

Report

| | final.contigs |
|--------------------------------|---------------|
| # contigs (≥ 0 bp) | 643 |
| # contigs (≥ 1000 bp) | 412 |
| Total length (≥ 0 bp) | 2584797 |
| Total length (≥ 1000 bp) | 2435209 |
| # contigs | 643 |
| Largest contig | 38656 |
| Total length | 2584797 |
| Reference length | 5547323 |
| GC (%) | 50.42 |
| Reference GC (%) | 50.48 |
| N50 | 8559 |
| N75 | 4250 |
| L50 | 89 |
| L75 | 197 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 46.220 |
| Duplication ratio | 1.008 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 422.16 |
| # indels per 100 kbp | 0.12 |
| Largest alignment | 38656 |
| NA50 | 8559 |
| NA75 | 4250 |
| LA50 | 89 |
| LA75 | 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

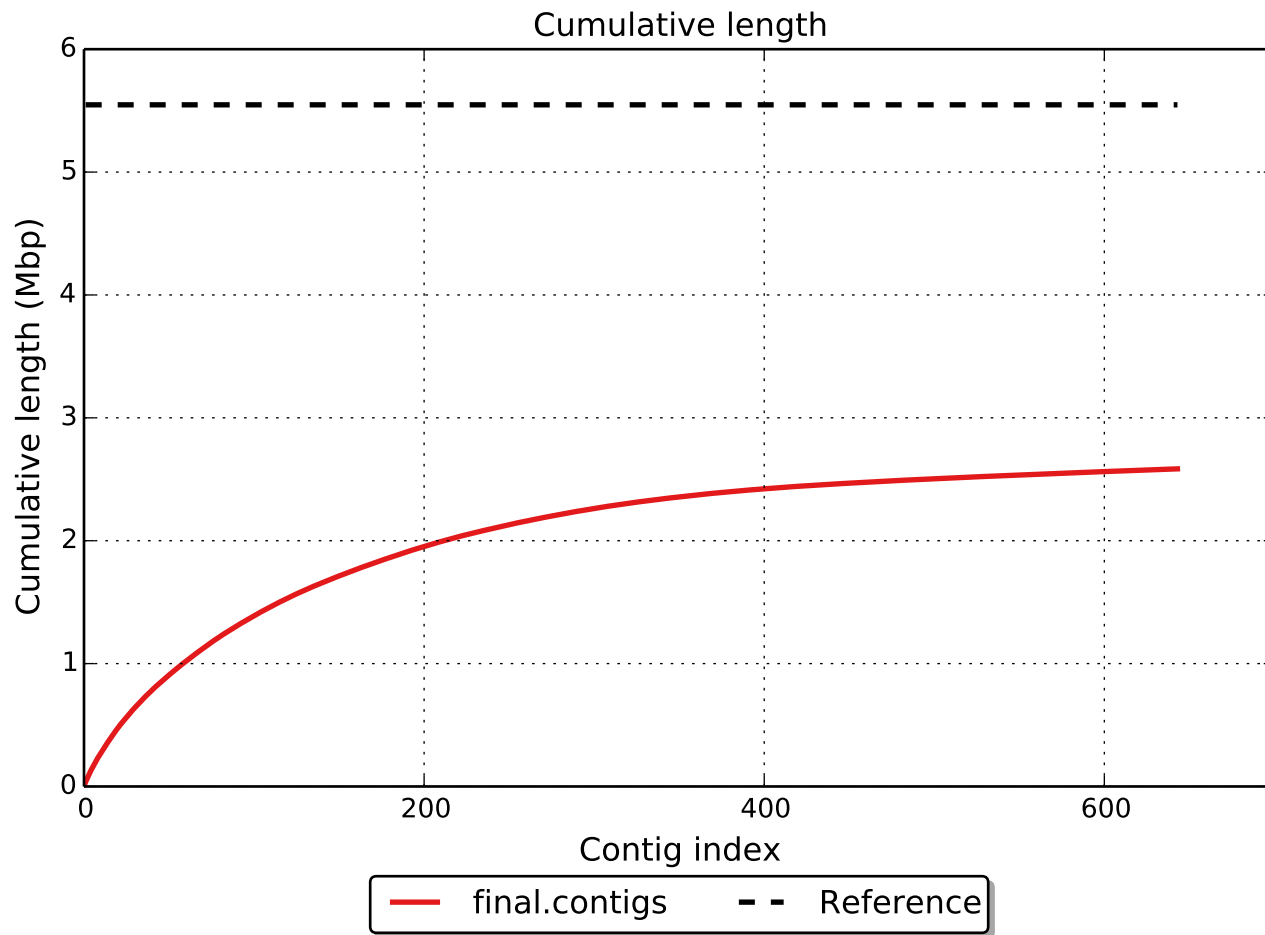
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 10824 |
| # indels | 3 |
| # short indels | 3 |
| # 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).

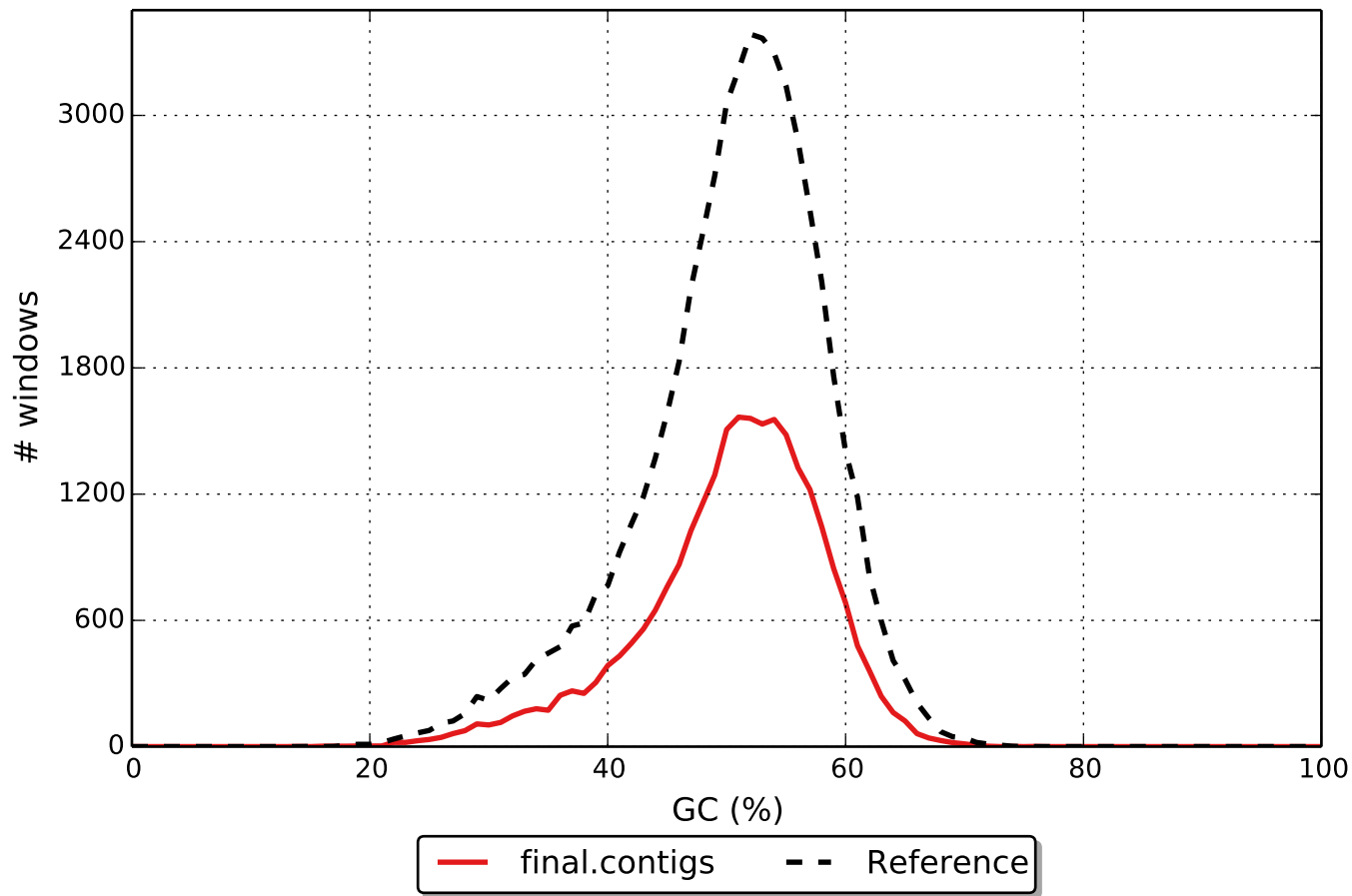
Unaligned report

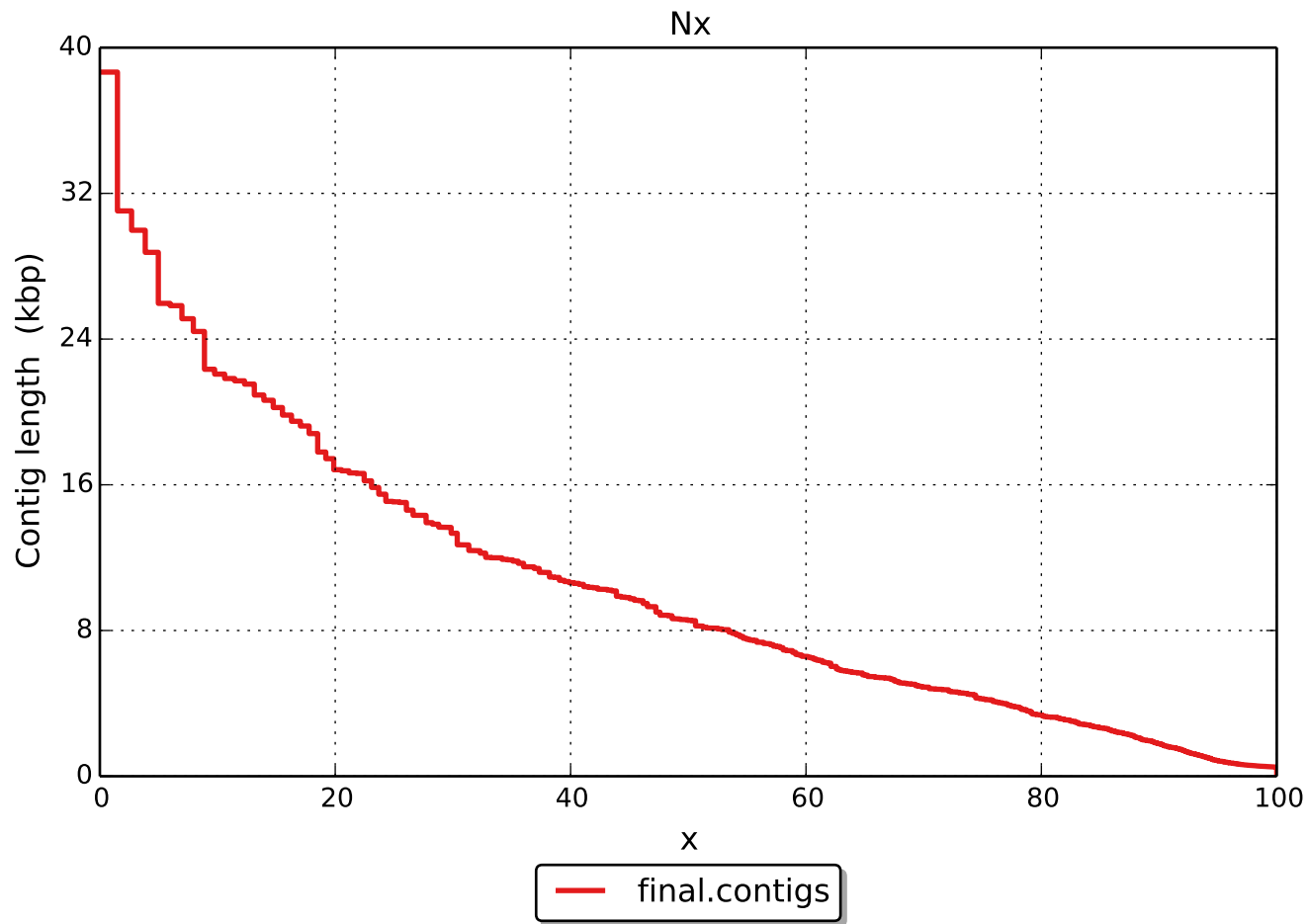
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

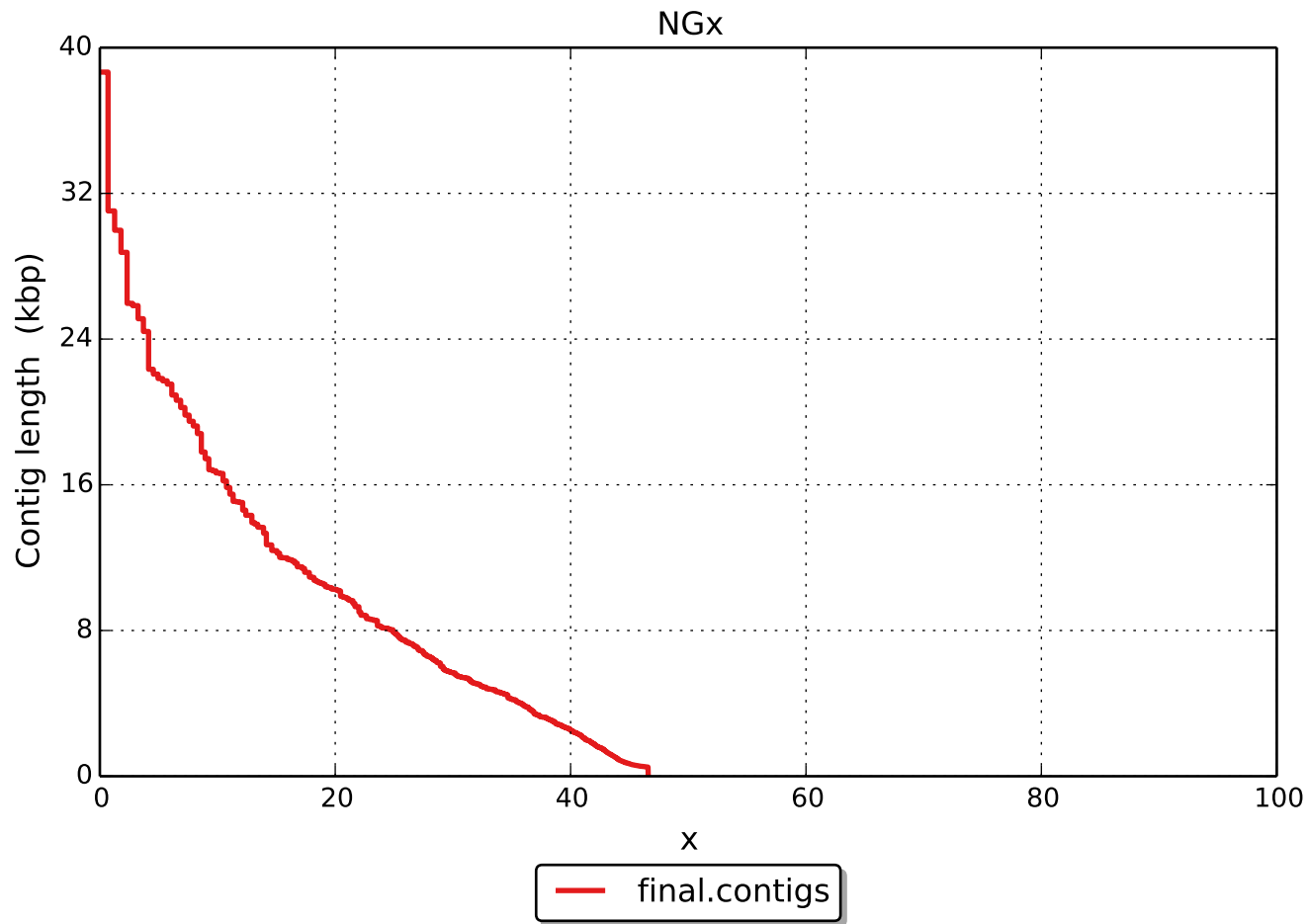
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

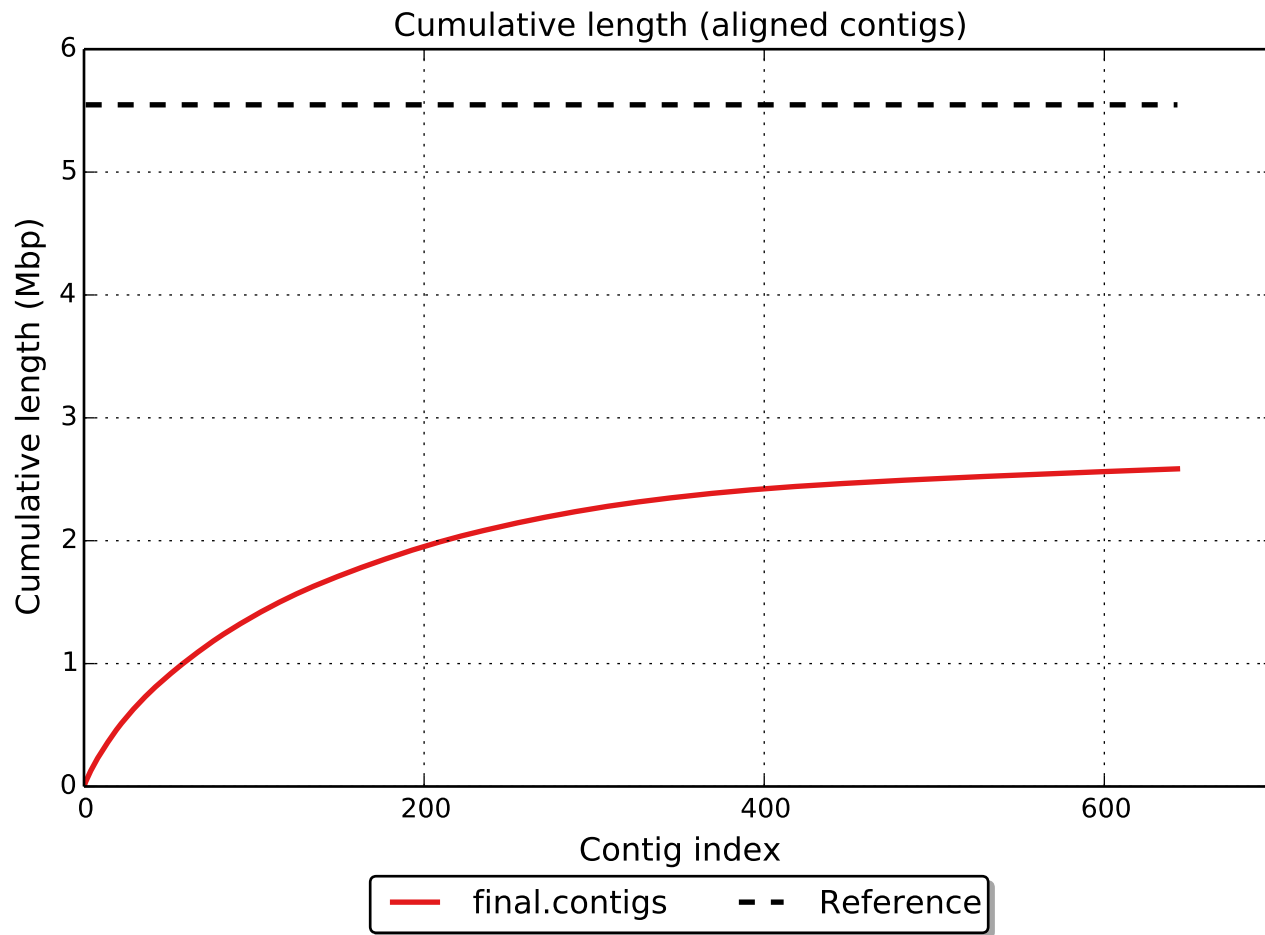


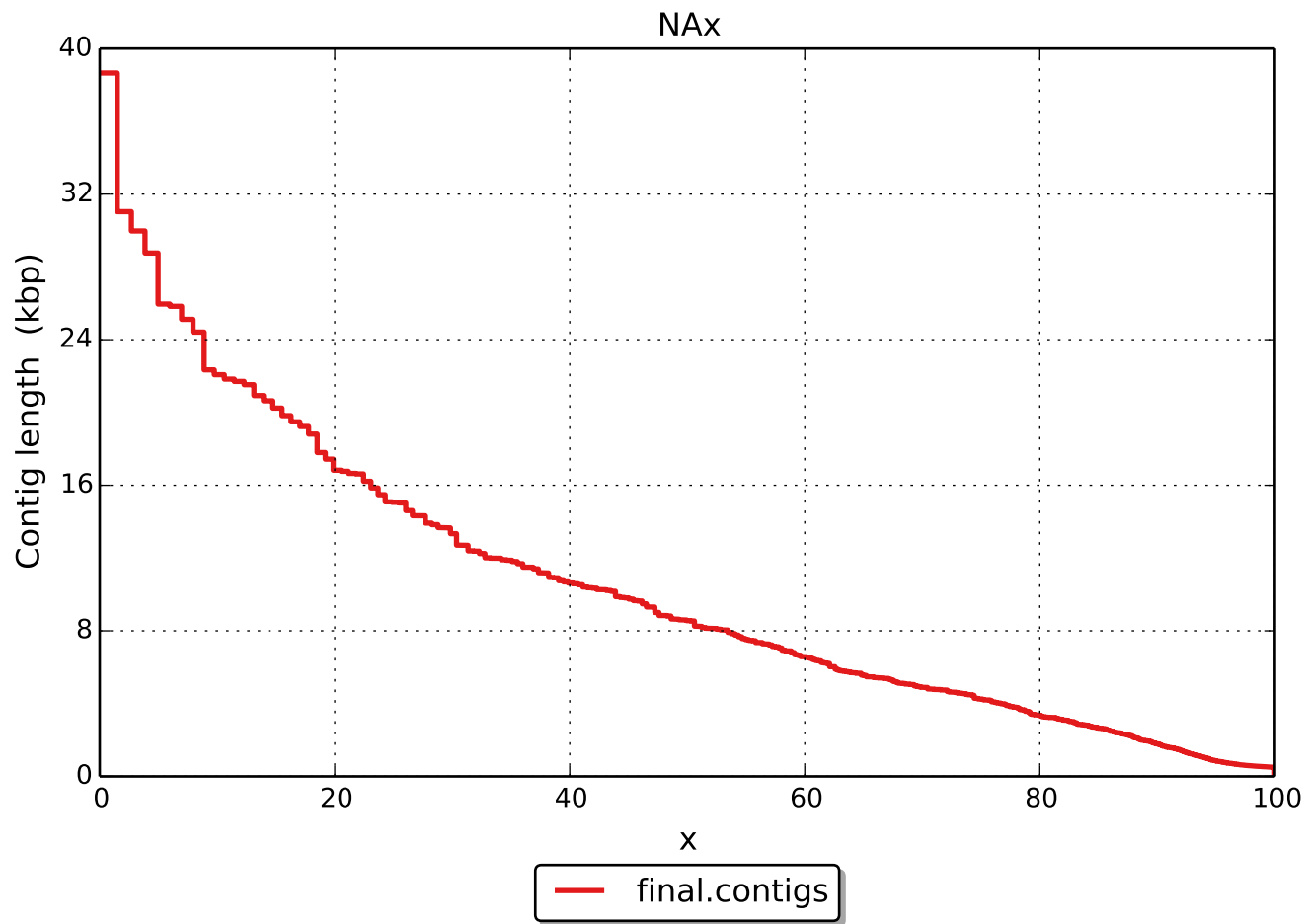




Misassemblies







NGAx

