

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 1047 |
| # contigs (>= 5000 bp) | 292 |
| # contigs (>= 10000 bp) | 63 |
| # contigs (>= 25000 bp) | 1 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 4325052 |
| Total length (>= 5000 bp) | 2393713 |
| Total length (>= 10000 bp) | 825519 |
| Total length (>= 25000 bp) | 26961 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1233 |
| Largest contig | 26961 |
| Total length | 4465552 |
| Reference length | 4641652 |
| GC (℥) | 50.74 |
| Reference GC (℥) | 50.79 |
| N50 | 5470 |
| NG50 | 5208 |
| N75 | 3081 |
| NG75 | 2841 |
| L50 | 262 |
| LG50 | 278 |
| L75 | 538 |
| LG75 | 583 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 1211 |
| # local misassemblies | 15 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (℥) | 96.057 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 4.37 |
| # indels per 100 kbp | 0.34 |
| Largest alignment | 26961 |
| NA50 | 5470 |
| NGA50 | 5208 |
| NA75 | 3081 |
| NGA75 | 2841 |
| LA50 | 262 |
| LGA50 | 278 |
| LA75 | 538 |
| LGA75 | 583 |

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

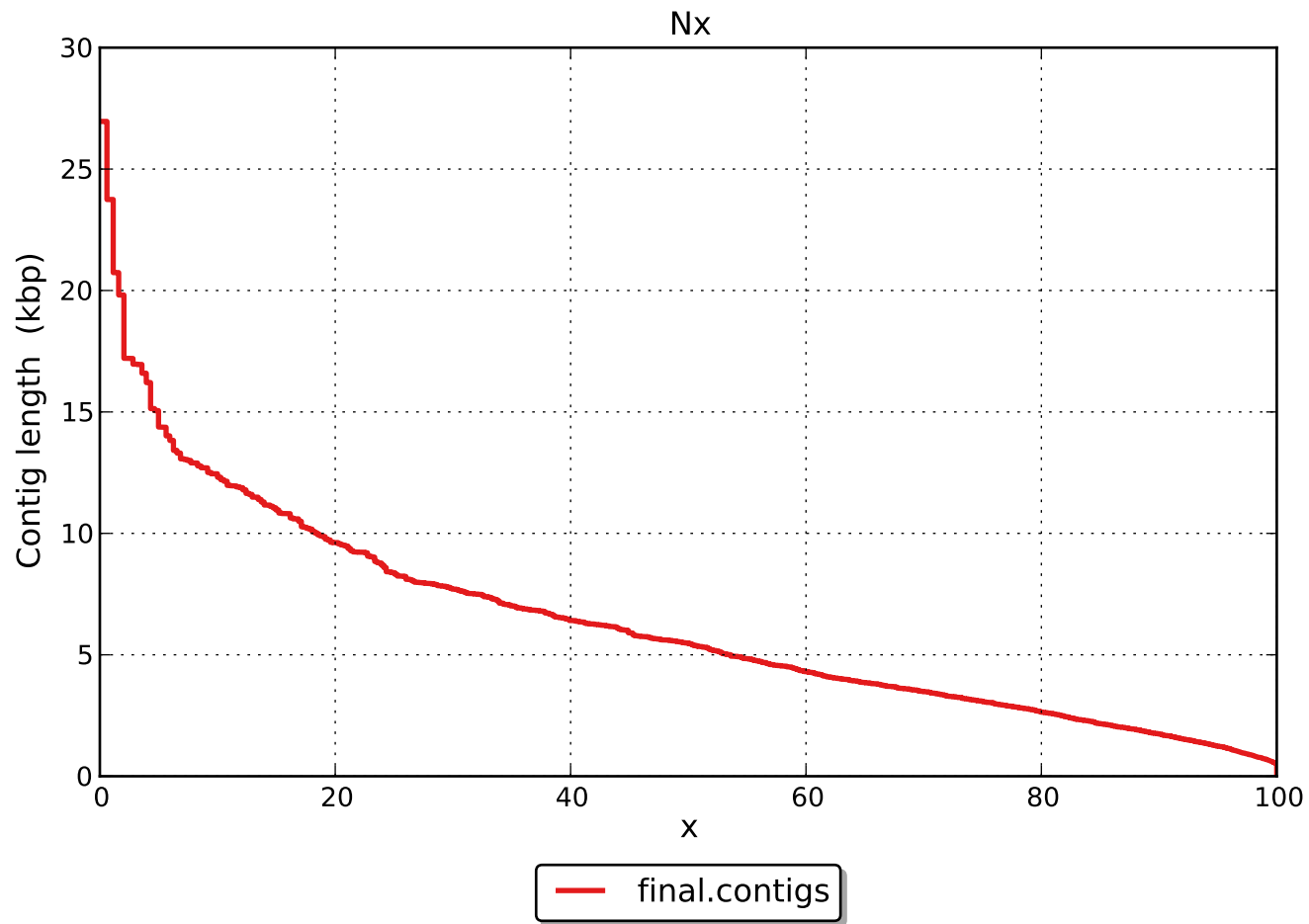
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 1 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 1 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 1211 |
| # local misassemblies | 15 |
| # mismatches | 195 |
| # indels | 15 |
| # short indels | 14 |
| # long indels | 1 |
| Indels length | 83 |

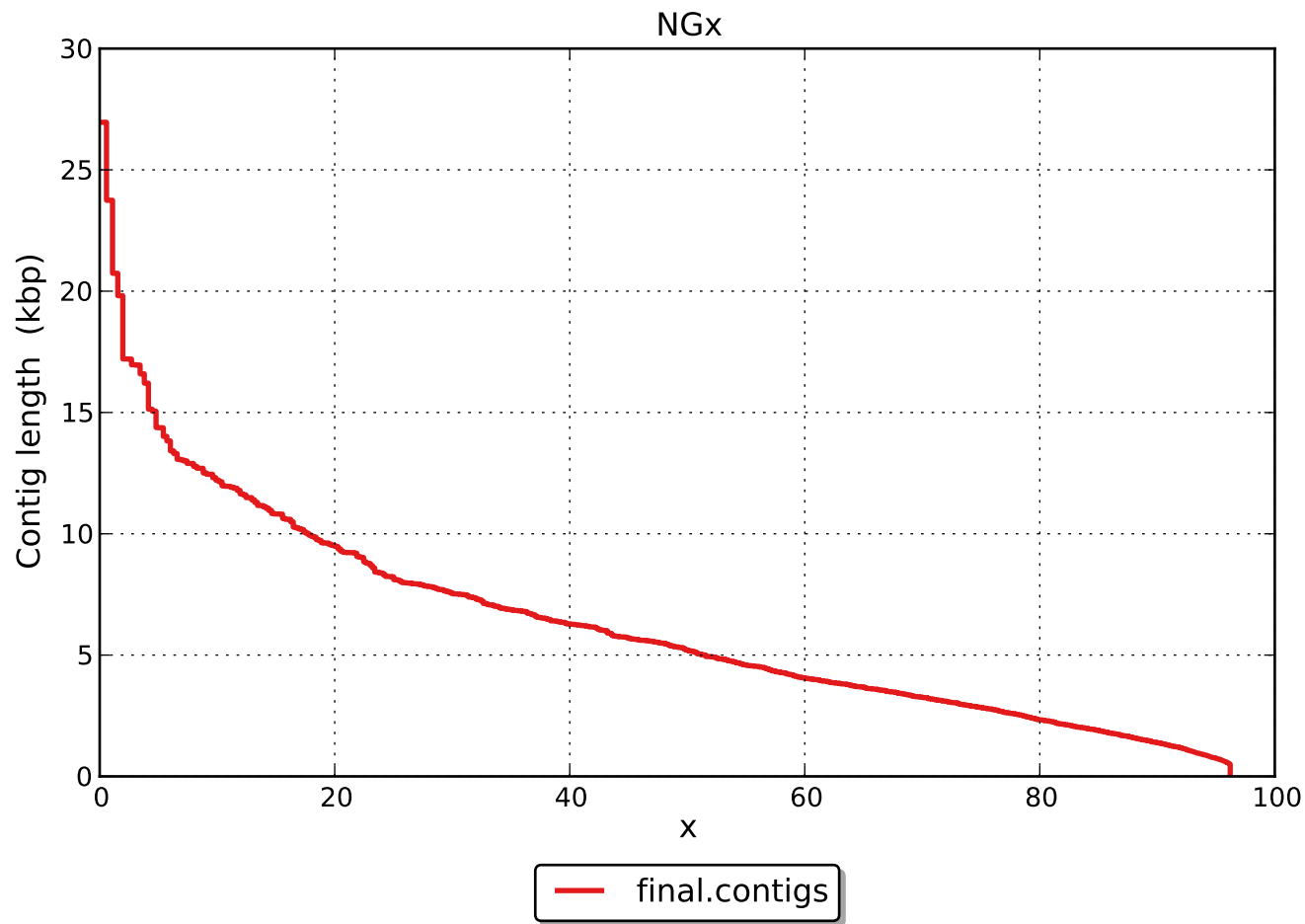
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

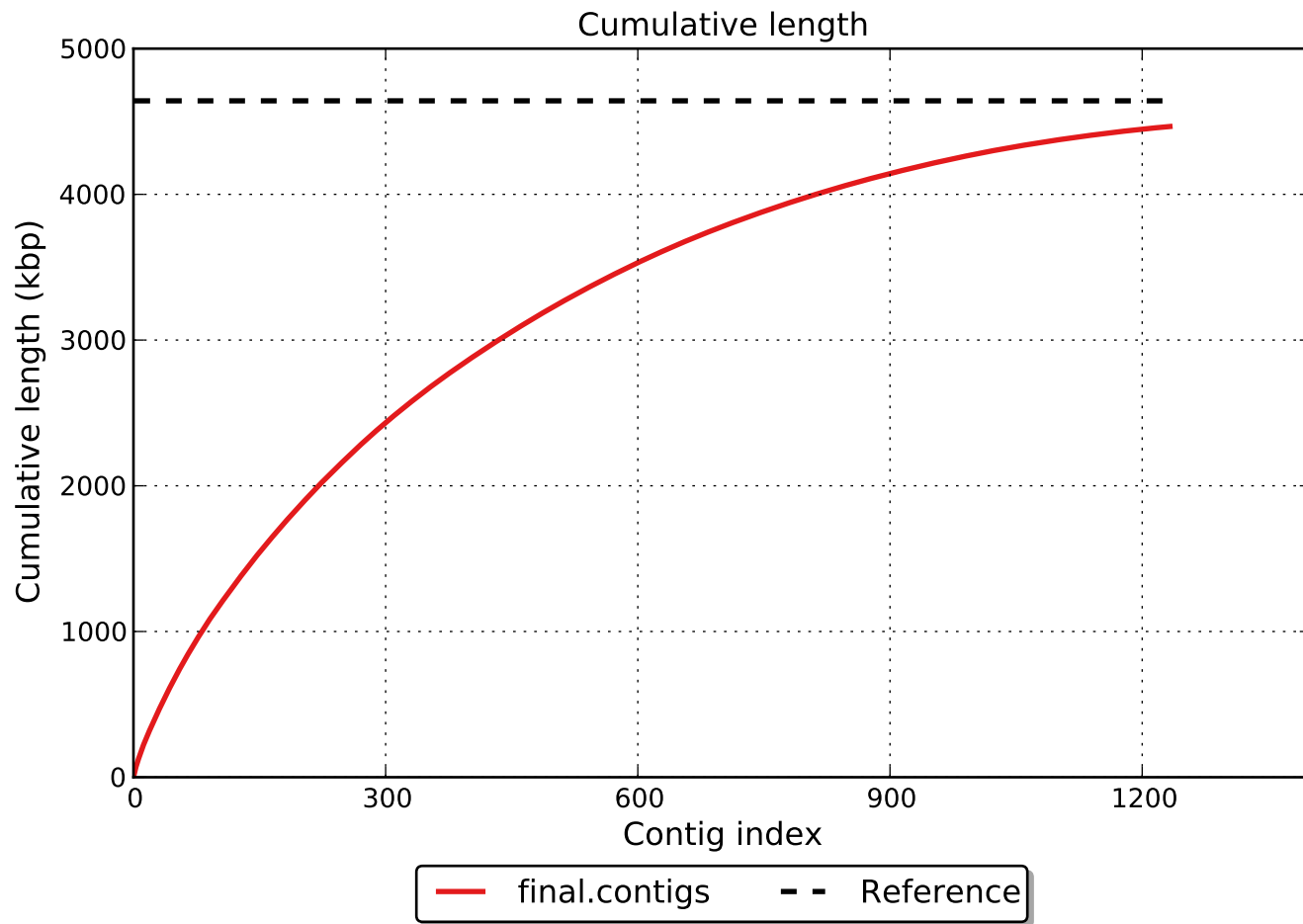
Unaligned report

| | 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 |

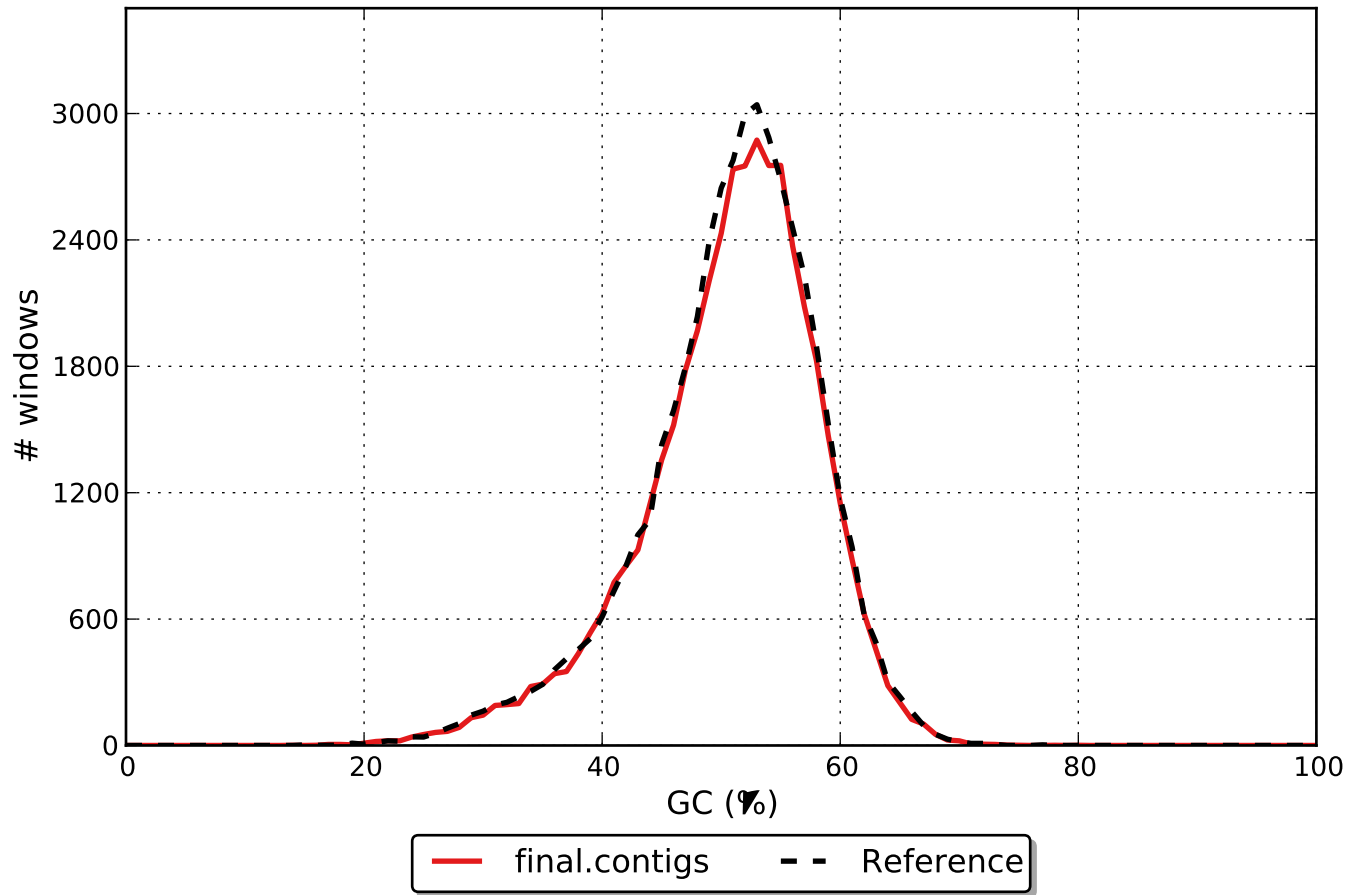
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

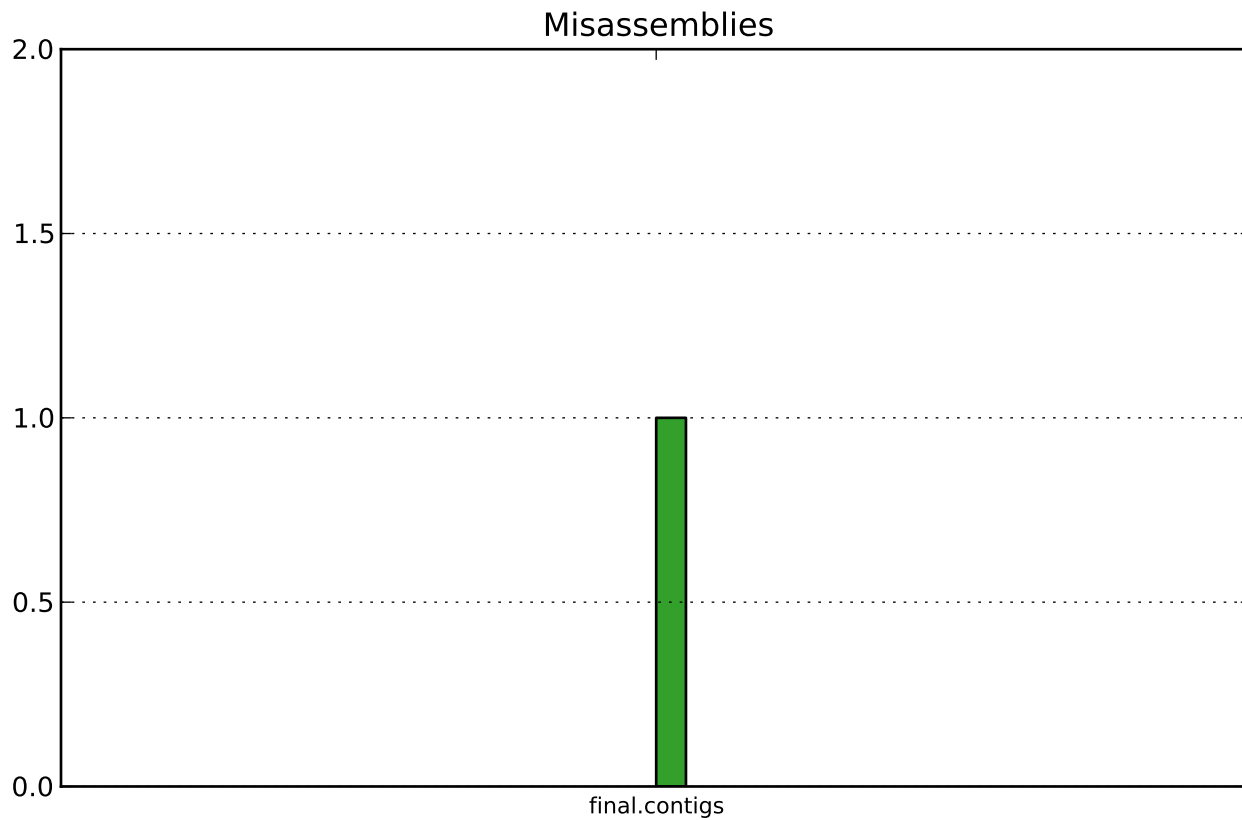




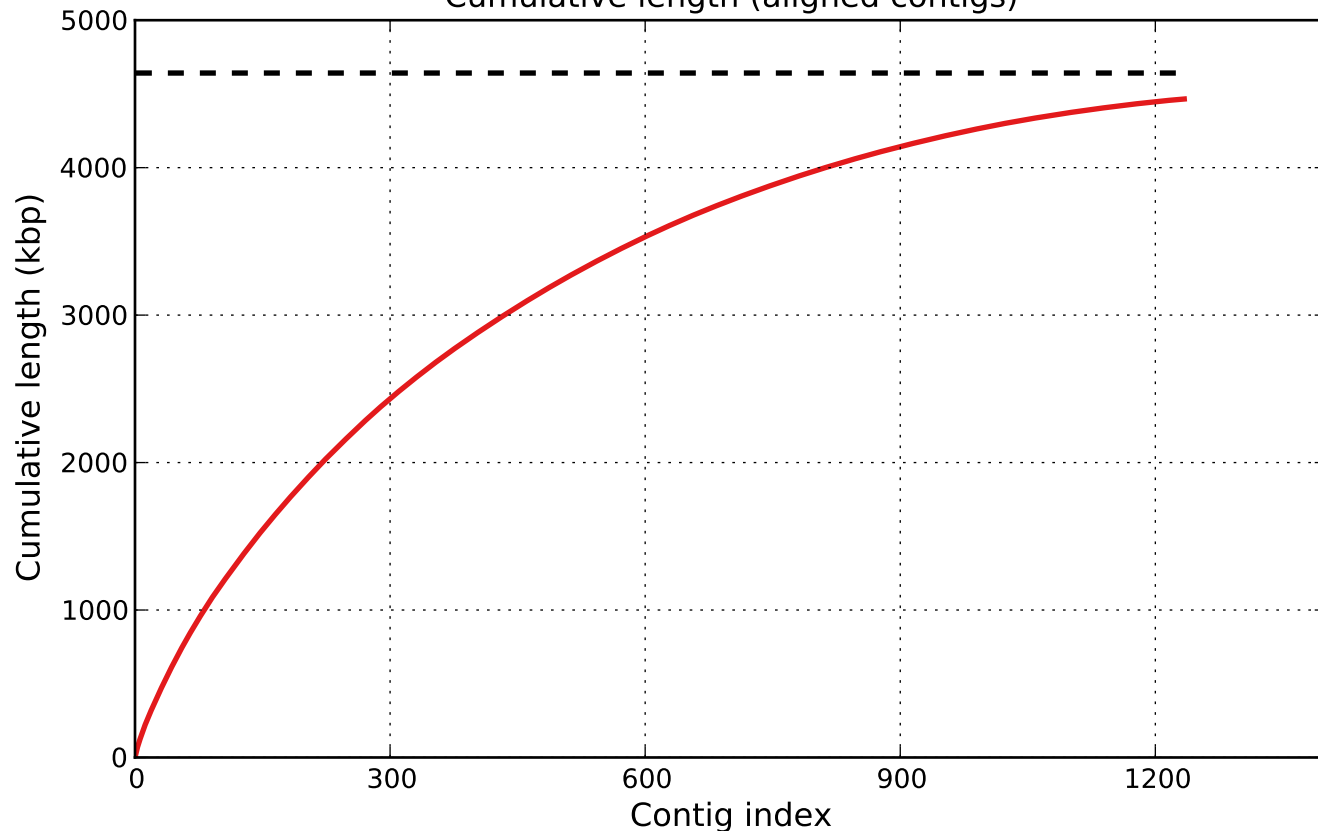


GC content

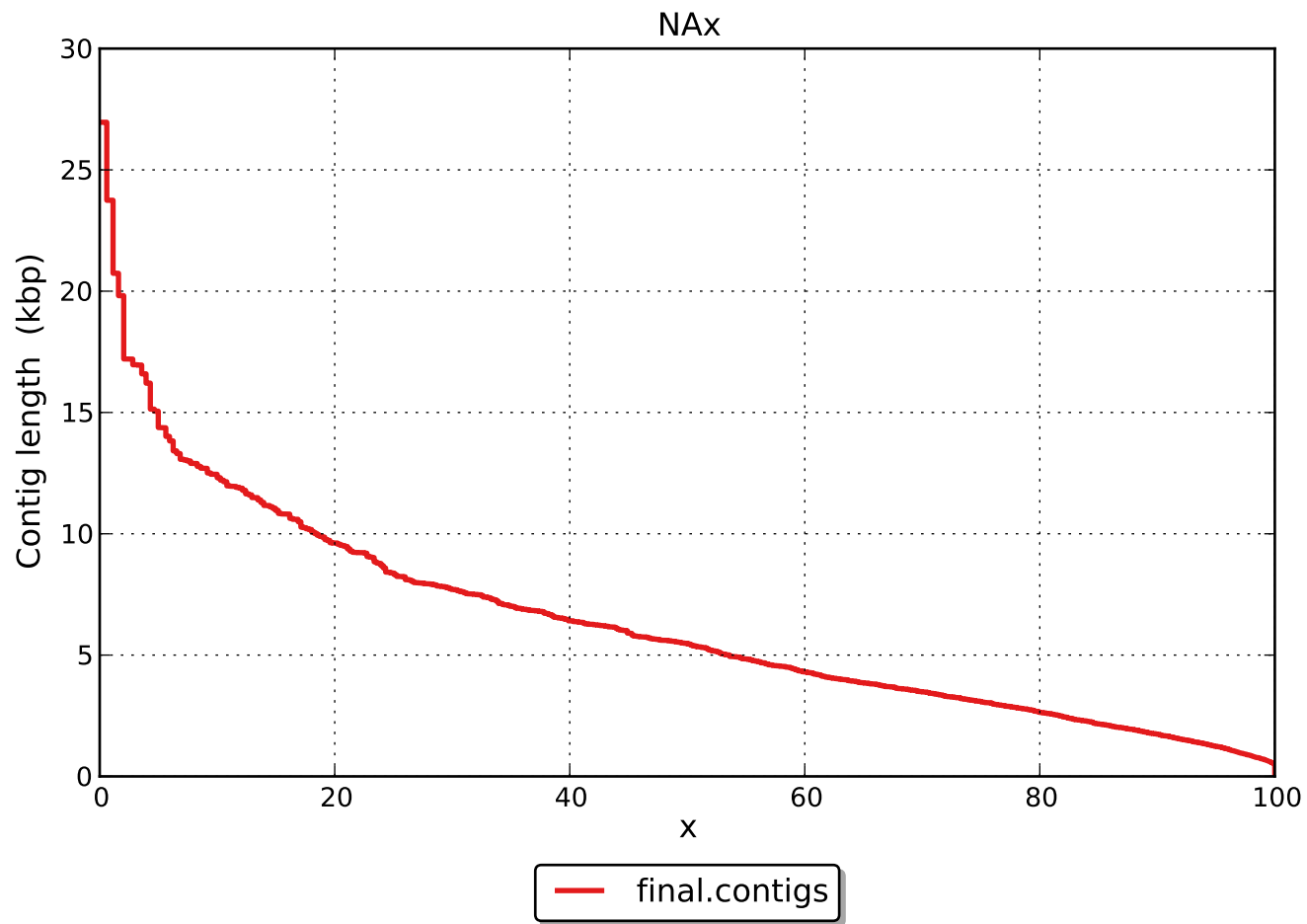




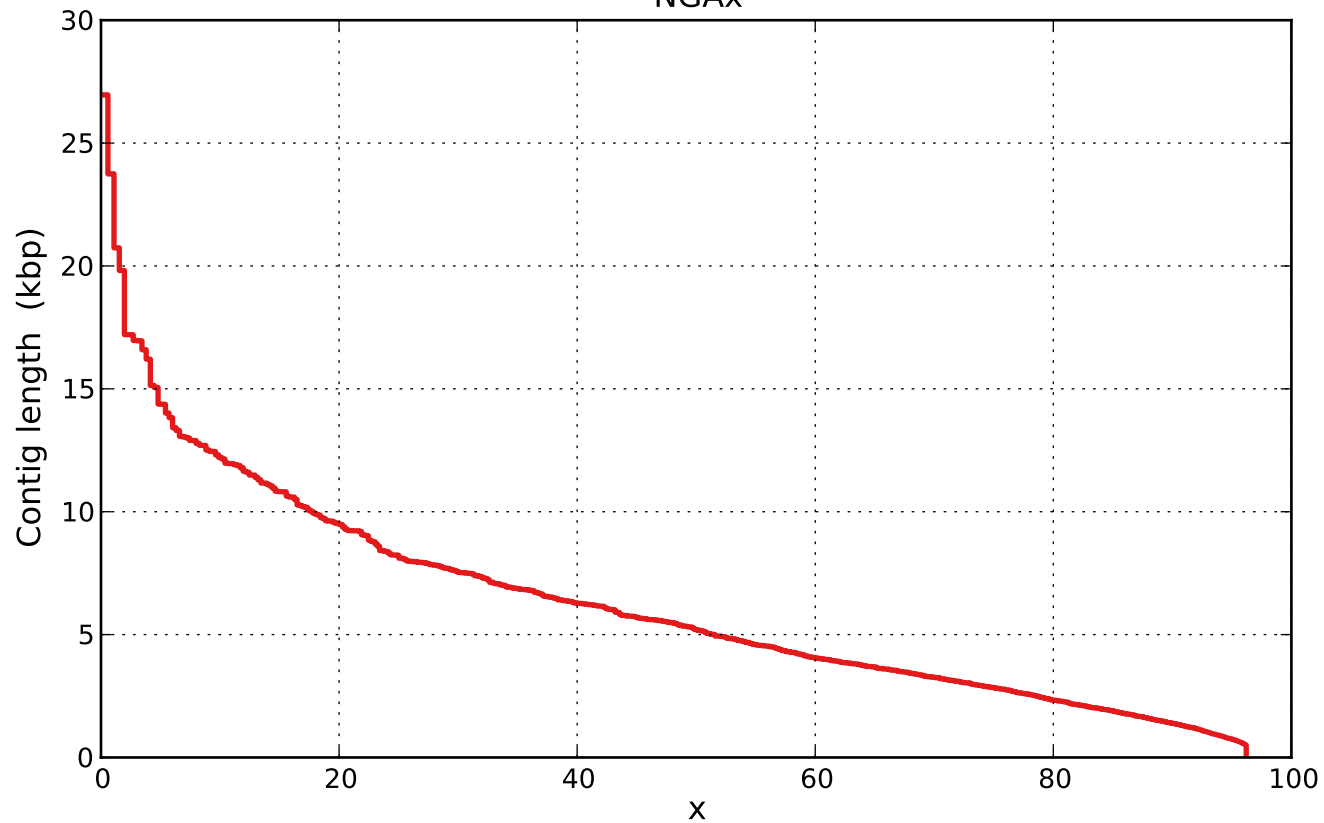
Cumulative length (aligned contigs)



— final.contigs - - Reference



NGAx



— final.contigs