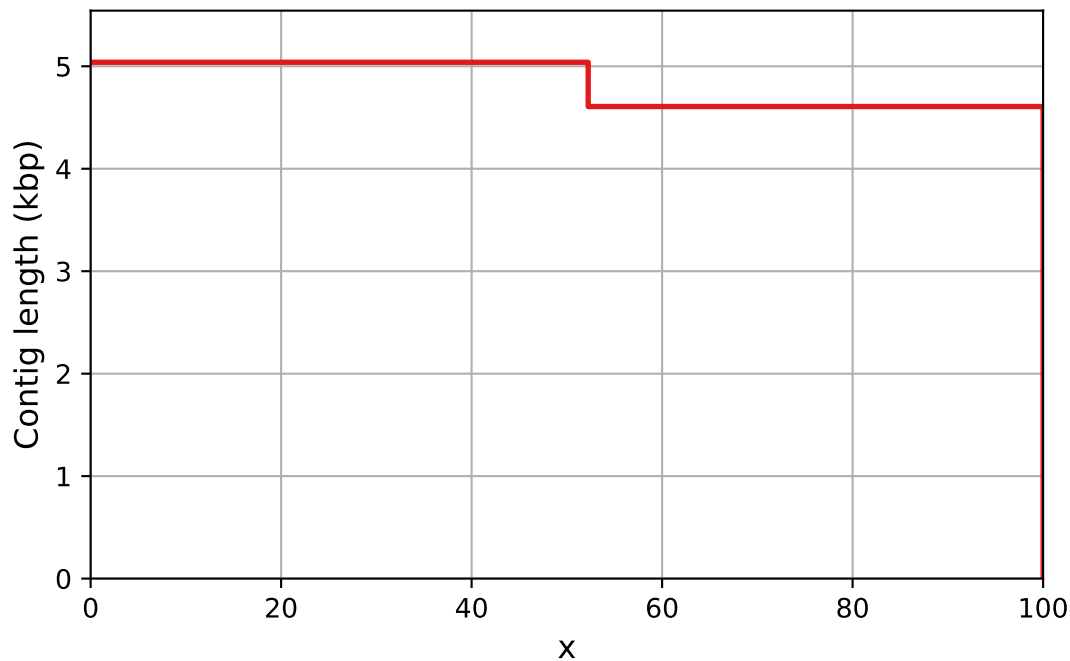


# Report

|                            | genome.nextpolish |
|----------------------------|-------------------|
| # contigs (>= 0 bp)        | 2                 |
| # contigs (>= 1000 bp)     | 2                 |
| # contigs (>= 5000 bp)     | 1                 |
| # contigs (>= 10000 bp)    | 0                 |
| # contigs (>= 25000 bp)    | 0                 |
| # contigs (>= 50000 bp)    | 0                 |
| Total length (>= 0 bp)     | 9646              |
| Total length (>= 1000 bp)  | 9646              |
| Total length (>= 5000 bp)  | 5039              |
| Total length (>= 10000 bp) | 0                 |
| Total length (>= 25000 bp) | 0                 |
| Total length (>= 50000 bp) | 0                 |
| # contigs                  | 2                 |
| Largest contig             | 5039              |
| Total length               | 9646              |
| GC (%)                     | 56.44             |
| N50                        | 5039              |
| N90                        | 4607              |
| auN                        | 4832.7            |
| L50                        | 1                 |
| L90                        | 2                 |
| # N's per 100 kbp          | 0.00              |
| Complete BUSCO (%)         | 0.00              |
| Partial BUSCO (%)          | 0.00              |
| # predicted rRNA genes     | 0 + 0 part        |

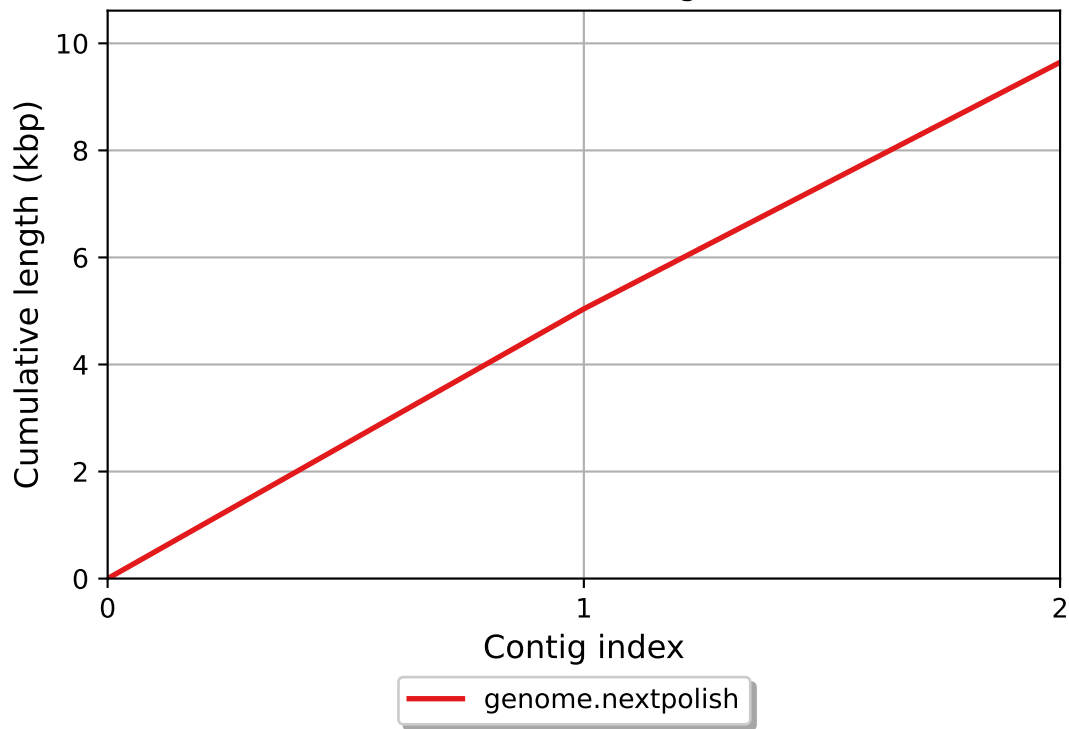
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

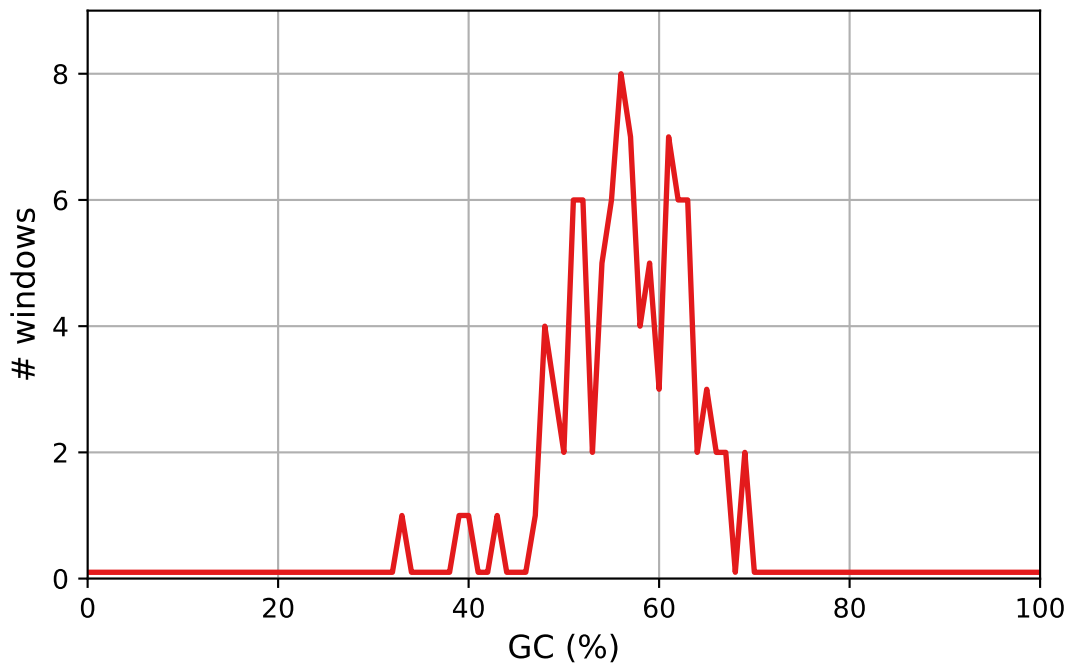


— genome.nextpolish

Cumulative length



## GC content



— genome.nextpolish

genome.nextpolish GC content

