

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 5 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 14119 |
| Total length (>= 5000 bp) | 5869 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 19 |
| Largest contig | 5869 |
| Total length | 22873 |
| Reference length | 4633577 |
| GC (%) | 45.70 |
| Reference GC (%) | 36.49 |
| N50 | 2207 |
| N75 | 666 |
| L50 | 3 |
| L75 | 10 |
| # 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 | 1 |
| # unaligned contigs | 3 + 8 part |
| Unaligned length | 17228 |
| Genome fraction (%) | 0.035 |
| Duplication ratio | 3.482 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 4565.08 |
| # indels per 100 kbp | 61.69 |
| Largest alignment | 495 |
| Total aligned length | 2285 |
| 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 | 1 |
| # mismatches | 74 |
| # indels | 1 |
| # indels (<= 5 bp) | 1 |
| # indels (> 5 bp) | 0 |
| Indels length | 1 |

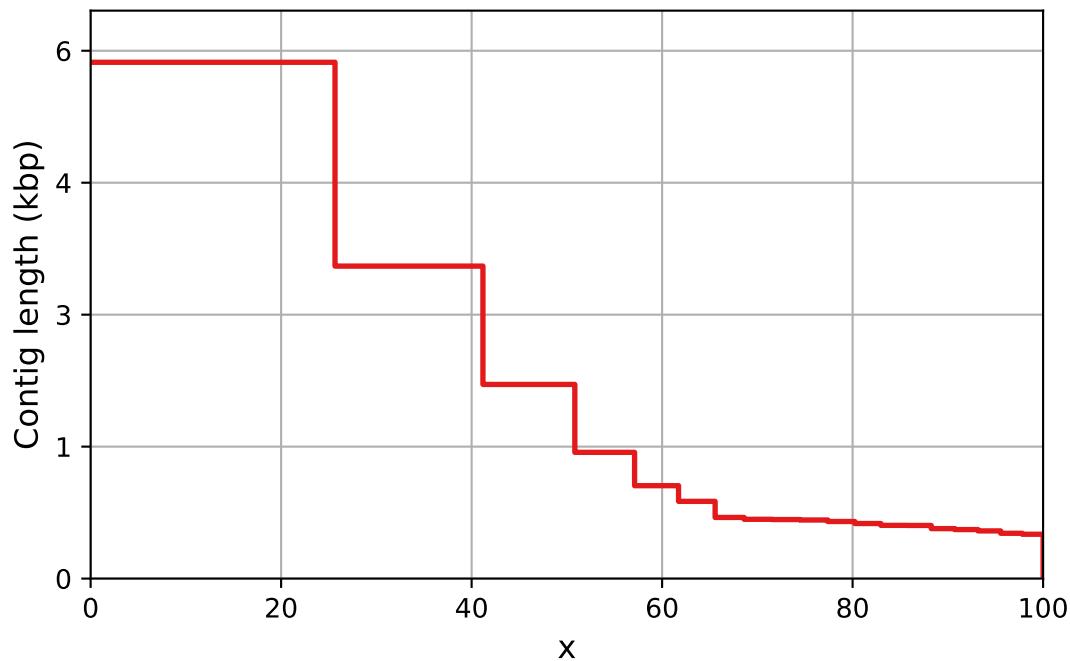
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 3 |
| Fully unaligned length | 2018 |
| # partially unaligned contigs | 8 |
| Partially unaligned length | 15210 |
| # N's | 0 |

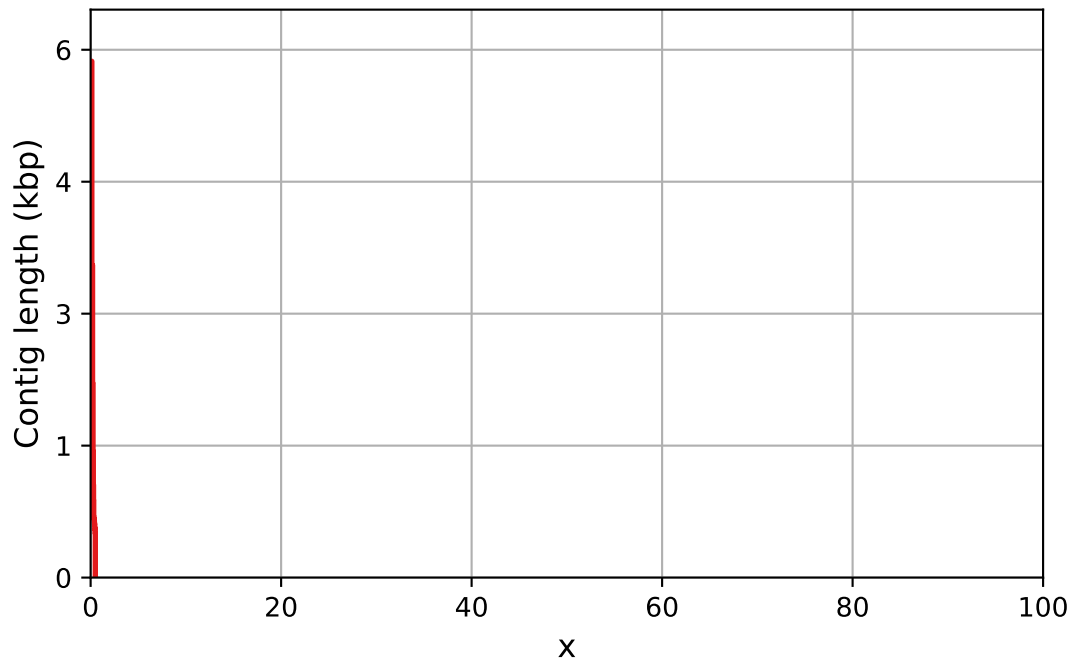
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

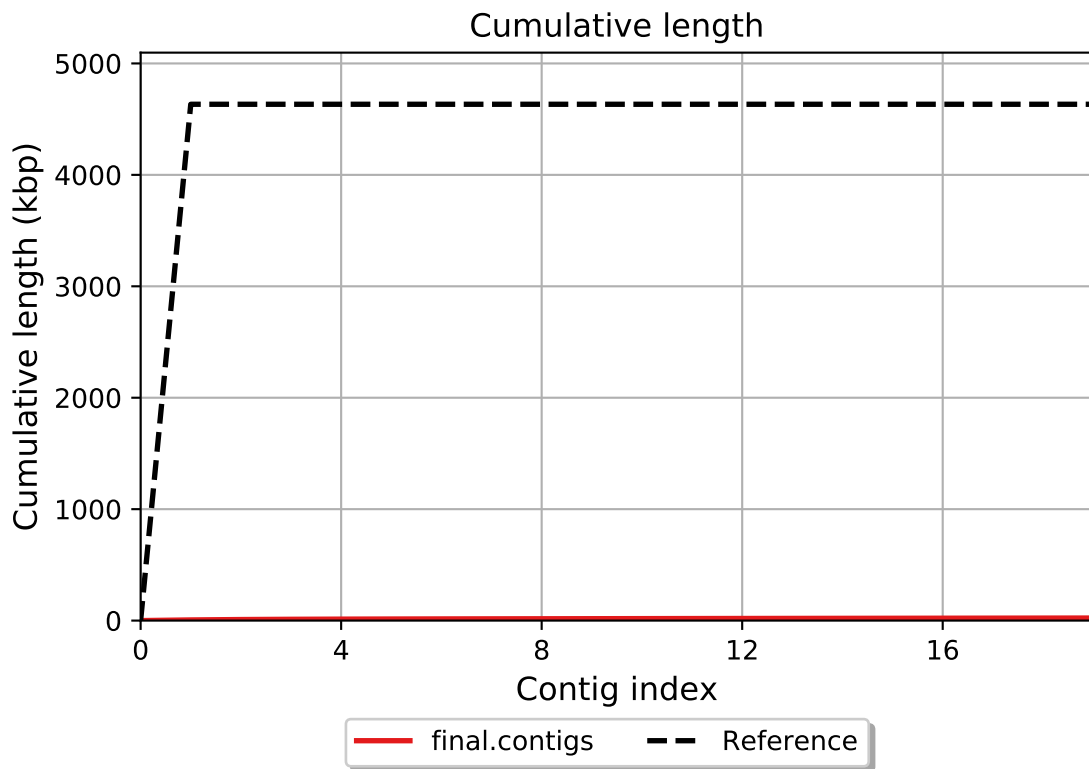


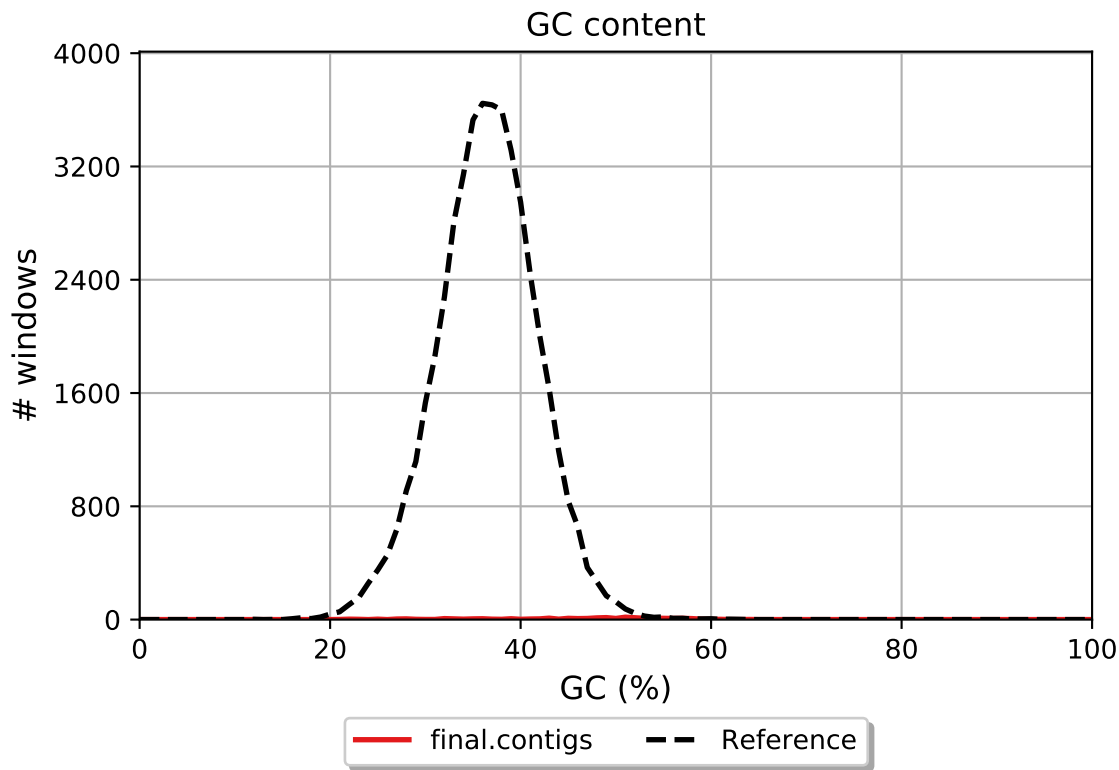
— final.contigs

NGx

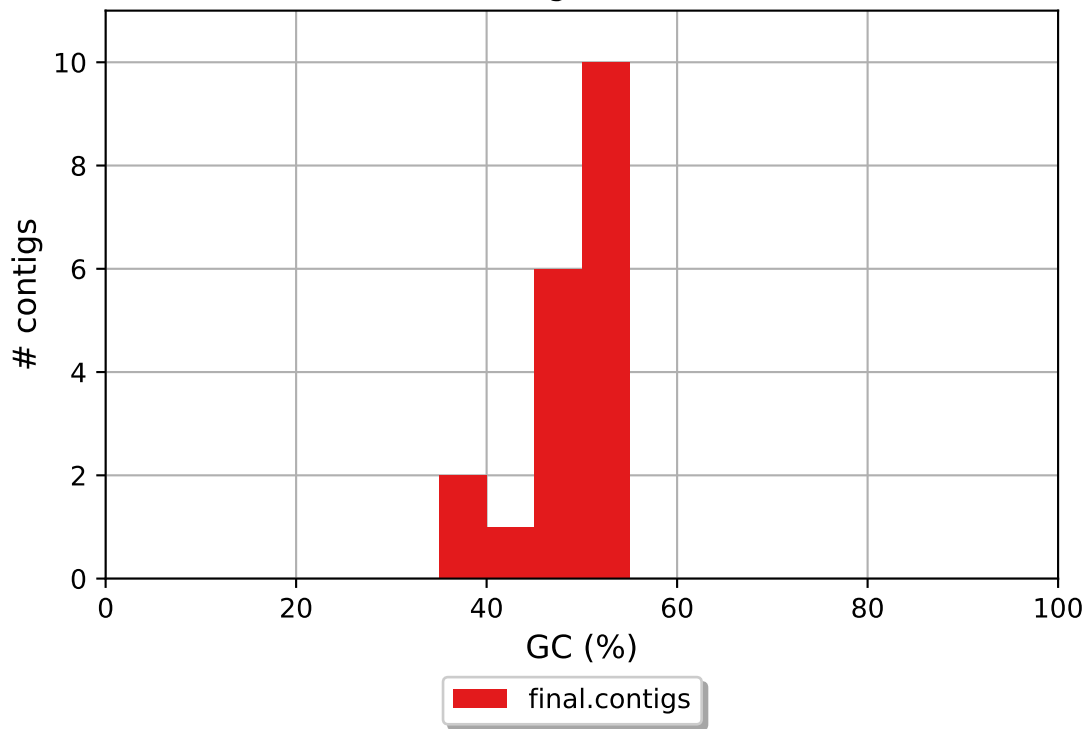


— final.contigs





final.contigs GC content

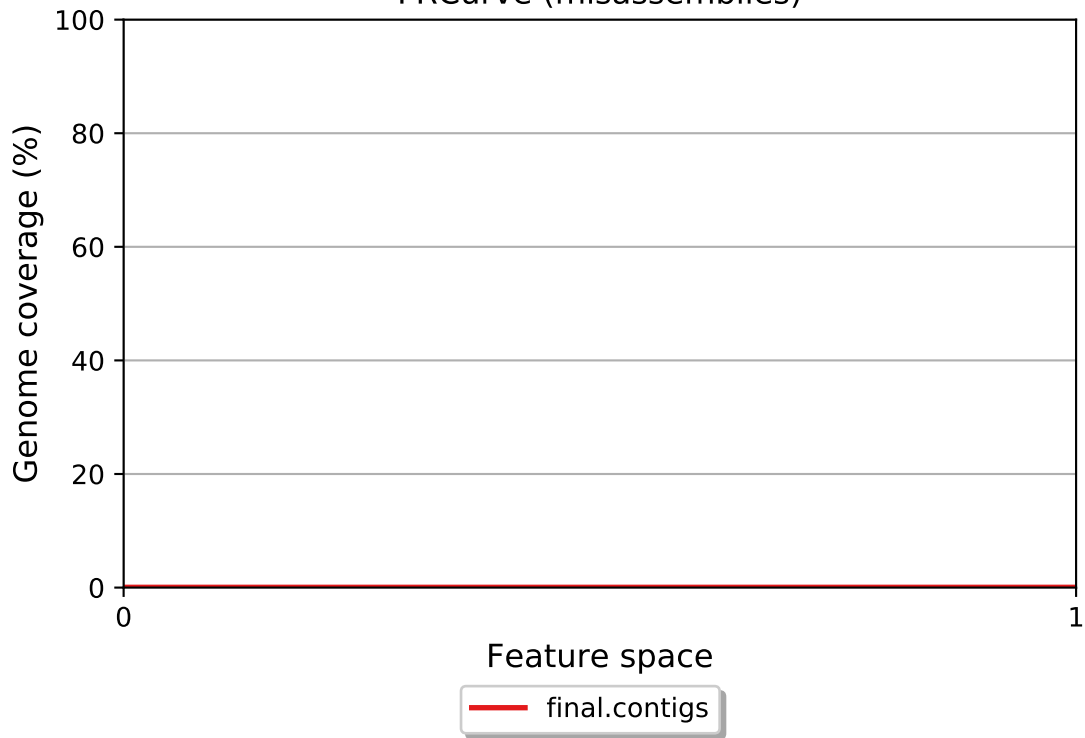


Misassemblies

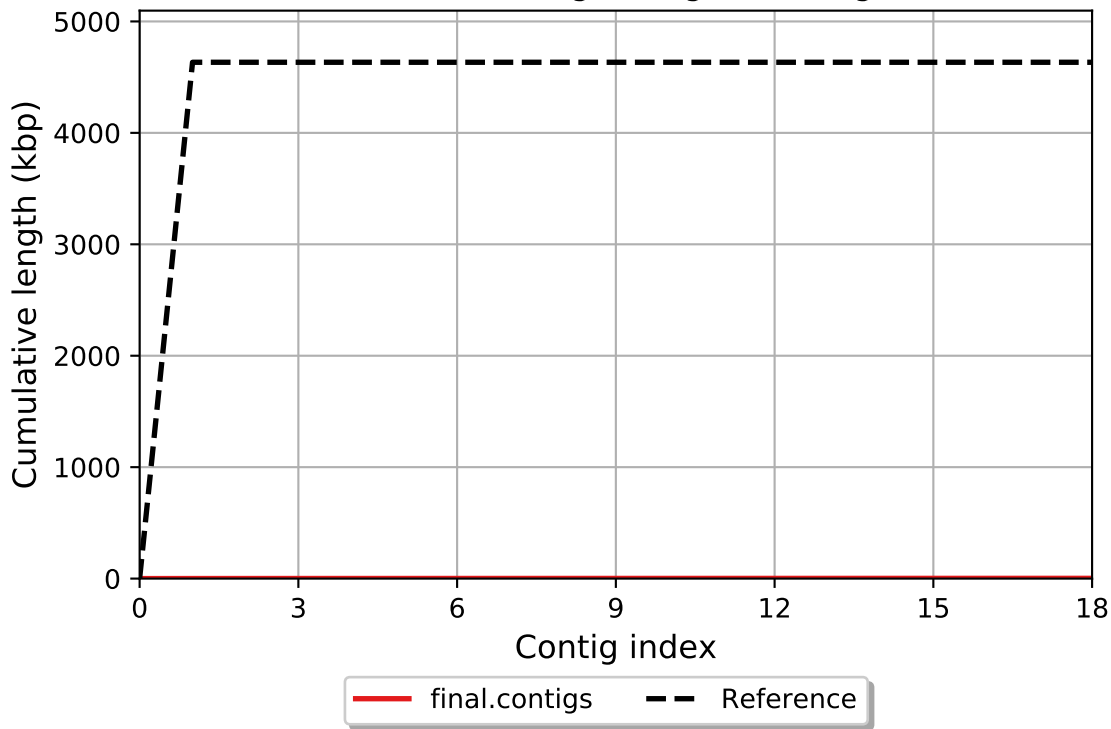


interspecies translocations

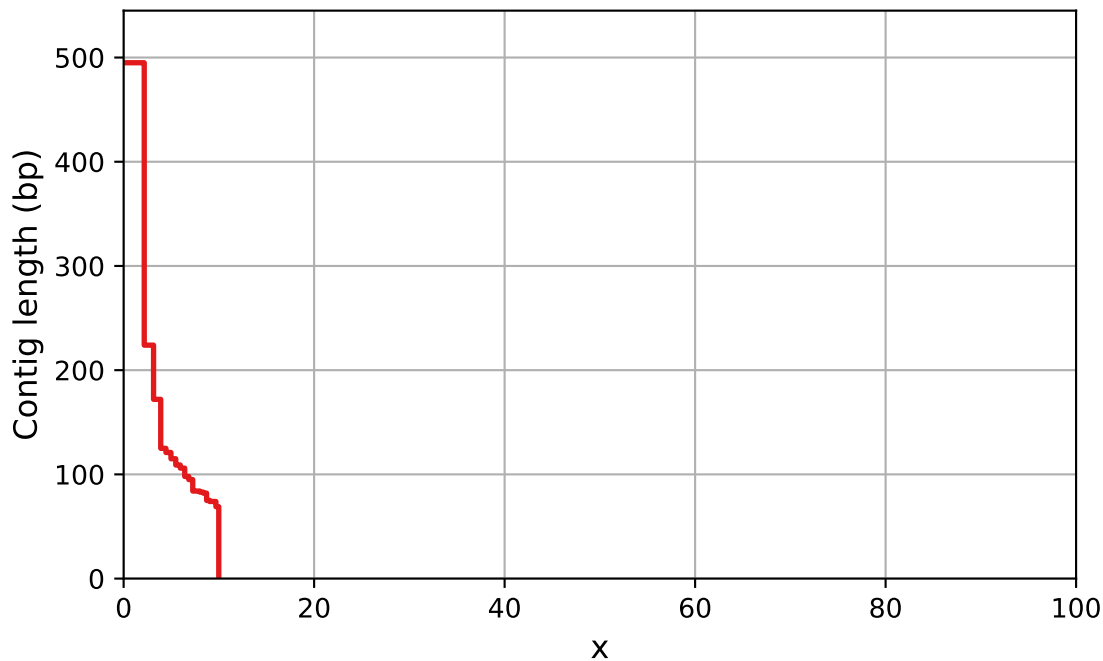
FRCurve (misassemblies)



Cumulative length (aligned contigs)

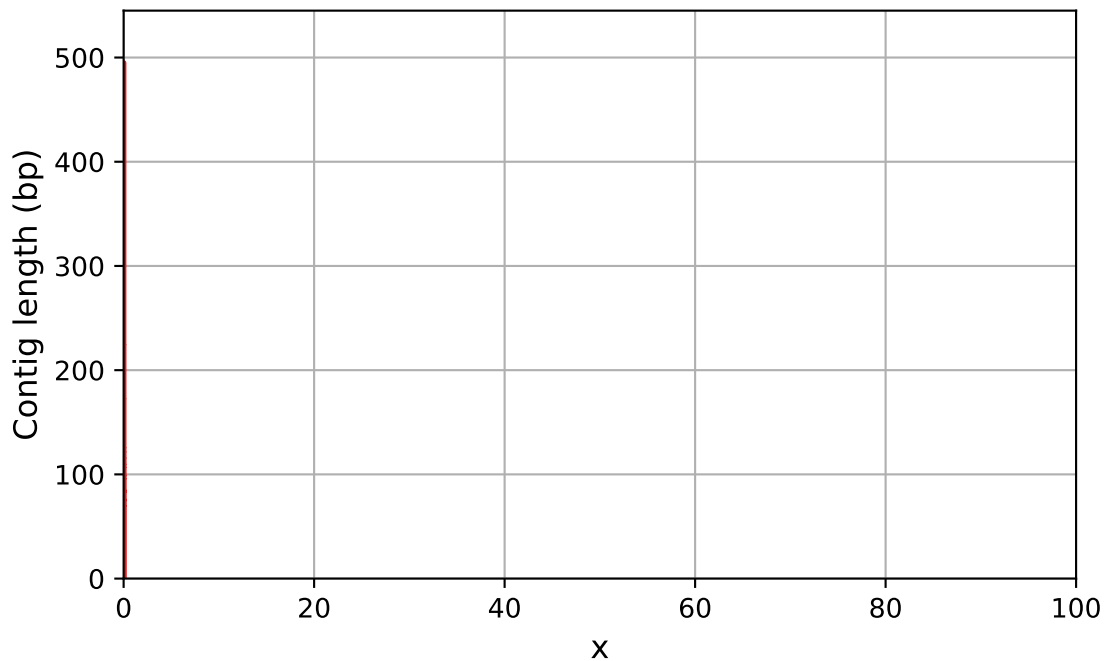


NAx



— final.contigs

NGAx



— final.contigs