# Report

| | final.contigs |
|---|---:|
| # contigs (>= 0 bp) | 1082 |
| # contigs (>= 1000 bp) | 522 |
| Total length (>= 0 bp) | 10903304 |
| Total length (>= 1000 bp) | 10700615 |
| # contigs | 617 |
| Largest contig | 168092 |
| Total length | 10764388 |
| Reference length | 11094646 |
| GC (%) | 50.40 |
| Reference GC (%) | 50.48 |
| N50 | 40236 |
| NG50 | 39095 |
| N75 | 21021 |
| NG75 | 20040 |
| L50 | 83 |
| LG50 | 87 |
| L75 | 175 |
| LG75 | 187 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 16523 |
| # local misassemblies | 3 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 96.573 |
| Duplication ratio | 1.005 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 8.73 |
| # indels per 100 kbp | 0.21 |
| Largest alignment | 168092 |
| NA50 | 40236 |
| NGA50 | 39095 |
| NA75 | 21021 |
| NGA75 | 20040 |
| LA50 | 83 |
| LGA50 | 87 |
| LA75 | 175 |
| LGA75 | 187 |

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).
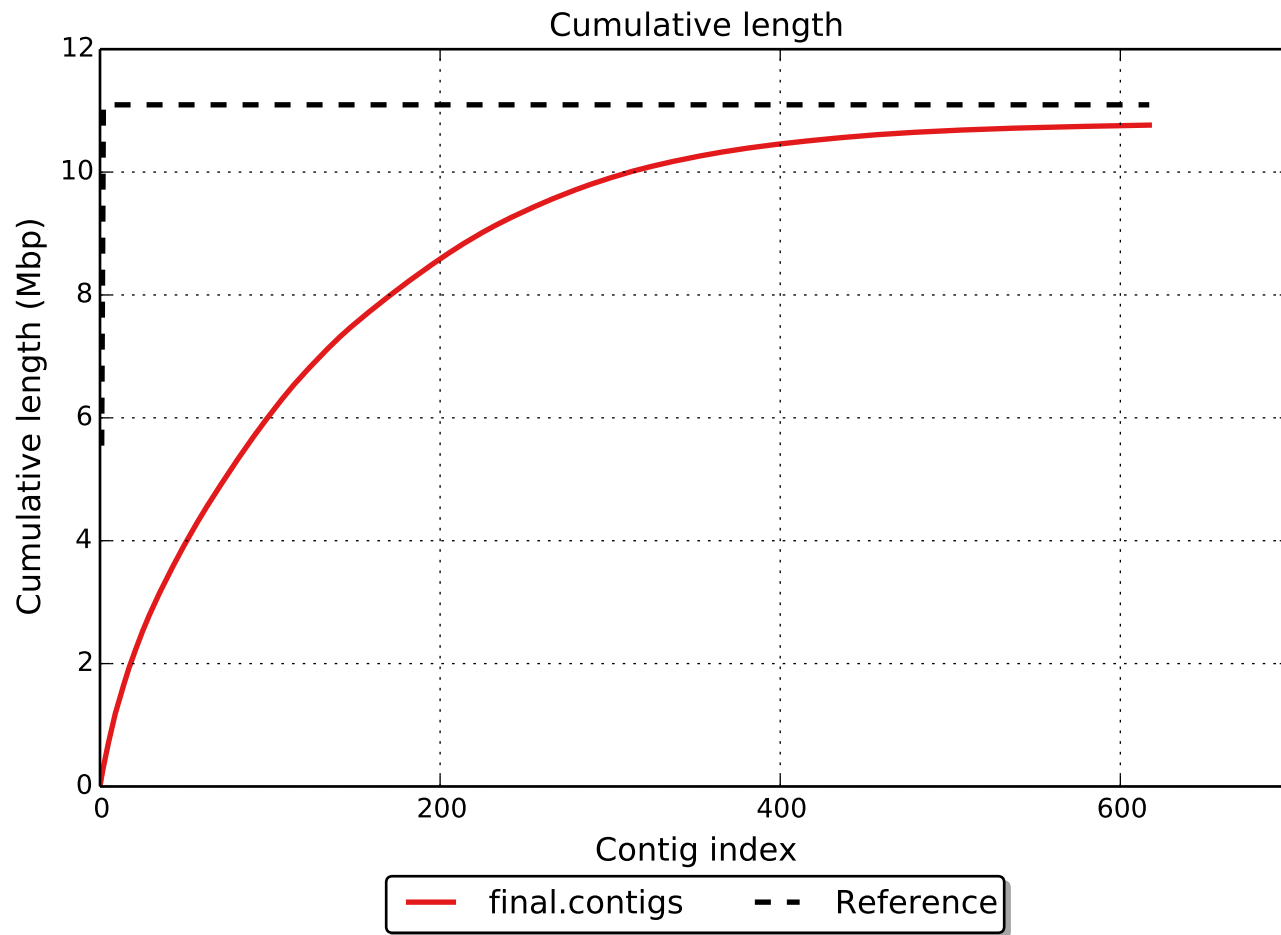
# Misassemblies report

| | final.contigs |
|---|---|
| # misassemblies | 1 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 16523 |
| # local misassemblies | 3 |
| # mismatches | 935 |
| # indels | 23 |
| # short indels | 21 |
| # long indels | 2 |
| Indels length | 35 |

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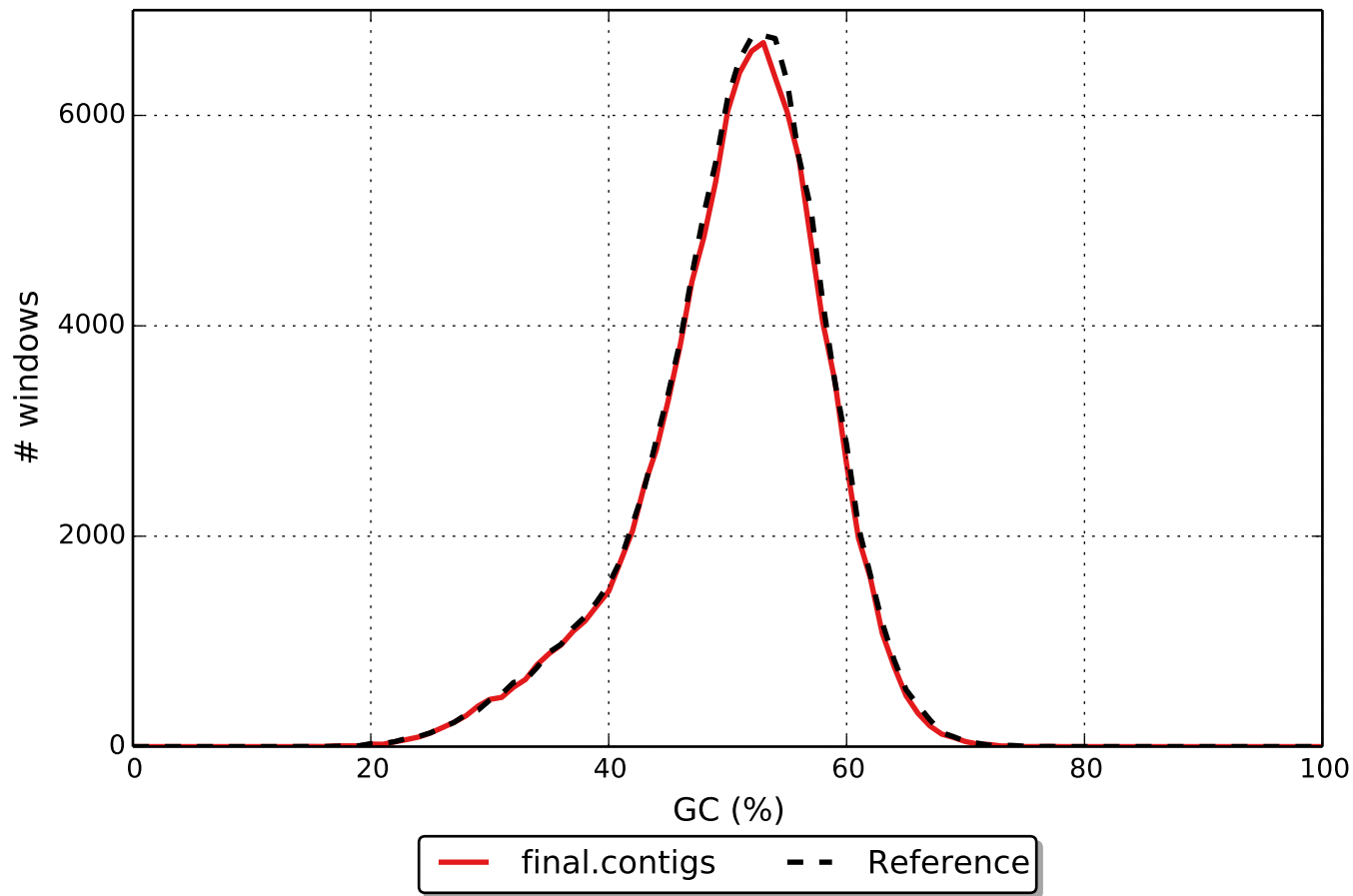(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
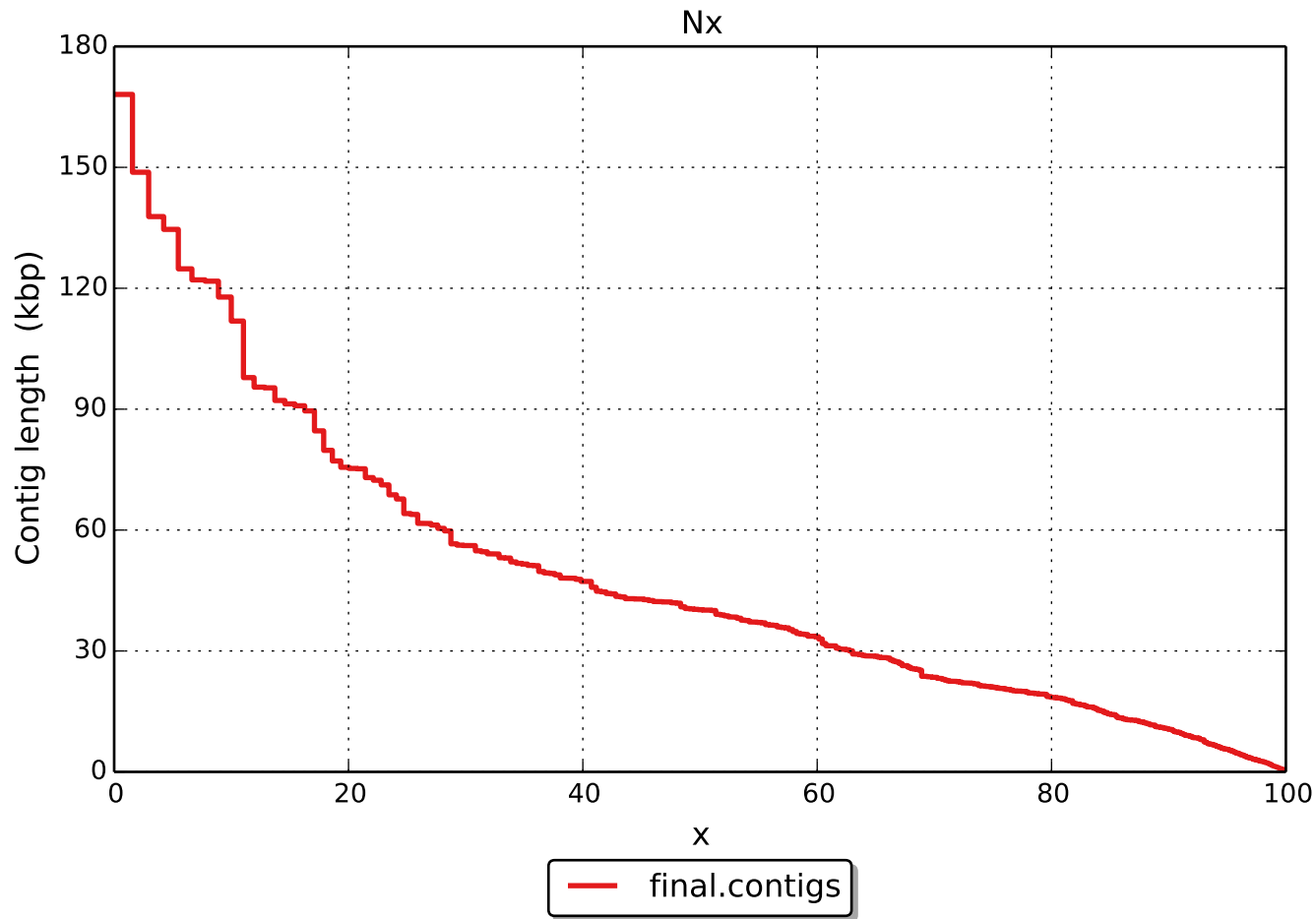
# Unaligned report

| | 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
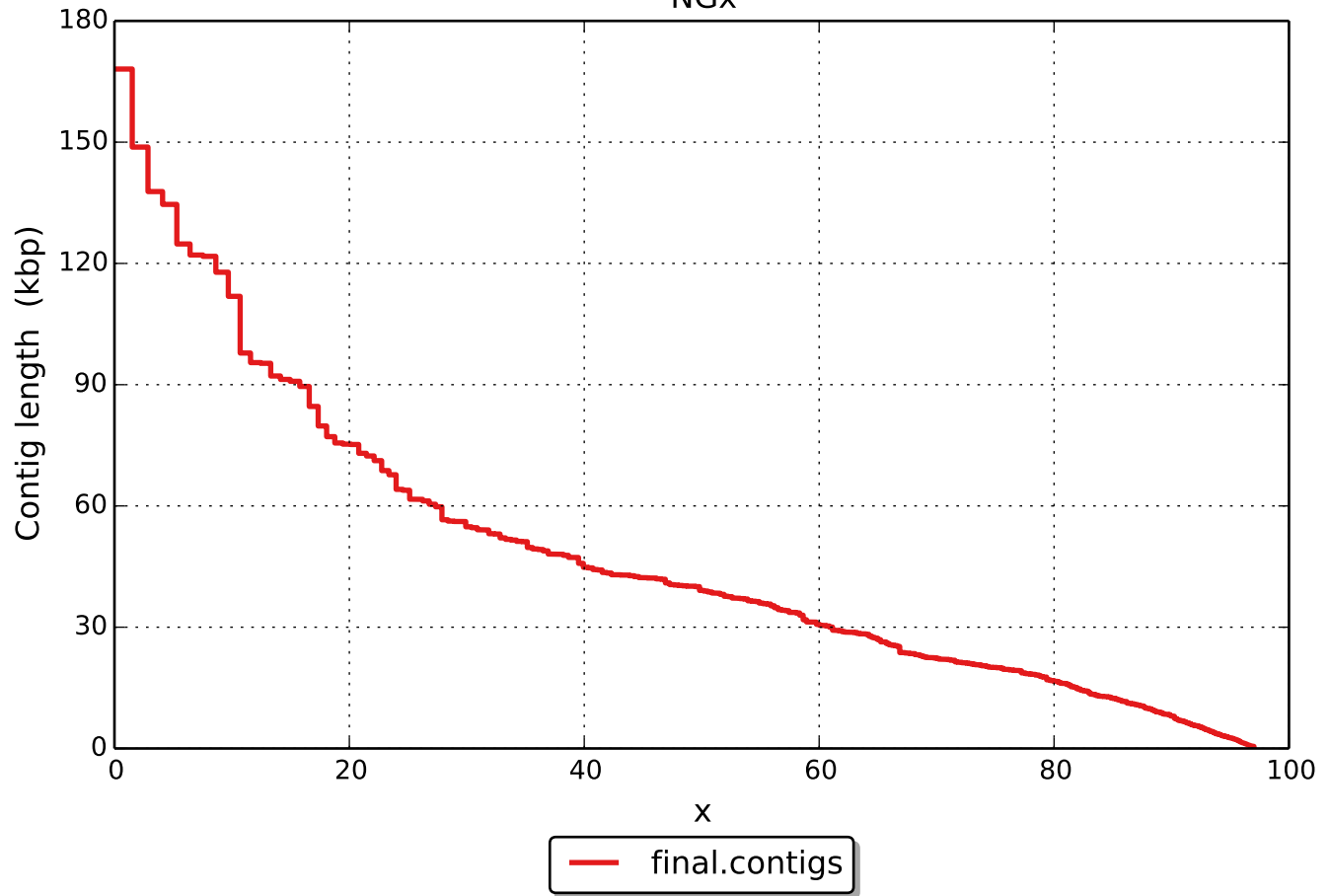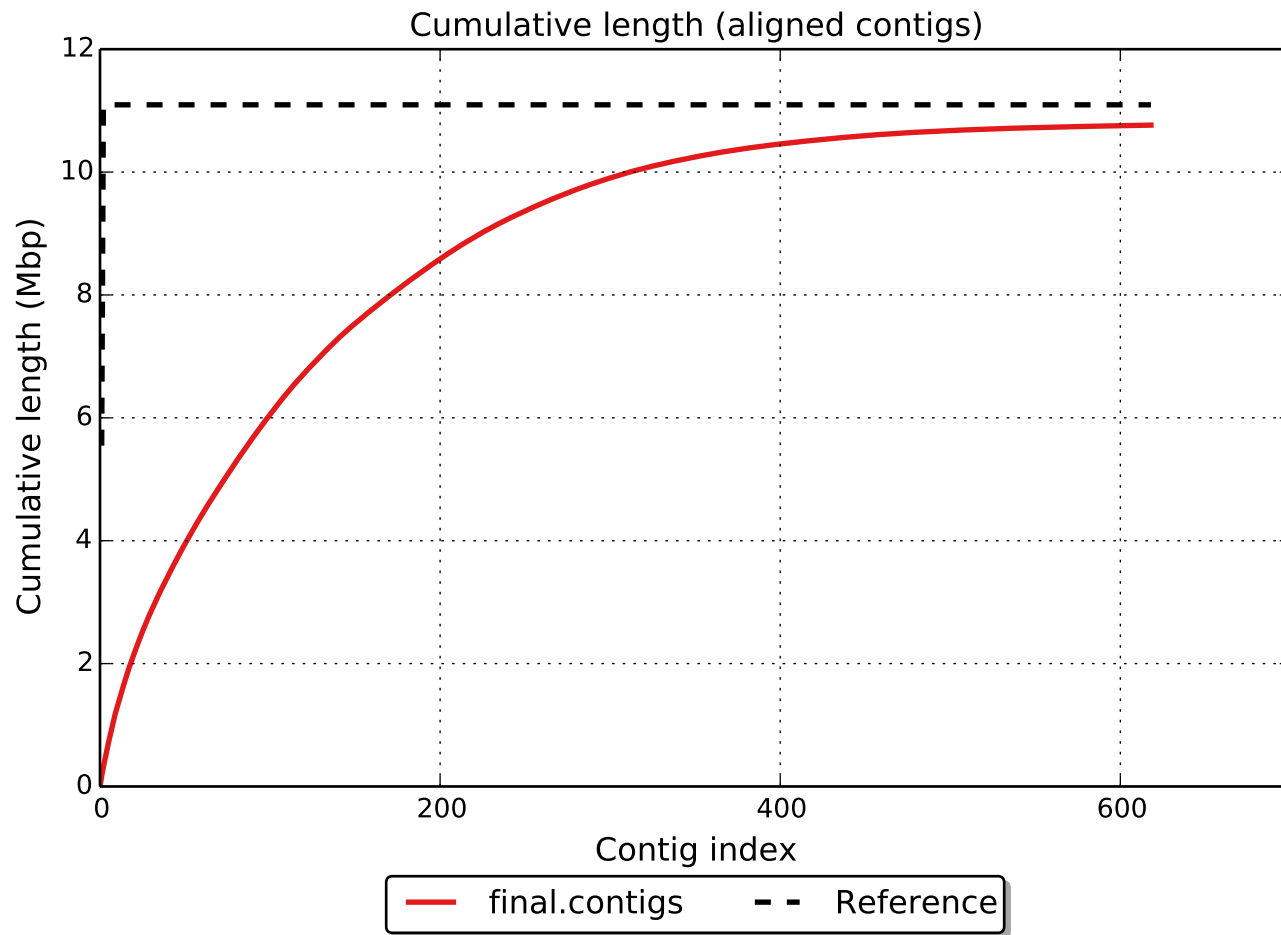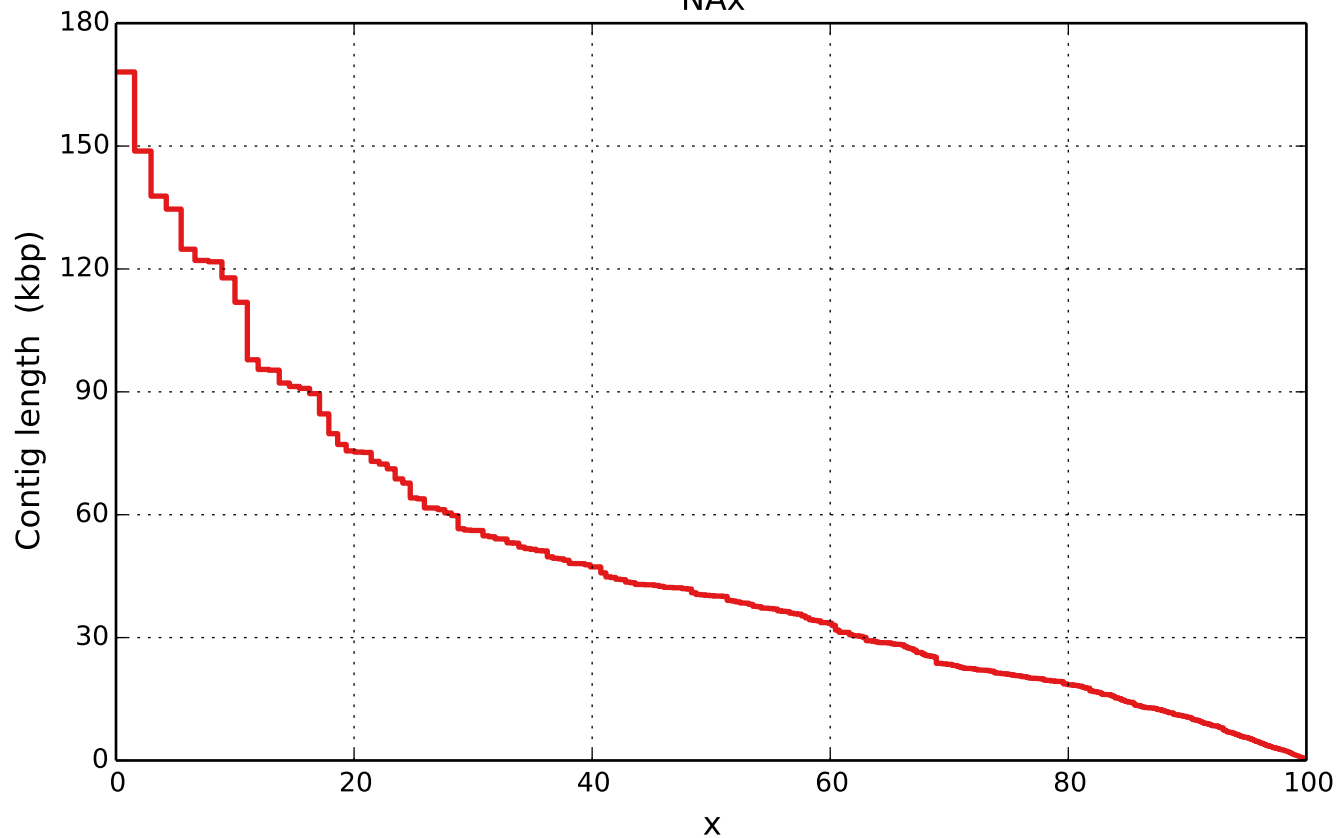(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

Nx

NGx

Misassemblies

final.contigs

# relocations

Cumulative length (aligned contigs)