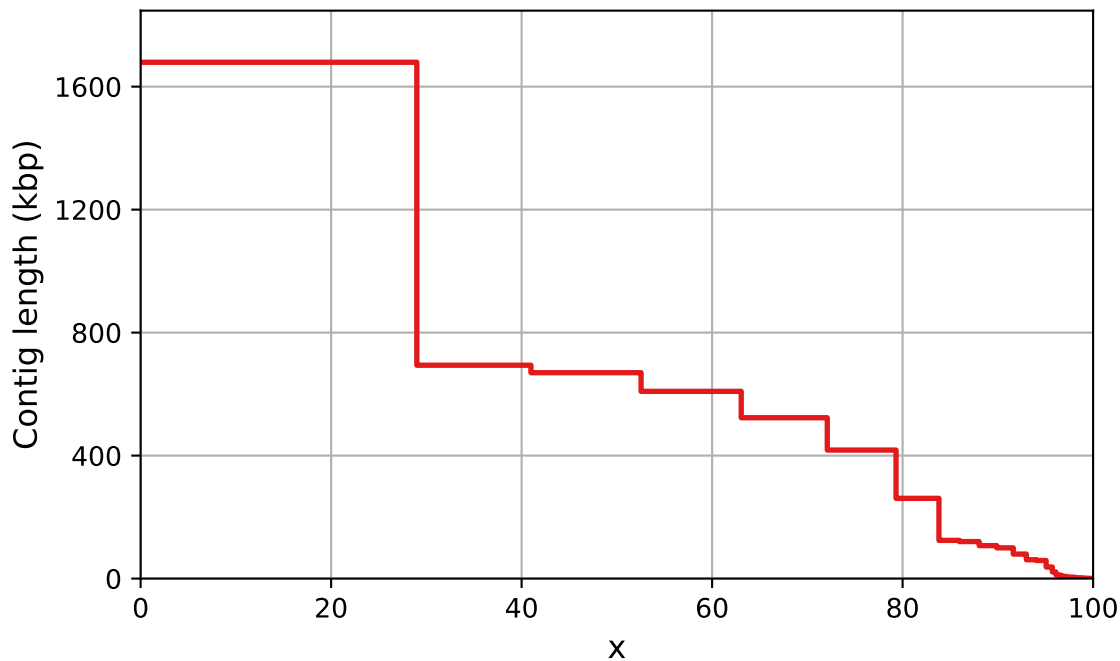


# Report

	genome.nextpolish
# contigs (>= 0 bp)	2514
# contigs (>= 1000 bp)	74
# contigs (>= 5000 bp)	28
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	14
Total length (>= 0 bp)	6381334
Total length (>= 1000 bp)	5757938
Total length (>= 5000 bp)	5654933
Total length (>= 10000 bp)	5598893
Total length (>= 25000 bp)	5543316
Total length (>= 50000 bp)	5505616
# contigs	124
Largest contig	1679237
Total length	5791117
GC (%)	56.83
N50	669601
N90	99943
auN	812464.5
L50	3
L90	11
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	21 + 1 part

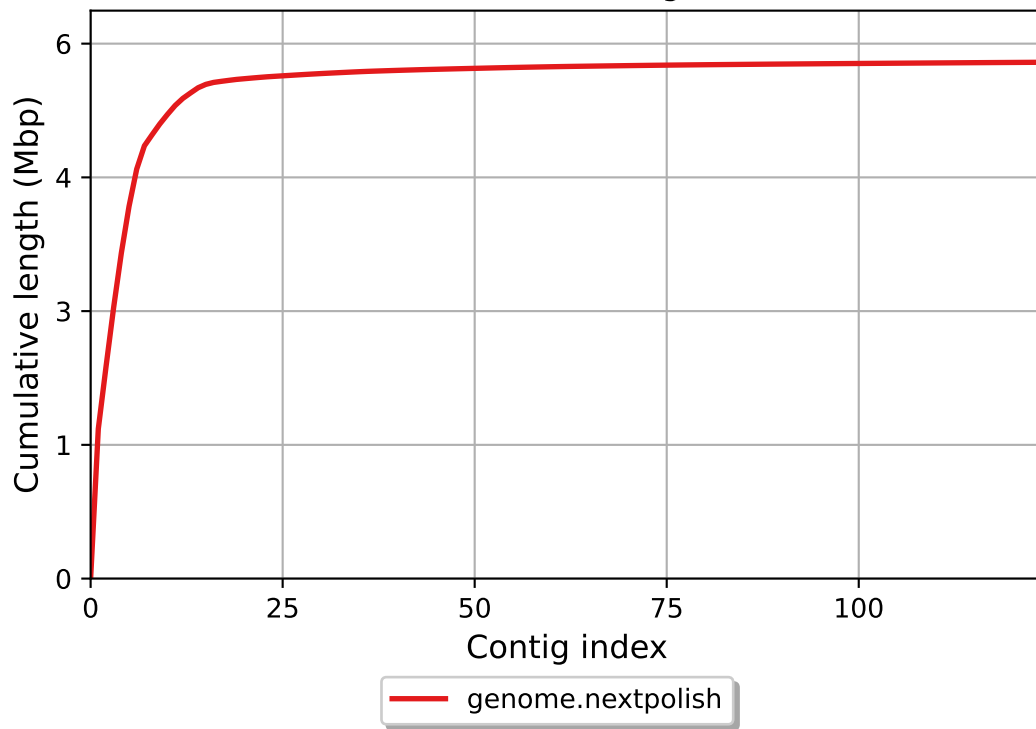
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

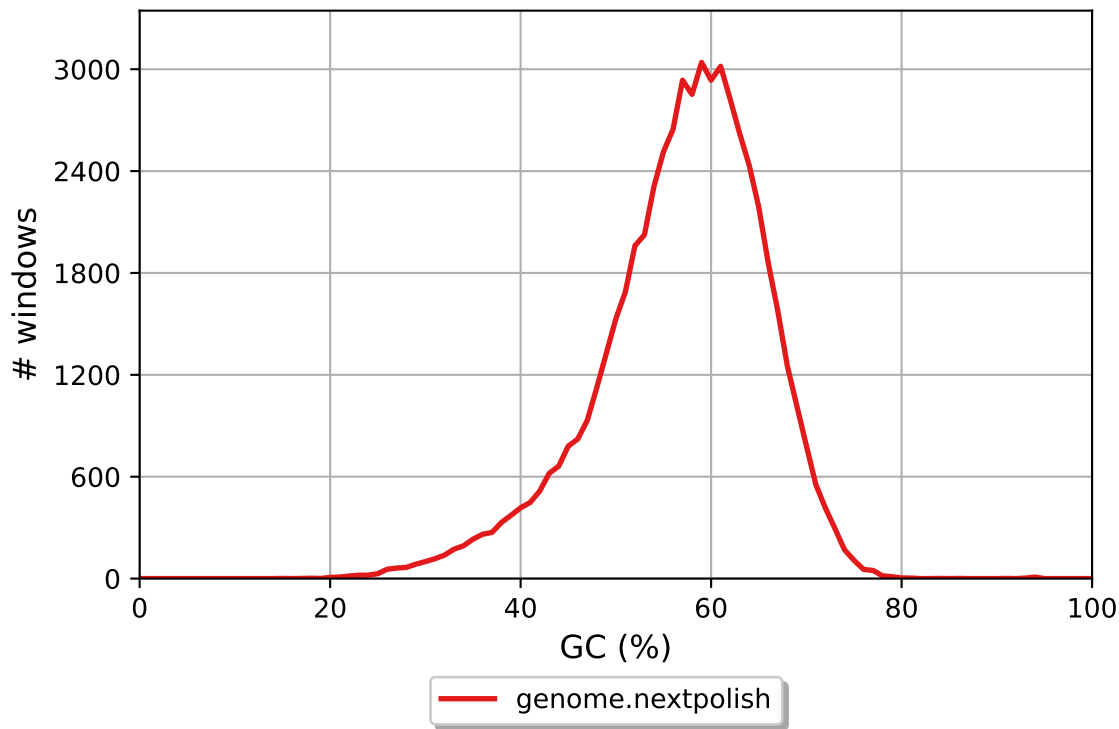


— genome.nextpolish

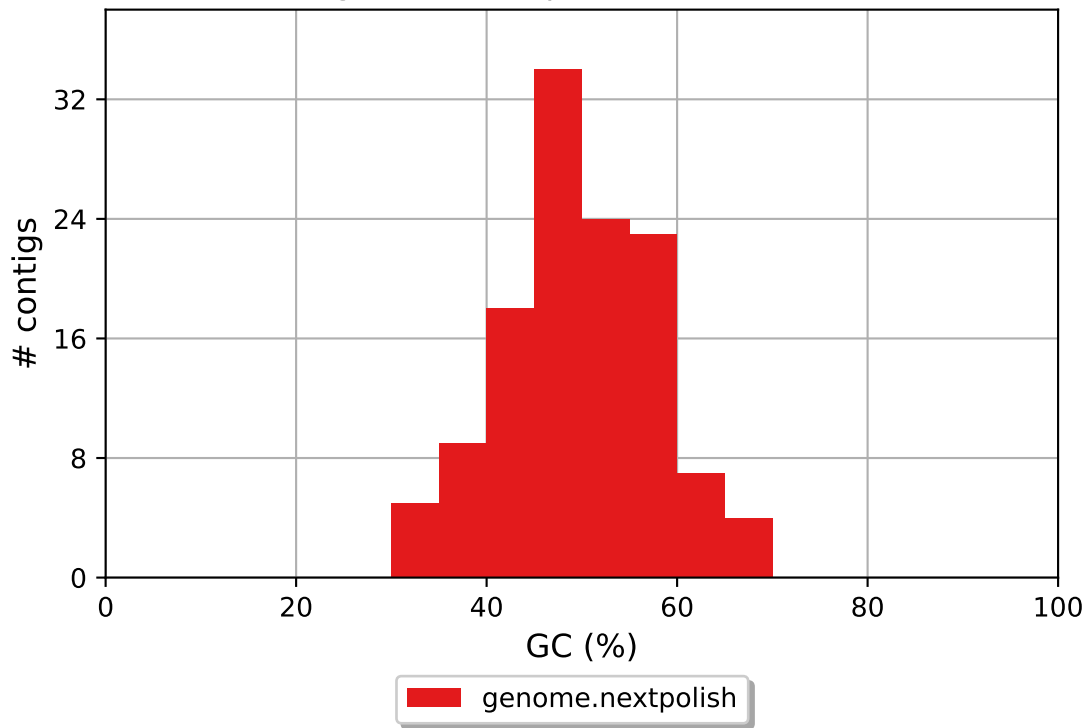
Cumulative length



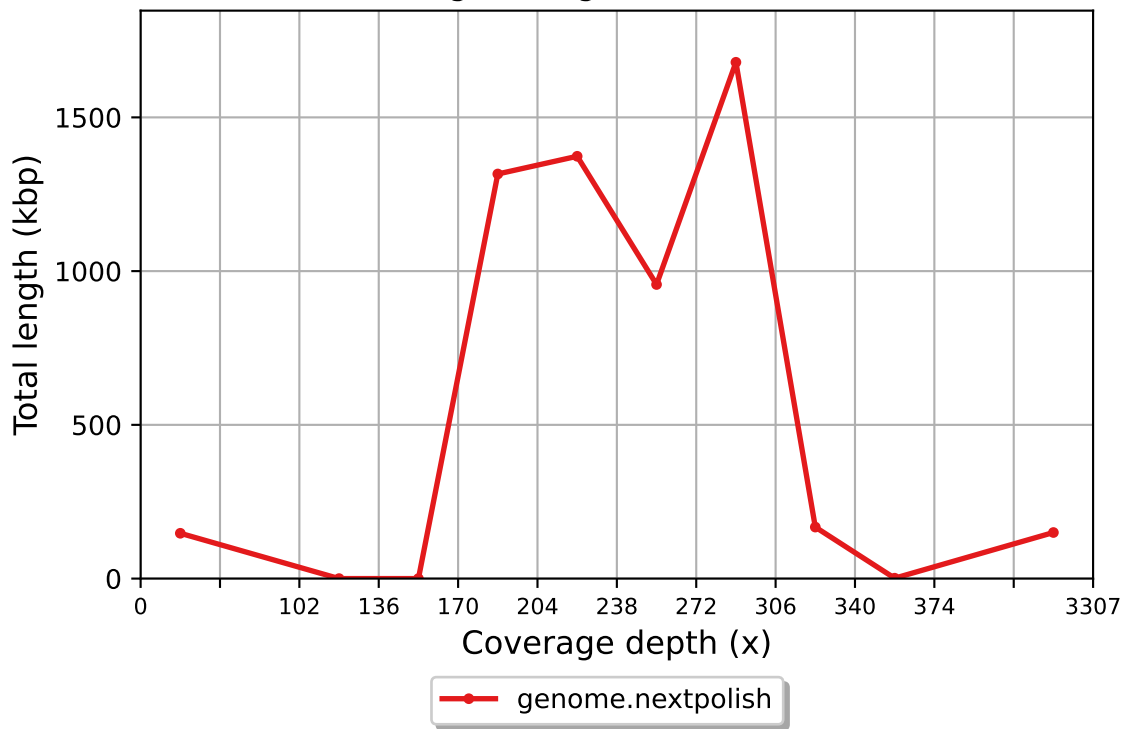
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 34x)



genome.nextpolish coverage histogram (bin size: 34x)

