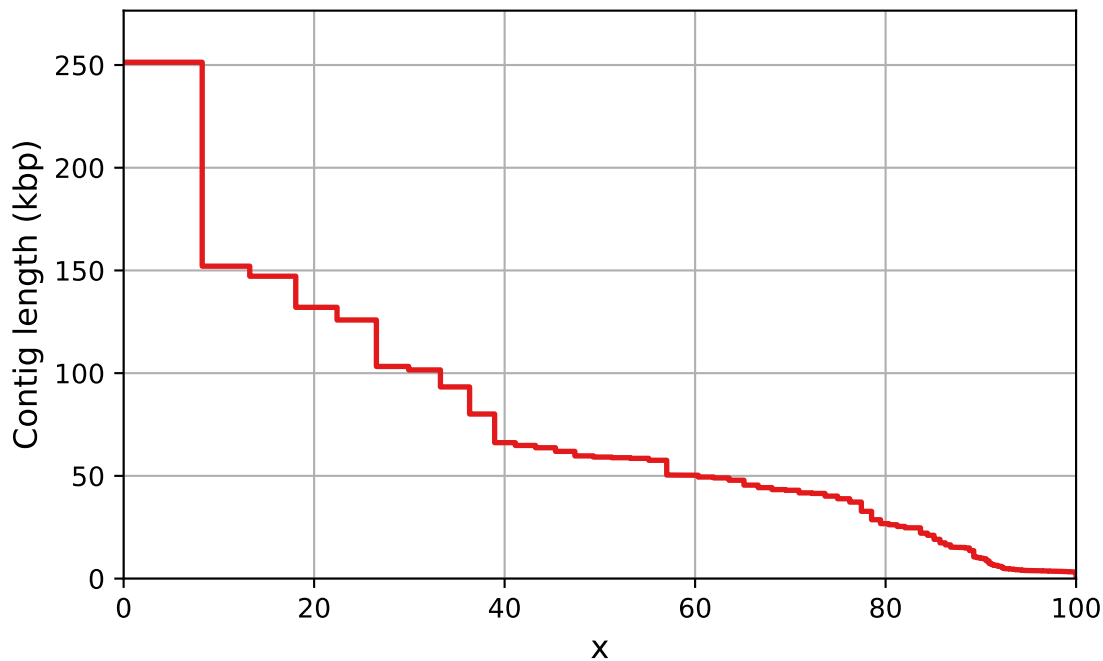


Report

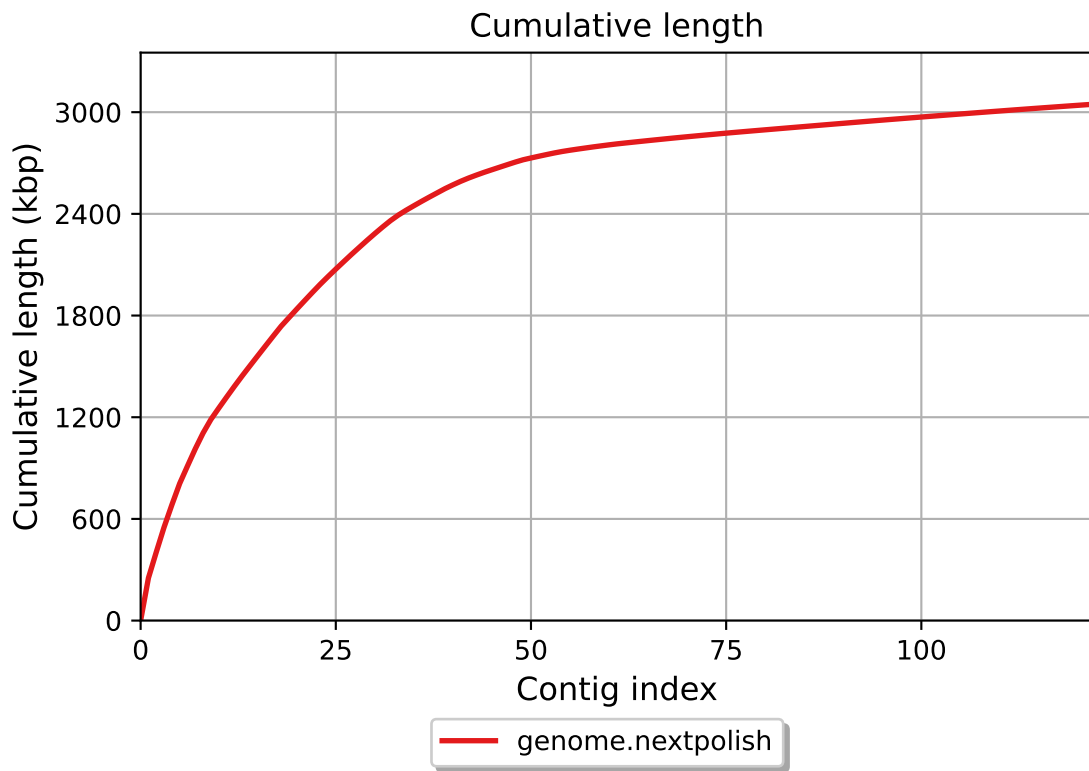
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 122 |
| # contigs (>= 1000 bp) | 122 |
| # contigs (>= 5000 bp) | 61 |
| # contigs (>= 10000 bp) | 51 |
| # contigs (>= 25000 bp) | 37 |
| # contigs (>= 50000 bp) | 20 |
| Total length (>= 0 bp) | 3046680 |
| Total length (>= 1000 bp) | 3046680 |
| Total length (>= 5000 bp) | 2812832 |
| Total length (>= 10000 bp) | 2739978 |
| Total length (>= 25000 bp) | 2499526 |
| Total length (>= 50000 bp) | 1837930 |
| # contigs | 122 |
| Largest contig | 251337 |
| Total length | 3046680 |
| GC (%) | 57.84 |
| N50 | 59154 |
| N90 | 9907 |
| auN | 81674.3 |
| L50 | 15 |
| L90 | 52 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 5 + 0 part |

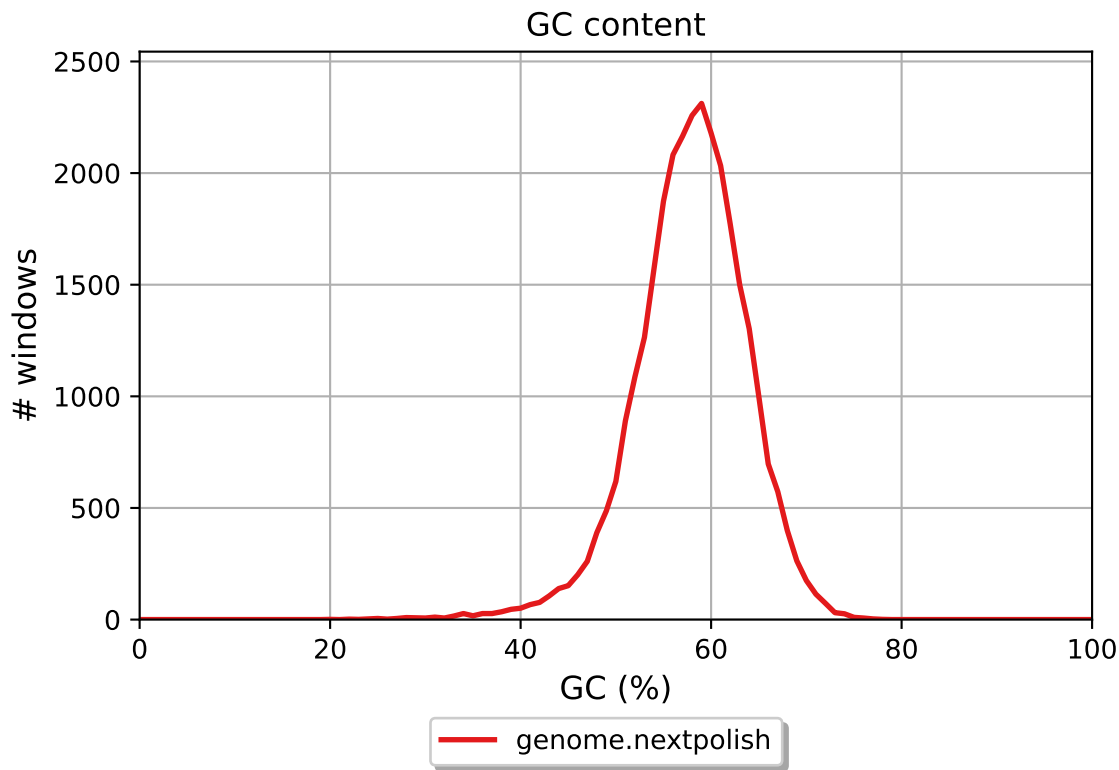
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx



— genome.nextpolish





genome.nextpolish GC content

