

# Report

|                                | final.contigs |
|--------------------------------|---------------|
| # contigs ( $\geq 0$ bp)       | 215           |
| # contigs ( $\geq 1000$ bp)    | 198           |
| Total length ( $\geq 0$ bp)    | 1267862       |
| Total length ( $\geq 1000$ bp) | 1254149       |
| # contigs                      | 215           |
| Largest contig                 | 36991         |
| Total length                   | 1267862       |
| Reference length               | 615980        |
| GC (%)                         | 25.34         |
| Reference GC (%)               | 25.35         |
| N50                            | 9274          |
| NG50                           | 16331         |
| N75                            | 5047          |
| NG75                           | 12035         |
| L50                            | 42            |
| LG50                           | 13            |
| L75                            | 86            |
| LG75                           | 25            |
| # misassemblies                | 1             |
| # misassembled contigs         | 1             |
| Misassembled contigs length    | 2187          |
| # local misassemblies          | 0             |
| # unaligned contigs            | 70 + 22 part  |
| Unaligned length               | 554414        |
| Genome fraction (%)            | 99.618        |
| Duplication ratio              | 1.163         |
| # N's per 100 kbp              | 0.00          |
| # mismatches per 100 kbp       | 173.23        |
| # indels per 100 kbp           | 0.33          |
| Largest alignment              | 36991         |
| NA50                           | 1725          |
| NGA50                          | 9274          |
| NGA75                          | 5569          |
| LA50                           | 94            |
| LGA50                          | 19            |
| LGA75                          | 39            |

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                 | 1             |
| # relocations                   | 1             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # possibly misassembled contigs | 16            |
| # misassembled contigs          | 1             |
| Misassembled contigs length     | 2187          |
| # local misassemblies           | 0             |
| # mismatches                    | 1063          |
| # indels                        | 2             |
| # short indels                  | 2             |
| # long indels                   | 0             |
| Indels length                   | 2             |

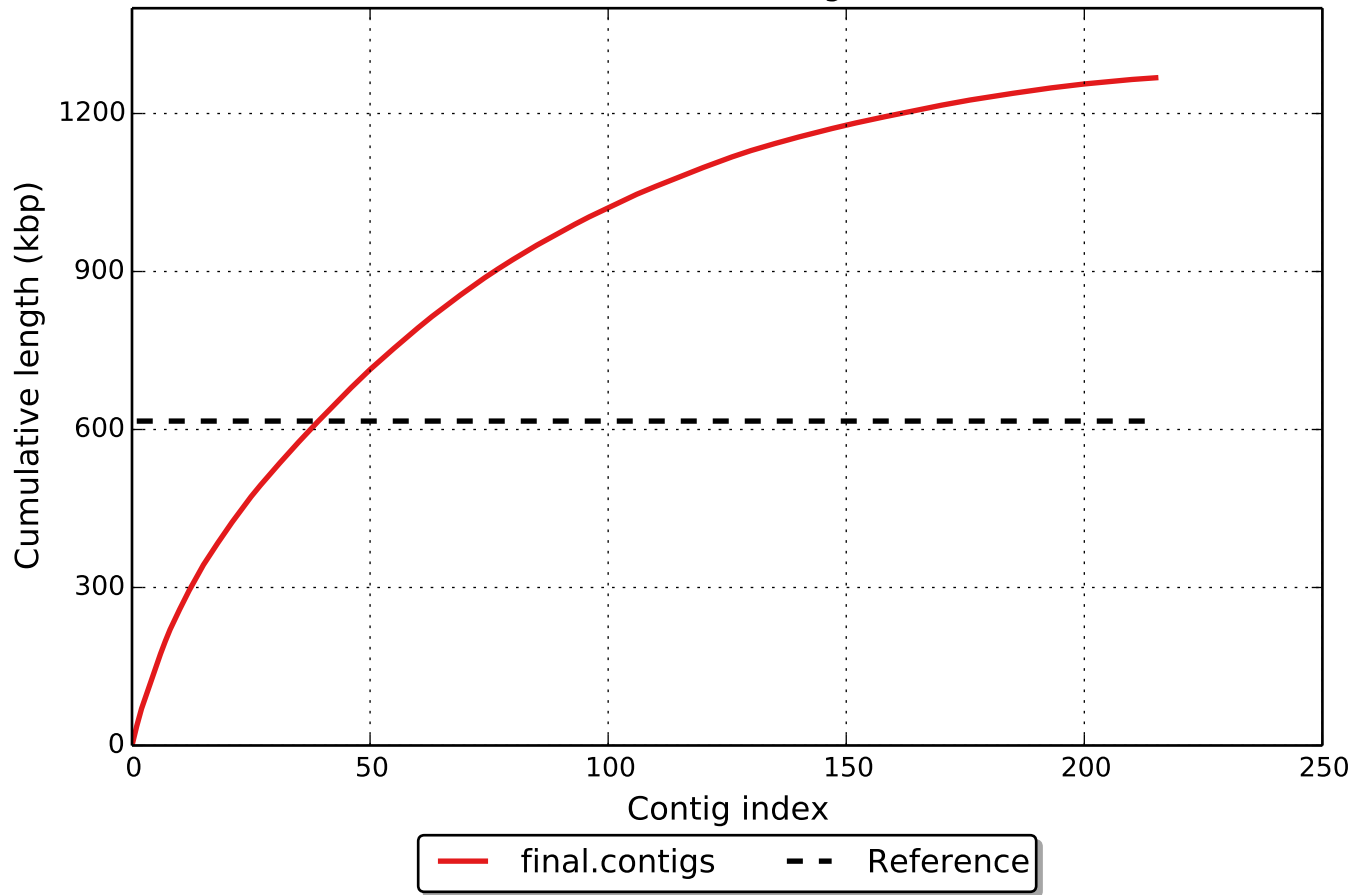
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

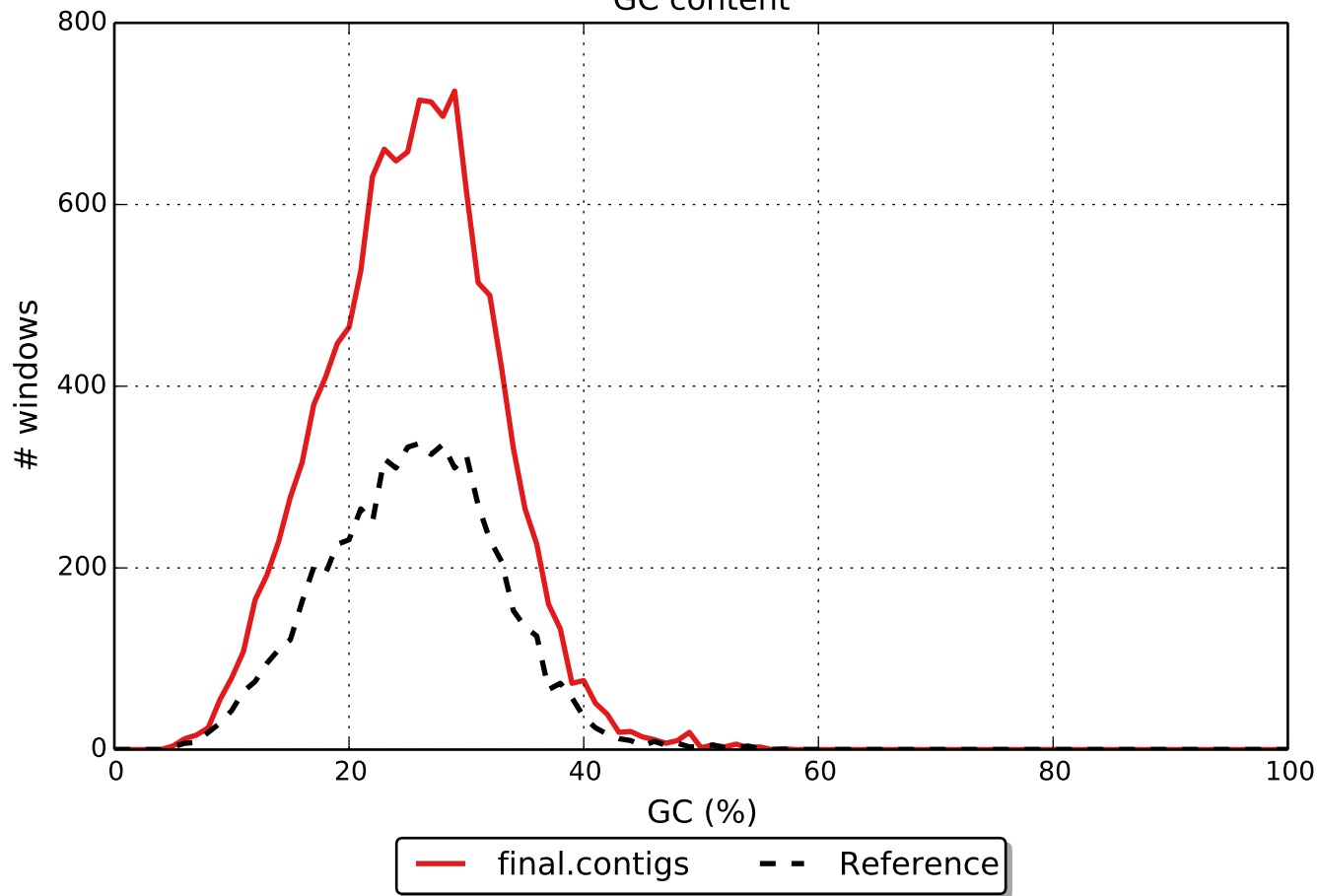
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 70            |
| Fully unaligned length        | 382062        |
| # partially unaligned contigs | 22            |
| # with misassembly            | 2             |
| # both parts are significant  | 16            |
| Partially unaligned length    | 172352        |
| # N's                         | 0             |

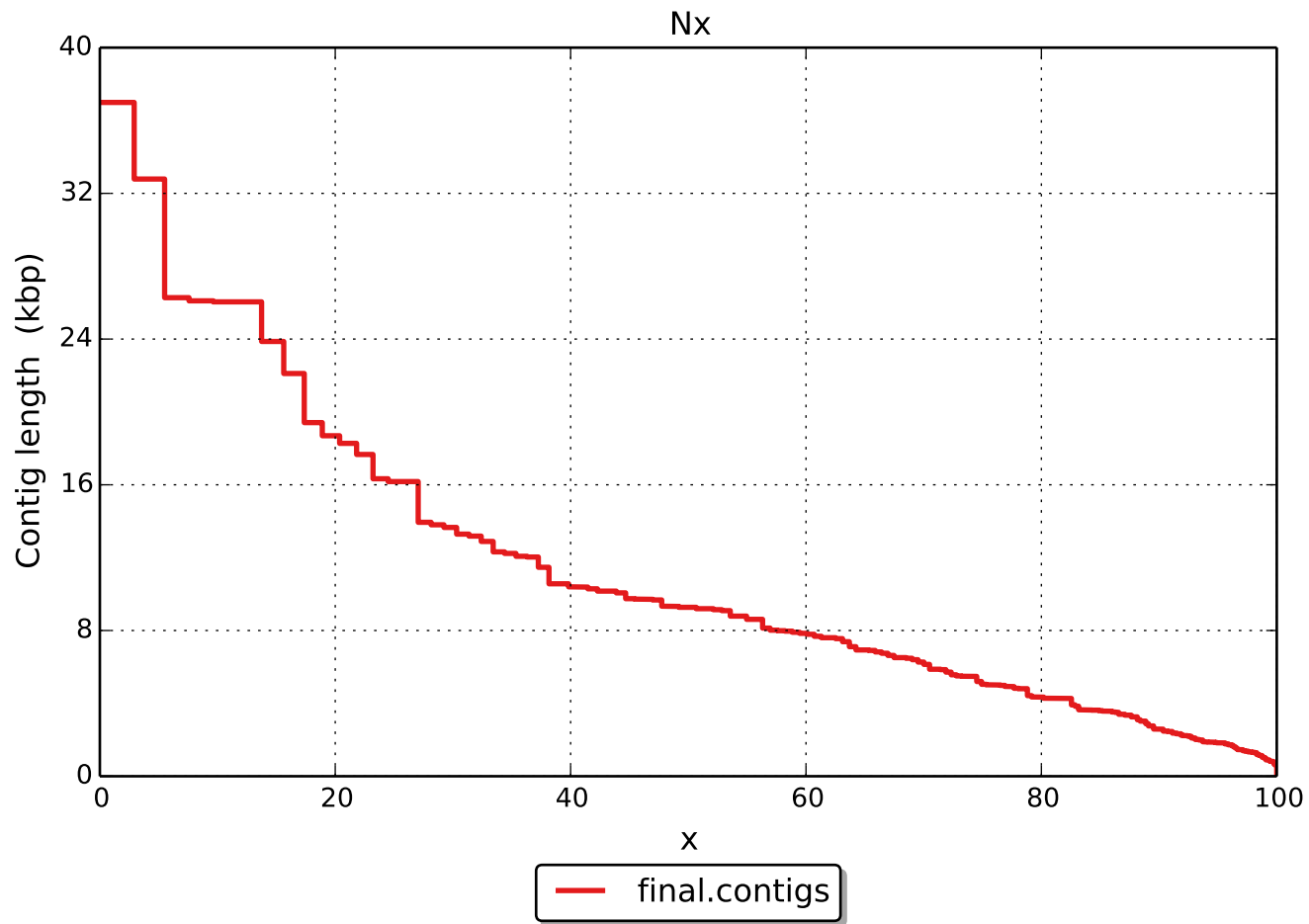
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

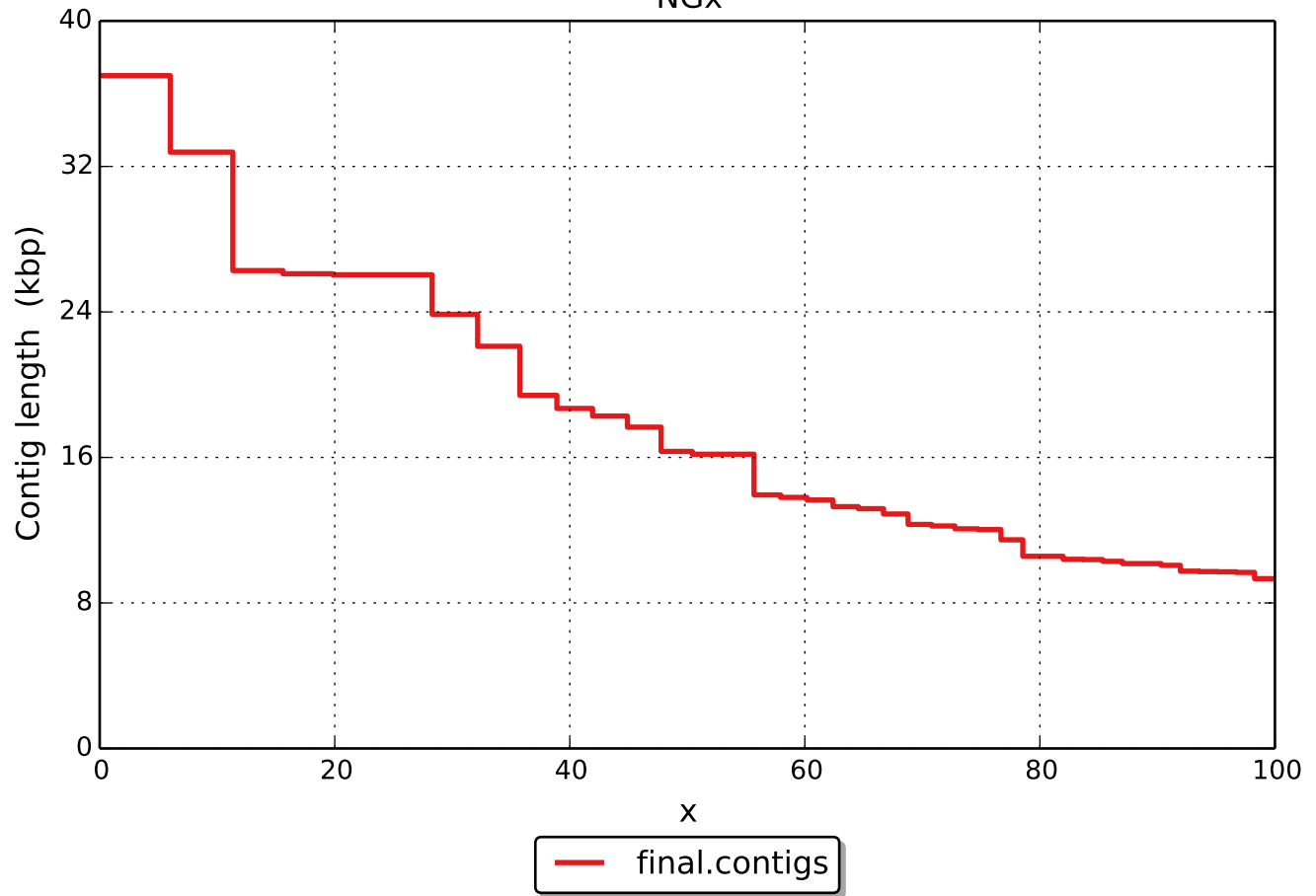


GC content





NGx

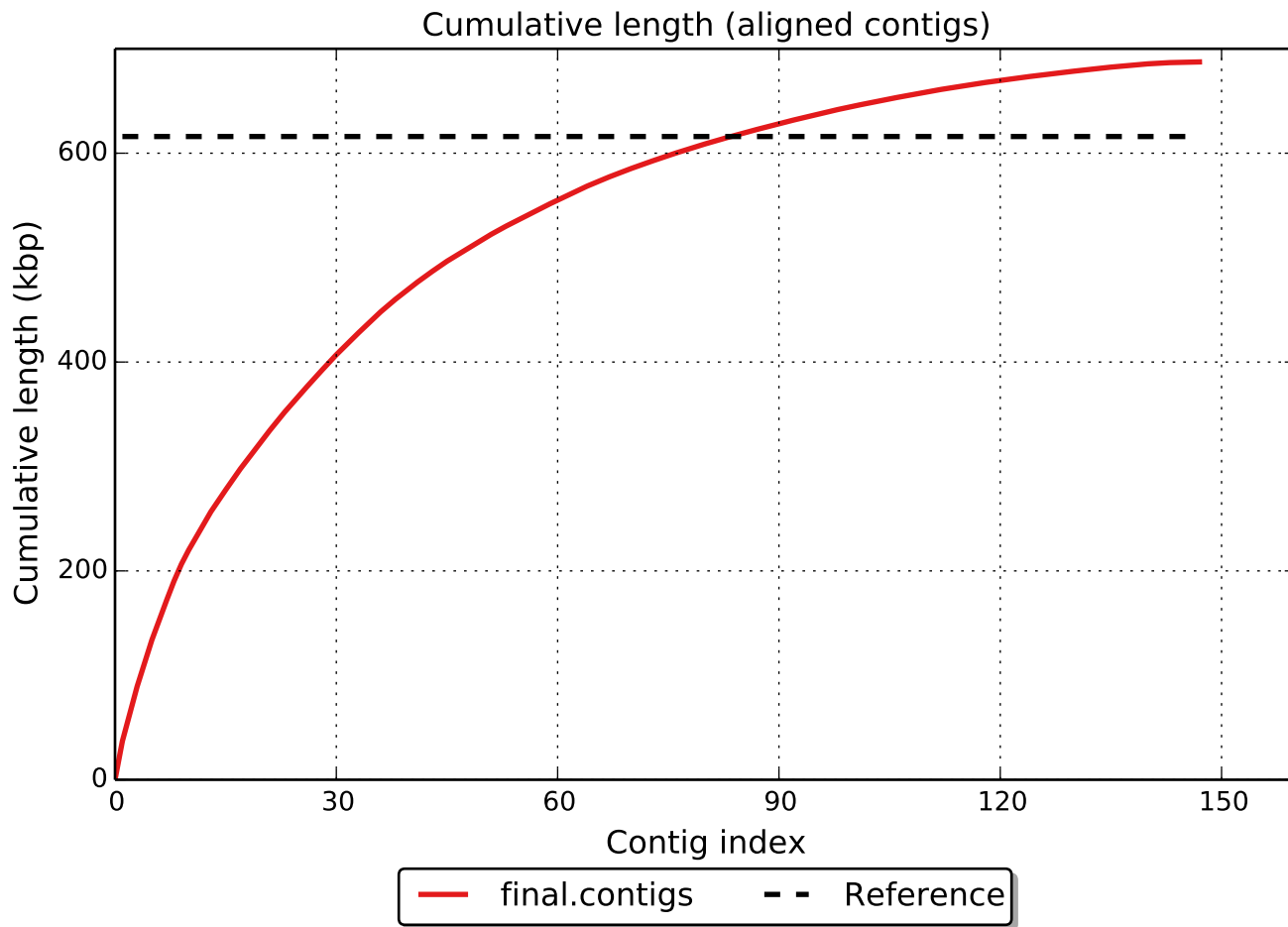


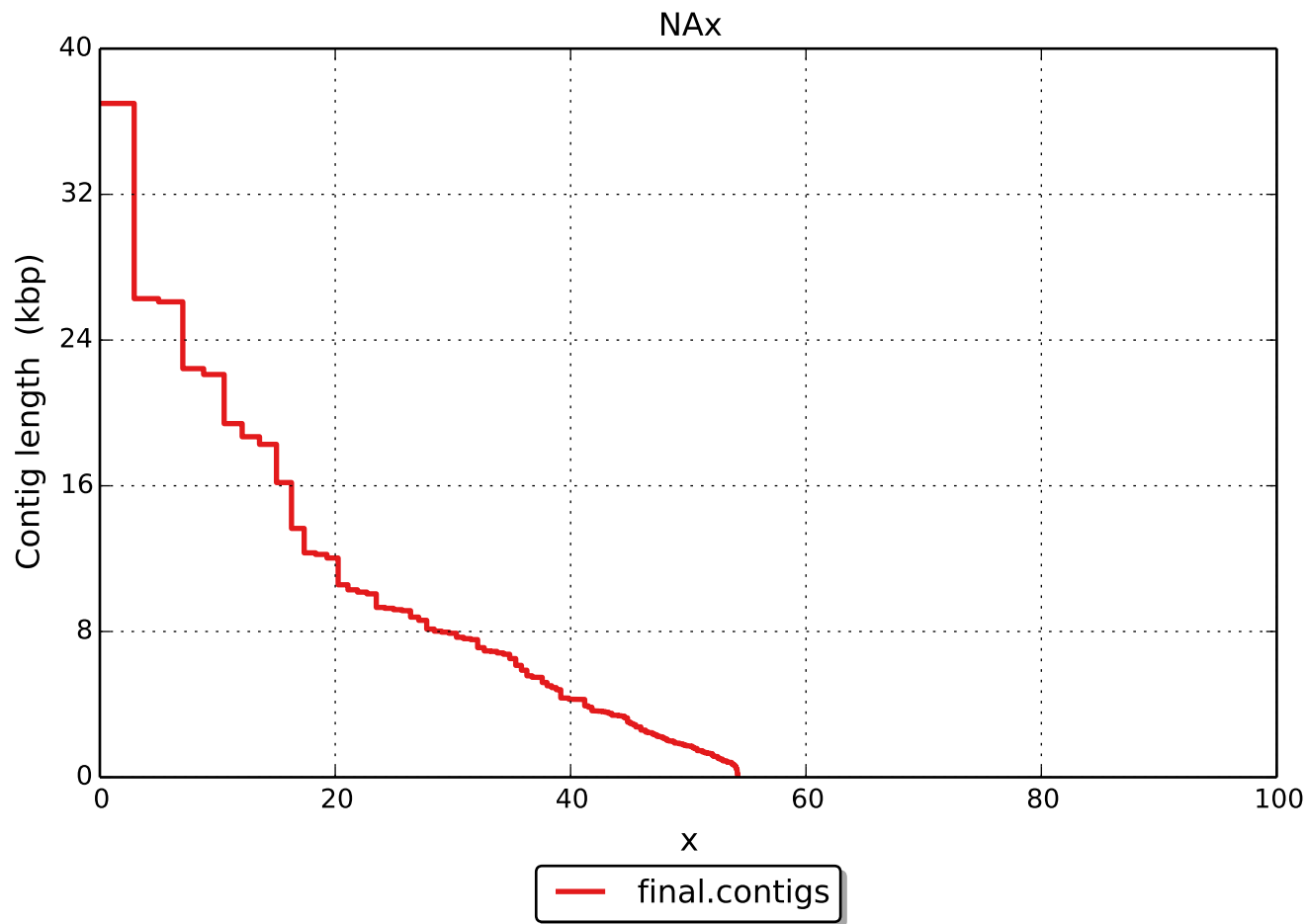
# Misassemblies



 # relocations







NGAx

