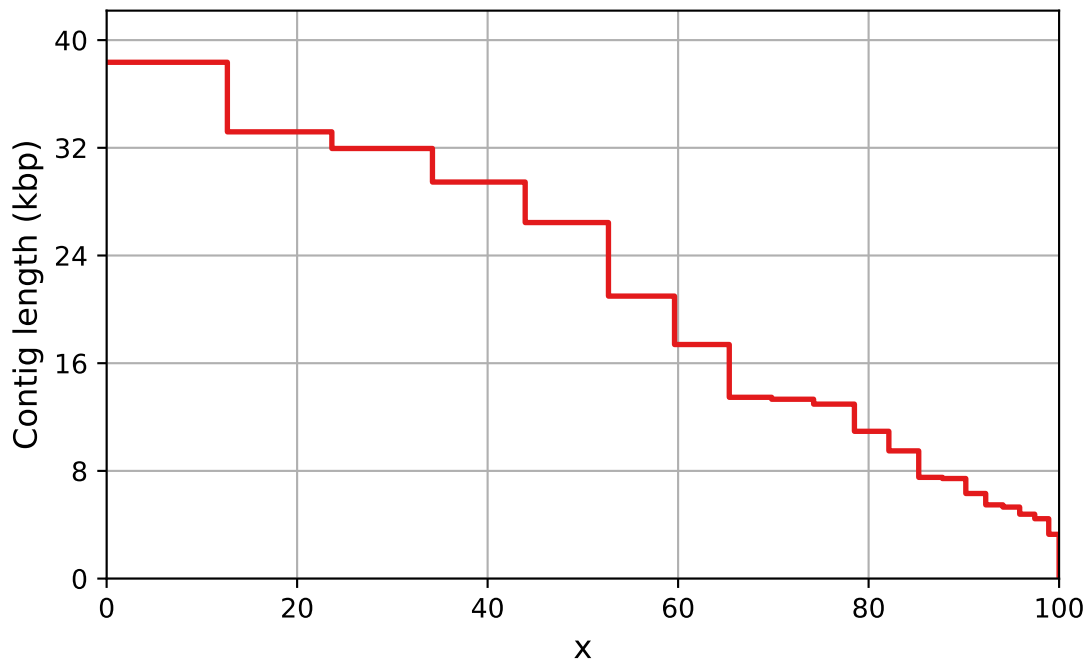


Report

| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 20 |
| # contigs (>= 1000 bp) | 20 |
| # contigs (>= 5000 bp) | 17 |
| # contigs (>= 10000 bp) | 11 |
| # contigs (>= 25000 bp) | 5 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 302529 |
| Total length (>= 1000 bp) | 302529 |
| Total length (>= 5000 bp) | 290009 |
| Total length (>= 10000 bp) | 248459 |
| Total length (>= 25000 bp) | 159396 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 20 |
| Largest contig | 38354 |
| Total length | 302529 |
| GC (%) | 25.32 |
| N50 | 26448 |
| N90 | 7433 |
| auN | 22817.9 |
| L50 | 5 |
| L90 | 14 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 1 + 1 part |

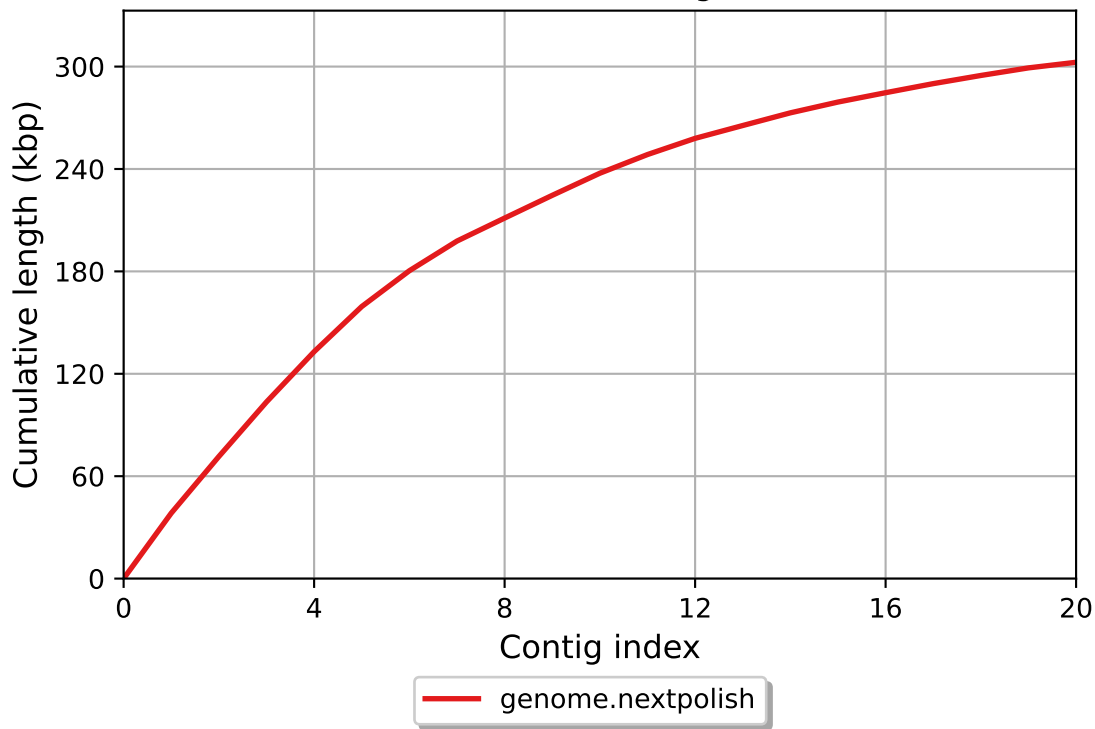
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

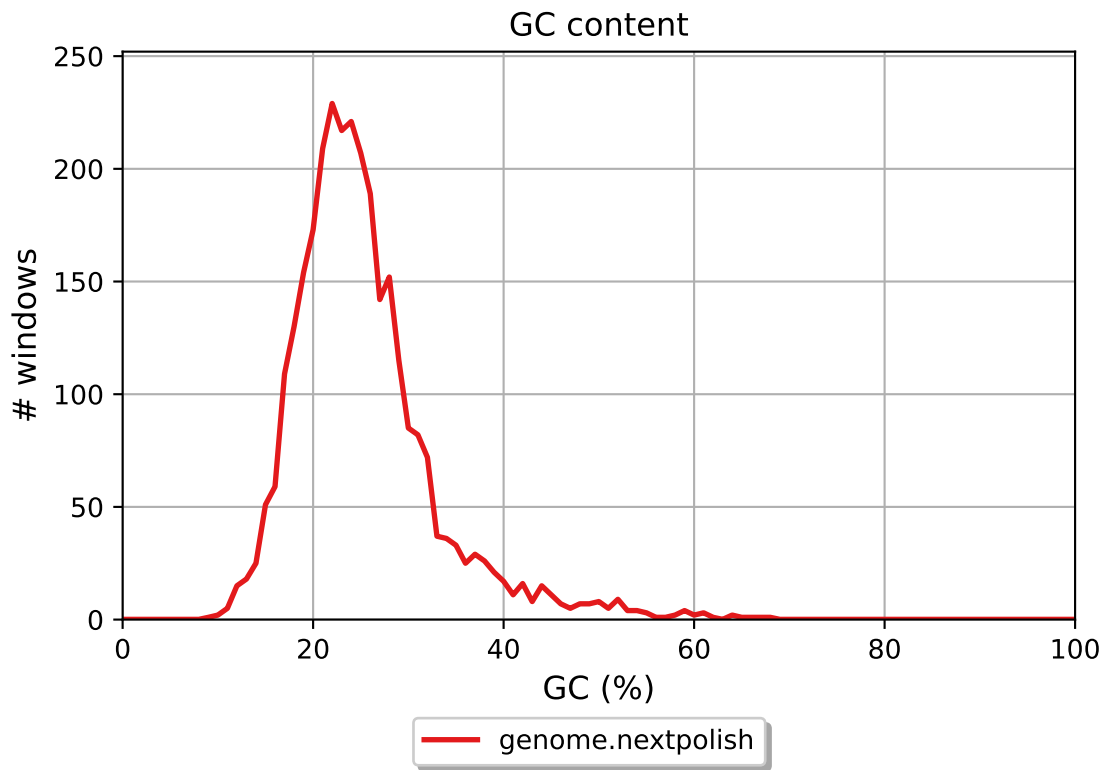
Nx



— genome.nextpolish

Cumulative length





genome.nextpolish GC content

