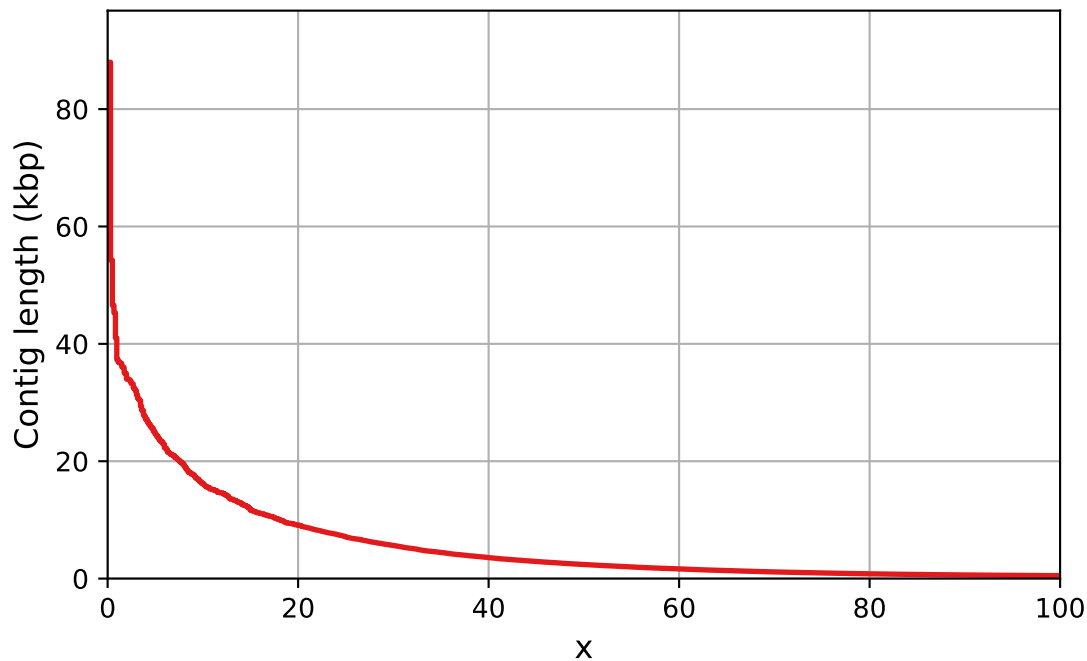


Report

	genome.nextpolish
# contigs (>= 0 bp)	165050
# contigs (>= 1000 bp)	6956
# contigs (>= 5000 bp)	894
# contigs (>= 10000 bp)	297
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	68313535
Total length (>= 1000 bp)	21060948
Total length (>= 5000 bp)	9276828
Total length (>= 10000 bp)	5151303
Total length (>= 25000 bp)	1416469
Total length (>= 50000 bp)	142259
# contigs	18175
Largest contig	87981
Total length	28537052
GC (%)	41.80
N50	2400
N90	615
auN	6092.1
L50	2390
L90	12993
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	27 + 10 part

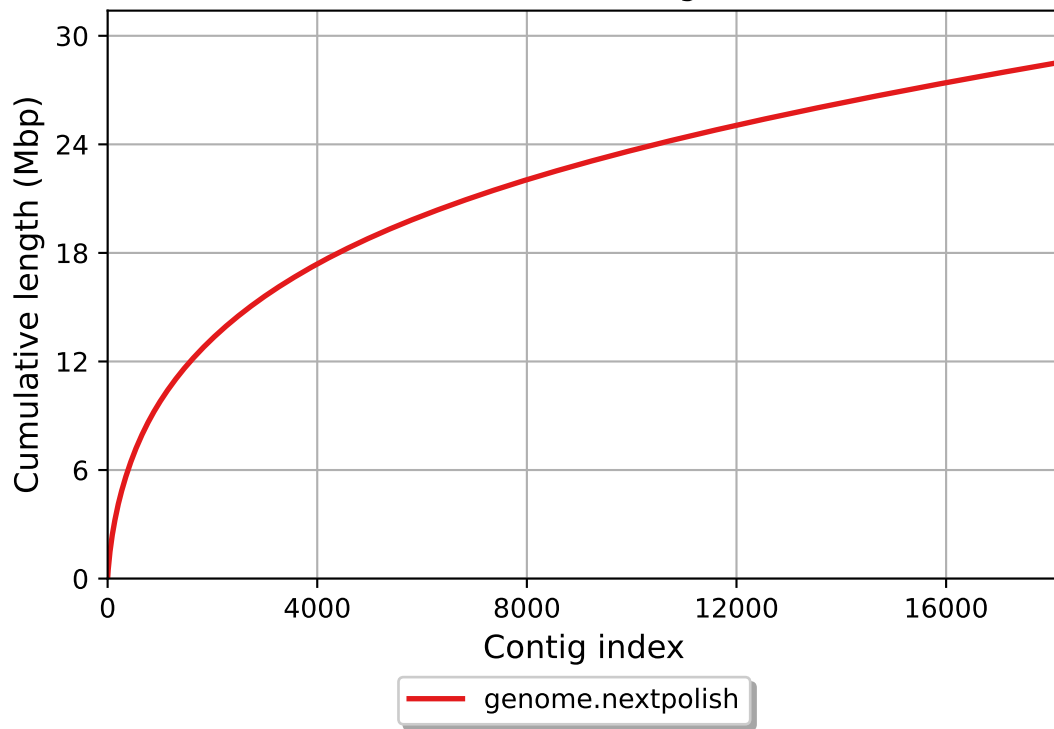
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

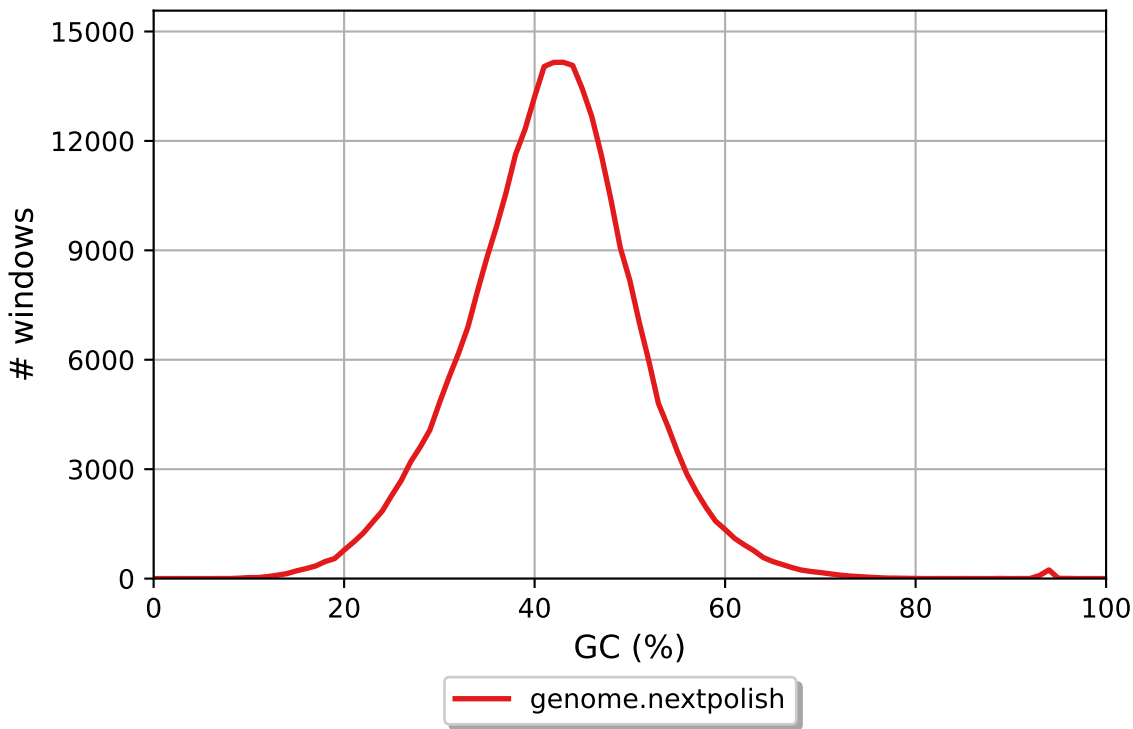


— genome.nextpolish

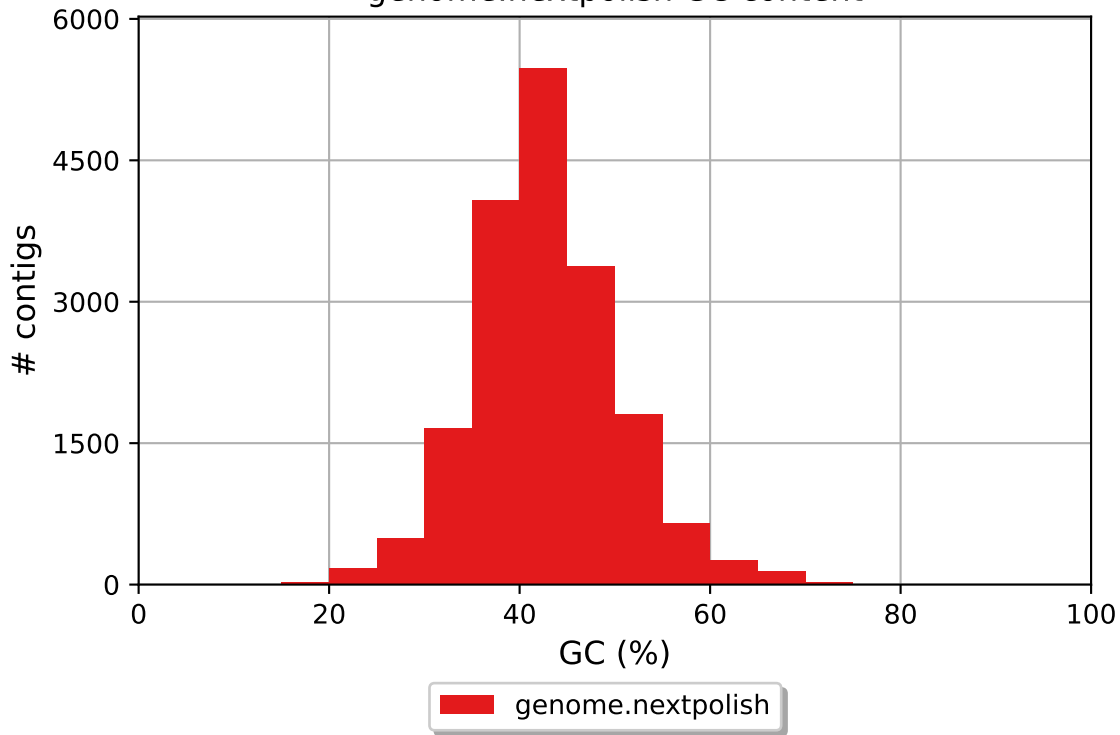
Cumulative length



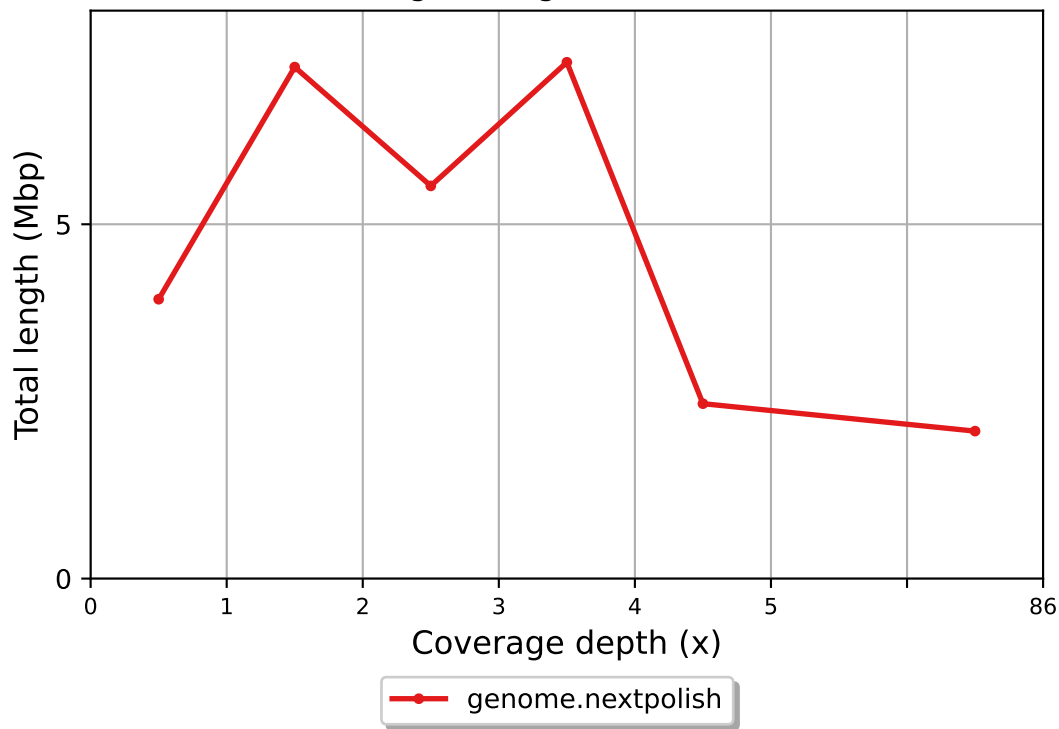
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

