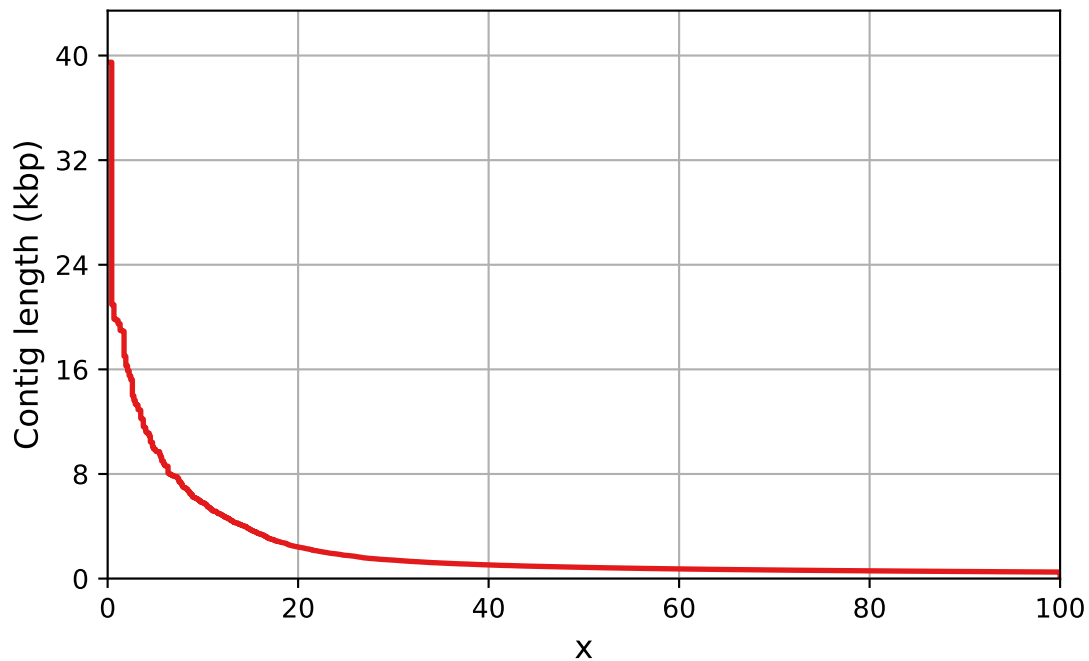


# Report

	genome.nextpolish
# contigs (>= 0 bp)	133404
# contigs (>= 1000 bp)	1808
# contigs (>= 5000 bp)	120
# contigs (>= 10000 bp)	29
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	42573932
Total length (>= 1000 bp)	3838308
Total length (>= 5000 bp)	1059816
Total length (>= 10000 bp)	440273
Total length (>= 25000 bp)	39485
Total length (>= 50000 bp)	0
# contigs	9898
Largest contig	39485
Total length	9127413
GC (%)	44.50
N50	858
N90	542
auN	2328.9
L50	2596
L90	8142
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	21 + 8 part

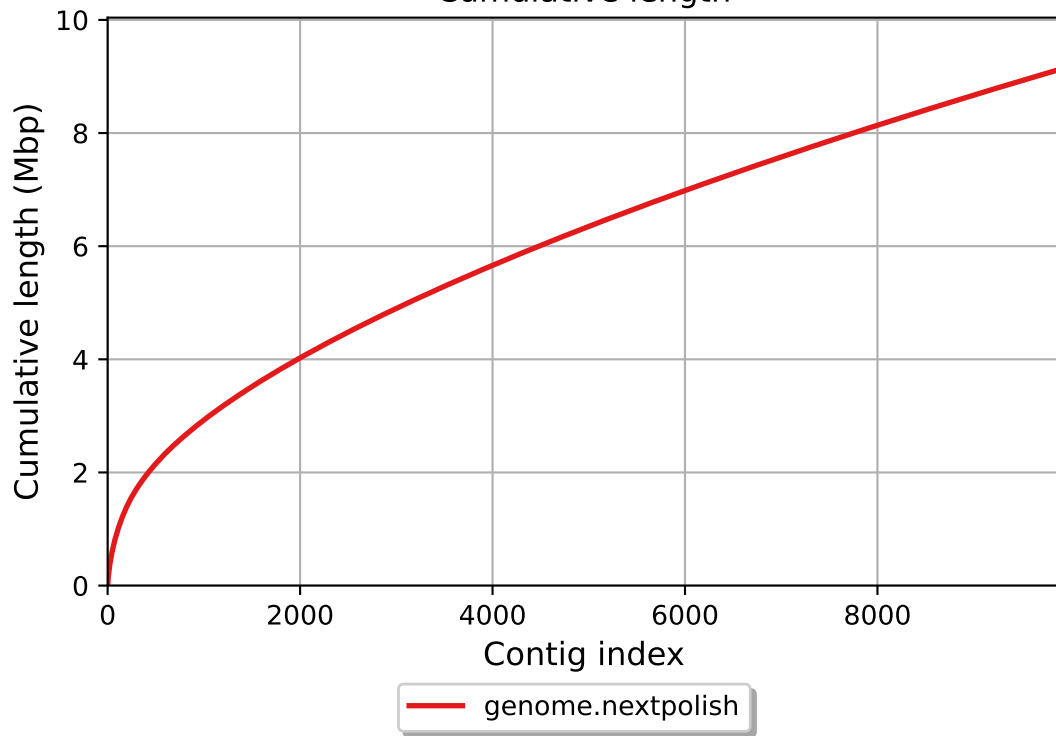
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

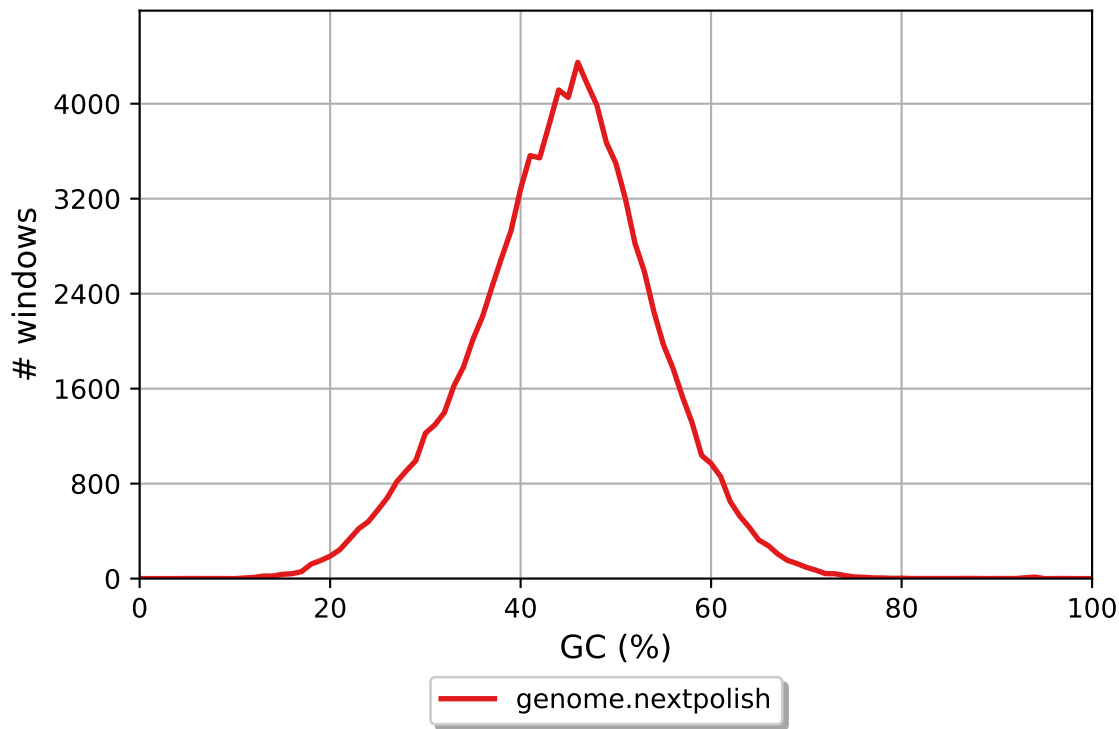


— genome.nextpolish

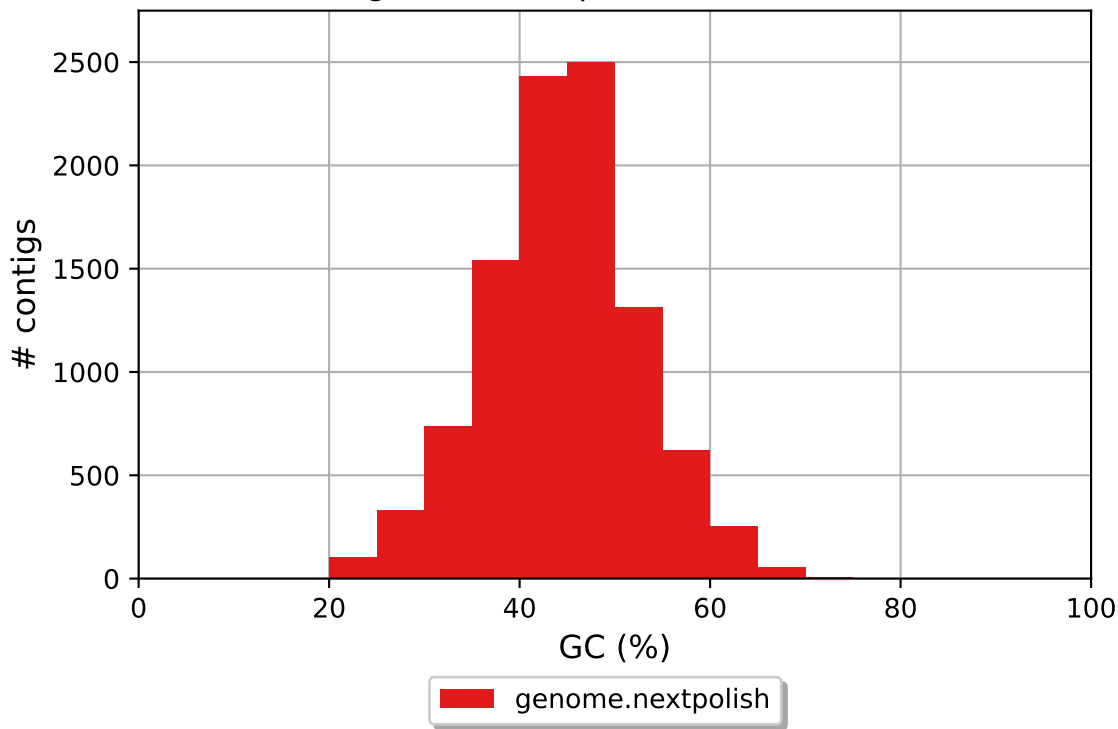
Cumulative length



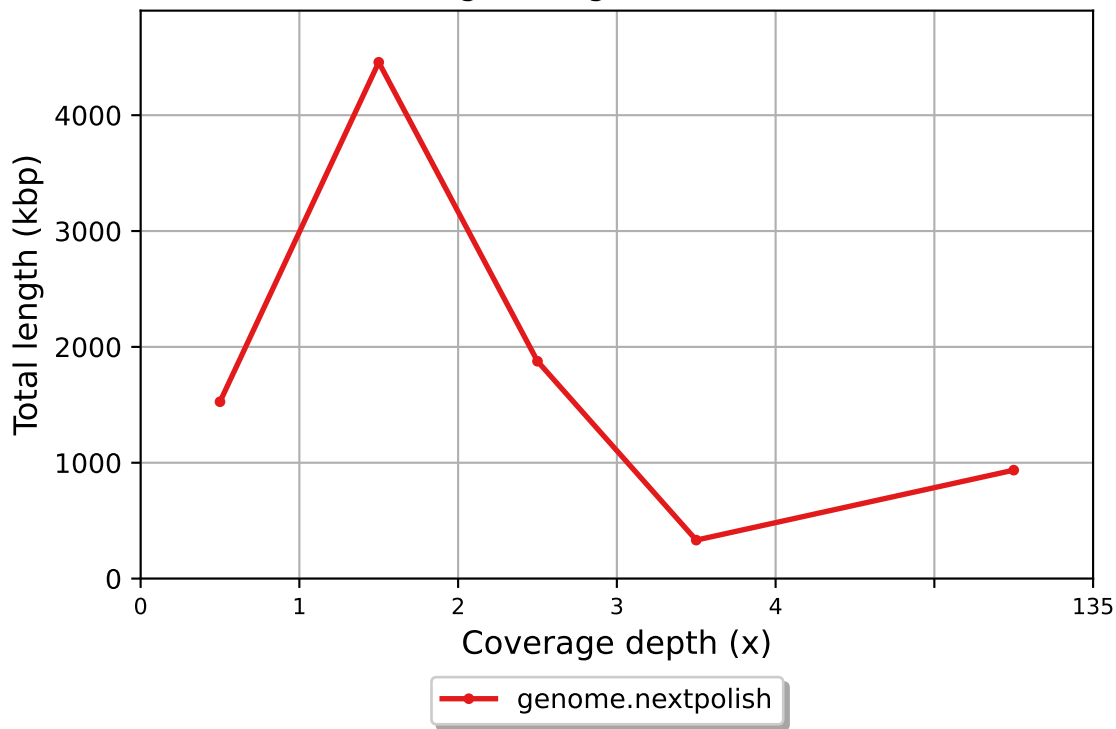
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



genome.nextpolish coverage histogram (bin size: 1x)

