

Report

| | TARA_SOC_RAW |
|-----------------------------|--------------|
| # contigs (>= 1000 bp) | 26 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 60158 |
| Total length (>= 5000 bp) | 5563 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 26 |
| Largest contig | 5563 |
| Total length | 60158 |
| Reference length | 3561038 |
| GC (%) | 46.30 |
| Reference GC (%) | 41.87 |
| N50 | 2487 |
| N75 | 1818 |
| L50 | 9 |
| L75 | 16 |
| # 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 | 8 + 18 part |
| Unaligned length | 58529 |
| Genome fraction (%) | 0.012 |
| Duplication ratio | 3.888 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 12887.83 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 147 |
| Total aligned length | 1629 |
| 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_SOC_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 | 24 |
| # possible misassemblies | 28 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 54 |
| # indels | 0 |
| # indels (<= 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 0 |

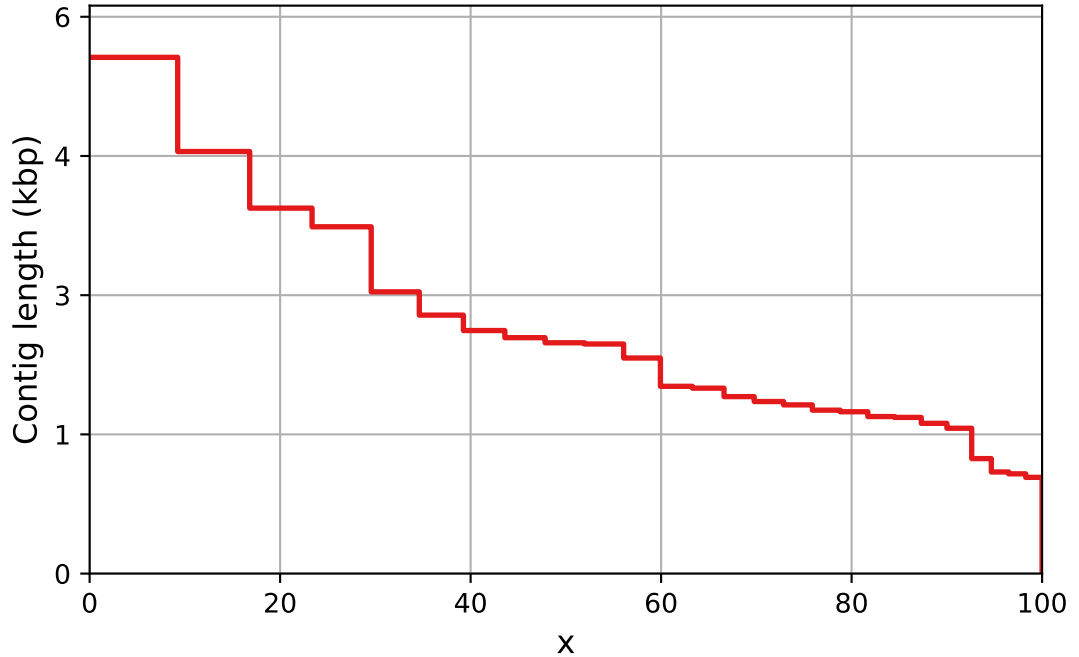
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | TARA_SOC_RAW |
|-------------------------------|--------------|
| # fully unaligned contigs | 8 |
| Fully unaligned length | 14087 |
| # partially unaligned contigs | 18 |
| Partially unaligned length | 44442 |
| # N's | 0 |

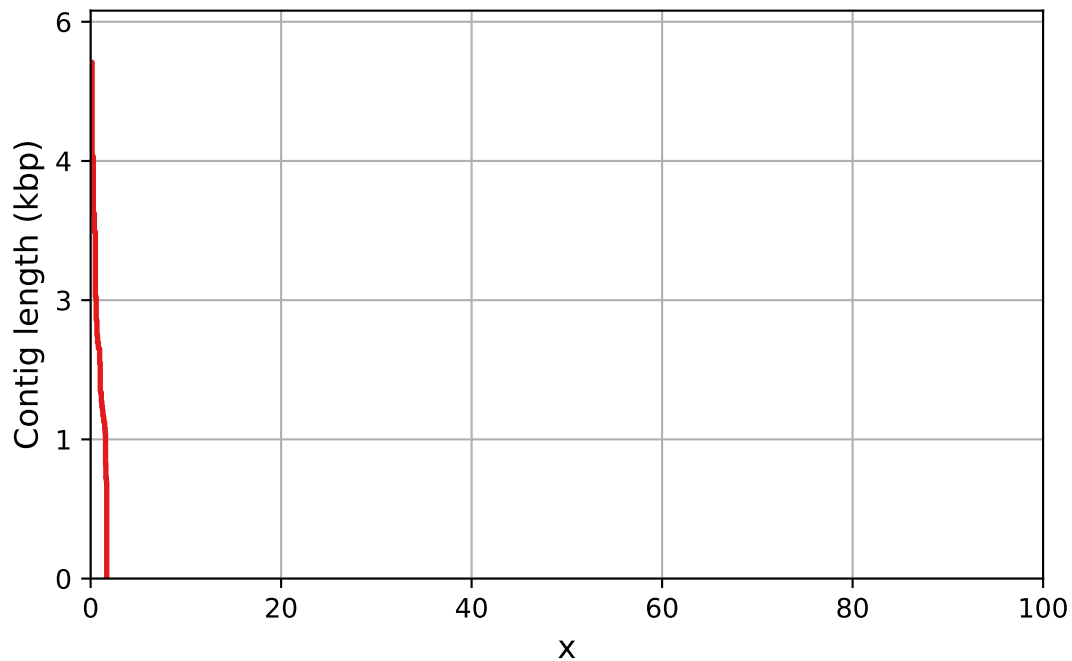
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

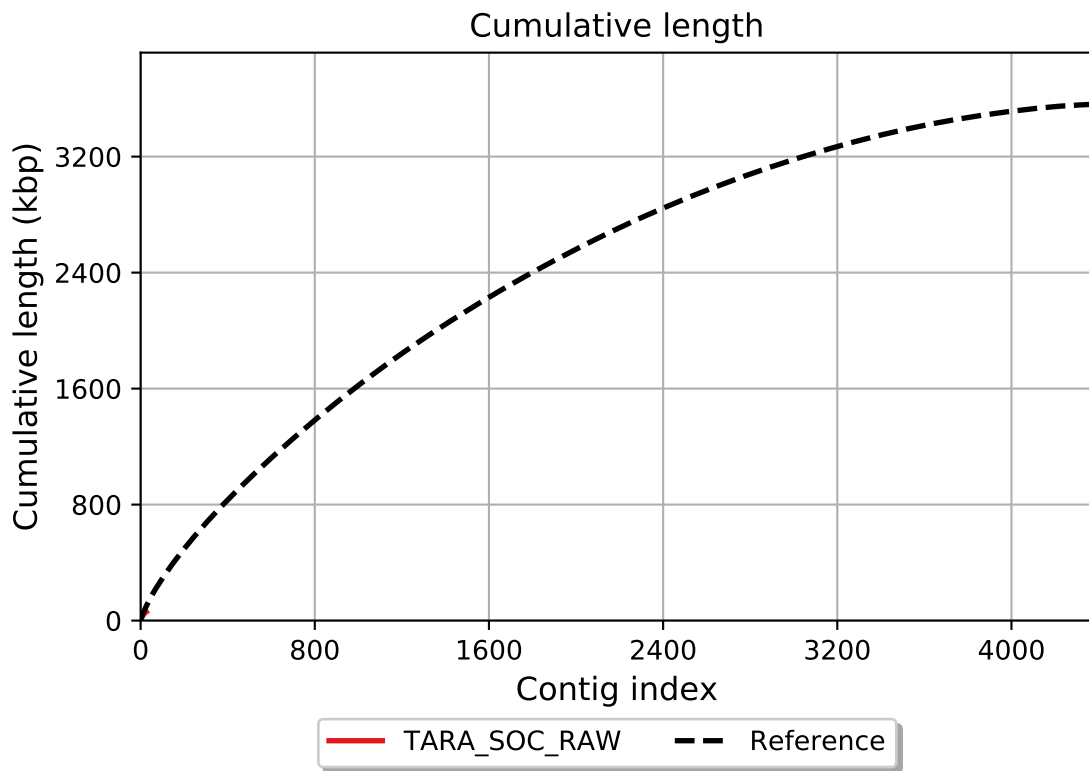


TARA_SOC_RAW

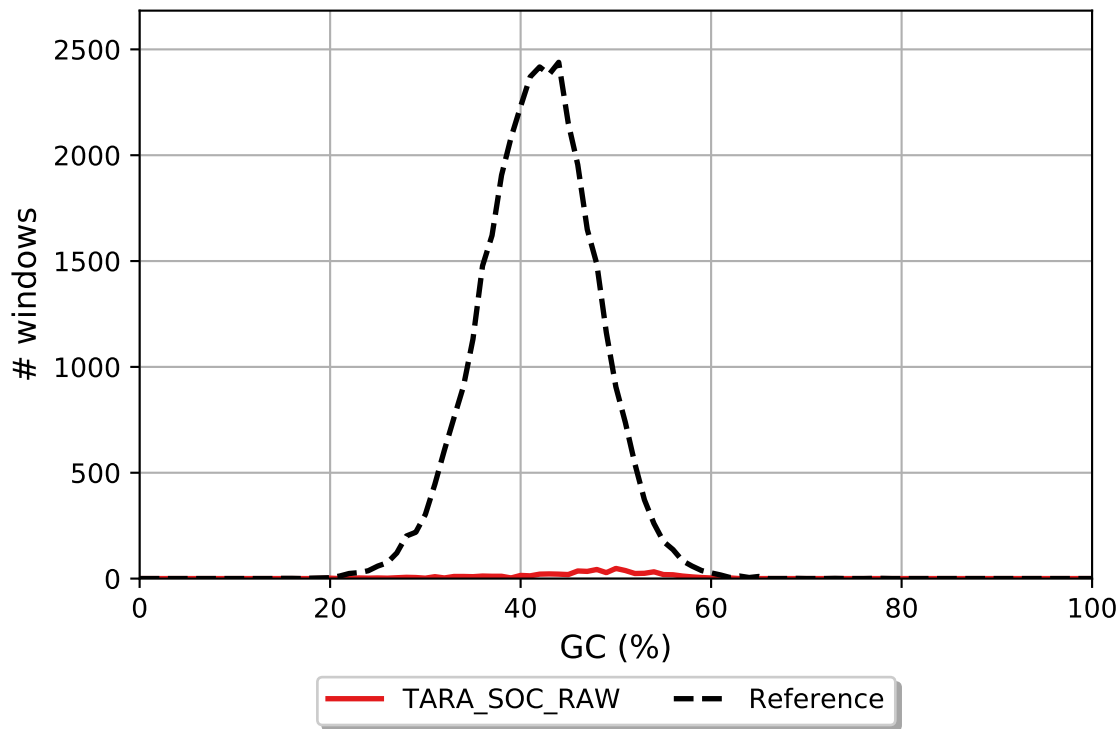
NGx



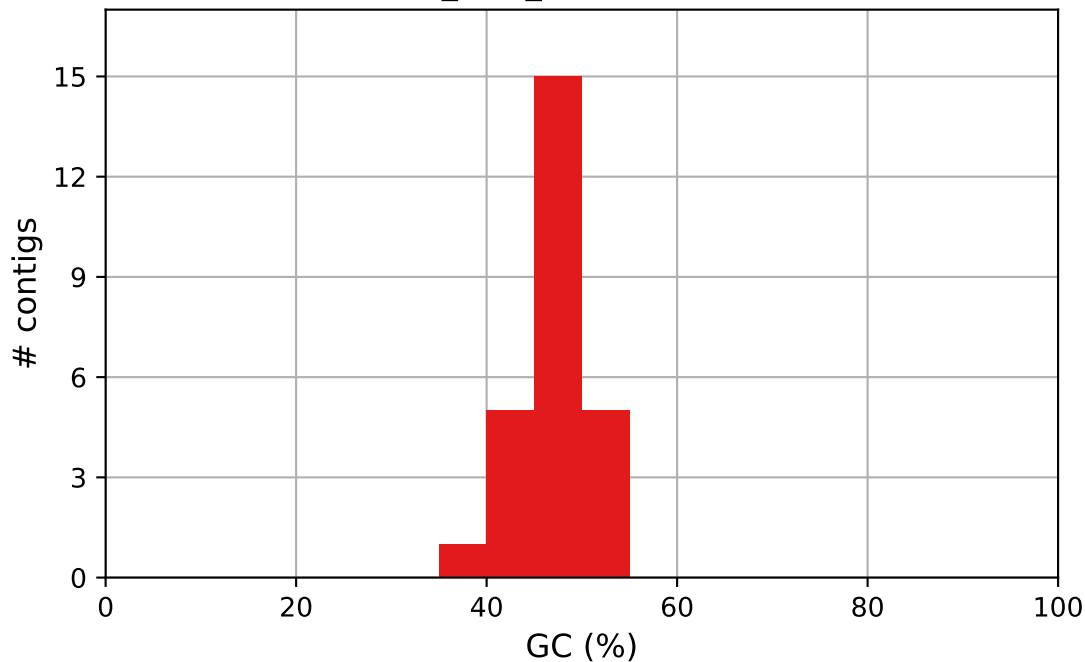
TARA_SOC_RAW



GC content

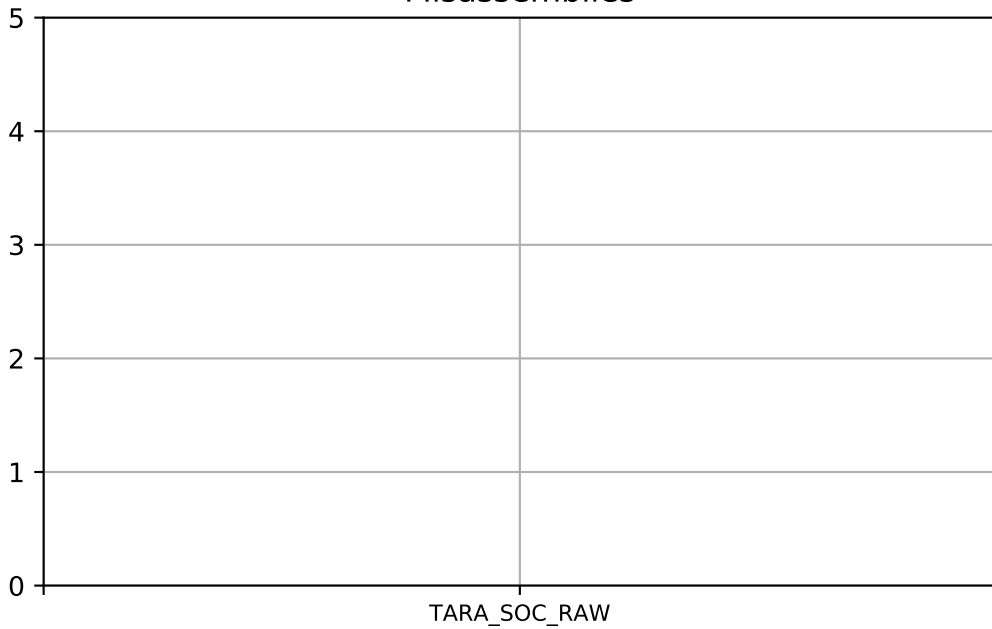


TARA_SOC_RAW GC content

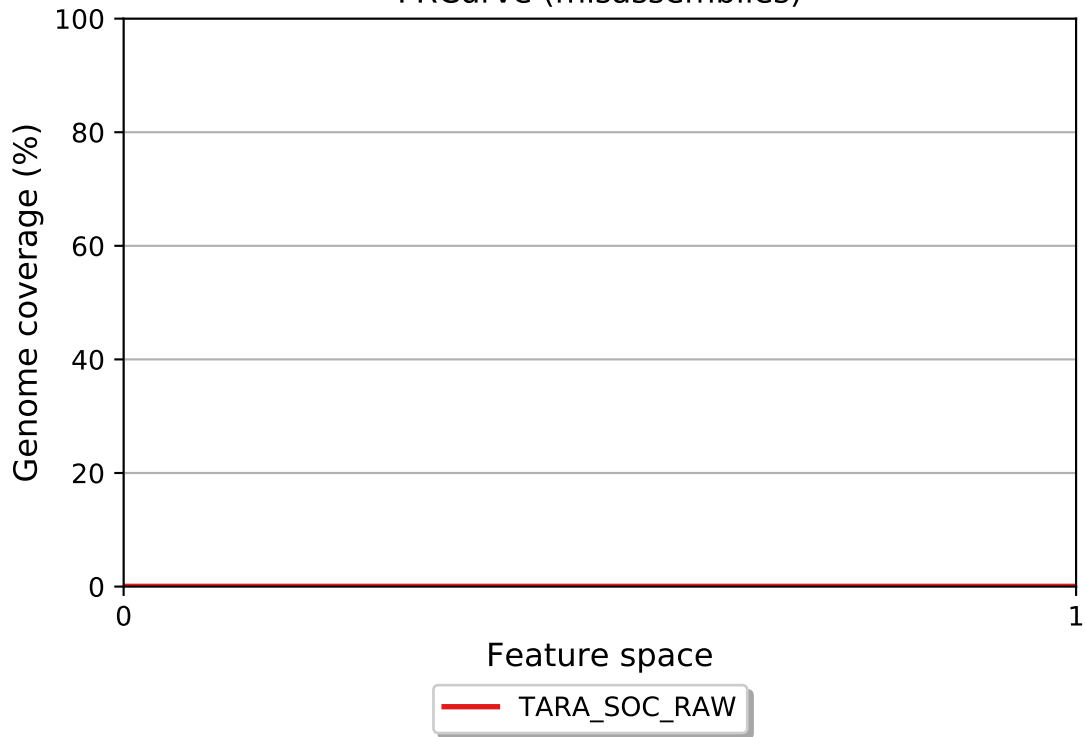


TARA_SOC_RAW

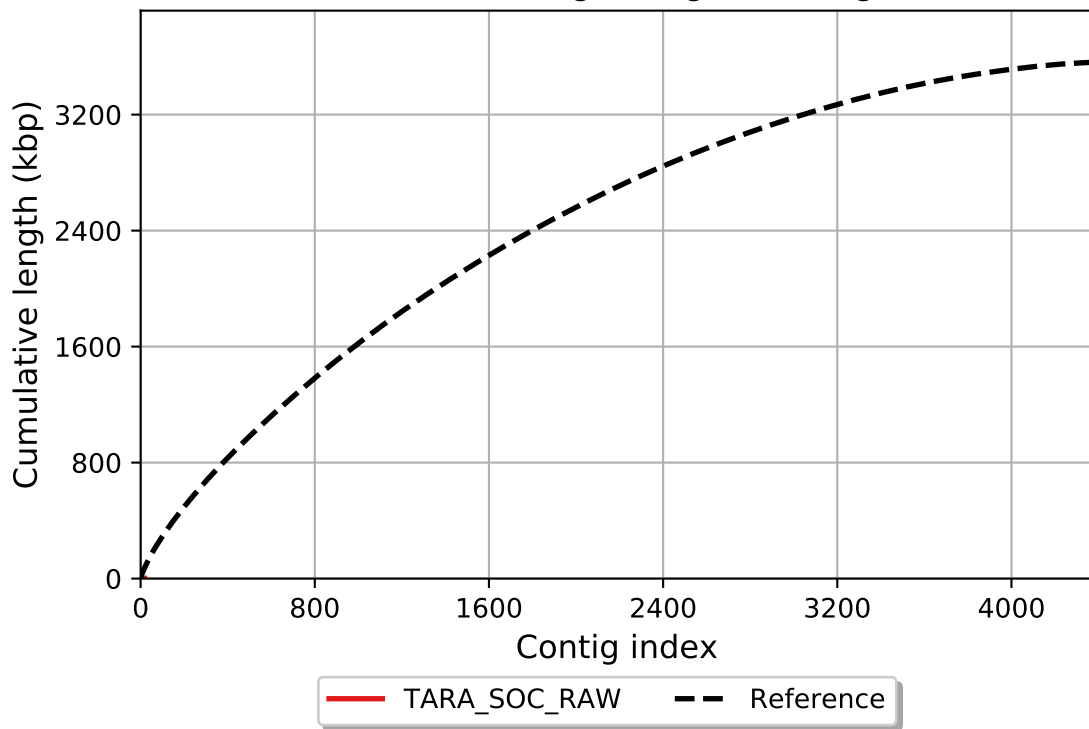
Misassemblies



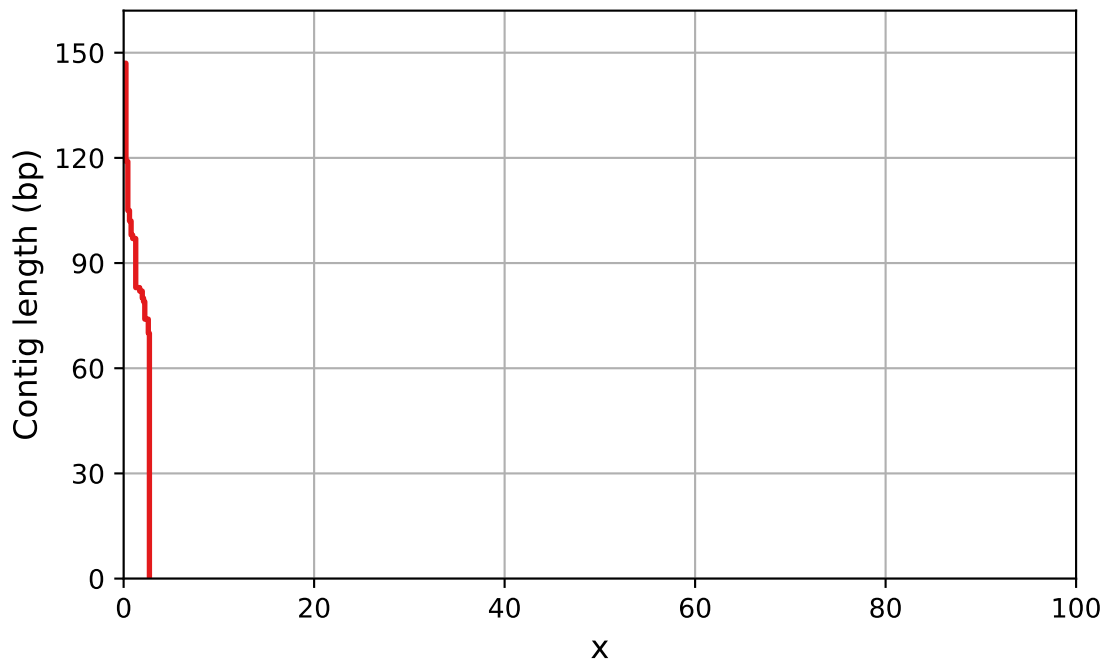
FRCurve (misassemblies)



Cumulative length (aligned contigs)

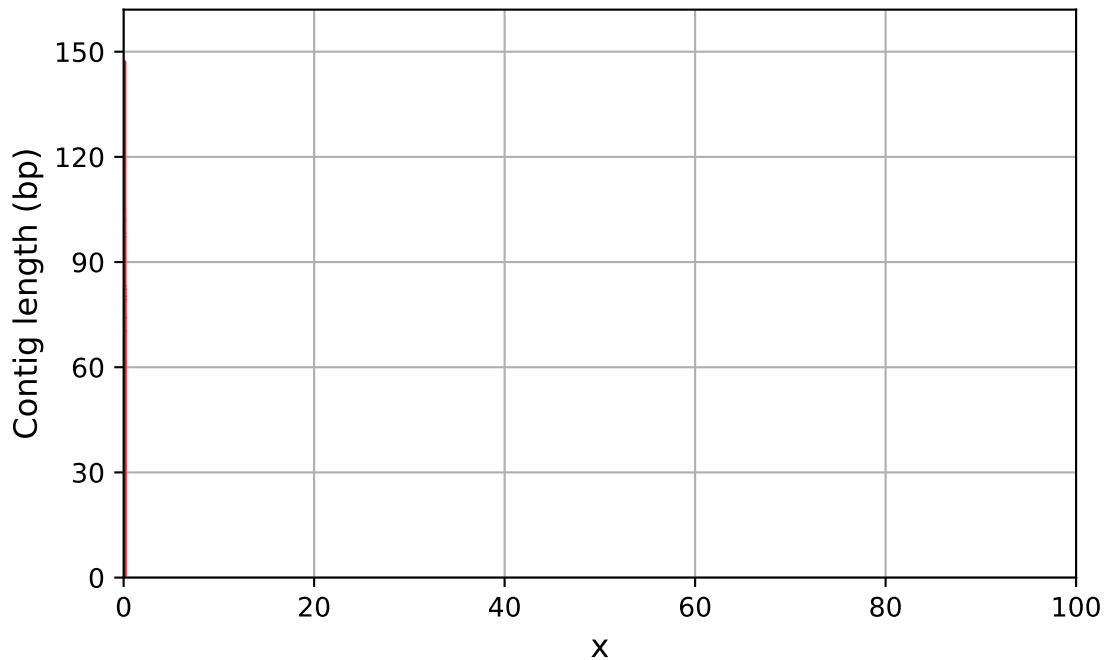


NAx



TARA_SOC_RAW

NGAx



TARA_SOC_RAW