

Report

| | contigs |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 117 |
| # contigs (≥ 1000 bp) | 73 |
| # contigs (≥ 5000 bp) | 53 |
| # contigs (≥ 10000 bp) | 48 |
| # contigs (≥ 25000 bp) | 42 |
| # contigs (≥ 50000 bp) | 27 |
| Total length (≥ 0 bp) | 4573823 |
| Total length (≥ 1000 bp) | 4559420 |
| Total length (≥ 5000 bp) | 4512299 |
| Total length (≥ 10000 bp) | 4474973 |
| Total length (≥ 25000 bp) | 4385233 |
| Total length (≥ 50000 bp) | 3871002 |
| # contigs | 84 |
| Largest contig | 327173 |
| Total length | 4567306 |
| Reference length | 4641652 |
| GC (%) | 50.75 |
| Reference GC (%) | 50.79 |
| N50 | 173566 |
| NG50 | 133063 |
| N75 | 87186 |
| NG75 | 78649 |
| L50 | 10 |
| LG50 | 11 |
| L75 | 20 |
| LG75 | 21 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 8 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 98.325 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2.48 |
| # indels per 100 kbp | 0.26 |
| Largest alignment | 327173 |
| NA50 | 172028 |
| NGA50 | 133063 |
| NA75 | 87186 |
| NGA75 | 78649 |
| LA50 | 10 |
| LGA50 | 11 |
| LA75 | 20 |
| LGA75 | 21 |

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

| | contigs |
|-----------------------------|---------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 8 |
| # mismatches | 113 |
| # indels | 12 |
| # short indels | 11 |
| # long indels | 1 |
| Indels length | 98 |

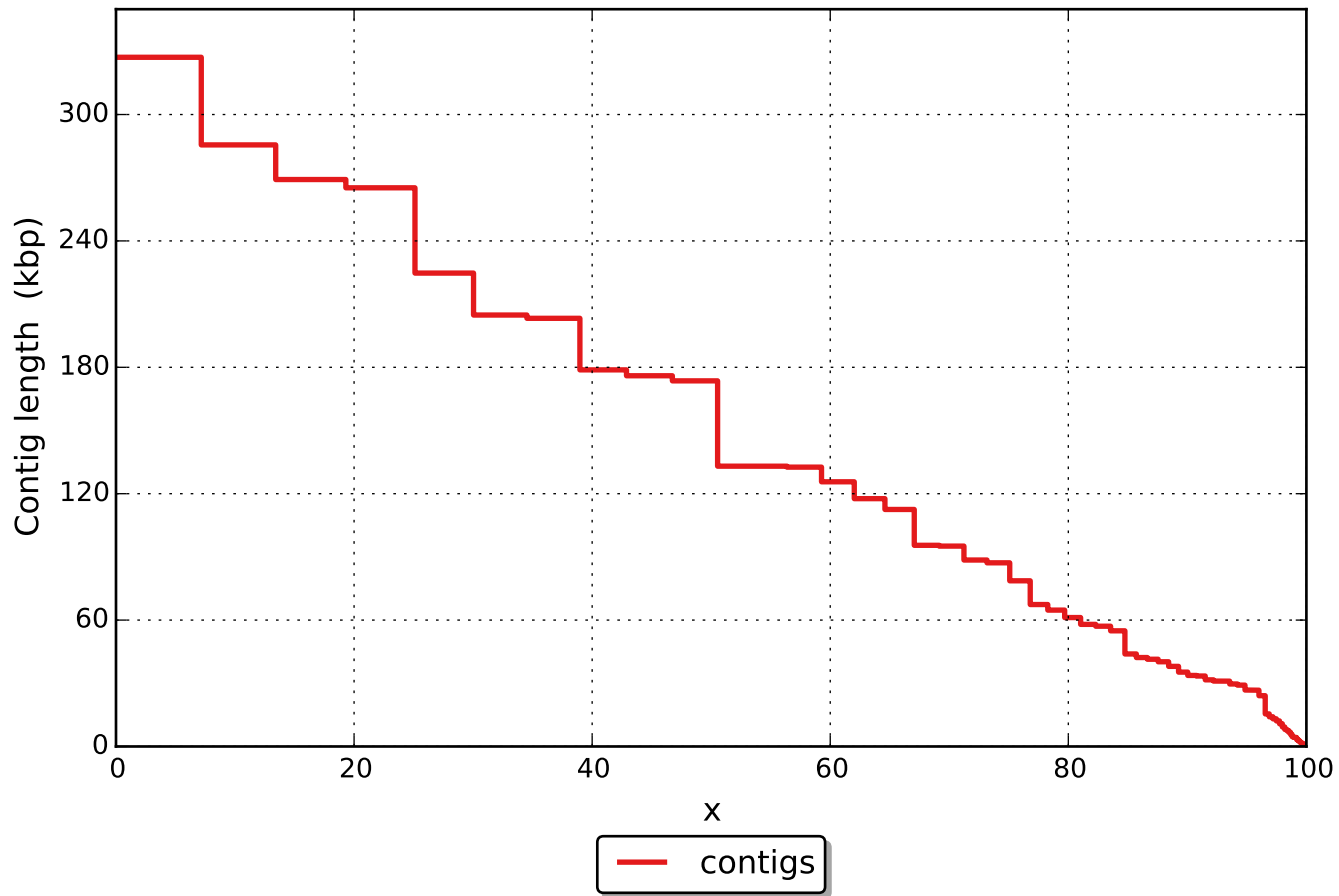
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

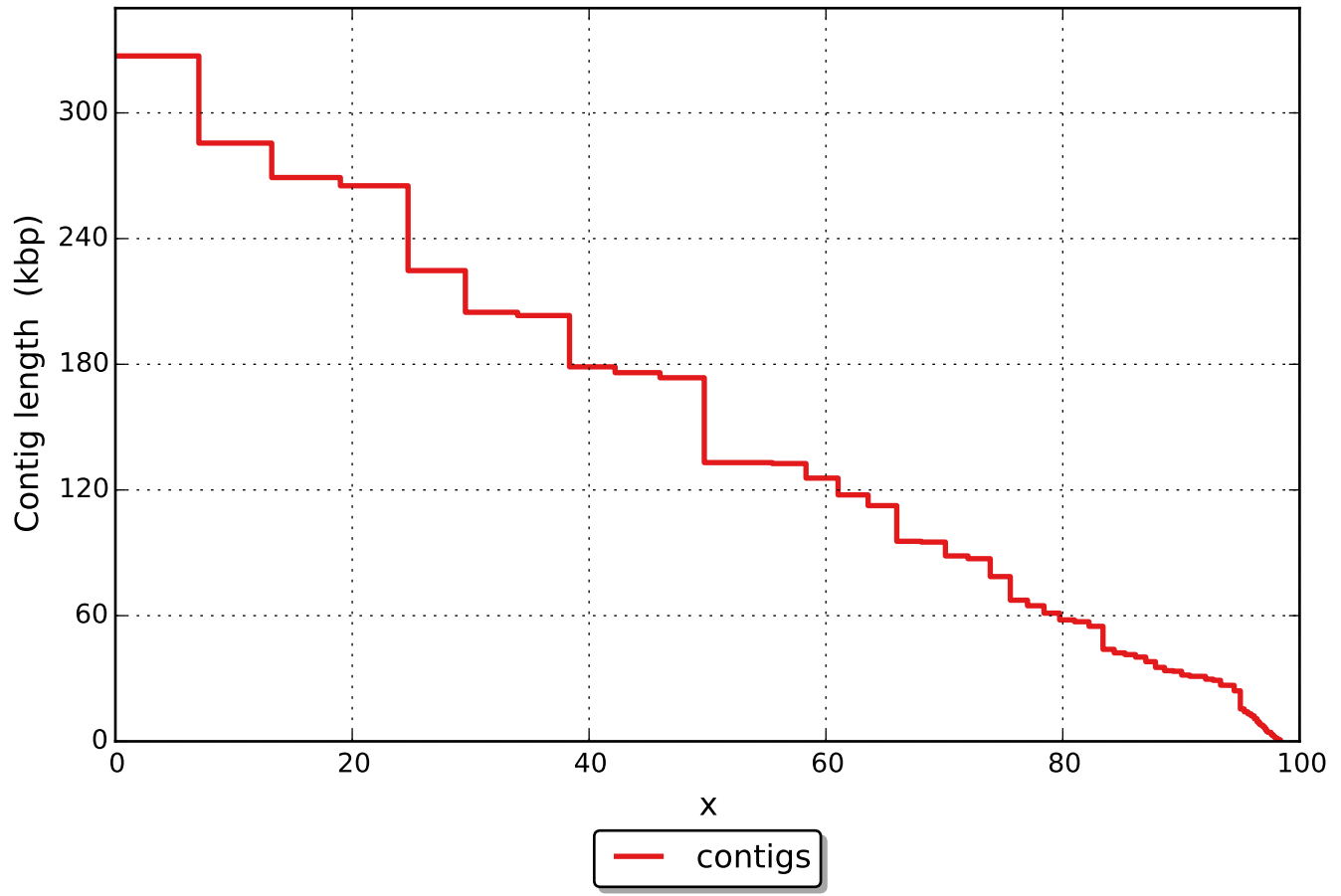
| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

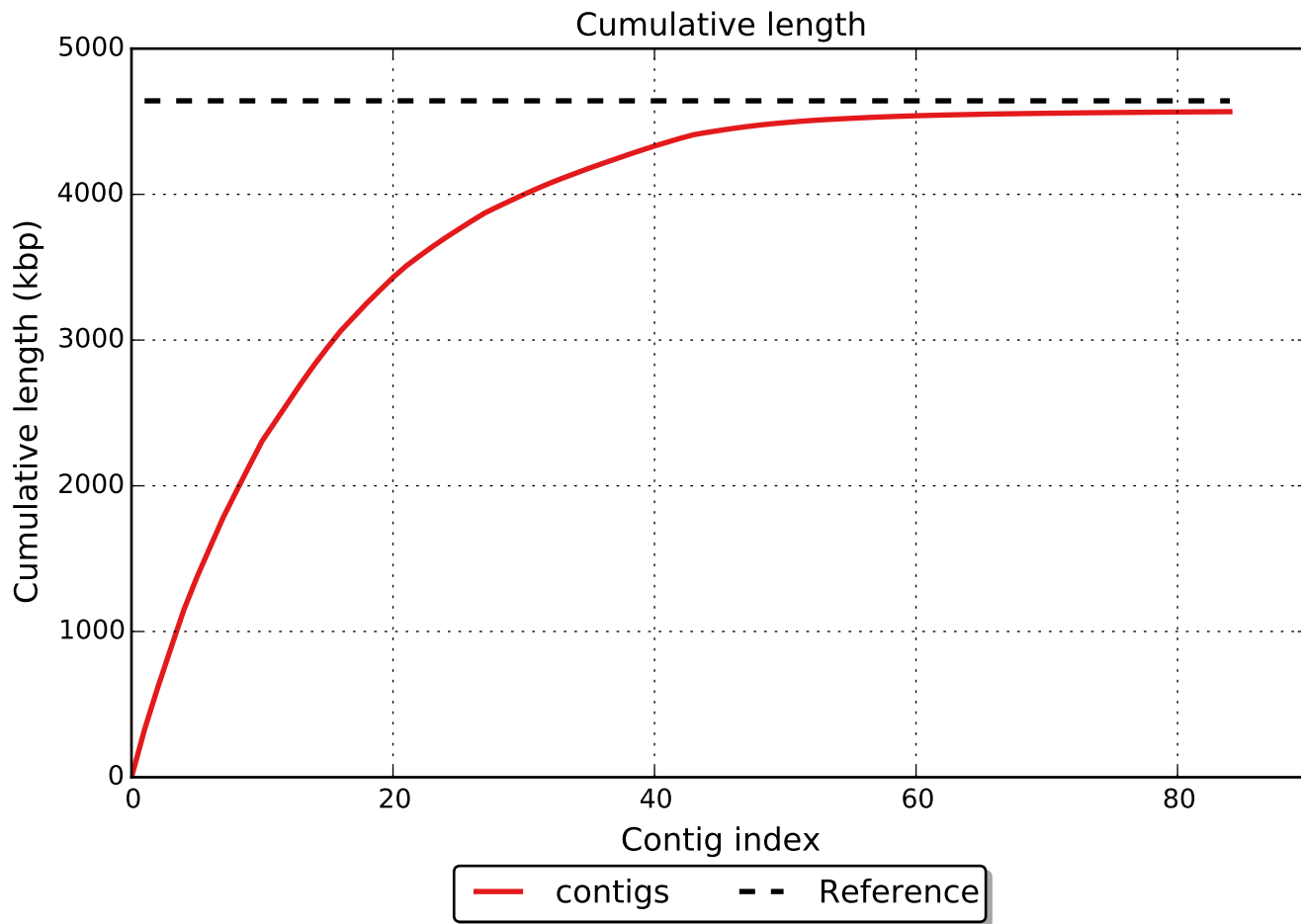
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

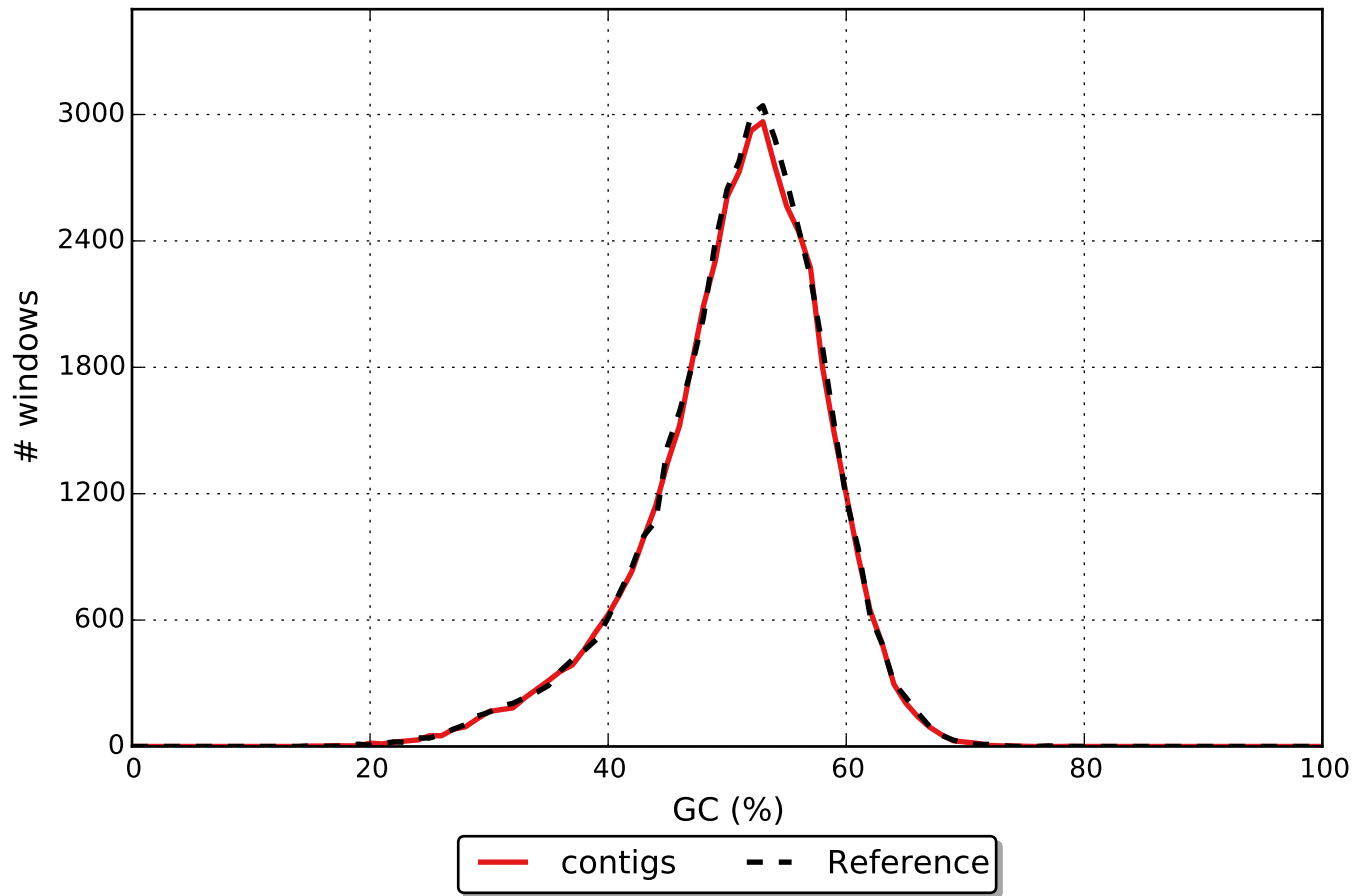


NGx





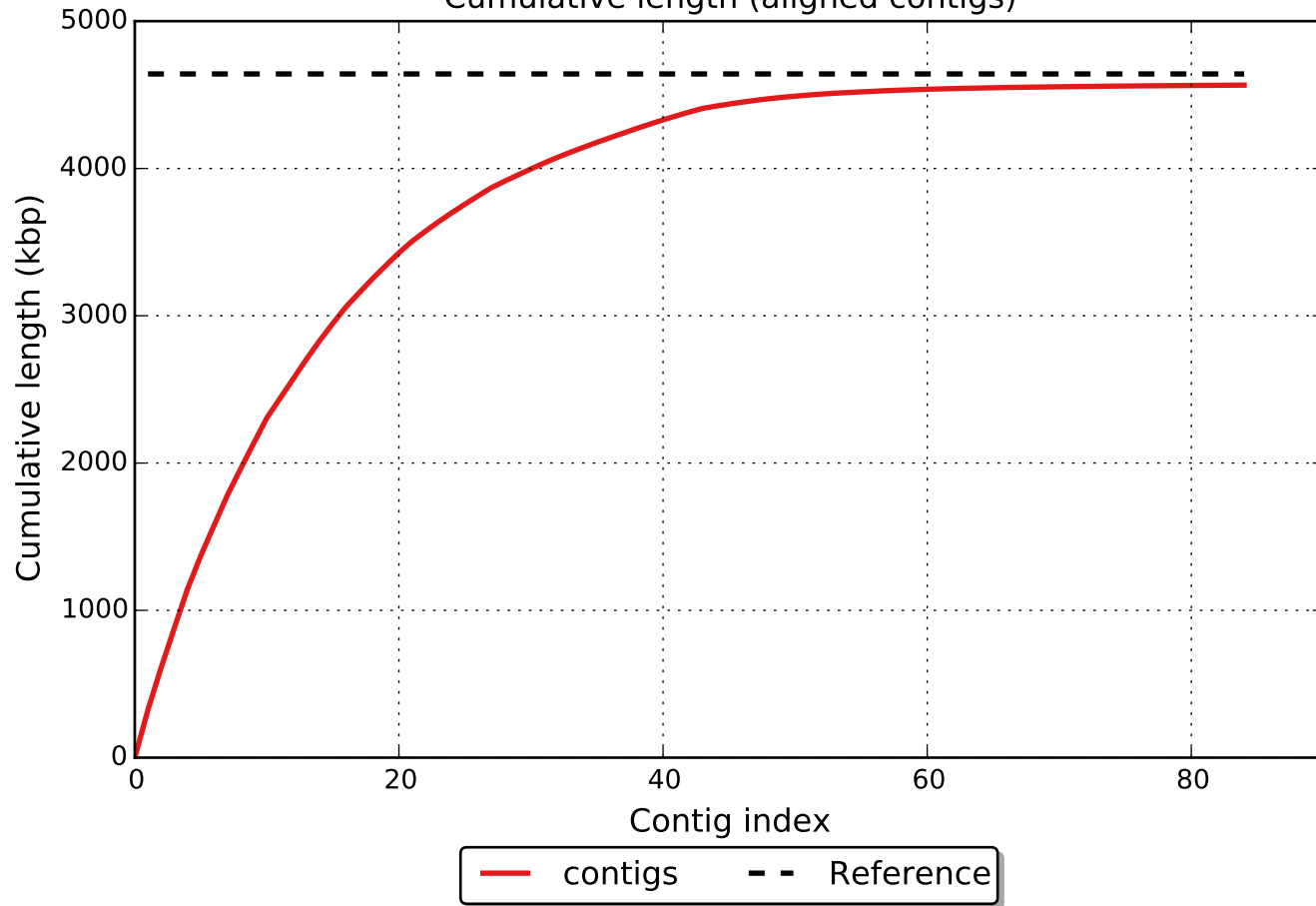
GC content



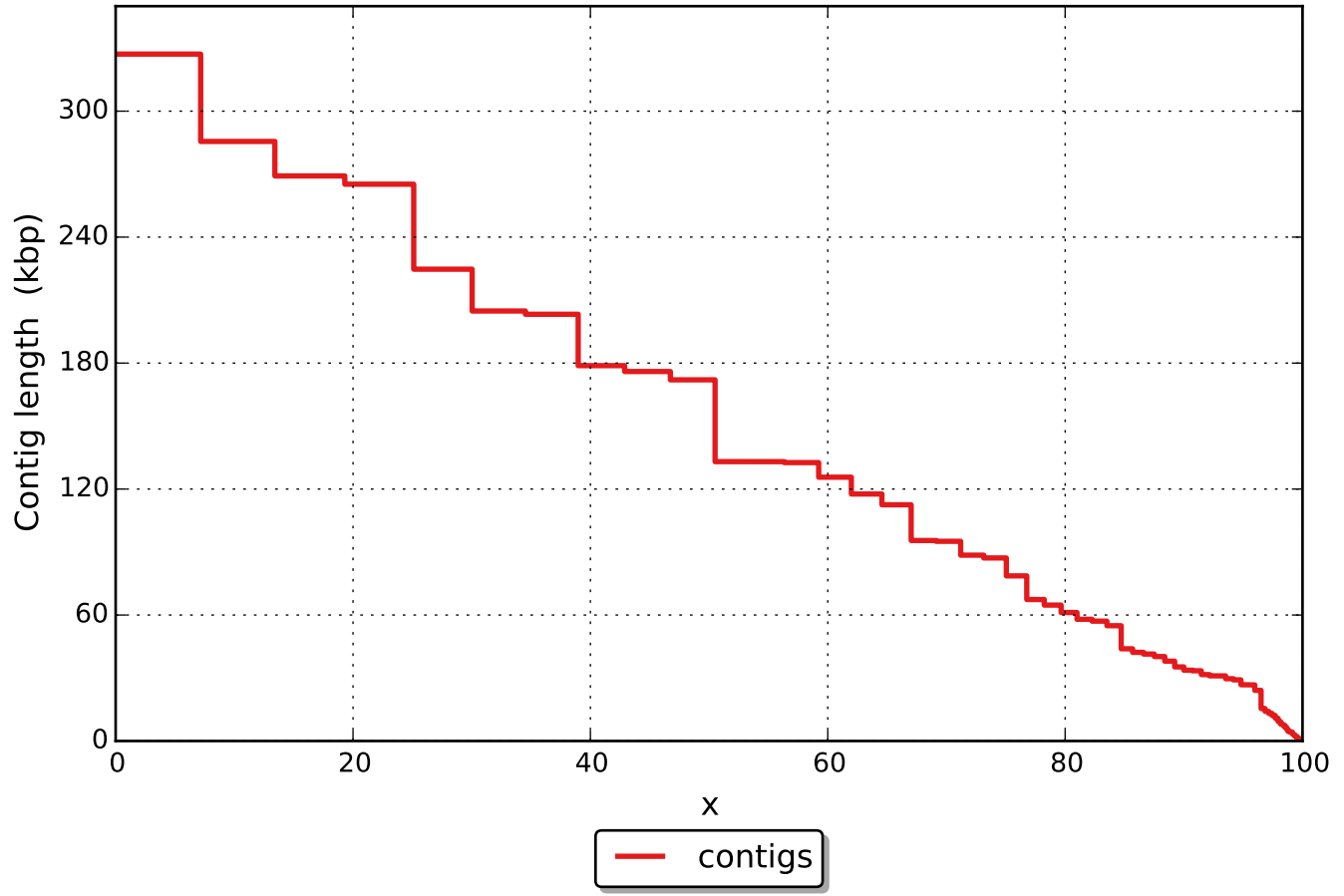
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

