

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 3 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 5025 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 6 |
| Largest contig | 2187 |
| Total length | 7326 |
| Reference length | 4306142 |
| GC (%) | 50.03 |
| Reference GC (%) | 53.59 |
| N50 | 1539 |
| N75 | 901 |
| L50 | 2 |
| L75 | 4 |
| # 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 + 4 part |
| Unaligned length | 6365 |
| Genome fraction (%) | 0.010 |
| Duplication ratio | 2.179 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2494.33 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 132 |
| Total aligned length | 441 |
| 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

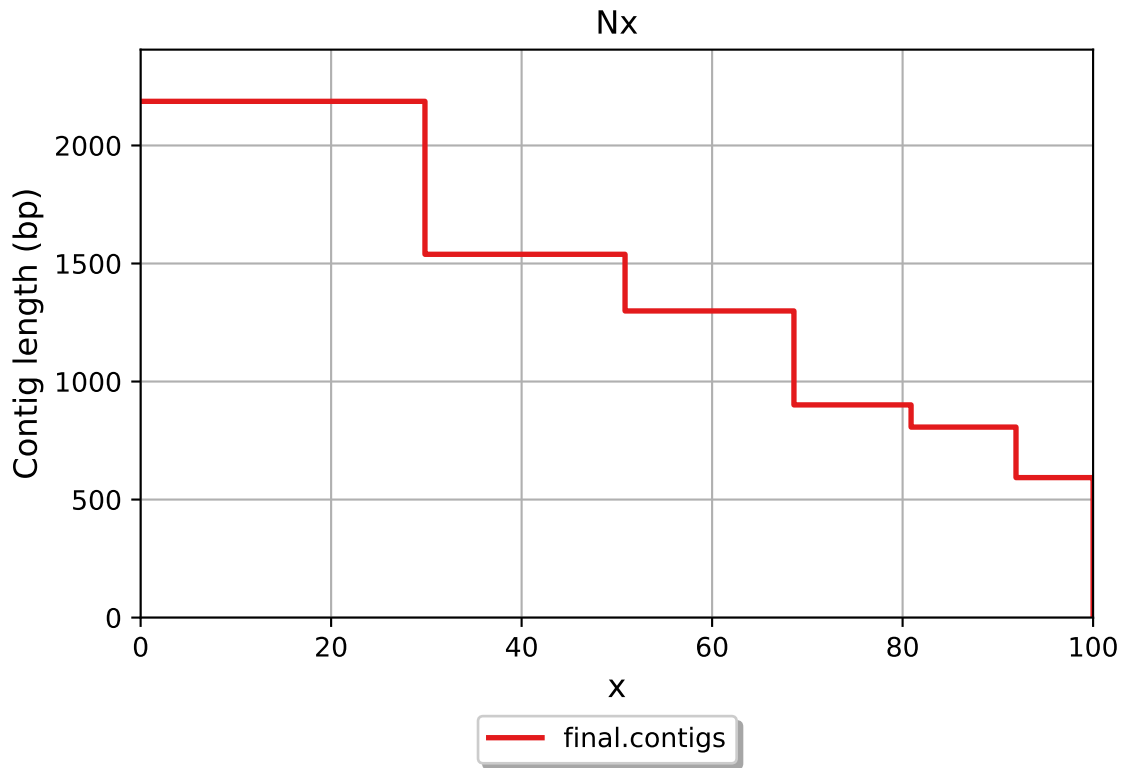
| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 2 |
| # possible misassemblies | 4 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 11 |
| # 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).

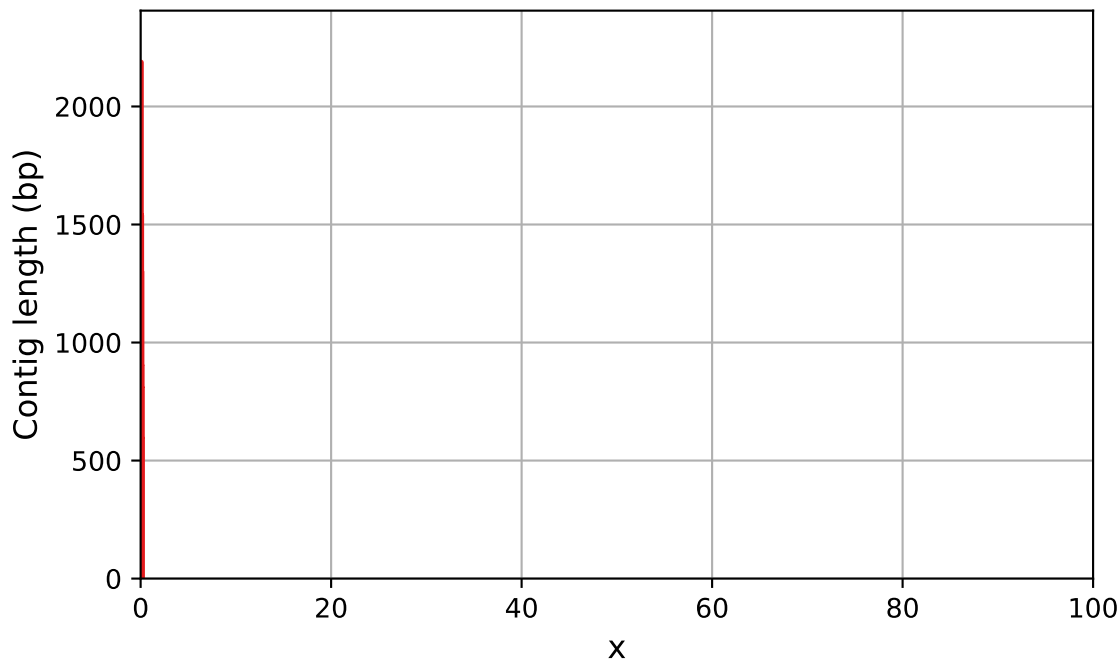
Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 1 |
| Fully unaligned length | 807 |
| # partially unaligned contigs | 4 |
| Partially unaligned length | 5558 |
| # N's | 0 |

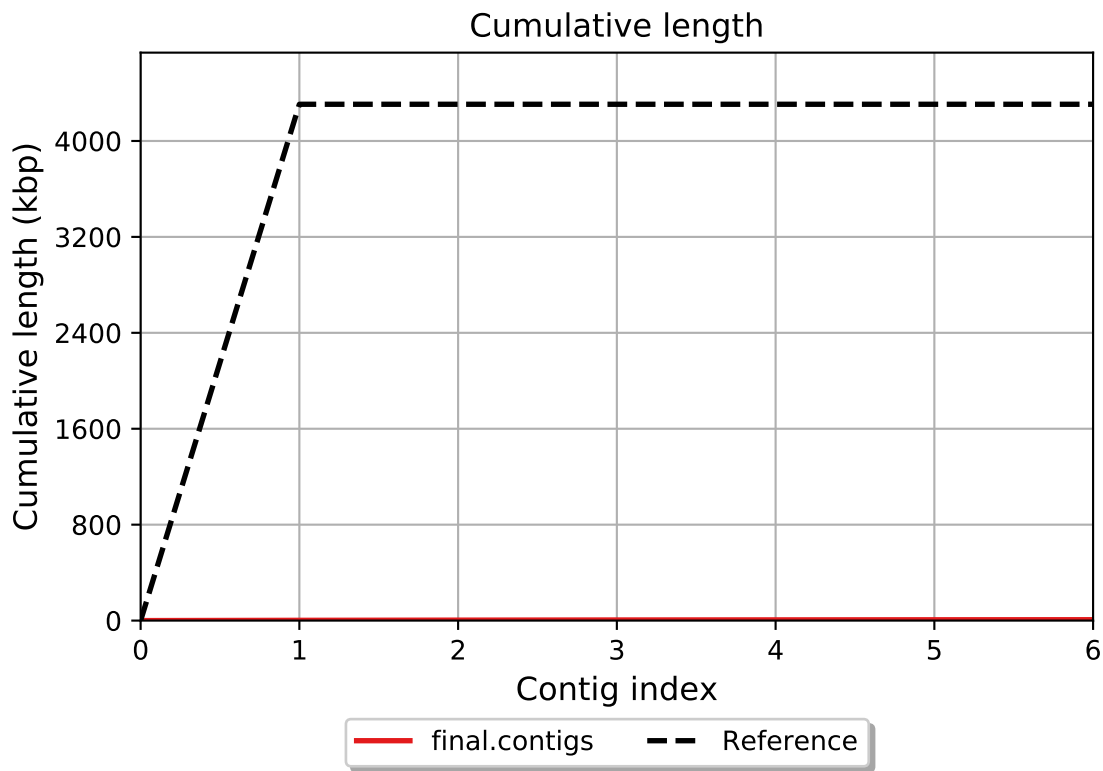
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



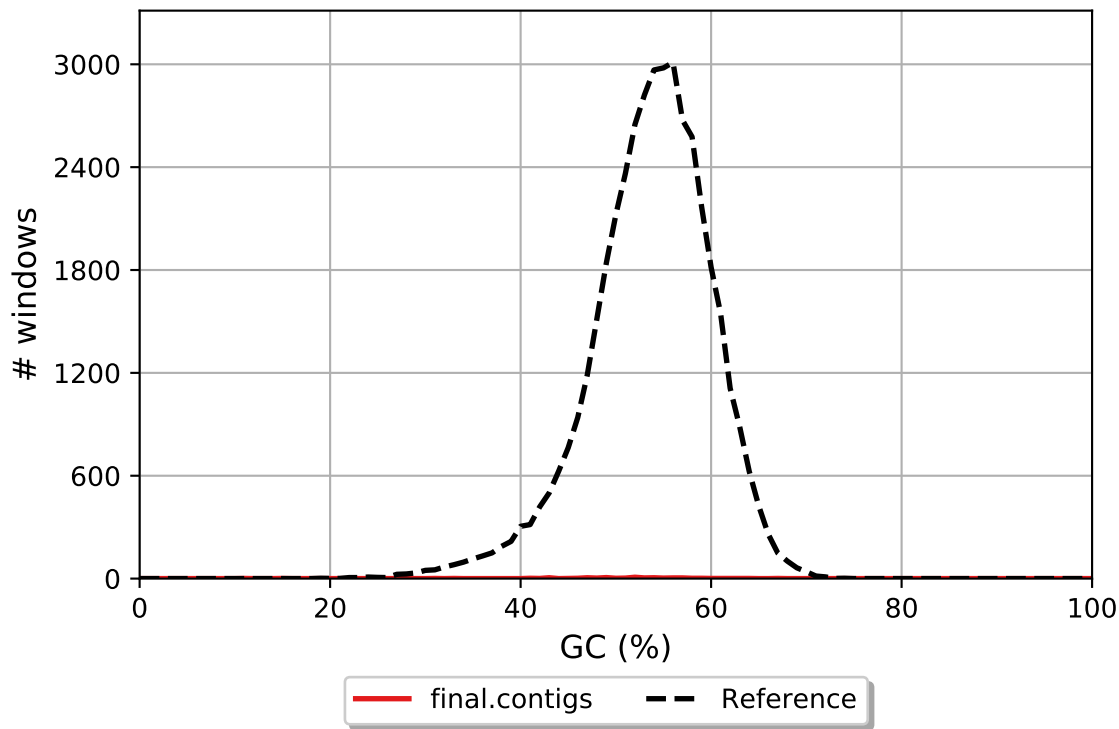
NGx



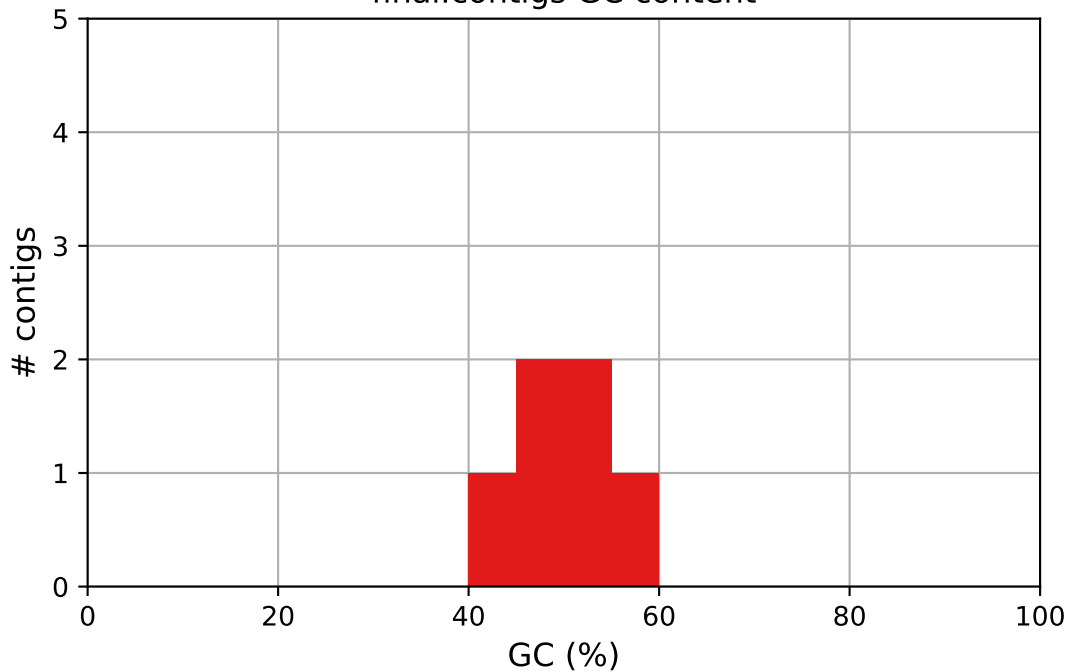
— final.contigs



GC content



final.contigs GC content



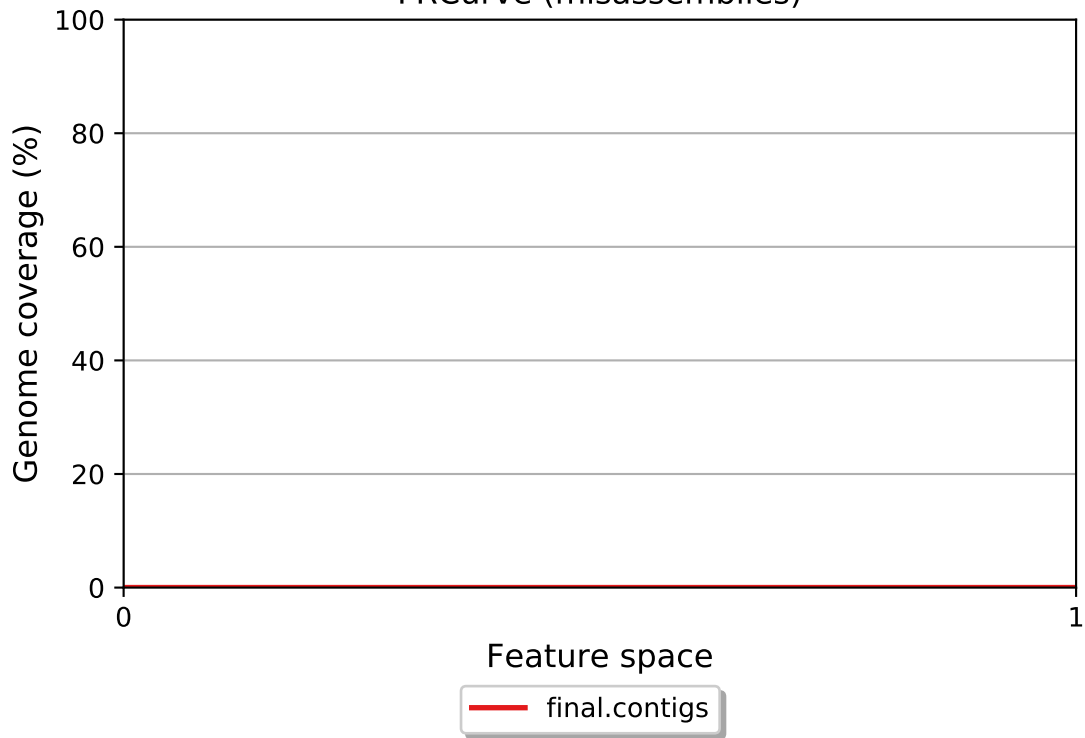
final.contigs

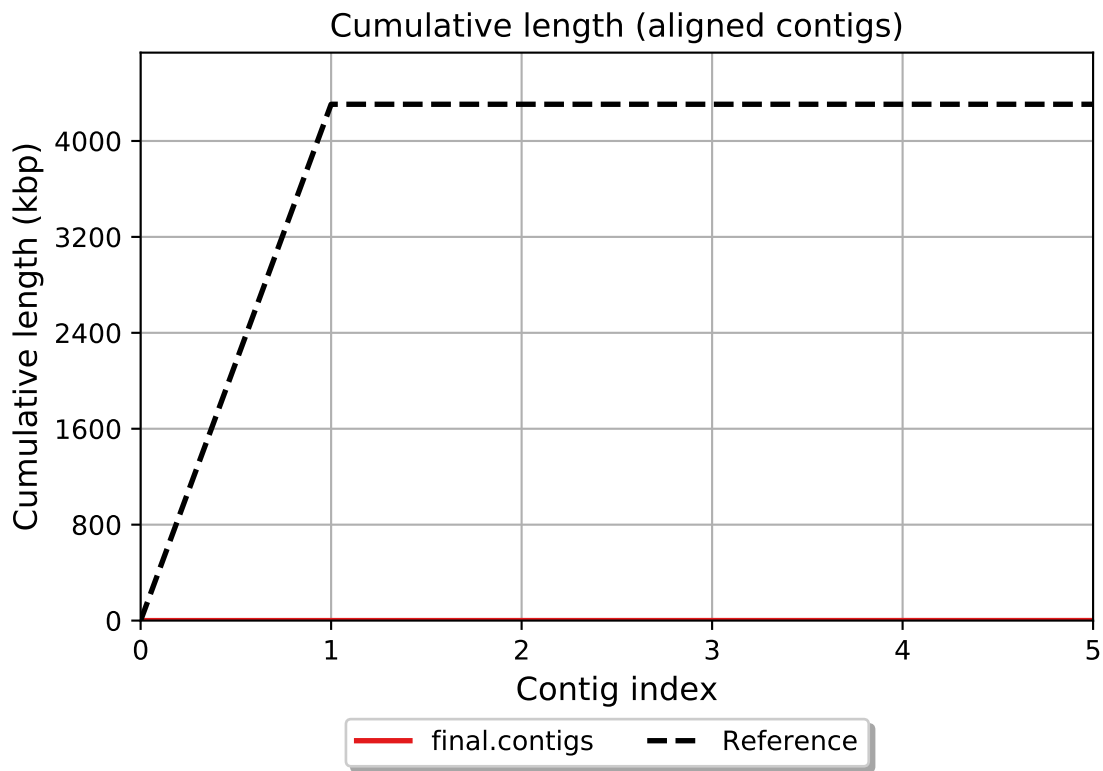
Misassemblies



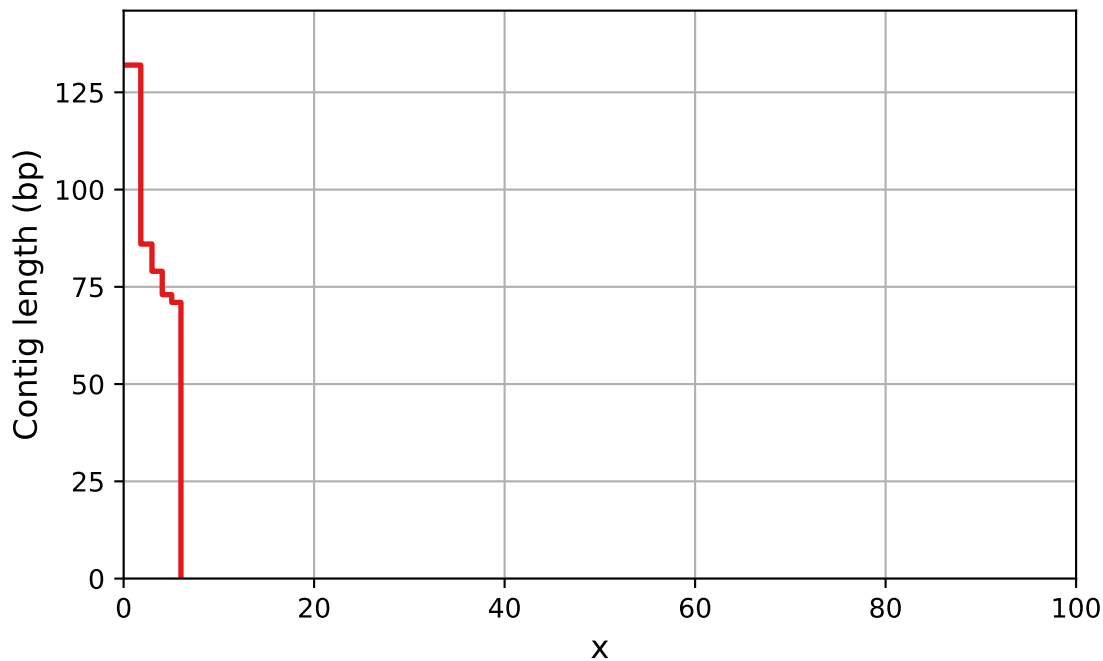
interspecies translocations

FRCurve (misassemblies)



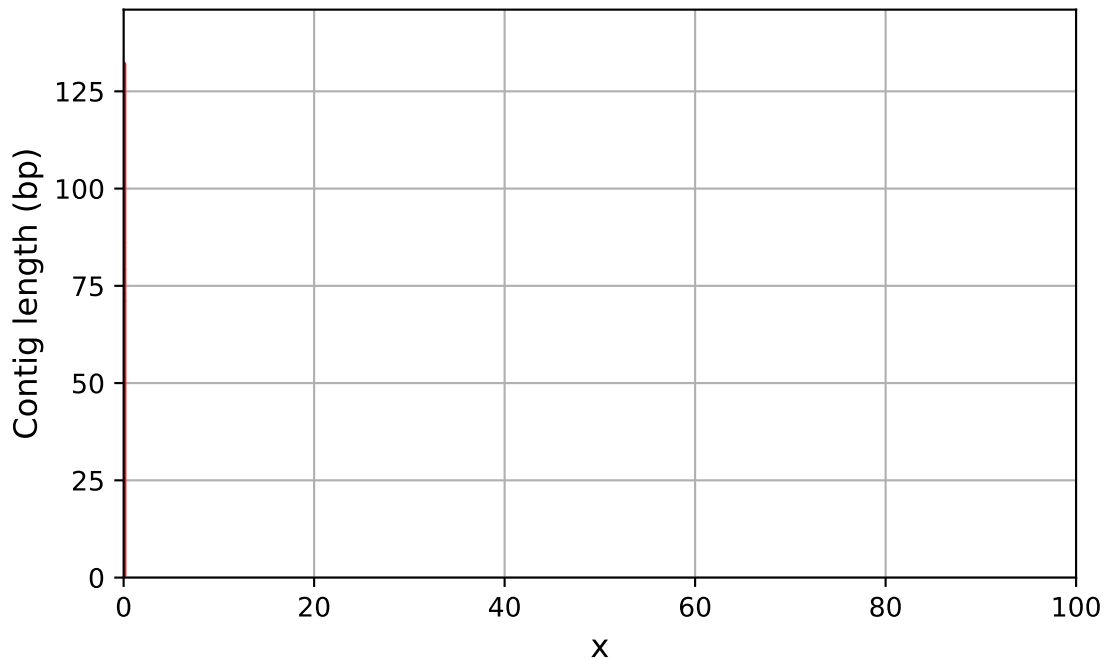


NAx



— final.contigs

NGAx



— final.contigs