

Report

|                             | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp)      | 150           |
| # contigs (>= 5000 bp)      | 130           |
| # contigs (>= 10000 bp)     | 109           |
| # contigs (>= 25000 bp)     | 73            |
| # contigs (>= 50000 bp)     | 33            |
| Total length (>= 1000 bp)   | 4868129       |
| Total length (>= 5000 bp)   | 4811579       |
| Total length (>= 10000 bp)  | 4654625       |
| Total length (>= 25000 bp)  | 4084167       |
| Total length (>= 50000 bp)  | 2708933       |
| # contigs                   | 153           |
| Largest contig              | 160557        |
| Total length                | 4870317       |
| Reference length            | 4857432       |
| GC (℥)                      | 52.22         |
| Reference GC (℥)            | 52.23         |
| N50                         | 56364         |
| NG50                        | 56364         |
| N75                         | 29888         |
| NG75                        | 29901         |
| L50                         | 28            |
| LG50                        | 28            |
| L75                         | 58            |
| LG75                        | 57            |
| # misassemblies             | 0             |
| # misassembled contigs      | 0             |
| Misassembled contigs length | 0             |
| # local misassemblies       | 0             |
| # unaligned contigs         | 0 + 0 part    |
| Unaligned length            | 0             |
| Genome fraction (℥)         | 99.998        |
| Duplication ratio           | 1.003         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 0.00          |
| # indels per 100 kbp        | 0.00          |
| Largest alignment           | 160557        |
| NA50                        | 56364         |
| NGA50                       | 56364         |
| NA75                        | 29888         |
| NGA75                       | 29901         |
| LA50                        | 28            |
| LGA50                       | 28            |
| LA75                        | 58            |
| LGA75                       | 57            |

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                    | 0             |
| # indels                        | 0             |
| # short indels                  | 0             |
| # long indels                   | 0             |
| Indels length                   | 0             |

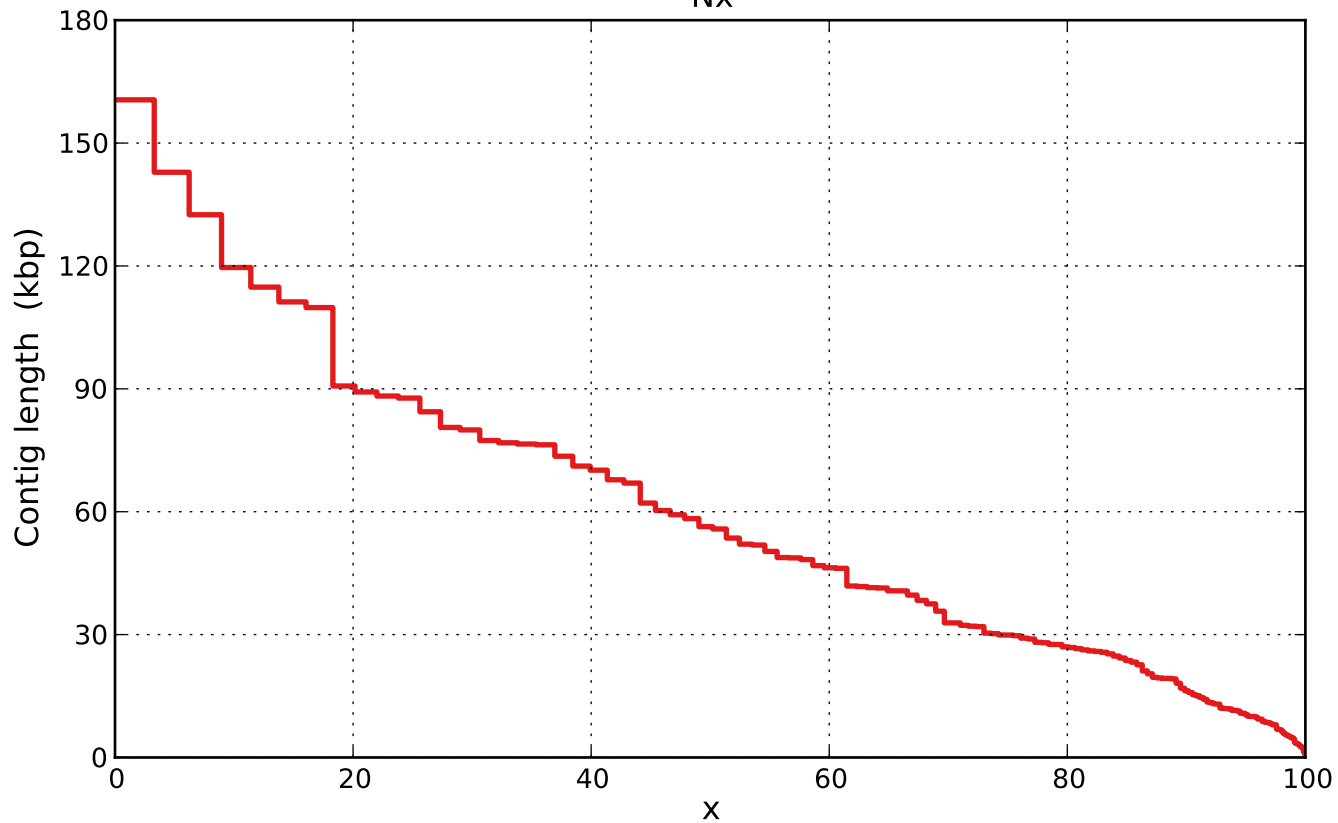
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

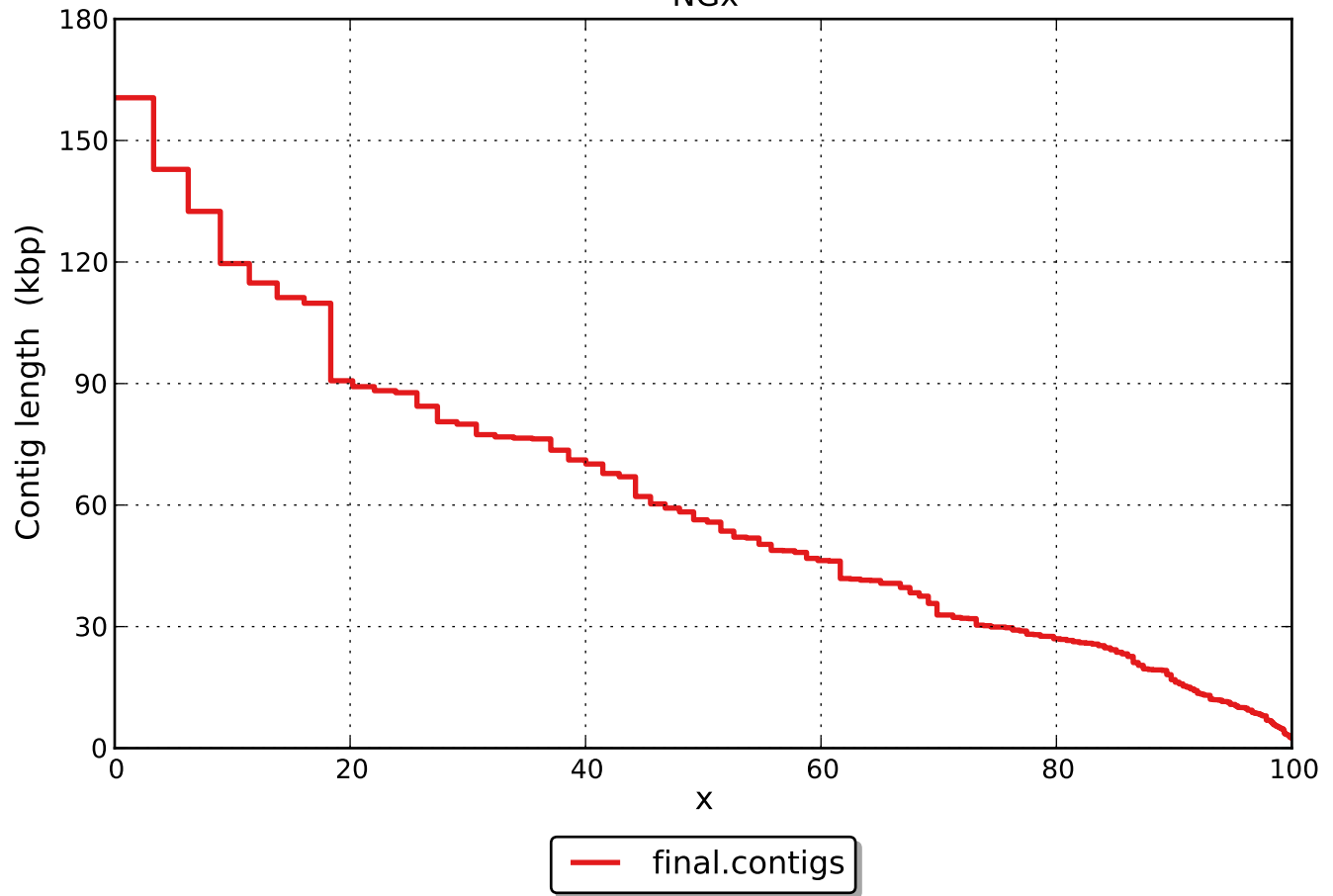
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 0             |
| # with misassembly            | 0             |
|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

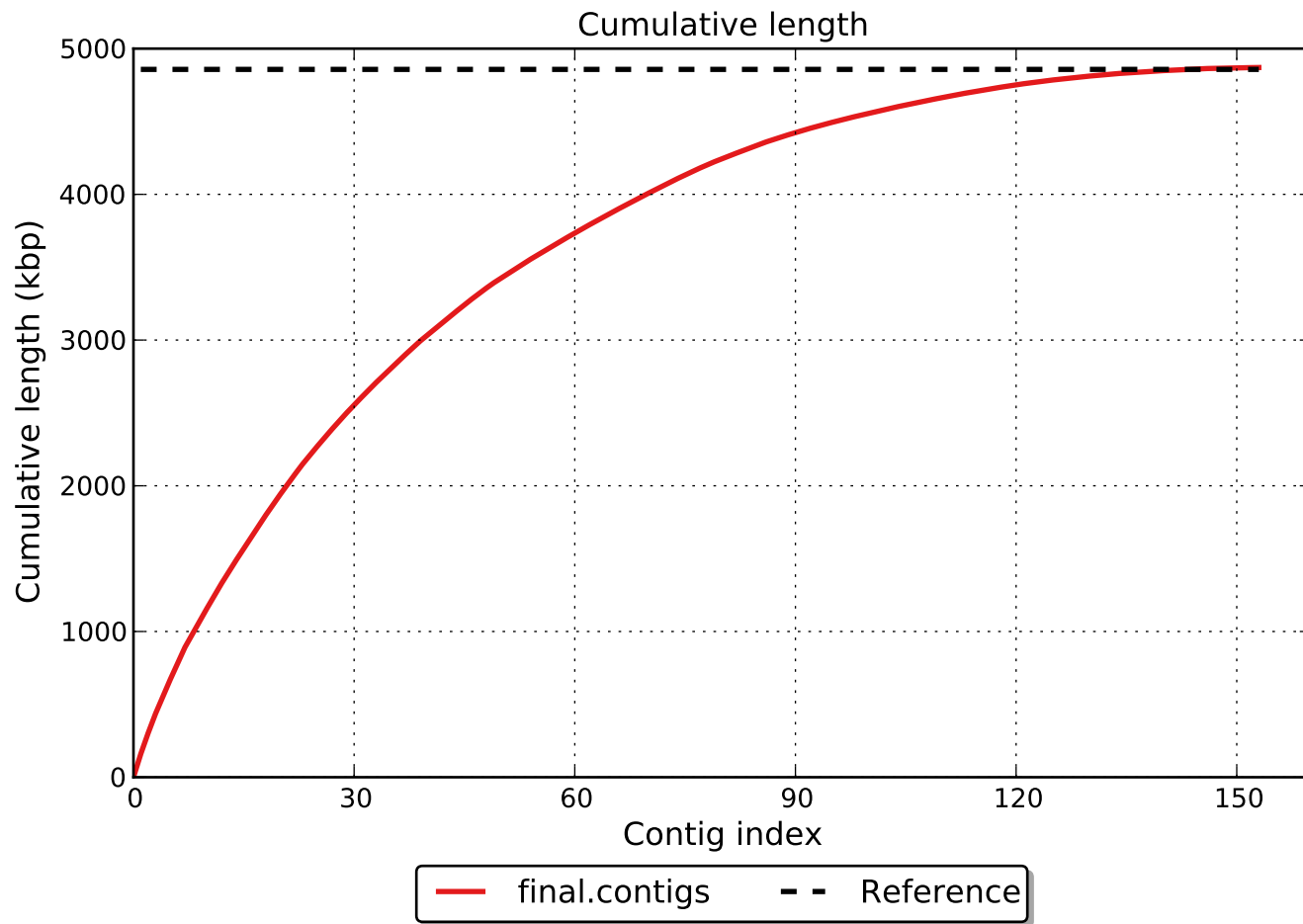
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

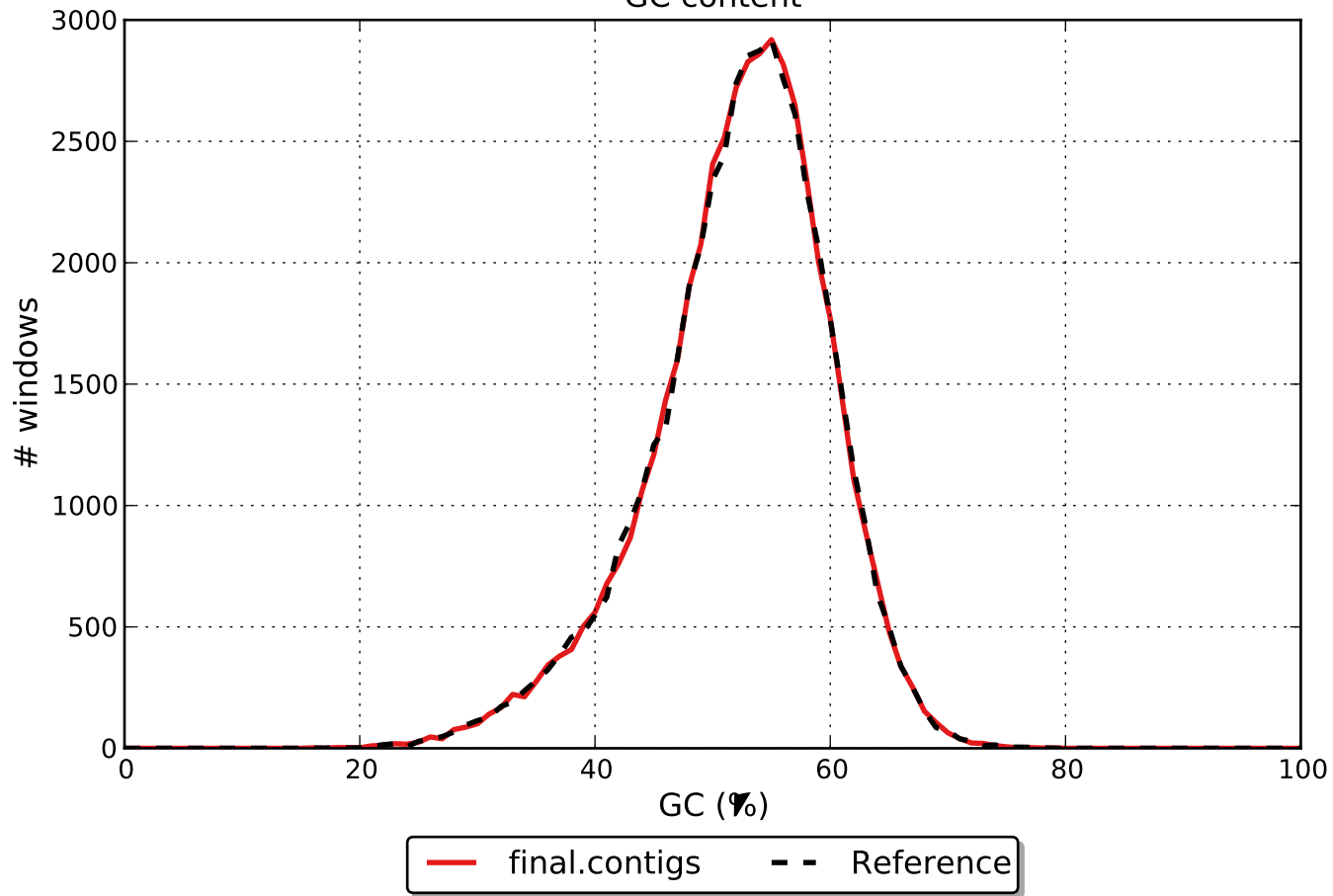


NGx

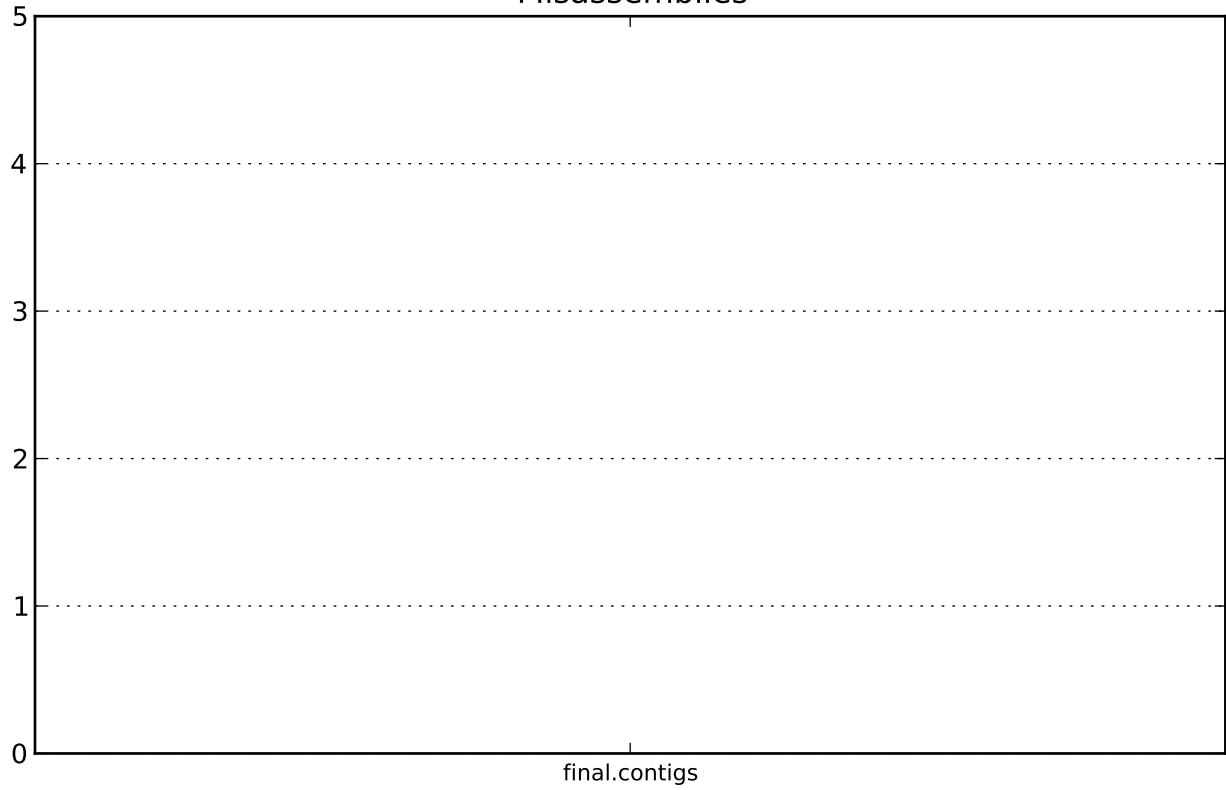




GC content

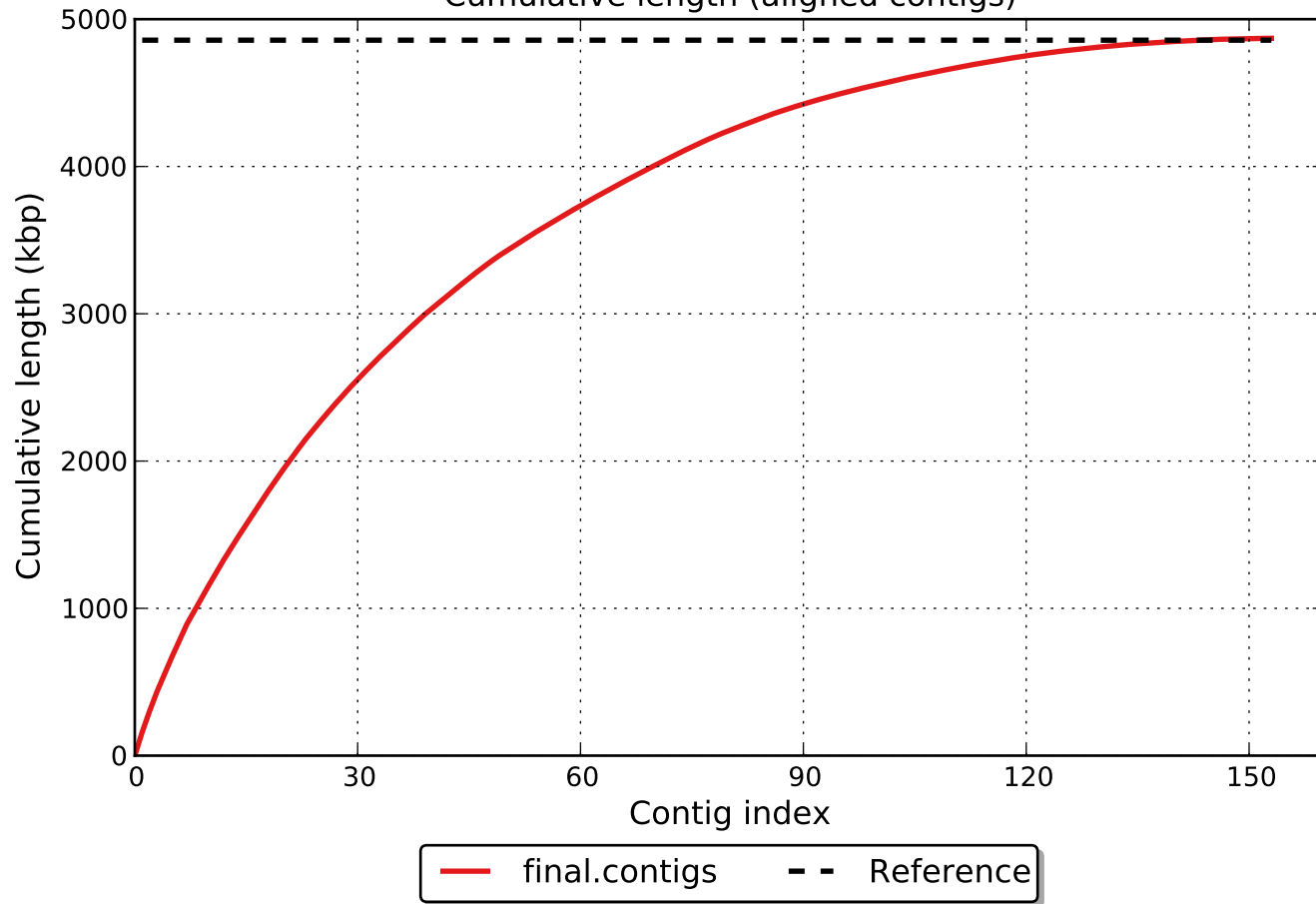


# Misassemblies

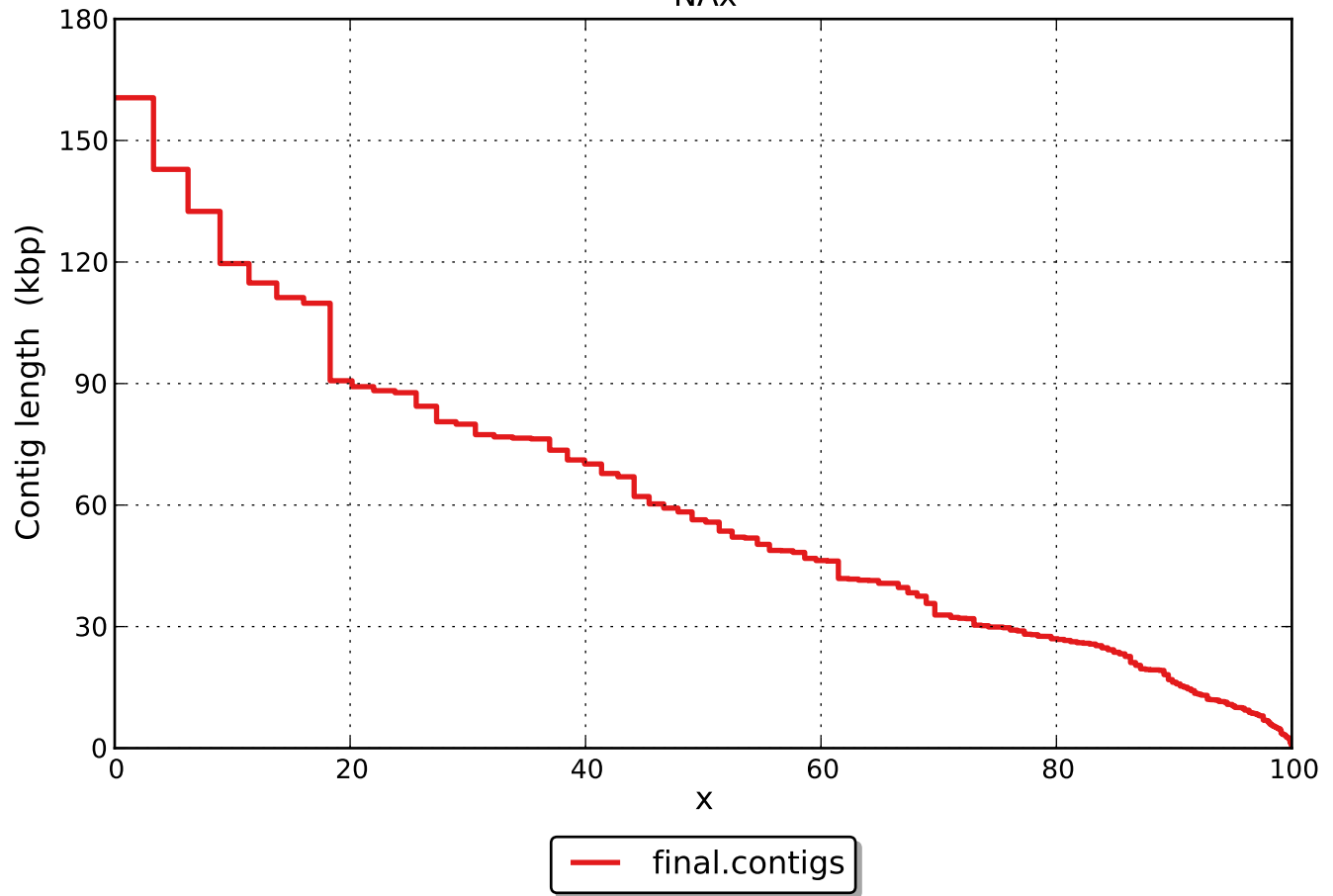




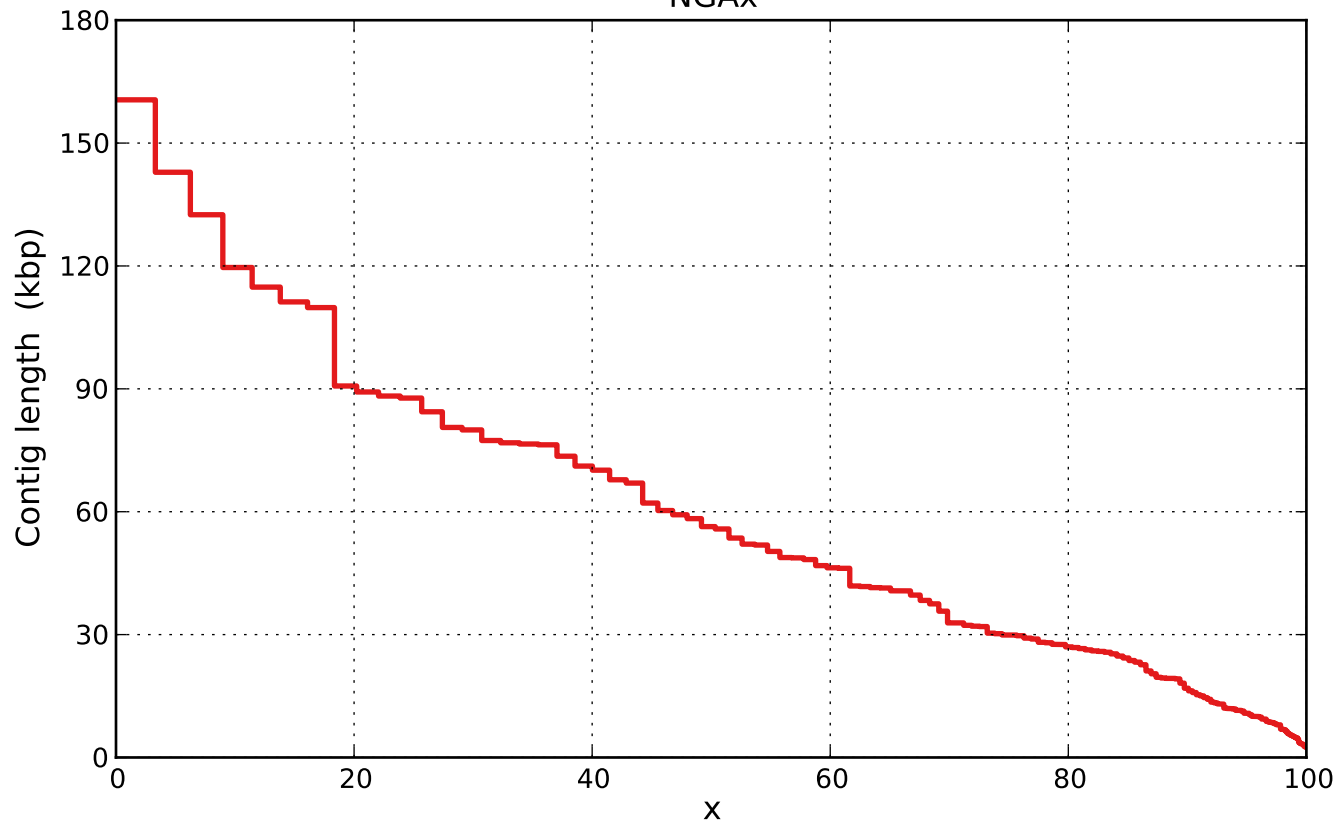
Cumulative length (aligned contigs)



NAx



# NGAx



— final.contigs