Report

	flye	hifiasm	lja
# contigs (>= 0 bp)	87	520	517
# contigs (>= 1000 bp)	67	520	517
# contigs (>= 5000 bp)	59	520	366
# contigs (>= 10000 bp)	58	520	248
# contigs (>= 25000 bp)	51	450	49
# contigs (>= 50000 bp)	42	76	24
Total length (>= 0 bp)	134695035	149560242	140518402
Total length (>= 1000 bp)	134682678	149560242	140518402
Total length (>= 5000 bp)	134662713	149560242	140079130
Total length (>= 10000 bp)	134654661	149560242	139214007
Total length (>= 25000 bp)	134534712	147975949	136198314
Total length (>= 50000 bp)	134217987	135512541	135377238
# contigs	86	520	517
Largest contig	16391882	24072003	24026988
Total length	134694543	149560242	140518402
Reference length	119667750	119667750	119667750
GC (%)	36.35	36.83	36.98
Reference GC (%)	36.06	36.06	36.06
N50	6958821	19060005	16449428
NG50	11020907	19188418	19188381
N90	2149576	53275	2784381
NG90	2890927	6256420	6671131
auN	7995031.3	13197880.5	14162262.1
auNG	8998975.0	16494654.6	16629864.3
L50	6	4	4
LG50	5	3	3
L90	21	59	12
LG90	16	8	8
# misassemblies	4103	5722	5623
# misassembled contigs	35	210	257
Misassembled contigs length	121368747	139560165	139066224
# local misassemblies	2305	2747	3010
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	12	0	0
# unaligned contigs	2 + 48 part	0 + 64 part	2 + 154 part
Unaligned length	20932083	20755069	20856581
Genome fraction (%)	90.632	87.597	90.663
Duplication ratio	1.046	1.225	1.098
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	686.49	627.27	686.29
# indels per 100 kbp	137.60	131.78	135.79
# genomic features	769654 + 6494 part	738636 + 6277 part	770190 + 6411 part
Largest alignment	871863	871863	871861
Total aligned length	113268902	128248289	118923055
NA50	83256	60358	77066
NGA50	102087	97260	103101
NA90	-	-	-
NGA90	6500	19961	9027
auNA	145471.2	131185.4	141881.7
auNGA	163738.2	163954.9	166602.9
LA50	359	485	392
LGA50	279	289	276
LA90	-	-	-
LGA90	1998	1445	1825

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

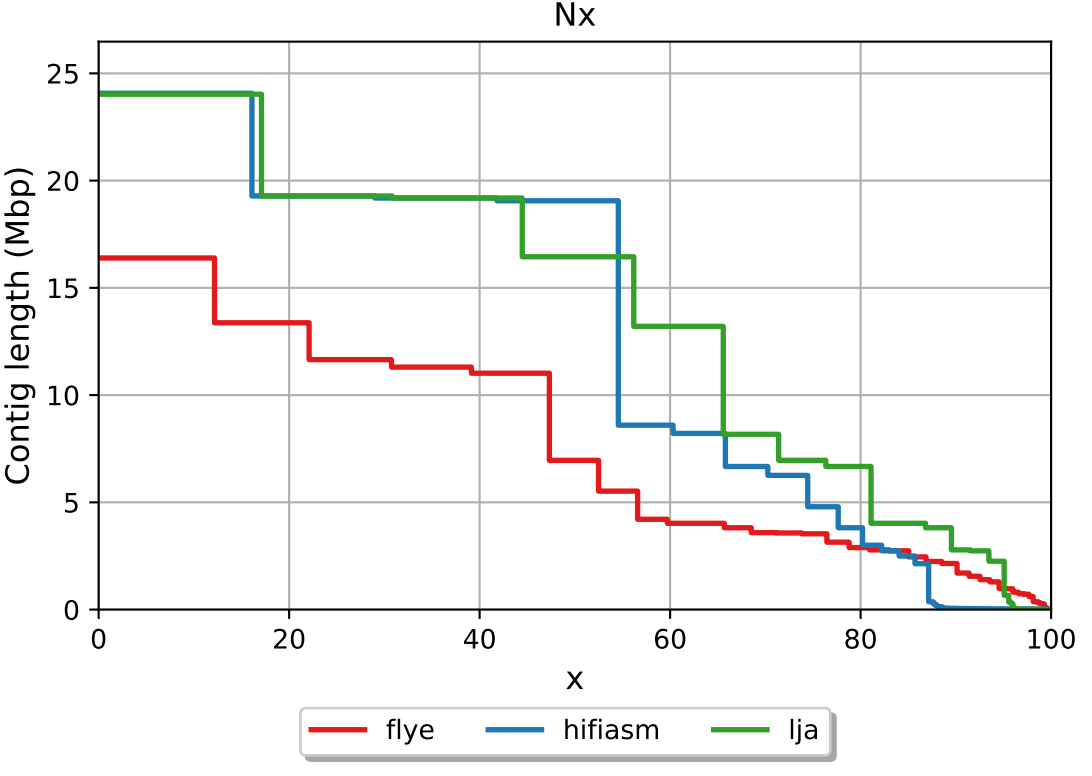
	flye	hifiasm	lja
# misassemblies	4103	5722	5623
# contig misassemblies	4103	5722	5623
# c. relocations	2536	3914	3761
# c. translocations	1529	1770	1832
# c. inversions	38	38	30
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	35	210	257
Misassembled contigs length	121368747	139560165	139066224
# local misassemblies	2305	2747	3010
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	12	0	0
# mismatches	777579	804465	816155
# indels	155856	169008	161484
# indels (<= 5 bp)	124812	136418	128635
# indels (> 5 bp)	31044	32590	32849
Indels length	907285	1022605	1034488

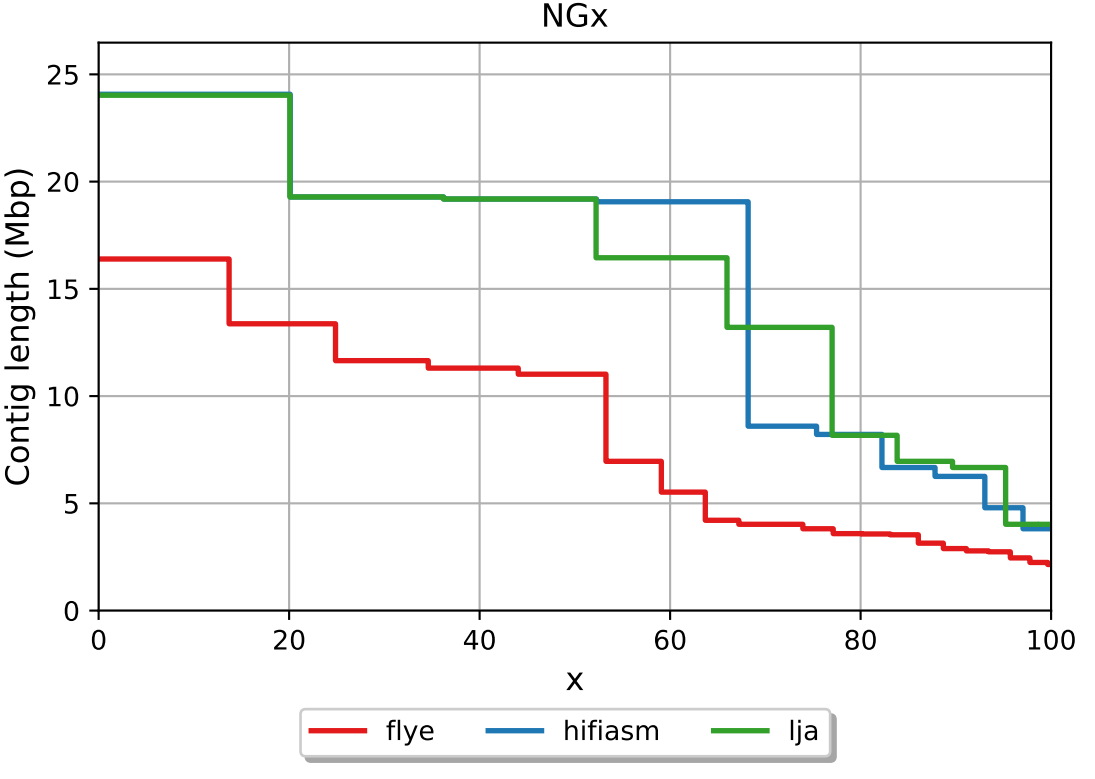
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

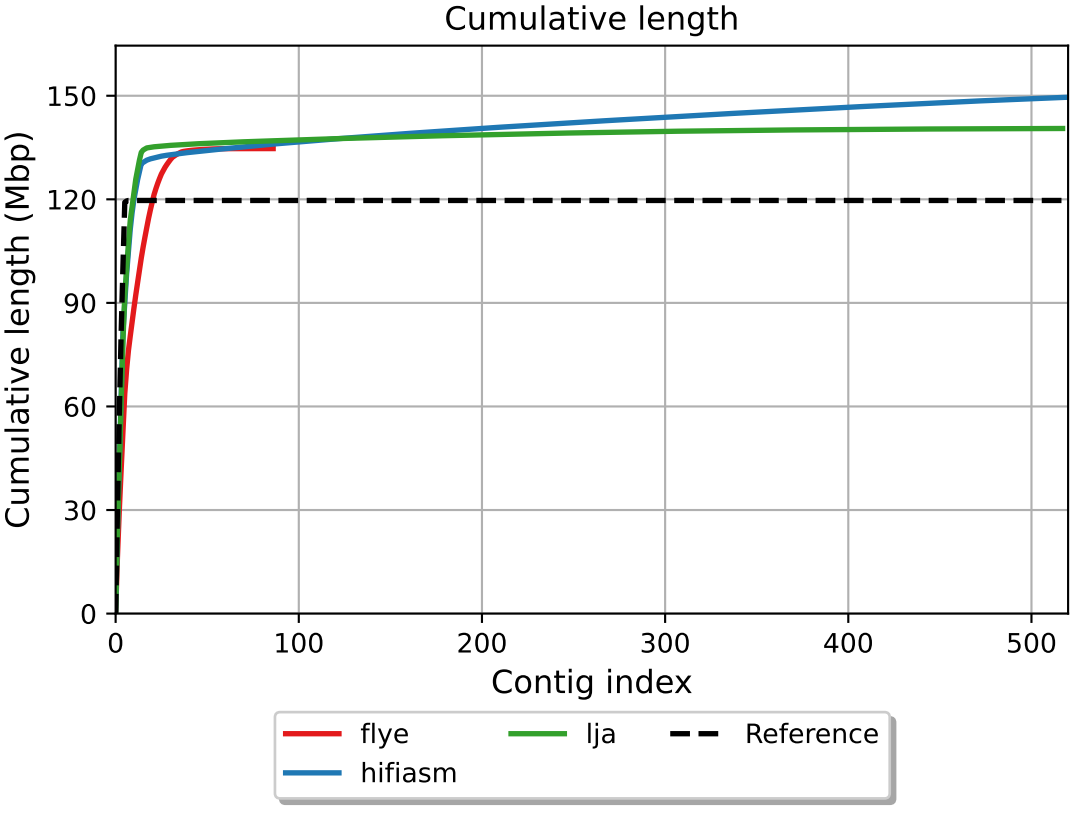
Unaligned report

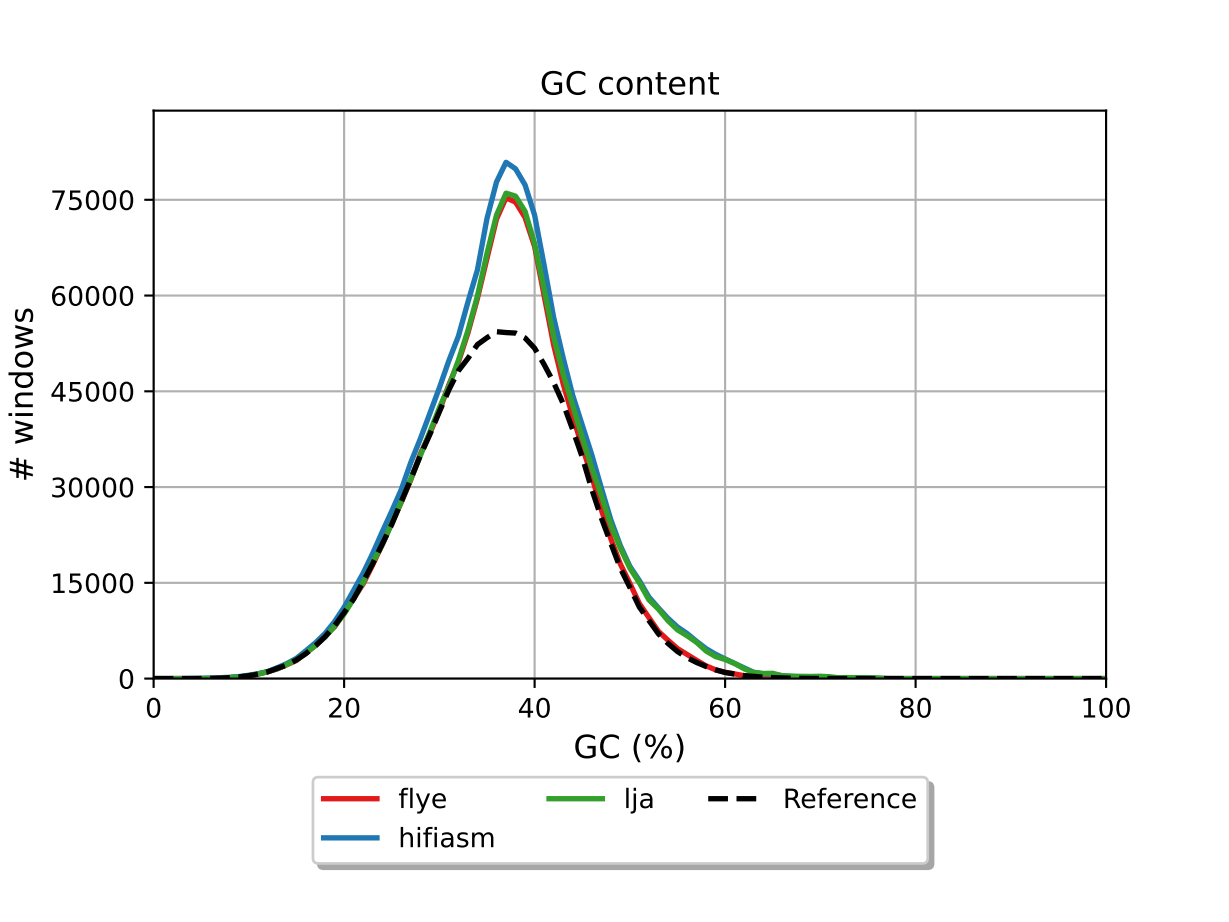
	flye	hifiasm	lja
# fully unaligned contigs	2	0	2
Fully unaligned length	627214	0	10190
# partially unaligned contigs	48	64	154
Partially unaligned length	20304869	20755069	20846391
# N's	0	0	0

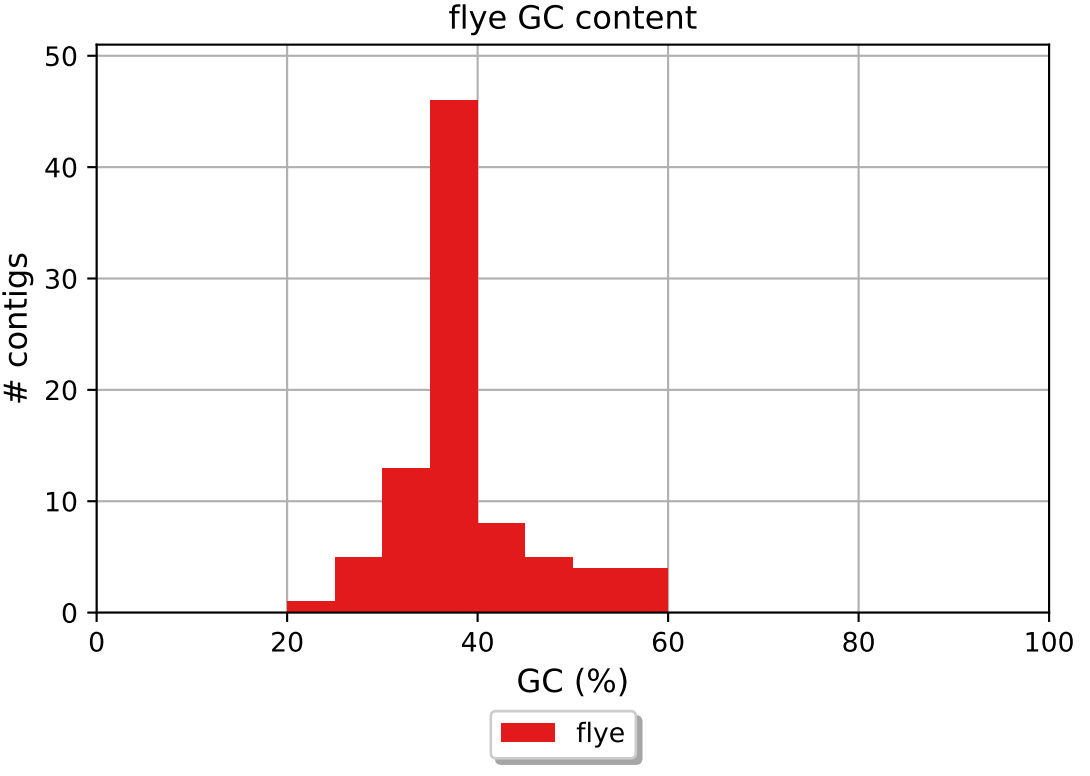
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

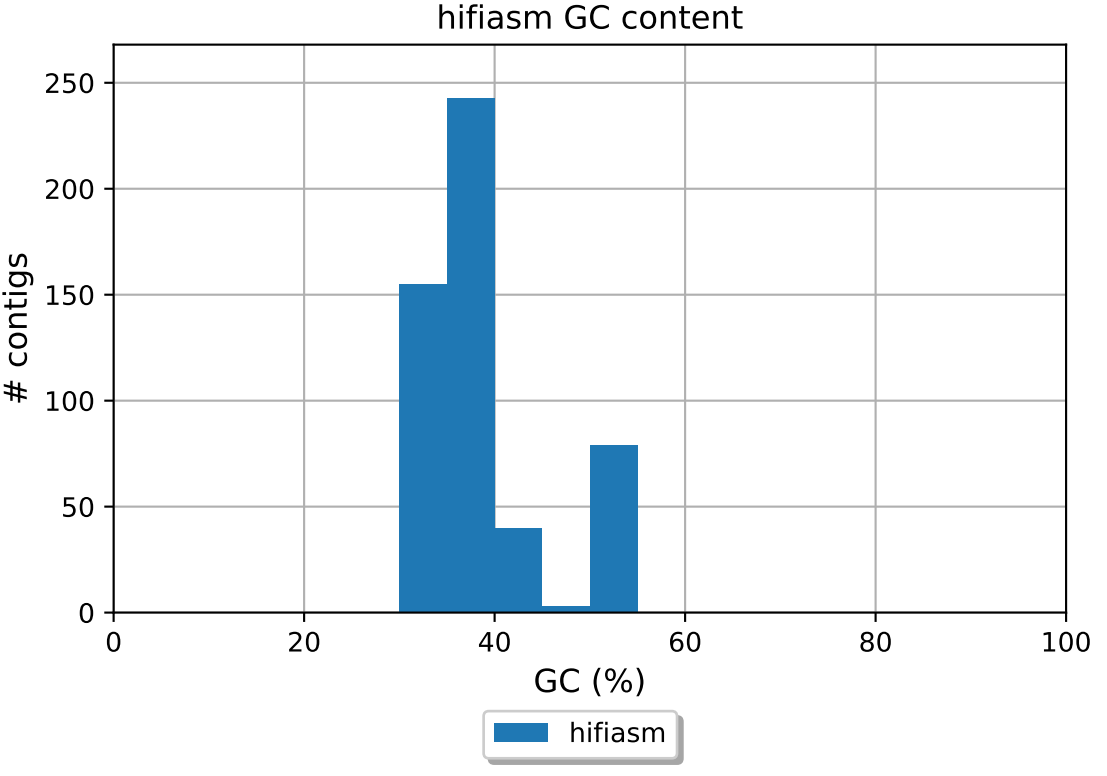

Nx
Contig length (Mbp)
0
5
10
15
20
25
0
20
40
60
80
100
x
flye
hifiasm
lja

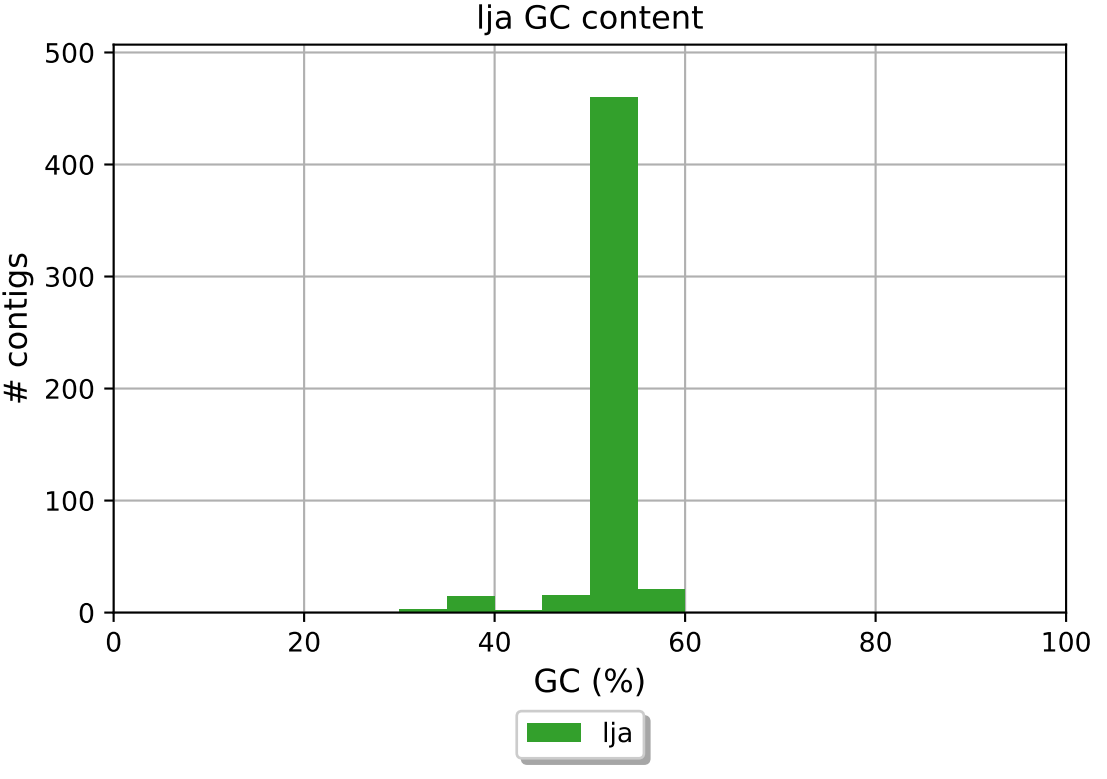

NGx
Contig length (Mbp)
0
5
10
15
20
25
0
20
40
60
80
100
x
flye
hifiasm
lja

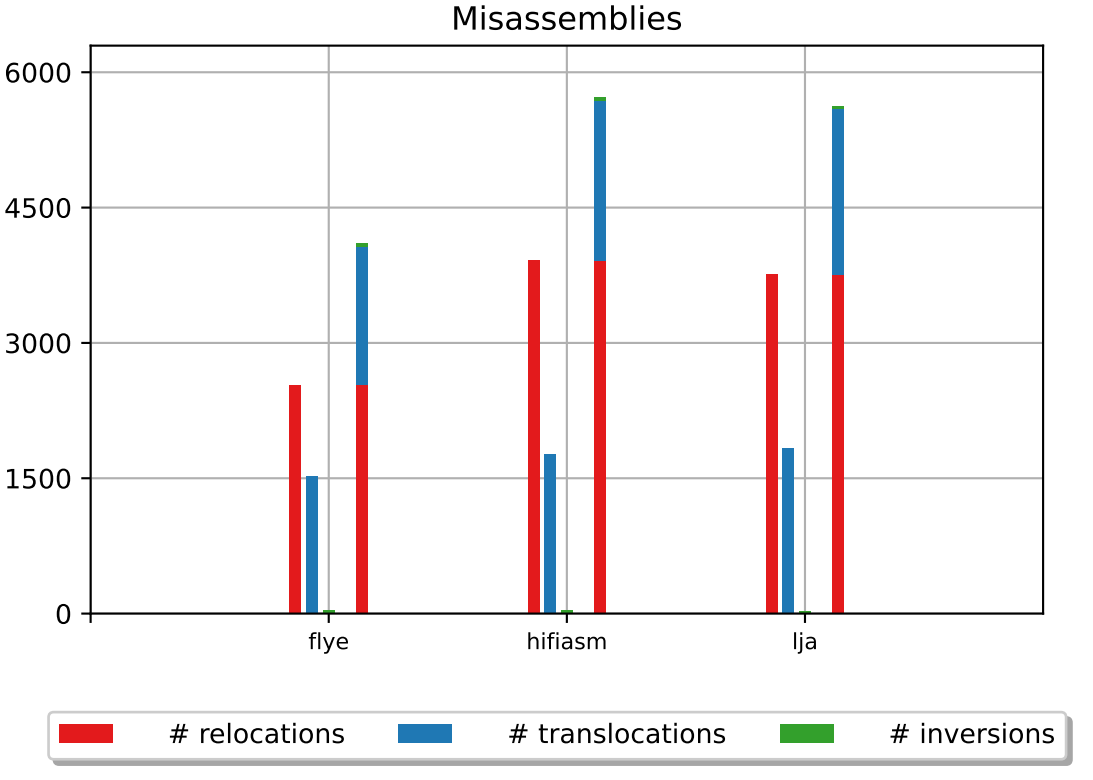

Cumulative length
Cumulative length (Mbp)
150
120
90
60
30
0
0
100
200
300
400
500
Contig index
flye
hifiasm
lja
Reference

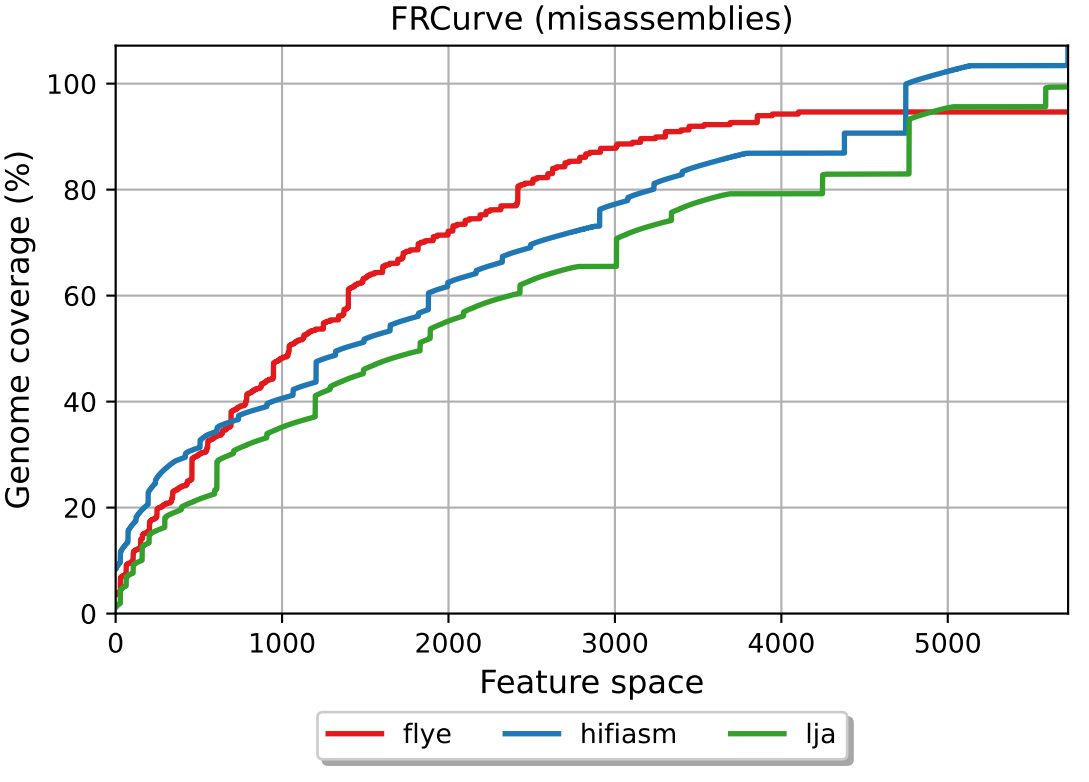

GC content
windows
75000
60000
45000
30000
15000
0
0
20
40
60
80
100
GC (%)
flye
hifiasm
lja
Reference

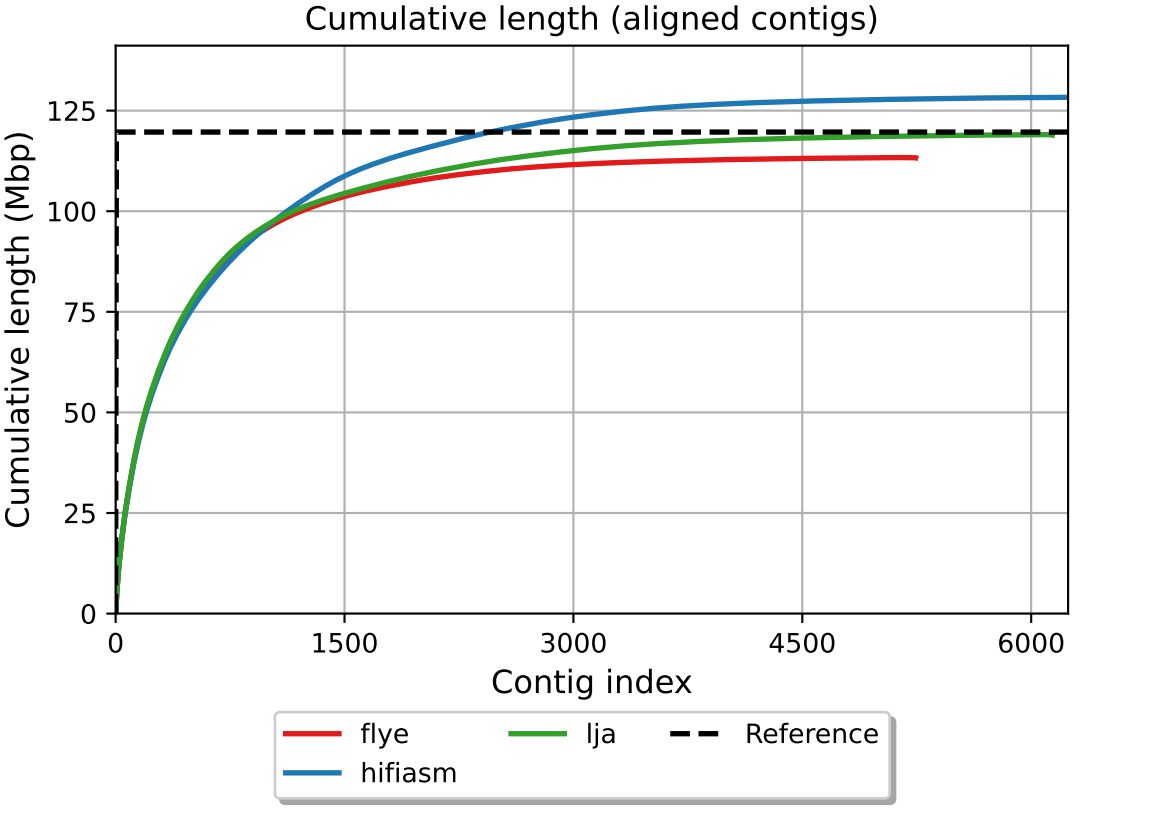

flye GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
flye

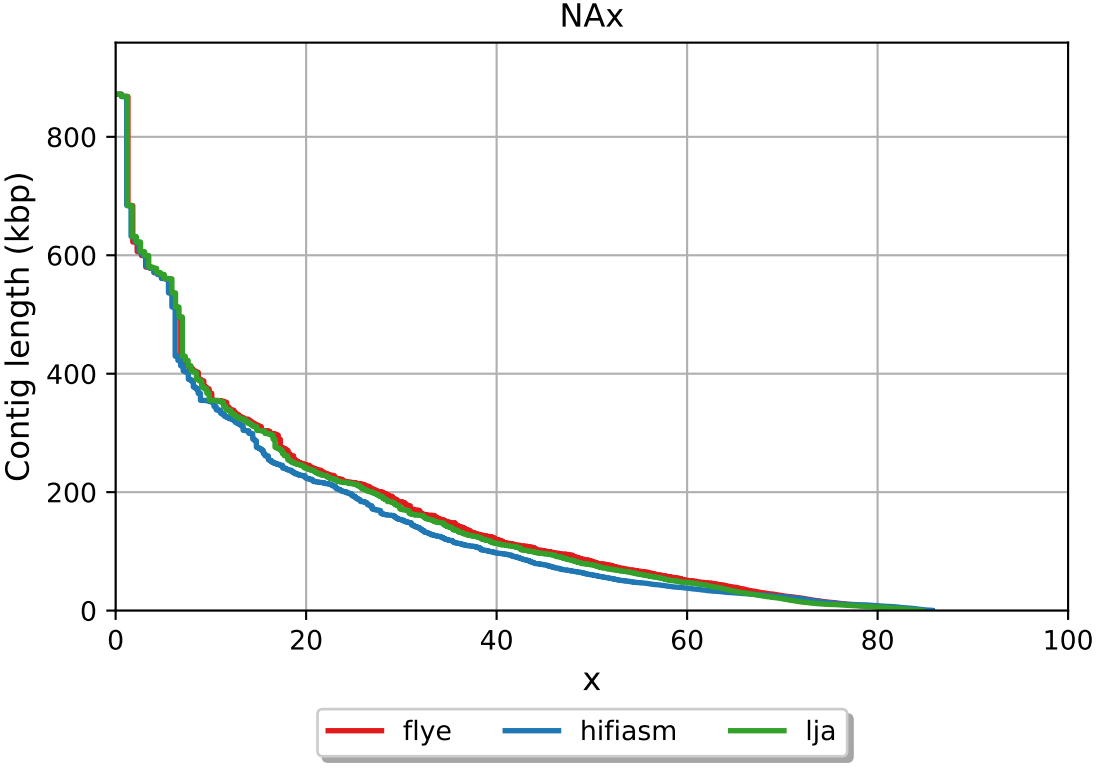

hifiasm GC content
contigs
GC (%)
0
50
100
150
200
250
0
20
40
60
80
100
hifiasm

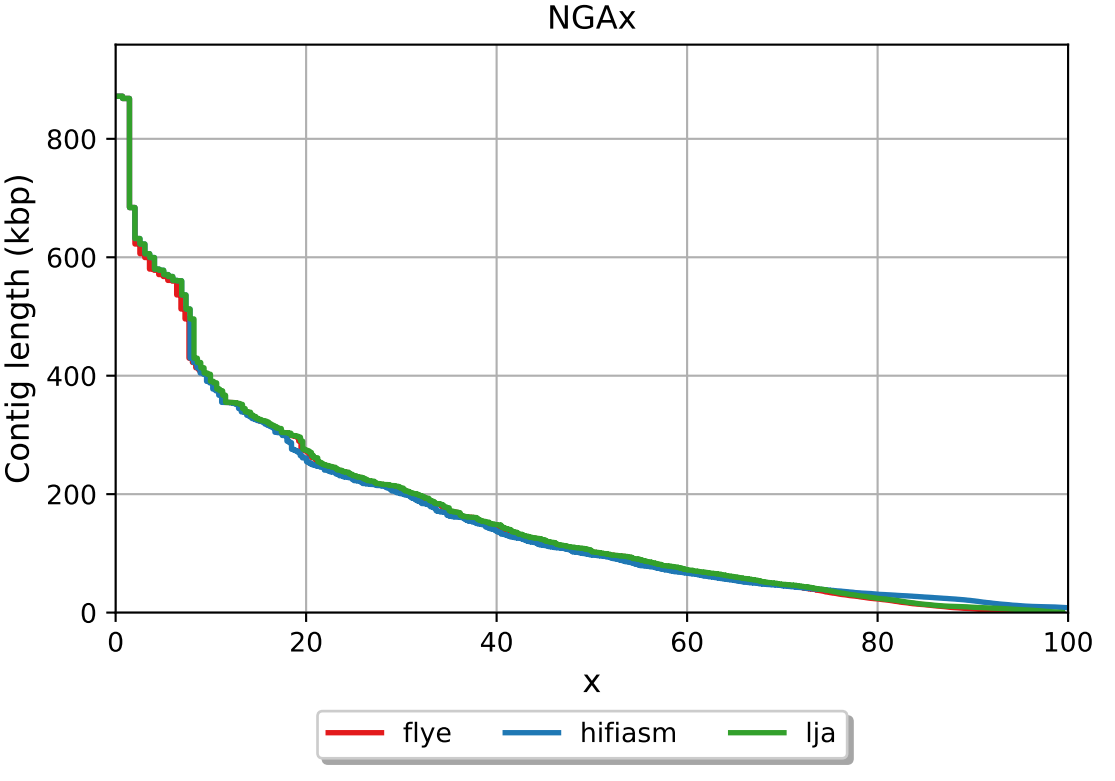

lja GC content
contigs
GC (%)
lja
0
100
200
300
400
500
0
20
40
60
80
100

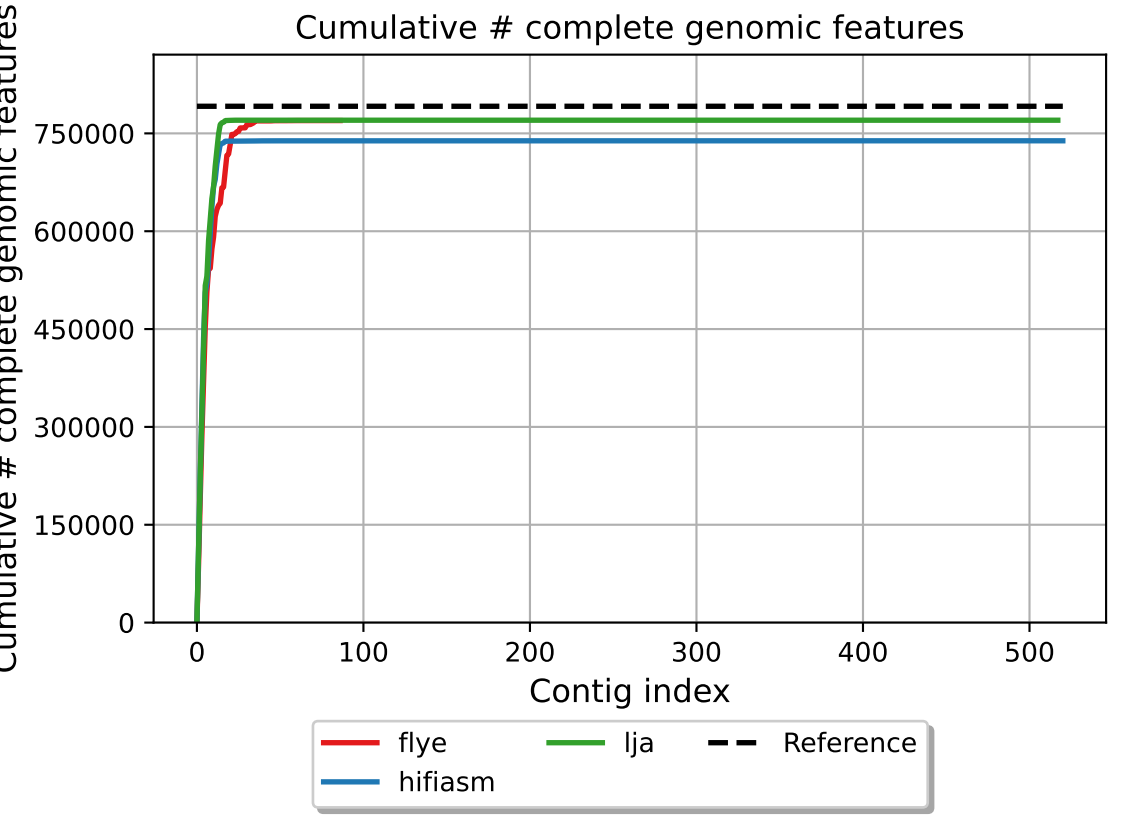

Misassemblies
6000
4500
3000
1500
0
flye
hifiasm
lja
relocations
translocations
inversions

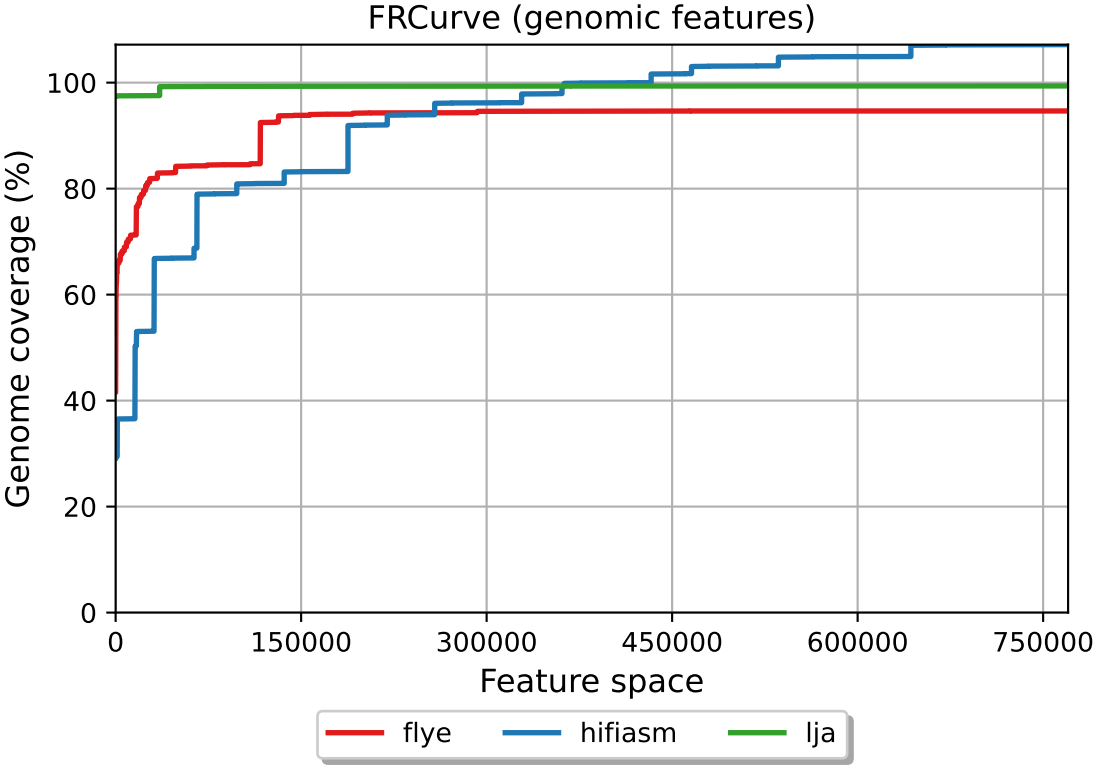

FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
1000
2000
3000
4000
5000
Feature space
flye
hifiasm
lja

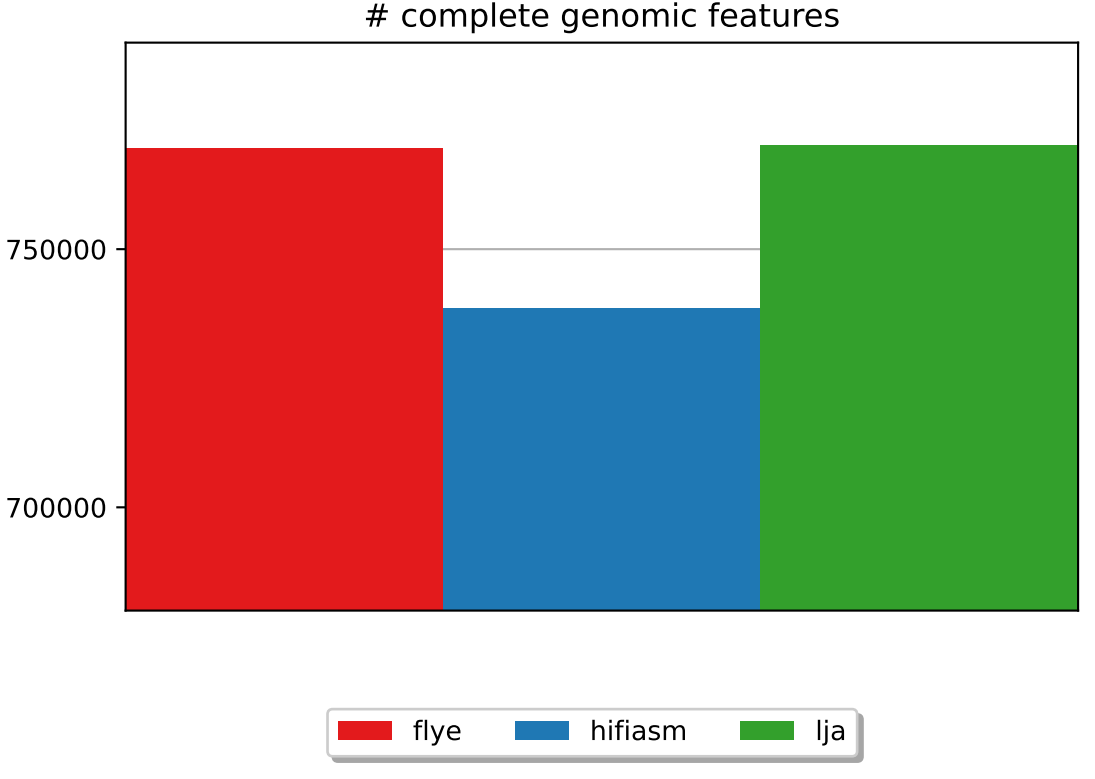

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
25
50
75
100
125
0
1500
3000
4500
6000
Contig index
flye
hifiasm
lja
Reference

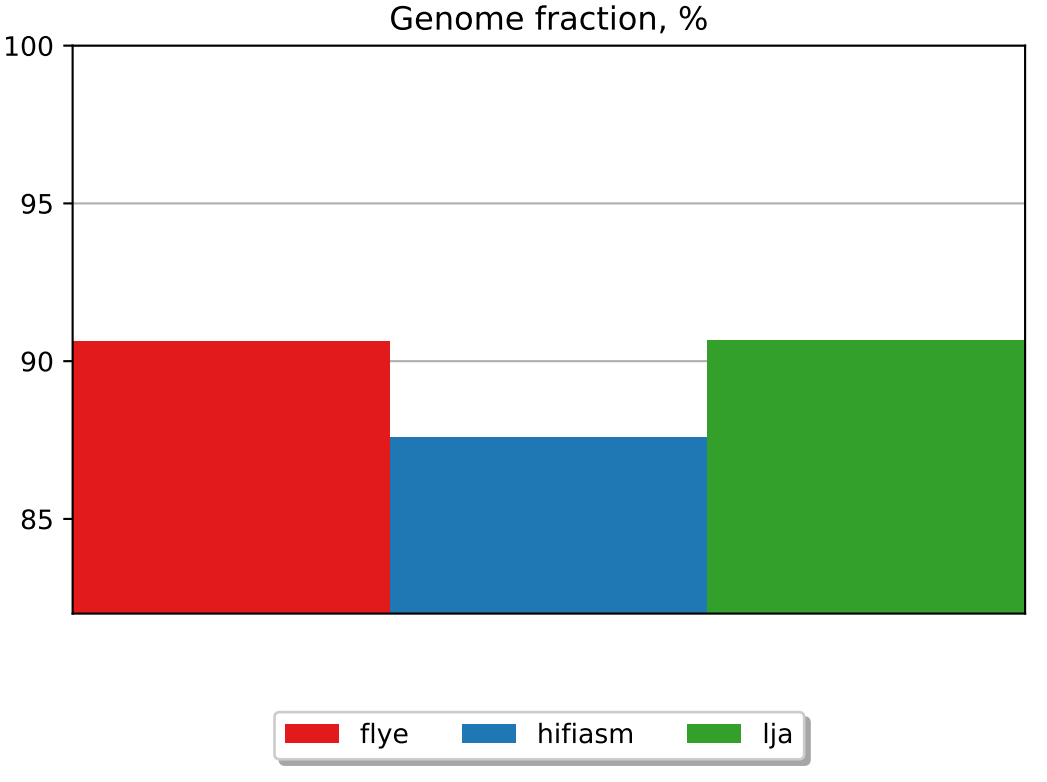

NAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
flye
hifiasm
lja


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
flye
hifiasm
lja


Cumulative # complete genomic features
Cumulative # complete genomic features
0
150000
300000
450000
600000
750000
0
100
200
300
400
500
Contig index
flye
hifiasm
lja
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
150000
300000
450000
600000
750000
Feature space
flye
hifiasm
lja


complete genomic features
750000
700000
flye
hifiasm
lja


Genome fraction, %
100
95
90
85
flye
hifiasm
lja