

Report

| | final.contigs |
|--------------------------------|---------------|
| # contigs (≥ 0 bp) | 215 |
| # contigs (≥ 1000 bp) | 198 |
| Total length (≥ 0 bp) | 1267862 |
| Total length (≥ 1000 bp) | 1254149 |
| # contigs | 215 |
| Largest contig | 36991 |
| Total length | 1267862 |
| Reference length | 615980 |
| GC (%) | 25.34 |
| Reference GC (%) | 25.35 |
| N50 | 9274 |
| NG50 | 16331 |
| N75 | 5047 |
| NG75 | 12035 |
| L50 | 42 |
| LG50 | 13 |
| L75 | 86 |
| LG75 | 25 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 2187 |
| # local misassemblies | 0 |
| # unaligned contigs | 70 + 22 part |
| Unaligned length | 554414 |
| Genome fraction (%) | 99.618 |
| Duplication ratio | 1.163 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 173.23 |
| # indels per 100 kbp | 0.33 |
| Largest alignment | 36991 |
| NA50 | 1725 |
| NGA50 | 9274 |
| NGA75 | 5569 |
| LA50 | 94 |
| LGA50 | 19 |
| LGA75 | 39 |

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 | 1 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 16 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 2187 |
| # local misassemblies | 0 |
| # mismatches | 1063 |
| # indels | 2 |
| # short indels | 2 |
| # long indels | 0 |
| Indels length | 2 |

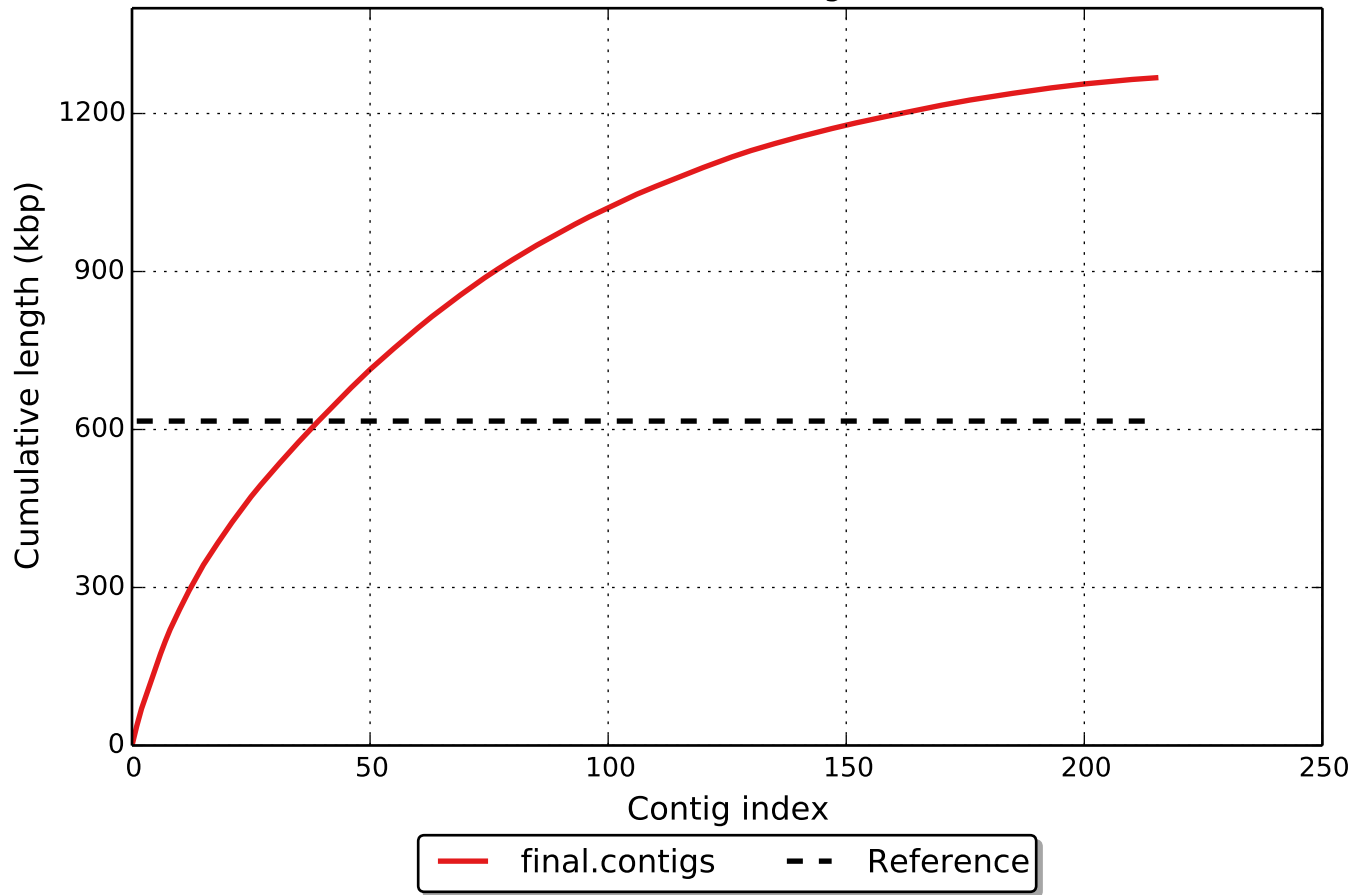
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

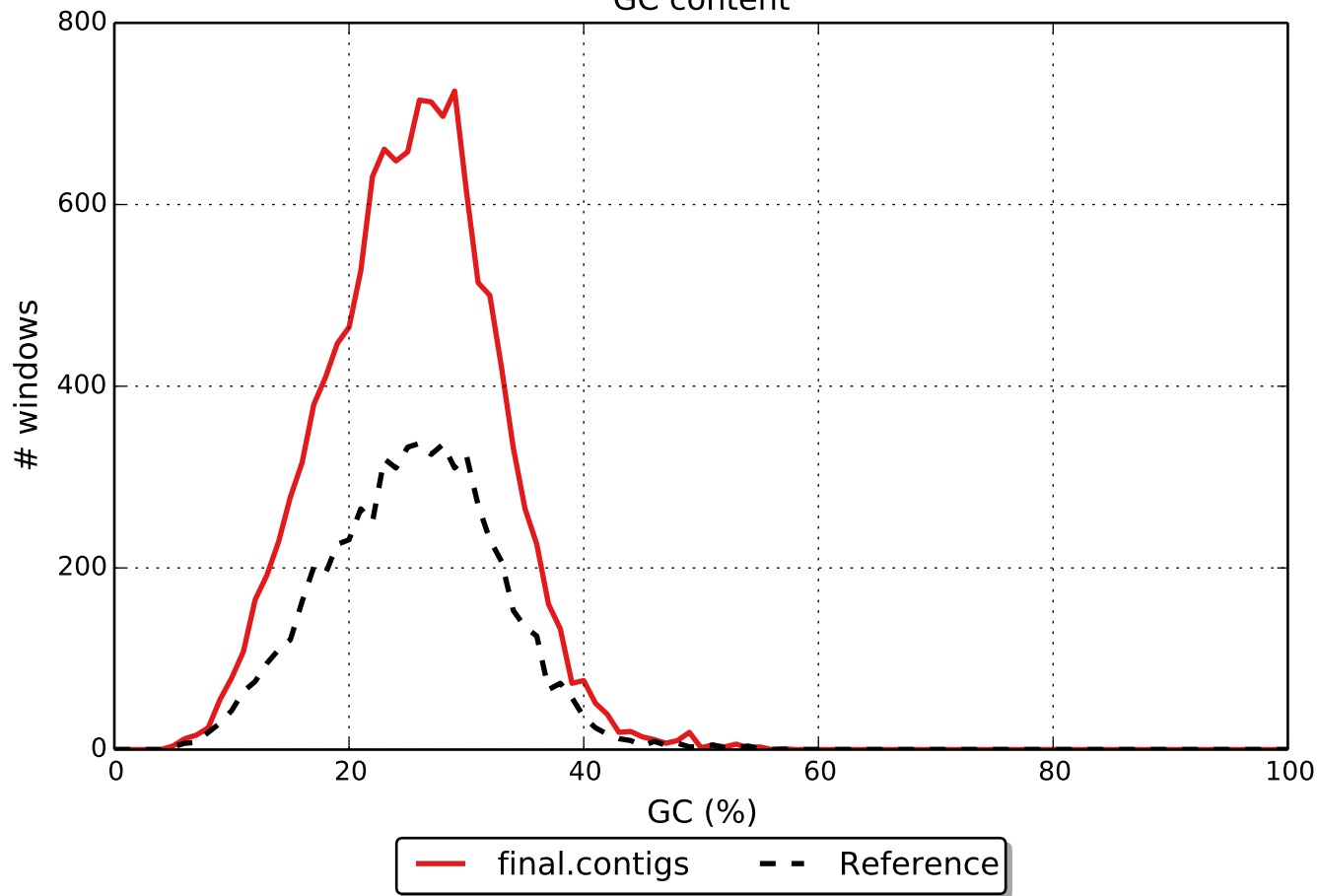
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 70 |
| Fully unaligned length | 382062 |
| # partially unaligned contigs | 22 |
| # with misassembly | 2 |
| # both parts are significant | 16 |
| Partially unaligned length | 172352 |
| # N's | 0 |

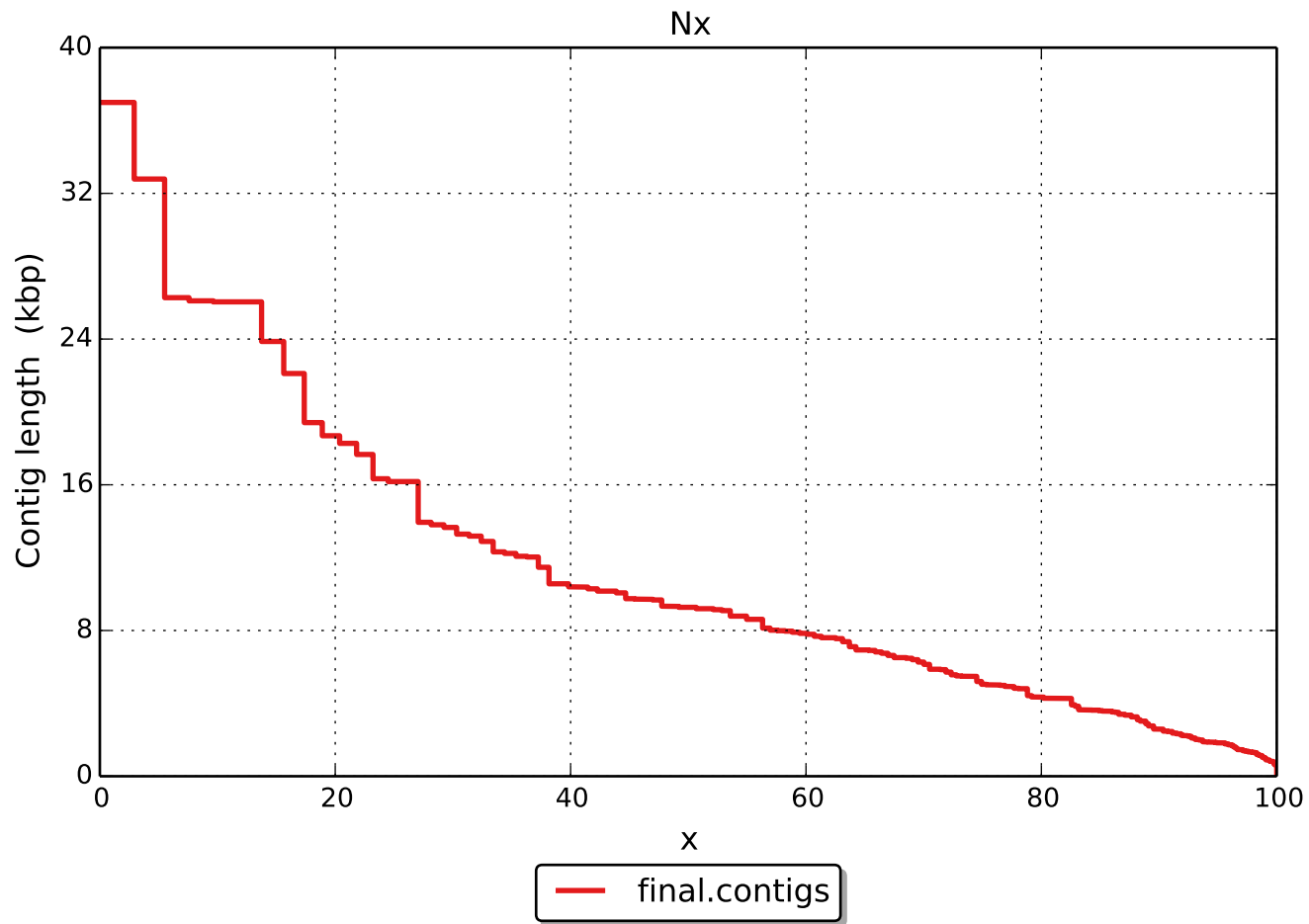
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

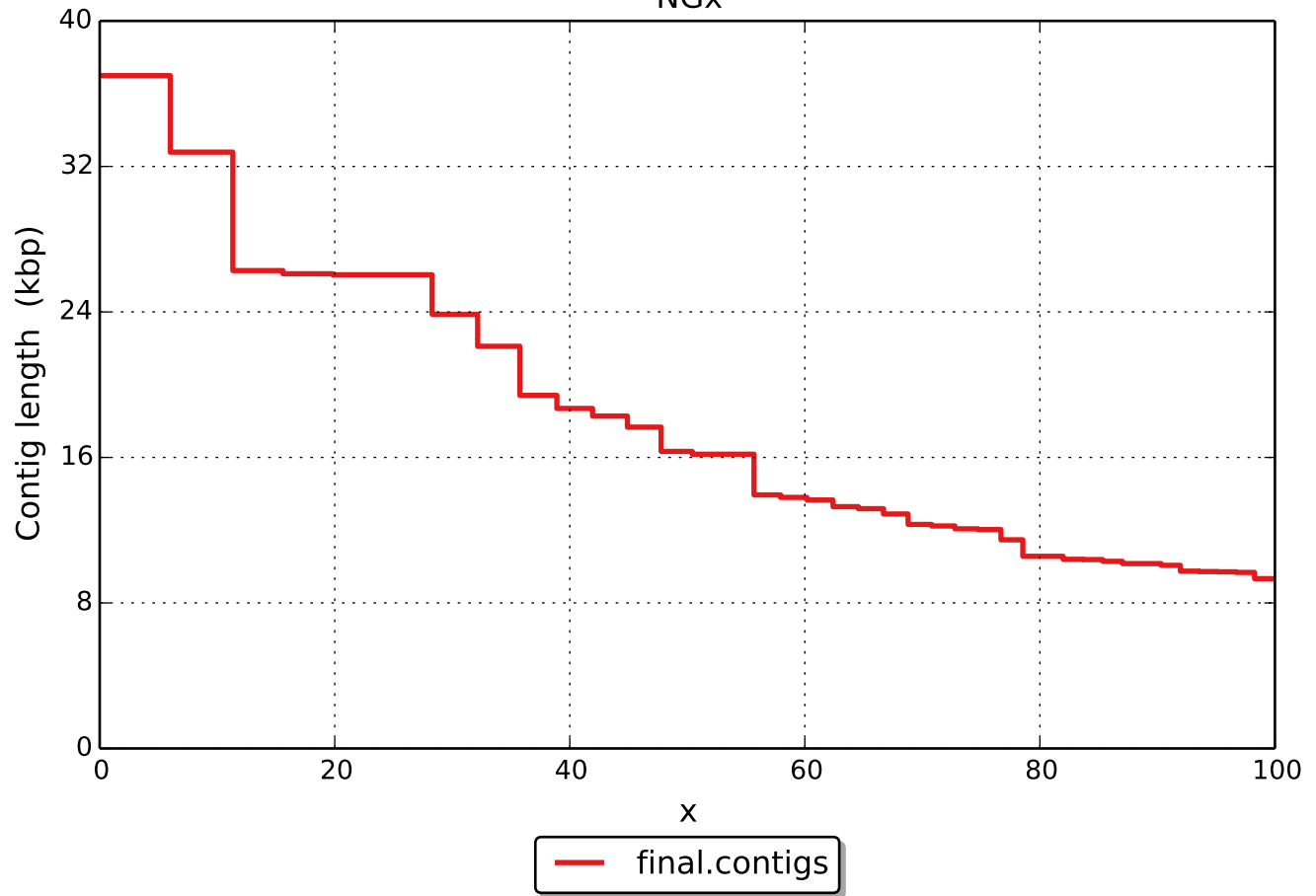


GC content

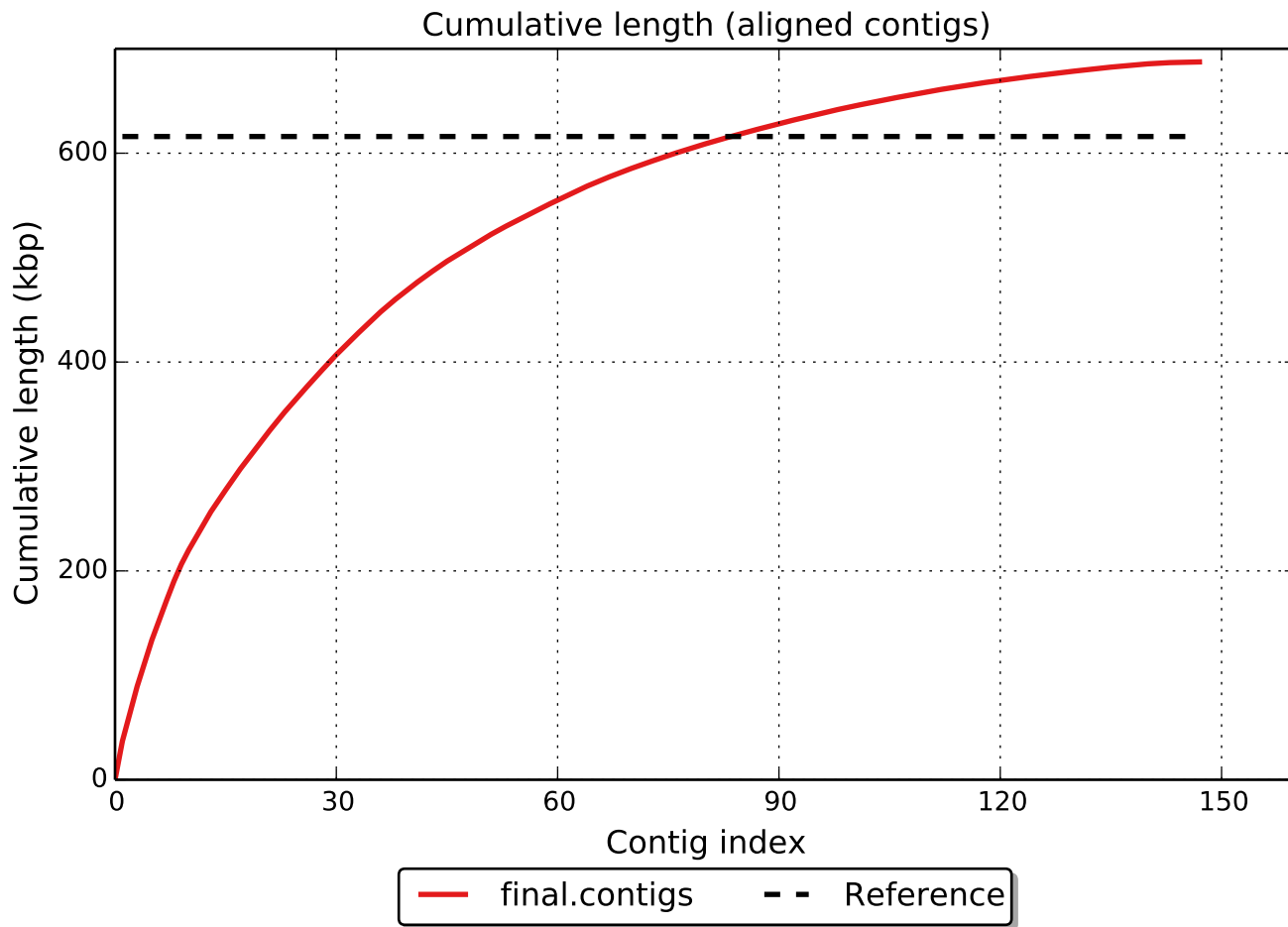


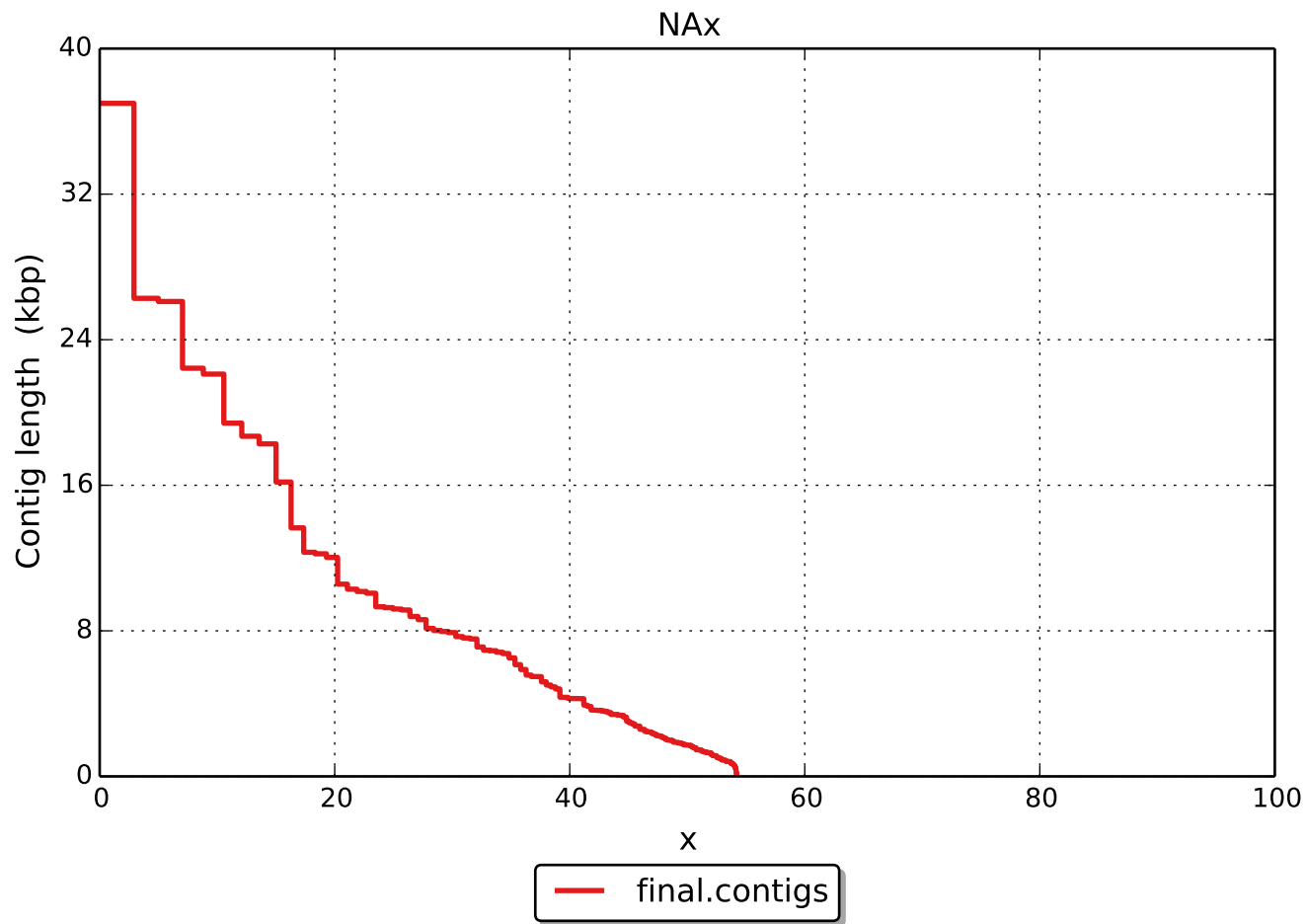


NGx









NGAx

