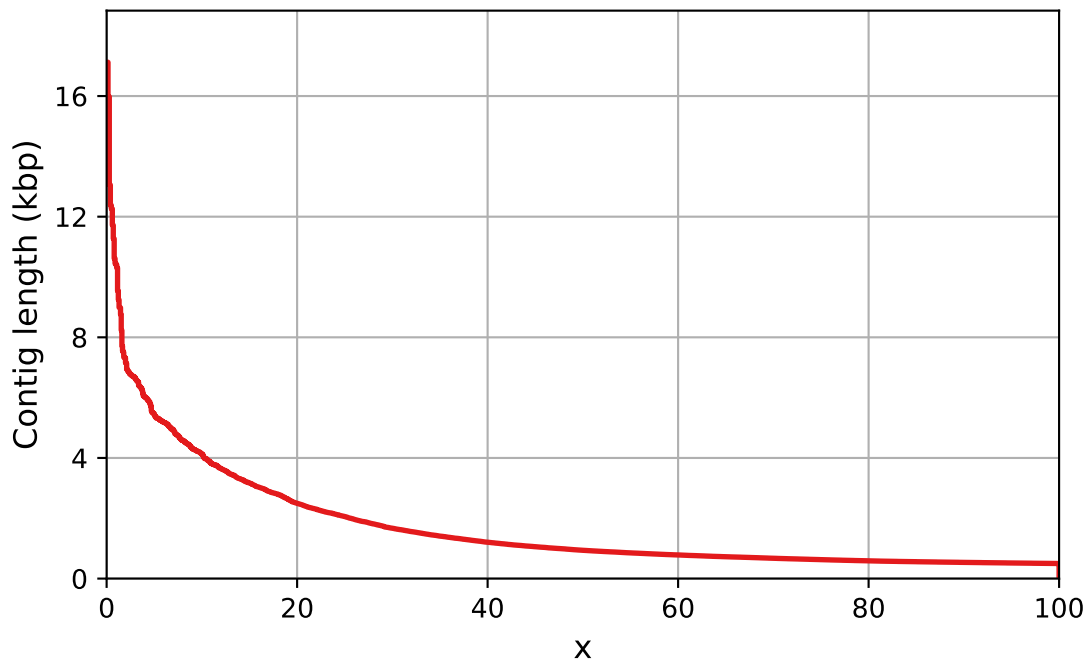


# Report

	genome.nextpolish
# contigs (>= 0 bp)	25395
# contigs (>= 1000 bp)	2793
# contigs (>= 5000 bp)	118
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	17133138
Total length (>= 1000 bp)	5589437
Total length (>= 5000 bp)	790307
Total length (>= 10000 bp)	135559
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12402
Largest contig	17120
Total length	11809773
GC (%)	45.14
N50	939
N90	537
auN	1747.1
L50	3119
L90	10121
# N's per 100 kbp	0.03
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	13 + 5 part

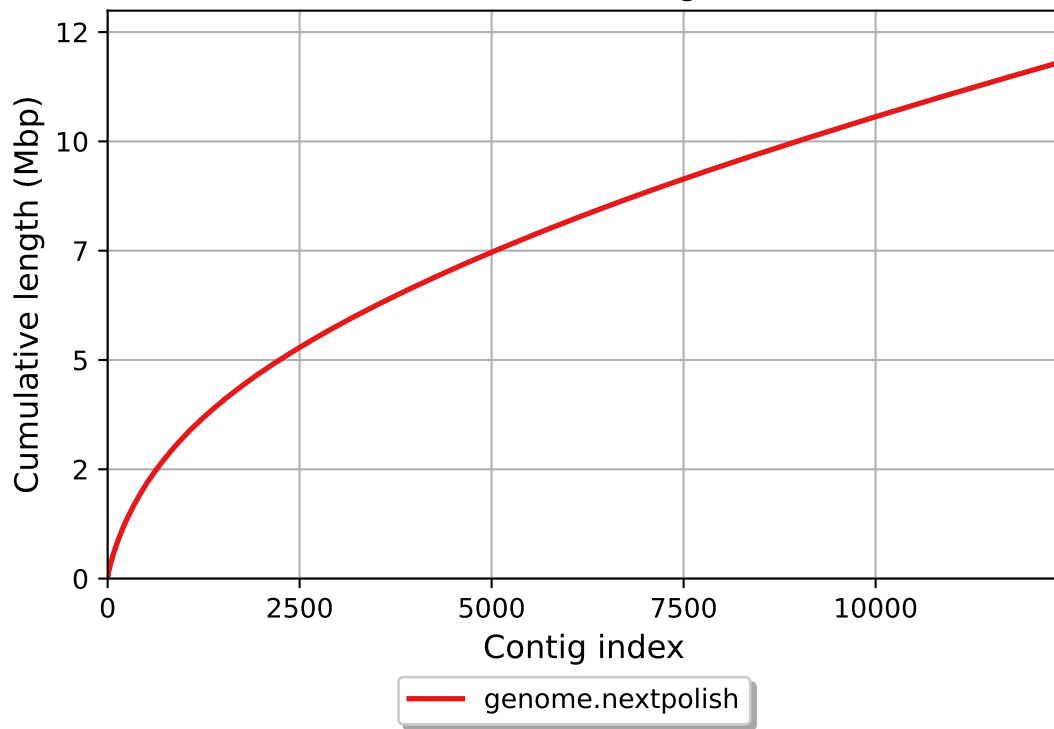
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

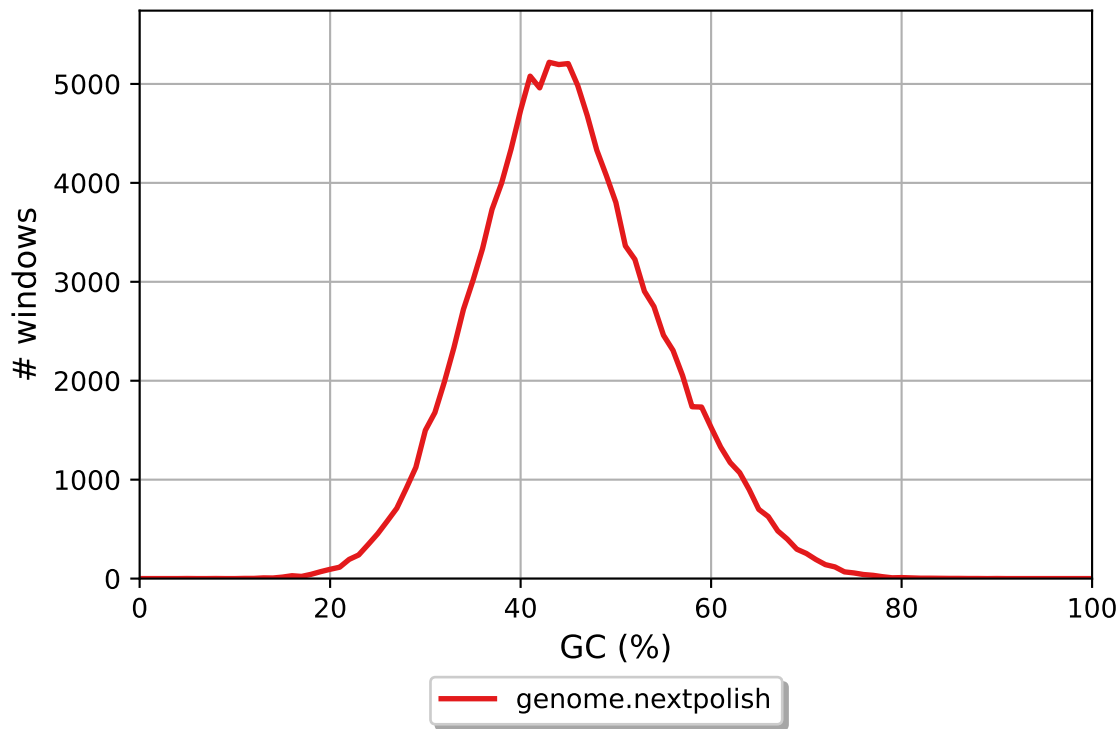


— genome.nextpolish

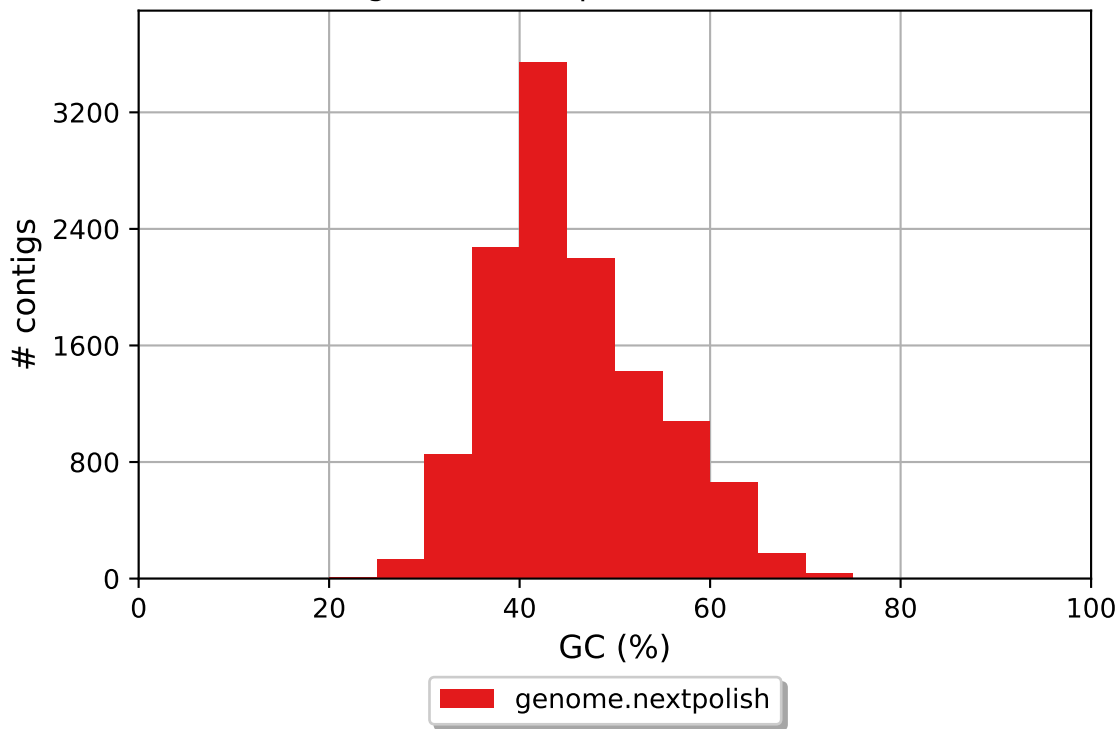
Cumulative length



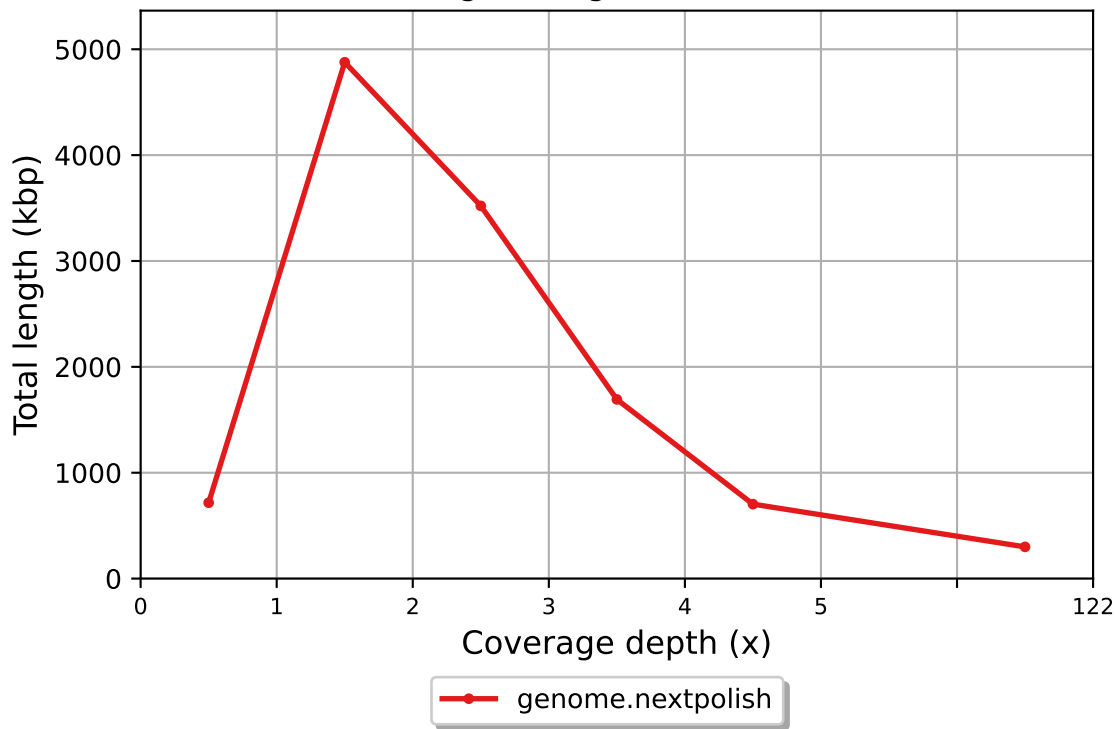
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

