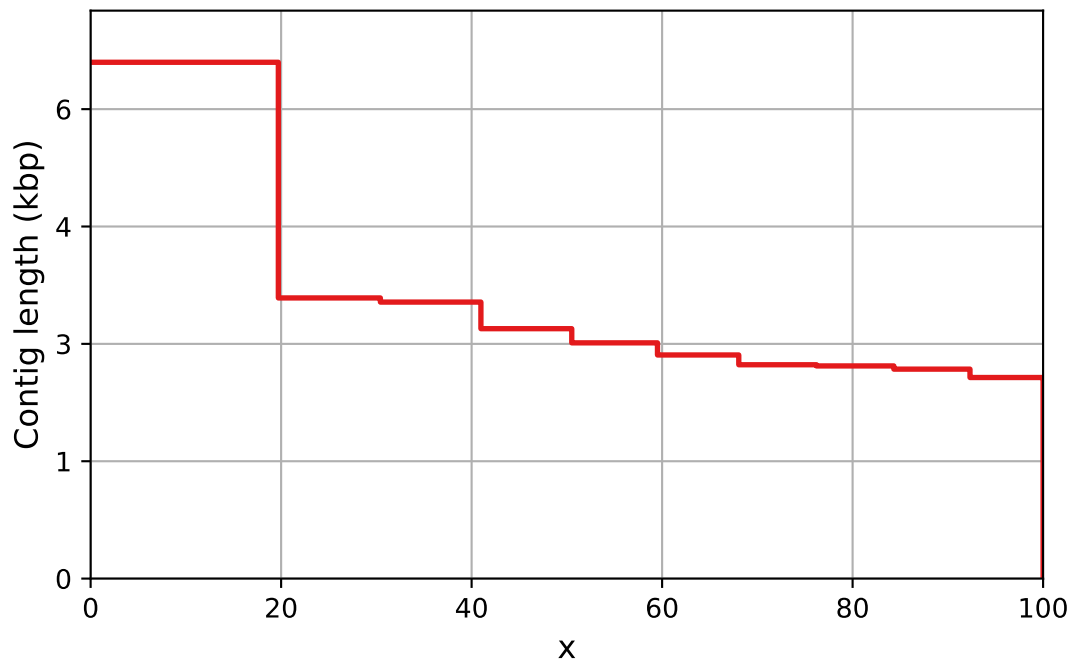


Report

| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 10 |
| # contigs (>= 1000 bp) | 10 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 33483 |
| Total length (>= 1000 bp) | 33483 |
| Total length (>= 5000 bp) | 6599 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 10 |
| Largest contig | 6599 |
| Total length | 33483 |
| GC (%) | 42.72 |
| N50 | 3194 |
| N90 | 2677 |
| auN | 3732.6 |
| L50 | 4 |
| L90 | 9 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 5 + 1 part |

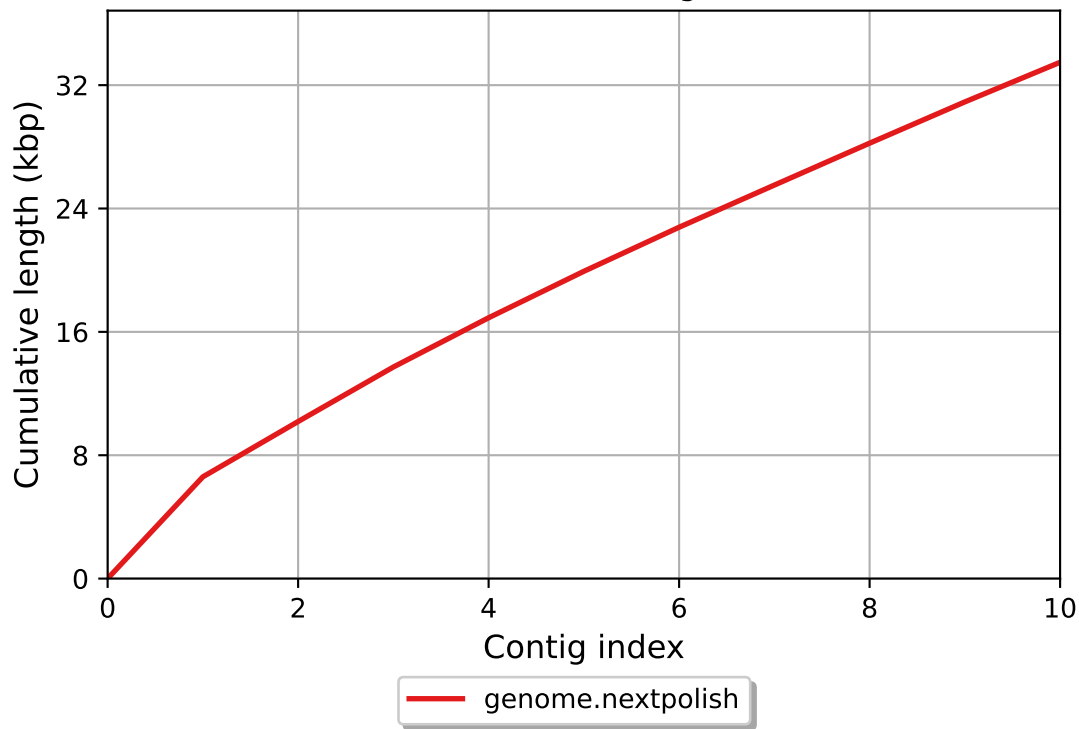
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

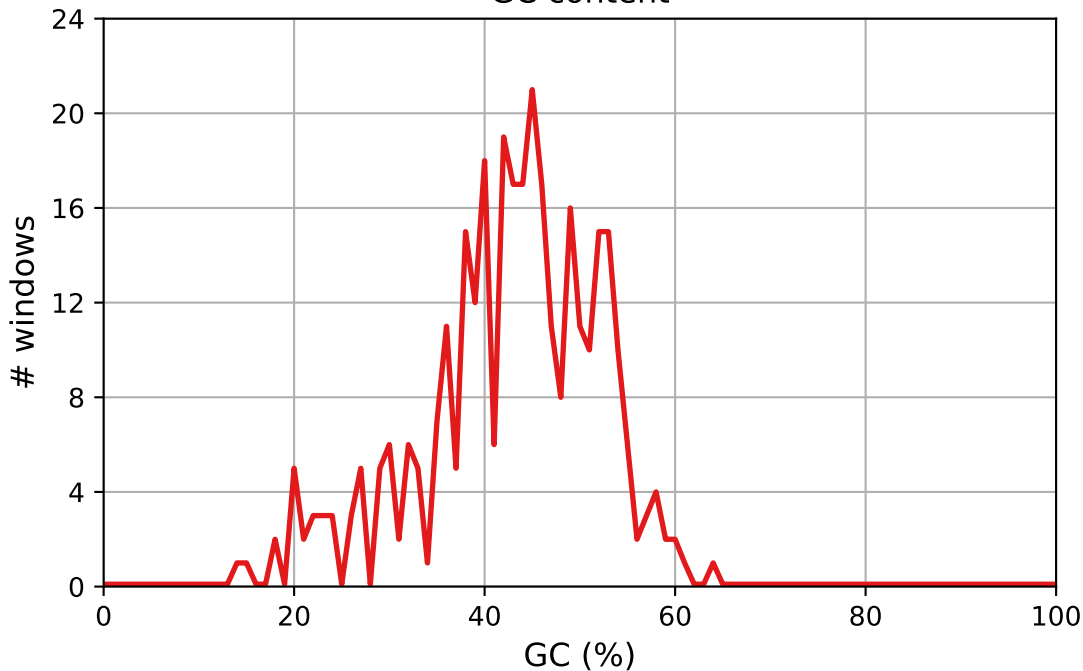


— genome.nextpolish

Cumulative length



GC content



— genome.nextpolish

genome.nextpolish GC content

