# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 12122 |
| # contigs (>= 1000 bp) | 1560 |
| # contigs (>= 5000 bp) | 14 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 6709677 |
| Total length (>= 1000 bp) | 2972934 |
| Total length (>= 5000 bp) | 88998 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 2811 |
| Largest contig | 9644 |
| Total length | 3879340 |
| Reference length | 4641652 |
| GC (%) | 50.83 |
| Reference GC (%) | 50.79 |
| N50 | 1672 |
| NG50 | 1390 |
| N75 | 1032 |
| NG75 | 724 |
| L50 | 755 |
| LG50 | 1005 |
| L75 | 1498 |
| LG75 | 2153 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 39 + 0 part |
| Unaligned length | 20817 |
| Genome fraction (%) | 82.161 |
| Duplication ratio | 1.012 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.08 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 9644 |
| NA50 | 1672 |
| NGA50 | 1390 |
| NA75 | 1032 |
| NGA75 | 724 |
| LA50 | 755 |
| LGA50 | 1005 |
| LA75 | 1498 |
| LGA75 | 2153 |

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).
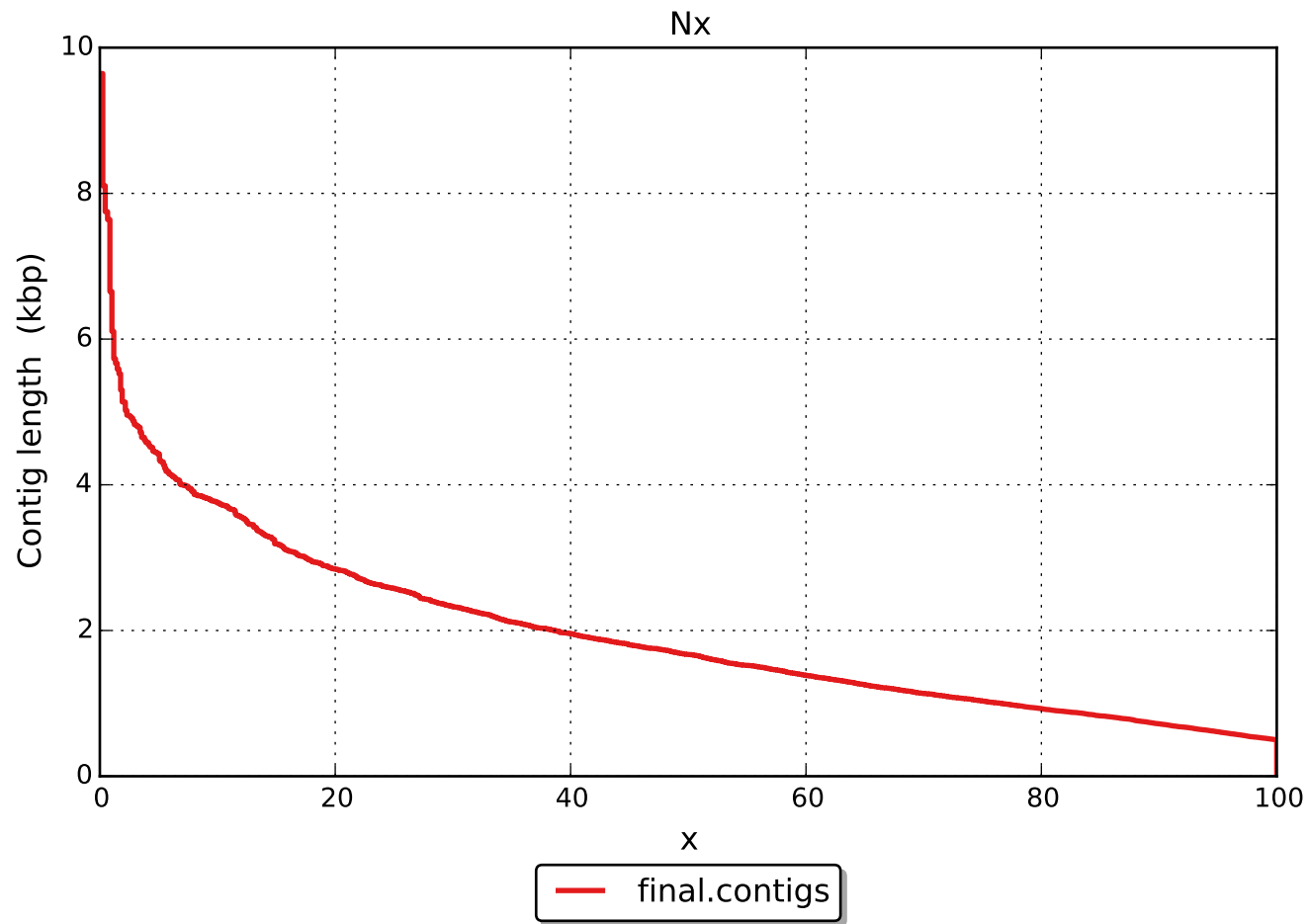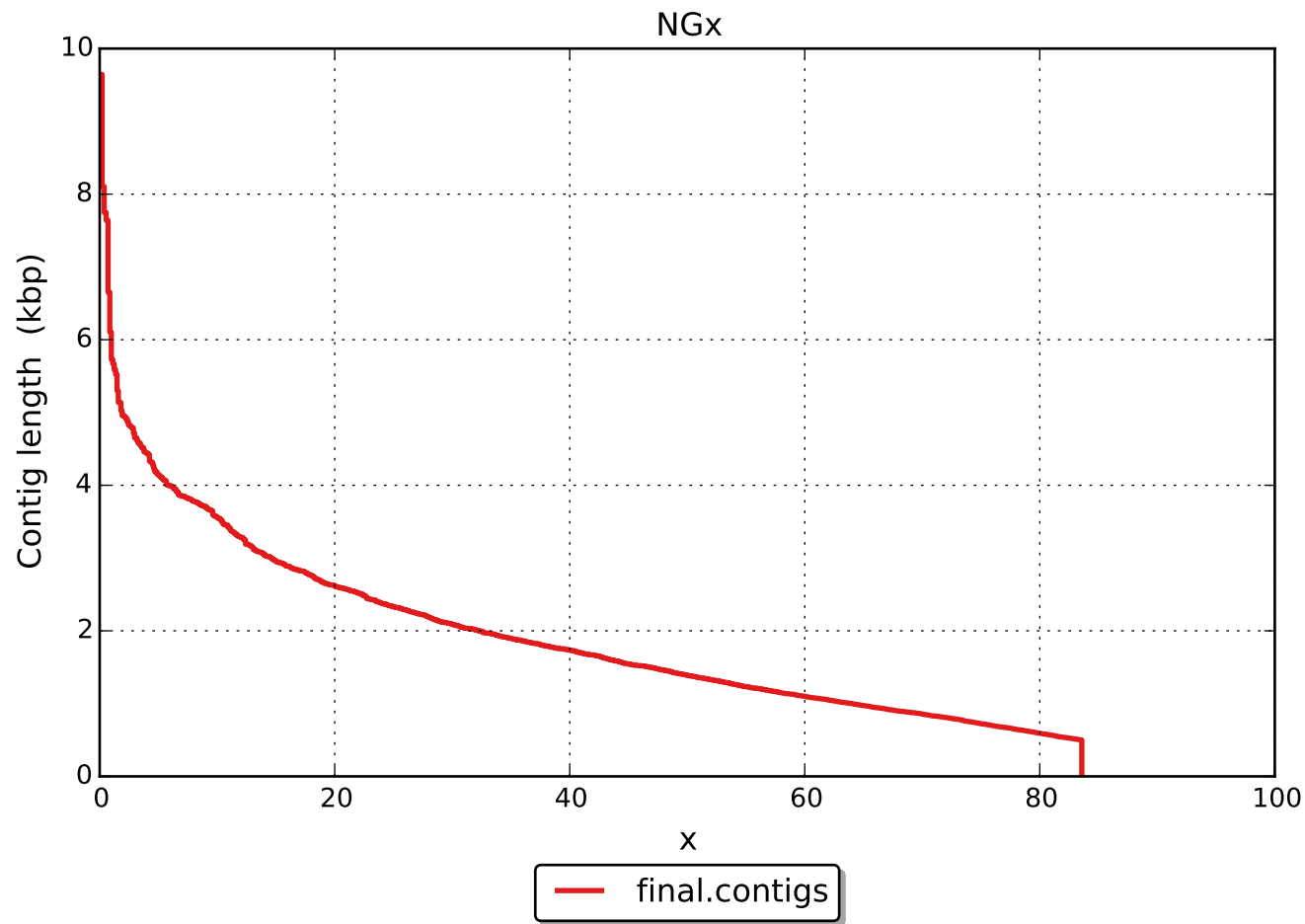
# Misassemblies report

| | final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 3 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

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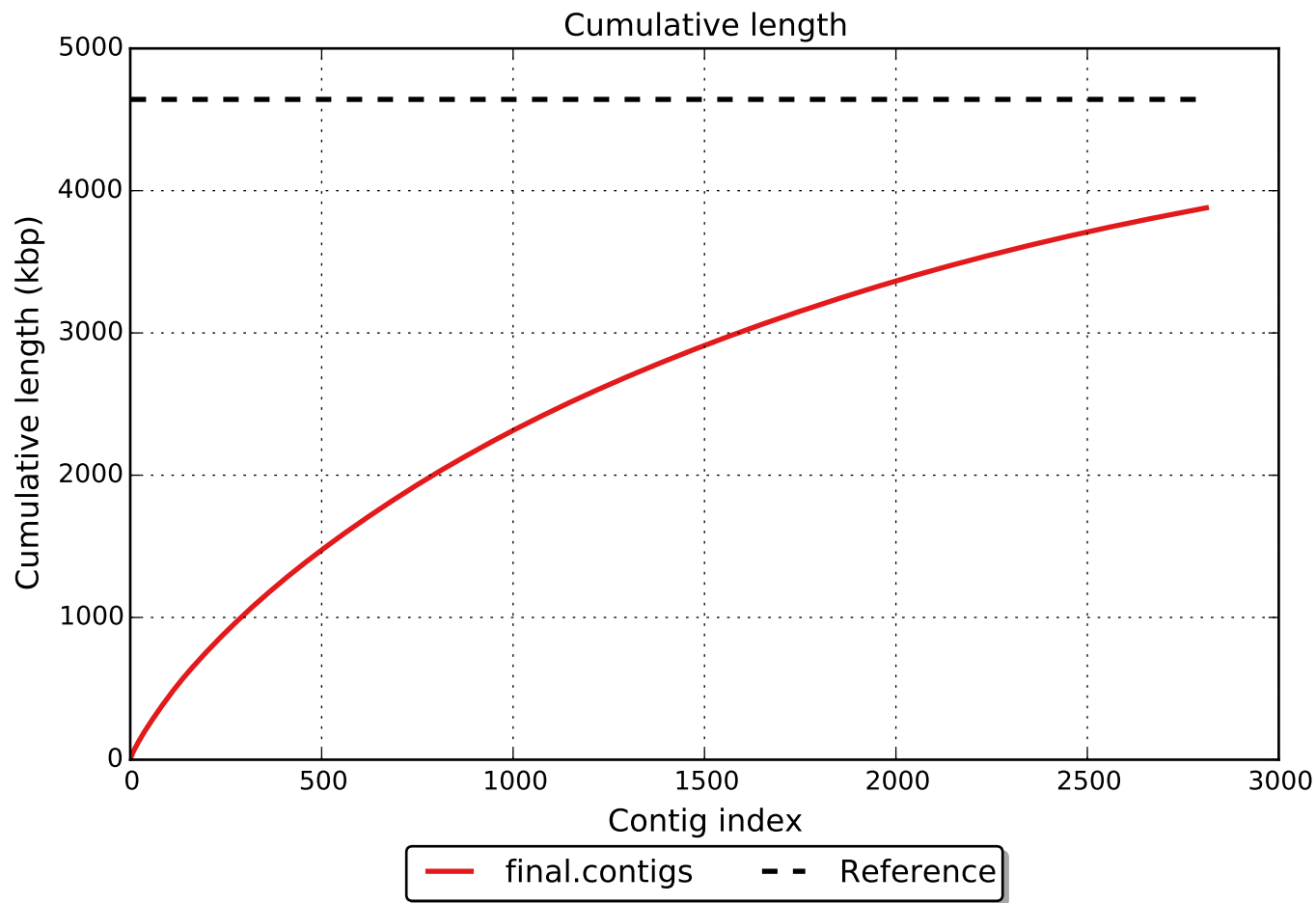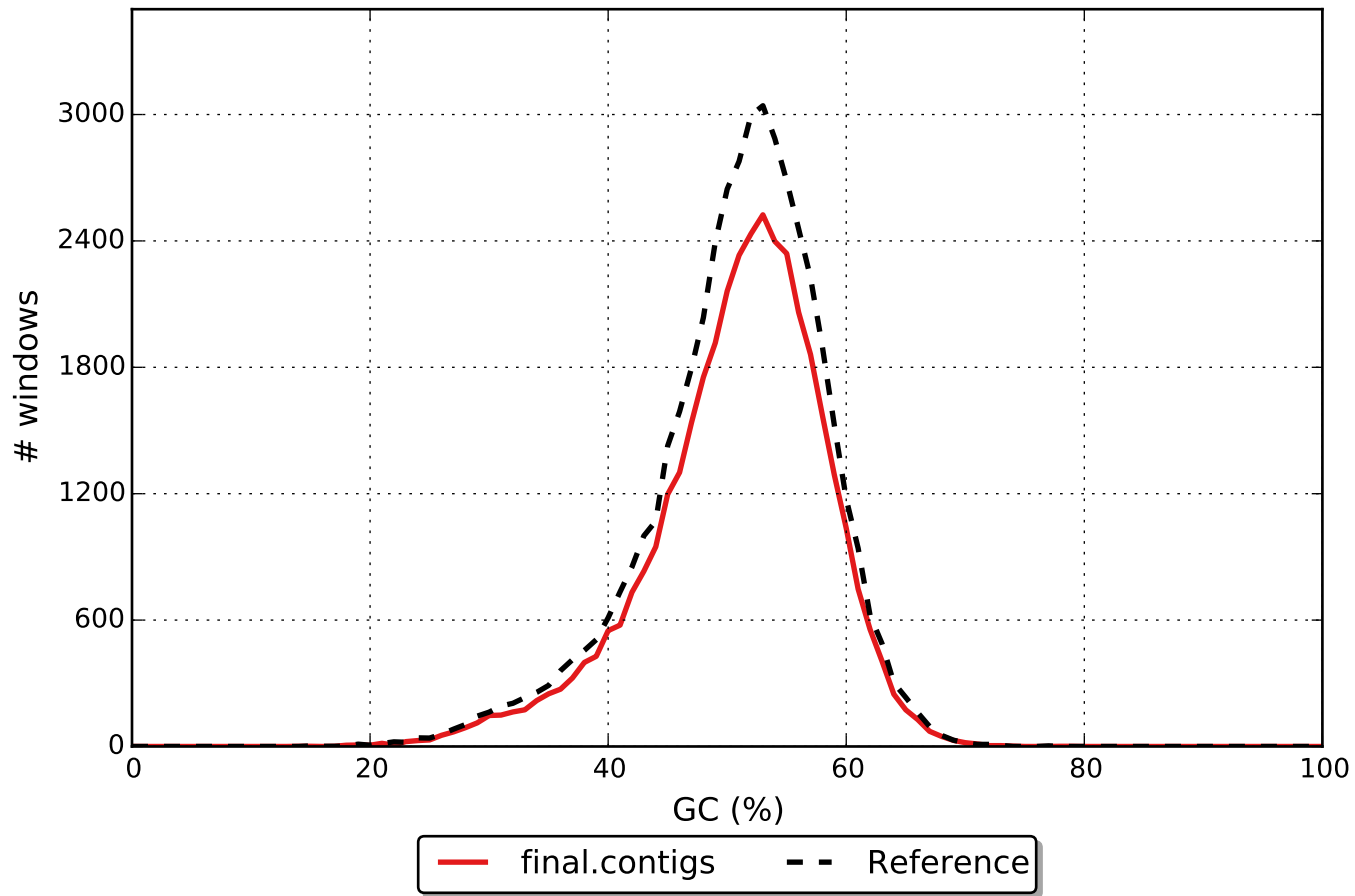(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

# Unaligned report

|  | final.contigs |
|---|---|
| # fully unaligned contigs | 39 |
| Fully unaligned length | 20817 |
| # 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).
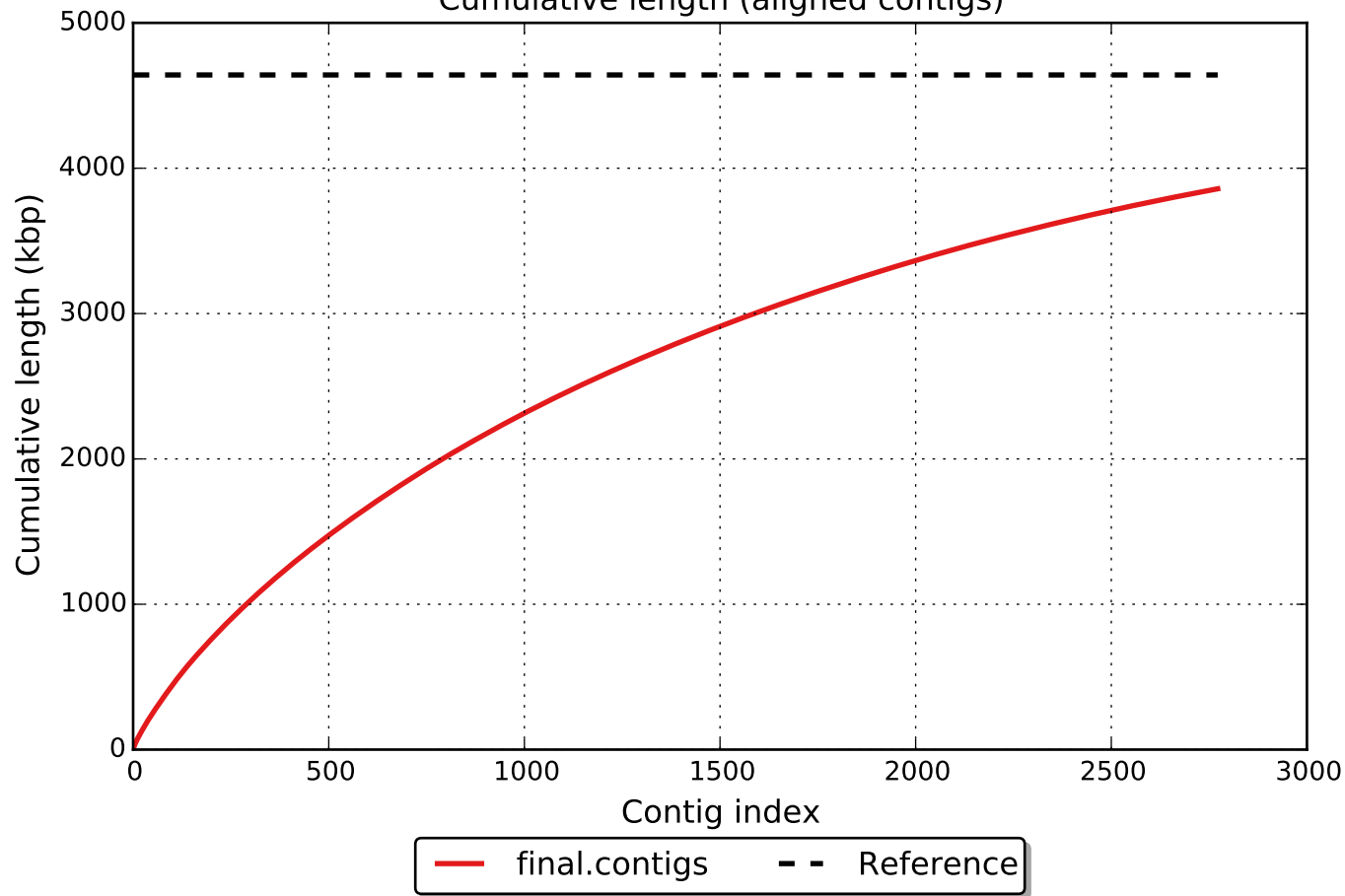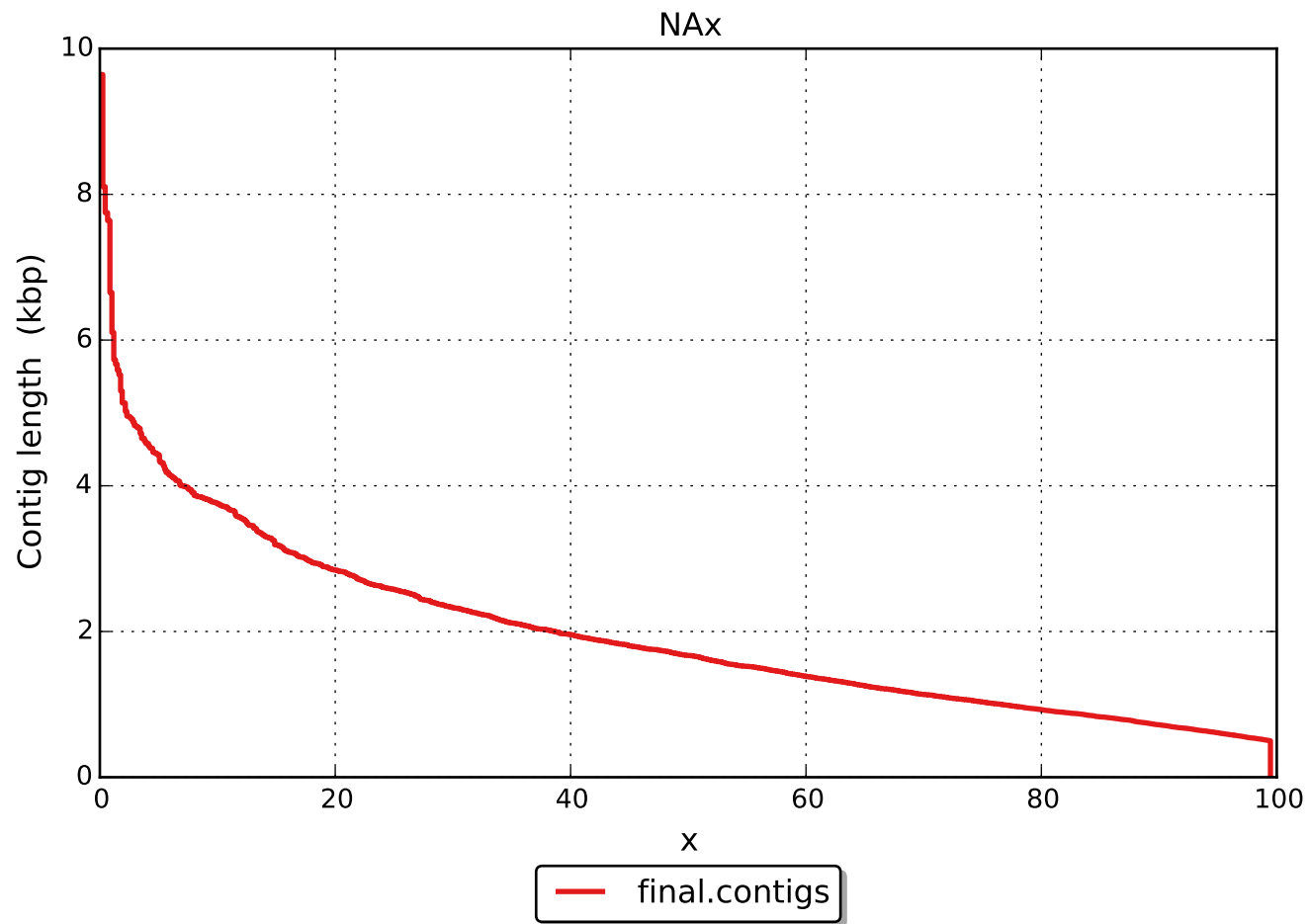
NGx

Contig length (kbp)

x

final.contigs

Cumulative length

GC content

# windows vs GC (%)

final.contigs — Reference

# Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs