# Report

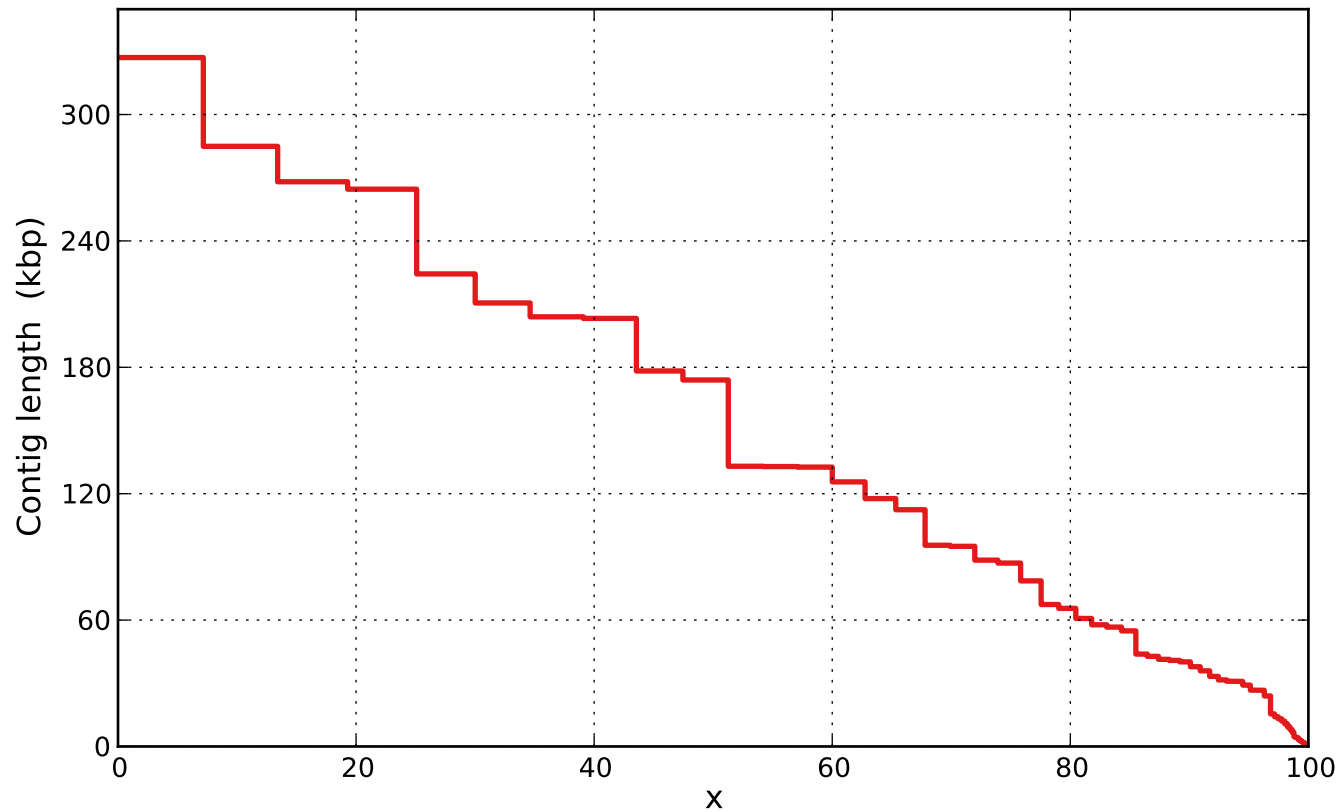| | scaffolds |
|---|---|
| # contigs (>= 0 bp) | 106 |
| # contigs (>= 1000 bp) | 72 |
| # contigs (>= 5000 bp) | 50 |
| # contigs (>= 10000 bp) | 47 |
| # contigs (>= 25000 bp) | 41 |
| # contigs (>= 50000 bp) | 27 |
| Total length (>= 0 bp) | 4566249 |
| Total length (>= 1000 bp) | 4556760 |
| Total length (>= 5000 bp) | 4506360 |
| Total length (>= 10000 bp) | 4482290 |
| Total length (>= 25000 bp) | 4392918 |
| Total length (>= 50000 bp) | 3900785 |
| # contigs | 79 |
| Largest contig | 327053 |
| Total length | 4562036 |
| Reference length | 4641652 |
| N50 | 173981 |
| N75 | 87064 |
| L50 | 10 |
| L75 | 20 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 98.228 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 59.26 |
| # indels per 100 kbp | 8.27 |
| Largest alignment | 327053 |
| NA50 | 173981 |
| NA75 | 87064 |
| LA50 | 10 |
| LA75 | 20 |

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

| | scaffolds |
|---|---|
| # 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 | 2702 |
| # indels | 377 |
| # short indels | 377 |
| # long indels | 0 |
| Indels length | 544 |

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

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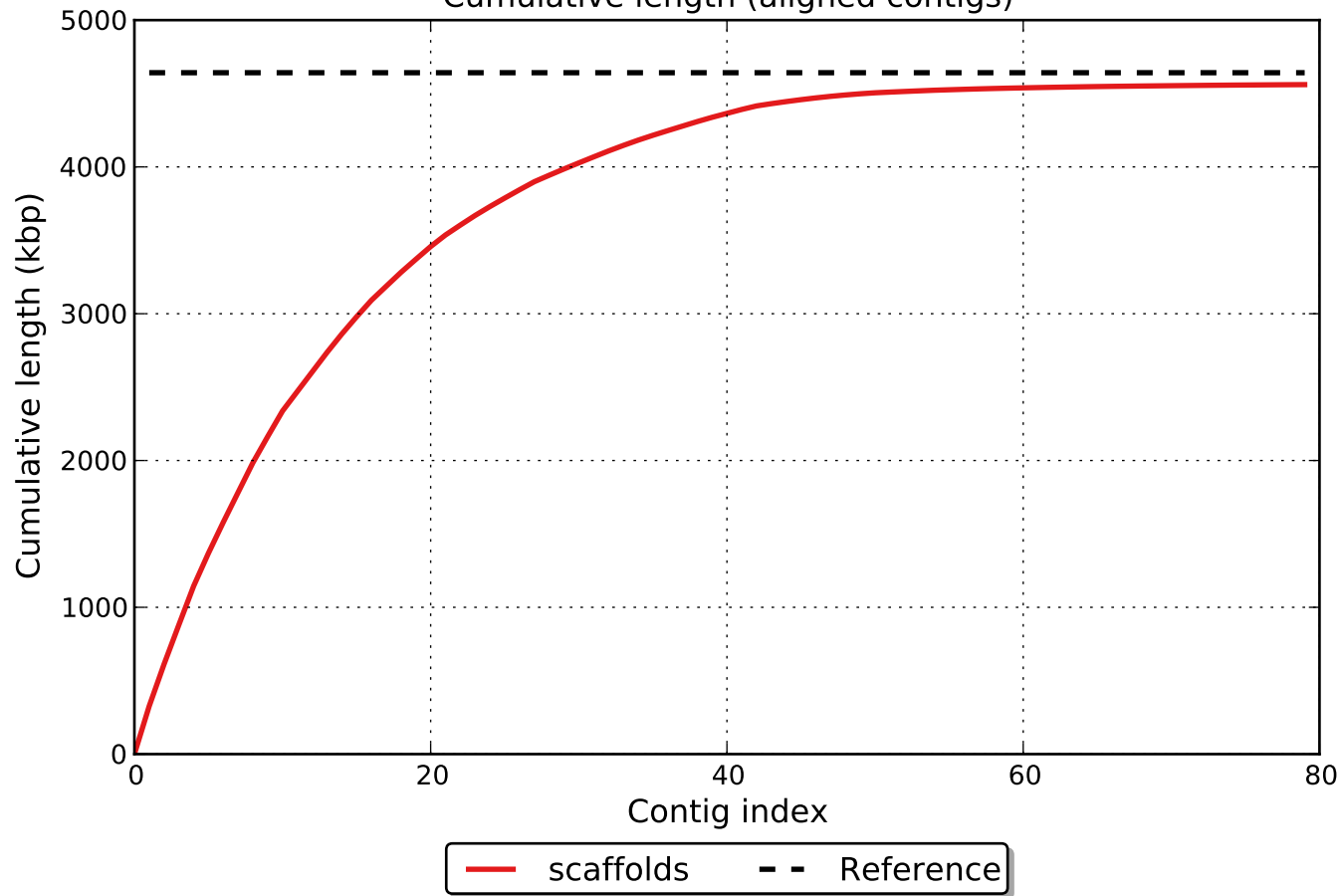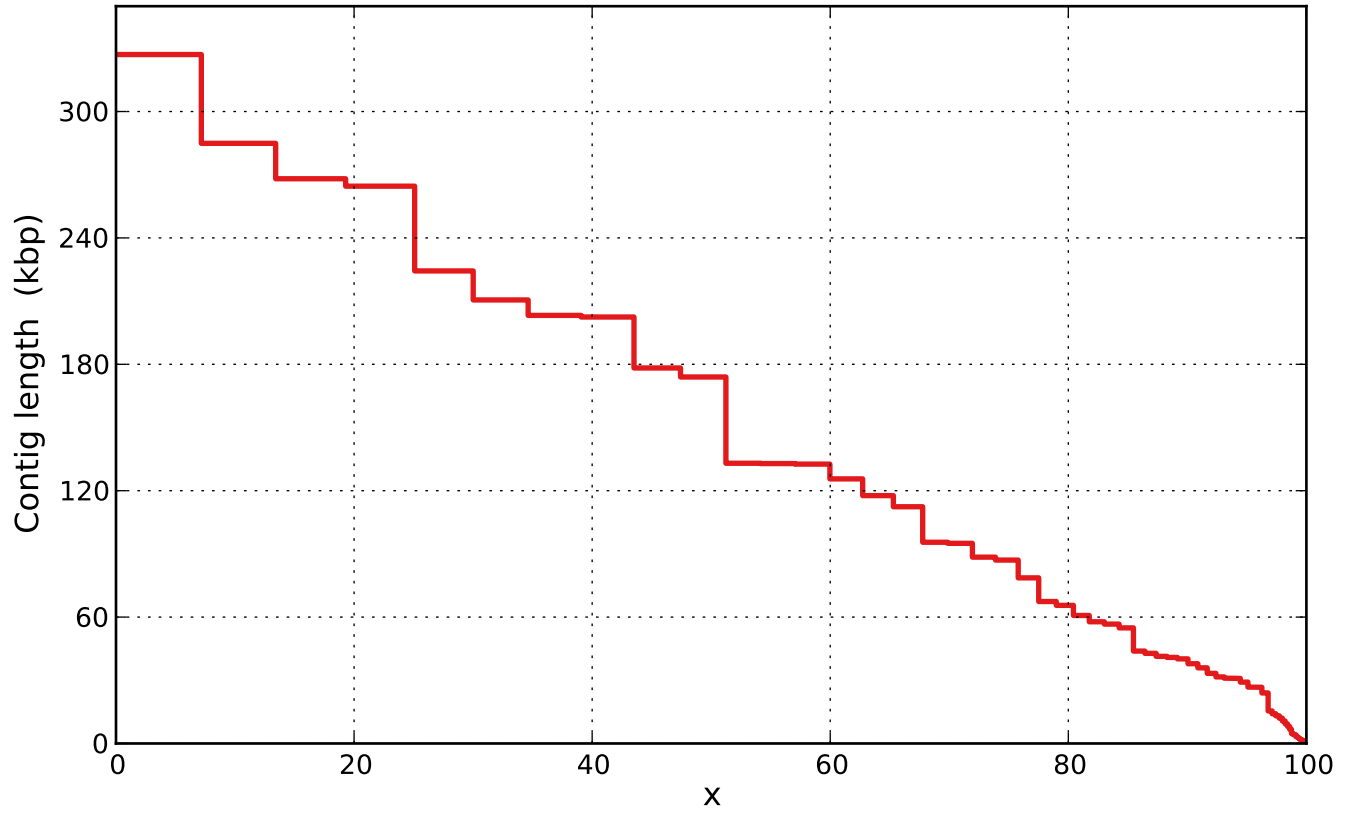(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length
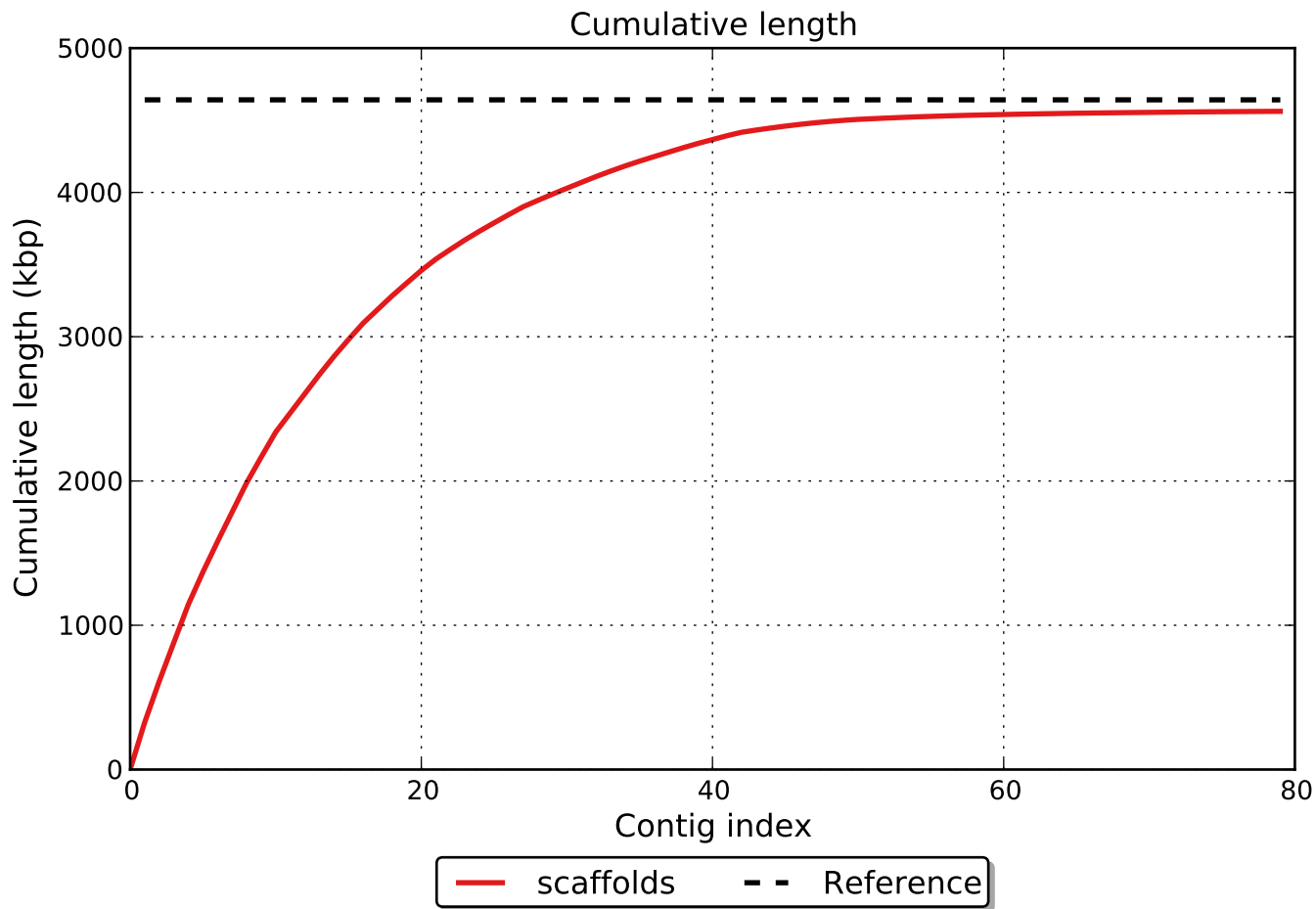
# Misassemblies
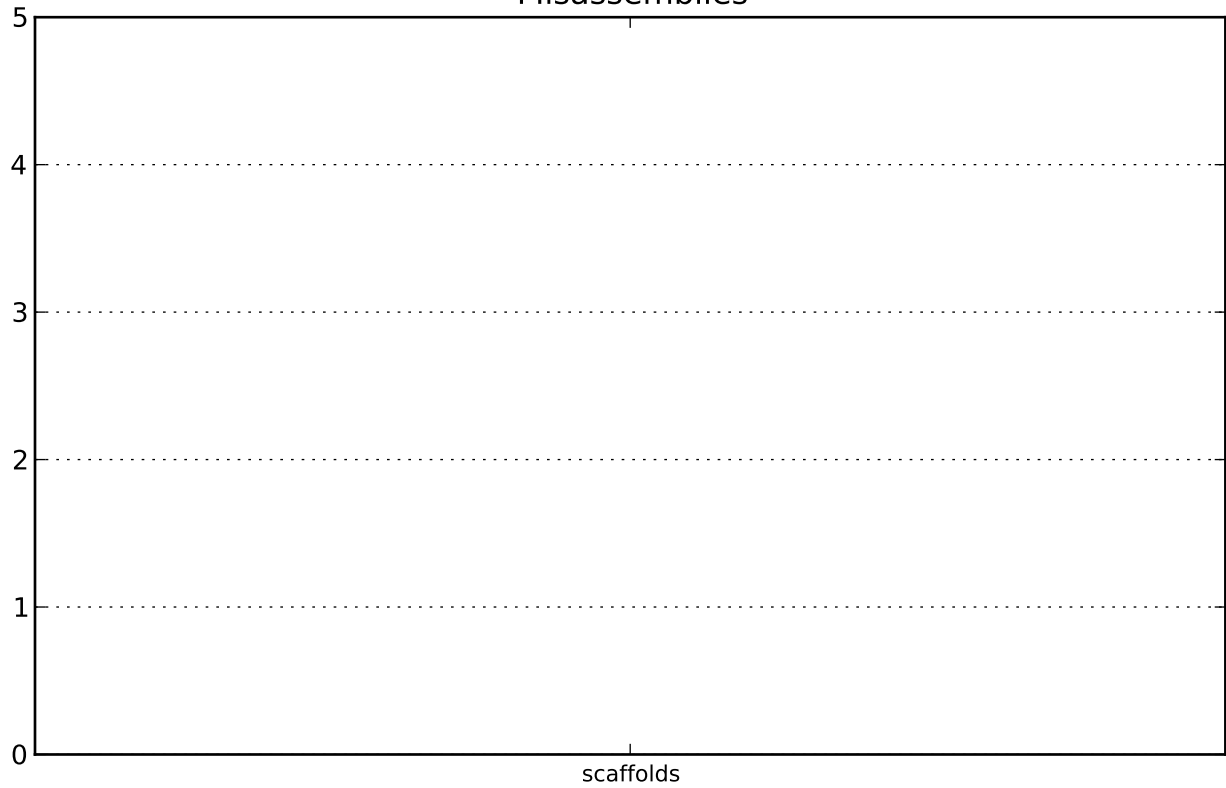
scaffolds

Cumulative length (aligned contigs)