

Report

| | final.contigs |
|---------------------------------|---------------|
| # contigs (≥ 1000 bp) | 2 |
| # contigs (≥ 5000 bp) | 1 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 1000 bp) | 10495 |
| Total length (≥ 5000 bp) | 9177 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 2 |
| Largest contig | 9177 |
| Total length | 10495 |
| Reference length | 3618700 |
| GC (%) | 46.09 |
| Reference GC (%) | 62.27 |
| N50 | 9177 |
| N75 | 9177 |
| L50 | 1 |
| L75 | 1 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 2 part |
| Unaligned length | 10341 |
| Genome fraction (%) | 0.004 |
| Duplication ratio | 1.000 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2597.40 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 86 |
| Total aligned length | 154 |
| NGA50 | - |

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

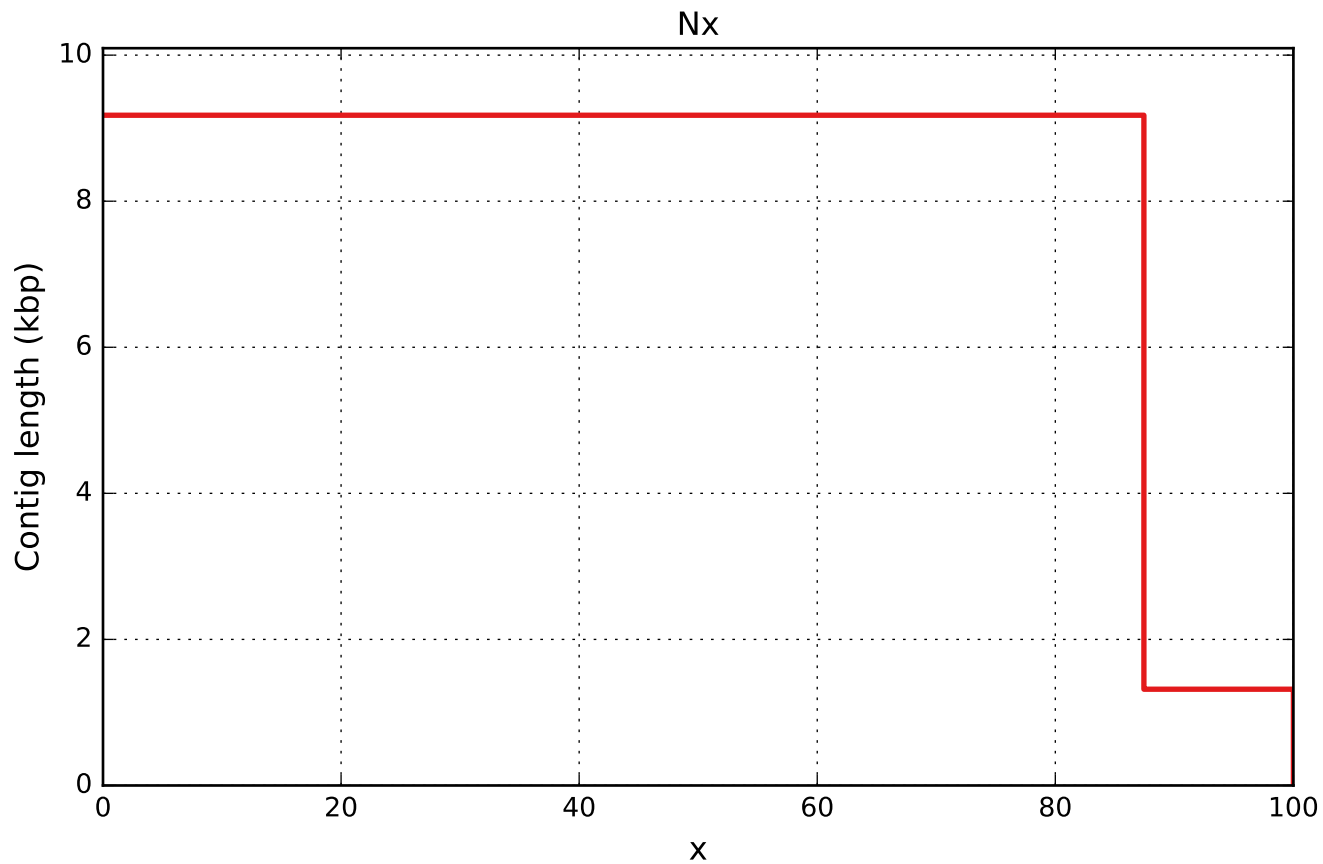
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 0 |
| # possible misassemblies | 0 |
| # local misassemblies | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 4 |
| # indels | 0 |
| # indels (<= 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 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).

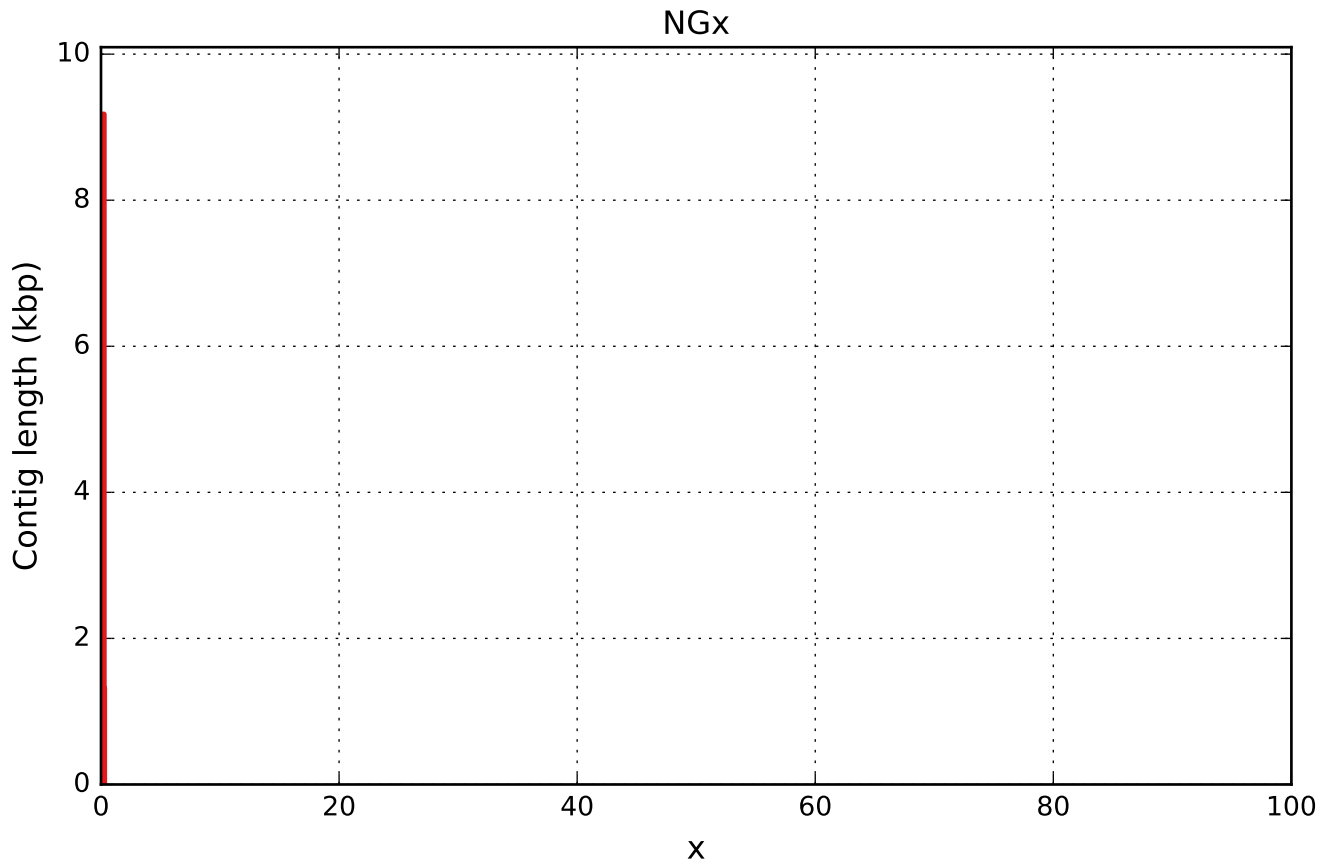
Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 2 |
| Partially unaligned length | 10341 |
| # N's | 0 |

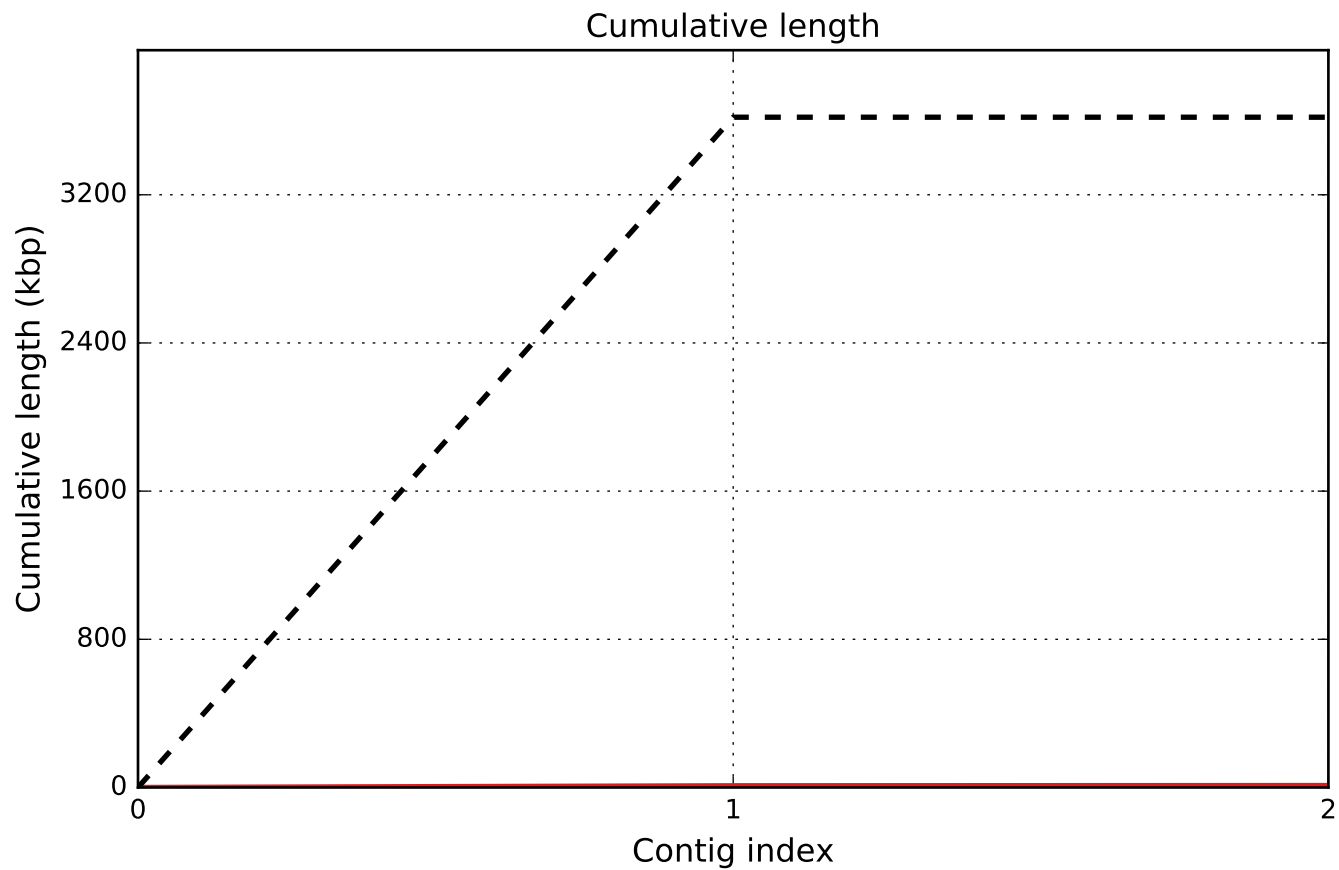
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



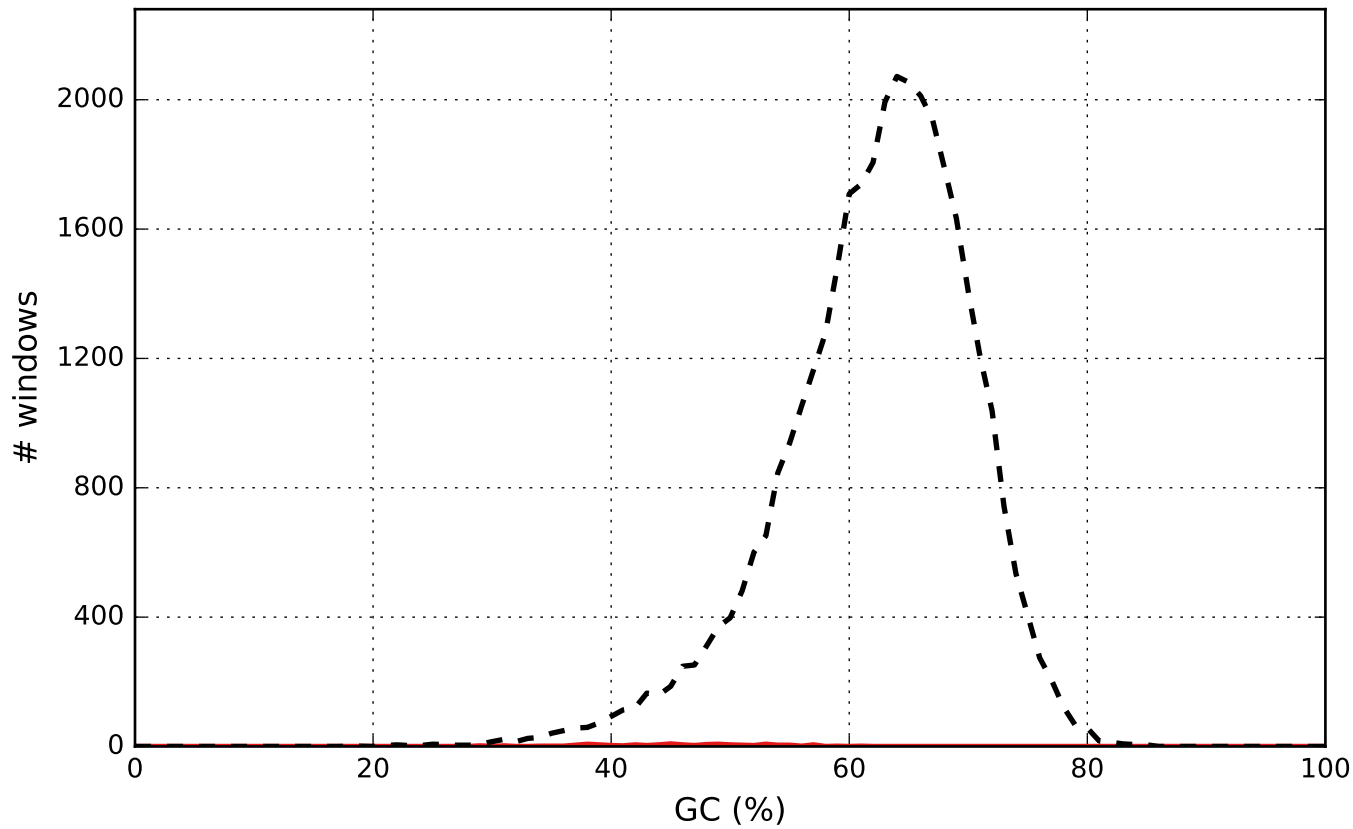
— final.contigs



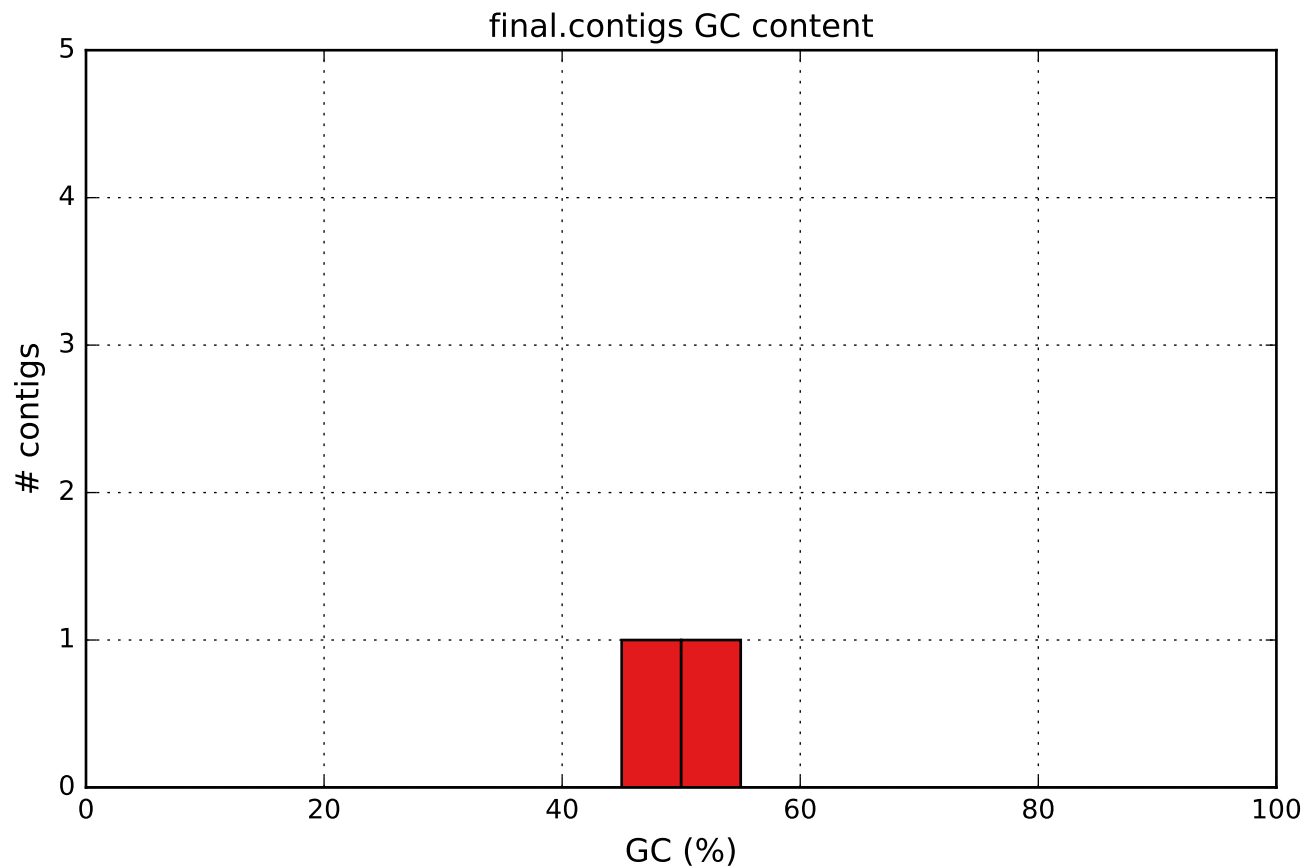
— final.contigs



GC content



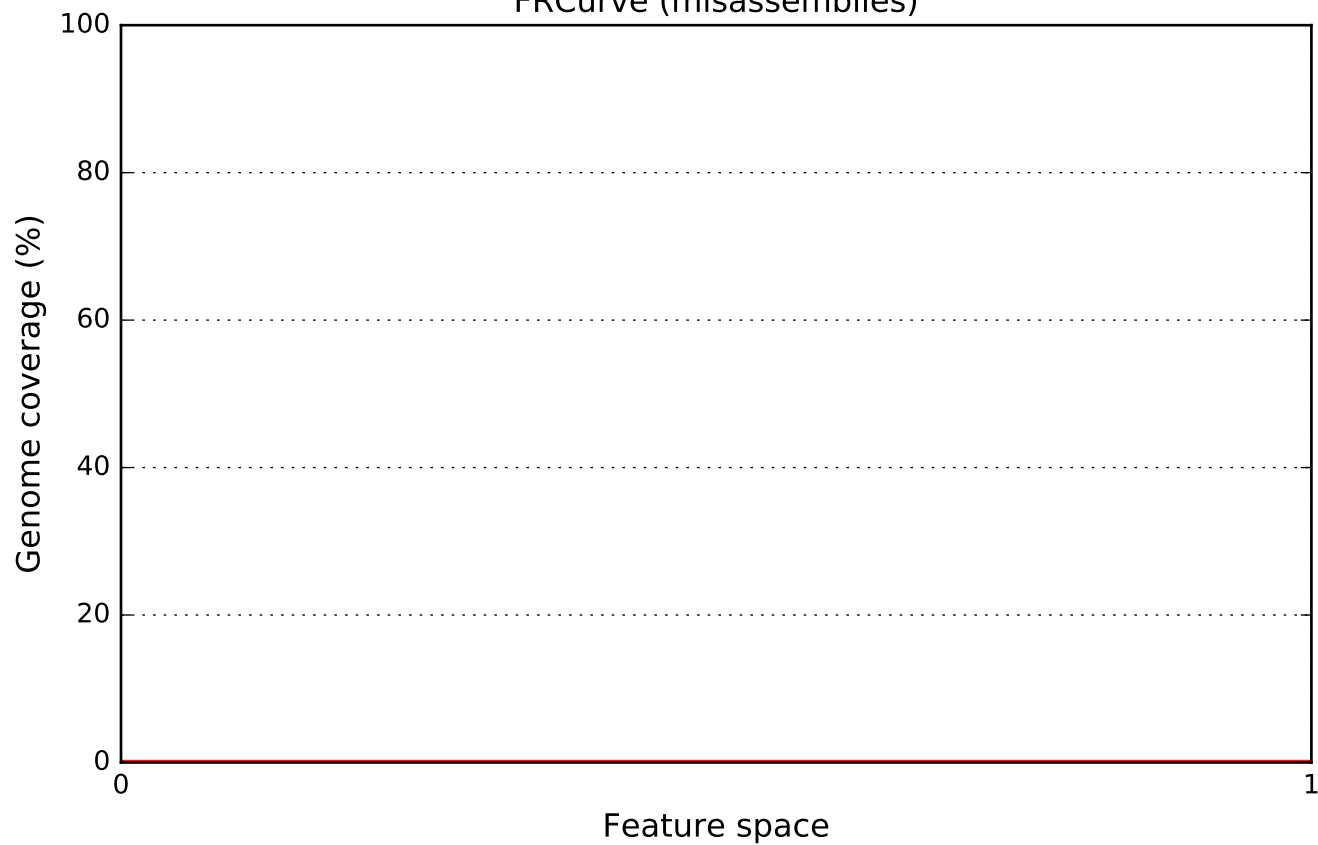
— final.contigs - - Reference



final.contigs

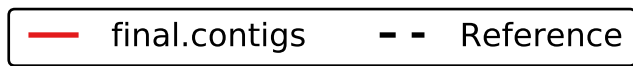
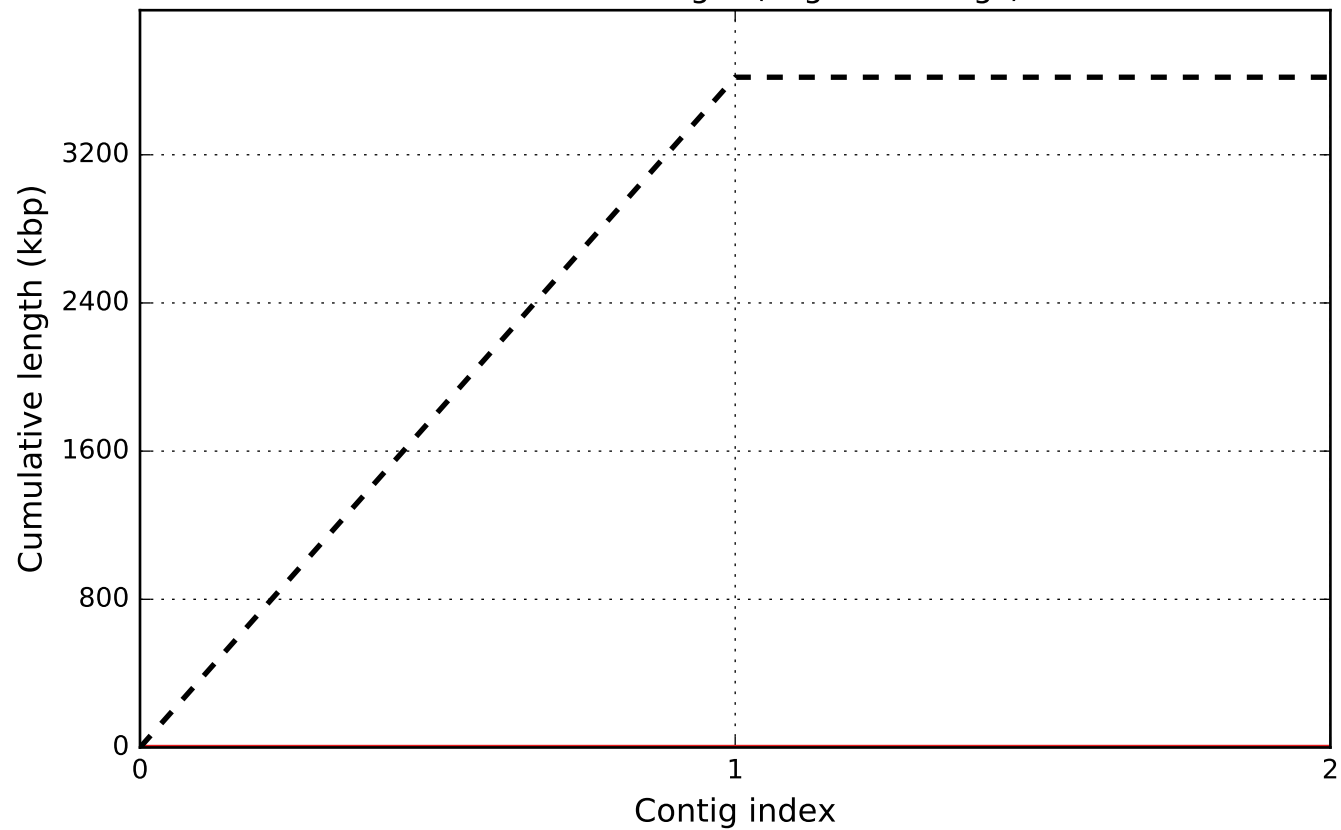


FRCurve (misassemblies)

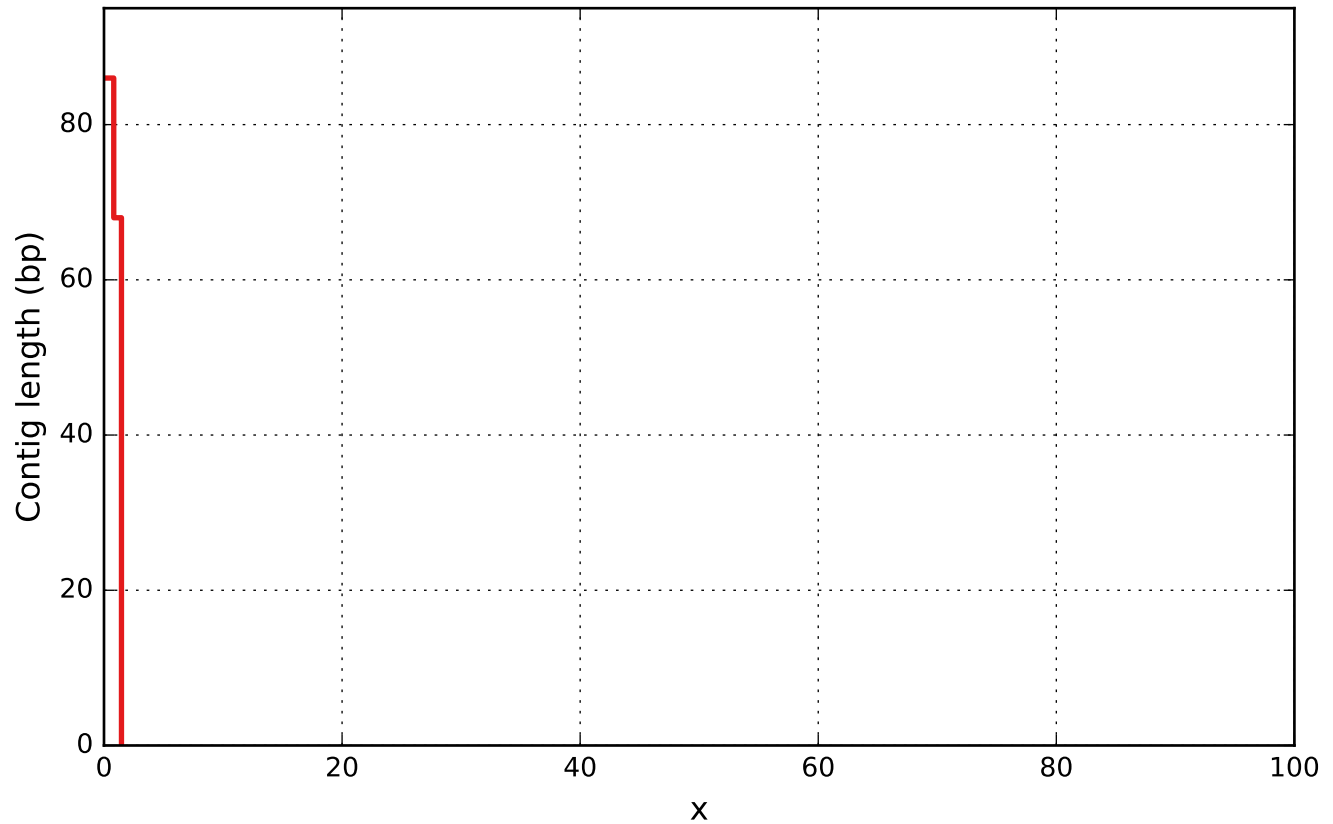


— final.contigs

Cumulative length (aligned contigs)

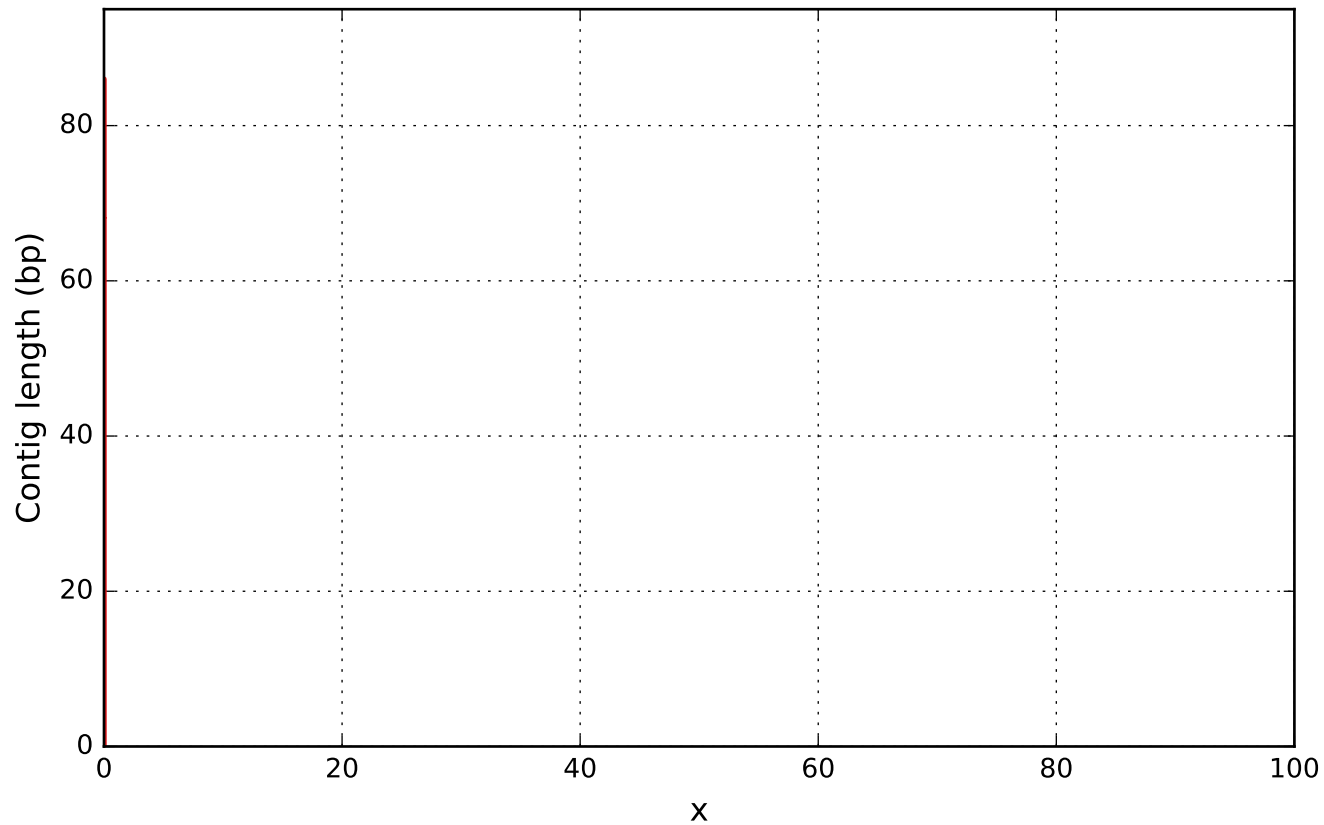


NAx



— final.contigs

NGAx



— final.contigs