

Report

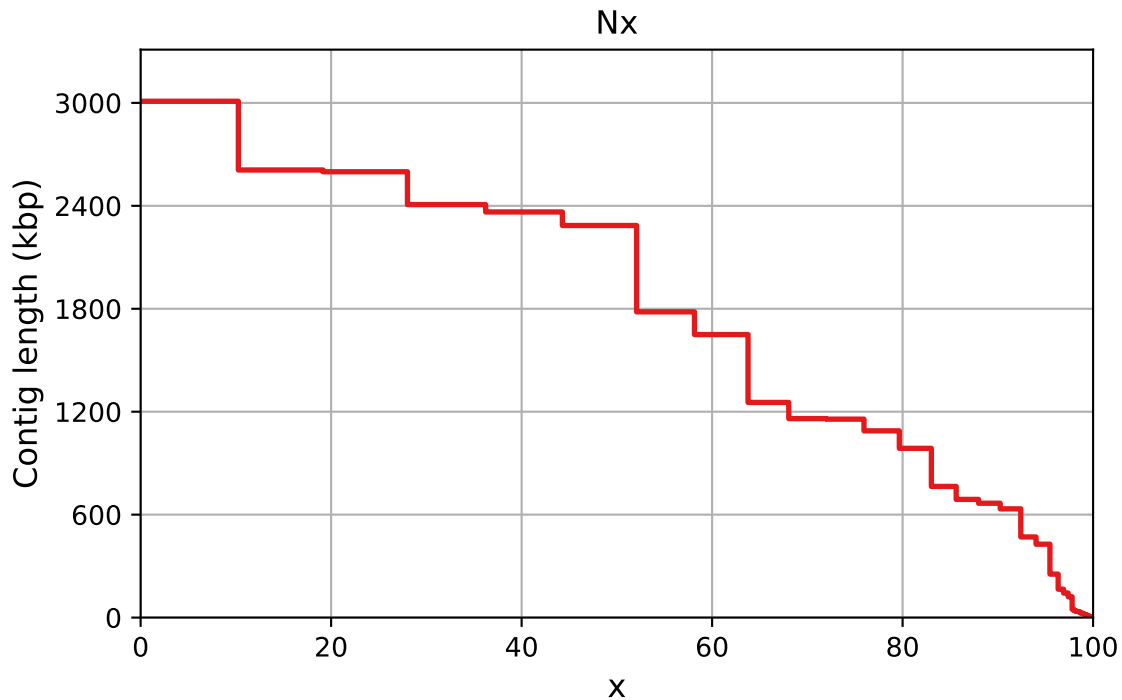
	flye_medaka_consensus
# contigs (>= 0 bp)	85
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	54
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	23
Total length (>= 0 bp)	29331139
Total length (>= 1000 bp)	29326657
Total length (>= 5000 bp)	29269595
Total length (>= 10000 bp)	29195274
Total length (>= 25000 bp)	29000428
Total length (>= 50000 bp)	28684946
# contigs	85
Largest contig	3009402
Total length	29331139
GC (%)	49.51
N50	2285325
N90	666529
auN	1840459.7
L50	6
L90	16
# total reads	409991
# left	0
# right	0
Mapped (%)	112.48
Properly paired (%)	0.0
Avg. coverage depth	48
Coverage >= 1x (%)	99.99
# N's per 100 kbp	0.00
# predicted rRNA genes	38 + 0 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

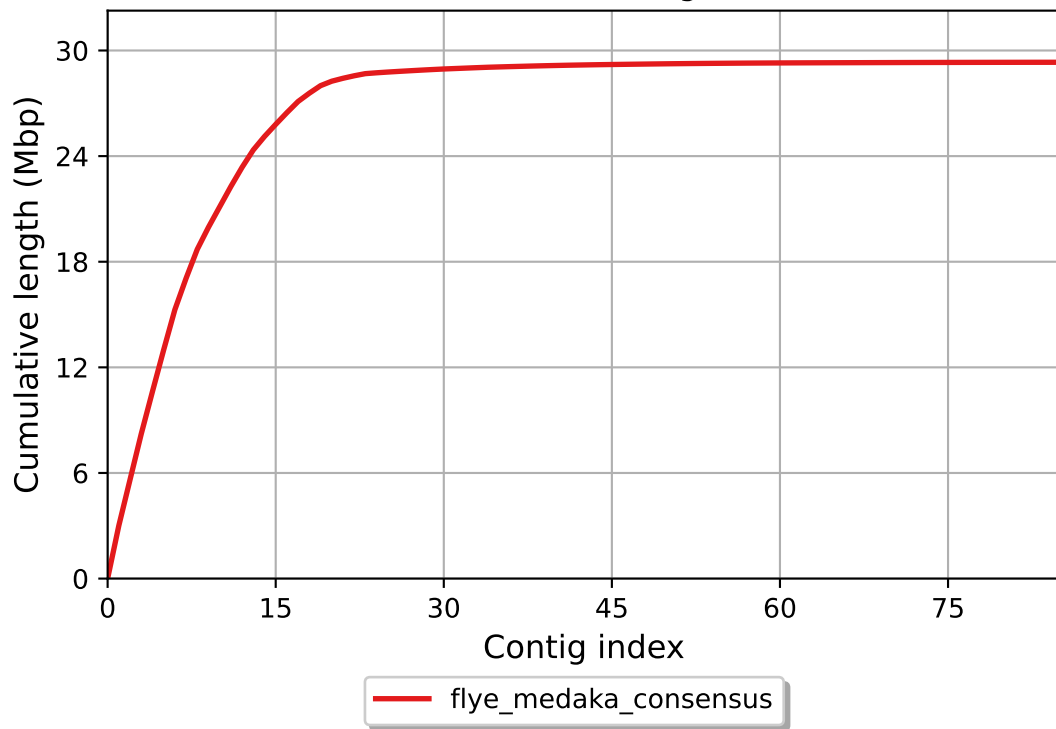
	flye_medaka_consensus
# total reads	409991
# left	0
# right	0
# mapped	461176
Mapped (%)	112.48
# properly paired	0
Properly paired (%)	0.0
# singletons	0
Singletons (%)	0.0
# misjoint mates	0
Misjoint mates (%)	0.0
Avg. coverage depth	48
Coverage >= 1x (%)	99.99
Coverage >= 5x (%)	99.95
Coverage >= 10x (%)	99.89

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).

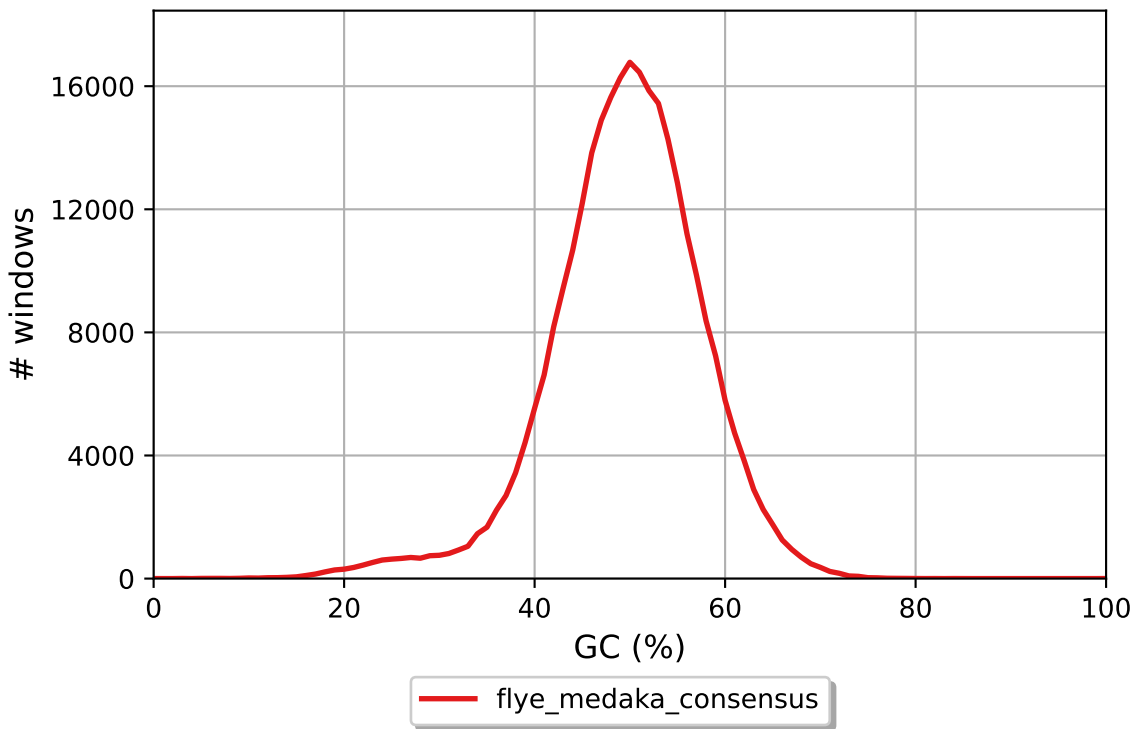


flye_medaka_consensus

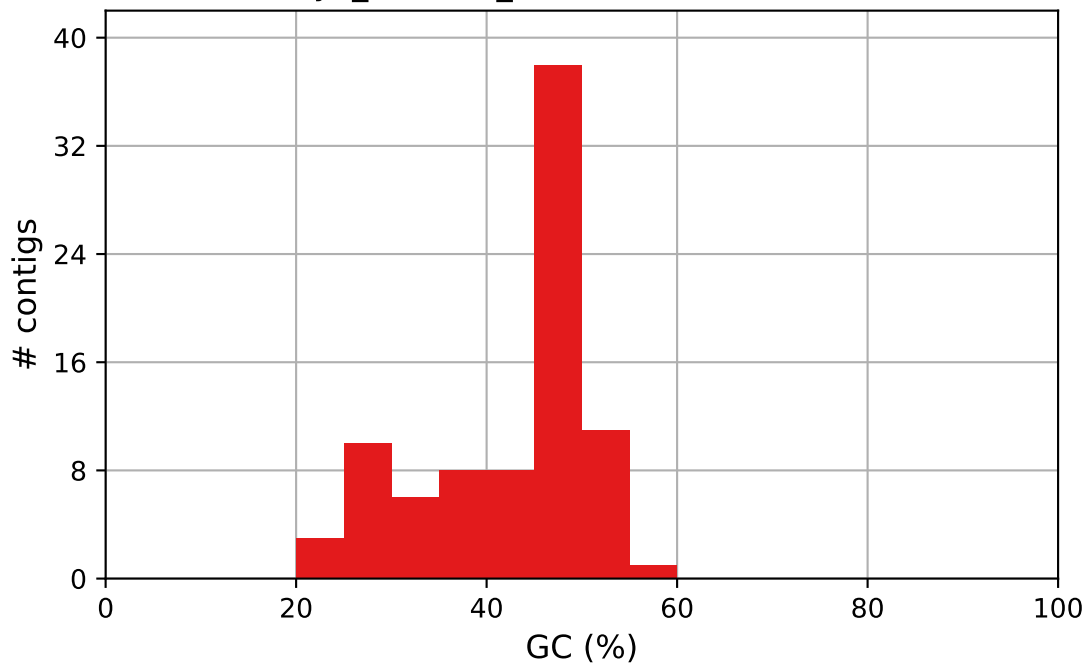
Cumulative length



GC content



flye_medaka_consensus GC content



flye_medaka_consensus