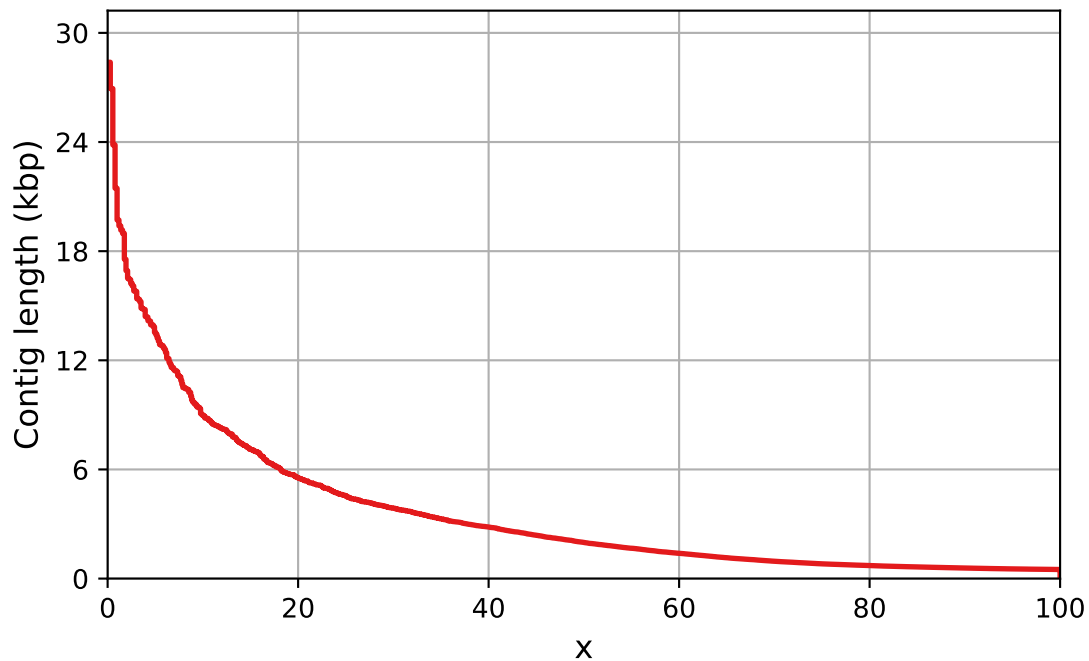


# Report

	genome.nextpolish
# contigs (>= 0 bp)	16461
# contigs (>= 1000 bp)	2548
# contigs (>= 5000 bp)	271
# contigs (>= 10000 bp)	63
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	13792115
Total length (>= 1000 bp)	6963172
Total length (>= 5000 bp)	2293783
Total length (>= 10000 bp)	892965
Total length (>= 25000 bp)	55323
Total length (>= 50000 bp)	0
# contigs	7397
Largest contig	28384
Total length	10127867
GC (%)	43.11
N50	1987
N90	580
auN	3682.2
L50	1180
L90	5502
# N's per 100 kbp	2.20
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	6 + 7 part

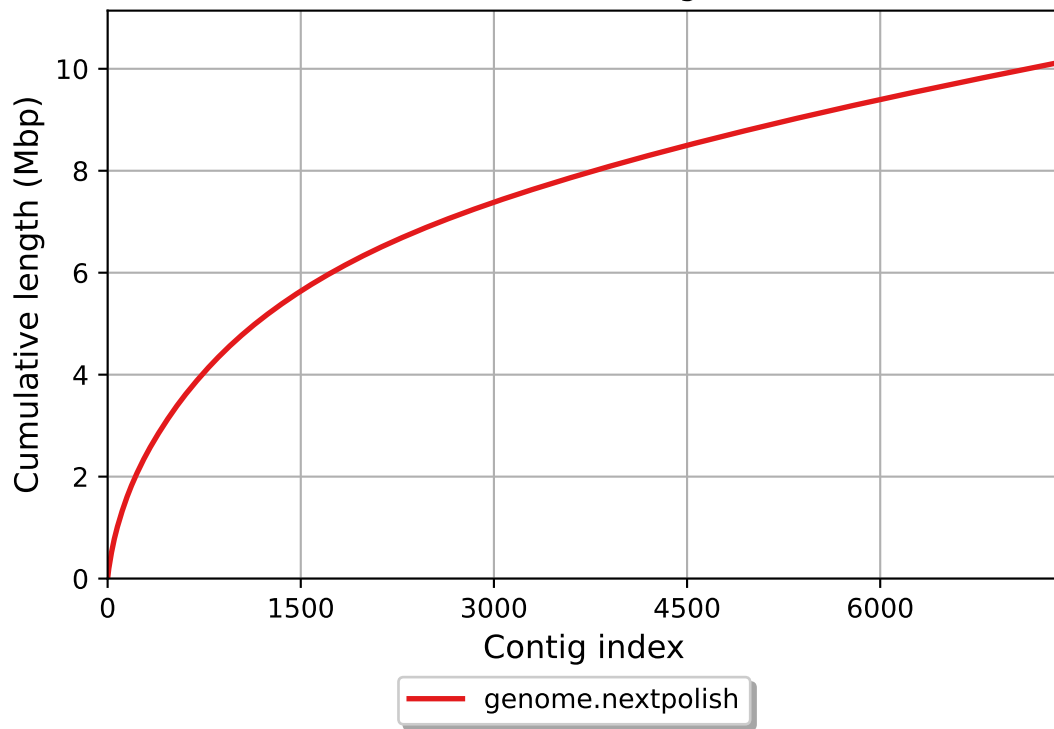
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

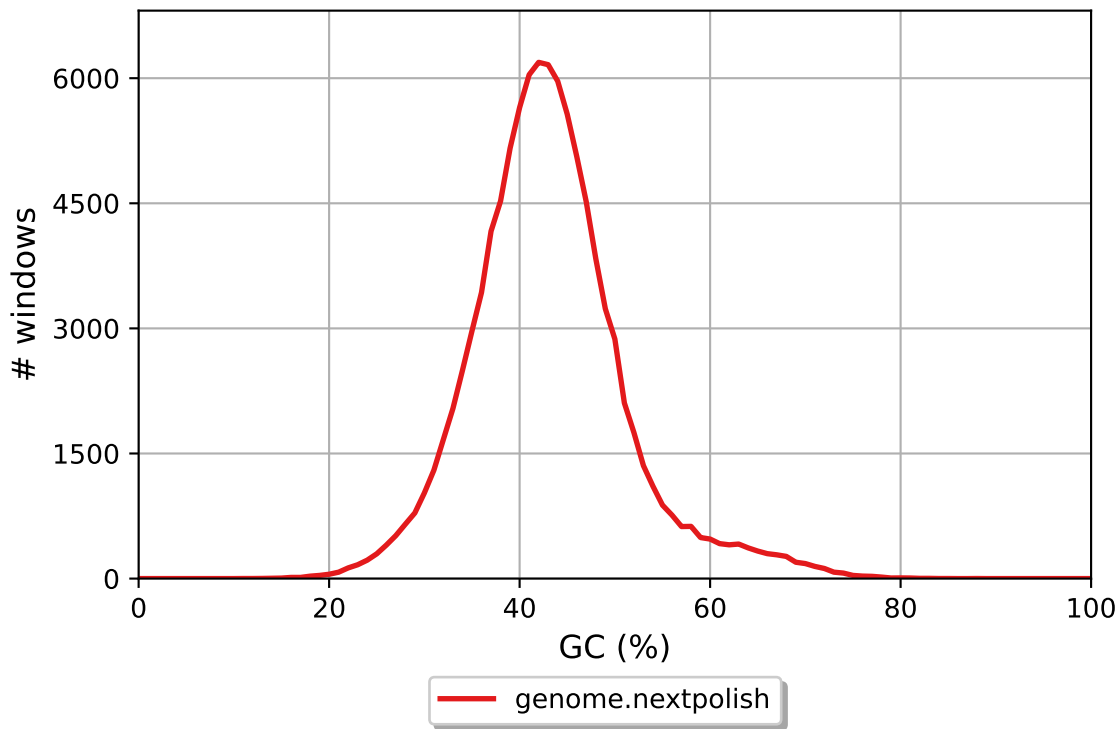


— genome.nextpolish

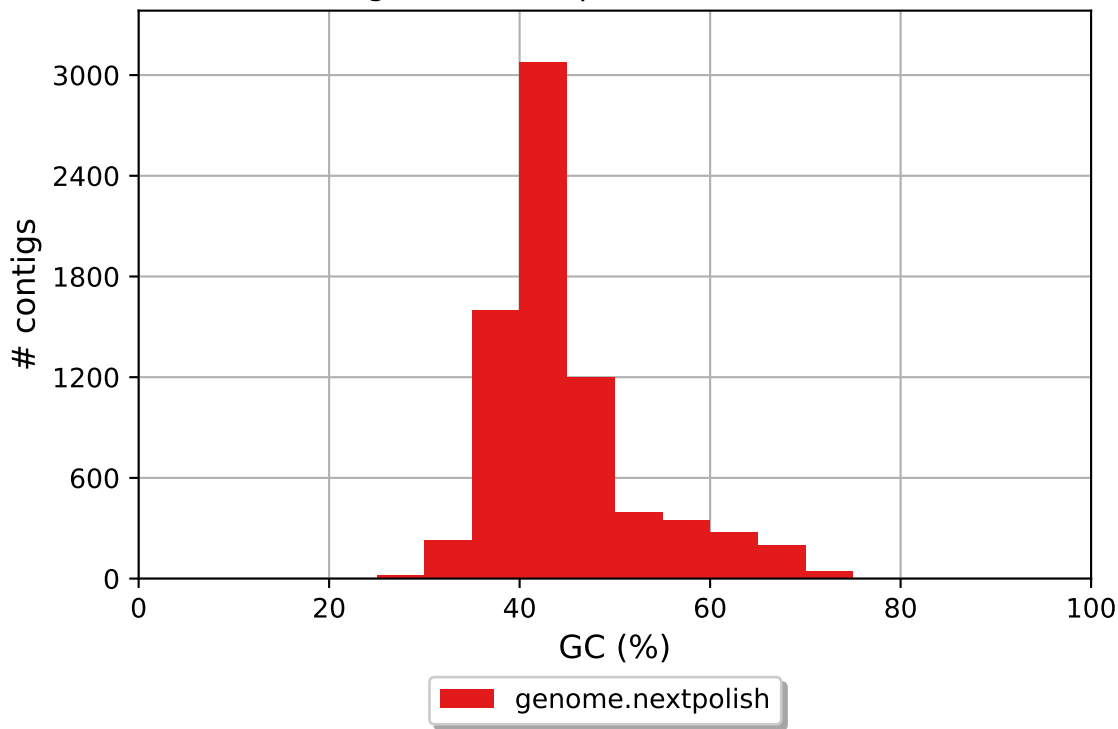
Cumulative length



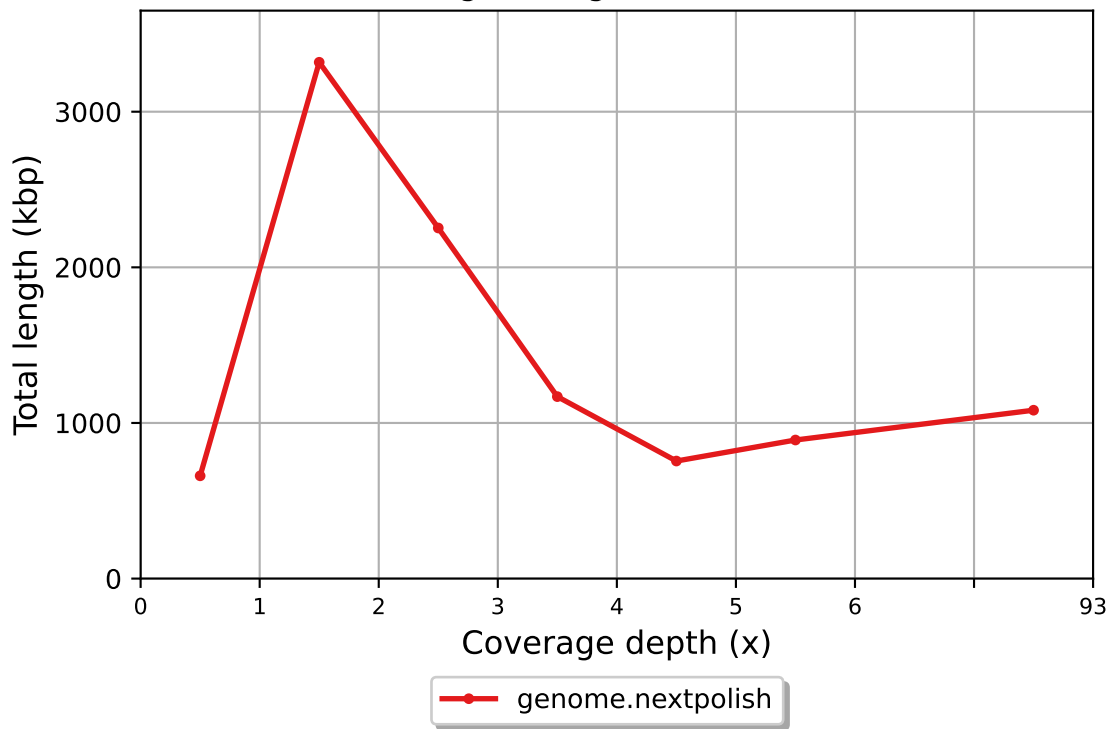
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

