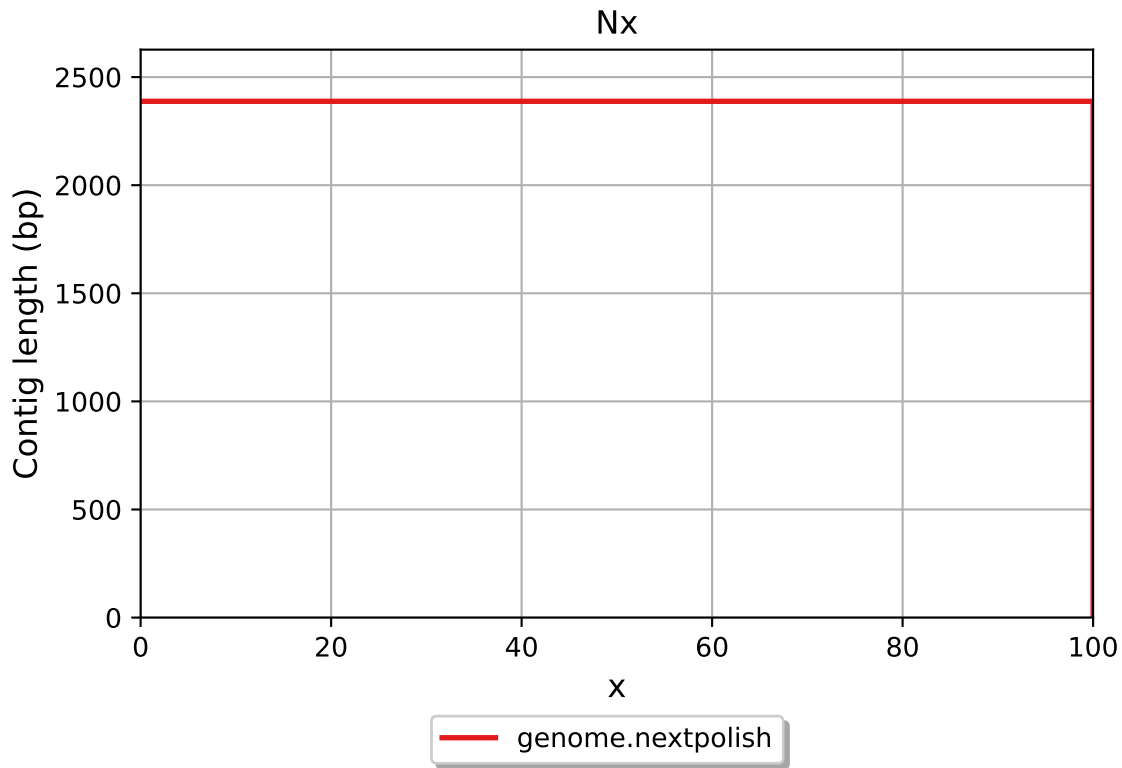
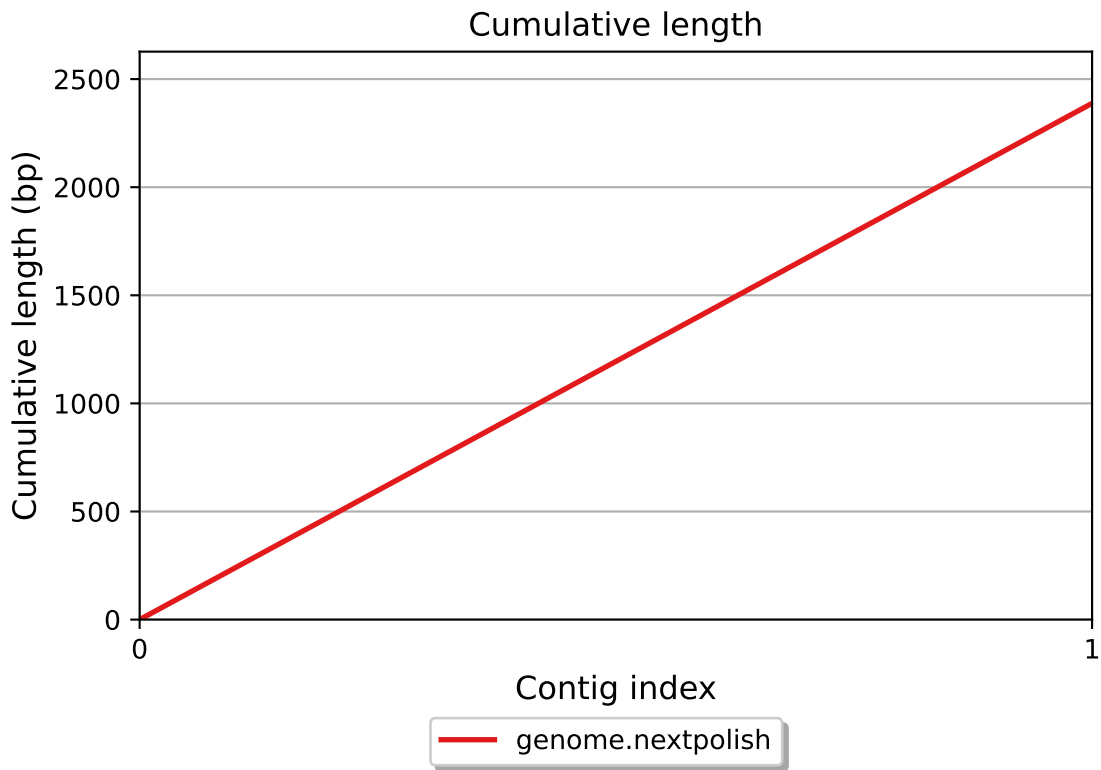


Report

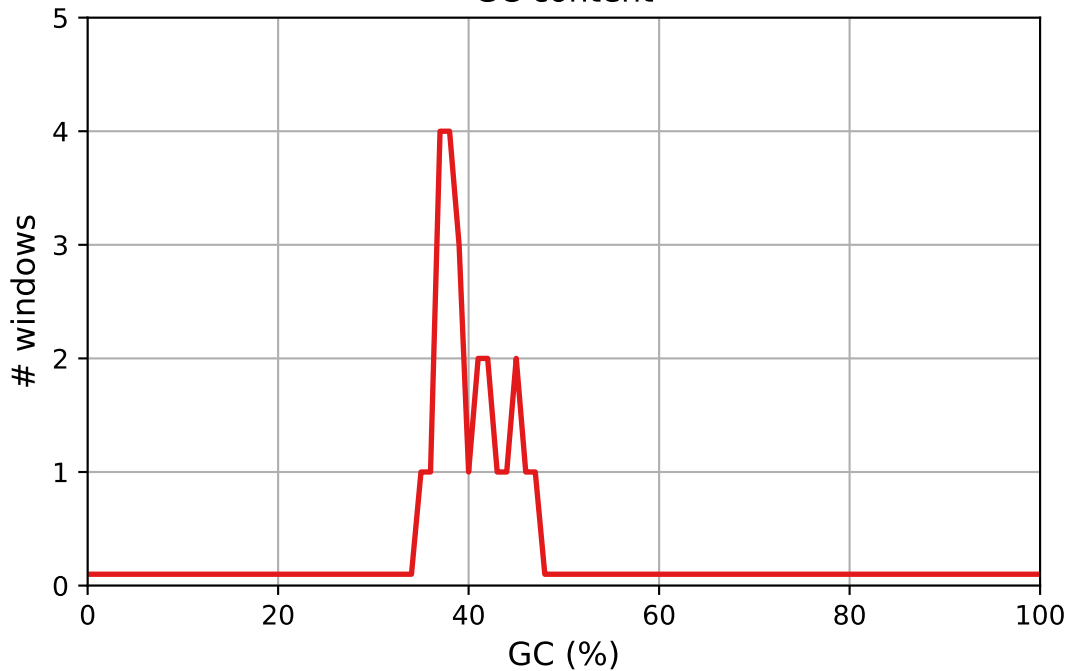
| | genome.nextpolish |
|---------------------------------|-------------------|
| # contigs (≥ 0 bp) | 1 |
| # contigs (≥ 1000 bp) | 1 |
| # contigs (≥ 5000 bp) | 0 |
| # contigs (≥ 10000 bp) | 0 |
| # contigs (≥ 25000 bp) | 0 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 0 bp) | 2388 |
| Total length (≥ 1000 bp) | 2388 |
| Total length (≥ 5000 bp) | 0 |
| Total length (≥ 10000 bp) | 0 |
| Total length (≥ 25000 bp) | 0 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 1 |
| Largest contig | 2388 |
| Total length | 2388 |
| GC (%) | 40.16 |
| N50 | 2388 |
| N90 | 2388 |
| auN | 2388.0 |
| 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).



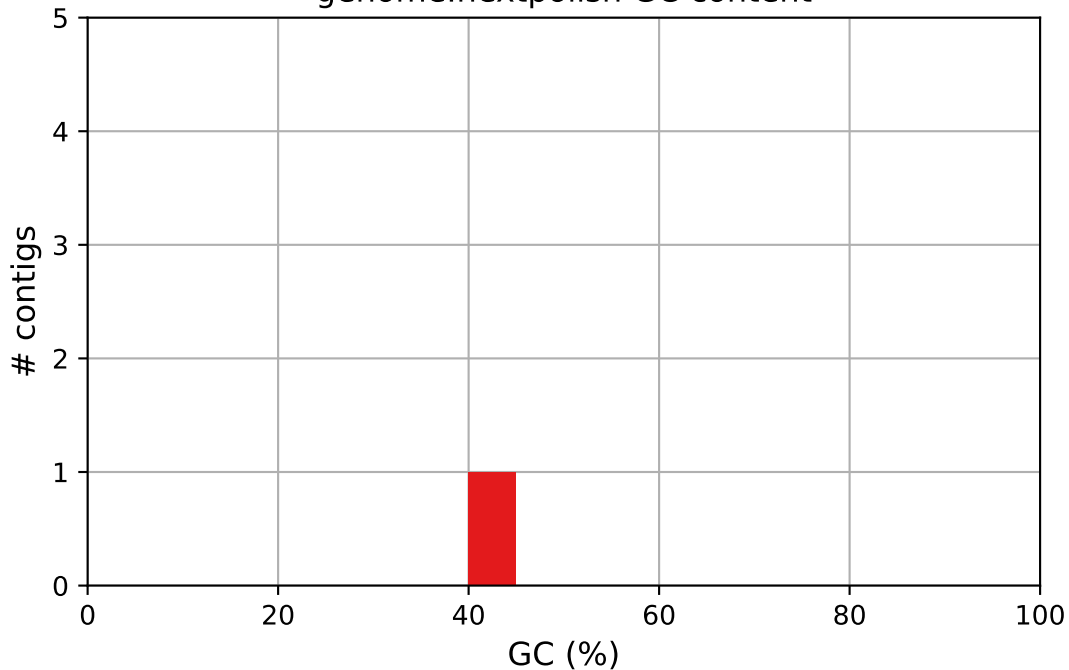


GC content



— genome.nextpolish

genome.nextpolish GC content



genome.nextpolish