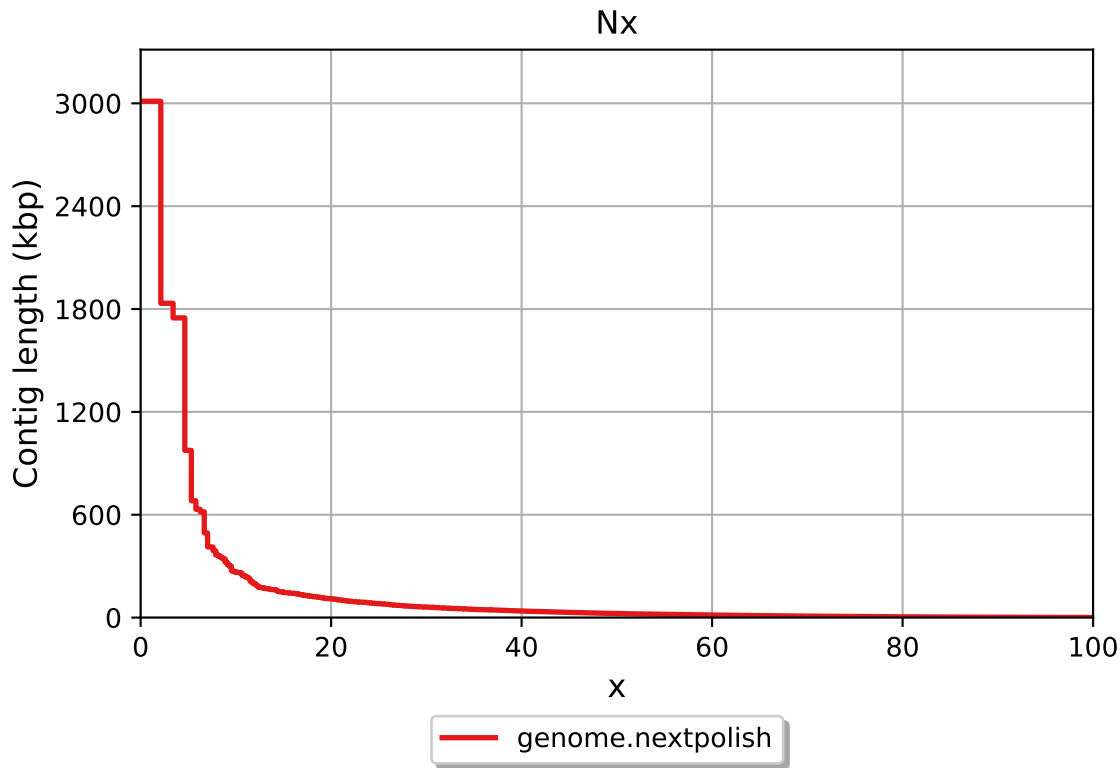
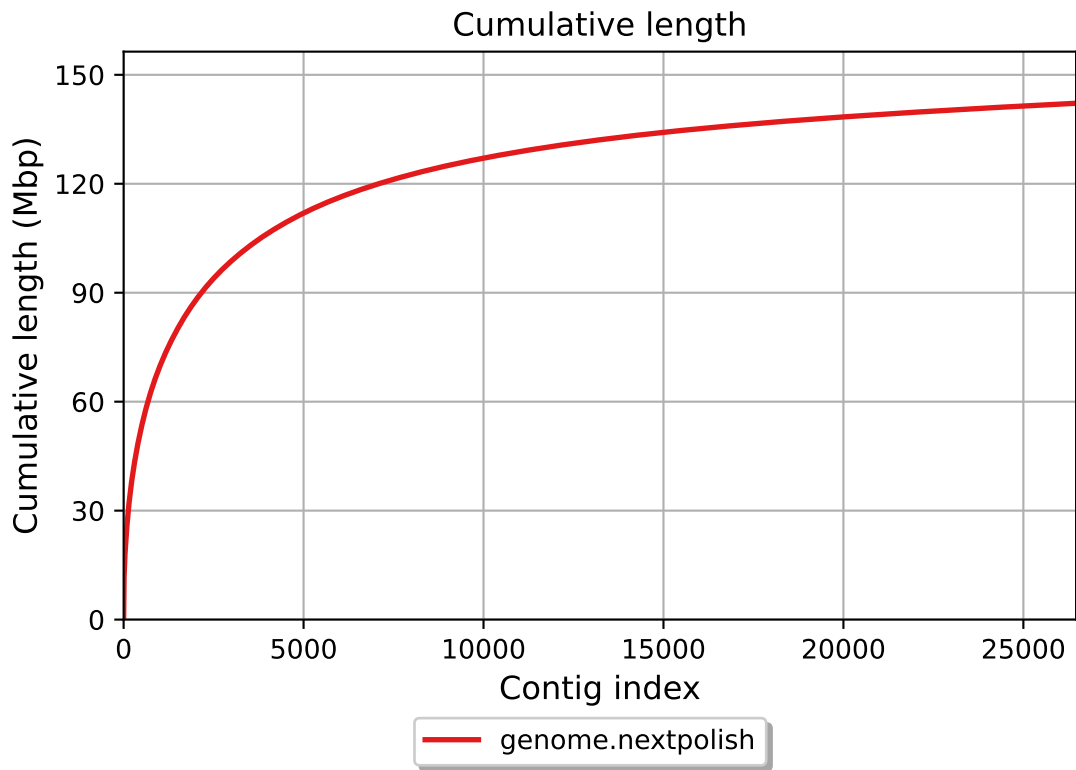


# Report

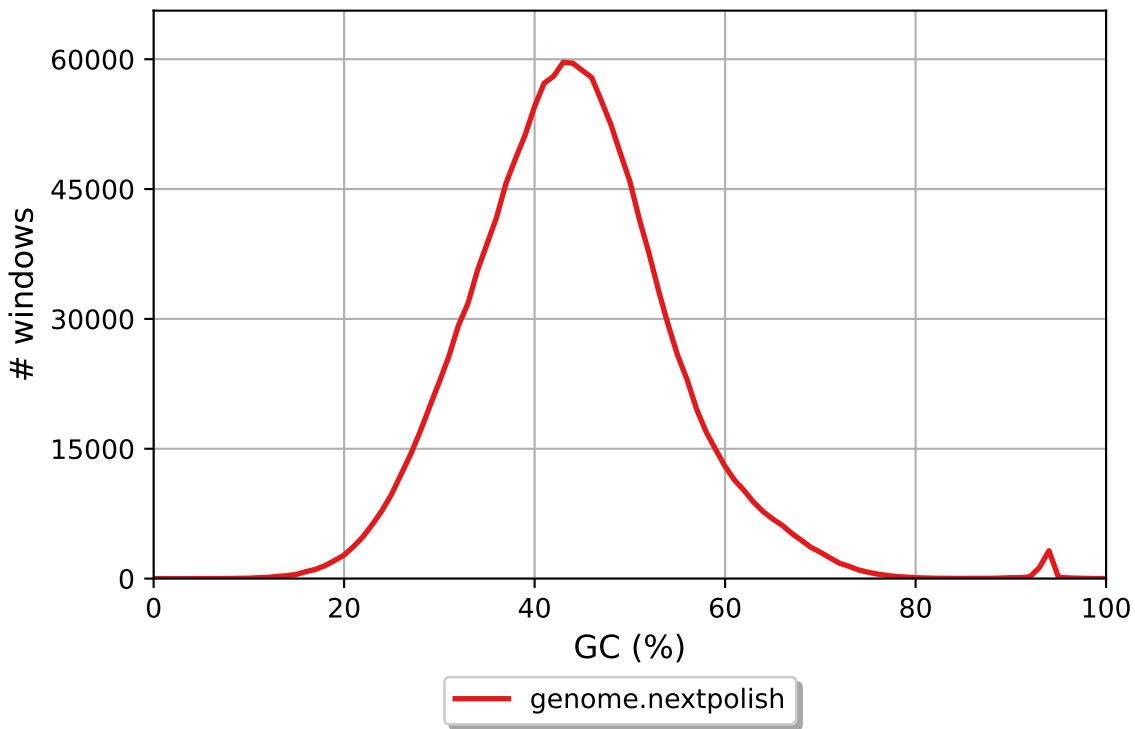
	genome.nextpolish
# contigs (>= 0 bp)	152572
# contigs (>= 1000 bp)	15548
# contigs (>= 5000 bp)	4935
# contigs (>= 10000 bp)	2661
# contigs (>= 25000 bp)	998
# contigs (>= 50000 bp)	400
Total length (>= 0 bp)	175525781
Total length (>= 1000 bp)	134727379
Total length (>= 5000 bp)	111608739
Total length (>= 10000 bp)	95626114
Total length (>= 25000 bp)	69529249
Total length (>= 50000 bp)	48606999
# contigs	26465
Largest contig	3012071
Total length	142165720
GC (%)	43.91
N50	23878
N90	1791
auN	172848.9
L50	1062
L90	10481
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	64 + 20 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).

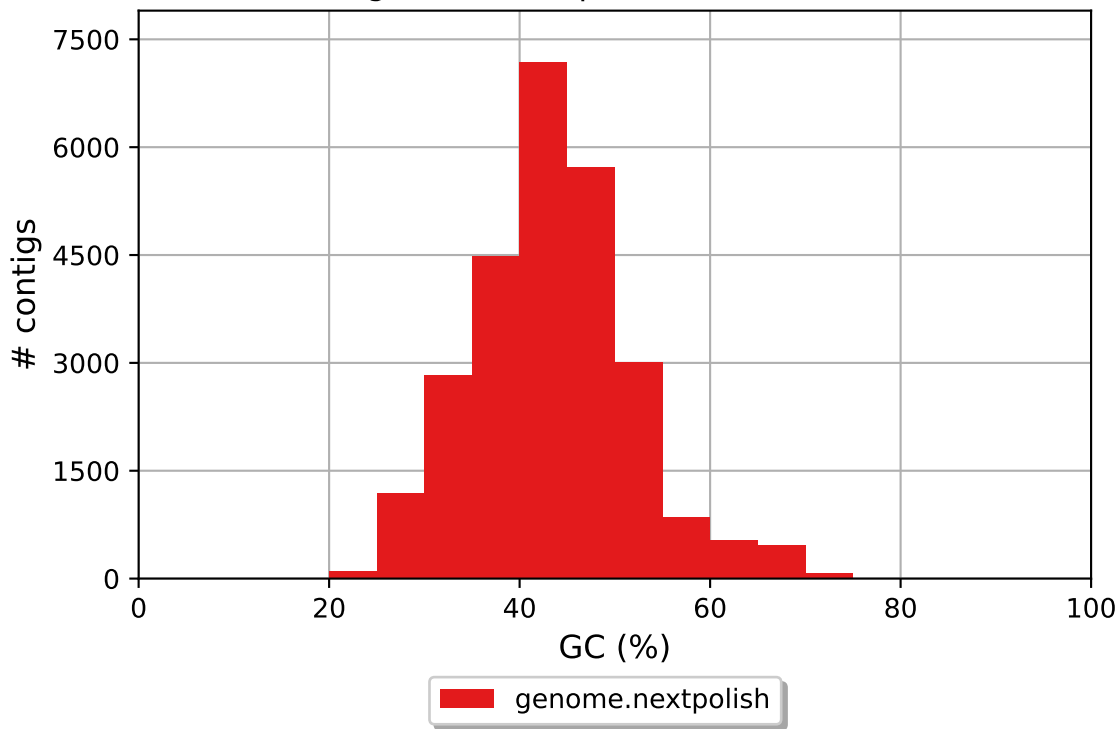




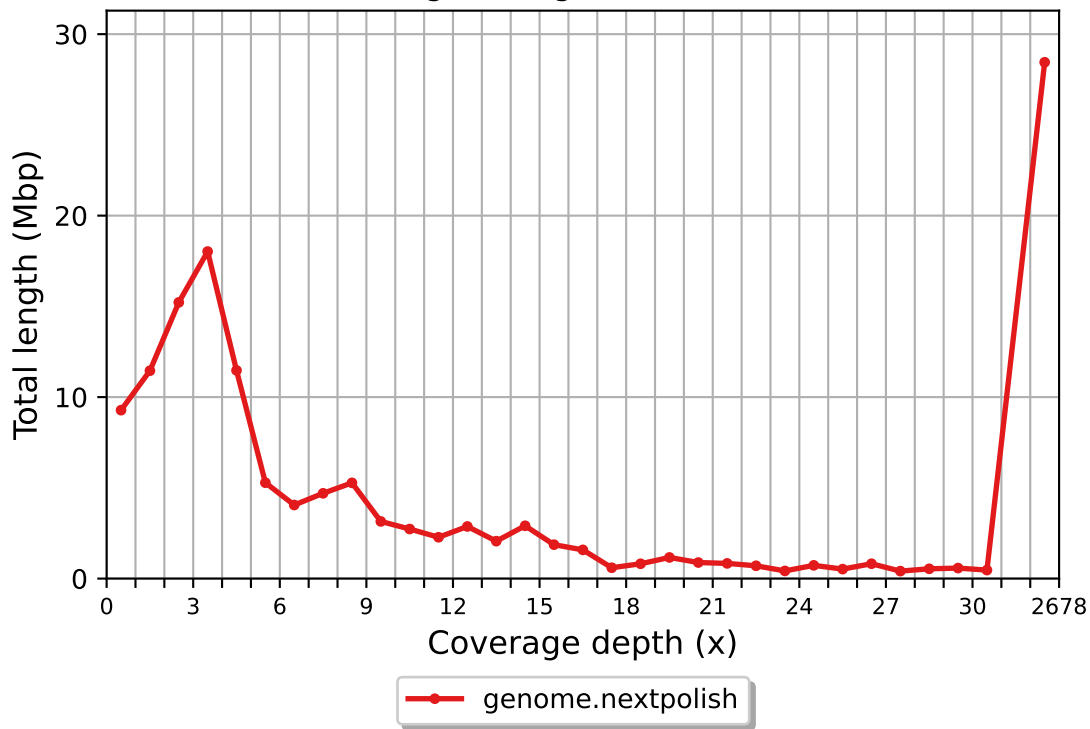
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

