

	Report	
	Flye	Hifiasm
# contigs (>= 0 bp)	81	1089
# contigs (>= 1000 bp)	59	1089
# contigs (>= 5000 bp)	54	1089
# contigs (>= 10000 bp)	53	1089
# contigs (>= 25000 bp)	49	1012
# contigs (>= 50000 bp)	40	126
Total length (>= 0 bp)	136225343	176354397
Total length (>= 1000 bp)	136211393	176354397
Total length (>= 5000 bp)	136202016	176354397
Total length (>= 10000 bp)	136195425	176354397
Total length (>= 25000 bp)	136109243	174605687
Total length (>= 50000 bp)	135786785	144121820
# contigs	80	1089
Largest contig	15970461	22724399
Total length	136224852	176354397
Reference length	119667750	119667750
GC (%)	36.32	36.54
Reference GC (%)	36.06	36.06
N50	8815587	8827965
NG50	10659865	19111340
N90	3126411	35225
NG90	4275163	7108853
auN	9135089.7	11356894.5
auNG	10399011.0	16736658.6
L50	6	6
LG50	5	3
L90	16	488
LG90	12	8
# misassemblies	4749	5637
# misassembled contigs	44	295
Misassembled contigs length	125584653	141376084
# local misassemblies	2928	3041
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	7	2
# unaligned contigs	0 + 36 part	49 + 22 part
Unaligned length	23011974	25458755
Genome fraction (%)	89.924	89.400
Duplication ratio	1.048	1.402
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	789.15	613.28
# indels per 100 kbp	159.20	139.26
# genomic features	791931 + 8471 part	785441 + 8372 part
Largest alignment	654106	654106
Total aligned length	112573538	149763755
NA50	64854	41241
NGA50	83085	81160
NA90	-	-
NGA90	5149	31411
auNA	112438.4	93321.9
auNGA	127995.2	137528.6
LA50	468	870
LGA50	355	359
LA90	-	-
LGA90	2377	1412

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).

## Misassemblies report

	Flye	Hifiasm
# misassemblies	4749	5637
# contig misassemblies	4749	5637
# c. relocations	3033	3857
# c. translocations	1697	1760
# c. inversions	19	20
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	44	295
Misassembled contigs length	125584653	141376084
# local misassemblies	2928	3041
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	7	2
# mismatches	888378	918476
# indels	179217	208564
# indels (<= 5 bp)	145339	172152
# indels (> 5 bp)	33878	36412
Indels length	1024961	1125286

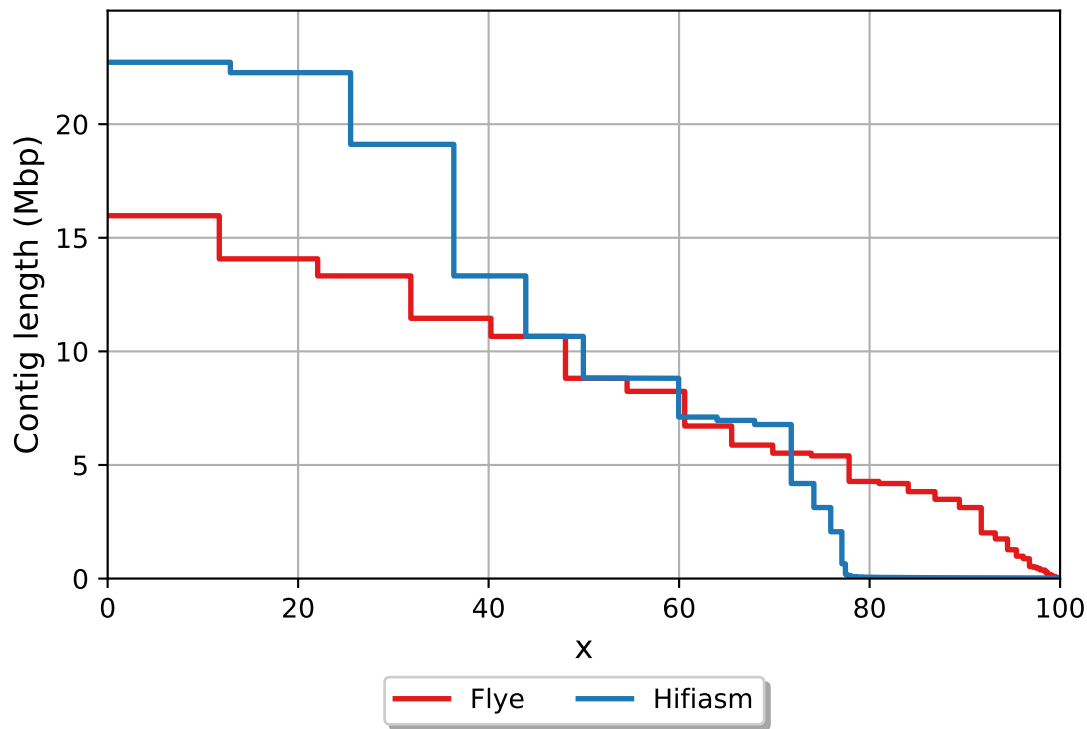
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

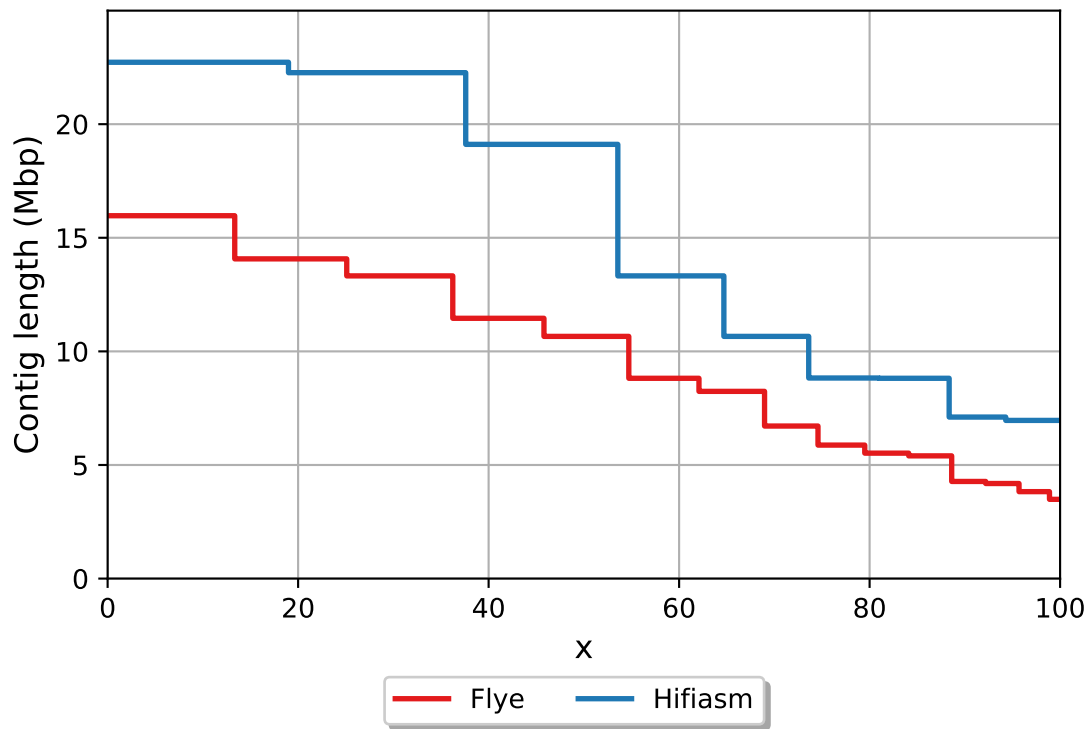
	Flye	Hifiasm
# fully unaligned contigs	0	49
Fully unaligned length	0	2321691
# partially unaligned contigs	36	22
Partially unaligned length	23011974	23137064
# N's	0	0

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

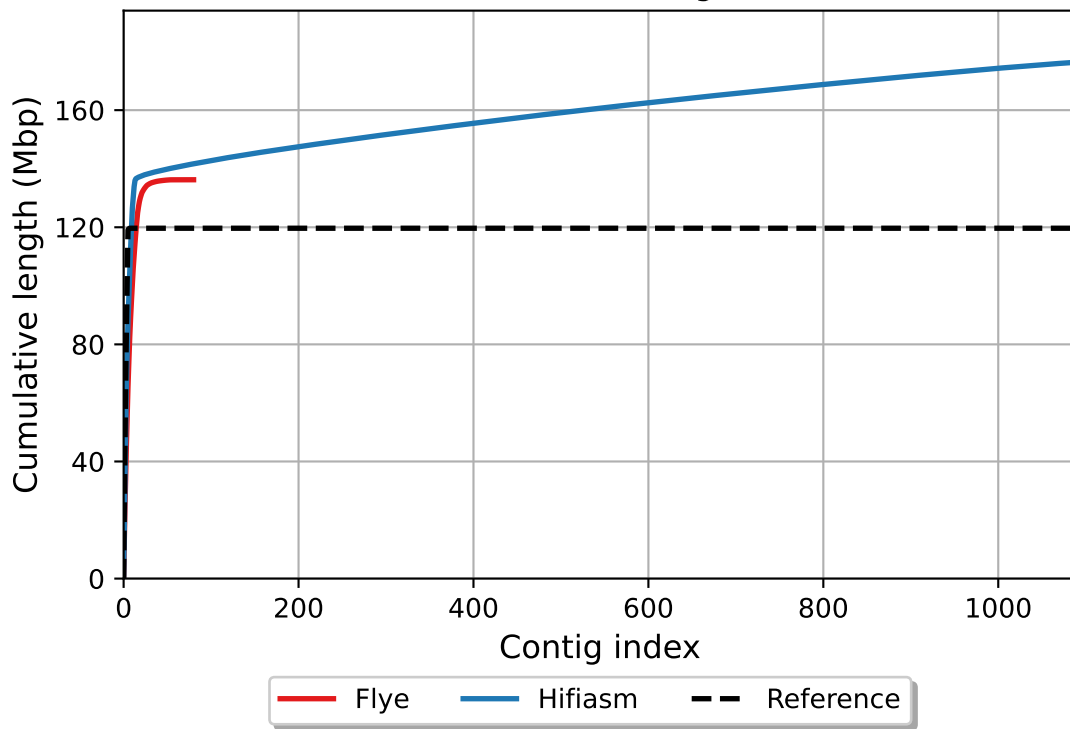
Nx

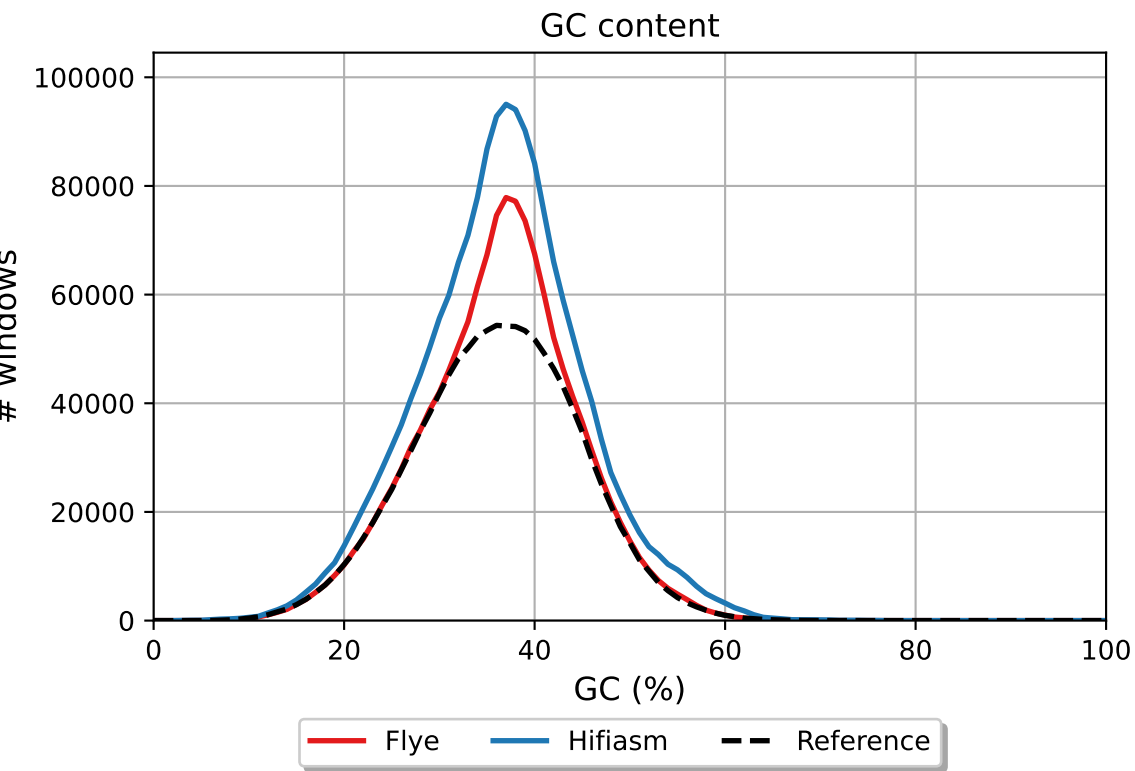


# NGx

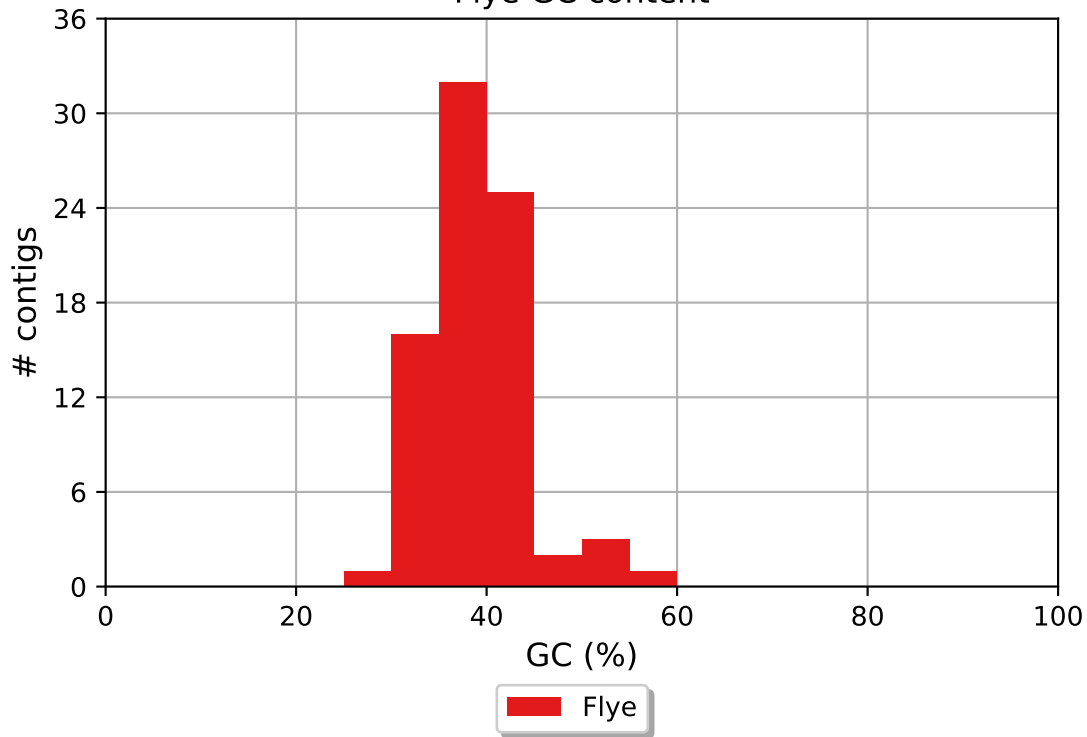


Cumulative length



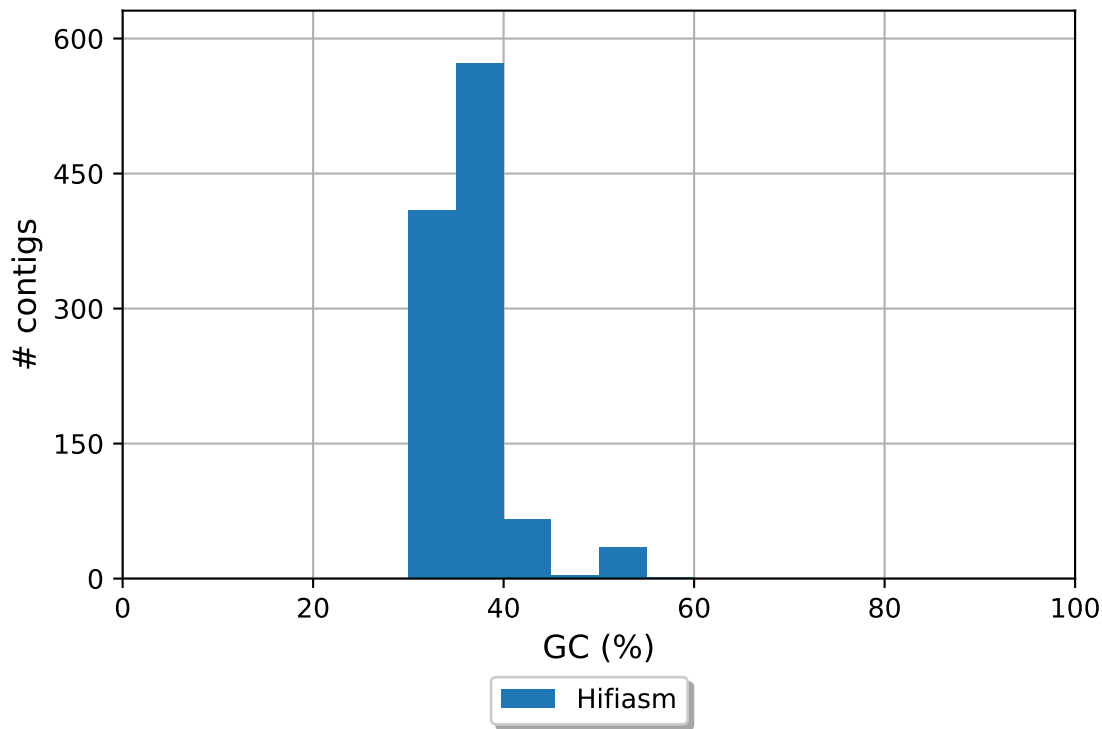


Flye GC content

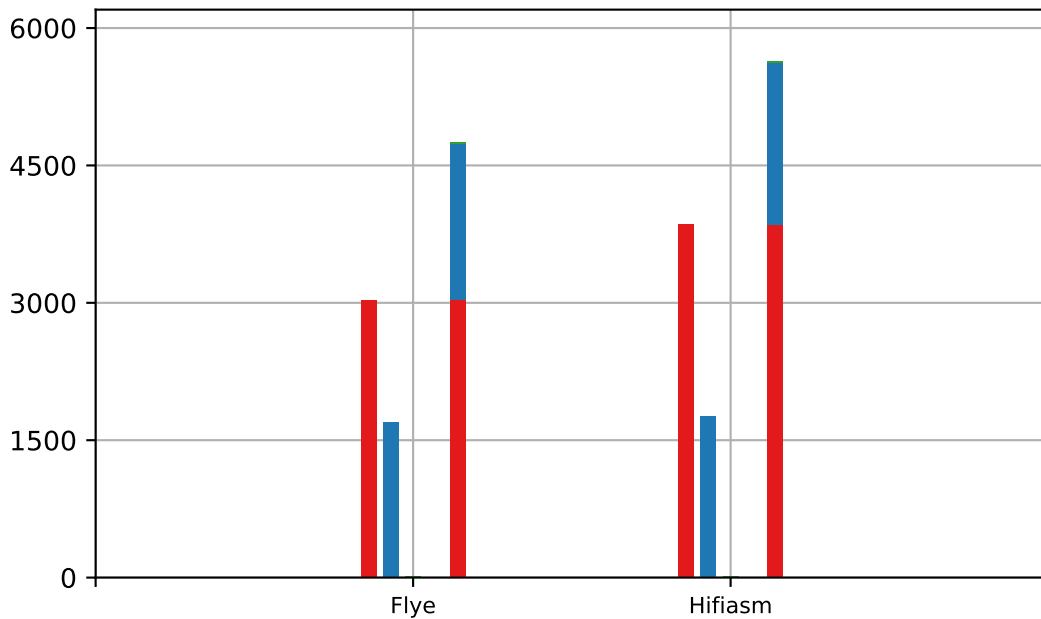




Hifiasm GC content



## Misassemblies



# relocations

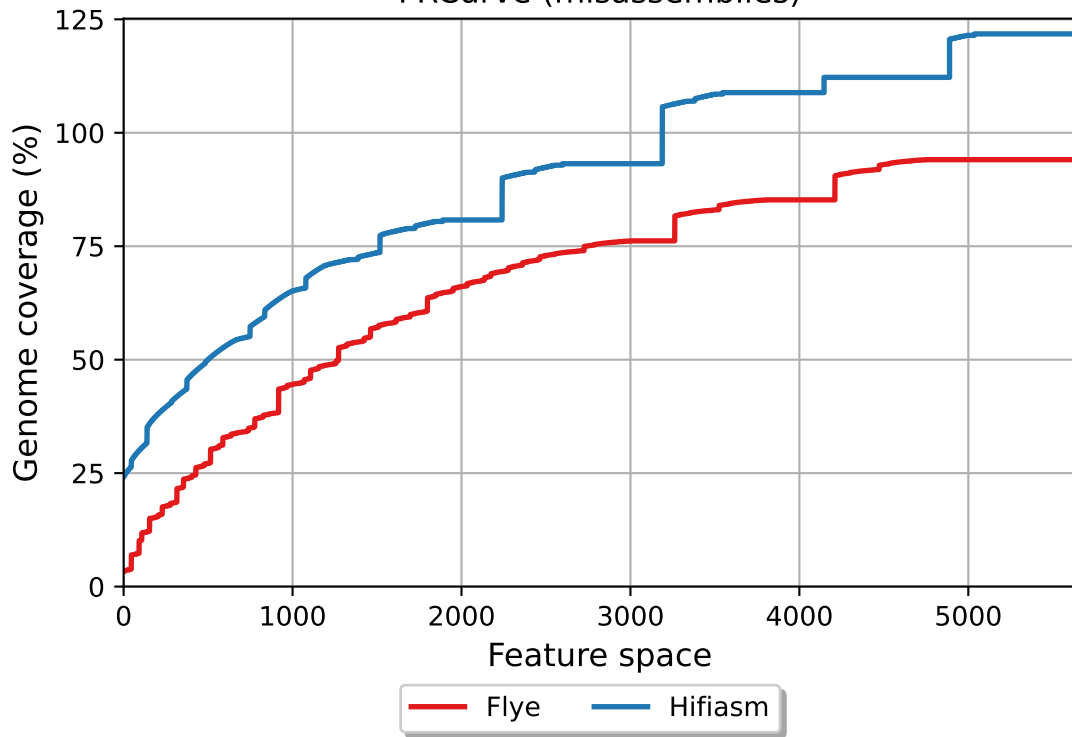


# translocations

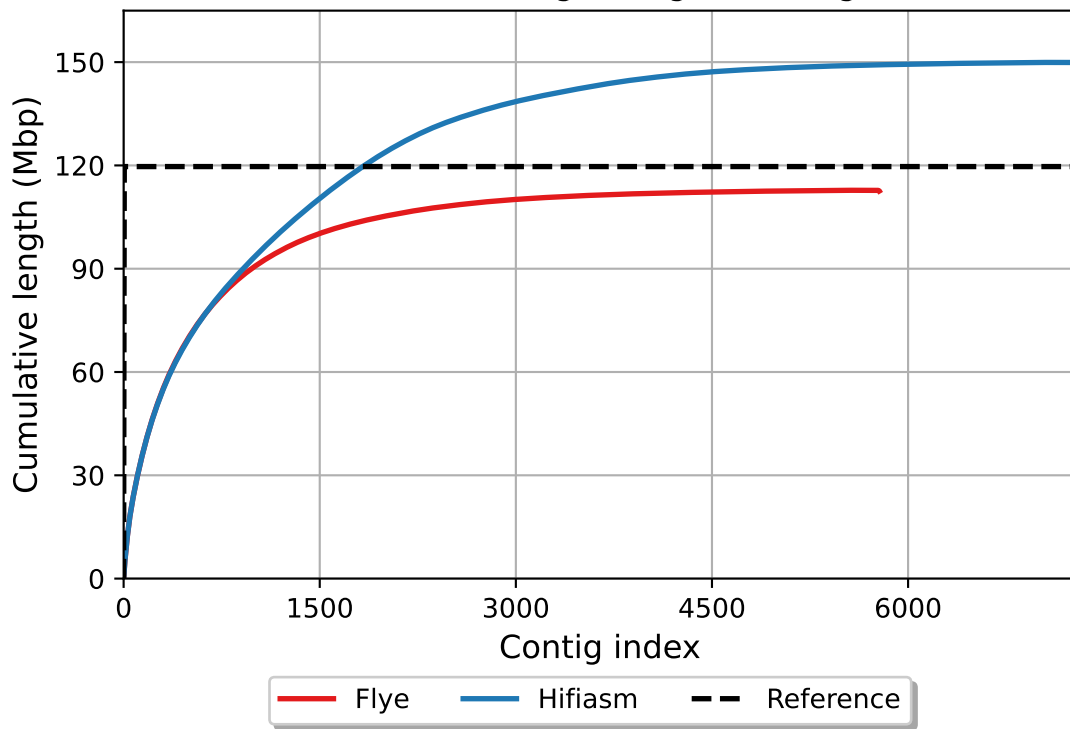


# inversions

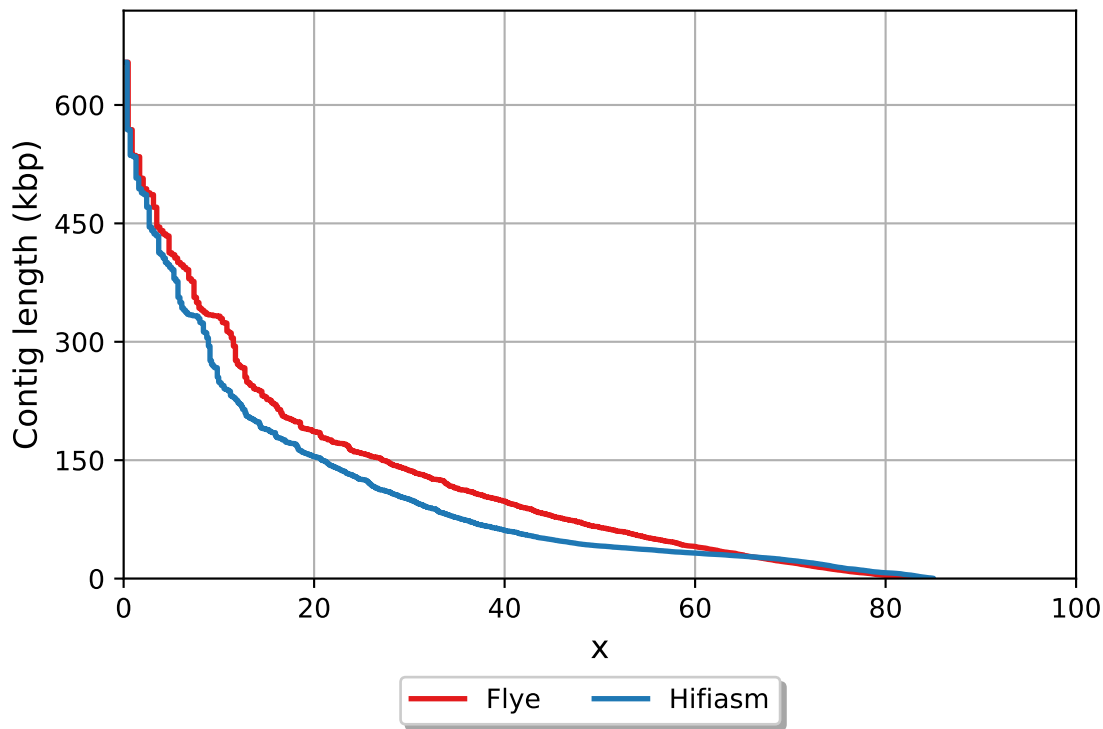
FRCurve (misassemblies)



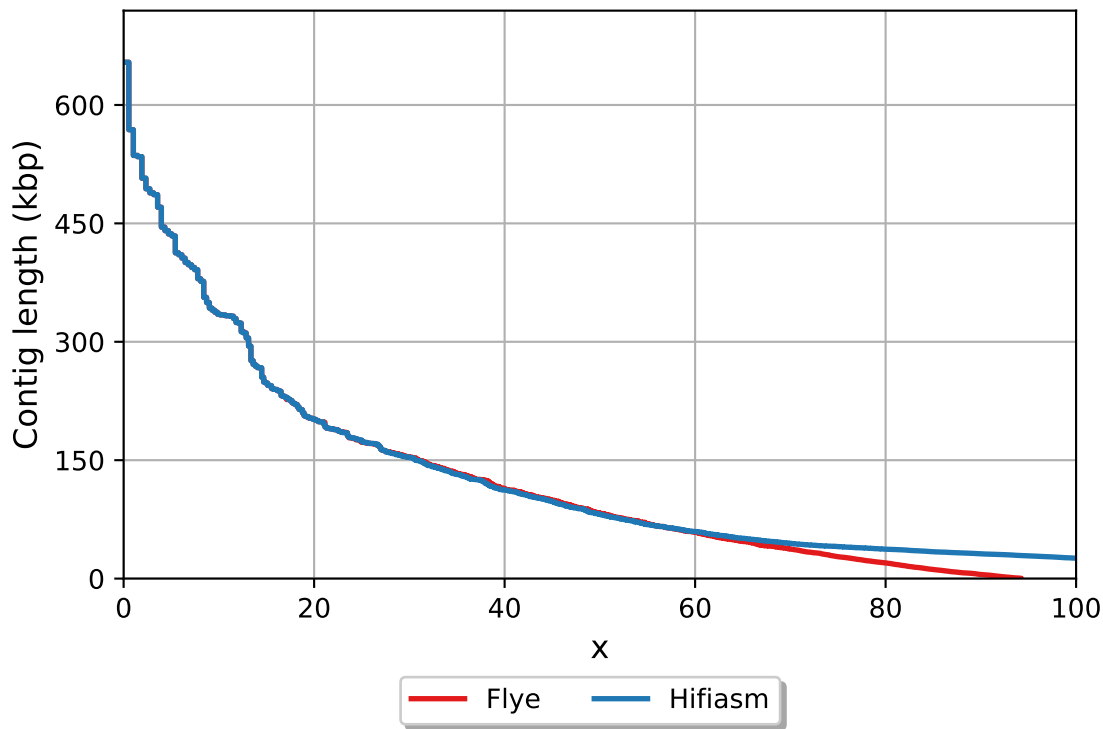
Cumulative length (aligned contigs)



NAx

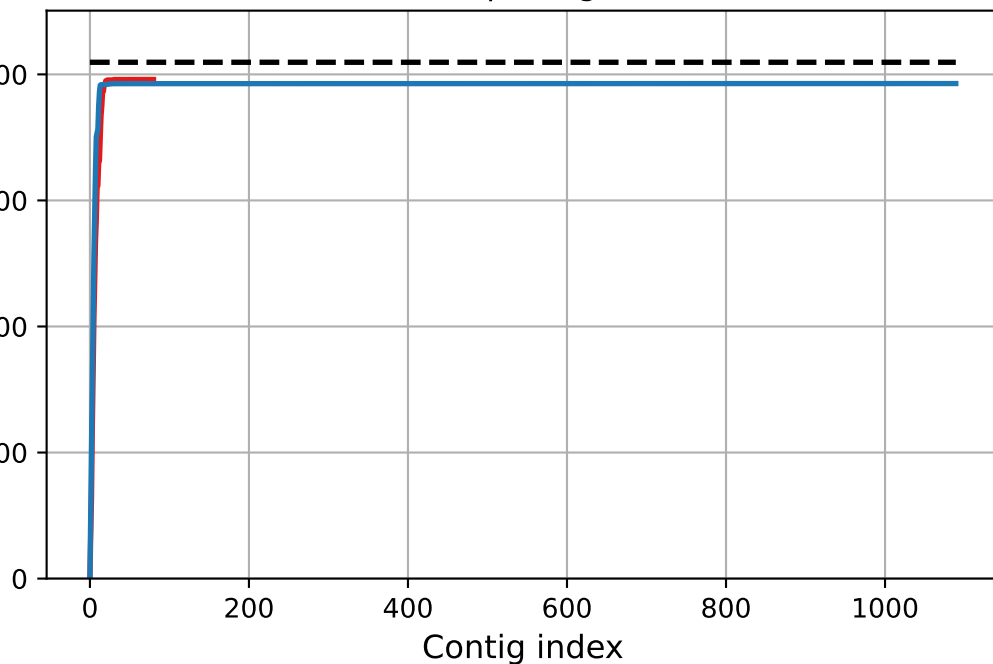


# NGAx



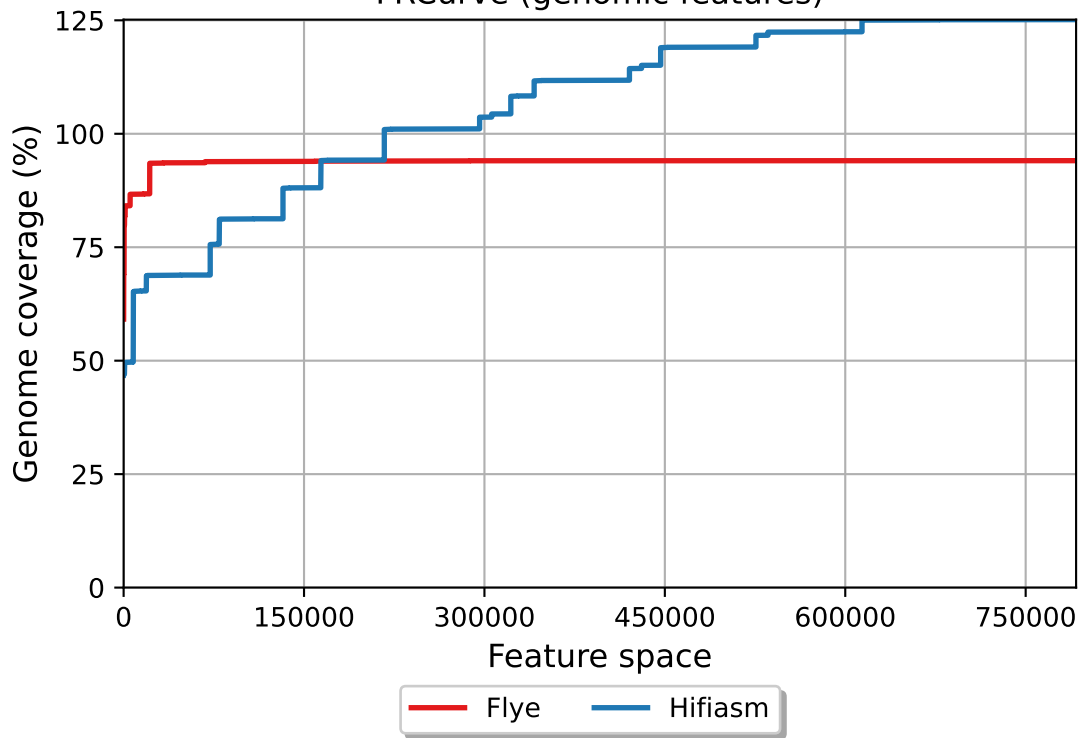
Cumulative # complete genomic features

Cumulative # complete genomic features



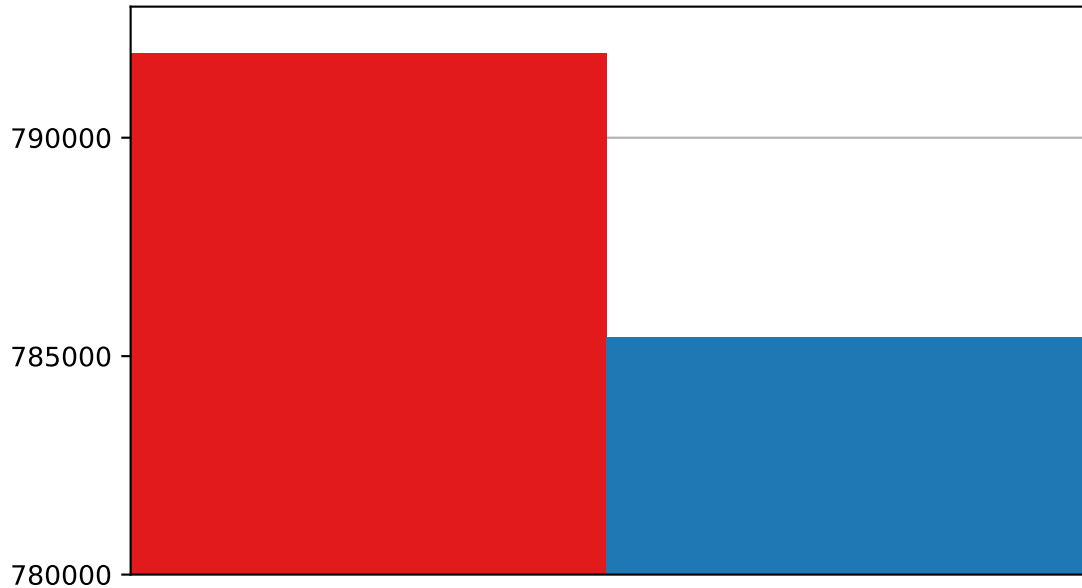
Flye Hifiasm Reference

FRCurve (genomic features)





# complete genomic features

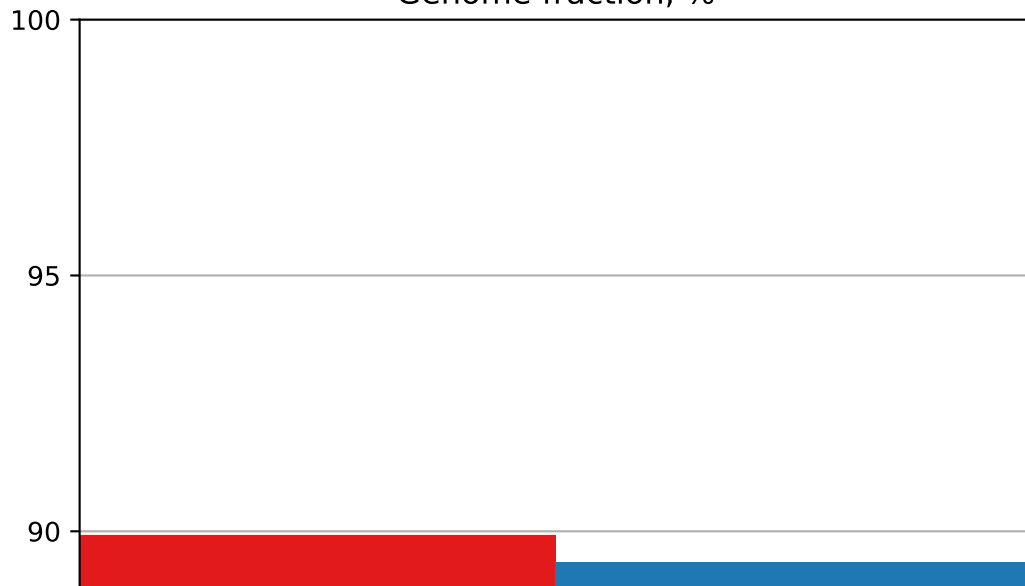


Flye



Hifiasm

Genome fraction, %



Flye



Hifiasm