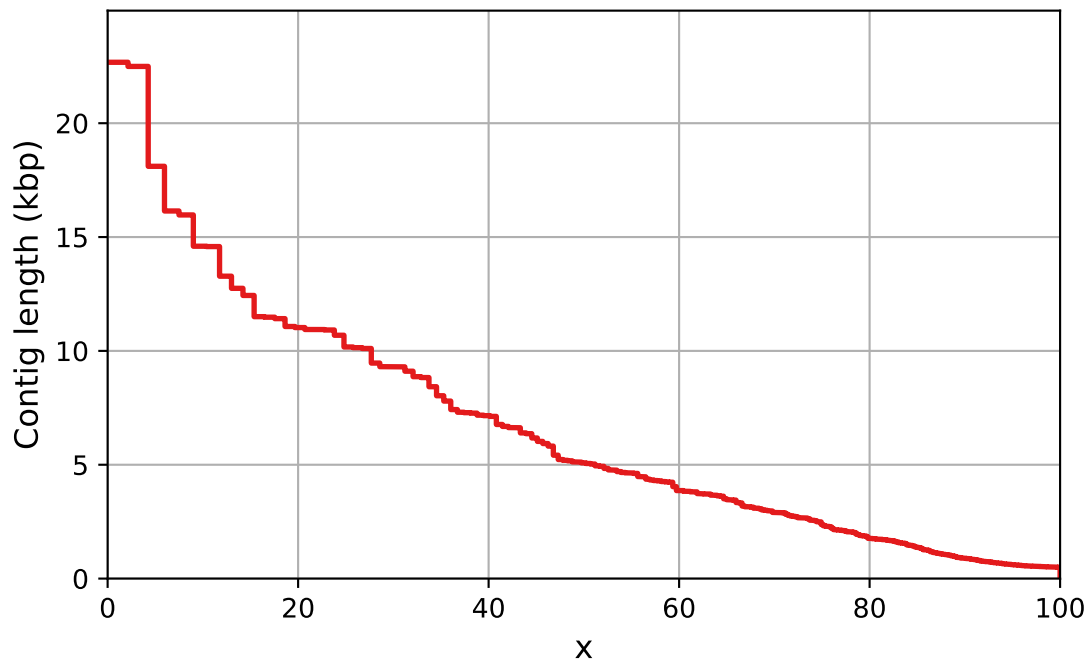


Report

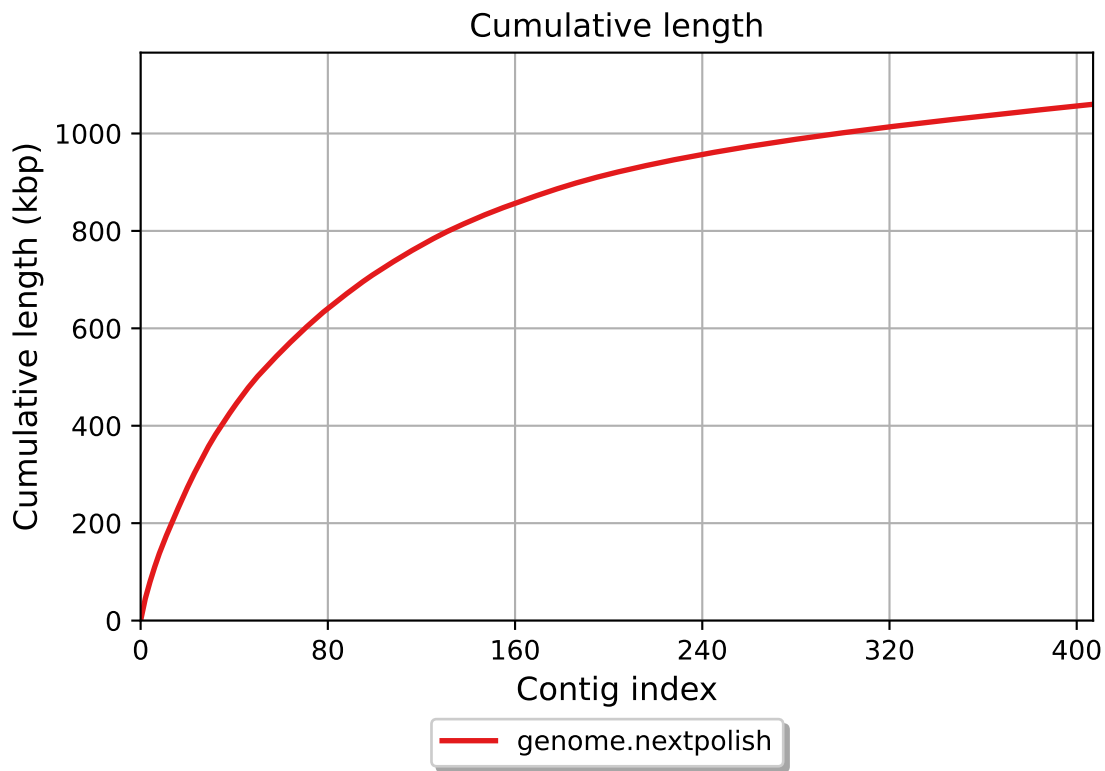
	genome.nextpolish
# contigs (>= 0 bp)	934
# contigs (>= 1000 bp)	221
# contigs (>= 5000 bp)	58
# contigs (>= 10000 bp)	22
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1249357
Total length (>= 1000 bp)	939285
Total length (>= 5000 bp)	542453
Total length (>= 10000 bp)	293437
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	407
Largest contig	22676
Total length	1059992
GC (%)	38.87
N50	5083
N90	896
auN	6842.6
L50	56
L90	237
# N's per 100 kbp	1.89
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	3 + 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).

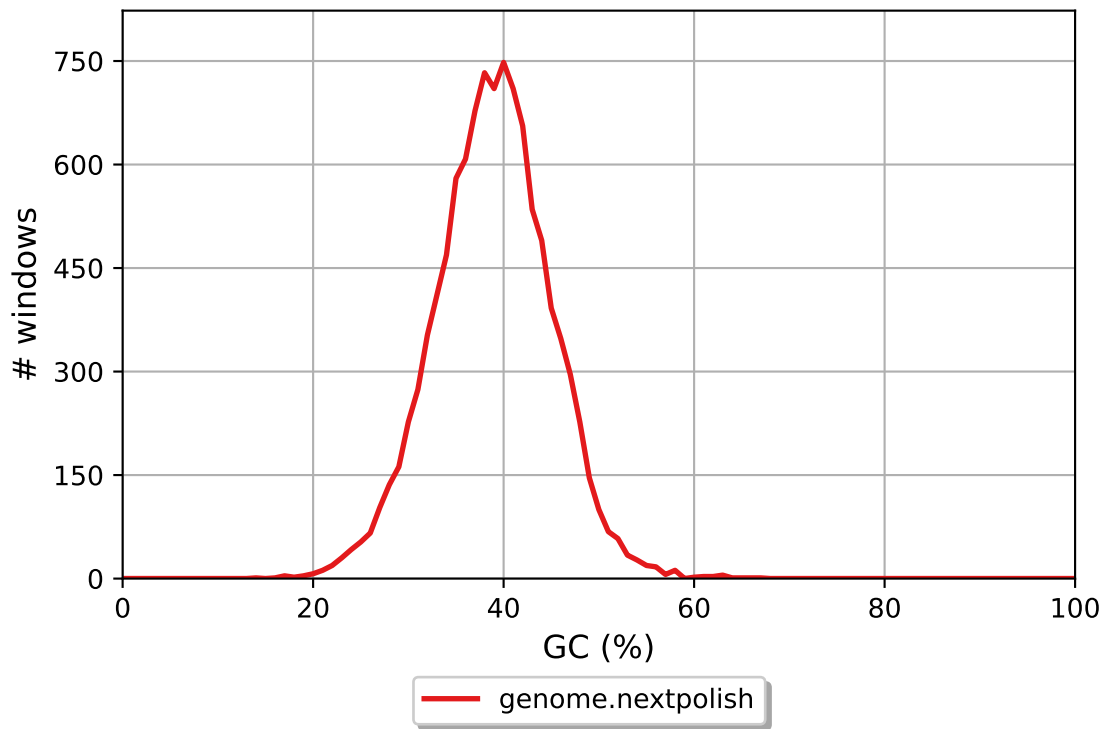
Nx



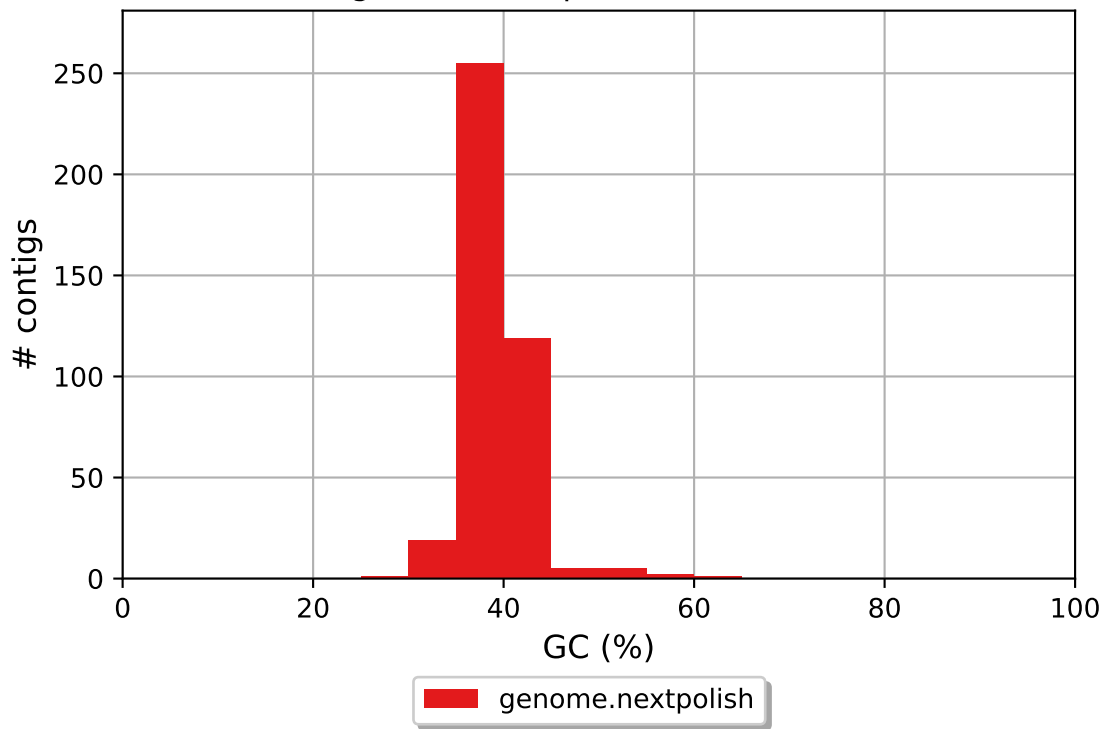
— genome.nextpolish



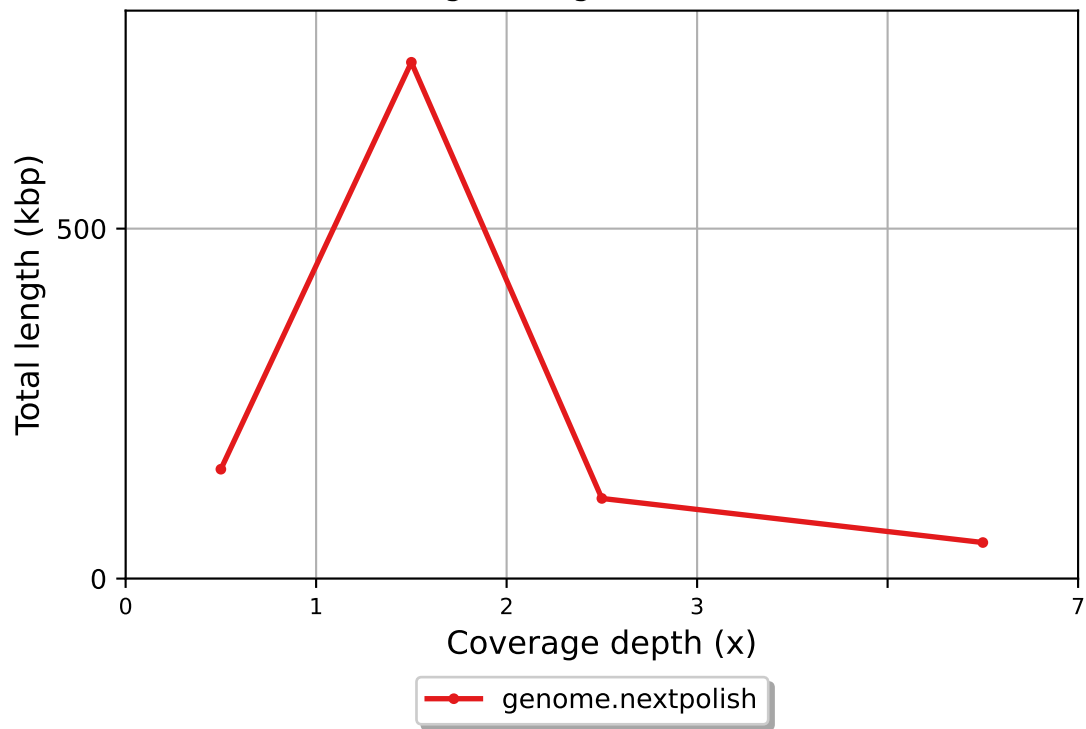
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

