

# Report

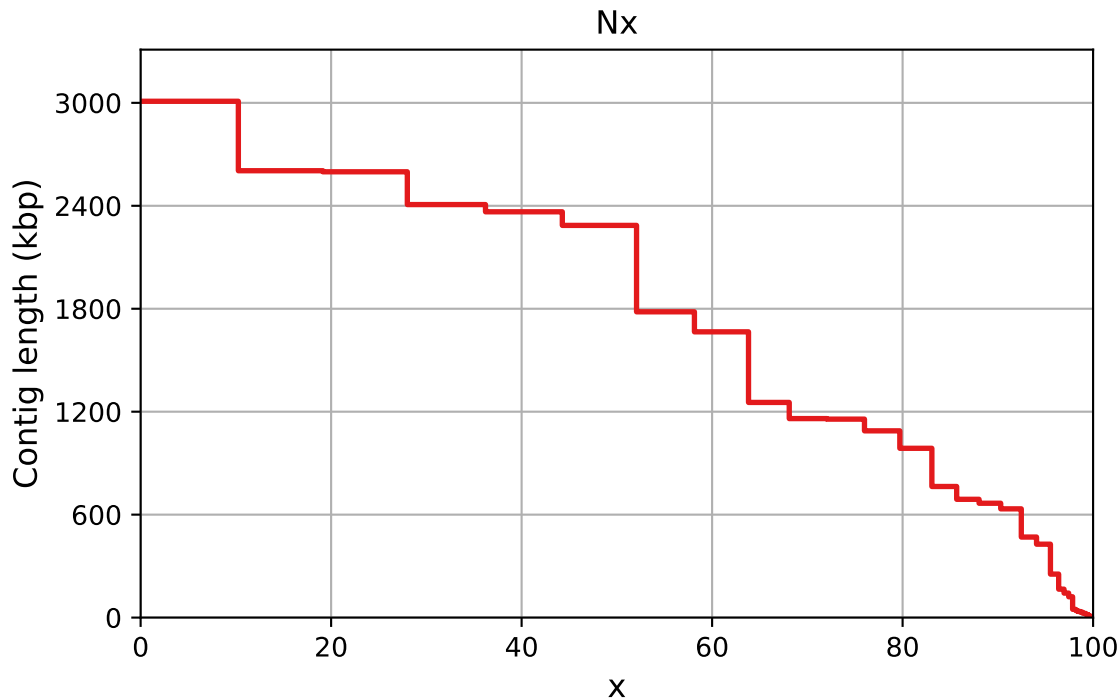
	flye_medaka_consensus
# contigs (>= 0 bp)	75
# contigs (>= 1000 bp)	73
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	42
# contigs (>= 25000 bp)	33
# contigs (>= 50000 bp)	23
Total length (>= 0 bp)	29326934
Total length (>= 1000 bp)	29325397
Total length (>= 5000 bp)	29281571
Total length (>= 10000 bp)	29211246
Total length (>= 25000 bp)	29056291
Total length (>= 50000 bp)	28696355
# contigs	75
Largest contig	3009198
Total length	29326934
GC (%)	49.50
N50	2285740
N75	1156631
L50	6
L75	11
# total reads	476124
# left	0
# right	0
Mapped (%)	98.14
Properly paired (%)	0.0
Avg. coverage depth	49
Coverage >= 1x (%)	100.0
# N's per 100 kbp	0.00
Complete BUSCO (%)	19.59
Partial BUSCO (%)	7.43
# predicted rRNA genes	38 + 6 part

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Reads report

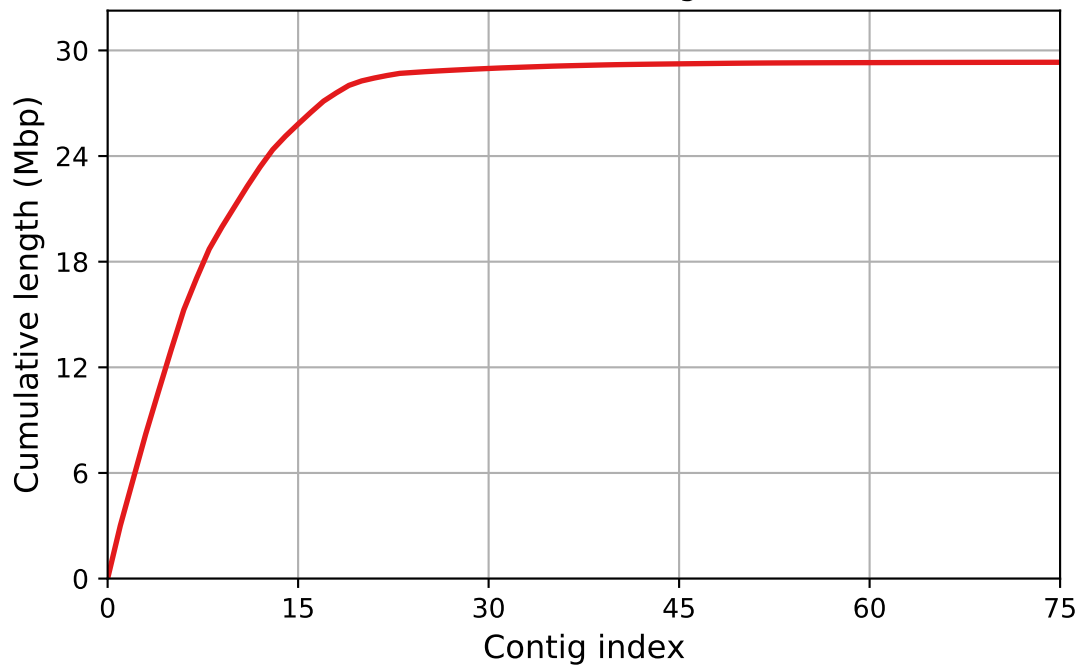
	flye_medaka_consensus
# total reads	476124
# left	0
# right	0
# mapped	467279
Mapped (%)	98.14
# properly paired	0
Properly paired (%)	0.0
# singletons	0
Singletons (%)	0.0
# misjoint mates	0
Misjoint mates (%)	0.0
Avg. coverage depth	49
Coverage >= 1x (%)	100.0
Coverage >= 5x (%)	99.96
Coverage >= 10x (%)	99.93

All statistics are based on contigs of size  $\geq 100$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



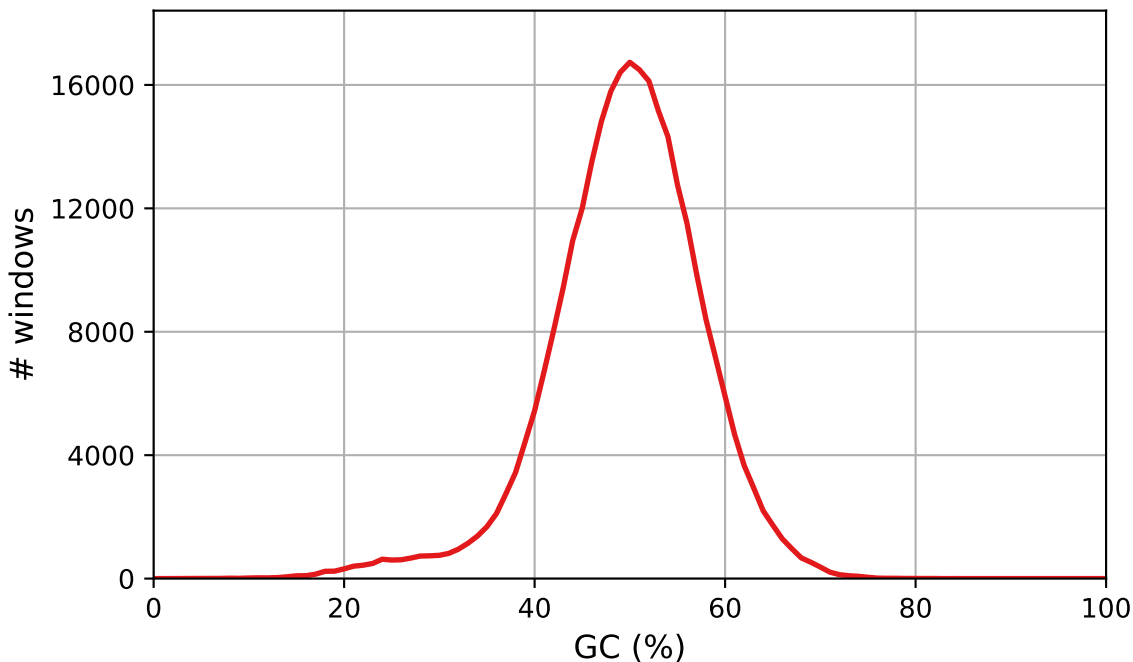
flye\_medaka\_consensus

Cumulative length



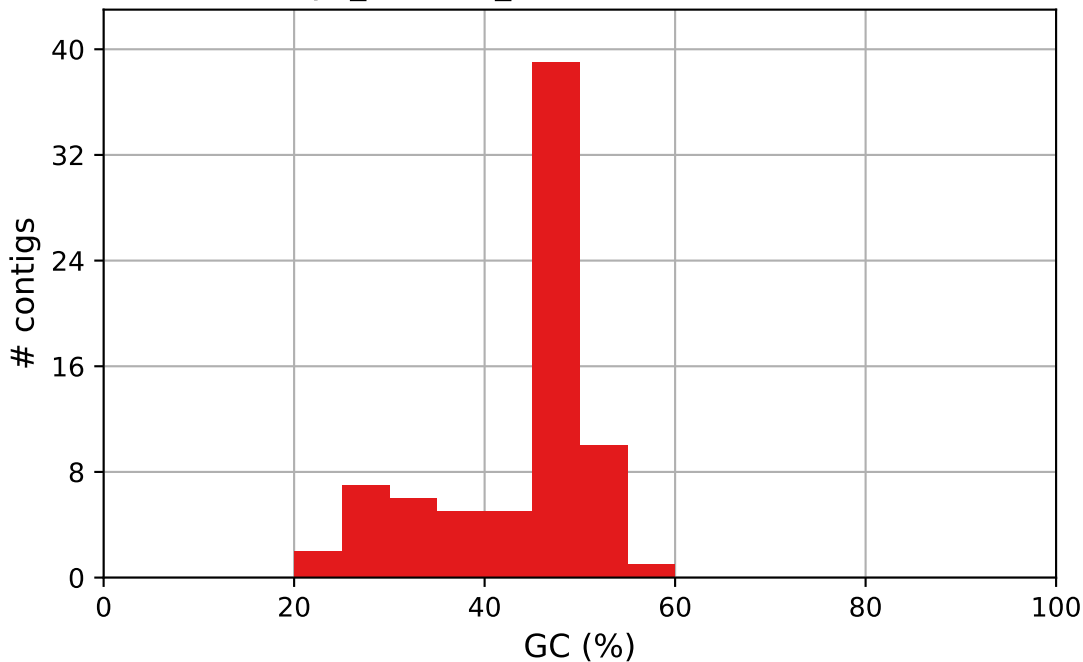
flye\_medaka\_consensus

GC content



flye\_medaka\_consensus

flye\_medaka\_consensus GC content



flye\_medaka\_consensus