

Report

| | contigs |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 544 |
| # contigs (≥ 1000 bp) | 136 |
| # contigs (≥ 5000 bp) | 99 |
| # contigs (≥ 10000 bp) | 80 |
| # contigs (≥ 25000 bp) | 57 |
| # contigs (≥ 50000 bp) | 33 |
| Total length (≥ 0 bp) | 4600775 |
| Total length (≥ 1000 bp) | 4554297 |
| Total length (≥ 5000 bp) | 4465913 |
| Total length (≥ 10000 bp) | 4319607 |
| Total length (≥ 25000 bp) | 3921952 |
| Total length (≥ 50000 bp) | 3043287 |
| # contigs | 148 |
| Largest contig | 204279 |
| Total length | 4562877 |
| Reference length | 4641652 |
| GC (%) | 50.75 |
| Reference GC (%) | 50.79 |
| N50 | 71453 |
| NG50 | 71453 |
| N75 | 39685 |
| NG75 | 38168 |
| L50 | 21 |
| LG50 | 21 |
| L75 | 42 |
| LG75 | 44 |
| # misassemblies | 3 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 29222 |
| # local misassemblies | 7 |
| # unaligned contigs | 0 + 1 part |
| Unaligned length | 35 |
| Genome fraction (%) | 98.150 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 20.81 |
| # indels per 100 kbp | 1.23 |
| Largest alignment | 204279 |
| NA50 | 71453 |
| NGA50 | 71453 |
| NA75 | 39685 |
| NGA75 | 38168 |
| LA50 | 21 |
| LGA50 | 21 |
| LA75 | 42 |
| LGA75 | 44 |

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

| | contigs |
|-----------------------------|---------|
| # misassemblies | 3 |
| # relocations | 3 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 29222 |
| # local misassemblies | 7 |
| # mismatches | 948 |
| # indels | 56 |
| # short indels | 56 |
| # long indels | 0 |
| Indels length | 70 |

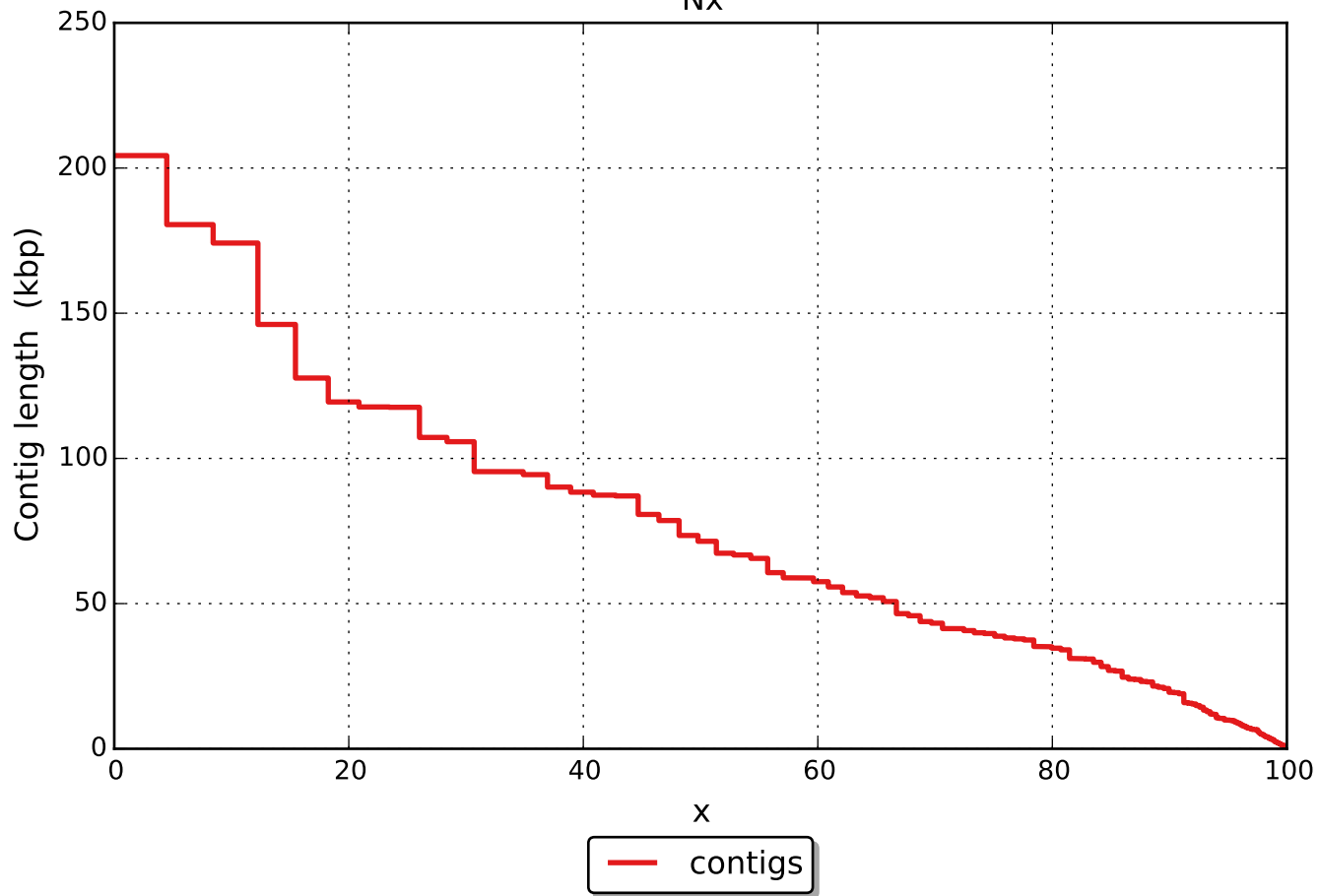
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

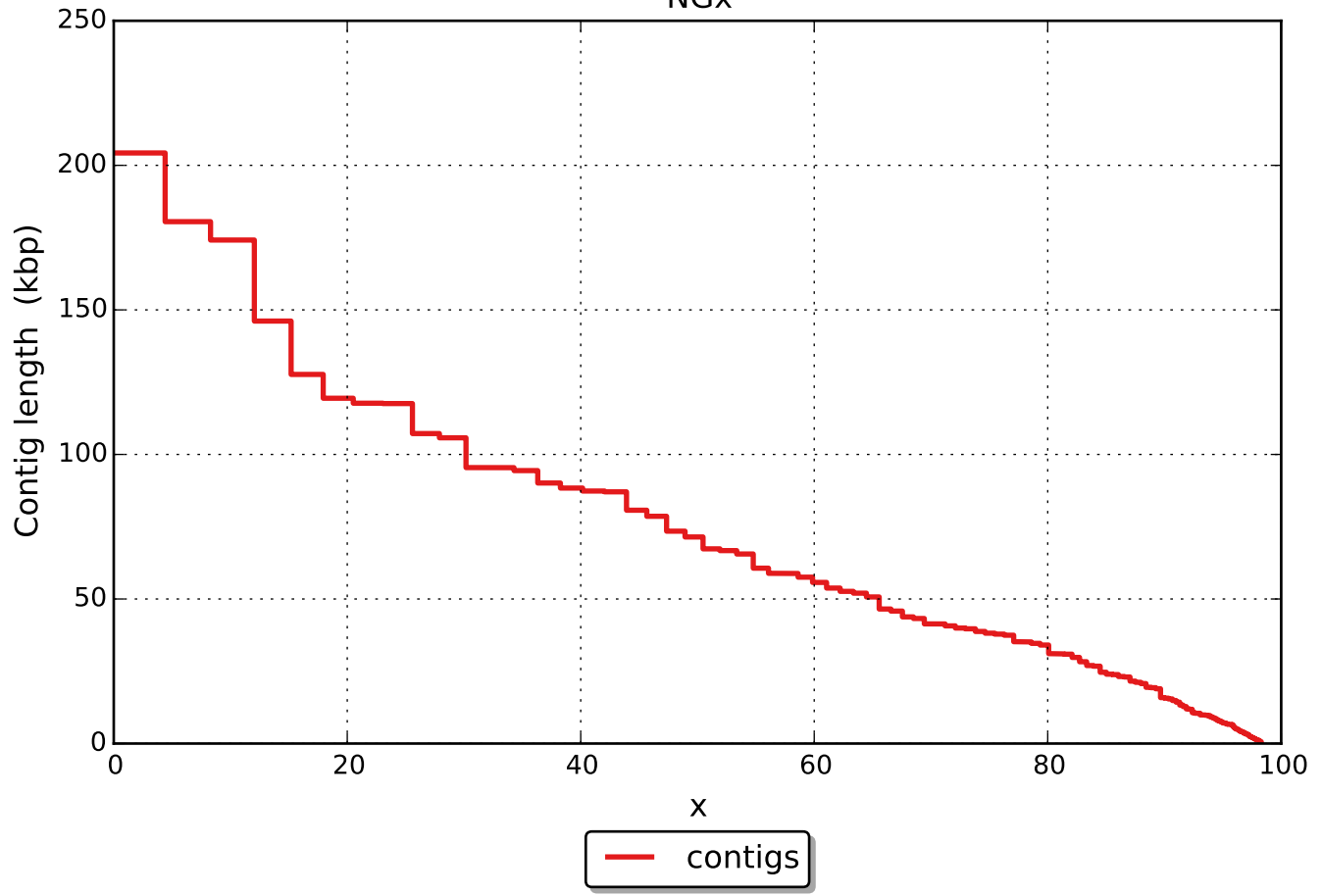
| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 35 |
| # N's | 0 |

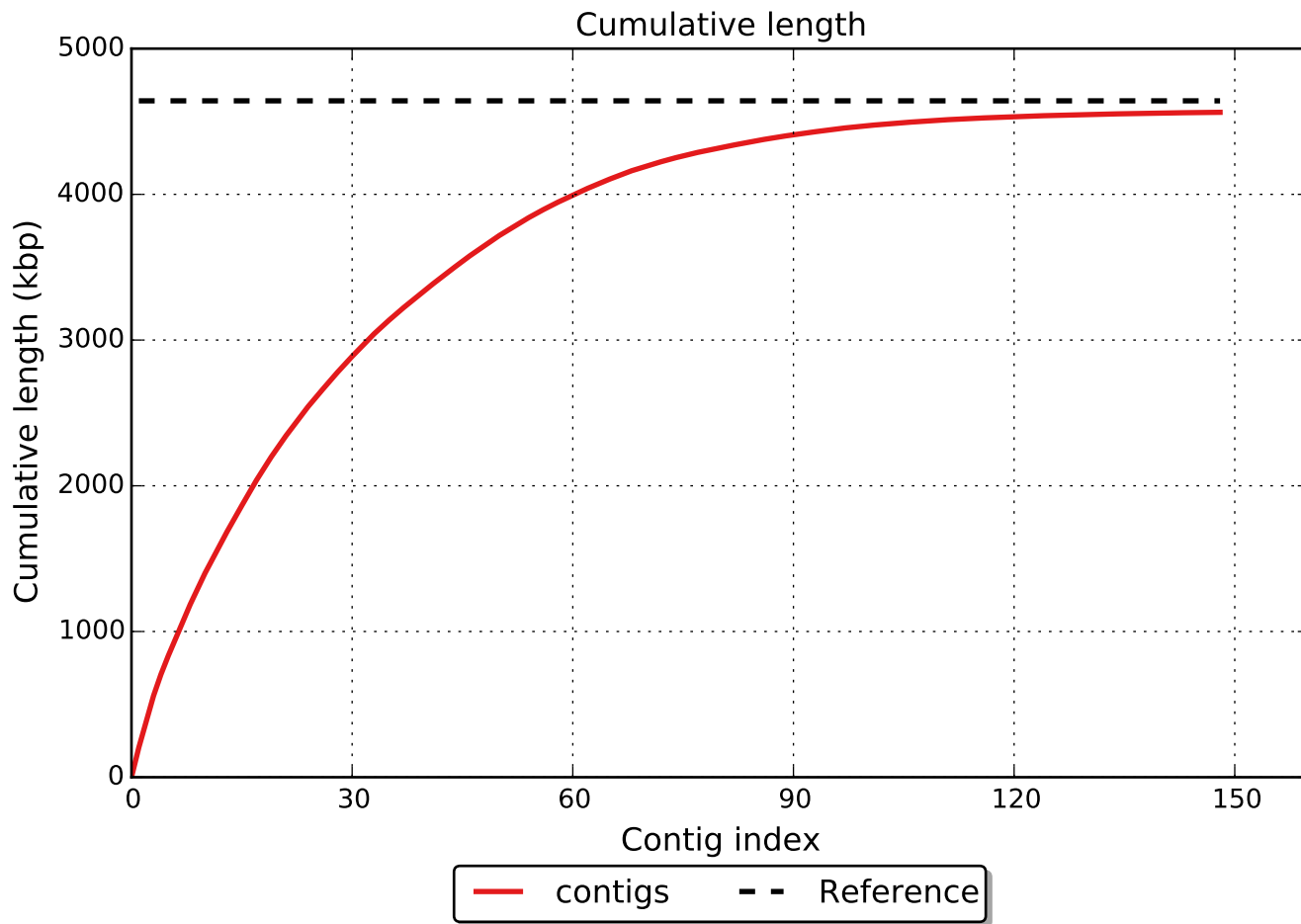
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

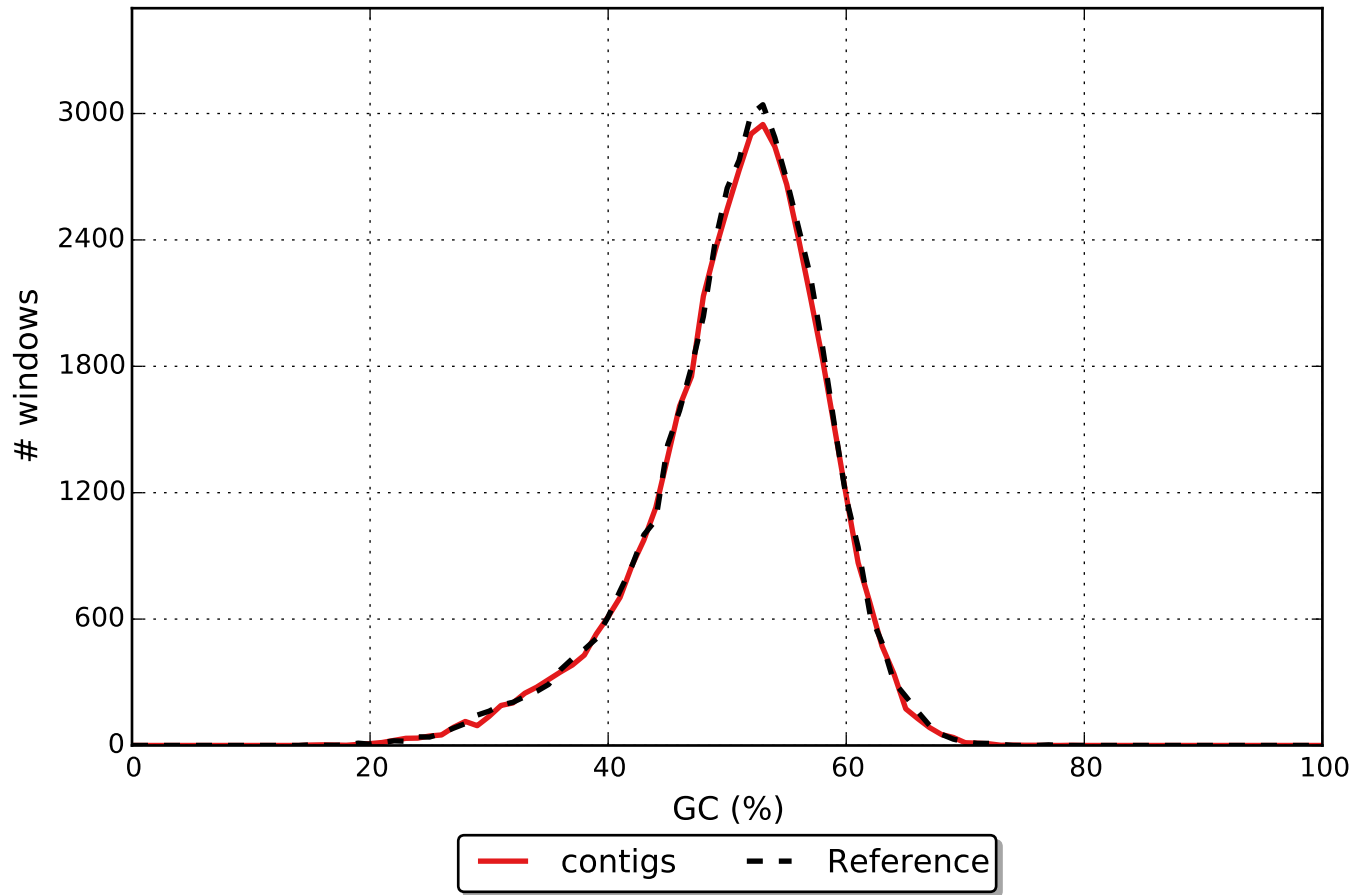


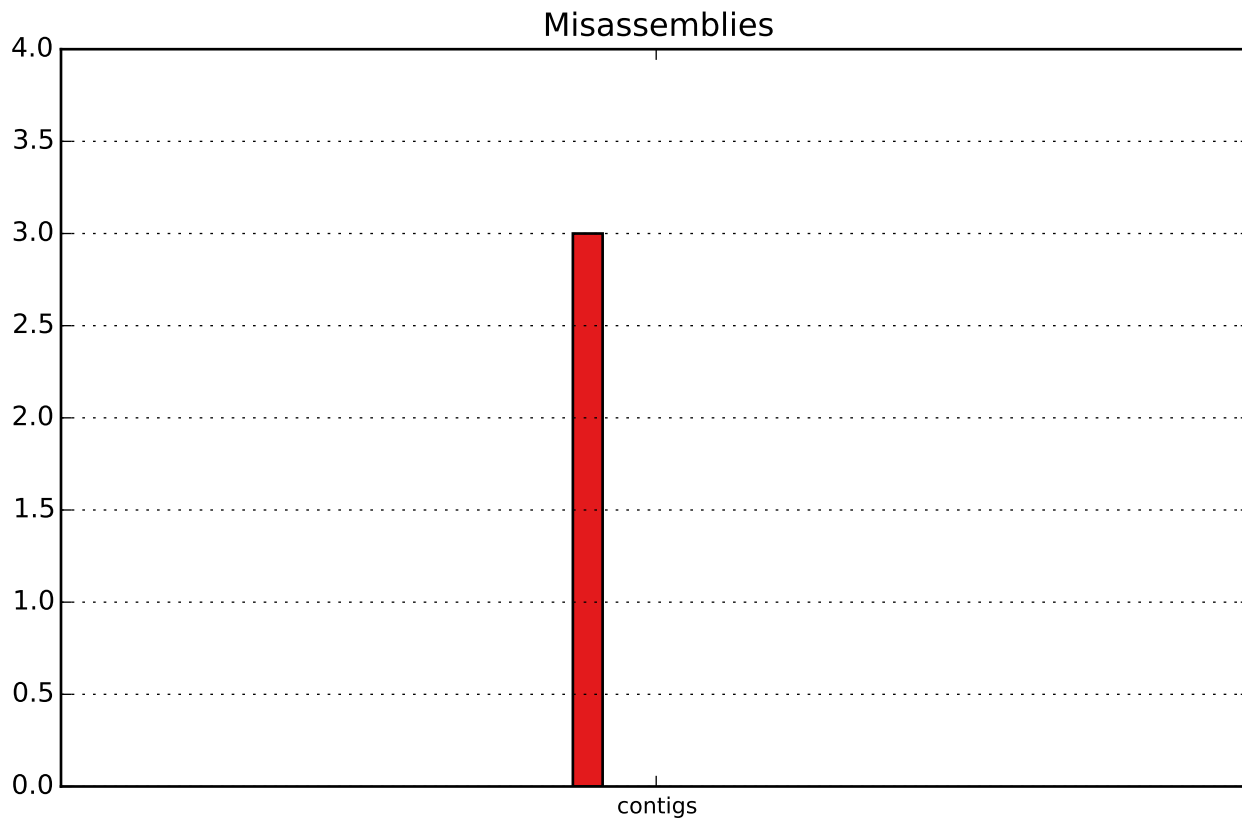
NGx



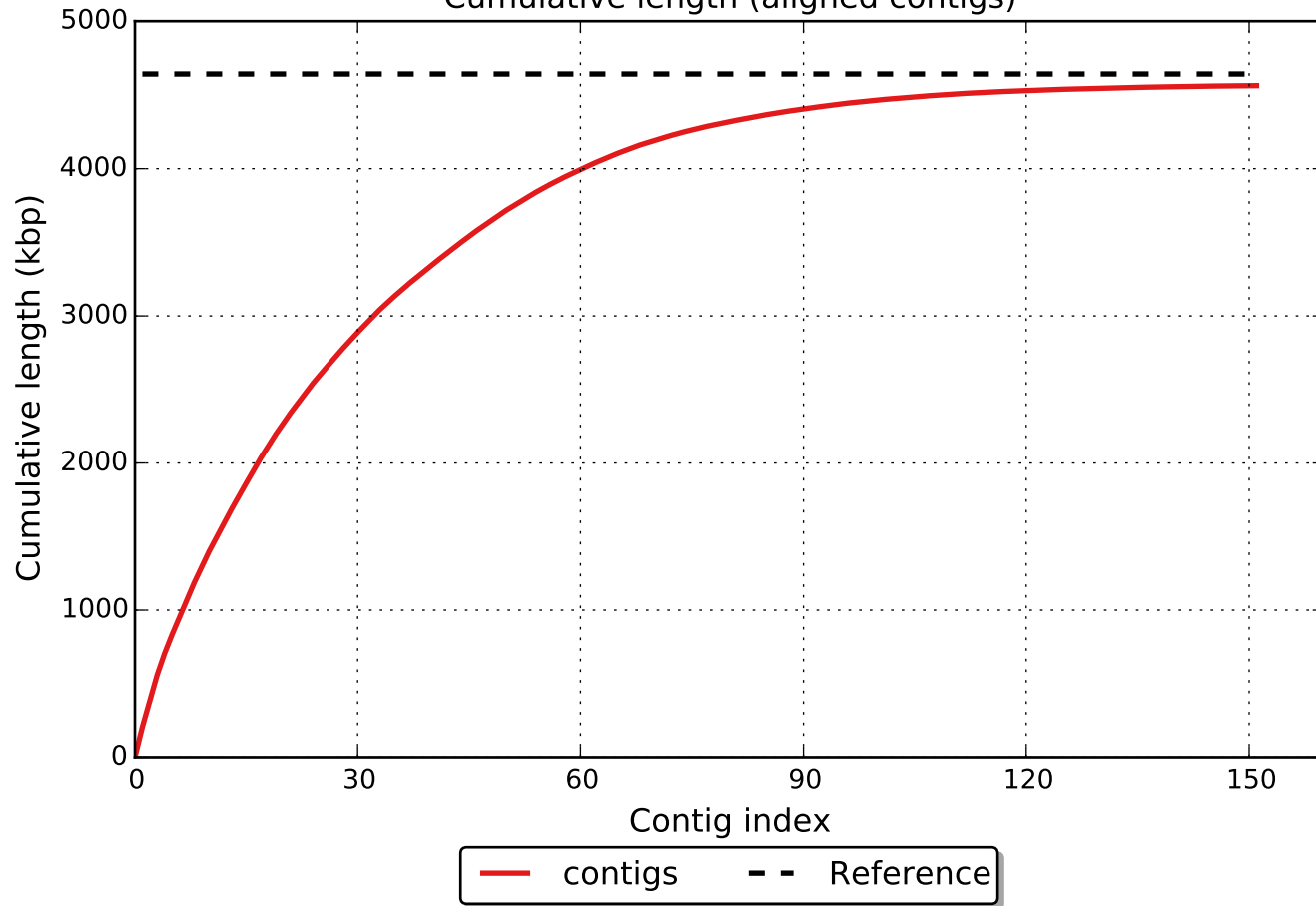


GC content

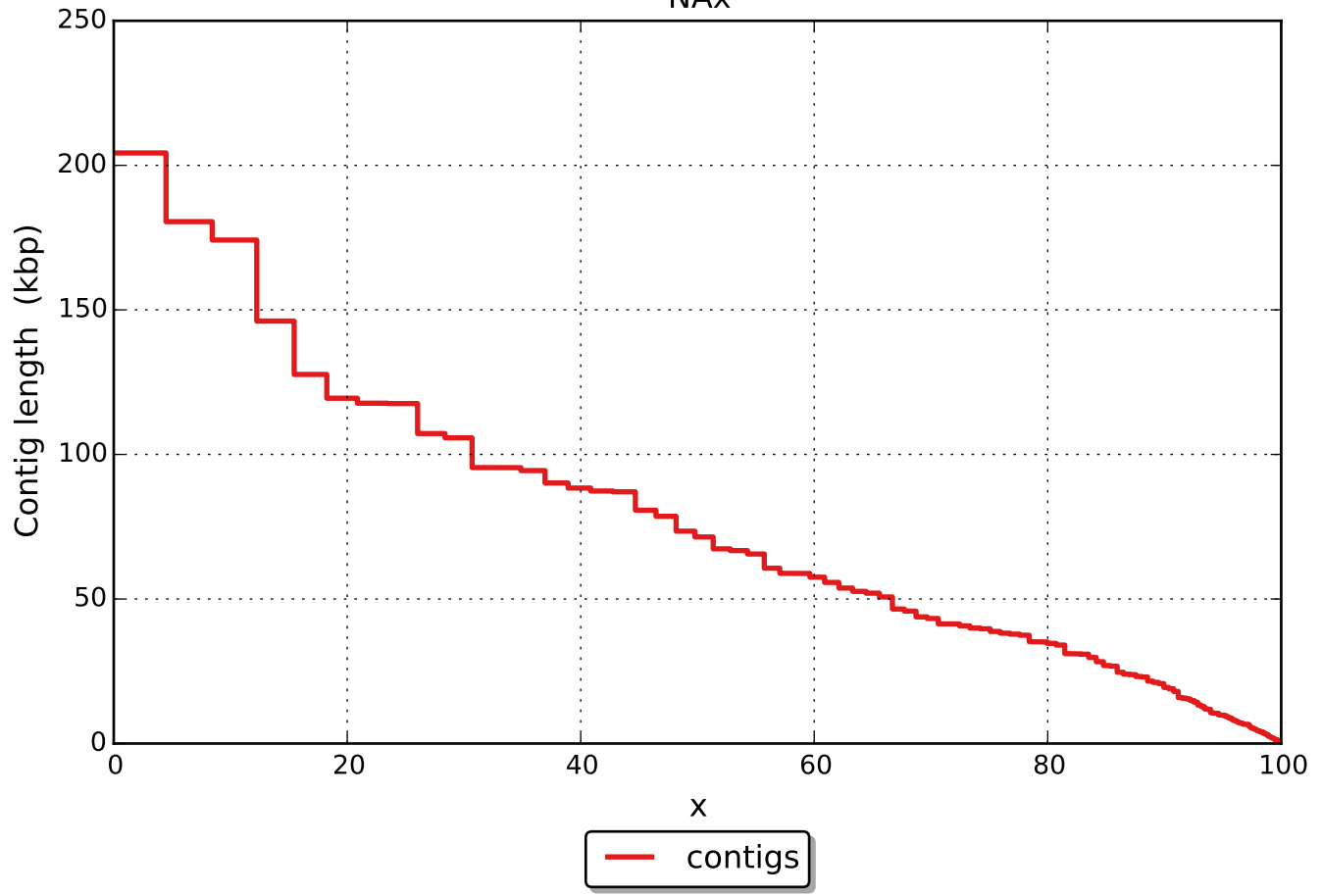




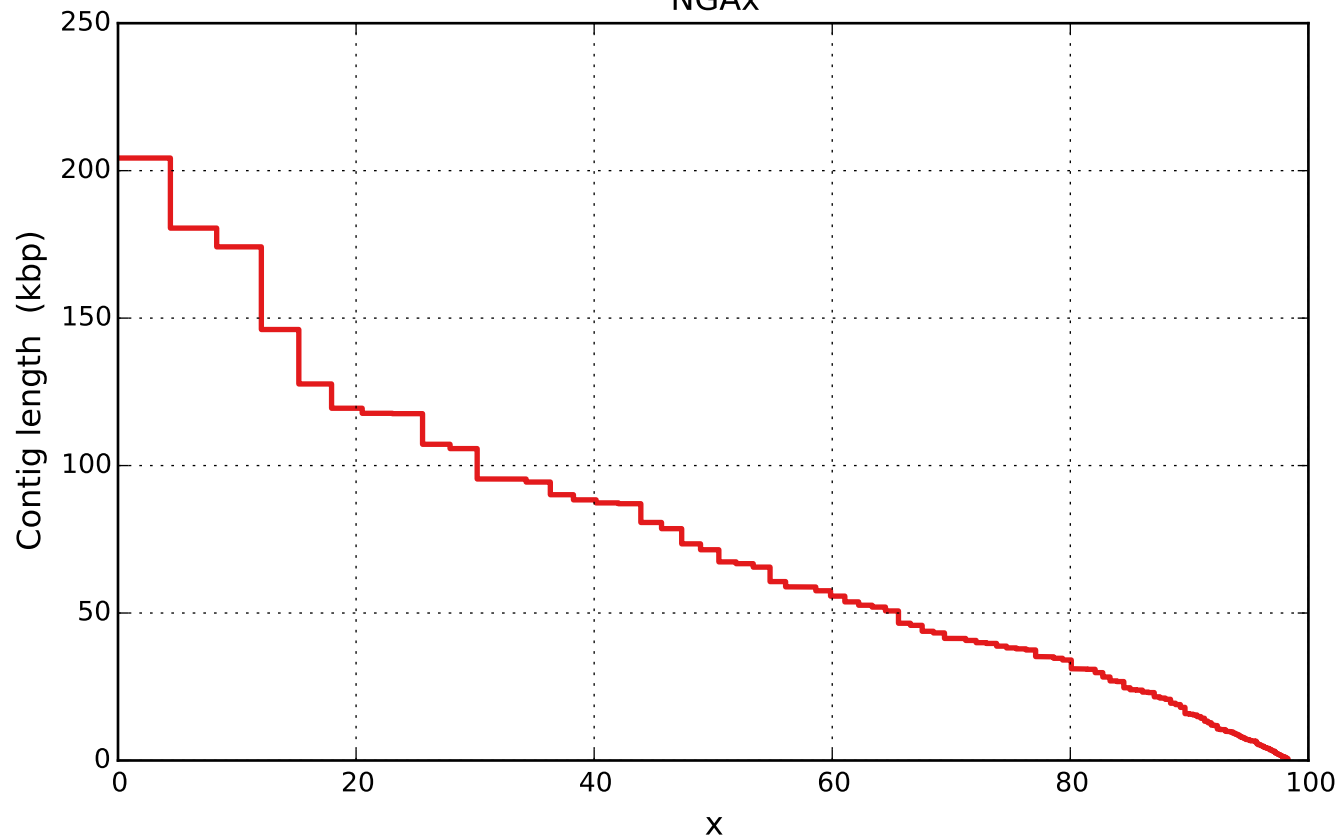
Cumulative length (aligned contigs)



NAx



NGAx



contigs