

Report

| | meta_contigs_1 | meta_contigs_2 |
|-----------------------------|----------------|----------------|
| # contigs (>= 1000 bp) | 2 | 2 |
| # contigs (>= 5000 bp) | 1 | 1 |
| # contigs (>= 10000 bp) | 1 | 1 |
| # contigs (>= 25000 bp) | 1 | 1 |
| # contigs (>= 50000 bp) | 1 | 1 |
| Total length (>= 1000 bp) | 56247 | 58868 |
| Total length (>= 5000 bp) | 55106 | 55421 |
| Total length (>= 10000 bp) | 55106 | 55421 |
| Total length (>= 25000 bp) | 55106 | 55421 |
| Total length (>= 50000 bp) | 55106 | 55421 |
| # contigs | 5 | 2 |
| Largest contig | 55106 | 55421 |
| Total length | 58663 | 58868 |
| Reference length | 59999 | 59999 |
| GC (%) | 50.17 | 50.19 |
| Reference GC (%) | 50.25 | 50.25 |
| N50 | 55106 | 55421 |
| NG50 | 55106 | 55421 |
| N75 | 55106 | 55421 |
| NG75 | 55106 | 55421 |
| L50 | 1 | 1 |
| LG50 | 1 | 1 |
| L75 | 1 | 1 |
| LG75 | 1 | 1 |
| # misassemblies | 0 | 0 |
| # misassembled contigs | 0 | 0 |
| Misassembled contigs length | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # unaligned contigs | 0 + 0 part | 0 + 0 part |
| Unaligned length | 0 | 0 |
| Genome fraction (%) | 97.575 | 98.115 |
| Duplication ratio | 1.002 | 1.000 |
| # N's per 100 kbp | 1.70 | 0.00 |
| # mismatches per 100 kbp | 23.91 | 25.48 |
| # indels per 100 kbp | 0.00 | 0.00 |
| Largest alignment | 55106 | 55421 |
| Total aligned length | 58663 | 58868 |
| NA50 | 55106 | 55421 |
| NGA50 | 55106 | 55421 |
| NA75 | 55106 | 55421 |
| NGA75 | 55106 | 55421 |
| LA50 | 1 | 1 |
| LGA50 | 1 | 1 |
| LA75 | 1 | 1 |
| LGA75 | 1 | 1 |

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

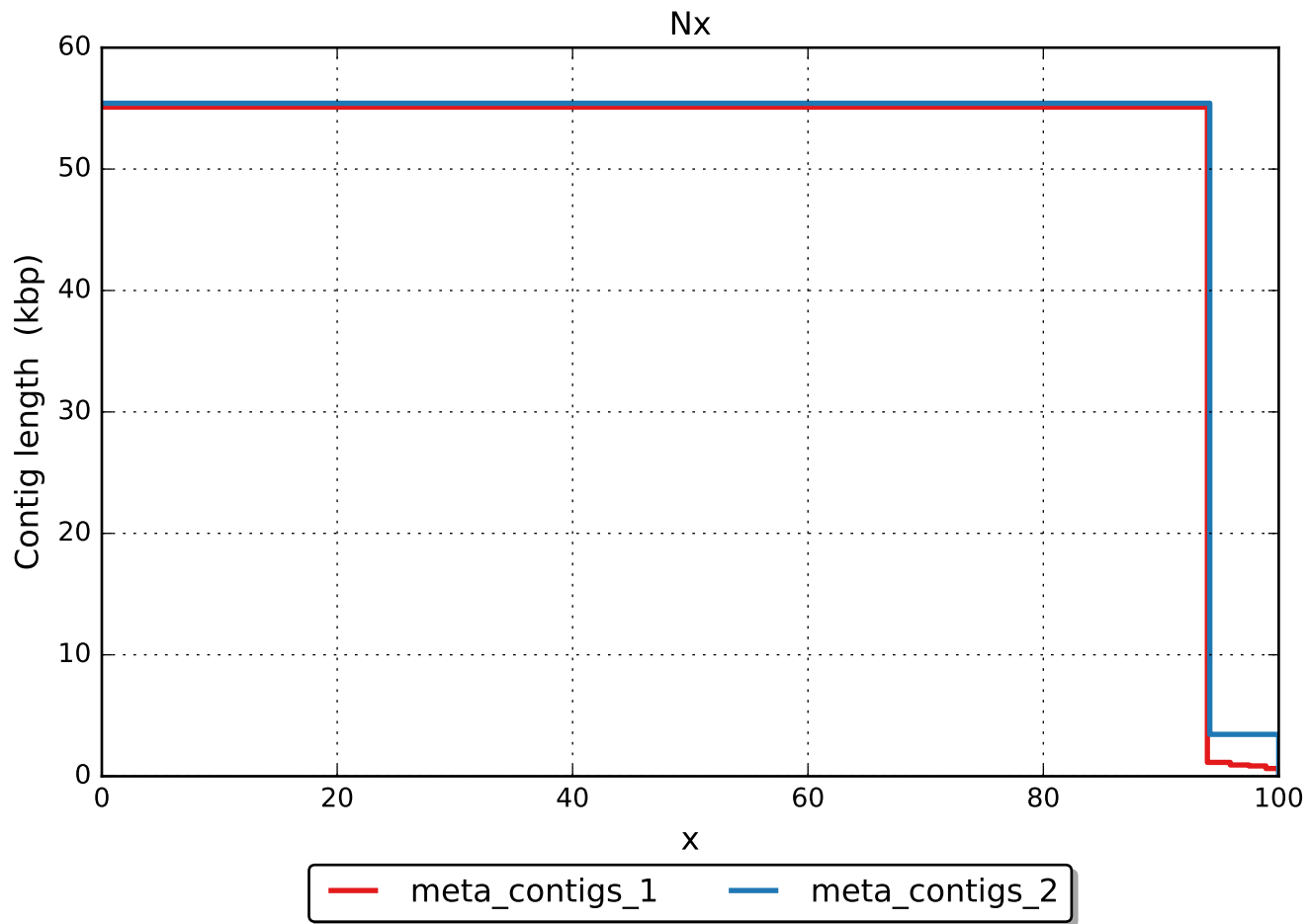
| | meta_contigs_1 | meta_contigs_2 |
|---------------------------------|----------------|----------------|
| # misassemblies | 0 | 0 |
| # relocations | 0 | 0 |
| # translocations | 0 | 0 |
| # inversions | 0 | 0 |
| # possibly misassembled contigs | 0 | 0 |
| # misassembled contigs | 0 | 0 |
| Misassembled contigs length | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # mismatches | 14 | 15 |
| # indels | 0 | 0 |
| # indels (≤ 5 bp) | 0 | 0 |
| # indels (> 5 bp) | 0 | 0 |
| Indels length | 0 | 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).

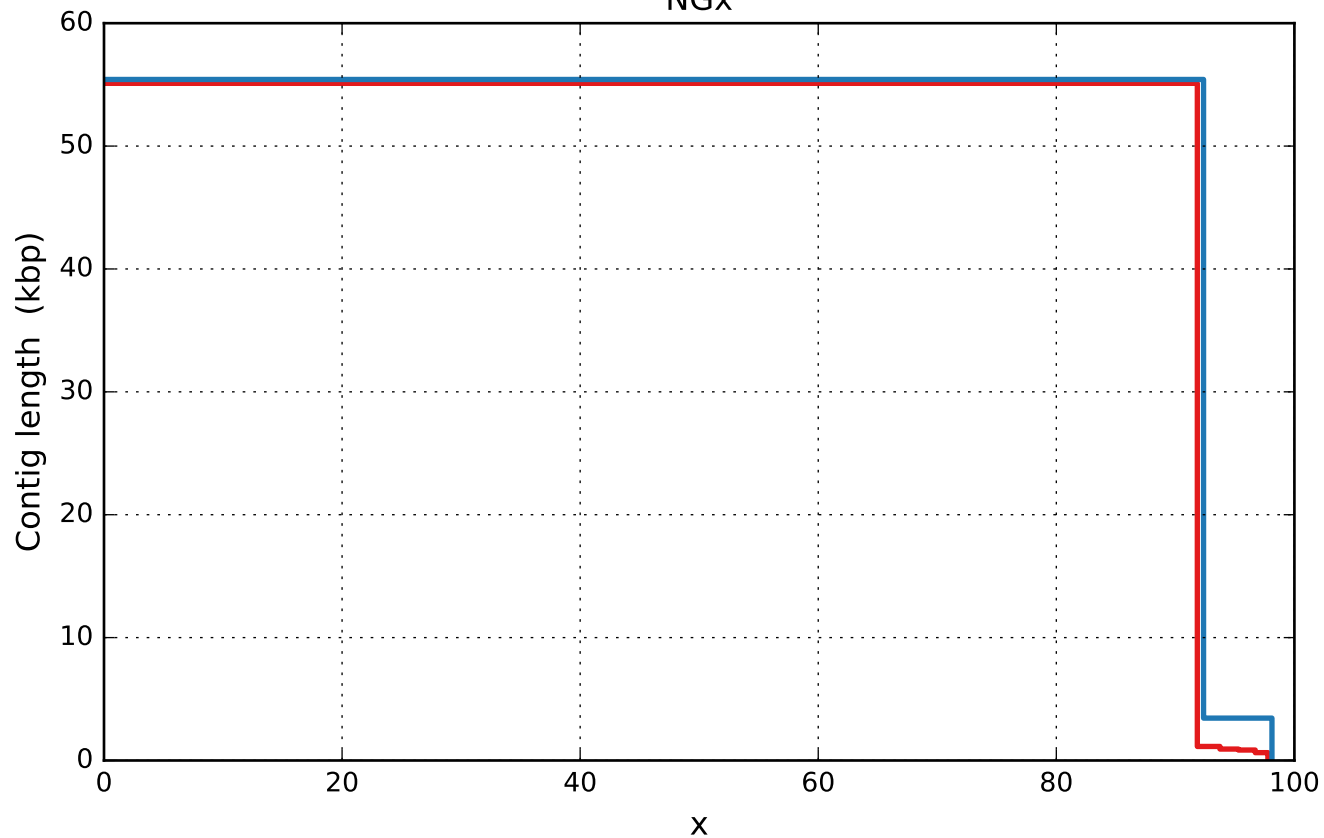
Unaligned report

| | meta_contigs_1 | meta_contigs_2 |
|-------------------------------|----------------|----------------|
| # fully unaligned contigs | 0 | 0 |
| Fully unaligned length | 0 | 0 |
| # partially unaligned contigs | 0 | 0 |
| # with misassembly | 0 | 0 |
| # both parts are significant | 0 | 0 |
| Partially unaligned length | 0 | 0 |
| # N's | 1 | 0 |

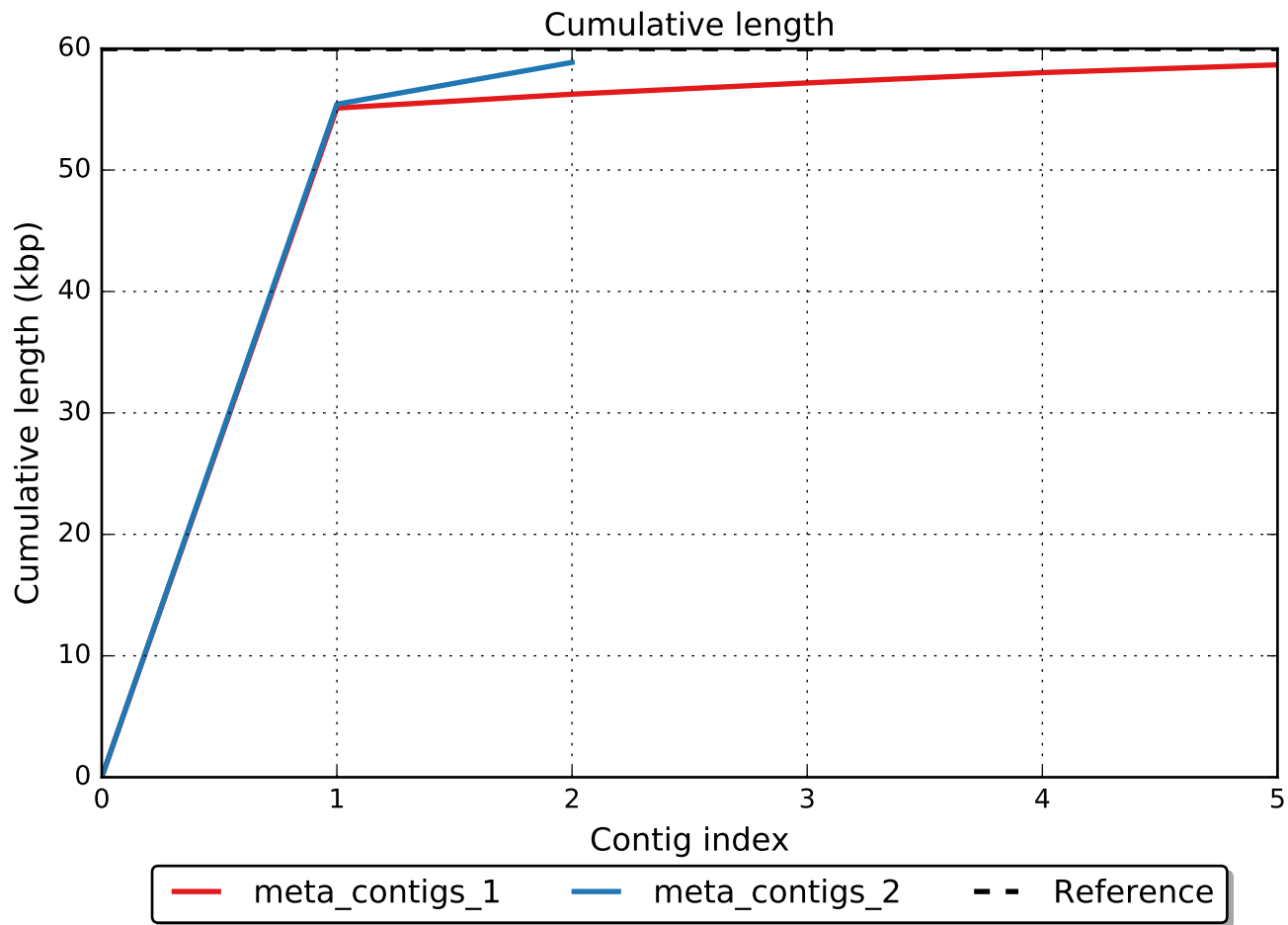
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

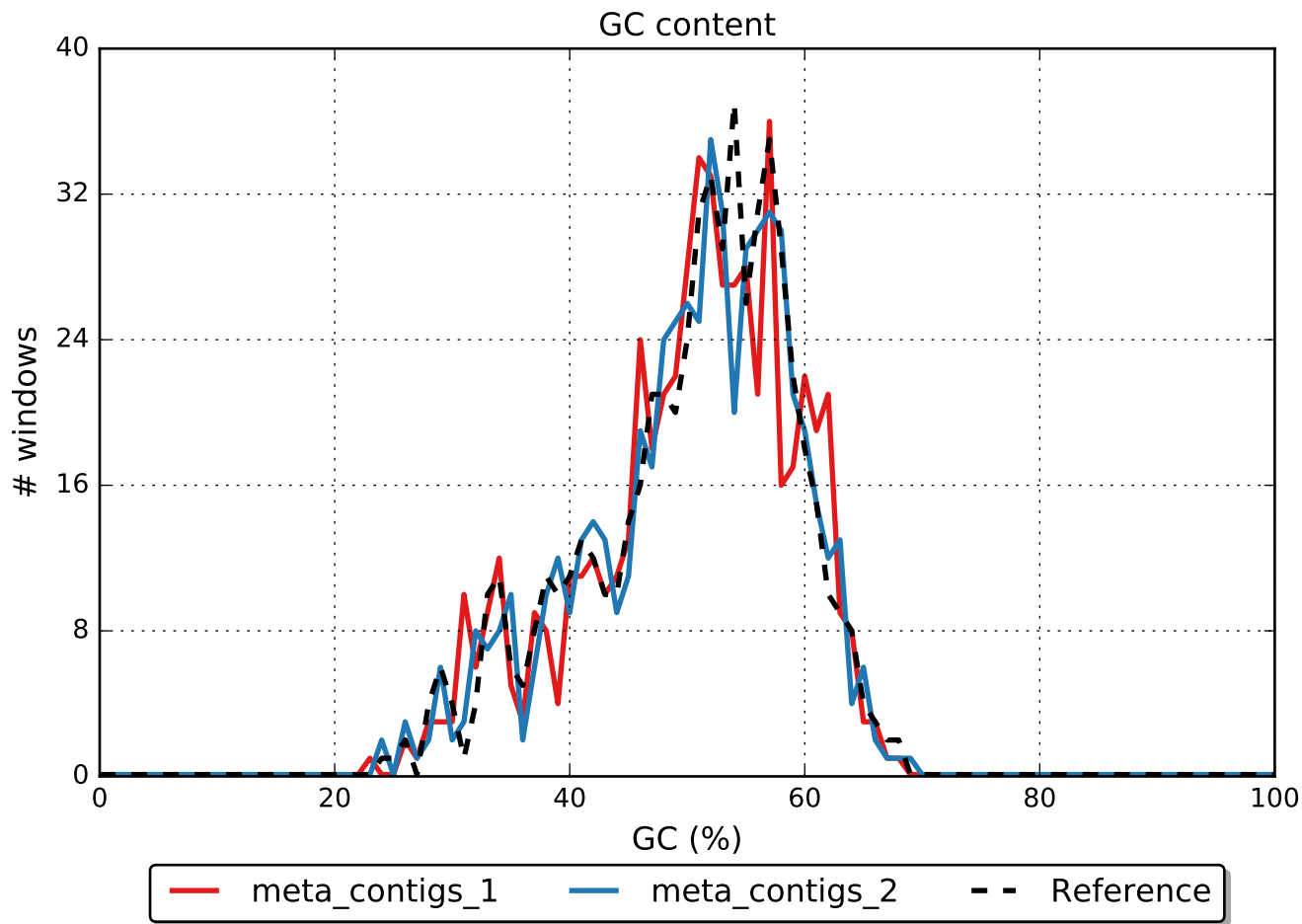


NGx

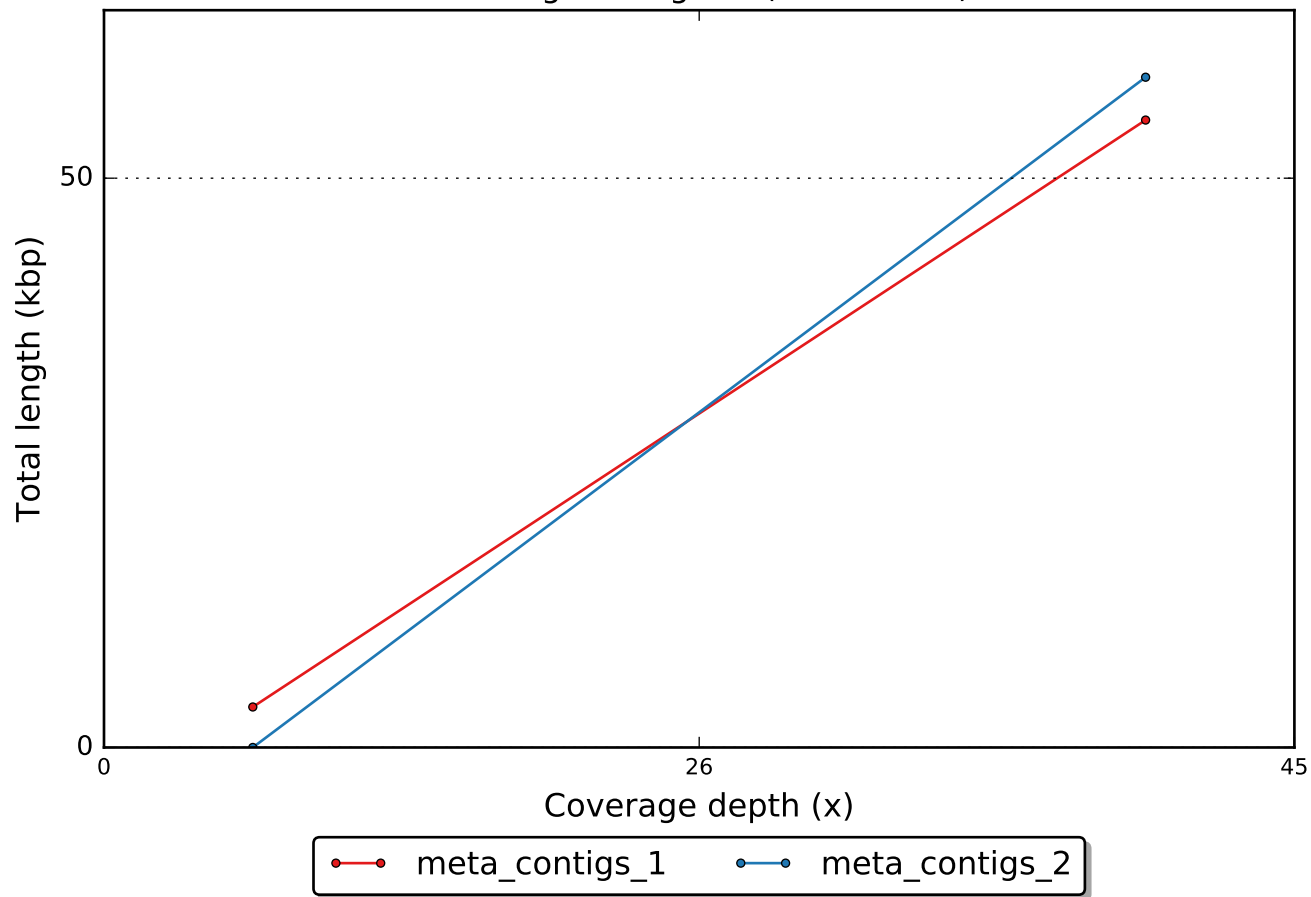


— meta_contigs_1 — meta_contigs_2

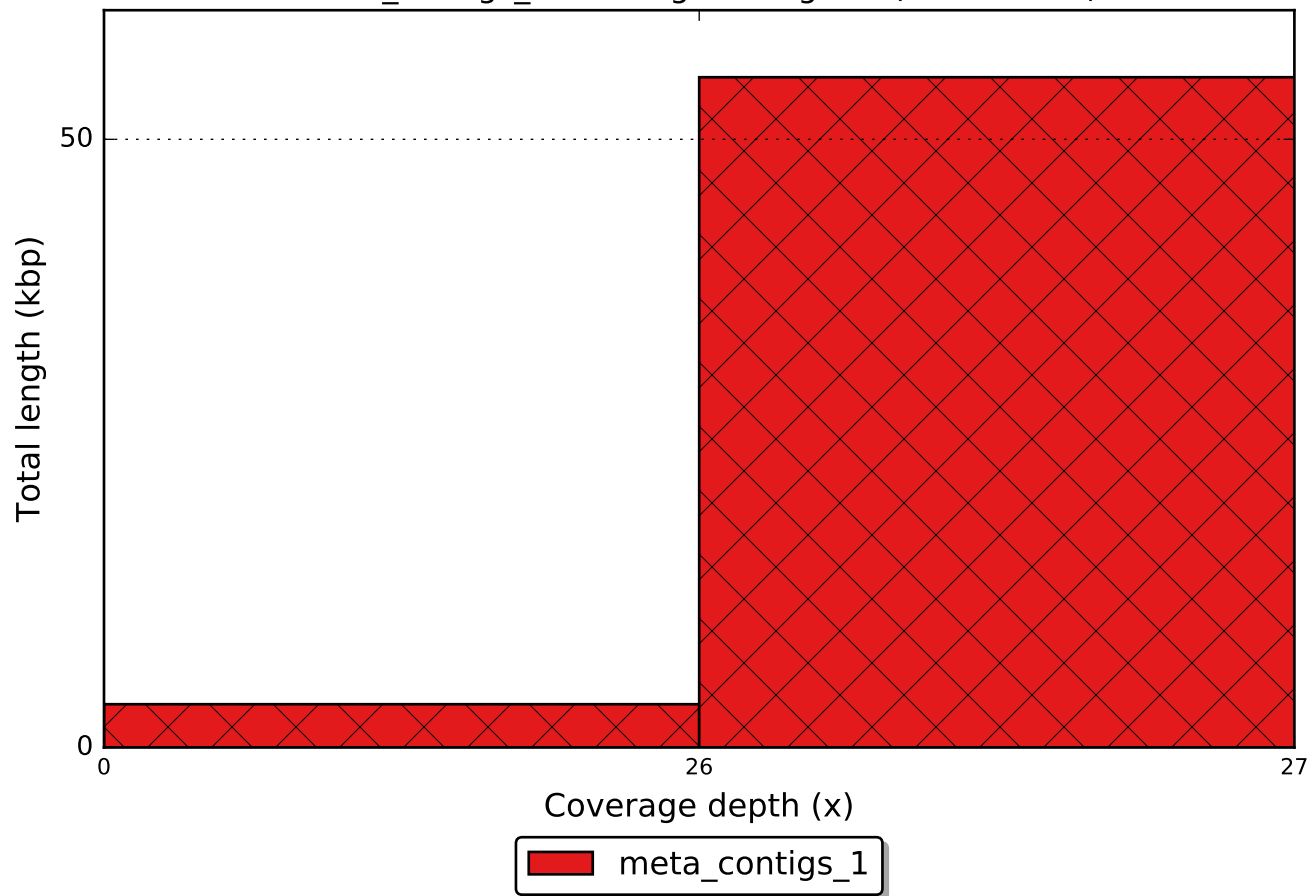




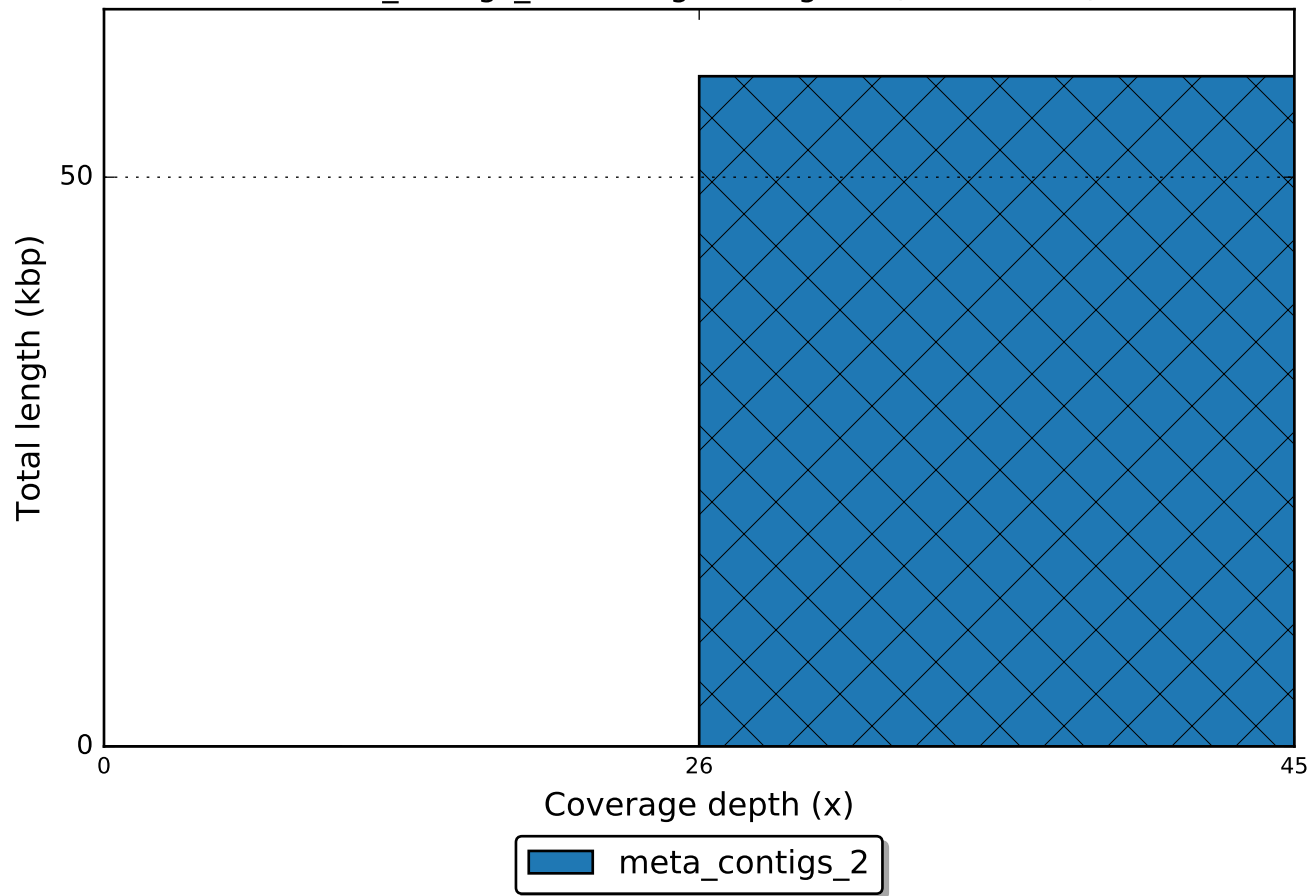
Coverage histogram (bin size: 1x)

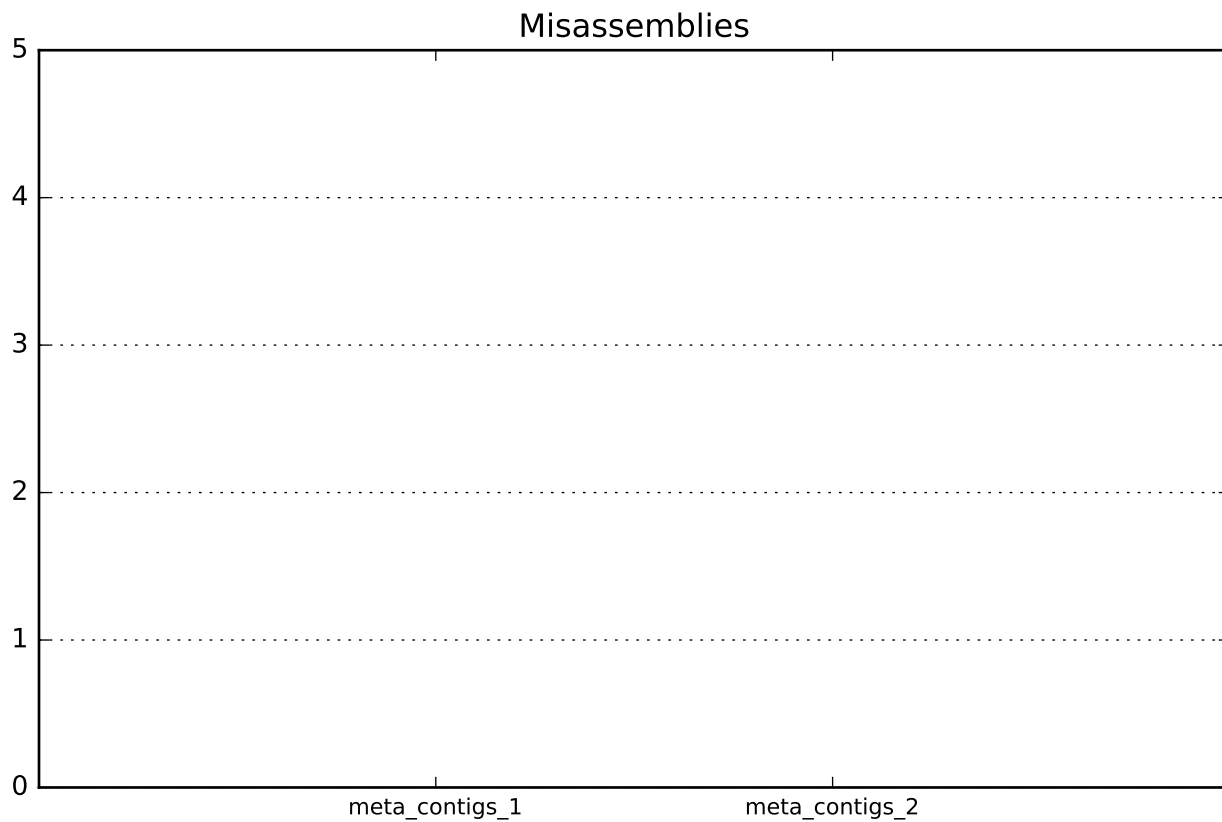


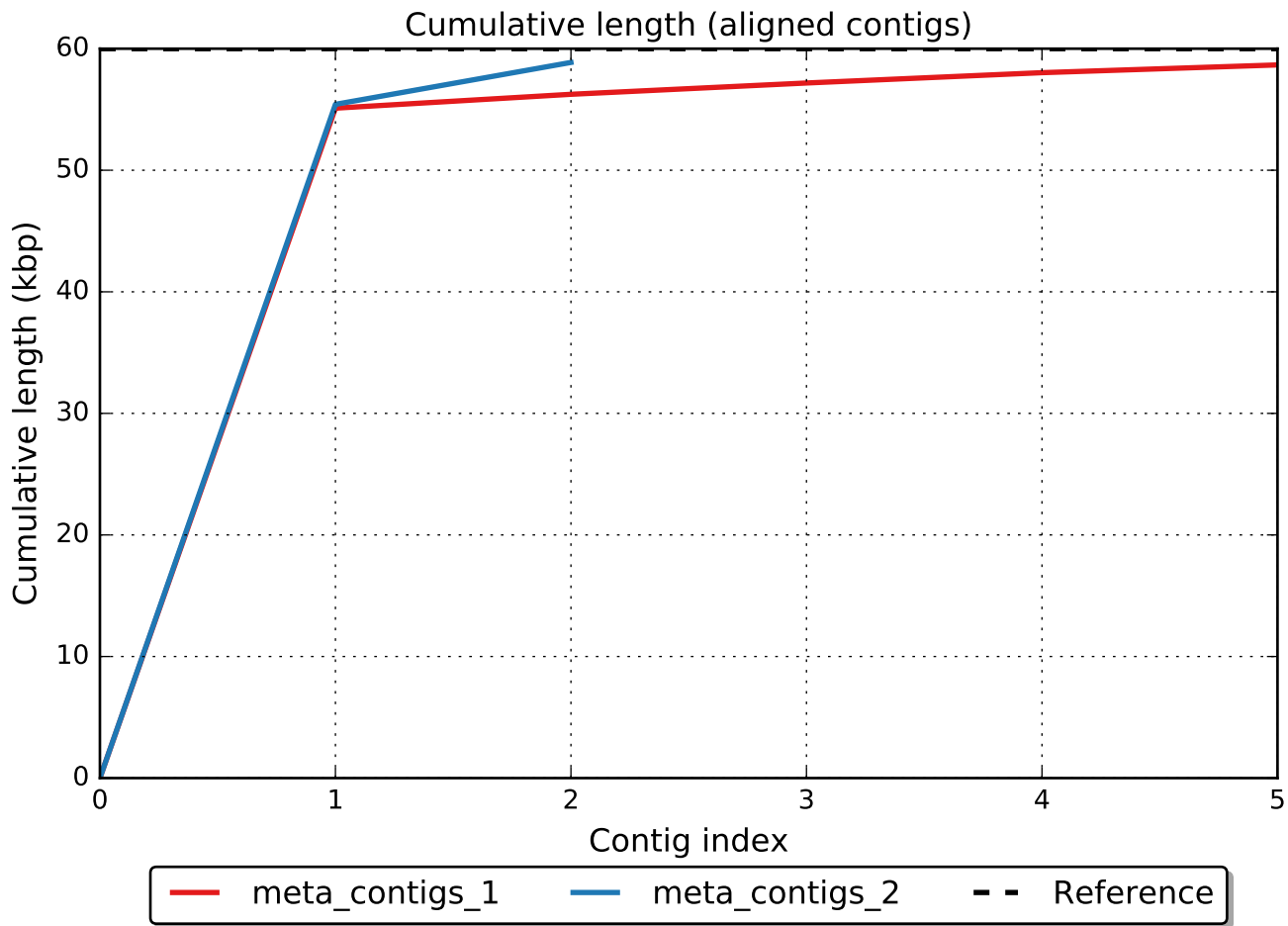
meta_contigs_1 coverage histogram (bin size: 1x)

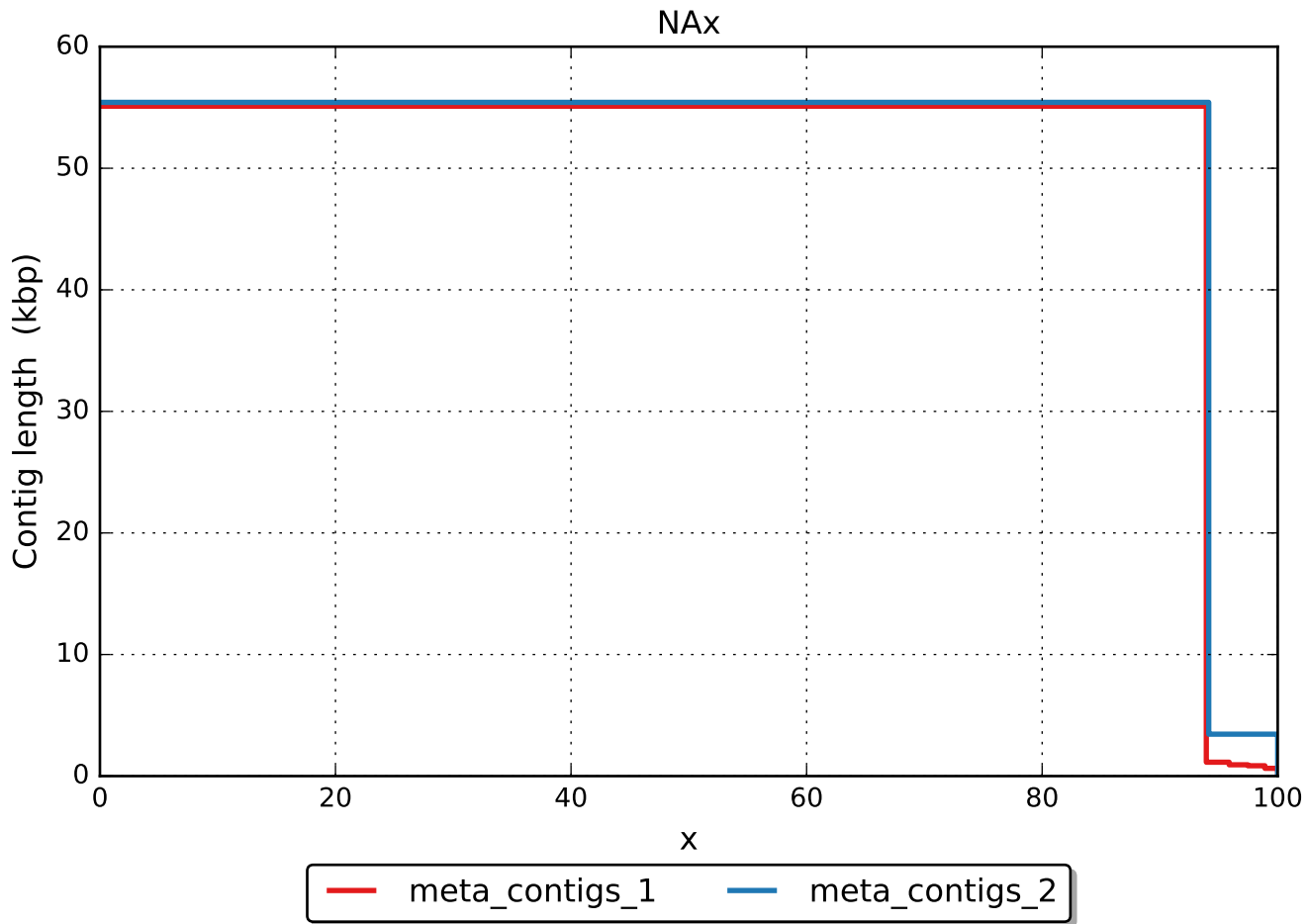


meta_contigs_2 coverage histogram (bin size: 1x)









NGAx

