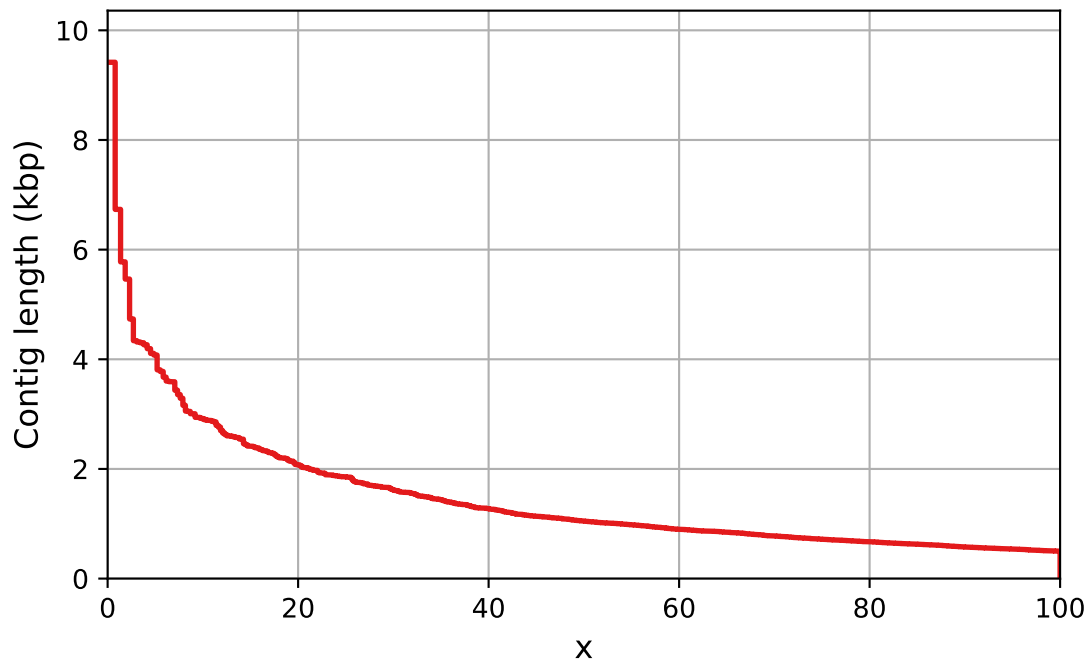


# Report

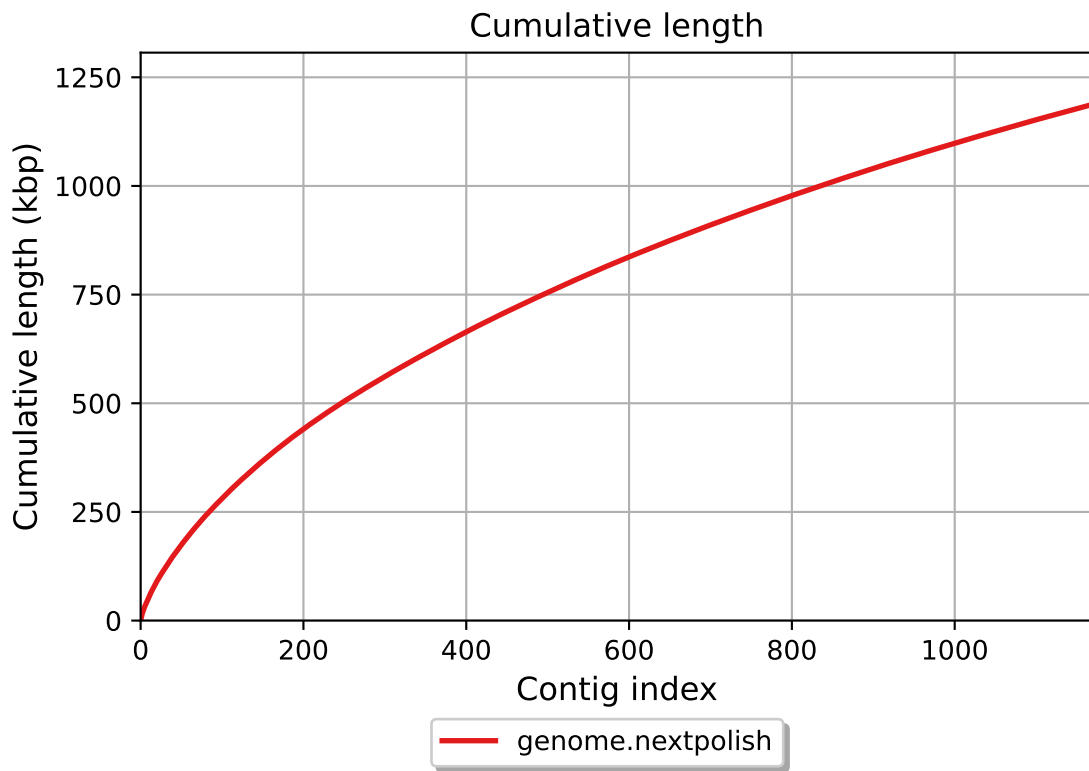
	genome.nextpolish
# contigs (>= 0 bp)	9324
# contigs (>= 1000 bp)	374
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3129532
Total length (>= 1000 bp)	638765
Total length (>= 5000 bp)	27391
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1170
Largest contig	9417
Total length	1187937
GC (%)	44.53
N50	1049
N90	576
auN	1508.6
L50	331
L90	949
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	1 + 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).

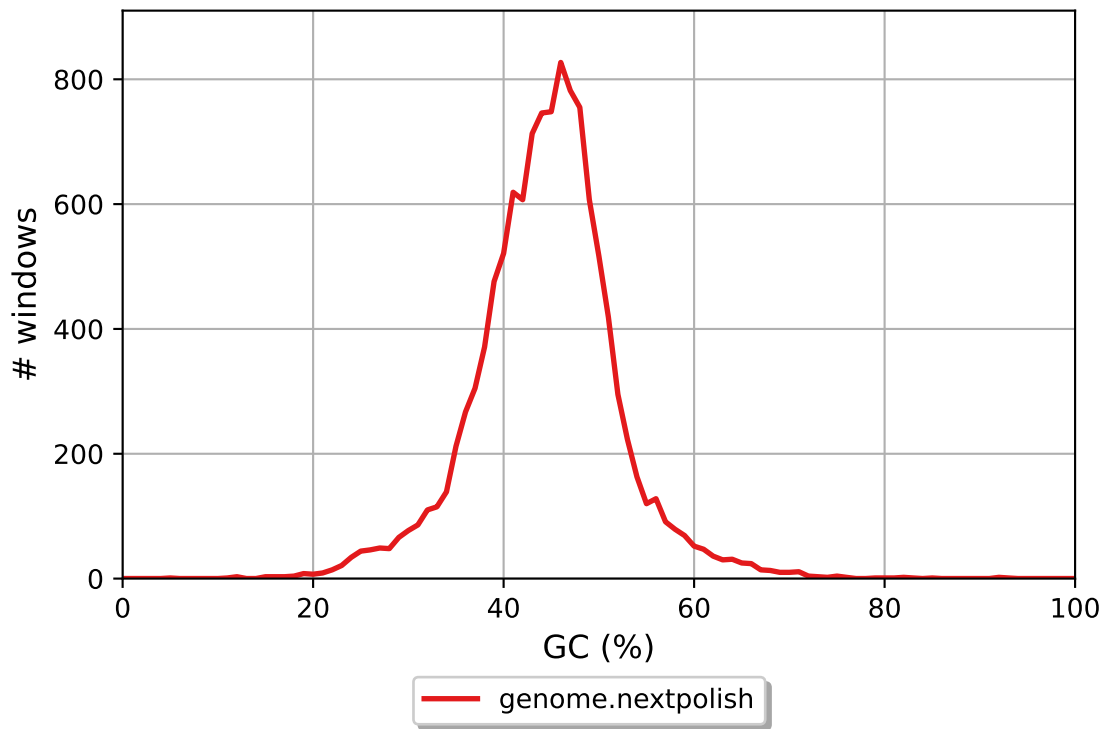
Nx



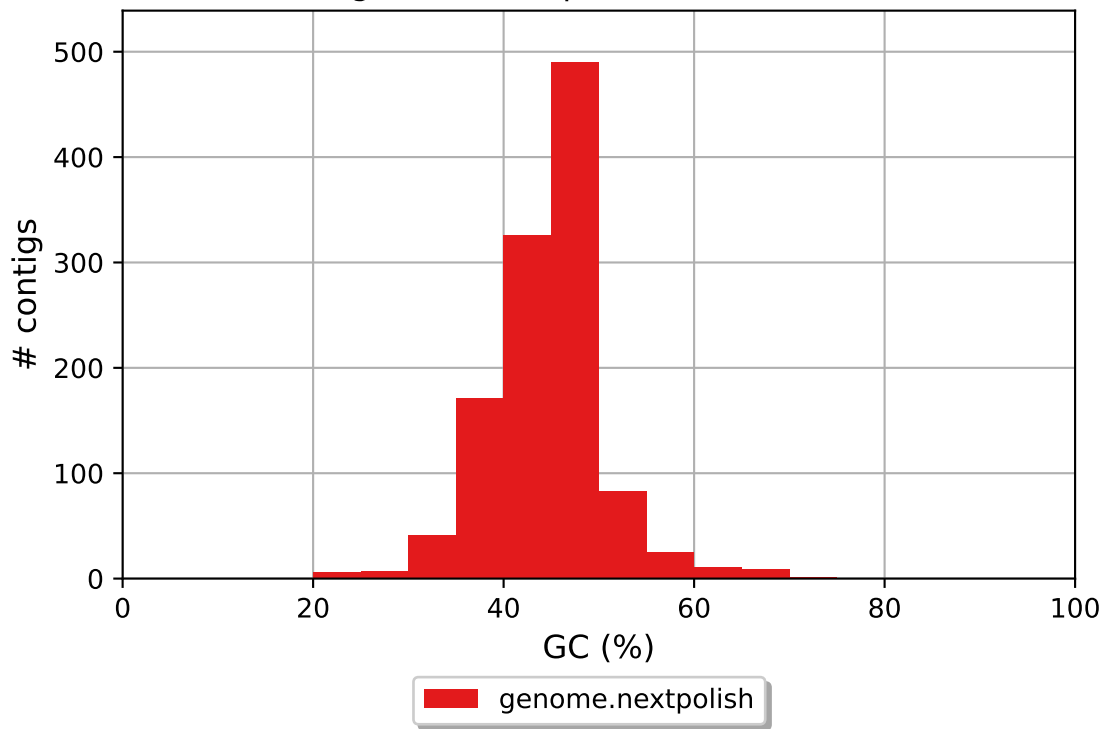
— genome.nextpolish



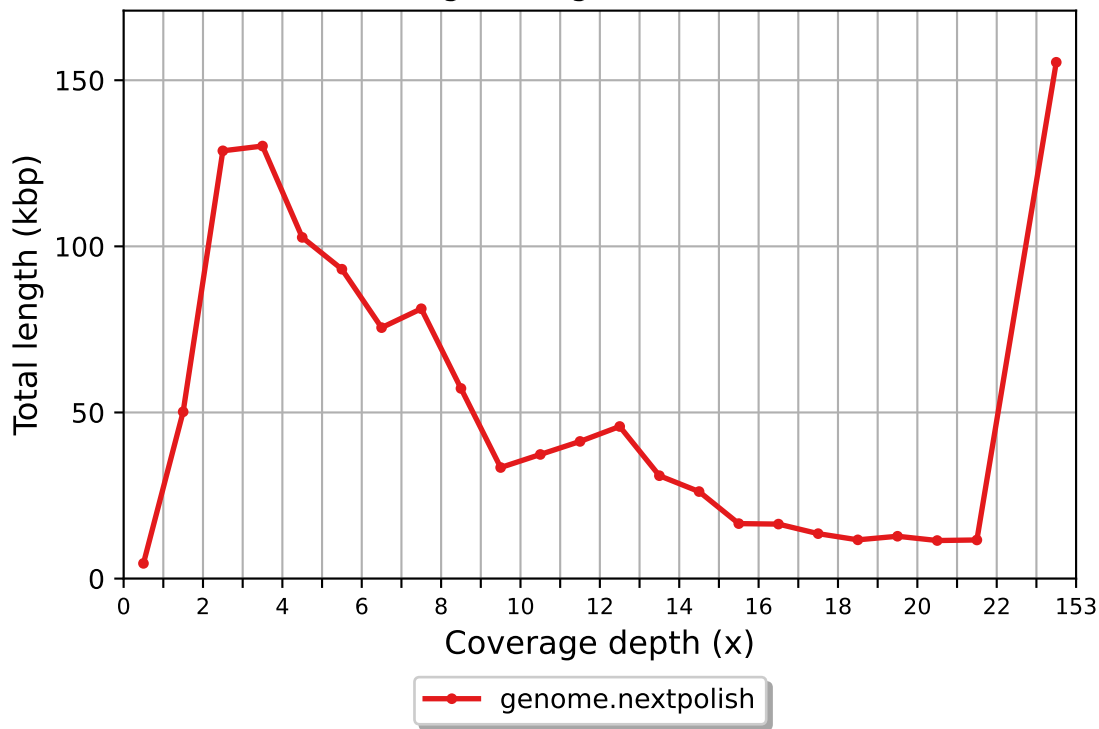
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

