

	canu_assembly	canu_assembly_polished	Report flye_assembly	flye_assembly_polished	UpperBound
# contigs (>= 0 bp)	192	192	164	164	4195
# contigs (>= 1000 bp)	192	192	103	103	1346
# contigs (>= 5000 bp)	185	185	59	59	565
# contigs (>= 10000 bp)	183	183	49	49	395
# contigs (>= 25000 bp)	162	162	37	37	291
# contigs (>= 50000 bp)	112	112	31	31	235
Total length (>= 0 bp)	122977739	123001103	119963782	119950311	117111587
Total length (>= 1000 bp)	122977739	123001103	119925361	119911914	116316331
Total length (>= 5000 bp)	122951239	122974598	119824915	119811844	114516181
Total length (>= 10000 bp)	122937652	122960987	119752542	119739466	113343980
Total length (>= 25000 bp)	122573799	122598770	119566446	119553357	111762551
Total length (>= 50000 bp)	120695097	120723224	119355633	119342541	109797276
# contigs	190	190	70	70	761
Largest contig	11567090	11570839	15013467	15013354	5908332
Total length	122973098	122996456	119869541	119856063	115282661
Reference length	119667750	119667750	119667750	119667750	119667750
GC (%)	36.27	36.26	36.05	36.05	36.03
Reference GC (%)	36.06	36.06	36.06	36.06	36.06
N50	3435125	3436535	14082887	14082808	1405724
NG50	3435988	3437141	14082887	14082808	1192680
N90	426854	427111	3443320	3443144	112503
NG90	566322	566539	3443320	3443144	81615
auN	4810862.4	4813051.9	12051185.8	12051151.6	1937457.2
auNG	4943743.4	4946932.9	12071507.2	12070115.7	1866461.2
L50	10	10	5	5	21
LG50	9	9	5	5	23
L90	45	45	9	9	161
LG90	39	39	9	9	203
# total reads	78141987	78254393	81407167	81260233	71399278
# left	38736252	38792384	40347157	40272685	35371023
# right	38636849	38693123	40291124	40218662	35259369
Mapped (%)	100.88	100.88	69.89	71.06	99.44
Reference mapped (%)	99.55	99.55	99.55	99.55	99.55
Properly paired (%)	91.03	90.97	63.86	64.52	87.5
Reference properly paired (%)	87.59	87.59	87.59	87.59	87.59
Avg. coverage depth	143	144	89	90	122
Reference avg. coverage depth	117	117	117	117	117
Coverage >= 1x (%)	100.0	100.0	100.0	100.0	99.81
Reference coverage >= 1x (%)	98.04	98.04	98.04	98.04	98.04
# misassemblies	757	754	563	567	0
# misassembled contigs	119	122	28	28	0
Misassembled contigs length	110796582	111026108	116362090	116354205	0
# local misassemblies	3552	3585	3413	3372	0
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	4	4	0
# possible TEs	66	66	34	34	0
# unaligned mis. contigs	38	33	11	10	0
# unaligned contigs	6 + 154 part	7 + 152 part	4 + 43 part	4 + 42 part	0 + 0 part
Unaligned length	13537717	13496215	13427090	13385889	0
Genome fraction (%)	88.649	88.680	88.536	88.561	96.166
Duplication ratio	1.032	1.032	1.006	1.006	1.003
# N's per 100 kbp	0.00	0.00	1.00	0.71	2.30
# mismatches per 100 kbp	808.35	810.05	777.67	779.47	0.04
# indels per 100 kbp	176.23	137.92	148.94	130.95	0.00
# genomic features	559066 + 11114 part	559299 + 10978 part	558308 + 11016 part	558522 + 10862 part	583368 + 1030 part
Largest alignment	4489636	4683090	5385170	6764147	5908332
Total aligned length	109333158	109380563	106439499	106466102	115282310
NA50	525319	525522	633886	633901	1405724
NGA50	589651	589824	633886	633901	1192680
NA90	-	-	-	-	112503
NGA90	7219	7392	-	-	81615
auNA	1011382.9	1100022.6	1418374.9	1580511.8	1937457.1
auNGA	1039318.4	1130621.1	1420766.6	1582998.9	1866461.2
LA50	46	45	36	35	21
LGA50	43	42	36	35	23
LA90	-	-	-	-	161
LGA90	695	678	-	-	203

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).

Reads report

	canu_assembly	canu_assembly_polished	flye_assembly	flye_assembly_polished	UpperBound
# total reads	78141987	78254393	81407167	81260233	71399278
# left	38736252	38792384	40347157	40272685	35371023
# right	38636849	38693123	40291124	40218662	35259369
# mapped	78829798	78940254	56896056	57742750	70997948
Mapped (%)	100.88	100.88	69.89	71.06	99.44
# properly paired	71134620	71190534	51989960	52428112	62473260
Properly paired (%)	91.03	90.97	63.86	64.52	87.5
# singletons	72621	72149	506790	488070	245983
Singletons (%)	0.09	0.09	0.62	0.6	0.34
# misjoint mates	4800590	4856466	2625018	2811540	4820392
Misjoint mates (%)	6.14	6.21	3.22	3.46	6.75
Avg. coverage depth	143	144	89	90	122
Coverage >= 1x (%)	100.0	100.0	100.0	100.0	99.81
Coverage >= 5x (%)	99.98	99.97	99.96	99.96	99.37
Coverage >= 10x (%)	99.94	99.92	99.94	99.94	98.89
# reference mapped	71199476	71199476	71199476	71199476	71199476
Reference mapped (%)	99.55	99.55	99.55	99.55	99.55
# reference properly paired	62641722	62641722	62641722	62641722	62641722
Reference properly paired (%)	87.59	87.59	87.59	87.59	87.59
# reference singletons	243547	243547	243547	243547	243547
Reference singletons (%)	0.34	0.34	0.34	0.34	0.34
# reference misjoint mates	4356194	4356194	4356194	4356194	4356194
Reference misjoint mates (%)	6.09	6.09	6.09	6.09	6.09
Reference avg. coverage depth	117	117	117	117	117
Reference coverage >= 1x (%)	98.04	98.04	98.04	98.04	98.04
Reference coverage >= 5x (%)	97.09	97.09	97.09	97.09	97.09
Reference coverage >= 10x (%)	96.39	96.39	96.39	96.39	96.39

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

	canu_assembly	canu_assembly_polished	flye_assembly	flye_assembly_polished	UpperBound
# misassemblies	757	754	563	567	0
# contig misassemblies	757	754	559	564	0
# c. relocations	571	568	458	464	0
# c. translocations	174	173	92	91	0
# c. inversions	12	13	9	9	0
# scaffold misassemblies	0	0	4	3	0
# s. relocations	0	0	4	3	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	119	122	28	28	0
Misassembled contigs length	110796582	111026108	116362090	116354205	0
# local misassemblies	3552	3585	3413	3372	0
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	4	4	0
# possible TEs	66	66	34	34	0
# unaligned mis. contigs	38	33	11	10	0
# mismatches	883797	886034	827753	829872	48
# indels	192674	150856	158529	139415	2
# indels (<= 5 bp)	160425	118571	126909	107775	1
# indels (> 5 bp)	32249	32285	31620	31640	1
Indels length	1885177	1878720	1809918	1832836	490

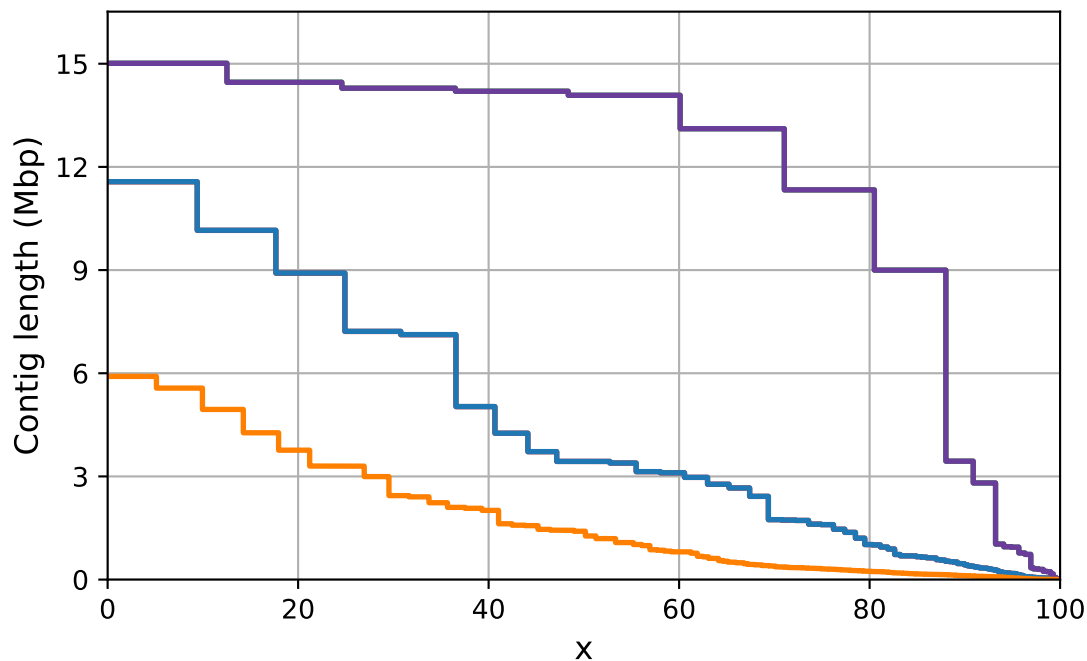
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	canu_assembly	canu_assembly_polished	flye_assembly	flye_assembly_polished	UpperBound
# fully unaligned contigs	6	7	4	4	0
Fully unaligned length	65902	80409	20876	20476	0
# partially unaligned contigs	154	152	43	42	0
Partially unaligned length	13471815	13415806	13406214	13365413	0
# N's	0	0	1200	855	2657

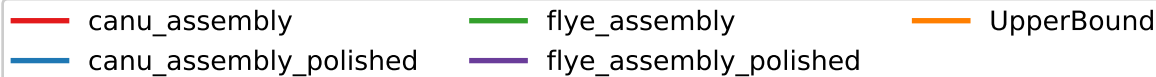
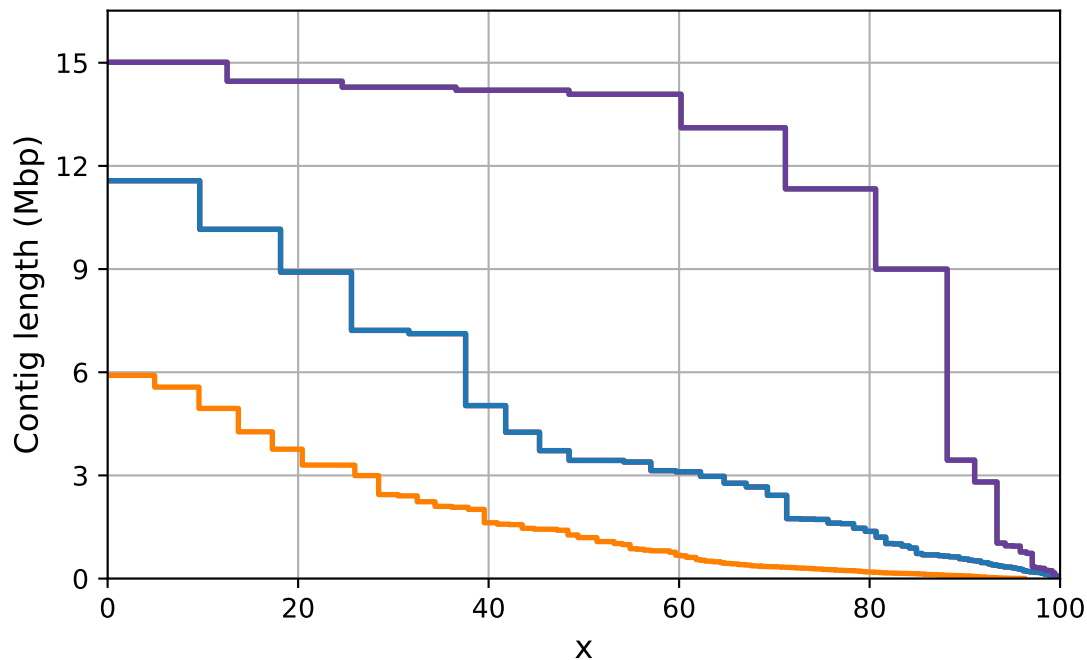
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

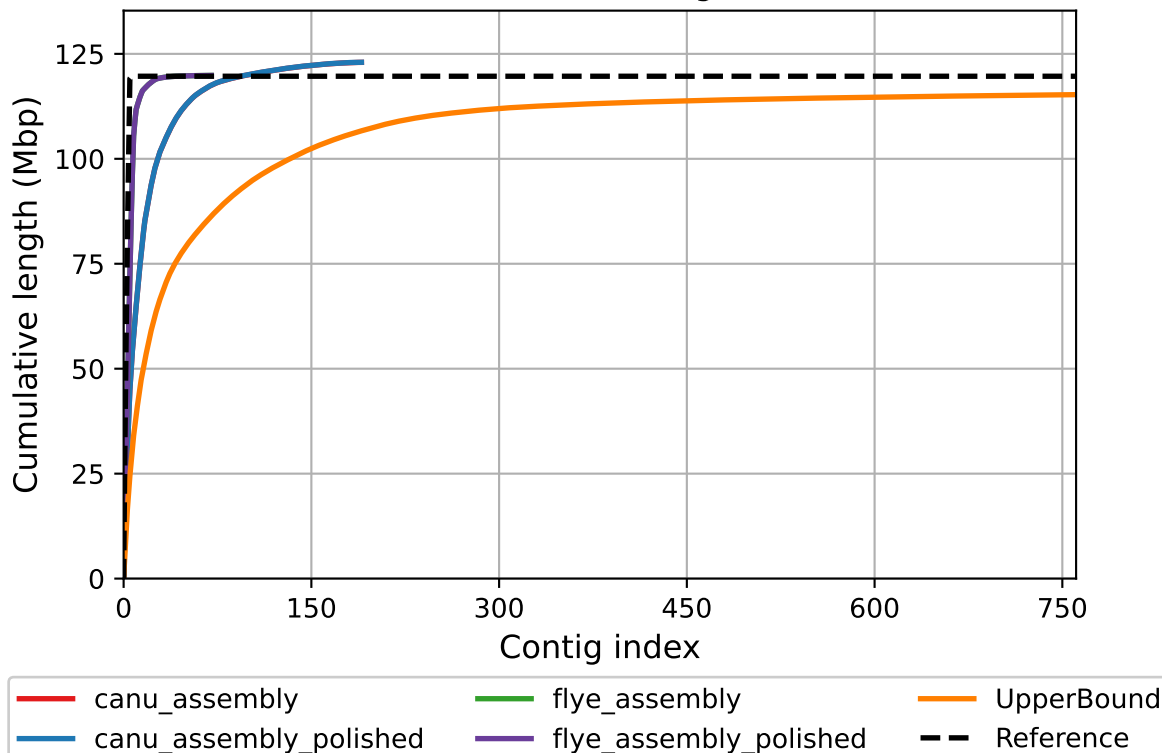


canu_assembly flye_assembly UpperBound
canu_assembly_polished flye_assembly_polished

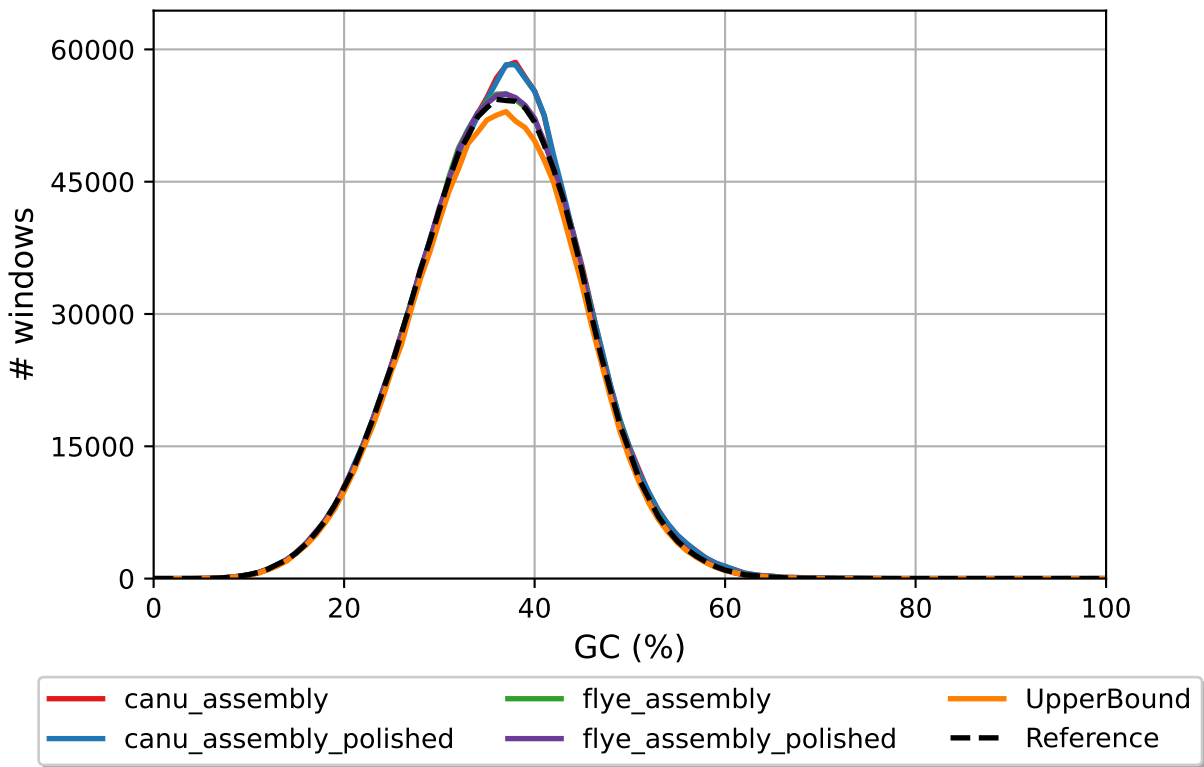
NGx



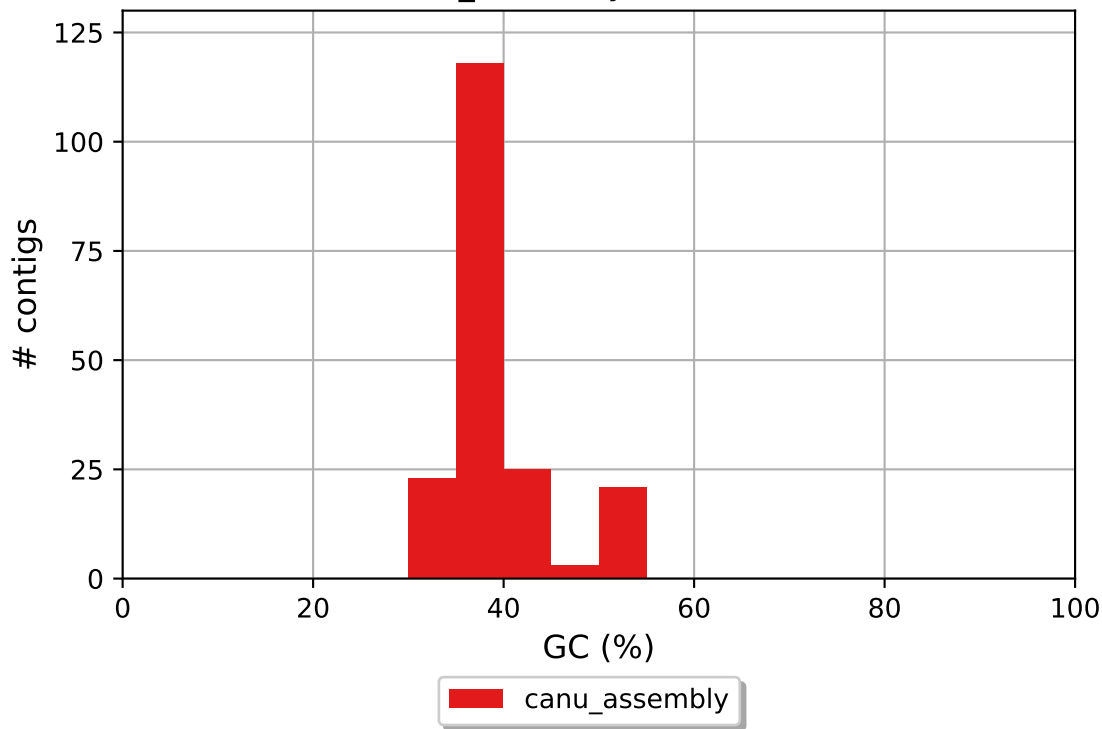
Cumulative length



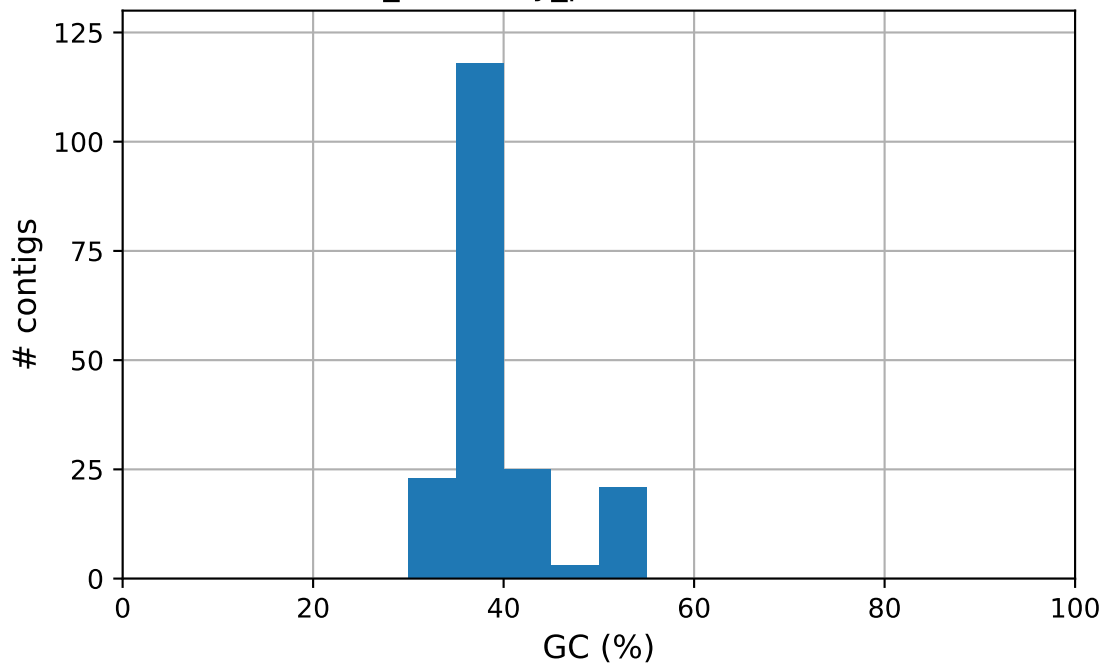
GC content



canu_assembly GC content

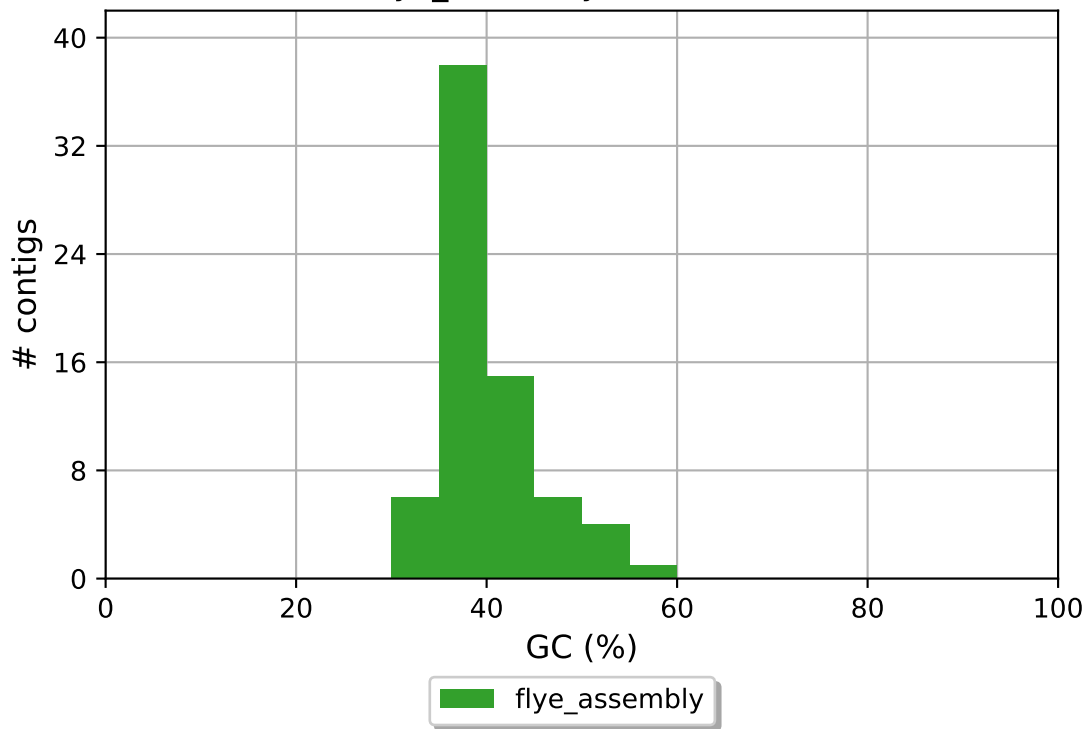


canu_assembly_polished GC content

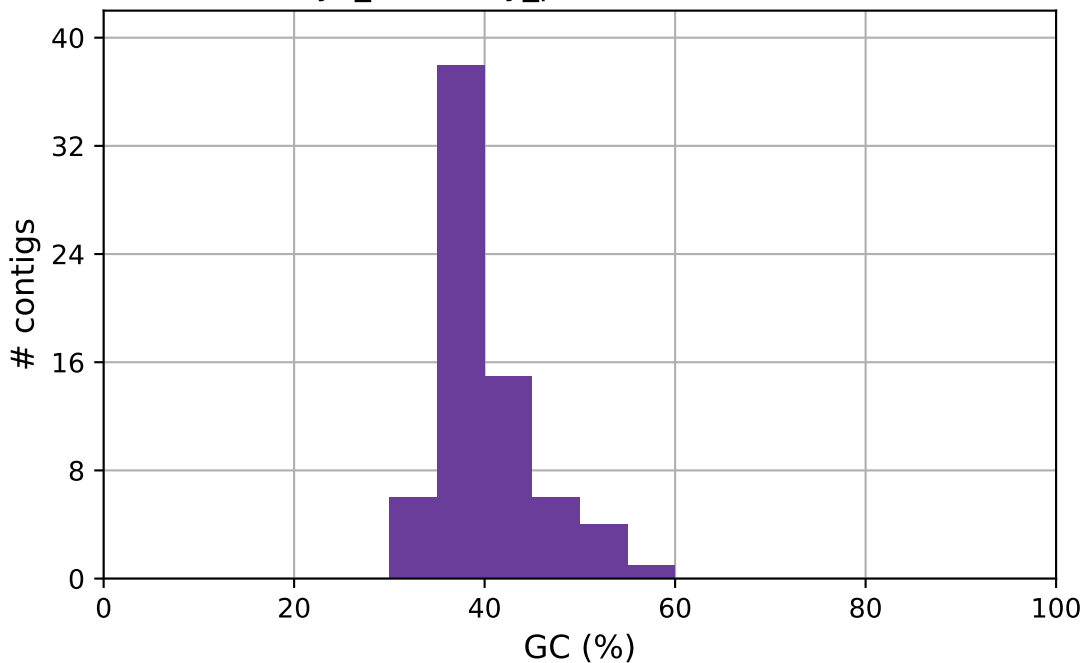


canu_assembly_polished

flye_assembly GC content

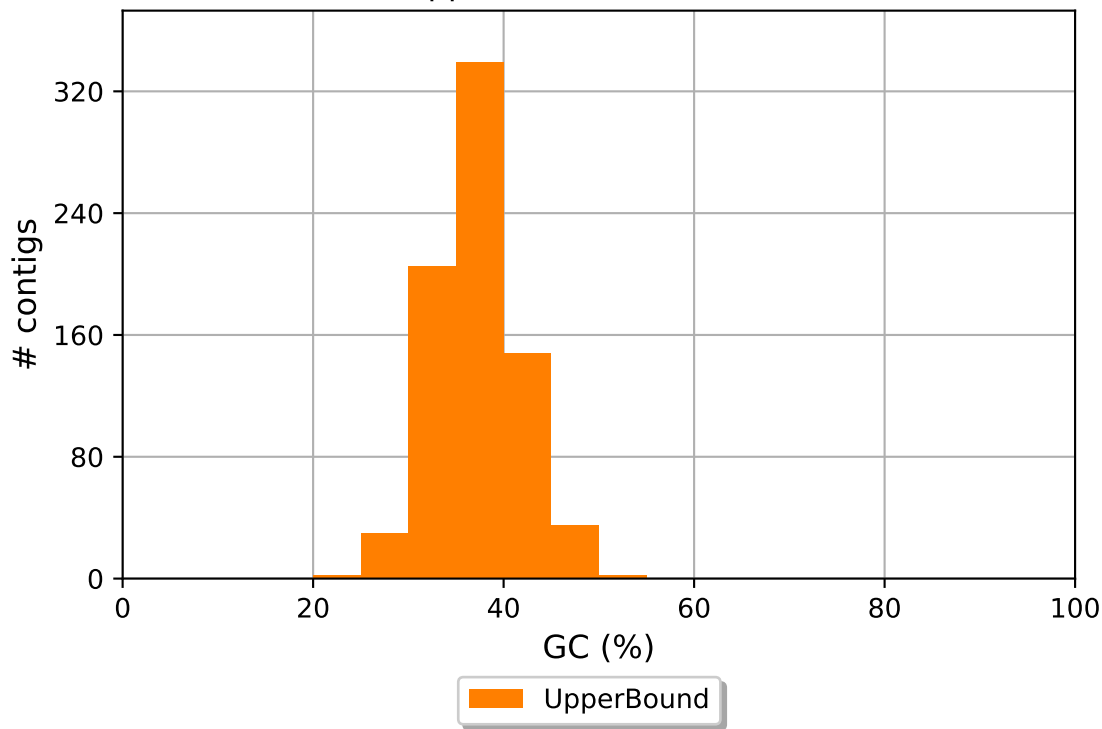


flye_assembly_polished GC content

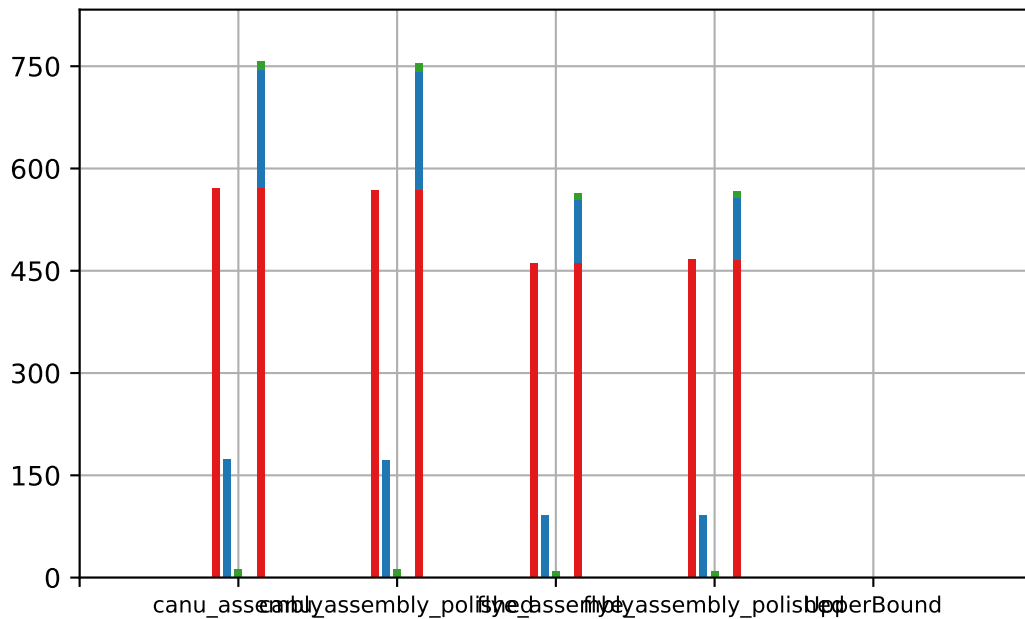


flye_assembly_polished

UpperBound GC content

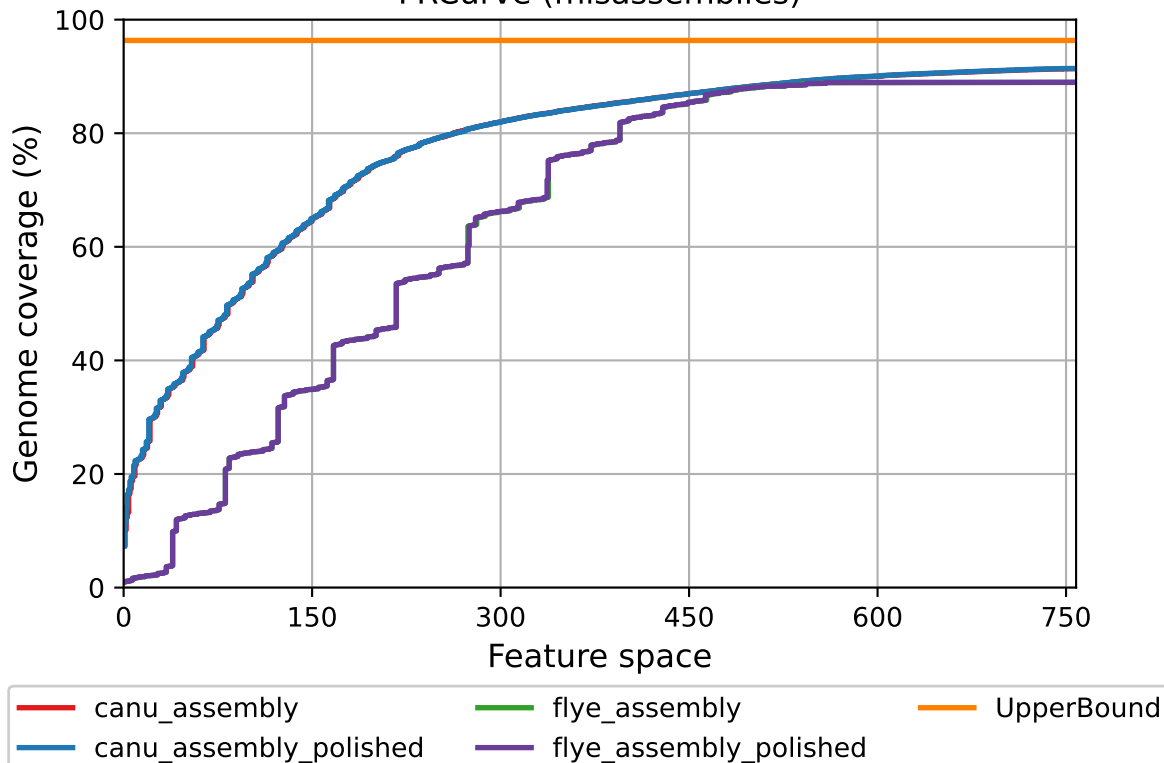


Misassemblies

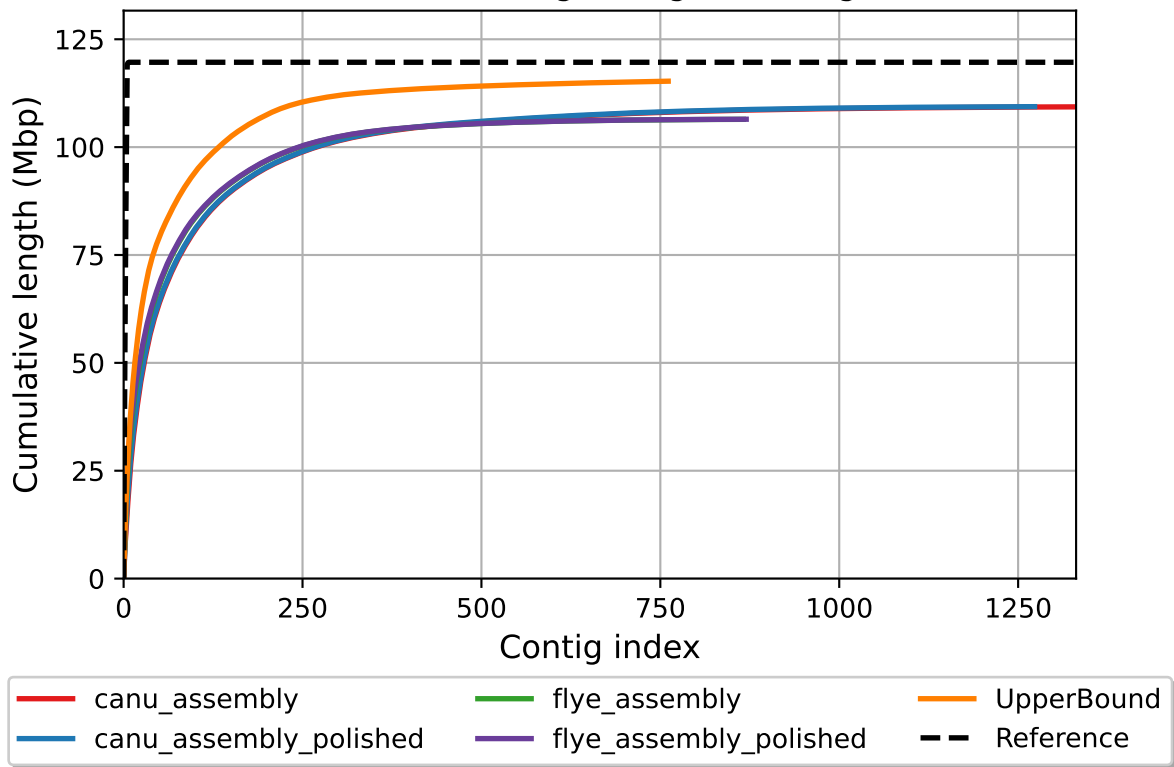


■ # relocations ■ # translocations ■ # inversions

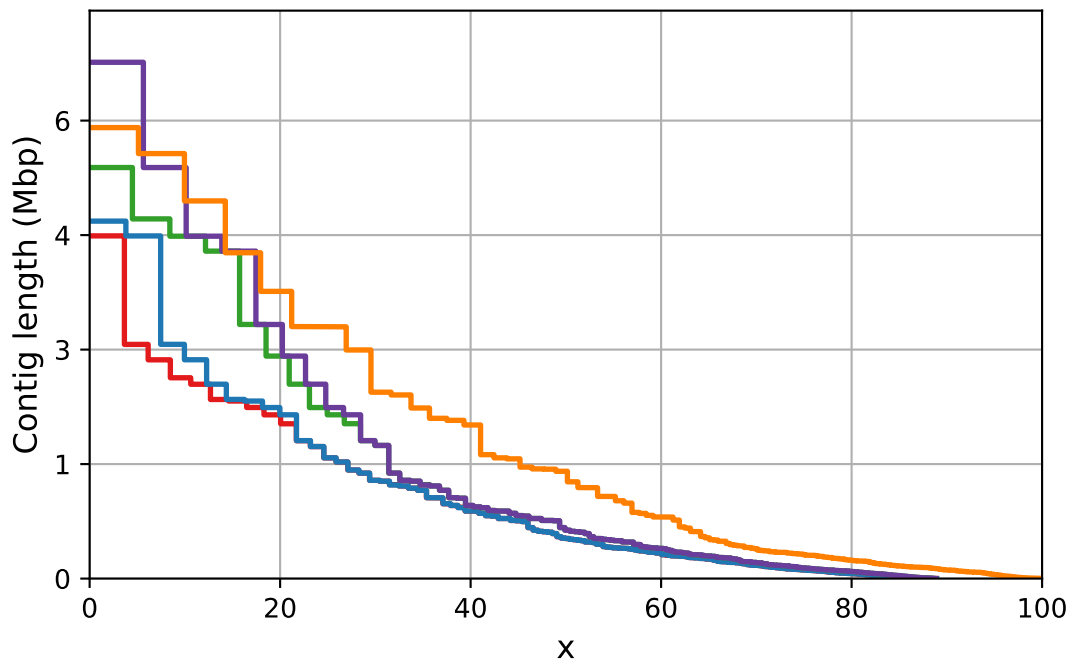
FRCurve (misassemblies)



Cumulative length (aligned contigs)

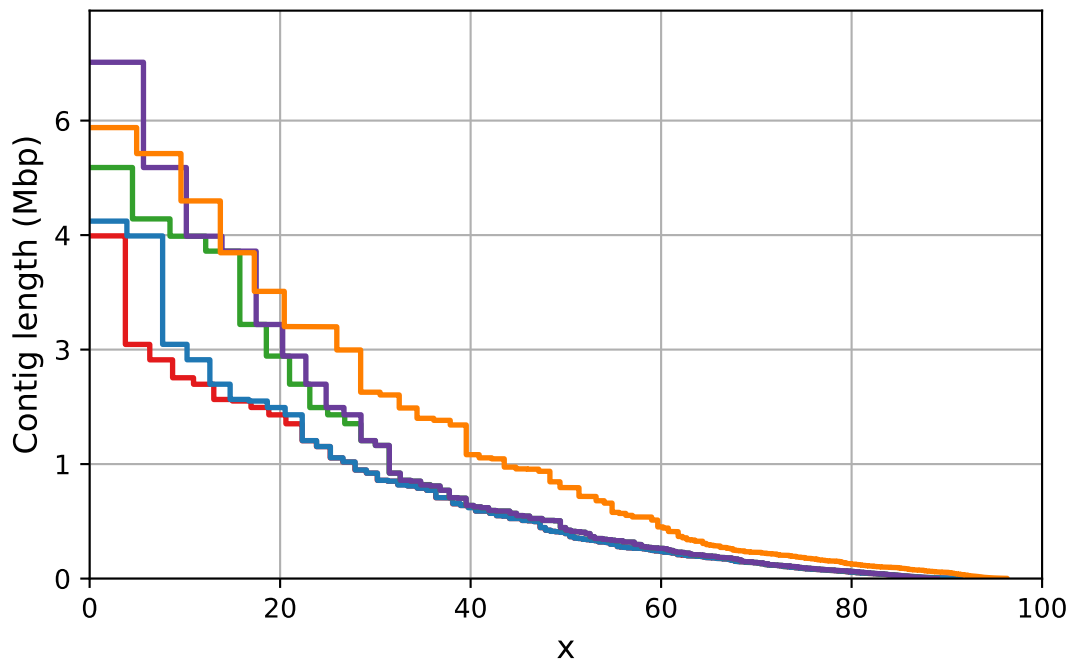


NAx



canu_assembly flye_assembly UpperBound
 canu_assembly_polished flye_assembly_polished

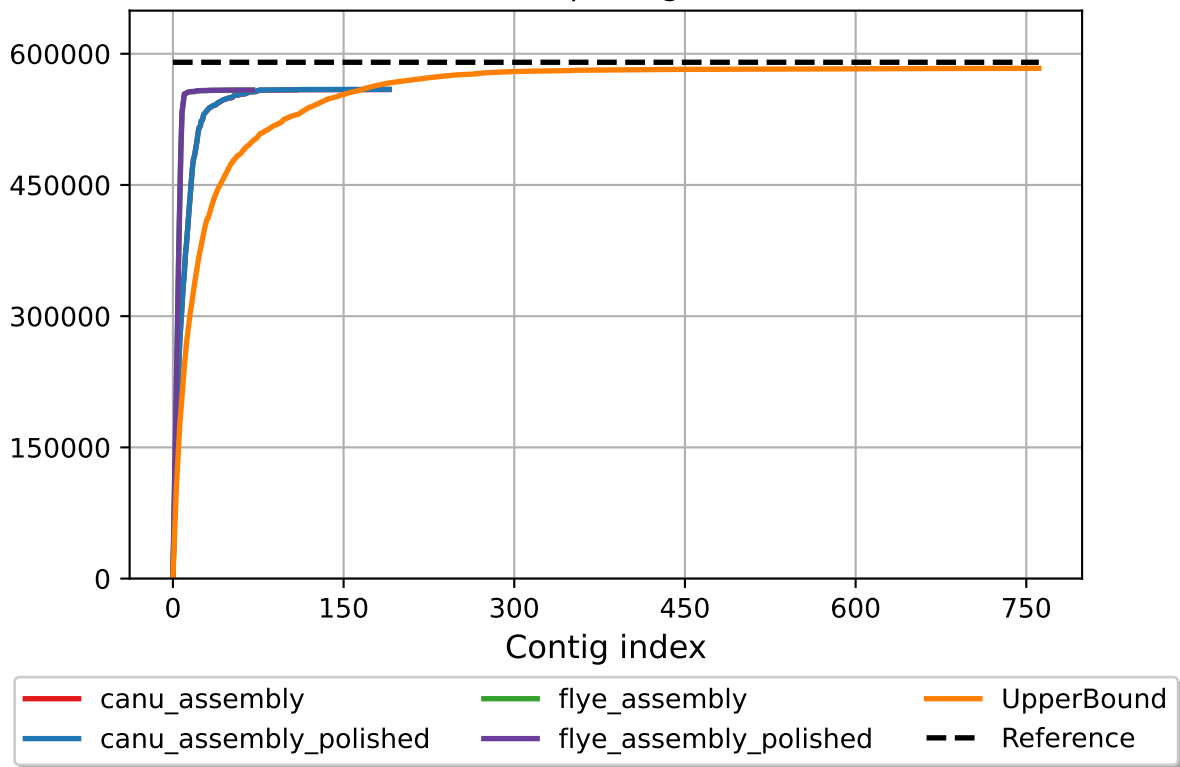
NGAx



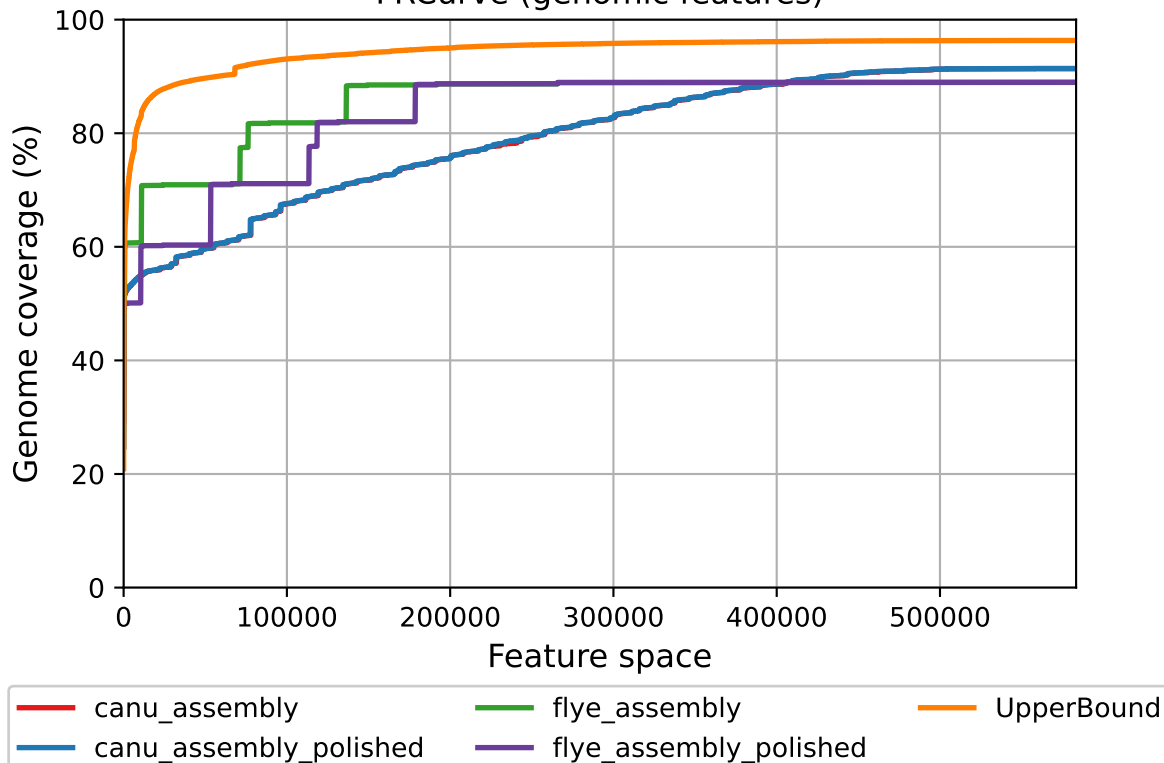
canu_assembly flye_assembly UpperBound
canu_assembly_polished flye_assembly_polished

Cumulative # complete genomic features

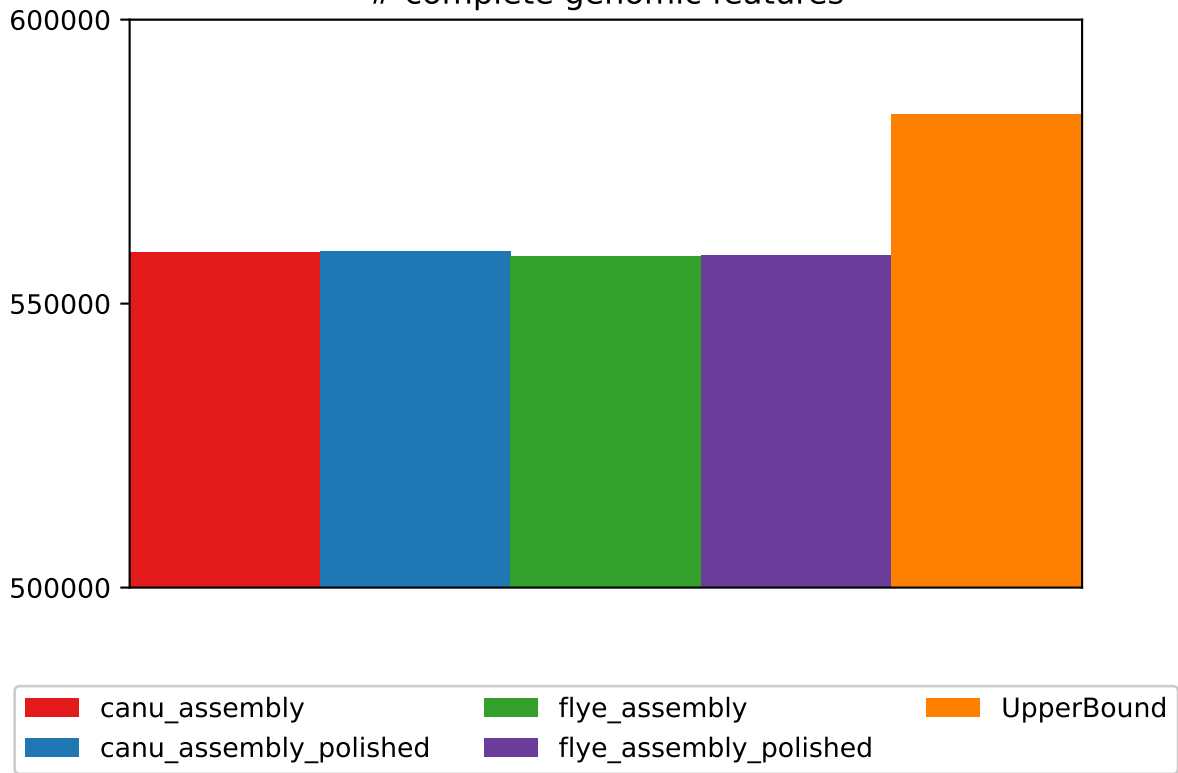
Cumulative # complete genomic features



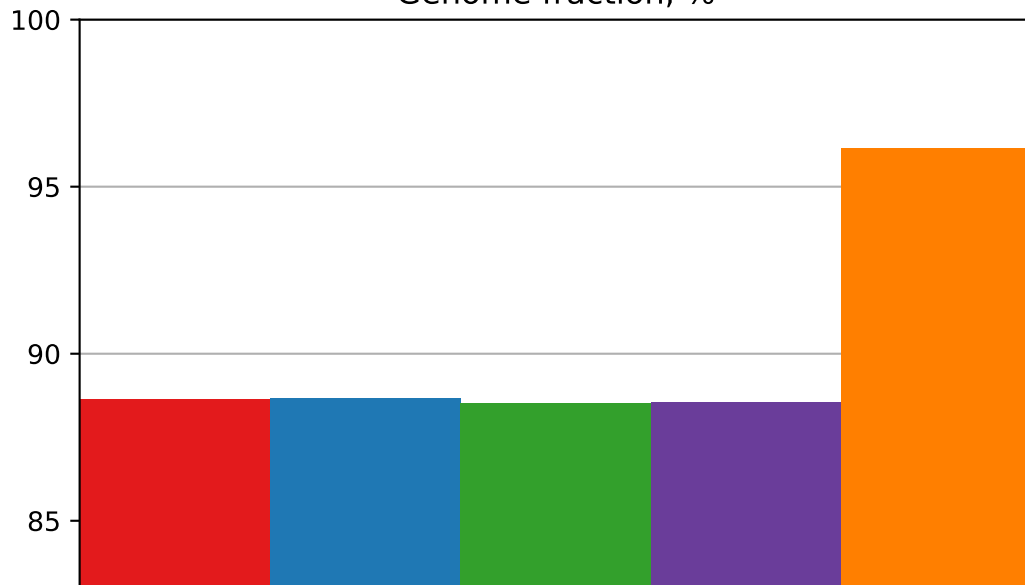
FRCurve (genomic features)



complete genomic features



Genome fraction, %



■ canu_assembly	■ flye_assembly	■ UpperBound
■ canu_assembly_polished	■ flye_assembly_polished	