Report

	merged_canu_flye_merged	flye	canu
# contigs (>= 0 bp)	21	11	29
# contigs (>= 1000 bp)	21	11	29
# contigs (>= 5000 bp)	21	10	29
# contigs (>= 10000 bp)	21	10	29
# contigs (>= 25000 bp)	21	10	28
# contigs (>= 50000 bp)	13	8	18
Total length (>= 0 bp)	40559038	34861082	35997303
Total length (>= 1000 bp)	40559038	34861082	35997303
Total length (>= 5000 bp)	40559038	34856925	35997303
Total length (>= 10000 bp)	40559038	34856925	35997303
Total length (>= 25000 bp)	40559038	34856925	35978808
Total length (>= 50000 bp)	40260229	34777534	35607977
# contigs	21	11	29
Largest contig	12245470	12197133	8143141
Total length	40559038	34861082	35997303
Reference length	34204973	34204973	34204973
GC (%)	22.74	22.74	22.76
Reference GC (%)	22.44	22.44	22.44
N50	8888792	8060236	5606788
NG50	8888792	8060236	5606788
N90	4959406	4039478	3926766
NG90	5510024	4039478	5028520
auN	8636202.9	8117212.2	5907817.2
auNG	10240501.6	8272914.0	6217385.0
L50	2	2	3
LG50	2	2	3
L90	5	5	6
LG90	4	5	5
# misassemblies	730	675	741
# misassembled contigs	19	9	26
Misassembled contigs length	40470480	34801372	35873046
# local misassemblies	162	161	163
# scaffold gap ext. mis.	2	1	2
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 10 part	0 + 9 part	0 + 14 part
Unaligned length	554802	426212	553592
Genome fraction (%)	97.120	97.172	97.059
Duplication ratio	1.202	1.035	1.066
# N's per 100 kbp	1.69	1.26	2.18
# mismatches per 100 kbp	130.37	139.15	142.25
# indels per 100 kbp	113.43	109.09	117.35
Largest alignment	1454560	1454451	1454400
Total aligned length	39906093	34374100	35379816
NA50	409129	404186	387049
NGA50	539282	404961	404880
NA90	57648	78783	34537
NGA90	208928	94427	90226
auNA	475347.1	476499.9	460561.4
auNGA	563649.7	485640.0	484694.7
LA50	30	27	28
LGA50	23	26	26
LA90	111	94	117
LGA90	68	87	89

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

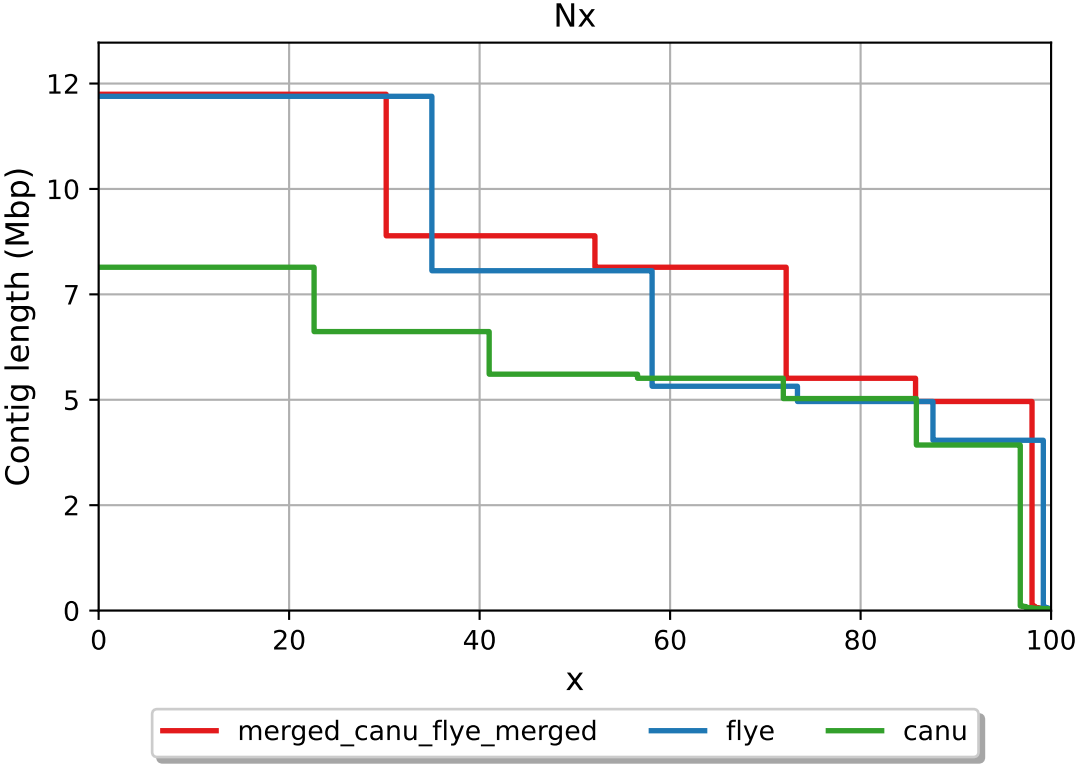
	merged_canu_flye_merged	flye	canu
# misassemblies	730	675	741
# contig misassemblies	723	671	731
# c. relocations	299	271	296
# c. translocations	410	388	424
# c. inversions	14	12	11
# scaffold misassemblies	7	4	10
# s. relocations	5	2	5
# s. translocations	2	2	5
# s. inversions	0	0	0
# misassembled contigs	19	9	26
Misassembled contigs length	40470480	34801372	35873046
# local misassemblies	162	161	163
# scaffold gap ext. mis.	2	1	2
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	52026	47831	50328
# indels	45266	37498	41517
# indels (<= 5 bp)	40112	33409	36525
# indels (> 5 bp)	5154	4089	4992
Indels length	150742	123237	143403

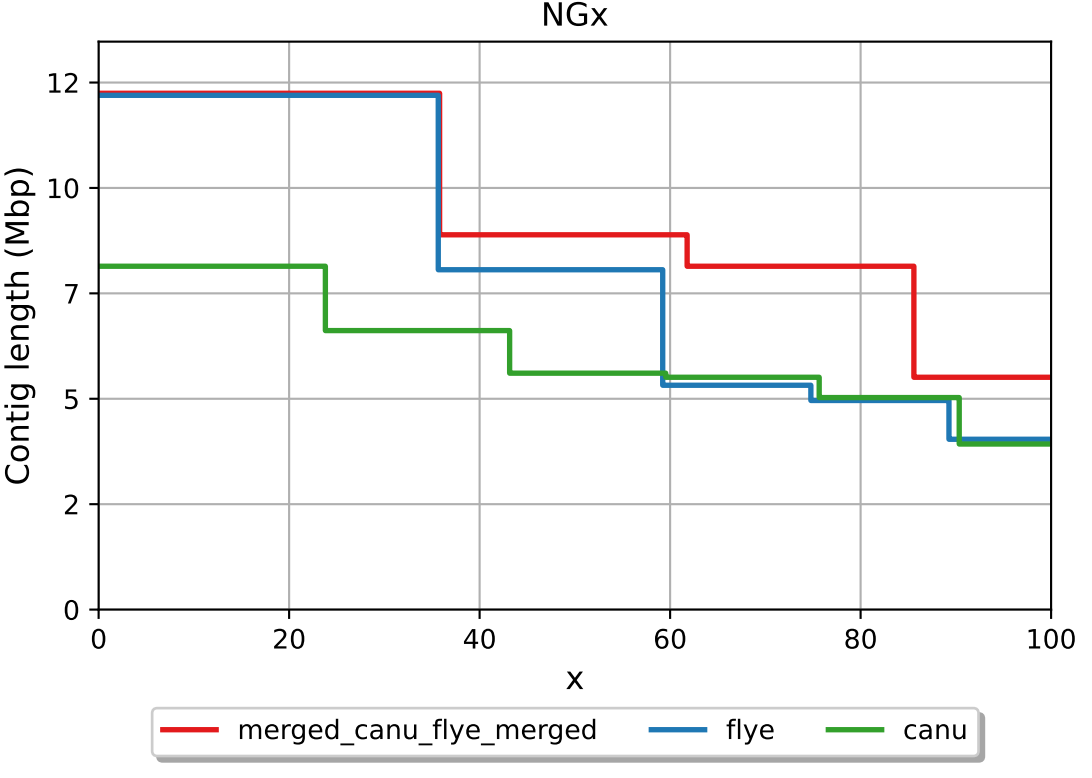
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

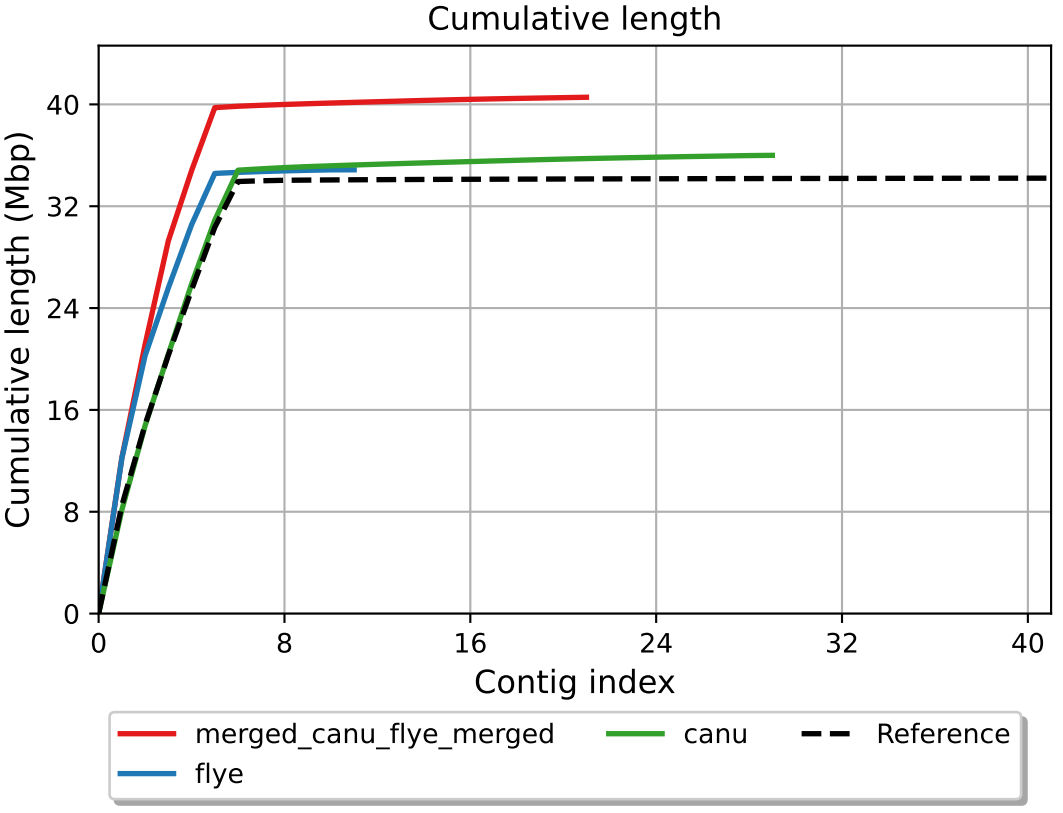
Unaligned report

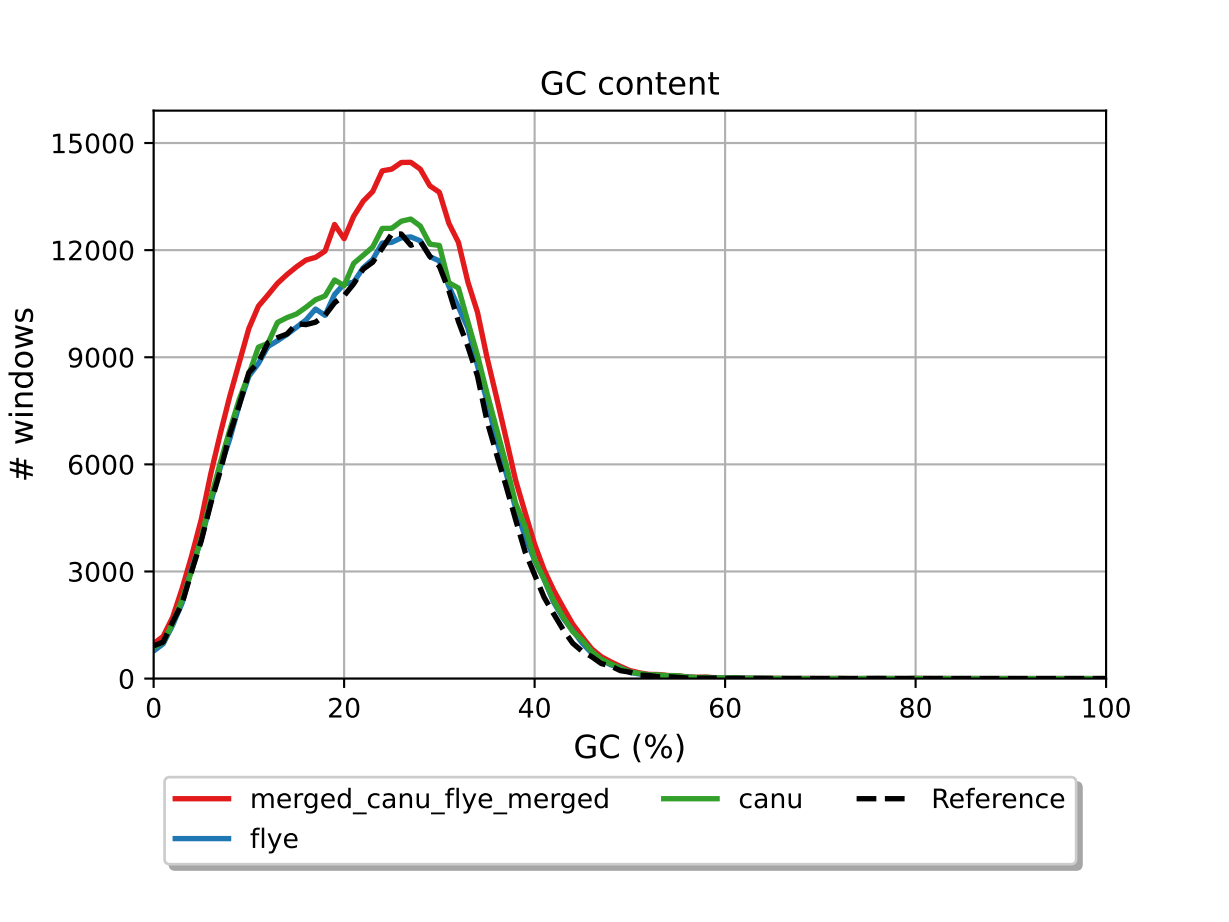
	merged_canu_flye_merged	flye	canu
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	10	9	14
Partially unaligned length	554802	426212	553592
# N's	687	438	786

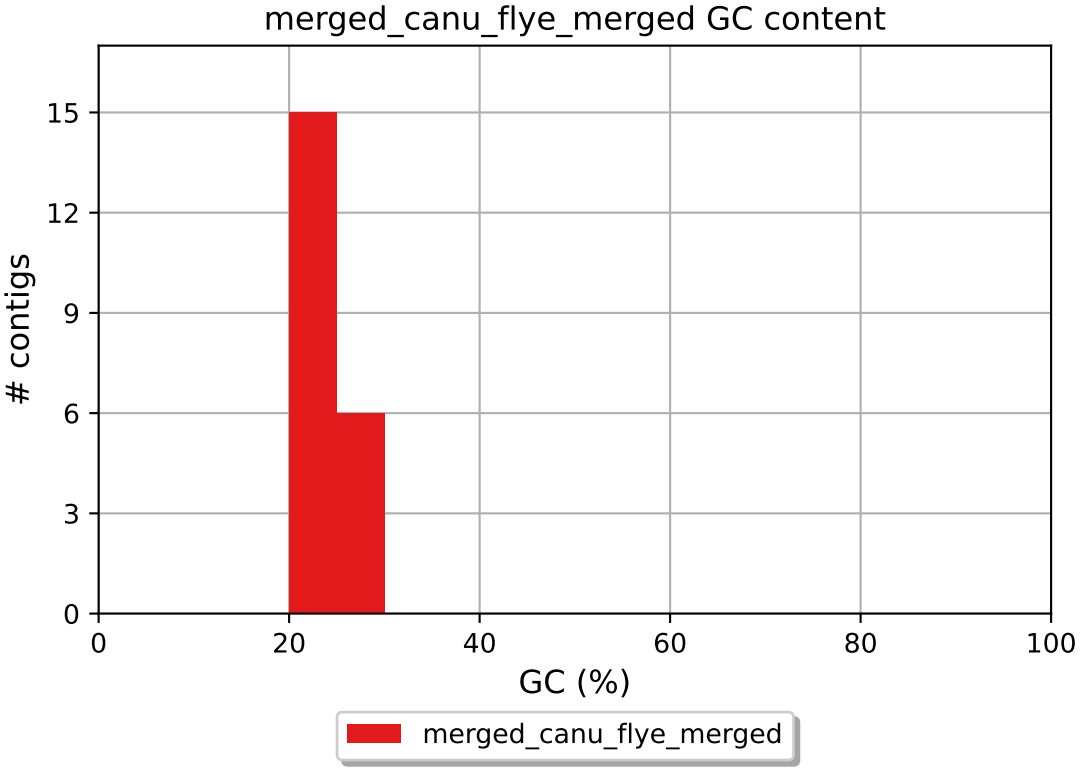
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

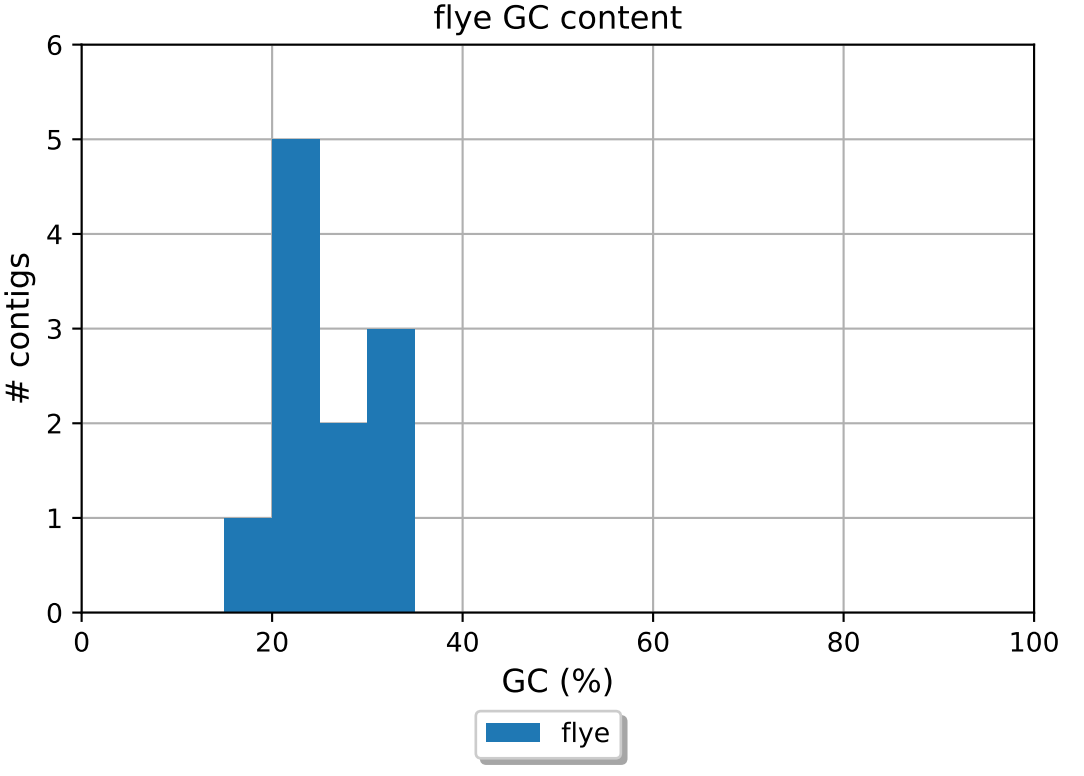

Nx
Contig length (Mbp)
12
10
7
5
2
0
0
20
40
60
80
100
x
merged_canu_flye_merged
flye
canu

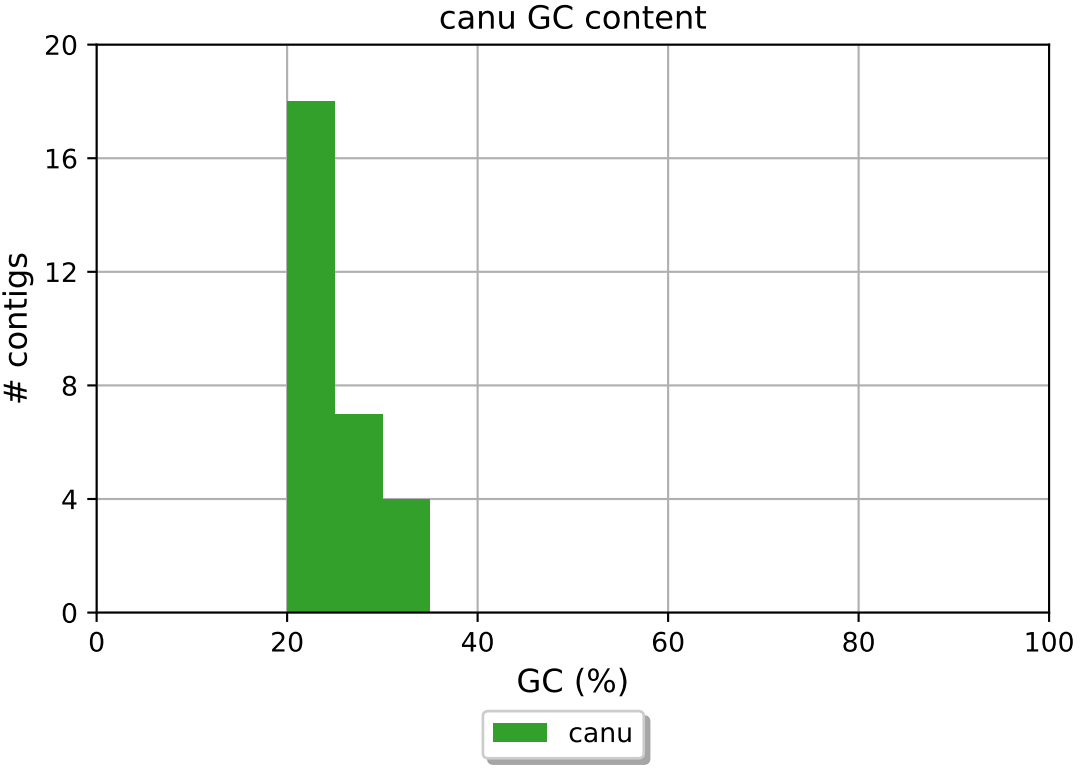

NGx
Contig length (Mbp)
12
10
7
5
2
0
0
20
40
60
80
100
x
merged_canu_flye_merged
flye
canu

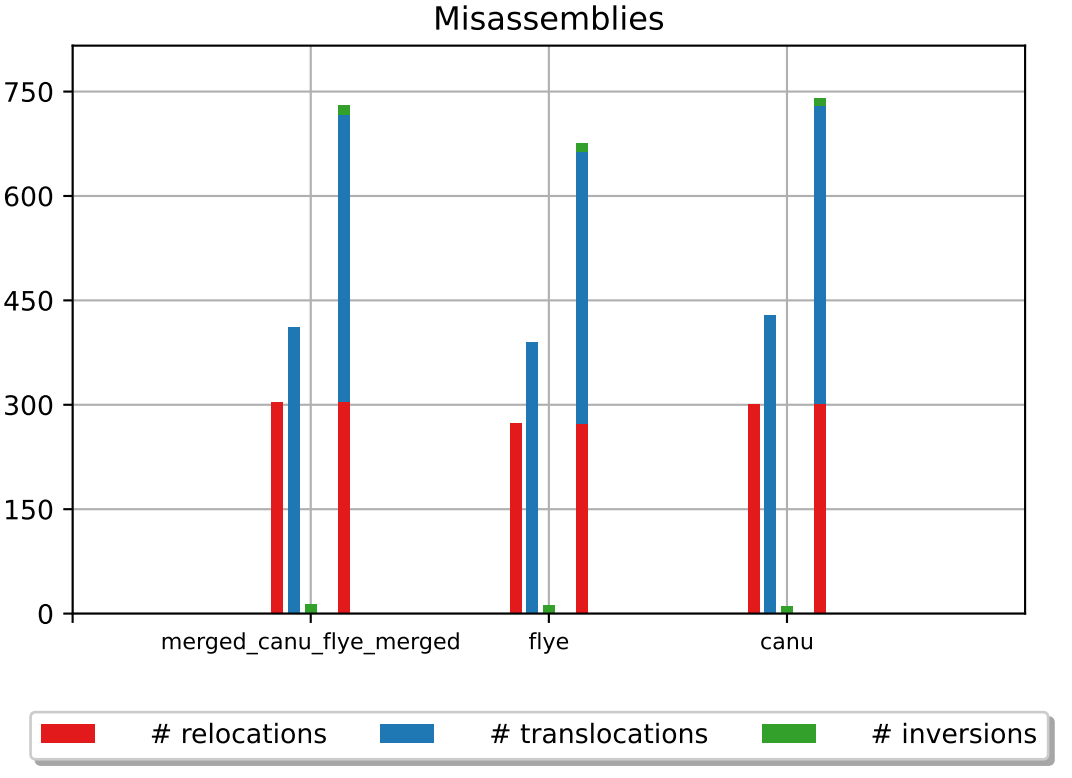

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
40
Contig index
merged_canu_flye_merged
flye
canu
Reference

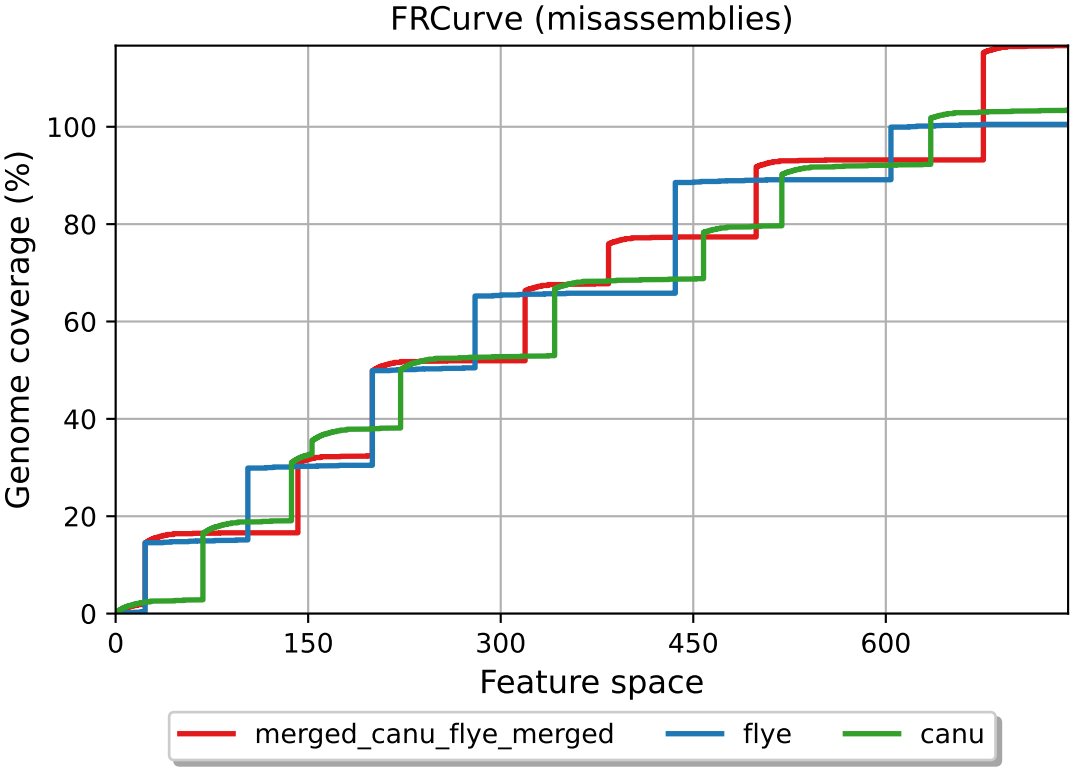

GC content
15000
12000
9000
6000
3000
0
windows
0
20
40
60
80
100
GC (%)
merged_canu_flye_merged
canu
Reference
flye

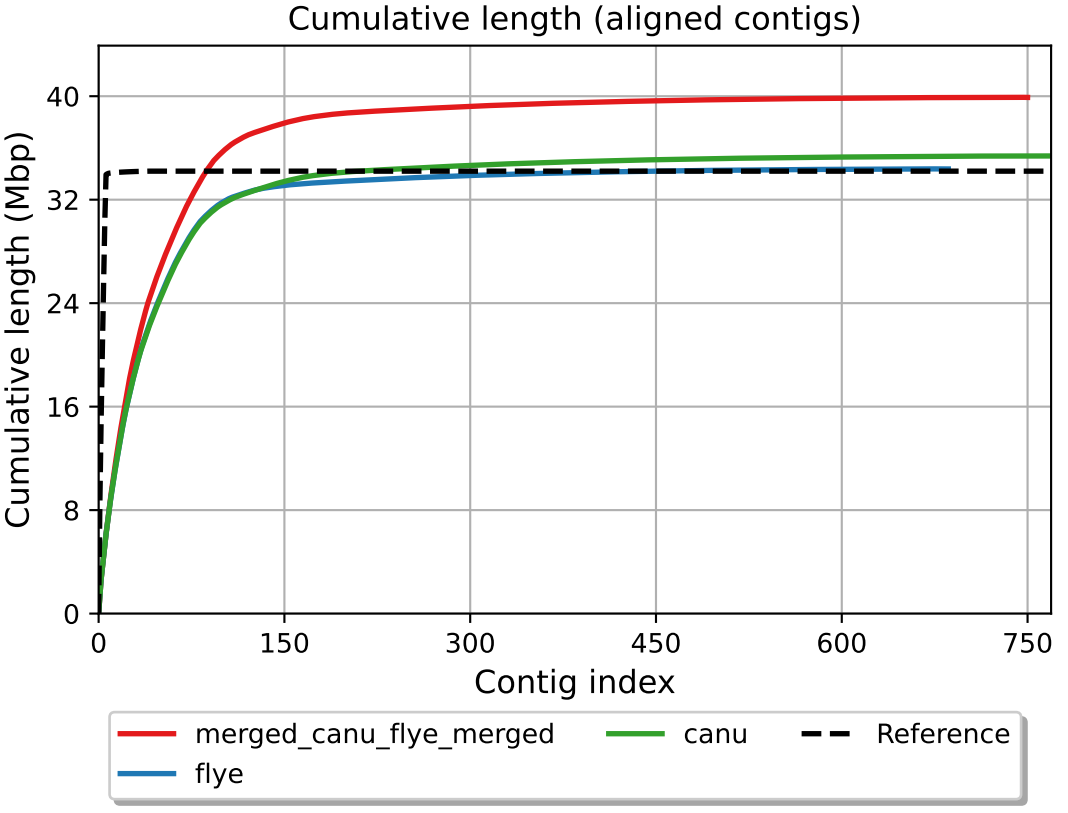

merged_canu_flye_merged GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
merged_canu_flye_merged

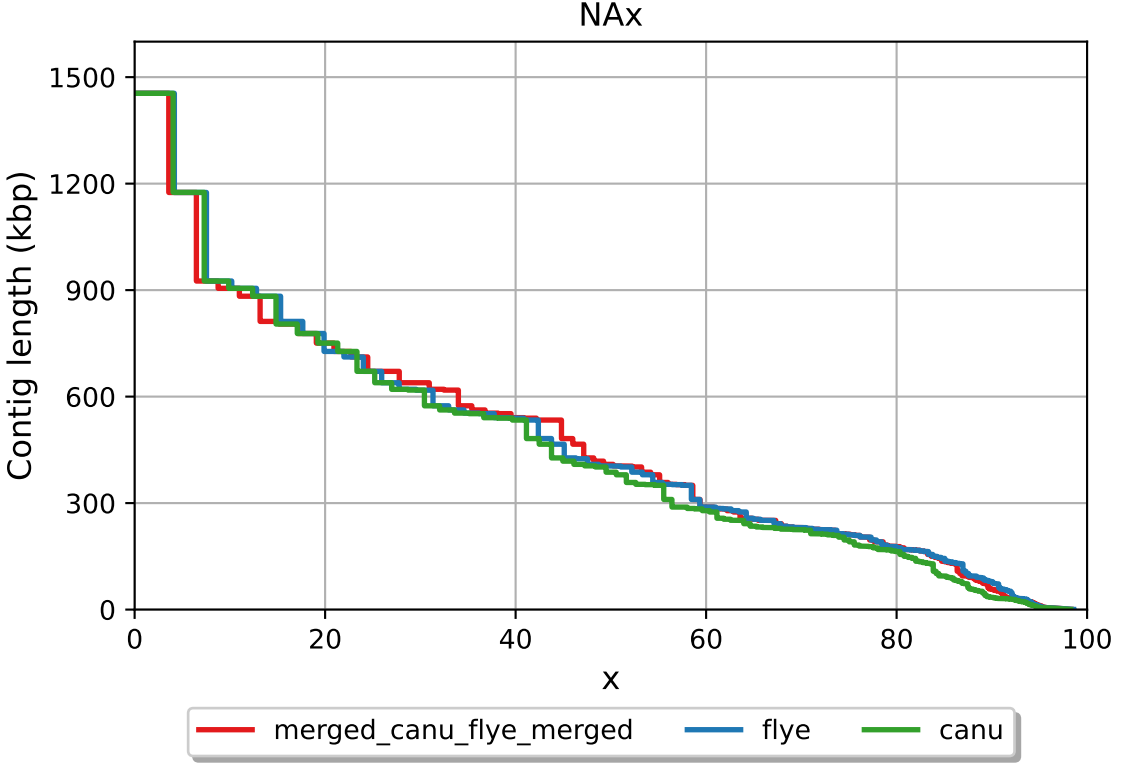

flye GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
flye

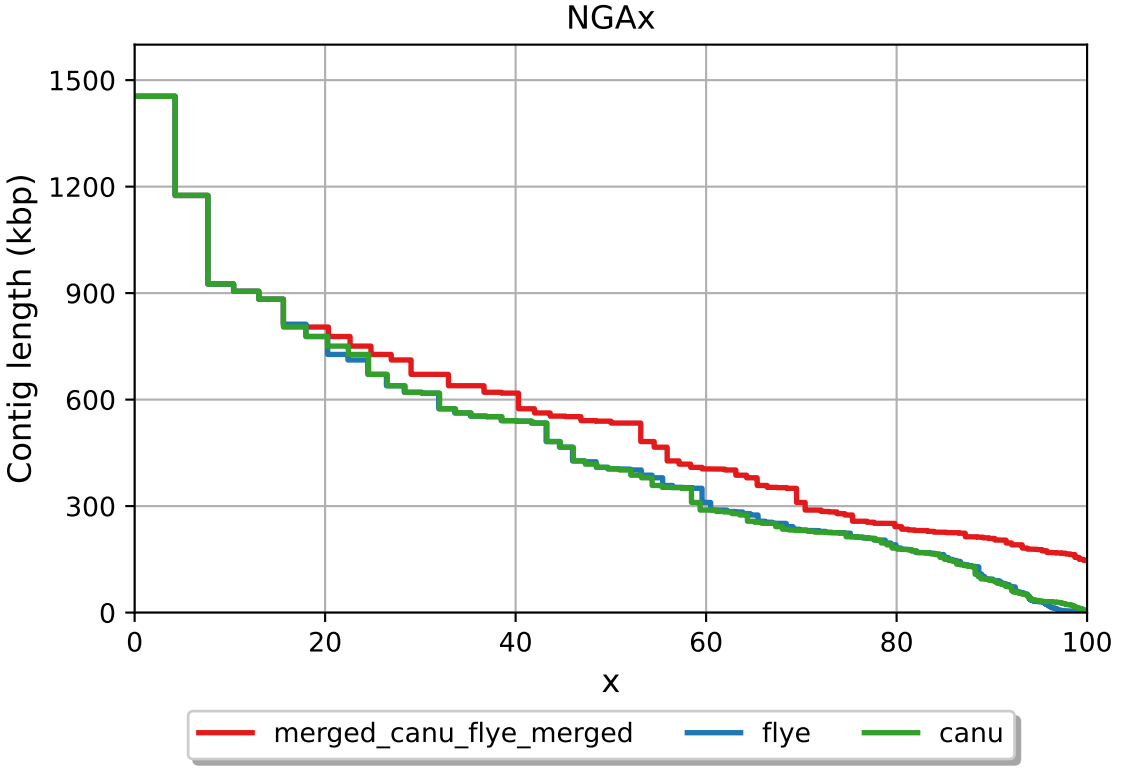

canu GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
canu

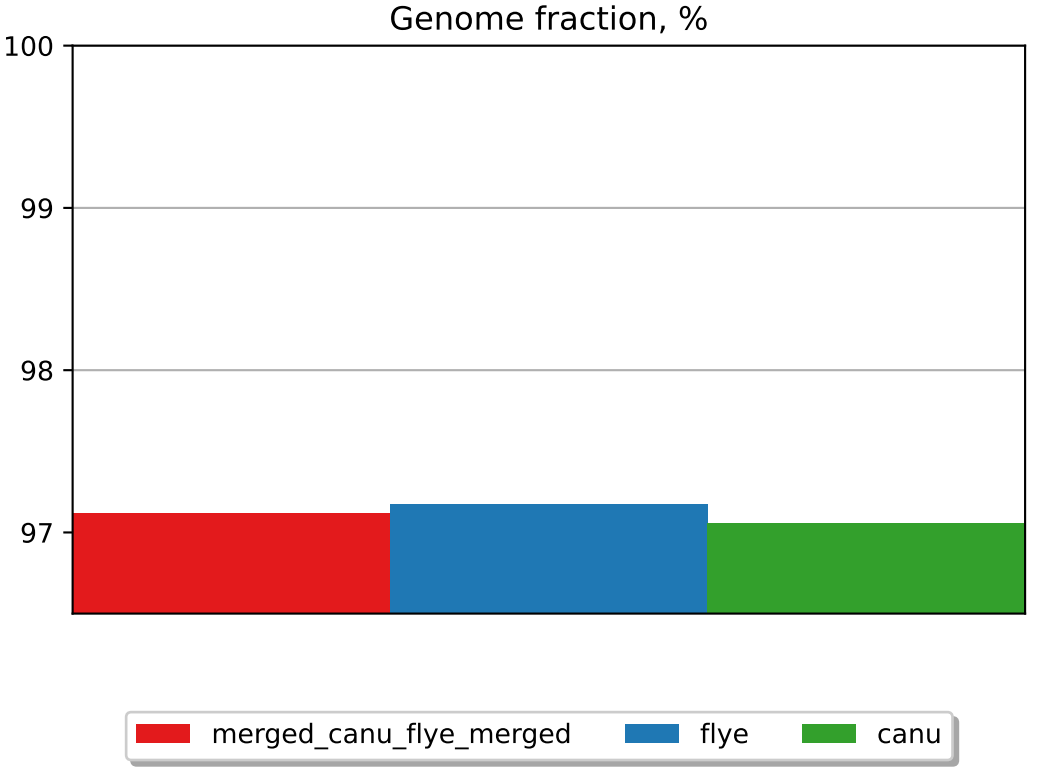

Misassemblies
750
600
450
300
150
0
merged_canu_flye_merged
flye
canu
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
150
300
450
600
Feature space
merged_canu_flye_merged
flye
canu


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
8
16
24
32
40
0
150
300
450
600
750
Contig index
merged_canu_flye_merged
canu
Reference
flye


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
merged_canu_flye_merged
flye
canu


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
merged_canu_flye_merged
flye
canu


Genome fraction, %
100
99
98
97
merged_canu_flye_merged
flye
canu