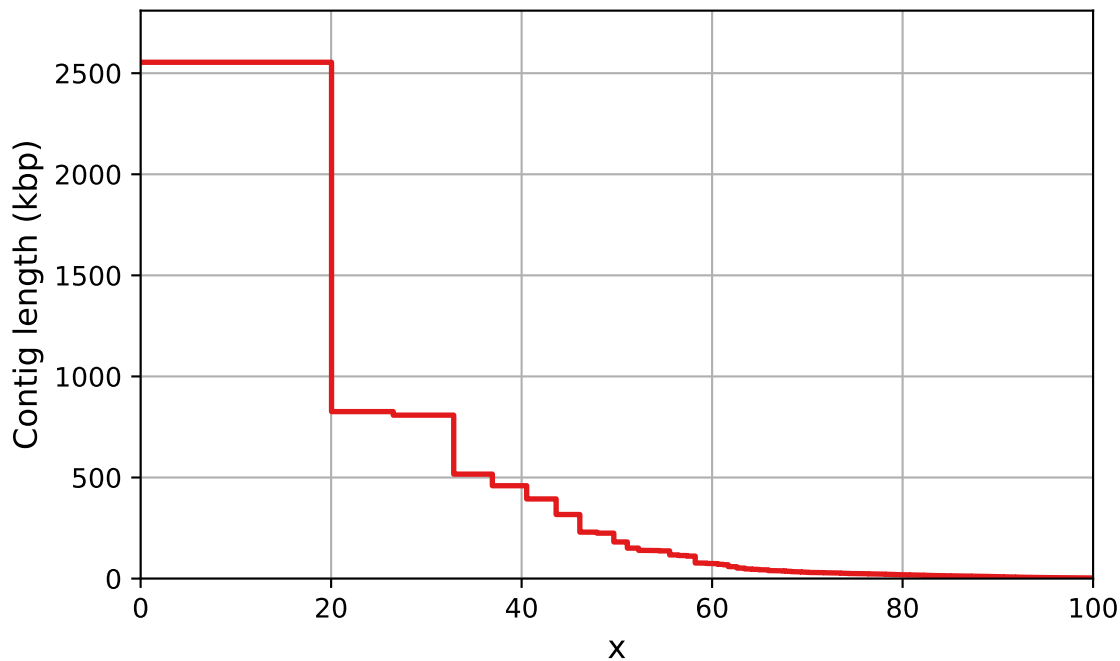


Report

| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 456 |
| # contigs (>= 1000 bp) | 456 |
| # contigs (>= 5000 bp) | 279 |
| # contigs (>= 10000 bp) | 186 |
| # contigs (>= 25000 bp) | 69 |
| # contigs (>= 50000 bp) | 27 |
| Total length (>= 0 bp) | 12742051 |
| Total length (>= 1000 bp) | 12742051 |
| Total length (>= 5000 bp) | 12041690 |
| Total length (>= 10000 bp) | 11376508 |
| Total length (>= 25000 bp) | 9495697 |
| Total length (>= 50000 bp) | 8082622 |
| # contigs | 456 |
| Largest contig | 2554075 |
| Total length | 12742051 |
| GC (%) | 50.37 |
| N50 | 181175 |
| N90 | 9382 |
| auN | 704964.8 |
| L50 | 10 |
| L90 | 196 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 20 + 13 part |

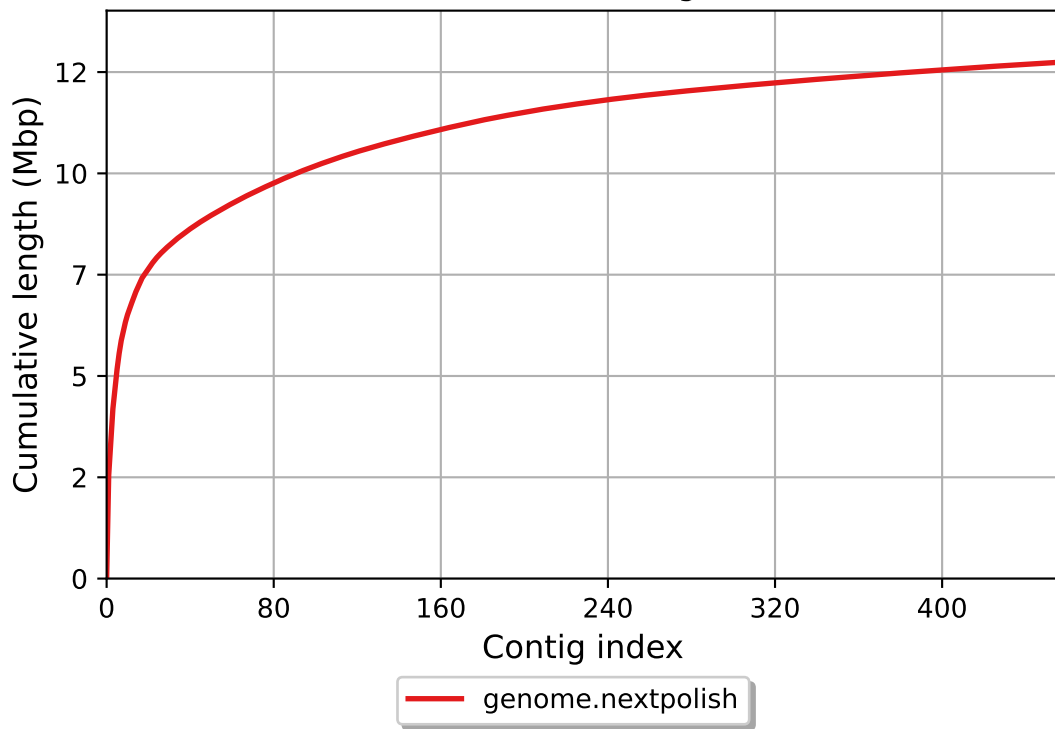
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

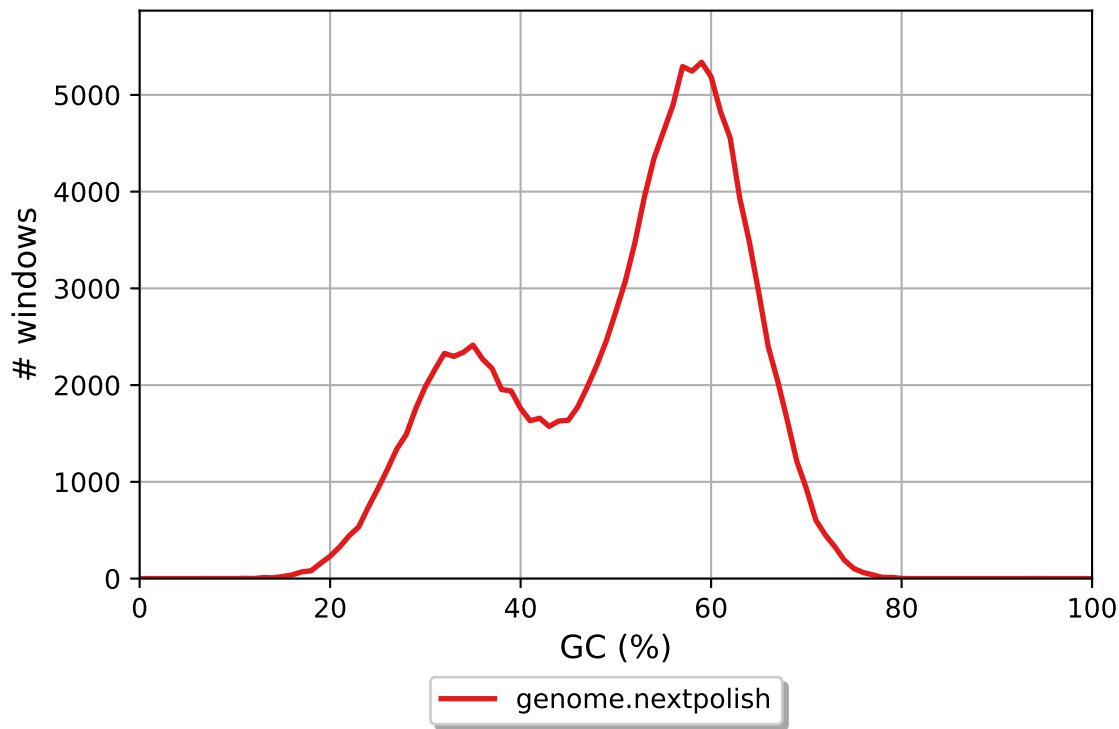


— genome.nextpolish

Cumulative length



GC content



genome.nextpolish GC content

