

Report

| | meta_contigs_1 | meta_contigs_2 |
|-----------------------------|----------------|----------------|
| # contigs (>= 1000 bp) | 2 | 1 |
| # contigs (>= 5000 bp) | 1 | 1 |
| # contigs (>= 10000 bp) | 1 | 1 |
| # contigs (>= 25000 bp) | 1 | 1 |
| # contigs (>= 50000 bp) | 0 | 0 |
| Total length (>= 1000 bp) | 49610 | 49658 |
| Total length (>= 5000 bp) | 48458 | 49658 |
| Total length (>= 10000 bp) | 48458 | 49658 |
| Total length (>= 25000 bp) | 48458 | 49658 |
| Total length (>= 50000 bp) | 0 | 0 |
| # contigs | 3 | 3 |
| Largest contig | 48458 | 49658 |
| Total length | 50324 | 51135 |
| Reference length | 54999 | 54999 |
| GC (%) | 45.77 | 45.73 |
| Reference GC (%) | 45.96 | 45.96 |
| N50 | 48458 | 49658 |
| NG50 | 48458 | 49658 |
| N75 | 48458 | 49658 |
| NG75 | 48458 | 49658 |
| L50 | 1 | 1 |
| LG50 | 1 | 1 |
| L75 | 1 | 1 |
| LG75 | 1 | 1 |
| # misassemblies | 1 | 0 |
| # misassembled contigs | 1 | 0 |
| Misassembled contigs length | 48458 | 0 |
| # local misassemblies | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 1 | 0 |
| # unaligned contigs | 0 + 1 part | 0 + 0 part |
| Unaligned length | 665 | 0 |
| Genome fraction (%) | 90.254 | 91.920 |
| Duplication ratio | 1.000 | 1.011 |
| # N's per 100 kbp | 39.74 | 0.00 |
| # mismatches per 100 kbp | 26.19 | 25.71 |
| # indels per 100 kbp | 0.00 | 0.00 |
| Largest alignment | 37178 | 49658 |
| Total aligned length | 49639 | 50555 |
| NA50 | 37178 | 49658 |
| NGA50 | 37178 | 49658 |
| NA75 | 11280 | 49658 |
| NGA75 | 11280 | 49658 |
| LA50 | 1 | 1 |
| LGA50 | 1 | 1 |
| LA75 | 2 | 1 |
| LGA75 | 2 | 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

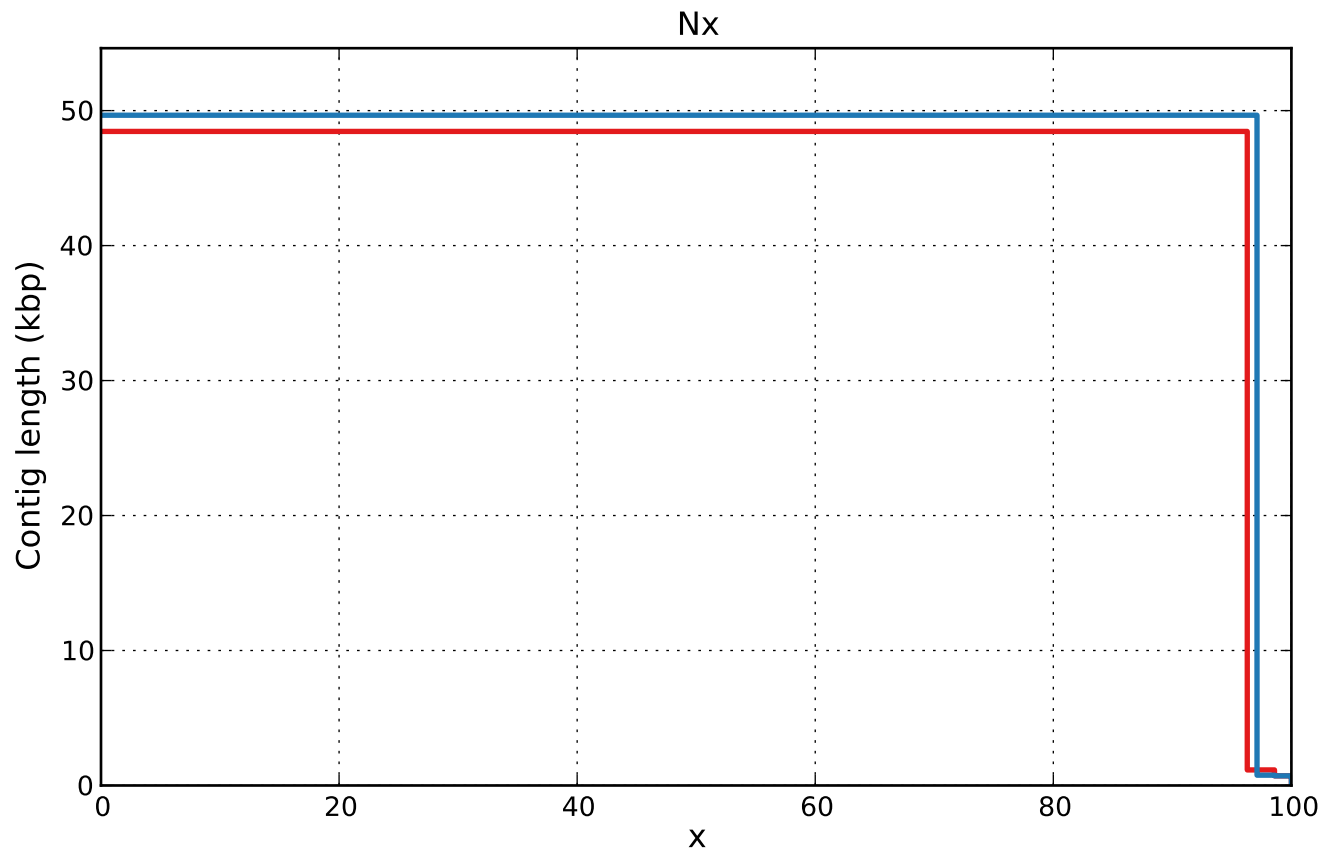
| | meta_contigs_1 | meta_contigs_2 |
|---------------------------------|----------------|----------------|
| # misassemblies | 1 | 0 |
| # contig misassemblies | 1 | 0 |
| # c. relocations | 1 | 0 |
| # c. translocations | 0 | 0 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 0 | 0 |
| # s. relocations | 0 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 1 | 0 |
| Misassembled contigs length | 48458 | 0 |
| # possibly misassembled contigs | 0 | 0 |
| # possible misassemblies | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 1 | 0 |
| # mismatches | 13 | 13 |
| # 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).

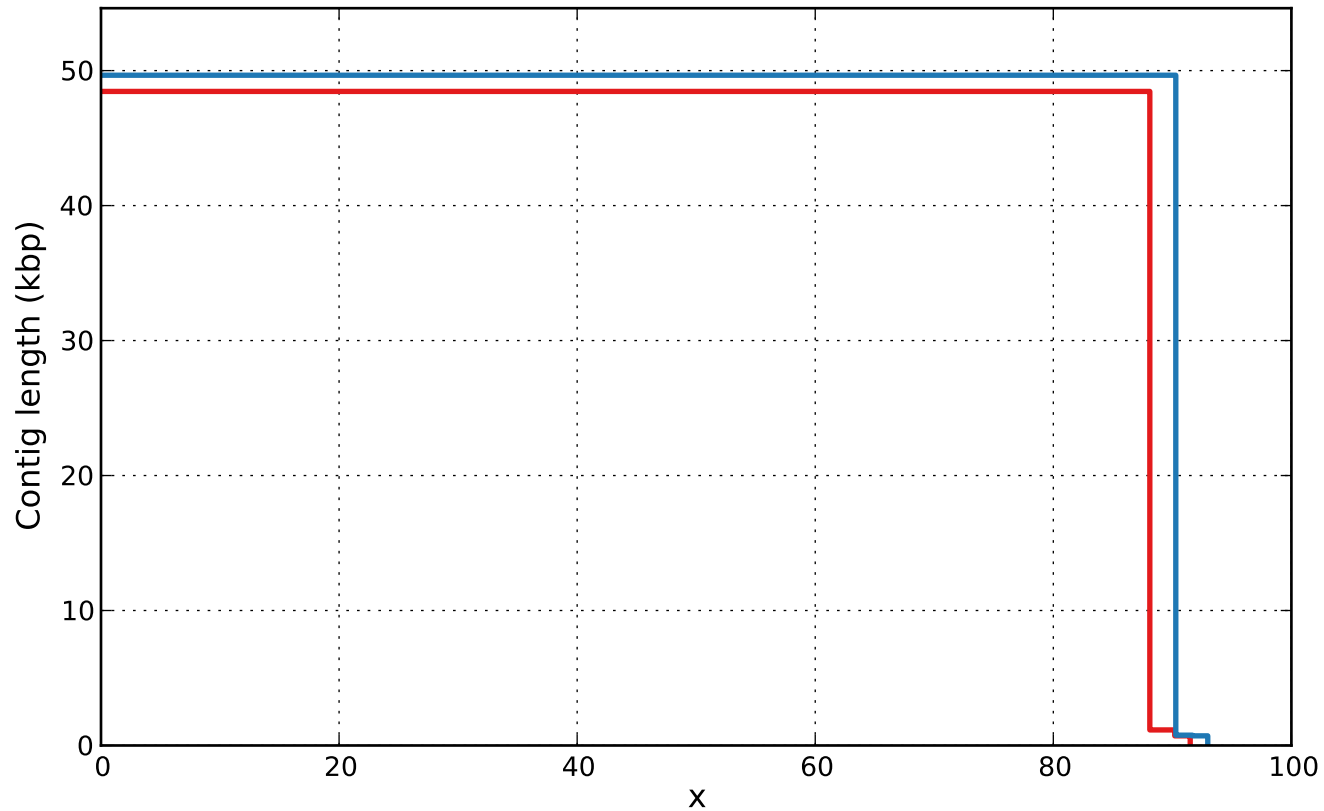
Unaligned report

| | meta_contigs_1 | meta_contigs_2 |
|-------------------------------|----------------|----------------|
| # fully unaligned contigs | 0 | 0 |
| Fully unaligned length | 0 | 0 |
| # partially unaligned contigs | 1 | 0 |
| Partially unaligned length | 665 | 0 |
| # N's | 20 | 0 |

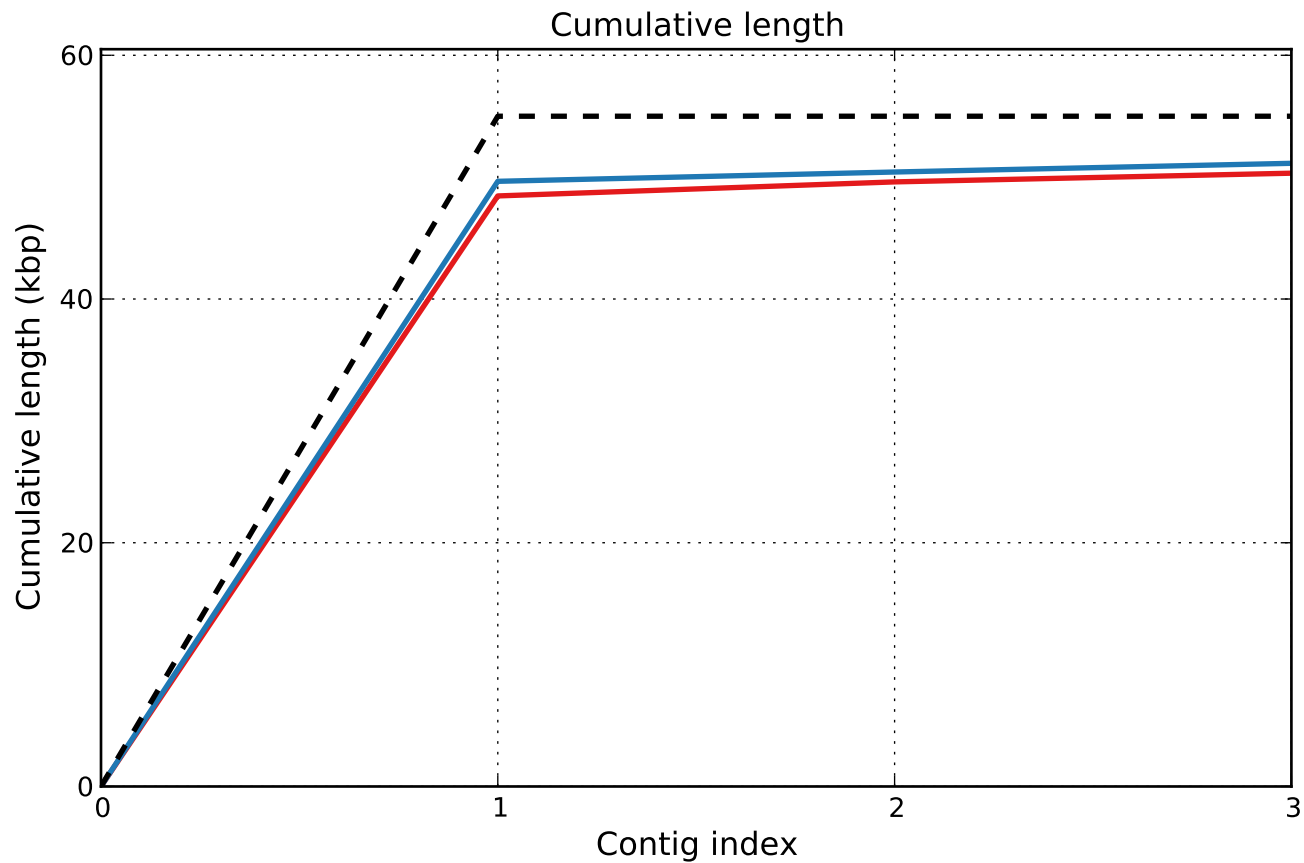
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



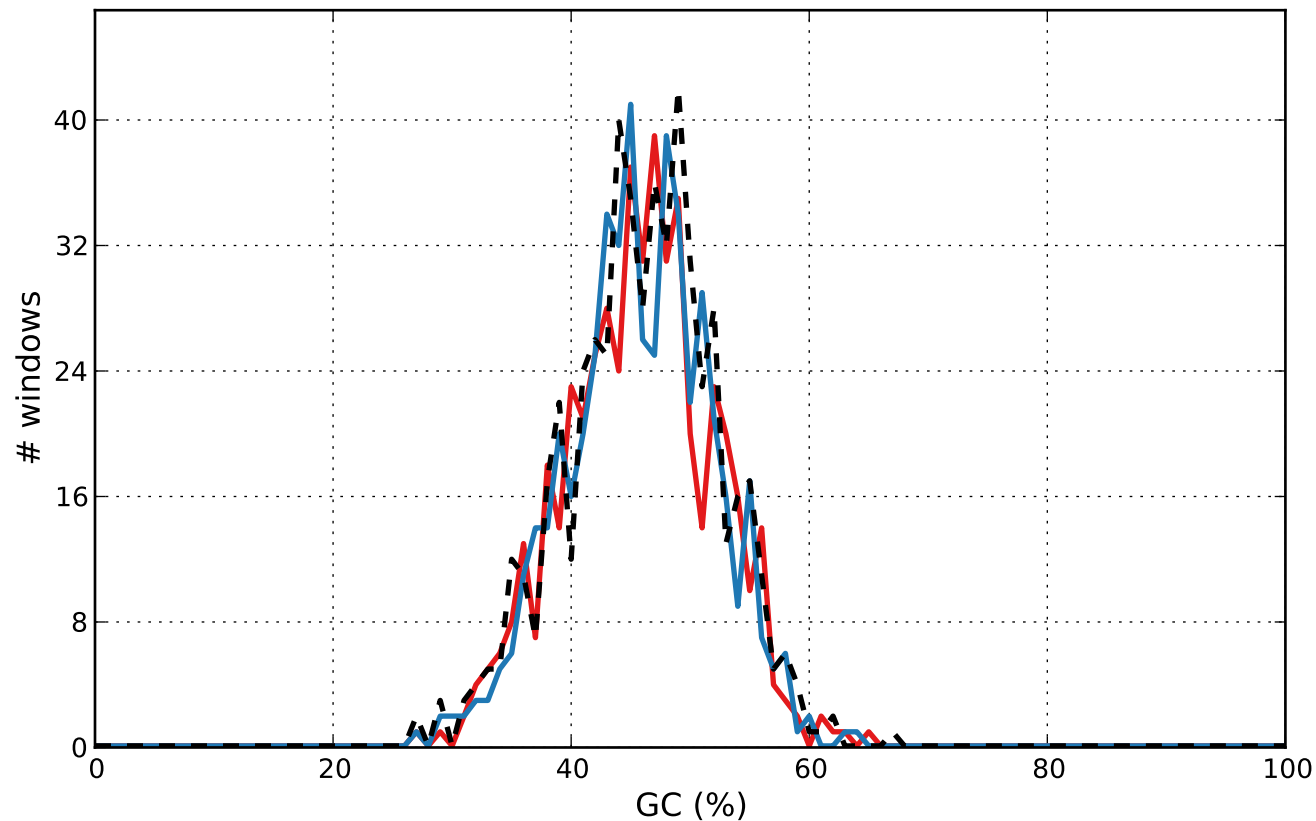
NGx



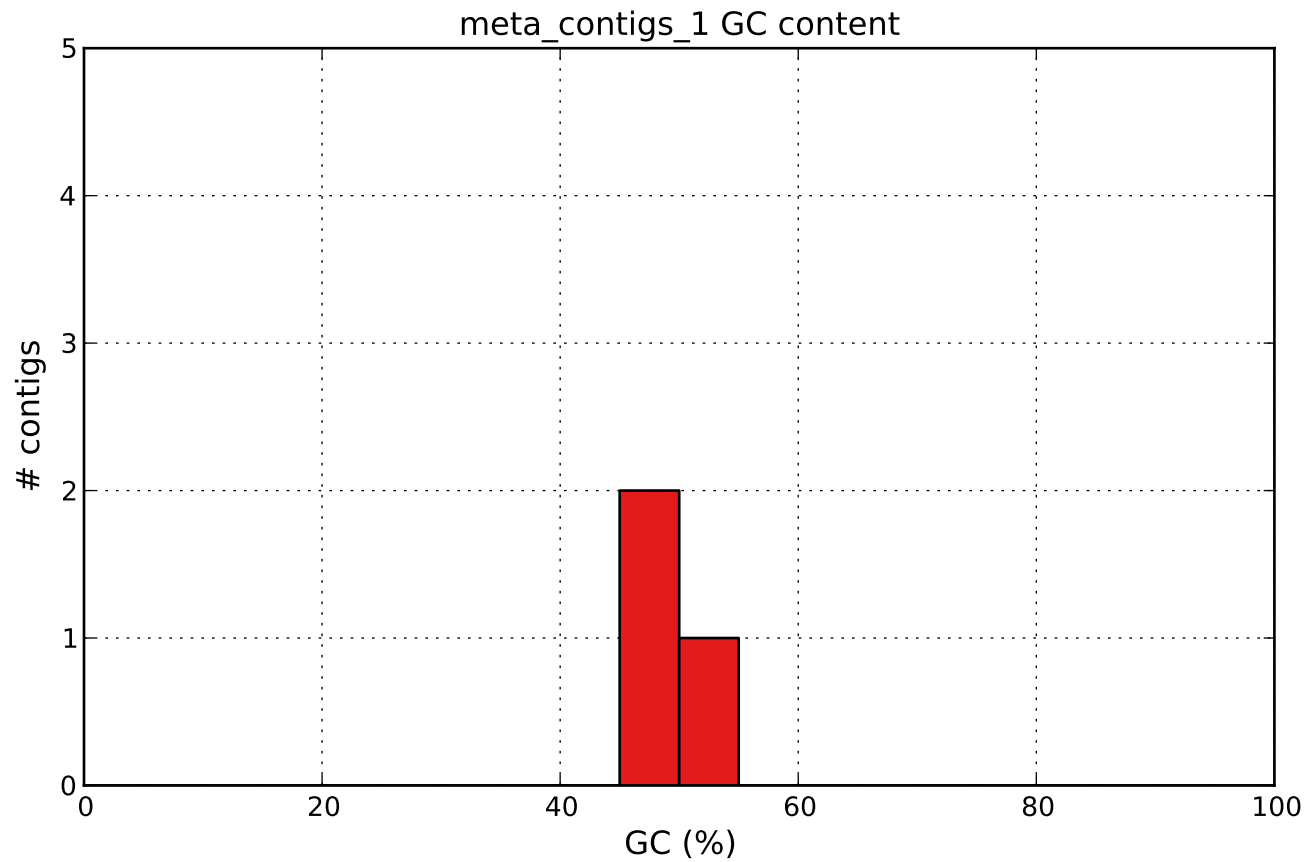
— meta_contigs_1 — meta_contigs_2



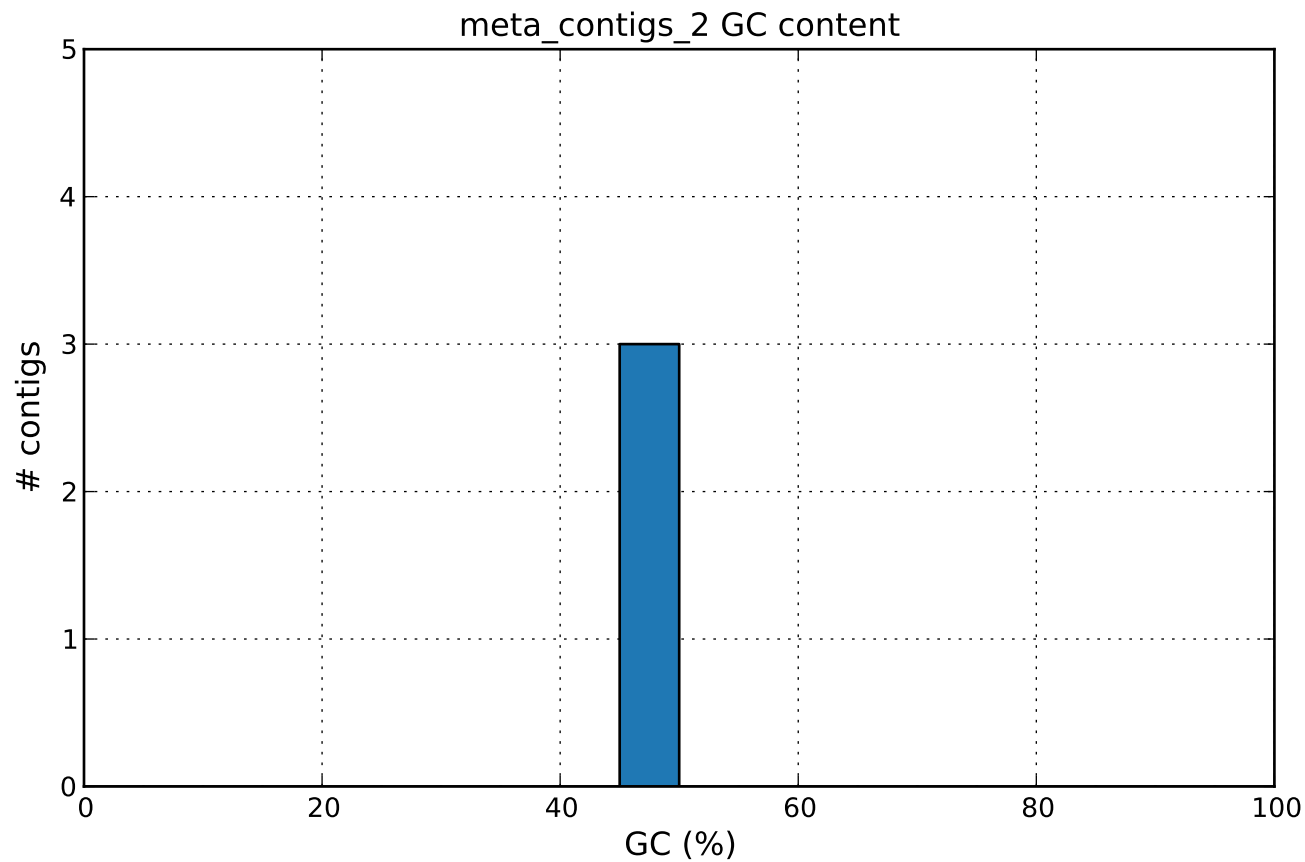
GC content



— meta_contigs_1 — meta_contigs_2 - - Reference

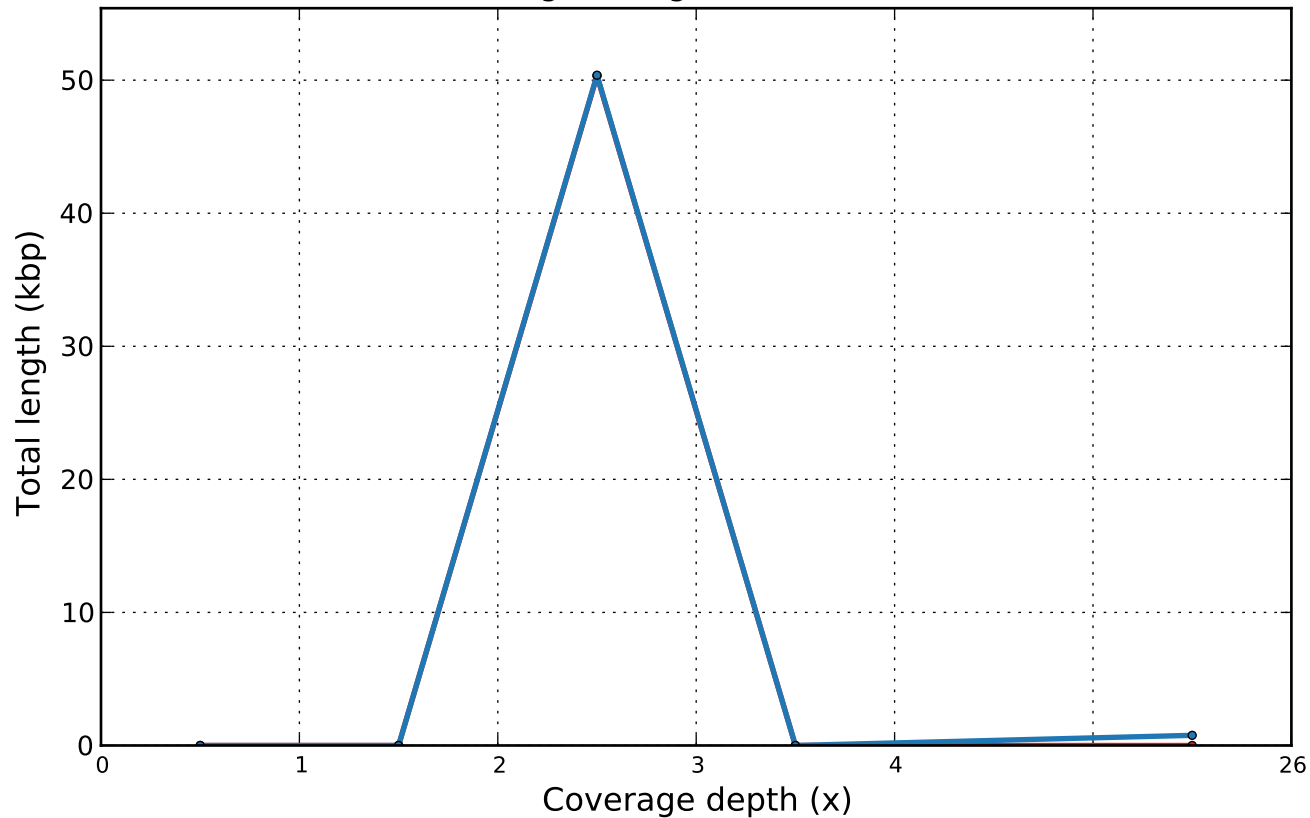


meta_contigs_1

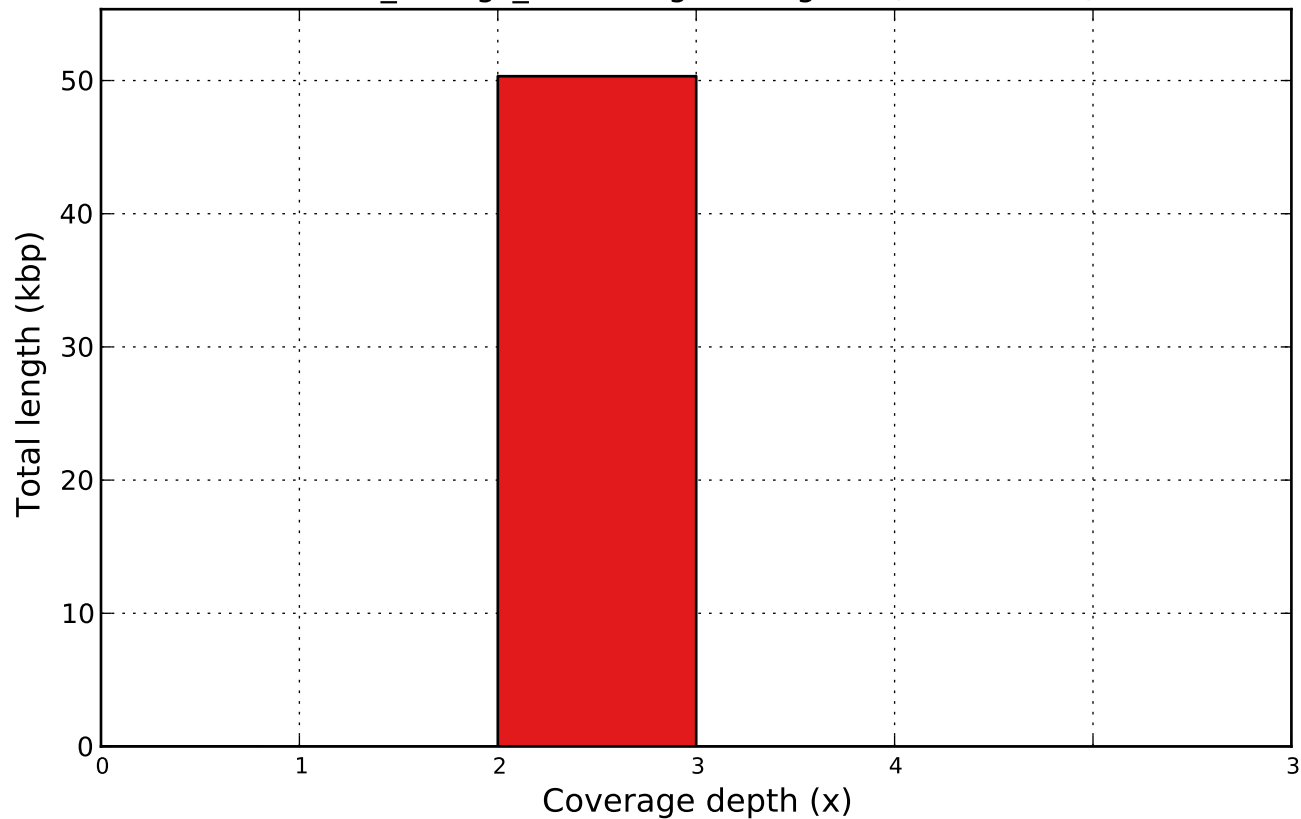


meta_contigs_2

Coverage histogram (bin size: 1x)

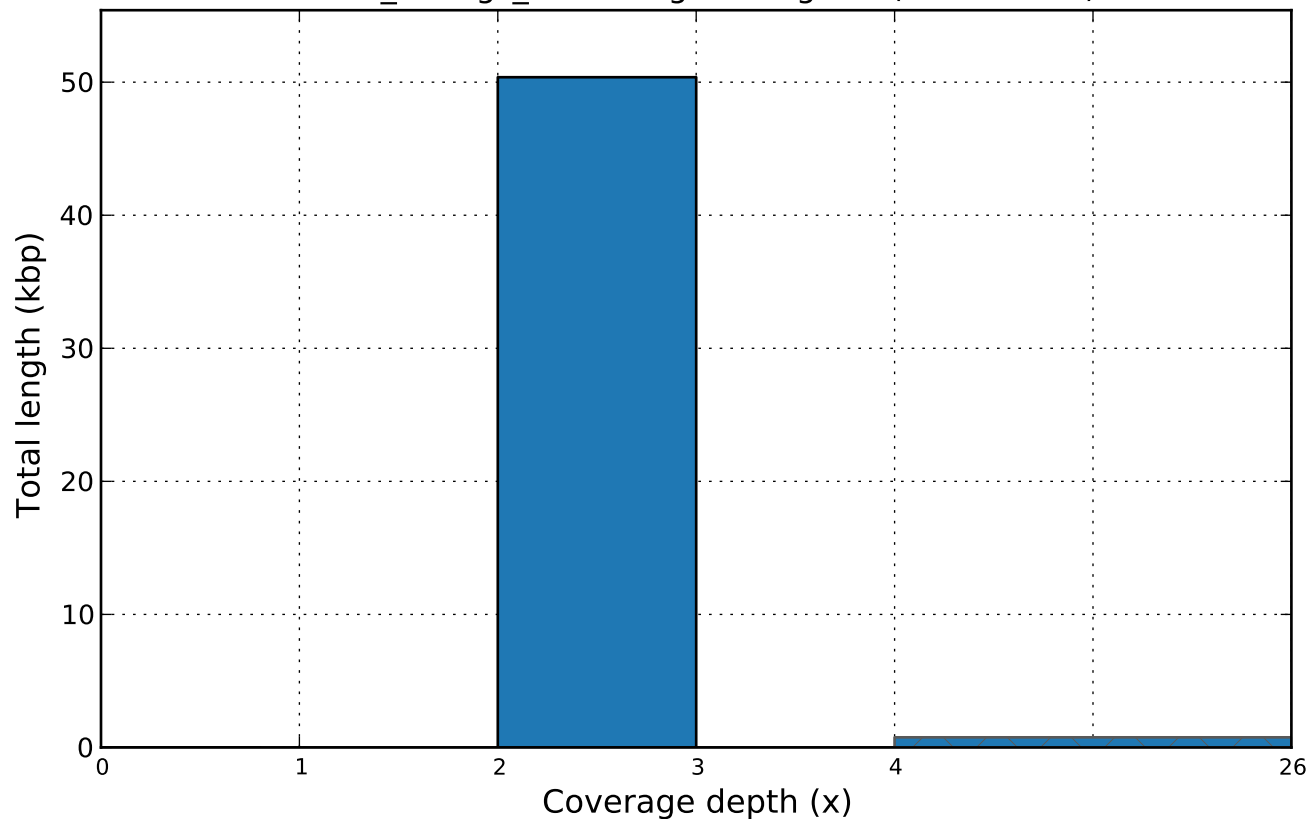


meta_contigs_1 coverage histogram (bin size: 1x)



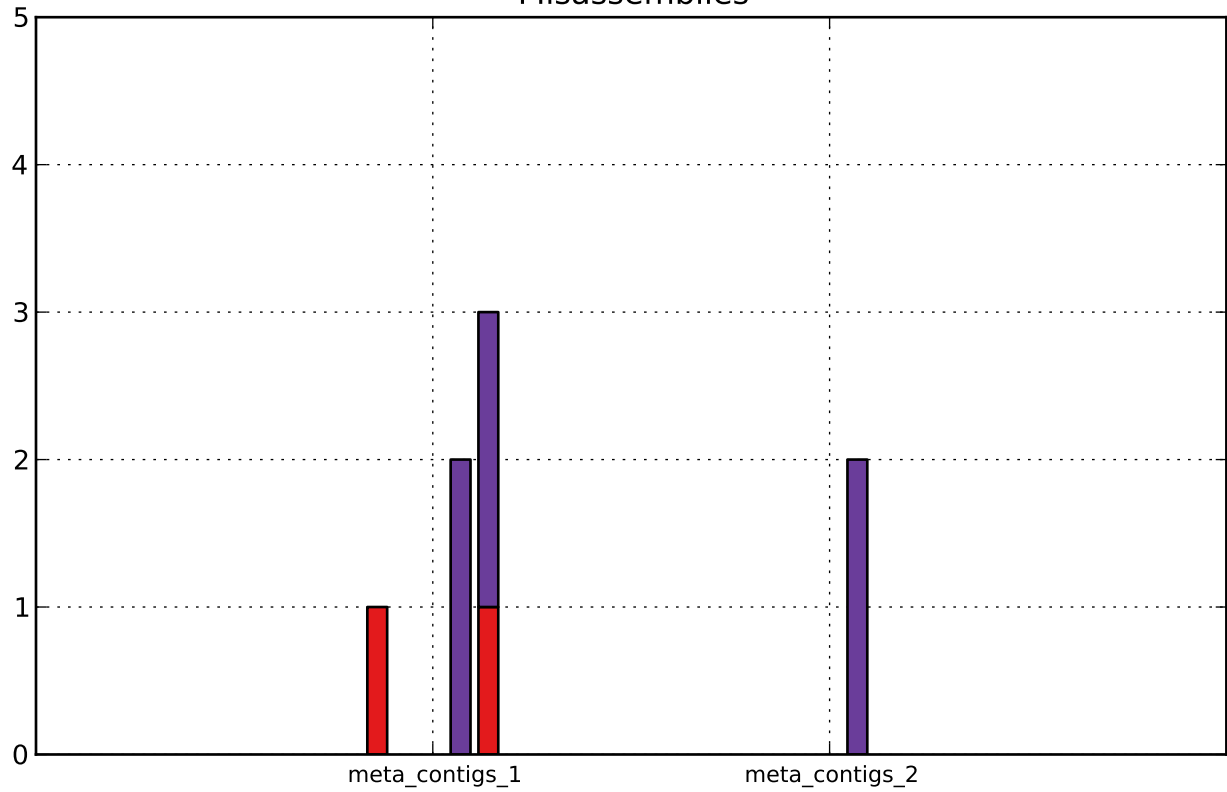
meta_contigs_1

meta_contigs_2 coverage histogram (bin size: 1x)

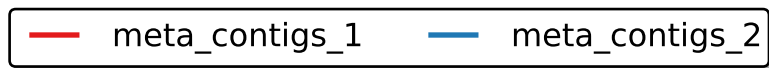
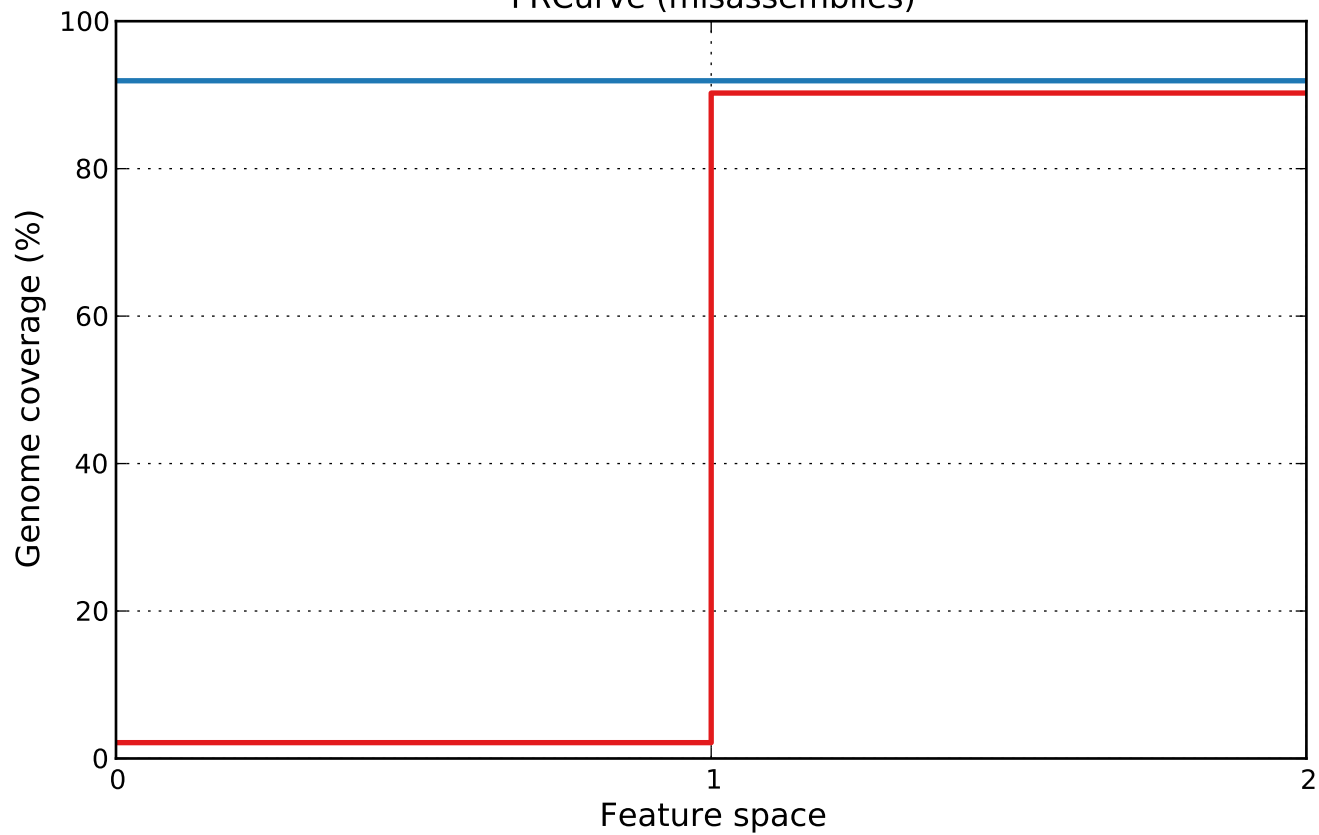


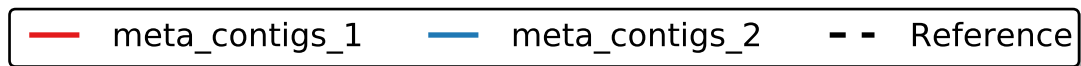
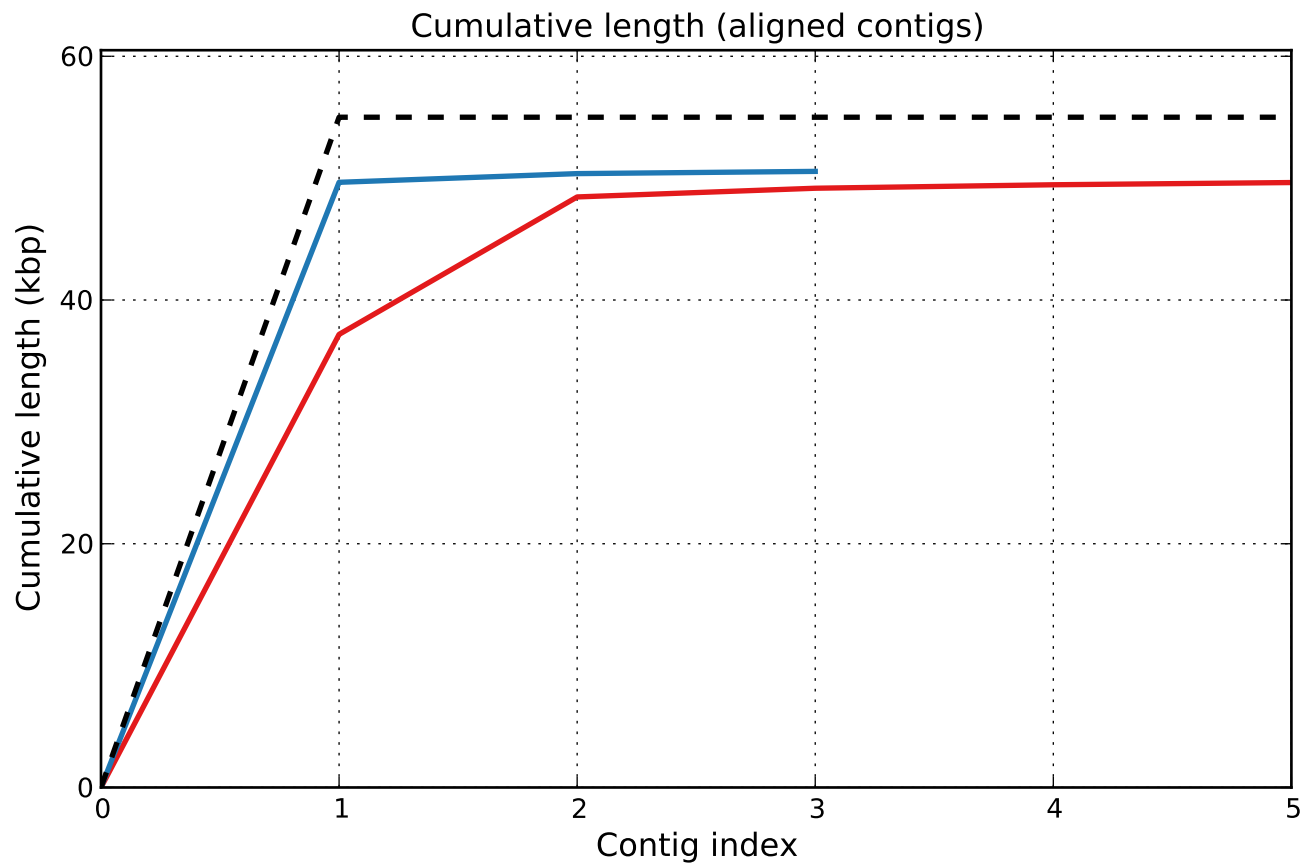
meta_contigs_2

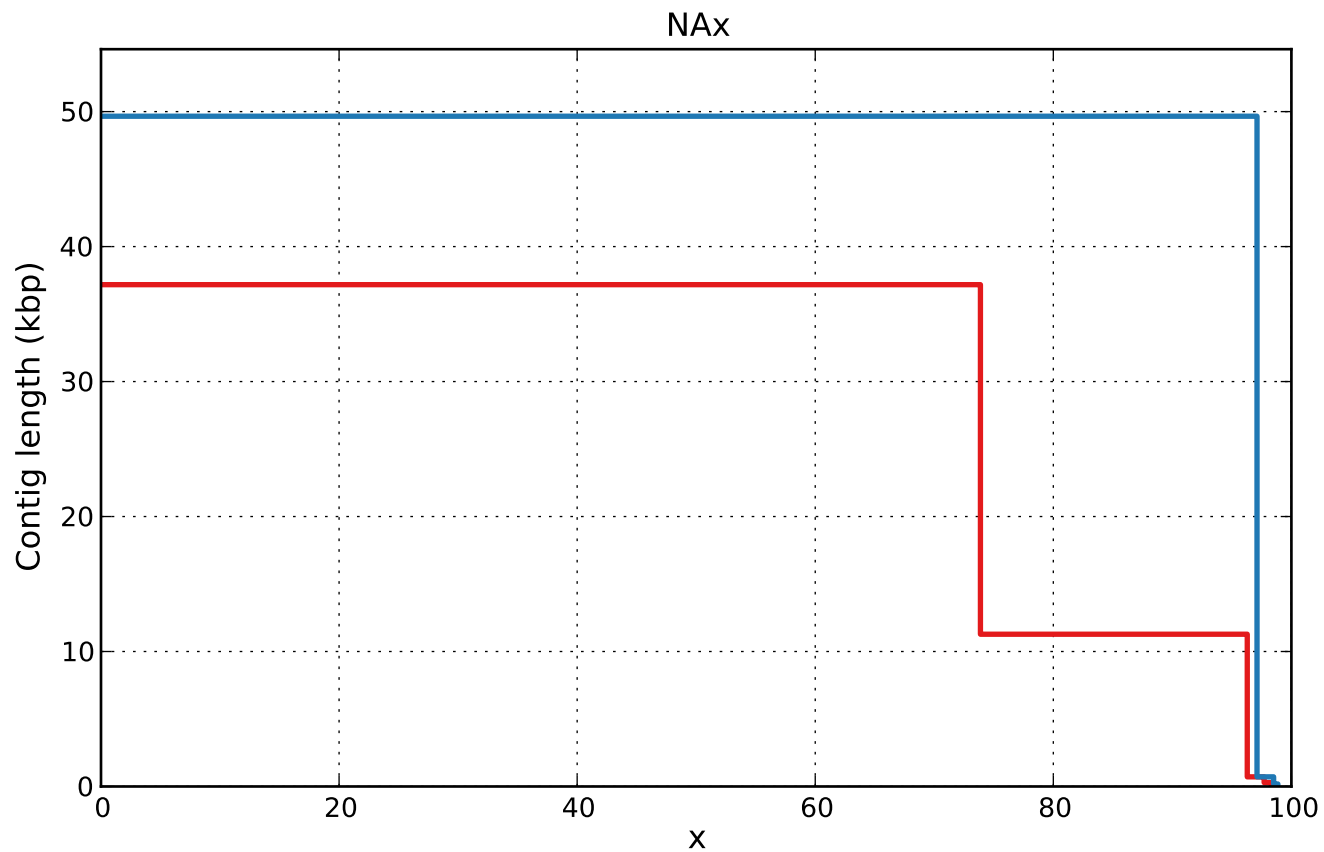
Misassemblies



FRCurve (misassemblies)







— meta_contigs_1 — meta_contigs_2

NGAx

