Report

	merged_final_merge_strict	flye_assembly_FIXED_v4.5	canu_polished_round1
# contigs (>= 0 bp)	10	12	29
# contigs (>= 1000 bp)	10	12	29
# contigs (>= 5000 bp)	9	11	29
# contigs (>= 10000 bp)	9	11	29
# contigs (>= 25000 bp)	9	11	28
# contigs (>= 50000 bp)	7	9	18
Total length (>= 0 bp)	34910524	34821575	35997303
Total length (>= 1000 bp)	34910524	34821575	35997303
Total length (>= 5000 bp)	34906367	34817418	35997303
Total length (>= 10000 bp)	34906367	34817418	35997303
Total length (>= 25000 bp)	34906367	34817418	35978808
Total length (>= 50000 bp)	34826976	34738027	35607977
# contigs	10	12	29
Largest contig	8060236	8060236	8143141
Total length	34910524	34821575	35997303
Reference length	34204973	34204973	34204973
GC (%)	22.70	22.73	22.76
Reference GC (%)	22.44	22.44	22.44
N50	5574931	5603593	5606788
NG50	5574931	5603593	5606788
N90	4039478	4039478	3926766
NG90	4039478	4039478	5028520
auN	6051143.3	5989400.2	5907817.2
auNG	6175961.2	6097369.2	6217385.0
L50	3	3	3
LG50	3	3	3
L90	6	6	6
LG90	6	6	5
# misassemblies	184	194	213
# misassembled contigs	9	11	22
Misassembled contigs length	34906367	34817418	35710739
# local misassemblies	198	201	226
# scaffold gap ext. mis.	0	0	1
# scaffold gap loc. mis.	0	0	1
# possible TEs	26	28	28
# unaligned mis. contigs	0	0	1
# unaligned contigs	0 + 8 part	0 + 10 part	0 + 17 part
Unaligned length	1152725	1023311	1389990
Genome fraction (%)	96.733	96.808	96.691
Duplication ratio	1.021	1.021	1.047
# N's per 100 kbp	1.07	1.26	2.18
# mismatches per 100 kbp	187.80	189.12	191.21
# indels per 100 kbp	99.73	99.11	104.05
Largest alignment	3686258	3681687	3686258
Total aligned length	33744426	33779572	34590925
NA50	2203526	2203804	1859030
NGA50	2203526	2203804	1859030
NA90	246854	247061	78431
NGA90	253709	253709	249410
auNA	1786957.1	1788035.6	1662451.9
auNGA	1823816.9	1820268.0	1749563.8
LA50	7	7	7
LGA50	7	7	7
LA90	29	29	39
LGA90	27	27	29

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

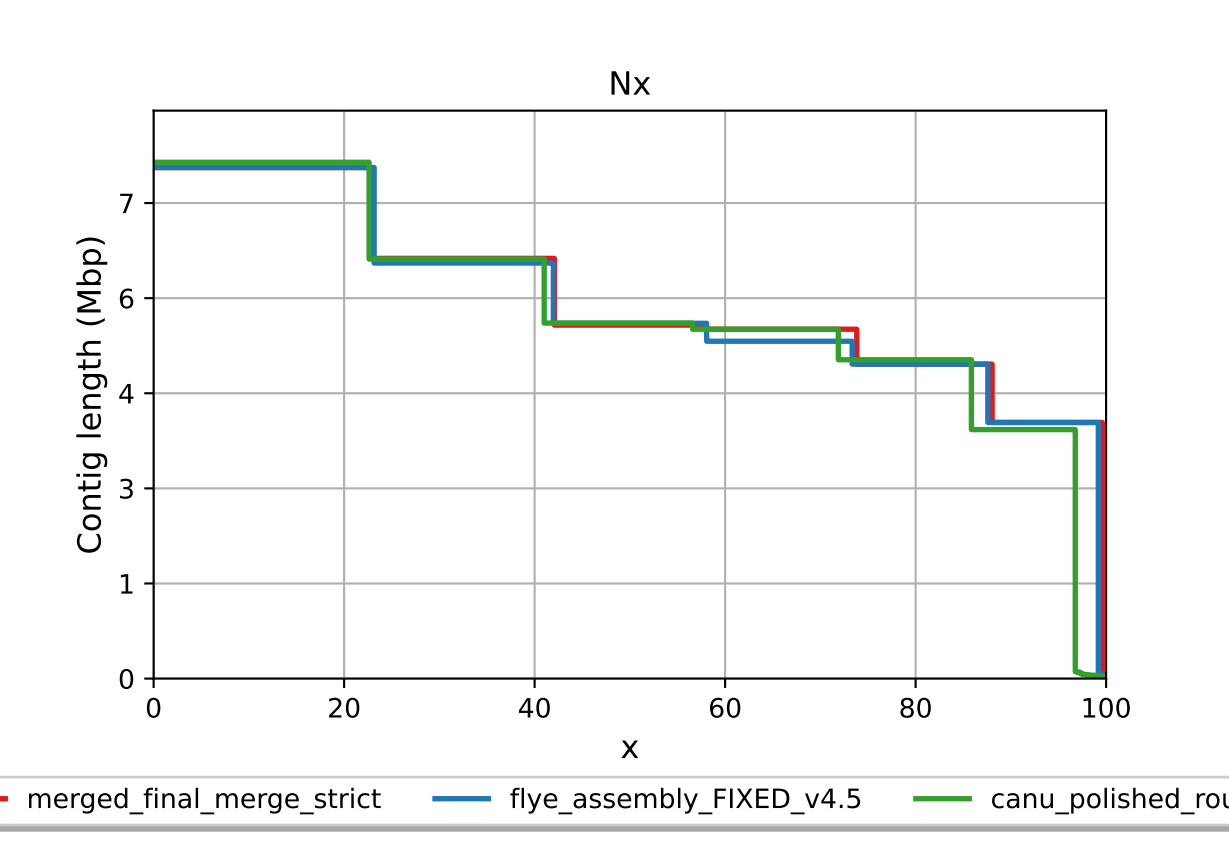
	merged_final_merge_strict	flye_assembly_FIXED_v4.5	canu_polished_round1
# misassemblies	184	194	213
# contig misassemblies	179	191	205
# c. relocations	105	108	117
# c. translocations	56	65	76
# c. inversions	18	18	12
# scaffold misassemblies	5	3	8
# s. relocations	3	2	4
# s. translocations	2	1	4
# s. inversions	0	0	0
# misassembled contigs	9	11	22
Misassembled contigs length	34906367	34817418	35710739
# local misassemblies	198	201	226
# scaffold gap ext. mis.	0	0	1
# scaffold gap loc. mis.	0	0	1
# possible TEs	26	28	28
# unaligned mis. contigs	0	0	1
# mismatches	63373	63883	66140
# indels	33653	33480	35991
# indels (<= 5 bp)	29302	29484	31106
# indels (> 5 bp)	4351	3996	4885
Indels length	392937	358495	387077

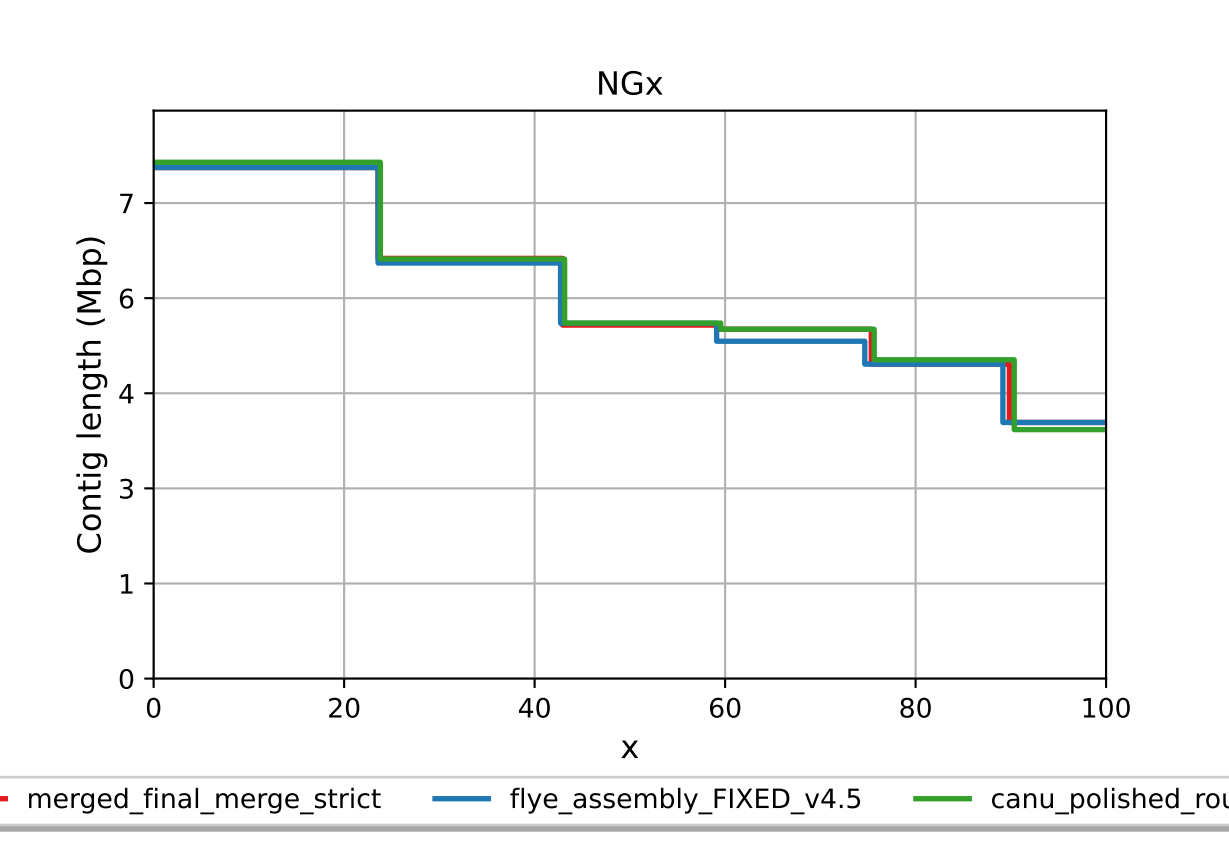
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

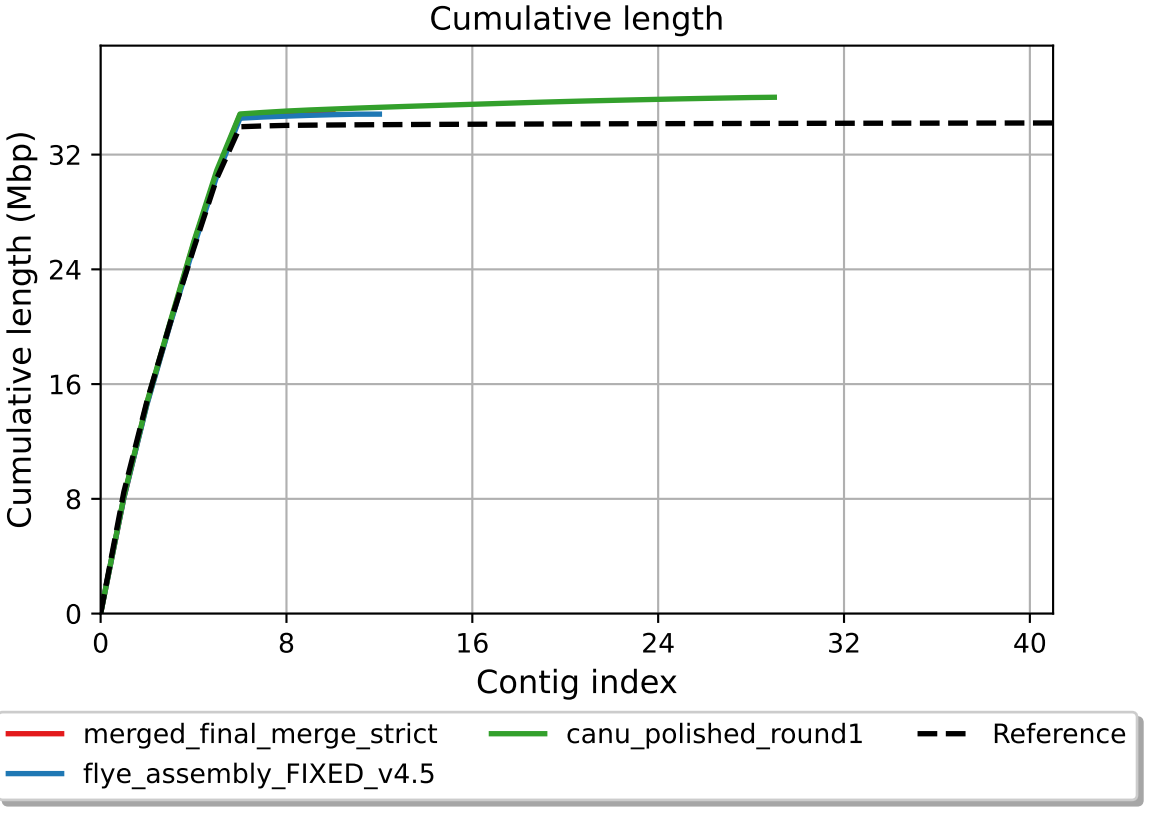
Unaligned report

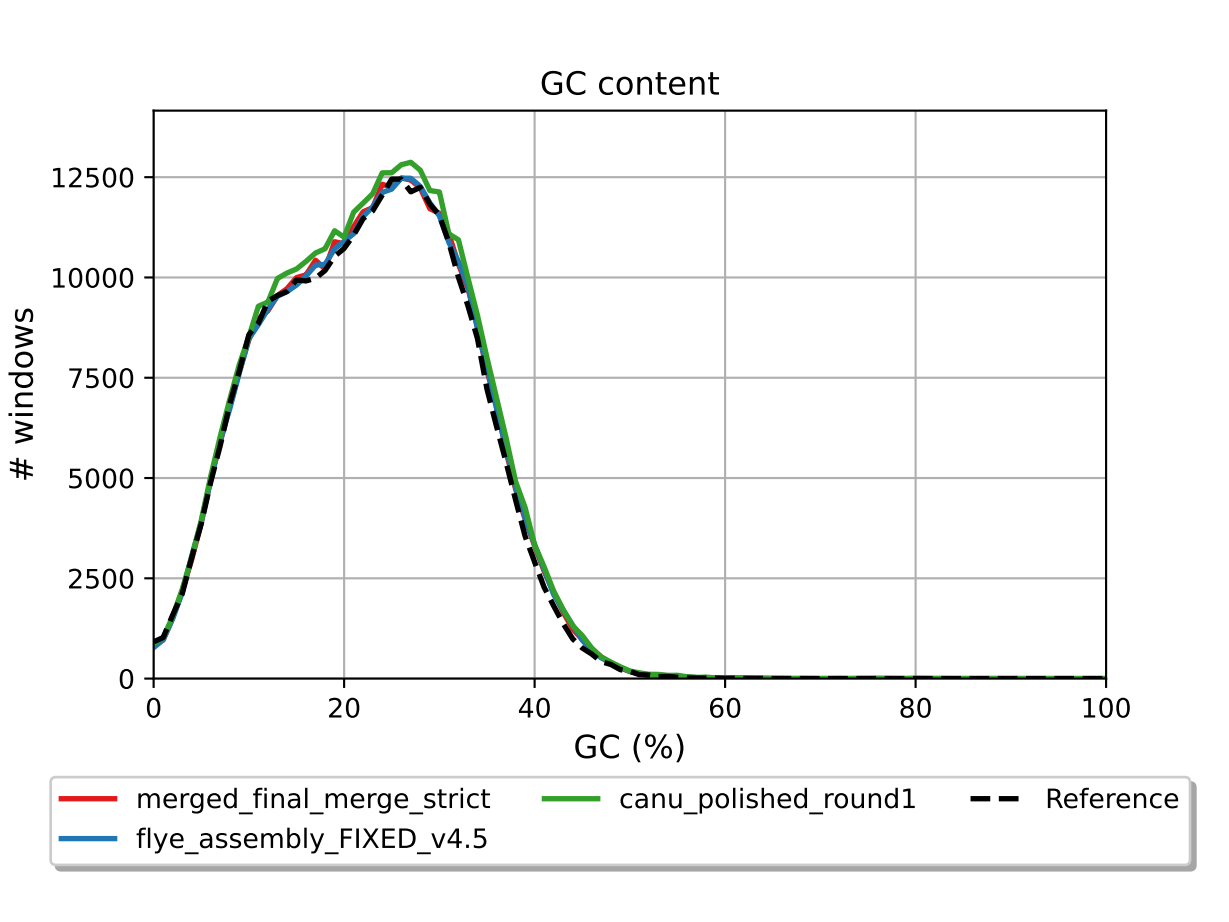
	merged_final_merge_strict	flye_assembly_FIXED_v4.5	canu_polished_round1
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	8	10	17
Partially unaligned length	1152725	1023311	1389990
# N's	375	438	786

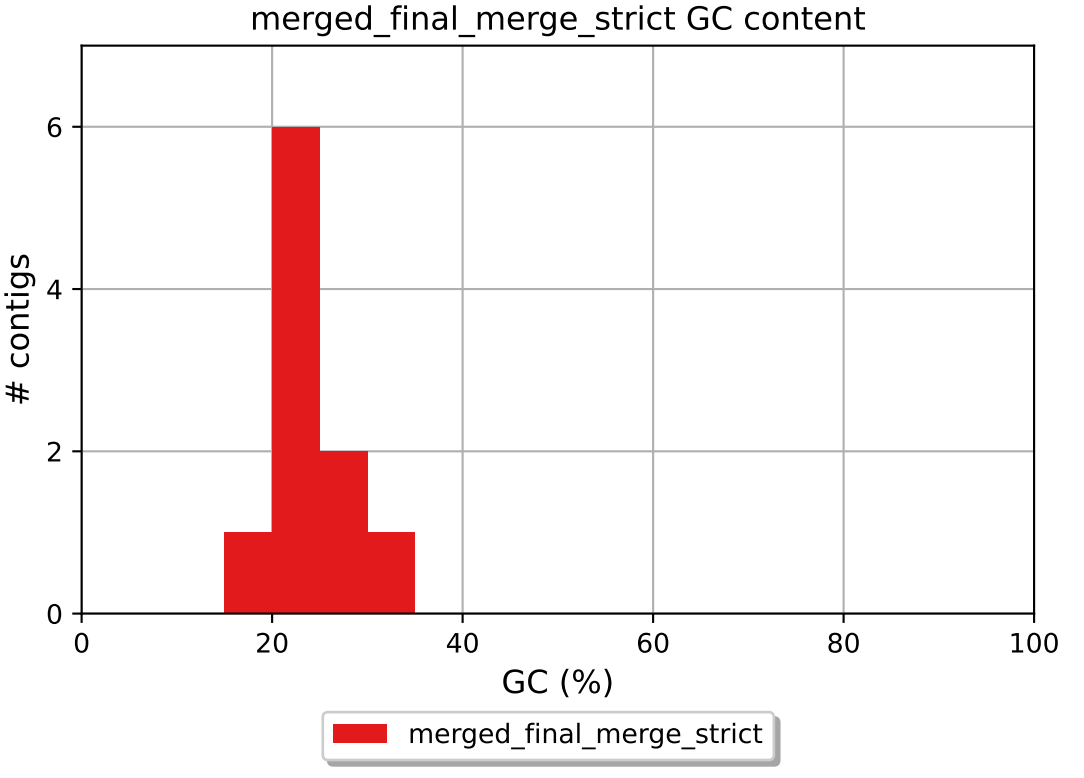
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

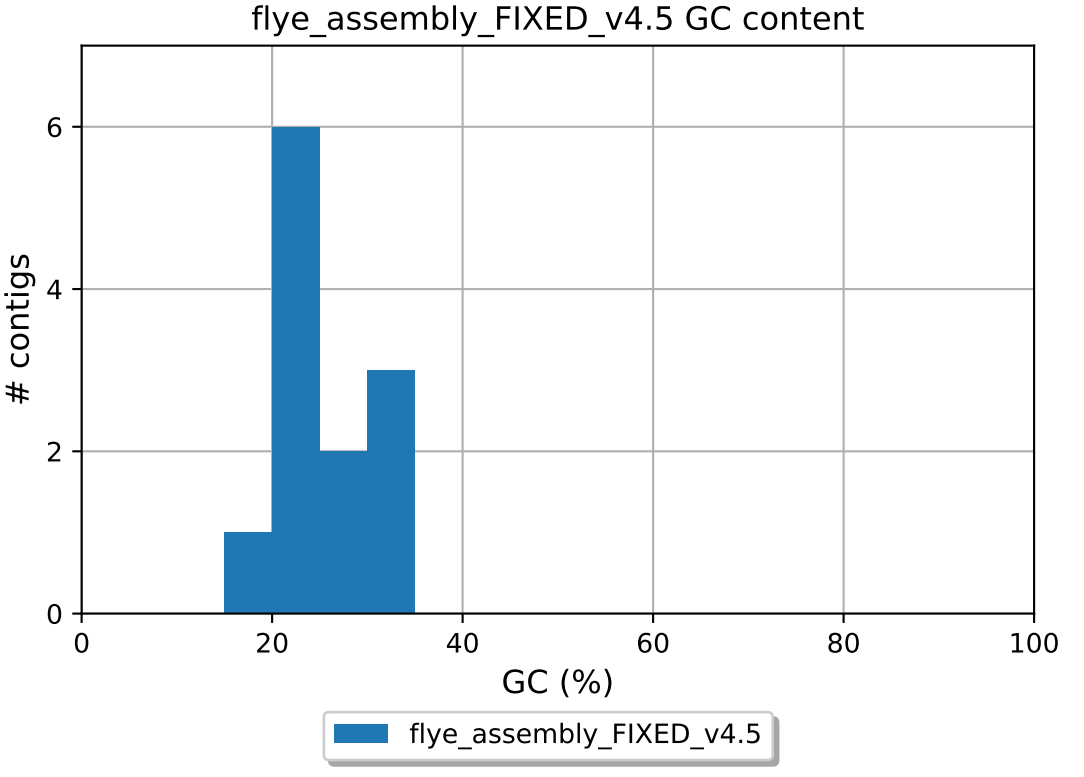

Nx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_rou

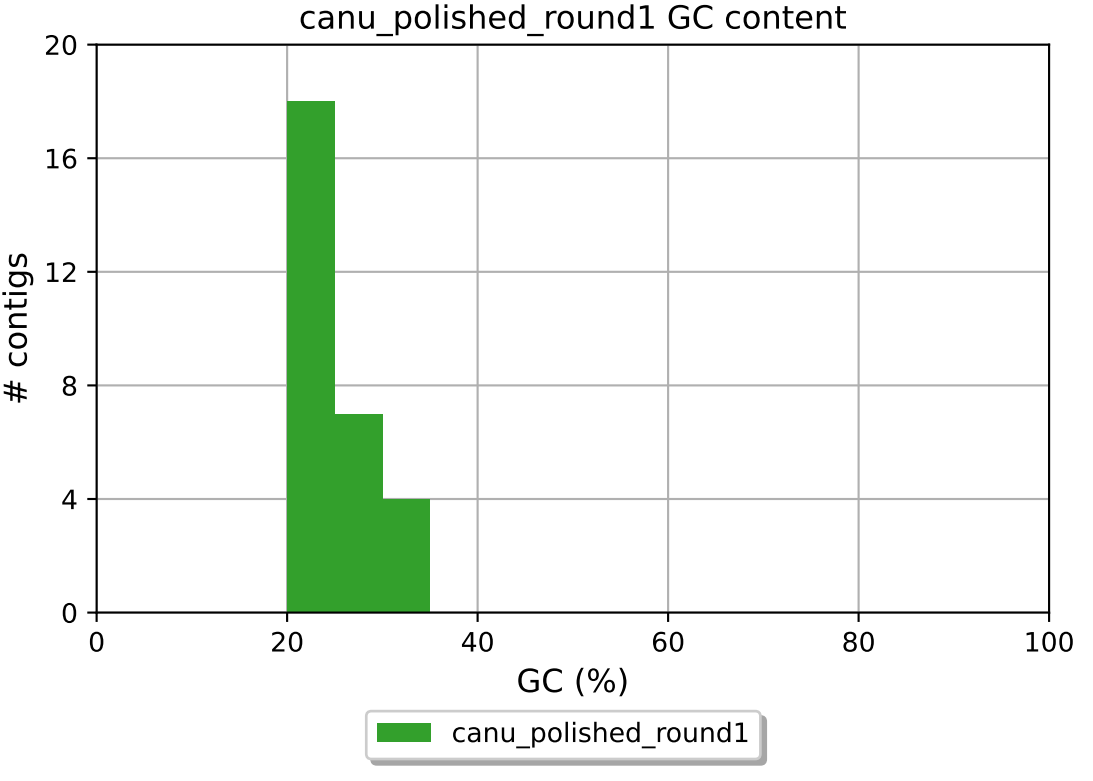

NGx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_rou

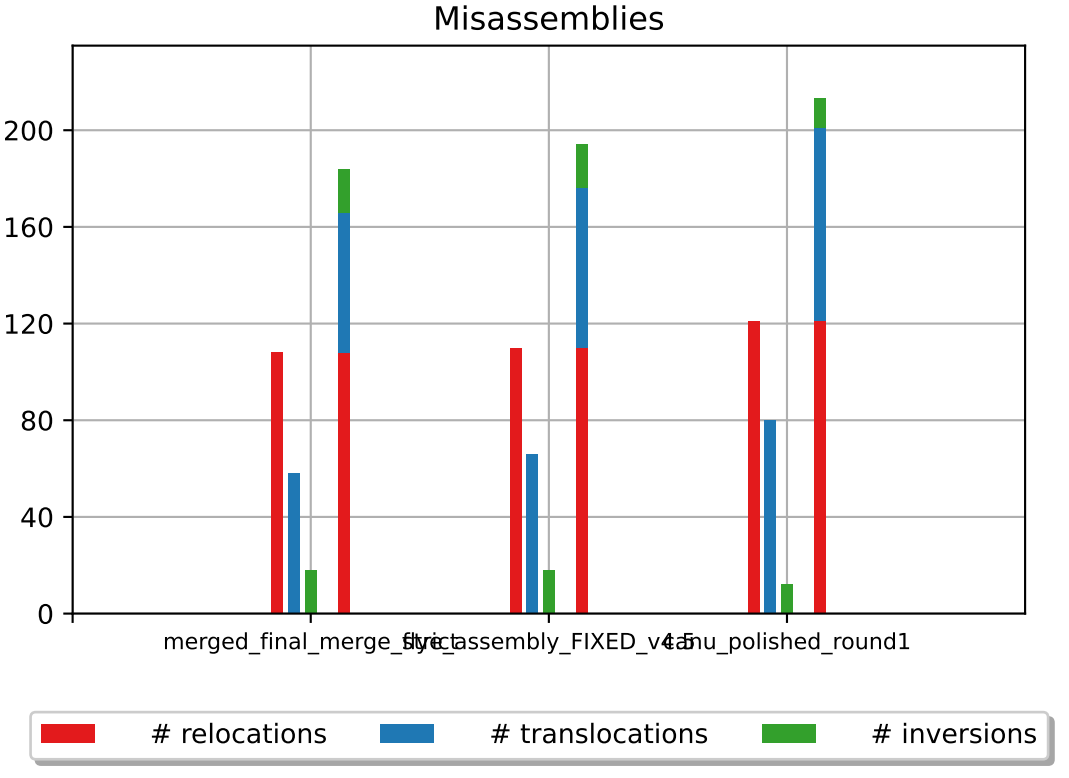

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_round1
Reference

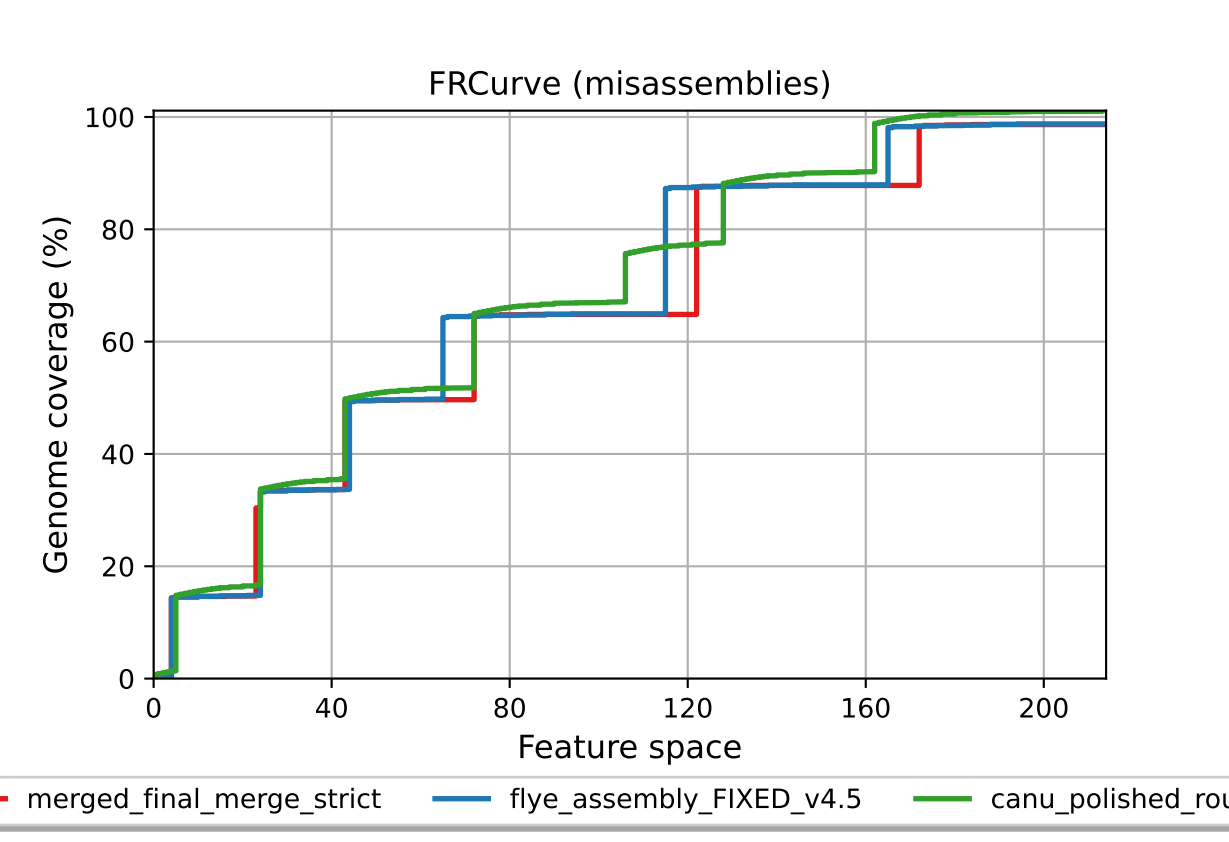

GC content
windows
12500
10000
7500
5000
2500
0
0
20
40
60
80
100
GC (%)
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_round1
Reference

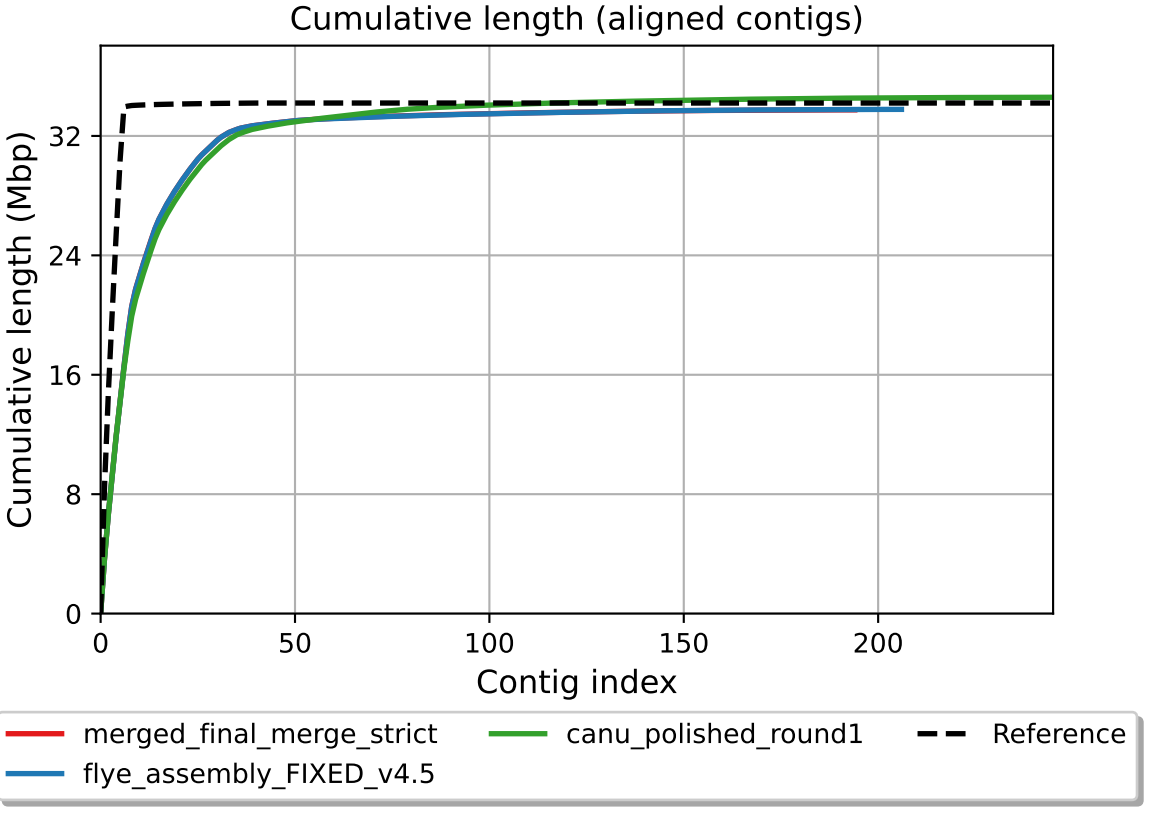

merged_final_merge_strict GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
merged_final_merge_strict

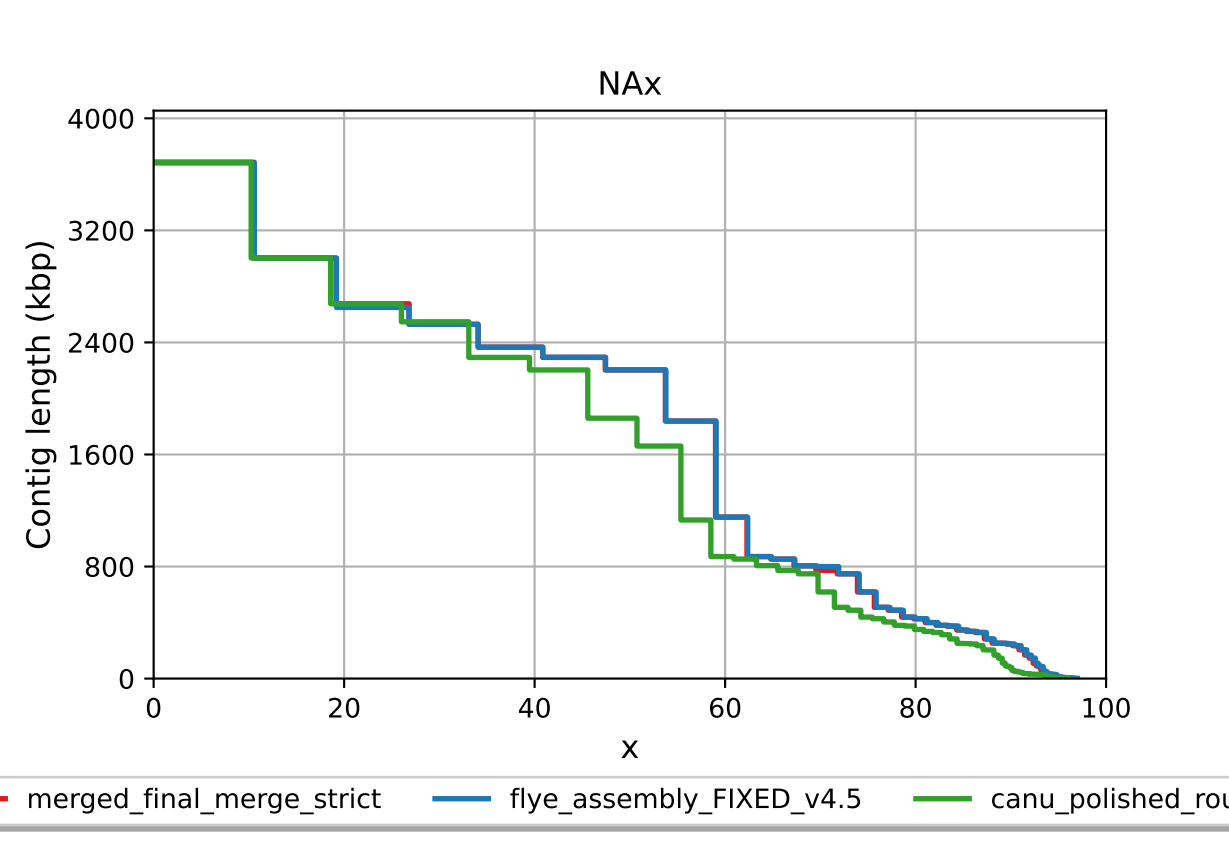

flye_assembly_FIXED_v4.5 GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
flye_assembly_FIXED_v4.5

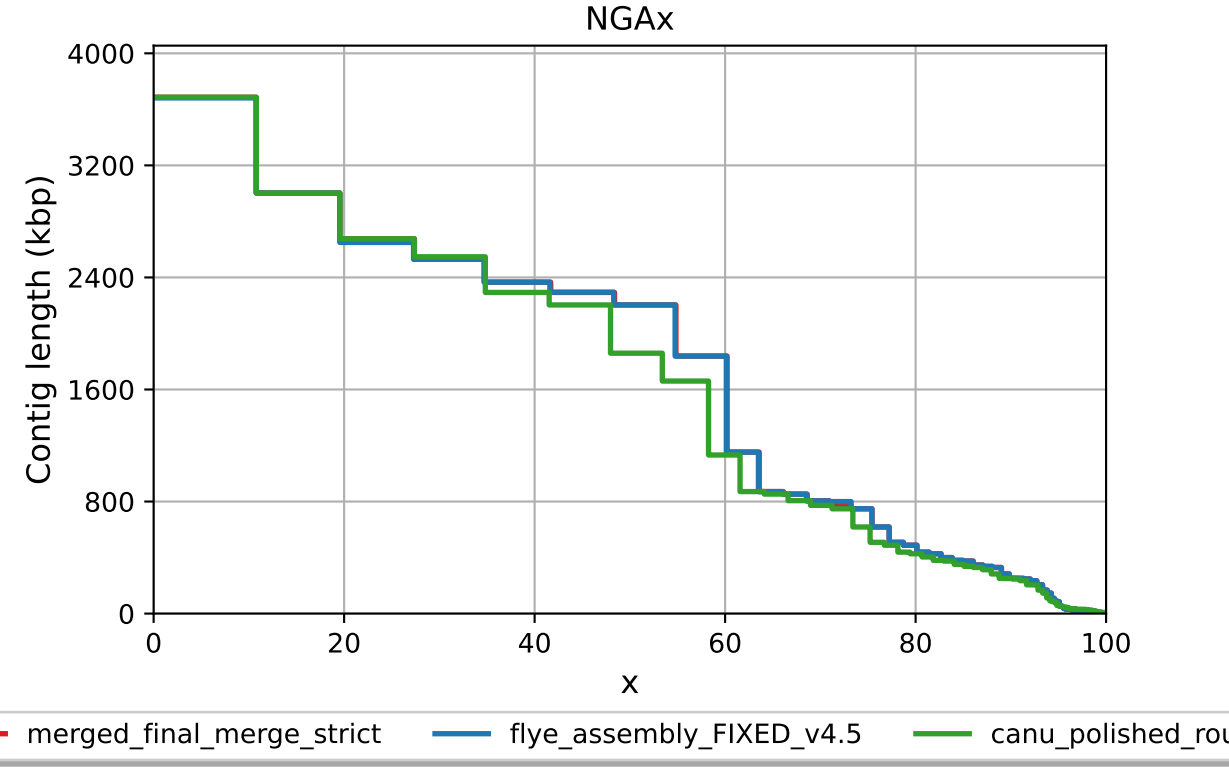

canu_polished_round1 GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
canu_polished_round1

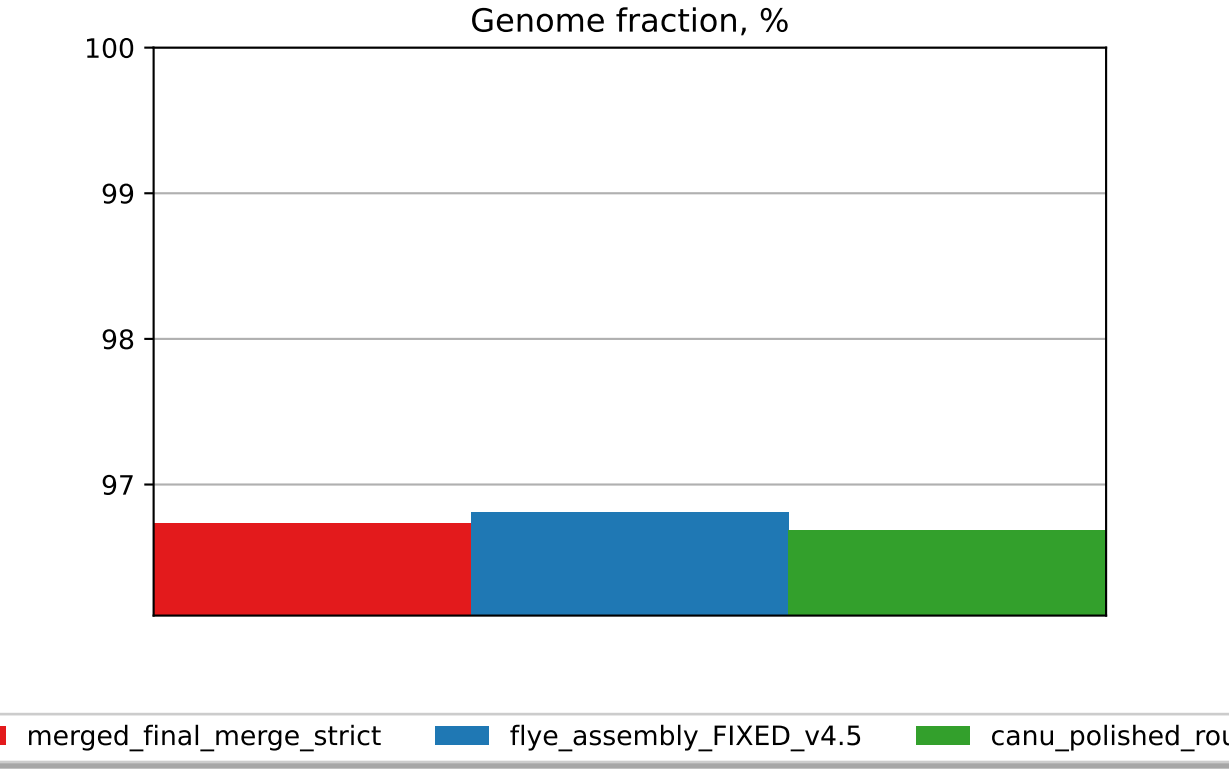

Misassemblies
200
160
120
80
40
0
merged_final_merge_style_t
strict_assembly_FIXED_v4.5
canu_polished_round1
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
40
80
120
160
200
Feature space
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_rou


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
8
16
24
32
0
50
100
150
200
Contig index
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_round1
Reference


NAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_rou


NGAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_rou


Genome fraction, %
100
99
98
97
merged_final_merge_strict
flye_assembly_FIXED_v4.5
canu_polished_rou