

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 0 bp) | 318 |
| # contigs (>= 1000 bp) | 233 |
| # contigs (>= 5000 bp) | 184 |
| # contigs (>= 10000 bp) | 146 |
| # contigs (>= 25000 bp) | 61 |
| # contigs (>= 50000 bp) | 17 |
| Total length (>= 0 bp) | 4569350 |
| Total length (>= 1000 bp) | 4535541 |
| Total length (>= 5000 bp) | 4410087 |
| Total length (>= 10000 bp) | 4121602 |
| Total length (>= 25000 bp) | 2746097 |
| Total length (>= 50000 bp) | 1198644 |
| # contigs | 255 |
| Largest contig | 94996 |
| Total length | 4551272 |
| Reference length | 4641652 |
| GC (%) | 50.75 |
| Reference GC (%) | 50.79 |
| N50 | 30931 |
| NG50 | 30566 |
| N75 | 17611 |
| NG75 | 16956 |
| L50 | 45 |
| LG50 | 46 |
| L75 | 94 |
| LG75 | 97 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 97.989 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.73 |
| # indels per 100 kbp | 0.09 |
| Largest alignment | 94996 |
| NA50 | 30931 |
| NGA50 | 30566 |
| NA75 | 17611 |
| NGA75 | 16956 |
| LA50 | 45 |
| LGA50 | 46 |
| LA75 | 94 |
| LGA75 | 97 |

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

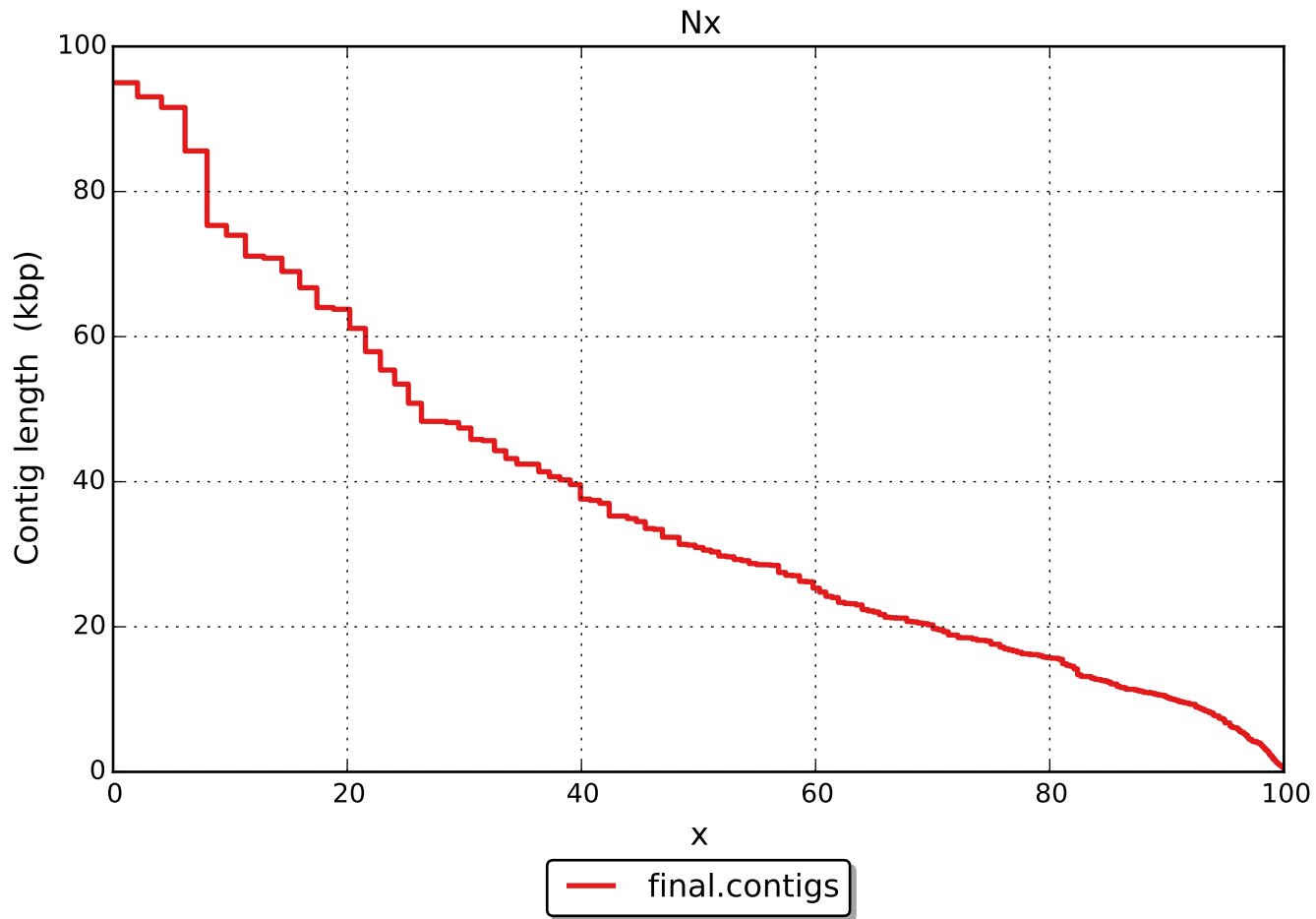
| | final.contigs |
|-----------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # mismatches | 33 |
| # indels | 4 |
| # short indels | 3 |
| # long indels | 1 |
| Indels length | 88 |

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).

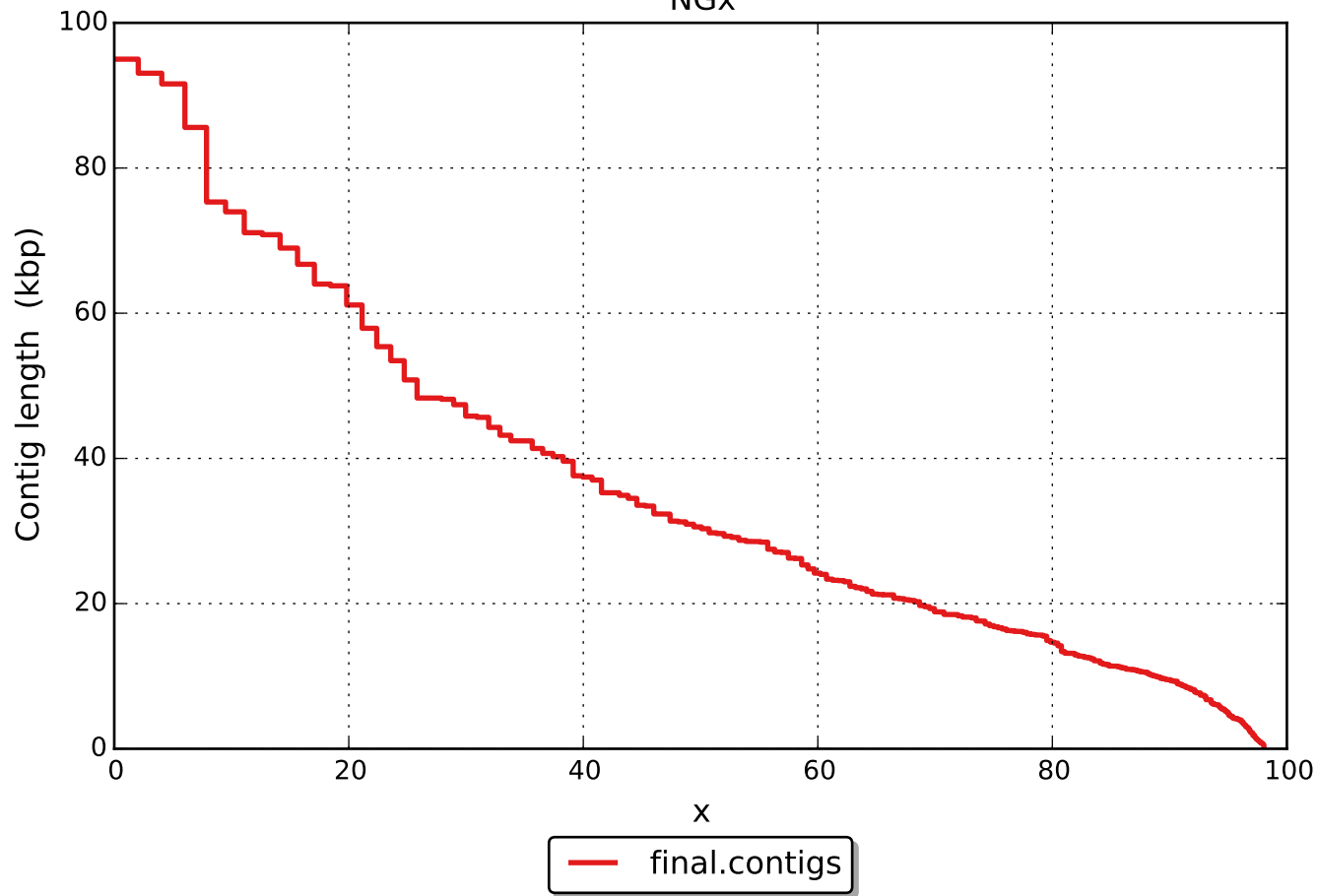
Unaligned report

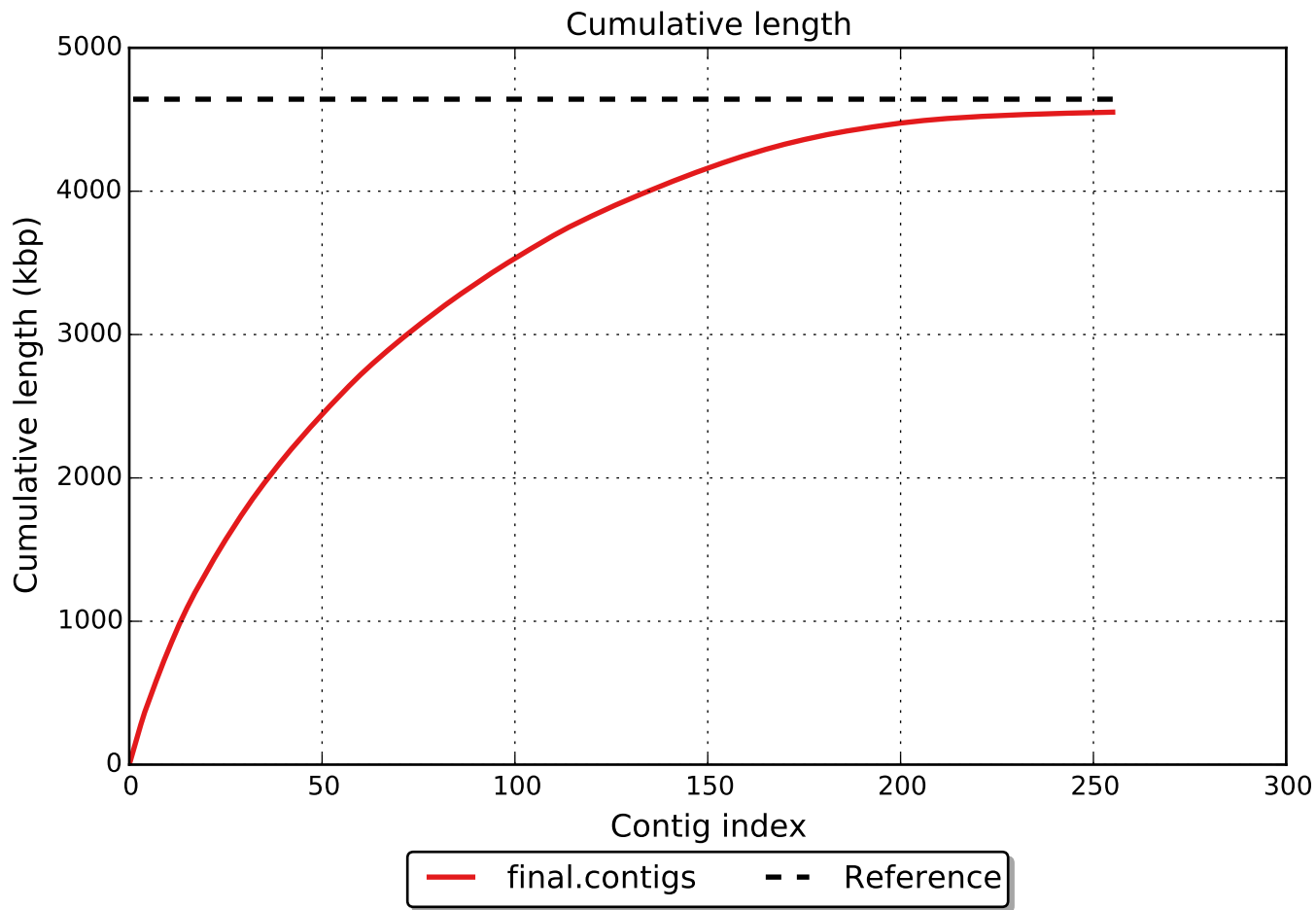
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

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).

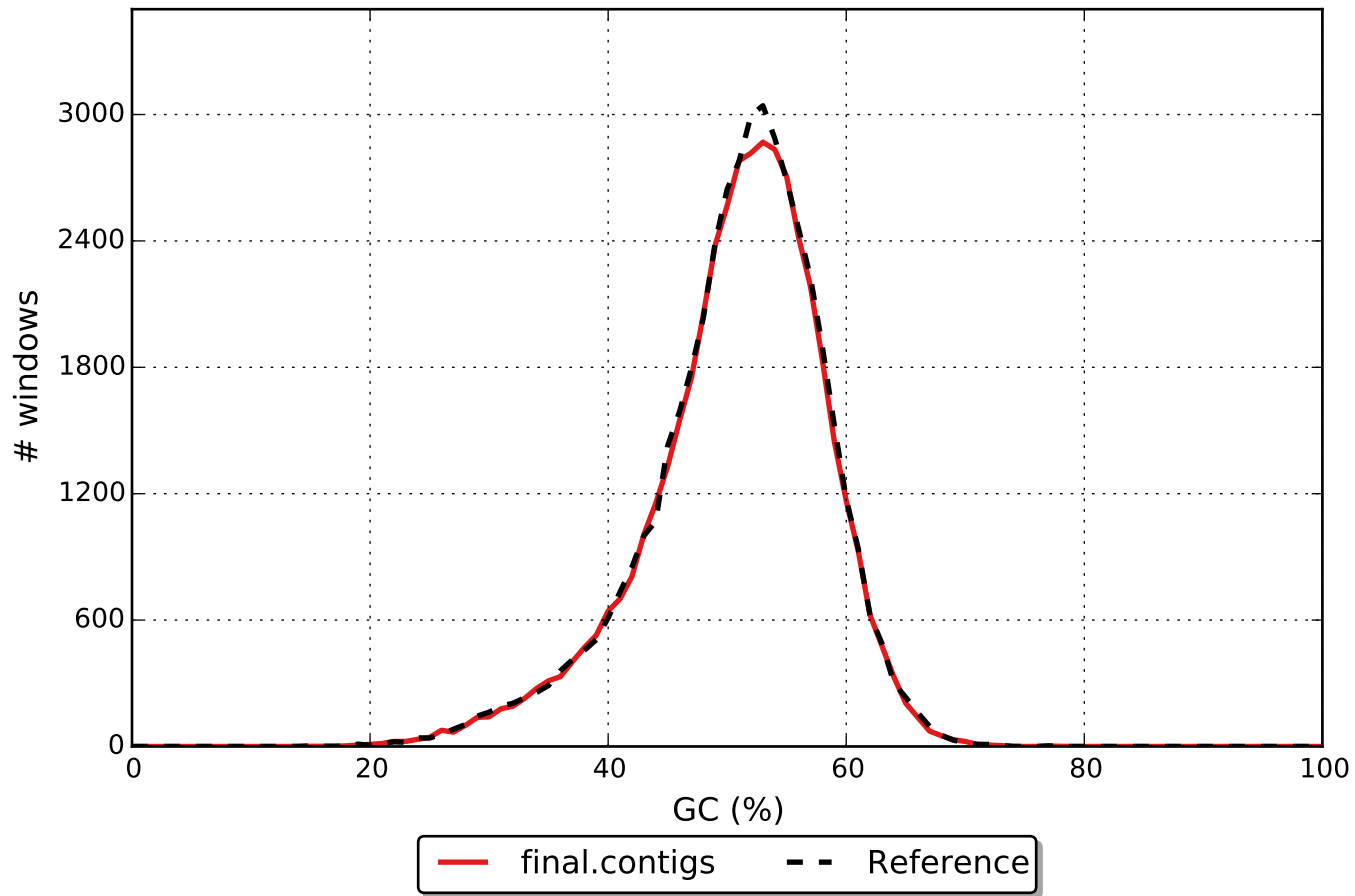


NGx





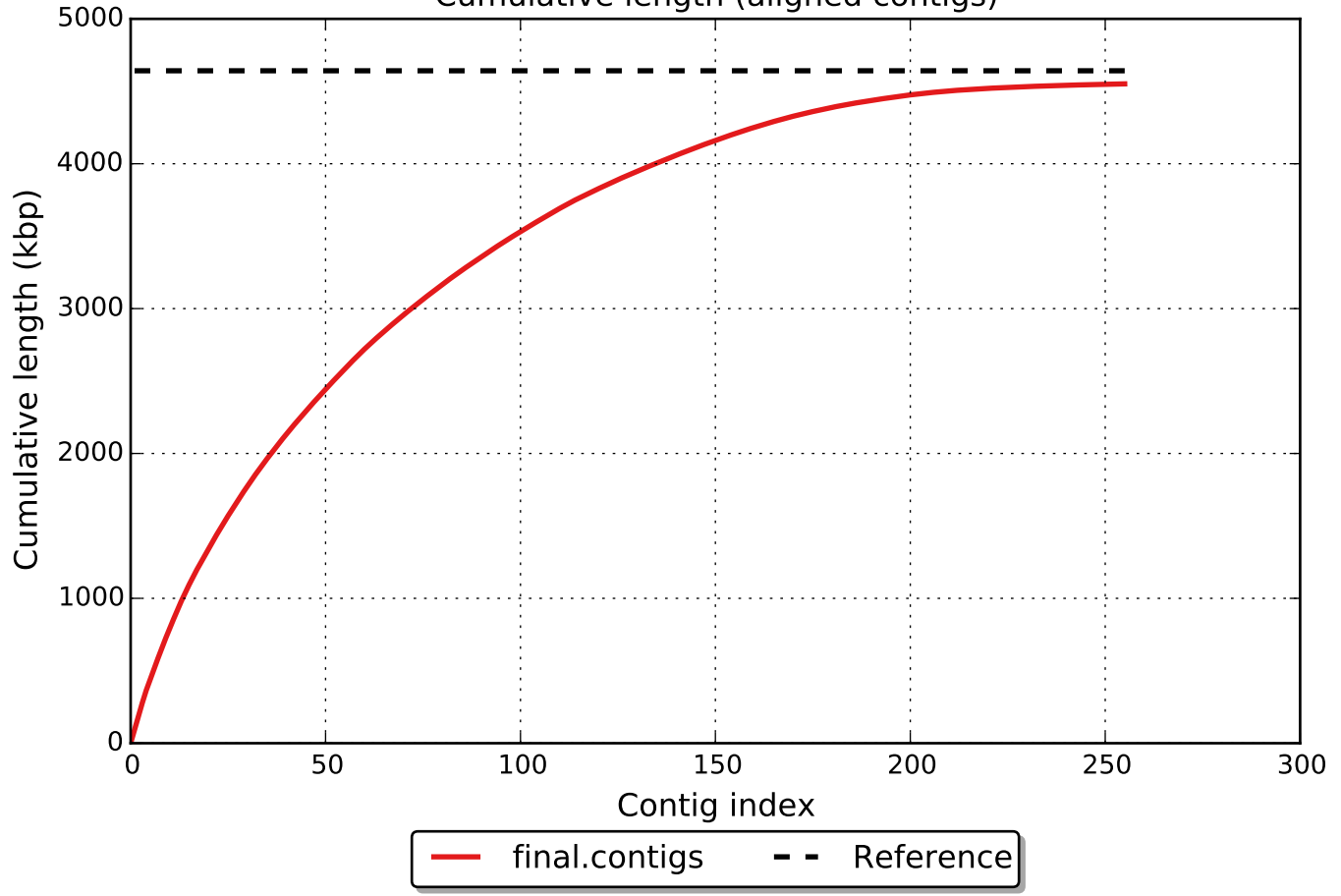
GC content



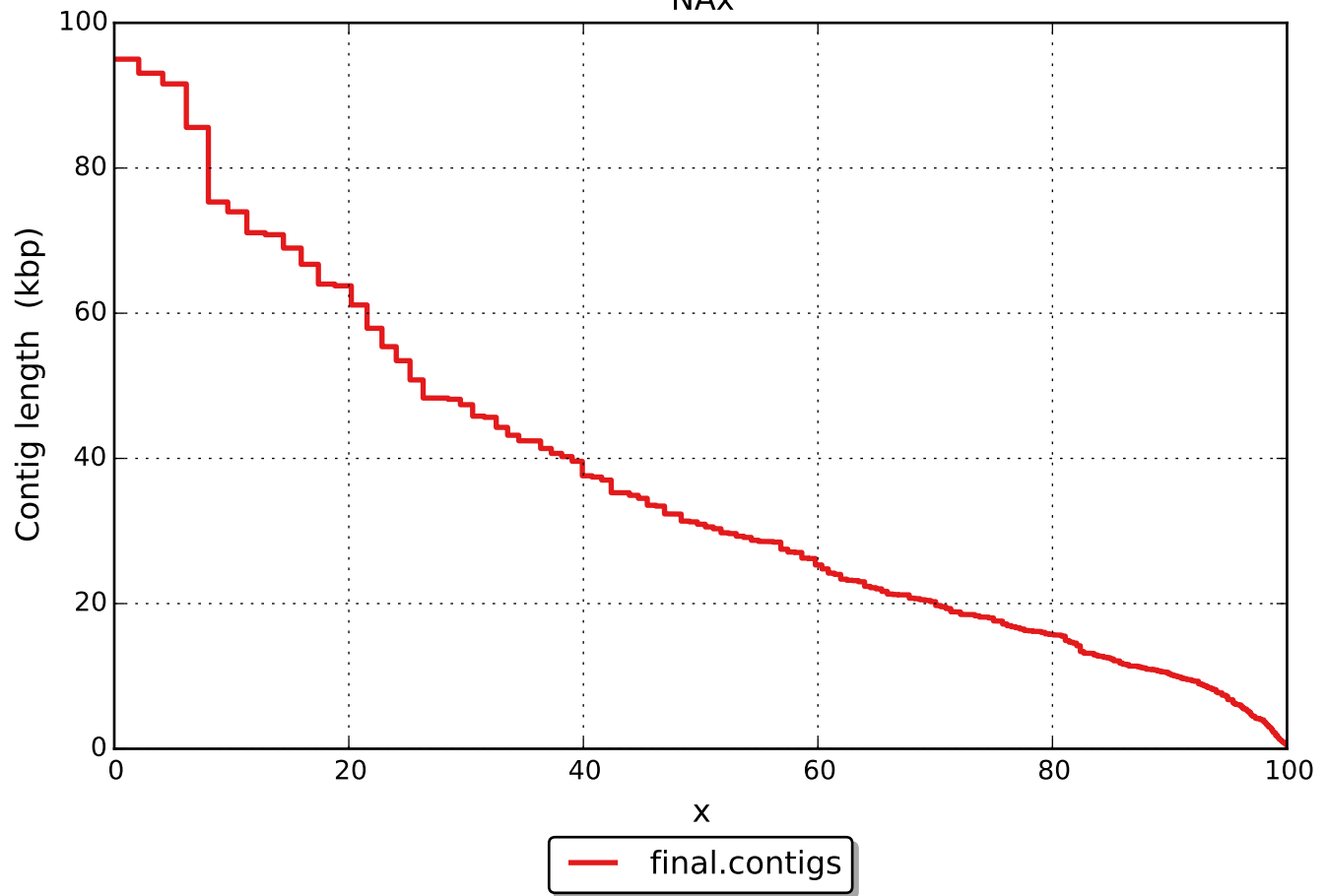
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

