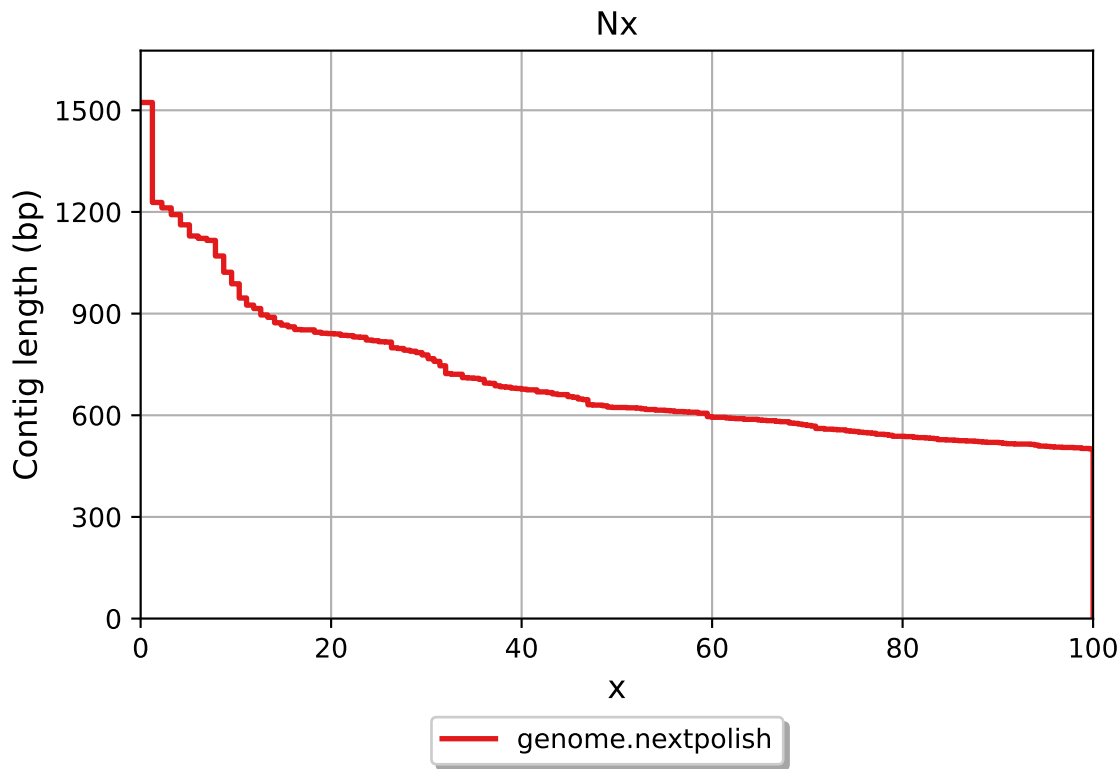


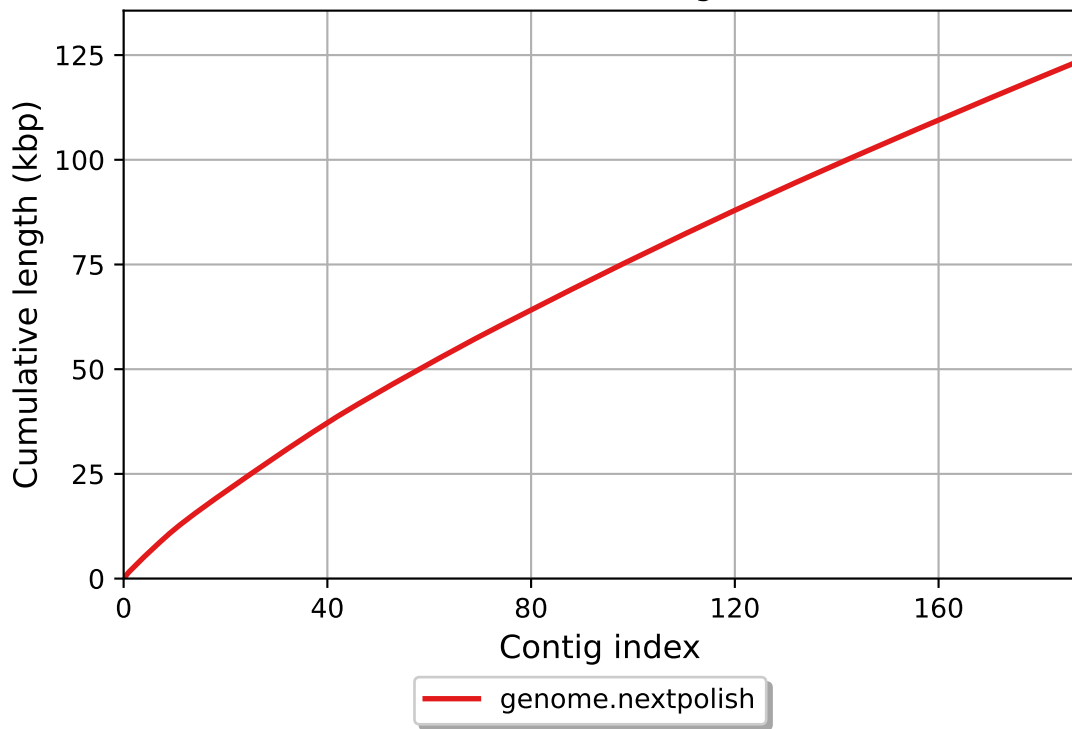
# Report

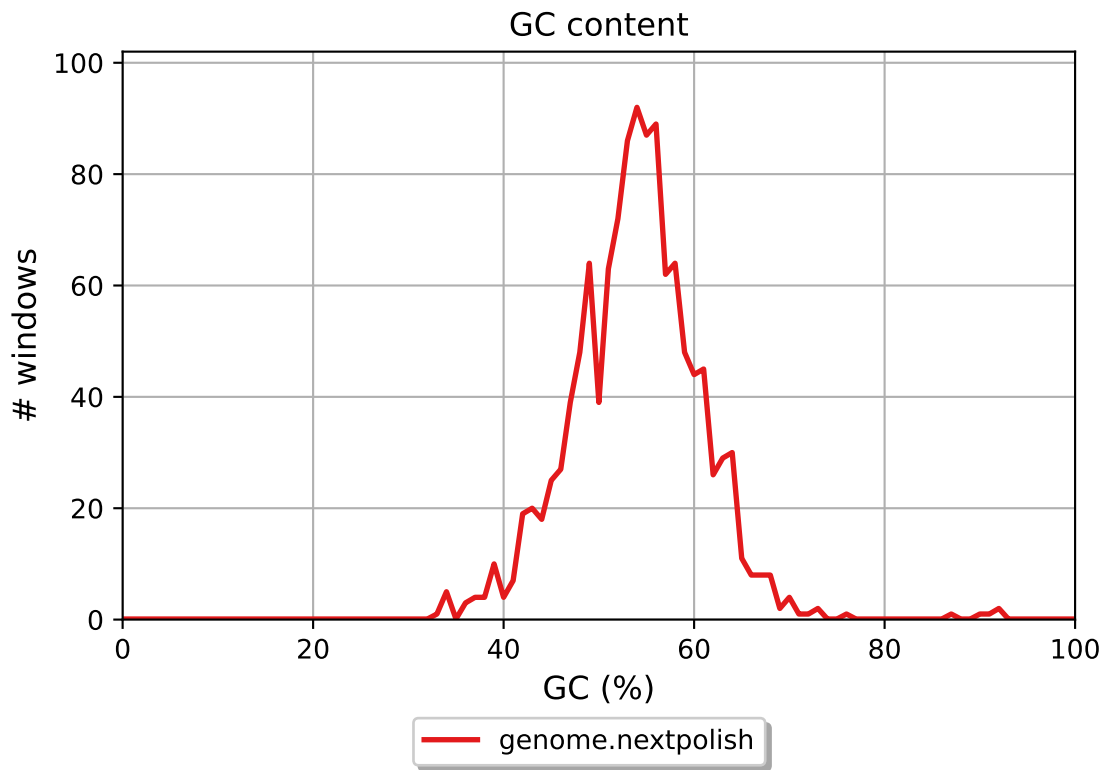
	genome.nextpolish
# contigs (>= 0 bp)	3669
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	815698
Total length (>= 1000 bp)	11776
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	187
Largest contig	1523
Total length	123286
GC (%)	54.00
N50	623
N90	520
auN	703.2
L50	76
L90	163
# 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).

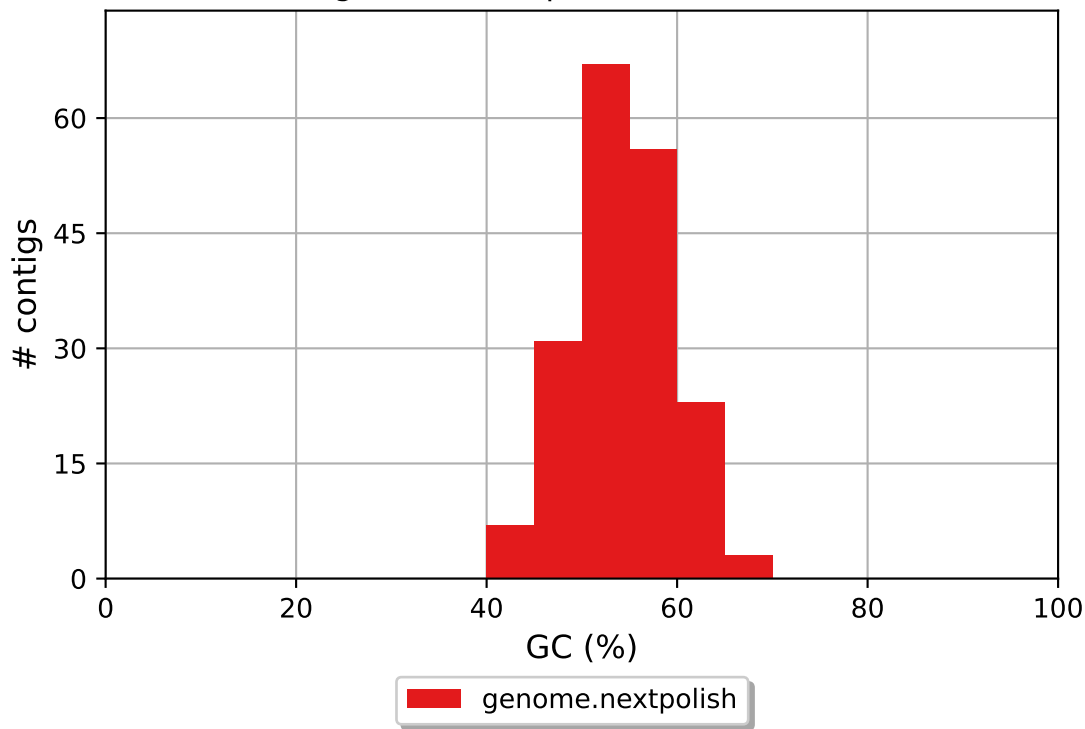


Cumulative length

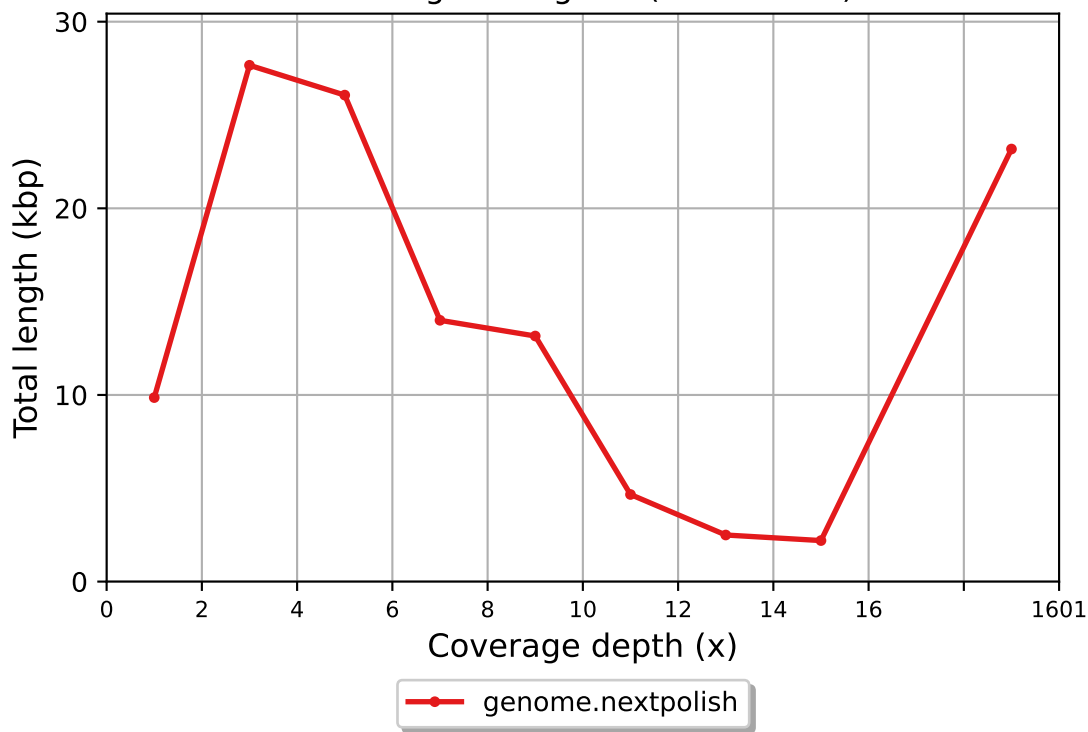




genome.nextpolish GC content



Coverage histogram (bin size: 2x)



genome.nextpolish coverage histogram (bin size: 2x)

