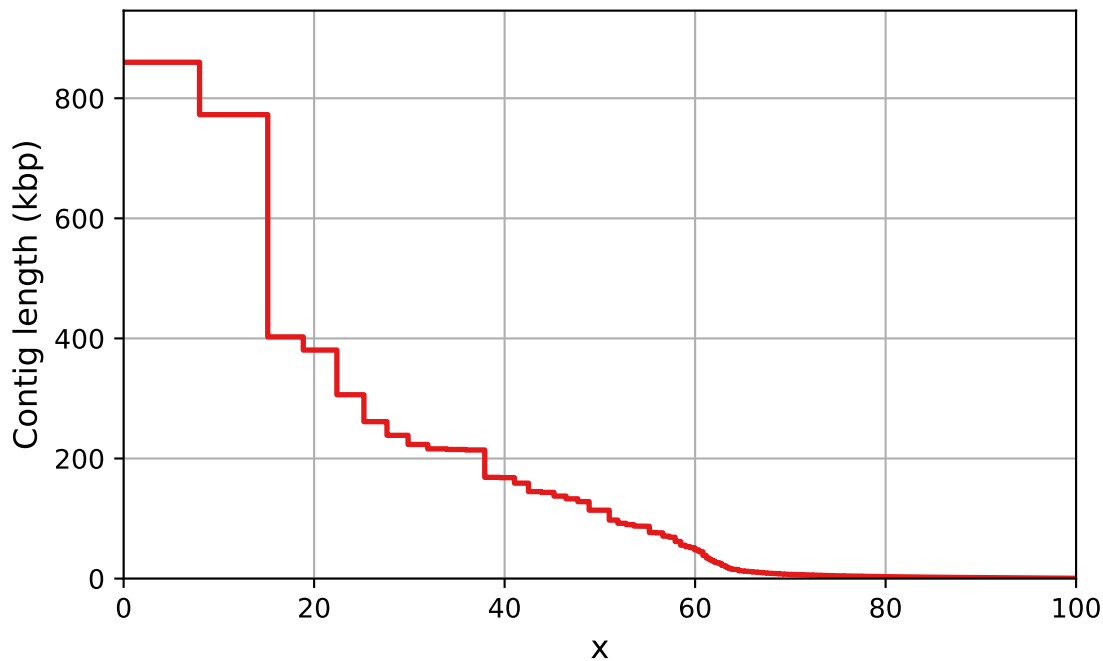


# Report

	genome.nextpolish
# contigs (>= 0 bp)	5521
# contigs (>= 1000 bp)	1299
# contigs (>= 5000 bp)	188
# contigs (>= 10000 bp)	78
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	11732751
Total length (>= 1000 bp)	10307391
Total length (>= 5000 bp)	7982360
Total length (>= 10000 bp)	7240989
Total length (>= 25000 bp)	6773831
Total length (>= 50000 bp)	6469581
# contigs	1986
Largest contig	859941
Total length	10789444
GC (%)	56.28
N50	113915
N90	1620
auN	218511.1
L50	21
L90	835
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	4 + 3 part

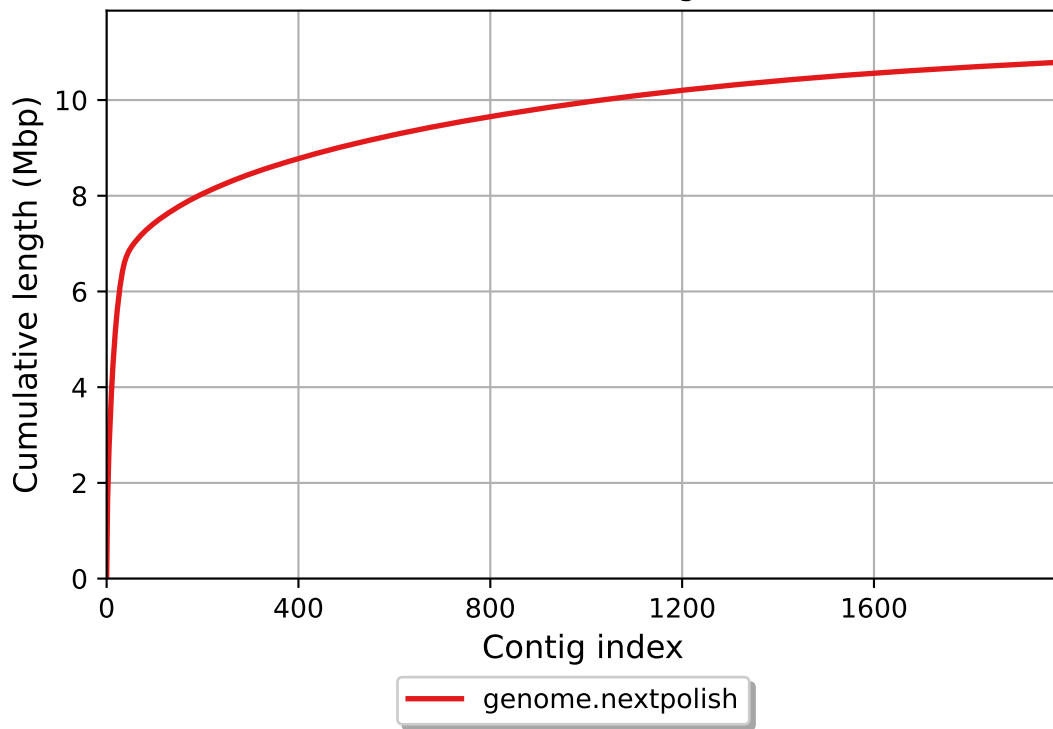
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

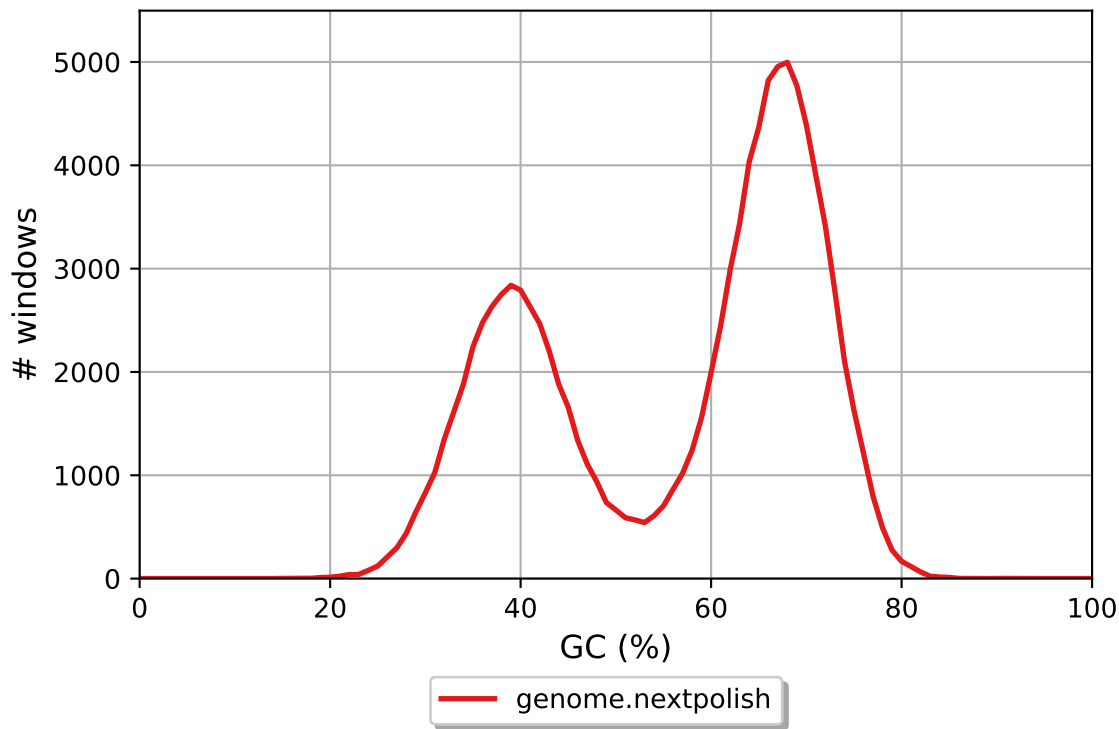


— genome.nextpolish

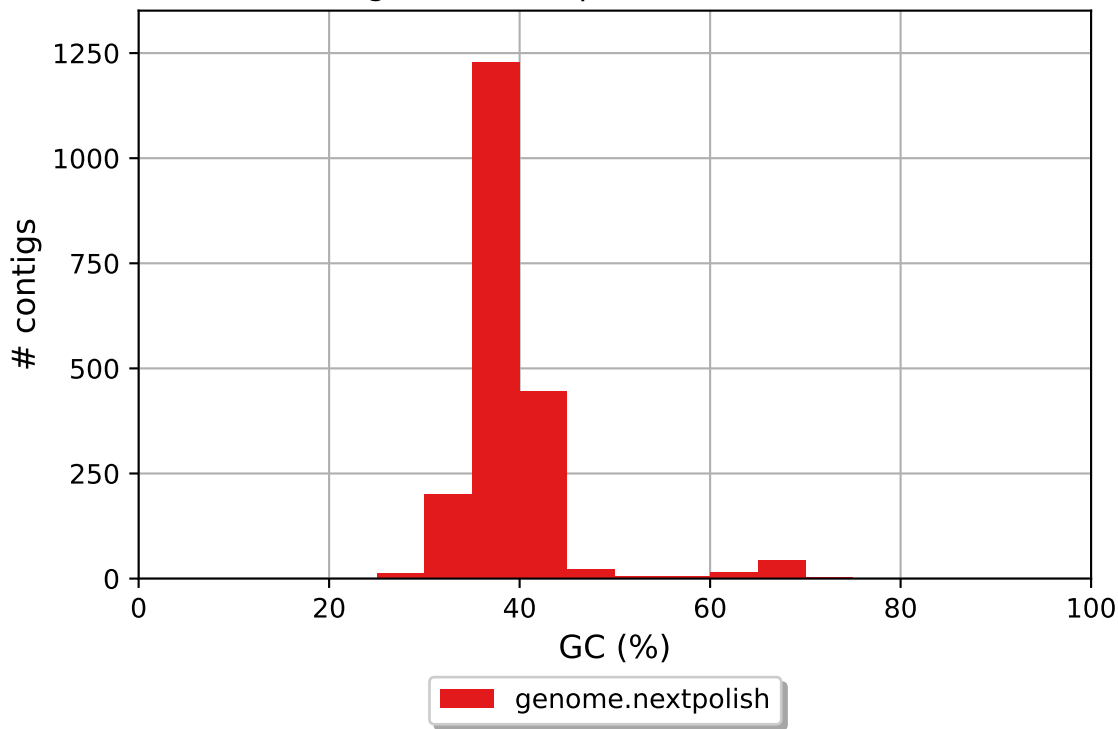
Cumulative length



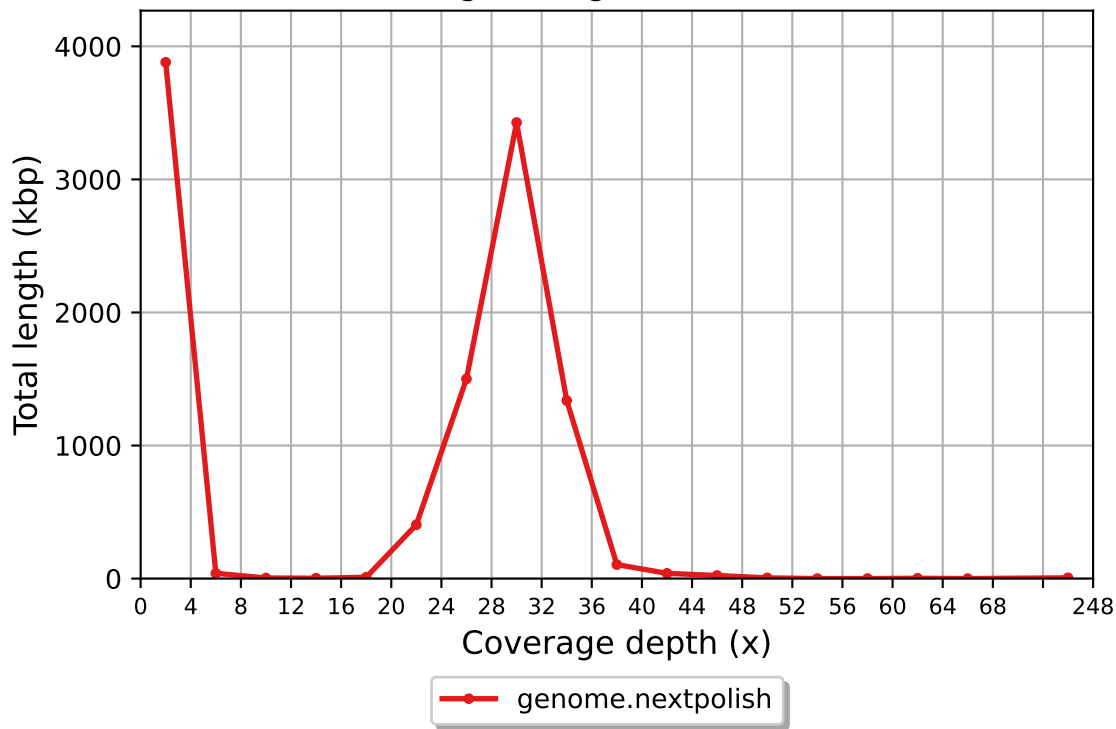
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 4x)



genome.nextpolish coverage histogram (bin size: 4x)

