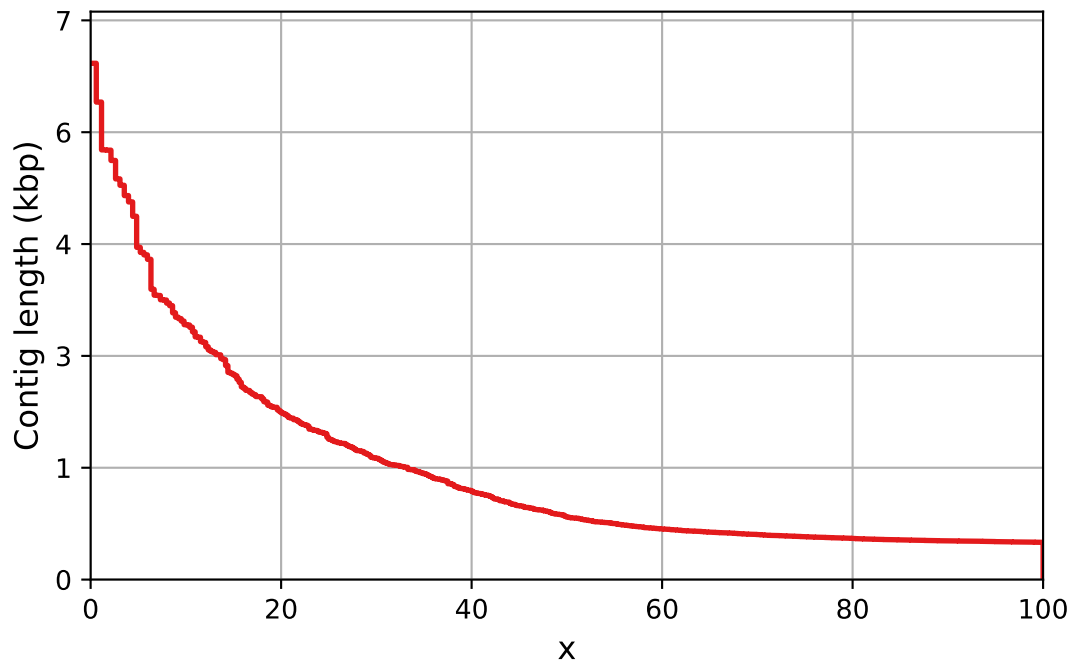


Report

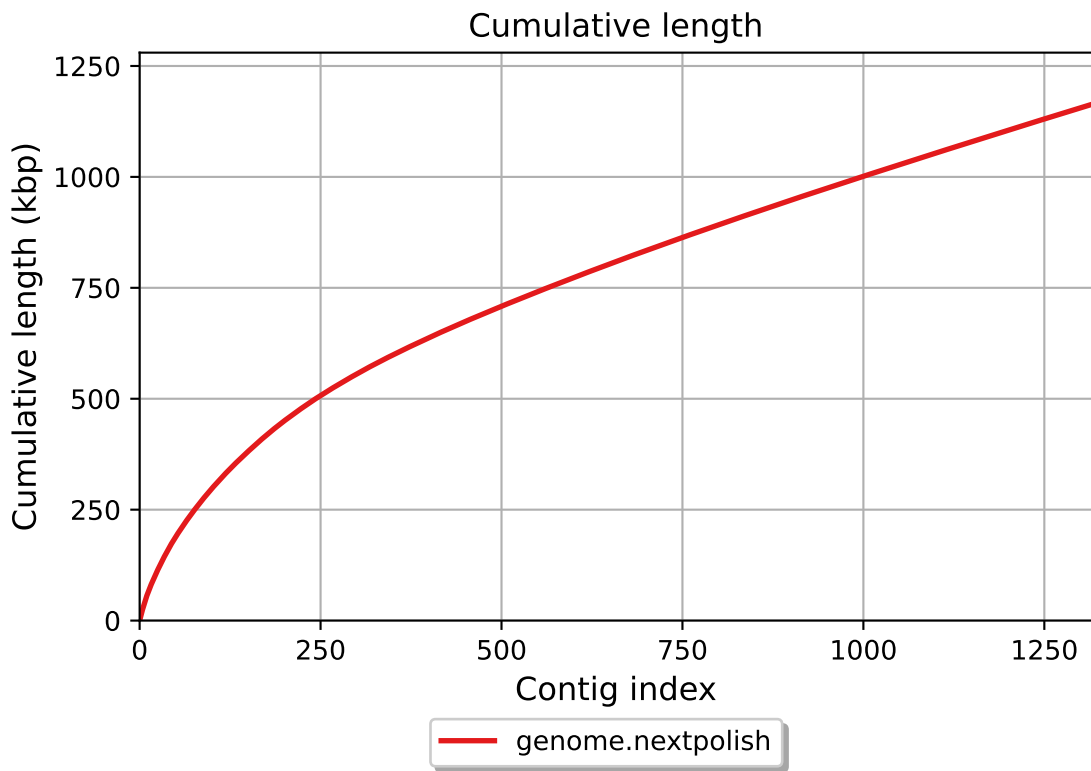
	genome.nextpolish
# contigs (>= 0 bp)	5468
# contigs (>= 1000 bp)	262
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	2837955
Total length (>= 1000 bp)	519498
Total length (>= 5000 bp)	51348
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1316
Largest contig	6924
Total length	1163702
GC (%)	45.56
N50	839
N90	520
auN	1487.9
L50	330
L90	1088
# N's per 100 kbp	0.60
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	6 + 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).

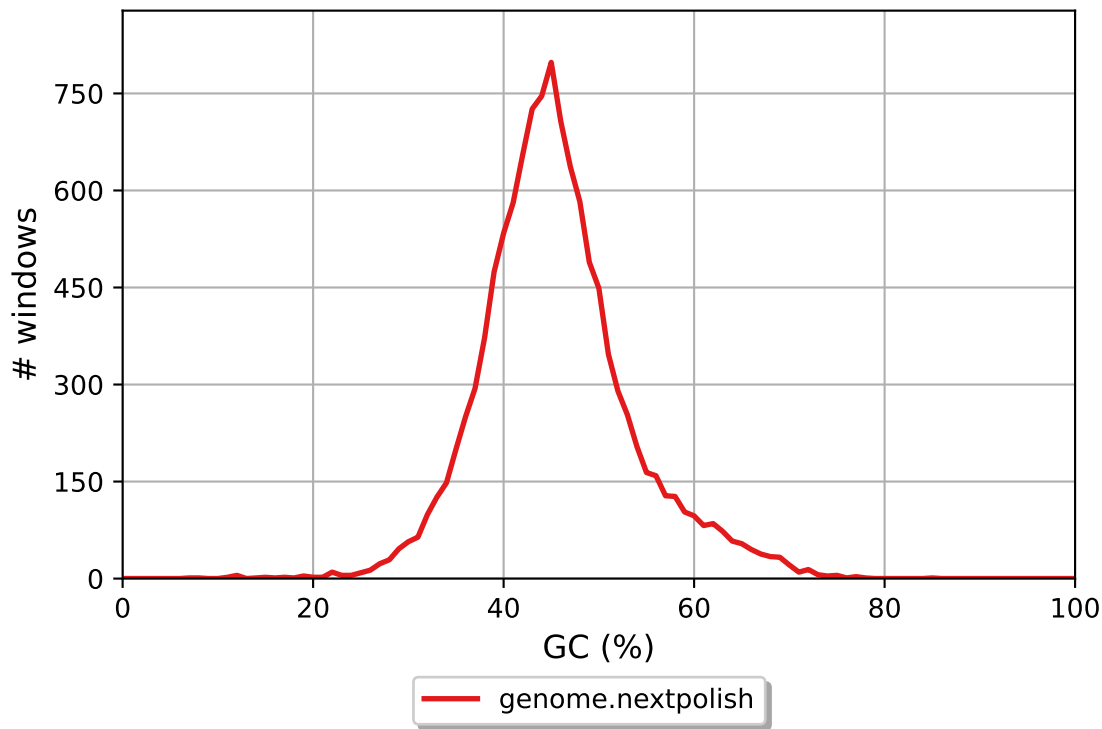
Nx



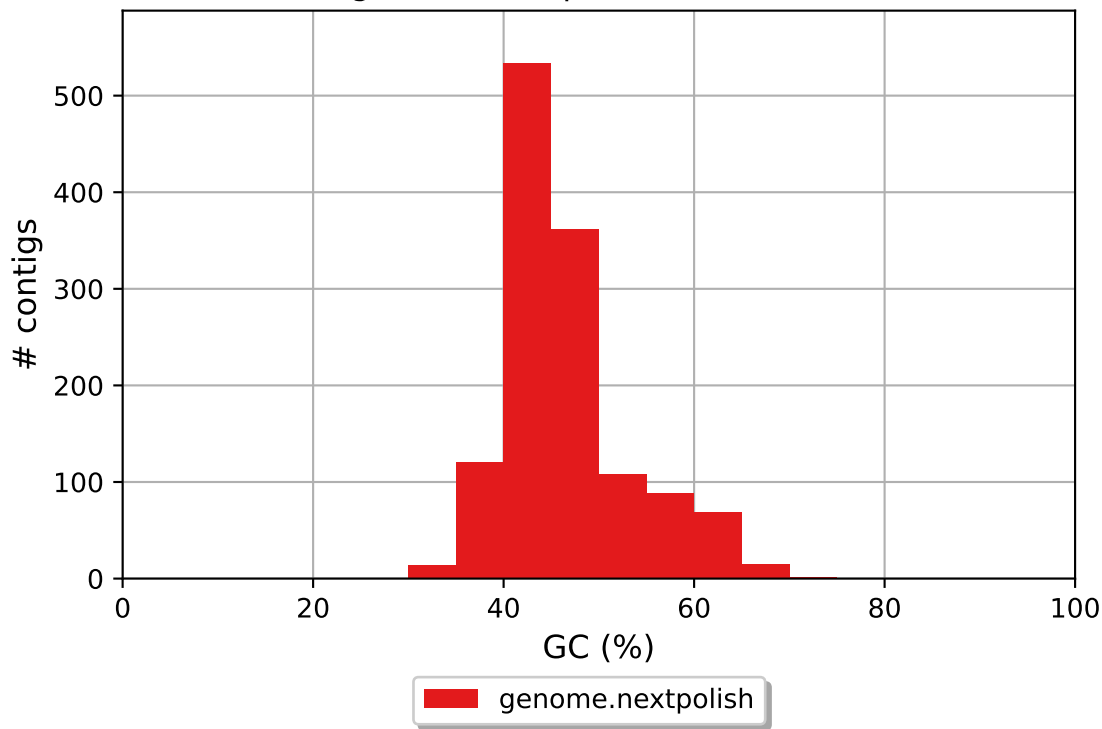
— genome.nextpolish



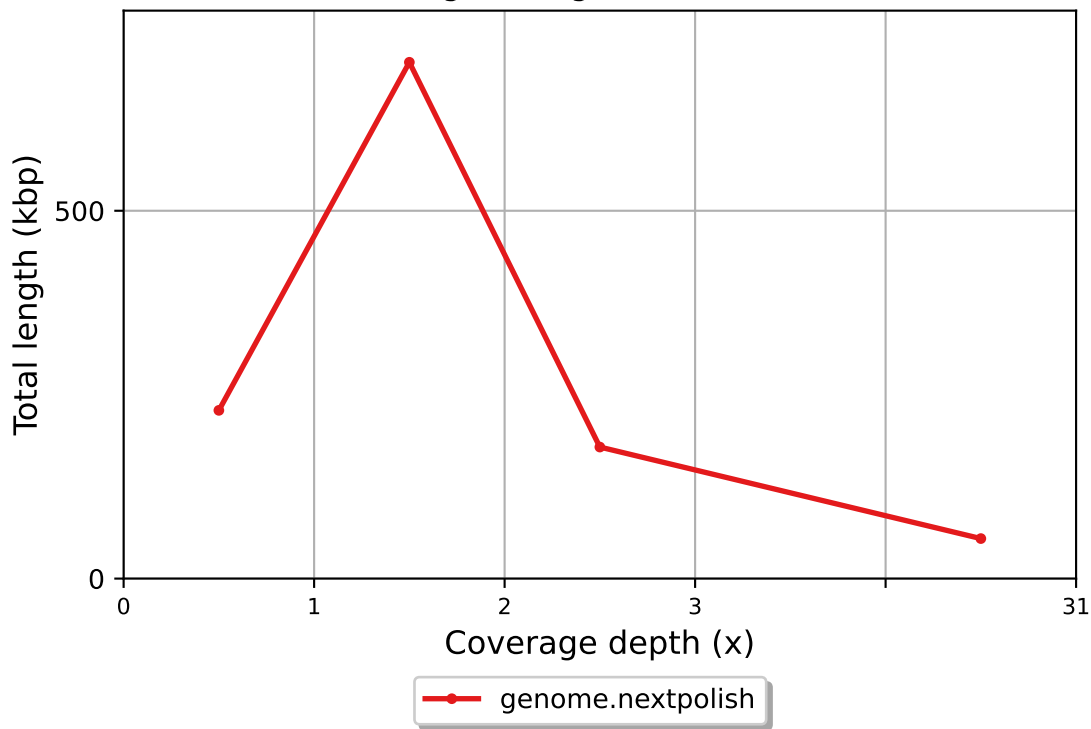
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

