# Report

| | final.contigs |
|---|---:|
| # contigs (>= 1000 bp) | 1415 |
| # contigs (>= 5000 bp) | 251 |
| # contigs (>= 10000 bp) | 29 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 4605243 |
| Total length (>= 5000 bp) | 1796369 |
| Total length (>= 10000 bp) | 342357 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1765 |
| Largest contig | 17106 |
| Total length | 4862807 |
| Reference length | 4857432 |
| GC (%) | 52.19 |
| Reference GC (%) | 52.22 |
| N50 | 3849 |
| NG50 | 3849 |
| N75 | 2241 |
| NG75 | 2242 |
| L50 | 397 |
| LG50 | 397 |
| L75 | 804 |
| LG75 | 802 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 9233 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 97.507 |
| Duplication ratio | 1.027 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 9.44 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 17106 |
| NA50 | 3838 |
| NGA50 | 3849 |
| NA75 | 2241 |
| NGA75 | 2242 |
| LA50 | 398 |
| LGA50 | 397 |
| LA75 | 804 |
| LGA75 | 802 |

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).
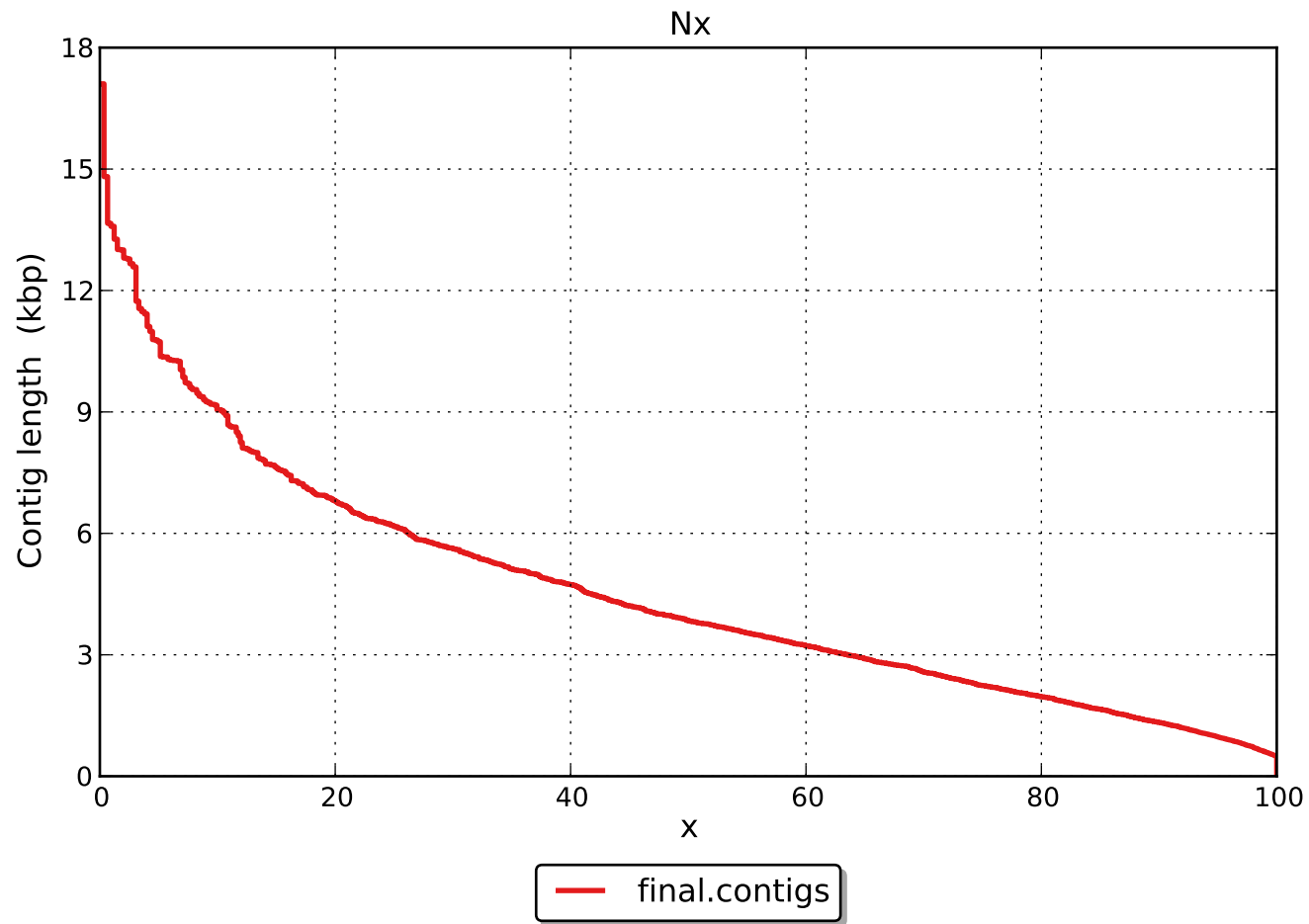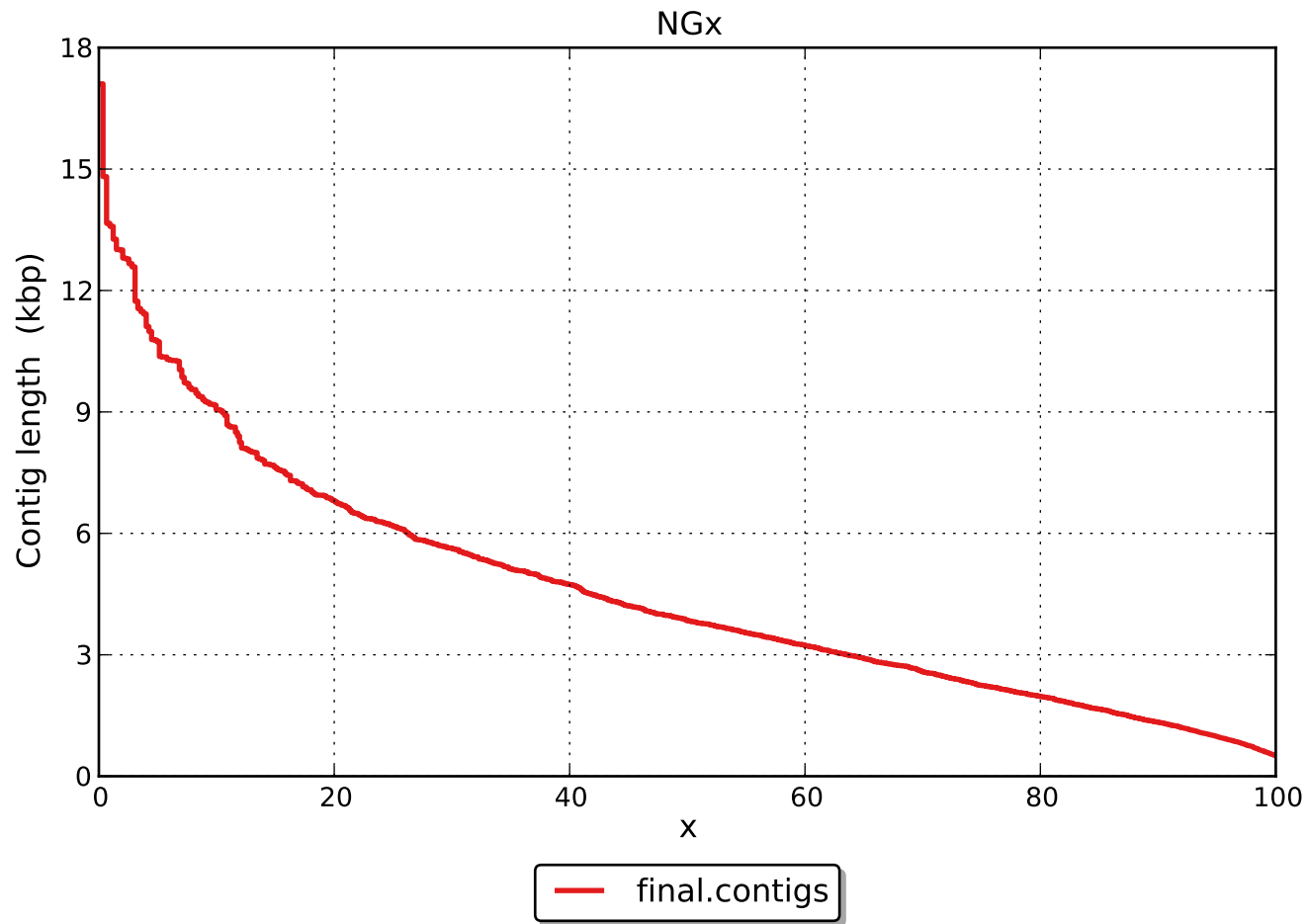
# Misassemblies report

|  | final.contigs |
|---|---|
| # misassemblies | 1 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 9233 |
| # local misassemblies | 0 |
| # mismatches | 447 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 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).

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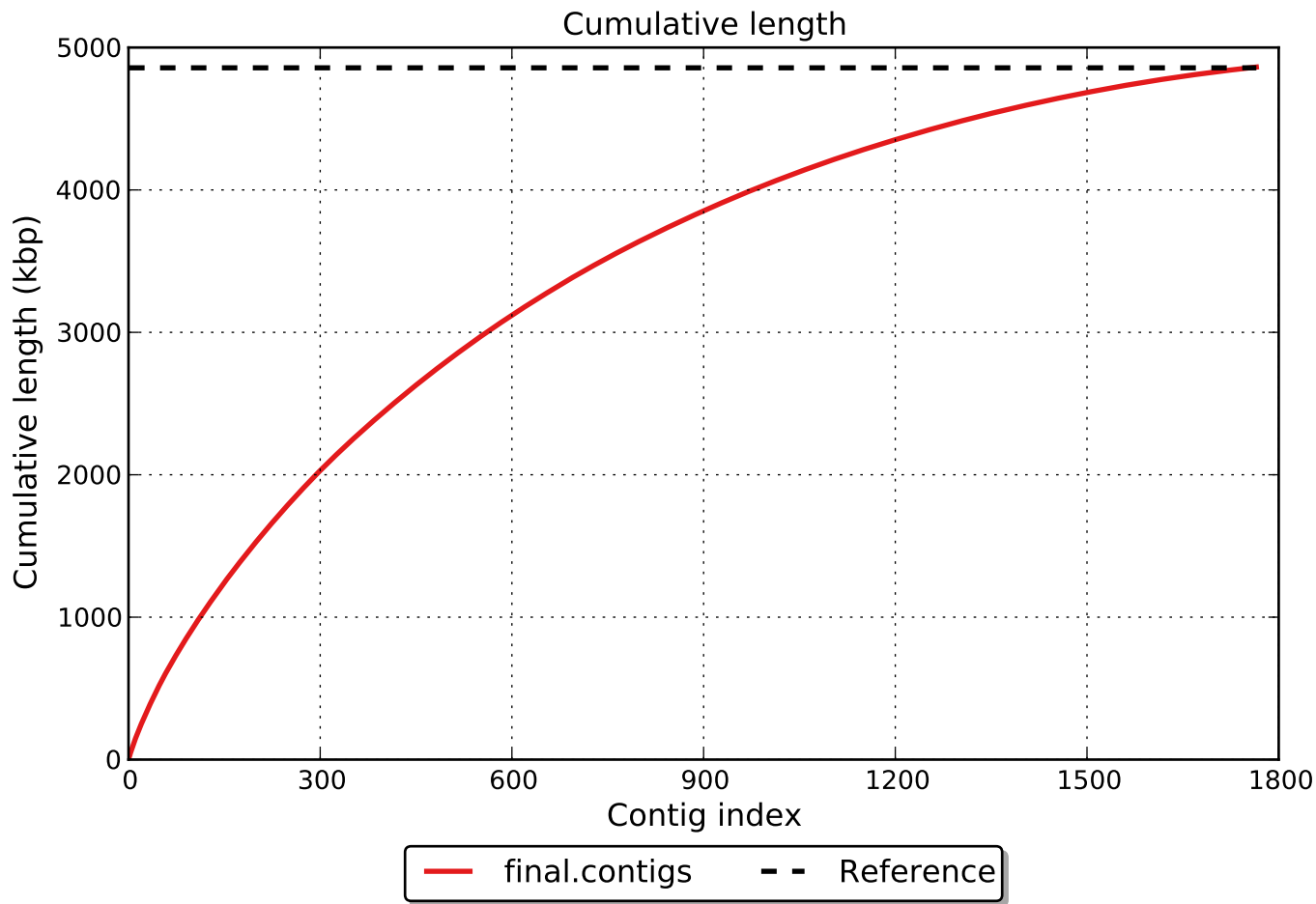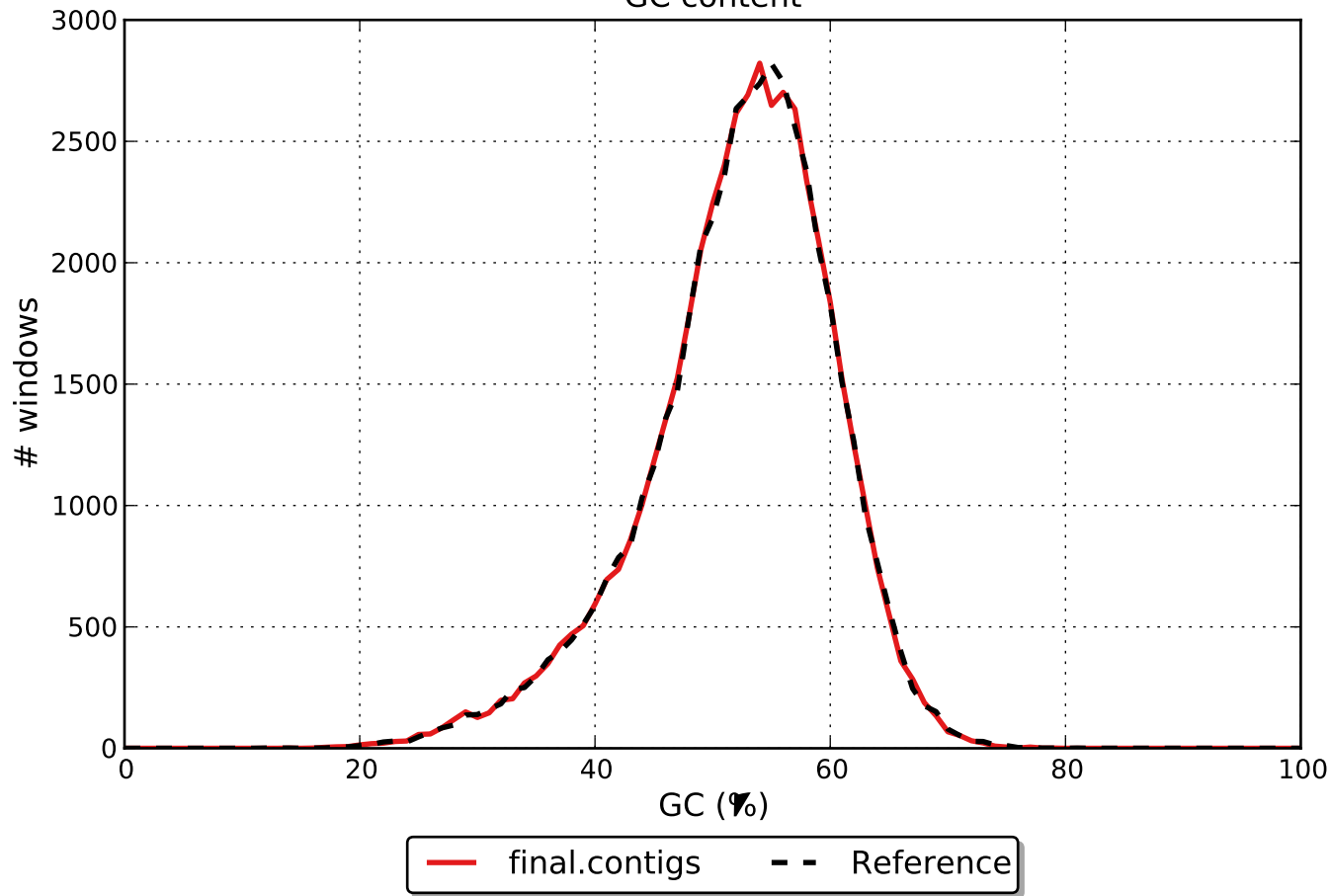
|  | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

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).

Nx

NGx

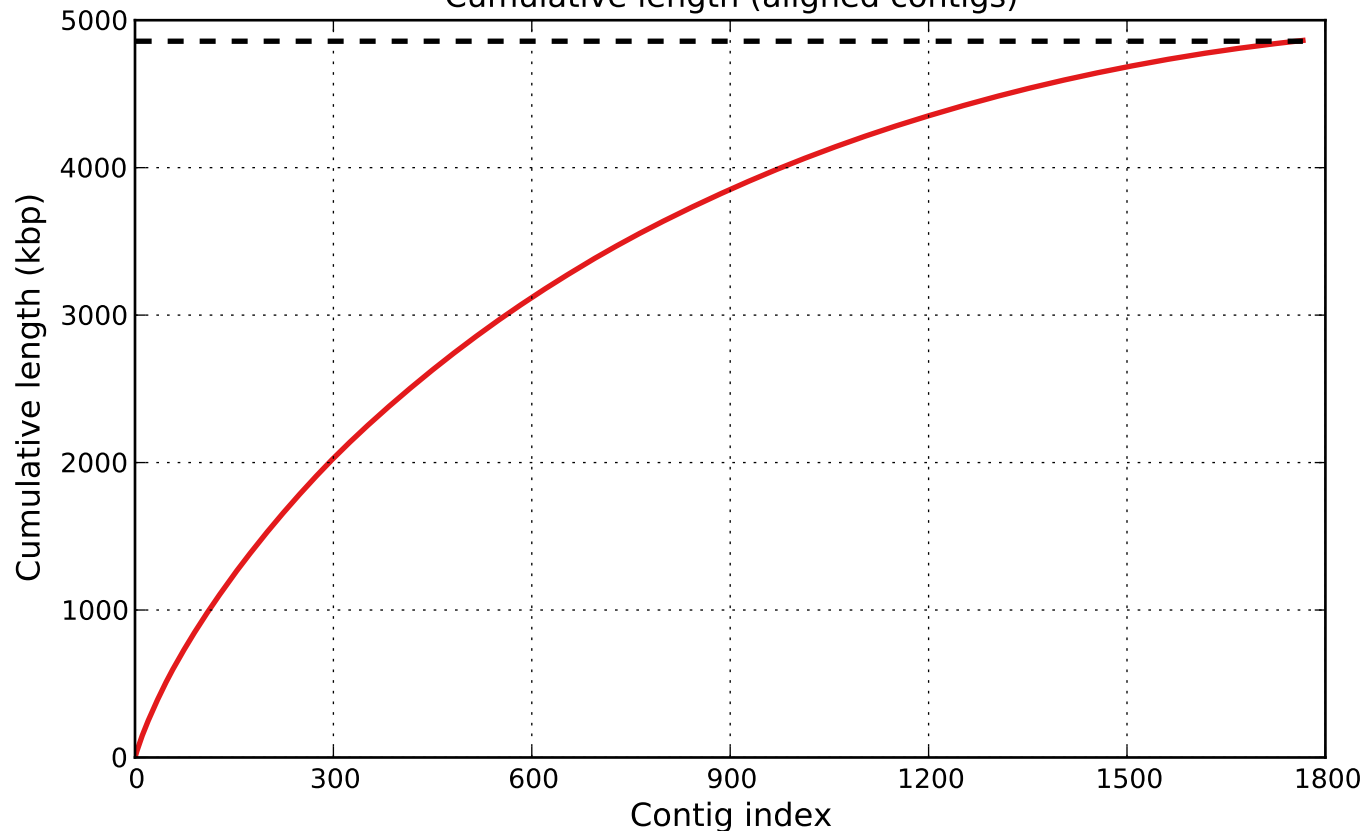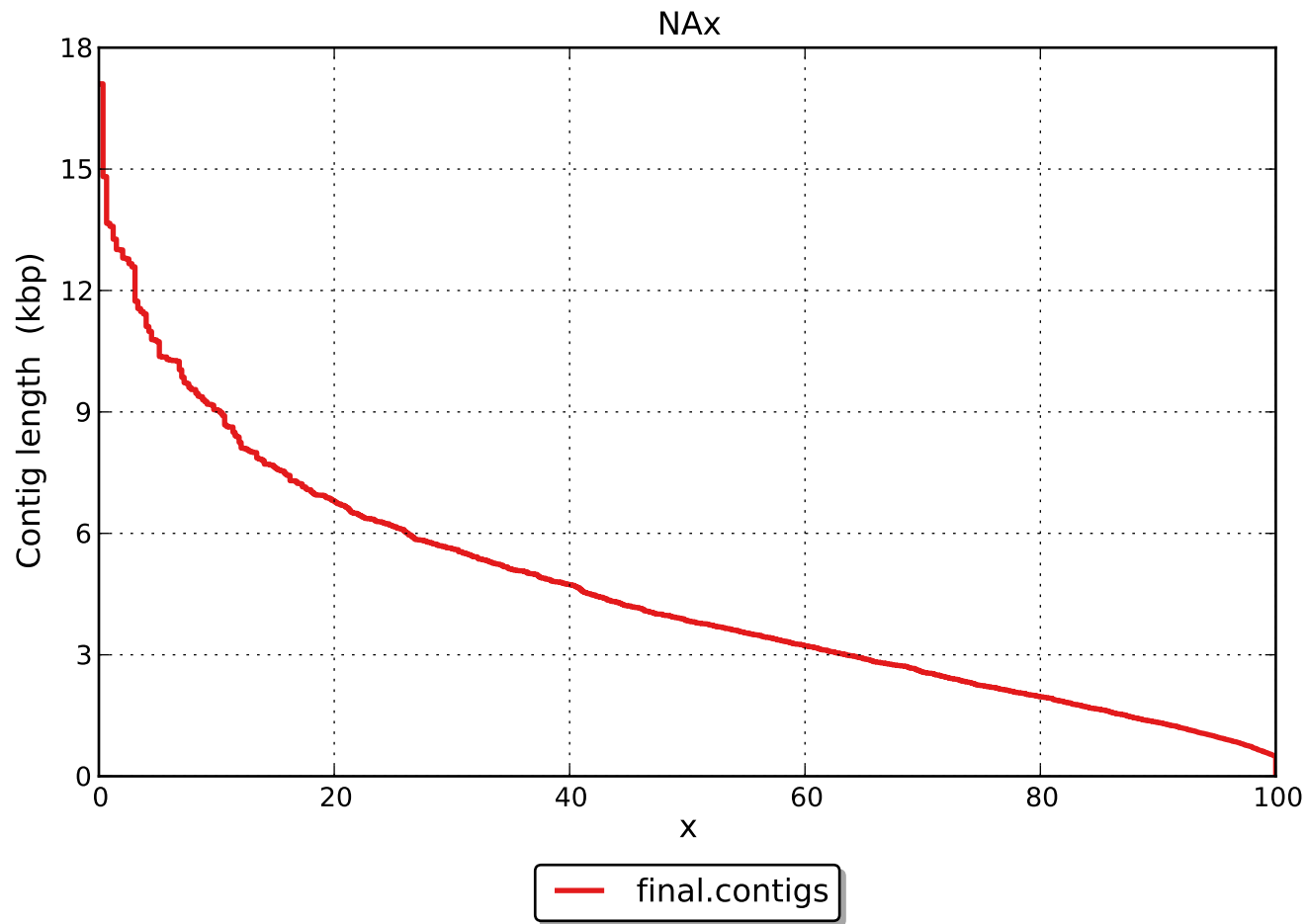final.contigs

Cumulative length

GC content

# windows

GC (%)

final.contigs — — Reference

# Misassemblies



final.contigs

# relocations

Cumulative length (aligned contigs)