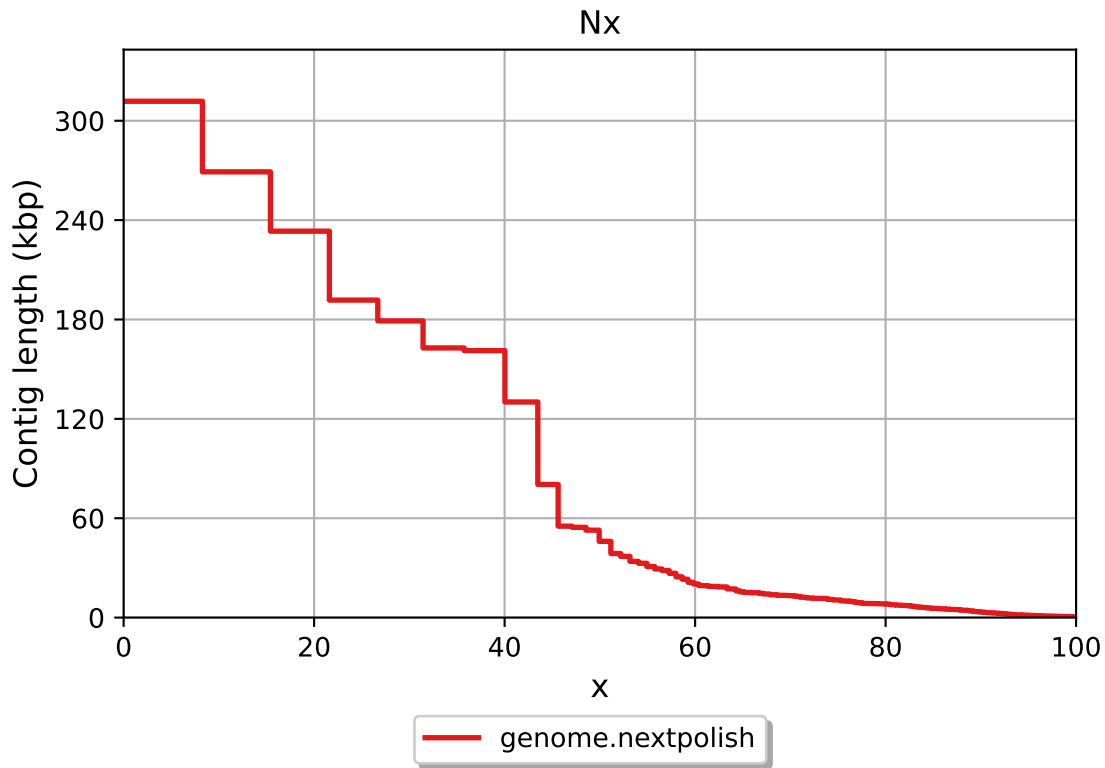


# Report

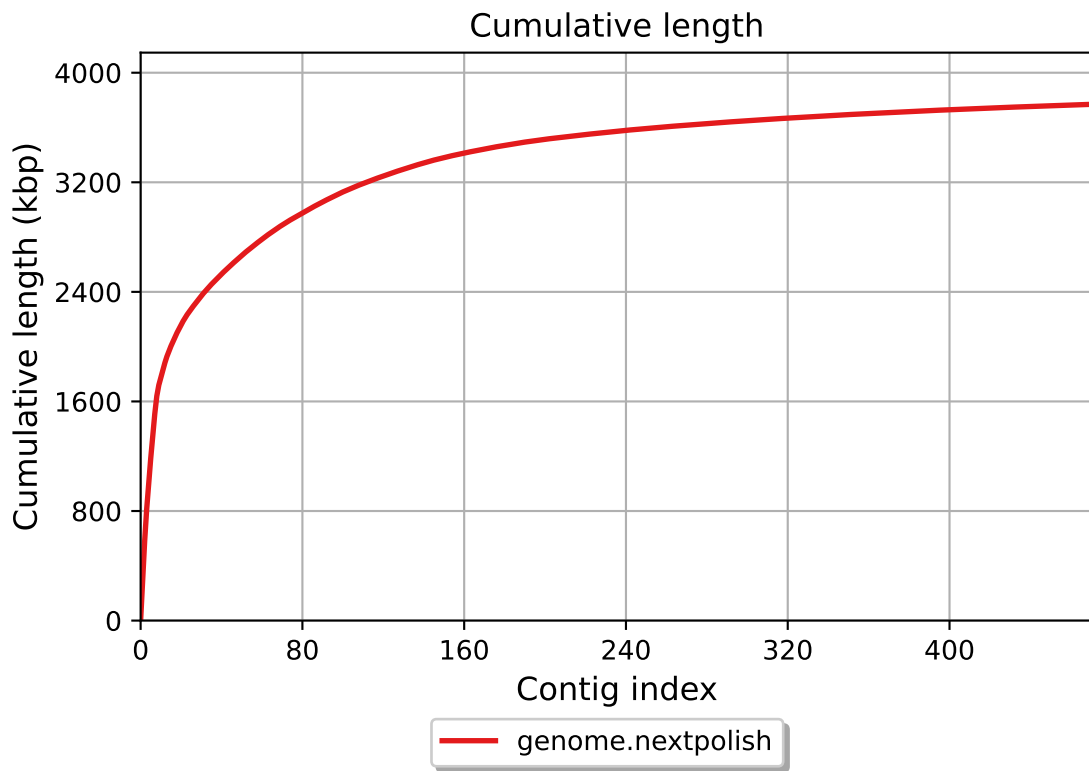
	genome.nextpolish
# contigs (>= 0 bp)	916
# contigs (>= 1000 bp)	297
# contigs (>= 5000 bp)	124
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	21
# contigs (>= 50000 bp)	12
Total length (>= 0 bp)	3888718
Total length (>= 1000 bp)	3646665
Total length (>= 5000 bp)	3266570
Total length (>= 10000 bp)	2858665
Total length (>= 25000 bp)	2185922
Total length (>= 50000 bp)	1882141
# contigs	471
Largest contig	311767
Total length	3769685
GC (%)	39.14
N50	46048
N90	3412
auN	106846.1
L50	13
L90	154
# N's per 100 kbp	0.95
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	18 + 2 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).

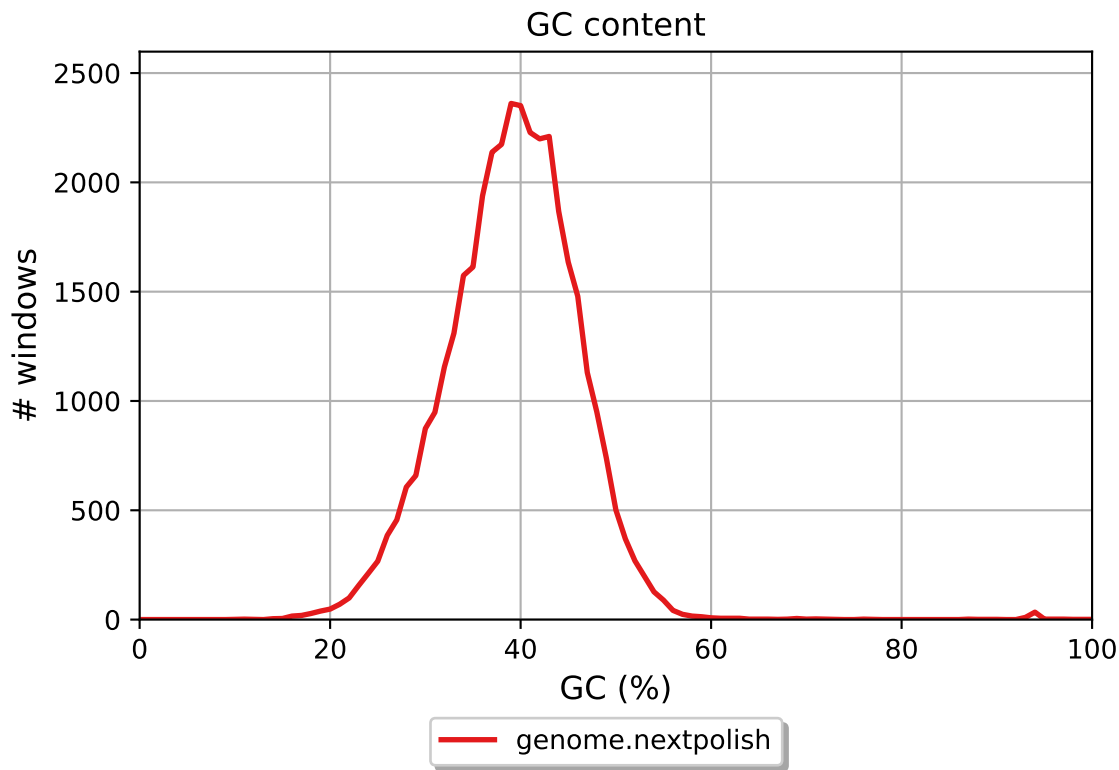






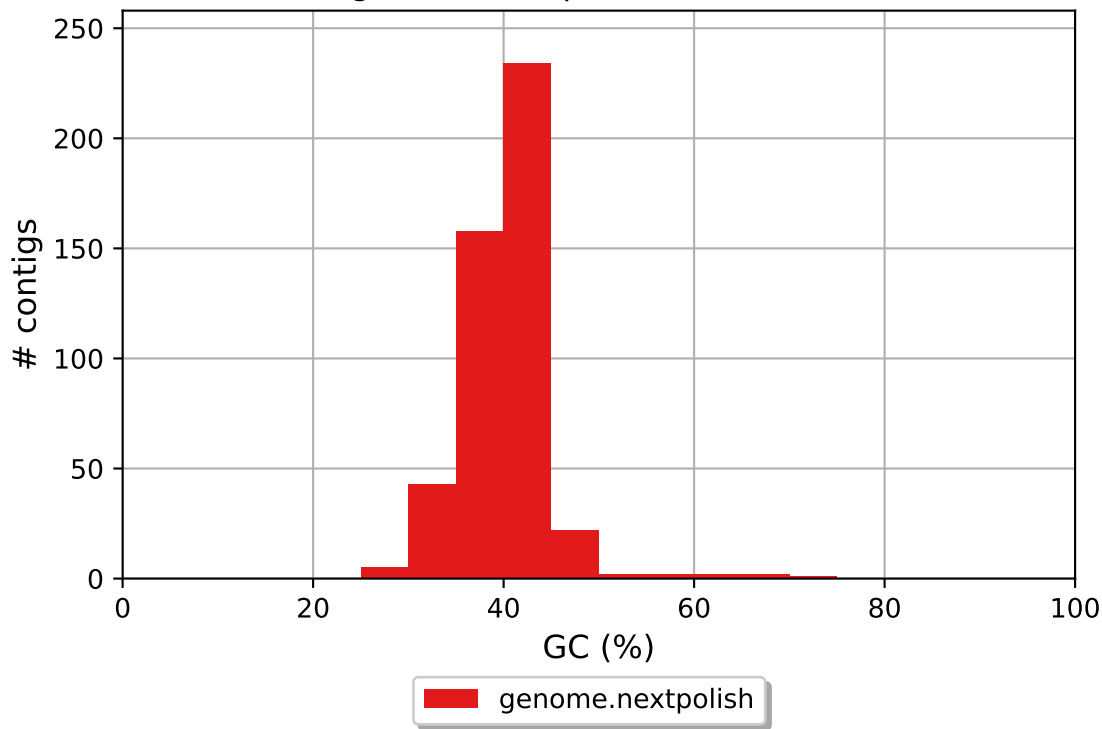






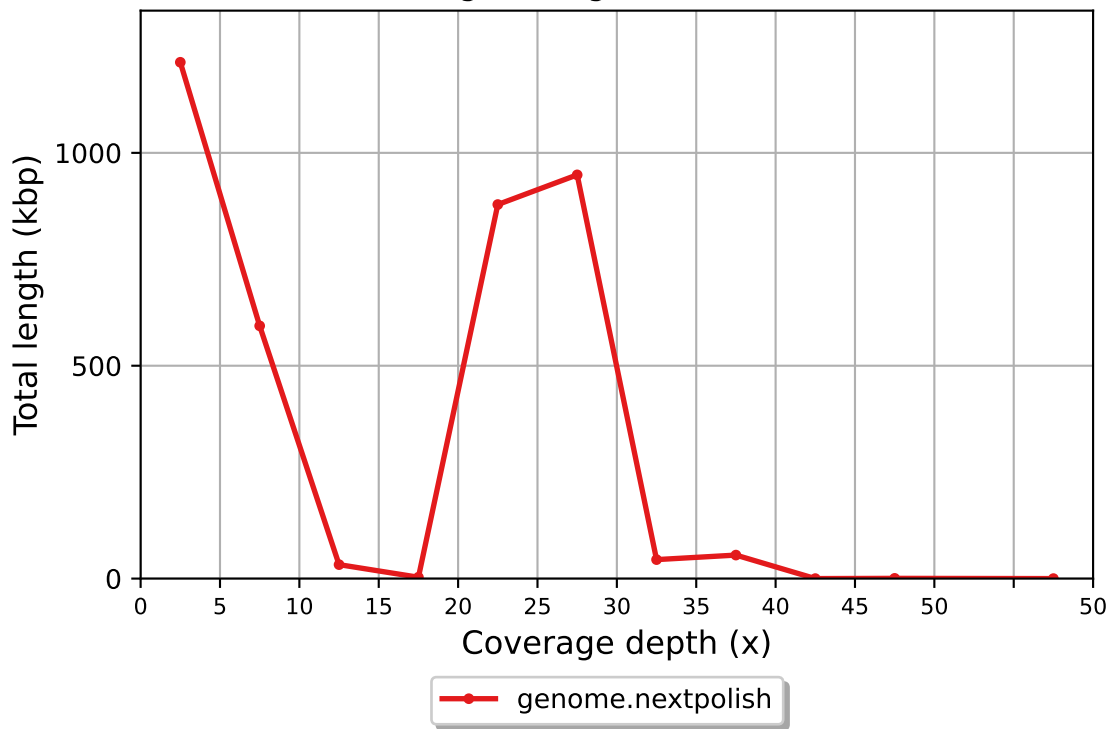


genome.nextpolish GC content





Coverage histogram (bin size: 5x)





genome.nextpolish coverage histogram (bin size: 5x)

