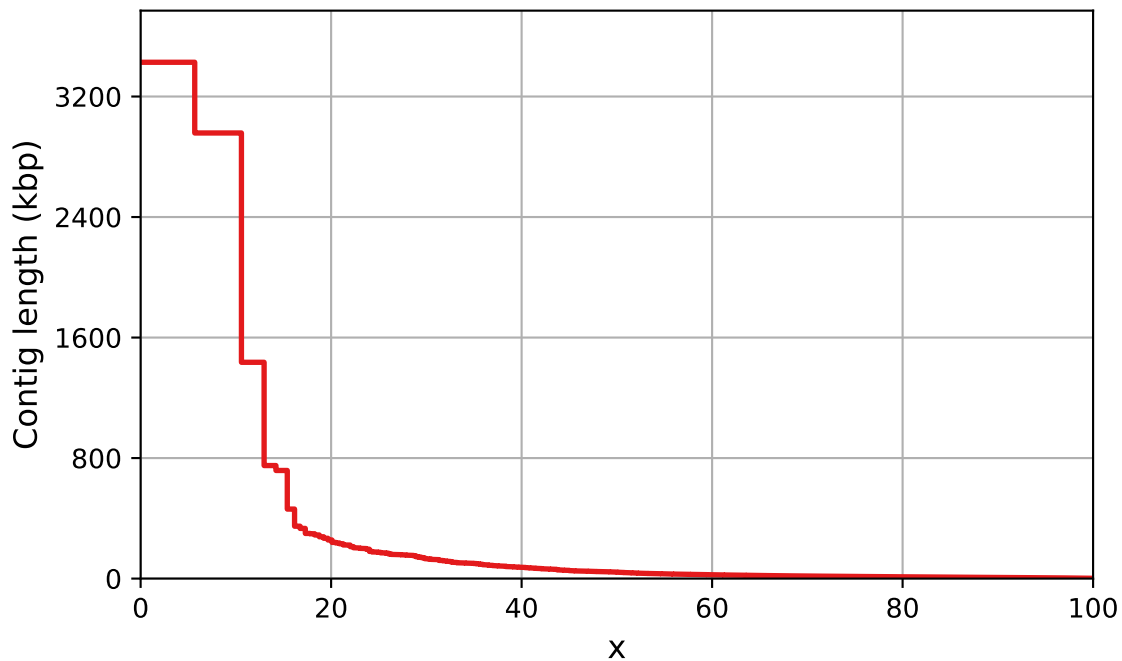


# Report

|                            | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp)        | 3121              |
| # contigs (>= 1000 bp)     | 3091              |
| # contigs (>= 5000 bp)     | 2326              |
| # contigs (>= 10000 bp)    | 1363              |
| # contigs (>= 25000 bp)    | 419               |
| # contigs (>= 50000 bp)    | 170               |
| Total length (>= 0 bp)     | 60328787          |
| Total length (>= 1000 bp)  | 60308180          |
| Total length (>= 5000 bp)  | 57733934          |
| Total length (>= 10000 bp) | 50795414          |
| Total length (>= 25000 bp) | 36380069          |
| Total length (>= 50000 bp) | 27810087          |
| # contigs                  | 3120              |
| Largest contig             | 3427368           |
| Total length               | 60328292          |
| GC (%)                     | 55.79             |
| N50                        | 42911             |
| N90                        | 7505              |
| auN                        | 448930.6          |
| L50                        | 221               |
| L90                        | 1769              |
| # N's per 100 kbp          | 0.00              |
| Complete BUSCO (%)         | 0.00              |
| Partial BUSCO (%)          | 0.00              |
| # predicted rRNA genes     | 91 + 15 part      |

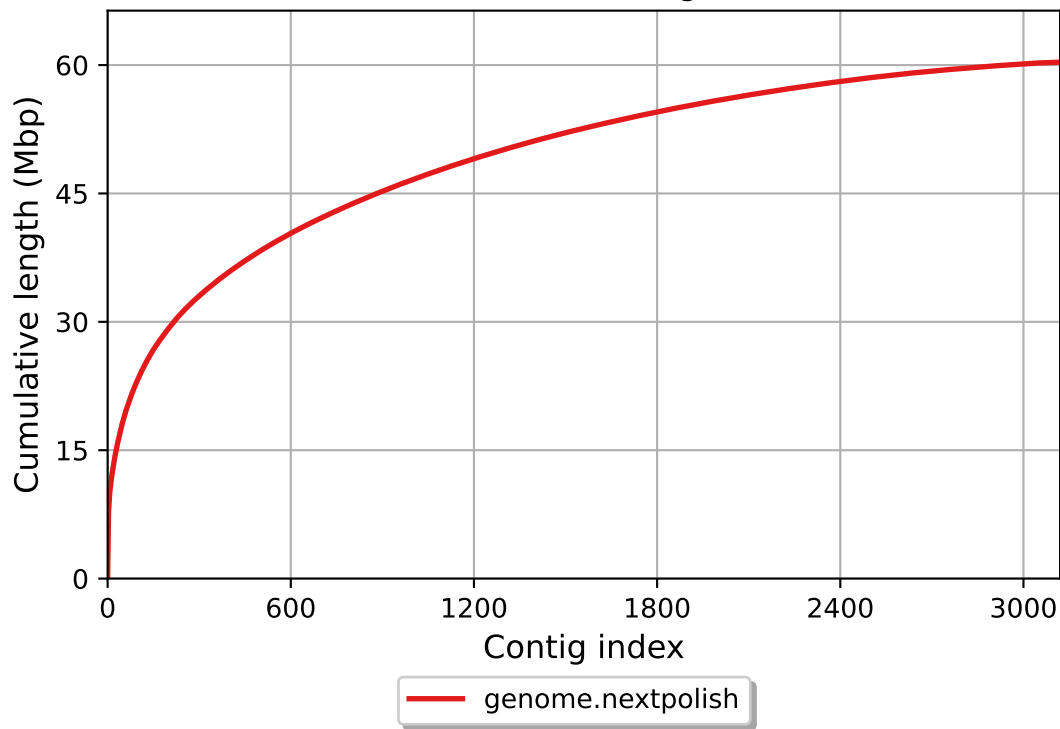
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

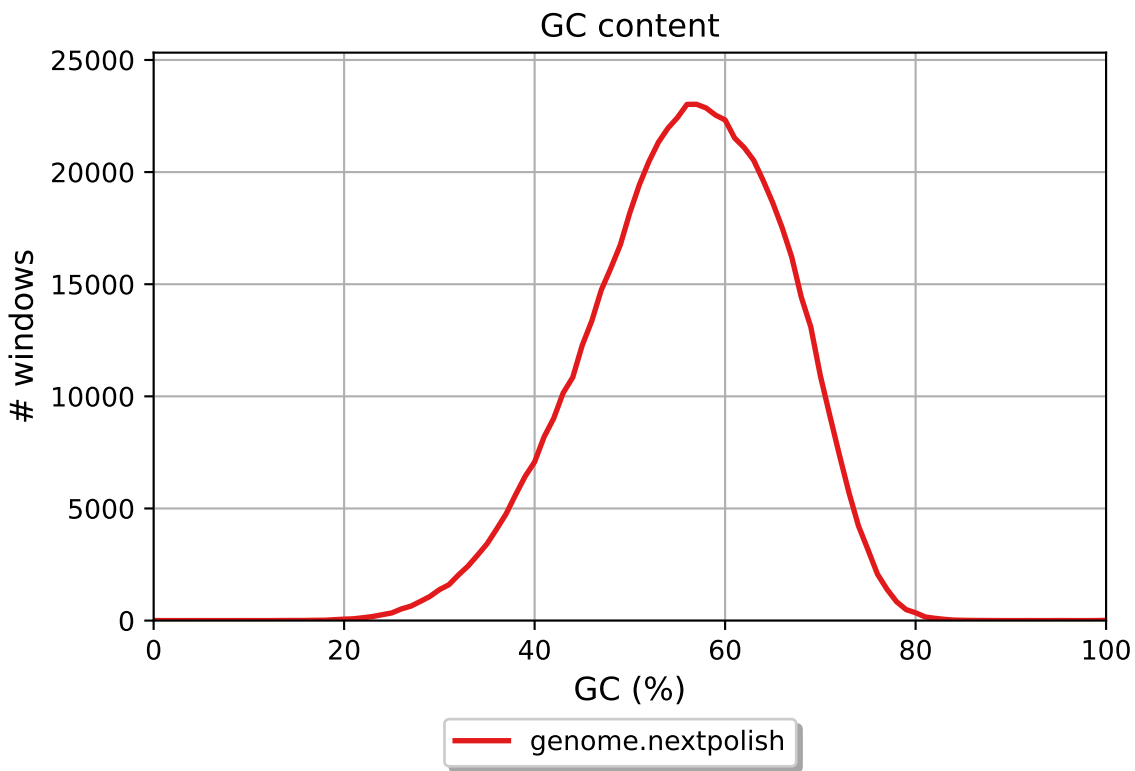
Nx



— genome.nextpolish

Cumulative length





genome.nextpolish GC content

