

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 1215 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 1729254 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 4169 |
| Largest contig | 4278 |
| Total length | 3810332 |
| Reference length | 4857432 |
| GC (%) | 52.22 |
| Reference GC (%) | 52.22 |
| N50 | 943 |
| NG50 | 807 |
| N75 | 705 |
| NG75 | 533 |
| L50 | 1397 |
| LG50 | 1998 |
| L75 | 2566 |
| LG75 | 3846 |
| # misassemblies | 4 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 4784 |
| # local misassemblies | 1 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 74.142 |
| Duplication ratio | 1.058 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 182.23 |
| # indels per 100 kbp | 0.06 |
| Largest alignment | 4278 |
| NA50 | 943 |
| NGA50 | 807 |
| NA75 | 704 |
| NGA75 | 533 |
| LA50 | 1398 |
| LGA50 | 1999 |
| LA75 | 2568 |
| LGA75 | 3848 |

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 | 4 |
| # relocations | 3 |
| # translocations | 0 |
| # inversions | 1 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 4784 |
| # local misassemblies | 1 |
| # mismatches | 6563 |
| # indels | 2 |
| # short indels | 2 |
| # long indels | 0 |
| Indels length | 2 |

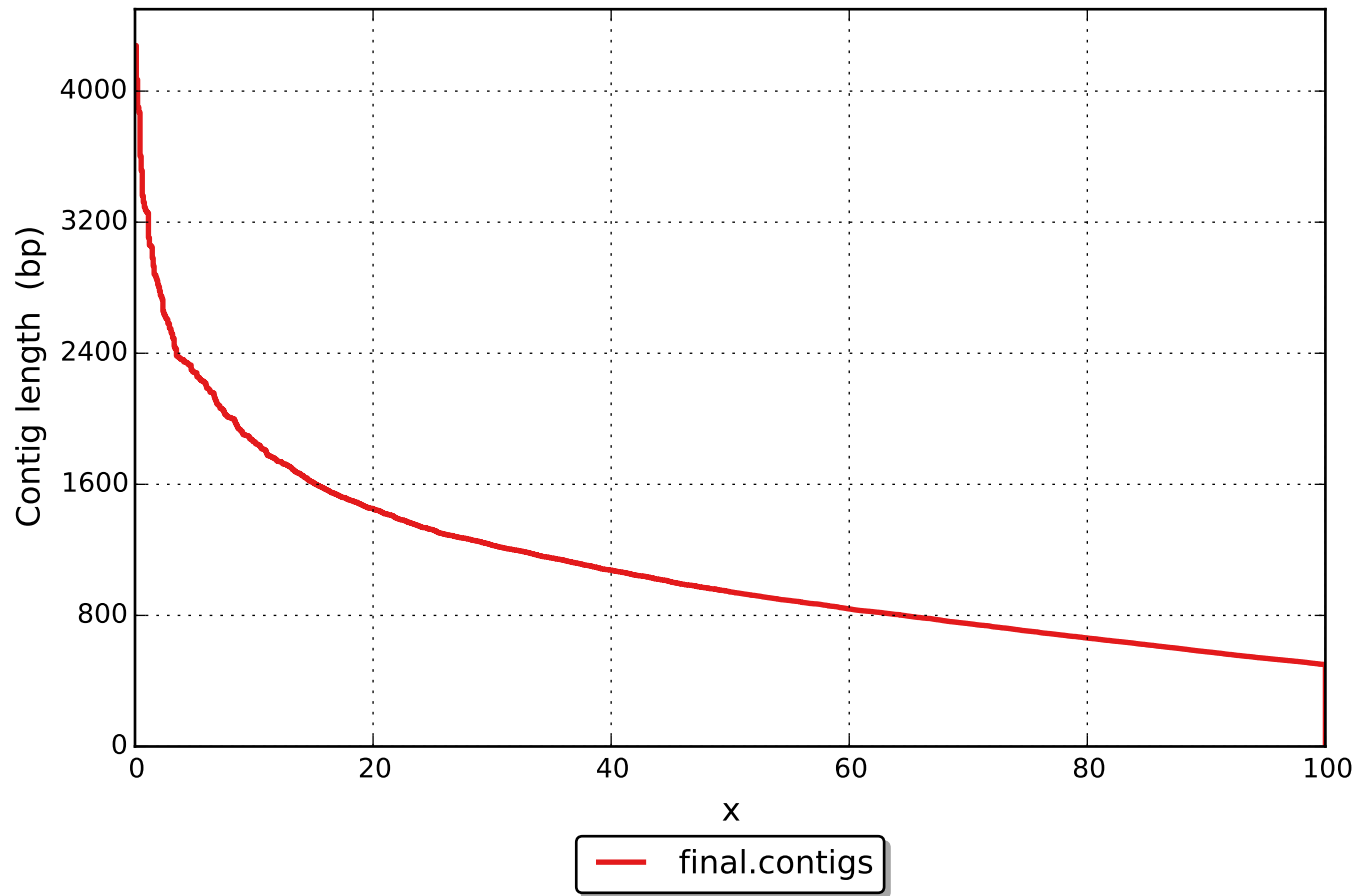
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

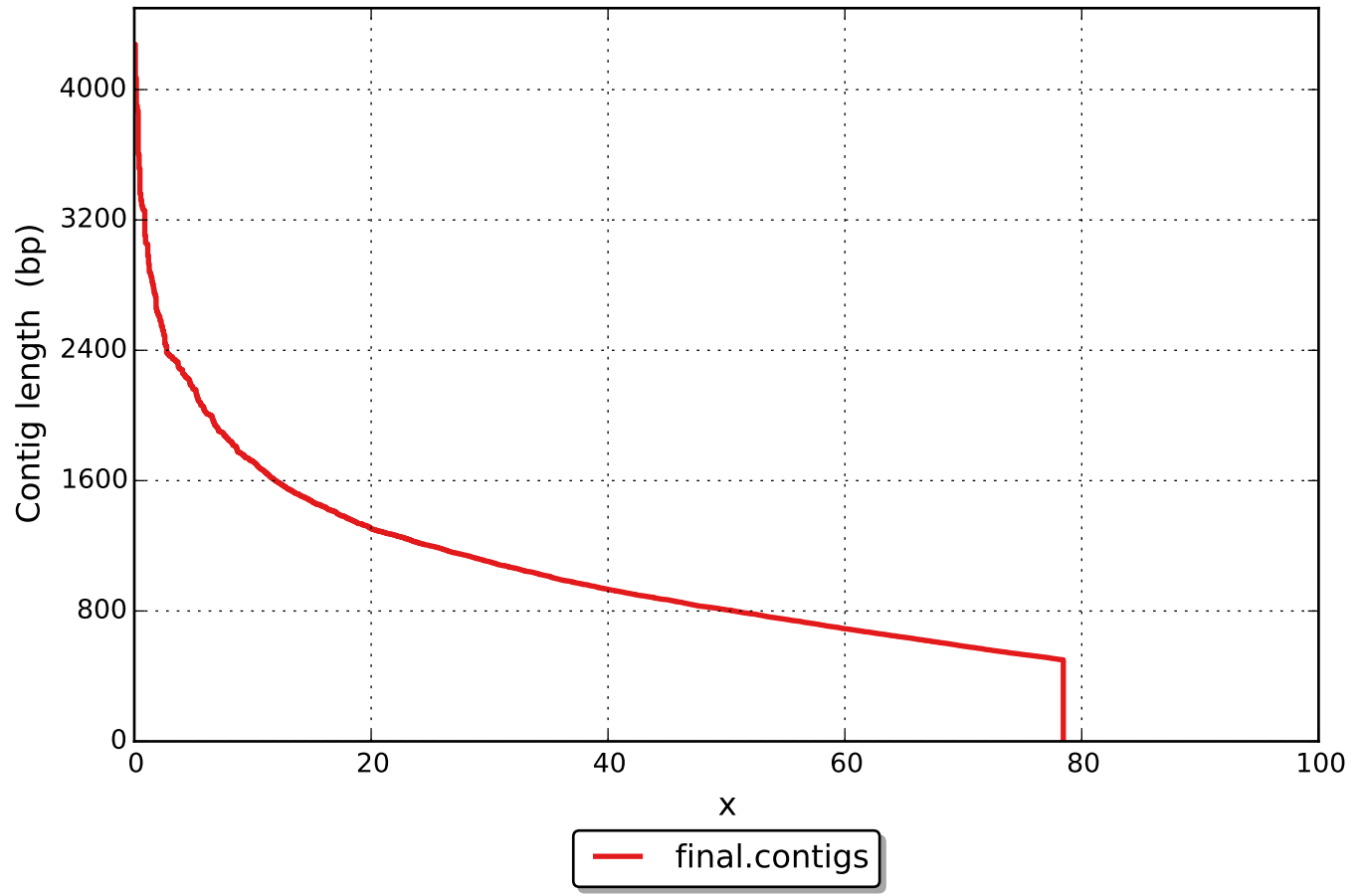
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

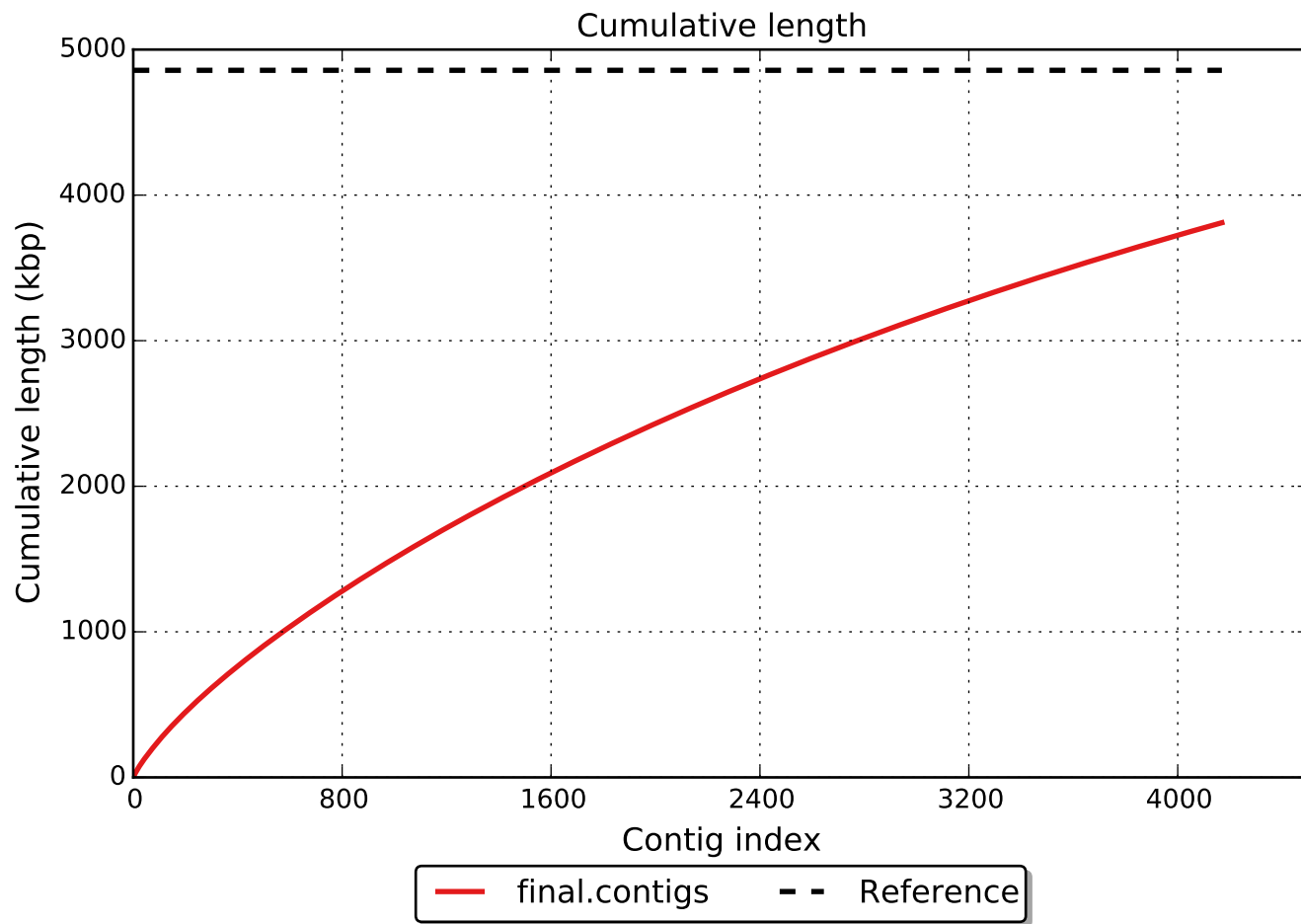
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

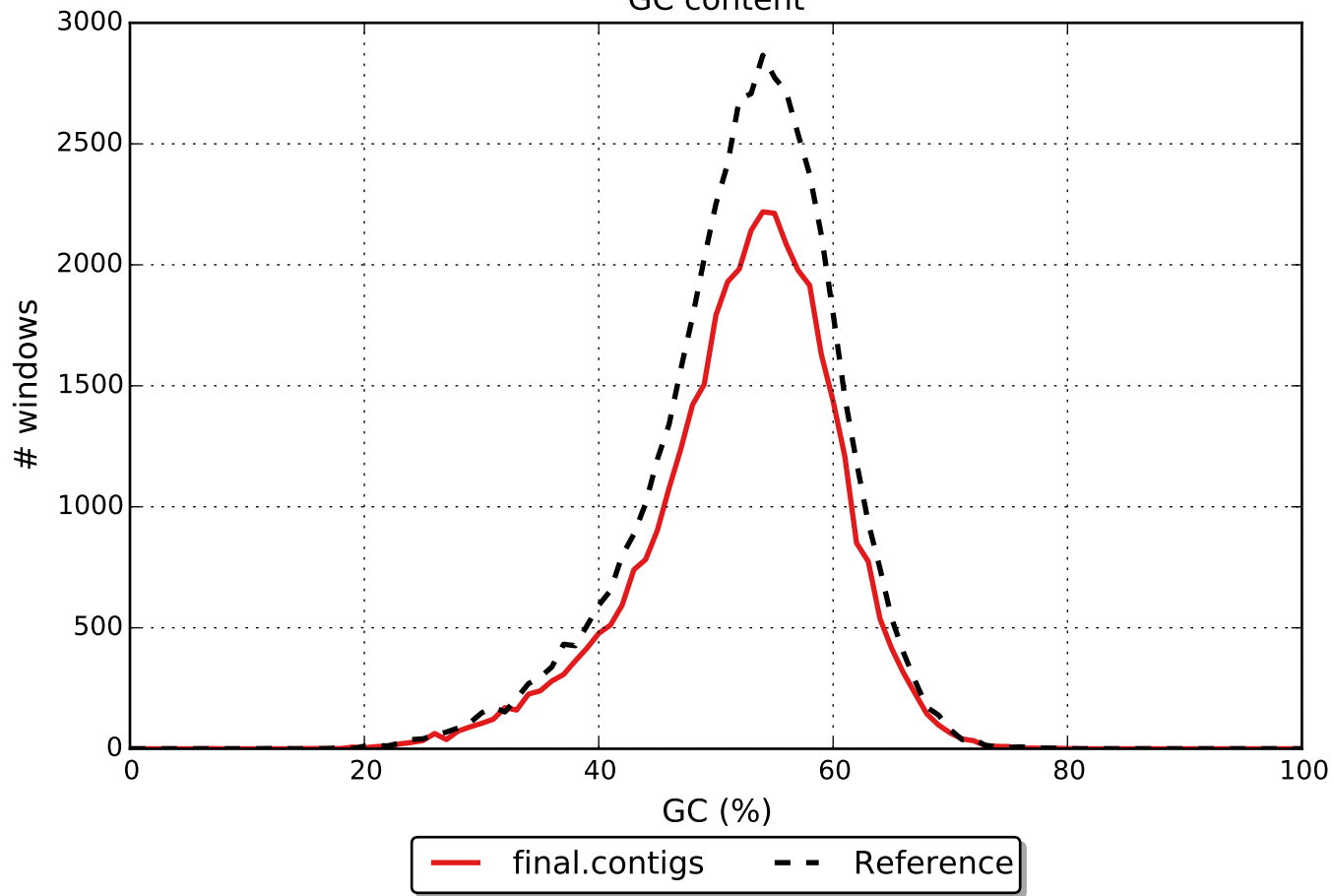


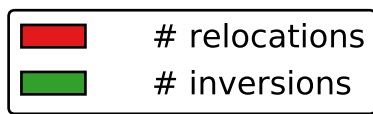
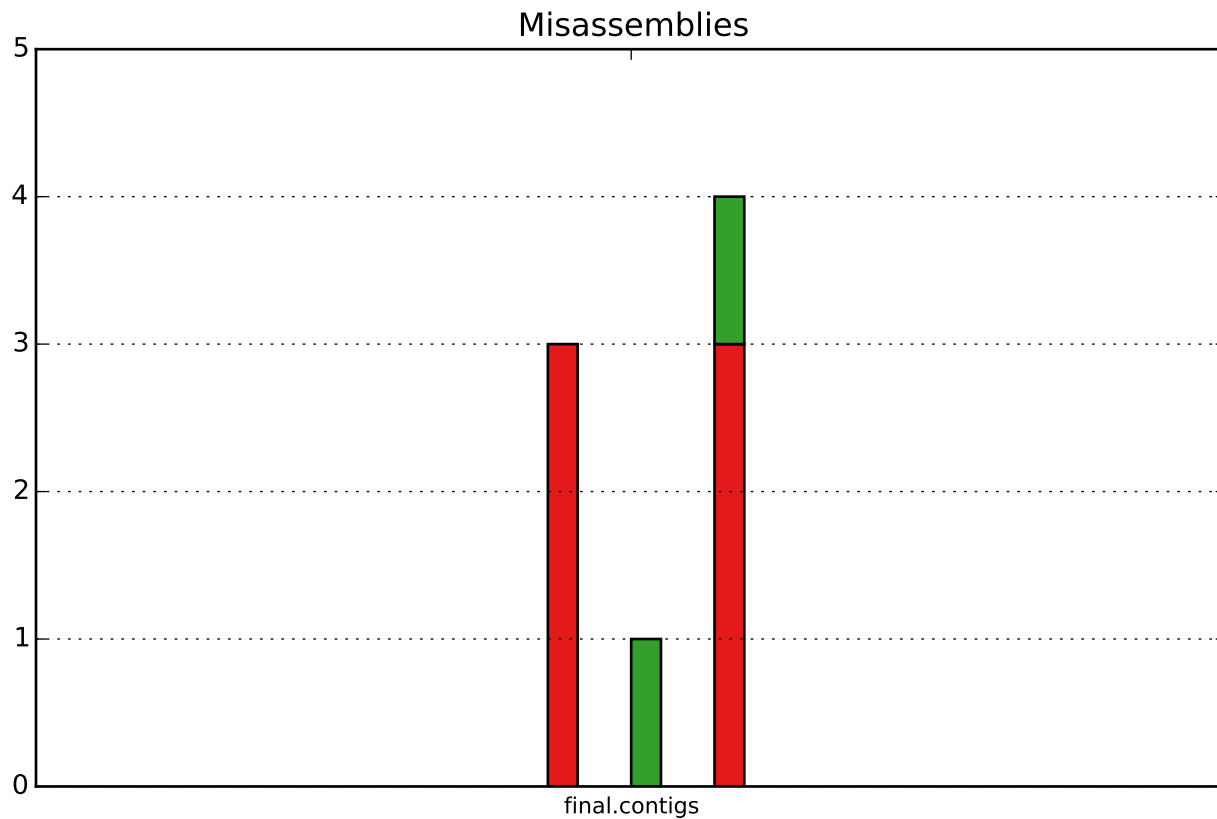
NGx



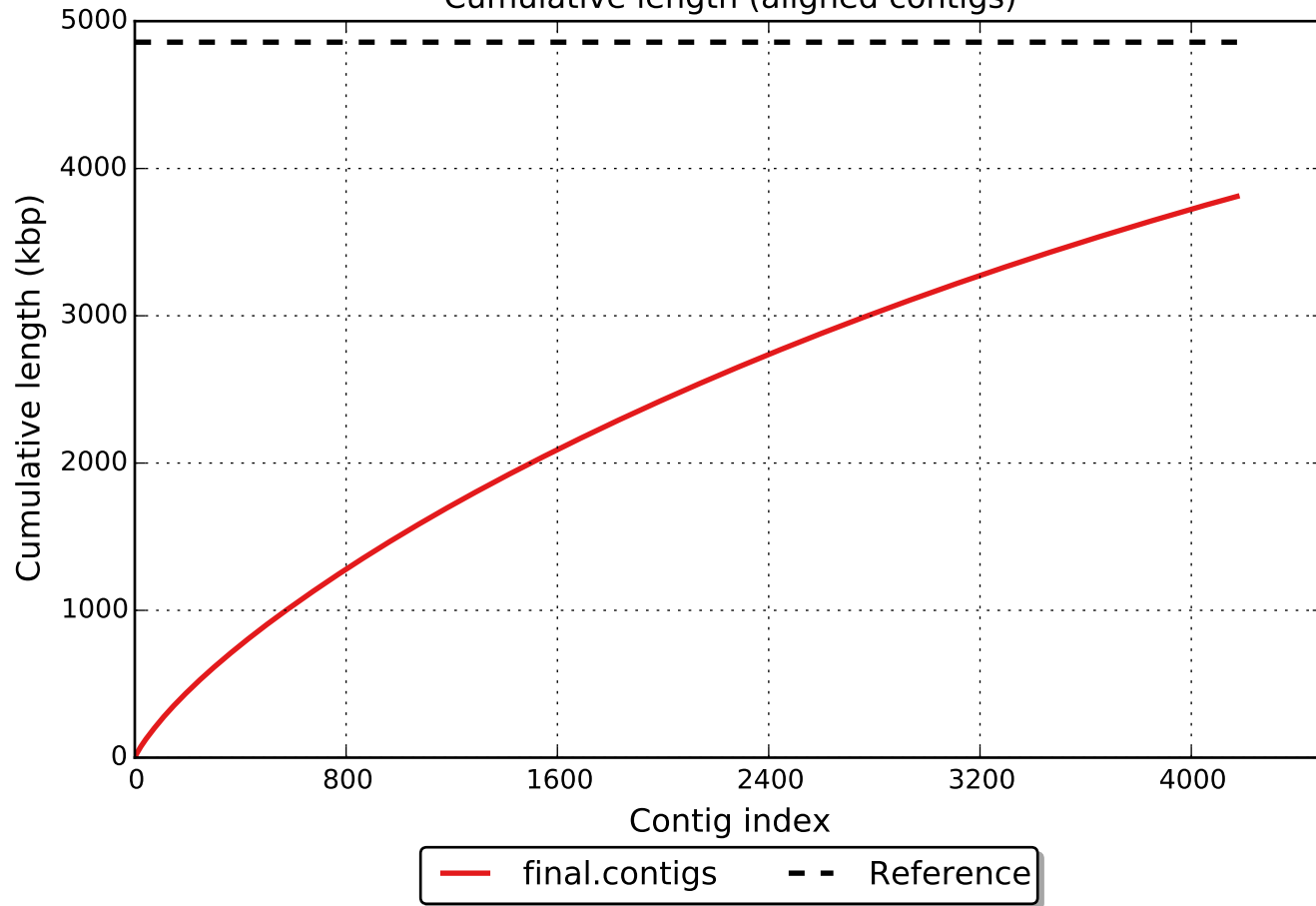


GC content

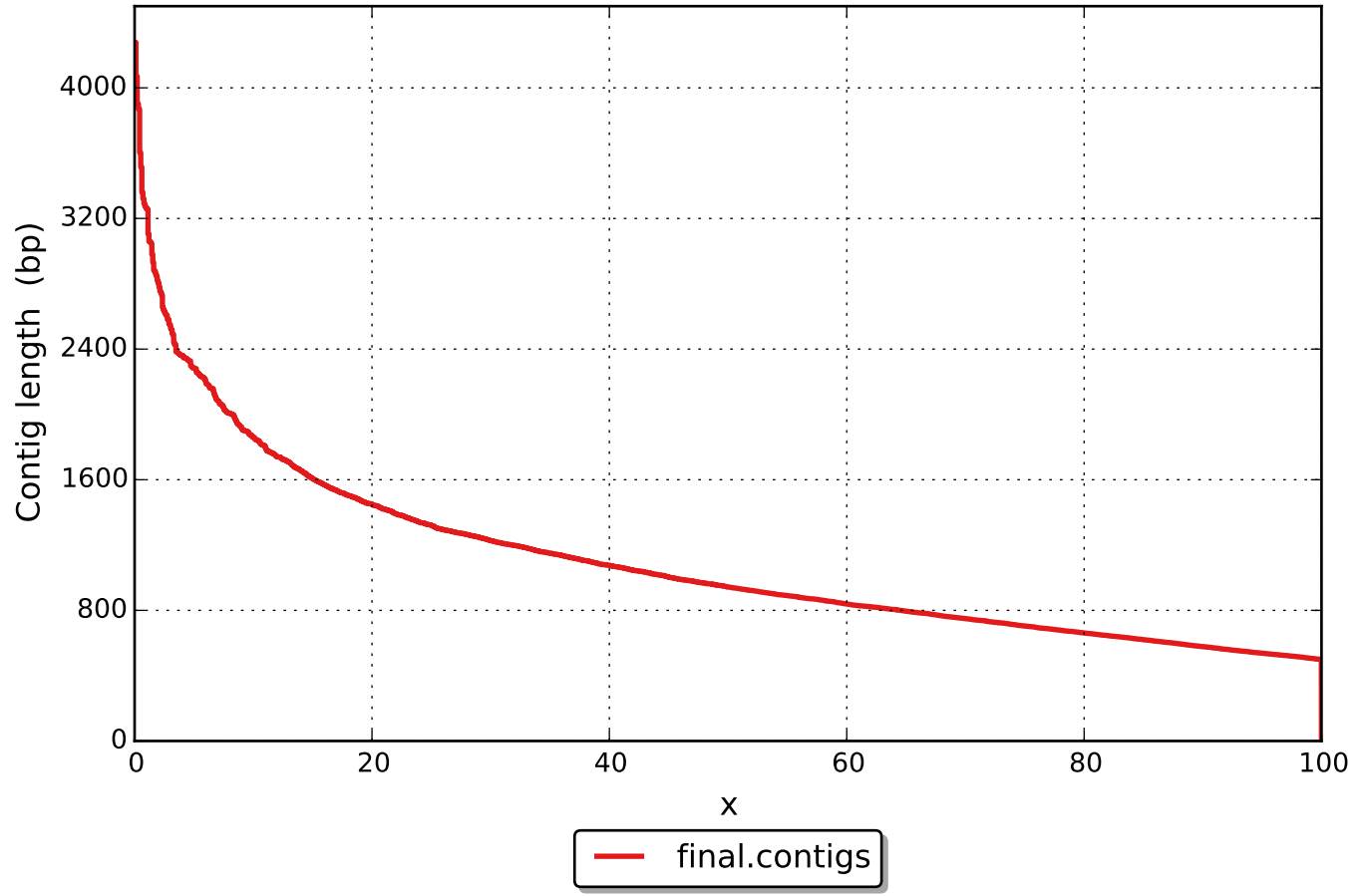




Cumulative length (aligned contigs)



NAx



NGAx

