

Report

| | contigs |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 4125 |
| # contigs (≥ 1000 bp) | 1581 |
| # contigs (≥ 5000 bp) | 15 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 0 bp) | 4254659 |
| Total length (≥ 1000 bp) | 2852440 |
| Total length (≥ 5000 bp) | 91563 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 2927 |
| Largest contig | 9678 |
| Total length | 3829739 |
| Reference length | 4641652 |
| GC (%) | 50.74 |
| Reference GC (%) | 50.79 |
| N50 | 1513 |
| NG50 | 1283 |
| N75 | 991 |
| NG75 | 682 |
| L50 | 818 |
| LG50 | 1109 |
| L75 | 1601 |
| LG75 | 2336 |
| # misassemblies | 28 |
| # misassembled contigs | 27 |
| Misassembled contigs length | 87605 |
| # local misassemblies | 9 |
| # unaligned contigs | 0 + 7 part |
| Unaligned length | 3000 |
| Genome fraction (%) | 81.862 |
| Duplication ratio | 1.007 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 906.16 |
| # indels per 100 kbp | 1.32 |
| Largest alignment | 9678 |
| NA50 | 1499 |
| NGA50 | 1271 |
| NA75 | 984 |
| NGA75 | 674 |
| LA50 | 833 |
| LGA50 | 1127 |
| LA75 | 1623 |
| LGA75 | 2364 |

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 | 28 |
| # relocations | 28 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 27 |
| Misassembled contigs length | 87605 |
| # local misassemblies | 9 |
| # mismatches | 34432 |
| # indels | 50 |
| # short indels | 48 |
| # long indels | 2 |
| Indels length | 145 |

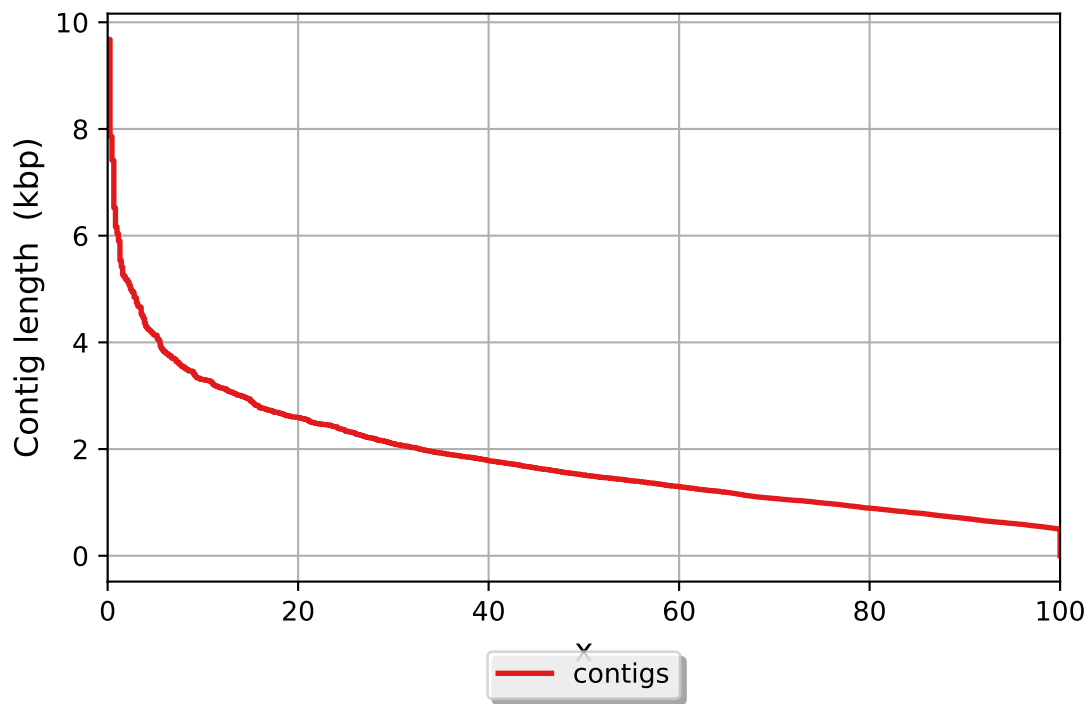
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

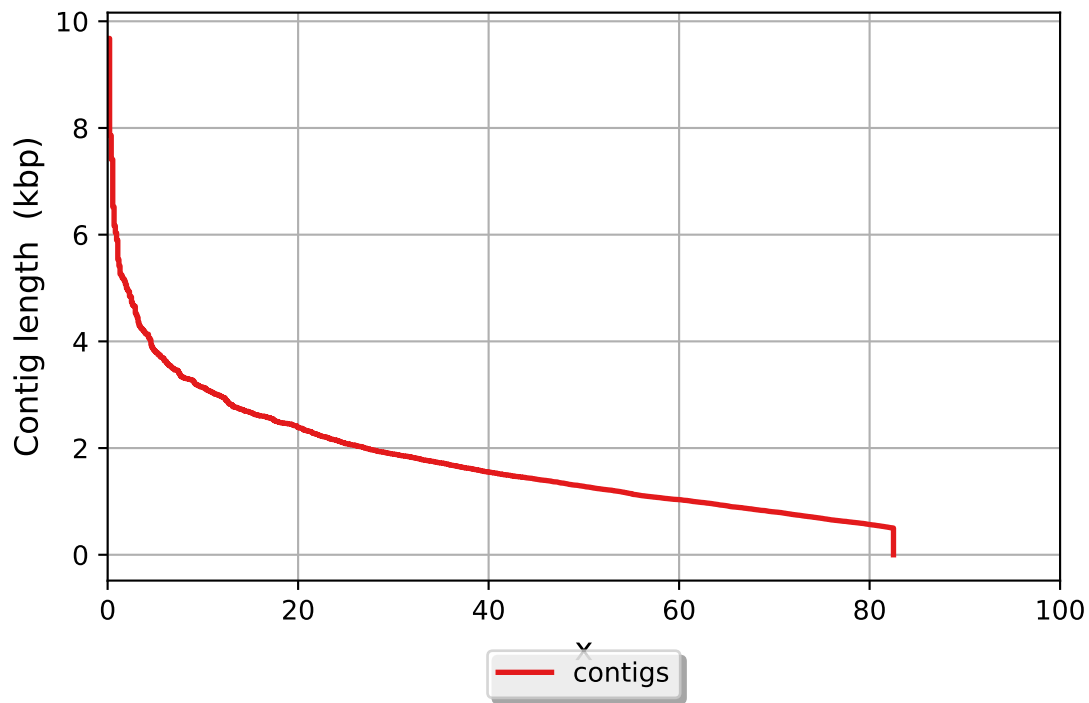
| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 7 |
| # with misassembly | 0 |
| # both parts are significant | 1 |
| Partially unaligned length | 3000 |
| # N's | 0 |

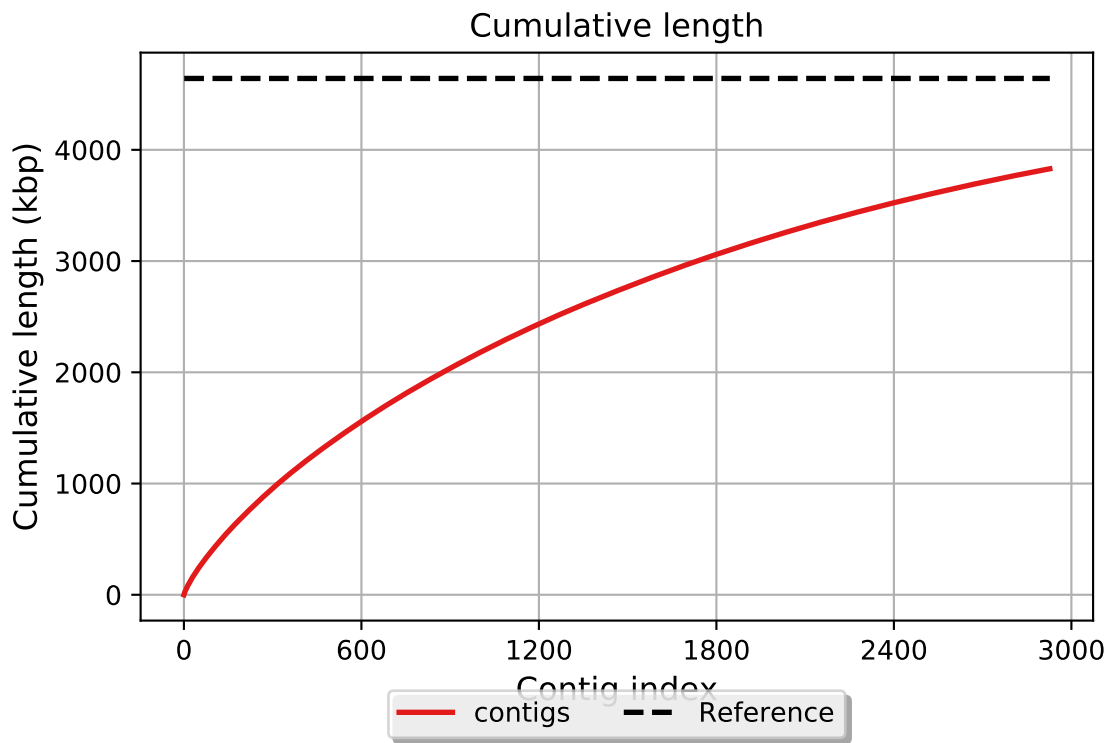
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

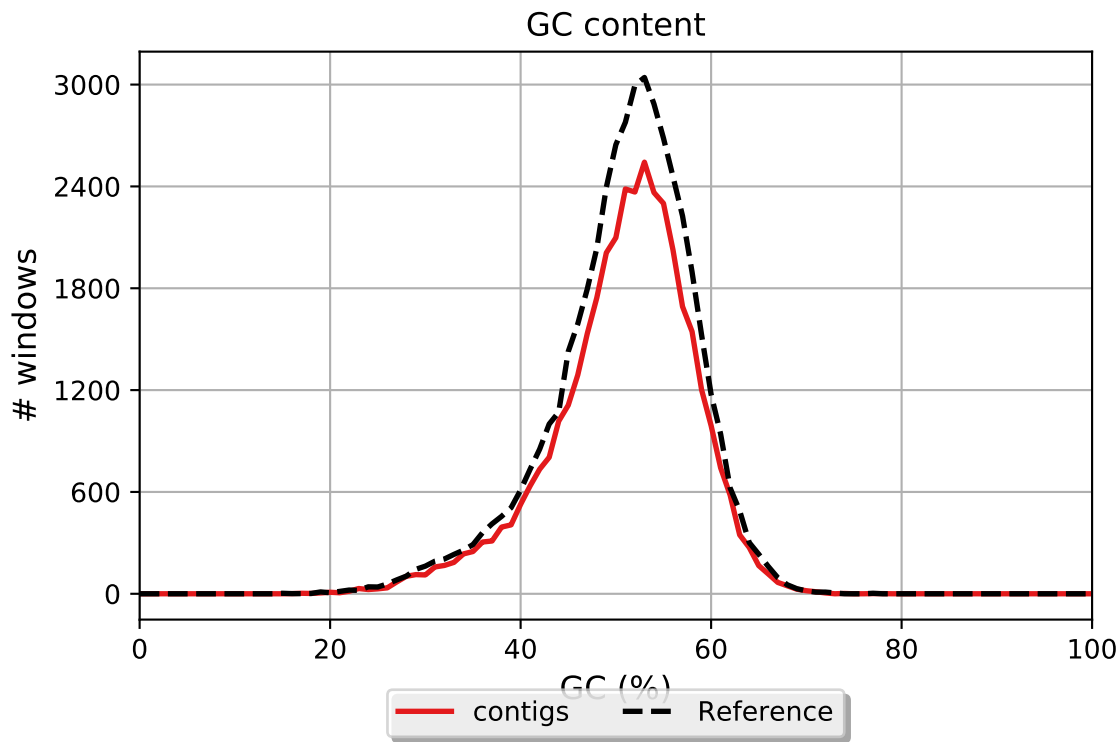
Nx



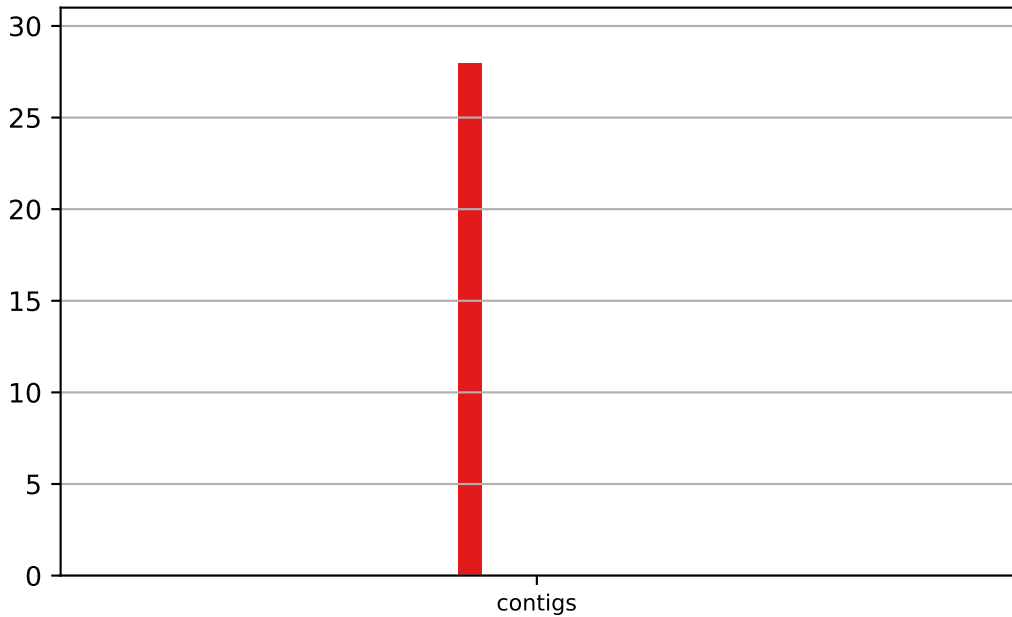
NGx



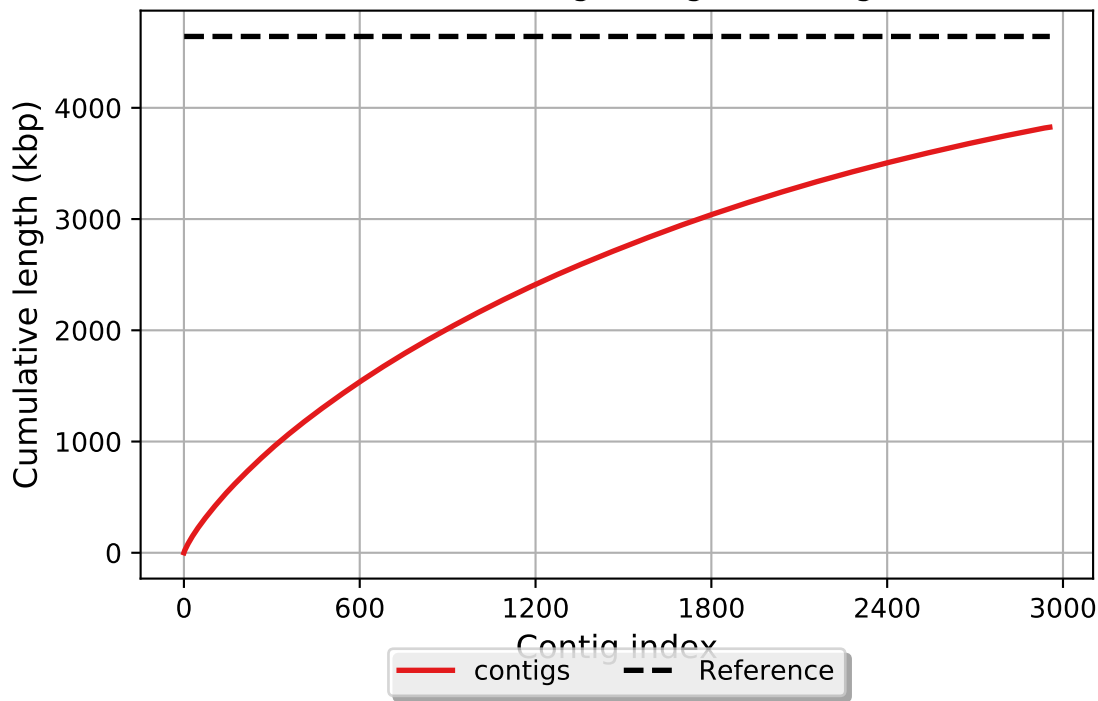




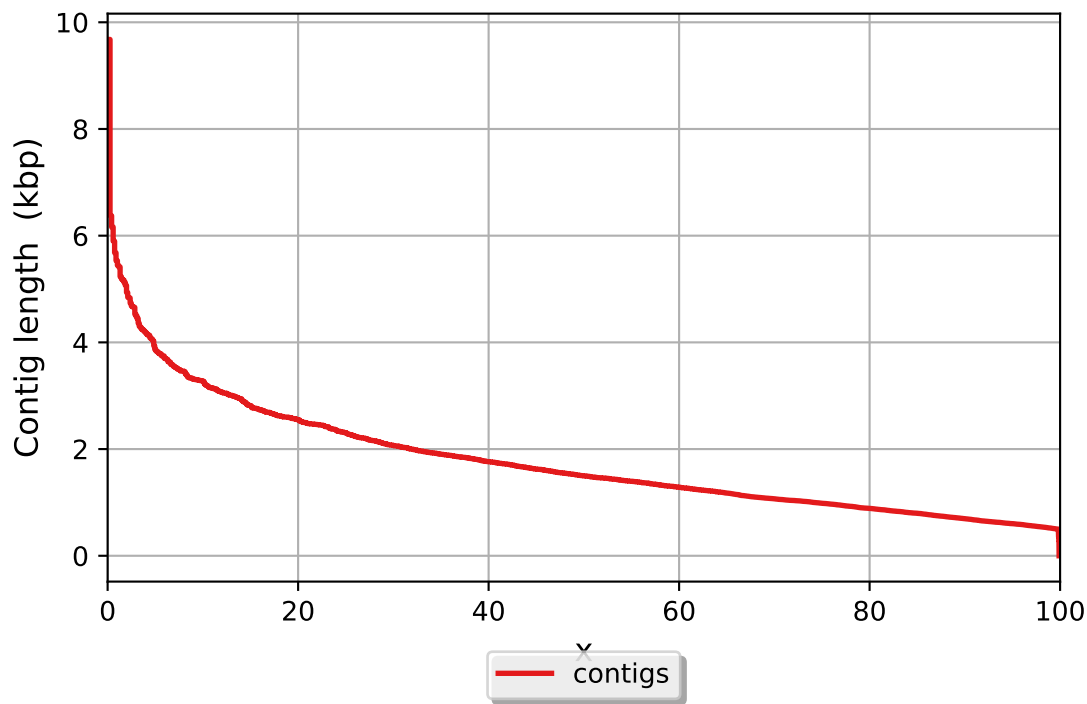
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

