

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp) | 522 |
| # contigs (>= 1000 bp) | 495 |
| Total length (>= 0 bp) | 5522502 |
| Total length (>= 1000 bp) | 5503535 |
| # contigs | 522 |
| Largest contig | 67238 |
| Total length | 5522502 |
| Reference length | 5478683 |
| GC (%) | 50.51 |
| Reference GC (%) | 50.50 |
| N50 | 17940 |
| NG50 | 18317 |
| N75 | 9618 |
| NG75 | 9821 |
| L50 | 95 |
| LG50 | 94 |
| L75 | 200 |
| LG75 | 197 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 99.911 |
| Duplication ratio | 1.009 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 8.26 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 67238 |
| NA50 | 17940 |
| NGA50 | 18317 |
| NA75 | 9618 |
| NGA75 | 9821 |
| LA50 | 95 |
| LGA50 | 94 |
| LA75 | 200 |
| LGA75 | 197 |

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

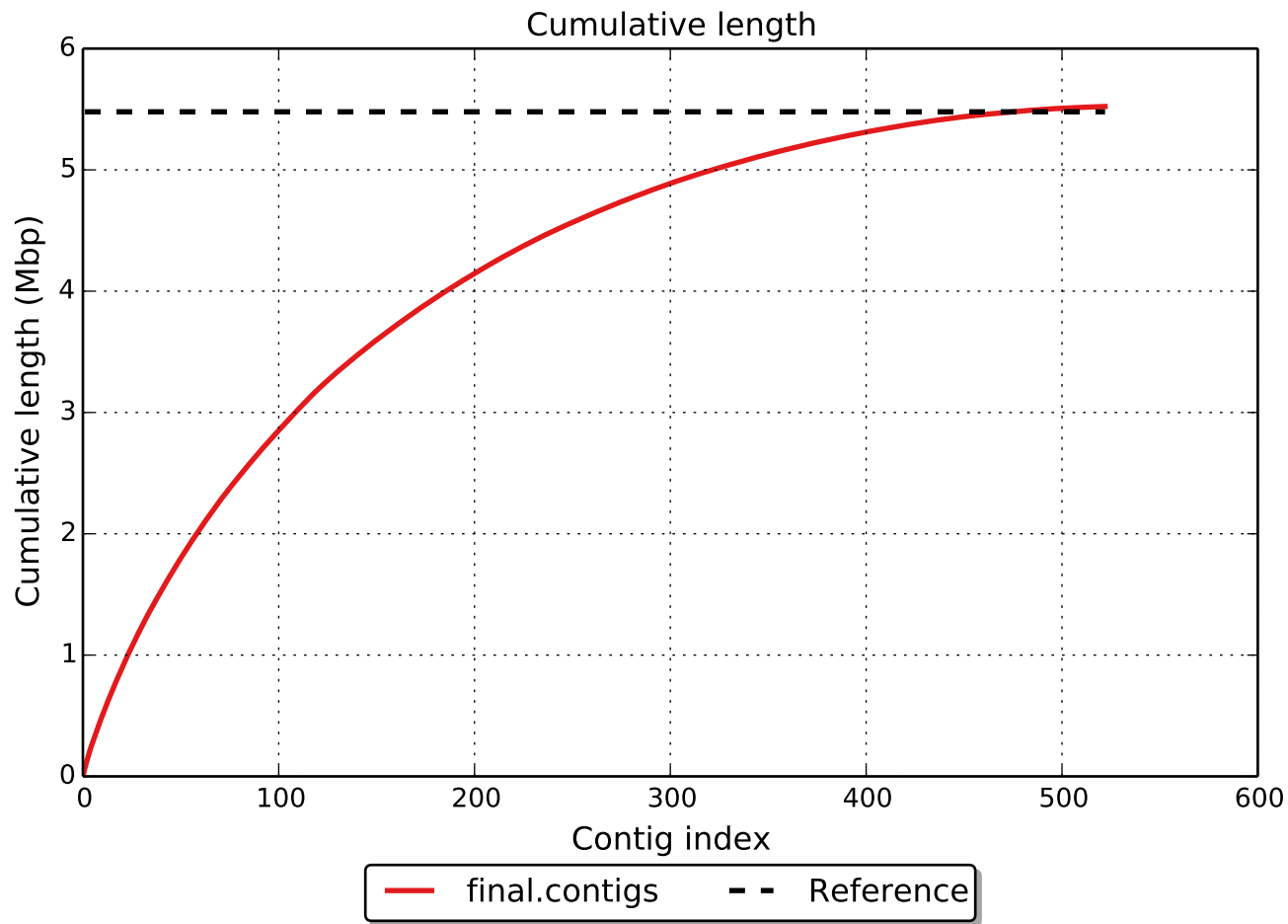
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 452 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 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).

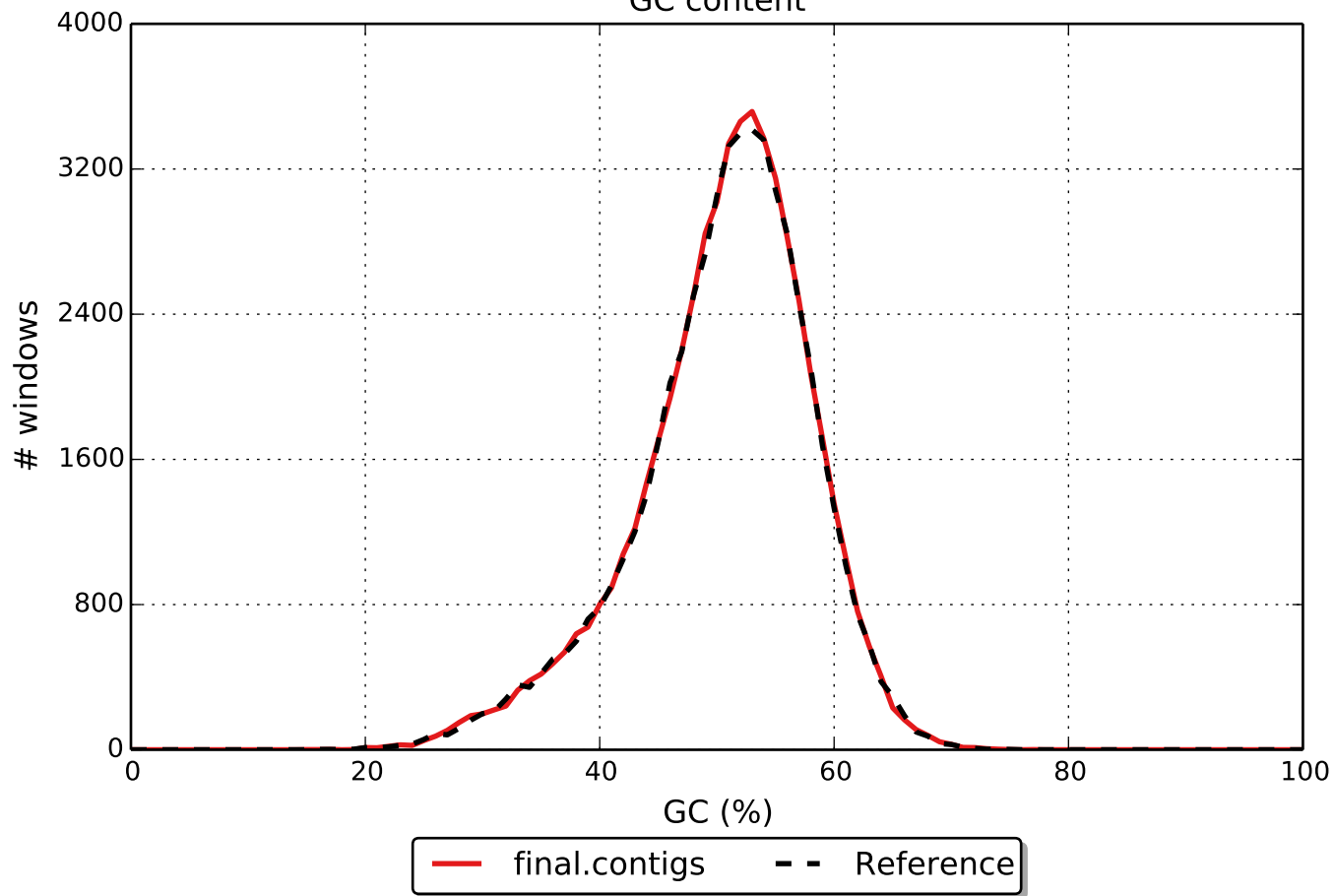
Unaligned report

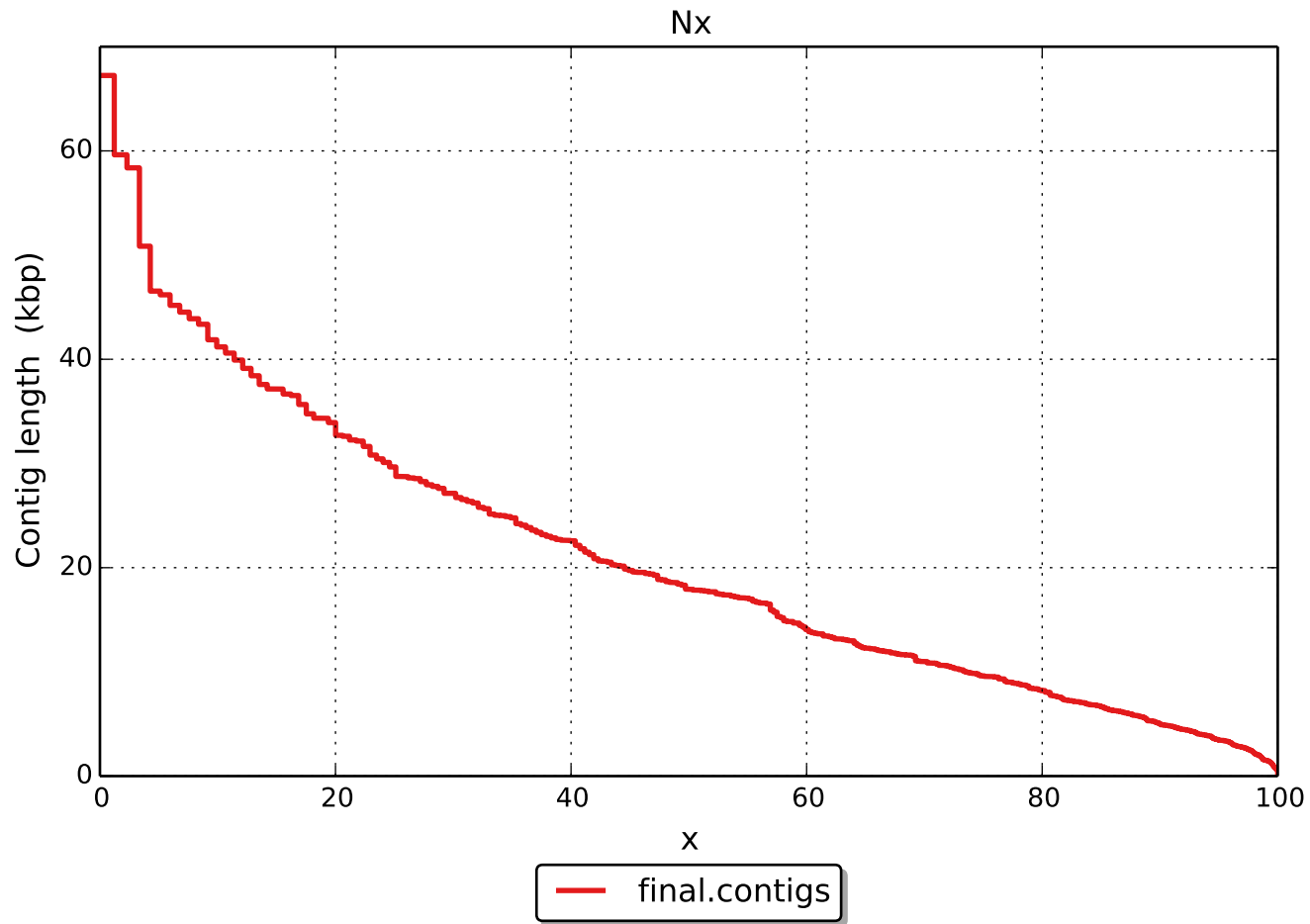
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

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).

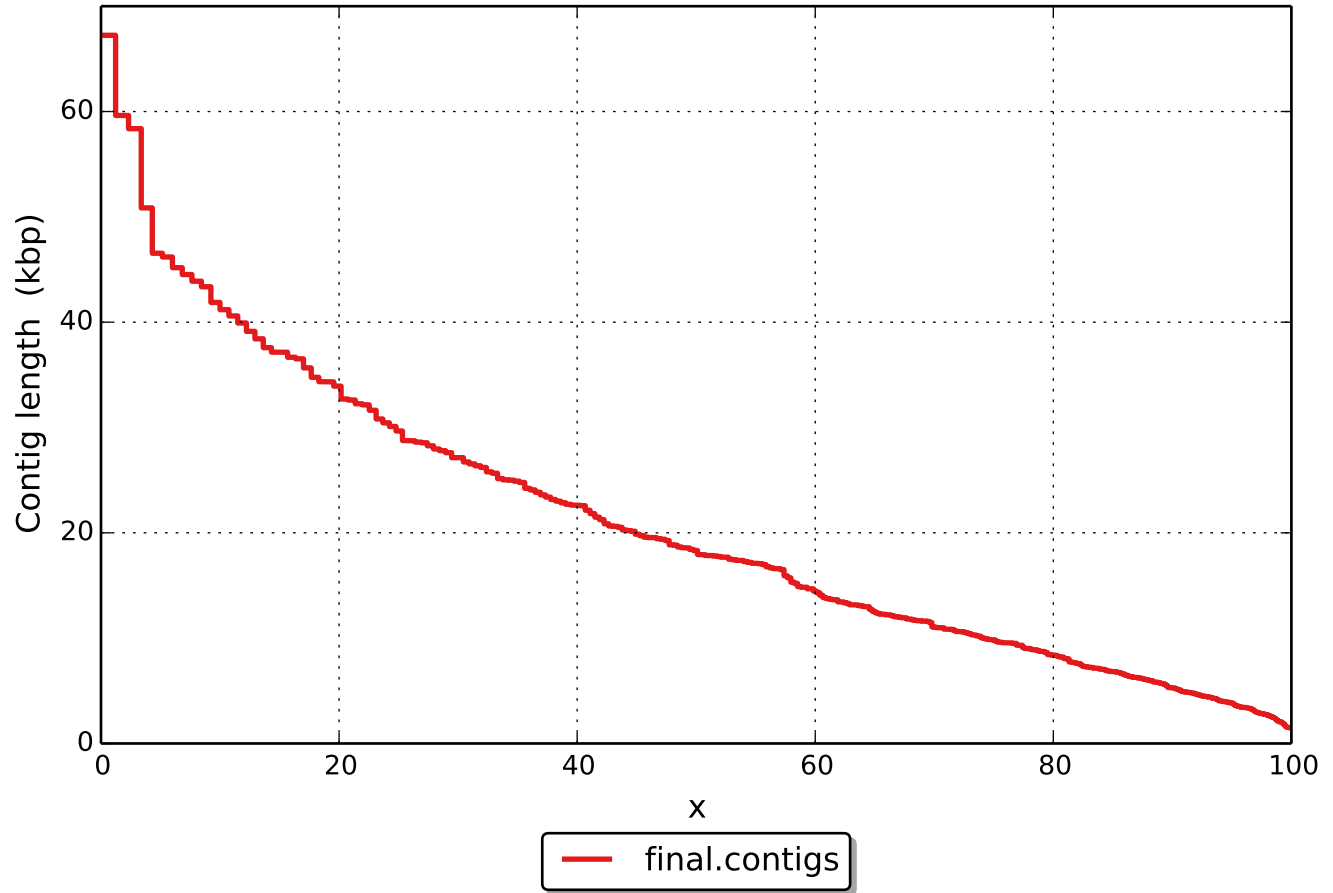


GC content



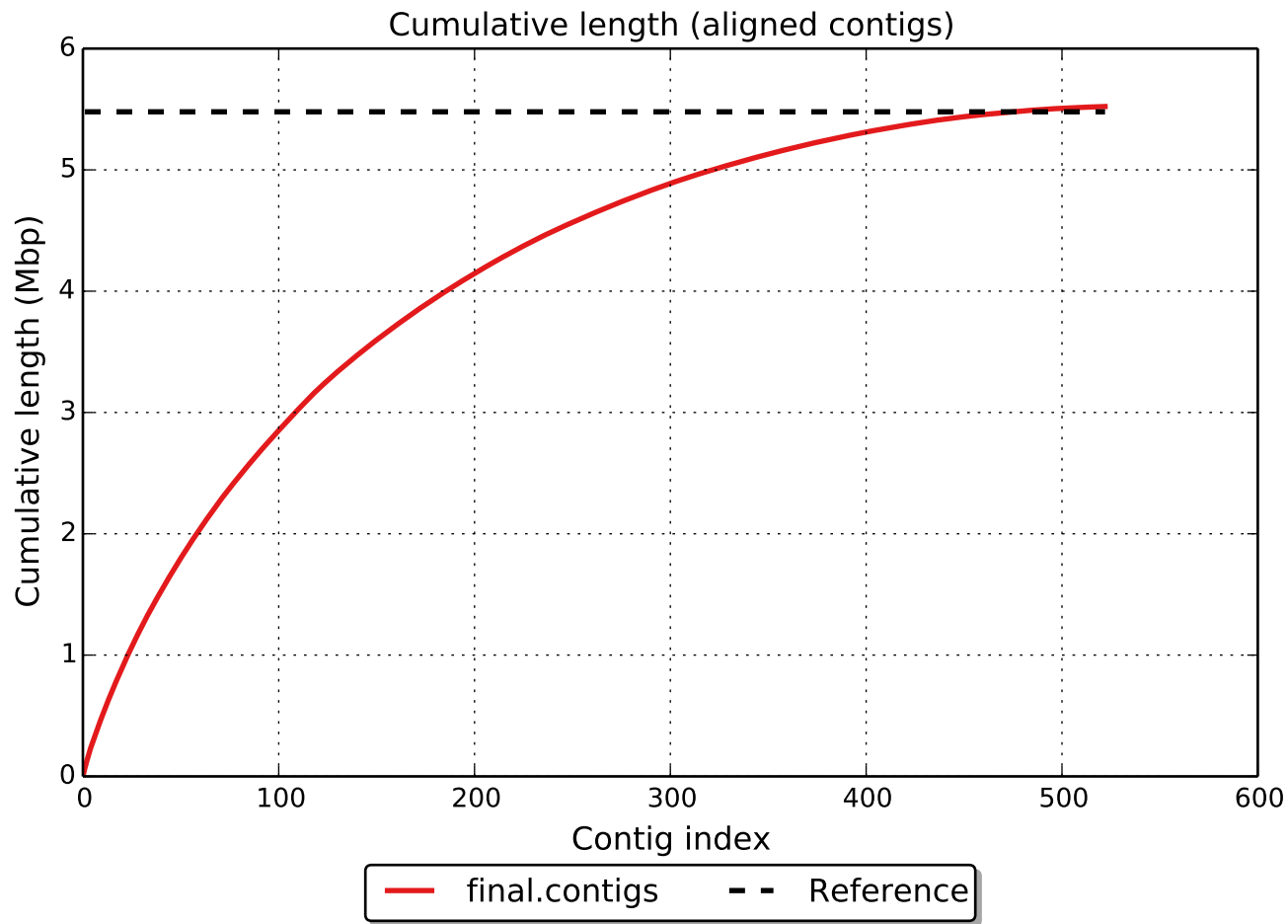


NGx

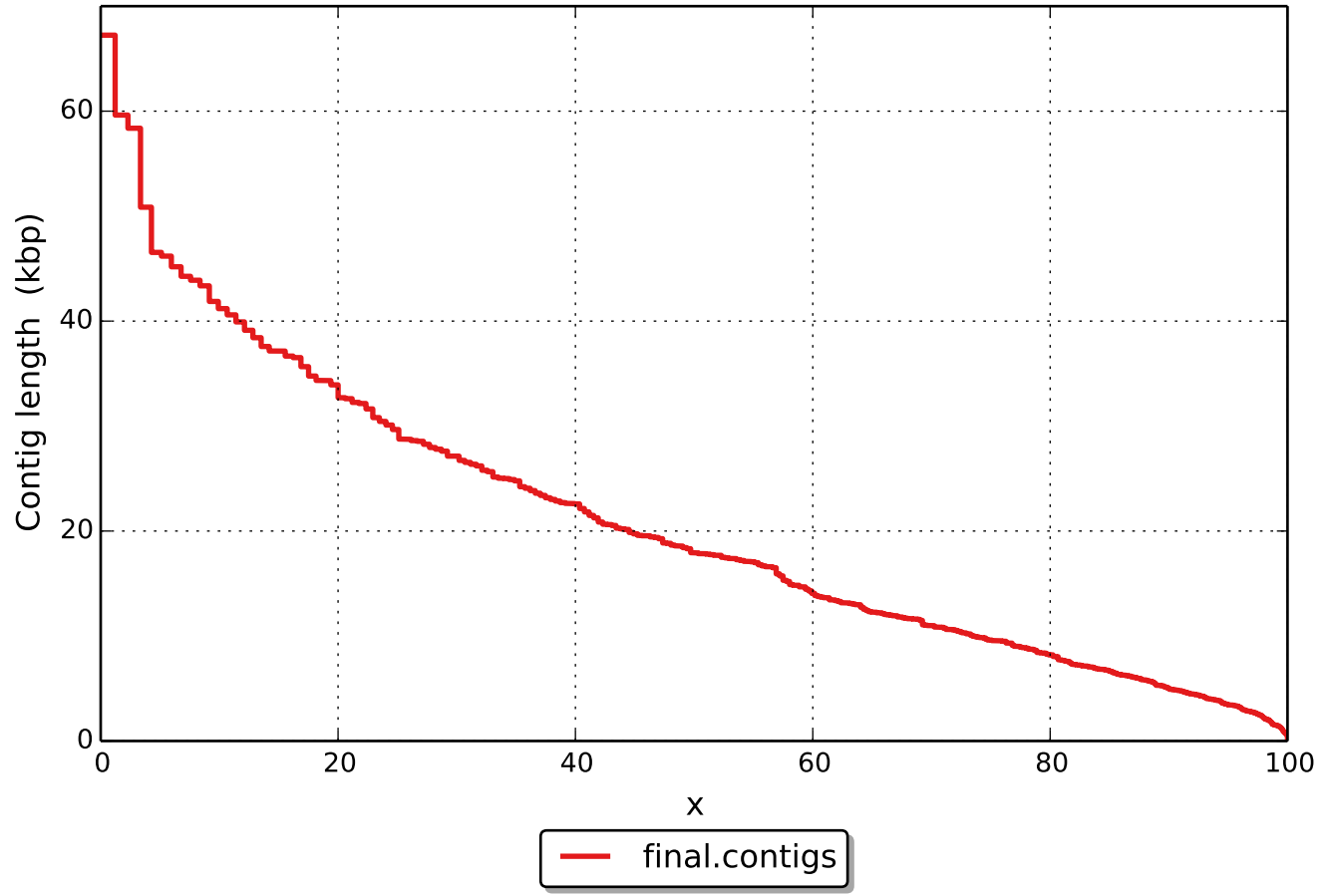


Misassemblies





NAx



NGAx

