

Report

| | final.contigs |
|--------------------------------|---------------|
| # contigs (≥ 0 bp) | 1674 |
| # contigs (≥ 1000 bp) | 351 |
| Total length (≥ 0 bp) | 1243657 |
| Total length (≥ 1000 bp) | 503853 |
| # contigs | 1101 |
| Largest contig | 2937 |
| Total length | 1035241 |
| Reference length | 1283598 |
| GC (%) | 26.39 |
| Reference GC (%) | 26.30 |
| N50 | 984 |
| NG50 | 849 |
| N75 | 720 |
| NG75 | 568 |
| L50 | 365 |
| LG50 | 502 |
| L75 | 674 |
| LG75 | 966 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 83.207 |
| Duplication ratio | 1.068 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 199.52 |
| # indels per 100 kbp | 0.19 |
| Largest alignment | 2937 |
| NA50 | 984 |
| NGA50 | 849 |
| NA75 | 720 |
| NGA75 | 568 |
| LA50 | 365 |
| LGA50 | 502 |
| LA75 | 674 |
| LGA75 | 966 |

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 | 2131 |
| # indels | 2 |
| # short indels | 2 |
| # long indels | 0 |
| Indels length | 2 |

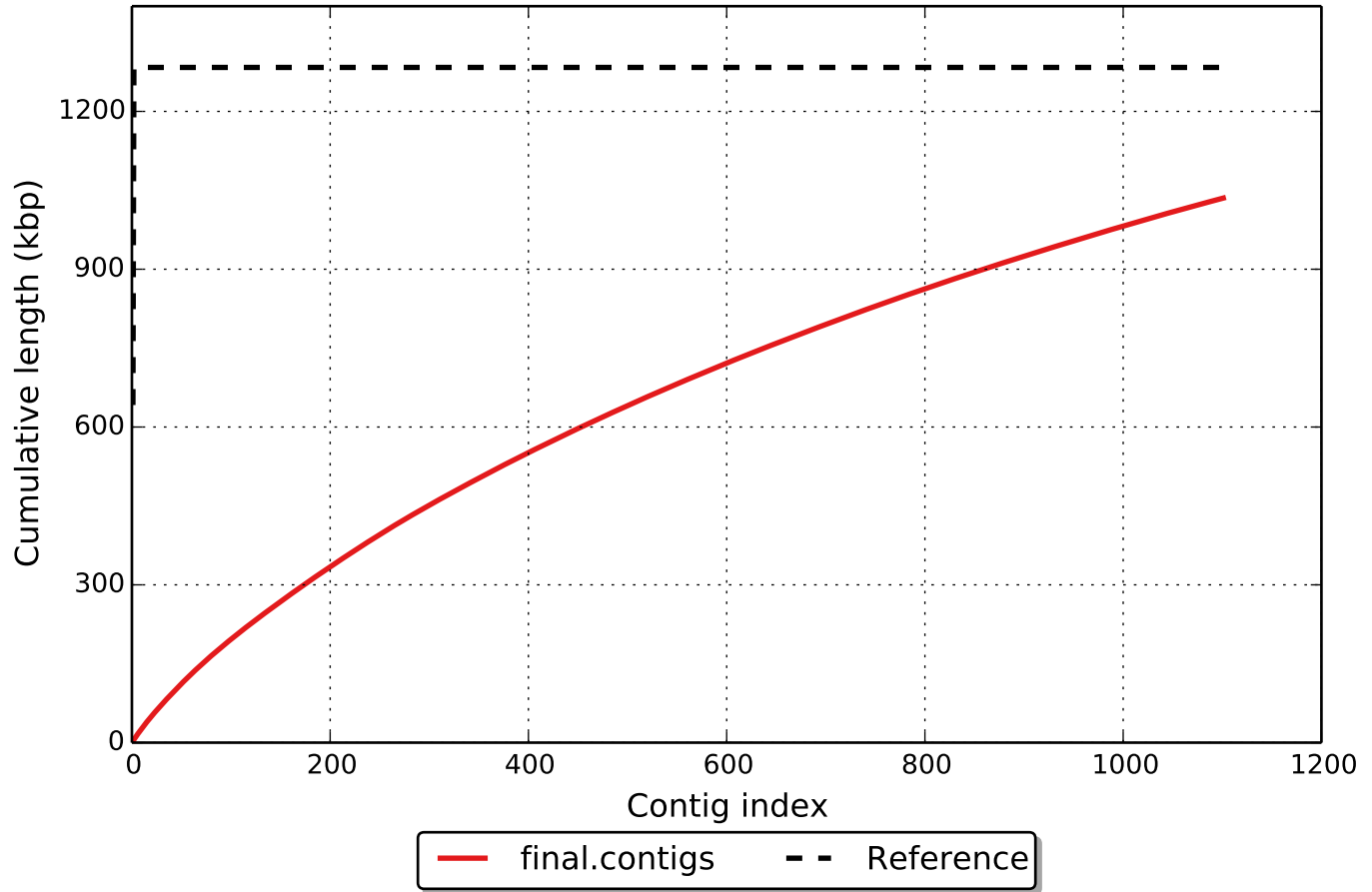
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

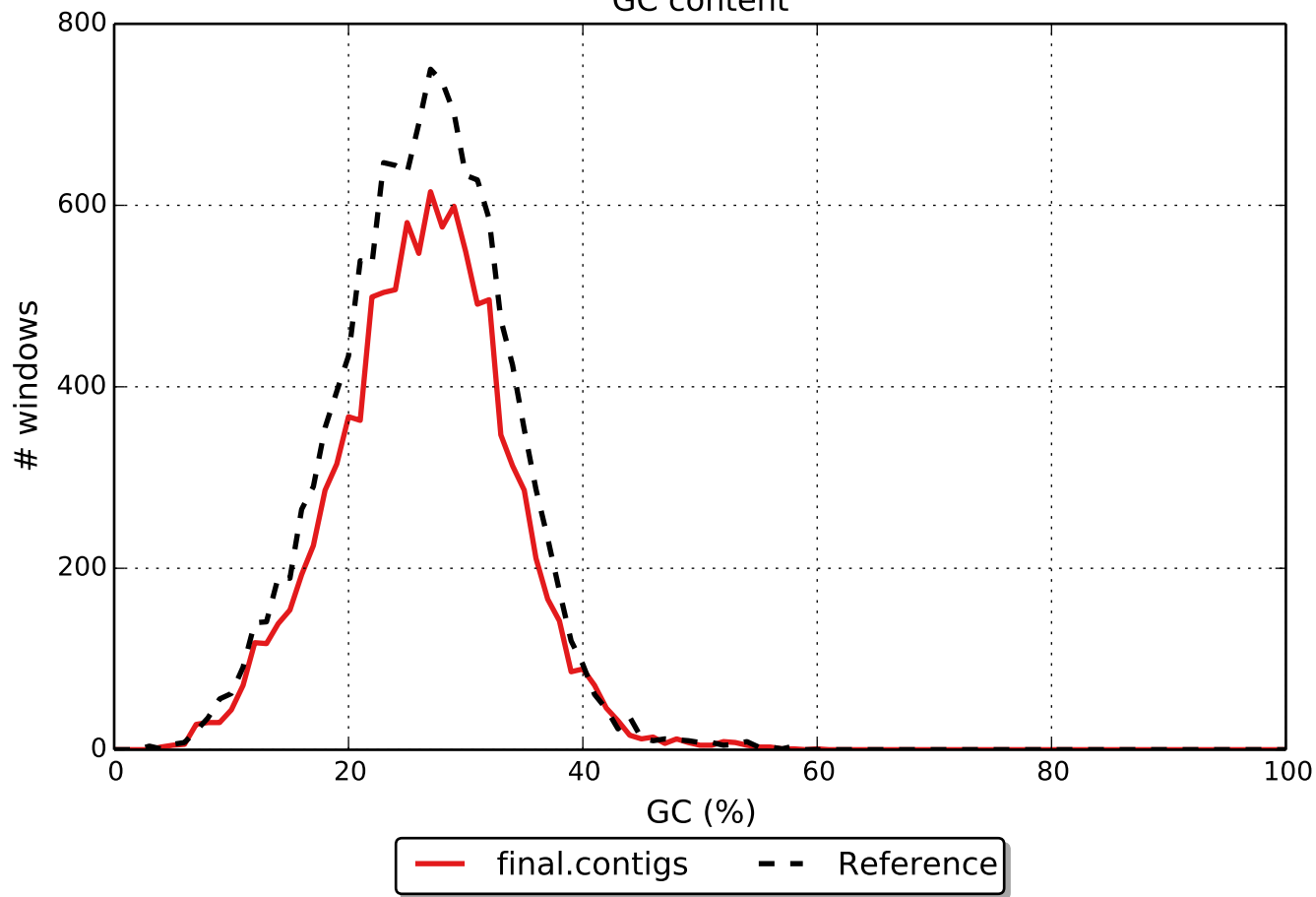
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

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).

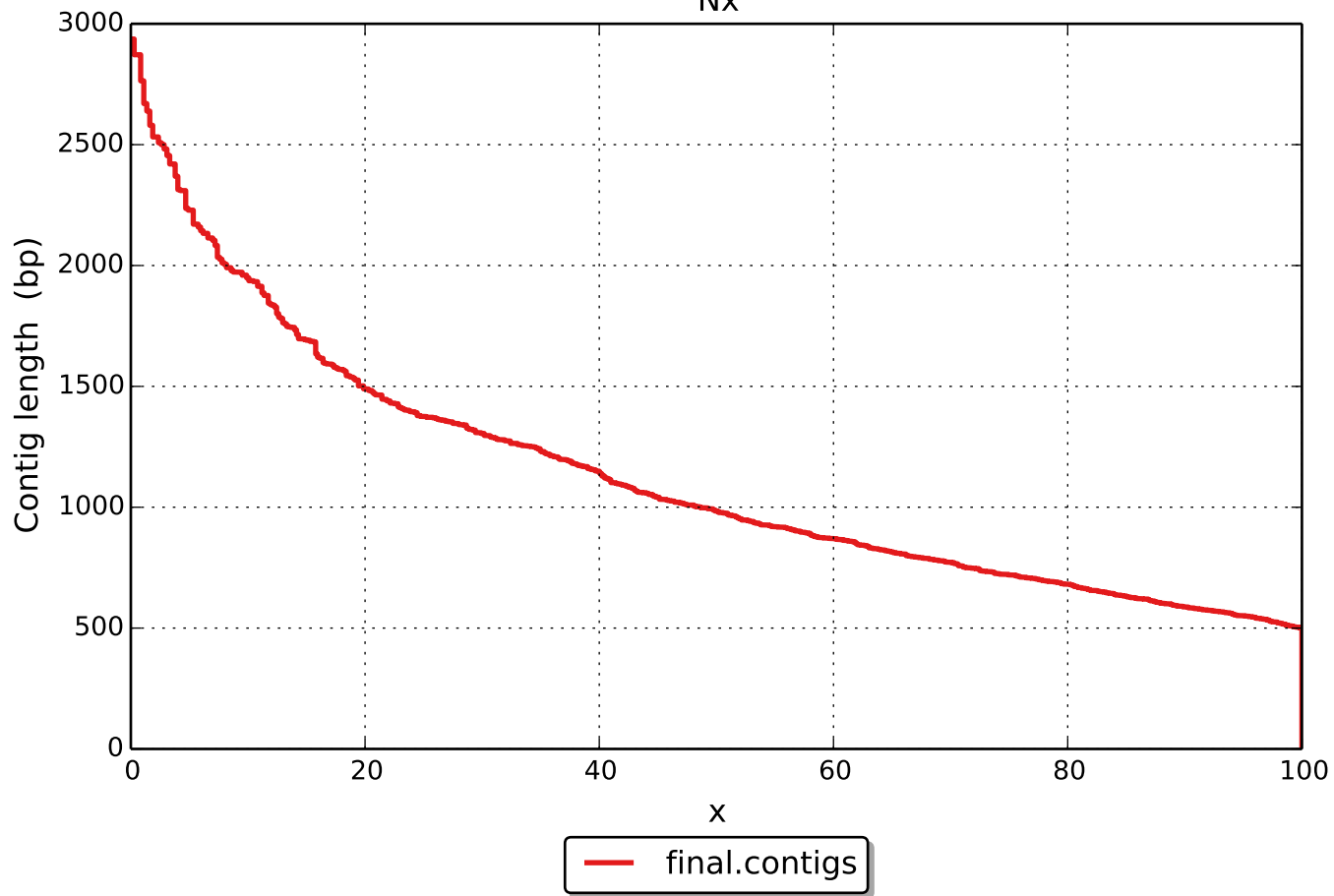
Cumulative length



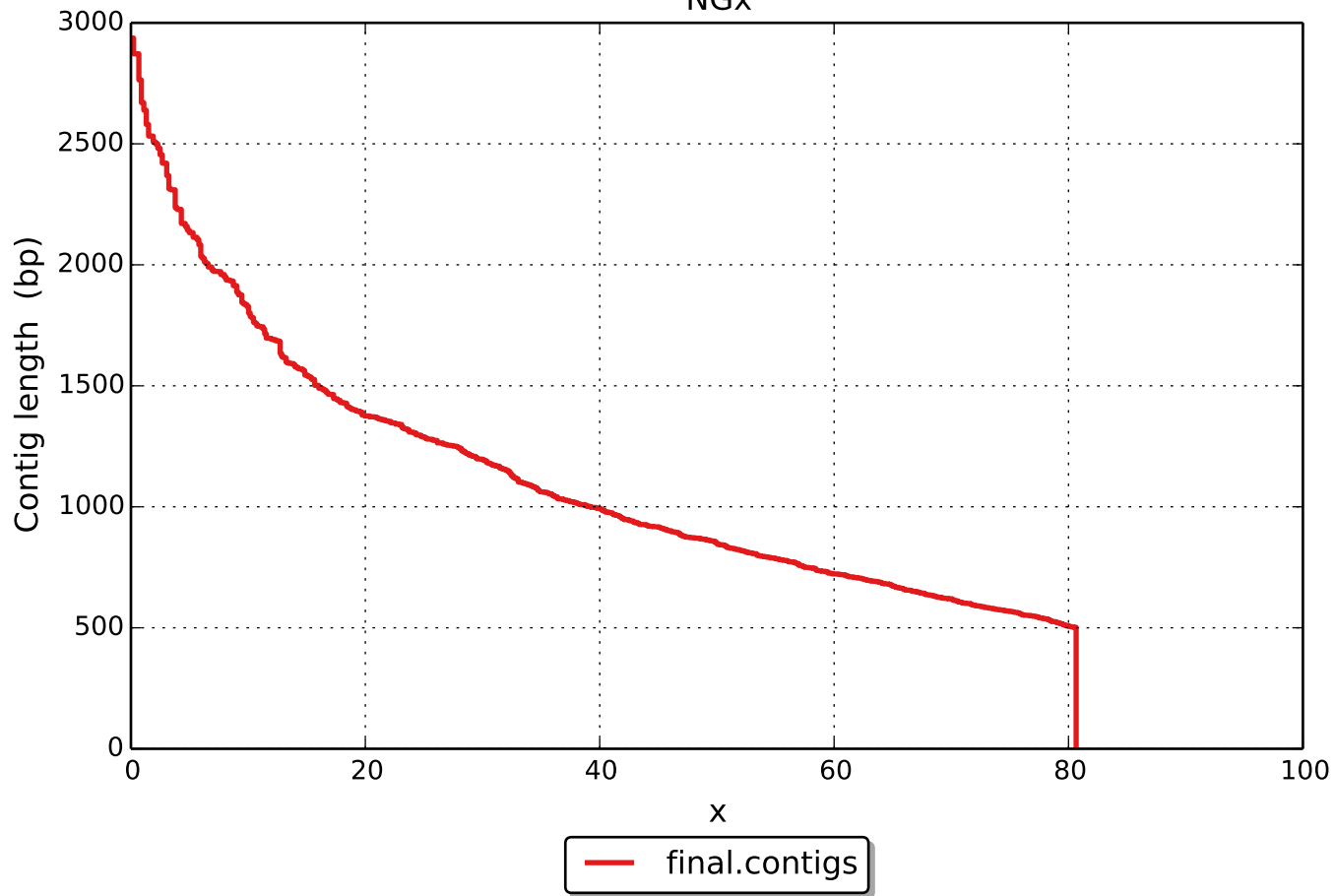
GC content



Nx



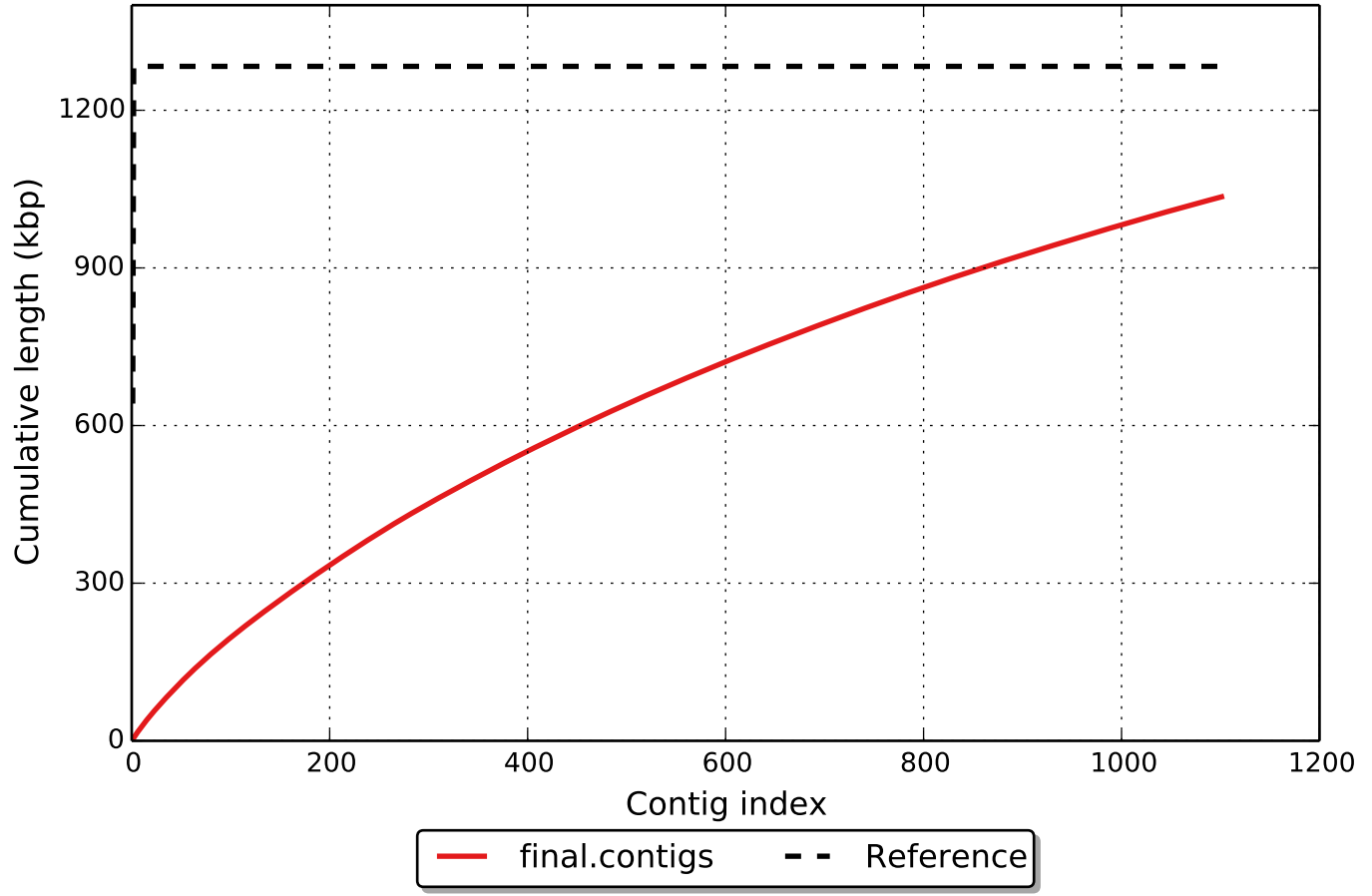
NGx



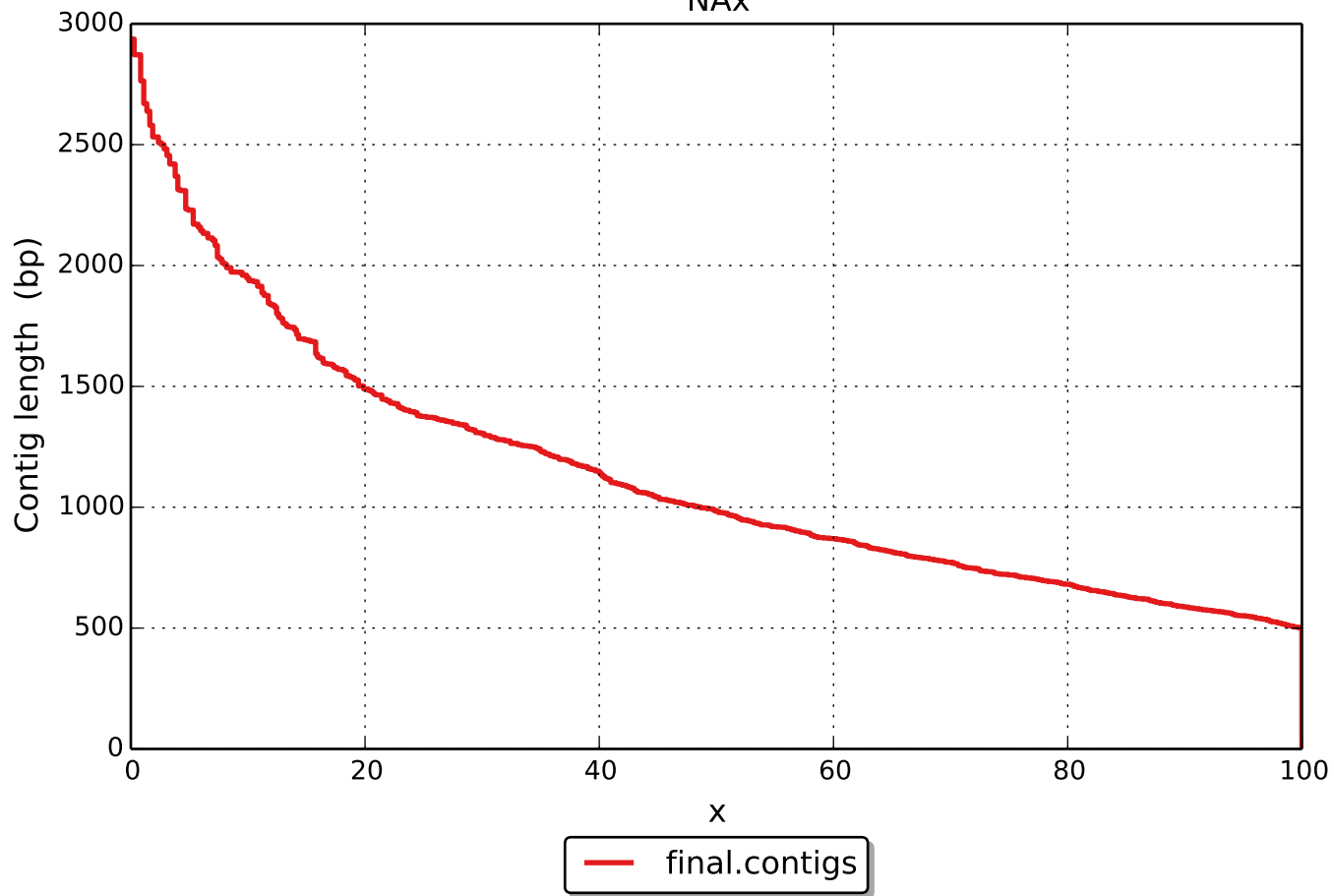
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

