Report

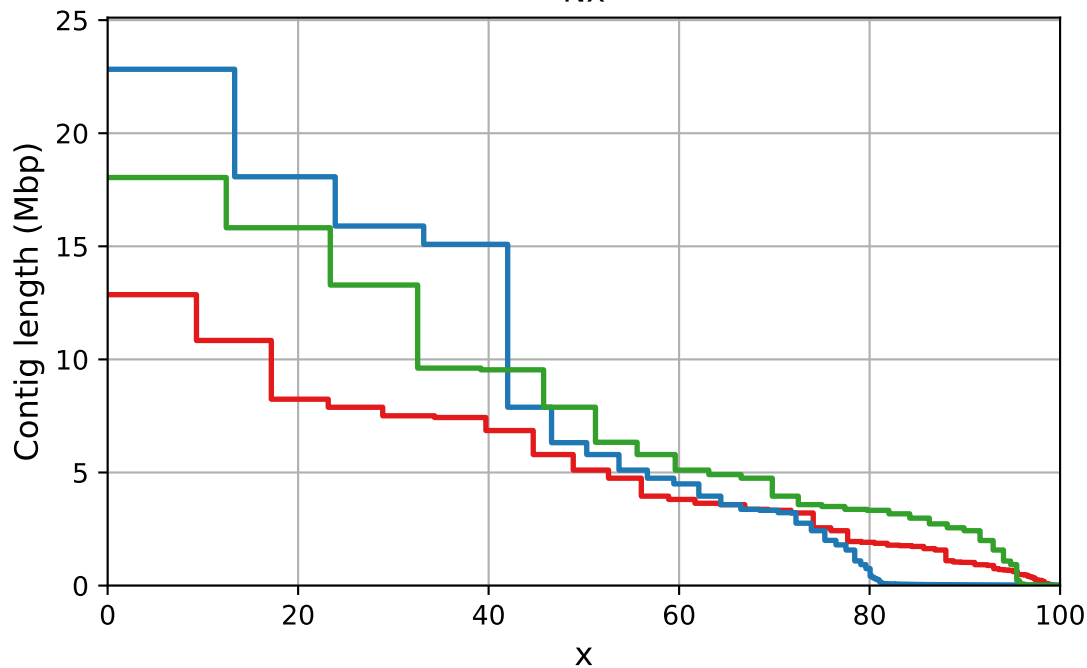|	flye_assembly_Altai-5	hifiasm_assembly_Altai-5	lja_assembly_Altai-5
# contigs (>= 0 bp)	163	958	490
# contigs (>= 1000 bp)	137	958	490
# contigs (>= 5000 bp)	129	958	383
# contigs (>= 10000 bp)	126	958	288
# contigs (>= 25000 bp)	80	810	79
# contigs (>= 50000 bp)	64	131	41
Total length (>= 0 bp)	137918295	171153468	144969763
Total length (>= 1000 bp)	137901329	171153468	144969763
Total length (>= 5000 bp)	137883904	171153468	144654871
Total length (>= 10000 bp)	137856628	171153468	143934847
Total length (>= 25000 bp)	137097964	167843313	140870442
Total length (>= 50000 bp)	136572216	145614642	139623094
# contigs	132	958	432
Largest contig	12861758	22827622	18041759
Total length	137894890	171153468	144849592
Reference length	119667750	119667750	119667750
GC (%)	36.39	36.69	37.01
Reference GC (%)	36.06	36.06	36.06
N50	5106113	6318855	7885885
NG50	6854838	15087710	9539496
N90	1028443	34662	2425861
NG90	1948952	3954529	3579029
auN	5737969.8	9474729.4	8664775.7
auNG	6611946.1	13551126.3	10488115.8
L50	9	6	6
LG50	7	4	5
L90	30	340	21
LG90	20	11	13
# misassemblies	639	1235	1067
# misassembled contigs	49	263	194
Misassembled contigs length	118865619	138399901	128402071
# local misassemblies	3545	3774	3766
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# possible TEs	50	34	30
# unaligned mis. contigs	26	4	5
# unaligned contigs	10 + 78 part	3 + 57 part	0 + 118 part
Unaligned length	28030381	29920167	29309094
Genome fraction (%)	88.902	88.493	88.902
Duplication ratio	1.035	1.334	1.087
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	831.60	630.75	797.36
# indels per 100 kbp	130.64	118.20	126.31
# genomic features	759335 + 11610 part	759601 + 11637 part	759590 + 11620 part
Largest alignment	4476808	4476799	4476805
Total aligned length	109943389	141080713	115473983
NA50	408200	212888	381769
NGA50	752903	788513	788515
NA90	-	-	-
NGA90	4356	41663	10341
auNA	1121548.0	935246.6	1097157.6
auNGA	1292376.1	1337626.0	1328033.9
LA50	52	103	59
LGA50	34	33	33
LA90	-	-	-
LGA90	778	385	667

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).
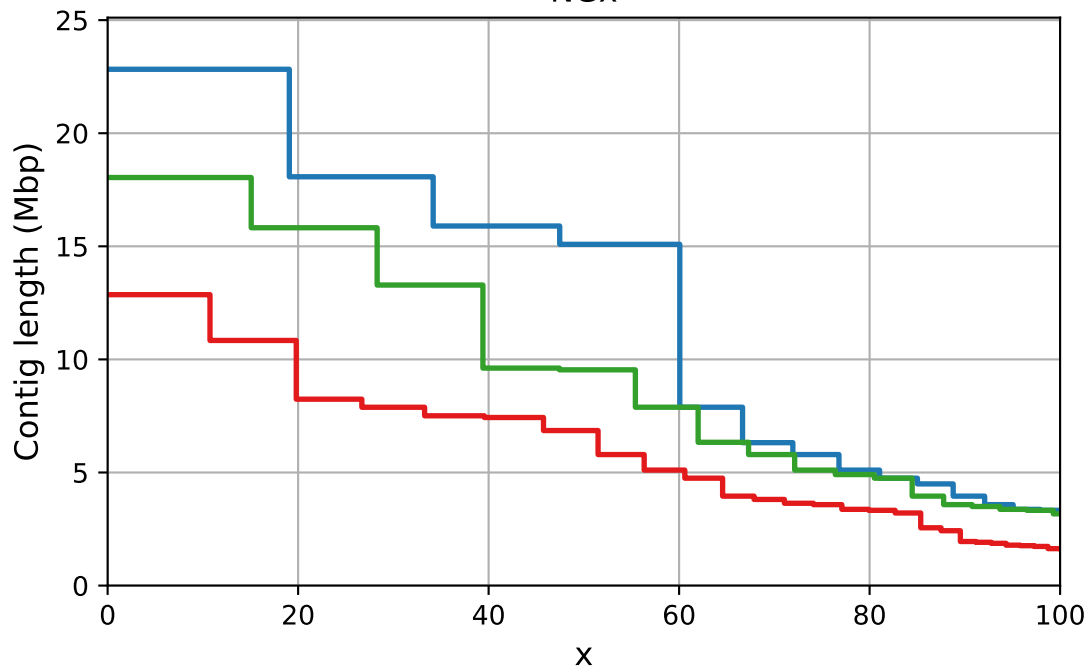
Misassemblies report

	flye_assembly_Altai-5	hifiasm_assembly_Altai-5	lja_assembly_Altai-5
# misassemblies	639	1235	1067
# contig misassemblies	639	1235	1067
# c. relocations	502	1083	905
# c. translocations	128	132	156
# c. inversions	9	20	6
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	49	263	194
Misassembled contigs length	118865619	138399901	128402071
# local misassemblies	3545	3774	3766
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# possible TEs	50	34	30
# unaligned mis. contigs	26	4	5
# mismatches	914289	889867	920745
# indels	143627	166753	145850
# indels (<= 5 bp)	111426	130699	112313
# indels (> 5 bp)	32201	36054	33537
Indels length	1833012	1937743	1912320

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).

Unaligned report

	flye_assembly_Altai-5	hifiasm_assembly_Altai-5	lja_assembly_Altai-5
# fully unaligned contigs	10	3	0
Fully unaligned length	654809	127906	0
# partially unaligned contigs	78	57	118
Partially unaligned length	27375572	29792261	29309094
# N's	0	0	0

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).

Nx

NGx

flye_assembly_Altai-5 — hifiasm_assembly_Altai-5 — lja_assembly_Altai-5

Cumulative length
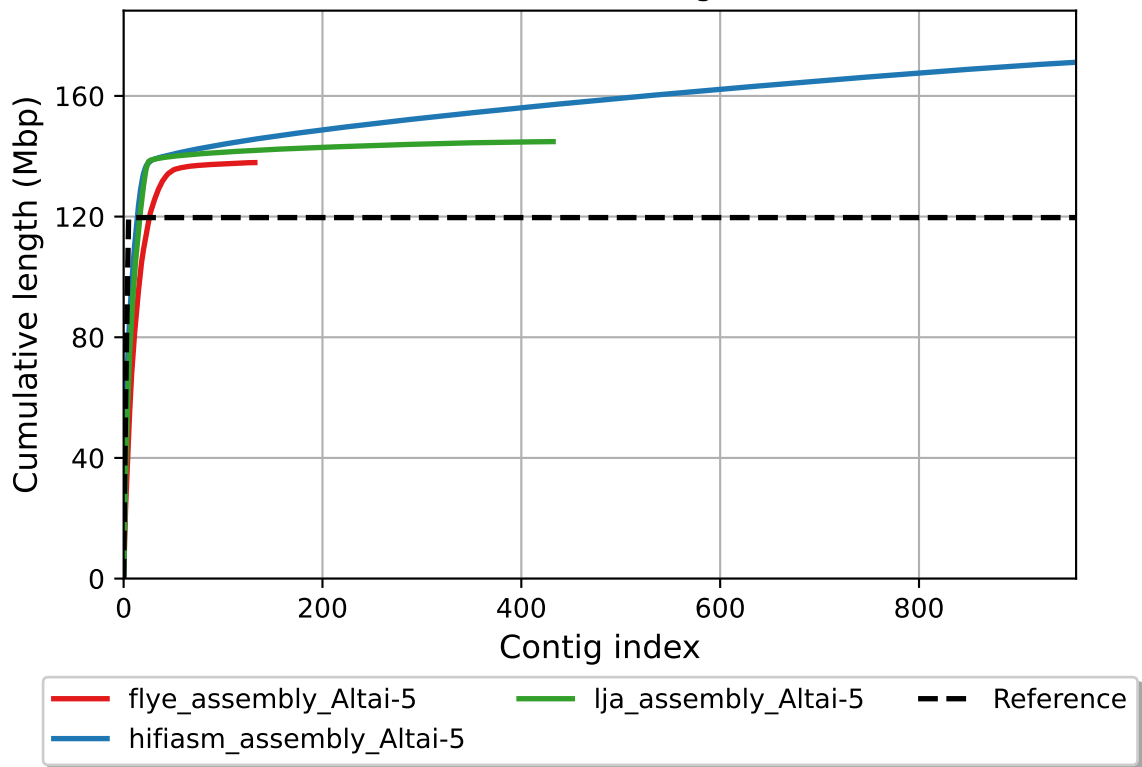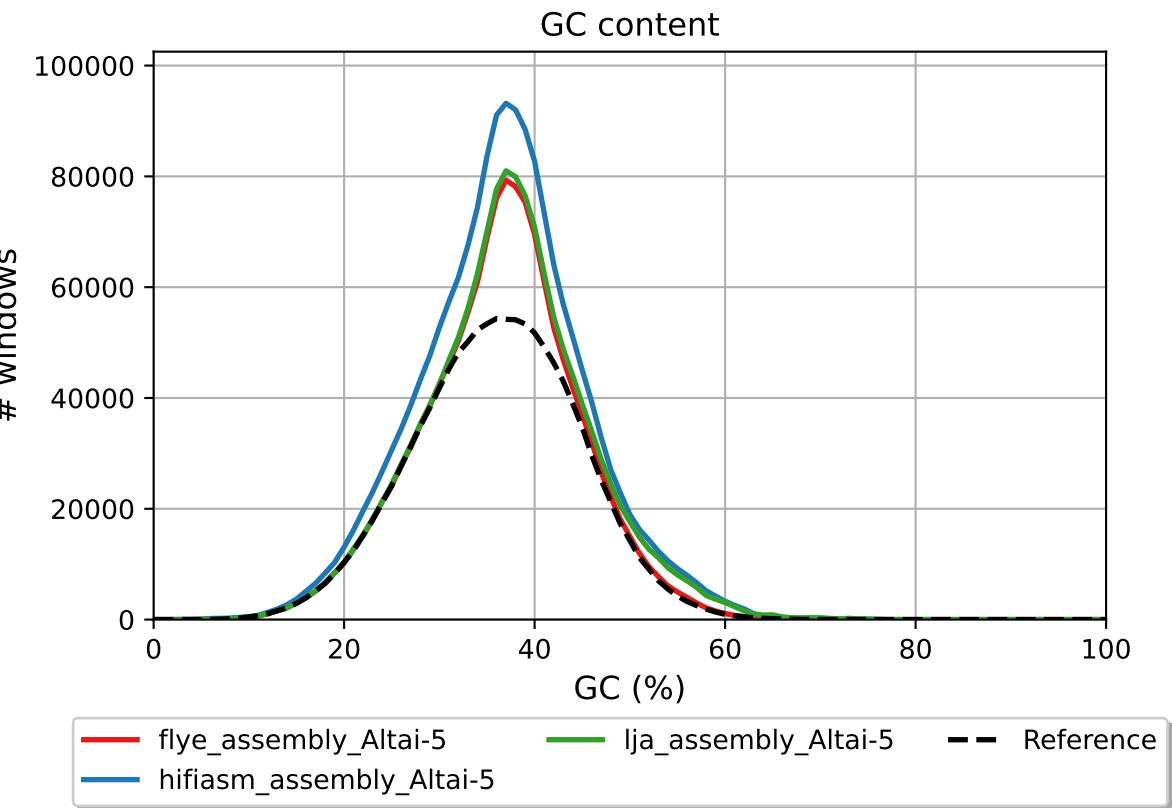
GC content
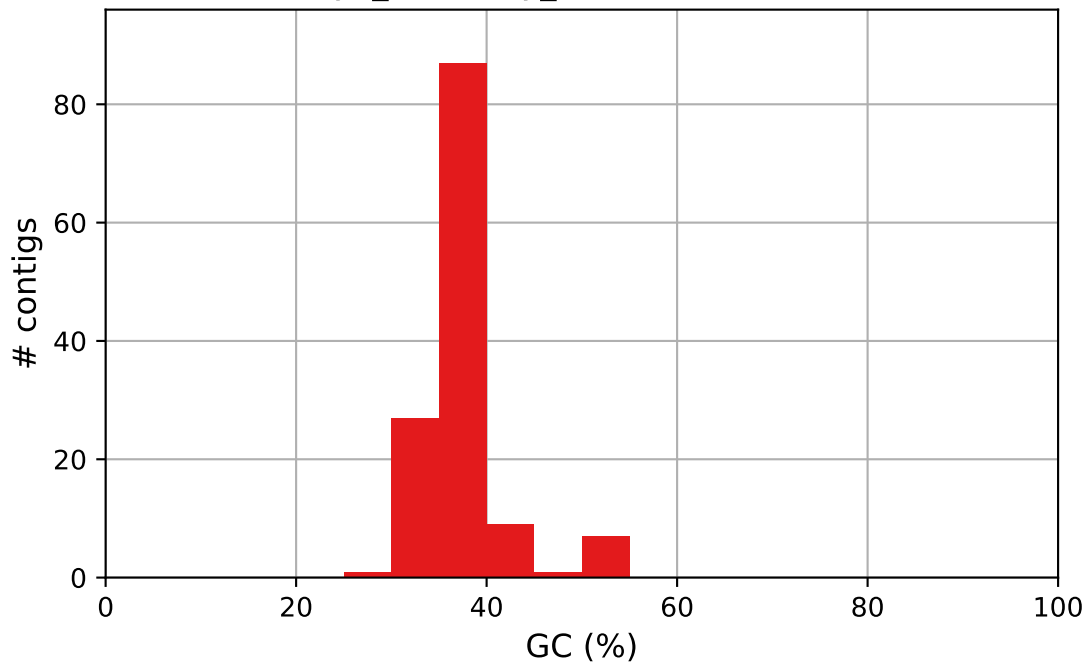
flye_assembly_Altai-5 GC content

hifiasm_assembly_Altai-5 GC content
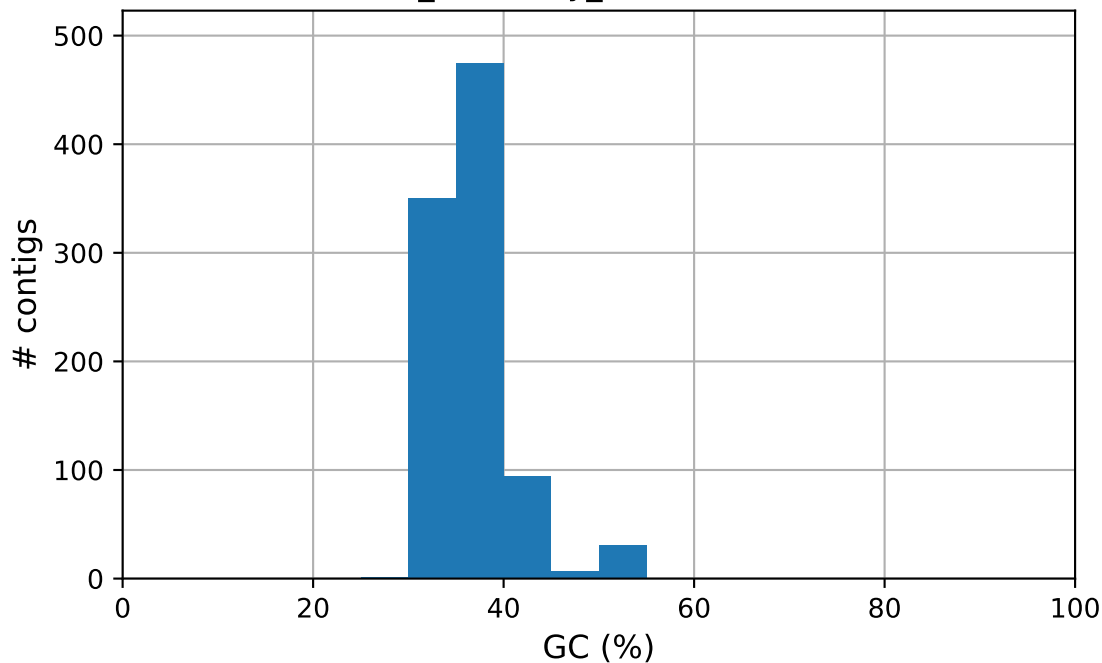
lja_assembly_Altai-5 GC content

Misassemblies

| # relocations | # translocations | # inversions |

FRCurve (misassemblies)

- flye_assembly_Altai-5
- hifiasm_assembly_Altai-5
- lja_assembly_Altai-5
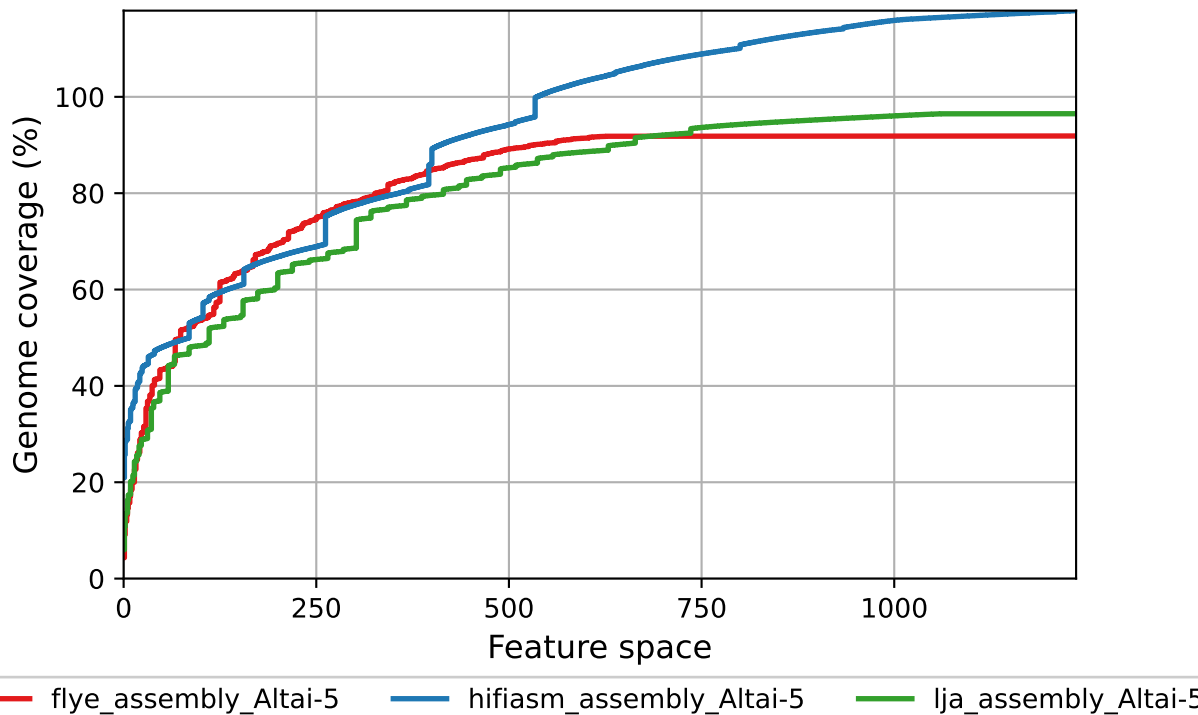
Cumulative length (aligned contigs)
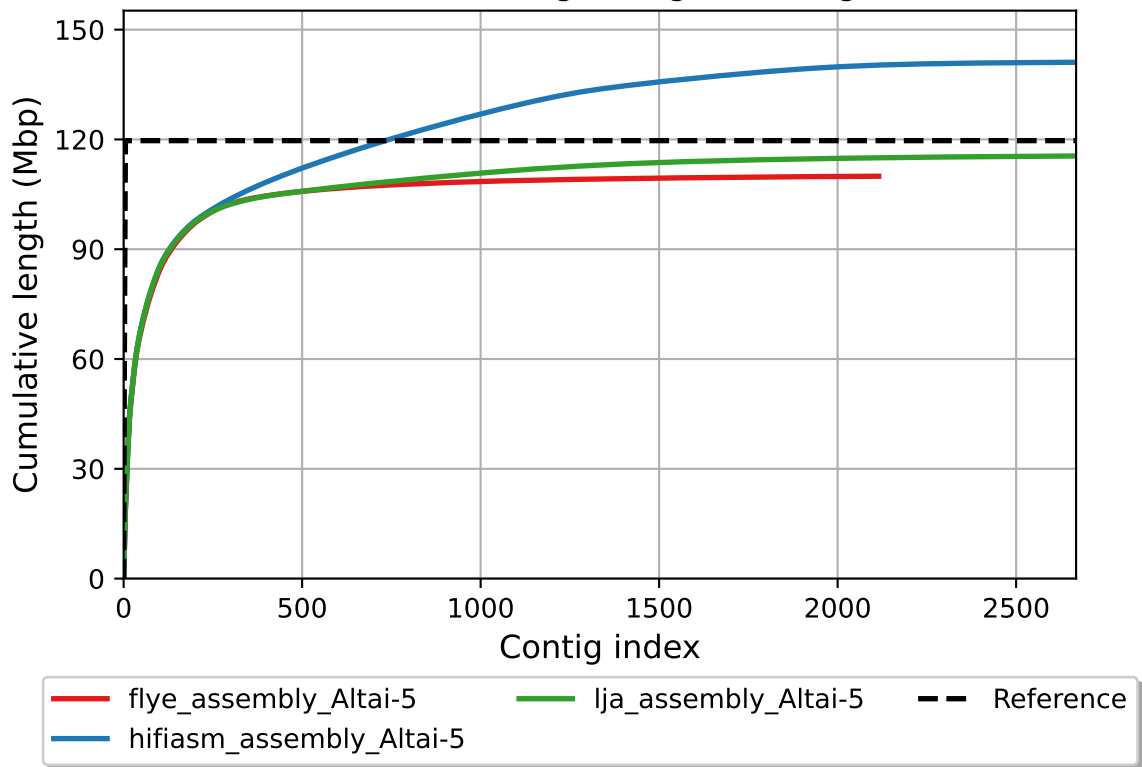
NAx
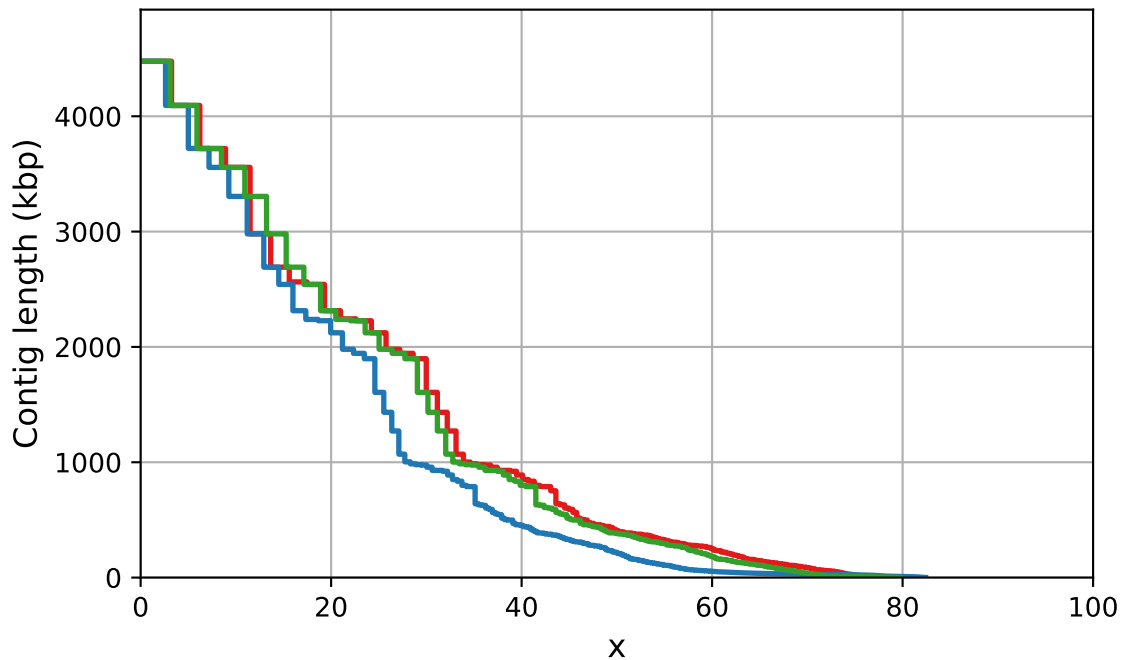
flye_assembly_Altai-5 — hifiasm_assembly_Altai-5 — lja_assembly_Altai-5
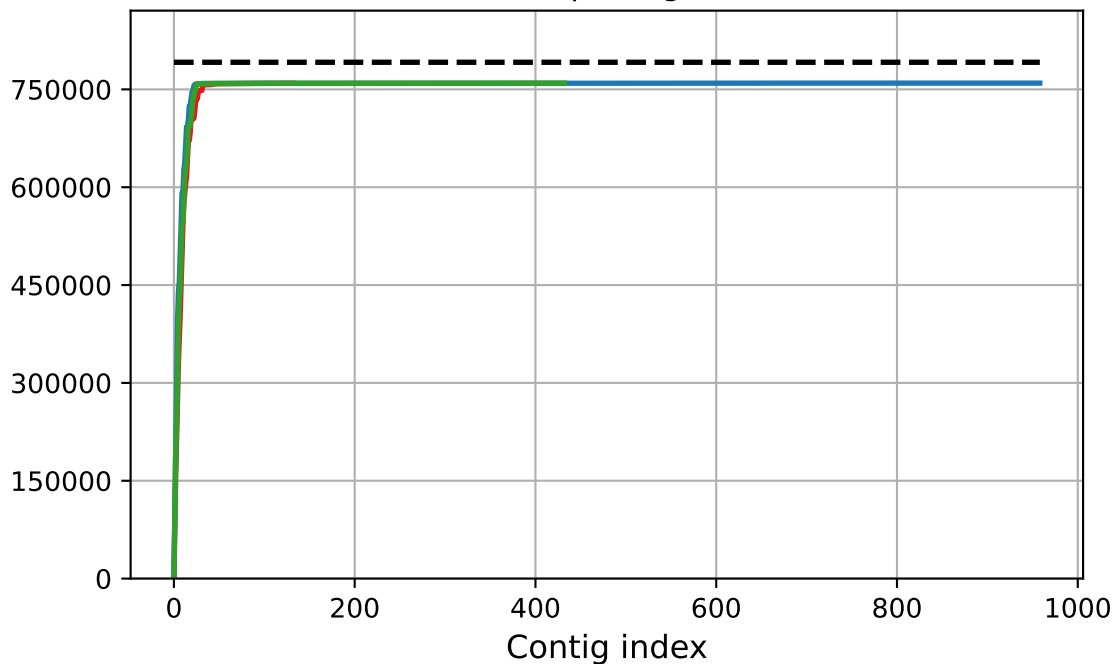
NGAx

Contig length (kbp) vs x
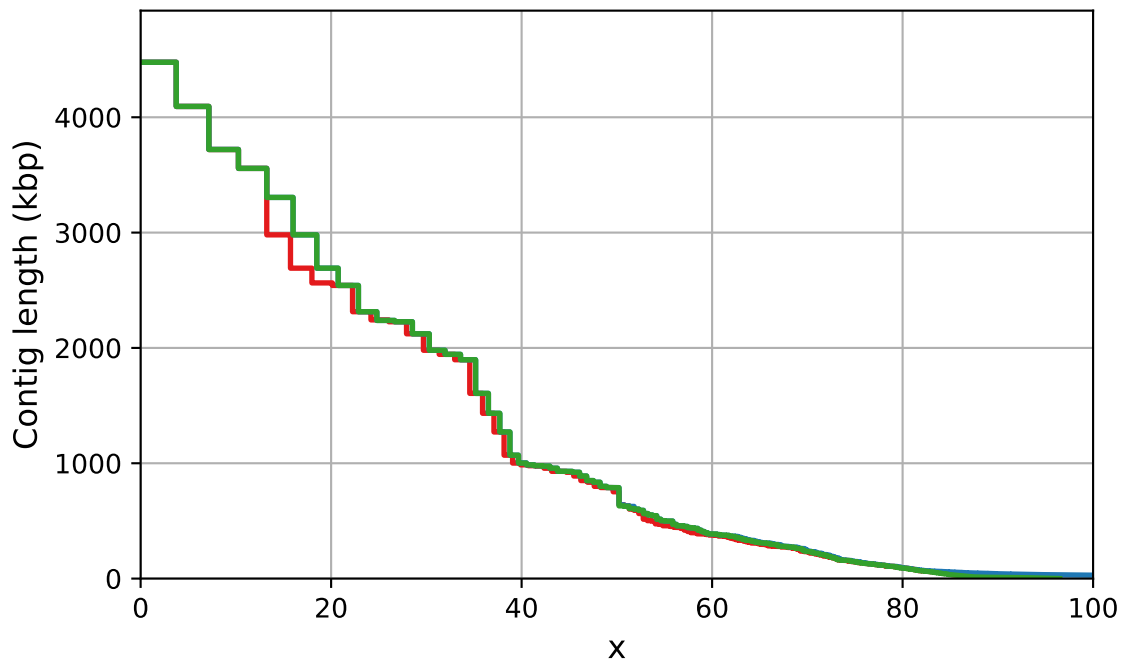
— flye_assembly_Altai-5
— hifiasm_assembly_Altai-5
— lja_assembly_Altai-5

Cumulative # complete genomic features

FRCurve (genomic features)
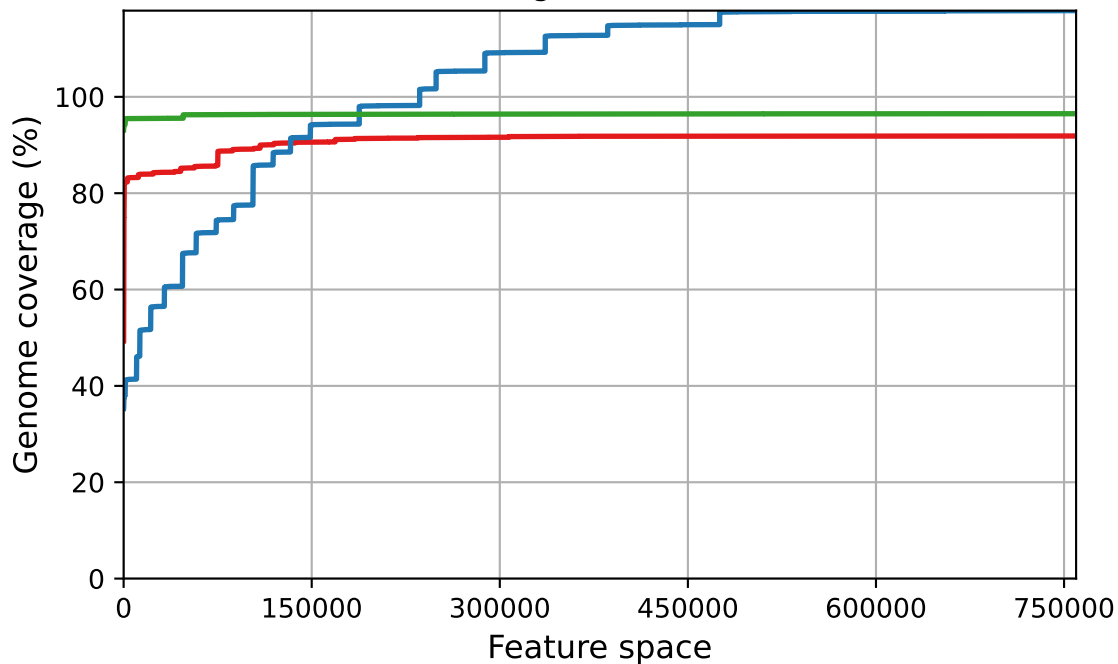
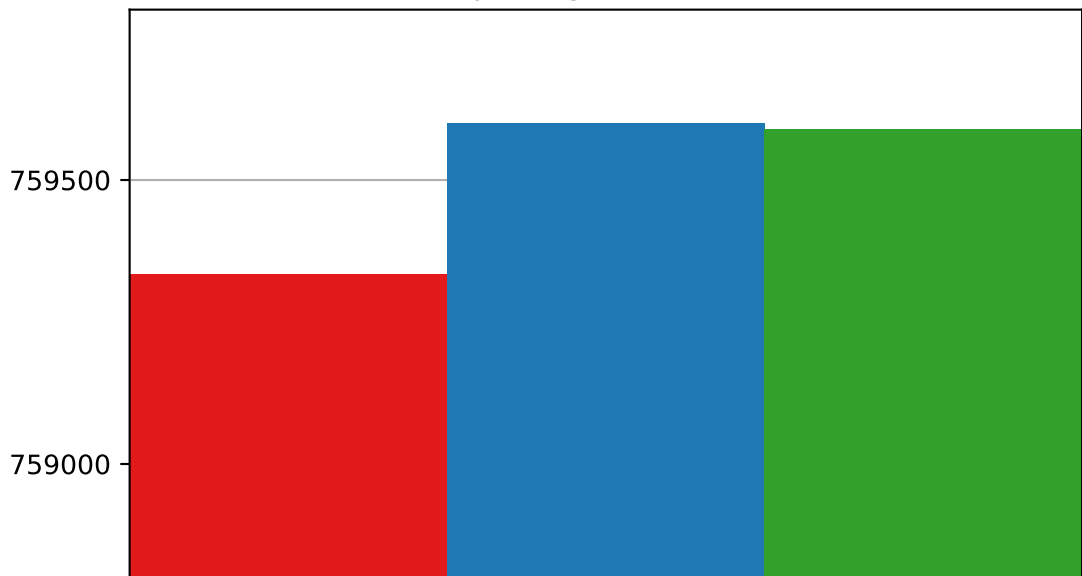Genome coverage (%) vs Feature space

Legend:
- flye_assembly_Altai-5 (red)
- hifiasm_assembly_Altai-5 (blue)
- lja_assembly_Altai-5 (green)

complete genomic features

flye_assembly_Altai-5	hifiasm_assembly_Altai-5	lja_assembly_Altai-5

Genome fraction, %

flye_assembly_Altai-5	hifiasm_assembly_Altai-5	lja_assembly_Altai-5