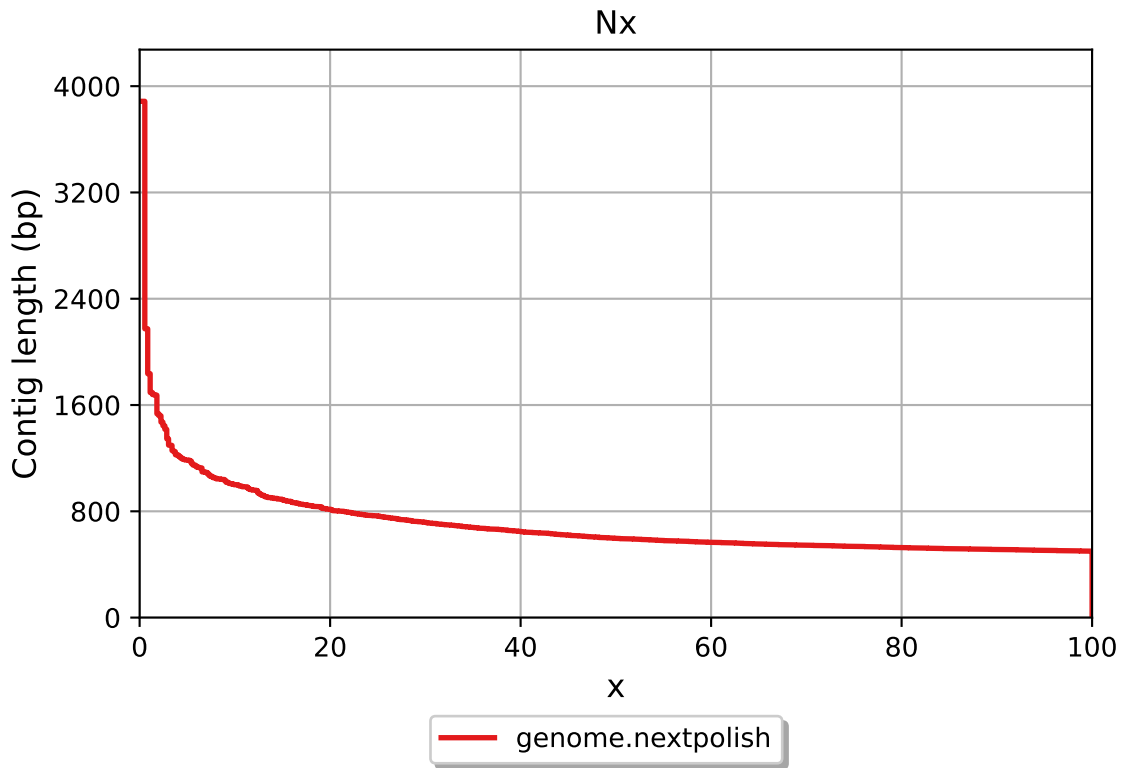
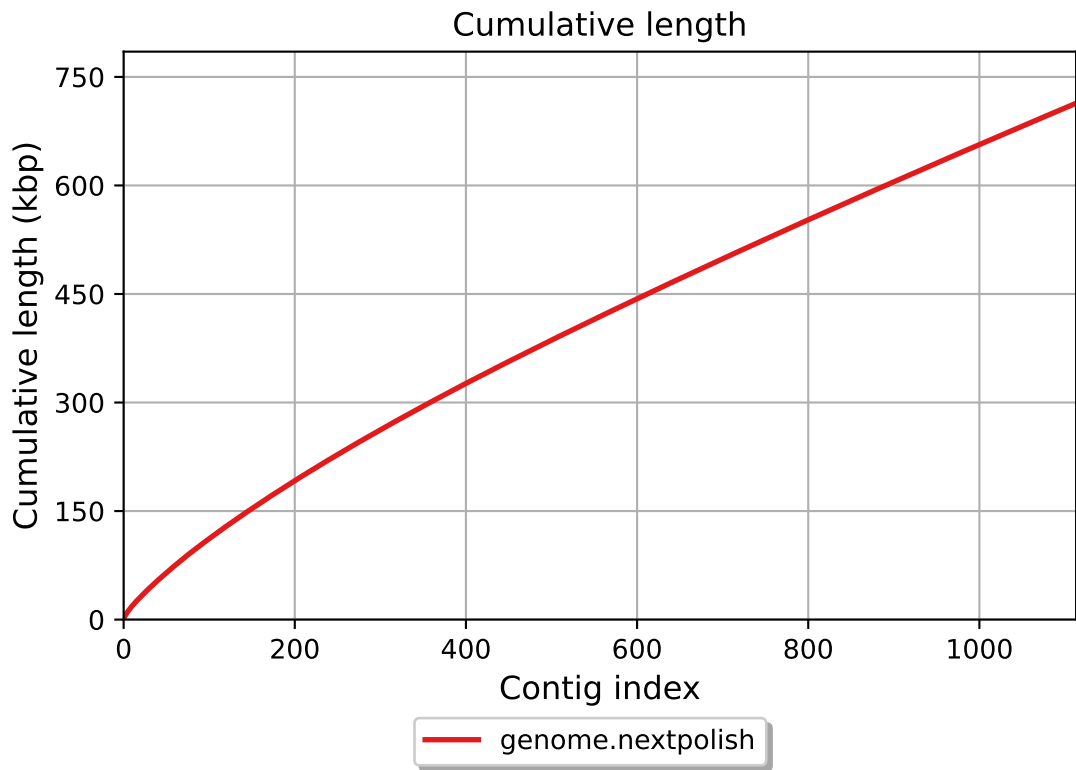


# Report

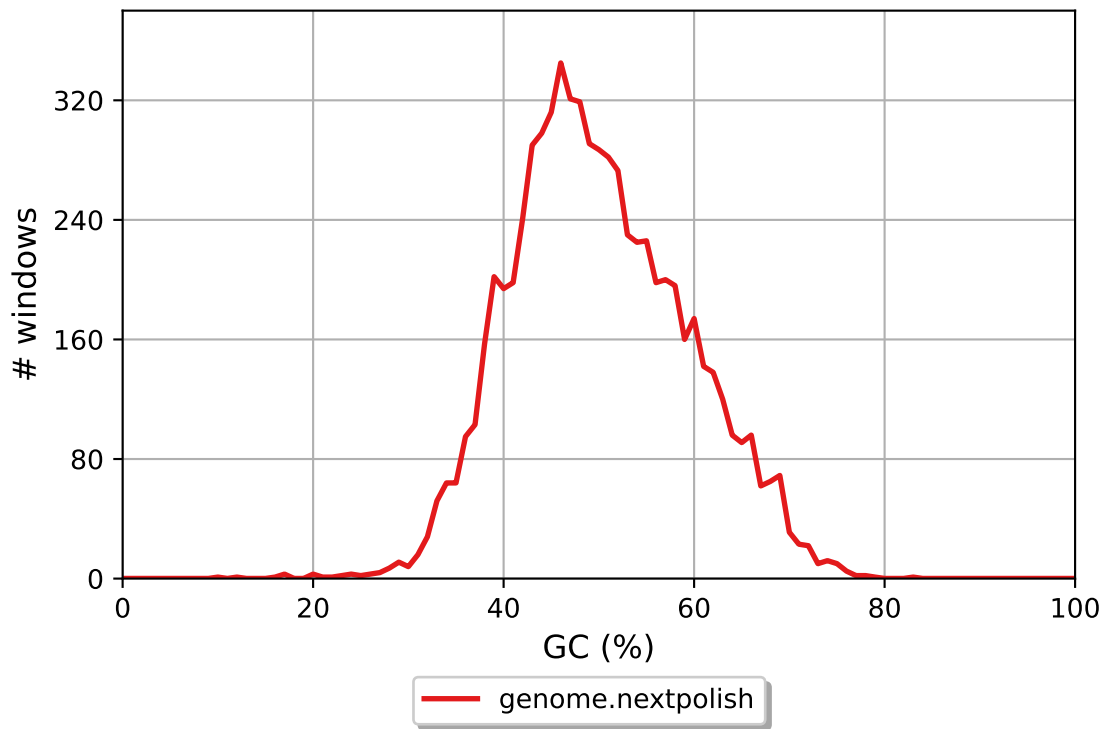
	genome.nextpolish
# contigs (>= 0 bp)	3732
# contigs (>= 1000 bp)	59
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1717873
Total length (>= 1000 bp)	73824
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1113
Largest contig	3886
Total length	713581
GC (%)	50.07
N50	597
N90	513
auN	706.1
L50	451
L90	973
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	1 + 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).

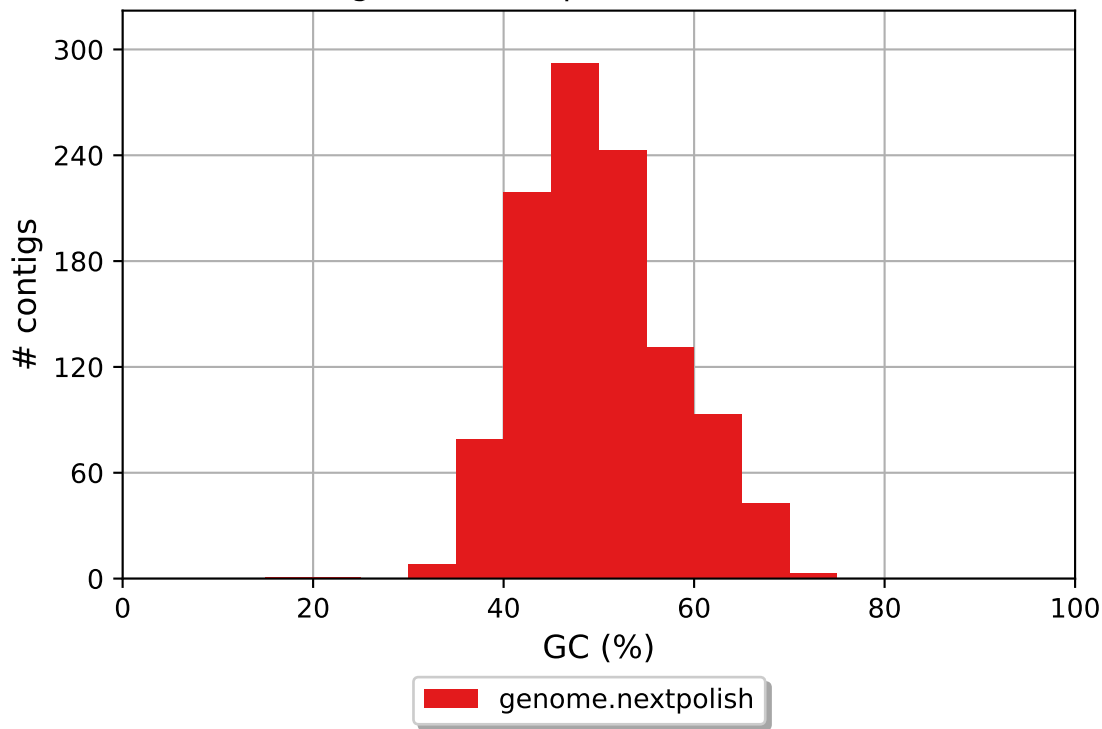




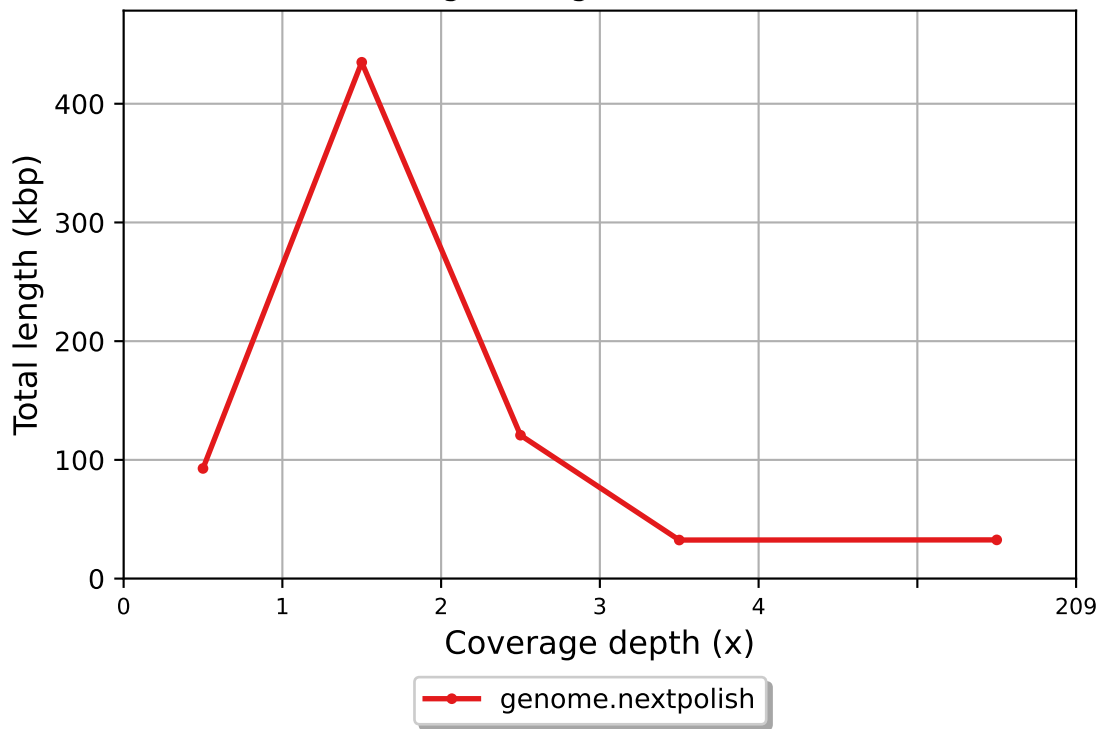
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

