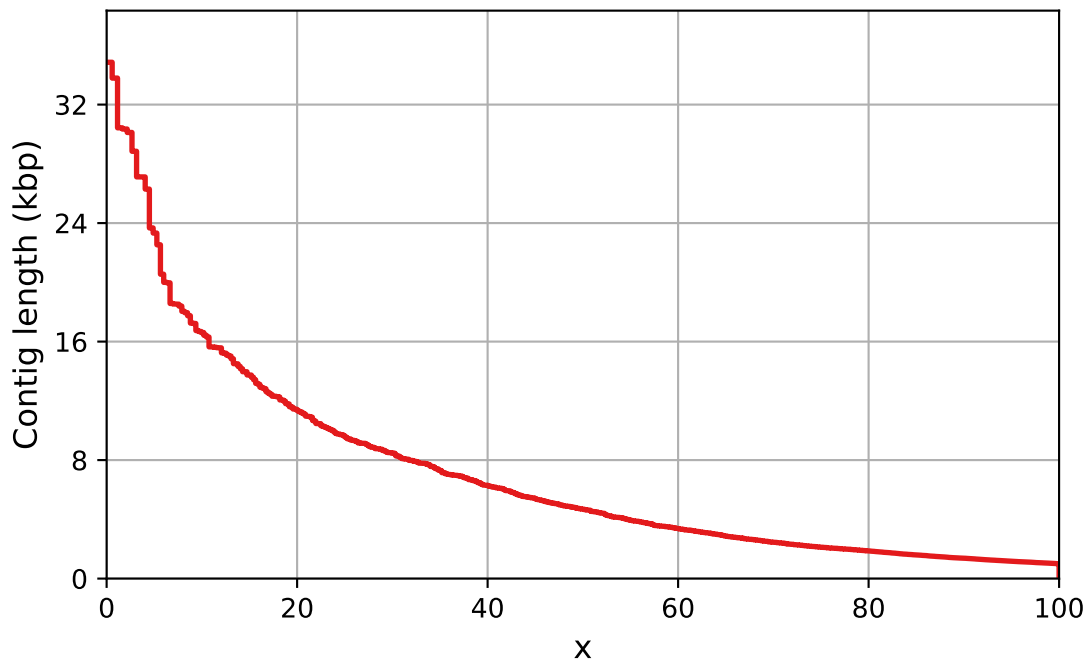


# Report

|                            | MEGAHIT-MaxBin2-3108596.005.fa |
|----------------------------|--------------------------------|
| # contigs (>= 0 bp)        | 1857                           |
| # contigs (>= 1000 bp)     | 1857                           |
| # contigs (>= 5000 bp)     | 295                            |
| # contigs (>= 10000 bp)    | 91                             |
| # contigs (>= 25000 bp)    | 9                              |
| # contigs (>= 50000 bp)    | 0                              |
| Total length (>= 0 bp)     | 5990934                        |
| Total length (>= 1000 bp)  | 5990934                        |
| Total length (>= 5000 bp)  | 2845893                        |
| Total length (>= 10000 bp) | 1418682                        |
| Total length (>= 25000 bp) | 268924                         |
| Total length (>= 50000 bp) | 0                              |
| # contigs                  | 1857                           |
| Largest contig             | 34857                          |
| Total length               | 5990934                        |
| GC (%)                     | 38.61                          |
| N50                        | 4697                           |
| N75                        | 2119                           |
| L50                        | 326                            |
| L75                        | 818                            |
| # N's per 100 kbp          | 0.00                           |
| # predicted rRNA genes     | 3 + 1 part                     |

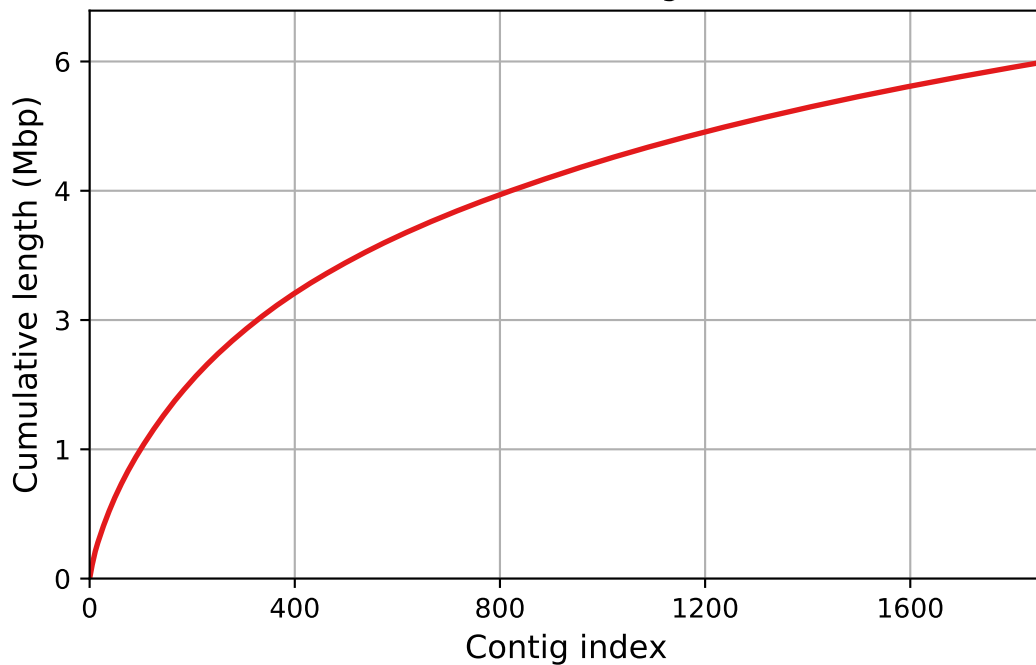
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

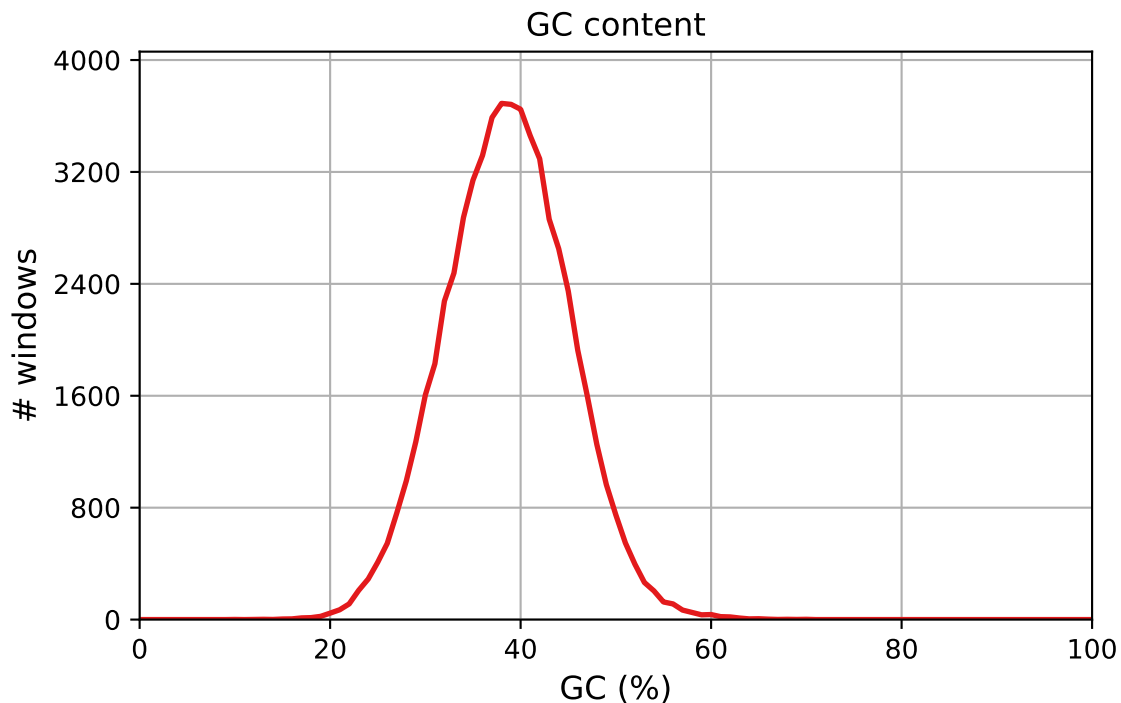


MEGAHIT-MaxBin2-3108596.005.fa

Cumulative length

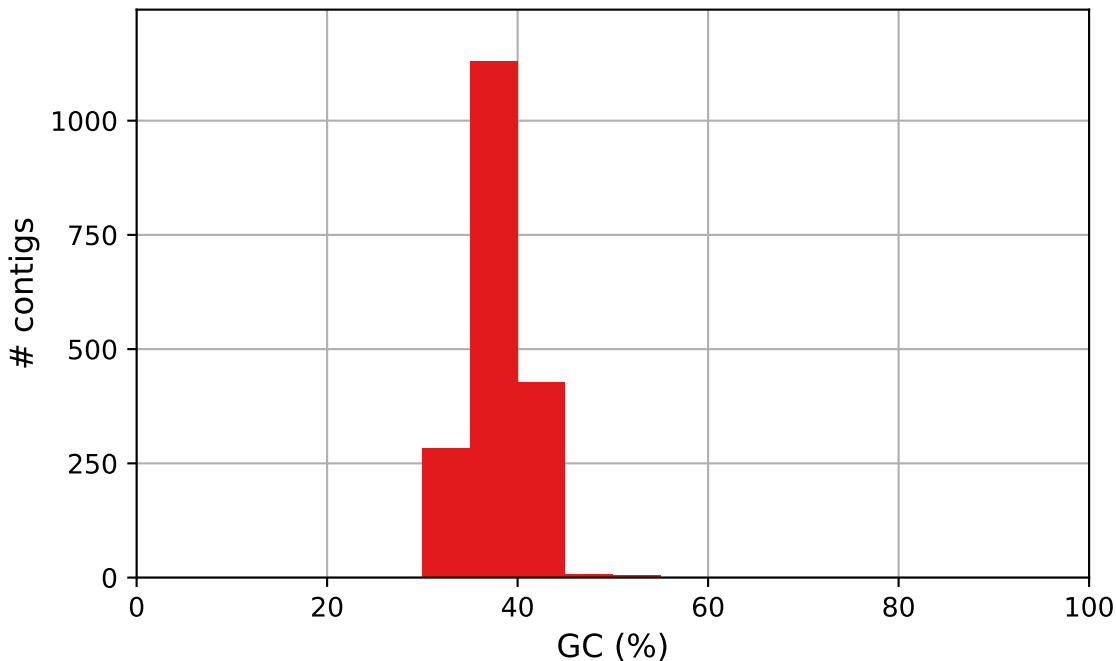


MEGAHIT-MaxBin2-3108596.005.fa



MEGAHIT-MaxBin2-3108596.005.fa

MEGAHIT-MaxBin2-3108596.005.fa GC content



MEGAHit-MaxBin2-3108596.005.fa