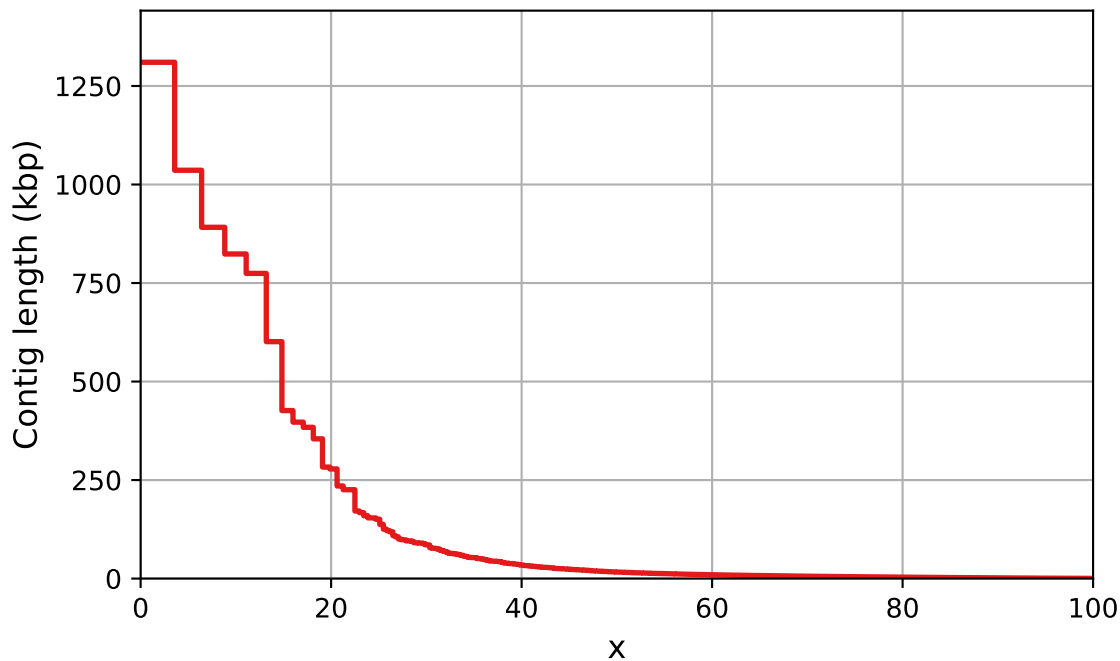


Report

	genome.nextpolish
# contigs (>= 0 bp)	15110
# contigs (>= 1000 bp)	4707
# contigs (>= 5000 bp)	1318
# contigs (>= 10000 bp)	545
# contigs (>= 25000 bp)	163
# contigs (>= 50000 bp)	72
Total length (>= 0 bp)	38855128
Total length (>= 1000 bp)	34978488
Total length (>= 5000 bp)	27179761
Total length (>= 10000 bp)	21826981
Total length (>= 25000 bp)	16212507
Total length (>= 50000 bp)	13107113
# contigs	7078
Largest contig	1310187
Total length	36653868
GC (%)	46.70
N50	16572
N90	1811
auN	187941.3
L50	268
L90	3219
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	24 + 6 part

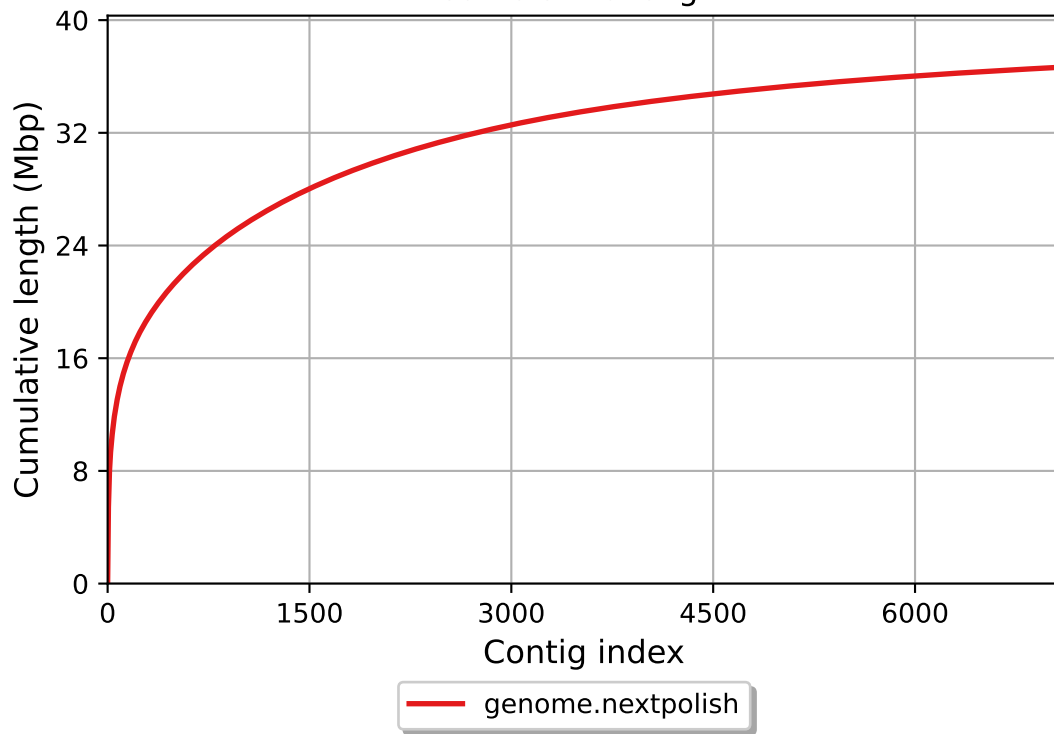
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

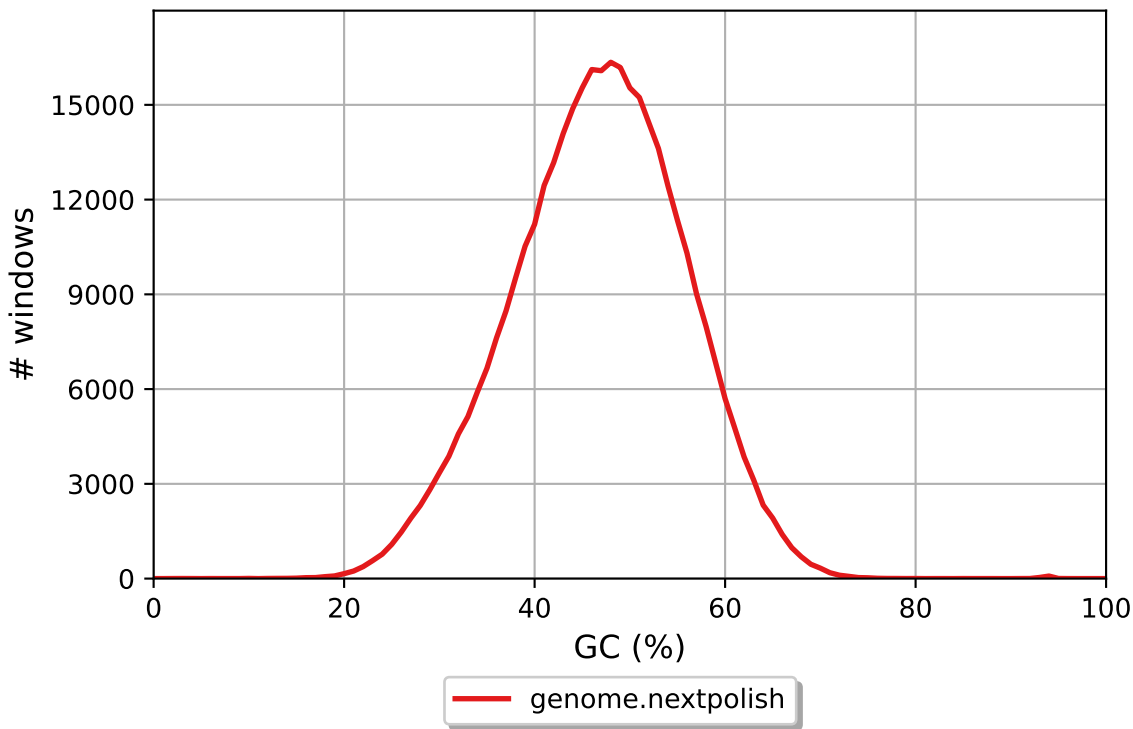


— genome.nextpolish

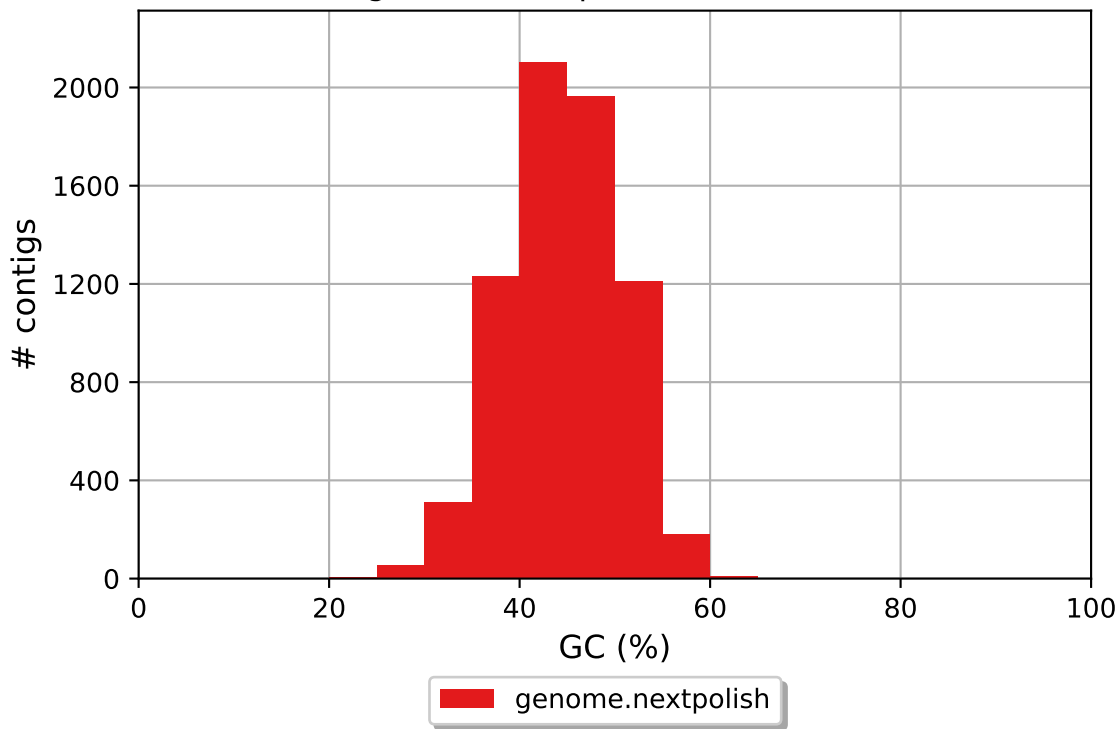
Cumulative length



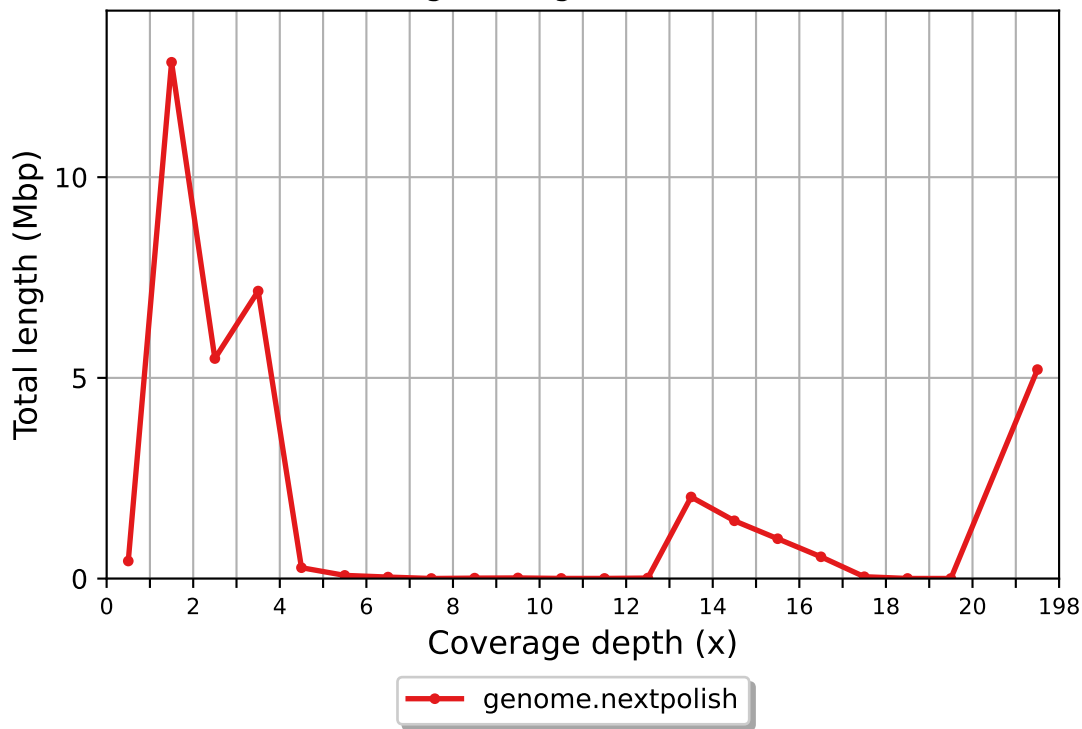
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

