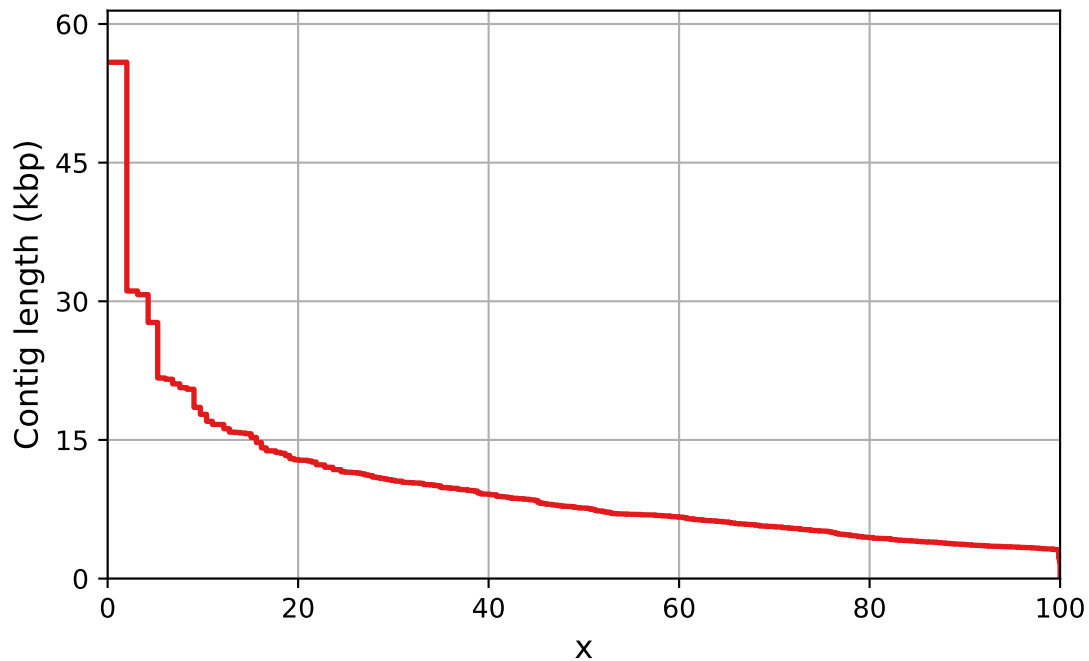


Report

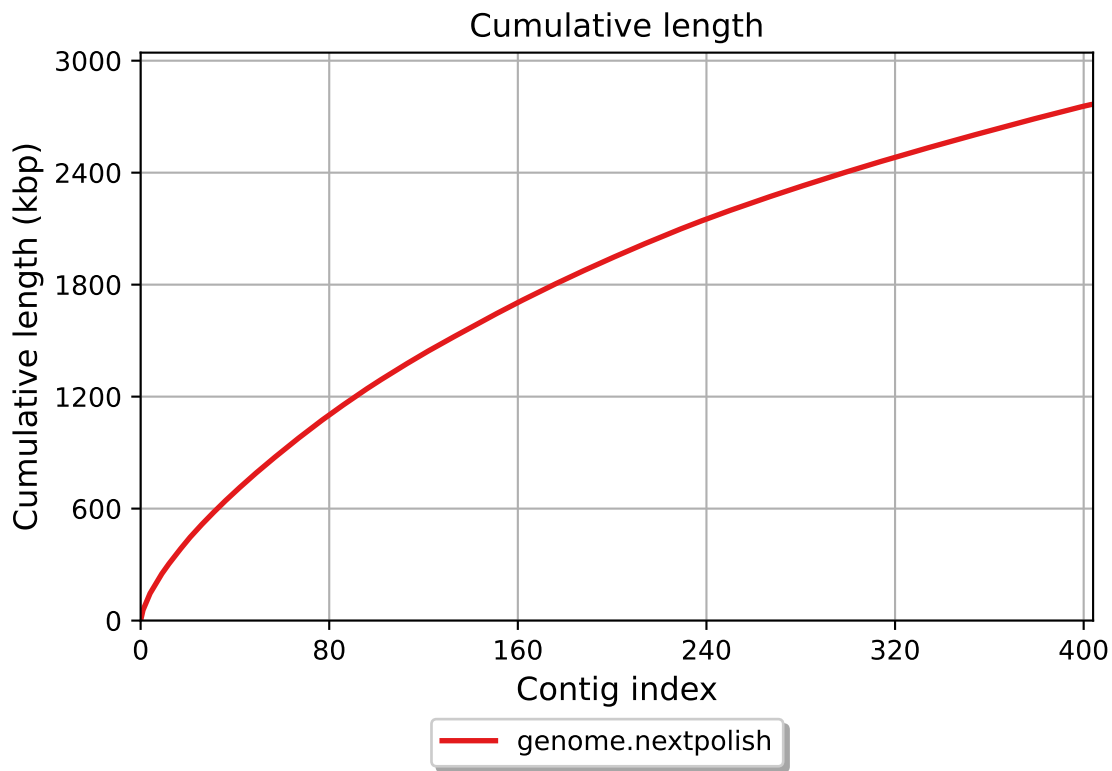
| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 404 |
| # contigs (>= 1000 bp) | 404 |
| # contigs (>= 5000 bp) | 230 |
| # contigs (>= 10000 bp) | 66 |
| # contigs (>= 25000 bp) | 4 |
| # contigs (>= 50000 bp) | 1 |
| Total length (>= 0 bp) | 2766496 |
| Total length (>= 1000 bp) | 2766496 |
| Total length (>= 5000 bp) | 2103110 |
| Total length (>= 10000 bp) | 967943 |
| Total length (>= 25000 bp) | 145399 |
| Total length (>= 50000 bp) | 55858 |
| # contigs | 404 |
| Largest contig | 55858 |
| Total length | 2766496 |
| GC (%) | 39.09 |
| N50 | 7635 |
| N90 | 3686 |
| auN | 10143.5 |
| L50 | 114 |
| L90 | 323 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 4 + 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).

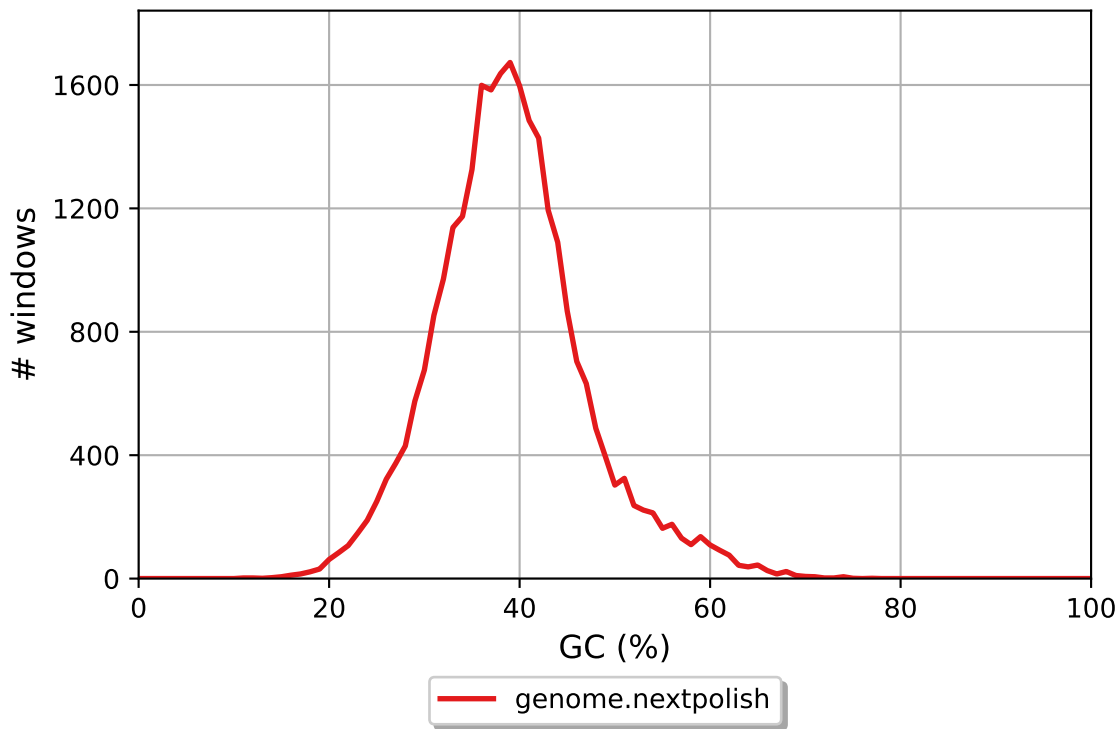
Nx



— genome.nextpolish



GC content



genome.nextpolish GC content

