

Report

| | SRR1191991_fw_80_complete |
|-----------------------------|---------------------------|
| # contigs (>= 1000 bp) | 43 |
| # contigs (>= 5000 bp) | 22 |
| # contigs (>= 10000 bp) | 11 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 249684 |
| Total length (>= 5000 bp) | 208527 |
| Total length (>= 10000 bp) | 141059 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 71 |
| Largest contig | 14979 |
| Total length | 270199 |
| Reference length | 30114 |
| GC (%) | 41.56 |
| Reference GC (%) | 41.12 |
| N50 | 10392 |
| NG50 | 14978 |
| N75 | 5018 |
| NG75 | 14978 |
| L50 | 11 |
| LG50 | 2 |
| L75 | 21 |
| LG75 | 2 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 4 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 82.782 |
| Duplication ratio | 10.839 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 4849.77 |
| # indels per 100 kbp | 20.06 |
| Largest alignment | 14978 |
| Total aligned length | 270133 |
| NA50 | 10391 |
| NGA50 | 14977 |
| NA75 | 5017 |
| NGA75 | 14977 |
| LA50 | 11 |
| LGA50 | 2 |
| LA75 | 21 |
| LGA75 | 2 |

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

| | SRR1191991_fw_80_complete |
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| # 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 | 0 |
| # possible misassemblies | 0 |
| # local misassemblies | 4 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 1209 |
| # indels | 5 |
| # indels (<= 5 bp) | 5 |
| # indels (> 5 bp) | 0 |
| Indels length | 14 |

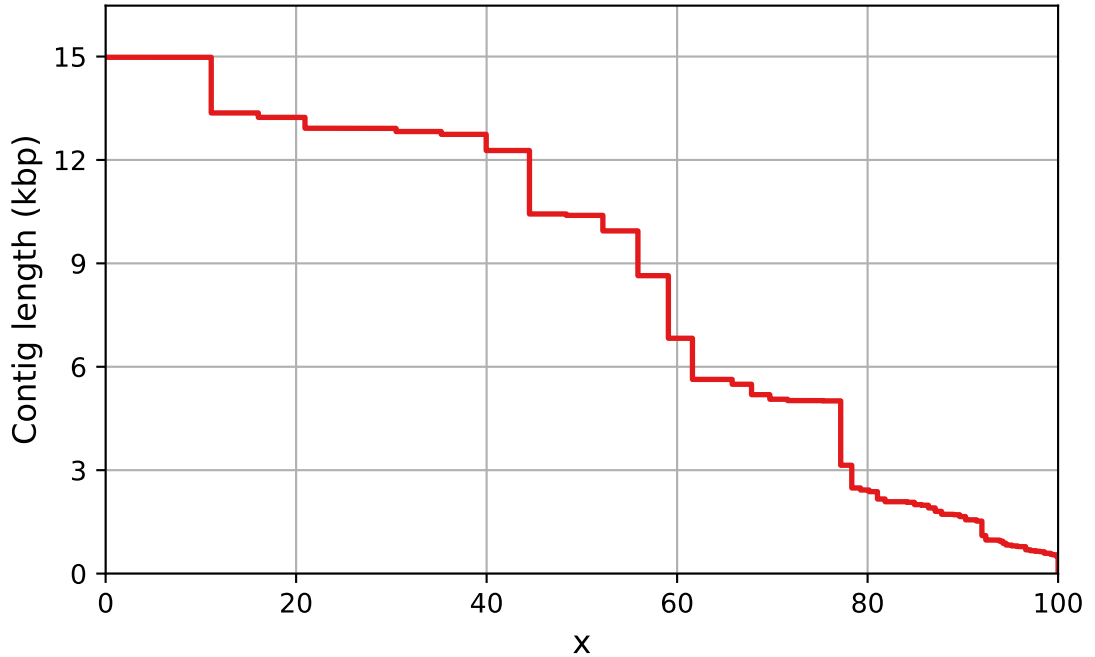
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | SRR1191991_fw_80_complete |
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| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

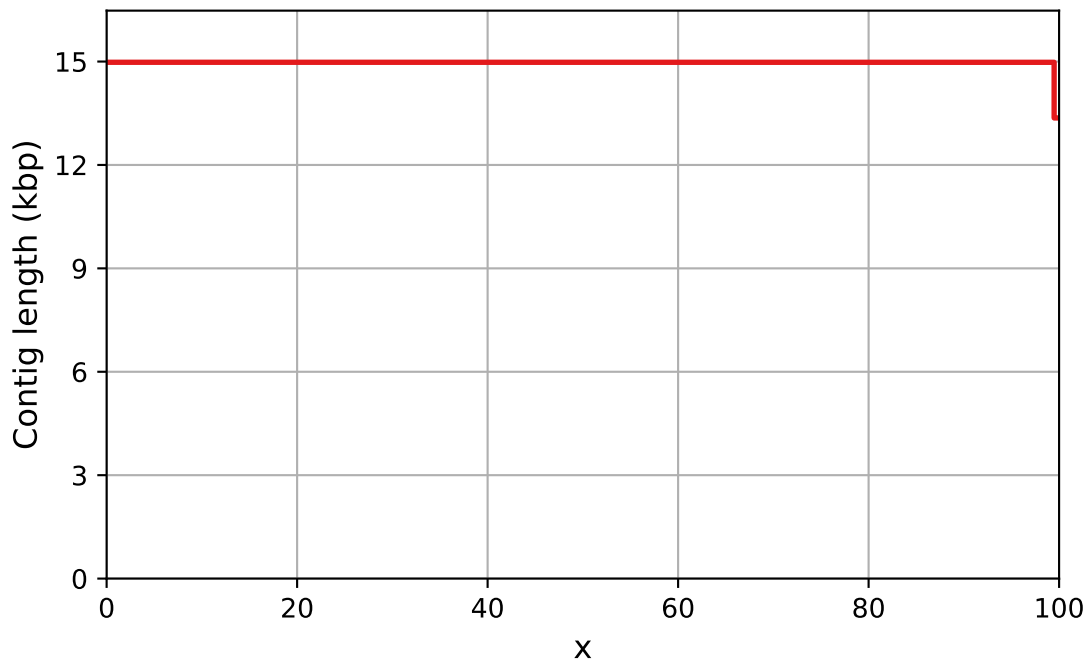
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



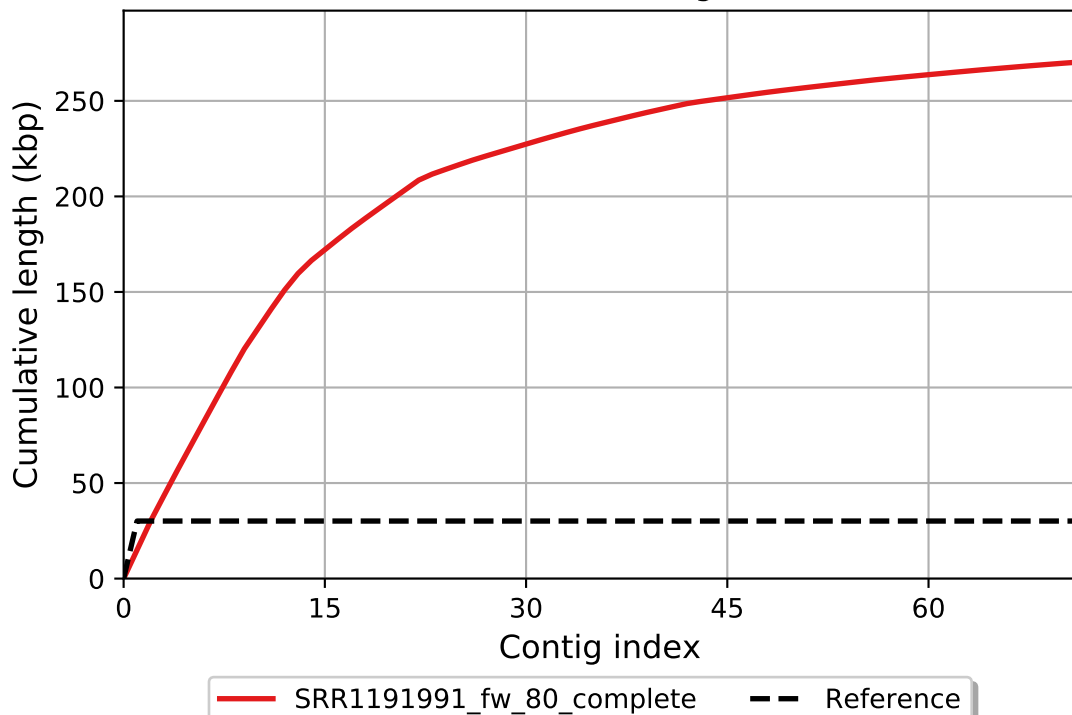
SRR1191991_fw_80_complete

NGx

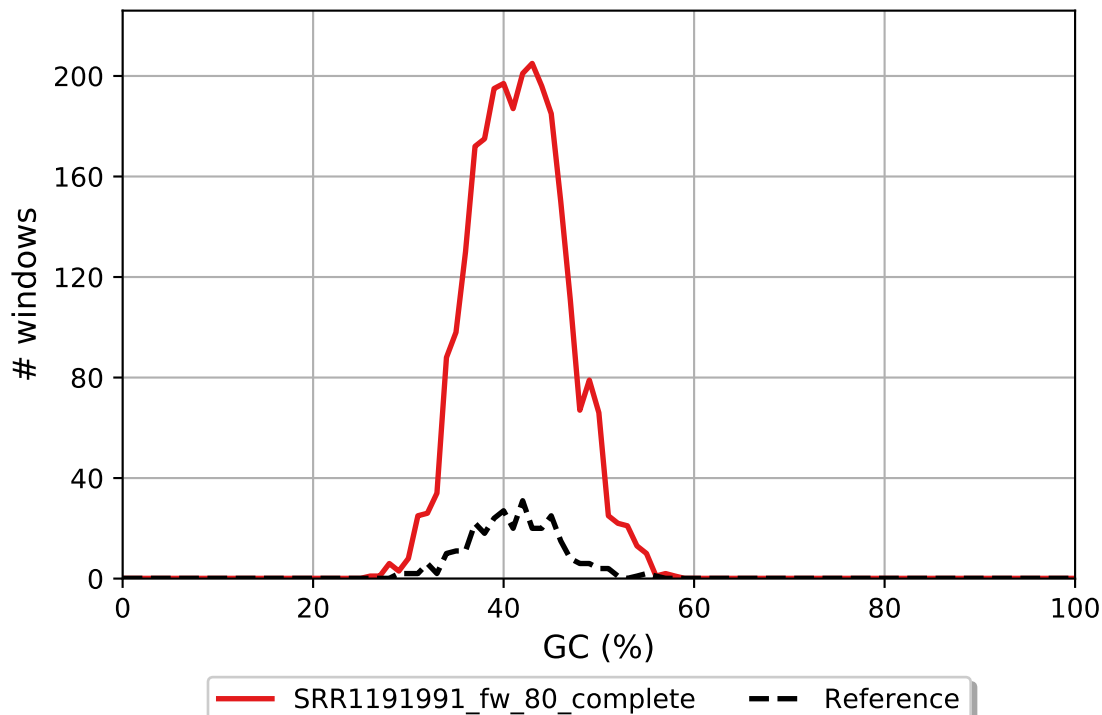


— SRR1191991_fw_80_complete

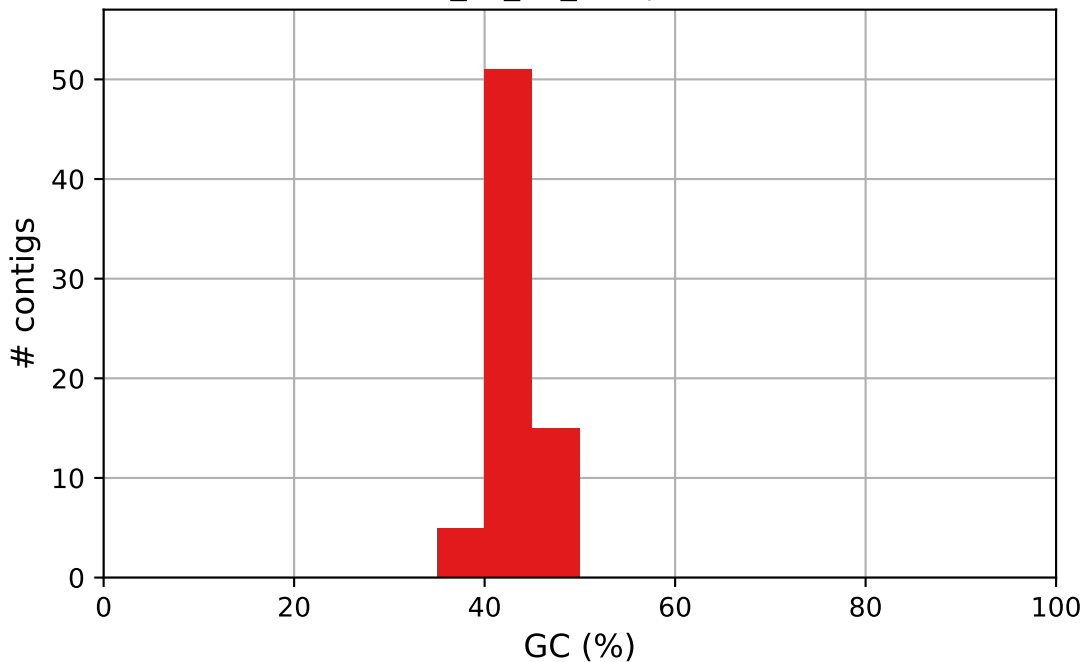
Cumulative length



GC content

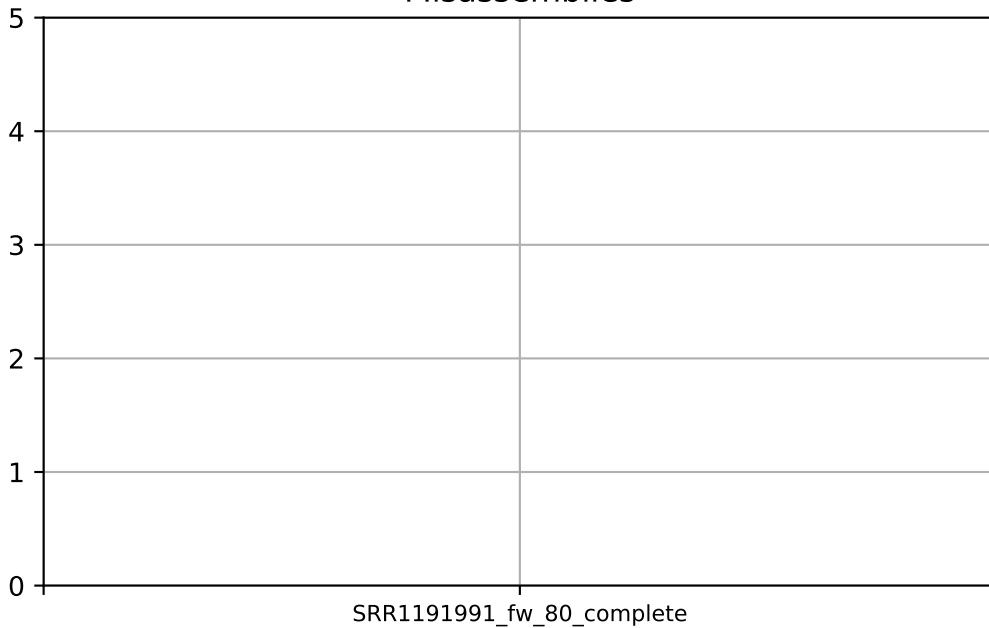


SRR1191991_fw_80_complete GC content

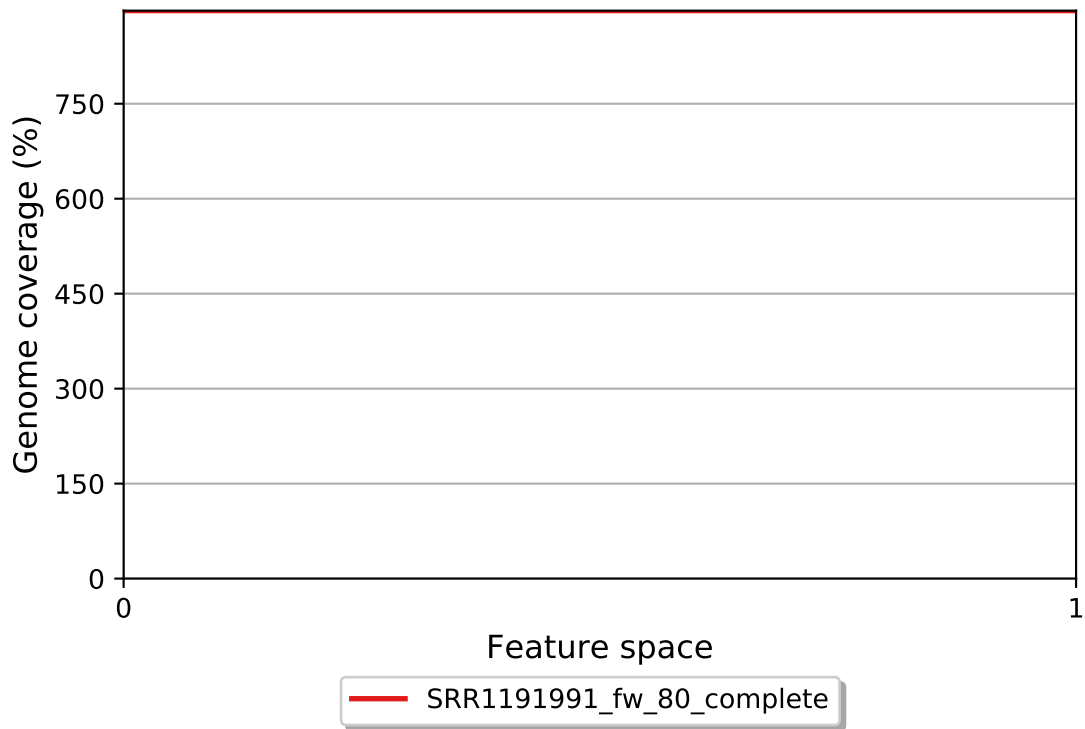


■ SRR1191991_fw_80_complete

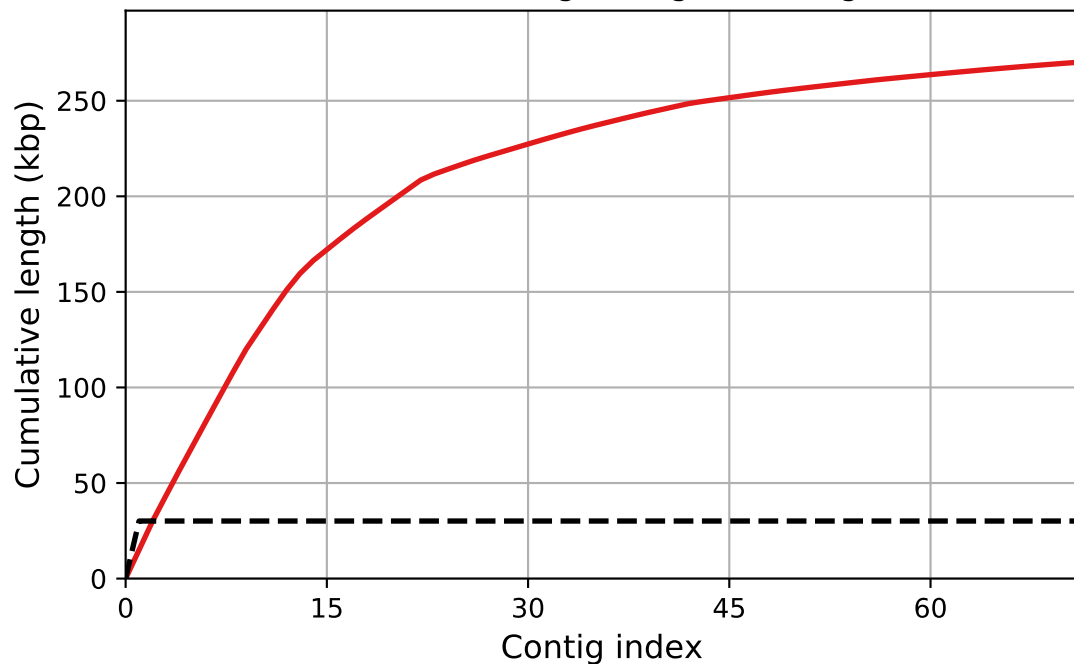
Misassemblies



FRCurve (misassemblies)

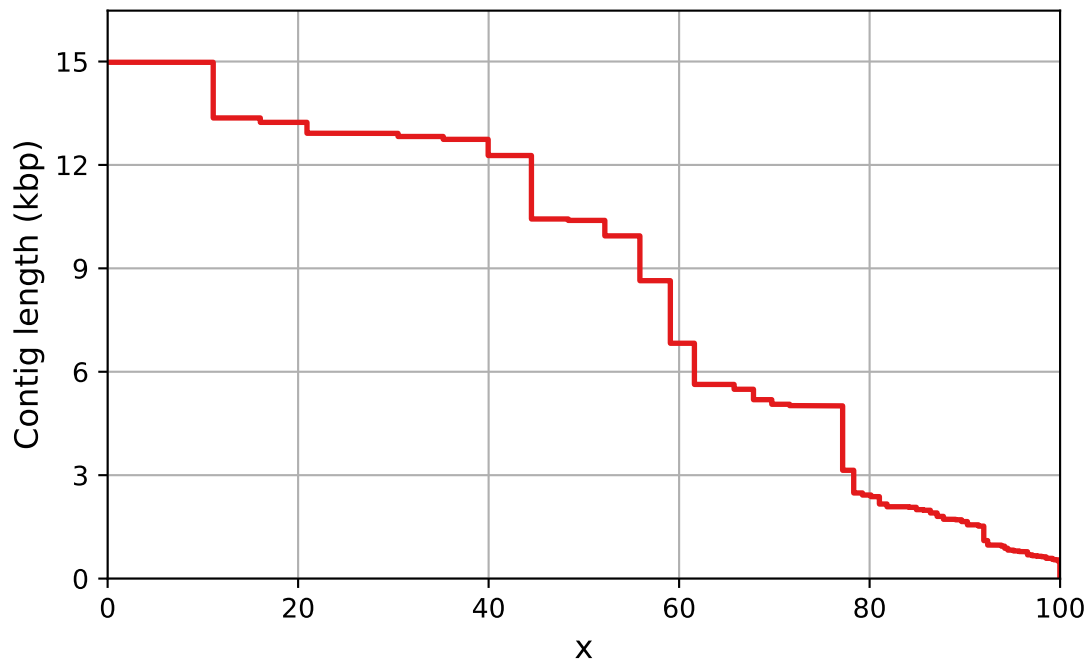


Cumulative length (aligned contigs)



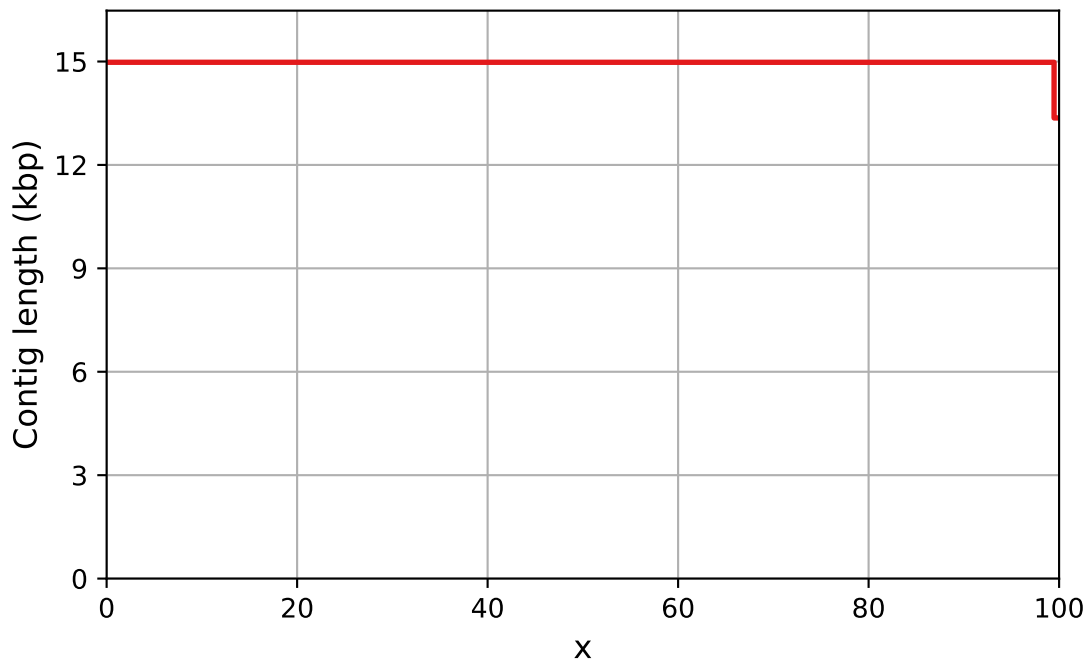
— SRR1191991_fw_80_complete - - Reference

NAx



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NGAx



— SRR1191991_fw_80_complete