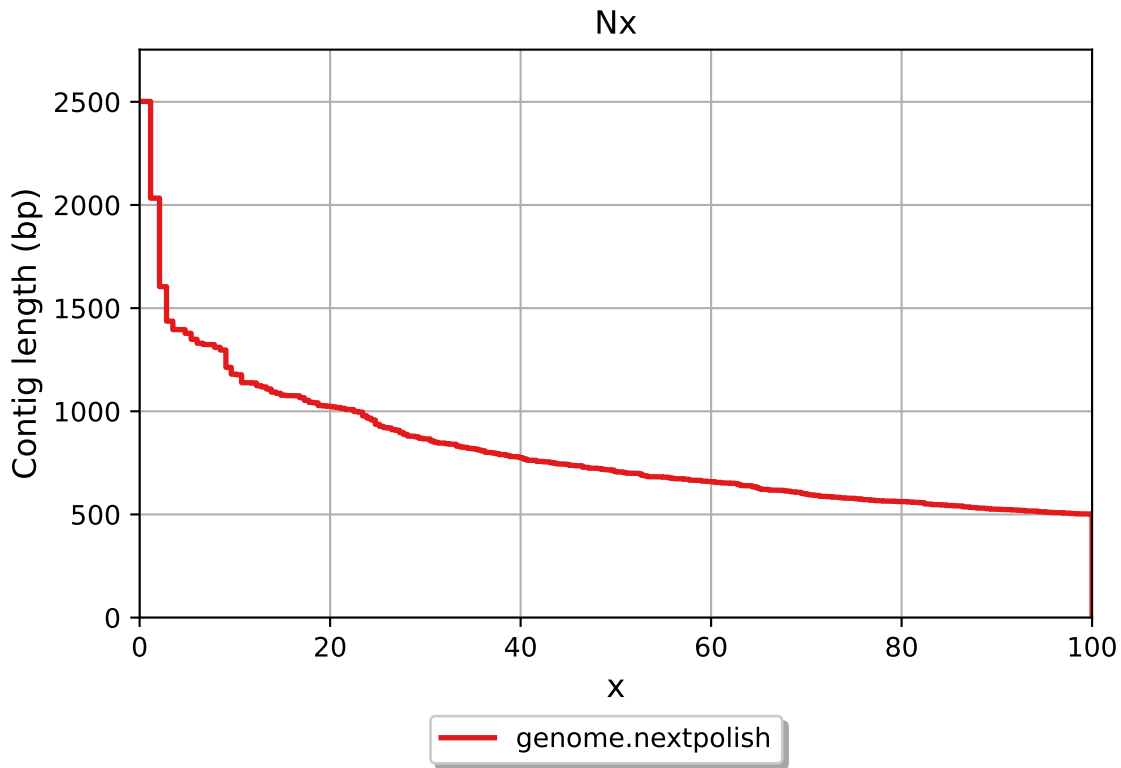
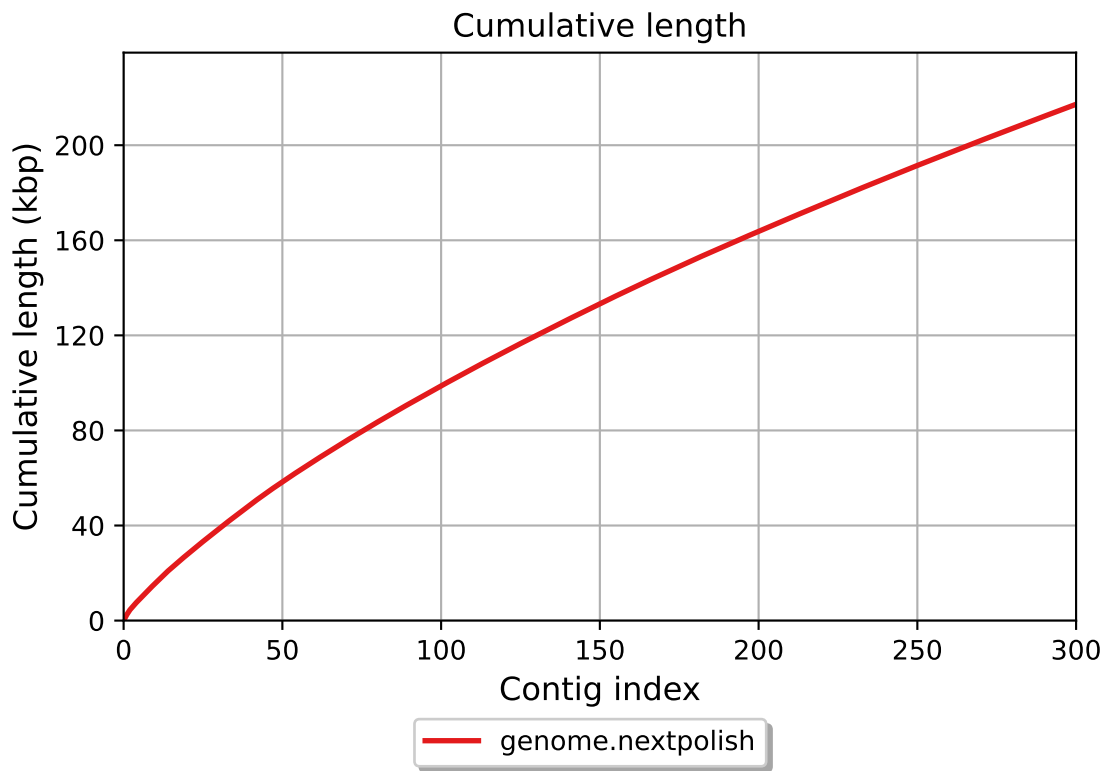


Report

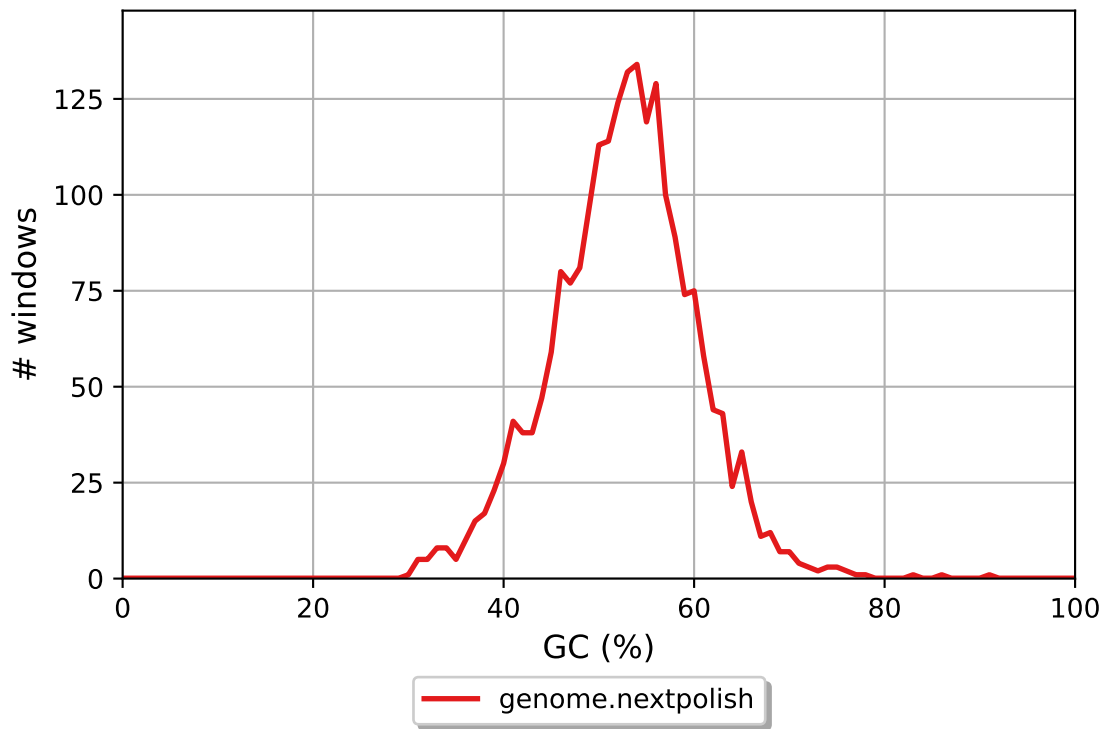
	genome.nextpolish
# contigs (>= 0 bp)	6056
# contigs (>= 1000 bp)	40
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1382159
Total length (>= 1000 bp)	48849
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	300
Largest contig	2502
Total length	217226
GC (%)	52.64
N50	708
N90	525
auN	809.5
L50	114
L90	258
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	0 + 1 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).

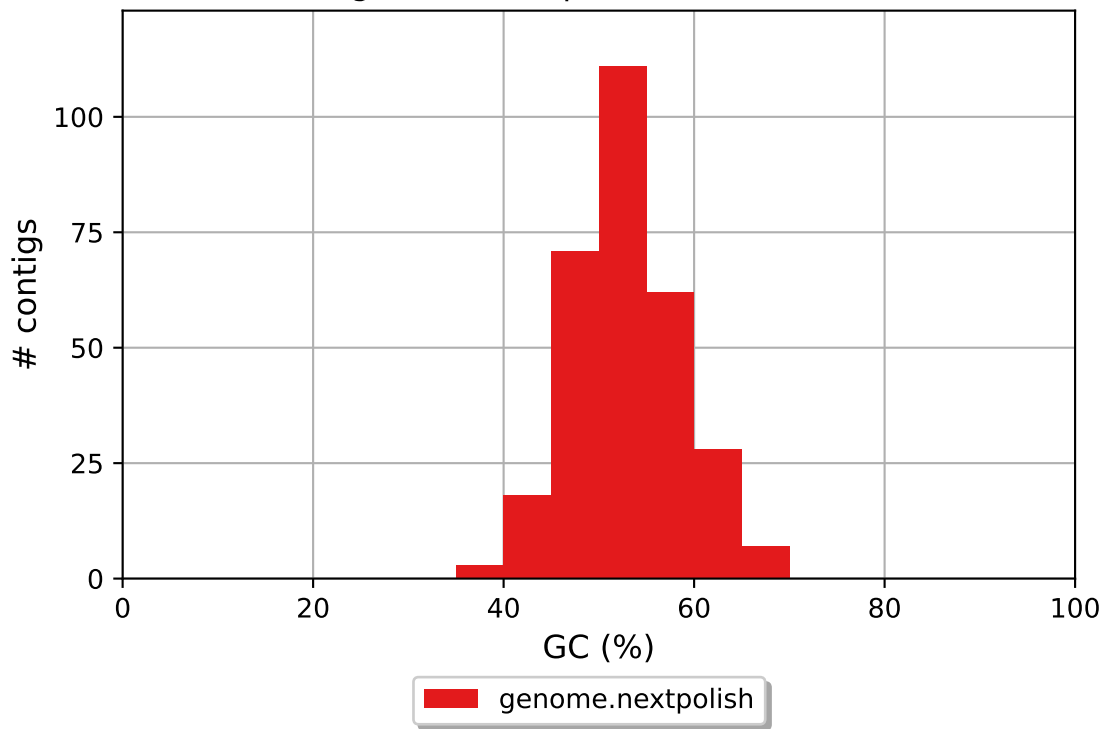




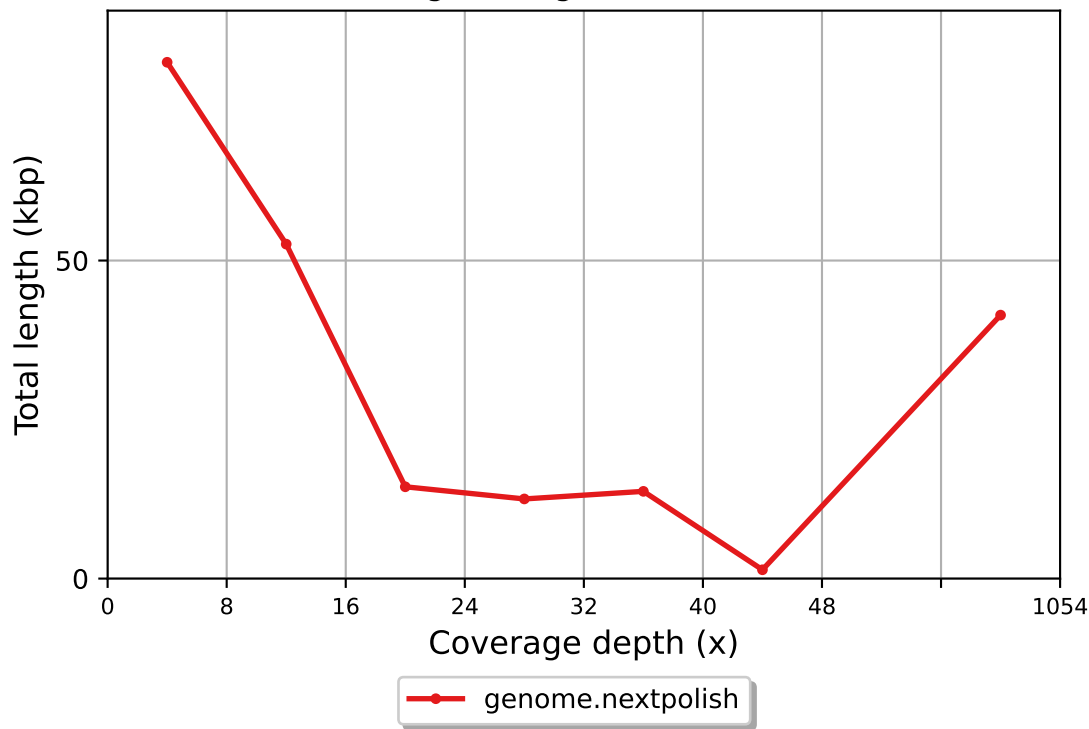
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 8x)



genome.nextpolish coverage histogram (bin size: 8x)

