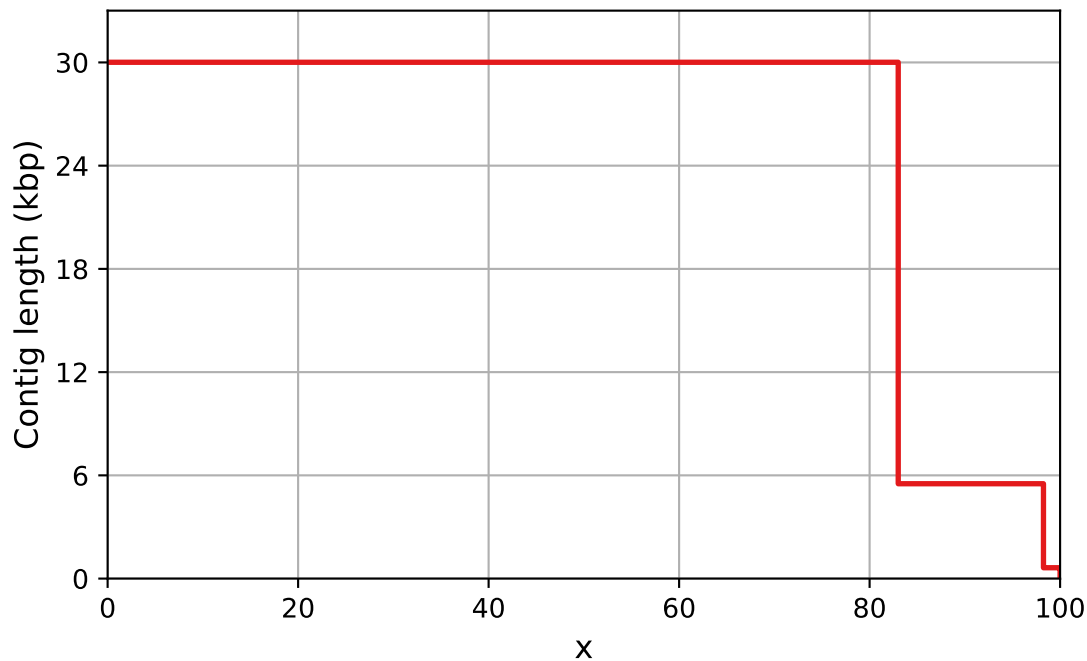


Report

	scaffolds
# contigs (≥ 0 bp)	4
# contigs (≥ 1000 bp)	2
# contigs (≥ 5000 bp)	2
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	36281
Total length (≥ 1000 bp)	35522
Total length (≥ 5000 bp)	35522
Total length (≥ 10000 bp)	30009
Total length (≥ 25000 bp)	30009
Total length (≥ 50000 bp)	0
# contigs	3
Largest contig	30009
Total length	36153
GC (%)	39.26
N50	30009
N75	30009
L50	1
L75	1
# N's per 100 kbp	0.00
# predicted genes (unique)	18
# predicted genes (≥ 0 bp)	18
# predicted genes (≥ 300 bp)	13
# predicted genes (≥ 1500 bp)	4
# predicted genes (≥ 3000 bp)	3

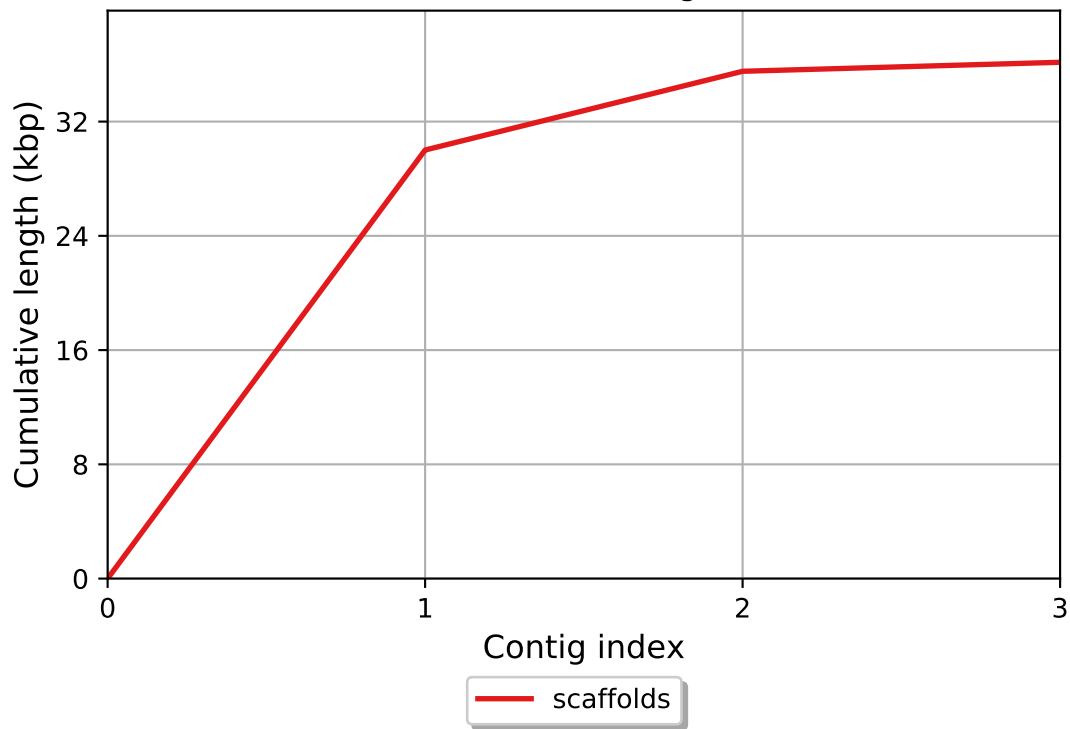
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

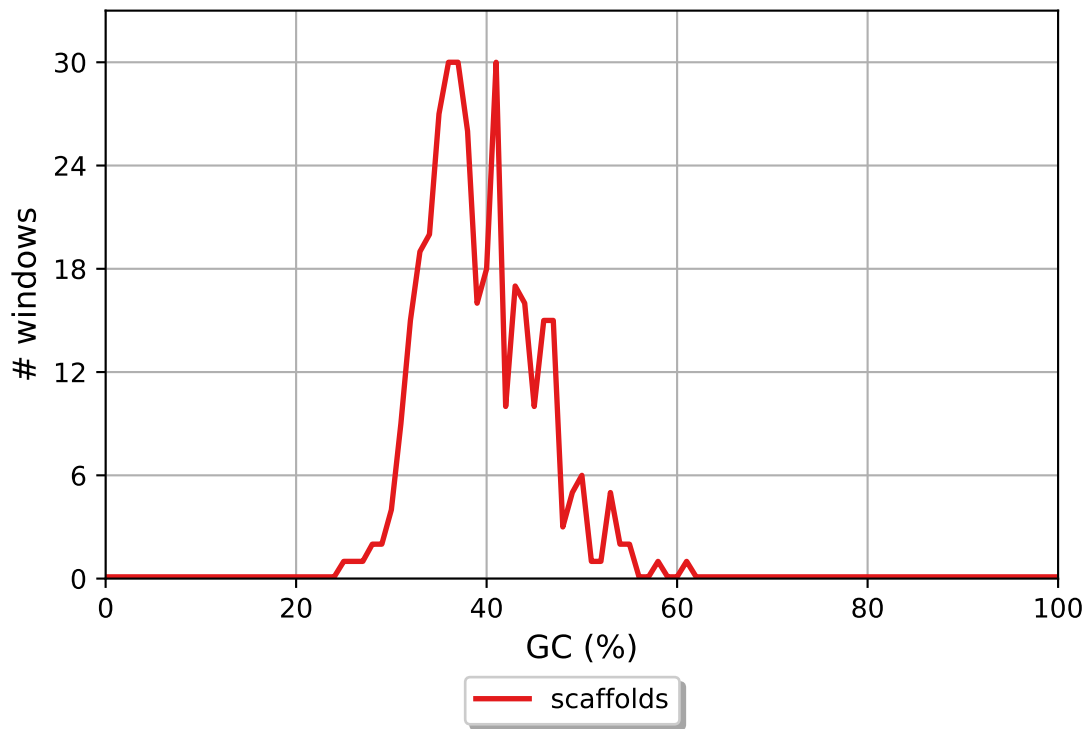


scaffolds

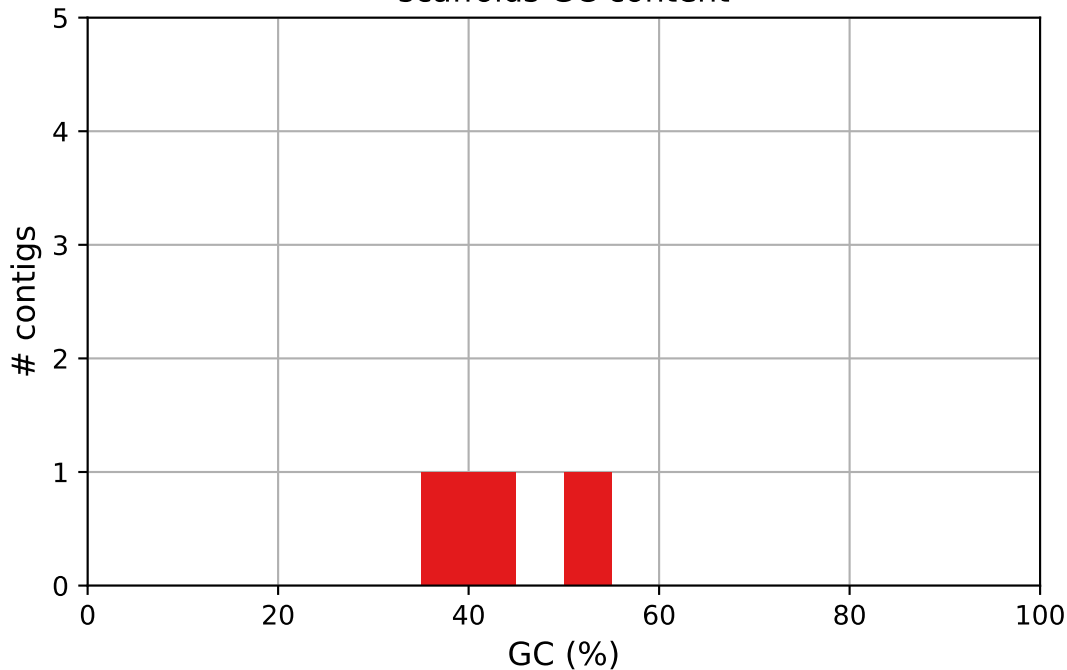
Cumulative length



GC content

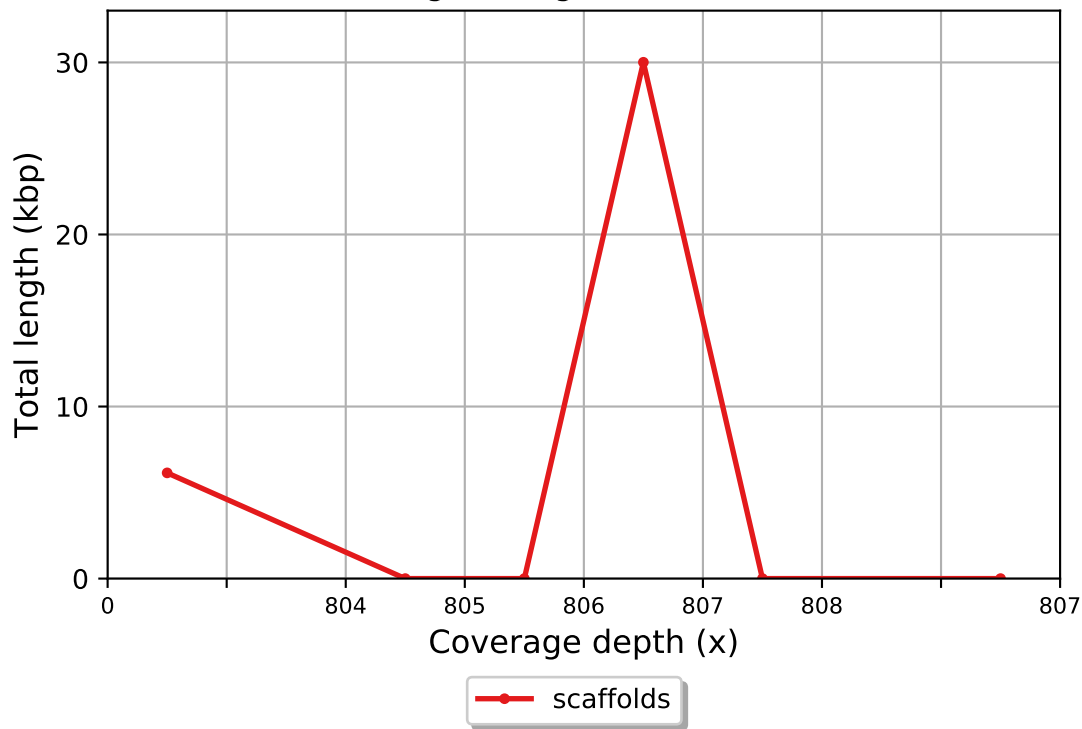


scaffolds GC content



scaffolds

Coverage histogram (bin size: 1x)



scaffolds coverage histogram (bin size: 1x)

