

Report

| | scaffolds |
|---------------------------------|-------------|
| # contigs (≥ 0 bp) | 425 |
| # contigs (≥ 1000 bp) | 150 |
| # contigs (≥ 5000 bp) | 109 |
| # contigs (≥ 10000 bp) | 99 |
| # contigs (≥ 25000 bp) | 86 |
| # contigs (≥ 50000 bp) | 64 |
| Total length (≥ 0 bp) | 8934170 |
| Total length (≥ 1000 bp) | 8823885 |
| Total length (≥ 5000 bp) | 8742657 |
| Total length (≥ 10000 bp) | 8670492 |
| Total length (≥ 25000 bp) | 8439598 |
| Total length (≥ 50000 bp) | 7717920 |
| # contigs | 203 |
| Largest contig | 431470 |
| Total length | 8858840 |
| Reference length | 9283304 |
| N50 | 105688 |
| N75 | 69219 |
| L50 | 22 |
| L75 | 47 |
| # misassemblies | 221 |
| # misassembled contigs | 44 |
| Misassembled contigs length | 4158295 |
| # local misassemblies | 11 |
| # unaligned contigs | 15 + 2 part |
| Unaligned length | 9815 |
| Genome fraction (%) | 49.301 |
| Duplication ratio | 1.933 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1308.63 |
| # indels per 100 kbp | 1.42 |
| Largest alignment | 431470 |
| NA50 | 58608 |
| NA75 | 25159 |
| LA50 | 40 |
| LA75 | 100 |

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 | 221 |
| # relocations | 179 |
| # translocations | 0 |
| # inversions | 35 |
| # interspecies translocations | 7 |
| # possibly misassembled contigs | 1 |
| # misassembled contigs | 44 |
| Misassembled contigs length | 4158295 |
| # local misassemblies | 11 |
| # mismatches | 59893 |
| # indels | 65 |
| # short indels | 64 |
| # long indels | 1 |
| Indels length | 75 |

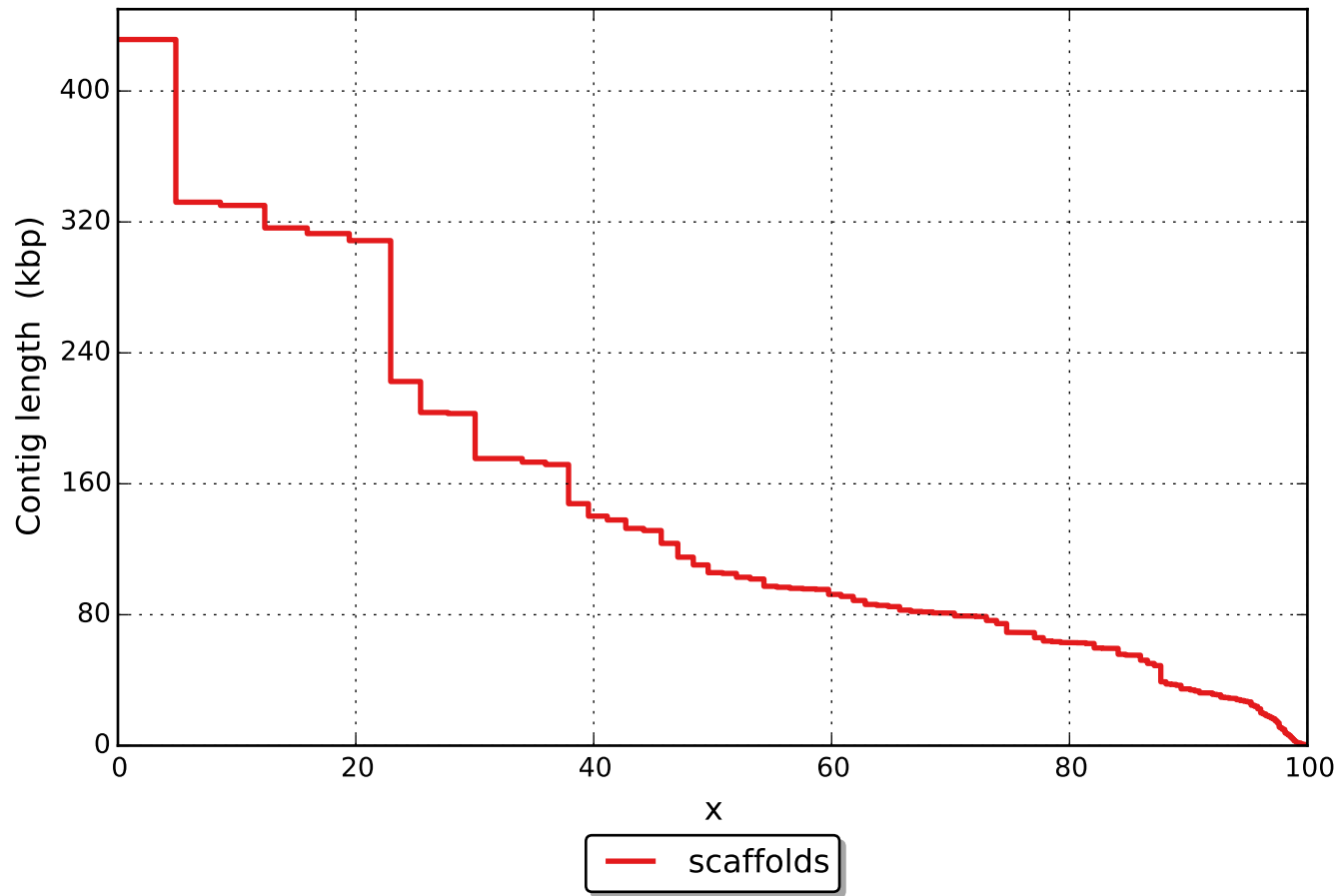
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

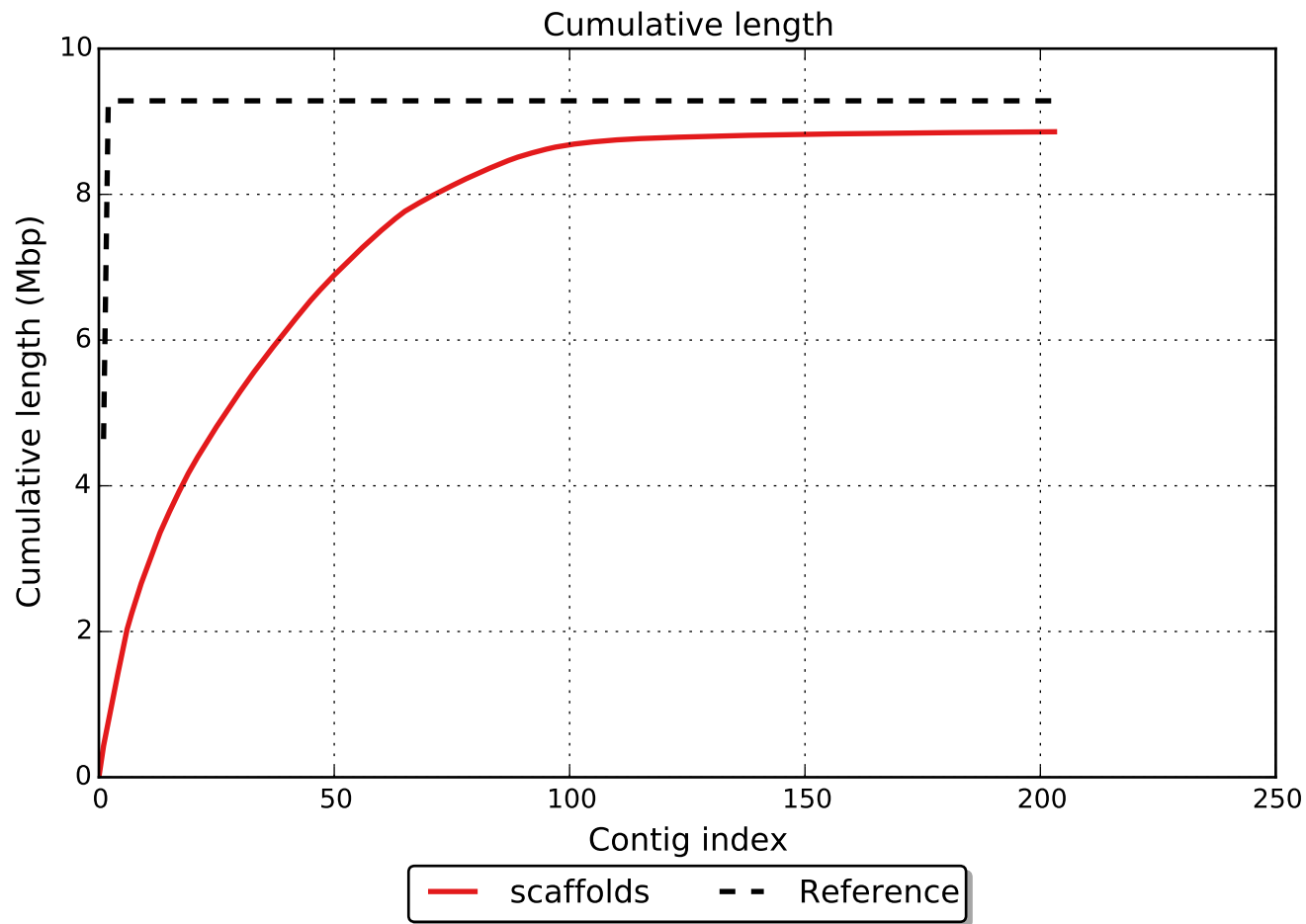
Unaligned report

| | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs | 15 |
| Fully unaligned length | 9425 |
| # partially unaligned contigs | 2 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 390 |
| # N's | 0 |

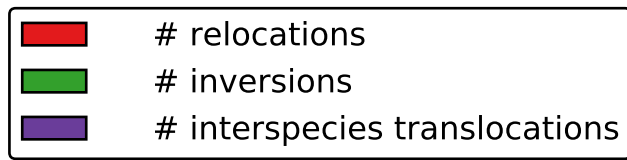
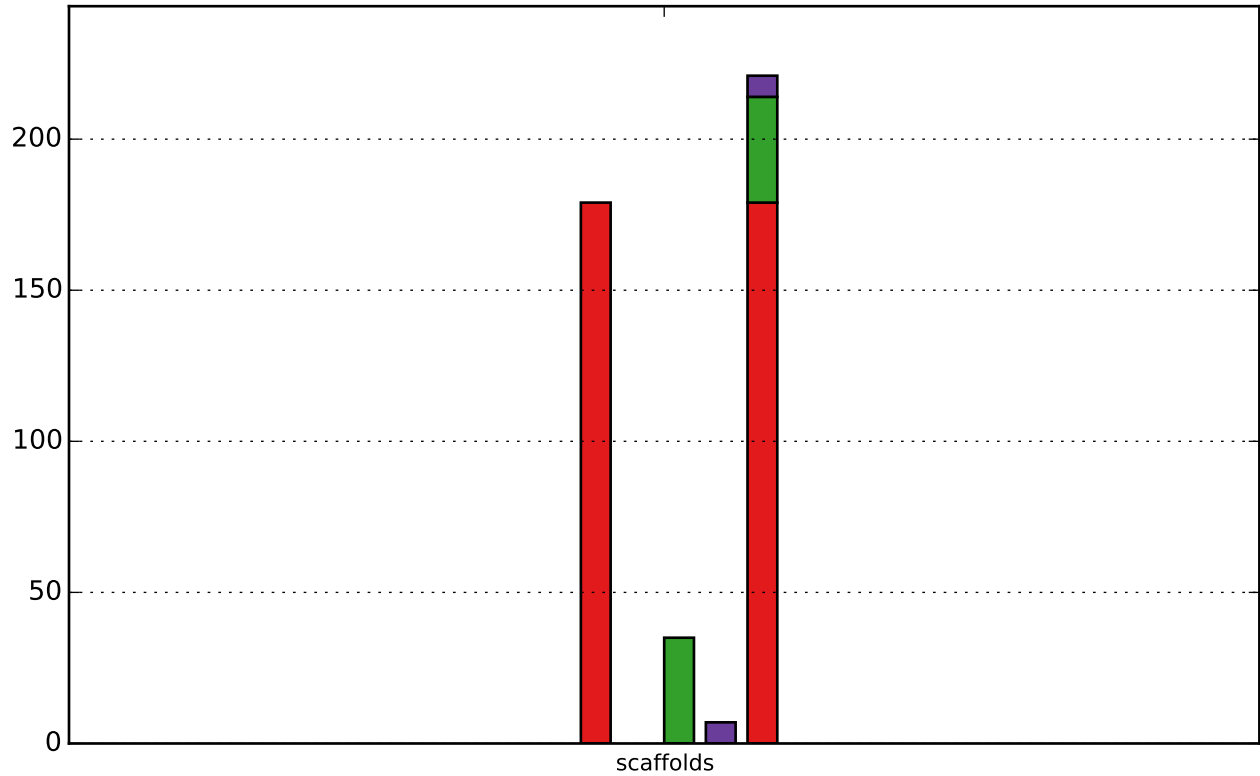
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

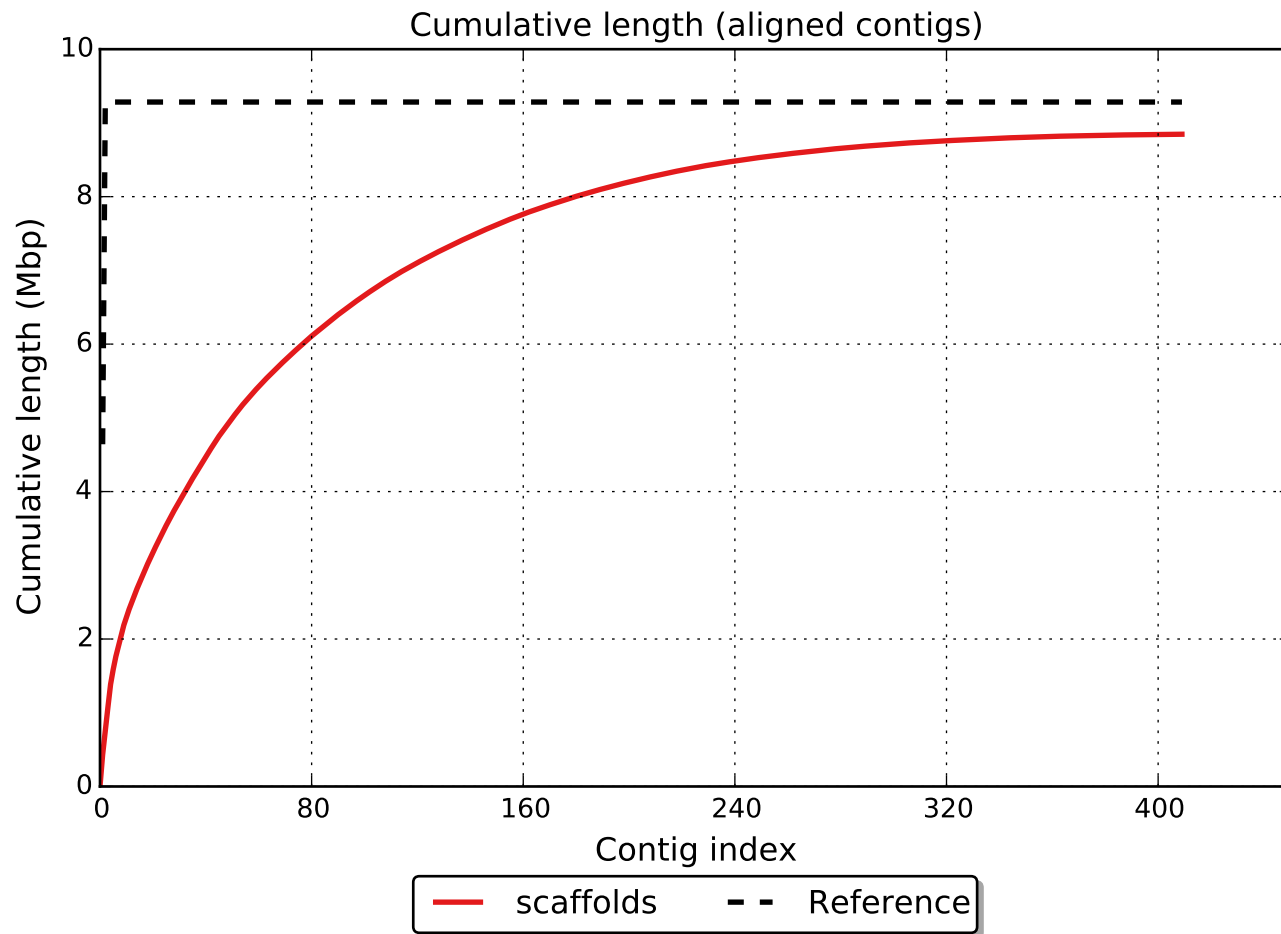
Nx





Misassemblies





NAx

