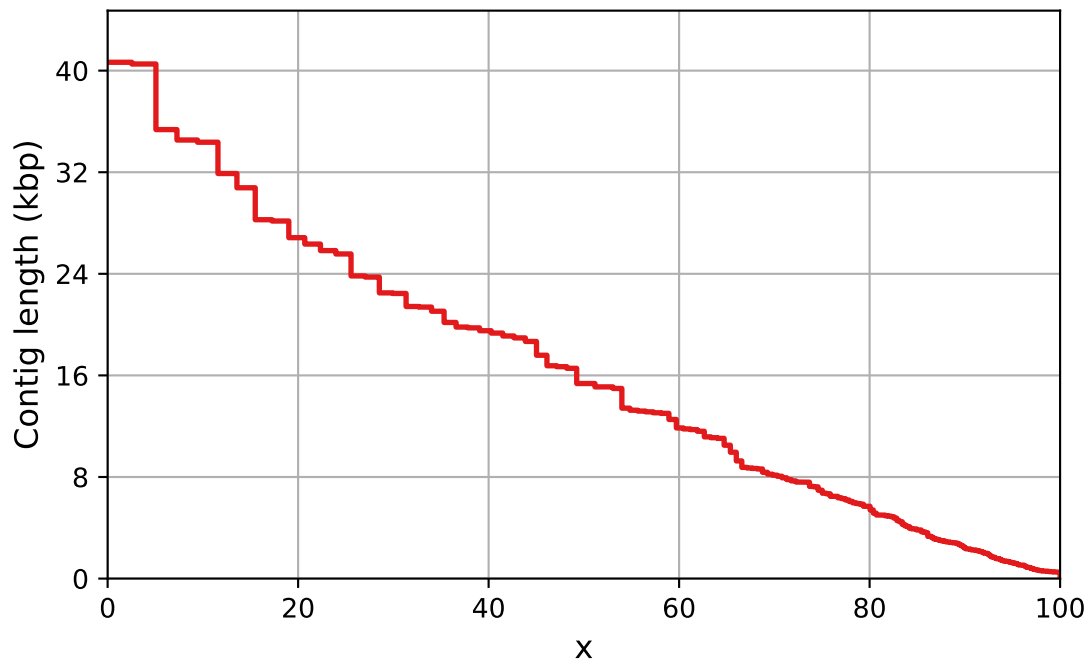


Report

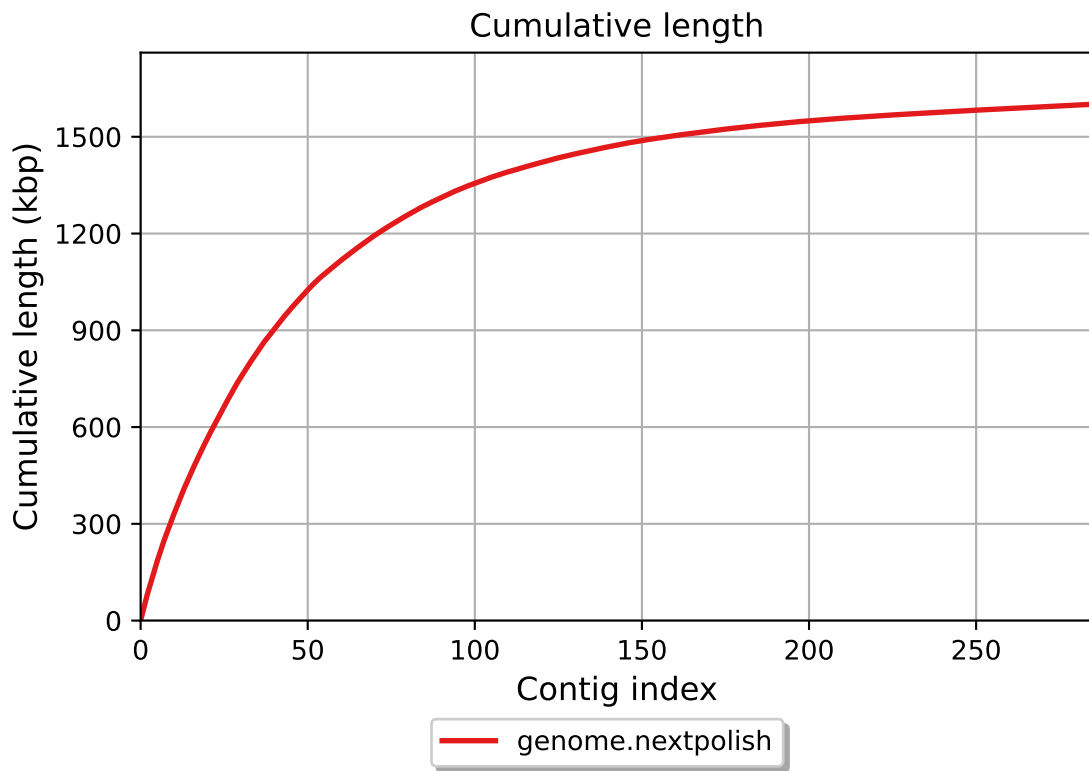
	genome.nextpolish
# contigs (>= 0 bp)	669
# contigs (>= 1000 bp)	191
# contigs (>= 5000 bp)	88
# contigs (>= 10000 bp)	52
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1734126
Total length (>= 1000 bp)	1541384
Total length (>= 5000 bp)	1302033
Total length (>= 10000 bp)	1046655
Total length (>= 25000 bp)	409106
Total length (>= 50000 bp)	0
# contigs	285
Largest contig	40658
Total length	1600830
GC (%)	38.80
N50	15361
N90	2420
auN	16769.1
L50	33
L90	128
# N's per 100 kbp	3.69
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	2 + 0 part

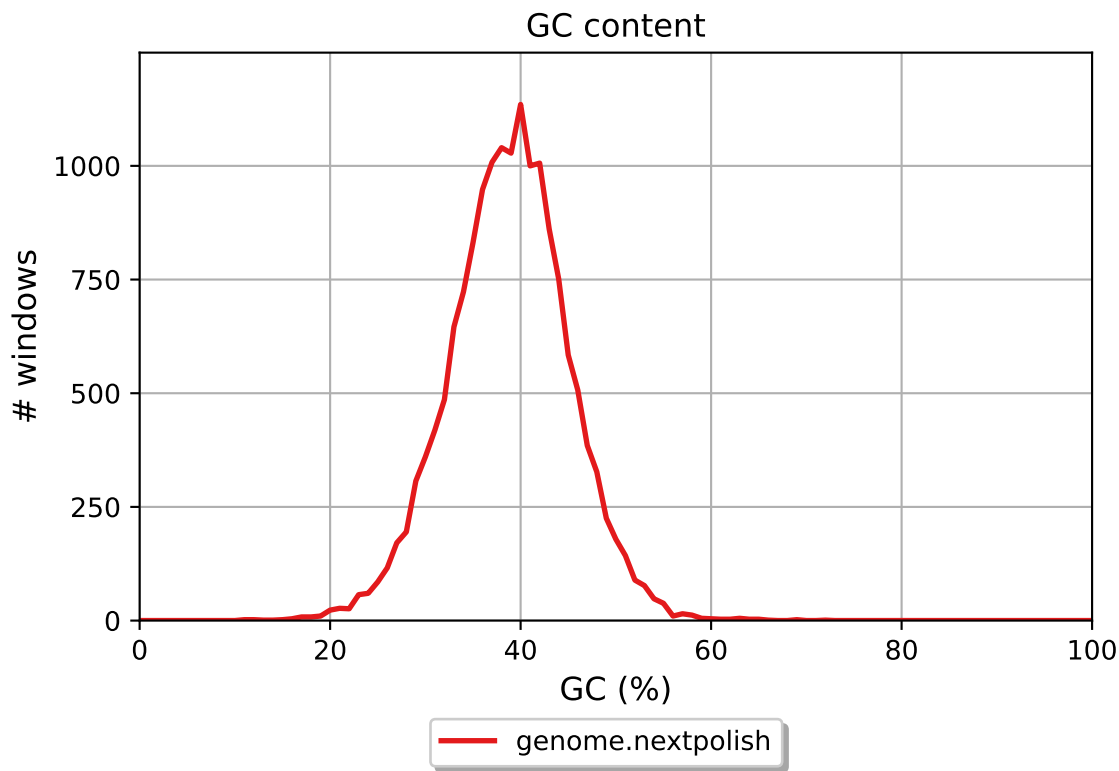
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

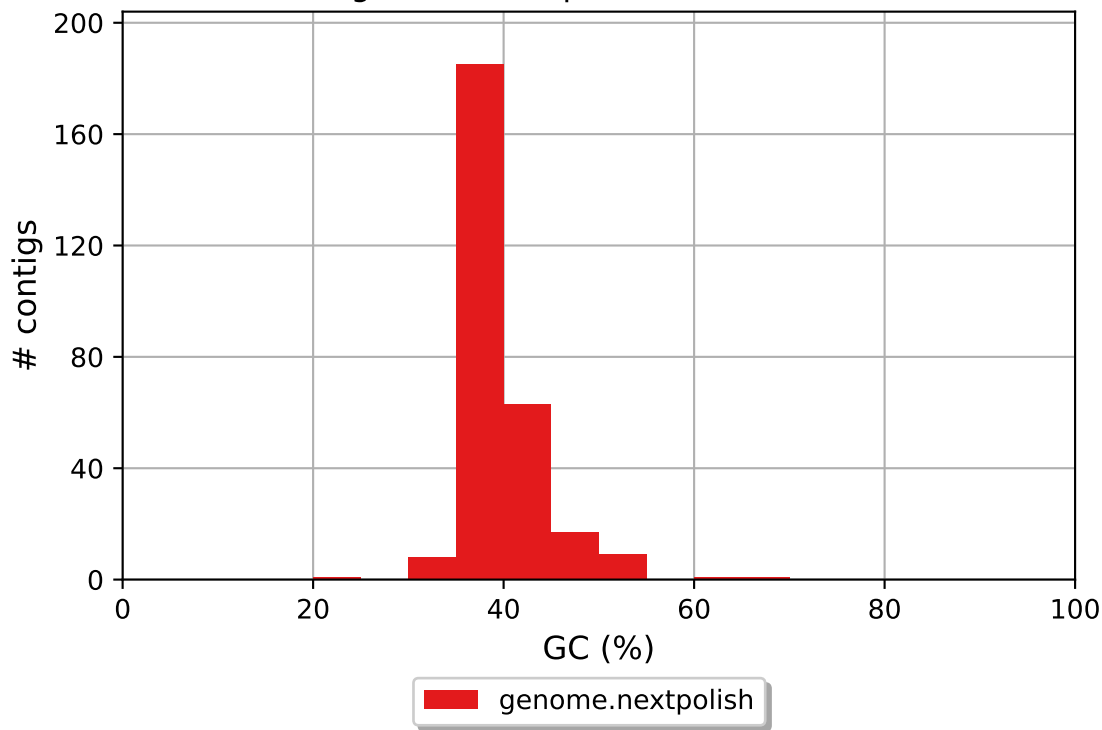


— genome.nextpolish

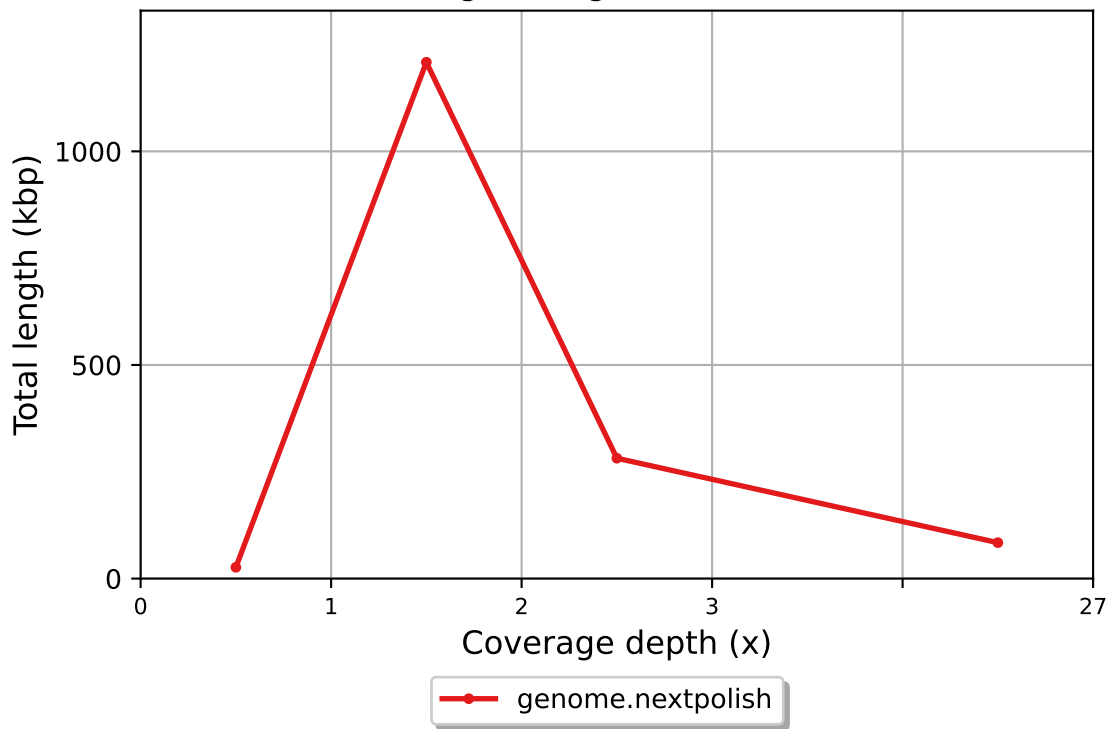




genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

