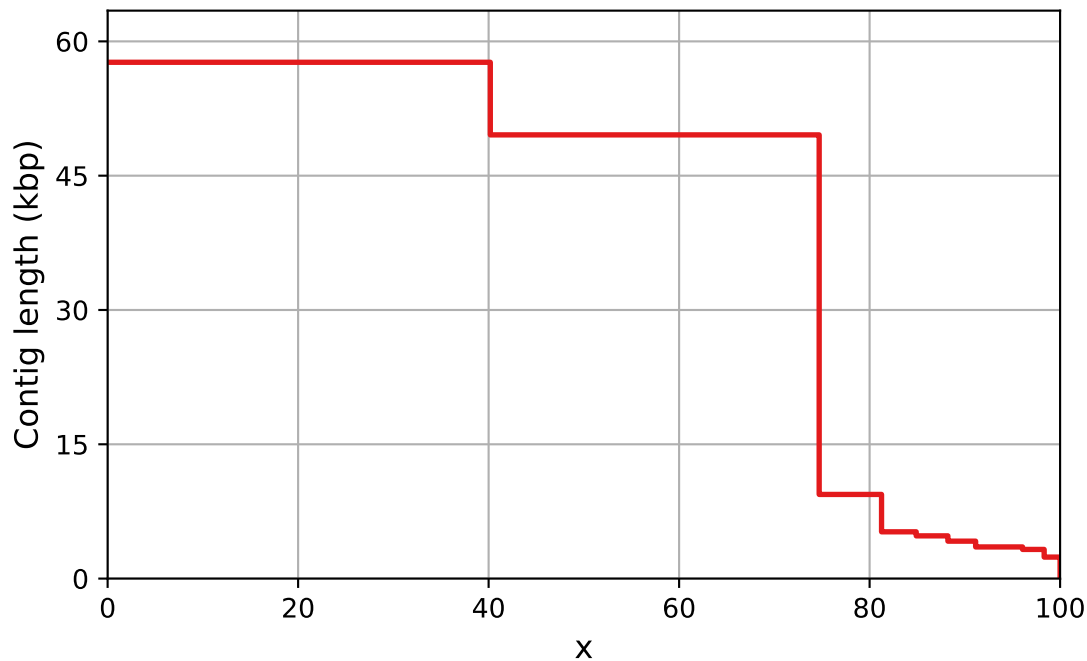


Report

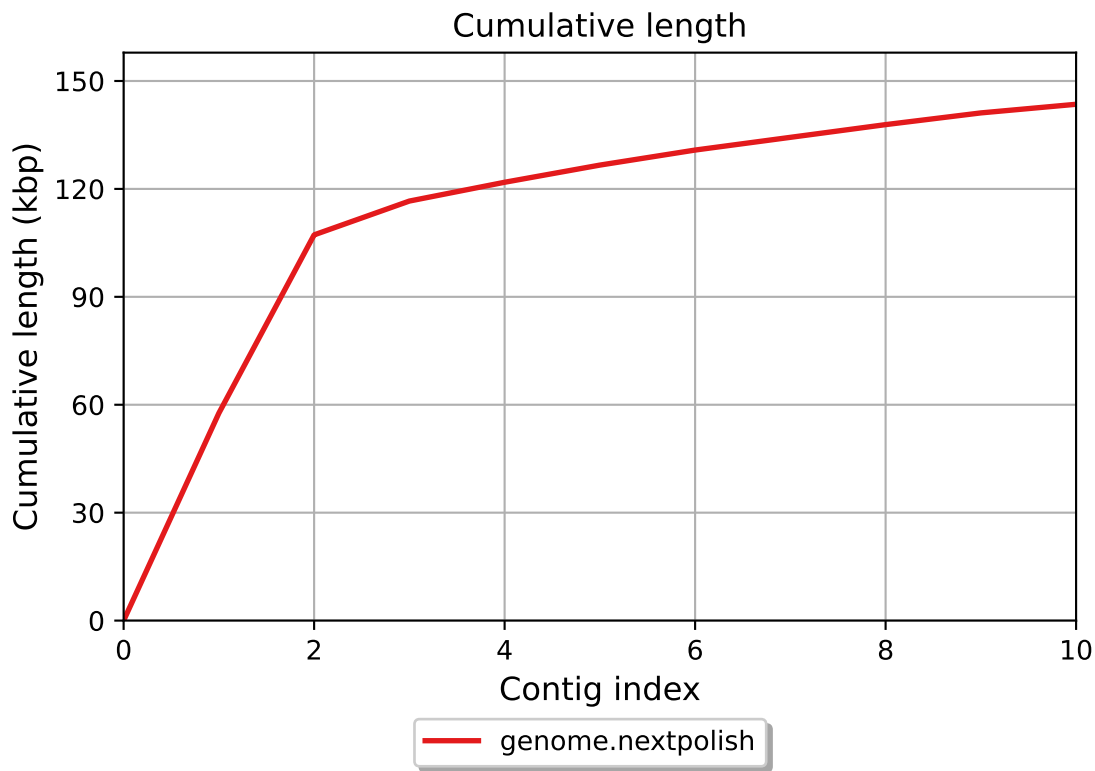
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 10 |
| # contigs (>= 1000 bp) | 10 |
| # contigs (>= 5000 bp) | 4 |
| # contigs (>= 10000 bp) | 2 |
| # contigs (>= 25000 bp) | 2 |
| # contigs (>= 50000 bp) | 1 |
| Total length (>= 0 bp) | 143528 |
| Total length (>= 1000 bp) | 143528 |
| Total length (>= 5000 bp) | 121847 |
| Total length (>= 10000 bp) | 107223 |
| Total length (>= 25000 bp) | 107223 |
| Total length (>= 50000 bp) | 57666 |
| # contigs | 10 |
| Largest contig | 57666 |
| Total length | 143528 |
| GC (%) | 58.43 |
| N50 | 49557 |
| N90 | 4180 |
| auN | 41654.1 |
| L50 | 2 |
| L90 | 6 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 0 + 0 part |

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).

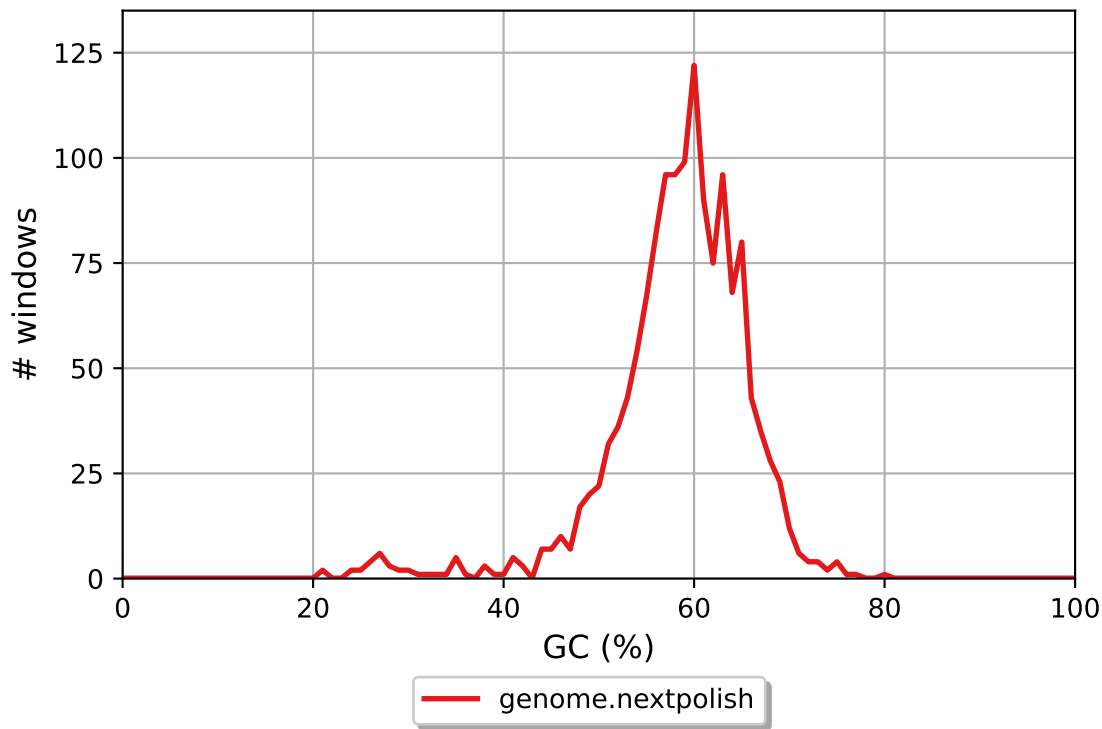
Nx



— genome.nextpolish



GC content



genome.nextpolish GC content

