

Report

| | final.contigs |
|--------------------------------|---------------|
| # contigs (≥ 0 bp) | 507 |
| # contigs (≥ 1000 bp) | 478 |
| Total length (≥ 0 bp) | 3744104 |
| Total length (≥ 1000 bp) | 3721380 |
| # contigs | 507 |
| Largest contig | 40013 |
| Total length | 3744104 |
| Reference length | 1892775 |
| GC (%) | 32.25 |
| Reference GC (%) | 32.27 |
| N50 | 12018 |
| NG50 | 18214 |
| N75 | 6586 |
| NG75 | 14480 |
| L50 | 103 |
| LG50 | 40 |
| L75 | 207 |
| LG75 | 69 |
| # misassemblies | 2 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 28614 |
| # local misassemblies | 0 |
| # unaligned contigs | 179 + 80 part |
| Unaligned length | 1749084 |
| Genome fraction (%) | 99.870 |
| Duplication ratio | 1.055 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 64.91 |
| # indels per 100 kbp | 0.58 |
| Largest alignment | 40013 |
| NA50 | 2025 |
| NGA50 | 13586 |
| NGA75 | 7962 |
| LA50 | 190 |
| LGA50 | 47 |
| LGA75 | 91 |

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

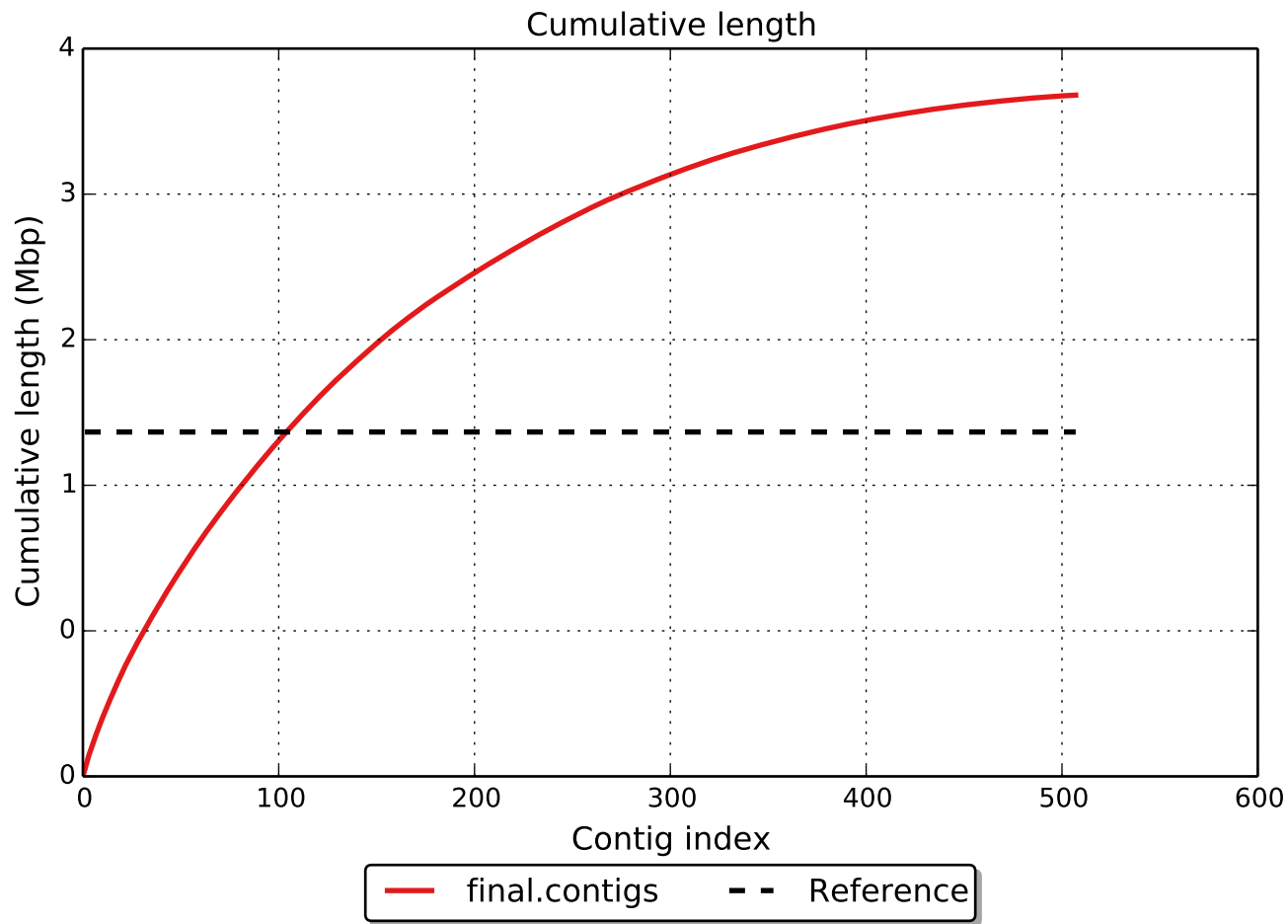
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 2 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 1 |
| # possibly misassembled contigs | 9 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 28614 |
| # local misassemblies | 0 |
| # mismatches | 1227 |
| # indels | 11 |
| # short indels | 5 |
| # long indels | 6 |
| Indels length | 73 |

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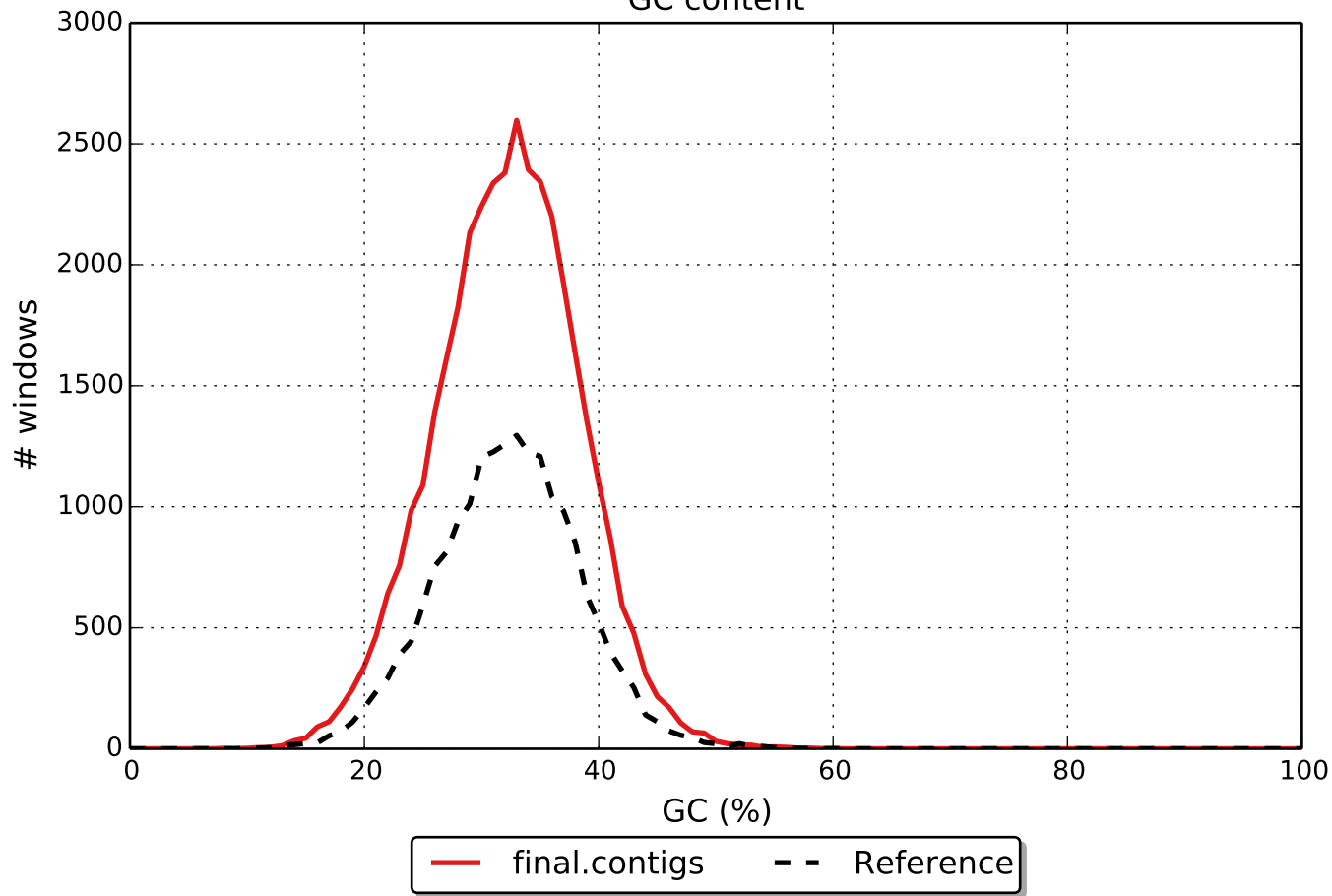
Unaligned report

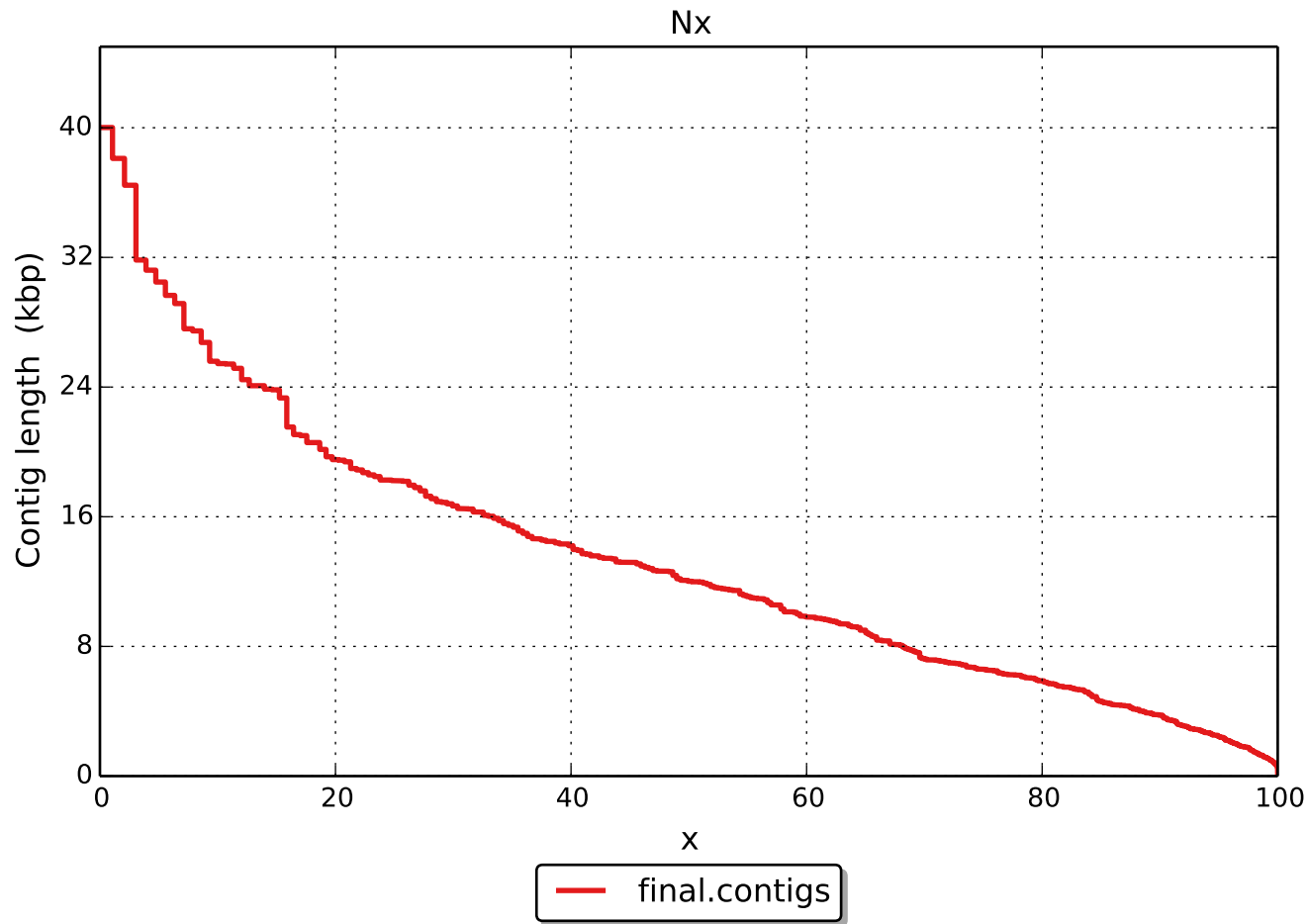
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 179 |
| Fully unaligned length | 1199989 |
| # partially unaligned contigs | 80 |
| # with misassembly | 5 |
| # both parts are significant | 7 |
| Partially unaligned length | 549095 |
| # N's | 0 |

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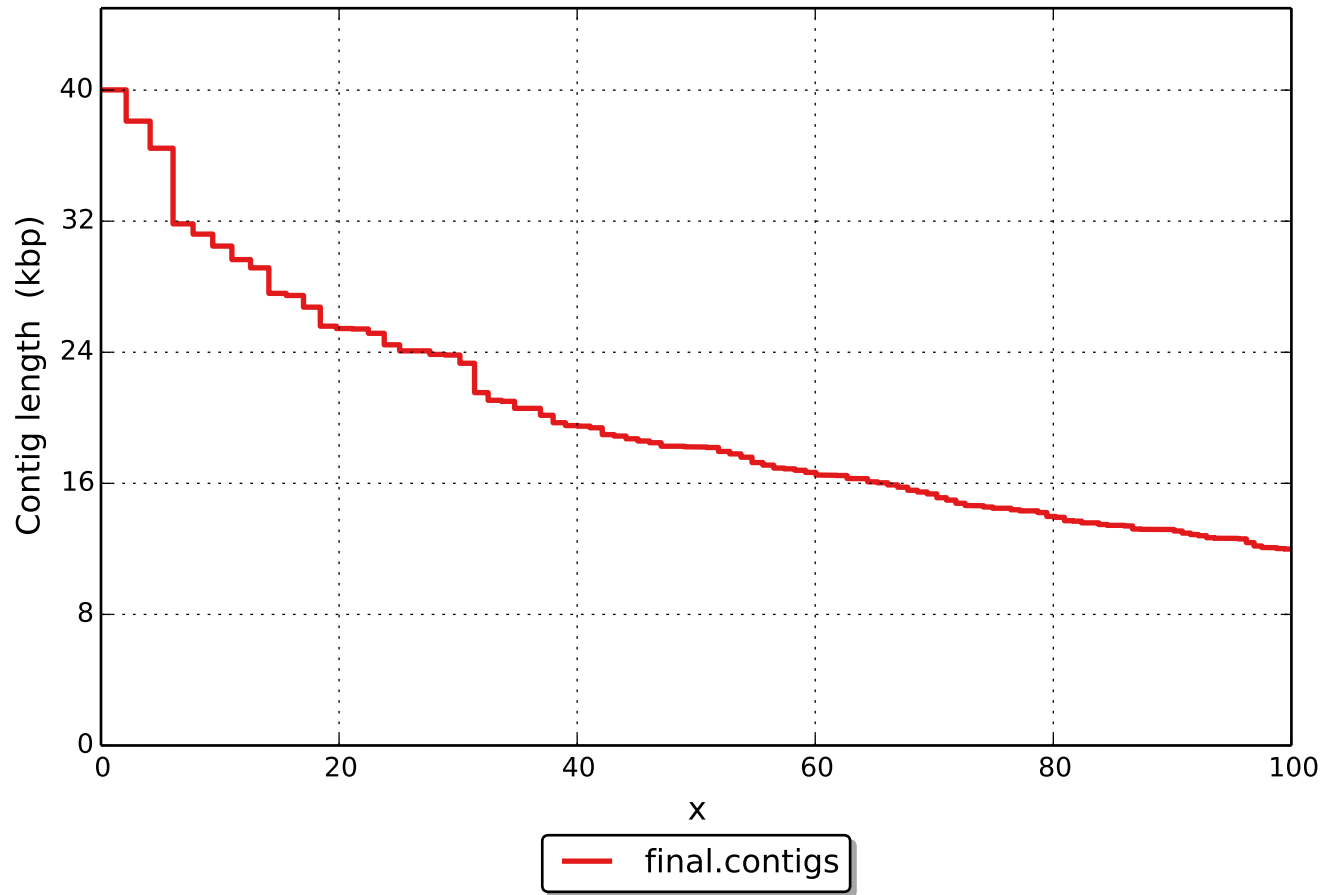


GC content

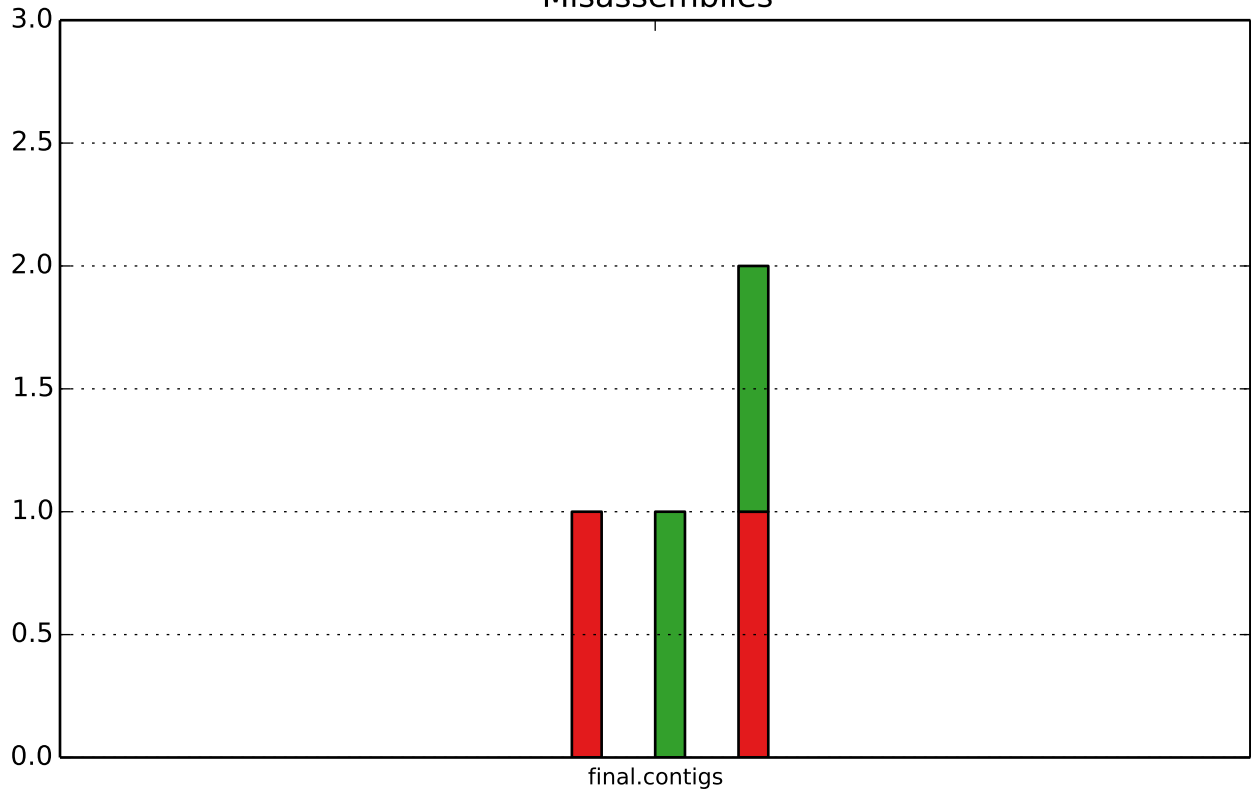




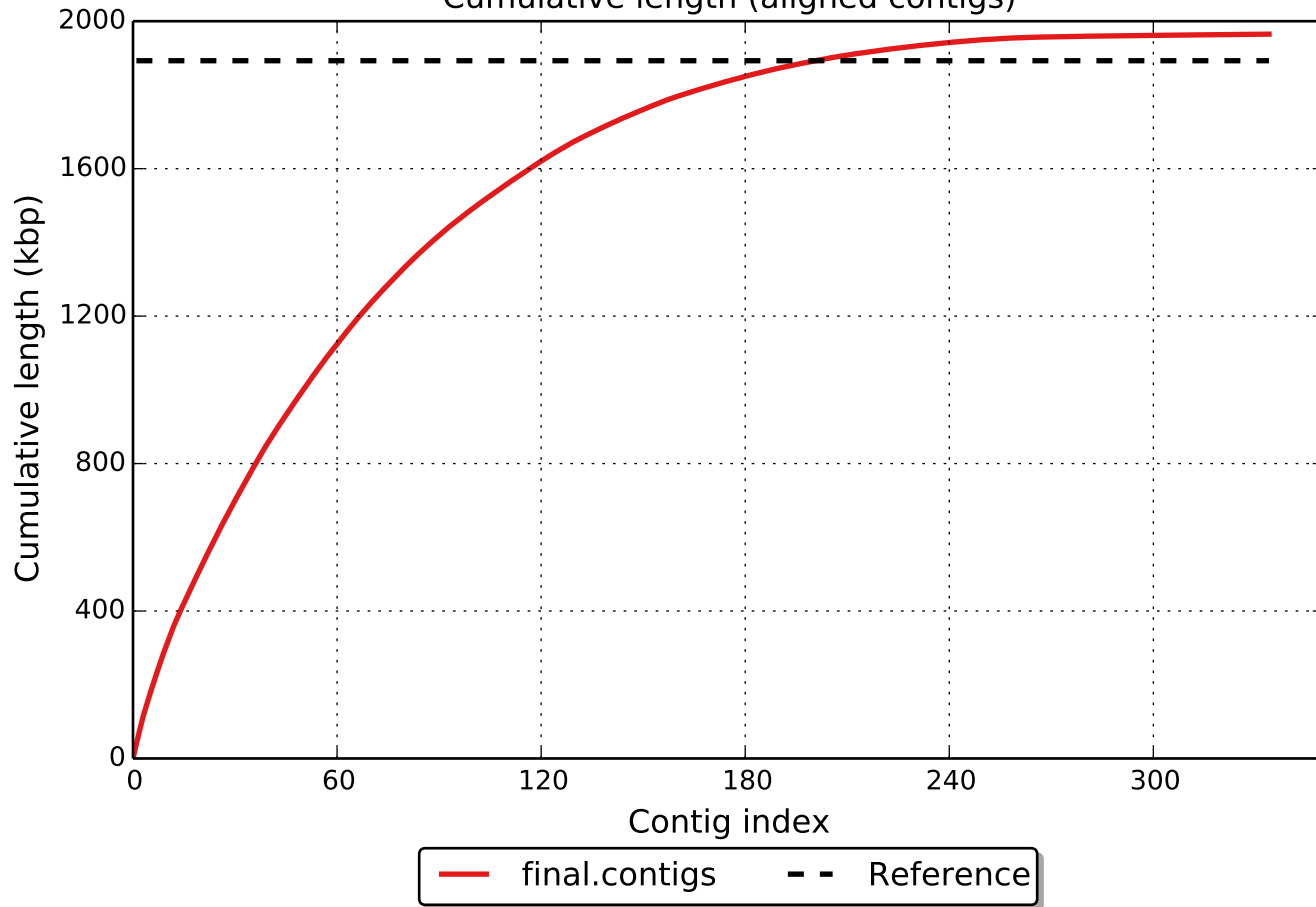
NGx



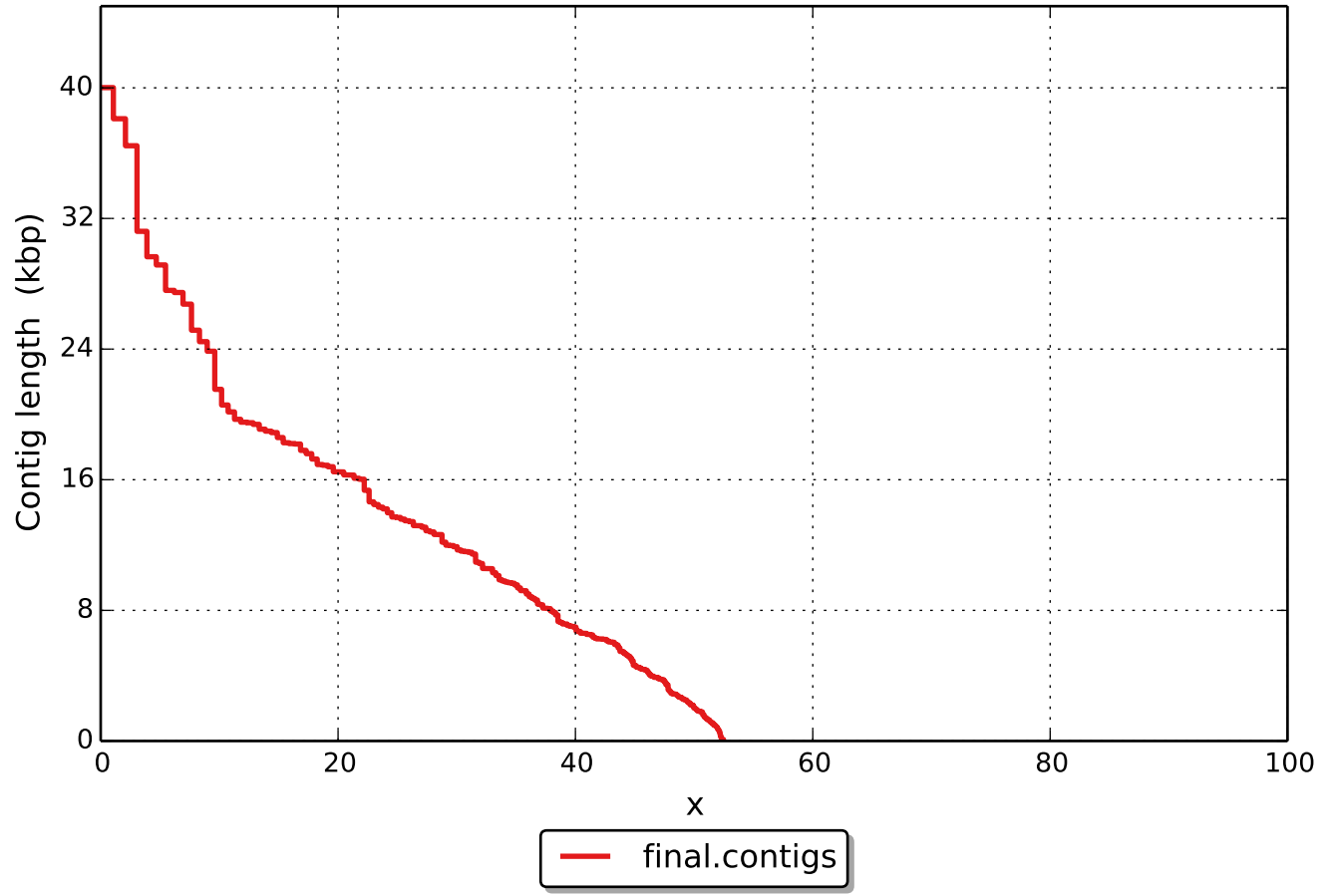
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

