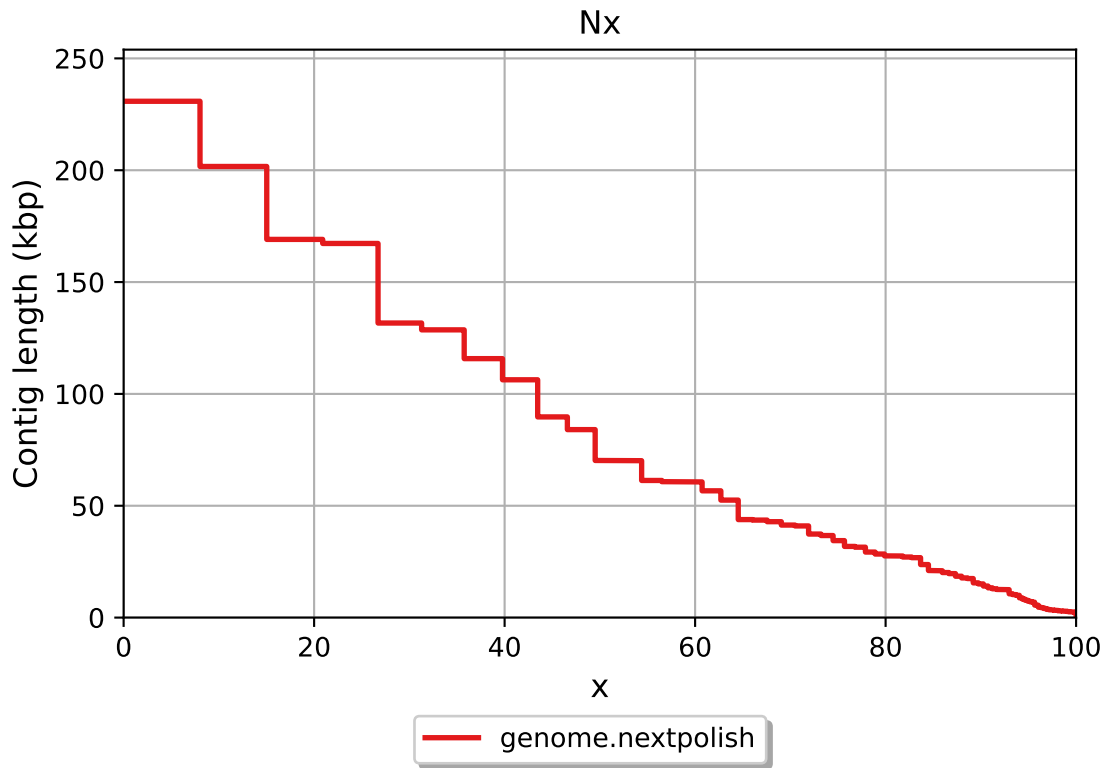
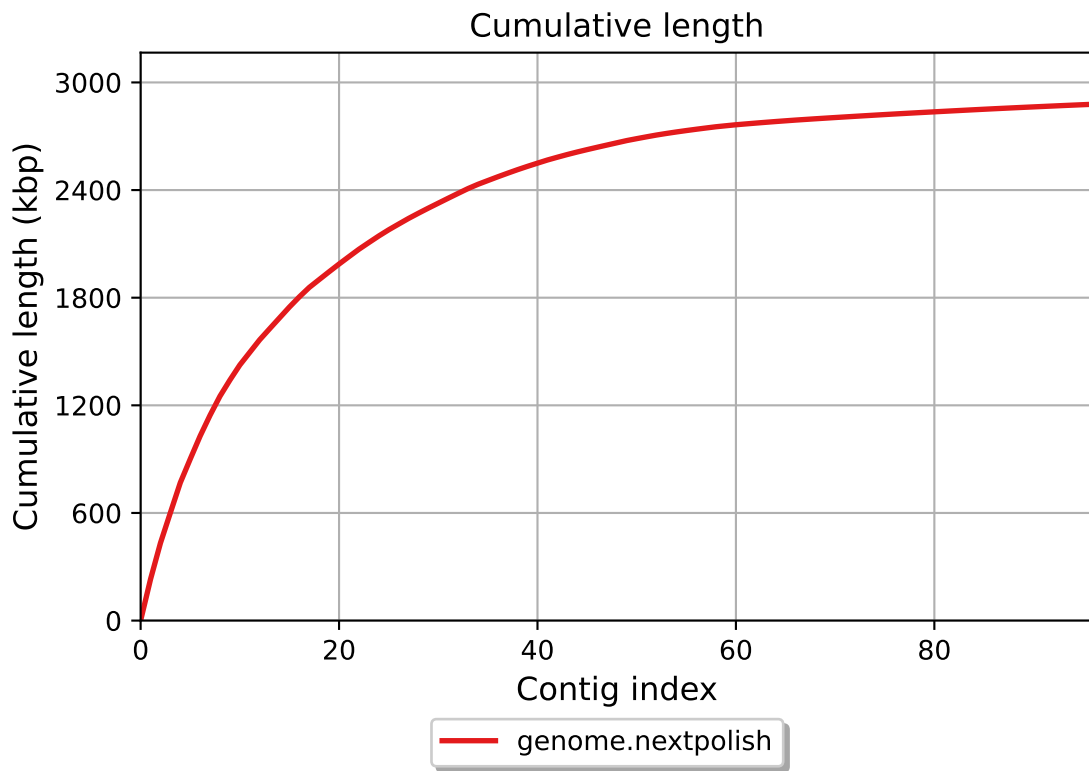


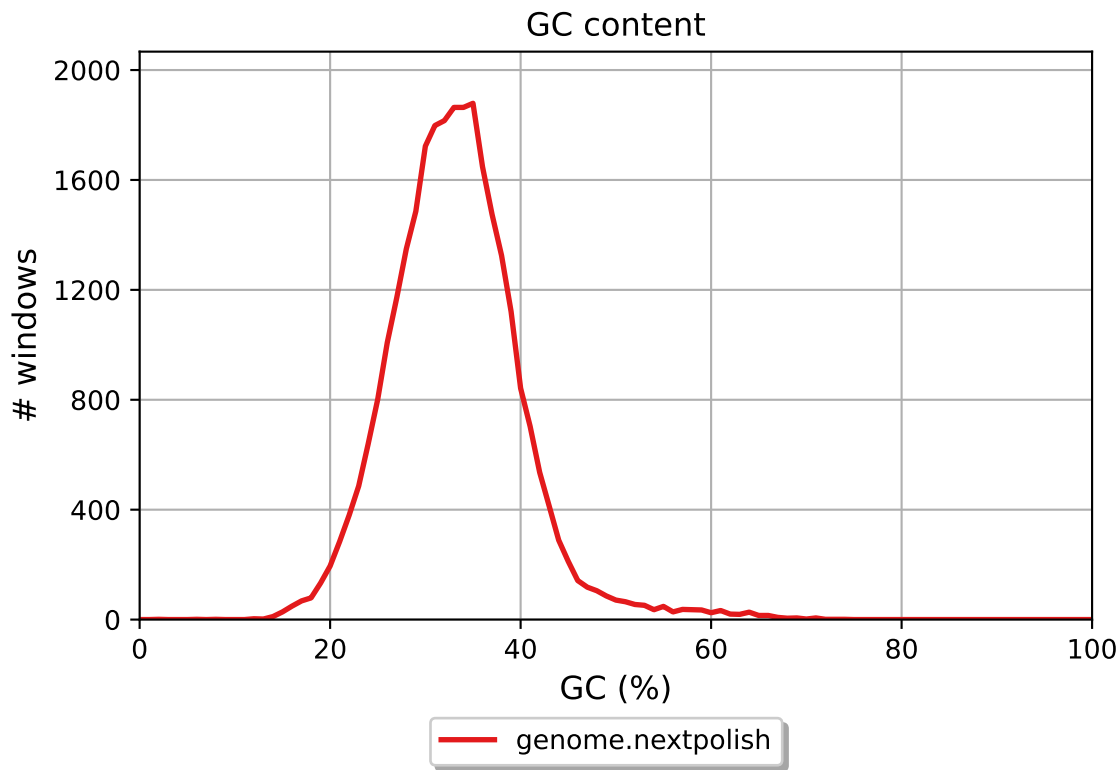
# Report

|                            | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp)        | 96                |
| # contigs (>= 1000 bp)     | 96                |
| # contigs (>= 5000 bp)     | 60                |
| # contigs (>= 10000 bp)    | 51                |
| # contigs (>= 25000 bp)    | 33                |
| # contigs (>= 50000 bp)    | 17                |
| Total length (>= 0 bp)     | 2878294           |
| Total length (>= 1000 bp)  | 2878294           |
| Total length (>= 5000 bp)  | 2764103           |
| Total length (>= 10000 bp) | 2696879           |
| Total length (>= 25000 bp) | 2408340           |
| Total length (>= 50000 bp) | 1857305           |
| # contigs                  | 96                |
| Largest contig             | 230829            |
| Total length               | 2878294           |
| GC (%)                     | 33.25             |
| N50                        | 70243             |
| N90                        | 15052             |
| auN                        | 96090.7           |
| L50                        | 11                |
| L90                        | 43                |
| # N's per 100 kbp          | 0.00              |
| Complete BUSCO (%)         | 0.00              |
| Partial BUSCO (%)          | 0.00              |
| # predicted rRNA genes     | 5 + 7 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).







genome.nextpolish GC content

