Report

	reference	flye_beforeRM	flye_afterRM	canu_beforeRM	canu_afterRM
# contigs (>= 0 bp)	41	11	11	29	29
# contigs (>= 1000 bp)	41	11	11	29	29
# contigs (>= 5000 bp)	20	10	10	29	29
# contigs (>= 10000 bp)	11	10	10	29	29
# contigs (>= 25000 bp)	8	10	10	28	28
# contigs (>= 50000 bp)	7	8	8	18	18
Total length (>= 0 bp)	34204973	34807692	34807692	35906896	35906896
Total length (>= 1000 bp)	34204973	34807692	34807692	35906896	35906896
Total length (>= 5000 bp)	34138341	34803535	34803535	35906896	35906896
Total length (>= 10000 bp)	34076491	34803535	34803535	35906896	35906896
Total length (>= 25000 bp)	34038432	34803535	34803535	35888397	35888397
Total length (>= 50000 bp)	33998636	34724309	34724309	35518355	35518355
# contigs	41	11	11	29	29
Largest contig	8484197	12181105	12181105	8126513	8126513
Total length	34204973	34807692	34807692	35906896	35906896
Reference length	34204973	34204973	34204973	34204973	34204973
GC (%)	22.44	22.77	22.77	22.80	22.80
Reference GC (%)	22.44	22.44	22.44	22.44	22.44
N50	5450249	8047075	8047075	5589158	5589158
NG50	5450249	8047075	8047075	5589158	5589158
N90	3602379	4033435	4033435	3917967	3917967
NG90	3602379	4033435	4033435	5009411	5009411
auN	6010706.9	8105654.3	8105654.3	5893519.9	5893519.9
auNG	6010706.9	8248482.4	8248482.4	6186761.4	6186761.4
L50	3	2	2	3	3
LG50	3	2	2	3	3
L90	6	5	5	6	6
LG90	6	5	5	5	5
# misassemblies	0	674	674	731	731
# misassembled contigs	0	9	9	26	26
Misassembled contigs length	0	34748006	34748006	35782662	35782662
# local misassemblies	0	154	154	167	167
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 9 part	0 + 9 part	0 + 14 part	0 + 14 part
Unaligned length	0	431209	431209	546647	546647
Genome fraction (%)	100.000	97.168	97.168	97.083	97.083
Duplication ratio	1.001	1.033	1.033	1.064	1.064
# N's per 100 kbp	67.66	0.29	0.29	1.31	1.31
# mismatches per 100 kbp	0.00	136.03	136.03	137.57	137.57
# indels per 100 kbp	0.00	246.06	246.06	255.48	255.48
Largest alignment	8483997	1452265	1452265	1451587	1451587
Total aligned length	34203973	34315382	34315382	35295972	35295972
NA50	5450149	403703	403703	400956	400956
NGA50	5450149	404264	404264	404265	404265
NA90	3602179	78641	78641	34573	34573
NGA90	3602179	90891	90891	90099	90099
auNA	6010371.9	475713.0	475713.0	462539.2	462539.2
auNGA	6010371.9	484095.4	484095.4	485553.5	485553.5
LA50	3	27	27	28	28
LGA50	3	26	26	26	26
LA90	6	94	94	115	115
LGA90	6	88	88	88	88

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

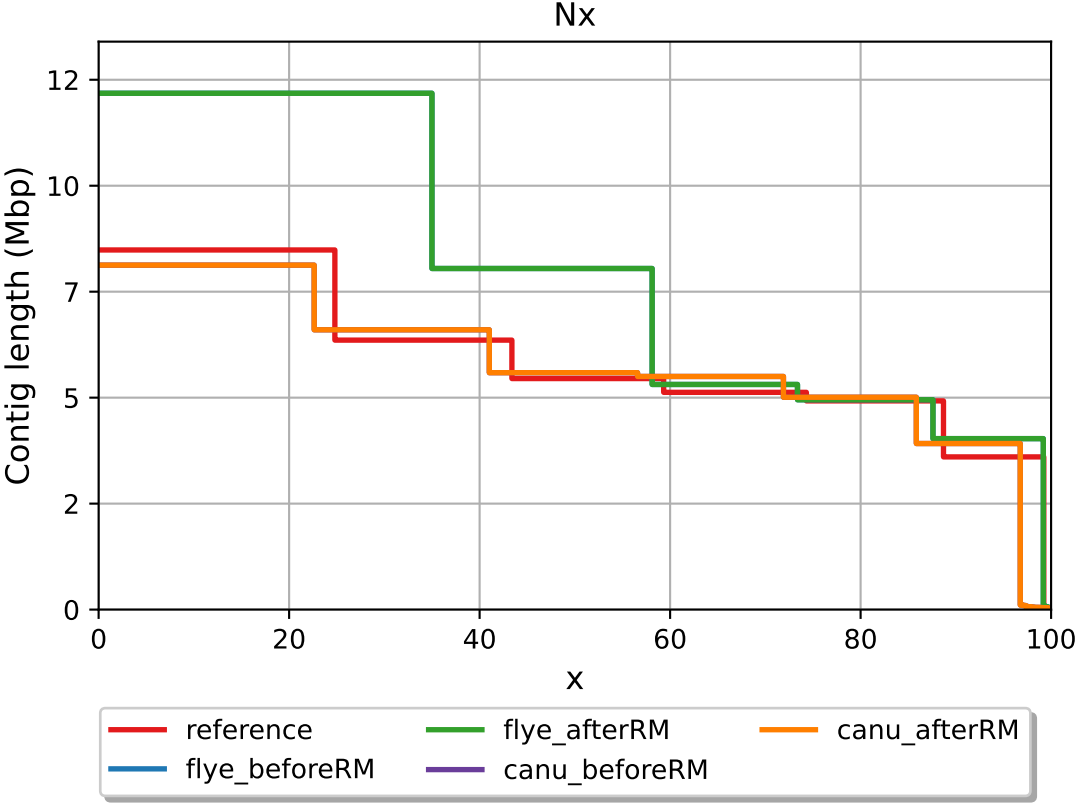
	reference	flye_beforeRM	flye_afterRM	canu_beforeRM	canu_afterRM
# misassemblies	0	674	674	731	731
# contig misassemblies	0	673	673	723	723
# c. relocations	0	276	276	297	297
# c. translocations	0	385	385	414	414
# c. inversions	0	12	12	12	12
# scaffold misassemblies	0	1	1	8	8
# s. relocations	0	1	1	4	4
# s. translocations	0	0	0	4	4
# s. inversions	0	0	0	0	0
# misassembled contigs	0	9	9	26	26
Misassembled contigs length	0	34748006	34748006	35782662	35782662
# local misassemblies	0	154	154	167	167
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# mismatches	0	46679	46679	48558	48558
# indels	0	84438	84438	90173	90173
# indels (<= 5 bp)	0	80327	80327	85085	85085
# indels (> 5 bp)	0	4111	4111	5088	5088
Indels length	0	196514	196514	217368	217368

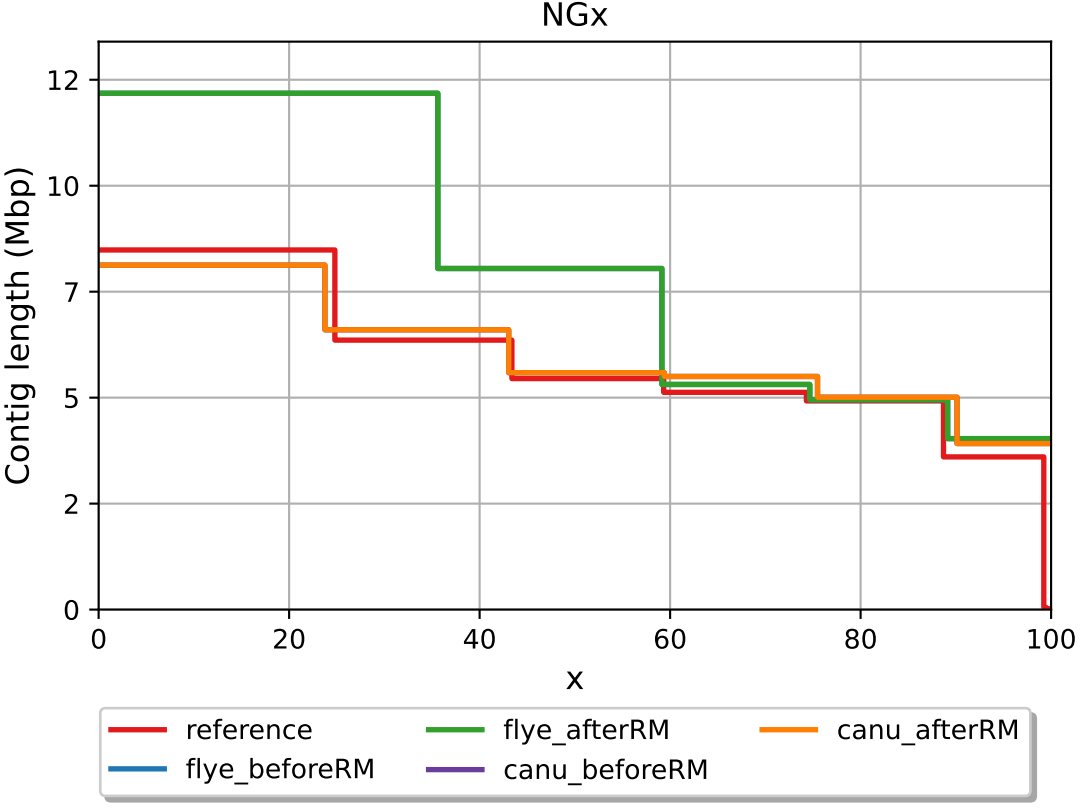
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

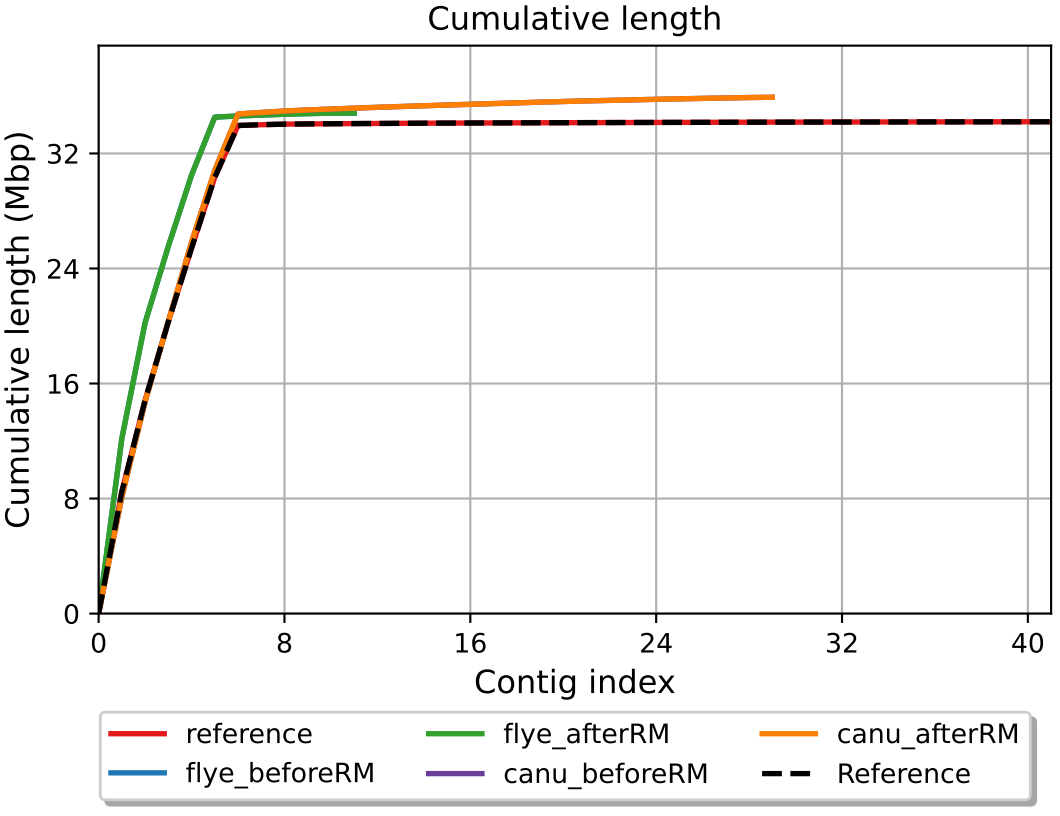
Unaligned report

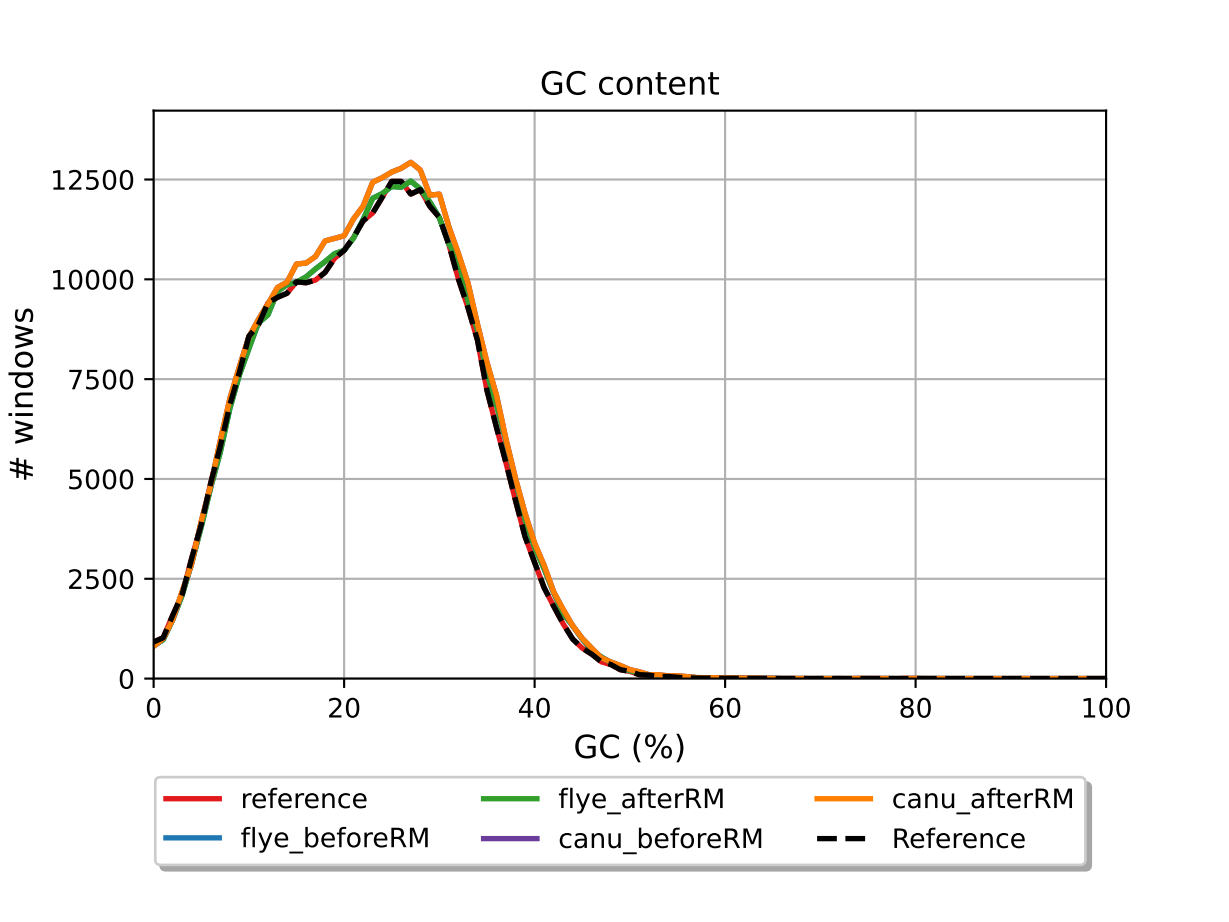
	reference	flye_beforeRM	flye_afterRM	canu_beforeRM	canu_afterRM
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	9	9	14	14
Partially unaligned length	0	431209	431209	546647	546647
# N's	23142	100	100	469	469

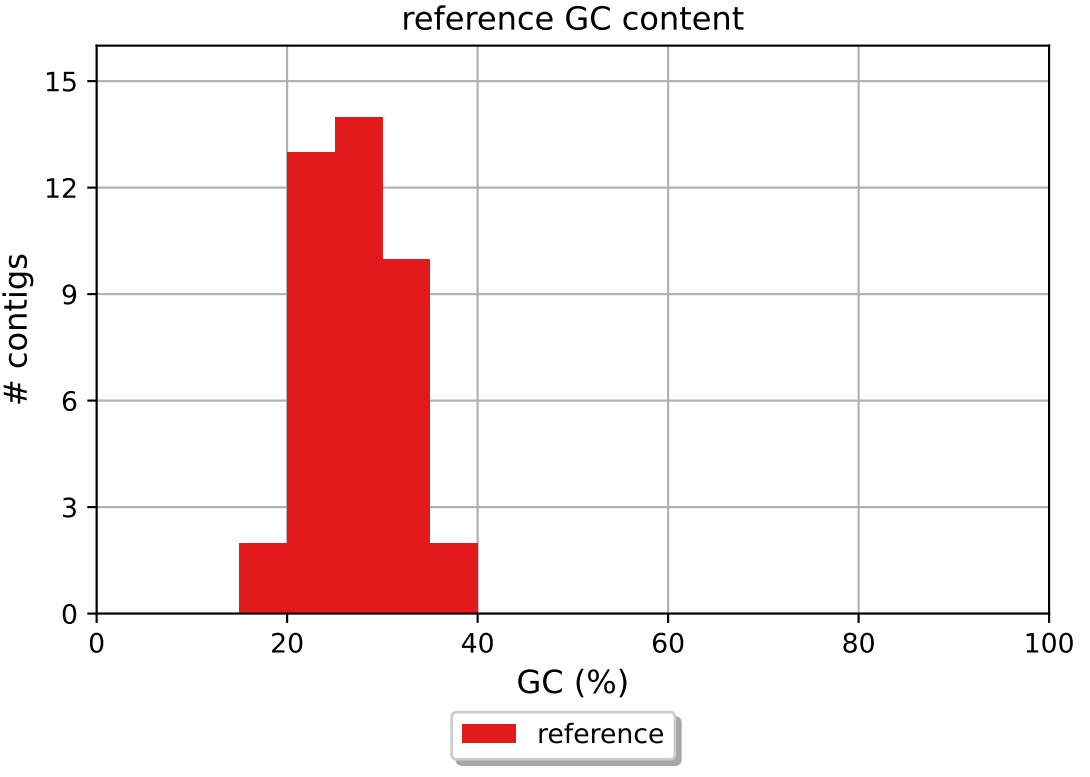
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

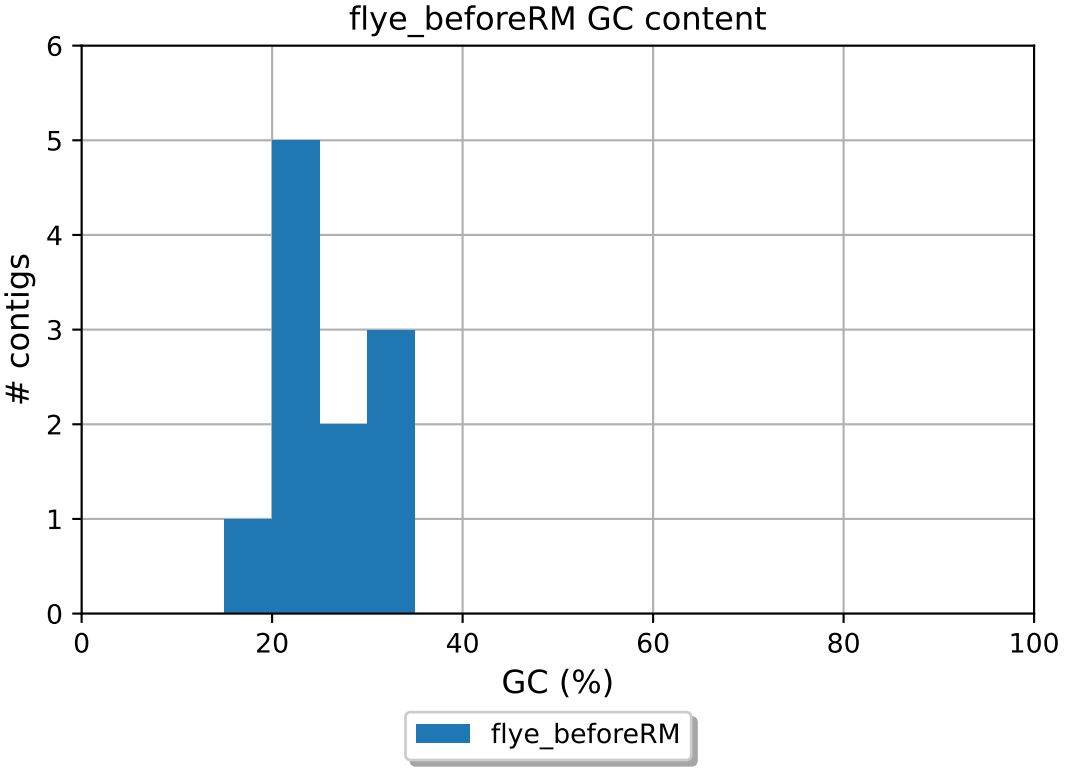

Nx
Contig length (Mbp)
12
10
7
5
2
0
0
20
40
60
80
100
x
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM

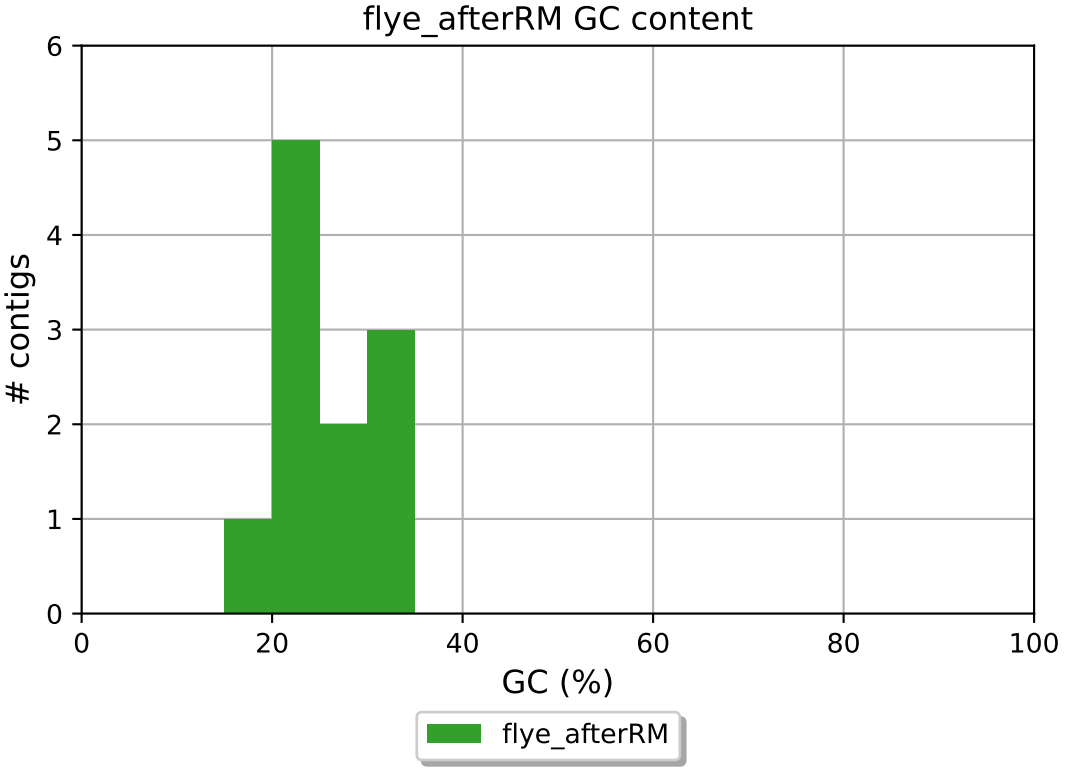

NGx
Contig length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
x
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM

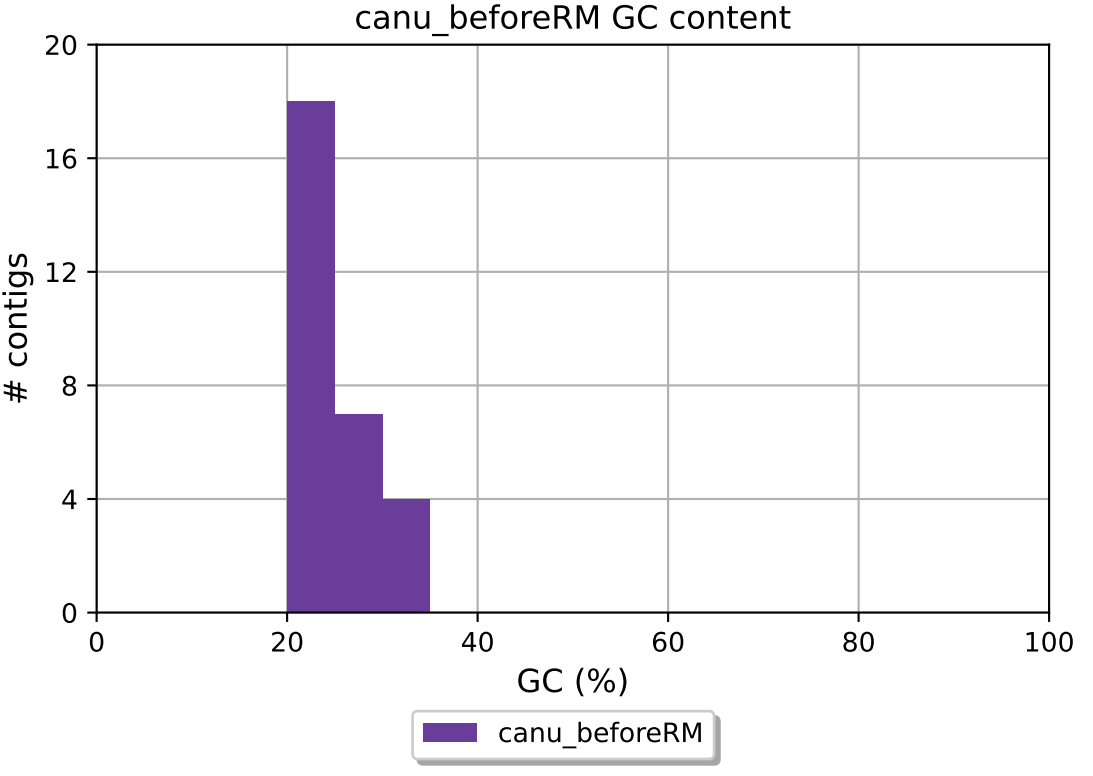

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM
Reference

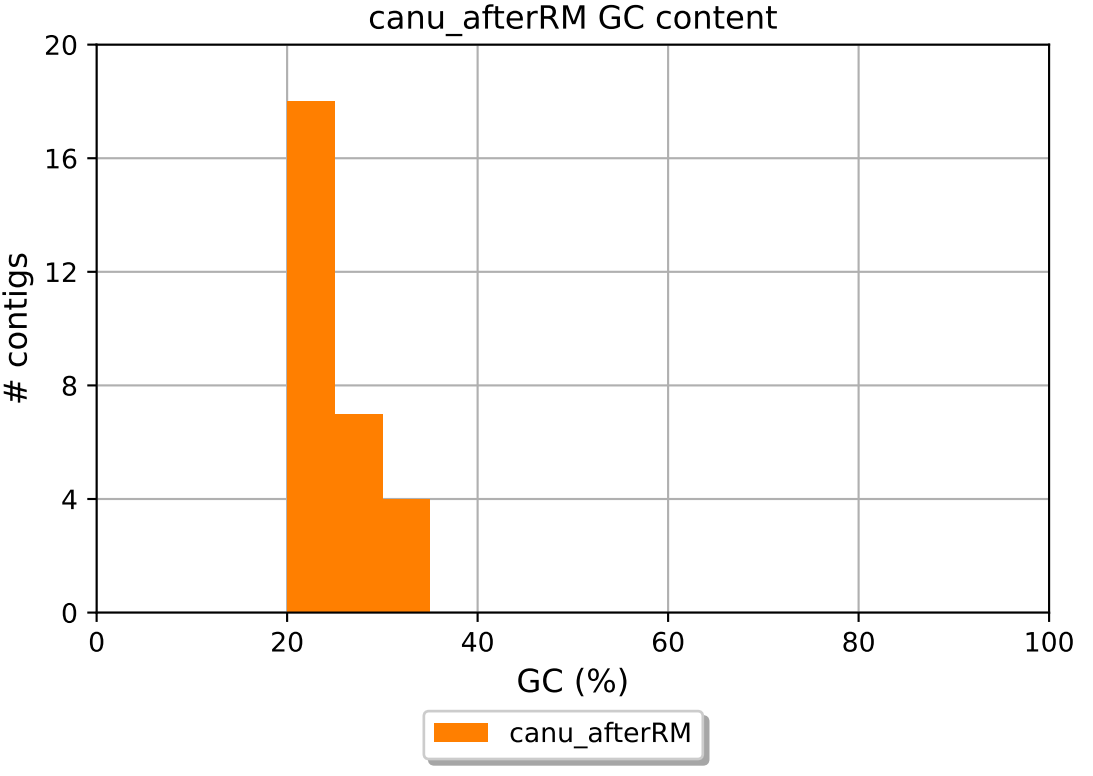

GC content
windows
GC (%)
0
2500
5000
7500
10000
12500
0
20
40
60
80
100
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM
Reference

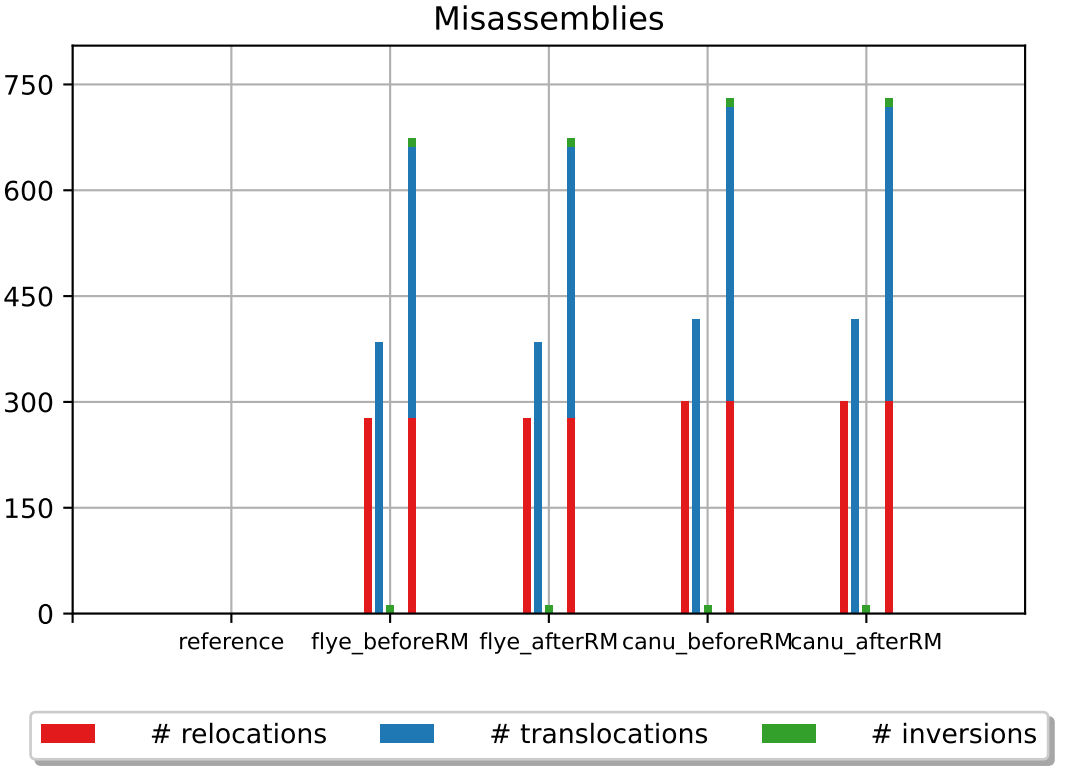

reference GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
reference

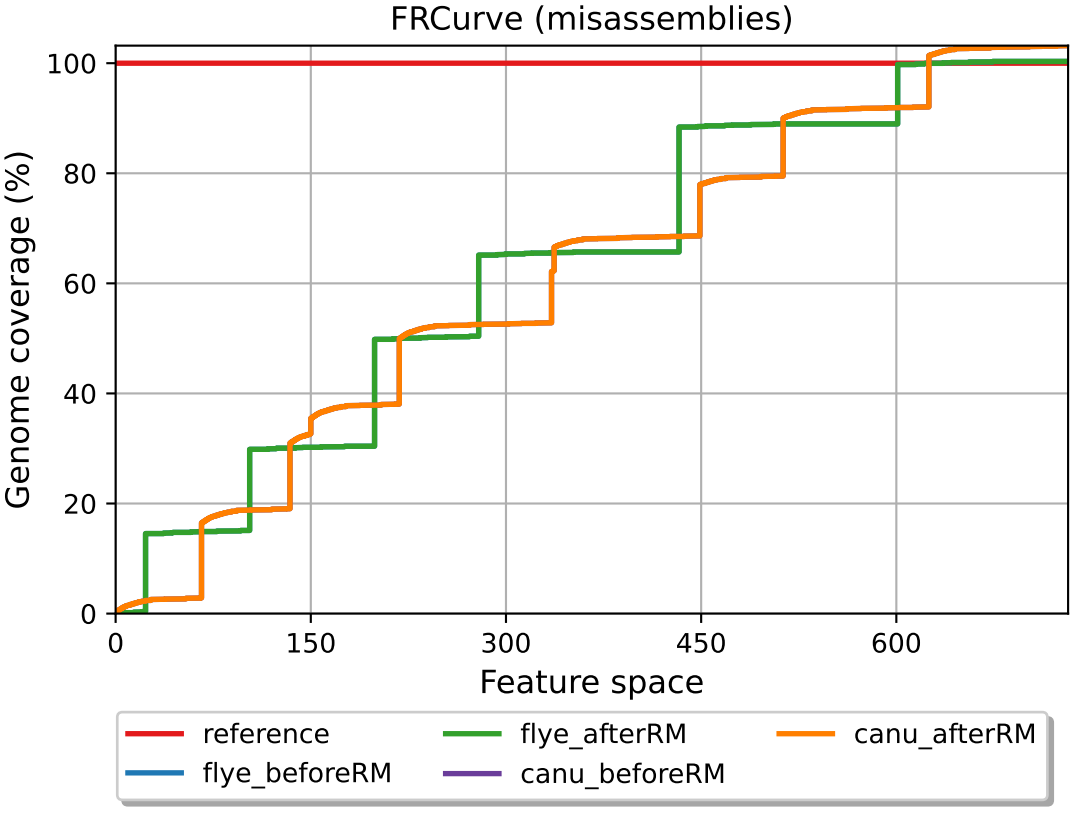

flye_beforeRM GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
flye_beforeRM

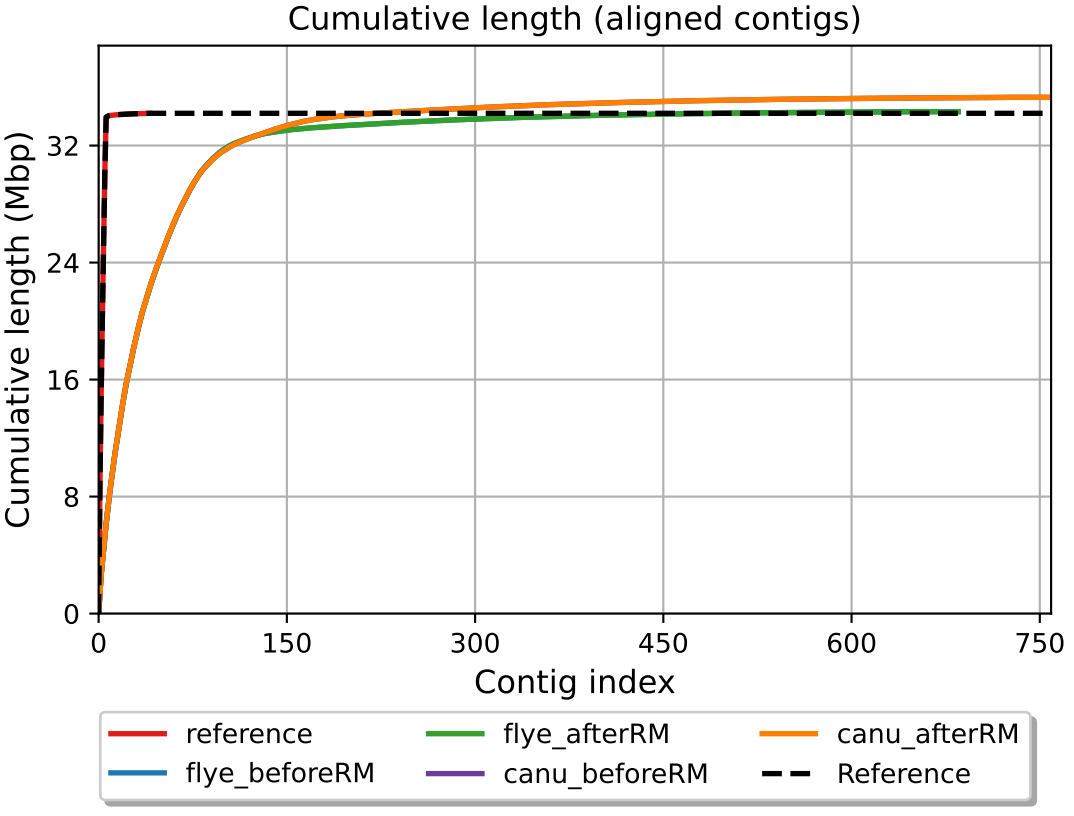

flye_afterRM GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
flye_afterRM

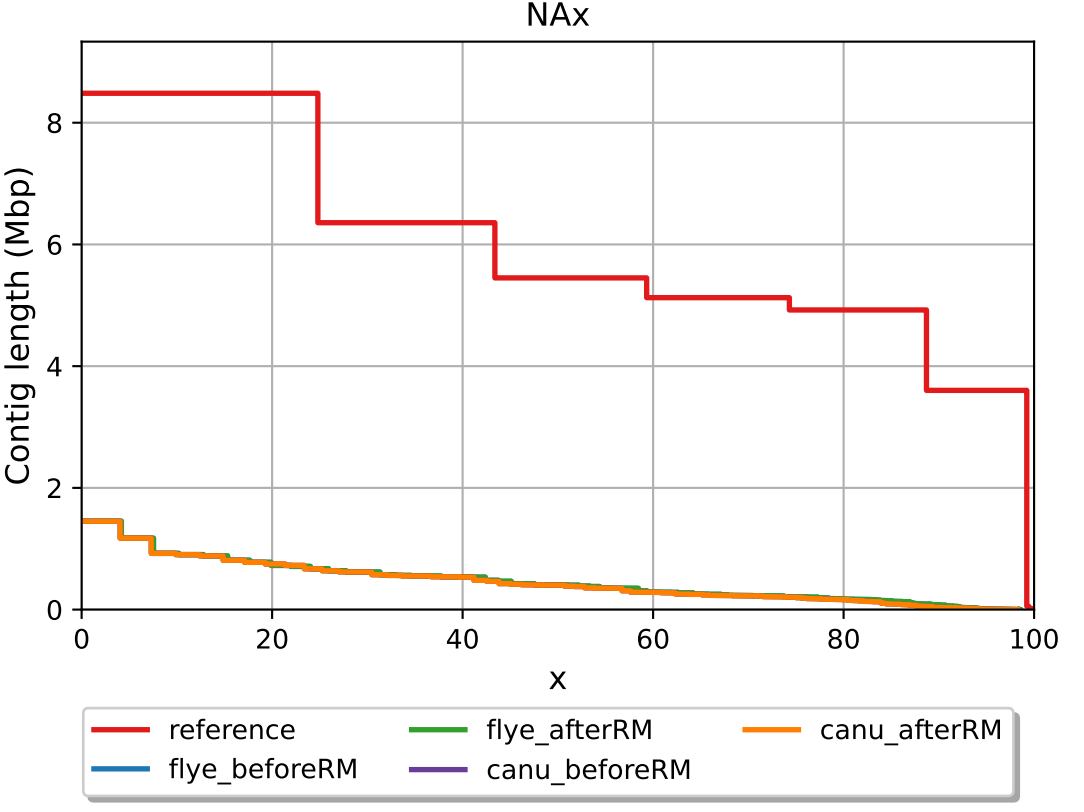

canu_beforeRM GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
canu_beforeRM

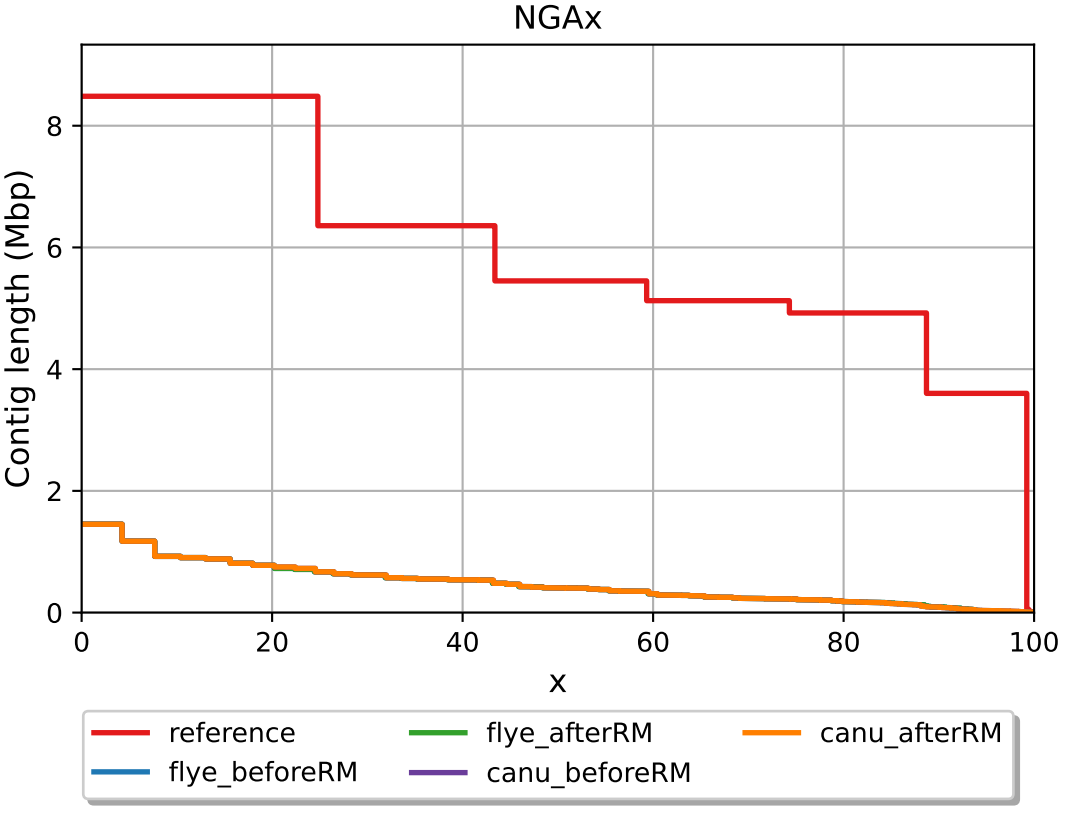

canu_afterRM GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
canu_afterRM

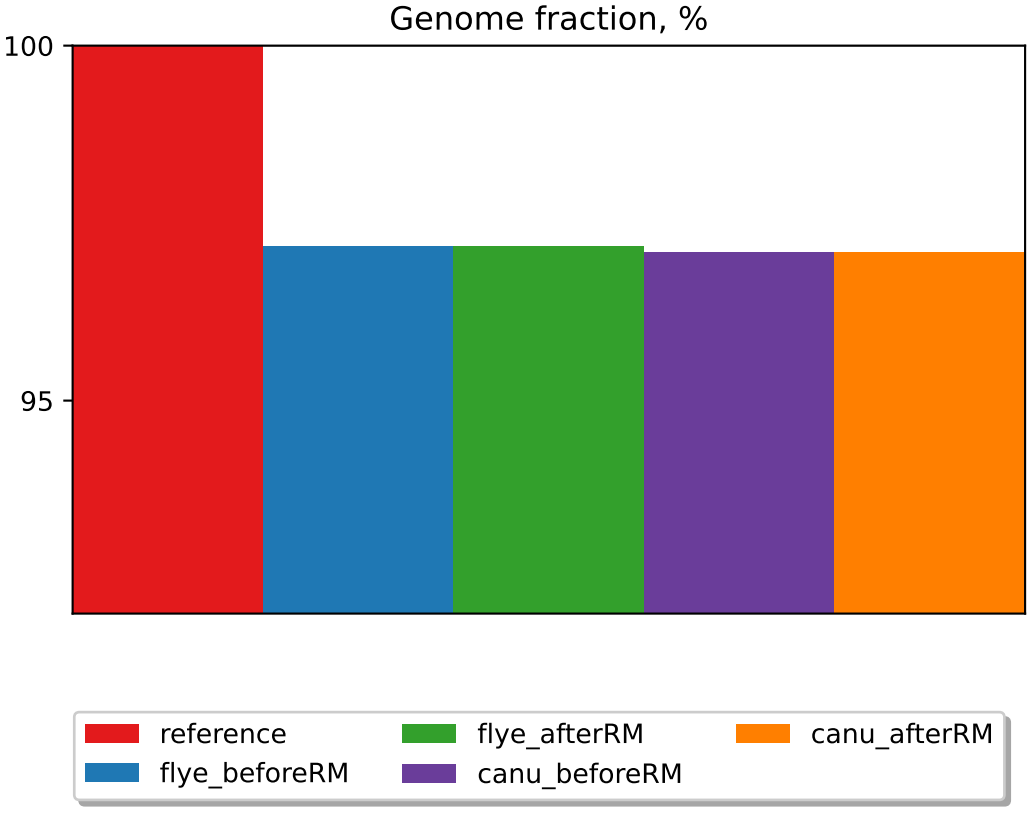

Misassemblies
750
600
450
300
150
0
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
150
300
450
600
Feature space
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
8
16
24
32
0
150
300
450
600
750
Contig index
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM
Reference


NAx
Contig length (Mbp)
0
2
4
6
8
0
20
40
60
80
100
x
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM


NGAx
Contig length (Mbp)
0
2
4
6
8
0
20
40
60
80
100
x
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM


Genome fraction, %
100
95
reference
flye_beforeRM
flye_afterRM
canu_beforeRM
canu_afterRM