Report

	flye	hifiasm	lja
# contigs (>= 0 bp)	127	836	481
# contigs (>= 1000 bp)	114	836	481
# contigs (>= 5000 bp)	109	836	375
# contigs (>= 10000 bp)	107	836	252
# contigs (>= 25000 bp)	72	687	59
# contigs (>= 50000 bp)	61	81	32
Total length (>= 0 bp)	134207120	161091237	140337274
Total length (>= 1000 bp)	134199441	161091237	140337274
Total length (>= 5000 bp)	134187049	161091237	140040306
Total length (>= 10000 bp)	134169439	161091237	139069129
Total length (>= 25000 bp)	133593672	157756048	136155293
Total length (>= 50000 bp)	133214476	137899189	135280631
# contigs	125	836	481
Largest contig	13151276	19422766	16485509
Total length	134206543	161091237	140337274
Reference length	119667750	119667750	119667750
GC (%)	36.33	36.58	36.79
Reference GC (%)	36.06	36.06	36.06
N50	7500357	11062720	12043709
NG50	8209526	12862929	12043709
N90	996742	35442	2102188
NG90	1932415	4694819	5243621
auN	7232448.8	9123339.2	9677957.7
auNG	8111140.7	12281420.8	11349575.8
L50	7	6	5
LG50	6	4	5
L90	26	253	16
LG90	17	10	11
# misassemblies	3810	4151	4876
# misassembled contigs	52	226	177
Misassembled contigs length	117924109	125520552	128502956
# local misassemblies	2345	2305	2735
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	26	9	6
# unaligned contigs	0 + 74 part	0 + 38 part	3 + 51 part
Unaligned length	20037147	19789151	20388123
Genome fraction (%)	90.982	90.973	91.066
Duplication ratio	1.046	1.296	1.096
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	673.00	557.50	660.74
# indels per 100 kbp	140.09	127.77	137.38
# genomic features	0 + 0 part	0 + 0 part	0 + 0 part
Largest alignment	888916	888916	888916
Total aligned length	113669062	140833533	119240646
NA50	79775	53636	73949
NGA50	100391	100366	102676
NA90	-	-	-
NGA90	7248	28267	9660
auNA	157695.1	135917.4	151514.1
auNGA	176853.9	182965.8	177684.2
LA50	349	555	386
LGA50	267	269	266
LA90	-	-	-
LGA90	1887	1288	1790

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

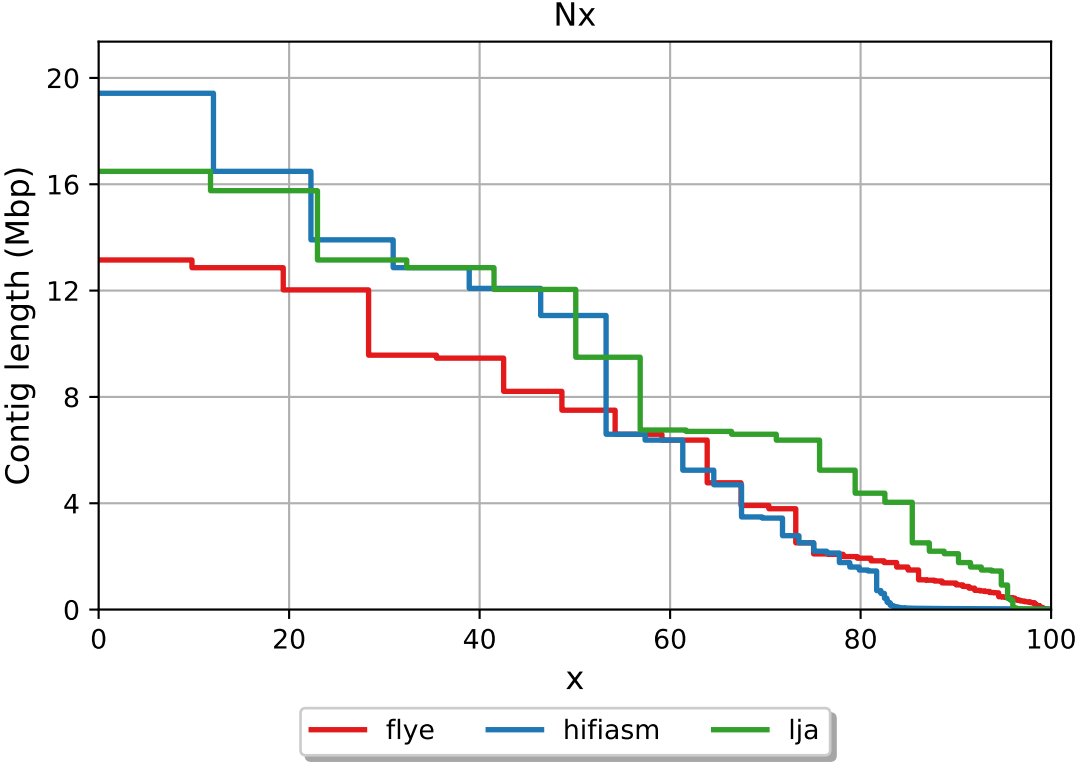
	flye	hifiasm	lja
# misassemblies	3810	4151	4876
# contig misassemblies	3810	4151	4876
# c. relocations	2405	2770	3329
# c. translocations	1386	1361	1527
# c. inversions	19	20	20
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	52	226	177
Misassembled contigs length	117924109	125520552	128502956
# local misassemblies	2345	2305	2735
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	26	9	6
# mismatches	764991	785152	787872
# indels	159238	179948	163811
# indels (<= 5 bp)	129250	147174	131934
# indels (> 5 bp)	29988	32774	31877
Indels length	900574	1028355	1004739

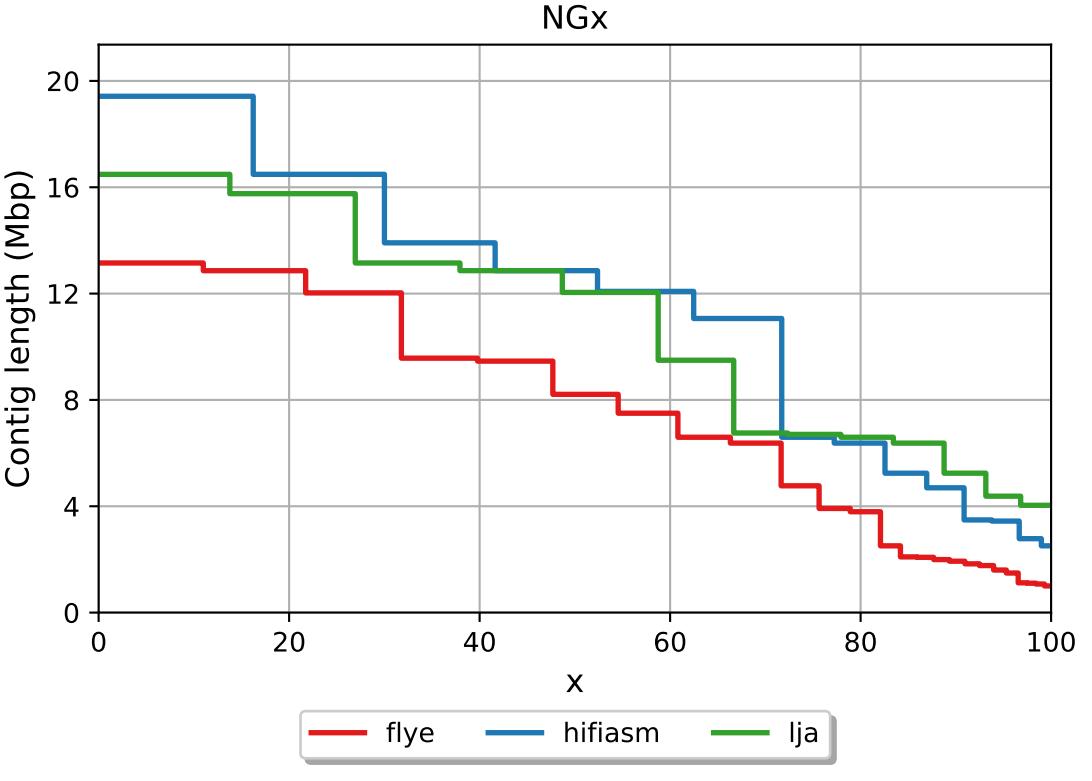
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

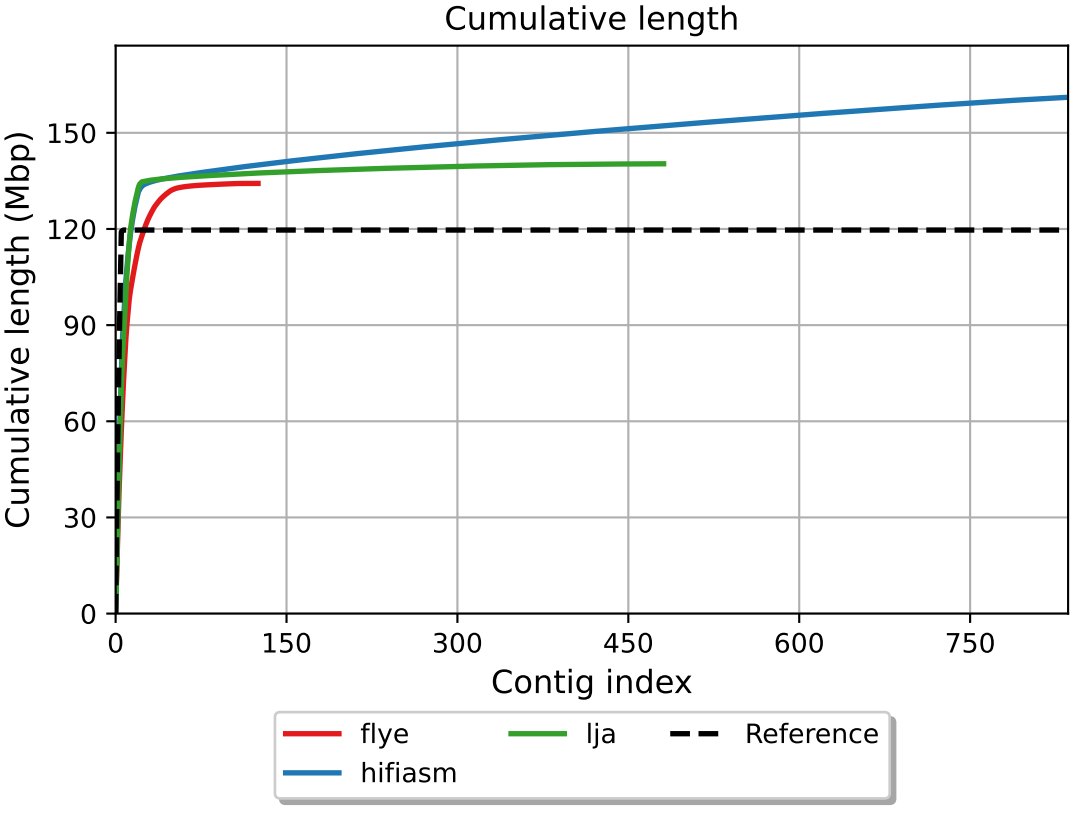
Unaligned report

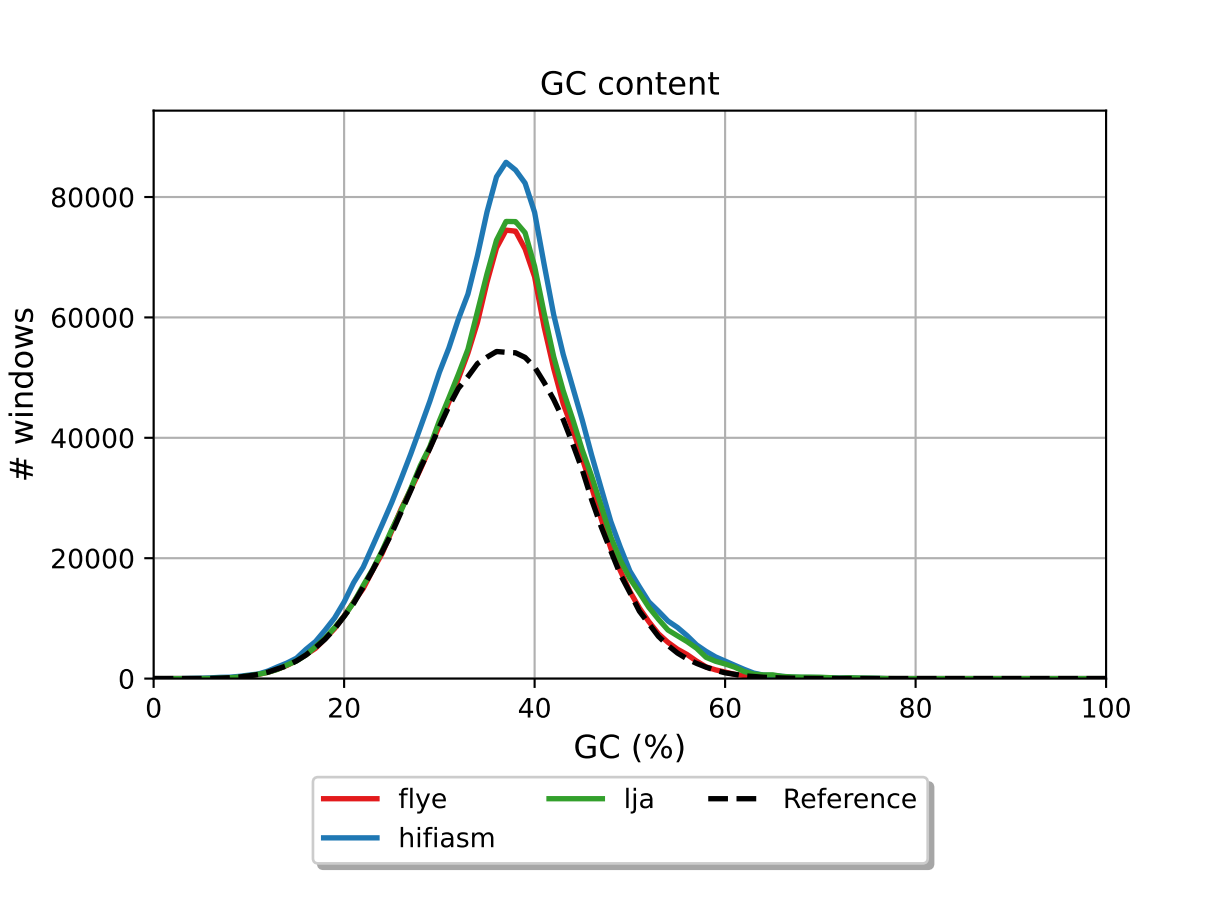
	flye	hifiasm	lja
# fully unaligned contigs	0	0	3
Fully unaligned length	0	0	9271
# partially unaligned contigs	74	38	51
Partially unaligned length	20037147	19789151	20378852
# N's	0	0	0

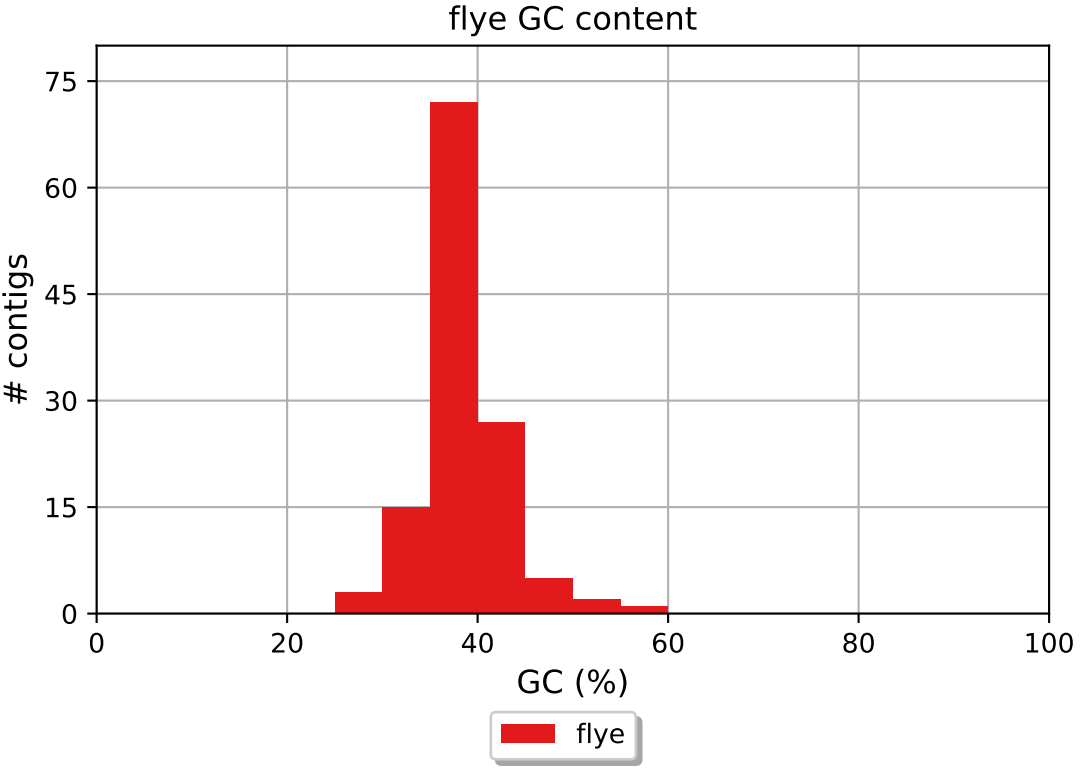
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

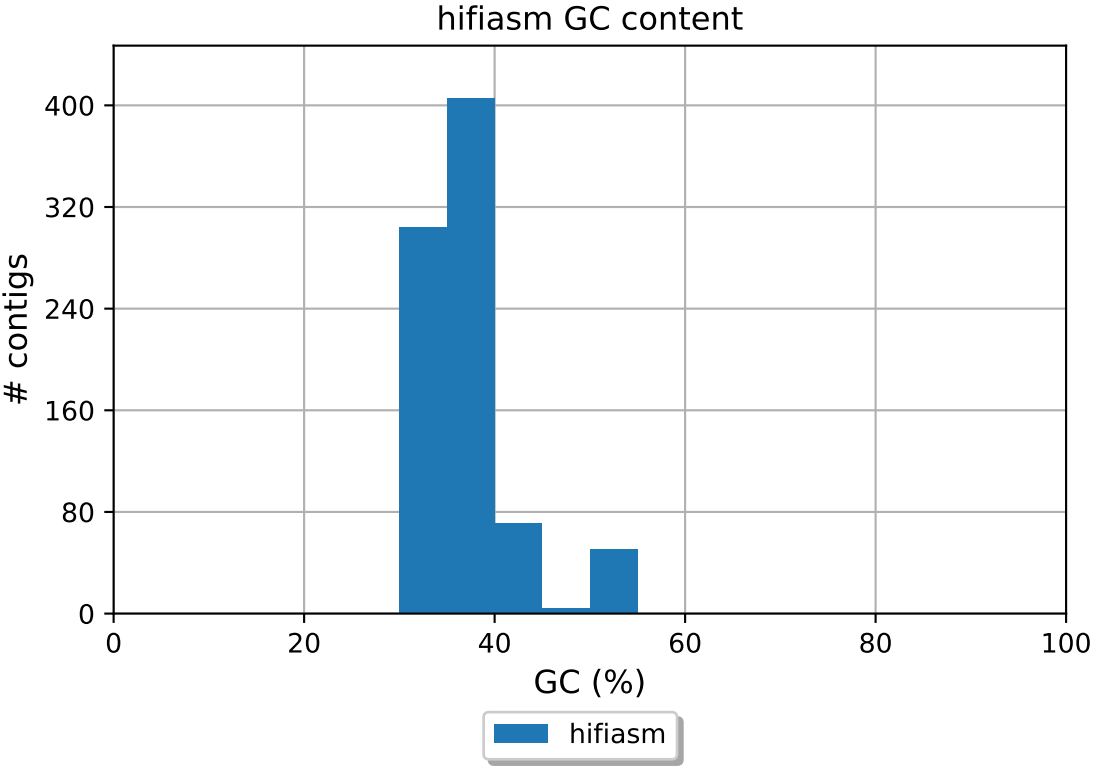

Nx
Contig length (Mbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
flye
hifiasm
lja

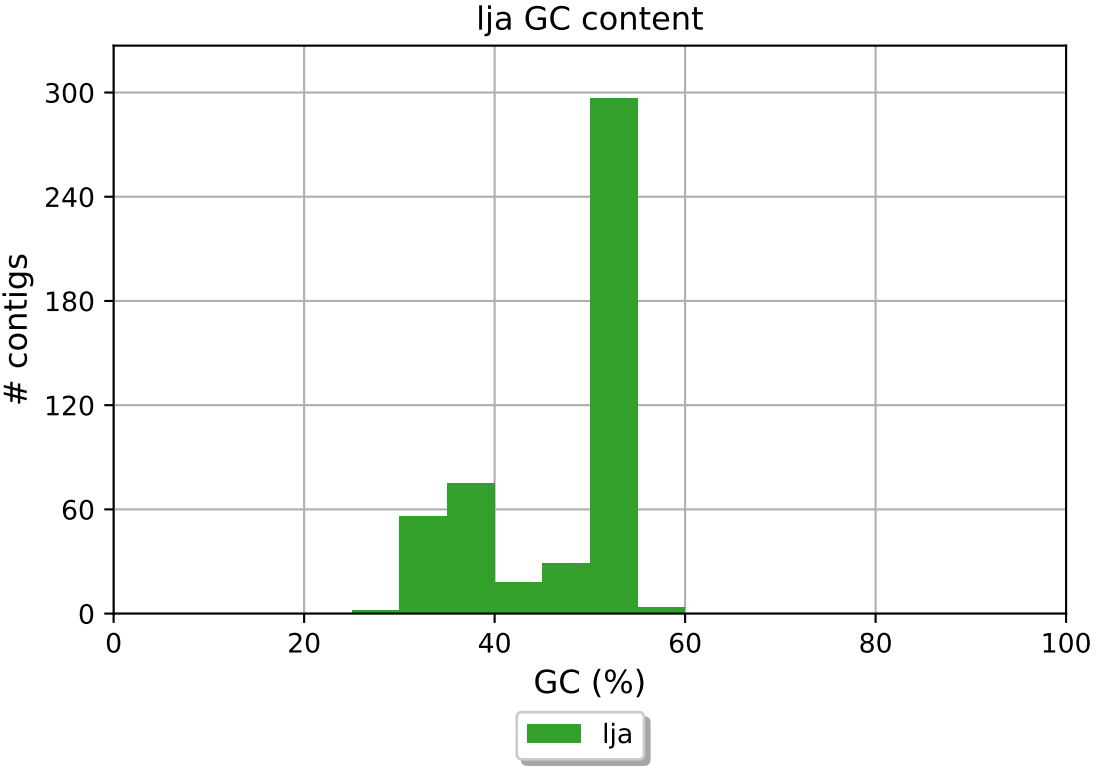

NGx
Contig length (Mbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
flye
hifiasm
lja

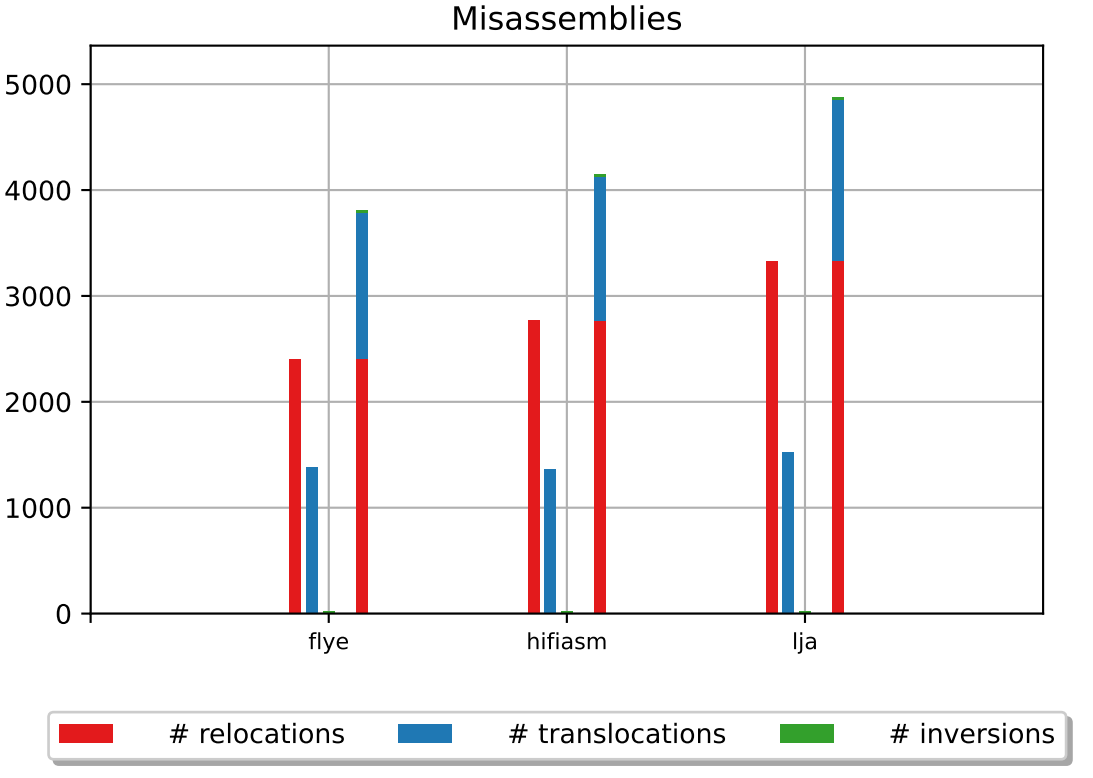

Cumulative length
Cumulative length (Mbp)
0
30
60
90
120
150
0
150
300
450
600
750
Contig index
flye
hifiasm
lja
Reference

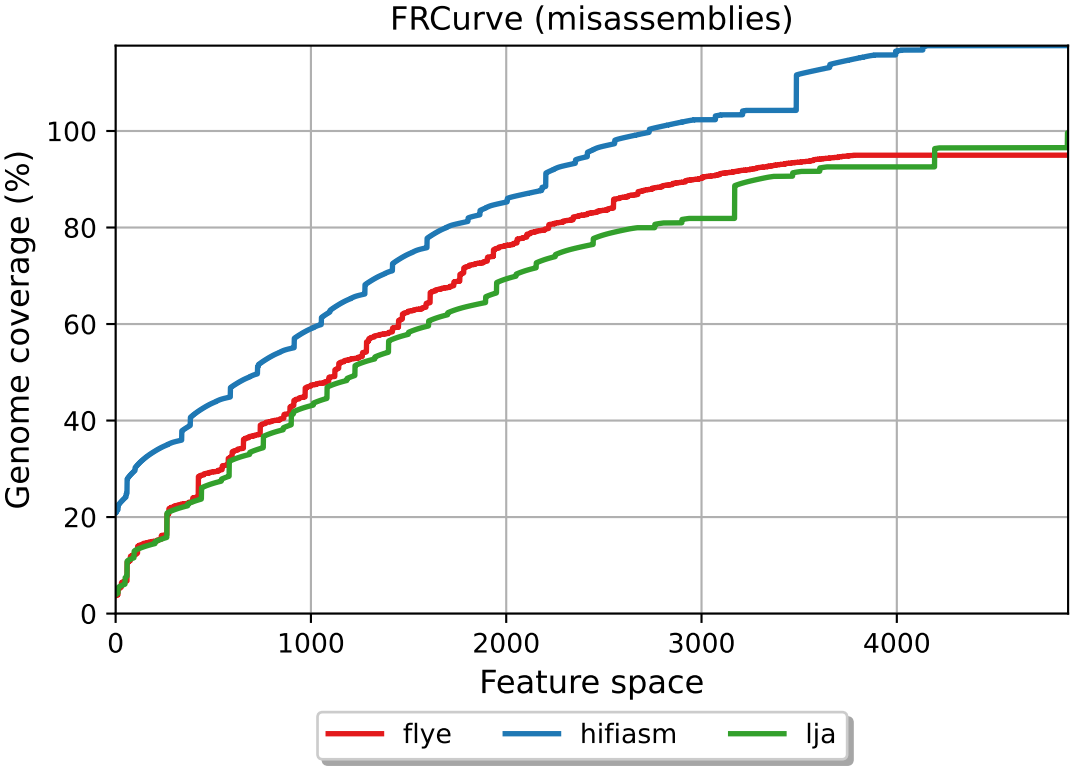

GC content
windows
GC (%)
0
20000
40000
60000
80000
0
20
40
60
80
100
flye
hifiasm
lja
Reference

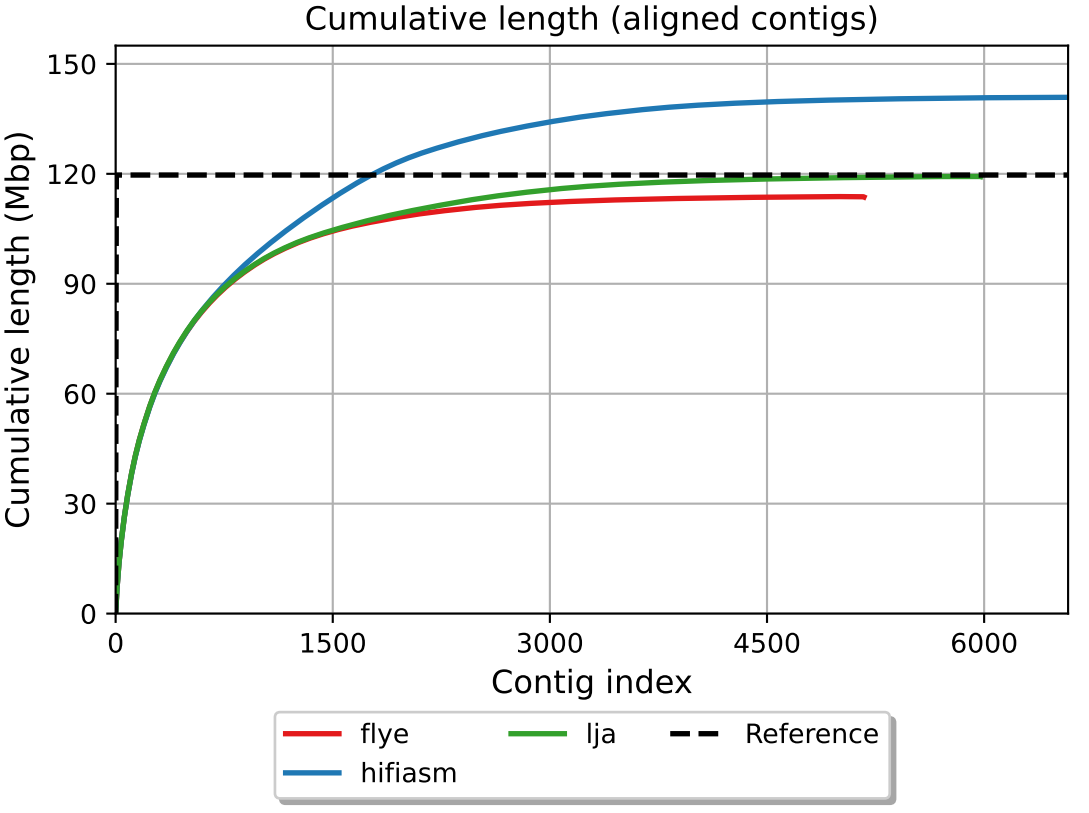

flye GC content
contigs
GC (%)
0
15
30
45
60
75
0
20
40
60
80
100
flye

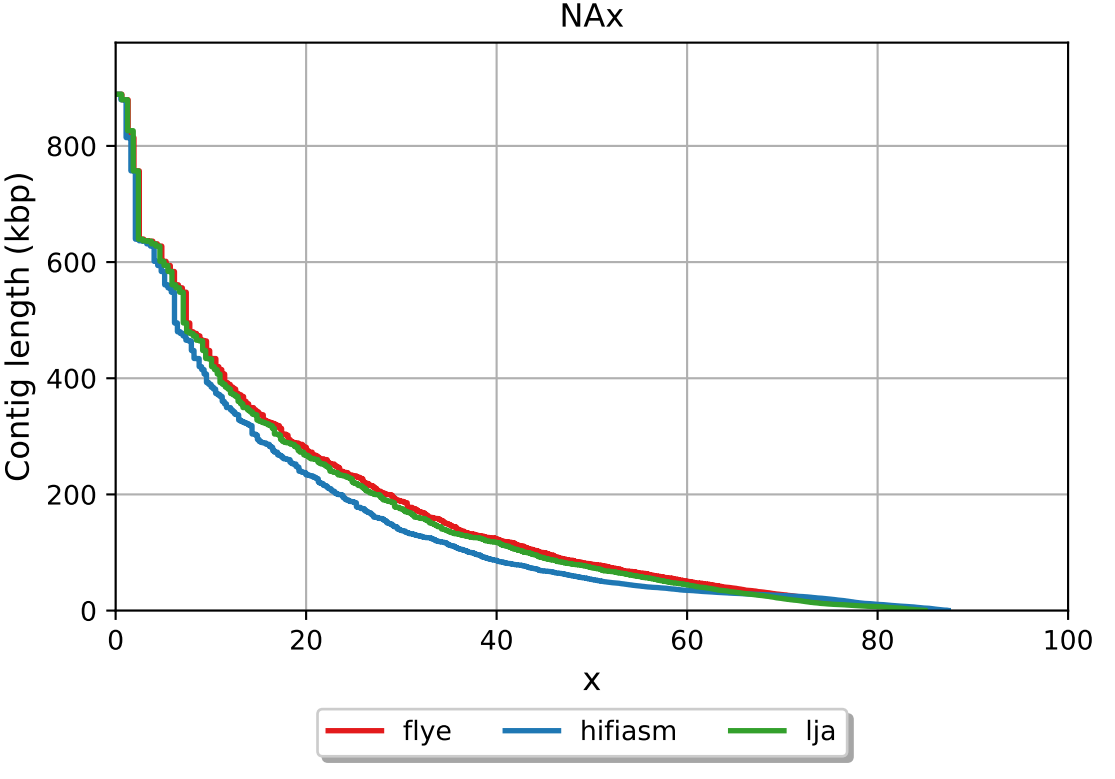

hifiasm GC content
contigs
400
320
240
160
80
0
0
20
40
60
80
100
GC (%)
hifiasm

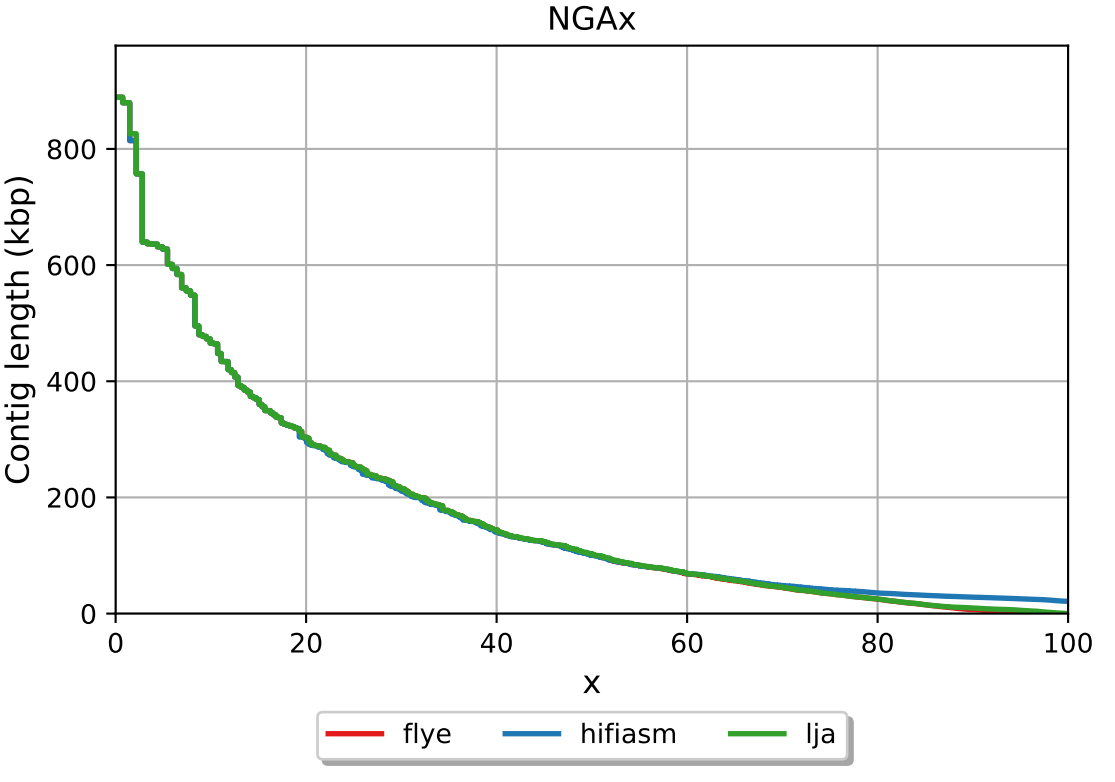

lja GC content
contigs
300
240
180
120
60
0
0
20
40
60
80
100
GC (%)
lja

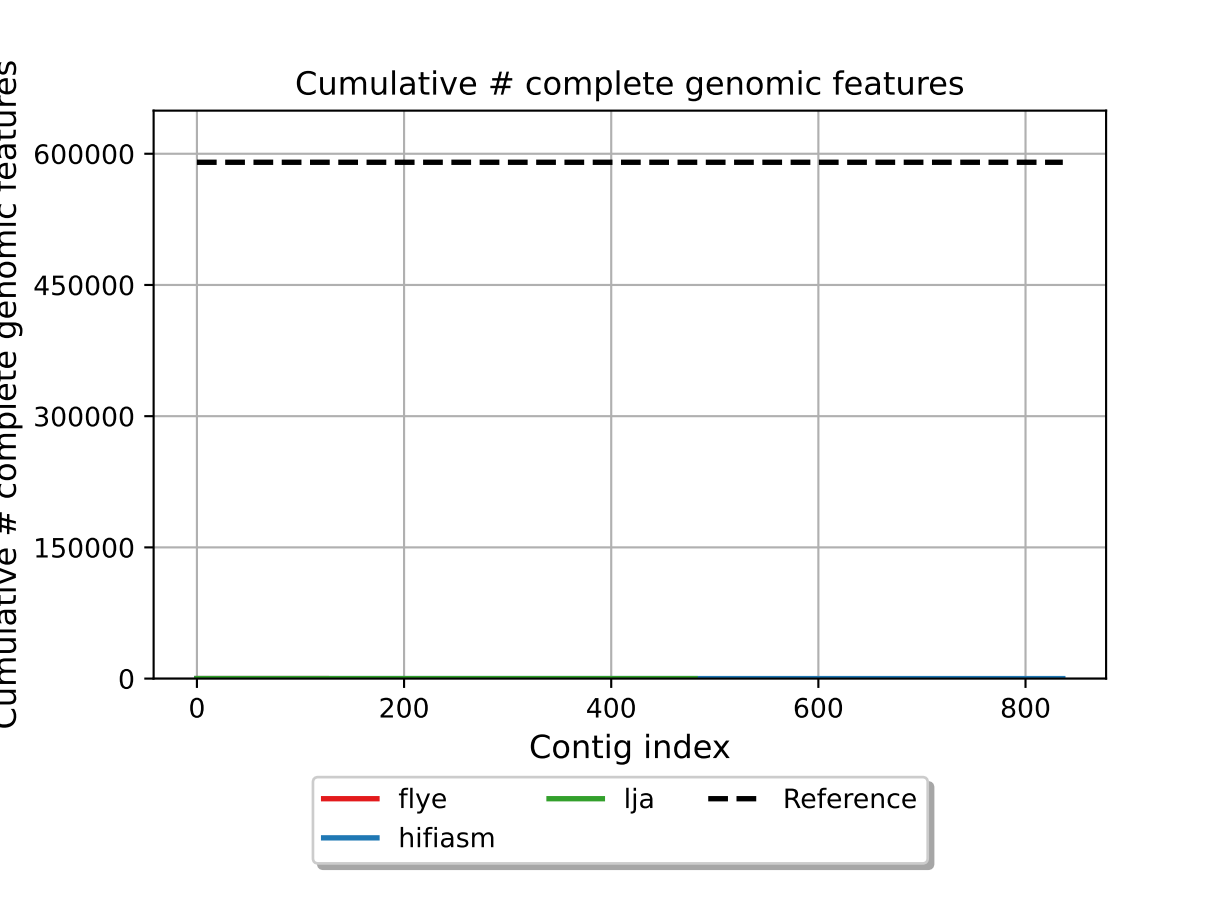

Misassemblies
5000
4000
3000
2000
1000
0
flye
hifiasm
lja
relocations
translocations
inversions

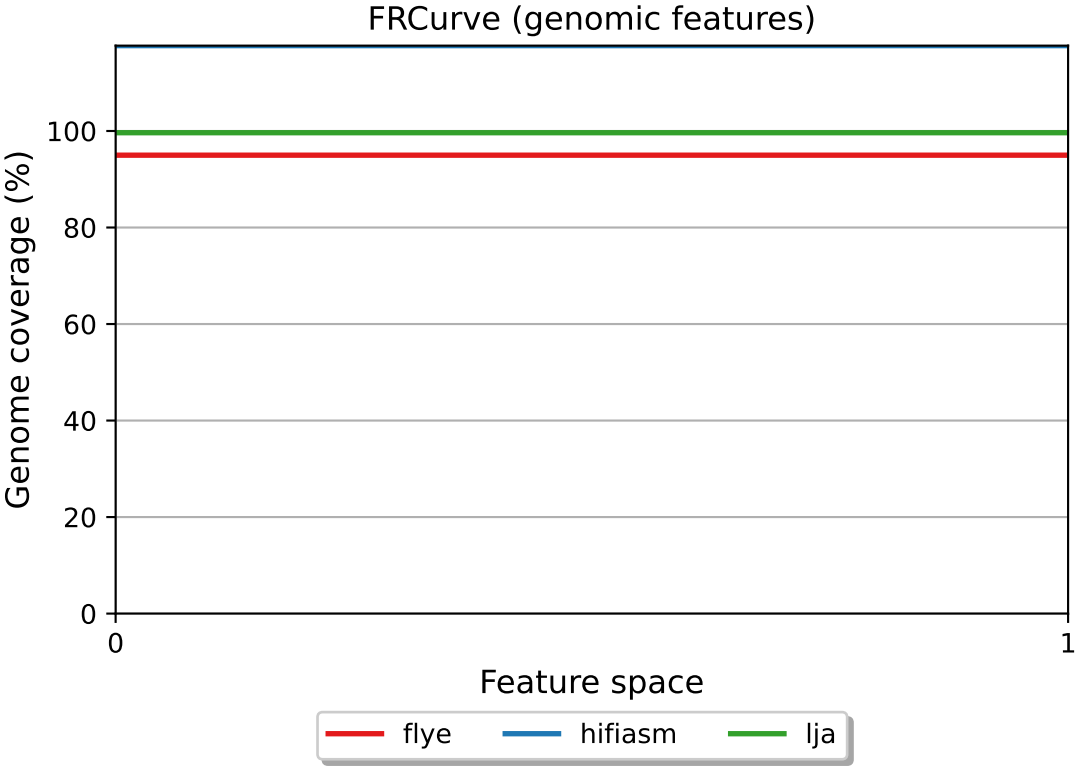

FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
1000
2000
3000
4000
Feature space
flye
hifiasm
lja

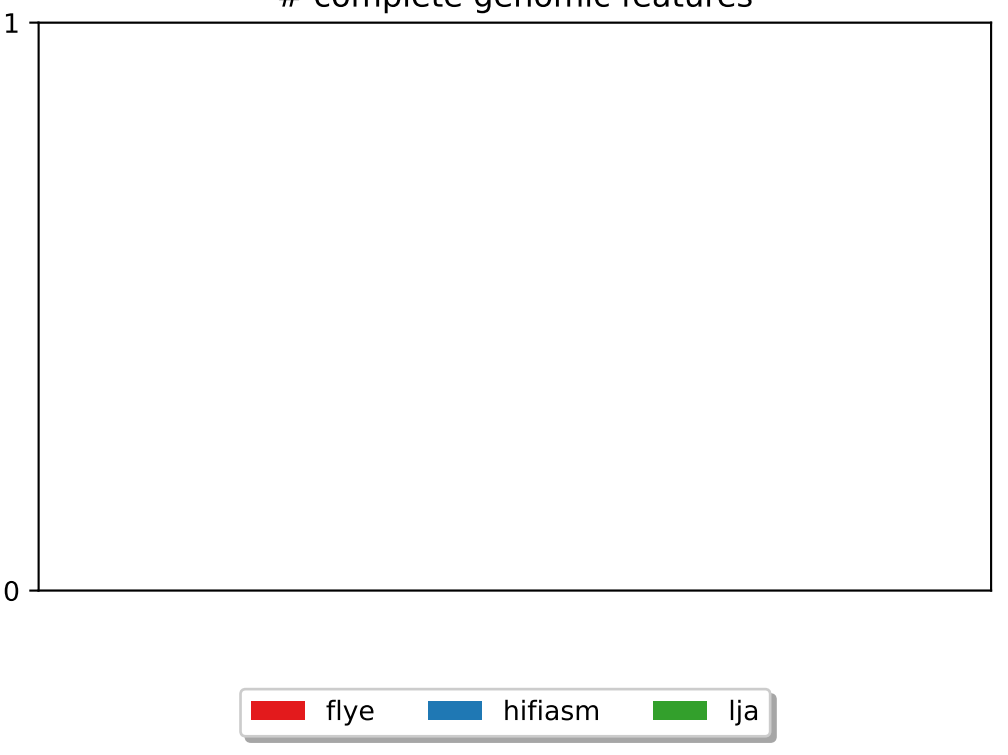

Cumulative length (aligned contigs)
Cumulative length (Mbp)
150
120
90
60
30
0
0
1500
3000
4500
6000
Contig index
flye
hifiasm
lja
Reference

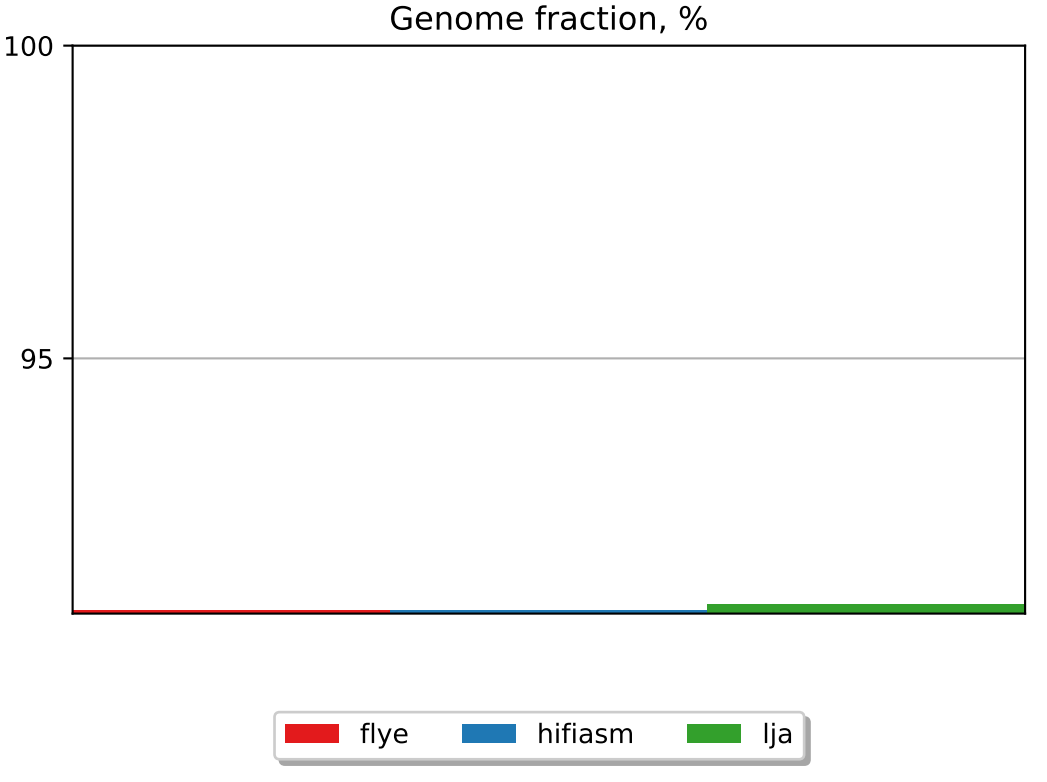

NAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
flye
hifiasm
lja


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
600000
450000
300000
150000
0
0
200
400
600
800
Contig index
flye
lja
Reference
hifiasm


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
flye
hifiasm
lja


complete genomic features
1
0
flye
hifiasm
lja


Genome fraction, %
100
95
flye
hifiasm
lja