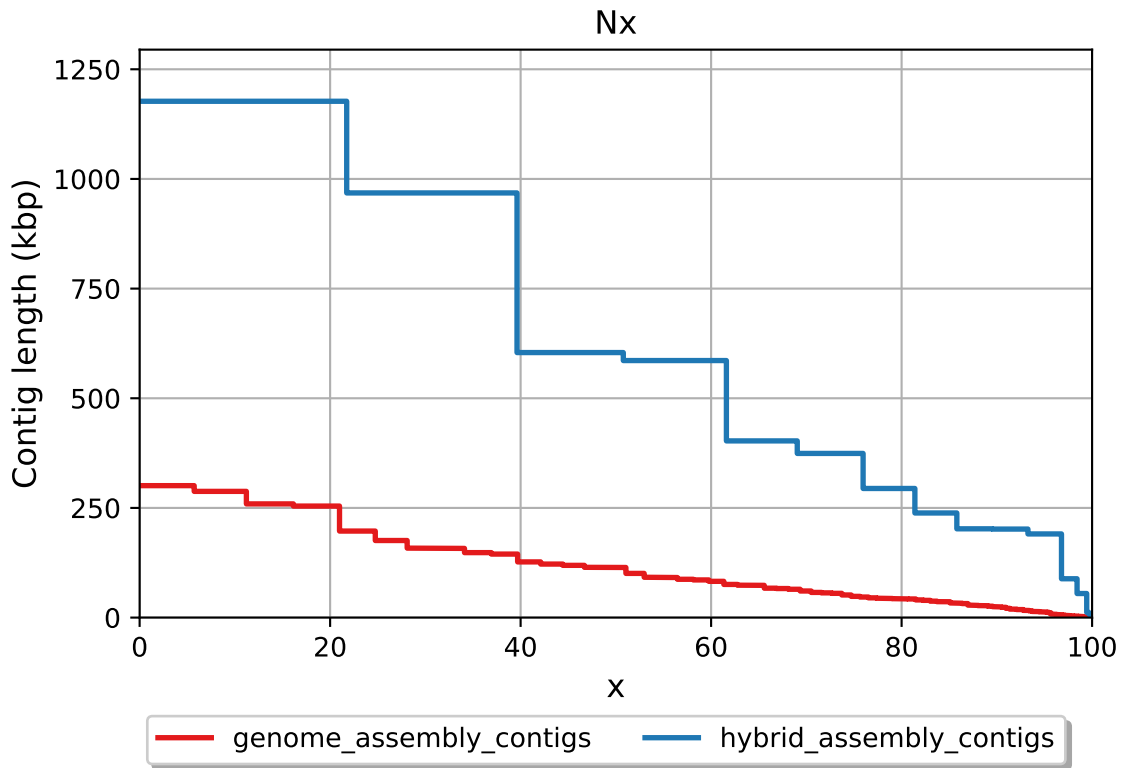


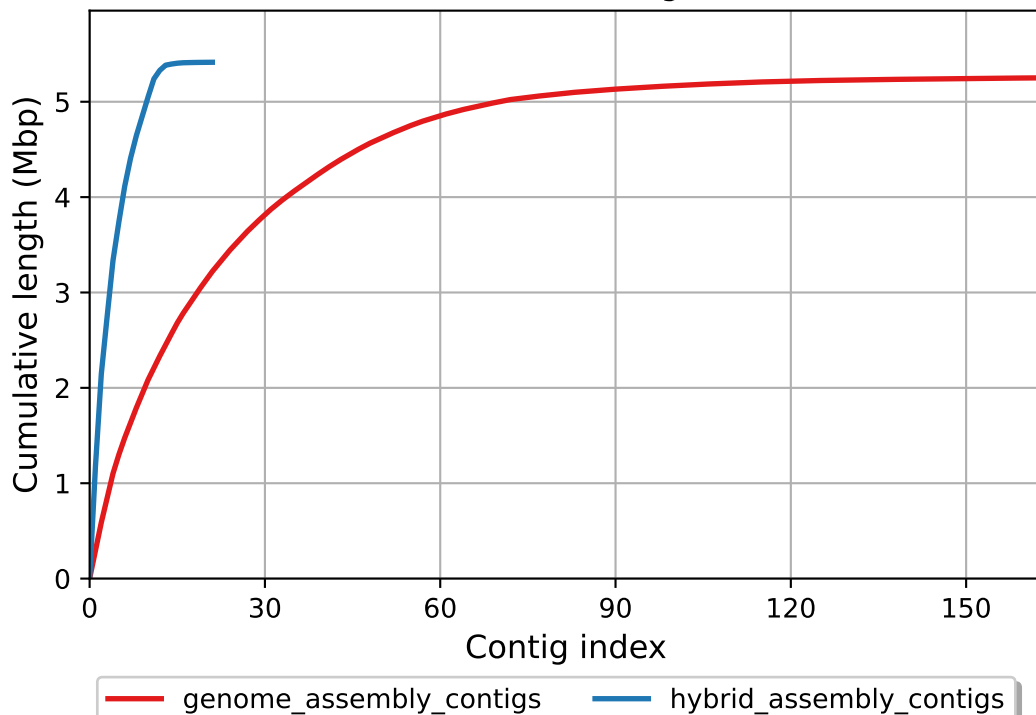
Report

	genome_assembly_contigs	hybrid_assembly_contigs
# contigs (≥ 0 bp)	901	91
# contigs (≥ 1000 bp)	128	18
# contigs (≥ 5000 bp)	84	15
# contigs (≥ 10000 bp)	72	14
# contigs (≥ 25000 bp)	53	13
# contigs (≥ 50000 bp)	32	13
Total length (≥ 0 bp)	5364110	5431368
Total length (≥ 1000 bp)	5226053	5411952
Total length (≥ 5000 bp)	5103995	5404168
Total length (≥ 10000 bp)	5022802	5395288
Total length (≥ 25000 bp)	4702489	5383440
Total length (≥ 50000 bp)	3922404	5383440
# contigs	163	21
Largest contig	300784	1177062
Total length	5250656	5414027
GC (%)	50.54	50.62
N50	114227	604190
N90	24915	201786
auN	127602.1	666056.4
L50	15	3
L90	54	10
# N's per 100 kbp	0.00	0.00

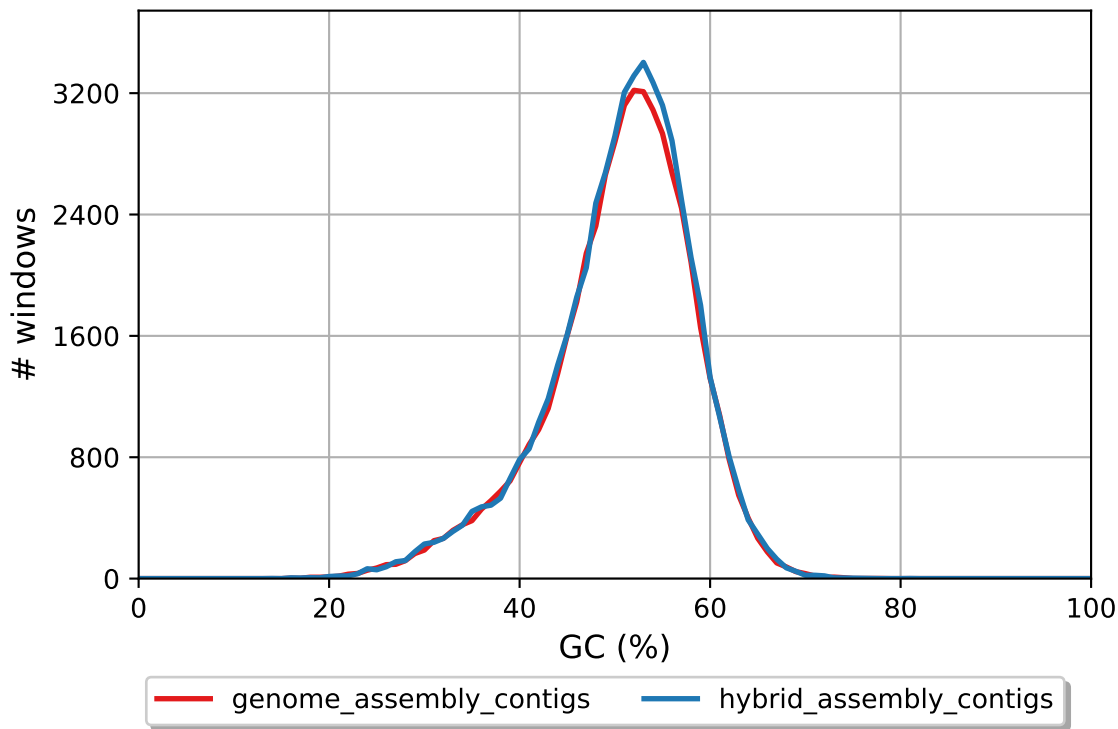
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



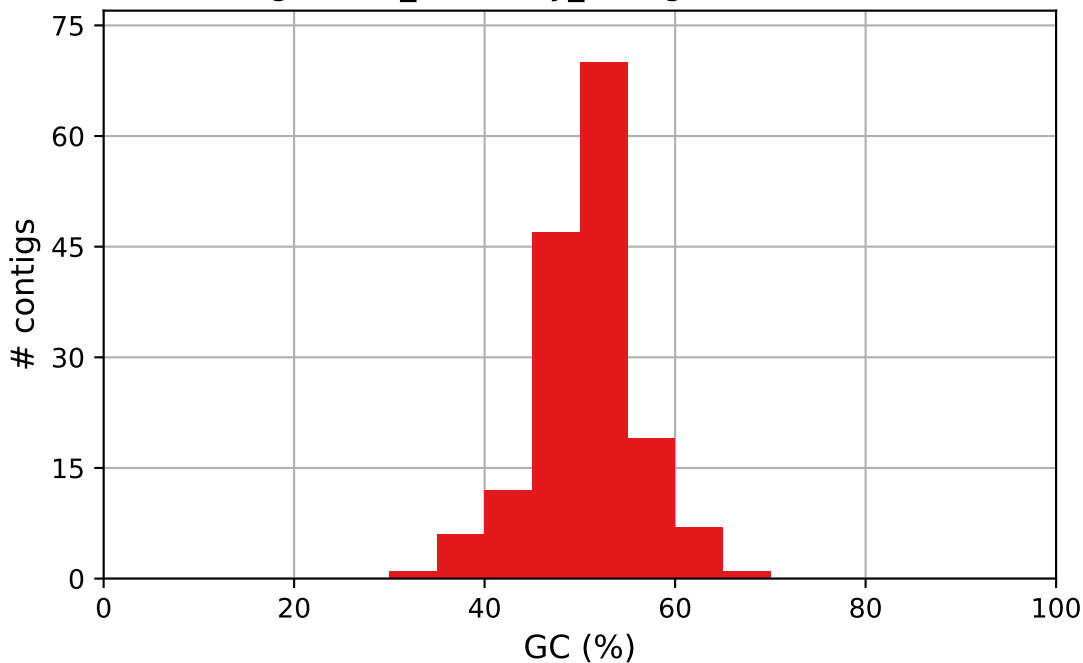
Cumulative length



GC content

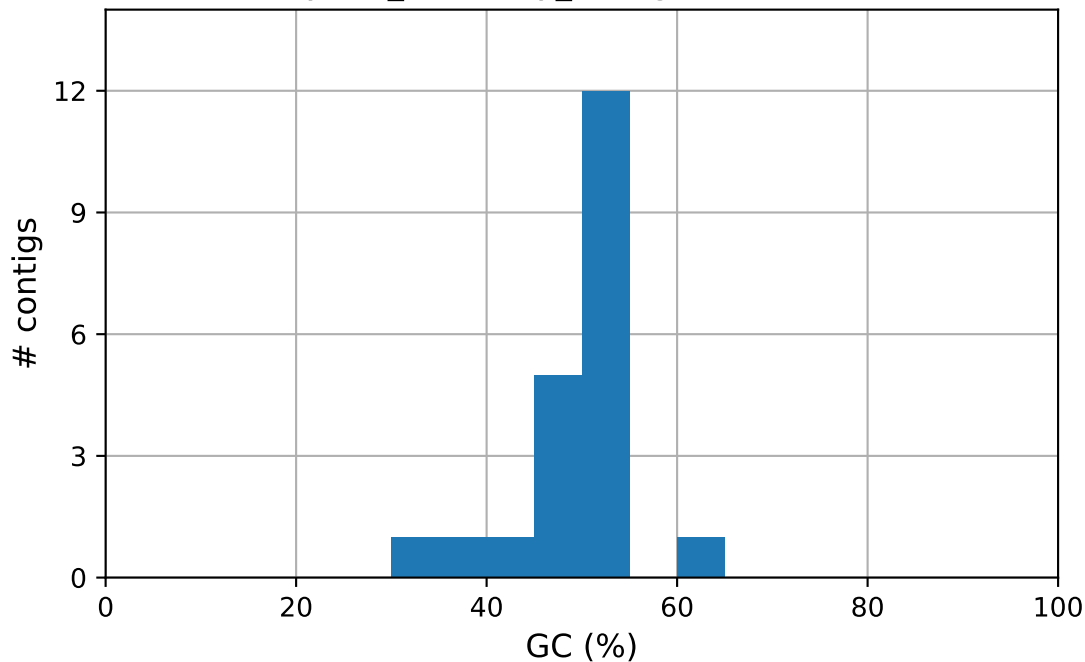


genome_assembly_contigs GC content



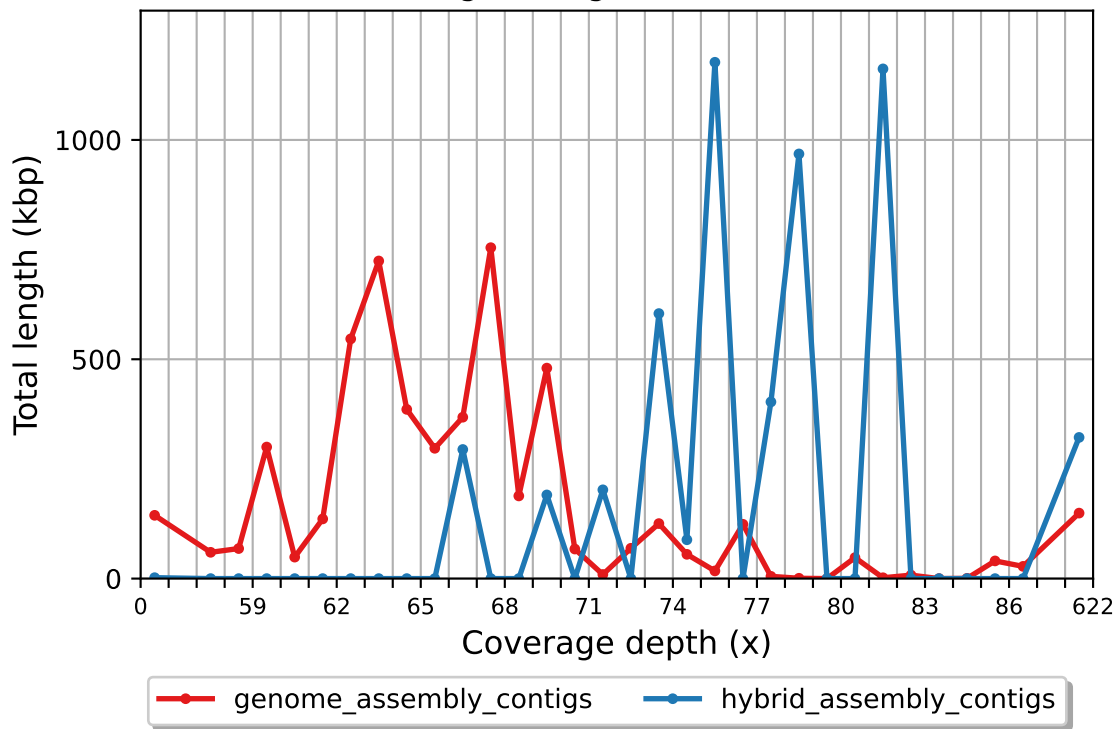
genome_assembly_contigs

hybrid_assembly_contigs GC content

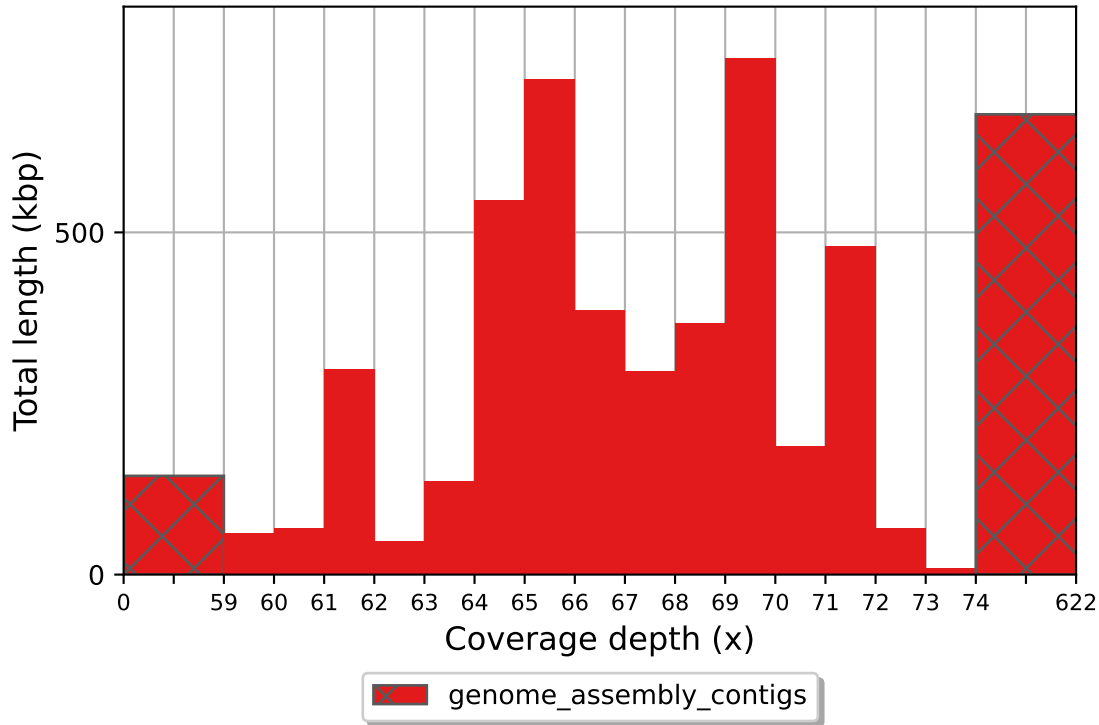


hybrid_assembly_contigs

Coverage histogram (bin size: 1x)



genome_assembly_contigs coverage histogram (bin size: 1x)



hybrid_assembly_contigs coverage histogram (bin size: 4x)

