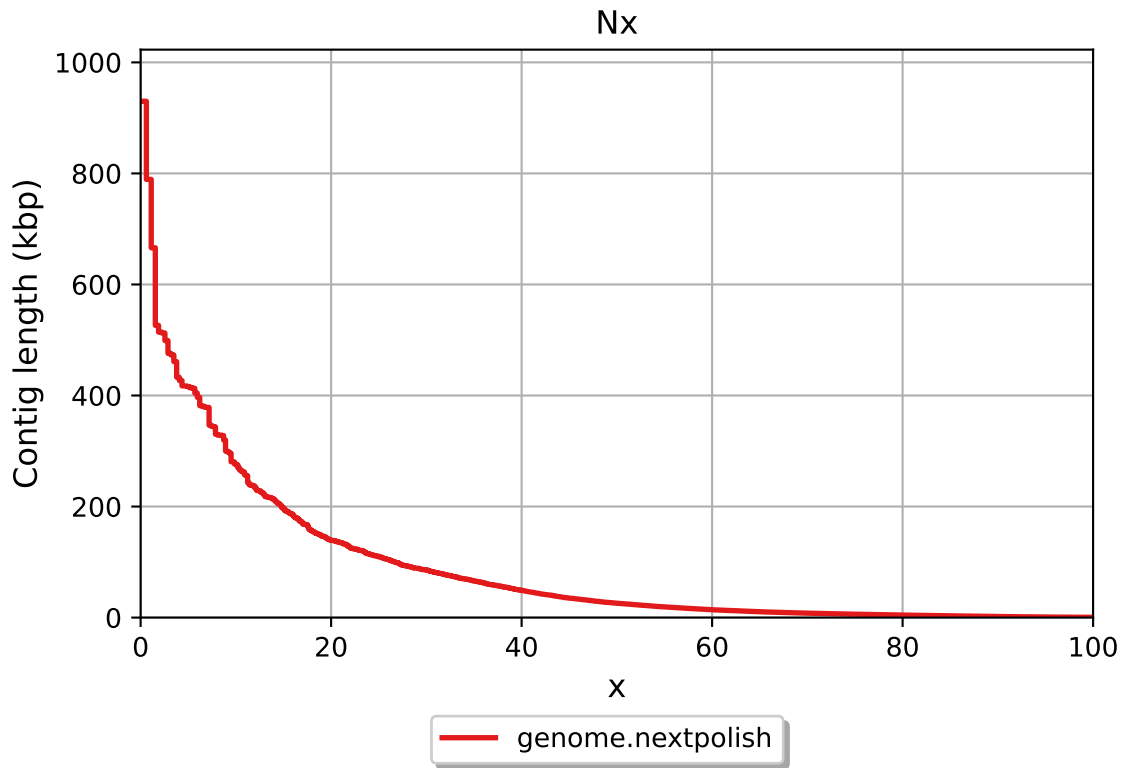


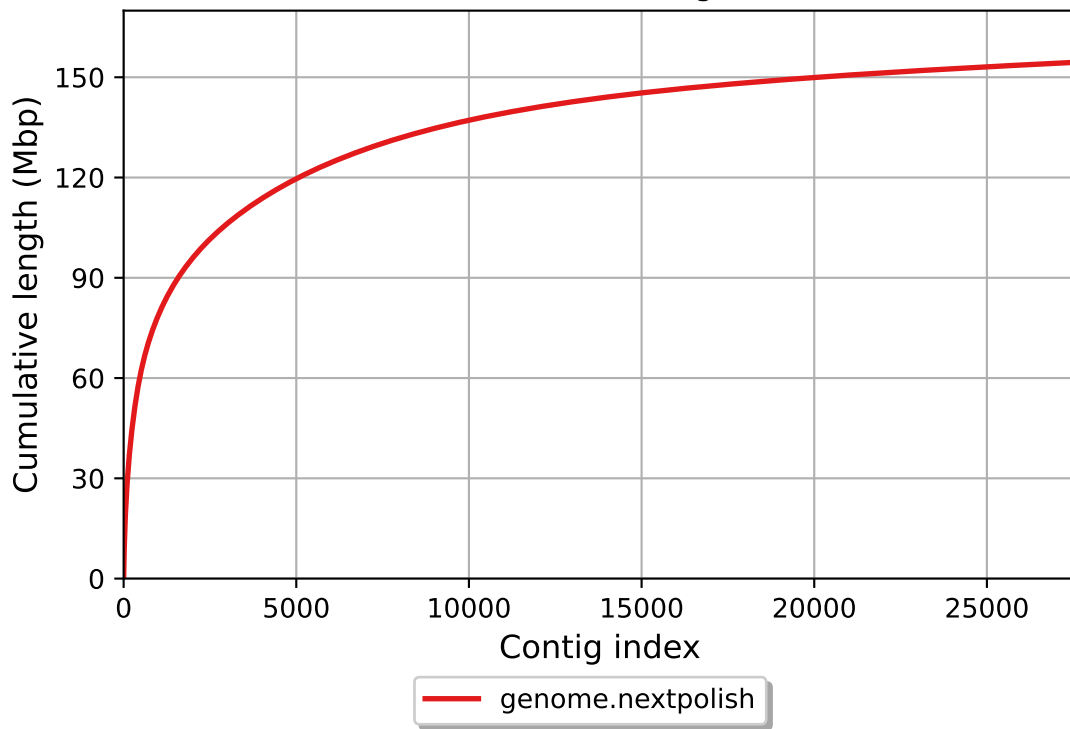
# Report

	genome.nextpolish
# contigs (>= 0 bp)	112378
# contigs (>= 1000 bp)	16481
# contigs (>= 5000 bp)	5312
# contigs (>= 10000 bp)	2519
# contigs (>= 25000 bp)	983
# contigs (>= 50000 bp)	487
Total length (>= 0 bp)	177577265
Total length (>= 1000 bp)	146914232
Total length (>= 5000 bp)	121244428
Total length (>= 10000 bp)	101766200
Total length (>= 25000 bp)	78256607
Total length (>= 50000 bp)	61189127
# contigs	27583
Largest contig	929961
Total length	154482985
GC (%)	48.08
N50	25878
N90	1982
auN	91533.7
L50	944
L90	10892
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	57 + 17 part

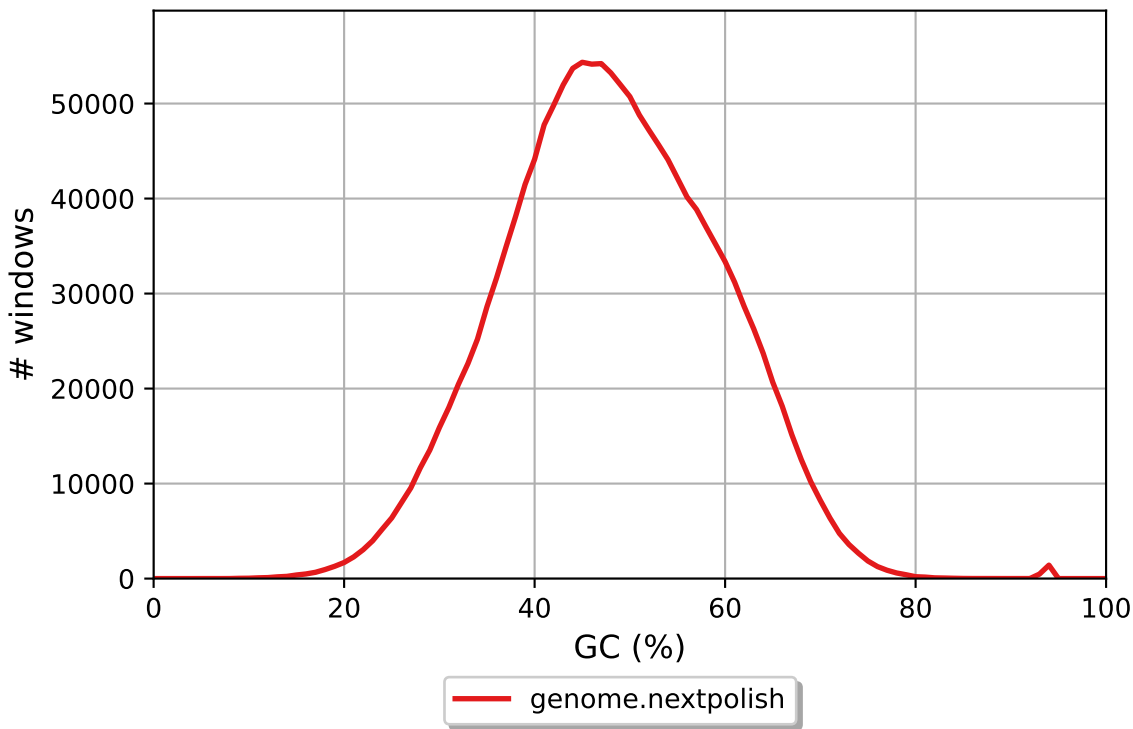
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



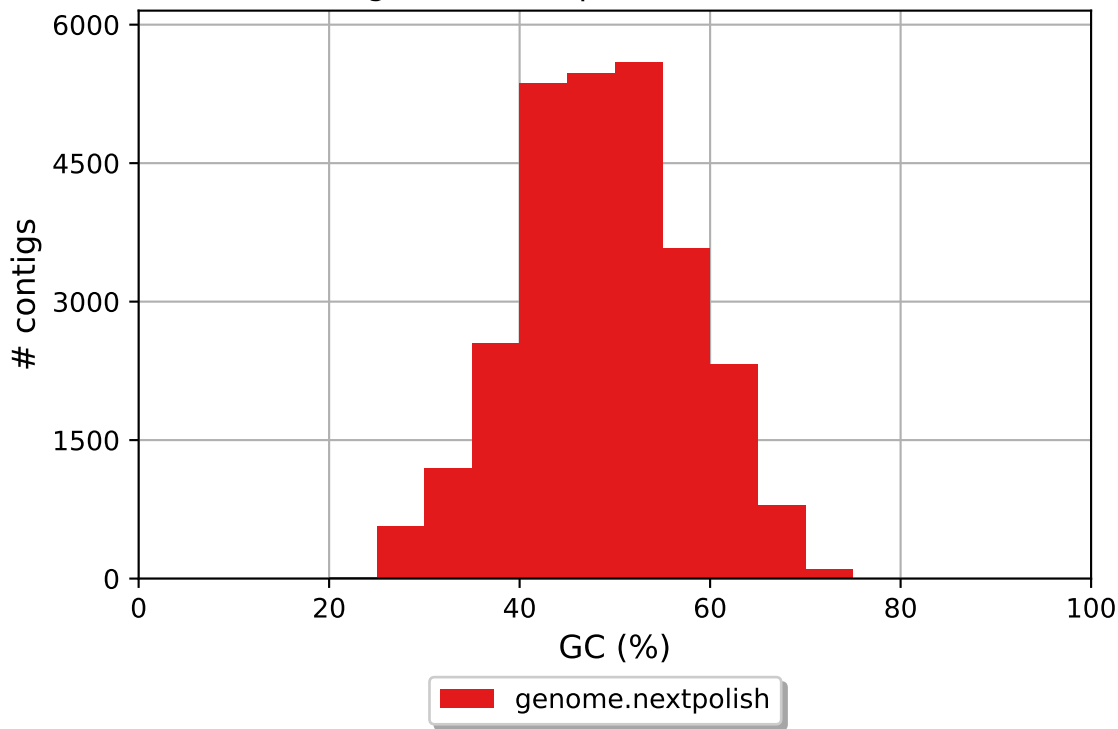
Cumulative length



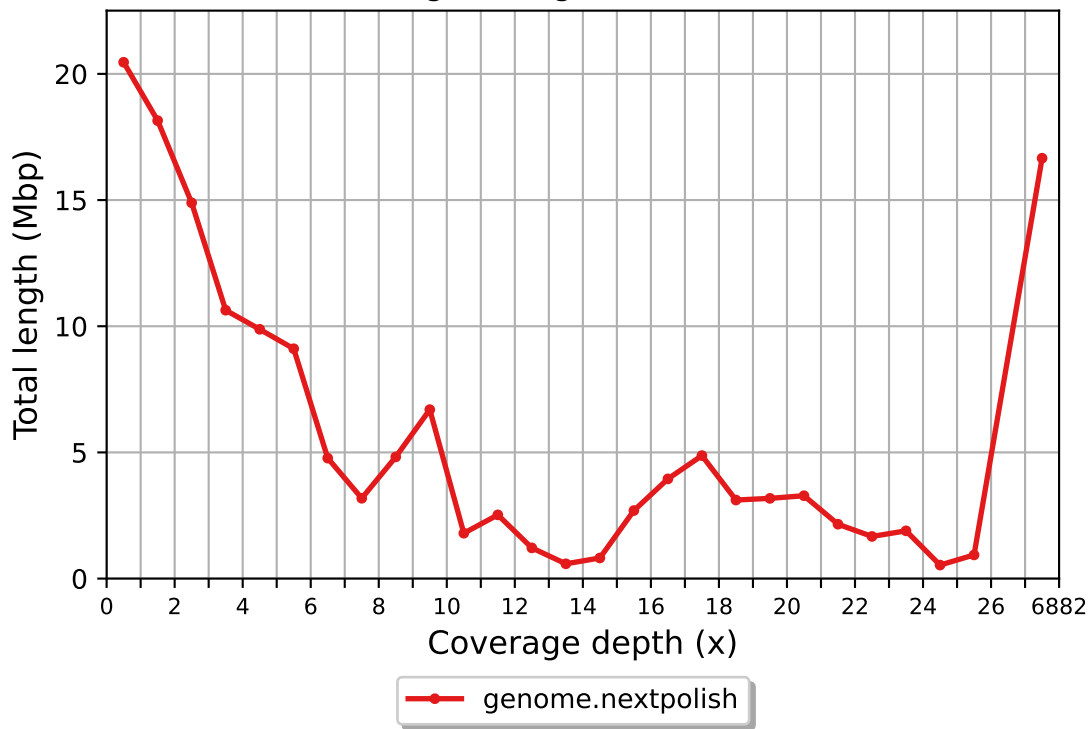
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

