

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 308 |
| # contigs (≥ 1000 bp) | 124 |
| # contigs (≥ 5000 bp) | 97 |
| # contigs (≥ 10000 bp) | 79 |
| # contigs (≥ 25000 bp) | 54 |
| # contigs (≥ 50000 bp) | 37 |
| Total length (≥ 0 bp) | 4603571 |
| Total length (≥ 1000 bp) | 4562517 |
| Total length (≥ 5000 bp) | 4491950 |
| Total length (≥ 10000 bp) | 4364624 |
| Total length (≥ 25000 bp) | 3974973 |
| Total length (≥ 50000 bp) | 3399888 |
| # contigs | 132 |
| Largest contig | 264572 |
| Total length | 4568391 |
| Reference length | 9283304 |
| N50 | 76208 |
| N75 | 43987 |
| L50 | 20 |
| L75 | 38 |
| # misassemblies | 5 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 310368 |
| # local misassemblies | 3 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 76.981 |
| Duplication ratio | 0.998 |
| # N's per 100 kbp | 13.44 |
| # mismatches per 100 kbp | 561.25 |
| # indels per 100 kbp | 0.63 |
| Largest alignment | 264572 |
| NA50 | 76208 |
| NA75 | 43384 |
| LA50 | 20 |
| LA75 | 39 |

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 | 5 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 4 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 310368 |
| # local misassemblies | 3 |
| # mismatches | 40109 |
| # indels | 45 |
| # short indels | 43 |
| # long indels | 2 |
| Indels length | 165 |

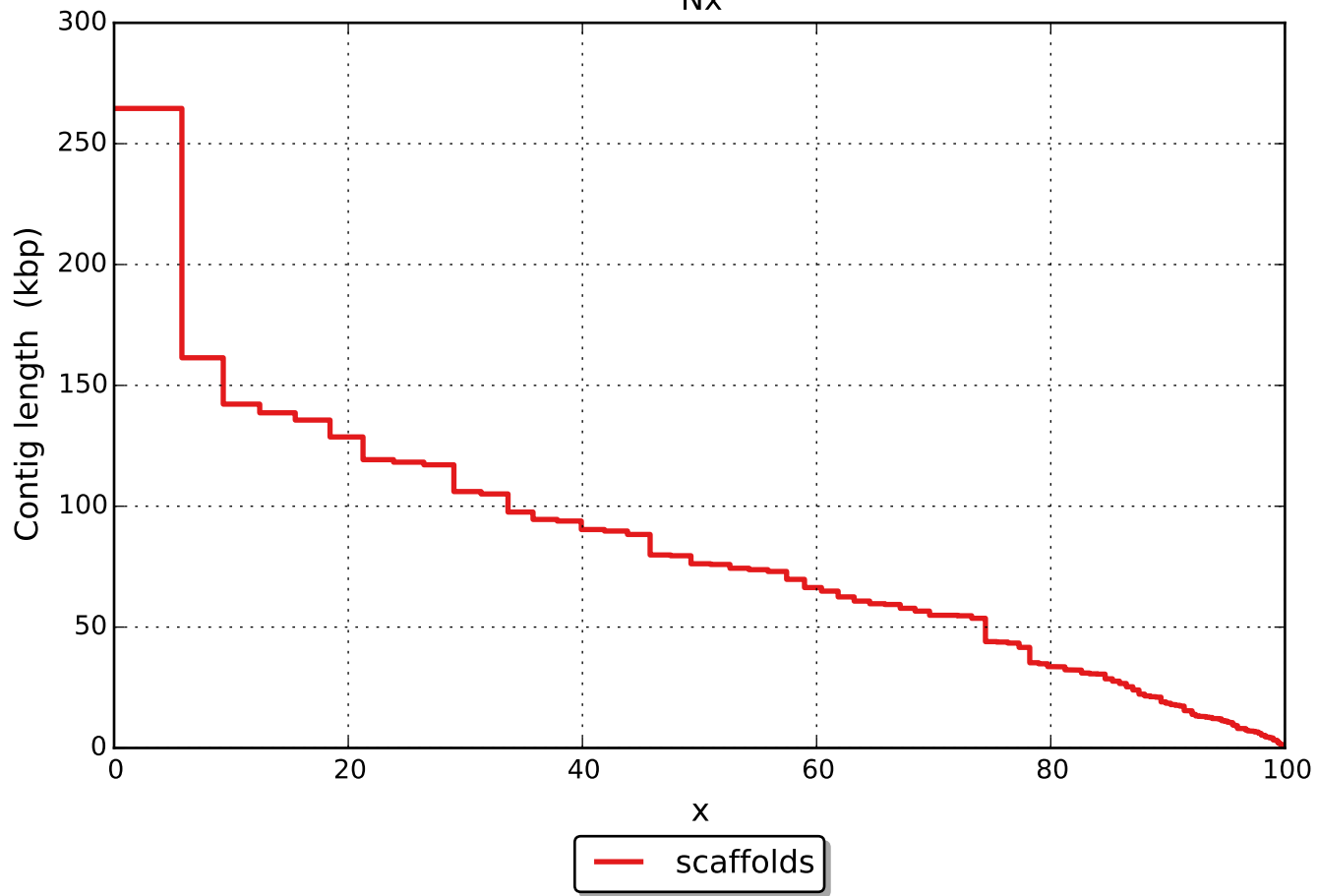
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

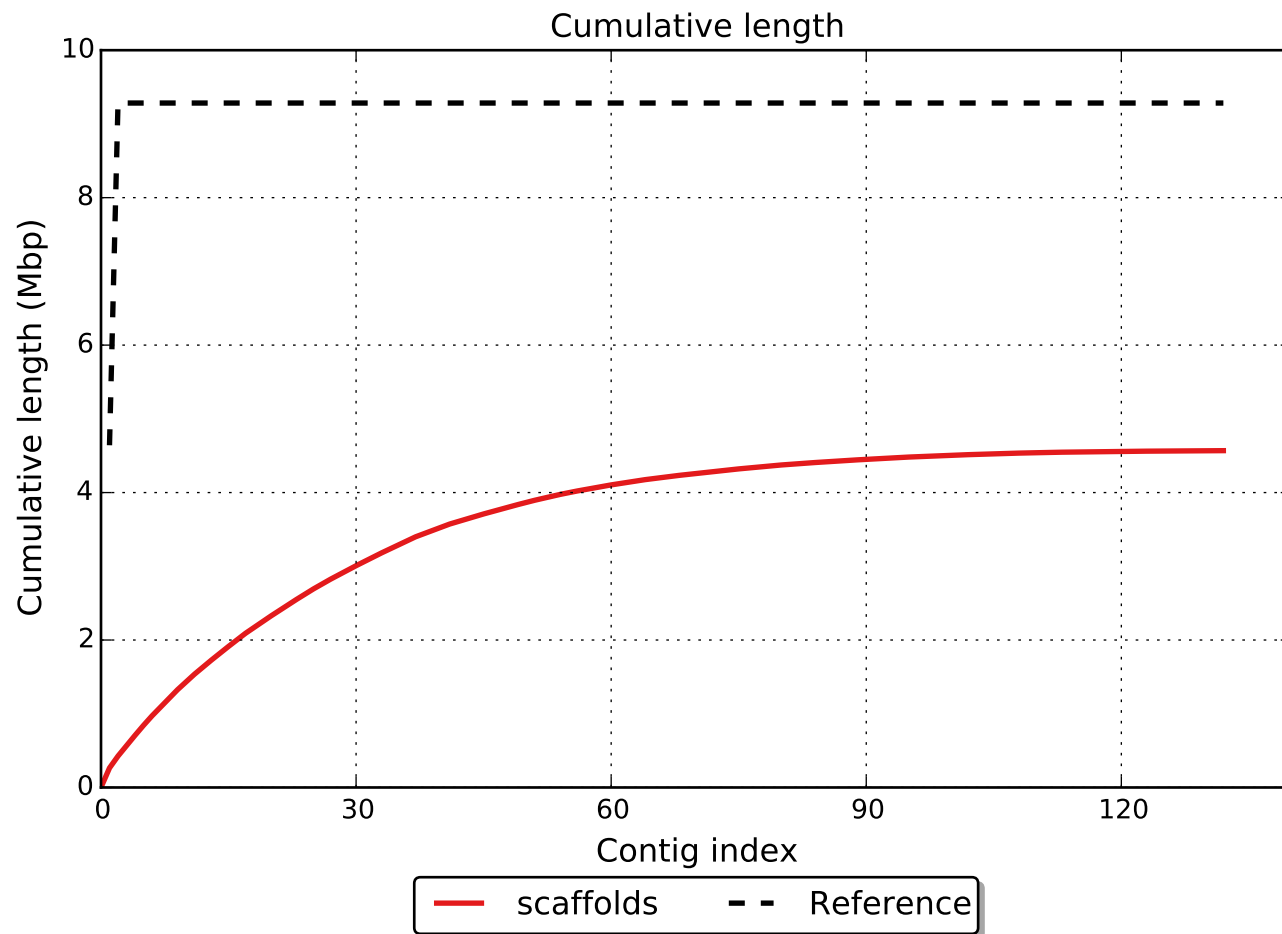
Unaligned report

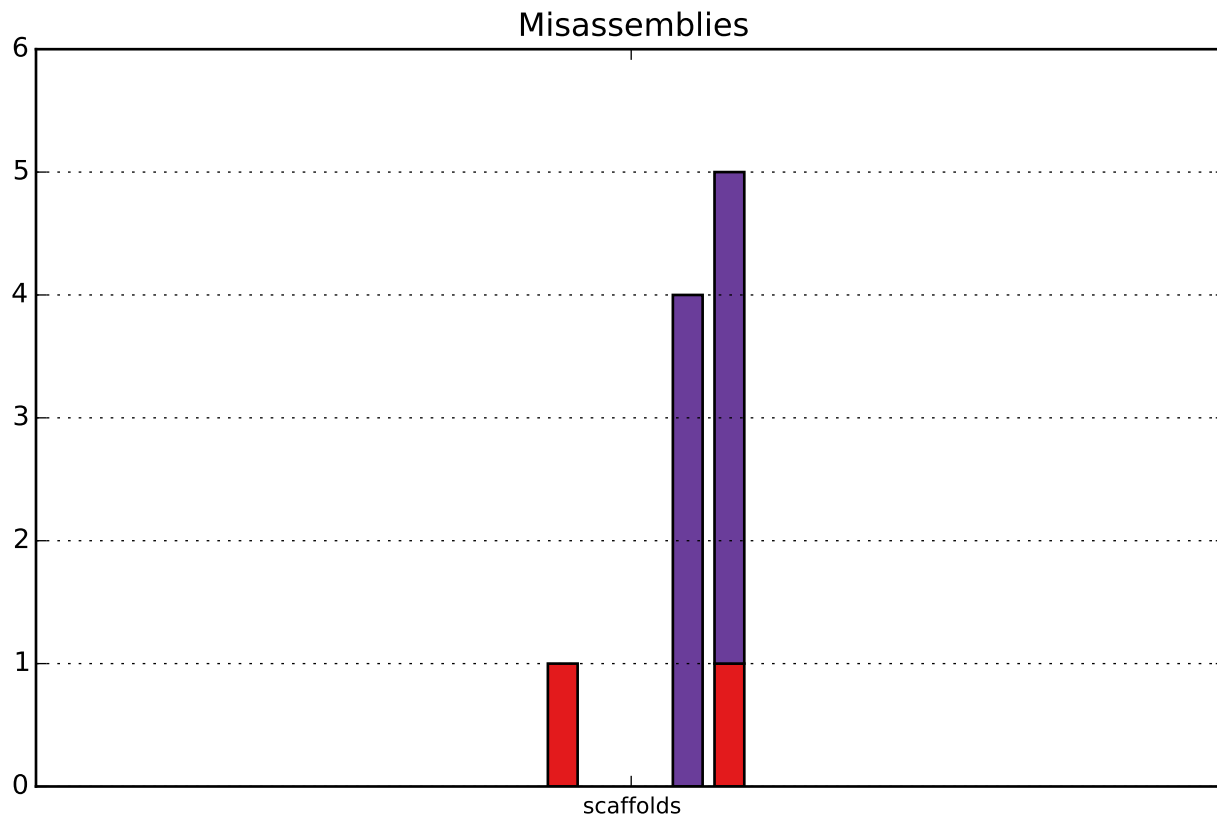
| | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 614 |

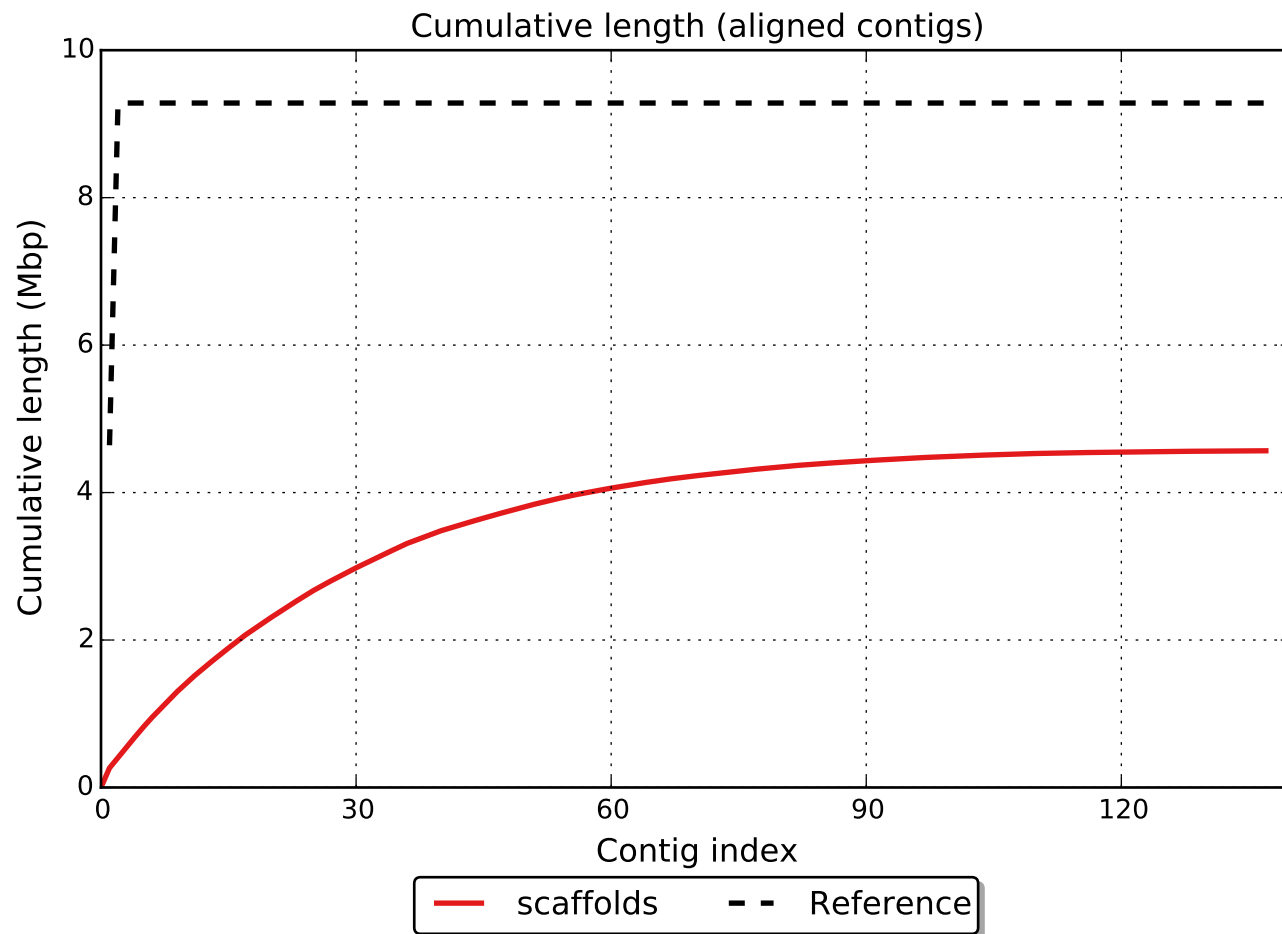
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

