

Report

| | final.contigs |
|--------------------------------|---------------|
| # contigs (≥ 0 bp) | 115 |
| # contigs (≥ 1000 bp) | 107 |
| Total length (≥ 0 bp) | 1292526 |
| Total length (≥ 1000 bp) | 1289546 |
| # contigs | 107 |
| Largest contig | 53647 |
| Total length | 1289546 |
| Reference length | 1283598 |
| GC (%) | 26.31 |
| Reference GC (%) | 26.31 |
| N50 | 18788 |
| NG50 | 18788 |
| N75 | 11480 |
| NG75 | 11480 |
| L50 | 23 |
| LG50 | 23 |
| L75 | 46 |
| LG75 | 45 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 25473 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 98.414 |
| Duplication ratio | 1.021 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 97.84 |
| # indels per 100 kbp | 0.47 |
| Largest alignment | 53647 |
| NA50 | 18788 |
| NGA50 | 18788 |
| NA75 | 11480 |
| NGA75 | 11480 |
| LA50 | 23 |
| LGA50 | 23 |
| LA75 | 46 |
| LGA75 | 45 |

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 | 0 |
| # interspecies translocations | 1 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 25473 |
| # local misassemblies | 0 |
| # mismatches | 1236 |
| # indels | 6 |
| # short indels | 6 |
| # long indels | 0 |
| Indels length | 6 |

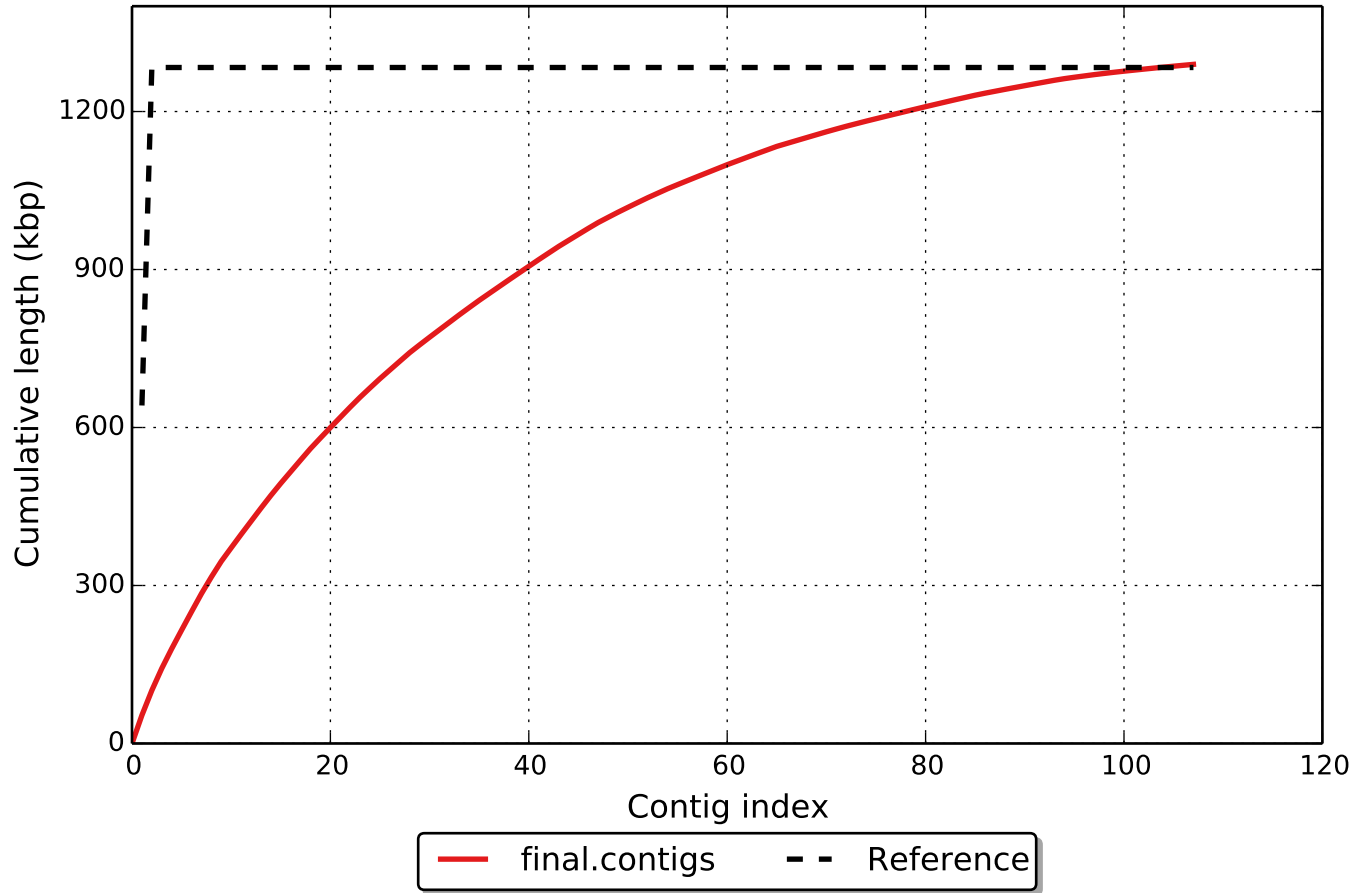
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

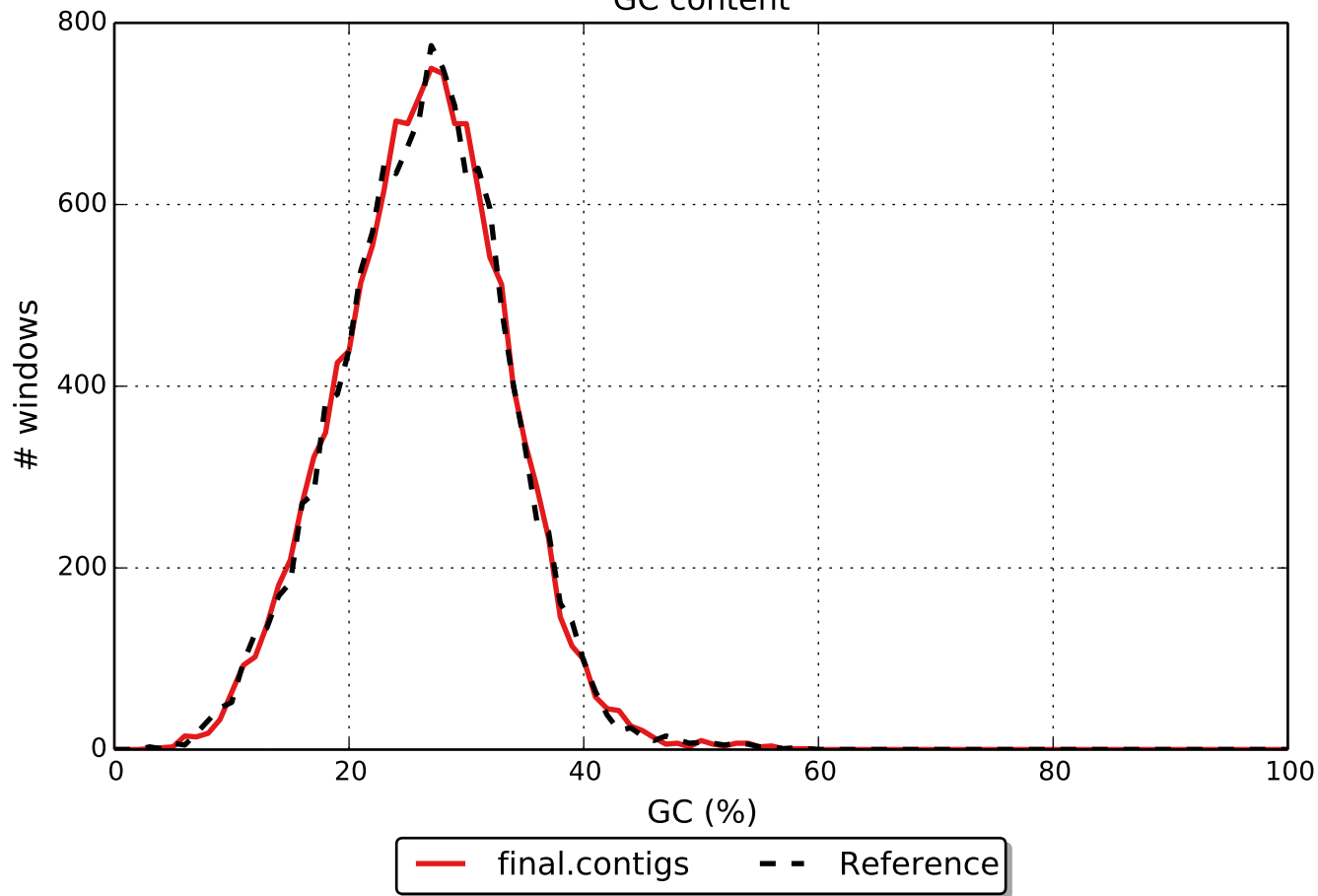
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

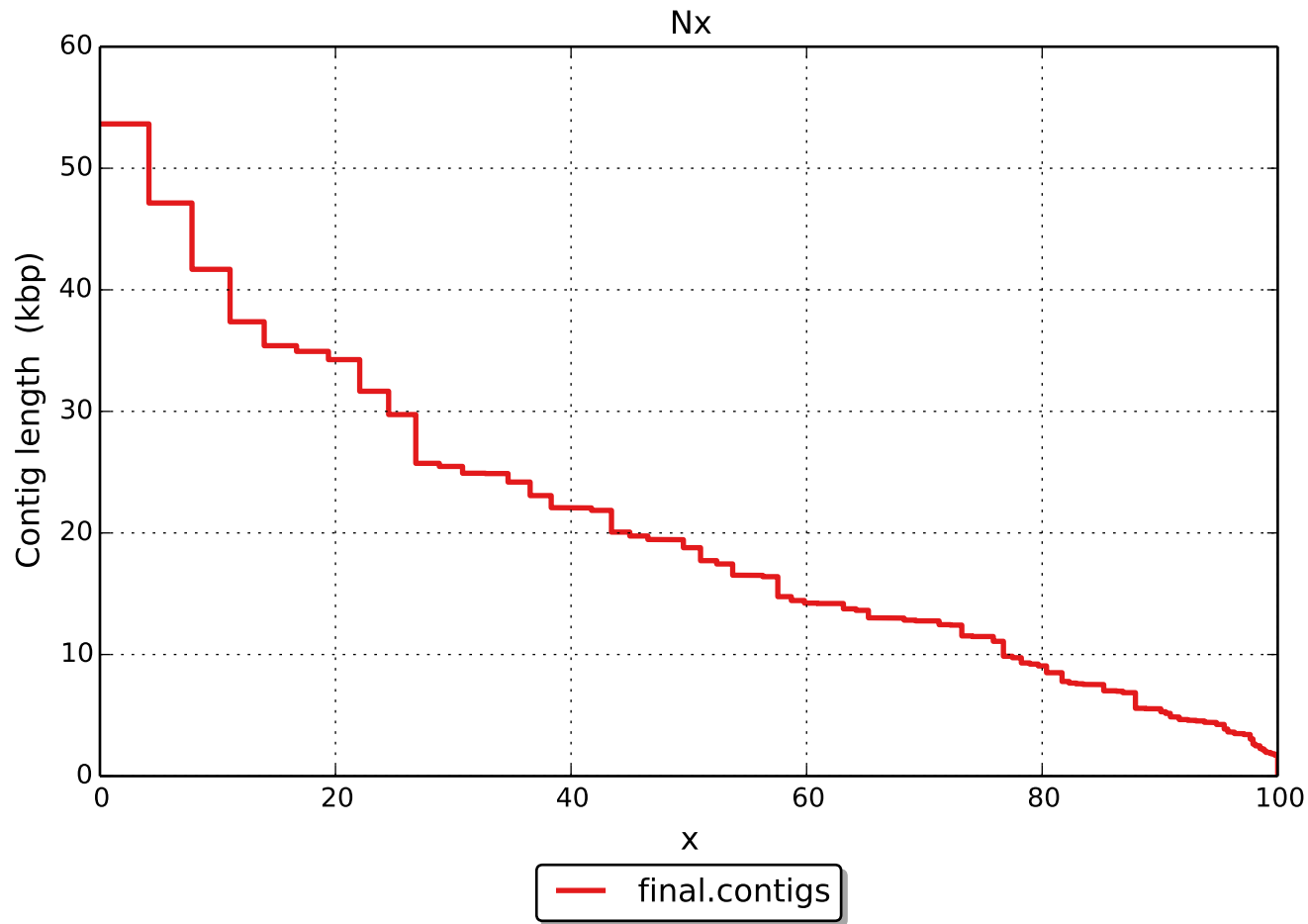
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

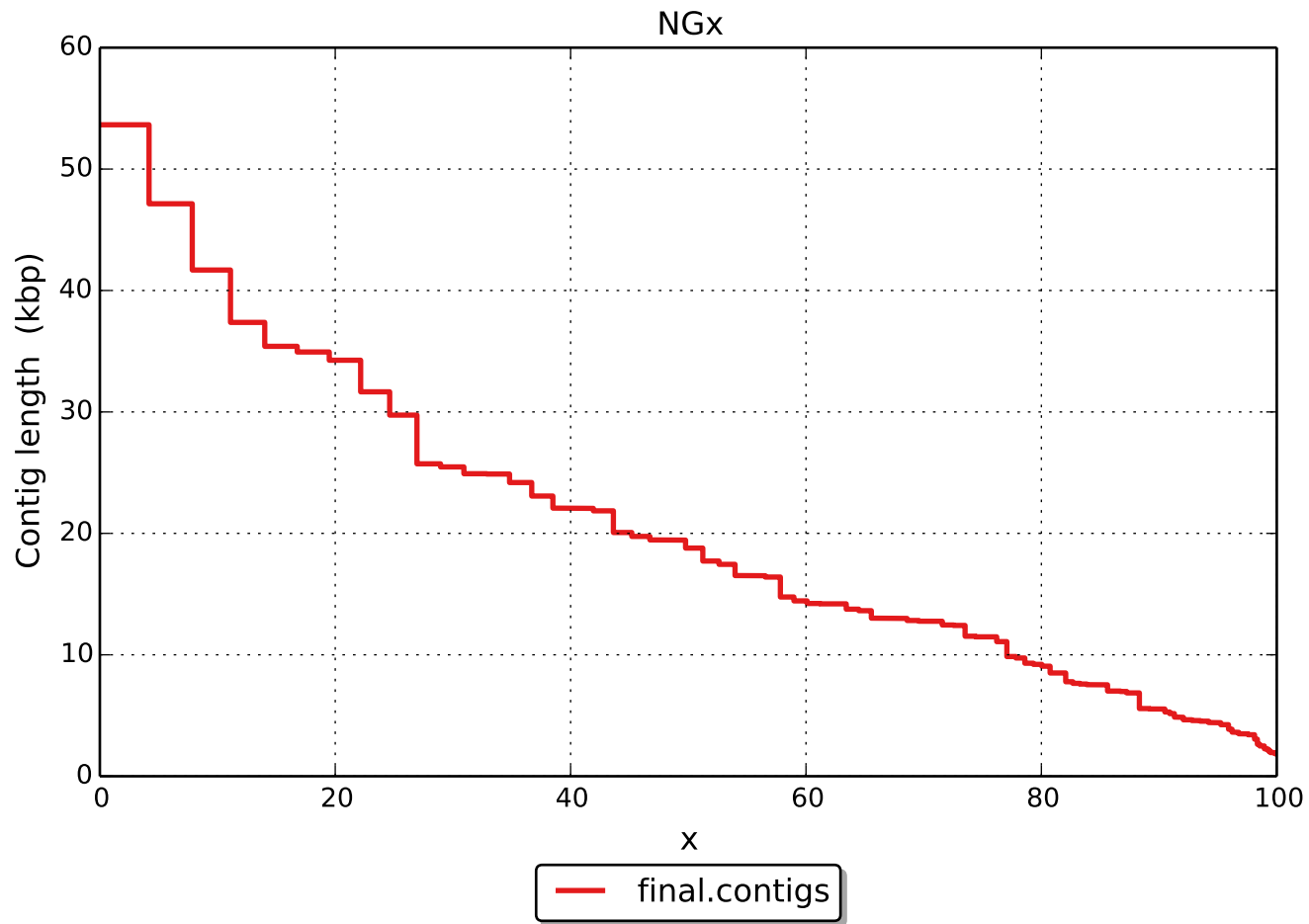
Cumulative length

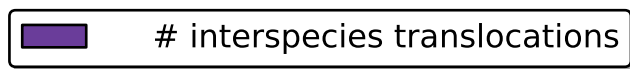
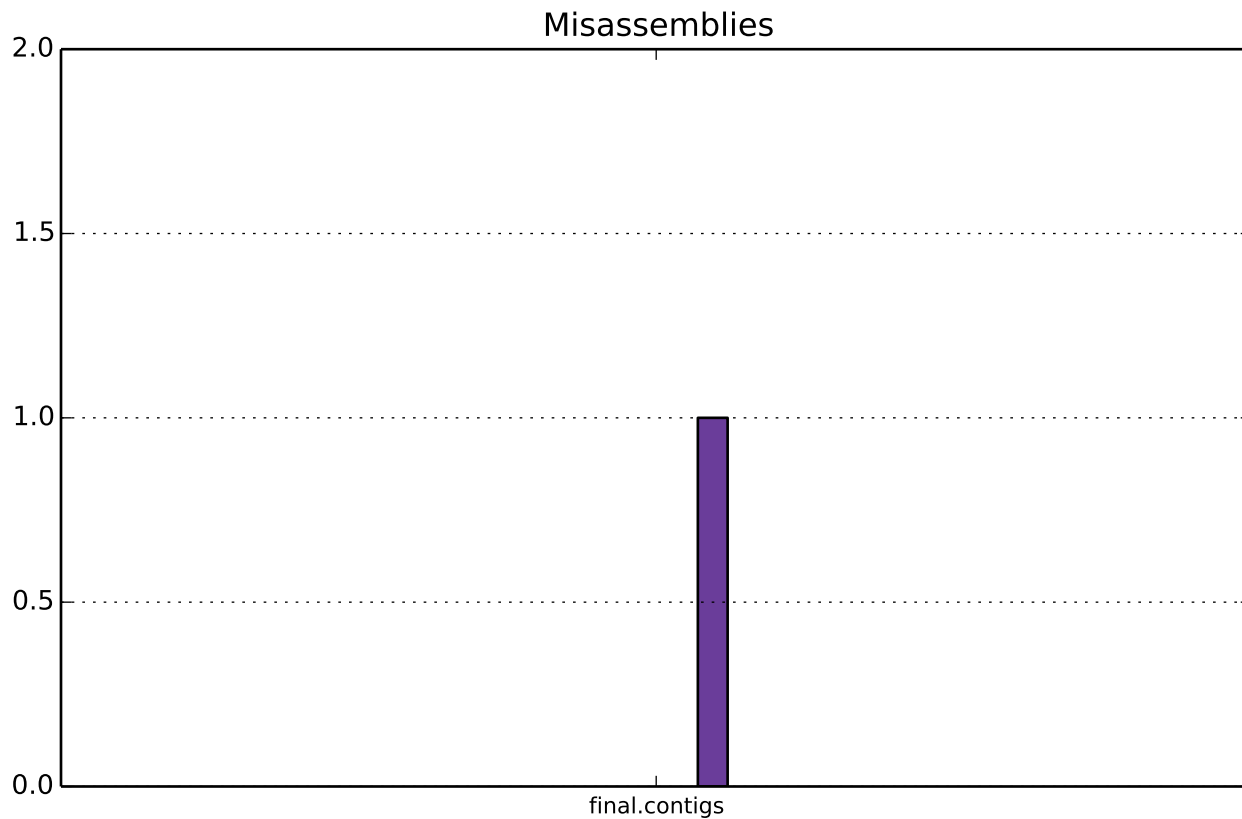


GC content

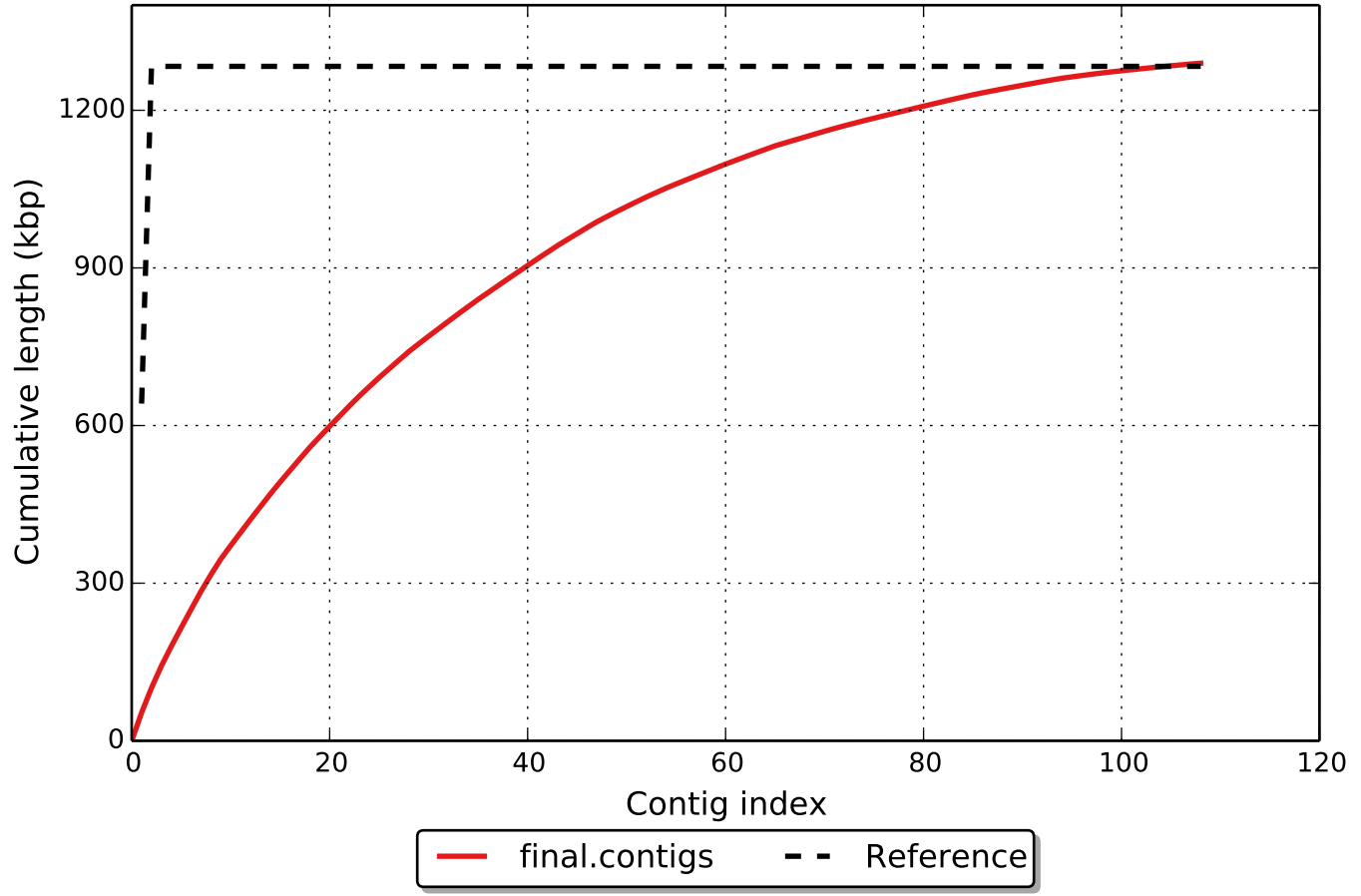


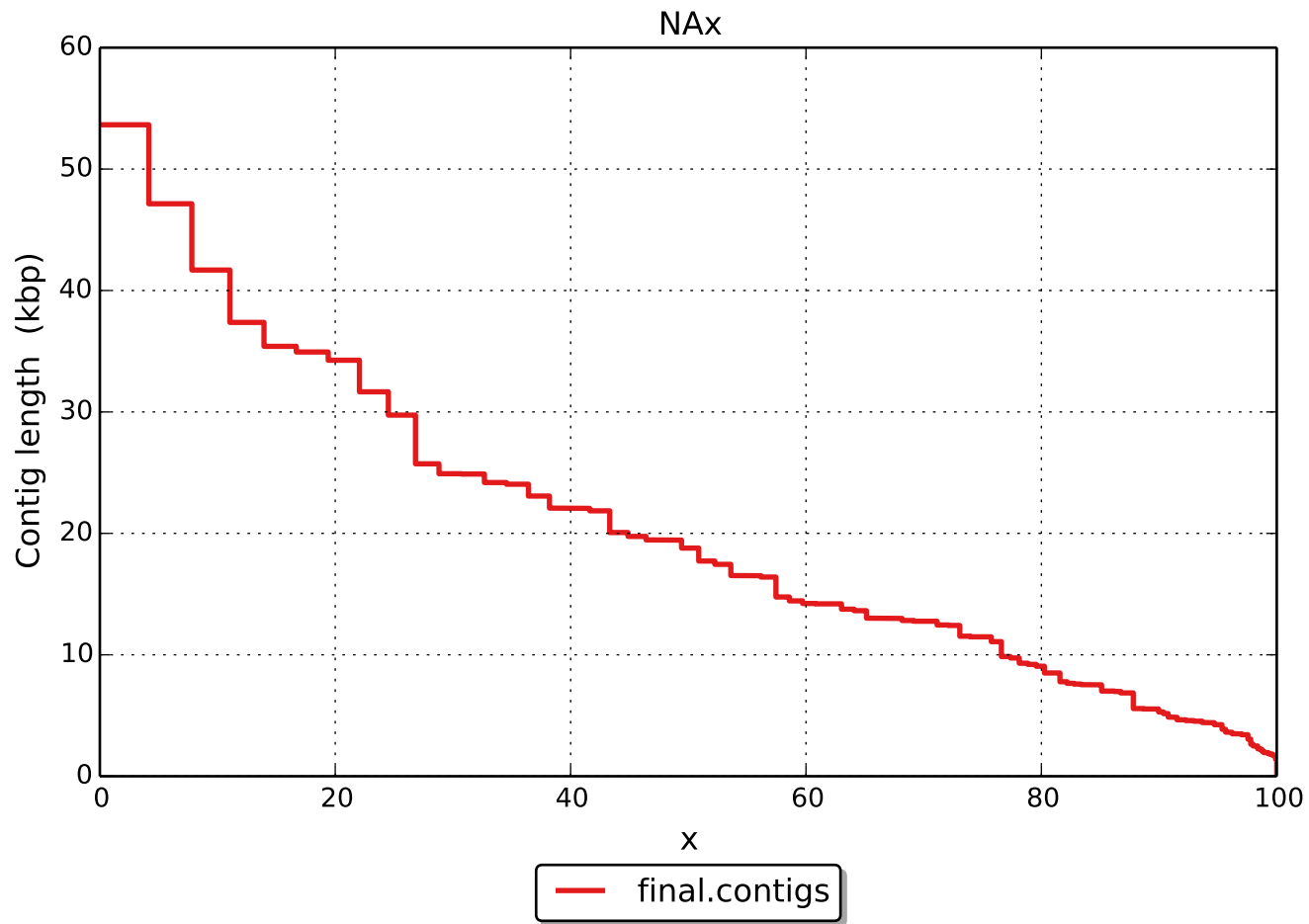






Cumulative length (aligned contigs)





NGAx

