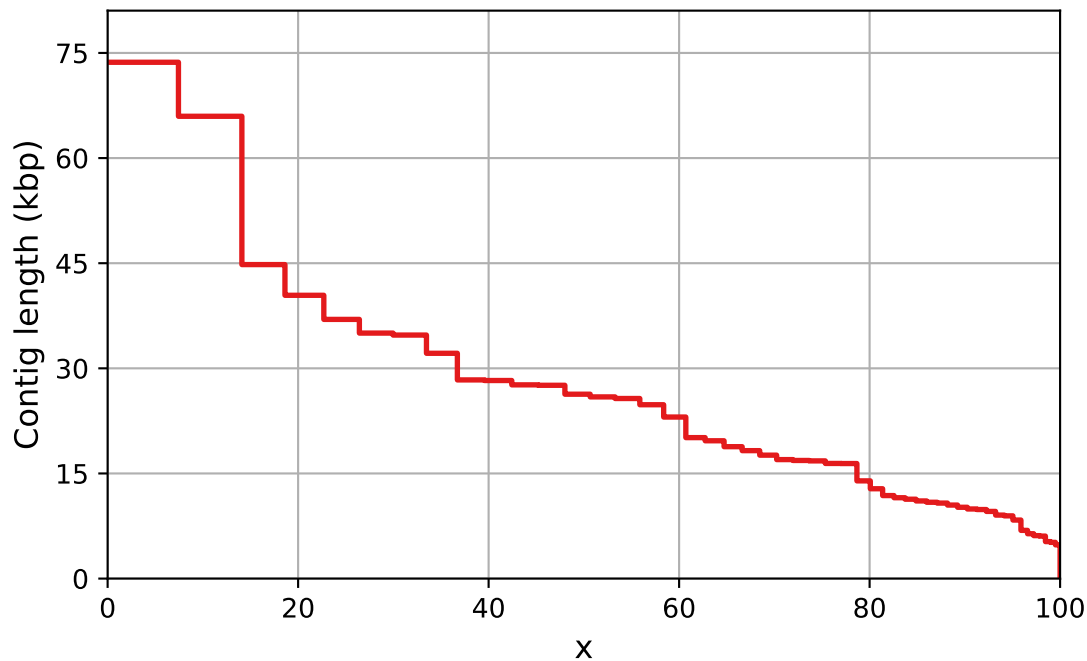


Report

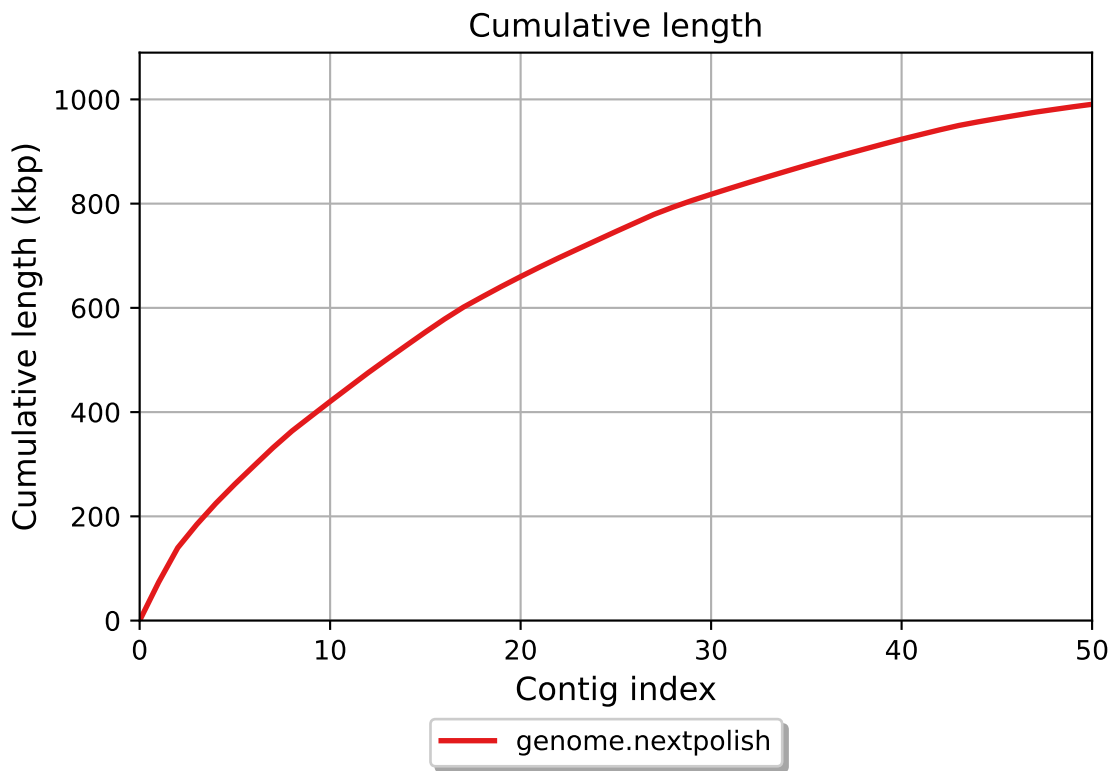
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 50 |
| # contigs (>= 1000 bp) | 50 |
| # contigs (>= 5000 bp) | 49 |
| # contigs (>= 10000 bp) | 37 |
| # contigs (>= 25000 bp) | 15 |
| # contigs (>= 50000 bp) | 2 |
| Total length (>= 0 bp) | 990641 |
| Total length (>= 1000 bp) | 990641 |
| Total length (>= 5000 bp) | 985828 |
| Total length (>= 10000 bp) | 894184 |
| Total length (>= 25000 bp) | 553520 |
| Total length (>= 50000 bp) | 139634 |
| # contigs | 50 |
| Largest contig | 73670 |
| Total length | 990641 |
| GC (%) | 42.75 |
| N50 | 26308 |
| N90 | 10175 |
| auN | 30108.6 |
| L50 | 13 |
| L90 | 37 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 5 + 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).

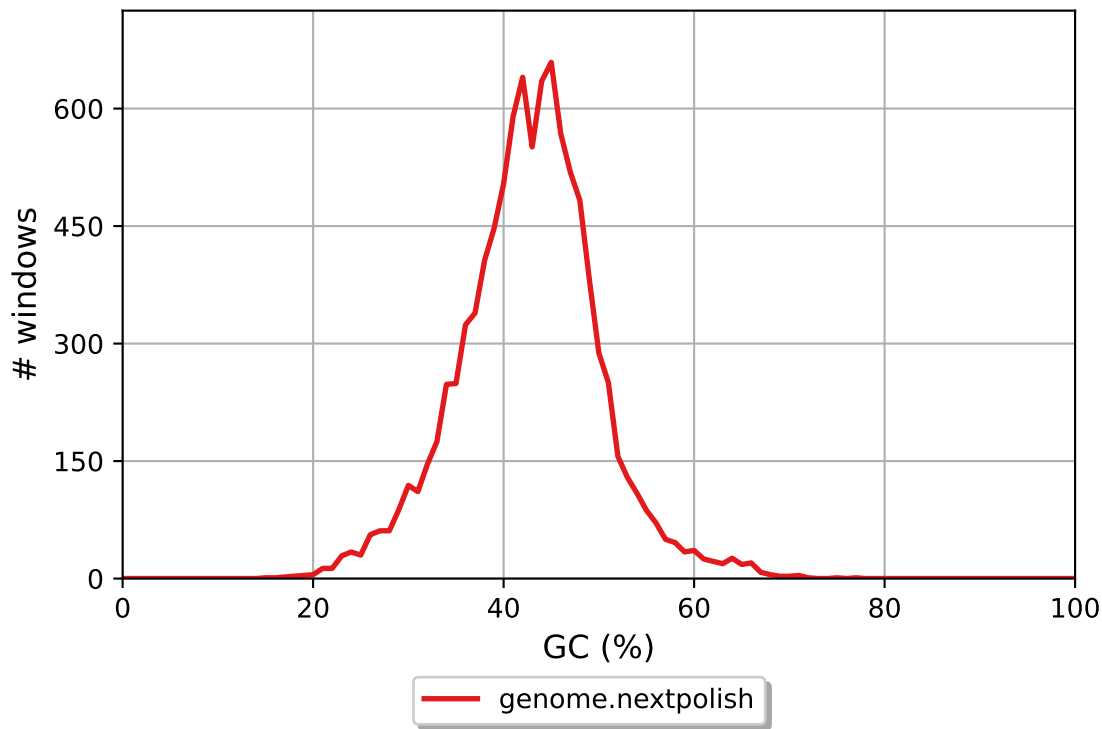
Nx



— genome.nextpolish



GC content



genome.nextpolish GC content

