

Report

	flye
# contigs (>= 0 bp)	237
# contigs (>= 1000 bp)	226
# contigs (>= 5000 bp)	187
# contigs (>= 10000 bp)	167
# contigs (>= 25000 bp)	124
# contigs (>= 50000 bp)	105
Total length (>= 0 bp)	115786471
Total length (>= 1000 bp)	115778864
Total length (>= 5000 bp)	115665068
Total length (>= 10000 bp)	115518973
Total length (>= 25000 bp)	114794082
Total length (>= 50000 bp)	114102592
# contigs	206
Largest contig	13644371
Total length	115742546
Reference length	119667750
GC (%)	36.06
Reference GC (%)	36.06
N50	10060011
NG50	10060011
N90	394722
NG90	224937
auN	7925817.5
auNG	7665843.9
L50	5
LG50	5
L90	32
LG90	45
# total reads	1128688
# left	0
# right	0
Mapped (%)	126.81
Reference mapped (%)	144.91
Properly paired (%)	0.0
Reference properly paired (%)	0.0
Avg. coverage depth	59
Reference avg. coverage depth	67
Coverage >= 1x (%)	99.99
Reference coverage >= 1x (%)	98.54
# misassemblies	487
# misassembled contigs	102
Misassembled contigs length	112403388
# local misassemblies	2993
# scaffold gap ext. mis.	2
# scaffold gap loc. mis.	8
# possible TEs	60
# unaligned mis. contigs	36
# unaligned contigs	19 + 158 part
Unaligned length	10178058
Genome fraction (%)	87.906
Duplication ratio	1.005
# N's per 100 kbp	0.86
# mismatches per 100 kbp	694.78
# indels per 100 kbp	160.29
# genomic features	0 + 0 part
Largest alignment	6929877
Total aligned length	105553966
NA50	784103
NGA50	688609
NA90	9199
NGA90	-
auNA	1702291.5
auNGA	1646454.9
LA50	28
LGA50	31
LA90	411
LGA90	-

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Reads report

	flye
# total reads	1128688
# left	0
# right	0
# mapped	1431321
Mapped (%)	126.81
# properly paired	0
Properly paired (%)	0.0
# singletons	0
Singletons (%)	0.0
# misjoint mates	0
Misjoint mates (%)	0.0
Avg. coverage depth	59
Coverage >= 1x (%)	99.99
Coverage >= 5x (%)	99.88
Coverage >= 10x (%)	99.84
# reference mapped	1635611
Reference mapped (%)	144.91
# reference properly paired	0
Reference properly paired (%)	0.0
# reference singletons	0
Reference singletons (%)	0.0
# reference misjoint mates	0
Reference misjoint mates (%)	0.0
Reference avg. coverage depth	67
Reference coverage >= 1x (%)	98.54
Reference coverage >= 5x (%)	96.96
Reference coverage >= 10x (%)	96.18

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

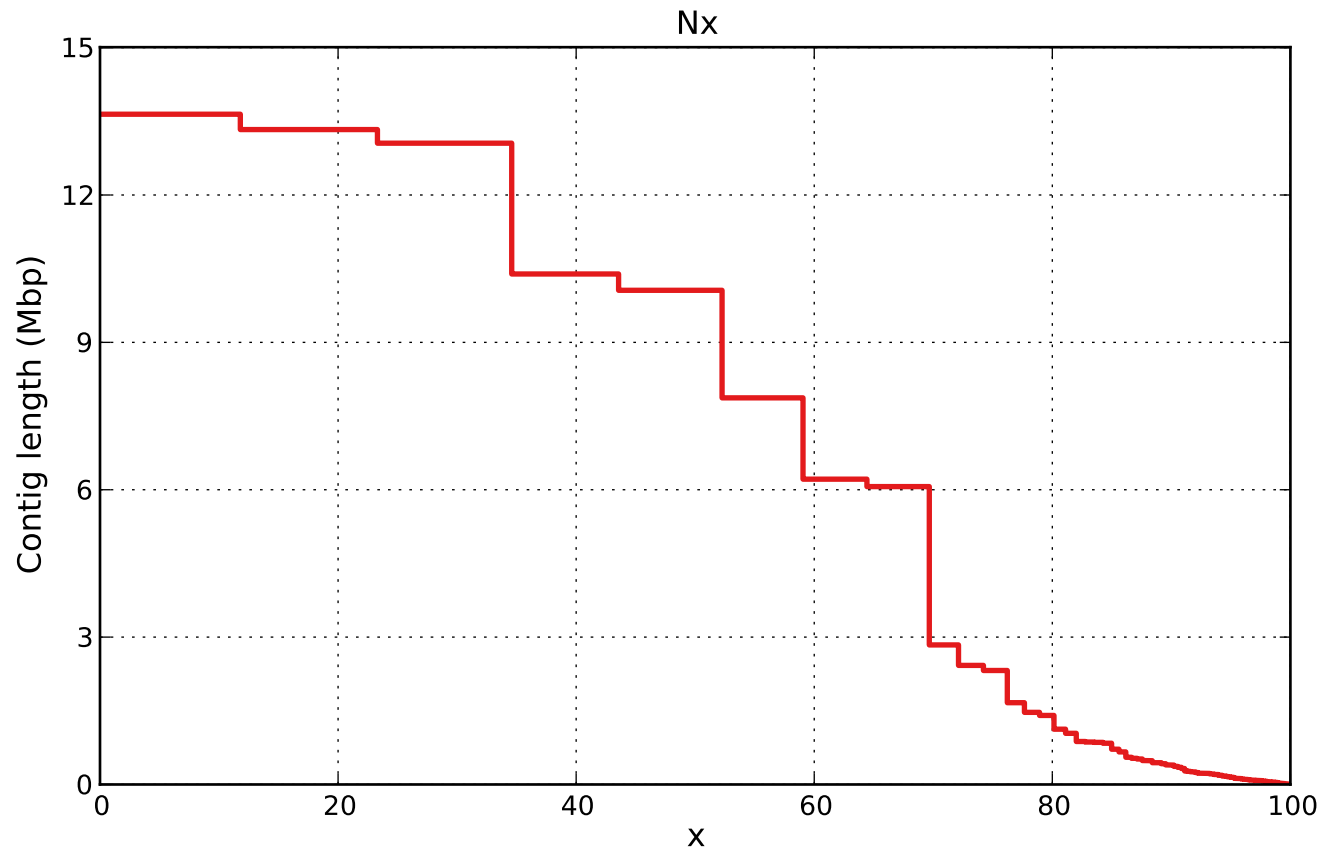
	flye
# misassemblies	487
# contig misassemblies	487
# c. relocations	359
# c. translocations	117
# c. inversions	11
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	102
Misassembled contigs length	112403388
# local misassemblies	2993
# scaffold gap ext. mis.	2
# scaffold gap loc. mis.	8
# possible TEs	60
# unaligned mis. contigs	36
# mismatches	733373
# indels	169189
# indels ( $\leq 5$ bp)	133600
# indels ( $> 5$ bp)	35589
Indels length	1870312

All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

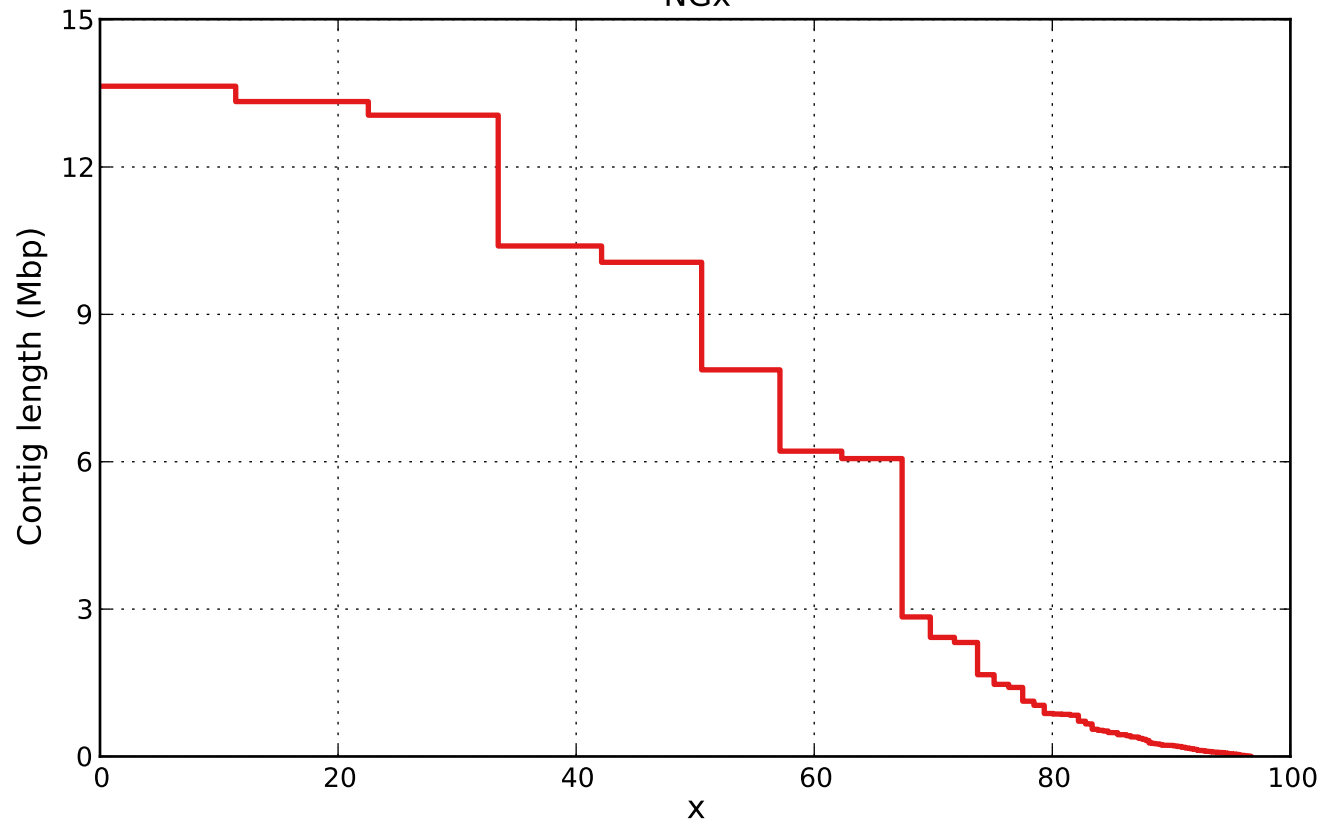
	flye
# fully unaligned contigs	19
Fully unaligned length	291146
# partially unaligned contigs	158
Partially unaligned length	9886912
# N's	1000

All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

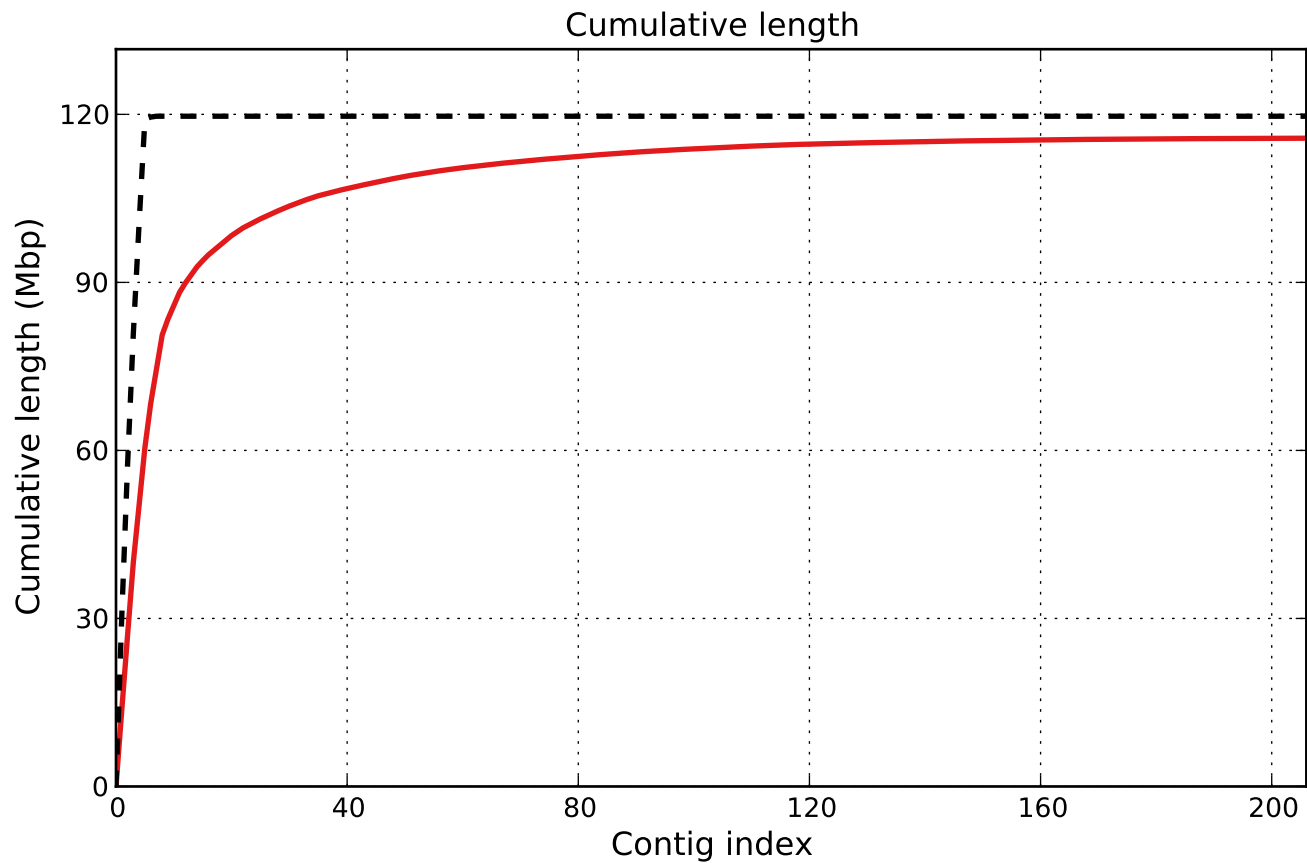


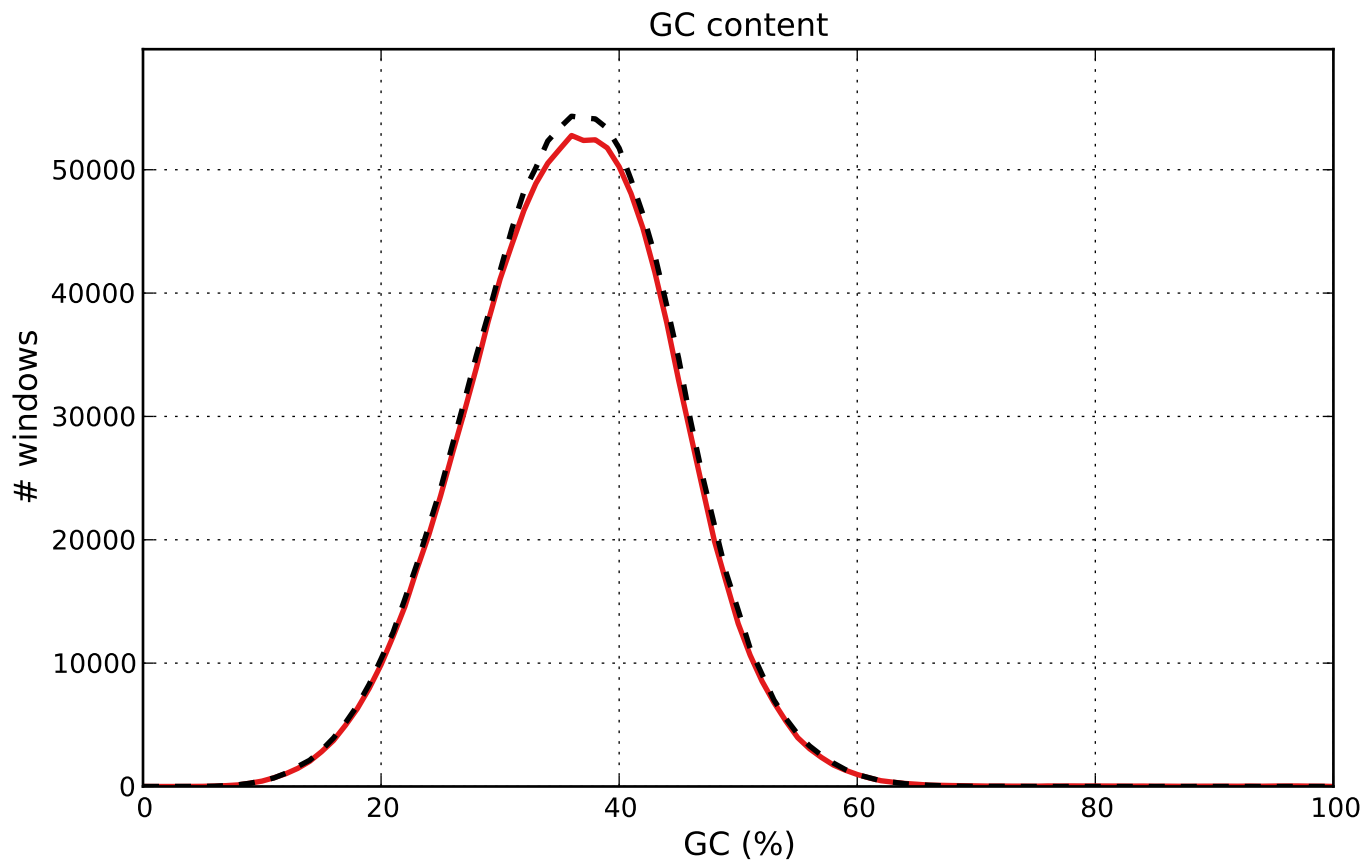
— flye

NGx



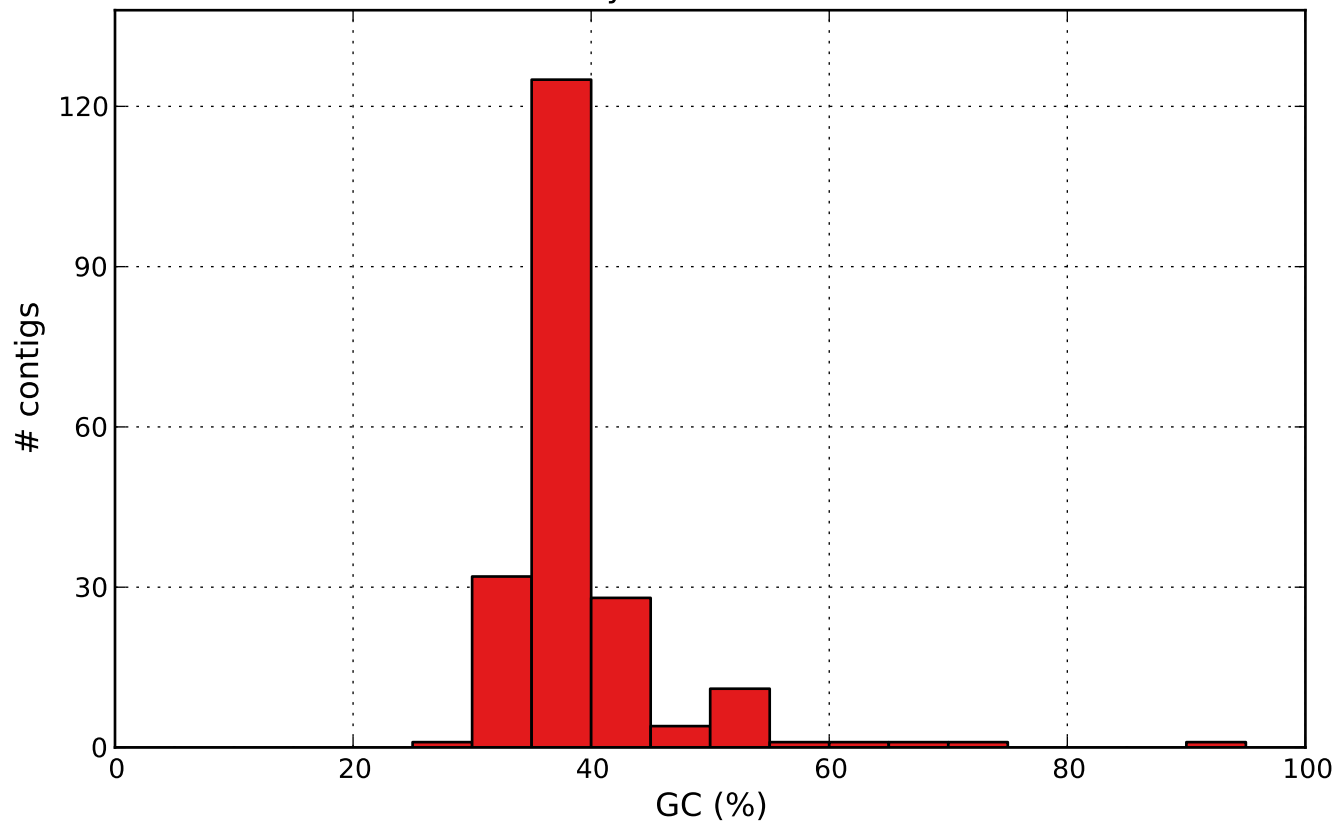
— flye





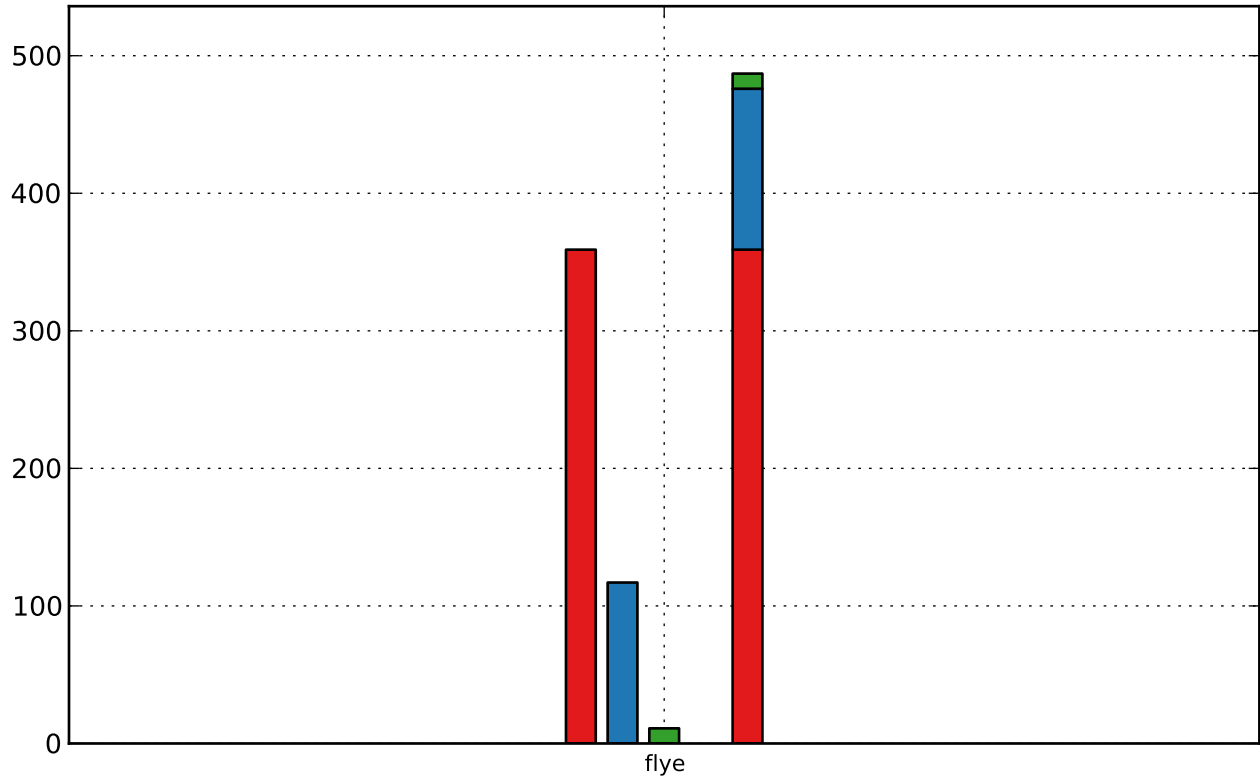


flye GC content

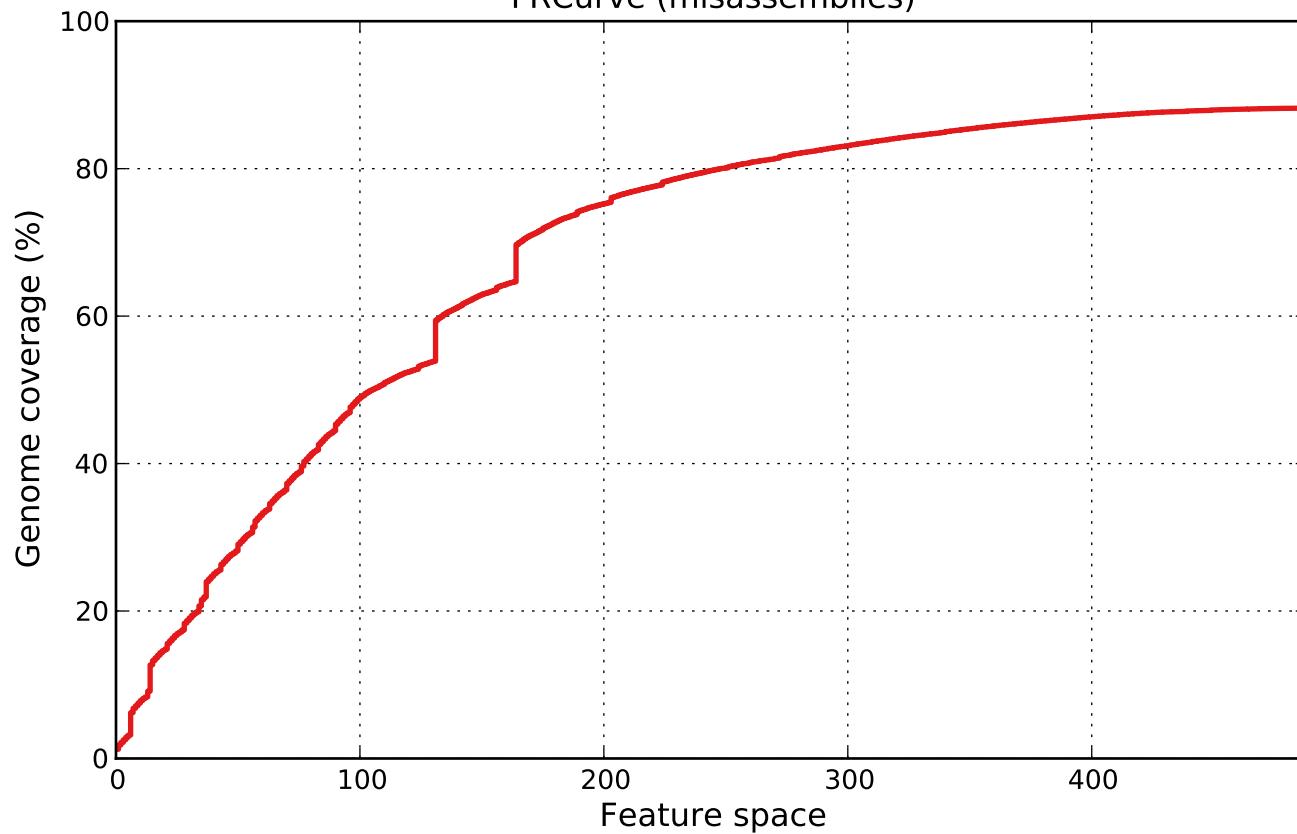


flye

# Misassemblies

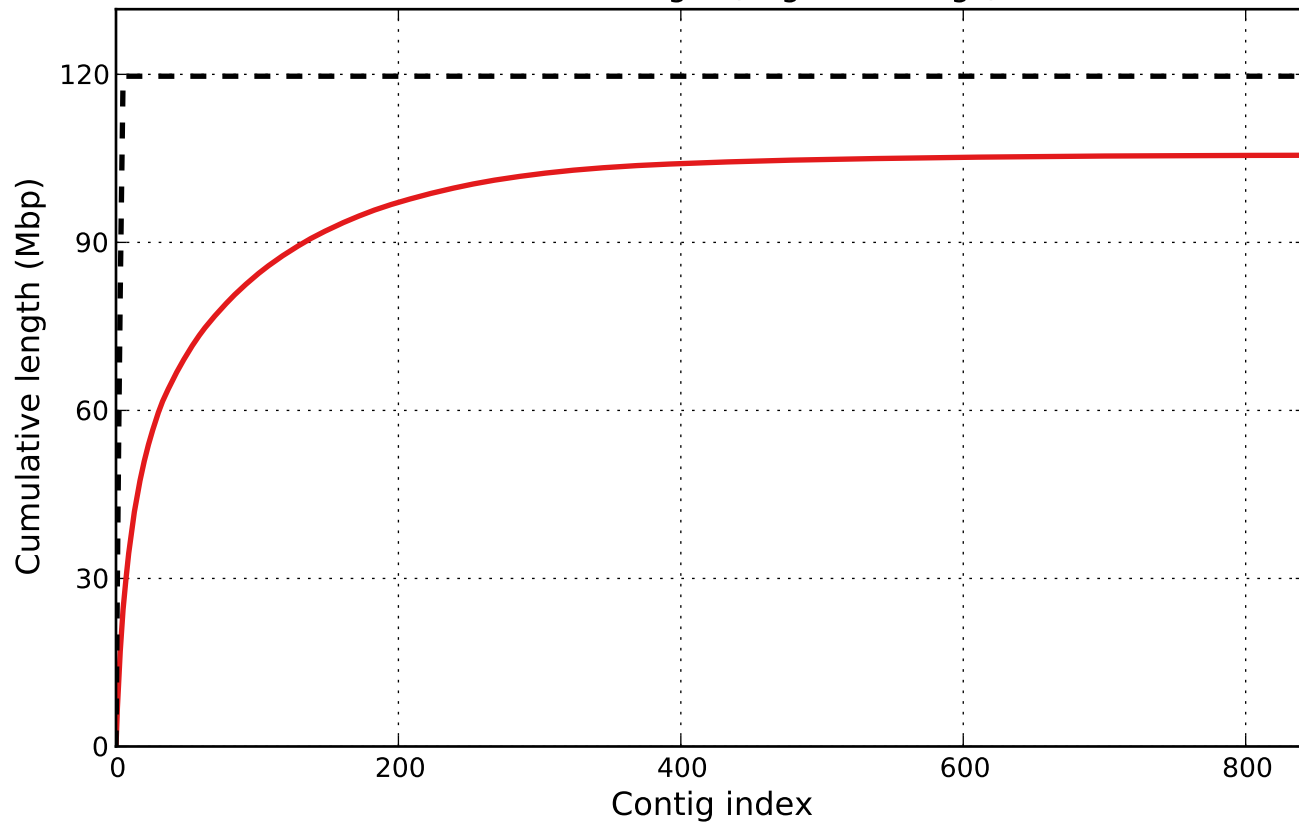


FRCurve (misassemblies)

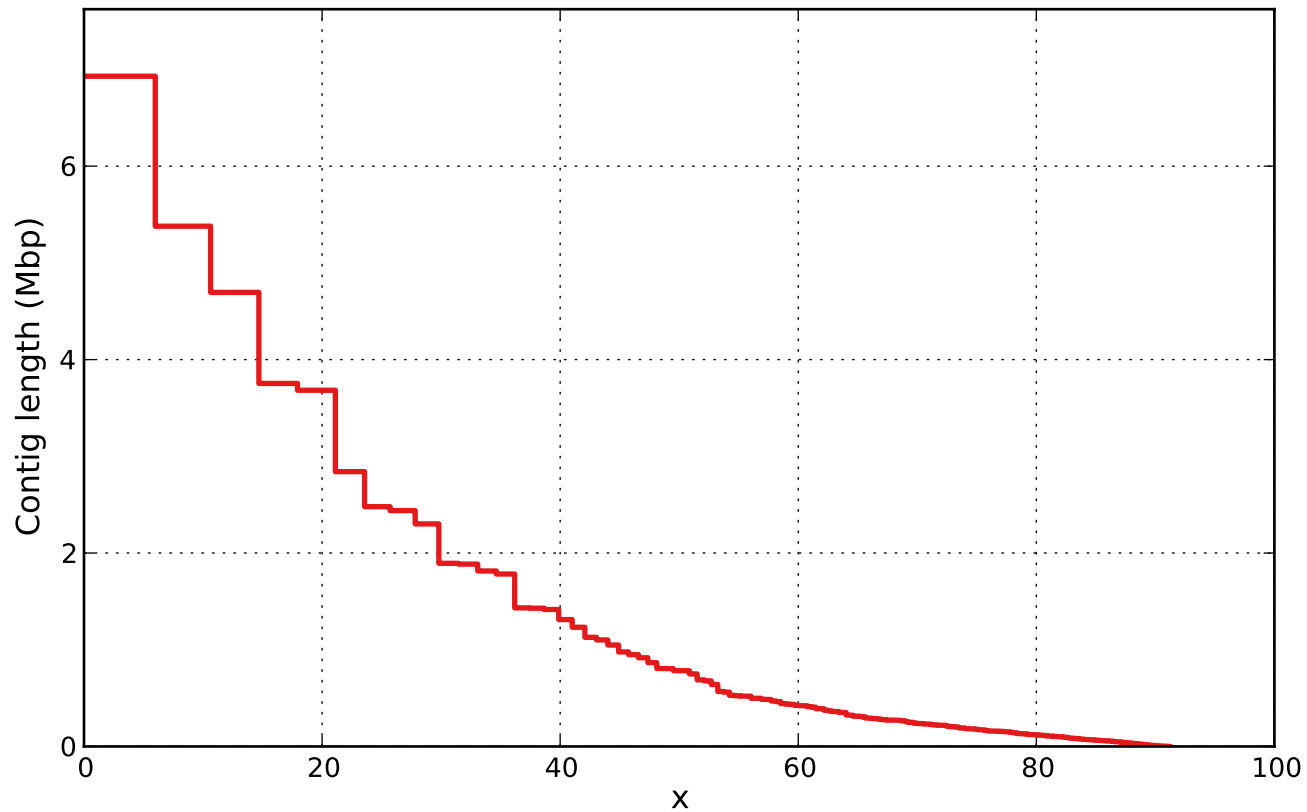


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Cumulative length (aligned contigs)

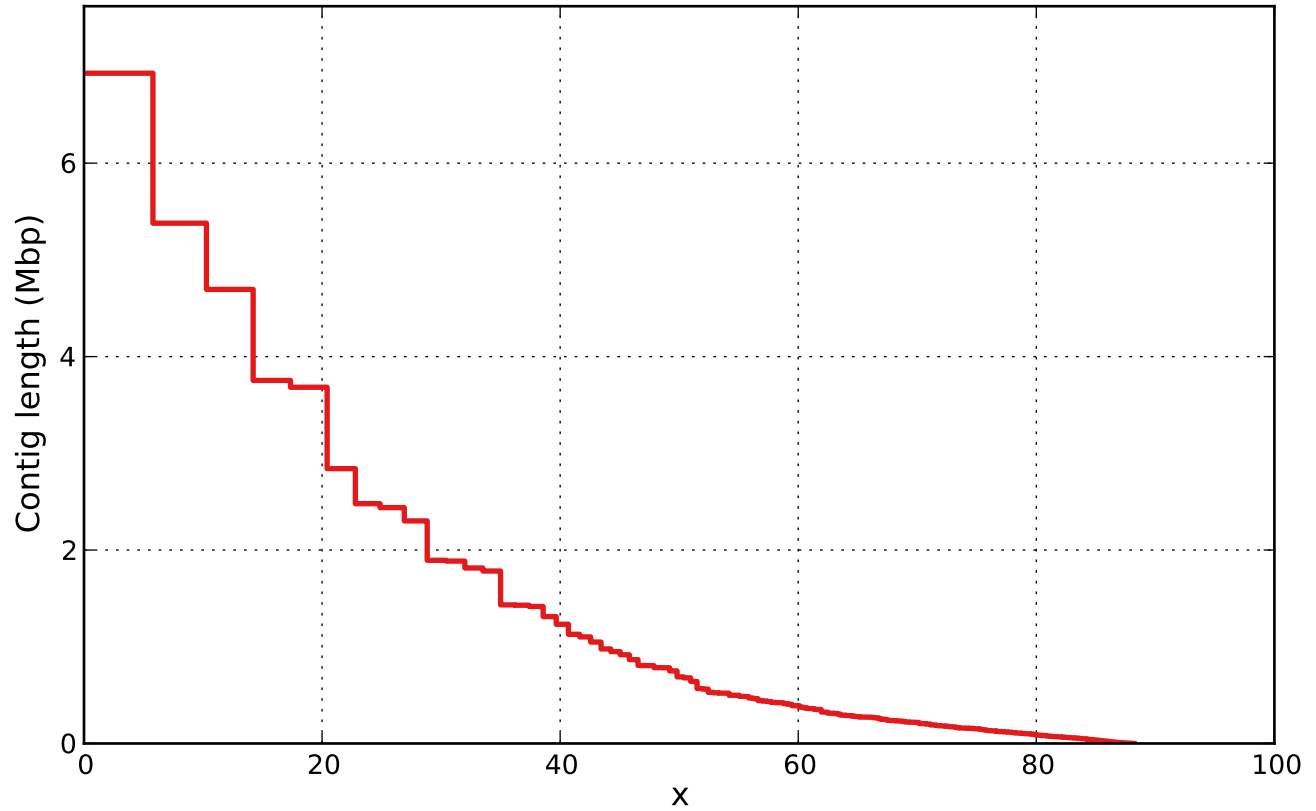


NAx

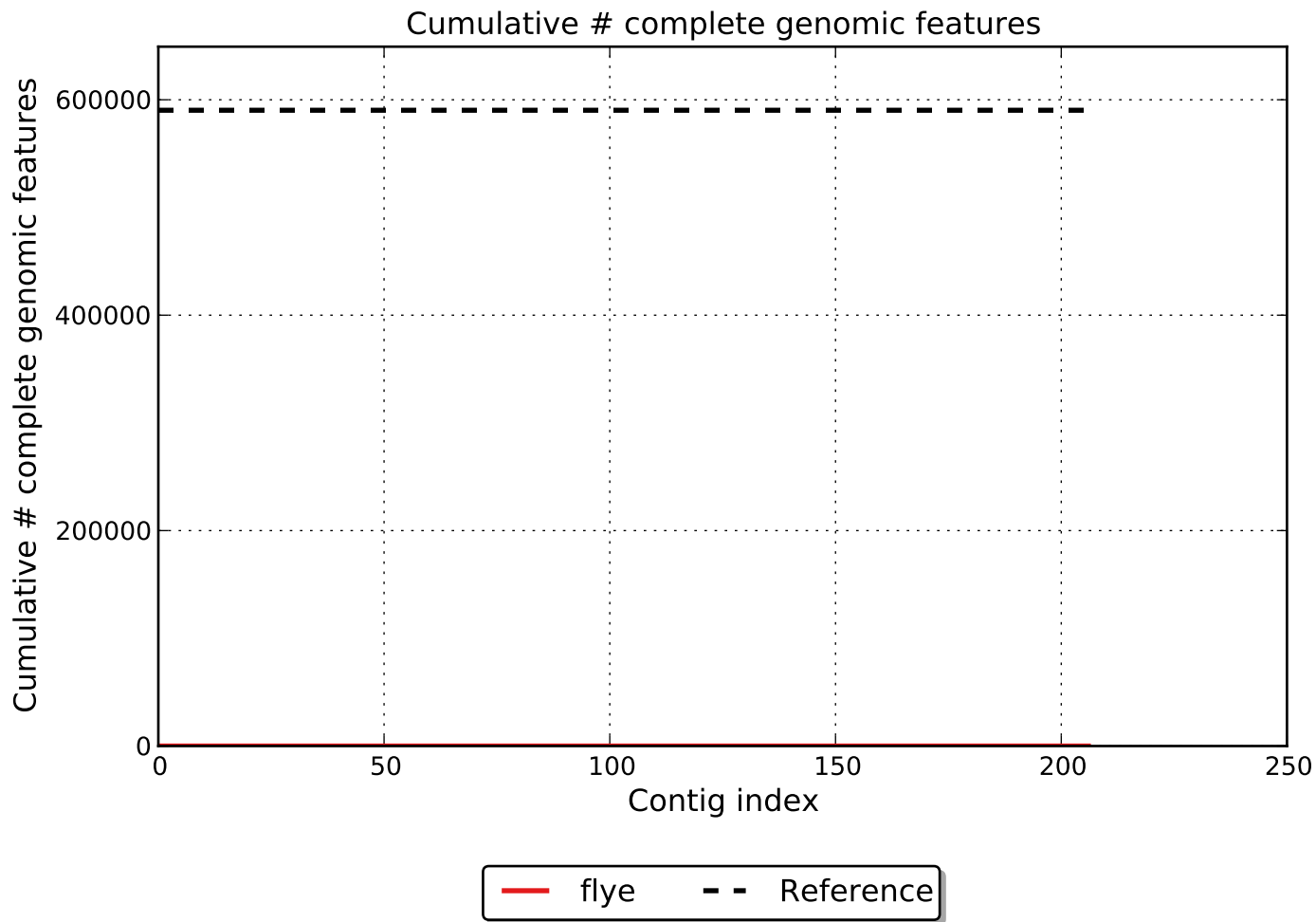


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NGAx



— flye



FRCurve (genomic features)

