

Report

| | final.contigs |
|--------------------------------|---------------|
| # contigs (≥ 0 bp) | 481 |
| # contigs (≥ 1000 bp) | 146 |
| Total length (≥ 0 bp) | 724691 |
| Total length (≥ 1000 bp) | 575096 |
| # contigs | 245 |
| Largest contig | 15816 |
| Total length | 641029 |
| Reference length | 1231960 |
| GC (%) | 25.36 |
| Reference GC (%) | 25.35 |
| N50 | 4661 |
| NG50 | 643 |
| N75 | 2314 |
| L50 | 42 |
| LG50 | 200 |
| L75 | 91 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 95.818 |
| Duplication ratio | 1.025 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 603.17 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 15816 |
| NA50 | 4661 |
| NGA50 | 643 |
| NA75 | 2314 |
| LA50 | 42 |
| LGA50 | 200 |
| LA75 | 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 | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 7120 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

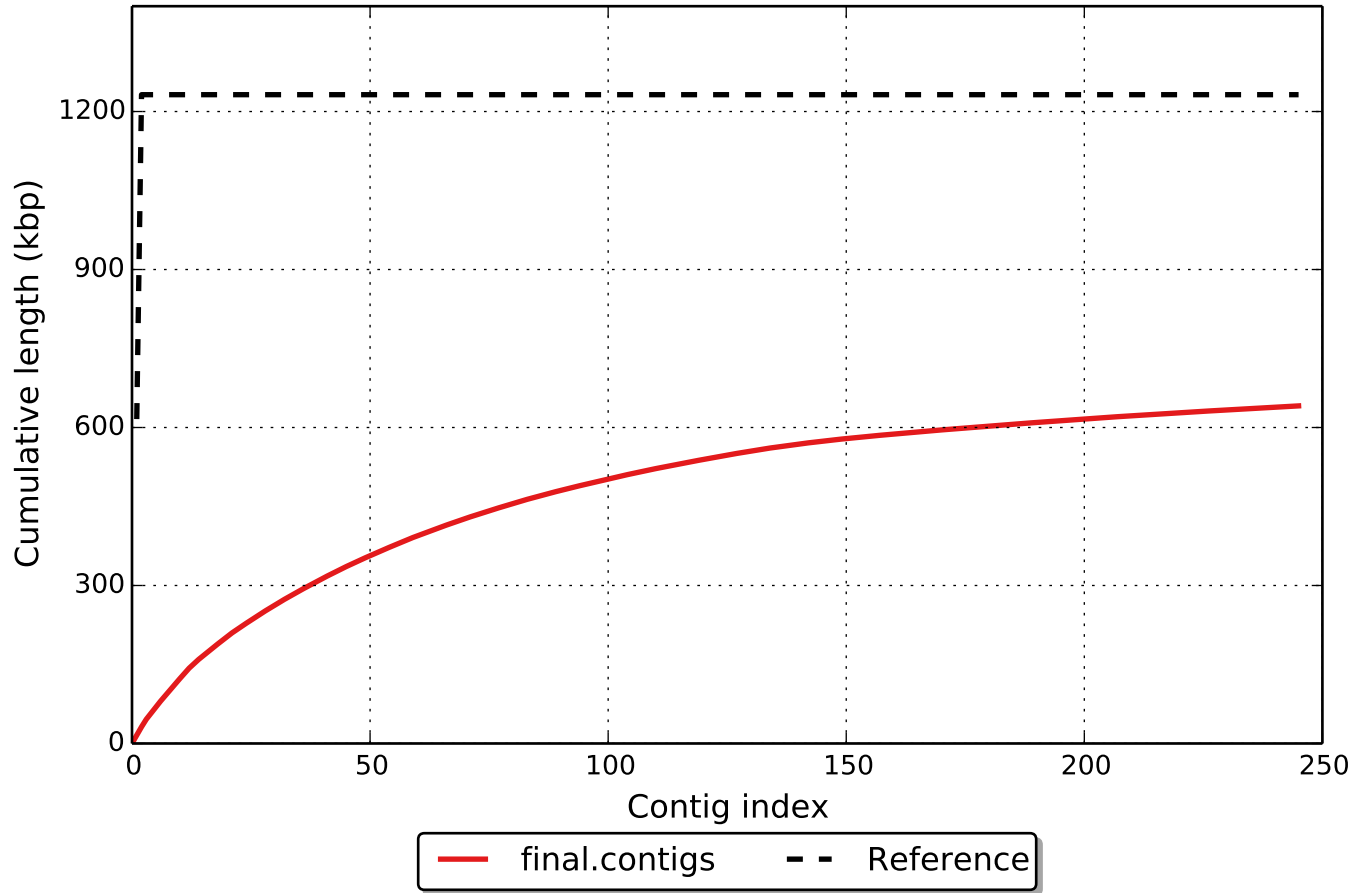
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

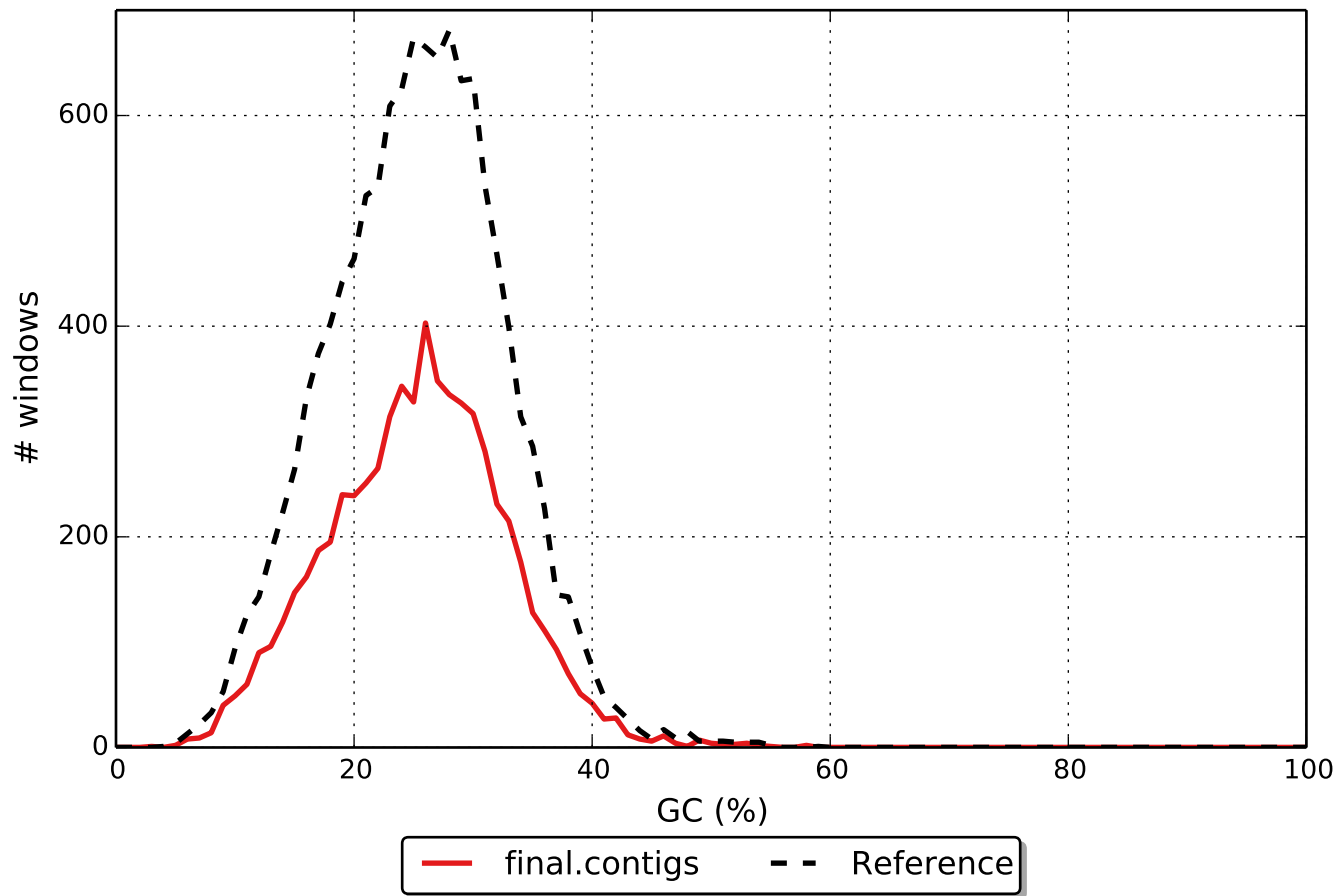
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

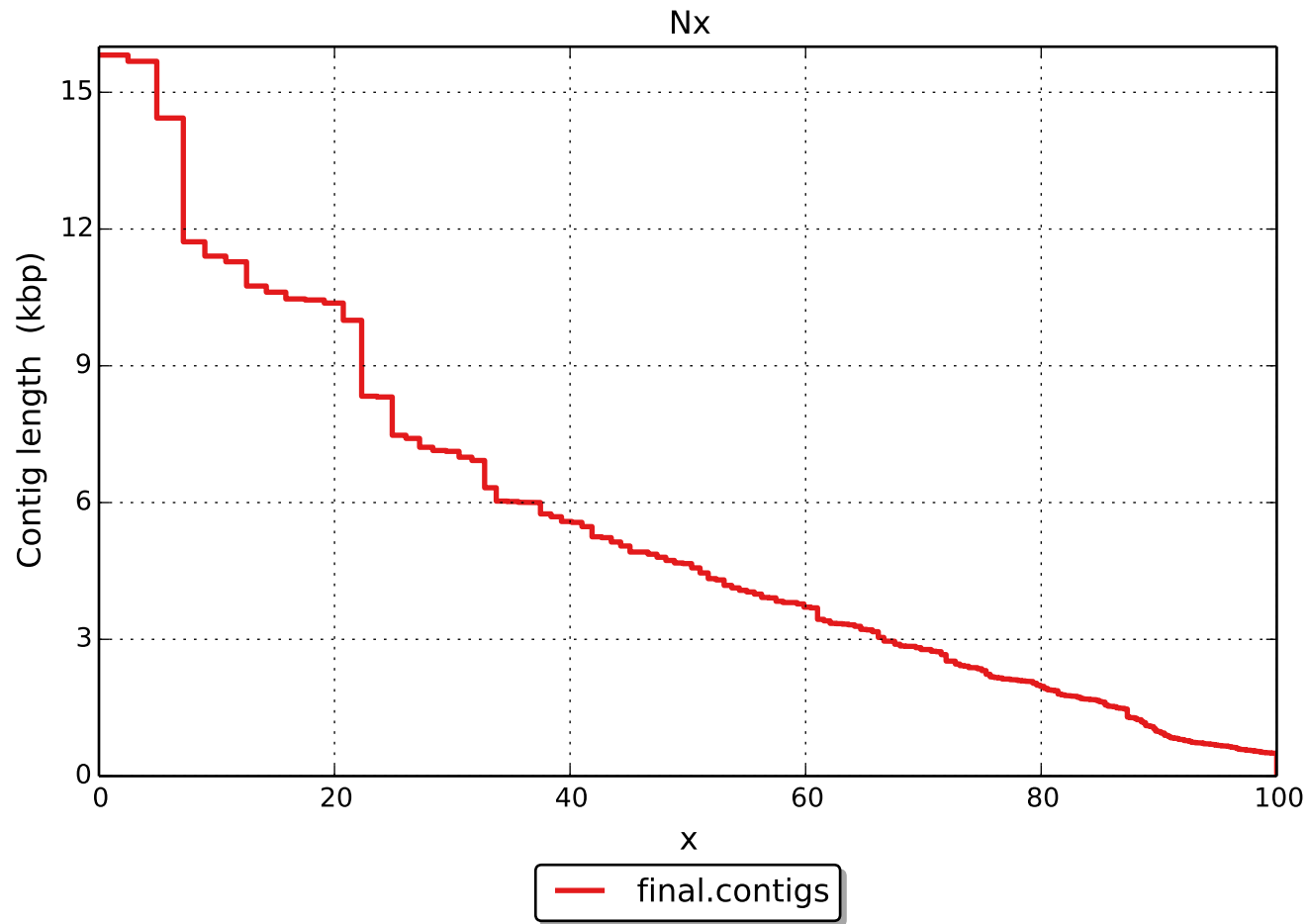
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

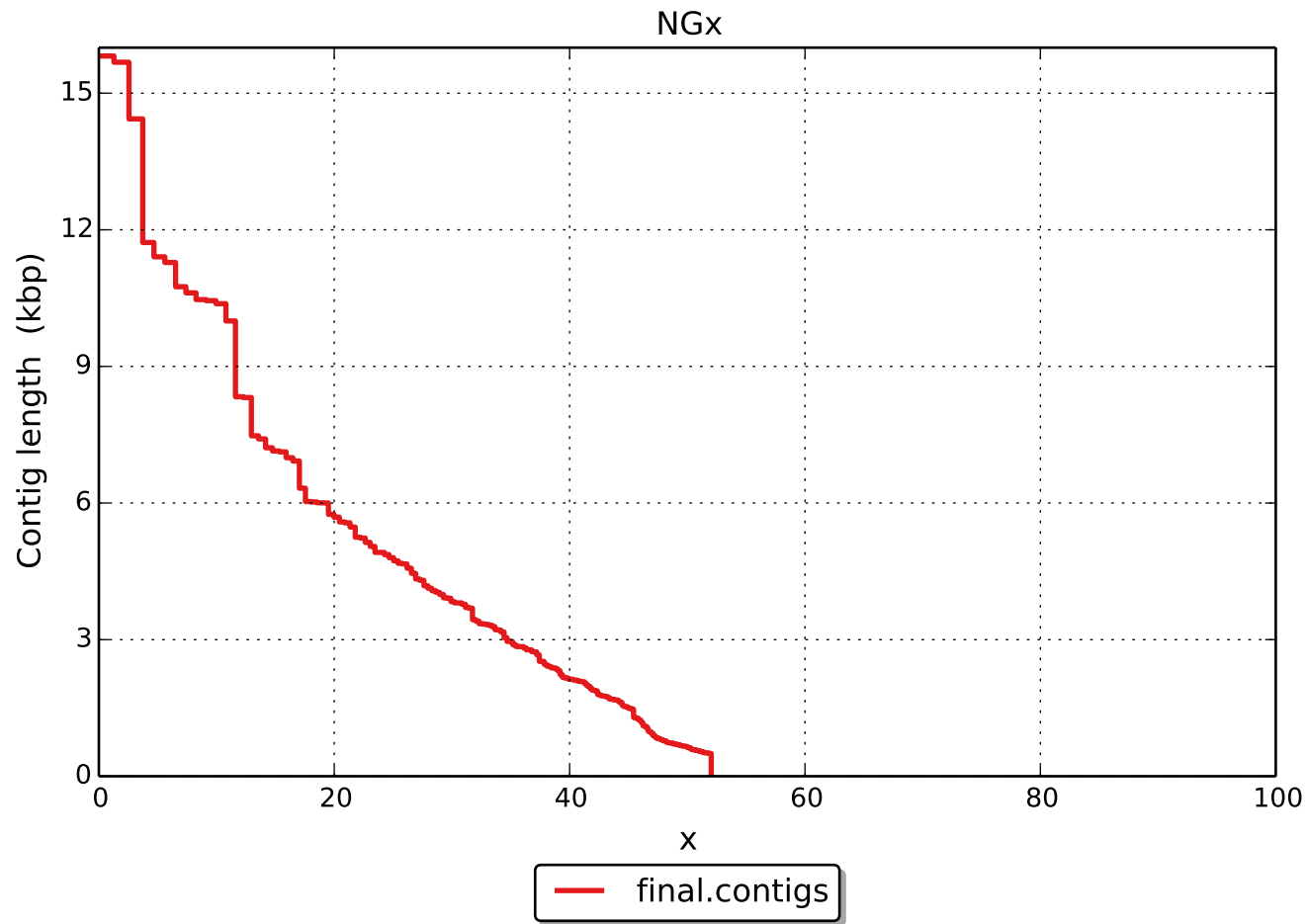
Cumulative length



GC content



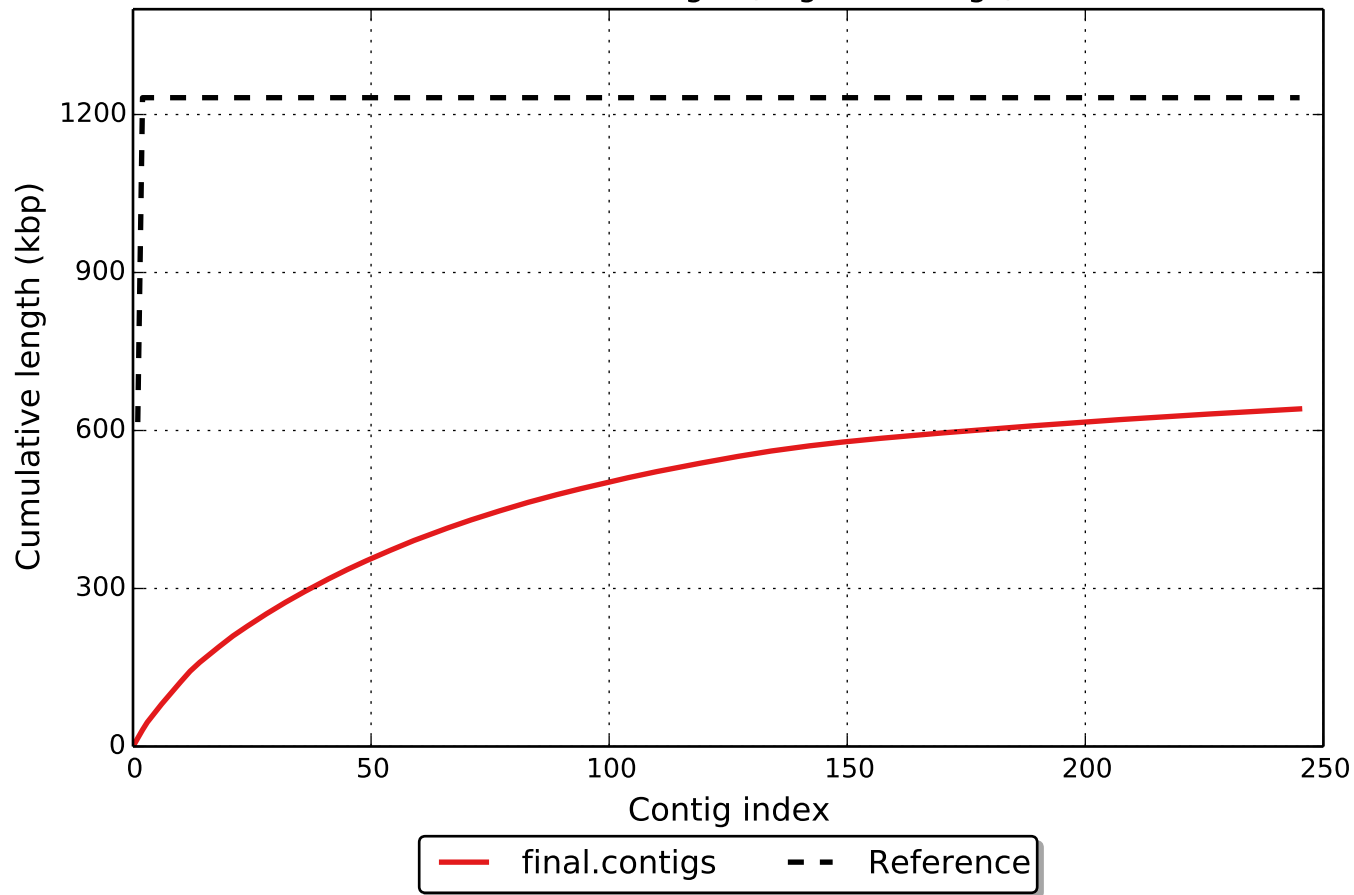


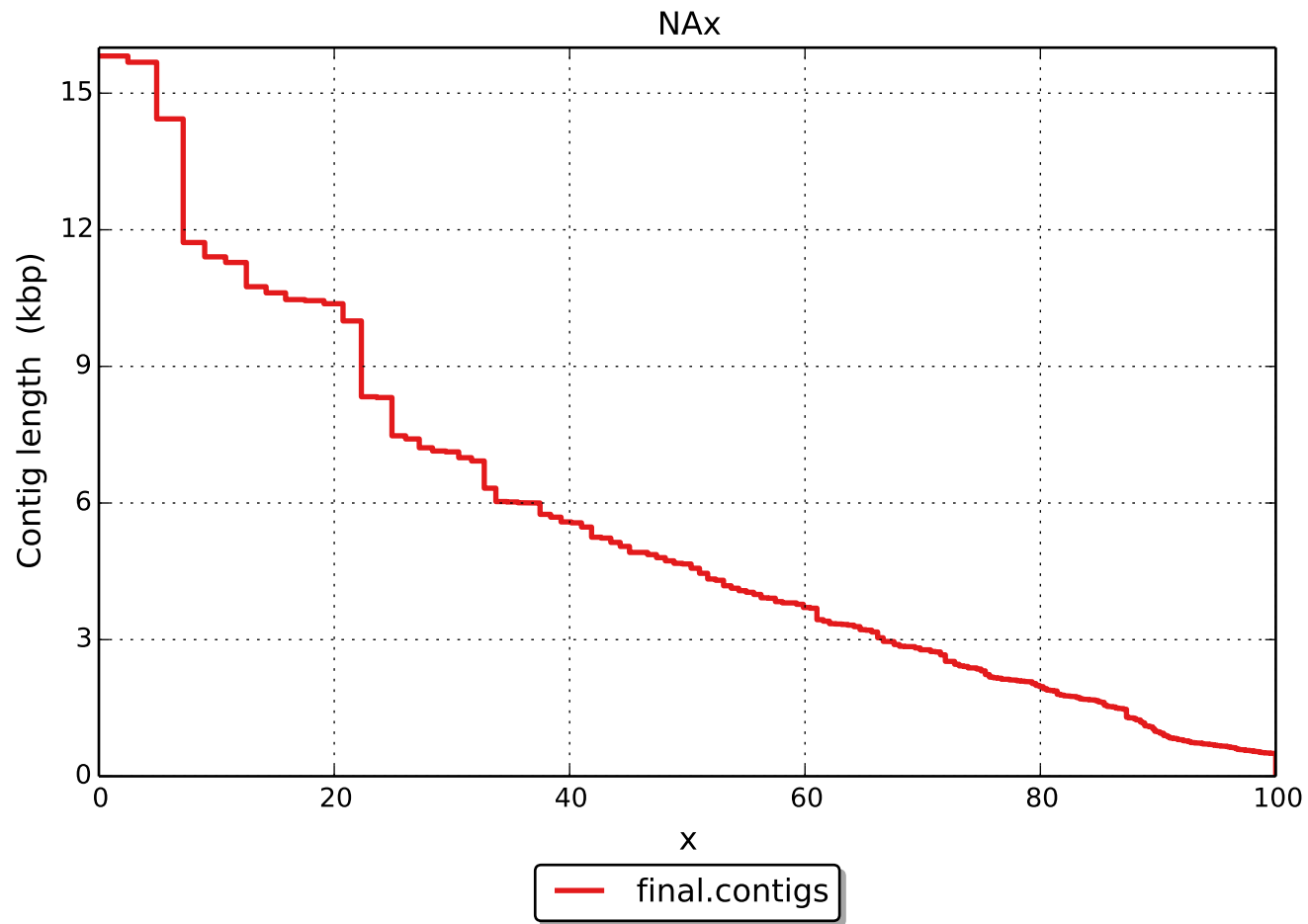


Misassemblies



Cumulative length (aligned contigs)





NGAx

