# Report

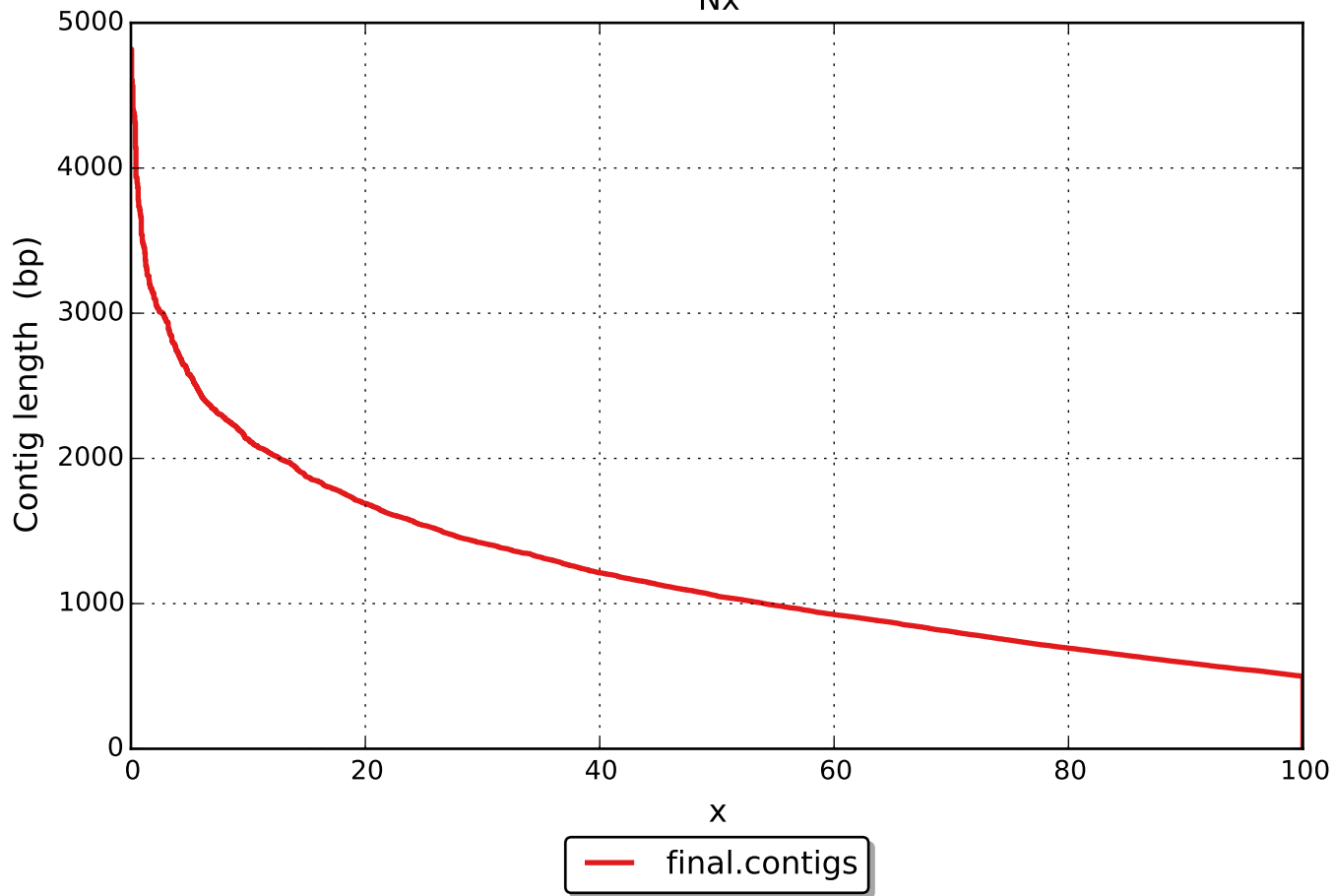| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 13917 |
| # contigs (>= 1000 bp) | 2993 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 10292436 |
| Total length (>= 1000 bp) | 4497321 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 8414 |
| Largest contig | 4818 |
| Total length | 8325679 |
| Reference length | 9714864 |
| N50 | 1052 |
| N75 | 748 |
| L50 | 2668 |
| L75 | 5009 |
| # misassemblies | 4 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 3459 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 2 part |
| Unaligned length | 112 |
| Genome fraction (%) | 81.334 |
| Duplication ratio | 1.054 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 133.43 |
| # indels per 100 kbp | 0.19 |
| Largest alignment | 4818 |
| NA50 | 1052 |
| NA75 | 748 |
| LA50 | 2668 |
| LA75 | 5010 |

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 | 4 |
| # relocations | 2 |
| # translocations | 0 |
| # inversions | 1 |
| # interspecies translocations | 1 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 3459 |
| # local misassemblies | 0 |
| # mismatches | 10543 |
| # indels | 15 |
| # short indels | 15 |
| # long indels | 0 |
| Indels length | 15 |

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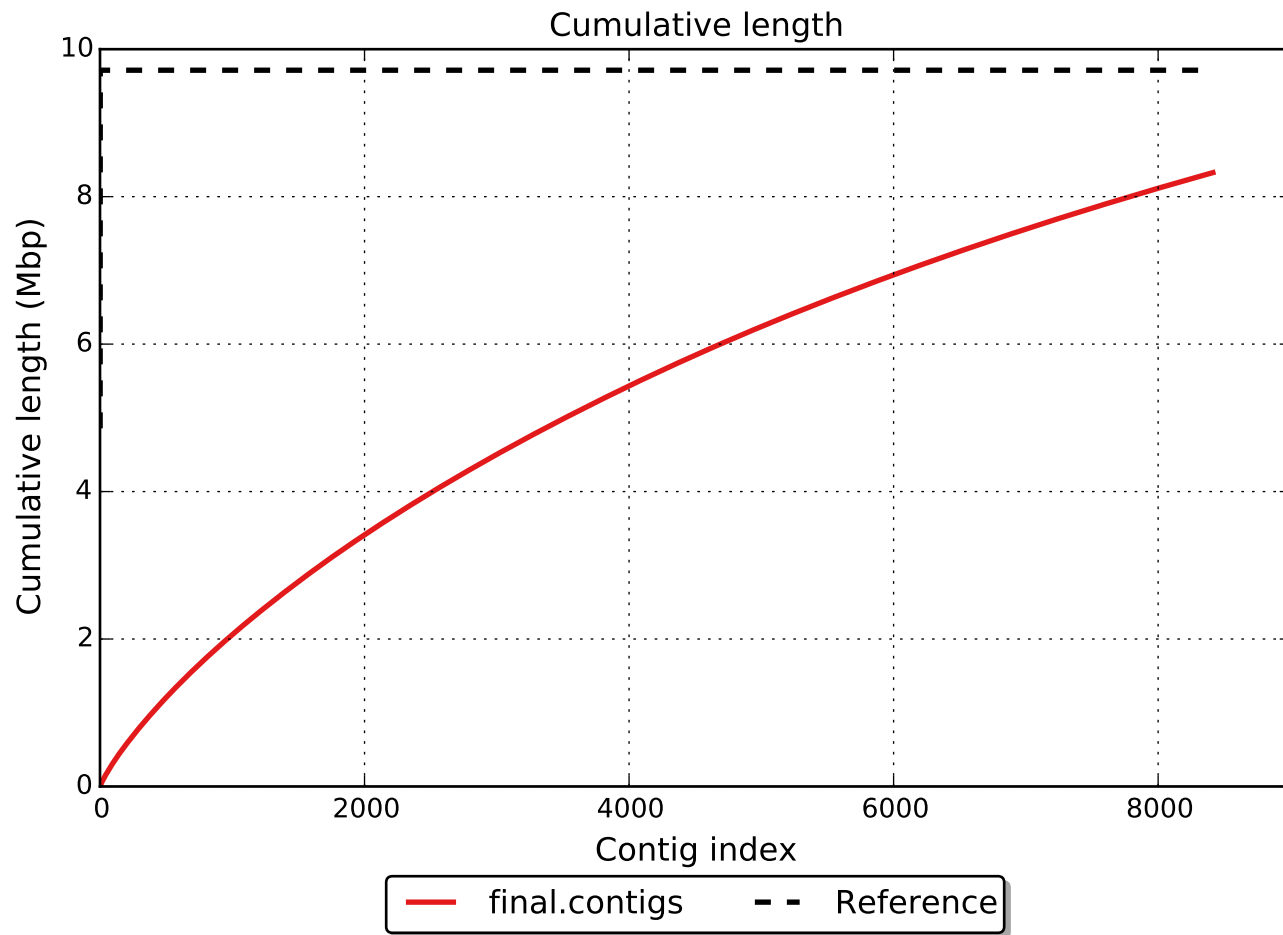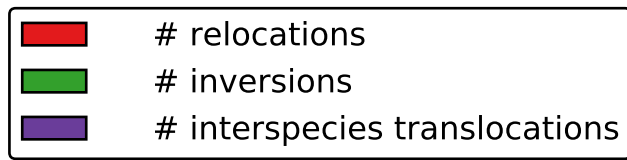(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

# Unaligned report

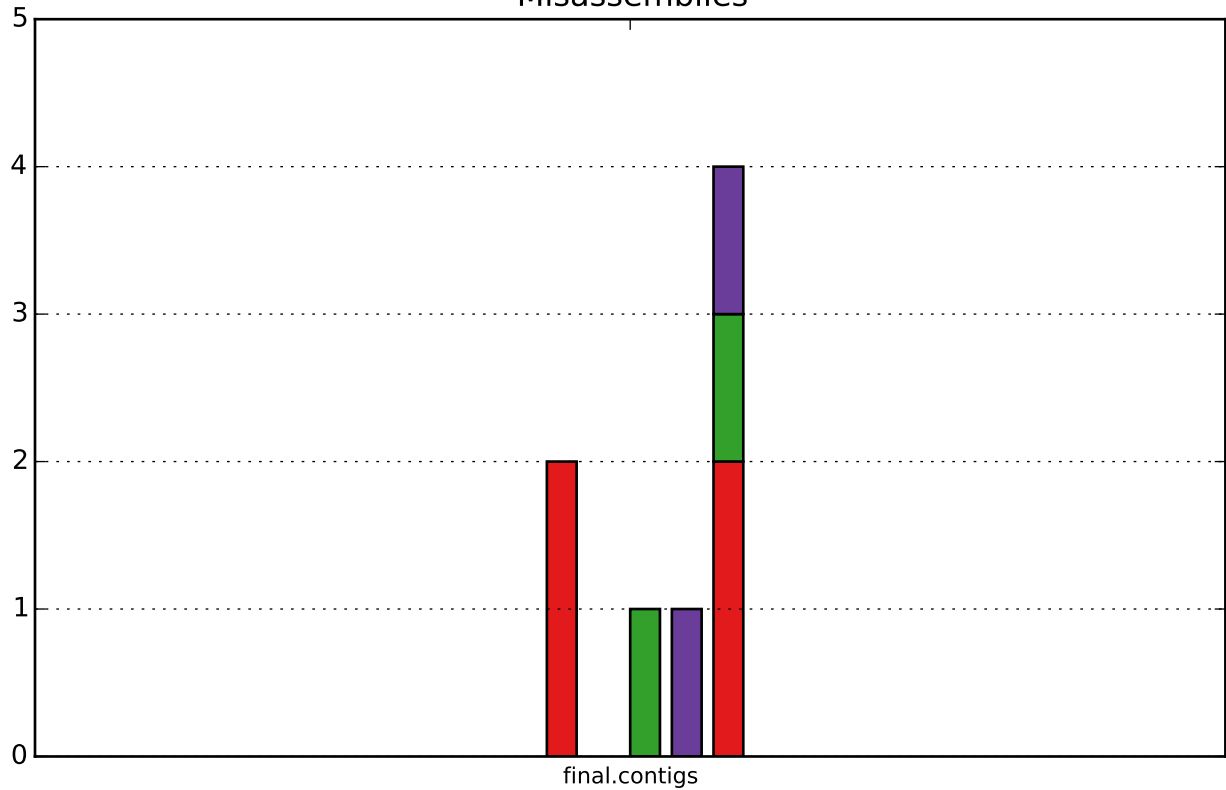| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 2 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 112 |
| # N's | 0 |

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).

Cumulative length
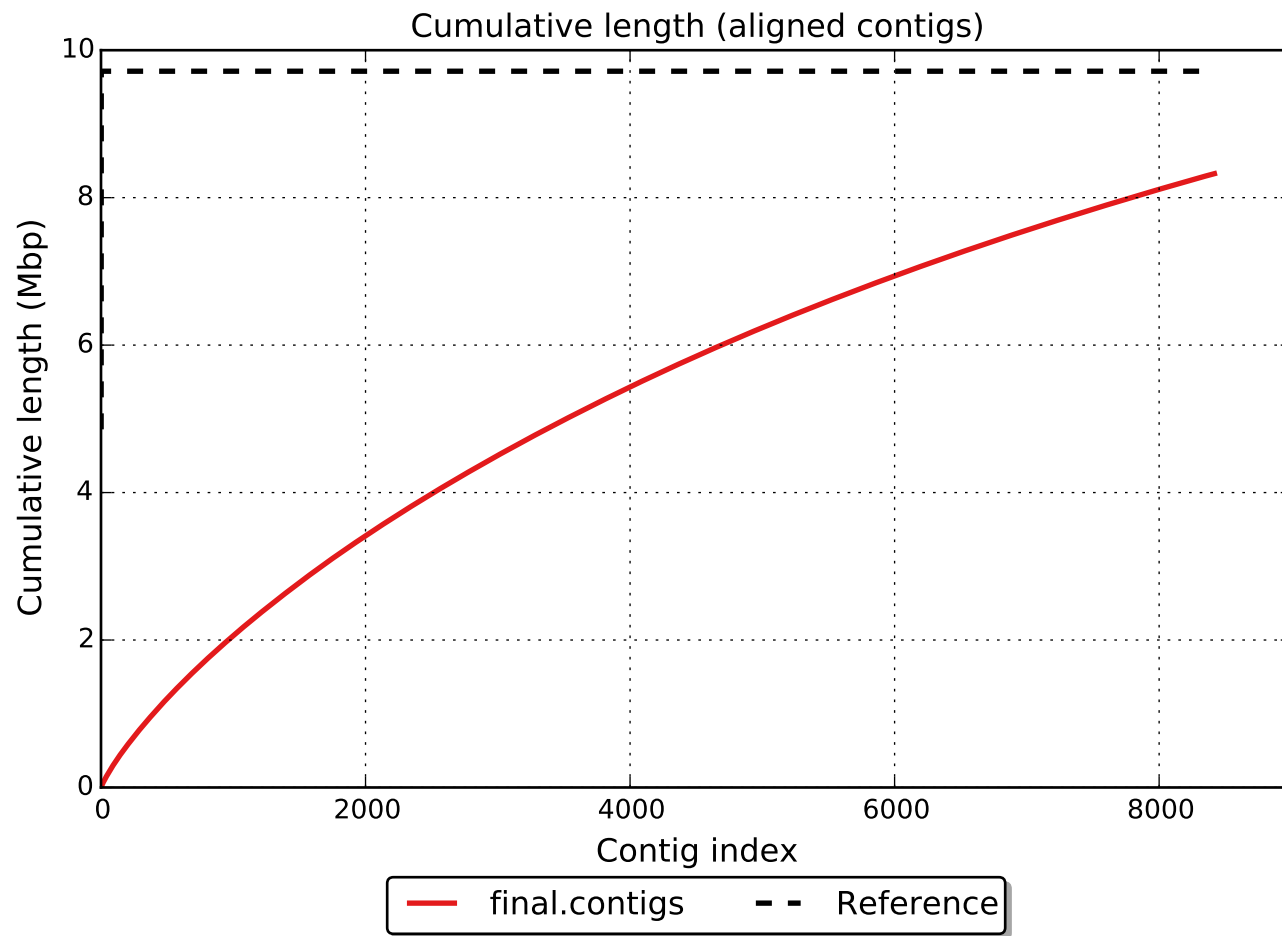
Misassemblies

final.contigs

- # relocations
- # inversions
- # interspecies translocations

Cumulative length (aligned contigs)