

# Report

|                             | TARA_PON_RAW |
|-----------------------------|--------------|
| # contigs (>= 1000 bp)      | 42           |
| # contigs (>= 5000 bp)      | 2            |
| # contigs (>= 10000 bp)     | 0            |
| # contigs (>= 25000 bp)     | 0            |
| # contigs (>= 50000 bp)     | 0            |
| Total length (>= 1000 bp)   | 93081        |
| Total length (>= 5000 bp)   | 11624        |
| Total length (>= 10000 bp)  | 0            |
| Total length (>= 25000 bp)  | 0            |
| Total length (>= 50000 bp)  | 0            |
| # contigs                   | 42           |
| Largest contig              | 6504         |
| Total length                | 93081        |
| Reference length            | 4234461      |
| GC (%)                      | 49.66        |
| Reference GC (%)            | 41.03        |
| N50                         | 2909         |
| N75                         | 1533         |
| L50                         | 12           |
| L75                         | 24           |
| # 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         | 10 + 32 part |
| Unaligned length            | 90202        |
| Genome fraction (%)         | 0.025        |
| Duplication ratio           | 2.673        |
| # N's per 100 kbp           | 0.00         |
| # mismatches per 100 kbp    | 6778.09      |
| # indels per 100 kbp        | 92.85        |
| Largest alignment           | 201          |
| Total aligned length        | 2879         |
| 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_PON_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 | 41           |
| # possible misassemblies        | 43           |
| # local misassemblies           | 0            |
| # scaffold gap ext. mis.        | 0            |
| # scaffold gap loc. mis.        | 0            |
| # unaligned mis. contigs        | 0            |
| # mismatches                    | 73           |
| # indels                        | 1            |
| # indels (<= 5 bp)              | 1            |
| # indels (> 5 bp)               | 0            |
| Indels length                   | 2            |

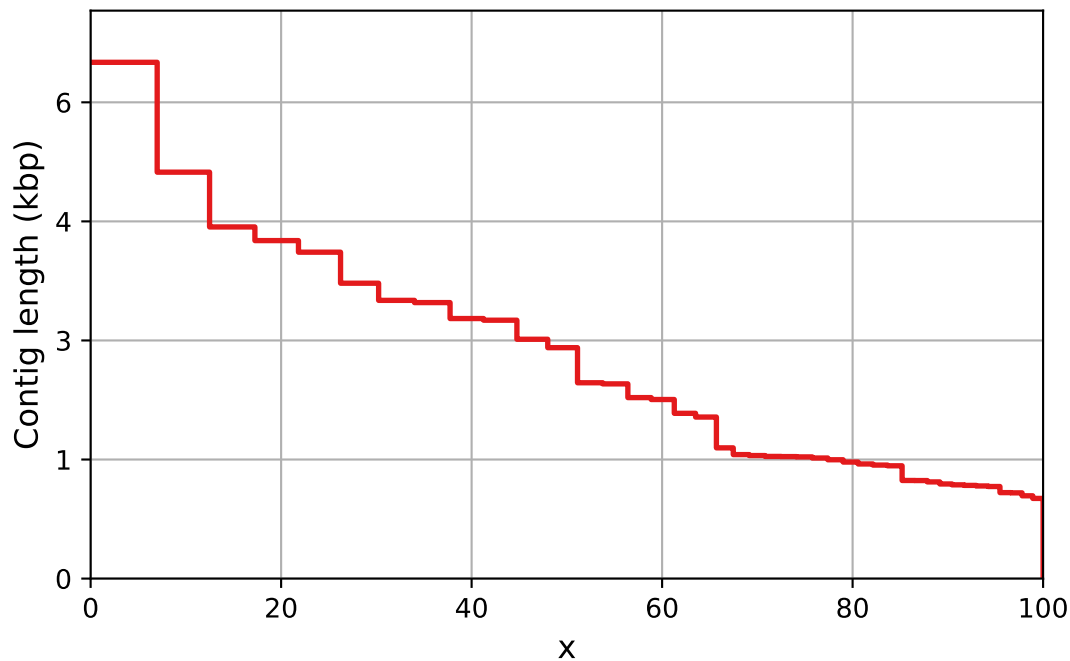
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

|                               | TARA_PON_RAW |
|-------------------------------|--------------|
| # fully unaligned contigs     | 10           |
| Fully unaligned length        | 21188        |
| # partially unaligned contigs | 32           |
| Partially unaligned length    | 69014        |
| # N's                         | 0            |

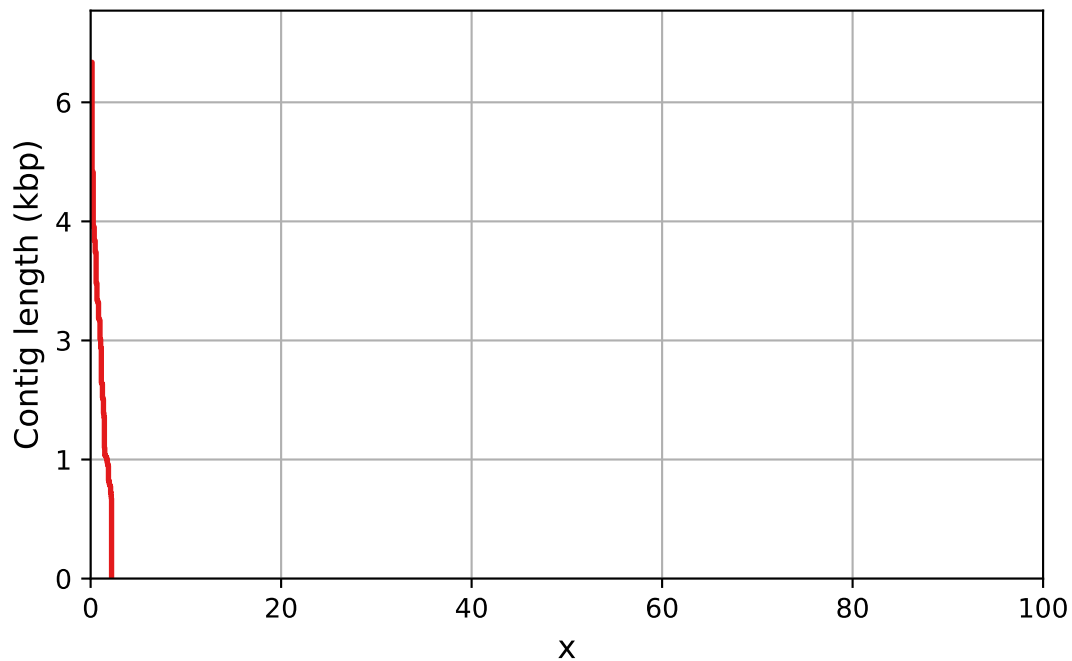
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

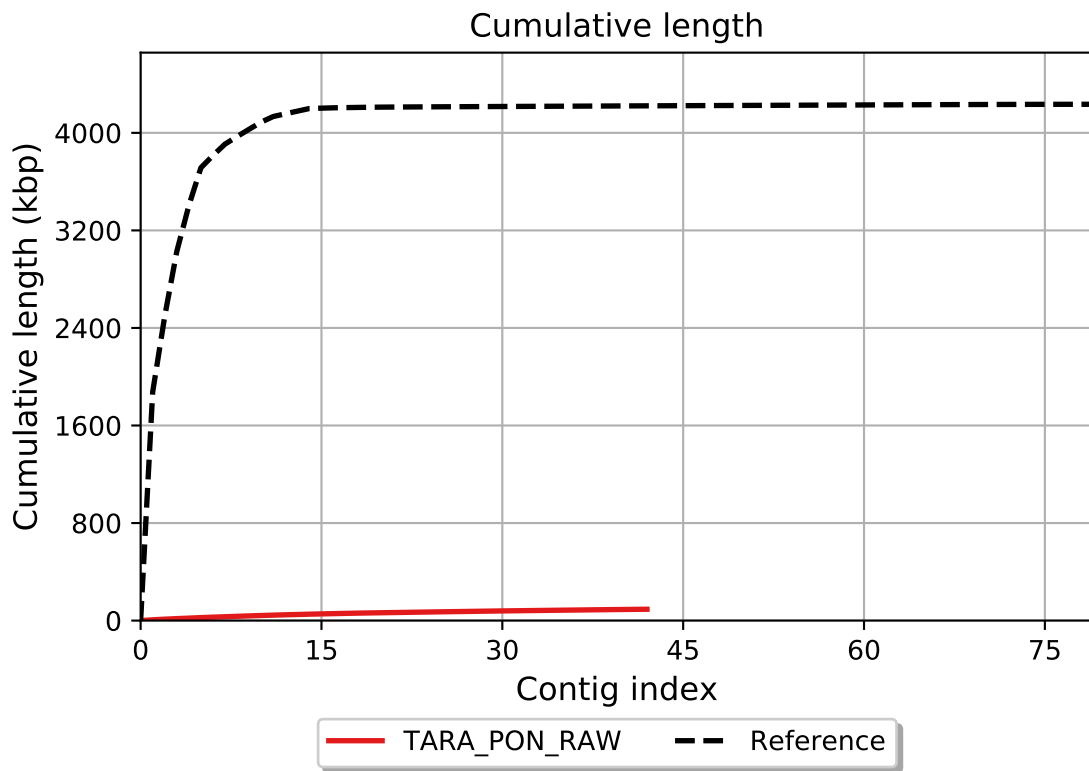


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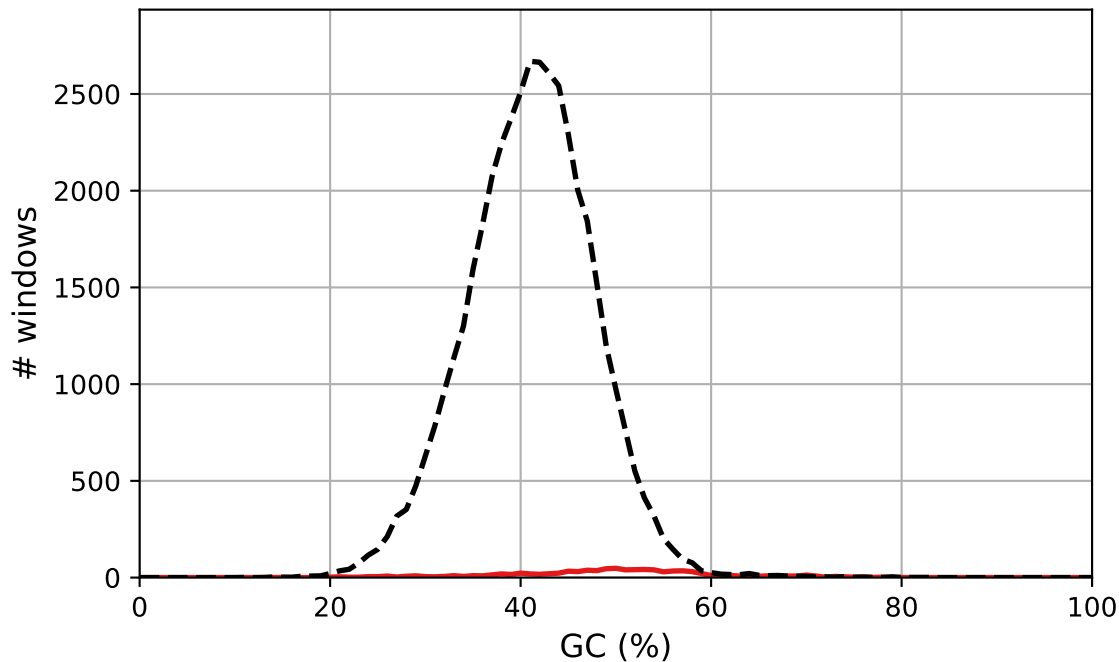
NGx



TARA\_PON\_RAW

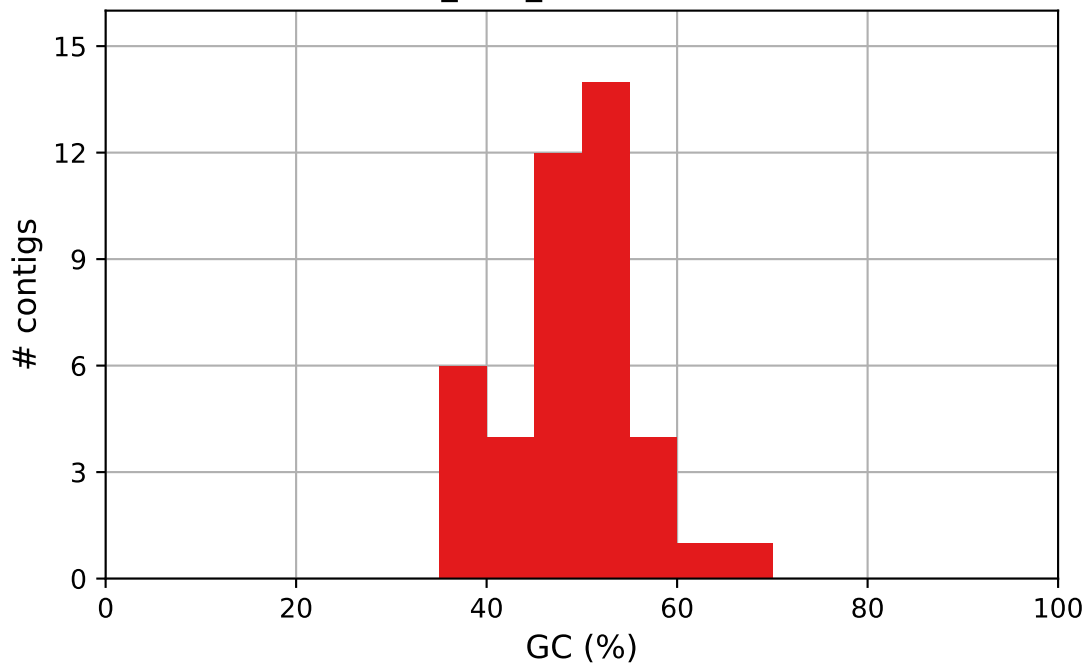


## GC content



— TARA\_PON\_RAW    - - Reference

TARA\_PON\_RAW GC content



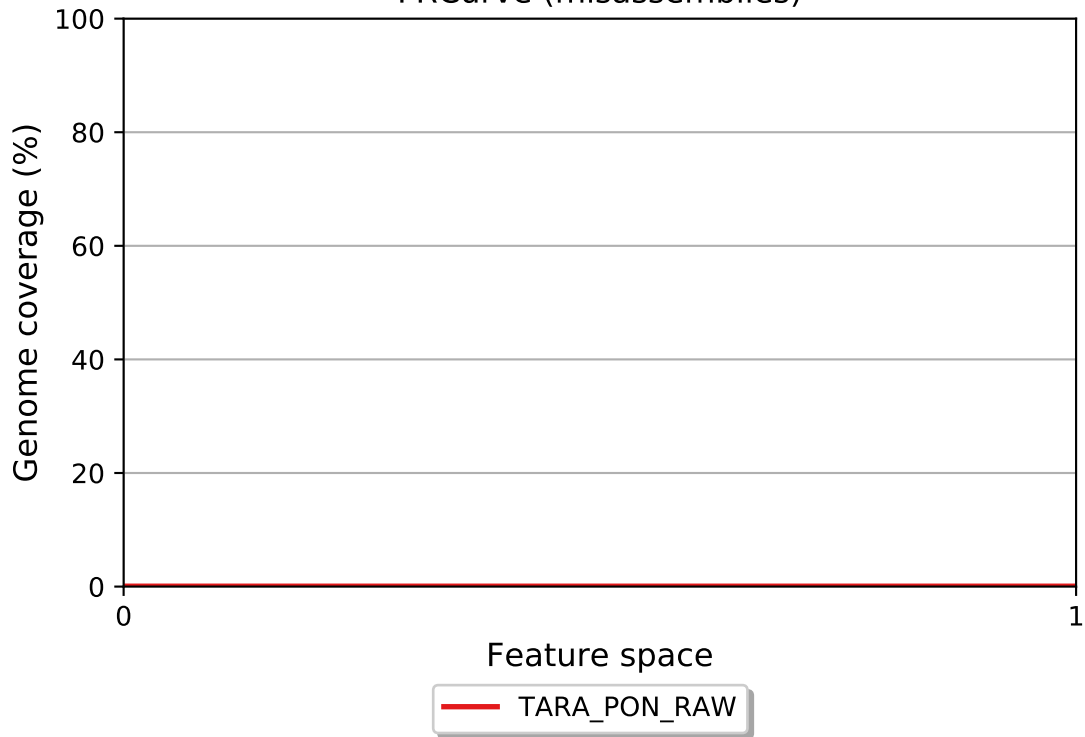
TARA\_PON\_RAW



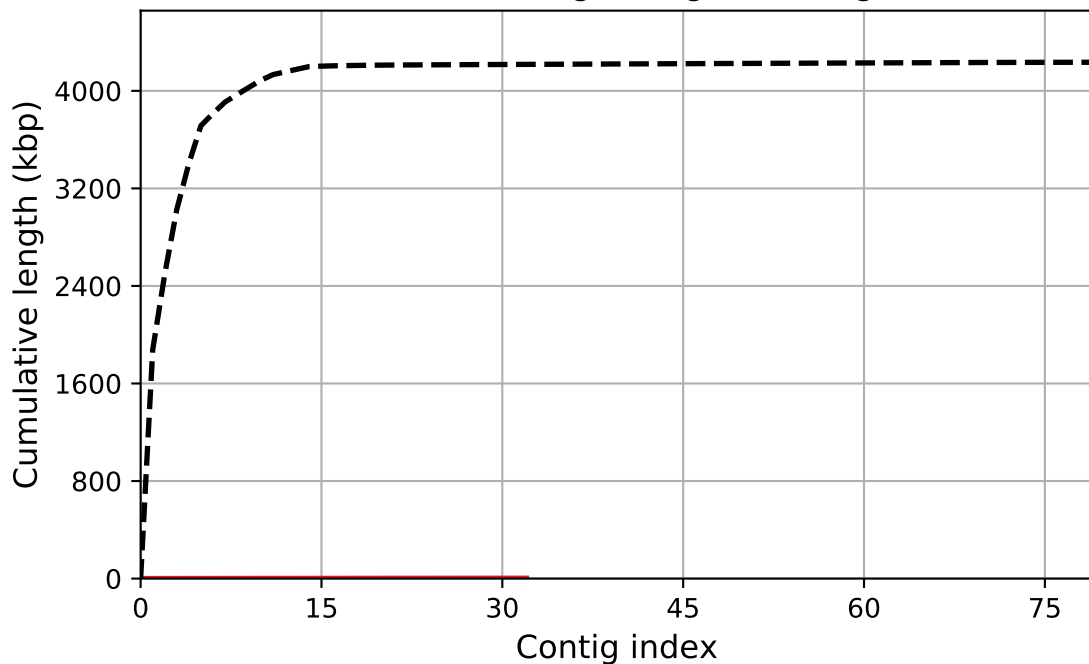
## Misassemblies



FRCurve (misassemblies)

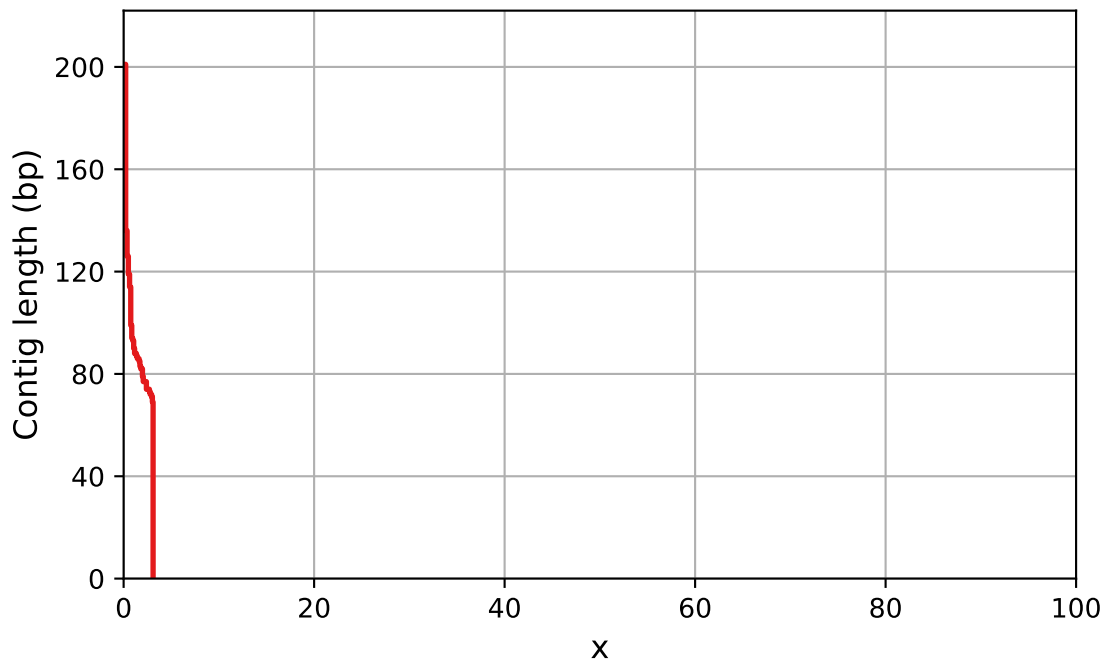


Cumulative length (aligned contigs)



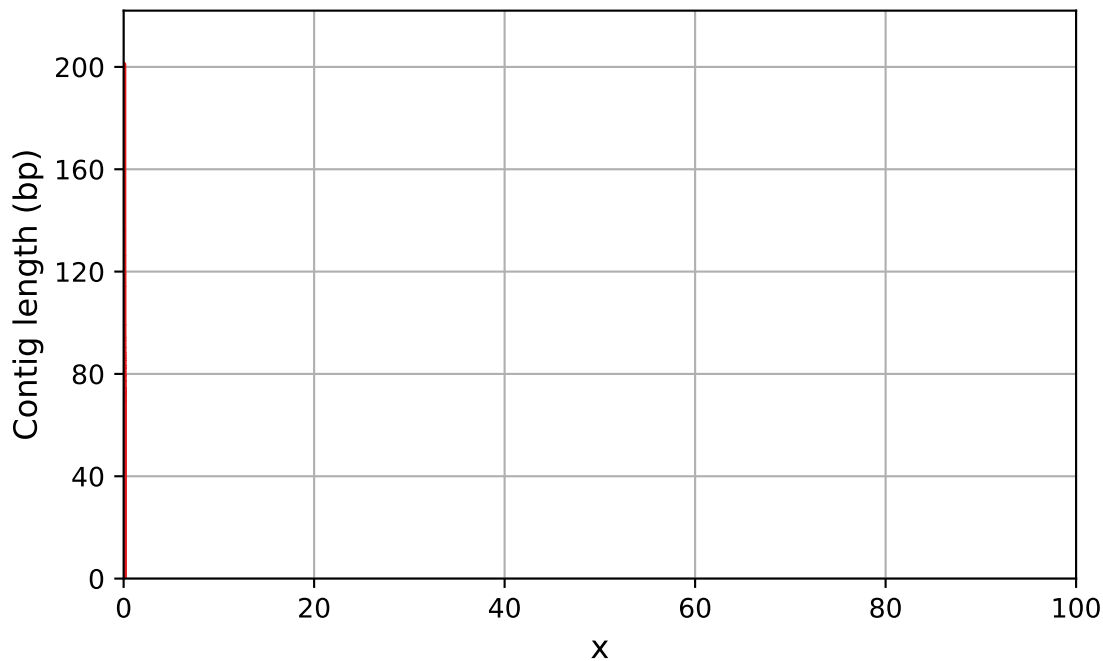
— TARA\_PON\_RAW    - - Reference

NAx



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# NGAx



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