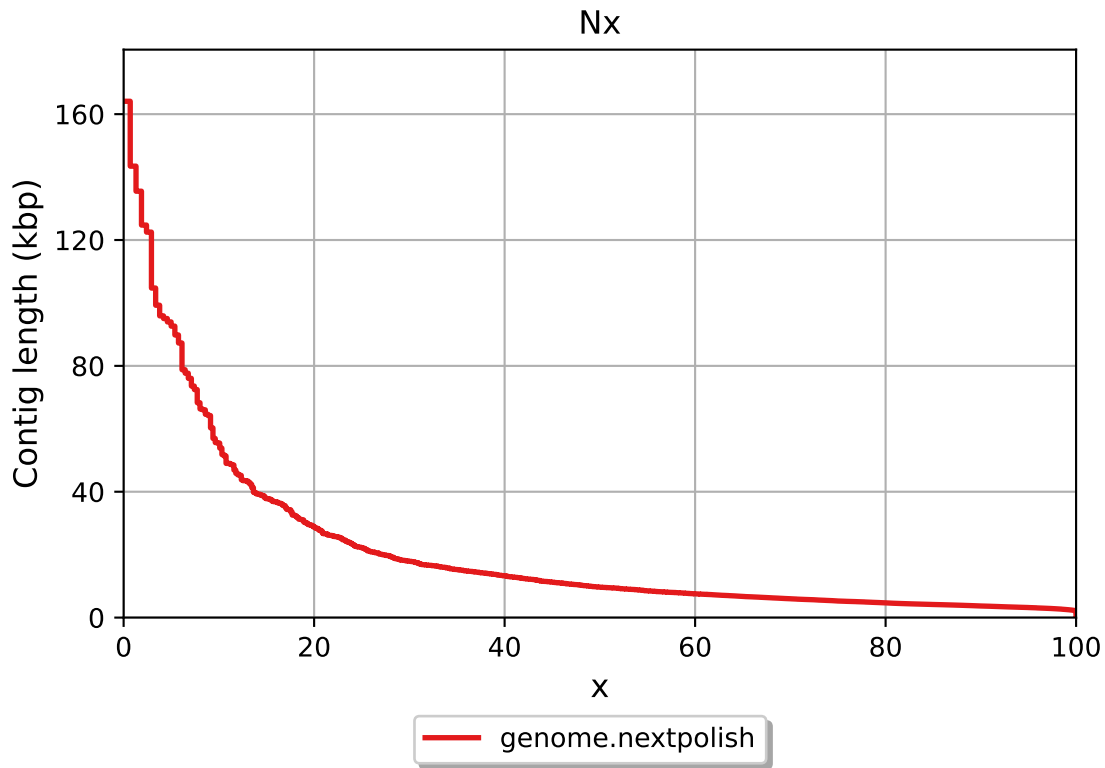


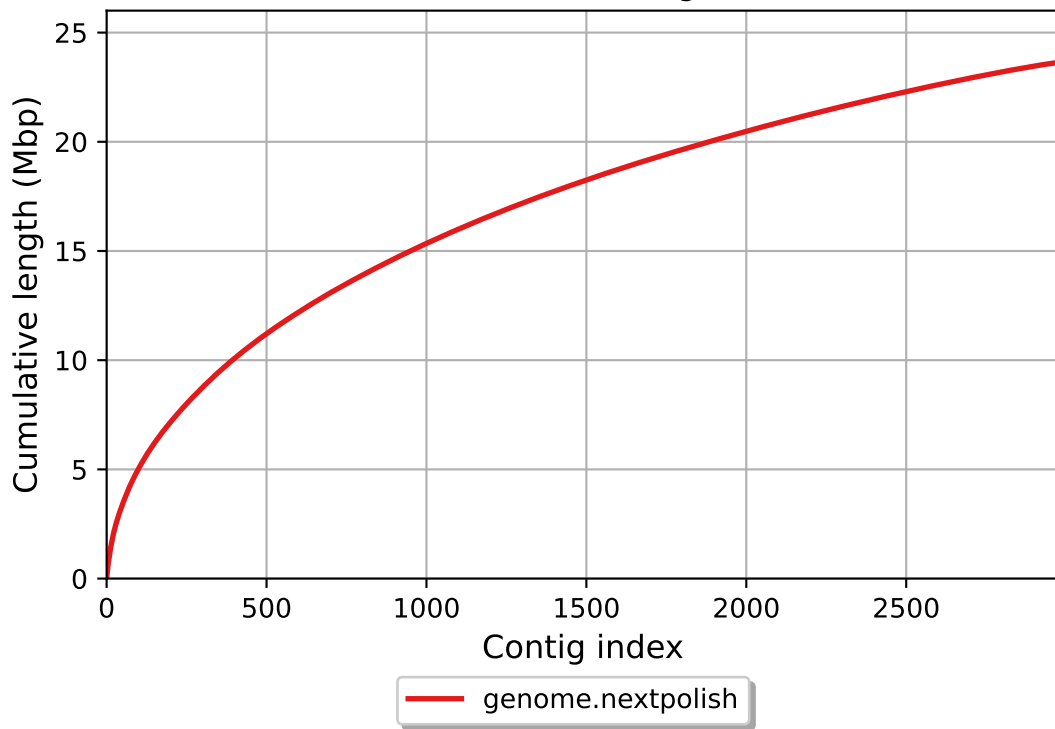
# Report

|                            | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp)        | 2978              |
| # contigs (>= 1000 bp)     | 2976              |
| # contigs (>= 5000 bp)     | 1520              |
| # contigs (>= 10000 bp)    | 535               |
| # contigs (>= 25000 bp)    | 115               |
| # contigs (>= 50000 bp)    | 30                |
| Total length (>= 0 bp)     | 23641355          |
| Total length (>= 1000 bp)  | 23640018          |
| Total length (>= 5000 bp)  | 18351327          |
| Total length (>= 10000 bp) | 11572312          |
| Total length (>= 25000 bp) | 5426523           |
| Total length (>= 50000 bp) | 2542265           |
| # contigs                  | 2978              |
| Largest contig             | 164093            |
| Total length               | 23641355          |
| GC (%)                     | 38.46             |
| N50                        | 9694              |
| N90                        | 3688              |
| auN                        | 21409.1           |
| L50                        | 561               |
| L90                        | 2206              |
| # N's per 100 kbp          | 0.00              |
| Complete BUSCO (%)         | 0.00              |
| Partial BUSCO (%)          | 0.00              |
| # predicted rRNA genes     | 10 + 3 part       |

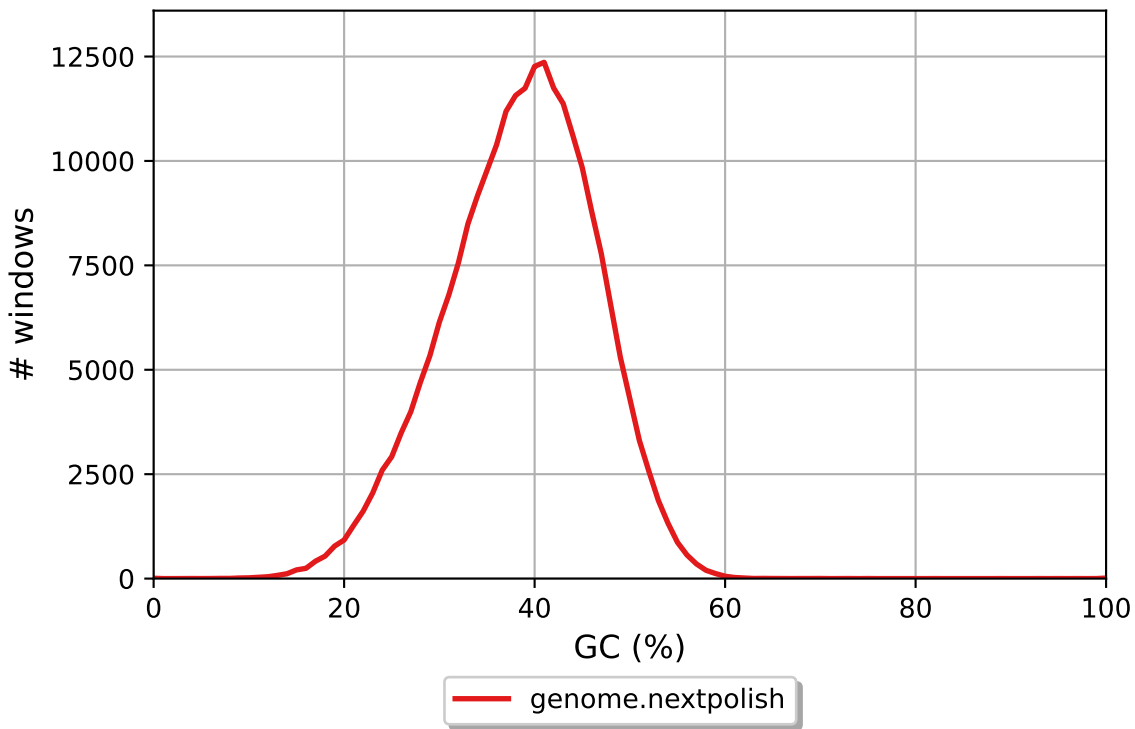
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



Cumulative length



## GC content



genome.nextpolish GC content

