

Report

| | contigs |
|---------------------------------|-------------|
| # contigs (≥ 0 bp) | 5809 |
| # contigs (≥ 1000 bp) | 422 |
| # contigs (≥ 5000 bp) | 2 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 0 bp) | 2987922 |
| Total length (≥ 1000 bp) | 567635 |
| Total length (≥ 5000 bp) | 14065 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 2202 |
| Largest contig | 8377 |
| Total length | 1791283 |
| Reference length | 4641652 |
| GC (%) | 50.67 |
| Reference GC (%) | 50.79 |
| N50 | 818 |
| N75 | 638 |
| L50 | 788 |
| L75 | 1408 |
| # misassemblies | 36 |
| # misassembled contigs | 34 |
| Misassembled contigs length | 54763 |
| # local misassemblies | 2 |
| # unaligned contigs | 2 + 31 part |
| Unaligned length | 7801 |
| Genome fraction (%) | 38.316 |
| Duplication ratio | 1.003 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1331.37 |
| # indels per 100 kbp | 3.20 |
| Largest alignment | 6837 |
| NA50 | 806 |
| NGA50 | - |
| NA75 | 629 |
| LA50 | 806 |
| LA75 | 1436 |

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 | 36 |
| # relocations | 36 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 34 |
| Misassembled contigs length | 54763 |
| # local misassemblies | 2 |
| # mismatches | 23678 |
| # indels | 57 |
| # short indels | 56 |
| # long indels | 1 |
| Indels length | 74 |

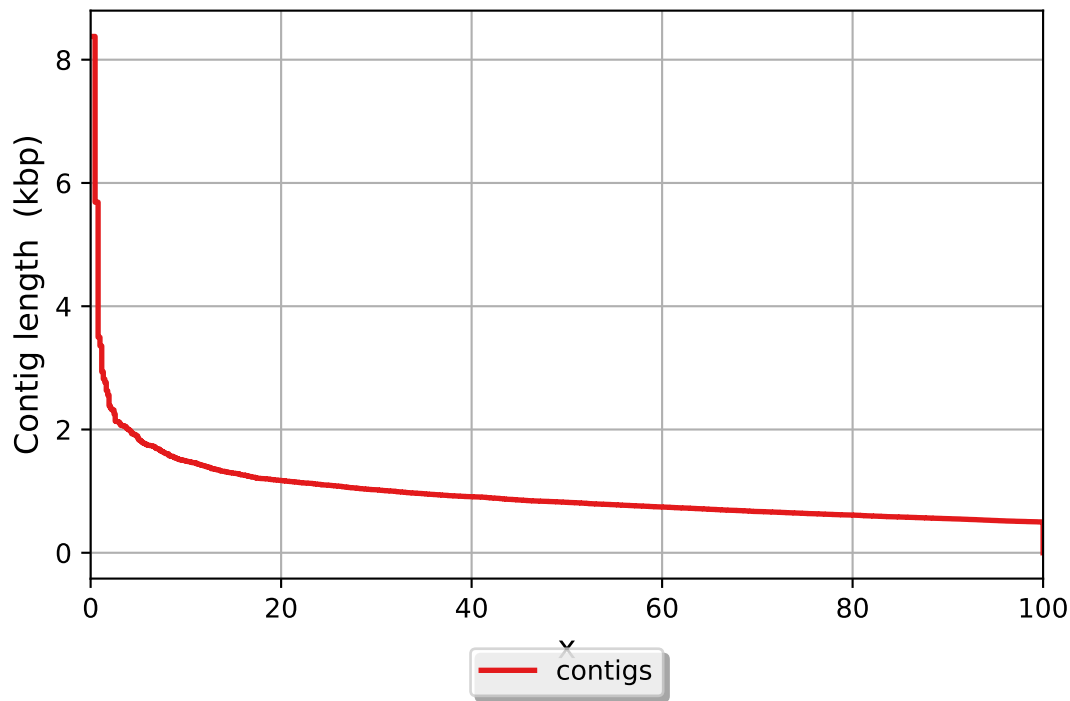
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

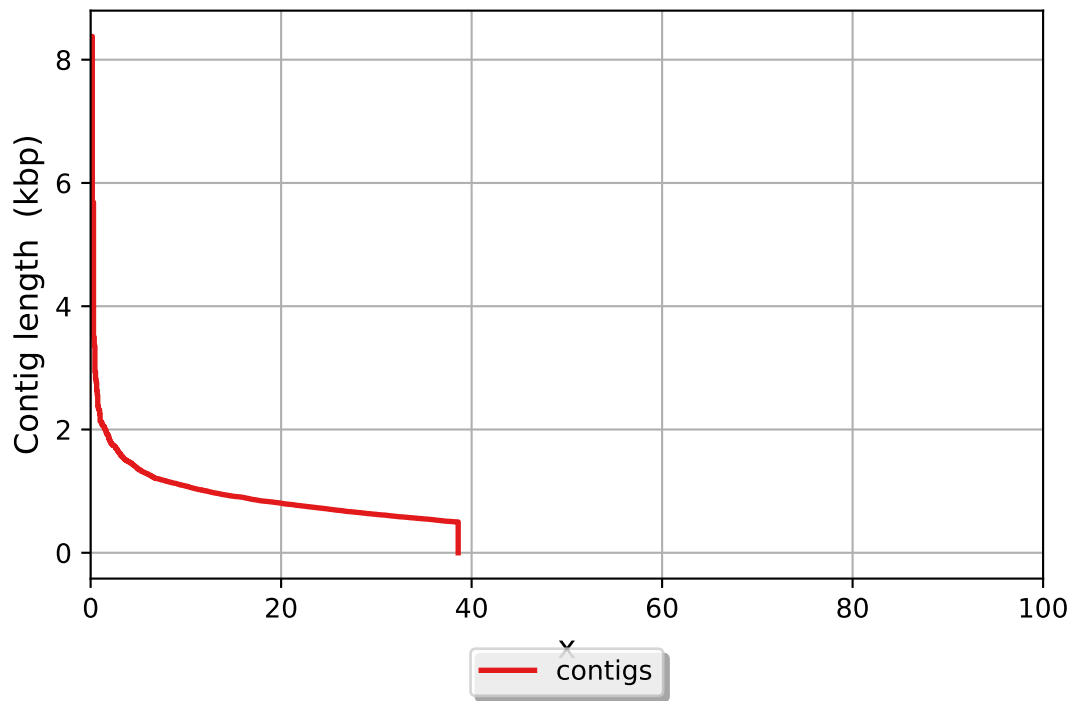
| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 2 |
| Fully unaligned length | 4448 |
| # partially unaligned contigs | 31 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 3353 |
| # N's | 0 |

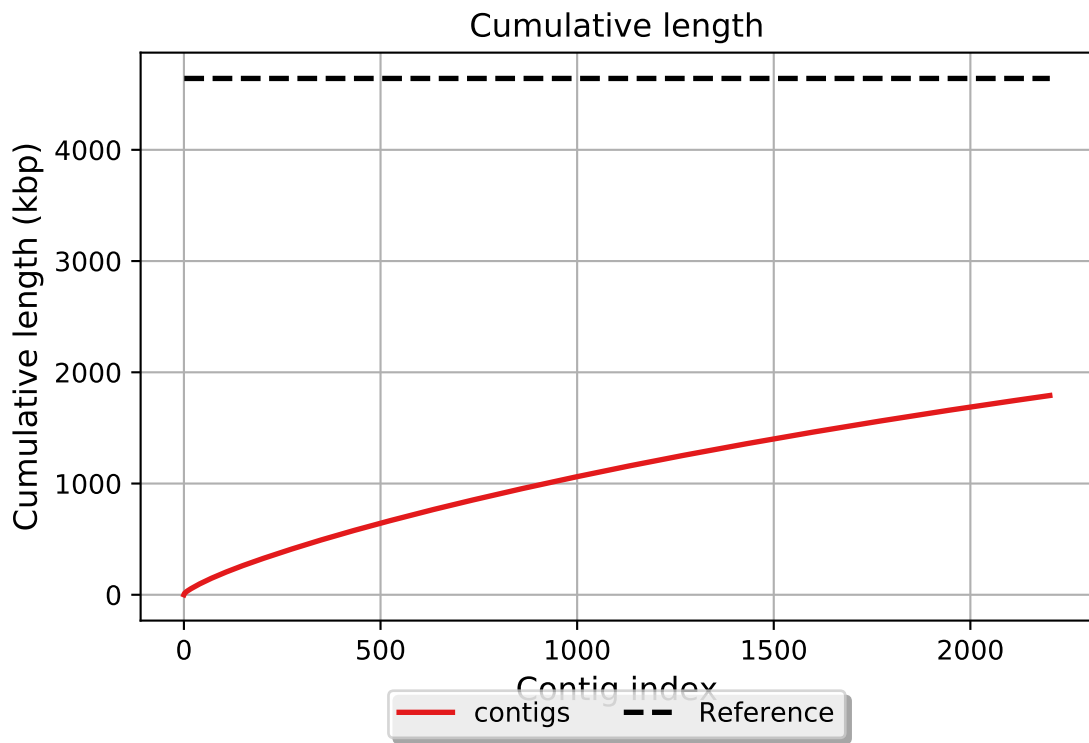
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

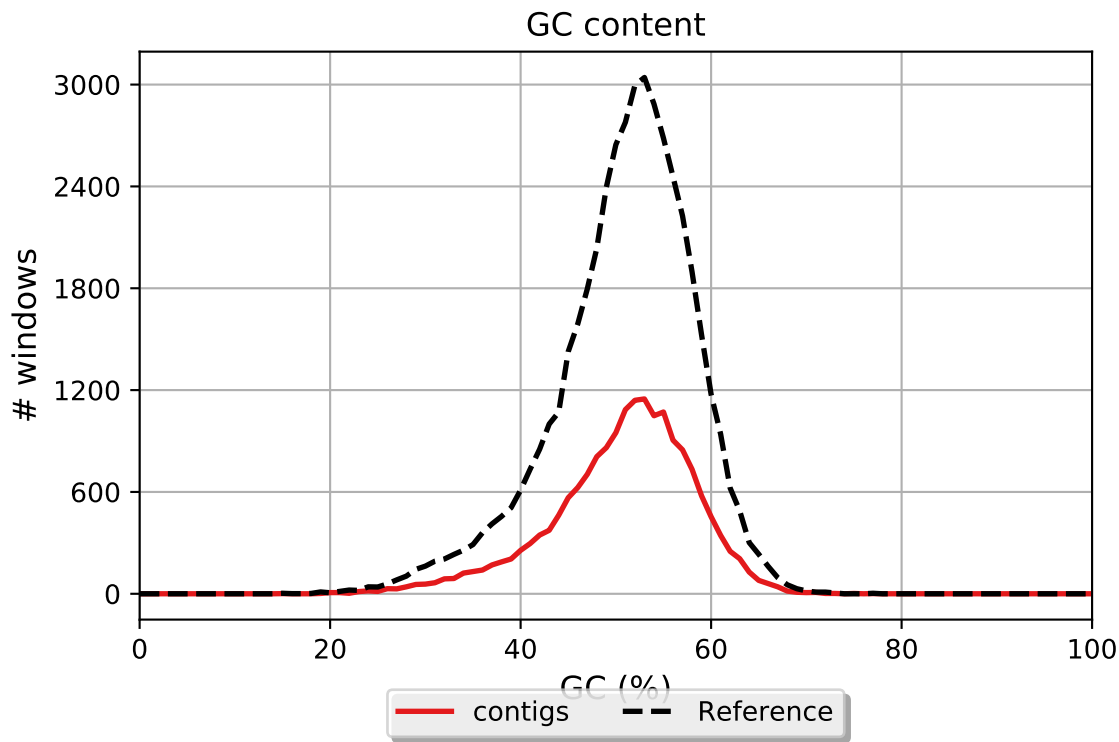
Nx



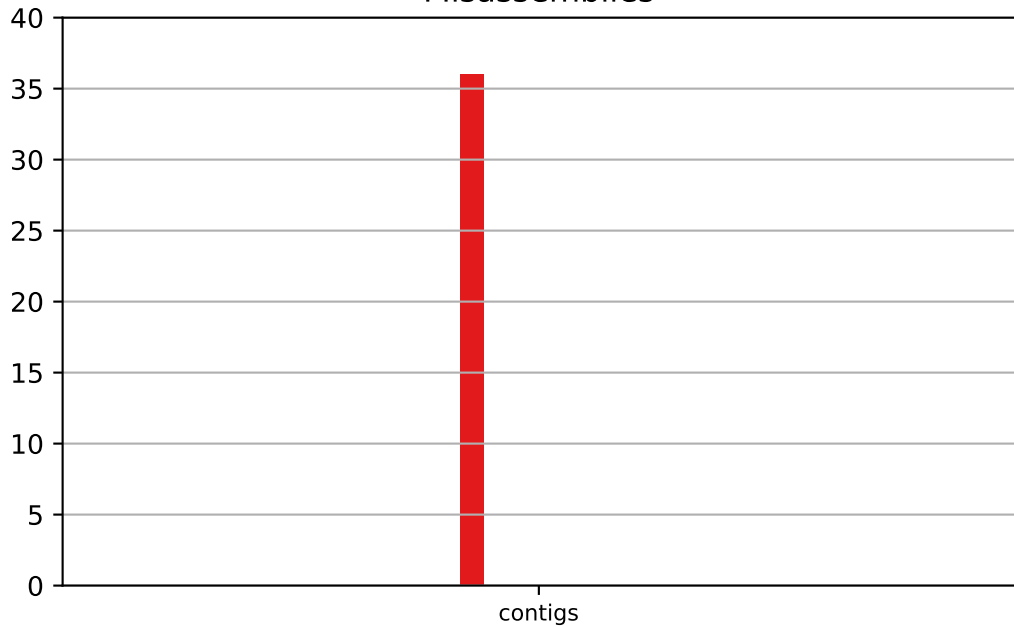
NGx



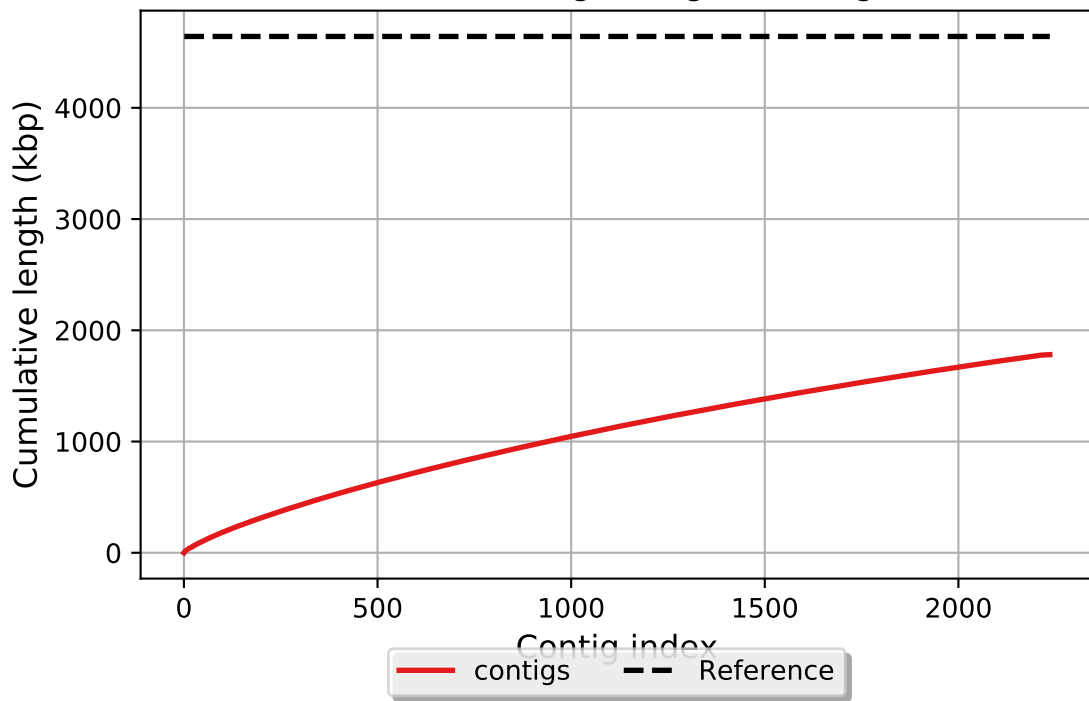




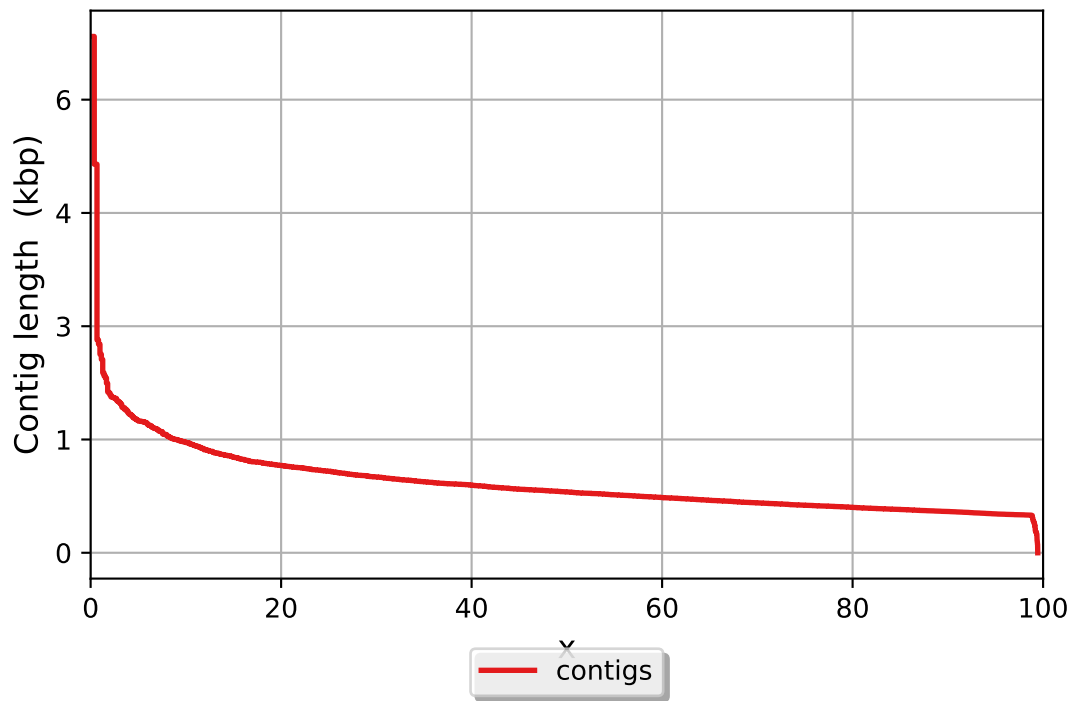
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

