

Report

| | final.contigs |
|---------------------------------|---------------|
| # contigs (≥ 0 bp) | 9808 |
| # contigs (≥ 1000 bp) | 3477 |
| # contigs (≥ 5000 bp) | 6 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 0 bp) | 9589939 |
| Total length (≥ 1000 bp) | 5981061 |
| Total length (≥ 5000 bp) | 32002 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 7153 |
| Largest contig | 5370 |
| Total length | 8617036 |
| Reference length | 9283304 |
| N50 | 1399 |
| N75 | 908 |
| L50 | 2063 |
| L75 | 3984 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (▼) | 89.983 |
| Duplication ratio | 1.045 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 32.92 |
| # indels per 100 kbp | 0.02 |
| Largest alignment | 5370 |
| NA50 | 1399 |
| NA75 | 908 |
| LA50 | 2063 |
| LA75 | 3984 |

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

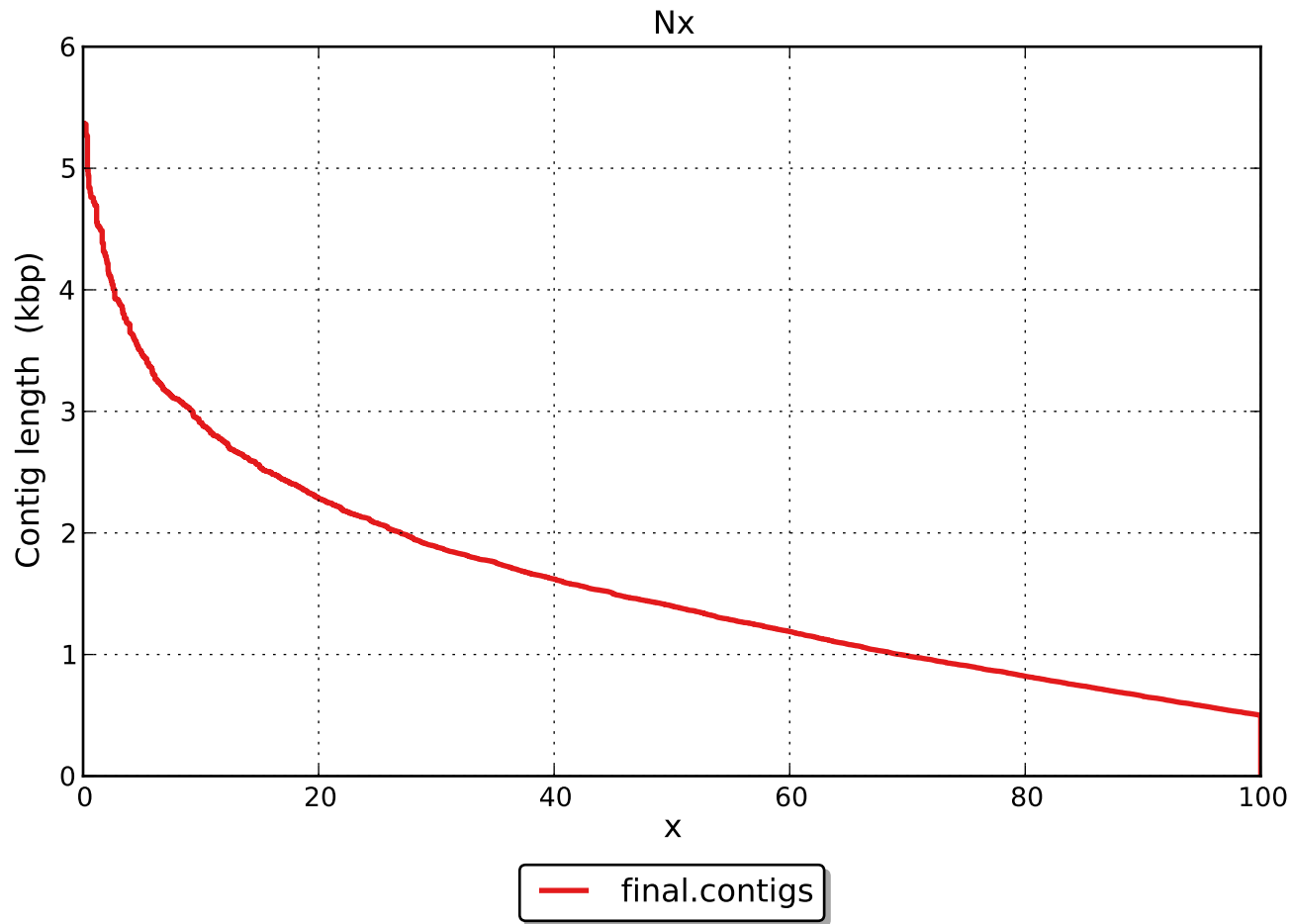
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 2750 |
| # indels | 2 |
| # short indels | 2 |
| # long indels | 0 |
| Indels length | 2 |

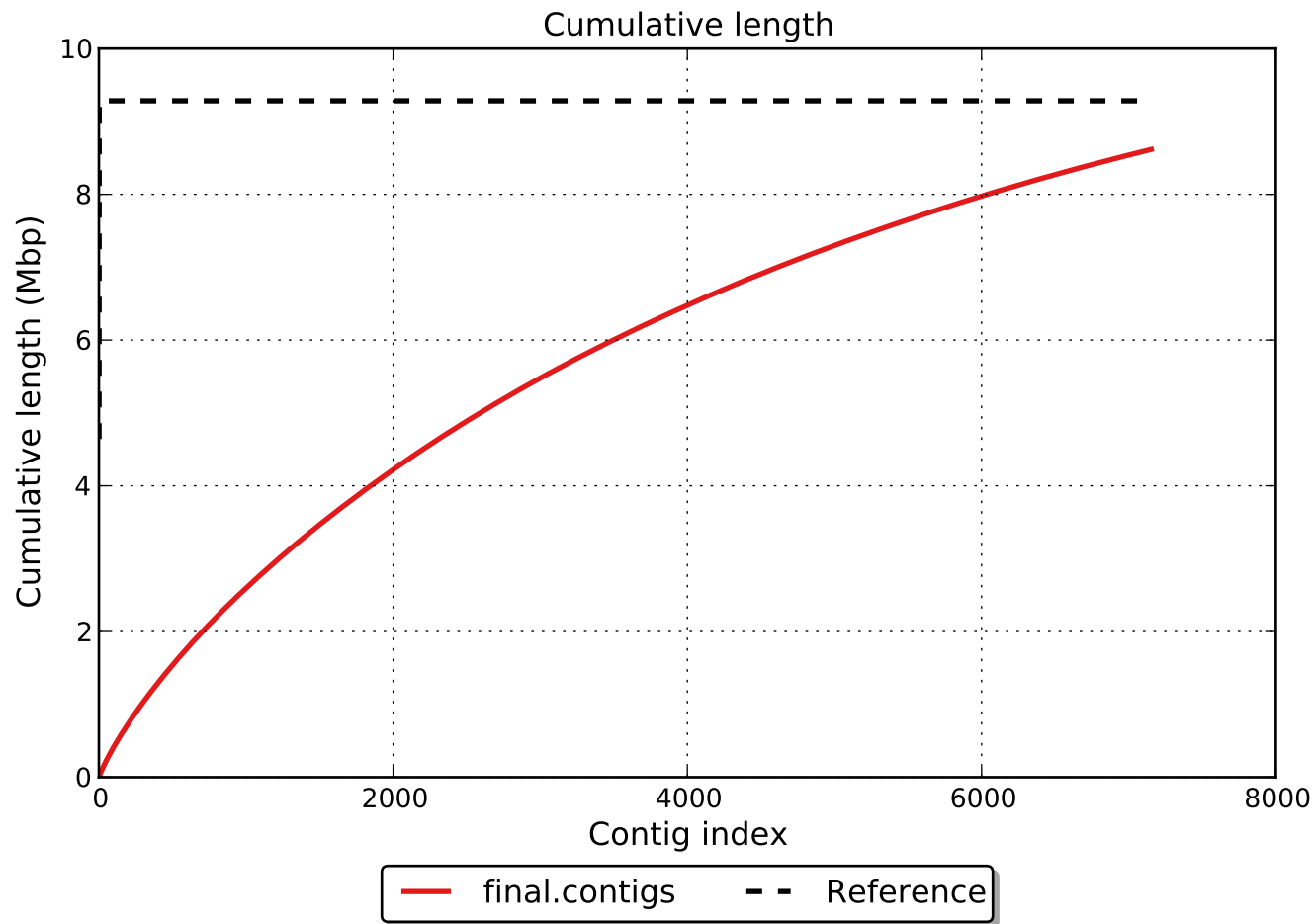
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # 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).





Misassemblies

