

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp) | 520 |
| # contigs (>= 1000 bp) | 364 |
| # contigs (>= 5000 bp) | 241 |
| # contigs (>= 10000 bp) | 160 |
| # contigs (>= 25000 bp) | 52 |
| # contigs (>= 50000 bp) | 5 |
| Total length (>= 0 bp) | 4655654 |
| Total length (>= 1000 bp) | 4594340 |
| Total length (>= 5000 bp) | 4266773 |
| Total length (>= 10000 bp) | 3679268 |
| Total length (>= 25000 bp) | 1936808 |
| Total length (>= 50000 bp) | 317938 |
| # contigs | 394 |
| Largest contig | 85460 |
| Total length | 4615600 |
| Reference length | 4641652 |
| GC (%) | 50.75 |
| Reference GC (%) | 50.79 |
| N50 | 21600 |
| NG50 | 21600 |
| N75 | 12033 |
| NG75 | 11932 |
| L50 | 69 |
| LG50 | 69 |
| L75 | 141 |
| LG75 | 142 |
| # misassemblies | 5 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 120242 |
| # local misassemblies | 3 |
| # unaligned contigs | 0 + 1 part |
| Unaligned length | 117 |
| Genome fraction (%) | 98.297 |
| Duplication ratio | 1.012 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 59.61 |
| # indels per 100 kbp | 0.24 |
| Largest alignment | 85460 |
| NA50 | 21513 |
| NGA50 | 21513 |
| NA75 | 11932 |
| NGA75 | 11546 |
| LA50 | 70 |
| LGA50 | 70 |
| LA75 | 142 |
| LGA75 | 144 |

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

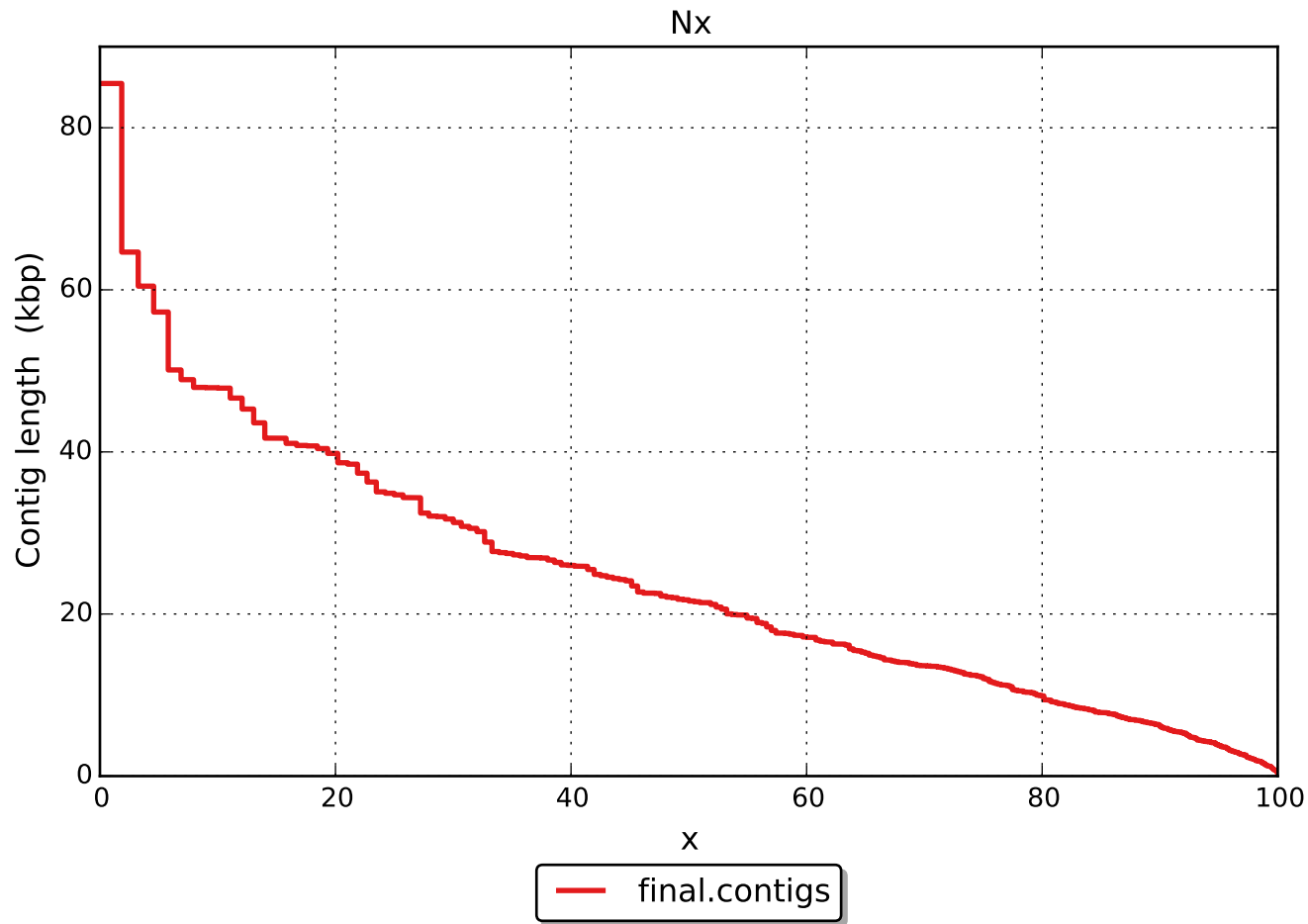
| | final.contigs |
|-----------------------------|---------------|
| # misassemblies | 5 |
| # relocations | 5 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 120242 |
| # local misassemblies | 3 |
| # mismatches | 2720 |
| # indels | 11 |
| # short indels | 10 |
| # long indels | 1 |
| Indels length | 92 |

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).

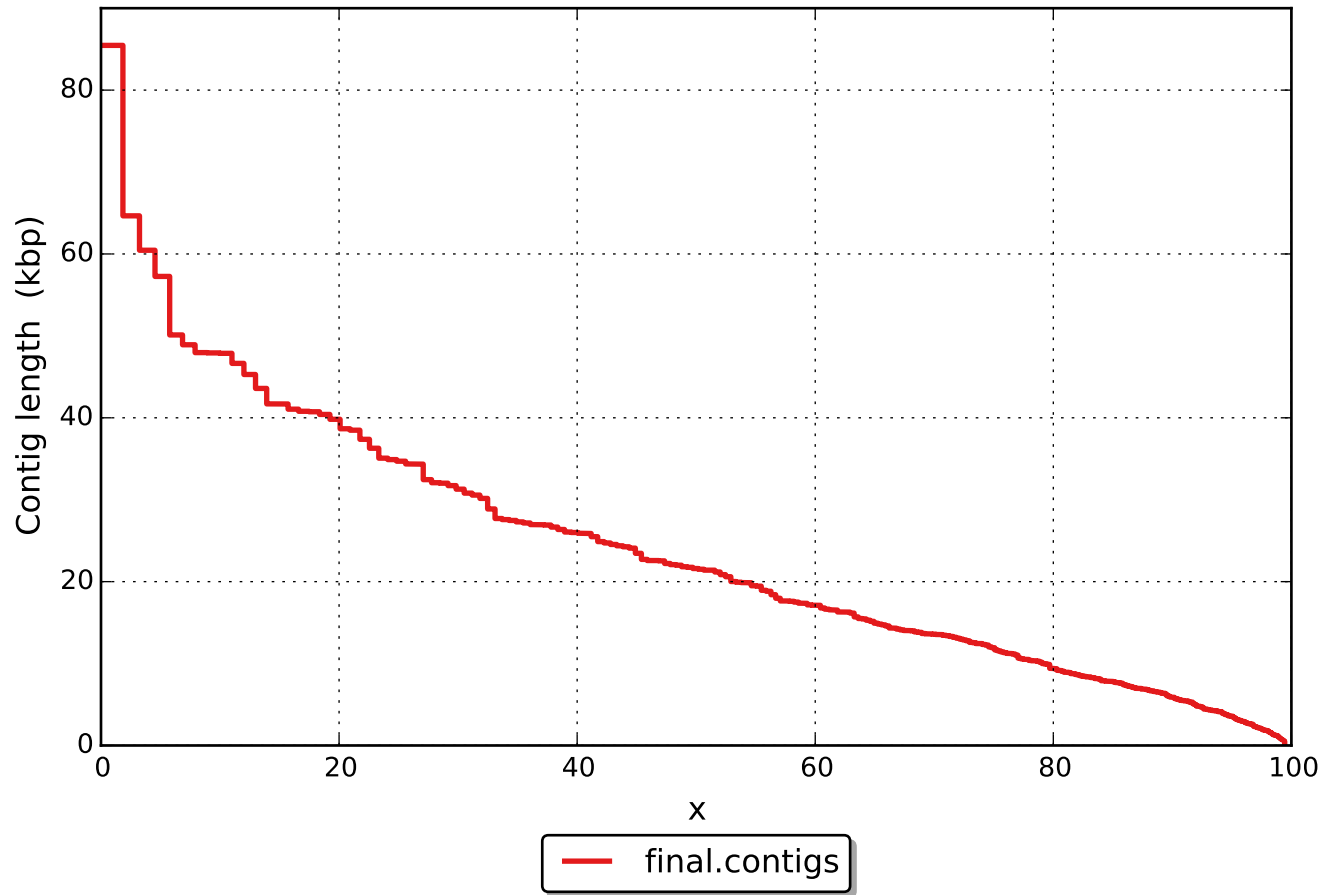
Unaligned report

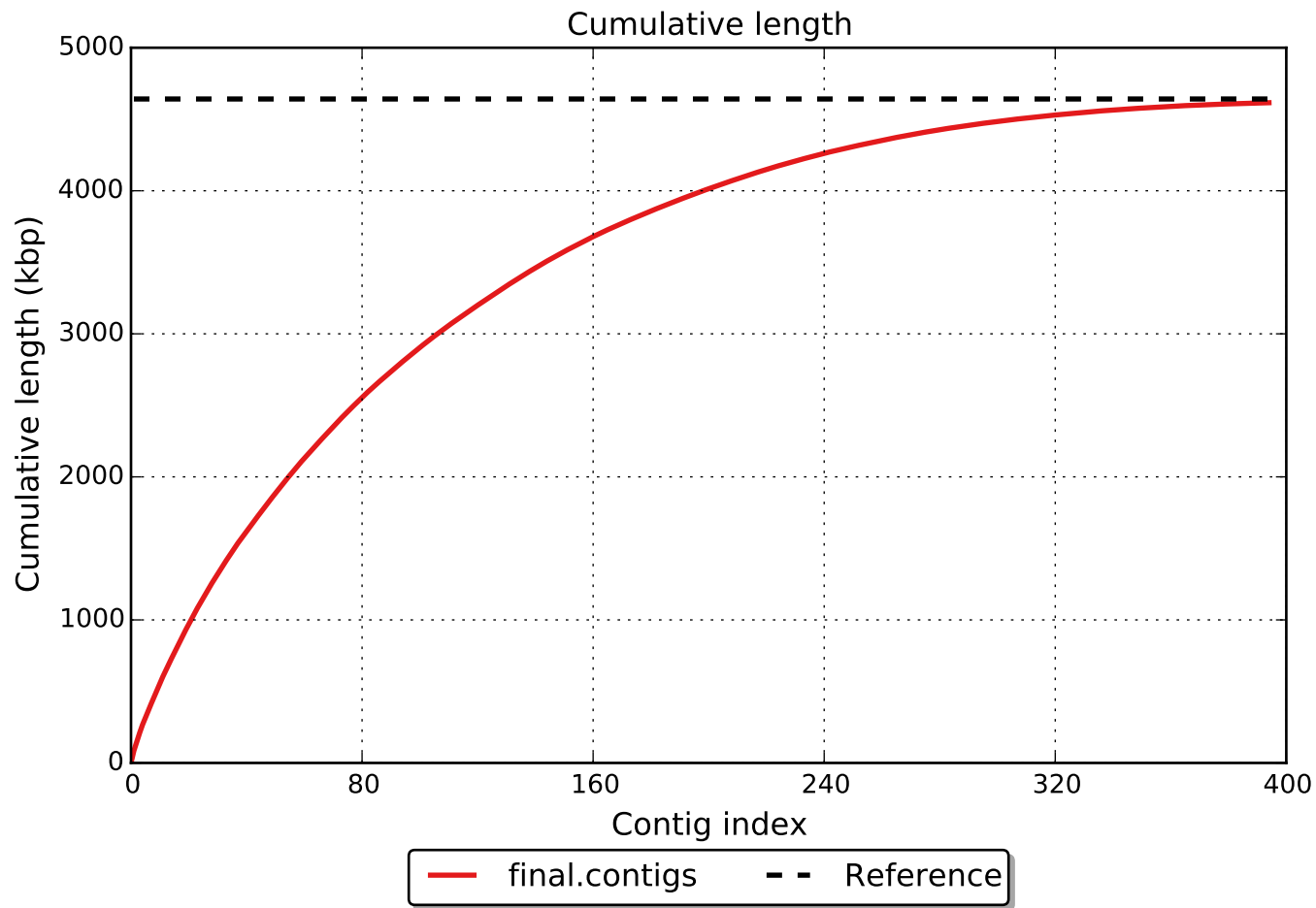
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 117 |
| # N's | 0 |

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).

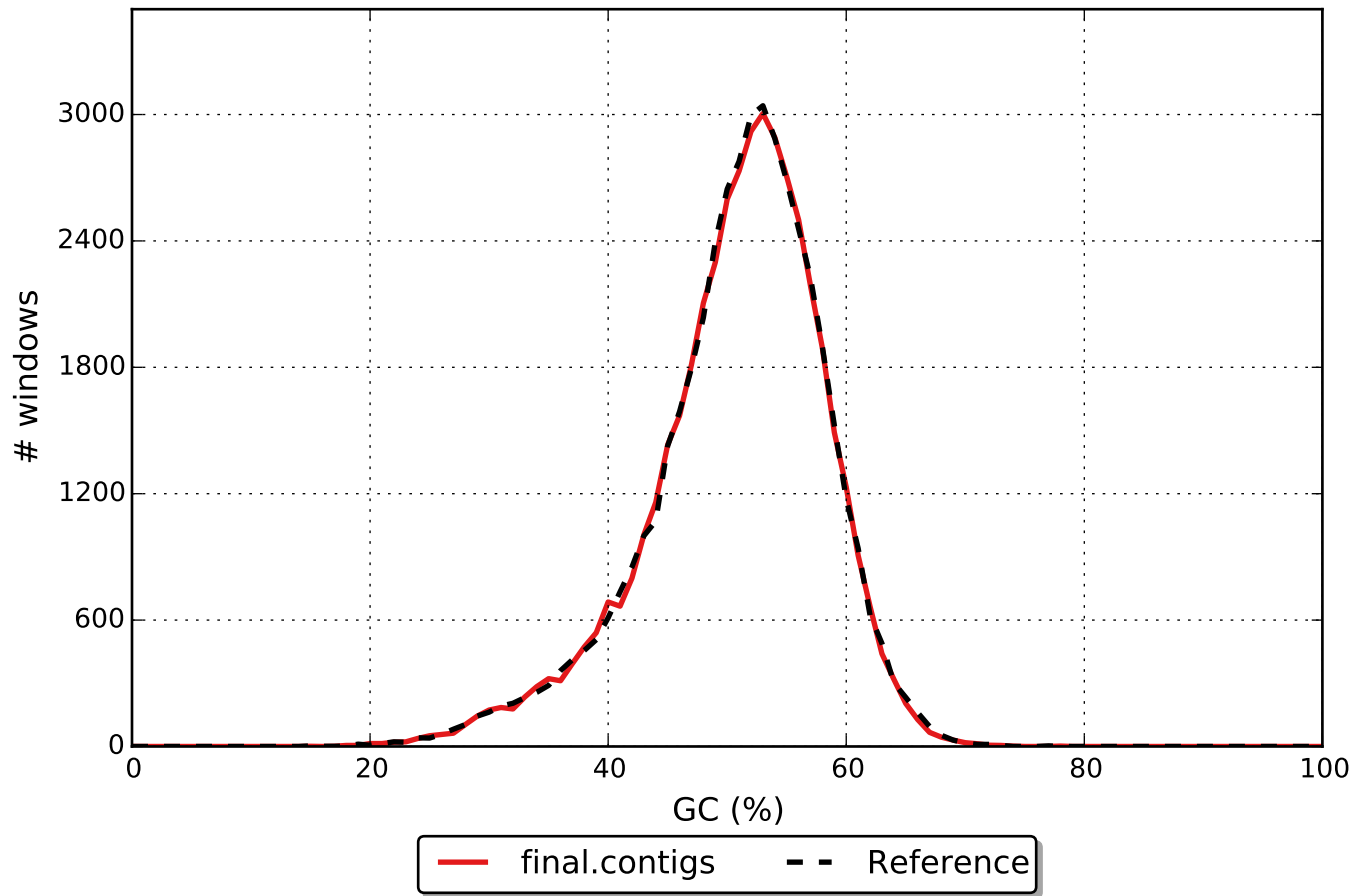


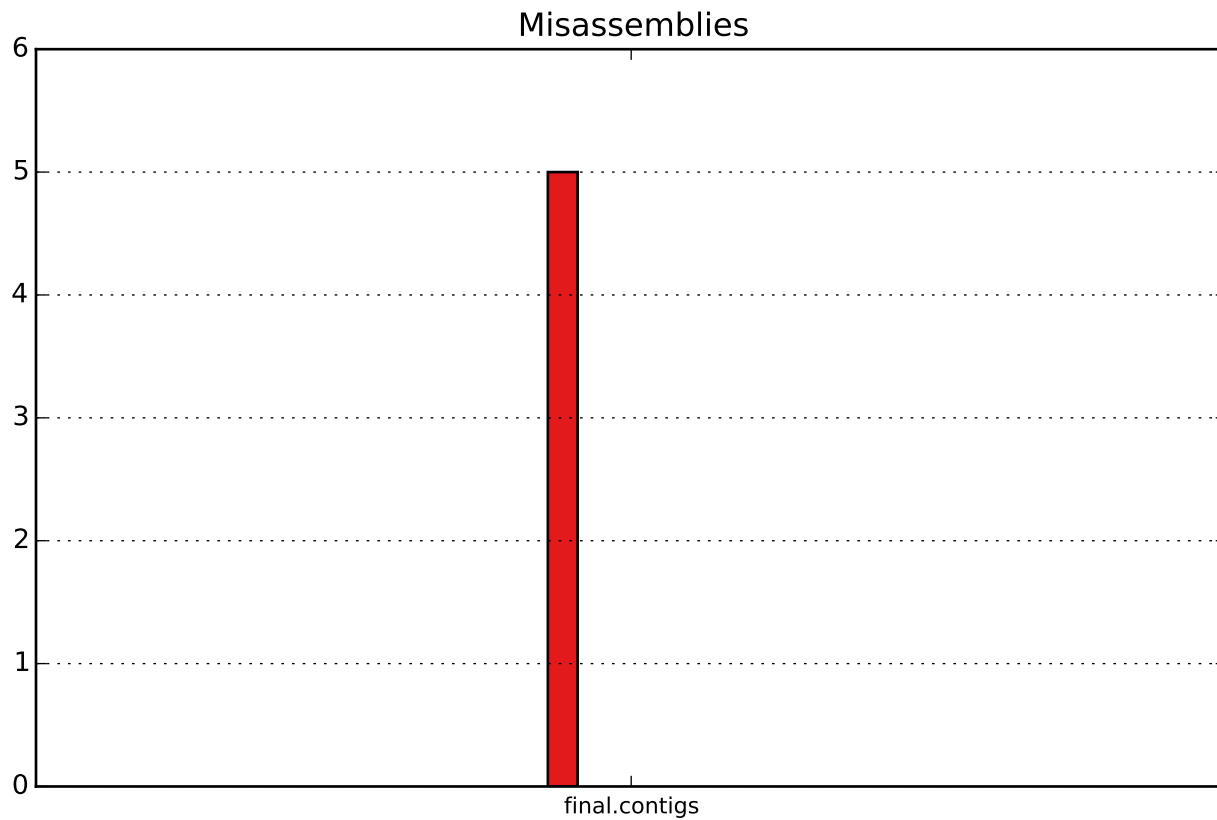
NGx



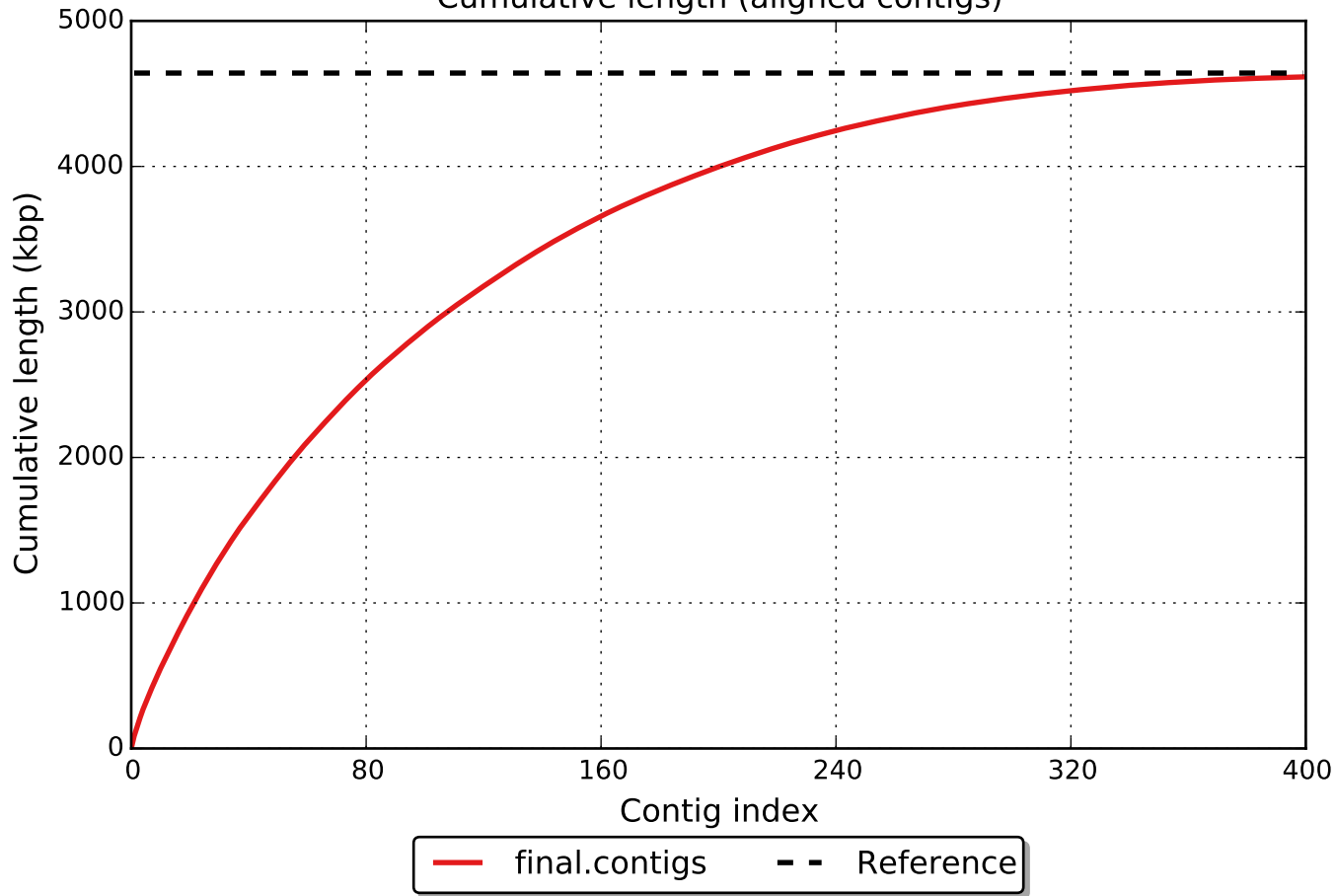


GC content

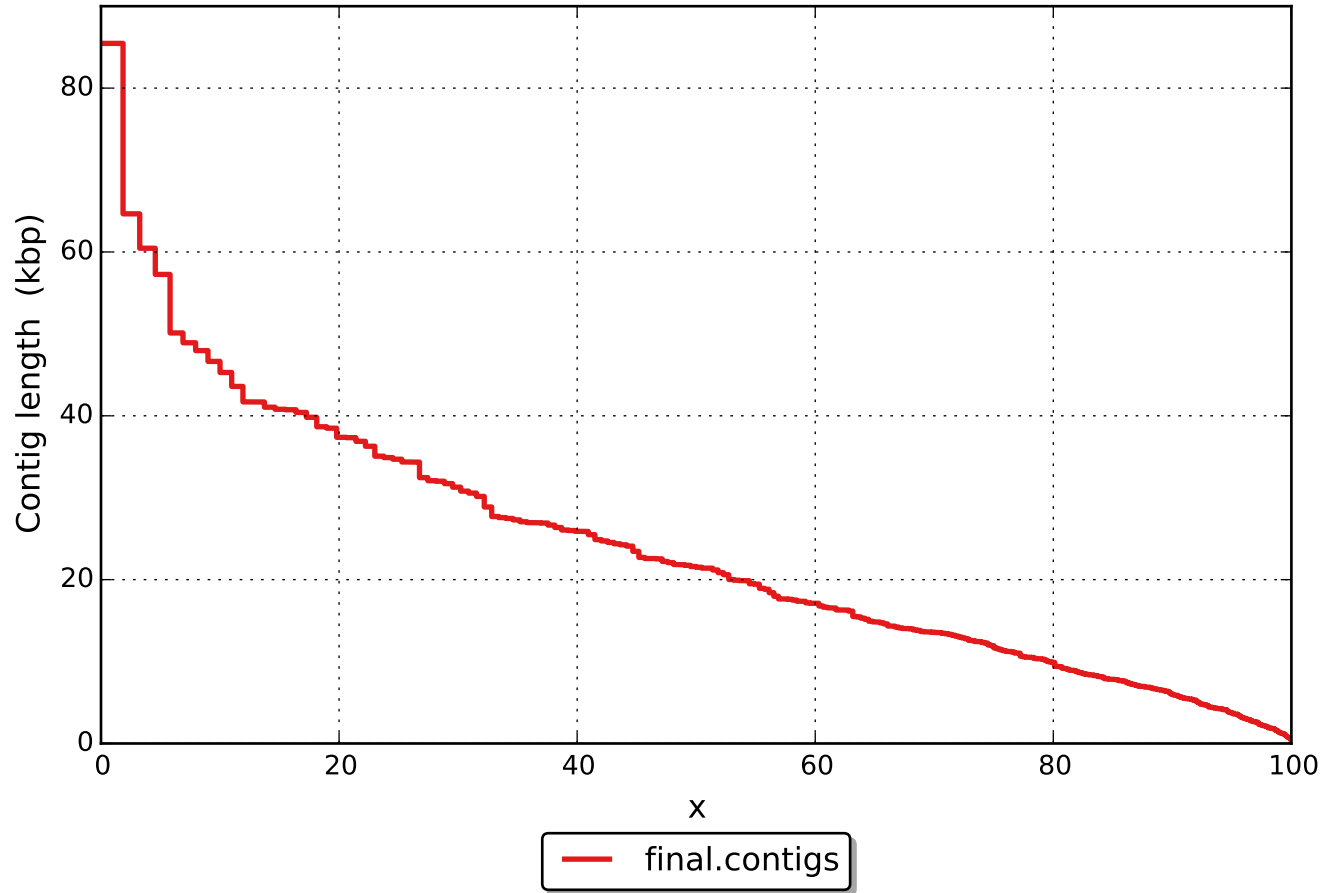




Cumulative length (aligned contigs)



NAx



NGAx

