

Report

| | assymbly_45 |
|-----------------------------|-------------|
| # contigs (>= 0 bp) | 1 |
| # contigs (>= 1000 bp) | 1 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 1040 |
| Total length (>= 1000 bp) | 1040 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1 |
| Largest contig | 1040 |
| Total length | 1040 |
| Reference length | 1040 |
| GC (%) | 51.25 |
| Reference GC (%) | 51.25 |
| N50 | 1040 |
| NG50 | 1040 |
| N90 | 1040 |
| NG90 | 1040 |
| auN | 1040.0 |
| auNG | 1040.0 |
| L50 | 1 |
| LG50 | 1 |
| L90 | 1 |
| LG90 | 1 |
| # 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 | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 100.000 |
| Duplication ratio | 1.000 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.00 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 1040 |
| Total aligned length | 1040 |
| NA50 | 1040 |
| NGA50 | 1040 |
| NA90 | 1040 |
| NGA90 | 1040 |
| auNA | 1040.0 |
| auNGA | 1040.0 |
| LA50 | 1 |
| LGA50 | 1 |
| LA90 | 1 |
| LGA90 | 1 |

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

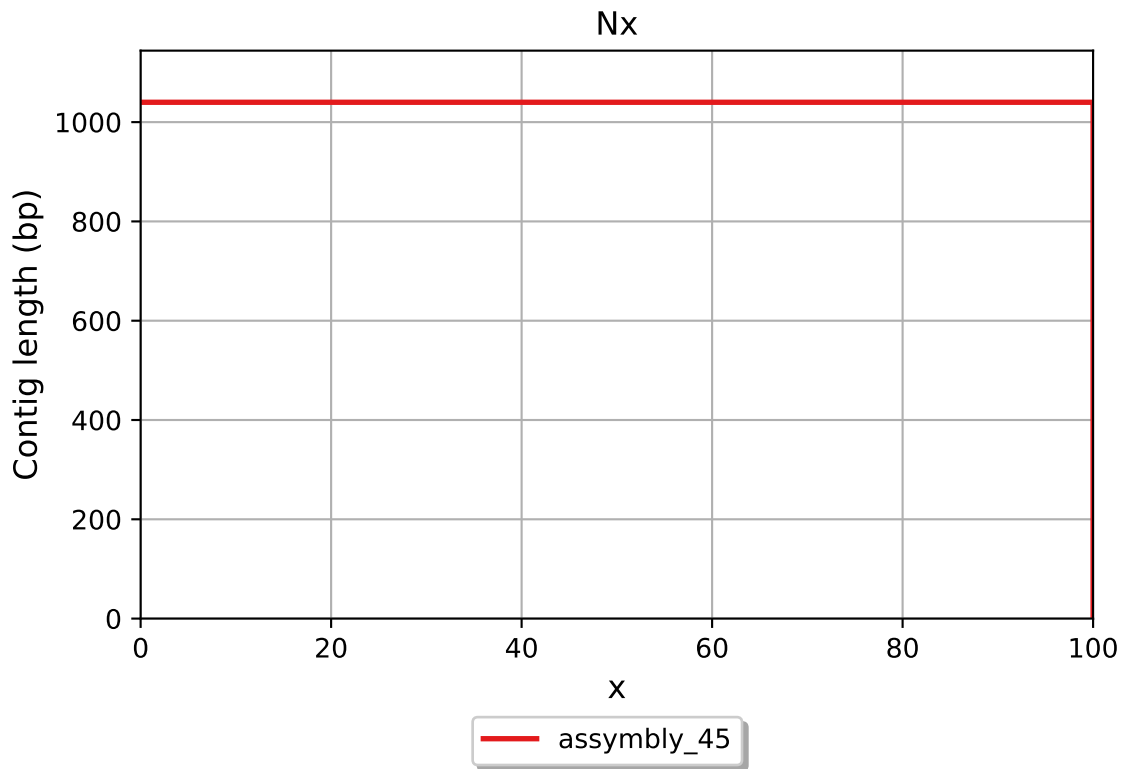
| | assembly_45 |
|-----------------------------|-------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 0 |
| # indels | 0 |
| # indels (<= 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 0 |

All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

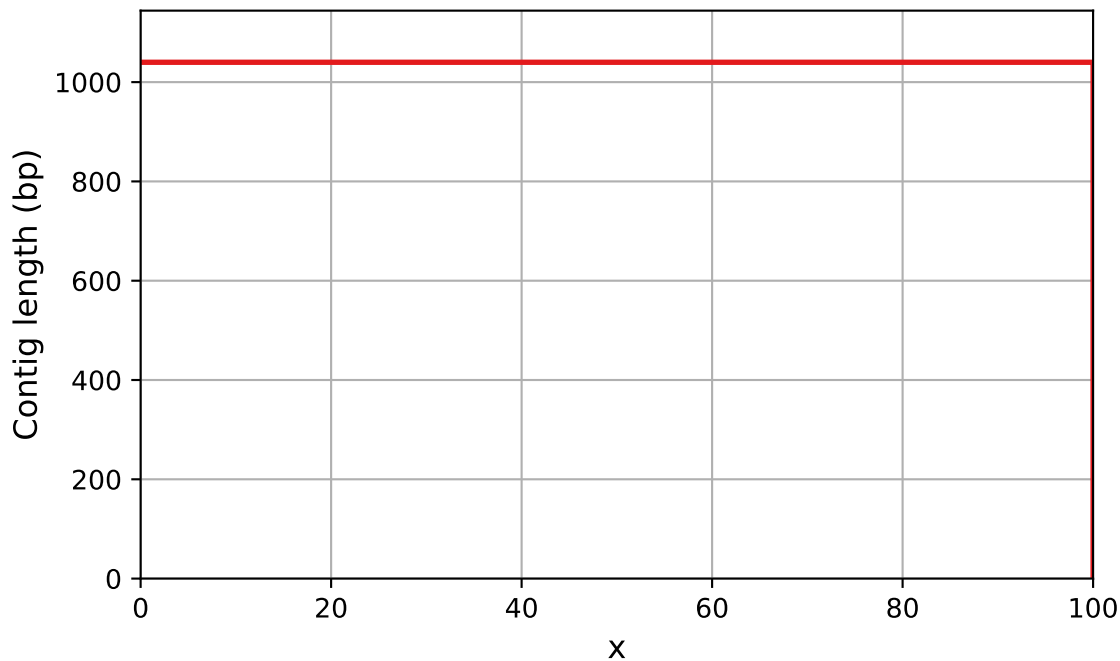
Unaligned report

| | assembly_45 |
|-------------------------------|-------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

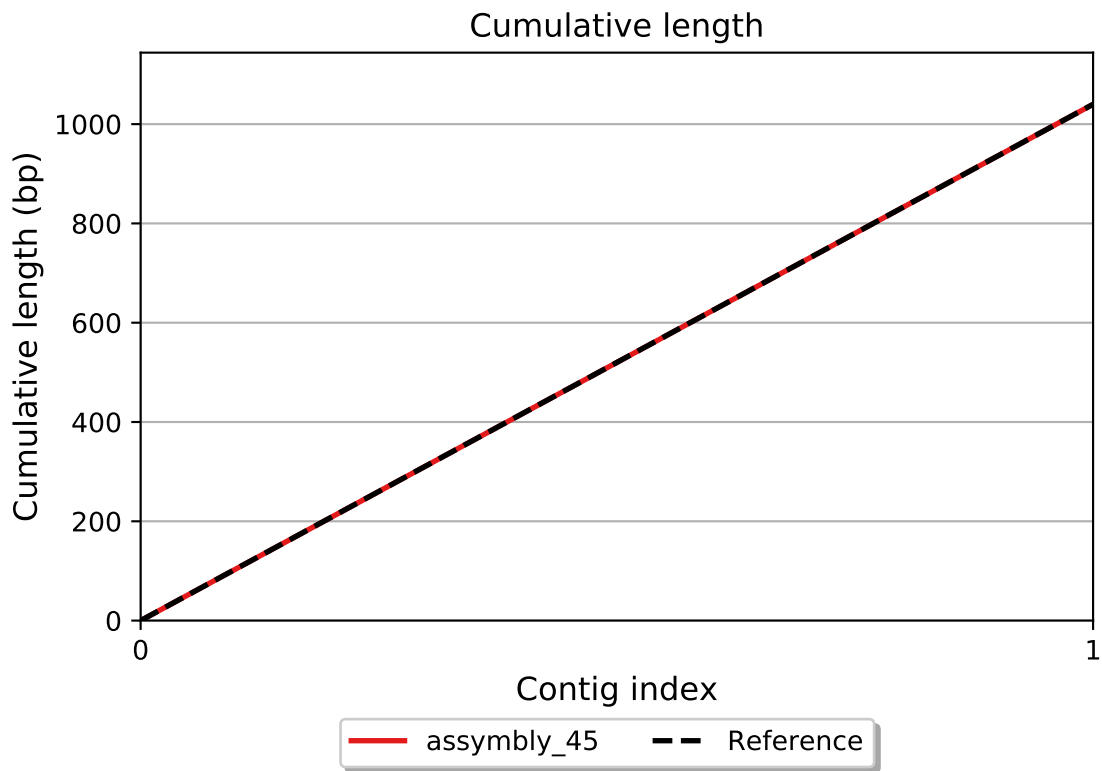
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



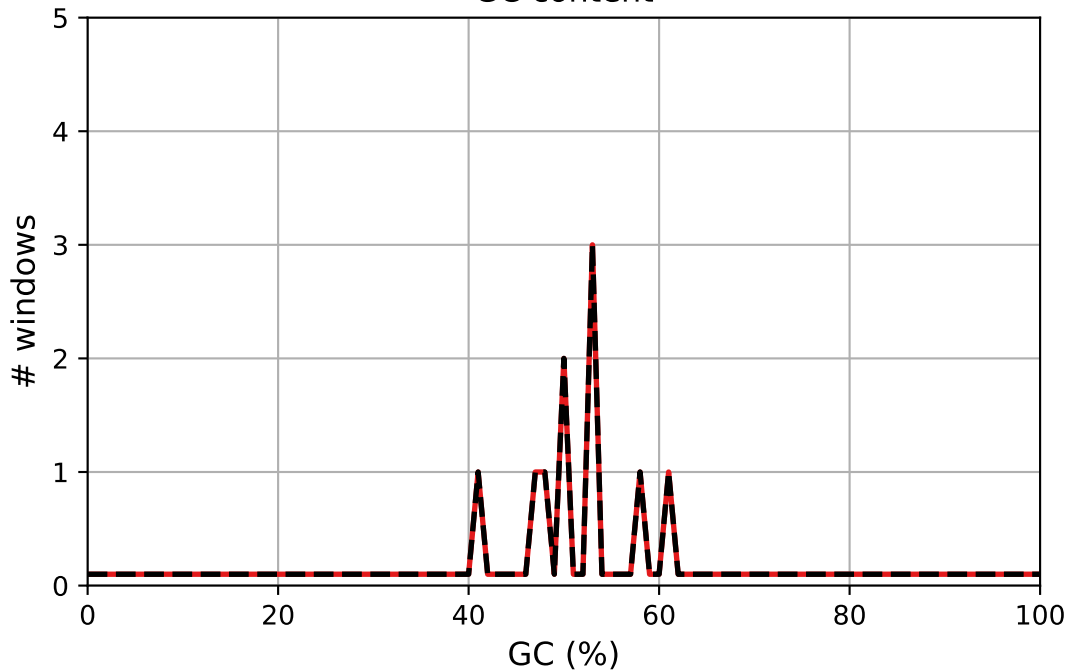
NGx



— assembly_45

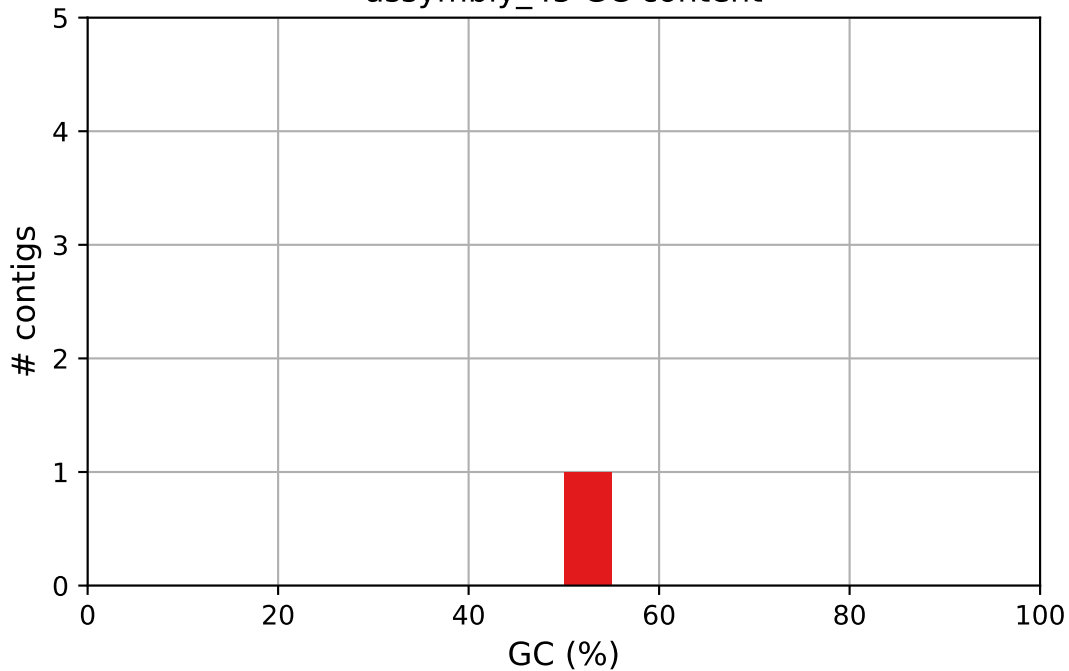


GC content



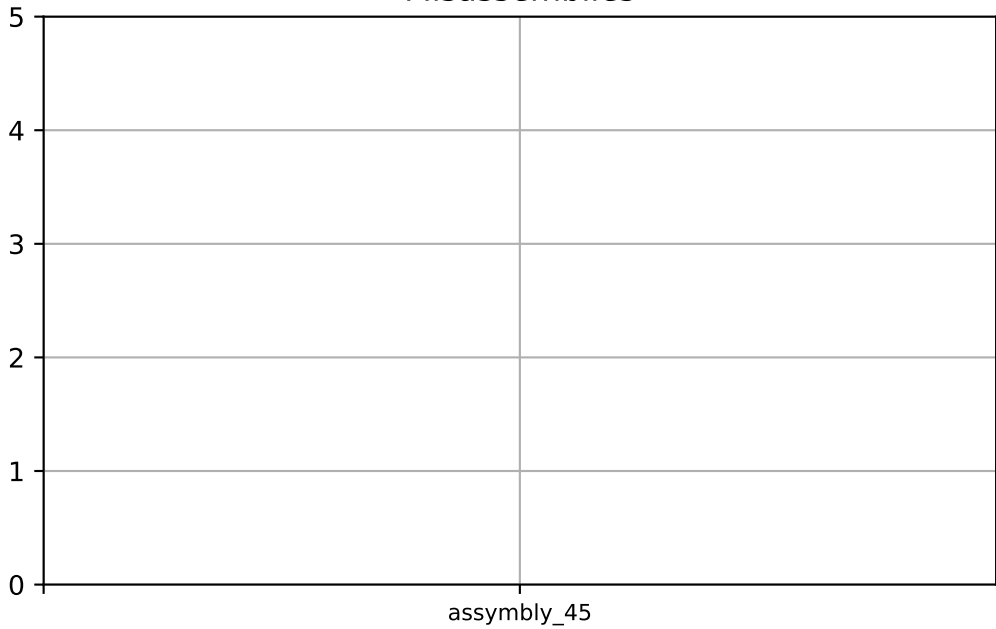
— assembly_45 - - Reference

assembly_45 GC content

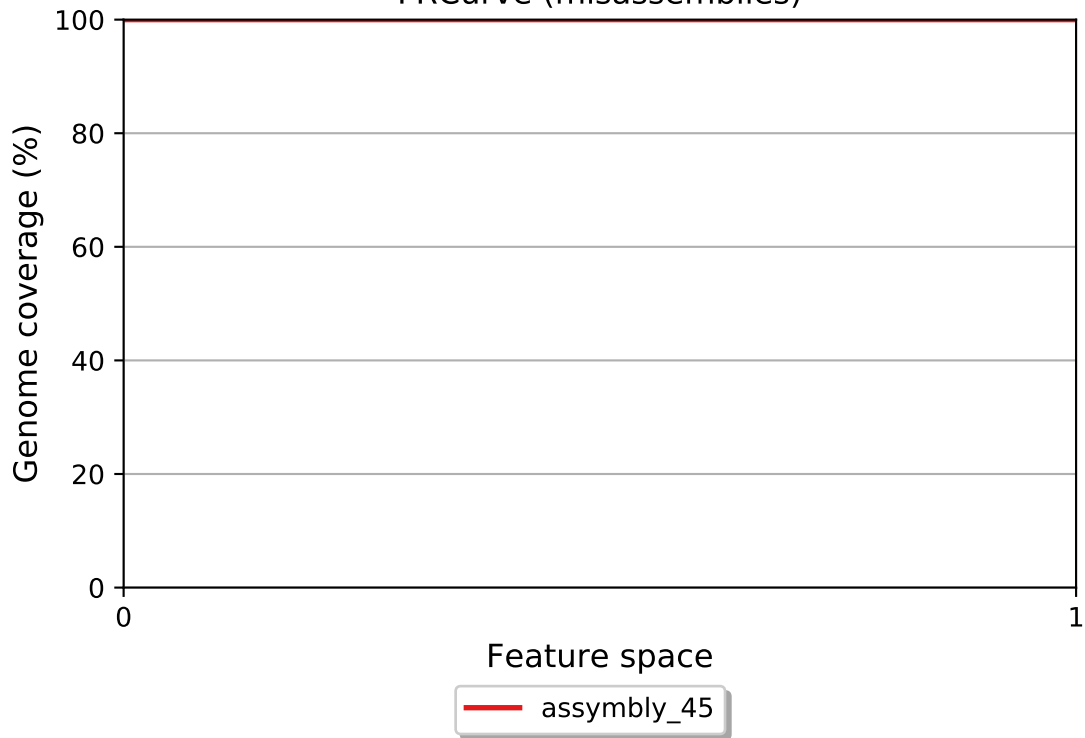


assembly_45

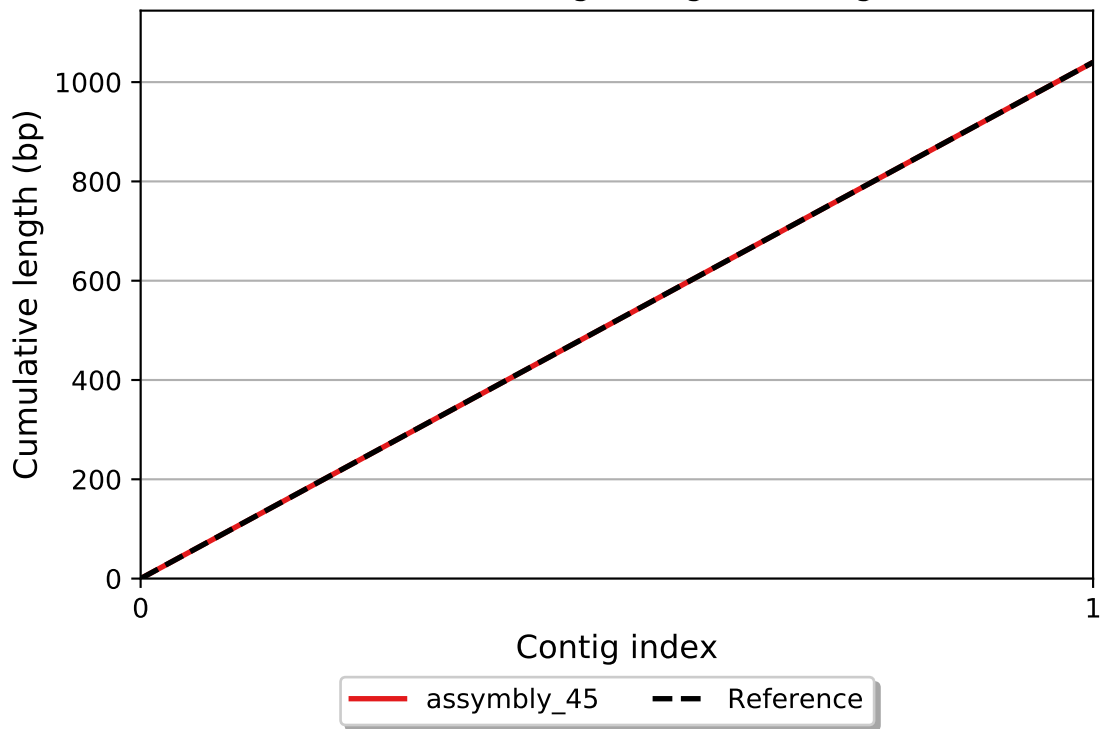
Misassemblies



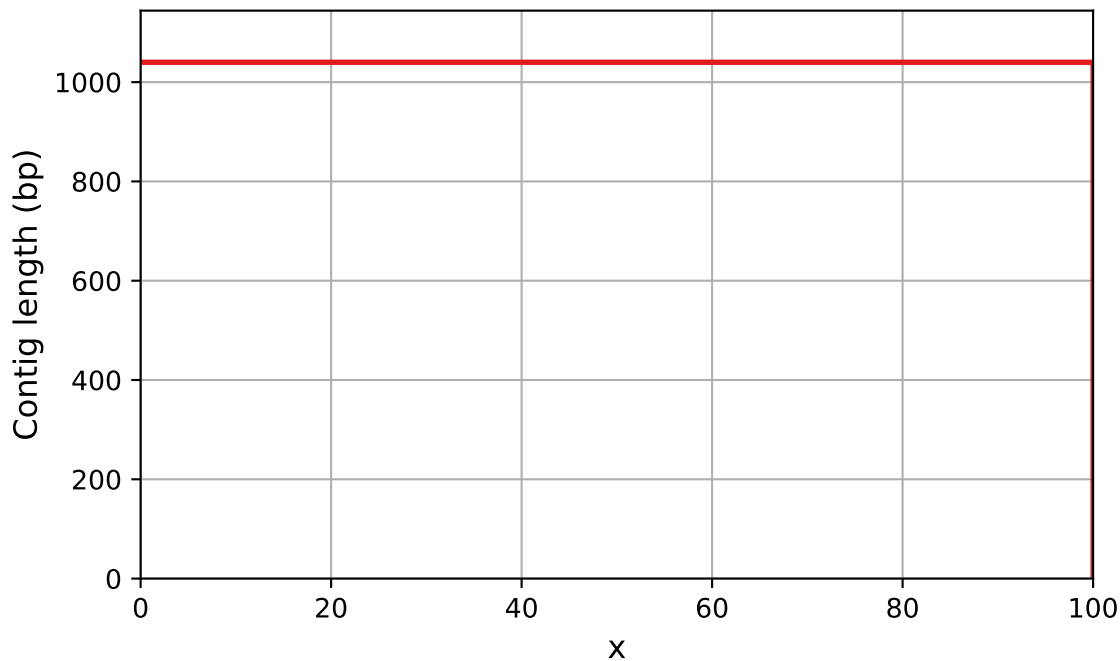
FRCurve (misassemblies)



Cumulative length (aligned contigs)

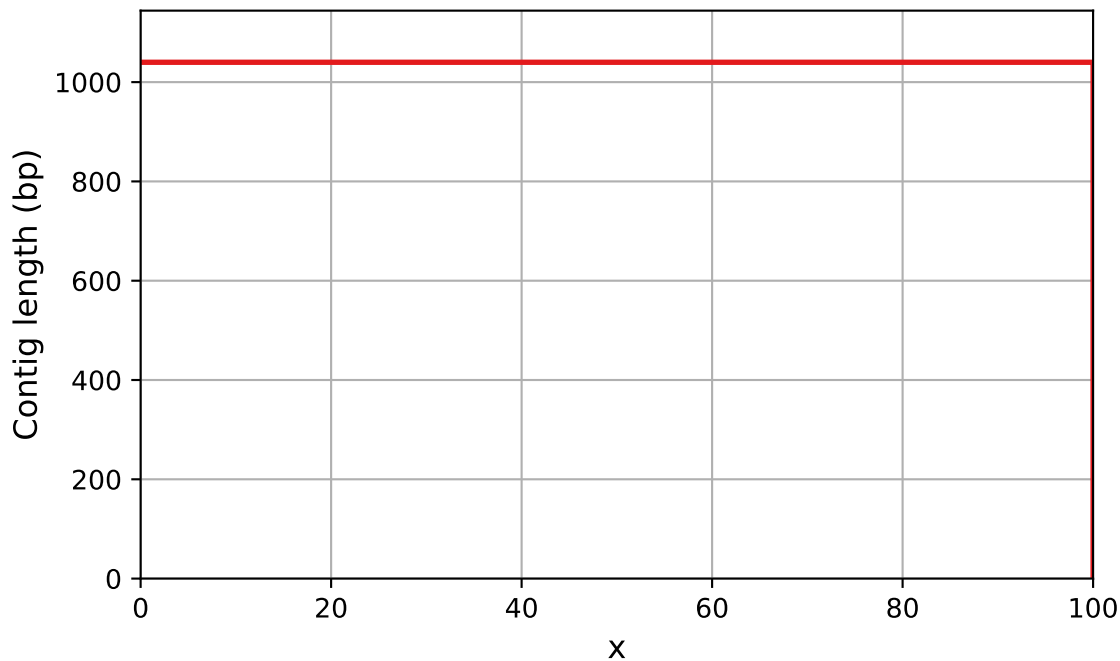


NAx



— assembly_45

NGAx



— assembly_45