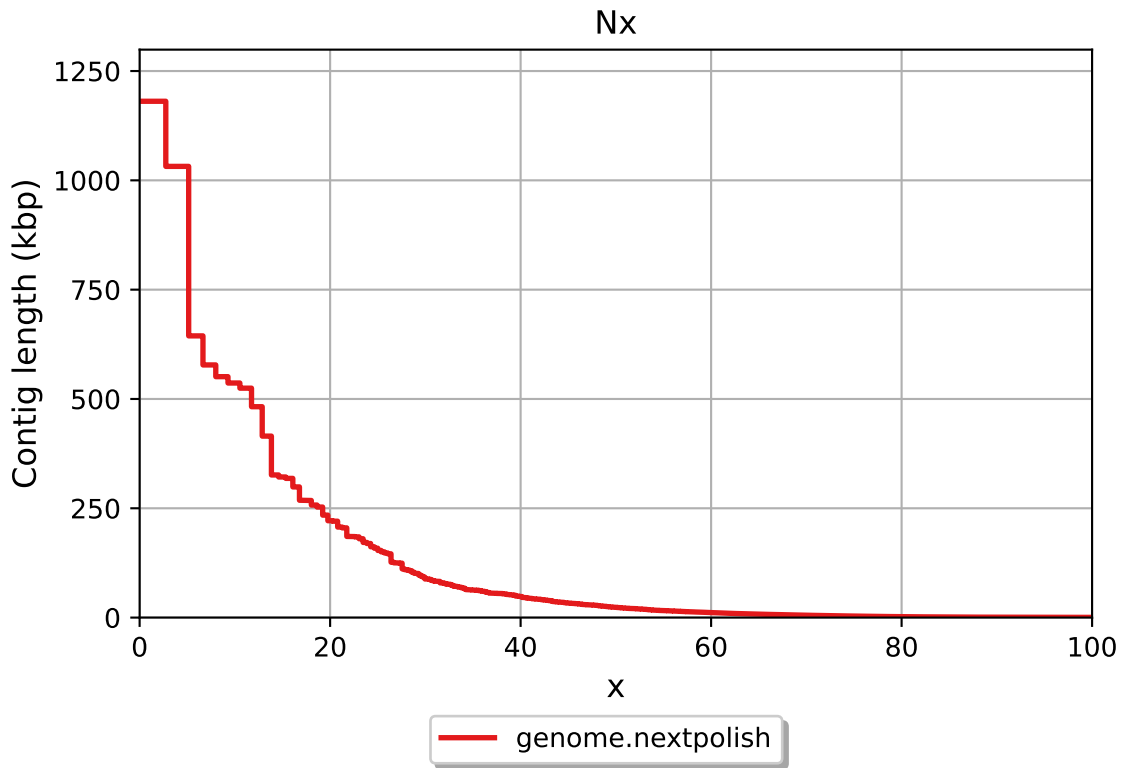


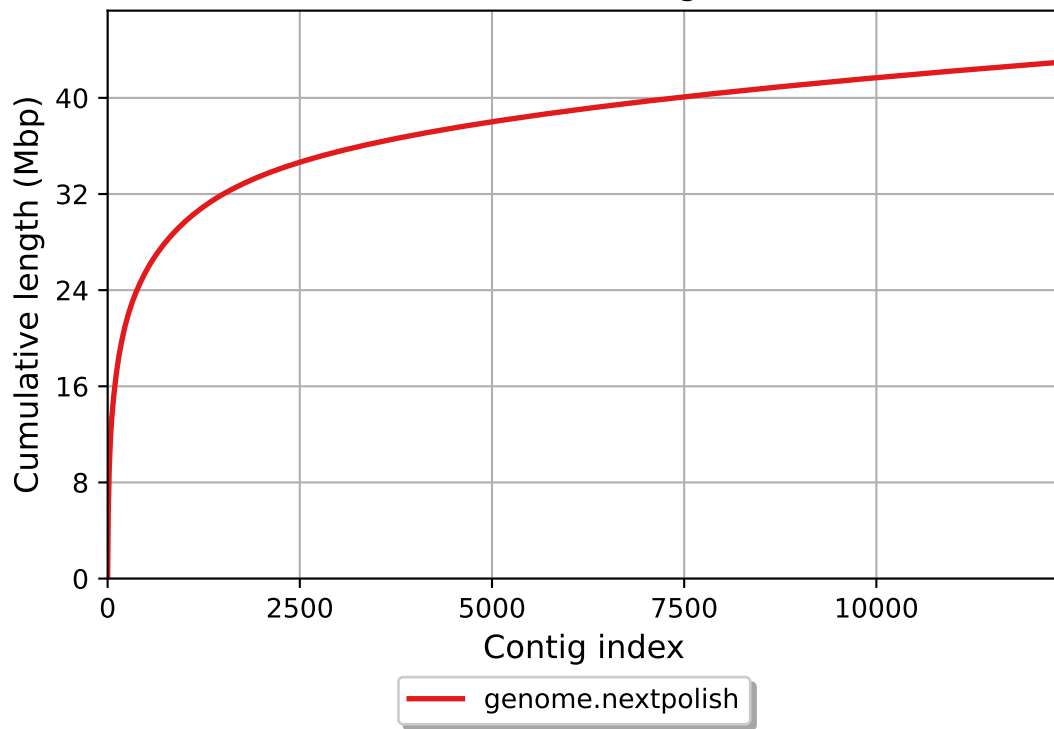
# Report

	genome.nextpolish
# contigs (>= 0 bp)	55773
# contigs (>= 1000 bp)	4909
# contigs (>= 5000 bp)	1159
# contigs (>= 10000 bp)	585
# contigs (>= 25000 bp)	232
# contigs (>= 50000 bp)	111
Total length (>= 0 bp)	55336184
Total length (>= 1000 bp)	37921314
Total length (>= 5000 bp)	30518995
Total length (>= 10000 bp)	26513070
Total length (>= 25000 bp)	21140776
Total length (>= 50000 bp)	16955072
# contigs	12390
Largest contig	1180851
Total length	42962136
GC (%)	44.65
N50	23407
N90	884
auN	150274.9
L50	247
L90	5702
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	62 + 6 part

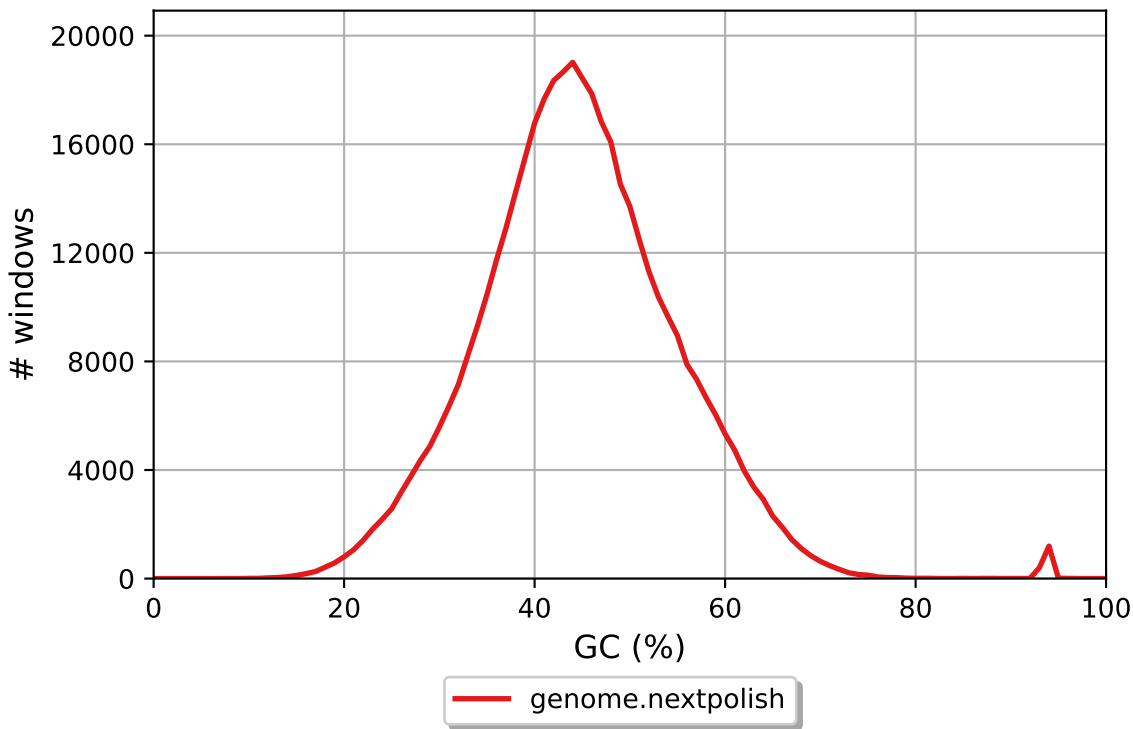
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



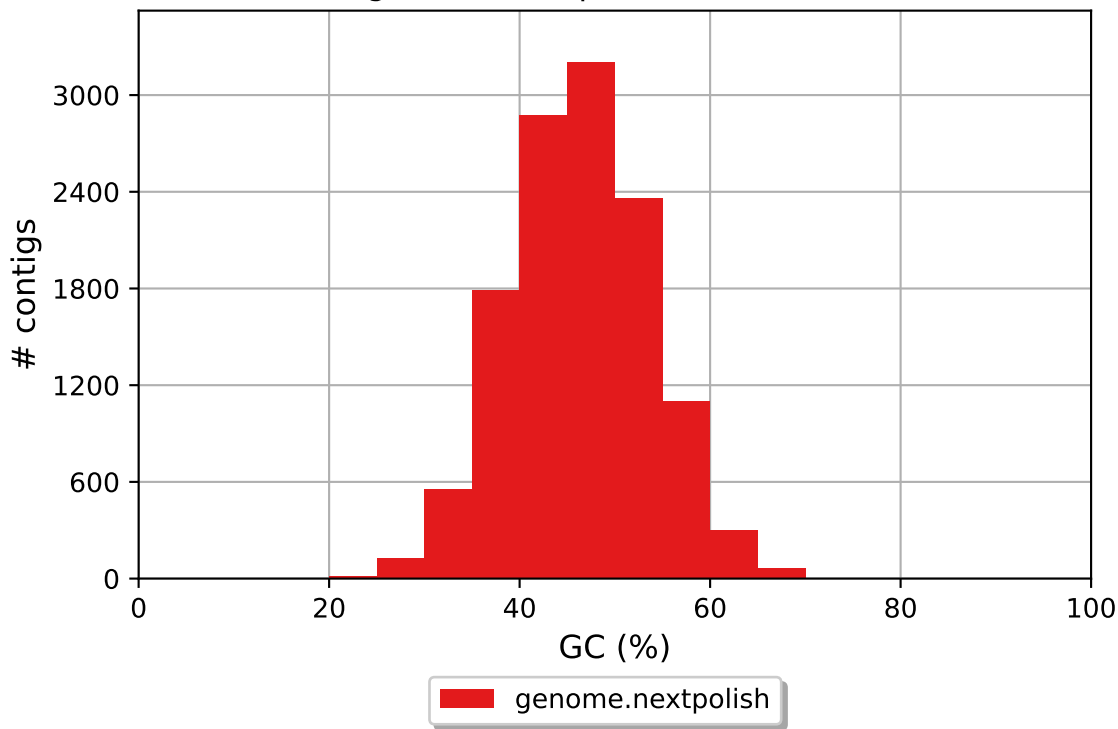
Cumulative length



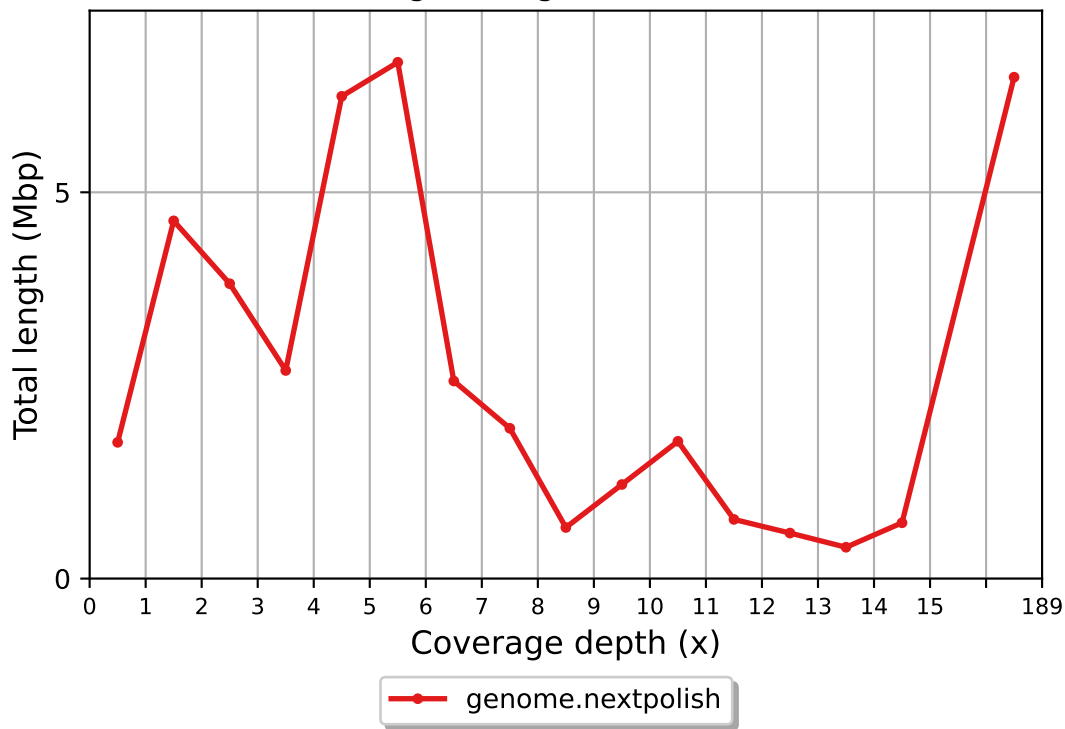
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

