

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 113 |
| # contigs (≥ 1000 bp) | 77 |
| # contigs (≥ 5000 bp) | 53 |
| # contigs (≥ 10000 bp) | 49 |
| # contigs (≥ 25000 bp) | 44 |
| # contigs (≥ 50000 bp) | 28 |
| Total length (≥ 0 bp) | 4566833 |
| Total length (≥ 1000 bp) | 4556812 |
| Total length (≥ 5000 bp) | 4502351 |
| Total length (≥ 10000 bp) | 4472445 |
| Total length (≥ 25000 bp) | 4399198 |
| Total length (≥ 50000 bp) | 3843225 |
| # contigs | 83 |
| Largest contig | 327064 |
| Total length | 4561322 |
| Reference length | 4641652 |
| N50 | 132876 |
| N75 | 78609 |
| L50 | 11 |
| L75 | 22 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 45411 |
| # local misassemblies | 3 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (▼) | 98.205 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 3.66 |
| # indels per 100 kbp | 0.37 |
| Largest alignment | 327064 |
| NA50 | 132876 |
| NA75 | 78609 |
| LA50 | 11 |
| LA75 | 22 |

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

| | scaffolds |
|---------------------------------|-----------|
| # misassemblies | 1 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 45411 |
| # local misassemblies | 3 |
| # mismatches | 167 |
| # indels | 17 |
| # short indels | 17 |
| # long indels | 0 |
| Indels length | 23 |

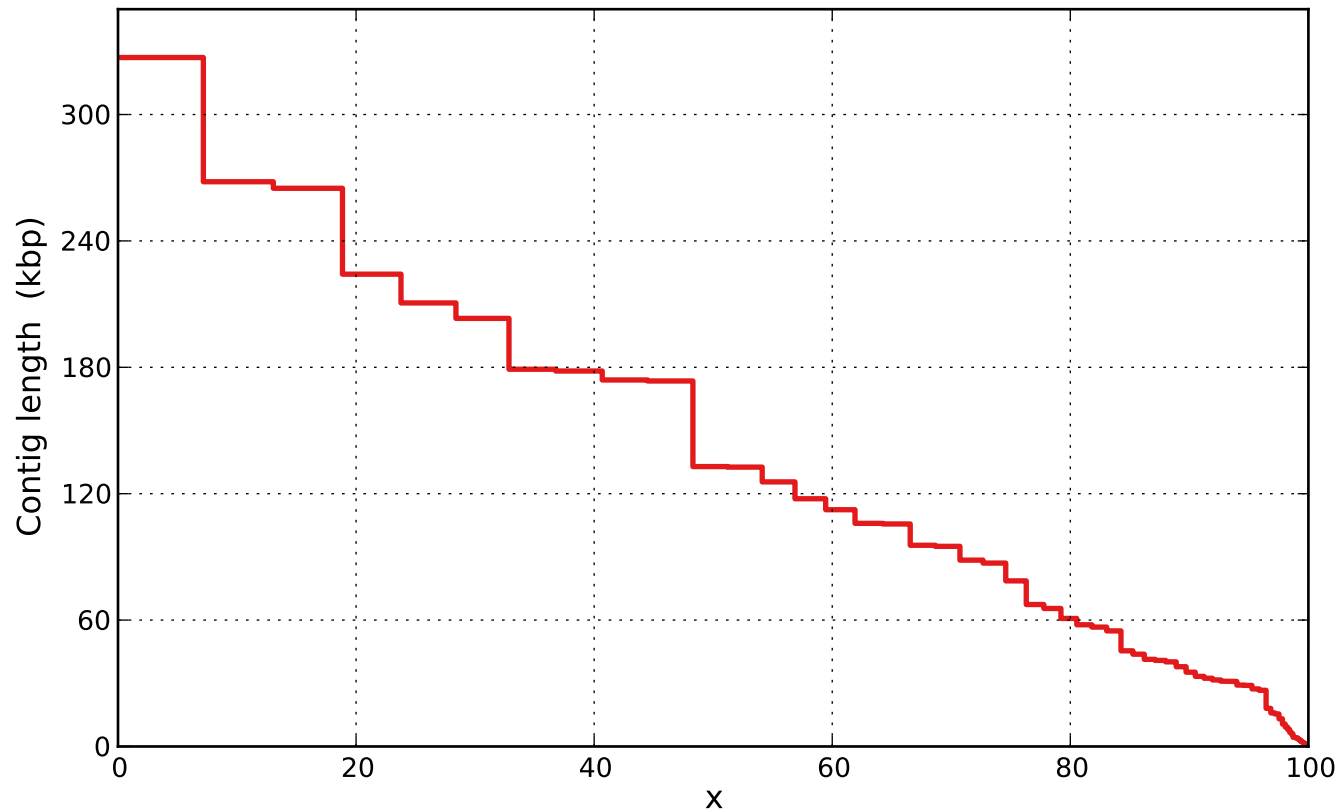
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

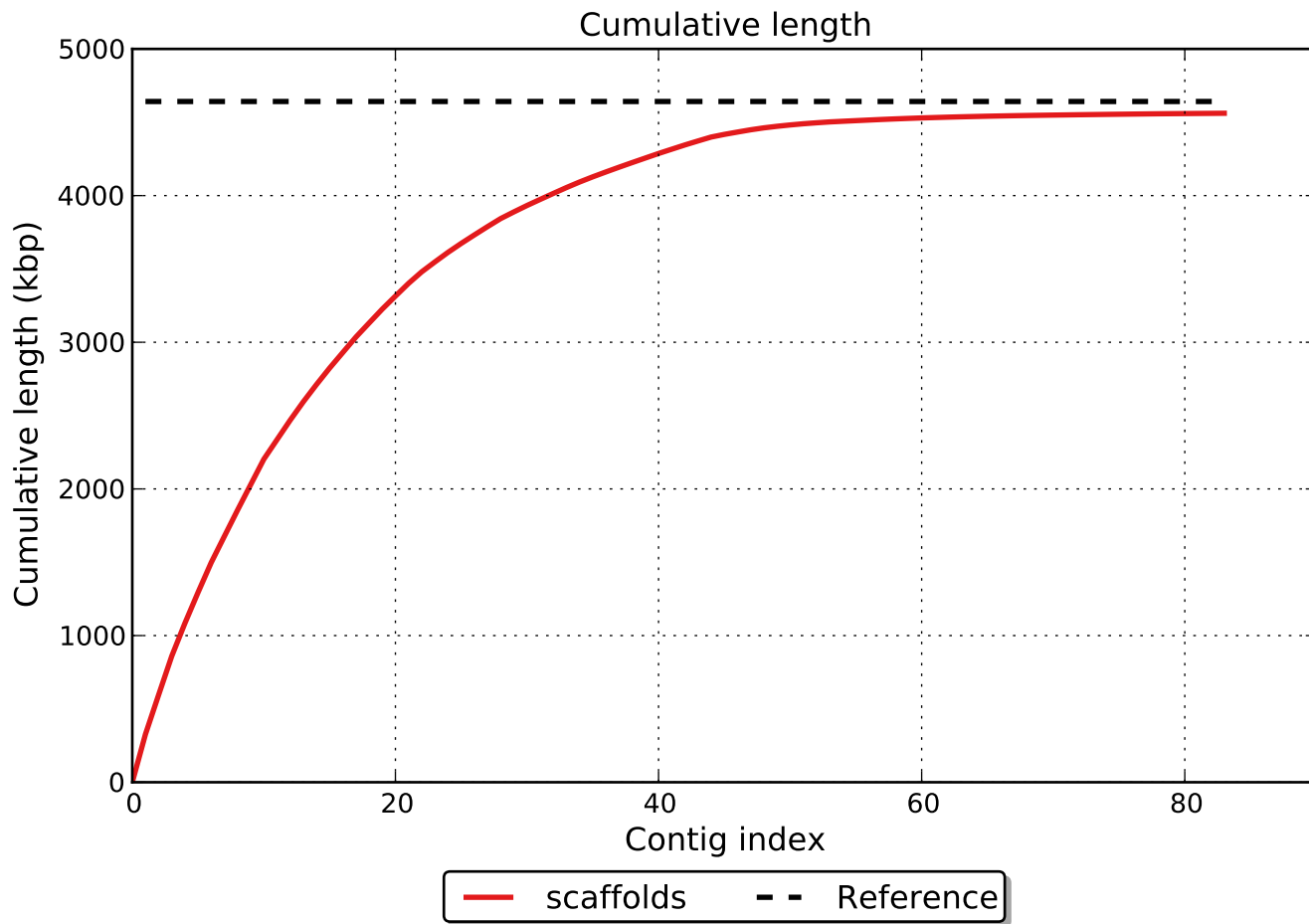
Unaligned report

| | scaffolds |
|-------------------------------|-----------|
| # 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).

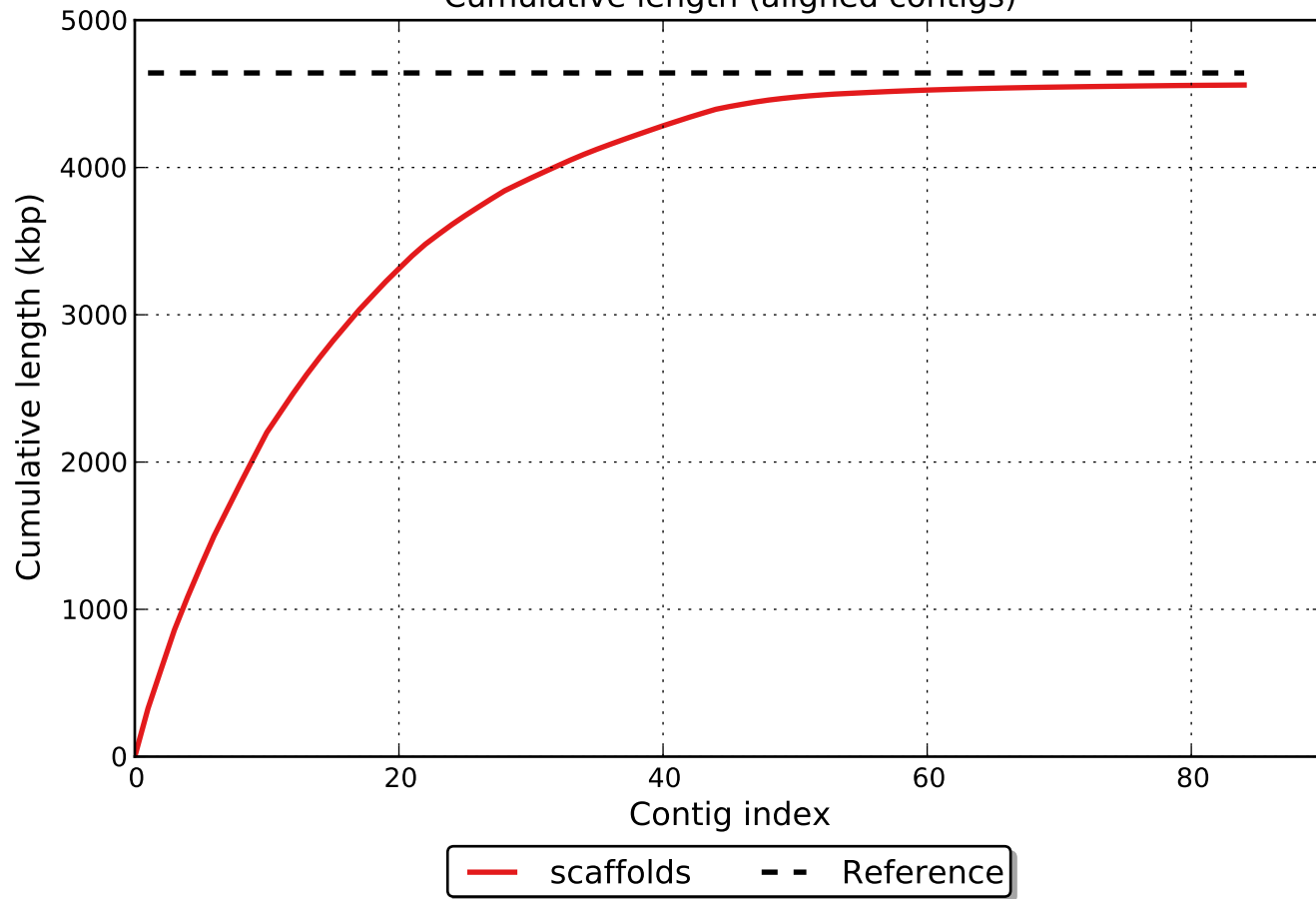
Nx







Cumulative length (aligned contigs)



NAx

