# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 10511 |
| # contigs (>= 1000 bp) | 4157 |
| Total length (>= 0 bp) | 11202559 |
| Total length (>= 1000 bp) | 7652287 |
| # contigs | 7654 |
| Largest contig | 6941 |
| Total length | 10201188 |
| Reference length | 10957366 |
| GC (%) | 50.37 |
| Reference GC (%) | 50.49 |
| N50 | 1567 |
| NG50 | 1467 |
| N75 | 1000 |
| NG75 | 897 |
| L50 | 2120 |
| LG50 | 2370 |
| L75 | 4156 |
| LG75 | 4756 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 89.348 |
| Duplication ratio | 1.042 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 38.06 |
| # indels per 100 kbp | 0.04 |
| Largest alignment | 6941 |
| NA50 | 1567 |
| NGA50 | 1467 |
| NA75 | 1000 |
| NGA75 | 897 |
| LA50 | 2120 |
| LGA50 | 2370 |
| LA75 | 4156 |
| LGA75 | 4756 |

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).
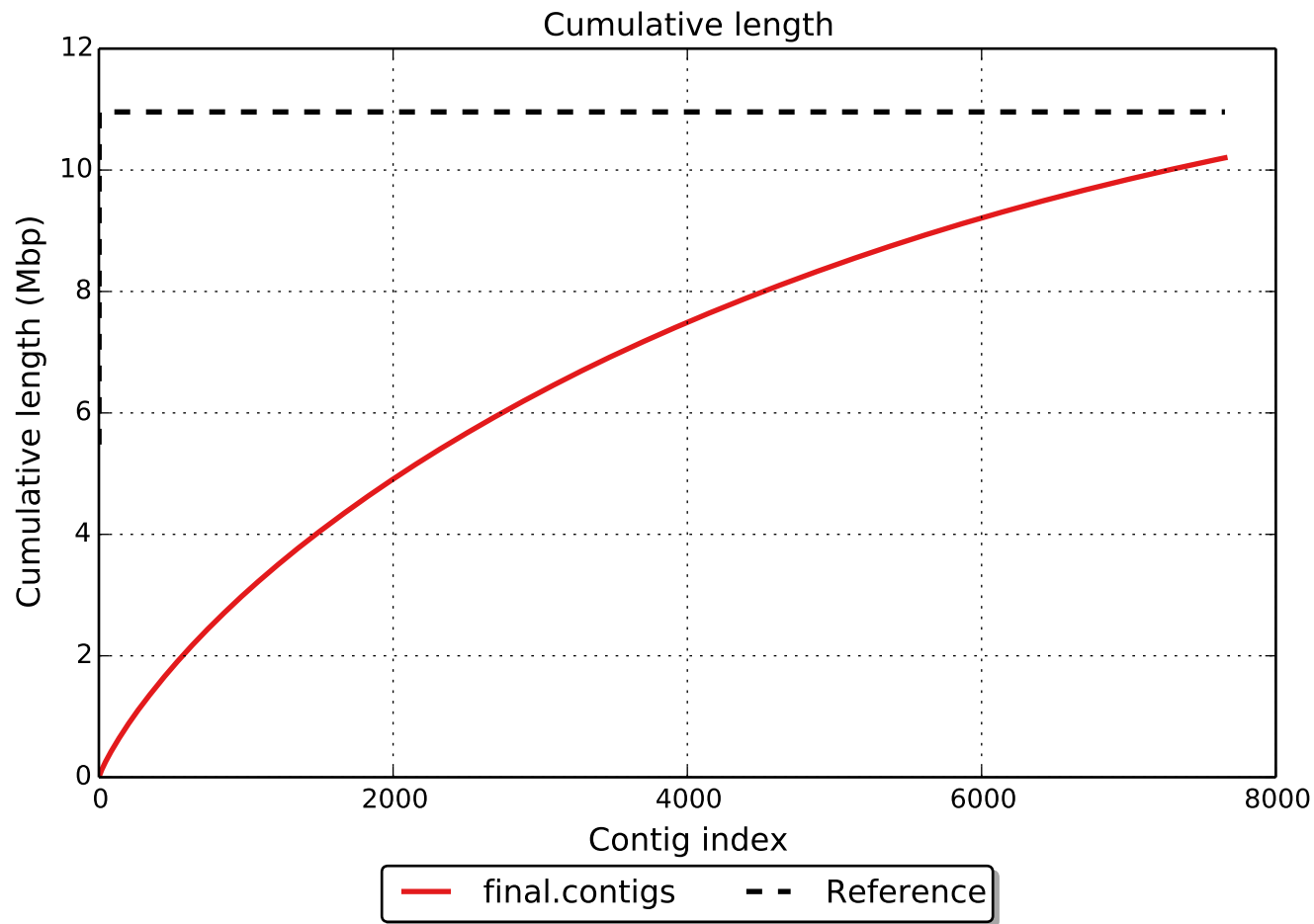
# Misassemblies report

| | 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 | 3726 |
| # indels | 4 |
| # short indels | 3 |
| # long indels | 1 |
| Indels length | 11 |

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
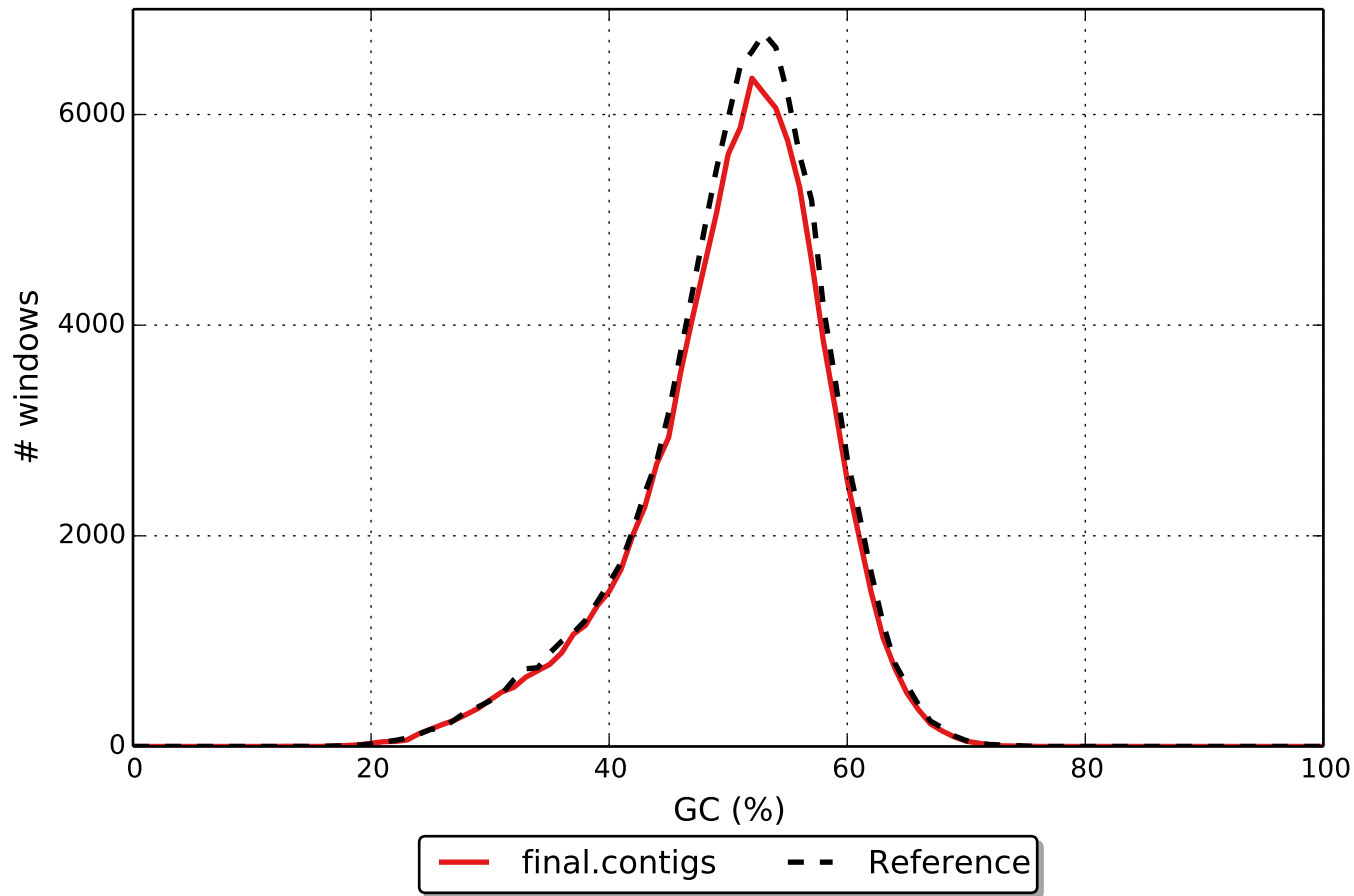(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
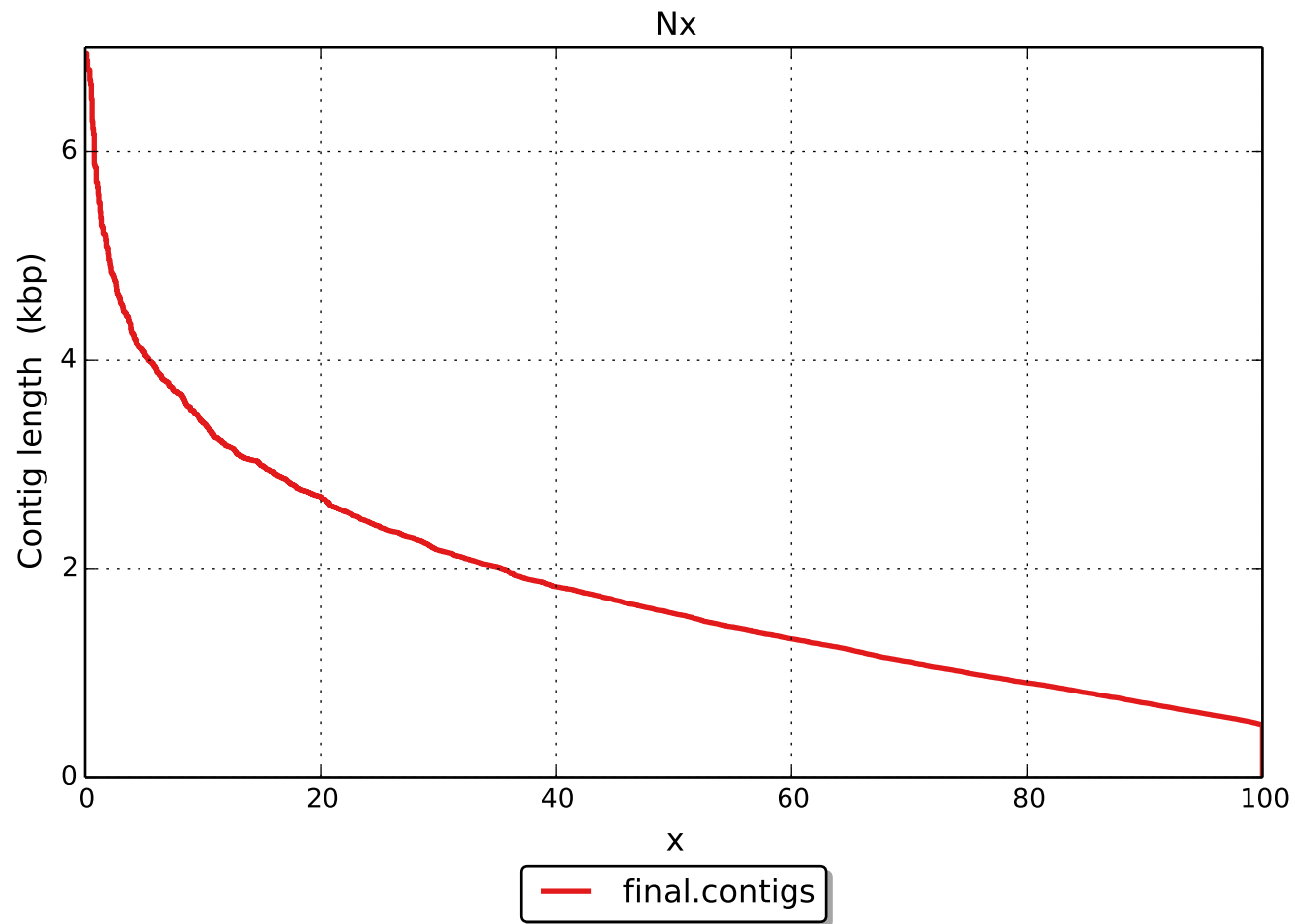
# Unaligned report

| | 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 >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
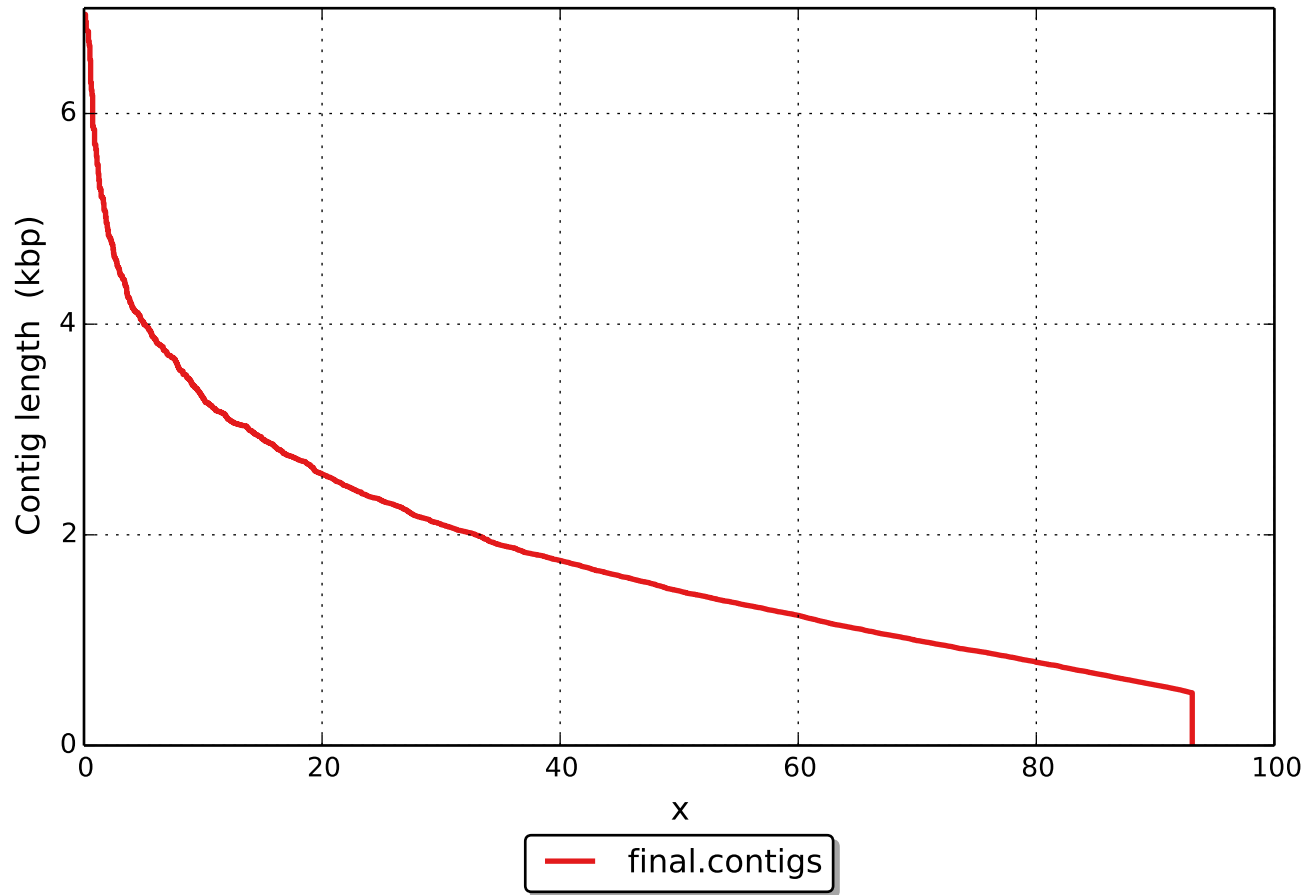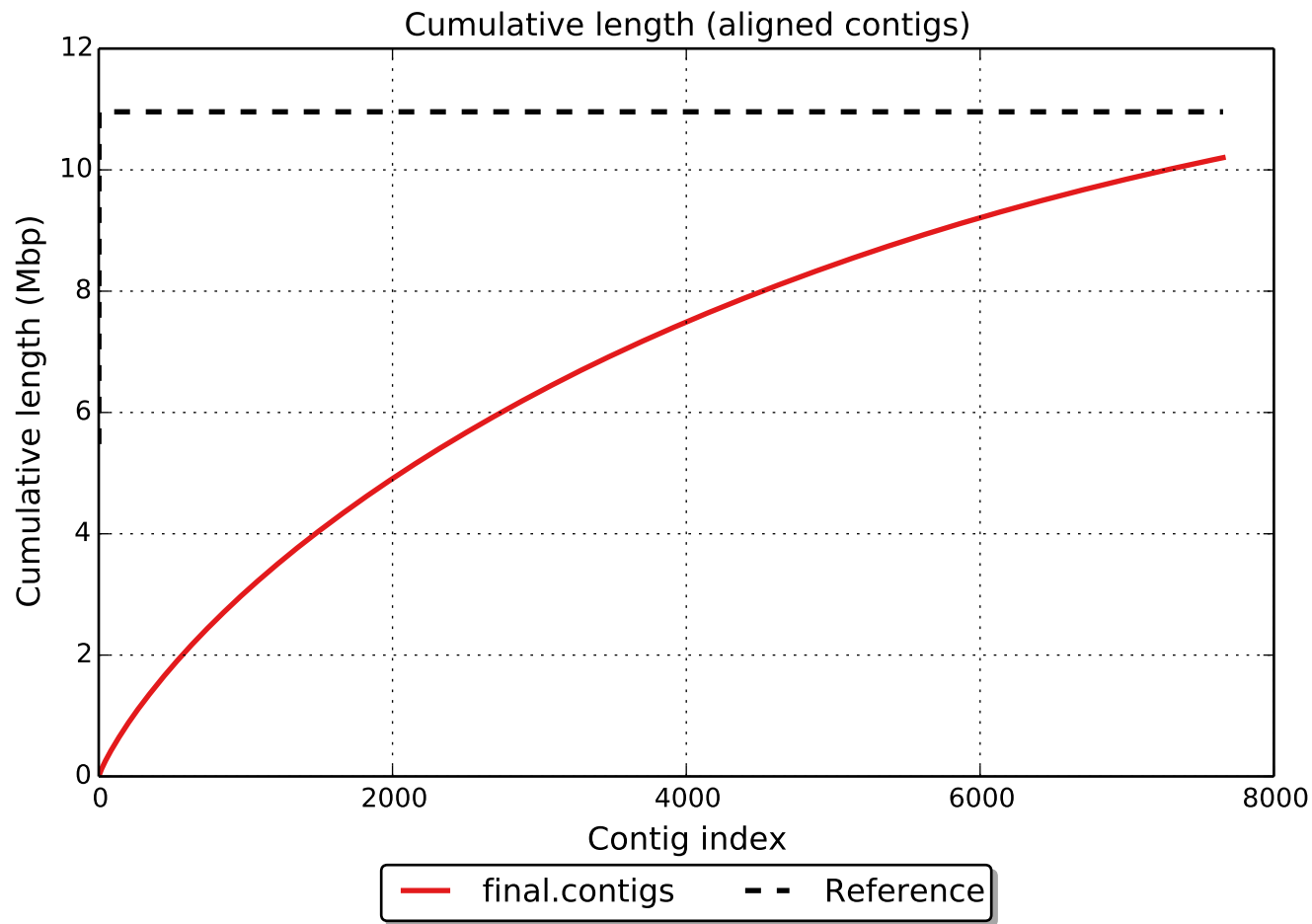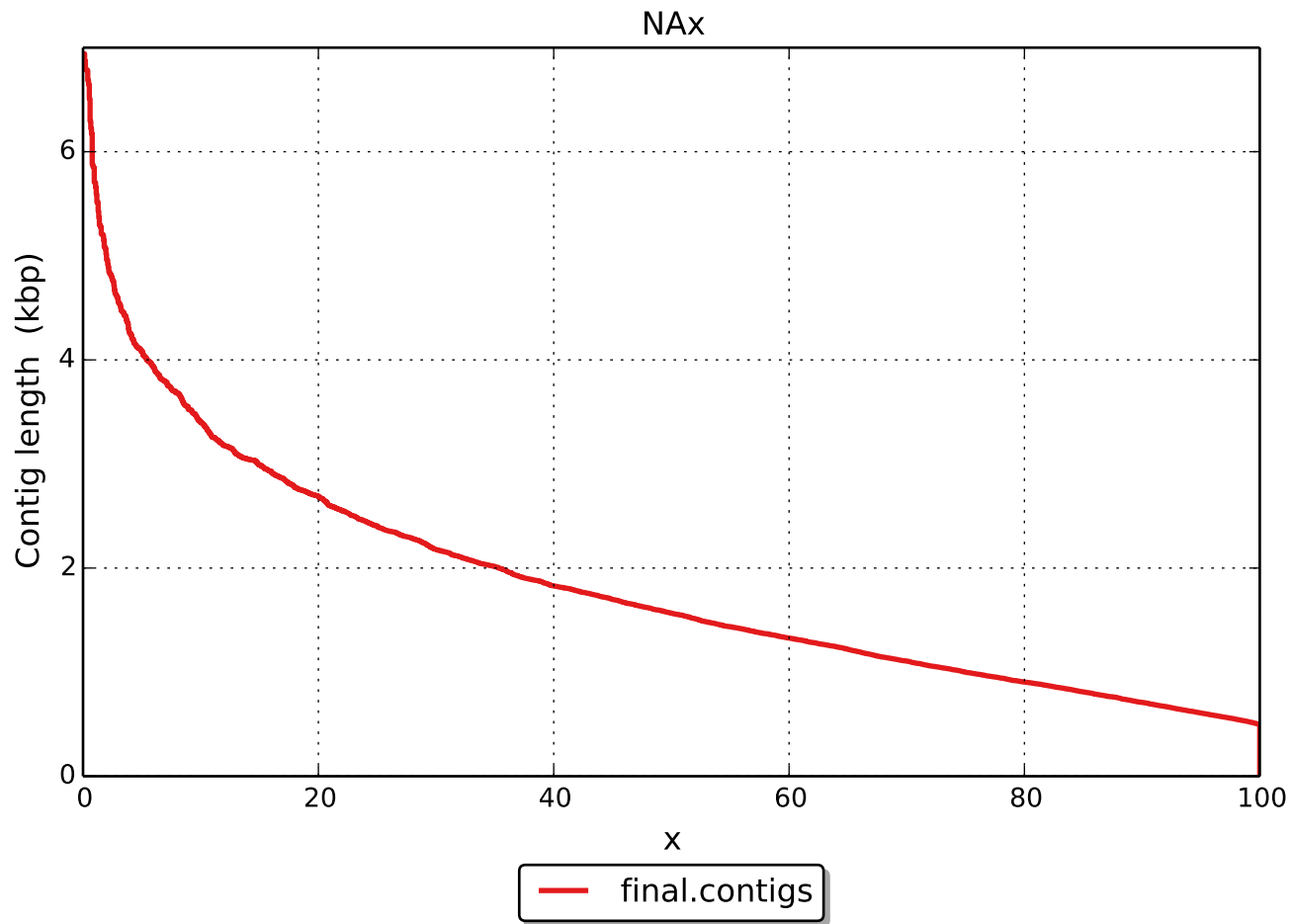
Cumulative length

GC content

# windows

GC (%)

— final.contigs  - - - Reference

# Misassemblies

final.contigs

Cumulative length (aligned contigs)