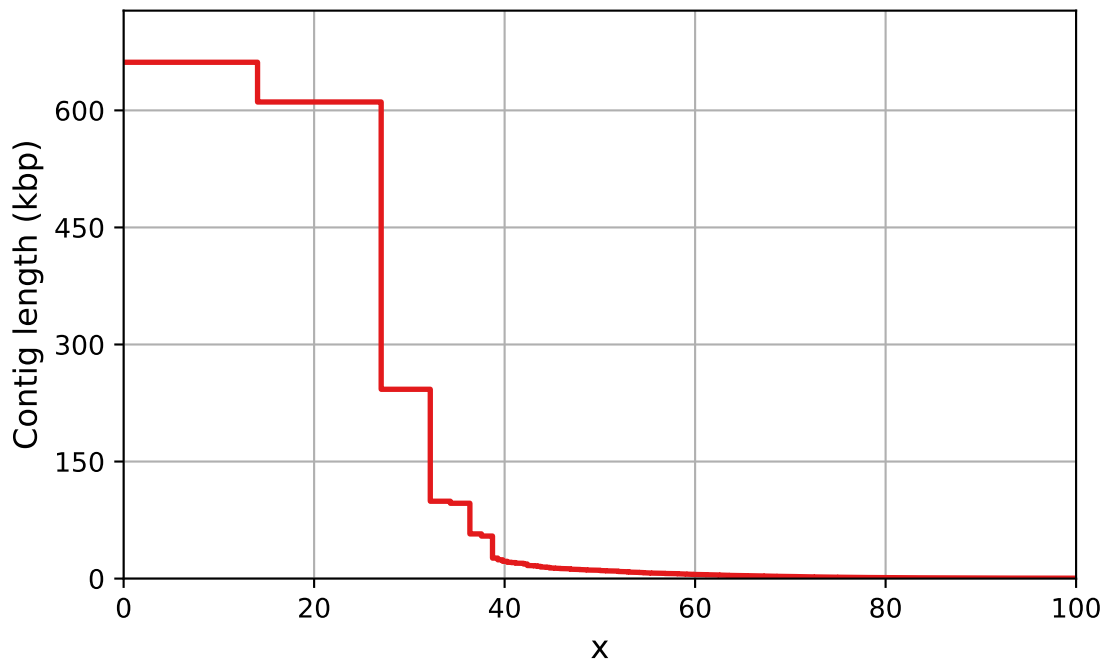


# Report

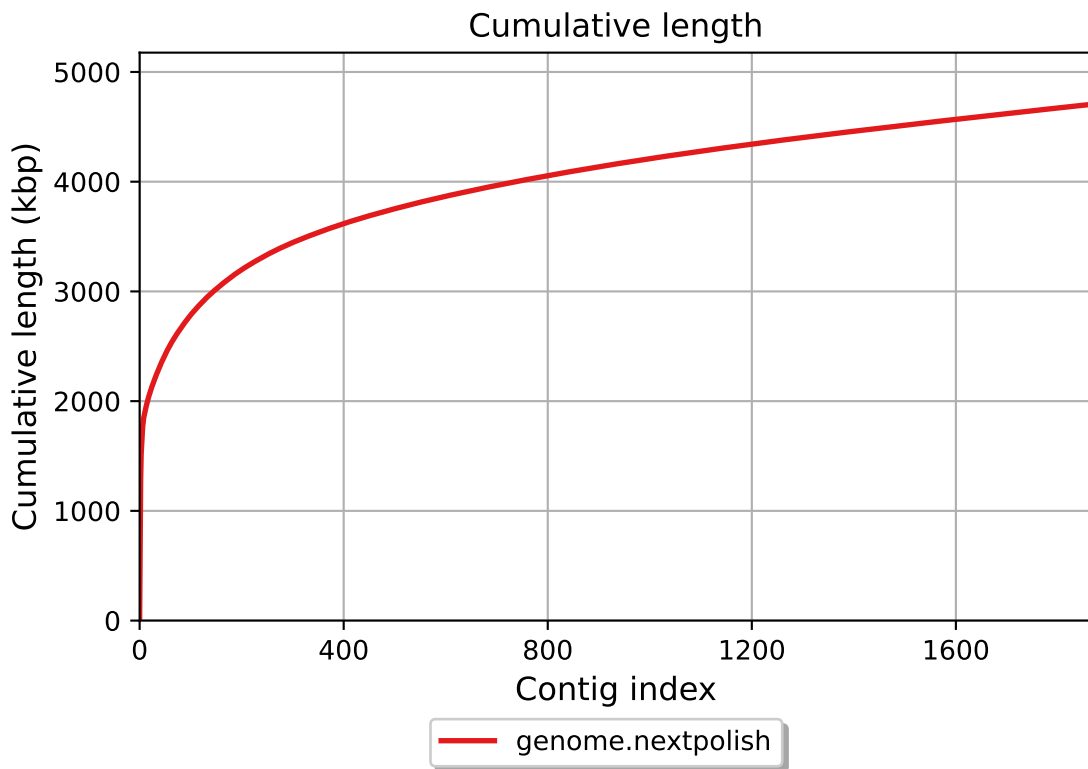
	genome.nextpolish
# contigs ( $\geq 0$ bp)	4197
# contigs ( $\geq 1000$ bp)	640
# contigs ( $\geq 5000$ bp)	117
# contigs ( $\geq 10000$ bp)	46
# contigs ( $\geq 25000$ bp)	8
# contigs ( $\geq 50000$ bp)	7
Total length ( $\geq 0$ bp)	5565080
Total length ( $\geq 1000$ bp)	3908358
Total length ( $\geq 5000$ bp)	2874650
Total length ( $\geq 10000$ bp)	2384391
Total length ( $\geq 25000$ bp)	1848699
Total length ( $\geq 50000$ bp)	1822446
# contigs	1867
Largest contig	661660
Total length	4705653
GC (%)	41.31
N50	10663
N90	690
auN	193485.5
L50	43
L90	1037
# N's per 100 kbp	0.09
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	20 + 0 part

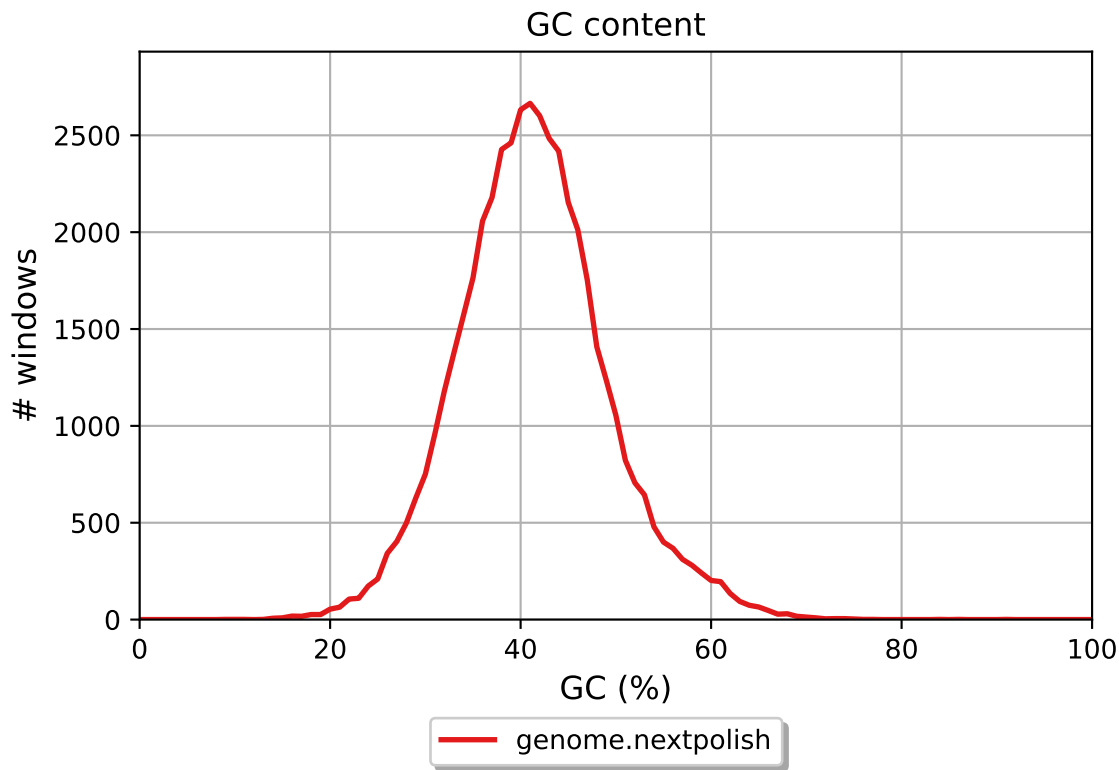
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

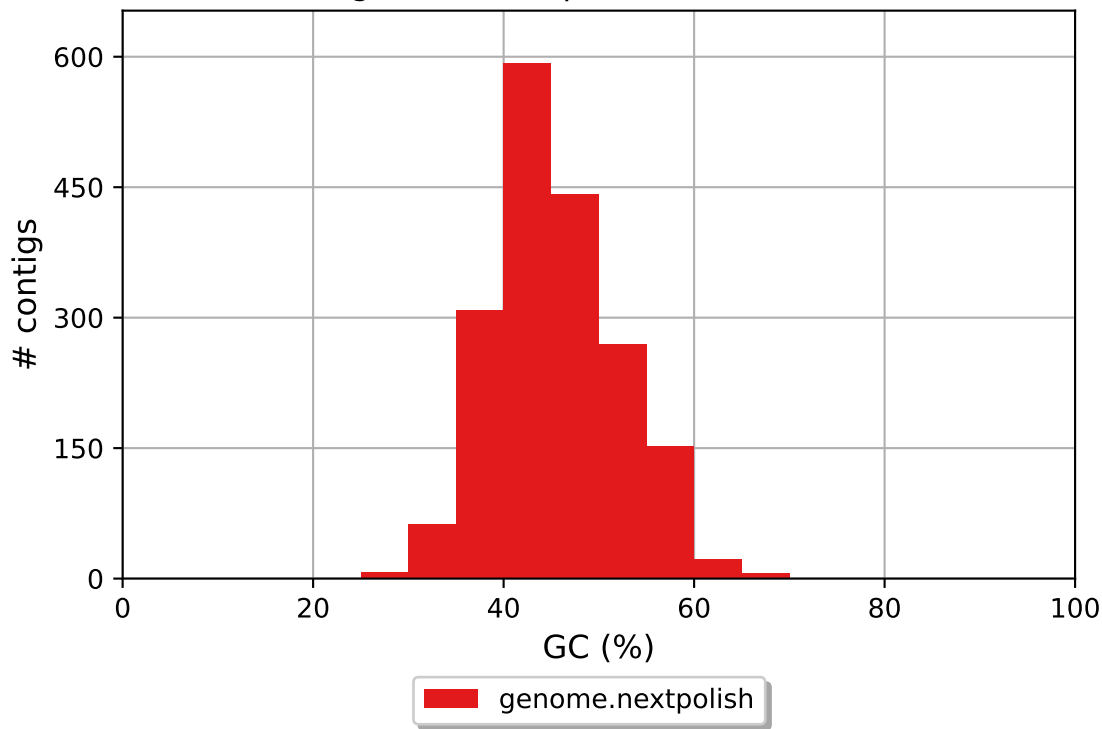


— genome.nextpolish

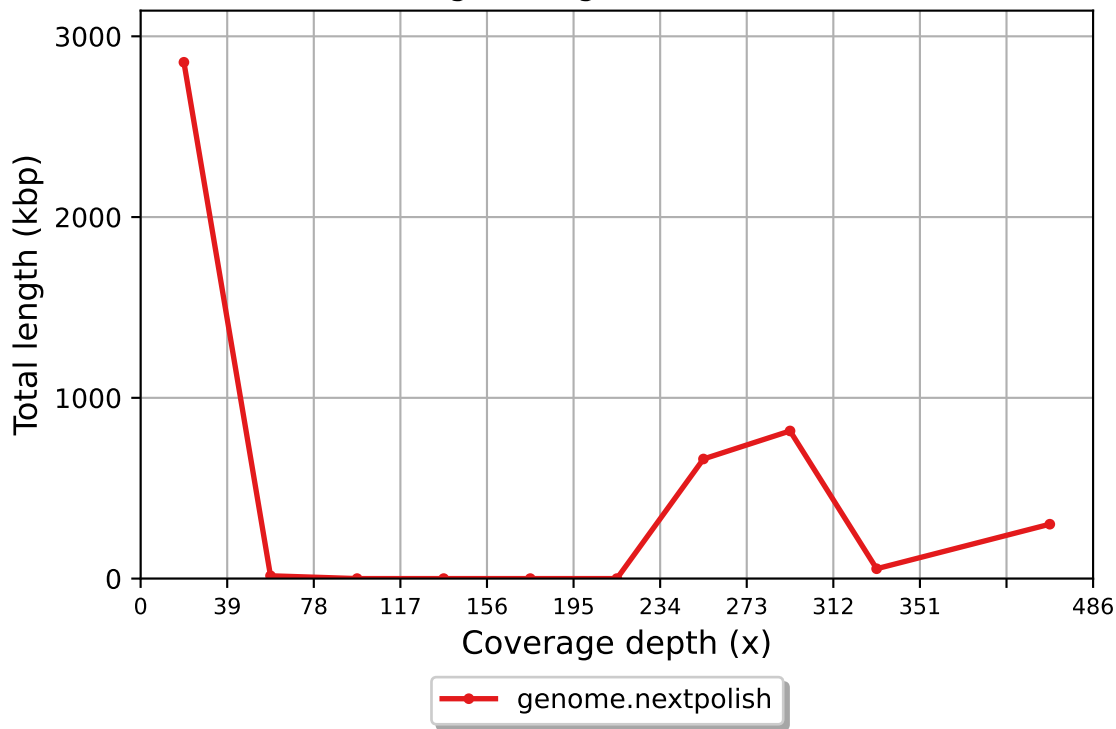




genome.nextpolish GC content



Coverage histogram (bin size: 39x)



genome.nextpolish coverage histogram (bin size: 39x)

