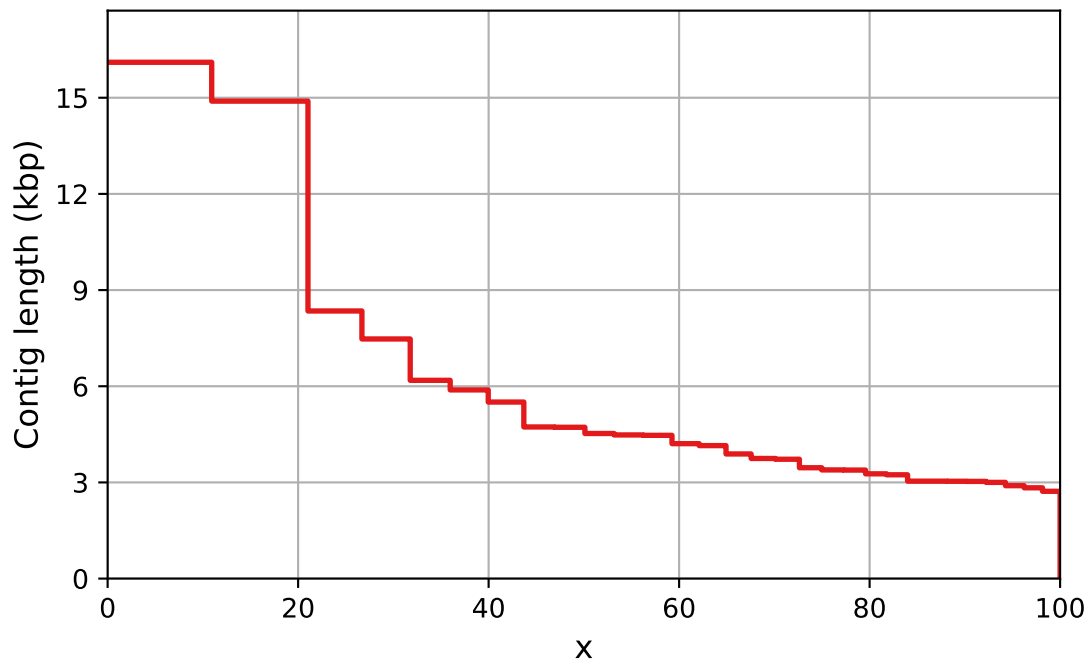


Report

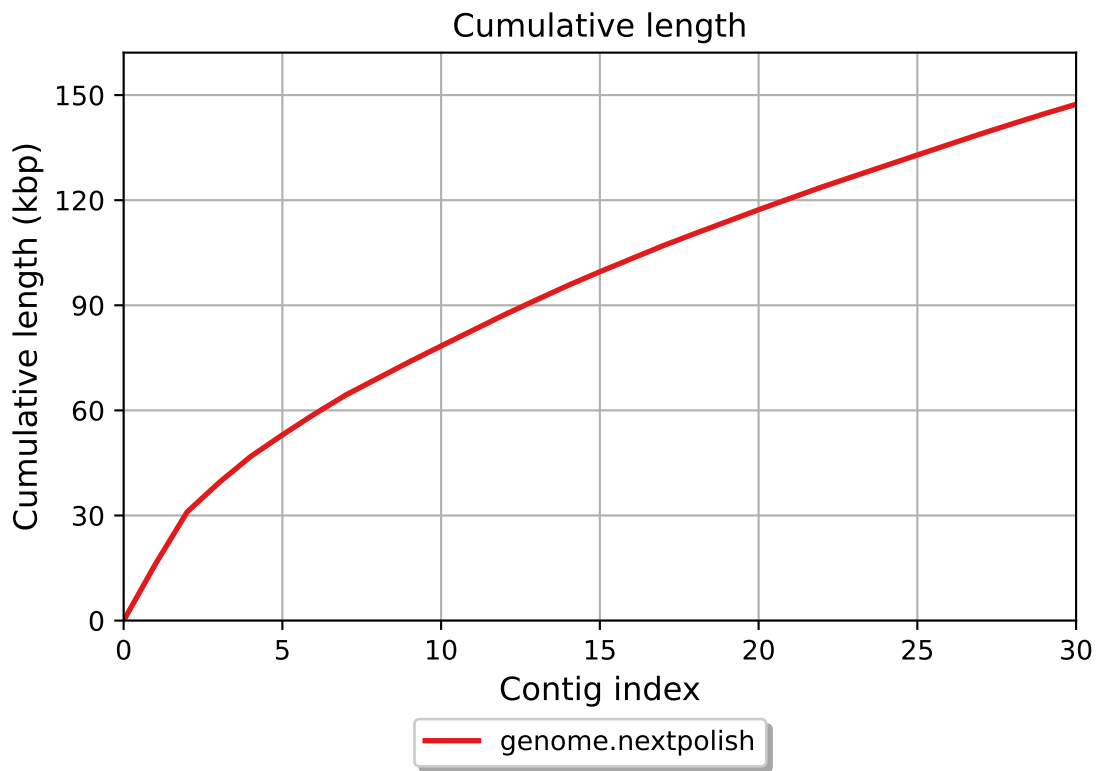
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 30 |
| # contigs (>= 1000 bp) | 30 |
| # contigs (>= 5000 bp) | 7 |
| # contigs (>= 10000 bp) | 2 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 147381 |
| Total length (>= 1000 bp) | 147381 |
| Total length (>= 5000 bp) | 64401 |
| Total length (>= 10000 bp) | 31000 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 30 |
| Largest contig | 16106 |
| Total length | 147381 |
| GC (%) | 45.04 |
| N50 | 4720 |
| N90 | 3036 |
| auN | 6913.7 |
| L50 | 9 |
| L90 | 25 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 1 + 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).

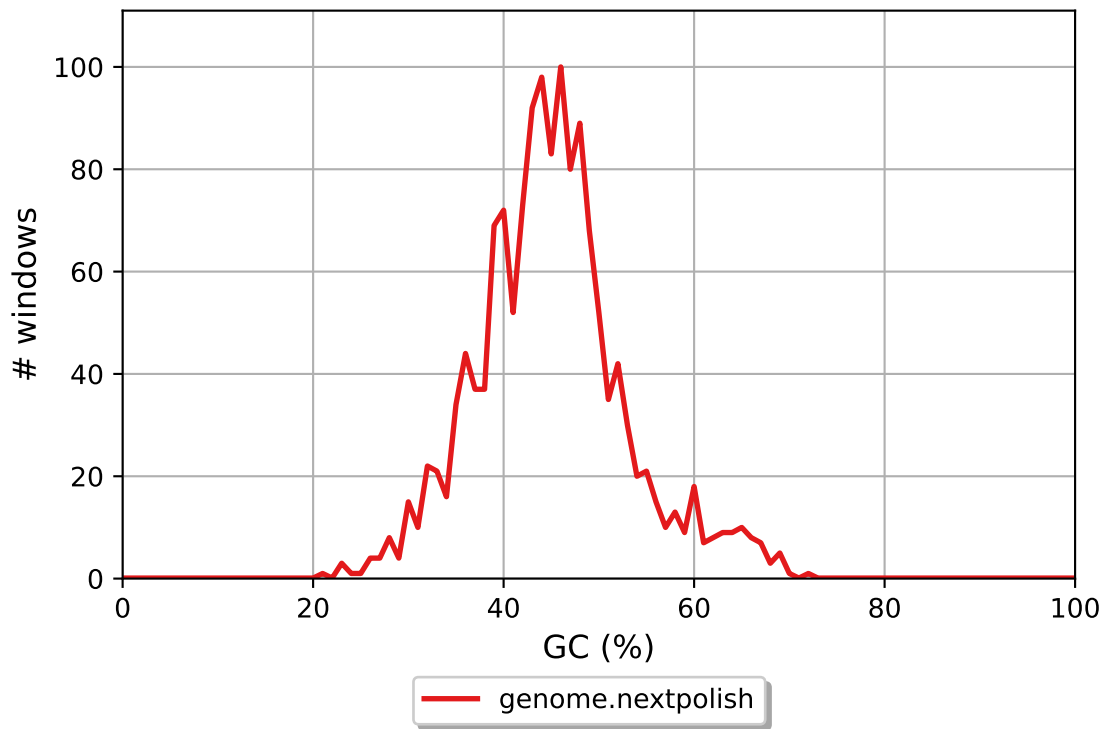
Nx



— genome.nextpolish



GC content



genome.nextpolish GC content

