

Report

| | TARA_PSW_RAW |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 387 |
| # contigs (>= 5000 bp) | 96 |
| # contigs (>= 10000 bp) | 53 |
| # contigs (>= 25000 bp) | 36 |
| # contigs (>= 50000 bp) | 15 |
| Total length (>= 1000 bp) | 3868949 |
| Total length (>= 5000 bp) | 3279405 |
| Total length (>= 10000 bp) | 2997829 |
| Total length (>= 25000 bp) | 2704483 |
| Total length (>= 50000 bp) | 1996739 |
| # contigs | 387 |
| Largest contig | 729901 |
| Total length | 3868949 |
| Reference length | 7658814 |
| GC (%) | 54.49 |
| Reference GC (%) | 63.29 |
| N50 | 54008 |
| NG50 | 1094 |
| N75 | 15846 |
| L50 | 14 |
| LG50 | 350 |
| L75 | 46 |
| # 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 | 4 |
| # unaligned contigs | 19 + 368 part |
| Unaligned length | 3837278 |
| Genome fraction (%) | 0.105 |
| Duplication ratio | 3.943 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 7993.03 |
| # indels per 100 kbp | 149.40 |
| Largest alignment | 427 |
| Total aligned length | 31671 |
| 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

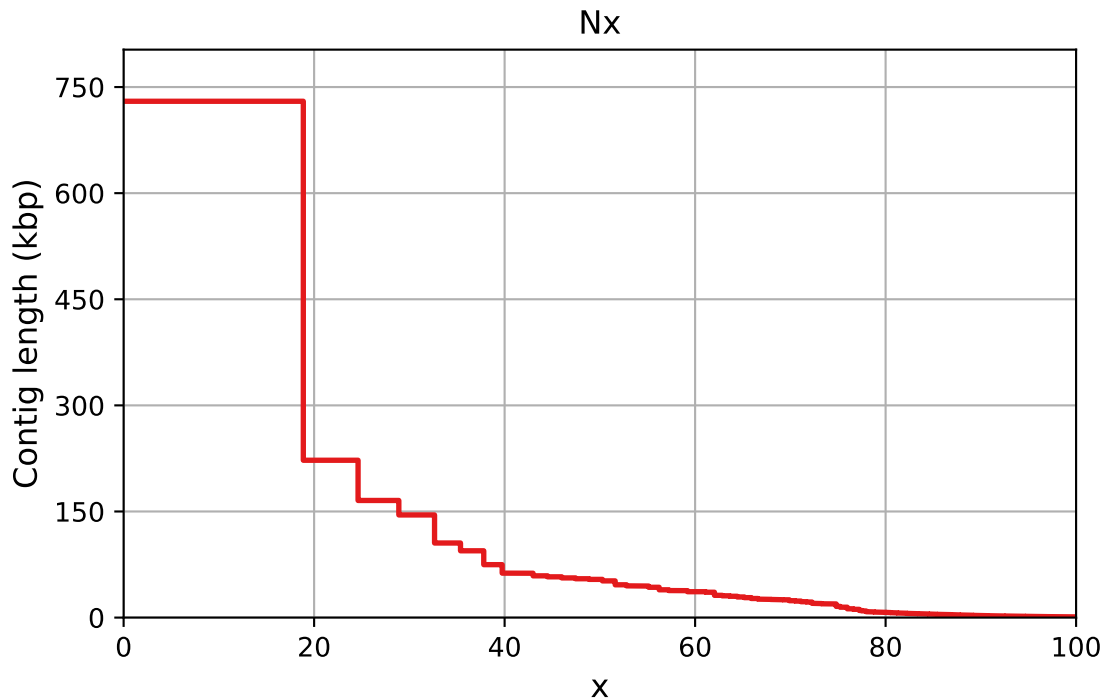
| | TARA_PSW_RAW |
|---------------------------------|--------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 378 |
| # possible misassemblies | 470 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 4 |
| # mismatches | 642 |
| # indels | 12 |
| # indels (<= 5 bp) | 12 |
| # indels (> 5 bp) | 0 |
| Indels length | 15 |

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

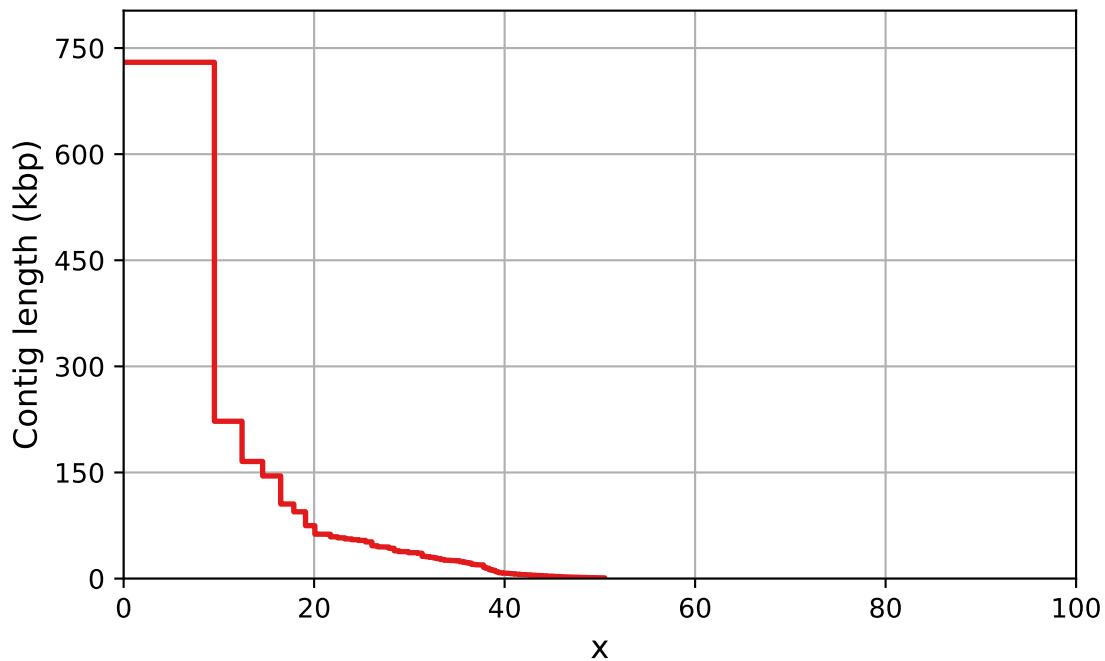
| | TARA_PSW_RAW |
|-------------------------------|--------------|
| # fully unaligned contigs | 19 |
| Fully unaligned length | 379784 |
| # partially unaligned contigs | 368 |
| Partially unaligned length | 3457494 |
| # N's | 0 |

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).



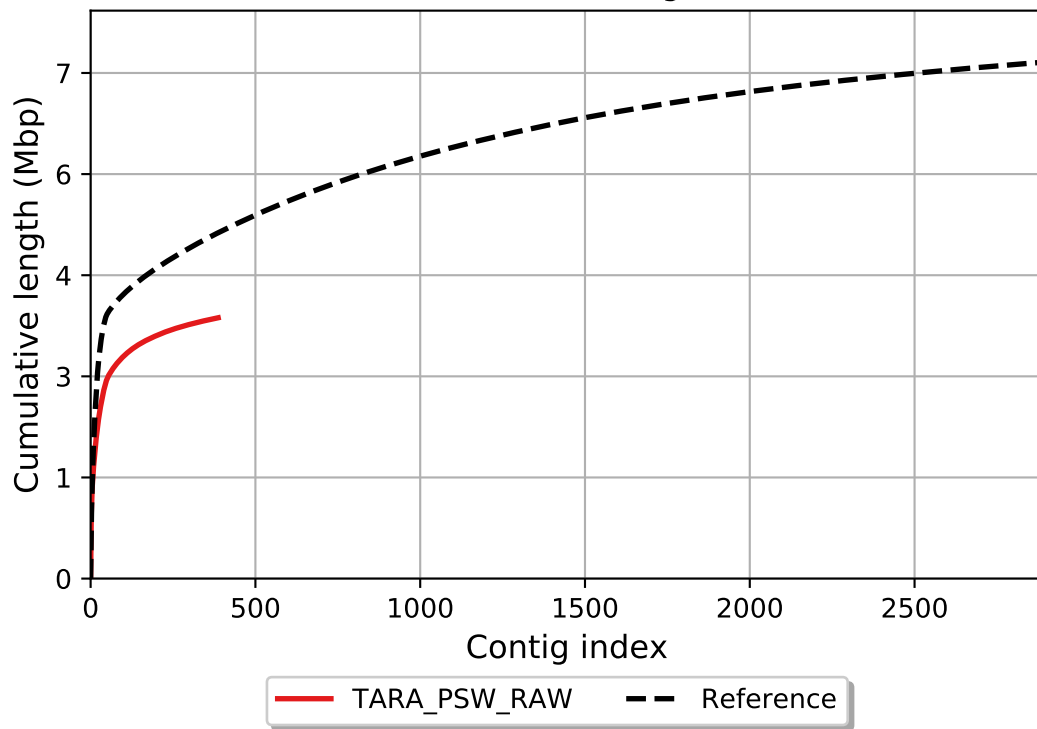
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NGx

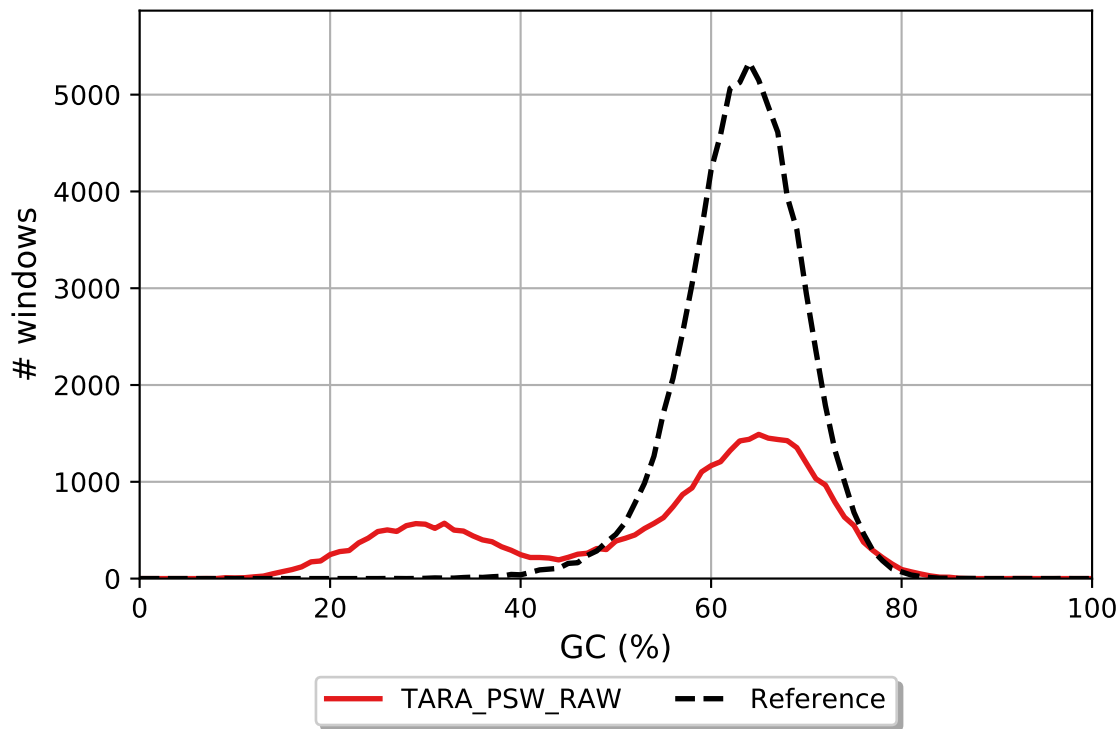


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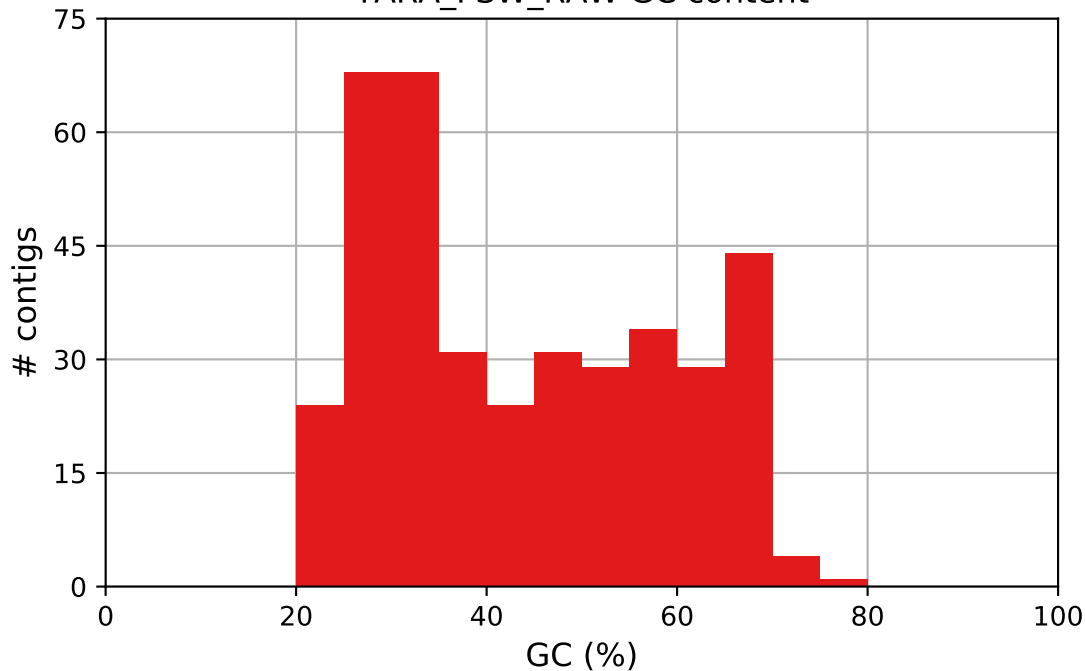
Cumulative length



GC content



TARA_PSW_RAW GC content

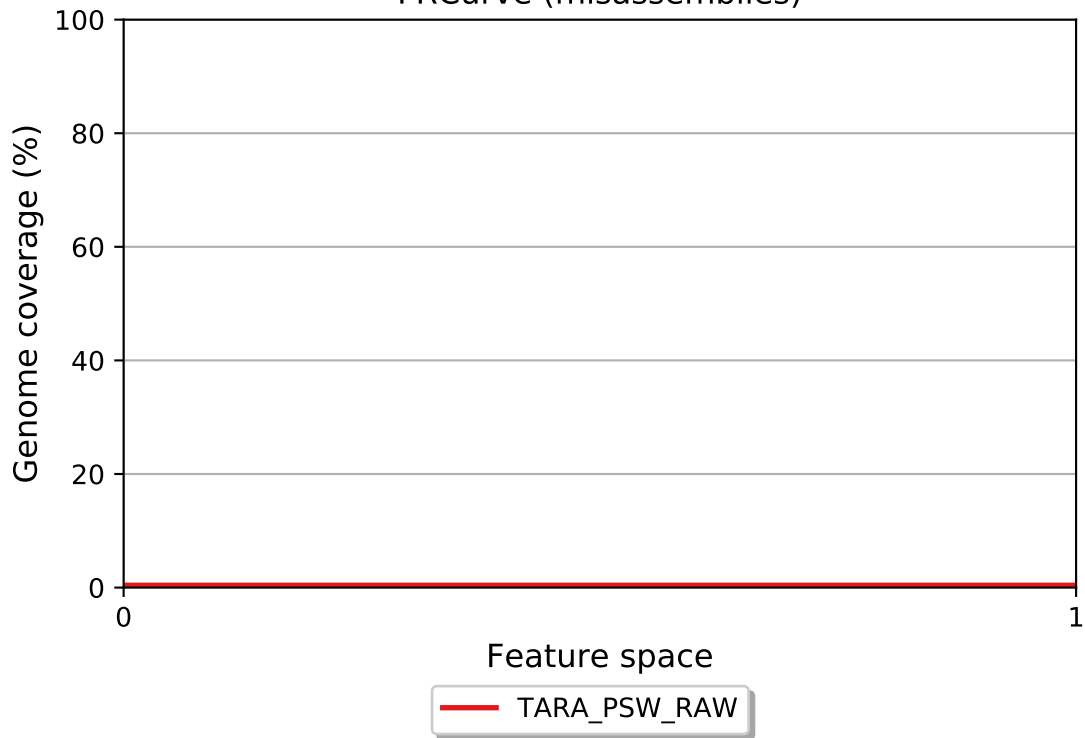


TARA_PSW_RAW

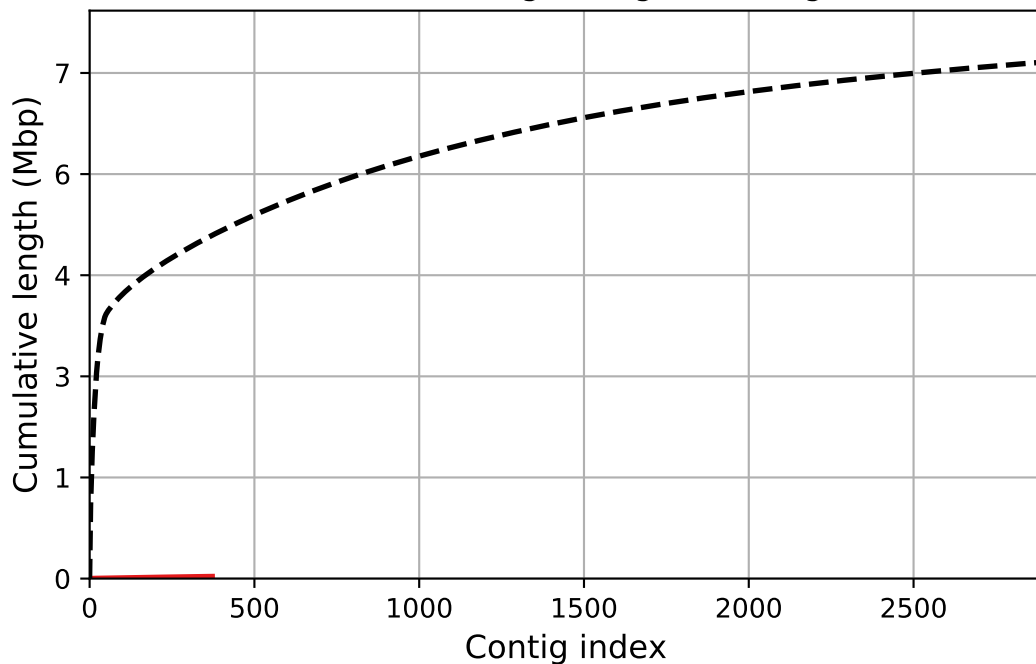
Misassemblies



FRCurve (misassemblies)

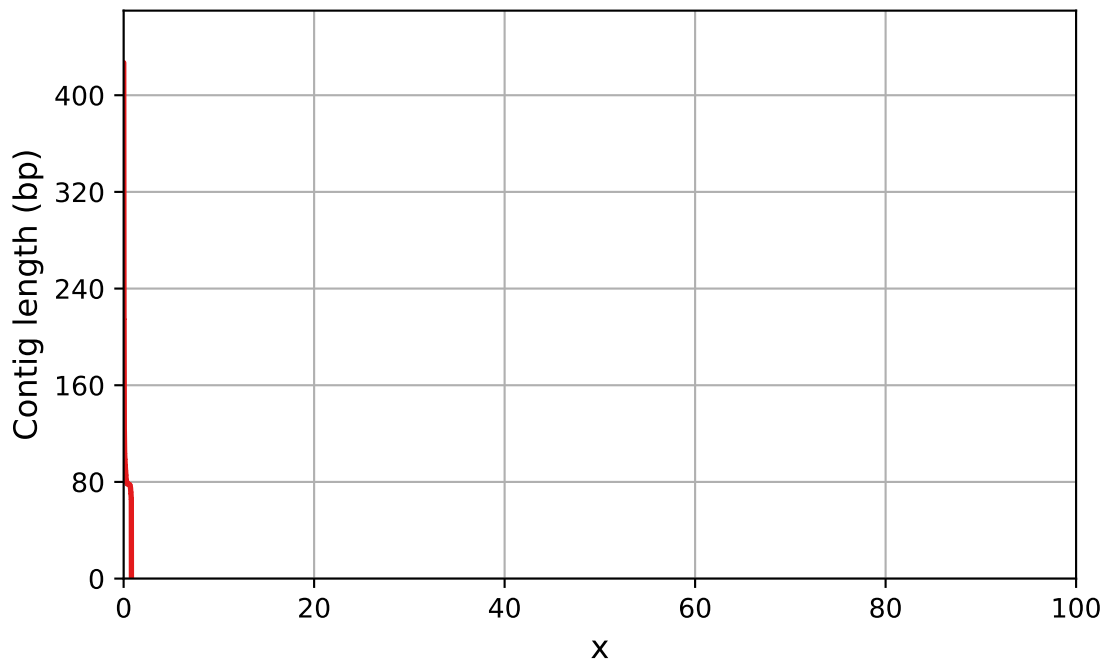


Cumulative length (aligned contigs)



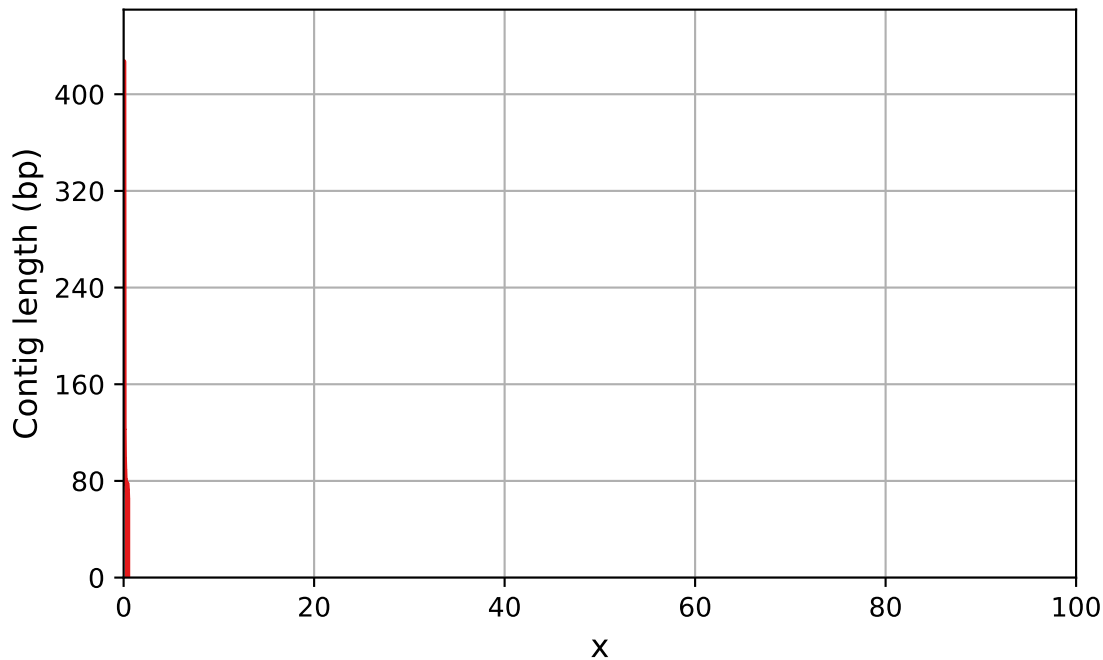
— TARA_PSW_RAW - - Reference

NAx



TARA_PSW_RAW

NGAx



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