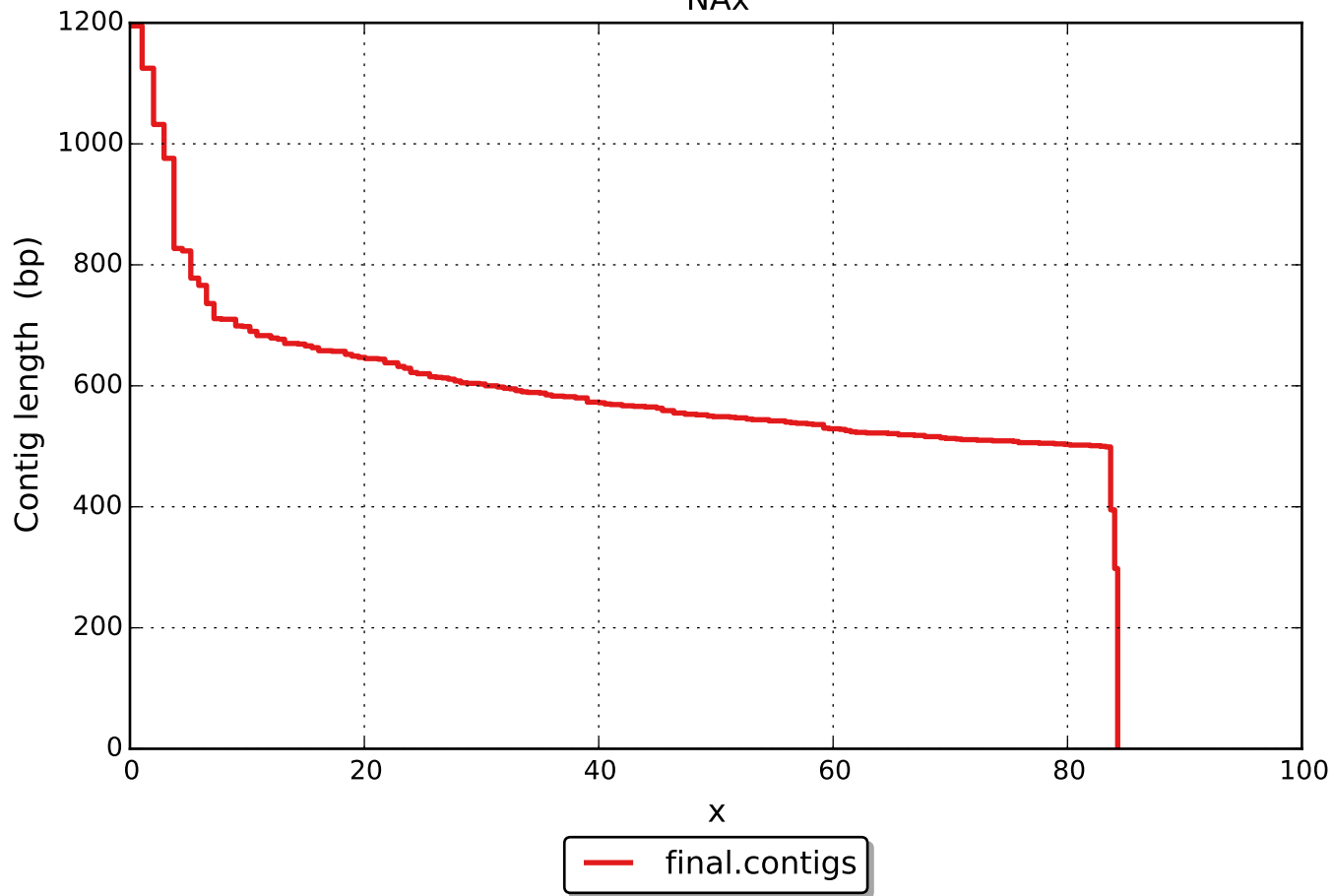




Cumulative length (aligned contigs)



NAx



NGAx

