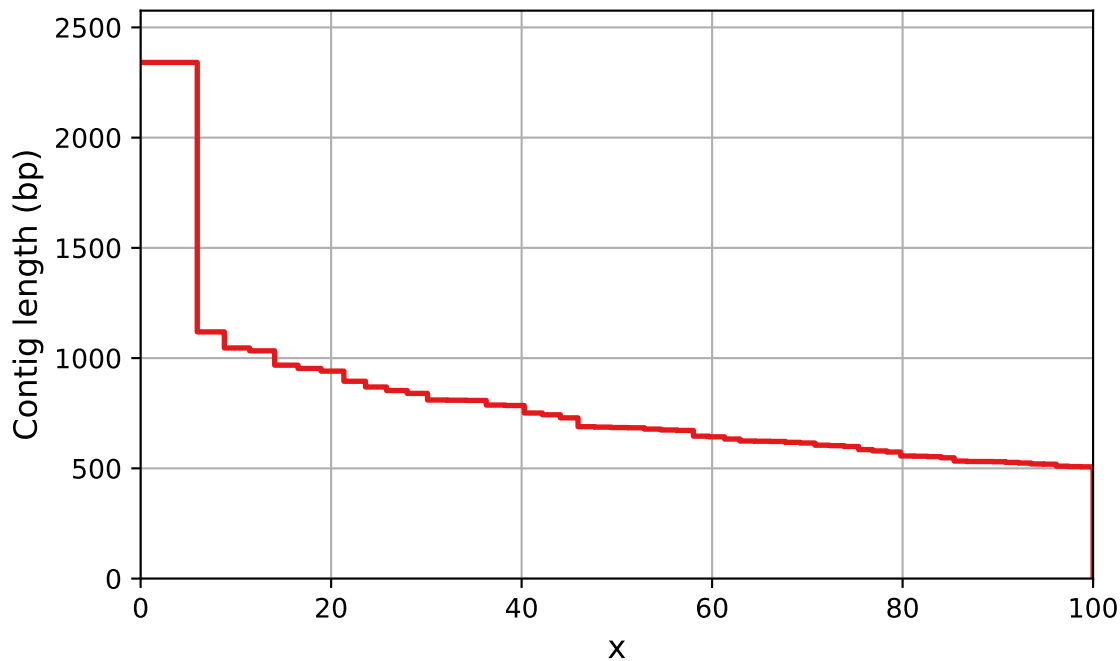


Report

	genome.nextpolish
# contigs (>= 0 bp)	2100
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	430026
Total length (>= 1000 bp)	5539
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	55
Largest contig	2341
Total length	39370
GC (%)	51.72
N50	685
N90	530
auN	817.4
L50	22
L90	48
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	0 + 2 part

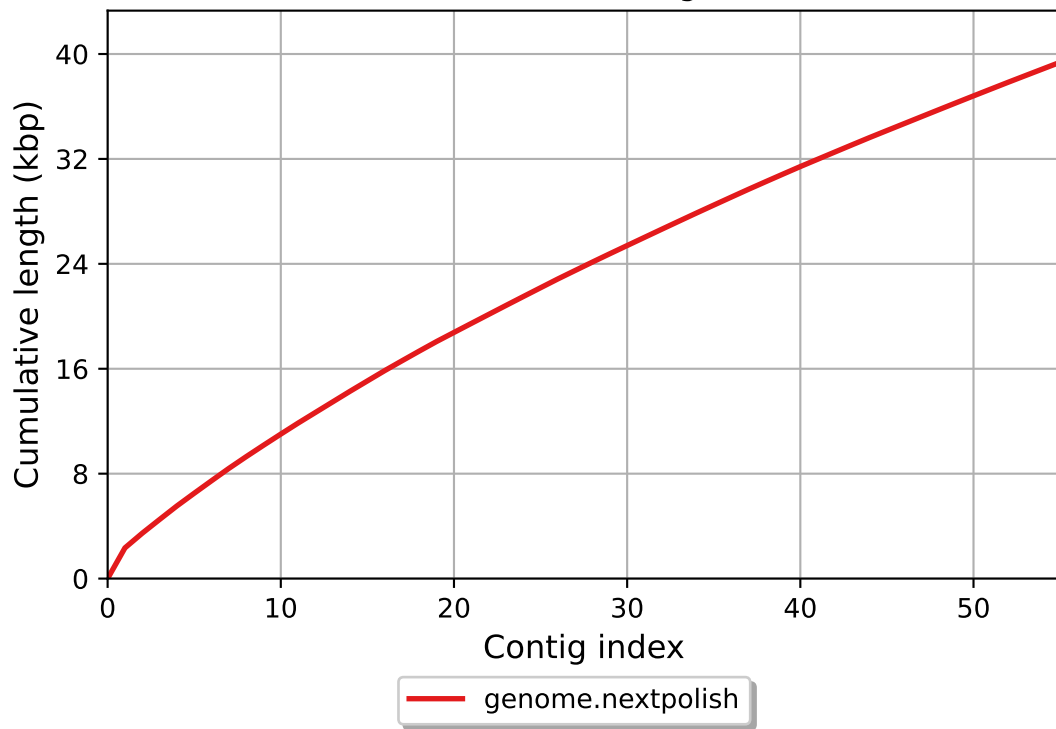
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

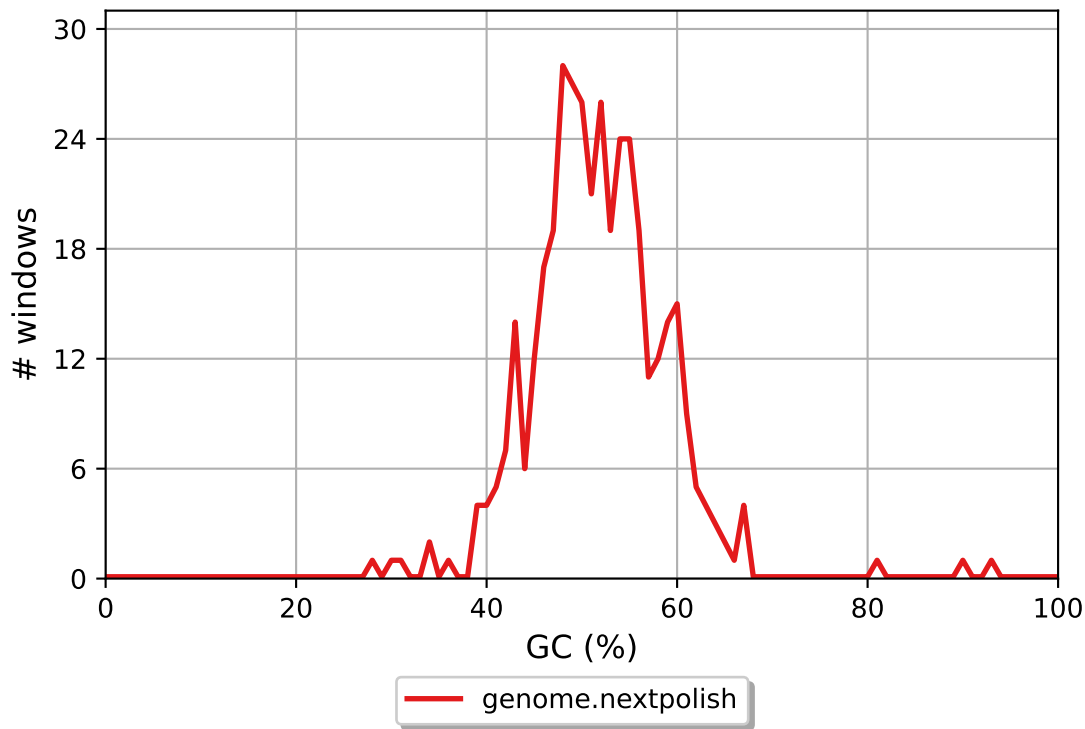


— genome.nextpolish

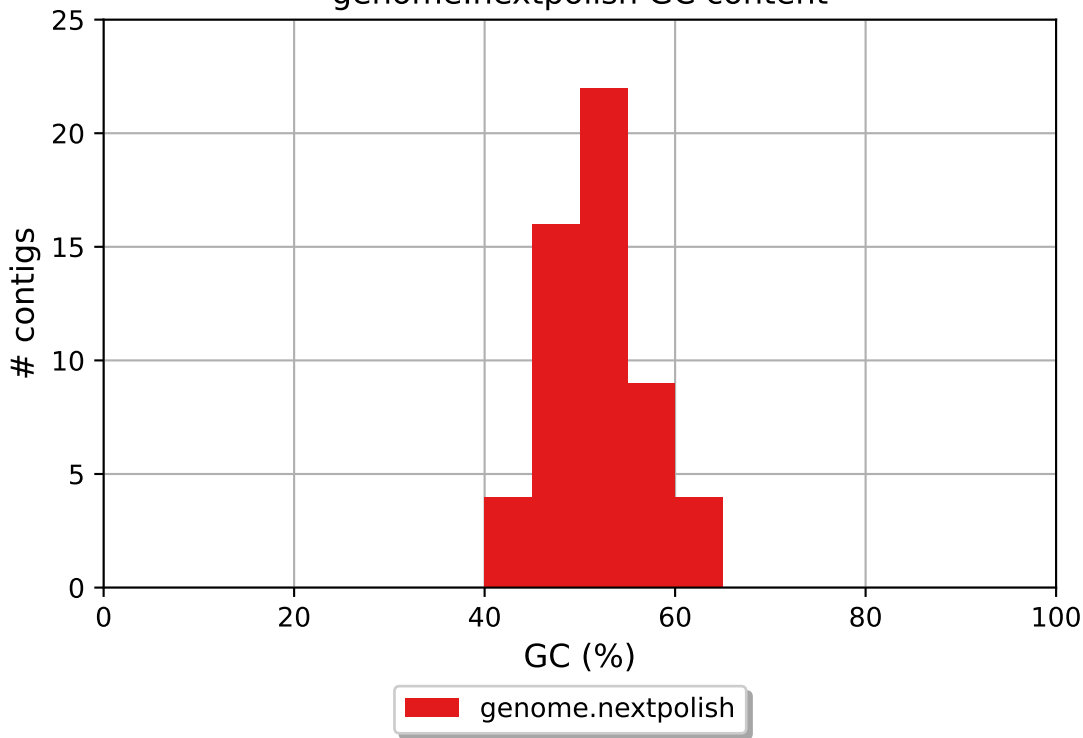
Cumulative length



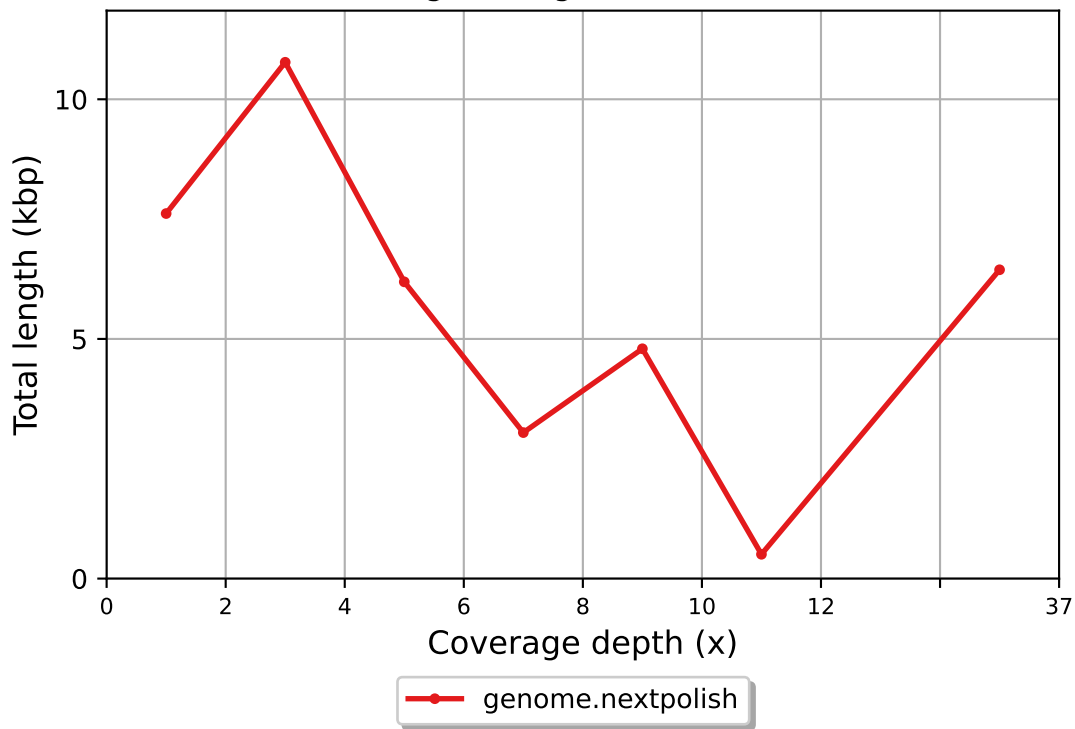
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 2x)



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

