

Report

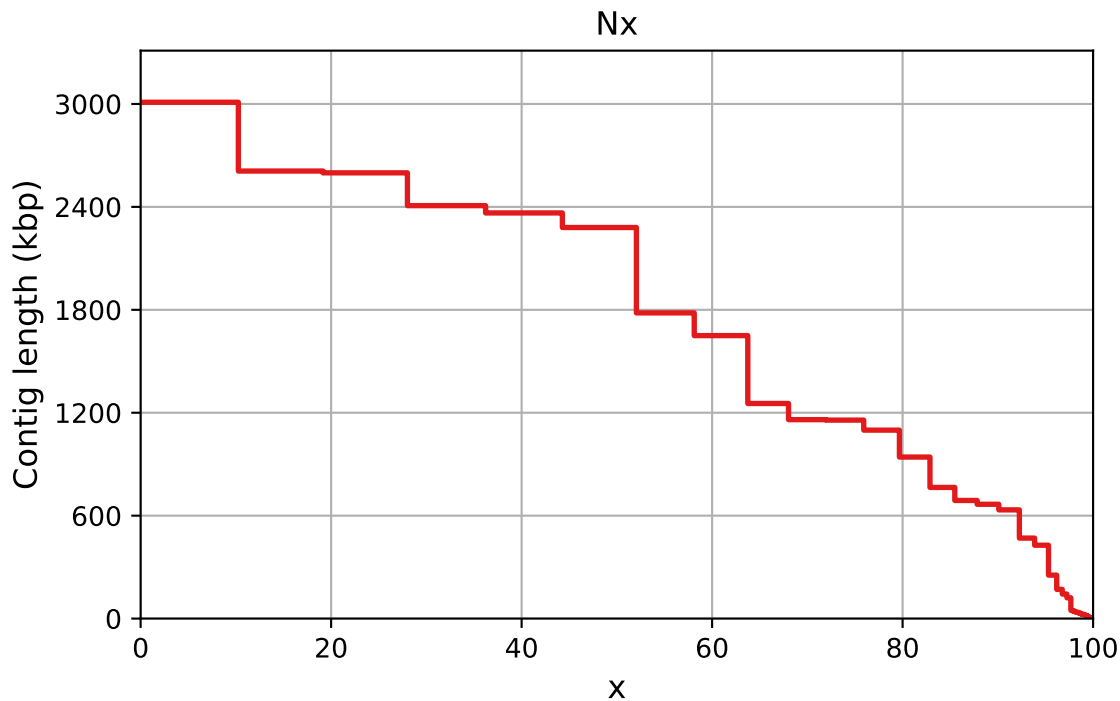
	flye_medaka_consensus
# contigs (>= 0 bp)	85
# contigs (>= 1000 bp)	76
# contigs (>= 5000 bp)	53
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	34
# contigs (>= 50000 bp)	23
Total length (>= 0 bp)	29335530
Total length (>= 1000 bp)	29329187
Total length (>= 5000 bp)	29274769
Total length (>= 10000 bp)	29205985
Total length (>= 25000 bp)	29036260
Total length (>= 50000 bp)	28650057
# contigs	85
Largest contig	3009856
Total length	29335530
GC (%)	49.50
N50	2279797
N90	666409
auN	1837446.5
L50	6
L90	16
# total reads	409991
# left	0
# right	0
Mapped (%)	111.01
Properly paired (%)	0.0
Avg. coverage depth	48
Coverage >= 1x (%)	99.99
# N's per 100 kbp	0.00
Complete BUSCO (%)	0.00
Partial BUSCO (%)	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

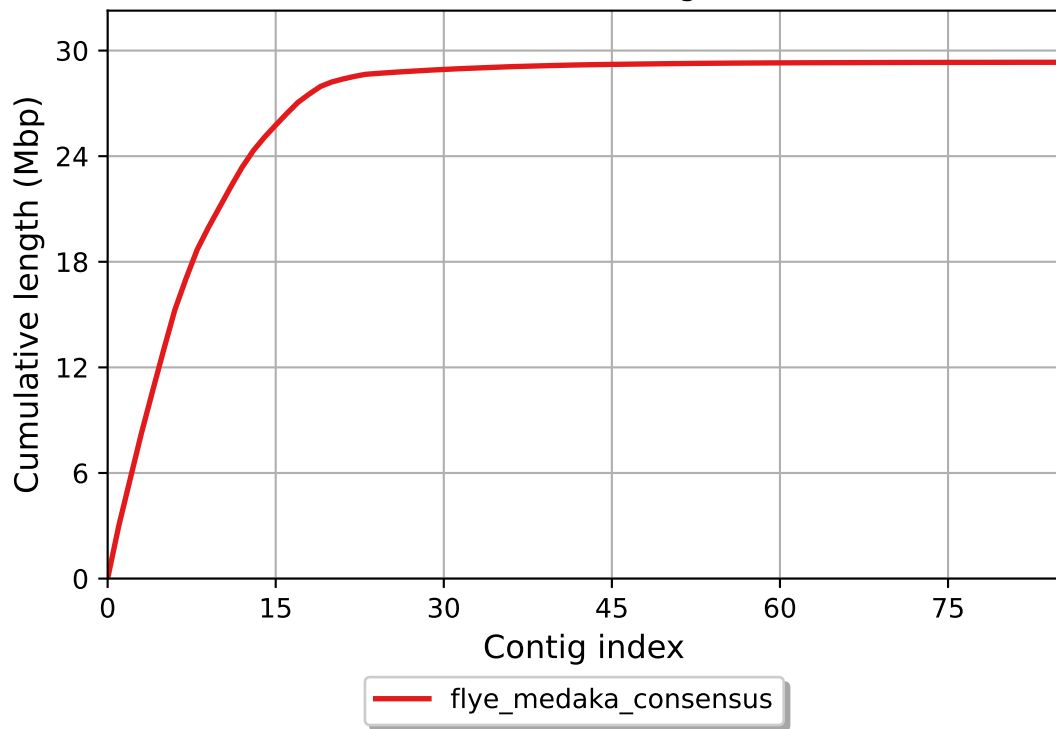
	flye_medaka_consensus
# total reads	409991
# left	0
# right	0
# mapped	455148
Mapped (%)	111.01
# properly paired	0
Properly paired (%)	0.0
# singletons	0
Singletons (%)	0.0
# misjoint mates	0
Misjoint mates (%)	0.0
Avg. coverage depth	48
Coverage >= 1x (%)	99.99
Coverage >= 5x (%)	99.94
Coverage >= 10x (%)	99.88

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).

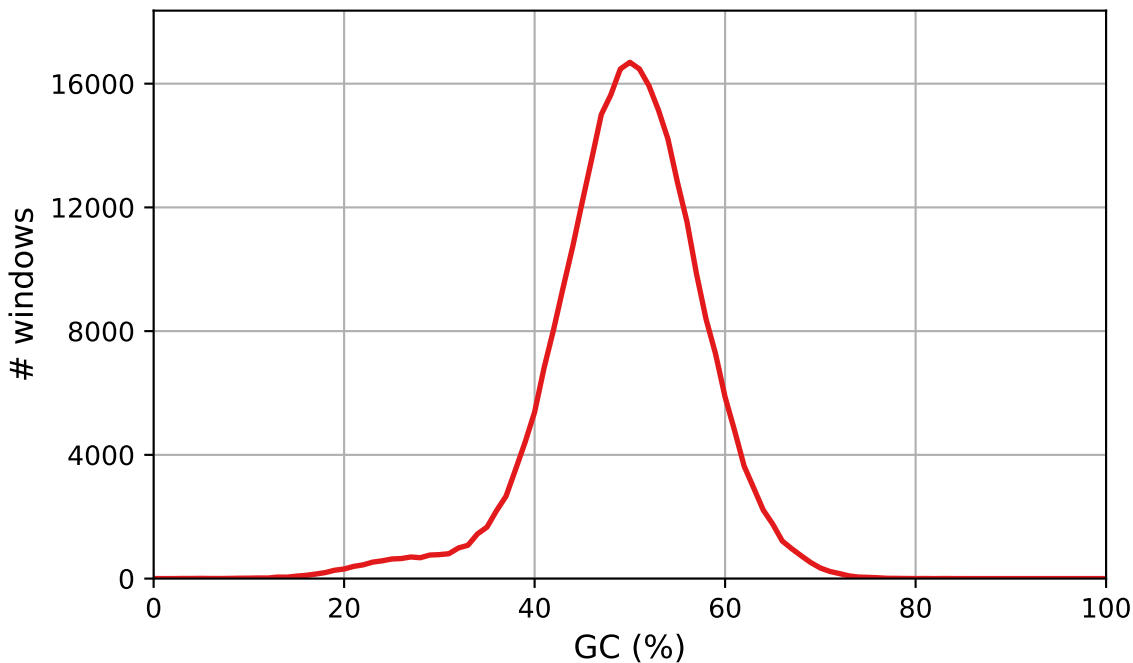


flye_medaka_consensus

Cumulative length

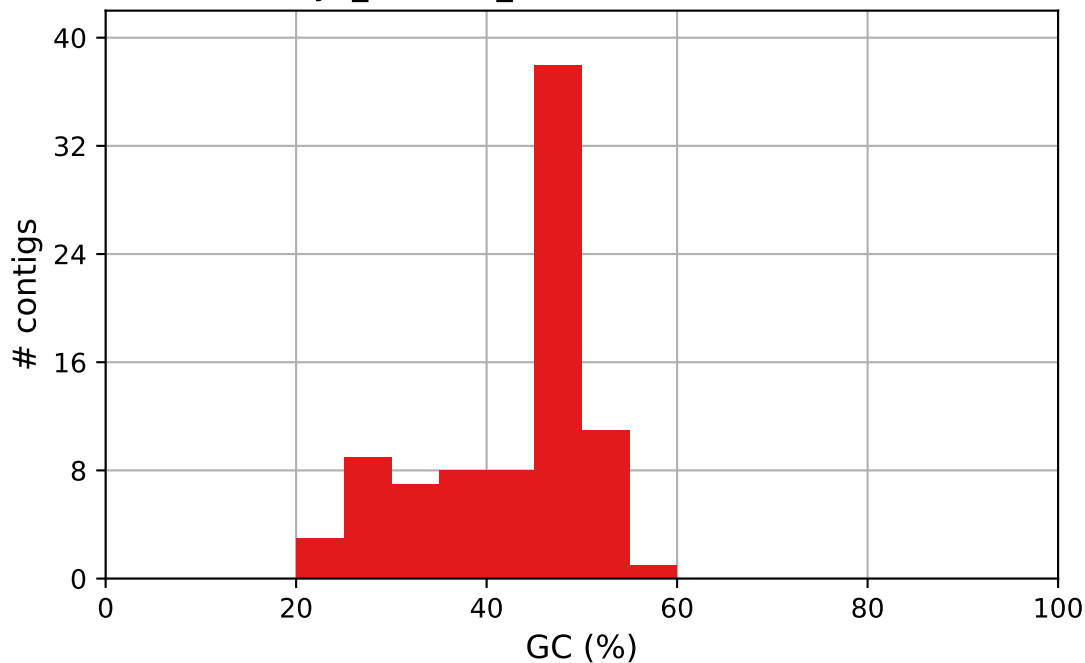


GC content



flye_medaka_consensus

flye_medaka_consensus GC content



flye_medaka_consensus