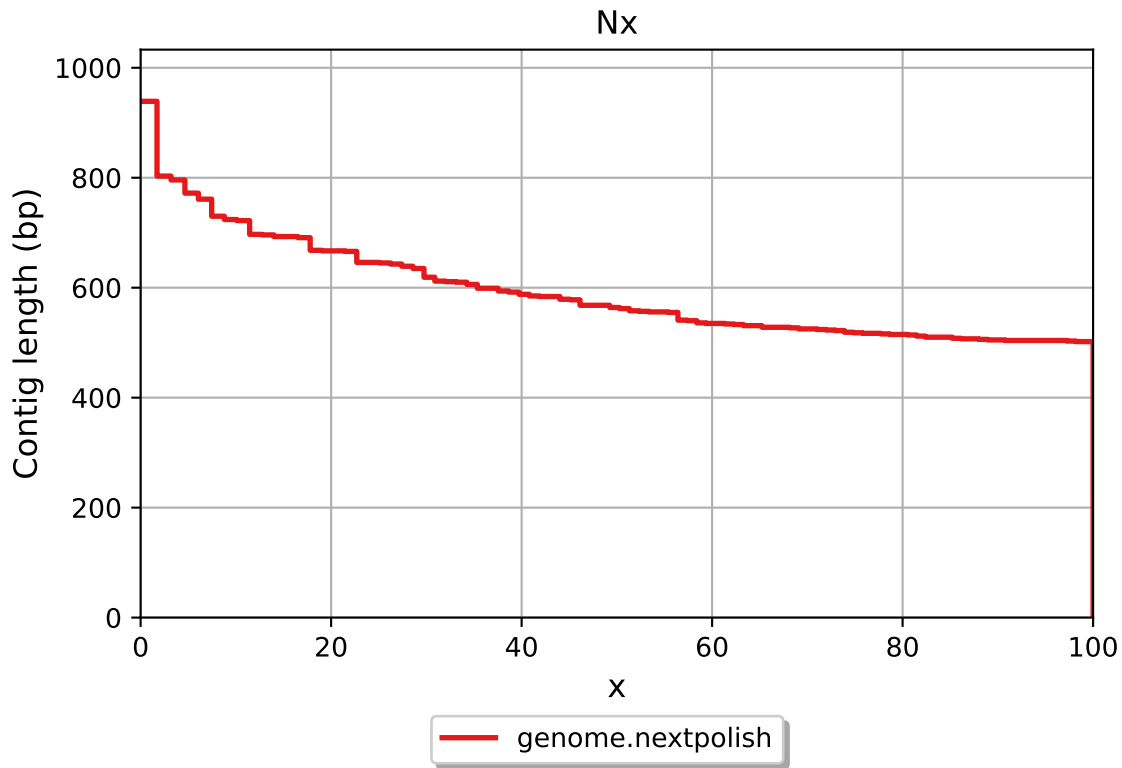


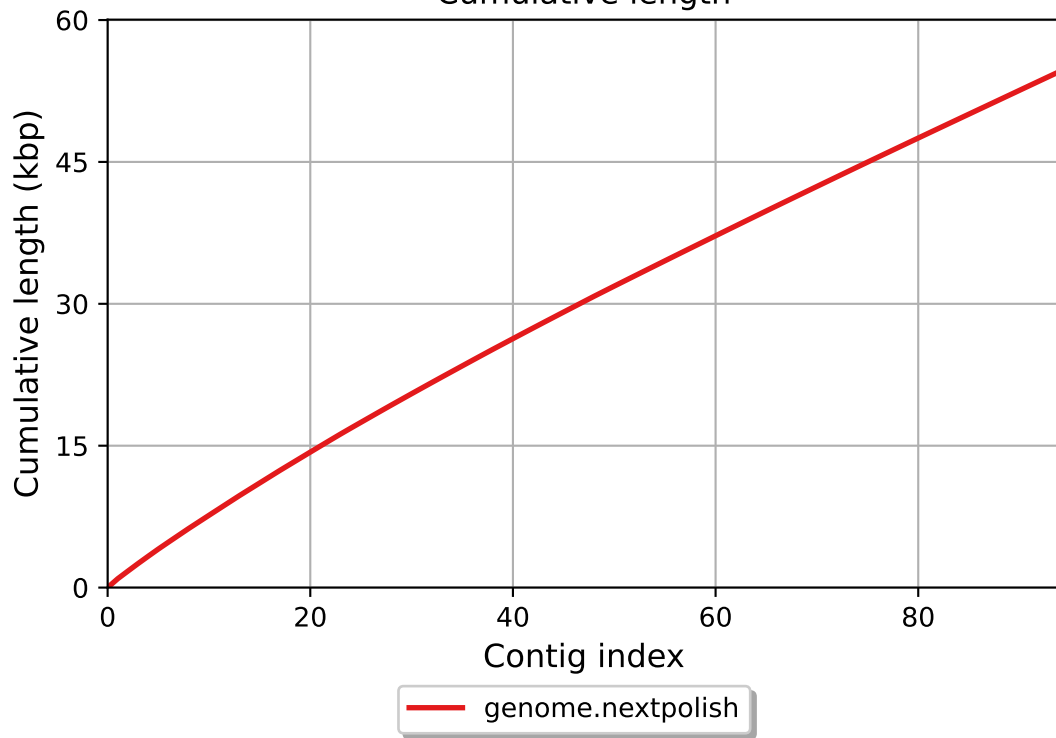
Report

	genome.nextpolish
# contigs (>= 0 bp)	1001
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	353834
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	94
Largest contig	939
Total length	54583
GC (%)	46.95
N50	564
N90	505
auN	593.0
L50	42
L90	84
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	0 + 0 part

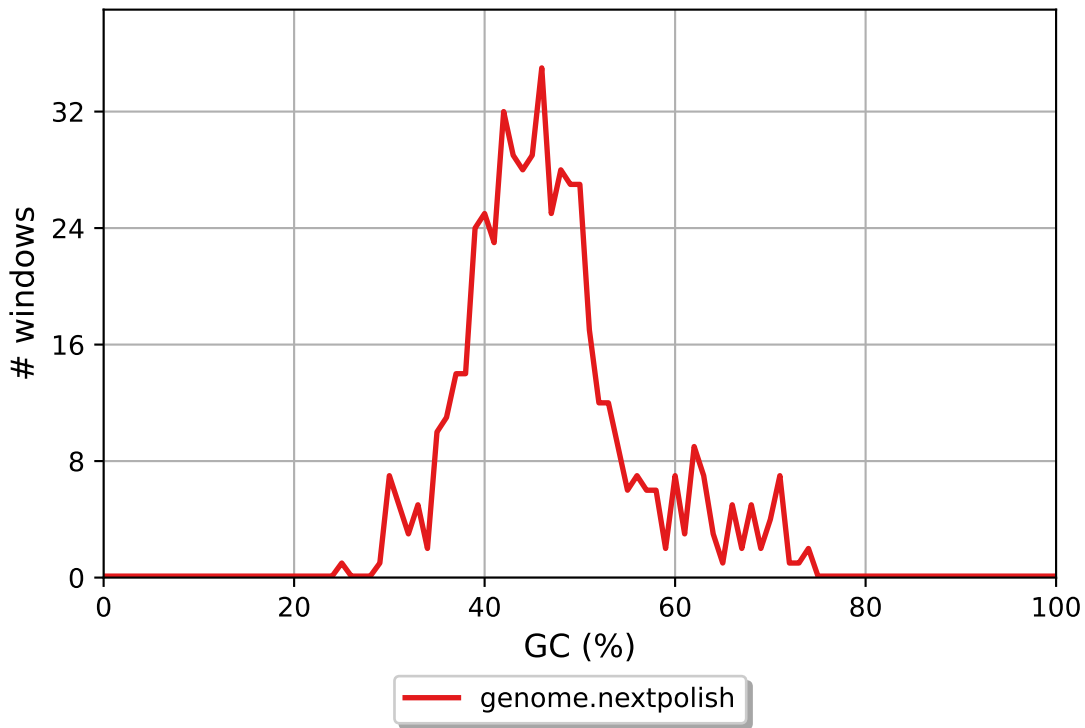
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



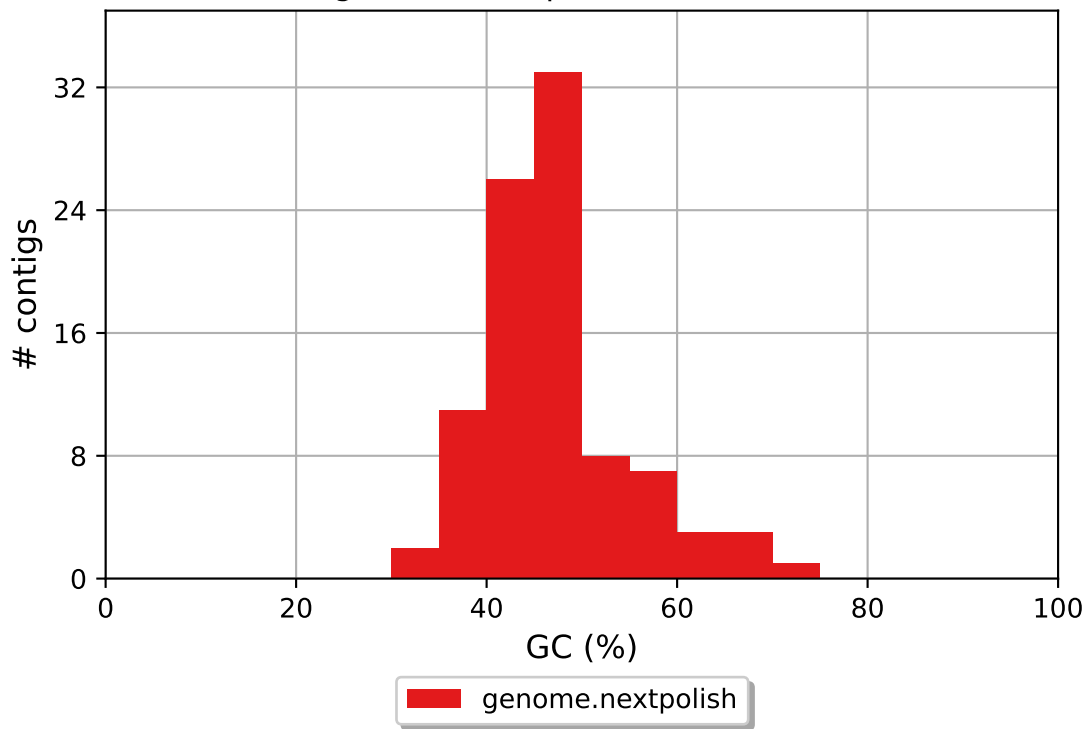
Cumulative length



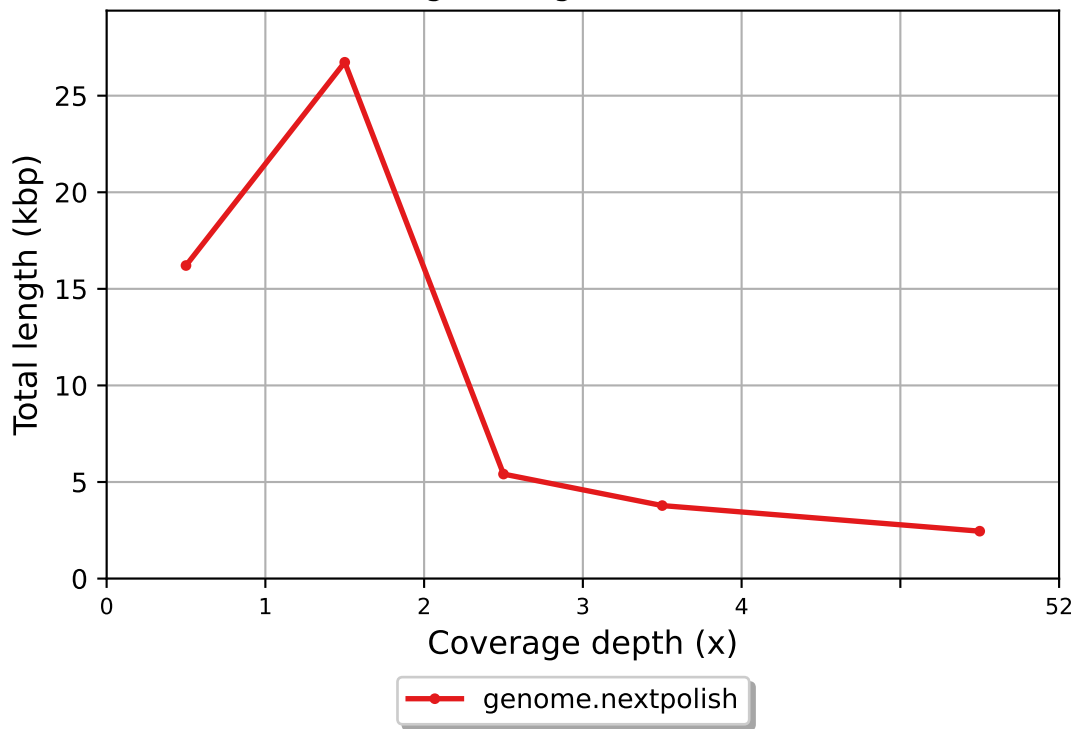
GC content



genome.nextpolish GC content



Coverage histogram (bin size: 1x)



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

