

Report

| | contigs |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 867 |
| # contigs (≥ 1000 bp) | 242 |
| # contigs (≥ 5000 bp) | 182 |
| # contigs (≥ 10000 bp) | 145 |
| # contigs (≥ 25000 bp) | 63 |
| # contigs (≥ 50000 bp) | 16 |
| Total length (≥ 0 bp) | 4663017 |
| Total length (≥ 1000 bp) | 4547320 |
| Total length (≥ 5000 bp) | 4388952 |
| Total length (≥ 10000 bp) | 4108610 |
| Total length (≥ 25000 bp) | 2752980 |
| Total length (≥ 50000 bp) | 1172712 |
| # contigs | 255 |
| Largest contig | 139697 |
| Total length | 4556041 |
| Reference length | 4641652 |
| GC (%) | 50.74 |
| Reference GC (%) | 50.79 |
| N50 | 30957 |
| NG50 | 30234 |
| N75 | 17627 |
| NG75 | 16604 |
| L50 | 46 |
| LG50 | 48 |
| L75 | 94 |
| LG75 | 98 |
| # misassemblies | 10 |
| # misassembled contigs | 10 |
| Misassembled contigs length | 317749 |
| # local misassemblies | 9 |
| # unaligned contigs | 0 + 3 part |
| Unaligned length | 210 |
| Genome fraction (%) | 97.815 |
| Duplication ratio | 1.003 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 126.23 |
| # indels per 100 kbp | 1.34 |
| Largest alignment | 139697 |
| NA50 | 28464 |
| NGA50 | 28280 |
| NA75 | 16604 |
| NGA75 | 15788 |
| LA50 | 48 |
| LGA50 | 49 |
| LA75 | 97 |
| LGA75 | 101 |

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

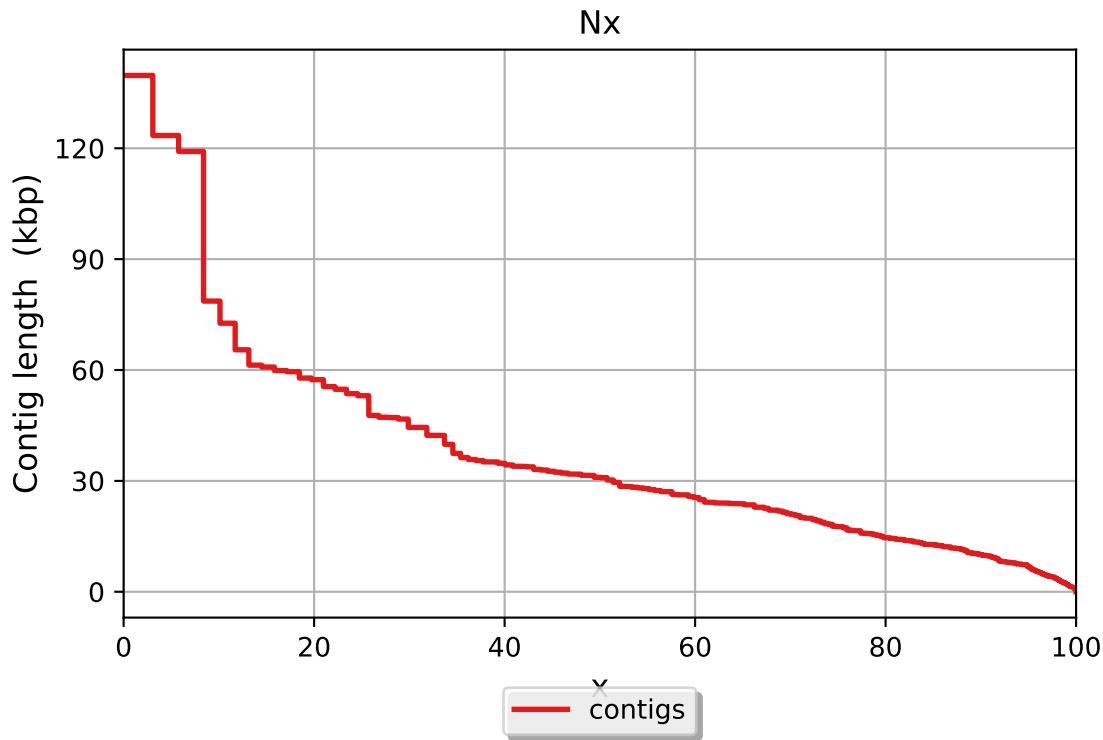
| | contigs |
|-----------------------------|---------|
| # misassemblies | 10 |
| # relocations | 10 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 10 |
| Misassembled contigs length | 317749 |
| # local misassemblies | 9 |
| # mismatches | 5731 |
| # indels | 61 |
| # short indels | 61 |
| # long indels | 0 |
| Indels length | 78 |

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).

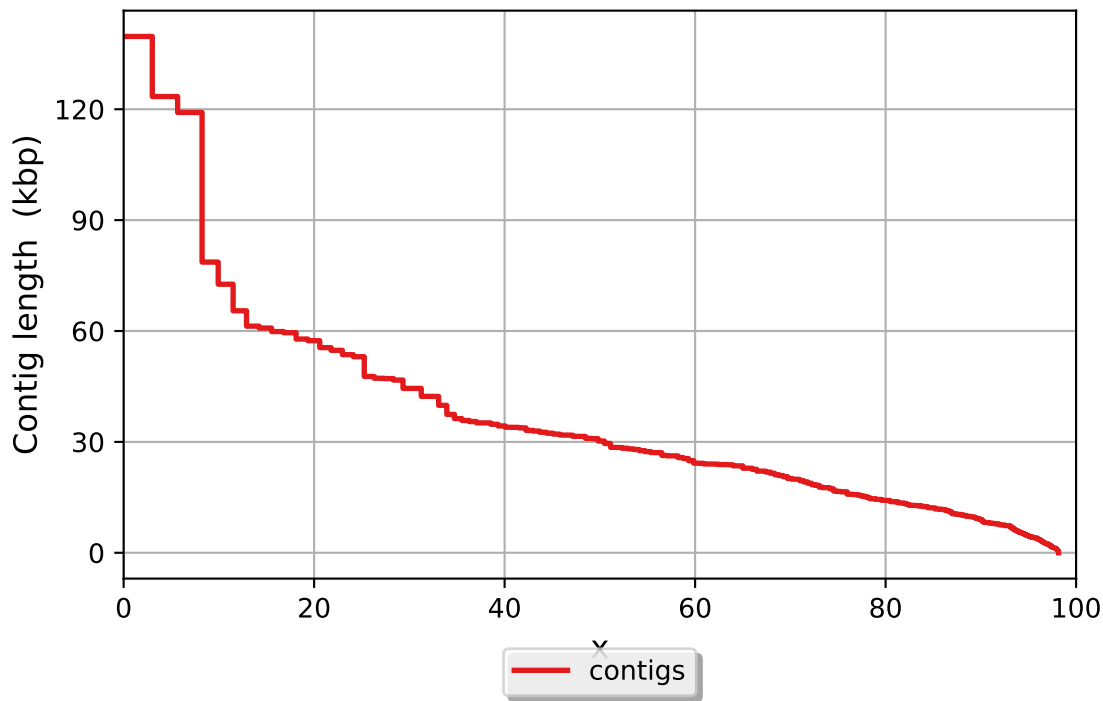
Unaligned report

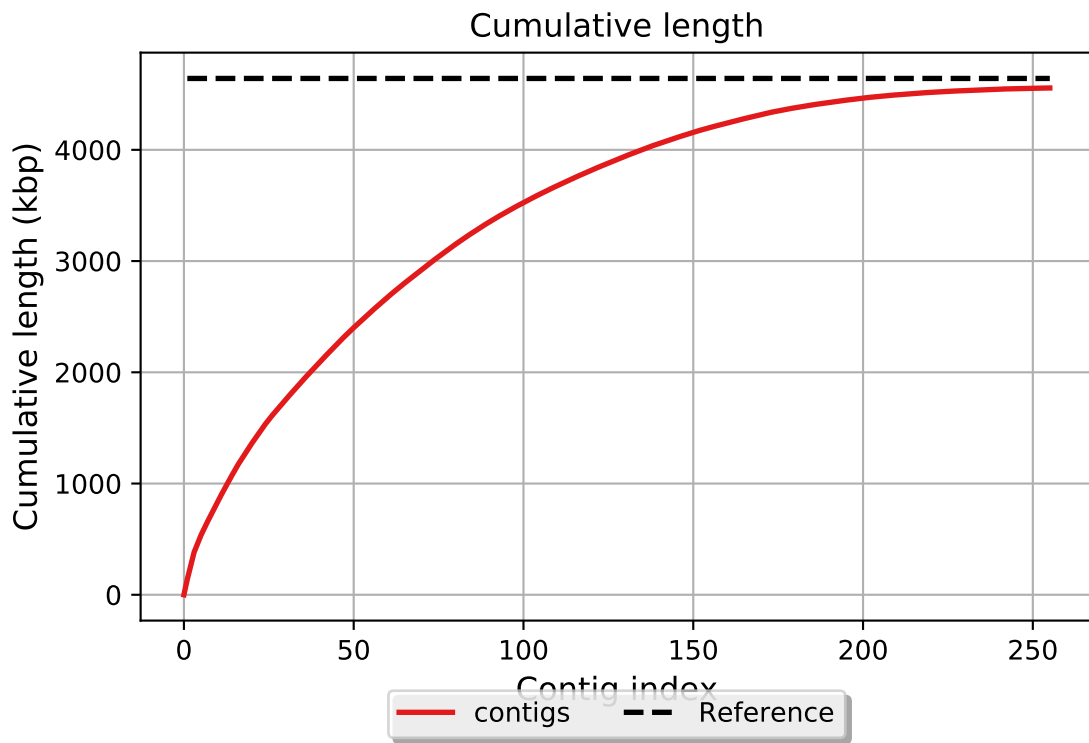
| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 3 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 210 |
| # N's | 0 |

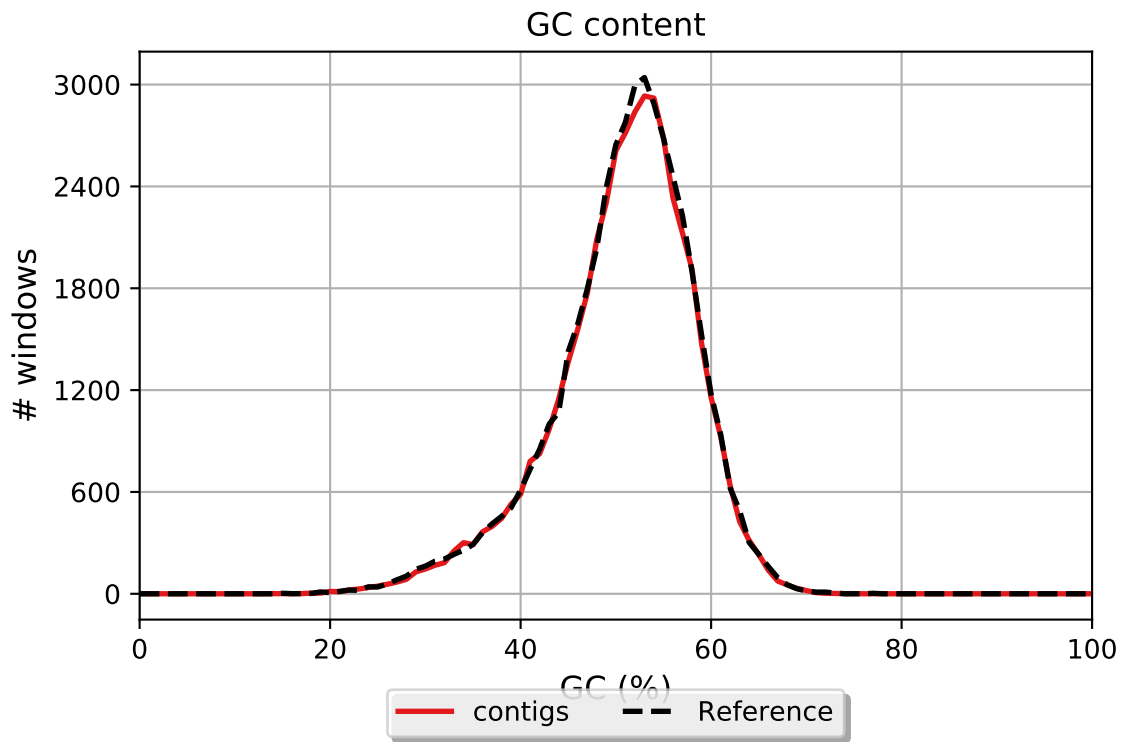
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



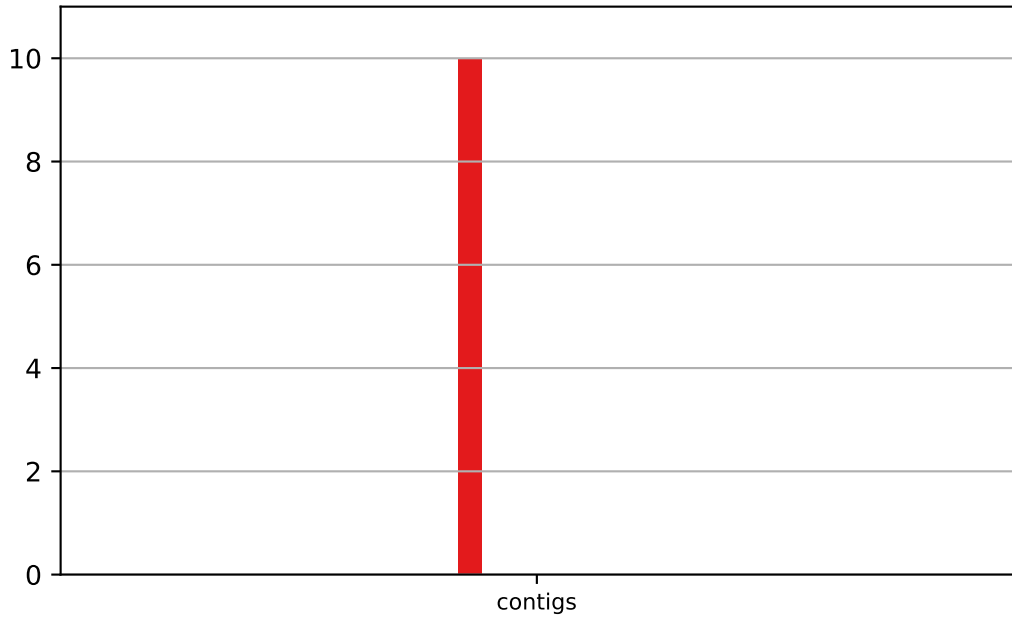
NGx



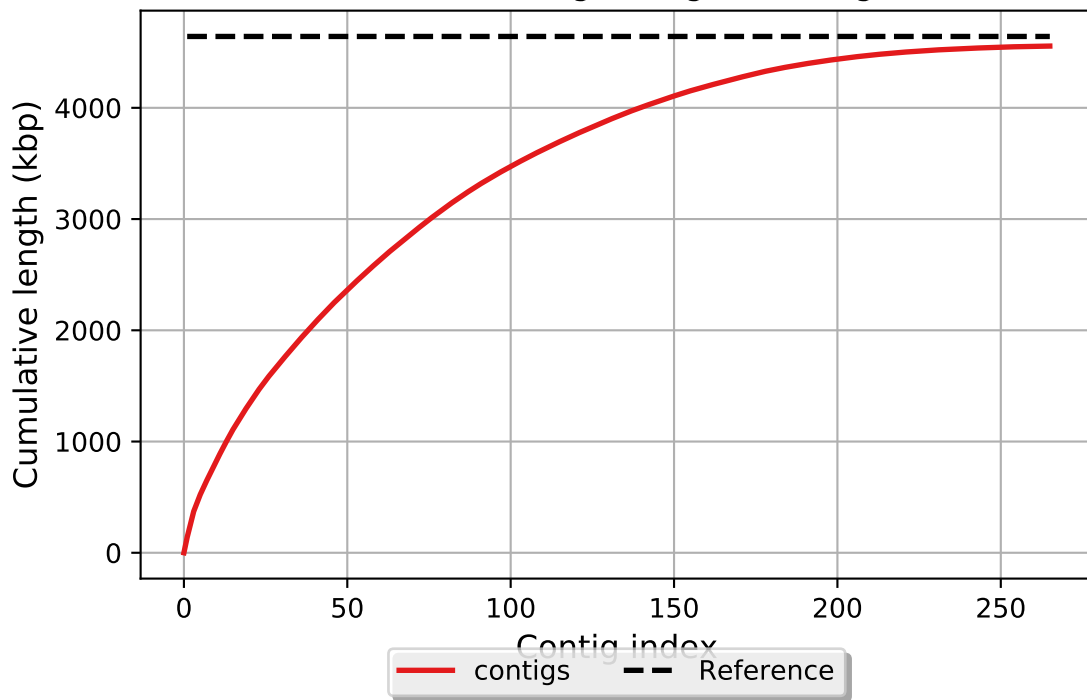




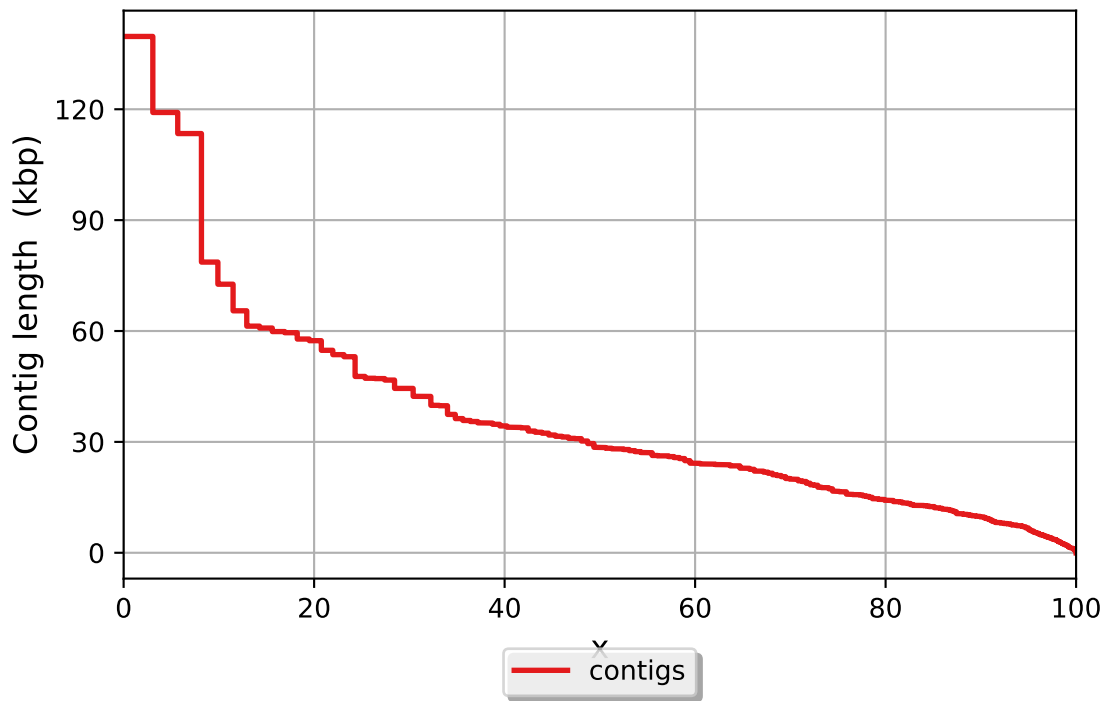
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

