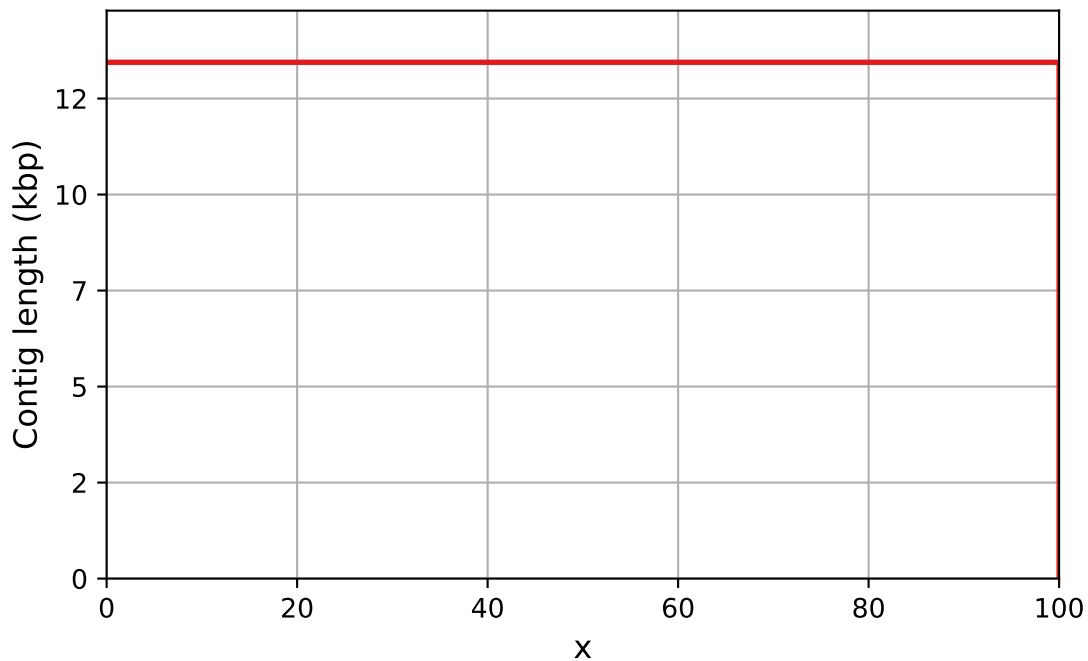


Report

| | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp) | 1 |
| # contigs (>= 1000 bp) | 1 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 1 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 13444 |
| Total length (>= 1000 bp) | 13444 |
| Total length (>= 5000 bp) | 13444 |
| Total length (>= 10000 bp) | 13444 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1 |
| Largest contig | 13444 |
| Total length | 13444 |
| GC (%) | 55.11 |
| N50 | 13444 |
| N90 | 13444 |
| auN | 13444.0 |
| L50 | 1 |
| L90 | 1 |
| # N's per 100 kbp | 0.00 |
| Complete BUSCO (%) | 0.00 |
| Partial BUSCO (%) | 0.00 |
| # predicted rRNA genes | 0 + 0 part |

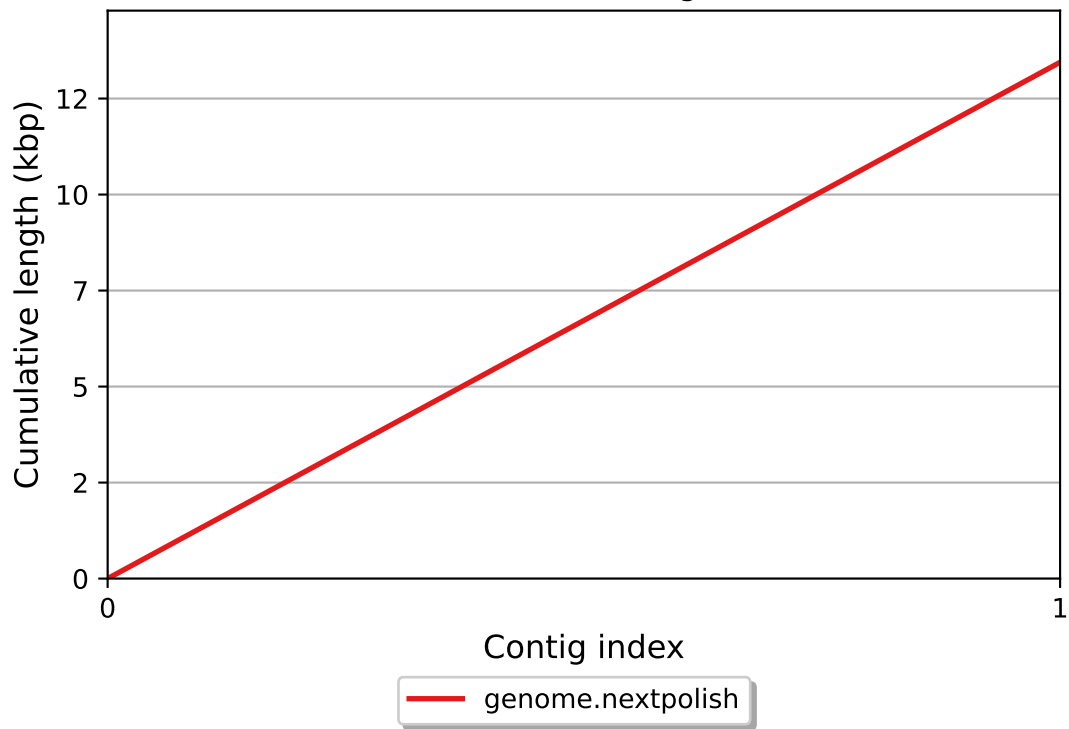
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

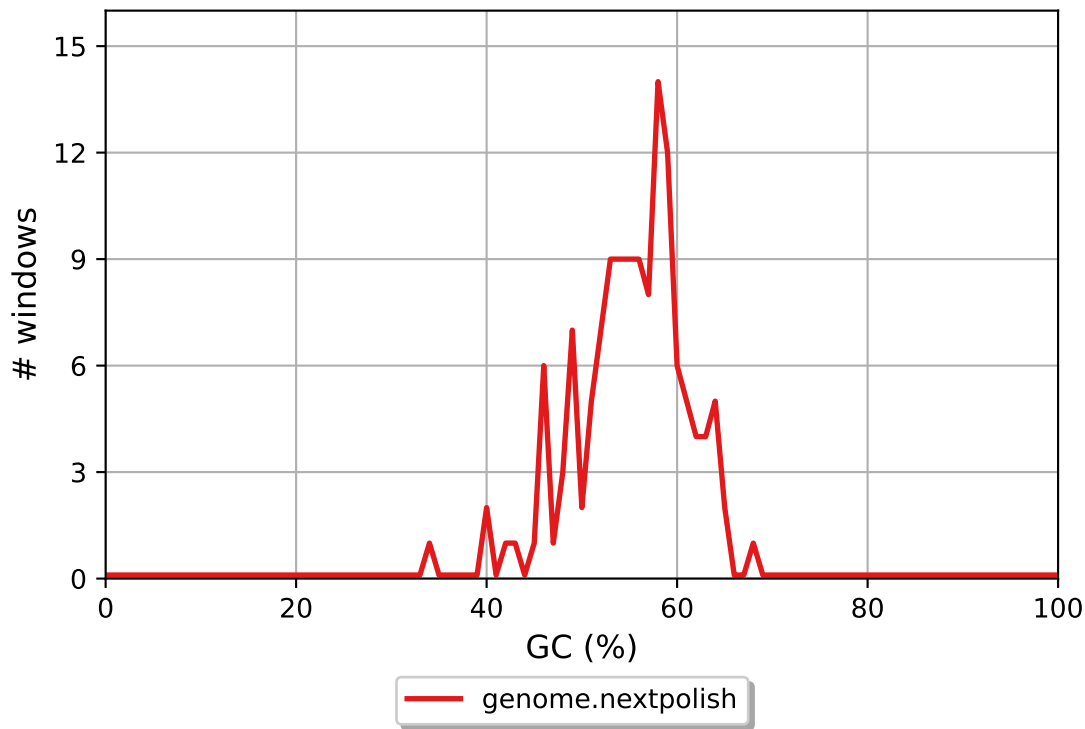


— genome.nextpolish

Cumulative length



GC content



genome.nextpolish GC content

