

Report

| | contigs |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 388 |
| # contigs (≥ 1000 bp) | 117 |
| # contigs (≥ 5000 bp) | 90 |
| # contigs (≥ 10000 bp) | 77 |
| # contigs (≥ 25000 bp) | 59 |
| # contigs (≥ 50000 bp) | 32 |
| Total length (≥ 0 bp) | 4592989 |
| Total length (≥ 1000 bp) | 4542438 |
| Total length (≥ 5000 bp) | 4479944 |
| Total length (≥ 10000 bp) | 4377299 |
| Total length (≥ 25000 bp) | 4094951 |
| Total length (≥ 50000 bp) | 3095598 |
| # contigs | 129 |
| Largest contig | 269647 |
| Total length | 4551504 |
| Reference length | 4641652 |
| GC (%) | 50.74 |
| Reference GC (%) | 50.79 |
| N50 | 66919 |
| NG50 | 66389 |
| N75 | 42988 |
| NG75 | 41323 |
| L50 | 19 |
| LG50 | 20 |
| L75 | 39 |
| LG75 | 41 |
| # misassemblies | 2 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 54189 |
| # local misassemblies | 1 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 97.997 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 12.00 |
| # indels per 100 kbp | 0.33 |
| Largest alignment | 269647 |
| NA50 | 66919 |
| NGA50 | 66389 |
| NA75 | 41690 |
| NGA75 | 41323 |
| LA50 | 19 |
| LGA50 | 20 |
| LA75 | 40 |
| LGA75 | 41 |

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

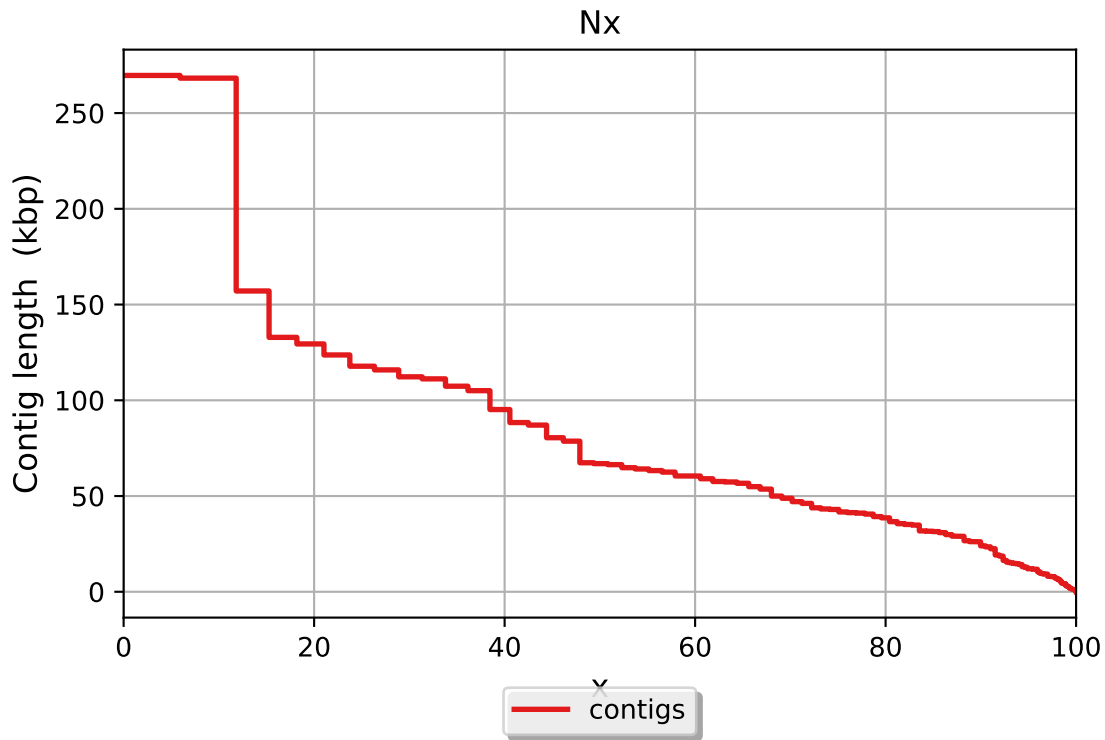
| | contigs |
|-----------------------------|---------|
| # misassemblies | 2 |
| # relocations | 2 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 54189 |
| # local misassemblies | 1 |
| # mismatches | 546 |
| # indels | 15 |
| # short indels | 15 |
| # long indels | 0 |
| Indels length | 17 |

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).

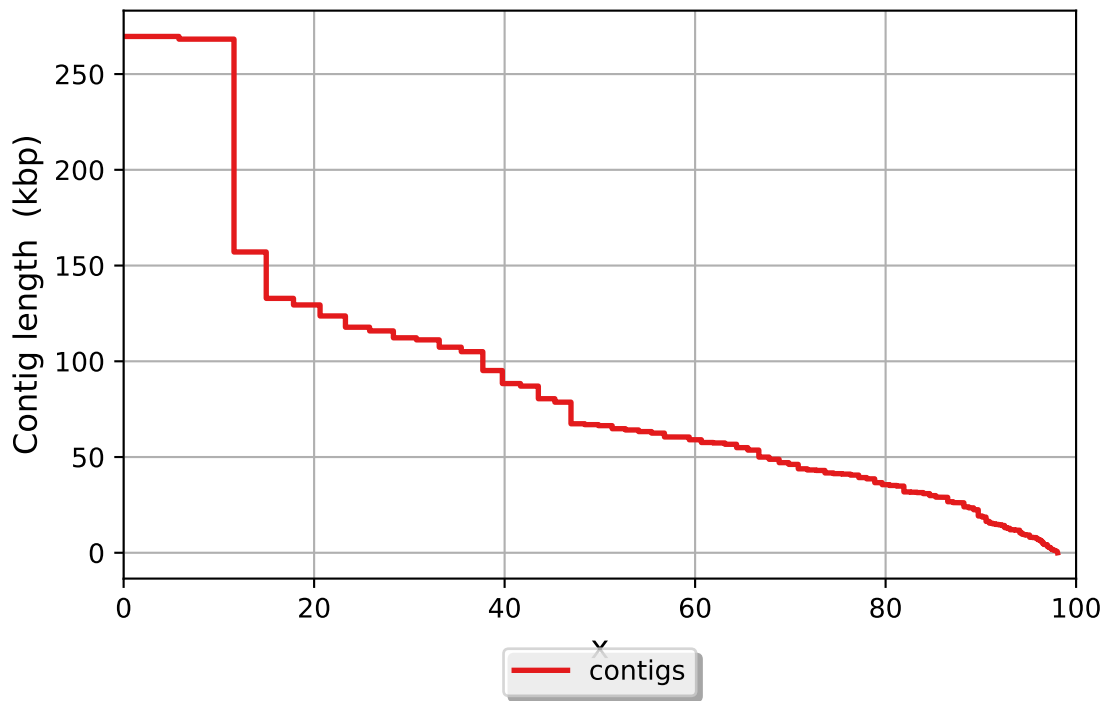
Unaligned report

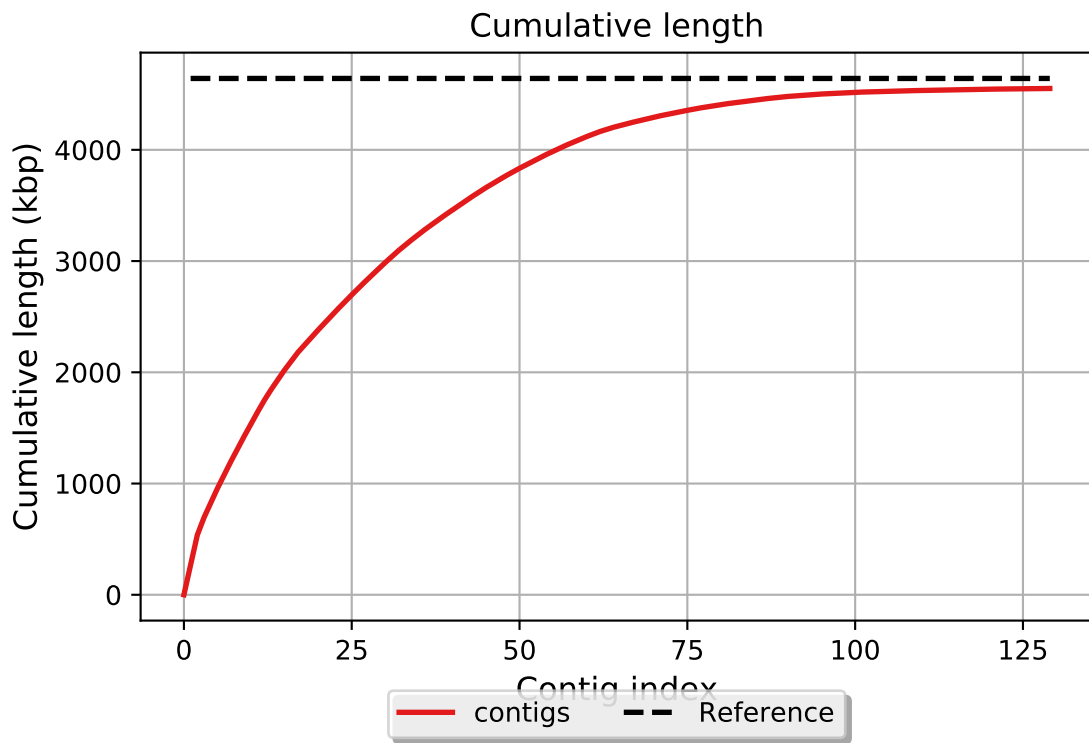
| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

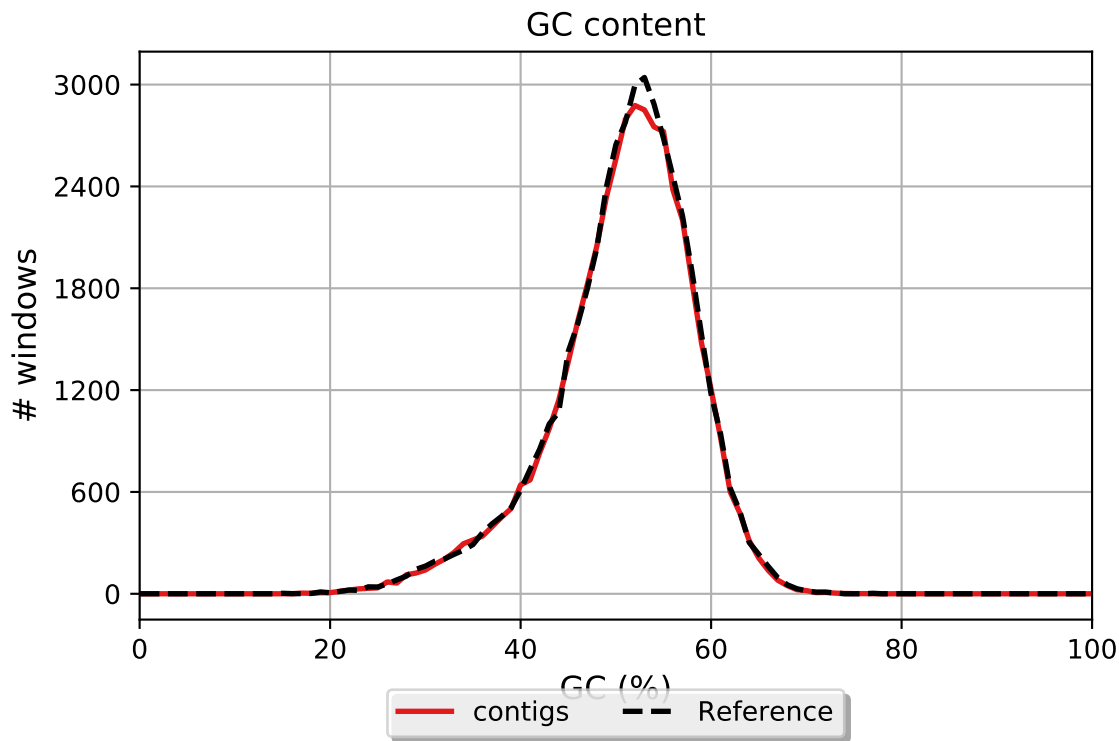
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



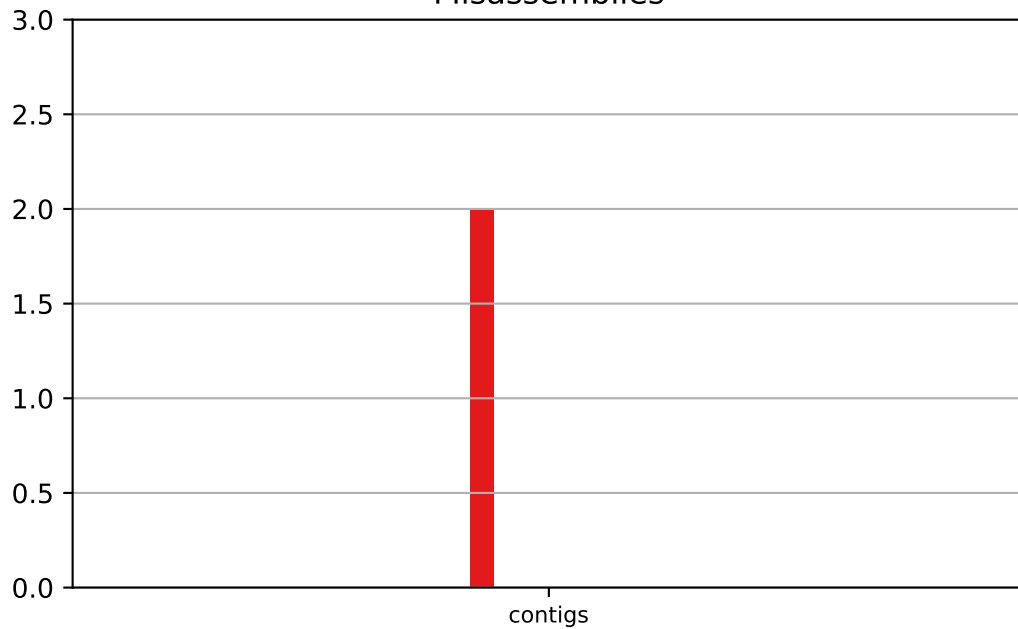
NGx



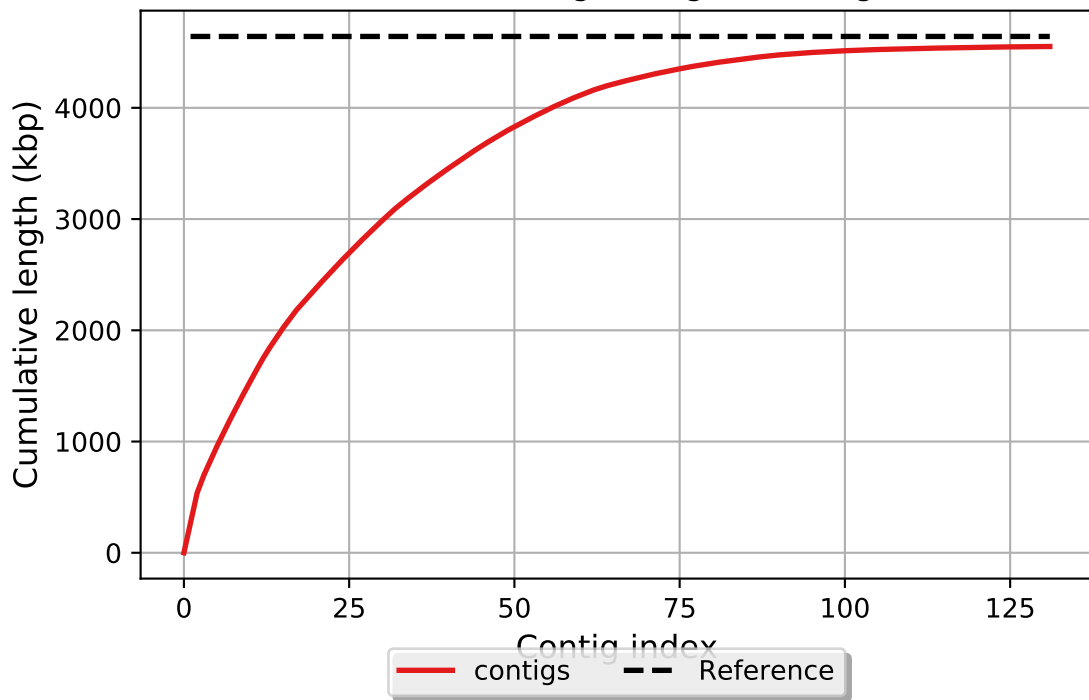




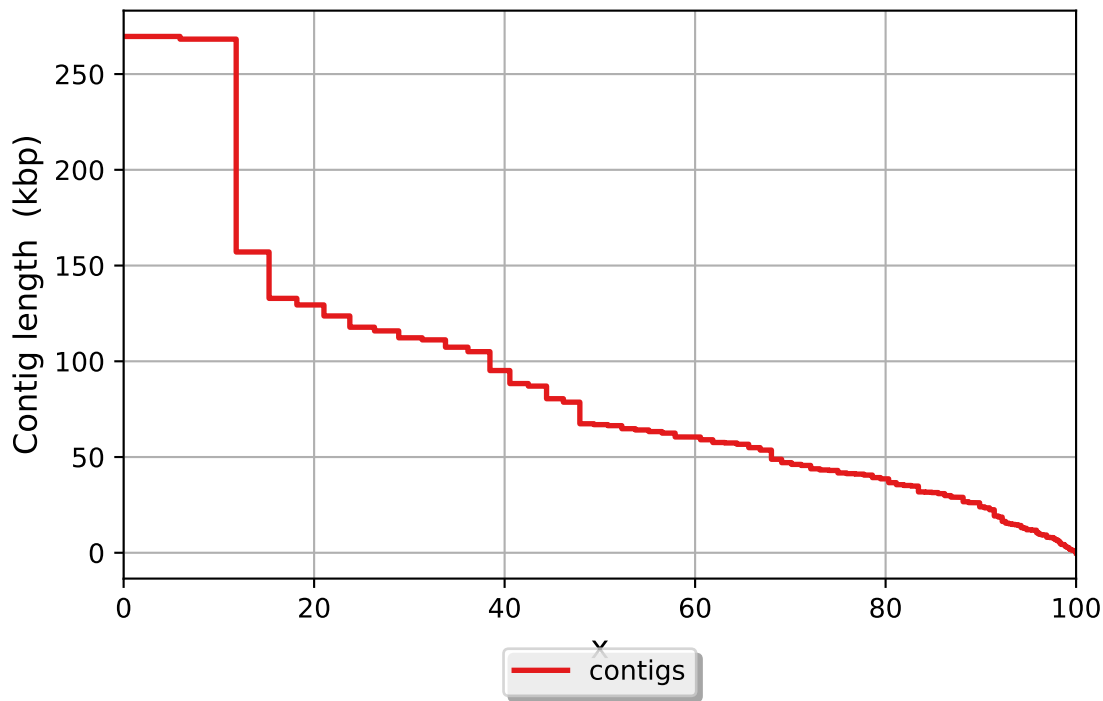
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

