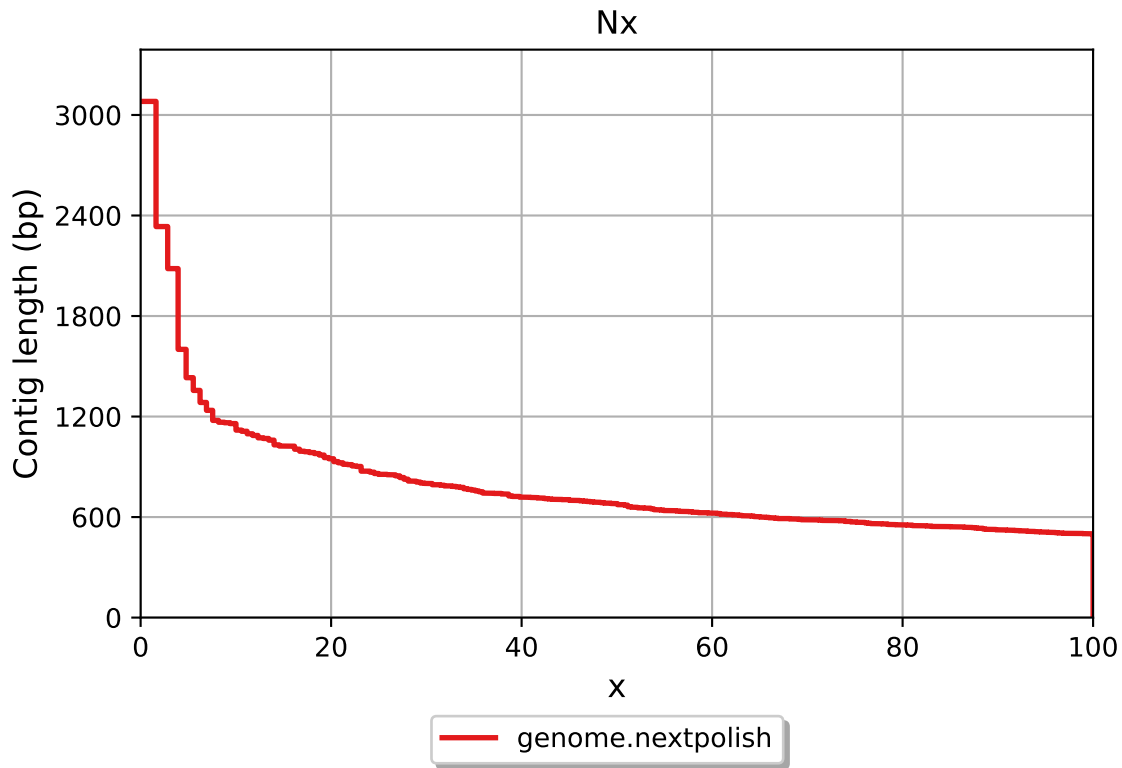
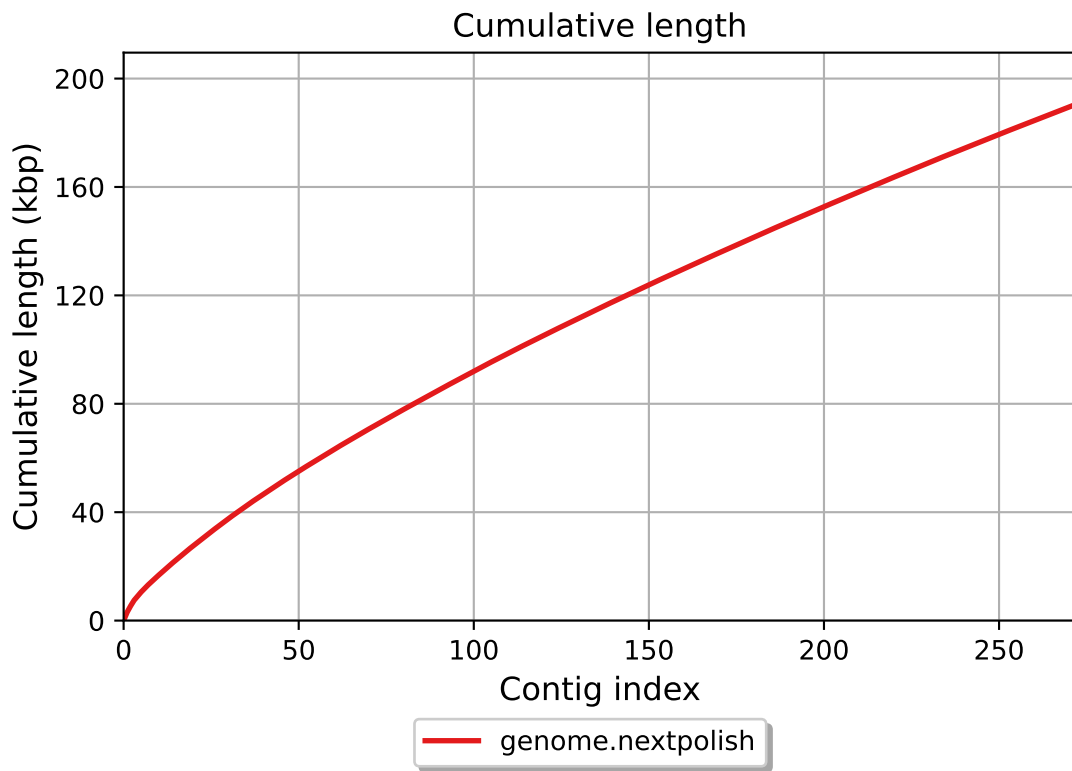


Report

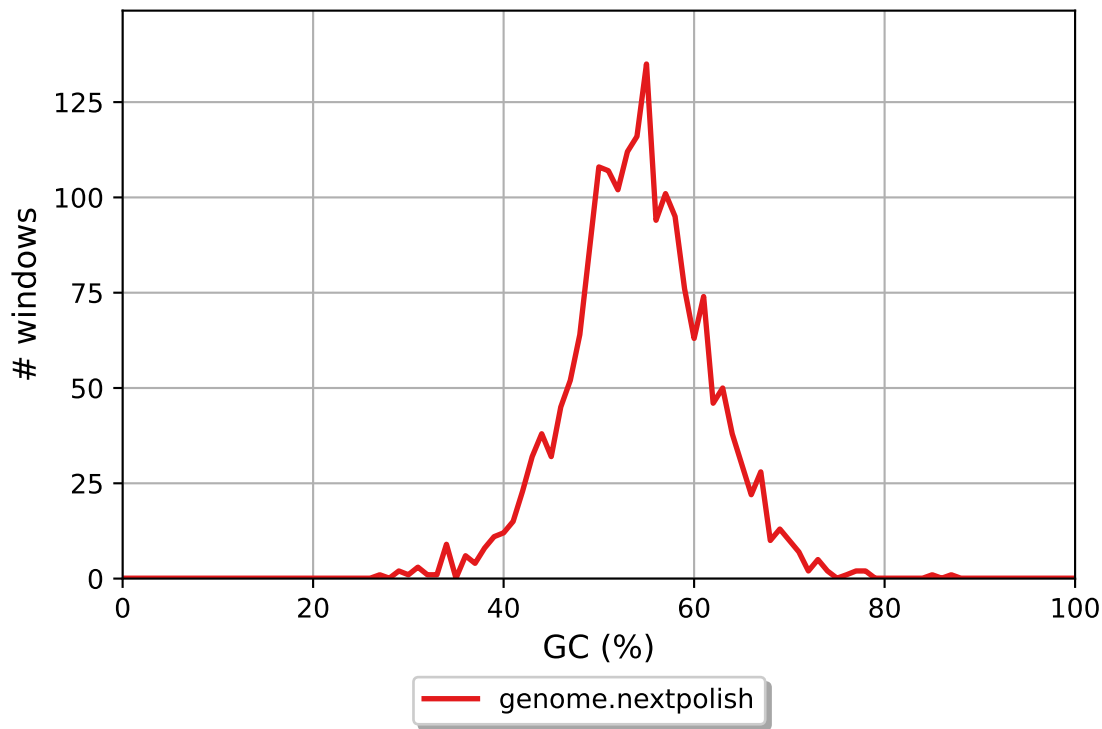
	genome.nextpolish
# contigs (>= 0 bp)	6017
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1295990
Total length (>= 1000 bp)	31795
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	272
Largest contig	3081
Total length	190518
GC (%)	54.15
N50	680
N90	524
auN	803.1
L50	105
L90	235
# 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).

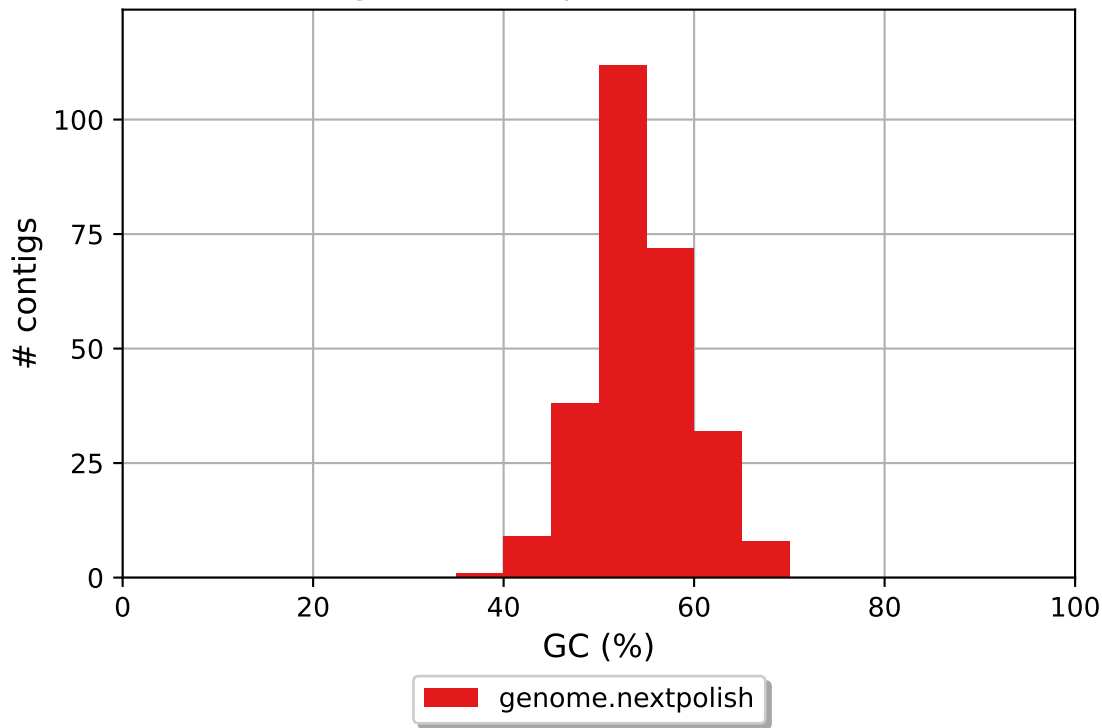




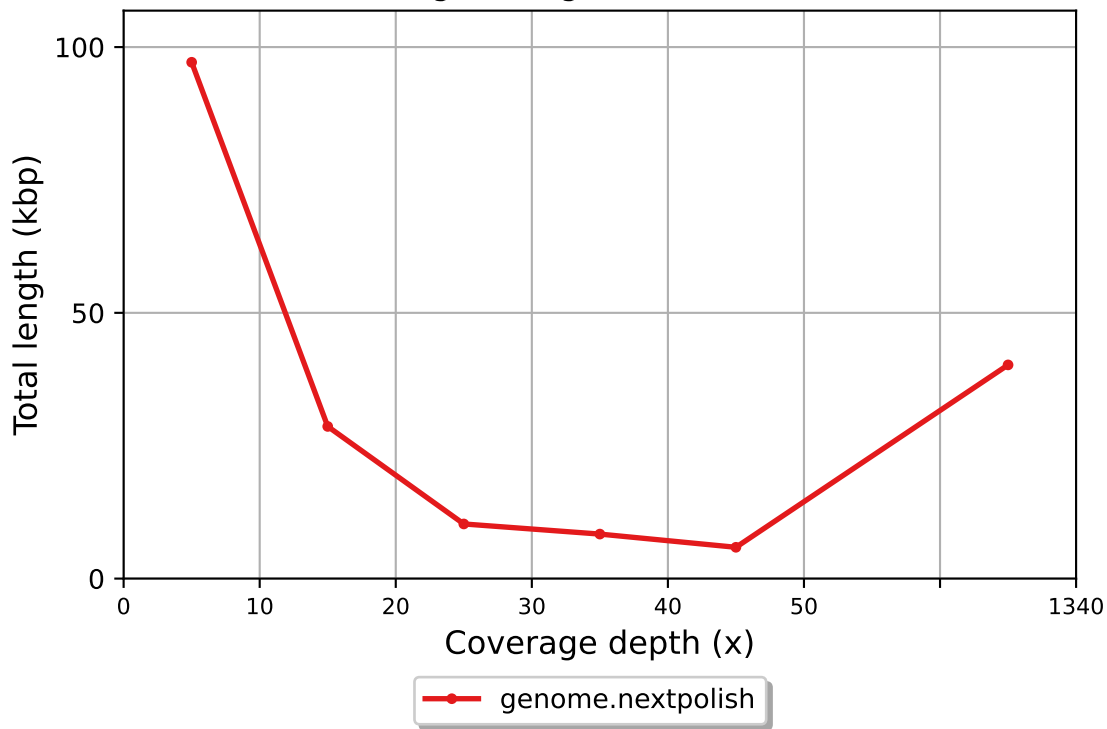
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 10x)



genome.nextpolish coverage histogram (bin size: 10x)

