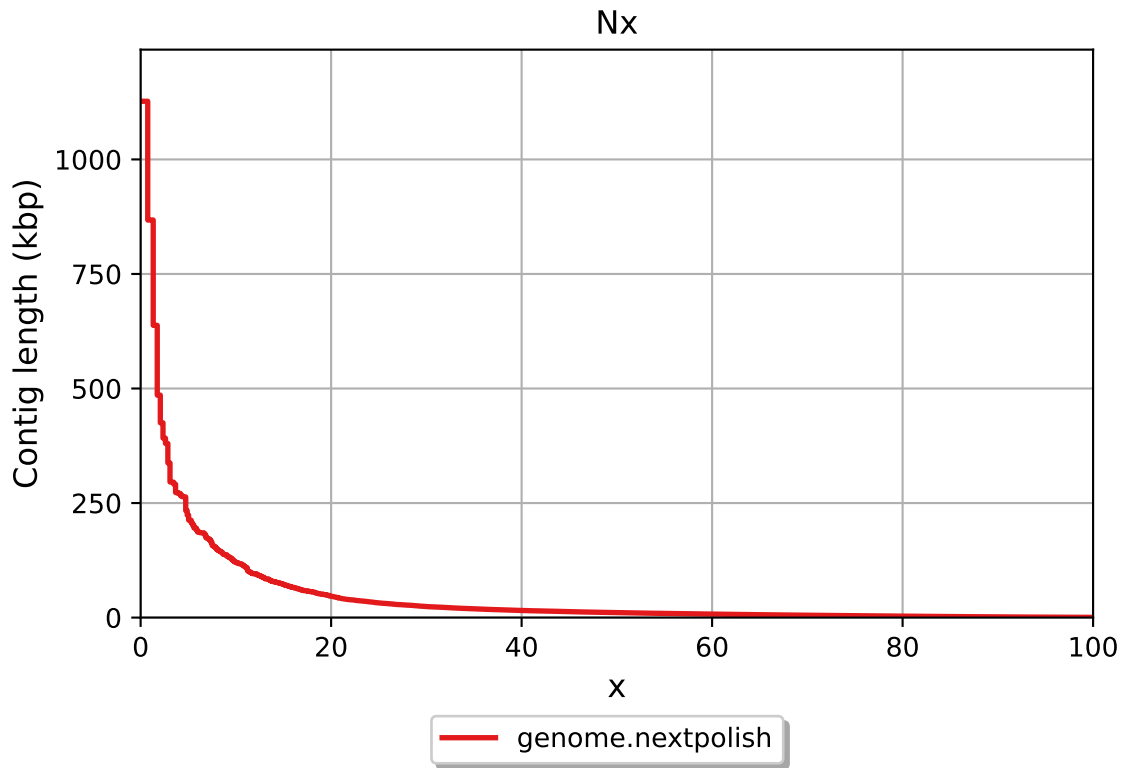


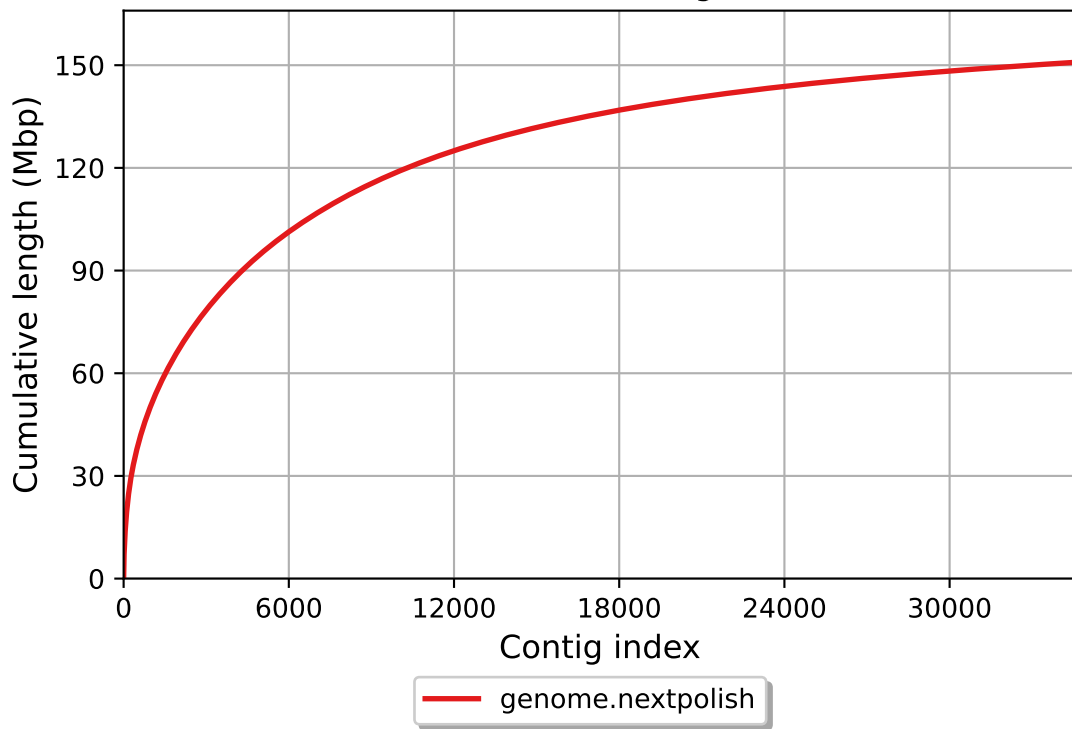
# Report

	genome.nextpolish
# contigs (>= 0 bp)	195906
# contigs (>= 1000 bp)	22727
# contigs (>= 5000 bp)	6972
# contigs (>= 10000 bp)	3046
# contigs (>= 25000 bp)	715
# contigs (>= 50000 bp)	259
Total length (>= 0 bp)	187315955
Total length (>= 1000 bp)	142600431
Total length (>= 5000 bp)	106529790
Total length (>= 10000 bp)	78945535
Total length (>= 25000 bp)	44399642
Total length (>= 50000 bp)	29172003
# contigs	34594
Largest contig	1126928
Total length	150857555
GC (%)	48.16
N50	10873
N90	1569
auN	51420.9
L50	2709
L90	17275
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	49 + 15 part

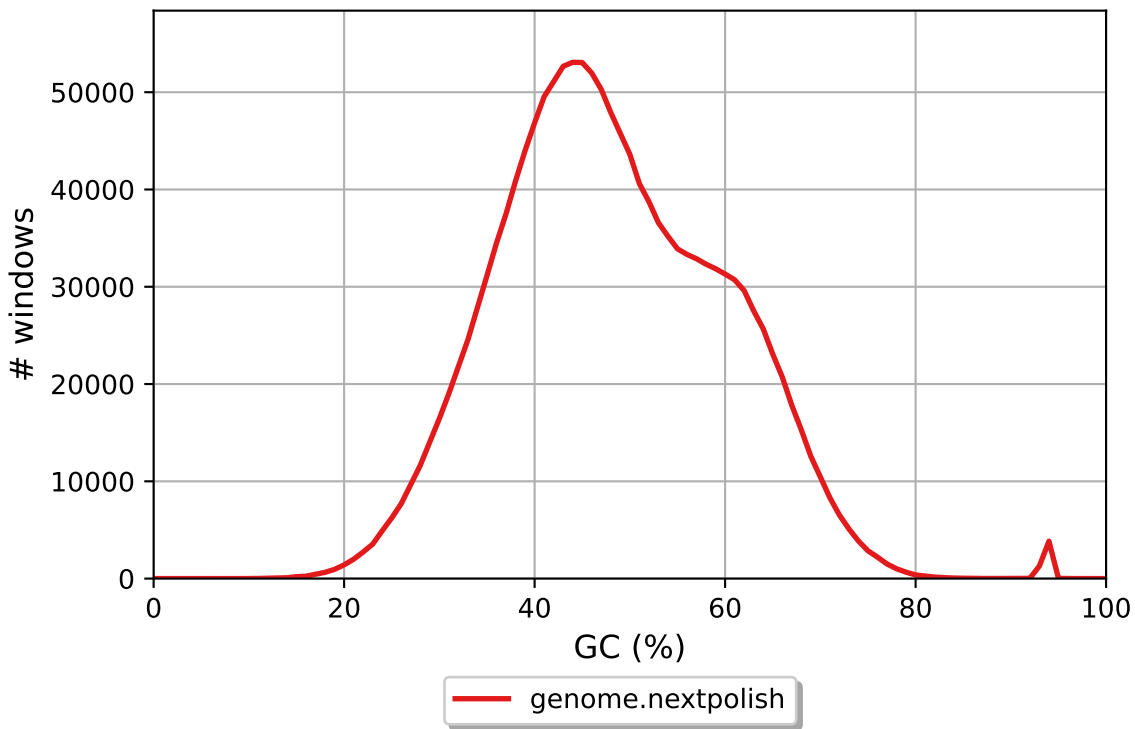
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



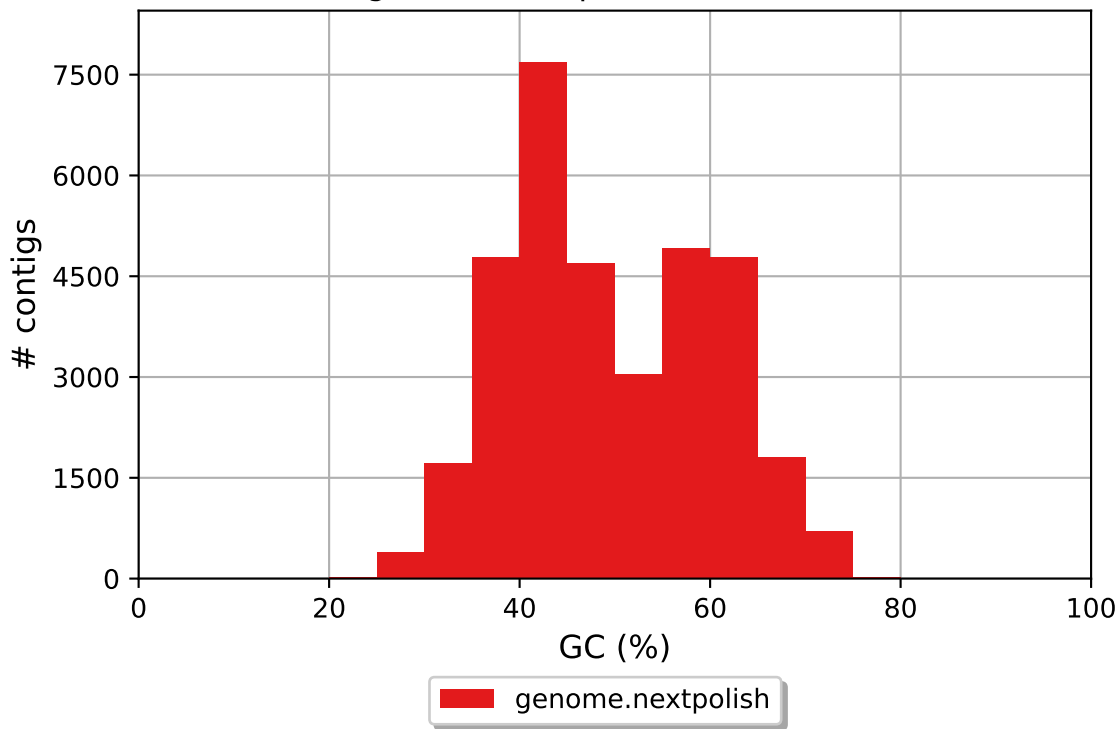
Cumulative length



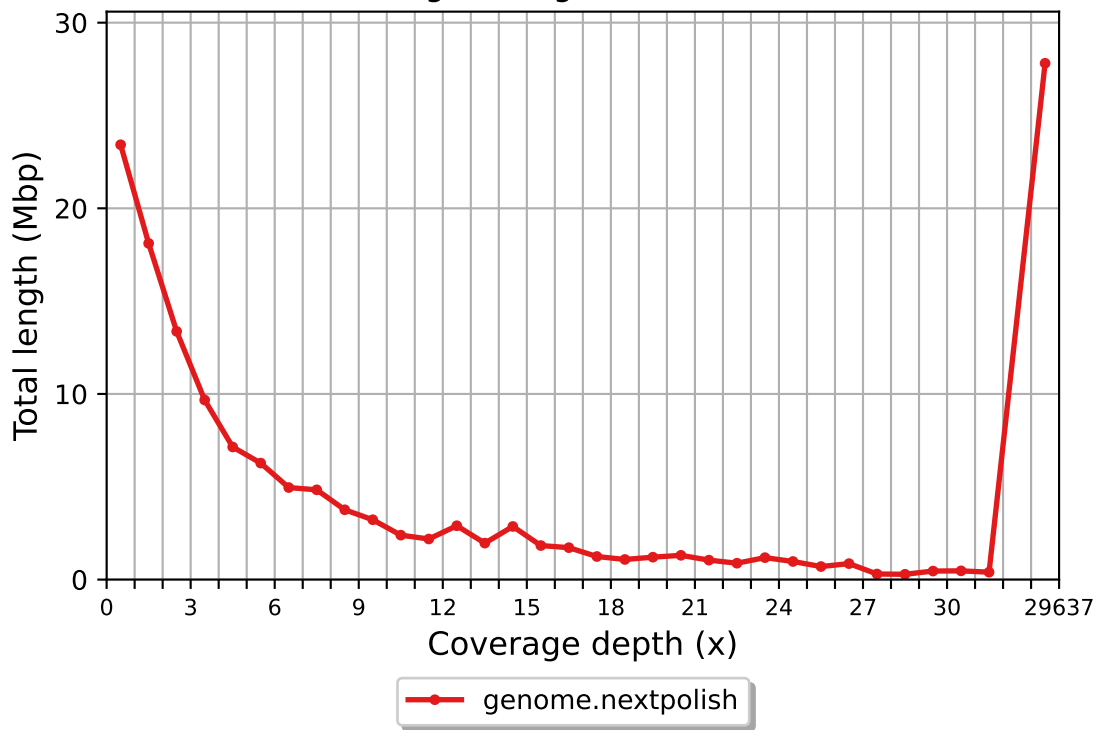
GC content



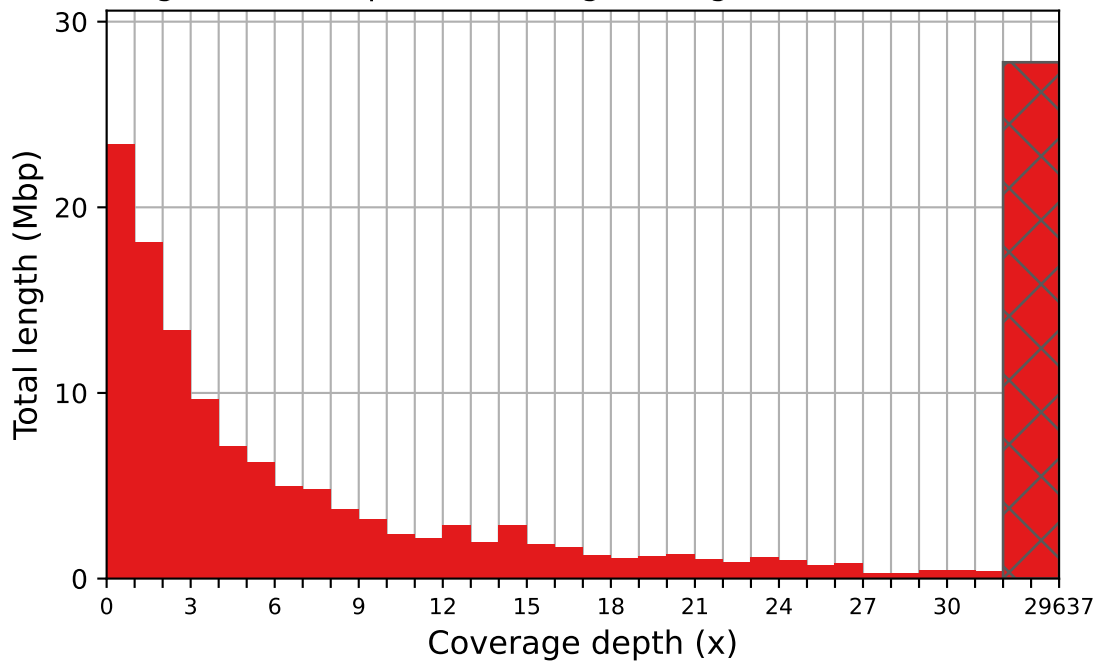
genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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



genome.nextpolish