

	Report	lja	hifiasm
# contigs (>= 0 bp)	133	1370	533
# contigs (>= 1000 bp)	112	1370	533
# contigs (>= 5000 bp)	103	1010	533
# contigs (>= 10000 bp)	102	703	533
# contigs (>= 25000 bp)	99	214	511
# contigs (>= 50000 bp)	82	113	171
Total length (>= 0 bp)	149786175	168417649	163570346
Total length (>= 1000 bp)	149772774	168417649	163570346
Total length (>= 5000 bp)	149751045	167330050	163570346
Total length (>= 10000 bp)	149745174	165026363	163570346
Total length (>= 25000 bp)	149696587	157151887	163076436
Total length (>= 50000 bp)	149103316	153824848	150691701
# contigs	133	1370	533
Largest contig	14984465	10926278	20513432
Total length	149786175	168417649	163570346
Reference length	119667750	119667750	119667750
GC (%)	36.35	37.68	36.96
Reference GC (%)	36.06	36.06	36.06
N50	5079472	5583654	7687602
NG50	6860403	6860363	10270435
N90	988575	78300	68797
NG90	2547681	2989757	3941965
auN	6024640.8	5185950.0	9008359.8
auNG	7540944.8	7298587.2	12313263.4
L50	9	11	7
LG50	7	7	4
L90	36	79	110
LG90	19	17	11
# total reads	476430	476430	173995
# left	0	0	0
# right	0	0	0
Mapped (%)	205.09	152.5	173.08
Reference mapped (%)	225.44	225.44	225.44
Properly paired (%)	0.0	0.0	0.0
Reference properly paired (%)	0.0	0.0	0.0
Avg. coverage depth	65	65	29
Reference avg. coverage depth	87	87	87
Coverage >= 1x (%)	100.0	98.27	98.63
Reference coverage >= 1x (%)	98.38	98.38	98.38
# misassemblies	4538	6022	5586
# misassembled contigs	66	564	226
Misassembled contigs length	129804080	150268466	146205324
# local misassemblies	2575	3290	2862
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	23	14	27
# unaligned contigs	1 + 87 part	3 + 189 part	0 + 118 part
Unaligned length	26023907	27367657	23660658
Genome fraction (%)	91.707	91.786	91.306
Duplication ratio	1.127	1.279	1.276
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	725.98	684.54	618.57
# indels per 100 kbp	141.58	134.52	134.71
Largest alignment	2063374	2063376	2063373
Total aligned length	123504517	140307117	139163604
NA50	66522	48868	55107
NGA50	104592	101474	103809
NA90	-	-	-
NGA90	15762	18649	29760
auNA	182582.8	164088.1	168957.7
auNGA	228536.0	230933.8	230943.4
LA50	441	613	558
LGA50	259	263	262
LA90	-	-	-
LGA90	1402	1353	1217

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).

Reads report

	flye	lja	hifiasm
# total reads	476430	476430	173995
# left	0	0	0
# right	0	0	0
# mapped	977119	726569	301156
Mapped (%)	205.09	152.5	173.08
# properly paired	0	0	0
Properly paired (%)	0.0	0.0	0.0
# singletons	0	0	0
Singletons (%)	0.0	0.0	0.0
# misjoint mates	0	0	0
Misjoint mates (%)	0.0	0.0	0.0
Avg. coverage depth	65	65	29
Coverage >= 1x (%)	100.0	98.27	98.63
Coverage >= 5x (%)	99.93	97.53	95.15
Coverage >= 10x (%)	99.76	96.96	91.92
# reference mapped	1074047	1074047	1074047
Reference mapped (%)	225.44	225.44	225.44
# reference properly paired	0	0	0
Reference properly paired (%)	0.0	0.0	0.0
# reference singletons	0	0	0
Reference singletons (%)	0.0	0.0	0.0
# reference misjoint mates	0	0	0
Reference misjoint mates (%)	0.0	0.0	0.0
Reference avg. coverage depth	87	87	87
Reference coverage >= 1x (%)	98.38	98.38	98.38
Reference coverage >= 5x (%)	97.75	97.75	97.75
Reference coverage >= 10x (%)	97.41	97.41	97.41

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	lja	hifiasm
# misassemblies	4538	6022	5586
# contig misassemblies	4538	6022	5586
# c. relocations	2814	4043	3837
# c. translocations	1708	1961	1726
# c. inversions	16	18	23
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	66	564	226
Misassembled contigs length	129804080	150268466	146205324
# local misassemblies	2575	3290	2862
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	23	14	27
# mismatches	896615	960457	860828
# indels	174861	188744	187467
# indels (<= 5 bp)	141831	151038	152685
# indels (> 5 bp)	33030	37706	34782
Indels length	1004879	1304211	1133275

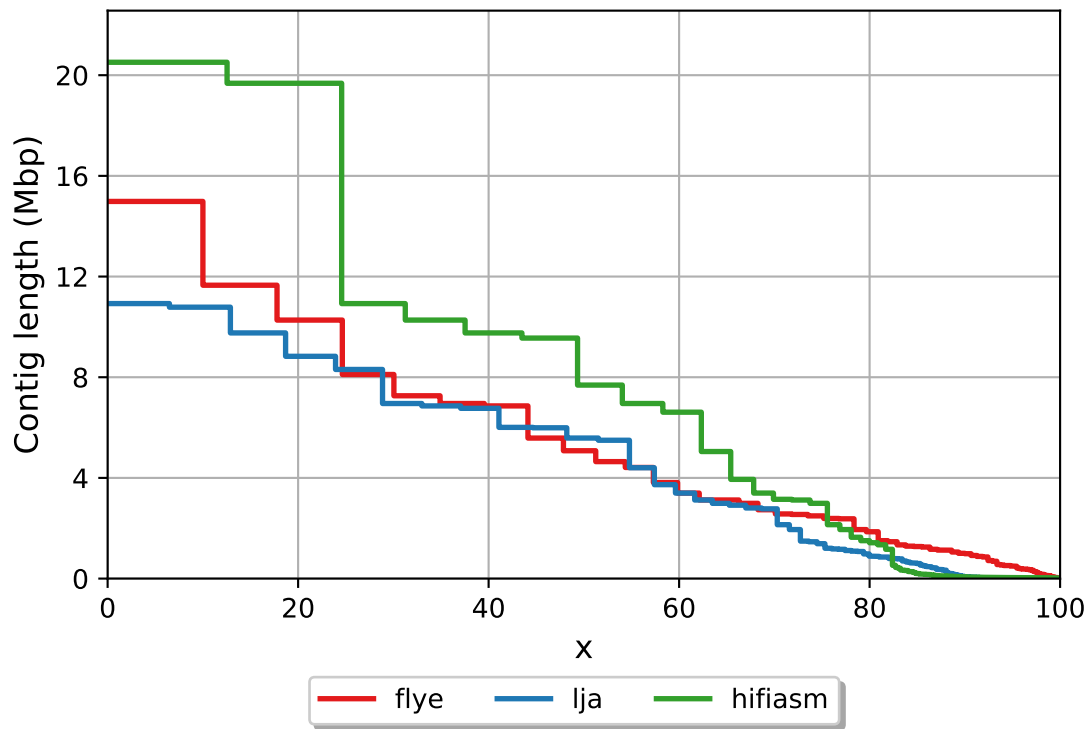
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

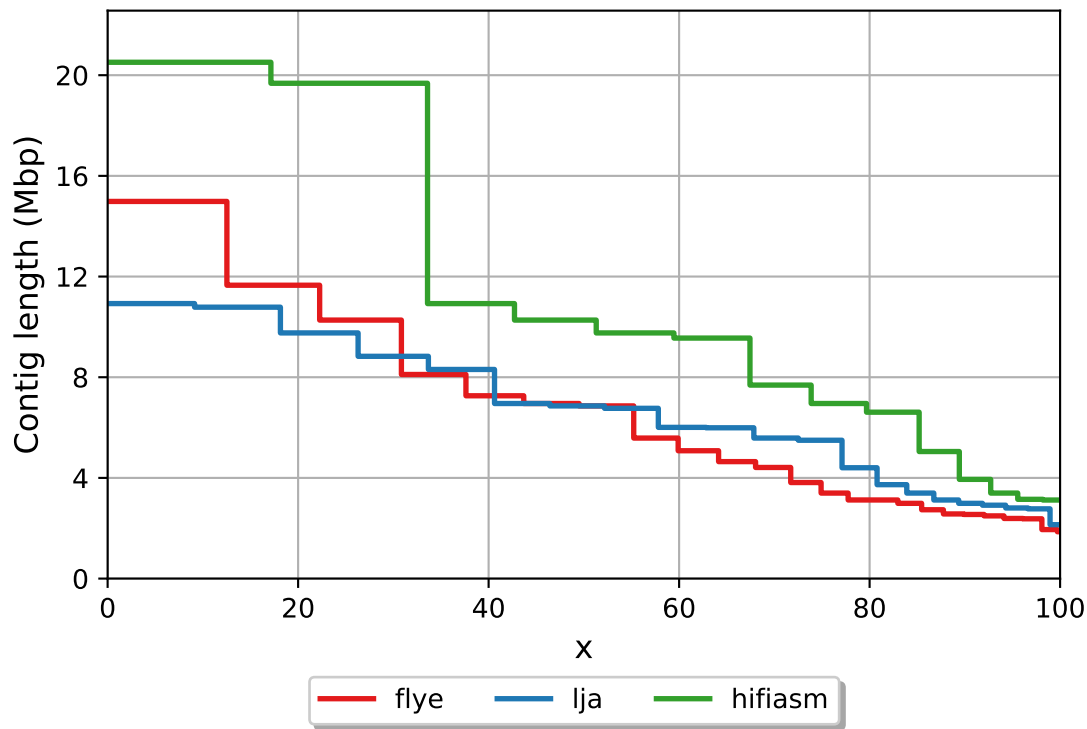
	flye	lja	hifiasm
# fully unaligned contigs	1	3	0
Fully unaligned length	31381	7633	0
# partially unaligned contigs	87	189	118
Partially unaligned length	25992526	27360024	23660658
# N's	0	0	0

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).

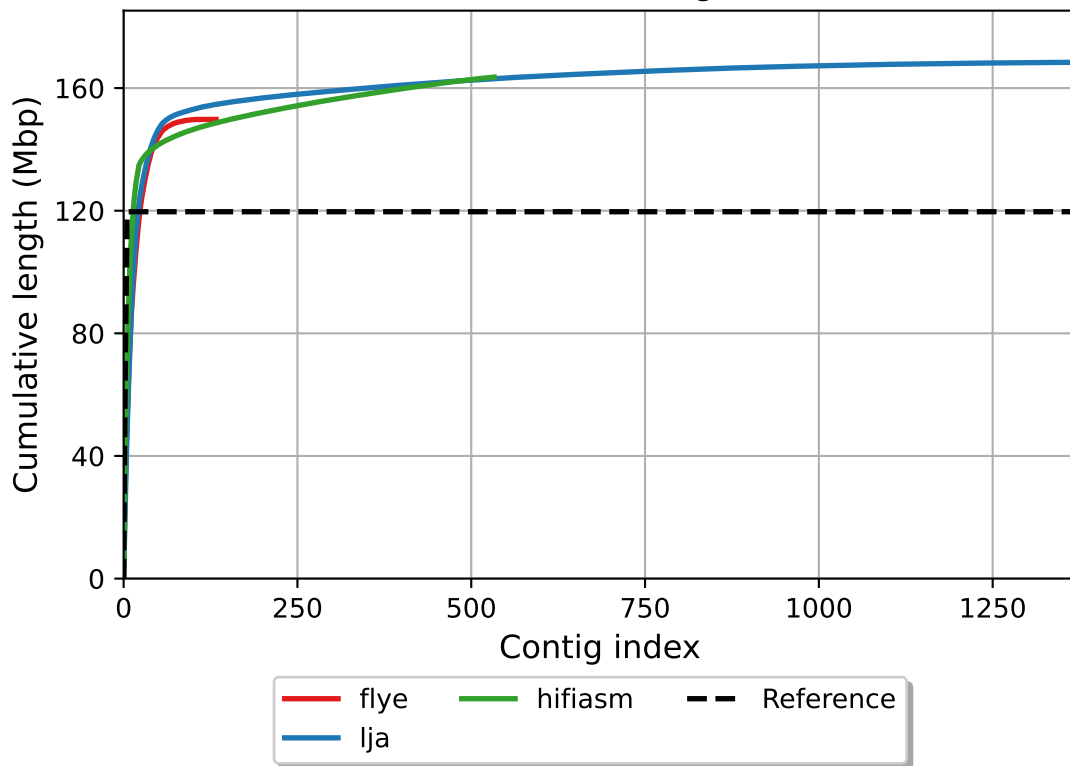
Nx



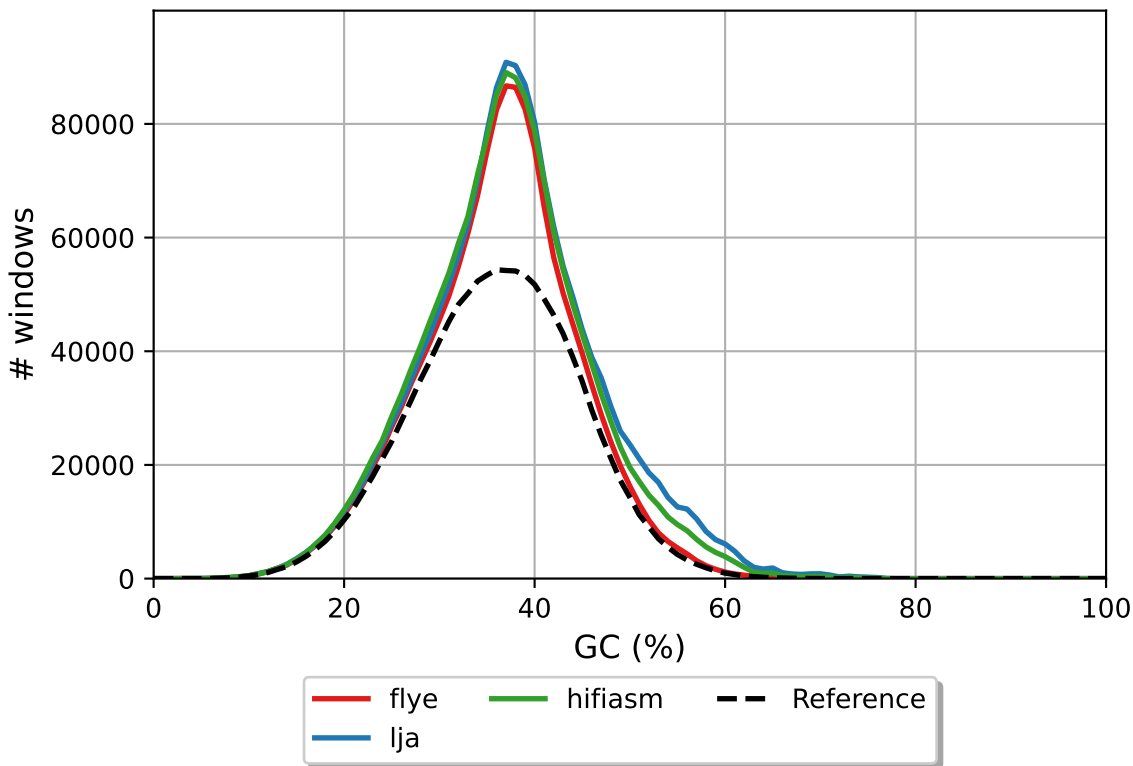
NGx



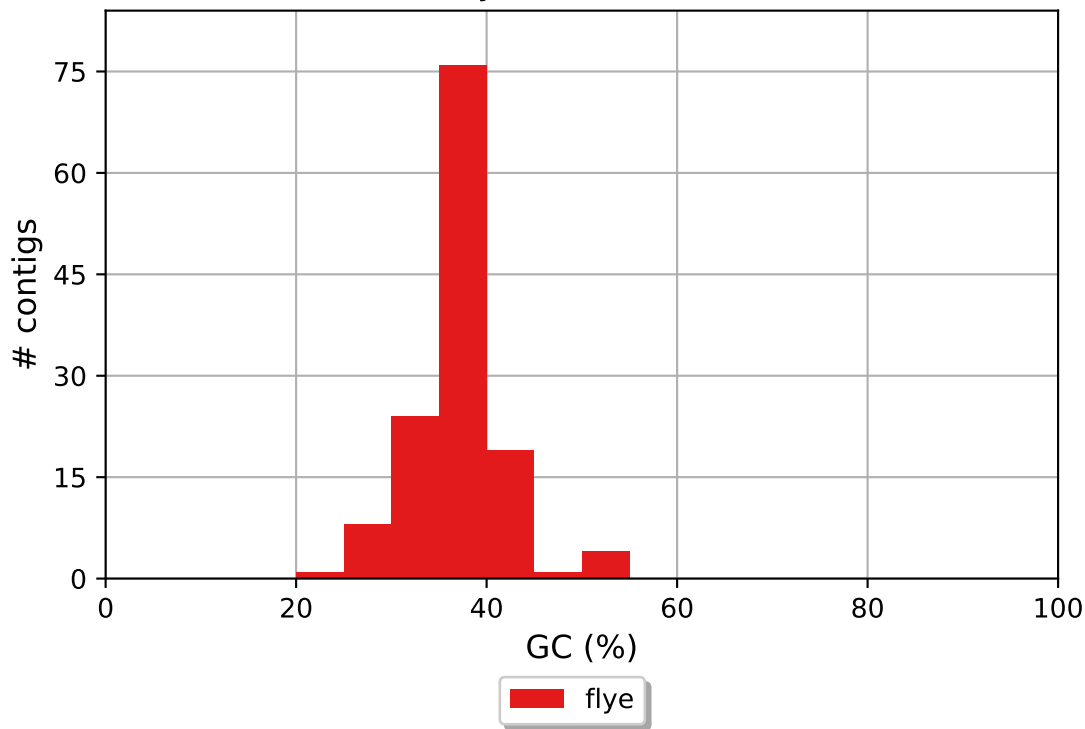
Cumulative length



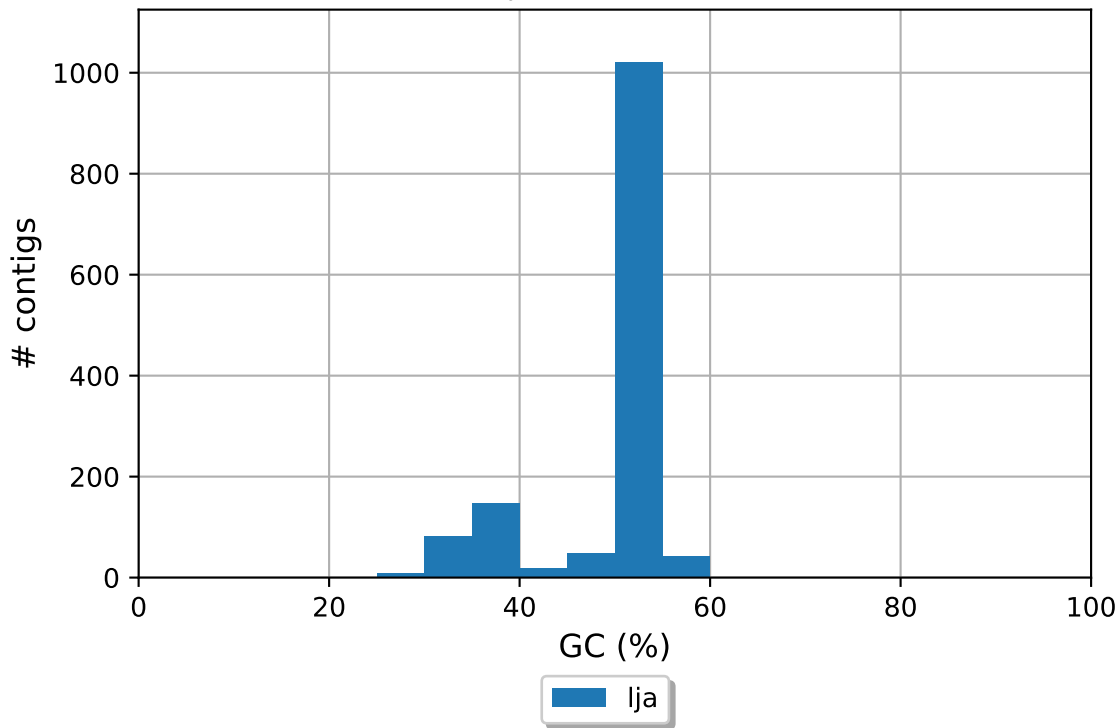
GC content



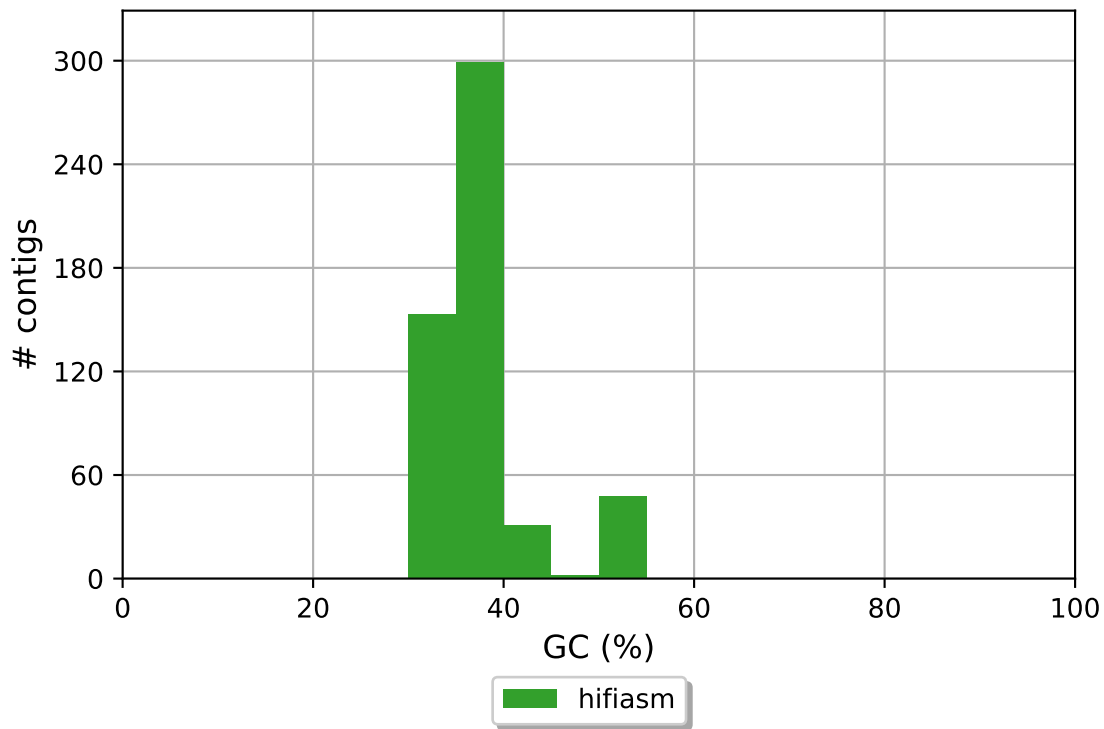
flye GC content



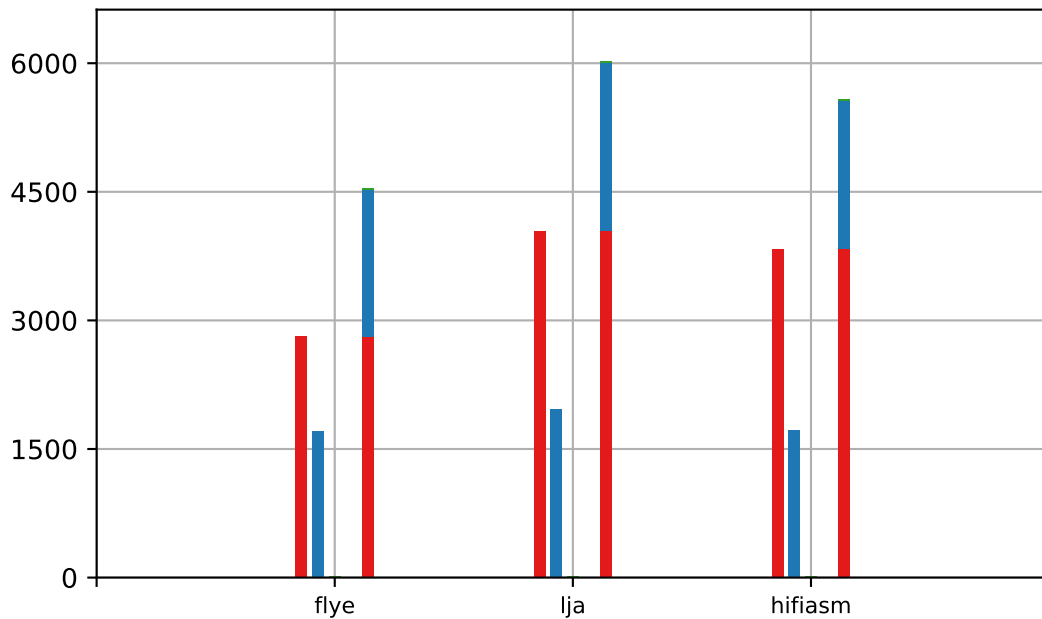
Ija GC content



hifiasm GC content



Misassemblies



relocations

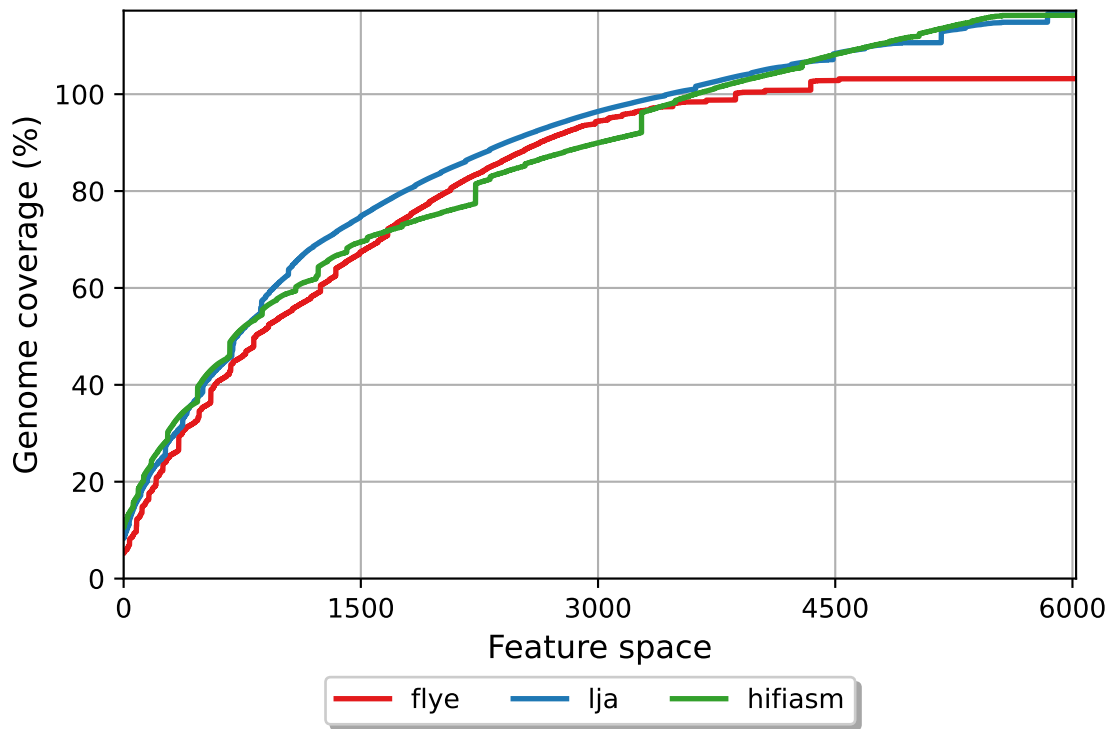


translocations

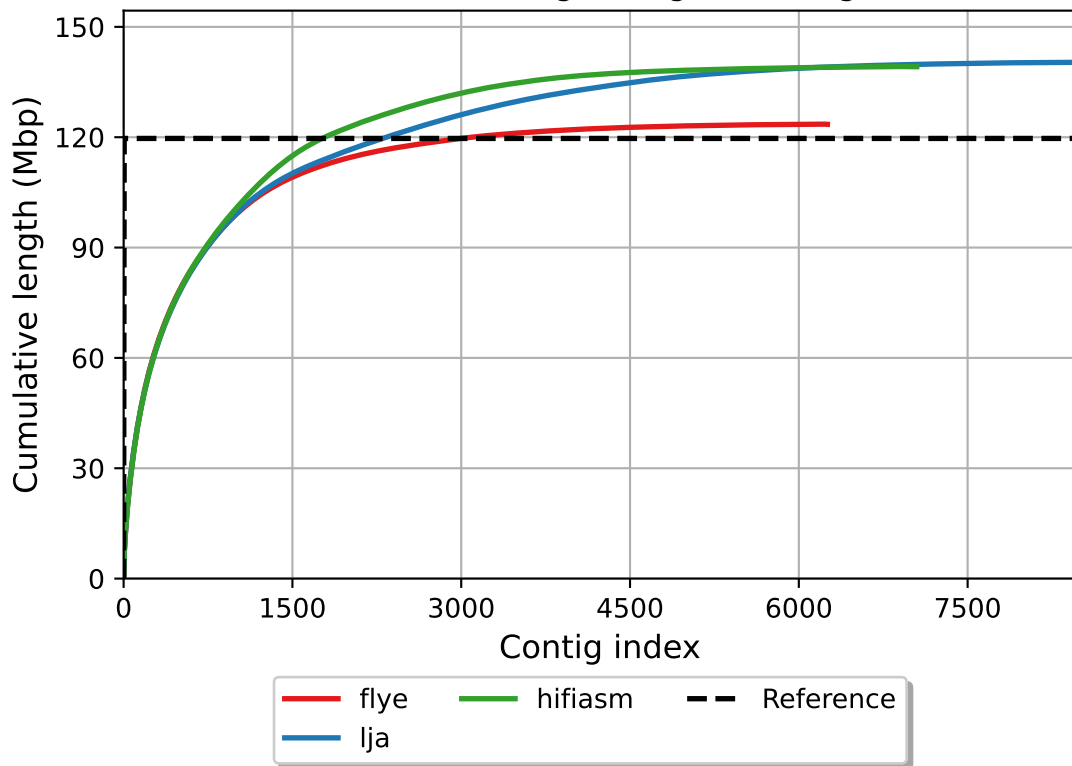


inversions

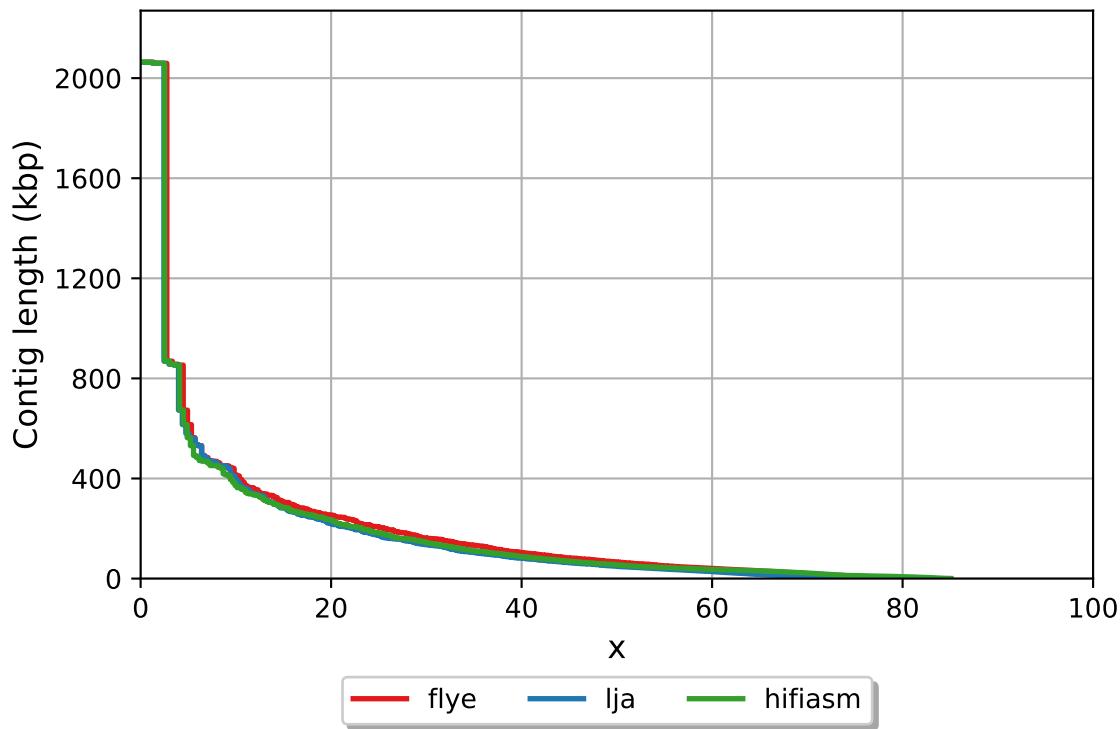
FRCurve (misassemblies)



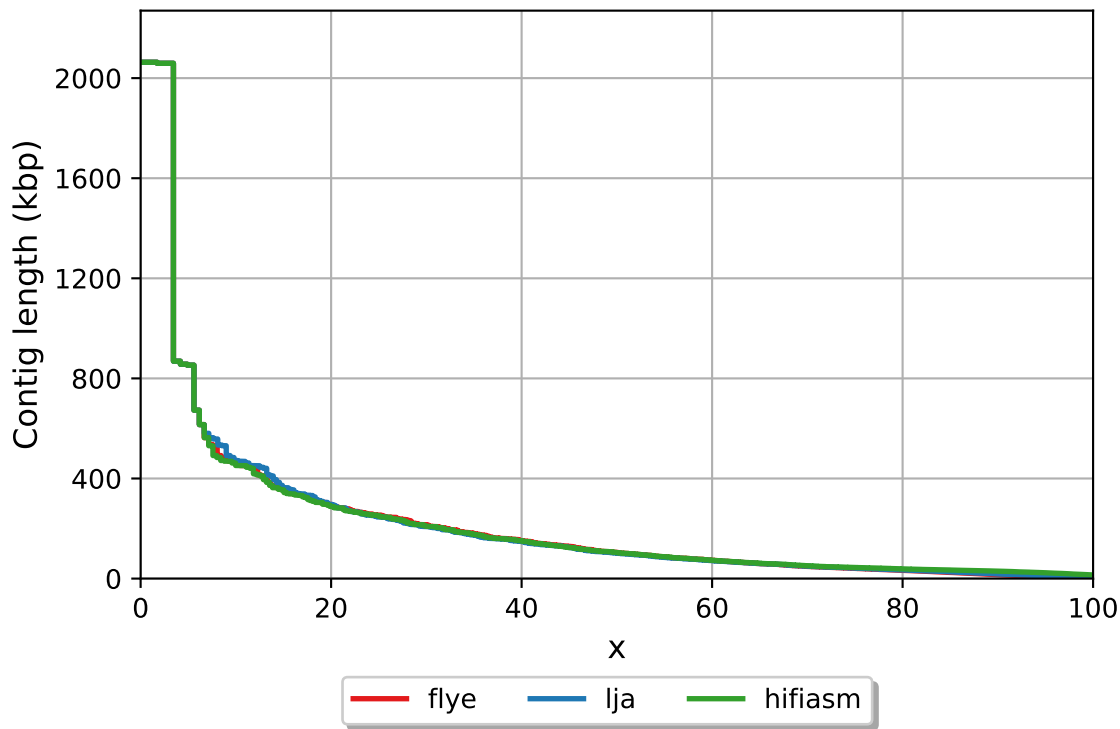
Cumulative length (aligned contigs)



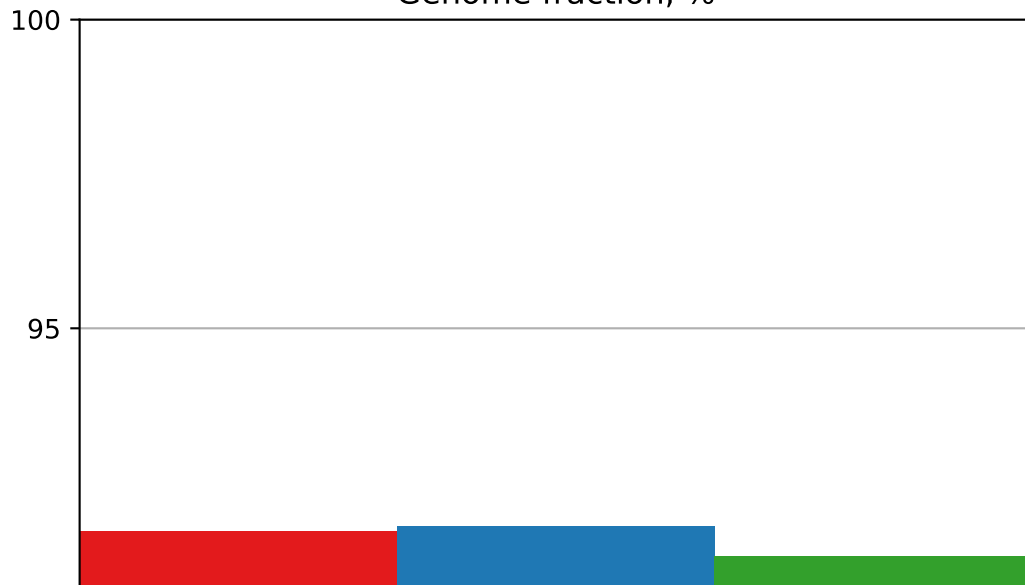
NAx



NGAx



Genome fraction, %



flye lja hifiasm