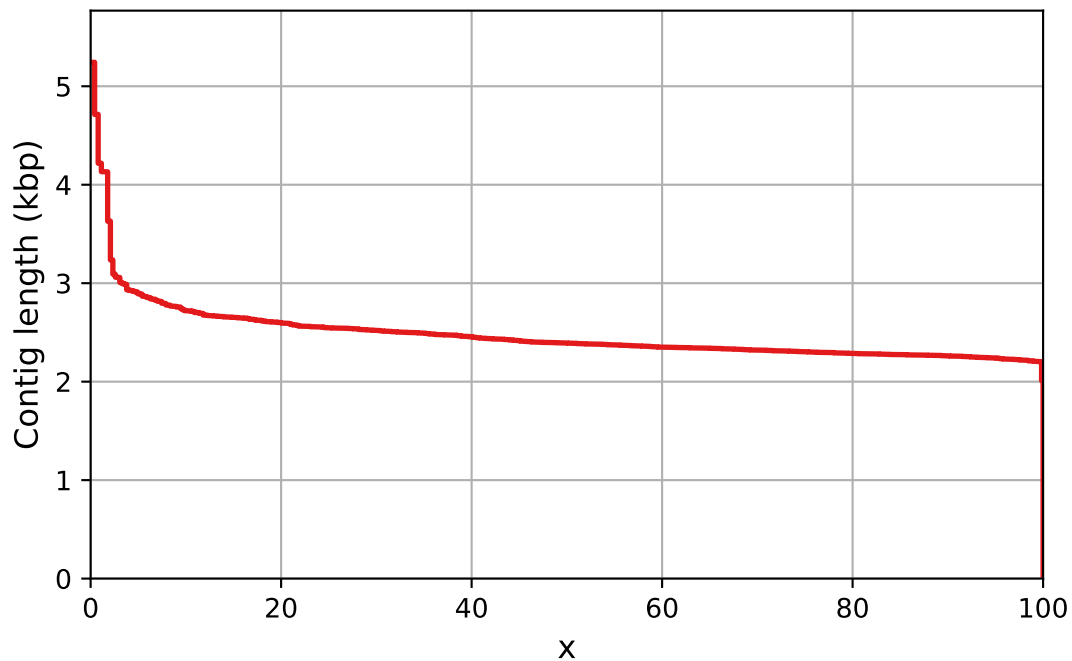


Report

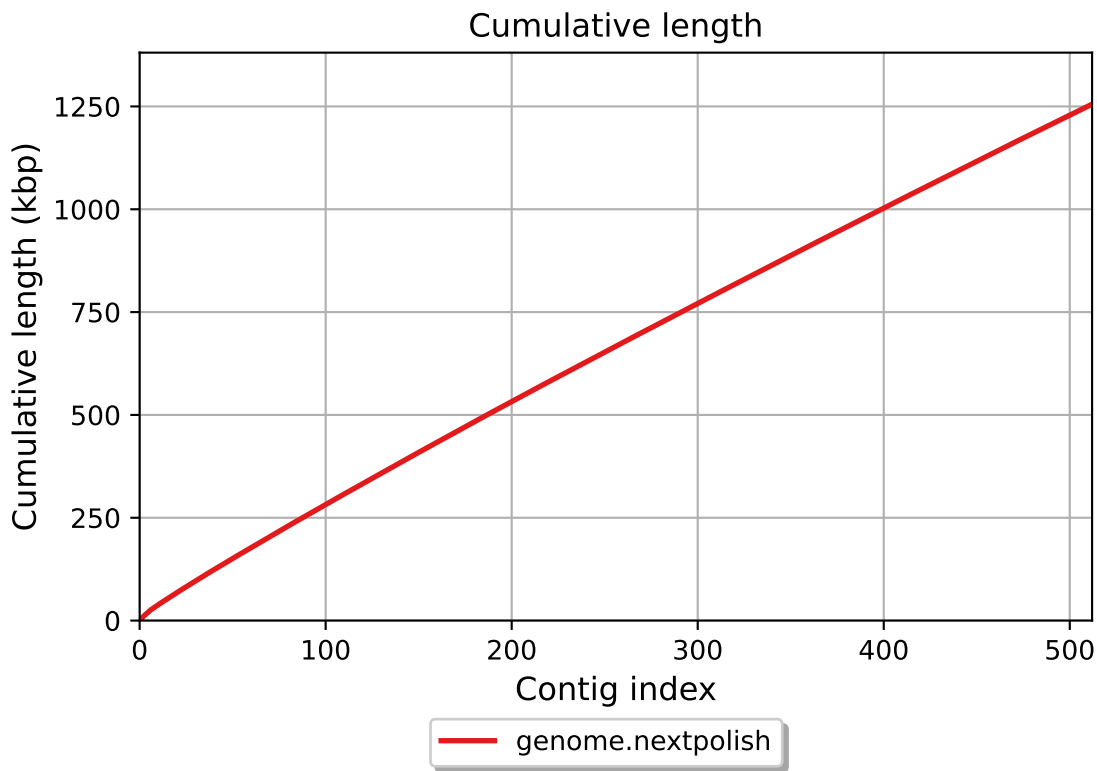
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 512 |
| # contigs (>= 1000 bp) | 512 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 1255268 |
| Total length (>= 1000 bp) | 1255268 |
| Total length (>= 5000 bp) | 5243 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 512 |
| Largest contig | 5243 |
| Total length | 1255268 |
| GC (%) | 51.35 |
| N50 | 2392 |
| N90 | 2261 |
| auN | 2482.9 |
| L50 | 240 |
| L90 | 456 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 2 + 4 part |

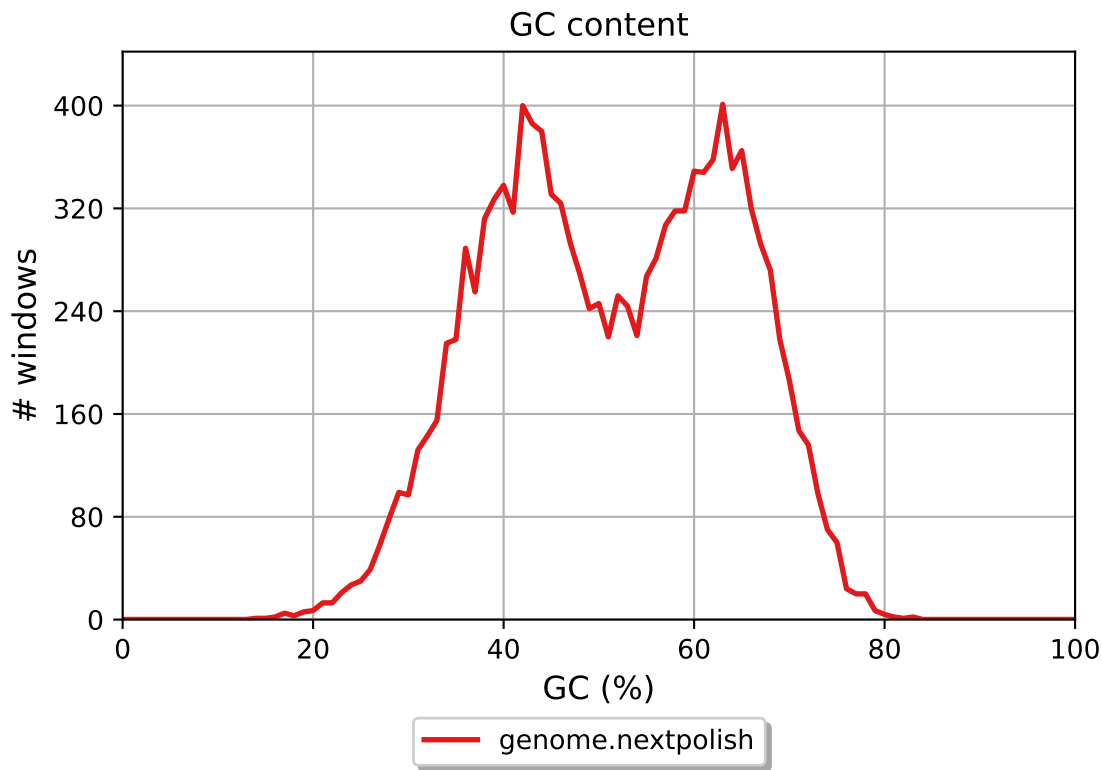
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx



— genome.nextpolish





genome.nextpolish GC content

