

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 1231 |
| # contigs (≥ 1000 bp) | 10 |
| # contigs (≥ 5000 bp) | 1 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 0 bp) | 372277 |
| Total length (≥ 1000 bp) | 18699 |
| Total length (≥ 5000 bp) | 5443 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 78 |
| Largest contig | 5443 |
| Total length | 60517 |
| Reference length | 4641652 |
| N50 | 657 |
| N75 | 560 |
| L50 | 25 |
| L75 | 50 |
| # misassemblies | 2 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 7077 |
| # local misassemblies | 1 |
| # unaligned contigs | 7 + 8 part |
| Unaligned length | 5117 |
| Genome fraction (▼) | 1.186 |
| Duplication ratio | 1.007 |
| # N's per 100 kbp | 1097.21 |
| # mismatches per 100 kbp | 694.15 |
| # indels per 100 kbp | 70.87 |
| Largest alignment | 5372 |
| NA50 | 627 |
| NA75 | 551 |
| LA50 | 27 |
| LA75 | 54 |

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

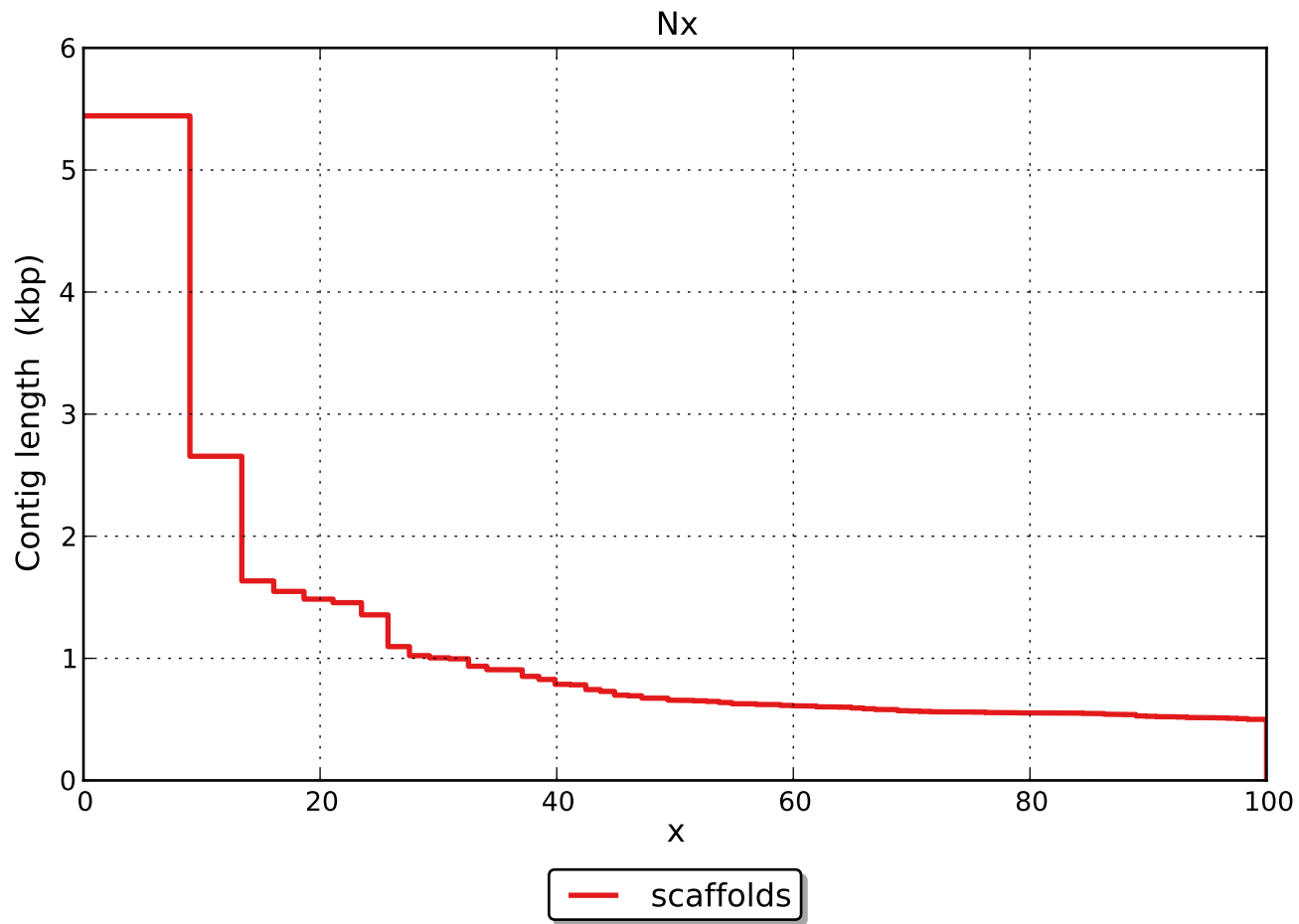
| | scaffolds |
|---------------------------------|-----------|
| # misassemblies | 2 |
| # relocations | 2 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 7077 |
| # local misassemblies | 1 |
| # mismatches | 382 |
| # indels | 39 |
| # short indels | 24 |
| # long indels | 15 |
| Indels length | 218 |

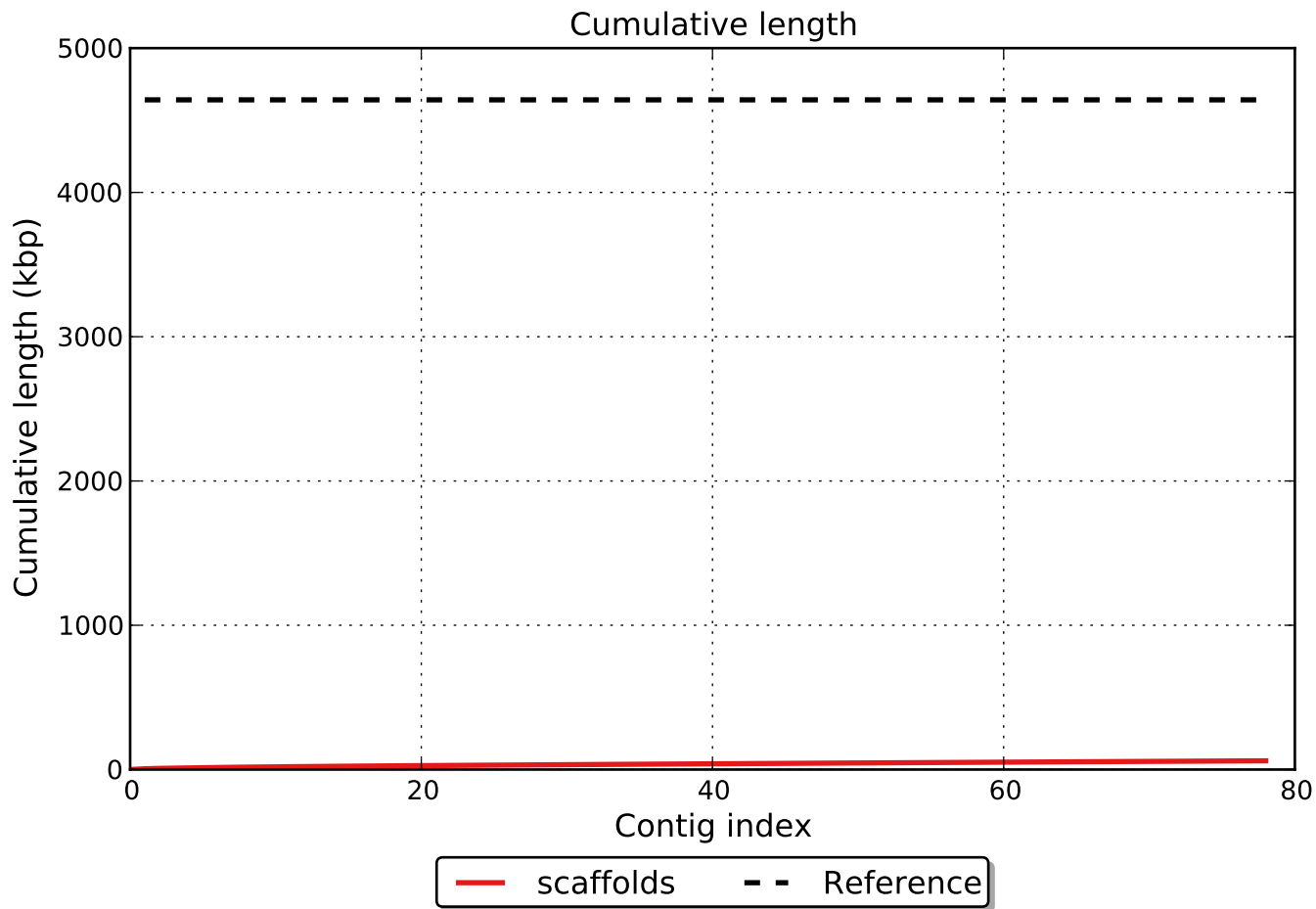
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

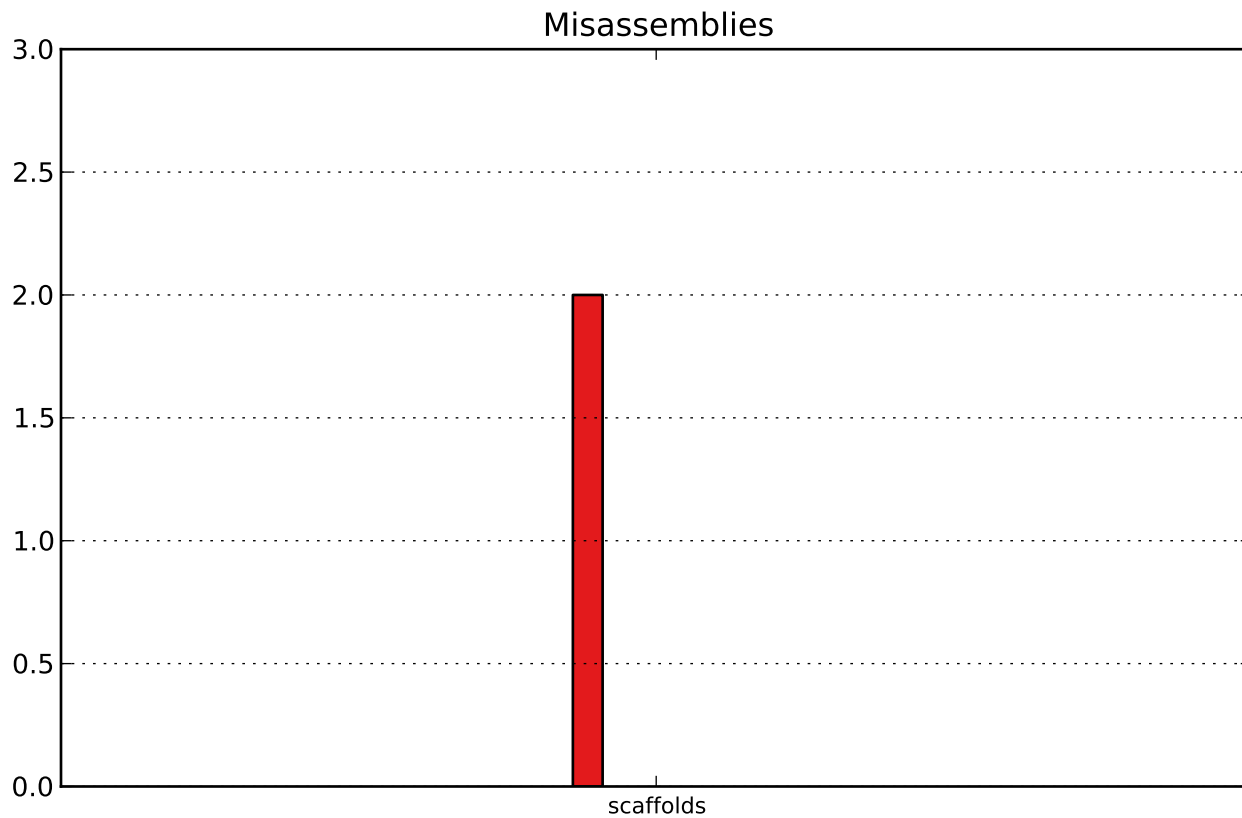
Unaligned report

| | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs | 7 |
| Fully unaligned length | 4322 |
| # partially unaligned contigs | 8 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 795 |
| # N's | 664 |

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).







Cumulative length (aligned contigs)

