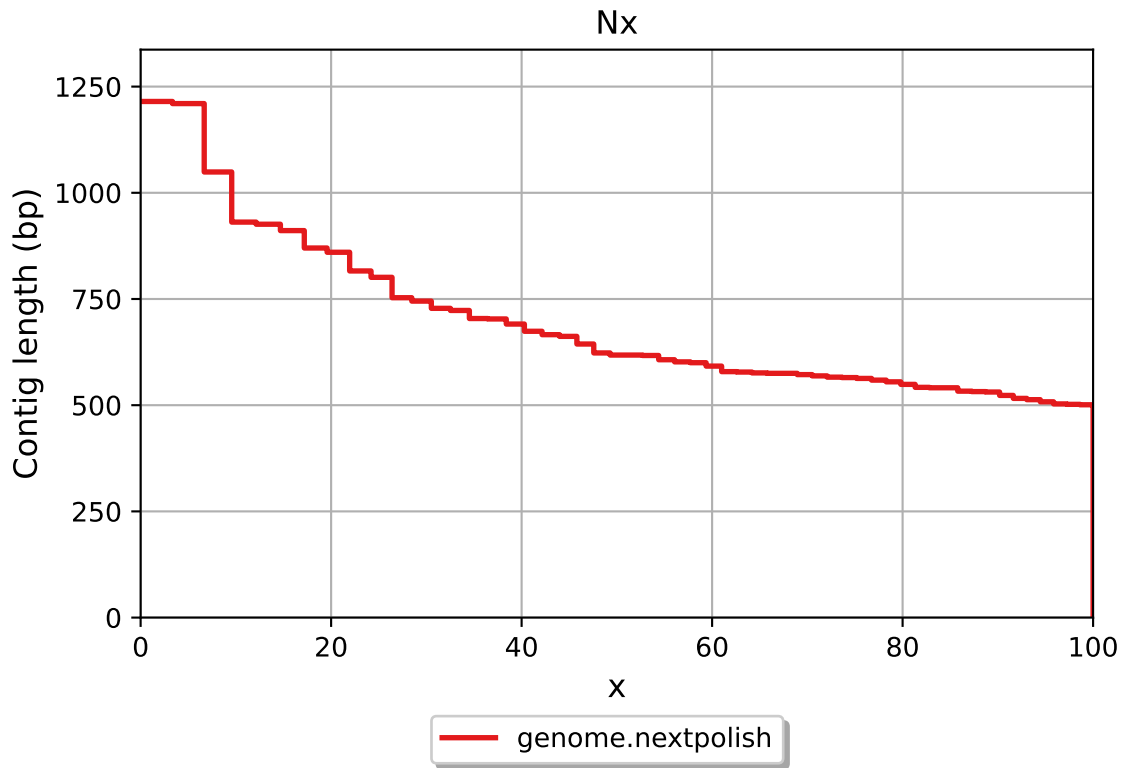


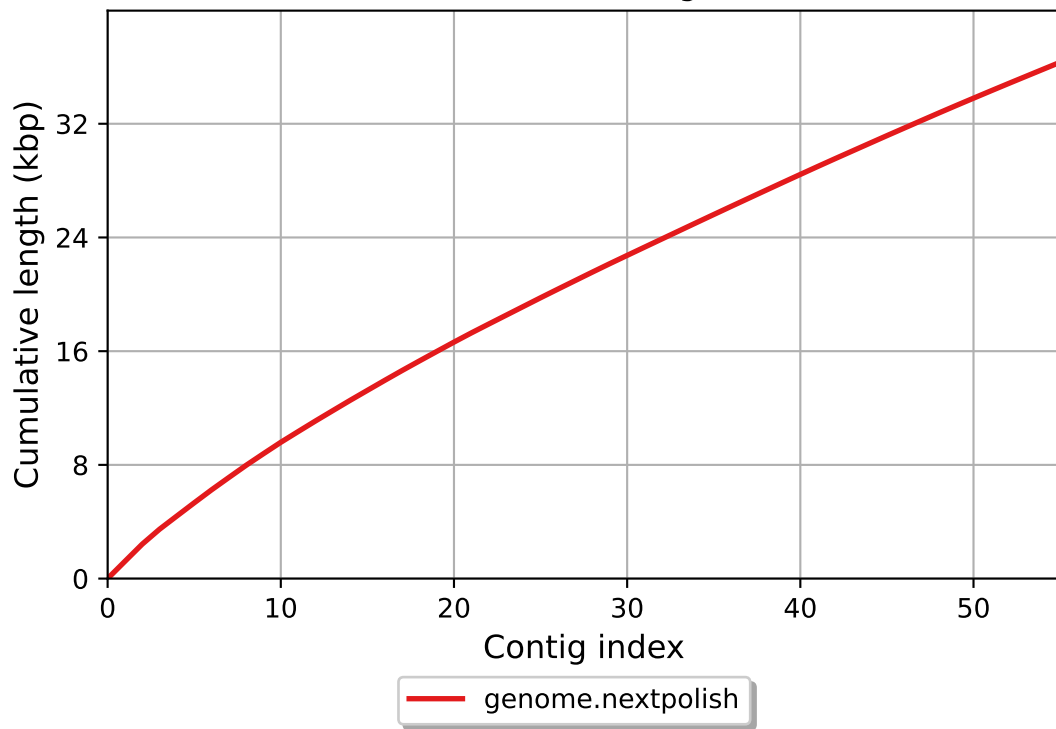
# Report

	genome.nextpolish
# contigs (>= 0 bp)	1921
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	363499
Total length (>= 1000 bp)	3474
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	55
Largest contig	1215
Total length	36326
GC (%)	53.56
N50	618
N90	531
auN	702.1
L50	23
L90	48
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	0 + 0 part

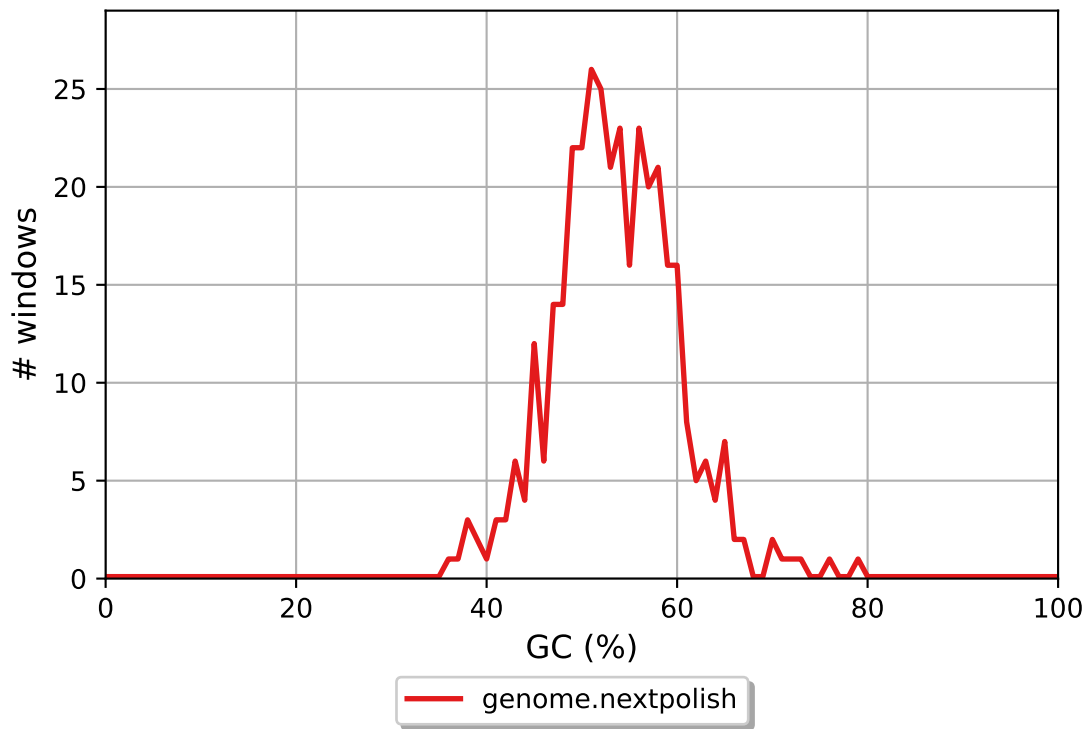
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



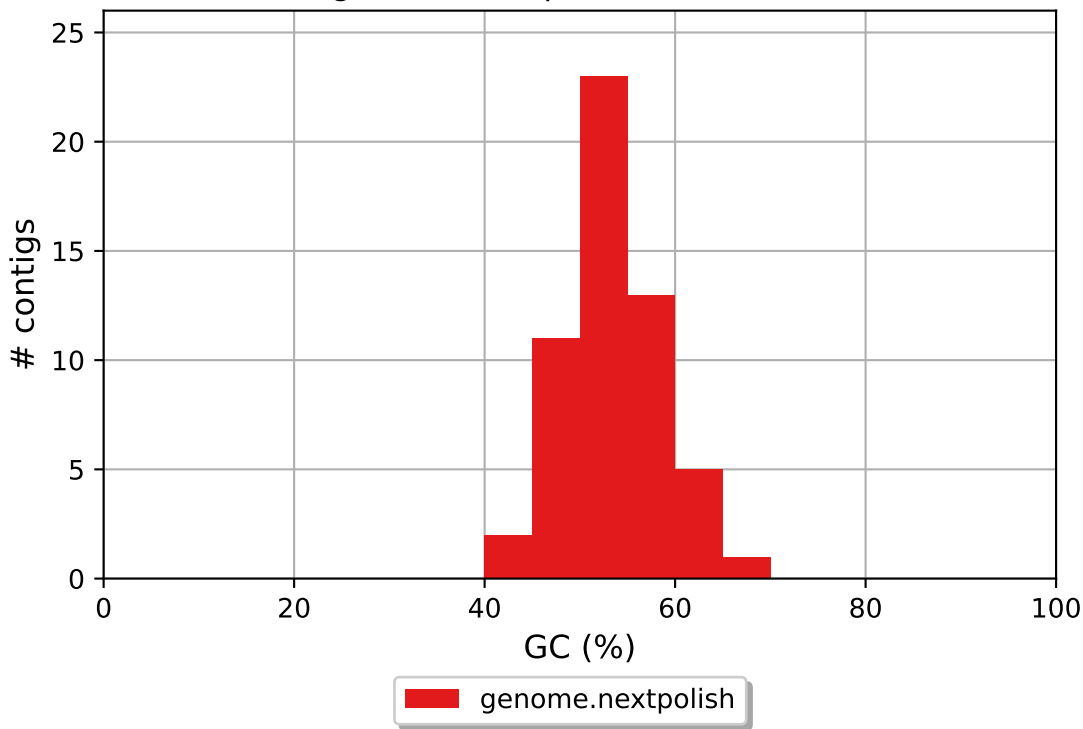
Cumulative length



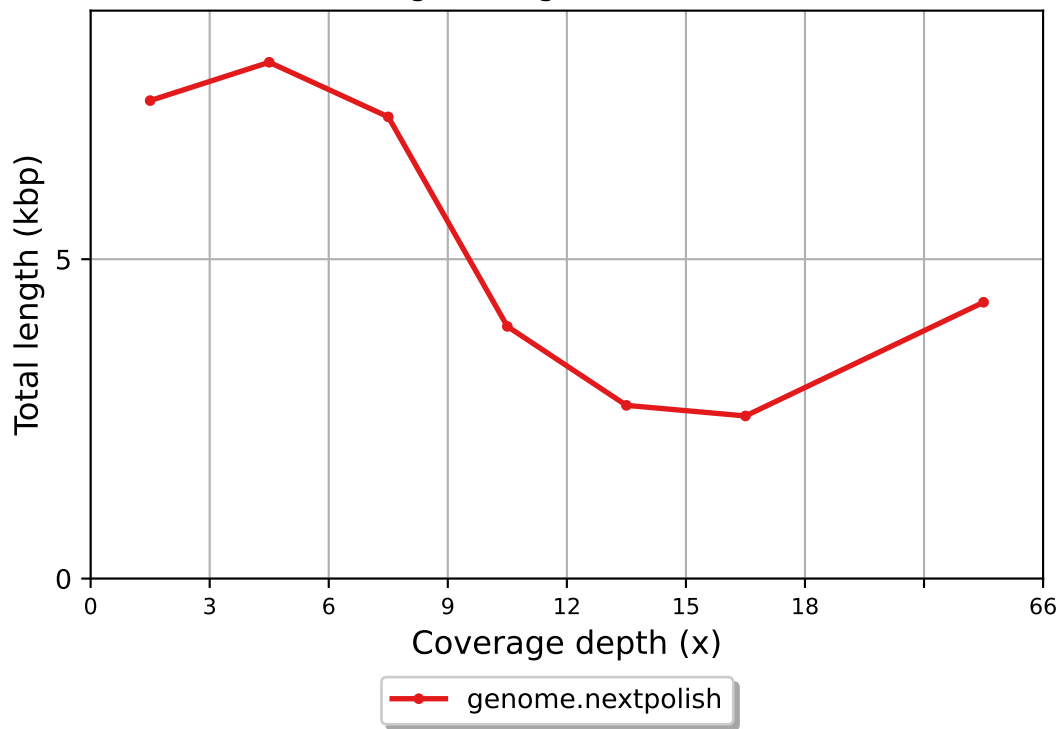
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 3x)



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

