

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 0 bp) | 229 |
| # contigs (≥ 1000 bp) | 99 |
| # contigs (≥ 5000 bp) | 77 |
| # contigs (≥ 10000 bp) | 74 |
| # contigs (≥ 25000 bp) | 66 |
| # contigs (≥ 50000 bp) | 48 |
| Total length (≥ 0 bp) | 9110170 |
| Total length (≥ 1000 bp) | 9058514 |
| Total length (≥ 5000 bp) | 9020683 |
| Total length (≥ 10000 bp) | 8998158 |
| Total length (≥ 25000 bp) | 8853949 |
| Total length (≥ 50000 bp) | 8231677 |
| # contigs | 132 |
| Largest contig | 600951 |
| Total length | 9079929 |
| Reference length | 9283304 |
| N50 | 200817 |
| N75 | 110783 |
| L50 | 16 |
| L75 | 31 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 3 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 97.788 |
| Duplication ratio | 1.000 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 548.81 |
| # indels per 100 kbp | 0.79 |
| Largest alignment | 600951 |
| NA50 | 200817 |
| NA75 | 110783 |
| LA50 | 16 |
| LA75 | 31 |

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 | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 3 |
| # mismatches | 49821 |
| # indels | 72 |
| # short indels | 72 |
| # long indels | 0 |
| Indels length | 72 |

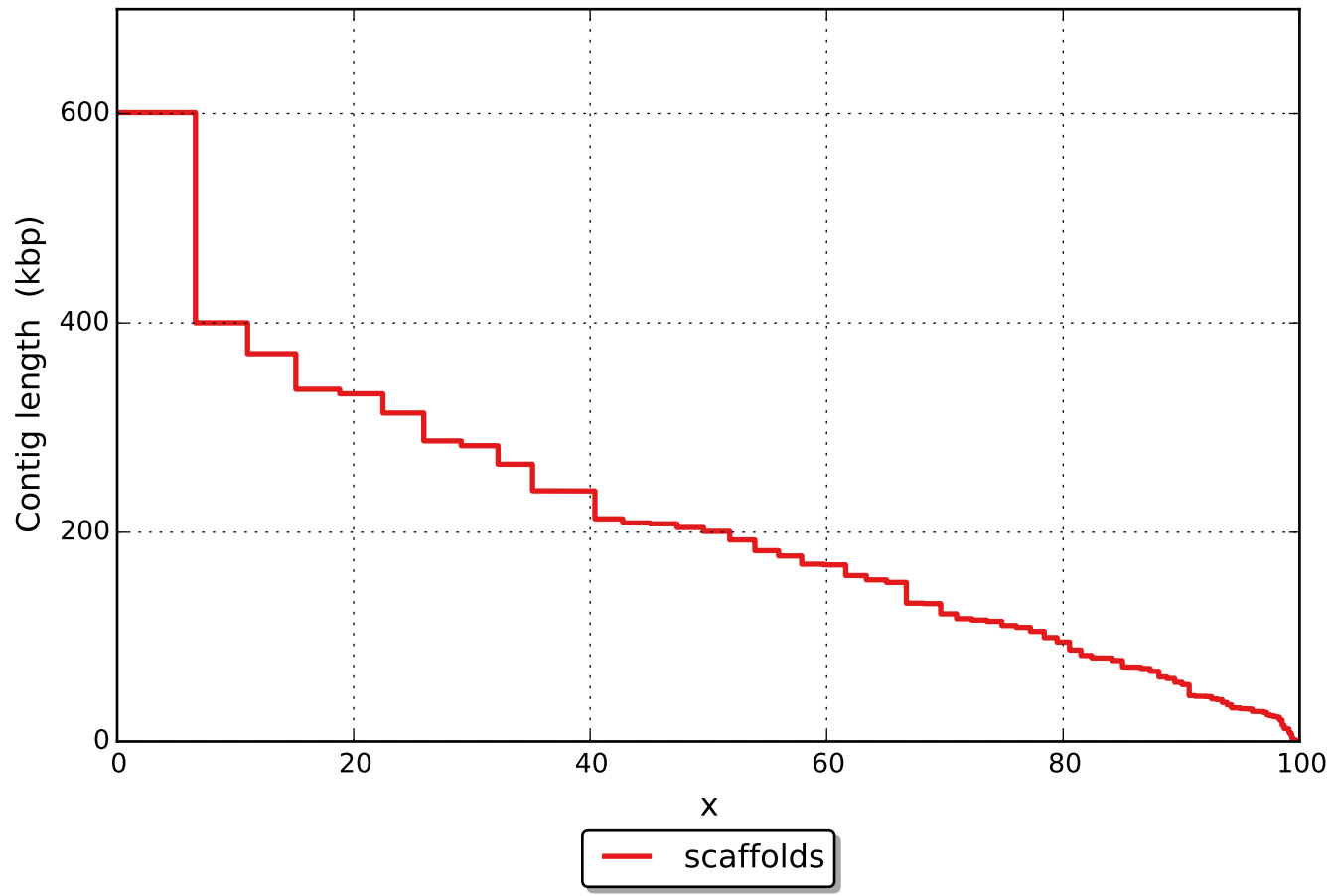
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

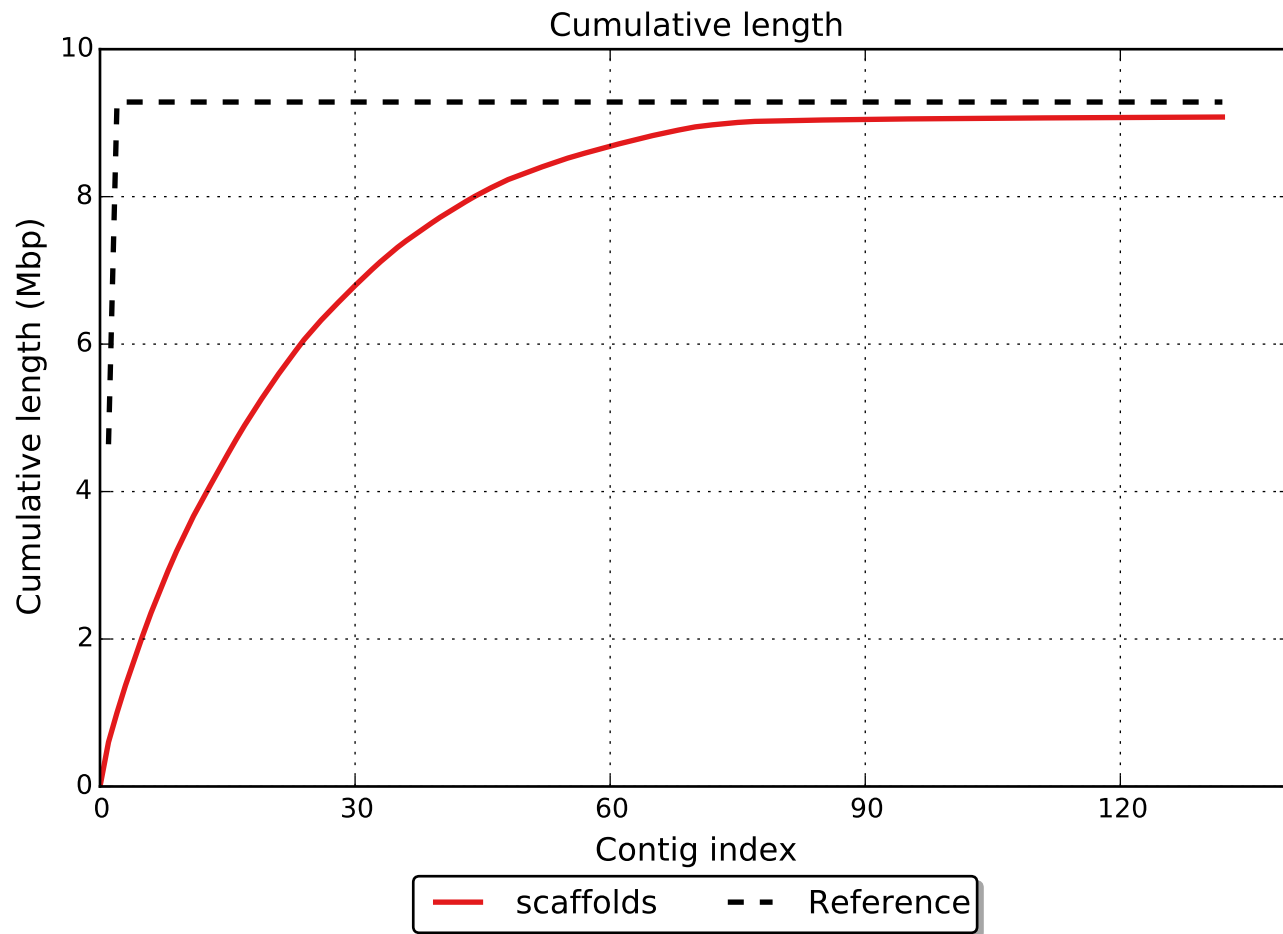
Unaligned report

| | 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 |

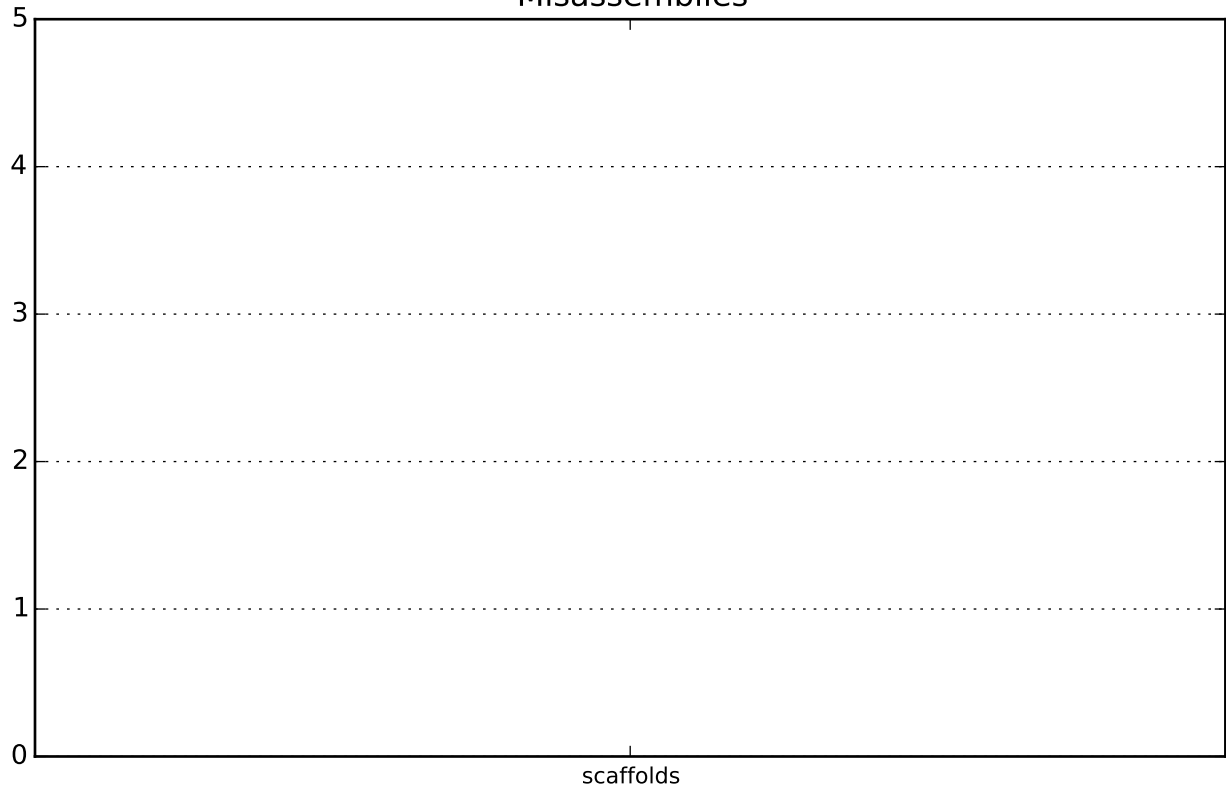
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

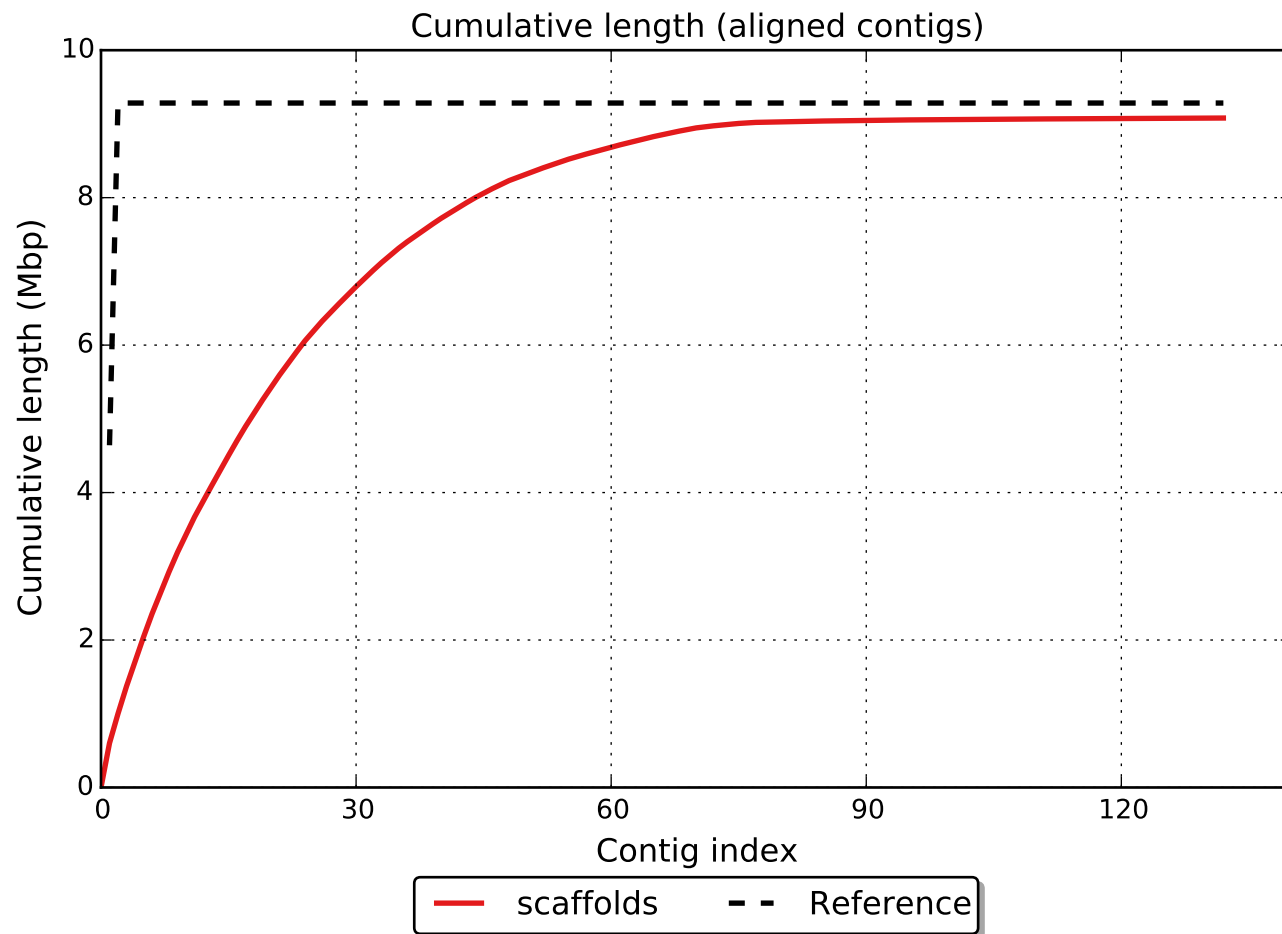
Nx





Misassemblies





NAx

