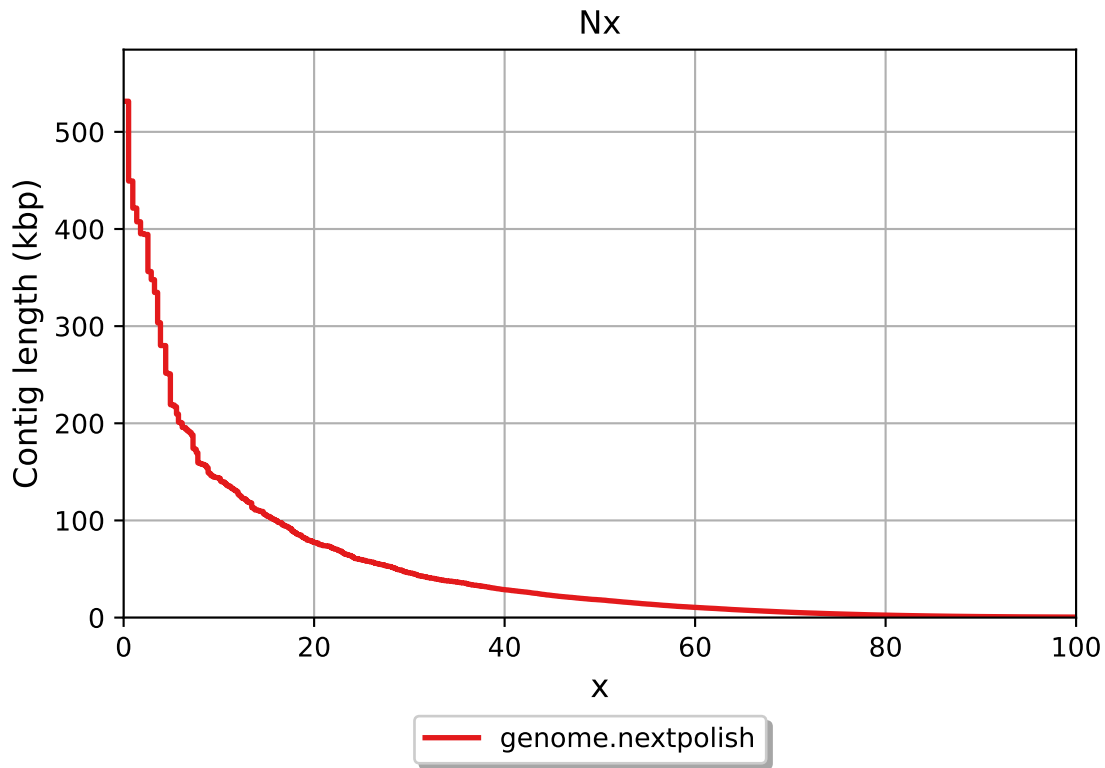


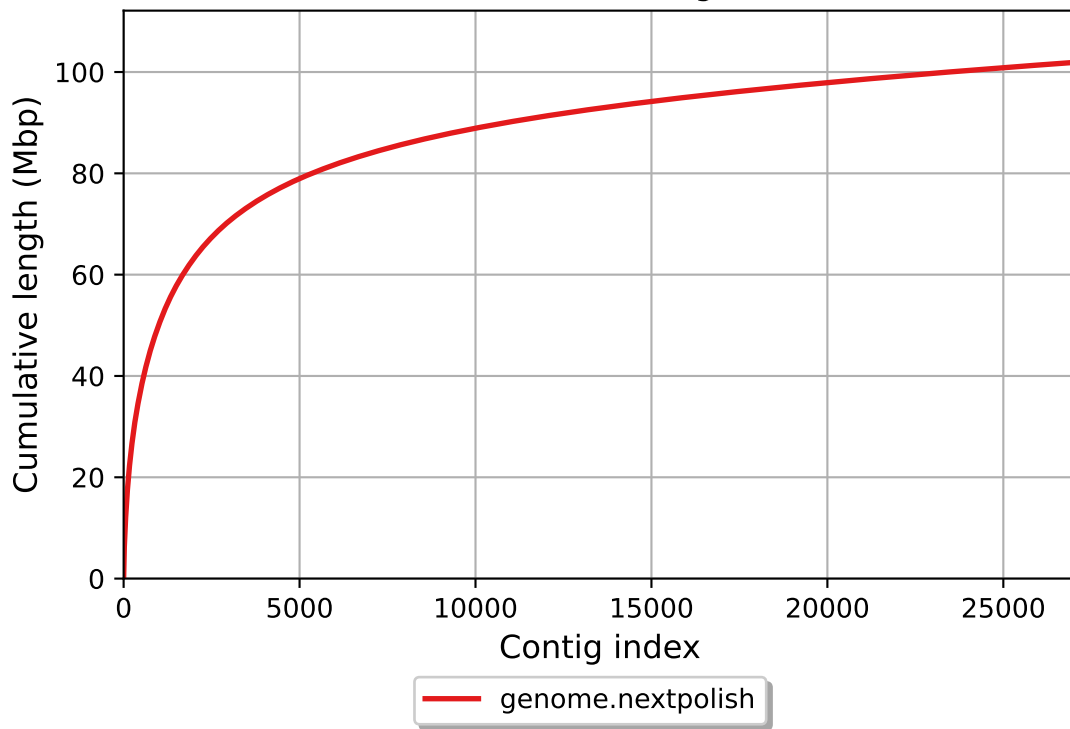
# Report

	genome.nextpolish
# contigs (>= 0 bp)	86368
# contigs (>= 1000 bp)	12921
# contigs (>= 5000 bp)	3373
# contigs (>= 10000 bp)	1880
# contigs (>= 25000 bp)	717
# contigs (>= 50000 bp)	284
Total length (>= 0 bp)	119081434
Total length (>= 1000 bp)	92277711
Total length (>= 5000 bp)	72592072
Total length (>= 10000 bp)	62091369
Total length (>= 25000 bp)	44019881
Total length (>= 50000 bp)	29196878
# contigs	27068
Largest contig	531483
Total length	101925546
GC (%)	47.26
N50	18269
N90	1047
auN	53044.3
L50	1047
L90	12390
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	32 + 18 part

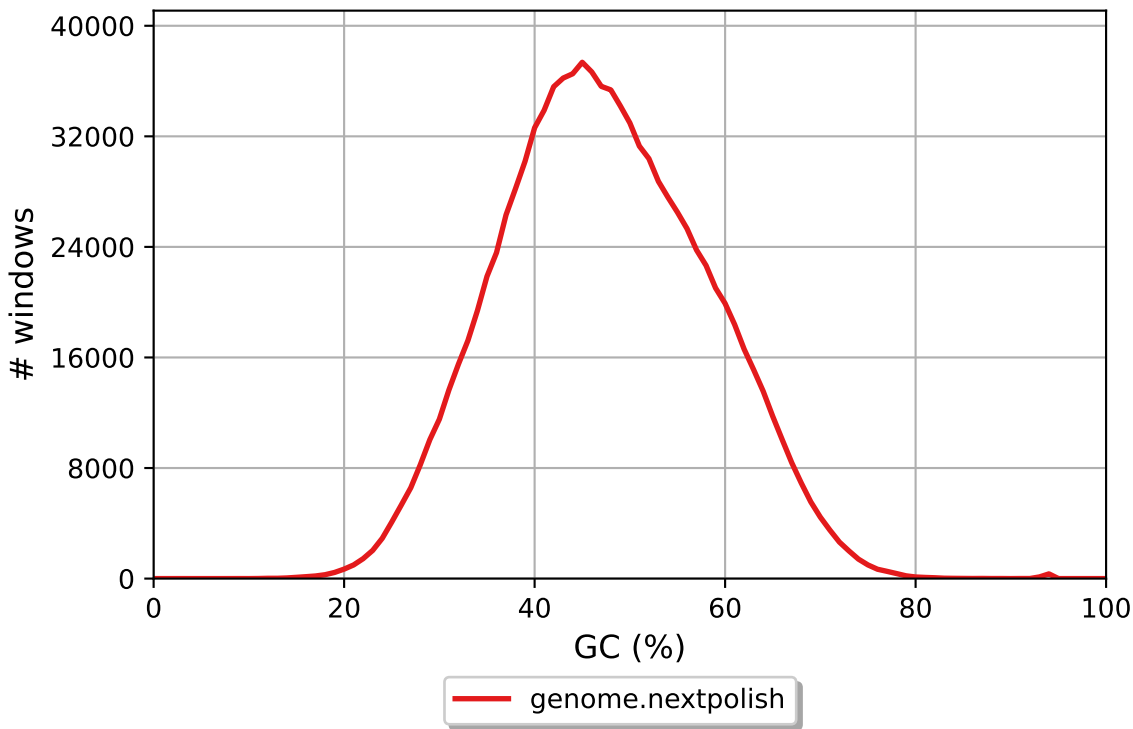
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



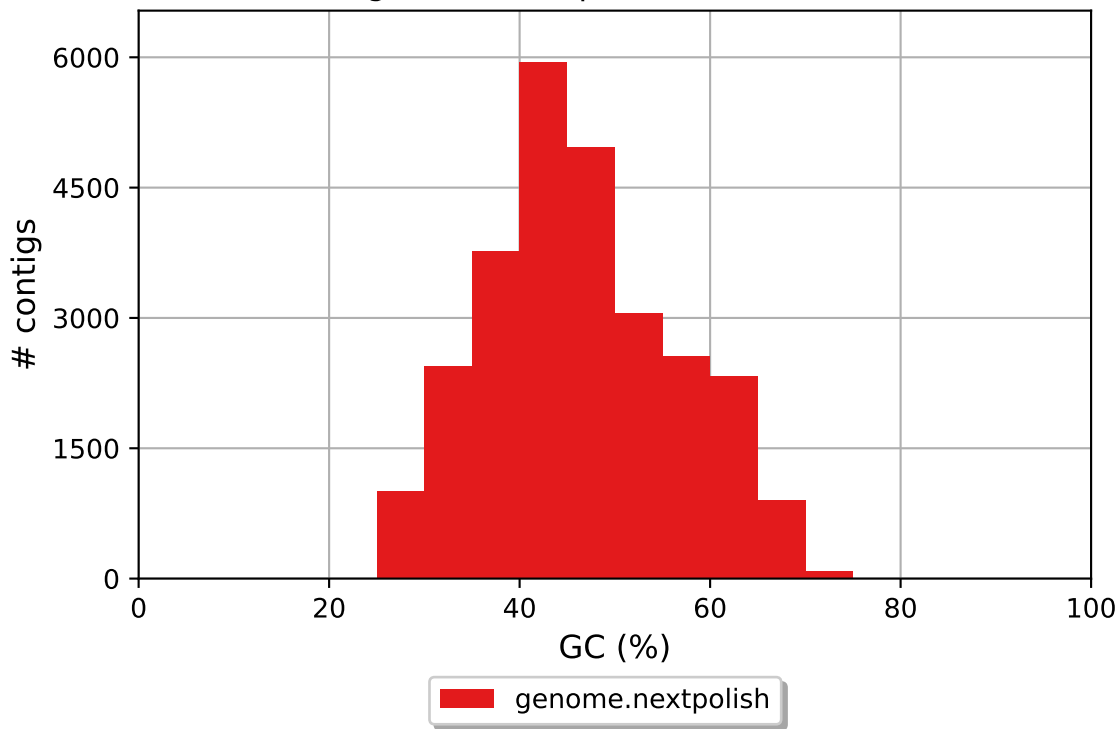
Cumulative length



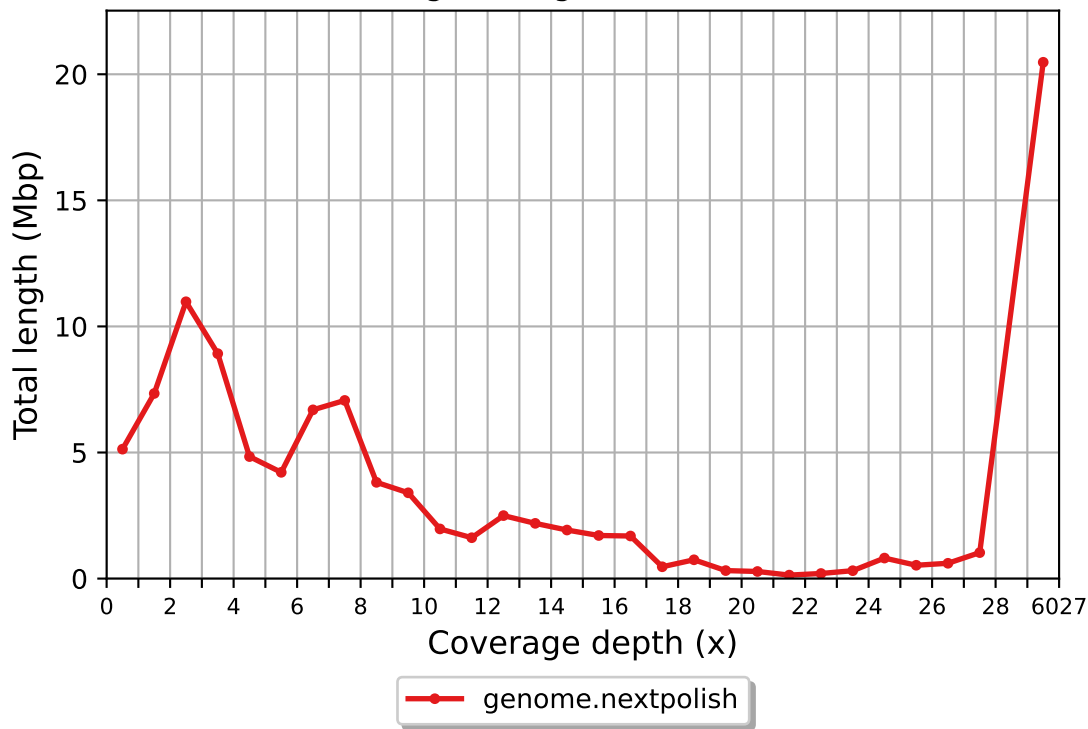
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



genome.nextpolish coverage histogram (bin size: 1x)

