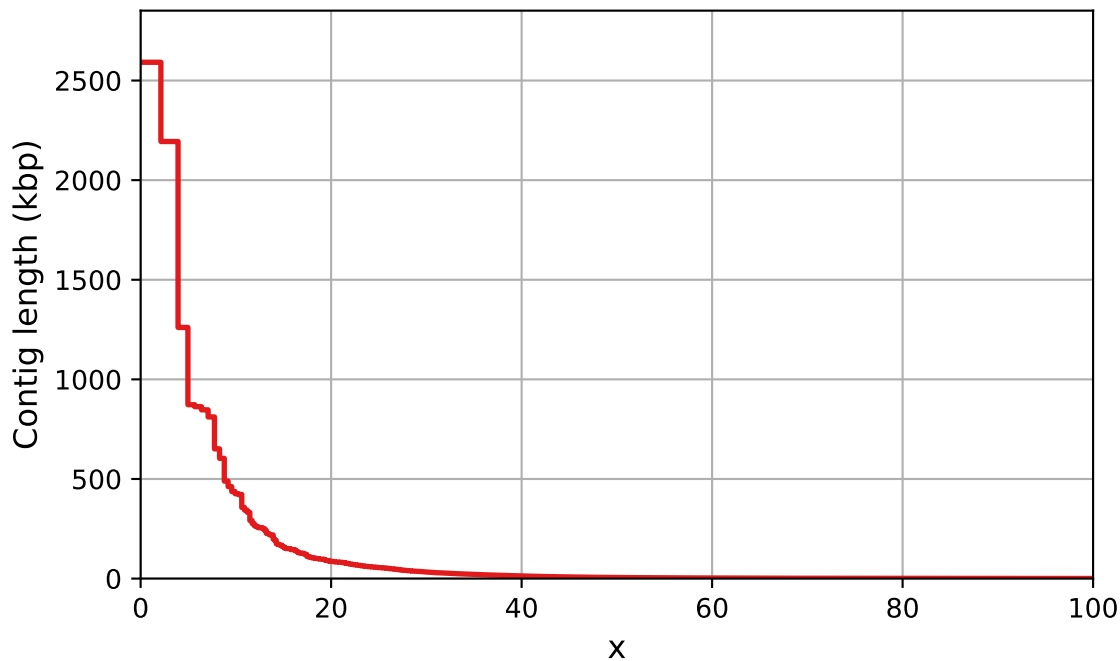


# Report

	genome.nextpolish
# contigs (>= 0 bp)	191080
# contigs (>= 1000 bp)	22331
# contigs (>= 5000 bp)	2721
# contigs (>= 10000 bp)	1233
# contigs (>= 25000 bp)	450
# contigs (>= 50000 bp)	204
Total length (>= 0 bp)	161298722
Total length (>= 1000 bp)	99284768
Total length (>= 5000 bp)	62409353
Total length (>= 10000 bp)	52292589
Total length (>= 25000 bp)	40220694
Total length (>= 50000 bp)	31839523
# contigs	55102
Largest contig	2591662
Total length	121783314
GC (%)	47.45
N50	5490
N90	716
auN	172659.9
L50	2432
L90	34597
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	75 + 17 part

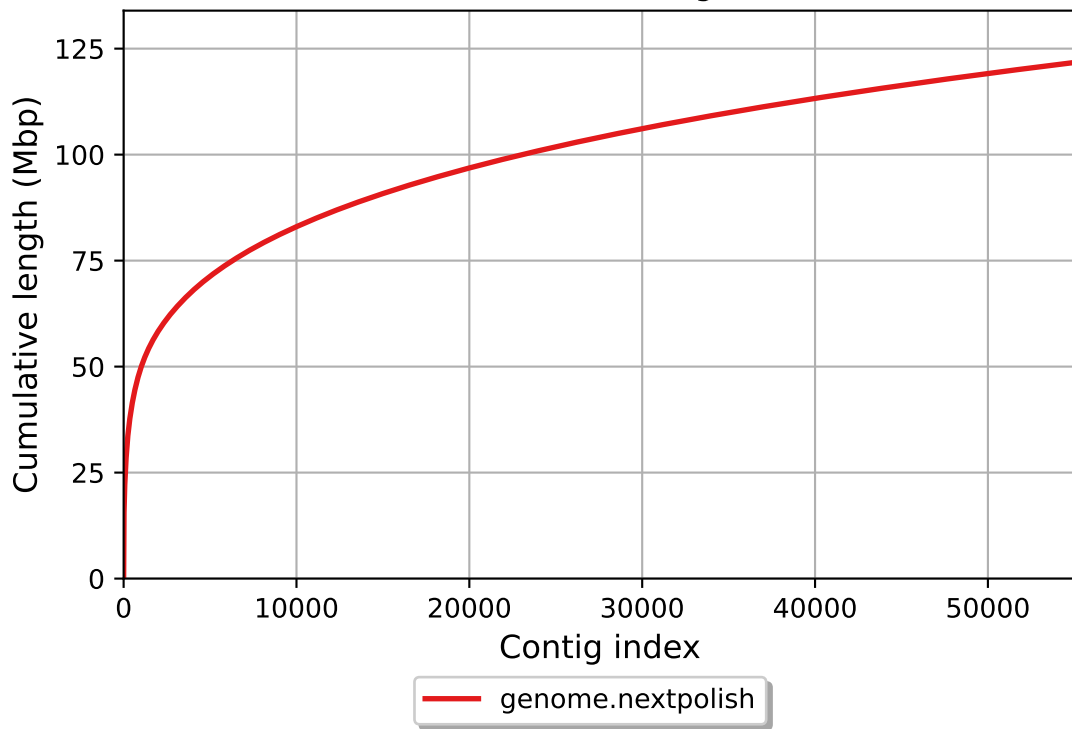
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

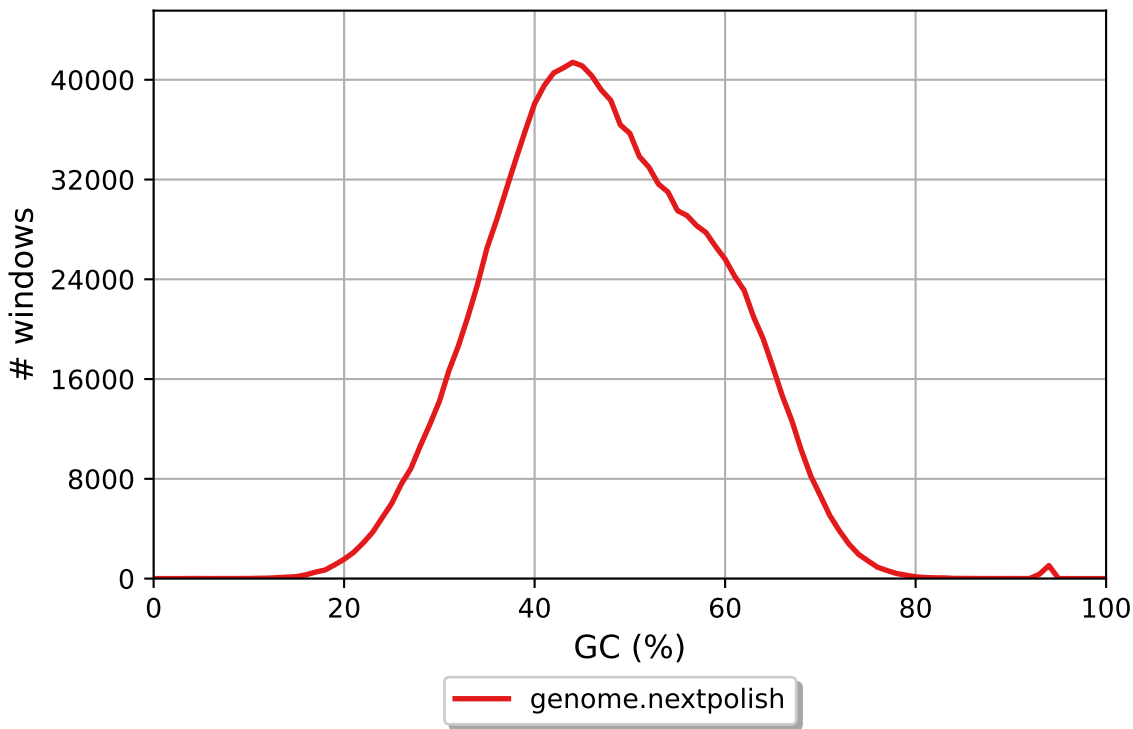


— genome.nextpolish

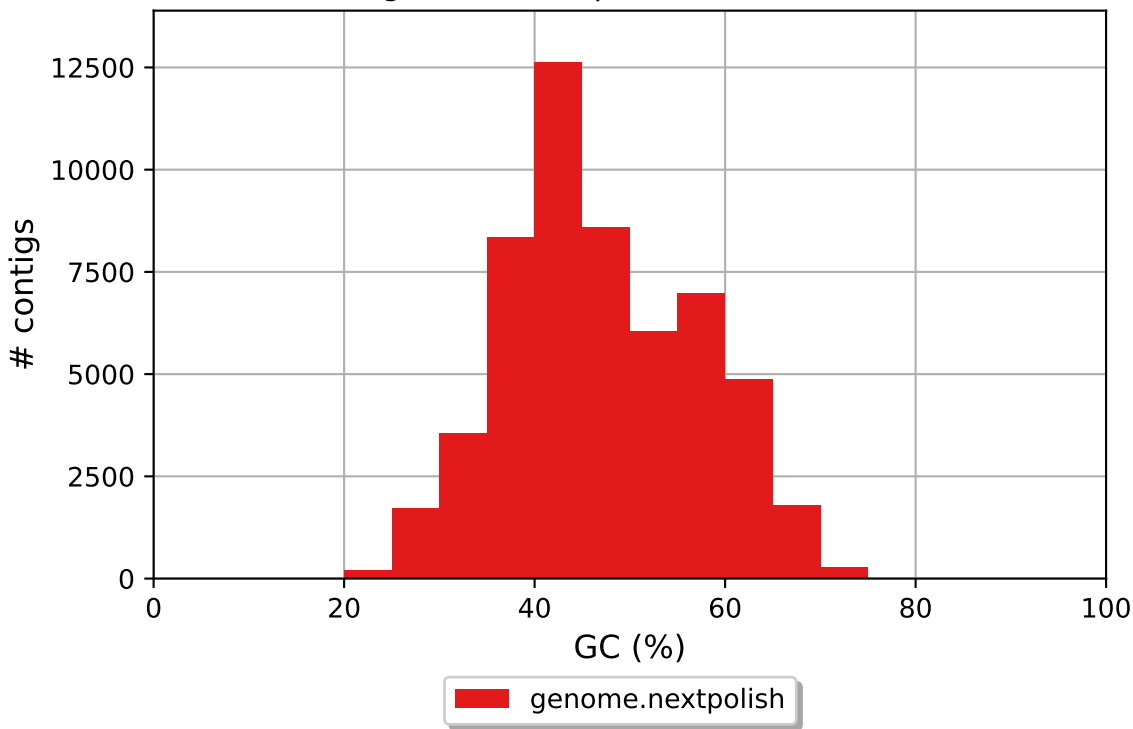
Cumulative length



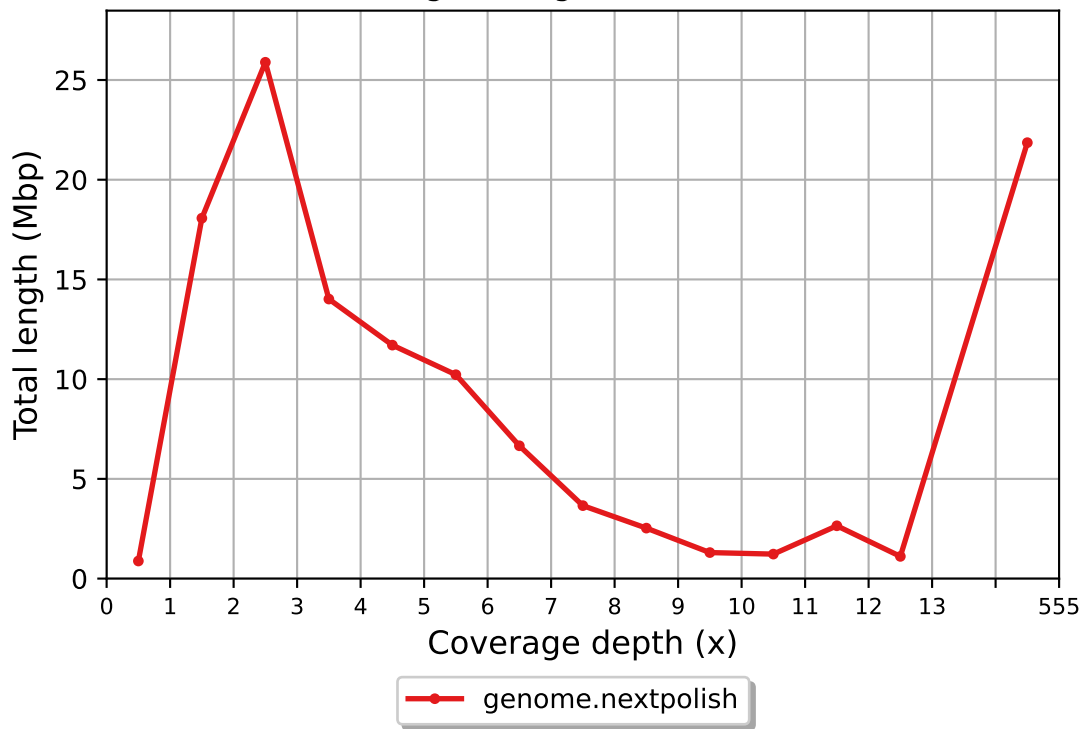
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

