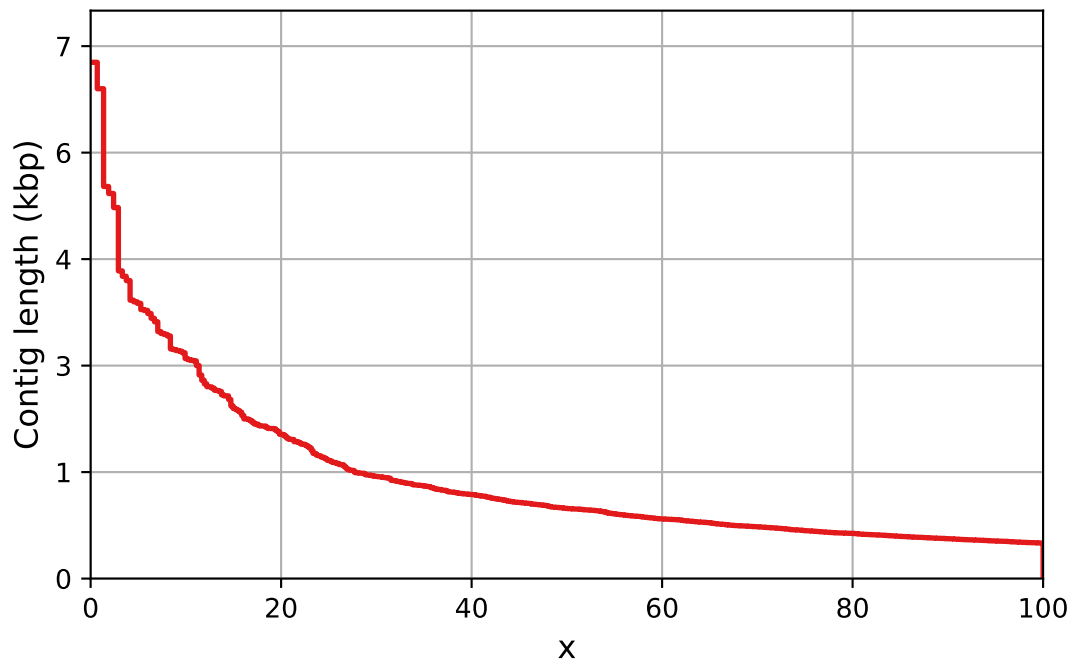


Report

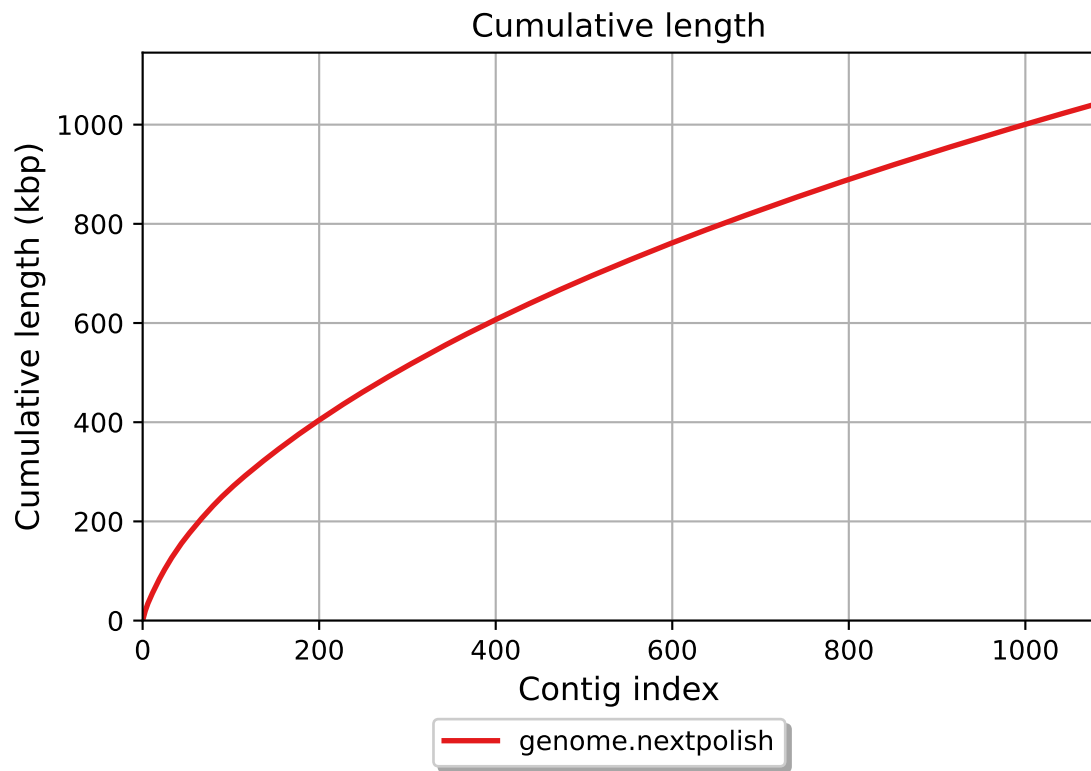
	genome.nextpolish
# contigs (>= 0 bp)	49159
# contigs (>= 1000 bp)	299
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	13009209
Total length (>= 1000 bp)	512625
Total length (>= 5000 bp)	30345
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1079
Largest contig	7272
Total length	1041085
GC (%)	43.98
N50	989
N90	561
auN	1447.3
L50	307
L90	883
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	2 + 2 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).

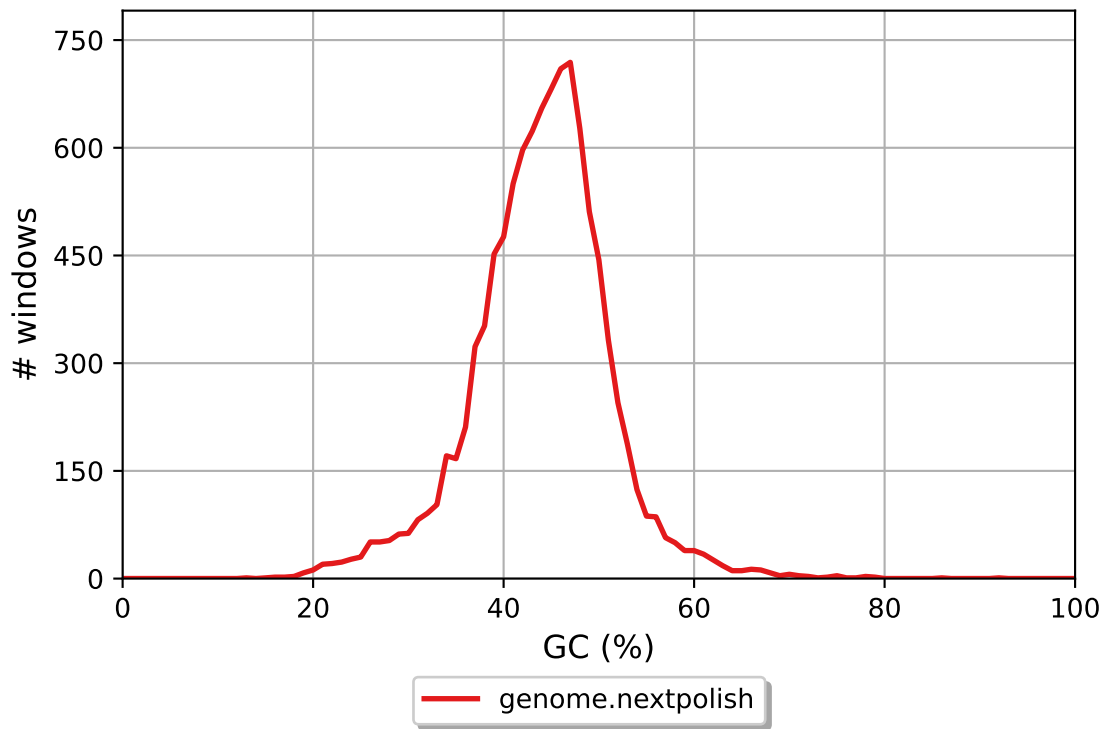
Nx



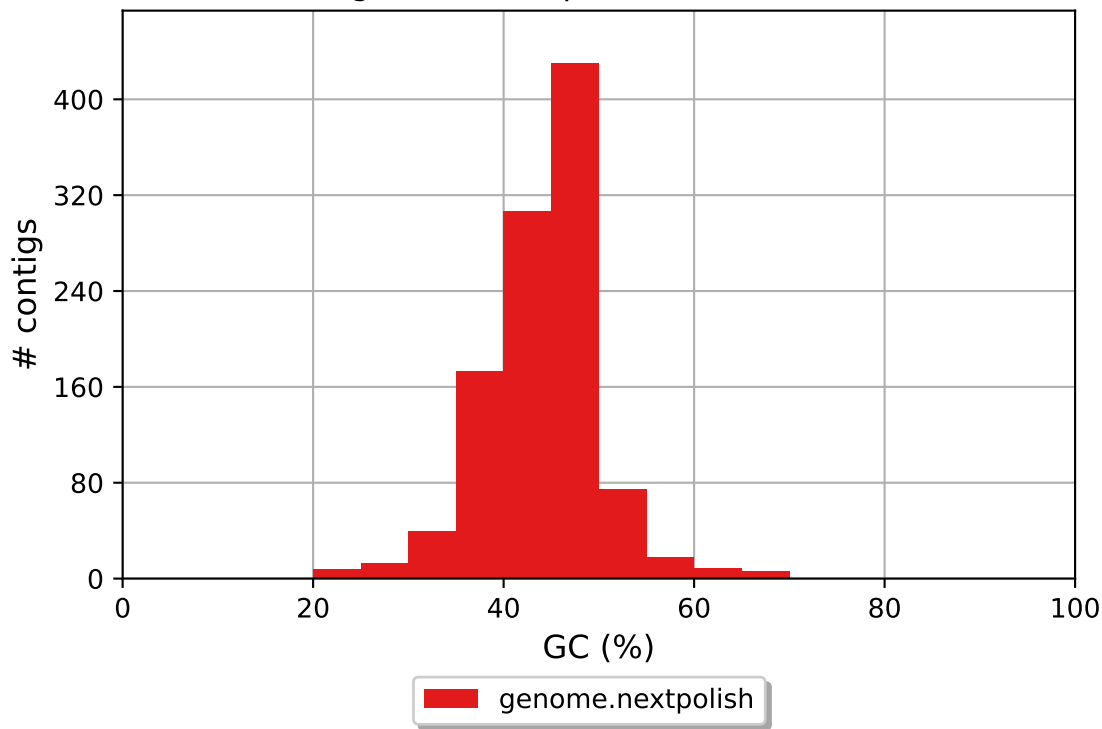
— genome.nextpolish



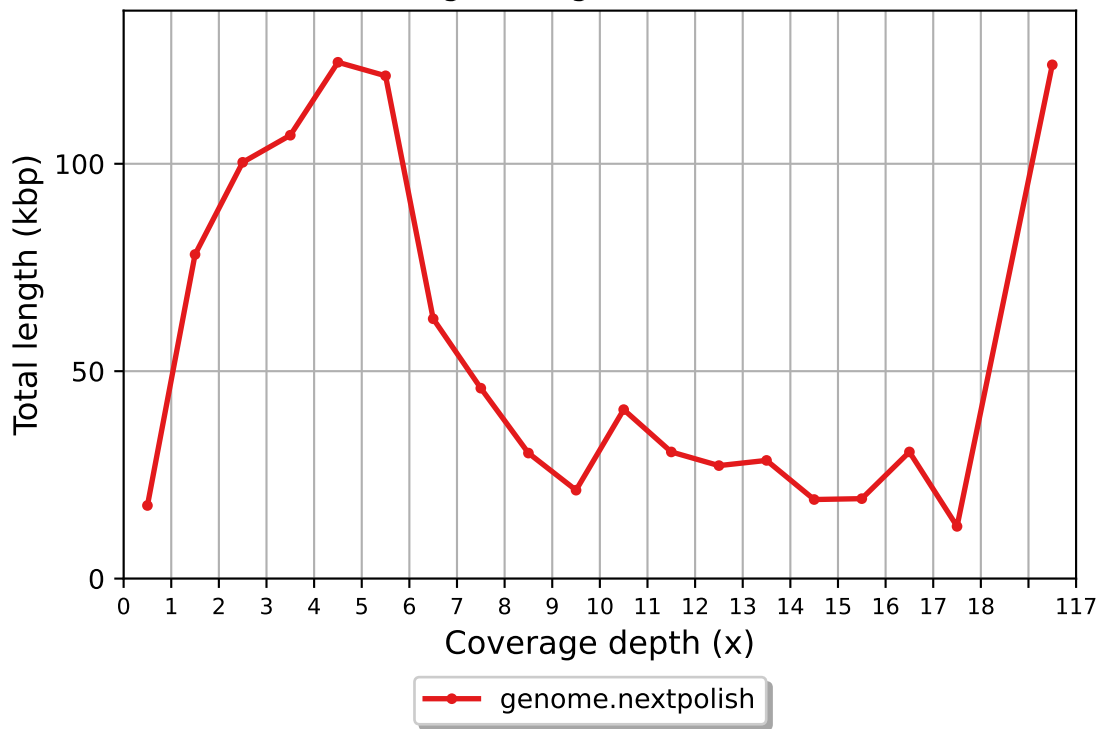
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

