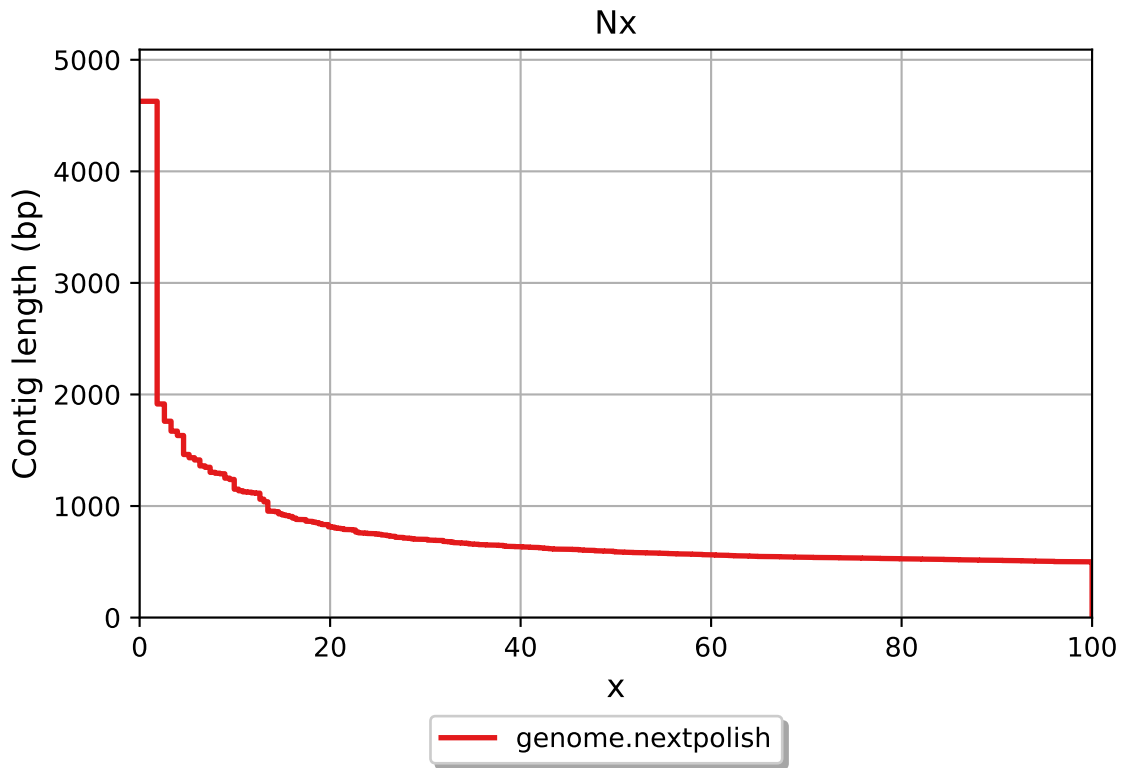
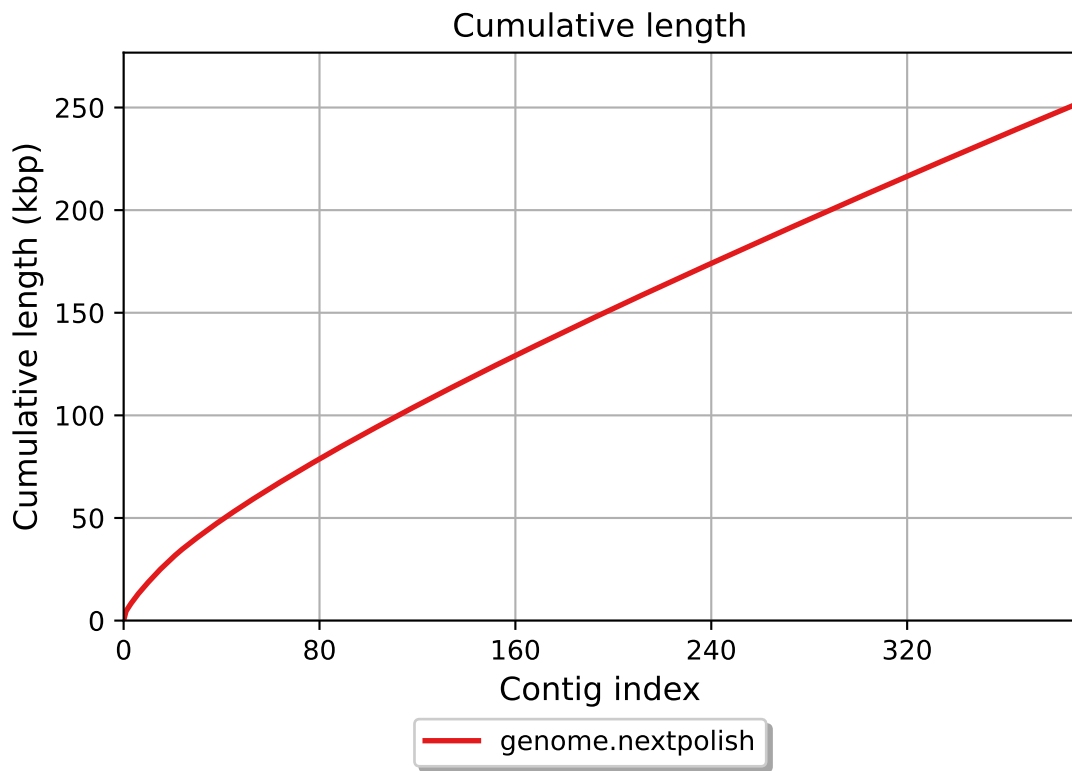


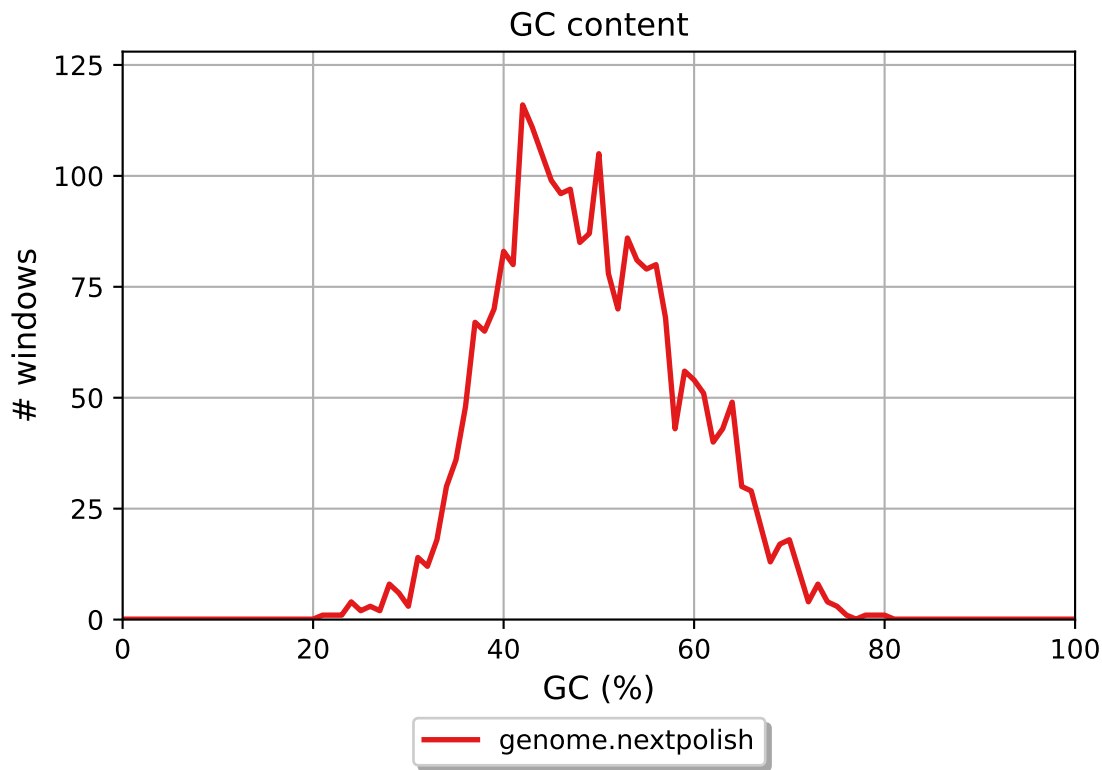
Report

	genome.nextpolish
# contigs (>= 0 bp)	2424
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1060050
Total length (>= 1000 bp)	33865
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	389
Largest contig	4628
Total length	251586
GC (%)	49.11
N50	589
N90	514
auN	773.4
L50	155
L90	340
# N's per 100 kbp	0.40
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	2 + 2 part

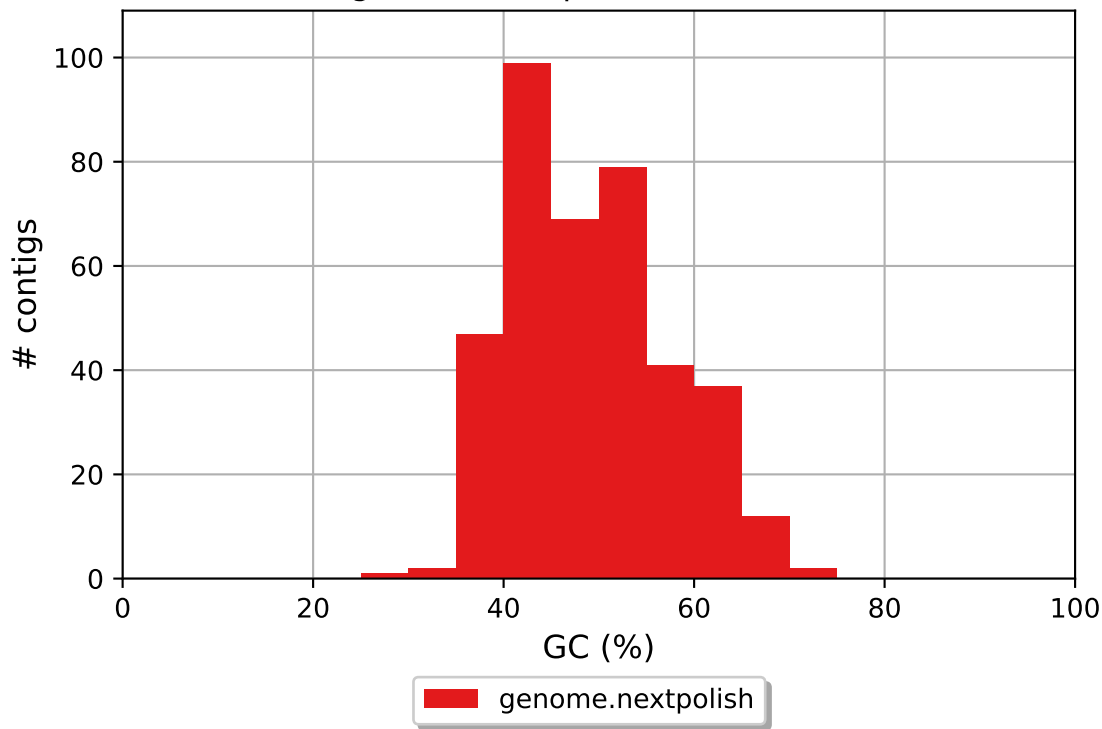
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



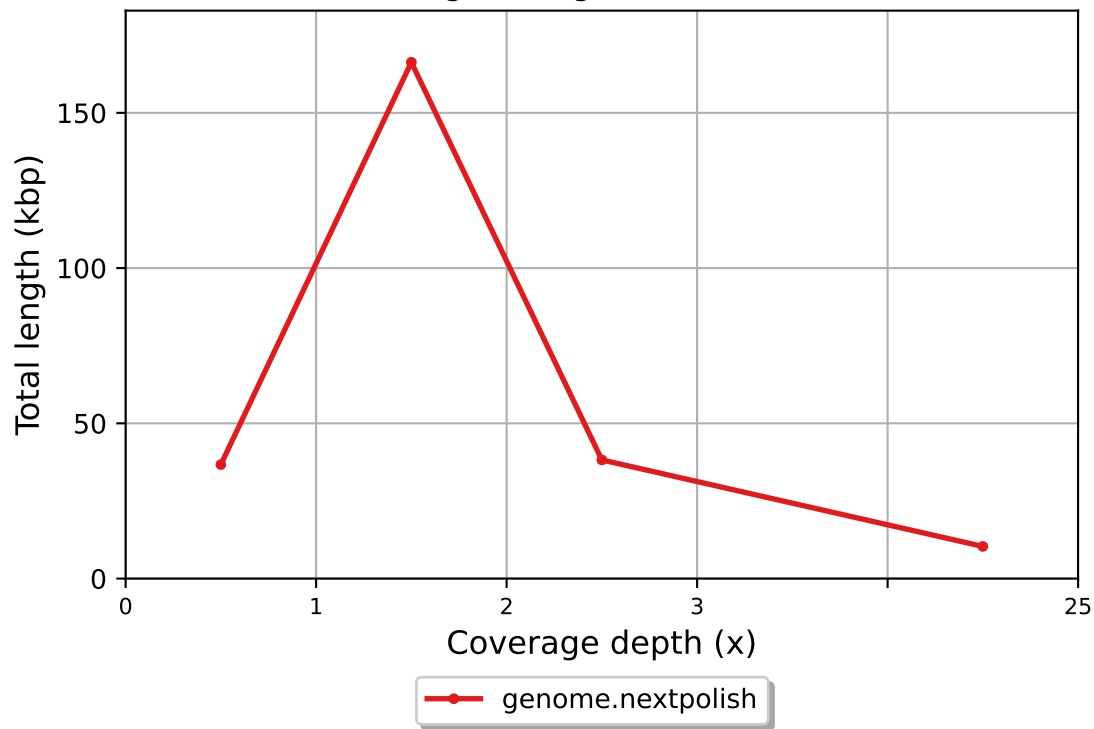




genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

