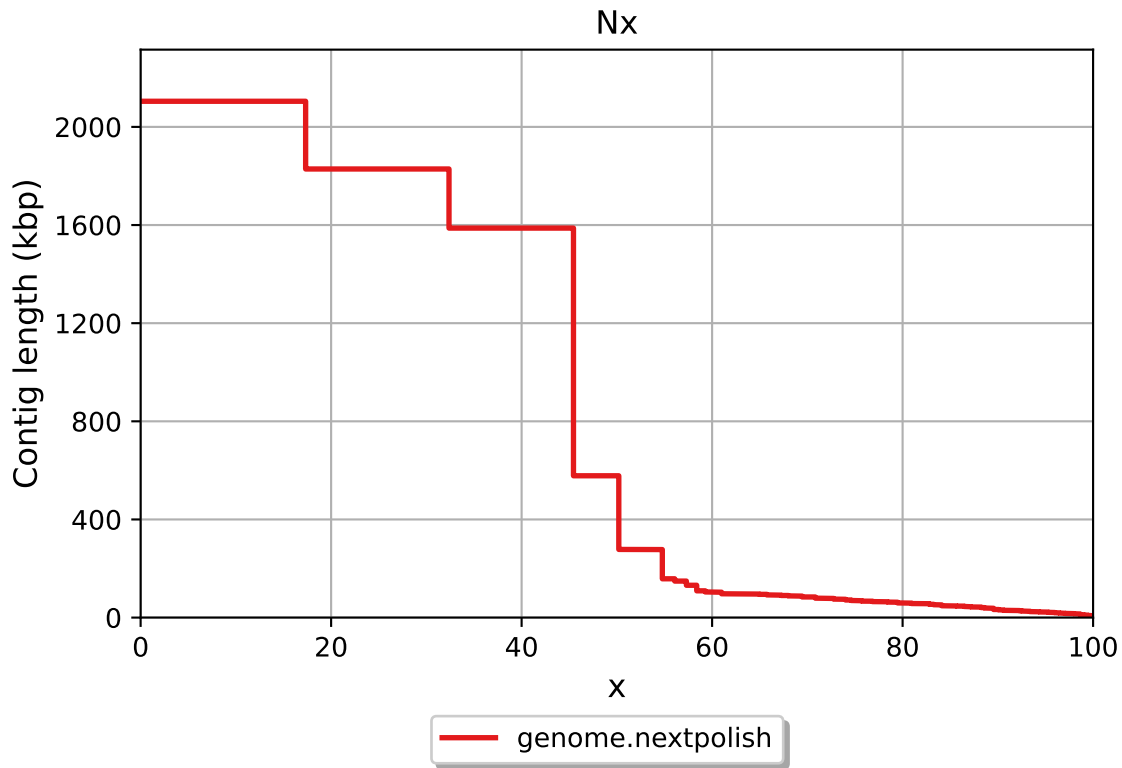


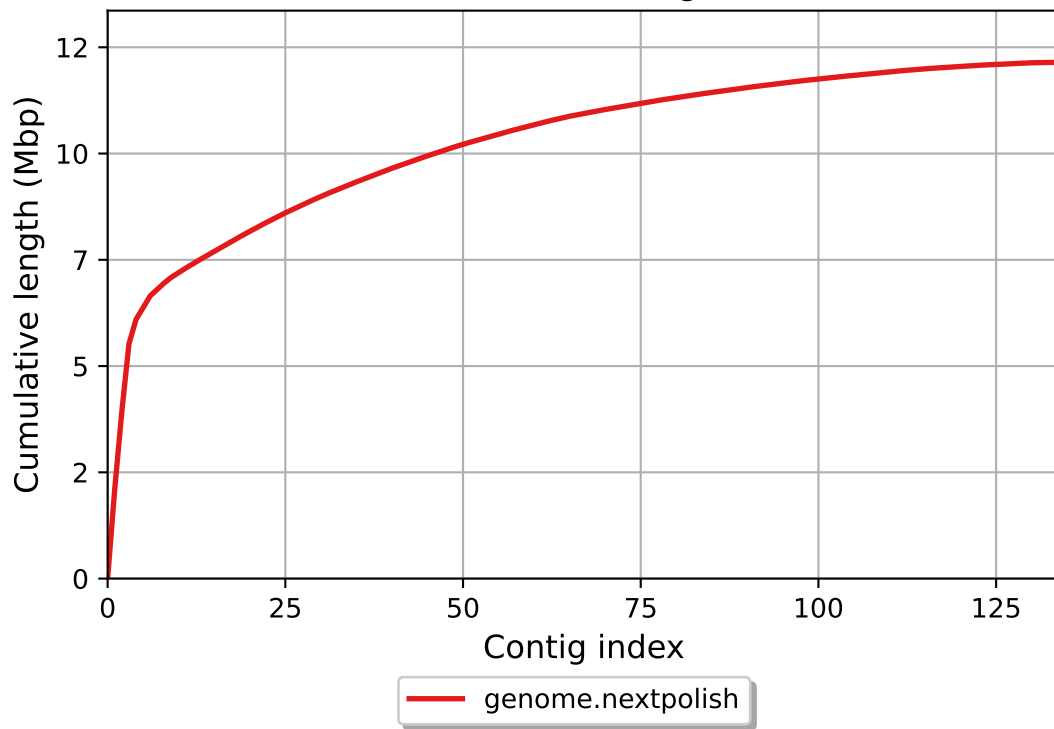
Report

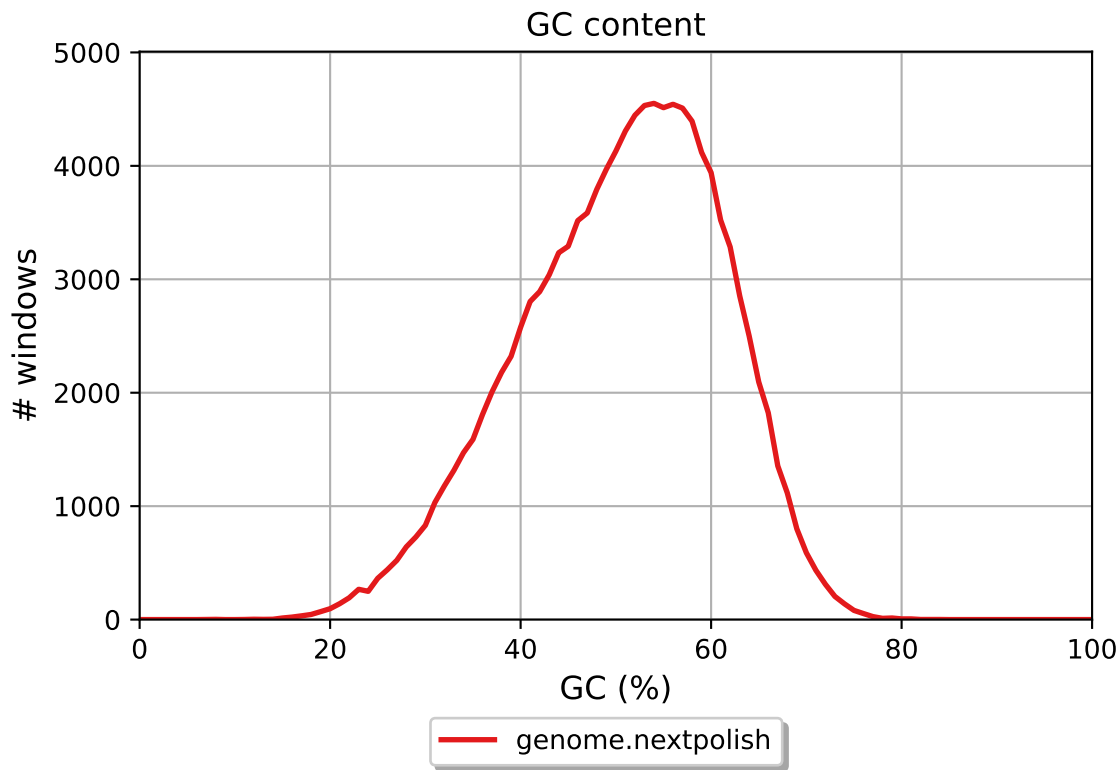
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 134 |
| # contigs (>= 1000 bp) | 134 |
| # contigs (>= 5000 bp) | 130 |
| # contigs (>= 10000 bp) | 122 |
| # contigs (>= 25000 bp) | 81 |
| # contigs (>= 50000 bp) | 50 |
| Total length (>= 0 bp) | 12147420 |
| Total length (>= 1000 bp) | 12147420 |
| Total length (>= 5000 bp) | 12135481 |
| Total length (>= 10000 bp) | 12070746 |
| Total length (>= 25000 bp) | 11342230 |
| Total length (>= 50000 bp) | 10217939 |
| # contigs | 134 |
| Largest contig | 2104478 |
| Total length | 12147420 |
| GC (%) | 50.47 |
| N50 | 578033 |
| N90 | 32884 |
| auN | 918009.2 |
| L50 | 4 |
| L90 | 67 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 38 + 5 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





genome.nextpolish GC content

