

Report

| | final.contigs |
|---------------------------------|---------------|
| # contigs (≥ 0 bp) | 173 |
| # contigs (≥ 1000 bp) | 93 |
| # contigs (≥ 5000 bp) | 69 |
| # contigs (≥ 10000 bp) | 63 |
| # contigs (≥ 25000 bp) | 49 |
| # contigs (≥ 50000 bp) | 30 |
| Total length (≥ 0 bp) | 4580210 |
| Total length (≥ 1000 bp) | 4552723 |
| Total length (≥ 5000 bp) | 4501501 |
| Total length (≥ 10000 bp) | 4455888 |
| Total length (≥ 25000 bp) | 4231053 |
| Total length (≥ 50000 bp) | 3587545 |
| # contigs | 173 |
| Largest contig | 327151 |
| Total length | 4580210 |
| Reference length | 4641652 |
| GC (%) | 50.76 |
| Reference GC (%) | 50.79 |
| N50 | 112430 |
| NG50 | 112430 |
| N75 | 58008 |
| NG75 | 54946 |
| L50 | 14 |
| LG50 | 14 |
| L75 | 28 |
| LG75 | 29 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 1 part |
| Unaligned length | 163 |
| Genome fraction (%) | 98.537 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.48 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 327151 |
| NA50 | 112430 |
| NGA50 | 112430 |
| NA75 | 58008 |
| NGA75 | 54946 |
| LA50 | 14 |
| LGA50 | 14 |
| LA75 | 28 |
| LGA75 | 29 |

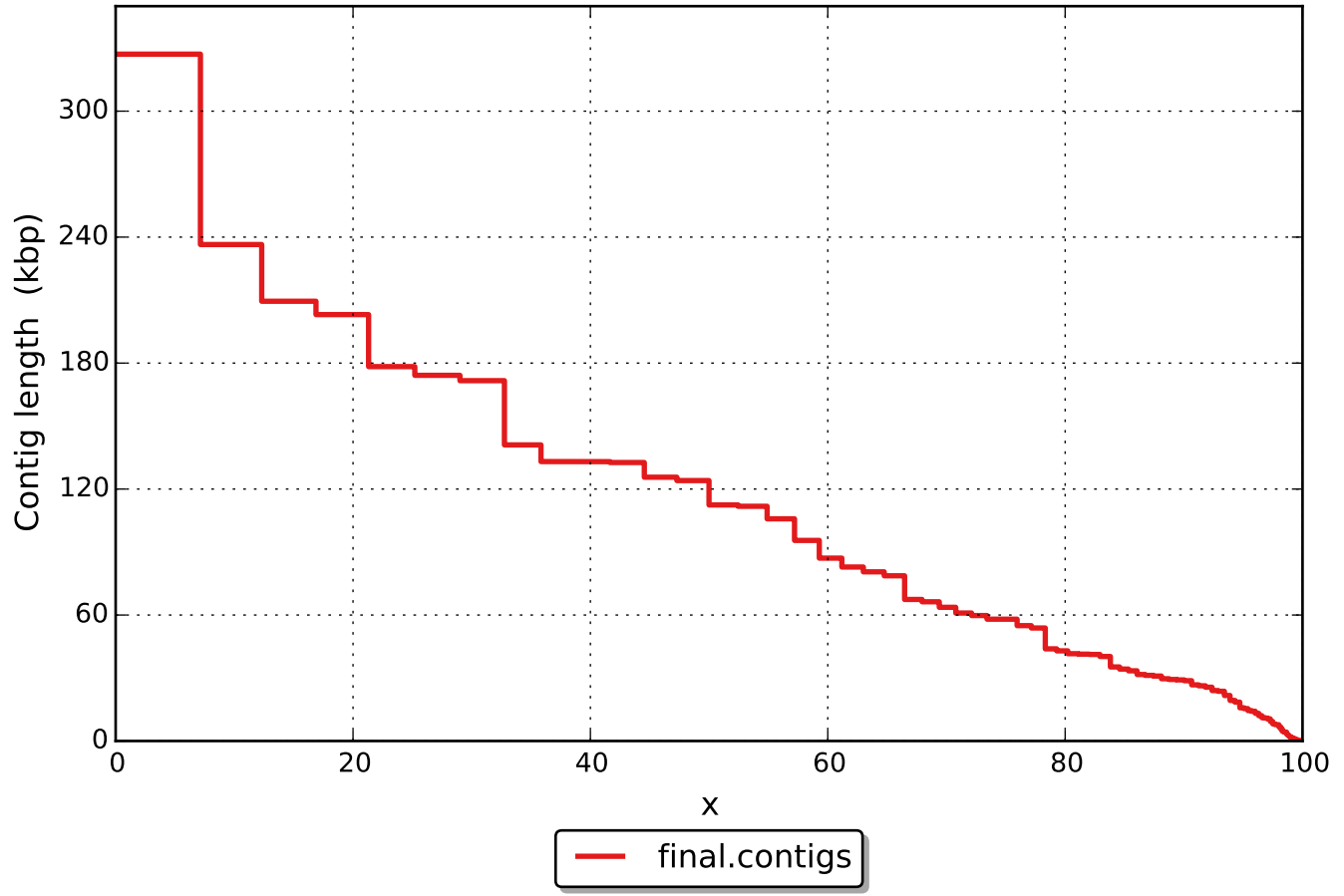
Misassemblies report

| | final.contigs |
|-----------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 22 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

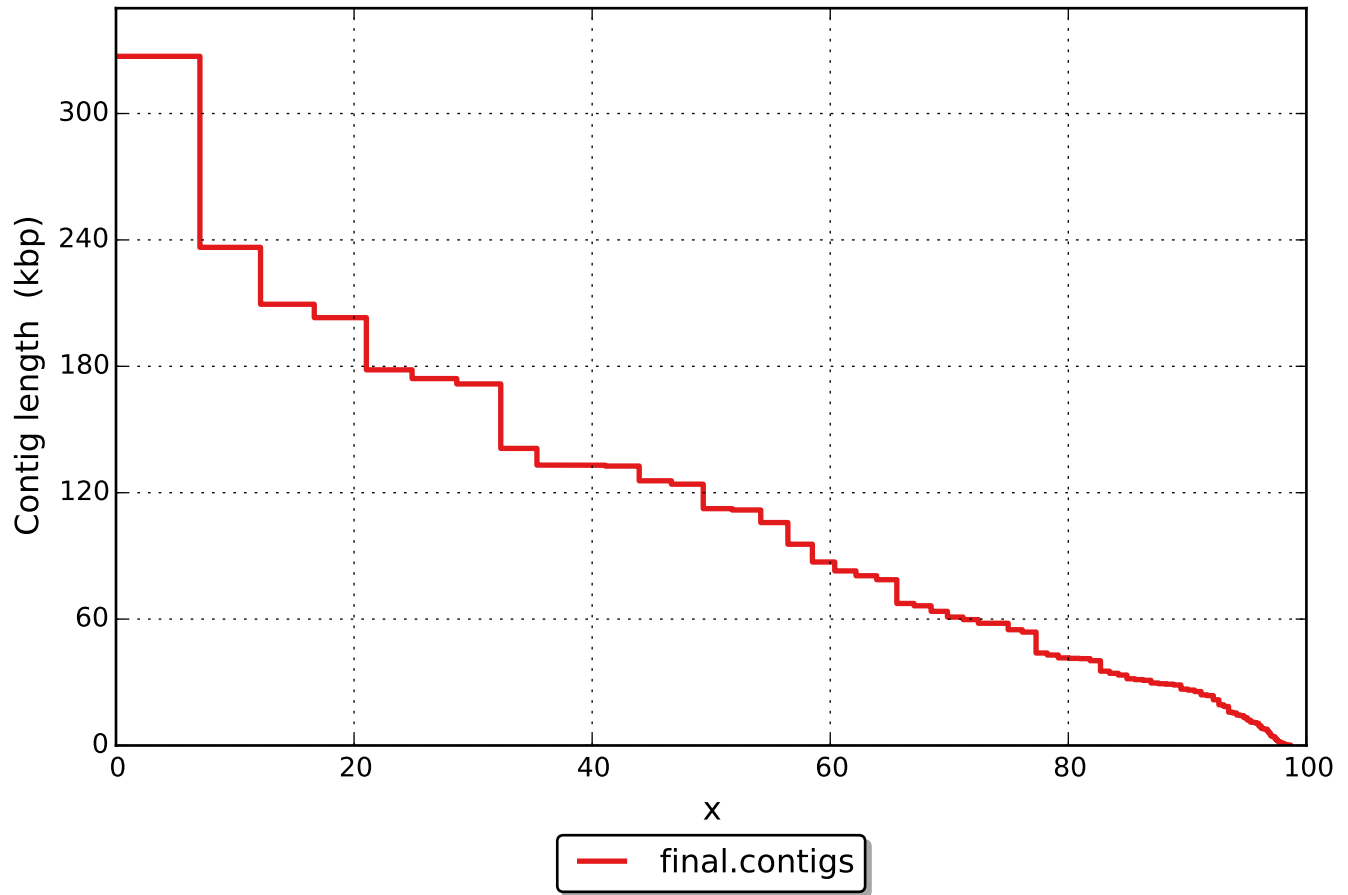
Unaligned report

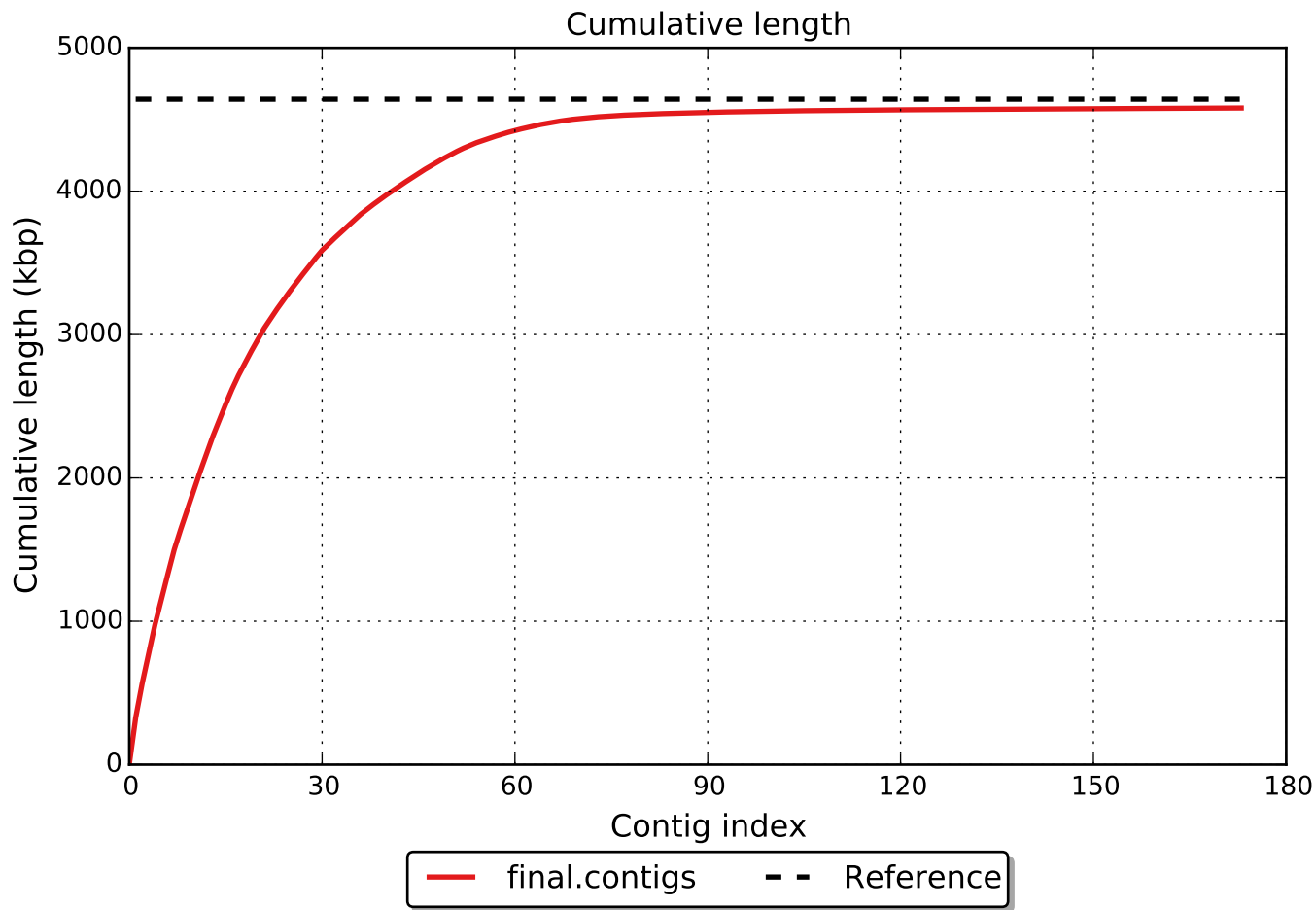
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 1 |
| Partially unaligned length | 163 |
| # N's | 0 |

Nx

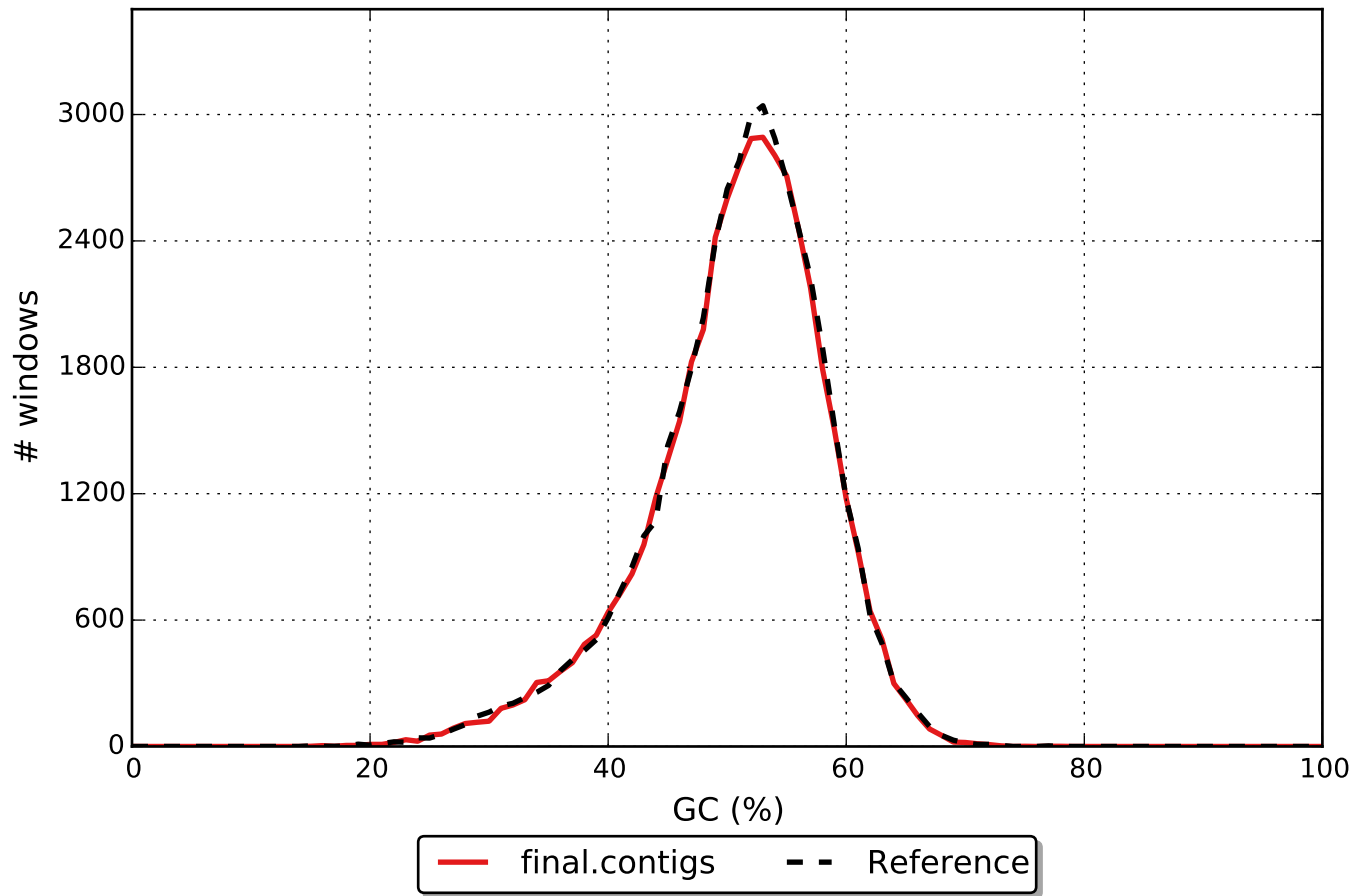


NGx





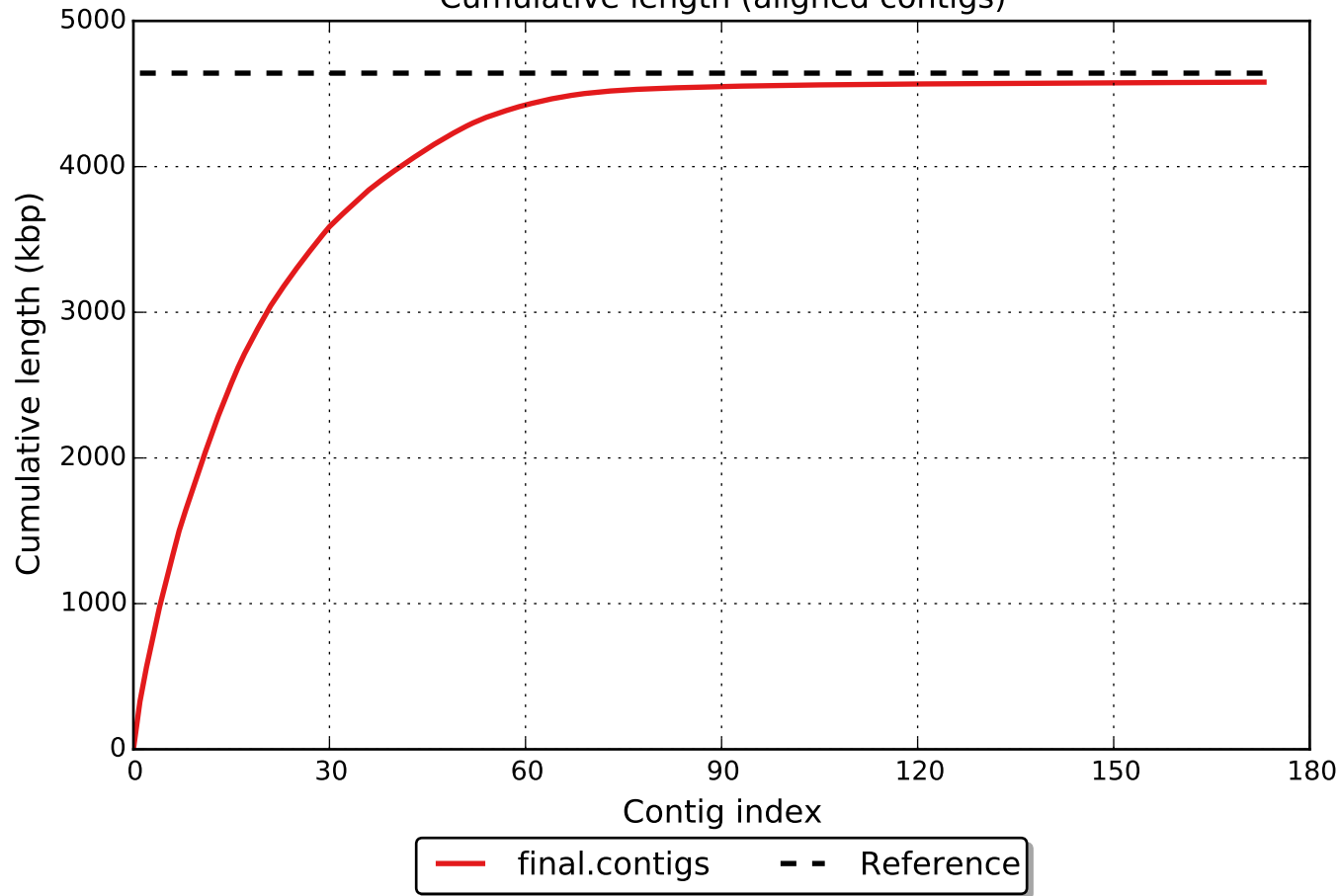
GC content



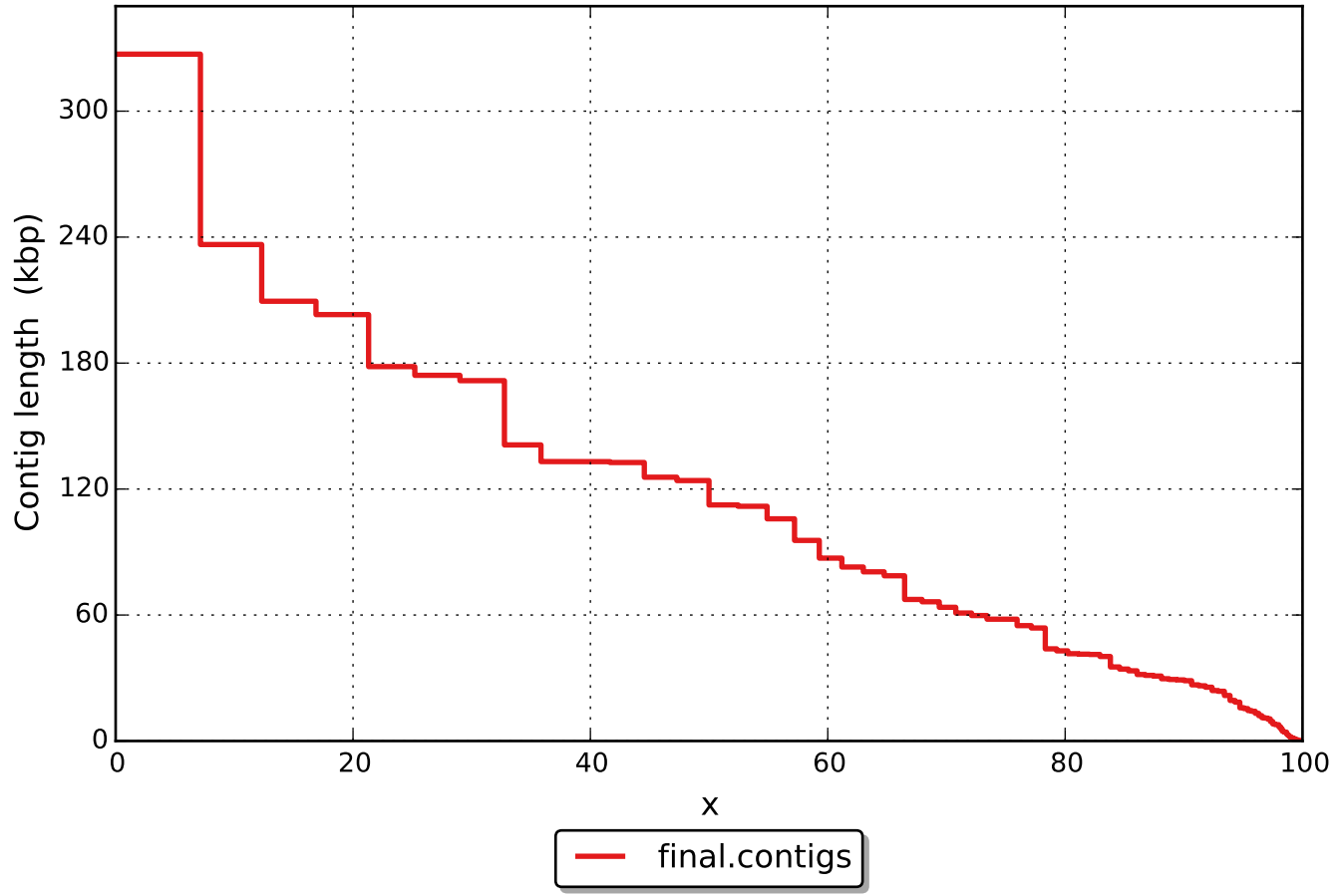
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

