

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 9 |
| # contigs (>= 5000 bp) | 3 |
| # contigs (>= 10000 bp) | 3 |
| # contigs (>= 25000 bp) | 2 |
| # contigs (>= 50000 bp) | 1 |
| Total length (>= 1000 bp) | 333388 |
| Total length (>= 5000 bp) | 324228 |
| Total length (>= 10000 bp) | 324228 |
| Total length (>= 25000 bp) | 299823 |
| Total length (>= 50000 bp) | 266140 |
| # contigs | 22 |
| Largest contig | 266140 |
| Total length | 342879 |
| Reference length | 3464554 |
| GC (%) | 59.39 |
| Reference GC (%) | 65.06 |
| N50 | 266140 |
| N75 | 266140 |
| L50 | 1 |
| L75 | 1 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 1 + 12 part |
| Unaligned length | 335606 |
| Genome fraction (%) | 0.059 |
| Duplication ratio | 3.536 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 3791.93 |
| # indels per 100 kbp | 145.84 |
| Largest alignment | 561 |
| Total aligned length | 2490 |
| 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

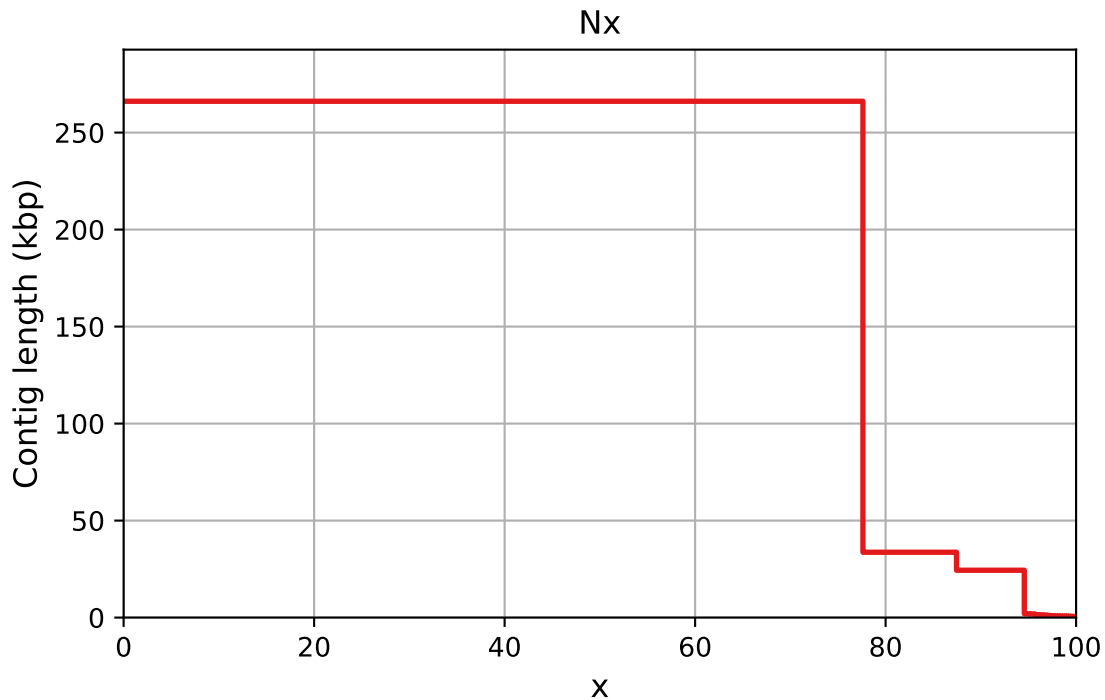
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 4 |
| # possible misassemblies | 6 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 78 |
| # indels | 3 |
| # indels (<= 5 bp) | 3 |
| # indels (> 5 bp) | 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

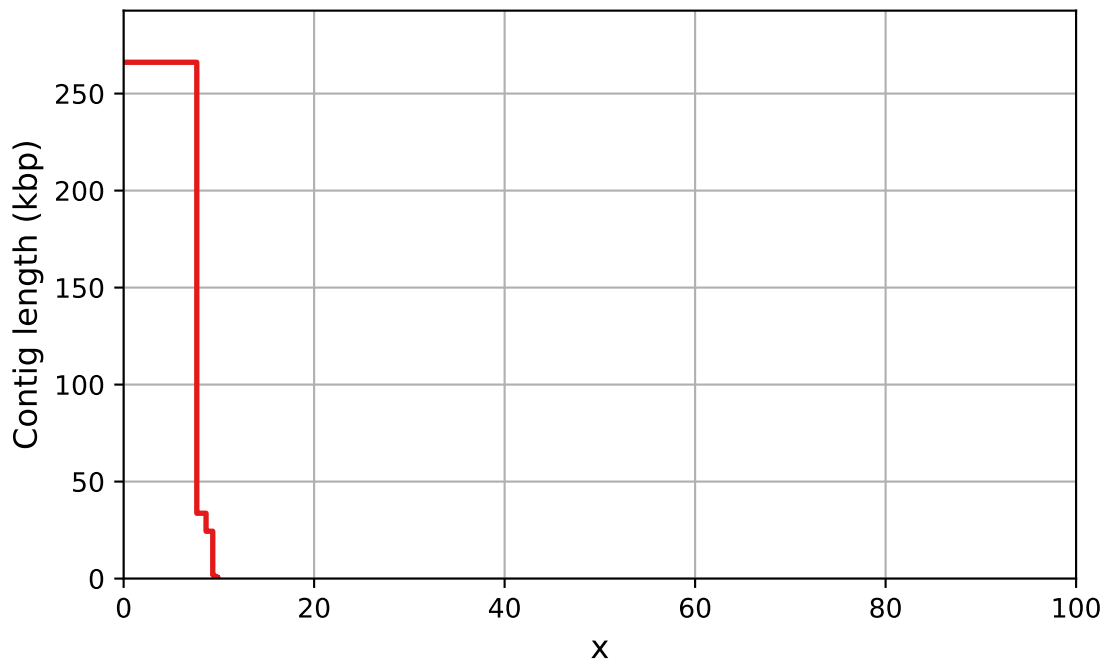
| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 1 |
| Fully unaligned length | 871 |
| # partially unaligned contigs | 12 |
| Partially unaligned length | 334735 |
| # N's | 0 |

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).

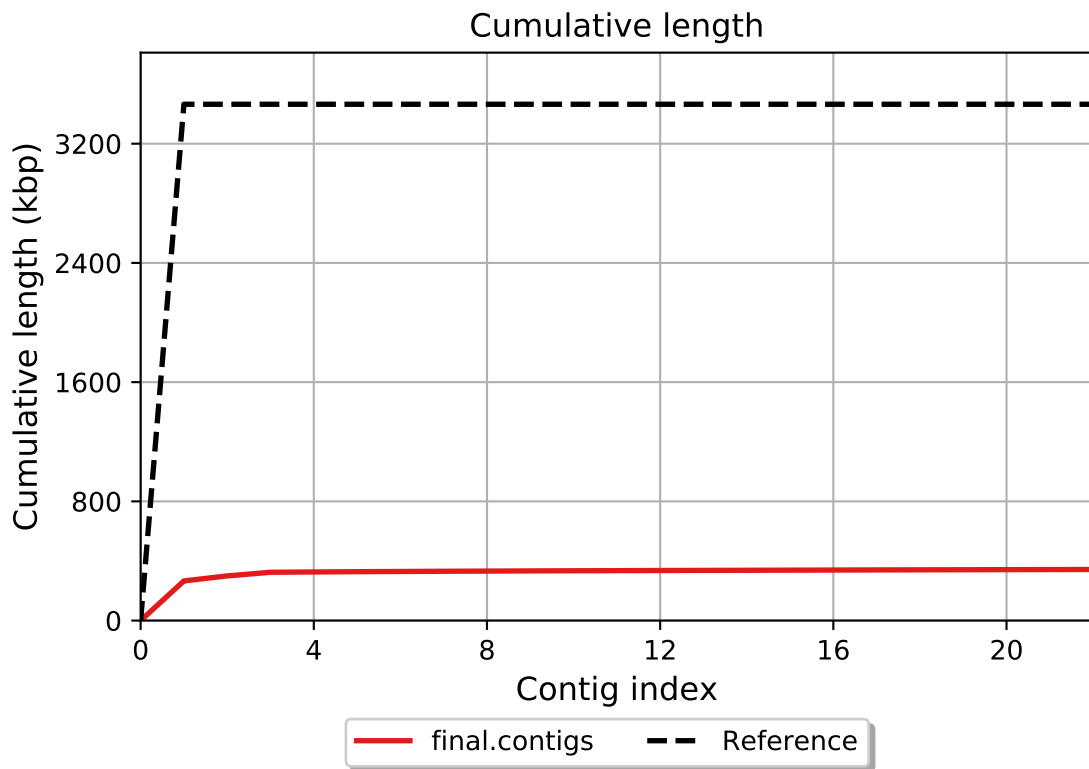


— final.contigs

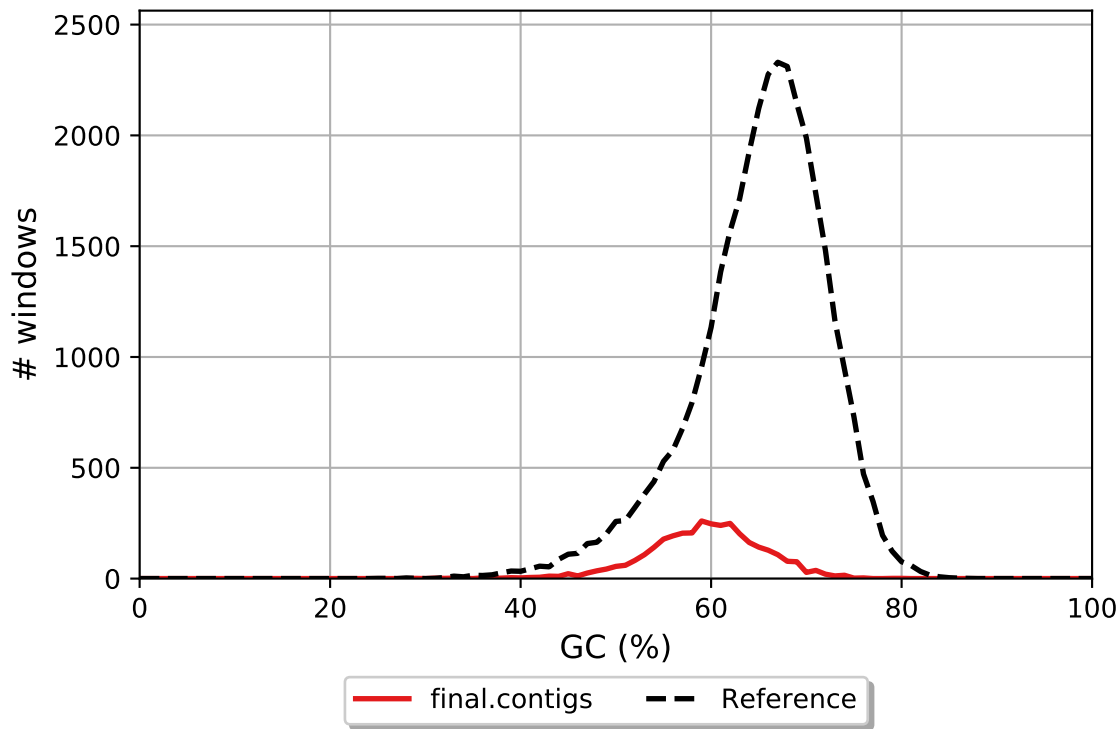
NGx



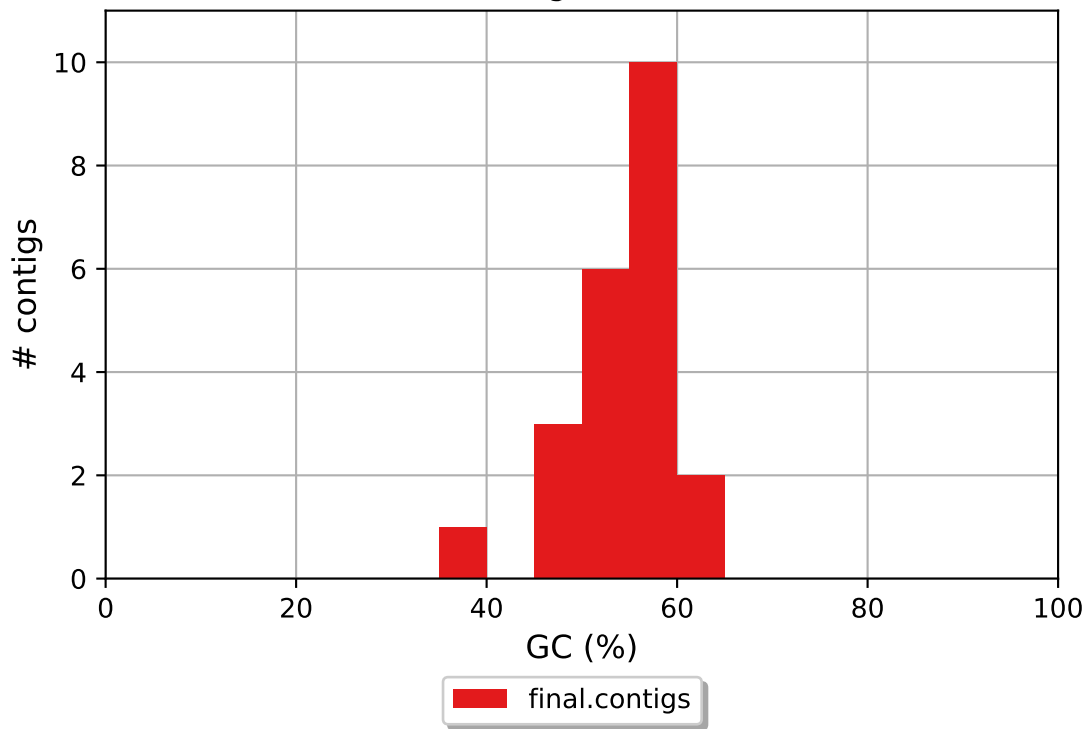
— final.contigs



GC content



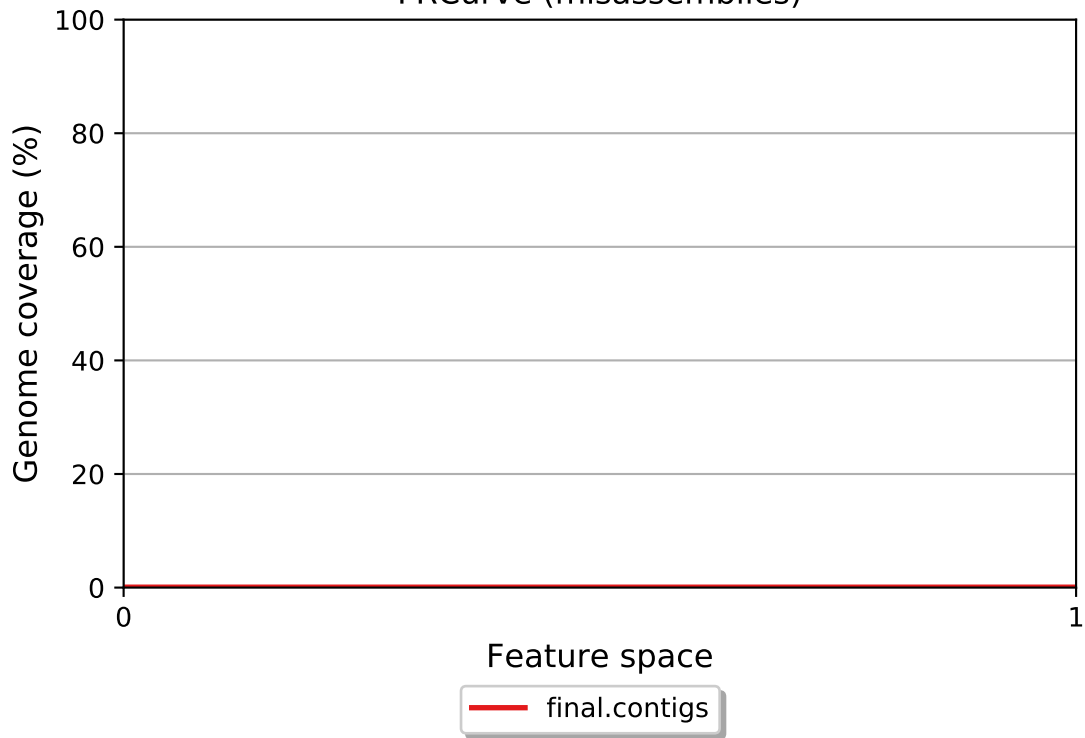
final.contigs GC content



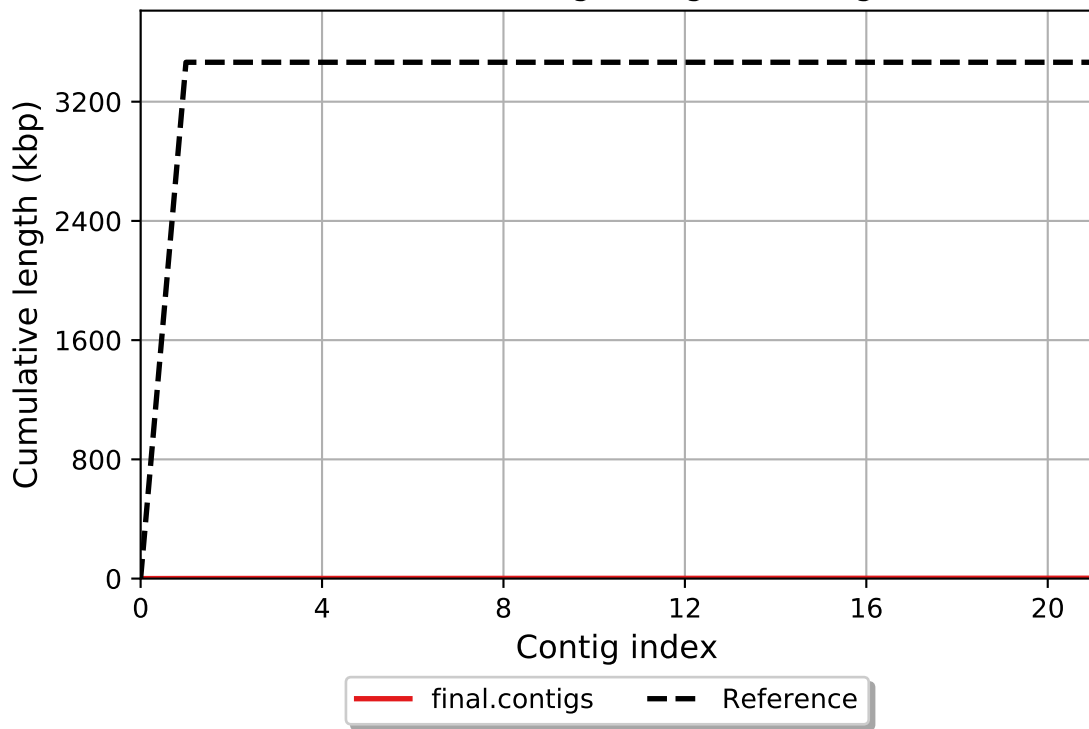
Misassemblies



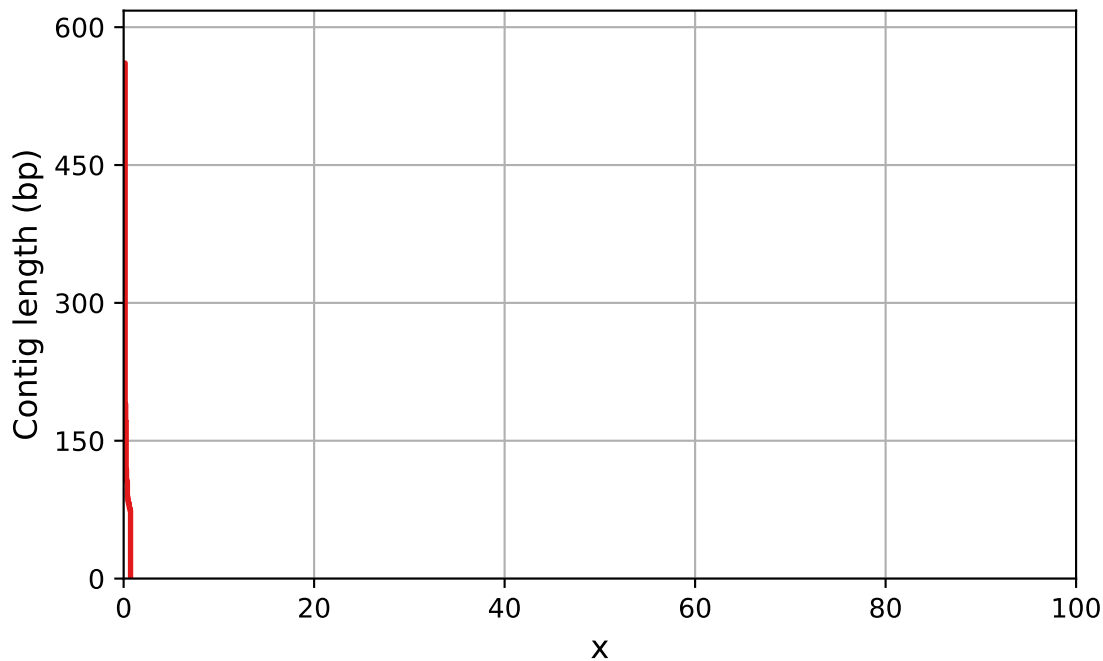
FRCurve (misassemblies)



Cumulative length (aligned contigs)

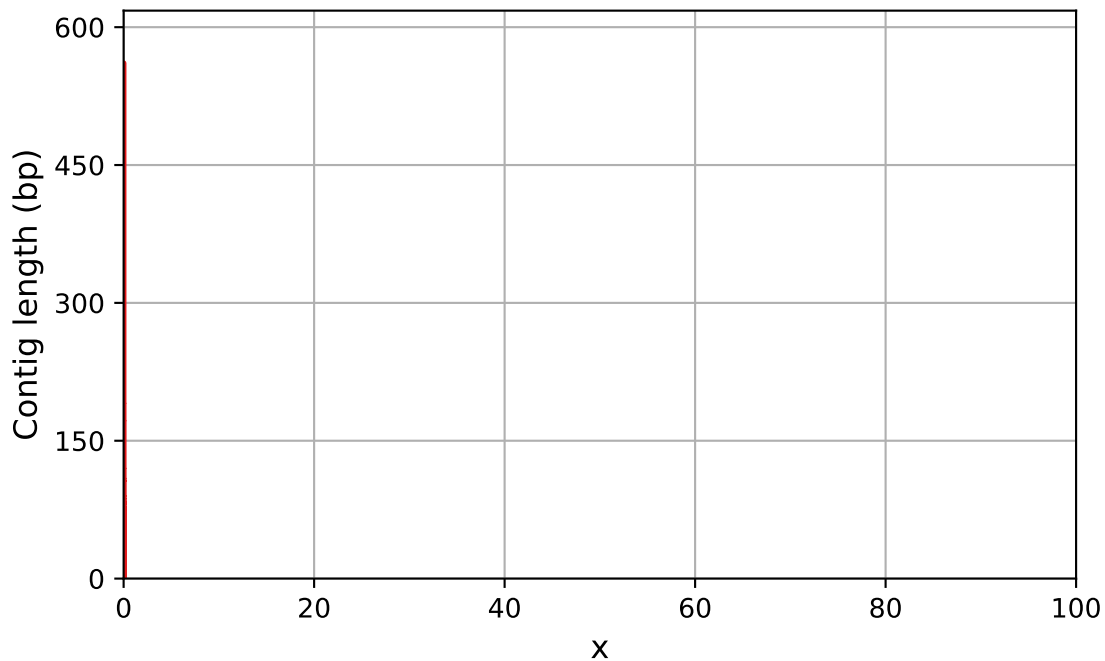


NAx



— final.contigs

NGAx



— final.contigs