# Report

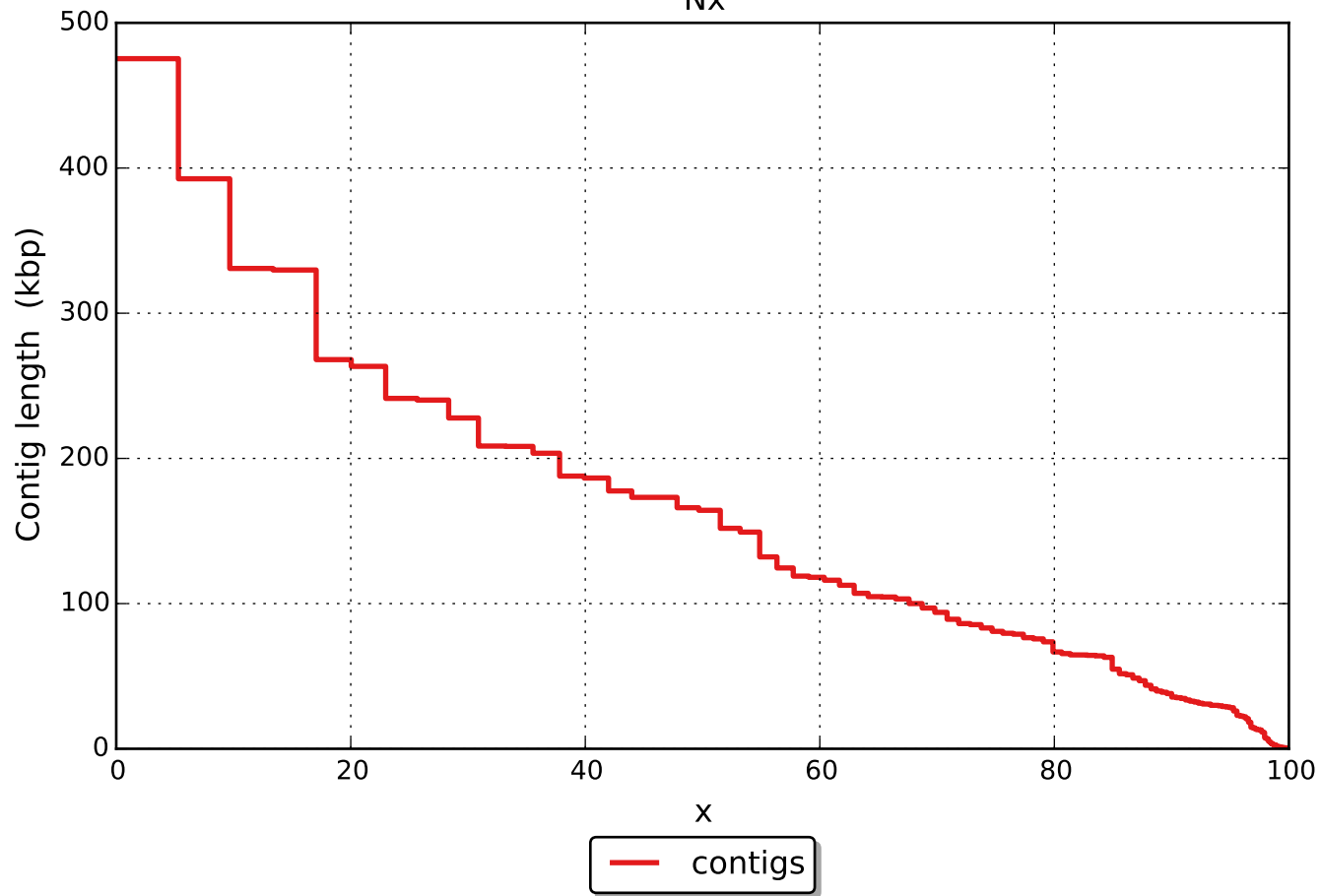| | contigs |
|---|---|
| # contigs (>= 0 bp) | 417 |
| # contigs (>= 1000 bp) | 149 |
| # contigs (>= 5000 bp) | 96 |
| # contigs (>= 10000 bp) | 90 |
| # contigs (>= 25000 bp) | 77 |
| # contigs (>= 50000 bp) | 54 |
| Total length (>= 0 bp) | 9029299 |
| Total length (>= 1000 bp) | 8920339 |
| Total length (>= 5000 bp) | 8818511 |
| Total length (>= 10000 bp) | 8779419 |
| Total length (>= 25000 bp) | 8567902 |
| Total length (>= 50000 bp) | 7771919 |
| # contigs | 217 |
| Largest contig | 475325 |
| Total length | 8965075 |
| Reference length | 9283304 |
| N50 | 164261 |
| N75 | 80872 |
| L50 | 19 |
| L75 | 39 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 96.365 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 835.53 |
| # indels per 100 kbp | 0.86 |
| Largest alignment | 475325 |
| NA50 | 164261 |
| NA75 | 80872 |
| LA50 | 19 |
| LA75 | 39 |

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

| | 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 | 2 |
| # mismatches | 74745 |
| # indels | 77 |
| # short indels | 75 |
| # long indels | 2 |
| Indels length | 96 |

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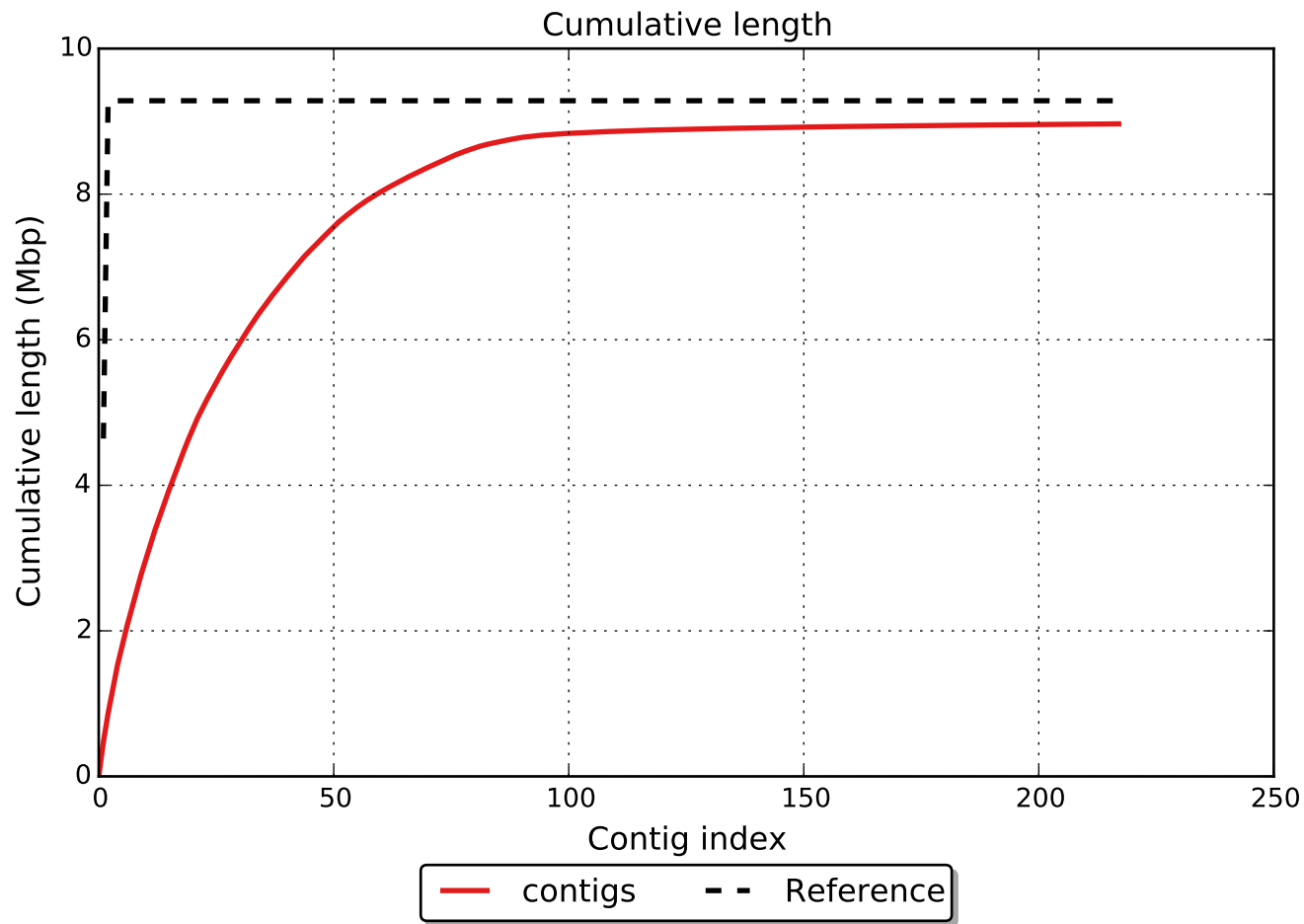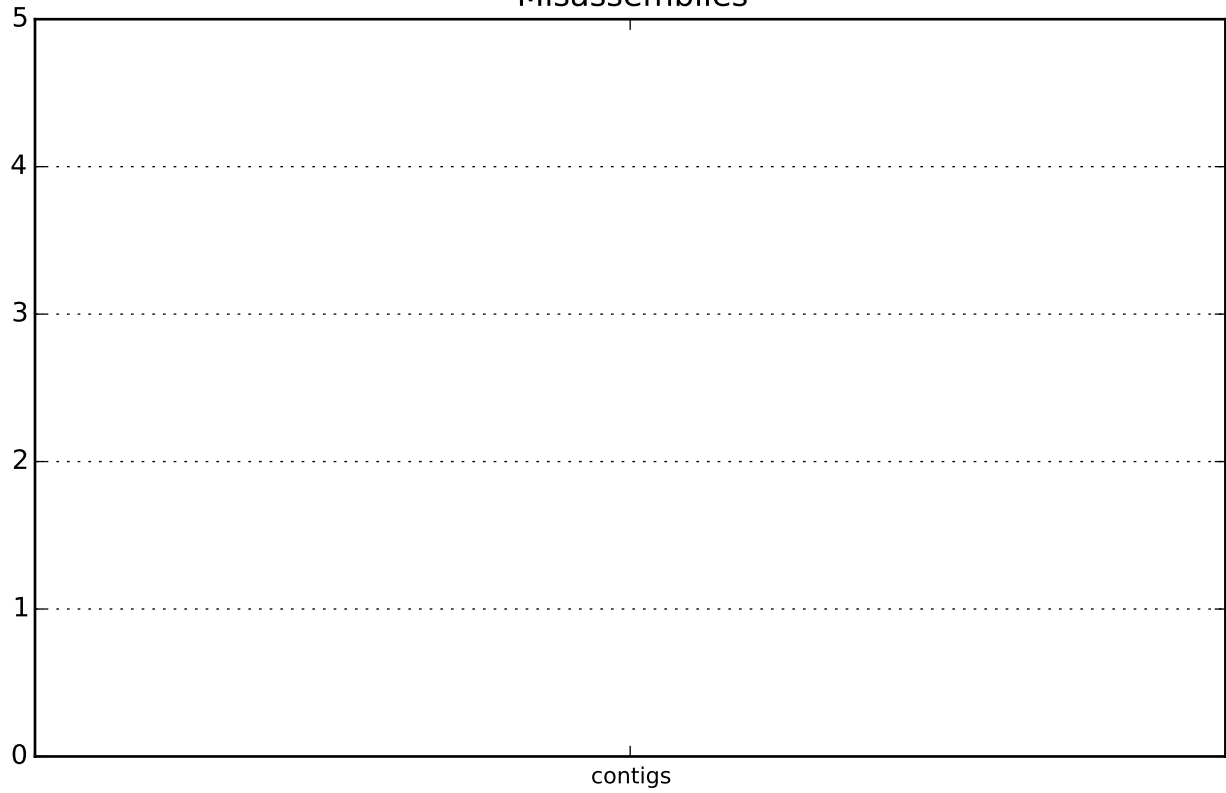(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

# Unaligned report

| | 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).
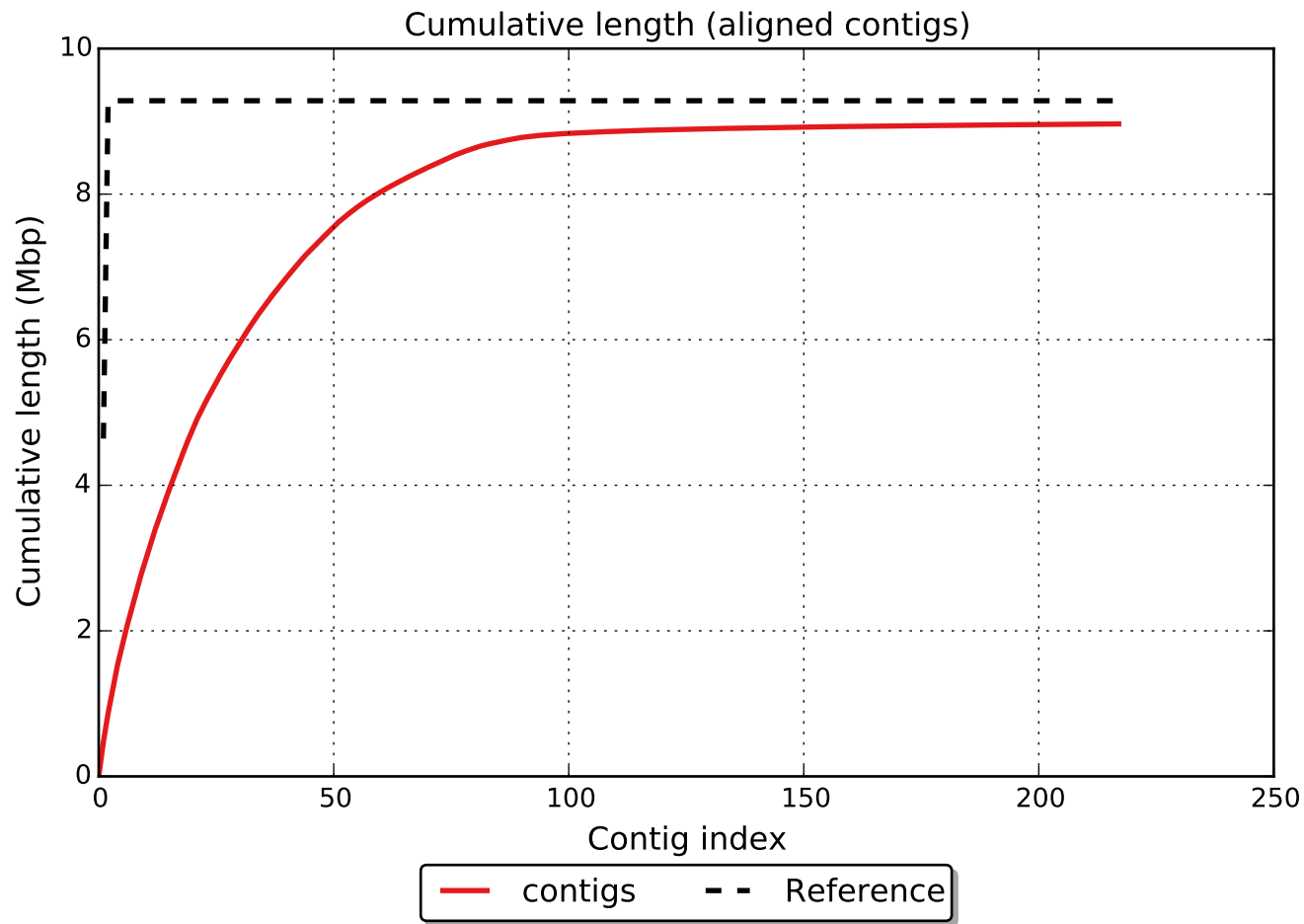
Nx

Cumulative length

# Misassemblies

contigs

Cumulative length (aligned contigs)