

Report

| | final.contigs |
|---------------------------------|---------------|
| # contigs (≥ 1000 bp) | 470 |
| # contigs (≥ 5000 bp) | 1 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 1000 bp) | 719036 |
| Total length (≥ 5000 bp) | 5037 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 1361 |
| Largest contig | 5037 |
| Total length | 1349428 |
| Reference length | 2224914 |
| GC (%) | 61.34 |
| Reference GC (%) | 60.84 |
| N50 | 1044 |
| NG50 | 666 |
| N75 | 736 |
| L50 | 427 |
| LG50 | 958 |
| L75 | 815 |
| # misassemblies | 5 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 6313 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 1 |
| # unaligned contigs | 5 + 42 part |
| Unaligned length | 63070 |
| Genome fraction (%) | 55.389 |
| Duplication ratio | 1.044 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1151.61 |
| # indels per 100 kbp | 5.76 |
| Largest alignment | 3896 |
| Total aligned length | 1269842 |
| NA50 | 981 |
| NGA50 | 611 |
| NA75 | 678 |
| LA50 | 455 |
| LGA50 | 1029 |
| LA75 | 873 |

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 | 5 |
| # contig misassemblies | 5 |
| # c. relocations | 5 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 6313 |
| # possibly misassembled contigs | 47 |
| # possible misassemblies | 55 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 1 |
| # mismatches | 14192 |
| # indels | 71 |
| # indels (<= 5 bp) | 62 |
| # indels (> 5 bp) | 9 |
| Indels length | 285 |

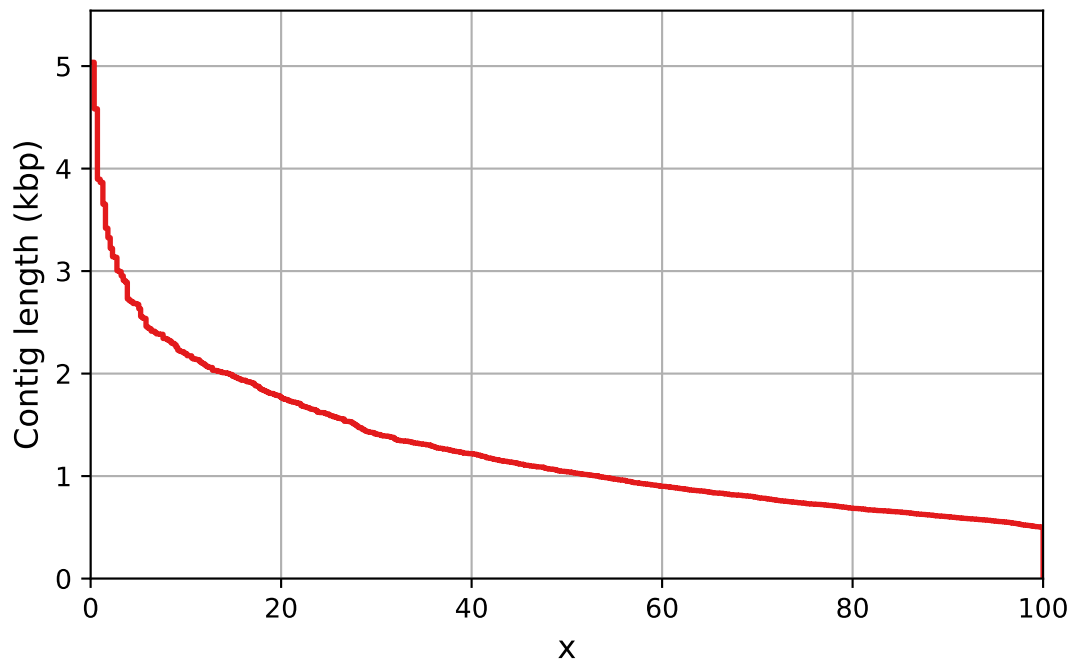
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 5 |
| Fully unaligned length | 6185 |
| # partially unaligned contigs | 42 |
| Partially unaligned length | 56885 |
| # N's | 0 |

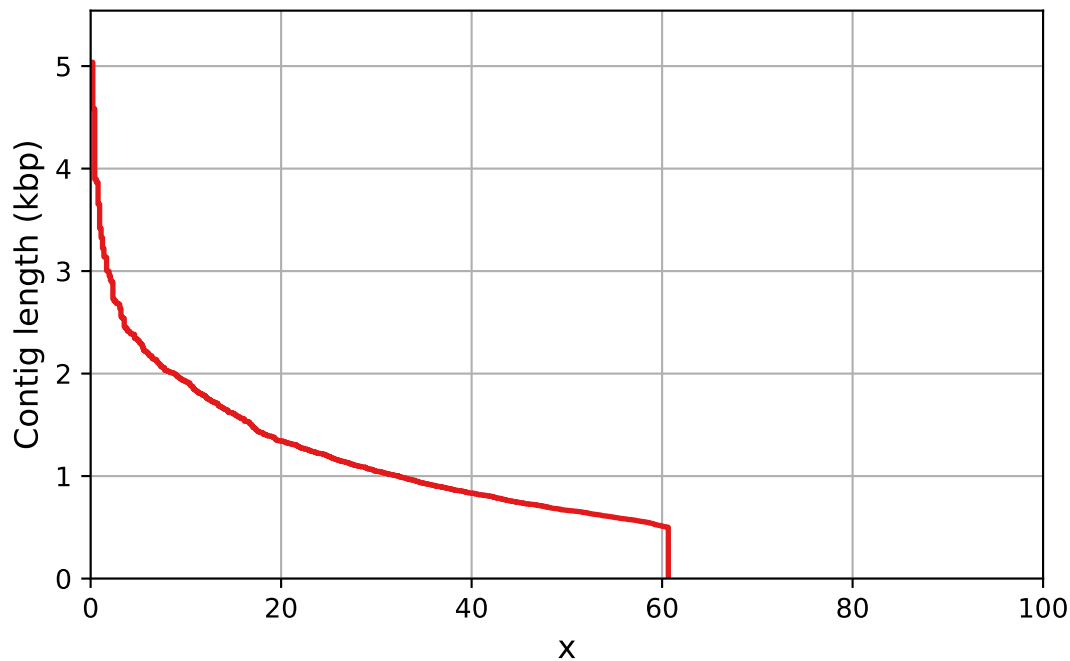
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

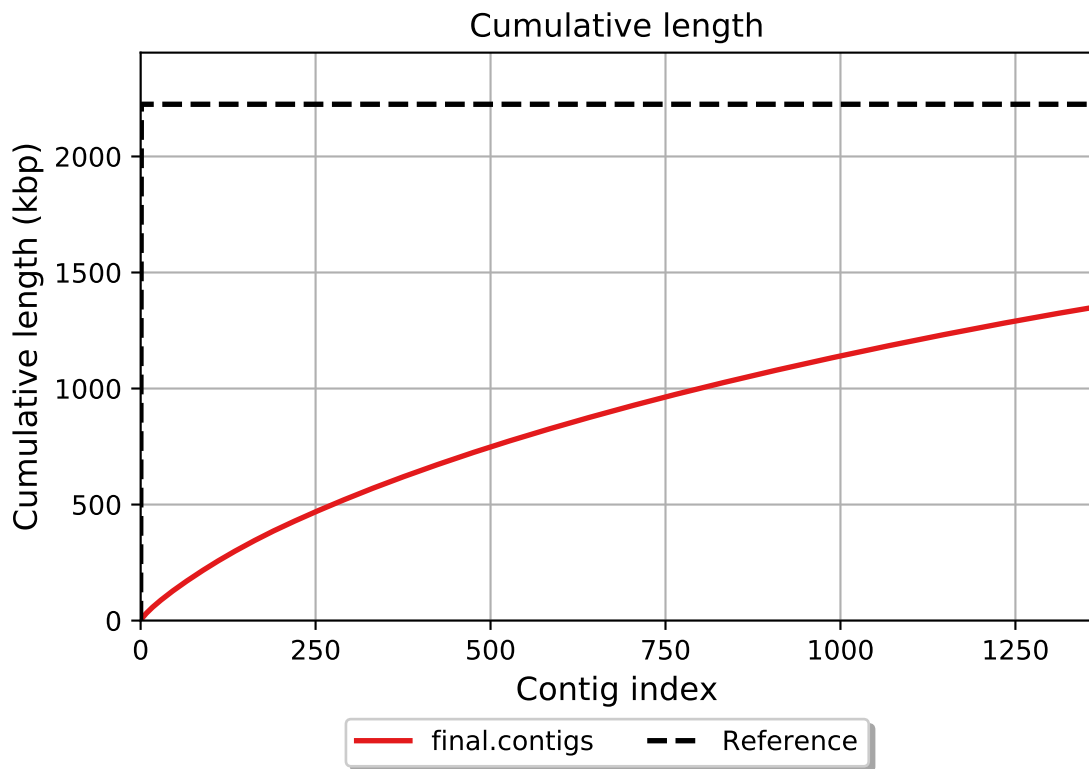


— final.contigs

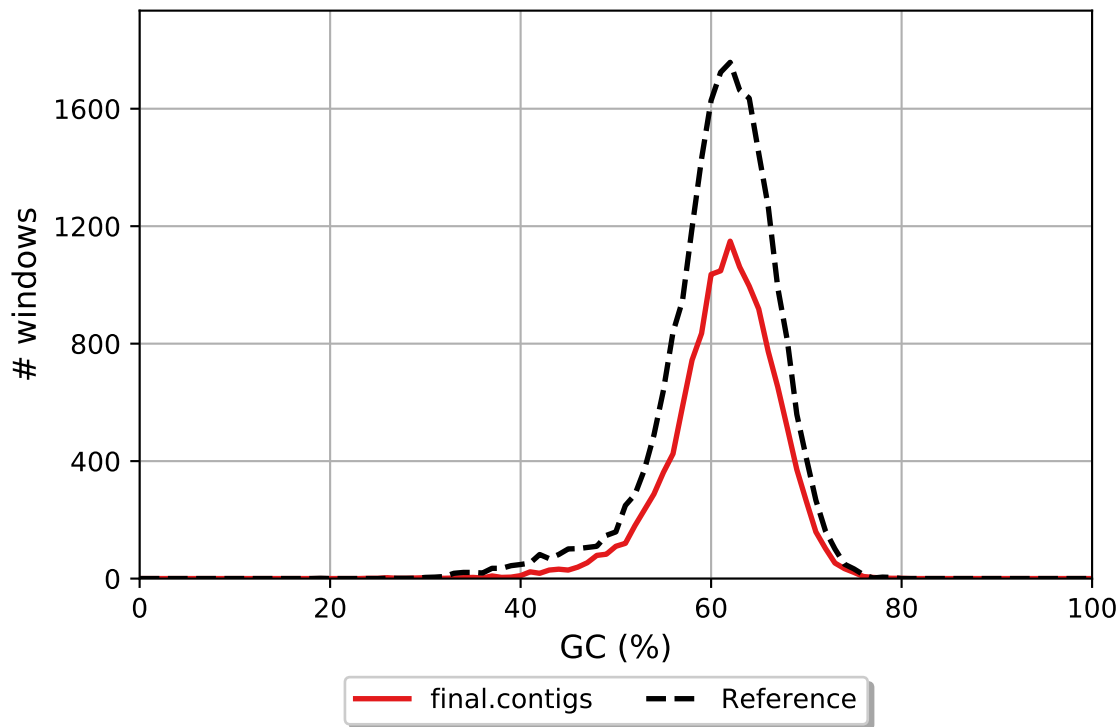
NGx



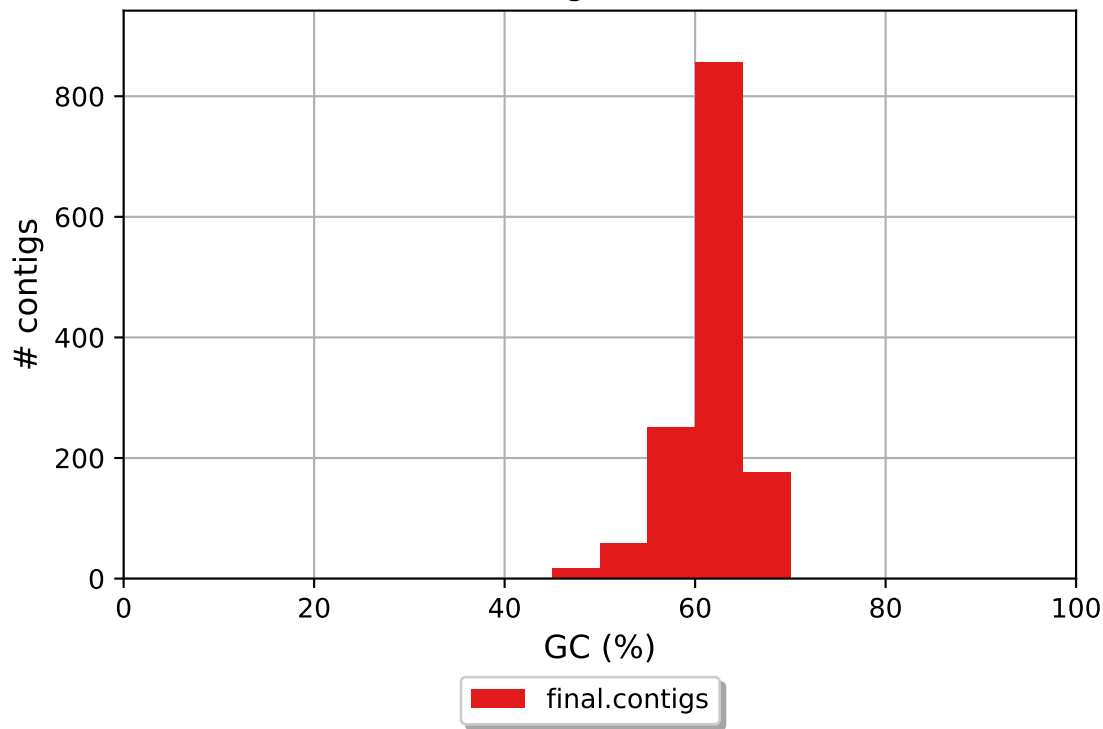
— final.contigs



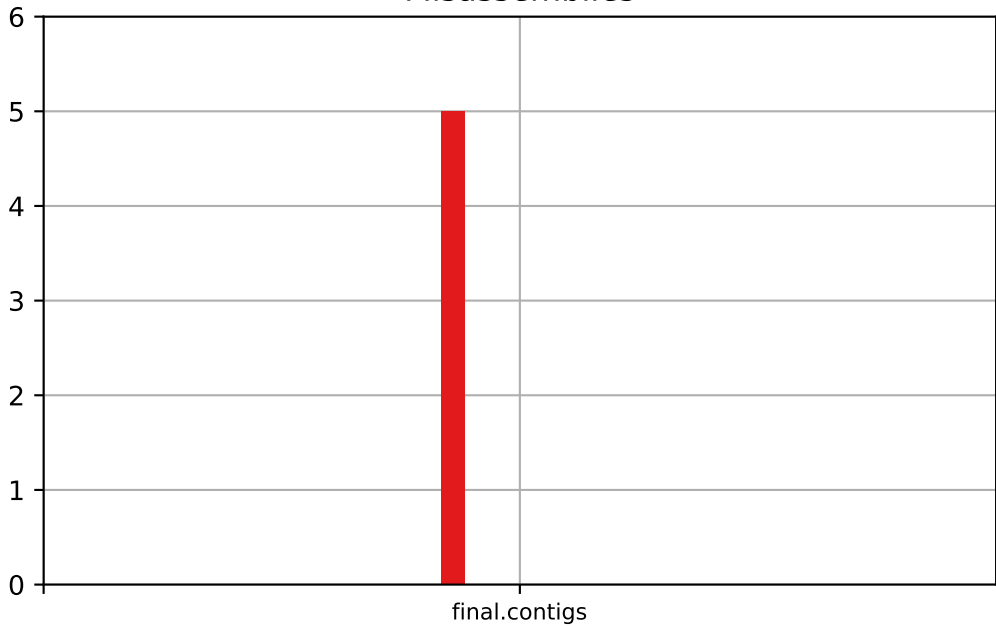
GC content



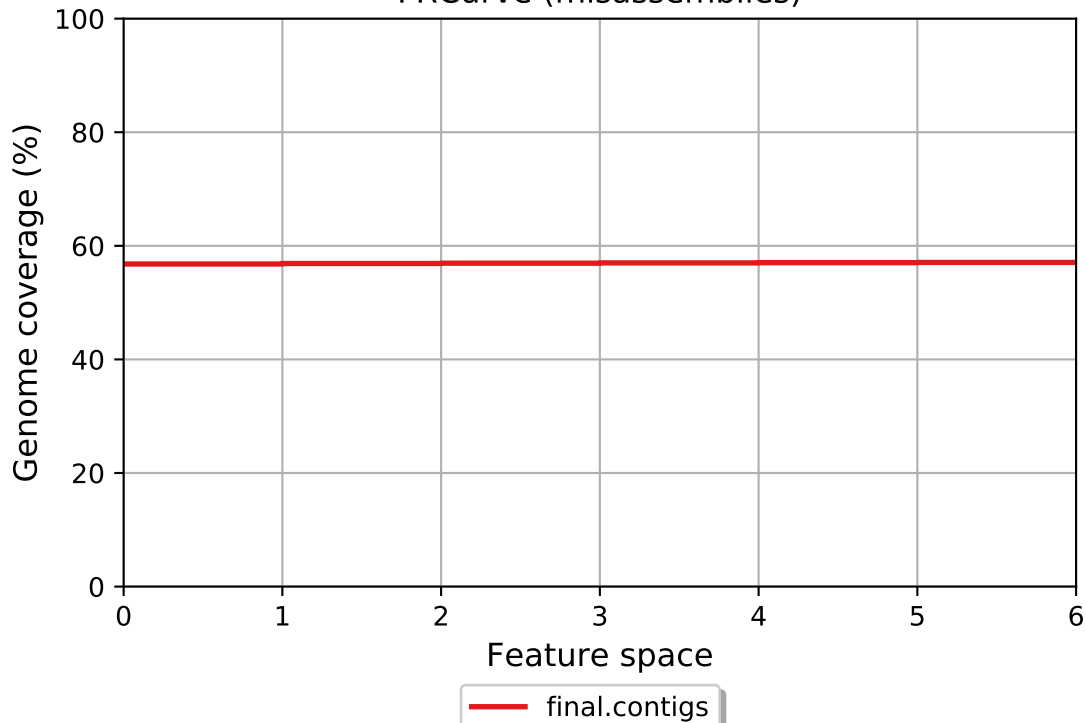
final.contigs GC content



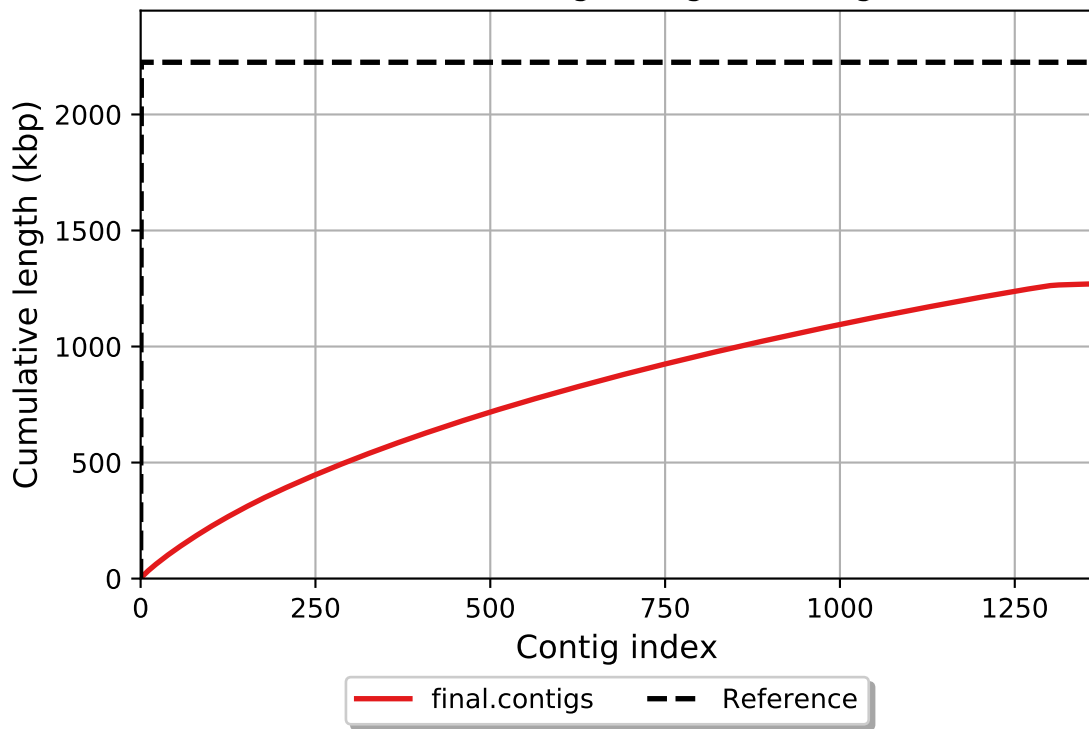
Misassemblies



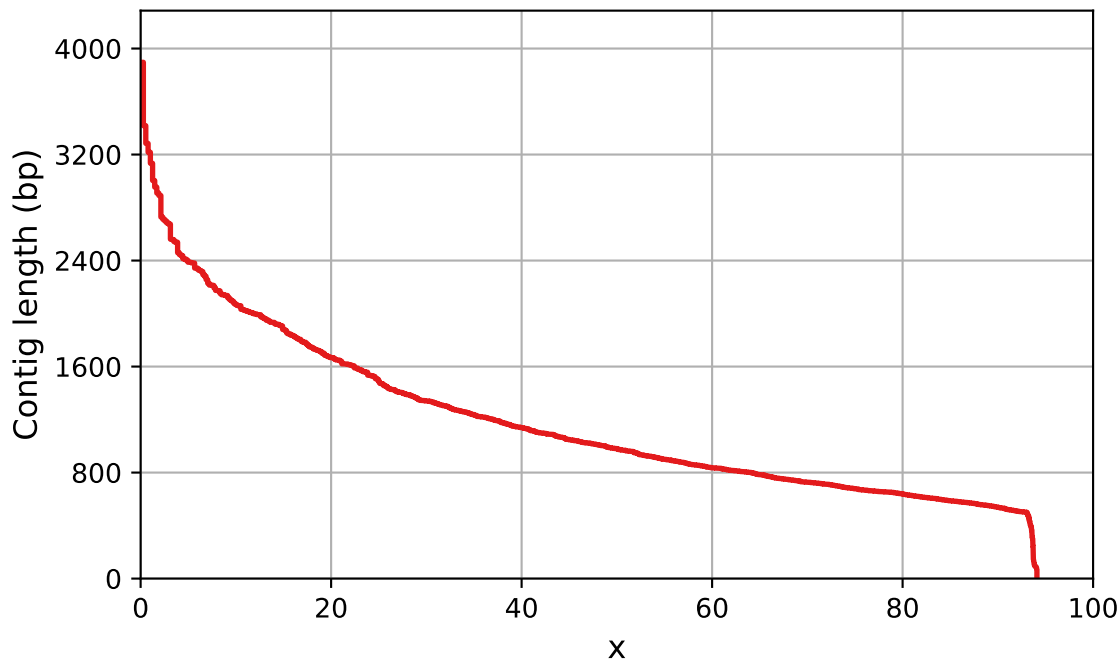
FRCurve (misassemblies)



Cumulative length (aligned contigs)

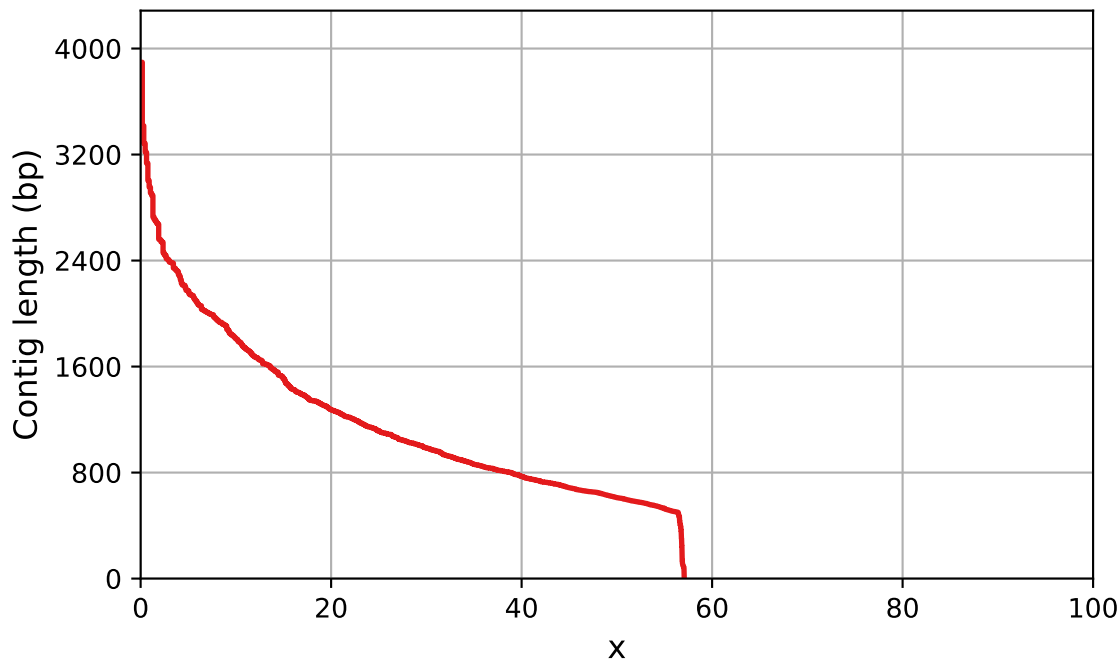


NAx



— final.contigs

NGAx



— final.contigs