Report

	canu	flye	shasta
# contigs (>= 0 bp)	41	16	16
# contigs (>= 1000 bp)	41	16	16
# contigs (>= 5000 bp)	41	15	15
# contigs (>= 10000 bp)	41	15	13
# contigs (>= 25000 bp)	40	15	11
# contigs (>= 50000 bp)	26	13	11
Total length (>= 0 bp)	35577586	34532450	33046224
Total length (>= 1000 bp)	35577586	34532450	33046224
Total length (>= 5000 bp)	35577586	34528293	33041364
Total length (>= 10000 bp)	35577586	34528293	33026887
Total length (>= 25000 bp)	35559156	34528293	33003033
Total length (>= 50000 bp)	35019221	34449109	33003033
# contigs	41	16	16
Largest contig	5884780	12078680	11062869
Total length	35577586	34532450	33046224
Reference length	34204973	34204973	34204973
GC (%)	23.04	22.95	22.91
Reference GC (%)	22.44	22.44	22.44
N50	3312350	3363344	6899527
NG50	3312350	3363344	6899527
N90	1236530	1717044	1199305
NG90	1756805	1717044	1177246
auN	3299140.5	6181024.9	6398498.1
auNG	3431531.9	6240201.8	6181738.5
L50	4	3	2
LG50	4	3	2
L90	11	8	7
LG90	10	8	8
# misassemblies	721	663	636
# misassembled contigs	38	14	11
Misassembled contigs length	35454535	34472865	33003033
# local misassemblies	164	157	136
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 20 part	0 + 14 part	0 + 8 part
Unaligned length	554700	426867	354940
Genome fraction (%)	97.060	97.163	93.504
Duplication ratio	1.054	1.024	1.020
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	125.02	127.02	131.07
# indels per 100 kbp	419.22	395.63	374.06
Largest alignment	1435619	1440049	1442157
Total aligned length	34961051	34002985	32597422
NA50	396866	400706	401295
NGA50	399719	401037	398753
NA90	33921	77988	78116
NGA90	77740	82801	30838
auNA	455858.8	471592.5	476557.5
auNGA	474152.0	476107.5	460413.4
LA50	28	27	25
LGA50	26	26	26
LA90	117	94	92
LGA90	93	91	112

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

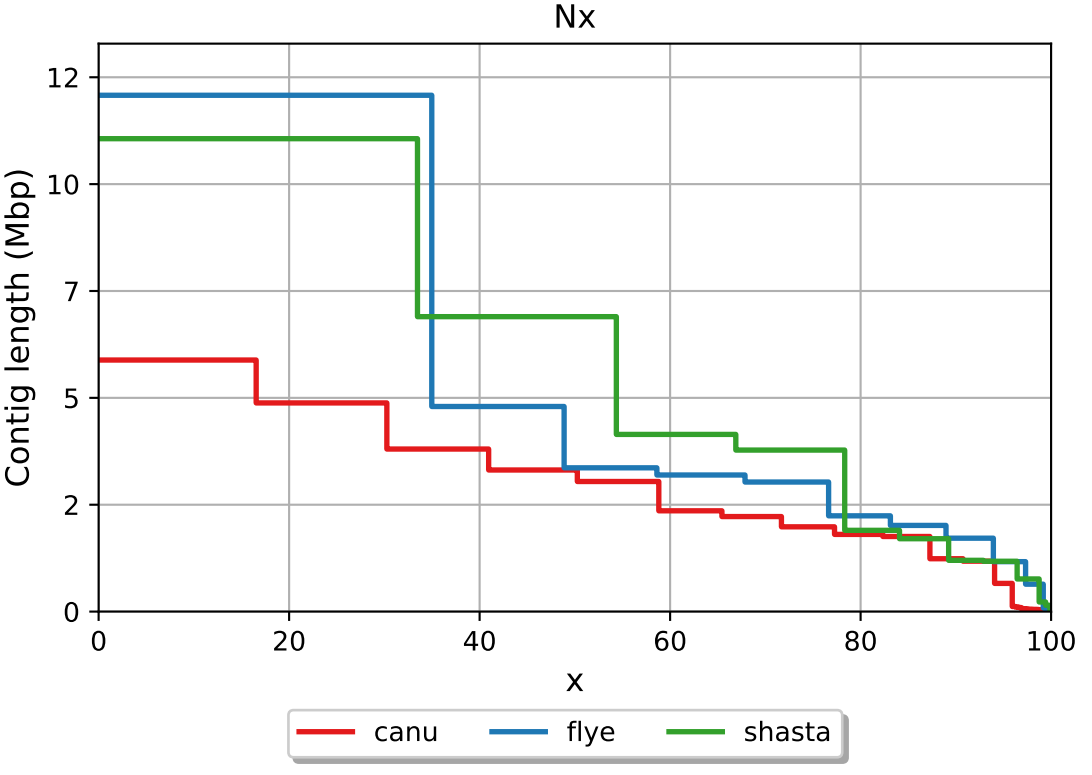
	canu	flye	shasta
# misassemblies	721	663	636
# contig misassemblies	721	663	636
# c. relocations	288	267	259
# c. translocations	421	386	365
# c. inversions	12	10	12
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	38	14	11
Misassembled contigs length	35454535	34472865	33003033
# local misassemblies	164	157	136
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	43709	43189	42725
# indels	146564	134525	121935
# indels (<= 5 bp)	122855	120385	111855
# indels (> 5 bp)	23709	14140	10080
Indels length	529209	415684	372359

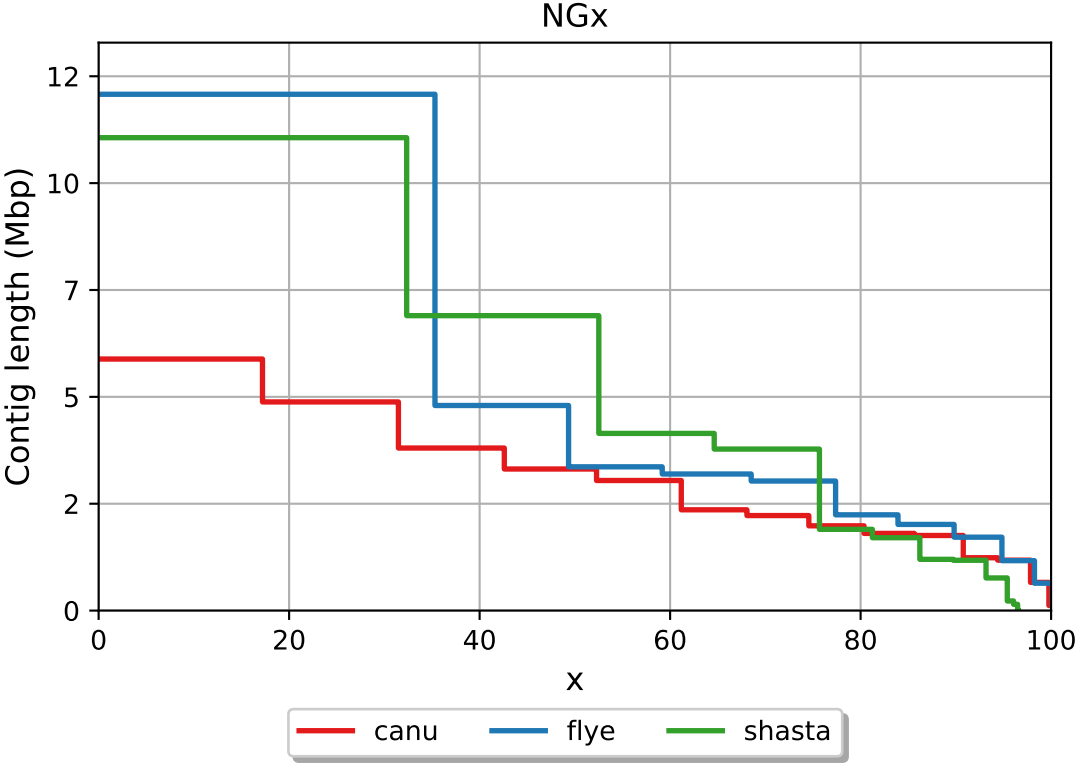
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

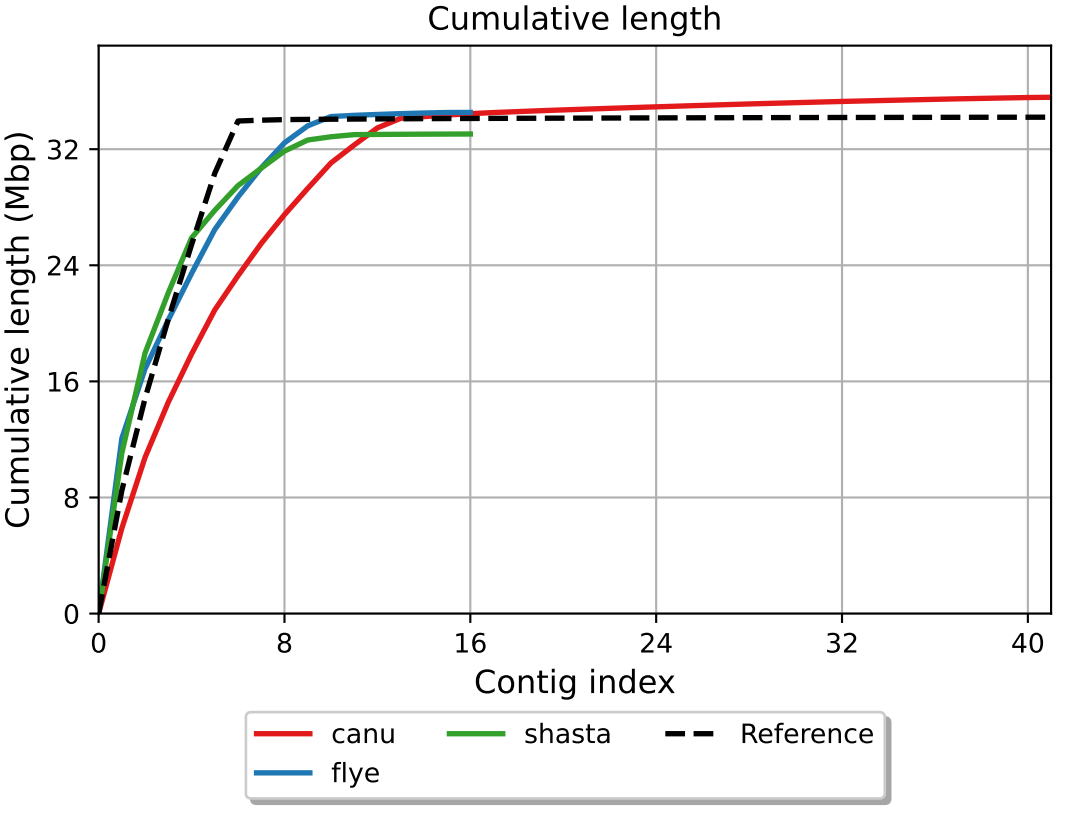
Unaligned report

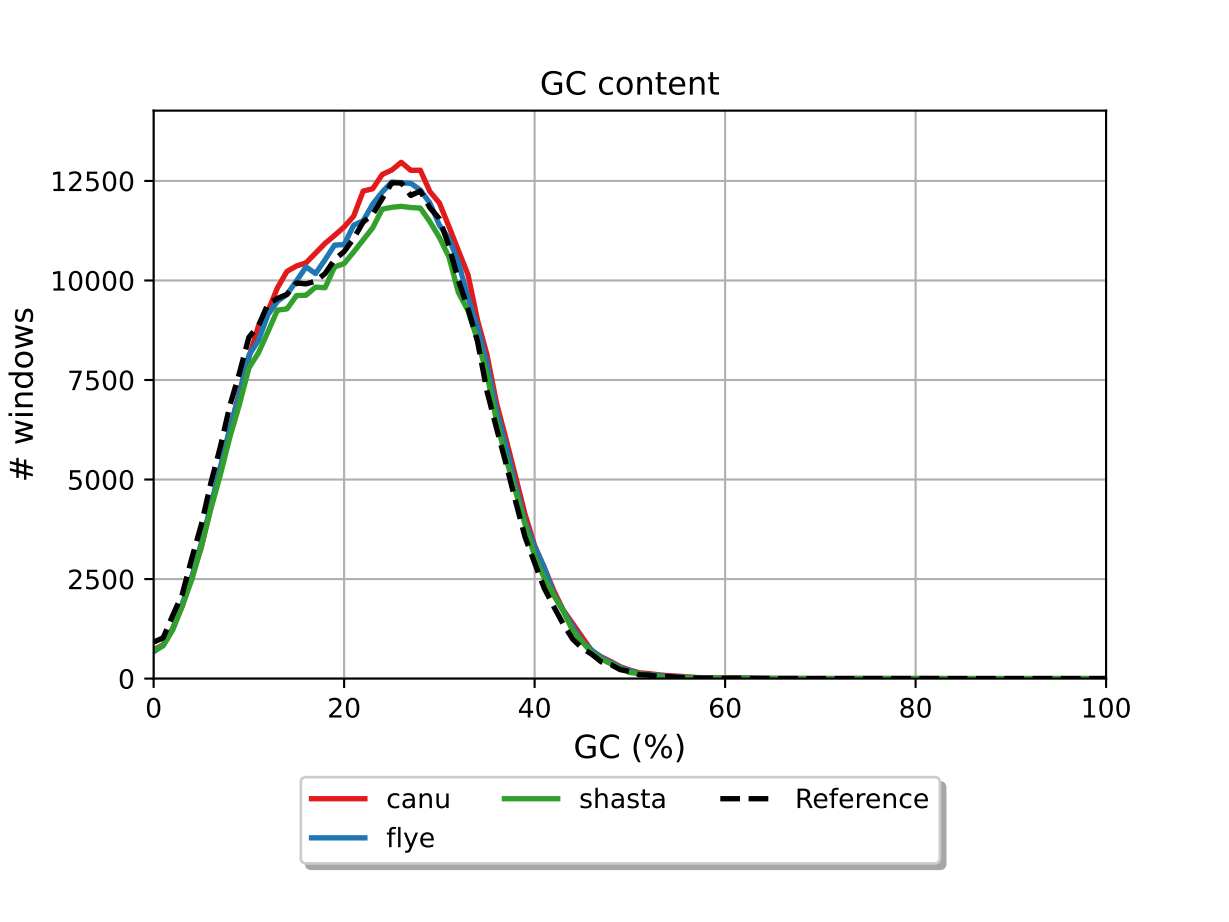
	canu	flye	shasta
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	20	14	8
Partially unaligned length	554700	426867	354940
# N's	0	0	0

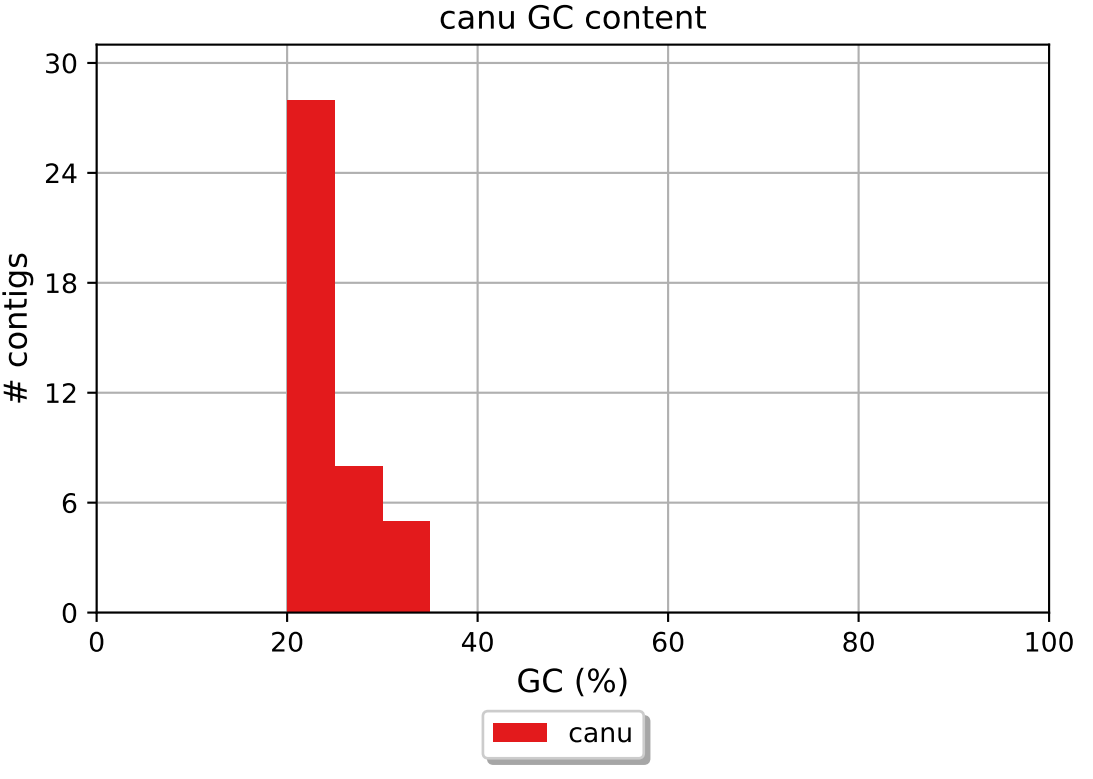
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

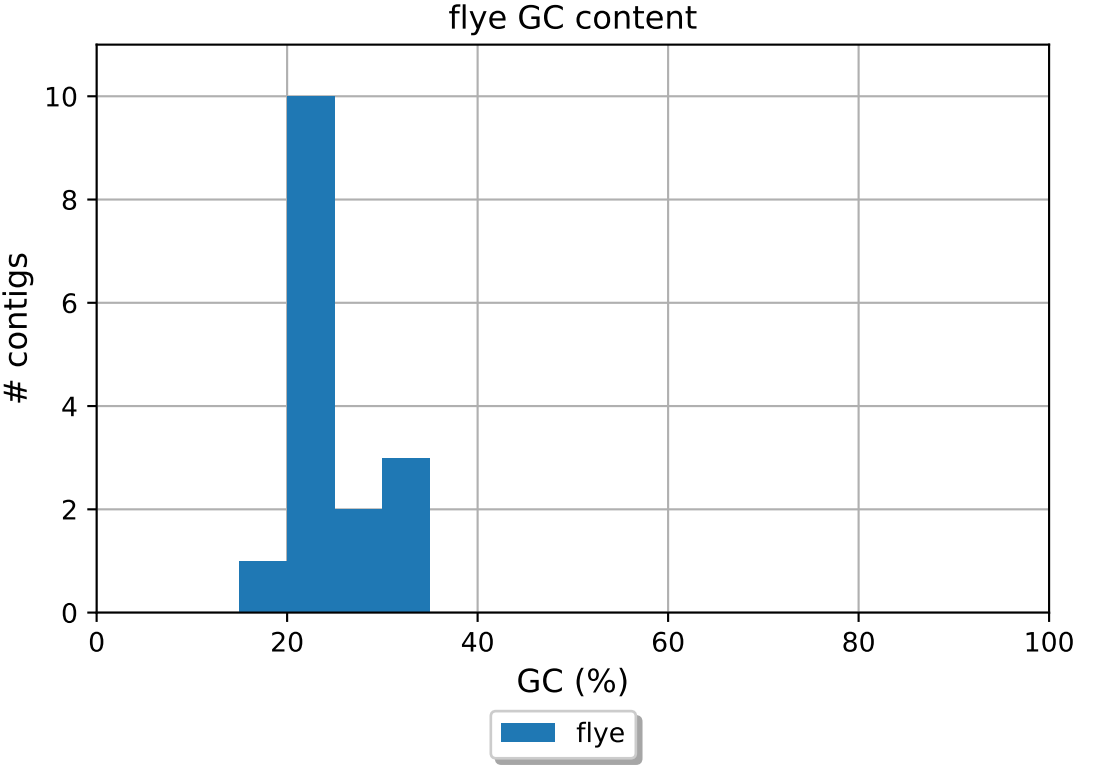

Nx
Contig length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
x
canu
flye
shasta

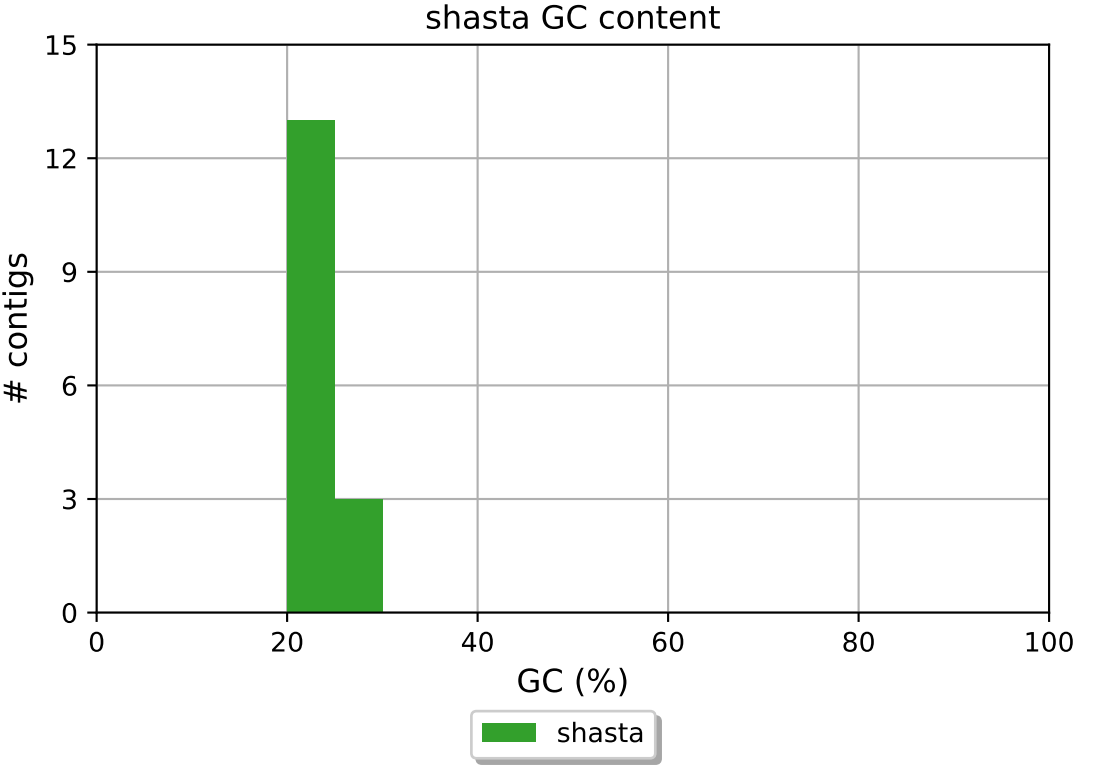

NGx
Contig length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
x
canu
flye
shasta

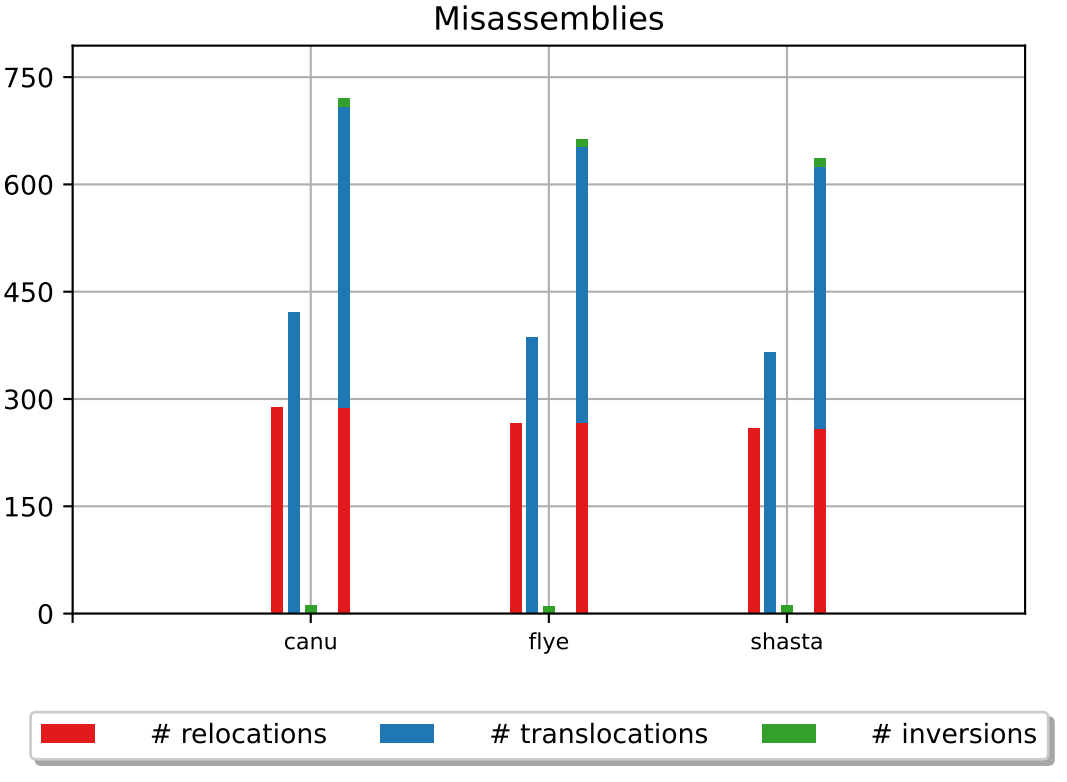

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
canu
flye
shasta
Reference

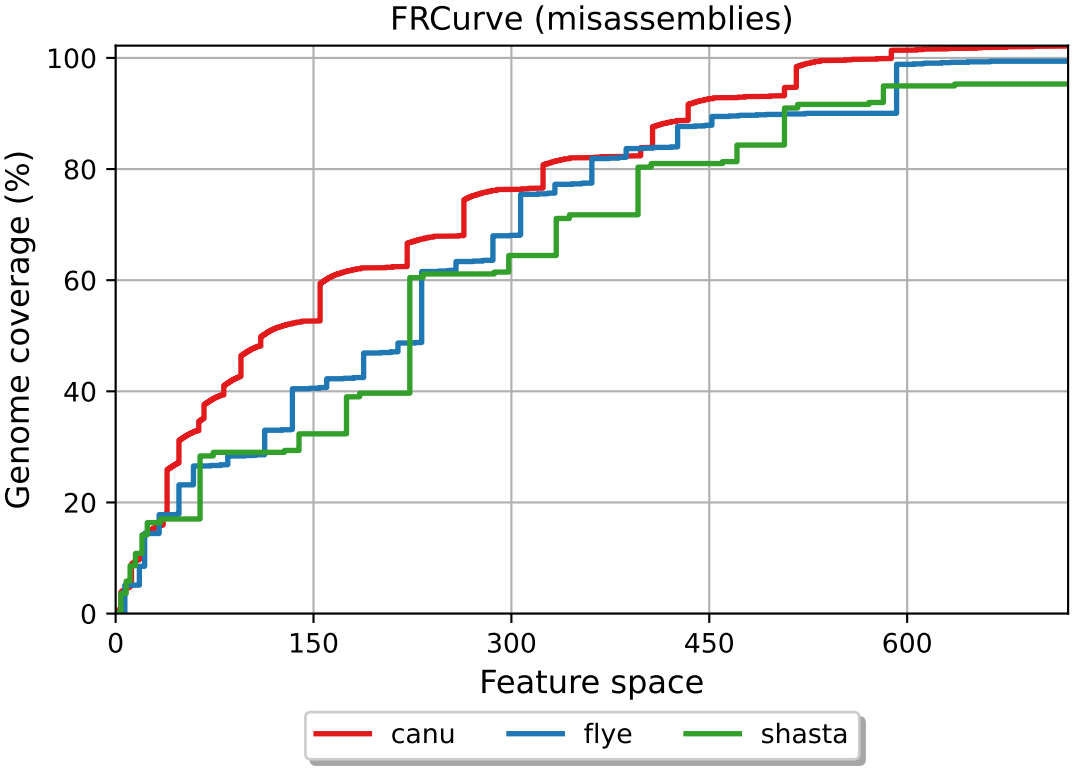

GC content
windows
GC (%)
0
2500
5000
7500
10000
12500
0
20
40
60
80
100
canu
flye
shasta
Reference

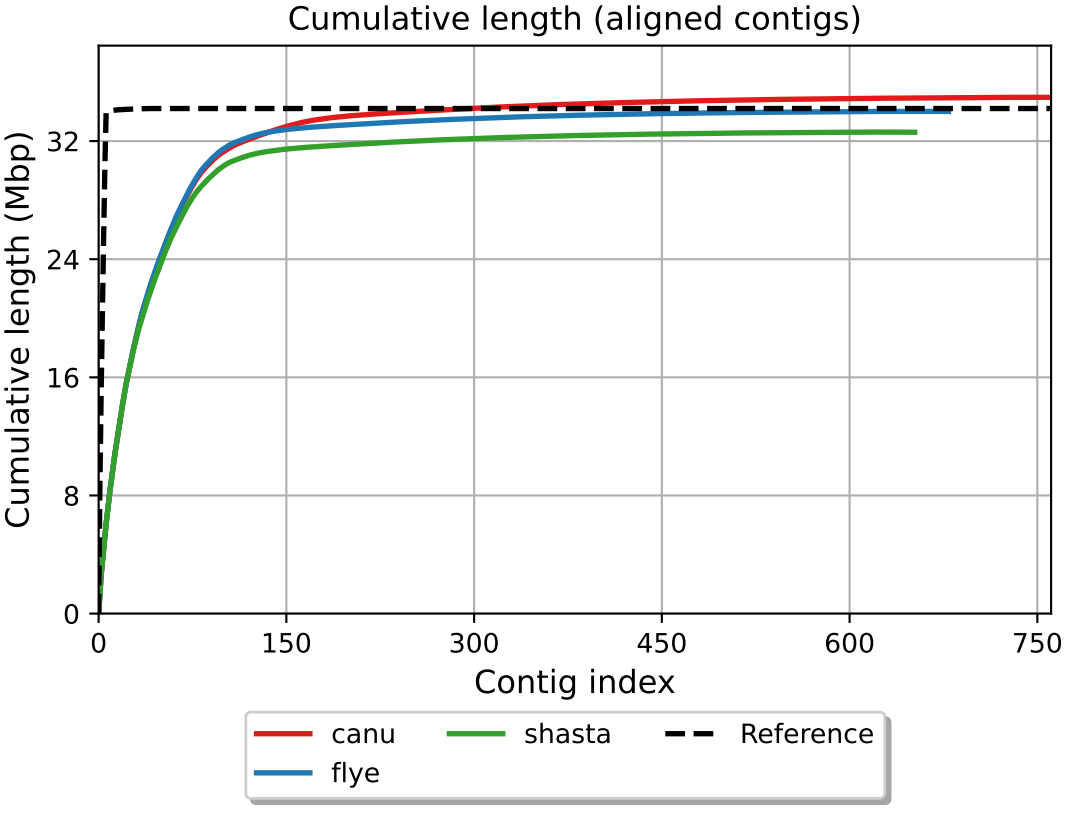

canu GC content
contigs
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
canu

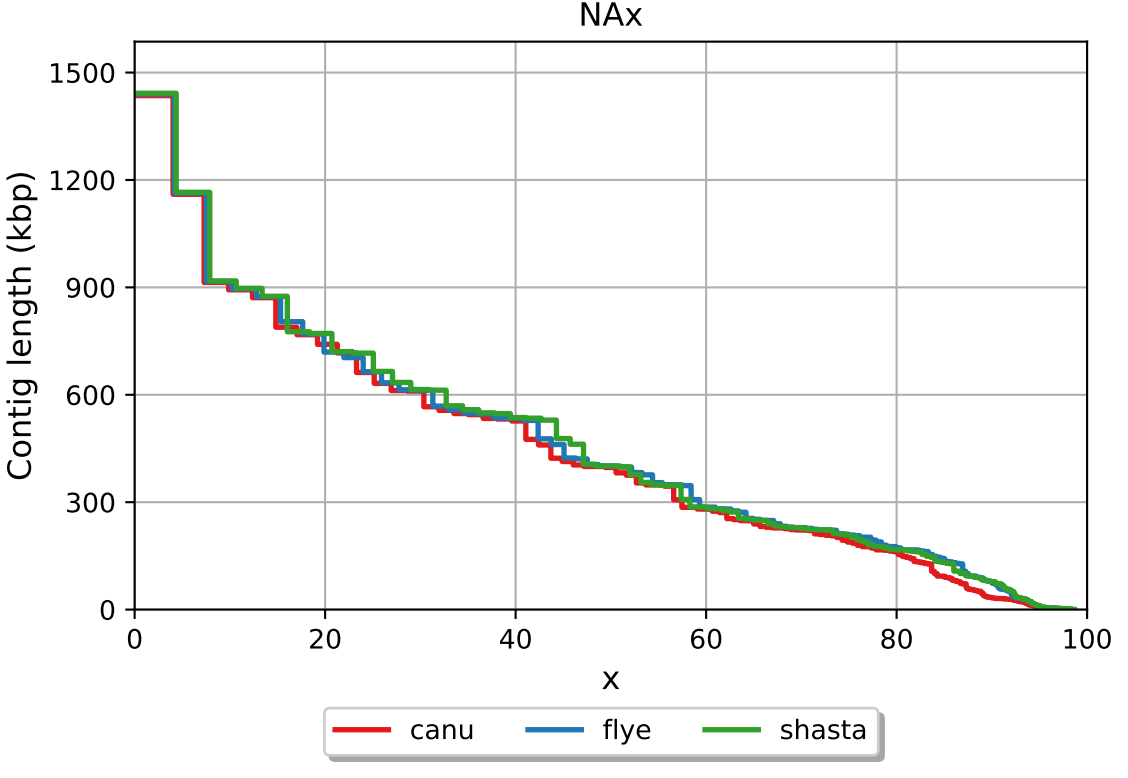

flye GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
flye

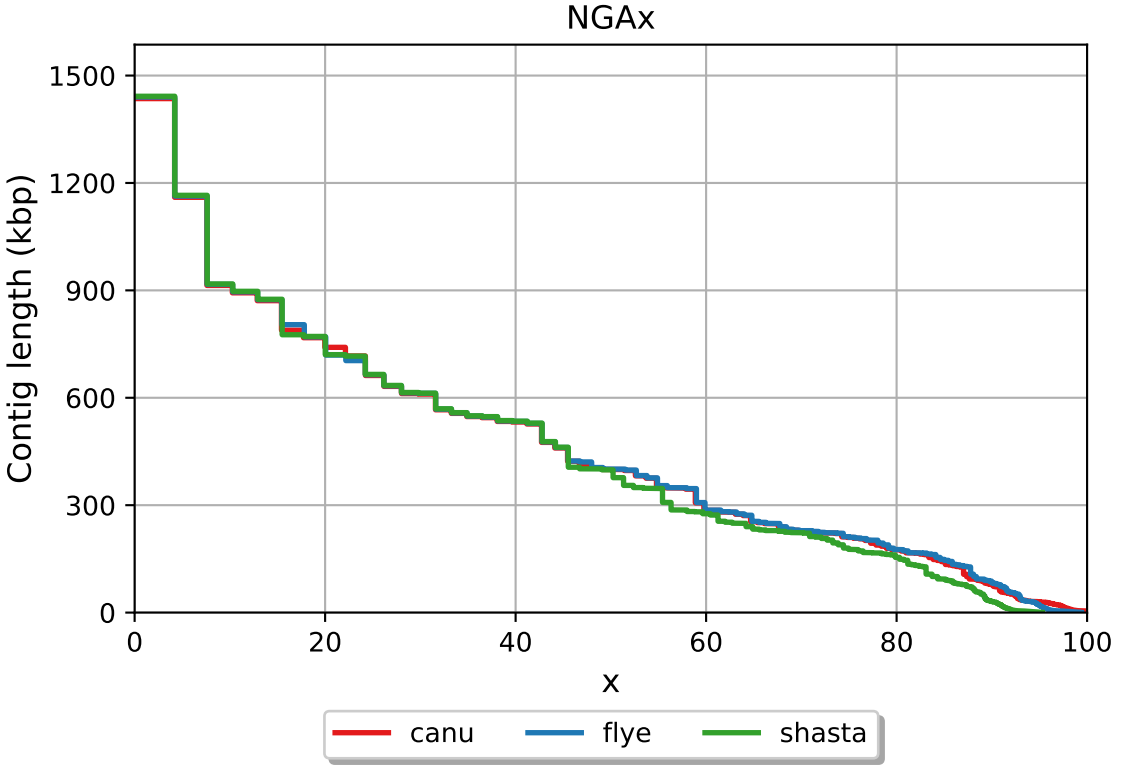

shasta GC content
contigs
GC (%)
shasta
0
3
6
9
12
15
0
20
40
60
80
100

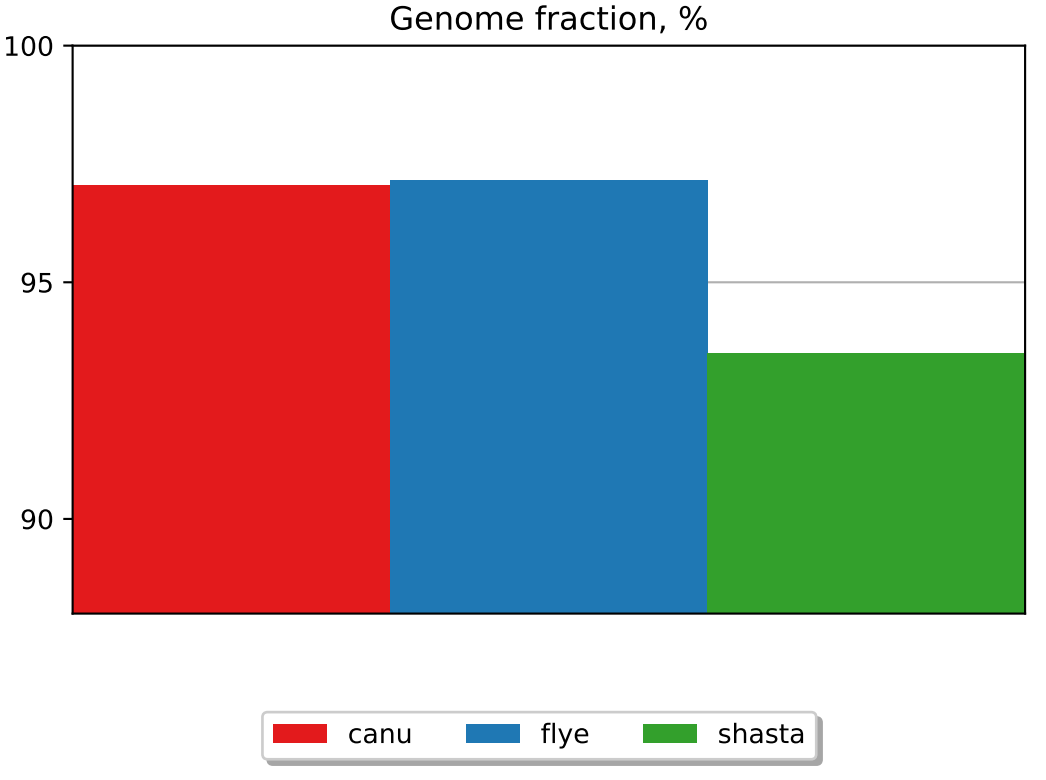

Misassemblies
750
600
450
300
150
0
canu
flye
shasta
relocations
translocations
inversions


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


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


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


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


Genome fraction, %
100
95
90
canu
flye
shasta