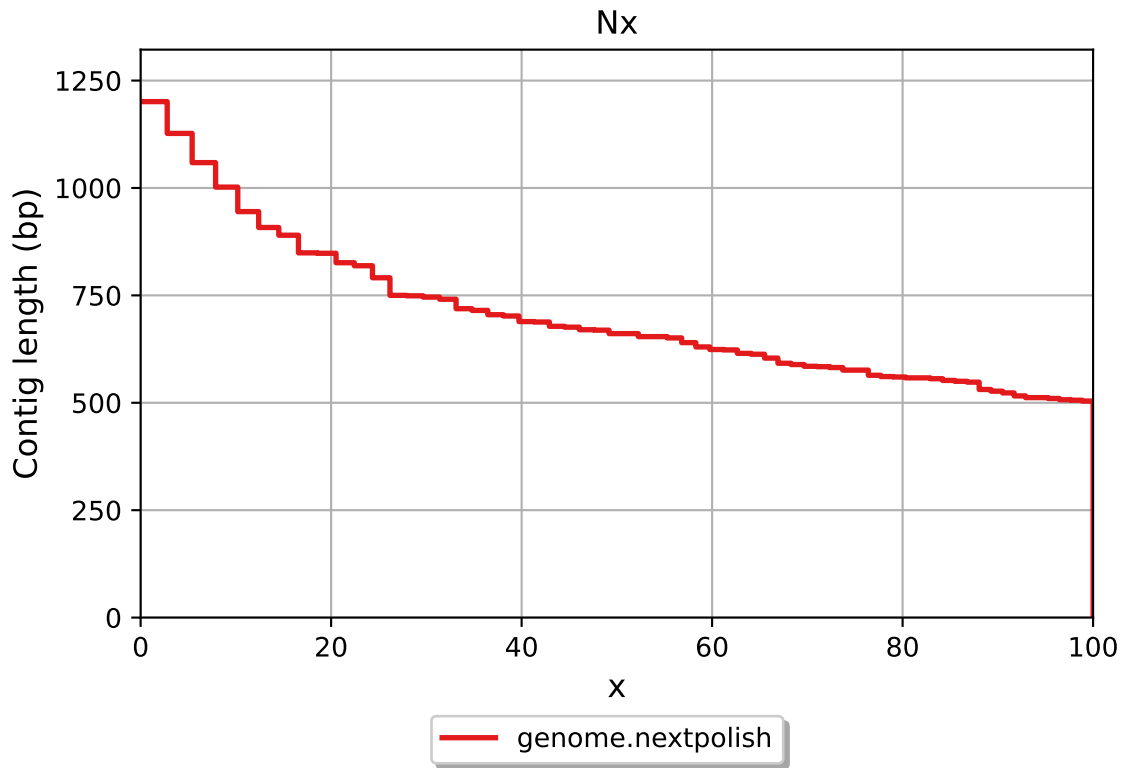


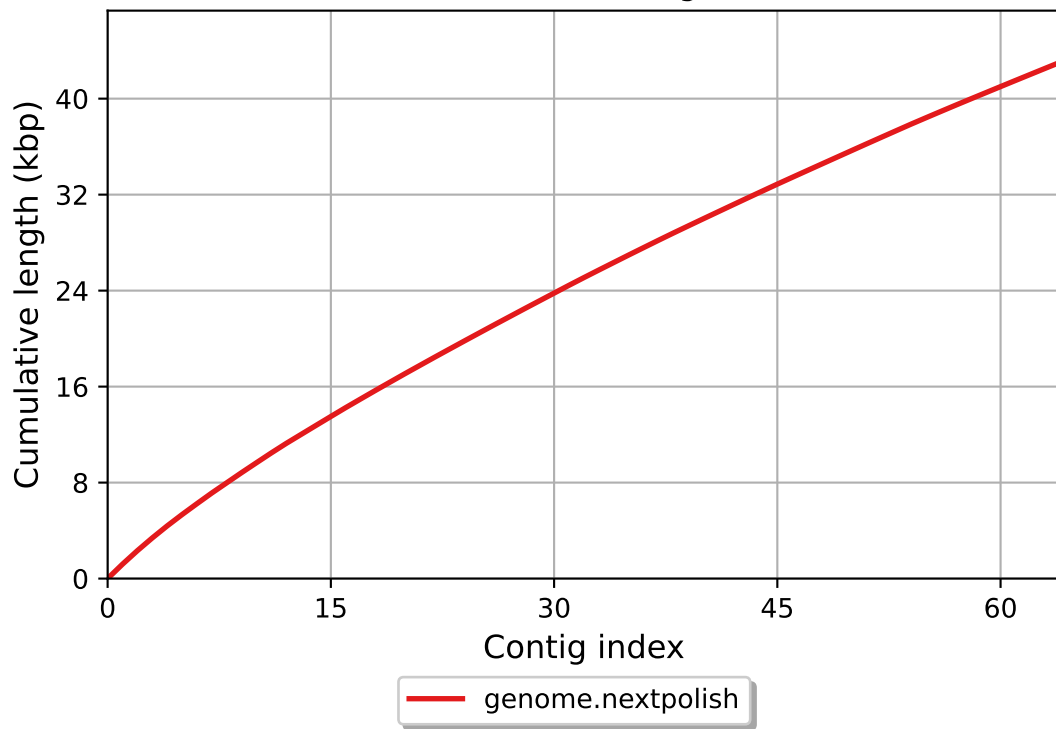
# Report

	genome.nextpolish
# contigs (>= 0 bp)	2171
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	433615
Total length (>= 1000 bp)	4389
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	64
Largest contig	1201
Total length	43031
GC (%)	54.64
N50	661
N90	527
auN	707.6
L50	27
L90	56
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	0 + 0 part

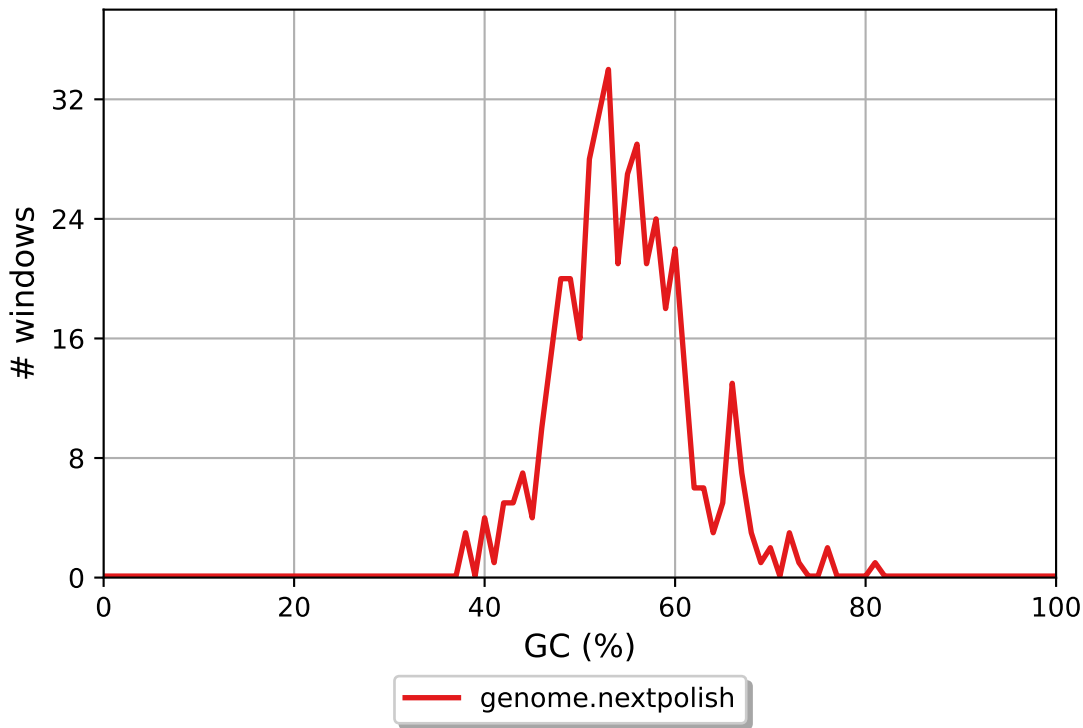
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



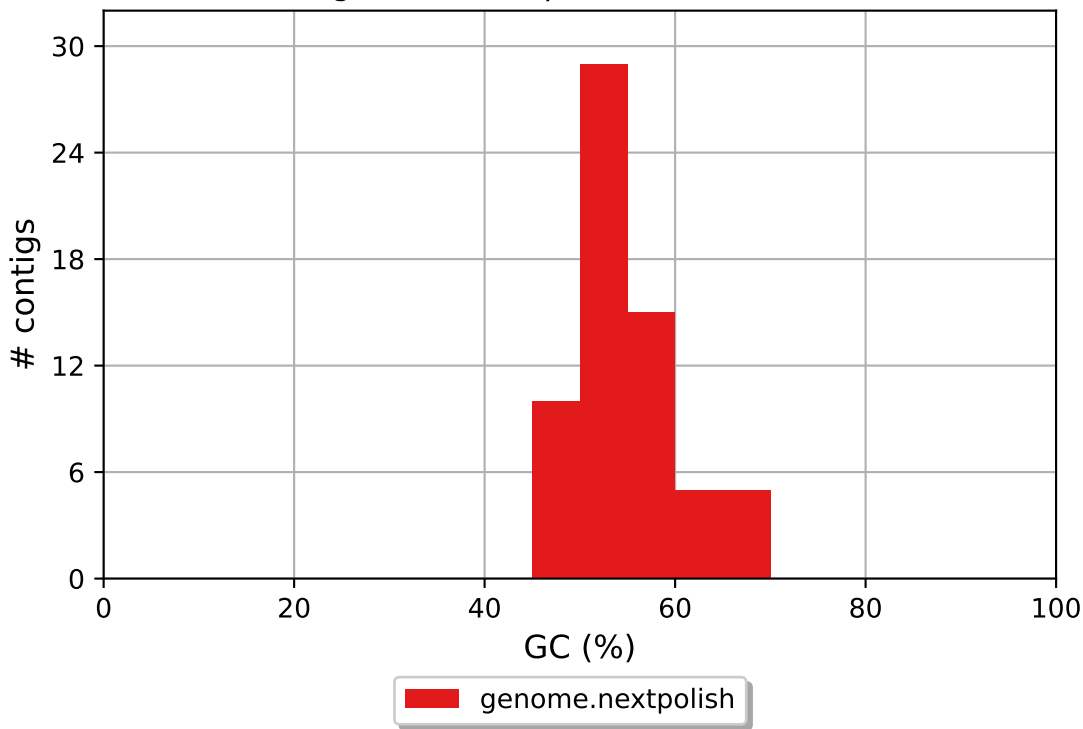
Cumulative length



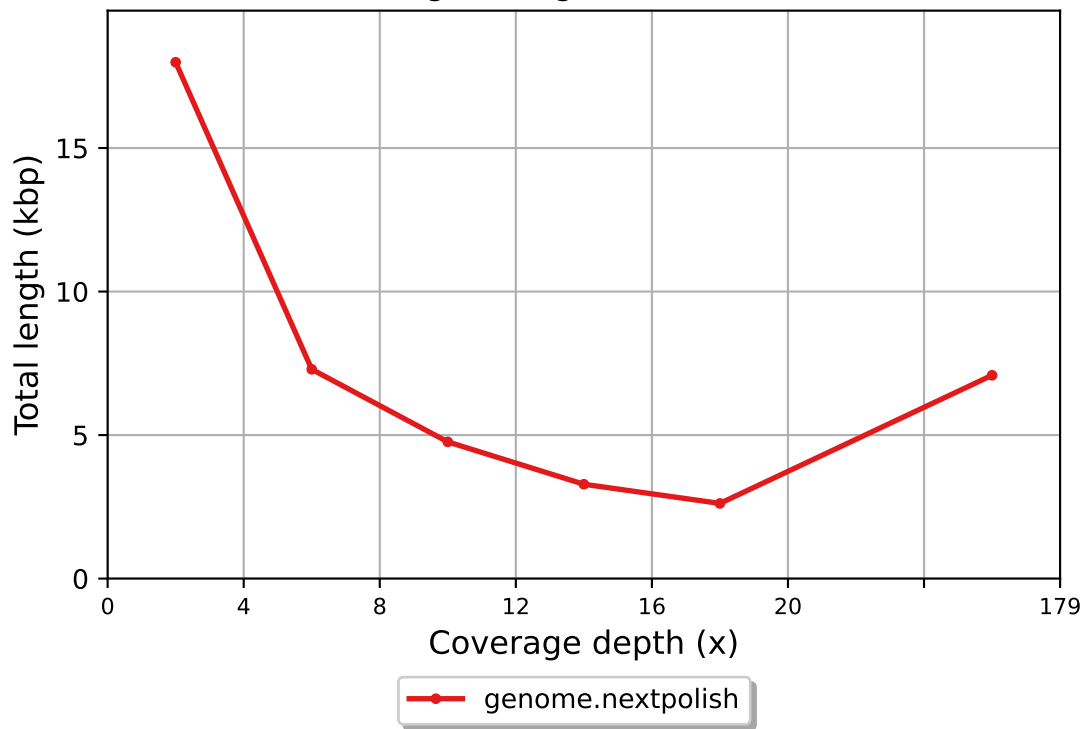
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 4x)



genome.nextpolish coverage histogram (bin size: 4x)

