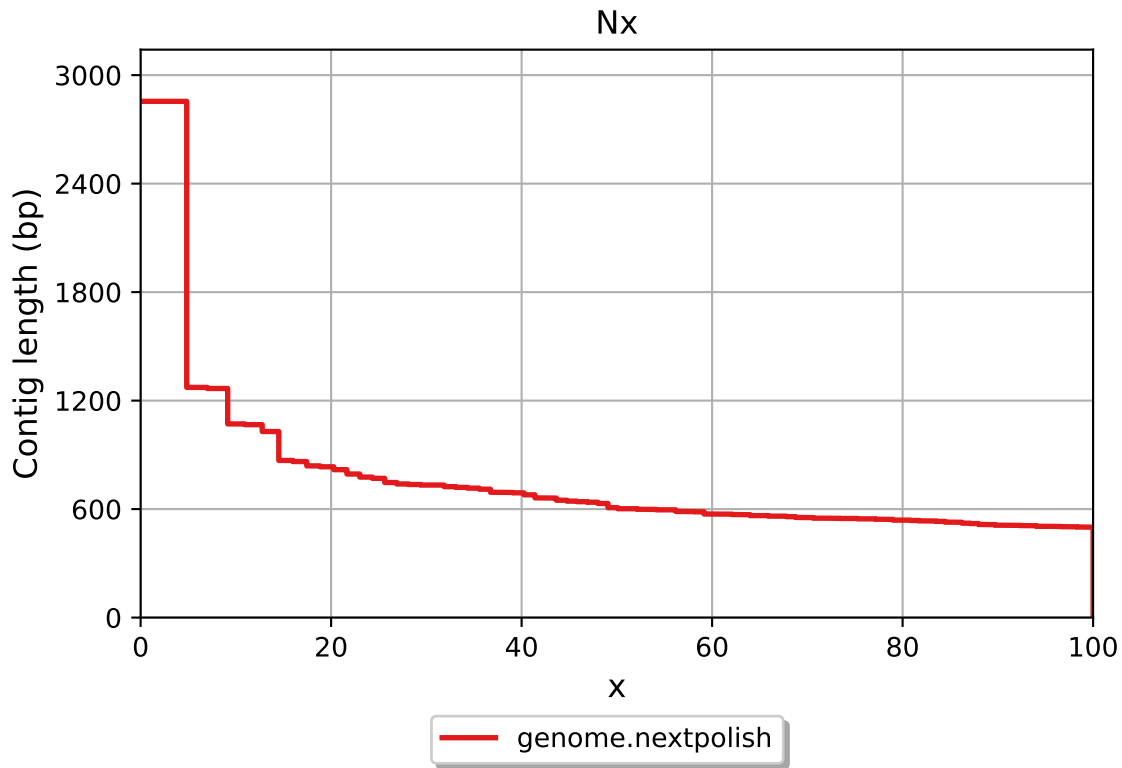


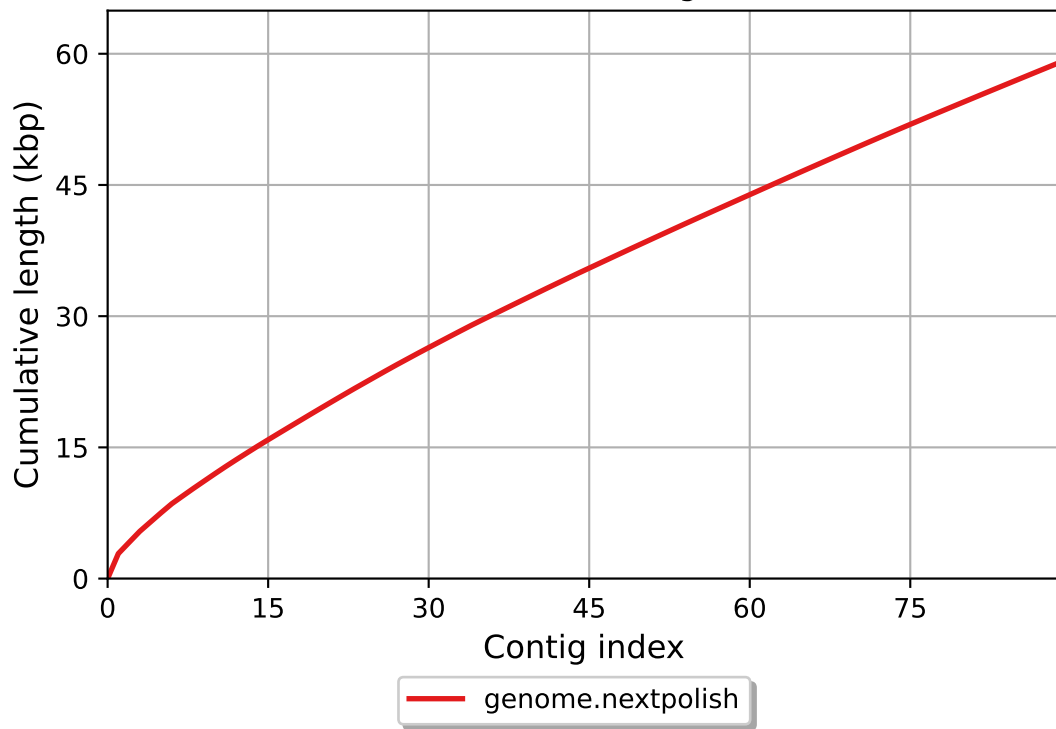
Report

| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 1994 |
| # contigs (>= 1000 bp) | 6 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 457475 |
| Total length (>= 1000 bp) | 8562 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 89 |
| Largest contig | 2855 |
| Total length | 59027 |
| GC (%) | 53.90 |
| N50 | 608 |
| N90 | 511 |
| auN | 782.8 |
| L50 | 35 |
| L90 | 78 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 0 + 0 part |

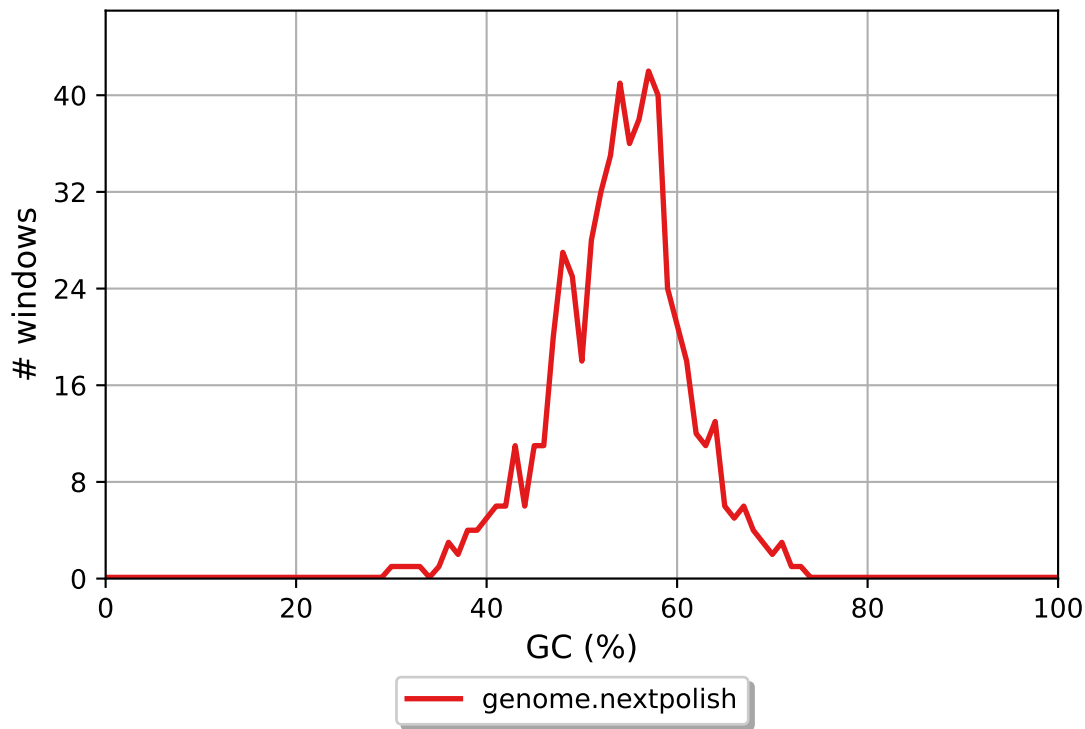
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



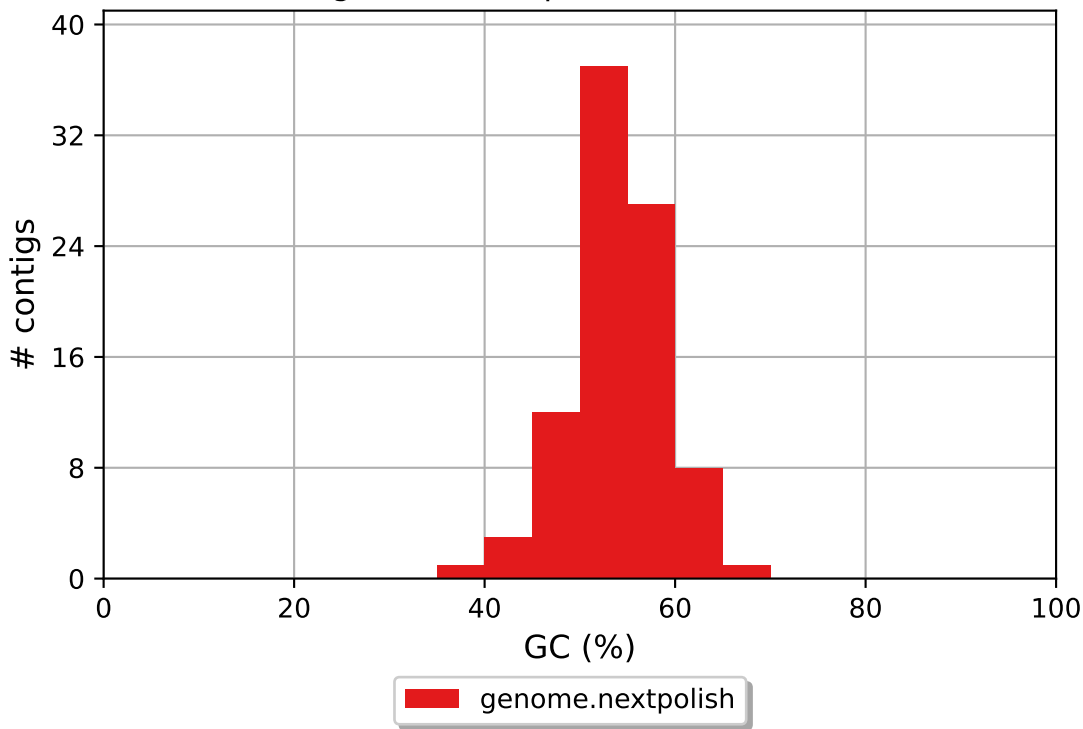
Cumulative length



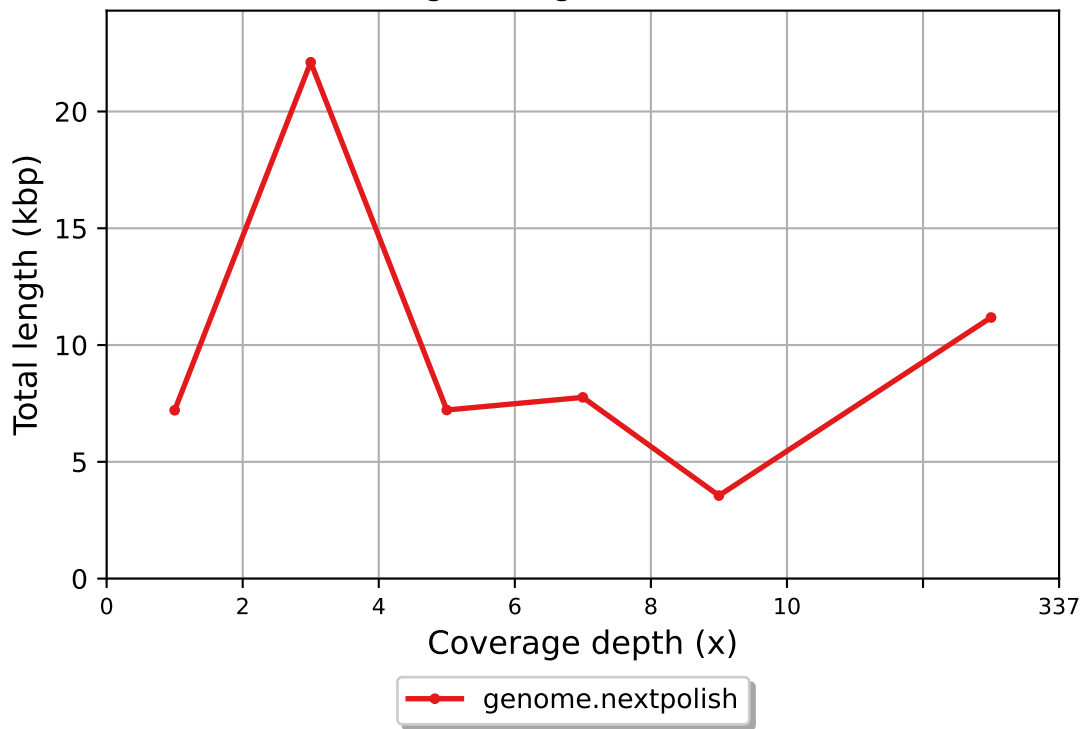
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 2x)



genome.nextpolish coverage histogram (bin size: 2x)

