

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp) | 129 |
| # contigs (>= 1000 bp) | 123 |
| Total length (>= 0 bp) | 1293350 |
| Total length (>= 1000 bp) | 1289336 |
| # contigs | 127 |
| Largest contig | 52933 |
| Total length | 1292592 |
| Reference length | 1283598 |
| GC (%) | 26.30 |
| Reference GC (%) | 26.30 |
| N50 | 16928 |
| NG50 | 16928 |
| N75 | 9299 |
| NG75 | 9306 |
| L50 | 25 |
| LG50 | 25 |
| L75 | 51 |
| LG75 | 50 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 99.538 |
| Duplication ratio | 1.012 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 26.06 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 52933 |
| NA50 | 16928 |
| NGA50 | 16928 |
| NA75 | 9299 |
| NGA75 | 9306 |
| LA50 | 25 |
| LGA50 | 25 |
| LA75 | 51 |
| LGA75 | 50 |

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 | 333 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

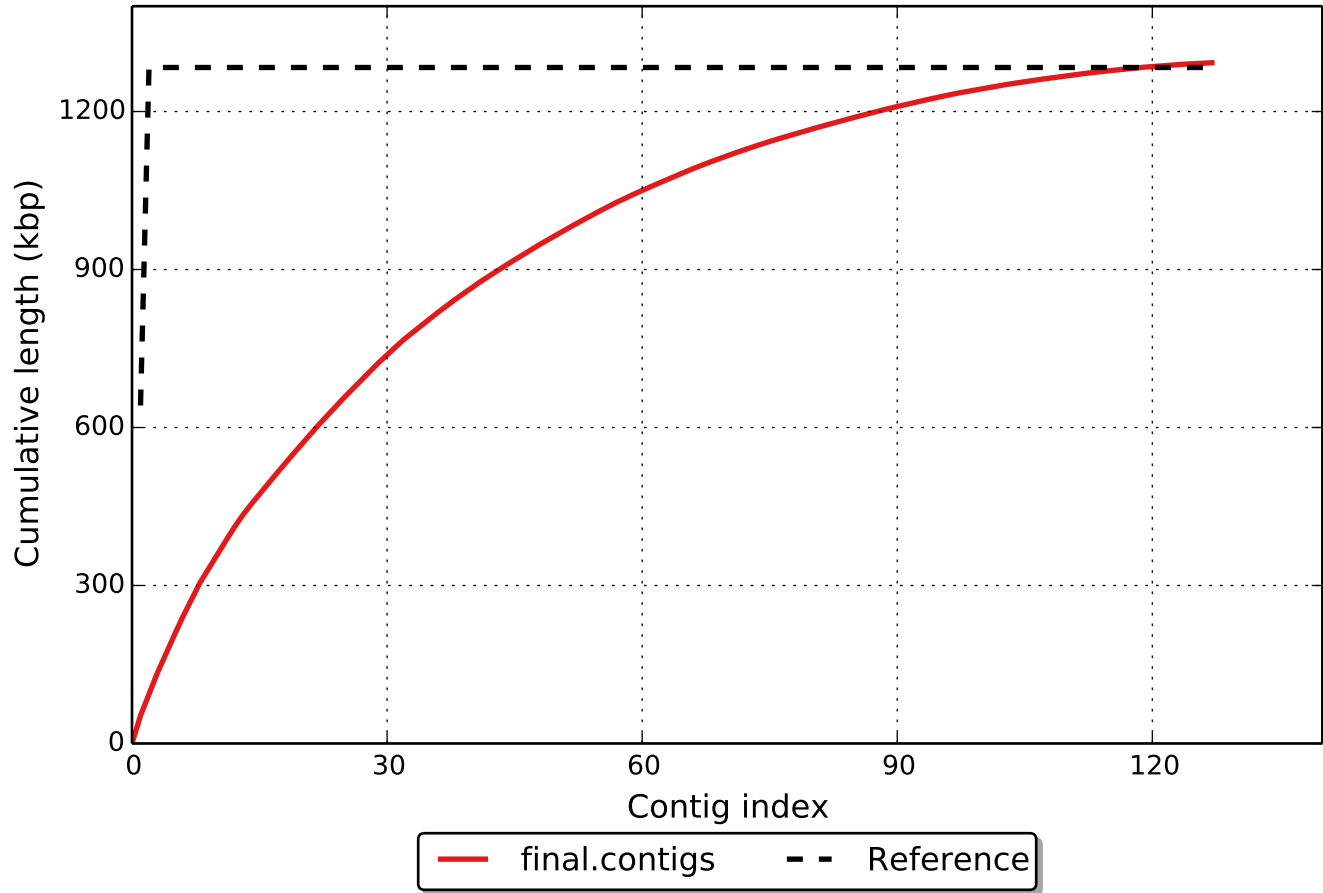
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

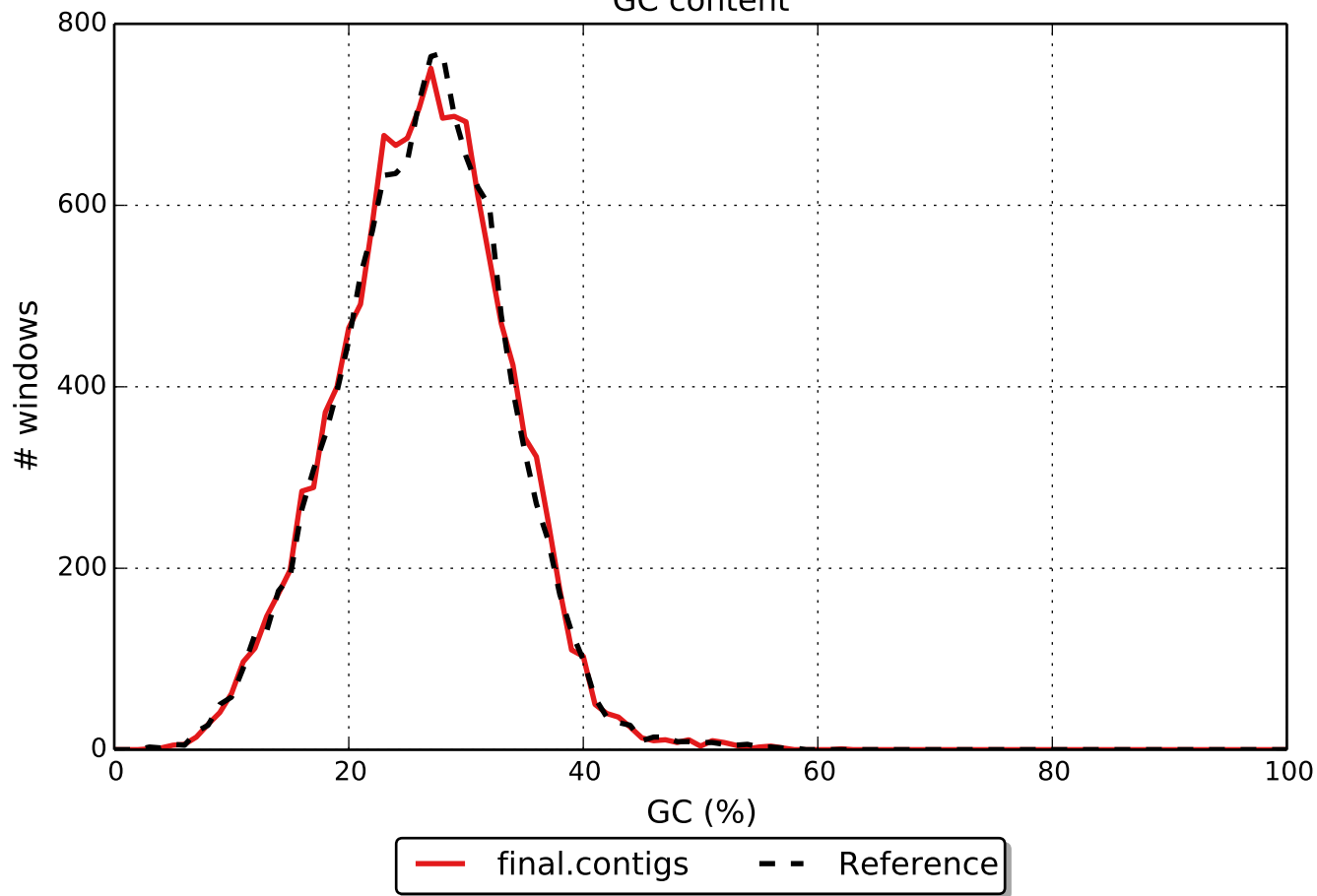
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

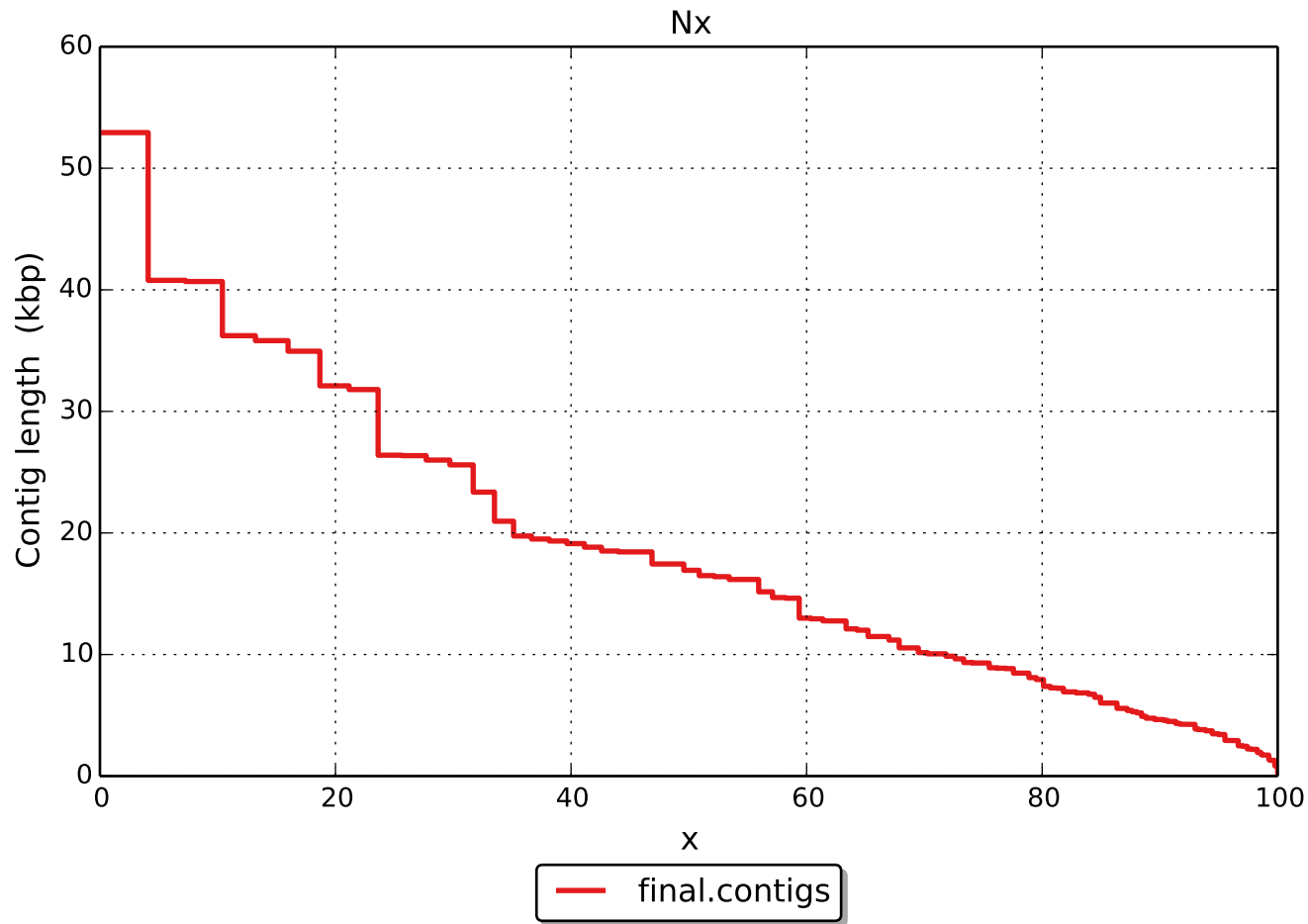
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

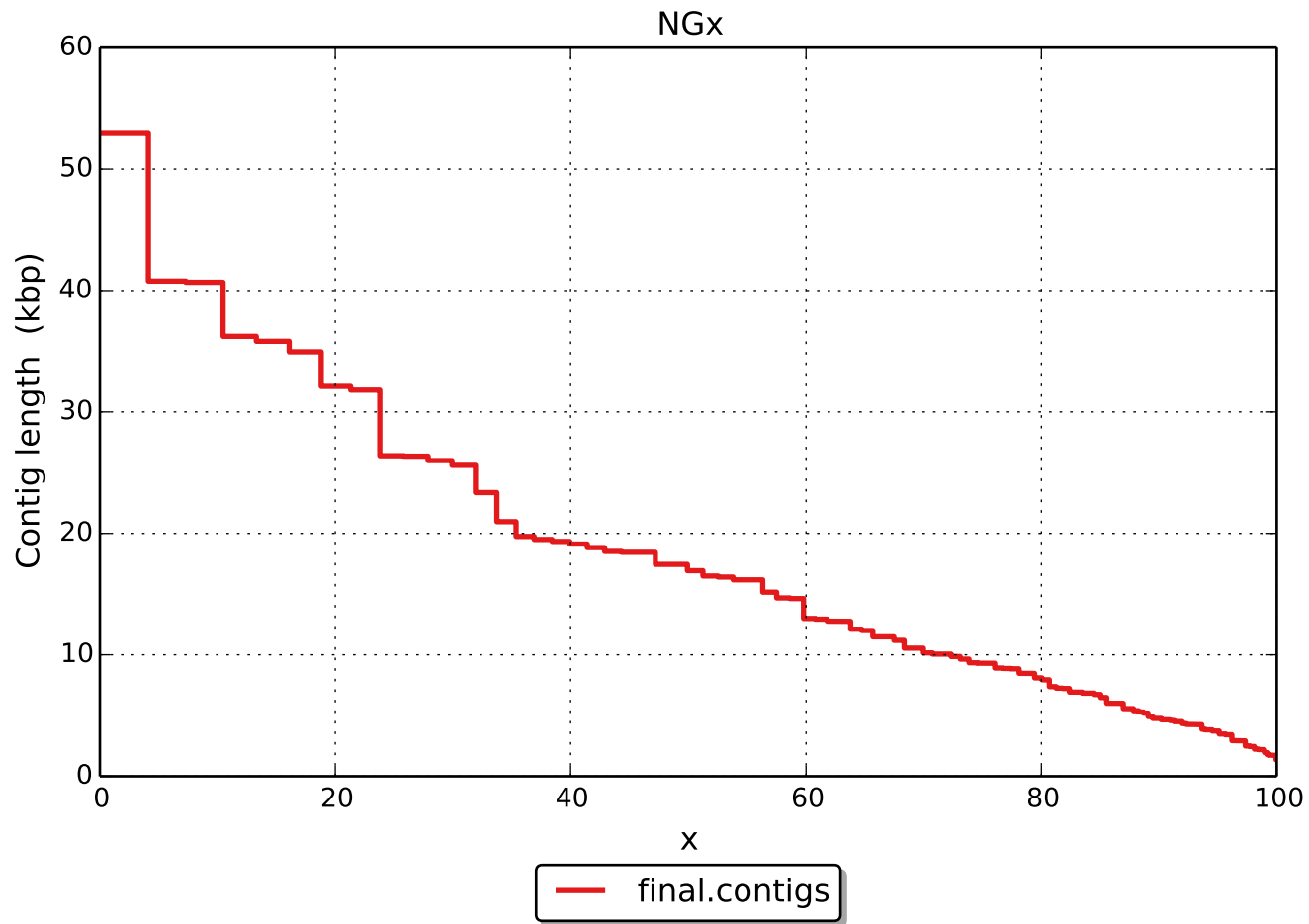
Cumulative length



GC content



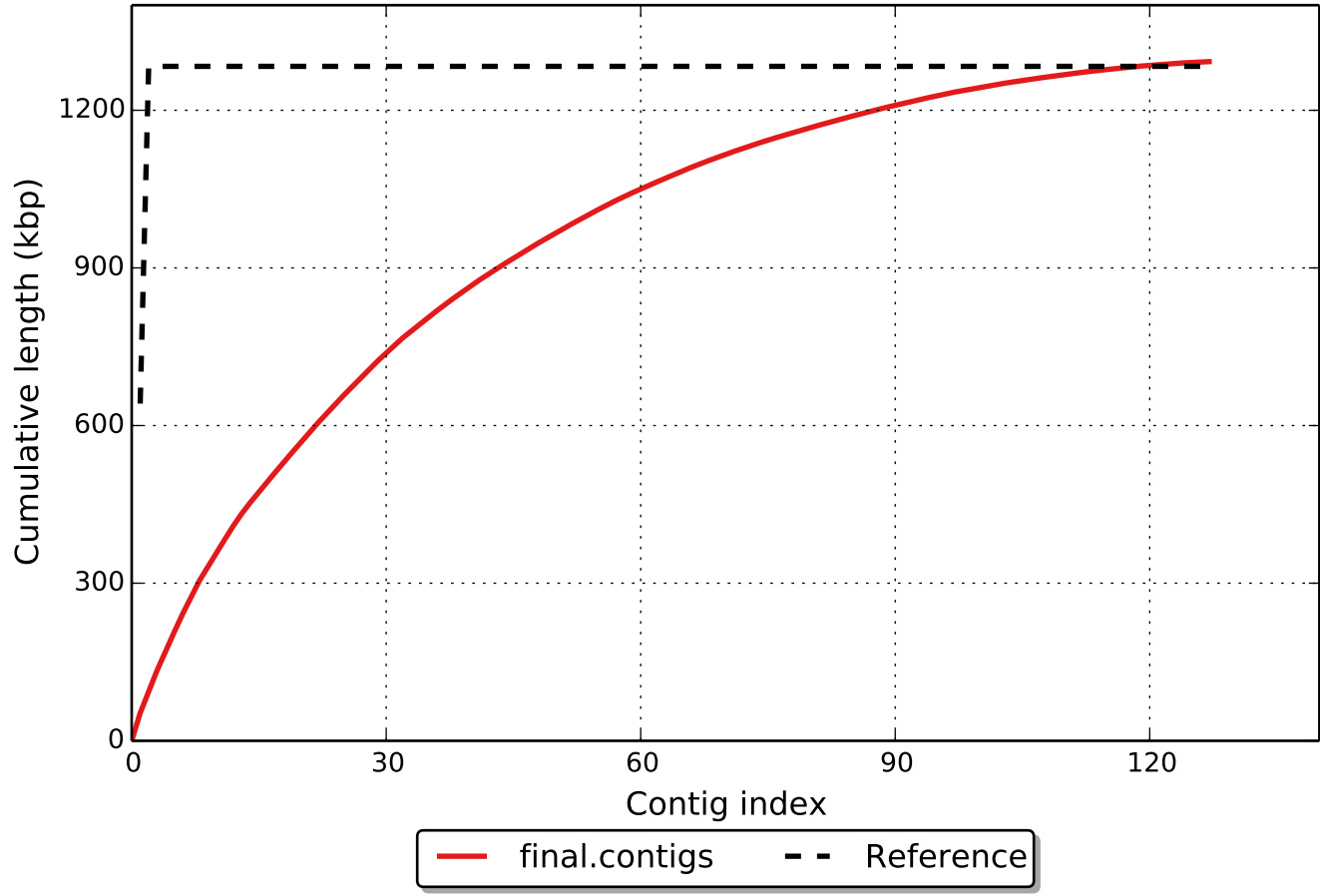


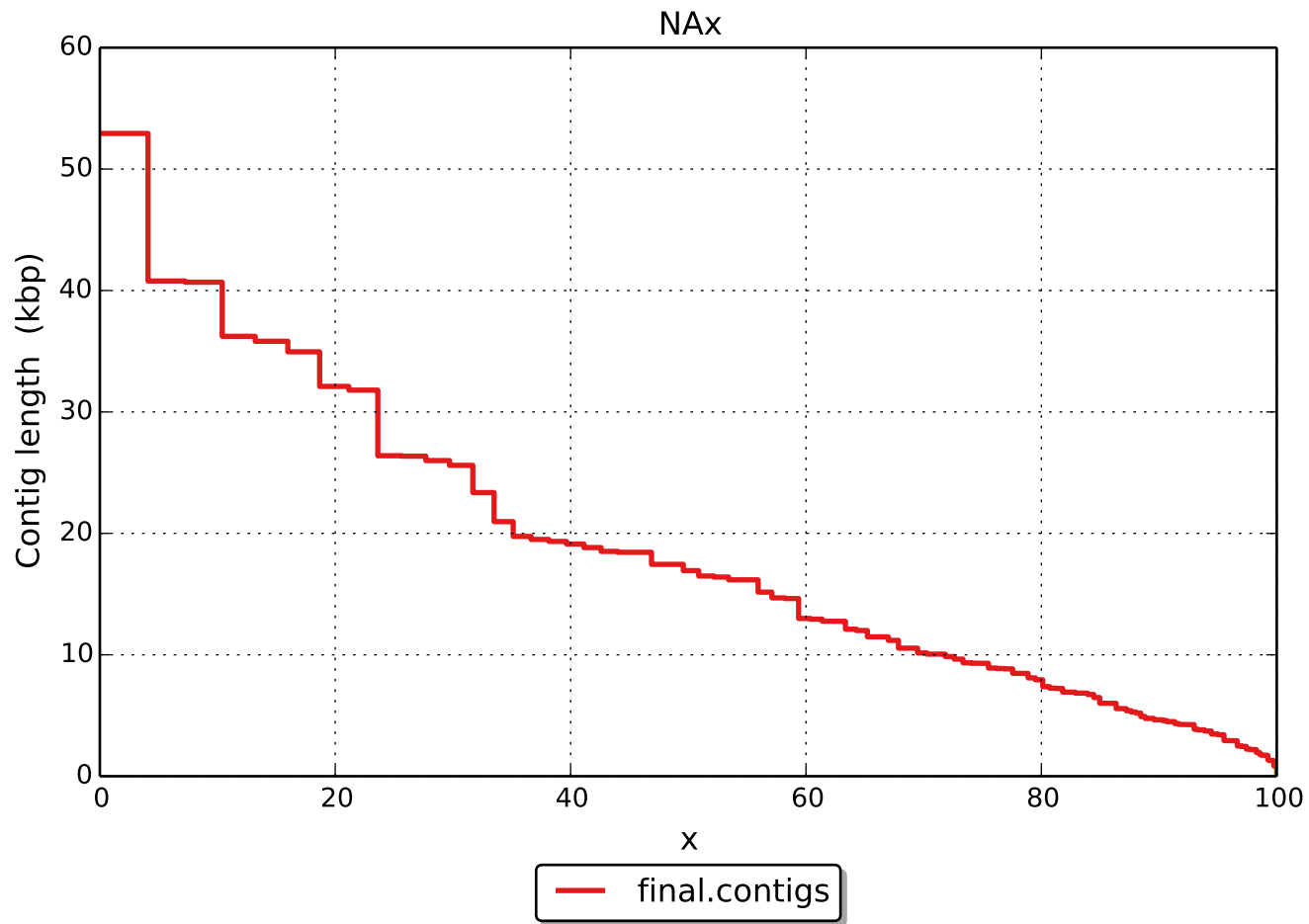


Misassemblies



Cumulative length (aligned contigs)





NGAx

