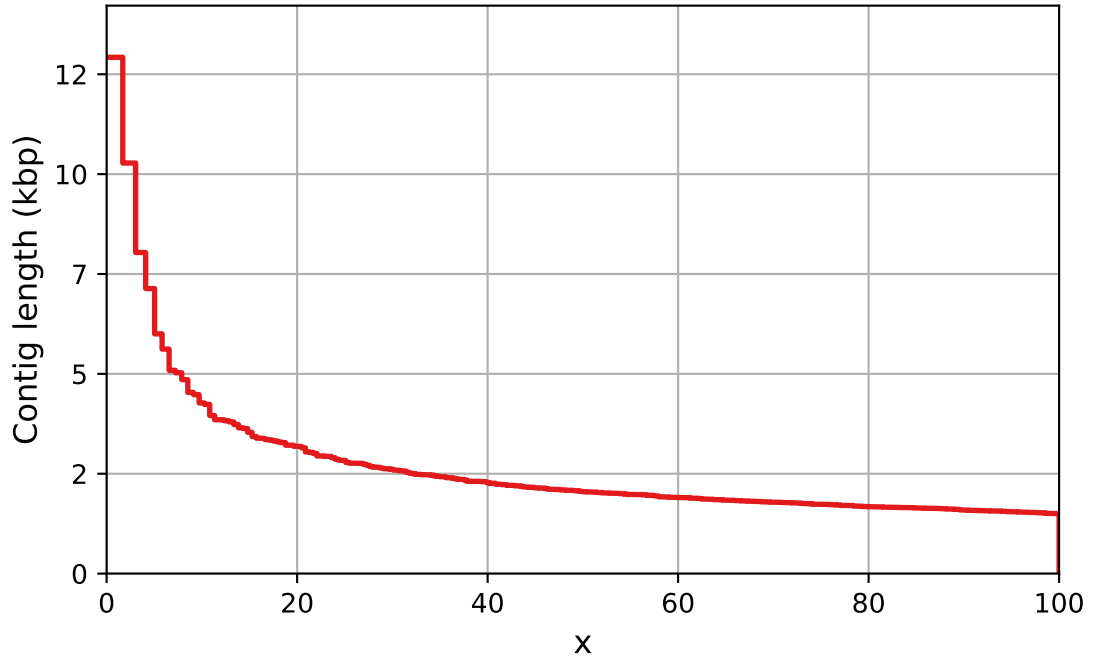


Report

| | MEGAHIT-MetaBAT2-3106237.6.fa |
|----------------------------|-------------------------------|
| # contigs (>= 0 bp) | 346 |
| # contigs (>= 1000 bp) | 346 |
| # contigs (>= 5000 bp) | 8 |
| # contigs (>= 10000 bp) | 2 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 762082 |
| Total length (>= 1000 bp) | 762082 |
| Total length (>= 5000 bp) | 60113 |
| Total length (>= 10000 bp) | 23203 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 346 |
| Largest contig | 12925 |
| Total length | 762082 |
| GC (%) | 42.71 |
| N50 | 2053 |
| N75 | 1736 |
| L50 | 127 |
| L75 | 229 |
| # N's per 100 kbp | 0.00 |
| # predicted rRNA genes | 0 + 0 part |

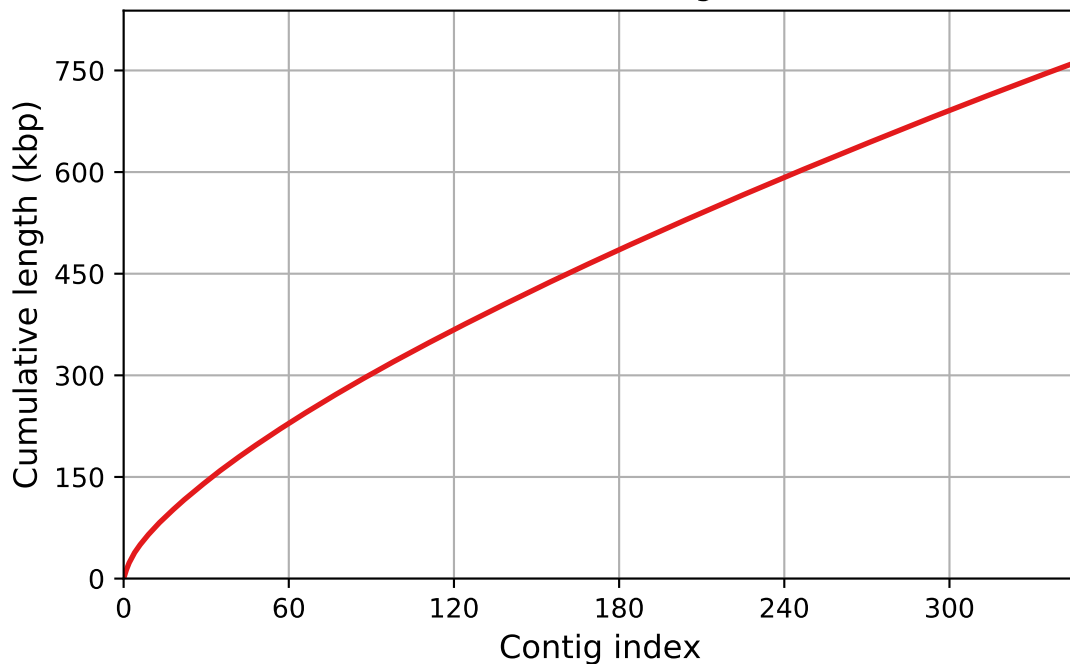
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

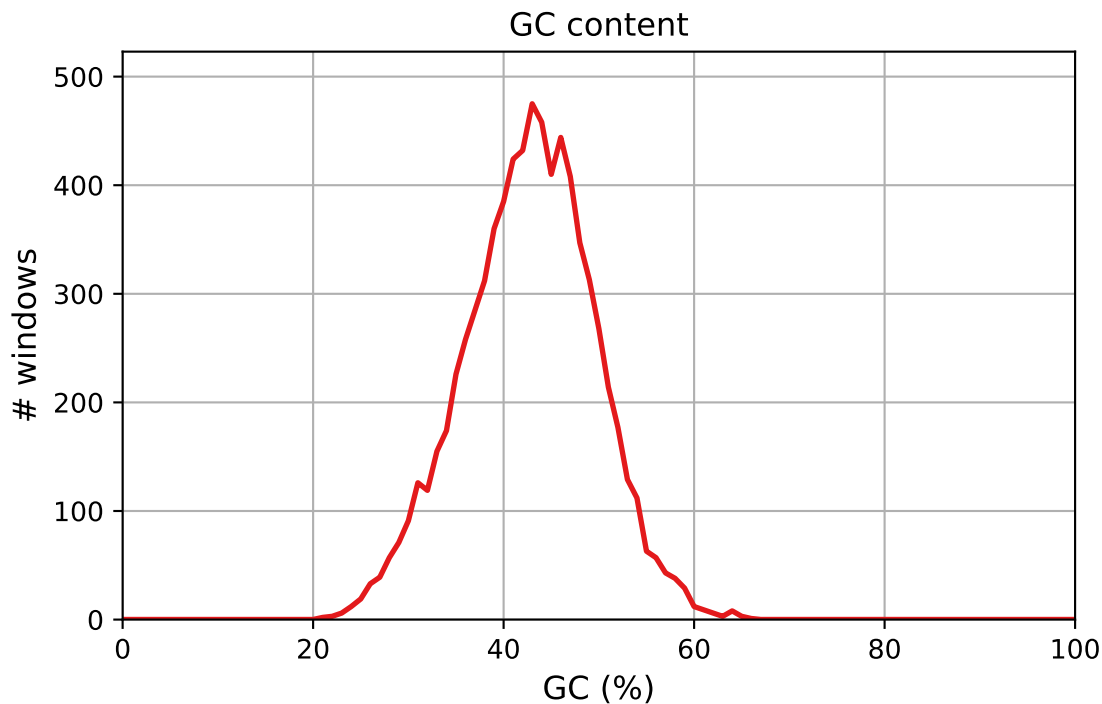


MEGAHIT-MetaBAT2-3106237.6.fa

Cumulative length

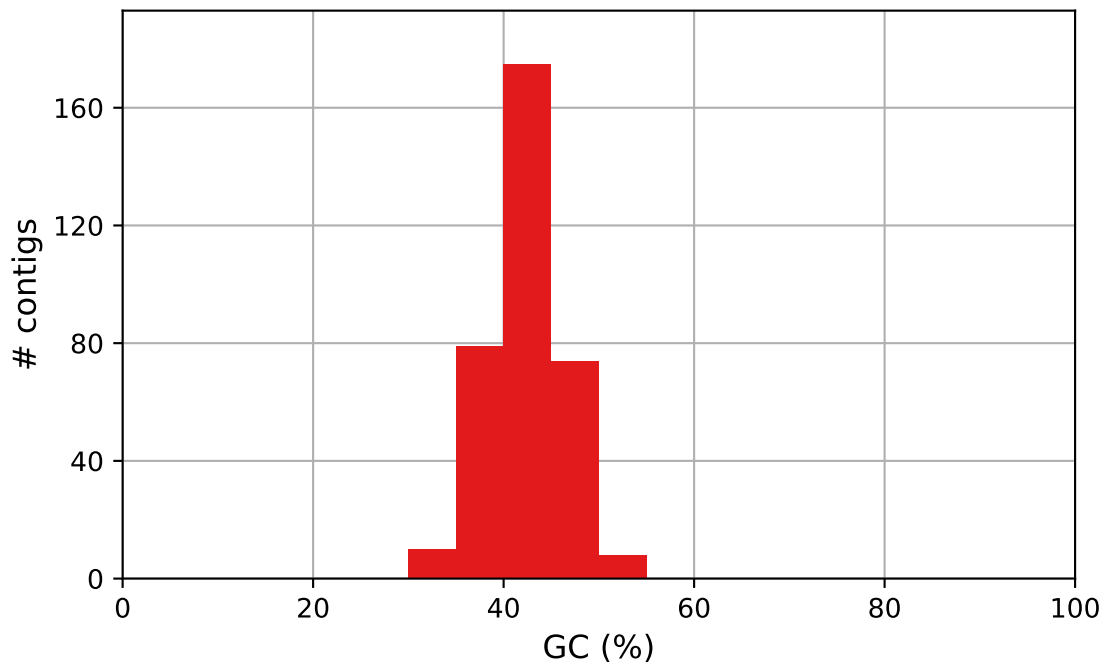


— MEGAHIT-MetaBAT2-3106237.6.fa



— MEGAHIT-MetaBAT2-3106237.6.fa

MEGAHIT-MetaBAT2-3106237.6.fa GC content



MEGAHIT-MetaBAT2-3106237.6.fa