# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 164 |
| # contigs (>= 1000 bp) | 86 |
| # contigs (>= 5000 bp) | 64 |
| # contigs (>= 10000 bp) | 57 |
| # contigs (>= 25000 bp) | 46 |
| # contigs (>= 50000 bp) | 30 |
| Total length (>= 0 bp) | 4605512 |
| Total length (>= 1000 bp) | 4571248 |
| Total length (>= 5000 bp) | 4522768 |
| Total length (>= 10000 bp) | 4473225 |
| Total length (>= 25000 bp) | 4300249 |
| Total length (>= 50000 bp) | 3733646 |
| # contigs | 109 |
| Largest contig | 327235 |
| Total length | 4585683 |
| Reference length | 4641652 |
| GC (%) | 50.75 |
| Reference GC (%) | 50.79 |
| N50 | 132730 |
| NG50 | 129572 |
| N75 | 58784 |
| NG75 | 58251 |
| L50 | 12 |
| LG50 | 13 |
| L75 | 25 |
| LG75 | 26 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 4 |
| # unaligned contigs | 1 + 1 part |
| Unaligned length | 576 |
| Genome fraction (%) | 98.586 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 7.60 |
| # indels per 100 kbp | 0.11 |
| Largest alignment | 327235 |
| NA50 | 132730 |
| NGA50 | 129572 |
| NA75 | 58784 |
| NGA75 | 58251 |
| LA50 | 12 |
| LGA50 | 13 |
| LA75 | 25 |
| LGA75 | 26 |

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).
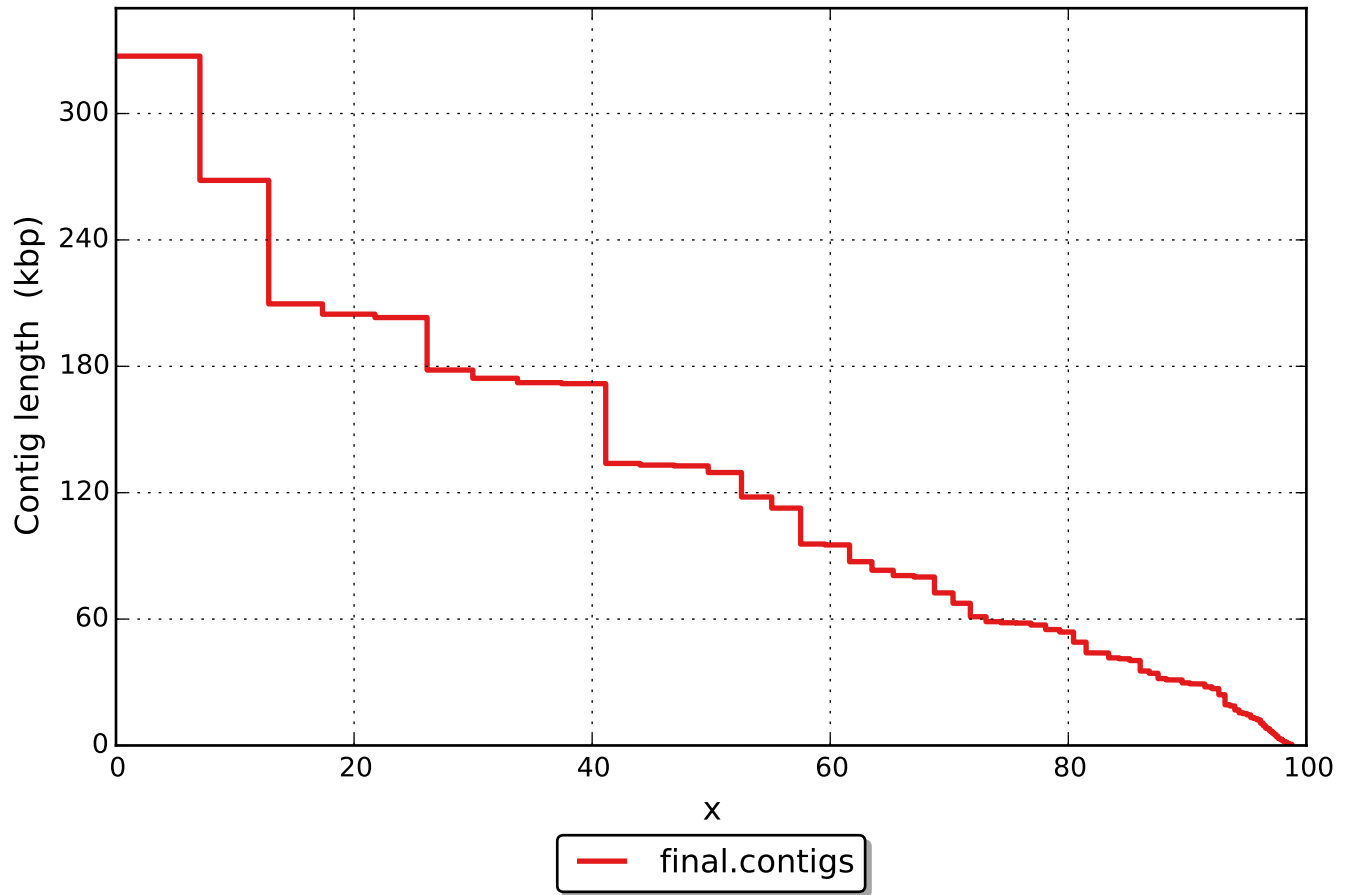
# Misassemblies report

| | final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 4 |
| # mismatches | 348 |
| # indels | 5 |
| # short indels | 5 |
| # long indels | 0 |
| Indels length | 5 |

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 | 1 |
| Fully unaligned length | 559 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 17 |
| # N's | 0 |

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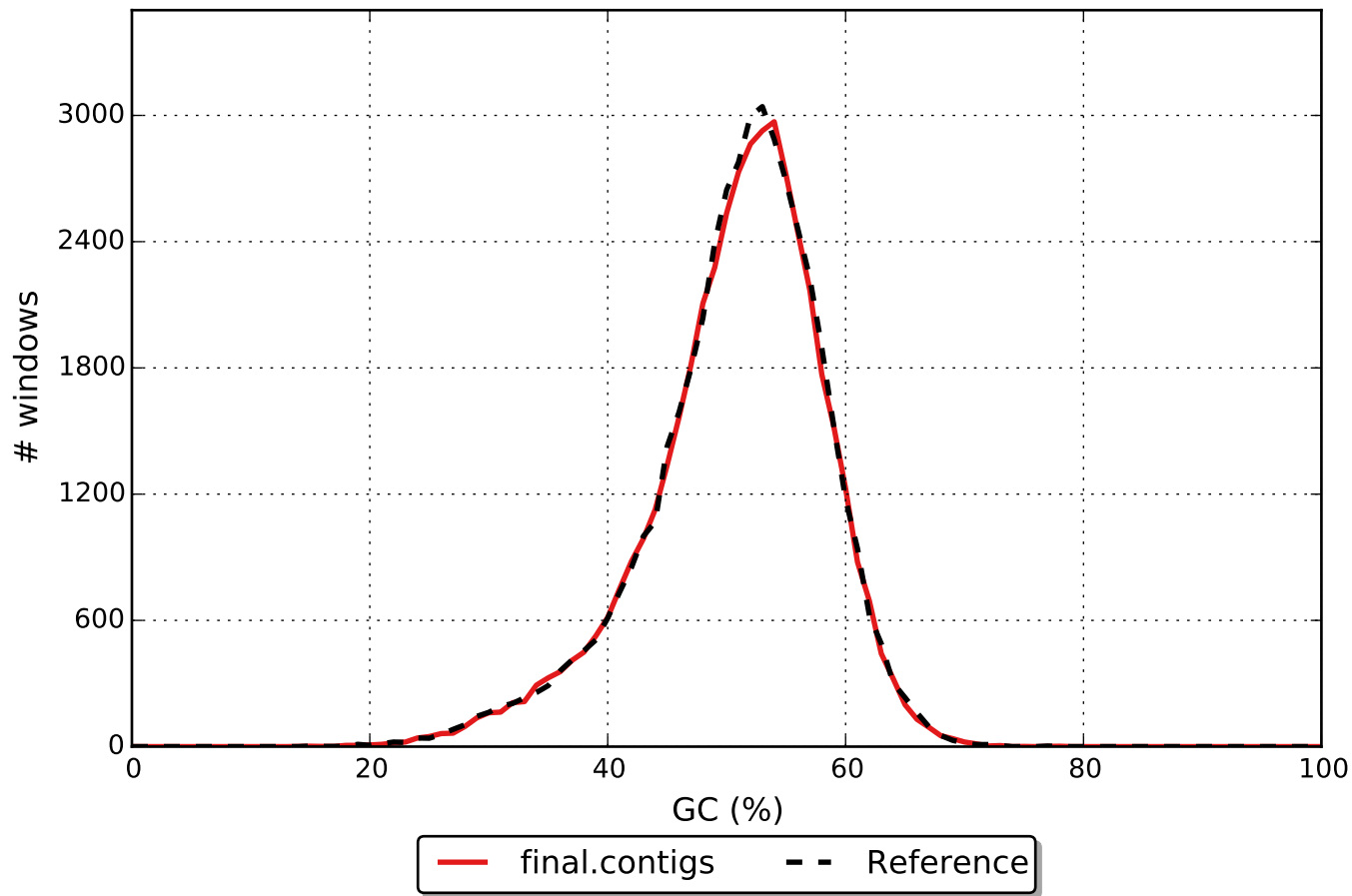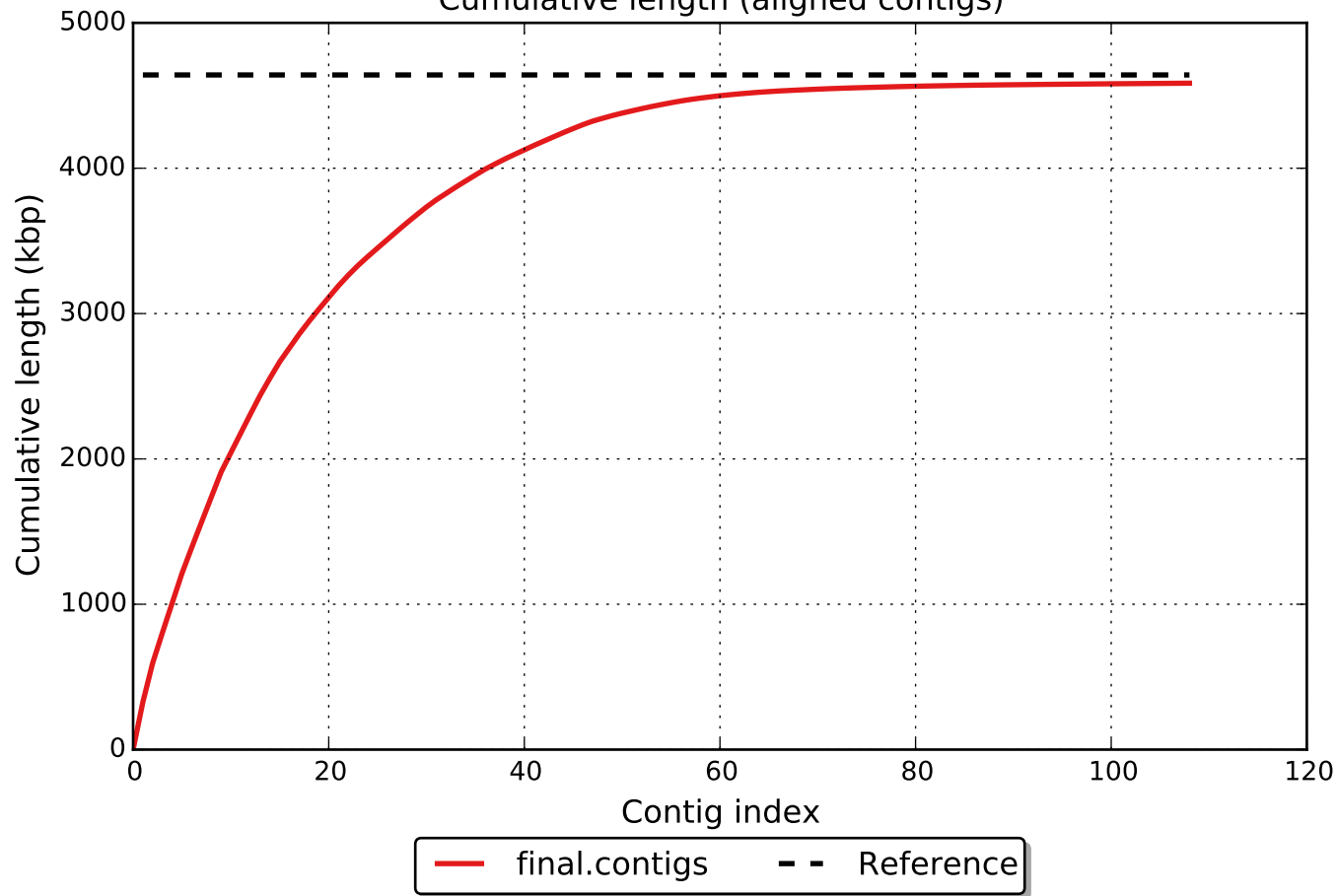(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length
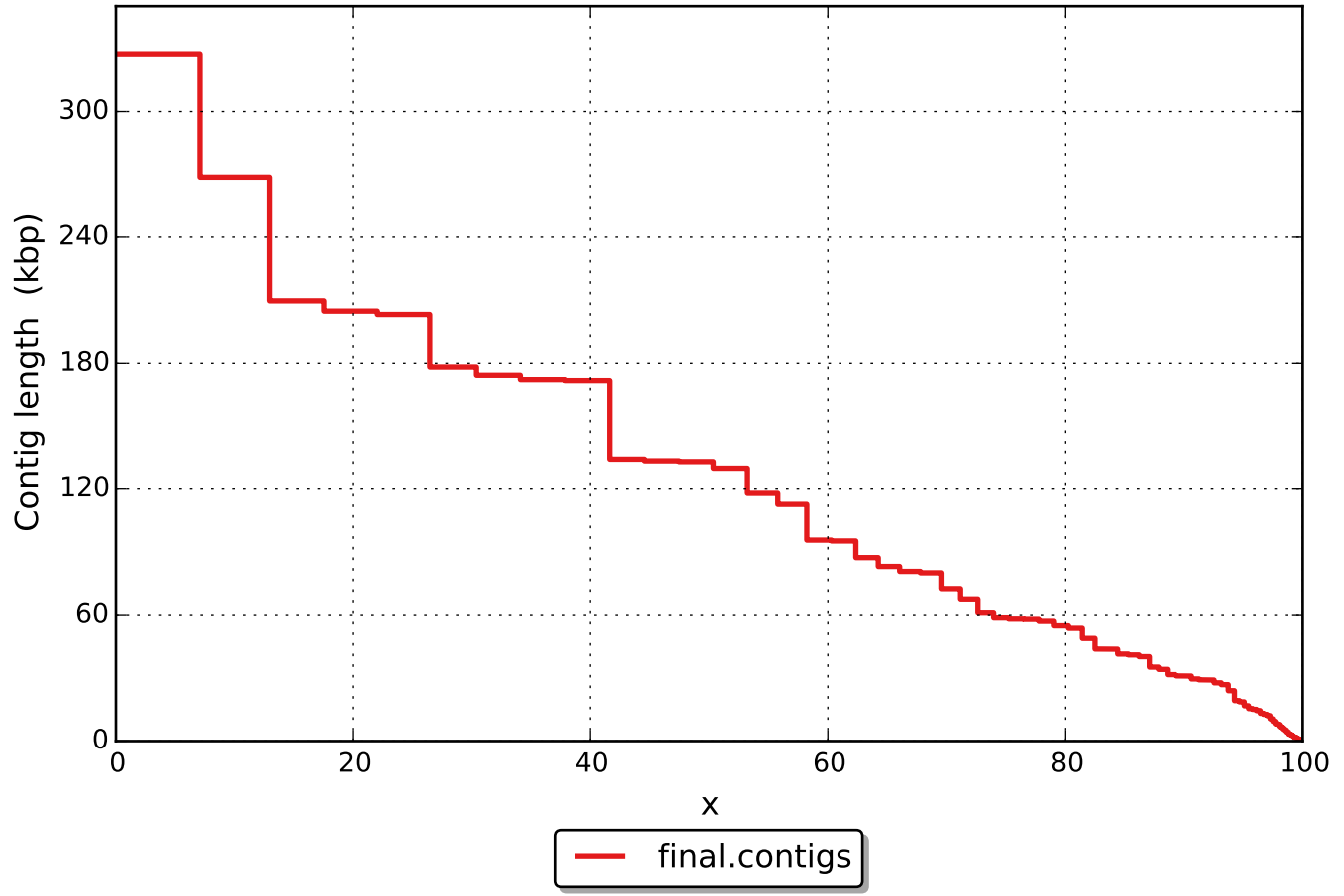
GC content

# windows vs GC (%)
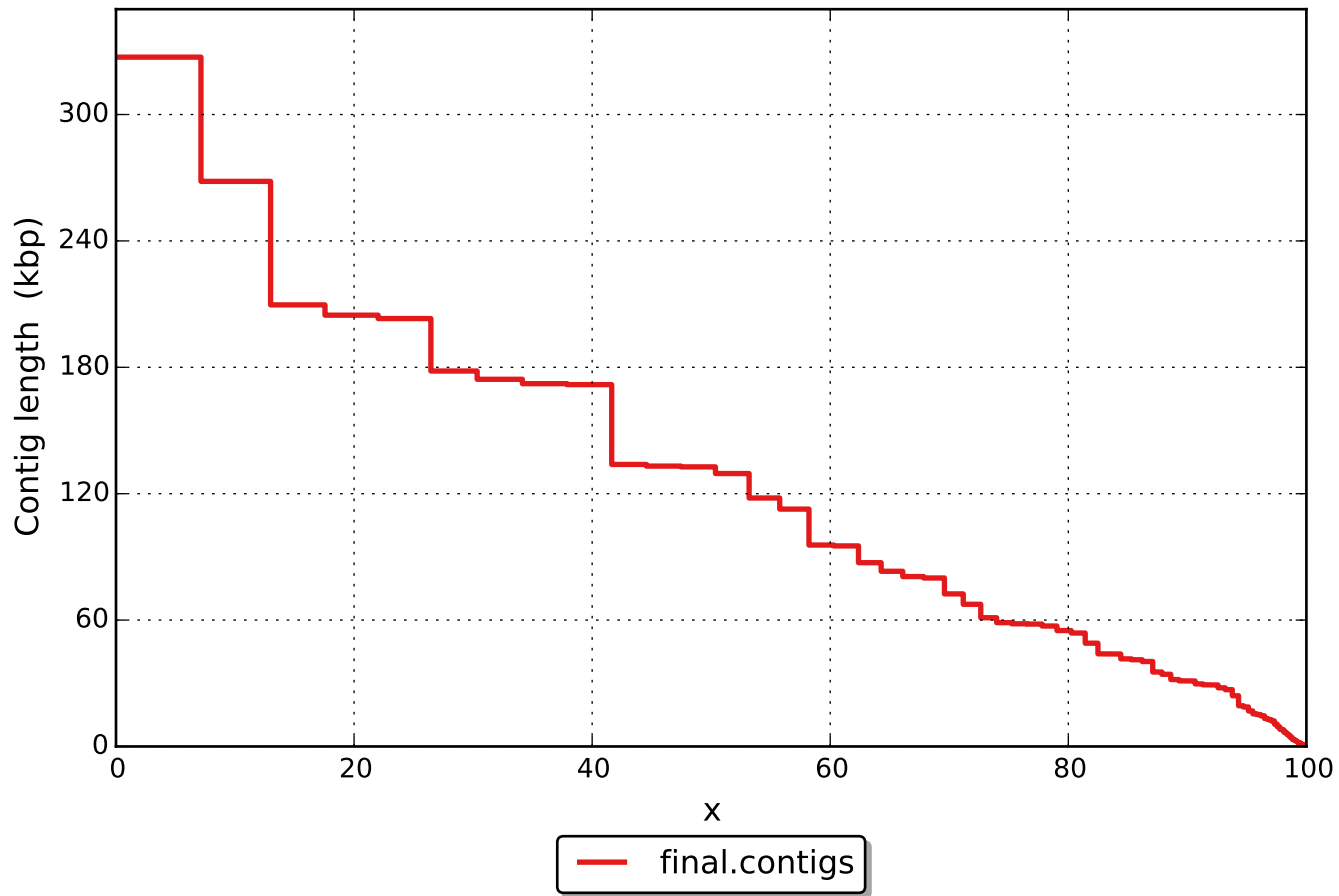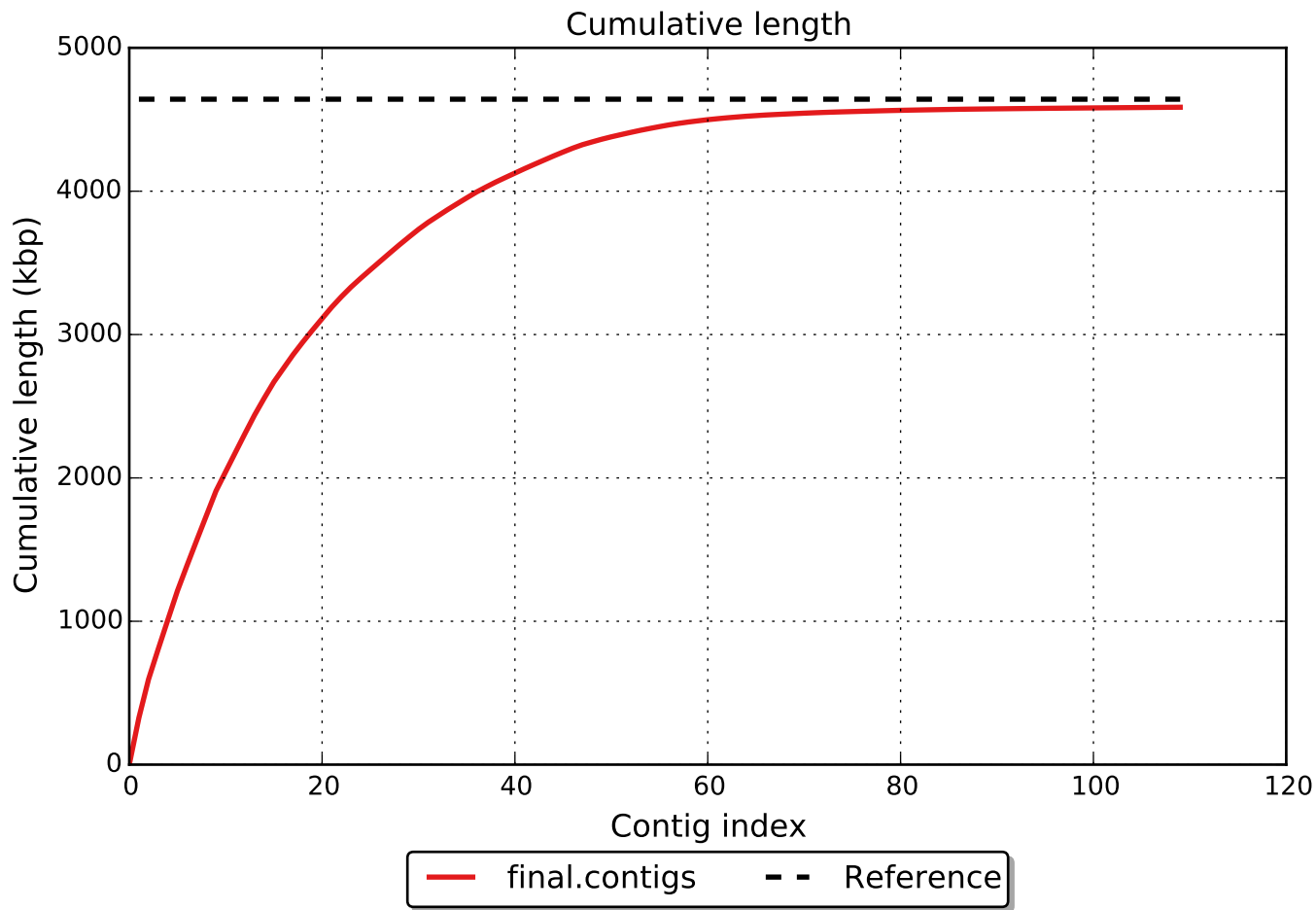
# Misassemblies

final.contigs

Cumulative length (aligned contigs)