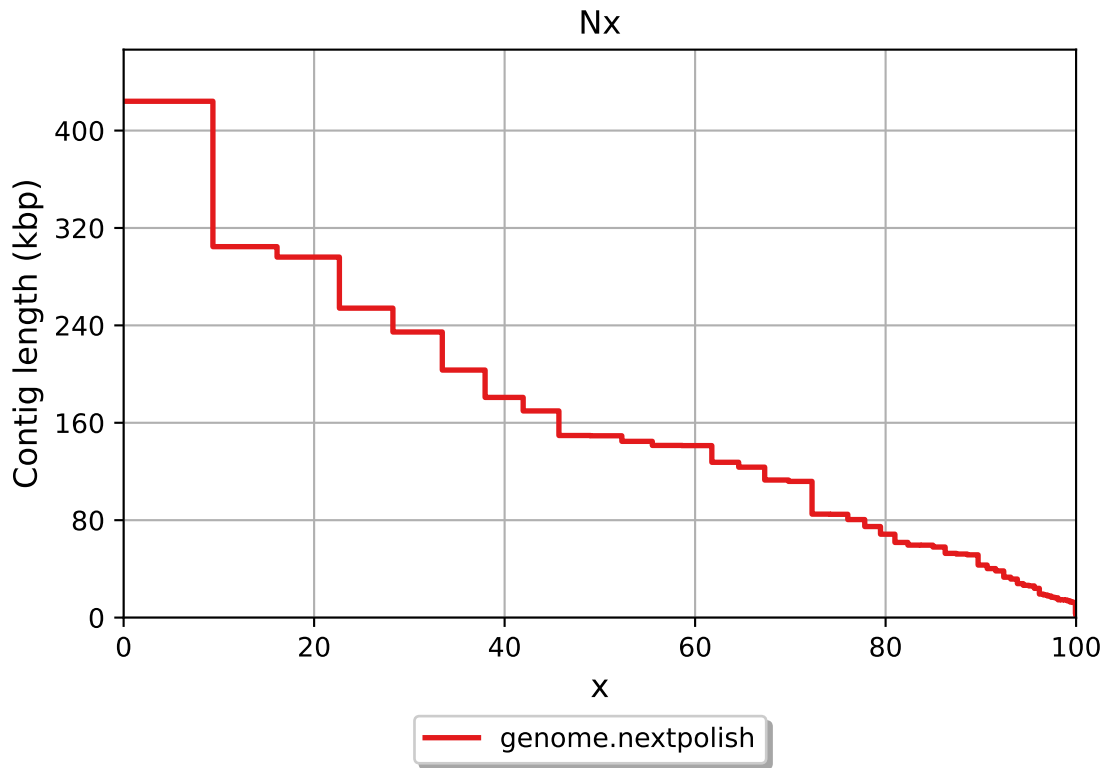
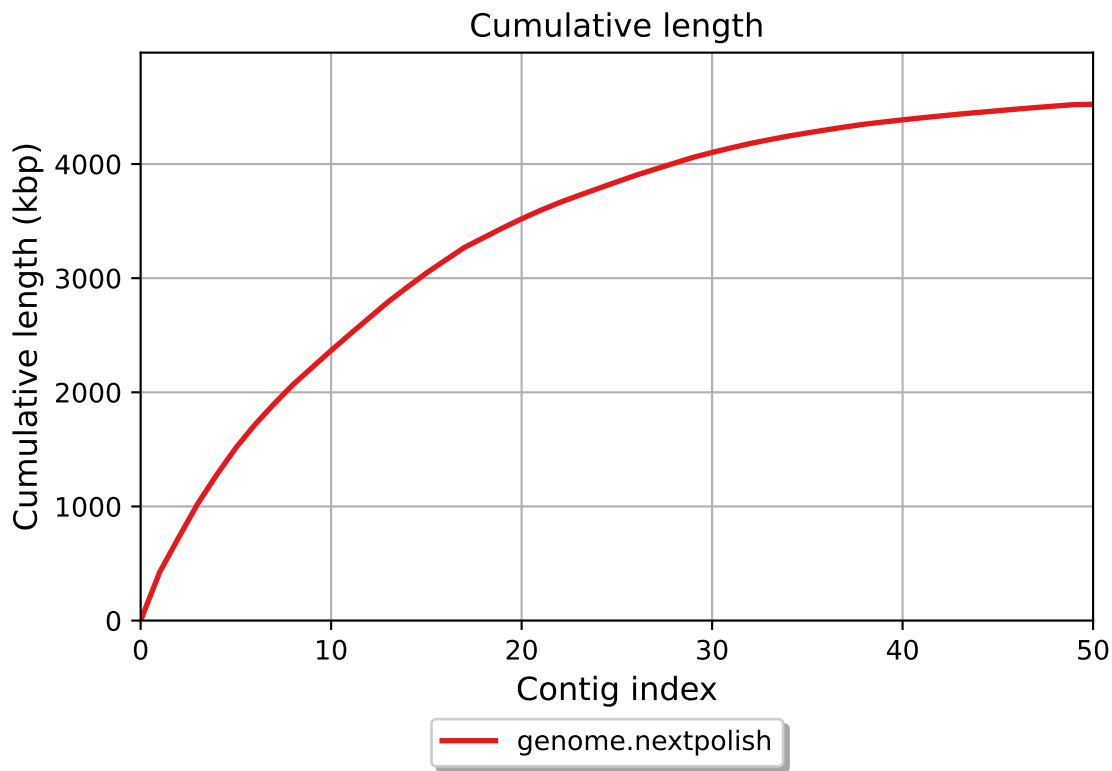


Report

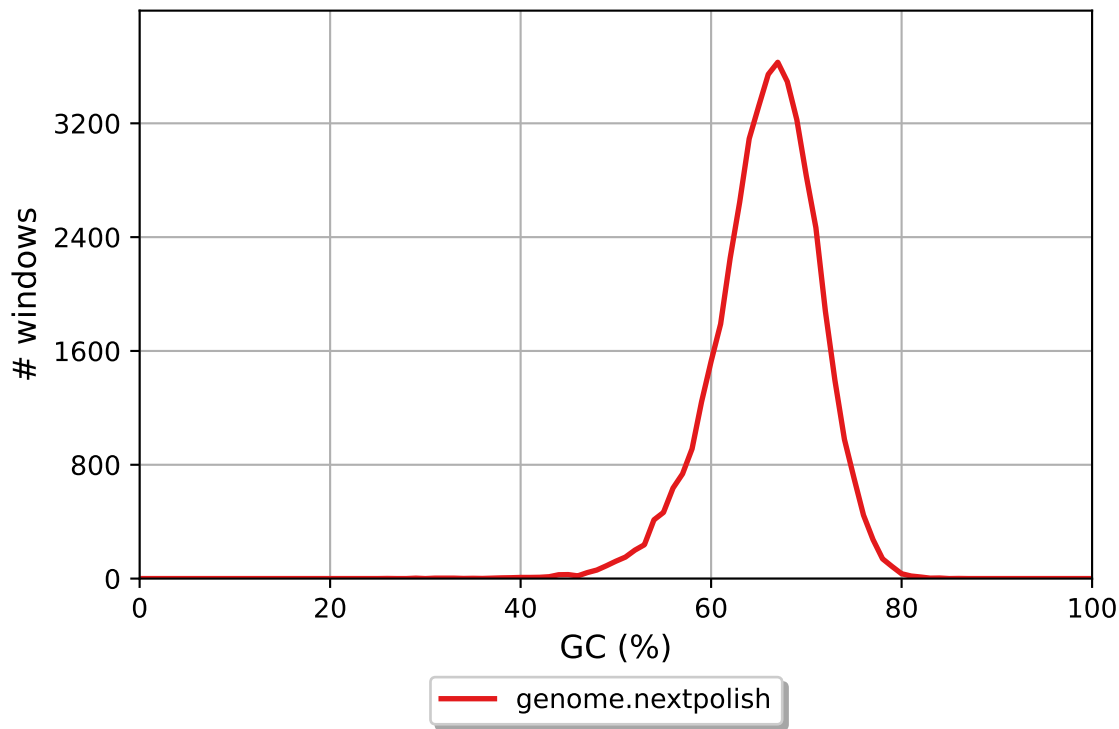
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 50 |
| # contigs (>= 1000 bp) | 50 |
| # contigs (>= 5000 bp) | 49 |
| # contigs (>= 10000 bp) | 49 |
| # contigs (>= 25000 bp) | 37 |
| # contigs (>= 50000 bp) | 29 |
| Total length (>= 0 bp) | 4523706 |
| Total length (>= 1000 bp) | 4523706 |
| Total length (>= 5000 bp) | 4520448 |
| Total length (>= 10000 bp) | 4520448 |
| Total length (>= 25000 bp) | 4325217 |
| Total length (>= 50000 bp) | 4058305 |
| # contigs | 50 |
| Largest contig | 424064 |
| Total length | 4523706 |
| GC (%) | 65.78 |
| N50 | 149325 |
| N90 | 43137 |
| auN | 179329.0 |
| L50 | 10 |
| L90 | 30 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 6 + 1 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).





GC content



genome.nextpolish GC content

