Report

	Flye_Medaka	Canu_Medaka
# contigs (>= 0 bp)	16	41
# contigs (>= 1000 bp)	16	41
# contigs (>= 5000 bp)	15	41
# contigs (>= 10000 bp)	15	41
# contigs (>= 25000 bp)	15	40
# contigs (>= 50000 bp)	13	27
Total length (>= 0 bp)	34875198	36010564
Total length (>= 1000 bp)	34875198	36010564
Total length (>= 5000 bp)	34871041	36010564
Total length (>= 10000 bp)	34871041	36010564
Total length (>= 25000 bp)	34871041	35992067
Total length (>= 50000 bp)	34791638	35496281
# contigs	16	41
Largest contig	12202900	5952923
Total length	34875198	36010564
Reference length	34204973	34204973
GC (%)	22.73	22.76
Reference GC (%)	22.44	22.44
N50	3394368	3355856
NG50	3394368	3355856
N90	1735621	1252116
NG90	2034585	1775321
auN	6245131.2	3340024.8
auNG	6367500.6	3516336.0
L50	3	4
LG50	3	4
L90	8	11
LG90	7	10
# misassemblies	669	726
# misassembled contigs	14	38
Misassembled contigs length	34815506	35886305
# local misassemblies	166	165
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 14 part	0 + 20 part
Unaligned length	424120	549856
Genome fraction (%)	97.171	97.082
Duplication ratio	1.034	1.067
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	141.98	144.04
# indels per 100 kbp	211.43	217.18
Largest alignment	1455312	1455185
Total aligned length	34350817	35400798
NA50	404380	401924
NGA50	405183	404979
NA90	78836	34342
NGA90	94458	90261
auNA	476715.4	462489.6
auNGA	486056.3	486903.2
LA50	27	28
LGA50	26	26
LA90	94	117
LGA90	87	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

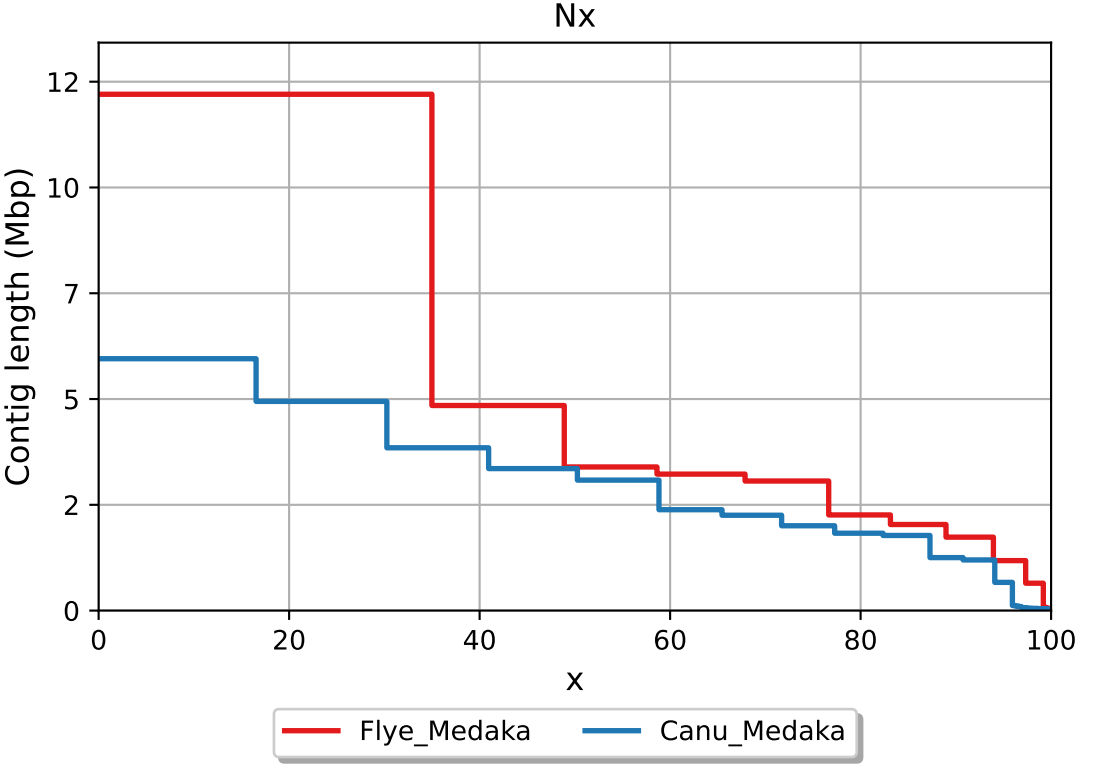
	Flye_Medaka	Canu_Medaka
# misassemblies	669	726
# contig misassemblies	669	726
# c. relocations	274	294
# c. translocations	385	422
# c. inversions	10	10
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	14	38
Misassembled contigs length	34815506	35886305
# local misassemblies	166	165
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	48771	50993
# indels	72627	76882
# indels (<= 5 bp)	68547	71800
# indels (> 5 bp)	4080	5082
Indels length	168677	191495

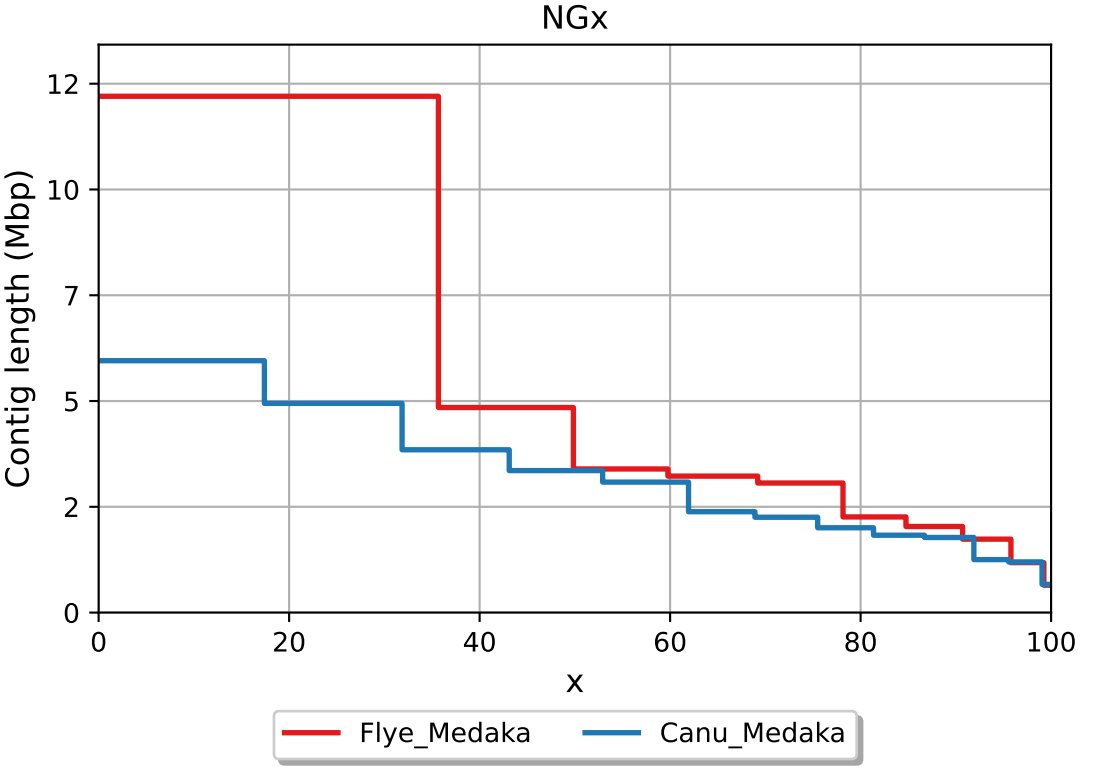
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

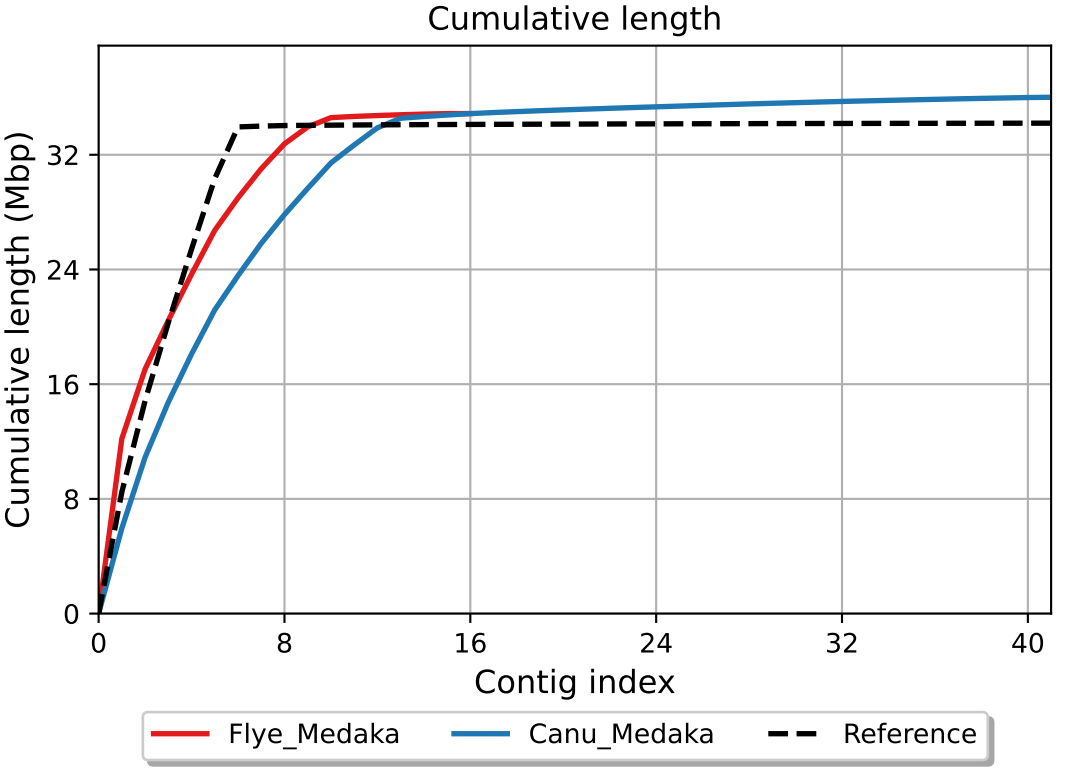
Unaligned report

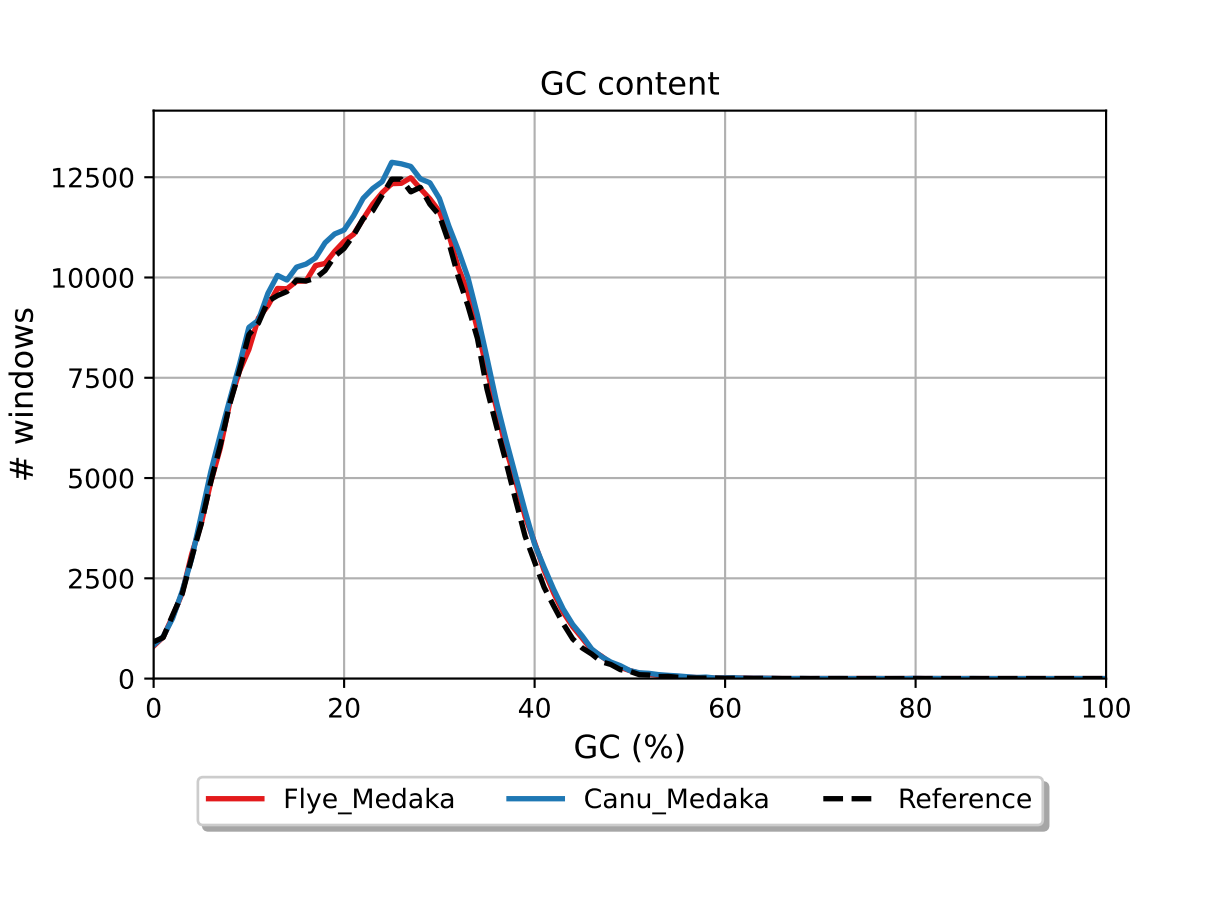
	Flye_Medaka	Canu_Medaka
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	14	20
Partially unaligned length	424120	549856
# N's	0	0

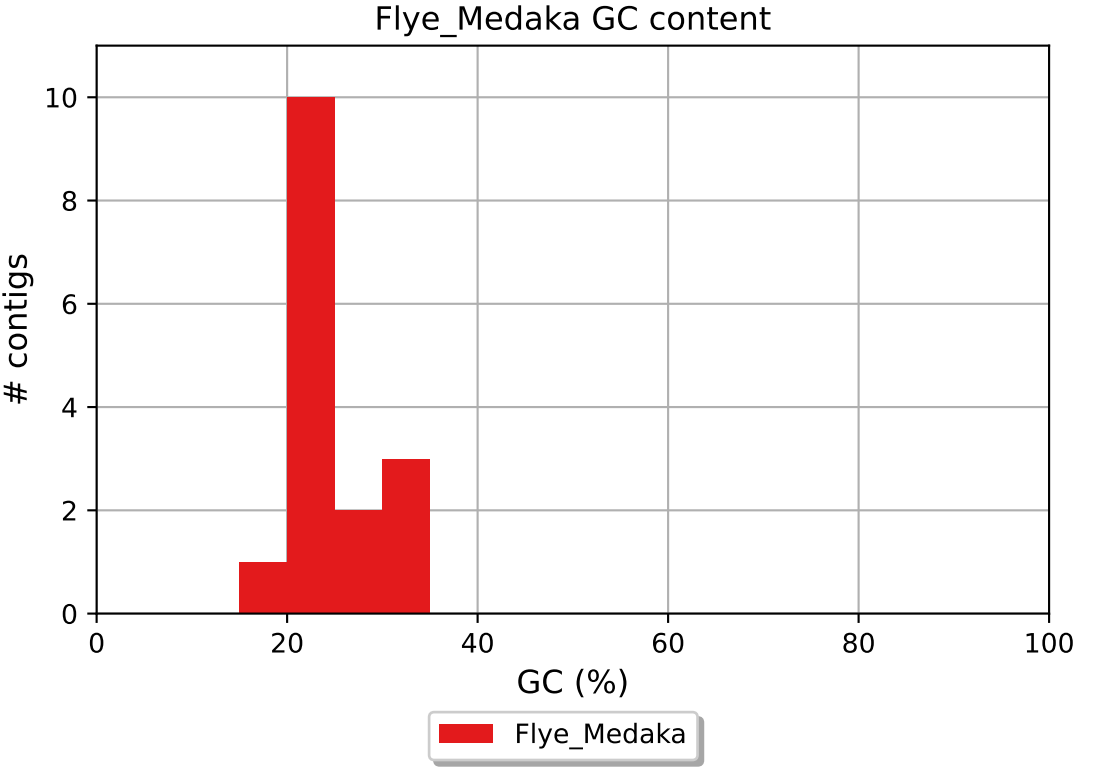
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

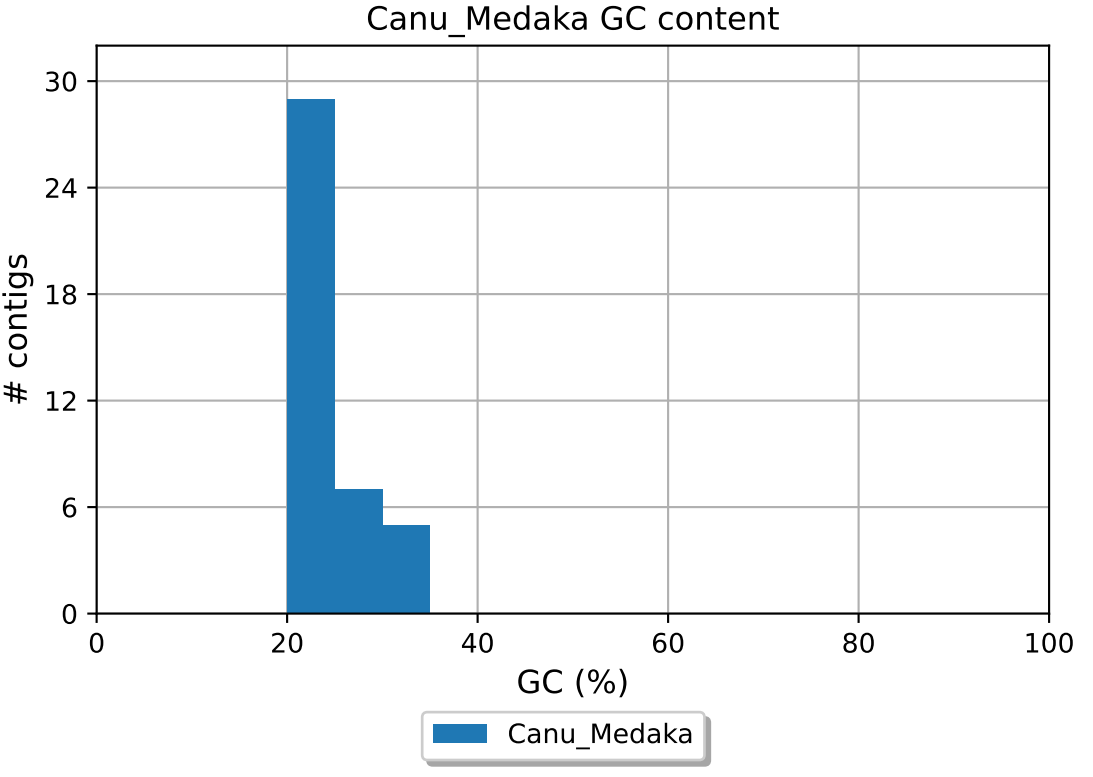

Nx
Contig length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
x
Flye_Medaka
Canu_Medaka

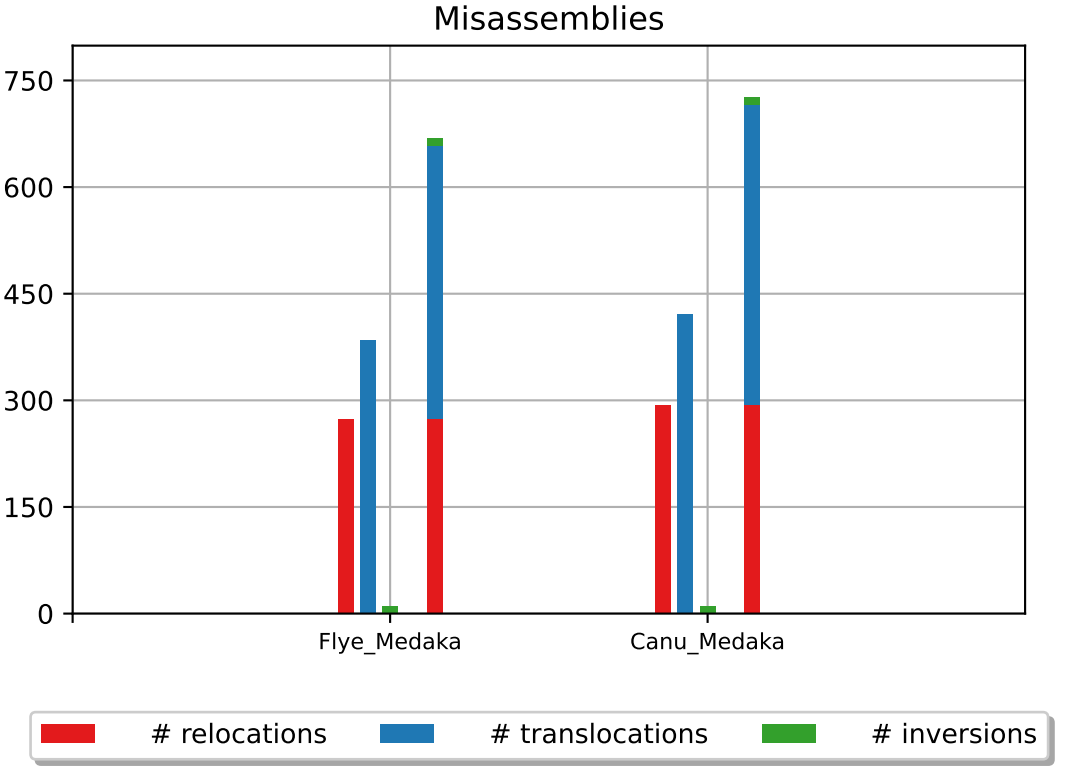

NGx
Contig length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
x
Flye_Medaka
Canu_Medaka

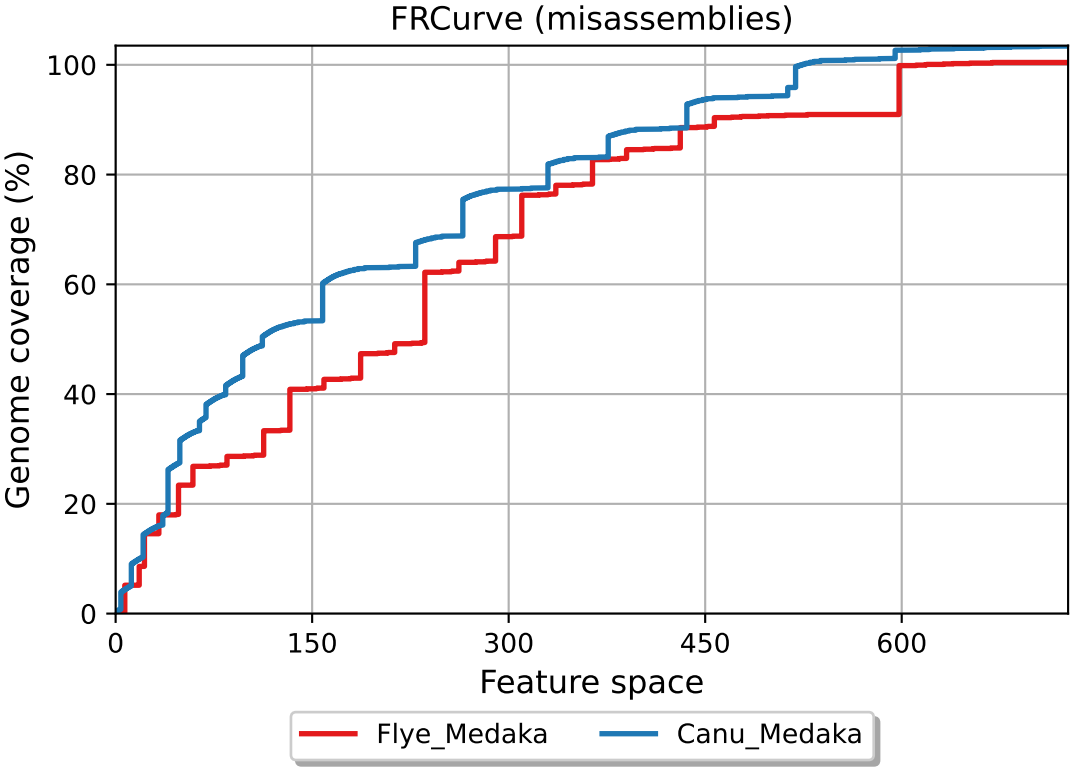

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
Flye_Medaka
Canu_Medaka
Reference

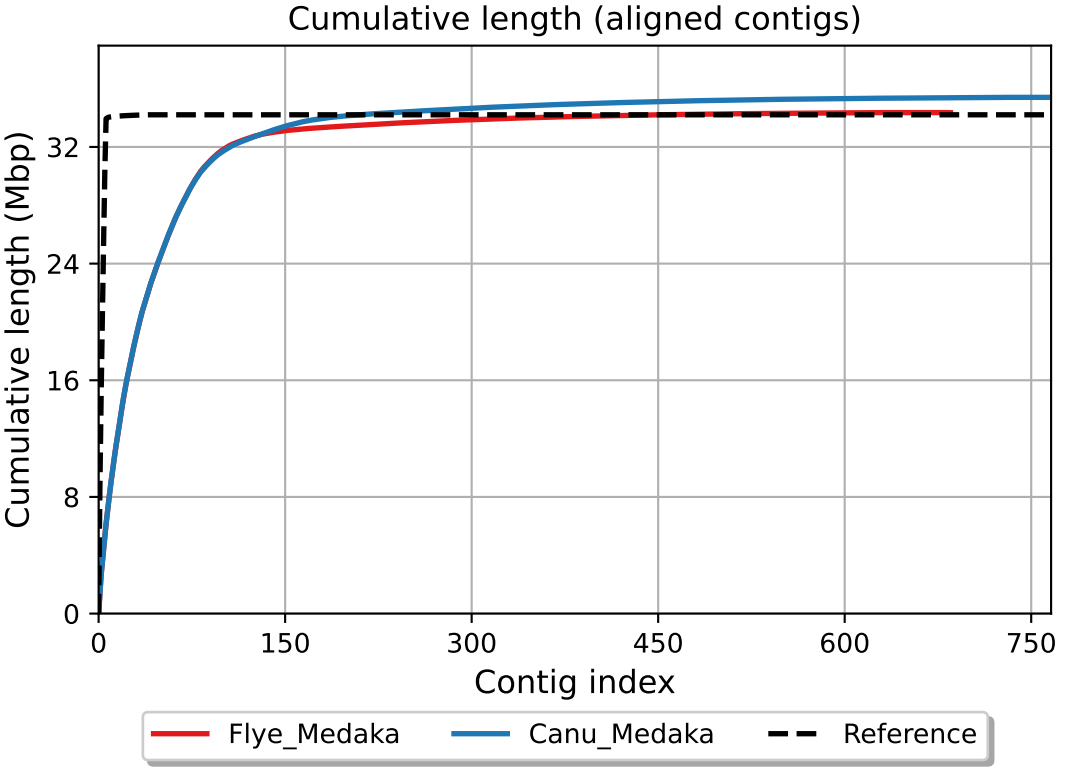

GC content
windows
12500
10000
7500
5000
2500
0
0
20
40
60
80
100
GC (%)
Flye_Medaka
Canu_Medaka
Reference

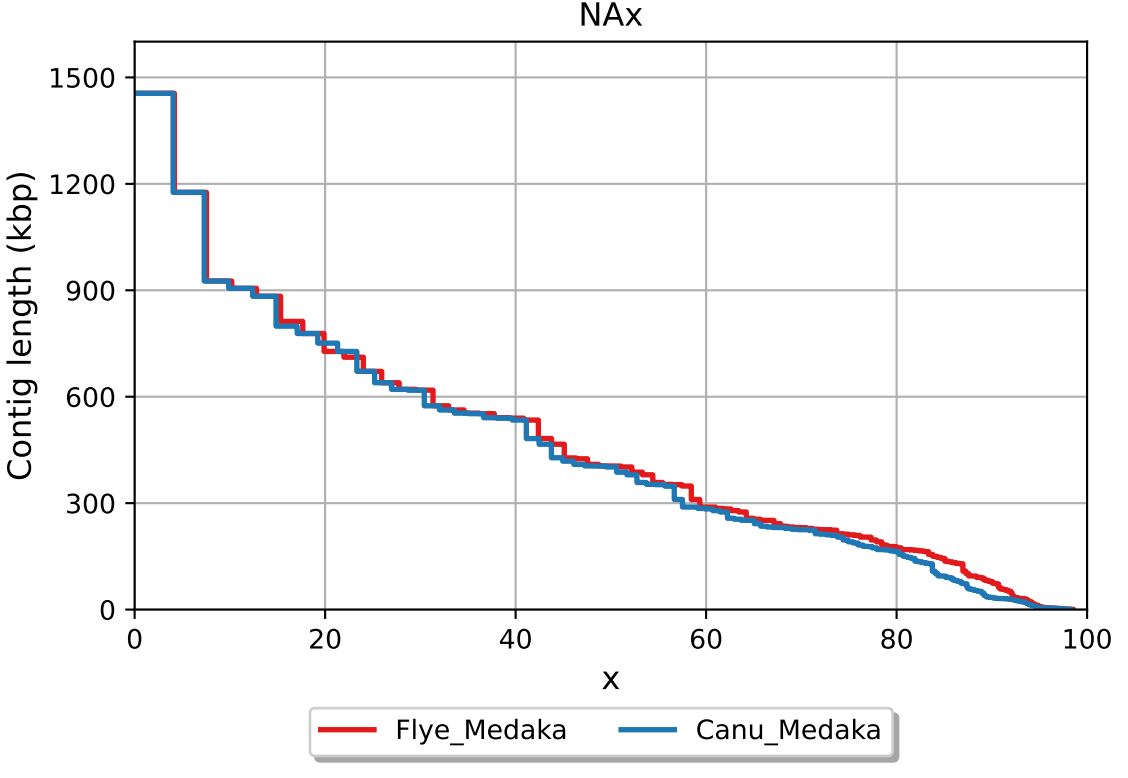

Flye_Medaka GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
Flye_Medaka

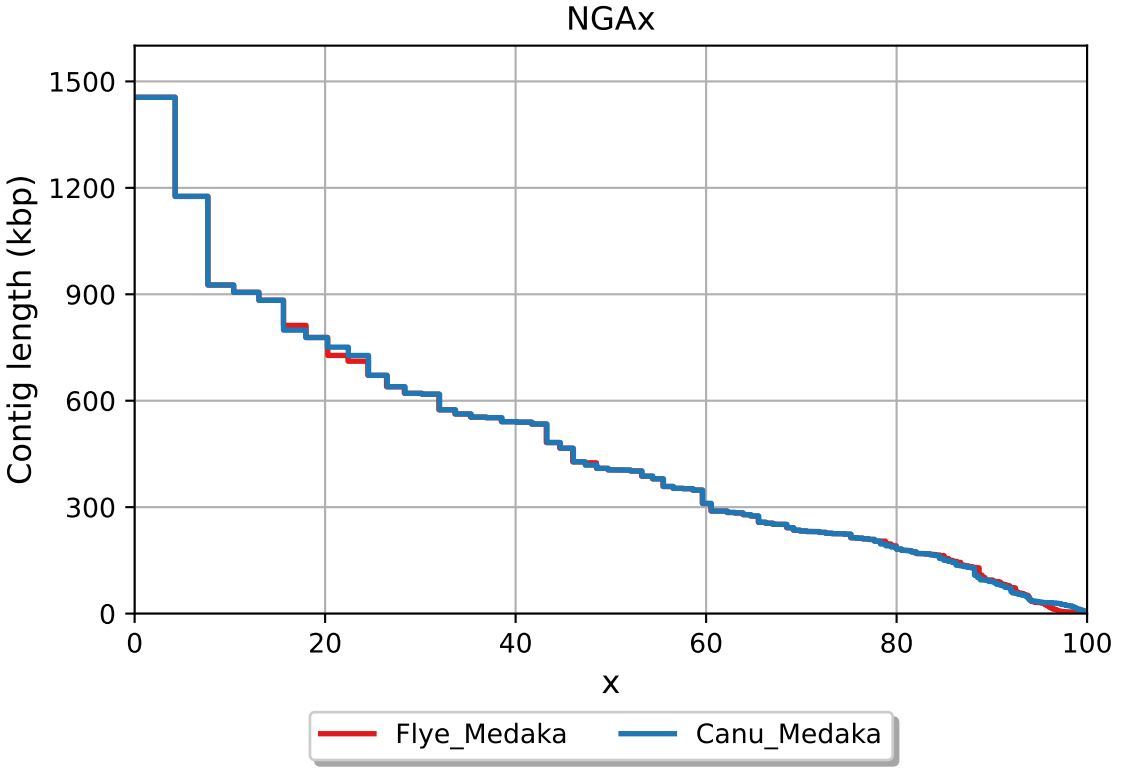

Canu_Medaka GC content
contigs
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
Canu_Medaka

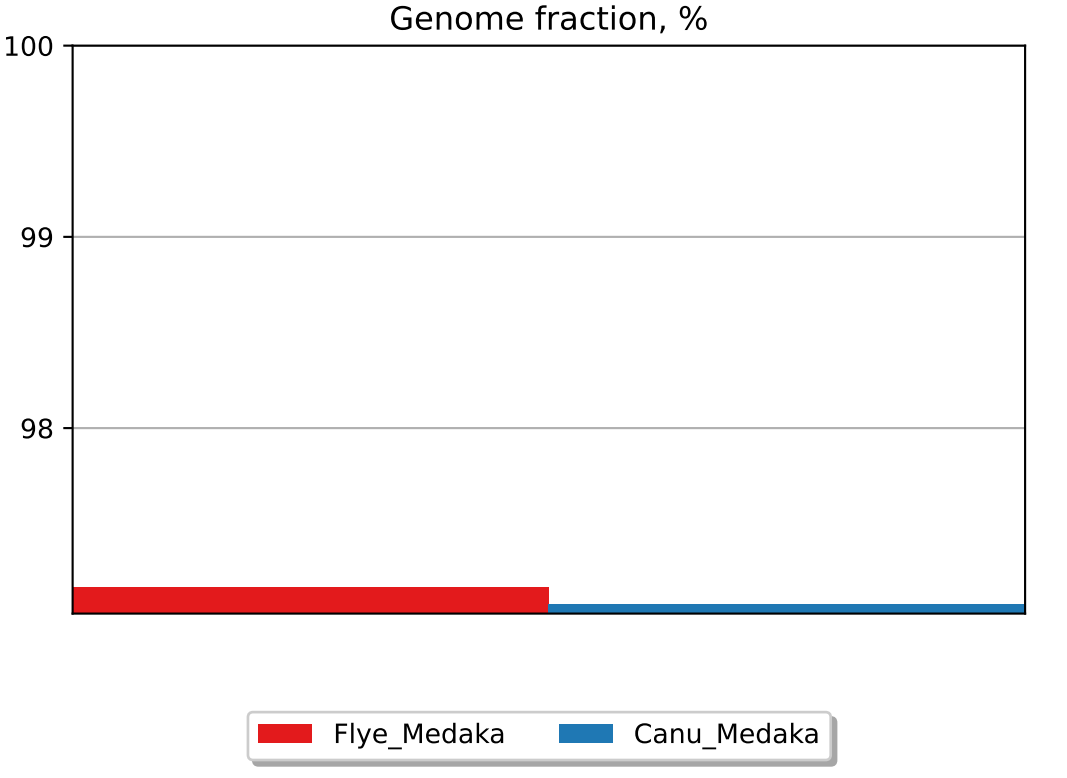

Misassemblies
750
600
450
300
150
0
Flye_Medaka
Canu_Medaka
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
150
300
450
600
Feature space
Flye_Medaka
Canu_Medaka


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


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
Flye_Medaka
Canu_Medaka


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
Flye_Medaka
Canu_Medaka


Genome fraction, %
100
99
98
Flye_Medaka
Canu_Medaka