

Report

| | final.contigs |
|---------------------------------|---------------|
| # contigs (≥ 0 bp) | 1239 |
| # contigs (≥ 1000 bp) | 731 |
| # contigs (≥ 5000 bp) | 500 |
| # contigs (≥ 10000 bp) | 316 |
| # contigs (≥ 25000 bp) | 104 |
| # contigs (≥ 50000 bp) | 10 |
| Total length (≥ 0 bp) | 9413043 |
| Total length (≥ 1000 bp) | 9226444 |
| Total length (≥ 5000 bp) | 8565283 |
| Total length (≥ 10000 bp) | 7213787 |
| Total length (≥ 25000 bp) | 3889345 |
| Total length (≥ 50000 bp) | 636325 |
| # contigs | 782 |
| Largest contig | 81775 |
| Total length | 9264828 |
| Reference length | 9283304 |
| N50 | 20423 |
| N75 | 10920 |
| L50 | 138 |
| L75 | 291 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 4 |
| # unaligned contigs | 0 + 1 part |
| Unaligned length | 21 |
| Genome fraction (%) | 99.046 |
| Duplication ratio | 1.008 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 11.46 |
| # indels per 100 kbp | 0.04 |
| Largest alignment | 81775 |
| NA50 | 20423 |
| NA75 | 10920 |
| LA50 | 138 |
| LA75 | 291 |

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

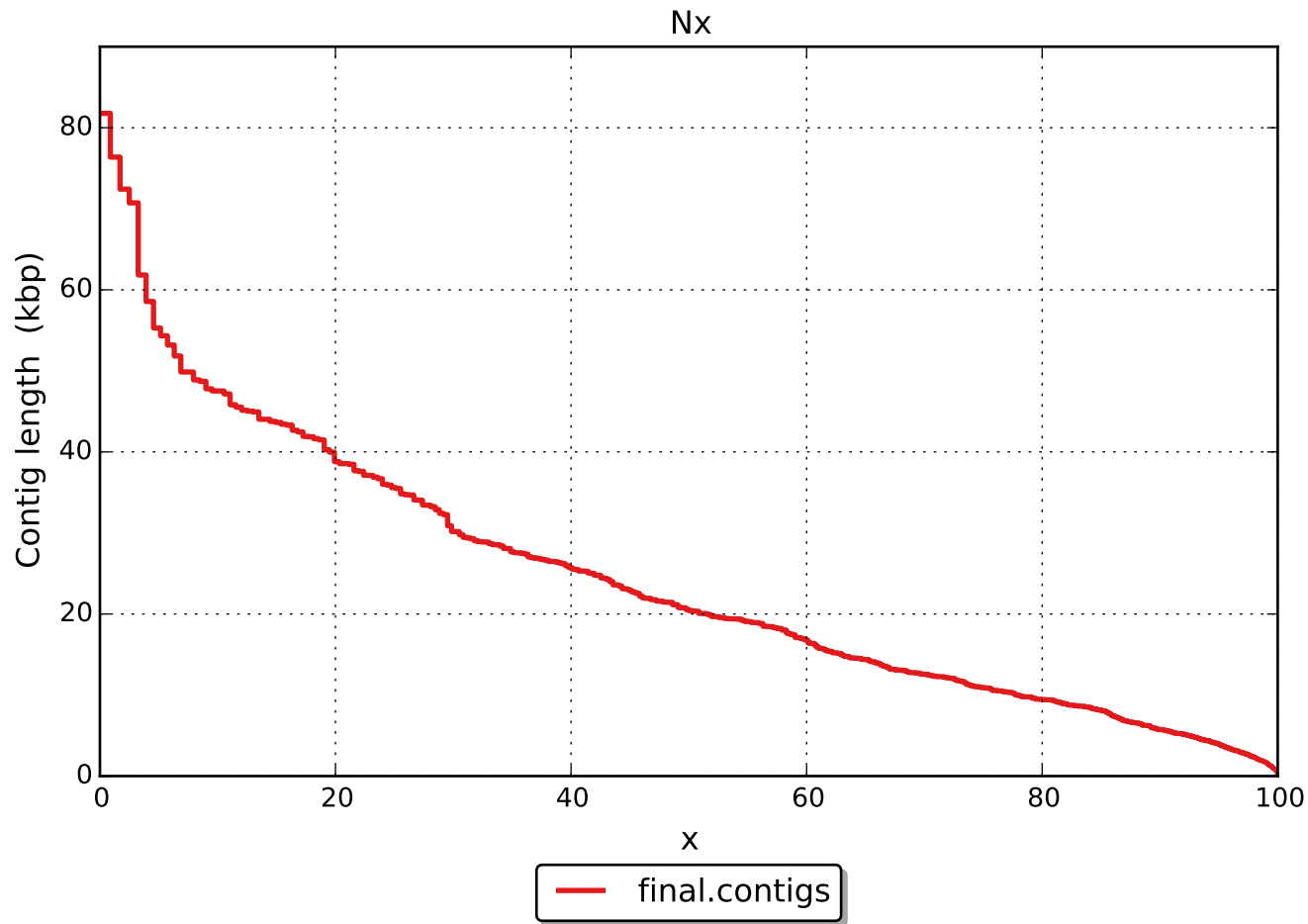
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 4 |
| # mismatches | 1054 |
| # indels | 4 |
| # short indels | 4 |
| # long indels | 0 |
| Indels length | 4 |

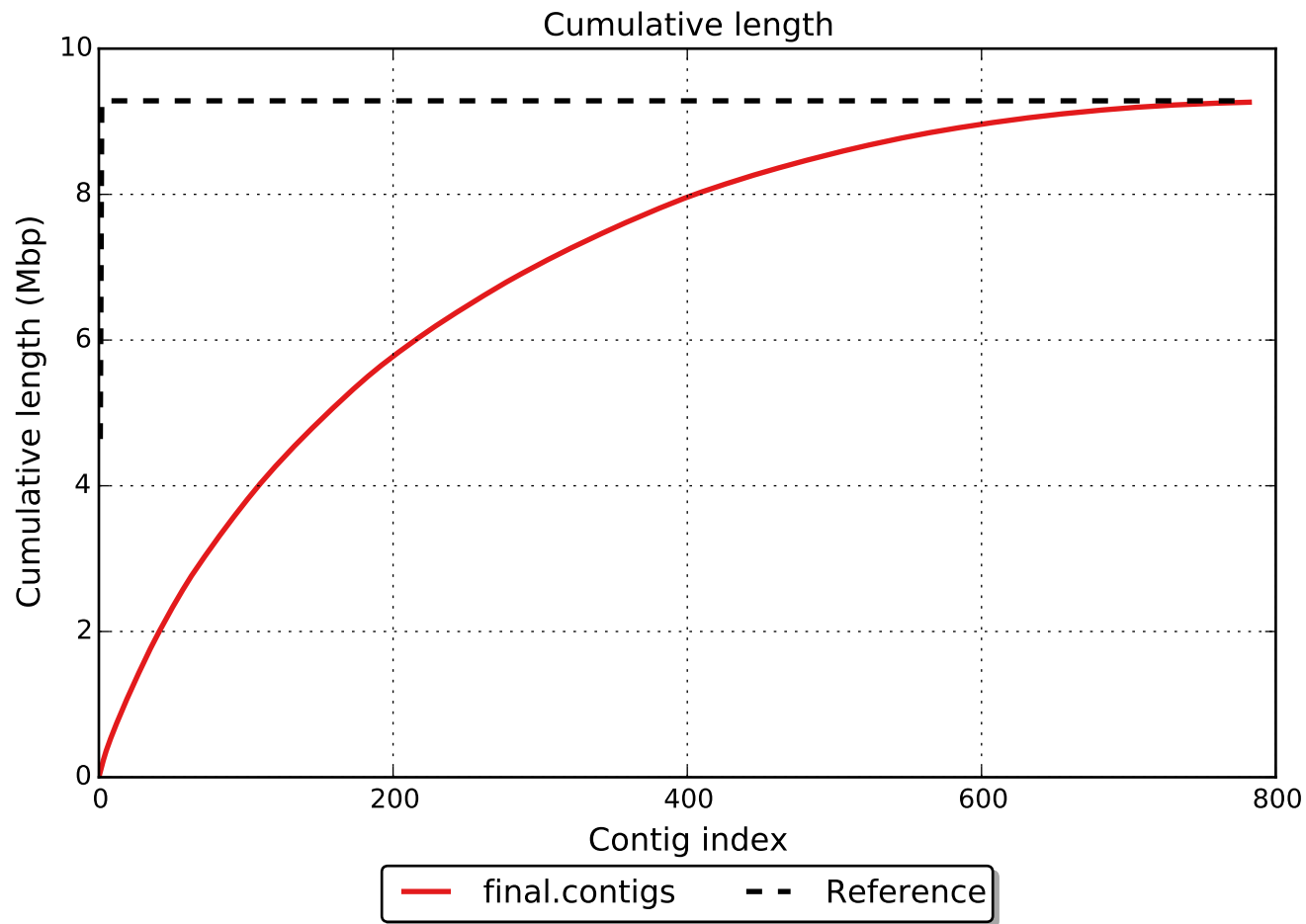
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

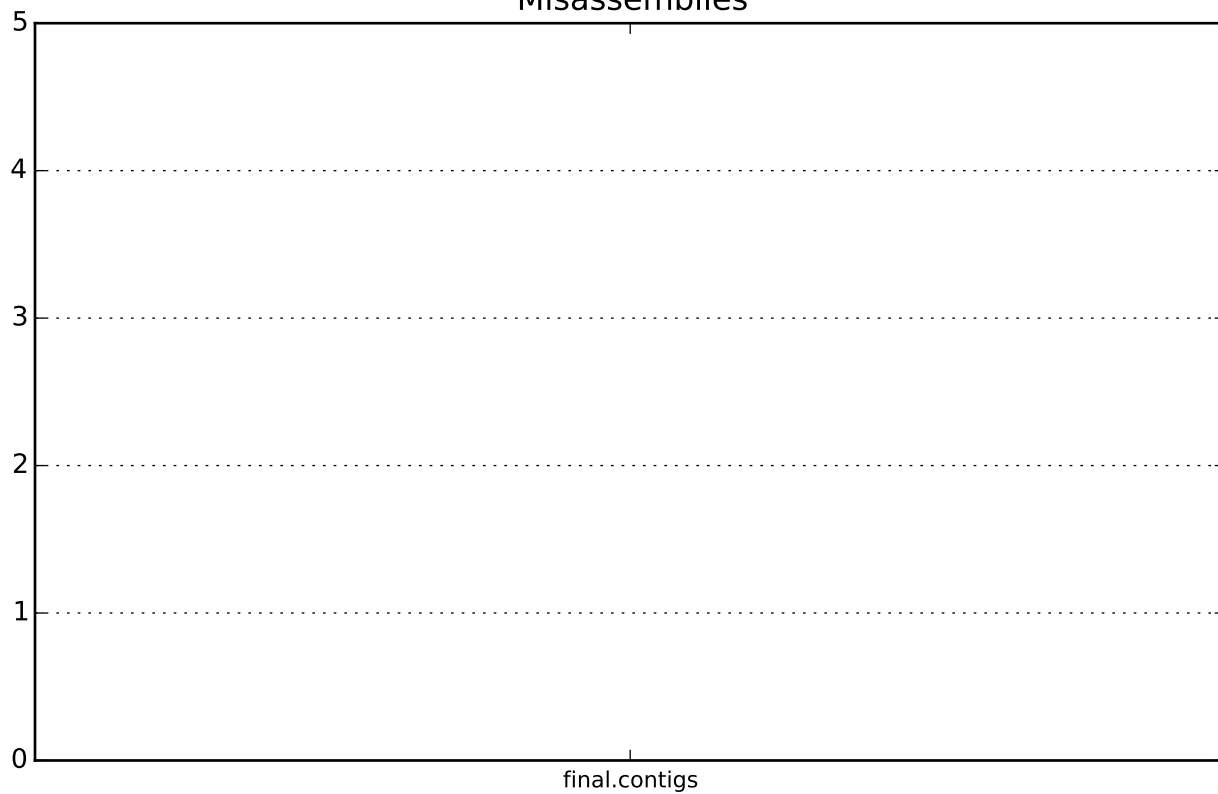
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 21 |
| # N's | 0 |

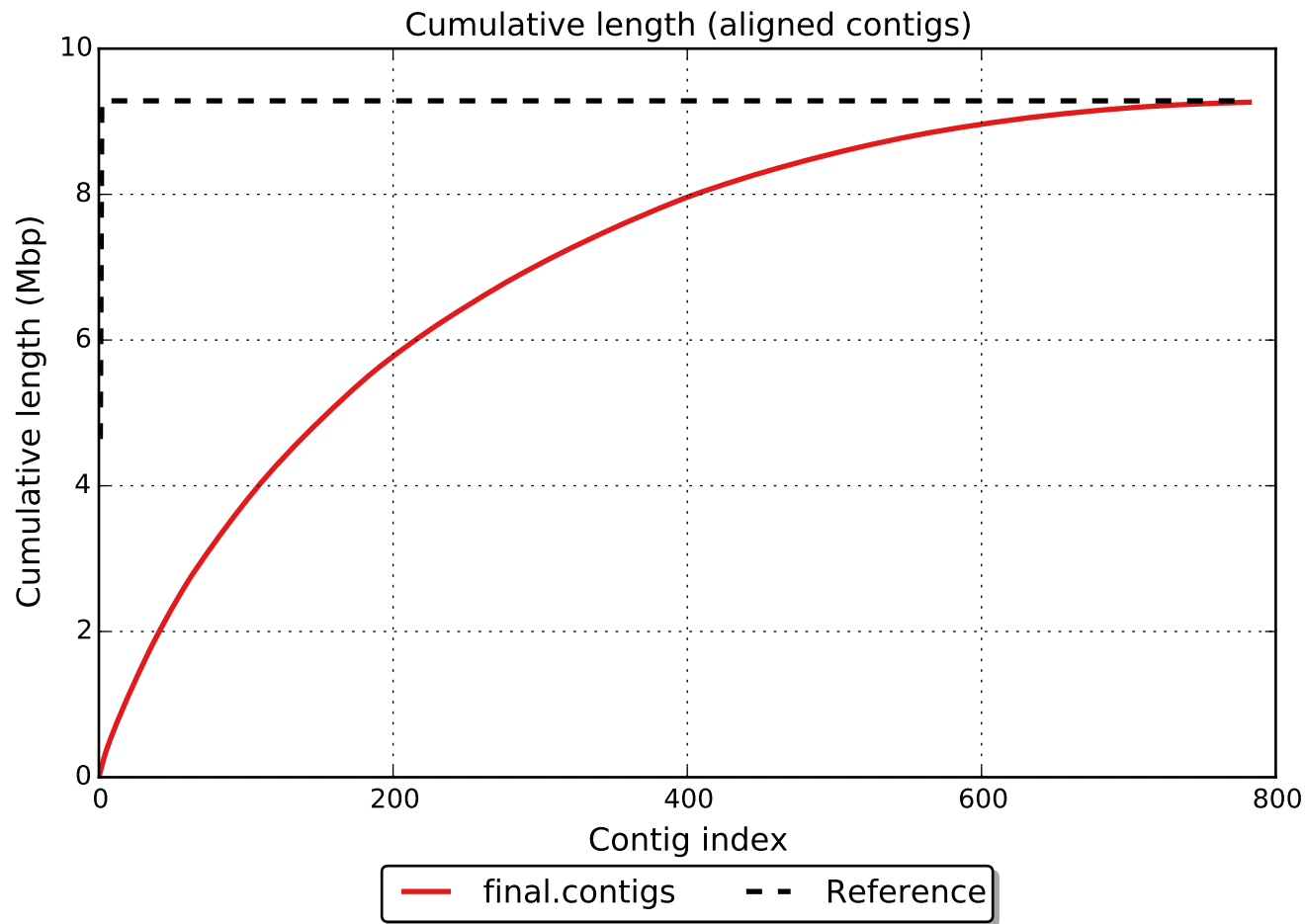
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

