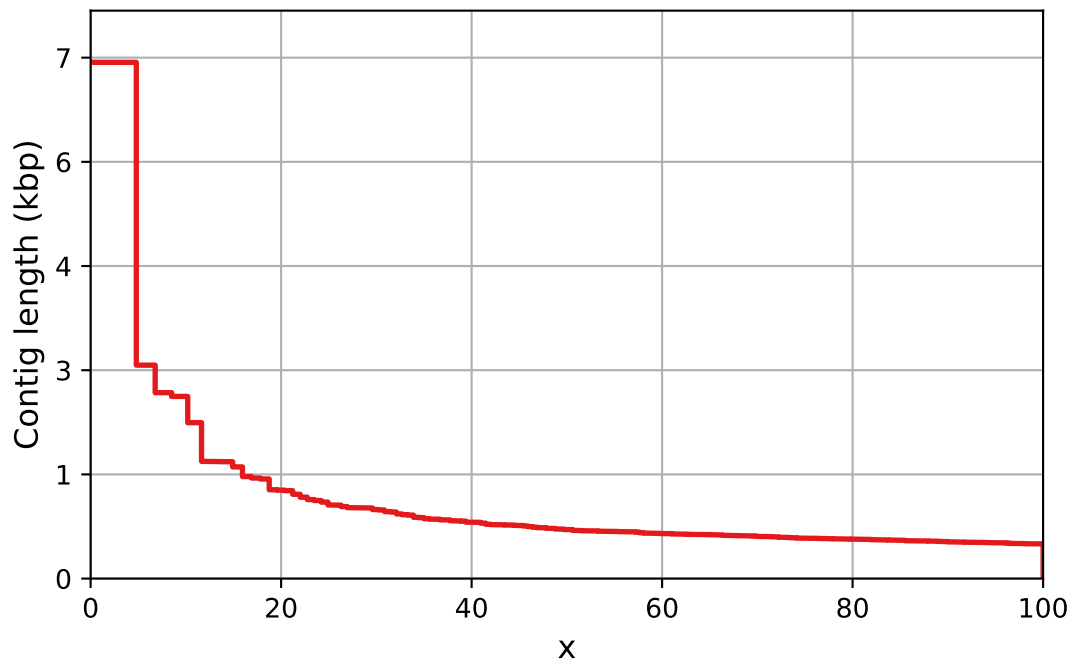


# Report

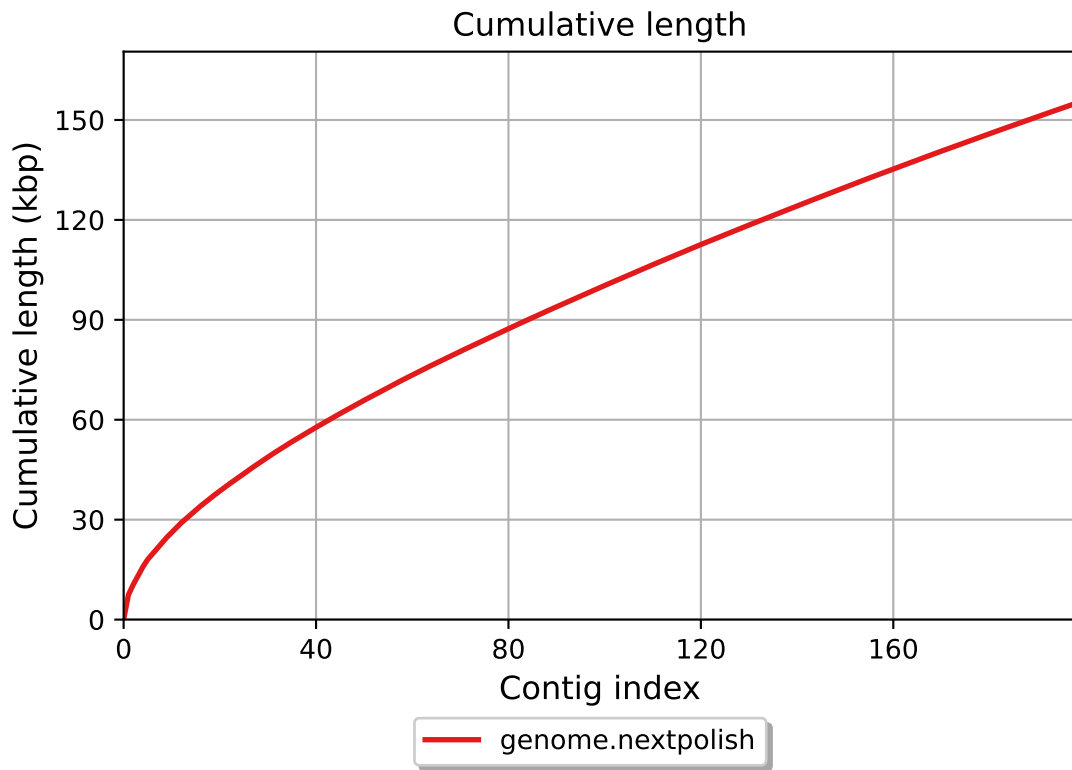
	genome.nextpolish
# contigs (>= 0 bp)	4551
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	990581
Total length (>= 1000 bp)	45860
Total length (>= 5000 bp)	7433
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	198
Largest contig	7433
Total length	155017
GC (%)	46.70
N50	706
N90	532
auN	1239.4
L50	66
L90	168
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	0 + 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).

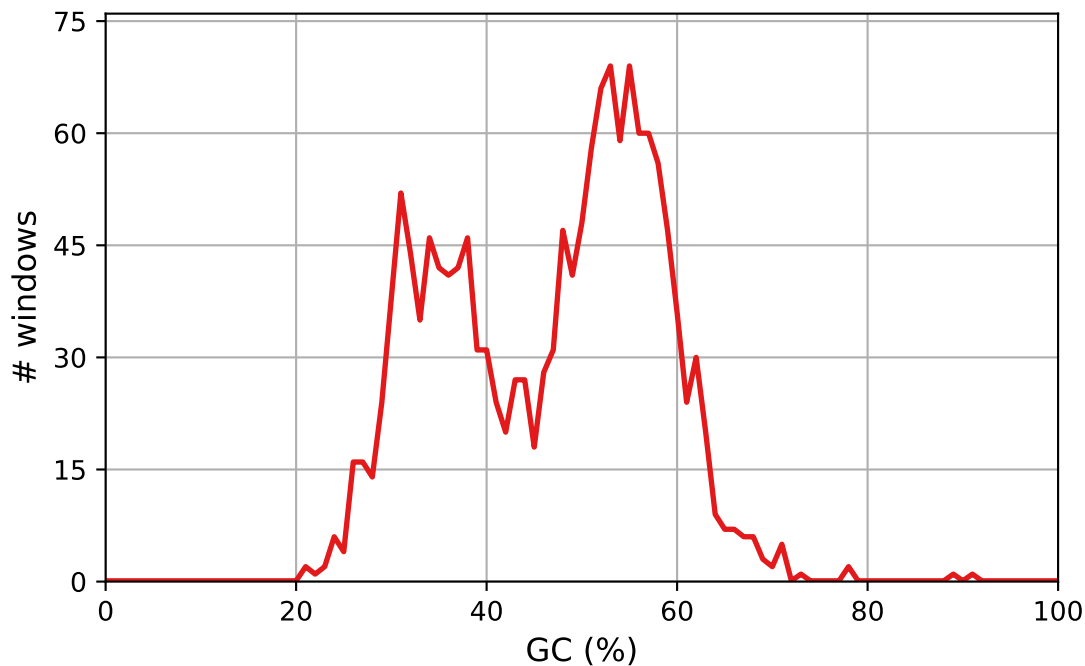
Nx



— genome.nextpolish

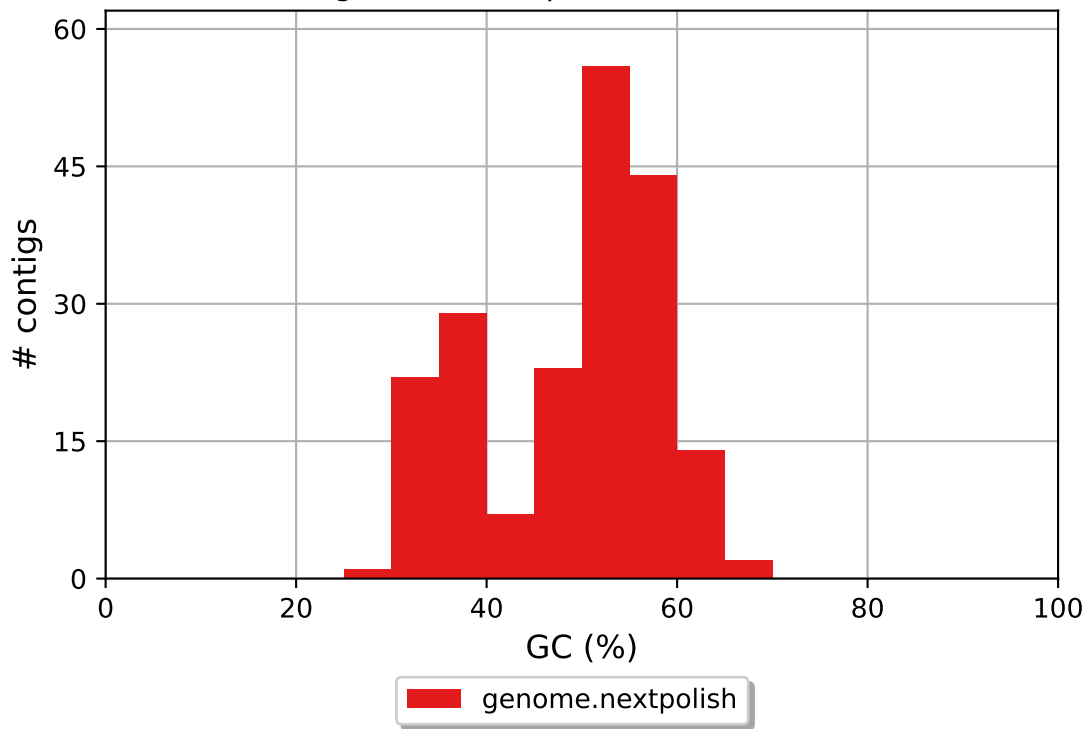


## GC content

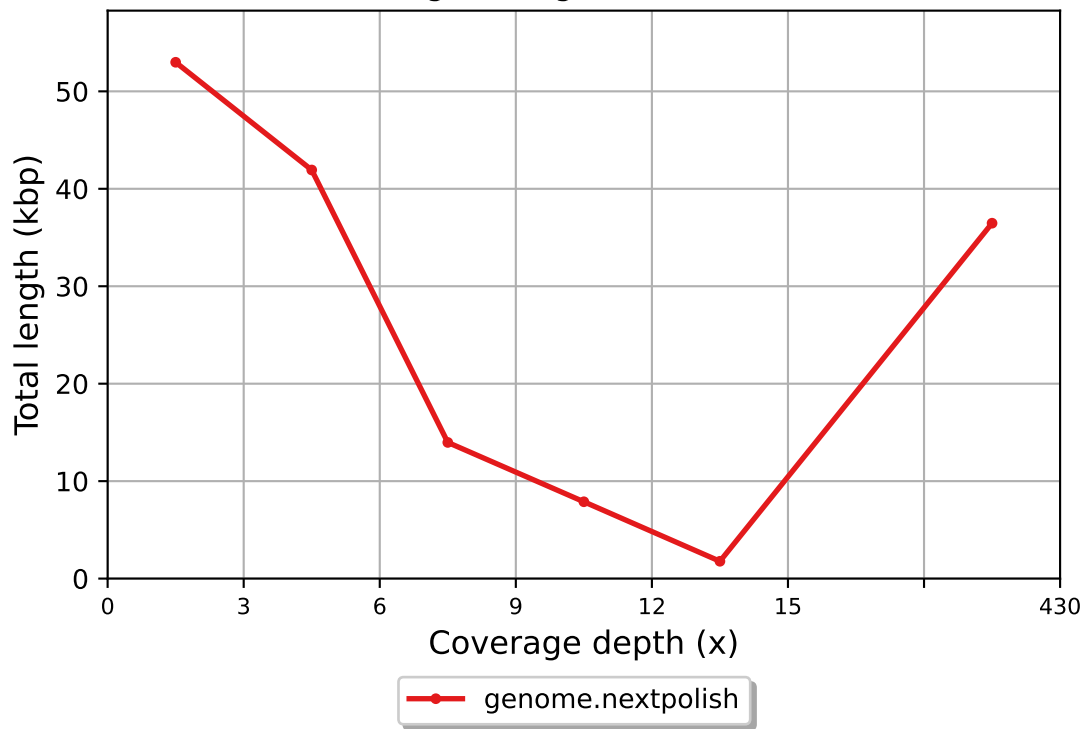


— genome.nextpolish

genome.nextpolish GC content



Coverage histogram (bin size: 3x)



genome.nextpolish coverage histogram (bin size: 3x)

