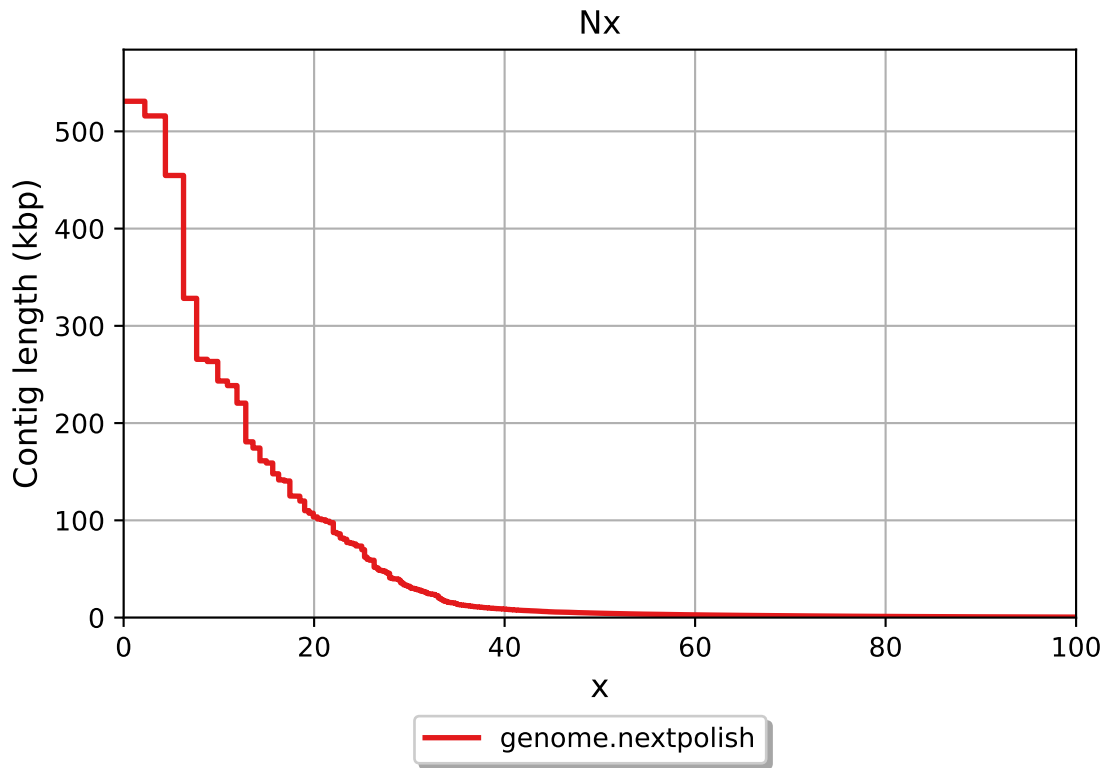


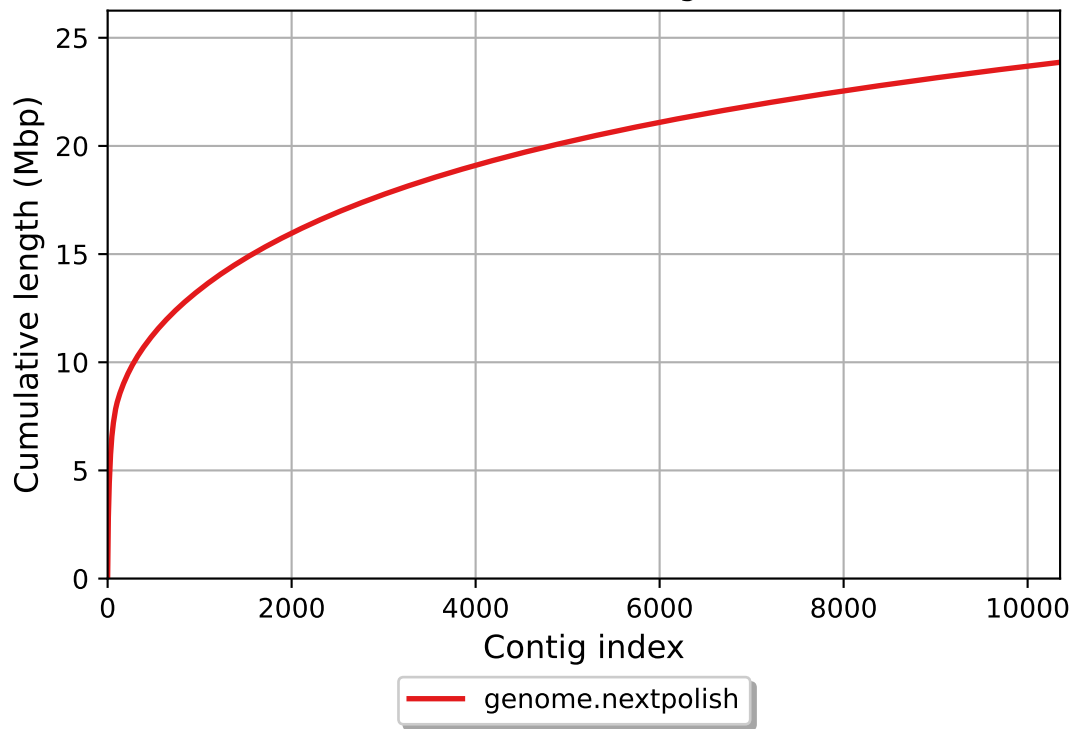
Report

	genome.nextpolish
# contigs (>= 0 bp)	28603
# contigs (>= 1000 bp)	4898
# contigs (>= 5000 bp)	535
# contigs (>= 10000 bp)	185
# contigs (>= 25000 bp)	78
# contigs (>= 50000 bp)	42
Total length (>= 0 bp)	29194245
Total length (>= 1000 bp)	20087897
Total length (>= 5000 bp)	11484565
Total length (>= 10000 bp)	9135955
Total length (>= 25000 bp)	7628324
Total length (>= 50000 bp)	6380241
# contigs	10353
Largest contig	530930
Total length	23867857
GC (%)	41.54
N50	4492
N90	774
auN	69208.4
L50	631
L90	6485
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	10 + 4 part

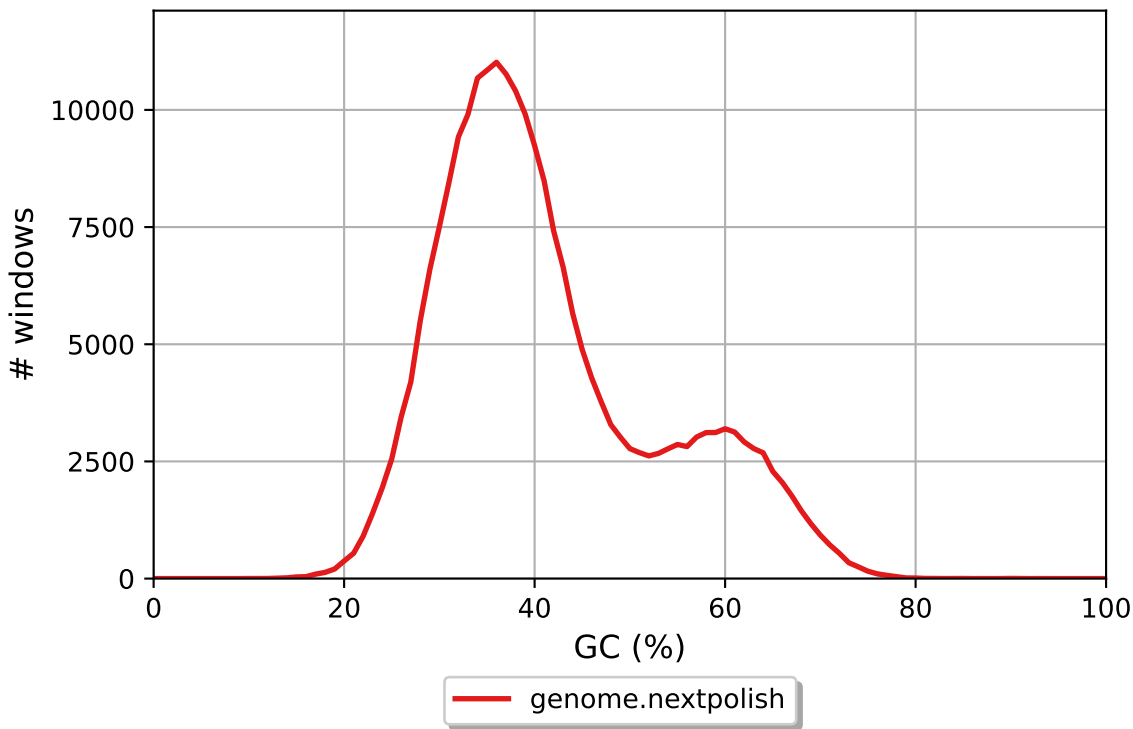
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



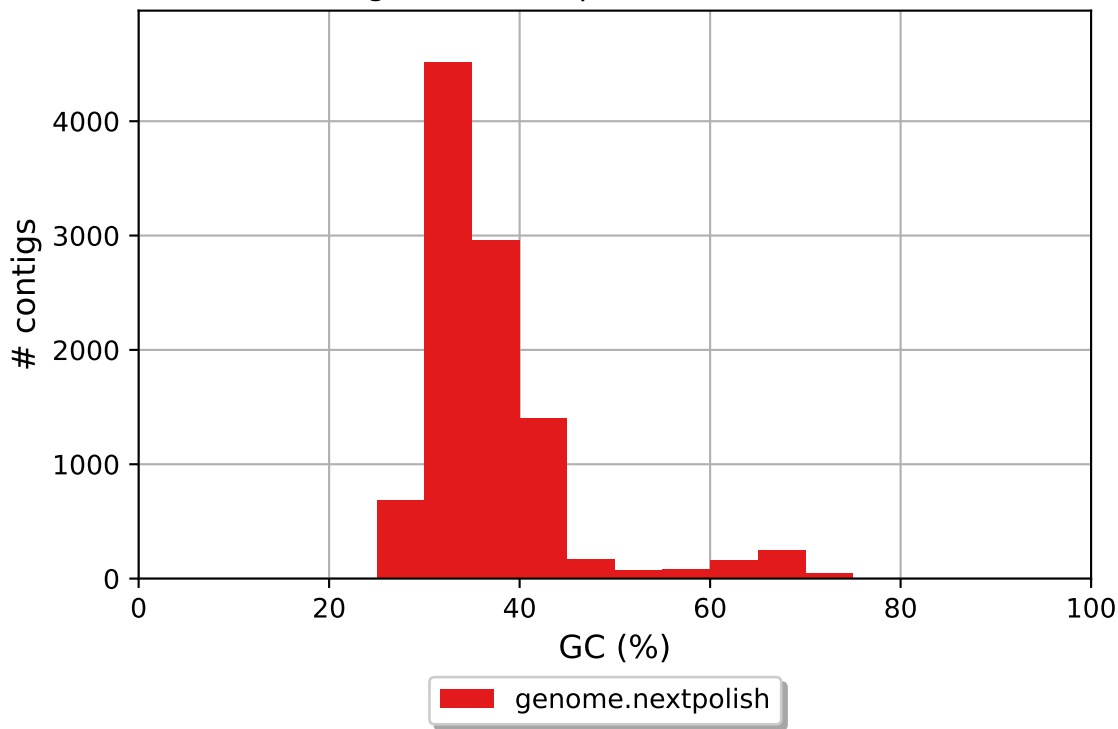
Cumulative length



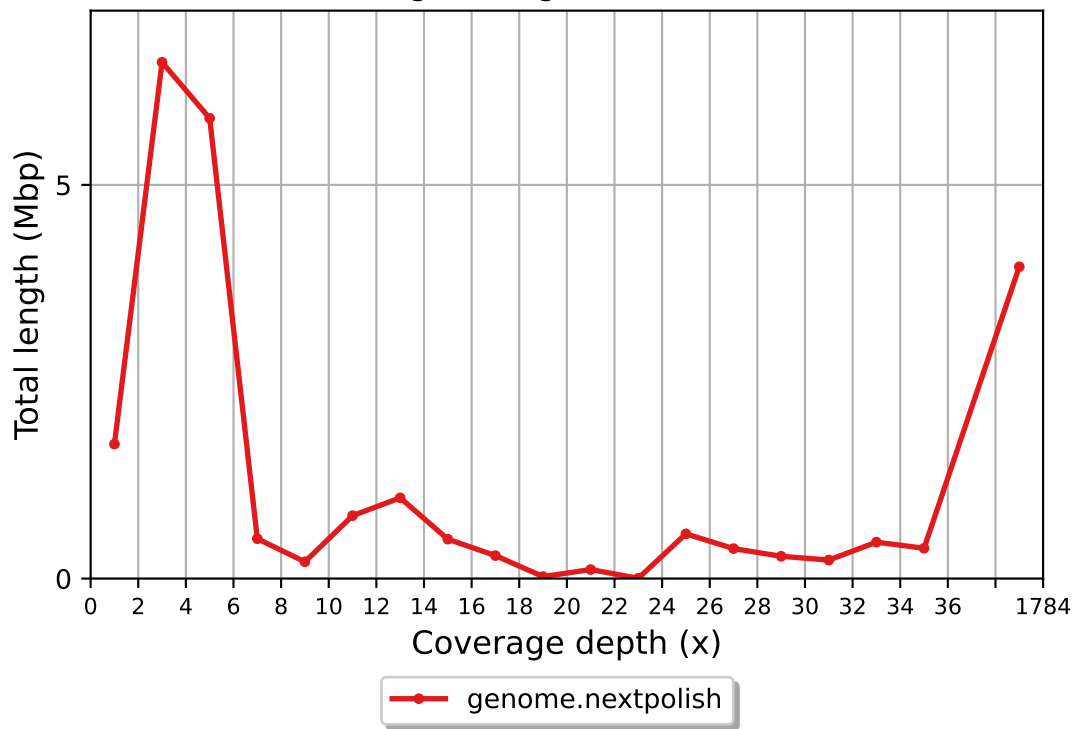
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 2x)



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

