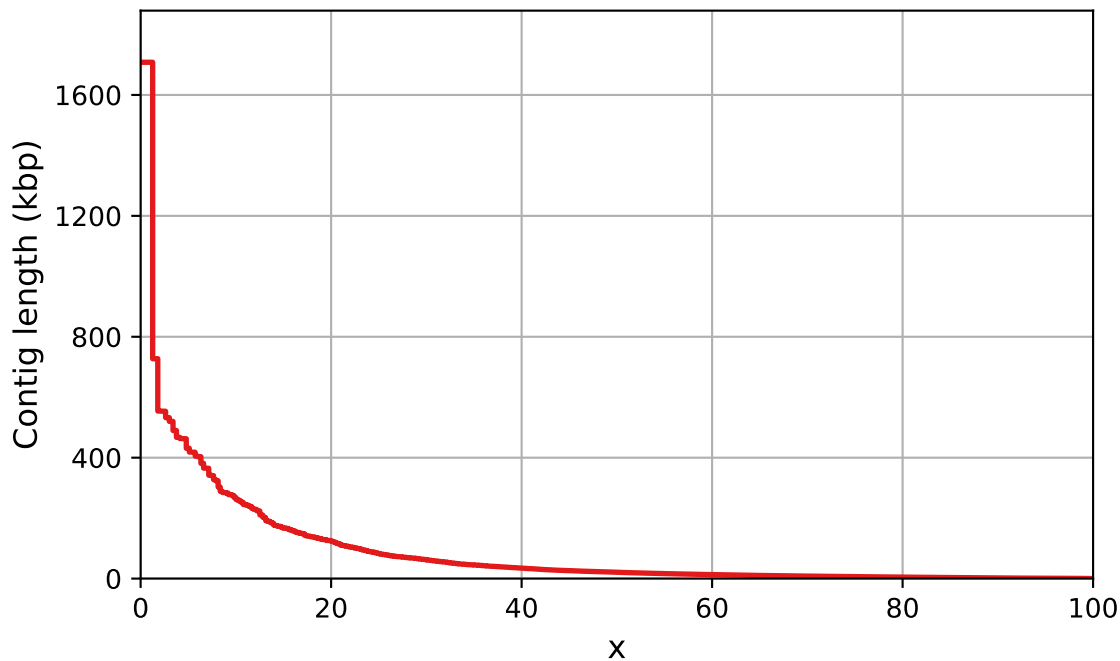


# Report

	genome.nextpolish
# contigs (>= 0 bp)	145307
# contigs (>= 1000 bp)	14064
# contigs (>= 5000 bp)	5232
# contigs (>= 10000 bp)	2595
# contigs (>= 25000 bp)	858
# contigs (>= 50000 bp)	349
Total length (>= 0 bp)	167581115
Total length (>= 1000 bp)	128498427
Total length (>= 5000 bp)	107595591
Total length (>= 10000 bp)	88925225
Total length (>= 25000 bp)	62311466
Total length (>= 50000 bp)	44820434
# contigs	24012
Largest contig	1708116
Total length	135167417
GC (%)	45.85
N50	21068
N90	2190
auN	96425.7
L50	1089
L90	9426
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	66 + 27 part

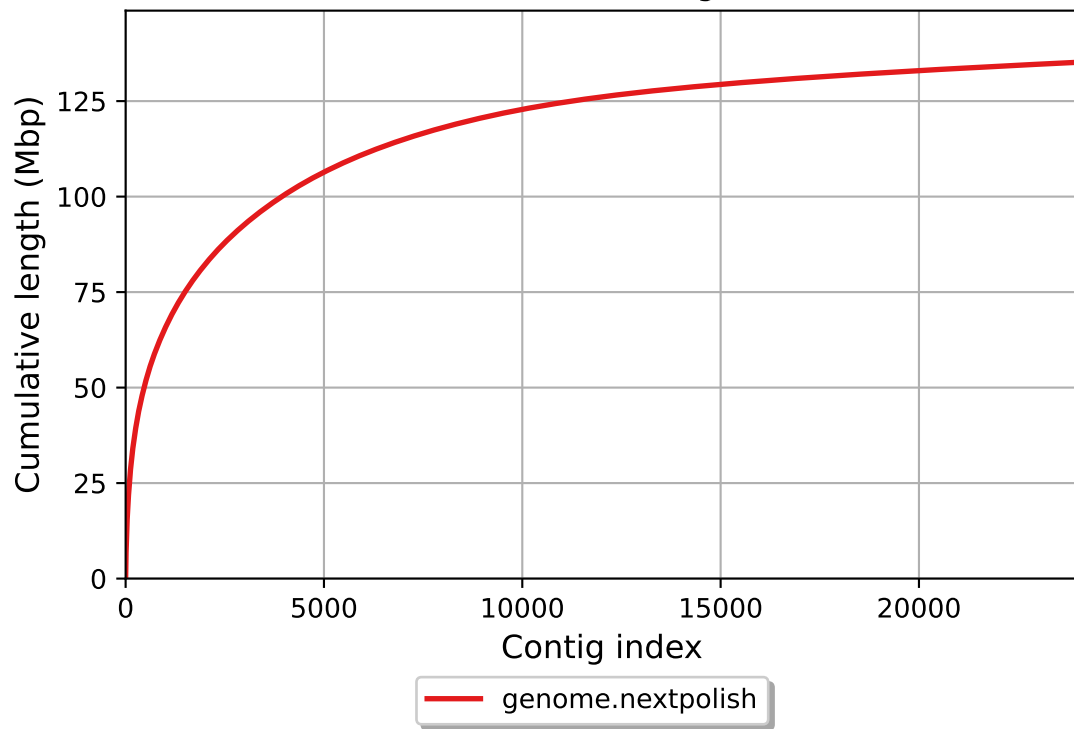
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

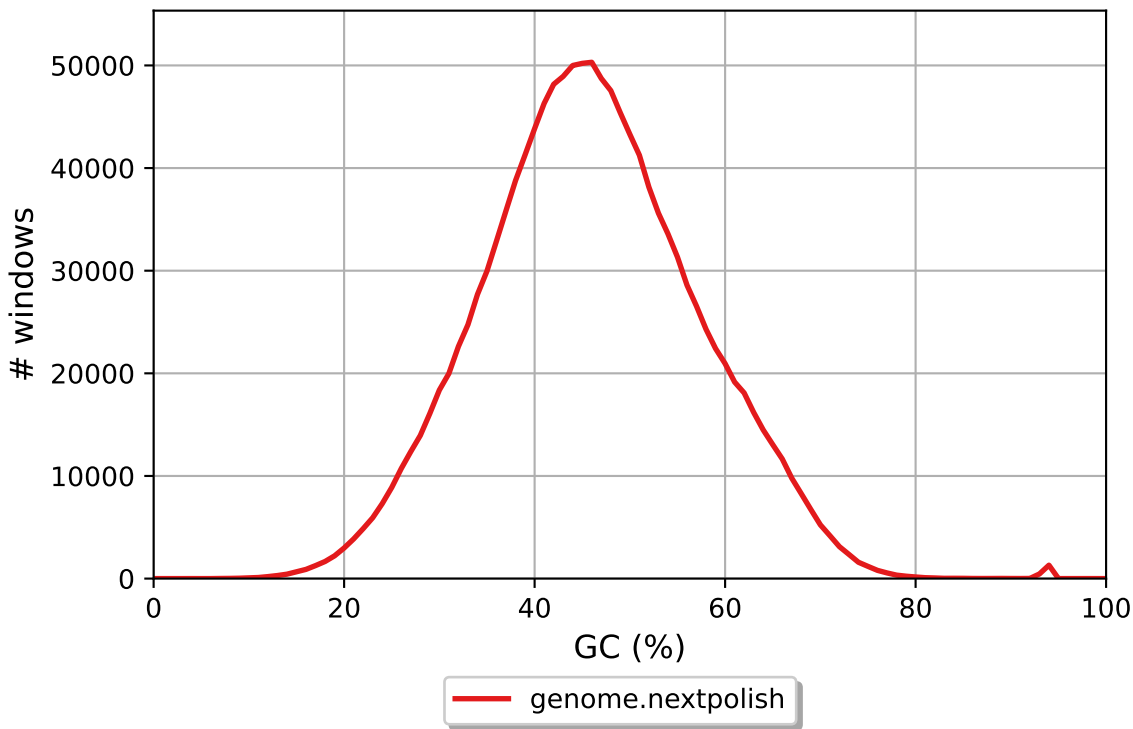


— genome.nextpolish

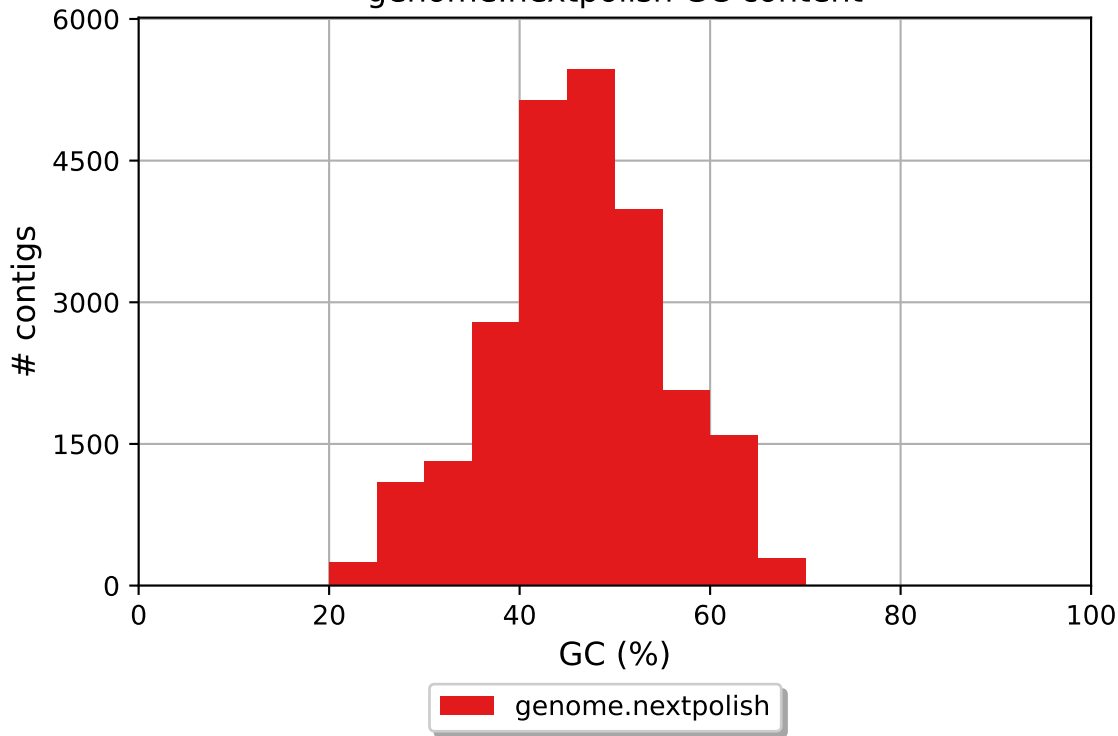
Cumulative length



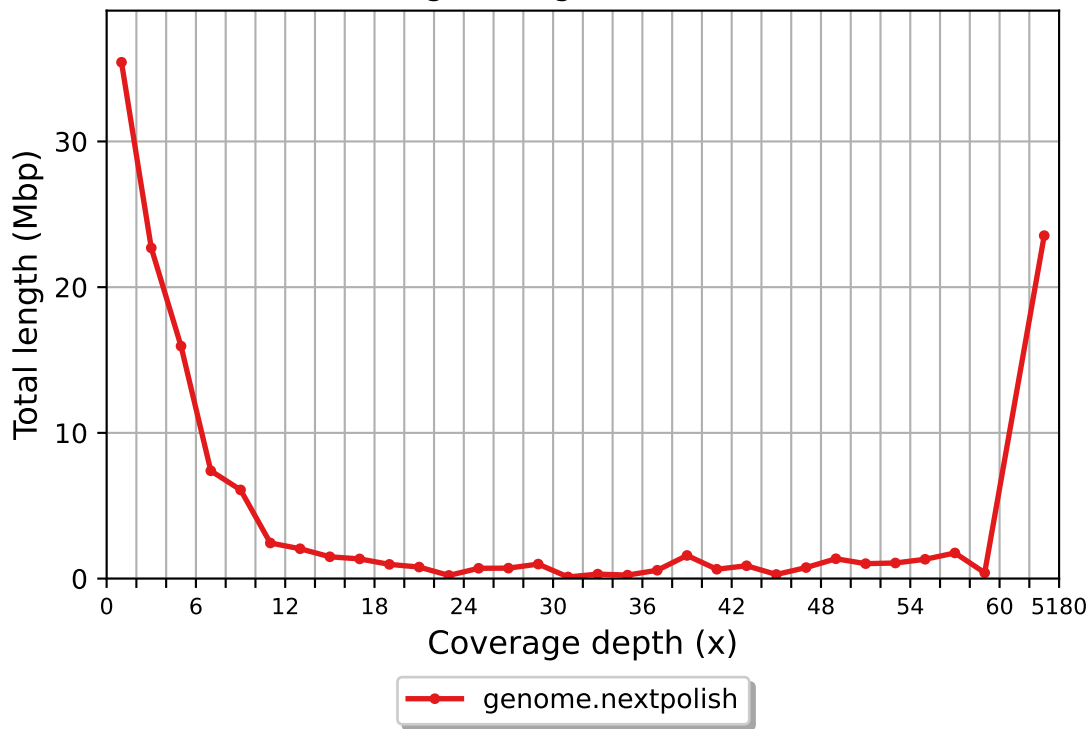
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 2x)



genome.nextpolish coverage histogram (bin size: 2x)

