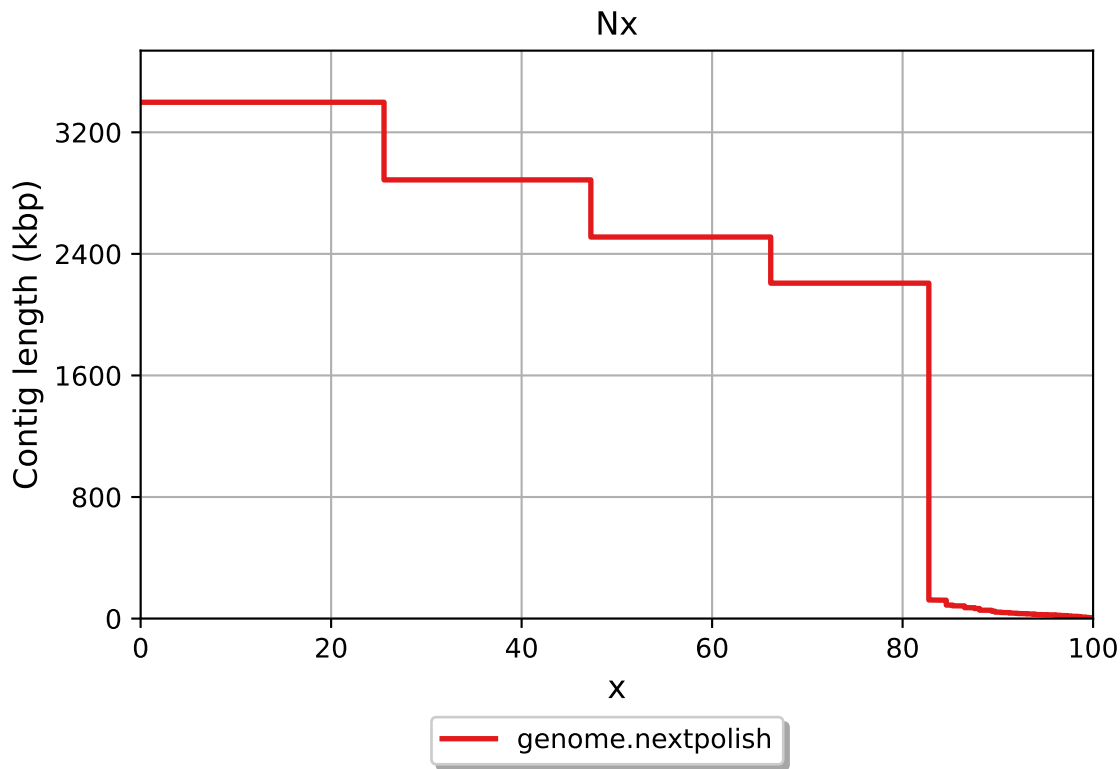


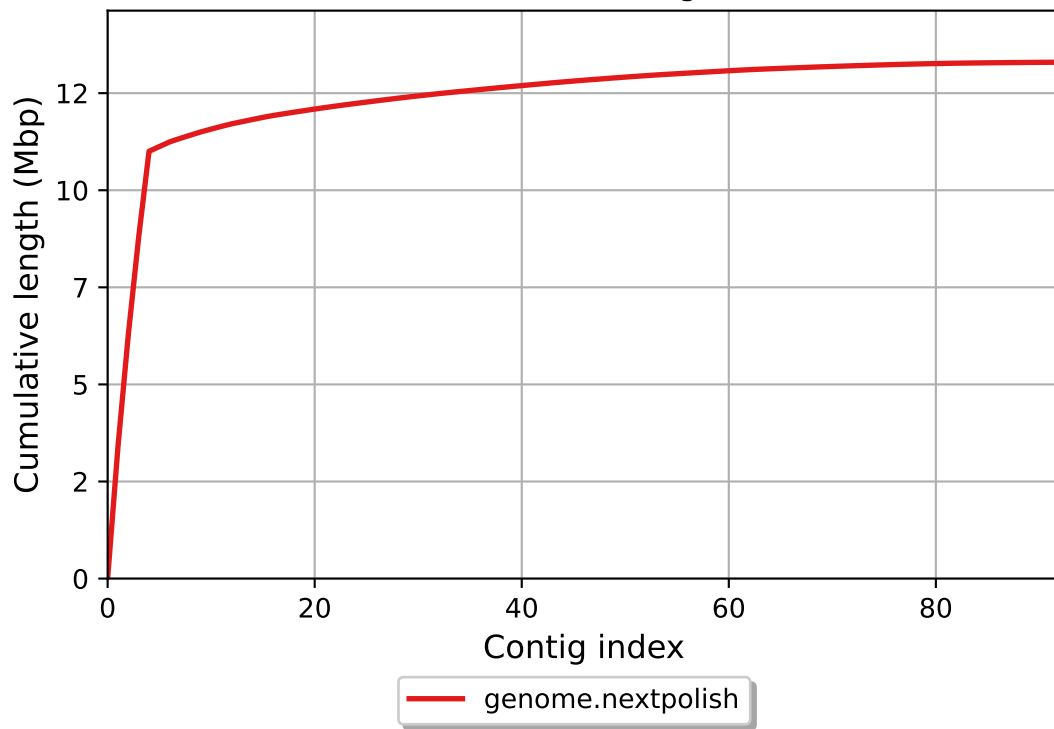
# Report

|                            | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp)        | 92                |
| # contigs (>= 1000 bp)     | 91                |
| # contigs (>= 5000 bp)     | 80                |
| # contigs (>= 10000 bp)    | 67                |
| # contigs (>= 25000 bp)    | 38                |
| # contigs (>= 50000 bp)    | 15                |
| Total length (>= 0 bp)     | 13295384          |
| Total length (>= 1000 bp)  | 13294721          |
| Total length (>= 5000 bp)  | 13262038          |
| Total length (>= 10000 bp) | 13158599          |
| Total length (>= 25000 bp) | 12644979          |
| Total length (>= 50000 bp) | 11876453          |
| # contigs                  | 92                |
| Largest contig             | 3397664           |
| Total length               | 13295384          |
| GC (%)                     | 53.35             |
| N50                        | 2510858           |
| N90                        | 42657             |
| auN                        | 2344195.4         |
| L50                        | 3                 |
| L90                        | 17                |
| # N's per 100 kbp          | 0.00              |
| Complete BUSCO (%)         | 0.00              |
| Partial BUSCO (%)          | 0.00              |
| # predicted rRNA genes     | 30 + 4 part       |

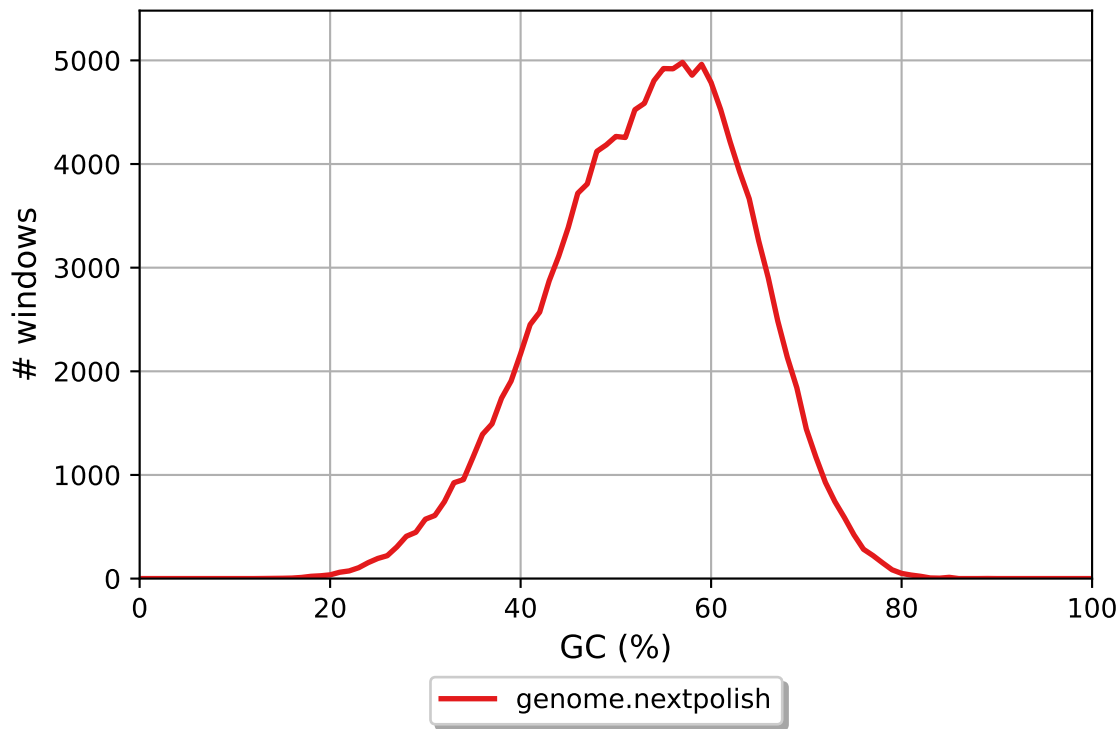
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



Cumulative length



## GC content



genome.nextpolish GC content

