

Report

| | scaffolds |
|---------------------------------|--------------|
| # contigs (≥ 0 bp) | 123 |
| # contigs (≥ 1000 bp) | 72 |
| # contigs (≥ 5000 bp) | 66 |
| # contigs (≥ 10000 bp) | 63 |
| # contigs (≥ 25000 bp) | 57 |
| # contigs (≥ 50000 bp) | 43 |
| Total length (≥ 0 bp) | 9152926 |
| Total length (≥ 1000 bp) | 9134576 |
| Total length (≥ 5000 bp) | 9121767 |
| Total length (≥ 10000 bp) | 9099134 |
| Total length (≥ 25000 bp) | 9008253 |
| Total length (≥ 50000 bp) | 8537401 |
| # contigs | 82 |
| Largest contig | 768359 |
| Total length | 9141550 |
| Reference length | 9283304 |
| N50 | 264356 |
| N75 | 131763 |
| L50 | 11 |
| L75 | 24 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 768359 |
| # local misassemblies | 1 |
| # unaligned contigs | 44 + 15 part |
| Unaligned length | 4340680 |
| Genome fraction (%) | 49.838 |
| Duplication ratio | 1.038 |
| # N's per 100 kbp | 1.05 |
| # mismatches per 100 kbp | 306.94 |
| # indels per 100 kbp | 1.04 |
| Largest alignment | 607862 |
| NA50 | 53885 |
| LA50 | 17 |

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 | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 1 |
| # possibly misassembled contigs | 8 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 768359 |
| # local misassemblies | 1 |
| # mismatches | 14201 |
| # indels | 48 |
| # short indels | 48 |
| # long indels | 0 |
| Indels length | 55 |

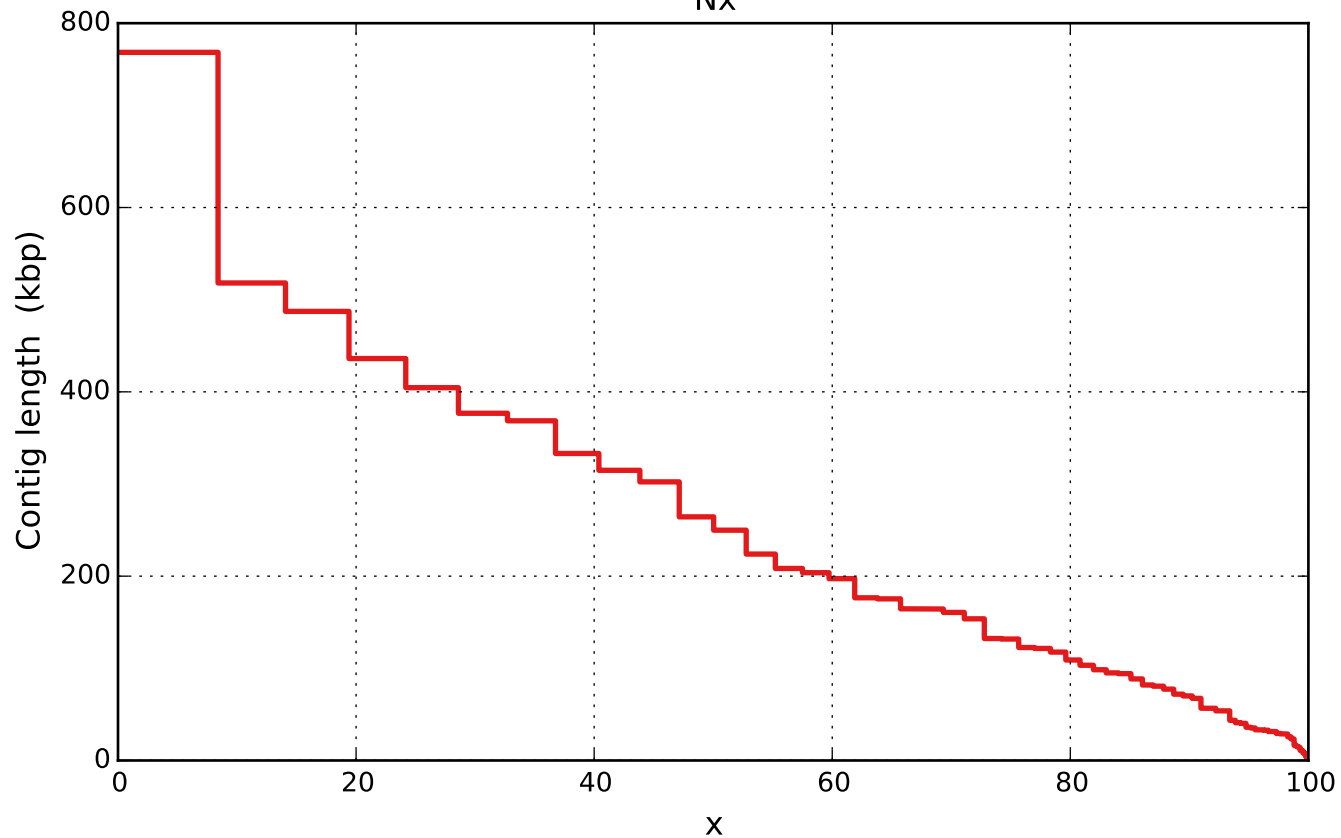
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

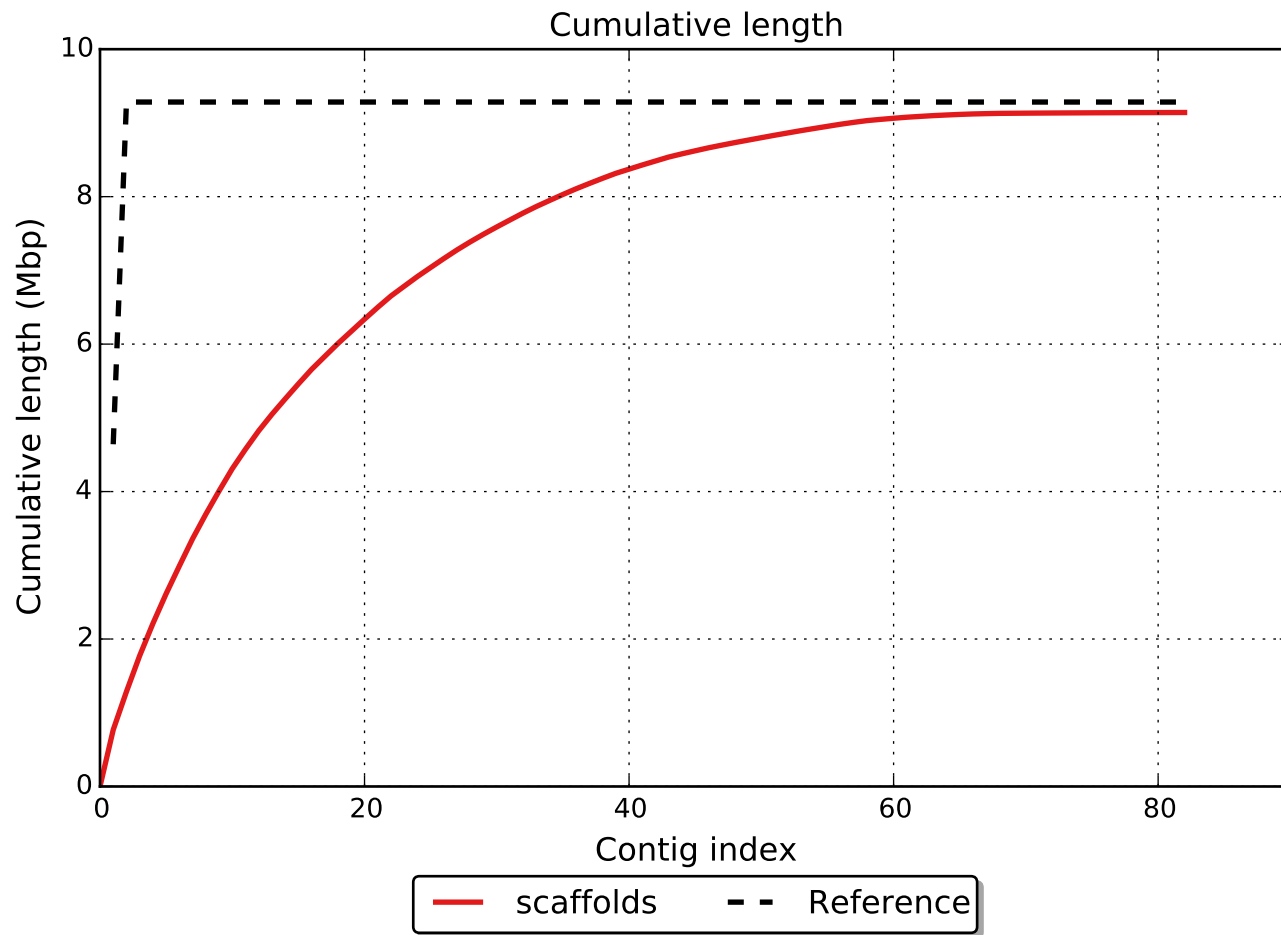
| | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs | 44 |
| Fully unaligned length | 2557407 |
| # partially unaligned contigs | 15 |
| # with misassembly | 3 |
| # both parts are significant | 7 |
| Partially unaligned length | 1783273 |
| # N's | 96 |

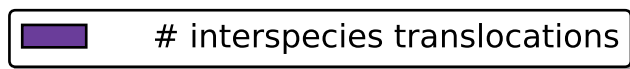
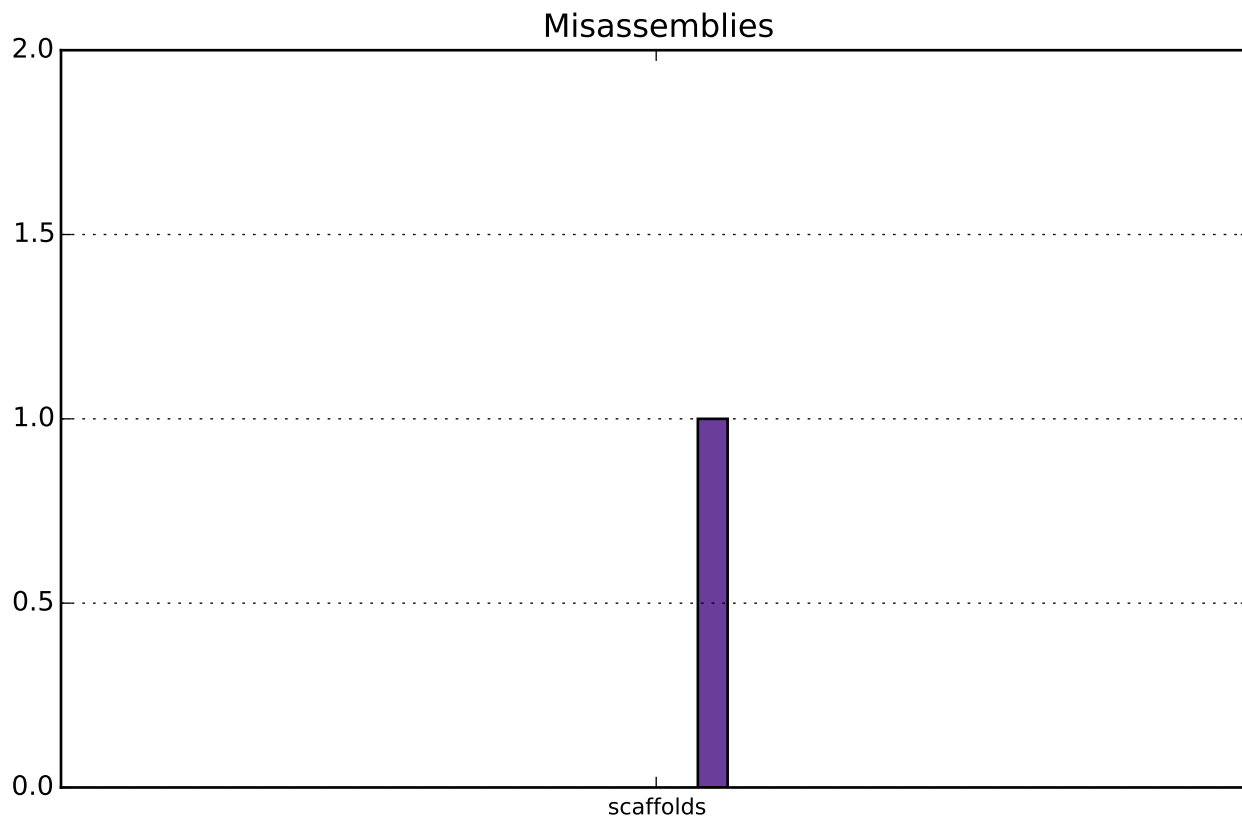
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

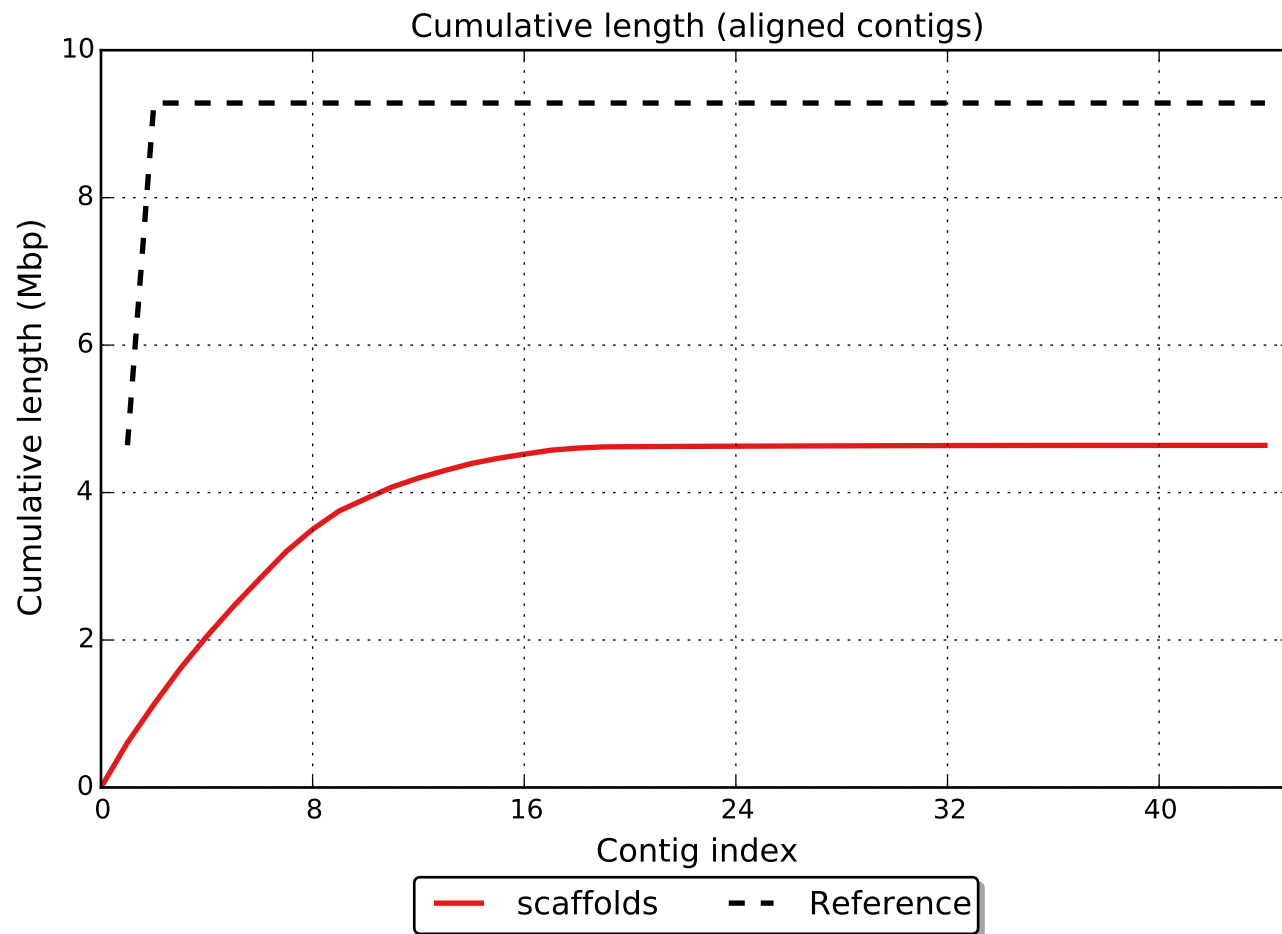
Nx



— scaffolds







NAx

